	(4)
Multiple Sequence alignment	(MsA)
Suppose 3 Sequences are:	
S1=ATTCGAT	ATT C G AT
$S_2 = TTGAG$ $S_2 = -$	TT - GA GJ JSON
53-ATGCT 353=1 F	
	miss ma
The Star Algorithm for W	15A Approximation to St
depend on distance every	pair séquence
	match
let δ(x/y)=0 if x=y δ(x/y)=1 if x+y	mismatch or Gap
	- GCCAT
SIEGCCAT	= GA _ = T
01100	distance - 3
distance = 2)	(1) × 101/10 = 5
distance included	
by alignment is defined	رت کی ت
(as) => d(si,sj) = 78(at	(b_t)
	match - > 9
	microstCh \leftarrow U
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/ /

S4 = ATT & C AT &C 351= A + G C - T - C D(S1, S4) = 3 S2 = AGAGC (S54 = A T T G C ATGC S3 = TT C TG (S1 = A - 1) G 1 A - GC D(S2, S4) = 4 D(52, 53) = 5 6) S4= A T T G C A T GC T - C - T G -()()3,54) =4 D(S1, S2) + D(S1, S3) + D(S1, S4) = 9 D(52,51) + D(52,53) 7 D(52,54) = 12 D(53, 51) + D(53 + 52) + D(53, 54) = 12 OCS4, S1) + D(S4, S2) + D(S4, S3) = 1 Son is Selected as the Center: SI is the most simillar to other distale 1

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	1 1
Alignment (S_1) S_2 S_3 (S_1+S_2) S_4	52 = AGAGC 53 = TT CTG 54 = ATTGCATGC
S1=A-GAGC S1=A-GAGC S1+S2+S2	
S1 = A T G C T C S1 = A - G A G C S3 = - T C T G	
[S1+S2+S3+S4]	
$S_1 = A T - G C - T - C$ $S_2 - A - G A - G - C$ $S_3 - T - T C - T - C$ $S_4 - A T T G C A T G$	3

ALADIB