

Gene/protein ID and description	Sequence	Pfam domains
MFS40622_RS06240_fs_MFS40622_RS06245 – fs-chlD gene with validated frameshifting signal from <i>Methanocaldococcus sp. FS406-22</i> (2039 bp)	ATGCAGTATATTTATCCATTCACTGCAATCGTTGGACAGGAAAAAGATGAAGAAGGCTTTAATTC TAAATGCTATAAAATCCAAAGATTGGTGGAGTTTAAATTAGGGGAGAGAAAGGAACAGC AAAATCCACTGCAGTTAGAGCTTTAGCTGATTTATTGCCAGAGATTGAAGTTGTGTAAGGATGCCCATTCAACTGCGAACCAAATGGAGAGTTGTGTGATATCTGCAAAGAAAAGAAAGAGA GAGGAGAGCTAAAAAGTAACAAAAAGAGATGAAGGTTGTTAATCTTCCAATTGGAGCTACTGGAAGATAGAGTTATTTGGAACCTTTGACATAGAAAAAGCTATAAAAAGAAAGGAATTAAAGCA TTAGAGCCGGGAATTTTGGCAGAGGCAAAATAGAAACATCCTCTACATTGATGAAGTTAATTTATTTGGATGACCATAATAATTGATGTTTTATTGGATGTTGCAGCAATGGGTTGGAACATCAT TGAGAGAGAGGGAGTTAAGATAAAGCATCCTTCAAGATTATATAGTAGGAACTTAATGAATCCAGAGGAGGGGAGTTAAGACCTCAAATTTTGGATAGATTGGTTTAAATGGTTGATGTTG AAGGATTAAATGATGTTAAAGATAGAGTAGAGGTTATAAAAGAGGTTTGAGGAATTTAACAACAATCCAGAAGAGTTCTATAAAAAAATTTGAAGAAGAACAGAAAAAATTAAGAGAAAAATA ATTAAAGCAAGAGAAATTTTAAATAAAGTTGAGATAAGCGATGAACCTCTAGAAATTTATATCAAAGTTTGTATTGAGTTAGGAATCAACAACAATAGGGCCGATATAACTGTTGTAGAAC AGCTAAAGCTTTAGCTGCCATATAACGGAAGGACTTATGTAACATATAGATGATGTCAAGGAGGCTATGGAGTTAGCTCTACCTCACAGAATGAGAAGAAAAACCATTTGAACCACCACAATTAA ACAAGAGAGAAGTTGGAGCAGATGATTAATGAGTTTAAACAGCAAAAAATAATAATGAAGAAGAAAAGGAAGAGCAAAAAATGATGACGTAAAAAAAACATGATGAAATAAGAAATGAGT TTGAAGAAGAAAAATGAGGATTCAAATAATCAAATAATAATAACAACCTCTAATAACCAAAATGAAGATACACCCGGGGACTTTGAAAAGAACGTTTGCCATAGATGAGAGCTTAAAGTAAAT CCCAAGCTTATACAATTTAAGCTTAAAGATAATATCCATAGATATGGCTCTGGAAGGCATATTTAAAGCTACAGCAAGAGAGGGAGGTATGTAAAATTCAGCTCCCAAAGGATAAAACTTC CGATATTGCCTTCGATGCTACATTTAGAAGAGCGGCAATACACCAAAAAAGAAAGAGAAAAATCCAATAAAAAATTAGCTATCTACTTTAGAAAAAGAGATATTGTAGAAAAGGTTAGAC AGAGGAAGATATCATCCCATATATTGTTGTTGTGATGTGAGTGGTTCAATGGGAGCTATGAGAAGAATGGAAGCCGCAAAAGGGGCTATAATCTCTCTACTCTTAGATGCCTATCAAAG AGGAACAAAAATGGGAATGATTGCATTTAGAAAAGATAGAGCTGAGTTGATTTTACCTTTTATCATCTTCAGTAGAGCTTTGGAGAGAACTACTTAAAGATTTACCAACTGGAGGGAAAACTCC TTTGGCTGATGCATTTAATTAAGAGCTATGAGGTCTTTGACAGAGAGCTATAGAAAAATCCAATATCATCCCAATAATGATTTGTAATAAGTGATTTCAAGCCGAATGTAGCTGTTAAGGAG ATTATGTTAAAGAGGTTTTTTGATGCGTGTGAGAAGATAGCTGAGAAGTGCAATTAACGTTATATTGATAGATACTGAGCGCAATCATTTATAAAAAATAGGGATTGGAAGAGAGATAGCCAAT AGATTTGGATTTAAGTATTATAAAATAGAGGAGTTAAGTGAAGAAAAATCTTAGATATTTGTAAGAGCTTAGAAATCAACTCTTAA	
MFS40622_RS06240 – the short product from the fs-chlD gene (362 aa)	MQYIYPFTAIVGQEKMKKALILNAINPKIGGVLRGEKGTAKSTAVRALADLLPEIEVVEGCPFNCDPNGELCDICKEKKERGE LKVTKKMKVNNLP IGATEDRVIGTLDIEKAIKEGIKA LEPGILAEANRNILYIDEVNLDDHIIDVLLDVAAMGWNI IREGVKKHPSRF ILVGTMNPEEGELRPQILDRFGLMVDVEGLNDVKDRVEV IKRVEEFNNNP EEFYKKFEEQKKLREKI IKAREILNKVEISDELLEFISKVIELGIQTNRADITVVRTAKALAAYNGRTYVTIIDVKEAMELALPHRMRKPFEPPLNKEKLEQMINEFKQQKNNNEEKEEQKND DVKKMMK	
MFS40622_RS06240_fs_MFS40622_RS06245 – the long product from the fs-chlD gene (679 aa)	MQYIYPFTAIVGQEKMKKALILNAINPKIGGVLRGEKGTAKSTAVRALADLLPEIEVVEGCPFNCDPNGELCDICKEKKERGE LKVTKKMKVNNLP IGATEDRVIGTLDIEKAIKEGIKA LEPGILAEANRNILYIDEVNLDDHIIDVLLDVAAMGWNI IREGVKKHPSRF ILVGTMNPEEGELRPQILDRFGLMVDVEGLNDVKDRVEV IKRVEEFNNNP EEFYKKFEEQKKLREKI IKAREILNKVEISDELLEFISKVIELGIQTNRADITVVRTAKALAAYNGRTYVTIIDVKEAMELALPHRMRKPFEPPLNKEKLEQMINEFKQQKNNNEEKEEQKND DRKKHDEIRNE FEEENEDSNNQNNNNNNNNQNE DTPGDFERTFGIDESFKVNP KLIQFKLKDN IHRYSGRH IKSYSKRGRYVKFKLPKDKTSDIAFDATFRRAAIHQKRRREKSNKKLA IYLEKEDI VEKVR QRKISSHILFVVDSVSGSMGAMRRMEAAKGAII SLLLDAYQKRNKIGMI AFRKDRAELI LPFTSSVEIGEKLLKDLPTGGKTPLADAFI KSYEVFDREL RKNPNI IPIMIVISDFKPNVAVKG DYVKEVFDAEKIAEKCINVILIDTEPQSFIKIGIGRE IANRFGFKYKIEELSEEKILIDICKSLEINF	
BAA17166.1 – ChlI protein (small Mg-chelatase subunit) from <i>Synechocystis sp. PCC 6803</i> (357 aa)	MTATLAAPSKTRRVFPFTAIVGQDEMKLALLLNVIDPKIGGVIMIMDRGTGKSTTIRALADLLPEIEVVANDP FNSSPSDPEMMSEEVRI RVD SQEPLSIVKKKVTMVDLPLGATEDRVCG TIDIEKALSEG VKAFEPGLLAKANRGILYVDEVNLLDDHLVDVLLDSAGGWNTVEREGISIRH PARFVLV GSGNP EEGELRPQLLDRFGMHAEIRTVREPELRV KIVEQRTEFDQNPHPFC DQYQTEQEALQAKI VNAQNLLPQVTIDYDYRVKVSE VCAELDVDGLRGDIVTNRAAKALAAFEGRTEVTDDISRVIVLCLRHRLRKDPLESIDSGSKVEKVKRVFGVVDEA	
BAA16787.1 – ChlD protein (medium Mg-chelatase subunit) from <i>Synechocystis sp. PCC 6803</i> (676 aa)	MTTLTPFIPLNFPITAI VQGEAIK LALLLG AIDPGLGGIV IAGRRGTAKSVMARIH TLLPPIEIIKGNRYQCDPKNPGSWDDDTLEKFADVPLDQLETVQVIPAPF IQIPLGVTEDRLLGSV DVEKSVKQGEAVFQPGLLAQAHRGVLYIDEINLLDDQIANQLLTVLTEGKNQIERGMSFQHP CQPLL IATYNPEEGPIRRHLLDR IAIALSADGILGLDQRVAAVDQV LAYADSPISFTID YDAELDDLKTTIILAREWLKEVSLTPEQVSYLVEEAI RGLLQHRGELFAMRVAKAIALDGRSDVQADDLRQAVELVIVPRSVLMNPPPEEQAPPPPPPPQNDQEGKDEQEDQQDDKEDD KDNEPEAEQDPPSIP EEFIFDPEGVSLDPSVLYFAQMAKQKGKSGRSVIFSDDRGRY LKPI LPKKGVRRIAVDATLRAASPYQKSRRLRHPDRQVIVEQGDIRGKKLVRKAGALIVFLVDA SGSMALNRMQAAGKAVMQLLTEAYENRDQVSLIPFQGENAEVLLPPTRSIAMAKKRL ETLPCGGGSLSHGLMQAVNVGMNAKRSGDIGQVVI VAITDGRGNIP LARSLGDEIPEGEKPD IK AELLEIAAKIRGLGMQLLVINTEKKFVSTGFGKELAQKAGGKYYQLPKATDQGIASMARQAIDMQ	