



NetPhosBac 1.0 Server - prediction results

Technical University of Denmark

>DHFR 159 amino acids

#

netphosbac-1.0a prediction results

#

# Sequence	# x	Context	Score	Kinase	Answer
# -----					
# DHFR	2 T	---MTLSIL	0.129	main	.
# DHFR	4 S	-MTLSILVA	0.409	main	.
# DHFR	36 S	VKKLSTGHT	0.715	main	Y
# DHFR	37 T	KKLSTGHTL	0.459	main	.
# DHFR	40 T	STGHTLVMG	0.508	main	Y
# DHFR	47 T	MGRKTFESI	0.289	main	.
# DHFR	50 S	KTFESIGKP	0.339	main	.
# DHFR	64 T	NVVLTSDDTS	0.188	main	.
# DHFR	65 S	VVLTSDDTSF	0.409	main	.
# DHFR	67 T	LTSDDTSFNV	0.203	main	.
# DHFR	68 S	TSDTSFNV	0.422	main	.
# DHFR	79 S	DVIHSIEDI	0.553	main	Y
# DHFR	97 T	FGGQTLFEE	0.396	main	.
# DHFR	112 T	DMYITVIEG	0.192	main	.
# DHFR	122 T	FRGDTFFPP	0.457	main	.
# DHFR	128 T	FPPYTFEDW	0.176	main	.
# DHFR	136 S	WEVASSVEG	0.541	main	Y
# DHFR	137 S	EVASSVEGK	0.522	main	Y
# DHFR	147 T	DEKNTIPHT	0.402	main	.
# DHFR	151 T	TIPHTFLHL	0.374	main	.

#

MTLSILVAHDLQRVIGFENQLPWHLPLNDLKHVKKLSTGHTLVLMGRKTFES

50

IGKPLPNRRNVVLTSDDTSFNVGVVDVIHSIEDIYQLPGHVFIFFGGQTLFE

100

EMIDKVDDMYITVIEGKFRGDTFFPPYTFEDWWEVASSVEGKLDEKNTIPH

150

TFLHLIRKK

200

%1S...T.....

50

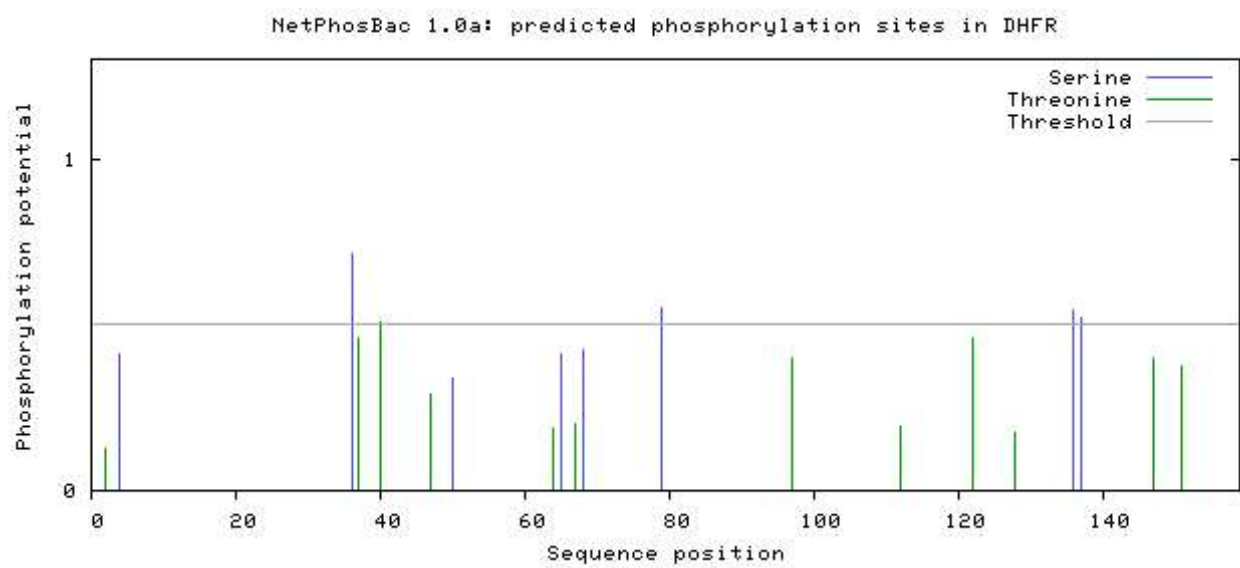
%1S.....

100

%1SS.....

150

%1



[Explain](#) the output. Go [back](#).
