

T-COFFEE, Version\_6.85 Tue Sep 9 14:03:25 WEST 2008

Cedric Notredame

CPU TIME:2 sec.

SCORE=80

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BAD AVG GOOD

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I : 80
II : 80
III : 81
con : 80

I 1 MMQESATETISNSSMNQNGMSTLSSQLDAGSRDGRSSGDTSS EVSTVELLHLQQQQA 57
II 1 MMQESATETISNSSMNQNGMSTLSSQLDAGSRDGRSSGDTSS EVSTVELLHLQQQQA 57
III 1 ----- 0
con 1 [color bar] 57

I 58 LQAARQLLLQQQTSGLKSPKSSDKQRPLQ-----VPV 89
II 58 LQAARQLLLQQQTSGLKSPKSSDKQRPLQ ELLPETKLCICGHSSGDGHPHNTFAVPV 114
III 1 ----- 0
con 58 [color bar] 114

I 90 SVAMMTPQVITPQQMQQILQQQVLS PQQQLQALLQQQ QAVMLQQQQQLQEFYKKQQEQL 146
II 115 SVAMMTPQVITPQQMQQILQQQVLS PQQQLQALLQQQ QAVMLQQQQQLQEFYKKQQEQL 171
III 1 ---MMTPQVITPQQMQQILQQQVLS PQQQLQALLQQQ QAVMLQQQQQLQEFYKKQQEQL 54
con 115 [color bar] 171

I 147 HLQLLQQHHPGKQAKEQQQQ 203
II 172 HLQLLQQHHPGKQAKEQQQQ 228
III 55 HLQLLQQHHPGKQAKEQQQQ 111
con 172 [color bar] 228

I 204 QQQQQQLAAQQLVFQQQLLQMQLQQQQHL LSLQRQGLISIPPGQAALPVQSLPQAG 260
II 229 QQQQQQLAAQQLVFQQQLLQMQLQQQQHL LSLQRQGLISIPPGQAALPVQSLPQAG 285
III 112 QQQQQQLAAQQLVFQQQLLQMQLQQQQHL LSLQRQGLISIPPGQAALPVQSLPQAG 168
con 229 [color bar] 285

I 261 LSPAIEIQQQLWKEVTGVHSMEDNGIKHGGLD LTTNNSSTTSSNTSKASPPITHHSIV 317
II 286 LSPAIEIQQQLWKEVTGVHSMEDNGIKHGGLD LTTNNSSTTSSNTSKASPPITHHSIV 342
III 169 LSPAIEIQQQLWKEVTGVHSMEDNGIKHGGLD LTTNNSSTTSSNTSKASPPITHHSIV 225
con 286 [color bar] 342

I	318	NGQSSVLSARRDSSSSHEETGASHTLYGHGVCKWPGCESICEDFGQFLKHLNNEHALD	374
II	343	NGQSSVLSARRDSSSSHEETGASHTLYGHGVCKWPGCESICEDFGQFLKHLNNEHALD	399
III	226	NGQSSVLSARRDSSSSHEETGASHTLYGHGVCKWPGCESICEDFGQFLKHLNNEHALD	282
con	343	*****	399
I	375	DRSTAQCRVQMQVVQQLEIQLSKERERLQAMMTHLHMRPSEP KPSPKPLNLVSSVTM	431
II	400	DRSTAQCRVQMQVVQQLEIQLSKERERLQAMMTHLHMRPSEP KPSPKPLNLVSSVTM	456
III	283	DRSTAQCRVQMQVVQQLEIQLSKERERLQAMMTHLHMRPSEP KPSPKPLNLVSSVTM	339
con	400	*****	456
I	432	SKNMLETSPQSLPQTPTTPTAPVTPITQGPSVITPASVPNVGAI RRRHSDKYNIPMS	488
II	457	SKNMLETSPQSLPQTPTTPTAPVTPITQGPSVITPASVPNVGAI RRRHSDKYNIPMS	513
III	340	SKNMLETSPQSLPQTPTTPTAPVTPITQGPSVITPASVPNVGAI RRRHSDKYNIPMS	396
con	457	*****	513
I	489	SEIAPNYEFYKNADV RPPFTYATLIRQAIMESSDRQLTLNEIYSWFTRTFAYFR RNA	545
II	514	SEIAPNYEFYKNADV RPPFTYATLIRQAIMESSDRQLTLNEIYSWFTRTFAYFR RNA	570
III	397	SEIAPNYEFYKNADV RPPFTYATLIRQAIMESSDRQLTLNEIYSWFTRTFAYFR RNA	453
con	514	*****	570
I	546	ATWKNAVRHNL SLHKCFVRVENVKGAVWTVDEVEYQKRRSQKITGSPTLVKNIPTSL	602
II	571	ATWKNAVRHNL SLHKCFVRVENVKGAVWTVDEVEYQKRRSQKITGSPTLVKNIPTSL	627
III	454	ATWKNAVRHNL SLHKCFVRVENVKGAVWTVDEVEYQKRRSQKITGSPTLVKNIPTSL	510
con	571	*****	627
I	603	YGAAALNASLQAALAESSLPLLSNPGLINNASSG LLQAVHEDLNGSLDHIDSNNGSS	659
II	628	YGAAALNASLQAALAESSLPLLSNPGLINNASSG LLQAVHEDLNGSLDHIDSNNGSS	684
III	511	YGAAALNASLQAALAESSLPLLSNPGLINNASSG LLQAVHEDLNGSLDHIDSNNGSS	567
con	628	*****	684
I	660	PGCSPQPHIHSIHVKEEPVIAEDED CPMSLVTTANHSPELEDDREIEEEPLSEDL E	715
II	685	PGCSPQPHIHSIHVKEEPVIAEDED CPMSLVTTANHSPELEDDREIEEEPLSEDL E	740
III	568	PGCSPQPHIHSIHVKEEPVIAEDED CPMSLVTTANHSPELEDDREIEEEPLSEDL E	623
con	685	*****	740