BIOLOGIC OXIDATIONS

1. Cells gain energy required for their functions:
2. Living organism can form ATP:
3. Human organism:
4. In cells of human organism ATP is formed
5. Cells can gain energy:
6. Oxidation of compounds in the cells:
7. Oxidation of compounds in vivo:
8. Glucose is compound which:
9. Glucose:
10. For synthesis of ATP from glucose:
11. Oxidation of compounds in the cells can be performed by:
12. Oxidation of compounds in vivo can proceed:
13. Reduction of compounds in the cells:
14. Reduction of compounds is possible:
15. Compound is oxidized:
16. Compound is reduced:
17. Dehydrogenation is reaction:
18. During dehydrogenation:
19. Dehydrogenation is:
20. During oxidation reduction reactions energy is released:
21. Energy rich compounds are compound which:
22. Energy rich bonds:
23. Compounds with energy rich bonds:
24. Which of following bonds belong to energy rich:
25. Bonds which belong to energy rich are:
26. Phosphoanhydride energy rich bond:
27. Which of statements about phosphoanhydride energy rich bond are correct:

28. Acylphosphate energy rich bond:
29. Acylphosphate energy rich bond is bond which:
30. Enolphosphate energy rich bond:
31. Phosphoenolpyruvate:
32. Compound with guanidiniumphosphate energy rich bond:
33. Guanidinium phosphate energy rich bond:
34. Thioester energy rich bond is present in:
35. Thioster bond is bond which:
36. Energy released by spliting of energy rich bonds can be used for:
37. Energy of guanidiniumphosphate energy rich bond can be used for:
38. Creatine phosphate is compound which:
39. Acetyl-CoA contains:
40. Which of following bonds belon to energy rich:
41. Oxidoreductases are enzymes which:
42. Which of following enzymes belongs to oxidoreductases:
43. Catalase is the enzyme which: 63
44. H_2O_2:
45. NAD is coenzyme which:
46. Monooxygenases are enzymes which:
47. FAD is coenzyme which:
48. FAD:
49. Monooxygenases:
50. Oxidation-reduction reactions in the cells:
51. Which of components of terminal oxidation transfers hydrogens:
52. Which of components of terminal oxidation transfers only electrons:
53. $NADH+H^+$ is coenzyme which:
54. Carriers of hydrogens and electrons in terminal oxidation:
55. Which of statements about carriers of electrons and hydrogens in terminal oxidation are correct:

56. When hydrogens are transfered to terminal oxidation by $NADH_2$:
57. Green complex I:
58. FeS protein in terminal oxidation:
59. Terminal oxidation is the process which:
60. Coenzyme Q is compound which:
61. ATP/ADP translocase:
62. ATP/ADP translocase is system which:
63. Cytochrome b in terminal oxidation:
64. Ubiquinone-cytochrome c reductase is system which:
65. Cytochrome c oxidase:
66. When $FADH_2$ is donor of hydrogens to respiratory chain, then:
67. Mitochondrial ATP-ase:
68. Mitochondrial ATP-ase is enzyme which:
69. Uncouplers for example dinitrophenol:
70. Process of terminal oxidation:

KREBS CYCLE

71. Acetyl-CoA is compound which:
72. Which offollowing statements about acetyl-CoA is correct:
73. Acetyl-CoA can be used:
74. Acetyl-CoA:
75. Conversion of oxaloacette into citrate:
76. Citrate synthase:
77. Citrate synthase catalyzes reaction which:
78. Which of statements about regulatory role of citrate synthase in Krebs cycle are correct:
79. Citrate synthase in regulation of Krebs cycle:
80. Aconitase is enzyme which:
81. Reaction catalyzed by aconitase:

82. Isomere of citrate in Krebs cycle in formed in reaction which:

83. Reaction catalyzed by isocitrate dehydrogenase:

84. Isocitrate dehydrogenase is enzyme which:

85. Reaction of conversion of isocitrate in Krebs cycle:

86. Conversion of isocitrate into2-ketoglutarate:

87. α-ketoglutarate in Krebs cycle is formed:

88. α-ketoglutarate dehydrogenase:

89. α-ketoglutarate dehydrogenase is enzyme which:

90. Enzyme which catalyzes convesrion of α-ketoglutarate to succinyl-CoA:

91. Succinyl-CoA:

92. Conversion of succinyl-CoA to succinate:

93. Substrate level phosphorylation in Krebs cycle:

94. Reaction of substrate level phosphorylation in Krebs cycle:

95. Further conversion of succinate in Krebs cycle:

96. Succinate dehydrogenase in Krebs cycle:

97. Conversion of fumarate in Krebs cycle:

98. Fumarase is enzyme which:

99. Conversion of fumarate into malate:

100. Malate dehydrogenase is the enzyme which:

101. Reaction cataylzed by malatedehydrogenase:

102. Regulators of isocitrate dehydrogenase are:

103. Isocitrate dehydrogenase in regulation of Krebs cycle:

104. By oxidation of acetyl-CoA in Krebs cycle:

105. Oxidation of acetyl-CoA in Krebs cycle:

106. Reaction of substrate level phosphorylation in Krebs cycle:

107. Reaction of Krebs cycle where substrate level phosphorylation occurs:

108. Reoxidation of reduced coenzymes formed in Krebs cycle allows synthesis of:

109. $NADH+H^+$ in Krebs cycle is formed:
110. Coenzyme by oxidation of which 3 ATP can be formed in Krebs cycle is formed:
111. Coenzyme by oxidation of which 2 ATP can be formed in Krebs cycle is synthesized:
112. Enzymes of Krebs cycle:
113. Enzyme complex required for conversion of pyruvate to acetyl-CoA:
114. Conversion of pyruvate into acetyl-CoA:
115. Pyruvate dehydrogenase catalyzes reaction which:
116. Lipoic acid in pyruvate dehydrogenase complex:
117. Compound required for utilization of ketone bodies in extrahepatic tissues:
118. In regulation of Krebs cycle participates:
119. Citrate synthase and isocitrate dehydrogenase are enzymes which:
120. High concentrations of ATP:

CARBOHYDRATES

121. In digestion of carbohydrates from the food:
122. Which statement about digestion of carbohydrates is correct:
123. Main source of glucose for newborn:
124. Product of the action of amylase into starch is:
125. Pyruvate:
126. Substrate for alcoholic fermentation is:
127. Activation of glucose:
128. During activation of glucose:
129. Glucokinase is enzyme which:
130. Glucokinase:
131. When glucose is activated before entering metabolic processes:
132. Glucose-6-phosphate is compound which:
133. Glucokinase and hexokinase are enzymes which:
134. Enzyme hexokinase:
135. Glucose-6-phosphate enters metabolic processes:

136. Processes which utilize glucose-6-phosphate:

137. Reaction of glucose with ATP:

138. Conversion of glucose-6-phosphate to fructose-6-phosphate:

139. Change of glucose-6-phosphate to fructose-6-phosphate:

140. Phosphofructokinase catalyzes reaction which:

141. Reaction catalyzed by phosphofructokinase:

142. Key regulatory reaction of glycolysis is:

143. Which of following compounds influence activity of phosphofructokinase I:

144. Inhibition of phosphofructokinase by ATP:

145. Glyceraldehyde-3-phosphate and dihydroxyacetonephosphate are compounds which:

146. Cleavage of fructose-1,6-bisphosphate in glycolysis:

147. Reaction of fructose-1,6-bisphosphate conversion in glycolysis:

148. Triosephosphate isomerase catalyzes reaction:

149. Intermediate of glycolysis which can be used for synthesis of triacylglycerols:

150. Change of dihydroxyacetonephosphate to glycerolphosphate:

151. Dihydroxyacetonephosphate is changed to glycerolphosphate:

152. Glycerolphosphate dehydrogenase is the enzyme which:

153. Reaction catalyzed by glycerolphosphate dehydrogenase:

154. During oxidation of glyceraldehyde-3-phosphate in glycolysis:

155. Product of reaction catalyzed by glyceraldehyde-3-phosphate dehydrogenase:

156. During oxidation of one glyceraldehyde-3-phosphate in aerobic conditions:

157. When glyceraldehyde-3-phosphate is oxidized in glycolysis:

158. Reaction of conversion glyceraldehyde-3-phosphate $\longrightarrow$ 1,3-bis-phosphoglycerate $\longrightarrow$ 3-phosphoglycerate allows synthesis of:

159. Different amounts of ATP by oxidation of glyceraldehyde-3-phosphate in aerobic and anaerobic conditions are formed because:

160. Glyceraldehyde-3-phosphate dehydrogenase is responsible for synthesis of:

161. Conversion of 1,3-bisphosphoglycerate in glycolysis:

162. Substrate for phosphoglyceratekinase is compound which:

163. Phosphoglycerate kinase in glycolysis catalyzes conversion of:

164. Phosphoglycerate kinase:

165. Phosphoglycerate mutase catalyzes::

166. 1,3-bisphosphoglycerate:

167. 2-phosphoglycerate in glycolysis is changed:

168. Conversion of 2-phosphoglycerate in glycolysis:

169. Compound formed by the action of enolase in glycolysis:

170. Enolase is enzyme which:

171. Compound with enolphosphate energy rich bond:

172. Enolphosphate energy rich bond contains:

173. Pyruvate kinase:

174. In regulation of pyruvate kinase activity:

175. Further conversion of phosphoenolpyruvate in glycolysis:

176. In conversion of phosphoenolpyruvate in glycolysis:

177. Fructose-1,6-bisphosphate influences enzymes of glycolysis that:

178. Pyruvate in glycolysis is synthesized by:

179. In aerobic conditions in glycolysis:

180. Reaction glucose + 2 ADP + 2 phosphates $\rightarrow$ 2 lactate + 2 ATP:

181. Summary reaction $C_6H_{12}O_6$ + 2 ADP + 2 P $\rightarrow$ 2 lactate + 2 ATP:

182. Reaction $C_6H_{12}O_6$ + 8 (6) ADP + 8 (6)P $\rightarrow$ 2 pyruvate+ 8 (6)ATP :

183. Reaction $C_6H_{12}O_6$ + 8 (6) ADP + 8 (6)P $\rightarrow$ 2 pyruvates + 8 (6)ATP :

184. Process which can be expressed by summary reaction $C_6H_{12}O_6 + 6\ O_2 \rightarrow$ 6 CO_2 + 6 H_2O + 38 ATP:

185. Process $C_6H_{12}O_6 + 6\ O_2 \rightarrow$ 6 CO_2 + 6 H_2O + 38 ATP:

186. Oxidation of glucose which is expressed by summary reaction:
$C_6H_{12}O_6 + 6\ O_2 \rightarrow$ 6 CO_2 + 6 H_2O + 38 ATP:

187. During complete aerobic oxidation of glucose:

188. Complete aerobic oxidation of glucose:

189. Glycerolphosphate is compound:

190. Compound glycerolphosphate:

191. Reaction of lactate with NAD^+:

192. Reaction of pyruvate with NADH:

193. Reaction of glucose with ATP:

194. Compound 1,3-bisphosphoglycerate: :

195. Reaction of phosphoenolpyruvate with ADP:

196. Which of following enzymes catalyzes reaction of cinversion of glyceraldehyde-3-phosphate to 1,3-bisphosphoglycerate::

197. Phosphorylation at the substrate level by means of utilization of acylphosphate energy rich bond:

198. Phosphorylation at the substrate level by means of utilization of enolphosphate energy rich bond:

199. Anaerobic glycolysis:

200. Aerobic glycolysis:

201. Which of statements about aerobic glycolysis are correct:

202. In metabolic regulation of glycolysis participate:

203. $NADH_2$ formed in reaction catalyzed by glyceraldehyde-3-phosphate dehydrogenase can be used for synthesis of ATP by oxidative phosphorylation:

204. Which of statements about transport of reduciong equivalents from cytosol into mitochondria is correct:

205. Which of following reactions of glycolysis are irreversible:

206. In the process of aerobic glycolysis.

207. During aerobic glycolysis:

208. Reaction typical for anaerobic glycolysis is:

209. Reaction of conversion of pyruvate to lactate:

210. Lactate dehydrogenase catalyzes reaction:

211. Anaerobic glycolysis produces less ATP than aerobic glycolysis because:

212. Conversion of pyruvate to lactate:

213. Production of lactate in working muscle::

214. Red blood cells gain energy in metabolic process which:
215. Source of energy for red blood cells can be:
216. Conversion of lactate to pyruvate:
217. Cori's cycle:
218. Compound with acylphosphate energy rich bond in glycolysis:
219. Which of statments about intermediates of glycolysis with energy rich bonds are true:
220. Intermediates of glycolysis with energy rich bond:
221. In the process of anaerobic glycolysis:
222. $NADH_2$ in anaerobic glycolysis is oxidized by:
223. Which cells of human body use glucose as the only source of energy:
224. Lactate:
225. Which of following tissues is almost completely dependent on glucose as source of energy:
226. Which statements about regulation of glycolysis are correct:
227. Gluconeogenesis is the process which:
228. Gluconeogenesis:
229. For glucose synthesis by gluconeogenesis can be used:
230. Organism can use for glucose synthesis by gluconeogenesis:
231. Pyruvate carboxylase is the enzyme which:
232. Phosphoenolpyruvate carboxykinase:
233. Phosphoenolpyruvate carboxykinase is the enzyme which:
234. For synthesis of free glucose in the process of gluconeogenesis is responsible enzyme:
235. Conversion of glucose-6-phopsphate into free glucose catalyzes enzyme:
236. Substrate for phosphoenolpyruvate carboxykinase is:
237. Enzyme of gluconeogenesis which produces compound with enolphosphate energy rich bond:
238. Reaction of pyruvate carboxylation::
239. Pyruvate carboxylase:
240. Synthesis of phosphoenolpyruvate from oxaloacetate proceeds:
241. Phosphoenolpyruvate carboxykinase:

242. Gluconeogenesis:

243. During long starvation:

244. During long starvation:

245. Process of gluconeogenesis:

246. Which of following enzymes are required for glucose synthesis by gluconeogenesis:

247. Acetyl-CoA cannot be for gluconeogenesis because:

248. Connection of proteins with gluconeogenesis:

249. Part of triacylglycerols which can be used for gluconeogenesis:

250. Connection of glycerol with process of gluconeogenesis requires:

251. Gluconeogenesis is influenced by:

252. Glygogen is compound:

253. Intermediate of glycogen synthesis is:

254. UDP-glucose is compound which:

255. Glucose-1-phosphate during glycogen synthesis:

256. Glucose-1-phosphate in metabolism of glycogen:

257. Further conversion of glucose-1-phosphate in glycogen synthesis:

258. Further conversion of glucose-1-phosphate in glycogen degradation:

259. Synthesis of UDP-glucose:

260. UDP-glucose is compound:

261. Glycogensynthase catalyzes synthesis of:

262. α-1,4 glycosidic bond:

263. Glycogensynthase is the enzyme which:

264. Compound glucose-1-phosphate:

265. Compound glucose-6-phosphate:

266. Uridinediphosphateglucose (UDPG):

267. Glycogensynthase:

268. Glucose-1-phosphate:

269. Compound which contians two glucoses bound by alpha-1,4-glycosidic bond:
270. Free gucose:
271. Reaction: of conversion of ATP into cAMP:
272. α-1,6 glycosidic bond:
273. Activity glycogensynthase in the liver decreases:
274. Activity of glycogensynthase in liver increases:
275. Glycogenphosphorylase is the enzyme which:
276. Glycogenphosphorylase catalyzes:
277. Glucose-1-phosphate:
278. Glucose-6-phosphate:
279. Free glucose during glycogen degradation can be formed:
280. Activation of glycogenphosphorylase mediates:
281. Regulatory enzymes of glycogen metabolism:
282. Glycogensynthase and glycogen phosphorylase are enzymes which:
283. Glycogensynthasephosphorylasekinase (GSPK) is enzyme which:
284. Comparing glycogen degradation in liver and in skeletal muscles we can say:
285. Pentose phosphate pathway:
286. In pentose phosphate pathway:
287. Ribose-5-phosphate is compound which:
288. Reaction of conversion of glucose-6-phosphate to 6-phosphogluconate:
289. Glucose-6-phosphate dehydrogenase:
290. Reaction catalyzed by lactonase:
291. Reaction of conversion of robulose-5-phosphate to ribose-5-phosphate:
292. Thiaminepyrophosphate in pentose phosphate patway is required for:
293. $NADPH+H^+$:
294. Conversion of glucose-6-phosphate to 6-phosphogluconate:
295. Glucose-6-phosphate dehydrogenase:23
296. Reaction of conversion of 6-phosphogluconate in pentose phosphate pathway:

297. Reaction of pentose phosphate pathway in which ribulose-5-phosphate is formed:
298. Increased production of ketone bodies in diabetes is caused by:
299. Which of following hormones participate in regulation of blood glucose:
300. Glucocorticoids are hormones which:
301. Insulin is the hormone which:
302. Epinephrine (adrenaline) is the hormone which:
303. In regulation of blood glucose level participate:
304. Insulin:
305. When level of glucose in blood increases:
306. Insulin decreases blood glucose level by:
307. Insulin participates in regulation of blood glucose level by:
308. Glucocorticoids:
309. Glucagon is the hormone which:
310. Which of following enzymes are activated in presence of glucagon:
311. Increased glucose concetration in blood causes:
312. Glycosuria:

LIPIDS

313. Cerebrosides:
314. Cerebrosides contain in their structure:
315. Ceramide is compound which:
316. Lipids with carbohydrate component:
317. Sphingosine:
318. C_{18} unsaturated aminoalcohol:
319. Compound which contains sphingosine, fatty acid, phosphate and choline:
320. Sphingomyelins are lipids which:
321. Phosphatidylinositols contain in their molecula:
322. Lecithines:

323. Fatty acid in sphingomyelins is bound:

324. Alcoholic component of cerebrosides:

325. During activation of palmitic acid:

326. Activation of fatty acids:

327. Activation of fatty acids can be catalyzed by:

328. During activation of fatty acids before β-oxidation:

329. Activated fatty acids are transported into mitochondria by help of:

330. For transport of activated fatty acid into mitochondria is required compound which:

331. Carnitine is compound which:

332. Carnitineacyltransferase I:

333. Carnitineacyltransferase I is enzyme which:

334. Carnitineacyltransferase II is enzyme which:

335. Tranport of activated fatty acids into place of β-oxidation:

336. Activated fatty acid is transported into mitochondria by:

337. Carnitine is compound which:

338. Reaction of β-oxidation which allows synthesis of 2 ATP by oxidative phosphorylation:

339. Adition of water in β-oxidation:

340. Reaction of β-oxidation which allows synthesis of 3 ATP by oxidative phosphorylation is:

341. Synthesis of 3 ATP from coenzyme formed in β-oxidatiopn allows:

342. Dehydrogenation reactions in β-oxidation are catalyzed by:

343. During oxidation of palmitic acid in β-oxidation:

344. During complete degradation of palmotoyl-CoA in β-oxidation are formed:

345. During β-oxidation of fatty acids with odd number of carbons as the last product is formed:

346. During oxidation of stearic acid in β-oxidation:

347. Complete oxidation of stearic acid allows:

348. Process of oxidation of myristic acid:

349. Acetyl-CoA in β-oxidation is formed:

350. Synthesis of acetyl-CoA in β-oxidation:
351. Acyl CoA dehydrogenase:
352. Compound containing acetyl residue bound to CoA:
353. Reaction during which fatty acids is changed to acyl-CoA:
354. EnoylCoA hydratase:
355. β-oxidation of fatty acids:
356. β-oxidation of fatty acids:
357. Acetyl-CoA in synthesis of fatty acids is formed in cytosol:
358. Acetyl-Co required for fatty acids synthesis is formed:
359. Citrate synthase and ATP-citrate lyase are enzymes which:
360. ATP citrate lyase and citrate synthase are enzymes which:
361. Carboxylation of acetyl-CoA to malonyl-CoA:
362. Synthesis of malonyl-CoA in synthesis of fatty acids:
363. β-hydroxyacyl-ACP in fatty acid synthesis is formed:
364. Synthesis of β-hydroxyacyl-ACP requires:
365. Regulatory step in fatty acid synthesis is:
366. Enzmye which plays key role in regulation of fatty acid synthesis is:
367. Reaction of acetyl-CoA carboxylation:
368. Synthesis of fatty acids:
369. Synthesis of fatty acids is the process about which we can say:
370. Reaction of fatty acid synthesis during which enoyl-ACP is changed to saturated acyl-ACP:
371. Malic enzyme is enzyme which:
372. Malonyl-CoA is compound which:
373. Acetyl-CoA carboxylase catalyzes reaction which:
374. Reaction of malonyl-CoA synthesis:
375. Acetyl-CoA carboxylase:
376. Acetyl-CoA carboxylase is enzyme which:

377. Source of hydrogens for reduction reactions of fatty acid synthesis is:
378. Condensing enzyme in fatty acid synthesis catalyzes reaction which:
379. β-ketoacylreductase:
380. β-hydroxyacyl-ACP is changed to enoyl-ACP:
381. Fatty acid synthase:
382. Thioesterase is the enzyme which:
383. Elongation of fatty acids:
384. Desaturation of fatty acids:
385. $NADPH_2$ in the process of synthesis of fatty acids:
386. Which of following reactions can be source of $NADPH_2$ for synthesis of fatty acids:
387. Fatty acid synthesis is regulated by:
388. Which statements about role of hormones in regulation of fatty acid synthesis are correct:
389. Which statements about role of glucagon in regulation of fatty acids synthesis are correct:
390. Which statements about regulatrion of fatty acid synthesis are correct:
391. Which of processes activated by insulin is important for conversion of glucose into fatty acids:
392. Triacylglycerol is compound which:
393. Which cells of human body synhesize and store triacylglycerols:
394. For triacylglycerol synthesis in is used:
395. Alcoholic component of triacylglycerols in adipose tissue:
396. In synthesis of triacylglycerols:
397. Hormone sensitive lipase is the enzyme which:
398. Degradation of triacylglycerols in adipose tissue:
399. In synthesis of lecithins:
400. CDP-diacylglycerol is compound which:
401. Synthesis of cholesterol in human body:
402. In the process of cholesterol synthesis:
403. Cholesterol is compound which:

404. HMG-CoA during cholesterol synthesis is changed:

405. Mevalonic acid is compound which:

406. Mevalonic acid in cholesterol synthesis:

407. HMG-CoA reductase is enzyxme which:

408. Which of statements about regulation of cholesterol synthesis are correct:

409. Chylomicrons:

410. Apoprotein A:

411. Apoprotein B:

412. Chylomicrons are lipoproteins which:

413. VLDL are lipoproteins which:

414. VLDL:

415. Apoprotein C:

416. Lipoprotein lipase is the enzyme which:

417. Lipoprotein lipase:

418. Lipoprotein lipase is enzyme which:

419. LDL are lipoproteins which:

420. LDL:

421. HDL are lipoproteins which:

422. HDL are lipoproteins which:

423. Which of statements about HDL are correct:

424. Lecithine-cholesterol acyltransferase (LCAT) is the enzyme which:

425. Lecithine-cholesterol acyltransferase (LCAT):

426. Which of following mechanisms participate in regulation of cholesterol content in cells:

427. When intracellular concentration of cholesterol increases:

ACETYL-CoA + KETONE BODIES

428. Acetyl-CoA is compound which:

429. Acetyl-CoA:

430. Acetyl-CoA can be utilized in the cells:

431. Utilization of acetyl-CoA is possible:

432. Acetyl-CoA can be formed:

433. Acetyl-CoA:

434. Utilization of acetyl-CoA for ketone bodies synthesis:

435. Which of statements about utilization of acetyl-CoA are correct::

436. Acetoacetyl-CoA:

437. Acetoacetyl-CoA is compound which:

438. Ketone bodies are compounds which:

439. Which of following compounds belong to ketone bodies:

440. Acetone is compound which:

441. β-hydroxy-β-methyl-glutaryl-CoA:

442. Under physiological conditions:

443. Acetoacetyl-CoA is broken by β-ketothiolase:

444. Which of following compounds is required for utilization of ketone bodies:

445. Synthesis of ketone bodies:

446. Ketegenesis is the process which:

447. Ketone bodies are compounds which: 69

448. Acetoacetate is compound which:

449. Acetoacetate is compound about which can be said:

450. Process of ketone bodies synthesis:

451. During process of ketone bodies synthesis:

452. HMG-CoA is compound which:

453. Hydroxybutyrate dehydrogenase:

454. β-hydroxybutyrate:

455. β-hydroxybutyrate is compound which:

456. Which cells of human body cannot utilize ketone bodies:

457. Extrahepatal utilization of ketone bodies:

458. Reaction of conversion of acetoacetate into acetoacetyl-CoA:

459. Malonyl-CoA is compound which:

460. Malonyl-CoA:

461. Increased synthesis of ketone bodies in diabetes is caused by:

462. Factors which stimulate synthesis of ketone bodies in diabetes and starvation are:

463. In regulation of ketone bodies synthesis participate:

464. In activation of ketone bodies synthesis participate:

465. Increased concentration of ketone bodies causes:

466. Increased concentration of ketone bodies in blood in diabetes:

467. Increased concetration of ketone bodies in blood:

AMINO ACIDS

468. Among glucogenic amino acids belong:

469. Glutamate:

470. Oxidases of amino acids:

471. Which of following amino acids enter Krebs cycle through succinyl-CoA:

472. Which of following amino acids enter Krebs cycle through ketoglutarate:

473. Glutamate dehydrogenase:

474. Glutamate dehydrogenaseis enzyme which:

475. Glutamate dehydrogenase:

476. Decarboxylation of glutamate:

477. Indirect deamination of amino acids requires:

478. Ammonia is transported from tissues to the liver in a form of:

479. Serine is deaminated:

480. Cysteine:

481. By decarboxylation:

482. Coenzyme of decarboxylases of amino acids is:

483. Essential amino acids:

484. Aspartate aminotransferase:

485. Ammonia:

486. Alanine aminotransferase:

487. Glutamine:

488. Decarboxylation of glutamate:

489. Glutamate dehydrogenase:

490. Ammonia:

491. Decarboxylation of serine:

492. Ammonia:

493. Pyruvate:

494. Alanine aminotransferase:

495. Carbamoylphosphate:

496. During urea cycle:

497. Urea $(NH_2)_2CO$:

498. Enzymes of urea cycle:

499. Universal acceptor of of amino group from majority of all amino acids can be:

500. Pyruvate:

501. During urea cycle:

502. Glutamine:

503. Aminoacid which is donor of one amino group in urea:

504. Ornithine transcarbamoylase:

505. Arginase:

506. Reaction of argininosuccinate conversion to arginine:

507. Reaction of arginine hydrolysis:

508. Urea:

509. Carbamolyphosphate:

510. Which of following statements about conversion of glutamate to glutamine are correct

511. Glutamine:

512. Reaction: of glutamine hydrolysis:

513. Reaction of ammonia binding to ketoglutarate:

514. Which of statements about conversion of glutamate to ketoglutarate are correct:

515. Aspartate aminotransferase

516. Four carbon dicarboxylic amino acid:

517. S-adenosylmethionine:

518. S-adenosylhomocysteine:

519. Decarboxylation of serine

520. Transamination of alanine:

521. Methionine is the amino acid which:

522. Phenyalanine hydroxylase:

523. S-adenosylmethinine:

524. Homocysteine:

525. Phenylalanine hydroxylase:

526. Tyrosine:

527. Phenylketonuria:

NUCLEOTIDES

528. Nucleotides are compounds which:

529. Nucleotides in human body:

530. Source of ribosephosphate in synthesis of purine nucleotides de novo is

531. PRPP is compound which:

532. PRDP-amidotransferase catalyzes reaction which:

533. Reaction of phosphoribosylamine synthesis:

534. PRPP-amidotransferase is enzyme which:

535. Reaction of phosphoribosylamine synthesis:

536. In the reaction of phosphoribosylamine with glycine: reaction:

537. Adenylosuccinate::

538. Further conversion of xanthosine monophospate in synthesis of purine nucleotides:

539. Synthesis of purine nucleotides de novo is the process which:

540. For conversion of IMP to AMP:

541. Source of energy in conversion of IMP into AMP is:

542. Source of NH_2 group in AMP:

543. In conversion of IMP into GMP:

544. GMP in de novo synthesis of purine nucleotides is formed:

545. For synthesis of GMP from IMP:

546. Source of NH_2 group in synthesis of GMP de novo is:

547. Source of energy in conversion of IMP into GMP is:

548. Nitrogen atoms in purine heterocycle:

549. Which of statements about origin of atoms in purine heterocycle are correct:

550. Main regulatory enzyme of purine nucleotide syntheisi de novo is:

551. Key regulatory enzyme of purine nucleotide synthesis de novo is:

552. Activity of PRPP-amidotransferase is influenced by:

553. Conversion of IMP into AMP is inhibited by:

554. Conversion of IMP into GMP is inhibited by:

555. Synthesis of GMP from IMP is inhibited by:

556. Source of NH_2 group for carbamoylphosphate synthesis in synthesis of pyrimidine nucleotides is:

557. Synthesis of carbamoylphosphate in de novo synthesis of pyrimidine nucleotides:

558. Carbamoylphosphate in synthesis of pyrimidine nucleotides is formed:

559. Reaction of condensation of aspartate with carbamoylphosphate:

560. Carbamoylphosphate synthase II:

561. Aspartate transcarbamoylase is the enzyme which:

562. Orotate is compound which:

563. Reaction of glutamine, CO2 + 2ATP:

564. Carbamoylaspartate is compound which:

565. Reaction of conversion dUMP into TMP

566. UMP in synthesis of pyrimidine nucleotides de novo:

567. For synthesis of cytidine nucleotides:

568. CTP is compound which:

569. Thymine nucleotides:

570. Synthesis of thymine nucleotides:

571. Main regulatory enzyme of pyrimidine nucleotide synthesis in eucaryotic cells is:

572. Amino acid glutamine in synthesis of nucleotidesis required:

573. Aspartate in synthesis of nucleotides is required:

574. Conversion of nucleotides into deoxynucleotides:

575. Ribonukleotidreductase is enzyme which:

576. In AMP degradation:

577. 5·-nucleotidase is enzyme which:

578. Adenosine is compound which:

579. Adenosine is changed to inosine:

580. During degradation of purine nucleotides:

581. Inosine during degradation of purine nucleotides:

582. Purine nucleoside phosphorylase is the enzyme which:

583. Hypoxanthine is compound which:

584. Xanthine oxidase is enzyme which:

585. Final product of degradation of purine nucletides is:

586. Uric acid is compound which:

587. Allopurinol is compound which:

588. Allopurinol is used in therapy of hyperuricemia because:

589. In the process of GMP degradation:

590. When AMP and water enter reaction:

591. Reaction of inosine with phosphate:

592. Reaction of hypoxanthine conversion in degradation of purine nucleotides:

593. Xanthine oxidase is the enzyme which:

594. Uric acid is compound which:

595. During CMP degradation:

596. Degradation of thymine nucleotides:

597. β-alanine is formed:

598. β-aminoisobutyrate is formed as final product of degradation of:

599. Synthesis of AMP from adenosine:

600. Adenosine kinase catalyzes reaction which:

601. GMP in salvage pathways is formed:

602. IMP in salvage pathways is formed:

603. Hypoxanthine-guanine phosphoribosyltransferase (HGPRT) is enzyme: 54

604. HGPRT in salvage pathways of nucleotide synthesis: 55

605. Conversion of hypoxanthine to IMP:

606. Adenosine kinase catalyzes reaction which:

607. In salvage pathways of nucleotide synthesis participate:

608. Primary metabolic hyperuricemia:

609. Causes of primary metabolic hyperuricemia can be:

610. Causes of secondary metabolic hyperuricemia can be:

611. What are differences between metabolic and renal hyperuricemia:

612. In primary renal hyperuricemia:

613. Primary renal hyperuricemia is result of:

614. Secondary renal hyperuricemia:

VITAMINS

615. Functions of riboflavine (vitamin B_2) are:

616. Riboflavine is vitamin which:

617. In amino acid metabolism vitamin B_2 is required for:

618. Vitamin B_2 is the component of the coenzyme for: 7

619. During reduction molecula of FAD binds:

620. Which of following vitamins is not required in oxidation-reduction reactions:

621. Which of following vitamins are present in coenzymes of oxidation-reduction reactions:

622. Thiamine pyrophosphate:

623. Which of following enzymes requires thiamine pyrophosphate:

624. In decarboxylation of amino acids participates:

625. Lipoate is the coenzyme required for:

626. Lipoic acid:

627. Which of following vitamins is the component of the enzyme system for oxidative decarboxylation of ketoglutarate in Krebs cycle:

628. Which of following coenzymes is the coenzyme for oxidative decarboxylation of pyruvate:

629. $NADPH_2$:

630. Nicotinamide:

631. Coenzyme form of nicotinamide:

632. NAD:

633. In amino acid metabolism vitamin B_6 is required for:

634. Pyridoxalphosphate is the coenzyme in reaction where ketoglutarate is the substrate. It is the reaction of:

635. Pyridoxalphosphate:

636. Indirect deamination of amino acids requires coenzymes derived from vitamins:

637. Transfer of CH_3 groups from methyl-tetrahydrofolate into homocysteine to regenerate methionine requires vitamin:

638. Vitamin B_{12} is required for:

639. Methylmalonyl-CoA is formed:

640. Methylmalonyl-CoA mutase:

641. Methylmalonyl-CoA in the presence of vitamin B_{12} is converted into:

642. Which of following compounds can be source of one carbon groups:

643. Panthotenic acid is vitamin which:

644. Coenzyme A:

645. Folic acid is vitamin which:

646. Folic acid:

647. Tetrahydrofolate:

648. One carbon groups are used for synthesis of:

649. Which of following reactions require biotin as a coenzyme:

650. Rate limiting reaction of fatty acid synthesis which requires biotin is the reaction:

651. Biotin is required as coenzyme:

652. Vitamin C (ascorbate) is required for:

653. Active form of vitamin B_6:

MOLECULAR BIOLOGY

654. During process of replication:

655. Synthesis of proteins:

656. Histones:

657. For replication are required:

658. Primase is the enzyme which:

659. During replication:

660. DNA polymerase III:

661. Okazaki fragments:

662. DNA polymerase I:

663. mRNA:

664. hnRNA:

665. Transcription is the process:

666. tRNA:

667. Synthesis of RNA:

668. Introns:

669. Exons:

670. Promoter is:

671. Transcription is the process:
672. During process of transcription:
673. Write which statement about tRNA and mRNA is true:
674. mRNA in eucaryotic cell:
675. 5th end of mRNA contains:
676. Polyadenylate tail:
677. Substrate for synthesis of RNA:
678. tRNA:
679. When proteins are formed in ribosomes:
680. For synthesis of proteins is required:
681. Aminoacyl-t-RNA synthase:
682. Lactose operon:
683. In tryptophane operone:
684. Steroid hormones can influence gene expression by:
685. Promoter is:
686. Reaction of amino acid activation:
687. Process of RNA synthesis:
688. Genetic code:
689. Anticodon:
690. Nucleotide GTP:
691. Compound TTP:
692. Nucleotide AMP:
693. Bond by which nucleotide are connected in RNA chain:
694. Bond by which nucleotide are connected in DNA chain:

REGULATIONS + RECEPTORS + HORMONES

695. Which of statements about hormones are correct:
696. Receptors for hormones:

697. Hydrophobic regulatory compounds can influence cellular processes by:

698. Cytosolic receptors:

699. Which of following receptors belongs to catalytic receptors:

700. Gi-protein:

701. Gi-protein is protein which:

702. Adenylatecyclase:

703. Adenylate cyclase is the enzyme which:

704. Hydrophobic regulatory compounds can influence functions of the cells:

705. Hydrophobic compounds can influence cellular metabolism by:

706. Protein hormones:

707. Phosphodiesterase:

708. G_p-protein:

709. α-subunit of G_s-protein:

710. α-subunit of G_p-protein:

711. α-subunit of G_i-protein:

712. Inositoltrisphosphate (IP_3) is compound which:

713. Receptor for insulin:

714. Phosphodiesterase is enzyme which:

715. Acetylcholine is compound which:

716. Acetylcholine:

717. Acetylcholine is inactivated:

718. Acetylcholine esterase:

719. Nicotinic receptors are receptors which:

720. Muscarinic receptors:

721. M_1 receptors:

722. M_2 receptorrs are receptors which:

723. Which of statements about cholinergic receptors are correct:

724. Activation of M_1 receptors causes:

725. Stimulation of muscarinic receptors in the heart causes:

726. Concentration of IP_3 and Ca^{2+} in the cells is increased after activation of:

727. Adrenaline (epinephrine):

728. The main degradation product of epinephrine is:

729. Acivation of nicotinic receptors:

730. Nerotransmitters of sympathetic nervous system are:

731. Adrenaline (epinephrine):

732. Monoaminooxidase is the enzyme which:

733. Degradation of catecholamines is catalyzed by:

734. Eprinephrine and norepinephrine cause:

735. Adrenergic receptors:

736. Activation of α_1-adrenergic receptors causes:

737. α_1-receptors:

738. α_2-adrenergic receptors:

739. Activation of α_2-receptors causes:

740. Adrenergic receptors:

741. β-adrenergic receptors:

742. Stimulation of β-adrenergic receptors causes:

743. Phospholipase C is enzyme which:

744. Which of following receptors is responsible for inhibition of adenylate cyclase:

745. Concentration of cAMP is increased after stimulation of:

746. Glucocorticoids:

747. Parathyroid hormone:

748. Aldosterone:

749. In adipose tissue:

750. Peptide hormones:

751. Insulin:

752. Glucagon:

753. Hormone receptors:

754. Glucocorticoids:

755. Insulin is hormone which

756. Glucagon is hormone which:

757. Which of the following hormones is required for transport of glucose into skeletal muscle cells:

758. We can say about renin-angiotensin system that:

759. In fatty acid metabolism:

760. Adrenaline (epinephrine):

761. Epinephrine:

762. In the group of steroid hormones can be included:

763. On cytoplasmic receptor binds:

764. The hormone with the structure of a peptide is:

765. Which of the following hormones influence level of calcium in blood:

766. Calcitonin is hormone:

767. Acive form of vitamin D:

768. Role of parathyroid hormone in kidneys is:

769. Calcium:

WATER + MINERALS, ACID-BASE BALANCE

770. Water:

771. Hyperhydration can be caused by:

772. Renin:

773. Angiotensin II:

774. Atrial natriuretic peptide:

775. Angiotensinogen is the compound which:

776. Sodium reabsorption in kidney is increased by:

777. Intracellular fluid:

778. Aldosteron secretion is stimulated by:
779. Which of statement about water in the body are correct::
780. Extracellular fluid:
781. Volume of water:
782. Which of following factors participates in regulation of water and minerals metabolism:
783. Dehydration may occur:
784. What is the meaning of Na^+ in the organism:
785. Vasopresin:
786. Receptor for vasopressin in kidneys:
787. Antiduiretic hormone in kidneys:
788. Main extracellular cation::
789. Sodium is cation which:
790. Which of statements about potassium are correct:
791. Potassium:
792. Hyperkaliemia occurs in:
793. Decreased potassium concentration:
794. Which of following factors participates in regulation of K^+:
795. What is range of pH compatible with life:
796. What is physiologic range of pH:
797. Which of following buffers is the most important in blood:
798. Which of following systems are important in regulation of acid-base balance:
799. HCO3:
800. Phosphate buffer:
801. Phosphate buffer consists of:
802. Respiratory system in regulation of acid base balance:
803. Carboanhydrase in tubular cells:
804. Carboanhydrase is enzyme which:
805. For regeneration of bocarbonate in kidneys is required:

806. Kidneys in regulation of acid base balance:

807. Glutaminase:

808. Protons secreted by tubular cells into urine can be boud to:

809. Glutamine in regulation of acid base balance:

810. In case of metabolic acidosis:

811. Which of following compounds may cause acidosis in diabetics:

812. Respiratory acidosis is compensated by:

813. Respiratory acidosis:

814. Metabolic acidosis is consequence of:

815. Respiratory alkalosis:

DIGESTION + LIVER + TETRAPYRROLS + IRON

816. Digestion of carbohydrates:

817. Alfa-amylase

818. Starch is digested

819. Pancreatic lipase

820. Lipids are absorbed from intestine:

821. Gastric juice:

822. For secretion of HCl is required:

823. Carboanhydrase is the enzyme which:

824. Which of following compounds is not formed by parietal cells:

825. Secretion of hydrochloric acid is regulated by:

826. Bile acids:

827. Pepsin:

828. Aminopeptidases

829. Intrinsic factor is:

830. Glucose is absorbed in the intestine:

831. Trypsinogen:
832. What is role of acetylcholine in regulation of digestion:
833. 1st phase of biotransformation:
834. Microsomal monooxygenase systen in the liver:
835. Cytochome p450 is important for:
836. UDP-glucuronate is required for:
837. Bile acids are conjugated with:
838. 2nd phase of biotransformation proceeds by:
839. Methylation processes:
840. Alcohol dehydrogenase:
841. By ethanol oxidation can be formed:
842. Aldehyde dehydrogenase:
843. Ethanol in the liver can be metabolized by:
844. Microsomal ethanol oxidizing system:
845. Coenzyme for MEOS is:
846. Enzyme typical for metabolism of ethanol in alcoholics is:
847. Bilirubin in the liver is conjugated by:
848. For heme synthesis are required:
849. Enzyme ALA-synthase:
850. Delta amino-levulinate is:
851. Porphobilinogen:
852. Which of the reaction of heme synthesis proceed in cytosol
853. Which of reactions of heme synthesis proceed in mitochondria
854. Hemoglobin is degraded:
855. Heme oxygenase:
856. Which of following enzymes is not required for hemoglobin synthesis
857. Biliverdin is formed:
858. Biliverdin reductase:

859. Bilirubin:

860. Non-conjugated bilirubin is transported:

861. Conjugation of bilirubin:

862. UDP-glucuronyl-transferase is the enzyme which:

863. Conjugated bilirubin is transported:

864. In prehepatic (hemolytic jaundice)

865. Increased concentration of non-conjugated bilirubin in blood:

866. Increased concentration of conjugated bilirubin in blood:

867. Bilirubin is excreted by urine:

868. Premicrosomal hepatic jaundice:

869. Microsomal hepatic jaundice:

870. Neonatal jaundice:

871. Posthepatic jaundice is caused by:

872. In posthepatic (obstructive jaundice):

873. Fe2+ ions:

874. Fe3+ ions

875. Form of iron which is absorbed the best is:

876. Divalent metal transporter is important for:

877. Transferrin:

878. Ferroportin:

879. Ferritin:

880. Iron is stored in the form of:

881. Transferrin receptors:

882. Amount of transferrin receptors increases in:

883. Hephaestin is:

884. Deficit of iron in the cells leads to:

885. Excess of iron in the cells leads to: