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## Biology of the Major Facilitative Folate Transporters SLC19A1 and SLC46A1

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### Abstract

This chapter focuses on the biology of the major facilitative membrane folate transporters, the reduced folate carrier (RFC), and the proton-coupled folate transporter (PCFT). Folates are essential vitamins, and folate deficiency contributes to a variety of health disorders. RFC is ubiquitously expressed and is the major folate transporter in mammalian cells and tissues. PCFT mediates intestinal absorption of dietary folates. Clinically relevant antifolates such as methotrexate (MTX) are transported by RFC, and the loss of RFC transport is an important mechanism of MTX resistance. PCFT is abundantly expressed in human tumors and is active under pH conditions associated with the tumor microenvironment. Pemetrexed (PMX) is an excellent substrate for PCFT as well as for RFC. Novel tumor-targeted antifolates related to PMX with selective membrane transport by PCFT over RFC are being developed. The molecular picture of RFC and PCFT continues to evolve relating to membrane topology, N-glycosylation, energetics, and identification of structurally and functionally important domains and amino acids. The molecular bases for MTX resistance associated with loss of RFC function, and for the rare autosomal recessive condition, hereditary folate malabsorption (HFM), attributable to mutant PCFT, have been established. From structural homologies to the bacterial transporters GltT and LacY, homology models were developed for RFC and PCFT, enabling new mechanistic insights and experimentally testable hypotheses. RFC and PCFT exist as homo-oligomers, and evidence suggests that homo-oligomerization of RFC and PCFT monomeric proteins may be important for intracellular trafficking and/or transport function. Better understanding of the structure and function of RFC and PCFT should facilitate the rational development of new therapeutic strategies for cancer as well as for HFM.

### 1. INTRODUCTION

The folates are members of the B family of vitamins that require active membrane transport systems for cellular uptake (Matherly & Goldman, 2003; Zhao, Diop-Bove, Visentin, &

Goldman, 2011). Studies of the membrane transport of folate cofactors over the past five decades have established its nutritional importance in providing cofactors for essential metabolic reactions required for cell proliferation and tissue repair. Transport is also required for uptake of antifolate drugs such as methotrexate (MTX) into tumor cells and is a major determinant of chemotherapeutic efficacy for these agents (Matherly, Hou, & Deng, 2007; Zhao & Goldman, 2003).

The reduced folate carrier (RFC; SLC19A1) belongs to the solute carrier (SLC) group of transporters and is the principal mechanism by which folates and clinically used antifolates are delivered to mammalian cells and tissues from the systemic circulation at neutral pH (Matherly et al., 2007). Although a transporter with unique properties from RFC was recognized for over 30 years to mediate intestinal absorption of folates, and more recently to drive uptake of the new generation antifolate pemetrexed (PMX) into tumor cells, it was not until 2006 that this system was cloned and characterized (Qiu et al., 2006). Thus, the proton-coupled folate transporter (PCFT; SLC46A1) was recognized as distinct from RFC or other known transporters capable of transporting folates such as the family of organic anion transporters (Matherly et al., 2007; Rizwan & Burckhardt, 2007). Identification of loss-of-function mutations in PCFT from human subjects with hereditary folate malabsorption (HFM) provided the molecular basis for this rare condition and unequivocally established PCFT as the principal mechanism for intestinal absorption of dietary folates (Qiu et al., 2006).

This review focuses on the biology of the major facilitative folate transporters, RFC and PCFT, including their physiology and structural and functional properties.

## 2. THE BIOLOGICAL ROLES OF FOLATES AND THERAPY WITH ANTIFOLATES

Folate is the generic term for water-soluble members of the B class of vitamins that are required for normal tissue growth and development in mammalian cells. The biological importance of reduced folates relates to their essential roles in one-carbon transfer reactions leading to thymidylate, purine nucleotides, serine, and methionine (Stokstad, 1990). Folates are also required for vitamin-B12-dependent synthesis of methionine, a precursor of *S*-adenosyl methionine, which is needed for methylation of DNA, histones, lipids, and neurotransmitters (Lu, 2000). Folic acid (Fig. 4.1) is the synthetic form of the metabolically important folates found in cells that differ in the level of oxidation of the pteridine ring, the nature of the one-carbon substituent at the N<sup>5</sup> and N<sup>10</sup> positions, and the extent of  $\gamma$ -glutamate conjugation (Stokstad, 1990). The major circulating folate is 5-methyl tetrahydrofolate (THF) (Fig. 4.1). Following cellular uptake, 5-methyl THF is converted to various THF polyglutamates required for folate-dependent metabolic reactions (Stokstad, 1990).

Mammalian cells, unlike bacteria, cannot synthesize folates *de novo*. Hence, folate requirements must be met entirely from dietary sources. Traditionally, folates are derived from foods such as liver and dark green leafy vegetables. In the United States and Canada, the fortification of cereals, grains, and bread with folic acid now represents an important

source of dietary folate and has resulted in a rise in folate levels in tissues and blood (Jacques, Selhub, Bostom, Wilson, & Rosenberg, 1999).

Folates are hydrophilic molecules that are anions at physiological pH and thus cross biological membranes poorly by diffusion. Reflecting this, mammalian cells have evolved sophisticated uptake systems for facilitating cellular uptake of folate cofactors (Kugel Desmoulin, Hou, Gangjee, & Matherly, 2012; Matherly & Goldman, 2003; Zhao et al., 2011). Major facilitative folate transporters include: (i) the RFC, an anionic exchanger and the major route of delivery of folates to systemic tissues at physiological pH (Matherly & Goldman, 2003; Matherly et al., 2007); and (ii) PCFT, like RFC, a member of the superfamily of solute carriers, but with an acidic pH optimum and distinct transport specificities (Kugel Desmoulin et al., 2012; Zhao & Goldman, 2007). In certain epithelial tissues such as renal cells and macrophages, folate receptors (FRs)  $\alpha$  and  $\beta$  are embedded in the plasma membrane by a glycosylphosphatidylinositol anchor and mediate uptake of folates into cells via receptor-mediated endocytosis at neutral to mildly acidic pHs (Elnakat & Ratnam, 2004; Kamen & Smith, 2004). Whereas RFC is ubiquitously expressed in human tissues (Whetstone, Flatley, & Matherly, 2002), PCFT is more narrowly expressed, although substantial levels of PCFT were detected in the duodenum and jejunum, kidney, and liver, as well as choroid plexus (Kugel Desmoulin et al., 2012). FR $\alpha$  is expressed in the proximal renal tubules, choroid plexus, uterus, and placenta, whereas FR $\beta$  is expressed in placenta and hematopoietic cells, and in activated macrophages (Elnakat & Ratnam, 2004).

Proliferating tumor cells have unique metabolic requirements characterized by enhanced nutrient uptake and metabolic pathways to support the biosynthesis of macromolecules needed for cell growth and division. These pathways include the folate-dependent *de novo* synthesis of purine nucleotides and thymidylate. Structural analogs of folate compounds (i.e., antifolates) have been developed and continue to be important drugs for treating a variety of cancers (Gonen & Assaraf, 2012a; Kugel Desmoulin et al., 2012; Visentin, Zhao, & Goldman, 2012a) and nonmalignant diseases such as psoriasis and rheumatoid arthritis (Chladek et al., 1998; Wessels, Huizinga, & Guchelaar, 2008). Clinically relevant antifolates include MTX, PMX, raltitrexed, and pralatrexate (Fig. 4.1). These classic antifolates use the same transporters as physiological folates to enter tumor cells, particularly RFC (Kugel Desmoulin et al., 2012; Matherly et al., 2007). Membrane transport of antifolates is an important determinant of clinical efficacy for cancer, and impaired transport is a common mechanism of drug resistance (Zhao & Goldman, 2003). In recent years, there has been emphasis on developing tumor-targeted folate-based therapies reflecting selective cellular uptake of folate-conjugated cytotoxins or cytotoxic antifolates by FRs or the PCFT by tumor cells (Deng, Wang, et al., 2008; Deng et al., 2009; Gibbs et al., 2005; Kugel Desmoulin et al., 2012, 2011a, 2010; Wang et al., 2012, 2010, 2011; Xia & Low, 2010; Yang, Vlashi, & Low, 2012). This has fostered a new paradigm, namely the rational development of tumor-targeted therapies based on tumor-specific expression and/or function of the major folate transporters.

In the following sections, we focus on biological properties of RFC and PCFT, including structure, function, and mechanisms of facilitative transport.

### 3. REDUCED FOLATE CARRIER (SLC19A1)

#### 3.1. Properties of RFC

As noted above, RFC is expressed ubiquitously and is widely considered to be the major transport system for folates in mammalian cells and tissues (Matherly et al., 2007). Very high levels of RFC transcripts are detected in liver and placenta, with appreciable levels in other tissues, including kidney, lung, bone marrow, intestine, brain, and portions of the central nervous system (Whetstone et al., 2002). By immunohistochemistry in mouse tissues, RFC was detected at the basolateral membrane of the renal tubule epithelium, the apical brush border membrane of the small intestine and colon, hepatocyte membranes, the apical surface of the choroid plexus, and the apical membrane of the cells lining the spinal canal (Wang, Zhao, Russell, & Goldman, 2001). Reflecting its physiological importance, low levels of RFC could result in a number of pathophysiological states associated with folate deficiency, ranging from cardiovascular disease, fetal abnormalities, neurological disorders, to possibly cancer (Matherly, 2004; Matherly et al., 2007). RFC is important for development since inactivating both RFC alleles by targeted homologous recombination in mice is embryonic lethal (Zhao, Russell, et al., 2001).

The properties of RFC-mediated transport in both human and rodent models have been comprehensively studied in numerous laboratories (Matherly et al., 2007). Investigators have used commercially available radioactive MTX as a surrogate substrate in functional studies on RFC because MTX is not metabolized over short intervals and because of the ease and accuracy of influx determinations and of distinguishing between free and protein-bound drug within cells (Goldman, Lichtenstein, & Oliverio, 1968). With minor exceptions, transport properties are remarkably conserved among species, in large part reflecting significant conservation of primary sequence (see below). The murine RFC was cloned in 1994 (Dixon, Lanpher, Chiu, Kelley, & Cowan, 1994), followed shortly thereafter by the human RFC by a number of laboratories (Moscow et al., 1995; Prasad, Ramamoorthy, Leibach, & Ganapathy, 1995; Williams & Flintoff, 1995; Wong, Proefke, Bhushan, & Matherly, 1995), thus paving the way to further detailed studies of RFC structure and function. The human RFC gene is localized to chromosome 21q22.3 (Moscow et al., 1995) and is subjected to complex regulation involving multiple promoters and noncoding exons that likely ensures its ubiquitous tissue expression (Matherly et al., 2007).

For most reduced folates and many antifolate substrates including clinically relevant drugs such as MTX and pralatrexate, transport by RFC is saturable at low micromolar concentrations ( $K_t \sim 1\text{--}5 \mu\text{M}$ ) (Matherly et al., 2007). The novel  $\delta$ -hemiphthaloylorinithine antifolate PT523 (Fig. 4.1) is one of the best substrates for human RFC with a  $K_t$  value less than  $1 \mu\text{M}$  (Rosowsky, Bader, Wright, Keyomarsi, & Matherly, 1994). Likewise, the benzoquinazoline antifolate GW1843U89 (Fig. 4.1) has a reported  $K_t$  of  $0.33 \mu\text{M}$  and is an excellent substrate for human RFC ( $V_{\text{max}}/K_t = 20.3$ ), although it is a surprisingly poor substrate for the murine RFC ( $V_{\text{max}}/K_t = 0.25$ ) (Duch et al., 1993). The affinity of RFC for folic acid is orders of magnitude less than for reduced folates (Goldman et al., 1968; Westerhof et al., 1995). While RFC transport is not stereospecific for 5-methyl THF (Fig. 4.1) (Sirotnak & Donsbach, 1974; White, Bailey, & Goldman, 1978), the (6*R*) isomer of 5-

formyl THF (Fig. 4.1) has a far lower affinity than the natural (6*S*) stereoisomer (Sirotnak et al., 1979). Thus, the (6*R*) stereoisomer of 5-formyl THF in leucovorin [(6*R,S*)5-formyl THF] should have no impact on cellular uptake of the (6*S*) stereoisomer of 5-formyl THF.

RFC is an anion transporter, and its activity is competitively inhibited by inorganic anions such as chloride, bicarbonate, and phosphate, or by structurally diverse organic anions such as adenine nucleotides and thiamine phosphate (Goldman, 1971a). Furthermore, replacing anionic buffers with nonanionic HEPES–sucrose buffers results in a dramatic stimulation of concentrative uptake of MTX (Henderson & Zevely, 1983b). When cells are incubated in anion-free buffers (without glucose) and preloaded with radio-labeled MTX, the rate of MTX efflux is inhibited. Efflux can be induced upon addition of both inorganic and organic anions (e.g., chloride, sulfate, phosphate, thiamine pyrophosphate, AMP, ADP, and 5-formyl THF) (Henderson & Zevely, 1980, 1981).

Folates include a glutamate moiety for which both  $\alpha$ - and  $\gamma$ -carboxyl groups are ionized at physiological pH. Replacing the glutamate with valine or 2-aminosuberate in the novel antifolate substrate ICI-198,583 preserved binding to RFC (Westerhof et al., 1995). Modifications of the glutamate  $\gamma$ -carboxyl group appear to be well tolerated; replacing either the glutamate with a  $\delta$ -hemiphthaloylornithine in PT523 (Fig. 4.1) or the  $\gamma$ -carboxyl with a tetrazole in ZD9331 (Fig. 4.1) preserved substrate activity (Jansen, 1999; Rosowsky et al., 1994). A series of diaminofuro[2,3-*d*]pyrimidine antifolates with hydrogen or methyl substitutions at the  $\alpha$ - or  $\gamma$ -carboxyl groups of the terminal glutamate were used to systematically assess the importance of these groups for substrate binding to RFC (Deng, Hou, et al., 2008). Analogs with only a single  $\alpha$ -carboxyl but no  $\gamma$ -carboxyl were potent inhibitors of MTX transport by RFC, whereas analogs with only a  $\gamma$ -carboxyl group but no  $\alpha$ -carboxyl group were poor inhibitors. Thus, the  $\alpha$ -carboxyl group is important for binding of (anti)folate substrates to RFC.

Transport by RFC is temperature-dependent and sodium-independent (Goldman, 1971a; Goldman et al., 1968) and shows a distinctly neutral pH optimum. Transport decreases dramatically below pH 7 (Sierra, Brigle, Spinella, & Goldman, 1997). Transport by RFC is concentrative, although the energy source for this uphill process is not directly linked to ATP hydrolysis (Goldman, 1971a; Henderson & Zevely, 1983a). Concentrative uptake by RFC is driven by gradients of organic anions that bind and exit cells via RFC and block folate export via this same mechanism (Goldman, 1971a). Consistent with this model, influx of radiolabeled MTX by RFC is enhanced (trans-stimulated) in cells “preloaded” with high concentrations of 5-formyl or 5-methyl THF (Goldman, 1971b). Similarly, in studies with membrane vesicles loaded with sulfate or phosphate anions, uptake of MTX in the “trans” compartment was dramatically stimulated via a counter-transport mechanism (Yang, Sirotnak, & Dembo, 1984). Finally, thiamine pyrophosphate and ZMP (5-aminoimidazole-4-carboxamide ribonucleotide) are *bona fide* RFC substrates, which, when present intracellularly, can trans-stimulate folate influx by RFC while inhibiting (anti)folate export (Visentin, Zhao, & Goldman, 2012b; Zhao, Gao, et al., 2001). Collectively, these studies support a model whereby concentrative folate uptake by RFC is driven by a counter-transport mechanism involving an anionic cellular metabolite, perhaps an organic phosphate.

However, neither the identity of the actual physiologic counter-anion(s) nor the detailed mechanism by which bidirectional anion fluxes are coupled is firmly established.

### 3.2. Structure and function of RFC

RFC belongs to the major facilitator superfamily (MFS) of transporters. MFS proteins transport an assortment of substrates including amino acids, neurotransmitters, sugars, vitamins, nucleosides, and organic phosphate in a uniport, symport, or antiport fashion (Chang, Lin, Keith Studley, Tran, & Saier, 2004). While no structure of RFC is yet available, three-dimensional crystal structures are available for RFC structural homologs including the bacterial lactose/proton symporter (LacY) (Abramson et al., 2003) and the inorganic phosphate/glycerol-3-phosphate antiporter (GlpT) (Huang, Lemieux, Song, Auer, & Wang, 2003) from which to draw mechanistic inferences and to generate predictive homology models (Hou, Ye, Haska, & Matherly, 2006) that can be experimentally tested. By analogy with these bacterial transporters, membrane transport of folates by RFC would be expected to involve a physical movement of the carrier within the plasma membrane accompanied by alternate accessibilities of the aqueous substrate-binding cavity between the intra- and extracellular compartments. For RFC, as noted above, transport is driven by extrusion of anions down a large (intra- to extracellular) concentration gradient.

While the functional properties of RFC in cultured murine leukemia cells were first documented over 40 years ago (Goldman et al., 1968), it was only following cloning of RFCs from multiple species (Dixon et al., 1994; Moscow et al., 1995; Prasad et al., 1995; Williams & Flintoff, 1995; Williams, Murray, Underhill, & Flintoff, 1994; Wong et al., 1995) that it became possible to explore structural determinants of RFC transport that impact its physiology and pharmacology. These include its membrane topology, N-glycosylation, functionally and structurally important domains and amino acids, and, more recently, tertiary and quaternary structures.

RFC is characterized by 12 transmembrane domains (TMDs) and cytoplasmically oriented N- and C-termini (Fig. 4.2) (Cao & Matherly, 2004; Ferguson & Flintoff, 1999; Liu & Matherly, 2002). Human RFC includes 591 amino acids and is N-glycosylated at Asn58 in the loop domain connecting TMD1 and TMD2 (Matherly, Czajkowski, & Angeles, 1991; Wong, Zhang, Proefke, & Matherly, 1998). RFCs from various species are conserved (64–66% between humans and rodents) with substantial conservation within the TMDs and the lowest homologies in the loop domain connecting TMD6 and TMD7, and in the N- and C-termini (Matherly & Hou, 2008). In structure–function studies of RFC, investigators have sought to identify domains and/or residues that contribute to binding and/or translocation of (anti)folate substrates, as well as TMD helix packing associations that facilitate folate substrate binding and translocation.

Deletions of the N- and C-termini exclusive of the TMDs from ectopically expressed human RFC did not impact surface targeting or transport activity in HEK-293 and HuTu-80 cells (Marchant, Subramanian, Parker, & Said, 2002). While the same findings were obtained with rodent RFCs for the N-terminus, the impact of deleting the C-terminal domain ranged from modest to a complete loss of expression (Sadlish, Williams, & Flintoff, 2002; Sharina, Zhao, Wang, Babani, & Goldman, 2002). Larger deletions of human RFC that included

TMD segments abolished surface targeting (Marchant et al., 2002). The linker domain connecting TMD6 and TMD7 in RFC (Fig. 4.2) is poorly conserved with the exception of a Lys204–Arg214 segment. Deleting segments (49 or 60 amino acids; positions 215–263 and 204–263, respectively) of the TMD6/TMD7 linker from human RFC abolished transport activity (Liu, Witt, & Matherly, 2003). Interestingly, replacing the deleted segments with 73 or 84 amino acid segments of nonhomologous sequence from SLC19A2 restored transport, although there was an absolute requirement for the human RFC 204–214 peptide sequence. Finally, when human RFC was expressed as individual TMD1–6 and TMD7–12 half molecules, transport activity was restored (Witt, Stapels, & Matherly, 2004). These studies establish that neither the N- or C-termini nor the TMD6/TMD7 linker is critical for folate substrate binding and membrane translocation. The primary role of the TMD6-TMD7 loop domain is to provide appropriate spacing between the TMD1–6 and TMD7–12 segments for optimal carrier function.

Studies with RFC mutants have implicated conserved amino acids in TMD1, TMD2, TMD4, TMD8, TMD10, and TMD11 as important for transport (Fig. 4.2) (Matherly et al., 2007). Structurally or functionally important amino acids identified from mutant studies include (numbers based on human RFC sequence) Val29, Gly44, Glu45, Ser46, Ile48, Val106, Trp107, Ser127, Ala132, Arg133, Tyr281, Ser313, and Arg373 (Brigle, Spinella, Sierra, & Goldman, 1995; Drori, Jansen, Mauritz, Peters, & Assaraf, 2000; Jansen et al., 1998; Liu & Matherly, 2001; Roy, Tolner, Chiao, & Sirotnak, 1998; Sadlish et al., 2002; Sharina et al., 2002; Wong et al., 1999; Zhao, Assaraf, & Goldman, 1998; Zhao, Gao, Babani, & Goldman, 2000; Zhao, Gao, & Goldman, 1999). Mutation of Lys404 in TMD11 of murine RFC (Lys411 in human RFC) to leucine resulted in 11- and 4-fold increases in  $K_i$  values for 5-methyl THF and 5-formyl THF, respectively (Sharina, Zhao, Wang, Babani, & Goldman, 2001). Binding of the  $\gamma$ -carboxyl group of MTX was localized to Lys411 of human RFC based on *N*-hydroxysuccinimide [ $^3$ H]MTX radioaffinity-labeling results (Deng, Hou, et al., 2008).

To identify domains that form the putative substrate-binding pocket/translocation pathway, Hou and coworkers (Hou, Stapels, Haska, & Matherly, 2005; Hou et al., 2006) used scanning cysteine accessibility methods (SCAM) with a functional “Cys-less” human RFC in which the 11 cysteine residues were replaced with serines (Cao & Matherly, 2003). In these studies, 282 cysteine mutants (in the Cys-less background) were individually expressed in RFC-null HeLa cells and treated with 2-sulfonatoethyl methanethiosulfonate (MTSES) so as to identify positions that are aqueous accessible (in spite of their TMD localization) and that may participate in folate substrate binding and/or translocation (Hou et al., 2005, 2006). From the patterns of transport inhibition by MTSES and protection from MTSES inhibition by leucovorin, residues localized in TMD4, TMD5, TMD7, TMD8, TMD10, and TMD11 were implicated in forming the putative substrate-binding pocket (Hou et al., 2005, 2006). Of the 282 RFC cysteine mutants tested, only 10 were completely inactive. Interestingly, these included a stretch of amino acids in TMD4 (Arg133, Ile134, Ala135, Tyr136, Ser138), Tyr281 in TMD7, Ser313 in TMD8, and Arg373 in TMD10. As described above, Arg133, Ser313, and Arg373 were previously implicated as structurally or

functionally important (Liu & Matherly, 2001; Sadlish et al., 2002; Sharina et al., 2002; Zhao et al., 1999).

From the solved structures of the LacY and GlpT proteins, a three-dimensional homology model for human RFC was generated that included a membrane translocation pathway formed from TMD1, TMD2, TMD4, TMD5, TMD7, TMD8, TMD10, and TMD11, and mechanistically important roles for Tyr281, Ser313, Arg373, and Lys411 (Fig. 4.3) (Hou et al., 2006). Based on this homology model, site-directed mutagenesis of Ser313 (localized to TMD8) and homo-bifunctional cross-linking between TMD8 and juxtaposed TMD5 were used to further examine the functional significance of Ser313 and TMD8 in RFC membrane transport (Hou, Wu, Ye, Cherian, & Matherly, 2010). The results showed that there are substantial differences between structurally diverse RFC (anti)folate substrates in their binding to RFCs with mutated Ser313, and in inducing conformational changes involving the proximal end of TMD8, determined by protein cross-linking. Thus, there is direct support for an essential role of TMD8 and Ser313 in binding and/or membrane translocation of (anti)folate substrates (Hou, Wu, et al., 2010).

Human RFC, like many MFS proteins, exists as a homo-oligomer (Hou & Matherly, 2009). RFC monomers appear to function independently (i.e., oligomerization is not a prerequisite for transport) (Hou, Cherian, Drews, Wu, & Matherly, 2010). Nonetheless, co-folding of RFC monomers to form oligomeric RFC seems to be functionally important for trafficking from the ER to the cell surface (Hou & Matherly, 2009). Co-expressing wild-type and inactive mutant S138C RFCs produces a dominant-negative phenotype due to decreased surface expression of both mutant and wild-type RFCs. Thus, it appears that RFC oligomerization may serve an important regulatory function. Clearly, further characterization of oligomeric RFC, including structural and regulatory determinants of oligomer formation, is essential, given its potential importance to understanding the broader physiologic and pharmacologic role of this transporter.

## 4. PROTON-COUPLED FOLATE TRANSPORTER (SLC46A1)

### 4.1. Properties of PCFT

In 2006, a new folate transporter was identified—PCFT (Qiu et al., 2006). While PCFT also belongs to the superfamily of solute carriers, it is functionally distinct from the RFC in that PCFT functions optimally at acidic rather than neutral pH, and it shows several differences in its specificities for particular(anti) folate substrates (Kugel Desmoulin et al., 2012; Zhao & Goldman, 2007).

The cloning of PCFT provided a molecular basis for the long-recognized but uncharacterized low pH folate transport activity in many normal and malignant cells, most notably in the small intestine (Assaraf, Babani, & Goldman, 1998; Henderson & Strauss, 1990; Kuhnel, Chiao, & Sirotnak, 2000; Sierra & Goldman, 1998; Zhao, Gao, Hanscom, & Goldman, 2004; Zhao & Goldman, 2007). The critical role of PCFT in intestinal absorption of dietary folates was confirmed by the demonstration of loss-of-function mutations in the human PCFT gene in patients with HFM (Atabay et al., 2010; Borzutzky et al., 2009; Diop-Bove, Jain, Scaglia, & Goldman, 2013; Lasry et al., 2008; Mahadeo et al., 2011, 2010;



Meyer et al., 2010; Min et al., 2008; Qiu et al., 2006; Shin et al., 2011, 2010; Zhao et al., 2007). PCFT knockout mice were developed that largely recapitulate the HFM syndrome seen in humans (Salojin et al., 2011). These mice fail to absorb dietary folates, resulting in undetectable levels of serum folate and elevated plasma homocysteine.

Within the intestine, the highest PCFT levels are found at the apical brush border membrane of the proximal jejunum and duodenum, while levels decrease markedly in other segments of the intestine and colon (Inoue et al., 2008; Qiu et al., 2006, 2007; Urquhart et al., 2010). Other major sites of PCFT expression include the kidney, placenta, spleen, the sinusoidal membrane of the liver, the basolateral membrane of the choroid plexus, and the retinal pigment epithelium (Inoue et al., 2008; Kugel Desmoulin et al., 2012; Qiu et al., 2006; Umapathy et al., 2007; Wollack et al., 2008; Zhao, Min, et al., 2009). PCFT is abundantly expressed in human tumor cell lines (e.g., breast, lung, ovarian, and lung) and at very low levels in human leukemia cell lines (Gonen, Bram, & Assaraf, 2008; Kugel Desmoulin et al., 2012). While PCFT is likely to be active in the acidic microenvironment characterizing the upper GI and in solid tumors, it seems unlikely that PCFT represents an important mechanism of folate uptake in most normal tissues in which it is expressed. From results in HFM patients, PCFT is important for folate transport across the choroid plexus (Wollack et al., 2008; Zhao, Min, et al., 2009). Clearly, the physiologic role of PCFT in tissues not normally associated with a low pH microclimate needs to be clarified. It is conceivable that PCFT transports 5-methyl THF and related folates in normal tissues in areas of localized acidification or when expressed at high levels (Zhao, Matherly, & Goldman, 2009). However, at comparatively neutral pHs of most tissues, RFC is more efficient at delivering reduced folates than PCFT (Zhao et al., 2008).

Investigators have extensively characterized the transport properties of PCFT expressed in transfected cell lines and in *Xenopus* oocytes microinjected with PCFT cRNAs (Kugel Desmoulin et al., 2011b, 2010; Nakai et al., 2007; Qiu et al., 2006; Wang et al., 2011; Zhao & Goldman, 2007). A distinguishing characteristic of PCFT is its acidic optimum (pH 5–5.5) (Nakai et al., 2007; Qiu et al., 2006; Zhao & Goldman, 2007). As the pH increases from pH 5.5, transport decreases dramatically. Above pH 7, transport is almost undetectable, although the extent of residual transport varies for different substrates (Kugel Desmoulin et al., 2011a, 2010; Wang et al., 2010, 2011; Zhao & Goldman, 2007; Zhao et al., 2008). RFC substrates including MTX, PMX, raltitrexed, aminopterin, pralatrexate, 5-methyl THF, and 5-formyl THF are all PCFT substrates (Deng et al., 2009; Kugel Desmoulin et al., 2012; Menter et al., 2012; Zhao et al., 2008). However, the antifolates PT523 and GW1843U89 do not appear to be transported by PCFT (Deng et al., 2009; Zhao & Goldman, 2007). In contrast to RFC, PCFT has similar  $K_{\text{T}}$ s for transport of reduced folates (5-methyl THF, 5-formyl THF) and folic acid (Zhao & Goldman, 2007). PCFT is stereospecific for (6*S*)5-formyl THF, and for L- over D-aminopterin (Menter et al., 2012; Zhao & Goldman, 2007). Whereas the 5-substituted pyrrolo[2,3-*d*]pyrimidine antifolate PMX is among the best substrates for transport by PCFT (Zhao & Goldman, 2007), a novel series of 6-substituted pyrrolo[2,3-*d*]pyrimidine thienoyl antifolate analogs were recently reported with affinities and transport activities for PCFT comparable to those for PMX (Kugel Desmoulin et al., 2011a; Kugel Desmoulin, Wang, et al., 2012; Wang et al., 2010, 2011). For the lead

compound of this series, PCFT transport by malignant mesothelioma xenografts in severe combined immunodeficient mice resulted in potent antitumor effects in early- and late-stage disease (Cherian et al., 2013). Notably, the binding affinities for both 5- and 6-substituted pyrrolo[2,3-*d*]pyrimidine analogs appear to be less affected by pH than for other PCFT substrates.

PCFT activity is not affected by removing extracellular  $\text{Na}^+$ ,  $\text{K}^+$ ,  $\text{Ca}^{2+}$ ,  $\text{Mg}^{2+}$ , or  $\text{Cl}^-$  (Qiu et al., 2006) or by changing membrane potential (Inoue et al., 2008), data consistent with an electroneutral mode of PCFT transport. However, there is a requirement for an inwardly directed proton gradient for PCFT-mediated folate transport based on the following observations. (i) Dissipation of the transmembrane proton gradient by a proton ionophore in *Xenopus* oocytes (Qiu et al., 2006) and a  $\text{K}^+/\text{H}^+$ -exchanging ionophore in HEK293 cells (Inoue et al., 2008) reduced transport by PCFT. (ii) A transvesicular pH gradient was reported to result in increased unidirectional folate transport and substantial transmembrane folate concentration gradients in rabbit jejunum, from the low pH to the high pH compartment, consistent with a proton-coupled process (Schron, Washington, & Blitzer, 1985). (iii) Treatment of HeLa cells with nitrate or bisulfite inhibited PCFT transport by abolishing the pH gradient (Zhao, Visentin, Suadicani, & Goldman, 2013). Finally, (iv) cellular acidification accompanied folate transport into *Xenopus* oocytes, confirming proton coupling (Unal, Zhao, et al., 2009).

Since folates are bivalent anions, this means that more than two protons must be co-transported with each folate molecule to account for the net positive charge of the PCFT–folate–proton complex (Qiu et al., 2006, 2007). Thus, PCFT functions as a folate–proton symporter such that the downhill flow of protons is coupled to the uphill flow of folates into cells. Interestingly, PCFT can also function in the absence of a transmembrane pH gradient. Under these conditions, folate transport is driven by membrane potentials (Qiu et al., 2006; Umaphathy et al., 2007), similar to the divalent metal-ion transporter DMT1 (Mackenzie, Ujwal, Chang, Romero, & Hediger, 2006). At low pH, PCFT exhibited channel-like activities (i.e., protons can flow independent of folates) (Mahadeo et al., 2010; Unal, Zhao, et al., 2009).

#### 4.2. Structure and function of PCFT

Human PCFT includes 459 amino acids and has a predicted molecular mass of 49.8 kDa. PCFT is predicted to contain 12 TMDs comprised of hydrophobic stretches of amino acids with cytosolic-oriented N- and C-termini (Fig. 4.4). This structure has been experimentally confirmed by immunofluorescence staining of hemagglutinin (HA)-tagged PCFT constructs and by SCAM with MTSEA (2-aminoethyl methanethiosulfonate)-biotin (Unal, Zhao, Qiu, & Goldman, 2008; Zhao, Unal, Shin, & Goldman, 2010). PCFT has two N-glycosylation sites (Asn58 and Asn68) in the loop domain between TMD1 and TMD2 (Unal et al., 2008). Mutating either of the asparagine residues to glutamine had no effect on PCFT expression and function (Unal et al., 2008). However, mutating both Asn58 and Asn68 to glutamine decreased transport activity to 40% of that for wild-type PCFT. In contrast to RFC which is expressed at the basolateral membrane (see above), PCFT (with a C-terminal, yellow fluorescent protein tag) was localized to the apical membrane of Madin-Darby canine

kidney and Caco-2 cells (Subramanian, Marchant, & Said, 2008). Truncating the C-terminus of human PCFT at position 449 did not impact apical membrane targeting or transporter activity (Subramanian et al., 2008).

A number of structurally and functionally important amino acids in human PCFT have been identified. This includes molecular characterization of human PCFT mutants that result in loss of function in HFM cases, and systematic mutagenesis of these HFM mutants. From considerations of species homologies and amino acid charge characteristics in relation to their TMD localization, other residues have been identified as important to PCFT transport. Thus, residues have been implicated as critical to proton coupling (i.e., Glu185 (TMD5); Unal, Zhao, & Goldman, 2009) or substrate binding (i.e., His281 (TMD7); Unal, Zhao, et al., 2009), or both (i.e., Arg376 (TMD10); Mahadeo et al., 2010) (Fig. 4.4).

His247, which is localized to the loop region separating TMD6 and TMD7, is predicted to lie in the cytoplasmic opening of the water-filled translocation pathway where it interacts with Ser172 to limit substrate access to the folate-binding pocket (thus determining substrate selectivity) (Unal, Zhao, et al., 2009). His281 faces the extracellular region in TMD7 (Fig. 4.4) and is believed to play an important role in PCFT protonation, which augments substrate binding to the carrier (Unal, Zhao, et al., 2009).

The conserved segment (DXXGRR) linking TMD2 and TMD3 (residues 109–114), including a  $\beta$ -turn, is of particular interest (Lasry et al., 2008; Shin et al., 2010; Subramanian et al., 2008; Zhao et al., 2007). Key residues in this stretch include Asp109 and Arg113 that are likely to play important roles in substrate binding and/or translocation since both conservative and nonconservative replacements completely abolish transport (Lasry, Berman, Glaser, Jansen, & Assaraf, 2009; Shin et al., 2010). According to a PCFT homology model based on the GlpT template, Arg113 protrudes into a hydrophobic cavity formed by TMD1, TMD3, TMD4, and TMD6 (Lasry et al., 2008). However, this has not been experimentally confirmed.

Other residues that may be functionally important in the human PCFT include Leu161 (TMD4), Glu232 (TMD6), and Ile304 (TMD8) (Fig. 4.4) (Zhao, Shin, Diop-Bove, Ovits, & Goldman, 2011). Loss of transport was associated with a reduced rate of carrier translocation (Glu232Gly mutant) or lower substrate affinities (Ile304Phe and Leu161Arg mutants). Mutating Pro425 to Arg in the loop junction flanking TMD12 (Fig. 4.4) eliminated binding of MTX and other substrates to PCFT, but preserved binding of PMX (Shin, Zhao, Yap, Fiser, & Goldman, 2012). Given its location, Pro425 is unlikely to directly participate in substrate binding. Rather, mutation at this position likely produces a conformational change that selectively inhibits binding of particular (anti)folate substrates. Finally, from mutant studies, Gly189 and Gly192 (TMD5) were implicated as functionally important (Zhao, Shin, Fiser, & Goldman, 2012).

In SCAM studies on human PCFT, membrane-impermeable methane-thiosulfonate reagents reacted with Cys replacements at positions 157, 158, and 161 in TMD4 and at position 188 in TMD5 (Shin, Zhao, Fiser, & Goldman, 2013; Zhao et al., 2012). Reactions could be

protected by PMX, placing these residues within or near the substrate-binding site(s) in human PCFT.

Based on the results with several complementary techniques, the human PCFT forms homooligomers both in detergent solution and *in situ* (Hou et al., 2012). Oligomerization of PCFT was demonstrated by protein cross-linking of the ectopically expressed carrier with 1,1-methanediyl bismethanethiosulfonate (MTS-1-MTS), and by fluorescence resonance energy transfer between co-expressed YPet- and ECFP\*-tagged PCFT monomers (Hou et al., 2012). Physical associations between HA- and His<sub>10</sub>-tagged PCFT monomers were established by co-expression in PCFT-null HeLa cells and co-binding to nickel affinity columns. Furthermore, the PCFT dimer was shown to be the dominant species by blue native gel electrophoresis (Hou et al., 2012). The functional significance of oligomerization was established by co-expression of wild-type and mutant Pro425Arg PCFT forms in PCFT-null HeLa cells. In these experiments, there was a “dominant-positive” functional phenotype, establishing positive cooperativity between PCFT monomers and a functional “rescue” of inactive mutant PCFT by wild-type protein (Hou et al., 2012). Based on these results, an “alternate access” model for PCFT transport, analogous to that suggested for LacY (Abramson et al., 2003) and adapted from that for monomeric PCFT (Unal et al., 2009), was proposed (Hou et al., 2012) that incorporates a role for PCFT oligomerization.

Duddempudi, Nakashe, Blanton, and Jansen (2013) suggested that PCFT may not oligomerize in plasma membranes prepared by polymerization with colloidal silica and polyacrylic acid from *Xenopus* oocytes or in Chinese hamster ovary cells. However, this conclusion was based on a limited number of methods. Furthermore, since different methods and metrics were employed in this report and the more extensive study of Hou et al. (2012), it is impossible to reconcile the conclusions of these reports.

The human PCFT primary sequence includes GXXXG motifs in TMD2 (amino acids 93–97) and TMD4 (amino acids 155–159) (Fig. 4.4) that are analogous to “dimerization motifs” in other amphipathic proteins (Duan, Wu, & You, 2011; Polgar et al., 2010). Mutating Gly93 and Gly97 to Ala did not inhibit transport activity or oligomer formation, based on thiol-reactive (MTS-1-MTS) protein cross-linking (Zhao et al., 2012). Unfortunately, parallel studies on the GXXXG motif in TMD4 were not performed. Interestingly, a TMD6 interface between PCFT monomers was suggested by the finding that MTS-1-MTS treatment generated cross-links between Cys229 (in TMD6) in individual PCFT monomers, but not when Cys229 was mutated to Ser (Zhao et al., 2012).

## 5. SUMMARY

This chapter focuses on the biology of the major facilitative membrane transport systems for folate cofactors, RFC and PCFT. Folate is an essential vitamin, and folate deficiency has been implicated in a variety of health disorders ranging from cardiovascular disease to neurodegenerative disease and cancer (Lucock, 2000; Matherly, 2004). Further, folate-based therapeutics (e.g., antifolates) continue to occupy an important niche for treating cancer as well as other pathological conditions (Gonen & Assaraf, 2012a; Kugel Desmoulin et al., 2012; Salojin et al., 2011; Visentin et al., 2012a). These include recent FDA-approved drugs

such as PMX and pralatrexate, with many more folate-based therapies in the pipeline. Losses of RFC or PCFT transport can have potential physiological and developmental consequences, particularly in the context of folate deficiency (Matherly, 2004; Matherly et al., 2007; Zhao et al., 2009), or may result in drug resistance with antifolates used for cancer therapy (Gonen & Assaraf, 2012b; Matherly et al., 2007; Zhao & Goldman, 2003).

RFC was functionally characterized beginning in the late 1960s as a neutral pH membrane transport mechanism for clinically relevant antifolates such as MTX that when lost resulted in MTX resistance (Goldman et al., 1968; Sirotiak, Kurita, & Hutchison, 1968). RFC was cloned and its molecular features were exhaustively documented beginning in the mid-1990s (Matherly & Hou, 2008; Matherly et al., 2007). It was soon recognized that RFC was the major folate transport system in mammalian cells, consistent with its ubiquitous tissue expression (Whetstone et al., 2002) and its absolute requirement for fetal development (Zhao, Russell, et al., 2001). By contrast, although an acidic pH transporter had long been recognized, the molecular characteristics of PCFT were not demonstrated until 2005 when it was originally classified as a heme transporter (Shayeghi et al., 2005). By 2006, PCFT was redefined as the molecular entity responsible for the acidic folate transport activity involved in intestinal uptake of dietary folates (Qiu et al., 2006). Studies soon followed that established that a low pH transport activity detected in many human solid tumor cells was in fact PCFT, and that PCFT was abundantly expressed in a wide range of human tumors and was highly active at pH conditions approximating those found in the tumor microenvironment (Kugel Desmoulin et al., 2011a). This soon led to the development of novel tumor-targeted therapies typified by 6-substituted pyrrolo [2,3-*d*]pyrimidine antifolates with selective membrane transport by PCFT over RFC (Kugel Desmoulin et al., 2012).

An important prerequisite for effective clinical applications of RFC and PCFT transport associated with folate deficiency or in targeted therapy of cancer is understanding of the structure and function of these critical transport systems. Indeed, since their cloning, structure–function research has led to remarkably detailed molecular information, including the membrane topology, N-glycosylation, energetics, and roles of functionally and structurally important domains and amino acids for both RFC and PCFT. These insights have shed important new light on the causal basis for chemotherapy resistance to MTX associated with the loss of RFC function, and for the rare autosomal recessive condition, HFM, involving mutations in the PCFT gene and protein. Based on structural homologies to the bacterial MFS transporters GlpT and LacY, homology models for human RFC and human PCFT have been developed. The models provide new mechanistic insights and experimentally testable hypotheses that could further facilitate efforts to design a new generation of targeted therapeutics with selective membrane transport by PCFT over RFC. Unfortunately, detailed X-ray diffraction studies on membrane proteins such as RFC and PCFT remain a formidable challenge.

Structure and function considerations for human RFC and human PCFT must now include higher-order structures such as homo-oligomers that may impact transport mechanisms and regulate transporter expression and function. Indeed, evidence suggests that formation of homo-oligomers between monomeric RFC and PCFT proteins may be essential for intracellular trafficking and/or for carrier function. Formation of PCFT or RFC oligomers,

including both wild-type and mutant forms, may also be important to clinical phenotypes involving mutant transporters in patients with HFM or in cancer patients being treated with cytotoxic antifolates. Clearly, better understanding of the broader significance and structural determinants of these higher-order oligomeric structures will be an important area for future study as these may lead to approaches for modulating the formation of oligomers for therapeutic impact.

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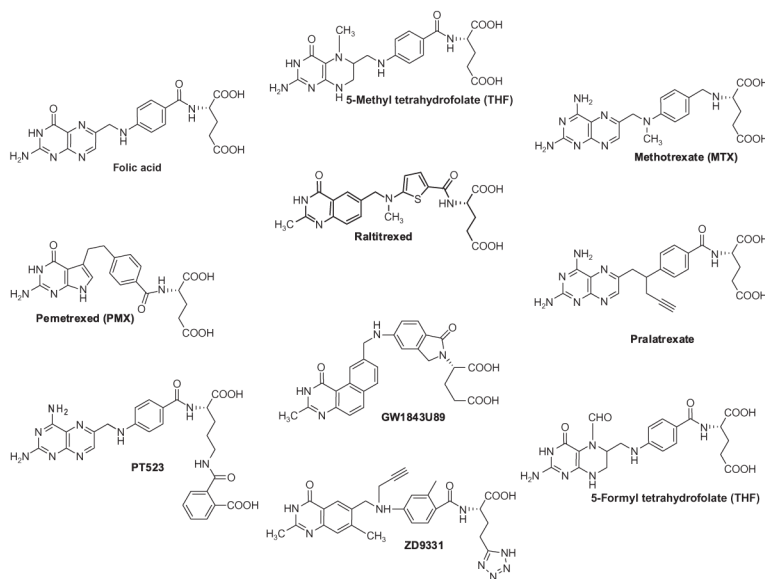
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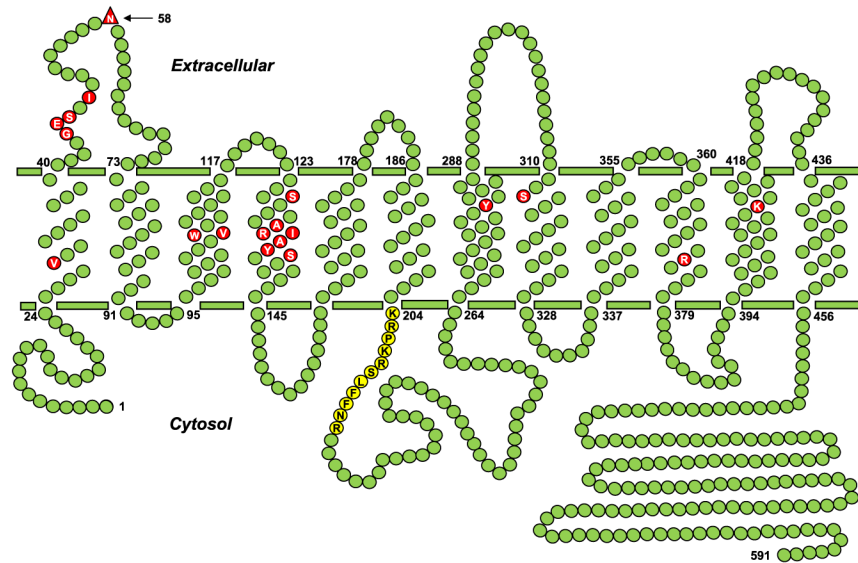
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**Figure 4.1.**

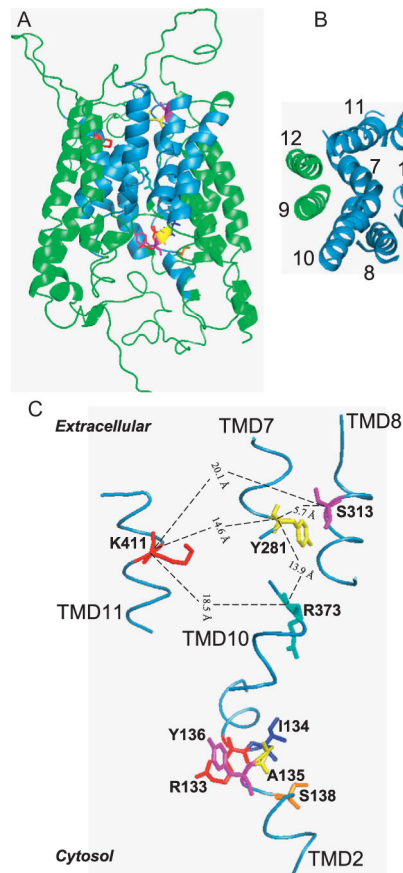
Structures of folates and clinically relevant antifolates. RFC substrates including MTX, PMX, raltitrexed, pralatrexate, 5-methyl THF, and 5-formyl THF are all excellent PCFT substrates. However, the antifolates PT523 and GW1843U89 do not appear to be transported by PCFT. RFC has a low affinity but PCFT has a high affinity for folic acid. GW1843U89 is an excellent substrate for human RFC, but a poor substrate for murine RFC.



**Figure 4.2.**

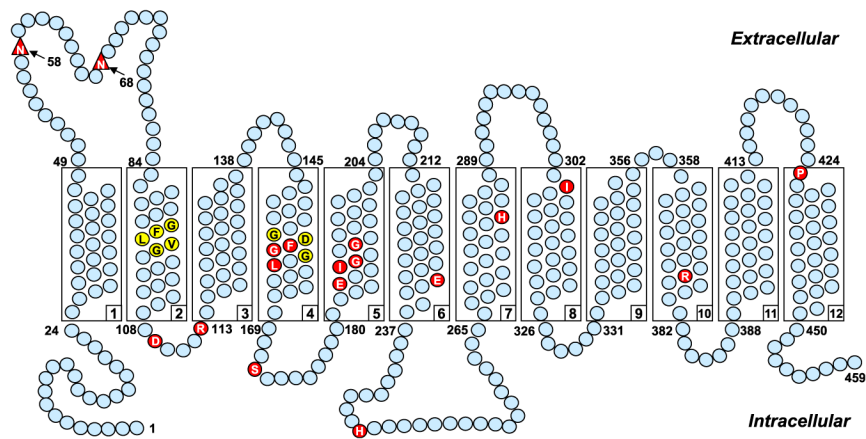
Human RFC topology model. A topology model is shown for human RFC, with 12 TMDs, internal N- and C-termini, and a loop domain connecting TMD6 and 7. The structurally and functionally important amino acids, as described in the text, are shown as red circles. A conserved stretch of amino acids (Lys204–Arg214) in the TMD6/TMD7 loop domain, which is important for transport activity, is shown as yellow circles. N-glycosylation occurs at Asn58, which is labeled as a red triangle.





**Figure 4.3.**

Three-dimensional (3D) homology models of human RFC. A 3D model for human RFC is presented, based on structure alignments between RFC and LacY/GlpT and experimental data. (A) A side view of the RFC for which the extended C-terminal segment is truncated at Lys479. TMD1, TMD2, TMD4, and TMD5 of the N-terminal region and TMD7, TMD8, TMD10, and TMD11 of the C-terminal region are involved in formation of the hydrophilic binding site for anionic folates (colored *sky blue*). TMD3, TMD6, TMD9, and TMD12 are buried in the lipid bilayer and do not directly participate in substrate binding (colored *green*). Panel (A) also depicts key amino acids (shown in assorted colors) that may contribute to the binding pocket for anionic folate substrates, as described in the text. (B) A cytosolic view of only the TMD segments of the human RFC molecule so that the order of helix packing can be seen easily. TMD coloring is the same as described in (A). (C) Enhanced view of the hypothetical substrate-binding site comprising the same key amino acids depicted in (A), including Lys411, Ser313, Tyr281, and Arg373, as described in the text. Other residues that may contribute to the substrate-binding pocket are also shown and include Arg133, Ile134, Ala135, Tyr136, and Ser138. The physical distances between the  $\alpha$ -carboxyl groups of Lys411, Ser313, Tyr281, and Arg373 are given in angstroms. *This figure was originally published in The Journal of Biological Chemistry, by Hou et al. (2006). © The American Society for Biochemistry and Molecular Biology.*



**Figure 4.4.**

Schematic structure of human PCFT membrane topology. A topology model is shown for human PCFT, with 12 TMDs and internal N- and C-termini. Structurally or functionally important amino acids, as determined from published mutagenesis studies and in patients with hereditary folate malabsorption (HFM), are shown as red circles. GXXXG putative oligomerization motifs (Phe157 and Gly158 in the  $G^{155}XXXG^{159}$  motif) are shown as yellow circles because they are also structurally and functionally important). N-glycosylation occurs at Asn58 and Asn68 (shown as red triangles).