IAP proteins as targets for drug development in oncology

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Abstract: The inhibitors of apoptosis (IAPs) constitute a family of proteins involved in the regulation of various cellular processes, including cell death, immune and inflammatory responses, cell proliferation, cell differentiation, and cell motility. There is accumulating evidence supporting IAP-targeting in tumors: IAPs regulate various cellular processes that contribute to tumor development, such as cell death, cell proliferation, and cell migration; their expression is increased in a number of human tumor samples, and IAP overexpression has been correlated with tumor growth, and poor prognosis or low response to treatment; and IAP expression can be rapidly induced in response to chemotherapy or radiotherapy because of the presence of an internal ribosome entry site (IRES)-dependent mechanism of translation initiation, which could contribute to resistance to antitumor therapy. The development of IAP antagonists is an important challenge and was subject to intense research over the past decade. Six molecules are currently in clinical trials. This review focuses on the role of IAPs in tumors and the development of IAP-targeting molecules for anticancer therapy.

Keywords: Smac mimetics, apoptosis, antitumor therapy

Introduction: IAP family of proteins

The inhibitors of apoptosis (IAPs) constitute a family of proteins highly conserved throughout evolution. IAPs were initially discovered in baculoviruses two decades ago,¹ as potent inhibitors of apoptosis in infected insect cells. The first human homologous neuronal apoptosis inhibitory protein (NAIP) and cellular IAP 1 and 2 (cIAP1 and cIAP2) were characterized 2 years later,²,³ followed by X-chromosome linked IAP (XIAP),⁴,⁵ survivin,⁶ Apollon (also called BRUCE),⁷ melanoma IAP (ML-IAP) (also called Livin),⁸ and IAP-like protein 2 (ILP2).⁹ The IAP family is defined by the presence of one to three conserved protein motifs named a baculoviral IAP repeat (BIR). Most of them form a surface hydrophobic groove that specifically binds a conserved tetrapeptide motif, called IAP binding motif (IBM), found in the active subunits of apoptotic protease caspase-3, -7, and -9 and in cellular IAP antagonists, such as the second mitochondria-derived activator of caspases (Smac) (also named direct IAP-binding protein with low isoelectric point [DIABLO])¹⁰–¹³ and the high temperature requirement protein A2 (HtrA2)¹²,¹⁴ (Figure 1). The first BIR of XIAP and cIAPs does not bind IBM but rather, the signaling molecule transforming growth factor beta (TGFB)-activated kinase 1-binding protein 1 (TAB1)¹⁵ or the tumor necrosis factor (TNF) receptor (TNFR) associated factors (TRAFs),¹⁶–¹⁸ connecting XIAP and cIAPs with the TGF and TNF signaling pathways, respectively. In addition to the BIRs, cIAPs, XIAP, ML-IAP and ILP2 also possess a C-terminal RING (really interesting new gene)
Numerous partners of IAPs have been identified, including some caspases,\textsuperscript{22–24} some signaling molecules,\textsuperscript{25,26} some regulators of the NF-κB: nuclear factor of kappa-light polypeptide gene enhancer in B-cell activating pathways,\textsuperscript{27} some regulators of the actin cytoskeleton,\textsuperscript{27} and some transcriptional regulators.\textsuperscript{28,29} Thus, although they were initially characterized as inhibitors of apoptosis, IAPs display additional nonapoptotic functions in the regulation of cell proliferation, cell division, cell differentiation, cell motility, and in proinflammatory and immune response (for review,\textsuperscript{25,26}), which could contribute to oncogenesis.

Expression of IAPs in tumors

The expression of IAPs or cellular IAP antagonists such as Smac,\textsuperscript{11} HtrA2, or the septin-like mitochondrial protein, ARTS,\textsuperscript{30,31} were shown to be altered in a number of human tumor samples (Table 1). Overexpression of IAPs or downregulation of the cellular IAP antagonists have been correlated with advanced progressive disease, aggressiveness, and poor prognosis or low response to treatment (Supplementary Table S1). The alterations of IAP expression can be associated or not, with gene mutations. The baculoviral IAP repeat containing protein (BIRC)2 and BIRC3 genes, encoding cIAP1 and cIAP2, respectively, are located on chromosome 11q21–22, a region found amplified in human hepatocarcinoma,\textsuperscript{32} mammary carcinoma,\textsuperscript{33} medulloblastoma,\textsuperscript{34} and in pancreatic,\textsuperscript{35} cervical,\textsuperscript{36} lung,\textsuperscript{37} oral squamous cell,\textsuperscript{38} and esophageal\textsuperscript{39} carcinomas. Some (30%) mucosa-associated lymphoid tissue (MALT) lymphoma are associated with the chromosomal translocation t(11;18) (q21;q21) generating a chimeric protein composed of the N-terminal sequences of cIAP2 fused to the C-terminal sequence of MALT1.\textsuperscript{17,40} Conversely, IAPs can also display antitumoral properties in lymphocytes. The BIRC2 and/or
Table 1 Expression of IAPs and IAP antagonists in human tumors

<table>
<thead>
<tr>
<th>IAPs and cellular IAP antagonists</th>
<th>Tumors</th>
</tr>
</thead>
<tbody>
<tr>
<td>XIAP overexpression</td>
<td>Acute myeloid leukemia, B-cell chronic lymphocytic leukemia, bladder carcinoma, breast carcinoma, cervical carcinoma, colorectal cancer, hepatocarcinoma, melanoma, non-small cell lung cancer, ovarian cancer, prostate carcinoma, renal carcinoma, thyroid carcinoma</td>
</tr>
<tr>
<td>clAP1 and clAP2 overexpression (amplicon 11q21-22)</td>
<td>Cervical cancer, esophageal squamous cell carcinoma, hepatocarcinoma, medulloblastoma, non-small and small cell lung cancer, oral squamous cell carcinoma, pancreatic cancer, B-cell chronic lymphocytic leukemia, bladder carcinoma, cervical carcinoma, chronic lymphocytic leukemia, colorectal cancer, head and neck squamous cell carcinoma, non-small and small cell lung cancer, prostate carcinoma, squamous carcinoma of tongue</td>
</tr>
<tr>
<td>clAP1 overexpression</td>
<td>Breast cancer, cervical carcinoma, chronic lymphocytic leukemia, colorectal carcinoma, prostate carcinoma</td>
</tr>
<tr>
<td>independently from amplicon 11q21-22</td>
<td>GAstric cancer, melanoma, neuroblastoma, osteosarcoma, testicular cancer</td>
</tr>
<tr>
<td>clAP2 overexpression</td>
<td>MALT myeloma, Multiple myeloma</td>
</tr>
<tr>
<td>independently from amplicon 11q21-22</td>
<td>Acute myeloid leukemia, childhood acute lymphoblastic leukemia, bladder carcinoma, colorectal carcinoma, gastric cancer, melanoma, neuroblastoma, renal cell carcinoma, testicular cancer</td>
</tr>
<tr>
<td>clAP2/MALT chimeric protein t(11,18)(q21,q21)</td>
<td>MALT myeloma</td>
</tr>
<tr>
<td>clAP1/clAP2 inactivation</td>
<td>Multiple myeloma</td>
</tr>
<tr>
<td>ML-IAP overexpression</td>
<td>Acute myeloid leukemia, breast carcinoma, cervical carcinoma, chronic lymphocytic leukemia, colorectal carcinoma, endometrioid endometrial cancer, esophageal carcinoma, lung cancer, rectal adenocarcinoma</td>
</tr>
<tr>
<td>Smac downregulation</td>
<td>Bladder carcinoma, esophageal adenocarcinoma, endometrial cancer, ovarian cancer, prostate carcinoma, stomach cancer, thyroid cancer</td>
</tr>
<tr>
<td>Smac overexpression</td>
<td>Endometrial cancer, ovarian cancer, testicular cancer</td>
</tr>
<tr>
<td>HtrA2 overexpression</td>
<td>Acute myeloid leukemia</td>
</tr>
<tr>
<td>ARTS overexpression</td>
<td>Testicular cancer</td>
</tr>
<tr>
<td>ARTS downregulation</td>
<td>Acute myeloid leukemia</td>
</tr>
<tr>
<td>Ratio IAP/IAP antagonists:</td>
<td></td>
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<tr>
<td>Increased XIAP/Smac</td>
<td>Renal adenocarcinoma</td>
</tr>
<tr>
<td>Reduced XIAP/Smac</td>
<td>Gastric carcinoma</td>
</tr>
<tr>
<td>Increased clAP1/HtrA2 and clAP1/Smac</td>
<td>Chronic lymphocytic leukemia</td>
</tr>
</tbody>
</table>

Abbreviations: ARTS, seopt-like mitochondrial protein; clAP1, cellular IAP; HtrA2, high temperature requirement protein A2; IAPs, inhibitors of apoptosis; MALT, mucosa-associated lymphoid tissue; ML-IAP, melanoma IAP; Smac, second mitochondria-derived activator of caspases; XIAP, X-chromosome linked IAP.

BIRC3 genes were found to be mutated in some multiple myeloma samples, and the BIRC4 encoding XIAP in X-linked lymphoproliferative disease. The expression and functions of the atypical IAP survivin in tumors, and the development of specific survivin-targeted therapy were recently reviewed by Coumar et al and won’t be discussed here.

Role of IAPs in cancer

IAPs as apoptotic regulators

IAPs were first characterized as inhibitors of apoptosis because of their ability to bind caspases. Indeed, clAP1s, XIAP and ML-IAP can bind caspase-3, -7, and -9 via the BIRs and can induce their ubiquitination or neddylation via the RING domain. The influence of the ubiquitination is still not very well established, triggering degradative or nondegradative consequences, while the neddylation of caspase-7, by XIAP, inhibits its activity. In addition, XIAP is able to directly inhibit the enzymatic activity of caspases (Figure 1). The XIAP BIR3 binds the dimer interface of caspase-9, and the linker region upstream of BIR2 binds across the substrate binding pocket of caspase-3 and -7, which hinder substrate accessibility and hide the catalytic residue of caspases. The capacity of XIAP to inhibit caspase activity could account for the resistance of cancer cells to antitumor therapy. Indeed, DNA-damaging treatments, such as ionizing irradiations, induce a translational upregulation of XIAP as a consequence of the presence of an internal ribosome entry site (IRES)-dependent translation mechanism, which results in the resistance of carcinoma cells to radiation-induced apoptosis.

IAPs can also inhibit cell death at an earlier step, preventing the assembly of caspase-8- or -10-activating platforms. Caspase-8 and -10 are initiator caspases recruited...
by the adaptor FADD in multiprotein complexes, which provide the proximity required for caspase homodimerization and self-activation (for review). These molecular platforms are assembled either in response to the engagement of death receptor from the TNFR superfamily (in which case, these referred to as death-inducing signaling complex [DISC] and complex II or in response to genotoxic stress, tumor necrosis factor-like weak inducer of apoptosis (TWEAK) engagement, or toll-like receptor (TLR) 3 stimulation (in which case, they are referred to as Ripoptosome). Complex II and Ripoptosome share, in addition to the caspase and the adaptor FADD, the serine/threonine kinase receptor interacting protein (RIP) (Figure 2). cIAPs and XIAP are potent regulators of proteins from the RIP family, catalyzing the conjugation of ubiquitin chains that control either protein degradation or signal transduction pathways (Figure 2). In the absence of cIAPs, non-ubiquitinated RIP1 promotes (through its kinase

**Figure 2** Mechanisms of action of Smac mimetics. **Notes:** IAPs are important regulators of NF-κB-activating signaling pathways. Upon TNFα stimulation, cIAPs and RIP1 are recruited to TNFR1 via the adaptors TRADD and TRAF2. cIAPs trigger self-ubiquitination and ubiquitination of RIP1. These ubiquitin chains serve as a scaffold for the recruitment of IKK, TAK, and LUBAC. Once activated, IKK complex triggers phosphorylation of IκBα, which is then degraded by the UPS and releases NF-κB dimer, which promotes the transcription of target genes. In the noncanonical pathway of NF-κB activation, cIAPs promote the degradative ubiquitination of NIK and associated TRAF proteins and prevent the activation of the IKK complex required for transcription factor activation. On the other hand, cIAPs and XIAP prevent the assembly of RIP1-containing initiator caspase-activating complexes, named complex-II and Ripoptosome; and XIAP inhibits, through a direct interaction via BIR2 and BIR3, the activity of caspase-3, -7, and -9. SMs bind to the BIR domains of cIAPs and stimulate their E3-ubiquitine ligase activity. This results first, in the ubiquitination of RIP1, leading to the canonical NF-κB activation, and second, in the rapid autoubiquitination and subsequent proteasome-mediated degradation of cIAPs. Depletion of cIAPs releases NIK, resulting in the noncanonical activation of NF-κB, and NF-κB target gene expression, including TNFα, MCP-1, and IL-6. TNFα engages TNFR1 via an autocrine pathway. In the absence of cIAP1, stimulation of TNFR1 triggers the assembly of the secondary RIP1-containing cytoplasmic complex (complex II), leading to cell death. SM-mediated IAP depletion can also favor the formation of the Ripoptosome, leading to cell death.

**Abbreviations:** BIR, baculoviral IAP repeat; cIAP, cellular IAP; IκBα, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha; IAPs, inhibitors of apoptosis; IL, interleukin; IκB, IκB kinase complex; LUBAC, linear ubiquitin chain assembly complex; MCP-1, monocyte chemoattractant protein; NF-κB, nuclear factor kappa-light-chain-enhancer of activated B cells; NIK, NF-κB-inducing kinase; RIP1, receptor interacting protein 1; SM, Smac mimetic; Smac, second mitochondria-derived activator of caspases; TAK, TGFβ-activated kinase; TGFβ, transforming growth factor beta; TNF, tumor necrosis factor; TNFR1, tumor necrosis factor receptor 1; TRADD, TNFR1-associated death domain; TRAF, TNFR-associated factor; UBA, ubiquitin proteasome system; XIAP, X-chromosome linked IAP; TAB, TAK1-binding partners; HOIL, heme-oxidized IRF2 ligase-1; HOIP, HOIL-1-interaction protein; NEMO, nuclear factor-κB (NF-κB) essential modulator; UPS, ubiquitin-proteasome system.
activity) the assembly of the caspase-activating platforms that leads to cell death.56,62 (Figure 2). Thus, cIAPs inhibit RIP1-containing caspase-activating platform assembly, either by promoting the ubiquitin-proteasome-mediated degradation of the components of the Ripoptosome54 or by inducing a nondegradative ubiquitination of RIP1, which inhibits the cell death complex assembly and promotes survival-signaling pathway transduction.56,59,63

IAPs as cell-signaling regulators
The role of IAPs in the regulation of the NF-κB-activating signaling pathways is well documented (for review,25,26). NF-κB is a transcription factor induced by the stimulation of antigen or cytokine receptors, by the recognition of microbiological patterns by the TLRs, the nucleotide-binding oligomerization domain-containing proteins (NODs), or the NOD-like receptors (NLRs), or in response to intracellular injuries, such as DNA damage or reactive oxygen species. NF-κB contributes to the adaptive response of cells, by mediating the expression of the proinflammatory molecules that counter microbial invasion and by promoting the expression of genes involved in cell survival, cell differentiation, and cell proliferation.64 The transcription factor consists of heterodimers formed by one Rel subunit (RelA [also called p65], RelB, or c-Rel) and one NF-κB subunit (the p50 subunit of NF-κB1 or the p52 subunit of NF-κB2). In resting cells, the p50/RelA dimer is sequestered into the cytoplasm by the inhibitor of κB (IκB) proteins. Upon stimulation of the cell surface or intracellular receptors, or DNA damage, p50/RelA is released as a consequence of the degradation of NF-kappa-B inhibitor alpha (IκB-α) and translocated into the nucleus to stimulate proinflammatory gene transcription (Figure 2). Degradation of IκB-α requires its phosphorylation by the IκB kinase (IKK) complex, which is activated by ubiquitination by the linear ubiquitin chain assembly complex (LUBAC) and by phosphorylation by TGFβ-activated protein kinase 1 (TAK1)64 (Figure 2). cIAPs and XIAP promote the steric proximity of TAK1, LUBAC, and IKK complex. In the TNF-R1-signaling pathway, cIAPs are recruited along with RIP1 to the receptor61 and trigger self-ubiquitination and the nondegradative polyubiquitination of RIP156,57,66 (Figure 2), and in NOD2-mediated inflammatory signaling, XIAP and cIAPs mediate the conjugation of ubiquitin chains to RIP2.67-69 These ubiquitin chains serve as a scaffold for the recruitment and activation of the signaling complexes leading to IKK activation56,61,68,70 (Figure 2). cIAPs can also modulate NF-κB activation by catalyzing the monoubiquitination of the IKK component NF-κB essential modulator (NEMO), which is required for IKK activation,71,72 and XIAP promotes the activation of TAK1 and the steric proximity of TAK1 and IKK complex71 during TGFβ and myelin basic protein (MBP) receptor signaling, or in response to DNA damage.15,71,73-75

A second NF-κB-activating signaling pathway, named the noncanonical pathway, involves NF-κB-inducing kinase (NIK), which catalyzes the phosphorylation of IKKα. In turn, IKKα induces the phosphorylation of the p100 NF-κB2 precursor, leading to its proteolytic activation into active p52 NF-κB2 (Figure 2). cIAPs prevent the noncanonical activation of NF-κB by mediating the ubiquitination and the proteasomal-mediated degradation of NIK70,76-79 (Figure 2). Mutations in cIAP-encoding genes leading to NIK stabilization and chronic NF-κB activation could facilitate B cell malignancy and lymphomagenesis, as observed in some multiple myelomas that harbor mutations in the cIAP1- or cIAP2-encoding genes81 and as observed in MALT lymphoma that is associated with a chromosomal translocation t(11;18)(q21;q21), generating a chimeric protein composed of the N-terminal sequence of cIAP2 fused to the C-terminal sequence of MALT1.17,40,80

Cell proliferation and migration
IAPs are positive regulators of cell proliferation, a function correlated with the nuclear localization of the proteins.79,81 Interestingly, the nuclear expression of cIAP1 has been associated with advanced disease stages and poor patient prognosis in human cervical and esophageal squamous cell carcinomas and bladder cancers36,82,83 (Supplementary Table S1). The influence of IAPs on cell proliferation can be explained by their capacity to stimulate the activity of the c-Myc and E2F1 transcription factors, which are important regulators of cell cycle progression and cell proliferation with oncogenic properties.28,29 IAPs have also been involved in the regulation of the invasive properties of mammalian cancer cells, as recently reviewed.84

Targeting IAPs in cancer therapy
Targeting IAPs in tumors is an important challenge and several strategies have been explored, including the use of antisense oligonucleotides and antagonist molecules. A synthetic antisense oligonucleotide to XIAP, named AEG35156, was developed by Aegera Therapeutics Inc (Montreal, QC, Canada).85 It demonstrated promising efficiency in the preclinical studies. It induced a decrease of XIAP expression in tumor cell lines and tumor xenograft models, and sensitized cells to various standard chemotherapeutic agents and Tumor Necrosis Factor-Related Apoptosis-Inducing Ligand
TRAIL) receptor agonists. AEG35156 entered into clinical trials (http://www.clinicaltrials.gov) in 2005, and to date, ten Phase 1, 2, or 1/2 clinical trials have been completed in solid tumors and in acute myeloid leukemia (AML) (Table 2) (for review). In the trials, AEG35156 appeared to accumulate in the liver and to have efficiently downregulated XIAP messenger ribonucleic acid (mRNA) in peripheral blood mononuclear cells and hepatocytes. AEG35156 is generally well tolerated except when administered in repeated high doses. Promising results were obtained with AEG35156 used as a single agent in solid tumors and in combination with cytarabine and idarubicin in AML in the Phase 1 studies, but it failed to show any significant antitumoral activity in the randomized Phase 2 studies in pancreatic adenocarcinoma, when combined with Gemcitabine, or in AML, when it was given in combination with cytarabine and idarubicin.

The structural characterization of the interaction of XIAP with caspases, or with Smac, or the drosophila Smac homologs has provided very potent tools for the design of synthetic IAP antagonists aiming to inhibit the capacity of XIAP with caspases, or with Smac, or the drosophila Smac motif of Smac inserts into the XIAP BIR2 and BIR3-caspase interaction pocket and abrogates XIAP-mediated caspase inhibition (Figure 1). The Smac N-terminal peptide was also derived to produce cell permeable peptides and was shown to mimic the activity of Smac and to sensitize human cancer cell lines to diverse chemotherapeutic agents, including etoposide, teniposide, cisplatin, paclitaxel, 7-ethyl-10-hydroxycamptothecin (SN-38), and TRAIL agonists. In xenograft models, a Smac-derived peptide, made permeable by linking to the shuttle peptide trans-activation of transcription (TAT) from HIV, enhanced the antitumoral effect of TRAIL in glioma, and a polyarginine-conjugated Smac peptide was shown to sensitize non-small cell lung carcinoma cells to cisplatin, with little toxicity to normal tissues. The pharmacological

Table 2 AEG35156 XIAP antisense oligonucleotide in clinical trials (http://www.clinicaltrials.gov)

<table>
<thead>
<tr>
<th>Phase</th>
<th>Drug combination</th>
<th>Start date</th>
<th>Condition</th>
<th>Observations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phase 1</td>
<td>Docetaxel</td>
<td>07/2006</td>
<td>Adult solid tumor</td>
<td>Generally well tolerated</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Cytarabine and idarubicin</td>
<td>08/2006</td>
<td>Refractory or relapsed acute myeloid leukemia (24 patients)</td>
<td>Toxicity included two cases of neuropathy in patients having received multiple AEG35316 doses</td>
</tr>
<tr>
<td>Phase 1</td>
<td>Docetaxel</td>
<td>09/2006</td>
<td>Adult solid tumor</td>
<td>Well tolerated</td>
</tr>
<tr>
<td>Phase 1</td>
<td>Single agent</td>
<td>10/2006</td>
<td>Advanced cancer (22 patients)</td>
<td>Evidence of efficiency (decreased XIAP mRNA in peripheral blood mononuclear cells)</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Gemcitabine</td>
<td>11/2007</td>
<td>Metastatic pancreatic adenocarcinoma (14 patients)</td>
<td>Clinical evidence of antitumoral activity</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Paclitaxel</td>
<td>11/2007</td>
<td>Mammary carcinoma</td>
<td>Toxicities include neutropenia, thrombocytopenia, peripheral neuropathy, fatigue, ascites, and nausea/vomiting</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Carboplatin and paclitaxel</td>
<td>11/2007</td>
<td>Non-small cell lung carcinoma</td>
<td>Faced to show significant antitumoral activity</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Single agent</td>
<td>10/2008</td>
<td>Refractory chronic lymphocytic leukemia and indolent B-cell lymphomas</td>
<td>Well tolerated</td>
</tr>
<tr>
<td>Phase 1/2</td>
<td>Sorafenib</td>
<td>04/2009</td>
<td>Advanced hepatocellular carcinoma</td>
<td>Did not improve rates of remission</td>
</tr>
<tr>
<td>Phase 2</td>
<td>Cytarabine and idarubicin</td>
<td>11/2009</td>
<td>Refractory or relapsed acute myeloid leukemia (27 patients)</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: RNA, ribonucleic acid; XIAP, X-chromosome linked IAP; IAPs, inhibitors of apoptosis; mRNA, messenger RNA.
properties of such Smac-derived peptides were not good enough to merit consideration of these molecules as therapeutic agents; however, they provided the bases for the structure-based design of IAP antagonists named Smac mimetics (SMs). Several approaches were used, including the screening of peptide or peptidomimetic libraries, and the structure-based design of conformationally constrained SMs (Figure 3). Considerable efforts were invested to improve the affinity of the compounds to the IAP BIR domains, to improve their ability to antagonize IAPs, to improve cellular delivery and activity (i.e., their capacity to induce apoptosis or to sensitize to apoptotic agents), and to improve their in vivo stability and bioavailability. The preclinical assays demonstrated their capacity to inhibit tumor growth in multiple solid tumors, acute lymphoblastic leukemia (ALL), and multiple myeloma xenograft models and to sensitize cells to TRAIL, proteasome inhibitors, B-cell lymphoma protein 2 (Bcl-2) family-targeting compounds, and more conventional therapeutic agents, such as radiation, melphalan, or cisplatin. Importantly, these compounds were well tolerated by animals and did not display toxicity against normal lymphocytes and bone marrow stromal cells or normal mammary epithelial cells. The analysis of binding affinity revealed that similarly to Smac, SMs can bind to XIAP-BIR2, preventing XIAP-caspase-7 and -3 binding, and to XIAP-BIR3, abrogating the XIAP-mediated inhibition of caspase-9. Structural and biochemical studies of the apoptotic activity of Smac cellular protein revealed, first, that it forms a symmetric dimer, second, that
<table>
<thead>
<tr>
<th>Compound</th>
<th>Structure</th>
<th>Preclinical assays in animals</th>
<th>Clinical trial</th>
<th>Conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>AT-406 (SM-406 – Debio 1143)</td>
<td>Monovalent</td>
<td>• Inhibited tumor growth and sensitized cells to carboplatin in ovarian cancer xenograft model[119]</td>
<td>Phase 1</td>
<td>Advanced solid tumors and lymphoma</td>
</tr>
<tr>
<td>Ascenta therapeutics/debiopharm SA</td>
<td></td>
<td>• Inhibited tumor growth in breast tumor xenograft model with no sign of toxicity[20]</td>
<td>Phase 1</td>
<td>Combination with daunorubicin and cytarabine in patients with poor-risk acute myelogenous leukemia</td>
</tr>
<tr>
<td>Birinapant (TL-32711) TetraLogic pharmaceuticals</td>
<td>Bivalent</td>
<td>• Tumor growth arrest or inhibition in patient-derived primary pancreatic cancer explant model[199]</td>
<td>Phase 1</td>
<td>Refractory solid tumors or lymphoma</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Remission in acute lymphoblastic leukemia xenograft models[200]</td>
<td></td>
<td>➔ Well tolerated with no dose limiting toxicities, potent and sustained target inhibition, apoptotic pathway activation in tumor and antitumoral activity in colon cancer and melanoma[203]</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Delayed the tumor growth and increases survival in combination with ionizing radiation in a glioblastoma multiform model in mice[201]</td>
<td>Phase 1/2</td>
<td>Combination chemotherapy (doxorubicin, paclitaxel, carboplatin, gemcitabine, irinotecan, docetaxel) in advanced and metastatic solid tumors</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Inhibited tumor growth in combination with the immunomodulatory agents IFNα or GM-CSF in a kidney carcinoma xenograft model[202]</td>
<td>Phase 1/2</td>
<td>Acute myelogenous leukemia, myelodysplastic syndrome and acute lymphoblastic leukemia</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Inhibited tumor growth in breast cancer xenograft without affecting normal mammary epithelial cells[204]</td>
<td>Phase 1</td>
<td>Combination with gemcitabine in patients with advanced solid tumor</td>
</tr>
<tr>
<td>GDC-0917 Genentech</td>
<td>Monovalent</td>
<td>• Inhibits tumor growth in breast cancer xenograft without affecting normal mammary epithelial cells[204]</td>
<td>Phase 1</td>
<td>Refractory solid tumors or lymphoma</td>
</tr>
<tr>
<td>GDC-0152 Genentech</td>
<td>Monovalent</td>
<td>• Induces an increased systemic level of cytokines and chemokines (TNFα and MCP-1), a systemic inflammatory response and hepatic injury when IV administered in dogs;[205] such effects were not observed in human[13]</td>
<td>Phase 1</td>
<td>Locally advanced or metastatic solid malignancies, or non-Hodgkin’s lymphoma without leukemic phase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>➔ Well tolerated, no signs of a systemic inflammatory response</td>
<td></td>
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<tr>
<td>HGS1029 (AEG-40826) Human Genome Sciences LCL161 Novartis pharmaceuticals</td>
<td>Bivalent</td>
<td>• Delays tumor growth in multiple solid tumor xenograft models as a single agent but is ineffective in acute lymphoblastic leukemia xenograft models[108]</td>
<td>Phase 1</td>
<td>Advanced solid tumors and refractory lymphoid malignancies</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Antitumor activity in combination with chemotherapy against a range of solid tumors including primary models of breast cancer (Novartis website)[9]</td>
<td>Phase 1</td>
<td>Relapsed or refractory lymphoid malignancies</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Inhibits tumor growth in combination with a Bcl-2 inhibitor in hepatocellular carcinoma xenograft models[10]</td>
<td>Phase 1</td>
<td>Solid tumors</td>
</tr>
<tr>
<td></td>
<td></td>
<td>➔ Well tolerated[15]</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>• Inhibits tumor growth and prolongs survival in combination with adenovirus bacteriophage-TNFα in melanoma xenograft models[11]</td>
<td>Phase 2</td>
<td>Combination with weekly paclitaxel in patients with advanced solid tumor</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Inhibits tumor growth in combination with the immunomodulatory agents IFNα or GM-CSF in a kidney carcinoma xenograft model[202]</td>
<td>Phase 1</td>
<td>Combination with weekly paclitaxel in patients with breast cancer</td>
</tr>
</tbody>
</table>


Abbreviations: GM-CSF, granulocyte-macrophage colony-stimulating factor; IFN, interferon; IV, intravenous; TNF, tumor necrosis factor; MCP-1, monocyte chemoattractant protein; Smac, second mitochondria-derived activator of caspases; SMs, Smac mimetics; Bcl-2, B-cell lymphoma 2.
dimerization is essential for Smac function, and third, that the capacity of Smac to abrogate XIAP-mediated caspase inhibition required the binding to both BIR2 and BIR3. Overall, these observations support the conclusion that compounds targeting both BIR domains could be more efficient as XIAP antagonists and lead to the development of bivalent small molecules containing two Smac AVPI IBM motif mimetics. As expected, these compounds appeared to be more potent than their monovalent counterparts, in antagonizing XIAP and in activating caspases. Like the monovalent versions, the bivalent molecules either inhibited tumor growth or sensitized cells to both conventional and nonconventional anticancer therapies in the preclinical assays and did not display toxicity to normal human primary cells, however, unlike the monovalent molecules, the bivalent SMs are not orally bioavailable. To date, more than 50 applications for patents related to IAP antagonists have been filed (for review, and six SMs have entered human clinical trials (http://www.clinicaltrials.gov/) for the treatment of cancer (described in Table 3).

Mechanisms of action of SMs

As expected, SMs abrogate XIAP-mediated caspase inhibition and therefore increase caspase-3 and -7 activities (Figure 1). However, in addition to binding XIAP BIRs, SMs also bind the BIR domains of ML-IAP, cIAP1 and cIAP2. SMs stimulate the E3-ubiquitine ligase activity of cIAPS, which results in the ubiquitination of RIP1, leading in turn, to canonical NF-κB activation and the rapid autoubiquitination and subsequent proteasome-mediated degradation of cIAPs (Figure 2). Depletion of cIAPs abolishes the cIAP-mediated ubiquitination and degradation of NIK and induces canonical activation of NF-κB. In turn, NF-κB induces the expression of proinflammatory cytokines and chemokines, including TNFα, which can trigger cell death by an autocrine pathway. Furthermore, depletion of cIAPs favors the assembly of the RIP1-containing cytoplasmic cell death complexes, such as complex II and Ripoptosome, resulting in cell death in some sensitive cancer cells, or in the sensitization to TNFα or DNA-damaging chemotherapeutic agents. SMs exert their activity through XIAP and cIAPs and both effects are required for their maximal antitumoral activity. Indeed, IAP antagonists displaying a high and selective affinity for cIAPs over XIAP appeared less potent than pan-IAP antagonists in promoting cancer cell death and in sensitizing cancer cells to TRAIL.

As a consequence of cIAP degradation and NF-κB activation, the administration of SMs such as LCL161, GDC-0152, and HGS1029, resulted in the upregulation of cytokines and chemokines, including TNFα, monocyte chemoattractant protein (MCP)-1, interleukin (IL)-7, IL-6, and interferon (IFN)γ. MCP-1 was used as a clinical biomarker for SMs efficiency in clinical programs. The analysis of the proinflammatory characteristics of cellular Smac-induced cell death suggests that the proinflammatory response elicited by SMs could activate the adaptive antitumor immune response in cancers. In dogs, intravenous (IV) administration of GDC-0152 induced an acute systemic inflammatory response with lung and hepatic injury, which are consistent with TNF-α mediated toxicity, however, a similar TNF-α-driven inflammatory response was not observed in humans. Although the first clinical trials did not reveal extensive toxicity of SMs when orally or intravenously administered, additional analysis of the consequences of cytokine and chemokine secretion are required. Because osteoclast differentiation and function are stimulated by activation of the noncanonical NF-κB pathway and because osteoclasts are susceptible to TNF-α, it will be interesting to target specific IAP functions in osteoporosis and specifically enhanced metastasis in bone.

Conclusion

SMs are a very promising new class of anticancer therapeutics. Results from preclinical studies have demonstrated an acceptable safety profile and some signs of antitumoral activity, in their use as a single agent or in combination with conventional or nonconventional therapies, such as dead receptor agonists, Bcl-2, or kinase-targeting therapies. The first clinical trials demonstrated a good tolerance and target inhibition. Ongoing and future clinical trials will determine the safety, appropriate indications, and drugs combinations. It will be important to determine the level and the site of production of TNFα and other cytokines and the consequences of cytokine production for tumoral and non-tumoral cells. Since IAPs are involved in the regulation of various cellular functions, it will be interesting to target specific IAP functions in order to limit possible adverse impacts. The consequences of SMs on the immune system in vivo and the use of cIAPs as potential therapeutic targets for inflammatory or immune disorders are still important questions that need to be addressed.
Acknowledgments

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Disclosure

The authors report no conflicts of interest in this work.

References


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Table S1 Role of IAPs in cancer

<table>
<thead>
<tr>
<th>Cohort</th>
<th>Observations</th>
</tr>
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</table>
| XIAP overexpression | AML 92
t 78eviewer 12
Correlated with poor cytogenetics
Inversely correlated with overall survival
Correlated with sensitivity to anticancer drugs (cytarabine)
Bladder carcinoma 176
Independent prognostic factor for early recurrence of invasive cancers
Associated with poor clinical outcome
Breast carcinoma 102
Nuclear expression
Cervical carcinoma 77
Independent negative prognostic factor for overall survival
Colorectal cancer 96
cytoplasmic expression
Independent negative prognostic factor
Correlated with tumor dedifferentiation, invasion, stage, and lower disease-free and overall survival
38
Correlated with resistance to irradiation
Hepatocellular carcinoma 69
Associated with shorter survival and increased risk of relapse and metastasis
Melanoma 55
cytoplasmic expression
Mainly expressed in the cytoplasm
NSCLC 144
Correlated with tumor grade and advanced tumor stage
55
No correlation with chemotherapy or radiotherapy
Ovarian cancer 226
Deregulation of XIAP occurs early in the pathogenesis of prostate cancer
Prostate carcinoma 226, 69
Deregulation of XIAP occurs early in the pathogenesis of prostate cancer
Renal carcinoma 145
Independent negative prognostic factor
66
Correlated with tumor grade and advanced tumor stage
NSCLC and SCLC 55
Cytoplasmic expression
No correlation with chemotherapy or radiotherapy
Pancreatic cancer 22, 28
Inversely correlated with patient survival

clIAP1 and clIAP2 overexpression associated with amplicon 11q21-22
Cervical cancer 70
Nuclear expression correlated with low overall survival
ESC 42
Correlated with resistance to cisplatin/camptothecin
Hepatocarcinoma 25
Mammary carcinoma 25
Medulloblastoma 17
NSCLC and SCLC 25
55
cytoplasmic expression
No correlation with chemotherapy or radiotherapy

clIAP1 overexpression independent from 11q21-22 amplicon
AML 22, 30
B-cell CLL 22, 30
Bladder cancer 102
Cervical carcinoma 70
Nuclear expression
Associated with resistance to several anticancer drugs
Correlated with resistance to irradiation
No correlation with fludarabine sensitivity
Nuclear expression correlated with proliferation index (Ki-67), tumor stage, and grade
Correlated with the resistance to irradiation
Inversely correlated with overall survival and recurrence-free survival
Inversely correlated with overall survival and recurrence-free survival
Correlated with advanced tumor stage

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<table>
<thead>
<tr>
<th>Table S1 (Continued)</th>
<th>Cohort</th>
<th>Observations</th>
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<tbody>
<tr>
<td>HNSCC</td>
<td>55&lt;sup&gt;54&lt;/sup&gt;</td>
<td>Nuclear expression correlated with metastasis, advanced stage, and poor patient prognosis</td>
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<tr>
<td>NSCLC and SCLC</td>
<td>55&lt;sup&gt;54&lt;/sup&gt;</td>
<td>Nuclear expression</td>
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<tr>
<td></td>
<td></td>
<td>No correlation with chemotherapy or radiotherapy</td>
</tr>
<tr>
<td>Prostate carcinoma</td>
<td>691&lt;sup&gt;17&lt;/sup&gt;</td>
<td>Inversely correlated with refractory disease</td>
</tr>
<tr>
<td>Squamous carcinoma</td>
<td>75&lt;sup&gt;75&lt;/sup&gt;</td>
<td>Nuclear and cytoplasmic expression</td>
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<tr>
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<td>Correlated with metastasis</td>
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<td>cIAP1/cIAP2 inactivation</td>
<td>Multiple myeloma 155&lt;sup&gt;56,57&lt;/sup&gt;</td>
<td>Correlated with a better response to treatment (cladribine, cyclophosphamide, fludarabine)</td>
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<tr>
<td>c-IAP1/ HtrA2</td>
<td>CLL 100&lt;sup&gt;3&lt;/sup&gt;</td>
<td>Correlated with tumor stage and with refractory disease</td>
</tr>
<tr>
<td>c-IAP1/Smac DIABLO</td>
<td>CLL 100&lt;sup&gt;3&lt;/sup&gt;</td>
<td>Associated with progressive disease</td>
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<td>Cytoplasmic expression</td>
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<td></td>
<td></td>
<td>No correlation with fludarabine sensitivity</td>
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<td>Colorectal cancer 46&lt;sup&gt;73&lt;/sup&gt;</td>
<td>Cytoplasmic expression</td>
</tr>
<tr>
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<td>Prostate carcinoma 691&lt;sup&gt;17&lt;/sup&gt;</td>
<td>Deregulation of c-IAP2 occurs early in the pathogenesis of prostate cancer</td>
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<td>Correlated with tumor stage and with refractory disease</td>
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<tr>
<td>c-IAP2/MALT chimeric protein t(11q21)</td>
<td>Breast cancer 144&lt;sup&gt;38&lt;/sup&gt;</td>
<td>Inversely correlated with overall survival</td>
</tr>
<tr>
<td></td>
<td>Cervical carcinoma 77&lt;sup&gt;7&lt;/sup&gt;</td>
<td>Inverse correlation with relapse-free survival and overall survival</td>
</tr>
<tr>
<td></td>
<td>CLL 100&lt;sup&gt;3&lt;/sup&gt;</td>
<td>Associated with progressive disease</td>
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<td>Cytoplasmic expression</td>
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<td>No correlation with fludarabine sensitivity</td>
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<td></td>
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<td>Deregulation of c-IAP2 occurs early in the pathogenesis of prostate cancer</td>
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<tr>
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<td>Correlated with tumor stage and with refractory disease</td>
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<td>ML-IAP overexpression</td>
<td>AML 34&lt;sup&gt;41&lt;/sup&gt;</td>
<td>Inversely correlated with overall survival</td>
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<td>Adults ALL 34&lt;sup&gt;41&lt;/sup&gt;</td>
<td>Inverse correlation with relapse-free survival and overall survival</td>
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<td></td>
<td>Childhood ALL 222&lt;sup&gt;42&lt;/sup&gt;</td>
<td>Correlated with relapse-free survival</td>
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<td>Bladder cancer 30&lt;sup&gt;43&lt;/sup&gt;</td>
<td>Correlated with relapse-free survival</td>
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<tr>
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<td>Colorectal cancer 8&lt;sup&gt;31&lt;/sup&gt;</td>
<td>Correlated with resistance to etoposide, vincristine, 5-fluorouracil&lt;sup&gt;44&lt;/sup&gt;</td>
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<td>Gastric cancer 40&lt;sup&gt;35&lt;/sup&gt;</td>
<td>Correlated with metastasis and dedifferentiation</td>
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<td>Melanoma 27&lt;sup&gt;36&lt;/sup&gt;</td>
<td>Resistance to etoposide</td>
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<td>Neuroblastoma 68&lt;sup&gt;37&lt;/sup&gt;</td>
<td>Associated with MYCN amplification → inversely correlated with patient survival</td>
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<td>Osteosarcoma 29&lt;sup&gt;40&lt;/sup&gt;</td>
<td>Nuclear expression: inverse correlation with overall survival</td>
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<td>Renal cell carcinoma 152&lt;sup&gt;44&lt;/sup&gt;,192&lt;sup&gt;40&lt;/sup&gt;</td>
<td>Nuclear expression&lt;sup&gt;30&lt;/sup&gt;</td>
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<td>204&lt;sup&gt;39&lt;/sup&gt;</td>
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<tr>
<td></td>
<td>Testicular cancer 131&lt;sup&gt;51&lt;/sup&gt;</td>
<td>Correlated with dedifferentiation</td>
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<tr>
<td>Smac downregulation</td>
<td>AML 71&lt;sup&gt;12&lt;/sup&gt;</td>
<td>Correlated with response to chemotherapy</td>
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<td>Bladder cancer 173&lt;sup&gt;53&lt;/sup&gt;</td>
<td>Inversely correlated with advanced tumor stage and tumor grade (serum)</td>
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<td>Breast cancer 62&lt;sup&gt;34&lt;/sup&gt;</td>
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<td>CLL 100&lt;sup&gt;3&lt;/sup&gt;</td>
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<td>Colorectal carcinoma 121&lt;sup&gt;56&lt;/sup&gt;</td>
<td>Inversely correlated with metastasis and advanced tumor stage</td>
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<td>Endometrioid 76&lt;sup&gt;67&lt;/sup&gt;</td>
<td>Inversely correlated with tumor grade and correlated with longer disease-specific survival</td>
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<td>Smac overexpression</td>
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<td>Bladder cancer 75&lt;sup&gt;50&lt;/sup&gt;</td>
<td>Correlated with postoperative recurrence-free period</td>
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<td>Gastric adenocarcinoma 46&lt;sup&gt;41&lt;/sup&gt;</td>
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<td>Renal carcinoma 66&lt;sup&gt;19&lt;/sup&gt;,85&lt;sup&gt;42&lt;/sup&gt;</td>
<td>Correlated with advanced tumor stage</td>
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<tr>
<td>XIAP/ Smac</td>
<td>Gastric adenocarcinoma 46&lt;sup&gt;41&lt;/sup&gt;</td>
<td>Low XIAP/ Smac ratio</td>
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<td>Renal carcinoma 66&lt;sup&gt;19&lt;/sup&gt;</td>
<td>High XIAP/ Smac ratio is correlated with advanced tumor stage</td>
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Table S1 (Continued)

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<td>Nuclear HtrA2 expression is elevated in poorly differentiated lymph node metastatic cancer</td>
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<td>Correlated with recurrence-free and tumor-specific survival</td>
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<td>Correlation with tumor grade and early-stage disease</td>
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<td>ARTS overexpression</td>
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<td>Resistance to S-azacytidine</td>
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<td>Astrocytoma</td>
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<td>Correlation with tumor grade and higher rate of apoptosis</td>
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**References**


