

Table S8. Stress response-related proteins in <i>D. deserti</i>, <i>D. radiodurans</i> and <i>D. geothermalis</i>				
Gene name ^a	<i>D. deserti</i>	<i>D. radiodurans</i>	<i>D. geothermalis</i>	Protein description
General/heat				
<i>groL</i>	Deide_22590 (549 aa)	DR_0607 (548 aa)	Dgeo_2231 (545 aa)	Hsp10, molecular chaperone
<i>grpE</i>	Deide_21980 (216 aa)	DR_0128 (221aa)	Dgeo_2077 (218 aa)	Hsp20, molecular chaperone
<i>groS</i>	Deide_22580 (95 aa)	DR_0606 (120 aa)	Dgeo_2230 (95 aa)	Hsp60, molecular chaperone
<i>dnaK</i>	Deide_21970 (628 aa)	DR_0129 (628 aa)	Dgeo_2076 (629 aa)	Hsp70, molecular chaperone
<i>dnaJ</i>	Deide_22000 (306 aa)	DR_0126 (313 aa)	Dgeo_2078 (302 aa)	Hsp70, chaperone cofactor
	Deide_07590 (373 aa)	DR_1424 (420 aa)	Dgeo_0451 (371 aa)	
<i>ibpA/ibpB</i>	Deide_18090 (164 aa)	DR_1114 (182 aa)	Dgeo_0505 (158 aa)	Small heat shock protein
	Deide_11290 (136 aa)	DR_1691 (166 aa)	Dgeo_0859 (134 aa)	
	Deide_1p01285 (129 aa)			
<i>hslJ</i>	Deide_07610 (221 aa)	DR_2056 (147 aa)	-	Related to heat shock protein
		DR_1940 (403 aa)	-	
<i>htpG</i>	-	-	-	Hsp90, molecular chaperone
<i>dksA</i>	-	-	-	DnaK suppressor protein
<i>clpA/clpB/clpC</i>	Deide_08490 (739 aa)	DR_0588 (741 aa)	Dgeo_1475 (737 aa)	ATPase subunits of Clp protease
	Deide_12640 (852 aa)	DR_1046 (875 aa)	Dgeo_1210 (861 aa)	
	Deide_12680 (747 aa)	DR_1117 (747 aa)	Dgeo_1215 (745 aa)	
<i>clpX</i>	Deide_19580 (401 aa)	DR_1973 (403 aa)	Dgeo_2152 (406 aa)	ATPase subunit of Clp protease
<i>clpP</i>	Deide_19570 (184 aa)	DR_1972 (204 aa)	Dgeo_2151 (200 aa)	ATP-dependent protease with chaperone activity
<i>lon</i>	Deide_19590 (808 aa)	DR_1974 (813 aa)	Dgeo_2153 (813 aa)	ATP-dependent Lon Serine protease
	Deide_05670 (820aa)	DR_0349 (821 aa)	Dgeo_0427 (820 aa)	
BS <i>hslU (clpY)</i>	-	-	-	ATPase subunit of Clp photolytic system
BS <i>hslV (clpQ)</i>	-	-	-	ATP-dependent protease HslV
<i>sms (radA)</i>	Deide_12660 (449 aa)	DR_1105 (503 aa)	Dgeo_121 (449 aa)	ATP-dependent serine protease COG1066 / DNA repair protein
<i>htrA</i>	Deide_21350 (391 aa)	DR_0327 (364 aa)	Dgeo_2185 (384 aa)	Do serine protease, with PDZ domain
	Deide_01170 (389 aa)	DR_0745 (366 aa)	Dgeo_2025 (375 aa)	
	Deide_04820 (387 aa)	DR_1599 (470 aa)	Dgeo_1495 (373 aa)	
	Deide_1p01286 (378 aa)	DR_1756 (441 aa)	Dgeo_0676 (426 aa)	
	Deide_06250 (417aa)	DR_0984 frameshift	Dgeo_0552 (423 aa)	
	Deide_10420 (434 aa)	DR_0300 frameshift	Dgeo_0103 (367 aa)	
<i>prc</i>	Deide_21230 (445 aa)	DR_1308 (447 aa)	Dgeo_0277 (447 aa)	Tail-specific periplasmic serine protease
	Deide_12780 (418 aa)	DR_1491 (445 aa)	Dgeo_1216 (438 aa)	
	Deide_10700 (438 aa)	DR_1551 (447 aa)	Dgeo_1479 (449 aa)	
<i>yaeL</i>	Deide_13240 (376 aa)	DR_1507 (377 aa)	Dgeo_1043 (372 aa)	Membrane-associated Zn-dependent protease I

<i>ftsH</i>	Deide_23310 (626 aa) Deide_18550 (618 aa) Deide_01120 (622 aa)	DR_0583 (618 aa) DR_1020 (655 aa) DR_A0290 (655 aa)	Dgeo_2075 (621 aa) Dgeo_1832 (623 aa) Dgeo_2182 (621 aa)	ATP-dependent Zn protease
<i>htpX</i>	Deide_21060 (354 aa) Deide_11220 (228 aa)	DR_0194 (227 aa)	Dgeo_1282 (226 aa)	Predicted Zn-dependent proteases (possible chaperone)
<i>sugE</i>	Deide_20500 (106 aa)	DR_1004 (103 aa) DR_1005 (113 aa)	Dgeo_2170 (106 aa) Dgeo_1957 (112 aa) Dgeo_1956 (111 aa)	Small multidrug resistance membrane protein
<i>hit</i>	Deide_15190 (115 aa) Deide_12650 (137 aa)	DR_1621 (118 aa)	Dgeo_1329 (114 aa) Dgeo_2064 (164 aa)	Diadenosine tetraphosphate (Ap4A) hydrolase, HIT family, cell cycle regulation
<i>yebL</i>	Deide_07330 (299 aa) Deide_3p02720 (322 aa)	DR_2523 frameshift	Dgeo_0534 (293 aa)	Zn-binding (lipo)protein of the ABC type Zn transport system (surface adhesin A)
<i>hflX</i>	Deide_19040 (569 aa) Deide_18500 (307 aa)	DR_0139 (525 aa) DR_0646 (311 aa)	Dgeo_2006 (569 aa) Dgeo_1825 (309 aa)	GTPase, protease modulator
BS <i>ytxJ</i>	Deide_14700 (217 aa)	DR_1832 (211 aa)	Dgeo_1464 (219 aa)	Thioredoxin-like
<i>thiJ</i>	Deide_04910 (189 aa)	DR_1199 (190 aa) DR_0491 (261 aa)	Dgeo_0863 (188 aa)	Protease I, related to general stress protein 18, ThiJ superfamily protein
<i>uspA</i>	Deide_22300 (177 aa) Deide_08840 (164 aa) Deide_3p00273 (301 aa) Deide_1p01770 (230 aa)	DR_2363 (160 aa) DR_2132 (150 aa)	Dgeo_0155 (177 aa) Dgeo_1279 (158 aa) Dgeo_2742 (157 aa)	Universal stress protein, nucleotide-binding
Starvation				
<i>spoT</i>	Deide_14760 (760 aa)	DR_1838 (787 aa)	Dgeo_1308 (766 aa)	Guanosine polyphosphate (ppGpp) pyrophosphohydrolase/synthetase
<i>mazF</i>	- -	DR_0417 (117 aa) DR_0662 (115 aa)	Dgeo_1937 (110 aa)	ppGpp regulated growth inhibitor
<i>mazE</i>	-	DR_0416 (80 aa)	Dgeo_1936 (88 aa)	Regulatory protein, MazF antagonist
<i>ppx</i>	Deide_01820 (500 aa)	DR_A0185 (515 aa)	-	Phosphatase of ppGpp
<i>dps</i>	Deide_21200 (203 aa)	DR_2263 (207 aa) DR_B0092 (241 aa)	Dgeo_0281 (222 aa)	Starvation inducible DNA-binding protein
<i>cstA</i>	-	-	-	Carbon starvation-induced protein, membrane
Osmotic				
<i>mscL</i>	Deide_02220 (131 aa)	DR_2422 (128 aa)	Dgeo_0305 (131 aa)	Large conductance mechano-sensitive channel
<i>yggB</i>	Deide_18560 (417 aa) -	DR_1995 (426 aa) DR_0211 (368 aa)	Dgeo_1833 (394 aa)	Membrane protein
<i>kdpD</i>	-	DR_B0088 (365aa)	Dgeo_0389 (557aa) Dgeo_2852 (365 aa)	Osmosensitive K ⁺ channel histidine kinase sensor domain
<i>trkA</i>	Deide_03820 (219 aa)	DR_1666 (226 aa)	Dgeo_1584 (219 aa)	Potassium uptake system, NAD-binding component

<i>trkH/trkG</i>	Deide_03830 (425 aa) Deide_3p00460 (451 aa)	DR_1667 (458 aa) DR_1668 (512 aa)	Dgeo_1583 (458 aa)	Potassium uptake component
<i>proW</i>	Deide_00160 (239 aa) Deide_00180 (393 aa)	DR_A0138 (247 aa) DR_A0136 (484 aa)	Dgeo_0171 (249 aa) Dgeo_0173 (397 aa)	Proline/glycine betaine ABC-type transport, permease subunit
<i>proV</i>	Deide_00170 (308 aa)	DR_A0137 (309 aa)	Dgeo_0172 (310 aa)	Proline/glycine betaine ABC-type transport, ATPase subunit
<i>yehZ</i>	Deide_00190 (301 aa)	DR_A0135 (369 aa)	Dgeo_0174 (300 aa)	Proline/glycine betaine ABC-type transport, periplasmic subunit
<i>otsA</i>	Deide_21370 (457 aa)	-	Dgeo_0059 (457 aa)	Trehalose-6-phosphate synthase
<i>otsB</i>	Deide_21360 (239 aa)	-	Dgeo_0060 (238 aa)	Trehalose-6-phosphatase
	Deide_16570 (954 aa)	DR_0463 (978 aa)	Dgeo_0539 (944 aa)	Maltooligosyltrehalose synthase TreY
	Deide_2p01290 (597 aa)	DR_0464 (600 aa)	Dgeo_0540 (603 aa)	Maltooligosyltrehalose trehalohydrolase TreZ
	Deide_07350 (552 aa)	DR_2036 (552 aa)	Dgeo_0537 (556 aa)	Trehalose synthase-like TreS
<i>aqpZ</i>	Deide_1p01582 (245 aa) Deide_3p02450 (232 aa)	- -	Dgeo_0516 (259 aa) Dgeo_1799 (221 aa)	Major intrinsic protein (aquaporin Z and glycerol uptake facilitator)
<i>glpF</i>	Deide_2p00230 (276 aa)	DR_1929 (274 aa)	Dgeo_2523 (274 aa)	
Oxidative / detoxication				
<i>oxyR</i>	Deide_03130 (301 aa) Deide_16400 (318 aa) Deide_3p01240 (298 aa)	DR_0615 (317 aa) - -	Dgeo_1888 (297 aa) Dgeo_1692 (329 aa) Dgeo_2711 (292 aa) Dgeo_2840 (299 aa)	Transcriptional regulator, LysR family
<i>soxR</i>	Deide_2p01800 (285 aa) - Deide_3p02530 (131 aa) Deide_3p02771 (139 aa) Deide_04091 (157 aa)	DR_2448 (280 aa) DR_2519 (127 aa) - - -	Dgeo_1424 (279 aa) - - - -	Transcriptional regulator, MerR family
<i>katE</i>	- Deide_2p00330 (540 aa)	DR_A0259 (772 aa) DR_1998 (536 aa)	- Dgeo_2728 (543 aa)	Catalase
<i>katA S. pombe</i>	-	DR_A0146 (361 aa)	-	Catalase; Eukaryotic type
-	-	DR_A0145 (460 aa)	-	Fe dependent peroxidase
<i>katG</i>	-	-	-	Catalase (peroxidase)
-	-	-	-	Mn-containing catalase
<i>sodA</i>	Deide_07760 (207 aa)	DR_1279 (211 aa)	Dgeo_0830 (212 aa)	Superoxide dismutase Mn or Fe dependent
<i>sodC</i>	- Deide_1p00740 (468 aa) Deide_19880 (182 aa)	DR_1546 (182 aa) DR_A0202 (462 aa) -	- - -	Superoxide dismutase Cu/Zn dependent
<i>fur</i>	Deide_16041 (116 aa) Deide_19480 (133 aa) Deide_2p00340 (142 aa)	DR_0865 (132 aa) Upstr DR_2342	Dgeo_0519 (135 aa) Dgeo_2141 (137 aa) Dgeo_2727 (135 aa)	Ferric uptake regulation protein
<i>bcp</i>	Deide_10900 (164 aa)	DR_0846 (175 aa)	Upstr Dgeo_1265	Peroxisredoxin, bacterioferritin comigratory protein, antioxidant

	Deide_09051 (170 aa) - -	DR_1209 (159 aa) DR_1208 (163 aa) -	(167-178 aa) Dgeo_0990 (152 aa) - Dgeo_2729 (159 aa)	protein
<i>tlp-like</i>	Deide_08290 (192 aa) - Deide_2p00420 (174 aa)	DR_0189 (185 aa) DR_0345 (188 aa) -	Dgeo_1248 (192 aa) - -	Peroxiredoxin, disulfide reductase
<i>osmC</i>	Deide_16090 (147 aa)	DR_1538 (172 aa) DR_1857 (139 aa)	Dgeo_0526 (145 aa) Dgeo_0446 (146 aa)	Protein involved in alkylperoxide and oxidative stress response, osmotically induced protein
<i>yhfA</i>	Deide_10790 (132 aa)	DR_1177 (140 aa)	Dgeo_1268 (132 aa)	Protein involved in alkylperoxide and oxidative stress response, osmotically induced protein
<i>msrA</i>	Deide_10980 (195 aa)	DR_1849 (206 aa)	Dgeo_0843 (209 aa)	Peptide methionine sulfoxide reductase A
<i>msrB</i>	Deide_04050 (150 aa)	DR_1378 (157 aa)	Dgeo_2072 (152 aa)	Peptide methionine sulfoxide reductase B
<i>ahpC/ahpE-like</i>	Deide_02430 (151 aa)	DR_2242 (151 aa)	Dgeo_0122 (151 aa)	Thioredoxin reductase/alkyl hydroperoxide reductase
<i>ahpf/trxB</i>	Deide_05800 (325 aa) Deide_23360 (336 aa) Deide_12541 (356 aa) Deide_09090 (321 aa)	DR_1982 (325 aa) DR_2623 (332 aa) DR_0412 (324 aa) DR_B0033 (833 aa)	Dgeo_1576 (327 aa) Dgeo_2772 (321 aa) Dgeo_1013 (331 aa) Dgeo_2331 (338 aa) Dgeo_0975 (320 aa)	Thiol-alkyl hydroperoxide reductase
<i>grxA</i>	Deide_06390 (81 aa) -	DR_2085 (81 aa) DR_A0072 (91 aa)	Dgeo_1508 (81 aa) Dgeo_2583 (84 aa)	Glutaredoxin
<i>nrdH</i>	Deide_13741 (92 aa)	DR_0057 (84 aa)	Dgeo_0729 (87 aa)	
<i>trx</i>	Deide_01140 (138 aa) Deide_18600 (121 aa)	DR_A0164 (142 aa) DR_0944 (141 aa)	Dgeo_2518 (141 aa) Dgeo_1837 (110 aa)	Thioredoxin
<i>btuE</i> /BS <i>bsaA</i>	-	-	-	Glutathione peroxidase
BS <i>cyp</i>	Deide_22920 (408 aa) Deide_01550 (421 aa) Deide_08170 (405 aa)	DR_2538 (409 aa) DR_2473 (381 aa) DR_1723 (445 aa) DR_C0001 (103 aa) DR_A0186 (fr.shift)	Dgeo_0143 (407 aa) Dgeo_0944 (405 aa)	Cytochrome P450
BS <i>yceH</i>	Deide_05270 (405 aa)	DR_1127 (416 aa)	Dgeo_0931 (406 aa)	Toxic anion resistance protein, possibly tellurite resistance
Desiccation				
-	Deide_09710 (166 aa)	DR_1372 (164 aa)	Dgeo_1551 (166 aa)	Desiccation-related protein, LEA 14 family
-	Deide_07540 (320 aa) Deide_08080 (312 aa)	DR_B0118 (337 aa)	Dgeo_0097 (311 aa) Dgeo_1323 (307 aa)	Desiccation-related protein
-	Deide_08510 (200 aa)	DR_1172 (298 aa) DR_0105 (163 aa)	Dgeo_1473 (236 aa)	LEA76 family desiccation resistance protein

Other				
<i>hupA</i>	Deide_2p01940 (125 aa)	DR_A0065 (122 aa)	Dgeo_2501 (149 aa)	Histone-like nucleoid DNA-binding protein
	Deide_00200 (115 aa)		Dgeo_0175 (116 aa)	
	Deide_3p00060 (121 aa)			
	Deide_3p00832 (166 aa)			
<i>pspA</i>	Deide_09450 (226 aa)	DR_1473 (223 aa)	Dgeo_0996 (227 aa)	Phage shock protein A, controls membrane integrity
BS_ylou/ BS_yqhY	Deide_12280 (116 aa)	DR_2068 (135 aa)	Dgeo_0697 (152 aa)	Alkaline shock protein, function unknown
	Deide_17570 (110 aa)	DR_0389 (110 aa)	Dgeo_1721 (110 aa)	
<i>cps</i>	Deide_3p00840 (87 aa)	DR_0907 (86 aa)	Dgeo_0638 (87 aa)	Cold shock protein, OB fold nucleic acid binding protein
	Deide_2p00490 (87 aa)		Dgeo_1006 (89 aa)	
	Deide_09930 (94 aa)			
<i>arsC</i>	Deide_3p02440 (153 aa)	DR_A0123 (180 aa)	Dgeo_0756 (153 aa)	Arsenate oxidoreductase (ArsC-like Rodanese protein)
	Deide_18400 (118 aa)	DR_0136 (127 aa)	Dgeo_0403 (118 aa)	
			Dgeo_2548 (153 aa)	
			Dgeo_2768 (153 aa)	
			Dgeo_2770 (143 aa)	

^aThe gene names are from *E. coli*, whenever an *E. coli* ortholog exists, or from *B. subtilis* (with the prefix BS_). Proteins in grey were identified in the proteome analysis after standard cultivation.