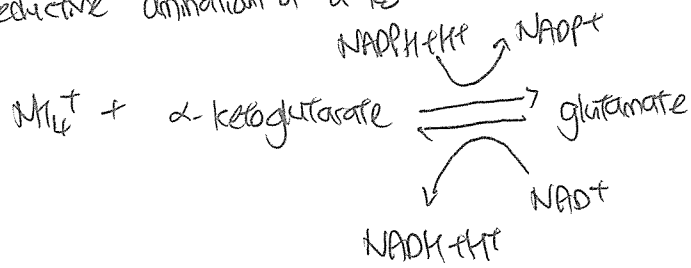


Glutamate dehydrogenase

- reductive amination of α -KG



- glutamate can be used to generate α -ketoglutarate for TCA cycle

reversible

Allosteric Regulation

- Synthesis of α -ketoglutarate from glutamate
- Inhibited by ATP / GTP, stimulated by ADP / GDP

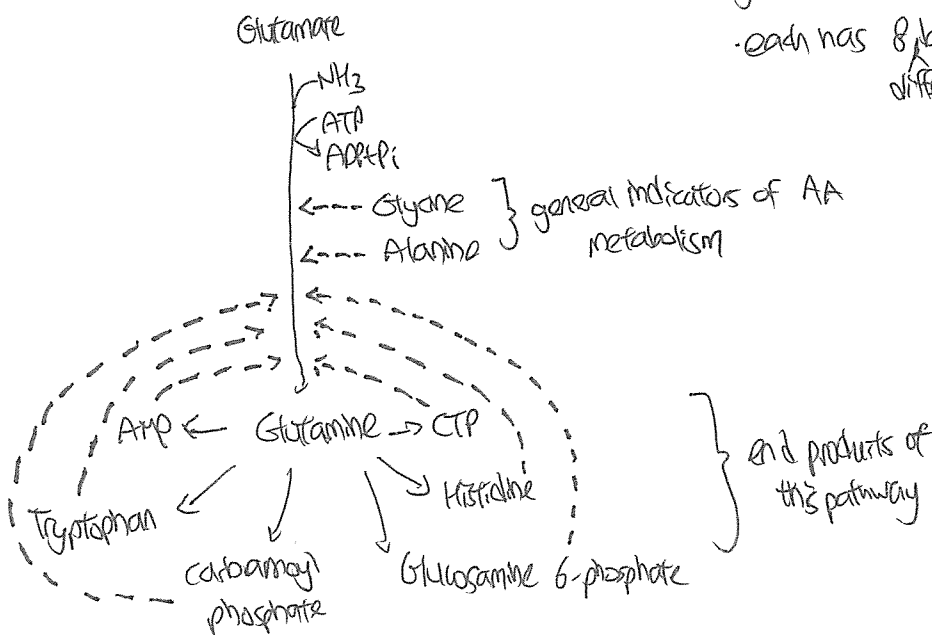
Regulation of Glutamine Synthetase (irreversible reaction)

- glutamate + NH_3 + ATP $\rightarrow$ glutamine + ADP + P_i
- central role in N metabolism
- biosynthesis of amino acids
- purines & pyrimidines
- detoxification of ammonia (particularly important in brain)
- depletion of α -KG
- tightly regulated
- allosteric regulation - cumulative feedback inhibition
- covalent modification
- Glu first reacts with ATP to form γ -glutamyl phosphate + ADP. The γ -glutamyl phosphate intermediate then reacts with NH_3 to form Gln + P_i

Feedback inhibition & specific inhibitors

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- glutamine synthetase has 12 subunits
- each has 8 binding sites, 96 total allosteric effector sites

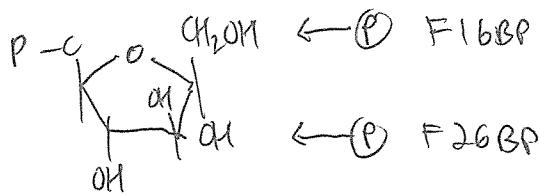


top view
hexagonal
sheet



side view
stacked
sheets

Phosphofructokinase: Co-enzyme and products



F26BP

• coordination of PFK and F16BPase activity via allosteric control (glycolysis and gluconeogenesis)

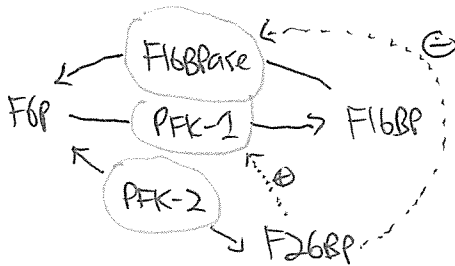
• PFK1: F6P $\rightarrow$ F16BP (major)

PFK2: F6P $\rightarrow$ F26BP

major: PFK1 (90%)

minor: PFK2 (10%)

PFK-2, F26BP and co-ordinate allosteric control



multiple PFK-2 isoforms

- tissue-specific expression
- activity modulated by phosphorylation
- activity modulated at level of expression
- bifunctional enzymes

* F26BP must be present

for glycolysis to proceed

PFK-2: bifunctional enzymes

$\rightarrow$ activated by shape change

(2 activities)

- single polypeptide chains, 2 enzymatic activities (only 1 enzymatic activity is active at any given time)



$\rightarrow$ a single gene in higher eukaryote, in lower prokaryote, where 2 enzymatic activities are encoded by 2 genes

glycolysis: activation of PFK-1

inhibition of PFK-1

gluconeogenesis: inhibition of F16BPase

activation of F16BPase

$\uparrow$ F26BP

$\downarrow$ F26BP

PFK-2: isoforms (PFKFB)

- single gene, alternative splicing (tissue-specific) generates isoforms that vary in terms of

$\rightarrow$ sensitivity to diff. protein kinases and control

$\rightarrow$ differential ratio of PFK-2 and F26BPase activities

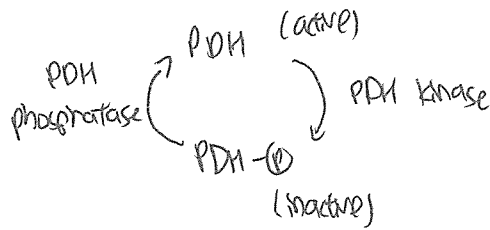
PFKFB-1: liver, heart, skeletal muscle (L-type)

2: lungs, brain, heart (H-type)

3: most tissues, low basal but inducible (I-type) $\rightarrow$ depends on hypoxia

4: most tissues, minor form

- Pyruvate Dehydrogenase
- multienzyme complex (3 units) - NADH
 - major control of activity via phosphorylation



PDH kinase regulated allosterically by metabolites

- activated by acetyl CoA, NADH (PDH products)
- inhibited by pyruvate, CoA, NAD (PDH substrates)
- inhibited by App (indicator of cellular energy state)

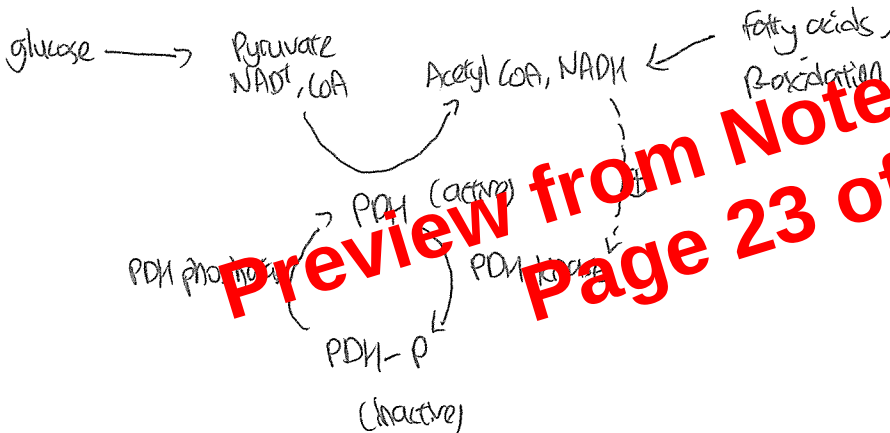
PDH products plentiful → feedback inhibition

PDH products eg: Acetyl CoA also produced from fatty acid oxidation — allows coordination of glucose and fat oxidation

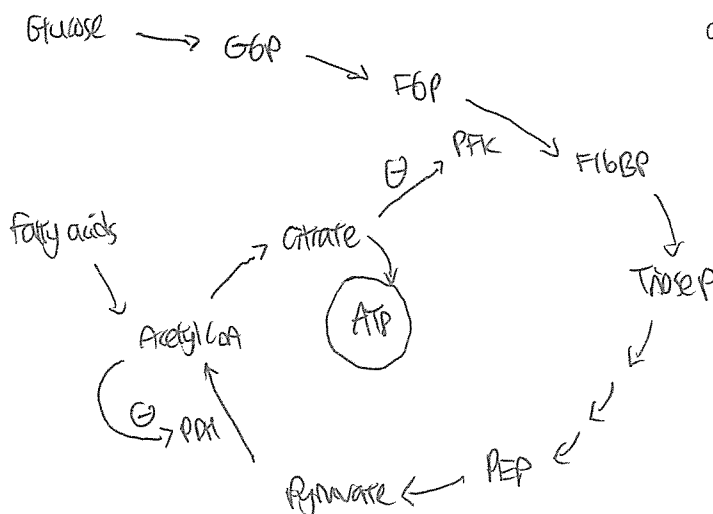
PDH substrates plentiful / energy status poor — favours continued PDH activity

PDH phosphatase activated by insulin signalling

- ↳ indicator of "incoming" glucose-derived pyruvate
- ↳ co-ordinates w fatty acid utilisation in starvation



Glucose-fatty acid cycle



In cancer, mutations in regulatory mechanisms allow hijack of body's glucose to grow into large tumours.

In normal cells, glucose utilisation is low

Pentose phosphate pathway (cytosol)

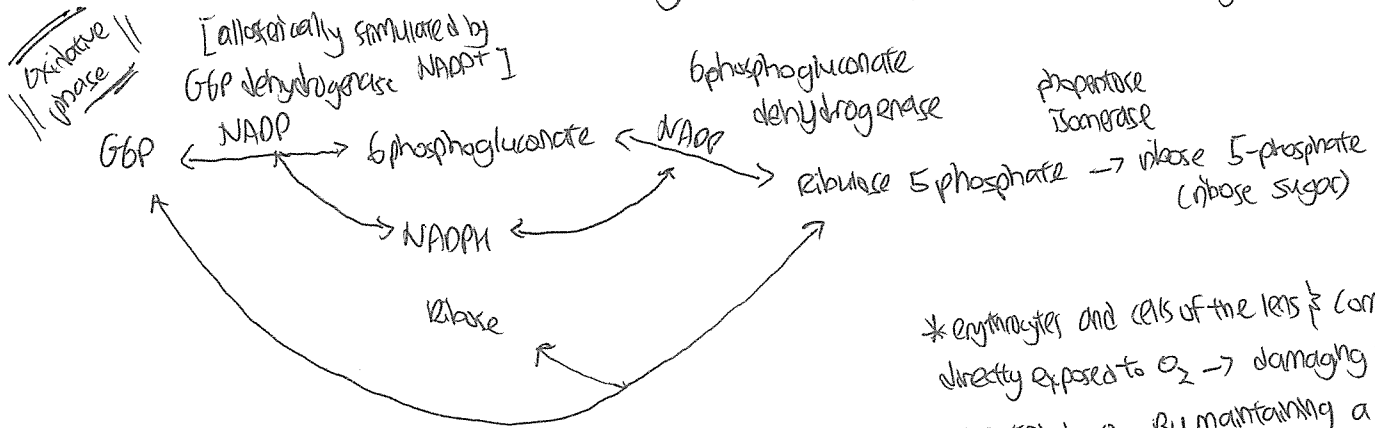
• alternate pathway of glucose catabolism

• 5-50% of all glucose ~~metabolism~~ ^{catabolism} (generally < 10%)

• high contribution in specific cells — active cell division eg: tumour cells
active fatty acid synthesis eg: adipose

adipose cells ≈ 50%
in tumour cells ≈ 50%

* NADPH used for
biosynthetic reaction



Pentose phosphate pathway: specific function and regulation

NADPH: for biosynthetic pathways eg: fatty acids, steroids

ribose sugars: for nucleotides, support DNA & RNA synthesis

Regulation: amount G6PDH and 6PGDH protein decreased in starvation

Transcription of both genes — activated by insulin
— inhibited by glucagon

Glycogen turnover: synthesis of glycogen (occurs at non-reducing end)

UDP provides activation

energy for glycogen synthesis

from glucose

Glycogen (10² ; 37 or 52kDa)

UDP-glucose → addition to ~~single~~ tyrosine ~~residues~~ on glycogen
glycogen-glucose
catalysed by glycogen's intrinsic
glucosyltransferase activity

UDP-glucose → autocatalysis

Glycogen - [glucose]_{6-p}

UDP-glucose → glycogen synthase (GS)

Glycogen - [glucose]₂₀ — after 20 C₆H₁₂O₆ residues attached,
branching occurs

↓ branching enzyme (BE) — little regulation

Glycogen

UDP-glucose ↓ GS & BE
glycogen → { glycogen }

Non-oxidative phase:

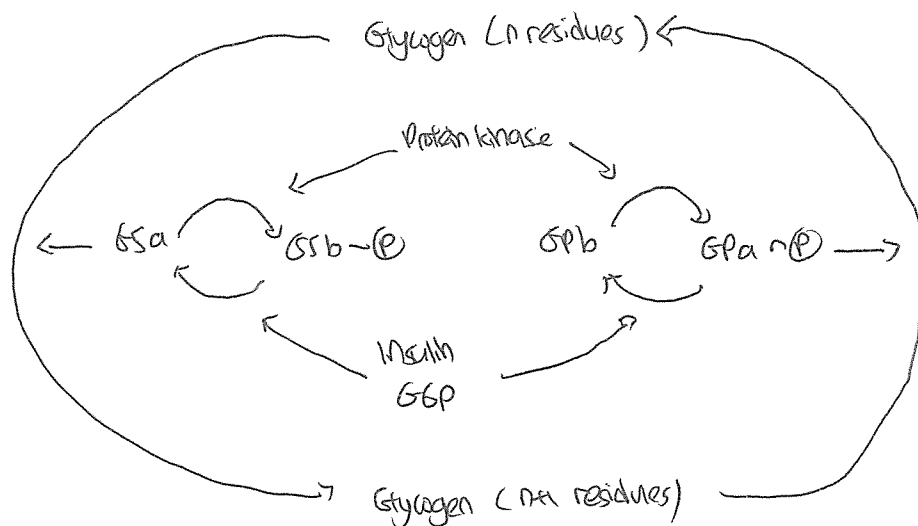
ribose 5-phosphate is converted
back to Glucose 6-phosphate by

Enzymes: transketolases, transaldolase

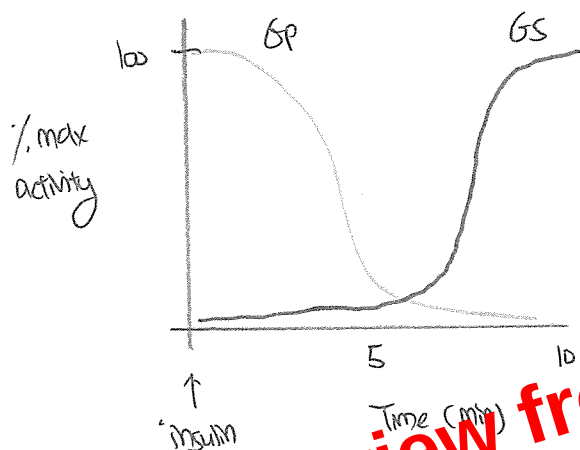
ribose 5-phosphate is first converted into
xylose 5-phosphate by ribose 5-phosphate
epimerase.

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Glycogen turnover: summary of regulation



Glycogen turnover: complexity of regulation

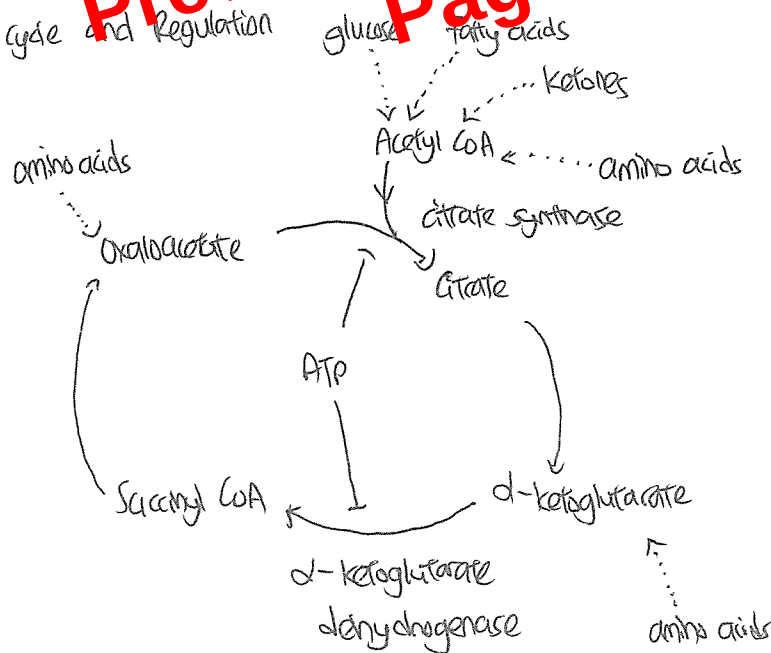


* latency coordination

Starved rats, liver extracts, liver cells

* All GP must be inactivated (dephosphorylated) for GS to be activated

Citric Acid Cycle and Regulation



Advantages of FAS1 organisation ^{enzyme} (hydrophobic intermediates, but in cytosol)

- Intermediates do not leave the ^{enzyme} complex - FA synthesis occurs in cytosol
- ↑ efficiency - intermediates concentrated, reactions coordinated
- coordinated regulation of expression - regulate levels of just ① polypeptide

Precursors for FA synthesis

Acetyl CoA - from glycolysis (pyruvate) and amino acids

- mainly generated in mitochondria

NADPH - from pentose phosphate pathway

- from transport of acetyl-CoA into cytosol (via citrate shuttle)
- from malic enzymes (malate → pyruvate)

Regulation of FA synthesis

- maximal when carbohydrate & ATP abundant
- excess carbohydrate converted to FA and stored as fat

Control mechanisms

- enzyme activity (fine control) - covalent modification, allostery (ACC)
- enzyme amount / coarse control - transcription, translation, degradation (this ↑ ACC)

Multi-level control of ACC

Global control: insulin, glucagon, adrenaline regulate enzyme activity according to status of whole organism

Local control: allosteric effectors (citrate, FA, AMP) regulate enzyme activity according to conditions in individual cells

Long-term control: regulation of ACC synthesis and degradation by changes in diet / nutritional status

Hormonal signals

insulin → signals for ↑ glucose, stimulates synthesis of fat, glycogen and protein
→ inhibits breakdown of fat, glycogen and protein
→ stimulate glucose transport into cells

glucagon - signal for ↓ glucose
- inhibit synthesis of fat, glycogen and protein
- stimulates breakdown of fat, glycogen and protein

For every Acetyl CoA transported across mitochondrial membrane, ① NADPH generated

- Acetyl CoA + oxaloacetate → citrate (citrate synthase)
- citrate transported from mitochondrial matrix into cytosol

by a citrate transporter on the inner mitochondrial membrane.

malate only transported back to mitochondria by malate-α-KG transporter (minor pathway)

Citrate Lyase then breaks down citrate into acetyl CoA + oxaloacetate (malate) oxaloacetate then converted to malate, then pyruvate, then transported back.

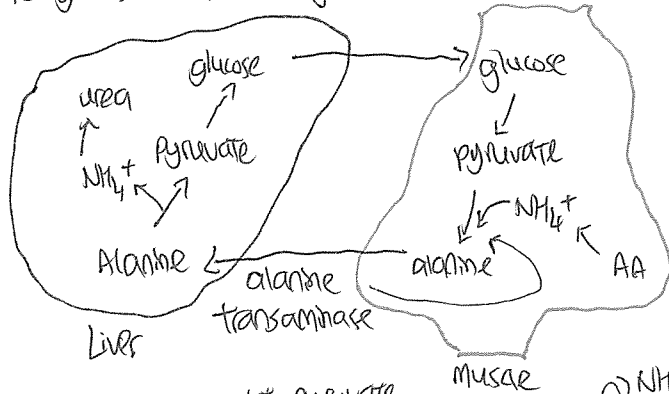
into mitochondria by pyruvate transporter in inner mitochondrial membrane (major pathway)

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Transporting Nitrogen to Liver

- urea is produced in liver
- The alanine cycle is used to transport nitrogen to the liver

The glucose - alanine cycle



- 1) transfer of amino groups to liver for disposal
- 2) transfer carbon from muscle protein to the liver for

glucose synthesis

in muscle
↳ catabolism of branched chain AA provide carbon for gluconeogenesis in the liver

- alanine transaminated to pyruvate
- amino group converted to urea
- pyruvate converted to glucose

→ NH_4^+ from AA transferred onto pyruvate
alanine transported to liver

and creatine kinase

* Serum levels of aspartate transaminase and Aspartate transaminase can be measured to determine severity of heart & liver damage after a heart attack.

Regulation of AA degradation

- Enzymes have high K_m → AA degraded & oxidised in proportion to concentration

- Supply of AA regulates activity

Fed: supply determined by delivery of AA

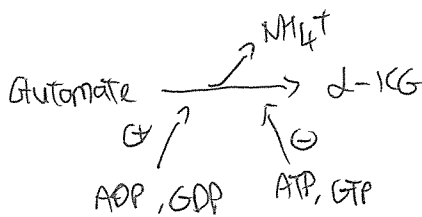
Fasted: supply determined by breakdown of body protein

- regulatory point: deamination - glutamate dehydrogenase

This is because these enzymes leak out of heart after heart attack.

Aminotransferases are also crucial in monitoring people who are exposed to chemicals like chloroform, CCl_4

Glutamate Dehydrogenase



- allosterically regulated by nucleotides
- AA degradation is regulated by energy charge

* mutation in ~~GDH~~ gene →

* mutation in GTP binding site of GDH leads to permanent activation of GDH → hyperammonemia - hyperammonemic syndrome

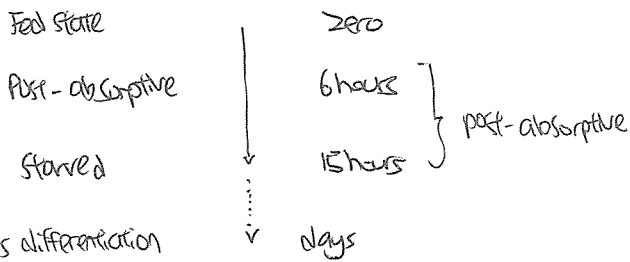
AA biosynthesis

- Assimilation of ammonia into glutamate / glutamine
- majority of AA obtain their nitrogen from Glu / Gln
- pathways for AA biosynthesis are diverse
- carbon skeletons come from intermediates of glycolysis, pentose phosphate pathway and Cit

[elevated levels of ammonia in blood stream & hypoglycaemia]

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Physiological Metabolic Integration: Starvation / feeding



* Species differentiation

* experimental model: rat, mouse

↓ pig = best model for metabolism

Calories and Nutrition

Daily minimum intake: 1000 - 2000 ~~calories~~ calories

balance

- regulation
- integration
- anabolism
- catabolism
- nutrient
- endocrine control

Composition (%)

	Diet	Body stores
carbohydrates	40-45	0.5
lipid	40	80
proteins	15-20	19.5

Body stores "reserves"

carbohydrate
1000 calories
(< 1 day, 2670 kJ)

- blood glucose (20g)
- liver glycogen (70g)
- muscle glycogen (200g)

protein
40,000 calories
(about 10 days, 100,000 kJ)

- tissue (muscles) (8-12kg)

lipid
180,000 calories
(about 60 days, 420,000 kJ)

adipose tissue triglyceride
(10-12kg)

Energy

Importance of glucose metabolism during starvation:

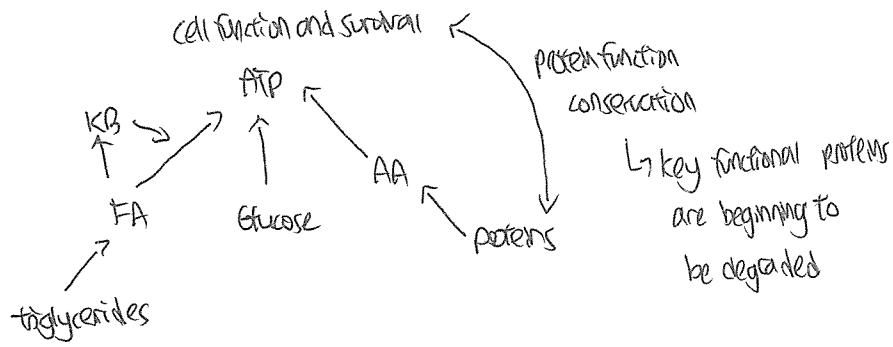
- ATP production - Anaerobic conditions (ETC, O_2)
- in terms of - cells without mitochondria (no citric acid cycle, ETC)
- cells without alternative nutrient supply

	Glucose used / day (g) during starvation	End product
brain (neurons) Blood-brain barrier	125	lactate, ATP (90%) CO_2 (10%)
RBC, renal medulla (no mitochondria)	50	lactate, pyruvate
Muscle (anaerobic exercise)	50	alanine

* these cells can only use glucose as energy source

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Prolonged starvation



Critical roles of insulin & glucagon in starvation

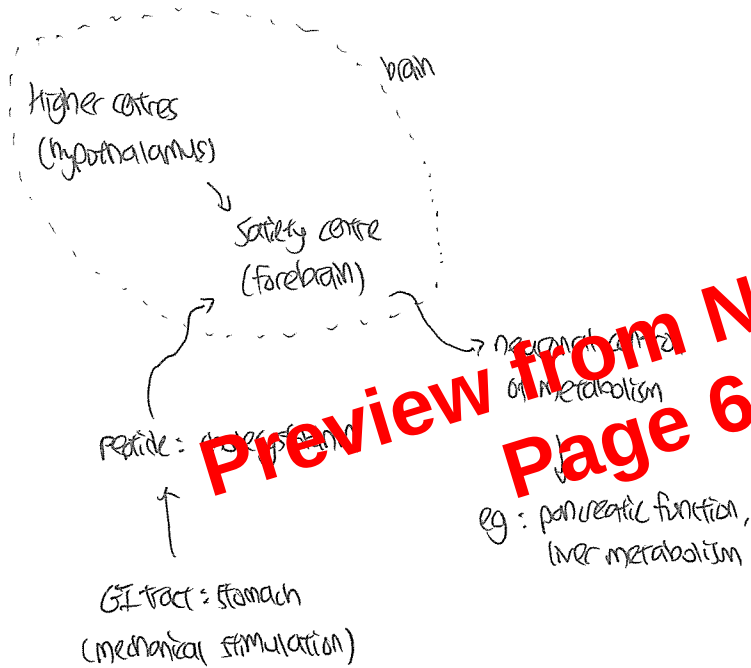
change in plasma in starvation

effects of injection on plasma: glucose conc.

FA concentration

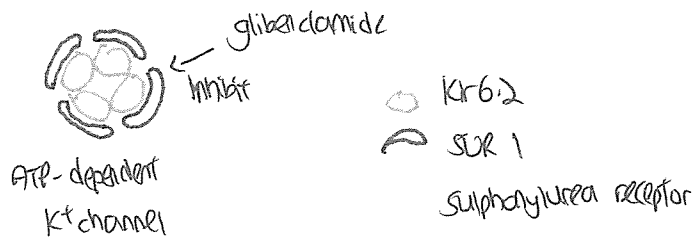
AA concentration

	insulin	glucagon
change in plasma in starvation	↓	↑
effects of injection on plasma: glucose conc.	↓	↑
FA concentration	↓	↑
AA concentration	↓	↑



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Insulin secretagogues

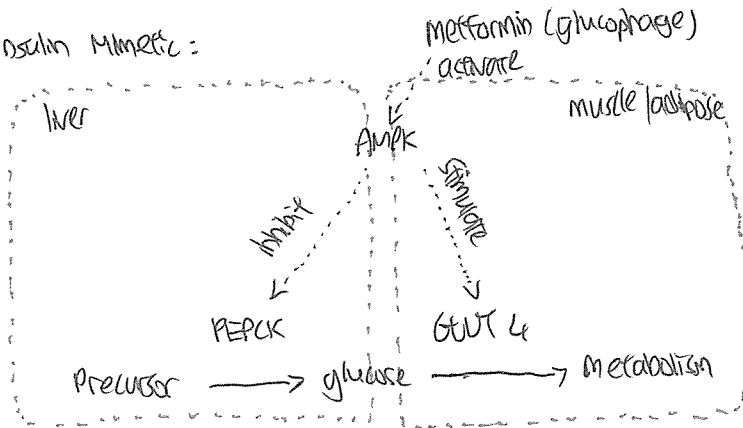


SUR 1 - binds sulphonylurea compounds (oral delivery)

↳ glibenclamide, tolbutamide

- closure of K⁺ channels, insulin release

Insulin Mimetic:

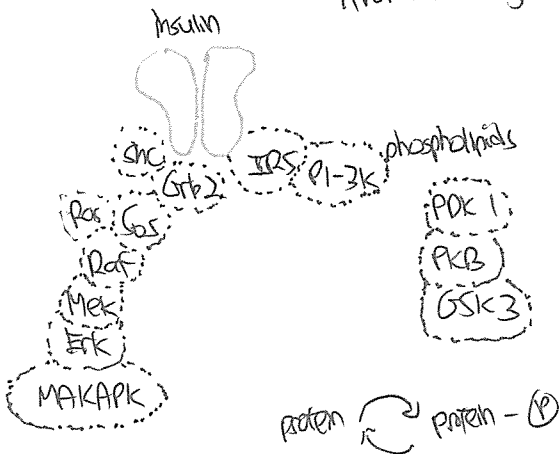


1st line of drug of choice for T2DM - especially overweight / obese

- intracellular insulin-mimetic signalling - stimulates AMPK signalling
- ↑ glucose uptake muscle / adipose
- ↓ glucose production in liver
- metformin ↑ AMP concentration

Insulin sensitisers

Avandia (rosiglitazone)



- metabolic changes
- protein turnover
- gene expression
- cell division
- apoptosis

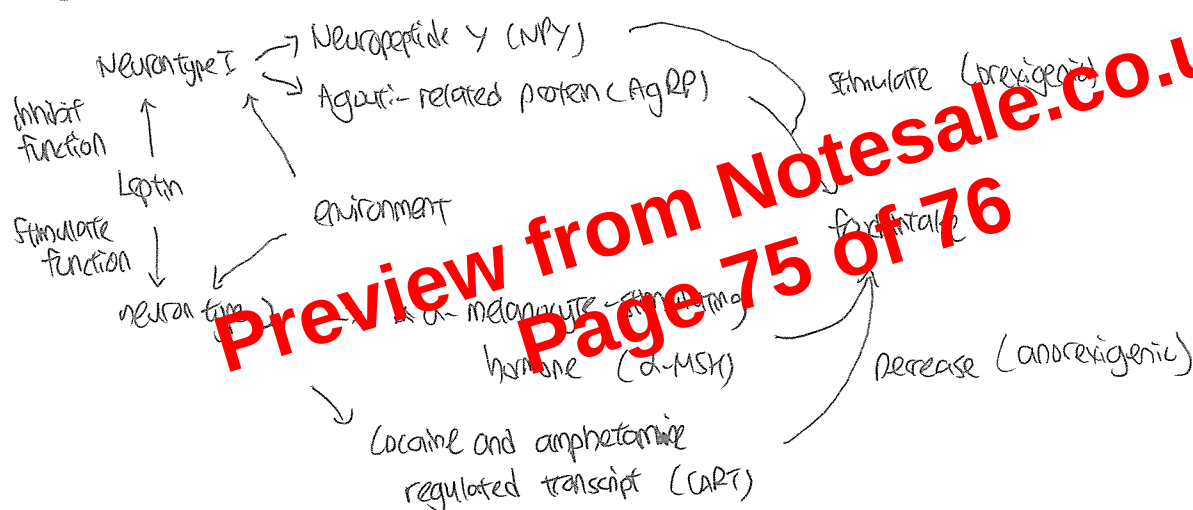
site of insulin resistance - human & animal diabetes

experimental "knock out" animals (KRS 2)

Therapies for obesity:

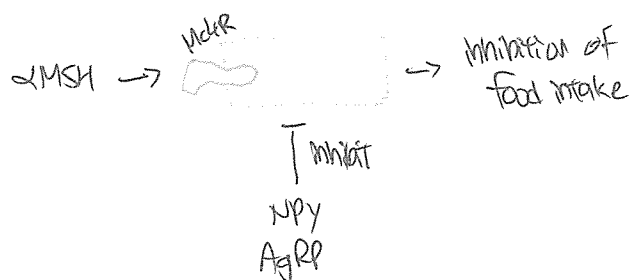
- 1) lifestyle and genetic background
- 2) decrease food intake -
 - Sibutramine (Meridia, Reductil)
 - ↳ inhibit neurotransmitter reuptake (SHT)
 - ↳ gastric bands (decrease stomach size)
- 3) block nutrients absorption from gut - Orlistat (Xenical)
 - ↳ inhibit pancreatic lipase - lipids not absorbed, flow through the GI tract
 - Dinitrophenol
- 4) ~~inhibit~~ ↑ thermogenesis - Ephedrine or caffeine, $\beta 3$ adrenergic receptor agonist
 - ↳ ↑ mitochondrial oxidation, UCP-1 expression
- 5) Modulate fat storage / metabolism (surgery)
 - ↳ maintain brown adipocyte phenotype (stem cell differentiation)
- 6) Modulate central controller system for body weight setting
 - ↳ Leptin? lack of knowledge of key factors

Primary target neurones: Arcuate nucleus of the hypothalamus (therapeutic target potential)



2° target neurones: lateral hypothalamus

↳ default function of neurones to inhibit food intake by unknown "downstream" mechanisms



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