

Table 2. Catalytic and molecular properties of human L-PGDS and H-PGDS

	L-PGDS/ β -trace	H-PGDS
Molecular weight of monomer	~26 000	~23 000
Tertiary structure	Monomer	Homodimer
Cofactor	Sulfhydryl compounds, such as dithiothreitol, β -mercaptoethanol, glutathione, cystein, cysteamine	Glutathione
Amino acid residues	190 (168 without signal sequence)	199
Activated thiol as an active site	Cys65	Glutathione bound to the enzyme
Inhibitor	SeCl ₄ , AT56	HQL79, TFC007, TAS204
Activator		Mg ²⁺
Gene name	ptgds	hpgds
Chromosomal localization	9q34.3 (Chr19: 136.98 Mb)	4q22.3
Post-translational modification	N-glycosylation (Asn29 and Asn56), a core-1-HexHexNAc-O-glycan at Ser7, acetylation at Lys16 and Lys138, sulfonation at Ser41 and Thr142, and dioxidation at Cys43 and Cys145 without signal sequence.	unknown
Subcellular localization	ER membrane, extracellular space (β -trace: CSF, inter-photoreceptor matrix, seminal plasma, plasma)	Cytosol (resting state), nuclear and ER membranes (active state after membrane trafficking)