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RdpA MHAALSPLSQRFERIAVQPLTGVLGAEITGVDLREPLDDSTWNEILDAFH 50
TauD ------------MSLTIQPISPALGAIVSGIDLGAPLDDTGQRAIEQALL 38
TfdA ------------MSVVANPLHPLFAAGVEDIDLREALGSTEVREIERLMD 38
SdpA ----------MQTTLQITPTGATLGATVTGVHLAT-LDDAGFAALHAAWL 39

RdpA TYQVIYFPGQAITNEQHIAFSRRFGPVDPVPLLKSIEGYPEVQMIRREAN 100
TauD EHQVLFFRDQSLEPRSQARFAARFGDLHIHPIYPSVPEQPEVIVLDTAVT 88
TfdA EKSVLVFRGQPLSQDQQIAFARNFGPLEGGFIKVNQRPSRFKYAELADIS 88
SdpA QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH 89

RdpA ESGRV----------------IGDDWHTDSTFLDAPPAAVVMRAIDVPEHG 135
TauD DVR-----------------DNAIWHTDVTFLETPALGAVLAAKQLPPYG 121
TfdA NVSLDGKVAQRDAREVVGNFANQLWHSDSSFQQPAARYSMLSAVVVPPSG 138
SdpA SPAEWDDMMKVIVG-------NMAWHADSTYMPVMAQGAVFSAEVVPAVG 132

RdpA GDTGFLSMYTAWETLSPTMQATIEGLNVVHSATRVFGSLYQAQNRRFSNT 185
TauD GDTLWASSTAAYEALSAPLRRLLDGLTATHDIGKSFP---RERFGVTEAD 168
TfdA GDTEFCDMRAAYDALPRDLQSELEGLRAEHYALNSRF---------LLGD 179
SdpA GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS----KLGHVQQAG 178

RdpA SVKVMDVDAGDRETVHPLVVTHPGSGRKGLYVNQVYCQRIEGMTDAESKP 235
TauD LARLEEARLKNPPRSHPVVRTHPVTGRKGLFVSDGFTTRINELEPAESDA 218
TfdA TDYSEAQRNAMPPVNWPLVRTHAGSGRKFLFIG-AHASHVEGLPVAEGRM 228
SdpA SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIG-RHAHAIPGMDAAESER 227

RdpA LLQFLYEHATRFDFTCRVRWKKDQVLVWDNLCTMHRAVPDYAGKFRYLTR 285
TauD LLKFLFAHATRPEFTVRWRWQENDVAFWDNRVTQHYAVDDYRPQRRVMHR 268
TfdA LLAELLEHATQREFVYRHRWNVGDLVMWDNRCVLHRGRRYDISARRELRR 278
SdpA FLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH 277

RdpA TTVGGVRPAR-----                                    295
TauD ATILGDKPF------                                    277
TfdA ATTLDDAVV------                                    287
SdpA SRLAGRPETEGAALV                                    292
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FIG. 2. Sequence alignment of RdpA and SdpA with other group II αKG-dependent dioxygenases. TfdA, *R. eutropha* 2,4-D/αKG dioxygenase (accession no. A27082); TauD, *P. aeruginosa* taurine/αKG dioxygenase (accession no. NP_252624). Conserved Fe(II)- and αKG-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.