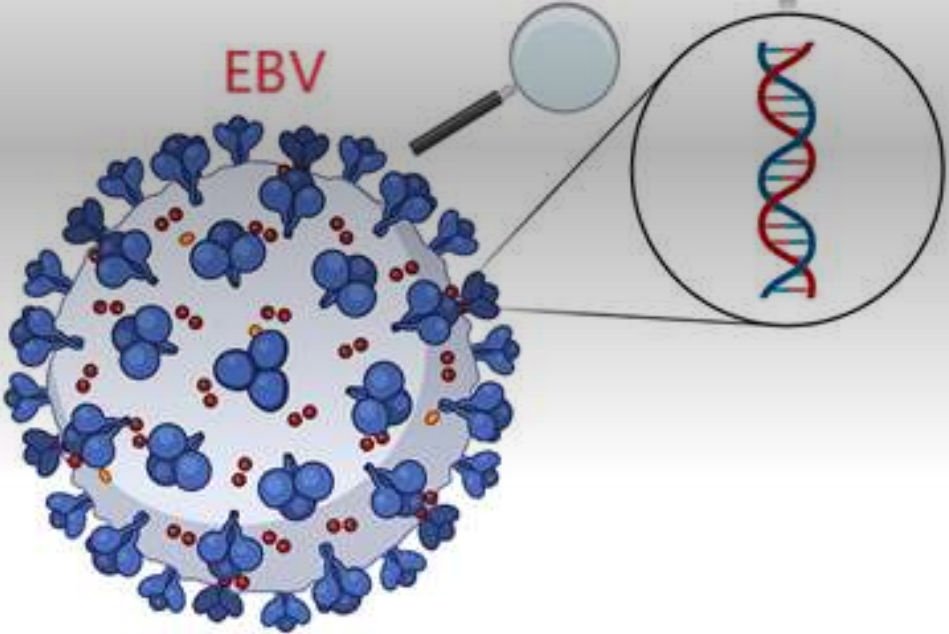


## Epstein–Barr Virusü ile Burkitt Lenfomanın Genetik İlişkininin Bioinformatik ve Gelişmiş Yapay Zeka Teknikleri ile Analizi

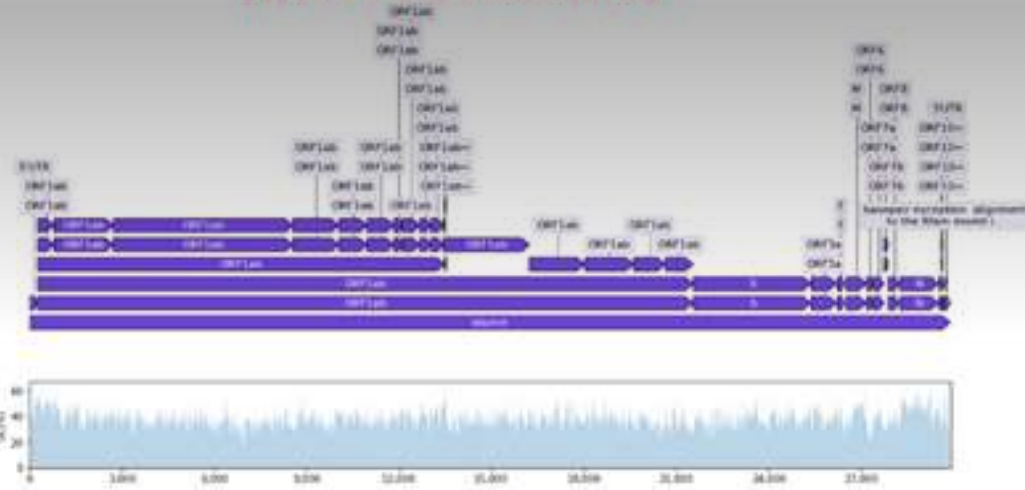
Rıza Aytaç Çetinkaya, Pınar Karadayı Ataş, Duygu Kırkık, Burak Sarıkaya

# GENETIC CODE

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# EBV: VIRAL PROTEINS



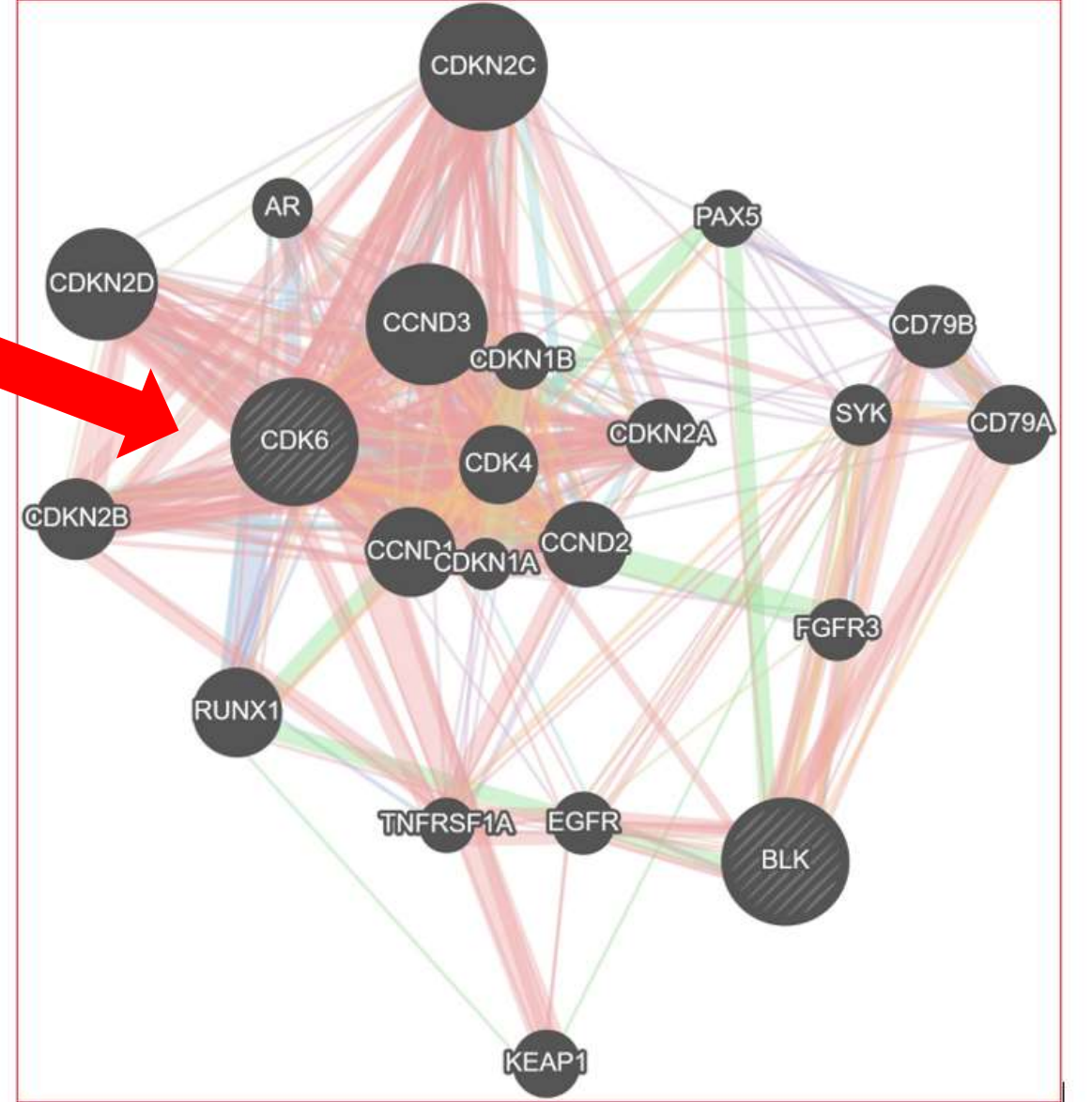




Resim 1. GeneMania veri tabanından elde edilen CDK6 geni ile diğer genler arasındaki ilişki

## Materyal

- EBV ve **Burkitt Lenfoma** arasında, apoptozla ilişkili genler bağlamında **cyclin dependent kinase 6 (CDK6)**



Co-expression lila rengi, ortak lokalizasyon mavi renkte, fiziksel etkileşim pembe ve paylaşılan protein alanları kahverengi renklerde gösterilmiştir.

# GENEMANIA

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GeneMANIA helps you predict the function of your favourite genes and gene sets.

Indexing 2,530 association networks containing 650,654,697 interactions mapped to 109,691 genes from 9 organisms.

# Materyal

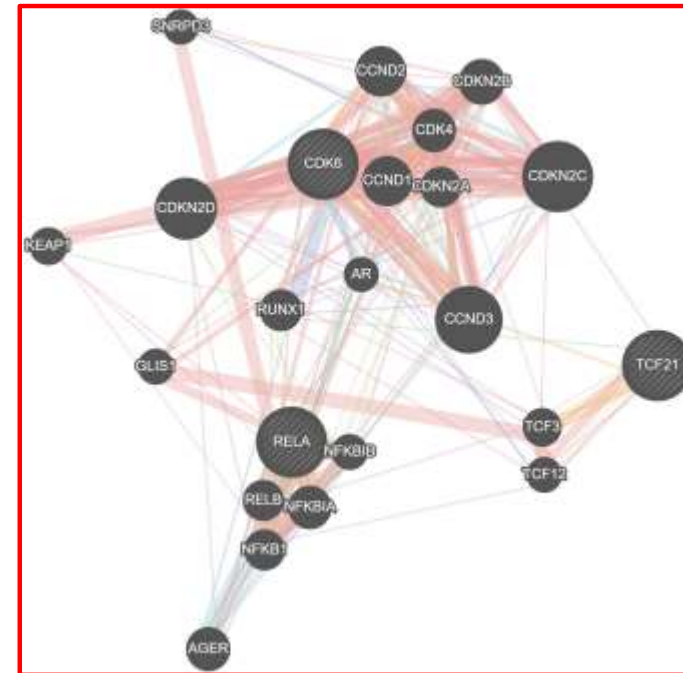
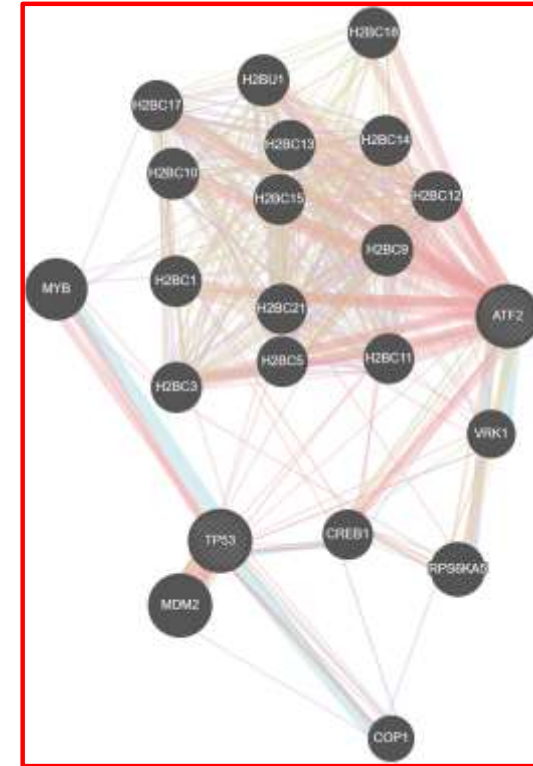
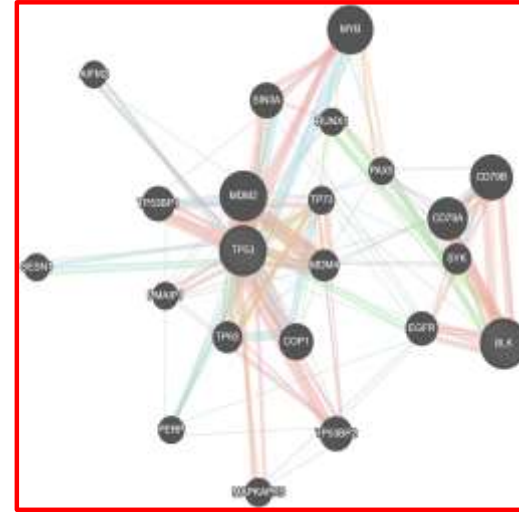
BH3 interacting domain death agonist (BID)

B-cell CLL/lymphoma 2 (BCL2),

Fas cell surface death receptor (FAS),

Myeloid cell leukemia sequence 1 (MCL1)

Tumor protein p53 (TP53)



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GeneMANIA helps you predict the function of your favourite genes and gene sets.

Including 2,830 association networks containing 960,664,667 interactions mapped to 100,661 genes from 8 organisms.

# Sonuçlar

	<b>Silhouette Score</b>	<b>Harabasz Index</b>	<b>Davies–Bouldin Index</b>
K- means	0.577	129.926	0.674
Generative Clustering	0.533	112.468	0.715
DBSCAN	0.425	41.429	0.962
Hierarchical Clustering	0.146	38.081	0.942

- ✓ K-means kümeleme algoritmasının Silhouette Skoru açısından diğer tekniklerden daha iyi performans gösterdiği
- ✓ Kümelerin makul derecede iyi ayrıldığını gösteren 0,577 puan elde ettiği
- ✓ Harabasz Endeksi ve Davies-Bouldin Endeksi dikkate alındığında, K-ortalamlar diğer yaklaşımlara göre daha yüksek değerlerde de olsa iyi performans göstermiştir.



Click here to contribute data to Geno<sub>2</sub>MP

HPO Browser  
Need to find the HPO term for a clinical finding?

Search for a gene, chromosomal position, region or HPO term

Search

- Gene (MYH3); chrom. position of variant (17:10534960); chrom. region of variants (17:10534960-10535460); dbSNP rsID (rs34393601)
- HPO term (oral cleft); HPO number (0000202)

Gene | CDK6,RNU6-10P

<https://geno2mp.gs.washington.edu/Geno2MP/#/>

**Description** cyclin-dependent kinase 6;RNA, U6 small nuclear 10, pseudogene  
**Number of variants** 2276  
**UCSC Browser** 7:92234235-92465941  
**GeneCards** CDK6 RNU6-10P  
**MalaCards** CDK6 RNU6-10P  
**OMIM** CDK6  
**ClinVar** CDK6

### Gene summary

Filter by annotation category All

Export table to TSV

Chr:Pos	Alleles	rsID	HPO Profiles	# het	# hom	Gene	mRNA	Annotations	cDNA Change	Protein Change	ESP AC	gnomAD AC	1K Genome AC	CADD Phred-scaled
7:92234241	T>C	NA	1	1	0	CDK6	NM_00114530...	3-prime-UTR	c.*10213A>G	NA	0	0	0	8.354
7:92234479	T>C	NA	1	1	0	CDK6	NM_00114530...	3-prime-UTR	c.*9975A>G	NA	0	0	0	12.74
7:92234626	G>C	rs149310804	5	7	0	CDK6	NM_00114530...	3-prime-UTR	c.*9828C>G	NA	0	0.00331454	0.000458	6.338
7:92234825	G>A	rs7810546	1	1	0	CDK6	NM_00114530...	3-prime-UTR	c.*9629C>T	NA	0	0.00487677	0.001374	4.352
7:92234939	A>C	NA	1	1	0	CDK6	NM_00114530...	3-prime-UTR	c.*9515T>G	NA	0	0.0000619444	0	5.766



**Tablo 1.** CDK6'da öngörülen kromozomların varyasyonları, tek nükleotid polimorfizmleri, cDNA ve protein değişiklikleri ile CADD puanları

<u>Chr:pos</u>	<u>Alleles</u>	<u>HPO profiles</u>	<u>het</u>	<u>hom</u>	<u>mRNA</u>	<u>Annotations</u>	<u>cDNA change</u>	<u>Protein Change</u>	<u>ESP AC</u>	<u>gnomAD AC</u>	<u>CADD Phred-scaled</u>
7:92462622	G>A	1	1	0	NM_001145306.1	synonymous	c.16C>T	p.(L6=)	0	0.00000473082	10.29
7:92462602	C>T	1	1	0	NM_001145306.1	synonymous	c.36G>A	p.(Q12=)	0	0	10.27
7:92462599	G>A	5	8	0	NM_001145306.1	synonymous	c.39C>T	p.(Y13=)	0	0.000704093	3.834
7:92462545	G>A	1	1	0	NM_001145306.1	synonymous	c.93C>T	p.(R31=)	0	0	1.665
7:92462500	C>A	4	4	0	NM_001145306.1	synonymous	c.138G>T	p.(R46=)	0	0.0000292503	10.46
7:92462470	G>A	4	7	0	NM_001145306.1	synonymous	c.168C>T	p.(L56=)	0	0.00000836918	0.056
7:92404076	G>A	1	1	0	NM_001145306.1	synonymous	c.303C>T	p.(V101=)	0	0.0000319875	10.34
7:92404019	T>C	1	1	0	NM_001145306.1	synonymous	c.360A>G	p.(E120=)	0	0	9.766
7:92355018	C>A	2	2	0	NM_001145306.1	synonymous	c.459G>T	p.(V153=)	0	0	13.28
7:92354985	G>A	1	1	0	NM_001145306.1	synonymous	c.492C>T	p.(F164=)	0	0.0000159162	13.32
7:92300823	G>C	1	1	0	NM_001145306.1	synonymous	c.564C>G	p.(P188=)	0	0.0000776458	9.306
7:92300781	G>A	1	1	0	NM_001145306.1	synonymous	c.606C>T	p.(L202=)	0	0	7.991
7:92252397	A>G	5	5	0	NM_001145306.1	synonymous	c.651T>C	p.(P217=)	0	0.000224898	5.664
7:92247521	G>A	1	1	0	NM_001145306.1	synonymous-near-splice	c.699C>T	p.(D233=)	0	0.000011955	3.657
7:92247515	A>G	1	2	0	NM_001145306.1	synonymous	c.705T>C	p.(I235=)	0	0	7.542
7:92247413	G>A	2	2	0	NM_001145306.1	synonymous	c.807C>T	p.(I269=)	0	0.00000796115	14.71
7:92244552	G>A	1	1	0	NM_001145306.1	synonymous	c.883C>T	p.(L295=)	0	0	9.21

Combined Annotation Dependent Depletion



## KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

KEGG2 PATHWAY BRITE MODULE KO GENES COMPOUND NETWORK DISEASE DRUG

Select prefix: map Organism: ebv Enter keywords: ebv [Go] [Help]

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### Pathway Maps

KEGG PATHWAY is a collection of manually drawn [pathway maps](#) representing our knowledge of the molecular interaction, reaction and relation networks for:

#### 1. Metabolism

Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid Other amino Glycan  
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Chemical structure

#### 2. Genetic Information Processing

#### 3. Environmental Information Processing

#### 4. Cellular Processes

#### 5. Organismal Systems

#### 6. Human Diseases

#### 7. Drug Development

The pathway map viewer linked from this page contains features of [KEGG mapping](#), especially for coloring map objects as described [here](#).

### Pathway Identifiers

Each pathway map is identified by the combination of 2-4 letter prefix code and 5 digit number (see [KEGG Identifier](#)). The prefix has the following meaning:

map	manually drawn reference pathway
ko	reference pathway highlighting KOs
ec	reference metabolic pathway highlighting EC numbers
rn	reference metabolic pathway highlighting reactions
<org>	organism-specific pathway generated by converting KOs to gene identifiers

and the numbers starting with the following:

011	global map (lines linked to KOs)
012	overview map (lines linked to KOs)
010	chemical structure map (no KO expansion)



## BH3 interacting domain death agonist (BID)

**Tablo 2.** BID'da öngörülen kromozomların varyasyonları, tek nükleotid polimorfizmleri, cDNA ve protein değişiklikleri ile CADD puanları

Chr:pos	Alleles	HPO profiles	het	hom	mRNA	Annotations	cDNA change	Protein Change	ESP AC	gnomAD AC	CADD Phred-scaled
22:18220891	G>A	2	2	0	NM_001196.3	synonymous	c.468C>T	p.(A156=)	0	0.00000795342	10.75
22:18220923	TCTC>T	1	1	0	NM_001196.3	coding	c.433_435del	p.(E145del1)	0	0.0000198881	-1
22:18220939	T>C	1	1	0	NM_001196.3	synonymous	c.420A>G	p.(R140=)	0	0	0.027
22:18220942	A>G	1	1	0	NM_001196.3	synonymous	c.417T>C	p.(P139=)	0	0	5.764
22:18222147	G>A	1	1	0	NM_001196.3	synonymous	c.331C>T	p.(L111=)	0	0.00000411702	6.457
22:18222165	G>GGC CCGGA GGGAT GCTACG GTCCAT GCT	2	2	0	NM_001196.3	coding	c.312_313in sAGCATGG ACCGTAGC ATCCCTCC GGGC	p.(G104_L105in sSMDRSIPPG)	0	0.00000807513	-1

## B-cell CLL/lymphoma 2 (BCL2),

**Tablo 3.** BCL2'de öngörülen kromozomların varyasyonları, tek nükleotid polimorfizmleri, cDNA ve protein değişiklikleri ile CADD puanları

Chr:pos	Alleles	HPO profiles	het	hom	mRNA	Annotations	cDNA change	Protein Change	ESP AC	gnomAD AC	CADD Phred-scaled
18:60795906	G>A	2	4	0	NM_000633.2	synonymous	c.672C>T	p.(A224=)	0	0.00000397902	10.04
18:60795933	C>A	1	1	0	NM_000633.2	synonymous	c.645G>T	p.(L215=)	0	0.00000398073	15.56
18:60985414	G>A	1	1	0	NM_000633.2	synonymous	c.486C>T	p.(V162=)	0	0	9.581
18:60985522	C>T	2	2	0	NM_000633.2	synonymous	c.378G>A	p.(A126=)	0	0	0.231
18:60985570	G>T	1	1	0	NM_000633.2	synonymous	c.330C>A	p.(R110=)	0	0	1.277
18:60985621	G>C	1	1	0	NM_000633.2	synonymous	c.279C>G	p.(V93=)	0	0.0000469748	10.36
18:60985636	C>T	1	1	0	NM_000633.2	synonymous	c.264G>A	p.(P88=)	0	0	10.85
18:60985648	A>C	3	3	0	NM_000633.2	synonymous	c.252T>G	p.(P84=)	0	0.0000073359	0.035
18:60985678	G>C	2	2	0	NM_000633.2	synonymous	c.222C>G	p.(T74=)	0	0.0000309866	0.192
18:60985693	G>A	2	2	0	NM_000633.2	synonymous	c.207C>T	p.(T69=)	0	0	5.551
18:60985746	GGGA>G	1	1	0	NM_000633.2	coding	c.151_153del3	p.(S51del1)	0	0	-1
18:60985756	G>A	1	1	0	NM_000633.2	synonymous	c.144C>T	p.(I48=)	0	0.0000146764	7.039
18:60985816	G>A	2	2	0	NM_000633.2	synonymous	c.84C>T	p.(Y28=)	0	0.00000832563	5.079
18:60985828	C>A	2	2	0	NM_000633.2	synonymous	c.72G>T	p.(S24=)	0	0.0000247439	9.462



# Fas cell surface death receptor (FAS)

**Tablo 4.** FAS'da öngörülen kromozomların varyasyonları, tek nükleotid polimorfizmleri, cDNA ve protein değişiklikleri ile CADD puanları

Chr:pos	Alleles	HPO profiles	het	hom	mRNA	Annotations	cDNA change	Protein Change	ESP AC	gnomAD AC	CADD Phred-scaled
10:90773883	C>T	1	1	0	NM_000043.4	synonymous	c.684C>T	p.(D228=)	0	0	12.14
10:90767506	C>T	2	2	0	NM_000043.4	synonymous	c.246C>T	p.(C82=)	0	0.0000119366	11.08
10:90767530	G>A	1	1	0	NM_000043.4	synonymous	c.270G>A	p.(E90=)	0	0.00000795551	9.766
10:90768647	C>G	1	1	0	NM_000043.4	synonymous-near-splice	c.336C>G	p.(G112=)	0	0	6.634
10:90774120	A>C	1	1	0	NM_000043.4	synonymous	c.921A>C	p.(A307=)	0	0	4.599
10:90767467	A>G	1	1	0	NM_000043.4	synonymous	c.207A>G	p.(K69=)	0	0	3.177
10:90774102	C>G	1	1	0	NM_000043.4	synonymous	c.903C>G	p.(A301=)	0	0	2.523
10:90762833	A>G	1	1	0	NM_000043.4	synonymous	c.78A>G	p.(Q26=)	0	0.0000119299	2.448
10:90774078	A>G	2	2	0	NM_000043.4	synonymous	c.879A>G	p.(T293=)	0	0.0000159213	2.222
10:90774192	C>T	3	3	0	NM_000043.4	synonymous	c.993C>T	p.(I331=)	0	0.0000309799	1.269
10:90771817	T>C	2	2	0	NM_000043.4	synonymous	c.630T>C	p.(H210=)	0	0.0000278596	1.088
10:90774024	T>C	1	1	0	NM_000043.4	synonymous	c.825T>C	p.(V275=)	0	0	0.218



# Myeloid cell leukemia sequence 1 (MCL1)

**Tablo 5.** MCL1'de öngörülen kromozomların varyasyonları, tek nükleotid polimorfizmleri, cDNA ve protein değişiklikleri ile CADD puanları

Chr:pos	Alleles	HPO profiles	het	hom	mRNA	Annotations	cDNA change	Protein Change	ESP AC	gnomAD AC	CADD Phred-scaled
1:150549863	A>G	1	1	0	NM_001197320.1	synonymous	c.582T>C	p.(Y194=)	0	0.0000119538	16.85
1:150551323	G>A	1	1	0	NM_001197320.1	synonymous	c.225C>T	p.(F75=)	0	0	11.27
1:150549950	G>A	1	1	0	NM_001197320.1	synonymous	c.495C>T	p.(F165=)	0	0.0000161374	9.483
1:150551341	G>A	1	3	0	NM_001197320.1	synonymous	c.207C>T	p.(R69=)	0	0.0000399393	7.1
1:150551347	C>A	1	1	0	NM_001197320.1	synonymous	c.201G>T	p.(V67=)	0	0	6.841
1:150551956	C>T	2	2	0	NM_001197320.1	synonymous	c.51G>A	p.(G17=)	0	0.00000459293	2.52
1:150551941	C>T	1	1	0	NM_001197320.1	synonymous	c.66G>A	p.(G22=)	0	0.00000468358	1.606
1:150551934	TGCC GGCC CCCAA >T	3	3	0	NM_001197320.1	coding	c.61_72del12	p.(L21_G24del4)	0	0.0000520952	-1
1:150551968	GTTGA GTCC GATTA CCGC GTTTC TT>G	2	2	0	NM_001197320.1	coding	c.15_38del24	p.(K5_N13delinsN)	0	0	-1

# THE HUMAN PROTEIN ATLAS

SECTIONS ABOUT NEWS LEARN DATA HELP

CDK6 Search Fields »

Search result (8 genes): CDK6 | CCND1 | CCND2 ...

## CDK6

SUMMARY TISSUE RNA BRAIN RNA SINGLE CELL RNA TISSUE CELL PATHOLOGY N/A DISEASE RNA IMMUNE MS BLOOD SUBCELL RNA CELL LINE STRUCTURE INTERACTION

### TISSUE

PRIMARY DATA  
TISSUES

ANTIBODIES AND VALIDATION

Dictionary

Tissue proteome

### GENERAL INFORMATION<sup>1</sup>

Gene name <sup>1</sup>	CDK6
Gene description <sup>1</sup>	Cyclin dependent kinase 6
Protein class <sup>1</sup>	Cancer-related genes Disease related genes Enzymes FDA approved drug targets Human disease related genes Plasma proteins
Predicted location <sup>1</sup>	Intracellular
Number of transcripts <sup>1</sup>	2

### HUMAN PROTEIN ATLAS INFORMATION<sup>1</sup>

Tissue expression cluster (RNA) <sup>1</sup>	Lymphoid tissue & Bone marrow - Cell proliferation (mainly)
Tissue specificity (RNA) <sup>1</sup>	Tissue enhanced (lymphoid tissue)
Tau specificity score (RNA) <sup>1</sup>	0.56
Tissue distribution (RNA) <sup>1</sup>	Detected in many
Protein evidence <sup>1</sup>	Evidence at protein level
Protein expression <sup>1</sup>	Cytoplasmic expression in several tissues, which in cases was combined with nuclear expression. Highest expression in bone marrow cells.

### IMMUNOHISTOCHEMISTRY DATA RELIABILITY

Data reliability description <sup>1</sup>	Medium consistency between antibody staining and RNA expression data.
Reliability score <sup>1</sup>	Enhanced
Antibodies <sup>1</sup>	HPA002637 , CAB004363

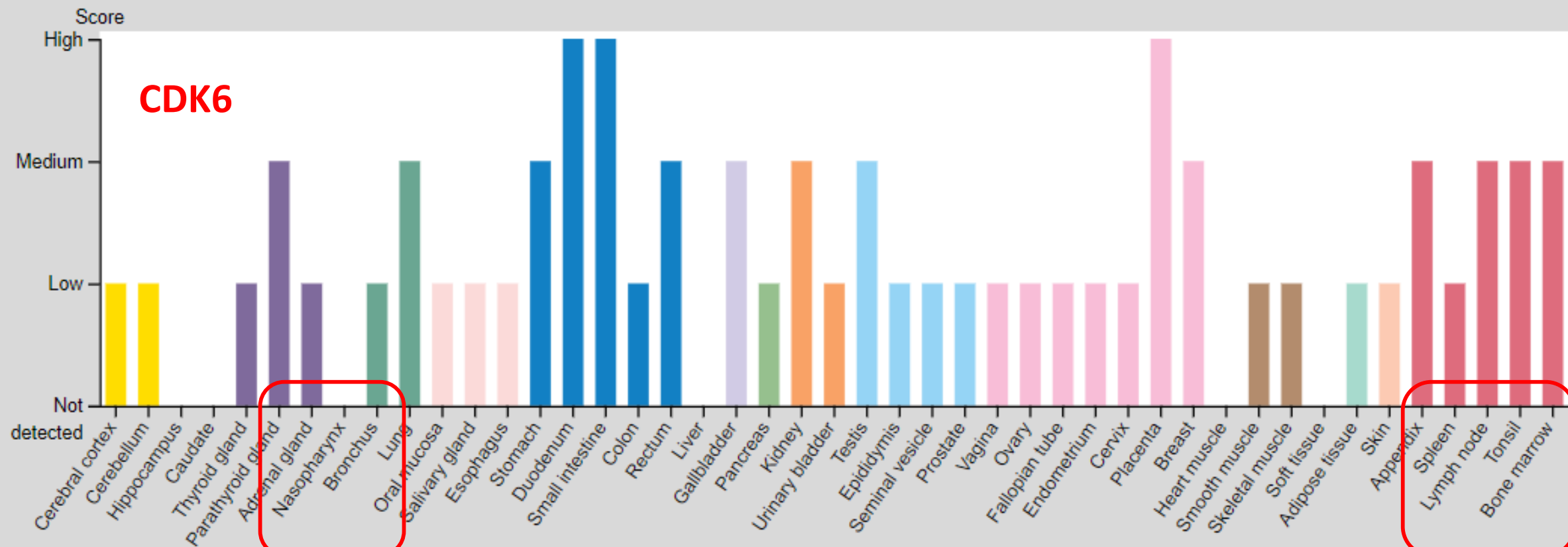
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### ASSAYS<sup>1</sup>

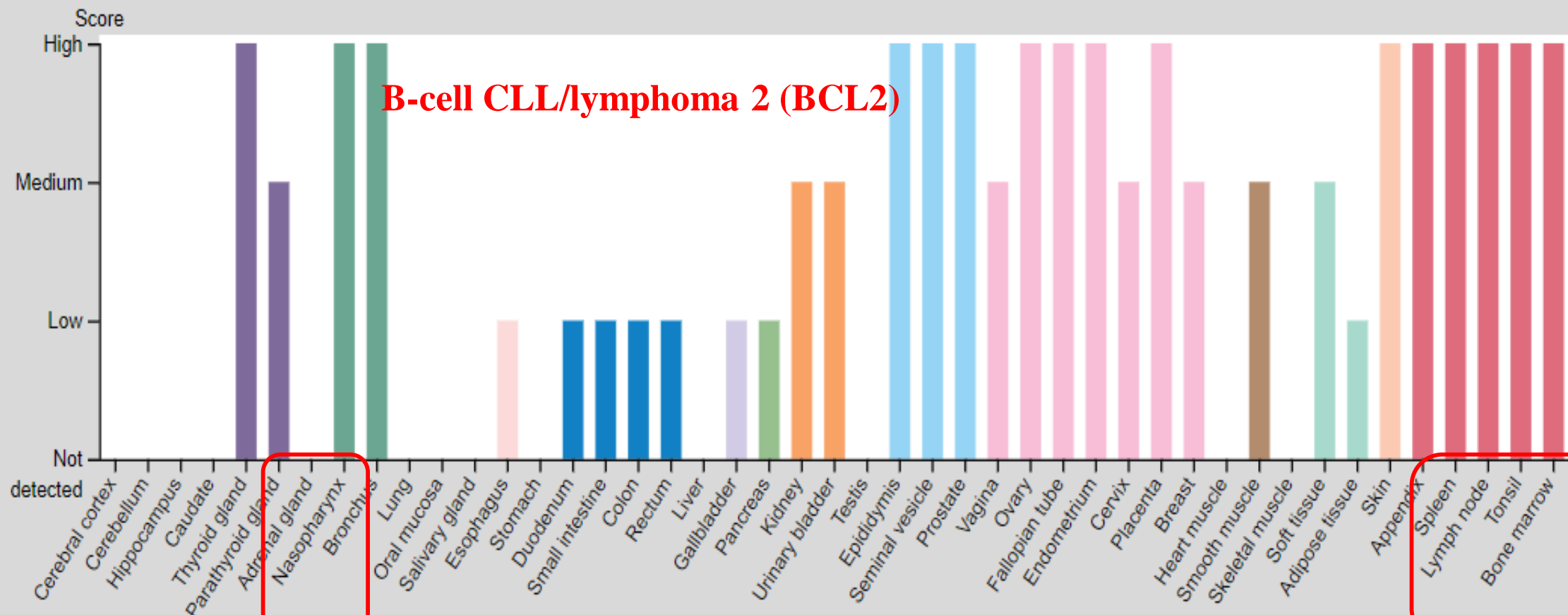


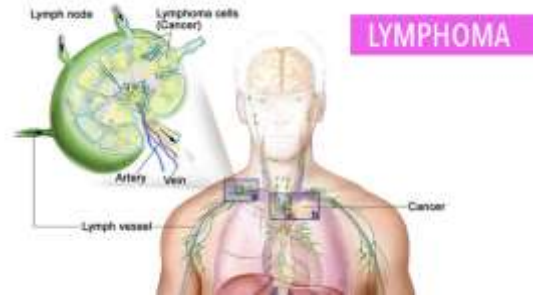
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**B-cell CLL/lymphoma 2 (BCL2)**





## Epstein–Barr Virusü ile Burkitt Lenfomanın Genetik İlişkinin Bioinformatik ve Gelişmiş Yapay Zeka Teknikleri ile Analizi

Rıza Aytaç Çetinkaya, Pınar Karadayı Ataş, Duygu Kırkık, Burak Sarıkaya