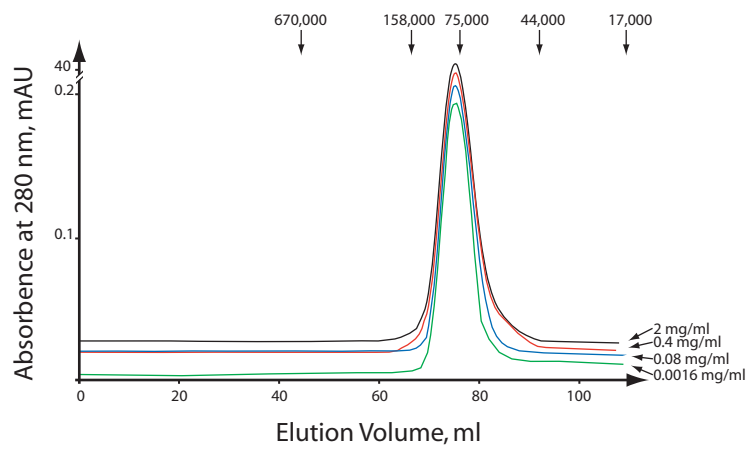


Legends to supplementary figures

SUPPLEMENTARY FIGURE S1. **Human SpmSyn is a dimer in solution.** 1 ml samples of purified SpmSyn solution of decreasing concentration were analyzed by size exclusion chromatography on a Superdex200 column. Arrows indicate the position of the size of standards: 670 kDa, thyroglobulin; 158 kDa, bovine γ -globulin; 75 kDa, conalbumin; 44 kDa, chicken ovalbumin; 17 kDa, equine myoglobin. All protein standards were purchased from BioRad.

SUPPLEMENTARY FIGURE S2. **Alignment of SpmSyn N-termini with prokaryotic AdoMetDCs.** Letters in brackets in the figure refer to eukaryotes (E), eubacteria (B), archaea (A) and bacteriophage (P) species. All the C-terminal aminopropyltransferase domains have been removed from the eukaryotic sequences and the bacterial fusion proteins from *Azoarcus* sp. EbN1, *Nocardia farcinica* IFM10152 and *Candidatus Pelagibacter ubique* HTCC1002. Amino acids have been truncated from the C-termini of some of the bacterial AdoMetDC sequences to facilitate the alignment. The bacterial phylum of each species is indicated after the accession number. Sequences shown are: H.sa, *Homo sapiens* (NP_004586); G.ga, *Gallus gallus* (NP_001025974 chicken); D.re, *Danio rerio* (NP_571831 zebra fish); D.me, *Drosophila melanogaster* (NP_729798 fruit fly); A.ga, *Anopheles gambiae* str. PEST (XP_315341 mosquito); A.me, *Apis mellifera* (XP_393567 bee); M.br, *Monosiga brevicollis* (JGI protein ID 30201 Choanoflagellida); S.pu, *Strongylocentrotus purpuratus* (XP_789223 sea urchin); C.sa, *Caldicellulosiruptor saccharolyticus* DSM 8903 (ZP_00884629 Firmicutes); C.te, *Clostridium tetani* E88 (NP_781940 Firmicutes); T.ma, *Thermotoga maritima* MSB8 (NP_228464 Thermotogae); M.ma, *Microscilla marina* ATCC 23134 (ZP_01693282 Bacterioidetes-Chlorobi); L.in, *Leptospira interrogans* serovar Copenhageni str. Fiocruz L1-130 (YP_003624 Spirochaetes); N.sp, *Nitratiruptor* sp. SB155-2 (YP_001356990 ϵ -Proteobacteria); L.sp, *Leptospirillum* sp. Group II UBA (EAY55693 Nitrospirae); P.fu, *Pyrococcus furiosus* DSM 3638 (NP_579659 Euryarchaeota, Thermococci); H.bu, *Hyperthermus butylicus* DSM 5456 (YP_001013262 Crenarchaeota, Thermoprotei); A.pe1, *Aeropyrum pernix* K1 (NP_147382 Crenarchaeota, Thermoprotei); A.pe2, *Aeropyrum pernix* K1 (NP_146946 Crenarchaeota, Thermoprotei); N.fa, *Nocardia farcinica* IFM10152 (YP_119998 Actinobacteria); S.er, *Saccharopolyspora erythraea* NRRL2338 (YP_001103517 Actinobacteria); H.au, *Herpetosiphon auranticus* ATCC 23779 (ZP_01423997 Chloroflexi); S.th, *Symbiobacterium thermophilum* IAM 14863 (YP_074250 Firmicutes); R.me, *Ralstonia metallidurans* CH34 (YP_585598 β -Proteobacteria); J.sp, *Jannaschia* sp. CCS1 (YP_510370 α -Proteobacteria); T.cr, *Thiomicrospira crunogena* XCL-2 (YP_390542 γ -Proteobacteria); T.ths, *Tetrahymena thermophila* (EAS07189 Ciliata); T.thr, *Tetrahymena thermophila* (EAR85566 Ciliata); P.ub, *Candidatus Pelagibacter ubique* HTCC1002 (ZP_01264992 α -Proteobacteria); S.el, *Synechococcus elongatus* PCC 6301 (YP_172760 Cyanobacteria); C.sp, Cyanophage S-PM2 (YP_195224); K.st, *Candidatus Kuenia stuttgartiensis* (CAJ71430 Planctomycetes); C.ps, Cyanophage P-SSM4 (YP_214675); A.ae, *Aquifex aeolicus* VF5 (NP_213175 Aquificales); A.sp, *Azoarcus* sp. EbN1 (YP_158219 β -Proteobacteria); M.hu, *Methanospirillum hungatei* JF-1 (YP_504294 Euryarchaeota, Methanomicrobia); T.th, *Thermus thermophilus* HB27 (YP_004448 Deinococcus-Thermus); T.ys, *Thermus thermophilus* phage YS40 (YP_874018); A.el, *Acidobacterium* bacterium Ellin345 (YP_589185 Acidobacteria).



Supplementary figure S1

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H.sa (E) : -----MAAARSTLDFMLGA---KADGETIHK-----GLOSI--F : 30
G.ga (E) : -----MAAARSTLDFMLGA---TADCNVTK-----ALQPV--F : 30
D.re (E) : -----MAVLVTLDFKLRA---PADVSATVR-----GLOSI--F : 29
D.me (E) : -----MAAQITLDFDTLTK---DKTAEDEARLQVAKILRNELEQL--F : 38
A.ga (E) : -----MSANSLLDFFSLDP---ARIIDEVSRKDIVRVCKEGLEKY--L : 38
A.me (E) : -----MVAHTVLLDFTVPS---NVIVDVEKRSTLKLAIITNVLOEY--F : 38
M.br (E) : -----MAALTLASRACLNALLCLLCT---MAALTLASRACLNALLCLLCT--- : 22
S.pu (E) : -----MDVVTVLLDFRVES---EILDNLCOQGSKINEQLKQALSSVVG-L : 40
C.sa (B) : -----MHALGRHIIAELYGCD---KEVLNRRERIKEMIVESALKAGAEV--R : 42
C.te (B) : -----MNNLGRHIIAELYGCD---ELIILNDKEYERIMVDSALKSGAEV--R : 42
B.su (B) * : -----MTMETMGRHIVISELWGCDFDKLNDMDFEKTFFVNAALKSGAEV--R : 44
T.ma (B) * : -----MKSLSGRHLVAEFYECD---REVLDNVQLIEQEMKQAAYESGATI--V : 42
M.ma (B) : -----MKALGQHLVLEFYGCP---EEMKDNHLEKVMNEAAKASGATI--V : 42
L.in (B) : -----MNALGKHVIAEFYECD---YETINNHELVEDIMLKSVDLSGATT--I : 42
N.sp (B) : -----MKSLGKHLVAEYRC---ENAINDVQKVEEALVKAAIAGATV--I : 42
L.sp (B) : -----MHALGTLLVELKDCQ---NERLNDVSPRQAMLDAALEAKATI--V : 42
P.fu (A) : -----MDTIGYVVVEAAGCD---PEVIADPNKREIFLEAAKVGNNMEV--K : 42
H.bu (A) : -----MKTIIATIRPRKPAEGEPRVYGMVFGNLYECN---VETLRDEKRREIVVEAAKVGNNMTL--L : 59
A.pe1 (A) : -----MAQIPSSR--TNGSQAQMRVPLGVYGNFYECAN---TELLKSPERKVVLEAAAREGGMTL--L : 58
A.pe2 (A) : -----MERR---EDVIVGKHYVGSYLVGP---REKATDEEYRGVVVRAAESAGATV--H : 47
N.fa (B) : -----TAEFTGHWLVAEFGVD---AALCDDLREPERESALRESLIAAGVTI--C : 48
S.er (B) : -----MS---IDTGTLPQVGLFTGQVLALEEGVD---PDLIDDEQFERTLQSLALDRSYATV--C : 53
H.au (B) : -----MSNFIQS---PIYPAAGRLLANLGGCS---AAILNDRDLQTIIVMOAANATNATV--L : 51
S.th (B) : -----MAYSTYGRHITMDLREVA---FEKLNDRVFRKEMVVEAAQCGATV--V : 44
R.me (B) : -----MNAPTLCAPPV---GRLLLDMQGV---AARLTDVAVLERVLYDAARVSGATV--V : 50
J.sp (B) : -----MKRHCETTQHRIRPCPCPHSHHNIPSMNTNTPPTVPHHTHLTHNGEDTYAGTLLIIDLH--N--AQNLNRRTHLEQALRDATKATGATL--L : 87
T.cr (B) : -----MPNSENVLVTGNDHFVEIKTTVIDDTPWTHDQAIEDQTLDFHFCRDKGTFTAGTLLIADFVW---ASHLLDLALREKALREAVEKAKATL--L : 88
T.ths (E) : -----MADEVVRNKMKGKLLIDFGQVVE---KVDLNSFAVLDKLFKDTLVSVDITV--E : 48
T.thr (E) : -----MGATMLDFHNVE---KIDLSDAKKQOGIFEAALKLTDCNV--C : 39
P.u (B) : -----MTKVGHEITLTDIIGTN---REYDPSVYENVIRKIAKAAEVTTI--L : 40
S.el (B) : -----MTVSLNPLLDAPPALGVGRCTLEIYGCA---GELLNDAAYVDRSIRREAAIAGATL--L : 55
M.ja (A) * : -----MLKYLKGLLILELWGCDFPKALDDIEGHEKMLVDSVKAAGATL--I : 43
C.sp (P) : -----MGDFLLNLFECD---SDRLDDEDLRKILINAATSADMTI--I : 39
K.st (B) : -----MALLGKHLILEMKGCC---RDIINNVSCKNILEKATEISNATL--V : 42
C.ps (P) : -----MN---APLNDEEYKETEIEAAKIGKLEV--L : 27
A.ae (B) : -----MAKTLGLHLLADLYGVD---ADKIDRVEDRELLEGAVKYANLTK--I : 43
A.sp (B) : -----MVHVNISPFPKFRDIERPMMGLHLLIADLYRCGTTAAALTBREARETELICVQCQREAGLTP--L : 60
M.hu (A) : -----MNGLHLLIADMYRCTCTADLLCDQSKIEKLCVSDACMNAGLTP--L : 42
T.th (B) : -----METVPGGRVVAEIVGCD---VDILEDPKMVEAALVDVMRLKGRAPDSA : 45
T.ys (P) : -----MWGLIFLTKLYNFVKNKQVPTGTEVILELRVME---GKDFRDKIKFFFYDILLKSNATI--L : 60
A.el (B) : -----MGIIEWIVEAQGCR---AADLRSLAAQELFADLTIRDLHDHVV--G : 41

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H.sa (E) : -----QEQGMAESVHTWDHGYLATYTNKNGSFANLRIYP-HGLVLLDIQSYDGDQAQ-----GKEEIDSILNKVVERMELSPDNK----- : 106
G.ga (E) : -----QEQGMTETVHNWEDHGYLATYTNKNGSFANLRIHP-HGLVLLDIQSYNDHTK-----GREETDQLLNNKVEERMKEFLHQLNG----- : 106
D.re (E) : -----QEQEMTENVHDSEGHGYLATYTNKNSRFALLRMHS-HGLVTFDLQCLEGDD-----AAQVNDLNLNALEKKLKALLDGNIQ----- : 103
D.me (E) : -----PQLELAYSMPESPENGYFAVHEN-KDTVITCRIFG-HGLLTLNVEYFLPDGK-----EPSISFDTRMTEMLILRQKFPDSD----- : 111
A.ga (E) : -----AGLKISYDMLTT-DGYLCISETGTGTIVTIRIFG-OGLITINVEYRKDDG-----EAKISFEQIRLENLILRQKLFKN----- : 111
A.me (E) : -----DSLKP--LTSSIDGSLVLYTGPRGSLITVRGYT-EGLITINVEYRKDEE-----EALLDFEQWRVLEADVAMALNSQ----- : 110
M.br (E) : -----DISFFQAQG---PKSAAALITSPNSPHSQIKAFETVTADIISLSLAAE-----EAAPDITDALERVRATATESLKAAPVQHL : 97
S.pu (E) : -----GDNIQVHSS---GEOLFCSFGHARSAMFEGHR-PDLVTFQFYDRKAKP-----SPTNENLPVLEEGSMEALKEELKVF : 112
C.sa (B) : -----EVAFHKFSP---QCVSGVVIISESHLIHTWPE-LGYAAVDVFCGGRVD-----PWQACNYTEMELKASHMTTTEVRRG----- : 113
C.te (B) : -----EVAFHKFSP---QCVSGVVIISESHLIHTWPE-LGYAAVDVFCGGRVNV-----PWDACNYGEKLNANKNITATEVRRG----- : 113
B.su (B) * : -----EVAFHKFSP---QCVSGVVIISESHLIHTWPE-HGYAADDVFCGQD-----LDPNVAADYIABAHADTR-ENIEIIPRGMGVPQIQRG : 123
T.ma (B) * : -----TSFTHRFELP---YCVSGVVIISESHLIHTWPE-YGYAADDVFCGQD-----PWKAFELHKKALKAKRVHVVHEHRGRVDEIG : 119
M.ma (B) : -----GSHFHTFNP---YCVSGVVIISESHLIHTWPE-YGYAADDVFCGQD-----NLLAFDYMKRHLKPQNTSTIEMKRGQLQNM : 119
L.in (B) : -----KSVFHRFSP---YCVSGVVIISESHLIHTWPE-YGYAADDVFCGDLID-----NQAADLYLKEKFGSKNVSVMEMKRG-VLNLG : 118
N.sp (B) : -----GKSPHRFSP---YCVSGVVIISESHLIHTWPE-YGYAADDVFCGQD-----PMKAEYHKEVFPQTQATVETILRG-VLNI-- : 117
L.sp (B) : -----DERFHFSP---FVSGVVIISESHLIHTWPE-YRYAADDVFCGDTLK-----PEVAALHAKKFPVSNNSPILSVKRGIGIQN : 119
P.fu (A) : -----ASYFFKFSP---MCVSGVVIISESHLIHTWPE-KGYAADDVFCGQKAD-----PEKAVDYLLEKPKAKYAHVSELKRG-IEEED : 118
H.bu (A) : -----DVKSWKIG---ECSVVVALVLESHLIHTWPE-YAFATVDVYSCGKHTN-----PEKAFNYVVALGAKR-----VERQATRHL : 130
A.pe1 (A) : -----DIKSWKI--G---ECSVVVALVLESHLIHTWPE-YRFATVDVYSCGQHTN-----PHRAFEVVAEALKPAR-----VEKQVATRHL : 129
A.pe2 (A) : -----AVNSWTI--PGE-K-GCSVVVALVLESHLIHTWPE-YDYATVDVYTCGEHTD-----PWKAFELHSELKPKRYTVHYVDRSQEKTVL : 126
N.fa (B) : -----DVVHKFSP---QCVTVLALLSESHASHTWPE-SGDIFVDVFCGSGIG-----AGATKAVELRDALAPANVRMQVQIR-----GH : 121
S.er (B) : -----EMIARRFSP---QCVTVLALLSESHASHTWPE-NGSIFVDVFCGHT-----AQPERAVALLAEALSPTAVNTQTIRH-----GH : 125
H.au (B) : -----EIVAHQFTP---HCVTVLALLSESHASHTWPE-HGAFAVDVFCGQY-----CQPEASLGVVVALHATNVHSQLIDRTISEVQT : 128
S.th (B) : -----GESFVQFSP---QCVTVLALLSESHLIHTWPE-EGFAADDVFCGQY-----VDPVAVACYLKAALGGRVVTAYALRRGSGAIED : 121
R.me (B) : -----DARFQHFSP---GLCVTVLALLSESHASHTWPE-YGFAADDVFCGGAQ-----PHRGIEMVAELAPAQWHVDAARGPASAGS : 127
J.sp (B) : -----SLSHHHFSP---QCVTVLALLSESHASHTWPE-IGFAADDVFCGQD-----PHAAIPVKAATDIDHVKELHRGLRQR-- : 161
T.cr (B) : -----HIHLHHFSP---NGSISGVALVAESHISVHSWPE-RNYAADDVFCGQD-----PAKAEVLEAAPTSPKVGVDNLRGBVTDND : 165
T.ths (E) : -----DIQKKEFVP---QGLTALYMLRSGLTIHHSWPE-SKACATDFHSHGVDTWNTVRHVEECLCDAMGWENCTSTVTIPRGVHSRLYCNENQAKC : 136
T.thr (E) : -----DKRVKVFPP---GQVSLIFLSESHMSFHSWPE-EKCATVDVFNCGQNSRFNCRTVBEEQLCNAPFGWECCTSNIMNRGTEAKLITNDYSKHT : 127
P.u (B) : -----EISKYKFP---QCVTVLALLSESHISHTWPE-KGIISEFFFCGQV-----PSALDIFVKEFKHKRIYTKAFDRDT : 111
S.el (B) : -----NOVCHEFSP---QCVTVLALLSESHASHTWPE-NGYAADDVFCGQHT-----QPEVACHHLLIQALNPKRIDQVHERPPIESPAADR : 132
M.ja (A) * : -----CVRTHKFSP---QCATGVALVAESHIAHTWPE-YGYAADDVFCGQEH-----TDPYKALEVIREFLKPKSIQIIDLKRGLMENGTFELK : 124
C.sp (P) : -----DMMSKHFSP---QCVTVLALLSESHASHTWPE-EYKAAVDVFCGQTKA-----KPRVACEIISHLNCIHFNKIHIVRN----- : 110
K.st (B) : -----DKRVKVFPP---YCVTVLALLSESHASHTWPE-HEYAADDVFCGQTMN-----PHNAASYISQAQHAKEFTFMELRGGDFDLHE : 119
C.ps (P) : -----KVDTHKFSP---HCVTVLALLSESHASHTWPE-DNVARCDELSCNPDTD-----YKAVIRYVQDRFNSMVEVKWGCDSRNWNL-- : 101
A.ae (B) : -----SSHYYQFQP---HCATGVALVAESHISHTWPE-HGLATVDVYFCGQPSK-----AYRAMDYITITQLNPKRIDQVHERPPIESPAADR : 120
A.sp (B) : -----GSFYQFRDESGAAAQVTVTVLALLSESHLIHTWPE-SGCVTVLVDVYVCNFSRDN-----DRARMVYRAVIDALRPAEIVGHEVVRGRLEPEKY : 146
M.hu (A) : -----GTYFHFQFMDENGNKAEVTVGNVVAESHLIHTWPE-NGVTVLVDVYVCNFSRDN-----DRARQTFQEVTSALAPEEMASHEVIRGAINAR : 128
T.th (B) : -----QSVVYQFHP---QCLSAAVVSPVAAVMVHTWPE-DNASATLDLVYFNRGDV-----PEEVLKGLTRAFGAKESAFRYWRGTEHAIK : 123
T.ys (P) : -----DCKHFVFPN---EASSGVCLLSESHLSHTWPE-ID-EGVSLDIYFCGNSFN-----HIKALSIKENVFIDDIKILKRGINKRGMKY : 137
A.el (B) : -----EMRWQHFPGS---NEVTFGALLSESHLAHTWPE-HQSLCLNLECCRPRN-----WDFVGELOVRLGADRNVRRVVERPYVADAD : 118

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Supplementary Figure S2