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Comparative thermophysiology of marine *Synechococcus* CRD1 strains isolated from different thermal niches in iron-depleted areas

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- 23 adaptation
- 24

25 Abstract

26 Marine Synechococcus cyanobacteria are ubiquitous in the ocean, a feature likely related to their 27 extensive genetic diversity. Amongst the major lineages, clades I and IV preferentially thrive in 28 temperate and cold, nutrient-rich waters, whilst clades II and III prefer warm, nitrogen or phosphorus-29 depleted waters. The existence of such cold (I/IV) and warm (II/III) thermotypes is corroborated by 30 physiological characterization of representative strains. A fifth clade, CRD1, was recently shown to 31 dominate the Synechococcus community in iron-depleted areas of the world ocean and to encompass 32 three distinct ecologically significant taxonomic units (ESTUs CRD1A-C) occupying different thermal 33 niches, suggesting that distinct thermotypes could also occur within this clade.

34 Here, using comparative thermophysiology of strains representative of these three CRD1 ESTUs we 35 show that the CRD1A strain MITS9220 is a warm thermotype, the CRD1B strain BIOS-U3-1 a cold 36 temperate thermotype, and the CRD1C strain BIOS-E4-1 a warm temperate stenotherm. Curiously, the 37 CRD1B thermotype lacks traits and/or genomic features typical of cold thermotypes. In contrast, we 38 found specific physiological traits of the CRD1 strains compared to their clade I, II, III and IV 39 counterparts, including a lower growth rate and photosystem II maximal quantum yield at most 40 temperatures and a higher turnover rate of the D1 protein. Together, our data suggests that the CRD1 41 clade prioritizes adaptation to low-iron conditions over temperature adaptation, even though the 42 occurrence of several CRD1 thermotypes likely explains why the CRD1 clade as a whole occupies 43 most iron-limited waters.

44

45 INTRODUCTION

46 Marine picocyanobacteria contribute to the biogeochemical cycling of various elements, most notably 47 carbon, contributing ~25% of ocean net primary productivity, of which the Synechococcus genus alone 48 is responsible for about 16% (Flombaum et al., 2013). The large geographic distribution of these 49 organisms, extending from the equator to subpolar waters, is largely attributable to their extensive 50 genetic and functional diversity (Zwirglmaier et al., 2008; Farrant et al., 2016; Doré et al., 2020). 51 Amongst the nearly 20 clades within subcluster (SC) 5.1, the most abundant and diversified 52 Synechococcus lineage in oceanic ecosystems (Dufresne et al., 2008; Scanlan et al., 2009; Ahlgren and 53 Rocap, 2012), only four (clades I, II, III and IV) were thought to largely dominate in situ. Clades I and 54 IV mainly thrive in temperate and cold, nutrient-rich waters, while clades II and III reside in warm, 55 oligotrophic or mesotrophic areas (Zwirglmaier et al., 2008; Mella-Flores et al., 2011), suggesting the 56 existence of cold (I/IV) and warm (II/III) Synechococcus 'thermotypes'. This hypothesis was 57 subsequently confirmed by work demonstrating that strains representative of these different clades 58 exhibit distinct thermal preferenda (Mackey et al., 2013; Pittera et al., 2014; Breton et al., 2020; Six et 59 al., 2021), a feature notably linked to differences in the thermostability of light-harvesting complexes 60 (Pittera et al., 2017), lipid desaturase gene content (Pittera et al., 2018) and the ability of some strains 61 to induce photoprotective light dissipation at colder temperatures using the orange carotenoid protein 62 (OCP; Six et al., 2021). Field studies using global ocean datasets have allowed to refine the respective 63 ecological niches of the different thermotypes, with clade I extending further north than clade IV 64 (Paulsen et al., 2016; Doré et al., 2022) and clades II and III predominating in N- and P-depleted waters, 65 respectively, but also to highlight the importance of a fifth clade within SC 5.1, the CRD1 clade 66 (Farrant et al., 2016; Sohm et al., 2016; Kent et al., 2019). Initially thought to be limited to the Costa 67 Rica dome area (Saito et al., 2005; Gutiérrez-Rodríguez et al., 2014), the latter clade was recently found 68 to be a major component of Synechococcus communities in Fe-depleted areas (Farrant et al., 2016; 69 Sohm et al., 2016; Ahlgren et al., 2020). Furthermore, analysis of the global distribution of these 70 organisms using high-resolution marker genes has highlighted large within-clade microdiversity 71 associated with niche differentiation in marine Synechococcus (Farrant et al., 2016; Larkin and Martiny, 2017; Xia et al., 2019), as also observed in Prochlorococcus (Kashtan et al., 2014; Larkin et 72 73 al., 2016). Using the *petB* gene encoding cytochrome b_6 , Farrant et al. (2016) showed that most major 74 clades encompassed several Ecologically Significant Taxonomic Units (ESTUs), i.e. genetically 75 related subgroups within clades occupying distinct oceanic niches. This is notably the case for ESTU 76 IIB that occupies a cold thermal niche in sharp contrast with IIA, the dominant ESTU within clade II 77 that occupies warm, mesotrophic, and oligotrophic iron (Fe)-replete waters. Similarly, three distinct 78 ESTUs with distinct thermal niches were identified within the CRD1 clade and the co-occurring clade 79 EnvB (a.k.a. CRD2; Ahlgren et al., 2020): i) CRD1B/EnvBB are found in cold mixed waters in co-80 occurrence with ESTUs IA, IVA and IVC, ii) CRD1C/EnvBC dominate in warm, high-nutrient low-81 chlorophyll (HNLC) regions such as the central Pacific Ocean, and iii) CRD1A/EnvBA are present in 82 both environments and thus span a much wider range of temperatures than CRD1B and C (Farrant et 83 al., 2016). This suggests that these three CRD1 ESTUs could correspond to different thermotypes.

In order to test this hypothesis, we used strains representative of each of the three CRD1 ESTUs to determine the fundamental thermal niches of these organisms as compared to typical cold (clades I and IV) and warm (clades II and III) thermotypes. Furthermore, given the strong influence of temperature 87 on optimal functioning of the photosynthetic apparatus in marine *Synechococcus* (Pittera et al., 2014, 88 2017; Guyet et al., 2020), we also examined the effect of temperature acclimation on the 89 photophysiology of CRD1 ESTUs compared to their clade I and IV counterparts and show that CRD1 90 thermotypes actually differ more strongly in this respect to members of clades I-IV than from each 91 other.

92 MATERIALS AND METHODS

93 Strains and growth conditions

94 The eight Synechococcus spp. strains used in this study were retrieved from the Roscoff Culture 95 Collection (RCC; https://roscoff-culture-collection.org/), including representative strains of the three 96 known CRD1 ESTUs (CRD1A - C) and one or two of each of the four dominant clades in the field 97 (clades I – IV) used as controls (Table 1 and Supplementary Fig. 1). Cells were grown in 50 mL flasks 98 (Sarstedt, Germany) in PCR-S11 culture medium (Rippka et al., 2000) supplemented with 1 mM 99 sodium nitrate. Cultures were acclimated for at least two weeks in temperature-controlled chambers 100 across a range of temperatures dependent on the thermal tolerance of each strain and under a continuous light of 75 µmol photons m⁻² s⁻¹ (hereafter $\mu E m^{-2} s^{-1}$) provided by a white-blue-green LED system 101 (Alpheus, France). For each experiment cultures were grown in triplicate, inoculated at an initial cell 102 103 density of $\sim 3 \times 10^6$ cells mL⁻¹, and samples harvested daily to measure growth rate and fluorescence 104 parameters as described below.

105 In order to compare the capacity of strains to repair the D1 subunit of photosystem II (PSII; see 106 'Measurement of PSII repair rate' section), cultures grown in 250 ml flasks at 75 µE m⁻² s⁻¹ were acclimated at 18, 22 and 25°C, temperatures at which all strains were able to grow, were subjected to 107 108 high light stress (375 μ E m⁻² s⁻¹). Exponentially growing cultures were sampled at T0 and after 15, 30, 109 60, and 90 min of stress, before shifting cultures back to the initial light conditions and then sampling 110 again after 15, 30, 60 min and 24h of recovery (R). While D1 repair measurements were performed at 111 all time points, cell concentrations were measured by flow cytometry only at T0, T30min, T90min, 112 R30min and R24h and liposoluble pigment content was determined only at T0.

113 Flow cytometry

Culture aliquots (200 µl) sampled for flow cytometry were fixed using 0.25% (v/v) glutaraldehyde (grade II, Sigma Aldrich, USA) and stored at -80°C until analysis (Marie et al., 1999). Cell concentrations were estimated using a Guava easyCyte flow cytometer (Luminex Corporation, USA)

117 and maximum growth rates (μ_{max}) were calculated as the slope of the linear regression of ln(cell

- 118 density) vs. time during the exponential growth phase. Synechococcus cells were identified based on
- their red (695 nm) and orange (583 nm) fluorescence, proxies for their chlorophyll *a* and phycoerythrin
- 120 content, respectively. Fluorescence, forward scatter and side scatter values were normalized to that of
- 121 standard 0.95 µm beads using Guavasoft software (Luminex Corporation, USA).

122 Fluorescence measurements

123 The maximum PSII quantum yield (F_v/F_M) was estimated using a Pulse Amplitude Modulation 124 fluorimeter (Phyto-PAM II, Walz, Germany) during the exponential growth phase after 10 min dark 125 acclimation followed by addition of 100 μ M of the PSII blocker 3-(3,4-dichlorophenyl)-1,1-126 dimethylurea (DCMU, Sigma-Aldrich, USA; Campbell et al., 1998).

127 The PSII quantum yield was calculated as:

128
$$F_V/F_M = (F_M - F_0)/F_M$$

129 where F_0 is basal fluorescence, F_M maximal fluorescence level and F_V variable fluorescence (Campbell 130 et al., 1998; Six et al., 2007).

Fluorescence excitation (with emission set at 580 nm) and emission (with excitation set at 530 nm) spectra were generated using a LS-50B spectrofluorometer (Perkin-Elmer, USA) as described in Six et al. (2004). The fluorescence excitation ratio (Exc_{495:550nm}) was used as a proxy for the PUB:PEB ratio. Phycobilisome (PBS) rod length and the degree of coupling of the PBS to PSII reaction center chlorophylls was then assessed using fluorescence emission spectra by calculating the phycoerythrin (PE, $F_{max} = 565-575$ nm) to phycocyanin (PC, $F_{max} = 645-655$ nm) ratio as well as the PC to PBS terminal acceptor (TA; $F_{max} = 680$ nm) ratio, respectively (Pittera et al., 2017).

138 **Pigment analyses**

- 139 Triplicate cultures were harvested during the exponential phase when F_v/F_M was maximum for each
- 140 temperature condition. Cultures (50 mL) were subjected to centrifugation in the presence of 0.01%
- 141 (v/v) pluronic acid (Sigma-Aldrich, Germany) at 4°C, 14,000 x g for 7 min, using an Eppendorf 5804R
- 142 (Eppendorf, France). Pellets were resuspended and transferred to 1.5 ml Eppendorf tubes and
- 143 centrifuged at 4°C, 17,000 x g for 2 min using an Eppendorf 5417R centrifuge (Eppendorf, France).
- 144 Once the supernatant was removed samples were stored at -80 °C until further analysis. Pigment

- 145 content was subsequently assessed using calibrated high-performance liquid chromatography (HPLC
- 146 1100 Series System, Hewlett Packard, St Palo Alto, CA), as previously described (Six et al., 2005).

147 Measurement of the photosystem II repair rate

Each culture acclimated to 75 µE m⁻² s⁻¹ and 18, 22 or 25 °C was split into two new 50 mL flasks 148 149 (Sarstedt Germany) with one used as a control and the other flask supplemented with lincomycin (0.5 150 mg mL⁻¹ final concentration, Sigma-Aldrich, USA) in order to inhibit protein synthesis and thus D1 151 repair (Guyet et al., 2020). Both sub-cultures were then subjected to light stress by exposing cultures 152 to 375 μ E m⁻² s⁻¹ continuous light (at the same temperature), and F_V/F_M measured at different time points as described above. The PSII repair rate for each strain at each temperature was determined from 153 154 the coefficient differences between the exponential curves fitted over the 90 min time course of F_V/F_M 155 measurements for control and +lincomycin samples. This light stress experiment was replicated on

156 four independent cultures.

157 Determination of the realized environmental niches of major Synechococcus ESTUs

158 The realized niches of CRD1 and clades I-IV ESTUs were determined using *petB* reads extracted from 159 metagenomic data from the Tara Oceans and Tara Polar circle expeditions, the Ocean Sampling Day 160 (OSD; June 21st 2014) campaign, and *petB* metabarcodes from i) various oceanographic cruises (CEFAS, BOUM, Micropolar, RRS Discovery cruise 368 and several in the northwestern Pacific 161 162 Ocean as detailed in Xia et al., 2017), ii) two individual sampling sites in the Mediterranean Sea 163 (Boussole, Point B) as well as iii) a bi-monthly sampling at the long-term observatory site SOMLIT 164 ("Service d'Observation en Milieu Littoral")-Astan located 2.8 miles off Roscoff between July 2009 165 and December 2011 (Supplementary Table 1).

petB metagenomic recruitment using the *Tara* Oceans and OSD datasets was performed as described previously (Farrant et al., 2016). *Synechococcus petB* sequences from both metagenomes and metabarcodes were used to define operational taxonomic units (OTUs) at 97% identity using Mothur v1.34.4 (Schloss et al., 2009) that were then taxonomically assigned using a *petB* reference database (Farrant et al., 2016). OTUs encompassing more than 3% of the total *Synechococcus* reads for a given sample were grouped into ESTUs and used to determine the whole temperature range occupied by each of the five major *Synechococcus* ESTUs.

173

174 Comparative genomics

175 The Cyanorak v2.1 information system (http://www.sb-roscoff.fr/cyanorak/; Garczarek et al., 2021)

176 was used to compare the phyletic pattern i.e., the presence/absence pattern of each cluster of likely

177 orthologous genes (CLOG) in each strain, for CRD1 strains and their clades I-IV counterparts for a

178 number of selected genes potentially involved in adaptation to low temperature based on previous

- 179 literature (see results).
- 180

181 **RESULTS**

182 The fundamental thermal niches of CRD1 vs. clades I to IV strains

183 In order to determine the temperature optima and boundary limits of the different CRD1 strains and to 184 compare them to those of typical cold and warm Synechococcus thermotypes, representative strains of 185 each of the three CRD1 ESTUs and strains of clades I, II, III and IV were grown over a range of 186 temperatures from 6 to 36°C. The growth responses of all strains to temperature followed a typical 187 asymmetric bell-shaped curve over the selected temperature range (Fig. 1), with a progressive rise in 188 growth rate (μ) until T_{opt} (the temperature associated with maximum μ : μ_{max}) was reached, and a sharp 189 decline above T_{opt}. BIOS-U3-1 (CRD1-B) was able to grow between 12 and 29°C with a T_{opt} at 25°C 190 $(\mu_{max} = 0.78 \pm 0.02 \text{ d}^{-1})$, a growth pattern most similar to that of the clade IV strain BL107, while the 191 clade I strain MVIR-18-1 was able to grow at much lower temperatures, down to 8°C but could not 192 grow above 25°C (Fig. 1A). MITS9220 (CRD1-A) and BIOS-E4-1 (CRD1-C) displayed thermal 193 growth characteristics more similar to the clade II (A15-62 and M16.1) and III (WH8102) strains, 194 representatives of warm thermotypes (Fig. 1B). While most strains in this category displayed a minimal 195 growth temperature of 16°C, large variations between strains were observed at the highest thermal 196 boundary limit (T_{max}). Maximum growth temperature was obtained for M16.1 (II; T_{max} : 34°C), then 197 A15-62 (II) and WH8102 (III; both with T_{max} at 32°C), MITS9220 (CRD1-A; T_{max} : 31°C) and finally 198 for BIOS-E4-1 (CRD1-C; T_{max}: 30°C). The latter strain also displayed the highest minimal growth 199 temperature (T_{min} : 18°C) and thus possesses the narrowest temperature range for growth of all the 200 strains studied (12°C vs. 15-18°C). It is also worth noting that CRD1 strains display a lower maximum 201 growth rate and more generally lower growth rates at most temperatures than their clade I, II, III and 202 IV counterparts.

203

204 The environmental realized niches of CRD1 vs. clades I to IV strains

205 We then compared the fundamental thermal niches of all studied strains, i.e. the whole temperature 206 range over which they can grow in a laboratory setting in the absence of biotic interactions (e.g. 207 competition or predation), with environmental realized niches (sensu Pearman et al., 2008) of the 208 corresponding ESTUs. For this, we determined the distribution limits of each of these ESTUs along 209 the Tara Oceans and Tara Polar circle transects, 203 samples from OSD2014 and additional 210 oceanographic cruises and individual sampling sites, altogether encompassing 413 samples worldwide 211 covering a wide range of temperature conditions (Fig. 1, Supplementary Fig. 2, Supplementary Table 212 1). This made it possible to have much finer estimates of the limits of the thermal niches of the different 213 ESTUs than in the study performed by Farrant et al. (2016), in particular for the cold adapted ESTUs, 214 which were poorly represented in the initial Tara Oceans dataset (Supplementary Fig. 2).

This analysis showed that the CRD1B ESTU displayed a reduced thermal tolerance range in the environment (14 to 24.5°C) compared to the BIOS-U3-1 strain in culture (12 to 29°C), while the typical cold thermotypes colonized larger thermal niches *in situ* than their representative strains (Fig. 1A). Environmental realized niches indeed ranged from 2.5 to 24°C for ESTU IA (compared to 8 to 25°C for MVIR-18-1) and from 8.5 to 25°C for ESTU IVA (compared to 12 to 29°C for BL107). Interestingly, the median temperature of the CRD1B ESTU is 3°C higher than that observed for ESTUs IA and IVA.

222 As concerns warm thermotypes, CRD1C displayed a fairly narrow thermal tolerance range in situ 223 (22 to 29.5°C), which, similar to the cold thermotype CRD1B, was even narrower than for its 224 representative strain BIOS-E4-1 (18 to 30°C; Fig. 1B). Comparatively, the CRD1A ESTU was detected 225 across a wider temperature range (14 to 30.5°C) than the other two CRD1 ESTUs and also slightly 226 larger than the corresponding strain in culture (MITS9220, 16 to 31°C). Still, the most extended 227 temperature range was observed for ESTU IIA and IIIA (12 to 32°C) that reached significantly lower 228 temperature limits than the corresponding clade II (16 to 32-34°C) and III (16 to 32°C) strains. Of note, 229 although both IIA and IIIA ESTUs displayed a similar temperature range, the median temperature of 230 ESTU IIA (25°C) was about 3°C higher than that of ESTU IIIA (22°C) and the maximum median 231 temperature was surprisingly observed for the CRD1C ESTU (26.5°C). In this context, it is also worth 232 mentioning that although clade II strains are clearly both warm thermotypes, M16.1 displays a

significantly higher temperature limit for growth than A15-62 and more generally than all other strains.

234 This suggests that ESTU IIA may encompass two distinct ESTUs, but such a high temperature niche

(>32 °C) where they could be discriminated is exceptional and not available in our dataset
(Supplementary Table 1).

237 Comparative genomics

238 In order to assess whether the cold, temperate thermotype BIOS-U3-1 (CRD1B) exhibits similar 239 adaptation mechanisms to those previously described for the cold-adapted clades I and/or IV, we 240 examined a number of clusters of likely orthologous genes (CLOGs) from all Synechococcus genomes 241 belonging to clades I-IV and CRD1 present in the Cyanorak v2.1 information system (Garczarek et al., 242 2021). First, we looked for the occurrence of two amino-acid substitutions in phycocyanin α - (RpcA) 243 and β -subunits (RpcB), which were shown to differ between cold- (Gly in clades I and IV for RpcA43; 244 Ser in RpcB42) and warm-thermotypes (Ala in clades II and III for RpcA43; Asp in RpcB42), these 245 substitutions being potentially responsible for the differential thermotolerance of this phycobiliprotein 246 between thermotypes (Pittera et al., 2017). In all three CRD1 strains, both sites displayed the warm-247 type residue (Supplementary Fig. 3A-B), suggesting that in contrast to typical cold and warm 248 thermotypes, the molecular flexibility of this phycobiliprotein does not differ between CRD1 249 thermotypes. We then looked at fatty acid desaturases that are essential for regulating membrane 250 fluidity and thus the activity of integral membrane proteins, including photosynthetic complexes 251 (Mikami and Murata, 2003; Pittera et al., 2018; Breton et al., 2020). All three CRD1 strains surprisingly 252 possess in addition to the core $\Delta 9$ -desaturase gene desC3, a second $\Delta 9$ -desaturase, desC4 253 (Supplementary Table 2), previously thought to be specific to cold-adapted strains as well as the $\Delta 12$ -254 desaturase desA3 found in both cold-adapted clades I and IV as well as in clade III, a warm thermotype 255 subjected to much stronger seasonal variability than its (sub)tropical clade II counterparts (Pittera et 256 al., 2018). Furthermore, BIOS-U3-1 also possesses desA2, thought to be specific to warm 257 environments, while this gene is in contrast absent from the other two CRD1 warm-adapted strains. 258 Thus, CRD1 strains exhibit a different desaturase gene set and potentially display a larger capacity to 259 regulate membrane fluidity than typical cold- or warm-adapted thermotypes. Finally, while all clades 260 I, III and IV genomes possess the ocp operon, involved in the protection of PSII against 261 photoinactivation through the dissipation of excess light energy (Kirilovsky, 2007) and which was 262 recently shown in marine Synechococcus to play a key role at low temperature (Six et al., 2021), none 263 of the three CRD1 genomes possess this operon.

265 **Photosynthetic activity and pigment content**

266 PSII quantum yield (F_V/F_M) , used as a proxy of photosynthetic activity, was measured for each strain 267 over their whole temperature growth range. Most strains displayed a decrease in this parameter at both 268 low and high boundary limits of their growth temperature range and this effect was particularly striking 269 for BIOS-U3-1, reaching values down to 0.11 at 14°C and 0.32 at 28°C (Fig. 2A). Besides MVIR-18-270 1 that exhibited a quite constant F_V/F_M over its whole temperature range, the decrease in F_V/F_M at high 271 temperature was stronger for cold than warm thermotypes that are able to maintain a quite high F_V/F_M 272 in the warmest growth conditions (Fig. 2B). Finally, as for growth rate, CRD1 strains exhibited lower 273 F_V/F_M at all temperatures than clade I to IV strains.

274 The Exc495:550nm fluorescence excitation ratio, used as a proxy for PUB:PEB ratio, was consistent 275 with the pigment type of each strain (Humily et al., 2013; Table 1; Supplementary Fig. 4A). This ratio 276 remained pretty constant over the whole temperature range for all strains except for the chromatic 277 acclimator BL107 (pigment type 3dA), for which a sharp increase was observed at its maximal growth 278 temperature (28°C) to reach a value (1.35) intermediate between that typically observed in green light 279 (or white light; 0.6-0.7) and blue light (1.6-1.7). This suggests that the chromatic acclimation process 280 could be affected by growth temperature, at least in this strain. The phycobilisome (PBS) rod lengths 281 and the degree of coupling of PBS to PSII reaction center chlorophylls, as estimated from PE:PC and 282 PE:TA ratios respectively, showed fairly limited variations over the temperature range, indicating that 283 the phycobiliprotein composition of PBS is quite stable over the growth temperature range of each 284 strain (Supplementary Fig. 4B-C). One notable exception was a rise in both ratios for strain A15-62 at 285 its minimal growth temperature, likely attributable to the partial decoupling of individual 286 phycobiliproteins and of the whole PBS from PSII, a phenomenon typically observed under stressful 287 conditions (Six et al., 2007; Guyet et al., 2020). It is also worth noting that MITS9220 and to some 288 extent BIOS-E4-1, exhibited a significantly higher PE:PC ratio than the five other strains, potentially 289 indicating a different phycobiliprotein composition and/or length of PBS rods.

In terms of liposoluble pigments, the β -carotene/chlorophyll *a* (β -car/Chl *a*) ratio tended to increase with temperature in BIOS-E4-1 and MITS9220, as observed for the other warm thermotypes, whilst this ratio was more stable in the cold thermotypes BIOS-U3-1 and BL107, and seemed to slightly increase in the lower part of the thermal range for the clade I strain MVIR-18-1 (Fig. 3). For all strains, 294 these ratios result from a concomitant increase with temperature of Chl a and β -car content per cell 295 (Supplementary Fig. 5), indicating an enhancement of the surface of thylakoids per cell at higher 296 temperatures that was particularly marked for BIOS-E4-1 and A15-62, whilst this variation was fairly 297 limited in the other two CRD1 strains. As these two pigments are present in different proportions in 298 PSI and II (Umena et al., 2011; Xu and Wang, 2017), the higher β -car/Chl a ratio measured in clades 299 I and IV strains also suggests that they may have a higher PSII:PSI ratio than all other strains, including 300 BIOS-U3-1, and that this ratio might be more strongly affected by temperature in warm than cold 301 thermotypes.

302 As concerns the zeaxanthin/chlorophyll a (Zea/Chl a) ratio, although an increase in this ratio was 303 measured at low temperature for all strains, the amplitude was globally larger for cold than for warm 304 thermotypes, with BIOS-U3-1 behaving very similarly to the clade IV strain BL107 that exhibits the 305 largest variation in this ratio (Fig. 3). Changes in this ratio likely originate partially from the decrease 306 in Chl a content in response to cold, a strategy typically used by cells to regulate light utilization under 307 slow growth conditions (Inoue et al., 2001). However, several strains also displayed an increase in their 308 Zea content per cell at low temperature, a response particularly striking in BIOS-U3-1 and A15-62, but 309 that also seems to occur in M16.1 and in the two other CRD1 strains BIOS-E4-1 and MITS9220 310 (Supplementary Fig. 5). Thus, although Zea has been hypothesized to be involved in the 311 photoprotection of cold-adapted strains by dissipating excess light energy under low temperature 312 conditions (Kana et al., 1988; Breton et al., 2020), this process seems to be present in both cold and 313 warm-adapted CRD1 strains and in most warm thermotypes as well. In this context, it is also worth 314 noting that the two clade II strains, A15-62 and M16.1, displayed fairly distinct temperature-induced 315 variations in their Zea:Chl a ratios and individual pigment contents, possibly linked to their different 316 isolation temperatures (see discussion below).

317 **Photosystem II repair capacity**

The ability of the different strains to repair PSII in response to light stress (375 μ E m⁻² s⁻¹) was determined in cultures acclimated to 18, 22 and 25°C by measuring changes in F_V:F_M over time after adding the protein synthesis inhibitor lincomycin, or not (Supplementary Fig. 6). While a decrease in F_V:F_M ratio during the 90 min light stress period was observed in both cultures supplemented with lincomycin and controls, this ratio only re-increased back up to initial F_V:F_M values, after shifting cultures back to standard light conditions (75 μ E m⁻² s⁻¹), in the control group in most strains and

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temperature conditions. Thus, all studied strains were able to recover from this light stress, as long as the D1 repair cycle was not inactivated by inhibition of protein synthesis. Yet, a fast decrease in $F_V:F_M$ was observed for all three CRD1 cultures supplemented with lincomycin, while the +/- lincomycin curves overlapped during the first 15-30 min of light stress in most other strains and conditions. This suggests that the initial decrease in $F_V:F_M$ in clades I-IV strains was not due to D1 damage but rather to dissipation of light energy as heat through non-photochemical quenching (Campbell et al., 1998), whilst the damage and hence repair of D1 proteins only occurred later on.

331 The PSII repair rate (R_{PSII}), as calculated from the time course of F_V:F_M with and without 332 lincomycin, increased with temperature in most strains, except for BIOS-U3-1 that displayed its highest 333 rate at 22°C (Fig. 4). Strikingly, all three CRD1 strains displayed significantly higher R_{PSII} than clade 334 I-IV strains at all three tested temperatures, a difference ranging from 3- to nearly 40-fold at the lowest 335 common temperature (18°C). Furthermore, CRD1 strains displayed fairly limited variation in RPSII with 336 temperature (ranging from 1.33 to 1.87-fold) compared to the other strains, the strongest increase in 337 RPSII being observed for the clade I strain MVIR-18-1 (21.5-fold) and the clade III strain WH8102 (5.5-338 fold). This indicates that CRD1 strains exhibit a constitutively high level of PSII repair compared to 339 the other strains whatever the growth temperature and only trigger a moderate increase in R_{PSII} in 340 response to temperature variations.

341

342 **DISCUSSION**

343 Temperature constitutes one the strongest driving factors that have shaped genetic diversification and 344 niche partitioning in marine cyanobacteria (Scanlan et al., 2009; Flombaum et al., 2013; Biller et al., 345 2015) and phytoplankton at large (Sunagawa et al., 2015; Delmont et al., 2020). While temperature has 346 caused one major diversification event in Prochlorococcus, resulting in the divergence of the cold-347 adapted HLI from the warm-adapted HLII clades (Johnson et al., 2006; Kettler et al., 2007), several 348 independent temperature-related diversification events also occurred in the Synechococcus SC 5.1 349 radiation, leading to the emergence of clades I and IV (Dufresne et al., 2008; Zwirglmaier et al., 2008). 350 Here, determination of the temperature optimum and boundary limits (i.e., the fundamental niche) of 351 strains representative of the three CRD1 ESTUs identified in the field (Farrant et al., 2016) showed 352 that different thermotypes can also be delineated within the CRD1 clade, which dominates the 353 Synechococcus populations in low-Fe areas of the world Ocean. Comparison with representative strains

of the cold-adapted *Synechococcus* ecotypes (clades I and IV) on the one hand, and warm-adapted ecotypes (clades II and III) on the other, made it possible to classify i) the CRD1A strain MITS9220, isolated from the equatorial Pacific Ocean, as a warm thermotype, ii) the CRD1B strain BIOS-U3-1, isolated from the Chilean upwelling, as a cold temperate thermotype, and finally iii) the CRD1C strain BIOS-E4-1, isolated from the edge of the South Pacific gyre, a stable, warm, Fe-depleted oceanic region (Claustre et al., 2008), as a warm temperate stenotherm.

360 As expected from theory (Pearman et al., 2008), the realized environmental thermal niches of 361 CRD1 ESTUs were narrower than their fundamental niches (or similar for MITS9220). In contrast, for 362 ESTUS IA to IVA, the realized environmental niche was significantly more extended towards the low 363 thermal limit than the fundamental niches of their representative strains, this expansion being 364 particularly marked for ESTU IA (Fig. 1). This could be due to passive transport of Synechococcus 365 populations by currents into water masses colder than their temperature limits for growth. 366 Alternatively, these ESTUs may exhibit a greater microdiversity than previously assessed (Farrant et 367 al., 2016) and could be subdivided into distinct ESTUs occupying slightly different thermal niches 368 from the current ones, although representative strains to test this hypothesis remain to be isolated. In 369 agreement with the latter hypothesis Paulsen et al. (2016) measured a positive growth rate of 370 Synechococcus natural populations dominated by clade I in waters as cold as 2°C in the vicinity of the 371 Svalbard island. Thus, CRD1 ESTUs appear to be strongly outcompeted by their ESTU IA to IVA 372 counterparts at their lower temperature limits. Consistent with this, comparison of their gene content 373 showed that CRD1 ESTUs, including the cold thermotype CRD1B, lack the main adaptation 374 mechanisms reported so far for typical cold thermotypes. Indeed, all CRD1 strains examined in this 375 study i) exhibit warm-type substitutions in their α and β -phycocyanin subunits, influencing the 376 thermotolerance of this phycobiliprotein (Pittera et al., 2017; Supplementary Fig. 3A-B); ii) possess a 377 different set of desaturase genes, involved in regulation of membrane fluidity (Pittera et al., 2018), than 378 typical warm and cold thermotypes (Supplementary Table 2) and iii) lack the OCP system, involved 379 in the protection of PSII against photoinactivation, which seemingly plays a key role at low temperature 380 (Kirilovsky, 2007; Six et al., 2021). Still, we cannot exclude that CRD1 strains could use alternative 381 strategies to cope with temperature variations and notably to deal with the generation of reactive 382 oxygen species, known to be generated by a variety of factors including low and high temperature 383 (Nishiyama et al., 2006; Latifi et al., 2009). For instance, all CRD1 strains possess the srxA gene 384 encoding sulfiredoxin catalyzing the reduction of 2-Cys peroxiredoxin involved in H₂O₂ detoxification

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(Findlay et al., 2005; Guyet et al., 2020) as well as *isiA* that, besides its role in increasing the lightharvesting efficiency of PSI under conditions of Fe-limitation, was also shown to provide photoprotection to PSII by dissipating excess light energy under oxidative stress conditions (Yeremenko et al., 2004; Ihalainen et al., 2005; Supplementary Table 2).

389 The ability of cyanobacteria to grow over a large temperature range largely relies on their capacity 390 to optimize the functioning of their photosynthetic apparatus, notably at low temperature that induces 391 a general slowing down of cell metabolism (Murata et al., 2007; Pittera et al., 2014, 2017). For this 392 reason, we also compared the photophysiology of CRD1 and clades I-IV strains at three growth 393 temperatures common to all strains. These analyses showed that all three CRD1 strains exhibit a lower 394 growth rate at most temperatures than clade I to IV strains (Fig. 1), possibly explaining why they are 395 easily outcompeted by other taxa when iron is no longer limiting, as observed for instance around the 396 Marquesas Islands (Caputi et al., 2019). Moreover, CRD1 strains also display a lower PSII maximum 397 quantum yield (Fig. 2), suggesting that PSII is partially photoinactivated, that is their D1 repair cycle 398 does not fully compensate damage to this protein, even under optimal growth temperatures. Consistent 399 with this, the very high turnover rate of the D1 protein measured in all CRD1 strains indicates that their 400 PSII is much more sensitive to light stress than other strains and can only trigger a moderate increase 401 in R_{PSII} in response to both light and temperature variations, possibly indicating that they are adapted 402 to live deeper in the water column than clades I to IV. This sensitivity could be partially linked to the 403 abovementioned absence of the OCP, potentially reducing their ability to dissipate excess light energy, 404 although it must be noted that the clade II strain A15-62 also lacks the OCP system. Interestingly in 405 this context, all cold thermotypes including the CRD1B strain BIOS-U3-1, possess more copies of the 406 D1:2 isoform (3-6 copies, average: 3.9 ± 1.1) than warm thermotypes (2-3 copies, average: 2.2 ± 0.4), 407 this isoform providing a lower quantum yield but higher PSII resistance to photoinhibition than D1:1 408 (Supplementary Table 2; Clarke et al., 1993a, 1993b; Campbell et al., 1995; Garczarek et al., 2008). 409 Moreover, A15-62 is one of the only Synechococcus strains to possess two complete copies of the D1:1 isoform, a duplication which could partly explain why, despite the absence of OCP, this atypical clade 410 411 II strain is able to maintain a high PSII quantum yield over its whole growth temperature range with 412 fairly low D1 repair rates. Interestingly, CRD1 strains also possess a paralog of *psbN*, which was found 413 to be required for the assembly of the PSII reaction centre in Nicotiana tabacum and would play an 414 important role in the D1 repair cycle (Torabi et al., 2014).

415 Taken together, both comparative genomics and photophysiological analyses highlighted a 416 number of specificities of CRD1 strains compared to their clade I-IV counterparts, rather than them 417 possessing traits distinctive of cold or warm thermotypes. In this context, it is worth noting that 418 although strains representative of ESTUs IVA and CRD1B exhibit a similar fundamental thermal niche 419 in culture, the higher median temperature of CRD1B in the field indicates that it preferentially thrives 420 in temperate waters (about 18°C, Fig. 1), where energetically costly temperature adaptation 421 mechanisms might not be essential. This suggests that for members of the CRD1 clade, adaptation to 422 low-Fe conditions likely prevails over adaptation to temperature variations, and/or that adaptation 423 mechanisms to temperature variations might be more complex and diversified than previously thought. 424 Still, in terms of a realized environmental thermal niche, the occurrence of several CRD1 thermotypes 425 likely explains why the CRD1 clade as a whole occupies most Fe-limited areas, a vast ecosystem 426 constituting about 30% of the world Ocean (Moore et al., 2013; Bristow et al., 2017). A notable 427 exception is the Southern Ocean, for which from the little available data shows that Synechococcus is 428 scarce south of the polar front (Wilkins et al., 2013; Farrant et al., 2016), consistent with the fairly high 429 low-temperature limit (14°C) of the CRD1B environmental realized niche (Fig. 1), while low-Fe 430 availability likely limits the growth of clades I and IV in this area. In contrast, CRD1 growth does not 431 currently appear to be limited by warm temperatures since most oceanic waters display a temperature 432 below 30°C (Supplementary Fig. 2B; Supplementary Table 1). However, one cannot exclude that with 433 global change, some areas of the world Ocean could become warmer than the highest limits determined 434 here for representative strains of CRD1A and C, i.e. 31°C and 30°C respectively. In this context, it is 435 worth mentioning that in the dataset used for this study, several coastal stations, sampled during the 436 OSD campaign reached 31.5 °C (Supplementary Table 1). Thus, although biogeochemistry global 437 models predict that *Synechococcus* could be one of the winners of the phytoplankton community in a 438 future world Ocean (Flombaum et al., 2013; Schmidt et al., 2020; Visintini et al., 2021), it might well 439 not be able to survive in the warmest low-Fe areas, an ecological niche that is currently expanding 440 (Polovina et al., 2008). Although a few studies have started to analyze the genomic bases of adaptation 441 of Synechococcus cells to Fe-limitation in the field (Ahlgren et al., 2020; Garcia et al., 2020), further 442 comparative genomic and physiological studies are still needed to decipher the specific capacity of 443 CRD1 clade members to deal with Fe-limitation which should help predict the future distribution and 444 dynamics of Synechococcus taxa in the world Ocean.

445

446 DATA AVAILABILITY STATEMENT

Unpublished metabarcoding data supporting the conclusions of this article are available as raw data
(SRA accession numbers) and processed data (number of *petB* reads per ESTU) in Supplementary
Table 1. The latter Table also encompasses the description of all environmental samples used in this
study.

451

452 **CONFLICT OF INTEREST**

453 The authors declare that the research was conducted in the absence of any commercial or financial

454 relationships that could be construed as a potential conflict of interest.

455

456 **AUTHOR CONTRIBUTIONS**

MF, HD and LG designed the experiments. MF, LD, HD, MR, AG, FRJ, TS, LC and GM collected the
samples and performed the physiological measurements. MF and DM ran the flow cytometry analyses.
FL isolated several CRD1 strains used in this study. HD, XX, DJS, HL and LG performed sequencing
and bioinformatics analyses of metabarcodes. MH, EC, FP and LG developed and refined the Cyanorak *v2.1* database. MF, HD, FP and LG made the figures. MF, LD, HD, FP and LG interpreted results. All
the authors contributed to the preparation of the manuscript, read and approved the final manuscript.

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468

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480

481 SUPPLEMENTARY MATERIAL

482 Supplementary Table 1 | Environmental samples used in this study for the determination of the
483 realized environmental niches of the major *Synechococcus* ESTUs

484 Supplementary Table 2 | Phyletic pattern of CRD1 and clade I-IV genes mentioned in this study
485 retrieved from the Cyanorak v2.1 database

486 Supplementary Figure 1. Isolation sites of the Synechococcus strains used in this study. Isolation 487 site of each strain is indicated on the map by a bubble arrow colored according to their corresponding 488 ESTUs indicated below the strain name. Longhurst provinces (Longhurst A., 2007, Ecological 489 Geography of the Sea, Academic Press, London) are shown as a colored background shown in the 490 insert. Only provinces from which at least one strain has been isolated are indicated on the map using 491 the following abbreviations: PEQD (Pacific equatorial divergence, Pacific, Trade wind), CHIL (Chile-492 Peru, current coastal province, Pacific, Coastal), NAST W (Northwest Atlantic subtropical gyral, 493 Atlantic, Westerly), CARB (Caribbean, Atlantic, Trade wind), MEDI (Mediterranean Sea, Atlantic, 494 Westerly), SARC (Atlantic sub-Arctic, Atlantic, Polar).

Supplementary Figure 2. Oceanwide environmental data used in this study to determine the
environmental realized thermal niches of the main ESTUs from clades CRD1 and I to IV. (A)
Map of the sampling sites, (B) Relative abundance of *Synechococcus* ESTUs IA to IVA and CRD1A

- 498 to C. (C) Temperature distribution of the sampling sites. The inserts specify (A, C) the name of
- 499 campaigns or datasets analyzed and **(B)** the *Synechococcus* ESTUs.
- 500 Supplementary Figure 3. Alignment of RpcA and RpcB, encoding phycocyanin α- and b-
- 501 subunits, from CRD1 and clades I-IV Synechococcus strains. (A) RpcA. (B) RpcB. Substitutions
- 502 potentially involved in thermotolerance are shown by a red rectangle in the alignment.
- 503 Supplementary Figure 4. Variation with growth temperature of phycobilins and 504 phycobiliproteins fluorescence excitation and emission ratios. (A) Average PUB:PEB ratios. (B)
- 505 Average phycoerythrin (PE) to phycocyanin (PC) ratios. (C) Average PC to terminal acceptor (TA)
- 506 ratios. The insert indicates the strain names, their corresponding ESTU (*sensu* Farrant et al., 2016) and
- 507 pigment type (*sensu* Humily et al., 2013) between brackets.
- 508 Supplementary Figure 5. Variation with growth temperature of the three main liposoluble
- 509 pigments per cell for CRD1 vs. clade I and IV strains. (A, D) Chlorophyll (Chl) *a* content (fg/cell).
- 510 (**B**, **E**) Zeaxanthin (Zea) content (fg/cell). (**C**, **F**) β-carotene (β-car) content (fg/cell). (**A-C**) CRD1-B
- 511 strain BIOS-U3-1 vs. cold thermotypes. (D-F) CRD1-A strain MITS9220 and CRD1-C strain BIOS-
- 512 E4-1 vs. warm thermotypes. Inserts indicate the strain names and their corresponding ESTU (sensu
- 513 Farrant et al., 2016) between brackets.
- 514 Supplementary Figure 6. Time course of photosystem II quantum yield (F_V/F_M) following light
- 515 stress in the presence or absence of lincomycin for CRD1 and clade I-IV strains acclimated to
- 516 **different temperatures.** Cultures acclimated to 75 μ E m⁻² s⁻¹ were shifted to 375 μ E m⁻² s⁻¹ at T0 for
- 517 90 min, then shifted back to the initial light conditions for 24h as indicated by a vertical dashed line on
- 518 each figure. Strain names and their corresponding ESTU between brackets (*sensu* Farrant et al., 2016)
- 519 are indicated on the right-hand side, acclimation temperatures are indicated on the top, whilst line
- 520 colour indicates the lincomycin treatment (i.e. -/+ linco).
- 521
- 522

523 **REFERENCES**

- Ahlgren, N. A., Belisle, B. S., and Lee, M. D. (2020). Genomic mosaicism underlies the adaptation of
 marine *Synechococcus* ecotypes to distinct oceanic iron niches. *Environ. Microbiol.* 22, 1801–
 1815. doi:10.1111/1462-2920.14893.
- 527 Ahlgren, N. A., and Rocap, G. (2012). Diversity and distribution of marine Synechococcus: Multiple 528 gene phylogenies for consensus classification and development of qPCR assays for sensitive 529 measurement of clades in the ocean. Front. Microbiol. 213-213. 3, 530 doi:10.3389/fmicb.2012.00213.
- Biller, S. J., Berube, P. M., Lindell, D., and Chisholm, S. W. (2015). *Prochlorococcus*: The structure
 and function of collective diversity. *Nat. Rev. Microbiol.* 13, 13–27. doi:10.1038/nrmicro3378.
- Breton, S., Jouhet, J., Guyet, U., Gros, V., Pittera, J., Demory, D., et al. (2020). Unveiling membrane
 thermoregulation strategies in marine picocyanobacteria. *New Phytol.* 225, 2396–2410.
 doi:10.1111/nph.16239.
- Bristow, L. A., Mohr, W., Ahmerkamp, S., and Kuypers, M. M. M. (2017). Nutrients that limit growth
 in the ocean. *Curr. Biol.* 27, R431–R510. doi:10.1016/j.cub.2017.03.030.
- Campbell, D., Hurry, V., Clarke, A. K., Gustafsson, P., and Öquist, G. (1998). Chlorophyll
 fluorescence analysis of cyanobacterial photosynthesis and acclimation. *Microbiol. Mol. Biol. Rev.* 62, 667–683. doi:10.1128/mmbr.62.3.667-683.1998.
- Campbell, D., Zhou, G., Gustafsson, P., Oquist, G., and Clarke, A. K. (1995). Electron transport
 regulates exchange of two forms of photosystem II D1 protein in the cyanobacterium
 Synechococcus. EMBO J. 14, 5457–5466. doi:10.1128/MMBR.62.3.667-683.1998.
- Caputi, L., Carradec, Q., Eveillard, D., Kirilovsky, A., Pelletier, E., Pierella Karlusich, J. J., et al.
 (2019). Community-level responses to iron availability in open ocean plankton ecosystems. *Glob. Biogeochem. Cycles* 33, 391–419. doi:10.1029/2018GB006022.
- 547 Clarke, A. K., Hurry, V. M., Gustafsson, P., and Oquist, G. (1993a). Two functionally distinct forms
 548 of the photosystem II reaction-center protein D1 in the cyanobacterium *Synechococcus* sp. PCC
 549 7942. *Proc. Natl. Acad. Sci. U. S. A.* 90, 11985–11989. doi:10.1073/pnas.90.24.11985.
- Clarke, A. K., Soitamo, A., Gustafsson, P., and Oquist, G. (1993b). Rapid interchange between two
 distinct forms of cyanobacterial photosystem II reaction-center protein D1 in response to
 photoinhibition. *Proc. Natl. Acad. Sci. U. S. A.* 90, 9973–9977. doi:10.1073/pnas.90.21.9973.
- Claustre, H., Sciandra, A., and Vaulot, D. (2008). Introduction to the special section bio-optical and
 biogeochemical conditions in the South East Pacific in late 2004: the BIOSOPE program.
 Biogeosciences 5, 679–691. doi:10.5194/bg-5-679-2008.
- Delmont, T. O., Gaia, M., Hinsinger, D. D., Fremont, P., Guerra, A. F., Eren, A. M., et al. (2020).
 Functional repertoire convergence of distantly related eukaryotic plankton lineages revealed by

- 558genome-resolved metagenomics.*BioRxiv*,2020.10.15.341214-2020.10.15.341214.559doi:10.1101/2020.10.15.341214.
- Doré, H., Farrant, G. K., Guyet, U., Haguait, J., Humily, F., Ratin, M., et al. (2020). Evolutionary
 mechanisms of long-term genome diversification associated with niche partitioning in marine
 picocyanobacteria. *Front. Microbiol.* 11, 567431. doi:10.3389/fmicb.2020.567431.
- Doré, H., Leconte, Jade, Breton, Solène, Demory, David, Hoebeke, Mark, Corre, Erwan, et al. (2022).
 Global phylogeography of marine *Synechococcus* in coastal areas unveils strikingly different communities than in open ocean. *BioRxiv*.
- Dufresne, A., Ostrowski, M., Scanlan, D. J., Garczarek, L., Mazard, S., Palenik, B. P., et al. (2008).
 Unraveling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. *Genome Biol.*9, R90. doi:10.1186/gb-2008-9-5-r90.
- 569 Farrant, G. K., Doré, H., Cornejo-Castillo, F. M., Partensky, F., Ratin, M., Ostrowski, M., et al. (2016). 570 Delineating ecologically significant taxonomic units from global patterns of marine 571 picocyanobacteria. Acad. U. S. Proc. Natl. Sci. Α. 113, E3365-E3374. 572 doi:10.1073/pnas.1524865113.
- Findlay, V. J., Tapiero, H., and Townsend, D. M. (2005). Sulfiredoxin: a potential therapeutic agent? *Biomed. Pharmacother.* 59, 374–379. doi:10.1016/j.biopha.2005.07.003.
- Flombaum, P., Gallegos, J. L., Gordillo, R. a, Rincón, J., Zabala, L. L., Jiao, N., et al. (2013). Present
 and future global distributions of the marine Cyanobacteria *Prochlorococcus* and *Synechococcus*. *Proc. Natl. Acad. Sci. U. S. A.* 110, 9824–9829. doi:10.1073/pnas.1307701110.
- Garcia, C. A., Hagstrom, G. I., Larkin, A. A., Ustick, L. J., Levin, S. A., Lomas, M. W., et al. (2020).
 Linking regional shifts in microbial genome adaptation with surface ocean biogeochemistry. *Philos. Trans. R. Soc. B Biol. Sci.* 375, 20190254. doi:10.1098/rstb.2019.0254.
- Garczarek, L., Dufresne, A., Blot, N., Cockshutt, A. M., Peyrat, A., Campbell, D. A., et al. (2008).
 Function and evolution of the *psbA* gene family in marine *Synechococcus*: *Synechococcus* sp.
 WH7803 as a case study. *ISME J.* 2, 937–953. doi:10.1038/ismej.2008.46.
- Garczarek, L., Guyet, U., Doré, H., Farrant, G. K., Hoebeke, M., Brillet-Guéguen, L., et al. (2021).
 Cyanorak v2.1: a scalable information system dedicated to the visualization and expert curation
 of marine and brackish picocyanobacteria genomes. *Nucleic Acids Res.* 49, D667–D676.
 doi:10.1093/nar/gkaa958.
- Gutiérrez-Rodríguez, A., Slack, G., Daniels, E. F., Selph, K. E., Palenik, B., and Landry, M. R. (2014).
 Fine spatial structure of genetically distinct picocyanobacterial populations across
 environmental gradients in the Costa Rica Dome. *Limnol. Oceanogr.* 59, 705–723.
 doi:10.4319/lo.2014.59.3.0705.
- Guyet, U., Nguyen, N. A., Doré, H., Haguait, J., Pittera, J., Conan, M., et al. (2020). Synergic effects
 of temperature and irradiance on the physiology of the marine *Synechococcus* strain WH7803.
 Front. Microbiol. 11, 1707. doi:10.3389/fmicb.2020.01707.

- Humily, F., Partensky, F., Six, C., Farrant, G. K., Ratin, M., Marie, D., et al. (2013). A gene island
 with two possible configurations is involved in chromatic acclimation in marine *Synechococcus. PLoS One* 8, e84459. doi:10.1371/journal.pone.0084459.
- Ihalainen, J. A., D'Haene, S., Yeremenko, N., van Roon, H., Arteni, A. A., Boekema, E. J., et al.
 (2005). Aggregates of the chlorophyll-binding protein IsiA (CP43') dissipate energy in cyanobacteria. *Biochemistry* 44, 10846–10853. doi:10.1021/bi0510680.
- Inoue, N., Taira, Y., Emi, T., Yamane, Y., Kashino, Y., Koike, H., et al. (2001). Acclimation to the
 growth temperature and the high-temperature effects on photosystem II and plasma membranes
 in a mesophilic cyanobacterium *Synechocystis* sp. PCC6803. *Plant Cell Physiol.* 42, 1140–
 1148. doi:10.1093/pcp/pce147.
- Johnson, Z. I., Zinser, E. R., Coe, A., McNulty, N. P., Woodward, E. M. S., and Chisholm, S. W.
 (2006). Niche partitioning among *Prochlorococcus* ecotypes along ocean-scale environmental
 gradients. *Science* 311, 1737–1740. doi:10.1126/science.1118052.
- Kana, T. M., Glibert, P. M., Goericke, R., and Welschmeyer, N. A. (1988). Zeaxanthin and β-carotene
 in *Synechococcus* WH7803 respond differently to irradiance. *Limnol. Oceanogr.* 33, 1623–
 1626. doi:10.4319/lo.1988.33.6part2.1623.
- Kashtan, N., Roggensack, S. E., Rodrigue, S., Thompson, J. W., Biller, S. J., Coe, A., et al. (2014).
 Single-cell genomics reveals hundreds of coexisting subpopulations in wild *Prochlorococcus*. *Science* 344, 416–420. doi:10.1126/science.1248575.
- Kent, A. G., Baer, S. E., Mouginot, C., Huang, J. S., Larkin, A. A., Lomas, M. W., et al. (2019). Parallel
 phylogeography of *Prochlorococcus* and *Synechococcus*. *ISME J.* 13, 430–441.
 doi:10.1038/s41396-018-0287-6.
- Kettler, G. C., Martiny, A. C., Huang, K., Zucker, J., Coleman, M. L., Rodrigue, S., et al. (2007).
 Patterns and implications of gene gain and loss in the evolution of *Prochlorococcus*. *PLoS Genet.* 3, e231. doi:10.1371/journal.pgen.0030231.
- Kirilovsky, D. (2007). Photoprotection in cyanobacteria: the orange carotenoid protein (OCP)-related
 non-photochemical-quenching mechanism. *Photosynth. Res.* 93, 7. doi:10.1007/s11120-007 9168-y.
- Larkin, A. A., Blinebry, S. K., Howes, C., Lin, Y., Loftus, S. E., Schmaus, C. A., et al. (2016). Niche
 partitioning and biogeography of high light adapted *Prochlorococcus* across taxonomic ranks
 in the North Pacific. *ISME J.* 10, 1555–1567. doi:10.1038/ismej.2015.244.
- Larkin, A. A., and Martiny, A. C. (2017). Microdiversity shapes the traits, niche space, and
 biogeography of microbial taxa: The ecological function of microdiversity. *Environ. Microbiol. Rep.* 9, 55–70. doi:10.1111/1758-2229.12523.
- Latifi, A., Ruiz, M., and Zhang, C. C. (2009). Oxidative stress in cyanobacteria. *FEMS Microbiol. Rev.* 33, 258-278-258–278. doi:10.1111/j.1574-6976.2008.00134.x.

- Mackey, K. R. M., Paytan, A., Caldeira, K., Grossman, A. R., Moran, D., McIlvin, M., et al. (2013).
 Effect of temperature on photosynthesis and growth in marine *Synechococcus* spp. *Plant Physiol.* 163, 815–829. doi:10.1104/pp.113.221937.
- Marie, D., Partensky, F., Vaulot, D., and Brussaard, C. (1999). Enumeration of phytoplankton, bacteria,
 and viruses in marine samples. *Curr. Protoc. Cytom.* 10, 11.11.1-11.11.15.
 doi:10.1002/0471142956.cy1111s10.
- Mella-Flores, D., Mazard, S., Humily, F., Partensky, F., Mahé, F., Bariat, L., et al. (2011). Is the
 distribution of *Prochlorococcus* and *Synechococcus* ecotypes in the Mediterranean Sea affected
 by global warming? *Biogeosciences* 8, 2785–2804. doi:10.5194/bg-8-2785-2011.
- Mikami, K., and Murata, N. (2003). Membrane fluidity and the perception of environmental signals in
 cyanobacteria and plants. *Prog. Lipid Res.* 42, 527–543. doi:10.1016/S0163-7827(03)00036-5.
- Moore, C. M., Mills, M. M., Arrigo, K. R., Berman-Frank, I., Bopp, L., Boyd, P. W., et al. (2013).
 Processes and patterns of oceanic nutrient limitation. *Nat. Geosci.* 6, 701–710.
 doi:10.1038/ngeo1765.
- Murata, N., Takahashi, S., Nishiyama, Y., and Allakhverdiev, S. I. (2007). Photoinhibition of
 photosystem II under environmental stress. *Biochim. Biophys. Acta Bioenerg.* 1767, 414–421.
 doi:10.1016/j.bbabio.2006.11.019.
- Nishiyama, Y., Allakhverdiev, S. I., and Murata, N. (2006). A new paradigm for the action of reactive
 oxygen species in the photoinhibition of photosystem II. *Biochim. Biophys. Acta BBA* -*Bioenerg.* 1757, 742–749. doi:10.1016/j.bbabio.2006.05.013.
- Paulsen, M. L., Doré, H., Garczarek, L., Seuthe, L., Müller, O., Sandaa, R.-A., et al. (2016). *Synechococcus* in the Atlantic gateway to the Arctic Ocean. *Front. Mar. Sci.* 3, 191.
 doi:10.3389/fmars.2016.00191.
- Pearman, P. B., Guisan, A., Broennimann, O., and Randin, C. F. (2008). Niche dynamics in space and
 time. *Trends Ecol. Evol.* 23, 149–158. doi:10.1016/j.tree.2007.11.005.
- Pittera, J., Humily, F., Thorel, M., Grulois, D., Garczarek, L., and Six, C. (2014). Connecting thermal
 physiology and latitudinal niche partitioning in marine *Synechococcus*. *ISME J.* 8, 1221–1236.
 doi:10.1038/ismej.2013.228.
- Pittera, J., Jouhet, J., Breton, S., Garczarek, L., Partensky, F., Maréchal, É., et al. (2018).
 Thermoacclimation and genome adaptation of the membrane lipidome in marine *Synechococcus. Environ. Microbiol.* 20, 612–631. doi:10.1111/1462-2920.13985.
- Pittera, J., Partensky, F., and Six, C. (2017). Adaptive thermostability of light-harvesting complexes in
 marine picocyanobacteria. *ISME J.* 11, 112–124. doi:10.1038/ismej.2016.102.
- Polovina, J. J., Howell, E. A., and Abecassis, M. (2008). Ocean's least productive waters are
 expanding. *Geophys. Res. Lett.* 35, L03618. doi:10.1029/2007GL031745.
- Rippka, R., Coursin, T., Hess, W., Lichtle, C., Scanlan, D. J., Palinska, K. A., et al. (2000).
 Prochlorococcus marinus Chisholm et al. 1992 subsp. *pastoris* subsp. nov. strain PCC 9511,

- 668 the first axenic chlorophyll a_2/b_2 -containing cyanobacterium (Oxyphotobacteria). *Int. J. Syst.* 669 *Evol. Microbiol.* 50, 1833–1847. doi:10.1099/00207713-50-5-1833.
- Saito, M. A., Rocap, G., and Moffett, J. W. (2005). Production of cobalt binding ligands in a *Synechococcus* feature at the Costa Rica upwelling dome. *Limnol. Oceanogr.* 50, 279–290.
 doi:10.4319/lo.2005.50.1.0279.
- Scanlan, D. J., Ostrowski, M., Mazard, S., Dufresne, A., Garczarek, L., Hess, W. R., et al. (2009).
 Ecological genomics of marine picocyanobacteria. *Microbiol. Mol. Biol. Rev.* 73, 249–299.
 doi:10.1128/MMBR.00035-08.
- Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., et al. (2009).
 Introducing Mothur: Open-source, platform-independent, community-supported software for
 describing and comparing microbial communities. *Appl. Environ. Microbiol.* 75, 7537–7541.
 doi:10.1128/AEM.01541-09.
- Schmidt, K., Birchill, A. J., Atkinson, A., Brewin, R. J. W., Clark, J. R., Hickman, A. E., et al. (2020).
 Increasing picocyanobacteria success in shelf waters contributes to long-term food web
 degradation. *Glob. Change Biol.* 26, 5574–5587. doi:10.1111/gcb.15161.
- Six, C., Joubin, L., Partensky, F., Holtzendorff, J., and Garczarek, L. (2007). UV-induced
 phycobilisome dismantling in the marine picocyanobacterium *Synechococcus* sp. WH8102.
 Photosynth. Res. 92, 75–86. doi:10.1007/s11120-007-9170-4.
- Six, C., Ratin, M., Marie, D., and Corre, E. (2021). Marine *Synechococcus* picocyanobacteria: Light
 utilization across latitudes. *Proc. Natl. Acad. Sci.* U. S. A. 118, e2111300118.
 doi:10.1073/pnas.2111300118.
- Six, C., Thomas, J., Brahamsha, B., Lemoine, Y., and Partensky, F. (2004). Photophysiology of the
 marine cyanobacterium *Synechococcus* sp. WH8102, a new model organism. *Aquat. Microb. Ecol.* 35, 17–29. doi:10.3354/ame035017.
- Six, C., Thomas, J.-C., Thion, L., Lemoine, Y., Zal, F., and Partensky, F. (2005). Two novel
 phycoerythrin-associated linker proteins in the marine cyanobacterium *Synechococcus* sp.
 strain WH8102. *J. Bacteriol.* 187, 1685–1694. doi:10.1128/JB.187.5.1685-1694.2005.
- Sohm, J. A., Ahlgren, N. A., Thomson, Z. J., Williams, C., Moffett, J. W., Saito, M. A., et al. (2016).
 Co-occurring *Synechococcus* ecotypes occupy four major oceanic regimes defined by
 temperature, macronutrients and iron. *ISME J.* 10, 333–345. doi:10.1038/ismej.2015.115.
- Sunagawa, S., Coelho, L. P., Chaffron, S., Kultima, J. R., Labadie, K., Salazar, G., et al. (2015).
 Structure and function of the global ocean microbiome. *Science* 348, 1261359–1261359.
 doi:10.1126/science.1261359.
- Torabi, S., Umate, P., Manavski, N., Plöchinger, M., Kleinknecht, L., Bogireddi, H., et al. (2014). PsbN
 is required for assembly of the photosystem II reaction center in *Nicotiana tabacum*. *Plant Cell* 26, 1183–1199. doi:10.1105/tpc.113.120444.

- Umena, Y., Kawakami, K., Shen, J.-R., and Kamiya, N. (2011). Crystal structure of oxygen-evolving
 photosystem II at a resolution of 1.9 Å. *Nature* 473, 55–60. doi:10.1038/nature09913.
- Visintini, N., Martiny, A. C., and Flombaum, P. (2021). *Prochlorococcus, Synechococcus*, and
 picoeukaryotic phytoplankton abundances in the global ocean. *Limnol. Oceanogr. Lett.* 6, 207–
 215. doi:10.1002/lol2.10188.
- Wilkins, D., Lauro, F. M., Williams, T. J., Demaere, M. Z., Brown, M. V., Hoffman, J. M., et al. (2013).
 Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics.
 Environ. Microbiol. 15, 1318–1333. doi:10.1111/1462-2920.12035.
- Xia, X., Cheung, S., Endo, H., Suzuki, K., and Liu, H. (2019). Latitudinal and vertical variation of
 Synechococcus assemblage composition along 170°W transect from the South Pacific to the
 Arctic Ocean. *Microb. Ecol.* 77, 333–342. doi:10.1007/s00248-018-1308-8.
- Xu, W., and Wang, Y. (2017). "Function and structure of cyanobacterial photosystem I," in *Photosynthesis: Structures, Mechanisms, and Applications*, eds. H. J. M. Hou, M. M. Najafpour, G. F. Moore, and S. I. Allakhverdiev (Cham: Springer International Publishing), 111–168. doi:10.1007/978-3-319-48873-8_7.
- Yeremenko, N., Kouřil, R., Ihalainen, J. A., D'Haene, S., van Oosterwijk, N., Andrizhiyevskaya, E.
 G., et al. (2004). Supramolecular organization and dual function of the IsiA chlorophyll-binding
 protein in cyanobacteria. *Biochemistry* 43, 10308–10313. doi:10.1021/bi0487721.
- Zwirglmaier, K., Jardillier, L., Ostrowski, M., Mazard, S., Garczarek, L., Vaulot, D., et al. (2008).
 Global phylogeography of marine *Synechococcus* and *Prochlorococcus* reveals a distinct
 partitioning of lineages among oceanic biomes. *Environ. Microbiol.* 10, 147–161.
 doi:https://doi.org/10.1111/j.1462-2920.2007.01440.x.
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TABLES

729

| Strains name | MVIR-18-1 | A15-62 | M16.1 | WH8102 | BL107 | BIOS-E4-1 | BIOS-U3-1 | MITS9220 |
|---------------------------|-----------|------------------------|-------------------|------------------|--------------|-----------------------|--------------------|-----------------------|
| RCC # ¹ | 2385 | 2374 | 791 | 539 | 515 | 2534 | 2533 | 2571 |
| Subcluster ² | 5.1 | 5.1 | 5.1 | 5.1 | 5.1 | 5.1 | 5.1 | 5.1 |
| Clade ² | Ι | II | II | III | IV | CRD1 | CRD1 | CRD1 |
| ESTU ² | IA | IIA | IIA | IIIA | IVA | CRD1C | CRD1B | CRD1A |
| Pigment type ³ | 3aA | 3dB | 3a | 3c | 3dA | 3cA | 3dA | 3dA |
| Ocean | Atlantic | Atlantic | Atlantic | Atlantic | Med. Sea | Pacific | Pacific | Pacific |
| Region | North Sea | Offshore Mauritania | Gulf of Mexico | Caribbean Sea | Balearic Sea | South East Pacific | Chile upwelling | Equatorial Pacific |
| Isolation latitude | 61°00' N | 17°37' N | 27°70' N | 22°48' N | 41°72' N | 31°52' S | 34°00' S | 0°00' N |
| Isolation longitude | 1°59' E | 20°57' W | 91°30' W | 65°36' W | 3°33' E | 91°25' W | 73°22' W | 140°00' W |

730 TABLE 1 | Characteristics of the Synechococcus strains used in this study

731 ¹Roscoff Culture Collection, ²Farrant et al. (2016), ³Humily et al. (2013).

732

733 **FIGURE LEGENDS** 734 735 FIGURE 1 | Fundamental thermal niches of CRD1 vs. clade I, II, III and IV strains and environmental 736 realized niches of the corresponding ESTUs. (A) CRD1-B strain BIOS-U3-1 vs. cold thermotypes. (B) 737 CRD1-A strain MITS9220 and the CRD1-C strain BIOS-E4-1 vs. warm thermotypes. The insert indicates 738 the strain names and their corresponding ESTU (sensu Farrant et al., 2016) between brackets. Each 739 data point is the average of at least 3 biological replicates. Environmental realized niches are indicated 740 as horizontal boxplots for each ESTU above each graph with the whiskers corresponding to 1.5-fold 741 the interquartile range and outliers being plotted as individual points. 742 743 FIGURE 2 | Variation with growth temperature of photosystem II quantum yield (F_V/F_M) for CRD1 744 vs. clade I, II, III and IV strains. (A) CRD1-B strain BIOS-U3-1 vs. cold thermotypes. (B) CRD1-A strain 745 MITS9220 and the CRD1-C strain BIOS-E4-1 vs. warm thermotypes. The insert indicates the strain

names and their corresponding ESTU (*sensu* Farrant et al., 2016) between brackets.

747

FIGURE 3 | Variation with growth temperature of cellular mass pigment ratios of CRD1 vs. clade I, II, III and IV strains. (A, B) β -carotene (β -car) to chlorophyll *a* (Chla) ratio. (C, D) Zeaxanthin (Zea) to Chl*a* ratio with (A, C) CRD1-B strain BIOS-U3-1 vs. cold thermotypes and (B, D) CRD1-A strain MITS9220 and the CRD1-C strain BIOS-E4-1 vs. warm thermotypes. Inserts indicate strain names and their corresponding ESTUs (*sensu* Farrant et al., 2016) between brackets.

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FIGURE 4 | Variation with growth temperature of cumulative photosystem II repair rate (RPSII) of
 CRD1 vs. clade I, II, III and IV strains. The insert indicates the strain names and their corresponding
 ESTU (sensu Farrant et al., 2016) between brackets.



Ferrieux et al., Figure 1



Ferrieux et al., Figure 2



Ferrieux et al., Figure 3



Ferrieux et al., Figure 4

Ferrieux et al. Supplementary Figures





Supplementary Figure 1. Isolation sites of the *Synechococcus* strains used in this study. Isolation site of each strain is indicated on the map by a bubble arrow colored according to their corresponding ESTUs indicated below the strain name. Longhurst provinces (Longhurst A., 2007, Ecological Geography of the Sea, Academic Press, London) are shown as a colored background shown in the insert. Only provinces from which at least one strain has been isolated are indicated on the map using the following abbreviations: PEQD (Pacific equatorial divergence, Pacific, Trade wind), CHIL (Chile-Peru, current coastal province, Pacific, Coastal), NAST W (Northwest Atlantic subtropical gyral, Atlantic, Westerly), CARB (Caribbean, Atlantic, Trade wind), MEDI (Mediterranean Sea, Atlantic, Westerly), SARC (Atlantic sub-Arctic, Atlantic, Polar).





Supplementary Figure 2. Oceanwide environmental data used in this study to determine the environmental realized thermal niches of the main ESTUs from clades CRD1 and I to IV. (A) Map of the sampling sites, (B) Relative abundance of *Synechococcus* ESTUs IA to IVA and CRD1A to C. (C) Temperature distribution of the sampling sites. The inserts specify (A,C) the name of campaigns or datasets analyzed and (B) the *Synechococcus* ESTUs.

A. RpcA

| | 1 10 | 20 | 30 4 | 40 5 | 0 60 | 70 | 80 90 | 100 11 | 0 | 120 130 | 140 | 150 163 |
|--|--|--|--|---|--|--|--|---|---|---|---|---|
| 1. CC9311 Ia IA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLD | AAKGLTAKADA | LVSSATQAVYTKFP | YTTQMEGPNYSAT | SEGKAKCSRD I GYYLRMI | TYCL VAGGTGPMDD Y | LIAGLDEI | NRTFELSPSWYVEALKE | IQSNHGL SGDA/ | ATEANSY INYA INALT* |
| 2. WH8020 Ia IA | MKTPLTEAVAAAD | OGRELSNTEVQAA | SGRENRAKASLE | AAKGLTAKADS | LVSSATQAVYTKFP | YTTQMEGPNYSAT | SEGKAKCSRD I GYYLRMI | TYCL VAGGTGPMDDY | LIAGLDEI | NRTFELSPSWYVEALKE | IQSNHGL SGDA/ | ATEANSY INYA INALT* |
| 3. MVIR-18-1 lb IA | MKTPLTEAVAAAD | SQGRFLSNTEVQAA | SGRENRAQASLE. | AAKGLTAKAD | LVSGATQAVYTKFP | YTTQMEGPNYSTT | PEGKAKCSRD I GYYLRMV | TYCLVAGGTGPMDDY | LIAGLDET | NRTFELSPSWYVEALKE | IKSNHGLSGDA/ | ATEANSY INYA INALT* |
| 4 PROS-9-1 Ib IA | MKTPLTEAVAAAD | OGREL SNTEVOAA | SGRENRAKASLE | AAKGLTSKAET | LVNSAAQAVYTKEP | FTTOMEGTNYAST | SEGKAKCSRD I GYYLRMI | TYCLVAGGTGPMDDY | LIAGLAET | NRTFELSPTWYVEALRN | KSNHGL SGDA | ATEANSY IDYAINALI* |
| 5 POS9604 IN IA | MKTPL TEAVAAAD | SOGREL SNTEVOAA | SCRENRAKASLE | AAKGI TAKADA | UVNGAADAVYTKEP | VITOMOGSNVSTT | SEGKAKCARD LGYVLRMI | TYCI VAGGTGPMDDY | LAGIDEL | NETEELSESWAVEALKY | IKANHGI SONA | STEANSY IDVAINAL I* |
| 6 SVN20 Ib IA | MKTRLTEAVAAAD | SOGREL SNTEVOAA | SCRENDAKASLE | AAKCI TAKADS | I VNGAAOAVYTKEP | YTTOMOGSNYSTT | PECKAKCAPDICYVIPMI | TYCL VAGGTGPMDDY | LAGEDEL | NOTEFI SPSWVVFALKE | KANHGI SONA | GTEANSY IDVAINAL I* |
| | NIK TPETEAVAAAAD | OCDEL SNTEVQAA | SCRENDAKASLE. | AAKGL TAKAD | | 111QWQG5N1511 | FEGRARCARD I GITTERMI | TICEVAGGTGFMDDI | LIAGEDET | INTERL COCHARGE AL KY | IKANHGE SGNA | GTEANSTIDIAINALI. |
| 7. WH8016_ID_IB | MKTPLTEAVAAAD | SQGRELSNIEVQAA | SGRENRARASLE. | AAKGLTAKAD | LVNGAAQAVTIKEP | TTTQMQGSNYSTT | TEGRARCARDIGTTERMI | TYCEVAGGTGPMDDY | LINGLUEI | NRIFELSPSWYVEALKY | I KANHGE SGNA | GTEANSTIDTAINALT* |
| 8. BL107_IVa_IVA | MKTPLTEAVAAAD | SQGRELSNIEVQAA | SGRENRAKASLE | AAKGLISKAEA | AL VNGAAQAVY I KEP | FILQMEGINYASS | PEGKAKCSRDVGYYLRMI | TYCEVAGGTGPMDDY | LIAGLSEI | NRIFELSPSWYVEALKE | TK INHGESGDA | ATEANSY IDYATNSLI* |
| 9. CC9902_IVa_IVA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKGLTSKADA | LVNGAAQAVYSKEP | YTTQMDGANYAST | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLSEI | NRTFELSPSWYVEALKE | IKANHGL SGDA/ | ATEANSY I DYAVNSLT* |
| 10. A15-44_IIa_IIA | MKTPLTEAVAAAD | SQGR F L SNTE I QGA | FGRENRAKAALE | AAKALTTKADI | LVNGAAQAVYSKFP | YTTQMQGPTYAST | PEGKAKCSRDIGYYLRMV | TYCLVAGGTGPMDDY | LIAGLDEI | NRTFELSPSWYVEALKY | IKANHGL SGEA/ | ATEANNYFDYAINALV* |
| 11. KORDI-52_IIa_IIA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYTKFP | YTTQMAGPNYSAS | PEGKAKCSRDVGYYLRMI | TYCL VAGGTGPMDD Y | LIAGLDEI | NRTFELSPSWYVEALKE | IKANHGLSGDA/ | ATEANSY IDYATNALT* |
| 12. M16.1 IIa IIA | MKTPLTEAVAAAD | OGRELSNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYTKFP | YTTQMEGSNYSAT | AEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDET | NRTFELSPSWYVEALKE | IKANHGL SGDA/ | ATEANSY IDYAINALI* |
| 13 RS9902 IIa IIA | MKTPLTEAVAAAD | OGREL SNTEVOAA | SGRENRAKASLE | AAKALTSKADS | | YTTOMAGPNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDET | NRTFELSPSWYVEALKE | IKANHGLSGDA | ATEANSY IDYAINALI* |
| 14 PS9007 IIa IIA | MKTPLTEAVAAAD | OGREL SNTEVOAA | SGRENRAKASLE | AAKAL TSKADS | I VNGAAOAVYTKEP | YTTOMEGSNYSAT | AEGKAKCSRDVGVVLRMI | TYCL VAGGTGPMDDY | LIAGUDEL | NRTEEL SPSWYVEALKE | IKANHGI SGDA | ATEANSY IDVAINAL I* |
| 15 TAK0803 Un UA | METRITEAVAAAD | OCREL SNTEVOAA | SCRENDAKASI E | AAVALTSKADS | UVNGAAOAVVTKER | VITOMEGENIVEAT | AEGKAKCSRDVGVVI PMI | TYCL VACGTORMODY | LINGLDEL | NOTE EL SOSWAVE AL KE | LKANHGI SODA | ATEANSY IDVALNAL I* |
| 15. TAK9602_IIA_IIA | NIK TPETEAVAAAD | OCDEL SNTEVQAA | SCRENDAKASLE. | AAKAL TOKAD | | VITTOME GONVEAT | ALGRARCSRDVGTTERMT | TYCL WAGGTGPWDD | LIAGEDET | NRTFEESF SHIVEALKE | IKANUGLOGDA | ATEANSY IDVALUAL I |
| 16. WH8109_IIa_IIA | MKTPLTEAVAAAD | SQGRELSNIEVQAA | SGRENRARASLE. | AARALISKAD | LVNGAAQAVTAKEP | TTTQMAGPINTSAT | PEGRARCSRDVGTTLRMI | TYCEVAGGTGPMDDY | LINGLUEI | NRIFELSPSWYVEALKP | INANHGE SGDA | ATEANST IDTAINAL I* |
| 17. A15-62_IIc_IIA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYTKEP | YTTQMAGPNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDEI | NRTFELSPSWYVEALKE | KANHGL SGDA/ | ATEANSY IDYA I NAL I * |
| 18. CC9605_IIc_IIA | MKTPLTEAVAAAD | SQGRFL SNTEVQAA | SGRENRAKASLE | AAKALTGKADS | LVNGAAQAVYTKFP | YTTQMAGPNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLAEI | NRTFELSPSWYVEALKE | TKANHGL SGDA/ | ATEANSY IDYA INALT* |
| 19. PROS-U-1_IIh_IIB | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYTKFP | YTTQMAGPNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLAEI | NRTFELSPSWYVEALKE | IKSNHGLSGDA/ | ATEANSY IDYATNAL I * |
| 20. A15-24 IIIa IIIA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYTKFP | YTTQMEGPNYSAT | PEGKAKCSRDVGYYLRMI | TYCL VAGGTGPMDD Y | LIAGLAET | NRTFELSPSWYVEALKE | IKSNHGLSGDA/ | ATEANSY IDYA I NALT* |
| 21. A18-40 IIIa 3IIIA | MKTPLTEAVAAAD | SQGRFLSNTEVQAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYSKEP | YTTQMEGSNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDET | NRTFELSPSWYVEALKE | IKANHGL SGDA/ | ATEANSY IDYAINALI* |
| 22 A18-46 1 IIIa IIIA | MKTPLTEAVAAAD | OGREL SNTEVOAA | SGRENRAKASLE | AAKALTSKADS | LVNGAAQAVYSKEP | YTTOMEGSNYSAT | PEGKSKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDET | NRTFELSPSWYVEALKE | IKANHGLSGDA | ATEANSY IDYAINALI* |
| 22. POLIM119 UID UIA | MKTPLTEAVAAAD | OGREL SNTEVOAA | SGRENRAKASLE | AAKAL TSKADS | I VNGAAOAVYSKEP | YTTOMEGSNYSAT | PEGKAKCSRDVGYYLRMI | TYCL VAGGTGPMDDY | LIAGUDEL | NRTEEL SPSWYVEALKE | IKANHGI SGDA | ATEANSY IDVAINAL I* |
| 23. DOOMTTO_IIIA_IIIA | METRITEAVAAAD | OCREL SNTEVOAA | SCRENDAKASI E | AAVALTSKADS | U VNGAAOAVVSKED | VTTOMEGENVEAT | DECKAKCS RDVGVVI PMI | TYCL VAGGTGRMDDY | LINGLDEL | NOTEEL COCHAVEAL KE | LKANHGI SGDA | ATEANSY IDVALNAL I* |
| 24. K59915_IIId_IIIA | NIK TPETEAVAAAD | OCDEL SNTEVQAA | SCRENDAKASLE. | AAKAL TOKAD | | VITTOME CONVERT | PEGKARCSRDVG11ERMI | TYCL WASGTGPWDD | LIAGLACI | NRTFEESF SHIVEALKI | IKANIIGE SODA | ATE ANGY I DYA I NALTA |
| 25. WH8102_IIIa_IIIA | MKTPLTEAVAAAD | SQGRELSNIEVQAA | SGRENRARASLE. | AARALISKAD | LVNGAAQAVTIKEP | TTTQMEGPINTSAT | PEGKSKCSRDVGTTERMI | TYCEVAGGTGPMDDT | LIAGLAET | NRIFELSPSWIVEALKE | INSINHGE SGDA | ATEANSTIDTAINALI* |
| 26. WH8103_IIIa_IIIA | MKTPLTEAVAAAD | SQGRELSNIEVQAA | SGRENRAKASLE | AAKALISKADS | LVNGAAQAVYSKEP | YTTQMEGSNYSAT | PEGKAKCSRDVGYYLRMI | TYCEVAGGTGPMDDY | LIAGEDET | NRTFELSPSWYVEALKE | TRANHGE SGDA | ATEANSY IDYATNALT* |
| 27. A15-28_IIIb_IIIA | MKTPLTEAVAAAD | SQGR F L SNTEVQAA | SGRENRAKASLE | AAKALTSKADA | LVNGAAQAVYSKEP | YTTQMEGSNYSAT | PEGKAKCSRDVGYYLRMI | TYCLVAGGTGPMDDY | LIAGLDEI | NRTFELSPSWYVEALKE | IKANHGL SGDA/ | ATEANSY IDYA I NAL I * |
| 28. MITS9220_CRD1_CRD1A | MKTPLTEAVAAAD | SQGR F L TNAE VQAA | SGRETRAKASLE | AAKALTSKGDA | LVNGAAQAVYTKFP | FTTQMEGSNYAST | TEGKAKCSRD I GYYLRMV | TYCLVAGGTGPMDDY | LIAGLAEI | NRTFELSPTWYVEALKE | IKANHGL SGDA/ | ATEANSYLDYAINALI* |
| 29. BIOS-U3-1_CRD1_CRD1B | MKTPLTEAVAAAD | AQGR F L SNTEVQAA | SGRFIRAKASLE. | AAKAL SAKADT | LVNGAAQAVYTKFP | YTTQMEGANYSAT | TEGKAKCSRDVGYYLRMV | TYCL VAGGTGPMDD Y | LIAGLDEI | NRTFELSPSWYVEALKE | IKANHGLSGDA/ | ATEANSYLDYATNALT* |
| 30. BIOS-E4-1 CRD1 CRD1C | MKTPLTEAVAAAD | OGRELTNAEVQAA | SGRETRAKASLE | AAKALTAKGDA | LVNSAAQAVYTKEP | FTTQMEGSNYAST | TEGKAKCSRD I GYYLRMV | TYCLVAGGTGPMDDY | LIAGLAET | NRTFELSPTWYVEALKE | IKANHGL SGDA/ | ATEANSYLDYAINALI* |
| | | | | | | | | | | | | |
| B. RpcB | | | | | | | | | | | | |
| B. RpcB | 1 10 | 20 | 30 40 | 50 | 60 | 70 80 | 90 100 | 110 | 120 | 130 140 | 150 | 160 173 |
| B. RpcB | | | 30 40 | 50 | | | 90 100 | | 120 | 130 140 | 150 DEAGLESSOCAS | 160 173 |
| B. RpcB | 1 10 MEDAFTKVVAQADA | 20 RGQFI SASEIDALAA | 30 40 MVSGSNKRLDAV | 50 SR I SNNAST I VA | 60 NAARELFAQQPALIS | 70 80 PGGNAYTSRRMAAC | 90 100 LIRDME I I LRYVTYSAFTGG | 110 ASVLEDRCLNGLRETT | 120 LALGTPGT | 130 140 SVATGVNLMKDAALSI VN | 150 DSAGI SSGDCASI | 160 173 LSSE IGTYFDRAAASVA* |
| B. RpcB | 1 10 MFDAFTKVVAQADAI MFDAFTKVVAQADAI | 20 RGQF I SASE I DALAA RGQF I STSE I DALAA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV | 50 SR I SNNAST I VA SR I SNNAST I VA | 60 NAARELFAQQPALIS SAARELFAQQPALIS | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LRDME I LRYVTYSAFTGC LRDME I LRYVTYSAFTGC | 110 ASVLEDRCLNGLRETT ASVLEDRCLNGLRETT | 120 LALGTPGT LALGTPGT | 130 140 SVATGVNLMKDAAL SI VN SVAAGVNLMKDAAL SI VN | 150 DSAGTSSGDCAS DRAGTSNGDCAS | 160 173 LSSE I GTYFDRAAASVA* LSSE I GTYFDRAAASVA* |
| B. RpcB 1. cc9311_la_IA 2. WH8020_la_IA 3. MWR-18-1_lb_IA | 1 10 MFDAFTKVVAQADAI MFDAFTKVVAQADAI MFDAFTKVVAQADAI | Z0 RGQF I SASE I DALAA RGQF I STSE I DALAA RGQF I SANE I DALAA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV | 50 SR I SNNAST I VA SR I SNNAST I VA SR I SNNAST I VA | 60 NAARELFAQQPALIS SAARELFAQQPALIS NAARQLFAQQPALIS | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LIRDME I LIRVYTYSAFTGD LIRDME I LIRVITYSAFTGD | 110 ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY | 120 LALGTPGT LALGTPGT LALGTPGA | 130 140 SVATGVNLMKDAAL STVN SVAAGVNLMKDAAL STVN SVATGVNLMKDAAL STVN | 150 DSAGI SSGDCASI DRAGI SNGDCASI DSAGI SSGDCASI | 160 173 LSSE I GTYFDRAAASVA* LSSE I GTYFDRAAASVA* |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. MVIR-18-1_lb_IA 4. PR05-9-1_lb_IA | 1 10 MFDAFTKVVAQADAI MFDAFTKVVAQADAI MFDAFTKVVAQADAI MFDAFTKVVAQADAI | 20 RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SANE I DALAA RGQF I SASE I DALAA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV | 50 SR I SNNAST IVA SR I SNNAST IVA SR I SNNAST IVA SR I SSNAST IVA | 60 NAARELFAQQPALIS SAARELFAQQPALIS NAARQLFAQQPALIS NAARELFAQQPALIS | 70 80 PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC | 90 100 LRDME I LRYVTYSAFTGU LRDME I LRYVTYSAFTGU LRDME I LRYTYSAFTGU LRDME I LRY I TYSAFTGU | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET | 120 'LALGTPGT 'LALGTPGT 'LALGTPGA 'LALGTPGA | 130 140 SVATGVNLMKDAAL S I VN SVASVVLMKDAAL S I VN SVATGVULMKDAAL S I VN SVATGVLMKDAAL S I VN | 150 DSAGI SSGDCASI DSAGI SSGDCASI DSAGI TNGDCASI DSAGI TNGDCASI | 160 173 LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSELGTYFDRAAASVA* |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WWR-18-1_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA | 1 MFDAFTKVVÁQADA MFDAFTKVVAQADA MFDAFTKVVAQADA MFDAFTKVVAQADA | 20 RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SSSE I DALSA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV MVSDSDKRLDAV | 50 SRISNNASTIVA SRISNNASTIVA SRISNNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAARELFAQOPALIS NAARELFAQOPALIS NAARELFAQOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LIROME I LIRVYTYSAFTG LIROME I LIRVYTYSAFTG LIROME I LIRVYTYSAFTG LIROME I LIRVYTYSAFTG | 110 ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLDDRCLNGLRETY | 120 'LALGTPGT 'LALGTPGT 'LALGTPGA 'LALGTPGA 'LALGTPGA | 130 140 SVATGVNLMKDAALS I VN SVATGVNLMKDAALS I VN SVATGVSLMKDAALS I VN SVATGVSLMKDAALS I VN | 150 DSAG I SSGDCASI DSAG I SNGDCASI DSAG I SSGDCASI DSAG I TNGDCASI DKAG I SSGDCSSI | 160 173 LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. MVIR-18-1_lb_IA 4. PR053-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_Jb_IA | 1 10 MEDAF TKVVAQADAI MEDAF TKVVAQADAI MEDAF TKVVAQADAI MEDAF TKVVAQADAI MEDAF TKVVAQADAI | 20 RGQFI SASEI DALAA RGQFI STSEI DALAA RGQFI SASEI DALAA RGQFI SASEI DALSA RGQFI SSSEI DALSA | 30 40 MVSGSNKRLDAVS MVSGSNKRLDAVS MVSGSNKRLDAVS MVSGSNKRLDAVS MVSDSKRLDSVS | 50 SR I SNNAST I VA SR I SNNAST I VA SR I SNNAST I VA SR I SSNAST I VA SR I SSNAST I VA SR I SSNAST I VA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAAROLFAQOPALIS NAAROLFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LRDMETTLRVYTYSAFTG LRDMETTLRVYTYSAFTG LRDMETTLRVTYSAFTG LRDMETTLRVTYSAFTG LRDMETTLRVTYSAFTG LRDMETTLRVTYSAFTG | 110 ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLDDRCLNGLRETY | 120 LALGTPGT LALGTPGT LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGVNLMKDAALS I VN SVATGVNLMKDAALS I VN SVATGVNLMKDAALS I VN SVATGVSLMKDAALS I VN SVATGVSLMKDAALS I VN SVAGVSLMK FAALA I N | 150 DSAGI SSGDCASI DRAGI SNGDCASI DSAGI SSGDCASI DSAGI TNGDCASI DKAGI SSGDCSSI DKAGI SSGDCSSI | 160 173 LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAAAVA+ |
| B. RpcB 1. CC9311_la_lA 2. WH8020_la_lA 3. WJR-B4_lb_lA 4. PROS-91_lb_lA 4. PROS-91_lb_lA 5. ROS8604_lb_lA 6. SYN20_lb_lA | 1 10 MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI | 20 RGQFI SASE I DALAA RGQFI STSE I DALAA RGQFI SASE I DALAA RGQFI SASE I DALSA RGQFI SSSE I DALSA RGQFI SSSE I DALSA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV MVSDSDKRLDAV MVSDSDKRLDSV MVSDSKRLDSV | 50 SRISNNASTIVA SRISNNASTIVA SRISNNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAARELFAQOPALIS NAARELFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LRDME I LRYVYTSAFTGC LRDME I LRYVYTSAFTGC LRDME I LRY I TYSAFTGC LRDME I LRY I TYSAFTGC LRDME I LRYVTSFSAFTGC LRDME I LRYVTSFSAFTGC | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLDDRCLNGLRET ASVLDDRCLNGLRET SVLDDRCLNGLRET | 120 LALGTPGT LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 140 140 SVAT GVINLIM DAALS I VIN SVAT GVINLIM DAALS I VIN SVAT GVINLIM DAALS I VIN SVAT GVINLIM DAALS I VIN SVAAGVINLIM EAALA I VIN SVAAGVINLIM EAALA I VIN | 150 DSAGI SSGDCASI DRAGI SNGDCASI DSAGI SSGDCASI DSAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI | 160 173 LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LSSE IGTYFDRAAASVA* LTSE IGTYFDRAAAVA* LTSE IGTYFDRAAAVA* |
| B. RpcB 1. cc9311_la_IA 2. wHe020_la_IA 3. MVIR-18-1 lb_IA 4. PPG5-9-1 lb_IA 5. ROS8604_lb_IA 6. SYN20_Jb_IA 7. WH8016_lb_IA 8. BL107_JVA_JVA | 1 10 MEDAF TKUVAQADA MEDAF TKUVAQADA MEDAF TKUVAQADA MEDAF TKUVAQADA MEDAF TKUVAQADA MEDAF TKUVAQADA | 20 GQF I SASE I DALAA GQF I SASE I DALAA GQF I SASE I DALAA GQF I SASE I DALSA GQF I SSSE I DALSA GQF I SSSE I DALSA GQF I SSSE I DALAA | 30 40 MVSGSNKRLDAVS MVSGSNKRLDAVS MVSGSNKRLDAVS MVSDSKRLDSV MVSDSKRLDSV MVSDSKRLDSV VVSDSNRLDSV | 50 SRISNIASTIVA SRISNIASTIVA SRISNIASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAARCLFAQOPALIS NAARQLFAQOPALIA NAARQLFAQOPALIA NAARQLFAQOPALIA NAARQLFAQOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LRDMETILRVYTSAFTG LRDMETILRVYTSAFTG LRDMETILRVTSAFTG LRDMETILRVYTSAFTG LRDMETILRVYTSAFTG LRDMETILRVYTSAFTG LRDMETILRVYTSAFTG | 110 ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLDDRCLNGLRETY ASVLDDRCLNGLRETY ASVLDDRCLNGLRETY | 120 'LALGTPGT 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA | 130 140 SVATGVNLMKDAAL SLVN SVATGVNLMKDAAL SLVN SVATGVSLMKDAAL SLVN SVAGVSLMKEAAL SL SVAGVNLMKEAAL SL SVAGVNLMKEAAL SL | 150 DSAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI | 160 173 LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAAAVA+ LSSE IGTYFDRAAAAVA+ LSSE IGTYFDRAAAAVA+ LSSE IGTYFDRAAASVA+ |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WWR-18-1_lb_IA 4. PROS-91_lb_IA 5. ROS&604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA_IVA | 1 10 MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI | 20 RGQ FI SASE I DALAA RGQ FI STSE I DALAA RGQ FI SASE I DALAA RGQ FI SASE I DALSA RGQ FI SSSE I DALSA RGQ FI SSSE I DALSA RGQ FI STSE I DALSA | 30 40 WVSGSNKRLDAV WVSGSNKRLDAV WVSGSNKRLDAV WVSGSNKRLDAV WVSDSDRLDSV WVSDSNRLDAV VVSDSNRLDAV | 50 SRISNNASTIVA SRISNNASTIVA SRISNNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAAROLFAQOPALIS NAAROLFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA | 70 80 PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC PGGNAYTSRIMAAC | 90 100 LRDME I LRYVTYSAFTGC LRDME I LRIVTYSAFTGC LRDME I LRVTYSAFTGC LRDME I LRVTYSAFTGC LRDME I LRVTYSAFTGC LRDME I LRVTYSAFTGC LRDME I LRVTYSVFTGC LRDME I LRVTYSVFTGC | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCNGLRET ASVLDDRCNGLRET ASVLDDRCLNGLRET ASVLDDRCLNGLRET ASVMEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVSLIMCDAALS I VN SVAGVSLIMC BALALI VN SVAGVNLIMC BALALI VN SVAGVNLIMCDAAL BMVN | 150 DSAG I SSGDCASI DRAG I SNGDCASI DSAG I SSGDCASI DSAG I SSGDCASI DSAG I SSGDCASI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SSGDCSSI | 160 173 LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ |
| B. RpcB 1. cc9311_la_A 2. wr8020_ls_LA 3. wr8020_ls_LA 4. procs-91_lb_LA 4. procs-91_lb_LA 5. srx20_lb_LA 7. wr8016_lb_LA 8. BL107_IVa_IVA 9. cc29902_IVa_IVA 10. 415-44_lla_ILA | 1 10 MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI MEDAETIK WAQADAI | 20 ROOFISASEIDALAA ROOFISASEIDALAA ROOFISASEIDALAA ROOFISASEIDALSA ROOFISSSEIDALSA ROOFISSSEIDALSA ROOFISSSEIDALAA ROOFISTSEIDALAA | 30 40 MVSGSNRLDAV MVSGSNRLDAV MVSGSNRLDAV MVSDSNRLDAV MVSDSNRLDAV VVSDSNRLDAV VVSDSNRLDAV VVSDSNRLDAV | 50 SRISNNASTIVA SRISNNASTIVA SRISNNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 NAARELFACOPALIS SAARELFACOPALIS NAAROLFACOPALIS NAAROLFACOPALIA NAAROLFACOPALIA NAAROLFACOPALIA NAAROLFACOPALIA NAAROLFACOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC | 90 100 LEDME ILLRYVTYSAFTOC LEDME ILLRYVTYSAFTOC LEDME ILLRYTYSAFTOC LEDME ILLRYTYSAFTOC LEDME ILLRYVTYSAFTOC LEDME ILLRYVTYSAFTOC LEDME ILLRYVTYSFTOC LEDME ILLRYVTYSFTOC | 110 ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLEDRCLNGLRETY ASVLDDRCLNGLRETY ASVLDDRCLNGLRETY ASVLDDRCLNGLRETY ASVMEDRCLNGLRETY ASVMEDRCLNGLRETY | 120 'LALGTPGT 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA 'LALGTPGA | 130 140 SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAAGVILINK EAALAI I NI SVAAGVILINK EAALAI I NI SVAAGVILINK BAALAI MIN SVAS GWILINKDAAL BINNI SVAS GWILINKDAAL BINNI | 150 DSAGI SSGDCASI DSAGI SNGDCASI DSAGI SSGDCASI DSAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI DRNG I TAGDCASI DRSGI TAGDCASI | 160 173 LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMAVA+ LSSE IGTYFDRAMAVA+ LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMAVA+ |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WIXF.18-1_Ib_IA 4. PROS-9-1_Ib_IA 5. ROS&60A_Ib_IA 6. SYN20_lb_IA 7. WH8016_Ib_IA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_IIa_IIA 11. KORPDE52_IIIa_IIA | 1 MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI MEDAFTKVVAQADAI | 20 RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SASE I DALAA RGQF I SSSE I DALSA RGQF I SSSE I DALSA RGQF I STSE I DALAA RGQF I STSE I DALAA RGQF I STSE I DALAA RGQF I DALAA | 20 40 WYSGSNKRLDAW WYSGSNRRLDAW WYSGSNRRLDAW WYSDSDRLDSW WYSDSDRRLDSW WYSDSDRRLDSW WYSDSNRLDAW WYSDSNRLDAW WYSDSNRLDAW | 50 SR I SNIAST I VA SR I SNIAST I VA SR I SNIAST I VA SR I SNIAST I VA SR I SSNAST I VA SR I SSNASS I VA | 60 NAARELFAQOPALIS SAARELFAQOPALIS NAAROLFAQOPALIS NAAROLFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA NAAROLFAQOPALIA SAAROLFAQOPALIA DAAROLFAQOPALIA | 70 80 PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC PGGIAYTSRIMAAC | 90 100 LRDME I LRYVTYSAFTGC LRDME I LRYVTYSAFTGC LRDME I LRYTYSAFTGC LRDME I LRYTYSAFTGC LRDME I LRYVTYSAFTGC LRDME I LRYVTYSAFTGC LRDME I LRYVTYSFTGC LRDME I LRYVTYSFTGC LRDME I LRYVTYSFTGC | 110 ASVLEDRCLNGLRETM ASVLEDRCLNGLRETM ASVLEDRCLNGLRETM ASVLEDRCLNGLRETM ASVLDDRCLNGLRETM ASVLDDRCLNGLRETM ASVMEDRCLNGLRETM ASVMEDRCLNGLRETM | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVSLIMCDAALS I VN SVATGVNLIMC BALAI VN SVAAGVNLIMC BALAI VN SVASGVNLIMCDAAL BINN SVASGVNLIMCDAAL BINN SVASGVNLIMCDAAL BINN | 150 DSAG I SSGDCASI DSAG I SNODCASI DSAG I SNODCASI DSAG I TNODCASI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SAGDCASI DKAG I SAGDCASI | 160 173 LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ LSSE IGTYFDRAAASVA+ |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR184-l_b_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 6. SYN20_lb_IA 8. BL107_VA_IVA 9. BL107_VA_ | 1 10 MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA MEDAETKVVAQADA | 20 GOF I SASE I DALAA GOF I SASE I DALAA GOF I SASE I DALAA GOF I SSSE I DALSA GOF I SSSE I DALSA GOF I SSSE I DALSA GOF I STSE I DALAA GOF I STSE I DALAA GOF I STSE I DALAA GOF I STSE I DALAA | 30 40 MVSGSNKRLDAV MVSGSNKRLDAV MVSGSNKRLDAV MVSDSDKRLDSV MVSDSDKRLDSV VVSDSNKRLDAV VVSDSNKRLDAV MVSDSNKRLDAV | 50 SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASTIVA SELSINASSIVA SELSINASTIVA | 60 NAARELFAOQPALIS SAARELFAOQPALIS NAAROLFAOQPALIS NAAROLFAOQPALIS NAAROLFAOQPALIA NAAROLFAOQPALIA NAAROLFAOQPALIA SAAROLFAOQPALIA SAAROLFAOQPALIA | 70 80 PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC PGGNAYTSRRIMAAC | 90 100 LEDKE IL RWY 15 AFTG LEDKE IL RWY 15 AFTG | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVMEDRCLNGLRET SSVMEDRCLNGLRET SSVMEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVAT GYNLINKDAAL 5 IVX VARGYNLINKDAAL 5 IVX SVAT GYNLINKDAAL 5 IVX SVAT GYNLINKDAAL 5 IVX SVAGYNLINK FAALAI IN SVAGYNLINK FAALAI INX SVAGYNLINK FAALAI INX SVAGYNLINK FAALAI INX SVAGYNLINK FAALAI INX SVAGYNLINK FAALAI INX SVAGYNLINK FAALAI INX | 150 DSAGI SSOCASI DSAGI SSOCASI DSAGI SSOCASI DSAGI TNGCASI DKAGI SSOCSI DKAGI SSOCSI DRNGI TAGCASI DKAGI TAGCASI DKAGI TAGCASI DKAGI TAGCASI | 190 173 LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA LSSE IGTYFORAMSVA |
| B. RpcB 1. CC9311_la_lA 2. WH8020_la_lA 3. WIR-18-1_lb_lA 4. PROS-91_lb_lA 5. ROS&604_lb_LA 6. SYN20_lb_LA 7. WH8016_lb_LA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_lla_lIA 11. KORD-52_lla_lIA 12. M16.1_IVA_IVA | 1 10 MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA | 20 GGOF ISASE IDALAA GGOF ISASE IDALAA GGOF ISASE IDALAA GGOF ISASE IDALSA GGOF ISSSE IDALSA GGOF ISSSE IDALSA GGOF ISSSE IDALSA GGOF ISSSE IDALAA GGOF ISSSE IDALAA GGOF ISSSE IDALAA GGOF ISSSE IDALAA GGOF ISSSE IDALAA | 20 40 WYSGSNRIDAW WYSGSNRIDAW WYSGSNRIDAW WYSDSNRIDAW WYSDSNRIDAW WYSDSNRIDAW WYSDSNRIDAW WYSDSNRIDAW WYSDSNRIDAW | 50 SRISNNASTIVA SRISNNASTIVA SRISNNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA SRISSNASTIVA | 60 SAARELEFAQOPALIS SAARELEFAQOPALIS NAARELEFAQOPALIS NAARELEFAQOPALIS NAARELEFAQOPALIA NAARELFAQOPALIA NAARELFAQOPALIA SAARELFAQOPALIA SAARELFAQOPALIS SAARELFAQOPALIS SAARELFAQOPSLIS | 70 80 PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC | 90 100 LEDME I LRVYTYSAFTO LEDME I LRVTYSAFTO LEDME I LRVTYSAFTO | 110 ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET ASVL EDRCLINGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGVNLIMCDAAL 51 VN SVATGVNLIMCDAAL 51 VN SVATGVNLIMCDAAL 51 VN SVATGVSLIMCDAAL 51 VN SVATGVSLIMCBAAL 51 VN SVAGVSLIMCBAAL 51 VN SVAGVSLIMCBAAL 51 VN SVAGVNLIMCBAAL 51 VN SVAGVNLIMCBAAL 51 VN SVAGVNLIMCBAAL 51 VN SVAGVNLIMCBAAL 51 VN SVAGVNLIMCBAAL 51 VN | 150 DSAG I SSGDCASI DSAG I SNGDCASI DSAG I SNGDCASI DSAG I TNGDCASI DKAG I SSGDCSSI DKAG I SSGDCSSI DKAG I SAGDCASI DKAG I SAGDCASI DKAG I SAGDCASI DKAG I SAGDCASI | 160 173 LSSE (GTYPDRAASSVA= LSSE (GTYPDRAASSVA= LSSE (GTYPDRAASSVA= LSSE (GTYPDRAASSVA= LSSE (GTYPDRAASVA= LSSE (GTYPDRAASVA= LSSE (GTYPDRAASVA= LSSE (GTYPDRAASVA= LSSE (GTYPDRAASVA= LSSE (GTYPDRAASVA= |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR-18-1_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVa_IA 9. CC9902_IVA_IAA 10. A15-44_lb_IA 11. KORCH-52_lb_IAA 11. KORCH-52_lb_IAA 11. KORCH-52_lb_IAA 13. MK1_IB_IAA | 1 10 HEDAFT XV ANADDA HEDAFT XV ANADDA | 20 GOPE 1545E1DALAA GOPE 1545E1DALAA GOPE 1545E1DALAA GOPE 1545E1DALAA GOPE 1555E1DAL5A GOPE 1555E1DAL5A GOPE 1555E1DALAA GOPE 1575E1DALAA GOPE 1575E1DALAA GOPE 1575E1DALAA GOPE 1575E1DALAA | 30 40 WYSGSNKRLDAW WYSGSNKRLDAW WYSGSNKRLDAW WYSDSDKRLDSW WYSDSDKRLDSW WYSDSNKRLDAW WYSDSNKRLDAW WYSDSNKRLDAW WYSDSNKRLDAW WYSDSNKRLDAW | 50 SELSNIASTIVA SELSNIASTIVA SELSNIASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA | 60 SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS MARCIEFACOPALIS MARCIEFACOPALIA MARCIEFACOPALIA MARCIEFACOPALIA SAATOLFACOPALIA SAATOLFACOPALIA SAATOLFACOPALIA SAATOLFACOPALIA SAATOLFACOPALIA | 70 80 Pedia Art SRIMAAA Pedia Art SRIMAAA | 90 100 LEDWE 11. RVV 17: SAFT 00 LEDWE 11. RVV 17: SAFT 00 | 110 AVLEDRCLAGERT AVLEDRCLAGERT AVLEDRCLAGERT AVLDRCLAGERT AVLDRCLAGERT AVLDRCLAGERT AVLDRCLAGERT SAWEDRCLAGERT SAWEDRCLAGERT SAWEDRCLAGERT SAWEDRCLAGERT SAWEDRCLAGERT | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVAT GVILINICDAL 5 IV0 SVAC VILINICDAL 5 IV0 SVAT GVILINICDAL 5 IV0 | 150 DSAGI SSGDCASI DRAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI TAGDCASI DKAGI TAGDCASI DKAGI SAGDCASI DKAGI SAGDCASI DKAGI SAGDCASI | 160 173 LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA LSSE IGTYFDRAAASVA |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WIR-18-1 lb_IA 4. PROS-91-lb_IA 5. ROS&604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA 9. CC9902_IVA_IVA 10. A15-44_IIa_IIA 11. KORD-52_IIa_IIA 12. W161_IIa_IIA 13. RS9907_IIa_IIA 14. RS9907_IIa_IIA 15. RS9907_IIa_IIA 15. RS9907_IIa_IIA 15. RS9907_IIA_IIA 16. | 1 10 MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA | 20 GGF I SASE I DALAA GGF I STSE I DALAA GGF I STSE I DALAA GGF I SSSE I DALSA GGF I SSSE I DALSA GGF I STSE I DALAA GGF I STSE I DALAA | 30 40 WYSGSNKRLDAW WYSGSNRLDAW WYSGSNRLDAW WYSDSDRLDSW WYSDSDRLDSW WYSDSNRLDAW WYSDSNRLDAW WYSDSNRLDAW WYSDSNRLDAW WYSDSNRLDAW WYSDSNRLDAW | 50 STISNIASTIVA STISNIASTIVA STISNIASTIVA STISNIASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA STISSNASTIVA | 60 SAAREELFAOOPALIS SAAREELFAOOPALIS NAARIOLFAOOPALIS NAARIOLFAOOPALIS NAARIOLFAOOPALIA NAARIOLFAOOPALIA NAARIOLFAOOPALIA SAARIOLFAOOPALIA SAARIOLFAOOPALIA SAARIOLFAOOPALIA SAARIOLFAOOPALIA SAARIOLFAOOPALIA SAARIOLFAOOPALIA | 70 80 PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC PGGNAYTSRRIMAC | 90 100 LEDME I LRYYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSAFTOL LEDME I LRYTYSFTOL LEDME I LRYTYSFTOL | 110 ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET SWLEDRCLMGLRET ASWLEDRCLMGLRET ASWLEDRCLMGLRET ASWLEDRCLMGLRET ASWLEDRCLMGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVNLMKDAAL 51 VM SVATGVNLMKDAAL 51 VM SVATGVSLMKDAAL 51 VM SVATGVSLMKDAAL 51 VM SVAGVNLMKDAAL 51 VM SVAGVNLMKDAAL 51 VA SVAGVNLMKDAAL 51 AA SVAGVNLMKDAAL 51 AA SVAGVNLMKDAAL 51 AA | 150 DSAG ISSGDCASI DRAG ISSGDCASI DSAG ISSGDCASI DSAG ISSGDCASI DSAG ISSGDCSSI DRAG ISSGDCSSI DRAG ISSGDCSSI DRAG ISAGDCASI DRAG ISAGDCASI DRAG ISAGDCASI DRAG ISAGDCASI DRAG ISAGDCASI DRAG ISAGDCASI | 160 173 LSSE (GTYPDRAMASVA= LSSE (GTYPDRAMASVA |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR184_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_lb_IIA 11. KORDL'52_lla_IIA 12. W161_IIA_IIA 13. RS9902_llA_IIA 14. RS9902_llA_IIA 15. TAK9802_llA_IIA | 1 10 НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА НЕРАКТКУЛАСАВА | 20 GGCF 15 45 E1 DALAA GGCF 15 45 E1 DALAA | 20 40 MVSGSNRIEDAV MVSGSNRIEDAV MVSGSNRIEDAV MVSDDRRIDAV VVSDDRRIDAV VVSDIRRIDAV MVSDIRRIDAV MVSDIRRIDAV MVSDIRRIDAV MVSDIRRIDAV MVSDIRRIDAV | 50 SELSNIASTIVA SELSNIASTIVA SELSNIASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA SELSSNASTIVA | 60 SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA | 70 80 Pediavt serihada Pediavt serihada | 90 100 LEDKE 11. RVV1V3 F100 LEDKE 11. RVV1V3 F100 LEDKE 11. RV1V3 F100 LEDKE 11. RV1 1V3 F100 LEDKE 11. RV1V3 F100 | 110 ASVLE BORCLANGLEFT ASVLE BORCLANGLEFT ASVLE BORCLANGLEFT ASVLE BORCLANGLEFT ASVLE BORCLANGLEFT ASVLEBORCLANGLEFT ASVMEDRICLANGLEFT ASVMEDRICLANGLEFT ASVMEDRICLANGLEFT ASVMEDRICLANGLEFT | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA VATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA SVATGVILIMICAALS IVA | 150 DSAGI SSGDCASI DRAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI SSGDCSSI DKAGI TAGDCASI DKAGI TAGDCASI DKAGI SAGDCASI DKAGI AGDCASI DKAGI AGDCASI DKAGI AGDCASI | 160 173 1555 1677 FDI AMAS VA 1558 1677 FDI AMAS VA |
| B. RpcB 1. CC9311_la_IA 2. WH800_la_IA 4. PRO5-9-1 lb_IA 4. PRO5-9-1 lb_IA 5. PRO58604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVa_IVA 9. CC9902_IVa_IVA 9. CC9902_IVa_IVA 10. A15-44_IIa_IIA 11. KORDI-52_IIa_IIA 12. M161_IIa_IIA 13. RS9902_IIa_IIA 14. RS9907_IIa_IIA 15. TAK\$8027_IIa_IIA 16. WH8109_IIa_IIA | 1 10 10 HEAFTWARDA MEDAFTWARD | 20 GGF I SASE I DALAA GGF I SASE I DALAA GGF I SASE I DALAA GGF I SSSE I DALSA GGF I SSSE I DALSA GGF I SSSE I DALSA GGF I SSSE I DALAA GGF I STSE I DALAA | 30 40 MVSGSNRLDAW MVSGSNRLDAW MVSGSNRLDAW MVSDSDRLDSV MVSDSDRLDSV MVSDSDRLDSV MVSDSNRLDAW | 50 R I SNNAST I VA R I SNNAST I VA R I SNNAST I VA R I SSNAST I VA R | AAAHELFAQOPALIS SAAAHELFAQOPALIS SAAAHELFAQOPALIS NAAAHELFAQOPALIS NAAAHELFAQOPALIS NAAAHELFAQOPALIA NAAAHELFAQOPALIA SAAHELFAQOPALIA SAAHELFAQOPALIA SAAHELFAQOPALIA SAAHELFAQOPALIA SAAHELFAQOPALIA SAAHELFAQOPALIA | 70 80 PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAAC PGGNAYTSRRMAC PGGNAYTSRRMAC PGGNAYTSRRMAC PGGNAYTSRRMAC PGGNAYTSRRMAC PGGNAYTSRRMAC PGGNAYTSRRMAC | 90 100 LEDME IL RVY VSAFTOC LEDME IL RVY VSAFTOC | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGVILMICAALS IVI SVATGVILMICAALS IVI SVATGVILMICAALS IVI SVATGVILMICAALS IVI SVAGVILMICAALS IVI S | 150 DSAG I SSGDCASI DRAG I SSGDCASI DSAG I SSGDCASI DSAG I SSGDCSSI DRAG I SSGDCSSI DRAG I SSGDCSSI DRAG I TAGDCASI DRAG I TAGDCASI DRAG I AGDCASI DRAG I AGDCASI DRAG I AGDCASI DRAG I AGDCASI | 160 173 LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMAVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ LSSE (GTYPDRAMSVA+ |
| B. RpcB 1. CC9311_la_lA 2. WH8020_la_lA 3. WWR-181_lb_lA 4. PROS-9-1.lb_lA 5. ROS&604_lb_lA 6. SYN20_lb_LA 7. WH8016_lb_LA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_lB_1IA 11. KORD-52_lB_1IA 12. W16.1_IB_1IA 13. RS9907_IB_1IA 14. RS9907_IB_1IA 15. TAKP802_IB_1IA 16. WH8109_IB_1IA 16. WH8109_IB_1IA 16. WH8109_IB_1IA | 1 10 MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA MEDAFTKVVA/ADA | 20 GGPE 15A5E I DALAA (GGPE 15A5E I DALAA (GGPE 15A5E I DALAA (GGPE 15A5E I DALAA (GGPE 15S5E I DALSA (GGPE 15S5E I DALAA (GGPE 15T5E I DALAA | 20 40 WVSGSNREDAV WVSGSNREDAV WVSGSNREDAV WVSGSNREDAV WVSDSNREDAV WVSDSNREDAV WVSDSNREDAV WVSDSNREDAV WVSDSNREDAV WVSDSNREDAV | 50 1 SINIAST IVA 2 I SINIATI IVA 2 I | 60 SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA | 70 SR0 PeGlayt SRIMAA PeGlayt SRIMAA | 90 100 LEDUE IL LRYVYSAFTGU LEDUE IL LRYVYSAFTGU LEDUE IL LRYVYSAFTGU LEDUE IL LRYVYSAFTGU LEDUE IL LRYVYSAFTGU LEDUE IL LRYVYSAFTGU LRDUE IL LRYVYSAFTGU | 10 ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT ASVLEDRCLAGGERT SSVLEDRCLAGGERT SSVLEDRCLAGGERT | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVINLIMCDAALS IVN SVAGVINLIMCDAALS IVN SVATGVINLIMCDAALS INN SVATGVINLIMCDAALS INN SVATGVINLIMCDAALS INN SVAGVINLIMCDAALS INN SVATGVINLIMCDAALS INN SVAGVINLIMCDAALS INN SVAGVINLIMCDAALS INN SVAGVINLIMCDAALS INN | 150 DEAGI SSCDCAS DEAGI SSCDCAS DEAGI SSCDCAS DEAGI SSCDCAS DEAGI SSCDCSS DRAGI SSCDCSS DRAGI SSCDCSS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS DRAGI SACDCAS | 160 173 LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAAVA* LSSE IGTYEDRAAAVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* LSSE IGTYEDRAAASVA* |
| B. RpcB 1. CC9311 Ja JA 2. WH8020 Ja JA 3. WMR 18-1 Jb JA 4. R0380-1 Jb JA 4. R0380-1 Jb JA 6. SVA20 Jb JA 6. SVA20 Jb JA 6. SVA20 Jb JA 8. BL107 JVa JVA 9. CC9902 JVa JVA 9. CC9902 JVa JVA 10. 415-44 Jla JIA 11. KORDI-52 Jia JIA 12. M16.1 Ja JIA 13. RS9902 JIa JIA 14. RS9907 JIa JIA 15. TAKS802 JIa JIA 15. TAKS802 JIa JIA 16. WH8109 JIa JIA 17. A15-62 JIC JIA | 1 10 10 HEDA FTVVACADA 10 HEDA | 20 GGP I SASE I DALAA GGP I SASE I DALAA GGP I SASE I DALAA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALAA GGP I STSE I DALAA | 20 40 MVSGSNRLDAV MVSGSNRLDAV MVSGSNRLDAV MVSDSDRLDSV MVSDSDRLDSV MVSDSDRRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV | R I SNNAST I V R I SNNAST IV SI SNNAST IV SI SNNAST IV SI SSNAST IV SI SSNASS IV SI SSNAST IV SI | 20 SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS NAATELFACOPALIA NAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA | 70 80 PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC PGGVAYTSRRIMAC | 90 100 LEDME IL RVV1YSAFTOC LEDME IL RVV1YSAFTOC LEDME IL RV1YSAFTOC LEDME IL RV1YSAFTOC LEDME IL RV1YSAFTOC LEDME IL RVV1YSAFTOC LEDME IL RVV1YSAFTOC | 10 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVAT GWILINKDAAL 5 I VI SVADGWILINK BALAI I IN SVADGWILINK BALAI I IN SVADGWILINK BALAI I VI SVADGWILINK BALAI I VI SVADGWILINK BALAI I VI SVADGWILINK BALAI VI | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TNOCCASI DSAGI TNOCCASI DRAGI SSCDCSSI DRAGI SSCDCSSI DRAGI TACDCASI DRAGI TACDCASI DRAGI TACDCASI DRAGI AACCASI DRAGI AACCASI DRAGI SACCASI DRAGI SACCASI DRAGI SACCASI DRAGI SACCASI | 160 173 LSSE IGTYFDRAMSVA+ LSSE IGTYFDRAMSVA+ |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR-18-1_lb_IA 4. PROS-91_lb_IA 5. ROS&604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_IIa_IIA 11. KORD-52_IIa_IIA 12. W16.1_IIA_IIA 13. RS9907_IIa_IIA 14. RS9907_IIa_IIA 15. TAKF802_IIa_IIA 16. WH8109_IIa_IIA 16. WH8109_IIa_IIA 17. A15-62_IIC_IIA 18. CC9605_IIC_IIA 19. PROS-04-1_IIA_IIB | 1 10 MEDAFTKVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA MEDAFTVVACADA | 20 GGF I SASE I DALAA GGF I SASE I DALAA GGF I SASE I DALAA GGF I SASE I DALAA GGF I SSE I DALAA | 30 40 WWSGSNRELDAW WWSGSNRELDAW WWSGSNRELDAW WWSDSDRELDSW WWSDSDRELDSW WWSDSDRELDSW WWSDSNRELDAW WWSDSNRELDAW WWSDSNRELDAW WWSDSNRELDAW WWSDSNRELDAW WWSDSNRELDAW | 50 51 SINASTIVA 51 SINASTIVA | 60 SAAREELFACOPALIS SAAREELFACOPALIS NAAREELFACOPALIS NAAREELFACOPALIS NAAREELFACOPALIA NAAREELFACOPALIA NAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA SAAREELFACOPALIA | 70 80 PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG PGGIAYTSRRIMAG | 90 100 LEDME ILRVYTYSAFTOL LEDME ILRVTYSAFTOL LEDME ILRVTYSAFTOL LEDME ILRVTYSAFTOL LEDME ILRVTYSAFTOL LEDME ILRVYTSAFTOL LEDME ILRVYTSAFTOL | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVHEDRCLNGLRET SSWHEDRCLNGLRET SSWHEDRCLNGLRET SSWHEDRCLNGLRET SSWHEDRCLNGLRET SSWHEDRCLNGLRET SSWHEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I VN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVATGVNLIMCDAALS I NN SVAGVNLIMCDAALS I NN SVAGVNLIMCDAALS A NN SVAGVNLIMCDAALS I NN SVAGVNLIMCDAALS A NN SVAGVNLIMCDAALS A NN SVAGVNLIMCDAALS A NN SVAGVNLIMCDAA | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TNCCASI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SACDCASI DKAGI SACDCASI | 160 173 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1556 I GTYPDRAASVA* 1556 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* 1555 I GTYPDRAASVA* |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WH8124-l_b_IA 4. PROS-9-1_lb_IA 5. ROS860_lb_IA 6. SYN20_lb_IA 6. SYN20_lb_IA 8. B1107_VG_IVA 9. B1107_VG_IVA 10. 415-44 lla_IIA 13. RS9902_lla_IIA 14. RS9907_lla_IIA 15. TAK9802_lla_IIA 16. WH8109_IIa_IIA 17. A15-62_llc_IIA 19. PROS-U-1_lIh_IB 20. A15-2_llG_IIA | 1 10 HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA HEDAFTWVARDAA | 20 GGPE1 SASE I DALAA GGPE1 SASE I DALAA GGPE1 SASE I DALAA GGPE1 SASE I DALAA GGPE1 SSSEI DALSA GGPE1 SSSEI DALSA GGPE1 SSSEI DALAA GGPE1 STSEI DALAA | 30 40 MVSGSNRLDAV MVSGSNRLDAV MVSGSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV MVSDSNRLDAV | 50 51 SINAAT IV 20 51 | 20 AMARIELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA | 70 80 PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC PGG14YTSRRIMAC | 90 100 LEDKE IL RYV173AFT0C LEDKE IL RYV173AFT0C | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVAT GYNLINKDAAL 5 I VI SVAT GYNLINKDAAL 5 I AN | 150 DSAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DSAGI TNGCASI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI TAGDCASI DRAGI TAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI | 160 173 155E 167YF0FAMASVA 155E 167YF0FAMASVA |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR-18-1_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_IIa_IIA 11. KORD-52_IIa_IIA 13. RS9907_IIa_IIA 14. RS9907_IIa_IIA 15. TAK7802_IIa_IIA 16. WH8109_IIa_IIA 16. WH8109_IIa_IIA 17. A15-62_IIC_IIA 18. CC9605_IIC_IIA 19. PROS-U-1_IIh_IIB 20. A15-24_IIIa_IIIA | 1 10 MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA MEDAFTKVVACADA | 20 20 20 20 20 20 20 20 20 20 | 30 40 WWSGSNRLDAW WWSGSNRLDAW WWSGSNRLDAW WWSDSDRLDSW WWSDSDRLDSW WWSDSNRLDAW WSSSNRLDAW WSSSNRLDAW WWSDSNRLDAW WWSDSNRLDAW WWSDSNRLDAW WWSDSNRLDAW WWSDSNRLDAW WWSDSNRLDAW | 50 50 51 51 51 51 51 51 51 51 51 51 | 60 SAAREE FAQOPAL IS SAAREE FAQOPAL IS NAARIO FAQOPAL IS NAARIO FAQOPAL IS NAARIO FAQOPAL IS NAARIO FAQOPAL IA NAARIO FAQOPAL IA SAARIO FAQOPAL IA | 70 80 PGGNAYTSRINAAC 90 PGGNAYTSRINAC 90 PGGNAYTSRINAC 90 | 90 100 LEDME I LRWYTYSAFT GC LEDME I LRWYTYSAFT GC LEDME I LRWYTYSAFT GC LEDME I LRWYTYSAFT GC LEDME I LRWYTSAFT GC | 110 SVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVNLMKDAAL 51 VM SVATGVNLMKDAAL 51 VM SVATGVNLMKDAAL 51 VM SVATGVSLMKDAAL 51 VM SVATGVSLMKDAAL 51 VM SVAGVNLMKDAAL 51 VM | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TNGCASI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SACDCASI DKAGI SACDCASI | 160 173 LSSE (GTYPDRAASSVA= LSSE (GTYPDRAASSVA= |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR-18-1_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_V0_JNA 9. CC9902_IV0_JNA 10. A15-04_lb_IA 11. KO16-05_IA 14. RS9902_lb_IA 14. RS9902_lb_IA 14. RS9902_lb_IA 15. TAK9802_lb_IA 15. TAK9802_lb_IA 16. WH8109_Ib_IA 18. CC9605_IC_IA 19. PROS-U-1_IIh_IB 20. A15-24_IIb_IIA 21. A18-40_IIb_IIA 21. A18-40_IIb_IIA 21. A18-40_IIb_IIA | 1 10 INERA FT VVA CARA INERA F | 20 GGPE13A5E1DALAA GGP13T5E1DALAA GGP13A5E1DALAA GGP13A5E1DALAA GGP13A5E1DALAA GGP1355E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA GGP13T5E1DALAA | 20 40 MVSGSNRILDAW MVSGSNRILDAW MVSGSNRILDAW MVSDSDRILDSW MVSDDRILDSW MVSDDRRLDSW MVSDDRRLDSW MVSDSNRILDAW | 50 51 SINA 31 V/ 51 V/ 51 SINA 51 V/ 51 V/ 5 | EQ SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIS SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA SAATELFACOPALIA | 70 80 P GGIAYT SRRMAC D GGIAYT SRRMAC | 90 100 LEDKE IL RYV1Y-SAFTOC LEDKE IL RYV1Y-SAFTOC | 110 AVLE DRCLNGLRET AVLEDRCLNGLRET AVLEDRCLNGLRET AVLEDRCLNGLRET AVLDRCLNGLRET AVLDRCLNGLRET SWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVAT GYNLINKDAAL SI VN YAAGYNLINKDAAL SI VN SVAT GYNLINKDAAL SI VN SVAT GYNLINKDAAL SI VN SVAT GYNLINKDAAL SI VN SVAGYNLINK BALLAI IN SVAGYNLINK BALLAI IN SVAGYNLINK BALLAI NN SVAGYNLINK BALLAI NN | 150 D SAG I S S CDCAS I D SAG I S S CDCAS I D SAG I S CDCAS I D SAG I S CDCAS I D SAG I TACCAS I D SAG I S CDCS SI D SAG I S CDCAS I D S C | 160 173 LSSE IGTYFDRAMSVA- LSSE IGTYFDRAMSVA- |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 4. PRO5-01_lb_IA 4. PRO5-01_lb_IA 5. ROS8604_lb_IA 6. SYR320_lb_IA 7. WH8016_lb_IA 8. BL107_IVa_IVA 9. CC9902_IVa_IVA 9. CC9902_IVa_IVA 9. CC9902_IVa_IVA 10. A15-44_IIa_IIA 11. KORDI-52_IIa_IIA 12. M161_IIa_IIA 13. RS902_IIa_IIA 14. RS902_IIa_IIA 15. TAK9802_IIa_IIA 15. TAK9802_IIa_IIA 16. WH8109_IIa_IIA 17. A15-62_IC_IIA 16. URL BID 16. A15-24_IIIa_IIA 17. A15-62_IC_IIA 16. A15-24_IIIa_IIIA 17. A15-62_IIC_IIA 16. A15-24_IIIA_IIIA 17. A15-62_IIC_IIA 17. A15-62_IIC_IIA 18. A15-74 18. A15-744 18. A15-744 18. A15-744 18. A15-744 | 1 10 MEDAFTWVACADA | 20 GGP I SASE I DALAA GGP I STASE I DALAA | 30 40 MWSGSNRLDAW MWSGSNRLDAW MWSGSNRLDAW MWSDSDRLDSW MWSDSDRLDSW MWSDSDRLDSW MWSDSNRLDAW | 50 51 51 51 51 51 51 51 51 51 51 | NAAREE FAQOPALE IS SAAREE FAQOPALE IS NAAREE FAQOPALE IS NAAREE FAQOPALE IS NAAREE FAQOPALE NAAREE FAQOPALE NAAREE FAQOPALE NAAREE FAQOPALE NAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE SAAREE FAQOPALE | 70 80 PGGNAYTSRRIMAG | 90 100 LEDME I LRVY1YSAFTOL LEDME I LRVY1YSAFTOL LEDME I LRV1YSAFTOL LEDME I LRV1YSAFTOL | 110 SVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET SWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGYNLMKDAAL 51W SVATGYNLMKDAAL 51W SVATGYNLMKDAAL 51W SVATGYNLMKDAAL 51W SVATGYNLMKDAAL 51W SVAGYNLMKCAAL 51W | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TNOCCASI DSAGI TNOCCASI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SACDCASI DKAGI SACDCASI | 160 173 LSSE (GTYFDRAMSVA+ LSSE (GTYFDRAMSVA+ |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR-1B-1_Ib_IA 4. PROS-9-1_Ib_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVa_IVA 9. CC9902_IVa_IVA 9. CC9902_IVa_IVA 10. A15-44_IA_IIA 11. KORD-52_IIa_IIA 12. W16.1_IIa_IIA 13. RS902_IIa_IIA 14. RS902_IIa_IIA 15. TAK9802_IIa_IIA 14. KS902_IIa_IIA 15. TAK9802_IIa_IIA 16. SC505_IIC_IIA 19. PROS-U-1_IIA_IIA 18. CC505_IIC_IIA 19. PROS-U-1_IIA_IIA 22. A18-40_IIB_IIIA 21. A18-40_IIB_IIIA 22. A18-40_IIB_IIIA 23. BOUM118_IIIB_IIIA 24. RS915_IIIA | 1 10 INFORMET VIVANCIDAD INFORMET VIVANCIDAD INF | 20 GGP I 345 E IDALAA GGP I 375 E IDALAA GGP I 375 E IDALAA GGP I 375 E IDALAA GGP I 355 E IDALAA GGP I 355 E IDALAA GGP I 375 E IDALAA | 20 40 MVX5SSNRILDAX MVX5SSNRILDAX MVX5SSNRILDAX MVX5SSNRILDAX MVX5DDRILD5X MVX5DDRILD5X MVX5DDRILD5X MVX5DSNRILDAX MV | 50 15 INAL TI VI 15 | 60 SAARIELFAQDPALIS SAARIELFAQDPALIS SAARIELFAQDPALIS MARIELFAQDPALIS MARIELFAQDPALIS MARIELFAQDPALIA MARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA SAARIELFAQDPALIA | 70 80 P GGIAVT SERIMACA 90 P GGIAVT SERIMACA 90 P GGIAVT SERIMACA 90 | 90 100 LEDBETLRWYTSAFTG LEDBE LLRWYTSAFTG LEDBE LLRWYTSAFTG | 110 AVL EDRCLAGGERT AVL EDRCLAGGERT AVL EDRCLAGGERT AVL EDRCLAGGERT AVL EDRCLAGGERT AVL EDRCLAGGERT AVL EDRCLAGGERT SSWIEDRCLAGGERT SSWIEDRCLAGGERT SSWIEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT AVMEDRCLAGGERT | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVAT GYNLINKDAAL S IVN VARGYNLINKDAAL SIVN | 150 0 546 1 5 500-651 0 546 1 5 500-551 0 546 1 5 500-551 0 546 1 5 500-551 0 546 1 5400-651 0 540 1 5400-651 0 5400 1 5400 1 5400-651 0 5400 1 5400-651 0 5400 1 5400 1 5400 1 5400 1 540000000000 | 190 173 1556 1674 PDF AMAS 184 1558 1574 PDF AMAS 184 1564 1574 PDF AMAS 184 1574 1574 PDF |
| B. RpcB 1. CC9311. Ja JA 2. WH80103. Ja JA 3. WH80103. Ja JA 4. PRG-9. Ja JA 4. PRG-9. Ja JA 4. PRG-9. Ja JA 5. WH8016. Jb JA 6. SYN20. Jb JA 7. WH8016. Jb JA 8. BL107. JVa, JVA 9. CC9902. JVa, JVA 10. 415-44. JIa, JIA 11. KORDI-52. JJa JIA 12. W161. JIA, JIA 13. RS9902. JIa, JIA 14. RS9902. JIa, JIA 15. TAK9802. JIa, JIA 15. TAK9802. JIa, JIA 16. WH8109. JIa, JIA 19. PROS-U-1, JIA, JIA 21. A18-46. JIA, JIA 22. HOLMO, JIA, JIA 23. KOLMO, JIA, JIA 24. KS9915. JIIA, JIIA 24. KS9915. JIIA, JIIA 25. WH81017. JIIA | 1 10 10 HEAFTWARDA 10 HEAFTWARDA | 20 GGP I SASE I DALAA GGP I SASE I DALAA GGP I SASE I DALAA GGP I SASE I DALAA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALAA GGP I SSSE I DALAA | 30 40 wws.csinkrldaw | 50 50 51 51 51 51 51 51 51 51 51 51 | 00 SAAREE FACOPALE IS SAAREE FACOPALE IS SAAREE FACOPALES NAAREE FACOPALES NAAREE FACOPALES NAAREE FACOPALE SAAREE FACOPALE | 70 80 PGGNAYT SRRMAAC 90 PGNAT SRRMAAC | 90 100 LEDME ILRVY1YSAFTOL LEDME ILLRVY1YSAFTOL LEDME ILLRVY1YSAFTOL | 110 ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVLEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET ASVHEDRCLMGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVATGWILMRDAALS IW SVATGWILMRDAALS IW SVATGWILMRDAALS IW SVATGWILMRDAALS IW SVATGWILMRDAALS IW SVAGWILMRDAALS IW | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TSCDCASI DSAGI TSCDCASI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SSCDCSSI DKAGI SACDCASI DKAGI SACDCASI | 160 173 LSSE (GTYPDRAMSVA- LSSE (GTYPDRAMSVA- |
| B. RpcB 1. CC9311_la_IA 2. WH8020_la_IA 3. WJR184_lb_IA 4. PROS-9-1_lb_IA 5. ROS8604_lb_IA 6. SYN20_lb_IA 7. WH8016_lb_IA 8. BL107_IVA_IVA 9. CC9902_IVA_IVA 10. A15-44_IJa_IIA 11. KORD-152_IIa_IIA 12. W161_IIA_IIA 13. RS9902_IIA_IIA 14. RS9907_IIA_IIA 15. TAK9902_IIA_IIA 15. TAK9902_IIA_IIA 16. WH8109_IIA_IIA 16. WH8109_IIA_IIA 17. A15-62_IC_IIA 18. CC9605_IC_IA 19. PROS-1-1_IIA 19. PROS-1-1_IIA 12. A15-22_IIA_IIA 12. A15-22_IIA_IIA 12. A15-22_IIA_IIA 13. PROS-1-1_IIA 14. RS9907_IIA_IIA 14. RS9907_IIA_IIA 15. TAK991_IA_IIA 16. WH8109_IIA_IIA 17. A15-63_IC_IIA 18. CC9605_II-IIA 19. PROS-1-1_IIA 21. A15-22_IIA_IIA 23. WH8102_IIA_IIA 24. RS9915_IIIA_IIA 25. WH8102_IIIA_IIA 25. WH8102_IIIA_IIA 26. WH8102_IIIA_IIA | 1 10 INFORMET VIVANOADO INFORMET VIVANOADO | 20 GGP I 375 E I DALAA GGP I 375 E I DALA GGP I 355 E I DALA GGP I 375 E I DALA | 20 40 MINUSSINRILDAN | 50 15 NA 3 T V 15 SNA 3 T V 15 | 60 SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIS SAAREELFACOPALIA | 70 80 P GGIANT SERIMAAC 90 P GGIANT SERIMAC 90 | 90 100 LEDME ILRWY1YSAFTG LEDME ILRWY1YSAFTG | 110 ASVLEDRCLAGURET | 120 LALGTPGT LALGTPGA | 120 140 VALCOVILING DAAL 5 19 VALCOVILING DAAL 5 VA | 150 D 345 15 300-451 D 345 15 3000-451 D 345 15 300-451 D 345 15 300-451 D 345 15 300-451 D | 190 173 1556 1674 197 1558 1674 197 157 157 157 157 157 157 157 157 157 15 |
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| B. RpcB 1. CC9311_la_JA 2. WH8020_la_JA 3. WJR184-l_b_JA 4. PROS-9-1_lb_JA 5. ROS8604_lb_JA 6. SYN20_lb_JA 6. SYN20_lb_JA 7. B107 VG_JVA 8. B107 VG_JVA 8. B107 VG_JVA 8. B107 VG_JVA 8. B107 VG_JVA 1. MILLA 1. KORDI-52_lb_JIA 1. KORDI-52_JIA 1. | 1 10 NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA NEDA FTV/VACIDA MEDA FTV/VACIDA | 20 GGP I SASE I DALAA GGP I SASE I DALAA GGP I SASE I DALAA GGP I SASE I DALAA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALSA GGP I SSSE I DALAA GGP I SSSE I DALAA | 20 40 MVSGSNRLDAW MVSGSNRLDAW MVSGSNRLDAW MVSDSNRLDAW MVSDSDRLDSW MVSDSDRLDSW MVSDSNRLDAW | 50 51 51 51 51 51 51 51 51 51 51 | AAATELEAOOPALIS SAAATELEAOOPALIS SAAATELEAOOPALIS SAAATELEAOOPALIS SAAATELEAOOPALIS SAAATELEAOOPALIS SAAATELEAOOPALIA SAAATELEAOOPALIA SAAATELEAOOPALIA SAATELEAOOPALIA | 70 80 PGGNAYT SRRMAC 90 PGGNATT SRRMAC 90 <th>90 100 LEDME IL RVV17SAFTGC LEDME IL RVV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RVV17SAFTGC LEDME IL RVV17SAFTGC</th> <th>110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET</th> <th>120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA</th> <th>130 140 SVAT GYNLINKDAAL 5 I VI SVAT GYNLINKDAAL 5 I VI SVAGYNLINK BALAI I I SVAGYNLINKDAAL 6 I SLA SVAGYNLINKDAAL 6 I VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 I VI</th> <th>150 DSAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DSAGI TNGDCASI DSAGI TNGDCASI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI TAGDCASI DRAGI TAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI</th> <th>160 173 LSSE IGTYFDRAMSVA- LSSE IGTYFDRAMSVA-</th> | 90 100 LEDME IL RVV17SAFTGC LEDME IL RVV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RV17SAFTGC LEDME IL RVV17SAFTGC LEDME IL RVV17SAFTGC | 110 ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET ASVLEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET SSWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET ASWIEDRCLNGLRET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 130 140 SVAT GYNLINKDAAL 5 I VI SVAT GYNLINKDAAL 5 I VI SVAGYNLINK BALAI I I SVAGYNLINKDAAL 6 I SLA SVAGYNLINKDAAL 6 I VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 VI SVAGYNLINKDAAL 1 I VI | 150 DSAGI SSGDCASI DSAGI SSGDCASI DSAGI SSGDCASI DSAGI TNGDCASI DSAGI TNGDCASI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI SSGDCSSI DRAGI TAGDCASI DRAGI TAGDCASI DRAGI SAGDCASI DRAGI SAGDCASI | 160 173 LSSE IGTYFDRAMSVA- LSSE IGTYFDRAMSVA- |
| B. RpcB 1. CC9311 Ja JA 2. WH800 Ja JA 4. PROS-9-1 Jb JA 4. PROS-9-1 Jb JA 4. PROS-9-1 Jb JA 5. ROS8604 Jb JA 6. SYN20, Jb JA 7. WH8016 Jb JA 8. BL107 JVa JVA 9. CC9902 JVa JVA 9. CC9902 JVa JVA 9. CC9902 JVa JVA 10. A15-44 JIa JIA 11. KORDI-52 JIa JIA 12. M161 JIA JIA 13. RS902 JIa JIA 14. RS9902 JIa JIA 15. TAK9802 JIa JIA 15. TAK9802 JIa JIA 15. TAK9802 JIa JIA 15. TAK9802 JIa JIA 16. WH8109 JIa JIA 17. A15-62 JIC JIA 19. PROS-11 JIA 12. A18-46 J JIIC JIA 23. BOUM118 JIIA JIA 24. RS9915 JIIA JIIA 25. WH8103 JIIA JIIA 26. WH8103 JIIA JIIA 27. A15-28 JID JIIA 28. MITS9220. CR01a_CR01A 28. MITS9220. CR01a_CR01A | 1 10 MEDAFTKVVACADA | 20 GGP I SASE I DALAA GGP I STS EI DALAA | 30 40 wws.cs.nkr.ldaw | 50 50 51 51 51 51 51 51 51 51 51 51 | AAAREE FAQOPAL I S SAAREE FAQOPAL I | 70 80 PGGNAYTSRINAAC 90 PGGNAYTSRINAC 90 | 90 100 LEDME I LRWYTYSAFT GC LEDME I LRWYTYSAFT GC LEDME I LRWTYSAFT GC | 110 SVL EDRCLAGURET ASVL EDRCLAGURET ASVL EDRCLAGURET ASVL EDRCLAGURET ASVL EDRCLAGURET ASVL EDRCLAGURET ASVLEDRCLAGURET SWEEDRCLAGURET SWEEDRCLAGURET SSWEEDRCLAGURET SSWEEDRCLAGURET SSWEEDRCLAGURET SSWEEDRCLAGURET SSWEEDRCLAGURET SSWEEDRCLAGURET ASWEEDRCLAGURET | 120 LALGTPGT LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA LALGTPGA | 120 140 SVATGVILMICABAL 51W SVATGVILMICABAL 51M SVATGVILMICABAL 51 | 150 DSAGI SSCDCASI DSAGI SSCDCASI DSAGI SSCDCASI DSAGI TNOCCASI DSAGI TNOCCASI DSAGI TNOCCASI DRAGI SSCDCSSI DRAGI SSCDCSSI DRAGI SSCDCSSI DRAGI SSCDCSSI DRAGI SACDCASI DRAGI SACDCASI | 160 173 LSSE (GTYPDRAMSVA- LSSE |

Supplementary Figure 3. Alignment of RpcA and RpcB, encoding phycocyanin a- and β -subunits, from CRD1 and clades I-IV Synechococcus strains. (A)

RpcA. (B) RpcB. Substitutions potentially involved in thermotolerance are shown by a red rectangle in the alignment.



Supplementary Figure 4. Variation with growth temperature of phycobilins and phycobiliproteins fluorescence excitation and emission ratios. (A) Average PUB:PEB ratios. (B) Average phycoerythrin (PE) to phycocyanin (PC) ratios. (C) Average PC to terminal acceptor (TA) ratios. The insert indicates the strain names, their corresponding ESTU (sensu Farrant et al., 2016) and pigment type (sensu Humily et al., 2013) between brackets.



Supplementary Figure 5. Variation with growth temperature of the three main liposoluble pigments per cell for CRD1 vs. clade I and IV strains. (A, D) Chlorophyll (Chl) a content (fg/cell). (B, E) Zeaxanthin (Zea) content (fg/cell). (C, F) β -carotene (β -car) content (fg/cell). (A-C) CRD1-B strain BIOS-U3-1 vs. cold thermotypes. (D-F) CRD1-A strain MITS9220 and CRD1-C strain BIOS-E4-1 vs. warm thermotypes. Inserts indicate the strain names and their corresponding ESTU (*sensu* Farrant et al., 2016) between brackets.



Supplementary Figure 6. Time course of photosystem II quantum yield (F_v/F_M) following light stress in the presence or absence of lincomycin for CRD1 and clade I-IV strains acclimated to different temperatures. Cultures acclimated to 75 µE m⁻² s⁻¹ were shifted to 375 µE m⁻² s⁻¹ at T0 for 90 min, then shifted back to the initial light conditions for 24h as indicated by a vertical dashed line on each figure. Strain names and their corresponding ESTU between brackets (*sensu* Farrant et al., 2016) are indicated on the right hand side, acclimation temperature are indicated on the top, whilst line colour indicates the lincomycin treatment (i.e. -/+ linco).