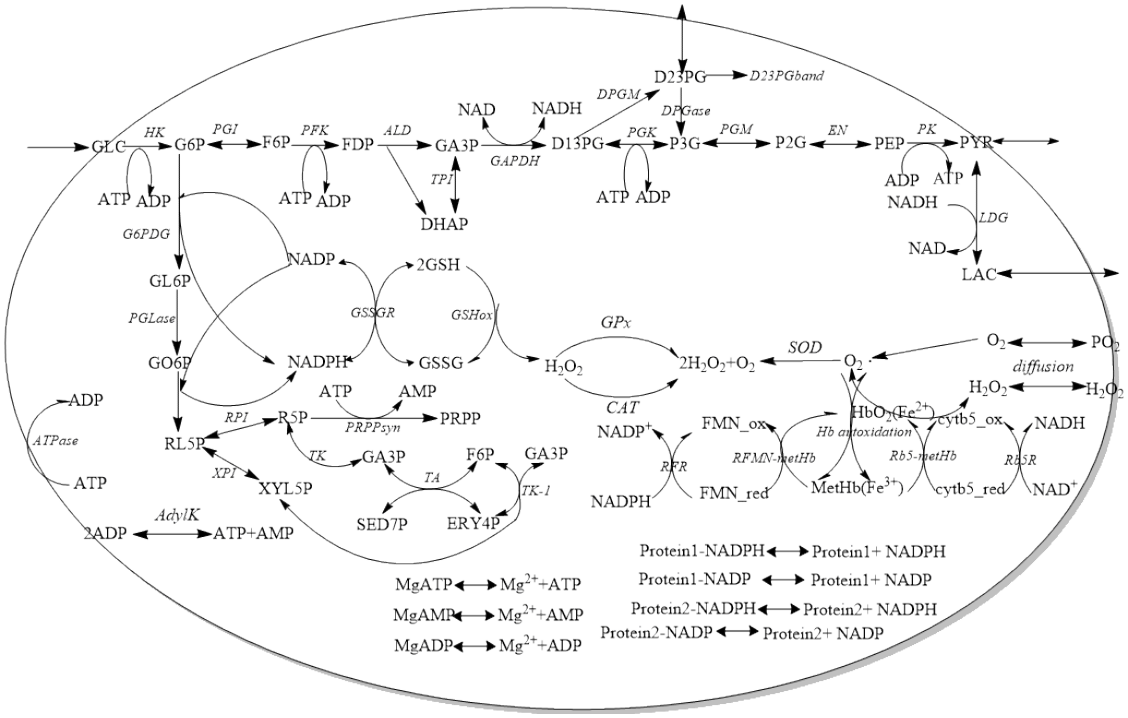
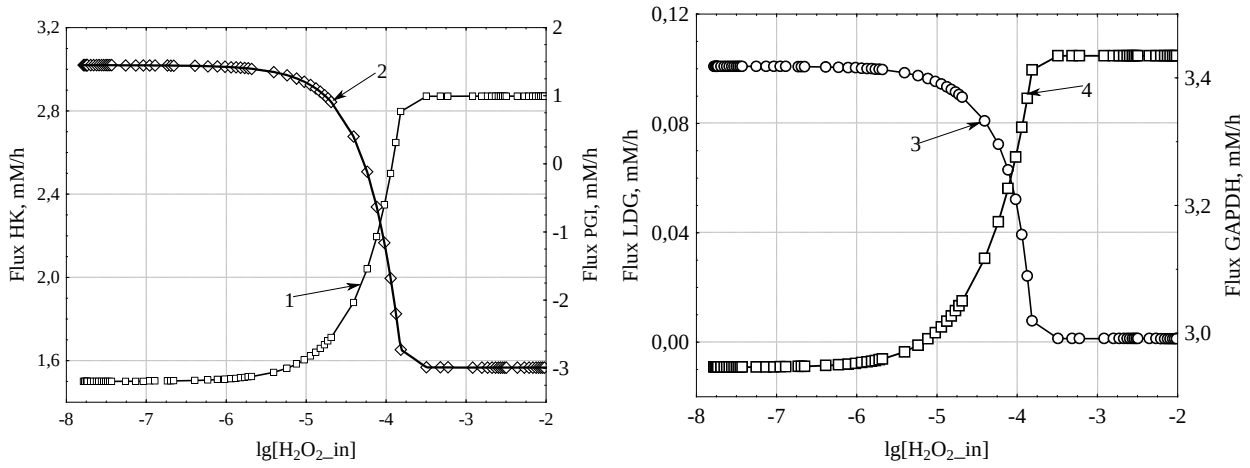
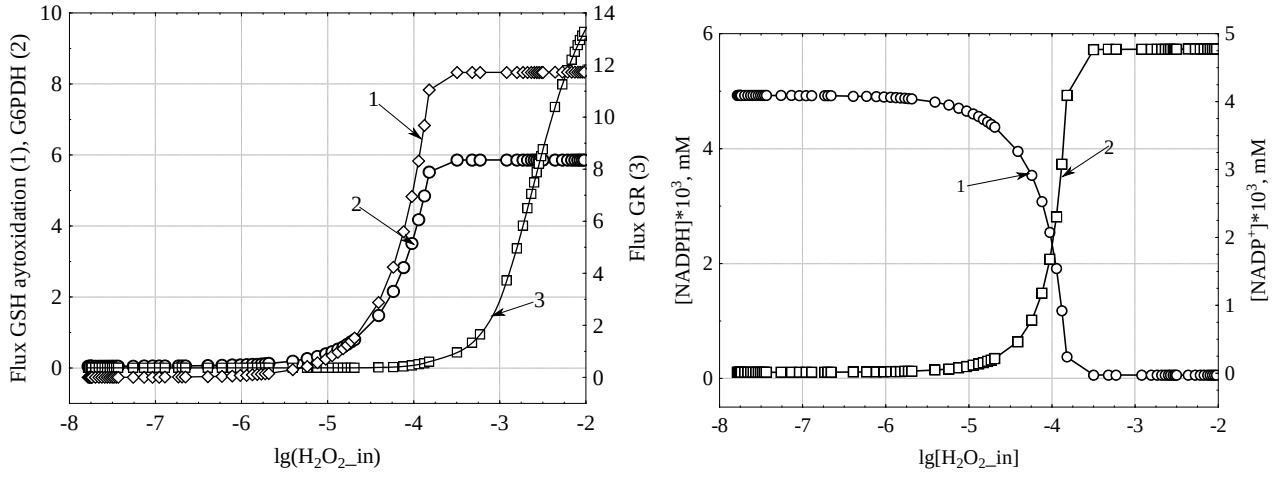


Fig. 1. Schematic representation of the pathways included in the model: **Metabolite**: GLC, glucose; G6P, glucose 6-phosphate; F6P, fructose 6-phosphate; FDP, fructose 1,6-diphosphate; DHAP, dihydroxyacetone phosphate; GA3P, glyceraldehyde 3-phosphate; D13PG, 1,3-diphosphoglycerate; D23PG, 2,3-diphosphoglycerate; D23PGband, band-form 2,3-diphosphoglycerate; P2G, 2-phosphoglycerate; P3G, 3-phosphoglycerate; PEP, phosphenolpyruvate; PYR, pyruvate; LAC, lactate; GL6P, gluconolactone 6-phosphate; GO6P, gluconate 6-phosphate; RU5P, ribulose 5-phosphate; R5P, ribose 5-phosphate; X5P, xylulose 5-phosphate; S7P, sedoheptulose 7-phosphate; E4P, erythrose 4-phosphate; GSH, reduced glutathione; GSSG, oxidized glutathione; H2O2, hydrogen peroxide, HbO2, oxyhemoglobin, MetHb , methemoglobin; O2, oxygen; , superoxide anion radical; cytb5_ox, oxidized cytochrome b5; cytb5_red, reduced form cytochrome b5. **Enzymes**: HK, hexokinase (EC 2.7.1.1), PGI, glucose-6-phosphate isomerase (EC 5.3.1.9); PFK, phosphofructokinase (EC 2.7.1.11); ALD, aldolase (EC 4.1.2.13); TPI, triosephosphate isomerase (EC 5.3.1.1); GAPDH, glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12); PGK, phosphoglycerate kinase (EC 2.7.2.3); DPGase, diphosphoglycerate phosphatase (EC 3.1.3.13); PGM, phosphoglycerate mutase (EC 5.4.2.1); EN, enolase (EC 4.2.1.11); PK, pyruvate kinase (EC 2.7.1.40); LDG, lactate dehydrogenase (EC 1.1.1.27); G6PDH, glucose-6-phosphate dehydrogenase (EC 1.1. 1.49) GAPDH, glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12); GL6PDH, phosphogluconate dehydrogenase (EC 1.1.1.44), RPI, ribose-5-phosphate isomerase (EC 5.3.1.6); XPI, ribulose phosphate epimerase (EC 5.1.3.1); TA, transaldolase (EC 2.2.1.2); TK, transketolase (EC 2.2.1.1); PRPPsyn, phosphoribosylpyrophosphate synthetase (EC 2.7.6.1); cytb5R, (NADH-dependent) cytochrome b5 reductase (EC 1.6.2.2); FR, (NADPH-dependent) flavin reductase (EC 1.5.1.30); GPx, glutathione peroxidase (EC 1.11.1.9); SOD, Superoxide dismutase (EC 1.15.1.1), CAT- catalase (1.11.1.6); GSSGR, glutathione-disulfide reductase (EC 1.8.1.7); GSHox –glutathione autoxidation reaction



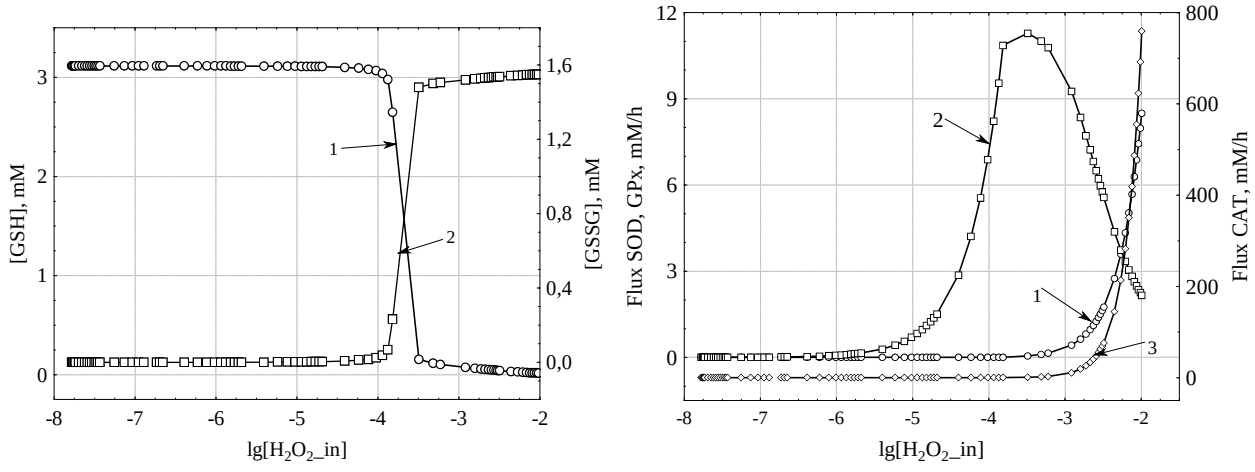
a *b*

Fig. 2. The change of enzyme activity in stationary state in conditions of oxidizing load: *a* – HK (1), PGI (2), *b* – LDG (3), GAPDH (4).



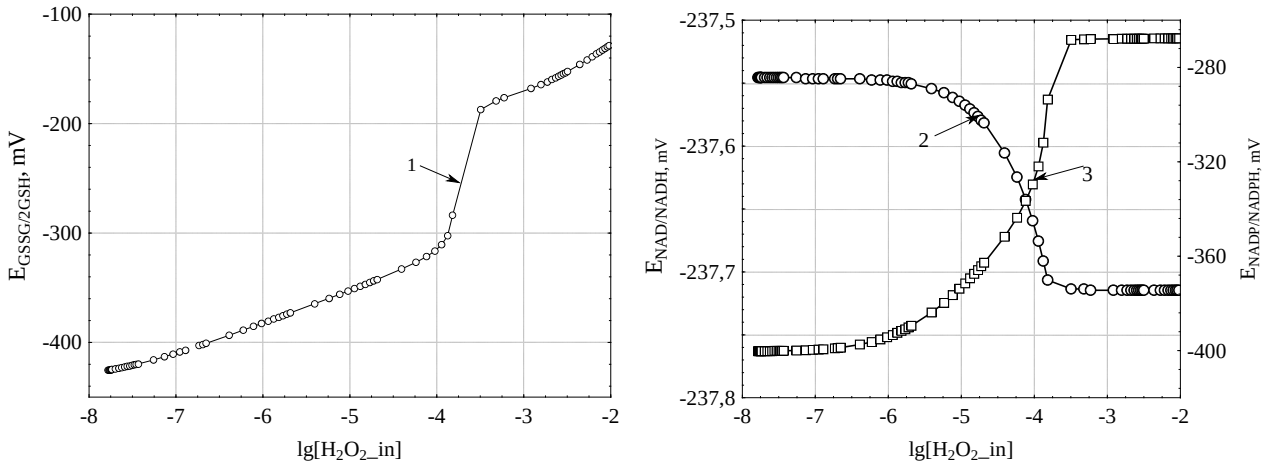
a *b*

Fig. 3. The change of flows and stationary concentrations of metabolites in conditions of oxidizing load: *a* – autoxidation GSH (1), G6PDH (2), *b* – [NADPH] (2) and [NADP+] (1)



a *b*

Fig. 4. The change of flows and stationary concentrations of metabolites in conditions of oxidizing load: *a* – [GSH] (1) and [GSSG] (2). b – CAT (1), GPx (2), SOD (3),



a *b*

Fig. 5. The change of redox-potentials at oxidizing load:
a – redox-potential GSSG/2GSH, *b* – NAD+/NADH (1) and NADP+/NADPH (2)