

*Supplementary material*

## **Genome analysis of a new sulfur disproportionating species *Thermosulfurimonas* strain F29 and comparative genomics of sulfur-disproportionating bacteria from marine hydrothermal vents**

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### **Supplementary Material S1:**

Table S1.1. References of the CDSs annotated by Prokka, RAST, MaGe and UniProtKB with the available protein sequences data on the NCBI's online automated prokaryotic genome annotation pipeline. CDSs were found with their associated loci, based on the assembly repository ASM1968873v1.

Gene name	Protein sequence accession number
<b>Genes related to carbon metabolism:</b>	
Formate dehydrogenase [EC 1.2.2.43]	WP_221172701 ; WP_221172702
5-methyltetrahydrofolate:corrinoid/iron-sulfur protein Co-methyltransferase (ascE) (EC 2.1.1.258)	WP_221172703
Acetyl-CoA synthase corrinoid iron-sulfur protein, large subunit ascC [EC:2.1.1.245]	WP_221172704
CO dehydrogenase/acetyl-CoA synthase, acetyl-CoA synthase subunit (EC 2.3.1.169)	WP_221172705
5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)	WP_221172706
5,10-methylenetetrahydrofolate reductase, small subunit (EC 1.5.1.20)	WP_221172707
CO dehydrogenase /acetyl-CoA synthase, CO dehydrogenase subunit cooS, acsA (EC 1.2.7.4),	WP_221172712
Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)	WP_221172713
Formate-tetrahydrofolate ligase [EC 6.3.4.3]	WP_221172714
Pyruvate: ferredoxin oxidoreductase [EC:1.2.7.1]	WP_221172159 ; WP_221172156
Glucokinase	WP_221173395
Glucose-6-phosphate isomerase (EC 5.3.1.9)	WP_221171986
Fructose 1,6-bisphosphatase (EC 4.1.2.13)	WP_221172601
ATP-dependent 6-phosphofructokinase (EC 2.7.1.11)	WP_221173515
Transketolase (EC 2.2.1.1)	WP_221173097
Transaldolase (EC 2.2.1.2)	WP_221171757
Triosephosphate isomerase (EC 5.3.1.1)	WP_221172452
NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	WP_221172665
Phosphoglycerate kinase (EC 2.7.2.3)	WP_221172669
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	WP_221172388
Phosphopyruvate hydratase	WP_221173282
Pyruvate phosphate dikinase	WP_221172666
Phosphoenolpyruvate synthase (EC 2.7.9.2)	WP_221172720
Ribulose-5-phosphate 4-epimerase	WP_221172245
Ribose-5-phosphate isomerase B (EC 5.3.1.6)	WP_221173605
Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	WP_221172369
Aconitate hydratase (EC 4.2.1.3)	WP_221172563
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	WP_221173063
2-oxoglutarate oxidoreductase	WP_221172104 ; WP_221172105 ; WP_221172386 ; WP_221172385
Fumarate hydratase	WP_221171610 ; WP_221173249
Malate dehydrogenase (EC 1.1.1.37)	WP_221173530
<b>Genes related to hydrogen metabolism:</b>	
[NiFe] Group 1a hydrogenase large subunit	WP_221172697
[NiFe] Group 1a hydrogenase small subunit	WP_221172699
[NiFe] Group 1c hydrogenase large subunit	WP_221173559
[NiFe] Group 1c hydrogenase small subunit	WP_221173558
[NiFe] Group 1c hydrogenase cytochrome subunit	WP_221173560
[NiFe] Group 1c hydrogenase putative iron-sulfur subunit	WP_221173557
[NiFe] Group 1c hydrogenase F420-non-reducing hydrogenase subunit G	WP_221173556
[NiFe] Group 1c hydrogenase maturation factor HypA	WP_221173563
[NiFe] Group 1c hydrogenase maturation factor HypB	WP_221173564
[NiFe] Group 1c hydrogenase maturation factor HypC	WP_221173562
[NiFe] Group 1c hydrogenase maturation factor HupD	WP_221173561

Gene name	Protein sequence accession number
<b>Genes related to nitrogen metabolism:</b>	
P-II family nitrogen regulator	WP_221172613 ; WP_221172620 ; WP_221172621
Ammonium transporter	WP_221172614
Nitrogenase FeMo-cofactor scaffold and assembly protein NifE	WP_221172615
Nitrogenase (molybdenum-iron) beta chain (EC 1.18.6.1)	WP_221172616
Nitrogenase (molybdenum-iron) alpha chain (EC 1.18.6.1) MBX6423085	WP_221172617
Nitrogenase FeMo-cofactor synthesis FeS core scaffold and assembly protein NifB	WP_221172618
Nitrogenase iron protein	WP_221172619
Ferredoxin-type protein NapH	WP_221171699
Ferredoxin-type protein NapG	WP_221171700
Periplasmic nitrate reductase chaperone NapD	WP_221171701
Periplasmic nitrate reductase NapA [EC:1.7.99.4]	WP_221171702
Periplasmic nitrate reductase subunit NapM	WP_221171703
Multiheme cytochrome c family protein, hydroxylamine oxidoreductase	WP_221171706
Polysulfide reductase NrfD	WP_221171707
Tetrathionate reductase subunit B	WP_221171708
Cytochrome c3 family protein	WP_221171709
Hydroxylamine reductase	WP_221173055
Ammonium transporter	WP_221171880 ; WP_221171881
4Fe-4S dicluster domain-containing protein NrfC	WP_221172692
Polysulfide reductase NrfD	WP_221172693
Cytochrome c family protein NrfH	WP_221172694
<b>Genes related to sulfur metabolism:</b>	
Sulfate adenylyltransferase	WP_221173271
Adenylyl-sulfate reductase subunit A	WP_221173268
Adenylyl-sulfate reductase subunit B	WP_221173269
Manganese-dependent inorganic pyrophosphatase	WP_221172681
DsrA	WP_221171921
DsrB	WP_221171920
DsrC	WP_221173469
DsrM	WP_221173160
DsrK	WP_221173159
DsrJ	WP_221173158
DsrO	WP_221173157
DsrP	WP_221173156
QmoA	WP_221173267
QmoB	WP_221173266
QmoC	WP_221173265
DsrD	WP_221172373
DsrT	WP_221173161
TorD/DmsD chaperon protein	WP_221171715
Molybdopterin oxidoreductase large subunit	WP_221171714
Molybdopterin oxidoreductase small subunit	WP_221171713
Tetrathionate reductase subunit A	WP_221172121
Tetrathionate reductase subunit B	WP_221172692 ; WP_221171708 ; WP_221171713
YeeE/YedE family protein	WP_221172062
Sulfurtransferase TusA	WP_221172063
putative DrsE domain-containing protein	WP_221172064
YTD cluster hp1	WP_221172065
YTD cluster hp2	WP_221172066
EscU/YscU/HrcU family type III secretion system export apparatus switch protein	WP_221172598

Table S1.2. Identity matrix of protein sequence homologies of the three CDSs from the MOLY cluster found by comparative genomics, namely the molybdopterin A subunits, the molybdopterin B subunits and the chaperone protein, between the genomes of strain F29, *T. marina*, *T. dismutans*, *T. ammonigenes*, *D. thermomarina* and *D. thermophilus*.

	<i>Thermosulfuriphilus ammonigenes</i> Molybdopterin subunit B	<i>Thermosulfurimonas dismutans</i> Molybdopterin subunit B	<i>Thermosulfurimonas</i> F29 Molybdopterin subunit B	<i>Thermosulfurimonas marina</i> Molybdopterin subunit B	<i>Dissulfurirhabdus thermomarina</i> Molybdopterin subunit B	<i>Dissulfuribacter thermophilus</i> Molybdopterin subunit B	<i>Thermosulfurimonas dismutans</i> Molybdopterin subunit A	<i>Thermosulfurimonas</i> F29 Molybdopterin subunit A	<i>Thermosulfurimonas marina</i> Molybdopterin subunit A	<i>Thermosulfuriphilus ammonigenes</i> Molybdopterin subunit A	<i>Dissulfurirhabdus thermomarina</i> Molybdopterin subunit A	<i>Dissulfuribacter thermophilus</i> Molybdopterin subunit A	<i>Dissulfuribacter thermophilus</i> Chaperone	<i>Thermosulfuriphilus ammonigenes</i> Chaperone	<i>Dissulfurirhabdus thermomarina</i> Chaperone	<i>Thermosulfurimonas</i> F29 Chaperone	<i>Thermosulfurimonas marina</i> Chaperone	<i>Thermosulfurimonas dismutans</i> Chaperone
<i>Thermosulfuriphilus ammonigenes</i> Molybdopterin subunit B	100.00	68.02	67.61	68.42	71.84	69.80	17.99	15.90	16.32	20.08	17.15	20.00	10.48	11.71	12.26	12.50	12.50	14.29
<i>Thermosulfurimonas dismutans</i> Molybdopterin subunit B	68.02	100.00	86.13	85.77	70.04	72.29	20.69	18.77	19.54	21.46	19.16	21.37	12.10	13.51	10.38	10.71	10.71	12.50
<i>Thermosulfurimonas</i> F29 Molybdopterin subunit B	67.61	86.13	100.00	89.45	71.66	68.67	22.14	20.23	20.61	22.52	20.99	22.81	12.80	14.41	11.32	13.27	13.27	14.16
<i>Thermosulfurimonas marina</i> Molybdopterin subunit B	68.42	85.77	89.45	100.00	72.06	69.48	21.67	20.53	20.91	22.43	21.29	22.35	12.00	14.41	10.38	11.50	10.62	13.27
<i>Dissulfurirhabdus thermomarina</i> Molybdopterin subunit B	71.84	70.04	71.66	72.06	100.00	77.33	19.49	17.80	18.22	21.19	18.22	21.94	12.10	13.51	12.26	13.39	13.39	15.18
<i>Dissulfuribacter thermophilus</i> Molybdopterin subunit B	69.80	72.29	68.67	69.48	77.33	100.00	19.58	16.67	17.08	20.00	17.50	21.58	8.94	10.00	10.48	9.91	11.71	12.61
<i>Thermosulfurimonas dismutans</i> Molybdopterin subunit A	17.99	20.69	22.14	21.67	19.49	19.58	100.00	83.72	84.24	70.73	69.88	69.65	14.68	15.30	14.69	17.30	16.76	17.84
<i>Thermosulfurimonas</i> F29 Molybdopterin subunit A	15.90	18.77	20.23	20.53	17.80	16.67	83.72	100.00	86.38	70.21	68.56	68.20	15.14	15.30	15.25	17.84	14.05	16.76
<i>Thermosulfurimonas marina</i> Molybdopterin subunit A	16.32	19.54	20.61	20.91	18.22	17.08	84.24	86.38	100.00	70.60	68.16	67.81	15.60	16.39	17.51	20.54	18.92	20.00
<i>Thermosulfuriphilus ammonigenes</i> Molybdopterin subunit A	20.08	21.46	22.52	22.43	21.19	20.00	70.73	70.21	70.60	100.00	70.98	70.60	17.13	16.02	17.71	20.22	19.13	20.22
<i>Dissulfurirhabdus thermomarina</i> Molybdopterin subunit A	17.15	19.16	20.99	21.29	18.22	17.50	69.88	68.56	68.16	70.98	100.00	72.24	14.42	16.67	18.39	18.13	18.13	19.23
<i>Dissulfuribacter thermophilus</i> Molybdopterin subunit A	20.00	21.37	22.81	22.35	21.94	21.58	69.65	68.20	67.81	70.60	72.24	100.00	13.49	16.67	13.22	15.93	14.29	15.93
<i>Dissulfuribacter thermophilus</i> Chaperone	10.48	12.10	12.80	12.00	12.10	8.94	14.68	15.14	15.60	17.13	14.42	13.49	100.00	36.46	45.14	33.33	34.97	37.16
<i>Thermosulfuriphilus ammonigenes</i> Chaperone	11.71	13.51	14.41	14.41	13.51	10.00	15.30	15.30	16.39	16.02	16.67	16.67	36.46	100.00	49.72	45.60	45.05	45.60
<i>Dissulfurirhabdus thermomarina</i> Chaperone	12.26	10.38	11.32	10.38	12.26	10.48	14.69	15.25	17.51	17.71	18.39	13.22	45.14	49.72	100.00	48.59	50.85	50.85
<i>Thermosulfurimonas</i> F29 Chaperone	12.50	10.71	13.27	11.50	13.39	9.91	17.30	17.84	20.54	20.22	18.13	15.93	33.33	45.60	48.59	100.00	78.38	77.30
<i>Thermosulfurimonas marina</i> Chaperone	12.50	10.71	13.27	10.62	13.39	11.71	16.76	14.05	18.92	19.13	18.13	14.29	34.97	45.05	50.85	78.38	100.00	77.30
<i>Thermosulfurimonas dismutans</i> Chaperone	14.29	12.50	14.16	13.27	15.18	12.61	17.84	16.76	20.00	20.22	19.23	15.93	37.16	45.60	50.85	77.30	77.30	100.00

Table S1.3. Putative homologs of the MOLY cluster associated proteins among the genomes of *Desulfurella amilsii*, *Caldimicrobium thiodismutans*, *Desulfocapsa sulfexigens*, *Dissulfurispira thermophila*, *Desulfofustis glycolicus* and *Desulfurivibrio alkaliphilus*.

Species	Protein subunit	Sequence
<i>Caldimicrobium thiodismutans</i>	Chaperone like protein	>OAF_LAKIJB_00480 hypothetical protein MKNLWFKYYSLLSYPKDWLYELENIERYLEKEKNDFKFSQFFKNSLQELQEEYTNLFISFPTLPCCPYEAYYREGLLGETSQEVLQDYVEKTFGFFKEGEPADHIAV ELEFCALTEDLTFIKRIKWNFNDLKECEVKSQIYSKIVKFISEELKWE
	Molybdopterin large subunit	>OAF_LAKIJB_00477 Perchlorate reductase subunit alpha MRVSRRTFLKALLGSAFLAGSKYFKKGFTEISRDEGIKYVRSTCSPNCTGACGFKAMVYRGRALVLIQAADYEEENPRGCLRQMSMNLNYGPRDKQLPVIRGKRG EGRFKAVSWDEALDYATKLAEMMKYGPESVAFIQVPGTGVYQKALMRSLSMGWSVIHAYTMNGDLPWFPIFGVQTEELESLEWANSKYTLUCGSNLIWTR VPAKFLHLSRERGGKIVVDPNYSPTAAAADWEIQINPSTDAAFALGLAHVLSGLYDENFVKYTDLLPLVRLDNQKKAEEVAGLSAQAKAMKSRLEPYRECYVY YDVKAKRFVIPNENLKRDFEPFLEGEIETLVLDGKKVYKVPFLLKKEILANYSPEKVAQIISPADRVKVEEYIKRIGREIATIKPLHIVYGASTYQVYVHGDLKGRAYSL LVALTGNLGSAGISTYAGQYRWRPLGAWWQFQKPLKVVSWFLLWLNKRESEEFKKYNKETYPPNDKALVFGWGNPFQDQHLNANLRKALNGELELIVN FDFQMATSVAVSDVILPGVAWYKDYTLATVLPVYLQQAPELFCQMPFIWICKELAKRVAEKLGDDELLKVEYREFVYVNPFLDKKEESARKKGEWNLRLAREIANQ ASLDAADMLKTGGPLVEGITLALKKGVPVRLNLPAPGRQLVYFEQIQEYKPPVSPALPKTARFVKSGRIFEYKEEDVFDLKTLPVHKDPIKTEHKNMKEKYSUIY ITRNLRLVYVTHSNITMELQDFRPRWIHPDPTAKKRGIKEGLDVEIYNERGKVVAYAVLDPGHPQIVTFEFGWWSRYLRGTSYNTLYPWIKTHIYFVPGIWEAST CWNEAACEIKKA
	Molybdopterin small subunit	>OAF_LAKIJB_00478 Tetrathionate reductase subunit B MPRWGMADLRCIGCRSACVIKHINALPPTGWVWRVETIGSKVHTHPVGRYDFSEVYLPVPCQCDNAPCVKVPVQATWQREDEGLVIDFERCIGCRYMTCAC PYGVRQFNWQPKNFKEAFKGLGYPQDFADSSYRPGYPLEHRTKDGRLVFTPKRPRGVEVEKTCVQYVDDQLPAPVCRGCPGNARIFGLDNDPHSLNSQVIKRR DVIRMREDLNTSPKVLYLPEKYSYRGRYIYERVLKAFEGKVVNL
<i>Desulfocapsa sulfexigens</i>	Chaperone like protein	>ELPILNN_01202 Chaperone protein TorD METANSYVSGLYGLLMMFFATEISPILLIQLRTPEFRETTELEMOLGQEFYKNPAQLVDELAIEAFGLIFGPRFISPHESVHRVRDDGDYGLKWAGADTVAVKFFVEA TGLSYQSDFGGMPDHIAGLEFMMQKLEERYAQAQVNDDETELAENLFSIKRRLFTEHLLAWAPEFFDKVINKANLPVREVAELAKTFDQESDILQKQQKQDCVAA
	Molybdopterin large subunit	>ELPILNN_01203 Thiosulfate reductase molybdopterin-containing subunit PhsA MKKISRNVLLKAAASGALLTAGKGMVGNALAGSVELAMGGDFNPDTGKERKAVPTVCYVTRDPKIAFVEDGRVVKIEGQPNRSRSLGKICAKGQAGVQVYFP DRILYPLKRAKRGDGKIKRISWDEALDLAARMKRLDDGHPKELMHYHGRAGKSSSLPCTVFMGTYSKTSIGTSHICEGKVVAAQELTWNHNYDNWDFDNTD VYLNFGSGLVEAHTNHIPTAQRLLKAMVERNVPCITFVDRLSYTAASKTKEPVRPGDGLAVLLAMNNVIMQENLYDREAFIRTTEDVNAPLDEKIAALKHLISYTP EWAEEKISGSAANIKKYAFKAKAAICISYRGLVAHYNGTDEGAAQMLGMITGNINSPPGRCKAVAPHWKYPKGPVKPKGKQLKTNTGSLALPNHGGECQSVLK MIKDGSHGRPDVLYWYCNVYVNGECQENIDVLSDEKLMPTFTVSNVYDESSRLADLIPDTSYLERWDWGDVNAVPTQTEFEFLRQPVPTLPGECRNFSDILCDLAK RMEMPLGFDTMEEFVLSCEMTPTKDLPGGGFEYLLKKGVVYHDPNEKPDFYSHKIVKADLKKEGILFDEATGVYVWNWKKSAKDEAEAMAKGYAKMAYSYKGY VGQIKGDVYKGFKPKDKNKTGYFELYSILKEKGFEPFPWSKAIPEHQELTKNQLTTLTYKVPVQIHSRSTHCKWLETFMHDNPAWINSKTAASLGKIDGLVLTLSKIG EISIKAYNVEMIVPGSIAISYHLGRTESSRYSYSGKSMIGSDNDPDLKLKWWDTYGVHPNVLIANAPPDIPSGQHRHVMDEVTVSKA
	Molybdopterin small subunit	>ELPILNN_01204 Tetrathionate reductase subunit B MTTNTRRDRREMLRVTVGSAAAGLASVLSQKPEAEAAVKTQVWVIMDLRRCCTGRACVACKAEYDVLGAFKTVIKQVDTGKYPDTRTLIPRRCNHCEGTE KVGDMTVPVCKACEYKPKDRRNVFVTAEGKRIYRGGATYKRPDGLIINDACTGCGKCIDACPYGARTFNKRSLGSKDKSKNAIVKSSCVHRHLEDEGIPACVNTCAP GARIFGLDNDPNSDVAKLAKEFNLLENRNKTTMKPEAKTMPNIYIDPEVLADYSYEDDKDLTEYRDIIVE
<i>Dissulfurispira thermophila</i>	Chaperone like protein	>BNAHJNJ_01148 Tat proofreading chaperone DmsD MHINEILNEKVRGDCYRLSACFYQPKSLMQLNLRNLVLEALRVCPASVFAEKMEGSIYRVEDDEDLIDYAKLVGPNELIAPPYSVYDLDRERRVMGDSLTKTME LYREAGLVIDDFKELPDHVAIELEFMYLVYFKEVEALEKSDMDTAHFKIMQQEFLNSFLGWINPFCEKIKEGEDNFKYHSLAEVCSVIMNISTPIYEMNKAQGVLYN
	Molybdopterin large subunit	>BNAHJNJ_01146 Thiosulfate reductase molybdopterin-containing subunit PhsA MEIKRRDFLKAGVAAGAVALTGPLLNAFAVTKPLAGEKVSSTDPGKWIPSTCGCTQWCPVEFVQNGRAVVRGNSLQKSVNNGVYCPRHMLLQELYDPDRIK VPMKRNTPKGRGVDKPFVPSVDEALGTADLADLKLRLKNNEPHKFLIRGRYSPTYPLAYGTLPKIIGSPNAISHAICAEAEKGFYTEGVYGRDYDQNLKMLCVW WGCPLSNRNVPTNINKIGDLDRGLTITVDPRLSAIAAKSMHWVVPKPGEDGALALIAHVLTEGLWSKEFIDFNDEKGNQFRTKTKTVDESAFAEKLHSLGVKWW NIELKDRTPWEAEEKIGSKIDQIKIAKTAAMAAAPQCAIWMGPGAVMSRPGAAASQAIIYANGLLGCVVDEGVVGLSHHPKSPNKLKIDDFLDDMAKKYKKEKIDQR GYKQFALNPDPKKGNKFPKGTAVITNNVATGILNADPEYKVVSNWANFNFSCTGAERWDRAMEKVFYVHGTNPESEAMAYADIVLPAHHATQKLSIDNKGNG YTHSIQPPVGRVLEEKADETEIMYMLAQLAEKGFNNIMFNYSFKDPETGKHPTEGPEAEIASKIISAVWPKPELPGDKLNGWEDFKAKGVNDESEPYKGLW EKGFPPTPKFEPYSEGLKIGLKAHAKEYKTTIDVDESAYTAKGEEVFVPHYEPKVVWGDVPPYFLLVDFKSLNREGRSQNTTWFFQFKVVDVDESDDVVRRINP EDAKLGIKTDGMYVSLTSGITVAKKLEFVGRPGTVSKFCQGHWAYGKATKFNKTRPGNNDMLPFDVERFTMGSCNRRNGGFRTRVIEKV
	Molybdopterin small subunit	>BNAHJNJ_01147 Menaquinone reductase, iron-sulfur cluster-binding subunit MPKYGMVIDLQKCVGACACIACTENNTQDRAGKQTVWADFVMTKEGKFDVFTMPVPLCNHCSDAACVACPVPKAMHKHEGEMTIHNMERICRGCQQ RACPYSSEDEKAGTQYSVIFNDFDEVHPFYKDTKEVIGPCTSSGADVSKRAGDMPHRTLYKHSYASVREKKEVKECMFCEHRLNQECPVACAPKARIFGD LSDPNSPEKLLKHKAVQLKNNKGLLPGKEGKTPQNVYYIRFSKAEAKKA
<i>Desulfofustis glycolicus</i>	Chaperone like protein	>MJEDABAB_01838 Tat proofreading chaperone DmsD MNSATEQLIRRGDTFKLLAACFYEPDKELGQHVCANLAGLLREIDPSAAAAEAAMVTAALTEEQQLSIDHAALFVGFPELPAAPYGSVYLERQRTMGDSTMV QRFYREAGLSIDVAEPPDIAIELEFLYLCRKEAEADASEQTRVTLQAFAFNQALLPWWKPFCSAIRSATGNPFYLAALAEQFIESCRPIYQRREGTRDVRVPTQV
	Molybdopterin large subunit	>MJEDABAB_01836 Thiosulfate reductase molybdopterin-containing subunit PhsA MKIKRRDFLKAAGATAALTGCCTADMNALKAAAGSTKNIGEAQGWLPTTCQGTQWCPVEFVQDGRAVVRGNSRQNDGNGVCPRHLSLQQLYDPDRIK LPMKRNTPKGRNEDPMFVPSVDEALNTIADKMMELRNSIPEKFLMIRGRYTHRDVYDLPKVFSPNLSRHPTLCLSSVIRGQVSGFTYPTDLKNARYVMAGANRAE LIWGCDPVASNRMPAAIKRLGNALDRATAVDPRLTSSAAKAEQVLPQPGTDGALALGIAHVILTDGGWDRDFVDFKDFGFRNFKPGAMVDEADFVDEKTYGL VKVWNNAVDMTAAKAAEISGPAEQIRVARGALAAAPNVVWMPGAAHARGGYSGMVHALGLVGLGIDNVGSSQTLAKIPVNLKDDGILKQHDLELAKK HTKKEIDQGRLELPTIKGSGGGVSTNNAPNGIINDPEYKLVGYMNNFVSSNGTDRWEKALSMPVFTVHLTHASEFMSFDILLPCASIKYERHGFGLTKA NRYATCTIQQPVVQPIVQVIEDETEFPFLIAEKLKRGFSNLHDLCLVEMYADPETGAAPKTAQELSNLAKYVTKPLWDGKDDHTGDTINGWNEMLSRGMWNSPEYA YKSHWGGKFSTKFFEFSETLKKALTAHAHRKVDVTVMEKVNRYARGEMAFVPHHEPRLRHSSEAEYLLFDYSKSLNREGRSQNPWYFFKHVDPGVDVGG QDTRLRHPTDQLGKIDGRVITSMGSGEAVARVWEGVRGPTVSKSYGGQHWAYGRATAASDFAGKTFARGINNITIPWELRLLSGSNARNGGHAARVREKI
	Molybdopterin small subunit	>MJEDABAB_01837 Menaquinone reductase, iron-sulfur cluster-binding subunit MTQYAMVIDLRKCVGACACIACTENNTAARKYQTHNWADFHEHTGSPNTGFRTLVPLCNHCSNAPVCEACPVEPKAMYKTAADGITMHNDRICGCRACQDA CPYSMDEVTKDGAAYGYSVISYNEEGESTQFFTKDELKIGCTSSGAEVLTGAIPPHQTRVQHPDYESVRRDNVIEKCFCHDRHKNDELPCYVACSPSARIFGLDLD AGSDVAKLLKQHSFVLEKEEGTKPNVYIRDYSAR
<i>Desulfurivibrio alkaliphilus</i>	Chaperone like protein	>JNICIFD_00427 Chaperone protein TorD MEATMHPGNSRQLLNLGCFDYSALRQLNVQLEQLENIHRLFINDRGGTKTPPYAGCYLDRDRRQFIMDFSGICEQGVIVSGHPDPHIMLETALLLAE KESPELIDSLQRYRGPWFPERAAALEHDEYGFYAAAAELKETLTLHRSXDKGLDH
	Molybdopterin large subunit	>JNICIFD_00426 Polysulfide reductase chain A MKVSRRKFLAGSVAAGLGAAGSAGLRVFRKAEAQGRAGEVKVYVSSCAICTSKVFRGQVNGIIRLEPEPDFPKSRGMMCARGNAGAWTPYDPRVYKPLIRT GRREGKWRKATWEEAYKIADTKNQVVEEGHRSQIFGASSEGTQEMYYHQFRREVFGSPNSLRHPTLCLSSVIRGQVSGFTYPTDLKNARYVMAGANRAE AIFTPTMDIFSRPKGSYKLYLDPRTKTKAAKADQLPKPGDVMFALALAHVIAENLDRDFVANFCFGDELVEHVHPKPSPEWAAEETGIAAADIRIARELATTHP SVFYPRSSWQGEVQTRAJIIVNALIGAFDRPGGLLPVADVPVMSRYFYFPAWYVQTRPRLESDDVMFLGRDGSVWVAVWRDLRALKADPYRIGFLFYKONVLEA VPDRDKSMKFLDQMDIIVCIDFMSDTAWYADVLPESNYLERLDPPQSLGGIETAVFRQPLIDRLDYTKPGFEVSELAAYFEDEGDKLSEYFEGSPEEHARNVADH PGAWELQREKAFITVVKVQFQYARQEGRRINTATGKVELYSEDFAGRLDPLPFRRCCEPQDFRFLVGRHAHITNSMATAFPELNVHQPENAVWLNPEAPARL GINDGLVQMQNRSQAQVTVKAVTAGIRPDCVYAPGYQKPVLYQRGASQAALIESHFEPISGNALMHETIIEIRV
	Molybdopterin small subunit	>JNICIFD_00425 Tetrathionate reductase subunit B MSQERKKRWVMDPKCIDCKACKRENGMDAGTDQVQYKRVNWTSGVETGYPKLKERFEPSCQCQCNQNPVCKVPTSASYQTEDGLVAIDYKRCIVCASC LACPVDARYKSPQTKIDKCTCAHRIAEGLKACVDTCTPKTRVFRGLDNDPNSVARLLATRHVRLKPEQGTKPSFLYLS

Table S1.4. BUSCA prediction of GO-terms and protein features for each of the 3 CDSs of *Dissulfuribacter thermophilus*, *Thermosulfurimonas* strain F29, *Thermosulfurimonas dismutans*, *Thermosulfurimonas marina*, *Thermosulfuriphilus ammonigenes* and *Dissulfurirhabdus thermomarina*.

▲ Protein Accession/ID	◆ GO-id	◆ GO-term	◆ Score	◆ Alternative Localization	◆ Features
⊕ Dissulfuribacter_thermophilus_Chaperone	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Dissulfuribacter_thermophilus_Molybdopterin_subunit_A	<a href="#">GO:0005886</a>	C:plasma membrane	0.36	-	1x Transmembrane Alpha Helix
⊕ Dissulfuribacter_thermophilus_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Dissulfurirhabdus_thermomarina_Chaperone	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Dissulfurirhabdus_thermomarina_Molybdopterin_subunit_A	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Dissulfurirhabdus_thermomarina_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_F29_Chaperone	<a href="#">GO:0005886</a>	C:plasma membrane	0.48	-	1x Transmembrane Alpha Helix
⊕ Thermosulfurimonas_F29_Molybdopterin_subunit_A	<a href="#">GO:0005615</a>	C:extracellular space	0.87	-	1x Signal Peptide
⊕ Thermosulfurimonas_F29_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_dismutans_Chaperone	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_dismutans_Molybdopterin_subunit_A	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_dismutans_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_marina_Chaperone	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfurimonas_marina_Molybdopterin_subunit_A	<a href="#">GO:0005615</a>	C:extracellular space	0.85	-	1x Signal Peptide
⊕ Thermosulfurimonas_marina_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfuriphilus_ammonigenes_Chaperone	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	
⊕ Thermosulfuriphilus_ammonigenes_Molybdopterin_subunit_A	<a href="#">GO:0005615</a>	C:extracellular space	0.8	-	1x Signal Peptide
⊕ Thermosulfuriphilus_ammonigenes_Molybdopterin_subunit_B	<a href="#">GO:0005737</a>	C:cytoplasm	0.7	-	