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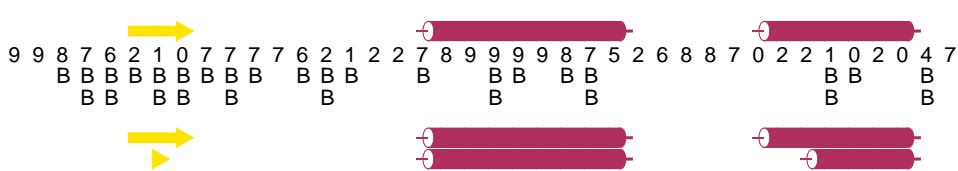
50 60

This figure displays a multiple sequence alignment of UniRef90 proteins. The alignment shows the conservation of amino acids at specific positions, with positions 50 and 60 highlighted in yellow. The sequences vary significantly, reflecting the diversity of the UniRef90 database. The alignment is presented in a grid format where each row represents a different protein sequence.

UniRef90_W9Y4R4
 UniRef90_U1PIH0
 UniRef90_X1U7J7
 UniRef90_T0L1W0
 UniRef90_X0SDQ5
 UniRef90_C5PCA3
 UniRef90_K1WLD7
 UniRef90_X0U1A6
 UniRef90_Q4A2W7
 UniRef90_K4MA03
 UniRef90_O55725
 UniRef90_G1U3I3

1	10	20	30	40
M I P I K C F T C G N V L A D K Y R Y Y E Q E V R K D K T P E G E V L D K L Q	M V G E H W E E F K R R T K E D P E D P E A V L D D L G	M K L L E E G V P D G E A M D Q V G		
M I I P I R C F T C G K E I S S K W E A Y C Y L V N T N K S K E E S L N E L D	M I I P I R C V T C N K I L G D K Q S K Y T E M I E N G I S I E E A L N K L G	M I I P I R C F S C G K V I G D L W E R Y L R R L L D D G R C N G P T R L		
M I I P V R C F S C G K V I G D L W E R Y L K L I D D Q Q V Q D G	M I I P V R C F S C G K V I G D L W E R Y L K L I D D Q Q V Q D G	Y D N Y K K A V E A G E E N P Q K I L D D L G		
M L P P I R C C T C N D L I	K F R E Y D E Q L R	N K S S Q S D A L S N I G		
M I S P L R C F S C N K I M K S P N E K G M V F V R N K K E D R E Q F F K K F N	N E G E D A A K V L D S L G			
M I S P L R C S T C S Q I T G N K W E A C L G L L Q A	K H T E G D A S V S L D			

lupas_21
 lupas_14
 lupas_28
 jnet
 conf
 sol25
 sol5
 solo
 jhmm
 jpssm



The figure shows two protein sequences aligned horizontally. The top sequence is UniRef90_W9Y4R4 and the bottom sequence is UniRef90_O55725. A highly conserved region is highlighted in yellow, spanning from position 50 to approximately 75. Both sequences show a high degree of conservation in this region, with identical or very similar amino acids at most positions.

The diagram illustrates the distribution of components across different variants. Components are represented by arrows (jnet) or colored bars (conf, sol). The variants are listed on the left, and their component counts are shown on the right.

Variant	jnet	conf	sol25	sol5	sol0
lupas_21	6	0	1	1	0
lupas_14	0	B	B	B	B
lupas_28	4	B	B	B	B
jnet	1	0	0	0	1
conf	1	1	0	0	1
sol25	1	1	0	0	1
sol5	3	2	2	4	8
sol0	9	9	9	8	8
jhmm	9	8	6	1	5
ipssm	9	B	B	B	B