Figure S3. Multiple sequence alignments of PTP3 and PTP3b in *A. algerae*. Both sequences share 29.1% of identity. Alignments were performed with Clustal Omega. Identical positions are highlighted in grey. Amino acid number are indicated in the right.

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PTP3       MNLSINAIHLFLVLQGIKLRGHLGTLAEMGDRVRHPSRESIQDMRRRTHAN---------      51
PTP3b      ----MLILKILLLKYSITKGHLGRLEEMHSRKDLPGANTSRLN-DSAGNNQNKHHGRQP      55

PTP3       -RNDRHHNDLHASFRKGNTASHGGSKGGVFGPTGSMSTNLLRDDILNDLGEHAM------     104
PTP3b      PGAGLKSGGNHSSFGKPDSTTHGGPKGGVFGPNGRASDKAVAEMVAADRASNPLPLGSLK     115

PTP3       ------------NGNVFAQHALNDIAEGRDNPGLSHSMGMMNKMNADKKAQDRKEYGGMD     152
PTP3b      DEVNAALGDAEKAGNQDIGNPLTDKAGGAPPSPL----------------------AAAN     153

PTP3       DLDEMNGLDEAMHHAVDHMTNNGLEEMKGHMQLEGNIADAIAAQENDPRIAEAANKEEAM     212
PTP3b      EAGENAALDAALSGASP-------EEAA----AAGQN--AAASTPKTPTTPEEAAARA-A     199

PTP3       SQLAKASGFKRPEEEIKAIAHKVGEAARAALKNGASIEEAEEA-----G--KRQEAAAA     265
PTP3b      QDAANTPTTPTPEEVAAAQA-------AEDAANAGASPAEQQAAADNAAGAPPTPEEAAA     252

PTP3       RELNEANN-------------------------NDKFVEESANFGGGHQNEENSGRQFNA     300
PTP3b      QAAQDAANAGASPAEQQAAADNAARNAAGVPPTPEEAAQDANAGASPAEQQAAAEQAAG     312

PTP3       AEGAEMGSGSDIDVPVNMIPRSKEDQQAQAAMQAEAALDNGATPEEAKNAGLEAAKAAA     360
PTP3b      LPPKPPGKGAGPS----RTP-EIEAAANDAGNKAEADALNKGATPEEAKAIGDEAAEKAR     367

PTP3       IAGERAAAGGAEKGAIMAGNIAHDKALAEGATPLEAHIAGDSEAQVQAAAGGAAMAGKMA     420
PTP3b      ENMNRDMDAGDE------GLAAEEAAKAAGASPQDAKDAGDAAEQAAKNW---PTSSEMA     418

PTP3       HDEVLENG----------------ATPFEAN--MAGEQAAKGKAA--AMAGKIARDKALA     460
PTP3b      EAPGQGQGEGQGQGQGQGQGQGQGQGEGQGEGQGEGQGEGQGEGQGEGEGQGEG     478

PTP3       NGATPFEANMAGEQAAKDTLNALGANQELAKAQGEEIAAKEEAKEADKMNAMHSAAEKAA     520
PTP3b      QGEDDFDNGLANENQDKDKEDQ-------------------------------AAAEK--     505

PTP3       GNAAMESAASGLPERKALTNADKAGREAAAGMAGESAAADAMEKGATAEEAEAIGNLAAD     580
PTP3b      --AAEEAAANGASPEEAEAAADEAGKGNAAERAGEGAAAQAAAGGASPEEAEAAGQAAAG     563

PTP3       STKALGMGAQVDPALH-------------------------------------------     596
PTP3b      DSLGNGNGGQNSPEEGNAQAAGDEAAKKALQNGDTIPEAAAKGNEAAQNALAGAGAGEGE     623

PTP3       ---EANKQE--EEANLAEAEKEIEGSMKSRVKEKAKGLAADIKNADSQEAFGVIGTVPDD     651
PTP3b      GAGEGQGQGQGQGQGQGQGEGQGEGQGQGQGQGEGYLEGDGNHAGEDSPQEEFGIIGTVPDD     683

PTP3       SNAVNLSKGHIDLPLKSFSGENPKTEEEKEAKNEQDALAEKLRNKITKDHIPSPLNVIKG     711
PTP3b      AKEVDINDGEISLPMKNFQKEKSQDEEGAANNALDDKLADKLRNKVTAGDIPSHLNKVKG     743

PTP3       EDGYMNIPESAKKIEIKEGTVYYPESAKEEMKKAGKDVSQLKHKFNTGERKDRPMGEGYY     771
PTP3b      KDGIFNIPESAKKLQISDGEVYFPKNAVEEMEANGEDTSDLEKRNNKGERSDIPIGEEYY     803

PTP3       IANASGFEMDLPSPLNKSPLKVLSGKNGVLDISGASGIDILSGKLNLIPWKQYSKGLHPD     831
PTP3b      VKDASGSEMLLPSPKHKSSPETINIKGTCSRIKKADKIHVKKGKILMTPWKDFSKLLKPV     863

PTP3       FNLETFAKEGVERTKEQRNFEEQLETLANTKAEVITNPSGKQFVKFTPPVGVSEQIPANE     891
PTP3b      LNFINKFKCPGKKPE---------DCEDLPKAELIYNPDGTPIAVLTPKLGAPEQVSLTD     914

PTP3       LASAEEVEFNKNNDSGQDGLSMLQSKSSKEPARSLNIAQNAPHG-EGAMEGAFEKKVEQN     950
PTP3b      LVSTPP---NGSGDYGQTNMPNLQQGPEPLPKRSLNIAKKVGNKDPKSFEELFQDKIIDK     971

PTP3       AKKDSEASLIVSETNSFDPTKE-------TKPKTKKAEKAE-------------------     984
PTP3b      AKKIKDAASILTKKNPFESKNVNSKPPSKPMPKEEPSKVLEITTKNLLKNGQRIGGSKKV     1031

PTP3       IT----EKAGEDENDQKCPATEKMLKNINDILKENSEKFGAALGMTQTVFATTMAKIPES     1040
PTP3b      VTAKKGSLNSNTKKNESCPKGPEMSKEVKGILHENAGKFSKSIGMSKEDFINKFRKIPEP     1091

PTP3       AMKVFLQYECKKESKEYQEEYRKAYDDLKTVFDKNAEPMIKIIGNVMNAAKQRSRPARVI     1100
PTP3b      SLQIIYDYKCKNKDPNYMKKYTNAYKDLSAIYQNLSEPFAKLLGNAIYLAQRRLNPQRNG     1151

PTP3       STRIVRRPVTRKIAVY-PKIIRSAKTNKIIQPKVVSSKTIINFKPTLVEKKVLTPVKEVV     1159
PTP3b      KTKIVVRPSVKRKGPRKVSILKKGKIYKKVTEQ----TAPNALKSTFNQK----------     1197

PTP3       IRKGPLLSNKNPPVLKPIKNHVVLNSDGSVAKESTQRDLPPNPK                     1203
PTP3b      ---------------------------------------------                    1197
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