*strings 2,3*: colored secondary structure

*string 4*: secondary structure in letters format (alpha-helix – H, beta-sheet – B, coil – C, turn (very conservative structure) – T, loop (very variable structure) – L)

*string 5*: extremely conservative aminoacids, bind Mn or Mg during oligomerisation

*string 6*: aminoacids that participate in oligomerisation

*string 7*: probably participated in binding sites

*string 9-20*: segment 1 – segment 12

1: >Scer|YOR202W|model1

2: TEQKALVKRITNETKIQIAISLKGGPLAIEHSIFPEKEAEAVAEQATQSQVINVHTGIGFLDHMIHALAKHSGWSLIVECIGDLHIDDHHTTEDCGIALGQAFKEALGAVRGVKRFGSGFAPLDEALSRAVVDLSNRPYAVVELGLQREKVGDLSCEMIPHFLESFAEASRITLHVDCLRGKNDHHRSESAFKALAVAIREATSPNGTNDVPSTKGVLM

3: TEQKALVKRITNETKIQIAISLKGGPLAIEHSIFPEKEAEAVAEQATQSQVINVHTGIGFLDHMIHALAKHSGWSLIVECIGDLHIDDHHTTEDCGIALGQAFKEALGAVRGVKRFGSGFAPLDEALSRAVVDLSNRPYAVVELGLQREKVGDLSCEMIPHFLESFAEASRITLHVDCLRGKNDHHRSESAFKALAVAIREATSPNGTNDVPSTKGVLM

4: CCBBBBBBBBTTTBBBBBBBBBLLLLLLLLLLLLLLLLLLLLLLLLLLLLBBBCCCTTHHHHHHHHHHHHHHTTBBBBBBBBLLLLLCHHHHHHHHHHHHHHHHHHHCCCCCCCCCBBBBBCCTTBBBBBBBBCCCCCBBBBBLLLLLLLLLLLLLHHHHHHHHHHHHHHTTBBBBBBBBTTHHHHHHHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCC

5: ------------E-------------------------------------------------H-------H-----------------HH--E-------------------------------E-----------------------------------H-----------------------HH--E------------------------------

6: ------------E-------------------------------------------------H-------------------------HH--E-----------------R---R---------E-----------R-----------------------H-----------------------HH--E-----------------------S-K----

7: -------K--T-E-K-Q-----------------------------------NVHT------H--HA--KH-------EC--------HH--EDC---------------R---RFG------DEA----VVD---R--A-V------------------H-L-S----------------KNDHH--E---K----------S-N------STKG---

8: >Segments 1-12

9: --------------------------------------------------------------------------------------------------------EALGAVRGVK---------------------------------------------------------------------------------------------------------

10: --------------------------------------------------------------------------------------------------------------------------------------SNRPYAVVE----------------------------------------------------------------------------

11: -----------------------------------------------------------------------------------------------------------------------------------------------LGLQREKVGD------------------------------------------------------------------

12: -------------------------------------------------------------------------------------------------------------------------------------------------------------------------SRITLHVDCL----------------------------------------

13: -----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------RGKNDHHRSE------------------------------

14: ----------------------------------------------------------------------------------------------CGIALGQAFK-------------------------------------------------------------------------------------------------------------------

15: ----------------------------------------------------------------IHALAKHSGW-------------------------------------------------------------------------------------------------------------------------------------------------

16: ------------------------------------------------------HTGIGFLDHM-----------------------------------------------------------------------------------------------------------------------------------------------------------

17: ----------------------------------PEKEAE-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

18: ----------------------------IEHSIF-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

19: -----------NETKIQ----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

20: ----ALVKRIT----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

Structural alignment between first and second parts of SCER protein with segments. It is easy to see that we have no repeated segments.

>Scer|YOR202W|, model1, 2-107

TE....QKALVKRITN..ETKIQIAISLKGGPLAIEHSIFPEKEAEAVAEQATQSQVINVHTGI..........GFLDHMIHALAKHSGWSLIVECIGDLHIDDHHTTEDCGIALGQAFKEALGAV

--....----------..----------------------------------------------..........----------------------------------------------EALGAV

--....----------..----------------------------------------------..........----------------------------------------------------

--....----------..----------------------------------------------..........----------------------------------------------------

--....----------..----------------------------------------------..........----------------------------------------------------

--....----------..----------------------------------------------..........----------------------------------------------------

--....----------..----------------------------------------------..........------------------------------------CGIALGQAFK------

--....----------..----------------------------------------------..........------IHALAKHSGW------------------------------------

--....----------..------------------------------------------HTGI..........GFLDHM----------------------------------------------

--....----------..----------------------PEKEAE------------------..........----------------------------------------------------

--....----------..----------------IEHSIF------------------------..........----------------------------------------------------

--....---------N..ETKIQ-----------------------------------------..........----------------------------------------------------

--....--ALVKRIT-..----------------------------------------------..........----------------------------------------------------

>Scer|YOR202W|, model1, 108-219

..RGVKRFGSGFA.P.LDEALSRAVVDLSN........................RPYAVVELGLQREKVGDLSCEMIPHFLESFAEASRITLHVDCLRG..KNDHHRSESAFKALAVAIREATSP.NGTNDVPSTKGVLM

..RGVK-------.-.-----------------------------------------------------------------------------------..------------------------.--------------

..-----------.-.------------SN........................RPYAVVE--------------------------------------..------------------------.--------------

..-----------.-.--------------........................-------LGLQREKVGD----------------------------..------------------------.--------------

..-----------.-.--------------........................---------------------------------SRITLHVDCL--..------------------------.--------------

..-----------.-.--------------........................-------------------------------------------RG..KNDHHRSE----------------.--------------

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