

CORRECTION

# Correction: Dramatic and concerted conformational changes enable rhodocetin to block $\alpha 2\beta 1$ integrin selectively

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The supplementary figures were incorrectly allocated and labelled:

- [S1 Fig](#) was mistakenly labelled and described as [S5 Fig](#)
- [S2 Fig](#) was mistakenly labelled and described as [S1 Fig](#)
- [S3 Fig](#) was mistakenly labelled and described as [S2 Fig](#)
- [S4 Fig](#) was mistakenly labelled and described as [S3 Fig](#)
- [S5 Fig](#) was mistakenly labelled and described as [S4 Fig](#)

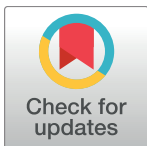
The authors have provided the correctly labelled supplementary figures. The legends remain the same.

## Supporting information

**S1 Fig. Asymmetric unit of the RC $\gamma\delta$ - $\alpha 2A$  crystal structure.** (A) Overall view of the asymmetric unit showing six RC $\gamma\delta$ - $\alpha 2A$  complexes. Individual  $\alpha 2A$  domains are shown in grey, with the Mn<sup>2+</sup> as pink spheres. RC $\gamma$  subunits are shown in red, whereas RC $\delta$  subunits are in yellow. (B) The different heterotrimeric assemblies can be subcategorized in three different interaction modi. Domain-domain contacts are mediated either via the core segment of the CLRP fold of RC $\gamma$  (top), the distal end of the  $\alpha 2A$  domain (middle) or the index finger loop segments (bottom). Remarkably, the overall r.m.s.d. in C $\alpha$  positions for all individual subdomains is 1.1Å demonstrating that the different RC $\gamma\delta$ - $\alpha 2A$  complexes are identical. (JPG)

**S2 Fig. Molecular model of the disulfide-locked conformation mutants of  $\alpha 2A$  domain.** By introducing disulfide bridges at the respective sites, helices 1 and 7 were fixed towards each other. Using this approach, the  $\alpha 2A$  domain is stabilized in either the “open” or “closed” conformation. (A) Model of K168C-E318C representing the open conformation. (B) Model of K168C-A325C showing the conformation. Residues involved in the formation of helix C are in red. To highlight the difference between the two conformations, amino acid residue positions 318 and 325 are coloured blue and green, respectively. Structures were modeled with Pymol using the pdb data sets of  $\alpha 2A$  domain in its “open” (1DZI) and “closed” (1AOX) conformation. (JPG)

**S3 Fig. Identification of the IIIG5 epitope within the RC $\gamma$  chain.** (A) Fragmentation scheme for the tryptic fragment of the RC $\gamma$  subunit containing the IIIG5 epitope. (B) NanoESI



## OPEN ACCESS

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fragment ion spectrum of the RC $\gamma$  peptide containing the IIIG5 epitope. It was obtained from a CID experiment on the ion mobility-separated doubly charged peptide precursor ions at m/z 942.40. The labelled peaks correspond to the fragmentation ions of this epitope peptide, as shown in (A).

(JPG)

**S4 Fig. Alignment of integrin  $\alpha$ 2A domains from different species.** Sequence comparison of the integrin  $\alpha$ 2 A-domain from different vertebrate species. The loop 2 sequence S214QYGGD is highlighted in yellow and shows a high degree of homology between different species. Multiple sequence alignment was carried out with Clustal Omega Software from EMBL-EBI.

(JPG)

**S5 Fig. Alignment of A-domain of different human integrin  $\alpha$ -chains.** A comparison of A-domains from different human integrin  $\alpha$  subunits. Integrin alpha subunits 1, 2, 10, and 11 belong to the subset of collagen binding integrins. They possess the characteristic helix C (yellow box, labelled  $\alpha$ -C), which is absent in the A-domain of the leukocyte  $\beta$ 2 integrins with their alpha subunits L, X, M, and D. Helix C of the integrin  $\alpha$ 2 subunit is the primary binding site for RC $\gamma\delta$  and is only present in the “closed” conformation of its A domain. The secondary RC contact site of  $\alpha$ 2A is located within the loop 2 sequence S214QYGGD, (yellow box, labelled loop 2) and is specific to the integrin  $\alpha$ 2 chain. The secondary structure elements are indicated by the red ( $\alpha$ -helices) and the blue ( $\beta$ -strands) boxes, respectively. The residue numbering refers to the integrin  $\alpha$ 2 sequence. Multiple sequence alignment was carried out with Clustal Omega Software from EMBL-EBI.

(JPG)

## Reference

1. Eble JA, McDougall M, Orriss GL, Niland S, Johanningmeier B, Pohlentz G, et al. (2017) Dramatic and concerted conformational changes enable rhodocetin to block  $\alpha$ 2 $\beta$ 1 integrin selectively. *PLOS Biology* 15(7): e2001492. <https://doi.org/10.1371/journal.pbio.2001492>. <https://doi.org/10.1371/journal.pbio.2001492> PMID: 28704364