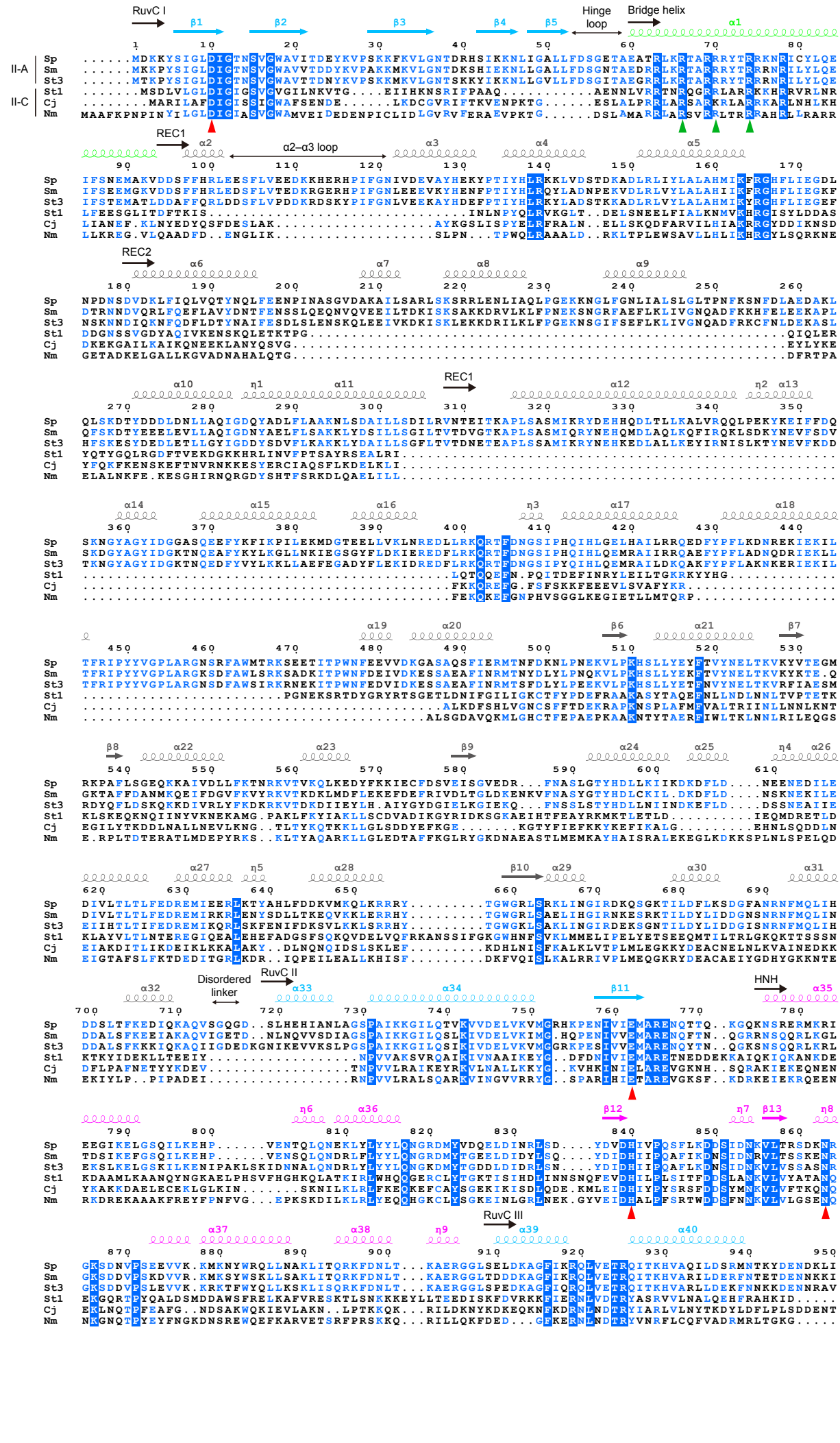
RuvC I
β1
β2
β3
β4
β5
Hinge loop
Bridge helix
α1
II-A
II-C
Sp
Sm
St3
St1
Cj
Nm
REC1
α2
α2–α3 loop
α3
α4
α5
REC2
α6
α7
α8
α9
α10
η1
α11
REC1
α12
η2
α13
α14
α15
α16
η3
α17
α18
α19
α20
β6
α21
β7
β8
α22
α23
β9
α24
α25
η4
α26
α27
η5
α28
β10
α29
α30
α31
Disordered linker
RuvC II
α32
α33
α34
β11
HNH
α35
η6
α36
β12
η7
β13
η8
RuvC III
α37
α38
η9
α39
α40

β14
α41
α42
End-capping loop
960 970 980 990 1000 1010 1020 1030
Sp R.....EVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKA
Sm R.....QVKIVTLKSNLVSNFRKEFELYKVREINDYHHAHDAYLNAVIGKALLGVYPQLEPEFVYGDYPHFHG.....HKENKA
St3 R.....TVKIITLKSTLVSQFRKDFELYKVREINDFHHAHDAYLNAVVASALLKKYPKLEPEFVYGDYPKYNS.....FREKSA
St1 .....TKVSVVRGQFTSQLRRHWGIEKTRDTYHHHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETG.....ELISDD
Cj KLNDTQKGSKVHVEAKSGMLTSALRHTWGFSAKDRNNHLHHAIDAVIIAYANNSIVKAFSDFKKEQESNSAELYAKK.....ISELDY
Nm .....KKRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVACSTVAMQQKITRFVRYKEMNAFDGKTID.....KETGEV
α43 α44 β15 β16 α45 β17 PI
1040 1050 1060 1070 1080 1090 1100 1110
Sp TAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKE.....SILP
Sm TAKKFFYSNIMNFFKKDDVRTD.....KNGEIIWKKDEHISNIKKVLSYPQVNIVKKVEEQTGGFSKE.....SILP
St3 TEKVYFYSNIMNIFKKSISLADGRVIERPLIEVNEETGESVWNKESDLATVRRVLSYPQVNVVKKVEEQNHGLDRGKPKGLFNANLSSKP
St1 EYKESVFKAPYQHFVDTLKSKE.....FEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADETYVLG.....KIKDIY
Cj KNKRKFFEP.....FSGFRQKVLDKIDEIFVS.....KPER
Nm LHQKTHFPQPWEFFAQEVMIRV.....FGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVS.....RAPN
β17–β18 loop β18 β19 α46 α47 η10
1120 1130 1140 1150 1160 1170 1180 1190
Sp KRNSDKLIARKKD...WDPKKYGGFDSPTVAYSVLVVAKVEKGKSK.....KLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDL
Sm KGNSDKLIPRKTKKFYWDTKKYGGFDSPIVAYSILVIADIEKGKSK.....KLKTVKALVGVTIMEKMTFERDPVAFLERKGYRNVQEEN
St3 KPNSNENLVGAKEY..LDPKKYGGYAGISNSFTVLVKGTIEKGAKK.....KITNVLEFQGISILDRINYRKDKLNFLLEKGYKDI..EL
St1 TQDGYDAFMKIYKK...DKSKFLMYRHDPQTFEKVIEPILENYPNKQINEK.GKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYD
Cj KKPSGALHEETFRK...EEEFYQSYGGKEGVLKALELGKIRKVNG.....
Nm RKMSGQGHMETVKS...AKRLDEGVSVLRVPLTQLKLKDLEKMVNREREPKLYEALKARLEAHKDDPAKAFAEPFYKYDKAGNRTQQVKA
β20 β21 η11 β22 β23 α48 α49 α50
1200 1210 1220 1230 1240 1250 1260 1270
Sp IIKLPKYSLFELENGRKRMLASAG.....ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
Sm IIKLPKYSLFKLENGRKRLLASAR.....ELQKGNEIVLPNHLGTLLYHAKNIHKV.....DEPKHLDYVDKHKDEFKELLDVVSNFS
St3 IIELPKYSLFELSDGSRRMLASILSTNNKRGEIHKGNQIFLSQKFVKLLYHAKRISNT.....INENHRKYVENHKKEFEELFYYILEFN
St1 SKLGNHIDITPKDSNNKVVLQSVSPWRADVYFNKTTGKYEILGLKYADLQFEKGTGTY.....KISQEKYNDIKKKEGVDSDSEFKFTLY
Cj .....KIVKNGDMFRVDIFKHKKTNKFYAVPIYTMDFALKVLPNKA.....VARSKKGEIKDWILMDENYEFCFSLY
Nm VRVEQVQKTGVWVRNHNGIADNATMVRVDVFE..KGDKYYLVPIYSWQVAKGILPDRA.....VVQGK..DEEDWQLIDDSFNFKFSLH
α51 α52 η12 β24 β25 η13 β26
1280 1290 1300 1310 1320 1330 1340 1350
Sp KRVILADANLDKVLSAYNKHRDKPIREQAENIIH.....LFTLTNLGAPAAFKYFDTTIDRKR.YTSTKEVLDATLIHQSITGLYE
Sm KKYTLAEGNLEKIKELYAQNNGEDLKELASSFIN.....LLTFTAIGAPATFKFFDKNIDRKR.YTSTTEILNATLIHQSITGLYE
St3 ENYVGAKKNGKLLNSAFQSWQNHSIDELCSSFIGPTGSERKG.LFELTSRGSAADFEFLGVKIPRYRDYTPSSLLKDATLIHQSVTGLYE
St1 KNDLLLVKDTETKEQQLFRFLSRTMPKQKHYVELKPYDKQKFEGGEALIKVLGNVANSGQCKKGLGKSNISIYKVRTDVLGNQHIIKNEG
Cj KDSLILIQTKDMQEPEFVYYNAFTSSTVSLIVSKHDNKFETL.SKNQKILFKNANEKEVIAKSIGIQNLKVFEKYIVSALG.EVTKAEFR
Nm PNDLVEVITKKAR..MFGYFASCHRGTGNINIRIHD.....LDHKIGKNGILEGIGVKTALSFQKYQIDELGKEIRPCRLK
β27 η14
1360
Sp TRIDLSQLGGD
Sm TRIDLNKLGGD
St3 TRIDLAKLGEG
St1 DKPKLDF....
Cj QREDFKK....
Nm KRPPVR.....

Figure S4