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p53 activates expression of HIC-1, a new candidate tumour suppressor gene on 17p13.3

DOI: 10.1038/nm0695-570 Nature Medicine, 1995, 1, 570-7.

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#	Paper I	F	Citations
396	No preferential loss of one parental allele of chromosome 17p13.3 in childhood medulloblastoma. 1995 , 63, 372-4		10
395	Genetic alterations distinguish different types of ovarian tumors. 1995, 64, 434-40		68
394	A microassay for measuring cytosine DNA methyltransferase activity during tumor progression. 1995 , 82-83, 335-40		7
393	A cDNA from the ovarian cancer critical region of deletion on chromosome 17p13.3. 1996 , 102, 85-90		40
392	Structure and methylation-associated silencing of a gene within a homozygously deleted region of human chromosome band 8p22. 1996 , 35, 55-65		108
391	DNA Methylation and Inactivation of Tumor Suppressor Genes. 1996 , 152-160		
390	Increased cytosine DNA-methyltransferase activity is target-cell-specific and an early event in lung cancer. 1996 , 93, 4045-50		217
389	The tumour suppressor gene p53 as a regulator of proliferative life-span and tumour progression. 1996 , 5, 139-53		16
388	De novo methylation of CpG island sequences in human fibroblasts overexpressing DNA (cytosine-5-)-methyltransferase. 1996 , 16, 4555-65		249
387	Allele loss from large regions of chromosome 17 is common only in certain histological subtypes of ovarian carcinomas. 1996 , 74, 1592-7		24
386	The DNA methylation machinery as a target for anticancer therapy. 1996 , 70, 1-37		70
385	Molecular analysis of the lissencephaly gene 1 (LIS-1) in medulloblastomas. 1996 , 22, 233-242		20
384	Aberrant DNA methylation on chromosome 16 is an early event in hepatocarcinogenesis. 1996 , 87, 1210-	·7	69
383	Molecular genetic approaches to non-melanoma and melanoma skin cancer. 1996 , 21, 253-62		13
382	Low frequency of loss of heterozygosity at the nevoid basal cell carcinoma locus and other selected loci in appendageal tumors. 1996 , 106, 1141-4		17
381	14-3-3 epsilon has no homology to LIS1 and lies telomeric to it on chromosome 17p13.3 outside the Miller-Dieker syndrome chromosome region. 1996 , 6, 735-41		18
380	Prognostic significance of p53 expression, chromosome 17 copy number, and DNA ploidy in non-metastasized colorectal carcinomas (stages IB and II). 1996 , 31, 481-9		14

379	Frequent aberrant methylation of p16INK4a in primary rat lung tumors. 1997 , 17, 1366-74	131
378	The human gene ZFP161 on 18p11.21-pter encodes a putative c-myc repressor and is homologous to murine Zfp161 (Chr 17) and Zfp161-rs1 (X Chr). 1997 , 43, 156-64	32
377	Arsenic alters cytosine methylation patterns of the promoter of the tumor suppressor gene p53 in human lung cells: a model for a mechanism of carcinogenesis. 1997 , 386, 263-77	226
376	Alterations in DNA Methylation: A Fundamental Aspect of Neoplasia. 1997 , 141-196	1277
375	Tumour-suppressor genes in prostatic oncogenesis: a positional approach. 1997 , 79 Suppl 1, 28-36	44
374	Adrenocortical carcinoma. 1997 , 8, 423-7	21
373	Inhibition of tumorigenesis by a cytosine-DNA, methyltransferase, antisense oligodeoxynucleotide. 1997 , 94, 684-9	154
372	Increased DNA methyltransferase expression is associated with an early stage of human hepatocarcinogenesis. 1997 , 88, 1165-70	79
371	Localization of a growth suppressor activity in MCF7 breast cancer cells to chromosome 17q24-q25. Oncogene, 1997, 14, 2339-45 9.2	28
370	Loss of heterozygosity of a locus on 17p13.3, independent of p53, is associated with higher grades of astrocytic tumours. <i>Oncogene</i> , 1997 , 15, 871-4	44
369	DNA hypomethylation in breast cancer: an independent parameter of tumor progression?. 1997 , 97, 83-9	71
368	Hypermethylation in the retinoblastoma gene is associated with unilateral, sporadic retinoblastoma. 1997 , 98, 43-9	113
367	A novel p53-inducible gene, PAG608, encodes a nuclear zinc finger protein whose overexpression promotes apoptosis. 1997 , 16, 4384-92	126
366	Molecular neuropathology of astrocytic brain tumors. 1997 , 35, 211-22	20
365	Multistep carcinogenesis of breast cancer and tumour heterogeneity. 1997 , 75, 429-39	190
364	p53 abnormalities in CLL are associated with excess of prolymphocytes and poor prognosis. 1997 , 99, 848-57	77
363	Localization of prostate cancer metastasis-suppressor activity on human chromosome 17. 1997 , 33, 271-80	30
362	Genetic markers for early detection of lung cancer and outcome measures for response to chemoprevention. <i>Journal of Cellular Biochemistry</i> , 1997 , 67, 64-73	12

361	Recurrent chromosomal abnormalities in hepatocellular carcinoma detected by comparative genomic hybridization. 1997 , 18, 59-65	204
360	No preferential parent of origin for the isochromosome 17q in childhood primitive neuroectodermal tumor (medulloblastoma). 1997 , 18, 143-146	9
359	Patterns of allelic loss on chromosome 17 in sporadic breast carcinomas detected by fluorescent-labeled microsatellite analysis. 1997 , 18, 181-92	60
358	Four regions of allelic imbalance on 17q12-qter associated with high-grade breast tumors. 1997 , 20, 354-362	36
357	Mutation analysis and loss of heterozygosity of PEDF in central nervous system primitive neuroectodermal tumors. 1997 , 72, 277-82	8
356	APM-1, a novel human gene, identified by aberrant co-transcription with papillomavirus oncogenes in a cervical carcinoma cell line, encodes a BTB/POZ-zinc finger protein with growth inhibitory activity. 1998 , 17, 215-22	77
355	Analysis of allelic imbalance on chromosome 17p13 in stage I and stage II epithelial ovarian cancers. 1998 , 71, 77-82	12
354	Identification of a commonly deleted region at 17p13.3 in leukemia and lymphoma associated with 17p abnormality. 1998 , 12, 510-6	40
353	Genetic instability leads to loss of both p53 alleles in a human glioblastoma. <i>Oncogene</i> , 1998 , 16, 321-6 9.2	33
352	Concordant methylation of the ER and N33 genes in glioblastoma multiforme. <i>Oncogene</i> , 1998 , 16, 3197-9292	65
351	Methylation of the HIC-1 candidate tumor suppressor gene in human breast cancer. <i>Oncogene</i> , 1998, 16, 2159-64	123
350	Detailed deletion mapping suggests the involvement of a tumor suppressor gene at 17p13.3, distal to p53, in the pathogenesis of lung cancers. <i>Oncogene</i> , 1998 , 17, 2095-100	49
349	Loss of heterozygosity for defined regions on chromosomes 3, 11 and 17 in carcinomas of the uterine cervix. 1998 , 77, 192-200	54
348	Molecular genetic analysis of easily accessible breast tumour DNA, purified from tissue left over from hormone receptor measurement. 1998 , 106, 371-7	21
347	The carboxy-terminal end of the candidate tumor suppressor gene HIC-1 is phylogenetically conserved. 1998 , 1443, 230-2	14
346	Increased expression of the LAZ3 (BCL6) proto-oncogene accompanies murine skeletal myogenesis. 1998 , 64, 33-44	19
345	Identification of deletions and insertions in the p53 gene using multiplex PCR and high-resolution fragment analysis: application to breast and ovarian tumors. 1998 , 12, 250-6	5
344	Genetic aspects of prostate cancer. 1998 , 432, 389-406	34

343	DNA hypermethylation at the D17S5 locus is associated with gastric carcinogenesis. 1998 , 122, 135-41	50
342	Short telomeres on human chromosome 17p. <i>Nature Genetics</i> , 1998 , 18, 76-80	286
341	Structure and methylation-based silencing of a gene (DBCCR1) within a candidate bladder cancer tumor suppressor region at 9q32-q33. 1998 , 48, 277-88	118
340	The human ROX gene: genomic structure and mutation analysis in human breast tumors. 1998 , 49, 275-82	18
339	Inactivation of the E-cadherin-mediated cell adhesion system in human cancers. 1998 , 153, 333-9	720
338	RP58 associates with condensed chromatin and mediates a sequence-specific transcriptional repression. 1998 , 273, 26698-704	72
337	DNA methylation in urological malignancies (review) 1998 , 13, 151	1
336	Allelic imbalance at chromosome 17p13.3 (YNZ22) in breast cancer is independent of p53 mutation or p53 overexpression and is associated with poor prognosis at medium-term follow-up. 1998 , 77, 797-800	16
335	High-risk myelodysplastic syndromes and hypermethylation of the p15Ink4B gene. 1998 , 32, 9-18	23
334	A Novel BTB/POZ Transcriptional Repressor Protein Interacts With the Fanconi Anemia Group C Protein and PLZF. <i>Blood</i> , 1999 , 94, 3737-3747	119
333	Isolation and embryonic expression of the novel mouse gene Hic1, the homologue of HIC1, a candidate gene for the Miller-Dieker syndrome. 1999 , 8, 697-710	44
332	Molecular basis of multistep hepatocarcinogenesis: genetic and epigenetic events. 1999 , 34, 737-42	17
331	Recruitment of SMRT/N-CoR-mSin3A-HDAC-repressing complexes is not a general mechanism for BTB/POZ transcriptional repressors: the case of HIC-1 and gammaFBP-B. 1999 , 96, 14831-6	101
330	Cancer-specific region of hypermethylation identified within the HIC1 putative tumour suppressor gene in acute myeloid leukaemia. 1999 , 13, 877-83	52
329	PA26, a novel target of the p53 tumor suppressor and member of the GADD family of DNA damage and growth arrest inducible genes. <i>Oncogene</i> , 1999 , 18, 127-37	191
328	Multiple target sites of allelic imbalance on chromosome 17 in Barrett@oesophageal cancer. Oncogene, 1999 , 18, 987-93	31
327	Correlation between the status of the p53 gene and survival in patients with stage I non-small cell lung carcinoma. <i>Oncogene</i> , 1999 , 18, 1007-14	73
326	Overexpressed BCL6 (LAZ3) oncoprotein triggers apoptosis, delays S phase progression and associates with replication foci. <i>Oncogene</i> , 1999 , 18, 5063-75	57

325	Loss of heterozygosity (LOH), malignancy grade and clonality in microdissected prostate cancer. 1999 , 79, 551-7		34
324	Prognostic significance of loss of heterozygosity at loci on chromosome 17p13.3-ter in sporadic breast cancer is evidence for a putative tumour suppressor gene. 1999 , 80, 821-6		18
323	Integration of a growth-suppressing BTB/POZ domain protein with the DP component of the E2F transcription factor. 1999 , 18, 212-28		66
322	Study of allelic losses on 3p, 6q, and 17p in human urothelial cancer. 1999 , 112, 42-5		10
321	New insights into p53 protein stabilisation in oral squamous cell carcinoma. 1999 , 35, 45-55		35
320	DNA hypermethylation at the D17S5 locus and reduced HIC-1 mRNA expression are associated with hepatocarcinogenesis. 1999 , 29, 703-9		97
319	Nuclear receptor co-repressor gene localizes to 17p11.2, a frequently deleted band in malignant disorders. 1999 , 25, 191-193		7
318	Analysis of the Max-binding protein MNT in human medulloblastomas. 1999 , 82, 810-6		23
317	Evolutionary divergence in the broad complex, tramtrack and bric [brac/poxviruses and zinc finger domain from the candidate tumor suppressor gene hypermethylated in cancer. <i>FEBS Letters</i> , 1999 , 451, 253-6	3.8	8
316	Molecular cloning and chromosomal mapping of the human homologue of MYB binding protein (P160) 1A (MYBBP1A) to 17p13.3. 1999 , 62, 483-9		16
315	Fold prediction and evolutionary analysis of the POZ domain: structural and evolutionary relationship with the potassium channel tetramerization domain. 1999 , 285, 1353-61		146
314	The catenin p120(ctn) interacts with Kaiso, a novel BTB/POZ domain zinc finger transcription factor. 1999 , 19, 3614-23		345
313	Increased expression of deoxyribonucleic acid methyltransferase gene in human astrocytic tumors. 2000 , 40, 564-70; discussion 570-1		
312	Role of 17p13.3 chromosomal region in determining p53 protein immunopositivity in human astrocytic tumors. 2000 , 32, 84-8		8
311	The role of DNA hypermethylation in human neoplasia. 2000 , 21, 329-33		48
310	Down-regulation of thediphthamide biosynthesis protein 2-like gene during retinoid-induced differentiation and apoptosis: Implications against its tumor-suppressor activity. 2000 , 88, 356-362		3
309	p53 allele deletion and protein accumulation occurs in the absence of p53 gene mutation in T-prolymphocytic leukaemia and Sezary syndrome. 2000 , 110, 180-7		21
308	Allelotyping defines minimal imbalance at chromosomal region 17q25 in non-serous epithelial ovarian cancers. <i>Oncogene</i> , 2000 , 19, 1466-72	9.2	22

(2001-2000)

307	Three new regions on chromosome 17p13.3 distal to p53 with possible tumor suppressor gene involvement in lung cancer. 2000 , 91, 589-96	14
306	Extensive intra-tumor heterogeneity in primary human glial tumors as a result of locus non-specific genomic alterations. 2000 , 48, 1-12	25
305	Ovarian Cancer. 2000,	3
304	The molecular pathogenesis of ovarian cancer. 2001 , 39, 25-36	1
303	High frequency allelic loss on chromosome 17p13.3-p11.1 in esophageal squamous cell carcinomas from a high incidence area in northern China. 2000 , 21, 2019-26	33
302	Suppression of tumorigenicity in breast cancer cells by the microfilament protein profilin 1. 2000 , 191, 1675-86	121
301	Mice deficient in the candidate tumor suppressor gene Hic1 exhibit developmental defects of structures affected in the Miller-Dieker syndrome. 2000 , 9, 413-9	96
300	Functional studies of the BTB domain in the Drosophila GAGA and Mod(mdg4) proteins. 2000 , 28, 3864-70	19
299	In-depth mutational analysis of the promyelocytic leukemia zinc finger BTB/POZ domain reveals motifs and residues required for biological and transcriptional functions. 2000 , 20, 6550-67	154
298	Myoneurin, a novel member of the BTB/POZ-zinc finger family highly expressed in human muscle. Biochemical and Biophysical Research Communications, 2000, 273, 385-91	12
298 297		12 78
	Biochemical and Biophysical Research Communications, 2000 , 273, 385-91	
297	Biochemical and Biophysical Research Communications, 2000, 273, 385-91 Characterization of the human TESTIN gene localized in the FRA7G region at 7q31.2. 2000, 68, 1-12 Physical and transcriptional mapping of the 17p13.3 region that is frequently deleted in human	78
² 97	Biochemical and Biophysical Research Communications, 2000, 273, 385-91 Characterization of the human TESTIN gene localized in the FRA7G region at 7q31.2. 2000, 68, 1-12 Physical and transcriptional mapping of the 17p13.3 region that is frequently deleted in human cancer. 2000, 70, 26-33	78 11
297 296 295	Characterization of the human TESTIN gene localized in the FRA7G region at 7q31.2. 2000, 68, 1-12 Physical and transcriptional mapping of the 17p13.3 region that is frequently deleted in human cancer. 2000, 70, 26-33 Expression and genetic analysis of XIAP-associated factor 1 (XAF1) in cancer cell lines. 2000, 70, 113-22	78 11 181
297 296 295	Characterization of the human TESTIN gene localized in the FRA7G region at 7q31.2. 2000, 68, 1-12 Physical and transcriptional mapping of the 17p13.3 region that is frequently deleted in human cancer. 2000, 70, 26-33 Expression and genetic analysis of XIAP-associated factor 1 (XAF1) in cancer cell lines. 2000, 70, 113-22 APC mutations in sporadic medulloblastomas. 2000, 156, 433-7 Aberrant DNA methylation precedes loss of heterozygosity on chromosome 16 in chronic hepatitis	78 11 181 215
297 296 295 294 293	Characterization of the human TESTIN gene localized in the FRA7G region at 7q31.2. 2000, 68, 1-12 Physical and transcriptional mapping of the 17p13.3 region that is frequently deleted in human cancer. 2000, 70, 26-33 Expression and genetic analysis of XIAP-associated factor 1 (XAF1) in cancer cell lines. 2000, 70, 113-22 APC mutations in sporadic medulloblastomas. 2000, 156, 433-7 Aberrant DNA methylation precedes loss of heterozygosity on chromosome 16 in chronic hepatitis and liver cirrhosis. 2000, 148, 73-80 Diminished expression of ING1 mRNA and the correlation with p53 expression in breast cancers.	78 11 181 215

289	Aberrant patterns of DNA methylation, chromatin formation and gene expression in cancer. 2001 , 10, 687-92	661
288	Monoclonal antibodies to Kaiso: a novel transcription factor and p120ctn-binding protein. 2001 , 20, 159-66	20
287	Cloning, structure, and expression of the mouse Ovca1 gene. <i>Biochemical and Biophysical Research Communications</i> , 2001 , 286, 1019-26	14
286	Characterization of HRG22, a human homologue of the putative tumor suppressor gene HIC1. Biochemical and Biophysical Research Communications, 2001, 287, 427-34	26
285	Loss of heterozygosity in tumour-adjacent normal tissue of breast and bladder cancer. 2001 , 37, 1372-80	68
284	Use of Monozygotic Twins in Search for Breast Cancer Susceptibility Loci. 2001 , 4, 251-259	5
283	Use of monozygotic twins in search for breast cancer susceptibility loci. 2001 , 4, 251-9	
282	Methylation and colorectal cancer. <i>Journal of Pathology</i> , 2001 , 195, 111-34 9.4	107
281	Detailed deletion mapping in sporadic breast cancer at chromosomal region 17p13 distal to the TP53 gene: association with clinicopathological parameters. <i>Journal of Pathology</i> , 2001 , 194, 318-26	23
2 80	Deletions of the YNZ22and Alu-VpA/MycL1Loci and Post-Surgery Prognosis in Human Colorectal Adenocarcinoma. 2001 , 35, 676-681	
279	Possible prediction of myeloid and lymphoid crises in chronic myelocytic leukemia at onset by determining the methylation status of the major breakpoint cluster region. 2001 , 126, 102-10	11
278	Allelic imbalance and fine mapping of the 17p13.3 subregion in sporadic breast carcinomas. 2001 , 129, 145-9	14
277	Genetic alterations in hepatocellular carcinoma and intrahepatic cholangiocarcinoma. 2001, 130, 22-8	46
276	Expression of the Hypermethylated in Cancer gene (HIC-1) is associated with good outcome in human breast cancer. 2001 , 85, 1878-82	34
275	Promoter hypermethylationcan this change alone ever designate true tumor suppressor gene function?. 2001 , 93, 664-5	34
274	Identification in the human candidate tumor suppressor gene HIC-1 of a new major alternative TATA-less promoter positively regulated by p53. 2001 , 276, 3078-89	61
273	Heterogeneity of DNA methylation status analyzed by bisulfite-PCR-SSCP and correlation with clinico-pathological characteristics in colorectal cancer. 2001 , 39, 121-8	23
272	Methylation matters. 2001 , 38, 285-303	393

(2003-2001)

271	P53-responsive genes and the potential for cancer diagnostics and therapeutics development. 2001 , 7, 131-64	30
270	Hepatocellular carcinoma: an update. 2001 , 25, 497-516	91
269	Class II histone deacetylases are directly recruited by BCL6 transcriptional repressor. 2002 , 277, 22045-52	133
268	The human candidate tumor suppressor gene HIC1 recruits CtBP through a degenerate GLDLSKK motif. 2002 , 22, 4890-901	83
267	Arsenic-related chromosomal alterations in bladder cancer. 2002 , 94, 1688-96	56
266	Comparative genomic hybridization analysis of adrenocortical tumors. 2002 , 87, 3467-74	103
265	Tumour suppressor genes in sporadic epithelial ovarian cancer. 2002 , 123, 341-53	18
264	Global and gene-specific methylation patterns in cancer: aspects of tumor biology and clinical potential. 2002 , 75, 1-16	48
263	Characteristic promoter hypermethylation signatures in male germ cell tumors. 2002 , 1, 8	77
262	Allelic loss in breast cancer. 2002 , 26, 426-34	13
261	Loss of heterozygosity analysis: practically and conceptually flawed?. 2002, 34, 349-53	63
260	Comprehensive allelotyping of well-differentiated human hepatocellular carcinoma with semiquantitative determination of chromosomal gain or loss. 2002 , 35, 329-39	33
259	Molecular alterations in sporadic breast cancer. 2002 , 44, 121-41	29
258	CpG island hypermethylation and tumor suppressor genes: a booming present, a brighter future. Oncogene, 2002 , 21, 5427-40 9.2	952
257	A genomic screen for genes upregulated by demethylation and histone deacetylase inhibition in human colorectal cancer. <i>Nature Genetics</i> , 2002 , 31, 141-9	766
256	The fundamental role of epigenetic events in cancer. 2002 , 3, 415-28	4311
255	Abnormal Methylation of Several Tumor Suppressor Genes in Sporadic Breast Cancer. 2003 , 37, 591-597	3
254	Structure, function and evolution of haspin and haspin-related proteins, a distinctive group of eukaryotic protein kinases. 2003 , 60, 446-62	37

253	Loss of heterozygosity of a locus in the chromosomal region 17p13.3 is associated with increased cell proliferation in astrocytic tumors. 2003 , 144, 156-64		14
252	Ambivalent role of BCL6 in cell survival and transformation. <i>Oncogene</i> , 2003 , 22, 507-16	9.2	49
251	Detailed characterization of a homozygously deleted region corresponding to a candidate tumor suppressor locus at distal 17p13.3 in human lung cancer. <i>Oncogene</i> , 2003 , 22, 1892-905	9.2	31
250	Physical and transcript map of the minimally deleted region III on 17p implicated in the early development of Barrett@oesophageal adenocarcinoma. <i>Oncogene</i> , 2003 , 22, 4134-42	9.2	5
249	Heterozygous disruption of Hic1 predisposes mice to a gender-dependent spectrum of malignant tumors. <i>Nature Genetics</i> , 2003 , 33, 197-202	36.3	182
248	Gene silencing in cancer in association with promoter hypermethylation. 2003 , 349, 2042-54		2694
247	Frequent promoter methylation of CDH1, DAPK, RARB, and HIC1 genes in carcinoma of cervix uteri: its relationship to clinical outcome. 2003 , 2, 24		166
246	Effects of cadmium on DNA-(Cytosine-5) methyltransferase activity and DNA methylation status during cadmium-induced cellular transformation. 2003 , 286, 355-65		364
245	Multigene methylation analysis of gastrointestinal tumors: TPEF emerges as a frequent tumor-specific aberrantly methylated marker that can be detected in peripheral blood. 2003 , 7, 201-7		17
244	Epigenetic silencing of the HIC-1 gene in human medulloblastomas. 2003 , 62, 1192-201		54
243	Role of the insulin-like growth factor system in adrenocortical growth control and carcinogenesis. 2004 , 36, 397-405		64
242	Targeted disruption of the 3p12 gene, Dutt1/Robo1, predisposes mice to lung adenocarcinomas and lymphomas with methylation of the gene promoter. 2004 , 64, 6432-7		56
241	The tumor suppressor gene HIC1 (hypermethylated in cancer 1) is a sequence-specific transcriptional repressor: definition of its consensus binding sequence and analysis of its DNA binding and repressive properties. 2004 , 279, 38313-24		63
240	Chromosome 17p deletion in human medulloblastoma: a missing checkpoint in the Hedgehog pathway. 2004 , 3, 1263-6		30
239	The tumor suppressor HIC1 (hypermethylated in cancer 1) is O-GlcNAc glycosylated. 2004 , 271, 3843-54		26
238	Identification of a second G-C-rich promoter conserved in the human, murine and rat tumor suppressor genes HIC1. <i>Oncogene</i> , 2004 , 23, 4023-31	9.2	17
237	Current treatment of medulloblastoma: recent advances and future challenges. 2004, 31, 666-75		74
236	Epigenetic and genetic loss of Hic1 function accentuates the role of p53 in tumorigenesis. 2004 , 6, 387-9	98	141

235	Supratentorial glioblastoma in adults: identification of subsets and their clinical correlation. 2004 , 21, 7-12		10
234	Role of epigenetic changes in hematological malignancies. 2004 , 83, 137-52		29
233	Two variants of the human hepatocellular carcinoma-associated HCAP1 gene and their effect on the growth of the human liver cancer cell line Hep3B. 2004 , 39, 48-58		16
232	Analysis of HIC-1 methylation and transcription in human ependymomas. 2004 , 110, 542-9		62
231	Gene expression microarray analysis and genome databases facilitate the characterization of a chromosome 22 derived homogeneously staining region. 2004 , 41, 17-38		20
230	Nuclear import of the BTB/POZ transcriptional regulator Kaiso. 2004 , 117, 6143-52		40
229	Oncogenes and tumor suppressor genes in breast cancer: potential diagnostic and therapeutic applications. 2004 , 9, 361-77		150
228	Aberrant methylation profile of human malignant mesotheliomas and its relationship to SV40 infection. <i>Oncogene</i> , 2005 , 24, 1302-8	9.2	69
227	Diagnostic clinical application of two-color fluorescence in situ hybridization that detects chromosome 1 and 17 alterations to direct touch smear and liquid-based thin-layer cytologic preparations of endometrial cancers. 2005 , 15, 70-80		9
226	Epigenetic changes in solid and hematopoietic tumors. 2005 , 32, 521-30		103
225	Skin Cancer Prevention. 2005 , 161-201		O
224	The BTB Domain Zinc Finger Proteins. 2005 , 134-150		2
223	Enhancement of in vitro and in vivo tumor cell radiosensitivity by the DNA methylation inhibitor zebularine. 2005 , 11, 4571-9		92
222	Molecular genetics of adrenocortical tumours, from familial to sporadic diseases. 2005 , 153, 477-87		133
221	Inactivation of tumor suppressor genes: choice between genetic and epigenetic routes. 2005 , 4, 10-2		18
220	Analysis of promoter methylation in stool: a novel method for the detection of colorectal cancer. 2005 , 3, 142-9		98
219	DNA Methylation, Epigenetics and Metastasis. 2005,		1
218	CpG Island Hypermethylation in Breast Cancer Progression and Metastasis. 2005 , 81-132		1

217	DNA methylation and gene silencing in cancer. 2005 , 2 Suppl 1, S4-11		835
216	25 Years of p53 Research. 2005 ,		12
215	Genetic profile of hepatocellular carcinoma revealed by array-based comparative genomic hybridization: identification of genetic indicators to predict patient outcome. 2005 , 43, 863-74		61
214	Hedgehog checkpoints in medulloblastoma: the chromosome 17p deletion paradigm. 2005 , 11, 537-45		64
213	OVCA1: tumor suppressor gene. 2005 , 15, 49-54		21
212	Tumor suppressor HIC1 directly regulates SIRT1 to modulate p53-dependent DNA-damage responses. 2005 , 123, 437-48		528
211	HIC1 promoter methylation and 17p13.3 allelic loss in invasive ductal carcinoma of the breast. 2005 , 222, 75-81		22
210	Zinc Finger Proteins. 2005,		17
209	[Chromosome arm 17p13.3: could HIC1 be the one ?]. 2006 , 22, 54-61		7
208	A L225A substitution in the human tumour suppressor HIC1 abolishes its interaction with the corepressor CtBP. 2006 , 273, 2879-90		16
207	[New therapeutic approaches for solid tumors: histone deacetylase, methyltransferase and proteasome inhibitors]. 2006 , 4, 108-13		4
206	Neue Therapieanstze bei der Behandlung von Tumoren: Histondeacetylase-, Methyltransferase-und Proteasominhibitoren. 2006 , 4,		
205	Epigenetic gene silencing in cancer - a mechanism for early oncogenic pathway addiction?. <i>Nature Reviews Cancer</i> , 2006 , 6, 107-16	31.3	1372
204	Identification of the p53 family-responsive element in the promoter region of the tumor suppressor gene hypermethylated in cancer 1. <i>Oncogene</i> , 2006 , 25, 2030-9	9.2	44
203	POZ for effectPOZ-ZF transcription factors in cancer and development. 2006 , 16, 578-87		205
202	Structural and functional properties of genes involved in human cancer. <i>BMC Genomics</i> , 2006 , 7, 3	4.5	63
201	Silencing of the UCHL1 gene in human colorectal and ovarian cancers. 2006, 119, 1338-44		83
200	The cancer epigenomecomponents and functional correlates. 2006 , 20, 3215-31		295

(2007-2006)

199	Mnt-deficient mammary glands exhibit impaired involution and tumors with characteristics of myc overexpression. 2006 , 66, 5565-73		29
198	Identification and functional characterization of a novel unspliced transcript variant of HIC-1 in human cancer cells exposed to adverse growth conditions. 2006 , 66, 10466-77		11
197	Methylation of serum DNA is an independent prognostic marker in colorectal cancer. 2006 , 12, 7347-52		154
196	Metabolic regulation of SIRT1 transcription via a HIC1:CtBP corepressor complex. 2007 , 104, 829-33		153
195	An acetylation/deacetylation-SUMOylation switch through a phylogenetically conserved psiKXEP motif in the tumor suppressor HIC1 regulates transcriptional repression activity. 2007 , 27, 2661-75		132
194	NSAIDs modulate CDKN2A, TP53, and DNA content risk for progression to esophageal adenocarcinoma. 2007 , 4, e67		209
193	SIRT1 is significantly elevated in mouse and human prostate cancer. 2007 , 67, 6612-8		367
192	Nucleoredoxin, a novel thioredoxin family member involved in cell growth and differentiation. 2007 , 9, 1035-57		84
191	Extensive methylation is associated with beta-catenin mutations in hepatocellular carcinoma: evidence for two distinct pathways of human hepatocarcinogenesis. 2007 , 67, 4586-94		50
190	Genome-epigenome interactions in cancer. 2007 , 16 Spec No 1, R96-105		50
189	Highly methylated genes in colorectal neoplasia: implications for screening. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007 , 16, 2686-96		105
188	Alterations of DNA methylation associated with abnormalities of DNA methyltransferases in human cancers during transition from a precancerous to a malignant state. 2007 , 28, 2434-42		160
187	Epigenetic control of tumor suppression. 2007 , 17, 295-316		29
186	Human SIRT1: a potential biomarker for tumorigenesis?. 2007 , 31, 636-7		37
185	Gene amplification is a relatively frequent event leading to ZBTB7A (Pokemon) overexpression in non-small cell lung cancer. <i>Journal of Pathology</i> , 2007 , 213, 294-302	·4	51
184	RPS6KA2, a putative tumour suppressor gene at 6q27 in sporadic epithelial ovarian cancer. Oncogene, 2007 , 26, 683-700	.2	78
183	Dancing in and out of the nucleus: p120(ctn) and the transcription factor Kaiso. 2007 , 1773, 59-68		88
182	Dual targeting of epigenetic therapy in cancer. 2007 , 1775, 76-91		60

181	Array CGH identifies distinct DNA copy number profiles of oncogenes and tumor suppressor genes in chromosomal- and microsatellite-unstable sporadic colorectal carcinomas. 2007 , 85, 293-304	118
180	Genomic deletion and promoter methylation status of Hypermethylated in Cancer 1 (HIC1) in mantle cell lymphoma. 2008 , 1, 85-95	4
179	Detailed mapping of chromosome 17p deletions reveals HIC1 as a novel tumor suppressor gene candidate telomeric to TP53 in diffuse large B-cell lymphoma. <i>Oncogene</i> , 2008 , 27, 2613-25	22
178	HIC1 tumour suppressor gene is suppressed in acute myeloid leukaemia and induced during granulocytic differentiation. 2008 , 141, 179-87	29
177	Alterations of DNA methylation and clinicopathological diversity of human cancers. 2008, 58, 544-58	67
176	The Genetics and Molecular Biology of Neural Tumors. 2008,	6
175	Skin Cancer Prevention. 2008, 239-289	
174	Novel and highly recurrent chromosomal alterations in SZary syndrome. 2008 , 68, 2689-98	148
173	Proteomic analysis of laser-captured paraffin-embedded tissues: a molecular portrait of head and neck cancer progression. 2008 , 14, 1002-14	168
172	Human gastric adenocarcinoma allelotype on chromosomes 17 and 18. 2008 , 36, 279-88	9
171	Just say no to ATOH: how HIC1 methylation might predispose medulloblastoma to lineage addiction. 2008 , 68, 8654-6	19
170	Specific 50@pG island methylation signatures of FHIT and p16 genes and their potential diagnostic relevance in Indian breast cancer patients. 2008 , 27, 517-25	7
169	Novel systemic therapies for small cell lung cancer. 2008 , 6, 315-22	23
168	DNA repair, insulin signaling and sirtuins: at the crossroads between cancer and aging. 2008 , 13, 6966-90	8
167	Implication of HIC1 (Hypermethylated In Cancer 1) in the DNA damage response. 2009 , 96, E66-72	19
166	Scavenger chemokine (CXC motif) receptor 7 (CXCR7) is a direct target gene of HIC1 (hypermethylated in cancer 1). 2009 , 284, 20927-35	55
165	The conserved NAD(H)-dependent corepressor CTBP-1 regulates Caenorhabditis elegans life span. 2009 , 106, 1496-501	49
164	Frequent epigenetic inactivation of the SLIT2 gene in chronic and acute lymphocytic leukemia. Epigenetics, 2009 , 4, 265-9 5-7	41

163	Epigenetics of neurological cancers. 2009 , 5, 1615-29		19
162	Identification of Smyd4 as a potential tumor suppressor gene involved in breast cancer development. 2009 , 69, 4067-72		54
161	The tumor suppressor gene hypermethylated in cancer 1 is transcriptionally regulated by E2F1. <i>Molecular Cancer Research</i> , 2009 , 7, 916-22	6.6	23
160	ECRG4 is a candidate tumor suppressor gene frequently hypermethylated in colorectal carcinoma and glioma. <i>BMC Cancer</i> , 2009 , 9, 447	4.8	66
159	HIC1 (Hypermethylated in Cancer 1) epigenetic silencing in tumors. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 26-33	5.6	62
158	HIC1 interacts with a specific subunit of SWI/SNF complexes, ARID1A/BAF250A. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 385, 586-90	3.4	43
157	Stem cells, cancer, and epigenetics. 2009,		11
156	Molecular, Clinical and Environmental Toxicology. <i>Exs</i> , 2009 ,		10
155	Distinct HIC1-SIRT1-p53 loop deregulation in lung squamous carcinoma and adenocarcinoma patients. 2009 , 11, 763-70		79
154	DNA hypermethylation markers of poor outcome in laryngeal cancer. 2010 , 1, 61-69		25
153	Demethylation treatment restores hic1 expression and impairs aggressiveness of head and neck squamous cell carcinoma. 2010 , 46, 678-83		16
152	Epigenetic alterations differ in phenotypically distinct human neuroblastoma cell lines. <i>BMC Cancer</i> , 2010 , 10, 286	4.8	20
151	SIRT1 and p53, effect on cancer, senescence and beyond. 2010 , 1804, 1684-9		197
150	A potential tumor suppressor role for Hic1 in breast cancer through transcriptional repression of ephrin-A1. <i>Oncogene</i> , 2010 , 29, 2467-76	9.2	37
149	Characterization of №p73 expression and regulation in gastric and esophageal tumors. <i>Oncogene</i> , 2010 , 29, 5861-8	9.2	20
148	Maternal genes and facial clefts in offspring: a comprehensive search for genetic associations in two population-based cleft studies from Scandinavia. <i>PLoS ONE</i> , 2010 , 5, e11493	3.7	33
147	IGFBP7 is a p53-responsive gene specifically silenced in colorectal cancer with CpG island methylator phenotype. 2010 , 31, 342-9		81
146	Differential regulation of HIC1 target genes by CtBP and NuRD, via an acetylation/SUMOylation switch, in quiescent versus proliferating cells. 2010 , 30, 4045-59		70

The Role of the Epigenome in Human Cancers. **2010**, 471-486

-13		
144	IGFBP7 is a p53 target gene inactivated in human lung cancer by DNA hypermethylation. 2011 , 73, 38-44	34
143	Epigenetics in Pediatric Cancers. 2011 , 163-252	
142	The human LIS1 is downregulated in hepatocellular carcinoma and plays a tumor suppressor function. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 409, 193-9	16
141	HIC1 (hypermethylated in Cancer 1). 2011 ,	
140	Loss of a single Hic1 allele accelerates polyp formation in Apc(116) mice. <i>Oncogene</i> , 2011 , 30, 2659-69 9.2	21
139	CpG-island methylation study of liver fluke-related cholangiocarcinoma. 2011 , 104, 1313-8	41
138	DSC3 expression is regulated by p53, and methylation of DSC3 DNA is a prognostic marker in human colorectal cancer. 2011 , 104, 1013-9	50
137	Protected from the inside: endogenous histone deacetylase inhibitors and the road to cancer. 2011 , 1815, 241-52	27
136	Identification of novel subregions of LOH in gastric cancer and analysis of the HIC1 and TOB1 tumor suppressor genes in these subregions. 2011 , 32, 47-55	19
135	Promoter hypermethylation of RASSF1A, MGMT, and HIC-1 genes in benign and malignant colorectal tumors. <i>Tumor Biology</i> , 2011 , 32, 845-52	30
134	Generation of two modified mouse alleles of the Hic1 tumor suppressor gene. 2011 , 49, 142-51	16
133	Classification of Epstein-Barr virus-positive gastric cancers by definition of DNA methylation epigenotypes. 2011 , 71, 7187-97	161
132	Systems analysis of immune responses in Marek@disease virus-infected chickens identifies a gene involved in susceptibility and highlights a possible novel pathogenicity mechanism. 2011 , 85, 11146-58	60
131	The dual role of sirtuins in cancer. 2011 , 2, 648-62	233
130	Pharmacological genome demethylation increases radiosensitivity of head and neck squamous carcinoma cells. 2012 , 29, 505-9	17
129	The important molecular markers on chromosome 17 and their clinical impact in breast cancer. 2011 , 12, 5672-83	25
128	Hypermethylated in cancer 1 (HIC1) recruits polycomb repressive complex 2 (PRC2) to a subset of its target genes through interaction with human polycomb-like (hPCL) proteins. 2012 , 287, 10509-10524	35

127	Emerging roles of microRNA-22 in human disease and normal physiology. 2012 , 12, 247-58		39
126	The receptor tyrosine kinase EphA2 is a direct target gene of hypermethylated in cancer 1 (HIC1). 2012 , 287, 5366-78		29
125	Loss of Hypermethylated in Cancer 1 (HIC1) in breast cancer cells contributes to stress-induced migration and invasion through № adrenergic receptor (ADRB2) misregulation. 2012 , 287, 5379-89		23
124	Pancreatic ductal cells acquire mesenchymal characteristics through cell fusion with bone marrow-derived mesenchymal stem cells and SIRT1 attenuates the apoptosis of hybrid cells. 2012 , 196, 129-36		1
123	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. 2012 , 22, 837-49		196
122	Prognostic and diagnostic relevance of hypermethylated in cancer 1 (HIC1) CpG island methylation in renal cell carcinoma. 2012 , 40, 1650-8		15
121	Promoter CpG island methylation markers in colorectal cancer: the road ahead. <i>Epigenomics</i> , 2012 , 4, 179-94	4.4	32
120	Cervical cancer pathogenesis is associated with one-carbon metabolism. <i>Molecular and Cellular Biochemistry</i> , 2012 , 369, 1-7	4.2	22
119	Alterations in promoter methylation status of tumor suppressor HIC1, SFRP2, and DAPK1 genes in prostate carcinomas. 2012 , 31, 826-32		18
118	Molecular dissection of the interaction between HIC1 and SIRT1. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 421, 384-8	3.4	9
117	Knock-down of Kaiso induces proliferation and blocks granulocytic differentiation in blast crisis of chronic myeloid leukemia. 2012 , 12, 28		19
116	The BTB-ZF transcription factors. 2012 , 11, 3358-69		73
115	DNA Methylation Alterations in Human Cancers. 2012 , 29-52		2
114	Signification of Hypermethylated in Cancer 1 (HIC1) as Tumor Suppressor Gene in Tumor Progression. 2012 , 5, 285-93		23
113	Primary Liver Cancer. 2012 ,		3
112	Cys2His2 zinc finger protein family: classification, functions, and major members. 2012 , 77, 217-26		107
111	A small molecule Inauhzin inhibits SIRT1 activity and suppresses tumour growth through activation of p53. 2012 , 4, 298-312		77
110	Metastasis-associated protein 1/nucleosome remodeling and histone deacetylase complex in cancer. 2012 , 72, 387-94		97

Primary Tumors of the Nervous System. **2013**, 1-22

108	Cellular reprogramming to reset epigenetic signatures. 2013 , 34, 841-8		22
107	Maintaining the unmethylated state. 2013 , 5, 17		1
106	DNA double-strand breaks lead to activation of hypermethylated in cancer 1 (HIC1) by SUMOylation to regulate DNA repair. 2013 , 288, 10254-64		32
105	Identification of p21 (CIP1/WAF1) as a direct target gene of HIC1 (Hypermethylated In Cancer 1). <i>Biochemical and Biophysical Research Communications</i> , 2013 , 430, 49-53	3.4	12
104	The Reelin receptors ApoER2 and VLDLR are direct target genes of HIC1 (Hypermethylated In Cancer 1). <i>Biochemical and Biophysical Research Communications</i> , 2013 , 440, 424-30	3.4	9
103	Regulation of the cyclin-dependent kinase inhibitor 1A gene (CDKN1A) by the repressor BOZF1 through inhibition of p53 acetylation and transcription factor Sp1 binding. 2013 , 288, 7053-64		8
102	Deciphering HIC1 control pathways to reveal new avenues in cancer therapeutics. 2013 , 17, 811-27		27
101	Developmentally programmed 3QCpG island methylation confers tissue- and cell-type-specific transcriptional activation. 2013 , 33, 1845-58		38
100	HIC1 modulates prostate cancer progression by epigenetic modification. 2013 , 19, 1400-10		41
99	HIC1 interacts with and modulates the activity of STAT3. 2013 , 12, 2266-76		16
98	References. 2013 , 217-288		
97	The Roles of SIRT1 in Cancer. 2013 , 4, 97-104		129
96	Small activating RNA restores the activity of the tumor suppressor HIC-1 on breast cancer. <i>PLoS ONE</i> , 2014 , 9, e86486	3.7	12
95	Anticancer agents targeted to sirtuins. <i>Molecules</i> , 2014 , 19, 20295-313	4.8	41
94	Genes suppressed by DNA methylation in non-small cell lung cancer reveal the epigenetics of epithelial-mesenchymal transition. <i>BMC Genomics</i> , 2014 , 15, 1079	4.5	37
93	miR-212 and miR-132 are dispensable for mouse mammary gland development. <i>Nature Genetics</i> , 2014 , 46, 802-4	36.3	16
92	The molecular significance of methylated BRCA1 promoter in white blood cells of cancer-free females. <i>BMC Cancer</i> , 2014 , 14, 830	4.8	29

91	Pathology of Pediatric Gastrointestinal and Liver Disease. 2014 ,		5
90	A novel p53/microRNA-22/Cyr61 axis in synovial cells regulates inflammation in rheumatoid arthritis. <i>Arthritis and Rheumatology</i> , 2014 , 66, 49-59	9.5	99
89	Metastatic tumor antigen in hepatocellular carcinoma: golden roads toward personalized medicine. <i>Cancer and Metastasis Reviews</i> , 2014 , 33, 965-80	9.6	21
88	P53 induction accompanying G2/M arrest upon knockdown of tumor suppressor HIC1 in U87MG glioma cells. <i>Molecular and Cellular Biochemistry</i> , 2014 , 395, 281-90	4.2	11
87	Molecular cloning and expression of high GC-rich novel tumor suppressor gene HIC-1. <i>Molecular Biotechnology</i> , 2014 , 56, 1040-8	3	2
86	Transcriptional regulation of the human thromboxane A2 receptor gene by WilmsQumor (WT)1 and hypermethylated in cancer (HIC) 1 in prostate and breast cancers. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014 , 1839, 476-92	6	12
85	Physical and functional interaction of the proto-oncogene EVI1 and tumor suppressor gene HIC1 deregulates Bcl-xL mediated block in apoptosis. <i>International Journal of Biochemistry and Cell Biology</i> , 2014 , 53, 320-8	5.6	3
84	Genome-wide DNA methylation profiling of recurrent and non-recurrent chordomas. <i>Epigenetics</i> , 2015 , 10, 213-20	5.7	15
83	HIC1 Tumor Suppressor Loss Potentiates TLR2/NF- B Signaling and Promotes Tissue Damage-Associated Tumorigenesis. <i>Molecular Cancer Research</i> , 2015 , 13, 1139-48	6.6	18
82	The multifaceted functions of sirtuins in cancer. <i>Nature Reviews Cancer</i> , 2015 , 15, 608-24	31.3	289
81	Hypermethylation of the HIC1 promoter and aberrant expression of HIC1/SIRT1 contribute to the development of thyroid papillary carcinoma. <i>Oncotarget</i> , 2016 , 7, 84416-84427	3.3	18
80	HIC1 controls cellular- and HIV-1- gene transcription via interactions with CTIP2 and HMGA1. <i>Scientific Reports</i> , 2016 , 6, 34920	4.9	14
79	HIC1 Expression Distinguishes Intestinal Carcinomas Sensitive to Chemotherapy. <i>Translational Oncology</i> , 2016 , 9, 99-107	4.9	2
78	Epigenetic Determinants of Cancer. Cold Spring Harbor Perspectives in Biology, 2016, 8,	10.2	501
77	Multiple functions of p21 in cell cycle, apoptosis and transcriptional regulation after DNA damage. <i>DNA Repair</i> , 2016 , 42, 63-71	4.3	498
76	HIC1 epigenetically represses CIITA transcription in B lymphocytes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 1481-1489	6	7
75	HIC1 modulates uveal melanoma progression by activating lncRNA-numb. <i>Tumor Biology</i> , 2016 , 37, 127	77 9 :927	78 9 4
74	KDM6B histone demethylase is an epigenetic regulator of estrogen receptor Expression in human pleural mesothelioma. <i>Epigenomics</i> , 2016 , 8, 1227-38	4.4	14

73	Molecular and Cellular Changes During Cancer Progression Resulting From Genetic and Epigenetic Alterations. <i>Progress in Molecular Biology and Translational Science</i> , 2016 , 144, 3-47	4	17
72	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. <i>Nature</i> , 2016 , 531, 471-475	50.4	142
71	promoter methylation in peripheral blood cells and predisposition to breast cancer. <i>Journal of Taibah University Medical Sciences</i> , 2017 , 12, 189-193	1.7	2
70	HIC1 loss promotes prostate cancer metastasis by triggering epithelial-mesenchymal transition. <i>Journal of Pathology</i> , 2017 , 242, 409-420	9.4	14
69	Regulation of Active DNA Demethylation through RAR-Mediated Recruitment of a TET/TDG Complex. <i>Cell Reports</i> , 2017 , 19, 1685-1697	10.6	32
68	The transcriptional repressor HIC1 regulates intestinal immune homeostasis. <i>Mucosal Immunology</i> , 2017 , 10, 1518-1528	9.2	14
67	Role of Sirtuin1-p53 regulatory axis in aging, cancer and cellular reprogramming. <i>Ageing Research Reviews</i> , 2018 , 43, 64-80	12	106
66	The tumor suppressor Hic1 maintains chromosomal stability independent of Tp53. <i>Oncogene</i> , 2018 , 37, 1939-1948	9.2	12
65	Narrower insight to SIRT1 role in cancer: A potential therapeutic target to control epithelial-mesenchymal transition in cancer cells. <i>Journal of Cellular Physiology</i> , 2018 , 233, 4443-4457	7	29
64	Hypermethylated in cancer 1 (HIC1) mediates high glucose induced ROS accumulation in renal tubular epithelial cells by epigenetically repressing SIRT1 transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018 , 1861, 917-927	6	37
63	Gestational oral low-dose estradiol-17 Induces altered DNA methylation of CDKN2D and PSAT1 in embryos and adult offspring. <i>Scientific Reports</i> , 2018 , 8, 7494	4.9	14
62	HIC1 links retinoic acid signalling to group 3 innate lymphoid cell-dependent regulation of intestinal immunity and homeostasis. <i>PLoS Pathogens</i> , 2018 , 14, e1006869	7.6	15
61	Zwitterion-functionalized dendrimer-entrapped gold nanoparticles for serum-enhanced gene delivery to inhibit cancer cell metastasis. <i>Acta Biomaterialia</i> , 2019 , 99, 320-329	10.8	45
60	HIC2, a new transcription activator of SIRT1. FEBS Letters, 2019, 593, 1763-1776	3.8	3
59	Hic1 Defines Quiescent Mesenchymal Progenitor Subpopulations with Distinct Functions and Fates in Skeletal Muscle Regeneration. <i>Cell Stem Cell</i> , 2019 , 25, 797-813.e9	18	64
58	Hypermethylated in cancer 1 (HIC1) suppresses bladder cancer progression by targeting yes-associated protein (YAP) pathway. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 6471-6481	4.7	4
57	Loss of hypermethylated in cancer 1 (HIC1) promotes lung cancer progression. <i>Cellular Signalling</i> , 2019 , 53, 162-169	4.9	3
56	Molecular mechanisms underlying eicosapentaenoic acid inhibition of HDAC1 and DNMT expression and activity in carcinoma cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194481	6	12

(2005-2020)

55	Opposite Roles of the JMJD1A Interaction Partners MDFI and MDFIC in Colorectal Cancer. <i>Scientific Reports</i> , 2020 , 10, 8710	4.9	6
54	The transcription factor Hypermethylated in Cancer 1 (Hic1) regulates neural crest migration via interaction with Wnt signaling. <i>Developmental Biology</i> , 2020 , 463, 169-181	3.1	O
53	Development and function of smooth muscle cells is modulated by in mouse testis. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	3
52	Hepatocellular Expression of SIRT1 and Its Effect on Hepatocellular Carcinoma Progression: A Future Therapeutic Perspective. <i>International Journal of Hepatology</i> , 2020 , 2020, 2374615	2.7	2
51	Association between Gene Promoter Methylation and Cervical Cancer Development: Global Distribution and A Meta-analysis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 450-459	4	4
50	Nkx2.5 Functions as a Conditional Tumor Suppressor Gene in Colorectal Cancer Cells Acting as a Transcriptional Coactivator in p53-Mediated p21 Expression. <i>Frontiers in Oncology</i> , 2021 , 11, 648045	5.3	1
49	A Computational and Biochemical Study of -1 Ribosomal Frameshifting in Human mRNAs.		
48	Phosphorylation of HIC1 (Hypermethylated in Cancer 1) Ser694 by ATM is essential for DNA repair. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 553, 51-57	3.4	3
47	Proline oxidase silencing inhibits p53-dependent apoptosis in MCF-7 breast cancer cells. <i>Amino Acids</i> , 2021 , 53, 1943-1956	3.5	1
46	Chemoresistance mechanisms in mouse models of glioblastoma. 2021 , 497-506		
45	Analysis of p53 Gene Alterations in Cancer: A Critical View. 2007 , 255-292		4
44	Hepatic Tumors in Childhood. 2004, 300-346		4
43	Epigenetics of colorectal cancer. <i>Methods in Molecular Biology</i> , 2015 , 1238, 405-24	1.4	16
42	CpG-island methylation in aging and cancer. <i>Current Topics in Microbiology and Immunology</i> , 2000 , 249, 101-18	3.3	215
41	Mapping the epigenomeimpact for toxicology. <i>Exs</i> , 2009 , 99, 259-88		13
40	Short telomeres on human chromosome 17p. <i>Nature Genetics</i> , 1998 , 18, 76-80	36.3	162
39	Epigenetic regulation of cell life and death decisions and deregulation in cancer. <i>Essays in Biochemistry</i> , 2010 , 48, 121-46	7.6	9
38	Aberrant gene silencing in tumor progression: implications for control of cancer. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2005 , 70, 427-33	3.9	41

37	HIC1 deletion promotes breast cancer progression by activating tumor cell/fibroblast crosstalk. <i>Journal of Clinical Investigation</i> , 2018 , 128, 5235-5250	15.9	32
36	A Novel BTB/POZ Transcriptional Repressor Protein Interacts With the Fanconi Anemia Group C Protein and PLZF. <i>Blood</i> , 1999 , 94, 3737-3747	2.2	8
35	A systematic analysis on DNA methylation and the expression of both mRNA and microRNA in bladder cancer. <i>PLoS ONE</i> , 2011 , 6, e28223	3.7	30
34	Chordoma characterization of significant changes of the DNA methylation pattern. <i>PLoS ONE</i> , 2013 , 8, e56609	3.7	27
33	HIC1 (hypermethylated in cancer 1) SUMOylation is dispensable for DNA repair but is essential for the apoptotic DNA damage response (DDR) to irreparable DNA double-strand breaks (DSBs). <i>Oncotarget</i> , 2017 , 8, 2916-2935	3.3	9
32	(Hypermethylated in Cancer 1) modulates the contractile activity of prostate stromal fibroblasts and directly regulates expression. <i>Oncotarget</i> , 2020 , 11, 4138-4154	3.3	1
31	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. <i>Oncotarget</i> , 2015 , 6, 19132-47	3.3	37
30	Epigenetic silencing of HIC1 promotes epithelial-mesenchymal transition and drives progression in esophageal squamous cell carcinoma. <i>Oncotarget</i> , 2015 , 6, 38151-65	3.3	17
29	Hypermethylated in cancer 1(HIC1) suppresses non-small cell lung cancer progression by targeting interleukin-6/Stat3 pathway. <i>Oncotarget</i> , 2016 , 7, 30350-64	3.3	15
28	DNA Methylation Profiles of MGMT, DAPK1, hMLH1, CDH1, SHP1, and HIC1 in B-Cell Lymphomas. <i>Korean Journal of Pathology</i> , 2009 , 43, 420		2
27	Aberrant promoter CpG methylation and its translational applications in breast cancer. <i>Chinese Journal of Cancer</i> , 2013 , 32, 12-20		33
26	FBXW11 contributes to stem-cell-like features and liver metastasis through regulating HIC1-mediated SIRT1 transcription in colorectal cancer. <i>Cell Death and Disease</i> , 2021 , 12, 930	9.8	2
25	p53 and Its Targets. 2002 , 77-96		
24	Chromosome 17.		
23	Role of DNA Methylation in Cancer Progression. 2008 , 79-93		
22	The Insulin-Like Growth Factor System in Adrenocortical Growth Control and Carcinogenesis. 2009 , 23	35-262	
21	Biomarkers of Hepatocellular Carcinoma. 2012 , 79-154		
20	Skin Cancer Prevention. 2014 , 321-376		

19	Hepatic Tumors in Childhood. 2014 , 547-614		1
18	The transcriptional repressor HIC1 regulates intestinal immune homeostasis.		O
17	HIC1 links retinoic acid signalling to group 3 innate lymphoid cell-dependent regulation of intestinal immunity and homeostasis.		
16	Skin Cancer Prevention. 2019 , 405-472		
15	Cell Cycle, Neurological Disorders, and Reactive Gliosis. 2006, 163-175		
14	Medulloblastoma, Primitive Neuroectodermal Tumors, and Pineal Tumors. 2008, 343-430		1
13	Molecular genetics of prostate cancer: clinical applications. <i>Journal of the National Medical Association</i> , 1998 , 90, S728-31	2.3	1
12	Association between HIC1 promoter methylation and solid tumor: A meta-analysis. <i>EXCLI Journal</i> , 2020 , 19, 476-489	2.4	1
11	Prx1 + and Hic1+ Mesenchymal Progenitors Are Present Within the Epidural Fat and Dura Mater and Participate in Dural Injury Repair Stem Cells Translational Medicine, 2022,	6.9	1
10	The promoter methylation drives down-regulation mode of HIC1 in gastric cancer, its molecular characteristics and downstream functional pathways <i>Gene</i> , 2022 , 824, 146380	3.8	O
9	Epigenetic Regulation in Cancer and Cancer Therapies.		
8	Myoneurin regulates BMP signaling by competing with Ppm1a for Smad binding. <i>IScience</i> , 2022 , 104495	6.1	
7	Tumor suppressor Hypermethylated in Cancer 1 represses expression of cell cycle regulator E2F7 in human primary cells.		
6	Characterization of EAminobutyric Acid Type A Receptor Associated Protein, a Novel Tumor Suppressor, Showing Reduced Expression in Breast Cancer. 2005 , 65, 394-400		20
5	Cellular taxonomy of Hic1+ mesenchymal progenitor derivatives in the limb: from embryo to adult. 2022 , 13,		O
4	Insights into Regulators of p53 Acetylation. 2022 , 11, 3825		2
3	MicroRNAs in doxorubicin-induced cardiotoxicity: The DNA damage response. 13,		O
2	COX-2/PGE2 upregulation contributes to the chromosome 17p-deleted lymphoma. 2023 , 12,		O

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