

Supplementary Table S5. Physicochemical Properties, secondary structure, and solubility analysis of final vaccine construct as predicted by ProtParam tool, PSIPRED, and SOLpro server.

Parameters	Vaccine Construction Sequence		
Number of amino acids	207		
Molecular weight	23.68 KDa		
Theoretical pI	9.46		
Total number of negatively charged residues (Asp + Glu)	13		
Total number of positively charged residues (Arg + Lys)	22		
Instability index	12.73 (Stable)		
Aliphatic index	108.50		
Grand average of hydropathicity (GRAVY)	0.502		
The estimated half-life	30 hours (mammalian reticulocytes, in vitro). >20 hours (yeast, in vivo) >10 hours (Escherichia coli, in vivo).		
Extinction coefficients	23840		
Amino acid composition	Ala (A)	27	13.0%
	Arg (R)	2	1.0%
	Asn (N)	8	3.9%
	Asp (D)	6	2.9%
	Cys (C)	0	0.0%
	Gln (Q)	2	1.0%
	Glu (E)	7	3.4%
	Gly (G)	12	5.8%

	His (H)	2	1.0%
	Ile (I)	24	11.6%
	Leu (L)	17	8.2%
	Lys (K)	20	9.7%
	Met (M)	9	4.3%
	Phe (F)	14	6.8%
	Pro (P)	10	4.8%
	Ser (S)	0	0.0%
	Thr (T)	18	8.7%
	Trp (W)	0	0.0%
	Tyr (Y)	16	7.7%
	Val (V)	13	6.3%
	Pyl (O)	0	0.0%
	Sec (U)	0	0.0%
Atomic composition	Carbon	C	1098
	Hydrogen	H	1709
	Nitrogen	N	247
	Oxygen	O	278
	Sulfur	S	9
Secondary structure analysis	Alpha helix (Hh)	53.14%	
	Extended strand (Ee)	25.12%	
	Random coil (Cc)	21.73%	
Solubility (SOLpro Server)	SOLUBLE with probability 0.994267		