A

```
Pf SufS   ------------------------MLRGPRCLYI------YLFFV---FLPFSFCYIRNNDNR   30
Bs SufS   ------------------------------------------------------------    0
Ec SufS   ------------------------------------------------------------    0
At cNif1  ------------------MEGVAMK-----------LP---SFPNA---ISIGHRS        21
Pf IscS   MKFLQIIKHL-KL-QNKKNALDNFVNCRTYEHISNINKLFLNNFSSTKEHSEHGQVKHEN   58
Bs YrvO   ------------------------------------------------------------    0
Ec IscS   ------------------------------------------------------------    0
At mNif1  MASKVIS---ATIRRTLTKPHGTFSRCR-----------YL----STA---AA-------   32
Sc Nfs1   MLKSTATRSITRLSQVYNVPAATYRACLVSRR-------FY----SPP---AAGVKLDDN   46


Pf SufS   FVY-----------------------------------IVKSIRKGPNIK-------LR----   47
Bs SufS   ------------------------------------------------------------     0
Ec SufS   ------------------------------------------------------------     0
At cNif1  FSR------------------------VRCSSSLSV----CSAA---                37
Pf IscS   FLNSTLKYEENSQNGSTNNLKNGKYNMYVSEGNVNINEEKYKDNNISSNNTQYNNNSSNS  118
Bs YrvO   ------------------------------------------------------------     0
Ec IscS   ------------------------------------------------------------     0
At mNif1  ------------------------------------------------------------    32
Sc Nfs1   FS-------------------------LETHTDIQA---------AAKAQASARASAS     70


Pf SufS   -LTKDEKPNIDNHIIDYFKNVREHFPFFKE---NKSLIYFDSAATTHKPSCVIEKMSEFY  103
Bs SufS   --------------MNITDIREQFPILHQQVNGHDLVYLDSAATSQKPRAVIETLDKYY    45
Ec SufS   ------------MIFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFY    47
At cNif1  -AASSATISTDSESVSLGHRVRKDFRILHQEVNGSKLVYLDSAATSQKPAAVLDALQNYY   96
Pf IscS   GSLNDEGPL-WKEHID--------DVVNENKKKKMNRFYLDSQATTMIDPRVLDKMLPYM  169
Bs YrvO   --------------------------MERIYLDHAATSPMDERVLEQMIPHF           26
Ec IscS   -------------------------MKLPIYLDYSATTPVDPRVAEKMMQFM           27
At mNif1  ---ATEV----NYEDE--------SIMMKGVRISGRPLYLDMQATTPIDPRVFDAMNASQ   77
Sc Nfs1   GTTPDAVVASGSTAMS-------HAYQENTGFGTRPIYLDMQATTPTDPRVLDTMLKFY  122


Pf SufS   --KKENSNIHRGIYKLSHNATNNYEKVRETIKEYINCEKNDNIIFTNGSTYGLNVVCKMM  161
Bs SufS   --NQYNSNVHRGVHTLGTRATDGYEGAREKVRKFINAKSMAEIIFTKGTTTSLNMVALSY  103
Ec SufS   --RHGYAAVHRGIHTLSAQATEKMENVRKRASLFINARSAEELVFVRGTTEGINLVANSW  105
At cNif1  --EFYNSNVHRGIHYLSAKATDEFELARKKVARFINASDSREIVFTRNATEAINLVAYSW  154
Pf IscS   --TYIYGNAHSRNHFFGWESEKAVEDARTNLLNLINGKNNKEIIFTSGATESNNLALIGI  227
Bs YrvO   --SGSFGNPSS-IHSFGRESRKWVDEARAQIAAEIG-AAEQEIIFTSGGTEADNLAIMGT   82
Ec IscS   TMDGTFGNPASRSHRFGWQAEEAVDIARNQIADLVG-ADPREIVFTSGATESDNLAIKGA   86
At mNif1  --IHEYGNPHSRTHLYGWEAENAVENARNQVAKLIE-ASPKEIVFVSGATEANNMAVKGV  134
Sc Nfs1   --TGLYGNPHSNTHSYGWETNTAVENARAHVAKMIN-ADPKEIIFTSGATESNNMVLKGV  179


                                  *
Pf SufS   IEEI--IKKEEDEIYLSYMEHHSNIIPWQEYINKEKKGRIKYVPLNKSGYINIKKLISNM  219
Bs SufS   ARAN---LKPGDEVVITYMEHHANIIPWQQAVKA-TGATLKYIPLQEDGTISLEDVRETV  159
Ec SufS   GNSN---VRAGDNIIISQMEHHANIVPWQMLCAR-VGAELRVIPLNPDGTLQLETLPTLF  161
At cNif1  GLSN---LKPGDEVILTVAEHHSCIVPWQIVSQK-TGAVLKFVTLNEDEVPDINKLRELI  210
Pf IscS   CTYYNKLNKQKNHIITSQIEHKCILQTCRFLQ-T-KGFEVTYLKPDTNGLVKLDDIKNSI  285
Bs YrvO   ALARKD---LGRHIITTKIEHHAVLHTCEKLE-G-DGFDITYLDVDQNGRVSAKQVKEAL  137
Ec IscS   ANFYQK---KGKHIISKTEHKAVLDTCRQLE-R-EGFEVTYLAPQRNGIIDLKELEAAM  141
At mNif1  MHFYKD---TKKHVITTQTEHKCVLDSCRHLQ-Q-EGFEVTYLPVKTDGLVDLEMLREAI  189
Sc Nfs1   PRFYKK---TKKHIITTRTEHKCVLEAARAMM-K-EGFEVTFLNVDDQGLIDLKELEDAI  234


Pf SufS   NINTKVISICHASNVIGNIQNIEKIIKKIKNVYPHIIIIIDASQSFAHIKYDIKKMKKNK  279
Bs SufS   TSNTKIVAVSHVSNVLGTVNPIKEMAKIAHDNG--AVIVVDGAQSTPHMKIDVQDLD---  214
Ec SufS   DEKTRLLAITHVSNVLGTENPLAEMITLAHQHG--AKVLVDGAQAVMHHPVDVQALD---  216
At cNif1  SPKTKLVAVHHVSNVLASSLPIEEIVVWAHDVG--AKVLVDACQSVPHMVVDVQKLN---  265
Pf IscS   KDNTIMASFIFVNNEIGVIQDIENIGNLCKEKN--ILFHTDASQAAGKVPIDVQKMN---  340
Bs YrvO   RDDTILVTVMYGNNEVGTVQPIEEIGELLKEHK--AYFHTDAVQAFGLLPIDVKNSH---  192
Ec IscS   RDDTILVSIMHVNNEIGVVQDIAAIGEMCRARG--IIYHVDATQSVGKLPIDLSQLK---  196
At mNif1  RPDTGLVSIMAVNNEIGVVQPMEEIGMICKEHN--VPFHTDAAQAIGKIPVDVKKWN---  244
Sc Nfs1   RPDTCLVSVMAVNNEIGVIQPIKEIGAICRKNK--IYFHTDAAQAYGKIHIDVNEMN---  289
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Pf SufS   SCPDILITSGHKFCASLGTGFIFINKELSSKYKFKPLLYGSNIITNVSKYKSKFVTSLSE   339
Bs SufS   --CDFFALSSHKMCGPTGVGVLYGKKALLE--NMEPAEFGGEMIDFVGLYE-STWKELPW   269
Ec SufS   --CDFYVFSGHKLYGPTGIGILYVKEALLQ--EMPPWEGGGSMIATVSLSEGTTWTKAPW   272
At cNif1  --ADFLVASSHKMCGPTGIGFLYGKSDLLH--SMPPFLGGGEMISDVFLDH-STYAEPPS   320
Pf IscS   --IDLMSMSGHKLYGPKGIGALYIKRKKP-NIRLNALIHGGGQ-------------ER   382
Bs YrvO   --IDLLSVSGHKLNGPKGTGFLYASK----DVKLSPLLFGGEQ-------------ER   231
Ec IscS   --VDLMSFSGHKIYGPKGIGALYVRR-KP-RVRIEAQMHGGGH-------------ER   237
At mNif1  --VALMSMSAHKIYGPKGVGALYVRR-RP-RIRLEPLMNGGGQ-------------ER   285
Sc Nfs1   --IDLLSISSHKIYGPKGIGAIYVRR-RP-RVRLEPLLSGGGQ-------------ER   330

Pf SufS   LLETGTQNIPGILSMGISLEFFKKINWNYVYQYEMYLYDLFIYYMNKYMKNHFV-QLPNL   398
Bs SufS   KFEAGTPIIAGAIGLGAAIDFLEEIGLDEISRHEHKLA--------AYALERFR-QLDGV   320
Ec SufS   RFEAGTPNTGGIIGLGAALEYVSALGLNNIAEYEQNLM--------HYALSQLE-SVPDL   323
At cNif1  RFEAGTPAIGEAIALGAAVDYLSGIGMPKIHEYEVEIG--------KYLYEKLS-SLPDV   371
Pf IscS   GLRSGTLPTHLIVGFGEAAKVCSLEMN-R----DEKKVRYFF----NYVKDYLTKHLDYI   433
Bs YrvO   KRRAGTENVPGIVGLKEAIKLSSEERD-E----KNEKYQSFK----AIFADTLRDAGVAF   282
Ec IscS   GMRSGTLPVHQIVGMGEAYRIAKEEMA-T----EMERLRGLR----NRLWNGIKDI-EEV   287
At mNif1  GLRSGTGATQQIVGFGAACELAMKEME-Y----DEKWIKGLQ----ERLLNGVREKLDGV   336
Sc Nfs1   GLRSGTLAPPLVAGFGEAARLMKKEFD-N----DQAHIKRLS----DKLVKGLLSA-EHT   380

Pf SufS   NLSYKKENINYKSHMQTHPPVHKYNDEQNFTNDHNITQSKQTKSIHSQHDTFKIYTHDTR   458
Bs SufS   TVYGPEE-----------------------------------------------------   327
Ec SufS   TLYGPQN-----------------------------------------------------   330
At cNif1  RIYGPRP-----------------------------------------------------   378
Pf IscS   VFNGCQINR---------------------------------------------------   442
Bs YrvO   EVNGDKEHS---------------------------------------------------   291
Ec IscS   YLNGDLEHG---------------------------------------------------   296
At mNif1  VVNGSMDSR---------------------------------------------------   345
Sc Nfs1   TLNGSPDHR---------------------------------------------------   389

Pf SufS   KYGLKKIGILPLWSNTFSSFDLVTFLDF-KNICIRAGHHCASLLH--KYYLKV-------   508
Bs SufS   -----RAGLVTFNLDDVHPHDVATVLDA-EGIAVRAGHHCAQPLM--KW-LDV-------   371
Ec SufS   -----RLGVIAFNLGKHHAYDVGSFLDN-YGIAVRTGHHCAMPLM--AY-YNV-------   374
At cNif1  SESVHRGALCSFNVEGLHPTDLATFLDQQHGVAIRSGHHCAQPLH--RY-LGV-------   428
Pf IscS   -----YYGNMNISFLFVEGESLLMSL---NEIALSSGSACTSSTLEPSYVLRSI-GISED   493
Bs YrvO   -----LPHVLNLYFPGVSVEALLVNLDM-AGVAVSSGSACTAGSVLPSHVLTAMFGEESD   345
Ec IscS   -----APNILNVSFNYVEGESLIMAL---KDLAVSSGSACTSASLEPSYVLRAL-GLNDE   347
At mNif1  -----YVGNLNLSFAYVEGESLLMGL---KEVAVSSGSACTSASLEPSYVLRAL-GVDED   396
Sc Nfs1   -----YPGCVNVSFAYVEGESLLMAL---RDIALSSGSACTSASLEPSYVLHAL-GKDDA   440

Pf SufS   --PDTSRISIYFYNTPQEIKYLAQQIASTSFMLNEMKNEK-----------------   566
Bs SufS   --TATARASFYLYNTEEEIDKLVEALQKTKEYFTNVF----------------------   429
Ec SufS   --PAMCRASLAMYNTHEEVDRLVTGLQRIHRLLG------------------------   432
At cNif1  --NASARASLYFYNTKDDVDAFIVALADTVSFFNSFK----------------------   486
Pf IscS   IAHTSIRIGFNRFTTFFEVQQLCINLVKSVERLRSISPLYEMELEKKNPSNDDIPKFIWT   553
Bs YrvO   RLTSSIRISFGLGNTAEQVKTAAKHVADVVKRLT------------------------   405
Ec IscS   LAHSSIRFSLGRFTTEEEIDYTIELVRKSIGRLRDLSPLWEMYKQGV-----DLNSIEWA   402
At mNif1  MAHTSIRFGIGRFTTKEEIDKAVELTVKQVEKLREMSPLYEMVKEGI-----DIKNIQWS   451
Sc Nfs1   LAHSSIRFGIGRFSTEEEVDYVVKAVSDRVKFLRELSPLWEMVQEGI-----DLNSIKWS   495

Pf SufS   --   546
Bs SufS   --   406           Class II
Ec SufS   --   406
At cNif1  --   463
Pf IscS   --   553
Bs YrvO   --   379
Ec IscS   HH   404           Class I
At mNif1  QH   453
Sc Nfs1   GH   497
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B

Percentage (%) sequence identity among the cysteine desulfurases									
	Pf SufS	*Bs* SufS	*Ec* SufS	*At* cNif1	*Pf* IscS	*Bs* YrvO	*Ec* IscS	*At* mNif1	*Sc* Nfs1
Pf SufS		**45.57**	**41.53**	**40.98**	**28.41**	**33.89**	**34.37**	**29.62**	**29.73**
Bs SufS	**45.57**		67.08	67.23	36.13	42.68	39.95	38.21	38.55
Ec SufS	**41.53**	67.08		63.11	35.66	38.86	36.95	36.56	35.75
At cNif1	**40.98**	67.23	63.11		30.24	38.82	37.62	36.65	34.31
Pf IscS	**28.41**	36.13	35.66	30.24		58.91	69.25	54.95	55.94
Bs YrvO	**33.89**	42.68	38.86	38.82	58.91		62.76	59.42	60.47
Ec IscS	**34.37**	39.95	36.95	37.62	69.25	62.76		76.30	73.51
At mNif1	**29.62**	38.21	36.56	36.65	54.95	59.42	76.30		66.87
Sc Nfs1	**29.73**	38.55	35.75	34.31	55.94	60.47	73.51	66.87	

Figure 7- figure supplement 1- source data 1. (A) Multiple sequence alignment used for **Figure 7- figure supplement 1**. **(B)** Table showing the percentage sequence identity among cysteine desulfurase orthologs based on the sequence alignment shown in panel (A).