	Construct 1	Construct 2
	Alpha helix: 22.46%	Alpha helix: 23.92%
Secondary structure	Extended strand: 26.84%	Extended strand: 26.16%
	Random coil: 50.7%	Random coil: 49.91%
Domochondron nlot	Favored regions: 81.2%	Favored regions: 4.2%
Kamachanuran piot	Disallowed regions: 82.2%	Disallowed regions: 1.6%
QMEAN scores	0.74	0.74
ERRAT Overall Quality Factor	86.5731	89.4212
VERIFY 3D averaged 3D-1D score of >= 0.1	73.84%	73.84%

Appendix 1. The quality scores for predicted secondary and tertiary structures of the Construct 1

and construct 2.

Appendix 2. Physicochemical properties of the Construct 1 and construct 2.

	Construct 1	Construct 2
Molecular weight	62246.31 Da	63524.67 Da
Pi	9.07	8.97
Extinction coefficient	77615 M ⁻¹ cm ⁻¹	77615 M ⁻¹ cm ⁻¹
	mammalian reticulocytes, in vitro: 30 hours	mammalian reticulocytes, in vitro: 30 hours
Estimated half-life	yeast, in vivo: >20 hours	yeast, in vivo: >20 hours
	Escherichia coli, in vivo: >10 hours	Escherichia coli, in vivo: >10 hours
Instability index	39.33 meaning as a stable protein	38.65 meaning as a stable protein

Appendix 3. Docking results and binding affinity assessment of the Construct 1 and construct 2.

	Construct 1 and EphA2	Construct 2 and EphA2
HADDOCK score	914.6 +/- 47.0	926.1 +/- 47.1
Prodigy binding affinity	ΔG : -19.1 kcal/mol	ΔG : -20.9 kcal/mol
	Kd: 9.2e-15M	Kd: 4.6e-16M

Appendix 4. allergencity and antigenicity results of the Construct 1 and construct 2.

	Construct 1	Construct 2
Allergencity	-1.29	-1.32
antigenicity	probable antigen	probable antigens



Appendix 5. The energy plot of predicting mRNA structures of the Construct 1 (a) and construct 2 (b).