Resonant Recognition Model (RRM)

All proteins can be considered as a linear sequence of their constitutive elements, i.e. amino acids and biological function of proteins is determined primarily by this linear sequence. The Resonant Recognition Model (RRM) has been previously presented in detail [4-17] and interprets this linear information by transforming a protein sequence into a numerical series and then into the frequency domain using digital signal processing method i.e. Fast Fourier Transform (FFT).

Protein primary structure can be presented as a numerical series by assigning the relevant physical parameter value to each amino acid. Our investigations have shown that the best correlation can be achieved with parameters which are related to the energy of delocalised electrons of each amino acid (calculated as Electron Ion Interaction Potential (EIIP)), as electrons delocalised from the particular amino acid, have the strongest impact on the electronic distribution of the whole protein [4-8]. The resulting numerical series represents the distribution of the free electron's energies along the protein molecule.

Such numerical series are then analysed by digital signal analysis methods, using FFT, to extract information pertinent to the biological function. As the distance between amino acid residues in a polypeptide chain is 3.8Å, it can be assumed that the points in the numerical sequence are equidistant. For further numerical analysis, the distance between points in these numerical sequences is set at an arbitrary value of d=1. Therefore, the maximum frequency in the spectrum is F=1/2d=0.5. The total number of points in the sequence influences the resolution of the spectrum only. Therefore, for N-point sequence the resolution in the spectrum is equal to 1/N. The n-th point in the spectral function corresponds to the frequency f=n/N.

To extract common spectral characteristics of sequences having the same or similar biological function, the multiple cross-spectral function is used. Peak frequencies in such a multiple cross-spectral function present common frequency component for all sequences analysed. Such common frequency components are found to be related to the common biological function of the analysed proteins leading to the conclusion that each specific biological function within the protein or DNA or RNA is characterised by one frequency [4-17].

Each biological function and/or process is driven by proteins that selectively interact with other proteins, DNA regulatory segments or small molecules. Using the RRM, it has been shown that proteins and their targets share the same matching characteristic frequency [4-6, 16]. The matching of periodicities within the distribution of energies of free electrons along the interacting proteins can be regarded as the resonant recognition and is highly selective. Thus, the RRM frequencies characterise not only protein function, but also recognition and interaction between a protein and its targets: receptors, binding proteins and inhibitors. In addition, it has been also shown that interacting proteins have opposite phases at their characteristic recognition frequency [4-6, 16]. Every frequency can be presented by one sinusoid characterised with its frequency, amplitude and phase. The phase is presented in radians and can be between $-\pi$ and $+\pi$ (-3.14 and +3.14). The phase difference of or about 3.14 is considered opposite phase. The phase value can be presented in the phase circle where it is easier to observe graphically opposite phases.

As it has been proposed that the RRM frequencies characterize, not only a general function, but also a recognition and interaction between the macromolecule and its target, which then can be considered as resonant recognition. This could be achieved with resonant energy transfer between the interacting macromolecules through oscillations of a physical field, which is electromagnetic in nature. Since there is evidence that proteins and DNA have certain conducting or semi-conducting properties, a charge moving through the macromolecular backbone and passing different energy stages, caused by different amino acid or nucleotide side groups, can produce sufficient conditions for a specific electromagnetic radiation or absorption. The frequency ranges of this field depend on the charge velocity. The RRM proposes that the charge is travelling through the macromolecular backbone at the estimated velocity of 7.87×10^5m/s [4-6, 9]. For this velocity and with the distance between amino acids in a protein molecule of 3.8Å, the frequency of protein interactions was estimated to be in the range

between 10^{13}Hz and 10^{15}Hz. Therefore, the estimated frequency range for both amino acid and nucleotide macromolecules includes infra-red, visible and ultra-violet light. To support this idea, we compared our computational predictions with number of published experimental results [4-6]:

- Laser light growth promotion of cells, by using the frequencies of light to produce the similar effect to that of growth factor proteins;
- Chymotrypsin activation (increase of enzyme activity) achieved by laser light radiation in a range of 850-860nm;
- Activation of highly homologous plant photoreceptors which, although being very homologous, absorb different wavelengths of light;
- Photo activated proteins, e.g. rhodopsin, flavodoxin, etc.

These comparisons have shown a strong linear correlation between frequencies, as calculated using the RRM method and experimentally measured characteristic frequencies, with the slope factor of K=201 [4-6, 9-17]. This finding parallel with the frequency range previously associated with the RRM numerical frequency spectrum that has been calculated from the charge velocities through the protein backbone. This correlation can be represented as following:

$$\lambda = K / f_{rrm}$$

where λ is the wavelength of light irradiation in nm, which can influence particular biological process, f_{rrm} is RRM numerical frequency and K is coefficient of this linear correlation.

We applied this concept on number of proteins and DNA examples [4-6, 9-17]. The concept has been also experimentally tested by predicting the electromagnetic frequencies for L-Lactate Dehydrogenase [17], where by radiating L-Lactate Dehydrogenase with predicted calculated electromagnetic frequencies the significant change in enzyme activity was achieved. The concept has also been tested independently on experimental measurements of photon emission from dying melanoma cells [18], on photon emission from lethal and non-lethal Ebola strains [19], as well as on classic signaling pathway, JAK-STAT, traditionally composed of nine sequential protein interactions [20].

Keeping all this in mind, we propose that the RRM concept is excellent predictor for proteins and DNA selective interactions, biological processes and pathways in living cells. In our previous work, we have calculated large number of specific frequencies for different protein and DNA biological functions and interactions [4-6, 9-17].