

	XXXXXXXXDLXXXXXXXXDXFX-----XXXXXXXXEXXX--VXYXXX	Majority
	10 20 30 40 50	
1	PGLNGMDLAKVETTAEEYSWTQGSWTLTGGLPQAKKEDLFPFHVVAYDFG	CPS.pro
1	MKFAVLVFPGSNCDRDMFN-----AAIKSGVEAEY--VDYRET	SapurQ.PRO
1	-----MDLTLIIDNYDSF-----VYNIA	anthranilatesynthase.pro
	XXXXXXXXIXGLXXXGXXXXIXXXXXSXXXXXXXXXPDXXLXSGPGXPXXX-D	Majority
	60 70 80 90 100	
51	AKRNILRMLVDRGCRLTIVPAQTS AEDVLKMNPDGIFLSNGPGDPAPC-D	CPS.pro
37	SLSGFDGVLIPGGSFSGD-----YLRSGAMASVA---	SapurQ.PRO
19	---QIVGELG--SYPIVIRNDEISIKGIERIDPDRLIISP GPGTPEKRED	anthranilatesynthase.pro
	XXIXXXVXKXLXXXXPVLGVCLGHQXL---GLAXGAKXXXXXXXXXFHGXNX	Majority
	110 120 130 140 150	
100	YAIT-AIQKFLFETDIPVFGIXLGHQLL---ALASGAKTVKMKFGHHGGNH	CPS.pro
66	-PIISEVKRLAAEGKPVLGVCNGFQILTEIGLLPGALLHNDSHLFI SRNE	SapurQ.PRO
64	IGVSLDVIKYL GKRTPI LGVCLGHQAI---GYAFGAKIRRARKV FHGKIS	anthranilatesynthase.pro
	XXXXVNN-XXXXXXXXXXXXX--XXXAXXHG--XXVDEXXXP----XXLIV	Majority
	160 170 180 190 200	
146	PVKDVEK-NVVM-----TAQNHG--FAVDEATLP----ANLRV	CPS.pro
115	ELEIVNNQTAFTNLVEQGEKVIYPVAHGE GHYYCTDEIYQQLKANNQIIL	SapurQ.PRO
111	NIILVNN-SPLSLYYGIAKE--FKATRYHS--LVVDEVHRP-----LIV	anthranilatesynthase.pro
	XXXXXXXDG---XIXGIHXEXXPXXGXQXHPE-AXXTXLGXXXLXXXFXXX	Majority
	210 220 230 240 250	
178	THKSLFDG---TLQGIHRTDKPAFSFQGNPE-ASPGPHDAAPLFDHFIEL	CPS.pro
165	KYVNNPNGSYDDIAGIVNEKGNVCGMMPHPERALETLLGTDSGVKLF EAM	SapurQ.PRO
150	DAIS AEDN---EIMAIHHEEYPIYGVQFHPE-SVGTSLGYKILYN-FLN-	anthranilatesynthase.pro
	XXXXRX---X	Majority
	260	
224	IEQYRK---T	CPS.pro
215	VKSWREQHV.	SapurQ.PRO
194	-----R---V	anthranilatesynthase.pro

Decoration 'Decoration #1': Shade (with solid bright yellow) residues that match the Consensus exactly.

