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## **Supporting Information**

## Screen and Optimization of Phage Display Cyclic Peptides Against WDR5 WBM Site

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Table S1. P	hage titer and recovery efficiency of three rounds in the biopanning; recovery efficiency = output titer /

input titer

Round	Input Titer (pfu)	Output Titer (pfu) Recovery Efficiency		Fold Increase				
	Subtractive panning with Ni-NTA magnetic agarose beads							
1	1.0×10 <sup>11</sup>	1.0×10 <sup>4</sup>	1.0×10 <sup>-7</sup>	1				
2	2.0×10 <sup>11</sup>	7.0×10 <sup>4</sup> 3.5×10		3.5				
3	2.0×10 <sup>11</sup>	1.0×10 <sup>4</sup> 0.5×10 <sup>-7</sup>		0.5				
Alternant panning with two kinds of magnetic beads								
1	1.0×10 <sup>11</sup>	2.0×10 <sup>6</sup>	2.0×10 <sup>-3</sup>	1				
2	2.0×10 <sup>11</sup>	4.0×10 <sup>5</sup>	2.0×10 <sup>-4</sup>	0.1				
3	2.0×10 <sup>11</sup>	2.5×10 <sup>8</sup>	1.25×10 <sup>-1</sup>	62.5				

No.	Peptide Sequence	Reads (Sanger)	PSBinder (SAROTUP)	Affinity (ADCP)
A1	CAHQRWVTC	4/33	0.93	-
A2	CPWQVHRDC	3/33	0.53	error
A3	*CADTNWLVC	2/33	0.52	-22.7
A4	CSSNTVPAC	2/33	0.04	-19.6
A5	CPWKTHQSC	2/33	0.17	error
A6	CSEARWMRC	2/33	0.12	-20.2
A7	*CSQAWWYQC	1/33	0.24	-22.7
A8	CPWKVHSYC	1/33	0.81	-
A9	*CPNQWKSYC	1/33	0.27	-22.0
A10	CNNLNAILC	1/33	0.08	-20.2
A11	*CFLNVSNAC	1/33	0.25	-21.1
A12	CDMPPTQKC	1/33	0.55	-19.7
A13	CWHAGRWTC	1/33	0.78	-
A14	CLPNDHLRC	1/33	0.20	error
A15	CGSSRWLEC	1/33	0.79	-

**Table S2.** The peptide sequences derived from the third round in the subtractive panning; \*: the sequence with an affinity value lower than -21.0

No.	Peptide Sequence	Reads (Sanger)	PSBinder (SAROTUP)	Affinity (ADCP)
B1	*CGSLDWPHC	5/124	0.69	-22.8
B2	CMTPNPTTC	2/124	0.35	-17.2
B3	CRAYDFPSC	2/124	0.97	-
B4	CDARGGLRC	2/124	0.37	-20.2
B5	CRVYEWPKC	1/124	0.98	-
B6	CRALPFNTC	1/124	0.34	-18.6
B7	CRVLPYGSC	1/124	0.94	-
B8	CRVHPVGEC	1/124	0.97	-
B9	CRDKPSNVC	1/124	0.21	-18.7
B10	CGTNPIKKC	1/124	0.27	-17.9
B11	CGSNTTVEC	1/124	0.57	-20.6
B12	CSSNTVPAC	1/124	0.04	-19.6
B13	CVSTATNGC	1/124	0.39	-19.1
B14	*CNSLNWFWC	1/124	0.30	-22.2
B15	CSKKNPSWC	1/124	0.25	-19.1
B16	CYGLSNSRC	1/124	0.40	-19.9
B17	*CGEGEADVC	1/124	0.50	-22
B18	CAIGETSTC	1/124	0.89	-
B19	CLNVSSPTC	1/124	0.10	-18.3
B20	CNNPAQPWC	1/124	0.19	-17.8
B21	CEPRSLANC	1/124	0.10	-19.2
B22	CNWRLSNYC	1/124	0.18	error
B23	CMNEDKFHC	1/124	0.53	error
B24	CTGPWIWHC	1/124	0.96	-
B25	CVNSMTYPC	1/124	0.04	error
B26	CINNLPKSC	1/124	0.12	-19.1
B27	CFPNVYHAC	1/124	0.24	error
B28	CSRSMNMAC	1/124	0.34	-18.6
B29	CHMYHNATC	1/124	0.00	error
B30	CHLTHQASC	1/124	0.00	error

**Table S3.** The peptide sequences derived from the third round in the alternant panning; \*: the sequence with an affinity value lower than -21.0

Product	Purify	Theoretical M.W.	Calculated M.W.	Observed [M+H] <sup>+</sup>	Intensity
CYC1	-	1273.50	1274.50	1274.59	1.87E+08
CYC2	-	1273.50	1274.50	1274.52	4.51E+07
CYC3	92.90%	1273.50	1274.50	1274.53	2.43E+06
CYC4	80.98%	1223.49	1224.49	1224.58	5.74E+06
CYC5	-	1225.47	1226.47	1294.37	8.03E+06
CYC6	-	1264.44	1265.44	1462.38	8.17E+06
CYC7	89.00%	1274.50	1275.50	1275.56	4.91E+06
CYC8	-	1269.47	1270.47	1170.51	1.59E+08
CYC9	-	1223.49	1224.49	1170.60	5.70E+07

Table S4. Purify and molecular weight of cyclization products with 9 different chemical linkers

Time (min)	Mobile Phase A (%)	Mobile Phase B (%)
0.0	20.0	80.0
2.0	95.0	5.0
5.0	60.0	40.0
6.5	5.0	95.0
8.0	5.0	95.0
8.5	95.0	5.0

 $\label{eq:table_state} \textbf{Table S5.} \ \text{The HPLC gradient elution condition}$ 



**Figure S1.** The characterization of purified his-tagged WDR5. (A) Gel-filtration chromatogram of his-tagged WDR5 with a single peak at 89 ml. (B) The elution volume of aggregated WDR5 at 47 ml. (C) SDS-PAGE of purified his-tagged WDR5 protein migrating above the band 35.0 kDa.

Α	B			
A 1 CADTNWLVC 2 CADTNWLVC 3 CSSNTVPAC 4 CSSNTVPAC 5 CSQAWWYQC 6 CPWKTHQSC 7 CPWKTHQSC 8 CPWKVHSYC 9 CPNQWKSYC 10 CNNLNAILC 11 CFLNVSNAC 12 CDMPPTQKC 13 CPWQVHRDC 14 CPWQVHRDC 15 CPWQVHRDC 16 CAHQRWVTC 17 CAHQRWVTC 19 CAHQRWVTC 19 CAHQRWVTC 20 CSEARWMRC 21 CSEARWMRC 22 CGSSRWLEC 23 CWHAGRWTC 24 CLPNDHLRC 25 CRTLPYKWC 26 CRTLPYKWC 26 CRTLPYKWC 27 CRTLPYKWC 30 CRTLPYKWC 31 CRTLPYKWC 32 CRTIPYNNC 33 CRTIPYNNC	B	1CGSLDWPHC2CGSLDWPHC3CGSLDWPHC4CGSLDWPHC5CGSLDWPHC6CHLTHQASC7CSRSMNMAC8CHMYHNATC9CMTPNPTTC10CMTPNPTTC11CRAYDFPSC12CRAYDFPSC13CDARGGLRC14CDARGGLRC15CRVYEWPKC16CRALPFNTC17CRVLPYGSC18CRVHPVGEC19CRDKPSNVC20CGTNP IKKC21CGSNTTVEC22CSSNTVPAC23CVSTATNGC24CNSLNWFWC25CSKKNPSWC26CYGLSNSRC27CGEGEADVC28CA I GETSTC29CLNVSSPTC30CNWRLSNYC34CMNEDKFHC35CTGPW IWHC36CFPNVYHAC37C INNLPKSC38CRTGSAWSC39CRTLT INQC	42 CRT IPFPTC 43 CRT IPFPTC 44 CRT IPFPTC 45 CRT IPFPHC 46 CRTLPFPEC 47 CRTLPFPC 48 CRTLPFPC 49 CRTWPFPTC 50 CRT0PFPNC 51 CRT0PFPNC 52 CRT0PFPNC 53 CRTLPFNTC 54 CRTLPFNTC 55 CRTLPFNTC 56 CRTLPFNTC 57 CRTLPFNTC 57 CRTLPFTC 58 CRTVPFNLC 59 CRTLPFTQC 60 CRTLPFTQC 61 CRTLPFTQC 62 CRTVPFGQC 63 CRTLPFGSC 64 CRTLPFGSC 64 CRTLPFGSC 65 CRTLPFGSC 66 CRTLPFHC 70 CRTLPFHC 70 CRTLPFHC 70 CRTLPYHC 70 CRTLPYHC 70 CRTLPYHC 70 CRTLPYHC 71 CRTLPYHC 72 CRTLPYHC 73 CRTLPYTC 74 CRTMPYKQC 75 CRTLPYMSC 79 CRTVPYMSC 80 CRTVPYMSC 81 CRTVPYMSC 81 CRTVPYMSC 82 CRTLPYLGC	83CRTLPYQGC84CRTLPYWGC85CRTMPWDFC86CRTLPWMTC87CRTLPWMTC88CRTLPWNQC89CRTLPWSMC90CRTLPHNMC91CRTLPHNMC92CRTLPHORC93CRTLPHGAC94CRTLPHGAC95CRTLPYGUC96CRTLPYGUC97CRTMPMSLC98CRTLPYGUC99CRTMPVGTC100CRTMPVGTC101CRTLPIGTC102CRTLPTVC103CRTEPFMHC104CRTEPFMHC105CRTAPFMHC106CRTAPFMHC107CRTVPYMHC108CRTQPYLYC110CRTVPIMQC111CRTMPINAC113CRTVPLQQC114CRTTPLMQC115CRTEPLMKC116CRTQPIYEC117CRTLPVKEC118CRTEPVKLC119CRTLQYMSC120CRTLQYMSC121CRTLSYGSC122CRTVAYMKC123CRTLEFSVC
				124 CRIVEMEAC

**Figure S2.** Phage-displayed cyclic peptide sequences picked from the third round of biopanning; numbers of the enriched sequences are marked by green colour. (A) 33 sequences picked from the subtractive panning with Ni-NTA magnetic agarose beads. (B) 124 sequences picked from the alternant panning with two kinds of magnetic beads.



Figure S3. Binding affinity derived from HTRF assay of the positive control peptide SV-10.



Figure S4. HPLC chromatogram and LC-MS spectrum of the cyclic peptide CYC3.



Figure S5. HPLC chromatogram and LC-MS spectrum of the cyclic peptide CYC4.



Figure S6. HPLC chromatogram and LC-MS spectrum of the cyclic peptide CYC7.





Peak#	Ret. Time	Area	Height	Area %	Height %
1	6.273	78470	7265	0.197	0.327
2	6.742	61991	7093	0.156	0.319
3	8.071	50498	4607	0.127	0.207
4	9.156	54310	5946	0.137	0.267
5	9.466	24090	2487	0.061	0.112
6	11.153	178661	10682	0.449	0.480
7	11.384	38383568	2098752	96.570	94.339
8	12.137	738204	71198	1.857	3.200
9	12.562	91685	8386	0.231	0.377
10	13.027	85431	8272	0.215	0.372
Total		39746908	2224690	100.000	100.000



Figure S7. The analysis certification of the synthetic peptide DH226015.





Figure S8. The analysis certification of the synthetic peptide D210012.







Figure S9. The analysis certification of the synthetic peptide D210014.



Figure S10. The analysis certification of the synthetic peptide DH226016.





Peak#	Ret. Time	Area	Height	Area %	Height %
1	7.062	7656	1792	0.039	0.113
2	7.459	174838	12325	0.880	0.776
3	7.833	188577	21560	0.949	1.358
4	8.291	18978190	1490478	95.475	93.887
5	8.617	198911	26678	1.001	1.681
6	8.942	201543	21990	1.014	1.385
7	9.296	127843	12693	0.643	0.800
Total		19877557	1587516	100.000	100.000



Figure S11. The analysis certification of the synthetic peptide DH210901.

uV



Figure S12. The analysis certification of the synthetic peptide DH226027.



Figure S13. The analysis certification of the synthetic peptide DH226027-L.