A

Predicted nuclease of Sir2 family

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1j8f                                                    EEEE   HH                HHHH        EEEEEE    HHHH              EEE  EEEEEEEE                HHHHHHHHH       EEEEE      HHHHHH
                                                         B1    a2                a3          b2        a8                b3   b4                          a10          b7         a11
157878472|Metaz|Homo sapiens                         47 ICLVGAGISTSAGIPDFRSPSTGLYDNLEK 48 KGLLLRCYTQNIDTLERIAGLEQ--  0 EDLVEAHGTFYTSHC 35 DIVFFGESLPARFFSCMQSDFLK--VDLLLVMGTSLQVQPFASLISK 242
229540344|Planc|Planctomyces limnophilus DSM 3776  27 MWMLGAGASASAGIPTASDMIWEFKQRLFV 80 SDLTRILWTTNFDSLVADACAKVYG 25 PIEIKLHGDFRSRRL  0 KNTDDELRHQDVRLRQLLVECCR--RFGLVVAGYSGRDSIMDALEE 246
148266052|delta|Geobacter uraniireducens Rf4       27 MWLLGAGASASAGIPTAGDMVWEFKQQLFI 80 AQLTRLVWTTNFDSLVADACAKVYD 25 PIEVKLHGDFRSRRL  0 KNTGDELRYQDQRDLRQLLVDSCK--RFGLVVVGYSGRDSIMDALEE 246
146337911|Alpha|Bradyrhizobium sp- ORS278          27 MWLLGAGASAAAGIPTAWDMIWEFKQQLYV 80 GARCQLVWTTNFDPLVADGCAKVYG 25 PVEVKLHGDFRSRRL  0 KNTGDELREQDAKLRALLIDSCC--RWGLVATGYSGRDASVMDTLEA 246
188992492|Gamma|Xanthomonas campestris B100        60 AWLLGAGASAASGIPTGYMILDFKAKLYC 79 SSKAPCVFTTNFDPLIEESLFASS 30 PLIVKLHGDYRSTSL  0 KNTTSELASQDKDMRRAMVEACK--RFGLVVVGYSGRDSSVMEALES 283
146283522|Gamma|Pseudomonas stutzeri A1501         22 AWLLGAGASAAAGIPTGYSMILDFKKRLFC 79 TRRIPCVFTTNFDQLVETATTLTDQ 30 PFLAKLHGDFQSVEL  0 KNTTDELREQDVRMRNALGASCA--RFGLVIVGYSGRDSSVMAALTE 245
192360229|Gamma|Cellvibrio japonicus Ueda107       22 AWFLGAGASASAGIPTGYSMILDFKKHLFC 79 TRRIPCAFTTNFDQLIETATTLTDQ 30 PFLAKLHGDFQSVEL  0 KNTTDELKEQDARMRRVLGAACA--RFGLVIVGYSGRDSSIMAALTQ 245
209515879|Betap|Burkholderia sp. H160                1 ------------MPSAQRCIWEWKRDIFV 80 AGFLRTIWTTNFDGLVSRACTAANV 21 VRLVSLHGDFRYDLL  0 KNTANELREQDLARELLHELK--DYDLVVIGYSGRDSLMCVLSA 203
171321418|Betap|Burkholderia ambifaria MEX-5       34 CLLLGAGASITSGMPSAQRCIWEWKRDIFI 80 AGCVRTIWTTNFDGLVARACTAADV 21 LRLVSLHGDFRYDAL  0 KNTADELREQDAALRKEFLHELK--DYDLIVIGYSGRDSLMRVLSA 249
91783256|Betap|Burkholderia xenovorans LB400       34 MLFLGAGASMTSGMPSANQCIWEWKRDIFL 80 SGLIQTVWTTNFDGLIARAAVATNL 21 LACVSMHGDYRYDRL  0 KNSPGELAQVEVQLRDSLIEALR--THTVVVAGYSGRDSVMCAFRQ 249
170696578|Betap|Burkholderia graminis C4D1M         1 MLFLGAGASMTSGMPSANQCIWEWKRDIFL 80 SGLIQTVWTTNFDGLIARAAAATNL 21 LACVSMHGDYRYDRL  0 KNSSGELAQVEVQLRDSLIEALR--THTVVVAGYSGRDSVMCAFHQ 216
218130589|Bacte|Bacteroides eggerthii DSM 20697   25 GFLLGAGTSLSSGVQSASDCIWDWKREIYC 80 YSIVESVWTTNFDGMTERAAHQMNI 21 LMCISLHGDYKYSTL  0 KNTSSELDNQSEVFCQVMTYYFT--TRHLVVLGYSGRDSLMSALKN 240
154490798|Bacte|Parabacteroides merdae ATCC 43184  27 GVLLGAGASISSGIQSANDCIWDWKFLIYQ 80 YGIVKSVWSTNFDGLVERAAQQANI 21 LLYIALHGDCKFRTL  0 KNTEKELDSQNSEFVSALRRYFV--DKNLIIIGYSGRDSLMSALKE 242
39996462|delta|Geobacter sulfurreducens PCA         21 MWFLGAGTSRSAGLPTASDIIWDLKHRYYC 81 MNQTKVVFTTNFDDVIETAFSDISG 23 PIYAKTHGDFRYQKI  0 KNLTPDLQTNDREIHKCFLAAAI--RFGLVVSGYSGRDPSVMEMLRA 239
84701998|Alpha|Parvularcula bermudensis HTCC2503  37 MWLLGAGASRAAGIKTGWDMIWDFKRSIYR 80 KNLCDIVWTTNFDRLVEDAAAAKFE 25 PVYGKLHGDFQSRSL  0 KNTASELQSQDETLRRALVDACR--TRGLAIVGYSGRDSSVMEALTH 256
189499315|Chlor|Chlorobium phaeobacteroides BS1   25 IWFLGAGTSRTAGMPTANDITWDLKRRYYC 81 LGLTRMVFTTNFDPLVELAAFSNVAE 23 PIYCKLHGDFRYQSV  0 KNLSVDLRDNDKQIEKCFLAAGN--RFGMVVSGYSGRDNVMAMFFS 243
229871911|Bacte|Spirosoma linguale DSM 74           9 LFLLGAGCSRDAGIPVSSEMVDRVQNLILH 113 LGIGLKVFSLNYDLCFEKIVGQKTE 23 YTLYKLHGSLLDWYTD 22 INKLRAIDPYLFYIYEFRRFCFHPDLKLIICIGYSFSDHINDISQ 283
229204038|Bacte|Pedobacter heparinus DSM 2366     11 IILLGAGASCDAGMRNSTQMITDIESLLKG 111 YTMPLRIFSLNYDMCVEENLGMENI 24 YFLYKLHGSLDWKRN 25 QNKLQSYDPYLFYFYAFREACIRSE--LIVISGYGFYDHINDNLSS 285
Consensus 80%:                                         hhhlGAGhS.s.Gh.s..phhhchpp.h.........h..h@chN@D.hh.p.h.........hhphHGshp.pph........ppL......h..h..hh......hhh.GYS.pDpshhphhp.
PSIPRED:                                                EEEE     HH     HHHHHHHHHHHHHH          EEEE  HHHHHHHHHHH        EEEEEEEE     HHH        HHHHHHHHHHHHHHHHHHH     EEEEE      HHHHHH
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61679607|Archa|Archaeoglobus fulgidus (1Y88)          17 LYFQGHMVARLLEEHGFETKTNVIVQGN---CVEQEDDVV----AER---------DGERYMIEGKFHNIPVYTGL---KEAMYTY-ARFLDVEKHG--FTQ---------PWIFTNTKFS 106
194365750|Gamma|Stenotrophomonas maltophilia R551-3  16 YRQFERLGSALLASA------GYSTIDPLGGTGDEGDDAI----IR---------ADSAGRTICFAYTVRA------DWRTKLRSDCNRVRDAGH--TPD---------VFVFACTEVI  98
150378393|Alpha|Sinorhizobium medicae WSM419        10 PDDFENLSRDLVGAE----TGVRFEATV-GADEGDDGR----HAK---------ADGSIILQAKHYLRSGFS-----KLKSKM--REERVSIDEL--APQ---------RYLLTTSVPL  93
16519676|Alpha|Rhizobium sp- NGR234                  10 PDDFENLSRDLVGAE----TGVRFEATV-GADEGDDGR----HAK---------ADGSIILQAKHYLRSGFS-----KLKSKM--REERVSIDEL--APQ---------RYLLTTSVPL  93
162145848|Alpha|Gluconacetobacter diazotrophicus PAl 5  10 HSQFEDLCRDLIGAE----LEVRFEAFPE-GPDDGDDGR----HVT---------ADGAIILQAKHYLRSGSV-----KLLSKM--KAERASIDGL--GPS---------RYLLTTSATL  93
119855143|Actin|Mycobacterium sp. KMS                 10 SAHIGDAGIALIHMR--VSAMGHVWHAR---GLDAGDDGM--IELRDPGT----GVVGNCHLLVQGKASDRQ-FPGETPEKFHFVVD-ERDLEYWLQA--TLP---------VILVCSHPNT 107
223934404|Verru|bacterium Ellin514                   21 NQITGQKGINLIERF--VLEMGFTWTSTSG-ANDAGDDGI--IEIRDPAT----GEANNLIVQVQGKATETE-FESETATSFVYRVK-ERDLNYWLQG--NAP---------VLLVVSRPSK 120
94311100|Betap|Ralstonia metallidurans CH34           9 SQLLGTQGTGLIELT--VSRMGLVWRFTA--QHDAGDDGE--IEIRDAAN----GRMTGMLLKVQGKAVSEF--KNETNAGFDYWPD-SRDMDYWLGH--SVP---------VILIVSRPST 106
154244390|Alpha|Xanthobacter autotrophicus Py2       8 SQVIGEGLETAIKKI--VLETGFLYEQRG--RLEAGDDGI--IELRDPKS----GAPLGKLLGVQGKSTESGQYVRENDNSFEYLLK-PDDLKYWRTS--NIP---------VIIVLWRKSD 107
13475182|Alpha|Mesorhizobium loti MAFF303099        41 NQLLGQIGEIAVQLR--FLTMGFQFDVRS--RLESGDDGI--AEVMIE------GQPTARMIAVQGKSATDAGIYAGEDASGFTYLLR-SEDLAYWRGS--NLP---------IIIVLFRKSD 138
182676906|Alpha|Beijerinckia indica ATCC 9039        8 SQLIGELGEAAVRKR--FLSMGFQFDLRG--RLEAGDDGI--AEIMIE------GEPTARMIAVQGKSTRAGTYTSETDSGFSYLLN-SKDLYYWRTS--NLP---------VILVLYRESD 105
84686688|Alpha|Rhodobacterales bacterium HTCC2654    8 SQRIGEIGEKAANLQ--FLRIGFQFDGRS--RLEAGDDGI--AEVMDD------DQPTAKMIAVQGKSTERGSYVGETDAGFTYRVR-ASDFDYWRGS--NLP---------VILVLYRQSD 105
83954753|Alpha|Sulfitobacter sp. NAS-14-1            8 NQITGEAGEAIIKAE--FLKVGLIYQCFG--RLESGDDGV--VELRDPNT----GVTSSQFVAVQGKPTVKGRYSFETDTSFDYLID-PKDLANWKQA--NLP---------VIIALHRLED 107
223987887|Gamma|Providencia rettgeri DSM 1131        33 NLSLEDALIPVLKEV--FNLPRLVNLNSKQ-KNFEGDDGD------LGD---------EYDRIAFQVTSTSGIDKV-------------KKTLSVFLEHGFENNFD--------ELFILILSEK 115
227332661|Gamma|Citrobacter youngae ATCC 29220       33 NLALEDAFIPVLKEV--FQLPHLFNLNSQQ-KNFEGDDGD------LGD---------EYDRVAFQVTSSTGLEKV-------------KKTLSQFIEKRFYESFD--------ELYILTLVEK 115
117922289|Gamma|Shewanella sp. ANA-3                 33 NLISEDAWIPILKEV--YQCPNLVNLNRKH-KNFEGDDGD------LGD---------EQDRVAFQVTSSTDIEKV-------------KSTLEQFKKRNYKNAFD--------ELYIFMLRSK 115
84702494|Alpha|Parvularcula bermudensis HTCC2503     7 NKICEDLVCGLIREL--YGFDGLRNLNAEEKQNFEGDDGD------LAD---------DRARVAIQVTSDRSLDKI-------------KDTLAKCVKYKHYEKYD--------RIIVYILTKK  90
124262647|Betap|Methylibium petroleiphilum PM1        7 HRASEGLVLGLLREL--YGWPRLRNLNTEERTNFEGDDGD------LAD---------DEARVAVQVTGTPTLDKI-------------KGTVSTFLTHGLDKRYD--------RLVIYVLTRK  90
149175029|Planc|Planctomyces maris DSM 8797           8 SKFTELRGLDRISHI--THEMNCLFRVIS--QDDVGGDDGE--IEVVTPKVDGNGYETSGGIIKVQGKSGTSYVKKD-HGLTFATPVR-MDDLEYWNHC--TFP---------VFFIVYHPDD 110
222476010|Halob|Halorubrum lacusprofundi ATCC 49239  14 ARRGEDYKEVVIEY--------MEGLN-----YMVEEDSAFHSTLDDIQFVNK---ATGDKVVAEAKAYSTGLSPN------DFRDELARYFIEYIKQ--PQPHRF-------DFYIFTETLS 105
20089857|Metha|Methanosarcina acetivorans C2A        14 TQNSKEYGKKIIEF--------LNLQG-----YHLEEDSNIEGIFSDKVFRNPKL-DGYKRTVWEAKETKLSLSDT------DFLKEFAKYFMSSLKE--EFN---------LFIFVREVA 103
Consensus 80%:                                         .....phs..hhp.......sh.h.s.......s.hD.....h.............s...hhhphp.....................p.h..h..h.p.................hhhh.p...
PSIPRED:                                               HHHHHHHHHHHHHH  HH   EEE              EE       EEEE        EEEEEEEE                HHHHHHHH                eeeeeee
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61679607|Archa|Archaeoglobus fulgidus (1Y88)          17 LYFQGHMVARLLEEHGFETKTNVIVQGNCV---EQEDDVVAER-------------DGERYMIEGKFHNIPVYTGLKEAMYTY----ARFLDVEKH------------GFTQPWIFTNTKFS 106
1Y88                                                   HHHHHHHHHHHH    EEEEEEEEEE          EEEEEEEEE                EEEEEEE          HHHHHHHH    HHHHHHHH                EEEEE
110639331|Bacte|Cytophaga hutchinsonii ATCC 33406     230 EYDVQDVLHTMLIGIFPDLKFEEQVQRTGAK--NTRMDFALD---------------SEGILLEAKMISDNY---------------KDEKEFIEQLKKDIESYFVYP-NLKDVIFFVYAPD 318
116749910|delta|Syntrophobacter fumaroxidans MPOB     289 EYHVQNLLCALLAPIFPDLDDEQYLTKIGQK--SPRADLYIF---------------SMKFIVFTKFIRTG---------------DKMQKVIDESIADASLYNAMGNECAGIIPFIWDDS 377
147677057|Clost|Pelotomaculum thermopropionicum SI  301 EYHVQDLLWVILAPIFPDLEDEENLPSLGHK--HPRQDLGIP---------------SLRLIIEKGKIYNGTS--------------SEFSRIIEEVASDASLYLSNDSGYDKIIVFVWDNS 391
84702442|Alpha|Parvularcula bermudensis HTCC2503    260 EYHVQNLLWTILRPIFPDLVDEETLKKLGHT--SPRQDLGIP---------------SLSTIIEKGKVVRRRGQ--------------SALKAITDEIAADHSLYLREGTGFARMIAFIWDEQ 350
21225131|Actin|Streptomyces coelicolor                296 EREIQNILWLMLRPVFDDLVDEETLRRIGHS--TYRADFGIP---------------SLELLIEKGKARKA---------------ADFKSFEKEIFEDYIGYLSDNTAYRHMTVFIYDES 384
225874784|Acido|Acidobacterium capsulatum ATCC 51196 279 EREVQDILWLILRSYFNDVVDEDTLPKLGHS--TYRADFGIG---------------SLKLIIEKGKFANSK---------------DDFKKIEKEVQEDCIPYLRD-LRYEALIVFIYDDS 366
222110534|Betap|Diaphorobacter sp. TPSY              278 EYHFQNLLCAVLAPVVPDLRDEEWLASVGQK--KPRADLVIF---------------SLHLVIEKGKWRTR---------------SSPQDLISQIGEDVSLYLKRGSPYRKVLPIIWDQG 366
Consensus 80%:                                         .....phhh.hh..h.ssh.sEp.h.h.pp..p.RhDhshs...................phhIEhKhhp.................sp..ph..ph..ph..Yh.....h.hh.h.@s.s
PSIPRED:                                               HHHHHHHHHHHHHHH      HHHHHHHH       HHH                    EEEEEEEE                HHHHHHHHHHHHHHHHHH       EEEEEEE
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