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## FAD binding site

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                *           20           *           40           *           60           *           80           *           100           *
AtYUCCA2 : ME--EVTETLGRRIHDE-----YVEETRCIMYEGPIIIVGSGPSGLATAAACLKSRDTPSLILERSCTASLWQHKTYPDRLRHLHPKDFCELPMPFFSSYPYPTKQOFV : 102
AtYUCCA6 : MDFCKKREMEGKLAHD----HRGMTSPRRICVWPGPIVVGAGPSGLATAAACLKSRGITSVLLERSNCTASLWQLKTYDRLRHLHPKQFCLELPPIPFPCDFPTYPTKQOFI : 106
ToFZY2 : MDSYLK-ELQGKTSHDYFNHNNKMINRCVFNWGPVIVGAGPSGLAAACLTSKGVQSLVLRBNCIASLWQLKTYDRLRHLHPKQFCLELPMPFFPHDFPTYPTKQOFI : 109
VvYUCCA2 : MD--MLKEVEGKRVHDE--LGRKMSKSERRIIVGPIVIVGAGPSGLAVAAACLKERTISSLILERSNCTASLWNLKTYDRLRHLHPKDFCELPMPFFPDPFRYPTKHQFL : 106
VvYUCCA6 : MD--BLRELEGKRAHDEIFNDKAMSCGR--SLIILGPIVIVGAGPSGLATAAACLKRVSVILERSNRITASLWQLNTPYDRLRHLHPKQFCLELPMPFFBNDFPTYPTKQOFI : 106

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## NADPH binding site

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                120           *           140           *           160           *           180           *           200           *           220
AtYUCCA2 : QYLESYAEHFDLKRFVFNQTVEEAKEDRRCCGLWRVVRTGGKKDEITMSYVSRMLVVAATGENABEVMPEIDGIPDFGCP--IHTSSYKSGEIESEKKILVVVCGNSGMEVCL : 210
AtYUCCA6 : EYLEDYARRFDIKRBFNQTVESAAFDENLCMWRVTSVGE--EGTTPYVCRMLVVAATGENABPVVRFEGCWDKFAAAGVVKHTCHYKTCGDRAGKRVLVVCGNSGMEVCL : 214
ToFZY2 : KYLESYALTENIRDFNQTVVSACVDRNLGLWRIRTDIT--TSSTREVTREMLIVATGENABAVVDEDEGMEBEDCS--IHHTSLYKSGEIEPKRKKVVLVCGNSGMEVCL : 215
VvYUCCA2 : NYLBAYAKRFDIRBFNKTVVSABEDPRSRIWQVKTTRGFKKEEIVYQCWLIIVATGENABEVMPEIQGMNFAFCP--IHTSSYKSGDSYRGRKRVLVVCGNSGMEVCL : 214
VvYUCCA6 : EYLBAYABREDIQRENEFSVARABYDHTLEFWRVKTET-----TEYLCRMLVVAARGENABAVVPEIEGRKKEGCP--IVHTSSYKSGDVMYRGRKRVLVVCGNSGMEVCL : 208

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                *           240           *           260           *           280           *           300           *           320           *
AtYUCCA2 : DLCNPNAPESLAVRDSVHVLEPQEMLGRSTFGISTSLKWFPEVHVVDRELLRMSRLVLDGTDRLGLRPRPLGPLERKKIKCGKTPVLDVGTLAKIRSGHIKVVYBELKR-VMH : 319
AtYUCCA6 : DLCNFGAQPESLAVRDAVHVLPREMLGRSTFGLSMFLKMLPIRLVDRLLVSRFLLGDTTLUGLNRPALGPLELKNLSGKTPVLDVGTLAKIKTGDIKVCSSGIRR-LKR : 323
ToFZY2 : DLCNHHAPESLAVRDTVHVLPREMLGRSTFGLSMFLKMLPMLRVDRLELLITSRILLGDTSRILGLDRPEITGLELKNLSGKTPVLDVGTLAKIKSGDIKVCPSGIKRLKH : 325
VvYUCCA2 : DLCNHNAPESLAVRDSVHVLEPQEMLGRSTFGLSMFLKWFPEVRLVDQELLLVSRMLLDGTARIGLRPRPLGPLQLKSLSGKTPVLDVGTLAKIKTGNIKVGRIKQ-LSC : 323
VvYUCCA6 : DLCNHNAPESLAVRDSVHILPRQMLGRSTFGLSMFLKMLPMLRVLDHLLLVSRFMLGDTARIGLRPRPALGPLELKNLSGKTPVLDVGTLAKIKSGDIKICPPIRQ-LKC : 317

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                340           *           360           *           380           *           400           *           420
AtYUCCA2 : YSABEYVDCRVDFDAIILATGYKSNVPMWLKGVNMFSEKDGEPHKRFPNGWKGESGLYAVGFTKRLGLLGAATDAKKIABDIEVQRHFLPLARPOHC--- : 415
AtYUCCA6 : EYVEFDNGKTERFDAIILATGYKSNVPSWLKKNKMFSEKDGEPHQBFEPGWRGEGCLYAVGFTKRGLISGASMDAKRIABDIHKCKQDEQVKKI----- : 417
ToFZY2 : HTEVFVNGQTEBYDAIILATGYKSNVPSWLKKEKMFSEKDGELPKRFPNGWKGEGCLYAVGFTKRGLLIGASIDAKKIABDIIHQYEQ----- : 411
VvYUCCA2 : HTEVFVDCRVDFDAIILATGYKSNVPSWLKGVNMFSEKDGELPKRFPNGWKGEGCLYAVGFTKRGLLIGASLDARRIABEELSVHSWPFQHFHRDNDHL : 422
VvYUCCA6 : HAVVEYVDCRVDFDAIILATGYKSNVPSWLKERDLESEKDGELPKRFPNGWKGEGCLYAVGFTKRGLLIGASMDAKRIABDIEBRCWKADAKRLTVKSHT- : 415

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