



INTRODUCTION

Inhibiting interleukin-4 receptor alpha (IL-4Rα) with targeted antibodies is major mechanism for alleviating Type II immune responses underlying atopic dermatitis (AD) and asthma [1-5]. Dupilumab is a first-generation IL-4Rα antibody inhibitor that binds to IL-4Rα to block its interaction with IL-4 and IL-13/IL-13Rα1 [1]. Despite much clinical success with dupilumab in the treatment of AD and asthma, many patients fail to respond, experience incomplete response, suffer waning efficacy over time or experience adverse effects such as conjunctivitis and arthralgias [6]. This raises the question, "What is it about dupilumab's molecular function that limits its clinical efficacy and potentially contributes to adverse events?" To answer this question, we performed a detailed molecular analysis of dupilumab compared to a new, second-generation IL-4Rα blocker, rademikibart.

Rademikibart (formally, CBP-201) is an optimized next-generation human monoclonal antibody targeting IL-4Rα. Compared to dupilumab, rademikibart demonstrated better inhibition of STAT6 intracellular signaling, provided similar potency in prohibiting both IL-4-induced TARC release and IL-4-induced B cell activation and has more than 2-fold higher binding affinity to IL-4Rα compared to dupilumab (20.7 pM vs 45.8 pM, respectively) [7]. Phase 3 clinical trials demonstrated that ~48% of dupilumab-treated patients achieve EASI-75 at Week 16 [8], in contrast to ~63% for rademikibart [9].

Here, we determined the 2.71Å x-ray crystal structure of rademikibart Fab bound to IL-4Rα and compared it to the complex of dupilumab Fab and IL-4Rα. Molecular dynamics simulations of rademikibart Fab and dupilumab Fab bound to IL-4Rα demonstrated the third interface loop (loop L5, residues 148 to 152) of IL-4Rα interacts directly with rademikibart, which is absent in the dupilumab/IL-4Rα complex. This finding is confirmed by analysis of the hydrogen bond interactions at the interface between the antibodies and IL-4Rα, demonstrating superior binding energy for rademikibart. Our data provides a molecular and structural rationale for the enhanced IL-4Rα inhibition by rademikibart over dupilumab [10-11], which corresponds to rademikibart's optimized epitope on IL-4Rα that overlaps more closely with the natural IL-4 epitope.



Alignment of IL-13-IL-4Rα complex and IL-4-IL-4Rα complex (**B**). Importantly, both IL-4 and IL-13 engage three major loops (L) on domains 1 (D1) and 2 (D2) of IL-4Rα.

RADEMIKIBART BINDING INTERFACE WITH IL-4R α CONTAINS MORE HYDROGEN BONDS THAN THE DUPILUMAB-IL-4R α COMPLEX



Figure 3. Comparison of the aligned (via IL-4Rα) dupilumab and rademikibart complexes with IL-4Rα. There is a 59.17° rotation of rademikibart on IL-4Rα compared to dupilumab (A). H bond interactions at the binding interface of dupilumab Fab and IL-4Rα at equilibrium (B). Note how dupilumab does not engage IL-4Rα D2. Close-up views of dupilumab and rademikibart complexes with IL-4Rα showing that the interacting residues at L5 loop of IL-4Rα (D150 and Y152, highlighted in red) are unique to rademikibart and provide enhanced antibody-antigen stability (**C**, **D**).



• IL-4 and IL-13 use a conserved structural mechanism to bind IL-4R α , which spans both domains 1 and 2 of IL-4R α . • Dupilumab binds to IL-4Rα through only domain 1, the consequence being it incompletely engages the natural IL-4/IL-13 epitope on IL-4Rα. • Molecular dynamics studies revealed that the binding interface between dupilumab Fab and IL-4Rα is highly mobile and weaker than that of rademikibart. • The x-ray crystal structure of rademikibart Fab-IL-4Rα complex revealed an ~60 degree rotation of rademikibart on IL-4Rα compared to dupilumab, optimizing its interference with the natural IL-4/IL-13 epitope. • Molecular dynamics studies showed rademikibart forms a very strong and stable interaction with IL-4Rα, confirmed structurally by lower B-factors (less motion) and more hydrogen bonds (stronger binding) than dupilumab. • Rademikibart is a next-generation, optimized antibody inhibitor of IL-4Rα with 2-fold stronger binding affinity than dupilumab and clinically significant and durable EASI-75 responses over 52 weeks of treatment.

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DISCLOSURES

CGB has served as investigator or consultant for AbbVie, Apogee, Connect BioPharma, Eli Lilly, Incyte, LEO Pharma, Pfizer, and Sanofi-Regeneron RC is an employee of Connect Biopharma. Other authors report no conflicts.

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Optimized Second-Generation IL-4Ra Inhibition: Structural and Molecular Dynamics Properties of Rademikibart Fab-IL-4Ra Complex Yuanjun Shi¹, Minh Ho², Haote Li¹, Raúl Collazo³, and Christopher G. Bunick^{2,4}

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Figure 2. Superposition of rademikibart-Fab crystal structure complexed with IL-4Rα at **2.71** Å resolution and the equilibrated structure of the same complex derived from MD simulations (A). Multiple H bond interactions comprise the binding interface of rademikibart-Fab and IL-4R α at equilibrium (**B**).

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STABLE COMPLEX THAN DUPILUMAB



Α	EASI-75 over 52 weeks of treatment (NRI-MI)	B	Pr
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	Week Rademikibart Q2W (n=219) Placebo (n=111) Rademikibart Q2W/Q2W (n=91) Rademikibart Q2W/Q4W (n=91)		