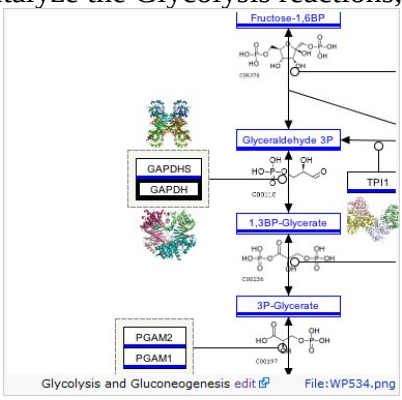
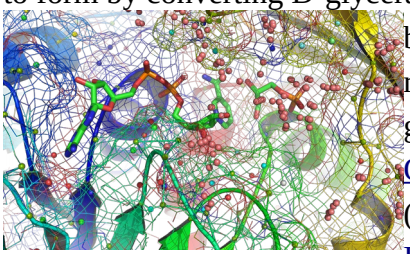
GAPDH USING A STRUCTURE-BASED DESIGN MODULATES AND AMPLIFIES A MECHANISTIC INSIGHT INTO A CRYSTAL STRUCTURES PHOTOCHEMICAL REACTION.
Authors: Mark R. Brenneman

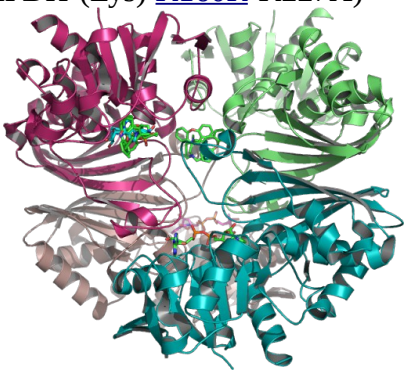
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) GAPDH/G3PD, is located in band 12p13.31; (§, ‡) related to both glycolysis and gluconeogenesis-pathways. G3PD catalyzes reversible oxidative phosphorylation of inorganic phosphate and nicotinamide adenine dinucleotide (NAD) converting in glycolysis the glycolytic protein GAPDH in which adenosine-triphosphate (ATP) is generated when phosphoglycerate kinase (PGK) is produced in the GAPDH-catalyzed reaction. These intermediate metabolites (aldolase, triose-phosphate-isomerase (TPI)) catalyze the Glycolysis reactions, in the sequence of the ten enzyme-catalyzed Embden-Meyerhof reactions in the metabolic pathway. Converting phosphoglycerate mutase 1 (PGM) catalyzing the internal steps by 2,3-BPG phosphatase to form by converting D-glyceraldehyde 3-phosphate (G3P) into 1,3-bisphosphoglycerate (1,3-BPG) from its role as 3-Phosphoglyceric acid (3PG) in glycolysis as the glycolytic protein GAPDH that catalyzes the first step (G3P into 1,3-BPG) of the pathway.

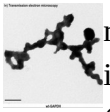




Plant cells contain several reactions of photosynthesis participating in glycolysis and the Calvin-Benson cycle signaling pathways in plants (cytosolic-GAPC (Arabidopsis thaliana) functions in plant cells.) its final byproduct is also another Glyceraldehyde-3-P. GAPDH is a band 3 protein that associates with the cytoplasmic face of human erythrocyte (RBC) membranes. The cytoplasmic GAPDH exists primarily as a tetrameric isoform, 4 identical 37 kDa subunits. By subcellular translocation GAPDH participates in nuclear events [In nuclear membrane the vesicular* tubular cluster fractions (VTCs) - anterograde transport or retrograde membrane transport complexes between the intermediates, these are the Golgi complex and the endoplasmic reticulum (ER), in the nucleus a function is lost in disease* that exploits this process.], this a change to a non-cytosolic localization due to the signal transduction pathways (considering LmGAPG L. mexicana-like functions.) involved in s-nitrosylase activity that mediates, governed by the equilibrium between four cysteine residues (nitrosylation and denitrosylation reactions), inhibition of GAPDH nuclear translocation, as a basis for its multifunctional activities relating to the extraglycolytic functions of GAPDH. Nuclear GAPDH promotes glucose metabolism to sustain cellular ATP levels, or potentially by inhibiting targets of p300/CBP such as p53 dependent phosphorylation. Nitric oxide synthase or neuronal NOS (involved in cellular and human intracellular nuclei events, in addition to the cytoplasm) could generate nitric oxide (NO). GAPDH has four cysteine residues which are associated with S-nitrosylation-yielding NOS-GAPDH which “recruited” its glycolysis subunit from the three molecular axes translocation roles (S-thiolation, S-nitrosylation or aggregated enzymes (Cys-152 and nearby 156 converted into a 'cross-linked soluble' states)), and (SNO-GAPDH) nitrosylated S-nitrosoglutathione (GSNO) the active site cysteine residue in GAPDH at its Cys 150 residue that binds

to Siah1 (seven in absentia homolog 1) acquisition and the translocation of GAPDH into the nucleus, and denitrosylation using a combination of approaches, including G3P. And NADPH may play a role in (VTC) vesicle function. The complex would function in the apoptosis cascade by its molecules translocation, this may depend on lysine 227 in the human GAPDH-Siah interaction to another intracellular position induced by apoptotic stimuli, augments p300/CREB binding protein (CBP)-associated acetylation of nuclear proteins. 'Engineering the cofactor (GAPDH-(Lys) K160R-K227A) availability prevents activation of p300/CBP that interferes with GAPDH-Siah1 binding'-prevents the ternary (GAPDH-Siah1) complex associations translocation; that CGP-3466 can reduce independently with both cofactors. Dysregulation of protein S-nitrosylation (S-nitrosocysteine - 247) by lipopolysaccharide (LPS) is associated with pathological conditions which contributes to disease phenotype, where GAPDH protects ribosomal protein RP-L13a from degradation, L13a and GAPDH forms a functional GAIT complex. One of the functions of GAPDH proteins role in glycolysis in relation to DNA synthesis is nuclear accumulation associated by the NAD(+)-dependent s-nitrosylation and denitrosylation





reactions both of these isforms are distinct parallel to the uracil DNA glycosylase (UDG) gene in mitochondria and in the nucleus is N-terminally processed is the 37-kDa subunit of the (GAPDH) glyceraldehyde-3-phosphate dehydrogenase protein. This enzyme is an example of moonlighting protein which is validated and replaced by alternative reference genes that link (in their nuclear forms) on the multifunctional properties of the enzyme GAPDH known as a key enzyme in glycolysis that contributes to a number of diverse cellular functions unrelated to glycolysis depending upon its subcellular location. GAPDH is a key enzyme in glycolysis the most commonly used expression is as a housekeeping gene.

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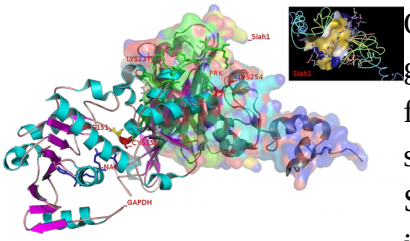
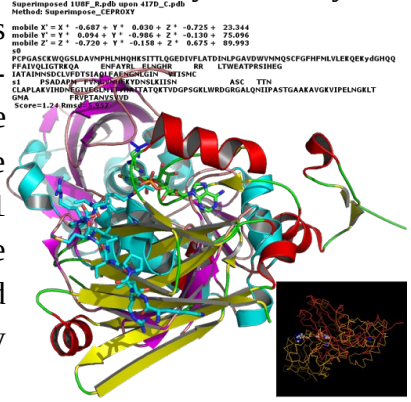


Cytotoxic stimuli [1a.] or Programmed cell death, via nitric oxide generation, lead to the binding of GAPDH from its usual tetrameric form to a dimeric form, to the protein Siah1 [1.] intracellular G-3-P [2.] substrate [3.] protects GAPDH from S-nitrosylation [4.]. The GAPDH-Siah interaction depends on lysine 227 [5.], in human GAPDH that interacts with a large groove [6.] of the Siah1 dimer, that connects the GAPDH dimer to PGK in the cytoplasm. The S-nitrosylation [7.,8.] abolishes catalytic activity and confers upon GAPDH the ability to bind to Siah [9.]. (GAPDH) is physiologically nitrosylated at its Cys 150 residue. GAPDH (SNO-GAPDH) [10.] binds to Siah1 [11.] by forming a protein complex. In the nucleus [12.] GAPDH is acetylated at Lys 160 [13.] and binds to the protein acetyltransferase p300/CBP. Under these conditions siah-1 formed a complex with GAPDH (PDB:4O63) and localized in the nucleus of Müller cells [14.]. GAPDH mutants [15.] that cannot bind Siah1 prevents translocation [16.] to the nucleus to elicit neurotoxicity



[17.] and cell apoptosis. (Figure 7.)

[1a.] 16492755, 8769851 [1.]16391220, [2.]19542219, 22534308, 3350006, 19937139, [3.]22847419, [4.]15951807, [5.]20601085, [6.]16510976, 20392205, [7.,8.]22817468, 16505364, [9.]16633896, [10.]16574384, [11.]20972425, [12.]19607794, [13.]18552833, [14.]19940145, [15.]23027902, [16.]24362262, [17.]16492755.

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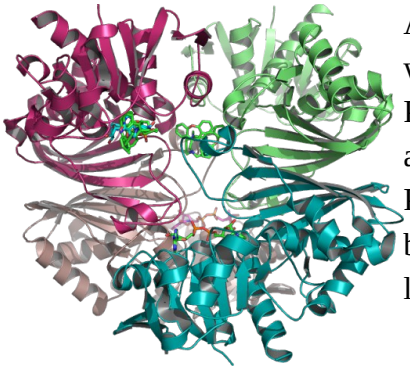

Analysis of CGP-3466 Docking (NAD) to Human Placental GAPDH which decreases the synthesis of pro-apoptotic proteins is N-terminally PMID:10677844, processed to which a Rossmann NAD(P) binding fold as seen in figure 1 is a C-terminal domain as seen on this page, PMID:10617673, 26022259, 16510976 ...The structure is also used to build a model of the complex between GAPDH and the E3 ubiquitin ligase Siah1. (Purple Ribbon-1U8F_Q Figure 1.)

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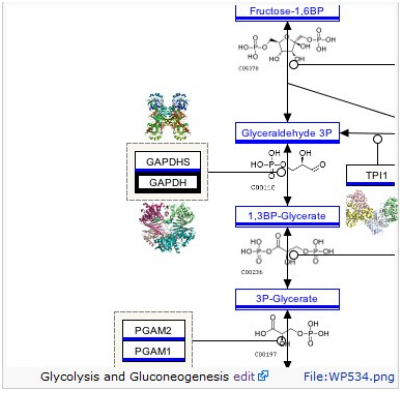

In the GAPDH-catalyzed reaction these intermediate metabolites (aldolase, triose-phosphate-isomerase Glycolysis and Glyconeogenesis (TPI)) catalyze the Glycolysis reactions, in the sequence of the ten enzyme-catalyzed Embden-Meyerhof reactions in the metabolic pathway. Converting phosphoglycerate mutase 1 (PGM) catalyzing the internal steps by 2,3-BPG phosphatase to form by converting D-glyceraldehyde 3-phosphate g3p(G3P) into 1,3-bisphosphoglycerate (1,3-BPG) from its role as 3-Phosphoglyceric acid (3PG) in glycolysis as the glycolytic protein GAPDH that catalyzes the first step (G3P into 1,3-BPG) of the pathway.

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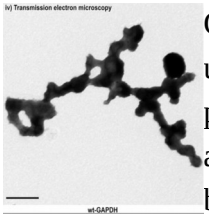

GAPDH homotetramer was studied as represented an assembly of repeating spherical units that harbored a distinct birefringent crystal structure to the optic axis for the p polarization, also discernible via transmission electron microscopy. of the relative amount of soluble monomeric GAPDH to G3P in the binding pocket of the NAD(+)-binding site residue located at the active site linked to GAPDH in Figures 5 and 6. PMID:25086035

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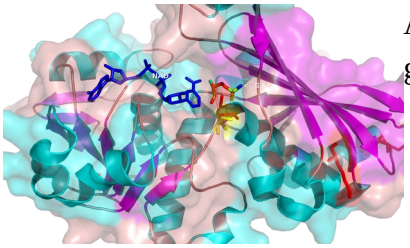

Another model building studie indicates that a structure obtained where glyceraldehyde 3-phosphate PDB:3CMC_Q binds in the P(s) pocket of

the natural substrate G3P phosphorylating GAPDH (PDB:1U8F_Q) at the catalytic cysteine residue site. To define the conditions suitable for affinity for the cosubstrate, the isolation and accumulation of the intermediate metabolites per G3P monomer found in Figure 8 of the equivalent Glc-3-P structure in the binding pocket of the NAD(+)-binding site residue located at the active site linked to GAPDH. PMID:19542219, 22534308

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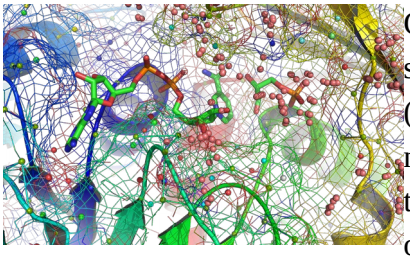

Correctly known binding sites on ((GAPD/NAD)) structures, polar spheres of the binding catalytic pocket that corresponds to G3P (glyceraldehyde 3-phosphate) aligned to the holographical structure nonbounded spheres (salmon color), these apoenzymes together with the cofactor(s) Cys 151, 152 which corresponds as below the Ps pocket of G3P, on the Green ribbon required for cofactor activity. Together with eliminated crystallographic waters and other possible spheres, these are at least one atom of a amino acid residue in contact with at least one alpha sphere of one binding pocket on the holo protein NAD structure 1U8F_Q needed to align holo and apo structures included in this data set with G3P (PDB:3CMC_Q) was tested only on holo structure (NAD), obtained via Pea Green spheres (link) aligned to 1U8F_Q ribbons/ligand structure which provide structural recognition insights into the biological 1U8F-Q assembly this includes 29 asymmetric units of its dimeric form, along the tetrameric 1U8F biological forms axis. PMID:9461340

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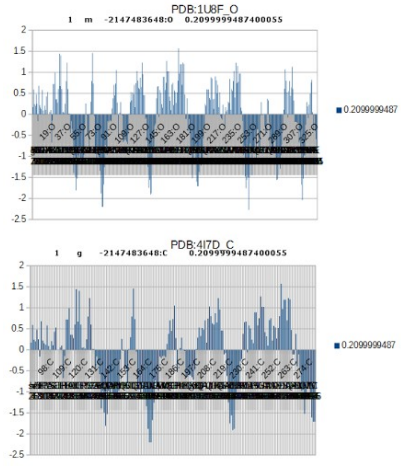

(Figure 8.) These are the results without the liquid chromatography coupled mass spectrometer, that are known 3D products by two-dimensional sequence analyses with the STRAP alignment tools data sets and which may have any effect on the functions of further analysis involved in more ordered results than this study attempts to show, of the analysis that may be included are identified separated into multiple gradients here in these paired graphs. Therefore in the present work to uncover the exact coincidence of 1U8F_R and 4I7D_C, the 3D coordinates of GAPDH (PDB:1U8F_Q) to the protein Siah1 4I7D were not presenting when subjected to STRAP alignment this apparent discrepancy (Figure 1.) was partially resolved by a (Figure 7) rendering from a more reactive native GAPDH_R homotetramer model.