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1 **Anterior Gradient proteins in gastrointestinal cancers: from cell**  
2 **biology to pathophysiology**

3

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25



27 **Abstract**

28 Most of the organs of the digestive tract comprise secretory epithelia which require  
29 specialized molecular machines to achieve their functions. As such Anterior GRradient  
30 (AGR) proteins, which comprise AGR1, AGR2 and AGR3 belong to the Protein  
31 Disulfide Isomerase family, and are involved in secretory and transmembrane protein  
32 biogenesis in the endoplasmic reticulum (ER). They are generally expressed in  
33 epithelial cells with high levels in most of the digestive tract epithelia. To date, the vast  
34 majority of the reports concerns AGR2, which has been shown to exhibit various  
35 subcellular localizations and to exert pro-oncogenic functions. AGR2 overexpression  
36 has recently been associated to a poor prognosis in digestive cancers. AGR2 is also  
37 involved in epithelial homeostasis. Its deletion in mice results in severe diffuse gut  
38 inflammation, whereas in inflammatory bowel diseases, the secretion of AGR2 in the  
39 extracellular milieu participates to the reshaping of cellular microenvironment. AGR2  
40 thus plays a key role in inflammation and oncogenesis and may represent a therapeutic  
41 target of interest. In this review, we summarize the already known roles and  
42 mechanisms of action of the AGR family proteins in digestive diseases, their  
43 expression in the healthy digestive tract and in digestive oncology. At last, we discuss  
44 the potential diagnostic and therapeutic implications underlying the biology of AGR  
45 proteins.

46

## 47 **1. Introduction**

48 The digestive system is composed of organs with specific differentiated cells, each of  
49 which having specific functions in the digestion process. Beyond these differences, all  
50 these organs show common secretory properties essential for homeostasis.  
51 Alterations in the secretory pathway have been implicated in oncogenesis. Digestive  
52 cancers, like most cancers, often result from a chronic inflammation that dysregulates  
53 the cell metabolism, gene expression and epigenetics. Chronic inflammation can be  
54 responsible for precancerous lesions, before the evolution toward invasive cancer, like  
55 in Barrett metaplasia in the esophagus, inflammatory bowel diseases (IBD) in the gut  
56 or pancreatic intraepithelial neoplasia (PanIN) in the pancreas. Among the cellular  
57 dysregulations that favor carcinogenesis, alterations of endoplasmic reticulum (ER)  
58 homeostasis and the subsequent adaptive mechanisms activated to cope with it were  
59 shown to significantly contribute to these processes. The ER is the first compartment  
60 of the secretory pathway that enables the proper biogenesis, folding, and maturation  
61 of secretory and transmembrane proteins (1). Beyond its role in protein homeostasis,  
62 the ER also maintains calcium and lipid homeostasis. As part of the ER folding and  
63 quality control machinery, the Protein Disulfide Isomerase (PDI) family is involved in  
64 the formation of inter and intra-molecular disulfide bridges in client proteins, productive  
65 protein folding, redox activity, and disulfide exchange through their thioredoxin-like  
66 domain (1-3). Although the roles of most PDI family members in protein folding have  
67 been well characterized, their function in ER homeostasis control and proteostasis  
68 maintenance is still unclear (4). Along with glutaredoxins and thioredoxins, PDI are  
69 members of the thioredoxin (TRX) superfamily which are characterized by the  
70 presence of a thioredoxin fold (5). So far, 20 PDIs have been identified (4,6). Most of  
71 them are located in the lumen of the ER, while others are transmembrane proteins

72 (TMX 1 to TMX 5) (6). PDI are defined as “proteins that can react with cysteine side  
73 chains”, but it includes also “proteins that contain non-thiol-reactive thioredoxin-like  
74 domains with chaperone-like activities for ER folding and secretion of proteins” (7).  
75 Therefore, the PDIs can be divided between thiol-non reactive (ERp27 and ERp29)  
76 and thiol-reactive proteins.

77 The AGR family is composed of three PDI-like proteins: AGR1 (also known as  
78 Thioredoxin domain-containing protein 12 (TXNDC12)), AGR2 (protein disulfide  
79 isomerase family A member 17 (PDIA17)), and AGR3 (Protein disulfide isomerase  
80 family A, member 18 (PDIA18)) (7,8). AGR1 is expressed in the ER and plays a role  
81 in the formation of mixed disulfide bounds with proteins (9). The expression of AGR2  
82 is induced upon disruption of ER homeostasis, through the activation of the ATF6 and  
83 IRE1 arms of the unfolded protein response (UPR) (1). AGR2 is shown to contribute  
84 to protein folding and maturation (10,11) and to participate in the elimination of  
85 misfolded proteins through ER-associated degradation (ERAD) (12). Several studies  
86 in the last decade have shown that AGR2 expression is associated with poor prognosis  
87 in solid cancers and may play pro-oncogenic roles through yet uncharacterized  
88 mechanisms. AGR3 is also an ER resident protein involved in the formation of disulfide  
89 bonds but its expression is independent of ER stress (13). Compared to AGR2, less is  
90 known about the functions and regulations of both AGR1 and AGR3 as well as their  
91 respective roles in the digestive tract. In this review, we cover the most recent data on  
92 the AGR family from biochemical and cell biology perspectives; we next connect these  
93 properties to the functions of these proteins in both normal and pathological gastro-  
94 intestinal tract and lastly discuss the potential theranostic aspects related to the AGR  
95 family.

96

## 97 2. The AGR family

### 98 2.1. Genes, structures and regulators

99 AGR2 is the most documented member of the AGR family. It was initially identified in  
100 the anterior region of the ectoderm of *Xenopus laevis* as XAG-2 (14–16). XAG-2 plays  
101 important roles in the endodermal patterning and in forebrain maturation by  
102 anteroposterior migration of the cement gland (mucus-secreting organs) during  
103 embryogenesis (14,17). In human, AGR2 is also expressed during embryonic  
104 development in the endoderm derived tissues like esophagus, trachea, lung, liver,  
105 stomach, and in the gut (18). In adult human tissues, the highest levels of AGR2  
106 expression are observed in the gastrointestinal tract from the stomach to the rectum,  
107 in the genitourinary tract (urinary bladder), and in the respiratory system (see Figure  
108 3). Human AGR2 is located on chromosome 7 (19) and is composed of 8 exons and 7  
109 introns. Seven different AGR2 transcripts are reported in the Ensembl database. In  
110 cancer, the most recurrent AGR2 anomaly is amplification; only few mutations or  
111 deletions were described (20). AGR2 predominant isoform is 175 amino acid long  
112 resulting in a molecular weight of ~20 kDa. Three other isoforms have been described  
113 [B5MC07, C9J3E2 and H7C3Z9 (UniProt)] but so far, there is no information on their  
114 functions. Its structure is composed of an N-terminal cleavable signal peptide, a non-  
115 canonical thioredoxin domain CXXS, a peptide binding loop and a C-terminal domain  
116 ER-retention (KTEL) motif (**Figure 1a, b**) (1). AGR1 has a high similarity with the  
117 thioredoxin domain CXXC motif in invertebrates, but is lost in higher vertebrates where  
118 it is replaced by the CXXC containing protein TXNDC12 (21–25). It is a 18kDa ER  
119 resident protein composed of 146 amino-acid in its mature sequence (Human Protein  
120 Atlas - (26)). AGR1 gene is located on chromosome 1 unlike AGR2 and AGR3. Similar  
121 to other PDI, it is involved in disulfide bond formation (24). AGR2 and AGR3 are

122 present in both amphibians and higher vertebrates (8). AGR proteins ER retention  
123 motifs differ (i.e. EDEL for AGR1, KTEL for AGR2, QSEL for AGR3) as do their  
124 thioredoxin-like motifs (**Figure 1a, b**) (27). Even though both proteins are very similar  
125 (>90% identity) and highly conserved in mammals (e.g. mouse and human – **Figure**  
126 **1b**), the role of AGR3 is less documented than AGR2 but its expression seems  
127 correlated with AGR2 and plays similar roles in some aspects, for instance promoting  
128 migration and metastasis (28). However, expression of AGR3 is independent of ER  
129 stress suggesting that the regulation of the two proteins differs each of another. AGR3  
130 gene is located on chromosome 7p21.1, it is composed of 10 exons and can produce  
131 three different transcripts (AGR3-201, AGR3-202, AGR3-203). The molecular weight  
132 of AGR3-201 is 19.2 kDa and contains 166 amino acids (Human Protein Atlas – (29)).  
133 AGR3 was first identified in breast cancer cell membrane and in breast tumors, where  
134 its expression correlates with estrogen receptor expression (30,31). It is expressed in  
135 airway epithelium where it is required for muco-ciliary clearance and for regulation of  
136 ciliary beat frequency (32). It is also expressed in prostate, as well as stomach and  
137 liver tissues of the digestive tract (33).

138 AGR2 exists in monomeric or homodimeric forms (34). AGR2 dimerizes through  
139 E60 and K64-dependent salt bridges, far from the thioredoxin domain (35,36) (**Figure**  
140 **1c**). It was also reported that AGR2 could form cysteine 81-dependent dimers but the  
141 precise functions of these dimers remain elusive (37). AGR2 was also found to form  
142 hetero dimers with AGR3 *in vitro*, but again the functions associated with this complex  
143 are unknown (38) (**Figure 1d**). AGR2 thioredoxin-like domain is found at position 81-  
144 84 (CXXS) and is conserved in mouse and human. It may be involved in the formation  
145 of mixed disulfide bridges with client proteins (39). ER stress conditions were shown  
146 to induce AGR2 monomerization, which was correlated with its secretion to the



147 extracellular milieu (34,40). Interestingly, AGR3 thioredoxin-like domain is not  
148 conserved in human and mouse, exhibiting a CXXS sequence in human and a  
149 canonical CXXC site in mouse (**Figure 1b**). This might reflect a difference in AGR3  
150 redox functions between the species. The AGR2 peptide binding loop (VDPSL,  
151 conserved in AGR3, **Figure 1b**) interacts with proteins such as the AAA+ protein  
152 RuvBL2/Reptin (41). The AGR2 C-terminal domain contains a non-canonical ER  
153 retention motif (KTEL), that enables a partial retention of AGR2 in the ER through  
154 KDEL receptors (27).

155

## 156 **2.2. AGR proteins functions and subcellular locations**

157 AGR proteins exhibit various sub-cellular locations, associated with different roles  
158 (**Figure 2**). So far most if not all functions of AGR1 were associated with the ER  
159 localization (24) and in particular in the regulation of the ATF6 arm of the UPR (42,43).  
160 Even though AGR2 and AGR3 show all the features of ER-resident luminal proteins  
161 (*i.e.* signal peptide and ER-retention motif), both proteins are released in the  
162 extracellular environment and AGR2 was also found in the cytosol (44). In the ER,  
163 AGR2 (erAGR2) participates in protein folding, maturation and secretion. It is also  
164 involved in ER-associated protein degradation (1). In particular, erAGR2 contributes to  
165 the productive folding of i) mucins (MUC2, MUC5A/C) most likely through the formation  
166 of mixed disulfide bonds (13), ii) low affinity, Ca<sup>2+</sup>-binding, multiple EF-hand proteins  
167 such as CALU and RCN1 (45–48), iii) proteases such as Cathepsins B and D (45), iv)  
168 adhesion molecules such as EpCAM (49) or v) other PDIs (50). In contrast to AGR2,  
169 the ER functions of AGR3 remain to be fully characterized. The contribution of AGR2  
170 to the productive folding of proteins whose functions are associated with cancer  
171 development, thereby sustaining their functions upon overexpression might represent

172 a pro-oncogenic feature (**Table 1**). In addition to the “canonical” ER localization of  
173 AGR2 and AGR3, both proteins were also found to be secreted extracellularly (eAGR2,  
174 eAGR3). Although the underlying mechanisms have not been studied for AGR3, it  
175 appears that ER stress is a driver of AGR2 secretion. Indeed, we demonstrated that  
176 upon ER stress induction either overexpression of AGR2 or dimer disruption (or both)  
177 correlated with enhanced AGR2 secretion (34). AGR2 dimer regulation was found to  
178 depend on the p24 cargo receptor family member TMED2 (34). It was also shown that  
179 the Cys81Ser mutation in the CXXS domain also prompted AGR2 secretion (51).  
180 Moreover, AGR2 KTEL motif binds to KDEL-R in a non-canonical manner, enabling an  
181 easier secretion of AGR2 compared to other proteins KDEL-containing motifs  
182 (1,52,53). This was confirmed upon replacement of KTEL by KDEL in AGR2 which led  
183 to its ER sequestration (52). The extracellular AGR2 (eAGR2) as well as eAGR3 plays  
184 multiple pathophysiological roles in inflammation, cell proliferation, angiogenesis, cell  
185 migration and metastasis, through autocrine, paracrine and maybe endocrine secretion  
186 (**Table 1**). The third sub-cellular localization in which AGR2 was detected is the cytosol.  
187 The mechanism by which AGR2 might relocate from the ER lumen to the cytosol was  
188 identified to be an ER stress-induced reflux of properly folded proteins initially identified  
189 in yeast and also found in mammalian cells (44). Although not demonstrated yet for  
190 AGR3, this phenomenon is likely to occur in the same manner as for AGR2 as  
191 suggested by the large number (12 out of 39) of cytosolic/nuclear proteins found  
192 associated with AGR3 in large scale protein-protein interaction experiments (54).  
193 These observations remain however to be confirmed experimentally with minimized  
194 experimental biases. Thus far the most important studies on the role of cytosolic AGR2  
195 (cAGR2) have focused on its capacity to inhibit p53 protein tumor suppressor activity.  
196 Indeed, beyond the demonstrated genetic alterations associated with alterations of p53

197 functions, AGR2 could exert a non-genetic inhibition of p53 (44,55). Indeed, AGR2-  
198 p53 co-immunoprecipitation experiments performed on the cytosolic fraction extracted  
199 from A549 cells, showed that inhibition of p53 phosphorylation and activity resulted  
200 from interaction of p53 with AGR2 consecutive to a reflux of AGR2 into the cytosol in  
201 response to treatment with tunicamycin, thapsigargin, Brefeldin-A, or etoposide, a  
202 Topoisomerase II inhibitor (44,55). Moreover, preventing the association of cAGR2  
203 with p53 by using specific AGR2 nanobodies expressed in the cytosol, resulted in the  
204 restoration of p53 activation upon stress (44,55). Cytosolic p53-dependent pro-  
205 oncogenic roles of AGR2 might also be mediated indirectly, for instance through the  
206 Dual Specificity Phosphatase 10 (DUSP-10) (56), Tumor-Susceptibility-Gene 101  
207 (TSG-101) (53) or RuvbL2/Reptin (41), but the underlying mechanisms remain to be  
208 identified. Cytosolic roles of AGR2, and possibly AGR3 might as well (as for p53) be  
209 associated to pro-oncogenic gains-of-functions which need to be experimentally  
210 validated in relevant models (**Table 1**).

211

### 212 **3. AGR family proteins expression in the gastrointestinal tract**

#### 213 **3.1. Organ specificity**

214 Analyses of the literature and databases (Human Protein Atlas – (57), (58)) showed that AGR2  
215 mRNA and protein is expressed from the stomach to the rectum in healthy human digestive  
216 tract with the highest expression detected in the ileum and colon (59). It is mostly found in  
217 luminal mucosal cells, witnessing its secretion with mucins in the intestinal lumen (51). We  
218 confirmed that the AGR2 protein is not detected in the liver and in the two malpighian tissues  
219 of the digestive tract which are the esophagus and the anus, while it is strongly expressed in  
220 all the other parts of the digestive system including pancreas and gallbladder (**Figure 3a**).  
221 The highest expression of AGR2 is observed in both stomach, colorectal and ileum epithelia  
222 (**Figure 3a, b**). AGR1 is ubiquitously expressed in all human tissues and, in the gastrointestinal

223 tract it is particularly abundant in the liver and rectum (Human Protein Atlas - (26), (22)). In  
224 contrast, AGR3 is highly and almost exclusively expressed in the digestive tube, liver,  
225 respiratory system and female organs (Human Protein Atlas - (29)).

### 226 **3.2. Cell specificity**

227 AGR2 is expressed in epithelial cells from various tissues. It is essential in the  
228 production of gel-forming mucins and for the protection of the gastrointestinal tract.  
229 Cells exhibiting the highest expression of AGR2 throughout the entire gastrointestinal  
230 tract, and especially in the rectum, colon, ileum, and stomach, are mucus-secreting  
231 cells, namely goblet cells and gastric mucocytes. Undifferentiated cells, Paneth cells  
232 and enterocytes are other specialized cells with high expression of AGR2 in the  
233 digestive tube. Both Paneth and goblet cells deregulation, especially downregulation,  
234 are involved in inflammatory bowel diseases. Indeed, the loss of protective mucus layer  
235 participates to the aggression of the intestinal epithelium by pathogens and is involved  
236 in the genesis and maintenance of these diseases (60). AGR2 expression is also  
237 reported in intestinal enteroendocrine cells. In the gallbladder, biliary tract and liver,  
238 AGR2 is specifically expressed by cholangiocytes. AGR1 is ubiquitously expressed in  
239 all organs; single cell analysis show highest expression for exocrine pancreatic cells,  
240 ductal cells and pancreatic endocrine cells among all the digestive cells from a RNA  
241 single cell analysis. Regarding AGR3 mRNA expression, proximal enterocytes are the  
242 highest expressers, followed by Paneth cells, goblet cells and distal enterocytes. There  
243 is a low expression of AGR3 in enteroendocrine cells, gastric mucocytes, exocrine  
244 glandular cells. A very weak signal is found for ductal cells, cholangiocytes and  
245 pancreatic endocrine cells, while there is no expression in hepatocytes (Human Protein  
246 Atlas, Single cell - (26,57,57)).

247

248

249

### 3.3. Roles in the gastrointestinal tract

250 AGR2 is essential for the maintenance of homeostasis and the protection of the  
251 digestive tract, as it has a key role in mucus production, secretion, proliferation, and  
252 differentiation. AGR2 is known to interact with different mucins of the intestinal  
253 epithelial layer (MUC1, MUC2, MUC5AC, MUC5B) and is indispensable for their  
254 proper folding and secretion through its PDI-like domain (61). AGR2 could be secreted  
255 with MUC-2, but its role within the mucus layer in the intestinal lumen remains obscure  
256 (62). In the stomach, AGR2 participates to calpain production and secretion, which is  
257 indispensable for mucosa protection (28). It is also involved in mucus production in  
258 other organs such as lung (60) or pancreas (63). Mice knock-out for *Agr2* show a large  
259 intestinal hyperplasia, from the antrum to the colon, causing multiple nutrient  
260 deficiencies and a shorter lifespan compared to *Agr2*<sup>+/+</sup> mice (median survival 20  
261 weeks vs. 60 weeks) (64). In the stomach of *Agr2*<sup>-/-</sup> mice, parietal and enteroendocrine  
262 cells are slightly present, and goblet cells expressing different gastric mucosal cell  
263 markers such as Trefoil factor family 2 (TFF2) and Griffonia Simplicifolia II (GSII)+ are  
264 overexpressed. As TFF2 and GSII marker normally disappear at birth, it is thought that  
265 AGR2 plays a key role in the maturation of gastric goblet cells. The gastric cells from  
266 *Agr2*<sup>-/-</sup> mice showed increased Ki67 expression and overexpressed SOX9 responsible  
267 for the maintenance of stem cell pluripotency. All these gastric features of *Agr2*<sup>-/-</sup> mice  
268 correspond to preneoplastic lesions known as spasmolytic protein expressing  
269 metaplasia (64). In the intestine, goblet cells of *Agr2*<sup>-/-</sup> mice lose their normal  
270 morphology and functions, likely associated with defects in the production of mucus  
271 and MUC-2 (59). A dramatic expansion of the Paneth cell compartment and abnormal  
272 Paneth cell localization were observed in their small intestine. Mice developed a severe  
273 terminal ileo-colitis with neutrophil infiltration in the lamina propria, hyperplastic

274 submucosa and crypt base, Peyer's patch hyperplasia, and granulomatous  
275 inflammation. Paneth, goblet, and progenitor cells experienced ER stress (61,64,65).  
276 In conclusion, these experiments provide important information on the key roles of  
277 AGR2 in the digestive tract and especially its protective and anti-inflammatory roles.

278

#### 279 **4. AGR proteins in digestive cancers**

280 AGR2 is overexpressed in numerous digestive solid cancers such as pancreas (66),  
281 biliary tract (67), esophagus (68), stomach (69), and colon (70,71) cancers. Analysis  
282 using the pan-cancer TCGA data from cBioportal data sets reports mainly  
283 amplifications of AGR2, but also AGR3 and AGR1 in cancers, whereas few deletions  
284 are observed (72). From a meta-analysis of 3,285 cases of different solid tumors,  
285 AGR2 is associated with the occurrence of metastasis and to a poor prognosis (73,74).  
286 Analysis of both the Human Protein Atlas and Cancer Genome Atlas (57) shows an  
287 overexpression of AGR2 at both mRNA and protein levels in most digestive neoplasia,  
288 especially gastric, colorectal, pancreatic, and biliary tract adenocarcinoma with the  
289 highest overexpression in stomach cancer. Cholangiocarcinoma (CCA) data have  
290 been grouped with those of the hepatocellular carcinoma, in which RNA and protein  
291 expression are poorly to not detected. However, a case per case analysis shows that  
292 for CCA, AGR2 is highly expressed. As AGR2 and AGR3 have similar roles in some  
293 aspects, we have compared their differential protein expression (tumors with high to  
294 moderate expression of proteins) in digestive cancers from the Human Protein Atlas  
295 **(Figure 4a, b)**.<sup>1</sup> In intestinal and pancreatic cancers, high and moderate expression of  
296 AGR2 and AGR3 is noted in 80 to 70% of the cases, respectively. In stomach cancer,  
297 100% of tumors have high or moderate expression of AGR2, and 80% of tumors  
298 express AGR3. Among the liver tumors of the Human Protein Atlas, one third

299 expresses AGR2 whereas only 1 tissue sample out of 11 express AGR3. In the liver,  
300 all tumors expressing AGR2 and AGR3 are emanating from the biliary tract (**Figure**  
301 **4a, b**).

302 *i. Esophagus adenocarcinoma*

303 Although anomalies are very unlikely, amplification is the most recurrent anomaly in  
304 AGR2 and 3 genes in esophagus adenocarcinoma and only one mutation in AGR1  
305 gene was observed in this cancer subtype. Regarding esophageal squamous cell  
306 carcinoma, no alterations of AGR1, 2 and 3 have been observed (20). AGR2 is  
307 overexpressed in esophagus adenocarcinoma and in Barrett metaplasia (55,75).  
308 Overexpression of AGR2 in Barrett metaplasia may be a consequence of chronic ER  
309 stress secondary to a permanent reflux of bile acid. Furthermore,  
310 immunohistochemical analysis of AGR2 has been found positive in 68 out of 69  
311 esophagus adenocarcinoma but only focally in 15 out of 41 cases of squamous cell  
312 carcinoma, making it a marker to differentiate them in combination with other markers  
313 in the context of esophageal carcinoma of uncertain differentiation (76). Interestingly,  
314 in a whole genome array, Barrett metaplasia and esophagus adenocarcinoma tissues  
315 showed an increase of AGR2 mRNA, among other functional elements of the ER and  
316 Golgi apparatus and among secreted glycoproteins like MUC2B and MUC6, compared  
317 to healthy esophagus tissue. Among these genes, some of them are involved in the  
318 formation of a protective mucous membrane to protect the esophagus tissue against  
319 acidity. This indicates an increase of the glycosylation capacities of Barrett and  
320 esophagus adenocarcinoma compared to normal esophagus mucosa, and the  
321 potential implication of AGR2 in this increased glycosylation capacity (68).

322

323

324 *ii. Gastric adenocarcinoma*

325 Analysis of the pan-cancer TCGA data indicates that amplification of AGR2 and 3  
326 genes is the most common observed alteration with very few deletions or missense  
327 mutations, while nearly no missense mutations and no amplification anomaly are found  
328 for AGR1 (20). Gastric adenocarcinoma cell lines, particularly SNU-520, HUG-1N,  
329 MKN-45 and IM-95 are the cancer cell lines with highest expression of AGR2 in  
330 cbioportal.org (20) and Depmap.org (77). A proteomic analysis comparing two gastric  
331 cancer cell lines with differential potential of metastasis showed that AGR2 was the  
332 most differentially overexpressed protein, supporting the capacity of AGR2 to predict  
333 the risk of developing metastasis in gastric cancer (78). *In vitro* analyses carried out  
334 on the gastric cancer cell line Tu-Kato III (*TP53* deleted) showed that AGR2 favors cell  
335 growth and resistance to apoptosis under stress or hypoxia (79). In a murine xenograft  
336 model of Tu-Kato-III treated with an AGR2 targeting miRNA, tumor growth was 8 fold  
337 lower and there was much less mice with peritoneal metastases than in the control  
338 group, suggesting AGR2 could contribute to gastric cancer aggressiveness and  
339 metastasis (79). Expression of AGR2 has a prognostic value in gastric  
340 adenocarcinoma, especially in the early stages of the disease. In a retrospective study  
341 of 436 gastric cancer and 92 non-cancerous gastric samples (69) patients with low  
342 expression of tumor AGR2 had a longer survival than those with high expression of  
343 tumor AGR2 in TNM stages I, II and III groups, but not for those at stage IV. In this  
344 study, 46,8% of gastric cancer samples had a correlation between high expression of  
345 AGR2 and Cathepsin-D, a marker of tumorigenesis associated to the process of  
346 metastasis (80). Increased tumor size, depth of invasion, tumor stage (based on UICC  
347 TNM classification) and positive vessel invasion and lymphatic metastasis were also  
348 significantly associated with high expression of AGR2 (69). However, another



349 immunohistochemistry analysis performed on 145 biopsies of patients with gastric  
350 adenocarcinoma didn't find a prognostic value of AGR2 (81). There was even a  
351 tendency for a poorer prognosis for patients with low expression of AGR2. This may  
352 be due to a difference in the proportion of patients with stages I-II-III vs IV. AGR1 might  
353 act as a pro-oncogenic protein in gastric cancers. Its expression was measured by  
354 immunohistochemistry and qPCR in GC tissues of patients and found to be significantly  
355 more expressed in tumor tissues than in normal tissues. Moreover, AGR1 expression  
356 was found to be correlated with tumor size and poor clinical prognosis (82).

357 *iii. Primary liver cancers*

358 Neither AGR2 nor AGR3 are expressed in hepatocytes and reports describing their  
359 roles in hepatocellular carcinoma (HCC) or models of HCC might be due to specificities  
360 of the samples studied. A recent study based on the analysis of transcriptomic profiles  
361 of tissue specimen of patients with HCC or intrahepatic cholangiocarcinoma (iCCA)  
362 demonstrated the existence of 4 liver cancer (LC) subtypes (LC1-LC4) showing distinct  
363 genetic variations. LC1 was a typical HCC, whereas LC2 were iCCA-like HCC, LC3  
364 were HCC-like iCCAs and LC4 corresponded to iCCAs. Gene expression of AGR2 was  
365 absent in LC1 and appeared with the iCCA component, AGR2 being a marker of intra-  
366 hepatic CCA-like HCC associated with *TP53* mutation, ER stress and unfavorable  
367 prognosis (83). In the normal biliary tract, AGR2 is expressed in the mucus secreting  
368 tall cells that covers the large bile ducts, and its expression was found enhanced in  
369 100% of hilar and extra-hepatic cholangiocarcinoma (eCCA) and in 50% of the iCCA  
370 (67). No data about the type of alteration are available in cbiportal.org. In addition, a  
371 cancer specific isoform of AGR2 (AGR2vH) has been identified in metastatic CCA,  
372 conferring migrating and adhesion ability to metastatic cells (84). The expression of  
373 AGR3 was analyzed on tissue sections of 74 patients diagnosed with either HCC or

374 iCCA by immunohistochemistry. A negative or very weak heterogeneously expression  
375 of AGR3 was observed in HCC patients, whereas AGR3 expression was moderate or  
376 strong in iCCA tissues. Thus, AGR3 was proposed to be used as a complementary  
377 marker in liver cancers to distinguish between HCC and iCCA for diagnosis (85).  
378 Fibrolamellar carcinoma (FLHCC), is a rare liver cancer that can arise in young patients  
379 without any previous liver disease. AGR2 was found often overexpressed in FLHCC  
380 (86). At last, 75% of primary FLHCC and 75% of metastatic FLHCC were positive for  
381 AGR2 (87). At last, AGR1 protein expression was evaluated in 106 human HCC tissues  
382 by immunohistochemistry and was significantly higher compared to corresponding  
383 adjacent normal tissues. In addition, its expression was correlated with HCC  
384 metastasis and AGR1 was found to promote metastasis through the induction of the  
385 epithelial–mesenchymal transition process (88), however the precise underlying  
386 molecular mechanisms remain unclear.

#### 387 *iv. Pancreatic cancer*

388 Few amplifications of AGR2 and AGR3 genes (<1%) have been demonstrated in  
389 pancreatic adenocarcinoma as well as very few missense mutations (<1%) have been  
390 observed for AGR2 (20). So far, no alterations have been demonstrated for the AGR1  
391 gene. Prolonged chronic ER stress induces the overexpression of AGR2 in  
392 normal Human Pancreatic Duct Epithelial (HPDE) cell line (66), and may be involved  
393 in development of pancreatic adenocarcinoma. In *LSL-Kras<sup>G12D</sup>;Pdx1-Cre (KC)*  
394 mouse, the induction of AGR2 expression precedes the formation of PanIN, whereas  
395 PanIN do not develop in *Agr2<sup>-/-</sup>* mice, suggesting the involvement of AGR2 in the  
396 development of pancreatic neoplasms (66). In human, AGR2 is highly expressed in  
397 PanIN compared to normal pancreatic tissue, and its expression is higher in PanIN  
398 than in invasive pancreatic adenocarcinoma (45,89–91). According to a retrospective

399 analysis of 57 biopsy samples, AGR2 mRNA expression is 14 times higher in  
400 pancreatic adenocarcinoma than normal pancreatic or pancreatitis tissues, with similar  
401 tendency for AGR2 protein expression (92). These data thus suggest that AGR2  
402 overexpression caused by ER stress is an early event in pancreatic cancer genesis  
403 and may be important for the progression from normal pancreas tissue to invasive  
404 pancreatic cancer. The prognostic value of AGR2 in pancreatic cancer is debated, with  
405 discordant results (89,90). A high expression was found to correlate with poor  
406 prognosis in one study (89), whereas in another study, a low expression related to poor  
407 prognosis only using univariate analysis, but could not be confirmed using multivariate  
408 analysis (91). However, a high expression of AGR2 may be correlated to poor  
409 differentiation of pancreatic ductal adenocarcinoma, and therefore to pancreatic cancer  
410 aggressiveness (91). In pancreatic cancer cell line MPanc-96, AGR2 is involved in cell  
411 proliferation and invasion, resistance to gemcitabine and to apoptosis. In an *in vivo*  
412 murine orthotopic pancreas tumor model, the silencing of AGR2 resulted in a 4 fold  
413 reduction of tumor volume compared to control, tumor sensitization to gemcitabine,  
414 and fewer metastases in the group treated with gemcitabine and silenced for AGR2  
415 (92). Interestingly, cell proliferation, migration and chemoresistance in different  
416 cultured pancreatic cells may be favored by the soluble form of AGR2 (93). All these  
417 data suggest AGR2 is involved in pancreas cancer proliferation and chemoresistance.

#### 418 *v. Colorectal cancer*

419 AGR2 is one of the most overexpressed proteins in human colorectal cancer (CRC),  
420 especially in mucinous forms (94). In CRC, the expression and prognostic role of AGR2  
421 remains to be fully understood. Indeed, Tian et al. (74), performed a comprehensive  
422 meta-analysis using data of 2 colorectal cancer studies (70,95) selected based on their  
423 high methodological quality (Newcastle-Ottawa Scale (NOS) scores between 8 and 9).

424 For the first study, blood samples of 54 stages I-IV CRC patients were collected and  
425 AGR2 expression was analyzed by qPCR. High and low AGR2 expressers were  
426 defined based on the mean relative AGR2 mRNA expression (high expressers > mean  
427 expression level and low expresser  $\leq$  mean expression level). Independently, this  
428 study found that AGR2 expression was correlated with stage III and high-grade tumors.  
429 In addition, progression-free survival (PFS) of patients with high AGR2 expression was  
430 decreased (Hazard Ratio: 2.32;  $p = 0.037$ ) (95). For the second study, AGR2  
431 expression was measured by immunohistochemistry in 432 CRC cases and a scoring  
432 system was used to make the classification based on the staining intensity: negative  
433 (0), weakly (1), moderately (2) and strongly positive (3). Low and high expressers were  
434 defined according to their AGR2 expression as either low (score 0 or 1) or high (score  
435 2 or 3). Low expression of AGR2 in CRC tissue samples was significantly associated  
436 with high tumor grade, left primary tumor localization as well as shorter patient survival  
437 times. 78% of patients had a lower AGR2 tumor expression compared to normal  
438 colonic mucosa (70). Interestingly, when combined together, pooled hazard ratio  
439 between the two studies, AGR2 overexpression could not predict poor outcomes in  
440 colorectal cancer: Hazard Ratio 0.80, 95% Confidence Interval: 0.41–1.53 (74). CRC  
441 cell proliferation and metastatic process may be favored by the secreted form of AGR2  
442 (71), For example, mice injected with CRC cell line HT-29 *Agr2*<sup>-/-</sup> developed  
443 significantly more metastases after treatment with eAGR2 than control. In different  
444 CRC cell lines, it has also been shown that eAGR2 can inhibit the canonical Wnt/b-  
445 catenin pathway (involved in proliferation) and stimulate the non-canonical Wnt/ b-  
446 catenin CAMKII-JNK pathway by promoting Wnt11 overexpression, which is a  
447 regulator of cell polarity and motility, stimulating the metastatic process (71). In induced  
448 CRC stem cells, the canonic Wnt/b-catenin pathway stimulates AGR2 expression

449 through b-catenin binding to the *AGR2* promoter (96). *AGR2* could also be involved in  
450 maintaining stem cells stemness potential since its silencing using shRNA induced the  
451 loss of their stem cell characteristics (96). The implication of *AGR2* in maintaining  
452 cancer stem cell potential has also been reported in head and neck squamous-cell  
453 carcinoma cells (97). *AGR2* might act as a tumor suppressor in CRC tumors however,  
454 future experimental verifications in bigger sample size studies are required. The  
455 functional role of *AGR3* in CRC was investigated in 8 CRC tissue samples by  
456 immunohistochemistry and 24 CRC tumor tissues by western blot. *AGR3* was  
457 significantly more expressed in CRC tumors tissues than in the adjacent normal tissues  
458 for the 8 patients. In addition, western blot results highlighted higher expression of  
459 *AGR3* in cancer tissue in 13 out of 24 tumors compared with matched adjacent normal  
460 tissues. High expression of *AGR3* was also significantly associated with poorer overall  
461 survival and *AGR3* expression was identified as an independent prognostic factor for  
462 poor survival (98). Although the results regarding the role of *AGR3* in CRC are  
463 quantitatively insufficient and need further experimental validation, they suggest an  
464 overexpression of *AGR3* in CRC which is associated with poor prognosis.

465

#### 466 **5. AGR proteins in IBD and colitis associated cancer**

467 IBD are characterized by deficiencies in mucus layer that is part of the intestinal  
468 epithelial barrier leading to incomplete protection against microbial aggression.  
469 Consequently, excessive immune responses are triggered which results in chronic  
470 inflammation. *AGR2* has been shown to be crucial for the protection of the mucus  
471 barrier in several studies. Whole genome sequencing performed in two siblings  
472 presenting infantile IBD, revealed a new *AGR2* variant which results in *AGR2* loss of  
473 function. *AGR2* deficiency led to increased ER stress and a decrease of MUC2

474 processing which impairs the proper formation of the mucus barrier and thus induces  
475 intestinal inflammation (99). AGR2 expression was measured by qPCR in small and  
476 large bowel biopsies of 56 Crohn's disease (CD) and 57 ulcerative colitis (UC) patients  
477 and shown to be significantly lower in both disease groups compared to 25 healthy  
478 controls. Unfortunately, this study does not specify if the patients were undergoing  
479 treatment at the time of the study (100). In contrast, AGR2 gene expression was  
480 significantly upregulated in rectal biopsies of active patients with UC compared to both  
481 the remission and control groups. However, AGR2 gene expression might be  
482 modulated with the use of anti-inflammatory drugs and AGR2 higher expression in  
483 active patients could be a consequence of therapeutic improvement (101). In addition,  
484 AGR2 monomers homodimers ratio homeostasis was shown to be altered in CD. This  
485 imbalance results in AGR2 secretion leading to monocytes recruitment and  
486 inflammation (34). Patients with IBD are 2 to 3 times more likely to develop CRC cancer  
487 than the general population. They are also at increased risk for CRC death (102,103).  
488 Mice genetically deficient in Muc2 developed tumors in the small and large intestine  
489 including the rectum (104). AGR2 is essential for the production of intestinal MUC2  
490 (61) indicating a critical role of AGR2 expression for protection to colitis associated  
491 cancer. To our knowledge, the contribution of AGR1 and AGR3 in IBD has never been  
492 demonstrated.

493

## 494 **6. Theranostic perspectives**

495 AGR2 has a physiological role in ER and interacts with a number of cellular partners  
496 depending on the cell type considered. Fourteen AGR2-interacting proteins overlapped  
497 in three independent studies (50,105,106). These proteins are involved predominantly  
498 in processes into the ER which contribute to maintaining of intracellular metabolic

499 homeostasis and/or to responses to ER stress (UPR, protein folding, changes in  
500 cellular metabolism, and redox state). Given the importance of the AGR2 interaction  
501 network in maintaining cellular homeostasis, the specific targeting of ER-resident  
502 AGR2 by potential therapeutic tools is difficult to envisage, as demonstrated by the  
503 deleterious effects observed in mice invalidated for this gene. On the contrary, secreted  
504 or cytosolic forms of AGR2 that play pro-oncogenic and pro-inflammatory functions  
505 appear to be more relevant to consider and open new avenues from a therapeutic point  
506 of view.

507 *i Development of monoclonal antibodies and immunotherapies*

508 Monoclonal antibodies (mAbs) directed against AGR2 have already been  
509 experimented in animal models with promising results. The main therapeutic objective  
510 is to specifically target the extracellular AGR2, without impacting the ER-resident  
511 protein. Promising results have been reported in experimental models. 18A4Hu, an  
512 anti-AGR2 mAb, reduced tumor volume and tumor weight as much as Bevacizumab,  
513 without significant side effects, in a mammary breast cancer xenograft model (107).  
514 However, the combination with Bevacizumab was not studied, which would have been  
515 interesting as we already know that AGR2 and VEGF-A act in synergy (71,108–110).  
516 The 18A4Hu mAb is also effective on lung cancer (A549 and H460) and melanoma  
517 (B16F10) cell lines by inhibiting tumor cell growth and migration, disrupting cell  
518 morphology and junctions, and increasing p53 and p21 expression (111). A murine  
519 xenograft model of A549 and H460 cells treated with 18A4Hu showed a 3 times fold  
520 reduction of tumor volume and tumor weight compared to untreated mice. Tumor  
521 analysis of treated mice showed an increase in apoptotic markers and p53 expression,  
522 and a reduction of tumor blood vessels compared to untreated mice, suggesting that  
523 18A4Hu has antiangiogenic properties. Similarly, mice with lung metastasis of

524 melanoma cell line B16F10, treated with 18A4Hu exhibits 10 times less metastasis in  
525 lungs, and their survival was significantly improved (24 vs. 20 days). Again, it was well  
526 tolerated, and there was neither reduction of intestinal mucus nor occurrence of  
527 intestinal inflammation. P1G4 and P3A5 are two other anti-AGR2 humanized mAbs.  
528 P1G4 is not efficient in monotherapy on a xenograft model of pancreatic  
529 adenocarcinoma (112). However, its association with gemcitabine decreased  
530 significantly tumor volume and increased survival compared to gemcitabine alone.  
531 P3A5 is not efficient alone or combined with gemcitabine to reduce tumor volume but  
532 it increased survival in combination with gemcitabine. A combination of mouse mAbs  
533 directed against AGR2 and C4.4A in a murine xenograft model of pancreatic cancer  
534 resulted in a 50% objective response rate, a 50% reduction of the occurrence of  
535 metastasis, and an increase in OS. Their efficacy was similar or better than  
536 gemcitabine alone or combined with the two mAbs (93). These preliminary results are  
537 promising as they prove that mAbs anti-AGR2 have *in vivo* effects in diverse cancers,  
538 and should be investigated further. Therapeutic progresses in digestive oncology  
539 remains challenging since, with the exception of immunotherapy in microsatellite  
540 instability (MSI) or deficient Mismatch Repair (MMR) CRC and oeso-gastric cancers,  
541 most of the targeted therapies currently used have been developed more than ten  
542 years ago and no other important progresses in terms of survival have been made. In  
543 addition to the development of anti-AGR2 therapeutic antibodies, dendritic cell (DC)  
544 vaccines with AGR2 as a potent antigen could improve cancer immunotherapy. DCs  
545 were transduced with a recombinant adenovirus encoding AGR2 and these  
546 engineered DCs both increased the number of T cells secreting IFN $\gamma$  and induced the  
547 lysis of AGR2-expressing colorectal cancer cell lines through the activation of potent  
548 AGR2-specific cytotoxic T cells (113). Although limitations persist and impede the



549 application of DCs vaccines immunotherapy, these in vitro experiments highlight the  
550 potential of AGR2 to trigger efficient immune responses against some cancers. Further  
551 research in animals is required to validate the therapeutic relevance of these findings.

552

553 *ii AGR2 and AGR3 as biomarkers?*

554 The identification of biomarkers using non-invasive sampling in digestive cancer is  
555 crucial to improve efficacy of diagnostic, predict prognosis and treatment outcome (or  
556 clinical management of patients). AGR2 gene expression has been assessed in whole  
557 blood of CRC patients before therapy by qPCR. AGR2 mRNA expression was  
558 significantly increased in the blood of patients with CRC compared to controls. In  
559 addition, the level of AGR2 gene expression was correlated with some invasive and  
560 high-grade tumor prognostic factors (95). Thus, high AGR2 gene expression in the  
561 blood of CRC patients might be a sign of poor patient outcome. However, this would  
562 need to be confirmed with a longitudinal study, while its relevance in therapeutic  
563 strategy would remain to be defined. AGR2 protein level has been measured in the  
564 plasma of pancreatic cancer patients before treatment using ELISA and is significantly  
565 higher compared to healthy controls (114). A diagnostic score comprising CA19.9,  
566 AGR2 and Regenerating islet-derived 1 beta (REG1B) serum levels was shown to be  
567 more efficient than CA19.9 dosage alone in differentiating pancreatic ductal  
568 adenocarcinoma (PDAC) from benign pancreatic tumor or healthy controls, making it  
569 a potential interesting score to avoid systematic biopsies in pancreatic tumor, of which  
570 are often difficult to perform with a diagnostic performance not optimal, which often  
571 necessitates to perform additional biopsies. However, this score has not been  
572 confirmed by a prospective study. In addition, AGR2 was significantly more elevated  
573 in the serum of patients with PDAC than in other tumors, while AGR2 alone was the

574 best marker for pancreas cancer diagnostic after CA19.9 (114). Although these results  
575 need to be validated in larger cohorts of samples, AGR2, in combination with other  
576 biomarkers, could be used for better patient management through early disease  
577 detection. To improve cancer diagnosis (/for early cancer detection), several research  
578 teams have developed high sensitive assays for rapid and ultrasensitive detection of  
579 AGR2 protein (115,116). Nevertheless, the application of these highly sensitive assays  
580 to plasma samples needs to be evaluated for non-invasive early detection of cancer.  
581 However, as AGR2 is not specific to one of the digestive organs, it cannot be used  
582 alone for early cancer detection as a serum biomarker, and it needs to be integrated  
583 in diagnostic scores. Overall, very few studies have investigated AGR2 protein level in  
584 the serum of digestive cancer patients. AGR2 might be a good candidate to predict  
585 clinical outcome such as metastatic potential or relapse but it needs to be  
586 demonstrated with longitudinal studies in cohort of patients. There is no data regarding  
587 AGR2 efficacy as treatment outcome predictor in digestive cancers. Moreover, the  
588 presence of AGR3 in the serum of patients with digestive cancer has never been  
589 explored. There are also limited data on AGR3 expression in healthy and digestive  
590 cancer tissues. Only one study investigated the potential role of AGR3 as a diagnostic  
591 biomarker to distinguish between iCCA and HCC in digestive cancer (as previously  
592 described in the primary liver cancers part of this review). AGR3 expression was  
593 measured in tissues of iCCA and HCC patients by immunohistochemistry and AGR3  
594 was found to be expressed only by intrahepatic bile duct cholangiocytes but not  
595 hepatocytes (91). Thus, AGR3 could be used as a new biomarker for differential  
596 diagnosis between these two cancers.  
597

598        **7 Conclusion**

599    The AGR2 protein has gained significant interest in oncology during the last years.  
600    This holds to its multiple pro-oncogenic properties and to the particularity that its  
601    pathological roles mostly depend on its cellular or extracellular localization. AGR2 is  
602    highly expressed in the digestive system. It is overexpressed at early stages in most  
603    cancer lesions and adenocarcinoma of the digestive tube and is often associated to a  
604    poor prognosis. Less studied than in cancer, AGR2 deregulation may also play an  
605    important role in inflammation, particularly in inflammatory bowel diseases (100,117).  
606    However, the role of extracellular AGR2 in the tumor microenvironment, its influence  
607    on the immune infiltrate, its autocrine and paracrine roles remain to be more clearly  
608    characterized. The development of anti-AGR2 therapies has already shown interesting  
609    results in animals and plasma/serum AGR2 could serve as prognostic/diagnostic  
610    biomarker. In the future, their development may have prospects in diverse pathologies  
611    like cancer and inflammatory diseases and may enter into the therapeutic arsenal of  
612    the treatment of these patients.

613

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625

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644 **Author contribution statement**

645 EB, EC, EOD and CP wrote the first draft of the manuscript, made the figures and  
646 finalized the document. LAE carried out the structural analyses presented in Figure 1.

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Localization	Protein	Function	References
Extracellular	AGR1	<i>Found in extracellular vesicles</i>	(118)
	AGR2	Angiogenesis/ VEGF potentialization <i>EMT Induction</i> Non canonic Wnt dependent cell migration AREG secretion and EGFR activation Binds to C4.4 and promote cell migration <i>Pro-inflammatory</i>	(71,108–110) (71,119) (71) (120) (31,93) (34)
	AGR3	Pro-migratory through SRC activation Binds to C4.4 and promote cell migration	(28) (31)
ER	AGR1	Activation of ATF6alpha Folding of PTX3	(42,43) (121)
	AGR2	<i>Productive protein folding and quality control</i> ERAD Regulation of PDI in cancer cells Deregulates proteins of the ubiquitin-proteasome degradation pathway CDX2 expression induction	(1,10,45) (10) (45) (45) (122)
	AGR3	ND	
Cytosol	AGR1	ND	
	AGR2	Inhibition of p53 <i>Modulation of RuvbL2/Reptin functions</i> Stimulates cell proliferation by overexpression of cyclin D1, c-myc, p-SRC, survivin and AREG Facilitates EMT by stabilizing p65 and activation of NFkB	(44,55,56) (41) (108,120) (110)
	AGR3	ND	

1049

1050 **Table 1: Pro-oncogenic gains-of-functions associated with the different**  
1051 **subcellular localizations of AGR proteins** – *Italic* type setting is indicative of potential  
1052 indirect pro-oncogenic functions.  
1053

1054 **Figure legends**

1055

1056 **Figure 1 – the mammalian AGR proteins - structural aspects.** a) Phylogram  
1057 representation of human and mouse AGR1, 2, 3 proteins (performed using  
1058 ClustalOmega). b) Amino-acid (aa) sequence alignment of human and mouse AGR1,  
1059 2 and 3 proteins. Three functional domains are indicated (Signal peptide for the  
1060 targeting to the ER; thioredoxin domain; peptide binding and ER retention). Polar and  
1061 basic aa are indicated in pink, polar and acidic aa in blue, polar and neutral aa in green,  
1062 non-polar and neutral in red. AA identity is indicated by “\*”, conservation by “:”. c)  
1063 Structure of the E60-K64 interaction dependent AGR2 dimer. d) Structure of the C81  
1064 interaction dependent AGR2 dimer.

1065

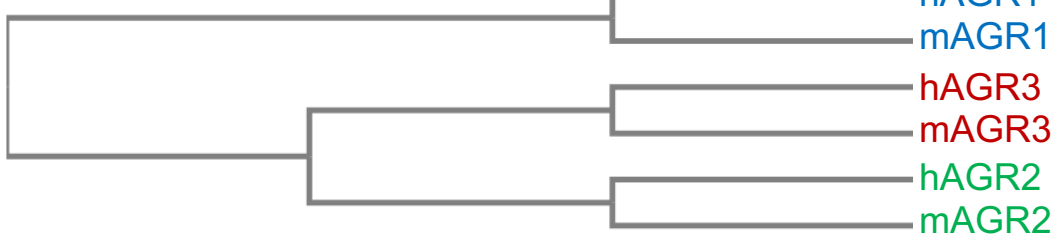
1066 **Figure 2 – Sub-cellular functions of AGR proteins: structural aspects.**  
1067 Demonstrated sub-cellular localizations of AGR1 (Blue), AGR2 (green) and AGR3  
1068 (red) and associated functions. ERQC: Endoplasmic Reticulum Quality Control; EV:  
1069 extracellular vesicle, EMT: Epithelial-to-Mesenchymal Transition; PDI: Protein  
1070 Disulfide Isomerase; UPR: Unfolded Protein Response.

1071

1072 **Figure 3 – Expression of AGR family members in the normal gastro-intestinal**  
1073 **tract.** a) AGR2 expression measured by immune-histochemistry. Black borders  
1074 indicate images obtained in-house and orange borders indicate data from the Human  
1075 Protein Atlas (<https://www.proteinatlas.org/> - 50, 51). b) AGR1, AGR2 and AGR3 gene  
1076 expression data extracted from the Human Protein Atlas measured by RNA-  
1077 sequencing in the colon, stomach, liver and pancreas of healthy tissues.

1078

1079 **Figure 4 – Expression of AGR family members in gastro-intestinal cancers. a)**  
1080 Percentage of tumors from liver, pancreas, stomach and intestinal sphere displaying a  
1081 positive AGR2 (pink) or AGR3 (blue) immune-histochemistry staining (full circle =  
1082 100%). **b)** AGR1, AGR2 and AGR3 gene expression data extracted measured by RNA-  
1083 sequencing in the colon, stomach, liver and pancreas of cancer tissues. Data extracted  
1084 from the Human Protein Atlas (<https://www.proteinatlas.org/> - 50, 51).  
1085



**b**

	Signal peptide			
hAGR1	METRPRLGATCLL--GFSFLL	-----	LVISSDGHNGLGKGFGDHIHWRTLE	44
mAGR1	--MSLRFGATCLL--SFSFLL	-----	LITSSDGRITGLGKGFGDHIHWRTLE	42
hAGR3	MMLHSALGL-CLLLVTVSSNLA	-----	IAIKKEKRPPQTL SRGWGDDITWVQTY	48
mAGR3	-MLHSALAL-CLLLITVSSNLA	-----	IAIKKEKRPPQTL SRGWGDDITWVQTY	47
hAGR2	-MEKIPVSA-FLLLVALS YTLARDTTVKPGAKKDTKDSRPKLPQTL SRGWGDQLIWTQTY	-----	-----	58
mAGR2	-MEKFSVSA-ILLLV AISGTLAKDTTVKSGAKKDPKDSRPKLPQTL SRGWGDQLIWTQTY	-----	-----	58
	.. ** .* *		*.:*:*:*: *	
			Thioredoxin	
hAGR1	DGKKEAA	-----	ASGLPLMVI IHKSWCGACKALPKPKFAESTEISEL	85
mAGR1	DGKKEAAARILGLFGLGWRLNPELVQADGLPLMVI IHKSWCGACKALPKPKFAESTEISEL	-----	-----	102
hAGR3	EEGL	-----	FYAQKSKKPLMVIHHL EDCQYSQALKKVFAQNEEIQEM	90
mAGR3	EEGL	-----	FHARKSNKPLMVIHHL EDCQYCQALKKEFAKNEEIQEM	89
hAGR2	EEAL	-----	YKSKTSNKPLMVIHHL EDCPHSQALKKVFAENKEIQKL	100
mAGR2	EEAL	-----	YRSKTSNRPLMVIHHL EDCPHSQALKKVFAEHKEIQKL	100
:			. **:* * . * .:*** **:	**..:
hAGR1	S-HNFVMVNLEDEE EPKDED FSPDGGYIPRILFLDPSGKVHPEIINENGNPSYKYFYVSA	-----	-----	144
mAGR1	S-HNFVMVNLEDEE EPKDED FSPDGGYIPRILFLDPSGKVRPEIINESGNPSYKYFYVSA	-----	-----	161
hAGR3	AQNKFIMLNLMH--ETTDKNLSPDGQYVPRIMFVDPSLTVRADIAGRYSNRLYTYEPRDL	-----	-----	148
mAGR3	AQNDFIMLNLMH--ETTDKNLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYTYEPQDL	-----	-----	147
hAGR2	A-EQFVLLNLVY--ETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADT	-----	-----	157
mAGR2	A-EQFVLLNLVY--ETTDKHLSPDGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDT	-----	-----	157
:	: ..*:*** * * :*:*** * ***:*** * **:		*: * .. * * *	
			ER retention motif	
hAGR1	EQVVQGMKEAQERLTGDAFRKKHLEDEL	-----	-----	172
mAGR1	EQVVQGMKEAQERLTGDAFREKHFQDEL	-----	-----	189
hAGR3	PLLIENMKKALRLIQSEL	-----	-----	166
mAGR3	PMLVDNMKKALRLIQSEL	-----	-----	165
hAGR2	ALLLDNMKKALKLLKTEL	-----	-----	175
mAGR2	ALLYDNMKKALKLLKTEL	-----	-----	175
:	: :.***: * : :			

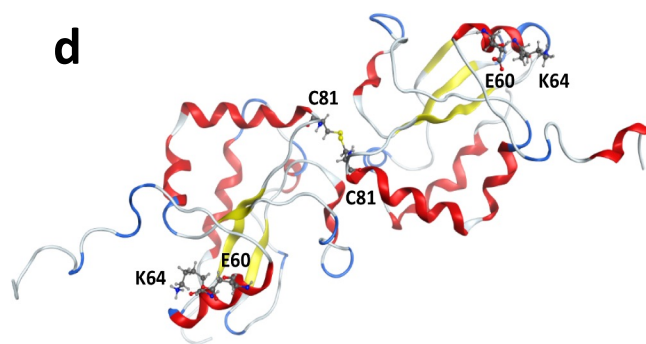
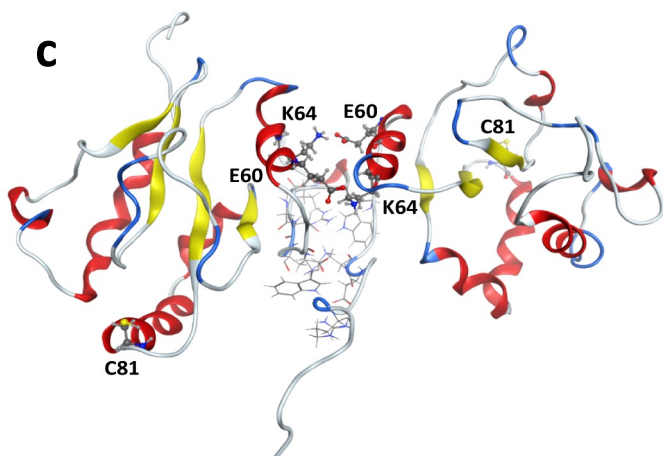


Figure 1

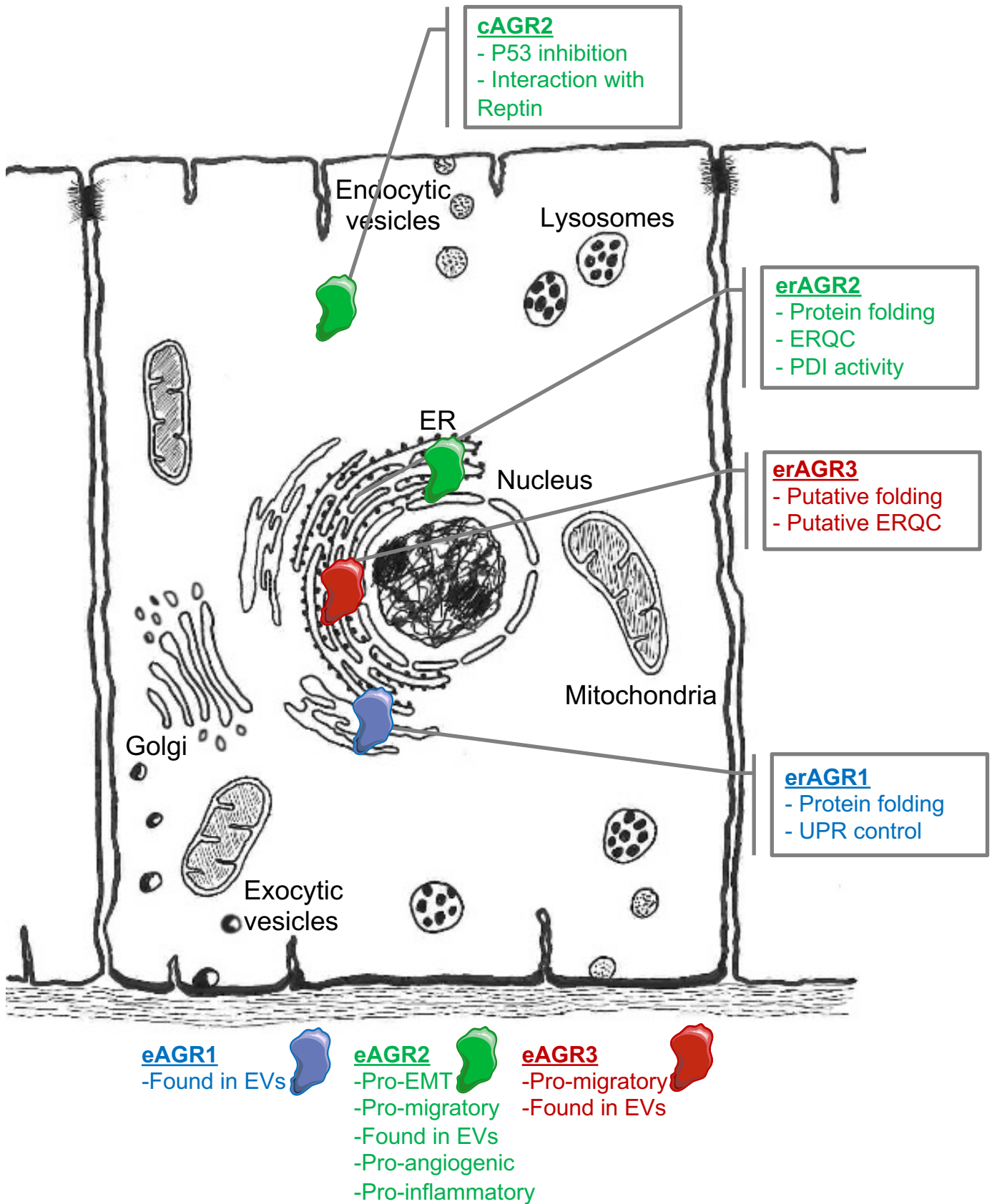
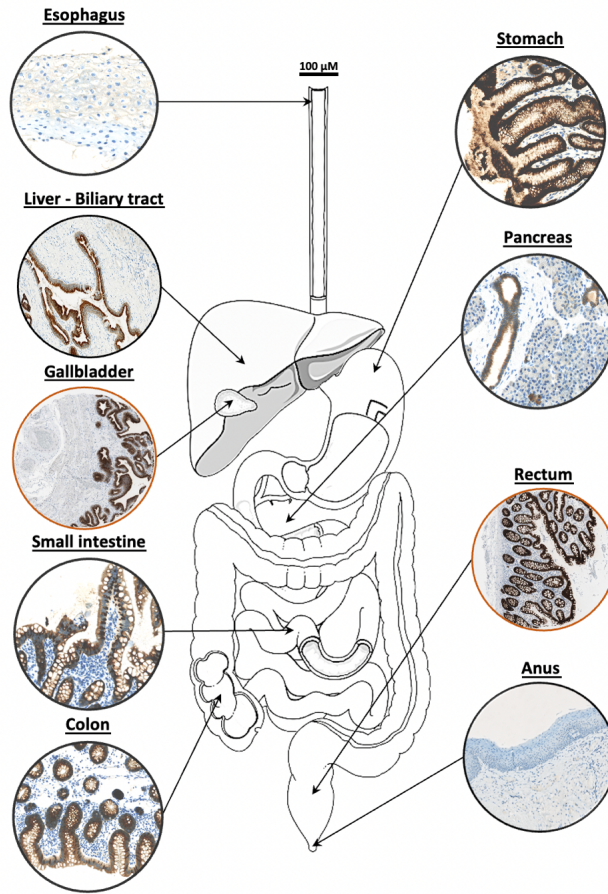


Figure 2

**a**



**b**

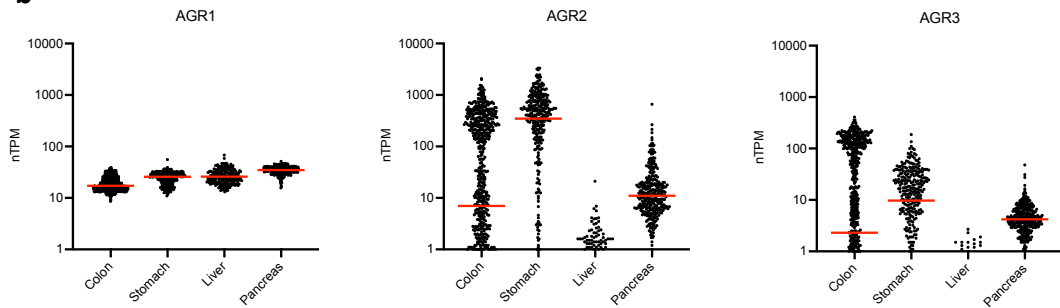


Figure 3

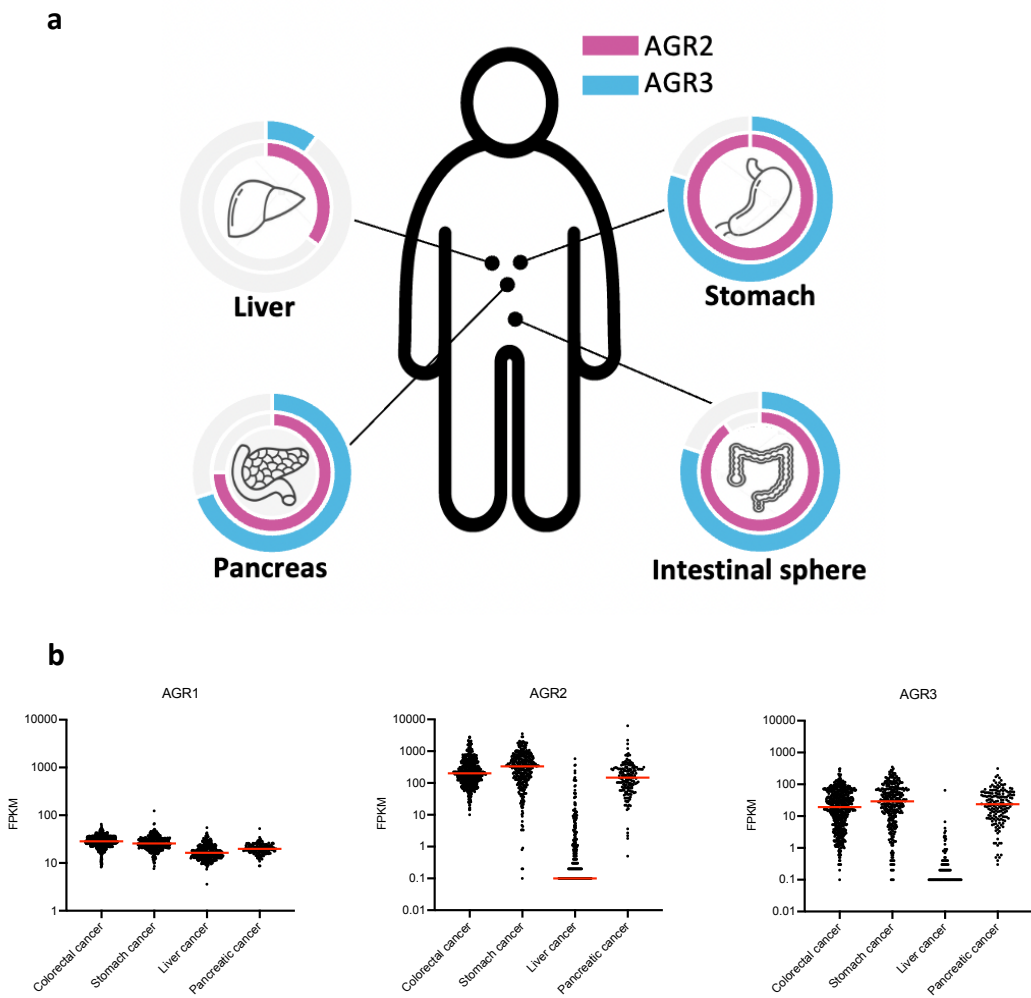


Figure 4