

Review

# Brief history of thermodynamic research on microorganisms

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**Abstract:** Pathogen-host interaction (virus-host, bacteria-host and fungi-host) is analyzed from the perspective of biothermodynamics. A mechanistic model of pathogen-host interactions, which was earlier applied to virus-host interactions, was applied for the first time to bacteria-host and fungi-host interactions. Through a mechanistic model suggested in this research, it is possible to explain the phenomenon of tropism of microorganisms to develop infections in certain tissues. Gibbs energy of biosynthesis represents the driving force for growth of bacteria inside host organisms. A growing bacterial colony represents a thermodynamic system, while the host organism is its surroundings. The permissiveness coefficient determines the possibility of growth of bacteria in an appropriate environment (tissue).

**Keywords:** Viruses; Escherichia coli; Klebsiella aerogenes; Candida utilis; Gibbs energy of biosynthesis; Biosynthesis reaction; Enthalpy; Entropy; Pathogen-host interaction

## 1. Introduction

Microorganisms have surrounded us and interacted with plants, animals and humans, causing diseases [Burkovski, 2022; Altermann and Kazmierczak, 2003; Cavalier-Smith, 2006; Schopf, 2006]. Microorganisms have surrounded us for a long time. A closer encounter with microorganisms has started during the early 18th century [van Leeuwenhoek, 1700; Lane, 2015; Payne, 1970].

The first thermodynamic research on living organisms, which represent hosts for microorganisms, has been made by Lavoisier and Laplace [Lavoisier and marquis de Laplace, 1783; Lavoisier and DeLaplace, 1994]. The germ theory of disease has been proved by Pasteur [Bordenave, 2003]. Robert Koch has showed in 1886 that microorganisms (bacteria) cause diseases [Nobel Prize, 2023]. Ivanovsky in 1892 and Beijerinck in 1898 have described and discovered the tobacco mosaic virus [Zaitlin, 1998; Beijerinck, 1898].

By the early 20th century, science has identified subcellular and cellular microorganisms, as causes of diseases in humans, animals and plants. Diseases appear as a consequence of interactions of microorganisms with host organisms. However, chemical and biothermodynamic backgrounds of interactions of microorganisms with multicellular host organisms have not been elucidated in full for the next 100 years, even though assumptions existed for this.

Clausius has founded thermodynamics, with desire to achieve better energy utilization by machines [Clausius, 1867, 1870, 1976]. Clausius has set the philosophical framework and developed the mathematical tools for research on energetics of processes performed in nature. Von Bertalanffy has made thermodynamics closer to biology, through the theory of open systems in biology [von Bertalanffy, 1950, 1971]. Boltzmann was the first to apply the entropy concept in analysis of organisms [Boltzmann, 1974]. This work was extended by Schrödinger, who made the first physical definition of life based on entropy [Schrödinger, 1944].

Morowitz made a great contribution to application of thermodynamics in life sciences, including explanation of biological order and complexity [Morowitz, 1955, 1968,

1995; Morowitz et al., 2000, 1988], as well as the emergence of life [Morowitz, 1992]. Prigogine has developed nonequilibrium thermodynamics, which found many applications in characterization of microorganisms and multicellular organisms [Prigogine, 1977, 1947; Prigogine and Wiamme, 1946; Glansdorff and Prigogine, 1971; Popovic, 2018; Demirel, 2014]. Moreover, nonequilibrium thermodynamics has been used in research on interactions of microorganisms with multicellular organisms and other microorganisms [Prigogine, 1977, 1947; Prigogine and Wiamme, 1946; Glansdorff and Prigogine, 1971; Popovic, 2018; Demirel, 2014]. Von Stockar found that the physical driving force for growth and metabolism of microorganisms is Gibbs energy [von Stockar, 2013a, 2013b; von Stockar and Liu, 1999; von Stockar et al., 2013, 2008, 2006; von Stockar and Marrison, 1993; Patiño et al., 2007]. Thermodynamics has been applied to study various metabolic processes [Greinert et al., 2020a, 2020b, 2020c; Meurer et al., 2017, 2016; Wangler et al., 2018; Niebel et al., 2019; Popovic et al., 2019; Du et al., 2018a, 2018b; Smeaton et al., 2018; Alazmi et al., 2019; Barros, 2021; Nagai et al., 2018]. Hansen et al. [2021, 2018, 2009] and Skene [2015] worked on relating the laws of thermodynamics and theory of evolution. Changes in entropy and information during growth and biosynthesis in organisms has been discussed in [Popovic, 2014a, 2014b].

Virions consist of genetic material (DNA or RNA) that encodes the information for the primary structure of proteins and a capsid that consists of viral structural proteins. Some viruses possess an envelope that consists of lipids. Thus, virions consist of a certain amount of substance, clearly separated from the virus's environment [Popovic, 2022b, 2022c, 2022d]. Thus, viruses represent thermodynamic systems [Popovic, 2022b, 2022c, 2022d]. Viruses perform biological processes of replication, transcription, translation, self-assembly, mutation etc. These processes have their chemical and thermodynamic background. Replication, transcription and translation represent chemical reactions of polymerization of monomers (nucleotides or amino acids) into polymers (nucleic acids or proteins) [Lee et al., 2020; Pinheiro et al., 2008; Dodd et al., 2020; Johansson and Dixon, 2013]. The driving force for reactions of polymerization is Gibbs energy of biosynthesis [Popovic, 2022a; Demirel, 2014]. This is why Gibbs energy determines biosynthesis rate, according to the phenomenological equation [Popovic, 2023c, 2023d; von Stockar, 2013a; Demirel, 2014].

Biosynthesis rate is a chemical term, which is related to the biological term of multiplication rate [Popovic and Minceva, 2020a]. Hypothetically, the thermodynamic driving force has a supreme position over information content. The proof for this is the fact that viroids represent circular RNA molecules that do not contain any information, but are still able to hijack the cellular metabolic machinery and perform replication driven by Gibbs energy of biosynthesis [Popovic, 2022a]. Moreover, parts of RNA of viroids serve as antigens that viroids use to enter host cells [Venkataraman et al., 2021]. Thus, viroids possess no information for biosynthesis of proteins. However, led by Gibbs energy of biosynthesis of nucleic acid, they are able to perform all processes as viruses, except for self-assembly.

From the perspective of biology and medicine, microorganisms represent causes of various diseases that appear as a consequence of interaction with host organisms. From the perspective of chemistry, these interactions represent chemical reactions, driven by Gibbs energy. From the perspective of thermodynamics, they represent processes that change the state of systems, related to changes in thermodynamic properties of enthalpy, entropy, Gibbs energy etc. Microorganisms represent open thermodynamic systems performing growth and accumulation of substances [Popovic, 2019]. State parameters of microorganisms as thermodynamic systems have been calculated [Battley, 1999a, 1992; Şimşek et al., 2021; Popovic, 2019; Popovic and Minceva, 2020a] and determined experimentally [Battley, 1999b, 1998; Battley et al., 1997; Popovic et al., 2021; Wimmer, 2006; Molla et al., 1991].

Mutations represent a process described in biology, during which there is spontaneous replacement of nucleotides with other nucleotides. This changes the information content in the nucleic acid. As a consequence of changed information in the nucleic acid, there

are changes in proteins during the process of translation. Every nucleotide has its empirical formula. Replacement of one or more nucleotides with another (which is the basis of mutation) leads to change in empirical formula of the thermodynamic system (bacteria or virus). Empirical formulas of viruses have been reported in the literature [Degueldre, 2021; Şimşek et al., 2021; Popovic, 2023b, 2023c, 2023d].

Thermodynamics has been applied to study various aspects of SARS-CoV-2. This includes the empirical formula and energy content of SARS-CoV-2 particles [Şimşek et al., 2021; Degueldre, 2021; Popovic, 2022a], energy cost of infection for the host organism [Yilmaz et al., 2020; Özilgen and Yilmaz, 2021], interaction with host cells [Lucia et al., 2021, 2020a; Popovic, 2022a], epidemiology [Lucia et al., 2020b; Kaniadakis et al., 2020], impact on society [Nadi and Özilgen, 2021]. The importance of thermodynamics for research on interactions between SARS-CoV-2 and the human organism, and its application in design of medicines has been discussed [Head et al., 2022].

Mutations that appeared during 3 years on SARS-CoV-2, from the Hu-1 to XBB.1.5 variant, have been reported in the literature [Degueldre, 2021; Şimşek et al., 2021; Popovic, 2023b, 2023c, 2023d, 2022b, 2022c, 2022d, 2022e, 2022f, 2022g, 2022h; Popovic and Popovic, 2022; Popovic and Minceva, 2021a, 2020b]. Chemical and thermodynamic properties of various viruses can be found in the literature [Popovic, 2022i, 2022j, 2022k, 2023e]. Moreover, phage-bacteria interactions have been characterized through the thermodynamic approach and calorimetry [Maskow et al., 2010; Guosheng et al., 2003; Tkhilaishvili et al., 2020a, 2020b, 2018a, 2018b, 2018c; Tkhilaishvili, 2022; Wang et al., 2020a, 2020b; Sigg et al., 2022; Popovic, 2023f].

Until 2019, the empirical formula was known only for the poliovirus [Wimmer, 2006; Molla et al., 1991]. During the last 3 years, the atom counting method has been developed for calculating empirical formulas of microorganisms [Popovic, 2022m]. Empirical formulas of SARS-CoV-2 virus particles have been reported by [Degueldre, 2021; Şimşek et al., 2021; Popovic, 2023b, 2023c, 2023d, 2022c, 2022d, 2022f, 2022h; Popovic and Minceva, 2020b]. Thermodynamic properties of human host tissues have been reported in the literature [Xu et al., 2022; Popovic, 2022i; Popovic and Minceva, 2020c]. In that way, conditions were formed for research on virus-host interactions from the perspective of thermodynamics. Models were developed for hijacking of host cell metabolism [Popovic and Minceva, 2020a] and for thermodynamic consequences of virus mutations [Popovic, 2023b, 2022f]. Thermodynamic background of virus-host interactions is available in the literature [Casasnovas and Springer, 1995; Gale, 2022, 2020, 2019, 2018; Mahmoudabadi et al., 2020; Ceres and Zlotnick, 2002; Katen and Zlotnick, 2009; Tzlil et al., 2004].

Interactions at the membrane (antigen-receptor binding) influences infectivity [Popovic, 2022a]. A virus characterized by a more negative Gibbs energy of binding exhibits greater infectivity [Popovic, 2022a]. A more negative Gibbs energy of biosynthesis of viruses leaves consequences on virus multiplication rate and damage to host cells (pathogenicity) [Popovic, 2022a].

The goal of this paper is to shed more light onto microorganism-host interactions from the perspective of biothermodynamics and to relate the biological phenomena with their thermodynamic driving forces and mechanisms that make them possible.

## 2. Materials and Methods

### 2.1. Data sources

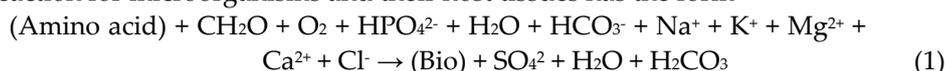
Elemental composition of human tissues, in the form of empirical formulas, was obtained from [Popovic and Minceva, 2020c]. The information on empirical formulas of live matter of different human tissues is given in Table 1. Thermodynamic properties of human tissues were taken from [Popovic and Minceva, 2020c] and are given in Table 2.

Data on elemental composition of microorganism live matter, in the form of empirical formulas, was taken from [Popovic, 2019]. They are shown in Table 3. Thermodynamic

properties of microorganism live matter were taken from [Popovic, 2019] and are given in Table 4.

## 2.2. Biosynthesis reactions

Biosynthesis reactions are macrochemical equations that summarize conversion of nutrients into new live matter [von Stockar, 2013b; Battley, 1999b, 1998; Popovic, 2022a]. The reactants in biosynthesis reactions are nutrients. Every nutrient contributes one or more elements to the formation of new live matter [Riedel et al., 2019]. A general biosynthesis reaction for microorganisms and their host tissues has the form



where (amino acid) represents a mixture of amino acids with the empirical formula  $\text{CH}_{1.798}\text{O}_{0.4831}\text{N}_{0.2247}\text{S}_{0.022472}$ ,  $\text{CH}_2\text{O}$  carbohydrates, and (Bio) represents the empirical formula of live matter [Popovic, 2022a, 2022c, 2022h]. Amino acids represent a source of energy, carbon, nitrogen and sulfur [Popovic, 2022a, 2022c, 2022h].  $\text{CH}_2\text{O}$  are an additional source of carbon and energy [Popovic, 2022a, 2022c, 2022h].  $\text{O}_2$  is the electron acceptor, which takes excess electrons when carbon from nutrients is oxidized into the oxidation state in live matter [Popovic, 2022a, 2022c, 2022h].  $\text{HPO}_4^{2-}$  is the source of phosphorus [Popovic, 2022a, 2022c, 2022h]. The ions  $\text{Na}^+$ ,  $\text{K}^+$ ,  $\text{Mg}^{2+}$ ,  $\text{Ca}^{2+}$  and  $\text{Cl}^-$  are the sources of sodium, potassium, magnesium, calcium and chlorine, respectively [Popovic, 2022a, 2022c, 2022h]. On the product side, the main product is new live matter (Bio). Additional metabolic products are  $\text{SO}_4^{2-}$  which takes excess sulfur that is not incorporate into live matter [Popovic, 2022a, 2022c, 2022h].  $\text{HCO}_3^-$  and  $\text{H}_2\text{CO}_3$  form a bicarbonate buffer that takes excess hydrogen ions produced during biosynthesis, but also take excess carbon that is not incorporated into new live matter [Popovic, 2022a, 2022c, 2022h].

## 2.3. Thermodynamic properties of biosynthesis

Biosynthesis stoichiometry can be used to find thermodynamic properties of biosynthesis, through Hess's law. Biosynthesis reactions are chemical equations and have characteristic thermodynamic properties, which include standard enthalpy of biosynthesis,  $\Delta_{bs}H^0$ , standard entropy of biosynthesis,  $\Delta_{bs}S^0$ , and standard Gibbs energy of biosynthesis,  $\Delta_{bs}G^0$ . These can be found using the Hess's law

$$\Delta_{bs}H^0 = \sum_{products} \nu \Delta_f H^0 - \sum_{reactants} \nu \Delta_f H^0 \quad (2)$$

$$\Delta_{bs}S^0 = \sum_{products} \nu S_m^0 - \sum_{reactants} \nu S_m^0 \quad (3)$$

$$\Delta_{bs}G^0 = \sum_{products} \nu \Delta_f G^0 - \sum_{reactants} \nu \Delta_f G^0 \quad (4)$$

where  $\Delta_f H^0$  is standard enthalpy of formation,  $S_m^0$  standard molar entropy,  $\Delta_f G^0$  standard Gibbs energy of formation, and  $\nu$  stoichiometric coefficient [Atkins and de Paula, 2011, 2014].

**Table 1:** Empirical formulas of live matter of human tissues. The general empirical formula of live matter for human tissues has the form  $C_nH_nHO_nN_nNnP_nP_nS_nS_nNa_nNaK_nKMG_nMGCa_nCaCl_nCl$ . Data taken from [Popovic and Minceva, 2020c].

Name	Live matter composition										
	n <sub>c</sub>	n <sub>H</sub>	n <sub>o</sub>	n <sub>N</sub>	n <sub>P</sub>	n <sub>s</sub>	n <sub>Na</sub>	n <sub>K</sub>	n <sub>Mg</sub>	n <sub>Ca</sub>	n <sub>Cl</sub>
Human body 1 (average)	1	1.7296	0.2591	0.1112	0.0134	0.0030	0.0027	0.0031	0.0000	0.0173	0.0018
Human body 2 (average)	1	1.7131	0.2674	0.0965	0.0189	0.0033	0.0033	0.0027	0.0006	0.0187	0.0020
Adipose tissue 1	1	1.8005	0.1218	0.0216	0.0000	0.0007	0.0010	0.0000	0.0000	0.0000	0.0007
Adipose tissue 2	1	1.8024	0.1124	0.0100	0.0000	0.0006	0.0009	0.0000	0.0000	0.0000	0.0006
Adipose tissue 3	1	1.8083	0.1066	0.0025	0.0000	0.0006	0.0008	0.0000	0.0000	0.0000	0.0005
Adrenal gland	1	1.7391	0.1627	0.0785	0.0014	0.0026	0.0000	0.0011	0.0000	0.0000	0.0024
Aorta	1	1.5313	0.2917	0.2450	0.0106	0.0076	0.0071	0.0021	0.0000	0.0082	0.0000
Blood-erythrocytes	1	1.4984	0.3047	0.2663	0.0020	0.0059	0.0000	0.0049	0.0000	0.0000	0.0036
Blood-plasma	1	1.7117	0.2767	0.2301	0.0000	0.0091	0.0382	0.0000	0.0000	0.0000	0.0331
Blood-whole	1	1.5408	0.2919	0.2572	0.0035	0.0068	0.0047	0.0056	0.0000	0.0000	0.0092
Brain-grey matter	1	1.9096	0.2590	0.1625	0.0122	0.0079	0.0110	0.0097	0.0000	0.0000	0.0107
Brain-white matter	1	1.8361	0.2017	0.1105	0.0080	0.0039	0.0054	0.0048	0.0000	0.0000	0.0052
Connective tissue	1	1.5480	0.3087	0.2568	0.0000	0.0109	0.0151	0.0000	0.0000	0.0000	0.0049
Eye lens	1	1.5143	0.2934	0.2507	0.0020	0.0058	0.0027	0.0000	0.0000	0.0000	0.0017
Gallblader - wall	1	1.6101	0.2757	0.2013	0.0055	0.0079	0.0037	0.0087	0.0000	0.0000	0.0024
Gastrointestinal tract - oesophagus	1	1.7041	0.2256	0.1640	0.0034	0.0033	0.0045	0.0027	0.0000	0.0000	0.0059
Gastrointestinal tract - small intestine (wall)	1	1.6480	0.2310	0.1789	0.0028	0.0054	0.0038	0.0044	0.0000	0.0000	0.0024
Gastrointestinal tract - stomach	1	1.6419	0.2140	0.1519	0.0044	0.0043	0.0030	0.0053	0.0000	0.0000	0.0039
Heart 1	1	1.6861	0.2340	0.1789	0.0056	0.0054	0.0038	0.0066	0.0000	0.0000	0.0049
Heart 2	1	1.6327	0.2689	0.2248	0.0075	0.0073	0.0051	0.0089	0.0000	0.0000	0.0066
Heart 3	1	1.6415	0.2689	0.2268	0.0032	0.0062	0.0043	0.0051	0.0000	0.0000	0.0084
Kidney 1	1	1.6151	0.2452	0.1949	0.0059	0.0057	0.0079	0.0047	0.0000	0.0023	0.0051

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Kidney 2	1	1.6364	0.2581	0.2184	0.0073	0.0071	0.0099	0.0058	0.0000	0.0028	0.0064
Kidney 3	1	1.6891	0.2593	0.1484	0.0075	0.0077	0.0067	0.0059	0.0000	0.0000	0.0043
Liver 1	1	1.6480	0.2904	0.1851	0.0084	0.0081	0.0075	0.0066	0.0000	0.0000	0.0049
Liver 2	1	1.6079	0.3277	0.2246	0.0092	0.0089	0.0083	0.0073	0.0000	0.0000	0.0054
Liver 3	1	1.5863	0.2866	0.2462	0.0077	0.0111	0.0103	0.0061	0.0000	0.0000	0.0101
Lung - parenchyma	1	1.6268	0.2836	0.2532	0.0074	0.0107	0.0100	0.0059	0.0000	0.0000	0.0097
Mammary gland 1	1	1.7549	0.1585	0.0775	0.0012	0.0023	0.0016	0.0000	0.0000	0.0000	0.0010
Mammary gland 2	1	1.6091	0.2502	0.2008	0.0025	0.0047	0.0033	0.0000	0.0000	0.0000	0.0021
Mammary gland 3	1	1.6184	0.2580	0.1805	0.0045	0.0066	0.0031	0.0072	0.0000	0.0000	0.0020
Muscle - skeletal 1	1	1.6390	0.2695	0.2039	0.0054	0.0079	0.0037	0.0086	0.0000	0.0000	0.0024
Muscle - skeletal 2	1	1.5606	0.3106	0.2297	0.0069	0.0100	0.0047	0.0110	0.0000	0.0000	0.0030
Muscle - skeletal 3	1	1.6659	0.2583	0.2213	0.0083	0.0081	0.0112	0.0066	0.0000	0.0000	0.0073
Ovary	1	1.7316	0.1885	0.1116	0.0046	0.0022	0.0062	0.0036	0.0000	0.0000	0.0040
Pancreas	1	1.6663	0.2830	0.2409	0.0044	0.0084	0.0117	0.0069	0.0000	0.0000	0.0000
Prostate	1	1.7527	0.1561	0.0704	0.0009	0.0018	0.0000	0.0015	0.0000	0.0000	0.0016
Skeleton - red marrow	1	1.8135	0.1107	0.0093	0.0000	0.0006	0.0008	0.0000	0.0000	0.0000	0.0005
Skeleton - yellow marrow	1	1.8135	0.1107	0.0093	0.0000	0.0006	0.0008	0.0000	0.0000	0.0000	0.0005
Skin 1	1	1.6631	0.2195	0.1578	0.0016	0.0045	0.0042	0.0012	0.0000	0.0000	0.0041
Skin 2	1	1.6032	0.2376	0.1765	0.0019	0.0037	0.0051	0.0015	0.0000	0.0000	0.0050
Skin 3	1	1.5756	0.2571	0.2008	0.0025	0.0047	0.0066	0.0019	0.0000	0.0000	0.0064
Spleen	1	1.6405	0.2753	0.2428	0.0103	0.0066	0.0046	0.0082	0.0000	0.0000	0.0060
Testis	1	1.6986	0.2342	0.1732	0.0039	0.0076	0.0106	0.0062	0.0000	0.0000	0.0068
Thyroid	1	1.6913	0.3035	0.1729	0.0033	0.0031	0.0088	0.0026	0.0000	0.0000	0.0057
Urinary bladder - wall	1	1.6101	0.2757	0.2013	0.0055	0.0079	0.0037	0.0087	0.0000	0.0000	0.0024

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**Table 2:** Thermodynamic properties of live matter of human tissues. This table shows standard enthalpies of formation,  $\Delta_f H^\circ$ , standard molar entropies,  $S_m^\circ$ , and standard Gibbs energies of formation,  $\Delta_f G^\circ$ . Data taken from [Popovic and Minceva, 2020c].

Name	$\Delta_f H^\circ$ (kJ/C-mol)	$S_m^\circ$ (J/C-mol K)	$\Delta_f G^\circ$ (kJ/C-mol)
Human body 1 (average)	-75.75	29.48	-37.54
Human body 2 (average)	-81.14	29.26	-43.21
Adipose tissue 1	-33.36	25.78	0.06
Adipose tissue 2	-31.32	25.41	1.62
Adipose tissue 3	-30.19	25.24	2.52
Adrenal gland	-40.53	26.90	-5.66
Aorta	-69.48	30.01	-30.58
Blood-erythrocytes	-65.03	30.14	-25.95
Blood-plasma	-75.88	32.48	-33.77
Blood-whole	-66.01	30.45	-26.54
Brain-grey matter	-73.32	32.83	-30.76
Brain-white matter	-55.50	29.61	-17.11
Connective tissue	-67.79	30.78	-27.89
Eye lens	-61.97	29.76	-23.39
Gallblader – wall	-63.06	29.88	-24.33
Gastrointestinal tract – oesophagus	-55.44	29.36	-17.38
Gastrointestinal tract - small intestine (wall)	-53.75	29.00	-16.16
Gastrointestinal tract – stomach	-50.63	28.15	-14.14
Heart 1	-56.99	29.62	-18.59
Heart 2	-63.88	30.56	-24.27
Heart 3	-63.78	30.66	-24.04
Kidney 1	-59.18	29.29	-21.21
Kidney 2	-63.82	30.31	-24.53
Kidney 3	-62.85	29.63	-24.44
Liver 1	-68.92	30.42	-29.49
Liver 2	-76.24	31.39	-35.55
Liver 3	-66.50	30.83	-26.53
Lung – parenchyma	-66.99	31.37	-26.32
Mammary gland 1	-40.07	26.96	-5.12
Mammary gland 2	-55.95	29.21	-18.08
Mammary gland 3	-59.12	29.22	-21.24
Muscle - sceletal 1	-62.58	30.16	-23.50
Muscle - sceletal 2	-69.68	30.52	-30.12
Muscle - sceletal 3	-63.52	30.76	-23.65
Ovary	-48.80	28.04	-12.46
Pancreas	-67.09	31.41	-26.37
Prostate	-39.80	26.78	-5.09

Skeleton - red marrow	-31.29	25.50	1.77
Skeleton - yellow marrow	-31.29	25.50	1.77
Skin 1	-51.46	28.57	-14.43
Skin 2	-54.25	28.55	-17.25
Skin 3	-58.17	29.08	-20.48
Spleen	-65.95	31.09	-25.65
Testis	-58.18	29.78	-19.59
Thyroid	-73.20	30.90	-33.14
Urinary bladder – wall	-63.06	29.88	-24.33

**Table 3:** Empirical formulas of microorganism live matter. The general empirical formula of microorganism live matter is  $C_nH_mO_pN_q$ . Data taken from [Popovic, 2019].

Name	C	H	O	N
Bacteria (general)	1	1.666	0.270	0.200
Escherichia coli	1	1.770	0.490	0.240
Klebsiella aerogenes	1	1.750	0.430	0.220
Candida utilis	1	1.830	0.540	0.100

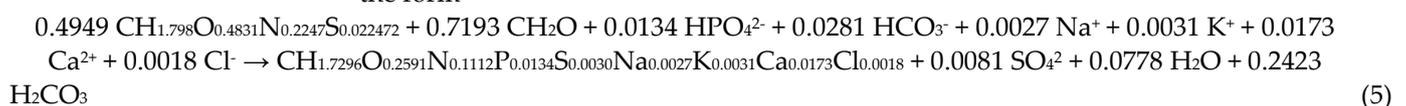
**Table 4:** Thermodynamic properties of formation of microorganism live matter. This table shows standard enthalpies of formation,  $\Delta_f H^0$ , standard molar entropies,  $S_m^0$ , and standard Gibbs energies of formation,  $\Delta_f G^0$ . Data taken from [Popovic, 2019].

Name	$\Delta_f H^0$ (kJ/C-mol)	$S_m^0$ (J/C-mol K)	$\Delta_f G^0$ (kJ/C-mol)
Bacteria (general)	-61.90	30.15	-22.82
Escherichia coli	-114.11	36.36	-66.98
Klebsiella aerogenes	-100.14	34.60	-55.28
Candida utilis	-127.13	35.54	-81.06

### 3. Results

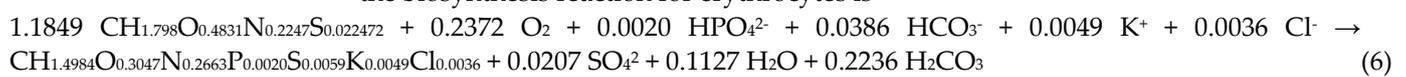
#### 3.1. Biosynthesis reactions and thermodynamic properties of human tissues

Based on empirical formulas from Table 1, biosynthesis reactions were formulated for different human tissues. In a biosynthesis reaction every nutrient contributes one or more elements to the formation of new live matter. The biosynthesis reactions for human tissues are given in Table 5. The biosynthesis reaction for the entire human organism has the form



where the empirical formula  $\text{CH}_{1.798}\text{O}_{0.4831}\text{N}_{0.2247}\text{S}_{0.022472}$  represents a mixture of amino acids [Popovic, 2022a],  $\text{CH}_2\text{O}$  carbohydrates [Popovic, 2022a], while  $\text{CH}_{1.7296}\text{O}_{0.2591}\text{N}_{0.1112}\text{P}_{0.0134}\text{S}_{0.0030}\text{Na}_{0.0027}\text{K}_{0.0031}\text{Ca}_{0.0173}\text{Cl}_{0.0018}$  is the empirical formula of the human organism from Table 1.

Biosynthesis reactions have also been formulated for various tissues. For example, the biosynthesis reaction for erythrocytes is



where  $\text{CH}_{1.4984}\text{O}_{0.3047}\text{N}_{0.2663}\text{P}_{0.0020}\text{S}_{0.0059}\text{K}_{0.0049}\text{Cl}_{0.0036}$  is the empirical formula of erythrocytes (Table 1).

**Table 5:** Biosynthesis reactions of human tissues. The general biosynthesis reaction has the form: (Amino acid) + CH<sub>2</sub>O + O<sub>2</sub> + HPO<sub>4</sub><sup>2-</sup> + H<sub>2</sub>O + HCO<sub>3</sub><sup>-</sup> + Na<sup>+</sup> + K<sup>+</sup> + Mg<sup>2+</sup> + Ca<sup>2+</sup> + Cl<sup>-</sup> → 1  
(Bio) + SO<sub>4</sub><sup>2-</sup> + H<sub>2</sub>O + H<sub>2</sub>CO<sub>3</sub>, where (Amino acids) represents a mixture of amino acids with the empirical formula CH<sub>1.798</sub>O<sub>0.4831</sub>N<sub>0.2247</sub>S<sub>0.022472</sub> and (Bio) represents the empirical formula 2  
of live matter from Table 1. 3

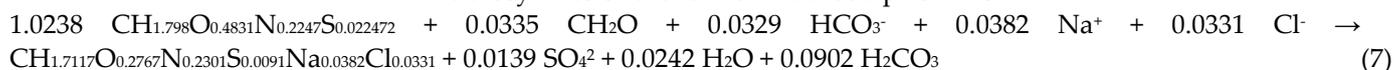
Name	Reactants											→	Products			
	Amino acid	CH <sub>2</sub> O	O <sub>2</sub>	HPO <sub>4</sub> <sup>2-</sup>	H <sub>2</sub> O	HCO <sub>3</sub> <sup>-</sup>	Na <sup>+</sup>	K <sup>+</sup>	Mg <sup>2+</sup>	Ca <sup>2+</sup>	Cl <sup>-</sup>		Bio	SO <sub>4</sub> <sup>2-</sup>	H <sub>2</sub> O	H <sub>2</sub> CO <sub>3</sub>
Human body 1 (average)	0.4949	0.7193	0.0000	0.0134	0.0000	0.0281	0.0027	0.0031	0.0000	0.0173	0.0018	→	1	0.0081	0.0778	0.2423
Human body 2 (average)	0.4293	0.8007	0.0000	0.0189	0.0000	0.0175	0.0033	0.0027	0.0006	0.0187	0.0020	→	1	0.0064	0.1008	0.2475
Adipose tissue 1	0.0960	1.2713	0.0000	0.0000	0.0000	0.0032	0.0010	0.0000	0.0000	0.0000	0.0007	→	1	0.0014	0.0884	0.3704
Adipose tissue 2	0.0447	1.3400	0.0000	0.0000	0.0000	0.0011	0.0009	0.0000	0.0000	0.0000	0.0006	→	1	0.0004	0.0937	0.3857
Adipose tissue 3	0.0245	1.3715	0.0000	0.0000	0.0000	0.0092	0.0008	0.0000	0.0000	0.0000	0.0005	→	1	0.0000	0.0888	0.4052
Adrenal gland	0.3493	0.9250	0.0000	0.0014	0.0000	0.0064	0.0000	0.0011	0.0000	0.0000	0.0024	→	1	0.0052	0.0926	0.2808
Aorta	1.0902	0.0000	0.0856	0.0106	0.0000	0.0381	0.0071	0.0021	0.0000	0.0082	0.0000	→	1	0.0169	0.1103	0.1284
Blood-erythrocytes	1.1849	0.0000	0.2372	0.0020	0.0000	0.0386	0.0000	0.0049	0.0000	0.0000	0.0036	→	1	0.0207	0.1127	0.2236
Blood-plasma	1.0238	0.0335	0.0000	0.0000	0.0000	0.0329	0.0382	0.0000	0.0000	0.0000	0.0331	→	1	0.0139	0.0242	0.0902
Blood-whole	1.1448	0.0000	0.1672	0.0035	0.0000	0.0319	0.0047	0.0056	0.0000	0.0000	0.0092	→	1	0.0189	0.0997	0.1766
Brain-grey matter	0.7230	0.4799	0.0000	0.0122	0.0229	0.0022	0.0110	0.0097	0.0000	0.0000	0.0107	→	1	0.0084	0.0000	0.2051
Brain-white matter	0.4917	0.7647	0.0000	0.0080	0.0000	0.0033	0.0054	0.0048	0.0000	0.0000	0.0052	→	1	0.0072	0.0346	0.2597
Connective tissue	1.1429	0.0000	0.1675	0.0000	0.0000	0.0399	0.0151	0.0000	0.0000	0.0000	0.0049	→	1	0.0148	0.0905	0.1828
Eye lens	1.1154	0.0000	0.1416	0.0020	0.0000	0.0356	0.0027	0.0000	0.0000	0.0000	0.0017	→	1	0.0193	0.1133	0.1510
Gallblader - wall	0.8957	0.1737	0.0000	0.0055	0.0000	0.0235	0.0037	0.0087	0.0000	0.0000	0.0024	→	1	0.0122	0.0954	0.0929
Gastrointestinal tract - oesophagus	0.7300	0.4163	0.0000	0.0034	0.0000	0.0209	0.0045	0.0027	0.0000	0.0000	0.0059	→	1	0.0131	0.0654	0.1672
Gastrointestinal tract - small intestine (wall)	0.7961	0.3211	0.0000	0.0028	0.0000	0.0252	0.0038	0.0044	0.0000	0.0000	0.0024	→	1	0.0125	0.0843	0.1423
Gastrointestinal tract - stomach	0.6760	0.4773	0.0000	0.0044	0.0000	0.0173	0.0030	0.0053	0.0000	0.0000	0.0039	→	1	0.0109	0.1042	0.1706
Heart 1	0.7961	0.3325	0.0000	0.0056	0.0000	0.0194	0.0038	0.0066	0.0000	0.0000	0.0049	→	1	0.0125	0.0695	0.1480

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Heart 2	1.0003	0.0540	0.0000	0.0075	0.0000	0.0228	0.0051	0.0089	0.0000	0.0000	0.0066	→	1	0.0152	0.0749	0.0771
Heart 3	1.0092	0.0366	0.0000	0.0032	0.0000	0.0276	0.0043	0.0051	0.0000	0.0000	0.0084	→	1	0.0165	0.0650	0.0733
Kidney 1	0.8672	0.2233	0.0000	0.0059	0.0000	0.0279	0.0079	0.0047	0.0000	0.0023	0.0051	→	1	0.0138	0.0938	0.1184
Kidney 2	0.9720	0.0968	0.0000	0.0073	0.0000	0.0298	0.0099	0.0058	0.0000	0.0028	0.0064	→	1	0.0148	0.0722	0.0986
Kidney 3	0.6604	0.4955	0.0000	0.0075	0.0000	0.0077	0.0067	0.0059	0.0000	0.0000	0.0043	→	1	0.0072	0.0885	0.1636
Liver 1	0.8236	0.2692	0.0000	0.0084	0.0000	0.0134	0.0075	0.0066	0.0000	0.0000	0.0049	→	1	0.0104	0.0902	0.1061
Liver 2	0.9994	0.0248	0.0000	0.0092	0.0000	0.0188	0.0083	0.0073	0.0000	0.0000	0.0054	→	1	0.0135	0.0902	0.0430
Liver 3	1.0956	0.0000	0.0791	0.0077	0.0000	0.0180	0.0103	0.0061	0.0000	0.0000	0.0101	→	1	0.0135	0.0909	0.1136
Lung - parenchyma	1.1266	0.0000	0.1070	0.0074	0.0000	0.0206	0.0100	0.0059	0.0000	0.0000	0.0097	→	1	0.0146	0.0661	0.1472
Mammary gland 1	0.3448	0.9363	0.0000	0.0012	0.0000	0.0092	0.0016	0.0000	0.0000	0.0000	0.0010	→	1	0.0055	0.0837	0.2903
Mammary gland 2	0.8936	0.1782	0.0000	0.0025	0.0000	0.0269	0.0033	0.0000	0.0000	0.0000	0.0021	→	1	0.0153	0.0929	0.0987
Mammary gland 3	0.8033	0.2958	0.0000	0.0045	0.0000	0.0222	0.0031	0.0072	0.0000	0.0000	0.0020	→	1	0.0115	0.1008	0.1213
Muscle - skeletal 1	0.9073	0.1696	0.0000	0.0054	0.0000	0.0241	0.0037	0.0086	0.0000	0.0000	0.0024	→	1	0.0125	0.0794	0.1010
Muscle - skeletal 2	1.0221	0.0000	0.0073	0.0069	0.0000	0.0246	0.0047	0.0110	0.0000	0.0000	0.0030	→	1	0.0129	0.1075	0.0467
Muscle - skeletal 3	0.9847	0.0898	0.0000	0.0083	0.0000	0.0220	0.0112	0.0066	0.0000	0.0000	0.0073	→	1	0.0141	0.0606	0.0966
Ovary	0.4967	0.7324	0.0000	0.0046	0.0000	0.0145	0.0062	0.0036	0.0000	0.0000	0.0040	→	1	0.0089	0.0790	0.2437
Pancreas	1.0719	0.0000	0.0330	0.0044	0.0000	0.0413	0.0117	0.0069	0.0000	0.0000	0.0000	→	1	0.0157	0.0400	0.1131
Prostate	0.3134	0.9749	0.0000	0.0009	0.0000	0.0084	0.0000	0.0015	0.0000	0.0000	0.0016	→	1	0.0052	0.0882	0.2967
Skeleton - red marrow	0.0415	1.3475	0.0000	0.0000	0.0000	0.0010	0.0008	0.0000	0.0000	0.0000	0.0005	→	1	0.0004	0.0886	0.3899
Skeleton - yellow marrow	0.0415	1.3475	0.0000	0.0000	0.0000	0.0010	0.0008	0.0000	0.0000	0.0000	0.0005	→	1	0.0004	0.0886	0.3899
Skin 1	0.7021	0.4433	0.0000	0.0016	0.0000	0.0208	0.0042	0.0012	0.0000	0.0000	0.0041	→	1	0.0113	0.0878	0.1662
Skin 2	0.7856	0.3149	0.0000	0.0019	0.0000	0.0258	0.0051	0.0015	0.0000	0.0000	0.0050	→	1	0.0140	0.1070	0.1264
Skin 3	0.8936	0.1666	0.0000	0.0025	0.0000	0.0279	0.0066	0.0019	0.0000	0.0000	0.0064	→	1	0.0153	0.1091	0.0881
Spleen	1.0806	0.0000	0.0447	0.0103	0.0000	0.0215	0.0046	0.0082	0.0000	0.0000	0.0060	→	1	0.0177	0.0649	0.1021
Testis	0.7709	0.3692	0.0000	0.0039	0.0000	0.0216	0.0106	0.0062	0.0000	0.0000	0.0068	→	1	0.0098	0.0639	0.1616
Thyroid	0.7696	0.3258	0.0000	0.0033	0.0000	0.0274	0.0088	0.0026	0.0000	0.0000	0.0057	→	1	0.0141	0.0644	0.1228
Urinary bladder - wall	0.8957	0.1737	0.0000	0.0055	0.0000	0.0235	0.0037	0.0087	0.0000	0.0000	0.0024	→	1	0.0122	0.0954	0.0929

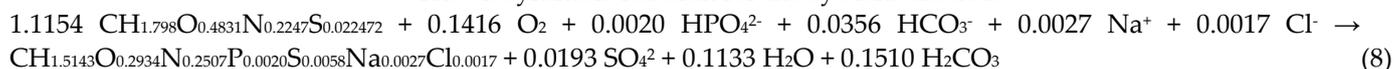
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The biosynthesis reaction for the blood plasma is



where  $\text{CH}_{1.7117}\text{O}_{0.2767}\text{N}_{0.2301}\text{S}_{0.0091}\text{Na}_{0.0382}\text{Cl}_{0.0331}$  is the empirical formula of the blood plasma (Table 1).

The biosynthesis reaction for the eye lens tissue is



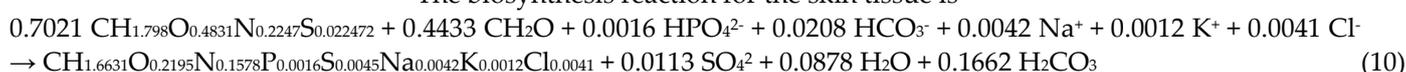
where  $\text{CH}_{1.5143}\text{O}_{0.2934}\text{N}_{0.2507}\text{P}_{0.0020}\text{S}_{0.0058}\text{Na}_{0.0027}\text{Cl}_{0.0017}$  is the empirical formula of the eye lens tissue (Table 1).

The biosynthesis reaction of the small intestine tissue, constituting a part of the gastrointestinal tract, is



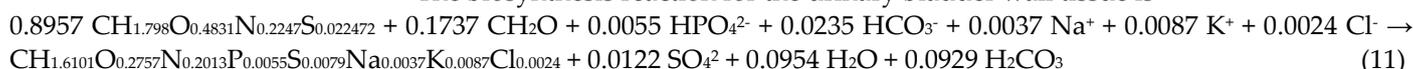
where  $\text{CH}_{1.6480}\text{O}_{0.2310}\text{N}_{0.1789}\text{P}_{0.0028}\text{S}_{0.0054}\text{Na}_{0.0038}\text{K}_{0.0044}\text{Cl}_{0.0024}$  is the empirical formula of the small intestine tissue (Table 1).

The biosynthesis reaction for the skin tissue is



where  $\text{CH}_{1.6631}\text{O}_{0.2195}\text{N}_{0.1578}\text{P}_{0.0016}\text{S}_{0.0045}\text{Na}_{0.0042}\text{K}_{0.0012}\text{Cl}_{0.0041}$  is the empirical formula of the skin tissue (Table 1).

The biosynthesis reaction for the urinary bladder wall tissue is



where  $\text{CH}_{1.6101}\text{O}_{0.2757}\text{N}_{0.2013}\text{P}_{0.0055}\text{S}_{0.0079}\text{Na}_{0.0037}\text{K}_{0.0087}\text{Cl}_{0.0024}$  is the empirical formula of the urinary bladder wall tissue (Table 1).

**Table 6:** Thermodynamic properties of biosynthesis of human tissues. This table shows standard enthalpies of biosynthesis,  $\Delta_{bs}H^\circ$ , standard entropies of biosynthesis,  $\Delta_{bs}S^\circ$ , and standard Gibbs energies of biosynthesis,  $\Delta_{bs}G^\circ$ .

Name	$\Delta_{bs}H^\circ$ (kJ/C-mol)	$\Delta_{bs}S^\circ$ (J/C-mol K)	$\Delta_{bs}G^\circ$ (kJ/C-mol)
Human body 1 (average)	-21.59	34.71	-31.37
Human body 2 (average)	-22.80	37.61	-33.44
Adipose tissue 1	-37.48	52.61	-51.88
Adipose tissue 2	-39.21	55.10	-54.28
Adipose tissue 3	-39.88	57.11	-55.78
Adrenal gland	-27.97	39.84	-38.93
Aorta	-42.41	1.08	-42.85
Blood-erythrocytes	-113.09	-15.73	-108.40
Blood-plasma	0.72	5.75	-0.96
Blood-whole	-79.52	-9.41	-76.74
Brain-grey matter	-13.05	23.99	-19.86
Brain-white matter	-22.50	34.45	-32.09
Connective tissue	-79.55	-9.14	-76.81
Eye lens	-69.40	-6.84	-67.37
Gallbladder – wall	-6.45	12.02	-9.93
Gastrointestinal tract – oesophagus	-14.30	21.42	-20.30

Gastrointestinal tract - small intestine (wall)	-11.68	18.34	-16.85
Gastrointestinal tract – stomach	-15.27	23.59	-21.87
Heart 1	-11.32	18.73	-16.64
Heart 2	-3.20	8.47	-5.76
Heart 3	-3.67	7.41	-5.88
Kidney 1	-8.30	15.13	-12.65
Kidney 2	-4.60	11.13	-7.91
Kidney 3	-14.14	23.06	-20.60
Liver 1	-8.04	14.62	-12.23
Liver 2	-1.40	5.41	-3.10
Liver 3	-37.09	-0.90	-36.91
Lung – parenchyma	-50.51	-2.80	-49.76
Mammary gland 1	-28.64	40.69	-39.84
Mammary gland 2	-8.61	12.87	-12.30
Mammary gland 3	-10.08	16.42	-14.73
Muscle - skeletal 1	-6.60	12.37	-10.18
Muscle - skeletal 2	-4.30	4.46	-5.71
Muscle - skeletal 3	-3.87	10.51	-7.01
Ovary	-22.26	33.11	-31.44
Pancreas	-18.09	4.71	-19.54
Prostate	-29.53	41.76	-41.01
Skeleton - red marrow	-39.47	55.48	-54.65
Skeleton - yellow marrow	-39.47	55.48	-54.65
Skin 1	-15.06	22.33	-21.29
Skin 2	-11.57	17.13	-16.38
Skin 3	-7.23	11.57	-10.54
Spleen	-22.74	3.10	-23.78
Testis	-11.39	19.96	-17.01
Thyroid	-11.19	15.52	-15.53
Urinary bladder – wall	-6.45	12.02	-9.93

The biosynthesis reactions were combined with thermodynamic properties of live matter of human tissues, from Table 2. This gave standard thermodynamic properties of biosynthesis of human tissues, which are given in Table 6. They include standard enthalpy of biosynthesis,  $\Delta_{bs}H^0$ , standard entropy of biosynthesis,  $\Delta_{bs}S^0$ , and standard Gibbs energy of biosynthesis,  $\Delta_{bs}G^0$ . For example, for the entire human organism, standard enthalpy of biosynthesis is -21.59 kJ/C-mol, standard entropy of biosynthesis is 34.71 J/C-mol K and standard Gibbs energy of biosynthesis is -31.37 kJ/C-mol. For erythrocytes, standard enthalpy of biosynthesis is -113.09 kJ/C-mol, standard entropy of biosynthesis is -15.73 J/C-mol K and standard Gibbs energy of biosynthesis is -108.40 kJ/C-mol. For blood plasma, standard enthalpy of biosynthesis is 0.72 kJ/C-mol, standard entropy of biosynthesis is 5.75 J/C-mol K and standard Gibbs energy of biosynthesis is -0.96 kJ/C-mol. For the eye lens tissue, standard enthalpy of biosynthesis is -69.40 kJ/C-mol, standard entropy of biosynthesis is -6.84 J/C-mol K and standard Gibbs energy of biosynthesis is -67.37 kJ/C-mol. For the small intestine wall tissue, standard enthalpy of biosynthesis is -11.68 kJ/C-mol,

standard entropy of biosynthesis is 18.34 J/C-mol K and standard Gibbs energy of biosynthesis is -16.85 kJ/C-mol. For the skin tissue, standard enthalpy of biosynthesis is -15.06 kJ/C-mol, standard entropy of biosynthesis is 22.33 J/C-mol K and standard Gibbs energy of biosynthesis is -21.29 kJ/C-mol. For the urinary bladder wall tissue, standard enthalpy of biosynthesis is -6.45 kJ/C-mol, standard entropy of biosynthesis is 12.02 J/C-mol K and standard Gibbs energy of biosynthesis is -9.93 kJ/C-mol.

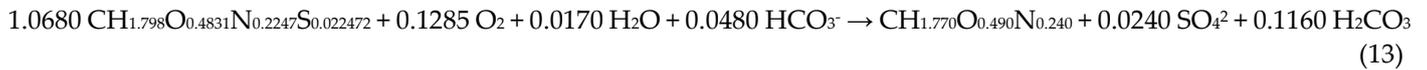
### 3.2. Biosynthesis reactions and thermodynamic properties of microorganisms

Based on empirical formulas in Table 3, biosynthesis reactions were formulated for microorganism live matter, which are presented in Table 7. For live matter of bacteria in general, biosynthesis of new live matter can be described through the macrochemical equation



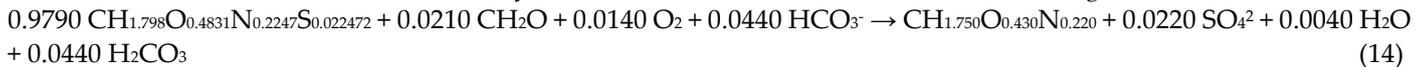
where the empirical formula  $\text{CH}_{1.798}\text{O}_{0.4831}\text{N}_{0.2247}\text{S}_{0.022472}$  represents a mixture of amino acids [Popovic, 2022a],  $\text{CH}_2\text{O}$  carbohydrates [Popovic, 2022a], and  $\text{CH}_{1.666}\text{O}_{0.270}\text{N}_{0.200}$  represents the empirical formula of bacterial live matter (Table 3).

Production of new live matter of *Escherichia coli* can be described by the biosynthesis reaction



where  $\text{CH}_{1.770}\text{O}_{0.490}\text{N}_{0.240}$  is the empirical formula of *E. coli* live matter (Table 3).

The biosynthesis reaction for the bacterium *Klebsiella aerogenes* is



where  $\text{CH}_{1.750}\text{O}_{0.430}\text{N}_{0.220}$  is the empirical formula of the *K. aerogenes* live matter (Table 3).

The biosynthesis reaction for the fungus *Candida utilis* is



where  $\text{CH}_{1.830}\text{O}_{0.540}\text{N}_{0.100}$  is the empirical formula of live matter of *C. utilis* (Table 3).

**Table 7:** Biosynthesis stoichiometry of microorganisms. The general biosynthesis reaction for microorganism live matter has the form (Amino acid) +  $\text{CH}_2\text{O} + \text{O}_2 + \text{H}_2\text{O} + \text{HCO}_3^- \rightarrow (\text{Bio}) + \text{SO}_4^{2-} + \text{H}_2\text{O} + \text{H}_2\text{CO}_3$ , where (Amino acids) represents a mixture of amino acids with the empirical formula  $\text{CH}_{1.798}\text{O}_{0.4831}\text{N}_{0.2247}\text{S}_{0.022472}$  and (Bio) represents the empirical formula of live matter from Table 3.

Name	Reactants					→	Products			
	Amino acid	CH <sub>2</sub> O	O <sub>2</sub>	H <sub>2</sub> O	HCO <sub>3</sub> <sup>-</sup>		Bio	SO <sub>4</sub> <sup>2-</sup>	H <sub>2</sub> O	H <sub>2</sub> CO <sub>3</sub>
Bacteria (general)	0.8900	0.1765	0.0000	0.0000	0.0400	→	1	0.0200	0.0570	0.1065
Escherichia coli	1.0680	0.0000	0.1285	0.0170	0.0480	→	1	0.0240	0.0000	0.1160
Klebsiella aerogenes	0.9790	0.0210	0.0140	0.0000	0.0440	→	1	0.0220	0.0040	0.0440
Candida utilis	0.4450	0.6350	0.0000	0.0000	0.0200	→	1	0.0100	0.0300	0.1000

The microbial biosynthesis reactions were combined with thermodynamic properties of microbial live matter from Table 4. This gave thermodynamic properties of biosynthesis of microorganisms, which are given in Table 8. They include standard enthalpy of biosynthesis,  $\Delta_{bs}H^0$ , standard entropy of biosynthesis,  $\Delta_{bs}S^0$ , and standard Gibbs energy of biosynthesis,  $\Delta_{bs}G^0$ . For bacteria in general, standard enthalpy of biosynthesis is -10.35 kJ/C-mol, standard entropy of biosynthesis is 12.19 J/C-mol K and standard Gibbs energy of biosynthesis is -13.81 kJ/C-mol. For *E. coli*, standard enthalpy of biosynthesis is -64.34 kJ/C-mol, standard entropy of biosynthesis is -12.25 J/C-mol K and standard Gibbs energy of biosynthesis is -60.68 kJ/C-mol. For *Klebsiella aerogenes*, standard enthalpy of biosynthesis is -12.06 kJ/C-mol, standard entropy of biosynthesis is 0.28 J/C-mol K and standard Gibbs

energy of biosynthesis is -12.13 kJ/C-mol. For *Candida utilis*, standard enthalpy of biosynthesis is -18.94 kJ/C-mol, standard entropy of biosynthesis is 16.11 J/C-mol K and standard Gibbs energy of biosynthesis is -23.11 kJ/C-mol.

**Table 8:** Thermodynamic properties of biosynthesis of microorganisms. This table shows standard enthalpies of biosynthesis,  $\Delta_{bs}H^0$ , standard entropies of biosynthesis,  $\Delta_{bs}S^0$ , and standard Gibbs energies of biosynthesis,  $\Delta_{bs}G^0$ .

Name	$\Delta_{bs}H^0$ (kJ/C-mol)	$\Delta_{bs}S^0$ (J/C-mol K)	$\Delta_{bs}G^0$ (kJ/C-mol)
Bacteria (general)	-10.35	12.19	-13.81
Escherichia coli	-64.34	-12.25	-60.68
Klebsiella aerogenes	-12.06	0.28	-12.13
Candida utilis	-18.94	16.11	-23.11

#### 4. Discussion

Microbial population number of cellular [Casadevall and Pirofski, 2000] and subcellular [Domingo, 2020] microorganisms are extremely large, compared with those of their host species. Host organisms are surrounded with various virus species, which exhibit great specificity. Viruses can infect host organisms, but can also exist passively in the environment and wait for a new host.

Specificity of viruses is exhibited on antigen-receptor interactions that are performed on the cell membrane. The *conditio sine qua non* for successful virus-host interaction is presence of an appropriate antigen on the virus surface and an appropriate receptor on the host cell surface [Riedel et al., 2019]. Various viruses use various receptors for binding and entrance into the host cell [Maginnis, 2018]. For example, all SARS-CoV-2 variants use the ACE2 receptor [Shirbhate et al., 2021; Gawish et al., 2022]. Antigen-receptor interactions proceed through a mechanism similar to protein-ligand interactions [Du et al., 2016; Popovic and Popovic, 2022]. The driving force for antigen-receptor interactions is Gibbs energy of binding [Gale, 2022, 2020, 2019, 2018; Casanovas and Springer, 1995; Popovic and Popovic, 2022; Popovic, 2022b]. The antigen-receptor binding reaction is competitive. If two virus species or variants use the same receptors, then they compete [Popovic and Minceva, 2021a]. For example, several dozen variants of SARS-CoV-2 use the same ACE2 receptor. During the COVID-19 pandemic, the phenomenon was noticed that multiple SARS-CoV-2 variants appeared in the same population at the same time in the same place. Competition between the variants for “soil” occurs. The result of competition was the suppression of the old variants with newer ones, which exhibited greater infectivity [Eales et al, 2022]. All variants of SARS-CoV-2 have been chemically and thermodynamically characterized [Popovic, 2023b, 2023c, 2023d, 2022b, 2022c, 2022d, 2022e, 2022f, 2022g, 2022h; Popovic and Popovic, 2022; Popovic and Minceva, 2021a, 2020b; Şimşek et al., 2021; Deguelde, 2021].

During the time evolution of the virus, through acquisition of mutations, changes occurred in the elemental composition, information content in the genome and spike glycoprotein, towards formation of a greater binding affinity for the receptor [Makowski et al, 2022]. An increase in binding affinity resulted in a greater antigen-receptor binding rate. This gave an advantage to the mutated variants to spread within the population. Some of the new variants caused pandemic waves. Some of the mutated variants have exhibited the ability of immune evasion [Gao et al., 2021; Cao et al., 2022a; Barton et al., 2021]. This phenomenon has exhibited an additional reason for the advantage of the new variants during the competition with older ones.

A virus represents an obligate intracellular parasite, which hijacks host cell metabolism [Summers, 2009; Thaker et al., 2019; Popovic and Minceva, 2020a; Proal and VanElzakker, 2021; Sumbria et al., 2021]. A virus performs biological processes of replication, transcription, translation and self-assembly. Replication, transcription and translation

represent chemical processes of polymerization of nucleotides and amino acids into nucleic acids, and structural and functional proteins of the virus [Lee et al., 2020; Pinheiro et al., 2008; Dodd et al., 2020; Johansson and Dixon, 2013]. The driving force for replication, transcription and translation is Gibbs energy of biosynthesis [Demirel, 2014; Balmer, 2010; Popovic, 2022a]. Gibbs energy of biosynthesis for various viruses is available in the literature [Popovic, 2023b, 2023c, 2023d, 2022c, 2022d, 2022f, 2022h; Popovic and Minceva, 2021a, 2020b]. According to the phenomenological equation, biosynthesis rate depends on Gibbs energy of biosynthesis [Demirel, 2014; Balmer, 2010; von Stockar, 2013a; Popovic, 2022a].

Gibbs energy of biosynthesis is, according to the phenomenological equations, directly proportional to the rate of biosynthesis of building blocks [Popovic, 2023a, 2023b, 2023c, 2022h]. The newly synthesized virions lead to damage of host cells. Greater damage to host cells indicates greater pathogenicity. Through analysis of evolution of SARS-CoV-2 from Hu-1 to the new BA.5.2, BF.7 and XBB.1.5 variants, it was shown that Gibbs energy of biosynthesis of Hu-1 is the most negative, while the variants that appeared through various mutations exhibited a less negative Gibbs energy of biosynthesis than that of Hu-1. Thus, we can conclude that SARS-CoV-2 has evolved towards an increase in infectivity, accompanied by a slight decrease or maintenance of constant pathogenicity.

A virus consists of a nucleic acid, a capsid and sometimes an envelope. Thus, a virus is clearly bordered from its surroundings [Popovic and Minceva, 2020a]. A virion exchanges substances with its environment and performs metabolic processes by using the host cell's machinery, in processes of replication, transcription and translation, accumulating matter during the multiplication process. Thus, the environment of the virus is the host cell, while the wider environment is the host organism. However, the virocell concept has been suggested [Forterre, 2011, 2013; Forterre and Krupovic, 2012; Howard-Varona et al., 2020; Rosenwasser et al., 2016]. According to the virocell concept, a virus and its host cell represent a system, while the surrounding is the tissue. This concept would require formulation of new mechanistic models and defining of state parameters of the thermodynamic system – virocell. Such a model seems to be less accurate, since the obtained Gibbs energy as the driving force for multiplication would not reflect only the multiplication of viruses, but also include biosynthesis of building blocks of the host cell. The building blocks of the host cell have their own Gibbs energy of biosynthesis, just like viruses have their own. Reactions of biosynthesis of viruses and those of host cell components are competitive. Due to a difference in Gibbs energies of biosynthesis of viruses and host cells, it is possible to explain the phenomenon of hijacking of host cell machinery. If we accept the virocell concept, then we would not be able to use the mechanistic model for hijacking of cell metabolic machinery.

It is obvious that mechanistic models of virus-host interactions on the membrane (antigen-receptor binding) and virus-host interactions in the cytoplasm can significantly contribute to better understanding of virus-host interactions and explain the phenomena like infectivity, pathogenicity, interference and coinfection [Gale, 2022, 2020, 2019, 2018; Lucia et al., 2021, 2020a, 2020b; Özilgen and Yilmaz, 2021, Yilmaz et al., 2020; Mahmoudabadi et al., 2017; Popovic, 2022a; Popovic and Minceva, 2021a].

Cellular microorganisms (bacteria, archaea, yeast) represent open thermodynamic systems with the property of growth [Popovic, 2019]. The driving force for growth of cellular microorganisms is Gibbs energy of biosynthesis [von Stockar, 2013a, 2013b]. Thermodynamic system can be a single microbial cell or microbial colony that appears due to multiplication of microorganisms through accumulation of matter taken from the environment [von Stockar, 2013a, 2013b]. The environment for a growing microbial colony, as a thermodynamic system, is the growth medium or tissue on which the microorganism is a parasite. Elemental composition and thermodynamic properties of live matter (enthalpy, entropy, Gibbs energy) have been reported in the literature for over 35 microorganism species [Popovic, 2019; Popovic et al., 2021; Calabrese et al., 2021]. These data have enabled a better understanding of microorganism-host interactions, through development of

mechanistic models. Having in mind the universality of nature and the fact that similar models apply to viroids [Popovic, 2023a], viruses [Popovic, 2022a] and bacteria [Popovic, 2019; Calabrese et al., 2021], it can be expected that development of mechanistic models with the application of thermodynamic properties of biosynthesis, it is possible to shed more light on other parasite-host interactions.

The biothermodynamic background of virus-host cell interaction is available in the literature [Popovic and Minceva, 2020a]. Let us try to analyze the biothermodynamic background of bacteria-host tissue interaction in this paper. In Tables 1-4, data are given on chemical and thermodynamic properties of biosynthesis for human tissues. In Tables 5-8, chemical and thermodynamic properties are given for biosynthesis for microorganisms that interact with humans: bacteria in general, *Escherichia coli*, *Klebsiella aerogenes* and *Candida utilis*. The biothermodynamic mechanisms of pathogen-host interactions are universal and are based on fundamental laws of thermodynamics and kinetics. Biosynthesis reactions for host cell components and pathogens are competitive. The rate at which these reactions occur depends on Gibbs energy of biosynthesis, for both subcellular and cellular parasites. Both subcellular and cellular parasites represent thermodynamic systems, clearly separated from the environment, which exchange and accumulate substances taken from the environment. In that way, they achieve growth of the microorganism population.

To describe the biothermodynamic background of interactions between bacteria and human host tissues, we must compare Gibbs energies of biosynthesis of bacteria to Gibbs energies of biosynthesis of host cell building blocks. In that way, we will calculate the permissiveness coefficients for multiplication of bacteria in certain tissues. Gibbs energy of biosynthesis for the entire human organism is around -31.37 kJ/C-mol. Gibbs energy of biosynthesis of *Escherichia coli* is -60.68 kJ/C-mol. Since the rate of biosynthesis of building blocks depends on the driving force – Gibbs energy of biosynthesis, according to phenomenological equations, it is obvious that *Escherichia coli* can multiply in a human host. The permissiveness coefficient for *E. coli* is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-60.68 \frac{\text{kJ}}{\text{C-mol}}}{-31.37 \frac{\text{kJ}}{\text{C-mol}}} = 1.93 \quad (16)$$

where  $\Delta_{bs}G$  is Gibbs energy of biosynthesis [Popovic, 2022a]. The permissiveness coefficient is greater than 1, which represents a thermodynamic confirmation of the observation that *E. coli* can be found in the human organism [Riedel et al., 2019]. Moreover, it is known that *E. coli* very often causes urinary infections. Gibbs energy of biosynthesis for the urinary bladder walls is -9.93 kJ/C-mol. The permissiveness coefficient is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-60.68 \frac{\text{kJ}}{\text{C-mol}}}{-9.93 \frac{\text{kJ}}{\text{C-mol}}} = 6.11 \quad (17)$$

It is obvious that the urinary pathways represent the predilected tissue for multiplication of *E. coli*, which is indicated by the greater permissiveness coefficient. However, Gibbs energy of biosynthesis for the eye lens is -67.37 kJ/C-mol. Thus, the permissiveness coefficient is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-60.68 \frac{\text{kJ}}{\text{C-mol}}}{-67.37 \frac{\text{kJ}}{\text{C-mol}}} = 0.90 \quad (18)$$

Since the permissiveness coefficient is lower than unity, the biosynthesis reaction for the eye lens live matter has an advantage and it can be expected that *E. coli* is not able to multiply on the eye lens. Furthermore, Gibbs energy of biosynthesis of erythrocytes is -108.40 kJ/C-mol. This means that the permissiveness coefficient is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-60.68 \frac{\text{kJ}}{\text{C-mol}}}{-108.40 \frac{\text{kJ}}{\text{C-mol}}} = 0.56 \quad (19)$$

The permissiveness coefficient for biosynthesis (multiplication of *E. coli*) is lower than 1. Thus, multiplication of *E. coli* on pure erythrocytes is difficult. On other tissues, multiplication of *E. coli* is possible, with different dynamics. The rate of multiplication depends on, according to the phenomenological equations, on Gibbs energy of biosynthesis

$$r_{bs} = -\frac{L_{bs}}{T} \Delta_{bs}G \quad (20)$$

where  $r_{bs}$  is biosynthesis rate,  $T$  is temperature,  $L_{bs}$  the biosynthesis phenomenological coefficient. Since the environment is the same for both the microorganism and host cells, the  $L_{bs}$  coefficient is the same for both. Thus, the biosynthesis reactions for different tissues, which are characterized by approximately equal or less negative Gibbs energy, enable growth of *E. coli* on that tissue.

Gibbs energy of biosynthesis of *Klebsiella aerogenes* is -12.13 kJ/C-mol. The less negative Gibbs energy of biosynthesis of *Klebsiella* makes its biosynthesis reaction much slower than that of *E. coli*. Thus, infections with *Klebsiella* are much less frequent. This is in very good agreement with the observation that infections with *Klebsiella* are opportunistic infections [Ssekatawa et al., 2021]. The pathogen-host interaction of *Klebsiella* with human tissues can occur only under changes in chemical and thermodynamic properties of human tissues. This is the case under various pathological states (diseases) of human tissues, when their elemental composition and thermodynamic properties change. This could be an explanation for the opportunistic character of *Klebsiella*. However, Gibbs energy of biosynthesis of urinary bladder wall is -9.93 kJ/C-mol. This means that the permissiveness coefficient for *Klebsiella* in the urinary pathways is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-12.13 \frac{\text{kJ}}{\text{C-mol}}}{-9.93 \frac{\text{kJ}}{\text{C-mol}}} = 1.22 \quad (21)$$

Moreover, if during cateterization *Klebsiella* enters the blood, it is able to multiply in the blood plasma. Gibbs energy of biosynthesis of the blood plasma is -0.96. This means that the permissiveness coefficient is

$$P = \frac{\Delta_{bs}G(\text{pathogen})}{\Delta_{bs}G(\text{host})} = \frac{-12.13 \frac{\text{kJ}}{\text{C-mol}}}{-0.96 \frac{\text{kJ}}{\text{C-mol}}} = 12.64 \quad (22)$$

The high permissiveness coefficient allows rapid multiplication of *K. aerogenes*, but only if it passes the barriers of other tissues, in which multiplication is much more difficult.

*Candida utilis* interacts with various human tissues in immunocompromised patients [Sreelekshmi et al., 2021]. The biothermodynamic background of this interactions can be explained in a similar way to that with bacteria-host and virus-host interactions. Gibbs energy of biosynthesis of *Candida utilis* is -23.11 kJ/C-mol. Very close values of Gibbs energy of biosynthesis are those of the urinary tract, gastrointestinal tract and skin. This makes infections of these organs the most likely. The fact that most other organs (Table 4) have a more negative Gibbs energy of biosynthesis, makes multiplication of *Candida* in these tissues difficult.

## 5. Conclusions

Biothermodynamics and mechanistic models have proved themselves as powerful tools in research on interactions of microorganisms with their hosts (e.g. virus-host interactions, bacteria-host interactions) and inanimate matter (e.g. bioreactors). Chemical and thermodynamic characterization of microorganisms (determination of empirical formula, enthalpy, entropy and Gibbs energy) has significantly contributed to shedding more light on virus-host interactions.

Until now, over 50 virus species and variants have been characterized: SARS, MERS, SARS-CoV-2 (from Hu-1 to BA.5.2, BF.7 and XBB.1.5), Ebola virus, Monkeypox, HIV-1, Herpes simplex, bacteriophages, viroids etc. It is important to continue the thermodynamic research on biothermodynamic background of various viruses and their interactions with their environment.

This paper reports biosynthesis reactions and thermodynamic properties of biosynthesis of the bacteria *E. coli* and *Klebsiella aerogenes*, and the fungus *Candida utilis*. Moreover, the biothermodynamic background of bacteria-host interaction and fungi-host interactions were analyzed. It was found that these interactions occur through the same model as the virus-host interactions.

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## References

1. Alazmi, M., Kuwahara, H., Soufan, O., Ding, L., & Gao, X. (2019). Systematic selection of chemical fingerprint features improves the Gibbs energy prediction of biochemical reactions. *Bioinformatics (Oxford, England)*, 35(15), 2634–2643. <https://doi.org/10.1093/bioinformatics/bty1035>
2. Altermann, W., & Kazmierczak, J. (2003). Archean microfossils: a reappraisal of early life on Earth. *Research in microbiology*, 154(9), 611–617. <https://doi.org/10.1016/j.resmic.2003.08.006>
3. Atkins, P. W., & de Paula, J. (2011). *Physical Chemistry for the Life Sciences* (2nd edition), W. H. Freeman and Company. ISBN-13: 978-1429231145
4. Atkins, P.W. & de Paula, J. (2014). *Physical Chemistry: Thermodynamics, Structure, and Change*, 10th Edition. New York: W. H. Freeman and Company. ISBN-13: 978-1429290197
5. Balmer, R.T. (2010). *Modern Engineering Thermodynamics*, Cambridge, MA: Academic Press. <https://doi.org/10.1016/C2009-0-20199-1>
6. Barros, N. (2021). Thermodynamics of Soil Microbial Metabolism: Applications and Functions. *Applied Sciences*, 11(11), 4962. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/app11114962>
7. Barton, M. I., MacGowan, S. A., Kutuzov, M. A., Dushek, O., Barton, G. J., & van der Merwe, P. A. (2021). Effects of common mutations in the SARS-CoV-2 Spike RBD and its ligand, the human ACE2 receptor on binding affinity and kinetics. *eLife*, 10, e70658. <https://doi.org/10.7554/eLife.70658>
8. Battley, E.H. (1999a). An empirical method for estimating the entropy of formation and the absolute entropy of dried microbial biomass for use in studies on the thermodynamics of microbial growth. *Thermochimica Acta*, 326(1-2), 7-15. [https://doi.org/10.1016/S0040-6031\(98\)00584-X](https://doi.org/10.1016/S0040-6031(98)00584-X)
9. Battley, E.H. (1999b). The thermodynamics of microbial growth. In: *Handbook of Thermal Analysis and Calorimetry*, vol. 4: From Macromolecules to Man; E.B. Kemp, ed., Amsterdam: Elsevier, 219-235. [https://doi.org/10.1016/S1573-4374\(99\)80008-9](https://doi.org/10.1016/S1573-4374(99)80008-9)
10. Battley, E.H. (1998). The development of direct and indirect methods for the study of the thermodynamics of microbial growth. *Thermochimica Acta*, 309 (1-2), 17-37. [https://doi.org/10.1016/S0040-6031\(97\)00357-2](https://doi.org/10.1016/S0040-6031(97)00357-2)
11. Battley, E.H., Putnam, R.L. and Boerio-Goates, J. (1997). Heat capacity measurements from 10 to 300 K and derived thermodynamic functions of lyophilized cells of *Saccharomyces cerevisiae* including the absolute entropy and the entropy of formation at 298.15 K. *Thermochimica Acta*, 298(1-2), 37-46. [https://doi.org/10.1016/S0040-6031\(97\)00108-1](https://doi.org/10.1016/S0040-6031(97)00108-1)
12. Battley, E.H. (1992). On the enthalpy of formation of *Escherichia coli* K-12 cells, *Biotechnology and Bioengineering*, 39, 5-12. <https://doi.org/10.1002/bit.260390103>
13. Beijerinck, M. W. (1898). Ueber ein contagium vivum fluidum als Ursache der Fleckenkrankheit der Tabaksblätter. *Verhandelingen der Koninklijke akademie van Wetenschappen te Amsterdam*, 65 (2) 3-21. Available at: <https://www.apsnet.org/edcenter/apsnetfeatures/Documents/1998/BeijerckSpotDiseaseTobaccoLeaves.PDF> (Accessed on February 18, 2023)
14. Boltzmann, L. (1974). The second law of thermodynamics. In: *Theoretical physics and philosophical problems*, McGuinness, B., ed., Boston, MA: D. Riedel Publishing Company, LLC. ISBN 978-90-277-0250-0 (translation of the original version published in 1886)
15. Bordenave G. (2003). Louis Pasteur (1822-1895). *Microbes and infection*, 5(6), 553–560. [https://doi.org/10.1016/s1286-4579\(03\)00075-3](https://doi.org/10.1016/s1286-4579(03)00075-3)
16. Burkovski A. (2022). Host-Pathogen Interaction 3.0. *International journal of molecular sciences*, 23(21), 12811. <https://doi.org/10.3390/ijms232112811>
17. Calabrese, S., Chakrawal, A., Manzoni, S., & Van Cappellen, P. (2021). Energetic scaling in microbial growth. *Proceedings of the National Academy of Sciences of the United States of America*, 118(47), e2107668118. <https://doi.org/10.1073/pnas.2107668118>
18. Cao, Y. R., Yisimayi, A., Jian, F., Song, W., Xiao, T., Wang, L., ... & Xie, X. S. (2022a). BA. 2.12. 1, BA. 4 and BA. 5 escape antibodies elicited by Omicron infection. *bioRxiv*. <https://doi.org/10.1101/2022.04.30.489997>
19. Casadevall, A., & Pirofski, L. A. (2000). Host-pathogen interactions: basic concepts of microbial commensalism, colonization, infection, and disease. *Infection and immunity*, 68(12), 6511–6518. <https://doi.org/10.1128/IAI.68.12.6511-6518.2000>
20. Casasnovas, J.M. and Springer, T.A. (1995). Kinetics and thermodynamics of virus binding to receptor: Studies with rhinovirus, intercellular adhesion molecule-1 (ICAM-1), and surface plasmon resonance. *Journal of Biological Chemistry*, 270(22), 13216-13224. <https://www.doi.org/10.1074/jbc.270.22.13216>

21. Cavalier-Smith T. (2006). Cell evolution and Earth history: stasis and revolution. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 361(1470), 969–1006. <https://doi.org/10.1098/rstb.2006.1842>
22. Ceres, P. and Zlotnick, A. (2002). Weak protein-protein interactions are sufficient to drive assembly of hepatitis B virus capsids. *Biochemistry*, 41(39), 11525-11531. <https://doi.org/10.1021/bi0261645>
23. Clausius, R. (1867). *The Mechanical Theory of Heat – with its Applications to the Steam Engine and to Physical Properties of Bodies*, London: John van Voorst. OCLC Number: 1547121
24. Clausius, R. (1870). On a Mechanical Theorem Applicable to Heat, *Philosophical Magazine Series 4*, 40(265), p. 122-127. <https://doi.org/10.1080/14786447008640370>
25. Clausius, R. (1976). On different forms of the fundamental equations of the mechanical theory of heat and their convenience for application, In: *The Second Law of Thermodynamics*; J. Kestin, ed., Stroudsburg, PA: Downen, Hutchinson and Ross, Inc. ISBN-13: 978-0470989449
26. Degueldre, C. (2021). Single virus inductively coupled plasma mass spectroscopy analysis: A comprehensive study. *Talanta*, 228, 122211. <https://doi.org/10.1016/j.talanta.2021.122211>
27. Demirel, Y. (2014). *Nonequilibrium Thermodynamics: Transport and Rate Processes in Physical, Chemical and Biological Systems*, 3rd ed. Amsterdam: Elsevier. ISBN: 9780444595812
28. Dodd, T., Botto, M., Paul, F. et al. (2020). Polymerization and editing modes of a high-fidelity DNA polymerase are linked by a well-defined path. *Nat Commun* 11, 5379. <https://doi.org/10.1038/s41467-020-19165-2>
29. Domingo E. (2020). Interaction of virus populations with their hosts. *Virus as Populations*, 123–166. <https://doi.org/10.1016/B978-0-12-816331-3.00004-0>
30. Du, B., Zhang, Z., Grubner, S., Yurkovich, J. T., Palsson, B. O., & Zielinski, D. C. (2018a). Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. *Biophysical journal*, 114(11), 2691–2702. <https://doi.org/10.1016/j.bpj.2018.04.030>
31. Du, B., Zielinski, D. C., & Palsson, B. O. (2018b). Estimating Metabolic Equilibrium Constants: Progress and Future Challenges. *Trends in biochemical sciences*, 43(12), 960–969. <https://doi.org/10.1016/j.tibs.2018.09.009>
32. Du, X., Li, Y., Xia, Y. L., Ai, S. M., Liang, J., Sang, P., ... & Liu, S. Q. (2016). Insights into protein–ligand interactions: mechanisms, models, and methods. *International journal of molecular sciences*, 17(2), 144. <https://doi.org/10.3390/ijms17020144>
33. Duboc, P., Marison, I. and von Stockar, U. (1999). Quantitative calorimetry and biochemical engineering. In: *Handbook of Thermal Analysis and Calorimetry vol. 4: From Molecules To Man*; R.B. Kemp, Ed., Amsterdam: Elsevier, pp. 267-365. [http://dx.doi.org/10.1016/S1573-4374\(99\)80009-0](http://dx.doi.org/10.1016/S1573-4374(99)80009-0)
34. Durnin, J.V.G.A. (1981). Basal Metabolic Rate in Man. Joint FAO/WHO/UNU Expert Consultation on Energy and Protein Requirements. (ESN: FAO/WHO/UNU EPR/81/5 August 1981) Available at: <https://www.fao.org/3/m2845e/m2845e00.htm>
35. Eales O, de Oliveira Martins L, Page AJ, Wang H, Bodinier B, Tang D, Haw D, Jonnerby J, Atchison C, Ashby D, Barclay W, Taylor G, Cooke G, Ward H, Darzi A, Riley S, Elliott P, Donnelly CA, Chadeau-Hyam M. Dynamics of competing SARS-CoV-2 variants during the Omicron epidemic in England. *Nat Commun*. 2022 Jul 28;13(1):4375. doi: 10.1038/s41467-022-32096-4. PMID: 35902613; PMCID: PMC9330949.
36. Forterre, P. (2013). The virocell concept and environmental microbiology. *ISME J* 7, 233–236. <https://doi.org/10.1038/ismej.2012.110>
37. Forterre, P., Krupovic, M. (2012). The Origin of Virions and Virocells: The Escape Hypothesis Revisited. In: Witzany, G. (eds) *Viruses: Essential Agents of Life*. Springer, Dordrecht. [https://doi.org/10.1007/978-94-007-4899-6\\_3](https://doi.org/10.1007/978-94-007-4899-6_3)
38. Forterre, P. (2011). Manipulation of cellular syntheses and the nature of viruses: the virocell concept. *Comptes Rendus Chimie*, 14(4), 392-399. <https://doi.org/10.1016/j.crci.2010.06.007>
39. Gale P. (2022). Using thermodynamic equilibrium models to predict the effect of antiviral agents on infectivity: Theoretical application to SARS-CoV-2 and other viruses. *Microbial risk analysis*, 21, 100198. <https://doi.org/10.1016/j.mran.2021.100198>
40. Gale P. (2020). How virus size and attachment parameters affect the temperature sensitivity of virus binding to host cells: Predictions of a thermodynamic model for arboviruses and HIV. *Microbial risk analysis*, 15, 100104. <https://doi.org/10.1016/j.mran.2020.100104>
41. Gale P. (2019). Towards a thermodynamic mechanistic model for the effect of temperature on arthropod vector competence for transmission of arboviruses. *Microbial risk analysis*, 12, 27–43. <https://doi.org/10.1016/j.mran.2019.03.001>
42. Gale P. (2018). Using thermodynamic parameters to calibrate a mechanistic dose-response for infection of a host by a virus. *Microbial risk analysis*, 8, 1–13. <https://doi.org/10.1016/j.mran.2018.01.002>
43. Gao, X., Zhu, K., Qin, B., Olieric, V., Wang, M., & Cui, S. (2021). Crystal structure of SARS-CoV-2 Orf9b in complex with human TOM70 suggests unusual virus-host interactions. *Nature communications*, 12(1), 2843. <https://doi.org/10.1038/s41467-021-23118-8>
44. Greinert, T., Baumhove, K., Sadowski, G. and Held, C. (2020a). Standard Gibbs energy of metabolic reactions: IV. Triosephosphate isomerase reaction. *Biophysical Chemistry*, 258, 106330. <https://doi.org/10.1016/j.bpc.2020.106330>
45. Greinert, T., Vogel, K., Seifert, A.I., Siewert, R., Andreeva, I.V., Verevkin, S.P., Maskow, T., Sadowski, G. and Held, C. (2020b). Standard Gibbs energy of metabolic reactions: V. Enolase reaction, *Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics*, 1868(4), 140365. <https://doi.org/10.1016/j.bbapap.2020.140365>

46. Greinert, T., Vogel, K., Mühlenweg, J. K., Sadowski, G., Maskow, T., & Held, C. (2020c). Standard Gibbs energy of metabolic reactions: VI. Glyceraldehyde 3-phosphate dehydrogenase reaction. *Fluid Phase Equilibria*, 517, 112597. <https://doi.org/10.1016/j.fluid.2020.112597>
47. Riem Gawish, Philipp Starkl, Lisabeth Pimenov, Anastasiya Hladik, Karin Lakovits, Felicitas Oberndorfer, Shane JF Cronin, Anna Ohradanova-Repic, Gerald Wirnsberger, Benedikt Agerer, Lukas Endler, Tümay Capraz, Jan W Perthold, Domagoj Cikes, Rubina Koglguber, Astrid Hagelkruys, Nuria Montserrat, Ali Mirazimi, Louis Boon, Hannes Stockinger, Andreas Bergthaler, Chris Oostenbrink, Josef M Penninger, Sylvia Knapp (2022) ACE2 is the critical in vivo receptor for SARS-CoV-2 in a novel COVID-19 mouse model with TNF- and IFN $\gamma$ -driven immunopathology *eLife* 11:e74623. <https://doi.org/10.7554/eLife.74623>
48. Glandsdorff, P. and Prigogine, I. (1971). *Thermodynamic Theory of Structure, Stability and Fluctuations*. Hoboken, NJ: Wiley. ISBN-13: 978-0471302803
49. Guosheng, L., Yi, L., Xiangdong, C., Peng, L., Ping, S., & Songsheng, Q. (2003). Study on interaction between T4 phage and *Escherichia coli* B by microcalorimetric method. *Journal of virological methods*, 112(1-2), 137–143. [https://doi.org/10.1016/s0166-0934\(03\)00214-3](https://doi.org/10.1016/s0166-0934(03)00214-3)
50. Hansen, L. D., Tolley, H. D., & Woodfield, B. F. (2021). Transformation of matter in living organisms during growth and evolution. *Biophysical Chemistry*, 271, 106550. <https://doi.org/10.1016/j.bpc.2021.106550>
51. Hansen, L. D., Popovic, M., Tolley, H. D., & Woodfield, B. F. (2018). Laws of evolution parallel the laws of thermodynamics. *The Journal of Chemical Thermodynamics*, 124, 141-148. <https://doi.org/10.1016/j.jct.2018.05.005>
52. Hansen, L. D., Criddle, R. S., & Battley, E. H. (2009). Biological calorimetry and the thermodynamics of the origination and evolution of life. *Pure and Applied Chemistry*, 81(10), 1843-1855. <https://doi.org/10.1351/PAC-CON-08-09-09>
53. Head, R. J., Lumbers, E. R., Jarrott, B., Tretter, F., Smith, G., Pringle, K. G., Islam, S., & Martin, J. H. (2022). Systems analysis shows that thermodynamic physiological and pharmacological fundamentals drive COVID-19 and response to treatment. *Pharmacology research & perspectives*, 10(1), e00922. <https://doi.org/10.1002/prp2.922>
54. Howard-Varona, C., Lindback, M. M., Bastien, G. E., Solonenko, N., Zayed, A. A., Jang, H., Andreopoulos, B., Brewer, H. M., Glavina Del Rio, T., Adkins, J. N., Paul, S., Sullivan, M. B., & Duhaime, M. B. (2020). Phage-specific metabolic reprogramming of virocells. *The ISME journal*, 14(4), 881–895. <https://doi.org/10.1038/s41396-019-0580-z>
55. Johansson, E., & Dixon, N. (2013). Replicative DNA polymerases. *Cold Spring Harbor perspectives in biology*, 5(6), a012799. <https://doi.org/10.1101/cshperspect.a012799>
56. Kaniadakis, G., Baldi, M. M., Deisboeck, T. S., Grisolia, G., Hristopoulos, D. T., Scarfone, A. M., Sparavigna, A., Wada, T., & Lucia, U. (2020). The  $\kappa$ -statistics approach to epidemiology. *Scientific reports*, 10(1), 19949. <https://doi.org/10.1038/s41598-020-76673-3>
57. Katen, S., & Zlotnick, A. (2009). The thermodynamics of virus capsid assembly. *Methods in enzymology*, 455, 395–417. [https://doi.org/10.1016/S0076-6879\(08\)04214-6](https://doi.org/10.1016/S0076-6879(08)04214-6)
58. Lane N. (2015). The unseen world: reflections on Leeuwenhoek (1677) 'Concerning little animals'. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 370(1666), 20140344. <https://doi.org/10.1098/rstb.2014.0344>
59. Lavoisier, AL, & marquis de Laplace, PS (1783). *Mémoire sur la chaleur: Lù à l'Académie royale des sciences, le 28 Juin 1783*. Paris, France: De l'Imprimerie royale. (English translation: "Memoir on Heat Read to the Royal Academy of Sciences, 28 June 1783")
60. Lavoisier, A. L., & DeLaplace, P. S. (1994). Memoir on heat read to the royal academy of sciences, 28 june 1783. *Obesity research*, 2(2), 189-202. <https://doi.org/10.1002/j.1550-8528.1994.tb00646.x> (Modern translation in English)
61. Lee, J., Schwarz, K. J., Kim, D. S., Moore, J. S., & Jewett, M. C. (2020). Ribosome-mediated polymerization of long chain carbon and cyclic amino acids into peptides in vitro. *Nature communications*, 11(1), 4304. <https://doi.org/10.1038/s41467-020-18001-x>
62. Lucia, U., Grisolia, G., & Deisboeck, T. S. (2021). Thermodynamics and SARS-CoV-2: neurological effects in post-Covid 19 syndrome. *Atti della Accademia Peloritana dei Pericolanti*, 99(2), A3. <https://doi.org/10.1478/AAPP.992A3>
63. Lucia, U., Grisolia, G., & Deisboeck, T. S. (2020a). Seebeck-like effect in SARS-CoV-2 bio-thermodynamics. *Atti della Accademia Peloritana dei Pericolanti-Classe di Scienze Fisiche, Matematiche e Naturali*, 98(2), 6. <https://doi.org/10.1478/AAPP.982A6>
64. Lucia, U., Deisboeck, T. S., & Grisolia, G. (2020b). Entropy-based pandemics forecasting. *Frontiers in Physics*, 8, 274. <https://doi.org/10.3389/fphy.2020.00274>
65. Makowski EK, Schardt JS, Smith MD, Tessier PM. Mutational analysis of SARS-CoV-2 variants of concern reveals key tradeoffs between receptor affinity and antibody escape. *PLoS Comput Biol*. 2022 May 31;18(5):e1010160. doi: 10.1371/journal.pcbi.1010160. PMID: 35639784; PMCID: PMC9223403.
66. Maginnis MS. (2018). Virus-Receptor Interactions: The Key to Cellular Invasion. *J Mol Biol*. 2018 Aug 17;430(17):2590-2611. doi: 10.1016/j.jmb.2018.06.024. Epub 2018 Jun 18. PMID: 29924965; PMCID: PMC6083867.
67. Mahmoudabadi, G., Milo, R. and Phillips, R. (2017). Energetic cost of building a virus. *PNAS*, 114(22), E4324-E4333. <https://doi.org/10.1073/pnas.1701670114>
68. Maskow, T., Kiesel, B., Schubert, T., Yong, Z., Harms, H., & Yao, J. (2010). Calorimetric real time monitoring of lambda prophage induction. *Journal of virological methods*, 168(1-2), 126–132. <https://doi.org/10.1016/j.jviromet.2010.05.002>

69. Meurer, F., Bobrownik, M., Sadowski, G. and Held, C. (2016). Standard Gibbs energy of metabolic reactions: I. Hexokinase reaction, *Biochemistry*, 55(40), 5665-5674. <https://doi.org/10.1021/acs.biochem.6b00471>
70. Meurer, F., Do, H.T., Sadowski, G. and Held, C. (2017). Standard Gibbs energy of metabolic reactions: II. Glucose-6-phosphatase reaction and ATP hydrolysis. *Biophysical Chemistry*, 223, 30-38. <https://doi.org/10.1016/j.bpc.2017.02.005>
71. Molla, A., Paul, A. V., & Wimmer, E. (1991). Cell-free, de novo synthesis of poliovirus. *Science (New York, N.Y.)*, 254(5038), 1647-1651. <https://doi.org/10.1126/science.1661029>
72. Morowitz, H. J., Kostelnik, J. D., Yang, J., & Cody, G. D. (2000). The origin of intermediary metabolism. *Proceedings of the National Academy of Sciences*, 97(14), 7704-7708. <https://doi.org/10.1073/pnas.110153997>
73. Morowitz, H. (1995). The emergence of complexity. *Complexity*, 1(1), 4-5. <https://doi.org/10.1002/cplx.6130010102>
74. Morowitz, H.J. (1992). *Beginnings of Cellular Life: Metabolism Recapitulates Biogenesis*. New Haven, CT: Yale University Press. ISBN-13: 978-0300102109
75. Morowitz, H.J., Heinz, B. & Deamer, D.W. The chemical logic of a minimum protocell. *Origins Life Evol Biosphere* 18, 281-287 (1988). <https://doi.org/10.1007/BF01804674>
76. Morowitz, H.J. (1968). *Energy Flow in Biology: Biological Organization as a Problem in Thermal Physics*. New York: Academic Press. <https://lccn.loc.gov/67031041>
77. Morowitz, H.J. (1955). Some order-disorder considerations in living systems. *Bulletin of Mathematical Biophysics*, 17, 81-86. <https://doi.org/10.1007/BF02477985>
78. Nadi, F., & Özilgen, M. (2021). Effects of COVID-19 on energy savings and emission reduction: a case study. *International Journal of Global Warming*, 25(1), 38-57. <https://doi.org/10.1504/IJGW.2021.117432>
79. Nagai, H., Masuda, A., Toya, Y., Matsuda, F., & Shimizu, H. (2018). Metabolic engineering of mevalonate-producing *Escherichia coli* strains based on thermodynamic analysis. *Metabolic engineering*, 47, 1-9. <https://doi.org/10.1016/j.ymben.2018.02.012>
80. Niebel, B., Leupold, S. & Heinemann, M. (2019). An upper limit on Gibbs energy dissipation governs cellular metabolism. *Nat Metab* 1, 125-132. <https://doi.org/10.1038/s42255-018-0006-7>
81. Nobel Prize (2023). The Nobel Prize in Physiology or Medicine 1905. [Online] NobelPrize.org. Nobel Prize Outreach AB 2023. Sat. 18 Feb 2023. <https://www.nobelprize.org/prizes/medicine/1905/summary/>
82. Özilgen, M., & Yilmaz, B. (2021). COVID-19 disease causes an energy supply deficit in a patient. *International journal of energy research*, 45(2), 1157-1160. <https://doi.org/10.1002/er.5883>
83. Patiño, R., Janssen, M., & von Stockar, U. (2007). A study of the growth for the microalga *Chlorella vulgaris* by photo-biocalorimetry and other on-line and off-line techniques. *Biotechnology and bioengineering*, 96(4), 757-767. <https://doi.org/10.1002/bit.21182>
84. Payne, A.S. (1970). *The Cleere observer, a biography of Antoni van Leeuwenhoek*. New York: Macmillan. ASIN: B000LX18TI
85. Pinheiro, A. V., Baptista, P., & Lima, J. C. (2008). Light activation of transcription: photocaging of nucleotides for control over RNA polymerization. *Nucleic acids research*, 36(14), e90. <https://doi.org/10.1093/nar/gkn415>
86. Popovic, M. (2023a) Simple but Powerful: Viroids can Hijack their Host Cells' Metabolism due to Greater Gibbs Energy Dissipation. Preprints, 2023010085. <https://doi.org/10.20944/preprints202301.0085.v1>
87. Popovic M. (2023b). Never ending story? Evolution of SARS-CoV-2 monitored through Gibbs energies of biosynthesis and antigen-receptor binding of Omicron BQ.1, BQ.1.1, XBB and XBB.1 variants. *Microbial risk analysis*, 23, 100250. <https://doi.org/10.1016/j.mran.2023.100250>
88. Popovic M. (2023c). The SARS-CoV-2 Hydra, a tiny monster from the 21st century: Thermodynamics of the BA.5.2 and BF.7 variants. *Microbial risk analysis*, 23, 100249. <https://doi.org/10.1016/j.mran.2023.100249>
89. Popovic, M.E. (2023d). XBB.1.5 Kraken cracked: Gibbs energies of binding and biosynthesis of the XBB.1.5 variant of SARS-CoV-2. *Microbiological Research*, 270, 127337. <https://doi.org/10.1016/j.micres.2023.127337>
90. Popovic, M. (2023e). Closer look into HIV-host interactions: Standard Gibbs energy of binding of the gp120 antigen of HIV-1 to the CD4 receptor and monoclonal antibodies. *Life in Silico*, 1(1), 8-12. Retrieved from <https://life-insilico.com/index.php/pub/article/view/2>
91. Popovic, M. (2023f). Thermodynamics of Bacteria-Phage Interactions: T4 and Lambda Bacteriophages, and E. Coli Can Coexist in Natural Ecosystems due to the Ratio of their Gibbs Energies of Biosynthesis. *Thermal Science*, 27(1), 411-431. <https://doi.org/10.2298/TSCI2301411P>
92. Popovic, M., & Popovic, M. (2022). Strain Wars: Competitive interactions between SARS-CoV-2 strains are explained by Gibbs energy of antigen-receptor binding. *Microbial risk analysis*, 21, 100202. <https://doi.org/10.1016/j.mran.2022.100202>
93. Popovic, M. (2022a). Biothermodynamics of Viruses from Absolute Zero (1950) to Virothermodynamics (2022). *Vaccines*, 10(12), 2112. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/vaccines10122112>
94. Popovic M. (2022b). Strain wars 2: Binding constants, enthalpies, entropies, Gibbs energies and rates of binding of SARS-CoV-2 variants. *Virology*, 570, 35-44. <https://doi.org/10.1016/j.virol.2022.03.008>
95. Popovic M. (2022c). Strain wars 3: Differences in infectivity and pathogenicity between Delta and Omicron strains of SARS-CoV-2 can be explained by thermodynamic and kinetic parameters of binding and growth. *Microbial risk analysis*, 22, 100217. <https://doi.org/10.1016/j.mran.2022.100217>

96. Popovic M. (2022d). Strain wars 4 - Darwinian evolution through Gibbs' glasses: Gibbs energies of binding and growth explain evolution of SARS-CoV-2 from Hu-1 to BA.2. *Virology*, 575, 36–42. <https://doi.org/10.1016/j.virol.2022.08.009>
97. Popovic, M. (2022e). Strain Wars 5: Gibbs energies of binding of BA.1 through BA.4 variants of SARS-CoV-2. *Microbial Risk Analysis*. <https://doi.org/10.1016/j.mran.2022.100231>
98. Popovic, M. (2022f). Beyond COVID-19: Do biothermodynamic properties allow predicting the future evolution of SARS-CoV-2 variants?. *Microbial risk analysis*, 22, 100232. <https://doi.org/10.1016/j.mran.2022.100232>
99. Popovic, M. (2022g). Omicron BA.2.75 Subvariant of SARS-CoV-2 Is Expected to Have the Greatest Infectivity Compared with the Competing BA.2 and BA.5, Due to Most Negative Gibbs Energy of Binding. *BioTech*, 11(4), 45. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/biotech11040045>
100. Popovic, M. (2022h). Omicron BA.2.75 Sublineage (Centaurus) Follows the Expectations of the Evolution Theory: Less Negative Gibbs Energy of Biosynthesis Indicates Decreased Pathogenicity. *Microbiology Research*, 13(4), 937–952. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/microbiolres13040066>
101. Popovic, M. (2022i). Why doesn't Ebola virus cause pandemics like SARS-CoV-2? *Microbial Risk Analysis*, 100236. <https://doi.org/10.1016/j.mran.2022.100236>
102. Popovic, M. (2022j). Formulas for death and life: Chemical composition and biothermodynamic properties of Monkeypox (MPV, MPXV, HMPXV) and Vaccinia (VACV) viruses. *Thermal Science*, 26(6A). <https://doi.org/10.2298/TSCI220524142P>
103. Popovic, M. (2022k). Everything you Always Wanted to Know about the Biothermodynamic Background of Herpes Simplex Virus Type 1 – Host Interaction. *Preprints*, 2022120063. <https://doi.org/10.20944/preprints202212.0063.v1>
104. Popovic M. (2022m). Atom counting method for determining elemental composition of viruses and its applications in biothermodynamics and environmental science. *Computational biology and chemistry*, 96, 107621. <https://doi.org/10.1016/j.compbiolchem.2022.107621>
105. Popovic, M., Stenning, G., Göttlein, A., & Minceva, M. (2021). Elemental composition, heat capacity from 2 to 300 K and derived thermodynamic functions of 5 microorganism species. *Journal of biotechnology*, 331, 99–107. <https://doi.org/10.1016/j.jbiotec.2021.03.006>
106. Popovic, M., & Minceva, M. (2021a). Coinfection and Interference Phenomena Are the Results of Multiple Thermodynamic Competitive Interactions. *Microorganisms*, 9(10), 2060. <https://doi.org/10.3390/microorganisms9102060>
107. Popovic, M., & Minceva, M. (2020a). A thermodynamic insight into viral infections: do viruses in a lytic cycle hijack cell metabolism due to their low Gibbs energy?. *Heliyon*, 6(5), e03933. <https://doi.org/10.1016/j.heliyon.2020.e03933>
108. Popovic, M., & Minceva, M. (2020b). Thermodynamic insight into viral infections 2: empirical formulas, molecular compositions and thermodynamic properties of SARS, MERS and SARS-CoV-2 (COVID-19) viruses. *Heliyon*, 6(9), e04943. <https://dx.doi.org/10.1016%2Fj.heliyon.2020.e04943>
109. Popovic, M. E., & Minceva, M. (2020c). Thermodynamic properties of human tissues. *Thermal Science*, 24(6 Part B), 4115–4133. <https://doi.org/10.2298/TSCI200109151P>
110. Popovic, M., Woodfield, B.F. and Hansen, L.D. (2019). Thermodynamics of Hydrolysis of Cellulose to Glucose from 0 to 100°C: Cellulosic Biofuel Applications and Climate Change Implications. *Journal of Chemical Thermodynamics*, 128, 244–250. <https://doi.org/10.1016/j.jct.2018.08.006>
111. Popovic M. (2019). Thermodynamic properties of microorganisms: determination and analysis of enthalpy, entropy, and Gibbs free energy of biomass, cells and colonies of 32 microorganism species. *Heliyon*, 5(6), e01950. <https://doi.org/10.1016/j.heliyon.2019.e01950>
112. Popovic, M. (2018). Living organisms from Prigogine's perspective: an opportunity to introduce students to biological entropy balance. *Journal of Biological Education*, 52(3), 294–300. <https://doi.org/10.1080/00219266.2017.1357649>
113. Popovic, M. (2014a). Comparative study of entropy and information change in closed and open thermodynamic systems. *Thermochimica Acta*, 598, 77–81. <https://doi.org/10.1016/j.tca.2014.11.002>
114. Popovic, M. (2014b). Entropy change of open thermodynamic systems in self-organizing processes. *Thermal Science*, 18(4), 1425–1432. <https://doi.org/10.2298/TSCI140424065P>
115. Prigogine, I. and Wiame, J.M. (1946). *Biologie et thermodynamique des phénomènes irréversibles*. *Experientia*, 2, 451–453. <https://doi.org/10.1007/BF02153597>
116. Prigogine, I. (1977). Nobel lecture: Time, Structure and Fluctuations. [Online] Available at: <https://www.nobelprize.org/prizes/chemistry/1977/prigogine/lecture/> (Accessed on: January 5, 2023)
117. Prigogine I. (1947). *Etude thermodynamique des phénomènes irréversibles*. Paris: Dunod. WorldCat ID: 421502786
118. Proal, A. D., & VanElzakker, M. B. (2021). Pathogens hijack host cell metabolism: intracellular infection as a driver of the Warburg effect in cancer and other chronic inflammatory conditions. *Immunometabolism*, 3(1). <https://doi.org/10.20900/immunometab20210003>
119. Rosenwasser, S., Ziv, C., Creveld, S. G. V., & Vardi, A. (2016). Virocell Metabolism: Metabolic Innovations During Host-Virus Interactions in the Ocean. *Trends in microbiology*, 24(10), 821–832. <https://doi.org/10.1016/j.tim.2016.06.006>
120. Sreelekshmi, T. S., Ninan, M. M., Premanand, A., Chacko, A., Sahni, R. D., & Michael, J. S. (2021). *Candida utilis*: a rare cause of septicemia in children. *Access microbiology*, 3(10), 000281. <https://doi.org/10.1099/acmi.0.000281>
121. Shirbhate, E., Pandey, J., Patel, V. K., Kamal, M., Jawaid, T., Gorain, B., Kesharwani, P., & Rajak, H. (2021). Understanding the role of ACE-2 receptor in pathogenesis of COVID-19 disease: a potential approach for therapeutic intervention. *Pharmacological reports : PR*, 73(6), 1539–1550. <https://doi.org/10.1007/s43440-021-00303-6>

122. Skene, K. (2015). Life's a Gas: A Thermodynamic Theory of Biological Evolution. *Entropy*, 17(12), 5522–5548. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/e17085522>
123. Smeaton, C. M., & Van Cappellen, P. (2018). Gibbs Energy Dynamic Yield Method (GEDYM): Predicting microbial growth yields under energy-limiting conditions. *Geochimica et Cosmochimica Acta*, 241, 1-16. <https://doi.org/10.1016/j.gca.2018.08.023>
124. Sterner, R.W., Elster, J.J. (2002). *Ecological Stoichiometry: The Biology of Elements from Molecules to the Biosphere*, Princeton, NJ: Princeton University Press. ISBN-13: 978-0691074917
125. Sumbria, D., Berber, E., Mathayan, M., & Rouse, B. T. (2021). Virus Infections and Host Metabolism-Can We Manage the Interactions?. *Frontiers in Immunology*, 11, 594963. <https://doi.org/10.3389/fimmu.2020.594963>
126. Summers W. C. (2009). Virus Infection. *Encyclopedia of Microbiology*, 546–552. <https://doi.org/10.1016/B978-012373944-5.00323-0>
127. Thaker, S. K., Ch'ng, J., & Christofk, H. R. (2019). Viral hijacking of cellular metabolism. *BMC biology*, 17(1), 59. <https://doi.org/10.1186/s12915-019-0678-9>
128. Tzllil, S., Deserno, M., Gelbart, W.M. and Ben-Shaul, A. (2004). A statistical-thermodynamic model of viral budding. *Biophysical Journal*, 86(4), 2037-2048. [https://doi.org/10.1016/S0006-3495\(04\)74265-4](https://doi.org/10.1016/S0006-3495(04)74265-4)
129. Schopf J. W. (2006). Fossil evidence of Archaeal life. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 361(1470), 869–885. <https://doi.org/10.1098/rstb.2006.1834>
130. Schrödinger, E. (1944). *What is life? The physical aspect of the living cell*, Cambridge: Cambridge university press. ISBN: 0-521-42708-8
131. Ssekatawa, K., Byarugaba, D.K., Nakavuma, J.L. et al. (2021). Prevalence of pathogenic *Klebsiella pneumoniae* based on PCR capsular typing harbouring carbapenemases encoding genes in Uganda tertiary hospitals. *Antimicrob Resist Infect Control* 10, 57. <https://doi.org/10.1186/s13756-021-00923-w>
132. Sigg, A. P., Mariotti, M., Grütter, A. E., Lafranca, T., Leitner, L., Bonkat, G., & Braissant, O. (2022). A Method to Determine the Efficacy of a Commercial Phage Preparation against Uropathogens in Urine and Artificial Urine Determined by Isothermal Microcalorimetry. *Microorganisms*, 10(5), 845. MDPI AG. Retrieved from <http://dx.doi.org/10.3390/microorganisms10050845>
133. Şimşek, B., Özilgen, M., & Utku, F. Ş. (2021). How much energy is stored in SARS-CoV-2 and its structural elements?. *Energy Storage*, e298. <https://doi.org/10.1002/est2.298>
134. Skoog, D.A., West, D.M., Holler, F.J. and Crouch, S.R. (2013). *Fundamentals of Analytical Chemistry*, 9th ed., Boston, MA: Cengage Learning. ISBN: 978-0-495-55828-6
135. Tkhilaishvili, T., Wang, L., Tavanti, A., Trampuz, A., & Di Luca, M. (2020a). Antibacterial Efficacy of Two Commercially Available Bacteriophage Formulations, Staphylococcal Bacteriophage and PYO Bacteriophage, Against Methicillin-Resistant *Staphylococcus aureus*: Prevention and Eradication of Biofilm Formation and Control of a Systemic Infection of *Galleria mellonella* Larvae. *Frontiers in microbiology*, 11, 110. <https://doi.org/10.3389/fmicb.2020.00110>
136. Tkhilaishvili, T., Wang, L., Perka, C., Trampuz, A., & Gonzalez Moreno, M. (2020b). Using Bacteriophages as a Trojan Horse to the Killing of Dual-Species Biofilm Formed by *Pseudomonas aeruginosa* and Methicillin Resistant *Staphylococcus aureus*. *Frontiers in microbiology*, 11, 695. <https://doi.org/10.3389/fmicb.2020.00695>
137. Tkhilaishvili, T., Di Luca, M., Abbandonato, G., Maiolo, E. M., Klatt, A. B., Reuter, M., Möncke-Buchner, E., & Trampuz, A. (2018a). Real-time assessment of bacteriophage T3-derived antimicrobial activity against planktonic and biofilm-embedded *Escherichia coli* by isothermal microcalorimetry. *Research in microbiology*, 169(9), 515–521. <https://doi.org/10.1016/j.resmic.2018.05.010>
138. Tkhilaishvili, T., Lombardi, L., Klatt, A. B., Trampuz, A., & Di Luca, M. (2018b). Bacteriophage Sb-1 enhances antibiotic activity against biofilm, degrades exopolysaccharide matrix and targets persisters of *Staphylococcus aureus*. *International journal of antimicrobial agents*, 52(6), 842–853. <https://doi.org/10.1016/j.ijantimicag.2018.09.006>
139. Tkhilaishvili, T., Di Luca, M., & Trampuz, A. (2018c). SIMULTANEOUS AND SEQUENTIAL APPLICATIONS OF PHAGES AND CIPROFLOXACIN IN KILLING MIXED-SPECIES BIOFILM OF *PSEUDOMONAS AERUGINOSA* AND *STAPHYLOCOCCUS AUREUS*. In *Orthopaedic Proceedings* (Vol. 100, No. SUPP\_17, pp. 65-65). The British Editorial Society of Bone & Joint Surgery.
140. Tkhilaishvili, T. (2022). *Bacteriophages as an alternative strategy in the treatment and prevention of implant-associated infections* (Doctoral dissertation). <http://dx.doi.org/10.17169/refubium-32604>
141. van Leeuwenhoek, A. (1700). IV. Part of a letter from Mr Antony Van Leeuwenhoek, concerning the worms in Sheeps livers, Gants and animalcula in the excrements of Frogs. *Philosophical Transactions of the Royal Society of London*, 22(261). <https://doi.org/10.1098/rstl.1700.0013>
142. Venkataraman, S., Badar, U., Shoeb, E., Hashim, G., AbouHaidar, M., & Hefferon, K. (2021). An Inside Look into Biological Miniatures: Molecular Mechanisms of Viroids. *International journal of molecular sciences*, 22(6), 2795. <https://doi.org/10.3390/ijms22062795>
143. Von Bertalanffy, L. (1950). The theory of open systems in physics and biology. *Science*, 111(2872), 23-29. <https://doi.org/10.1126/science.111.2872.23>
144. Von Bertalanffy, L. (1971). *General System Theory: Foundations, Development, Applications*. New York, NY: George Braziller Inc. ISBN-13: 978-0807604533

145. Von Stockar, U. (2013a). Live cells as open non-equilibrium systems. In Urs von Stockar, ed., *Biothermodynamics: The Role of Thermodynamics in Biochemical Engineering*, Lausanne: EPFL Press, 475-534.
146. Von Stockar, U. (2013b). Biothermodynamics of live cells: energy dissipation and heat generation in cellular structures. In: *Biothermodynamics: the role of thermodynamics in Biochemical Engineering*, von Stockar, U., ed., Lausanne: EPFL Press, pp. 475-534.
147. Von Stockar, U., Maskow, T. and Vojinovic, V. (2013). Thermodynamic analysis of metabolic pathways. In: *Biothermodynamics: the role of thermodynamics in Biochemical Engineering*, von Stockar, U., ed., Lausanne: EPFL Press, pp. 581-604.
148. von Stockar, U., Vojinović, V., Maskow, T., & Liu, J. (2008). Can microbial growth yield be estimated using simple thermodynamic analogies to technical processes?. *Chemical Engineering and Processing: Process Intensification*, 47(6), 980-990. <https://doi.org/10.1016/j.cep.2007.02.016>
149. Von Stockar, U., Maskow, T., Liu, J., Marison, I. W., & Patino, R. (2006). Thermodynamics of microbial growth and metabolism: an analysis of the current situation. *Journal of Biotechnology*, 121(4), 517-533. <https://doi.org/10.1016/j.jbiotec.2005.08.012>
150. von Stockar, U., & Liu, J. (1999). Does microbial life always feed on negative entropy? Thermodynamic analysis of microbial growth. *Biochimica et biophysica acta*, 1412(3), 191-211. [https://doi.org/10.1016/s0005-2728\(99\)00065-1](https://doi.org/10.1016/s0005-2728(99)00065-1)
151. Von Stockar, U., & Marison, I. W. (1993). The definition of energetic growth efficiencies for aerobic and anaerobic microbial growth and their determination by calorimetry and by other means. *Thermochimica acta*, 229, 157-172. <https://doi.org/10.1002/bit.1176>
152. Wang, L., Tkhilaishvili, T., Trampuz, A., & Gonzalez Moreno, M. (2020a). Evaluation of Staphylococcal Bacteriophage Sb-1 as an Adjunctive Agent to Antibiotics Against Rifampin-Resistant Staphylococcus aureus Biofilms. *Frontiers in microbiology*, 11, 602057. <https://doi.org/10.3389/fmicb.2020.602057>
153. Wang, L., Tkhilaishvili, T., Bernal Andres, B., Trampuz, A., & Gonzalez Moreno, M. (2020b). Bacteriophage-antibiotic combinations against ciprofloxacin/ceftriaxone-resistant Escherichia coli in vitro and in an experimental Galleria mellonella model. *International journal of antimicrobial agents*, 56(6), 106200. <https://doi.org/10.1016/j.ijantimicag.2020.106200>
154. Wangler, A., Schmidt, C., Sadowski, G. and Held, C. (2018). Standard Gibbs energy of metabolic reactions: III. The 3-phosphoglycerate kinase reaction. *ACS Omega*, 3(2), 1783-1790. <https://doi.org/10.1021/acsomega.7b01704>
155. Wimmer E. (2006). The test-tube synthesis of a chemical called poliovirus. The simple synthesis of a virus has far-reaching societal implications. *EMBO reports*, 7 Spec No(Spec No), S3-S9. <https://doi.org/10.1038/sj.embor.7400728>
156. Xu, X., Rioux, T. P., & Castellani, M. P. (2022). The specific heat of the human body is lower than previously believed: The Journal Temperature toolbox. *Temperature*, 1-5. <https://doi.org/10.1080/23328940.2022.2088034>
157. Yilmaz, B., Ercan, S., Akduman, S., & Özilgen, M. (2020). Energetic and exergetic costs of COVID-19 infection on the body of a patient. *International Journal of Exergy*, 32(3), 314-327. <https://doi.org/10.1504/IJEX.2020.108602>
158. Zaitlin, M. (1998). The Discovery of the Causal Agent of the Tobacco Mosaic Disease. In: *Discoveries in Plant Biology*, S.D Kung and S. F. Yang (eds), pp.: 105-110. Hong Kong: World Publishing Co., Ltd.

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