

**Different genome-wide transcriptome responses of *Nocardioides simplex* VKM Ac-2033D to phytosterol and cortisone-21-acetate**

Victoria Yu. Shtratnikova<sup>1</sup>, Mikhail I. Schelkunov<sup>2,3</sup>, Victoria V. Fokina<sup>4,5</sup>, Eugeny Y. Bragin<sup>4</sup>, Andrei A. Shutov<sup>4,5</sup>, Marina V. Donova<sup>4,5</sup>.

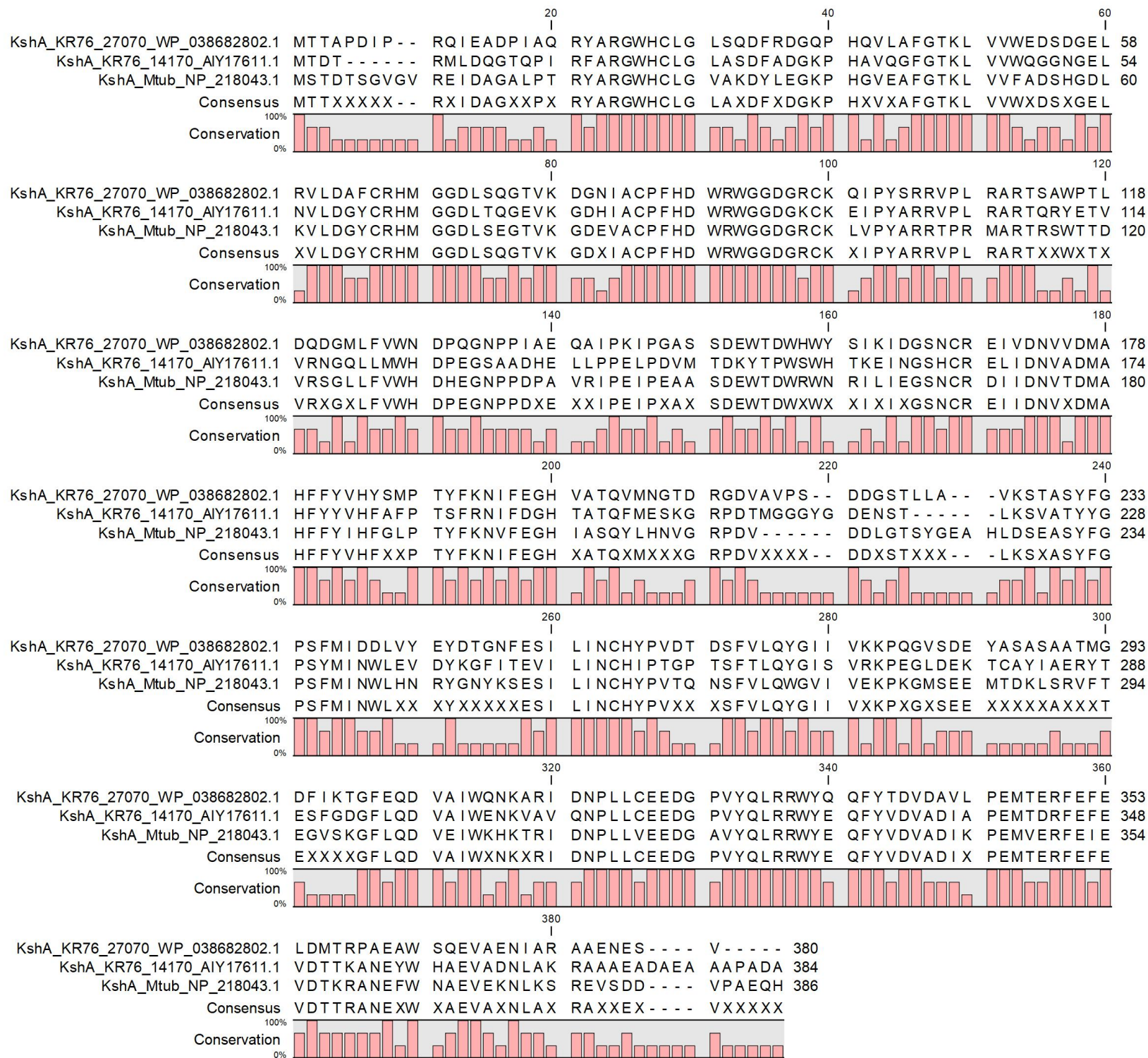
<sup>1</sup>Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Leninskie gory, h. 1, b. 40, Moscow, Russian Federation, 119991

<sup>2</sup>Skolkovo Institute of Science and Technology, Nobelya str., 3, Moscow, Russian Federation, 121205

<sup>3</sup>Institute for Information Transmission Problems, Russian Academy of Sciences, Bolshoy Karetny per., h. 19, b. 1, Moscow, Russian Federation, 127994

<sup>4</sup>G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms, Federal Research Center “Pushchino Center for Biological Research of the Russian Academy of Sciences”, pr. Nauki, 5, Pushchino, Moscow Region, Russian Federation, 142290

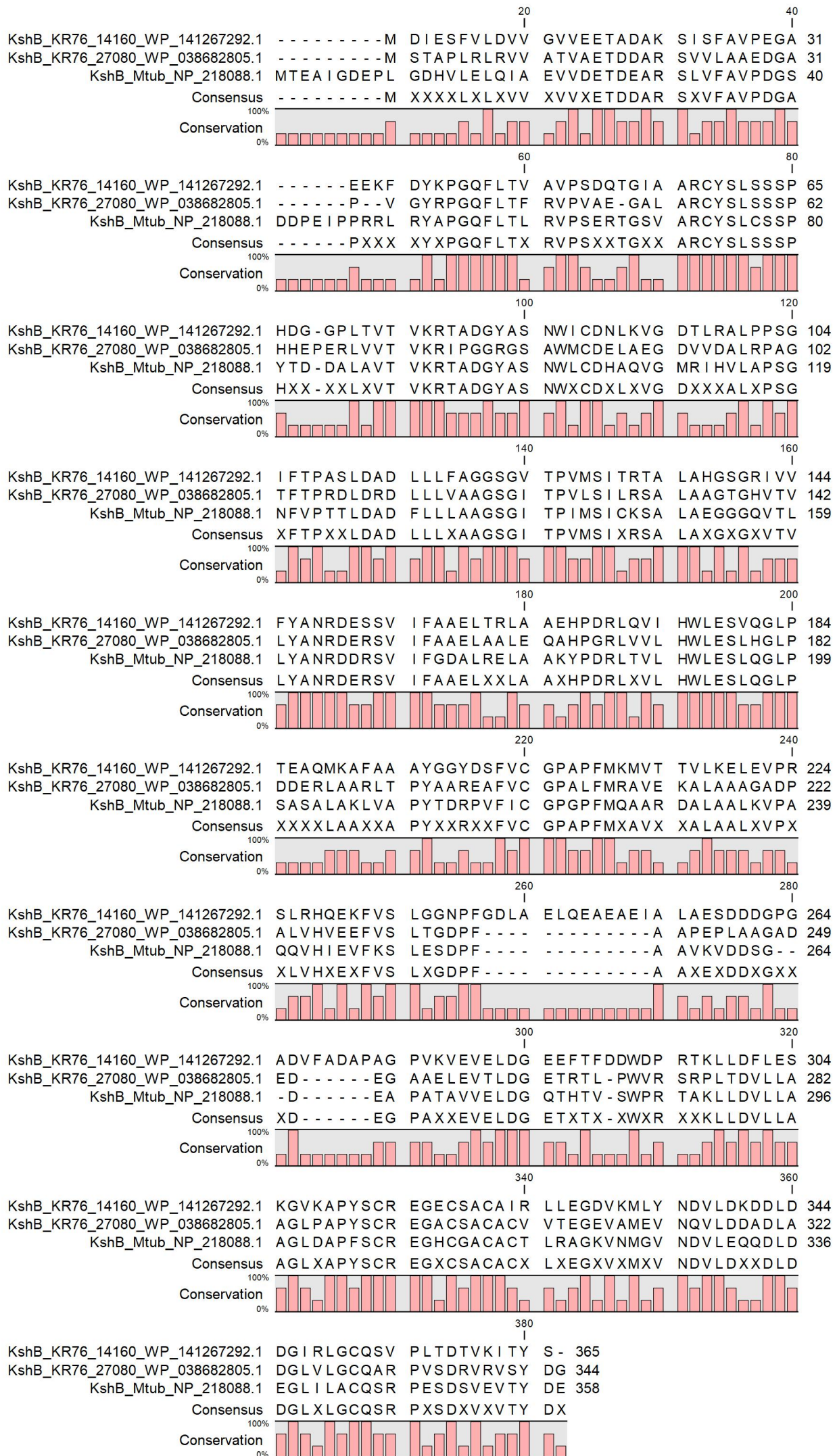
<sup>5</sup>Pharmins, Ltd., R&D, Institutskaya str., 4, Pushchino, Moscow Region, Russian Federation, 142290



### **Supplementary Figure S1. KshA alignment**

KshA from *M. tuberculosis* consists of conservative Rieske domain (amino acid residues 24-153), where C67 and C86 are responsible for one Fe<sup>2+</sup> ion binding, and H69 and H89 — for another [71]. The catalytic domain (amino acid residues 154-374) contains conserved amino acid residues V176, D178, H181, H186, Q204, Y232, M238, N240, N257, F301, D304 and W308. In *KR76\_27070* of *N. simplex*, N240 is replaced with D240 in this protein.

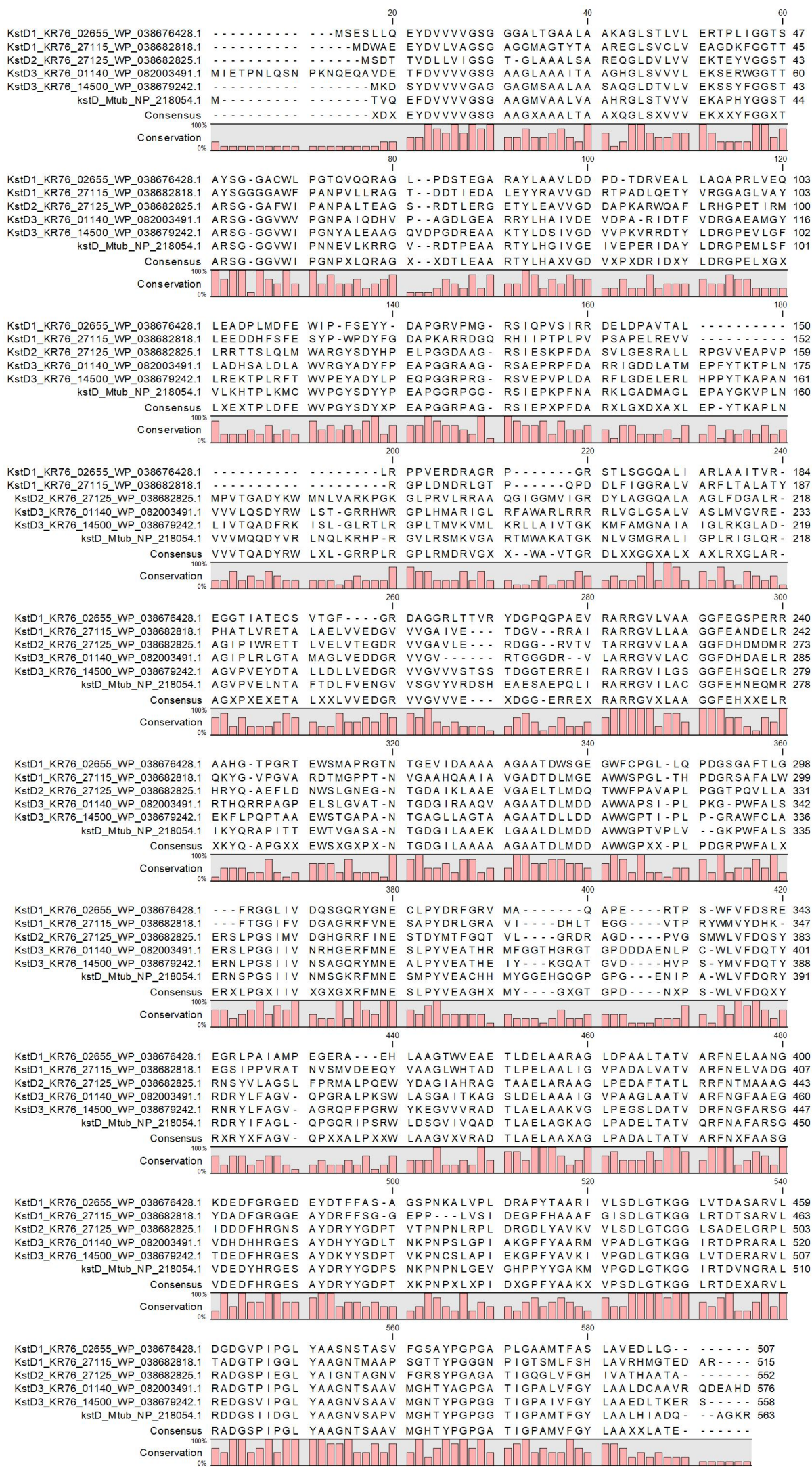




## Supplementary Figure S2. KshB alignment

There are three domains in KshB containing a number of conservative amino acid residues, namely, a flavin binding domain RxYSL (72-76 in product of Rv3571 *M. tuberculosis*), a NAD binding domain GGIGITP or AGSGITP (135-141 in product of Rv3571 *M. tuberculosis*), and a 2Fe2S-cluster binding domain C<sub>x4</sub>C<sub>x2</sub>C<sub>x29</sub>C (305-344 in product of Rv3571 *M. tuberculosis*) [85]. All three domains were also found in ortholog of KshB in *N. simplex* with two





### Supplementary Figure S3. KstD alignment

The important residues of KstD2 from *R. erythropolis* SQ1 [86] are the following: FAD-binding domain (12-35 in product of Rv3537 of *M. tuberculosis*), consensus GSG(A/G)(A/G)(A/G)X<sub>17</sub>E; Ser325 (318A in product of Rv3537 of *M. tuberculosis* or T in other actinomycetal KSTD enzymes, i.e., small residue at this position); and Thr503 (497 in product of Rv3537 of *M. tuberculosis*). KR76\_27125 of *N. simplex* contains Ala in position corresponding to 318A in *M. tuberculosis* and 325S in *R. erythropolis*; but FAD-binding domain is different from consensus: GSGT-GX<sub>17</sub>E.