Epigenetics-related ELISA kits

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Epigenetics research focuses on the regulation of gene activity and expression. It refers to heritable changes in gene expression that occur without alterations in the gene sequence. These changes are dynamic and reversible. Epigenetic research encompasses various molecular mechanisms, including DNA methylation, histone modification, chromatin remodeling, non-coding RNAs, and more. These molecular mechanisms can transmit genetic information within cells, activating or inhibiting gene expression, thereby influencing an organism's growth, development, health, and disease progression.

CUSABIO is dedicated to providing researchers with high-precision, high-sensitivity ready-to-use epigenetics ELISA kits that cater to a variety of sample types. These kits assist in the in-depth analysis of key regulatory mechanisms such as DNA methylation, histone modifications, chromatin remodeling, and non-coding RNA, offering accurate and reliable data support for your scientific research. We aim to empower you to achieve breakthroughs in the field of epigenetics.

DNA methylation

DNA methylation is a chemical modification process where methyl groups are added to the genomic DNA molecules under the action of DNA methyltransferases, and it is the most important form of epigenetic modification. In eukaryotes, there are primarily two types of DNA methyltransferases, namely DNMT1 (DNA methyltransferase 1) and DNMT3a and DNMT3b. DNA methylation can affect chromatin structure, the accessibility of gene promoters, and the interaction between transcription factors and DNA. It plays a crucial role in biological processes such as cell differentiation, gene silencing, maintenance of genome stability, and responses to the environment.

Aberrant DNA methylation is closely associated with the development of cancer. On one hand, a decrease in the overall level of genome methylation can lead to the activation of proto-oncogenes, abnormal transposon expression, and genome instability, promoting tumorigenesis. On the other hand, abnormal high methylation in CpG islands (cytosine-phosphate-guanine) within gene promoter regions can result in gene silencing, leading to decreased expression of tumor suppressor genes and also contributing to the formation and progression of tumors. High methylation in certain cancers, such as colorectal cancer, can serve as a biomarker for early diagnosis.

Histone modification

DNA exists in the form of chromatin in the cell nucleus, and apart from DNA, chromatin also contains histones, non-histone proteins, and a small amount of RNA. Histones are the fundamental structural proteins of chromatin, found in the chromatin of eukaryotic and prokaryotic cells. Histone modification refers to post-translational modifications of histones, such as methylation, acetylation, ubiquitination, and phosphorylation, which occur under the action of specific enzymes. These modifications are reversible covalent changes, and their occurrence, removal, and functional effects are mainly regulated by histone-modifying enzymes and corresponding cofactors, including three major categories: Writers, Erasers, and Readers.

Histone modifications not only regulate gene expression but also influence the development of various diseases, including some immune-related diseases and cancers. Lower levels of histone methylation or acetylation are associated with poor prognosis in prostate cancer, lung cancer, and kidney cancer. Conversely, higher levels of specific histone modifications (such as H3K9ac) are correlated with lower survival rates in lung cancer[1].

Table 1. Main histone modifying enzymes of Writer and Eraser

Modification type	Writer	Eraser
Methylate	Histone lysine methyltransferases (HKMTs) and protein arginine methyltransferases (PRMTs)	lysine-specific demethylase 1 (KDM1/LSD1) and demethylase containing Jumonji C domain (JMJ)
Acetylization	Histone acetyltransferase (HATs)	Histone deacetylase (HDACs)
Phosphorylation	Kinases	Phosphatases

Chromatin remodeling

Chromatin remodeling refers to the phenomenon where the packaging state of chromatin, the histones within nucleosomes, and the corresponding DNA molecules undergo a series of changes, resulting in alterations in the position and structure of chromatin. The mechanisms involved typically include histone modifications and ATP-dependent chromatin remodeling. ATP-dependent chromatin remodeling refers to the use of ATP hydrolysis energy to move, loosen, evict, or rebuild nucleosomes, thereby regulating the packaging state of chromatin.

Chromatin remodeling can regulate gene transcription and is involved in normal cellular growth and development. However, abnormal chromatin remodeling can lead to the development of diseases such as cancer. For example, mutations in genes encoding chromatin remodeling complexes such as ARID1A, SMARCA4, SMARCB1, ACTL6A, CHRAC1, and RSF1 have been shown to be associated with various types of ovarian cancer[2].

Non-coding RNA

Non-coding RNA (ncRNA) refers to RNA molecules that do not encode proteins. Functional non-coding RNAs mainly include miRNA, siRNA, lncRNA, and circRNA, among others.

1. MiRNA is a class of small ncRNAs, approximately 18 to 22 nucleotides in length, involved in post-transcriptional gene expression regulation. Their mechanism of action involves complementarity with mRNA, leading to mRNA silencing or degradation. Any changes in the structure and function of miRNA can potentially lead to the development of diseases, and some miRNAs that exhibit oncogenic functions are referred to as onco-miRs.

2. SiRNA, with a length of 20-25 nucleotides, exhibits strong specificity and can effectively inhibit the expression of target genes. It has a significant inhibitory effect on various cancers such as lung cancer and glioblastoma.

3. LncRNA is a class of ncRNAs with a length greater than 200 nucleotides, comprising 70%-98% of the total cellular RNA. They play roles in coordinating DNA methylation, chromatin structure remodeling, and histone chemical modifications, among others. The mechanism of action of lncRNAs still has many ambiguities, but research has found that some lncRNAs are highly sensitive in tumors, providing new insights into cancer treatment.

4. CircRNA is a type of circular RNA with a stable closed-loop structure. Due to its unique circular and stable structure, it not only plays important biological roles in the development processes of organisms, such as serving as miRNA sponges and functioning as endogenous RNAs, but also participates in the development of various diseases. CircRNA has become a new hotspot in the field of RNA research.

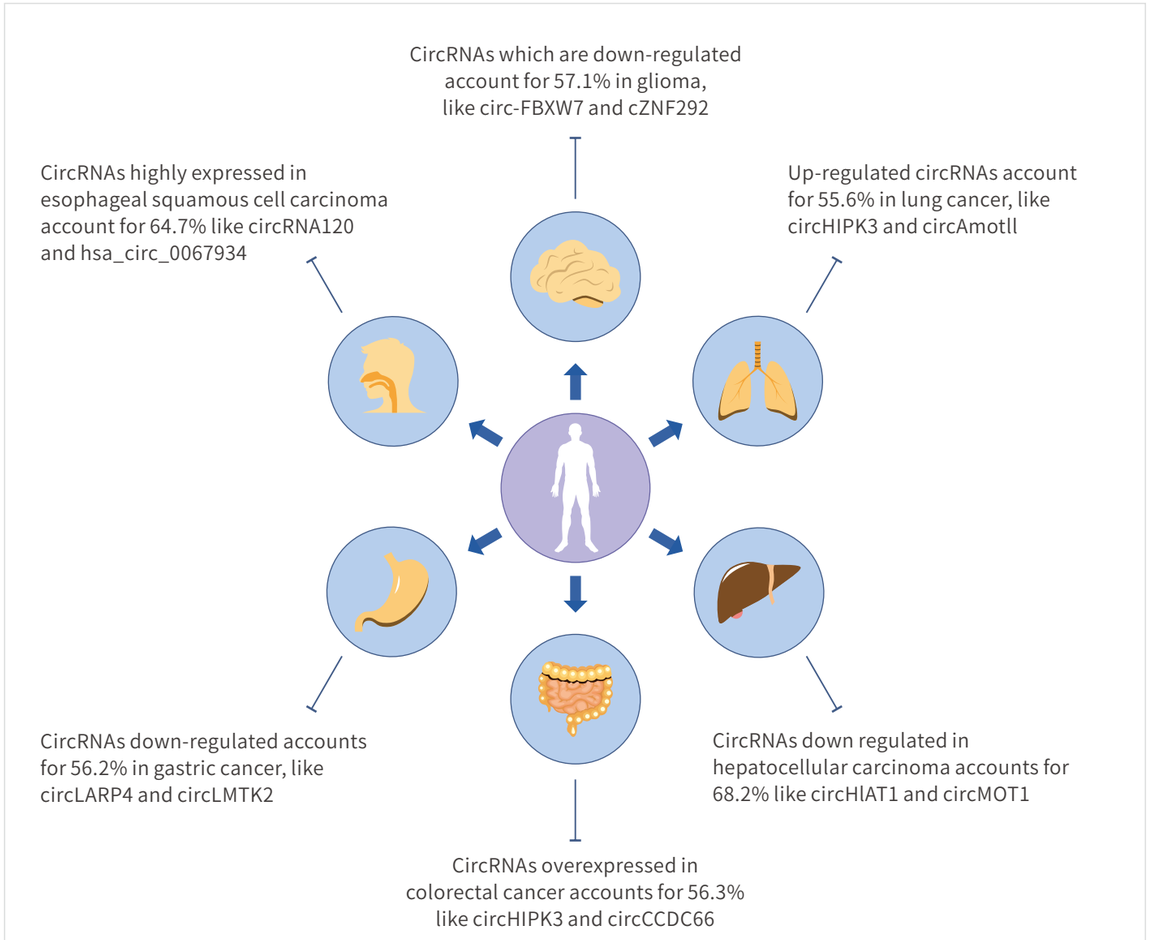

Fig 1. CircRNAs distribution in cancer[3]

The list of CUSABIO's epigenetics-related ELISA kits

Code	Product Name	Sensitivity	Target
CSB-EL002802HU	Human Bromodomain-containing protein 4(BRD4) ELISA kit	4.68 pg/mL	BRD4
CSB-EL004976HU	Human Cytidine deaminase(CDA) ELISA kit	3.9 pg/mL	CDA
CSB-EL006590HU	Human DNA damage-inducible transcript 4 protein(DDIT4) ELISA kit	0.039 ng/mL	DDIT4
CSB-EL006710HU	Human Protein DEK(DEK) ELISA kit	5.86 pg/mL	DEK
CSB-E09068h	Human deoxyribonuclease Ⅰ,DNase- Ⅰ ELISA Kit	0.39 ng/mL	DNASE1
CSB-EL007049BO	Bovine Deoxyribonuclease-1(DNASE1) ELISA kit	3.1 pg/mL	DNASE1
CSB-EL007052HU	Human Deoxyribonuclease gamma(DNASE1L3) ELISA kit	5.86 pg/mL	DNASE1L3
CSB-EL007520HU	Human Protein argonaute-2(EIF2C2) ELISA kit	6.25 pg/mL	EIF2C2
CSB-EL007520MO	Mouse Protein argonaute-2(EIF2C2) ELISA kit	7.81 pg/mL	EIF2C2
CSB-EL007681HU	Human Ectonucleotide pyrophosphatase/phosphodiesterase family member 3(ENPP3) ELISA kit	0.039 ng/mL	ENPP3
CSB-EL009161HU	Human Growth arrest and DNA damage-inducible protein GADD45 alpha (GADD45A) ELISA kit	6.25 pg/mL	GADD45A
CSB-E14145m	Mouse growth arrest-specific gene-6(gas-6)ELISA Kit	17.086 pg/mL	GAS6
CSB-EL010418HU	Human Histone H3.1(HIST1H3A) ELISA kit	5.8 pg/mL	HIST1H3A
CSB-E13159h	Human histidine-rich glycoprotein (HRG) ELISA kit	1.56 μg/mL	HRG
CSB-EL010736MO	Mouse Histidine-rich glycoprotein(HRG) ELISA kit	3.12 ng/mL	HRG
CSB-EL011843MO	Mouse Ubiquitin-like protein ISG15(ISG15) ELISA kit	0.078 ng/mL	ISG15
CSB-E12075h	Human ubiquitin-like modifier (ISG15) ELISA kit	0.195 ng/mL	ISG15
CSB-EL011843BO	Bovine Ubiquitin-like protein ISG15(ISG15) ELISA kit	0.078 ng/mL	ISG15
CSB-EL012147HU	Human Kelch-like ECH-associated protein 1(KEAP1) ELISA kit	6.25 pg/mL	KEAP1
CSB-EL012394HU	Human Krueppel-like factor 4(KLF4) ELISA kit	4.6 pg/mL	KLF4
CSB-E15769h	Human melanoma-associated antigen 3 (MAGE-3) ELISA Kit	0.156 ng/mL	MAGEA3
CSB-E09260h	Human c-myc Oncogene product,c-myc ELISA Kit	0.078 ng/mL	MYC
CSB-EL015278HU	Human N-myc proto-oncogene protein(MYCN) ELISA kit	3.9 pg/mL	MYCN
CSB-EL015319HU	Human E3 ubiquitin-protein ligase MYLIP(MYLIP) ELISA kit	3.9 pg/mL	MYLIP
CSB-EL017379MO	Mouse Protein-arginine deiminase type-4(PADI4) ELISA kit	1.17 pg/mL	PADI4
CSB-E16219h	Human protein-arginine deiminase type-4(PADI4) ELISA kit	0.039 ng/mL	PADI4
CSB-EL017722HU	Human Protein disulfide-isomerase A4(PDIA4) ELISA kit	5.8 pg/mL	PDIA4
CSB-E11308h	Human protein(peptidylprolyl cis/trans isomerase)NIMA-interacting 1, PIN1 ELISA Kit	0.39 pg/mL	PIN1
CSB-EQ027833HU	Human RNA polymerase III (Pol III) antibody ELISA kit	Request Information	Pol III Ab
CSB-EL019571HU	Human RE1-silencing transcription factor(REST) ELISA kit	7.81 pg/mL	REST
CSB-EL019798HU	Human Ribonuclease 7(RNASE7) ELISA kit	0.39 ng/mL	RNASE7
CSB-EL020818MO	Mouse Secretoglobin family 3A member 1(SCGB3A1) ELISA kit	15.6 pg/ml	SCGB3A1
CSB-EL020819MO	Mouse Secretoglobin family 3A member 2(SCGB3A2) ELISA kit	2.35 pg/mL	SCGB3A2
CSB-EL021142HU	Human Serine/arginine-rich splicing factor 1(SFRS1) ELISA kit	7.81 pg/mL	SFRS1
CSB-E16187m	Mouse NAD-dependent deacetylase sirtuin-1(Sirt1)ELISA Kit	0.039 ng/mL	SIRT1
CSB-E15058h	Human NAD-dependent deacetylase sirtuin-1 (SIRT1/SIR2L1) ELISA kit	0.039 ng/mL	SIRT1
CSB-EL021339RA	Rat NAD-dependent protein deacetylase sirtuin-1(SIRT1) ELISA kit	8.5 pg/mL	SIRT1
CSB-E17018h	Human NAD-dependent deacetylase sirtuin-6 (SIRT6/SIR2L6) ELISA kit	0.78 pg/mL	SIRT6
CSB-EL021860MO	Mouse E3 ubiquitin-protein ligase SMURF1(SMURF1) ELISA kit	7.8 pg/mL	SMURF1
CSB-E17858h	Human thiopurine S-methyltransferase (TPMT) ELISA kit	0.39 mU/mL	TPMT
CSB-EL024502HU	Human E3 ubiquitin-protein ligase TRIM63(TRIM63) ELISA kit	3.1 pg/mL	TRIM63
CSB-E13238h	Human Protein Gene Product 9.5 (PGP 9.5) ELISA Kit	1.56 ng/mL	UCHL1
CSB-E11789h	Human tryptophanyl-tRNA synthetase,WARS ELISA Kit	0.078 ng/mL	WARS
CSB-EL027165HU	Human Zyxin(ZYX) ELISA kit	5.8 pg/mL	ZYX

Research prospect of epigenetics

1. Early Cancer Diagnosis and Treatment: Epigenetics research helps us better understand the mechanisms of cancer development, which can aid in the development of more effective cancer treatments, including drug therapies targeting epigenetic modifications. Additionally, epigenetics can provide new biomarkers for the early diagnosis of cancer.

2. Precision Medicine: Epigenetics research provides additional tools and resources for precision medicine. By analyzing epigenetic markers in patients, doctors can gain a better understanding of disease risk, disease progression, and treatment responses, leading to more personalized treatment plans.

3. Environment and Health: Epigenetics also contributes to the study of how environmental factors impact health. Lifestyle choices, environmental exposures, and dietary decisions can all regulate epigenetic modifications, influencing human health. This helps us better understand the interplay between environmental factors and genetics.

4. Brain Science: Epigenetics research is of significant importance in the field of neuroscience. It can help us better understand mechanisms related to neural development, learning and memory, and neurodegenerative diseases.

5. Aging and Longevity: Epigenetics research also touches on the mechanisms of human aging and longevity. Understanding the role of epigenetic modifications in the aging process can contribute to the search for methods to extend lifespan and improve elderly health.

In summary, the prospects for research in the field of epigenetics are very promising. It has the potential to make significant breakthroughs in areas such as medicine, life sciences, and environmental science, contributing to improved health, disease treatment, and scientific progress.

References

[1] Fardi M, Solali S, Farshdousti Hagh M. Epigenetic mechanisms as a new approach in cancer treatment: An updated review[J]. Genes&Diseases, 2018, 5(4): 304-311.

[2] Ieva V, Rasa S, Rimantas J L, et al. The Emerging Role of Chromatin Remodeling Complexes in Ovarian Cancer[J]. International Journal of Molecular Sciences, 2022, 23(22).

[3] Cheng D, Wang J, Dong Z, et al. Cancer-related circular RNA: diverse biological functions[J]. Cancer Cell International, 2021, 21 (1): 11.