

atum.bio

Bispecifics & Fc fusion Developability Analytics

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in silico Predictions



		<i>in silico</i> Analysis				
	Protein Name	Mol. Wt. (MW)	Isoelectric point (PI)	N-Glycans*	GRAVY – Hydrophobicity*	Number of Cysteines
4 chain bslgG1	bsAb 1 - pool	145671	6.48	[299], [295], N/A	-0.45, -0.49, -0.56	27
	bsAb1 - clone	145671	6.48	[299], [295], N/A	-0.45, -0.49, -0.56	27
3 chain bslgG4	bsAb 2- pool	146942	7.99	N/A, [312], [302], N/A	-0.27, -0.53, -0.39, -0.44	34
	bsAb 2 - clone	146942	7.99	N/A, [312], [302], N/A	-0.27, -0.53, -0.39, -0.44	34
Fc fusion	Fc fusion	102476	7.2	[148,170,316]	-0.53	29

*Heavy chain, Light chain (H,L)

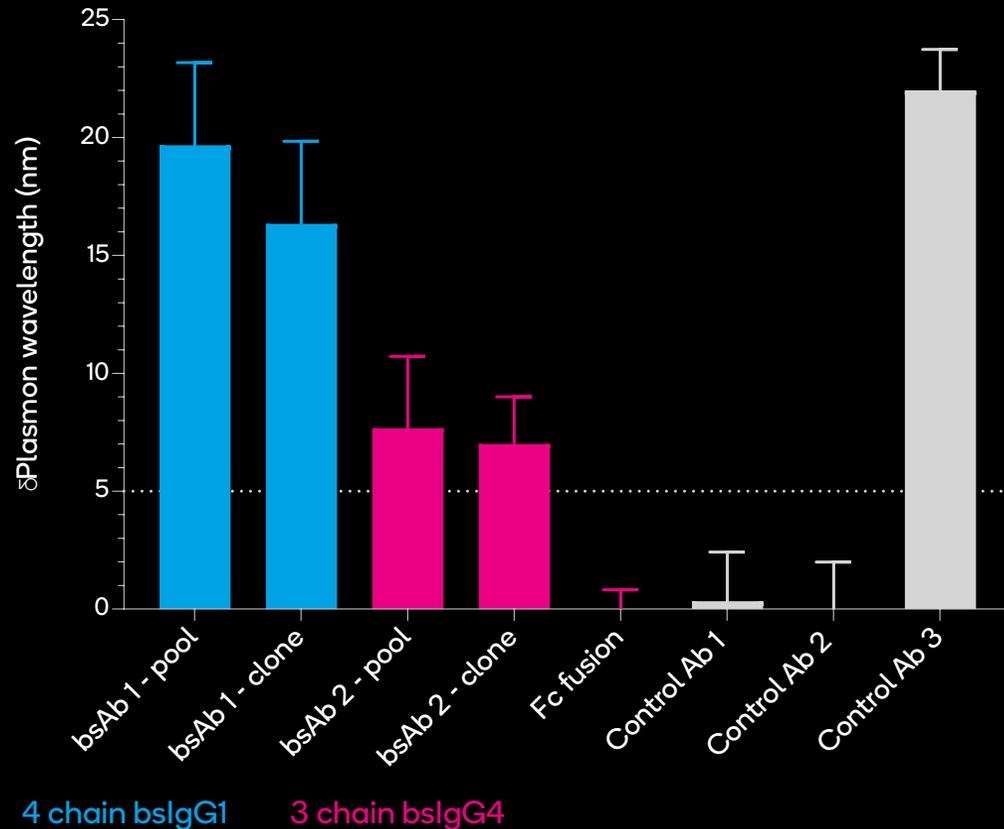
N-Glycans - N-X-S/T motif (X is any amino acid except proline)

Positive GRAVY values indicate hydrophobic, negative values indicate hydrophilic

Cysteines - Could be a potential issue to folding and cause aggregation

Aggregation Propensity: AC-SINS

(Affinity Capture - Self Interaction Nanoparticle Spectroscopy)

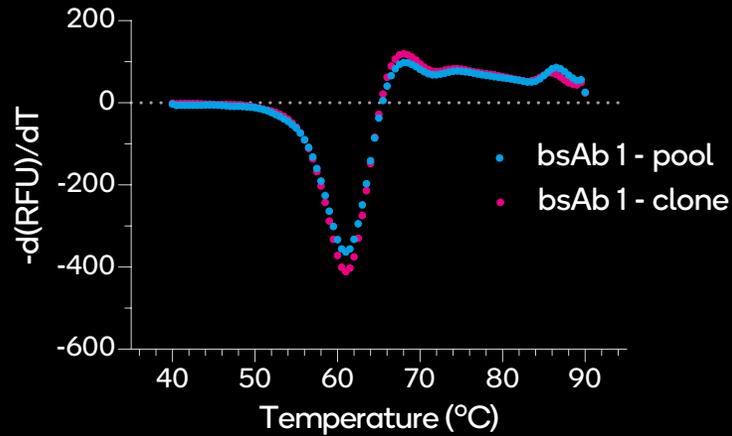


mAb	Protein Name	δ Plasmon wavelength (nm)	Standard Deviation
4 chain bsIgG1	bsAb 1 - pool	20	3.51
	bsAb 1 - clone	16	3.51
3 chain bsIgG4	bsAb 2 - pool	8	3.06
	bsAb 1 - clone	7	2.00
Fc fusion	Fc fusion	0	1.15

Higher signal = Higher aggregation

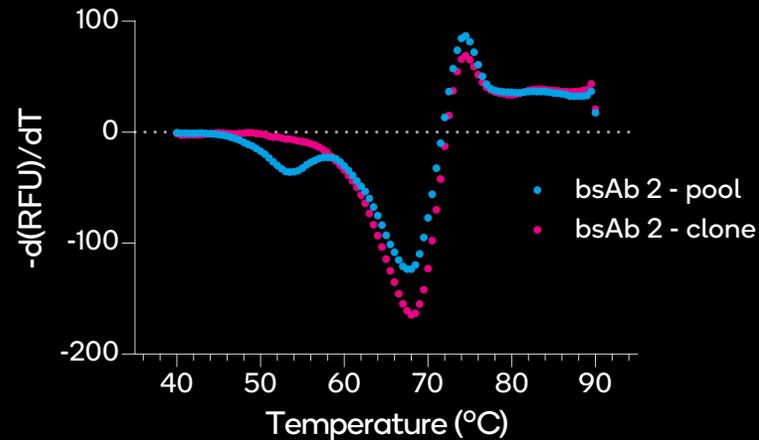
Thermo Stability: Tm

4 chain bsIgG1



Protein Name	Tm (°C)
bsAb 1 - pool	61.0
bsAb 1 - clone	61.0

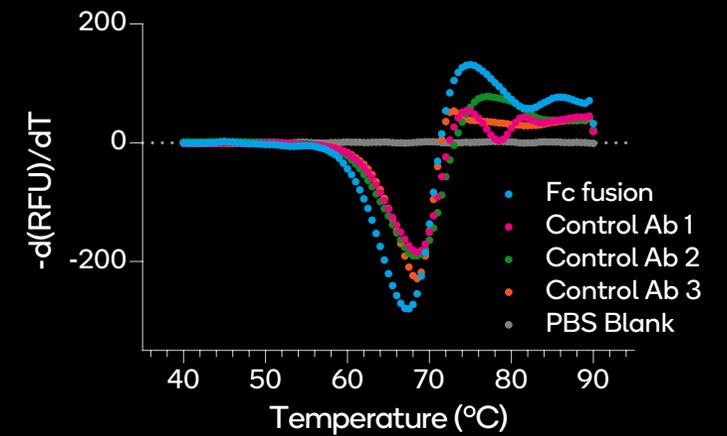
3 chain bsIgG4



Protein Name	Tm (°C)
bsAb 2 - pool	53.5 ; 68*
bsAb 2 - clone	68.0

*The protein undergoes multiple unfolding, resulting in more than one Tm value.

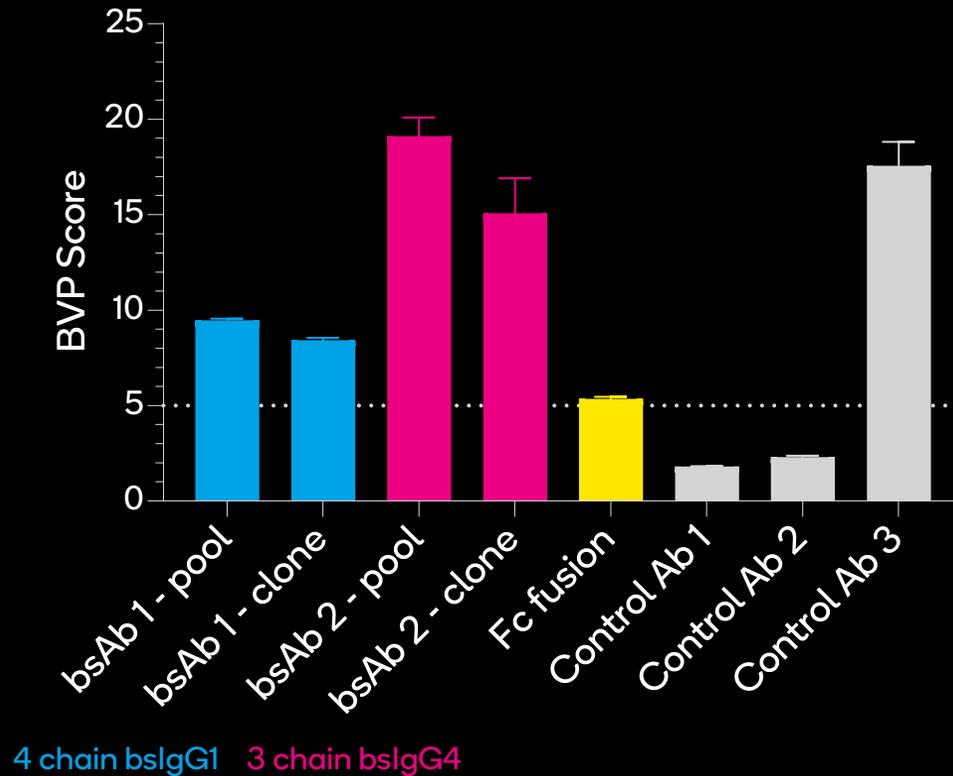
Fc fusion



Protein Name	Tm (°C)
Fc fusion	67.5
Control Ab 1	68.5
Control Ab 2	68.0
Control Ab 3	68.5

Polyspecificity: BVP-ELISA

(BaculoViral Particle – ELISA)



	Protein Name	BVP Score	Standard Deviation
4 chain bsIgG1	bsAb 1 - pool	9.47	0.082
	bsAb 1 - clone	8.43	0.109
3 chain bsIgG4	bsAb 2 - pool	19.11	0.982
	bsAb 2 - clone	15.08	1.826
Fc fusion	Fc fusion	5.36	0.104

Higher BVP score = Poorer *in vivo* PK