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RdpA MHAALSPLSQRFERIAVQPLTGVLGAEITGVDLREPLDDSTWNEILDAPH 50
TauD -----MSLTIQPISPALGAIIVSGIDLGLAPLDDTGQRAIEQALL 38
TfdA -----MSVVANPLHPLFAAGVEDIDLREALGSTEVREIERLMD 38
SdpA -----MQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWL 39

RdpA TYQVIYFPGQAITNEQHIAFSRRFGFVDPVPLLKSTIEGYPEVQMIRREAN 100
TauD EHQVLFRRDQSLEPRSQAARFAGDLHIHPYPSVPEQPEVIVLDTAVT 88
TfdA EKSVLVFRGQPLSQDQQTAFARNFGFLEGGFIKVNQRPSRFKYAELADIS 88
SdpA QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH 89
      ↑

RdpA ESGRV-----IGDDWHTDSTFLDAPPAAVVMRAIDVPEHG 135
TauD DVR-----DNAIWHTDVTFLETPALGAVLAQKQLPPYG 121
TfdA NVSLDGKVAQRDAREVVGNFANQLWHSDDSSFFQQPAARYSMLS AVVPPSG 138
SdpA SPAEWDMMKVIVG-----NMAWHADSTYMPVMAQGAVFSAEVVPAVG 132
      ↑      ↑      ↑

RdpA GDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRFRSNT 185
TauD GDTLWASSTAAYEALSAPLRRLDGLTATHDIGKSFP---RERFGVTEAD 168
TfdA GDTFCDMRAAYDALPRDLQSELEGLRAEHYALNSRF-----LLGD 179
SdpA GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS---KLGHVQQAG 178
      ↑

RdpA SVKVMVDVADGRET VHP LVVTHFGSGRKGLYVNQVYCQRIEGMTDAESKP 235
TauD LARLEEARLKNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDA 218
TfdA TDYSEAQRNAMPPVNWPLVRTHAGSGRKFLFIG-AHASHVEGLPVAEGRM 228
SdpA SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESES 227
      ↑

RdpA LLQFLYEHAATRFDFTCRVRWKKDQVLVWDNLCTMERAVPDYAGKFRYLTR 285
TauD LLKFLFAHATRPEFTVRWRWQENDVAFWDNRVTQHYAVDDYRPPQRRVMHR 268
TfdA LLAELLEHAATQREFVYRHRWNVGD LVWWDNRVCLHRGRYDISARRELRR 278
SdpA FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 277
      ↑      ↑      ↑

RdpA TTVGGVRPAR----- 295
TauD ATILGDKPF----- 277
TfdA ATTLD DAVV----- 287
SdpA SRLAGRPETEGAALV 292

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FIG. 2. Sequence alignment of RdpA and SdpA with other group II α KG-dependent dioxygenases. TfdA, *R. eutropha* 2,4-D/ α KG dioxygenase (accession no. A27082); TauD, *P. aeruginosa* taurine/ α KG dioxygenase (accession no. NP_252624). Conserved Fe(II)- and α KG-binding residues are shaded in black; other conserved regions are shaded in gray. Black arrows indicate 2,4-D binding residues in TfdA; gray arrows indicate residues undergoing posttranslational hydroxylation in TauD or TfdA. Amino acid positions numbers are shown to the right of each line. The alignment was created with CLUSTAL W.