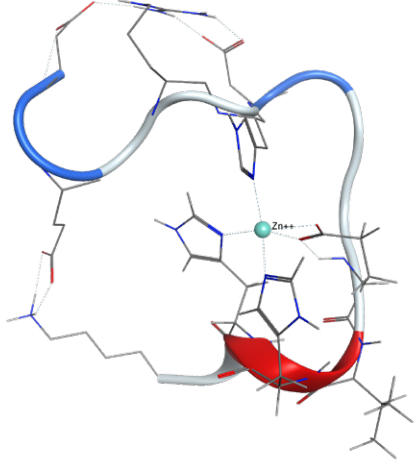
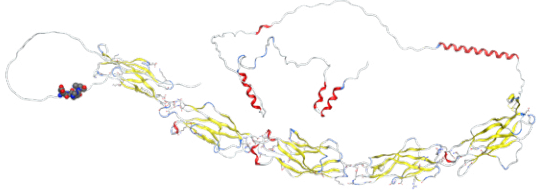
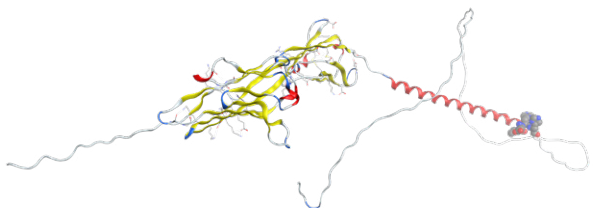
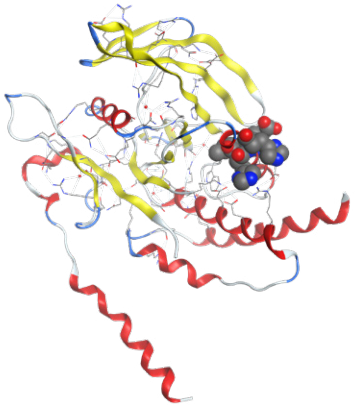
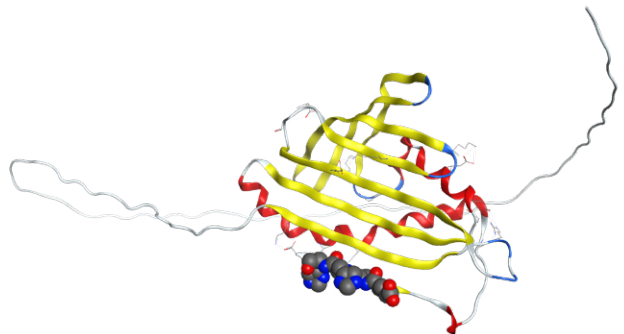
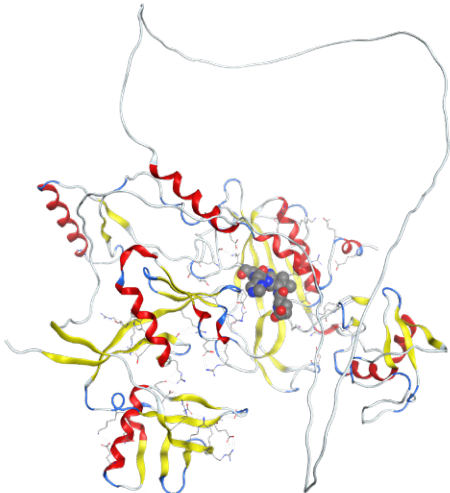
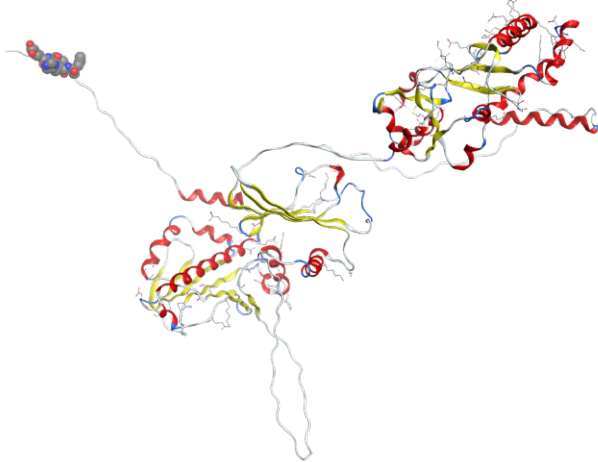
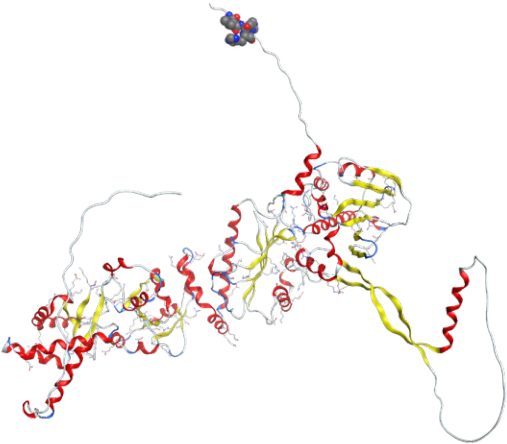
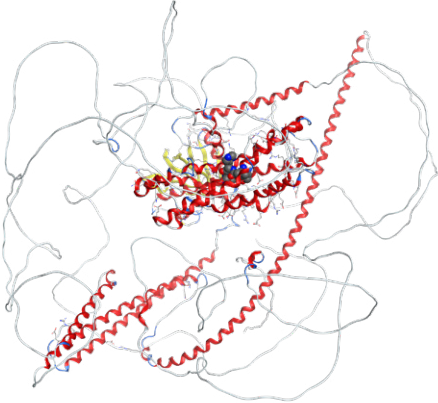


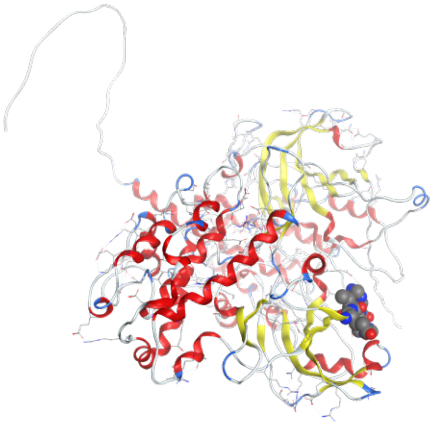
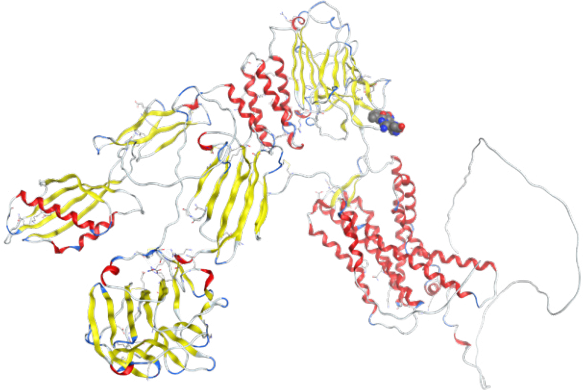
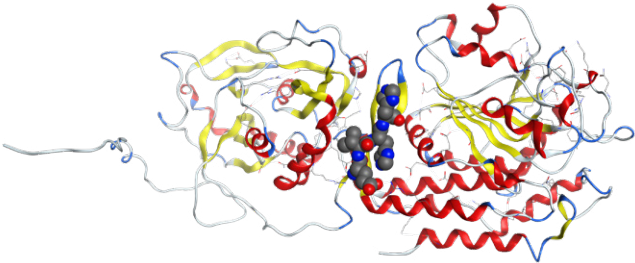
Table S1. Conservativity of the EVHH fragment in human proteins. The entries are listed in descending order of conservativity all isoforms containing the EVHH fragment

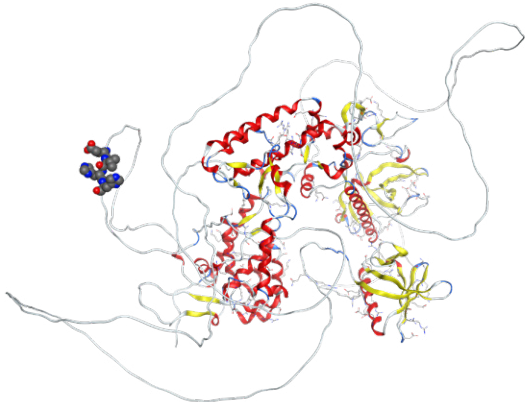
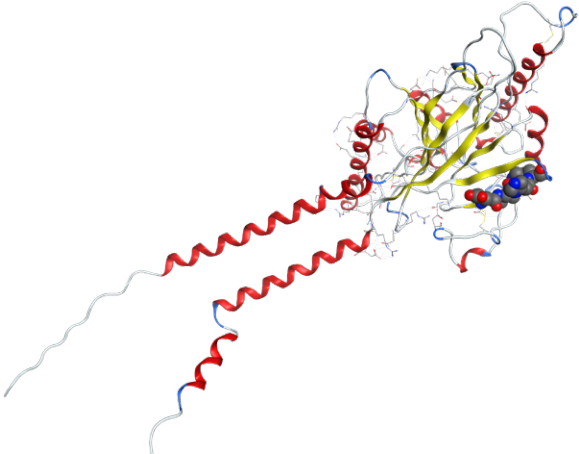
N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
1	885/985 (89.8%)	P05067 P05067-3 P05067-4 P05067-5 P05067-6 P05067-7 P05067-8 P05067-9 P05067-10 P05067-11	Amyloid-beta precursor protein	682-685	1ZE9: Zn ²⁺ binding domain	YEVHHQ	 1ZE9 - with Zn ²⁺
2	683/800 (85.4%)	Q13634 Q13634-2	Cadherin-18	46-49	AF-Q13634-F1: EVHH site is part of propeptide 25-53, in the structure of the AF model it is located in a disordered loop, on the protein surface	TEVHHR	
3	667/930 (71.7%)	P78310 P78310-2 P78310-6 P78310-7	Coxsackievirus and adenovirus receptor	272-275	AF-P78310-F1: EVHH site is located in the α-helix, on the protein surface	KEVHHH	

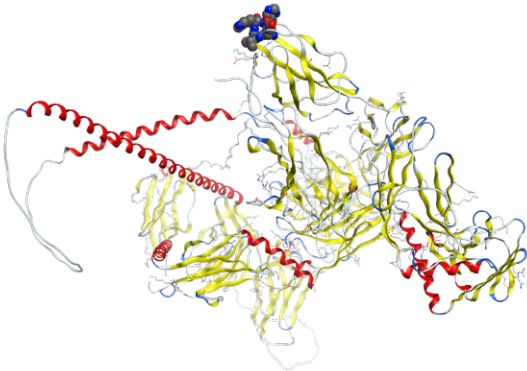
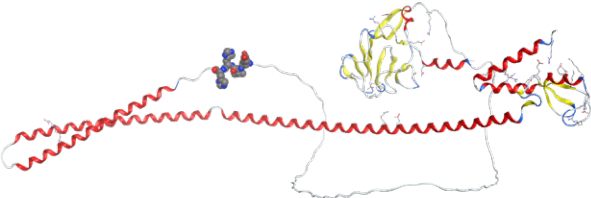
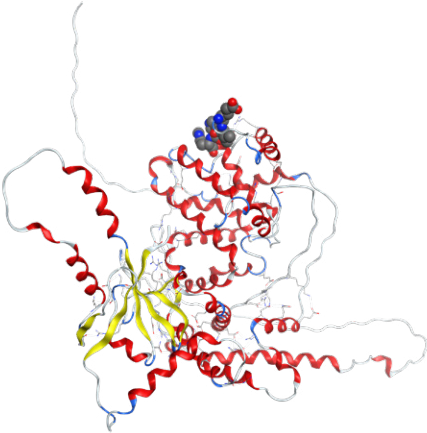
N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
4	437/995 (43.9%)	Q06124 Q06124-1 Q06124-3	Tyrosine-protein phosphatase non-receptor type 11	441-444	3b7o: Tyrosine-protein phosphatase domain, EVHH site is part of α -helix, on the protein surface	EEVHHK	
5	405/950 (42.6%)	Q9H8M1 Q9H8M1-2	Coenzyme Q-binding protein COQ10 homolog B, mitochondrial	234-237	AF-Q9H8M1-F1: EVHH site is a part of β -strand, on the protein surface	HEVHHT	

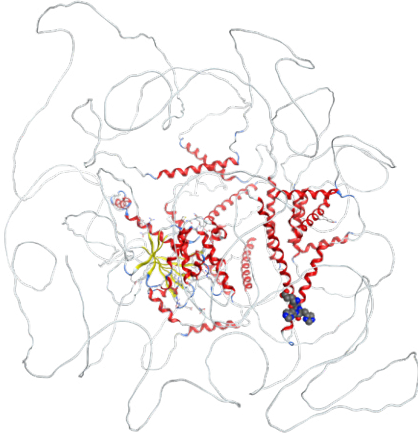
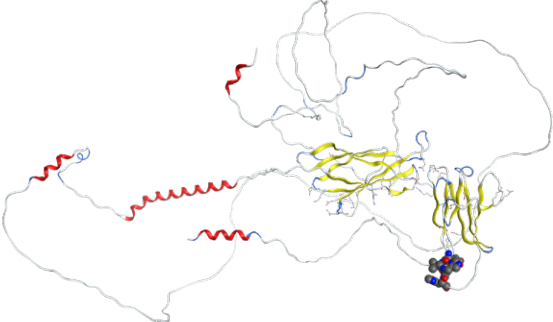
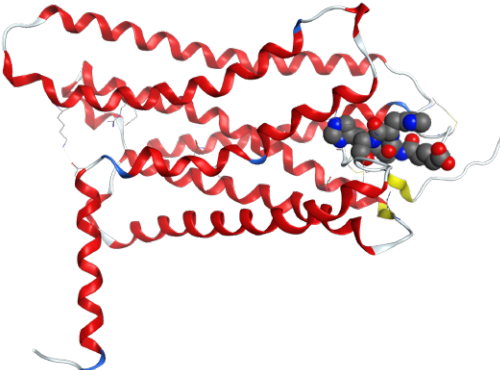
N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
6	276/965 (28.6%)	Q9Y2E6 Q9Y2E6-2	E3 ubiquitin-protein ligase DTX4	575-578	AF-Q9Y2E6-F1: EVHH site is located in disordered loop in extended conformation, on the protein surface	NEVHHK	
7	168/779 (21.6%)	Q03001-11	Dystonin	101-104	No AlphaFold structure	VEVHHQ	No AlphaFold structure
8	154/844 (18.2%)	Q58FF7	Putative heat shock protein HSP 90-beta-3	4-7	AF-Q58FF7-F1: EVHH site is a part of the N-terminal disordered region in extended conformation, on the protein surface	EEVHHG	

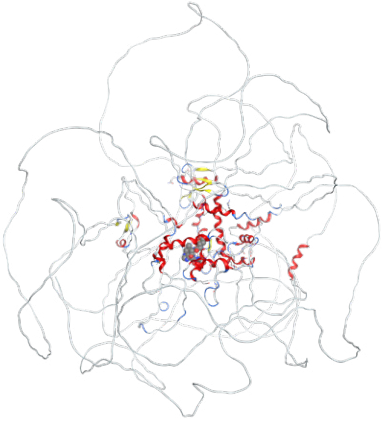
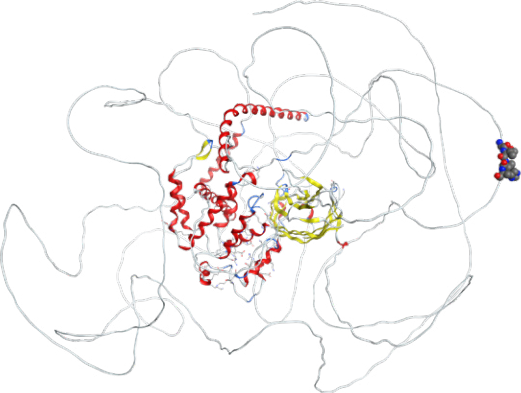
N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
9	133/859 (15.5%)	P08238	Heat shock protein HSP 90-beta	4-7	3nmq, 1uym: absent, AF-P08238-F1: EVHH site is a part of the N-terminal disordered region in extended conformation, on the protein surface	EEVHHG	
10	134/990 (13.5%)	Q6ZSZ5 Q6ZSZ5-1 Q6ZSZ5-2 Q6ZSZ5-5 Q6ZSZ5-6	Rho guanine nucleotide exchange factor 18	459-462	AF-Q6ZSZ5-F1: EVHH site is a part of α-helix inside protein globule	TEVHHV	

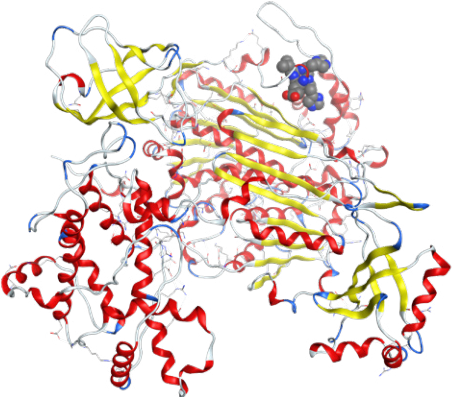
N	Con- serva- tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
11	105/1000 (10.5%)	O75676 O75676-2	Ribosomal protein S6 kinase alpha-4	471-474	AF-O75676-F1: EVHH site is a part of β -strand on the protein surface	HEVHHH	
12	100/991 (10.1%)	Q86SQ4 Q86SQ4-2 Q86SQ4-3 Q86SQ4-4	Adhesion G-protein coupled receptor G6	797-800	AF-Q86SQ4-F1: EVHH site is located in the loop of β -stranded GAIN B domain (PRU00098) which mediates interaction with laminin-2, on the protein surface	QEVHHHP	
13	81/872 (9.6%)	Q7Z3D6 Q7Z3D6-2 Q7Z3D6-3 Q7Z3D6-4 Q7Z3D6-5	D-glutamate cyclase, mito- chondrial	273-276	AF-Q7Z3D6-F1: EVHH site is a part of β -strand on the protein surface	PEVHHI	

N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
14	47/522 (9.0%)	Q9Y4G2	Pleckstrin homology domain-containing family M member 1	233-236	AF-Q9Y4G2-F1: EVHH site is a part of disordered region in extended conformation, on the protein surface	IEVHHS	
15	87/974 (8.9%)	Q53F39 Q53F39-2 Q53F39-3 Q53F39-4	Metallo-phosphoesterase 1	309-312	AF-Q53F39-F1: EVHH site is a part of β-strand on the protein surface	CEVHHG	

N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
16	60/1000 (6.0%)	P54296	Myomesin-2	751-754	AF-P54296-F1: EVHH site is a β -hair-pin turn of fibronectin type-III 4 domain, on the protein surface	REVHHK	
17	48/959 (5.0%)	O76064 O76064-3	E3 ubiquitin-protein ligase RNF8	229-232	AF-O76064-F: EVHH site is a part of disordered region in extended conformation, on the protein surface	TEVHHE	
18	48/1000 (4.8%)	Q5TG30	Rho GTPase-activating protein 40	392-395	AF-Q5TG30-F1: EVHH site is located in the loop after α -helix of Rho-GAP domain, on the surface	DEVHHN	

N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
19	43/998 (4.3%)	Q2M3C7 Q2M3C7-2	A-kinase anchor protein SPHKAP	682-685	AF-Q2M3C7-F1: EVHH site is a part of α -helix, surrounded by unstructured loops	DEVHHK	
20	25/960 (2.7%)	P10912 P10912-2 P10912-3 P10912-4	Growth hormone receptor	71-74	1axi: absent AF-P10912-F1: EVHH site is located in disordered loop, on the protein surface	DEVVHG	
21	26/999 (2.6%)	Q8NH48	Olfactory receptor 5B3	171-174	AF-Q8NH48-F1: EVHH site is located in the loop connecting two α -helices on the protein surface.	NEVHHF	

N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
22	4/262 (1.5%)	Q9H0D2 Q9H0D2-2	Zinc finger pro- tein 541	218-221	AF-Q9H0D2-F1: EVHH site is a part of α-helix of C2H2-type 3 domain, on the protein surface	YEVHHG	
23	9/949 (0.9%)	Q5VT97 Q5VT97-2	Rho GTPase- activating protein SYDE2	567-570	AF-Q5VT97-F1: EVHH site is a part of disordered region in extended conformation, on the protein surface	REVHHT	

N	Con-serva-tivity	Uniprot IDs	Protein name	Position in sequence	Structure ID, location	Sequence context	Position in structure
24	4/998 (0.4%)	P41226	Ubiquitin-like modifier-activating enzyme 7	283-286	8se9: EVHH site is a part of α -helix, on the protein surface	Q <u>E</u> VHHA	

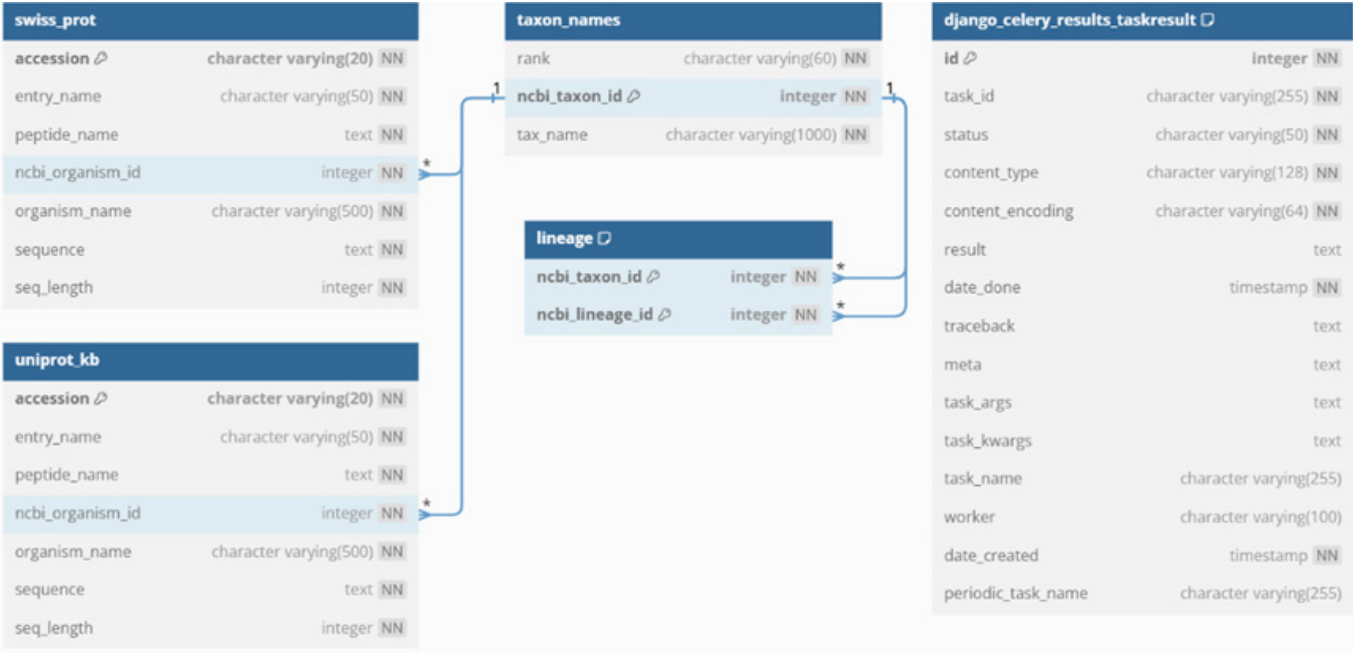


Fig. S1. PepString database structure (made by <https://dbdiagram.io/d>)