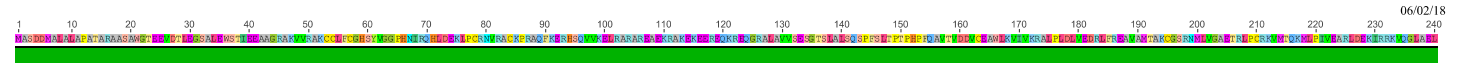


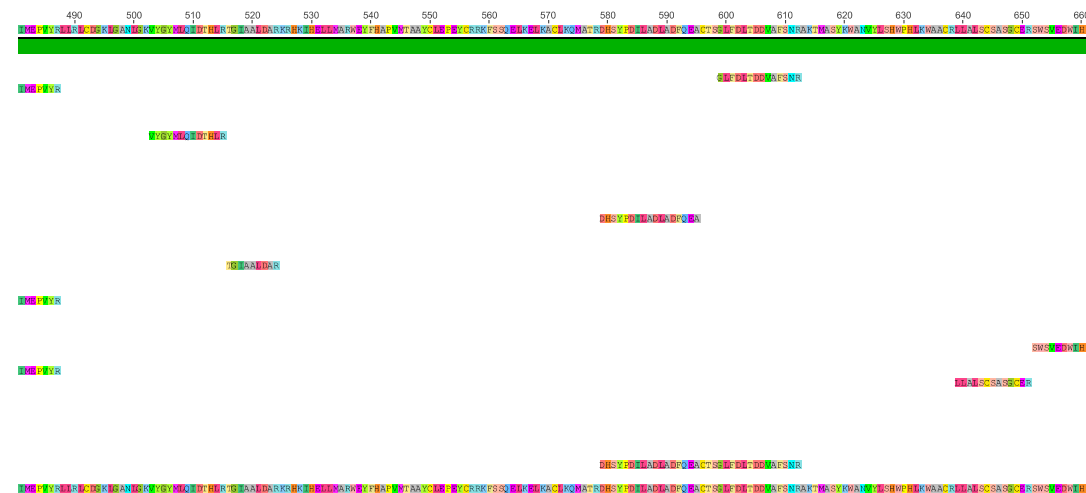
Consensus Identity

Consensus Identity

37. hAT2_Ace_protein



2. P65.01 Pep5801
3. P65.01 Pep5800
4. P65.01 Pep5799
5. P65.01 Pep5798
6. P65.01 Pep5797
7. P65.01 Pep5796
8. P65.01 Pep5795
9. P65.01 Pep5794
10. P65.01 Pep5792
11. P65.01 Pep5791
12. P65.01 Pep5790
13. P65.01 Pep5789
14. P65.01 Pep5788
15. P65.01 Pep5787
16. P65.01 Pep5786
17. P65.01 Pep5785
18. P65.01 Pep5784
19. P65.01 Pep5783
20. P65.01 Pep5782
21. P65.01 Pep5781
22. P65.01 Pep5780
23. P65.01 Pep5779
24. P65.01 Pep5778
25. P65.01 Pep5777
26. P65.01 Pep5776
27. P65.01 Pep5775
28. P65.01 Pep5774
29. P65.01 Pep5773
30. P65.01 Pep5772
31. P65.01 Pep5771
32. P65.01 Pep5768
33. P65.01 Pep5767
34. P65.01 Pep5766
35. P65.01 Pep5765
36. P65.01 Pep5770
37. hAT2 Ace protein



Consensus	1 10 20 30 40 50 60 70 80 90
Identity	MMTWDASGWN YGVQLVVKRKWATGDM LIECPPGECTFDDRVDVTR LQTRSCLPVHSAEGMQTEETFLHYIHR LDEWISQ RSAVEEAA TGGEP I Q
1. P942.01_Pep26259	
2. P942.01_Pep26260	
3. P942.01_Pep26262	
4. P942.01_Pep26263	
5. P942.01_Pep26265	SAVEEAA TGGEP I Q
6. P942.01_Pep26266	
7. Mariner3_Luffy_protein	MMTWDASGWN YGVQLVVKRKWATGDM LIECPPGECTFDDRVDVTR LQTRSCLPVHSAEGMQTEETFLHYIHR LDEWISQ RSAVEEAA TGGEP I Q
Consensus	100 110 120 130 140 150 160 170 180
Identity	RPVVLMLDNHCSRFSDELLRKTSGPAAELGIRIFTEESGTS GF LQALDQFNSSFHRSY NKARDAYKDAHLAVHGHPLSHLALADFLGILGGSK
1. P942.01_Pep26259	
2. P942.01_Pep26260	
3. P942.01_Pep26262	IFTEESGTS GF LQALDQFNSSFH R
4. P942.01_Pep26263	
5. P942.01_Pep26265	R
6. P942.01_Pep26266	FSDELLR
7. Mariner3_Luffy_protein	RPVVLMLDNHCSRFSDELLRKTSGPAAELGIRIFTEESGTS GF LQALDQFNSSFHRSY NKARDAYKDAHLAVHGHPLSHLALADFLGILGGSK
Consensus	190 200 210 220 230 240 250 260 270
Identity	RLGVPGMWF SWCDRYDILKAWKR VGIAGNR LCPQLVDRS NFWDQDAELAAARRDASVSSPGPSSLAFAKRTPPGLRRGSLAAANAKLQOLEQF
1. P942.01_Pep26259	
2. P942.01_Pep26260	SNFWDQDAELAAAR
3. P942.01_Pep26262	
4. P942.01_Pep26263	DASVSSPGPSSLAFAK
5. P942.01_Pep26265	
6. P942.01_Pep26266	
7. Mariner3_Luffy_protein	RLGVPGMWF SWCDRYDILKAWKR VGIAGNR LCPQLVDRS NFWDQDAELAAARRDASVSSPGPSSLAFAKRTPPGLRRGSLAAANAKLQOLEQF
Consensus	280 290 300 310 320 330 340 350 360 370
Identity	AKKLEEK AQAPYDPSRGVLSLS SDAPSARQGGTGSDDSDAADGDSASPVRRARRRLVQLSGSFTLRDMWGEKQKRQQFAAKVEDAAQRKKAAR
1. P942.01_Pep26259	
2. P942.01_Pep26260	GVLSLS SDAPSAR
3. P942.01_Pep26262	
4. P942.01_Pep26263	
5. P942.01_Pep26265	
6. P942.01_Pep26266	
7. Mariner3_Luffy_protein	AKKLEEK AQAPYDPSRGVLSLS SDAPSARQGGTGSDDSDAADGDSASPVRRARRRLVQLSGSFTLRDMWGEKQKRQQFAAKVEDAAQRKKAAR
Consensus	380 390 400 410 420 430 440 450 460 463
Identity	LEKRAEDEFERSRVRRDAFVACKDVCMCAIVPCPWEGFMLCDNCGNLKKGWCKKRFCVKWRKSPVSVASALVVGLESGVCASGAASDVGACP
1. P942.01_Pep26259	
2. P942.01_Pep26260	
3. P942.01_Pep26262	
4. P942.01_Pep26263	
5. P942.01_Pep26265	
6. P942.01_Pep26266	
7. Mariner3_Luffy_protein	LEKRAEDEFERSRVRRDAFVACKDVCMCAIVPCPWEGFMLCDNCGNLKKGWCKKRFCVKWRKSPVSVASALVVGLESGVCASGAASDVGACP