

Supplementary Information

The amino acid coding introduced by Ghosh and Chaudhuri and used in the present work is shown in Table S1 . The evolution code of number 84, as defined by Xiao et al.¹, is illustrated in Fig. S1.

Aminoacid	Code	Aminoacid	code
Glycine (G)	00000000	Cysteine (C)	01000100
Alanine (A)	00000100	Threonine (T)	00110100
Proline (P)	00100110	Asparagine (N)	00101110
Valine (V)	00110110	Glutamine (Q)	00101111
Methionine (M)	00110110	Tyrosine (Y)	10100100
Tryptophan (W)	10110110	Histidine (H)	01111110
Phenylalanine (F)	10000100	Lysine (K)	00110111
Isoleucine (I)	00011110	Arginine (R)	01111111
Leucine (L)	00010111	Aspartic Acid (D)	01110110
Serine (S)	00100100	Glutamic Acid (E)	01110110

Table S1 . Aminoacid coding from Ghosh and Chaudhuri².

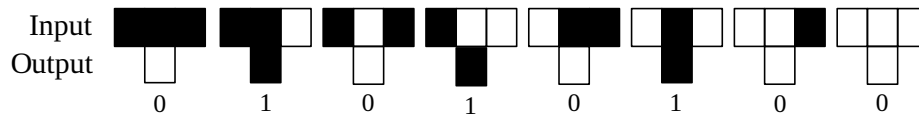


Figure S1. Evolution rule for the cellular automata.

The Table S2 is the dissimilarity matrix using the p-distance between aligned Lysozyme protein sequences that was calculated using MEGA software.

Species	Bullfrog	Salamander	Microcaecilia	Peafowl	Chicken	Pheasant	Crow	Fruit Fly	House Fly	Wax Moth	Orangutan	Human	Gorilla	Gymnodraco	Perca Flavescens	Salmo Salar	Alligator	Pelodiscus
Bullfrog																		
Salamander	0.513																	
Microcaecilia	0.393	0.449																
Peafowl	0.492	0.341	0.414															
Chicken	0.527	0.374	0.465	0.038														
Pheasant	0.500	0.372	0.429	0.054	0.069													
Crow	0.451	0.586	0.500	0.547	0.569	0.555												
Fruit Fly	0.688	0.647	0.700	0.639	0.637	0.655	0.678											
House Fly	0.683	0.633	0.669	0.619	0.630	0.636	0.637	0.357										
Wax Moth	0.621	0.619	0.588	0.608	0.600	0.625	0.537	0.620	0.620									
Orangutan	0.430	0.398	0.438	0.395	0.428	0.418	0.486	0.625	0.618	0.586								
Human	0.594	0.560	0.589	0.523	0.561	0.515	0.576	0.708	0.708	0.641	0.589							
Gorilla	0.423	0.398	0.431	0.395	0.428	0.418	0.479	0.625	0.604	0.586	0.027	0.589						
Gymnodraco	0.485	0.437	0.500	0.453	0.461	0.460	0.528	0.659	0.666	0.566	0.409	0.570	0.409					
Perca	0.457	0.458	0.464	0.437	0.468	0.453	0.471	0.637	0.659	0.550	0.381	0.556	0.381	0.251				
Salmo Salar	0.452	0.407	0.471	0.429	0.420	0.448	0.528	0.625	0.653	0.523	0.333	0.594	0.333	0.324	0.317			
Alligator	0.538	0.344	0.438	0.317	0.376	0.333	0.569	0.702	0.695	0.611	0.455	0.589	0.455	0.479	0.465	0.472		
Pelodiscus	0.448	0.290	0.387	0.310	0.307	0.333	0.543	0.669	0.666	0.611	0.374	0.573	0.366	0.407	0.407	0.416	0.229	
Pogona	0.545	0.503	0.534	0.500	0.534	0.507	0.590	0.656	0.620	0.616	0.513	0.557	0.513	0.535	0.500	0.434	0.527	0.480

Table S2 . Matrix from the p-distance in the MEGA package³ for the complete Lysozyme protein between each pair from the 19 species considered here.

References

1. Xiao, X. *et al.* Using cellular automata to generate image representation for biological sequences. *Amino Acids* **28**, 29–35, DOI: <https://doi.org/10.1007/s00726-004-0154-9> (2005).
2. Ghosh, S. & Chaudhuri, P. P. Cellular automata model for proteomics and its application in cancer immunotherapy. In *Cellular Automata.*, 3–15, DOI: https://doi.org/10.1007/978-3-319-99813-8_1 (Springer International Publishing, Cham, 2018).
3. Tamura, K., Stecher, G. & Kumar, S. MEGA11: Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* **38**, 3022–3027, DOI: <https://doi.org/10.1093/molbev/msab120> (2021).