

Supplementary Figures S1 to S16 for:

Thiol reductases in *Deinococcus* bacteria and roles in stress tolerance

by:

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Figure S1. Multiple sequence alignment of *Deinococcus*, *E. coli* and *B. subtilis* NADPH thioredoxin reductases.

Figure S2. Multiple sequence alignment of *Deinococcus*, *E. coli* and *B. subtilis* thioredoxins.

Figure S3. Gene clusters with additional *trxR*, *trxA* and *ahpD* genes in *D. peraridilitoris*.

Figure S4. 3D models of Trx and Trx-like proteins of *D. radiodurans*.

Figure S5. Sequence alignments of Trx-like proteins from *Deinococcus*.

Figure S6. Multiple sequence alignment of *Deinococcus* FrnE reductases.

Figure S7. Putative operons encoding DsbA, DsbB and UvrA.

Figure S8. Multiple sequence alignments of *Deinococcus* Dsb oxidoreductases.

Figure S9. Gene clusters encoding CcdA and DsbE/CcmG homologs.

Figure S10. Multiple sequence alignment of *Deinococcus* Msr proteins.

Figure S11. Multiple sequence alignments of BCP peroxiredoxins from *Deinococcus*.

Figure S12. Multiple sequence alignment of *Deinococcus* AhpE and AhpD proteins.

Figure S13. 3D models of BCPs and OsmC of *D. radiodurans*.

Figure S14. Multiple sequence alignment of *Deinococcus* OsmC, Ohr and YhfA proteins.

Figure S15. Multiple sequence alignment of *Deinococcus* bacillithiol reductases.

Figure S16. Multiple sequence alignment of *Deinococcus* bacilliredoxins.

Figure S1

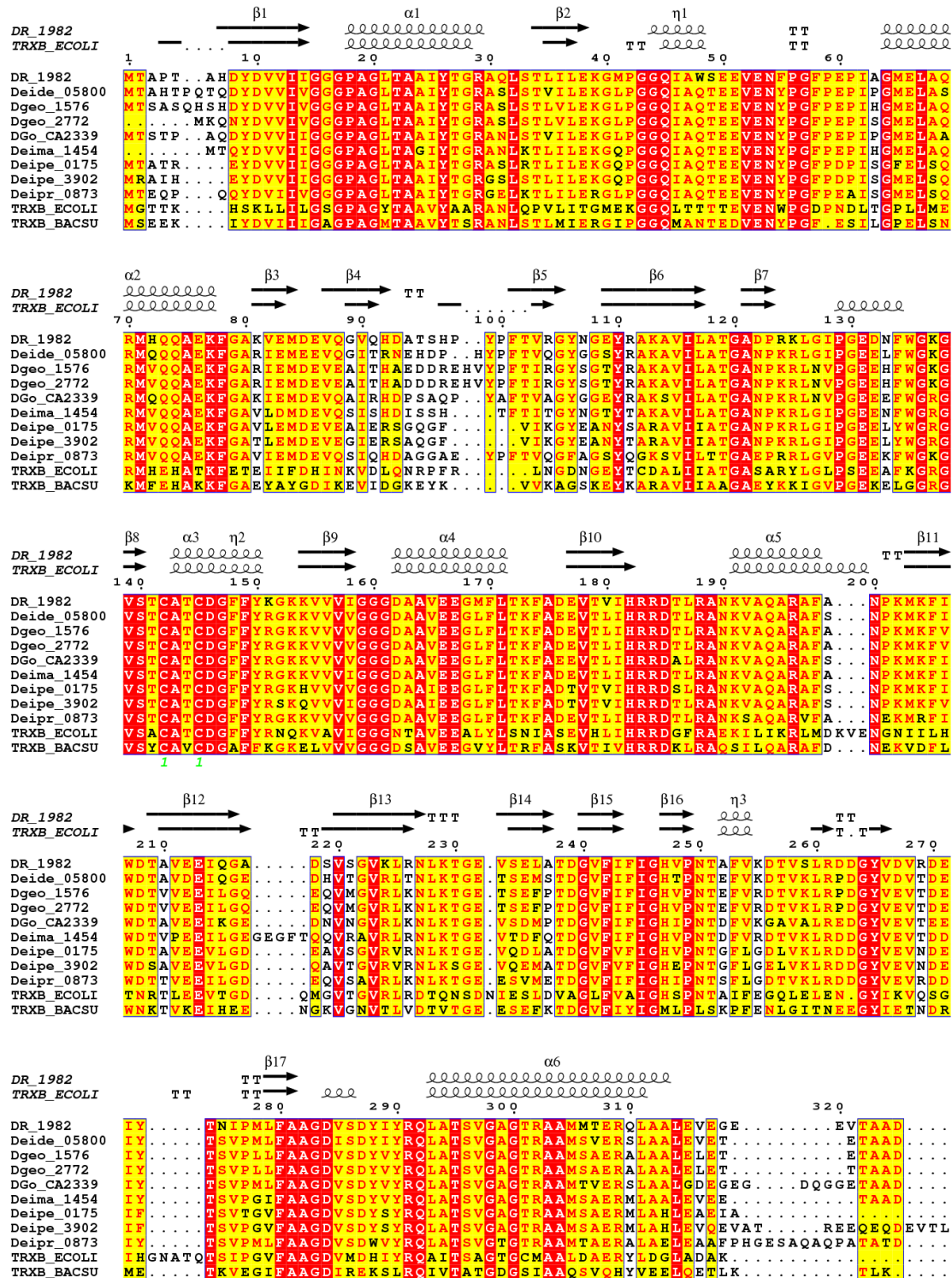
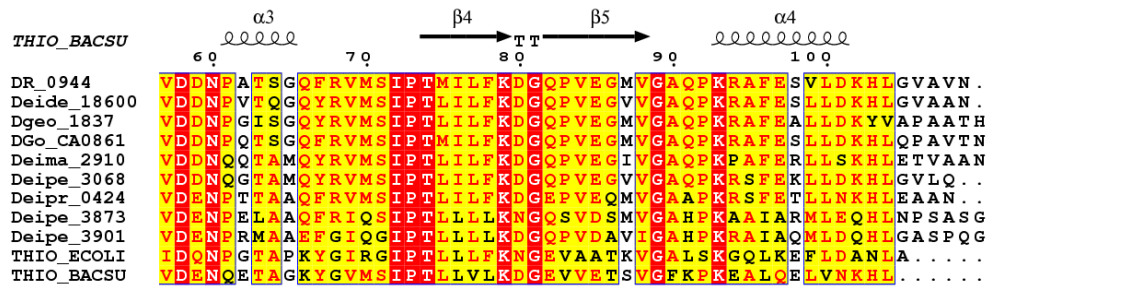
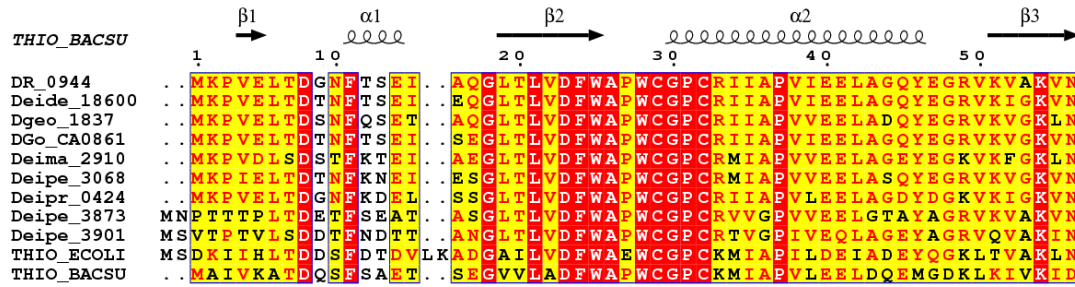


Figure S1. Multiple sequence alignment of *Deinococcus*, *E. coli* and *B. subtilis* NADPH thioredoxin reductases. Abbreviations of *Deinococcus* species names (*i.e.* the first part of the locus tags (gene numbers)) are as specified in Table 1. TRXB_ECOLI and TRXB_BACSU, thioredoxin reductases from *E. coli* and *B. subtilis*, respectively. The alignment was made with ClustalW at NPS@ [178] and ESPript [179].

Figure S2

(a)



(b)

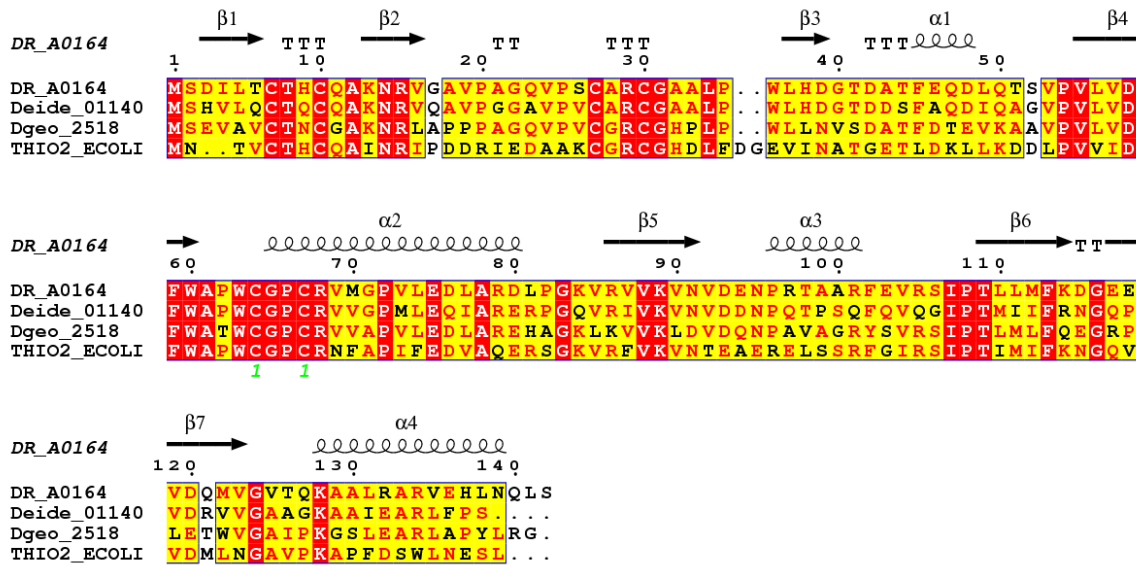


Figure S2. Multiple sequence alignment of *Deinococcus*, *E. coli* and *B. subtilis* thioredoxins. **(a)** Alignment of Trx1 sequences. **(b)** Alignment of Trx2 sequences. Abbreviations of *Deinococcus* species names are as specified in Table 1. THIO_ECOLI and THIO_BACSU, thioredoxins 1 from *E. coli* and *B. subtilis*, respectively. THIO2_ECOLI, thioredoxin 2 from *E. coli*. Alignment was made as in Figure S1.

Figure S3

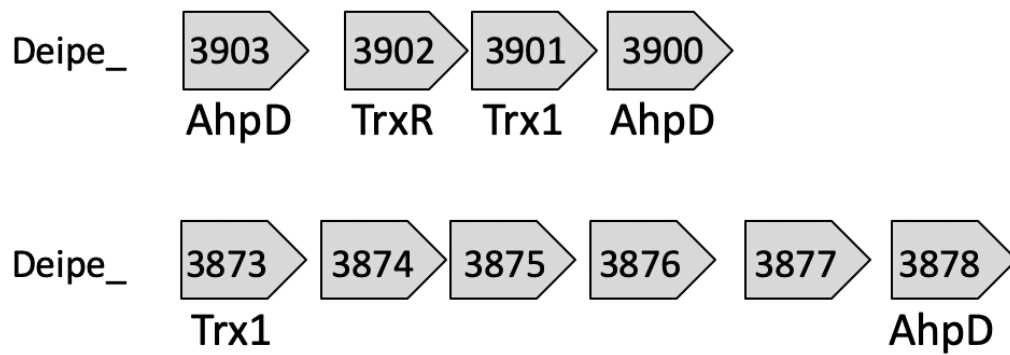
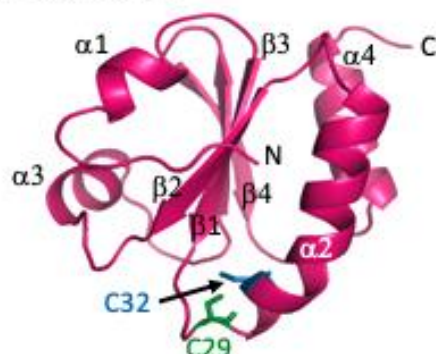


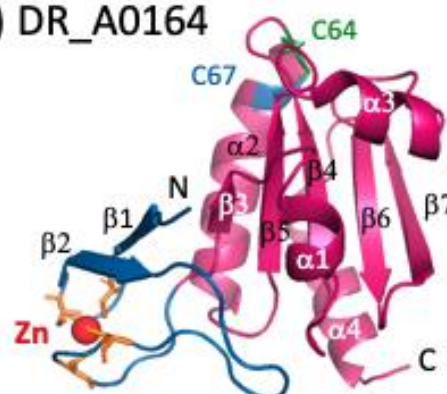
Figure S3. Gene clusters with additional *trxR*, *trxA* and *ahpD* genes in *D. peraridilitoris*. The two clusters shown are both located on plasmid pDEIPE01. Locus tags (Deipe_3903 etc.) are indicated. Gene sizes not drawn to scale.

Figure S4

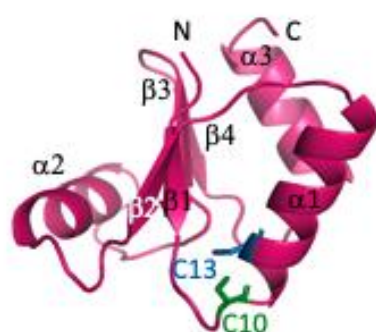
(a) DR_0944



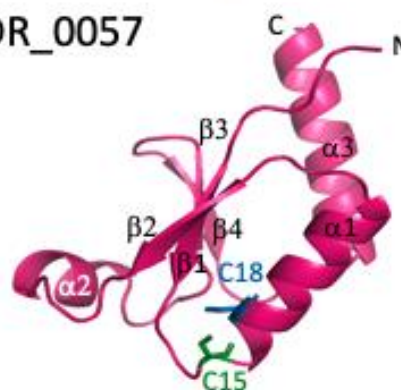
(b) DR_A0164



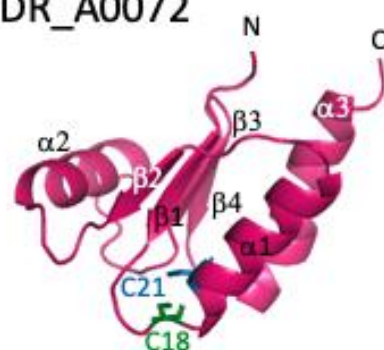
(c) DR_2085



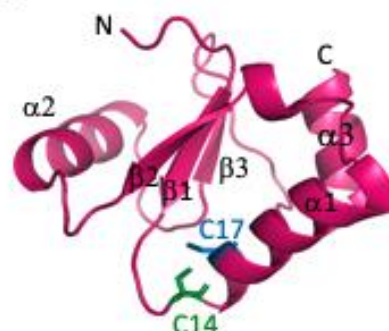
(d) DR_0057



(e) DR_A0072



(f) DR_B0110



(g) DR_0948

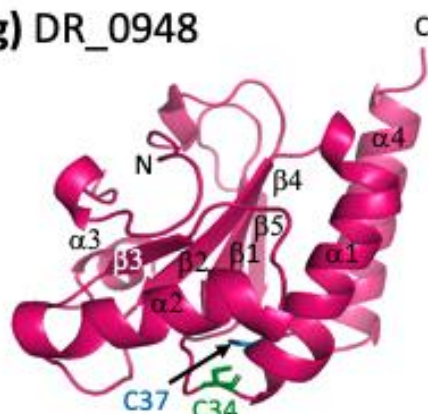


Figure S4. 3D models of Trx and Trx-like proteins of *D. radiodurans*. Models in panels **(a)** (Trx1) and **(c)** to **(g)** (Trx-like) were obtained with AlphaFold2_Advanced [180]. **(b)** Crystal structure of Trx2 (PDB 7DL6) showing the extra N-terminal zinc binding domain in dark blue [60]. Catalytic and resolving cysteine residues are shown in green and blue, respectively. 3D structure or model images were generated using PyMOL (PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC).

Figure S5 (panels a to e)

(a)

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DR_0057      -----MTPLP-TLTLYHRPGCHLCEQAQTHLDELGFAYQLHDISGDAALTA 45
Deide_13741  MTGRTGPDQQDPVQRPVP-ALTLYSRLGCHLCEQAESHKALAFTFQVVDVDTDPLLKA 59
Dgeo_0729    -----MLP-VLTLYTRAGCHLCEQAQANLQALEYRYEPLDVRVPALQA 43
DGo_CA0407   -----MPEP-GLRLYSRVGCHLCEQAEEERLDYGFYERLEVSGDPERER 44
Deima_1186   -----MTAAP-TLTLYTRAGCHLCEDAEATLTRLGVPYTPVDVTGHADLEA 45
Deipe_0565   ----MAPA-ELKAGQPGTQ-GLVLYSRAGCHLCEDAERMLASLSVPFTRIEVSSDDDLER 54
Deipr_1451   MTD----S--AAAPLPSTPLIPVFYTRASCKLCQQAALLRAWEVFPQRVDIAGDEDLIA 54
              : * * . * : * : * : * : * : * : * : * : * : * : * : * : * :
DR_0057      RHGDHIPVLALG-----DRVLLRGVLSRSRLSTLKLRLLLREQEA----- 84
Deide_13741  RYGDVPVPLASG-----GRVLGKGAFSRSRLSQIKLLLLRETRTQPDSPG--- 104
Dgeo_0729    RYGDDVPVPLALG-----ERVLLKGVLRSRGLSALKLQLLREQAGQRKRV---- 87
DGo_CA0407   LYGHDVPVLTDR-----AGRVLLRGVFGPGRLGELRLRLRRELAP--GGAGDV- 90
Deima_1186   RYGWDVPVPLARG-----DQVLLKGVLSAARITA-KLRVHRLT----- 81
Deipe_0565   RYGWDVPVLTTRSPSAGHPPEVLLKGVSFRARILARLA-----GRP----- 94
Deipr_1451   RYGHVVPVLTLPPLPGG--ERTLHRGPLTRSSLPALQLRLIRLRRELSSAPRQLH 106
              : * . : * * : . . * : * : . . :

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(b)

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DR_A0072     MPERSAPDITVYTVPDCPDCEAVQALLRRRGLTPTVRNVRGDPAAALAEMQRRADGVRIA 60
Dgeo_2583    -----MSMTVTVYTVPNCSSCEAVKRFLRSRGVPFTEKNIREDPAAALAEMQARA-NVRIA 54
Deipr_2424   -----MKNLEVTLYTVPDCADEIAIKRLLKRENVPFTEKNVRGDPAAALAEMQLRADGVRIA 56
DGo_PC0211   -----MPDITLYTVPQCADCEAIKRLLQHEGAPFTEKNVRGDPQALAEMQARRA-DVRIA 53
DGo_PC0201   -----MKTVTVYTVPGCASCEAIKRFLAARRVPYTEKNVREDPAALAEMQAKA-RVRIA 53
Deipr_2732   -----MPKVILYATPTCPDCHALRLWFNRKGIEFEERNLTIP-AVADEAKA-RYGVRVA 52
              : : * : . * . * . * : : . . : * : . * : * : * :
DR_A0072     PVTIIEQVFYGFDEQRPRLAALERQGTQ- 91
Dgeo_2583    PVTVIGDQAFYGTFFDDQRPLLEAALGENGI-- 84
Deipr_2424   PVTMIGQQAIFYGRFDEQRPQILAALAEQNHG 88
DGo_PC0211   PVTIIDEHIFYGPFSDQRPRIILAELEKRA--- 82
DGo_PC0201   PVTVIGEEAFFGTFFDDQRPFLAALREND-- 83
Deipr_2732   PITVVGDDQFFYGTFFEQQRPELEPLFA----- 78
              * : * : * : . * : * : * : * : * : * :

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(c)

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DR_B0110     ----MSDRPFLLLTQGA CPGCERLKKMLAGPLRGQFDSHIEVIHRQSAQERFDALSAHFG 56
Dgeo_1776    -----MLLTQANCPACVRLERMLSGPLRGAYWEQIEVVRREDDERQFLALAGEYG 50
DGo_PA0204   MTDPAKPAEVLMLTQDACPDCERLKLMLDKPLRGQFAGLIRPVHRQGQPDDEFESVVALYG 60
Deipr_2190   MTEPAVQTRFVLLTQDNCPNCEERLKLMLAKPLRGQFDDQIVTVHREQAASEFEALAAEYS 60
              : : * * * * * * * * : * * * * : * : * : . * : : . . :
DR_B0110     VRSVPALIRVSDGTRAHDPGSLGAVRAFLQG----- 87
Dgeo_1776    VRSTPALVERGTGRQITGAGSLHEVRLLLG----- 81
DGo_PA0204   VQKTPALIDTASGRVLLNTGGLGEVKAFLTAQAEPVGS 100
Deipr_2190   VQSTPALIDRERGEVLRNTGGLGEVKNFLTA----- 91
              * : . . * * : * . * * * : * :

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(d)

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DR_0948      -----MRWPDFADFVHGSPLPPTTEWGRPGLLMTFNLECPGCVSRGIPFLKRLHAHEY 52
Deide_06780  -----MEWPSQEDFVHGDPVAPPCGWDPRGLVMTFNLECSGCVSRGIPFLKRLHSEF 52
Dgeo_1960    -----MDWPAPEDFVHGDPPLPPDQWTRPGLVMVFNLECPGCVSRGLPFLRQLHTEF 52
DGo_CA2541   -----MLWPAPADFVHGSPLPPTTGWTRPGLVMTFNLECPGCVSRGVFPFLKRLHGEF 52
Deima_2994   -----MTLWPSIDTFVHGTPVPSPEQVNRPMMLVMTFNLECAGCVSRGIPFMKRLHAEF 53
Deipr_1792   MTPESSPPLPWPAAAGDFVWRAADV---PARPSLLMFFHLECAGCVSRGIPFMKRLHAHEY 57
              **      **                      ** *: * *:*** *****:***::** *:

DR_0948      GEQVHLLAVHTSFGHRQLTREEVEPTLVKFARDFAKLPFPVALDLGSGFAREWQTEGTPH 112
Deide_06780  GGRVQLLAVHTSWGHRQLPREDVEPTLLKFSRDFARLPFPVALDLGSGFARHWNTGTPH 112
Dgeo_1960    GDRVHLLALHTSRGHRRLPREDVEPTLVRFAREYARLPFPVALDLGDLARTWATEGTPH 112
DGo_CA2541   GDRVNLLAVHTSLGHRDLARGDVEPTLVKFARDFARLPFAVALDLGSGFARHWHTGTPY 112
Deima_2994   GEAVQMLVIHTAHGHRQLPRQDVEPTLVRFQAQSFARLPFPVALDLGEGIAQAWRTGTPH 113
Deipr_1792   GEQVNFIAVHTSRGHRQLPRADILPTLLHFAERFARLPFPVALDETALAAAYATEGTPH 117
              *  *:::.*: *** * * :: ***:*. . :*:*** ***** * :* : *****:

DR_0948      WLAFAPGGELLRSVYGSQENAQTRLEYLLAEWAAASRP- 150
Deide_06780  WLAFAPGGELLRSVYGSQENAQTRLQYLLQEWAGQGDP 151
Dgeo_1960    WLAFAPGGELLRSVYGSQENAQTRLQYLLLEELVGPA--- 148
DGo_CA2541   WLAFAPGGELLRSVYGSQENAQTRLQYLLLEWTGQAE- 150
Deima_2994   WLAFAPGGELLRSVYGSQENAQTRLEYLLAELATSS--- 149
Deipr_1792   WIAL-EGGEVRSIYGSQENAQTRLEYWLAELTSAGDA- 154
              *:.. ***:.*:*****:.* * * . .
```

(e)

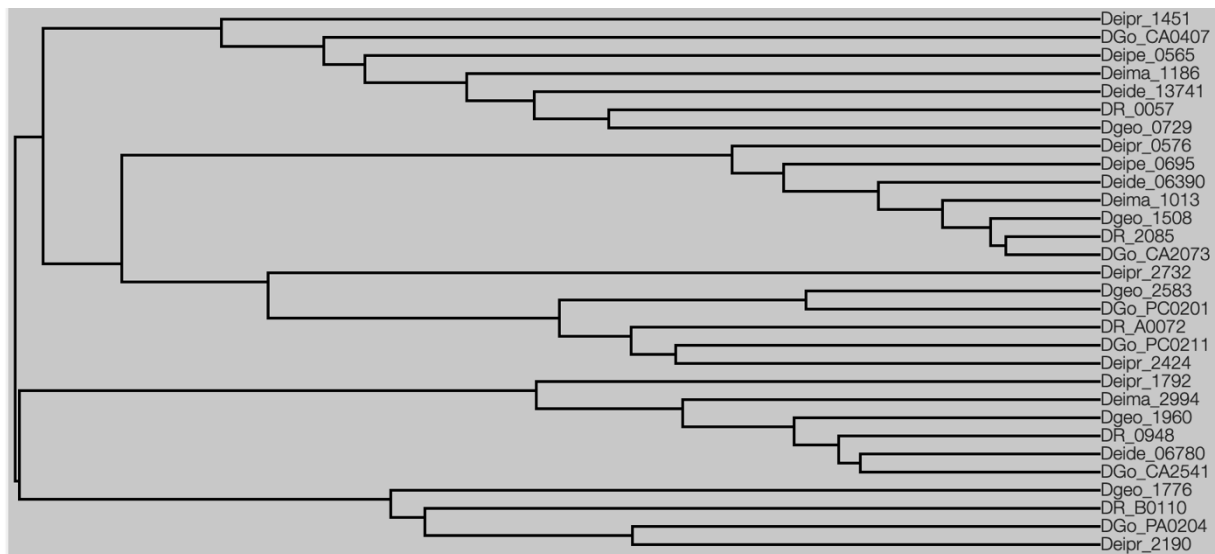
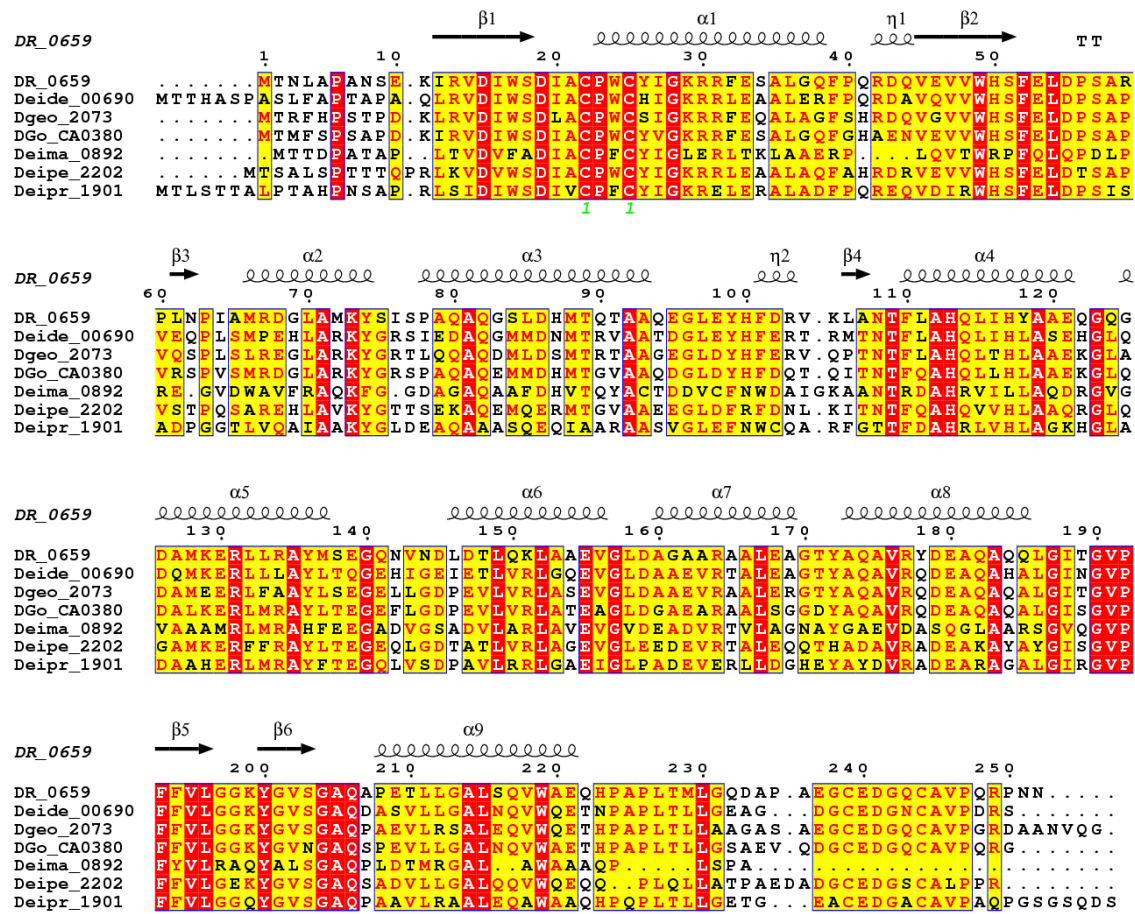


Figure S5. Sequence alignments of Trx-like proteins from *Deinococcus*. **(a)** Alignment of *Deinococcus* DR_0057-type sequences. **(b)** Alignment of *Deinococcus* DR_A0072-type sequences. **(c)** Alignment of *Deinococcus* DR_B0010-type sequences **(d)** Alignment of *Deinococcus* DR_0948-type sequences. **(e)** Tree showing sequence relationship between Trx-like proteins shown in Figure 2 and in panels (a)-(d). The guide tree is calculated based on the distance matrix that is generated from the pairwise scores. Trx active site sequences are highlighted in yellow, residues highlighted in cyan in Deipr sequences differ in the proximity of the active site. Abbreviations of *Deinococcus* species names are as specified in Table 1. Alignments and tree were obtained with UniProt ClustalO (<https://www.uniprot.org/align/>) [181].

Figure S6 (panels a to c)

(a)



(b)

Deide_3p01230 MSDLHLLYVTDAYCGWCWGFAPTL SAFHARH-PHLPLRLISGGIFTGEKIAPIAAYPHIP 59
Deipr_1559 MTKTKLTYVTDYCIWCWGFGEALRGFAQQNADRIELEVLPGGLLVGDRVQPVGKPRVL 60
* : . : * * * * . * * * * . : * . : : : * : : * * * : . * : : * : :

Deide_3p01230 GANDRITHLTGVTFGDAYQARLQEGILVLNSDDAAAGLAALRALAPDRALEAFHAIQHAF 119
Deipr_1559 ESAARVANMTGVPTGEGFRRSVEEGSTVLD SGVAARAYWALHSLAPSRGLDIAHALQHAW 120
: * : : : * * * * : : : : : * * * * : . * * : * * * : * * : * * * :

Deide_3p01230 YMEGQSLSDPRTYRAVAQTNLNDPDAEEAAFHGPQARTEAAQDYQLARTLGVD SYPTLLA 179
Deipr_1559 YWDGLDLHDPVIGGVARELG L D A A A A A R A L A D P A A E I Q A L A G F E R R Q T L D I S G Y P T L L V 180
* : * . * * * . : * : * * * * * * : . * * . : * : : * * : : * * : . * * * * :

Deide_3p01230 QQDGQRTVLARGAATVEQVETRIQLRALNPATP----- 211
Deipr_1559 HGP HGTQRIGGARATPAKLTA AFEQVVLAGETVEEED E E 218
: : . . * * : : : : : * *

(c)

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DR_2335      MTPQPTDAQPTDAQPTDLYDFDLC PYAWRGVEMAHVLRG-----SGEGFRLRHFSLVQGN 55
Deide_22890  -----MTSTDLEFFDFIC PYAWRGLELVNALRA-----EGETFRLRHFSLVQGN 43
DGo_CA0030   -----MLASAMTDVYFDFLC PYAWRGLELANVLRALPGDAGGETFRLRHFSLAQGN 51
Deima_0620   -----MTQTQPLQVYIDFLC PFAWRGVELALILRET----RGLNVQLRHYSLVQGN 47
Deipe_1019   -----MQPSSVYFDFLC PYAWRGLELVS----Q----LGVRLPQLKHFSLVQGN 40
              .:::***:**:****:*. .          *      *:***:**.***

DR_2335      HPQNK---DQETVQWWLTDQPLGAEGSGYMKYQRPSLNAFLAAHAAARQGEEKSWAFAL 112
Deide_22890  HADNA---GQPEPRWWLTDQPPGEGTV-----SQSSSLAAFLAAGAAARQGEAAWAFSL 95
DGo_CA0030   HPDNAAAKGAGDVRWWLSDQPQGEAA-----HQSSSLDAFLAHTAAARQGEERSWAFAL 106
Deima_0620   HPENP---DRKQPTWWLTDQTADSGSD----MQRGSLLAAFLAAGAAARQGEQERFTFTV 99
Deipe_1019   HAQNP---DRKNPVWKLAAQPLTEGPD----SQQASLRSFLAAQAARLQGNELQFTL 92
              * : *      .      * * : *          * : * * : *** * * * * : * :

DR_2335      ALFRLHHEDKRDLEA-AFQDAATRAGLDLSQWKQDRQDEAGLRRELRLADLEAAALGVF 171
Deide_22890  ALLRIRHEDGQPLDEA-ALTQAAQTAGLDSGRWAADRADETGLREGLRDLSEAHRLGVF 154
DGo_CA0030   ALFRRRHEHGQALDEA-AIQGAAGDAGLDTAQFAADRQDDGGLRAALRRELEEAADLGVF 165
Deima_0620   ELFRLRHQDGRALHDPTTLHAAAERAGLDAAARFAQDLQDDAGLRAALTEDLRAAAALGVF 159
Deipe_1019   QLLRLRHDGRRDLNDPQTAREAANQAGLDTGRFETDLADEASLRESLARDLNDAAQLGVF 152
              *: * : * : : * : : : * * * * * . : : * * : . * * * : * * * * *

DR_2335      GTPTFDLGGGDVAYFKFEELTRDPQAARDLWNLFTSTLRSEARVATIRRPVPPKG--- 226
Deide_22890  GTPTFVLPDGHAAYYRFDHLTRDPQVARERWQLYRDVLQSEAGIGTIKRTRMTR--- 209
DGo_CA0030   GTPTFVLEDGGAAYYRFENLTRDPQTARAWWDLYRTVLD SGAGIATIKRARNRPAKKA 223
Deima_0620   GTPTFVLGDGANAAYFRFARLPESPEAAHALWELYVQTLLNDARIETIKRPR----- 210
Deipe_1019   GTPTFVLPDQAAAYLRFSQLPADESAARRLWD TYVTVLTSDAN IETIKRPR----- 203
              ***** * .. . * * : * . * . . . : * : : . * . * : * * : *

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Figure S6. Multiple sequence alignment of *Deinococcus* FrnE reductases. **(a)** FrnE proteins (DsbA family, FrnE subfamily). The N-terminal CxxC corresponds to residues 22-25 in *D. radiodurans* FrnE (DR_0659), and the C-terminal CxxxxC to residues 239-244. **(b)** FrnE-like proteins found in two *Deinococcus* species (DsbA family, FrnE-like subfamily). The CxxC motif is highlighted in yellow. **(c)** Proteins containing a DSBA-like Trx domain. The single Cys is highlighted in yellow. Alignments were made as in Figures S1 & S5.

Figure S7

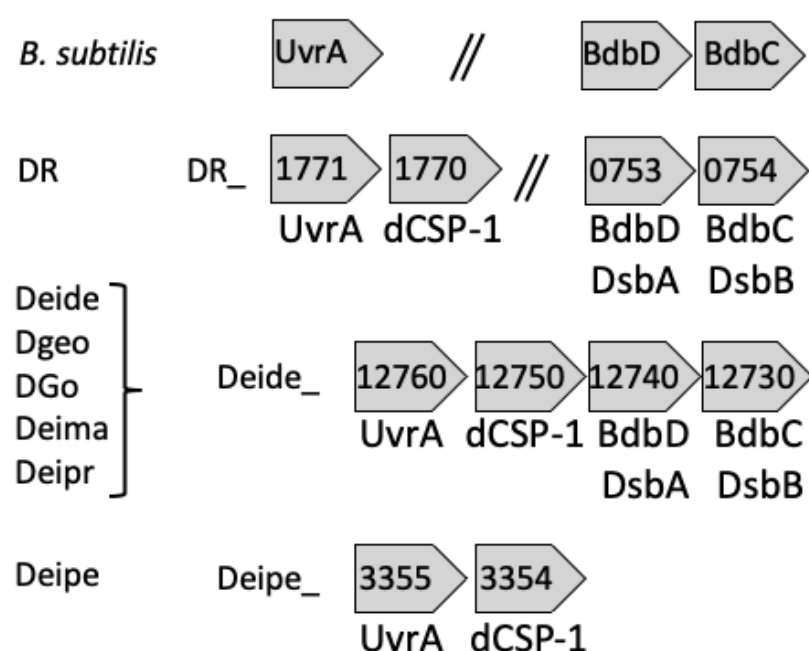


Figure S7. Putative operons encoding DsbA, DsbB and UvrA. Similar to the *B. subtilis* *bdbDC* operon encoding DsbA and DsbB homologs, putative operons encoding DsbA and DsbB family proteins are present in most *Deinococcus* species. In five of the seven analyzed species, these genes are likely in operon with genes encoding DNA repair protein UvrA and a membrane protein designated dCSP-1 (*Deinococcus*-specific conserved signature protein-1). In *D. radiodurans* (DR), the *uvrA*-*dCSP-1* genes are located separate from the *bdbDC* genes. *D. peraridilitoris* (Deipe) lacks the *bdbDC* homologs. Gene numbers (locus tags) for *D. radiodurans*, *D. deserti* and *D. peraridilitoris* are indicated.

(a) (DsbA family with N-terminal transmembrane helix)

Dataset	Reads (approx.)
Deipr_2421	1000
BDBD_BACSU	950
Deima_1749	850
Deipr_0493	750
Dgeo_0692	650
DR_0753	600
Deide_12740	550
DGo_CA1008	500

(b) (DsbB family, BdbC subfamily)

DR_0754	--MNRDRLRYLAWLVALAATLGSLYFSEIRHFNP	CPLCWAQRIFMYPLAVILGIAAFVGD	58
Deide_12730	MLSSADNR IYA A W V V A L V A T L G S L Y L S N V L G F K P	CVL C W Y Q R I C M Y P L A L W L G I A A L R G D	60
Dgeo_0691	--MTRDNR L Y L A W V V A L L A T L G S L W F S E V R Q F V P	CVL C W F Q R I A M Y P L A L L L G I A A L R A D	58
DGo_CA1007	--MSRDNR L Y A A W V V A L V A T L G S L Y F S E V R G F N P	CVL C W Y Q R I C M Y P L A L L L G V A A F R G D	58
Deima_1748	--MTREN R Y A A W V V A I L A T M G S L Y F S E V R Q F V P	CVL C W F Q R I C M Y P L V L V L G V A A F R D	58
Deipr_0492	--MNRSTR L Y A W V V A L V A T L G S L Y S E V L G Y R P C K L C	W Y Q R I A M Y P L A M L G I A A F R D D	58
BDBC_BACSU	-MKNR I V F L Y A S W V V A L I A M L G S L Y F S E I R K F I P	C E L C W Y Q R I L M Y P L V L I L G I A T F Q G D	59
	.	: * : * : * : * : * : * : : * * * * * * * : * : * : *	
DR_0754	HGVR R Y V L P L A A L G L G F A I F Q N L E T W G - F V Q S I K A C T V N A A - A A C N T P W P V W G T S - - - Q -		112
Deide_12730	TG I R V Y A W P L A A V G W I I A L V Q N A E D W G - W I P T L K A C A P D P T T V A C N I P W P L W G S G - - - A L		116
Dgeo_0691	L G I R V Y A L P L A A I G W V I A L I Q N L E D W G - V I P T L R V C S A R A A - A P C D V H W P V W G A G - - - A -		112
DGo_CA1007	L G I R A Y A L P L A V V G W L T A L Y Q N A E T W G - W V P V L K A C T T N P A - A S C G T P W P V W G V G - - - N -		112
Deima_1748	P G G R A Y A L P L A V A G W L V A M V H N L E D W G - V I Q A L K V C G V G Q T T A G C D A K W P I F G D A - - - - N		113
Deipr_0492	L R V R L Y A A A L I G A I T A L V Q N A E I W G - W I P T L K S C S I D A G Q E P C T T I W P L W S T L F G E G A		117
BDBC_BACSU	T R V K K Y V L P M A I I G A F I S I M H Y L E Q K V P G F S I K P V S - - - G V P C S G Q Y I N W - - - - -		108
	: * . : * * : : : * . : * . : :		
DR_0754	DTLNRALTIPVLSMIAFALILALLSWPRQRVTVPESAAVQG----		153
Deide_12730	SGLNSVITIPVLSMIAFTLILALLSWRRERFI-----		148
Dgeo_0691	-SLNSVLTIIPVLSLVAFTLIIIGLLSWARERKV-----		143
DGo_CA1007	DALNTTITIPVLSMIAFTLIIALLSWRRVARTTADQTVAAQA----		154
Deima_1748	KAVSDIITIPVLSFVAFTLVIALLTWRERPGR-----		146
Deipr_0492	SALNSILTIPVLSMIAFSLILALLAWPRMRPEEQAQATYTEPHDRV		163
BDBC_BACSU	---FGFITIPFLALIAFIILIFMCLLKGEKSE-----		138
	: * * * : * : * * : * : : :		

(c) (DsbA family with N-terminal signal peptide)

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DR_2019      MPSFSLSFLSGRGLVAAALLALS GAPAQAQLWETPQTT-ARQPLLRGVSVQPGGKVLRLG 59
DR_0560      MLW-----AMKRLLAALLGALLLPSAHAQLG-QPTDALLKSPLFVGAQTSRAGIITLKS 53
Deide_06420  MNK-----VLLGLVWGVVALAPVASAQLWETPQAT-VRQEVLKDFS--AGNVLQGP 48
Dgeo_0747    MNRVIG-----LVAGALLAANLGSQASQALLATPAAT-AAQPLLAGFRV--SGSTLTRG 51
DGo_CA1399   MTH-----FARRFFALGLLAALSGAAHAQVG-GQVAPVRAAPAFQGAQVAGGGLLTLD 53
Deima_1134   MNRTL-----LTAALSVLG--VAAQV-AYPASNYARLTGGTAASATASTTSVRVG 48
Deipr_0943   MK-----PHMSFLVAALLLPGAQAQLWNTPQAT-ASQPLLRSFKA--EGDVLTHG 47
              *               * **

DR_2019      STTLTLDVVAGRVVGVLIIEG--RDTASVARA-----LAAVWDS 95
DR_0560      GNVNVLGQRGGRLTTVTITTPYTEPQGISGSSDTAVAAGSVEQRVGGSALAAQTVGAVTG 113
Deide_06420  ETRVTLDVSGGRVVGVLVEA--ATGTALARG-----VAAAWGM 84
Dgeo_0747    TTTLTLDTAGGRVVGVLVQA--DNPQDVARA-----LVAAWGG 87
DGo_CA1399   GAQVTL SQKAGYLAGASVSV-----PASGAARAAELLGVLSG 90
Deima_1134   GGTVTVTTAGGLAARFAYSGPTDDTASAARA-----LIATETD 86
Deipr_0943   QTRAE LDRIGQRVIGVYVRAPKANTEDVARA-----ILSAWGA 85
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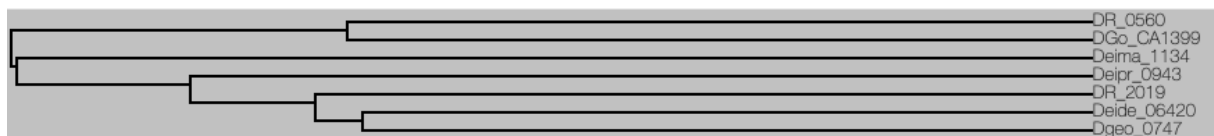
DR_2019      TAEGAA-----SLQQA FARPAFQDRARLGSVQPSDENGTDLLAIRLTGRGAEQRWRVYA- 149
DR_0560      YGEGLS----APLLQFLRQPDV---VKQLPQGVTVDAPPLTIQAQVQGRALVLK-----L 161
Deide_06420  READLP-----QLVRLQSSSELLASARRGFTEFTDESEQDMITVKVGTGGAQVRWRAYL- 138
Dgeo_0747    PEQNV A-----AVAQALGRDDL-QREARGAQGLRDDSEGTLRLVKLNGTGGAQRWTAYT- 140
DGo_CA1399   YDGLA-----EPL EAF LKRSV---AGRLPQGVTVDAEPFTVTARLTGGRLNVS-----L 138
Deima_1134   MDAPVTAAQAKQLAGAFDKIR---AQVLGKGVPVPLG-----FADGLDFTLDWTASRL 135
Deipr_0943   PEDAVP-----DLKGVLD DPGFQQQAQQLFEEVSEDGGS AV-YVRL----QDGTWQAYT- 134
              :               :

DR_2019      AVNVLP E--SDFPVTRNVT---GQSKAPNVIHVLSDFC CPAC RQLWAEQ-IPGWRA---Q 200
DR_0560      SMTQVPA--GQFTATKNLRPAA-KPGKDVVLRVYSDFC CPYC QKLELET-MPALLRA--L 215
Deide_06420  ALKIWD--AAFPATRNVS---GRADAPNSIRIFSDFC CPYC RDLWHET-LPGWAR---Q 189
Dgeo_0747    ALLIFPD--RAFPATANVQ---GSAQAPNVLRIFSDFC CPYC KELWDTA-HPKWAA---Q 191
DGo_CA1399   VLAQVPA--AQFAPVKTAAARTATASPVVLRVYSDFC CPYC QQFETQT-LPELQKA--L 193
Deima_1134   TFTVAPHEYTGF GADRYVL---GKG--GPVIREFSDFC CPYC RELHDDV-FPALQRDLIG 189
Deipr_0943   ALKVYPH--SAFPQVSAPL---GNDGAPARLNIVSDYQ CPYC NQLWNSASMAEWS---K 186
              .   *       *               :..  **:* ** *..:

DR_2019      PAKYRLFYHHFPL-SYHANAFAAAEASE CAAK QGQFWTYADRLFGGV EEWGRASAPQATR 259
DR_0560      PDDVRVEFHQFPLEQIHPLARPAAEASE CAAQ QGRFWDYKDALFRDRSWLQ----NNPNE 271
Deide_06420  TTQYRV AHYHFPL-DFHKNAFAAAEASE CAAQ GAFWKMDQIFAGFDVWNRLSARDAAT 248
Dgeo_0747    PNRYRVMHYHFPL-SFHKN AEPAAIASE CAAE QGKFWPYADLLFRHTAEWTGLPS--ASA 248
DGo_CA1399   PADVRIEFHQFPLESIHPRARAAAEASE CASA QGKFWAYKDALFADRSWLS----GDAAT 249
Deima_1134   KGLARFSYRHFPPL-SFHQNAMPLALGGE CAAQ QGKFWAYHDAFTVTSP-----237
Deipr_0943   PGVYRLNYHHFPL-SFHPLALPAAQFSE CAAQ QGRFEFSDAVNADFAHWTTQQPEAEARQ 245
              * . . :*** . * * * .***: ** * * *

DR_2019      LFGTYAGKCLKLDRTAFDRCLNTHQLKAKVQRQIQGAGKTYLRGTPTVYLNQVKNLSFSDE 319
DR_0560      TFLRLAGDLKLDPGKFKDCLALRGKGAGVDAGLAE AQQLGLNATPTVFVDGYRVGNPFD 331
Deide_06420  QFRTYAGNAKLT PATFEKMTQRSSRAVVDAQIKAGLT LGVKGTPTVFLNGMKLQNYTDA 308
Dgeo_0747    KFSEYAQAAGLNVA AFQTCLTSAAPKAVVRAQQAAGLKLGVQGTPTVYLNQVQLRNYSD 308
DGo_CA1399   AFTATAGKAGLNLTAFKGC LAARGGRAAVDAGLAEADRLGLQGTSPSVFVNGYAVADPYDA 309
Deima_1134   --VTA AKQLGLNLTTFQ TCLKDPAVQALVKADMKVGDAVDVQGTPSLYVGPFKVQNWTD 295
Deipr_0943   SFTRYAVSAGVTQAE LDKCLAQDRSRDIMATADQLQRQLNVRGTPSVYLNQIKLNNYND 305
              *       :       :. *:       :       : ..**:::.. : . *

DR_2019      -ELASVQAVTRAQPSAASV---IAA--RFKSFR-----346
DR_0560      AAVLQLIDVARATR-----345
Deide_06420  SEWAQVQAVTTAKPSAAQL---IES--RLAQFR-----336
Dgeo_0747    NELA AVRAVTAASPGAVEV---IAA--RLKRF-----335
DGo_CA1399   PALLRLIAYARAVDTAPAAATPVTAPSPLSPKAVPATPPATR 352
Deima_1134   ASIGNYVKLVLTALGK-----310
Deipr_0943   AQIRAIRAVTEAGPGA EKV---IEQ--RLKGLR-----333
              .   *
```



(d) (Cytochrome c biogenesis protein CcdA, DsbD family)

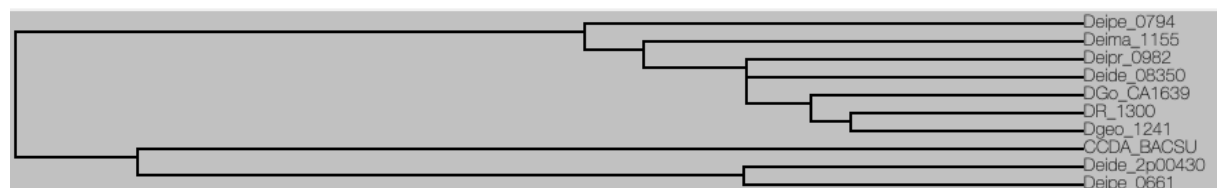
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DR_1300      MLPGVNVSAAPSLTVAFLAGLISFLSPCVLPLLPVSYLGVLGGA-----KAPL 47
Deide_08350  ----MMSTGAPTLTVAFLAGLVSLSPCVLPLVPSYLGAIIGT-----RAPL 43
Dgeo_1241    ---MFASPGAPSVTVAFLAGLISFLSPCVLPLVPSYLGVLGGA-----RAPL 44
DGo_CA1639   --MLAQALAAPTLAVAFVAGLVSLSPCVLPLVPSYLGVLGGA-----RAPL 45
Deima_1155   -----MSSAPTVTIAFLAGLVSLSPCVLPLVPSYLGVLGGA-----RAPM 41
Deipe_0794   --MNPQAQAEVLPALGIAFAAGLLSLSPCVLPLVPSYLGVLGGG-----RSPL 46
Deipr_0982   ---MVEAASAPTLTVAFVAGLLSLSPCVLPLVPSYLGVLGGT-----RAPL 44
Deide_2p00430 -----MTDSPGFLFAFGAGLLSLSPCVLPLPAYLGFLTGMMSGELAGPQ--ARRLAL 52
Deipe_0661   -----MISSPSFLFAFGAGLLSLSPCVLPLPAYLGFLTGMMSGELSER--ARRPAL 52
CCDA_BACSU   -----MGDVNYFLTTFGAGFLSFISPCCLPLYPAFLSYITGVSMDDVKTEKLLQKRSL 53
          .:* **::*:*** **::*: .: *
          : *
          :
```

```
DR_1300      GRALGFIAGFGLVFVALGATASTLGAFLAPHKLLLGQLAAVLIVFFGLVMLGVIRLPFLM 107
Deide_08350  ARALGFIAGFGLVFIALGATASTLGSVLAPHKILLGQVAGGLIVFFGLVMLGLIRVPLLM 103
Dgeo_1241    LRALGFILGFGLVFIALGATASSLGALLAPHKLLGRVAAVLIIFFGLVMLGVIRLPWLM 104
DGo_CA1639   LRAAGFILGFGLVFMALGATASTLGAALAPHKALLAQLAGVLILFFGLVMLGALRLPFLM 105
Deima_1155   TRALGFVLGFGLVFVALGATASSLGALLQYKYLIGRVAAVLIIFFGLVMLGVIRLPFLM 101
Deipe_0794   VRALGFVVMGFGLVFIALGATASYLGALLAPHKIVLGRAGAILIIAFGLFMLGLRPRGLM- 105
Deipr_0982   VRALGFIAGFGLVFVALGATASALGALLAPHKLLLGRLAGALIVFFGLVMLGVIRLPWMM 104
Deide_2p00430 SHAVAFLAGFSVVFLALGALVESAAVVLTTYGTPVRVIGGAMVLMMLGFTLGVLRVNALY 112
Deipe_0661   KHALAFLAGFGVVFLALGALVESASIIILTTYGTPVRVLGGVIVLLGLVTLGALRAPWLK 112
CCDA_BACSU   FHTLCFLLGFSVIFIALGYGTSFIGSLFRDYHDAIRQIGALLIILFGFITLGVFRPEAMM 113
          :: * : **::*:*** .. . : : : .. :: :*: *
          :
```

```
DR_1300      RDTRQ-LA--DAGGYGPVALGAAFAFGWSPCLGPTLGSILGLAASSASLGSVRLVAYT 164
Deide_08350  RDTRA-LA--GAGSYSPVALGAAFAFGWSPCLGPALGSILGLAASSASLSSGVVLLAAYT 160
Dgeo_1241    RDTRA-LA--DAGGYGPVALGAAFAFGWSPCLGPALGSILGLAASSASLSTGVGLLAAYT 161
DGo_CA1639   RDTRQ-LA--DAGGYGPVALGAAFAFGWSPCLGPALGSILGLAASTASLQTVGLLAAYT 162
Deima_1155   RDTRTALY--GADRYGAVALGAAFAFGWSPCLGPVLGSILGLAASGASLPLGVGLLAAYT 159
Deipe_0794   LDSRR-MR--GAERYGAVVLGAAFAFGWSPCLGPILGSILSLAASSANLPRGVSLGAYT 162
Deipr_0982   RDTRQ-LS--AADRYGPVALGAAFAFGWSPCLGPALGSILGLAASTSSLSQGVVLLTYT 161
Deide_2p00430 LERRVQLKSKPAGYLGSAVVLGAFAGWTPCMGPILAGVLFMAAQQP--ALGVPLLLTYA 170
Deipe_0661   MERRTHLARKPAGYLGSAVVLGAFAGWTPCMGPILAGVLFVAAQQP--GLGVPLLLTYA 170
CCDA_BACSU   KERRIHFKHKPSGFLGSVLIGMAFAAGWTPCTGPILAAVITLAGTNP--GSAVPYMMLYV 171
          : * : : . . : * ** * : * * * . . : : * . * : *
```

```
DR_1300      LGLALPFLLAALLWDRNLNRLNRYAGIFEKVGGAVLVIVGVMMLTGQFTRLATFFFSVM 224
Deide_08350  LGLAVPFLLAALLWHRNLNRLNRYSPVFEKVGGVVLVAMGLLMLSGEFTRLASFFFTIM 220
Dgeo_1241    LGLAVPFLLAALLWHRNLNRLNRYAGVFEKVGGAVLVLVGMLMLTGQFTRLATFFYEVM 221
DGo_CA1639   AGLALPFLLAALLWDRNLNRLNRYAGVFEKVGGALLVVVGVLMLTGQFTRLASFFYSVM 222
Deima_1155   LGLAVPFLLAGLLWNRLNRLNRYSPVFEKIGGALLVLVGTILVITGAFTRLNSFFFEVT 219
Deipe_0794   VGLAVPFLLAALLWRRNLNRLNRYSPVFEKIGGAILVVVGLLIFSGETRLAGFFFEIT 222
Deipr_0982   LGLAAPFLLAALLWDRINLRLNRYAGIFEKVGGAILVAVGLLMLSGYFTVLAFFYSVM 221
Deide_2p00430 LGFSVPFLLGALFLERV--RALHRTPTLERAGGALMVVAGILLITNGFAWISRLVNV- 227
Deipe_0661   LGFSVPFLLGALFLERV--RLLGRFTPTLERVGGVMVAVGVLITNGFAVMSQYLVNV- 227
CCDA_BACSU   LGFAVPFLLSFFITKL--KWIRKNQLFIMKAGGVLMIVIGVLLFFNWMSLIIILSDLF 229
          *:: **** .:: :: : : : : : * : * : * : : : : :
```

```
DR_1300      PEWLKV-- 230
Deide_08350  PDWMRI-- 226
Dgeo_1241    PAWLRV-- 227
DGo_CA1639   PAWLIS-- 228
Deima_1155   PAWLRL-- 225
Deipe_0794   PAWLRYL 230
Deipr_0982   PQWLRV-- 227
Deide_2p00430 VGFQGF-- 233
Deipe_0661   LGFQGF-- 233
CCDA_BACSU   GGTGTF-- 235
          :
```



(e) (DsbE/CcmG homologs, TlpA-like family)

```

DR_0189      MTEPA-----PASPAPAWTRALPPLAALVGGGLGWALLKPAG-NA--A-NGPLVG 48
DR_0345      MTSPTPPT-SPSLSPQPRRASWTRWIVPAVMVGLVGLLAYGLFTDPD-EG----GPALLG 54
Deide_08290  MTQ----PAASS-TNSAPVPANWRLLPPLIAAGLVGVLGVALFRPAD-DA--TTGGPLVG 52
Dgeo_1248    MTE----LPSTS-KPAAPAPLWRRLLPPLAALVAVLGIALLNPAH-NA--TDGGPLVG 52
DGo_CA2017  MTE----KTAPSNPAPAARFSPWRRFVPLLAAGLVAVLGVTLRLPAR-TA--TDGGPLIG 53
DGo_PC0193  -----M-TPDRPPPLWKRLPPLLAAGLATSLAVALLNPAR-NA--TSGGPLVG 45
Deima_1148  -----MTTSPSPPAVPTWRRLLPPLAFLLVVFAVALTRQSD-SARTGATGPLVG 51
Deipe_0801  -----MKRWIPPLAGLLVIVLAAALLRSGS-----DATGPLVG 34
Deipe_4366  -----MPRSPVRCLLRRWIPPLSALLVIVLAAALLRSGA-----E-GVPLLG 42
Deipr_0892  MTRPAPHDPADLQPTSPSPGPAWKWLPPLAAGLVAAALGTALFSPTR-NE--TAGGPLVD 57
Deide_2p00420 -----MRL-RIKGRITQKQLTLLFLITS-L---ASAVRPG 32
Deipe_0660  -----MRVLTLLLSLGV-V---AQAVRPG 21
YNEN_BACSU  -----MLKKWLAGILLIMLVGYTGNLYQYYS-KK---EVGIQEG 36
RESA_BACSU  -----MKKKRRLFIRTGILLVLICALGYTINAVF-AG---KESISEG 39
DSBE_ECOLI  -----MKRKVLLIPLIIFLAIAAALLWQLARNAEGDDPTNLESALIG 42
      :
      .

DR_0189      KPAPQFNLTGLDGGQPVALA---DYRGRPVVLFNWASWCGPCREEAPLFAKLAHP----- 100
DR_0345      KPAPAFLEDLGGRTHALT---AAQGKPVVFNFWASWCVPCRQEAPLFSKLSQET-----A 107
Deide_08290  KTAPDFILQSLDGGPELRRLS---SLKGRPVVFNFWASWCVPCRQEAPLFRDLSARQ---APG 107
Dgeo_1248    KPAPFETTLTSLDGTFPVSLA---SLRGRPVVLFNWASWCGPCREEAPLFRELSTRQ---SAG 107
DGo_CA2017  KAAPEFDLQTLDDGTLSLA---SLKGRPVVFNFWASWCVPCRQEAPLFRELGARPANAGG 110
DGo_PC0193  RPAPDFTLSDGVDVRLA---ALKGRPVVLFNWASWCVPCRQEAPLFRELSEKQ---TAG 100
Deima_1148  KAAPNFTLKDNLGNTVTSLA---SLRGRPVVLFNWASWCVPCRNEAPLLSDVARQ---RA 105
Deipe_0801  KTAPDFHLQTLDDGGDVRLS---DLRGRPVVFNFWASWCVPCRQEAPLLREIAEQ---AE 88
Deipe_4366  QAAPNFKLETLDGSSLEFA---QLRGRPVVLFNWASWCVPCRQEAPLLQELARQ---DD 96
Deipr_0892  KAAPDFRLTSLDGTFPVSLA---DFRGRPVVLFNWASWCGPCREEAPLFRELSEKQ---GA 111
Deide_2p00420 DVAPDFTLNDPSGKKTLS---ALRQGPVLTFWATWCLVCKEELPELNQEARA---84
Deipe_0660  DVAPNFSLKTEAGKTVSLN---SLRGPVLTFWATWCLVCKEELPELNQEARA---73
YNEN_BACSU  QQAPDFSLKTLSDGKSSLSQ---DAKGGKVVLFNWATWCKPCRQEMPAMEKQKEY---A 89
RESA_BACSU  SDAPNFVLEDTNGKRIELS---DLKGGKGVFLNFWGTWCEPCKEFPYMANQYKHF---KS 93
DSBE_ECOLI  KVPVFRFRLSDNPGQFYQADVLTKGKPVLLNVATWCPTRAEHQYLNQLSA----- 95
      * * *      : * . . . * : * : * : .

DR_0189      GAPAVLGILF--NETKPNQARDFARQYGL--TYP-NLQDP-----GVATAIAYQVTGI 148
DR_0345      GKAEFFGVYI--NDQP-ADARRFMDQYGL--IYP-ALLDP-----GSRTALSYGVGKL 154
Deide_08290  TGLAVVGVLF--QEPREDAARTFIQEYAL--AYP-NLRDP-----KARTAINYGVAGI 155
Dgeo_1248    QGLAVVGVLF--QETNEQNARDFIREYAL--AYP-SLRDP-----GIQTGINYGVSGI 155
DGo_CA2017  QGLAVVGVLF--NETREQDARDFIREYAL--AYP-NLRDP-----GISTGINYGVSGV 158
DGo_PC0193  RGLAVIGILF--QEPKEANARTFIREFSL--AYP-NLRDP-----KSATAINYGVAGI 148
Deima_1148  QGLAVVGVYI--ADDNVSAIRDIFIYEYNL--AYP-NVRDP-----GSRTAIDYGVAAV 153
Deipe_0801  GGLVIVGIMY--QDRE-ADARKFIEDYGL--TFP-SLIDK-----DLSTADYGVGAV 135
Deipe_4366  RGLVVGVGVF--QDTL-KNARAFRDEFNL--TFP-SVDFP-----GSRTAIDYGVSAI 143
Deipr_0892  GGLAVVGVLF--EEKNEQNARDFIREYAL--AYP-NLRDQ-----NLNTAIDYGVGAI 159
Deide_2p00420 KVKNMFAV---SATDTPKAALDYFKQAKLGAITP-LVDAPKAKGPGTGAGVAKSYRIIGQ 140
Deipe_0660  KLKNMYAV---SATDSAKDALAYFRKNELGSVTP-LVDAPGKTGTSTAASVARAYRIIGQ 129
YNEN_BACSU  DKLAVVAVNFTSAEKSEKQVRAFADTYDL--TFP-ILIDK-----KG-INADYNVMSY 138
RESA_BACSU  QGVEIVAVNV---GESKIAVHNFMKSYGV--NFP-VVLDL-----DRQVLDAYDVVSPL 140
DSBE_ECOLI  QGIRVVMGNY---KDDRQKAIKSWLKEGLN--PYALSFDG-----DGMGLGLDLGVYGA 143
      . . :      :      :      :

DR_0189      PRTVFIDAQGVVRHIDQGGDLTARLNAGLSKIGVPGL----- 185
DR_0345      PITFIVDQGGKVHHKDGPIEEPRLRAALKQAGL----- 188
Deide_08290  PETVFIDAKGVVIQHVDRGGLDRARLNVGLEKIGVKGL----- 192
Dgeo_1248    PETFFIDREGVIRHVRGGLTRERLNVGLKKIGVPGL----- 192
DGo_CA2017  PETVFIDKNGVQVHMDRGGLDRARLNVGLAKIGVPGL----- 195
DGo_PC0193  PETVFIDRQGVQFMDRGGLTRERLNMGLTIGVPGL----- 185
Deima_1148  PETFFIDKTGVIRAHVRQEVTRDVLTRQLKTIGVSQ----- 189
Deipe_0801  PETFLIDRDGVVQRHLRQPLTRELLRDELPKIGVRL----- 171
Deipe_4366  PETFFVDRHGVVRAVFGQTLTREHLTRELPKIGVTP----- 179
Deipr_0892  PETFFIDKGVIRYKDKGGLDRARLNAKLTIGVEPL----- 196
Deide_2p00420 PVSVFIDSKGKVTAHVSGYLPPEQFRVYLKQIRP----- 174
Deipe_0660  PVSVFIDKAGKVASVHSGYMPPEQFRVYLKTIQTP----- 164
YNEN_BACSU  PTTYILDEKGVQIDIHVGTMKKEMEQLDL----- 170
RESA_BACSU  PTTFLINPEGKVVVGTGMTESMIHDMNLKPGETSG--- 179
DSBE_ECOLI  PETFLIDNGIIRYRHAGDLNPRVWEEIEKPLWEKYSKEAAQ 185
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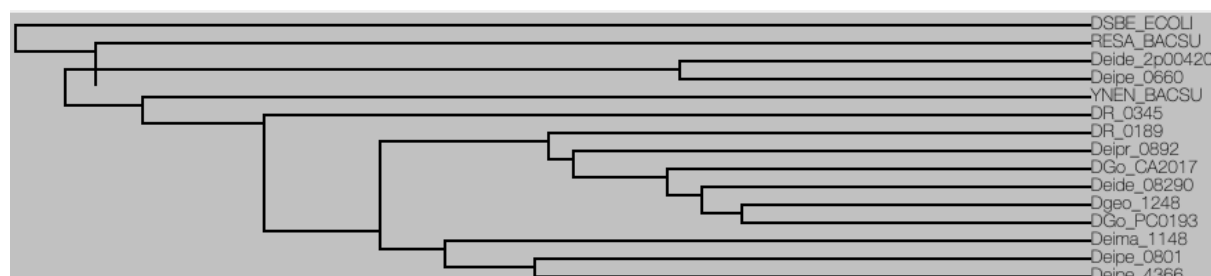
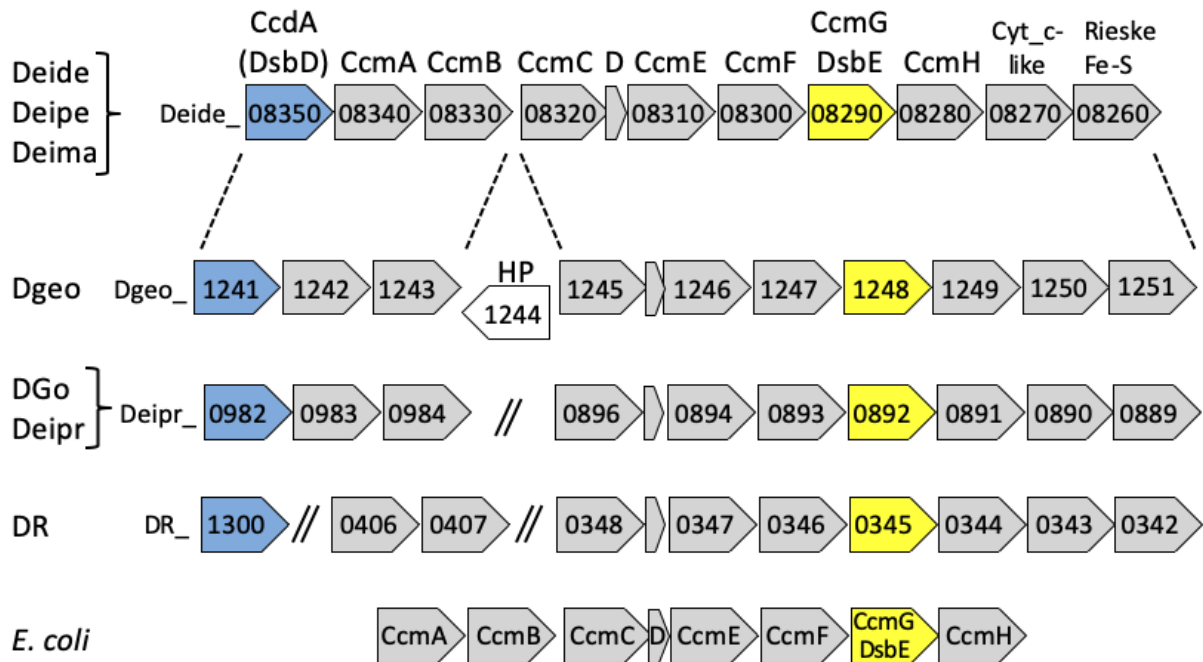


Figure S8. Multiple sequence alignments of *Deinococcus* Dsb oxidoreductases. **(a)** DsbA family proteins with an N-terminal transmembrane helix from *Deinococcus* species aligned with *B. subtilis* BdbD. Except for the second homolog of *D. proteolyticus* (Deipr_2421), the genes are adjacent to a gene encoding the DsbB/BdbC homologs shown in panel **(b)** (see also Figure

S7). Residues highlighted in cyan in Deipr_2421 differ in the proximity of the active site. **(c)** DsbA family proteins with N-terminal signal peptide. **(d)** Homologs of the DsbD family protein CcdA from *Deinococcus* aligned with *B. subtilis* CcdA. The deinococcal *ccdA* homologs are in gene clusters also encoding DsbE/CcmG homologs (see Figure S9). **(e)** DsbE/CcmG homologs from *Deinococcus* encoded by gene clusters also encoding CcdA and by isolated genes aligned with the TlpA-like family proteins ResA and YneN from *B. subtilis* and DsbE/CcmG from *E. coli*. Cys residues and CxxC motifs are highlighted in yellow. Guide trees showing sequence relationship between various proteins are included in case more than one homolog is present in the same *Deinococcus* species. Alignments and trees were obtained with UniProt ClustalO as in Figure S5.

Figure S9

(a)



(b)

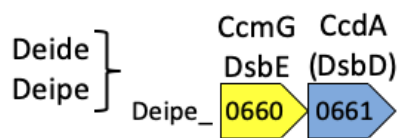


Figure S9. Gene clusters encoding CcdA and DsbE/CcmG homologs. **(a)** The seven analyzed *Deinococcus* species possess *ccdA* (DsbD family) and *dsbE/ccmG* homologs in gene clusters containing other cytochrome c biogenesis genes. Different genetic organisations are present in the different species, as shown. The *ccm* cluster from *E. coli* is also shown for comparison. Gene numbers (locus tags) for the indicated *Deinococcus* species are indicated. HP, hypothetical protein. **(b)** Additional two-gene cluster encoding CcdA and DsbE/CcmG found in two *Deinococcus* species.

Figure S10 (panels a & b)

(a)

```

DR_1849      -----MTQQTNSQGTQPGAAQEQAIFAGGCFWCTEAVM 33
Deide_10980  -----MTDTAMQGMQQAILAGGCFWCTEAVM 26
DGo_CA1541   -----MTNGTQGKEQAIFAGGCFWCTEAVL 25
Dgeo_0843    -----MTSAQSEQTQQAIFAGGCFWCTEAVM 26
Deima_1788   -----MNQVILASGCFWCTEAVF 18
Deipe_3499   -----MAQEIATLAGGCFWCTEAVF 20
Deipr_1412   -----MTQAHPSQAIFAGGCFWCTEAVM 24
MSRA_ECOLI   MSLFDKKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMETIAIFAMGCFWGVVERLF 60
MSRA_BACSU   -----MSEKKEIATFAGGCFWCMVKPF 22
              : . : * * * * :

DR_1849      QDLRGVQKVESGYIGGTVPNPDYRSVCGGQTGHAEAVRVTFDPNQISYRDLLGLFFATHD 93
Deide_10980  KDLRGVHKVESGYIGGHTARPDYRSVCSGTTGYAEAVRVTFDPAQVSFRDLLGLFFATHD 86
DGo_CA1541   KDIQGVDKVESGYIGGDVPDPTYRAVCGGDTGHAEAVRVTFDPAQVSYKDLLGLFMATHD 85
Dgeo_0843    KDVRGVTRVESGYIGGHVPNPDYAAVCSGETGHAEAVRVTFDPAQVSFRDLLMLFFATHD 86
Deima_1788   KNVRGVQRVESGYIGGHVPNPNTYNQVCGGDTGHAEAVRLTYDPNVISSRDLLGIFATHD 78
Deipe_3499   QEVLGVSSESVEGYIGGADPNPTYEQVCGGRTGHAEAVRITYDSQVISYEDILGIFATHD 80
Deipr_1412   LRVRGVQQVESGYIGGRRPNPSYEQVCTGVTGHAEAVRVTFDPAEVSYRDLLHIFFGTHD 84
MSRA_ECOLI   WQLPGVYSTAAGYTGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHD 120
MSRA_BACSU   DEQPGIEKVVSQYTGHTENPTYEEVCSSETTGHREAVQITFHPDVPFYEKLLLEFWQQID 82
              * : . : * * * * * * * : * * : : : . . : * : *

DR_1849      PTSLNRQGADVGTQYRSALFPLTQEQEQTAREMIEQLGTED---VFGRPIVTSIEPASTF 150
Deide_10980  PTTLNRRQGADVGTQYRSVFPPLTPEQERETREMIADLNAQN---IFEAPIVTTIEPASEF 143
DGo_CA1541   PTSLNRQGADVGTQYRSVFPPLSAEQERETREVFADLGAQN---VFDRPIVTTIEPASEF 142
Dgeo_0843    PTSLNRQGADVGTQYRSVFPPLNEEQERETREVI GELTAQG---VFERPIVTTIEPAGPF 143
Deima_1788   PTQLNRQGADVGTQYRSVIFYANDEERQTAQAVIDELNAGN---VFDAPVVTTLPEATTF 135
Deipe_3499   PTTLNRRQGADVGTQYRSAIFAHGDSQRVTAERVIAELNDAH---IWEAPIVTTIESDGP 137
Deipr_1412   PTTLNRRQGADRGTQYRSALFPLTDAQRAEAQAVIEELNTS----TFGGAIVTSIEEPSEF 140
MSRA_ECOLI   PAQGMRRQGNHGTQYRSALFYPLTPEQDAAARASLERFQAAMLAADDDRHHITTEIANATPF 180
MSRA_BACSU   PTDAGGQFADRGSSYRAAIFYHNDKQKELAEASKQRLAESG---IFKDPIVTDILKAEPF 139
              * : * * * : * * : : : : : : : * : *

DR_1849      YVAEDYHQNYKNNPGQGYCMA-V---ISPKVAKLRQYYGDKLR----- 190
Deide_10980  FVAEAYHQDYANNPNPDGYCRA-V---IAPKVAKLRQYYGEKLRA----- 184
DGo_CA1541   YVAEDYHQDYFANNPRQPYCAA-V---IAPKVAKLRKYYGDRLKAHARA 187
Dgeo_0843    YVAEDYHQDYARNPYQPYCMA-V---ITPKVAKFRKAYS DRLRG----- 184
Deima_1788   YVAEGYHQDYERNPGQPYCMA-V---ITPKVIKFRKQFSSYLS----- 175
Deipe_3499   YKAEPYHQDFFRRNPGQGYCLA-V---VAPKVVKFRRQFAQRLKSA--- 179
Deipr_1412   YVAEYHQDYANNPNQNPYCSA-V---VGPKVAKLRQSYARFLNE---- 181
MSRA_ECOLI   YYAEDDHQYLLHKNPYG-YCGIGGIGVCLPPEA----- 212
MSRA_BACSU   YEAEGYHQHFYKKNPAHYQRYRTGSG---RAGFISEHWGAK----- 177
              : ** ** : . **

```

(b)

```
DR_1378      ----MTQDTKTDFQKPSDNDLRERLTPIQYQVTQHEGTERAFTGEYWDHDEGIIYVDVVS 56
Deide_04050  -----MSKADFRKPADAELRERLTPIQYQVTQHEGTERAYTGEYWDHTEEGIIYVDVVS 53
DGo_CA0919   ---MTQSPPKKTYSKPSDSELRERLSPIQYQVTQHEGTERAFTGEYWDTDDEGIIYVDVVS 57
Dgeo_2072    -----MTRDFVKPSEAE LRQKLTPEQYRVTTQEGTERAFTGEYWDHDEPGIIYVDVVS 52
Deima_1441   -----MSEYVKPTDAELRERLT PQQYAVTQHEATERAFTGEFWDHEEPGIYVDVVS 51
Deipe_4299   MTNSTDNDTFLTGLPSTEA EWRERLSPEQFRVLRQAGTERAFTGEYVDTDEEGSYHQAAC 60
Deipr_1900   --MTKPNWTPEGYRKPADADLRAQLTPEQYQVTQHEGTERAFTGEYWDTAEDGIIYVDVVS 58
MSRB_ECOLI   -----MANKPSAEELKKNLSEM QFYVTQNHGTEPPFTGRLLHNKR DGVYHCLIC 49
MSRB_BACSU   -----MAYNKEEKIKSLNRMQYEV TQNNGTEPPFQNEYWDHKEEGLYVDIVS 47
              :      * .  * : * : : . ** : .. . . * * .

DR_1378      GEPLFSSLDKYDAGCGWPSFTQPIPDVALENTDYKIGYARTEVRSASADSHLGHVFPDG 116
Deide_04050  GEPLFSSRDKYDAGCGWPSFTTRPIQNMSLTENTDYKIGYPRTEVRSPVADSHLGHVFPDG 113
DGo_CA0919   GEPLFSSDKKYDAGCGWPSFTTRPLKDVSLTENTDYKIGYARTEVRSRGVDSHLGHVFPDG 117
Dgeo_2072    GEPLFSSLDKYDAGCGWPSFTTRPIPGVTLTERTDHKIGYPRTEVRSGLDADSHLGHVFPDG 112
Deima_1441   GEPLFSSTDKYDAGCGWPSFTTRPITDHGITERVDRQYGMVRTEVRSTQADSHLGHVFDDG 111
Deipe_4299   GNLLFDSSSKYHSGCGWPSFTEAVAPS AVELLED RSHGMIRTEVRQARCHSHLGHVFDDG 120
Deipr_1900   GEPLFSSRDKYDAGCGWPSFTTRPIAQ--LTEKTD FKLMPRTEVRSQVADSHLGHVFPDG 116
MSRB_ECOLI   DAPLFHSQTKYDSGCGWPSFYEPVSEESIRYIKDL SHGMQRIEIRGNCDAHLGHVFPDG 109
MSRB_BACSU   GKPLFTSKDKFDSQCGWPSFTKPIEEE-VEEKLDT SHGMIRTEVRSTADSHLGHVFNDG 106
              .  ** *  * : : : ***** . : : : * .  * * : . : ***** **

DR_1378      PRDRGGLRYCINSAALRFVPLSELDAQGYGQYRALFEGRQG 157
Deide_04050  PQEHGGLRYCINSASLRFVPVQGLEAEGYADYLP LFR---- 150
DGo_CA0919   PQEEGGLRYCINSASLRFVPAGQLEAEGYGEYAPMFR---- 154
Dgeo_2072    PSEAGGLRYCINSAALRFVPLERLEEEG YGEYRKLFEQQD- 152
Deima_1441   PREHGGLRYCINSAALRFIPVEQLEAEGYGEYQRLFVGG-- 150
Deipe_4299   PRDRGGQRYCMNSVALNLEER----- 141
Deipr_1900   PQDQGGLRYCINSAALRFVPLSQLDAEGYGEYRQLFG---- 153
MSRB_ECOLI   PQP-TGERYCVNSASLRFTDGENGEEING----- 137
MSRB_BACSU   PGP-NGLRYCINSAALRFVPKHKLKEEGYESYLHLFNK--- 143
              *      *  *** : ** : : : :
```

Figure S10. Multiple sequence alignment of *Deinococcus* Msr proteins. **(a)** Alignment of *Deinococcus*, *E. coli* and *B. subtilis* MsrA sequences. MSRA_ECOLI and MSRA_BACSU, MsrAs from *E. coli* and *B. subtilis*, respectively. **(b)** Alignment of *Deinococcus*, *E. coli* and *B. subtilis* MsrB sequences. MSRB_ECOLI and MSRB_BACSU, MsrBs from *E. coli* and *B. subtilis*, respectively. Catalytic and resolving cysteines are highlighted in green and cyan, respectively. Extra cysteines present in some sequences are highlighted in yellow. The black lines indicate the consensus sequences proximal to catalytic cysteines and prevalent in MsrA and MsrB.

Figure S11 (panels a to c)

a

```

DR_0846      MTDSDSQSPDTPQEVARLQPGDTPDFSLPDAAGDLHSLGQYDGKYVVLVYYPKDDTPGCTREACDFRDHQ 71
Deide_10900  -----MTEPQRIEFGATFPEFSLPDASGKAHRLSEYAGRYVVLVYYPKDDTPGCTKEACDFRDHT 60
DgeoAM_1323  -----MTEVPPQPNAGRLTPGEFPNPFALPDAEGRTHRLSDYAGRYVVLVYYPKDDTPGCTKEACDFRDSA 66
DGo_CA1364   MTQSGEQ--PSPSPSPRLQPGGEAFPAFALPDAEGQTHRLGQYEGKYVVLVYYPKDDTPGCTREACDFRDSA 69
Deima_2368   -----MSDPTPDQAVKLTAGQPPDFALPDADGTVHRLADHAGHYVVLVYYPKDDTPGCTKEACDFRDNA 65
Deipe_0259   -----MTQEAALQAGQPPDFALPDADNHLHLRLADYGRYLVLVYYPKDDTPGCTKEACDFRDHA 50
Deipr_0703   -----MTNNRIQPGDPFPFASLPDAGQTHNLSYAGRYVVLVYYPKDDTPGCTREACDFRDSA 59
BCP_BACSU    -----MTIIGQKAPDLELKGHDGHTVTKLSYKGYIVLYYYPKDMTPGCTTEACDFRDHSH 56
BCP_ECOLI    -----MNPLKAGDIAPKFSLPDQDGEQVNLDFQGGQVVLVYYPKAMTPGCTVQACGLRDNM 57
          : * * * * . . * .. * : : : * * * * * : * : *

DR_0846      -LLRQHGAIVLGVSRDDAASHQQAADKYSLFPFLSDPDAEFLRAIGSYGPKTMYGKTSEGVKRRQTFLIGP 141
Deide_10900  -LLKSLNAVILGVSRDDAASHQAFAEKYSLFPFLSDPDAEFLKSIGSYGPKTLYGKVTEGVKRRQTFLIGP 130
DgeoAM_1323  -RLKALGAVILGVSRDDAASHQAFAEKHSLFPFLSDPEAEFLKSVGAYGPKNLYGKIVEGVKRRQTFLIGP 136
DGo_CA1364   -TLRAHGAAIILGSRDDAASHQKFAEKYSLFPFLSDPEAEYIRAIAGAWGTKNMYGKVSEGIKRRQTFLIGP 139
Deima_2368   -TLRAHGAQVILGVSRDDADSHAKFAEKYSLFPFLSDPNAEFLRSIGAYGTKNMYGKVTEGIKRRSTFLIGP 135
Deipe_0259   -ELRAEGAAIILGSRDDAASHAGFAQKFSNFPFLVSDPDATFIRTIGAWGTKNLYGKVSEGLKRSTFLIAP 130
Deipr_0703   -RLREMGVQILGISQDDAASHQRFSEKFSLPFLFLTD-DGEFLASIGAYGEKNSYGVVTQGVKRRSTFIIDP 128
BCP_BACSU    ESFAELDAVIIIGVSPDSQEKHGKFKKHNLPFLFLVDDEHKLAEAFDVWKLKKNFGKEYMGIERSTFLIDK 127
BCP_ECOLI    DELKKAGVDVLGISDTPKPEKLSRFAEKELLNFTLLSDEDHQVCEQFGVWGEKSFMGKTYDGIHRSIFLIDA 128
          : .. : : * * . . * * * * * : .. : * . ** * : * : * :

DR_0846      DGKLVKSWLAVQVDGHADAVAAAIKDLQKKGQA 175
Deide_10900  DGRLVKSWLAVTVDGHADAVADAIREHQSKEPVA 164
DgeoAM_1323  DGKLVKAWNRNVSVDGHADAVAAAEADRKTRGEA 170
DGo_CA1364   DGRLVKSWLAVQVDGHADAVAAAIKDRAAHE-- 171
Deima_2368   DGKLVKAWYAVKVDGHADAVVNAIETDQKVRSA- 168
Deipe_0259   DGTLVKVSNSNVKVDGHADAVLRELREHKARRG-- 162
Deipr_0703   QGKLLKSWLAVKVDGHAEAVADAIAADMETSA-- 160
BCP_BACSU    EGRLIKEWRKVKVDHVAEALQTLKDMSEK---- 157
BCP_ECOLI    DGKIEHVFDDEKTSNHDVVLNWLKEHA----- 156
          : * : : : . . . * . :

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b

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DR_1209      MTPRVGPAPPFRARSDDGRLIDLAE LRGRWVVLVYYPFRAGTPGCSVEAQRFEALPEFERLGAEVIGVST 71
Deide_09051   MSLQVGRQAPPDVRSDDGRRVSLSAMRGQVVLVYYPKANTPACSIEAQRFEAVLPEFERLGATVIGVST 71
Dgeo_0990     MPLHPGQPAPEFDVRSDDGQVRVLADLRGRWVVLVYYPFRANTPGCSVEARRFEALPEFERLNAVIGVST 71
Dgeo_2729     MSPRPGDPAPEFETRSDDGRLADLFRGHWLVLFYFPFRANTTHCQLQARRFEALAPAFGALNARILGVSS 71
DGo_CA1403    MAPRVGQPAPEFARSDDGRALSLGTLRGQWIALVFWPGAQGPACP-EAQAFERAQPEFGALGAVLVAVSR 70
Deima_1714    MTPRVGDLAPDFRARSDDGDVSLAALRGRWVVLVYYPFRASSPGCSVEARAFETALPEFERRGATVIGVST 71
Deipe_3580    MGLRVGETAPAFARSDDGRAVELSALRGRWVVLVYYPFKAGSMGCALEAGRFESSLPEFERLNATVIGVST 71
Deipr_1557    MKLQLGQPAPEFSAVSDDGRHVRLQDLRGQWTVLYYYPFRANSYGC SIEAQRFEQFLPQFAALGAQVIGIST 71
Deima_0169    MTIQVGDLAPDVP---DTPPLALSAWRGQWVVLVYYPFRAHATHCQMQRFFQALMPEFQALGANIVGVSS 68
Deipe_3178    MALQVGAQVPDAV---SGAEVLRFSWRGQWVVLVYYPFRSNTTHCQLQARRFQALLPEFEHLHARLLGIS 68
DR_1208      MTLPLGYAPAFKPLPGDDGRWGLPDLRGQAALVYYPFLAHSRDCALEAMAFEVLLGEFAAGARVLGIST 71
          * * * * . : * : * : * : * : * : * : * : * : * : * :

DR_1209      DTEAQQARFRDRCGLSFPLLPDGDRAVAEAYGVLGG-V--GKLLGMT---ARQTFLLIDPAGRLAFHWKRVN 137
Deide_09051   DTEARQASFRDQCRLSFPLIPDGRKRLARDYGVVVG-L--RGLLGIA---SRETFLIDPEGELAHWRVTN 137
Dgeo_0990     DTEARQANFRDTCGLSFPLIPDGRTLRSAYGIVGG-L--GGLLGVA---ARQTFLLIDPEGRIAQHWRTVN 137
Dgeo_2729     DARAQQVAFRNLCCLSFPLIPDTHQLSERYGVVVG-L--PFPGEETRIA---RRETFLISPEGRVVRHWTEVI 139
DGo_CA1403    DTEAHLAQLRDRCGLSFPLLPDQAQVVARAYGVGGFRLWPERWGLGRRETGTFTFLIDPRGRLAHWPRAAD 141
Deima_1714    DTEAKQALFRDRCGLSFPLLPDGDKVIARAYGAVGV-V--GGLLNMA---SRRFTFLIDPGGRVAHVYRVLN 137
Deipe_3580    DTEASQAKFRQKCSLSFPLLPDGDQRQIAAAYGVMMGG-L--MKVFGRS---SRQTFLLIDPAGNIVHHWSRVN 137
Deipr_1557    DAAPGQAARFRKCGLSFPLLPDQDTIRAYGVVGG-L--TGLLGVS---GRASFVIDPQGLLVHQHRLDN 137
Deima_0169    DTGAQMTFRDVCVRSFPLLPDAGERIGGVYGVLEDAVEDEETRL---KRQTFLLIDPQGVVVEHHTVEVD 137
Deipe_3178    DTVAQQTFRFETCRLQFPLFTDSTQQLIELFGVREDDLLIDGESTHRA---KRQTFLLISPEGVIAHHWVQVD 137
DR_1208      DSRAQLARFRHAQGLTFPLLPDAGREVSRLYGARRS-P--WGLVGRA---GRQTYLLDERGRVHVHPQVD 137
          * : : : * : : : * : : : * : : : * : : : * : : :

DR_1209      PLGHAAEVLQTLQEQRTDPPTS---- 159
Deide_09051   PATHAAEVLSELEERTGAY----- 155
Dgeo_0990     PATHAADVLQALQERV----- 152
Dgeo_2729     PKTHAAEVLLEELRKVLGQPAA----- 159
DGo_CA1403    AAGL-PEVLAQIRQRQTPA----- 159
Deima_1714    VGGHATEVLADLDRRAEQPARASLS- 162
Deipe_3580    PLRHATDVLAELERIQQRHNAG----- 158
Deipr_1557    HTVHVQAALQAIREKQEQLA----- 156
Deima_0169    PNTHAGEVLAALRQHEAPLA----- 156
Deipe_3178    PNTHASEVLEYLAHSSARRPDLLG-- 161
DR_1208      PAWHAQAVLDTLRRWRDGDQDGAUTLGA 163
          . * :

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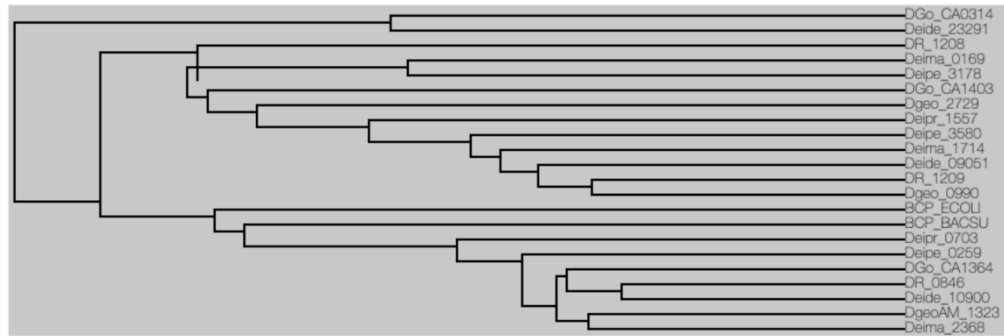

c

Figure S11. Multiple sequence alignments of BCP peroxiredoxins from *Deinococcus*. **(a)** Alignment of *Deinococcus* DR_0846-type, *B. subtilis* and *E. coli* BCP sequences. **(b)** Alignment of other *Deinococcus* BCP sequences. **(c)** Tree showing sequence relationship between BCP proteins shown in panels (a) and (b) and two more distant proteins from *D. gobiensis* and *D. deserti*. BCP, bacterioferritin comigratory protein. BCP_ECOLI and BCP_BACSU, BCP peroxiredoxins from *E. coli* and *B. subtilis*, respectively. Peroxidatic and resolving cysteines are highlighted in green and cyan, respectively. The black line indicates the sequence proximal to peroxidatic cysteine prevalent in BCPs, PKxxTPGCTxEAC [118]. The two other residues of the catalytic triad are highlighted in grey. Residues highlighted in yellow are highly conserved in bacterial BCPs [128]. Extra cysteines present in some sequences are highlighted in pink. Alignments and tree were obtained with UniProt ClustalO as in Figure S5.

Figure S12

(a)

```
DR_2242      -----MTLVGQPAPDFTLPA-----STGQDITLSSYRGQ-SHVVLVIFYPLDFSPVCSMQLP 50
Deide_02430  -----MSLLGQPAPDFTLPS-----STGENITLGSYRGQ-KHVVLVIFYPLDFSPVCSMQLP 50
Dgeo_0122    -----MSLLGQPAPDFTLPS-----TLGEPVTLSSYRGQ-QHVVLVIFYPLDFSPVCSMQLP 50
DGo_CA2657   -----MSLVGQPAPDFTLPA-----STGQAVTLSSYRGH-SAVVLVIFYPLDFSPVCSMQLP 50
Deima_0618   -----MSLLGQAPDFTLPS-----TLGEPITLSSYRGQ-KHVVLVIFYPLDFSPVCSMQLP 50
Deipe_1016   -----MSLLGQNAPDFALPS-----TEGREIRLSDFKGQ-QHVVLVIFYPLDFSPVCSMQLP 50
Deipr_0175   MIASPQALLNQTPDFTLNAVQPGLWQPVTLSSYAAAGRWAIVIFYPLDFSPGTAQVP 60
AHPE_MYCTU   -----MLNVGATAPDFTLRD-----QNQLVTLRGYRGA-KNVLLVFFPLAFTGIQQGELD 50
              :.  ****:*          . : * .: .      .:***:** * : *   ::

DR_2242      EYSGSQDDFTEAGAVVLGINRDSVYAHRAWAAEYGIEVPLLADMQ--LEVARQYGAIDE 108
Deide_02430  EYSGRQDDFADAGAVILGINRDSVHAHKAWAADYGIEVPLLADMK--CDVARQYGVTVDE 108
Dgeo_0122    EYSGRQDDFAEAGAVVLGVNRDSVYTHKAWAAEYGIEVPLLADMN--LNVARQYGAIDE 108
DGo_CA2657   EYSGRQDDFAEAGAAVLGINRDSVHAHKAWAAEYGIDVPLLADMR--LDVARLYGVAIDD 108
Deima_0618   EYSGRQDDFADADTVVLGVNRDSVYTHQAWAAEYGIDVPLLADLN--LAVARAYGVALDE 108
Deipe_1016   EYSGRQEDFAALDTTVLGVNRDSVYTHKAWAAEYGIEIPLLADLN--LKVAREYGAIDE 108
Deipr_0175   DYSRHAADFDAAGADVLCISRDSVYTHRAWSRELGLQVPLLADMN--LAVAAQYGVALPD 118
AHPE_MYCTU   QLRDHLPEFENDDSAALAISVGPPPTHKIWATQSGFTFPLLSDFWPHGAVSQAYGVFNEQ 110
              :      :*      .:  * .: .      *: * : : * : .***:* :      * :   ***   :

DR_2242      RGISGRAVFLIDREGVVRYQHVEEQTGQYTVRPGAVLEQLRGL-- 151
Deide_02430  RGVSGRAVFLIDREGVVRFHEHVEAKPSEYTIRPEVVLKITEL-- 151
Dgeo_0122    RGISGRAVFLIDKGGVVRFEYVEAQTGDYTVRPELVLAQLAEL-- 151
DGo_CA2657   RGISGRAVFLIDKEGVIRYAHVEEKTSDYTVRPEQVLAQLRAL-- 151
Deima_0618   RGISGRAVFLIDKGGVVQFEHVEEKTGDYTVRPADVLDRAVTLR-- 152
Deipe_1016   RAISKRAVFLIDKDGVVRFEGVEPSTGDYSVRPEQVLEQIRTL-- 151
Deipr_0175   QGCARRAIFVVGPDGRVRWLHLEEDPTEVTLSAREVLAQLP---- 159
AHPE_MYCTU   AGIANRGTFVVDRSGLIRFAEMKQPGEVRDQR--LWTDALAALTA 153
              . : *. *:: . * ::: ::          :
```

(b) (continues on next page)

```
DR_1765      ----MPTT-----QPLSFLAVPTEDNAHEGVKK-LWSKAEANM--GFVVPN 39
Deide_13030  -----MNRI SWLEVPDEHSAPEGVRK-LWGKAEANL--GFVVPN 35
Dgeo_1446    MTTTQPEA-----KDRISLPVPDATQVPEGVRK-LWAKAEANI--GFVVPN 43
DGo_CA1027   --MTHNPD-----AAPISFLPLPTEDTAPEGVRK-LWNKAQANL--GFVVPN 41
Deima_0298   -----MPSLSFLVPVTEAEVTPEIAT-LWRKAHGAL--GFTPN 35
Deipe_3296   -----M-----NPEISRLRLPRREDLPQEARE-LMSAAEDKF--SFVVPN 36
Deipe_4199   -----M-----KQFASWISVIPYEEATGKLKI-LYDRIKGP--NEIDN 36
Deipe_3903   -----MPRISPINPETASPELQQTLYTVKSKMG--GKLPN 33
Deipe_3878   -----MARIDQVTPEQATGRAKQLLDAV-QNQR--GMTPN 32
Deipe_3900   --MS-KPY-----HLQ--LPQVTLENAEPEARE-VLERAKRQV--GRLPN 37
Deipr_2741   --MT-VPD-----SSKARRLSVHTVESAPEGSRAQLEAVQKRNG--GYLPN 41
Deide_1p00700 --MSRVTA-----PSRLPWMARLA-----SRALTWR----F--GKPPF 30
AHPD_MYCTU   --MSIEKLKAALPEYAKDIKLNLSITRSSVLDQ-----EQLWGTTLLASAAATRNPQ 50

DR_1765      VF-----RAQALNGEQFLAWWNY-F-----NLLVNKEG 66
Deide_13030  VF-----RAQALNGEQFLAWWNY-F-----NLLVNKEG 62
Dgeo_1446    VF-----RAQAVNGEQFLAWWNY-F-----NLLLNKEG 70
DGo_CA1027   VF-----RAQALNGEQFLAWWGY-F-----NLLLNKEG 68
Deima_0298   VF-----RAQALNPAQFWAWWKY-Y-----DLLMNKEG 62
Deipe_3296   VL-----RAWAVRPDHLVKWRAY-Y-----DLIMQGES 63
Deipe_4199   IM-----LTHSLRPHSMEGHMAL-Y-----K--NVLHHHGN 64
Deipe_3903   LV-----TTFAQSPAALNGYLG-F-----N--GVQSG 58
Deipe_3878   IL-----QVMALSPNVLDAYLKF-T-----G--A-LGQ 56
Deipe_3900   MY-----LLMANHPGLLETYLNG-Y-----D-HLRKSS 63
Deipr_2741   LL-----GVLSNSPTVLESYLT--S-KLNGKT 66
Deide_1p00700 TV-----ALLSHHPAYPVPLYFM-A-----GIYNGNST 57
AHPD_MYCTU   VLADIGAEATDHL SAAARHAALGAAAIMGMNNVFYRGRGFLEGRYDDL RPGLRMNI IANP 110
              :
```

DR_1765	GLSNAERELLAVVVSGLNRCVYCAVSHGAALREFSG---- <td>118</td>	118
Deide_13030	QLSNTDRELLAVVVSGLNRCVYCAVSHGAALREYSA----DPVLADTVAIN----WRHAN	114
Dgeo_1446	YLTNAERELVAVVVSGLNRCVYCAVSHGAALREFLG----DPQKADAVAVN----WRHAD	122
DGo_CA1027	FLTVAERELVAVVVSGLNRCVYCAVSHGAALREATG----DARTADGAAVN----WRQAA	120
Deima_0298	HLPLEREMVATVVSSLNRCVYCLVSHASAVRVLG----DVRADTLAID----YRQAD	114
Deipe_3296	SLTRTQREMIHAVVSSVNRCVYCTSTTHPAFLRLRLQREGDPPLAHVLSNPDPHALHDER	123
Deipe_4199	SLPKWLLEVTGVVVSLLNGCEYQVEHHHAGLTRLLRDDR----AHAIREALENQTPEQV	120
Deipe_3903	TLSPQLREQIALVVAQANGCDYCLAASHMLGKMRGLDDQNV---RQA-R-----QG-QA	107
Deipe_3878	TLSPRLREQIAVLVAQLNNGCYCLAHTAAAKRAGIDSESEL---QAN-Y-----QA-DS	105
Deipe_3900	RLNPVEQEVVFLTLRSRENSCEYCTSVHSFIADQMSKVPTFV---TDAIR-----DGRPI	114
Deipr_2741	SLTPDEREVVQLMAATTHGCSFCVAGHTTLTAQKTTKLSAED---IEALR-----GHKTL	117
Deide_1p00700	KLNPTTKALVSHLVAQLNGCAFCIDLGQVRVARDKGLDTSKLQW-VLAF-----RERPE	109
AHPD_MYCTU	GIPKANFELWSFAVSAINGCSHCLVAHEHTLRTVGVVDREAI---FEALK-----AAAI	160
	: : : * *	

DR_1765	LSEREQAMCAYAEKLTLRPAEMTEADLAPLRAAGLSDEAILEAVQVIAMFNMTNRVSSAL	178
Deide_13030	LGARERAMCAYAEKLTTRPEAMTQEDLTPLRQAGLSDPQILELVQVVGFMFNMTNRVSSAL	174
Dgeo_1446	LTEREQALAAAYAEKLTTRHPAEVTAADLEPLRAVGLDDHQIMELVQVIGMFNLTNRVSSAL	182
DGo_CA1027	LSPREQAMCAYAEKLTLRPAEMTEADLAPLRGEGLSDAQILELVQVVGFMFNLTNRVSSAL	180
Deima_0298	LTARQRAILDYAAHLTRHPDRASRDDLTPLRDAGLDDHAILELTQVVGFMFNATNRVSSAL	174
Deipe_3296	FTPLERALLSFALDLTLRSHQLGQAHVEALRTAGLSDEGIFDAAQTAAMFNFTNRLANAT	183
Deipe_4199	FEGKELAILRYARALTETPASLHRDSLADMRAGMDDGEILEVNQVVSFYFAYANRTVLGL	180
Deipe_3903	SDPKVQAALGFAQAIVEQGRVNTMDLQAIRDAGYNDEEIVEITVNVAYNLTNYLNNVA	167
Deipe_3878	GDAKTKAALQFARIVTLERQIREDDLRVLLAGYSEQEVLEIIAHVALSVFTNYISNTT	165
Deipe_3900	PDARLEALRTFVRVMHDTGRPRDQAAAQAFDAGYSEQHILDVILAIKVTISNYANHFV	174
Deipr_2741	QDSKLAALASYTSAVIANRGAVSDEELQAFDAGYDQAQALEVVGLGVLATICNFGNNVA	177
Deide_1p00700	YSPAERALEYAWEATQVTAKVSDETYAT-LSSFYSEREIIELTVAVATENFFNRLTGPL	168
AHPD_MYCTU	VSGVAQALATI-EAL--SPS-----	177
	*	

DR_1765	GFVPNPPEYHIQSR-----	191
Deide_13030	GFAPNAEYHAQARPDSQS-----	192
Dgeo_1446	GFVPNPPEYRQAR-----	195
DGo_CA1027	GFVPNAEYHVMGR-----	193
Deima_0298	GFQPNEEYFHLGRTGQ-----	190
Deipe_3296	GLLPNDEYHAMGR-----	196
Deipe_4199	GVTTQGDMLGLSPSDSDDPDNWSHG---	205
Deipe_3903	DTDIDFPHA-----PPLSSAAD--	184
Deipe_3878	KPDVEFPVP-----RPLAAS---	181
Deipe_3900	NTPLDEAFS-----SREWRGEPVT	193
Deipr_2741	QTTLNPELE-----PYRWDGLS--	194
Deide_1p00700	NIESQGFCALPDRQ----P-----	183
AHPD_MYCTU	-----	

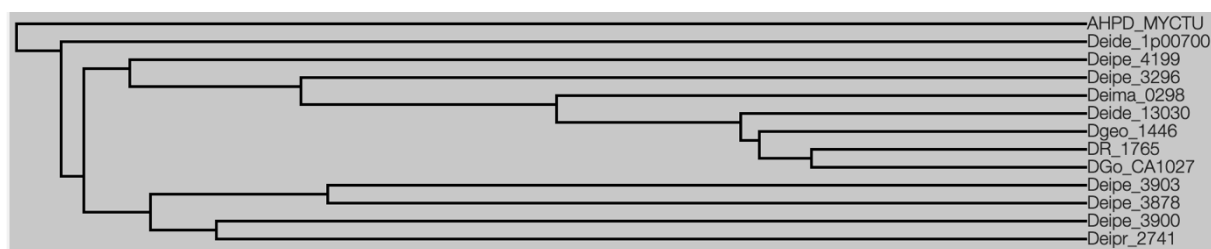
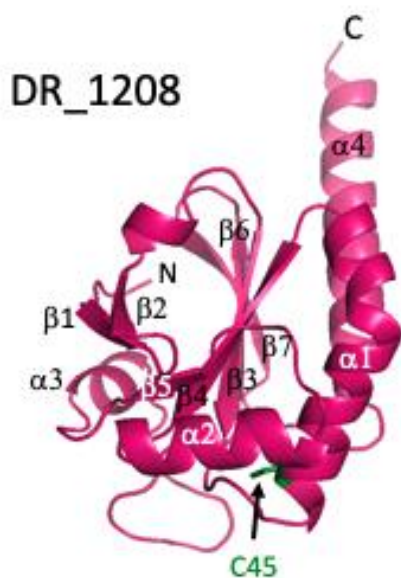
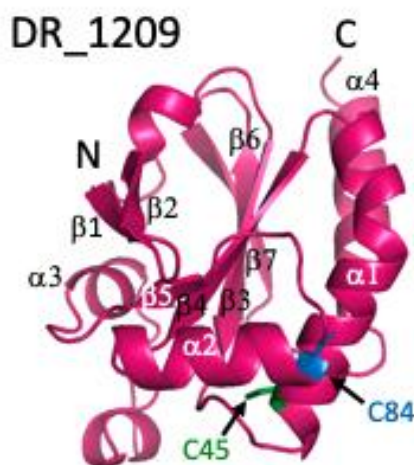
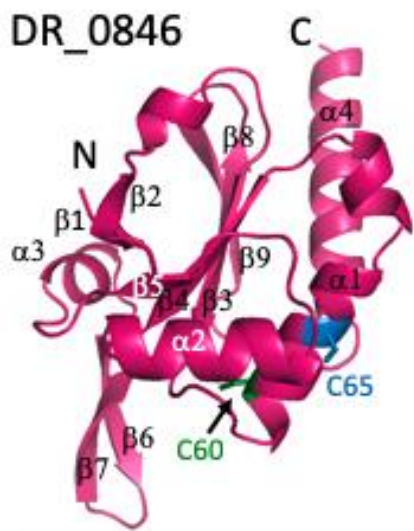


Figure S12. Multiple sequence alignment of *Deinococcus* AhpE and AhpD proteins. **(a)** Alignment of *Deinococcus* and *M. tuberculosis* AhpE sequences. AHPE_MYCTU, AhpE from *M. tuberculosis*. Peroxidatic cysteine (green) and other catalytic triad residues (grey) are highlighted. **(b)** Alignment of *Deinococcus*, and *M. tuberculosis* AhpD sequences. AHPD_MYCTU, AhpD from *M. tuberculosis*. Catalytic and resolving cysteines are highlighted in green and cyan, respectively. The residues highlighted in grey in AhpD sequences are involved in the catalytic mechanism. The guide tree showing sequence relationship between the various AhpD-like proteins is included. Alignments and tree were obtained with UniProt ClustalO.

Figure S13

(a) BCP



(b) OsmC/Ohr

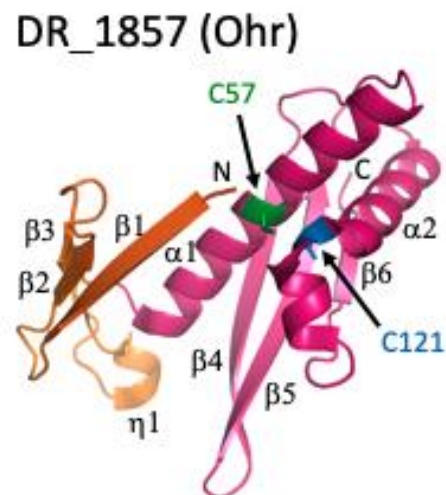
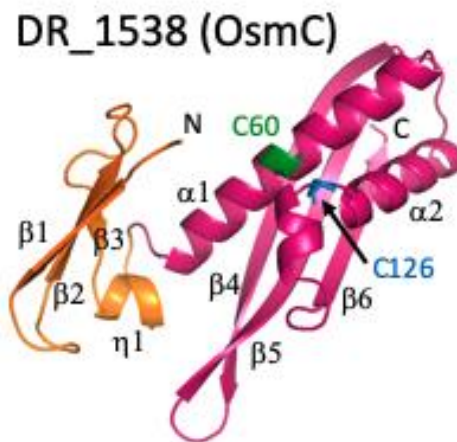


Figure S13. 3D models of BCPs and OsmC of *D. radiodurans*. **(a)** The three BCPs having a Trx-fold. **(b)** Model of OsmC and crystal structure of Ohr (PDB 1USP). Peroxidatic and resolving cysteine residues are shown in green and blue, respectively. The OsmC/Ohr monomer is composed of two distinct subdomains. The N-terminal domain (orange) consists of three β -strands folded into a β -sheet. In the C-terminal domain, helices $\alpha 1$ and $\alpha 2$ (the latter severely kinked) are stacked on a β -sheet formed by strands $\beta 4 - \beta 6$. The active OsmC and Ohr protein is formed by a homodimer [159]. Models and images were obtained as described in Figure S4.

Figure S14 (panels a to c)

(a)

```

DR_1538      MADIARKASAHWEGDLKSGNGTITTESGVLSQAQYSFKTRFEN--GKGTNP EELLASAHA 58
Deide_16090  MADISRKANAQWFGDLKSGNGTVSTESGALKDNSYSFKARFEQDKAPGTNP EELLAAAAHA 60
Dgeo_0526    MADIARKASAQWRGDLRSGQGTIRTESGVLKDAQYSFKTRFEN--GAGTNP EELLAAAAHA 58
DGo_CA1241   MADIARKANAQWMDLKS GKNISTESGTVKDAQYSFGTRFEN--GVGTNP EELLAAAAHA 58
Deima_0667   MANIHRKANAQWTGDLKSGSGTITTPSGVLQAAPYSFRTRFED--QPGTNP EELIAAAHA 58
Deipe_3743   MANIERKANAQWNGDLKSGNGTISL SGVLSDPYSFRTFEN--QPGTNP EELIAAAHA 58
OSMC_ECOLI   -MTIHKKGQAHWEGDIKRGKTVSTESGVLNQQPYGFNTRFEG--EKGTNP EELIGAAHA 57
              * :*.*.*: * **:: *.*.: : **.:. *. * :*** *****.:***

DR_1538      GFTMQLSALLAEHGHEIKALD TDATCEMVKDGP GFKINMHMLRVRAQLTGSDQADFEAH 118
Deide_16090  GFTMQLSAMLA AHGHQPEDLRTEATCEMVKDGP GFKVSTMRLTIRGKVGNI DQAEFEKH 120
Dgeo_0526    GFTMQLSALLA ADGHDPQDLRTEATCEMVREGQG FKV SAMRLVVRGRVGNIDQAEFERH 118
DGo_CA1241   GFTMQLSALLA AHGHDPQDVRTEATCEMVKDGP GFKVSTMRLQVRGKVGNI DQAEFEKH 118
Deima_0667   GFTMAFSNVLKTAGYEPRDLATEATLGMSMDG- GPKLT TMHLVVRGKADGLDQTQFQAL 117
Deipe_3743   ACFTMAFSNVLQQAGHAPRTLATDATLGMDASGGGFKIATMHLVVRGSAEGLDQQQFQQL 118
OSMC_ECOLI   ACFSMALSLMLGEAGFTPTS IDTTADVSLDKVDAGFAITKIALKSEVAVPGIDASTFDGI 117
              .**.* :* :* *. : * * : . * : : * . . * *:

DR_1538      VKDAAEK CPLSRIMQGNVEVTHEAILEG 146
Deide_16090  VAQAADACPLSRVMKGNVEITHEAVLE- 147
Dgeo_0526    VQQA AQMCPLSRVMQGNVEITHEAVLE- 145
DGo_CA1241   VAQAADMCPMSRVMKGNVEIVHEAVLE- 145
Deima_0667   AEQAEQGCPVSGALRGNLQITVEATLE- 144
Deipe_3743   AEKAEQGCPVSGALRGNLDITVEAIYEQ 146
OSMC_ECOLI   IQKAKAGCPVSQVLKAEITLDYQLKS-- 143
              . * **.* :.:.: : :

```

(b)

```

DR_1857      -----MANVYTAEATATGGRAGTTRSSDDR LNLDSVPAEMGG-DGGPGTNPEQLFAA 52
Dgeo_0446    MSGIMSAMSNLYTAEATATGGRGAVKSSDGR L DPLSSPRELGG-DGGPGTNPEQLFAA 59
DGo_CA0901   ---MPLMSNLYTAEAVATGGRAGKTRSTDGRMD L DLSVPA AIGG-DDGPGTNPEQLFAL 56
Deima_2331   -----MSNLYTAEATATGGRAGHARTSDGR L D VLSVPSEIGG-DGGTGTNPEQLFAA 52
Deipe_0225   -----MSNAIFHTQATAHGG RAGHIETPDHHL D V KLSVPGQLGG-KGGG GTNPEQLFAA 53
Deipr_0815   -----MANLYETT VKTQGAR GGTIQSEDGR L DLSVPKALGG-DDGQGTNPEQLFAA 52
DGo_CA1828   ----MTQNETLFETTSSAHGGRAGHVEG-EGGLN VRLAVPEAMGG-DGEGGSTPEGLFAA 54
Deipr_0816   -----MQKLYTATATAHGAPGQVATDDRRID L PLSLPTELGG-EGGDGTNPEQLLAA 52
Deima_0137   ----MTQELKPLFTATSLVTGGRSGDLQLGRDR TPLTLRPAR-----TRRAGTDPEELFAA 52
OHRA_BACSU   -----MSQPLFTATVSAVGGREGKVISSDRVLELDVAMPGT PRAKKLEKATNPEQLFAA 54
OHRB_BACSU   -----MALFTAKVTARGGRAGHITSDDGVLD FDI VMPNAKKE--GQTGTNPEQLFAA 50
              :: : . * . . : . : : ** *.*

DR_1857      GYAACFQ GAGLVVSRRQKIDVPADSTITARVGLQK--AGLAFALDVELEGHFPGLSREQA 110
Dgeo_0446    GYAACFQSALGVVARREKVELPEDSTVTARVGLQR--NGLAFALDVELEGHFPGLSSEQA 117
DGo_CA0901   GYAACFQ GAGLAVARRQKIEIPEGSTVTARVGLER--AGLAFALNVELVGSFPGLEREQA 114
Deima_2331   GYAACFQ GAGLVAARRQKVSA-DNSEVTAKVGLEK--EGLGFKLNVEIAVRLPGVERDVA 109
Deipe_0225   GYASCFQSAIGVIARQENIEF-GDSTVTALVGLLR--DEQGYGLDVELQITLPGLSREQA 110
Deipr_0815   GYGACFQGAMGLVARRQGIQLPEGSSITATVGMEK--DDVSFLLNAHLVGRFPGMDREQA 110
DGo_CA1828   ALAACFASAMGAVARAENYPEFGDMEVSATAGLSL--DGEAHTLHAALDIKLPGLSREQA 112
Deipr_0816   GYSSCFLAALGI VSKRREVSLSPDIQVQTRLELYE--NGDAYDFKVYLT VSGSDVDA AQL 110
Deima_0137   GYAACYLSALNEVADARRVRVSGAQAQ-LQVTLNV-TDAGEYILSV ALHVYLPDVAHDEA 110
OHRA_BACSU   GYAACFDSALQLVARTERVKVE--TEVTANVSL LKDEADQGYKLGVT LQVKGEGVSASEL 112
OHRB_BACSU   GYAACFGGALEHVAKEQNIEID--SEIEGQVSLMKDES DGGFKIGVT L VVNTKDL DREKA 108
              . . :*: .*: : . : : . : . : . :

DR_1857      EGLMHAHEVCPYSAATRNNVDVRLKVRE---- 139
Dgeo_0446    HALMHAHQVCPYSVALRDNVAVRLKVAG---- 146
DGo_CA0901   QALMDATYNVCPYSVATKGNVETTLTVA----- 142
Deima_2331   EKL VHAAHEVCPYSNATRGNI D VRLSVID---- 138
Deipe_0225   EDLVHKAHQVCPYSRITRGNL D VRLTVVES--- 140
Deipr_0815   QKLMEETLEVCPYSRATKGNMQTSVSVAD---- 139
DGo_CA1828   QHLVDGAKDICAYTRALKGNVDV D YRLHD---- 141
Deipr_0816   QPLLDET LKVCPI TRATQGA EIS---VSAG--- 137
Deima_0137   LDLMRAAHAVCPYSHAVRGNI E VTLVAADAPLS 143
OHRA_BACSU   EALVKKAHGVC PYSKATSGNI D VTL E VAE---- 141
OHRB_BACSU   QELVNAAHEFC PYSKATRGNV D V KLEL K---- 136
              *: : .* : .

```

(c)

```
DR_1177      MSTKKTLNVTWLGEQRYLGVSESGHQLLIDNSPV----KVGVSPEALLGALATCTAYDV 56
Deide_10790  --MKKTLNVTWLGEQRYLGVSESGHQLLIDNSPV----KVGVSPEALLGALATCTAYDV 54
Dgeo_1268    --MKKTLKVTWLGEQRYVGVSESGHQILIDNSSV----KIGVSPEALLGALATCTAYDI 54
DGo_CA1763   --MKKTLNVTWLGEQRYLGVSESGHQLLIDNSPV----KVGVSPEALLGALATCTAYDV 54
Deima_2343   --MKKRLTVHHLGDQRYVGFNETGQQLLIDNSDV----KVGVSPEALLGAVATCTAYDI 54
Deipe_0234   --MGTKMTMHYLGEQRYVGLNERGQQLLIDASPV----SVGVRPMEALLGALATCTAYDV 54
Deipr_0697   MANTKTVNIDWLGEQRYVGRSENGQQLLIDNSAN----KVGVSPEALLGALATCTAYDV 56
Deide_21170  --MQIEVQVRQISPATSQA-TARTHQVMIDRPLEKGGEDRGMMGGEQLLVSLGGCFISNL 57
Deipe_0648   --MQIQVQIHQVGVATAEG-VARTHHLIDRPLEKGGEDRGMMGGEYLLVALGGCFMSNL 57
YHFA_ECOLI   ----MQARVKWVEGLTFLGESASGHQILMDGNSG----DKAPSPMEMVLMAAGGCSAIDV 52
          :  :      .      : : : : *      . .      : : * : . *      : :

DR_1177      VEIMKKRRTPPLASYRIEVEGERADTDPKRYTRITVRHIAAGEGVTAEALSKAHLSHEKY 116
Deide_10790  VEIMKKRRTPPLSTYRIEVEGERADTDPKRYTTITVRHIASGEGITAEALEKAHLSHEKY 114
Dgeo_1268    VEIMKKRRTPPLTAYRIEVEGERADTDPKRYTTITVRHIASGEGLTEEALSKAHLSHEKY 114
DGo_CA1763   VEVMKKRRTPPLSAYRIEVEGERADTDPKRYTHITVRHIASGEGVTEEMLSKAHLSHEKY 114
Deima_2343   VEIMKKRKTPPLSTYRIEIEGDRAEEHPKRYTHIIVRHIAGGAGVTRDALEKAHLSHEKY 114
Deipe_0234   VGILAKRKTPPLSSYRIEVEGERAEHPKRYTTITVRHIAGGEGVLEALQKAVQLSHDKY 114
Deipr_0697   VGIMEKRKTPPLSSYRIEVEGERADTTPARYTRITVRHIAGGEGVTKEQLEKAHLSHEKY 116
Deide_21170  LAAIKAREADITDVQLTVTGTL-ESSPSRFSIAIEVVVD--AQAQDRALLEKLVEM-SDRA 113
Deipe_0648   LAAIRAREAEIHDVRLVETGTL-ASAPSRFTEIEVVVG--ARCADPALLEKLVEM-ADRA 113
YHFA_ECOLI   VSILQKGRQDVVDCEVKLTSEERREEAPRLFTHINLHFIVTGRDLKDAAVARAVIDLSAEKY 112
          :  :      .  :      . : : .      *  : : * :      .      : : . : : :

DR_1177      CSVAASLNSEIVVEAELAGEPAAS 140
Deide_10790  CSVAASLNSEIKLETQLE----- 132
Dgeo_1268    CSVAASLNSEIRLETRVE----- 132
DGo_CA1763   CSVAASLNSEISLETRVE----- 132
Deima_2343   CSAAASVNAEITLQVELVETA--- 135
Deipe_0234   CSVVASLNAEIHTDVQLEQAGVPV 138
Deipr_0697   CSVAASLNAEIVLDVRLAEGSEG- 139
Deide_21170  CIVSNTLRPAVALSFRLA----- 131
Deipe_0648   CICTNTLRPAVIPTFRISAIER-- 135
YHFA_ECOLI   CSVALMLEKAVNITHSYEVVAA-- 134
          *      : .      :
```

Figure S14. Multiple sequence alignment of *Deinococcus* OsmC, Ohr and YhfA proteins. **(a)** Alignment of *Deinococcus* and *E. coli* OsmC sequences. OSMC_ECOLI, OsmC from *E. coli*. **(b)** Alignment of *Deinococcus* and *B. subtilis* Ohr. OHRA_BACSU and OHRB_BACSU, OhrA and OhrB proteins, respectively, from *B. subtilis*. **(c)** Alignment of *Deinococcus* and *E. coli* YhfA sequences. YHFA_ECOLI, YhfA from *E. coli*. Peroxidatic and resolving cysteines are highlighted in green and cyan, respectively. The two residues highlighted in grey in Ohr and OsmC sequences are involved in the catalytic mechanism [154].

Figure S15

```

DR_2623      -----MSLYDVAIVGAGPVGLAAAICKRAGLSYVVLEKGCVVNAIFEYP 45
Deide_23360  -----MSGLVDAIIGAGPVGLAAAICKRAGLSYVVLEKGCVVNAIFEYP 46
Dgeo_2331    -----MSEMYDVAIVGAGPVGLAAAICKRAGLSYVVLEKGCVVNAIFEYP 46
DGo_CA0078   -----MSTLLDVAIVGAGPVGLAAAICKRAGLSYVVLEKGCVVNAIFEYP 46
Deima_0670   -----MFDVAIIGAGPVGLAAAICKRAGLSYVVLEKGCVVNAIFDYP 43
Deipe_2475   -----MMYDLAIVGGGFPVGLAAAIAAKRAGLSYTVLEKGCVVNAIFDYP 44
Deipr_1732   MTTEPNPGIPNPEPQGGLYDVAIVGGGFPVGLAAAICKRSGLSYVVLEKGCVVNAIFDYP 60
YPDA_BACSU   -----MIQEKAIIGGGFCGLSAAIHLKQIGIDALVIEKGNVNSIYNYP 45
BC_1495      -----MQKETVIIIGGGFCGLAAAISLQKVGINPLVIEKGNIVNAIYNYP 45
SACOL1520    -----MQKVESIIIGGGFCGLSAAIEQKRKGIDTLIIEKGNVVESIYNYP 45
              *:.*.* **:* ** : : * : : * : : * : : * : : *

DR_2623      TYMGFFTTAPELEIGNHPFVTGHDKPDRDALMYRLVTQRENINVRQYTTVNKVHAAPA 105
Deide_23360  TYMSFFTTAPELEIGNHPMVTGHDKPDRDALMYRLVTQREALNVEQYTEVTAVHAAPA 106
Dgeo_2331    TYMTFFTTSPRLEIGNHPFVTQREPRDRKEALHYRLVAEREALHIEQYTEVTAVHPAPA 106
DGo_CA0078   TYMGFFTTAPELEIGNHPMVTGHDKPDRDALMYRLVTQREELKVEQYTEVTKVHAAPA 106
Deima_0670   TYMSFFTTAPELEIGGHPMVTGHDKPDRDALMYRLVADREALNIEQYTEVTRVHAAPA 103
Deipe_2475   TYMTFFTTAPELEIGGHPMVSPREKPRKEALMYRLVAEREALDLQYQYTEVTNVHAAPA 104
Deipr_1732   TDMTFFTTAPELEIGGHPFVSPFDKPKRVDALQYRKYVQAEGLNVRQYTRVEKVHAAPA 120
YPDA_BACSU   THQTFSSSEKLEIGDVAFITENRKPVRIQALSYREVVRKKNIRVNAFEMVRKVTKTQN 105
BC_1495      THQTFSSSEKLEIGDVAFITENRKPVNRQALAYREVVRKKSVRVNAFERVEKVQKDGE 105
SACOL1520    THQTFSSSDKLSIGDVFFIVEESKPRNRQALVYREVVRKHQKLVNAFEEVLTVKKMNN 105
              * **::.*.*. : : : * : * * * * . : : : * *

DR_2623      GFTLEIEAQDGTGPVVEARRVVVATGYDNP LSMGIPGEDSENVSHYYTEAHFFMGLNVT 165
Deide_23360  GFTVQVEKRDGNSGVVEARRVVVATGYDNP MALGIPGEDSDNVSHYYTEAHFFMGLNVT 166
Dgeo_2331    GFTLAVNRKDGRLGLVEARRVIVATGYFDNPVLLGIPGEDSPNVSHYYTEAHFFWGLKVT 166
DGo_CA0078   GFTLEIERRDGTGPVVEARRVVVATGYDNP LGLGIPGEDSENVSHYYTEAHFFMGLNVT 166
Deima_0670   GFTVEAERRDGTPTFEARRVIVATGYDNP VQLGIPGEDAENVSHYYTEAHFFWKLNVT 163
Deipe_2475   GFTLEVNHKDGTPGVIARRVVVATGYDNP VMGIPGEERENVSHYYTEAHFFWNKLT 164
Deipr_1732   GFTLQVEAQDGRQDVVEARRVVVATGYDNP VPLDIPGEDSENVSHYYTEAHFFGLNVT 180
YPDA_BACSU   N----TFVITSKETYTTPYCIATGYDHPNMGVPGEDLPKFVHFYFKEGHPYFDKDVV 161
BC_1495      AFQVETTKRDGSKETIYAKYIVVATGYDNP NPMNVPGEELKKVAHYFKEGHPYFDRDVV 165
SACOL1520    KFT-----ITTKDVECRFLTATGYGQHTLEVEGADLPKFVHFYFKEAHPYFDQDVV 160
              :****. : : * : : * **.*.* : .

DR_2623      VIGAGNSAADAALDLWRSGVNVMTMVRAPELKSTIKYWVRPDLENRIKEGSIHAHFNSRV 225
Deide_23360  VIGAGNSAADAALDLWRGGANVTMVRAPELKPTIKYWVRPDLENRIKEGSTAHFNSQV 226
Dgeo_2331    VIGAGSSAADAALDLWRGGAHVTLVVRGAELKPTLKYWIRPDLENRIREGSIQAHFSSRV 226
DGo_CA0078   VIGAGNSAADAALDLWRGGAHVTLVVRGAELKPTIKYWVRPDLENRIKEGSIHAHFNSRV 226
Deima_0670   VIGAGNSAADAALDLWRGGANVTMVRAPELKSTIKYWVRPDLENRIREGSIQAHFNSRV 223
Deipe_2475   VIGAGNSAADAALDLWRGGAQVTMVRAPSVKNTVKYWVKPDLENRIKEGSTIAHFESRA 224
Deipr_1732   IIGAGNSAADAALDLMNAGANVTMVRGEGIRSTVKYWVKPNLENRIKEGRIGAHFRSQV 240
YPDA_BACSU   VIGGKNSSVDAALELVKSGARVTVLYRGNEYSPSIKPWILPEFEALVRNGTIRMEFGACV 221
BC_1495      VIGGKNSSVDAALELVKSGARVTVLYRGIEYSPSIKPWILPEFEALVRNGTIQMHFGAHV 225
SACOL1520    IIGGKNSAIDAALLEKAGANVTVLYRGDYSPSIKPWILPNFTALVNHEKIDMEFNANV 220
              :.*. : * : * : * : * : * : * : * : * : * : * : * : *

DR_2623      VEIHPEHVVVQGEDGRTFELPTDFTFALTGYRPDLSFLDGLNLATQPDE----CLVLTEN 281
Deide_23360  VEIHPLVVRVQRQDGTWDLPTHFTFALTGYRPDLSFLSGLGLAQHPDE----CLVLSDH 282
Dgeo_2331    TAILERDVVVEGPGQ-RWELPTDFTFALTGYRPQLSFLADLNLATQADQ----CLALSEH 281
DGo_CA0078   VEIHPEHVRVQREDGTTWELPTDFTFALTGYRPDLSFLAGLDLATQPDE----CLVLDEH 282
Deima_0670   TEIREDSVIVDGPDG-AWELPTHFTFALTGYRPDLSFLEGLGLAQHEDE----CLVLNEH 278
Deipe_2475   VEIGDDYVVVENQSGEKWLPTDFTFALTGYRPKLDLAGLGLAQHEDE----CLMLSdT 280
Deipr_1732   VEILPDVAVRQREDGTTFLPTHFTFAMTGYLPNLDLFLEGLDLRTLPE----CLVLSEH 296
YPDA_BACSU   EKITENEVVFERSGEKELITIKNDVFVAMTGYHPDHQFLEKIGVEIDKE--TGRPFFNEET 279
BC_1495      KEITEHTLTFTVD-GEALTIKNDVFVAMTGYHPDHSFLTKMGVQIDEE--TGRPPFYTEDR 282
SACOL1520    TQITEDVTVTEVN-GESKTIHNDYVFAMIGYHPDYEFLKSVGIQINTNEFGTAPMYNKET 279
              * . : : ...*: * * . * : : : : :

DR_2623      YESSVPGLFVVGSGAGFAGKTNQVFIENGRFHADHAVAEIERQLRSGELRPA----- 332
Deide_23360  YESSVPGLFVVGSGAGFAGKTNQVFIENGRFHADHAVAEIERQLRSGVLRQG----- 333
Dgeo_2331    YETSIPLGFVVGSGAGFAGRTNQVFIENGREHALLAVAEIERQLGALTEFFALPSPPR- 338
DGo_CA0078   YQSSVPGLFVVGSGAGFAGRTNQVFIENGRHHALLAVAEIEQQLGTRDLRPA----- 333
Deima_0670   FESSVPGLFVVGSGAGFAGRTNQVFIENGRHHAVVAEIEIVRQLASGTLAR----- 329
Deipe_2475   FESSVPGLFVVGSGAGFAGRTNQVFIENGREHALVALAEIARQLQAVRL----- 328
Deipr_1732   HESTVPGLFVVGSGAGYAGRTNQVFIENGRIHAEAVAEIARQLAQAEQATARSGEMA 354
YPDA_BACSU   METNVEGVFIAGVIAAGNNANEIFIENGRFHGGHIAEIAKRENH----- 324
BC_1495      METNAENIFIAGVIAAGNNANEIFIENGRFHGDAIAQTAISREK----- 326
SACOL1520    YETNIENCYIAGVIAAGNDANTIFIENGKFHGGIIAQSMLAKQTPLES----- 328
              :.. : :.* . . : * :***** : . : :

```

Figure S15. Multiple sequence alignment of *Deinococcus* bacillithiol reductases. Bdr homologs from *Deinococcus* are aligned with Bdr proteins YPDA_BACSU from *B. subtilis*, BC_1495 from *B. cereus*, and SACOL1520 from *S. aureus*. Cysteine residues are highlighted in yellow.

Figure S16

```
DR_1832      ----MTQGQDQVLSPLTTPDEV DQFLKDYPLAAVFK-AGTCHKTMQGFVLETFLLQ-RYE 54
Deide_14700  MTQATQAE NQQVLVPLTTPEEVDQFLTEYPLAAVFK-AGTCHKTMQGFVLETFLLQ-RHE 58
Dgeo_1464    MT-QNATQQEQVLVPLTTPDEVDRFLQAYPLAAIFK-AGTCHKTMQGFVLESFLQ-RHE 57
DGo_CA1021   MT-QTASQDPQVLVPLTTPEEVDQFLQDYPLAAVFK-AGTCHKTMQGFVLETFLLQ-NHE 57
Deima_1446   -----MSEQVLVPLTTPEEVDTFLEHPLAAVFK-AGTCHKTMQGFVLETFLLK-GHE 51
Deipe_3166   -----MTQLVPLTTPDEVETFLAQFPLAAIFK-AGTCHKTMQGFVLETYLLA-RHE 49
Deipr_0555   --MTQATQAEQVLLPLTTPEEVQTFLAEYPLAAVFK-AGTCHKTMQGFVLETFLLQ-RHE 56
YtxJ_BACCE   -----MNMTKLETIEELEVLVEKNEPYVLFKHSTTCPI SHGAYTEFQAYCSEERE 50
YTXJ_BACSU   -----MAKQLIQSEEEFKRIAEQEGVFVFLKHSTTCPI SQAAFHEFD AFANQHED 50
SACOL0804    -----MAIKLSSIDQFEQVIEENKYVFLKHSETCPI SANAYDQFNKFLY-ERD 48
              : : : : . . : * : * : : : : : : :

DR_1832      LPVGFIRVVDWRPASNHVAELTGLTHHSPQFILFKDQGAQYEVNNWDITPEALGPVFEQQ 114
Deide_14700  LPVGFIRVVDWRPASNHVAQRTGIVHHSPQFILFRDGEVQFEVNNWDITPEALRPVFD SQ 118
Dgeo_1464    LPVGFIRVVDWRPASNHVAELTGIVHHSPQFILFRNGQPLFEVNNWDITPEALAPVFEAQ 117
DGo_CA1021   LPVGFIRVVDWRPASNHVAQRTGITHQSPQFILFKQGE PQFEVNNWDITPEALSPVFESH 117
Deima_1446   LPVGFIRVVDWRPASNHVAERTGIVHHSPQFILFRE GQPVFDVDNWDITPGALTPVFDEF 111
Deipe_3166   LPVGFIRVVDWRPASNHVAERTGVRHHSPQFLLFKNGQSVFDVDNWDITPQALAPVFEAH 109
Deipr_0555   LPVGFIRVVDWRPASNFVAEMTGIIQHHS PQLIIFQEGQPRFEVNNWDITPEALAPVFEAL 116
YtxJ_BACCE   VPAYYLYVQDARDVSNRVAEQYSIRHES PQVLYIKDGMVVWNTSHWNIKKDALEENIK-- 108
YTXJ_BACSU   VPAYYLQVQEARPLSNFIAETYGVKHES PQIFIIQNGEVKWH TSHSQITEAAIEQHLS-- 108
SACOL0804    MDGYYLIVQQERDLSDYIAKKTNVKHES PQAFYFVNGEMVWNRDHGDINVSSLAQAE-- 106
              : : * : * * : : : : : * : : * : : : : :

DR_1832      VPQRSGAAQVDAGDSVEPYRQLMQAYLAGQLSDWAFQDQYVTMFRDDASLRSQREFELLS 174
Deide_14700  VPQRTGSAAIATDDNVEPYRRLMRDFVDGR LNEWAFQDQYVTMFRDDASLRSQREFELLS 178
Dgeo_1464    VPRRSTETAVATDDNVEPYRRLMAYLDGQLSDWAFQDQYVTLFRDDASLRSQREFEALS 177
DGo_CA1021   VPARSGEGAVATEDNAEPYRRLMHAFLD GQLSEWAFQDQYVTMFRDDASLRSQREFELLS 177
Deima_1446   VPARAEGQVRTQGNVEPYKRLMQDFLDGR LNEWAFQDQYVTMFRDDASLRSQAEFELLS 171
Deipe_3166   VPLRTDT-AEGISTNIEPYKQLMHQFLNDELNEWQFQEA YVNYFRDDANLRSQREFELLS 168
Deipr_0555   VPARAG-GNVETEGNIQPYLDLMDAYLGGQLNDFEFQDRWVPLFRDDASLRSQHEFELLS 175
YtxJ_BACCE   -----
YTXJ_BACSU   -----
SACOL0804    -----

DR_1832      RLFGDPDAYHGGLHQLGAPQDRGDLKARVQSVLDQLG----- 211
Deide_14700  RLFGDPDAYHGGLHQLGAPQDRGDLRARVQALLQEL----- 214
Dgeo_1464    RLFGDPDAYHGGLHQLGAPQARGDLKARVQALLNELSSRSLG-- 219
DGo_CA1021   RLFGDPDAYHGGLHQLGAPQERGDLKARVQTLNNDLG----- 214
Deima_1446   RLFGDPDAYHGGLHQLGAPAERGDLRGRVQELL AQL----- 207
Deipe_3166   RLFGDPDAYHGGLHQLGAPQSRGDLKTRVQELL AQL----- 204
Deipr_0555   RLFGDPDAYHGGLHQLGAPASRGDLRPRVEQLRTELLALRGQSA 219
YtxJ_BACCE   -----
YTXJ_BACSU   -----
SACOL0804    -----
```

Figure S16. Multiple sequence alignment of *Deinococcus* bacilliredoxins. The BrxC-type bacilliredoxins (also called AbxC for atypical BrxC) from *Deinococcus* are aligned with BrxC proteins YtxJ_BACCE from *B. cereus*, YTXJ_BACSU from *B. subtilis*, and SACOL0804 from *S. aureus*. Active site cysteine is highlighted in yellow.