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Supporting information for article:

New structural forms of a mycobacterial adenylyl cyclase Rv1625c

Deivanayaga Barathy, Rohini Mattoo, Sandhya Visweswariah and Kaza Suguna



Figure S1 (a) Gel filtration analysis of Rv1625c-F363R shows the presence of dimer (~60 kDa). (b) Crystals of Rv1625c-F363R obtained after optimization.



Figure S2 (a) The proximity of $\beta 3' - \alpha 3'$ loop region of the symmetry-related molecule (green) to the $\beta 7 - \beta 8$ loop and $\alpha 4$ helix of Rv1625c-F363R (blue) is shown. (b) The residues forming salt bridge and H-bonds between Rv1625c-F363R and its symmetry-related molecule are shown in sticks.



Figure S3 Interactions at the new interface of Rv1625c-Wt domain swapped dimer. Each monomer is coloured differently in orange (chain B) and green (chain A). The interacting residues along with suphate ion are shown in sticks.

Rv1625cWt monomer	GAGRLYSAFDALVAQHG-LEKIKV <mark>S</mark> GDSYMVVSGVPRPRPDHTQALADFAL
1cjk_a_chain	TLNELFARFDKLAAENH-CLRIKILGDCYYCVSGLPEARADHAHCCVEMGM
1cjk_b_chain	LLNEIIADFDDLLSKPKFSGVEKIKT <mark>IG</mark> STYMAATGLSAIR-QYMHIGTMVEFAY
2W01	VLNIYFGKMADVITHHG-GTIDEFMGDGILVLFGAPTSQQDDALRAVACGV
ЗЕТ6	LLDELYQRFDAAIEEYPQLYKVETIGDAYMVVCNVTVPCDDHADVLLEFAL
3R5G	LLNNYLNEMSKIALKYG-GTIDKFVGDCVMVFFGDPSTQGAKKDAVAAVSMGI
3UVJa_chain	MLNALYTRFDQQCGELD-VYKVETIGDAYCVAGGLHKESDTHAVQIALMAL
3UVJB_chain	LLNDLYTRFDTLTD-SRKNPFVYKVETVCDKYMTVSGLPEPCIHHARSICHLAL
1WC0	LLNEYLGEMTRAVFENQ-GTVDKF <mark>V</mark> GDAIMALYGAPEEMSPSEQVRRAIATAR
1YBT	LLDNHDTIVCHEIQRFG-GREVNTAGDGFVATFTSPSAAIACAD
1Y10	LAGRLAGLARDLTAPP-VWFIKTIGDAVMLVCPDPAPLLDTVL
1FX2	AVAAHHRMVRSLIGRYK-CYEVKTVGDSFMIASKSPFAAVQLAQ

Figure S4 Structure-based sequence alignment of Rv1625c-Wt with different AC and GC catalytic domains. The dimer interface of Rv1625c-Wt has a serine substituted in place of the hydrophobic residues found in other cyclases (highlighted in red).



Figure S5 Gel-filtration studies on monomeric and dimeric fractions of Rv1625c-Wt