



# 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	
NÉV	Anonymous

## BETEG ADATAI

Oncompass™ ID:

Név:

Születési dátum: 1959

Primer daganat lokalizációja: breast

Szöveti típus: invasive carcinoma NST

Metasztázis lokalizációja: bone, lymph node

## SZAKÉRTŐK

Molekuláris Farmakológus: Dr. Peták István

Genetikai Tanácsadó: Déri Júlia, MSc

Molekuláris Biológus: Várkonyi Edit, PhD

Konzulens Orvos: Dr. Pajkos Gábor

Szakértő: Dr. Szuszán Marianna

Betegút Koordinátor: Czető Réka

Info-bionikus Mérnök: Tihanyi Dóra, MSc

Molekuláris Bionikus Mérnök: Dirner Anna, MSc

## PATOLÓGIAI ÉS MOLEKULÁRIS DIAGNOSZTIKAI VIZSGÁLATOK

Mintaazonosító: XXX (szöveti minta)

Minta eredete: nyirokcsomó metastázis

Tumorarány: 50%

Tumortípus: invazív ductális emlő carcinoma

### Elvégzett vizsgálatok:

IHC - PD-L1 normál expresszió

MSI - MSS

TMB - magas: 6,44 mut/Mb

NGS - 591 gén

### Korábbi molekuláris vizsgálatok eredménye:

IHC - ER, PR, HER2 normál expresszió

IHC - PD-L1 overexpresszió (>1%)

## KORÁBBI KEZELÉSEK

Neoadjuváns kezelés: DOCETAXEL + DOXORUBICIN

1. vonal: PACLITAXEL + BEVACIZUMAB

2. vonal: CARBOPLATIN + DOCETAXEL

## ÖSSZEFOGLALÁS

Az Oncompass vizsgálat a következő mintából történt:

Mintaazonosító: XXX (szöveti minta), Minta eredete: nyirokcsomó metastázis. Tumorarány: 50%

Elvégzett vizsgálatok:

IHC - PDL1 (Normál expresszió)

MSI - MSS

TMB - HIGH

NGS - 591 gén

Korábbi molekuláris vizsgálatok eredménye:

IHC - ER (Normál expresszió), HER2 (Normál expresszió), PR (Normál expresszió)

## ÖSSZEFOGLALÁS

### IHC - PDL1 (Overexpresszió >1%)

591 gén NGS szekvenálása 5103 genetikai variánst mutatott ki a mintában. A molekuláris profilba feltöltött 34 variáns bioinformatikai és funkcionális szűrések eredményeként került kiválasztásra. Ezek a variánsok szerepelnek a Realtime Oncology Calculatorban további funkcionális interpretáció és orvosi döntéstámogatás céljából.

Az MTC algoritmus az aktuális evidencia adatbázis alapján **driverként** listázta a következő eltéréseket: TMB-H driver (AEL: 803,92, AF/TR: NA /50%), PDL1 protein overexpression driver (AEL: 475,62, AF/TR: NA/NA), BRCA1-K654fs\*47 driver (AEL: 85,31, AF/TR: 31.72%/50%), KMT2C-C391\* driver (AEL: 16,09, AF/TR: 7.24%/50%),

További driver gén ismeretlen variánsaként **-VUS, driver gén** jelöléssel -listázott alterációkra vonatkozólag nem szerepel információ az evidencia adatbázisban, de ismert, hogy a gén más mutációi hozzájárulhatnak a daganatképződéshez: TP53-M160\_A161dup VUS, driver gén (AEL: 22,52, AF/TR: 23.66% /50%), KIT-E930Q VUS, driver gén (AEL: 14,13, AF/TR: 12.1%/50%), CUL3-R162fs\*9 VUS, driver gén (AEL: 0,07, AF/TR: 8.62%/50%),

**TMB HIGH:** A vizsgált mintában a szekvenancia analízis (NGS) során kapott 1 megabázisra vonatkozó mutációk száma **(TMB): 6,44**. Az adatbázisunkban lévő kalkulált TMB értékek (n=585) eloszlása alapján az eseteink 90%-ában kaptunk ennél alacsonyabb TMB értéket.

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

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

A törzskönyv alapjául a KEYNOTE-158 fázis II klinikai vizsgálat (NCT02628067) előre tervezett retrospektív analízise szolgált.

### TMB-High tripla negatív emlődaganat

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

Az ATEZOLIZUMAB törzskönyvezett PD-L1 pozitív, irrezekábilis, lokálisan előrehaladott vagy metasztatikus tripla negatív emlődaganat (triple negative breast cancer, TNBC) indikációban nab-paclitaxellel kombinációban. (Impassion130 klinikai vizsgálat).

### PD-L1 overexpresszált tripla negatív emlődaganat

TNBC indikációban törzskönyvezett immunterápia az ATEZOLIZUMAB és a PEMBROLIZUMAB (csak az FDA által).

A PEMBROLIZUMAB (PD-1 inhibitor) az FDA által törzskönyvezett kemoterápiával kombinációban PD-L1 pozitív (10%), előrehaladott TNBC betegek számára.

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

Magasabb kópiaszámokban vannak jelen, a z FGFR1, CCNE1, RHPN2, CEBPA (n=8), TACC1 (n=7), ZNF703, BRCA1 (n=5).

Az NGS vizsgálat által detektált kópiaszám-változásokat klinikai relevancia esetében FISH vizsgálattal is javasoljuk megvizsgálni. Az FGFR1 gén FISH vizsgálata folyamatban van.

**FGFR1 amplifikáció emlődaganatban:** FGFR1 amplifikáció esetén az FGFR1 gátló gyógyszerek lehetnek hatékonyak. Törzskönyvezett multi-tirozin kináz gátlószerek, amelyek többek között az FGFR jelpályát is gátolják a LENVATINIB, a NINTEDANIB, a PAZOPANIB, a REGORAFENIB és a PONATINIB, illetve kevésbé specifikusak a SORAFENIB és a SUNITINIB. FDA által urothelialis daganatok indikációjában elfogadott FGFR gátló hatóanyag az ERDAFITINIB.

**CCNE1 amplifikáció:** CCNE1 amplifikáció esetén a CDK-k és a WEE1 említhetők pozitív asszociációban, mint indirekt targetek.

Egy preklinikai vizsgálat során PARP+ATR inhibitorok kombinációja CCNE1 amplifikált, PARPI- és platina-rezisztens ovárium daganat xenograft modellekben teljes terápiás választ és tumor regressziót eredményezett.

**BRCA1-K654fs\*47:** Ez a mutáció a ClinVar és a BRCA Exchange adatbázisok és a tudományos irodalom szerint patogén. Szerepel a COSMIC adatbázisban is. A leolvasási keretelődést okozó mutáció (frameshift mutation) a BRCA1 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti. A mutáns génről egy csonka fehérjevaltozat képződik, ezért feltételezhető, hogy funkcióvesztéssel jár. BRCA inaktiváció esetén a PARP inhibitorok említhetők pozitív asszociációban. Ováriumdaganatokban írták le, hogy BRCA mutáció esetén a PD-1/PD-L1 gátló immunterápiától is emelkedett hatékonyság várható.

### BRCA mutáció emlődaganatban

Csíravonalas BRCA mutáció esetén HER2 negatív emlődaganatos betegek részére törzskönyvezett PARP gátló gyógyszer az OLAPARIB és a TALAZOPARIB. Mindkét gyógyszer neoadjuváns/adjuváns/metasztatikus vonalban alkalmazott kemoterápia után adható.

### Frameshift mutációk

## ÖSSZEFOGLALÁS

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

## ÖSSZEGEZVE:

Molekuláris profil alapján-amennyiben klinikailag támogatható- szóba jöhet: **IMMUNTERÁPIA+PARP gátló (Atezolizumab+Olaparib/vagy Talazoparib)**, TMB-high/6,44, PDL1 pozitivitas és BRCA1 mutáció miatt,off label+EMK. Az FDA törzskönyvezte az atezolizumabot PD-L1 pozitív, irrezekábilis, lokálisan előrehaladott vagy metasztatikus tripla negatív emlődaganat indikációban nab-paclitaxellel kombinációban. Csírvonalas BRCA mutáció esetén HER2 negatív emlődaganatos betegek részére törzskönyvezett PARP gátló gyógyszer az OLAPARIB és a TALAZOPARIB. Mindkét gyógyszer neoadjuváns/adjuváns/metasztatikus vonalban alkalmazott kemoterápia után adható.

BRCA1 mutáció germline vizsgálata javasolható (vérből), illetve genetikai tanácsadás. A kezelőorvos kérésére BRCA1 mutáció vizsgálatát vérből elvégezzük.

## MOLEKULÁRIS CÉLPONT ELEMZÉS

### MOLEKULÁRIS ALTERÁCIÓK

TMB-H driver (AEL: 803,92, AF/TR: NA/50%),  
 PDL1 protein overexpression driver (AEL: 475,62, AF/TR: NA/NA),  
 BRCA1-K654fs\*47 driver (AEL: 85,31, AF/TR: 31.72%/50%),  
 TP53-M160\_A161dup VUS, driver gén (AEL: 22,52, AF/TR: 23.66%/50%),  
 KMT2C-C391\* driver (AEL: 16,09, AF/TR: 7.24%/50%),  
 KIT-E930Q VUS, driver gén (AEL: 14,13, AF/TR: 12.1%/50%),  
 NFE2L2-G589D VUS, driver gén (AEL: 1,18, AF/TR: 11.01%/50%),  
 GNAS-P459R driver (AEL: 0,85, AF/TR: 30.3%/50%),  
 KDM5C-S299R VUS, driver gén (AEL: 0,50, AF/TR: 55.89%/50%),  
 CUL3-R162fs\*9 VUS, driver gén (AEL: 0,07, AF/TR: 8.62%/50%),  
 FOXA1-L148V VUS, driver gén (AEL: 0,04, AF/TR: 69.51%/50%),  
 TENT5C-E299K driver (AEL: 0,01, AF/TR: 45.34%/50%),  
 GAS6-V673fs\*37 driver (AEL: 0,01, AF/TR: 3%/50%),  
 ZNF703-A514del ellentmondásos driver (AEL: 0,00, AF/TR: 4.27%/50%),  
 ZNF703-P307S ellentmondásos driver (AEL: 0,00, AF/TR: 9.4%/50%),  
 AKAP9-Q1373E ellentmondásos driver (AEL: 0,00, AF/TR: 11.97%/50%),  
 MAGI2-E867K ellentmondásos driver (AEL: 0,00, AF/TR: 12.5%/50%),  
 BRCA1-D430N ellentmondásos driver (AEL: 0,00, AF/TR: 38.74%/50%),  
 OTOP1-V69M ellentmondásos driver (AEL: 0,00, AF/TR: 23.08%/50%),  
 KLHL6-Q317L ellentmondásos driver (AEL: 0,00, AF/TR: 38.4%/50%),  
 SEC16A-T1001I ellentmondásos driver (AEL: 0,00, AF/TR: 58.21%/50%),  
 PCBPI-N84S ellentmondásos driver (AEL: 0,00, AF/TR: 42.56%/50%),  
 PIK3CG-Q1071E ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.09%/50%),  
 OTOP1-L104M ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 51.92%/50%),  
 AXL-P279Q ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 30.69%/50%),  
 SPEGR-R1621C ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 33.09%/50%),  
 BUB1B-Q487H ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 8.43%/50%),  
 AMPH-Q71fs\*4 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25.2%/50%),  
 FGF14-N242T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25%/50%),  
 CCNE1-R101S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 7.24%/50%),  
 KMT2C-R380L nem driver (AEL: -3,65, AF/TR: 7.5%/50%),  
 KIT-M541L nem driver (AEL: -4,20, AF/TR: 49.94%/50%),  
 GNAT2-A5V nem driver (AEL: -5,00, AF/TR: 50.15%/50%),  
 WNK2-H758N nem driver (AEL: -5,00, AF/TR: 61.82%/50%),  
 EPHA5-A672T nem driver (AEL: -10,00, AF/TR: 99.53%/50%),  
 NOTCH1-R1279H nem driver (AEL: -16,57, AF/TR: 61.04%/50%)

### INDIREKT CÉLPONT GÉNEK

CD274 vad típus (AEL: 1764,22),  
 • PDL1 protein overexpression driver (AEL: 475,62) ;  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TMB-H driver (AEL: 803,92) ;  
 • BRCA1-D430N driver (AEL: 0,00)

PD-1 vad típus (AEL: 1440,84),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TMB-H driver (AEL: 803,92) ;  
 • PDL1 protein overexpression driver (AEL: 475,62) ;  
 • BRCA1-D430N driver (AEL: 0,00)

CTLA4 vad típus (AEL: 809,26),  
 • TMB-H driver (AEL: 803,92)

PARP1 vad típus (AEL: 165,38),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • BRCA1-D430N driver (AEL: 0,00)

KIT vad típus (AEL: 121,53),  
 • KIT-E930Q driver (AEL: 14,13)

CHEK1 vad típus (AEL: 109,87),  
 • BRCA1-D430N driver (AEL: 0,00) ;  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PARP2 vad típus (AEL: 85,41),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • BRCA1-D430N driver (AEL: 0,00)

WEE1 vad típus (AEL: 26,32),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

ATR vad típus (AEL: 23,86),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK4 vad típus (AEL: 23,50),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

RARG vad típus (AEL: 23,41),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PLK1 vad típus (AEL: 23,00),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PRKDC vad típus (AEL: 22,92),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK1 vad típus (AEL: 22,85),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

MOLEKULÁRIS CÉLPONT ELEMZÉS	
	<p>CDK9 vad típus (AEL: 22,85),</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: 22,52)</li> </ul> <p>CDK2 vad típus (AEL: 22,85),</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: 22,52)</li> </ul> <p>AURKB vad típus (AEL: 22,80),</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: 22,52)</li> </ul> <p>BRD4 vad típus (AEL: 18,23),</p> <ul style="list-style-type: none"> <li>KMT2C-C391* driver (AEL: 16,09)</li> </ul> <p>JAK2 vad típus (AEL: 14,55),</p> <ul style="list-style-type: none"> <li>KIT-E930Q driver (AEL: 14,13)</li> </ul> <p>glutaminase vad típus (AEL: 4,45),</p> <ul style="list-style-type: none"> <li>NFE2L2-G589D driver (AEL: 1,18)</li> </ul> <p>PRKACA vad típus (AEL: 1,35),</p> <ul style="list-style-type: none"> <li>GNAS-P459R driver (AEL: 0,85)</li> </ul> <p>ATM vad típus (AEL: 0,72)</p> <ul style="list-style-type: none"> <li>CUL3-R162fs*9 driver (AEL: 0,07)</li> </ul>

DAGANAT MOLEKULÁRIS PROFILJÁVAL POZITÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK	DAGANAT MOLEKULÁRIS PROFILJÁVAL NEGATÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK
<p><b>FORGALOMBAN LÉVŐ</b> 4 listázott hatóanyag (összesen 95)</p> <p>PEMBROLIZUMAB (esophagus - squamous cell carcinoma [FDA]; lung - non-small cell carcinoma [FDA+EMA]; bármely tumor - renal cell carcinoma [FDA+EMA]; head-neck - squamous cell carcinoma [FDA+EMA]; rectum - bármely szövettan [FDA+EMA]; breast - bármely szövettan [FDA]; bármely tumor - mediastinal B-cell lymphoma [FDA]; gastroesophageal junction - adenocarcinoma [FDA]; gastric - adenocarcinoma [FDA]; bármely tumor - malignant melanoma [FDA+EMA]; skin - squamous cell carcinoma [FDA]; cervix - bármely szövettan [FDA]; lung - adenocarcinoma [FDA+EMA]; skin - Merkel cell carcinoma (MCC) [FDA]; bármely tumor - urothelial carcinoma [FDA+EMA]; liver - hepatocellular carcinoma [FDA]; endometrium - bármely szövettan [FDA]; bármely tumor - endometrioid carcinoma [FDA]; colon - bármely szövettan [FDA+EMA]; bármely tumor - Hodgkin lymphoma [FDA+EMA]) (AEL: 10455,98)</p> <ul style="list-style-type: none"> <li>TMB-H driver (AEL: 803,92);</li> <li>PD-1 vad típus target (AEL: 1440,84);</li> <li>PD-L1 protein overexpression driver (AEL: 475,62);</li> <li>PD-L1 vad típus target (AEL: 1764,23)</li> </ul> <p>ATEZOLIZUMAB (bármely tumor - malignant melanoma [FDA]; lung - small cell carcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]; bármely tumor - urothelial carcinoma [FDA+EMA]; breast - bármely szövettan [FDA+EMA]; liver - hepatocellular carcinoma [FDA+EMA]) (AEL: 3641,80)</p> <ul style="list-style-type: none"> <li>PD-L1 vad típus target (AEL: 1764,23);</li> <li>PD-L1 protein overexpression driver (AEL: 475,62)</li> </ul> <p>OLAPARIB (pancreas - bármely szövettan [FDA+EMA]; peritoneum - bármely szövettan [FDA+EMA]; prostate - bármely szövettan [FDA+EMA]; fallopian tube - bármely szövettan [FDA+EMA]; ovary - bármely szövettan [FDA+EMA]; breast - bármely szövettan [FDA+EMA]) (AEL: 766,00)</p> <ul style="list-style-type: none"> <li>PARP1 vad típus target (AEL: 165,38);</li> <li>BRCA1-D430N driver (AEL: 0,00);</li> <li>BRCA1-K654fs*47 driver (AEL: 85,31)</li> </ul> <p>NIRAPARIB (ovary - epithelial carcinoma [FDA+EMA]; fallopian tube - bármely szövettan [FDA+EMA]; peritoneum - bármely szövettan [FDA+EMA]) (AEL: 402,97)</p> <ul style="list-style-type: none"> <li>BRCA1-K654fs*47 driver (AEL: 85,31);</li> <li>PARP1 vad típus target (AEL: 165,38);</li> <li>BRCA1-D430N driver (AEL: 0,00);</li> <li>PARP2 vad típus target (AEL: 85,41)</li> </ul>	<p><b>FORGALOMBAN LÉVŐ</b> 10 listázott hatóanyag (összesen 13)</p> <p>DOXORUBICIN (bone marrow - multiple myeloma [FDA]; blood vessel - kaposi sarcoma [FDA]; ovary - carcinoma [FDA]; breast - carcinoma [FDA]) (AEL: -47,76)</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: -22,52);</li> <li>KMT2C-C391* driver (AEL: -16,09)</li> </ul> <p>CRIZOTINIB (lung - non-small cell carcinoma [FDA+EMA]; bármely tumor - anaplastic large cell lymphoma [FDA]) (AEL: -44,26)</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: -22,52);</li> <li>KIT-E930Q driver (AEL: -14,13)</li> </ul> <p>CHOP (AEL: -39,53)</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: -22,52)</li> </ul> <p>CYTARABINE (AEL: -24,65)</p> <ul style="list-style-type: none"> <li>KMT2C-C391* driver (AEL: -16,09)</li> </ul> <p>PACLITAXEL (AEL: -22,56)</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: -22,52)</li> </ul> <p>ETOPOSIDE (AEL: -22,56)</p> <ul style="list-style-type: none"> <li>TP53-M160_A161dup driver (AEL: -22,52)</li> </ul> <p>BAZEDOXIFENE (AEL: -16,16)</p> <ul style="list-style-type: none"> <li>ESR1 vad típus target (AEL: -16,38)</li> </ul> <p>GEFITINIB (lung - squamous cell carcinoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]; lung - non-small cell carcinoma [FDA+EMA]) (AEL: -1,40)</p> <p>MELPHALAN (AEL: -0,17)</p> <p>AFATINIB (lung - non-small cell carcinoma [FDA+EMA]; lung - squamous cell carcinoma [FDA+EMA]; lung - adenocarcinoma [FDA+EMA]) (AEL: -0,14)</p>

DAGANAT MOLEKULÁRIS PROFILJÁVAL POZITÍV KAPCSOLATBAN ÁLLÓ HATÓANYAGOK	DAGANAT MOLEKULÁRIS PROFILJÁVAL KAPCSOLATBAN ÁLLÓ HATÓANYAGOK NEGATÍV
<p><b>KLINIKAI FEJLESZTÉS ALATT</b> 10 listázott hatóanyag (összesen 108)</p> <p>TORIPALIMAB (AEL: 2056,45)</p> <ul style="list-style-type: none"> <li>• PD-L1 protein overexpression driver (AEL: 475,62) ;</li> <li>• PD-1 vad típus target (AEL: 1440,84)</li> </ul> <p>SINTILIMAB (AEL: 1956,45)</p> <ul style="list-style-type: none"> <li>• PD-1 vad típus target (AEL: 1440,84) ;</li> <li>• PD-L1 protein overexpression driver (AEL: 475,62)</li> </ul> <p>CS1001 (AEL: 1764,48)</p> <ul style="list-style-type: none"> <li>• PD-L1 vad típus target (AEL: 1764,23)</li> </ul> <p>BINTRAFUSP ALFA (AEL: 1764,22)</p> <ul style="list-style-type: none"> <li>• PD-L1 vad típus target (AEL: 1764,23)</li> </ul> <p>PACMILIMAB (AEL: 1764,22)</p> <ul style="list-style-type: none"> <li>• PD-L1 vad típus target (AEL: 1764,23)</li> </ul> <p>MDX-1105 (AEL: 1764,22)</p> <ul style="list-style-type: none"> <li>• PD-L1 vad típus target (AEL: 1764,23)</li> </ul> <p>camrelizumab (AEL: 1441,74)</p> <ul style="list-style-type: none"> <li>• PD-1 vad típus target (AEL: 1440,84)</li> </ul> <p>TISLELIZUMAB (AEL: 1441,32)</p> <ul style="list-style-type: none"> <li>• PD-1 vad típus target (AEL: 1440,84)</li> </ul> <p>GEPTANOLIMAB (AEL: 1441,04)</p> <ul style="list-style-type: none"> <li>• PD-1 vad típus target (AEL: 1440,84)</li> </ul> <p>ABBV-181 (AEL: 1440,84)</p> <ul style="list-style-type: none"> <li>• PD-1 vad típus target (AEL: 1440,84)</li> </ul>	<p><b>KLINIKAI FEJLESZTÉS ALATT</b> 7 listázott hatóanyag (összesen 7)</p> <p>R-CHOP (AEL: -63,80)</p> <ul style="list-style-type: none"> <li>• TP53-M160_A161dup driver (AEL: -22,52)</li> </ul> <p>PATUPILONE (AEL: -22,59)</p> <ul style="list-style-type: none"> <li>• TP53-M160_A161dup driver (AEL: -22,52)</li> </ul> <p>AZD9496 (AEL: -16,38)</p> <ul style="list-style-type: none"> <li>• ESR1 vad típus target (AEL: -16,38)</li> </ul> <p>SRN-927 (AEL: -16,38)</p> <ul style="list-style-type: none"> <li>• ESR1 vad típus target (AEL: -16,38)</li> </ul> <p>ELACESTRANT (AEL: -16,16)</p> <ul style="list-style-type: none"> <li>• ESR1 vad típus target (AEL: -16,38)</li> </ul> <p>BRILANESTRANT (AEL: -16,11)</p> <ul style="list-style-type: none"> <li>• ESR1 vad típus target (AEL: -16,38)</li> </ul> <p>FK866 (AEL: -1,82)</p>

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 LEÍRÁS

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 vettük össze a rendszerben található klinikai vizsgálatok beválogatási és kizárási feltételeivel. A manuálisan beállított keresési feltételek nem feltétlenül tartalmaznak minden szűrési 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

AKAP9-Q1373E, AMPH-Q71FS\*4, AXL-P279Q, BRCA1-D430N, BRCA1-K654FS\*47, BUB1B-Q487H, CCNE1-R101S, CUL3-R162FS\*9, EPHA5-A672T, FGF14-N242T, FOXA1-L148V, GAS6-V673FS\*37, GNAS-P459R, GNAT2-A5V, KDM5C-S299R, KIT-E930Q, KIT-M541L, KLHL6-Q317L, KMT2C-C391\*, KMT2C-R380L, MAGI2-E867K, NFE2L2-G589D, NOTCH1-R1279H, OTOPI-L104M, OTOPI-V69M, PCBP1-N84S, PIK3CG-Q1071E, SEC16A-T1001I, SPEG-R1621C, TENT5C-E299K, TP53-M160\_A161DUP, WNK2-H758N, ZNF703-A514DEL, ZNF703-P307S

### VAD TÍPUSÚ GÉNEK

ABCB1, ABCC2, ABL1, ABL2, ABRAXAS1, ACVR1B, ACVRL1, ADGRB3, AGTRAP, AIP, AKT1, AKT2, AKT3, ALK, AMER1, APC, APEX1, AR, ARAF, ARFRP1, ARID1A, ARID1B, ARID2, ASXL1, ATM, ATP11B, ATP4A, ATP6VOD2, ATR, ATRX, AURKA, AURKB, AXIN1, AXIN2, B2M, BAP1, BARD1, BAX, BAZ2B, BCL2, BCL2L1, BCL2L2, BCL6, BCL9, BCOR, BCORL1, BCR, BIM, BIRC2, BIRC3, BLM, BMPR1A, BRAF, BRCA2, BRD4, BRIP1, BTG1, BTK, CARD11, CASP8, CASR, CBF3, CBL, CBLB, CBLG, CCDC178, CCDC6, CCND1, CCND2, CCND3, CD74, CD79A, CD79B, CDA, CDC27, CDC73, CDH1, CDK12, CDK4, CDK6, CDK8, CDKN1A, CDKN1B, CDKN1C, CDKN2A, CDKN2B, CDKN2C, CEBPA, CEP57, CHD1, CHD2, CHD4, CHD7, CHEK1, CHEK2, CHIC2, CIC, CIT, CREBBP, CRKL, CRLF2, CSF1R, CSMD3, CSNK2A1, CTCF, CTNNA1, CTNNA2, CUBN, CYLD, CYP19A1, CYP2A6, CYP2B6, CYP2C19, CYP2C9, CYP2D6, DAXX, DCC, DCUN1D1, DDB2, DDR1, DDR2, DDX11, DDX3X, DICER1, DIS3L2, DMD, DNMT3A, DOT1L, DPH3, DPYD, DSE, ECT2L, EED, EGFR, ELMO1, EML4, EMSY, EP300, EPCAM, EPHA2, EPHA3, EPHA7, EPHB1, ERBB2, ERBB3, ERBB4, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ERG, ERFF1, ESR1, ESR2, ESRP1, ETV6, EXOC2, EXT1, EXT2, EZH2, EZR, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCL, FANCM, FAS, FAT1, FAT3, FBXO11, FBXO12, FBXW7, FGF10, FGF19, FGF23, FGF3, FGF4, FGF5, FGF6, FGF9, FGF11, FGF12, FGF13, FGF14, FGF15, FGF16, FGF17, FGF18, FGF19, FGF20, FGF21, FGF22, FGF23, FGF24, FGF25, FGF26, FGF27, FGF28, FGF29, FGF30, FGF31, FGF32, FGF33, FGF34, FGF35, FGF36, FGF37, FGF38, FGF39, FGF40, FGF41, FGF42, FGF43, FGF44, FGF45, FGF46, FGF47, FGF48, FGF49, FGF50, FGF51, FGF52, FGF53, FGF54, FGF55, FGF56, FGF57, FGF58, FGF59, FGF60, FGF61, FGF62, FGF63, FGF64, FGF65, FGF66, FGF67, FGF68, FGF69, FGF70, FGF71, FGF72, FGF73, FGF74, FGF75, FGF76, FGF77, FGF78, FGF79, FGF80, FGF81, FGF82, FGF83, FGF84, FGF85, FGF86, FGF87, FGF88, FGF89, FGF90, FGF91, FGF92, FGF93, FGF94, FGF95, FGF96, FGF97, FGF98, FGF99, FGF100, FGF101, FGF102, FGF103, FGF104, FGF105, FGF106, FGF107, FGF108, FGF109, FGF110, FGF111, FGF112, FGF113, FGF114, FGF115, FGF116, FGF117, FGF118, FGF119, FGF120, FGF121, FGF122, FGF123, FGF124, FGF125, FGF126, FGF127, FGF128, FGF129, FGF130, FGF131, FGF132, FGF133, FGF134, FGF135, FGF136, FGF137, FGF138, FGF139, FGF140, FGF141, FGF142, FGF143, FGF144, FGF145, FGF146, FGF147, FGF148, FGF149, FGF150, FGF151, FGF152, FGF153, FGF154, FGF155, FGF156, FGF157, FGF158, FGF159, FGF160, FGF161, FGF162, FGF163, FGF164, FGF165, FGF166, FGF167, FGF168, FGF169, FGF170, FGF171, FGF172, FGF173, FGF174, FGF175, FGF176, FGF177, FGF178, FGF179, FGF180, FGF181, FGF182, FGF183, FGF184, FGF185, FGF186, FGF187, FGF188, FGF189, FGF190, FGF191, FGF192, FGF193, FGF194, FGF195, FGF196, FGF197, FGF198, FGF199, FGF200, FGF201, FGF202, FGF203, FGF204, FGF205, FGF206, FGF207, FGF208, FGF209, FGF210, FGF211, FGF212, FGF213, FGF214, FGF215, FGF216, FGF217, FGF218, FGF219, FGF220, FGF221, FGF222, FGF223, FGF224, FGF225, FGF226, FGF227, FGF228, FGF229, FGF230, FGF231, FGF232, FGF233, FGF234, FGF235, FGF236, FGF237, FGF238, FGF239, FGF240, FGF241, FGF242, FGF243, FGF244, FGF245, FGF246, FGF247, FGF248, FGF249, FGF250, FGF251, FGF252, FGF253, FGF254, FGF255, FGF256, FGF257, FGF258, FGF259, FGF260, FGF261, FGF262, FGF263, FGF264, FGF265, FGF266, FGF267, FGF268, FGF269, FGF270, FGF271, FGF272, FGF273, FGF274, FGF275, FGF276, FGF277, FGF278, FGF279, FGF280, FGF281, FGF282, FGF283, FGF284, FGF285, FGF286, FGF287, FGF288, FGF289, FGF290, FGF291, FGF292, FGF293, FGF294, FGF295, FGF296, FGF297, FGF298, FGF299, FGF300, FGF301, FGF302, FGF303, FGF304, FGF305, FGF306, FGF307, FGF308, FGF309, FGF310, FGF311, FGF312, FGF313, FGF314, FGF315, FGF316, FGF317, FGF318, FGF319, FGF320, FGF321, FGF322, FGF323, FGF324, FGF325, FGF326, FGF327, FGF328, FGF329, FGF330, FGF331, FGF332, FGF333, FGF334, FGF335, FGF336, FGF337, FGF338, FGF339, FGF340, FGF341, FGF342, FGF343, FGF344, FGF345, FGF346, FGF347, FGF348, FGF349, FGF350, FGF351, FGF352, FGF353, FGF354, FGF355, FGF356, FGF357, FGF358, FGF359, FGF360, FGF361, FGF362, FGF363, FGF364, FGF365, FGF366, FGF367, FGF368, FGF369, FGF370, FGF371, FGF372, FGF373, FGF374, FGF375, FGF376, FGF377, FGF378, FGF379, FGF380, FGF381, FGF382, FGF383, FGF384, FGF385, FGF386, FGF387, FGF388, FGF389, FGF390, FGF391, FGF392, FGF393, FGF394, FGF395, FGF396, FGF397, FGF398, FGF399, FGF400, FGF401, FGF402, FGF403, FGF404, FGF405, FGF406, FGF407, FGF408, FGF409, FGF410, FGF411, FGF412, FGF413, FGF414, FGF415, FGF416, FGF417, FGF418, FGF419, FGF420, FGF421, FGF422, FGF423, FGF424, FGF425, FGF426, FGF427, FGF428, FGF429, FGF430, FGF431, FGF432, FGF433, FGF434, FGF435, FGF436, FGF437, FGF438, FGF439, FGF440, FGF441, FGF442, FGF443, FGF444, FGF445, FGF446, FGF447, FGF448, FGF449, FGF450, FGF451, FGF452, FGF453, FGF454, FGF455, FGF456, FGF457, FGF458, FGF459, FGF460, FGF461, FGF462, FGF463, FGF464, FGF465, FGF466, FGF467, FGF468, FGF469, FGF470, FGF471, FGF472, FGF473, FGF474, FGF475, FGF476, FGF477, FGF478, FGF479, FGF480, FGF481, FGF482, FGF483, FGF484, FGF485, FGF486, FGF487, FGF488, FGF489, 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FGF615, FGF616, FGF617, FGF618, FGF619, FGF620, FGF621, FGF622, FGF623, FGF624, FGF625, FGF626, FGF627, FGF628, FGF629, FGF630, FGF631, FGF632, FGF633, FGF634, FGF635, FGF636, FGF637, FGF638, FGF639, FGF640, FGF641, FGF642, FGF643, FGF644, FGF645, FGF646, FGF647, FGF648, FGF649, FGF650, FGF651, FGF652, FGF653, FGF654, FGF655, FGF656, FGF657, FGF658, FGF659, FGF660, FGF661, FGF662, FGF663, FGF664, FGF665, FGF666, FGF667, FGF668, FGF669, FGF670, FGF671, FGF672, FGF673, FGF674, FGF675, FGF676, FGF677, FGF678, FGF679, FGF680, FGF681, FGF682, FGF683, FGF684, FGF685, FGF686, FGF687, FGF688, FGF689, FGF690, FGF691, FGF692, FGF693, FGF694, FGF695, FGF696, FGF697, FGF698, FGF699, FGF700, FGF701, FGF702, FGF703, FGF704, FGF705, FGF706, FGF707, FGF708, FGF709, FGF710, FGF711, FGF712, FGF713, FGF714, FGF715, FGF716, FGF717, FGF718, FGF719, FGF720, FGF721, FGF722, FGF723, FGF724, FGF725, FGF726, FGF727, FGF728, FGF729, FGF730, FGF731, FGF732, FGF733, FGF734, FGF735, FGF736, FGF737, FGF738, FGF739, FGF740, FGF741, FGF742, FGF743, FGF744, FGF745, FGF746, FGF747, FGF748, FGF749, FGF750, FGF751, FGF752, FGF753, FGF754, FGF755, FGF756, FGF757, FGF758, FGF759, FGF760, FGF761, FGF762, FGF763, FGF764, FGF765, FGF766, FGF767, FGF768, FGF769, FGF770, FGF771, FGF772, FGF773, FGF774, FGF775, FGF776, FGF777, FGF778, FGF779, FGF780, FGF781, FGF782, FGF783, FGF784, FGF785, FGF786, FGF787, FGF788, FGF789, FGF790, FGF791, FGF792, FGF793, FGF794, FGF795, FGF796, FGF797, FGF798, FGF799, FGF800, FGF801, FGF802, FGF803, FGF804, FGF805, FGF806, FGF807, FGF808, FGF809, FGF810, FGF811, FGF812, FGF813, FGF814, FGF815, FGF816, FGF817, FGF818, FGF819, FGF820, FGF821, FGF822, FGF823, FGF824, FGF825, FGF826, FGF827, FGF828, FGF829, FGF830, FGF831, FGF832, FGF833, FGF834, FGF835, FGF836, FGF837, FGF838, FGF839, FGF840, FGF841, FGF842, FGF843, FGF844, FGF845, FGF846, FGF847, FGF848, FGF849, FGF850, FGF851, FGF852, FGF853, FGF854, FGF855, FGF856, FGF857, FGF858, FGF859, FGF860, FGF861, FGF862, FGF863, FGF864, 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FGF1657, FGF1658, FGF1659, FGF1660, FGF1661, FGF1662, FGF1663, FGF1664, F



## RÉSZLETES MOLEKULÁRIS PROFIL

### MOLEKULÁRIS ALTERÁCIÓK

TMB-H driver (AEL: 803,92, AF/TR: NA/50%),  
 PDL1 protein overexpression driver (AEL: 475,62, AF/TR: NA/NA),  
 BRCA1-K654fs\*47 driver (AEL: 85,31, AF/TR: 31.72%/50%),  
 TP53-M160\_A161dup VUS, driver gén (AEL: 22,52, AF/TR: 23.66%/50%),  
 KMT2C-C391\* driver (AEL: 16,09, AF/TR: 7.24%/50%),  
 KIT-E930Q VUS, driver gén (AEL: 14,13, AF/TR: 12.1%/50%),  
 NFE2L2-G589D VUS, driver gén (AEL: 1,18, AF/TR: 11.01%/50%),  
 GNAS-P459R driver (AEL: 0,85, AF/TR: 30.3%/50%),  
 KDM5C-S299R VUS, driver gén (AEL: 0,50, AF/TR: 55.89%/50%),  
 CUL3-R162fs\*9 VUS, driver gén (AEL: 0,07, AF/TR: 8.62%/50%),  
 FOXA1-L148V VUS, driver gén (AEL: 0,04, AF/TR: 69.51%/50%),  
 TENT5C-E299K driver (AEL: 0,01, AF/TR: 45.34%/50%),  
 GAS6-V673fs\*37 driver (AEL: 0,01, AF/TR: 3%/50%),  
 ZNF703-A514del ellentmondásos driver (AEL: 0,00, AF/TR: 4.27%/50%),  
 ZNF703-P307S ellentmondásos driver (AEL: 0,00, AF/TR: 9.4%/50%),  
 AKAP9-Q1373E ellentmondásos driver (AEL: 0,00, AF/TR: 11.97%/50%),  
 MAGI2-E867K ellentmondásos driver (AEL: 0,00, AF/TR: 12.5%/50%),  
 BRCA1-D430N ellentmondásos driver (AEL: 0,00, AF/TR: 38.74%/50%),  
 OTOP1-V69M ellentmondásos driver (AEL: 0,00, AF/TR: 23.08%/50%),  
 KLHL6-Q317L ellentmondásos driver (AEL: 0,00, AF/TR: 38.4%/50%),  
 SEC16A-T1001I ellentmondásos driver (AEL: 0,00, AF/TR: 58.21%/50%),  
 PCBP1-N84S ellentmondásos driver (AEL: 0,00, AF/TR: 42.56%/50%),  
 PIK3CG-Q1071E ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 9.09%/50%),  
 OTOP1-L104M ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 51.92%/50%),  
 AXL-P279Q ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 30.69%/50%),  
 SPEG-R1621C ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 33.09%/50%),  
 BUB1B-Q487H ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 8.43%/50%),  
 AMPH-Q71fs\*4 ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25.2%/50%),  
 FGF14-N242T ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 25%/50%),  
 CCNE1-R101S ismeretlen jelentőségű variáns (AEL: 0,00, AF/TR: 7.24%/50%),  
 KMT2C-R380L nem driver (AEL: -3,65, AF/TR: 7.5%/50%),  
 KIT-M541L nem driver (AEL: -4,20, AF/TR: 49.94%/50%),  
 GNAT2-A5V nem driver (AEL: -5,00, AF/TR: 50.15%/50%),  
 WNK2-H758N nem driver (AEL: -5,00, AF/TR: 61.82%/50%),  
 EPHA5-A672T nem driver (AEL: -10,00, AF/TR: 99.53%/50%),  
 NOTCH1-R1279H nem driver (AEL: -16,57, AF/TR: 61.04%/50%)

### INDIREKT CÉLPONT GÉNEK

CD274 vad típus (AEL: 1764,22),  
 • PDL1 protein overexpression driver (AEL: 475,62) ;  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TMB-H driver (AEL: 803,92) ;  
 • BRCA1-D430N driver (AEL: 0,00)

PD-1 vad típus (AEL: 1440,84),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TMB-H driver (AEL: 803,92) ;  
 • PDL1 protein overexpression driver (AEL: 475,62) ;  
 • BRCA1-D430N driver (AEL: 0,00)

CTLA4 vad típus (AEL: 809,26),  
 • TMB-H driver (AEL: 803,92)

PARP1 vad típus (AEL: 165,38),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • BRCA1-D430N driver (AEL: 0,00)

KIT vad típus (AEL: 121,53),  
 • KIT-E930Q driver (AEL: 14,13)

CHEK1 vad típus (AEL: 109,87),  
 • BRCA1-D430N driver (AEL: 0,00) ;  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PARP2 vad típus (AEL: 85,41),  
 • BRCA1-K654fs\*47 driver (AEL: 85,31) ;  
 • BRCA1-D430N driver (AEL: 0,00)

WEE1 vad típus (AEL: 26,32),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

ATR vad típus (AEL: 23,86),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK4 vad típus (AEL: 23,50),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

RARG vad típus (AEL: 23,41),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PLK1 vad típus (AEL: 23,00),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

PRKDC vad típus (AEL: 22,92),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK1 vad típus (AEL: 22,85),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK9 vad típus (AEL: 22,85),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

CDK2 vad típus (AEL: 22,85),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

AURKB vad típus (AEL: 22,80),  
 • TP53-M160\_A161dup driver (AEL: 22,52)

BRD4 vad típus (AEL: 18,23),  
 • KMT2C-C391\* driver (AEL: 16,09)

JAK2 vad típus (AEL: 14,55),  
 • KIT-E930Q driver (AEL: 14,13)

glutaminase vad típus (AEL: 4,45),  
 • NFE2L2-G589D driver (AEL: 1,18)

PRKACA vad típus (AEL: 1,35),  
 • GNAS-P459R driver (AEL: 0,85)

ATM vad típus (AEL: 0,72)  
 • CUL3-R162fs\*9 driver (AEL: 0,07)



## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

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

A vizsgált mintában a szekvenencia analízis (NGS) során kapott 1 megabázisra vonatkozó mutációk száma (TMB): 6,44. Az adatbázisunkban lévő kalkulált TMB értékek (n=585) eloszlása alapján az eseteink 90%-ában kaptunk ennél alacsonyabb TMB értéket.

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%. 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 tumorrall 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).

#### Referenciák:

- (1) Goodman AM et al., *Tumor Mutational Burden as an Independent Predictor of Response to Immunotherapy in Diverse Cancers. Mol Cancer Ther.* 2017 Nov;16(11):2598-2608. Epub 2017 Aug 23. PMID: 28835386
- (2) Goodman AM et al., *Microsatellite-Stable Tumors with High Mutational Burden Benefit from Immunotherapy. Cancer Immunol Res.* 2019 Oct;7(10):1570-1573. Epub 2019 Aug 12. PMID: 31405947
- (3) Samstein RM, et al. *Tumor mutational load predicts survival after immunotherapy across multiple cancer types. Nat Genet.* 2019 Feb;51(2):202-206. Epub 2019 Jan 14. PMID: 30643254
- (4) Marabelle A et al. *Association of tumour mutational burden with outcomes in patients with advanced solid tumours treated with pembrolizumab: prospective biomarker analysis of the multicohort, open-label, phase 2 KEYNOTE-158 study. Lancet Oncol.* 2020 Sep 10:S1470-2045(20)30445-9. Epub ahead of print. PMID: 32919526

### TMB-High tripla negatív emlődaganat

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

Az ATEZOLIZUMAB törzskönyvezett PD-L1 pozitív, irrezekábilis, lokálisan előrehaladott vagy metasztatikus tripla negatív emlődaganat (triple negative breast cancer, TNBC) indikációban nab-paclitaxellel kombinációban. Az IMpassion130 klinikai vizsgálat eredményei szerint az első vonalas nab-paclitaxel-hez adott atezolizumab kezelés a teljes betegpopuláción és a PD-L1 pozitív alcsoportban is szignifikánsan növelte a progressziómentes túlélést (progression-free survival, PFS). Teljes betegpopuláción a medián PFS az atezolizumab plusz nab-paclitaxel kombinációs karban 7,2 hónapnak, míg a placebo plusz nab-paclitaxel karban 5,5 hónapnak adódott (1). Ebben a tanulmányban nem vizsgálták a TMB sátuszt.

TNBC betegek között a neoadjuváns kemoterápiához adott durvalumab (PD-L1 gátló) 53%-ra emelte a teljes válaszadási arányt, a placebo + kemoterápia karban 44% volt ez az érték. A TMB-H betegcsoportban a betegek 58%-ánál figyeltek meg teljes patológiai válaszadást, míg a TMB-L (low) csoportban ez az érték 38% volt (2).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Egy fázis Ib klinikai vizsgálatban előrehaladott, TNBC betegeket kezeltek első vonalban ipatasertib, atezolizumab és kemoterápia kombinációjával. A vizsgálat előzetes eredményei szerint a betegek 73%-ánál értek el teljes vagy részleges választ, biomarker státuszról függetlenül (3).

Fázis II vizsgálatban magas TMB értékkel előrehaladott emlődaganatos betegek vettek részt. A válaszadási arány 21% volt, a medián PFS 10,6 hét, a medián teljes túlélés (overall survival, OS) 31,6 hét (4).

### Referenciák:

- (1) Schmid P et al., Atezolizumab and Nab-Paclitaxel in Advanced Triple-Negative Breast Cancer. *N Engl J Med.* 2018 Nov 29;379(22):2108-2121. Epub 2018 Oct 20. PubMed PMID: 30345906
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### PD-L1 overexpresszió

A PD-L1 overexpresszió több tumortípusban összefüggést mutat a PD-1 és PD-L1 gátló immunterápiák hatékonyságával (1, 2).

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

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### PD-L1 overexpresszált tripla negatív emlődaganat

A PD-L1 overexpresszió több tumortípusban összefüggést mutat a PD-1 és PD-L1 gátló immunterápiák hatékonyságával (1, 2).

Egy tanulmányban tripla negatív emlődaganatos (triple negative breast cancer, TNBC) betegek 19%-ában (20/105) mutattak ki >5% feletti PD-L1 expressziót (3). TNBC betegek körében intenzíven kutatott terület az immunterápiák alkalmazása (4).

TNBC indikációban törzkönyvezett immunterápia az ATEZOLIZUMAB és a PEMBROLIZUMAB (csak az FDA által).

Az ATEZOLIZUMAB (PD-L1 inhibitor) nab-paclitaxellel (nanorészecske albumin-kötött paclitaxel) kombinációban törzkönyvezett PD-L1 pozitív, irrezekábilis, lokálisan előrehaladott vagy metasztatikus TNBC betegek számára. Az IMpassion130 klinikai vizsgálat eredményei szerint a PD-L1 pozitív betegeknél a medián progressziómentes túlélés (progression-free survival, PFS) az atezolizumab plusz nab-paclitaxel kombinációs karban 7,5 hónapnak, míg a placebo plusz nab-paclitaxel karban 5,0 hónapnak adódott. A PD-L1 pozitív alcsoportban atezolizumab plusz nab-paclitaxel karban az esetek 59%-ában, míg a placebo plusz nab-paclitaxel karban az esetek 47%-ában értek el teljes vagy részleges választ. A teljes betegcsoporton a medián PFS és 7,2 hónap és 5,5 hónap, a medián teljes túlélés (overall survival; OS) 21,0 és 18,7 hónap, az objektív válaszadási ráta (objective response rate; ORR) 56% és 45,9% volt az atezolizumab és a placebo karban (5, 6).

Az IMpassion031 fázis III vizsgálat előzetes eredményei alapján az atezolizumab kombinálva nab-paclitaxellel majd doxorubicin+cyclophosphamide kemoterápiával (A-kemo) kedvezőbb patológiai teljes választ eredményezett a placebo és nab-paclitaxel majd kemoterápia (P-kemo) kombinációhoz képest előzetesen nem kezelt, korai stádiumú TNBC betegek körében, PD-L1 státuszról függetlenül (7).

Az IMpassion131 fázis III vizsgálat előzetes eredményei alapján az atezolizumab és paclitaxel kombináció nem eredményezett szignifikáns PFS és OS előnyt a placebo+paclitaxel terápiához képest elsővonalas kezelésként TNBC betegek számára (8).

Egy fázis I vizsgálatban (NCT01375842) metasztatikus TNBC betegek (n=112) részesültek atezolizumab terápiában. Az 1 éves OS ráta 45% volt a magas PD-L1 expressziójú tumor-infiltráló immunsejtekkel rendelkező betegek esetén és 37% a PD-L1-et alacsony szinten vagy nem expresszáló betegek között. A válaszadási ráta rendre 13% és 5% volt (9).

Egy fázis Ib klinikai vizsgálatban előrehaladott, TNBC betegeket kezeltek első vonalban ipatasertib, atezolizumab és kemoterápia kombinációjával. A vizsgálat előzetes eredményei szerint a betegek 73%-ánál értek el teljes vagy részleges választ, biomarker státuszról függetlenül (10).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Egy fázis Ib vizsgálatban (JAVELIN, NCT01772004), az avelumab (PD-L1 gátló) kezelés hatékonyságát tanulmányozták PD-L1 státusz alapján nem előszelektált, többszörösen előkezelt, metasztatikus emlődaganatos betegek (n=168) között. Az ORR a teljes csoportban 3,0% volt, a TNBC betegek (n=58) alcsoportjában 5,2%. Az ORR pozitív trendet mutatott a tumor asszociált immunsejtek PD-L1 expressziójával, TNBC betegek esetén 22,2% és 2,6% volt PD-L1 pozitív és negatív esetben (11).

A PEMBROLIZUMAB (PD-1 inhibitor) az FDA által törzskönyvezett kemoterápiával kombinációban PD-L1 pozitív (10%), előrehaladott TNBC betegek számára. A törzskönyv alapjául a fázis III KEYNOTE-355 vizsgálat szolgált, melyben a pembrolizumab vagy placebo és kemoterápia kombinációt hasonlították össze. A 10%-nál magasabb PD-L1 expresszióval rendelkező TNBC betegek alcsoportjában a medián PFS 9,7 hónap volt a pembrolizumab karban (n=220) és 5,6 hónap a placebo karban (n=103). PD-L1 státusztól függetlenül a medián PFS 7,5 hónap volt a pembrolizumab-karban (n=566), és 5,6 hónap a placebo-karban (n=281) (12).

Egy fázis II vizsgálatban (KEYNOTE-086, NCT02447003) a pembrolizumab (PD-1 inhibitor) hatékonyságát tanulmányozták előzetesen kezelt metasztatikus TNBC betegek között (kohort A). Az ORR 5,5% körüli értékű volt PD-L1 expressziótól függetlenül. A medián PFS 2,0 hónap, a medián OS 9,0 hónap volt, a 6-hónapos PFS és OS ráta rendre 14,9% és 69,1% volt (13).

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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.

Az eredmény alapján feltételezhető kópiaszám-növekedést okozó genetikai eltérés jelenléte. Daganatképződéssel összefüggésbe hozható gének, melyek feltehetően magasabb kópiaszámban vannak jelen, a z FGFR1, CCNE1, RHPN2, CEBPA (n=8), TACC1 (n=7), ZNF703, BRCA1 (n=5).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Az NGS vizsgálat által detektált kópiaszám-változásokat klinikai relevancia esetében FISH vizsgálatral is javasoljuk megvizsgálni. A kizárólag NGS-sel detektált kópiaszám-változások rutinszerűen nem szerepelnek a molekuláris profilban listázott azon variánsok között, amelyeket a digitális terápitervezés figyelembe vesz. Az FGFR1 gén FISH vizsgálata folyamatban van.

### FGFR1 amplifikáció emlődaganatban

Az FGFR1 amplifikáció ismert onkogenikus genetikai elváltozás emlőrákban. Egy tanulmányban a 880 vizsgált emlőtumor 8,7%-a mutatott FGFR1 amplifikációt. Az ösztrogénreceptor pozitív betegek között az FGFR1 amplifikáció rosszabb prognózissal korrelált (1).

Egy meta-analízis eredménye szerint az FGFR1 amplifikáció rövidebb betegségmentes túléléssel is korrelál (2).

FGFR1 amplifikáció esetén az FGFR1 gátló gyógyszerek lehetnek hatékonyak (3). Törzskönyvezett multi-tirozin kináz gátlószerek, amelyek többek között az FGFR jelpályát is gátolják a LENVATINIB, a NINTEDANIB, a PAZOPANIB, a REGORAFENIB és a PONATINIB, illetve kevésbé specifikusak a SORAFENIB és a SUNITINIB. FDA által urotheliális daganatok indikációjában elfogadott FGFR gátló hatóanyag az ERDAFITINIB.

Egy fázis I/IIa vizsgálatban 12 FGF aberrációval rendelkező előrehaladott emlőrákos beteg részesült LUCITANIB (fejlesztés alatt álló FGFR gátló hatóanyag) kezelésben. 6 beteg mutatott részleges tumorválaszt, és 6 betegnél írtak le stabil betegséget a kezelés hatására. A medián progressziómentes túlélés 40,4 hét volt (4). Egy fázis II vizsgálatban 178 metasztatikus emlődaganatos beteg részesült lucitanib kezelésben. A teljes válaszadási arány 3% volt, és nem írtak le különbséget a kezelés hatékonyságában az FGF aberrációk alapján (5). Egy másik lucitanibet tesztelő fázis II vizsgálatban (NCT02053636) 76 HR pozitív, HER2 negatív metasztatikus emlő carcinomás beteget vizsgáltak. A klinikai előny (azaz a teljes és részleges válaszadás, illetve a 24 hétnél hosszabb stabil betegség összesített aránya) 41% volt az FGFR1 amplifikált betegek esetén. A teljes válaszadási arány az FGFR1 erősen amplifikált páciensek esetében 25%, míg a gyengén amplifikált betegeknél 8% volt (6).

A DOVITINIB, fejlesztés alatt álló FGFR gátló hatóanyag, fázis II vizsgálatban 25%-os válaszadási arányt eredményezett FGFR1 amplifikált HR+ emlőrákos betegek körében, míg FGFR negatív HR+ emlőrákos betegek között a válaszadási arány 3% volt (7).

FGFR1 amplifikációt hordozó, emlőtumorból származó preklinikai modellekkel végzett kísérletekben specifikus FGFR1 gátlószerek (a ponatinib, illetve a klinikai fejlesztés alatt álló brivanib) aktivitást mutattak (8, 9). Kevésbé specifikus, az FGFR több típusát blokkoló tirozin kináz inhibitorok csökkentették az olyan emlő eredetű sejtvonalak osztódását, amelyekben a FGFR jelpálya aktiválódott, és ugyanezek a szerek hatástalanok voltak az aktiválódott jelátviteli útvonal jelenléte nélkül (9, 10).

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### CCNE1 amplifikáció

A CCNE1 által kódolt cyclin E1, a G1-S fázis tranzíciót irányítja a ciklin-dependens kináz 2 (CDK2) fehérjével komplexet képezve, és fontos szerepet játszik a sejtciklus szabályozás, DNS replikáció és kromoszóma szegregáció folyamatában (1).

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

A tudományos irodalom alapján a CCNE1 kópiaszám-növekedés és overexpresszió rossz prognózissal asszociált különböző daganattípusokban, különösen tripla-negatív emlőtumrok (TNBC) esetén (1-3). A CCNE1 amplifikáció TP53-mutáns gyomordaganatban májajtással asszociált egy tanulmány szerint (4).

CCNE1 amplifikáció esetén a CDK-k és a WEE1 említhetők pozitív asszociációban, mint indirekt targetek (5).

A CDK2 és pan-CDK gátlók ugyan ígéretesnek tűntek preklinikai kísérletekben CCNE1 amplifikáció esetén, azonban nem jutottak túl fázis II vizsgálatokon monoterápiaként az off-target gátlás okozta mellékhatások miatt. Jelenleg a CDK2 inhibitorokat PI3K inhibitorokkal vagy kemoterápiával kombinációban tanulmányozzák (5).

Egy tanulmányban a ciklin-E1 overexpressziója növelte a WEE1 aktivitást, CDK2-függő módon aktiválta a DNS replikációs stressz útvonalakat, és érzékenyítette a TNBC-s sejtvonalakat az adavosertib WEE1 inhibitorra (3).

Megnövekedett CCNE1 kópiaszámú ovarium tumoros sejtvonalak proliferációját gátolta, migrációját, kolóniaformáló képességét csökkentette DINACICLIB és az SDHA inhibitor 3NPA kombinációja egy preklinikai vizsgálat során (6).

Egy preklinikai vizsgálat során PARP+ATR inhibitorok kombinációja CCNE1 amplifikált, PARPi- és platina-rezisztens ovarium daganat xenograft modellekben teljes terápiás választ és tumor regressziót eredményezett (7).

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### TACC1 kópiaszám-nyerés

A TACC1 fehérjéről egérmodellekben kimutatták, hogy onkogenikus tulajdonságaival hozzájárulhat az emlődaganatok kialakulásához (1).

Prosztatadaganatokban a TACC1 gén expressziós szintje az androgén-független stádiummal asszociált (2).

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### ZNF703 kópiaszám-nyerés

A ZNF703 proto-onkogen emelkedett kópiaszáma overexpresszióval és rosszabb klinikai kimenetellel asszociál (1, 2). A ZNF703 overexpressziója jellemző luminal B típusú (hormon receptor pozitív) emlő daganatokban. Overexpressziója esetén az AKT/mTOR útvonal aktivációja és az ERalfa csökkent működése figyelhető meg (3, 4). Feltehetően hozzájárulhat tamoxifen hormonkezeléssel szemben való rezisztencia kialakulásához (3). mTOR gátló hatóanyag alkalmazása növelte a ZNF703 overexpresszálo sejtek érzékenységét tamoxifennel szemben (3). Preklinikai vizsgálatban az AKT inhibitor MK2206 és a PI3K inhibitor LY294002 egyaránt csökkentette a ZNF703 overexpresszálo sejtek proliferációját (4).

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### Az újgenerációs szekvenálás (NGS) eredménye

591 gén NGS szekvenálása 5103 genetikai variánst mutatott ki a mintában. A molekuláris profilba feltöltött 34 variáns bioinformatikai és funkcionális szűrések eredményeként került kiválasztásra. Ezek a variánsok szerepelnek a Realtime Oncology Calculatorban további funkcionális interpretáció és orvosi döntéstámogatás céljából.

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

- CONFIDENCE: Olvasási mélység, allél frakció, illetve genotípus minőség szerinti filterezést tesz lehetővé. A bioinformatikai szűrés során azokat a variánsokat zártuk ki, amelyeknek a jelenléte bizonytalan a szekvenálási minőségértékek alapján.
- COMMON VARIANTS: Segítségével kiszűrhetőek 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 összeállításánál 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).



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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.

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.

### BRCA1-K654fs\*47

Ez a mutáció a ClinVar és a BRCA Exchange adatbázisok és a tudományos irodalom (1) szerint patogén. Szerepel a COSMIC adatbázisban is. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) a BRCA1 gén nonsense-mediated decay (NMD) rezisztens pozícióját érinti, ezért nagy valószínűséggel az NMD folyamat nem vezet a mutáns mRNS lebomlásához (1). A mutáns génről egy csonka fehérjeváltozat képződik, ezért feltételezhető, hogy funkcióvesztéssel jár.

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### BRCA mutáns gén - célpontok

BRCA inaktiváció esetén a PARP inhibitorok említhetőek pozitív asszociációban (1, 2). Forgalomban lévő PARP gátló gyógyszerek az OLAPARIB, RUCAPARIB, NIRAPARIB és a TALAZOPARIB.

Egy meta-analízis szerint BRCA mutáns szolid daganatos betegek között az olaparib kezelés szignifikáns túlélési előnyt jelentett (3). Ováriumdaganatokban írták le, hogy BRCA mutáció esetén a PD-1/PD-L1 gátló immunterápiától is emelkedett hatékonyság várható (4, 5). Emlő- és pancreas daganatokban leírták már, hogy a BRCA mutáns tumorok jól reagálnak platina-alapú terápiára (6-8).

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## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

### BRCA mutáció emlődaganatban

Csíravonalas BRCA mutáció esetén HER2 negatív emlődaganatos betegek részére törzskönyvezett PARP gátló gyógyszer az OLAPARIB és a TALAZOPARIB. Mindkét gyógyszer neoadjuváns/adjuváns/metasztatikus vonalban alkalmazott kemoterápia után adható. Hormonreceptor pozitív betegeknél az előzetes hormonkezelés is szükséges.

Fázis III vizsgálatban HER2 negatív, deleterious vagy likely deleterious csíravonalas BRCA mutációt hordozó emlődaganatos betegeket kezeltek olaparibbal, vagy az orvos választása szerinti hatóanyaggal (treatment of physician's choice, PCT). Az objektív válaszadási arány (objective response rate, ORR) 59,9% volt az olaparib kezelésben részesülő csoportnál és 28,8% az egyéb kezelést kapó betegek körében. A medián progresszió mentes túlélés (progression-free survival, PFS) rendre 7,0 és 4,2 hónap volt az olaparibot és az egyéb kezelés kapó betegek csoportjában. Az olaparib kezelés hormonreceptor pozitív és negatív betegek körében is hatékonyabbnak bizonyult a standard kezelésnél (1).

Fázis III vizsgálatban a talazoparib monoterápia 8,6 hónapos PFS-t eredményezett BRCA mutáns előrehaladott emlőrákos betegek között, míg standard kemoterápia kezelés esetén a medián PFS 5,6 hónap volt. Az ORR 62,6% volt a talazoparib karon, 27,2% a kemoterápia karon (2).

Egy fázis III klinikai vizsgálatban HER2-negatív, csíravonalas BRCA1/2 mutációkat hordozó, előrehaladott emlődaganatos betegek talazoparib kezelést, vagy a kezelőorvos által választott kemoterápiát (PCT) kaptak. A talazoparib esetében statisztikailag szignifikáns becslést általános javulást tapasztaltak a kiindulási állapothoz képest a globális egészségi állapotban / életminőségben (GHS / QoL), szemben a PCT statisztikailag szignifikáns romlásával (3,0 és -5,4). A talazoparib hatására statisztikailag szignifikánsan nagyobb késést figyeltek meg a GHS / QoL végleges klinikailag jelentős romlásáig a PCT-hez viszonyítva (medián 24,3, illetve 6,3 hónap) (3).

Egy fázis II-es klinikai vizsgálatban BRCA1/2 mutációkat hordozó, előrehaladott emlődaganatos betegek talazoparib kezelést kaptak. Az ORR a BRCA1 (1-es csoport), illetve BRCA2 (2-es csoport) mutációkat hordozó betegeknél 23%-nak, valamint 33%-nak adódott. Tripla-negatív emlődaganatos és hormon-receptor pozitív betegek esetén az ORR 26% és 29% volt. A medián PFS és OS az 1-es csoportban 4 és 12,7 hónap, a 2-es csoportban 5,6 és 14,7 hónap volt (4).

Egy fázis I-es klinikai vizsgálatban 14 emlő-, és 12 ováriumdaganatos, csíravonalas BRCA1/2 mutációkat hordozó beteg talazoparib kezelést kapott. Az emlődaganatos betegeknél az ORR 50%-nak adódott. Egy betegnél teljes válaszadást, 6-nál részleges válaszadást, 5-nél pedig stabil betegséget figyeltek meg. A klinikai hasznosulási arány 86%-os volt, a medián PFS 34,6 hétnek adódott. Az ováriumdaganatos betegeknél az ORR 42%, a klinikai hasznosulási arány pedig 67%-os volt. Egy betegnél komplett választ, 6-nál részleges választ, 5-nél pedig stabil betegséget figyeltek meg. A medián PFS 36,4 hétnek bizonyult (5).

Egy fázis I-es klinikai vizsgálatban 19 emlődaganatos, csíravonalas BRCA1/2 mutációkat hordozó beteg neoadjuváns talazoparib kezelést kapott. 10 betegnél RCB-0-t (RCB-0 = CR), 2-nél RCB-I-et, 5-nél RCB-II-t és 3-nál RCB-III-mat figyeltek meg. Az RCB-0/CR arány 53%, az RCB-0/I/CR arány 63% volt (6).

Fázis II vizsgálatban molekulárisan nem szelektált tripla negatív emlődaganatos betegek között a niraparib (PARP gátló) és a pembrolizumab (PD-1 gátló) kombinációja 21%-os válaszadási arányt és 49%-os betegség kontroll arányt eredményezett. A BRCA mutáns alcsoportban a válaszadási arány 47%, a betegség kontroll arány 80%, a medián progressziómentes túlélés 8,3 hónap volt. A BRCA vad típusú alcsoportban a válaszadási arány 11%, a betegség kontroll arány 33%, a medián progressziómentes túlélés 2,1 hónap volt (7).

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#### Frameshift mutációk

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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 géneexpresszió 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 célpontjául 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 genomális 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 aminosavcserét 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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### KMT2C-C391\*

A variáns több, mint 100 alkalommal szerepel a COSMIC adatbázisban. Az NCBI ClinVar mutációs adatbázisban nem található bejegyzés az alteráció pathogenitására vonatkozóan. Az alteráció az egyik PHD-ujj régióban található. A korai STOP kodon megjelenését eredményező mutáció (nonsense mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló KMT2C variáns jön létre, amelyről hiányoznak a FYR és a SET domének is. Ezért a mutáció valószínűleg a szubsztrátfelismerés hibájához vezet, és ezáltal a KMT2C metiltranszferáz funkciójának elvesztését eredményezi (1, 2). A LOVD adatbázisban azonban benignus, vélhetően benignus besorolással szerepel.

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## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

**KMT2C mutáns gén - célpontok**

A tumorszupresszor funkciójú hiszton metiltransferáz KMT2C/MLL3 fehérje (1) funkcióvesztő mutációiról több daganattípusban leírták már, hogy hozzájárulhatnak a daganatképződéshez (2-4). MLL3 hiányos leukémia sejtek ellenállóak voltak hagyományos kemoterápiával szemben, de érzékenyek mutatkoztak a BET gátló JQ1 hatóanyagra (1).

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**ZNF703-P307S**

Ez a variáns alacsony frekvenciával szerepel a COSMIC adatbázisban (n<5). A tudományos irodalomban nem érhető el adat a funkcionális jelentőségéről.

**GNAS-P459R**

Ez a variáns alacsony frekvenciával szerepel a COSMIC adatbázisban (n<15). A SNPeffekt adatbázis szerint a mutáció GNAS hiperfunkció megbetegedést (GNASHYP) okoz.

**GNAS mutáns gén - célpontok**

A GNAS egy proto-onkogén (1), de bizonyos tumortípusokban tumorszupresszor szerepét is leírták (2). Egy kontroll nélküli GNAS mutáns xenograft modellen végzett kísérlet alapján a GNAS génben detektált funkcióvesztő driver mutációval kapcsolatban említhető indirekt target a PKA (PKACA) (1), melynek inhibitorai jelenleg klinikai fejlesztés alatt állnak.

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**CUL3-R162fs\*9**

A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló CUL3 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

**CUL3 mutáns gén - célpontok**

A CUL3 gén egy ubiquitin ligáz kódol. Funkcióvesztése TP53 mutáns sejtekben daganatképződéshez vezet. A TP53 és CUL3 együttes funkcióvesztése érzékenyít ATM gátló hatóanyagokra (1).

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**ZNF703-A514del**

A mutáció szerepel a COSMIC adatbázisban, azonban funkcionális jelentőségéről nem található adat a szakirodalomban.

**TENT5C-E299K**

Ez a variáns alacsony frekvenciával szerepel a COSMIC adatbázisban (n<15). A tudományos irodalomban nem érhető el adat a funkcionális jelentőségéről.

**GAS6-V673fs\*37**

## MOLEKULÁRIS BIOLÓGIAI INTERPRETÁCIÓ

Ez az alteráció szerepel a COSMIC adatbázisban.. A leolvasási kereteltolódást okozó mutáció (frameshift mutation) következtében egy jelentősen rövidebb fehérjeváltozatot kódoló GAS6 variáns jön létre, így a funkcióvesztés nagymértékben valószínűsíthető.

### KIT-M541L

A mutáció megtalálható a COSMIC adatbázisban. A szakirodalomban (1, 2), a ClinVar adatbázisban és az SNPEffect adatbázisban tumorigenikus hatás nélküli polimorfizmusként írják le, azonban összefüggésbe hozták gyermekkori mastocytosis (3). Sejtvonalas evidenciák alapján az imatinib KIT-inhibitorra a vad típushoz képest nagyjából kétszeres, növekedett érzékenységet mutat (3). Öt krónikus eozinofil leukémiás beteget bevonó tanulmányban alacsony dózisu (100 mg/nap) imatinib kezelés mellett teljes remissziót tapasztaltak mind az 5 beteg esetében (a medián követési idő 74 hónap volt). A tanulmányba bevont betegek közül négy páciens KIT-M541L variánst hordozott, de egy esetben sem detektáltak olyan genetikai elváltozást, amely érzékenységet mutatna imatinib kezelés esetén (BCR/ABL1, FIP1L1/PDGFR, illetve JAK2 mutáció) (4).

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### Molekuláris profiltól függetlenül törzskönyvezett hatóanyagok emlődagana indikációjában

Az angiogenezis gátló hatóanyag BEVACIZUMAB törzskönyvezett emlő tumor indikációjában.

Egy vizsgálat során 722 metasztatikus emlődagana betegben hasonlították össze a bevacizumab + paclitaxel kezelés és a paclitaxel monoterápia hatását (1). Egy másik vizsgálatban 1237 beteg esetében végeztek összehasonlítást a különböző kemoterápiás kezelésekkel (például capecitabine) kombinációban kapott bevacizumab illetve placebo hatása között (2). A vizsgálatok eredménye azt mutatta, hogy a bevacizumab adása növelte a progressziómentes túlélést (progression-free survival, PFS). A bevacizumab + paclitaxel kombináció esetében a PFS mediánja 11,4 hónap volt, szemben az önálló paclitaxel kezeléssel, ahol 5,8 hónapot mértek. A bevacizumabot capecitabine terápiával kombinálva a 8,6 hónapra nőtt a medián PFS a capecitabine + placebo kontroll csoportban megfigyelt 5,7 hónaphoz képest (2).

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# Oncompass Report

AZONOSÍTÓ  
NÉV Anonymous

A Realtime Oncology Molecular Treatment Calculator számításaival

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A Realtime Oncology Molecular Treatment Calculator számításaival

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A Realtime Oncology Molecular Treatment Calculator számításaival

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# Oncompass Report

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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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A Realtime Oncology Molecular Treatment Calculator számításaival

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A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ  
NÉV Anonymous

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AZONOSÍTÓ	
NÉV	Anonymous

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KMT2C-C391*	<p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Sanger Institute</p>
KIT-E930Q	<p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Vila L, Liu H, Al-Quran SZ, Coco DP, Dong HJ, Liu C. Identification of c-kit gene mutations in primary adenoid cystic carcinoma of the salivary gland. <i>Mod Pathol.</i> 2009 Oct;22(10):1296-302. doi: 10.1038/modpathol.2009.95. Epub 2009 Jul 17. PubMed PMID: 19617878; PubMed Central PMCID: PMC3746033.</p>
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GNAS-P459R	<p>Wellcome Trust 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>
KDM5C-S299R	<p><a href="https://www.ncbi.nlm.nih.gov/clinvar/variation/134493/">https://www.ncbi.nlm.nih.gov/clinvar/variation/134493/</a></p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>Wellcome Trust Sanger Institute</p> <p>Wellcome Sanger Institute</p> <p>NCBI ClinVar Database</p>

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TENT5C-E299K		Wellcome Trust Sanger Institute Wellcome Sanger Institute
GAS6-V673fs*37		Wellcome Trust Sanger Institute
ZNF703-A514del		Wellcome Sanger Institute
ZNF703-P307S		Wellcome Trust Sanger Institute Wellcome Trust Sanger Institute
AKAP9-Q1373E		Wellcome Trust Sanger Institute
MAGI2-E867K		Wellcome Sanger Institute
BRCA1-D430N		Wellcome Sanger Institute
OTOP1-V69M		Wellcome Trust Sanger Institute
KLHL6-Q317L		Wellcome Trust Sanger Institute
SEC16A-T1001I		Wellcome Trust Sanger Institute
PCBP1-N84S		Wellcome Trust Sanger Institute
KMT2C-R380L		Wellcome Trust Sanger Institute  Yang B, Luo L, Luo W, Zhou Y, Yang C, Xiong T, Li X, Meng X, Li L, Zhang X, Wang Z, Wang Z. The genomic dynamics during progression of lung adenocarcinomas. <i>J Hum Genet</i> . 2017 Aug;62(8):783-788. doi: 10.1038/jhg.2017.40. Epub 2017 Jan 06. PubMed PMID: 28381877; PubMed Central PMCID: PMC5537414.  Cho SJ, Yoon C, Lee JH, Chang KK, Lin JX, Kim YH, Kook MC, Aksoy BA, Park DJ, Ashktorab H, Smoot DT, Schultz N, Yoon SS. KMT2C Mutations in Diffuse-Type Gastric Adenocarcinoma Promote Epithelial-to-Mesenchymal Transition. <i>Clin Cancer Res</i> . 2018 Dec 15;24(24):6556-6569. doi: 10.1158/1078-0432.CCR-17-1679. Epub 2018 Aug 14. PubMed PMID: 30108106; PubMed Central PMCID: PMC6295255.
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GNAT2-A5V		NCBI ClinVar Database

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NÉV Anonymous

BIOMARKEREK DRIVEREK	ÉS	REFERENCIA
WNK2-H758N		NCBI ClinVar
EPHA5-A672T		Wellcome Sanger Institute
		<a href="http://snpeffect.switchlab.org/mutation/EPHA5_HUMAN/VAR_042144">http://snpeffect.switchlab.org/mutation/EPHA5_HUMAN/VAR_042144</a>
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		NCBI ClinVar

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## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
AMPH	May participate in mechanisms of regulated exocytosis in synapses and certain endocrine cell types. May control the properties of the membrane associated cytoskeleton.
AXL	Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding growth factor GAS6 and which is thus regulating many physiological processes including cell survival, cell proliferation, migration and differentiation. Ligand binding at the cell surface induces dimerization and autophosphorylation of AXL. Following activation by ligand, AXL binds and induces tyrosine phosphorylation of PI3-kinase subunits PIK3R1, PIK3R2 and PIK3R3; but also GRB2, PLCG1, LCK and PTPN11. Other downstream substrate candidates for AXL are CBL, NCK2, SOCS1 and TNS2. Recruitment of GRB2 and phosphatidylinositol 3 kinase regulatory subunits by AXL leads to the downstream activation of the AKT kinase. GAS6/AXL signaling plays a role in various processes such as endothelial cell survival during acidification by preventing apoptosis, optimal cytokine signaling during human natural killer cell development, hepatic regeneration, gonadotropin-releasing hormone neuron survival and migration, platelet activation, or regulation of thrombotic responses. Plays also an important role in inhibition of Toll-like receptors (TLRs)-mediated innate immune response. In case of filovirus infection, seems to function as a cell entry factor.

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
BRCA1	E3 ubiquitin-protein ligase that specifically mediates the formation of Lys-6-linked polyubiquitin chains and plays a central role in DNA repair by facilitating cellular responses to DNA damage. It is unclear whether it also mediates the formation of other types of polyubiquitin chains. The E3 ubiquitin-protein ligase activity is required for its tumor suppressor function. The BRCA1-BARD1 heterodimer coordinates a diverse range of cellular pathways such as DNA damage repair, ubiquitination and transcriptional regulation to maintain genomic stability. Regulates centrosomal microtubule nucleation. Required for normal cell cycle progression from G2 to mitosis. Required for appropriate cell cycle arrests after ionizing irradiation in both the S-phase and the G2 phase of the cell cycle. Involved in transcriptional regulation of P21 in response to DNA damage. Required for FANCD2 targeting to sites of DNA damage. May function as a transcriptional regulator. Inhibits lipid synthesis by binding to inactive phosphorylated ACACA and preventing its dephosphorylation. Contributes to homologous recombination repair (HRR) via its direct interaction with PALB2, fine-tunes recombinational repair partly through its modulatory role in the PALB2-dependent loading of BRCA2-RAD51 repair machinery at DNA breaks. Component of the BRCA1-RBBP8 complex which regulates CHEK1 activation and controls cell cycle G2/M checkpoints on DNA damage via BRCA1-mediated ubiquitination of RBBP8.
CCNE1	Essential for the control of the cell cycle at the G1/S (start) transition.
EPHA5	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 most probably constitutes the cognate/functional ligand for EPHA5. Functions as an axon guidance molecule during development and may be involved in the development of the retinotectal, entorhino-hippocampal and hippocamposeptal pathways. Together with EFNA5 plays also a role in synaptic plasticity in adult brain through regulation of synaptogenesis. In addition to its function in the nervous system, the interaction of EPHA5 with EFNA5 mediates communication between pancreatic islet cells to regulate glucose-stimulated insulin secretion (By similarity).
FGF14	Probably involved in nervous system development and function
GAS6	Ligand for tyrosine-protein kinase receptors AXL, TYRO3 and MER whose signaling is implicated in cell growth and survival, cell adhesion and cell migration. GAS6/AXL signaling plays a role in various processes such as endothelial cell survival during acidification by preventing apoptosis, optimal cytokine signaling during human natural killer cell development, hepatic regeneration, gonadotropin-releasing hormone neuron survival and migration, platelet activation, or regulation of thrombotic responses.2 Publications (Microbial infection) Can bridges virus envelope phosphatidylserine to the TAM receptor tyrosine kinase Axl to mediate viral entry by apoptotic mimicry (PubMed:21501828). Plays a role in Dengue cell entry by apoptotic mimicry (PubMed:23084921). Plays a role in Vaccinia virus cell entry by apoptotic mimicry (PubMed:21501828). Plays a role in ebolavirus and marburgvirus cell entry by apoptotic mimicry (PubMed:17005688).
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 adenylate 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 adenylate cyclase: it activates the cyclase in response to beta-adrenergic stimuli. Stimulates the Ras signaling pathway via RAPGEF2.
GNAT2	Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems. Transducin is an amplifier and one of the transducers of a visual impulse that performs the coupling between rhodopsin and cGMP-phosphodiesterase.
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).
KIT	Tyrosine-protein kinase that acts as cell-surface receptor for the cytokine KITLG/SCF and plays an essential role in the regulation of cell survival and proliferation, hematopoiesis, stem cell maintenance, gametogenesis, mast cell development, migration and function, and in melanogenesis. In response to KITLG/SCF binding, KIT can activate several signaling pathways. Phosphorylates PIK3R1, PLCG1, SH2B2/APS and CBL. Activates the AKT1 signaling pathway by phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase. Activated KIT also transmits signals via GRB2 and activation of RAS, RAF1 and the MAP kinases MAPK1/ERK2 and/or MAPK3/ERK1. Promotes activation of STAT family members STAT1, STAT3, STAT5A and STAT5B. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate. KIT signaling is modulated by protein phosphatases, and by rapid internalization and degradation of the receptor. Activated KIT promotes phosphorylation of the protein phosphatases PTPN6/SHP-1 and PTPRU, and of the transcription factors STAT1, STAT3, STAT5A and STAT5B. Promotes phosphorylation of PIK3R1, CBL, CRK (isoform Crk-II), LYN, MAPK1/ERK2 and/or MAPK3/ERK1, PLCG1, SRC and SHC1.
KLHL6	Involved in B-lymphocyte antigen receptor signaling and germinal center formation.
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.
NFE2L2	Transcription activator that binds to antioxidant response (ARE) elements in the promoter regions of target genes. Important for the coordinated up-regulation of genes in response to oxidative stress. May be involved in the transcriptional activation of genes of the beta-globin cluster by mediating enhancer activity of hypersensitive site 2 of the beta-globin locus control region.

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### DRIVER GÉNEK

Név	Leírás
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 HIF1A away from HIF1A. Required for the THBS4 function in regulating protective astrocytogenesis 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).
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).
PCBP1	Single-stranded nucleic acid binding protein that binds preferentially to oligo dC
PD-L1	Involved in the costimulatory signal, essential for T-cell proliferation and production of IL10 and IFNG, in an IL2-dependent and a PD-1-independent manner. Interaction with PD-1 inhibits T-cell proliferation and cytokine production.
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.
SEC16A	Defines endoplasmic reticulum exit sites (ERES) and is required for secretory cargo traffic from the endoplasmic reticulum to the Golgi apparatus. SARI1A-GTP-dependent assembly of SEC16A on the ER membrane forms an organized scaffold defining an ERES. Required for normal transitional endoplasmic reticulum (tER) organization.
SPEG	Isoform 3 may have a role in regulating the growth and differentiation of arterial smooth muscle cells.
TP53	Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. In cooperation with mitochondrial PPIF is involved in activating oxidative stress-induced necrosis; the function is largely independent of transcription. Induces the transcription of long intergenic non-coding RNA p21 (lincRNA-p21) and lincRNA-Mkn1. LincRNA-p21 participates in TP53-dependent transcriptional repression leading to apoptosis and seem to have an effect on cell-cycle regulation. Implicated in Notch signaling cross-over. Prevents CDK7 kinase activity when associated to CAK complex in response to DNA damage, thus stopping cell cycle progression. Isoform 2 enhances the transactivation activity of isoform 1 from some but not all TP53-inducible promoters. Isoform 4 suppresses transactivation activity and impairs growth suppression mediated by isoform 1. Isoform 7 inhibits isoform 1-mediated apoptosis. Regulates the circadian clock by repressing CLOCK-ARNTL/BMAL1-mediated transcriptional activation of PER2 (PubMed: 24051492).
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.
ZNF703	Transcriptional corepressor which does not bind directly to DNA and may regulate transcription through recruitment of histone deacetylases to gene promoters. Regulates cell adhesion, migration and proliferation. May be required for segmental gene expression during hindbrain development.



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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.
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.
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 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
CDK1	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, HMGA1, 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



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CDK2	<p>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> <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 dissociates 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 G1(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 G1(S) phase. Hypophosphorylates RB1 in early G1(S) 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>
CDK9	<p>Protein kinase involved in the regulation of transcription. Member of the cyclin-dependent kinase pair (CDK9/cyclin-T) complex, also called positive transcription elongation factor b (P-TEFb), which facilitates the transition from abortive to productive elongation by phosphorylating the CTD (C-terminal domain) of the large subunit of RNA polymerase II (RNAP II) POLR2A, SUPT5H and RDBP. This complex is inactive when in the 7SK snRNP complex form. Phosphorylates EP300, MYOD1, RPB1/POLR2A and AR, and the negative elongation factors DSIF and NELF. Regulates cytokine inducible transcription networks by facilitating promoter recognition of target transcription factors (e.g. TNF-inducible RELA/p65 activation and IL-6-inducible STAT3 signaling). Promotes RNA synthesis in genetic programs for cell growth, differentiation and viral pathogenesis. P-TEFb is also involved in cotranscriptional histone modification, mRNA processing and mRNA export. Modulates a complex network of chromatin modifications including histone H2B monoubiquitination (H2Bub1), H3 lysine 4 trimethylation (H3K4me3) and H3K36me3; integrates phosphorylation during transcription with chromatin modifications to control co-transcriptional histone mRNA processing. The CDK9/cyclin-K complex has also a kinase activity towards CTD of RNAP II and can substitute for CDK9/cyclin-T P-TEFb in vitro. Replication stress response protein; the CDK9/cyclin-K complex is required for genome integrity maintenance, by promoting cell cycle recovery from replication arrest and limiting single-stranded DNA amount in response to replication stress, thus reducing the breakdown of stalled replication forks and avoiding DNA damage. In addition, probable function in DNA repair of isoform 2 via interaction with KU70/XRCC6. Promotes cardiac myocyte enlargement. RPB1/POLR2A phosphorylation on Ser-2 in CTD activates transcription. AR phosphorylation modulates AR transcription factor promoter selectivity and cell growth. DSIF and NELF phosphorylation promotes transcription by inhibiting their negative effect. The phosphorylation of MYOD1 enhances its transcriptional activity and thus promotes muscle differentiation.</p>
CHEK1	<p>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 NEK1, which is required for polyubiquitination and degradation of CDC25A. Inhibition of CDC25</p>

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	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
CTLA4	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.
glutaminase	Catalyzes the first reaction in the primary pathway for the renal catabolism of glutamine. Plays a role in maintaining acid-base homeostasis. Regulates the levels of the neurotransmitter glutamate in the brain. Isoform 2 lacks catalytic activity.
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.
KIT	Tyrosine-protein kinase that acts as cell-surface receptor for the cytokine KITLG/SCF and plays an essential role in the regulation of cell survival and proliferation, hematopoiesis, stem cell maintenance, gametogenesis, mast cell development, migration and function, and in melanogenesis. In response to KITLG/SCF binding, KIT can activate several signaling pathways. Phosphorylates PIK3R1, PLCG1, SH2B2/APS and CBL. Activates the AKT1 signaling pathway by phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase. Activated KIT also transmits signals via GRB2 and activation of RAS, RAF1 and the MAP kinases MAPK1/ERK2 and/or MAPK3/ERK1. Promotes activation of STAT family members STAT1, STAT3, STAT5A and STAT5B. Activation of PLCG1 leads to the production of the cellular signaling molecules diacylglycerol and inositol 1,4,5-trisphosphate. KIT signaling is modulated by protein phosphatases, and by rapid internalization and degradation of the receptor. Activated KIT promotes phosphorylation of the protein phosphatases PTPN6/SHP-1 and PTPRU, and of the transcription factors STAT1, STAT3, STAT5A and STAT5B. Promotes phosphorylation of PIK3R1, CBL, CRK (isoform Crk-II), LYN, MAPK1/ERK2 and/or MAPK3/ERK1, PLCG1, SRC and SHC1.
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.
PARP2	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
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.
PLK1	Serine/threonine-protein kinase that performs several important functions throughout M phase of the cell cycle, including the regulation of centrosome maturation and spindle assembly, the removal of cohesins from chromosome arms, the inactivation of anaphase-promoting complex/cyclosome (APC/C) inhibitors, and the regulation of mitotic exit and cytokinesis. Polo-like kinase proteins acts by binding and phosphorylating proteins are that already phosphorylated on a specific motif recognized by the POLO box domains. Phosphorylates BORA, BUB1B/BUBR1, CCNB1, CDC25C, CEP55, ECT2, ERCC6L, FBXO5/EMI1, FOXM1, KIF20A/MKLP2, CENPU, NEDD1,

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### TARGET GÉNEK

Név	Leírás
	<p>NINL, NPM1, NUDC, PKMYT1/MYT1, KIZ, PPP1R12A/MYPT1, PRC1, RACGAP1/CYK4, SGOL1, STAG2/SA2, TEX14, TOPORS, p73/TP73, TPT1 and WEE1. Plays a key role in centrosome functions and the assembly of bipolar spindles by phosphorylating KIZ, NEDD1 and NINL. NEDD1 phosphorylation promotes subsequent targeting of the gamma-tubulin ring complex (γTuRC) to the centrosome, an important step for spindle formation. Phosphorylation of NINL component of the centrosome leads to NINL dissociation from other centrosomal proteins. Involved in mitosis exit and cytokinesis by phosphorylating CEP55, ECT2, KIF20A/MKLP2, CENPU, PRC1 and RACGAP1. Recruited at the central spindle by phosphorylating and docking PRC1 and KIF20A/MKLP2; creates its own docking sites on PRC1 and KIF20A/MKLP2 by mediating phosphorylation of sites subsequently recognized by the POLO box domains. Phosphorylates RACGAP1, thereby creating a docking site for the Rho GTP exchange factor ECT2 that is essential for the cleavage furrow formation. Promotes the central spindle recruitment of ECT2. Plays a central role in G2/M transition of mitotic cell cycle by phosphorylating CCNB1, CDC25C, FOXM1, CENPU, PKMYT1/MYT1, PPP1R12A/MYPT1 and WEE1. Part of a regulatory circuit that promotes the activation of CDK1 by phosphorylating the positive regulator CDC25C and inhibiting the negative regulators WEE1 and PKMYT1/MYT1. Also acts by mediating phosphorylation of cyclin-B1 (CCNB1) on centrosomes in prophase. Phosphorylates FOXM1, a key mitotic transcription regulator, leading to enhance FOXM1 transcriptional activity. Involved in kinetochore functions and sister chromatid cohesion by phosphorylating BUB1B/BUBR1, FBXO5/EM1 and STAG2/SA2. PLK1 is high on non-attached kinetochores suggesting a role of PLK1 in kinetochore attachment or in spindle assembly checkpoint (SAC) regulation. Required for kinetochore localization of BUB1B. Regulates the dissociation of cohesin from chromosomes by phosphorylating cohesin subunits such as STAG2/SA2. Phosphorylates SGOL1: required for spindle pole localization of isoform 3 of SGOL1 and plays a role in regulating its centriole cohesion function. Mediates phosphorylation of FBXO5/EM1, a negative regulator of the APC/C complex during prophase, leading to FBXO5/EM1 ubiquitination and degradation by the proteasome. Acts as a negative regulator of p53 family members: phosphorylates TOPORS, leading to inhibit the sumoylation of p53/TP53 and simultaneously enhance the ubiquitination and subsequent degradation of p53/TP53. Phosphorylates the transactivation domain of the transcription factor p73/TP73, leading to inhibit p73/TP73-mediated transcriptional activation and pro-apoptotic functions. Phosphorylates BORA, and thereby promotes the degradation of BORA. Contributes to the regulation of AURKA function. Also required for recovery after DNA damage checkpoint and entry into mitosis. Phosphorylates MISP, leading to stabilization of cortical and astral microtubule attachments required for proper spindle positioning (PubMed:8991084, PubMed:11202906, PubMed:12207013, PubMed:12447691, PubMed:12524548, PubMed:12738781, PubMed:12852856, PubMed:12939256, PubMed:14532005, PubMed:14734534, PubMed:15070733, PubMed:15148369, PubMed:15469984, PubMed:16198290, PubMed:16247472, PubMed:16980960, PubMed:17081991, PubMed:17351640, PubMed:17376779, PubMed:17617734, PubMed:18174154, PubMed:18331714, PubMed:18418051, PubMed:18477460, PubMed:18521620, PubMed:1).</p>
PRKACA	<p>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 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 Ca<sup>2+</sup>, leading to reduced amplitude and increased frequency of store overload-induced Ca<sup>2+</sup> release (SOICR) characterized by an increased rate of Ca<sup>2+</sup> release and propagation velocity of spontaneous Ca<sup>2+</sup> waves, despite reduced wave amplitude and resting cytosolic Ca<sup>2+</sup>. 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).</p>
PRKDC	<p>Serine/threonine-protein kinase that acts as a molecular sensor for DNA damage. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break (DSB) repair and V(D)J recombination. Must be bound to DNA to express its catalytic properties. Promotes processing of hairpin DNA structures in V(D)J recombination by activation of the hairpin endonuclease artemis (DCLRE1C). The assembly of the DNA-PK complex at DNA ends is also required for the NHEJ ligation step. Required to protect and align broken ends of DNA. May also act as a scaffold protein to aid the localization of DNA repair proteins to the site of damage. Found at the ends of chromosomes, suggesting a further role in the maintenance of telomeric stability and the prevention of chromosomal end fusion. Also involved in modulation of transcription. Recognizes the substrate consensus sequence [ST]-Q. Phosphorylates Ser-139 of histone variant H2AX/H2AFX, thereby regulating DNA damage response mechanism. Phosphorylates DCLRE1C, c-Abi/ABL1, histone H1, HSPCA, c-jun/JUN, p53/TP53, PARP1, POU2F1, DHX9, SRF, XRCC1, XRCC1, XRCC4, XRCC5, XRCC6, WRN, MYC and RFA2. Can phosphorylate C1D not only in the presence of linear DNA but also in the presence of supercoiled DNA. Ability to phosphorylate p53/TP53 in the presence of supercoiled DNA is dependent on C1D. Contributes to the determination of the circadian period length by antagonizing phosphorylation of CRY1 Ser-588 and increasing CRY1 protein stability, most likely through an indirect mechanism. Interacts with CRY1 and CRY2; negatively regulates CRY1 phosphorylation.</p>
RARG	<p>Receptor for retinoic acid. Retinoic acid receptors bind as heterodimers to their target response elements in response to their ligands, all-trans or 9-cis retinoic acid, and regulate gene expression in various biological processes. The RAR/RXR heterodimers bind to the retinoic acid response elements (RARE) composed of tandem 5'-AGGTCA-3' sites known as DR1-DR5. In the absence of ligand, acts mainly as an activator of gene expression due to weak binding to corepressors. Required for limb bud development. In concert with RARA or RARB, required for skeletal growth, matrix homeostasis and growth plate function (By similarity).</p>
WEE1	

## DRIVER ÉS TARGET GÉNEK LEÍRÁSA

### TARGET GÉNEK

Név	Leírás
	Acts as a negative regulator of entry into mitosis (G2 to M transition) by protecting the nucleus from cytoplasmically activated cyclin B1-complexed CDK1 before the onset of mitosis by mediating phosphorylation of CDK1 on Tyr-15. Specifically phosphorylates and inactivates cyclin B1-complexed CDK1 reaching a maximum during G2 phase and a minimum as cells enter M phase. Phosphorylation of cyclin B1-CDK1 occurs exclusively on Tyr-15 and phosphorylation of monomeric CDK1 does not occur. Its activity increases during S and G2 phases and decreases at M phase when it is hyperphosphorylated. A correlated decrease in protein level occurs at M/G1 phase, probably due to its degradation

## 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, IPIILUMUMAB, 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 VIZSGÁLTATBAN 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, AC0010MA, 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, AZD-7762, 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, GSK126458, 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, LESTAURTINIB, LGX818, LINIFANIB, LOP628, LORLATINIB, LUCITANIB, LXS196, LY2606368, LY287445, LY-2874455, LY2875358, LY294002, LY3023414, LY3039478, LY3076226, LY3164530, M344, MASITINIB, MATUZUMAB, MC1568, ME-344, ME-401, MEDI4276, MEHD79454, MEK162, MFG1877S, MGAH22, MGC0103, 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, MPTOE028, 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, P7170, PACRITINIB, PARECOXIB, PCI-34051, PD-0166285, PD0325901, PD184352, PD98059, PEFICITINIB, PEGDINETANIB, PELITINIB, PEPIDH1M, 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, POZITOTINIB, PQR309, PRT062070, PU-H71, PWT143, PWT33597, PX-478, PX-866, PYROTINIB, QUIZARTINIB, R547, RAF265, RDEA119, REBASTINIB, RG1530, RGB-286638, RIDAFOROLIMUS, RILOTUMUMAB, RINDOPEPIMUT, Ro3280, RO4929097, RO4987655, RO5045337, RO5083945, RO5126766, RO5212054, RO5503781, RO6839921, ROCILETINIB, RP6530, ROBOXISTAURIN, 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-0909, SU-014813, SU-11274, SU9516, SULFATINIB, Sym004, TAK-165, TAK-285, TAK-733, TANDUTINIB, TAREXTUMAB, TAS-120, TASELISIB, TELATINIB, TEPOTINIB, TESEVATINIB, TEW-7197, TG02, 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, XL888, XL-999, ZALUTUMUMAB, ZD4547, ZM336372, ZSTK474

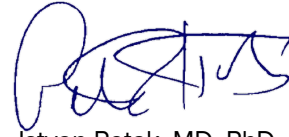
A gének funkcionális leírása a UniProt (Universal Protein Resource) adatbázisból származik.

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 felhasználásával információt szolgáltat a tumorok és a molekuláris profil közötti 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.

# Oncompass Report

A Realtime Oncology Molecular Treatment Calculator számításaival

AZONOSÍTÓ	
NÉV	Anonymous



Istvan Petak, MD, PhD

Molekuláris farmakológus, Igazgató