






Supplementary File 7. Ligand binding sites mapped on the sequence of wNsp16 protein aligned with the closest homologs found in UniProt.

Ligand BS:

-  S-ADENOSYLMETHIONINE (5YN6-SAM, MERS)
-  S-ADENOSYL-L-HOMOCYSTEINE (5YN8-SAH, MERS)
-  SINEFUNGIN (5YNB-SFG, MERS)
-  P1-7-METHYLGUANOSINE-P3-ADENOSINE-5',5'-TRIPHOSPHATE (5YNF-GTA, MERS)
-  7-METHYL-GUANOSINE-5'-TRIPHOSPHATE-5'-GUANOSINE (5YNI-GTG, MERS)

QHN73794		KVVKVTIDYTEISFMLWCKDGHVETTFYPKLQSSQAWQPGVAMPNLYKMQRMLLEKCDLQN	6827
SP	P0C6X7 R1AB_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
TR	Q6UZF5 Q6UZF5_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
TR	Q6UZF1 Q6UZF1_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
TR	Q6JH48 Q6JH48_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
TR	Q692E6 Q692E6_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
TR	A0A0K1YZY7 A0A0K1YZY7_CVHSA	KVVKVTIDYVEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6804
SP	P0C6W2 R1AB_BCHK3	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6798
SP	P0C6W6 R1AB_BCRP3	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6802
SP	P0C6V9 R1AB_BC279	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6810
TR	A0A0U1WHI4 A0A0U1WHI4_CVHSA	KVVKVTIDYAEISFMLWCKDGHVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6799
TR	A0A0U1WHG0 A0A0U1WHG0_CVHSA	KVVKVTIDYAEISFMLWCKDGYVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6799
TR	A0A166ZL34 A0A166ZL34_9NIDO	KVVKVTIDYAEISFMLWCKDGYVETTFYPKLQASQAWQPGVAMPNLYKMQRMLLEKCDLQN	6606
TR	R9QTB2 R9QTB2_CVHSA	-----	
TR	R9QTH2 R9QTH2_CVHSA	-----	
SP	P0C6U8 R1A_CVHSA	-----	
TR	Q6JH47 Q6JH47_CVHSA	-----	
TR	Q692E5 Q692E5_CVHSA	-----	
SP	P0C6F8 R1A_BCHK3	-----	
TR	A0A0K1Z0N1 A0A0K1Z0N1_CVHSA	-----	
SP	P0C6F5 R1A_BC279	-----	
SP	P0C6T7 R1A_BCRP3	-----	

QHN73794		YGDSATLPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6887
SP	P0C6X7 R1AB_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
TR	Q6UZF5 Q6UZF5_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
TR	Q6UZF1 Q6UZF1_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
TR	Q6JH48 Q6JH48_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
TR	Q692E6 Q692E6_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
TR	A0A0K1YZY7 A0A0K1YZY7_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6864
SP	P0C6W2 R1AB_BCHK3	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6858
SP	P0C6W6 R1AB_BCRP3	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6862
SP	P0C6V9 R1AB_BC279	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6870
TR	A0A0U1WHI4 A0A0U1WHI4_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6859
TR	A0A0U1WHG0 A0A0U1WHG0_CVHSA	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6859
TR	A0A166ZL34 A0A166ZL34_9NIDO	YGENAVIPKGIMMNVAKYTQLCQYLNLTTLAVPYNMRVIHFGAGSDKGVPAGTAVLRQWL	6666
TR	R9QTB2 R9QTB2_CVHSA	-----	
TR	R9QTH2 R9QTH2_CVHSA	-----	
SP	P0C6U8 R1A_CVHSA	-----	
TR	Q6JH47 Q6JH47_CVHSA	-----	
TR	Q692E5 Q692E5_CVHSA	-----	
SP	P0C6F8 R1A_BCHK3	-----	
TR	A0A0K1Z0N1 A0A0K1Z0N1_CVHSA	-----	
SP	P0C6F5 R1A_BC279	-----	
SP	P0C6T7 R1A_BCRP3	-----	



QHN73794			NYLGKPREQIDGYVMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKEGQIND	7067
SP	P0C6X7	R1AB_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7044
TR	Q6UZF5	Q6UZF5_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7044
TR	Q6UZF1	Q6UZF1_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7044
TR	Q6JH48	Q6JH48_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7044
TR	Q692E6	Q692E6_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7044
TR	A0A0K1ZY7	A0A0K1ZY7_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMFLKENQIND	7044
SP	P0C6W2	R1AB_BCHK3	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7038
SP	P0C6W6	R1AB_BCRP3	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7042
SP	P0C6V9	R1AB_BC279	NYLGKPREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7050
TR	A0A0U1WHI4	A0A0U1WHI4_CVHSA	NYLGKPKREQIDGYTMHANYVFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7039
TR	A0A0U1WHG0	A0A0U1WHG0_CVHSA	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	7039
TR	A0A166ZL34	A0A166ZL34_9NIDO	NYLGKPKREQIDGYTMHANYIFWRNTNPIQLSSYSFLDMSKFPLKLRGTAVMSLKENQIND	6846
TR	R9QTB2	R9QTB2_CVHSA	-----	
TR	R9QTH2	R9QTH2_CVHSA	-----	
SP	P0C6U8	R1A_CVHSA	-----	
TR	Q6JH47	Q6JH47_CVHSA	-----	
TR	Q692E5	Q692E5_CVHSA	-----	
SP	P0C6F8	R1A_BCHK3	-----	
TR	A0A0K1Z0N1	A0A0K1Z0N1_CVHSA	-----	
SP	P0C6F5	R1A_BC279	-----	
SP	P0C6T7	R1AB_BCRP3	-----	

QHN73794		MILSLLEKGRLLIIRENNRVVVISSDVLVNN	7096
SP	P0C6X7 R1AB_CVHSA	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7073
TR	Q6UZF5 Q6UZF5_CVHSA	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7073
TR	Q6UZF1 Q6UZF1_CVHSA	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7073
TR	Q6JH48 Q6JH48_CVHSA	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7073
TR	Q692E6 Q692E6_CVHSA	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7073
TR	A0A0K1YZY7 A0A0K1YZY7_CVHSA	MIYSLLEKGRLLIIRENNTVVVSSDVLVNH	7073
SP	P0C6W2 R1AB_BCHK3	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7067
SP	P0C6W6 R1AB_BCRP3	MIYSLLEKGRLLIIRENNRVVSSDILVNN	7071
SP	P0C6V9 R1AB_BC279	MIYSLLENGRLLIIRENNRVVSSDILVNN	7079
TR	A0A0U1WHI4 A0A0U1WHI4_CVHSA	MIYSLLEKGRLLIIRENNTVVVSSDVLVNH	7068
TR	A0A0U1WHG0 A0A0U1WHG0_CVHSA	MIYSLLEKGRLLIVRENNRVIVSSDVLVNN	7068
TR	A0A166ZL34 A0A166ZL34_9NIDO	MIYSLLEKGRLLIVRENNRVIVSSDVLVNN	6875
TR	R9QTB2 R9QTB2_CVHSA	-----	
TR	R9QTH2 R9QTH2_CVHSA	-----	
SP	P0C6U8 R1A_CVHSA	-----	
TR	Q6JH47 Q6JH47_CVHSA	-----	
TR	Q692E5 Q692E5_CVHSA	-----	
SP	P0C6F8 R1A_BCHK3	-----	
TR	A0A0K1Z0N1 A0A0K1Z0N1_CVHSA	-----	
SP	P0C6F5 R1A_BC279	-----	
SP	P0C6T7 R1A_BCRP3	-----	