|  |
| --- |
| a |
| *(a*) Fe-s cluster domain(N-terminal) DNA binding (C-terminal) 3 17 18 60KS WhiB1 ------------------MDWRSKAACLDEDPELFFPIGNT-GPA-IEQIEKAKKVCARCEVTETCLQWAIETGQDAGVWGGLSEDERRALKRRNA--RARRAS--- 82KS WhiB2 ----VHELQIVGHPEQAVPSWQERALCAQTDPEAFFPEKGG-S------TREAKRVCTGCDVRSECLDYALENDERFGIWGGLSERERRKLKRRAV--FTA------ 88KS WhiB3 ----MDSTARQPGPVADLWDWQFEGLCRTTDPEEFFHPEGERGSARRLRDERAKRVCQRCPVILECREHALAAKEPYGVWGGLSEDEREQELARRS---RRGLRGA- 99KS WhiB7 ----MLALADHQTLIDQARVAGRPLPCLENDPDTWFADTPT-G------VEYAKSLCHACPVRTLCLEGALERREPWGVWGGELIEAGRVLPRKRPRGRPRKHPIAA 96 3 17 18 60Mtb whiB1 ------------------MDWRHKAVCRDEDPELFFPVGNS-GPA-LAQIADAKLVCNRCPVTTECLSWALNTGQDSGVWGGMSEDERRALKRRNA--RTKARTGV- 93Mtb whiB2 LVPEAPAPFEEPLPPEATDQWQDRALCAQTDPEAFFPEKGG-S------TREAKKICMGCEVRHECLEYALAHDERFGIWGGLSERERRRLKRGII----------- 89Mtb whiB3 ----MPQPEQLPGPNADIWNWQLQGLCRGMDSSMFFHPDGERGRARTQREQRAKEMCRRCPVIEACRSHALEVGEPYGVWGGLSESERDLLLKGTM-GRTRGIRRTA 103Mtb whiB7 -------VSVLTVPRQTPRQRLPVLPCHVGDPDLWFADTPA-G------LEVAKTLCVSCPIRRQCLAAALQRAEPWGVWGGEIFDQGSIVSHKRPRGRPRKDAVA- 92 \* \* . :\* . \*\* :\* \* : \* \*: : \*:\*\*\* Variable region functional region |
| b |
|  *(* ND1Mtb SigA ------------------------------------------------------------------------------------------------------ 102 KS SigA VTPPTSEKSAETPTVSEPVTAVLGKQLLDKPGLIEFVERAVDNGKVATDKVQQAIEGASLTPTQAQRLLKNLRSQGVEVHFDQETAARLAQEQRGVKPRASR 0 ND1 Mtb SigA VAAT-----KASTATDEPVKRTATKSPAASASGAK-TGAKRTAAKSASGSPP-AKR—-ATKPAARSVKPASAPQDTTTSTIPKRKTRAAAKSAAAKAPSARG 203 KS SigA SRTTRSTTAKTATAKSTTAKSTATKSTTAKSTAAKSTTAKSTAAKSTAAKSTTAKSTTAKSTAAKSTTAASGTSAKGT-ASTTRKATTAAKGTAAKSTTAKG 93  :\* \*::\*\*.. .\* \*\*\*\*\* :\*.::.\*\* \* \*\* \*\*\*\*\*::.. \*\* \*.. \*\*:\*.. \*\*. . . \* : .\*\*: :\*\*\*.:\*\*\*: :\*:\*ND1Mtb SigA HATKPRAPKDAQHEAATDPEDALDSVEELDAEPDLDVEPGEDLDLDAADLNLDDLEDDVAPDADDDLDSGDDEDHEDLEAEAAVAPGQTADDDEEIAEPTEK 270 KS SigA RTAAKGTTKSAAE---TNARNA------AADAPELDEIAAEDEAEERAA-----------------LA-GK—-D------TVELVAGETSQAAPQKAESTEE 195  ::: : \*.\* . \*: .:\* \*:\*\* .\*\* : \* \* \*. \* . :. \*:\*:: : \*\* \*\*: ND1Mtb SigA DKASGDFVWDEDESEALRQARKDAELTASADSVRAYLKQIGKVALLNAEEEVELAKRIEAGLYATQLMTELSERGEKLPAAQRRDMMWICRDGDRAKNHLLE 367 KS SigA ESESRGFVLRADDEDDA-PAQQVVTAGATADAVKDYLKQIGKVALLNAEQEVDLAKRIEAGLFAEQRL----NSGDKIDAKLKRELWWVASDGKNAKNHLLE 297  :. \* .\*\* \*:.: \*:: . \*:\*\*:\*: \*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*:\*\*\*\*\*\*\*\*\*:\* \* : : \*:\*: \* :\*:: \*:. \*\*..\*\*\*\*\*\*\* ND1 ND2Mtb SigA ANLRLVVSLAKRYTGRGMAFLDLIQEGNLGLIRAVEKFDYTKGYKFSTYATWWIRQAITRAMADQARTIRIPVHMVEVINKLGRIQRELLQDLGREPTPEEL 469 KS SigA ANLRLVVSLAKRYTGRGMLFLDLIQEGNLGLIRAVEKFDYTKGYKFSTYATWWIRQAITRAMADQARTIRIPVHMVEVINKLARVQRQMLQDLGREPTPEEL 399  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*.\*:\*\*::\*\*\*\*\*\*\*\*\*\*\*\*\* ND2 LD CD Mtb SigA AKEMDITPEKVLEIQQYAREPISLDQTIGDEGDSQLGDFIEDSEAVVAVDAVSFTLLQDQLQSVLDTLSEREAGVVRLRFGLTDGQPRTLDEIGQVYGVTRE 571 KS SigA AKELDMTPEKVVEVQKYGREPISLHTPLGEDGDSEFGDLIEDSEAVVPSDAVSFTLLQEQLHSVLDTLSEREAGVVSMRFGLADGQPKTLDEIGRVYGVTRE 501  \*\*\*:\*:\*\*\*\*\*:\*:\*:\*.\*\*\*\*\*\*. :\*::\*\*\*::\*\*:\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*:\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\* :\*\*\*\*:\*\*\*\*:\*\*\*\*\*\*:\*\*\*\*\*\*\* CDMtb SigA RIRQIESKTMSKLRHPSRSQVLRDYLD 598 KS SigA RIRQIESKTMSKLRHPSRSQVLRDYLD 528  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* |
| c |
| KS SigB VIHDDFPARTHGASHAVPD----Q-ALVRRRLTAAHALPEQHRQQELIDVIADHIPFARR 55Mtb SigF -----MTARAAGGSASRANEYADVPEMFRELVGLPAGSPEFQR--HRDKIVQRCLPLADH 53 : \*\*: \*.\* : : :.\*. : . \*\* :\* . .:: :\*:\* :KS SigB LGRRFAPTPSLVDDCEQVACMALVLAVQRWDPAFDANLSSYAQPTILGELRRFLRDSTWW 115Mtb SigF IARRFEGRGEPRDDLIQVARVGLVNAAVRFDVKTGSDFVSFAVPTIMGEVRRHFRDNSWS 113 :.\*\*\* . \*\* \*\*\* :.\*\* \*. \*:\* .::: \*:\* \*\*\*:\*\*:\*\*.:\*\*.:\* KS SigB VRPPRRIQELAALVRSTEEELRHSTGREPTAQEVARAVGASPDEVSEARVAAAGRYVASV 175Mtb SigF VKVPRRLKELHLRLGTATADLSQRLGRAPSASELAAELGMDRAEVIEGLLAGSSYHTLSI 173 \*: \*\*\*::\*\* : :: :\* : \*\* \*:\*.\*:\* :\* . \*\* \*. :\*.:. :. \*:KS SigB DEEDPETG---RLVHL-----VHSPAVDEWVSLHPHIQALDPRDRCVLLRRYLEDETQAS 227Mtb SigF DSGGGSDDDARAITDTLGDVDAGLDQIENREVLRPLLEALPERERTVLVLRFFDSMTQTQ 233 \*. . . . :.. . ::: \*:\* ::\*\* \*:\* \*\*: \*:::. \*\*:.KS SigB IARALGISQAQVSRRLKRALDTLREQVPGGLSNA 261Mtb SigF IAERVGISQMHVSRLLAKSLARLRDQLE------ 261 \*\*. :\*\*\*\* :\*\*\* \* ::\* \*\*:\*:  |
| d |
| KS SigH MTPTTSEKPRSEVNSDPAEVDVATETPQERAARFEREALPHLDQLYSAALRTTRNPTDAE 60Mtb SigH MADIDGV-----TGSAGLQPGPSEETDEELTARFERDAIPLLDQLYGGALRMTRNPADAE 55 \*: . ..\* : . : \*\* :\* :\*\*\*\*\*:\*:\* \*\*\*\*\*..\*\*\* \*\*\*\*:\*\*\*KS SigH DLVQETYAKAYAAFHQYKPGTNLKAWMYRILTNTYINTYRKKQRQPLQSDAAEVEDYQLA 120Mtb SigH DLLQETMVKAYAGFRSFRHGTNLKAWLYRILTNTYINSYRKKQRQPAEYPTEQITDWQLA 115 \*\*:\*\*\* .\*\*\*\*.\*:.:: \*\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*\*\* : : :: \*:\*\*\*KS SigH AAESHTAKGLRSAETEALDHIADSQVTDALAQLSEEFRLAVYLADVEGFAYKEIAEIMDT 180Mtb SigH SNAEHSSTGLRSAEVEALEALPDTEIKEALQALPEEFRMAVYYADVEGFPYKEIAEIMDT 175 : .\*::.\*\*\*\*\*\*.\*\*\*: : \*:::.:\*\* \* \*\*\*\*:\*\*\* \*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*KS SigH PIGTVMSRLHRGRKQLRELLAEYGAERGFGRQSQGKEVSS- 220Mtb SigH PIGTVMSRLHRGRRQLRGLLADVARDRGFARGEQAHEGVSS 216 \*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\* \*\*\*: . :\*\*\*.\* .\*.:\* \*  |
| e |
| KS SigJ MEMSRVDLERFEVARGRLGAVAYRLLGSASEAEDVVQESFVRWQAADRGRIEVPVAWLTK 60Mtb SigJ -----MEVSEFEALRQHLMSVAYRLTGTVADAEDIVQEAWLRWDSPDT-VIADPRAWLTT 54 :::..\*\*. \* :\* :\*\*\*\*\* \*:.::\*\*\*:\*\*\*:::\*\*:: \* \* \* \*\*\*\*.KS SigJ VVTNLCLNQLTSARSRREEYVGQWLPEPLLDGDPMLGPAETLEQRGSVSLAMLMILETLS 120Mtb SigJ VVSRLGLDKLRSAAHRRETYTGTWLPEPVVTGLDATDPLAAVVAAEDARFAAMVVLERLR 114 \*\*:.\* \*::\* \*\* \*\*\* \*.\* \*\*\*\*\*:: \* .\* :: .. :\* :::\*\* \* KS SigJ PTERAVYVLREAFAVPHGEIAEILETTPAATQQALSRAKSRIASLSHRHRTEADPVAARA 180Mtb SigJ PDQRVAFVLHDGFAVPFAEVAEVLGTSEAAARQLASRARKAVTAQPALISGDPDPA-HNE 173 \* :\*..:\*\*::.\*\*\*\*..\*:\*\*:\* \*: \*\*::\* \*\*\*:. ::: : \*\*. . KS SigJ IVEEFLAAATSGRVENLVRLLTDDAFGIGDGGGAVPARPKPVLGAQSVAKMLRGLAVPSA 240Mtb SigJ VVGRLMAAMAAGDLDTVVSLLHPDVTFTGDSNGKAPTAVRAVRGSDKVVRFILGLVQRYG 233 :\* .::\*\* ::\* ::.:\* \*\* \*. \*\*..\* .\*: : \* \*::.\*.::: \*\*. .KS SigJ A------KRELAGGSLDCHFALVNTSPALVAVVAGRVVGVIVLDIADGRISVVRIQANPH 294Mtb SigJ PGLFGANQLALVNGELGAYTAGL---PGVDG-YRAMAPRITAITVRDGKVCALWDIANPD 289 : \*..\*.\*..: \* : \*.: . . . : .: : \*\*::..: \*\*\*.KS SigJ KLDRATR-RWAASPHGRPLLSGW 316Mtb SigJ KFTGSPLKERRAQPTGRGRHHRN 312 \*: : . \*.\* \*\*  |
| Supplementary fig 2: Alignment of Wbl and major sigma factor A,B, H and J proteins between *K. sedentarius* MBB13 (KS) and *M. tuberculosis* H37Rv (Mtb) amino acid sequences. (a) The conserved cysteines residues, unique G(I/V)WGG domain (tryptophan containing) and AT-hook (of Wbl7) of Wbl proteins are highlighted. The conserved residues, Trp3, Phe17, Phe18 and Trp60 of the [4Fe–4S] cluster binding pocket of WhiB1 are underlined. (b) The Sigma factor N-terminal 1 and 2, linker and C-terminal domains are indicated as ND1, ND2, LD and SD respectively. The conserved residues, His516 and Pro517 of Sigma factor ACTD are underlined (c, d and e) Sigma factors similarity B, H and J respectively. *Mycobacterium tuberculosis* H37Rv was obtained from [ncbi.nlm.nih.gov](file:///C%3A%5CUsers%5Cmahadlaq%5CDesktop%5C%D8%B1%D8%AF%20%D8%AC%D9%81%5Cncbi.nlm.nih.gov) (RefSeq NC\_000962.3). |