# Expert Opinion

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# Targeting the IGF1 axis in cancer proliferation

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The IGF network of ligands, cell-surface receptors and IGF-binding proteins has important roles at multiple levels, including the cellular, organ and organism levels. The IGF system mediates growth, differentiation and developmental processes, and is also involved in various metabolic activities. Dysregulation of IGF system expression and action is linked to diverse pathologies, ranging from growth deficits to cancer development. Targeting of the IGF axis emerged in recent years as a promising therapeutic approach in conditions in which the IGF system is involved. Specific IGF1 receptor (IGF1R) targeting, in particular, produced the best experimental and clinical results so far, and generated significant optimism in the field. This review provides a basic analysis of the role of the IGF1R in cancer biology and explores the functional interactions between the IGF signaling pathways and various cancer genes (e.g., oncogenes, tumor suppressors). In addition, we review a number of specific malignancies in which the IGF system is involved and summarize recent data on preclinical and clinical studies employing IGF1R-targeted modalities.

Keywords: IGF-1 receptor (IGF1R), insulin-like growth factors (IGF), monoclonal antibodies, targeted therapy, tyrosine kinase inhibitors

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### 1. The IGF system of ligands, receptors and binding proteins

The IGFs are a system of secreted hormones, cell-surface receptors and binding proteins that control normal growth and differentiation of most organs [1,2]. The IGFs are active at most stages of the life cycle, including the fetal period, infancy and adulthood. In addition, the IGF status of the organism (i.e., circulating hormone levels, tissue receptor activation, interactions with other signaling pathways, etc) affects critical aspects of the aging process and, hence, seems to have a marked effect on longevity [3]. Unlike most other growth factor systems, the IGF axis displays biological activities at both the cell and organism levels. At the cellular level, IGFs function as cell progression factors, 'pushing' the cell through the various phases of the cell cycle. At the organism level, IGFs participate in the control of multiple systems, including neuronal activity, kidney function, reproduction, etc. The IGF network is also involved in a wide range of pathological processes, such as diabetes and cancer [4-7]. In the specific context of cancer, the IGF axis emerged in recent years as a promising candidate for targeted therapies [8-10]. The aim of this review is i) to provide a brief analysis of the role of the IGF system in the biology of cancer; and ii) to review the current status of ongoing efforts to target the IGF axis for therapeutic purposes.

The IGF system consists of two ligands (IGF1 and IGF2), two receptors [IGF1R and IGF2/mannose 6-phosphate receptor (M6P-R)], and at least six IGF-binding proteins (IGFBPs) [11]. The IGF network includes, in addition, a series of IGFBP-related proteins and IGFBP proteases. The existence of the IGFs was postulated in the late 1950's, following the seminal observation by Salmon

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- 55 and Daughaday that growth hormone (GH) stimulated the incorporation of sulfate into cartilage in an indirect fashion, which involved activation of a specific serum factor [12]. The factor that was originally termed 'sulfation factor' and then 'somatomedin' is now accepted as IGF1. Circulating IGF1 60
- levels are mostly dependent on liver output, a process that is tightly regulated by GH. Both IGF1 and IGF2 activate a common cell-surface receptor, the IGF1R, which signals mitogenic, antiapoptotic and transforming activities [13,14]. The IGF1R is coupled to several intracellular second mes-65 senger pathways, including the ras-raf-MAPK and PI3K-PKB/Akt signaling cascades (Figure 1). IGF1R is vital for
- cell survival, as illustrated by the lethal phenotype of mice in which the IGF1R gene was disrupted by homologous recombination. The IGF2/M6P-R, on the other hand, is 70 apparently not involved in IGF signaling but is mainly responsible for targeting the highly mitogenic IGF2 for lysosomal degradation. In this respect, the IGF2/M6P-R functions as a tumor suppressor by protecting the organism from pervasive IGF2-induced IGF1R activation [15]. Importantly,
- 75 significant portions of the proliferative activities of IGF2 have been shown to be mediated by a particular isoform of the insulin receptor (InsR), termed InsR-A.
- Unlike insulin, which circulates in serum unbound, IGF1 and IGF2 are carried in serum and other body fluids (e.g., 80 cerebrospinal fluid, saliva, etc) by a family of IGFBPs [16,17]. In the serum, the majority of circulating IGFs are found in a ternary complex with IGFBP3 and an acid-labile subunit. This complex modulates IGF action by protecting the growth factors from proteolysis, thus prolonging their half-lives in 85 the circulation. The release of the IGFs from the IGFBPs involves IGFBPs protease action. The ratio between free and bound IGFs in serum is of major importance in terms of proliferation and mitogenic potential. Finally, some IGFBPs exert their biological effects in an IGF-independent manner, suggesting the existence of IGFBP receptors [18].

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### Similarities and differences between the IGF1 and insulin signaling pathways

- 95 The structural and functional similarities between insulin and IGF1 suggest that both molecules are derived from a common ancestral precursor that probably participated in food intake and nutritional regulation. A divergence of functions most probably occurred before the appearance of the 100 first vertebrates, with insulin mostly active in the regulation of metabolism and IGF1 in growth processes. However, in view of their common evolutionary origins and conserved architecture there is a certain degree of cross-talk between insulin, IGFs and their receptors [19]. Specifically, insulin 105 may interact with IGF1R with low affinity, thus mediating growth type of activities, whereas IGFs may stimulate metabolic activities via interaction with the InsR. The complexity of these interactions is further illustrated by the important 109
  - role of InsR-A in mediating the mitogenic actions of IGF2.

The specificity of insulin and IGF1 physiological activities, 110 despite marked structural similarities at both ligand and receptor levels, has been the topic of controversial research. In addition, the fact that the vast majority of the signaling modules downstream of IGF1R, InsR (A and B isoforms) and IGF1R-InsR hybrid receptors (composed of an IGF1R hemi- 115 receptor linked to an InsR hemireceptor) are shared by all of them raises the question as to how these receptors are able to engage in basically different biological activities. A number of potential mechanisms were postulated to explain this paradox, including a different tissue distribution of IGF1R and 120 InsR [20], different internalization kinetics and subcellular distribution of the hormone-receptor complex [21], and different hormone-receptor affinities [22]. Furthermore, various substrates and signaling mediators that are preferentially activated by insulin or IGF1 have been identified. For example, the 125 adapter protein Grb10 associates with InsR but not with IGF1R [23]. Differential activation of this and other substrates may partially explain the specificity of the receptors. Finally, and as mentioned above, the fact that IGF1, but not insulin, is carried in the circulation and extracellular fluids by IGFBPs 130 further contributes to the divergent actions of the ligands.

### 3. The involvement of the IGF1 axis in cancer development

A number of mechanisms have been proposed to rationalize the possible role/s of the IGF system in the initiation and/or progression of neoplasia [24,25]. Although IGF1 was shown to increase chromosomal fragility under experimental conditions, it is usually considered to be nongenotoxic [26]. A widely 140 accepted model of IGF1 action in cancer cells postulates that, while unable to induce oncogenic transformation by itself, once a malignant transformation has already occurred, cell survival of transformed cells depends on IGF1 action. The disruption of internal checks and control mechanisms associated with the 145 neoplastic phenotype is further emphasized by the finding that IGF1 action can override the cellular signals of apoptosis [13].

Unlike the IGF1 gene, overexpression of the IGF2 gene has been linked to the etiology of a number of overgrowth syndromes (e.g., Beckwith-Wiedemann Syndrome) and neo- 150 plasias (e.g., Wilms' tumor, rhabdomyosarcoma) [27]. The IGF2 gene is an imprinted one (i.e., it is only expressed from the paternal allele). Overexpression of IGF2 in cancer may be caused by a number of genetic events, including gene duplication, loss of heterozygosity, and loss of imprinting, leading to 155 biallelic IGF2 expression [28]. Furthermore, and in agreement with its cell survival role, the initial proliferative switch in oncogene-induced transformation was correlated with focal activation of IGF2 [29]. Transfection with an antisense oligonucleotide to the IGF2 mRNA interfered with tumor 160 cell proliferation in vitro, and transgenic mice homozygous for a disruption of the IGF2 gene developed tumors with reduced malignancy. Combined, these results suggest that IGF2 signaling is necessary to elicit hyperproliferation. 164



**Figure 1. IGF1 signaling pathways**. IGF1/2 binding to the extracellular domain of the IGF1R (or Type 1 IGF receptor) leads to autophosphorylation of its tyrosine kinase domain and subsequent activation of various cytoplasmic mediators. Particularly important pathways are the *Ras-Raf-MEK-ERK1*/2 and the *PDK-AKT-mTOR* signaling systems. The net consequences of the concerted activation of these pathways are, among other biological effects, an increase in proliferation and a marked reduction in apoptosis.

- 165 Among all growth factor receptors described, the IGF1R displays one of the most potent antiapoptotic activities. This inherent feature of the receptor confers upon IGF1R-expressing cells the capacity not to die, a quintessential feature of cancer cells [30]. On the other hand, IGF1R-null cells (R–, derived from IGF1R knockout embryos) are unable to undergo transformation when exposed to different cellular and viral onco-
- genes [31]. The IGF1R displays, in addition, pivotal roles in invasion, metastasis and angiogenesis [5]. Combined, these data support the notion that IGF1R expression is a funda-
- mental prerequisite for acquisition of a malignant phenotype. However, the presence of the IGF1R may not be an obligatory prerequisite, as demonstrated by the fact that certain oncogenes induce transformation via pathways that are IGF1R-independent. For example, transfection of R- cells
  with the GTPase-deficient mutant Gα<sub>13</sub> resulted in malignant

transformation in spite of the absence of the IGF1R [32].

# 4. IGF1R overexpression in cancer: the classical dogma and some new concepts

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Analysis of targeted disruption experiments, showing that disruption of the IGF1R gene is incompatible with life, 188 along with ontogenetic studies, demonstrating an almost universal pattern of distribution of the IGF1R during devel-189 opment, underscore its crucial role as a cell-survival and 190 proliferation factor in most organs [33,34]. In accordance with this role, most primary tumors and malignant cells express increased IGF1R mRNA and protein levels and augmented IGF binding. These tumors include, breast, ovarian, prostate, colon, hematopoietic, rhabdomyosarcoma, renal, etc. 195 Increased IGF1R expression in cancer reflects a reversal to a less differentiated, more primitive ontogenetic stage that, in most species and body organs, is characterized by very high IGF1R mRNA concentrations and IGF binding sites [35]. The molecular mechanisms responsible for the increased 200 expression of the IGF1R gene in tumors, however, remain largely unidentified. Amplification of the IGF1R locus at band 15q26 has been reported in a small number of breast and melanoma cases [36].

The dogma that emerged from these comprehensive analyses postulated that IGF1R expression is a fundamental prerequisite for cellular transformation [31,37]. The strength of this paradigm resided in the fact that enhanced IGF1R levels and IGF1 signaling were considered key factors, indispensable for the cell, in order to adopt proliferative pathways. While correct in most aspects, some of the above notions are interpreted today as overgeneralizations and, 212

- 213 therefore, a more balanced examination is required [38]. Specifically, IGF1R overexpression is a common theme in most
- 215 pediatric tumors (that are, in many cases, associated with recurring chromosomal translocations) and other solid cancers, including renal tumors [7,10]. The extent and biological significance of IGF1R overexpression in adult epithelial tumors is more complex. At the methodological level, the
- 220 large number of studies describing IGF1R overexpression in breast, prostate and other tumors have been, for the most part, based upon analyses of tissue homogenates or established cancer cell lines for which appropriate normal controls do not exist. The IGF1R content of homogenates, in
- 225 particular, can be affected by contamination with stroma, which would dilute IGF1R content in normal epithelium or small tumors.

More recent analyses of IGF1R expression in breast and prostate cancer revealed that expression is tightly dependent on tumor stage. Immunohistochemistry of primary breast tumors and matched control samples revealed that IGF1R and the downstream signaling molecule insulin receptor substrate-1 (IRS-1) were expressed at high levels in control tissues and in well and moderately differentiated carcinoma,

but at low levels in poorly differentiated cancers. InsR, on the other hand, did not show a significant correlation with the differentiation grade of the tumors [39]. Interestingly, a study by Papa *et al.* [40] demonstrated that InsR content (as measured by radioimmunoassay) in a collection of 159 breast cancer specimens was more than sixfold higher than in normal breast tissue. In addition, the receptor retained its capacity to bind insulin and to undergo phosphorylation, suggesting a role for the InsR in breast cancer.

In the prostate, IGF1R levels were significantly reduced in prostate carcinoma, as compared with benign prostate epithelium [41]. IGF1R expression was also diminished in a majority of human prostate cancer bone marrow metastases, although a recent study showed sustained upregulation of IGF1R in metastases [42]. While the molecular and biochemical nature of this reduction has not yet been established, the results of studies showing that androgens and estrogens control IGF1R levels can be interpreted to suggest that an IGF1R decrease might be linked to the acquisition

- of steroid hormone independence at advanced stages of the disease [43,44]. Another potential explanation for the decrease of IGF1R levels is the downregulation of the receptor by the very high levels of *in situ*-produced IGF2 and stroma-produced IGF1. Taken together, available data suggest that normal prostate and breast epithelial cells respond to circulating
- 260 IGF1 to maintain an appropriate balance between proliferation and differentiation. Disruption of this balance (e.g., excess of IGF secretion, IGF1R overexpression) leads to increased cellular proliferation, and the probability that cells become hyperplastic and premalignant. The transition to frank malignancy, at least in the case of breast and prostate cancer, seems to be associated with a reduction of IGF1R levels
  267 and, therefore, IGF responsiveness. Kim *et al.* [45] have

shown that a constitutively active IGF1R causes transformation and xenograft growth of immortalized mammary epithelial cells, accompanied by an epithelial to mesenchymal 270 transition. Interestingly, a recent study has shown that tumors initiated by IGF1R have the ability to become independent of this initiating oncogene, and IGF1R independence was associated with an epithelial to mesenchymal transition [46]. 275

# 5. Interactions between IGF1R and cancer genes

Cellular and viral oncogenes can induce transformation by 280 'recruiting' and activating the IGF signaling pathway. For example, transformation by  $pp60^{src}$ , the protein encoded by the *src* oncogene of Rous sarcoma virus, results in the constitutive tyrosine phosphorylation of the IGF1R tyrosine kinase domain [47]. It has been estimated that ~ 10 – 50% of the 285 receptors are phosphorylated in the unstimulated *src*-transformed cell, while addition of IGF1 synergistically increased the extent of phosphorylation. These results raise the possibility that  $pp60^{src}$  alters growth regulation by rendering the cells constitutively subject to a mitogenic signal.

Additional oncogenes were shown to exhibit a direct transactivating effect of the IGF1R gene. For instance, overexpression of c-myb (the cellular equivalent of the viral transforming oncogene v-myb) in Balb/c-3T3 cells induced an increase in the levels of both the IGF1R and IGF1 tran- 295 scripts [48]. This event led to abrogation of the requirement for IGF1 in the growth media, one of the distinctive hallmarks of a malignantly transformed cell. An additional oncoprotein shown to stimulate IGF1R gene transcription is the hepatitis B virus X (HBx) gene product. In hepatocellular- 300 carcinoma-derived cell lines containing HBx protein, IGF1R mRNA levels were approximately fivefold higher than in cells that do not express HBx transcripts [49]. Furthermore, expression of the HBx cDNA induced a large increase in IGF1R promoter activity, mRNA and IGF binding. These 305 findings support the notion that the mechanism of action of oncogene HBx in the specific context of hepatocellular carcinoma involves the transactivation of the IGF1R gene.

In summary, the fundamental requisite for a functional IGF1R in order for a cell to undergo oncogenic transformation can be explained, at a molecular level, by the fact that many oncogenes 'adopt' the IGF1R signaling pathway as their mechanism of transformation. Certain oncogenes (e.g., *c-myb*) are able to directly transactivate the IGF1R promoter, thus drastically increasing receptor congenes (e.g., pp60<sup>src</sup>) induce a large increase in IGF1R β subunit phosphorylation [47,48]. Regardless of the mechanism of action of the oncogene in the specific context of IGF1R control (i.e., regulation at the transcriptional or post-transcriptional levels), the transformed cells display essentially identical phenotypes. 322

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### <sup>323</sup> 6. The interplay between tumor suppressors and the IGF1R gene

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Molecular characterization of the IGF1R gene regulatory region identified a number of *cis*-acting elements and *trans*-acting factors that are directly involved in control of IGF1R gene expression [50]. Some of these transcription factors were identified as tumor suppressor gene products, and they

- 330 identified as tumor suppressor gene products, and they include p53, p63, p73, BRCA1, the von Hippel-Lindau protein (VHL), the Wilms' tumor protein (WT1) and the Kruppel-like factor-6 (KLF6) [51-58]. As described below, most of these tumor suppressors negatively regulate IGF1R
- 335 gene transcription. Accordingly, it has been postulated that inhibitory control of the IGF1R gene by tumor suppressors constitutes a mechanism that prevents from the cell from engaging in mitogenic activities.

A typical example of a tumor suppressor involved in regu-340 lation of the IGF1R gene is p53, a nuclear protein that, in its hyperphosphorylated state, blocks progression of cells through the cell cycle. The p53 protein functions as a transcription factor that binds specifically to DNA sequences in

- various promoters and stimulates their transcriptional activ-345 ity. Mutations of the p53 gene are the most frequent event in human cancers. In addition, p53 can also function as a transcriptional repressor of many growth-regulated genes. Thus, transient expression of wild type p53 in osteosarcoma and rhabdomyosarcoma cell lines suppressed the activity of
- 350 a cotransfected IGF1R promoter construct by ~ 90% [51]. On the other hand, cotransfection of tumor-derived, mutant p53 stimulated promoter activity by several-fold. In addition, wild type p53 decreased the IGF1-induced tyrosine phosphorylation of IGF1R and IRS-1, whereas mutant p53
- stimulated phosphorylation [59,60]. These results support the view that, at least part of, the effects of wild type p53 on apoptosis and cell cycle arrest are mediated via suppression of the IGF1R promoter. Lack of inhibition, or even stimulation, by mutant p53 may accelerate tumor growth and
  inhibit apoptosis, thus providing an increased survival

capacity to malignant cells. Inactivation of the VHL gene is a frequent event in the etiology of clear cell renal cell cancer (CC-RCC) [61]. The potential regulation of the IGF1R gene by VHL was recently examined [58]. IGF1R mRNA levels were significantly higher in CC-RCC biopsies than in benign kidney. IGF1R protein levels were unaffected by hypoxia, but were higher in CC-RCC cells harboring a mutant inactive VHL that in isogenic cells expressing a wild type VHL. Furthermore, IGF1R mRNA

- 370 and promoter activities were lower in CC-RCC cells expressing a wild type VHL, consistent with a transcriptional effect. In terms of the mechanism of action of VHL, it was shown that the negative effect of VHL involves interaction with and, potentially, sequestration of, zinc finger protein Sp1, a
- 375 potent transactivator of the IGF1R gene. In addition, VHL was shown to control IGF1R mRNA stability. Hence, this
- 377 study identified a new, hypoxia-independent role for VHL in

suppressing IGF1R transcription and mRNA stability. VHL 378 inactivation leads to IGF1R upregulation, contributing to renal tumorigenesis and, potentially, also to chemoresistance. 380

BRCA1 has been identified as a tumor suppressor gene that, when mutated, increases the risk of breast and ovarian cancer. BRCA1 participates in multiple biological pathways, including DNA damage repair, cell growth and apoptosis, and gene transcription The BRCA1 gene product has been 385 shown to inhibit IGF1R transcription in breast cancer cell lines, suggesting that a potential mechanism of action of BRCA1 involves suppression of IGFIR gene expression [56]. In contrast, mutant BRCA1 proteins lacking transcriptional activity are impaired in their ability to suppress the IGF1R 390 promoter, with resulting increments in IGF1R mRNA and IGF binding in mammary tumors [55,56]. Similar to the mechanism of action of VHL, BRCA1 was shown to specifically bind Sp1, thus preventing from the zinc finger from binding to, and transactivating, the IGF1R gene [56]. Finally, 395 and consistent with the postulate that mutant BRCA1 may lead to dysregulated IGF1R expression, a recent immunohistochemical analysis revealed a significant elevation of IGF1R levels in primary breast tumors derived from BRCA1 mutation carriers compared to non-carriers [62]. 400

# 7. Epidemiological evidence of the involvement of the IGF1 axis in cancer

The importance of IGF action in cancer biology is sup- 405 ported by epidemiological studies showing a correlation between circulating IGF1 values and cancer incidence. Seminal studies from the group of Michael Pollack published in 1998 identified IGF1 as a risk factor in breast and prostate cancers [63,64]. Specifically, in a prospective nested 410 control study (the Nurse's Health Study) the relative risk (RR) of breast cancer in premenopausal women was 4.6 in the upper tertile of IGF1 values, in comparison to women in the lower tertile. The RR increased to 7.3 when the concentrations of IGFBP3 were included in the analysis. 415 Likewise, the RR of prostate cancer in men (evaluated in the Physician's Health Study) in the upper quartile of IGF1 values was 2.4 (4.3 when normalized for IGFBP3). Noteworthy is that IGF1 levels were measured an average of seven years before the diagnosis of the disease. A meta-analysis 420 of 14 studies confirmed the association between IGF1 levels and prostate cancer [65]. In addition to hormone-dependent prostate and breast carcinomas, the importance of IGF1 as a risk factor was evaluated in various non-hormone-dependent types of cancers. Analysis of colon cancer risk in the Nurse's 425 and Physician's Health Studies showed an increased cancer risk in individuals with the highest IGF1 values [66,67]. A recent meta-regression analysis by Renehan and coworkers identified 21 eligible studies, which included 3609 cases and 7137 controls [68]. The study concluded that high concen-430 trations of IGF1 were associated with an increased risk of prostate cancer (odds ratio comparing 75th with 25th percentile 432

- 433 1.49, 95% CI 1.14 1.95) and premenopausal breast cancer (1.65, 1.26 – 2.08) and high concentrations of IGFBP3
- 435 were associated with increased risk of premenopausal breast cancer (1.51, 1.01 – 2.27). Associations were larger in assessments of plasma samples than in serum samples, and in standard case-control studies compared with nested studies. In summary, serum levels of IGF1 and IGFBP3 are associ-
- 440 ated with increased risk of common cancers, but associations seem to be smaller than those reported in earlier studies. Furthermore, the correlations vary between sites. Although laboratory methods need to be standardized, these epidemiological observations could have major implications for
- 445 assessment of risk and prevention of cancer. Finally, the importance of circulating IGF1 levels in cancer is further underscored by animal studies showing reduced susceptibility to skin and other types of cancer in mice with low serum IGF1 values [69]. Of interest, and in spite of its potent mitogenic potential, no epidemiological link has been reported
- between serum IGF2 and cancer risk.

## 8. Selected examples of IGF1R involvement in human cancer

#### 8.1 Breast cancer

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Epidemiological, clinical, and in vitro and in vivo experimental evidence support a key role for the IGF axis in breast cancer development. The expression of IGF ligands, 460 receptors, and IGFBPs is changed in breast cancer tissue compared with normal breast tissue. Moreover, many components of the IGF axis are altered in the circulation of breast cancer patients. Recent epidemiological studies indicate that evaluation of IGF1 levels in breast cancer patients 465 might be important both in terms of prognosis and diagnosis. However, the results of some of these studies are controversial. A number of systematic reviews and meta-analyses of prospective and case-control studies indicated a relationship between IGF1 and IGFBP3 regarding breast cancer risk in 470 premenopausal but not postmenopausal women [68,70-72]. However, a recent case-cohort study, which included 423 breast cancer cases and 1901 controls, reported that IGF1 and IGFBP3 were positively associated with breast cancer risk in patients older than 50, but not in younger women [73]. 475 Likewise, the European Prospective Investigation into Cancer and Nutrition (EPIC) study analyzed data from 1081 patients and 2098 controls, and reported that high levels of IGF1 or IGFBP3 are associated with a 40% increased risk for breast cancer in women older than 50 years of age, but not in

- 480 younger women [74]. On the other hand, the Nurses' Health Study II found no association between circulating IGF1, IGFBP1, and IGFBP3 levels and breast cancer risk in a large cohort of premenopausal women [75]. Moreover, a recent study including 835 incident breast cancer patients and 816
  485 controls from the Women's Health Initiative Observational Study (WHI-OS) found no association between total and free
- 487 IGF1 levels and breast cancer risk. Notably, a modest positive

association was reported between free IGF1 and risk of 488 breast cancer among nonusers of hormone replacement therapy [76]. Renehan *et al.* [77] suggested that these controversial findings may be a result of lack of standardization of assays, variation in study design, and/or variability in IGFBP3 proteolysis in serum samples.

Regarding IGF1R expression in primary tumors, previous studies have shown that the IGF1R gene is highly expressed 495 (39 – 93%) in breast carcinomas [78] yet conflicting data exists regarding its biological significance. Data have suggested lower IGF1R levels in benign lesions and normal breast tissue, compared with their malignant counterpart [79,80]. Shimizu *et al.* [81] demonstrated IGF1R overexpression in 48% of primary breast tumors, although expression levels did not correlate with tumor size, nodal status, hormone receptor status, histological grade, or prognosis. Finally, an additional study demonstrated that IGF1R expression in breast cancer was correlated with lower grade 505 and hormone receptor positivity [82].

Besides its role in cancer progression, the IGF1R has also a role in mediating resistance to various targeted and non-targeted cancer therapies [83]. Compared with HER2<sup>+</sup> breast cancers, which represent 20 - 25% of all breast cancers, the high-level-IGF1R-expression breast cancers represent a much broader potential group of patients that may be candidates for targeted therapy [84]. The IGF1R has been demonstrated to mediate resistance to radiotherapy in breast cancer, *in vitro* and *in vivo* [85]. Moreover, treatment of breast cancer cells with IGF1R antibody can sensitize these cells to the effect of doxorubicin [86]. Conversely, other *in vitro* studies showed that increased IGF1 signaling in breast cancer cell lines is correlated with increased response to various chemotherapies [87].

#### 8.2 Prostate cancer

Growing evidence has accumulated suggesting that the IGF1 axis plays an important role in normal prostate gland growth and development as well as in prostate cancer etiology. As 525 indicated above, multiple epidemiological studies have addressed the potential correlation between serum IGF1 levels and prostate cancer incidence. In terms of IGF1R expression in prostate cancer, Hellawel et al. [42] showed that IGF1R mRNA and protein were significantly upregulated, 530 compared with benign prostatic epithelium, in a study including 54 primary prostate specimens. In addition, in a study using frozen tissue sections, widespread IGF1R expression was found in normal prostate, prostate cancer, and metastases, with more intense staining in the stromal tissue 535 surrounding the tumor [88]. Upregulation of IGF axis components, including IGF1, IGF2, IGF1R and IRS-1, in prostatic intraepithelial neoplasia in a collection of 56 tissue specimens, has been shown to be correlated with tumor grade [89]. As discussed above, other studies reported a 540 marked reduction of IGF1R levels during progression of prostate cancer from a benign to a metastatic stage [40]. 542

- 543 IGF1R expression in prostate cancer seems to be dependent on androgen receptor (AR) status. A study by Pandini *et al.* [44]
- 545 has shown that androgens upregulate IGF1R levels in cultured prostate cancer cells and sensitize the cells to the biological effects of IGF1. In addition, IGF1R levels are also correlated with BRCA1 status, a tumor suppressor whose involvement in prostate cancer is still a controversial issue. Significantly ele-
- 550 vated BRCA1 levels were seen in prostate cancer in comparison to normal prostate tissue. In addition, an inverse correlation between BRCA1 and IGF1R levels was observed in the ARnegative P69 and M12 prostate cancer-derived cell lines. Coexpression experiments in M12 cells revealed that BRCA1 was
- 555 able to suppress IGF1R promoter activity and endogenous IGF1R levels. On the other hand, BRCA1 enhanced IGF1R levels in LnCaP C4-2 cells expressing an endogenous AR [90]. These findings are of relevance because they demonstrate a new mechanism for IGF and AR stimulation of prostate can-
- 560 cer and further support the relevance of targeting AR and IGF1R in prostate cancer with BRCA1 expression as a marker for defining the target activity.

#### 8.3 Cervical cancer

- 565 In vitro and in vivo data suggest a possible role for the IGF system in cervical tumorigenesis. Early studies by Steller *et al.* [91] found an elevation of IGF2, but not IGF1, mRNA levels following EGF stimulation in the cervical cancer cell line HT-3, and suggested that IGF2 plays a central role in
- 570 mediating cervical cancer. In a follow-up report, the same group reported overexpression of the IGF1R gene in primary cervical cancer cell cultures and cell lines, compared with normal cervical cells [92].
- A recent study evaluated IGF1R expression levels and activation status in patients with cervical intraepithelial neoplasia (CIN) and cervical cancer [93]. IGF1R expression was elevated in CIN-stage III and invasive cancer. Furthermore, IGF1R phosphorylation was promoted in all CIN and invasive cancers, and its intensity was related to tumor promotion. The authors suggested that human papilloma virus
- (HPV) infection contributes to upregulation of IGF1R expression in cervical cancer and to the initiation and progression of the tumors. Another study of 137 women assessed the correlation between serum IGF1 and IGFBP3 and the incidence of cervical oncogenic HPV and CIN [94]. Having a
- high IGF1:IGFBP3 ratio was associated with increased persistence of oncogenic HPV infection and women with high serum IGFBP3 had lower rates of oncogenic HPV detection and HPV-positive CIN. Finally, a recent study of 72 patients
- 590 with early cervical cancer investigated the clinical implication of the IGF system in this malignancy [95]. Notably, the 5-year recurrence free and overall survival rates were significantly lower among patients with high grade IGF1R expression [95]. Moreover, IGF1R expression was an independent predictor
- 595 of death and recurrence. Treatment with an IGF1R-blocking antibody decreased IGF1R phosphorylation and inhibited
- 597 tumor growth in SCID mice [95].

#### 8.4 Ovarian cancer

IGFs and their receptors play key roles in regulating the normal biology of ovarian epithelial cells and have been 600 implicated in the transformed phenotype of ovarian carcinoma cells [96]. IGF1, IGF2 and the IGF1R have been shown to be produced in vitro by ovarian cancer cell lines, displaying autocrine growth loops mediated through the IGF1R. In a recent study, Brokaw et al. [97] analyzed the 605 IGF1 mRNA expression and protein levels in 215 epithelial ovarian cancer (EOC) patients and reported that high IGF1 mRNA values are associated with increased risk of disease progression. Another study investigated the expression of IGF axis genes in relation to EOC outcome using microar- 610 ray profiles from 64 patients with advanced disease [98]. In this study, IGFBP4 and IGF2/M6PR gene expression were inversely associated with survival. Moreover, the expression patterns of several gene subsets of the IGF family were also associated with prognosis of EOC. 615

An important role of IGF1R signaling in resistance to chemotherapy in ovarian cancer was recently reported [99]. Specifically, the authors reported that IGF1R expression levels were correlated with cisplatin resistance and IGF1-induced cisplatin resistance. Finally, Gotlieb *et al.* [100] observed a growth inhibition of ovarian cancer cell lines treated with NVP-AEW541, a small molecular weight IGF1R inhibitor (see below), associated with decreased activity of the downstream IGF1R signaling pathway and enhanced apoptosis.

#### 8.5 Endometrial cancer

The elevated estrogen levels in obese women were suggested to explain the relationship between obesity and endometrial cancer. Recent hypotheses regarding this link, however, have focused on hyperinsulinemia, as insulin is a known mitogen. 630 In the uterus, cyclic changes in IGF1 expression and signaling play an important role in regulating the transition of the premenopausal endometrium through proliferative, secretory and menstrual cycles. In addition, a number of studies showed a correlation between components of the IGF system 635 and endometrial cancer risk. For example, Ayabe et al. [101] reported higher IGF1 and lower IGFBP1 levels in postmenopausal endometrial cancer patients compared with controls. Petridou et al. [102], in a study of 84 endometrial cancer patients and 84 control women, reported that endo- 640 metrial cancer was positively associated with IGF2 blood levels and inversely associated with IGF1. A recent study including 250 incident endometrial cancer patients and 465 controls from the WHI-OS assessed the association between endometrial cancer risk and serum levels of IGF1, IGFBP3, 645 insulin and estradiol [103]. Low levels of free IGF1 and high levels of insulin were associated with endometrial cancer risk. Both associations were stronger among obese patients.

Consistent with the important role of the IGF axis in endometrial cancer, McCampbell *et al.* [104] reported a significant 650 increase in IGF1R expression in biopsies from hyperplastic endometrium and endometrial carcinoma compared with 652

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- proliferative endometrium. Finally, the correlation between IGF1R and IGF2 expression and endometrial cancer stage was
  investigated in a study that included 59 endometrial adenocarcinomas, 10 endometrial hyperplasias and 7 normal tissues [105].
  - The expression of IGF1R and IGF2 was much higher in malignant tissue at advanced stages (stages III-IV) compared with early stages or endometrial hyperplasia.
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# 9. Approaches and methodological issues in IGF1R targeted therapy

- IGF1R targeting emerged in recent years as a very active 665 area in cancer therapeutics. IGF1R targeting is expected to result in: i) inhibition of IGF1R expression; ii) blockade of ligand-receptor interaction; and/or iii) impairment of receptor activation. Targeting methods are evaluated for their ability to: i) inhibit cancer cell proliferation, survival, and 670 anchorage independent growth in vitro; ii) reverse tumor growth and metastases formation in vivo; and iii) sensitize cancer cells to chemotherapy, radiotherapy, hormonal and biological therapies. Various experimental methods are currently being employed to downregulate IGF1R expres-675 sion and signaling (Figure 2). These approaches include, among others, IGF1R antibodies and IGF1R-specific low-molecular-weight tyrosine kinase inhibitors. A number
- of differences exist between the mechanisms of action of antibodies and kinase inhibitors, leading to different outcomes and, potentially, distinct side effects. Thus, humanized IGF1R antibodies are designed to prevent IGF1 binding, with ensuing receptor degradation whereas tyrosine kinase inhibitors, on the other hand, are designed to inhibit IGF1R's kinase activity without affecting IGF1R expression. A number of selected examples of recent attempts to target
- 685 A number of selected examples of recent attempts to targe the IGF1R are described below.

#### 9.1 IGF1R blocking antibodies

- Targeting of the IGF1R with specific monoclonal antibodies has been the most pursued method of blocking IGF signaling 690 employed in clinical investigations to date. The feasibility of this targeting approach was first demonstrated using a mouse monoclonal antibody directed against the IGF1R α-subunit (\alpha-IR3) [106]. It has been suggested that IGF1R antibodies 695 block signaling by two mechanisms: i) abrogation of ligand binding; and ii) induction of receptor internalization and degradation [107]. Several IGF1R antibodies have been developed in recent years and some of them are currently in Phase I and II clinical trials (Table 1) [108]. For example, monoclonal 700 antibody EM164 (Sanofi) has been shown to inhibit IGF1/2stimulated proliferation and survival of diverse cancer cell lines. Furthermore, its antitumoral effect was enhanced by combined treatment with a cytotoxic agent [109]. Similarly, Wu et al. [110], in a study using a human prostate cancer xenograft model, 705 showed that treatment with IM Clone's A12 antibody markedly decreased tumor size and also augmented the inhibitory effect
- 707 of docetaxel. Another extensively studied IGF1R monoclonal

antibody is CP-751,871 (Pfizer). A recent dose-escalation clinical trial including 47 patients with multiple myeloma revealed no significant response to single agent CP-751,871 therapy. 710

No significant response to single agent CP-/51,8/1 therapy. /10 However, 28 patients had stable disease and 9 had objective response when dexamethasone was added to the antibody [111]. In a Phase I study of AMG-479 (Amgen) that enrolled 33 patients, three objective responses and five incidences of stable disease were observed [112]. The dose-limiting toxicity of 715 this agent was thrombocytopenia while additional adverse effects included arthralgia, diarrhea and hyperglycemia.

Several *in vivo* studies evaluated the anti-tumor activity of anti-IGF1R as monotherapy as well as in combination with chemotherapy, radiotherapy or additional antibodies. As mentioned above, the potential effect of IGF1R antibodies on InsR signaling is of special concern given that these antibodies can co-target or alter InsR function, leading to insulin resistance and adverse effects on glucose and carbohydrate metabolism. On the other hand, InsR targeting (and, in particular, 525 isoform A) could become an advantage because specific inhibition of the InsR in the tumor could add to the effective antitumoral activity [113]. Preliminary results from Phase I trials in patients with advanced cancer treated with CP-751,871 or A12 antibodies showed only infrequent mild transient hyperglycemia with no dose-limiting toxicity [114-116].

#### 9.2 Small molecule IGF1R kinase inhibitors

In addition to IGF1R antibodies, a series of small-molecule IGF1R kinase inhibitors have been used in experimental 735 studies demonstrating tumor growth inhibitory properties (Table 1). However, a potential pitfall of these therapies is the fact that they might indiscriminately inhibit the kinase domains of all IGF/insulin receptors, as they share high homology at these domains [84]. Remarkable exceptions are the NVP-ADW742 and NVP-AEW541 pyrrolo[2,3-D] pyrimidine derivatives (Novartis), which display a 15 – 30-fold increased potency for IGF1R kinase inhibition compared with InsR kinase [117,118].

Mitsiades et al. [118] reported in vitro and in vivo antitu- 745 moral activity of NVP-ADW742 in multiple myeloma. Similarly, Garcia-Echeverria et al. [117] reported in vivo antitumoral activity of the NVP-AEW541 compound in the MCF-7 and NWT-21 cell lines. This orally bioavailable compound also inhibited IGF1R signaling in tumor xeno- 750 grafts and significantly reduced the growth of IGF1R-driven fibrosarcomas. In addition, Scotlandi et al. [119] reported that NVP-AEW541 effectively inhibited the in vitro tumor growth of Ewing sarcoma and displayed a synergistic effect with combined chemotherapy. Hopfner et al. [120] showed 755 in vitro growth inhibition of gastrointestinal neuroendocrine tumors and hepatocellular carcinoma cells by NVP-AEW541, both alone and in combination with chemotherapy. Finally, Gotlieb et al. [100] showed an inhibitory effect of NVP-AEW541 in ovarian cancer cell lines and this activity 760 was associated with decreased Akt phosphorylation and increased PARP cleavage. 762



**Figure 2. IGF1R targeted therapies**. This scheme depicts two of the most commonly used approaches for IGF1R targeting: anti-IGF1R monoclonal antibodies (centre) and small molecular weight IGF1R trosine kinase inhibitors (right). IGF1R blockade by specific antibodies (usually against the extracellular domain) leads to a decrease in ligand binding and IGF1R activation, followed by enhanced receptor internalization and degradation. Low-molecular-weight tyrosine kinase inhibitors prevent IGF1R activation and signaling, without major effect on IGF1R expression.

Compound	Company	Status	Ref.
Monoclonal antibodies			
IMC-A12	IMClone	Phase I/II	[110,115]
CP-751,871	Pfizer	Phase II	[111,114,116]
EM164	Sanofi	Preclinical	[109]
AMG479	Amgen	Phase I	[112]
MK-0646/h7C10	Merck	Preclinical/Phase I	[108]
Tyrosine kinase inhibitors			
NVP-AEW541-ADW742	Novartis	Preclinical	[117-120]
BMS-554417	Bristol-Myers Squibb	Preclinical	[121]
Picropodophyllin (PPP)	Karolinska	Preclinical	[122,123]

Table 1. Sciected for the monocional antibodies and small molecule tyrosine kinase ministers.
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Recently, Haluska *et al.* [121] reported the *in vitro* inhibition of colon, ovarian, and breast cancer cells, as well as of the *in vivo* growth of a mouse xenograft, using a dual IGF1R/InsR kinase inhibitor, BMS-554417. This small-molecule compound inhibited both InsR and IGF1R with similar potency. However, at the most effective dose tested, transient hyperglycemia and supraphysiologic elevation of secreted insulin was observed.

Another selective inhibitor of the IGF1R tyrosine kinase is 770 picropodophyllin (PPP). PPP efficiently blocked IGF1R activity and induced apoptosis and tumor regression in a xenograft mouse model [122]. PPP was shown to inhibit the IGF1R, but not the InsR, tyrosine kinase [123]. Finally, INSM18, a small-molecule IGF1R inhibitor that has also activity against 775 HER2, has been shown in clinical trials to be well tolerated 776 777 among 15 patients with prostate cancer and showed response in 2 patients [84].

#### 780 9.3 Molecular approaches to IGF1R targeting

A number of nucleic acid-based strategies, including antisense oligonucleotides and siRNAs, have been employed to target the IGF1R, mainly in experimental systems. For example, antisense oligomers against IGF1R mRNA led to 785 reduced receptor levels and inhibition of IGF signaling in various types of cancer, including lung, breast, prostate and melanoma [9,124]. The clinical use of these approaches, however, has been so far very limited. A pilot study published a few years ago investigated the effect of ex vivo treatment of autologous malignant astrocytoma with antisense oligomers 790 against IGF1R mRNA. Results of this study showed that this approach induced apoptosis and a host response in vivo, associated with radiographic and clinical improvements, without major side effects [125]. Likewise, injection of antisense oli-795 gomers into human psoriasis lesions grafted onto nude mice

led to reversal of epidermal hyperproliferation [126].

### 10. Conclusions

- The IGF network has a central role in normal and patho-800 logical growth. We have presented evidence suggesting that the mechanism of action of certain oncogenic agents are strongly linked to the IGF signaling pathways. The interplay between cancer genes and the IGF axis may involve oncogenic transactivation of the IGF1R promoter (with ensuing 805 increases in IGF1R mRNA), constitutive activation of the IGF1R kinase domain and downstream mediators by onco-
- genic agents, transcriptional dysregulation of the IGF1R promoter by mutated tumor suppressors and other mechanisms. 810 As a corollary to the involvement of the IGF axis in cancer biology, targeted therapy of the IGF1R emerged as a biologically plausible approach. Most experimental, preclinical and clinical data generated in the last few years corroborate the hypothesis that the IGF axis and, in particular, the IGF1R 815 are promising targets in cancer therapy.

### 11. Expert opinion

The huge amount of information accumulated in the IGF 820 field since the early 1980s led to the recognition that the IGF signaling network fulfills a pivotal role in cancer cells. Consequently, this paradigm led to the logical prediction that targeting of the IGF axis may constitute an important strategy in cancer therapy. While early studies attempted to 825 assess the clinical value of various candidate targets along

the GH-IGF axis (GH, GHR, IGF ligands, etc), most recent work focused on the IGF1R as a clinically relevant therapeutic target. As discussed in this review, the central role of this receptor as an important mediator of the proliferative and cell survival actions of IGF1 and IGF2 has been 830 831 amply validated.

Various technologies are currently being employed to 832 downregulate IGF1R expression and signaling. These approaches include, among others, anti-IGF1R antibodies and IGF1R-specific low-molecular-weight tyrosine kinase 835 inhibitors. However, a number of fundamental differences exist between the mechanisms of action of monoclonal antibodies and kinase inhibitors, leading to different outcomes and, potentially, complications. Thus, humanized IGF1-R antibodies (e.g., Pfizer's CP-751871, Sanofi's EM164, ImClone's 840 A12, etc) are designed to prevent IGF1 binding, with ensuing receptor degradation. On the other hand, tyrosine kinase inhibitors (e.g., tyrphostins, Novartis' pyrrolo [2,3-D]pyrimidine derivatives, Biovitrum's picropodophyllin, etc) are designed to inhibit IGF1R's kinase activity without affecting 845 IGF1R expression.

While most published preclinical data highlights the potential of IGF1R-targeted therapies, a number of obstacles must be resolved. These difficulties are primarily due to the large similarity between the mature forms of IGF1R and 850 InsR, reaching 84% homology in the kinase domain. In addition, and as indicated above, the downstream pathways elicited by IGF1R and InsR are almost identical. Thus, the potential effect of IGF1R targeting on insulin signaling, leading to potential complications such as the development 855 of insulin resistance, is of special concern. On the other hand, experts in the field advise that combined targeting of both IGF1R and InsR (and hybrid receptors) may have an added value in specific types of cancer.

Anti-IGF1R in combination therapy may also provide a 860 significant advantage over anti-IGF1R monotherapy. Combination therapies may include, in addition to anti-IGF1R, the use of a supplemental biological targeting reagent (e.g., epidermal growth factor receptor antibodies) or conventional chemotherapy and/or radiotherapy. A number of studies 865 have already demonstrated the benefit of the combined approach. It is expected that post genomic technological developments, including analyses of molecular signatures of tumors and identification of biomarkers linked to cancer response, will allow in the near future delivery of targeted 870 therapies in a more rational and personalized fashion.

In summary, the combined efforts of basic scientists and clinicians in the fields of IGF and cancer research, pharmacology, endocrinology, bioinformatics and others, for many years, are paving the way for important translational devel- 875 opments that will undoubtedly impinge on our ability to move on 'from the bench to the bedside'.

### **Declaration of interest**

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