

# Групповой проект H3K9me

## Эпигенетическая модификация - Histone methylation

Полыгалов Богдан	<a href="#"><u>HR</u></a>	Histone modification erase
Матирко Кирилл	<a href="#"><u>MINA</u></a>	Histone modification erase
Бондаренко Артём	<a href="#"><u>KDM1A</u></a>	Histone modification erase
Седых Александр	<a href="#"><u>KDM3A</u></a>	Histone modification erase
Ахунова Анастасия	<a href="#"><u>SUV39H1</u></a>	Histone modification write
Козлова Екатерина	<a href="#"><u>CBX3</u></a>	Histone modification read
Романова Анастасия	<a href="#"><u>POGZ</u></a>	Histone modification read
Баран София	<a href="#"><u>IMJD1C</u></a>	Histone modification erase
Варшавер Александра	<a href="#"><u>ERBB4</u></a>	Histone modification cofactor
Сидорова Татьяна	<a href="#"><u>UHRF1</u></a>	Histone modification read, Histone modification write cofactor

<a href="#"><u>HR</u></a>	We performed a series of in vitro demethylation assays, which demonstrated that HR can demethylate monomethylated or dimethylated histone H3 lysine 9 (H3K9me1 or me2)
<a href="#"><u>MINA</u></a>	Управляет онкогенезом глиобластомы, регулируя циклины и циклинзависимые киназы через деметилирование H3K9me3.
<a href="#"><u>KDM1A</u></a>	KDM1A способствует иммуносупрессии при гепатоцеллюлярной карциноме путем регуляции PD-L1 посредством деметилирования MEF2D. KDM1A может деметилировать H3K4me1/2 (Lys-4) и H3K9me1/2 (Lys-9), что означает, что он действует как коактиватор или корепрессор в зависимости от контекста.
<a href="#"><u>KDM3A</u></a>	KDM3A and KDM3B catalyze the demethylation of transcriptionally repressive mono- and di-methylated histone H3 lysine 9 (H3K9me1/me2) in vitro and in vivo with a preference for dimethylated residues, thereby mediating transcriptional activation
<a href="#"><u>SUV39H1</u></a>	Первая белковая метилтрансфераза. Вводит ди- и триметилирование в гистоне H3 лизин 9 (H3K9) и играет важную роль в поддержании гетерохроматина и экспрессии генов
<a href="#"><u>CBX3</u></a>	Chromobox protein 3 (i.e. CBX3) associated with the heterochromatin protein 1 (HP1) complex is a methyl reader that interprets H3K9me3 marks which are mediated by H3K9 methyltransferases (i.e., SUV39H1 or SUV39H2).
<a href="#"><u>POGZ</u></a>	POGZ is a potential reader of H3K9me3, as it contains a PHD finger that binds specifically to this histone mark. Chromatin immunoprecipitation followed by sequencing (ChIP-seq) is used to identify proteins that interact with various histone marks in bird cells, and POGZ was found to be enriched at genomic loci marked by H3K9me3.
<a href="#"><u>JMJD1C</u></a>	JMJD1A and JMJD1C belong to the KDM3 subfamily and both can demethylate H3K9
<a href="#"><u>ERBB4</u></a>	ErbB-4 — рецептор эпидермального роста семейства EGFR/ErbB. Было показано, что уровень H3K9me3 в клетках увеличивался при стимуляции рецепторов ErbB4 с помощью NRG-1 ( за счет внутриклеточного домена).
<a href="#"><u>UHRF1</u></a>	UHRF1: играет роль в поддержании метилирования ДНК в клетках млекопитающих. Он связывается с метилированными гистонами H3K9 и H3K27, а также с ДНК метилтрансферазой DNMT1, что помогает поддерживать метилирование ДНК во время клеточного деления.

## В какие комплексы входят выбранные белки?

<b>HR</b>	Функционирует сам по себе
<b>MINA</b>	Функционирует сам по себе
<b>KDM1A</b>	NuRD, BHC, SCL
<b>KDM3A</b>	Функционирует сам по себе
<b>SUV39H1</b>	eNoSc
<b>CBX3</b>	RING2-L3MBTL2, L3MBTL1
<b>POGZ</b>	Функционирует сам по себе
<b>JMJD1C</b>	Функционирует сам по себе
<b>ERBB4</b>	Функционирует сам по себе
<b>UHRF1</b>	Функционирует сам по себе

## Экспрессия (ткани)

Ген	Название ткани + средний TPM
HR	<b>Мозг:</b> мозжечок (66), полушарие мозжечка (57), кора (23); <b>кожа:</b> открытая часть (94), закрытая (102); <b>пищевод:</b> слизистая (31);
MINA	<b>Щитовидная железа</b> (28.66); <b>клетки:</b> культивированные фибробласты (19.56); <b>клетки:</b> EBV-transformed лимфоциты (16.46)
KDM1A	<b>Тестикулы:</b> (194.0); <b>Клетки:</b> EBV-transformed лимфоциты (96.4); <b>Яичник</b> (86.78)
KDM3A	<b>Тестикулы:</b> (46.66); <b>Кожа:</b> подверженная солнцу, голени (42.54), не подверженная солнцу, надлобковая (40.88); <b>Артерия:</b> большеберцовая (34.71)
SUV39H1	<b>Клетки:</b> EBV-transformed лимфоциты (20.93); <b>Тестикулы:</b> (11.07); <b>Селезенка</b> (10.24)

## Экспрессия (ткани)

CBX3	<b>Клетки:</b> EBV-transformed лимфоциты (175.7), <b>Мозг:</b> амигдала
POGZ	<b>Мозг:</b> мозжечок (123), полушарие мозжечка (116.5); <b>яичник</b> (105.3); <b>гипофиз</b> (91.65)
<u>IMJD1C</u>	<b>Мозг:</b> мозжечок (55,06), полушария мозжечка (48,78); <b>Легкие:</b> (25,05); <b>EBV-трансформированные лимфоциты</b> (30,30)
ERBB4	<b>Аорта</b> (8.631); <b>мозг:</b> мозжечок (9.091), передняя поясная кора (8.62); <b>тестикулы</b> (5.018)
UHRF1	<b>Культивируемые фибробласты</b> (14.89); <b>Лимфатические узлы</b> (24.58); <b>Пищевод</b> (4.284); <b>Мозг - Амигдала</b> (0.6221); <b>Кровь</b> (1.376).



## Доменная структура

[HR](#)

[MINA](#)

[KDM1A](#)

[KDM3A](#)

[SUV39H1](#)

[CBX3](#)

[POGZ](#)

[JMJD1C](#)

[ERBB4](#)

[UHRF1](#)



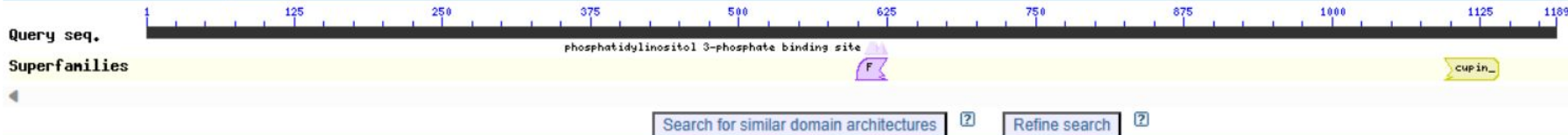
# Доменная структура белка гена HR

Conserved domains on [lcl|seqsig\_MESTP\_ece665434b20d6dac05583b96dd83863]

View Concise Results ?

NP\_005135.2 lysine-specific demethylase hairless isoform a [Homo sapiens]

Graphical summary ☐ Zoom to residue level show extra options > ?



## List of domain hits

	Name	Accession	Description	Interval	E-value
[+]	cupin_RmlC-like super family	cl40423	RmlC-like cupin superfamily; This superfamily contains proteins similar to the RmlC (dTDP ...	1095-1140	1.92e-07
[+]	FYVE_like_SF super family	cl28890	FYVE domain like superfamily; FYVE domain is a 60-80 residue double zinc finger ...	598-625	2.21e-04

## References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures.", **Nucleic Acids Res.**45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", **Nucleic Acids Res.**43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", **Nucleic Acids Res.**39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.



# Доменная структура белка гена MINA

Entry matches to this protein ⓘ



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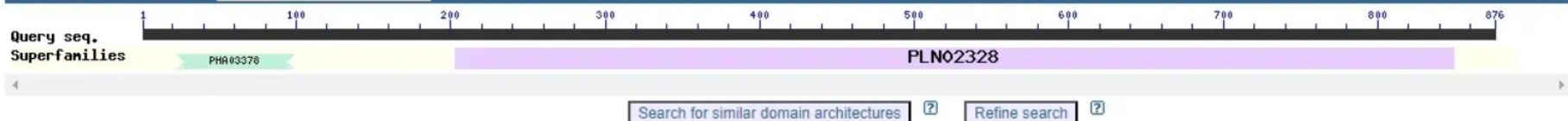
# Доменная структура белка гена KDM1A

Conserved domains on [lcl|seqsig\_MLSGK\_f383eb1a231064b352816220b25c9863]

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NP\_001009999.1 lysine-specific histone demethylase 1A isoform a [Homo sapiens]

**Graphical summary** ☐ Zoom to residue level [show extra options >](#) ?



## List of domain hits

	Name	Accession	Description	Interval	E-value
[+]	PLN02328 super family	cl33466	lysine-specific histone demethylase 1 homolog	203-849	7.61e-125
[+]	PHA03378 super family	cl33729	EBNA-3B; Provisional	23-98	1.28e-03

## References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures.", **Nucleic Acids Res.**45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", **Nucleic Acids Res.**43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", **Nucleic Acids Res.**39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.

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# Доменная структура белка гена KDM3A

Conserved domains on [lcl|seqsig\_MVLTL\_ca33e1b99aa48fe057054f12179026b4]

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NP\_001140160.1 lysine-specific demethylase 3A [Homo sapiens]

## Protein Classification

**cupin domain-containing protein** (domain architecture ID 1562428)

cupin domain-containing protein, part of a functionally diverse superfamily with the active site generally located at the center of a conserved domain forming a beta-barrel fold

## Graphical summary

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Query seq.

Superfamilies



[Search for similar domain architectures](#) ?

[Refine search](#) ?

## List of domain hits

	Name	Accession	Description	Interval	E-value
[+]	cupin_RmlC-like super family	cl40423	RmlC-like cupin superfamily; This superfamily contains proteins similar to the RmlC (dTDP ...	1151-1264	4.40e-22
[+]	cupin_RmlC-like super family	cl40423	RmlC-like cupin superfamily; This superfamily contains proteins similar to the RmlC (dTDP ...	1064-1134	7.35e-05

## References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures.", **Nucleic Acids Res.**45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", **Nucleic Acids Res.**43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", **Nucleic Acids Res.**39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.

# Доменная структура белка гена SUV39H1

Conserved domains on [lcl|seqsig\_MVGMS\_58871ec50b5410933e2a9f302907a53c]

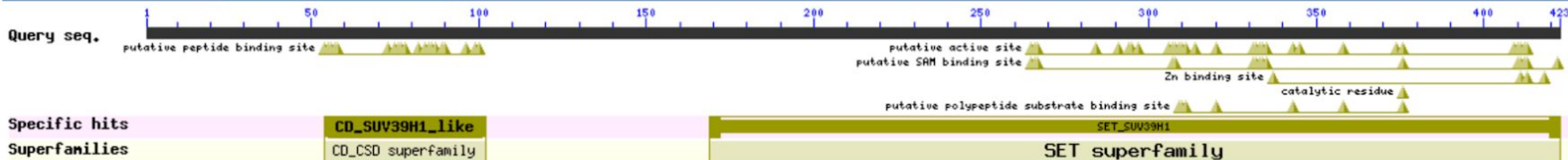
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NP\_001269095.1 histone-lysine N-methyltransferase SUV39H1 isoform 1 [Homo sapiens]

## Graphical summary

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## List of domain hits

	Name	Accession	Description	Interval	E-value
[+]	SET_SUV39H1	cd10525	SET domain (including pre-SET and post-SET domains) found in suppressor of variegation 3-9 ...	169-423	0e+00
[+]	CD_SUV39H1_like	cd18639	chromodomain of histone methyltransferase SUV39H1, and similar proteins; CHRomatin ...	54-102	3.62e-29

## References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLe: functional classification of proteins via subfamily domain architectures.", **Nucleic Acids Res.**45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", **Nucleic Acids Res.**43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", **Nucleic Acids Res.**39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.

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# Доменная структура белка гена CBX3

Conserved domains on [cl|seqsig\_MASNK\_b579573f517e186cac761691316c18e0]

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NP\_001397795.1 chromobox protein homolog 3 isoform b [Homo sapiens]

## Protein Classification

**chromo domain-containing protein**( [domain architecture ID 1001045](#))

chromo (chromatin organization modifier) domain-containing protein may bind methylated histone tails

## Graphical summary

☐ Zoom to residue level

[show extra options »](#)



[Search for similar domain architectures](#) [?](#)

[Refine search](#) [?](#)

## List of domain hits

<a href="#">+</a>	Name	Accession	Description	Interval	E-value
<a href="#">+</a>	CD_CSD super family	cl28914	CHROMO (CHRmatin Organization Modifier) domains and chromo shadow domains; Members of this ...	29-56	2.08e-12

# Доменная структура белка гена POGZ

Conserved domains on [lcl|seqsig\_MADTD\_eee4806359a31de965c8c1d41bfa6208]

View [Concise Results](#) [?](#)

NP\_001181866.1 pogo transposable element with ZNF domain isoform 4 [Homo sapiens]

## Protein Classification

**CENPB and rve domain-containing protein**( [domain architecture ID 13325336](#))

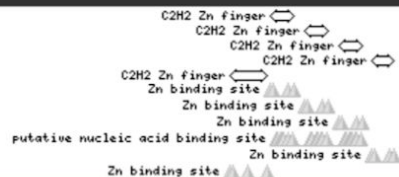
protein containing domains PLN02983, CENPB, and rve

## Graphical summary

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Query seq.



Specific hits

Superfamilies

PLN0

CENPB  
MTH\_Tnp\_T

rve superfamily

[Search for similar domain architectures](#) [?](#)

[Refine search](#) [?](#)

## List of domain hits

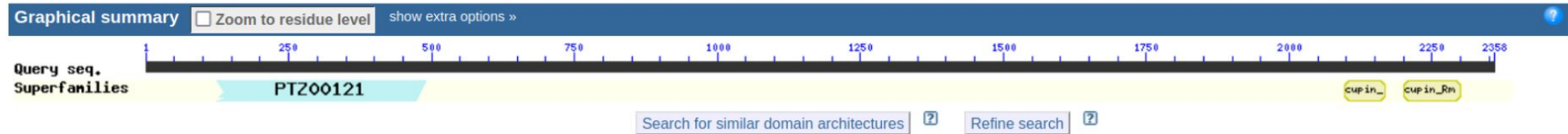
	Name	Accession	Description	Interval	E-value
[+]	CENPB	smart00674	Putative DNA-binding domain in centromere protein B, mouse jerky and transposases;	1012-1073	1.26e-13
[+]	rve super family	cl21549	Integrase core domain; Integrase mediates integration of a DNA copy of the viral genome into ...	1153-1264	8.84e-10
[+]	PLN02983 super family	cl33616	biotin carboxyl carrier protein of acetyl-CoA carboxylase	404-453	3.09e-03

# Доменная структура белка гена JMJD1C

**Conserved domains on** [Ic|seqsig\_MQGPY\_dc5146abb41e44c1e0a304579c55f269]

View Concise Results

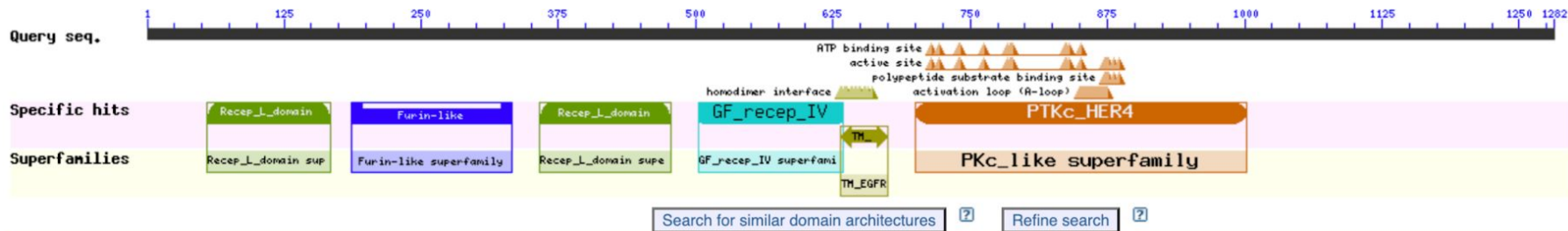
NP\_001269877.1 probable JmjC domain-containing histone demethylation protein 2C isoform c [Homo sapiens]



	Name	Accession	Description	Interval	E-value
+	cupin_RmlC-like super family	cl04023	RmlC-like cupin superfamily; This superfamily contains proteins similar to the RmlC (dTDP ...	2200-2299	1.56e-11
+	cupin_RmlC-like super family	cl04023	RmlC-like cupin superfamily; This superfamily contains proteins similar to the RmlC (dTDP ...	2096-2168	1.14e-05
+	PTZ00121 super family	cl31754	MAEBL; Provisional	125-490	2.02e-04



# Доменная структура белка гена ERBB4



List of domain hits					
	Name	Accession	Description	Interval	E-value
[+]	PTKc_HER4	cd05110	Catalytic domain of the Protein Tyrosine Kinase, HER4; PTKs catalyze the transfer of the ...	700-1002	0e+00
[+]	GF_recep_IV	pfam14843	Growth factor receptor domain IV; This is the fourth extracellular domain of receptor tyrosine ...	502-634	1.28e-70
[+]	Furin-like	pfam00757	Furin-like cysteine rich region;	186-332	1.58e-46
[+]	Recept_L_domain	pfam01030	Receptor L domain; The L domains from these receptors make up the bilobal ligand binding site. ...	55-167	7.56e-35
[+]	Recept_L_domain	pfam01030	Receptor L domain; The L domains from these receptors make up the bilobal ligand binding site. ...	358-478	1.46e-28
[+]	TM_ErbB4	cd12092	Transmembrane domain of ErbB4, a Protein Tyrosine Kinase; PTKs catalyze the transfer of the ...	632-675	2.10e-21

# Доменная структура белка гена UHRF1

