

## Engineering a Pure and Stable Heterodimeric IgA for the Development of Multispecific Therapeutics

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# Advances in IgG protein engineering have fueled rapid development and expansion of multispecific antibody formats and their applications



Bispecific IgG antibodies have been developed with broad application for cancer immunotherapy and the treatment of other diseases More than 30 mature commercial technology platforms have been used to develop bispecific antibodies



#### Target combinations of bispecific antibodies:



Making a Meaningful Difference

# IgG is not the only antibody isotype that can be leveraged for therapeutic design





Engineering a bispecific Fc can grant therapeutic tractability to new antibody isotypes by enabling multispecific design



### Recent work has highlighted the potential of IgA as a neutrophilengaging cancer therapeutic



 Antibody-driven mechanisms of cytotoxicity



• Differential Fc receptor engagement







Trogocytosis

Adapted from Avtenyuk et al, Int J Mol Sci, 2020

Brandsma et al, Front Immunol, 2019

Chan et al, Front Immunol, 2022

#### Making a Meaningful Difference



# Engineering for developability: Zymeworks' previous success engineering an IgG heterodimeric Fc

### Azymetric™

The foundation to how we build and design multi-functional and unique antibodies

Azymetric<sup>™</sup> is an IgG heterodimeric antibody technology developed using proprietary internal tools



Developability concepts and parameters for **purity and stability** introduced early in the engineering process



Use knowledge and tools used to develop IgG Azymetric<sup>™</sup> to build an **IgA heterodimeric Fc platform** 

### Rational design strategy used for IgA Fc interface engineering





### Crystal structure of homodimeric (wild-type) IgA Fc used for indepth analysis of IgA CH3-CH3 interface





PDB ID:10W0; from Herr et al, Nature, 2003

- Interface analysis to predict the energetic contribution of amino acid residues at the interface and the non-bonded contacts in the structure
- 2. Identify core interface positions (hot spots) where introduction of mutation is predicted to increase or decrease the strength of the interface
- 3. Mutations were introduced and modelled computationally



IgA Fc interface contact analysis

- Carbon-carbon contacts

### In silico tools employed to inform heterodimeric IgA Fc design



3. In silico design

Models of homodimeric and heterodimeric IgA CH3:CH3 variants were scored for affinity based on analysis of:

- Knowledge-based potential: probabilities of interactions between atoms based on known protein structures
- **Physics-based potential:** . energetic contribution of residue interactions across the interface

Variants were predominately selected based on affinity metrics



Top designs were selected based on the largest energetic difference between homodimer and heterodimer

**Negative designs** 

 Thresholds on stability metrics and clashes were used to further narrow down the search

**Positive designs** ("rescuing" heterodimerization)

Predicted affinity based on **Knowledge-Based Potential** 



### Example *in silico* models of steric vs electrostatic heterodimeric IgA **zymeworks** Fc designs





### Experimental *in vitro* evaluation of IgA heterodimeric Fc designs





## IgA Fc variants containing electrostatic design mutations did not have any detectable protein expression



Wildtype IgA CH3:CH3 interface



- All electrostatic designs included the replacement of the R372-R418 pi-pi interaction in the CH3:CH3 interface with a salt bridge.
- Mutations had the potential to skew the energetics of the CH3 interface to favour heterodimerization, but also carried significant risk of destabilization of the protein.

Design	Chain A Mutations	Chain B Mutations		
Electrostatic 1	T366D_L370D_ <b>R372D</b> _I416E	T366R_L370R		
Electrostatic 2	T366E_L370E_ <b>R372D_</b> I416D_ <b>R418E</b>	T366R_L370K		
Electrostatic 3	T366E_ <b>R372D_</b> I416D_ <b>R418D</b>	T366R_L370K_I416R		
Electrostatic 4	T366E_ <b>R372D_</b> I416E_ <b>R418E</b>	T366K_L370K_ <b>R372K</b> _I416R		
Electrostatic 5	R372D_E403D_I416D_R418E	L370K_ <b>R372K</b> _E403R_ I416K		
Electrostatic 6	R372D_E403D_I416D_R418E	L370K <b>_R372K_</b> I416K		

## High heterodimeric IgA Fc purity measured by CE-SDS and analytical SEC after affinity purification for steric 6 design







### Heterodimeric IgA Fc engineered for thermal stability and high purity



Thermal stability of purified heterodimeric IgA Fc designs assessed by differential scanning calorimetry



Summary of purity and stability for IgA Fc design

	Post affinity purification			Post prepSEC purification			
Design	HPLC-SEC OAA purity (%)	CE-SDS OAA purity (%)	,	HPLC-SEC OAA purity (%)		OAA yield (mg/L culture)	lgA CH3 Tm (°C)**
Wild-type	52	49	324	91	92	76	74.2
Steric 2	65	55	240	97	96	76	55
Steric 3	91	89	328	100	98	136	65.9
Steric 6 *	96	92	320	100	97	100	71.9
Steric 10 *	72	88	370	100	85	82	72
Steric 11 *	74	95	440	100	93	71	73.6

\*Lead designs

A crystal structure of the heterodimeric IgA Fc revealed that the IgA CH3 mutations do not perturb the overall IgA Fc structure and a heterodimeric IgA interface consistent with *in silico models* 

Chain A mutations



Heterodimeric IgA Fc (steric 6 design)



- Heterodimeric IgA Fc (steric 6) crystal structure was solved in complex with *Staphylococcus aureus* protein SSL7 (PDB ID: 7TTZ)
- A412F, T414Y L396V, W398T, I416L

Chain B mutations

• Heterodimeric IgA Fc (blue/green) superimposed with wildtype IgA Fc (grey) have RMSD of 0.94 Å across  $C_{\alpha}$  atoms in the Fc



Wildtype IgA Fc (PDB ID: 2QEJ)



In silico model

The RMSD of the heterodimeric IgA Fc CH3 crystal structure relative to the *in silico* model was 1.2 Å across  $C_{\alpha}$ atoms (residues 345-450)



### Heterodimeric IgA Fc designs show preserved binding to Fc $\alpha$ RI by SPR





**Kinetic value** ka (1/Ms) 2.76E+05 IgA OAA WT 20 Wild-type IgA 교 1 kd (1/s) 3.07E-03 Fc KD (M) 1.11E-08 200 300 ka (1/Ms) 6.46E+05 IaA OAA Steric 6 Heterodimeric 교 10 kd (1/s) 1.48E-02 IgA Fc steric 6 KD (M) 2.28E-08 200 300 400 30 ka (1/Ms) 1.08E+05 IgA OAA FcαRI-KO 1x 20 . IgA FcαRI-KO 22 2.96E-02 kd (1/s) 1x 2.73E-07 KD (M) 100 200 300 400 ka (1/Ms) IgA FcαRI-KO No binding kd (1/s) NA 2x KD (M)

Increasing the density of Fc $\alpha$ RI resulted in higher avidity-driven binding for wild-type and heterodimeric IgA Fc variants



### **Applications of heterodimeric IgA Fc**









### Dimeric IgA specifically disables intracellular mutated oncodrivers



Figure from Prince and Hollmen, Immunity Previews, 2023 Biswas *et al*, Immunity, 2023 Biswas *et al*, Nature, 2021



### **Applications of heterodimeric IgA Fc**







### **Summary**







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Zymeworks team members (past and present)

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Photo from CBRE



### Thank you