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Evidence for functional and regulatory cross-talk between the tricarboxylic acid cycle 2-oxoglutarate dehydrogenase complex and 2-oxoadipate dehydrogenase on the L-lysine, L-hydroxylysine and L-tryptophan degradation pathways from studies *in vitro*

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Abbreviations: hOGDHc, human 2-oxoglutarate dehydrogenase complex; hE1o, 2-oxoglutarate dehydrogenase, the first E1 component of hOGDHc; hE2o, dihydrolipoyl succinyltransferase, the second E2 component of hOGDHc; hE3, dihydrolipoyl dehydrogenase, the third E3 component of all 2-oxo acid dehydrogenase complexes; LDo, lipoyl domain of hE2o; hE1a, 2-oxoadipate dehydrogenase; *DHTKD1*, gene coding for 2-oxoadipate dehydrogenase; hOADHc, 2-oxoadipate dehydrogenase complex, assembled from hE1a+hE2o+hE3; TCA cycle, tricarboxylic acid cycle; H_2O_2, hydrogen peroxide; IPTG, isopropyl β-D-1-thiogalactopyranoside ; TCEP, Tris(2-carboxyethyl)phosphine hydrochloride; ThDP, thiamin diphosphate; DCPIP, 2,6-dichlorophenolindophenol; OG, 2-oxoglutarate; OA, 2-oxoadipate; KMV, α-keto-β-methyl-*n*-valeric acid; DANS-As, (4-((5-(dimethylamino) naphthalene)-1-sulfonamido) phenyl) arsenous acid; FT-MS, Fourier transform mass spectrometry; EPR, Electron Paramagnetic Resonance.