A few additional examples.

In **Fig.1**. various kinases are presented, with which the interactions of the active site of the MYC peptide were studied.

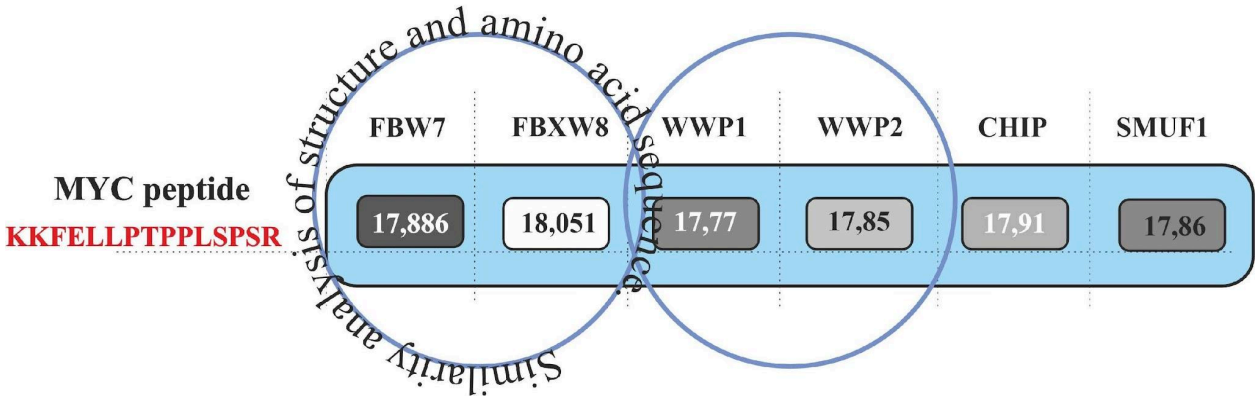


Figure 1.

The structures of the ligases **FBW7** and **FBXW8**, **WWP**1 and **WWP2** are somewhat similar, so they are studied in pairs. We are interested in the smallest numerical values obtained.

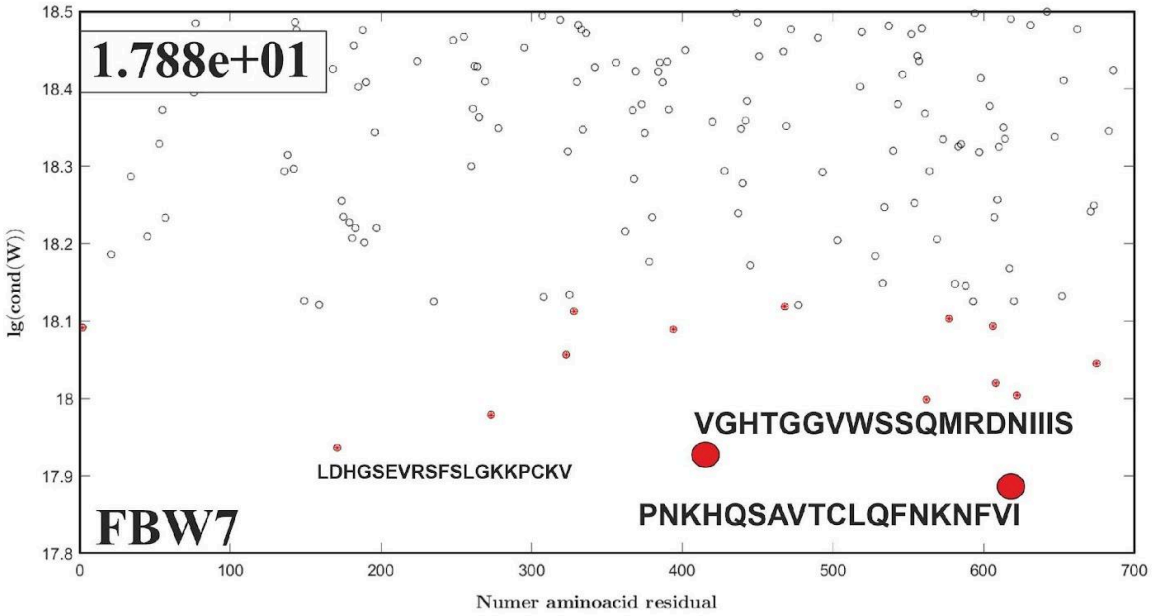
Figures 2 and **3** contain information about the results of numerical calculations, as well as the structure of **FBW7** and **FBXW8** ligases.

Figure 4 contains the results of numerical calculations indicating the domains and amino acid sequences that interact with the MYC peptide.

The second part of the **figure 4** contains an overlay of three-dimensional structures of two **FBW7** and **FBXW8** ligases in the region of the "propeller" domains.

Figures 5 and **6** contain the results of calculations for **WWP1** and **WWP2** molecules when interacting with the MYC peptide.

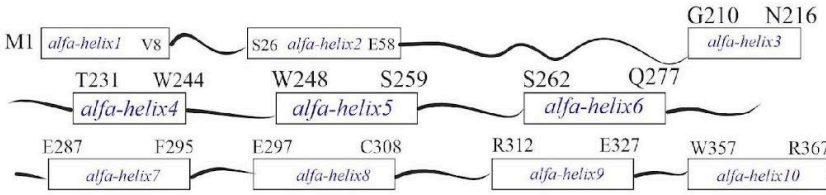
Figures 7 and **8** contain the results of calculations of the interaction of the MYC peptide with **CHIP** and **SMUF** ligases, indicating the structure of the molecules



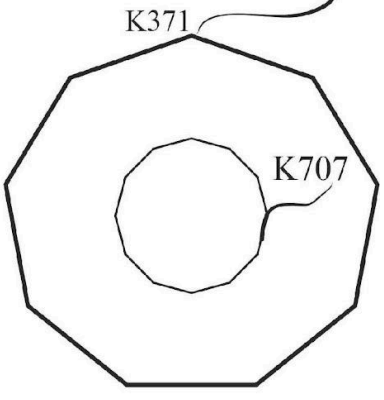
Shift plot of the MYC peptide along the amino acid sequence of the FBW7 ligase

619	**PNKHQSAVTCLQFNKNFVI**	**KKFELLPTPPLSPSRRSGL**	**1.788611e+01**
417	**VGHTGGVWSSQMRDNIIIS**	**KKFELLPTPPLSPSRRSGL**	**1.793076e+01**
171	**LDHGSEVRSFSLGKKPCKV**	**KKFELLPTPPLSPSRRSGL**	**1.793632e+01**
273	PQFQRDFISLLPKELALYV	KKFELLPTPPLSPSRRSGL	1.797889e+01
562	IRVWDVETGNCIHTLTGHQ	KKFELLPTPPLSPSRRSGL	1.799851e+01
622	HQSAVTCLQFNKNFVITSS	KKFELLPTPPLSPSRRSGL	1.800396e+01
608	KTGQCLQTLQGPNKHQSAV	KKFELLPTPPLSPSRRSGL	1.802002e+01
675	RASNTKLVCAVGSRNGTEE	KKFELLPTPPLSPSRRSGL	1.804516e+01

Sampling of the obtained results

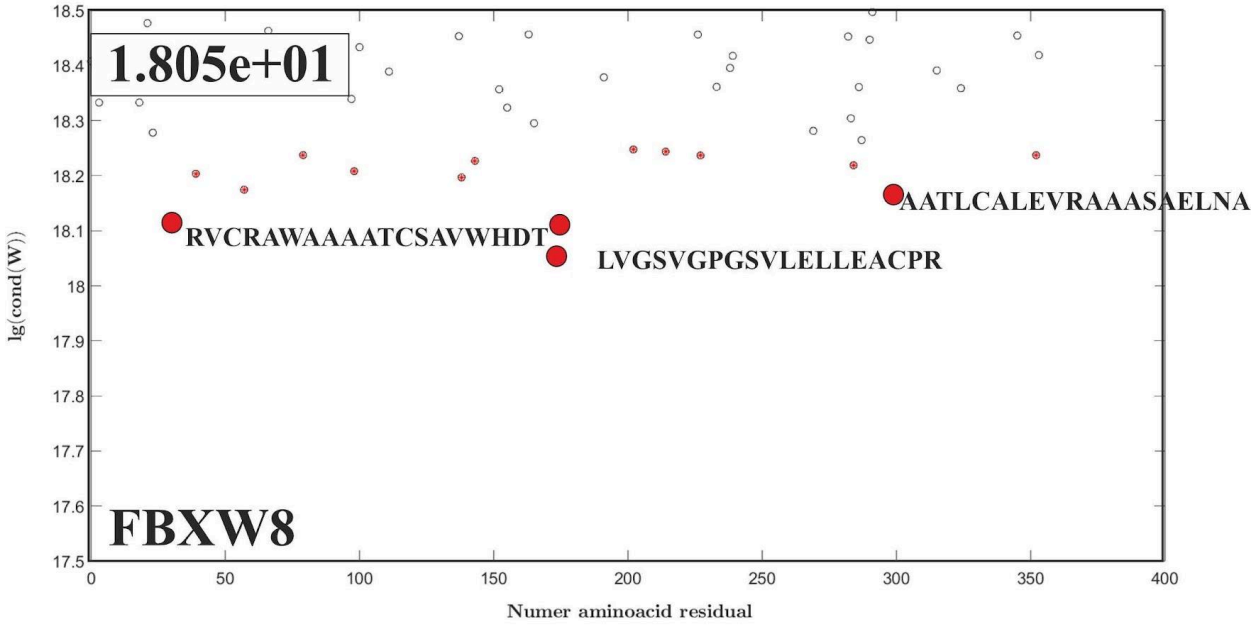


Structure of FBW7 Domain



MNQELLSVGSKRRRTGGSLRGNPSSSQVDEEQMNRVVEEEQQQQLRQQEEEHTAR
NGEVVGVEPRPGGQNDSQQGQLEENNNRFISVDEDSSGNQEEQEEDEEHAGEQDE
EDEEEEEMDQESDDFDQSDDSSREDEHTHTNSVTNSSSIVDLPVHQLSSPFYTKTTKM
KRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS
VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLL
PKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPG
FIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTL
KVWSAVTGKCLRTL**VGHTGGVWSSQMRDNIIIS**GSTDRTLKVWNAETGECIHTLYGH
TSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVS
GAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNC
IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQG**PNKHQSAVTCLQ**
FNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSR

Figure 2. The results of numerical analysis of the interaction of the MYC peptide with the **FBW7** ligase, indicating the amino acid sequences, as well as the structure of the " propeller" domain.



Shift plot of the MYC peptide along the amino acid sequence of the FBXW8 ligase

173	**LVGSVGPGSVLELLEACPR**	**KKFELLPTPPLSPSRRSGL**	**1.805165e+01**
174	**VGSVGPGSVLELLEACPRL**	**KKFELLPTPPLSPSRRSGL**	**1.811519e+01**
29	**RVCRAWAAAATCSAVWHDT**	**KKFELLPTPPLSPSRRSGL**	**1.811570e+01**
299	**AATLCALEVRAAASAELNA**	**KKFELLPTPPLSPSRRSGL**	**1.817078e+01**
57	GMLPPYLSACLDHIHNLRL	KKFELLPTPPLSPSRRSGL	1.817457e+01
138	HLDLRRLSFTLDDALVLQA	KKFELLPTPPLSPSRRSGL	1.819692e+01
39	TCSAVWHDTKISCECELEG	KKFELLPTPPLSPSRRSGL	1.820355e+01
98	RAPGLRGLRLECRGEKPLF	KKFELLPTPPLSPSRRSGL	1.820815e+01
284	SGDTVGPVRFAAHHYAATL	KKFELLPTPPLSPSRRSGL	1.821891e+01
143	RLSFTLDDALVLQAARSCP	KKFELLPTPPLSPSRRSGL	1.822686e+01
227	CPEDARASPLPNEAWVALR	KKFELLPTPPLSPSRRSGL	1.823675e+01
352	RLRTYTLKLTREPHPWRPT	KKFELLPTPPLSPSRRSGL	1.823720e+01
79	PSRKPSRRAAIELLMVLAG	KKFELLPTPPLSPSRRSGL	1.823744e+01
214	DRAPFALLALRCACPEDAR	KKFELLPTPPLSPSRRSGL	1.824370e+01
202	LSHAILEALAAPDRAPFAL	KKFELLPTPPLSPSRRSGL	1.824752e+01

Sampling of the obtained results

Figure 3. The results of numerical analysis of the interaction of the MYC peptide with the **FBXW8** ligase, indicating the amino acid sequences.

Color indicates the identified amino acid sequences that are involved in binding to the MYC peptide.

MNQELLSVGSKRRRTGGSLRGNPSSSQVDEEQMNRVVEEEQQQQLRQQEEEHTARNGEVVGVEPRPGGQNDSQQGQLEENNNRFISVDEDS
SGNQEEQEEDEEHAGEQDEEDEEEEEMDQESDDFDQSDDSSREDEHTHTNSVTNSSSIVDLPVHQLSSPFYTKTTKMKRKLDHGSEVRSFSLGKK
PCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFI
SLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHD
DHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVV
SGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDV
ETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLES
GGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK

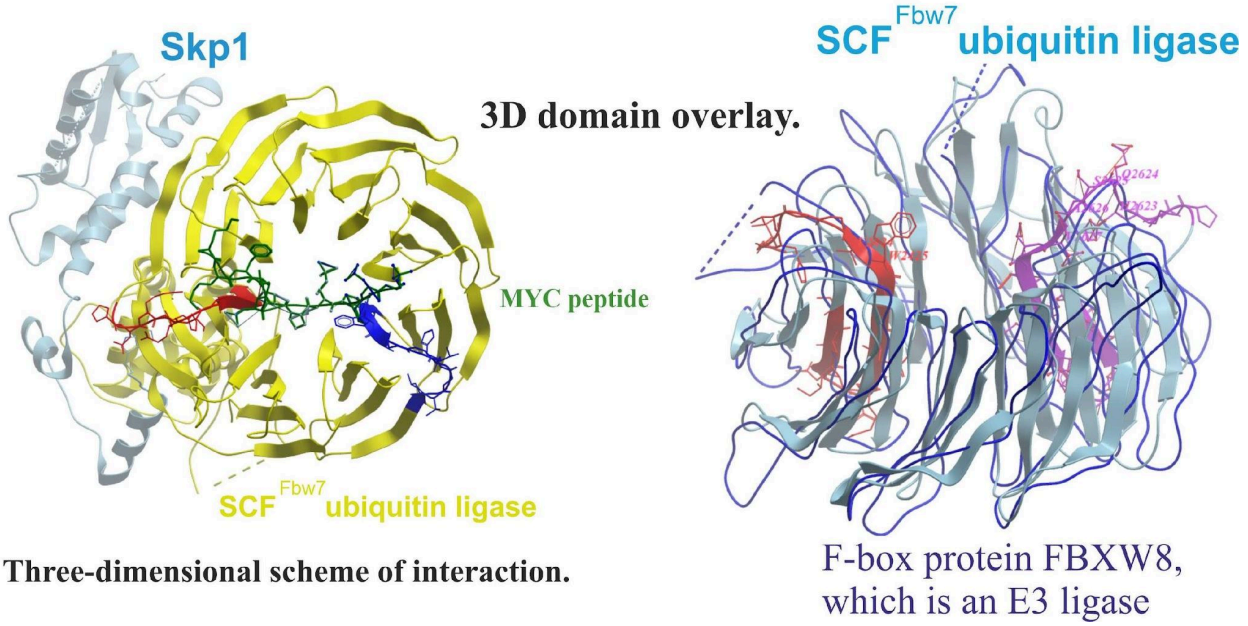
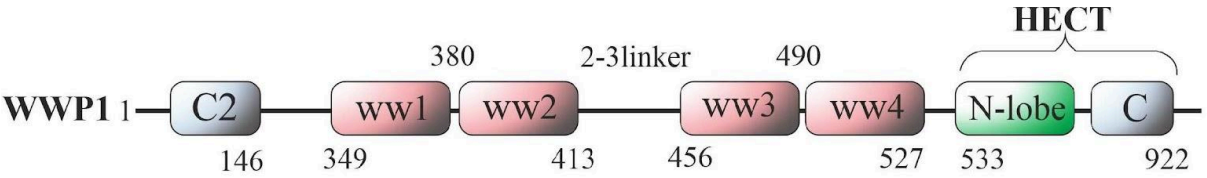
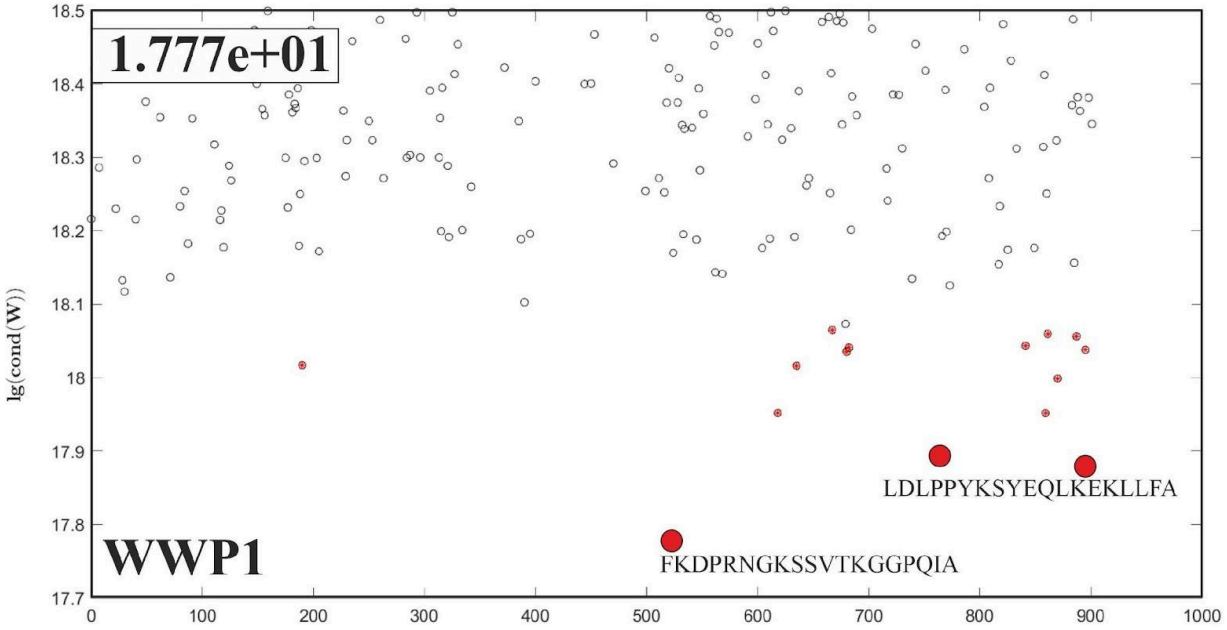


Figure 4. The assembled three-dimensional model involving Fbw7 ligase and MYC peptide, the amino acid sequence is shown with indication of the found sequences.

A three-dimensional comparison of the "propeller" domains of two ligases FBXW8 and **FBW7** is given.



Structure of WW Domain Containing E3 Ubiquitin Protein Ligase 1

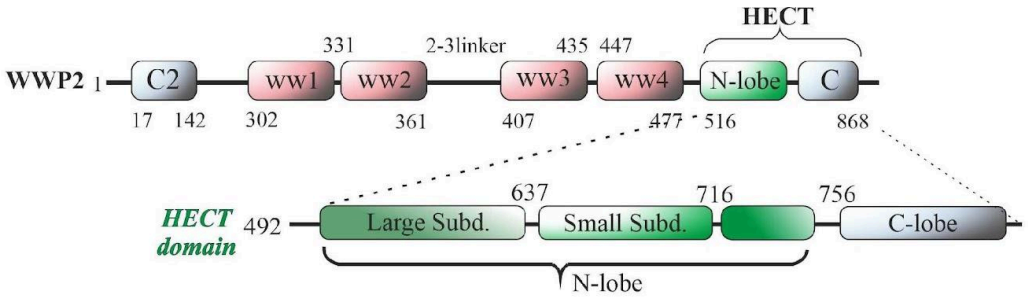


Shift plot of the MYC peptide along the amino acid sequence of the WWP1 ligase

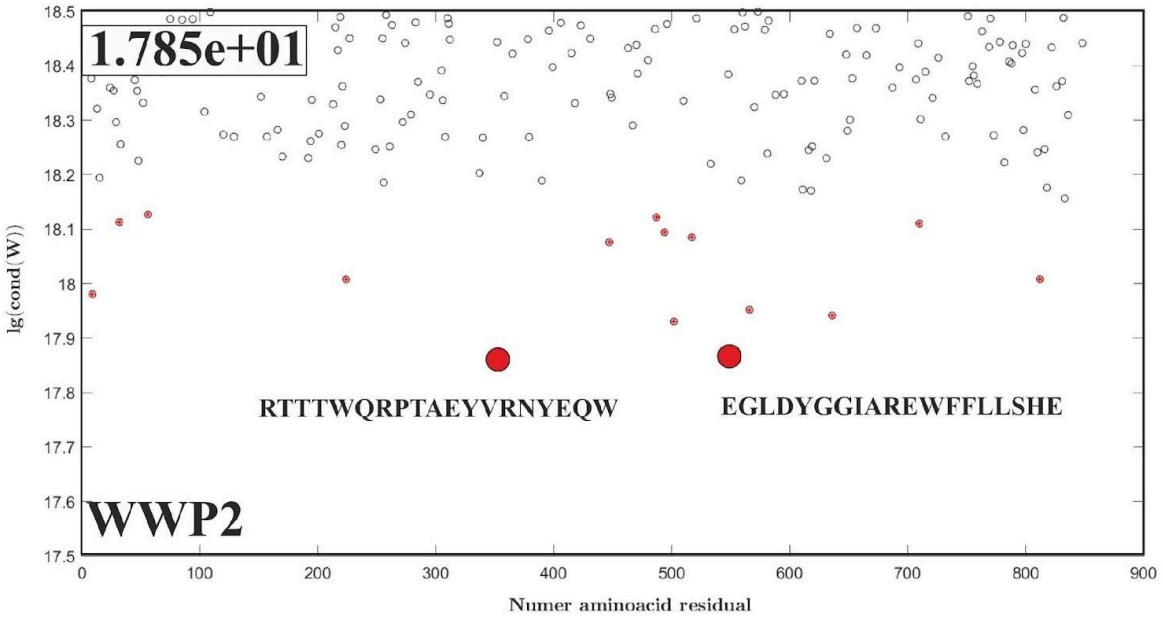
523	**FKDPRNGKSSVTKGGPQIA**	**KKFELLPTPPLSPSRRSGL 1.777744e+01**
893	**LDLPPYKSYEQLKEKLLFA**	**KKFELLPTPPLSPSRRSGL 1.787564e+01**
762	WRFSRGVQEQTKAFLDGFN	KKFELLPTPPLSPSRRSGL 1.789587e+01
859	GFAELMGSNGPQKFCIEKV	KKFELLPTPPLSPSRRSGL 1.795186e+01
618	LSHEVLNPMYCLFEYAGKN	KKFELLPTPPLSPSRRSGL 1.795195e+01
870	QKFCIEKVGKDTWLPRSHT	KKFELLPTPPLSPSRRSGL 1.799886e+01
635	KNNYCLQINPASTINPDHL	KKFELLPTPPLSPSRRSGL 1.801605e+01
190	NHVPTSTLVQNSCCSYVVN	KKFELLPTPPLSPSRRSGL 1.801677e+01
680	PFYKRMLSKKLTIKDLESI	KKFELLPTPPLSPSRRSGL 1.803545e+01
895	LPPYKSYEQLKEKLLFAIE	KKFELLPTPPLSPSRRSGL 1.803773e+01
682	YKRMLSKKLTIKDLESIDT	KKFELLPTPPLSPSRRSGL 1.804081e+01
841	VRMRLLQFVTGTCRLPLGG	KKFELLPTPPLSPSRRSGL 1.804322e+01
887	HTCFNRLDLPPYKSYEQLK	KKFELLPTPPLSPSRRSGL 1.805628e+01

Sampling of the obtained results

Figure 5. The results of numerical analysis of the interaction of the MYC peptide with the **WWP1** ligase, indicating the amino acid sequences, as well as the structure of the domain.



Structure of WW Domain Containing E3 Ubiquitin Protein Ligase 2

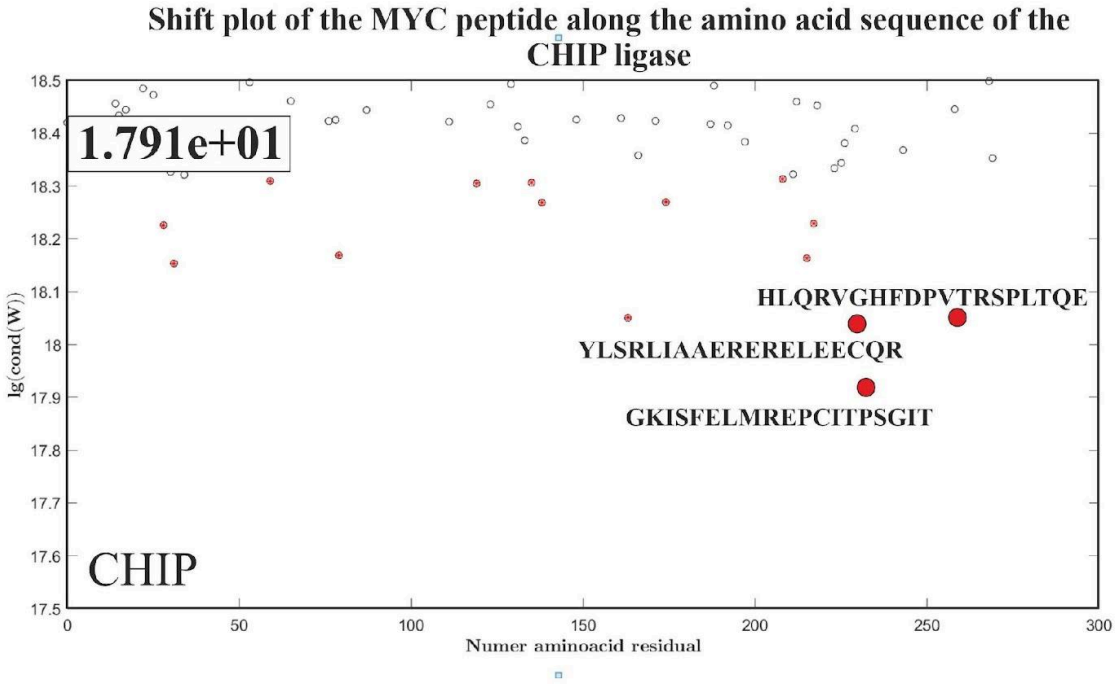


Shift plot of the MYC peptide along the amino acid sequence of the WWP2 ligase

353	**RTTTWQRPTAEYVRNYEQW**	**KKFELLPTPPLSPSRRSGL 1.785669e+01**
551	**EGLDYGGIAREWFFLLSHE**	**KKFELLPTPPLSPSRRSGL 1.786919e+01**
502	RFLCHSNALPSHVKISVSR	KKFELLPTPPLSPSRRSGL 1.793021e+01
636	KRPTLKDLESIDPEFYNSI	KKFELLPTPPLSPSRRSGL 1.794161e+01
566	LSHEVLNPMYCLFEYAGKN	KKFELLPTPPLSPSRRSGL 1.795195e+01
9	GVALPFEKSQLTLKVVSAK	KKFELLPTPPLSPSRRSGL 1.798044e+01
224	SGHSGLANGTVNDEPTTAT	KKFELLPTPPLSPSRRSGL 1.800744e+01
812	IGSNGPQKFCIDKVGKETW	KKFELLPTPPLSPSRRSGL 1.800780e+01
447	PGWEMKYTSEGVRYFVDHN	KKFELLPTPPLSPSRRSGL 1.807607e+01
517	SVSRQTLFEDSFQQIMNMK	KKFELLPTPPLSPSRRSGL 1.808469e+01
494	FRWKYHQFRFLCHSNALPS	KKFELLPTPPLSPSRRSGL 1.809416e+01
710	WRFTRGVEEQTKAFLDGFN	KKFELLPTPPLSPSRRSGL 1.811028e+01

Sampling of the obtained results

Figure 6. The results of numerical analysis of the interaction of the MYC peptide with the **WWP2** ligase, indicating the amino acid sequences, as well as the structure of the domain.



232	**GKISFELMREPCITPSGIT**	**KKFELLPTPPLSPSRRSGL**	**1.791670e+01**
230	**LCGKISFELMREPCITPSG**	**KKFELLPTPPLSPSRRSGL**	**1.803913e+01**
259	**HLQRVGHFDPVTRSPLTQE**	**KKFELLPTPPLSPSRRSGL**	**1.804961e+01**
163	YLSRLIAAERERELEECQR	KKFELLPTPPLSPSRRSGL	1.805057e+01
31	QGNRLFVGRKYPEAAACYG	KKFELLPTPPLSPSRRSGL	1.815352e+01
215	SQVDEKRKKRDIPDYLCGK	KKFELLPTPPLSPSRRSGL	1.816347e+01
79	LADCRRALELDGQSVKAHF	KKFELLPTPPLSPSRRSGL	1.816884e+01
28	LKEQGNRLFVGRKYPEAAA	KKFELLPTPPLSPSRRSGL	1.822608e+01

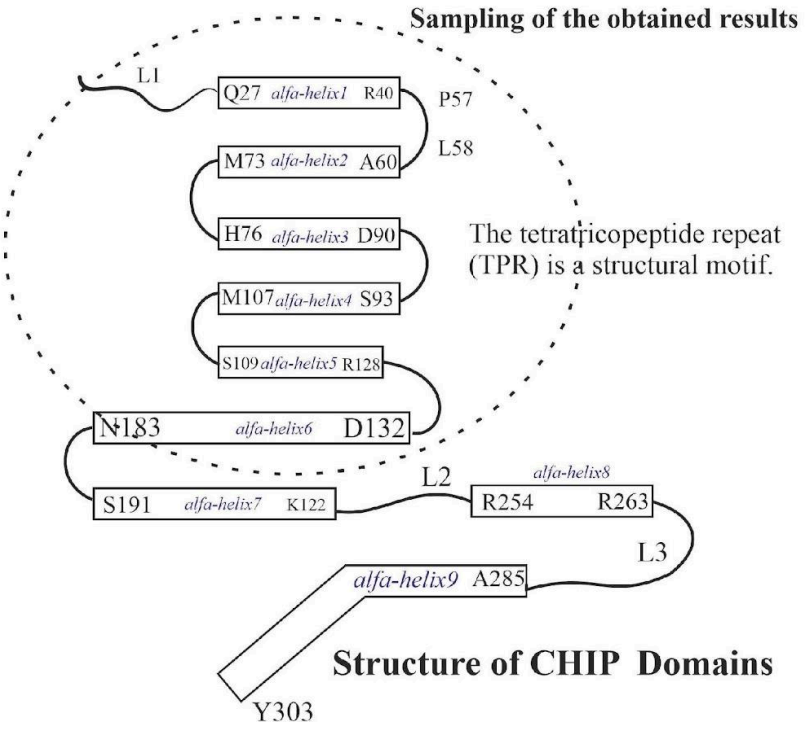
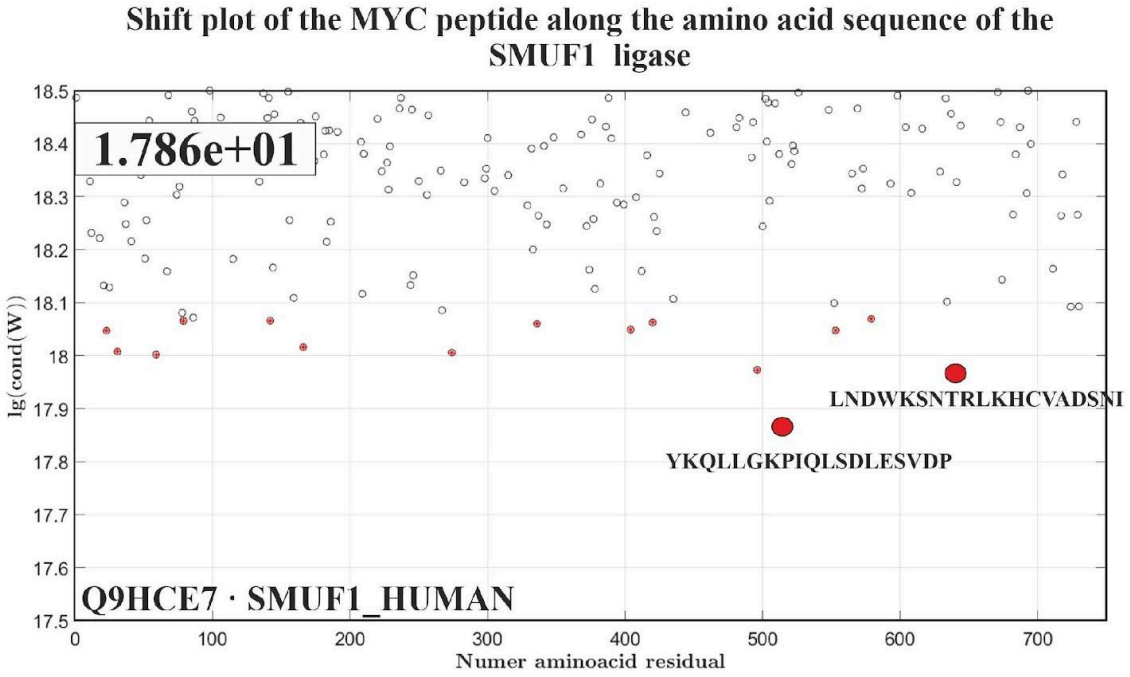


Figure 7. The results of numerical analysis of the interaction of the MYC peptide with the **CHIP** ligase, indicating the amino acid sequences, as well as the structure of the domain.



514	**YKQLLGKPIQLSDLESVDP**	**KKFELLPTPPLSPSRRSGL**	**1.786918e+01**
639	**LNDWKSNTRLKHCVADSNI**	**KKFELLPTPPLSPSRRSGL**	**1.796568e+01**
496	**GLAVFHGHYINGGFTVPFY**	**KKFELLPTPPLSPSRRSGL**	**1.797297e+01**
59	PKWNQHYDLYVGKTDSITI	KKFELLPTPPLSPSRRSGL	1.800196e+01
274	PGGDAAFLYEFLLQGHTSE	KKFELLPTPPLSPSRRSGL	1.800562e+01
31	RLPDPFAKIVVDGSGQCHS	KKFELLPTPPLSPSRRSGL	1.800731e+01
166	GPGRPLSCFMEEPAPYTDS	KKFELLPTPPLSPSRRSGL	1.801576e+01
23	NLAKKDFFRLPDPFAKIVV	KKFELLPTPPLSPSRRSGL	1.804675e+01
553	TFCVEHNAFGRILQHELKP	KKFELLPTPPLSPSRRSGL	1.804738e+01

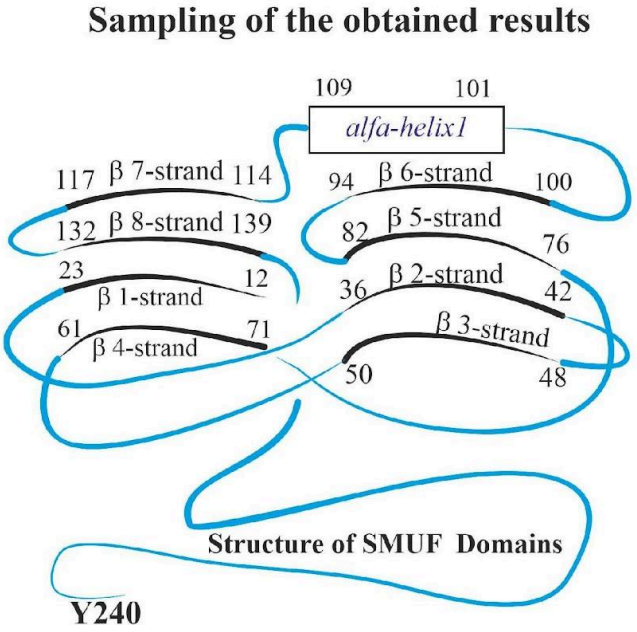


Figure 8. The results of numerical analysis of the interaction of the MYC peptide with the **SMUF1** ligase, indicating the amino acid sequences, as well as the structure of the domain.