Supplementary materials

Isolation and Cultivation of Carotenoid-Producing Strains from Tidal Flat Sediment and Proposal of *Croceibacterium aestuarii* sp. nov., a Novel Carotenoid-Producing Species in the Family *Erythrobacteraceae*

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Table S1. Genomic information of strain D39^{T} and other related *Erythrobacteraceae* type strains used in this study.

Strain	NCBI GenBank accession number	Contigs	Genomic size (bp)	DNA G+C content (%)	Gene count
Strain D39^{T}	GCA_030657335.1	1	3,347,658	65.8	3,297
Actirhodobacter atriluteus HHU K3-1^{T}	GCA_013370205.1	23	2,939,611	62.1	2,843
Alteraurantiacibacter aestuarii JCM 16339^{T}	GCA_009827405.1	5	2,241,463	62.6	2,138
Altererythrobacter epoxidivorans CGMCC 1.7731^{T}	GCA_001281485.1	1	2,786,256	61.5	2,785
Altericroceibacterium indicum DSM 18604^{T}	GCA_009828105.1	20	3,106,258	55.8	2,921
Alteripontixanthobacter maritimus HME9302^{T}	GCA_003340475.1	2	2,676,898	60.8	2,641
Alteriqipengyuania lutimaris S-5^{T}	GCA_003363135.1	12	3,290,764	65.4	3,181
Aurantiacibacter gangjinensis CGMCC 1.15024^{T}	GCA_001886695.1	2	2,724,951	62.7	2,701
Croceibacterium atlanticum DSM 100738^{T}	GCA_001008165.2	2	3,375,106	61.9	3,327
Croceibacterium ferulae KCTC 62090^{T}	GCA_003660445.1	36	3,608,511	66.5	3,362
Croceibacterium mercuriale DSM 29971^{T}	GCA_000802385.1	10	3,482,341	67.3	3,198
Croceibacterium salegens MCCC 1K01500^{T}	GCA_009827435.1	63	3,636,778	64.6	3,539
Croceibacterium selenioxidans MCCC 1K08007^{T}	GCA_018599195.1	4	3,438,177	63.6	3,318
Croceibacterium soli MCCC 1K02066^{T}	GCA_009828065.1	15	3,084,697	67.0	2,890
Croceibacterium xixiisoli CGMCC 1.12804^{T}	GCA_009827305.1	7	3,879,260	63.3	3,663
Croceicoccus marinus E4A9^{T}	GCA_001661675.2	3	4,109,188	64.5	3,869
Erythrobacter longus DSM 6997^{T}	GCA_000715015.1	14	3,602,162	57.4	3,377
Novosphingobium capsulatum NBRC 12533^{T}	GCA_001598375.1	70	4,836,455	65.7	4,352
Parapontixanthobacter aurantiacus MCCC 1A09962^{T}	GCA_009827635.1	7	2,895,130	61.2	2,799
Paraurantiacibacter namhicola JCM 16345^{T}	GCA_001687545.1	1	2,591,679	65.0	2,563
Parerythrobacter jejuensis JCM 16677^{T}	GCA_009827995.1	1	4,149,941	60.2	4,070

Strain	NCBI GenBank accession number	Contigs	Genomic size (bp)	DNA G+C content (%)	Gene count
Pelagerythrobacter marinus H32^T	GCA_009827515.1	16	3,001,465	68.2	2,888
Pontixanthobacter luteolus SW-109^T	GCA_009828095.1	3	2,887,613	59.3	2,788
Pseudopontixanthobacter vadosimaris JL3514^T	GCA_012979275.1	43	2,629,682	63.0	2,541
Qipengyuania sediminis CGMCC 1.12928^T	GCA_004358425.1	1	2,416,000	66.8	2,378
Rhodospirillum rubrum ATCC 11170^T	GCA_000013085.1	2	4,406,557	65.4	3,950
Tsuneonella dongtanensis KCTC 22672^T	GCA_001698205.1	1	3,009,495	65.8	2,953

Table S2. All Crt protein sequences of strain D39^T, seven *Croceibacterium* type strains and *Erythrobacter longus* DSM 6997^T.

Strain	Crt protein	Synthesized product	Protein sequence
Strain D39^T	CrtB	Phytoene synthase	MPGRILRFGNRRLVSSSILRQTPRQVGGGRERAALVRQAKKSIARGSKSFSLASKLFDKPTRERVWLLYAWC RRCDDIADGQDHGQSAPVSVLKLDDASNKQRILAIRILTERALQGQPTAELAFDAFNQVSAECRLTKEEAD DVIEGFALDAQGWRPRTEEDLMRYCFHVAGAVGVMMAKVMGVSGEDHETLDRACDLGLAFQLVNIAR DVSDDDAAGRCYIPTEWQAEADLPPGMRLRPEYREQLVELVGRMLDLAEVHEAAARYGANGLRFRQRW AVLSAANIYGAIGRKVRAAGPHAWDHRIHTGGLAKLGFVARAFVEALRGAPEPEEWPQHTRGSLMTAAR MAGPVAPMPMTPLPDEE
Strain D39^T	CrtG	2,2'-beta-ionone ring hydroxylase	MAIGILLSALAMTLIVGGRYLASSGLFALVTRRVRPGLYASLEPQIRREIGWSLASAAIYGVPAGVVAWGWR ERGWTLIYDGWSDYPLWYLPLSVFLYLLAHDTWFYWTHRLLHRPRWFRAAHAVHHASRPPTAWAAMSF HPLEALSGAIVIPALVFIVPIHVVMLLLVLTIMTVMGVTNHMGWEMFPRALVYSKAGNWLITASHHQRHH DEYKCNYGLYFRFWDRLCGTDRGLSPRSA
Strain D39^T	CrtI	Phytoene desaturase (lycopene-forming)	MTVESKRACVIGSGFGGLALAIRLQSAGVQTTIVEGRDKPGGRAYHWQREGFTFDAGPTVITDPACLEELW NLSGSDIRDDVELMKVMPFYRLNWPDGTNFDYSNDDKLLRGEIGKLDPADIAGYDAFLEYSAAVYEEGYV KLGTVPFLDFKSMLKAAPALAKHQAWRSVYSVVSKYVRNEKLREALSFHTLLVGGSPMTTSAIYALIHKLE KDGGVWWARGGTNRLVAGMVRLFERLGGTIRLGDPVVRVHTIGNRASEVQTESGWREAFHAAASNADI VHSYRDLLGGTKRGDEMGRSLAKKRFSPSLFVVHFGIEGTWPGIPHHMILFGPRYKGLLEDIYDRGVLPQD FSIYLHHPTVTDPSMAPQGKSTFYALIPVAHMGKLTIDWNEVGPKLEKRILDEVGRRLIPDIHDRIVTKFHYA PSDFAHDLHAHVGSAFSLEPILTQSAWFRGHNRDDVIGNFYLVGAGTHPGAGIPGVVGSAKATAGLMLED LAQ
Strain D39^T	CrtY	Lycopene beta-cyclase	MPGRTCDIAIVGGGLAGGLIALALRRARPEVSVRLIESGAAPGGNHRWSWFESDLDEAGRQLLGAFRTTR WGDGYDVAFPGRVRHLGTAYNSLSSEDFAAALQRELAPGAIMTKRKAKILLADGVFLEDGGWVGARAVI DCRGFAPTRHLSGGWQVFLGRHLRTERPHQVARPMIMDARVGQEDGYRFVYVLPLGADELFVEDTYYQD RPQLDRSLLSDRIDSYCEDNGWRGEDLGSETGVLPVVTGGSFARWQAEERTAGVARAGAGAGFLHPLTSY TLPFAAATANAIARAGDLTGERLSAMLGARARKHWSETKFYRRLGSMLFGAARSHERWRVFARFYSLDEG

Strain	Crt protein	Synthesized product	Protein sequence
			LVERFYAARSTRADRRRVVCGRPPVPISRAFAALTTSRPTLEPTE
Strain D39^{T}	CrtZ	Beta-carotene hydroxylase	MAPLPWQGKRGLSLRGQSPYLASMSWLAPVLIVLATALAMEAVAWSSHKYVMHGFGWGWHRDHHEPH DKLLEKNDLFGLVGAAVSIAFFAIGSPLVMGAGAWWPGTWIGLGVLFYGVIYTLVHDGLVHQRYFRWVPK RGYARRLVQAHKLHHATVSREGGVSFGFVFVRDPAALKADLKRQAATGQTRLRDSVPGAAELVPSGRNL GDRAG
Strain D39^{T}	CrtE	Geranylgeranyl pyrophosphate synthase	MGLVLASDILARAFERIQREVDDCFDGLLPLPDDARAPLIEAMRYAVIGGGKRARPLLLTATAEMYGVARD CAVLTGCAVEAIHAYSLIHDDLPCMDNDDVRHGKATLHREYDEAVAVLAGDSLHALAFEILAMPETSSDP YVRTELVYTLAGASGASGMAGGQMMDIVAESENFDLHTVTRLQQLKTGALLGAAVEMGAILGRVPEEGR AHLRAYARDIGLAFQIADDLLDISGDEAKAGKALRKDADAGKATFVSLMGEEKARDQAQALAAQAVGH LAQHGEEADILRALARFVVERDR
Croceibacterium atlanticum DSM 100738^{T}	CrtB	Phytoene synthase	MPRPRLLAPSRILRSTPRQIGGGRSREALVRRARESIEKGSKSFAMASRLFDRHTREKAWLLYAWCRRCDDI ADGQDHGGELKLDEADAKDRIEAIRVLTRRALDGQPTAELAFDALGQVAMEAGLTQDMTDDVIEGFALD AAGWRPRSELDMMRYCYHVAGAVGVMMAQVMGVPADDQDTLDRACDLGLAFQLNNIARDVWEDDA AGRCYLPMEWLVEADIPPGQHMKPQYRGKLVELVARMVGMAEQHEAAARLGAARLGFRQRWAILSAA NIYGAIGREVRARGAAAWDHRVHISKTAKLRHVARAFREALRKPPEPEQMPRWTRGEILVAVRMAGPVAP IPMTPLPDDF
Croceibacterium atlanticum DSM 100738^{T}	CrtG	2,2'-beta-ionone ring hydroxylase	MQAAIIVSAIAMTAIVALRYLAASGAFAFATSRTRPGLYAGLGPQIRREIGWSLASAAIYGVPAGIVAWGWQ EHGWTRIYADWGAYPLWYMPLSLFLYLFLHDTWFYWTHRLLHRPRWFRVAHAVHHASRPPTAWAAMSF HPIEALTGAIVIPALVFFVPIHVAMLGLVLTIMTVMGVTNHMGWEMFPRALVHSRLGNWLITASHHQRHH DEYRCNYGLYFRFWDRLCGTDRGLAKPR
Croceibacterium atlanticum DSM 100738^{T}	CrtI	Phytoene desaturase (lycopene-forming)	MMNDKGSTGKRACVIGSGFGGLALAIRLQSAGVATTIVEARDKPGGRAYFWERDGFTFDAGPTVITDPDC LKELWQLTGHDIAEDVELMPVFPFYRLNWPDGTNFDYSNDERDLRNQIAKLDPGDIAGYEAFLNYSAAVF EEGYVKLGTVPFLDFKSMIKAAPALAKQQAWRSVYGMVSKYVRNEKLREALSFHTLLVGGNPMTTSSIYAL

Strain	Crt protein	Synthesized product	Protein sequence
			IHKLEKDGGVWWARGGTNRLVAGMVRHFERLGGTIRLADPAVKVHTLGNRATEVETASGWRMAFDAVA SNGDIVHTYRELLGQTQRGSTYGRKLTQKKFSPSLFVVHFGIEGNWPGIPHHMILFGPRYKGLLDDIYVNG VLPQDFSIYLHHPTVTDPSMAPEGKSTFYALVPVAHMGKLAVDWKTLGPVLEKRVLDEVGRRLIPDIHDRV LTSFHYTPRDFAHDLGAHLGSAFSLEPVLTQSAFFRGHNRDDVFRNFYLVGAGTHPGAGIPGVVGSAKAT AGLMLEDMNQ
Croceibacterium atlanticum DSM 100738^{T}	CrtY	Lycopene beta-cyclase	MNGRDCDIAIAGGGLAGGLIALALARLRPDVSVRLLEAGTVPGGNHRWSWFASDLSPAARDLMNPFRKS RWEGGYDVRFPAHERHLATSYRSLTSLDFAYALQRELAPGTLRVNAVVATLDAGGVTLESGVRITARTVIDC RGFTPTAHLSGGWQVFMGRHLRMAEMHGVHRPIIMDARVAQHGGYRFLYVLPTGTNELFLEDTYYQDG PLLDRGALSARLDEYARAHGWVGETISSETGVLPVITGGDFGAWQASQRVPGVGMAGAKGGFVHPLTSY TLPFAAQTALAIVAGADLPGEEMSAMLEDRARAHWRATRFYRQLGGMLFGAAKPEERYRVFQRFYRLPEP LIERFYAARSTRADRMRILCGKPPVPIAGALRALATSRPALQEPA
Croceibacterium atlanticum DSM 100738^{T}	CrtZ	Beta-carotene hydroxylase	MEWIAPLLIVLASMAAMEWVAWASHKYIMHGFGWAWHRDHHEPHDKLLEKNDLYGLVGAVMSISMFA VGSPLVMGENAWWPGTWIGLGILGYGIIYTLIHDGLVHQRYFRWVPKRGYAKRLVQAHKLHHATIGKEG GVSFGFVLARDPAKLKAELKRQREAGIAVVRESAGG
Croceibacterium atlanticum DSM 100738^{T}	CrtE	Geranylgeranyl pyrophosphate synthase	MGLVLADDLLGRGLQRIQREIDATFDAILEVPEDSRAPLVDAMRHAVIGGGKRVRPLLLVTVGEIYGCSRAS AVRAGCALEAIHCYSLIHDDLPCMDDDDMRHGKPTVHKVFGEATAVLAGDALHALAFDLLSDPATSSDP FIRAELVHTLAIASGHKGMAGGQVMDMAAETTEFDLHSVTRLQQLKTGALLGAAVEMGAILGRVPNEGR AHLRNYARDIGLAFQIADDLLDHEGDEEKAGKALRKDAEQGKATFVSLMGPEKAREQARALSEQAVGHL CGHGSEADLLRALARFVVERDR
Croceibacterium ferulae KCTC 62090^{T}	CrtB	Phytoene synthase	MSTTPPIRPANRRPLTVPRRLLAPSRIMRPTPRQIGGGREREDLVAEAHRAIRKGSKSFAAASRLFDRDTREK AWLLYAWCRRCDDIADGQDSGFTLRPGTDGHERITGIRVLTGRALEGQPTAEPAFDAFGQVALEAGLKAD MAADVIEGFALDLAGWRPRTEMDLWRYCYHVAGAVGVMMARVMGVEADDEDLLDRACDLGLAFQLG NIVRDISEDDAGGRCYIPVEWLAEADIPPGEHMKPAFRPQLVALVARMVALAEEREASARIGAASLSFRQR WAVLAAANIYGAIGRKVRAKGAKAWDRRVRIGKLAKLRHVLAALFEALRSPAEPPAQWPTPSRGQILLAV

Strain	Crt protein	Synthesized product	Protein sequence
			RMAGPIAPMPMTPLPDEDSV
Croceibacterium ferulae KCTC 62090^T	CrtG	2,2'-beta-ionone ring hydroxylase	MLTALIASAAAMVAIVGLRYLLVSGAFALATARVRPGLYATLGPQIRREIAWSLSAAIIYGVPAGIIAWGWQE RGWTRIYAEWDAWPLWWLPASLFLYLFAHDTWFYWTHRLMHRPRWFKVMHAVHHASRPPTAWAAMA FHWTESLTGALVIPVLVFVLPVHVAVLGLVLTVMTVMGVTNHMGWEMFPPAFVNSRLGNWLITASHHQR HHEEYKCNYGLYFRFWDHLCGTDRGLSRRWQQP
Croceibacterium ferulae KCTC 62090^T	CrtI	Phytoene desaturase (lycopene-forming)	MIDPQAKRACIIGAGFGGLALAIRLQSAGIATTVVEARDKPGGRAYYWQRDGFTFDAGPTVVTDPACLQE LWAITGHDMARDIELMPVMPFYRLNWPDGVNFDYSNDDAQLKREIAKLDPGDIDGYERFLEYSAGVFQE GYVKLGSVPFLDFASMIKAAPALMKHQAWRSVYSVVSSYVKSEKLREALSFHTLLVGGNPMTTSSIYALIHK LEKDGGVWWARGGTNRLIAAMVRHFERLGGVVRLGDPVTAIGTMGDRASDVTCASGWNESFDAVASNG DIVHSYRDLLSGNQRGQREGRKLMKKRFSPSLFVVHFGVEGTWPGIPHHMILFGPRYKGLLDDIYTHGVLP EDFSIYLHHPSVSDPSMAPPGMSTFYALVPVAHMGKLAIDWSVVGPQLEKRILDEVGRRLIPDIHNRIVTKF HYAPPDFATDLNAHLGSAFSLEPMLTQSAFFRGHNRDDVIRNFYLVGAGTHPGAGIPGVVGSAKATAGLM LEDLAG
Croceibacterium ferulae KCTC 62090^T	CrtY	Lycopene beta-cyclase	MSSAPGSNGCDVAIVGGGLAGGLIALALATRCPQLHLRVIEEGARAGGNHRWSWFASDLNAAGTKLVAP LRKAEWQAGYEVDFPRFRRVLDTRYRSLASHDFAAHLAAALPAGTLVTGKRAEAVAADGVMLPGGERLP AGAVIDCRGFRPTRHLRGGWQVFLGRHLRVDRPHGLTRPTIMDARVDQTDGYRFVYVLPLAADELFIEDT YYQDSPVLDRALLSARLDAYAAAHGWTGTMLAEETGVLPVITGGDFAAWQAESRVPGVARAGAGAGFV HPLTSYTLPFAVETALAVADAFAQTPGLTGTALADLLERRGREHWQAMGFYRLLGTMLFGAADPAERYRV FERFYTLKPSLVERFYAGRSTWTDKARVLSGRPPVPVAAAVRALAGNRPRLYLGAQQQRDSA
Croceibacterium ferulae KCTC 62090^T	CrtZ	Beta-carotene hydroxylase	MTTEWLIPLLIVLASAAAMEWVAWASHKYIMHGWGWAWHRDHHEPHDHLLEKNDLYAIVGAVMSISMF ALGSEWMLGDAAWWPATWIGVGILVYGIIYTLIHDGLVHQRYFNWVPRRGYAKRLVQAHRLHHATIGKE GGVSFGFVLARDPAALKAELRRQREAGTATLRESERLEG
Croceibacterium ferulae	CrtE	Geranylgeranyl	MGTTMLDSDLLPRSLARIQAEVDETFDALLPIPDDARSRLVEAMRHAVIGGGKRMRPMLLITVAEMFNAD

Strain	Crt protein	Synthesized product	Protein sequence
KCTC 62090^T		pyrophosphate synthase	RDAAIRAACAIEAIHAYSLVHDDLPCMDDDAMRHGKPSTHVAYGEAIAVLAGDSLHALAFEILADTATSG DPFVRADLVRCLATASGHDGMAGGQMMDIAAEDGGFDLHTVIRLQELKTGALLGAAVEMGAILGHVPE DGRAPLRAYARDIGLAFQIADDLLDHEGDEALAGKALRKDAEAGKATFVSLMGSEAARAQARALSEQAI GHLVQHGSEADLLRALARYVVERDH
Croceibacterium mercuriale DSM 29971^T	CrtB	Phytoene synthase	MSSTPPLRPASRRPLTVPRRMLAPSRILRPTPRQIGGGRERDDLVAEAHRAIRKGSKSFAAASRIFDRDTREK AWLLYAWCRRCDDIADGQDSGFTLRPGTDGHERITGIRVLTARALEGQPTAEPAFDAFGQVALEAGLKAE MAADVIEGFALDLAGWRPRSEMDLWRYCYHVAGAVGVMMARVMGVDPDDDELLDRACDLGLAFQLG NIARDISEDAAGDRCYLPMEWLAEADIPPGEHMKPAFRPQLVALVAKLVALAEEREASARFGAASLSFRQR WAVLAAANIYGAIGRKVRARGAKAWDRRVRIGKLAKLRHVLTALFEALRSPGEPPAQWPQPARGQILLAV RMAGPIAPMPMTPLPDEDST
Croceibacterium mercuriale DSM 29971^T	CrtG	2,2'-beta-ionone ring hydroxylase	MLSALIASAAAMVAIVGVRYLLVSGAFALATARVRPGLYNGLKPQIRREIAWSLSAAVVYGVPAGIIAWGW QERGWTRIYAEWDAMPLWWLPVSLFLYLFAHDTWFYWTHRLMHRPRWFKVMHAVHHASRPPTAWAA MAFHWTESLTGALVIPVLVFLLPVHVSVLSLVLTIMTVMGVTNHMGWEMFPRALVHSRLGNWLITASHH QRHHEEYKCNYGLYFRFWDHLCGTDRGLSRRWQQP
Croceibacterium mercuriale DSM 29971^T	CrtI	Phytoene desaturase (lycopene-forming)	MIDPQAKRACIIGAGFGGLALAIRLQSAGIATTVVEARDKPGGRAYFWQRDGFTFDAGPTVVTDPACLQEL WAISGHDMARDIELMPVMPFYRLNWPDGSNFDYSNDEVSLKREIAKLDPADVAGYDRFLEYSAGVFQEG YVKLGSVPFLDFASMIKAAPALMKHQAWRSVYSVVSSYVKSEKLREALSFHTLLVGGNPMTTSSIYALIHKL EKDGGVWWARGGTNRLIAAMVRHFERLGGVVRLGDPVTAIGTMGDRASDVTCASGWNETFDAVASNG DIVHSYRDLLSGNQRGQREGRKLMKKRFSPSLFVVHFGVEGTWPGIPHHMILFGPRYKGLLDDIYTHGVLP EDFSIYLHHPSVTDPAMAPPGMSTFYALVPVAHMGKLAIDWSVVGPQLEKRILDEVGRRLIPDIHSRIVTKF HYAPTDFAADLNAHLGSAFSLEPMLTQSAFFRGHNRDDVIRNFYLVGAGTHPGAGIPGVVGSAKATAGL MLADLAA
Croceibacterium mercuriale DSM 29971^T	CrtW	Beta-carotene ketolase	MIATAPARVDATRGQAVVGVSLAAAIIAAWLAIHVTGIFFWHWSLSAVPLAALMVLVQTWLSTGLFIIAHD AMHGALAPGHPRLNRAIGTASLALYACLSYAALLPRHHLHHRHTGRDGDPDFHGGNPSLFGWFGQFFR

Strain	Crt protein	Synthesized product	Protein sequence
			NYYSHGQIVRITLVALVYTLLLGAPLGNIVIFWAVPALGAVAQLFVFGTWLPHRERDEPFADDHRAHSIRIA PVLSLLTCFHFGGYHHEHHLSPGTPWWGLPARRRADAATSRER
Croceibacterium mercuriale DSM 29971^T	CrtY	Lycopene beta-cyclase	MGTAAGSNGCDVAIVGGGLAGGLIALALATRCPDLHIRVIEEGAQPGGNHRWSWFASDLDEAGTRLLAP LTKAEWHAGYEVAFPHGGRVLETDYRSLGSDDFASHLTAVLPAGTLVTGQRAQDVAADGVTMADGARLP AGAVIDCRGFRPTRHLRGGWQVFMGRTLQLERPHGLTRPIIMDATVDQVDGYRFVYVLPMAADAVFIEDT YYQDSPVLDRALLSGRIDAYAAAHGWTGTMTHEETGVLPVITGGDFAAWQAEMRVPGVARAGAGAGLV HPLTSYTLPFAVETALIVAEAFANKPALTGTALADLLEQRGREHWRRTGFYRLLGKMLFGAAAPAERYRVF ERFYALKPSLIERFYAGRSTWADRVRVLSGKPPVPVGAAVRALAQDRPPLYLGAQTQRDSA
Croceibacterium mercuriale DSM 29971^T	CrtZ	Beta-carotene hydroxylase	MTWLERIAVVVFMVLFMECFAWAAHRYIMHGWGWGWHKSHHEAHEGWFEKNDLYAAVFAIVPIVLFV VGLWWEPLWWAALGITIYGLIYTFVHDMLVHQRGGFRWVPKRGYFKRLLQAHRLHHAVEGKDGTVSHG FLFARKPAVLKAQLRAHAEQQHKRAPQARNPAKTPAAADQ
Croceibacterium mercuriale DSM 29971^T	CrtE	Geranylgeranyl pyrophosphate synthase	MGTSLLDTDLLAHGLARIQGEVDATFDALLPVPEDARSRLVEAMRHAVIGGGKRVRPMLVITVAEMYNVD REAAIRAGCAIEAIHAYSLVHDDLPCMDDDAMRHGKPSTHAAFGEAIAVLAGDSLHALAFEILSDTATSG DPFVRADLVRCLATASGHDGMAGGQMMDIAAEGAGFDLHTVTRLQQLKTGALLCAAVEMGAILGHVPE EGRTLLRAYARDIGLAFQIADDLLDHEGDEALAGKALRKDAEAGKATFVSLMGAEAARAQARALSEQAI GHLVQHGPEADLLRALARYVVERDH
Croceibacterium salegens MCCC 1K01500^T	CrtB	Phytoene synthase	MAGRILRFGNRRLVSSSIIRQTPRQVGGGRERAALVRQAKKSITRGSKSFSLASKLFDRATRERVWLLYAWCR RCDDIADGQDHGASILKLDDATTKQRVLAIRILTERALQGQPTAELAFDAFNQVSAECRLTQEEANDVIEG FALDAQGWRPRTEEDLMRYCFHVAGAVGVMMAKVMGVSGEDHETLDRACDLGLAFQLVNIARDVSDD DAAGRCYIPLEWQAEADLPPGMRLRPEYREQLVALVARMLDIAEQHEAAARFGANGLRFRQRWAVLSAA GIYGAIGRKVRAAGPHAWDHRIHTSAWSKLGFVARGFVDAIRGAPEPEVWPKHTRGSLMTAARMAGPPA PMPMTPLPDEA
Croceibacterium salegens MCCC 1K01500^T	CrtG	2,2'-beta-ionone ring hydroxylase	MTAAVILSALAMTAIVALRYLAASGLFAWATRRVRPGLYAGLEPQIRREIGWSLASAAIYGVPAGVVAWGW DQRGWTQIYDGWGDYPLWYLPVSVLLYLFAHDTWFYWTHRLLHRPRWFRAAHAVHHASRPPTAWAAM

Strain	Crt protein	Synthesized product	Protein sequence
			SFHPLEAVSGAIVIPALVFLVPIHVAMLLIVLTIMTVMGVTNHMGWEMFPRALVYSKAGNWLITASHHQRH HDEYKCNYGLYFRFWDRLCGTDRGLSQRSA
Croceibacterium salegens MCCC 1K01500^T	CrtI	Phytoene desaturase (lycopene-forming)	MTFANKRACVIGSGFGGLALAIRLQSAGVQTTVVEGRDKLGGRAYHWQREGFTFDAGPTVITDPGCLLEL WNLSGSDMRDDVELMKVMPFYRLNWPDGTNFDYSNDDKLLRGEIGKLDPYDIAGYEAFLDYAAAVYEE GYVKLGTVPFLDFKSMIRAAPALMKHQAWRSVYSVVSQYVRNEKLREALSFHTLLVGGNPMTTSSIYALIH KLEKDGGVWWARGGTNRLVAGMVRLFERLGGTVRLGDPVVHVHTIGSRAAEVQAQSGWREAFDAVAS NADIVHTYRDLLRGSPRGEQMGRALAKKRFSPSLFVVHFGIEGSWPGIPHHMILFGPRYKGLLEDIYVRGV LPQDFSIYLHHPTVTDPSMAPQGKSTFYALVPVAHMGKLAVDWDQVGPVLEKRILDEVGRRLIPDIHDRIV TKFHYAPSDFAHDLHAHVGSAFSLEPILTQSAFFRGHNRDDVIGNFYLVGAGTHPGAGIPGVVGSAKATA GLMLEDLAK
Croceibacterium salegens MCCC 1K01500^T	CrtY	Lycopene beta-cyclase	MPGRTCDIAIVGGGLAGGLIALALRQSNPDISVRLIETGATPGGNHRWSWFESDLDDEARWLMRPFRTTR WDKGYDVAFPGHVRHLDTAYRSLSSEDFAAGLNRELAPGTIMANRSARSLMADGVYLEDGGWVGARAVI DCRGFTPTPHLTGGWQVFLGRHMRTEKPHDVTRPVIMDATVDQKDGYHFVYVLPLGADELFIEDTYYQD EPKLDRSKLSGRIDRYCEHHGWRGELLSSETGILPVVTGGNFSRWQAEQDVDGVARAGVHAGFLHPLTSY SLPFAAATANAVARYGDLPGDQLAAMLAARARRHWSDTKFYRRLGSMLFGAARSHERWRVFSHFYGLD EELVERFYAARSTRADRMRILWGRPPVPIRRAIAALATSRPSLEHAA
Croceibacterium salegens MCCC 1K01500^T	CrtZ	Beta-carotene hydroxylase	MSWLAPALIVIATVLAMECVAWSSHKYVMHGFGWGWHRDHHEPHDKRLEKNDLFGVVGAGISISFFAIG SPLVMGVNAWWPATWIGLGVLFYGIIYTLVHDGLVHQRYFRWVPKRGYARKLVQAHKLHHATVSKEGGV SFGFIFVRDPPALKADLRRQAAAGQTQLRDSAS
Croceibacterium salegens MCCC 1K01500^T	CrtE	Geranylgeranyl pyrophosphate synthase	MGLVLANDILARALERIQREVDARFDGLLPVPDDARARLIEAMRYATIGGGKRVRPLLLTATAEMYGVSRG CAVLAGCAVESIHAYSLIHDDLPCMDNDDMRHGKPTLHKAFDEATAVLAGDSLHALAFEILSMPEVSTDP YVRSDLVLALAAASGASGMAGGQMMDIVAEEQEFDLHTVTRLQQLKTGALLAASVEMGAILGRVSEEGR GHLRAYARDIGLAFQIADDLLDTSGDEAKAGKALRKDADAGKATFVSLMGEEKARDQAYALSEQAVGHL SQHGEEADVLRALARFIVERDR

Strain	Crt protein	Synthesized product	Protein sequence
Croceibacterium selenioxidans MCCC 1K08007^T	CrtB	15-cis-phytoene synthase	MGLVLANDILARALERIQREVDARFDGLLPVPDDARARLIEAMRYATIGGGKRVRPLLLTATAEMYGVSRG CAVLAGCAVESIHAYSLIHDDLPCMDNDDMRHGKPTLHKAFDEATAVLAGDSLHALAFEILSMPEVSTDP YVRSDLVLALAAASGASGMAGGQMMDIVAEEQEFDLHTVTRLQQLKTGALLAASVEMGAILGRVSEEGR GHLRAYARDIGLAFQIADDLLDTSGDEAKAGKALRKDADAGKATFVSLMGEEKARDQAYALSEQAVGHL SQHGEEADVLRALARFIVERDR
Croceibacterium selenioxidans MCCC 1K08007^T	CrtG	2,2'-beta-ionone ring hydroxylase	MTAAVILSALAMTAIVALRYLAASGLFAWATRRVRPGLYAGLEPQIRREIGWSLASAAIYGVPAGVVAWGW DQRGWTQIYDGWGDYPLWYLPVSVLLYLFAHDTWFYWTHRLLHRPRWFRAAHAVHHASRPPTAWAAM SFHPLEAVSGAIVIPALVFLVPIHVAMLLIVLTIMTVMGVTNHMGWEMFPRALVYSKAGNWLITASHHQRH HDEYKCNYGLYFRFWDRLCGTDRGLSQRSA
Croceibacterium selenioxidans MCCC 1K08007^T	CrtI	Phytoene desaturase (lycopene-forming)	MPGRTCDIAIVGGGLAGGLIALALRQSNPDISVRLIETGATPGGNHRWSWFESDLDDEARWLMRPFRTTR WDKGYDVAFPGHVRHLDTAYRSLSSEDFAAGLNRELAPGTIMANRSARSLMADGVYLEDGGWVGARAVI DCRGFTPTPHLTGGWQVFLGRHMRTEKPHDVTRPVIMDATVDQKDGYHFVYVLPLGADELFIEDTYYQD EPKLDRSKLSGRIDRYCEHHGWRGELLSSETGILPVVTGGNFSRWQAEQDVDGVARAGVHAGFLHPLTSY SLPFAAATANAVARYGDLPGDQLAAMLAARARRHWSDTKFYRRLGSMLFGAARSHERWRVFSHFYGLD EELVERFYAARSTRADRMRILWGRPPVPIRRAIAALATSRPSLEHAA
Croceibacterium selenioxidans MCCC 1K08007^T	CrtY	Lycopene beta-cyclase	MTFANKRACVIGSGFGGLALAIRLQSAGVQTTVVEGRDKLGGRAYHWQREGFTFDAGPTVITDPGCLLEL WNLSGSDMRDDVELMKVMPFYRLNWPDGTNFDYSNDDKLLRGEIGKLDPYDIAGYEAFLDYAAAVYEE GYVKLGTVPFLDFKSMIRAAPALMKHQAWRSVYSVVSQYVRNEKLREALSFHTLLVGGNPMTTSSIYALIH KLEKDGGVWWARGGTNRLVAGMVRLFERLGGTVRLGDPVVHVHTIGSRAAEVQAQSGWREAFDAVAS NADIVHTYRDLLRGSPRGEQMGRALAKKRFSPSLFVVHFGIEGSWPGIPHHMILFGPRYKGLLEDIYVRGV LPQDFSIYLHHPTVTDPSMAPQGKSTFYALVPVAHMGKLAVDWDQVGPVLEKRILDEVGRRLIPDIHDRIV TKFHYAPSDFAHDLHAHVGSAFSLEPILTQSAFFRGHNRDDVIGNFYLVGAGTHPGAGIPGVVGSAKATA GLMLEDLAK

Strain	Crt protein	Synthesized product	Protein sequence
Croceibacterium selenioxidans MCCC 1K08007^T	CrtZ	Beta-carotene hydroxylase	MSWLAPALIVIATVLAMECVAWSSHKYVMHGFGWGWHRDHHEPHDKRLEKNDLFGVVGAGISISFFAIG SPLVMGVNAWWPATWIGLGVLFYGIIYTLVHDGLVHQRYFRWVPKRGYARKLVQAHKLHHATVSKEGGV SFGFIFVRDPPALKADLRRQAAAGQTQLRDSAS
Croceibacterium selenioxidans MCCC 1K08007^T	CrtE	Geranylgeranyl pyrophosphate synthase	MAGRILRFGNRRLVSSSIIRQTPRQVGGGRERAALVRQAKKSITRGSKSFSLASKLFDRATRERVWLLYAWCR RCDDIADGQDHGASILKLDDATTKQRVLAIRILTERALQGQPTAELAFDAFNQVSAECRLTQEEANDVIEG FALDAQGWRPRTEEDLMRYCFHVAGAVGVMMAKVMGVSGEDHETLDRACDLGLAFQLVNIARDVSDD DAAGRCYIPLEWQAEADLPPGMRLRPEYREQLVALVARMLDIAEQHEAAARFGANGLRFRQRWAVLSAA GIYGAIGRKVRAAGPHAWDHRIHTSAWSKLGFVARGFVDAIRGAPEPEVWPKHTRGSLMTAARMAGPPA PMPMTPLPDEA
Croceibacterium soli MCCC 1K02066^T	CrtB	Phytoene synthase	MRRPRLLVMPRKPRPLVASGIMRAPPRQTGGGRERESLVQLAHQSMRRGSKSFALASRLFDKSTRERAWLL YAWCRRCDDIADGQDHGGGLKLDESTARNRIEAIRVLTRRALEGQPTAEVAFDAIGQVATEAGLSADMTE DVIDGFALDAEGWRPRSEADLMRYCYHVAGAVGVMLARAMGVPADDHDTLDRACDLGLYFQLVNIAR DVSEDDAAGRCYLPVEWLVEADIPPGEHMRPDFREQLVGMVARLLDMAEAHKAAALFGAGRLPFRQRW AVIAAAEIYGATARDIRQRGPAAWDHKPRTGYFAKLGLIAQAFFAAFKTAPQPDPMPRWTRGELMTMIRM AGPIAPMPTTPLPDEEM
Croceibacterium soli MCCC 1K02066^T	CrtI	Phytoene desaturase (lycopene-forming)	MTAEGKRACVVGSGFGGLALAIRLQAAGVATTVIEGRDRPGGRAYHLREDGFTFDAGPTAIADPAGLREL WELTGHDLALDVELMPVSPVCRLSWPDGTTFDFSADERAVRNEIARISPRDVAGYDALLGYSAIVREEATR LAGMPFLDRKSMAKATPALAKHQAWRSLYSHVARHVRHEKLREALSFHTLAIGGNPLTTSALQALACAP ARDGGVWWARGGMNRLVAGMARHFERLGGSVRLNDPAVRIHTIGNRVSEVETRGGWRERFDAVASNAD PVHTYRDLLASSHRGRQMARRLAKQRYSPGVFVVHFGIEGSWPGIPHHTVLFGPRFHGLLEDIYDRGVLPA DSLIYLHHPTVTDPSLAPEGMSTFHALVPVANMGKLTIDWQQIAPLLEKRILDEVGRRLIPDIHDRIVTKFSC SPRDMALEQNAHLGSAYGPEPLLTQSAFFRAHNRDDVIGNLYLVGAGTHPGAGVPGVVAGARITAGLML EDLAG

Strain	Crt protein	Synthesized product	Protein sequence
Croceibacterium soli MCCC 1K02066^{T}	CrtE	Geranylgeranyl pyrophosphate synthase	MGLILADDILARGFDRIQREVDAMFDGYLRVPKDARSRLVEAMRYAAIGGGKRVRPLLLTATAEIYGVSRD AAVRAGCAIEAIHAYSLIHDDLPCMDDDDMRHGKPTVHKAFDVATAVLAGDALHALAFELLTDDQTSAD PFVRAELVRALARASGHHGMAGGQMMDMAATDQQFDLHAVTRLQQLKTGALLAAAVEMGAILGRVVE EGRAHLRAYARDIGLAFQIADDLLDCEGDESKAGKALRKDDGAGKATFVSLMGAEKARDQAHALAEQAI GHLSTHGEEANLLRALARFVVERDR
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtB	15-cis-phytoene synthase	MARRPRLLAPSRILRTTPRQIGGGRPRPSLVEQARESINTGSASHALASKLFDKETRERAWLLFAWRRRCND IAGGRGMGSTMADESDPHDRIEAIRVLSLRALDGQPTADVAFDAFGQVSMEAGLDEQLADDVIEGFALDA DRWQPRDQDDLLRYCYHTAGAAGVMMARIMRVDRDDNDALDRACDMGIAFRLIDIARDLARDDALGR CHLPVHWLAEAGIPAQRPLDPVWRGQLAQIAVQLIALADIYAAAGRQVTTGLSFRQRWAVLSIANIFAAT GQKVIQRGEKAWDKRIRLSPLGKLTQVTRALGQALRSQPALEEWPPLTRGQILIAVRMTGPIPPVPMTPLPD EELE
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtG	2,2'-beta-ionone ring hydroxylase	MWSTLSAVIYGLPAGVVLWLWASGTGSAIYLDAAEYPWWWLVAAPIVYLLIHDAWFYWSHRLMHVPAVY RACHYVHHRSHPPTAWAAMSFHWTEALSGAWLIPVLALFIPIHVGALGFVMAVMTLFGVTNHMGWEIW PRWMVHGRLGGLIITATHHDNHHRKNKGNYGLYFRFWDRLCGTDVGFSRFGADRPDRRRHEGRGTGPG TSGHVAVDDNDRRAAQ
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtI	Phytoene desaturase (lycopene-forming)	MTDRRNAIVIGAGFGGLALAIRLQSAGISTTVLEARDRPGGRAYVWEKGGYTFDAGPTVITDPACLQELW GLTGADIAADVDLLEIAPFYRLLWNDGVRFDYTNDDATLLPQIAALDAGDVAGYKRFLEYAAGVYQEGY VKLGAVPFLDFSAMIRAAPALMKYQAWRSVYSIVAGFVKNEKLRQALSFHTLLVGGNPMATSSIYALIHKL ERDGGVWFARGGTNRLIAGMVRHFERLGGTLRLGDAVAQIHHSGDRVTGVTTRSGWHADADMIASNGD VVHSYGLITGSDYAQRKQARLKRKRFSPSLFVVHFGLKGTFPDIAHHSILFSDRYGSLLDDIYRHGNLPVDPS LYLHHPSATDPAMAPAGCSTFYALAPVPHLGKADVDWAAEVGPKYRDIVLDRVQDLLIPDLRDRLDQVFHY TPADFAGDLGAHLGNAFSLEPVLTQSAWFRTHNRDDHFGNLYFVGAGTHPGAGIPGVVGSAKATAGLML
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtY	Lycopene beta-cyclase	MTVAHAATPIATRVSDIASTPATYRVSRPLTELLPKVDTLIVGGGLAGVLCALATSRVAPDHVVMVVEQGK RLGGNHRWSWFDSDLDIHGHALLHGAEKSRWDGHELRFPAFGRAMQTGYNSMSSVAFHDWAAGLLQP

Strain	Crt protein	Synthesized product	Protein sequence
			DRLLLDTTVTQLDEGGVTLADGRRIEAERVIDARGPHAIAGAGAAQGVQVGWQKFAGFEIAVSSHGLVRP IIMDARVNQADGYRFIYTLPLTADRLFIEDTFYSSSPVIDATARREAVWRYAAQFGTPTTEYSREVGVLPIVQS GNPDLFWPAGGGIARAGMAGGFFHHTTGYSLPLAVRNALAFADEVAAGQAPDANWWRDRFLQHWRD QRYFRMLNTMLFRAAVPDERYRVFEHFYRLPEPLVQRFYAGQMTWADQLRVMTGRPPVPVTRAIRALLSE KDHA
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtZ	Beta-carotene hydroxylase	MLYALIILVTVLFMEGFAYAMHRWVMHGPGWFLHASHHRPRHGPFEWNDLYAVIFALPSIALIYAGVQGS WGPVATSLGVGIAMYGLIYFIFHDALVHQRVPIRYVPRSAYMKRIVQGHRLHHATHGRKGSVSFGFLYAPK AVVLKRQLRANAARAEKQS
Croceibacterium xixiisoli CGMCC 1.12804^{T}	CrtE	Geranylgeranyl pyrophosphate synthase	MTAELADDLLSEGLQRVQREIDDAFDAILDVPDDPRARLVEAMRYATIGGGKRVRPLLLVAVAEMYGVARP SAIRAGCAIEALHAYSLVHDDLPCMDDDERRHGKPTLHLAFDDATAVLAGDSLHALAFELLSDTQTSADP FVRAELVRCLAVASGSNGMAGGQMMDIIAETSQFDLHMITRLQQLKTGALLGAAVEMGAILGHVAQEGR THLRAYARDIGLAFQIADDLLDHEGDEQKAGKALRKDEGQGKATFVSLMGAEKAREQAFALSDQAIARL AQHGKEADLLRALARFVVERDR
Erythrobacter longus DSM 6997^{T}	CrtB	15-cis-phytoene synthase	MSVVGMDGDLLKDGLKRVQAEIDSVFDAFLPVPSDTRARLVEAMRYAAIGGGKRVRPLLLVTTAELFGVD RTSALRAGAAVEAIHCYSLIHDDLPCMDDDDLRHGKATLHHVYDEATAVLAGDALHALAFEILADHGTS SDPFVRSELIATLGTASGMNGMAGGQMMDMVADEEGVTYDLQAITRLQQLKTGALLSCAVEMGAVLGK VPVEGRAHLRAYSRDIGLAFQIADDLLDVEGDAQLAGKALRKDEGQGKQTFVTLMGADQARDQARMLV DQAIGHLSSHGSEADTLRALARFIVERDR
Erythrobacter longus DSM 6997^{T}	CrtG	2,2'-beta-ionone ring hydroxylase	MSDSEIDSVPNDDSCDCAIVGGGLAGGLIALALQRARPEFRIRVIEAGRTIGGNHRWSWFDSDLSDAGRAL LADFRQTDWEGGYEVRFPKYRRKLKTAYRSMASTDFHEGLLRALPEGSVILGRKAVGLDARGVDLAPSQY GPATRINARSVIDCRSFKPSAHLKGGWQVFLGRHMRLQEPHGVENPVIMDATVDQLAPHGNGGSYRFVY VLPLGSHDVFIEDTYYADDPLLDRNALSGRIDQYARANGWENGTPVHHEAGVLPVLTGGDFSAYQDEVRI PGVAIAGARGGFTHPLTSYTMCVAVENALAMAEQPDLSGEQLAAFFDSRARRHWSKTGYYRLLARFLFFA AKPEKRVKVFQRFYGLREGLIERFYAARSNTFDKVRVLWGEPPVAIHSAILAMFKSGPALKSEKSDRGVAQA

Strain	Crt protein	Synthesized product	Protein sequence
			ALDEELQTEKRP
Erythrobacter longus DSM 6997^T	CrtI	Phytoene desaturase (lycopene-forming)	MNADQNIAPGLDFAPANTGERGINPVIAEKYKGRTACVIGSGFGGLALALRLQSHGIQTTIVEARDKPGGR AYFWEKDGFTFDAGPTVITDPPCLKELWELTGHDISEDVELMKVHPFYRLNWPDGTNFDYSNVDEELNAE IAKLNPDDVIGYQKFLEYSARVHEEGYVKLGTVPFLDFKSMLKAAPALVKERAWRSVYDMVSSYIKDERLR EAFSFHTLLVGGSPMKTSAIYALIHKLEKDGGVWWARGGTNRLIAGMVRHFERLGGTMRIGDPVVQVHT QGTKATEVETKSGWKERFDAVCSNADIMHSYKELLGESDRGRKYAKSLARKSYSPSLFVVHFGLEGSWPGI AHHMILFGPRYKELVDDIYKHGVLPQDFSIYLHHPTVTDPSMAPKGMSTFYALVPVAHLGKMPIDWDVEG PKFEKAILDEIGRRLIPDIHDRIVTKFSYAPKDFQADLNAHMGSAFSLEPVLWQSAYMRGHNRDDVIDNFYL VGAGTHPGAGIPGVVGSAKATAGLMLEDLSVK
Erythrobacter longus DSM 6997^T	CrtW	Beta-carotene ketolase	MVNPERRAELVAHARATIKHGSQSFSAASQLFDSKTRERAWLLYAWCRQCDDIADNQVLGGELGDQSDL DERLAHIRRLTALAFEGKPTGDPAFDALGVVAEECGLTPAMAEDVIAGFALDADDWRPRTEADMMRYCY HVAGAVGVMMAVVMGVDPEDQDTLDRANDLGLAFQLSNIARDIVEDDAAGRCYLPINWLVEQDIEPGQ HTKPHHREELAEMAARLVALVEKHEAAARVGAERLPFRSRWAVLAAARIYGAIGRKVRDRGTEAWNSRT FVPRWEKALYGMRAFLSAAINREKHPDGEITWGIKDFRPA
Erythrobacter longus DSM 6997^T	CrtY	Lycopene beta-cyclase	MVPADTPVWLAFLIVGTAMSVMVALRYFASSGIFAWITKRARPGLYAKQRRQIASEIRYSLIAAVIYGVPAGA VFWLWRHHDFALIYTDWNAYPLWYLPFSVLIYLFAQDTWFYWSHRAMHHWPSLFQLAHKVHHDSKPPT AWTAMSFHPVESLTGAIVIPILVFFVPIHLAMLGVVLTVATVMGVVNHMGWEIFPRAFVHSPFGALVITASH HERHHEEYRCNFGLYFRFWDKVCGTDRGLSRRFDKQARSAP
Erythrobacter longus DSM 6997^T	CrtZ	Beta-carotene hydroxylase	MTWLEAIAVTLGALVFMEFFAWWAHKYIMHGWGWGWHRDHHEPHTNTFEKNDLYATVFGTINASMYIF GSLYWEWLWWAALGVNLYGVIYAIVHDGLVHQRFFKWVPKKGYAKRLVQAHKLHHATIGKEGGVSFGF VIARDPAKLKAELKKQAKAGVAVVRDSASAREDAANRITTLN
Erythrobacter longus DSM 6997^T	CrtE	Geranylgeranyl pyrophosphate	MLSPSVSSGMTPASLSLPSQTVQGVVGLALAALIAGGWLGIHAYAMFVFELSWQNLPFAIGMAIVQCWLS VGVFIVCHDAMHGTLVPSRPKLGGAIATVLLLLYAGFGWKNLRDAHHTHHRLAGHAGDPDFDEDNPAH

Strain	Crt protein	Synthesized product	Protein sequence
		synthase	FAKWYWTFFKRYFGWQSLLFVHTVVGIYWLIIGIPMVQIVLLYGAPALLSSLQLFYFGTYRPHAHIDGKSFA DDHNARSDGFGTLASLATCFHFGYHLEHHRRPDVPWWALPAARKAGIGNMPDNKAVKEQASV

Table S3. The 16S rRNA gene sequence identities (by using EzBioCloud websever) and colonial color of isolated bacterial strains in this study.

Strain	Closest relative	Sequence identity (%)	Colonial color	Phylum	Class	Order	Family	16S rRNA GenBank accession number
D1	*Shewanella marisflavi* SW-117^T	99.9	red	*Pseudomonadota*	*Gammaproteobacteria*	*Alteromonadales*	*Shewanellaceae*	OR871657
D3	*Bacillus amyloliquefaciens* NBRC 15535^T	99.9	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR835564
D6	*Rossellomorea vietnamensis* 15-1^T	99.8	pink	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871658
D7	*Cytobacillus firmus* IAM 12464^T	99.2	cream	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871659
D12	*Neobacillus niacini* IFO 15566^T	99.6	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871660
D15	*Virgibacillus halodenitrificans* ATCC 49067^T	99.9	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR603115
D16	*Fictibacillus enclensis* NIO-1003^T	99.5	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871661
D17	*Lysinibacillus composti* NCCP-36^T	99.0	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Caryophanaceae*	OR871664
D19	*Pontixanthobacter luteolus* SW-109^T	99.4	yellow	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Erythrobacteraceae*	OR875941
D21	*Priestia aryabhattai* B8W22^T	100.0	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871663
D24	*Vibrio natriegens* NBRC 15636^T	100.0	white	*Pseudomonadota*	*Gammaproteobacteria*	*Vibrionales*	*Vibrionaceae*	OR603134
D25	*Vibrio alginolyticus* ATCC 17749^T	99.4	yellow	*Pseudomonadota*	*Gammaproteobacteria*	*Vibrionales*	*Vibrionaceae*	OR603136
D31	*Oceanisphaera psychrotolerans* LAM-WHM-ZC^T	100.0	cream	*Pseudomonadota*	*Gammaproteobacteria*	*Aeromonadales*	*Aeromonadaceae*	OR871665
D32	*Kocuria indica* NIO-1021^T	100.0	yellow	*Actinomycetota*	*Actinomycetes*	*Micrococcales*	*Micrococcaceae*	OR871669
D33	*Micrococcus endophyticus* YIM 56238^T	98.9	yellow	*Actinomycetota*	*Actinomycetes*	*Micrococcales*	*Micrococcaceae*	OR871666

Strain	Closest relative	Sequence identity (%)	Colonial color	Phylum	Class	Order	Family	16S rRNA GenBank accession number
D34	*Maribacter dokdonensis* DSW-8^T	99.6	orange	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OR871667
D37	*Maribacter luteus* RZ05^T	98.6	yellow	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OP132875
D38	*Qipengyuania gaetbuli* SW-161^T	99.8	orange	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Erythrobacteraceae*	OR603149
D39	*Alteripontixanthobacter muriae* SALINAS58^T	97.6	yellow	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Erythrobacteraceae*	OP132876
D40	*Parasphingopyxis algicola* ATAX6-5^T	96.4	white	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	OR603151
D42	*Qipengyuania nanhaisediminis* T30^T	100.0	cream	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Erythrobacteraceae*	OR603153
D44	*Bacillus altitudinis* 41KF2b^T	100.0	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871668
D46	*Roseovarius indicus* B108^T	99.4	white	*Pseudomonadota*	*Alphaproteobacteria*	*Rhodobacterales*	*Roseobacteraceae*	OR871671
H3	*Marinovum algicola* NBRC 16653^T	99.1	white	*Pseudomonadota*	*Alphaproteobacteria*	*Rhodobacterales*	*Roseobacteraceae*	OR656552
H4	*Microbacterium aquimaris* JCM 15625^T	100.0	yellow	*Actinomycetota*	*Actinomycetes*	*Micrococcales*	*Micrococcaceae*	OR656553
H6	*Maribacter luteus* RZ05^T	97.9	orange	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OR656554
H9	*Christiangramia flava* JLT2011^T	96.6	orange	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OP132826
H11	*Modicisalibacter tunisiensis* R2A 31.P^T	97.9	yellow	*Pseudomonadota*	*Gammaproteobacteria*	*Oceanospirillales*	*Halomonadaceae*	OR656561
H13	*Alteriqipengyuania lutimaris* S-5^T	99.1	white	*Pseudomonadota*	*Alphaproteobacteria*	*Sphingomonadales*	*Erythrobacteraceae*	OR656562
H14	*Zunongwangia mangrovi* P2E16^T	95.8	yellow	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OP132872
H15	*Fluviibacterium aquatile* SM1902^T	97.8	white	*Pseudomonadota*	*Alphaproteobacteria*	*Rhodobacterales*	*Roseobacteraceae*	OP132873
H16	*Pseudomonas benzenivorans* DSM 8628^T	98.8	white	*Pseudomonadota*	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	OR656565

Strain	Closest relative	Sequence identity (%)	Colonial color	Phylum	Class	Order	Family	16S rRNA GenBank accession number
H18	*Mangrovibacterium lignilyticum* BM_7^T	97.2	red	*Bacteroidota*	*Bacteroidia*	*Bacteroidales*	*Prolixibacteraceae*	OR656566
H20	*Aequorivita antarctica* SW49^T	98.6	yellow	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OP132874
H22	*Pseudomonas peli* R-20805^T	99.2	white	*Pseudomonadota*	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	OR656569
H23	*Pseudoalteromonas lipolytica* LMEB 39^T	100.0	orange	*Pseudomonadota*	*Gammaproteobacteria*	*Alteromonadales*	*Pseudoalteromonadaceae*	OR656568
H24	*Mariniflexile aquimaris* HWR-17^T	99.9	yellow	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OR885467
H25	*Rheinheimera hassiensis* E48^T	99.6	cream	*Pseudomonadota*	*Gammaproteobacteria*	*Chromatiales*	*Chromatiaceae*	OR656570
Z5	*Celeribacter halophilus* ZXM137^T	100.0	white	*Pseudomonadota*	*Alphaproteobacteria*	*Rhodobacterales*	*Roseobacteraceae*	OR612978
Z6	*Aurantimonas coralicida* WP1^T	99.8	white	*Pseudomonadota*	*Alphaproteobacteria*	*Hyphomicrobiales*	*Aurantimonadaceae*	OR612977
Z8	*Arenibacter aquaticus* GUO^T	99.5	white	*Bacteroidota*	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	OR612979
Z10	*Pseudomonas leptonychotis* CCM 8849^T	99.8	white	*Pseudomonadota*	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	OR612980
Z12	*Aurantimonas coralicida* WP1^T	99.8	yellow	*Pseudomonadota*	*Alphaproteobacteria*	*Hyphomicrobiales*	*Aurantimonadaceae*	OR612981
Z14	*Paracoccus homiensis* DD-R11^T	99.8	yellow	*Pseudomonadota*	*Alphaproteobacteria*	*Rhodobacterales*	*Paracoccaceae*	OR612983
Z15	*Fictibacillus phosphorivorans* CCM 8426^T	100.0	cream	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR612982
Z16	*Mesobacillus subterraneus* COOI3B^T	99.8	yellow	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR612984
Z17	*Exiguobacterium aestuarii* NIO-Fe4^T	100.0	orange	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR612985
Z19	*Planococcus maritimus* TF-9^T	99.7	yellow	*Bacillota*	*Bacilli*	*Caryophanales*	*Caryophanaceae*	OR612986

Strain	Closest relative	Sequence identity (%)	Colonial color	Phylum	Class	Order	Family	16S rRNA GenBank accession number
Z21	*Rossellomorea marisflavi* TF-11^T	100.0	red	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR612990
Z24	*Brachybacterium ginsengisoli* T62^T	100.0	orange	*Actinomycetota*	*Actinomycetes*	*Micrococcales*	*Dermabacteraceae*	OR885466
Z28	*Mesobacillus jeotgali* YKJ-10^T	99.2	orange	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR871671
Z29	*Planococcus citreus* DSM 20549^T	99.2	white	*Bacillota*	*Bacilli*	*Bacillales*	*Planococcaceae*	OR612989
Z30	*Bacillus siamensis* KCTC 13613^T	100.0	white	*Bacillota*	*Bacilli*	*Caryophanales*	*Bacillaceae*	OR612987
Z31	*Psychrobacter celer* SW-238^T	98.9	white	*Pseudomonadota*	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	OR612988

Table S4. Comparison of cellular fatty acid compositions (%) in strain D39^T and its related reference strains. 1, strain D39^T; 2, *C. salegens* MCCC 1K01500^T; 3, *C. soli* MCCC 1K02066^T. Summed feature 3 contains $C_{16:1}\omega6c$ and/or $C_{16:1}\omega7c$; summed feature 6 contains $C_{19:1}\omega9c$ and/or $C_{19:1}\omega11c$; summed feature 8 contains $C_{18:1}\omega6c$ and/or $C_{18:1}\omega7c$. ND, not detected. TR, traces (< 0.5 %).

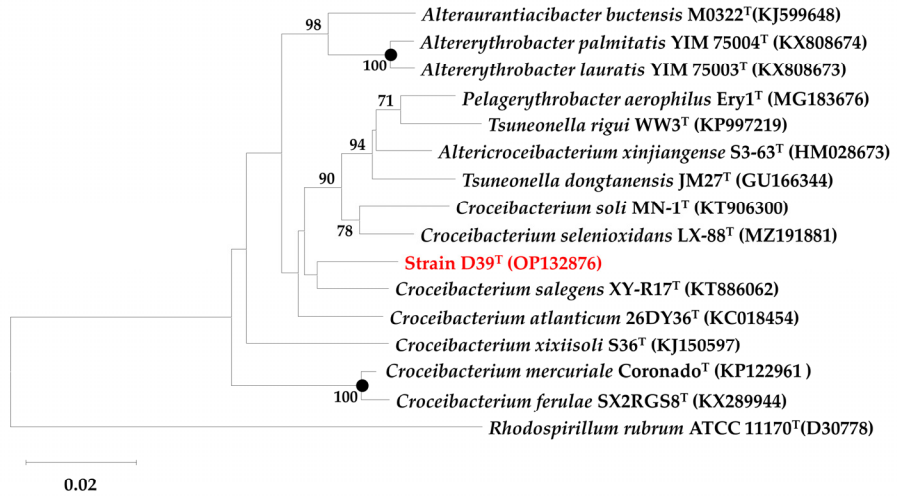
Fatty acid	1	2	3
Straight-chain			
$C_{12:0}$	TR	TR	0.5
$C_{14:0}$	0.6	0.5	0.7
$C_{16:0}$	15.8	3.5	24.2
$C_{17:0}$	2.2	0.6	0.6
$C_{18:0}$	1.5	0.6	2.0
Branched-chain			
iso-$C_{10.0}$	0.9	TR	1.8
Hydroxyl			
$C_{14:0}$ 2-OH	5.4	2.2	3.8
$C_{15:0}$ 2-OH	5.4	0.6	1.4
$C_{16:0}$ 2-OH	2.2	1.1	2.8
$C_{18:0}$ 3-OH	0.6	ND	1.0
$C_{16:1}$ 2-OH	ND	ND	0.8
Unsaturated			
$C_{16:1}$ $\omega5c$	1.0	6.1	1.2
$C_{17:1}$ $\omega6c$	7.3	10.8	4.2
$C_{17:1}$ $\omega8c$	0.6	0.9	0.7
$C_{18:1}$ $\omega5c$	0.5	0.9	TR
$C_{20:1}$ $\omega7c$	TR	ND	0.9
$C_{18:1}$ $\omega7c$ 11-methyl	22.3	ND	5.2
Summed feature			
Summed Feature 3	6.1	12.7	16.8
Summed Feature 6	ND	ND	2.2
Summed Feature 8	24.2	57.3	25.9

Table S5. Summary of relative abundance of *Pseudomonadota* members in other tidal flat regions.

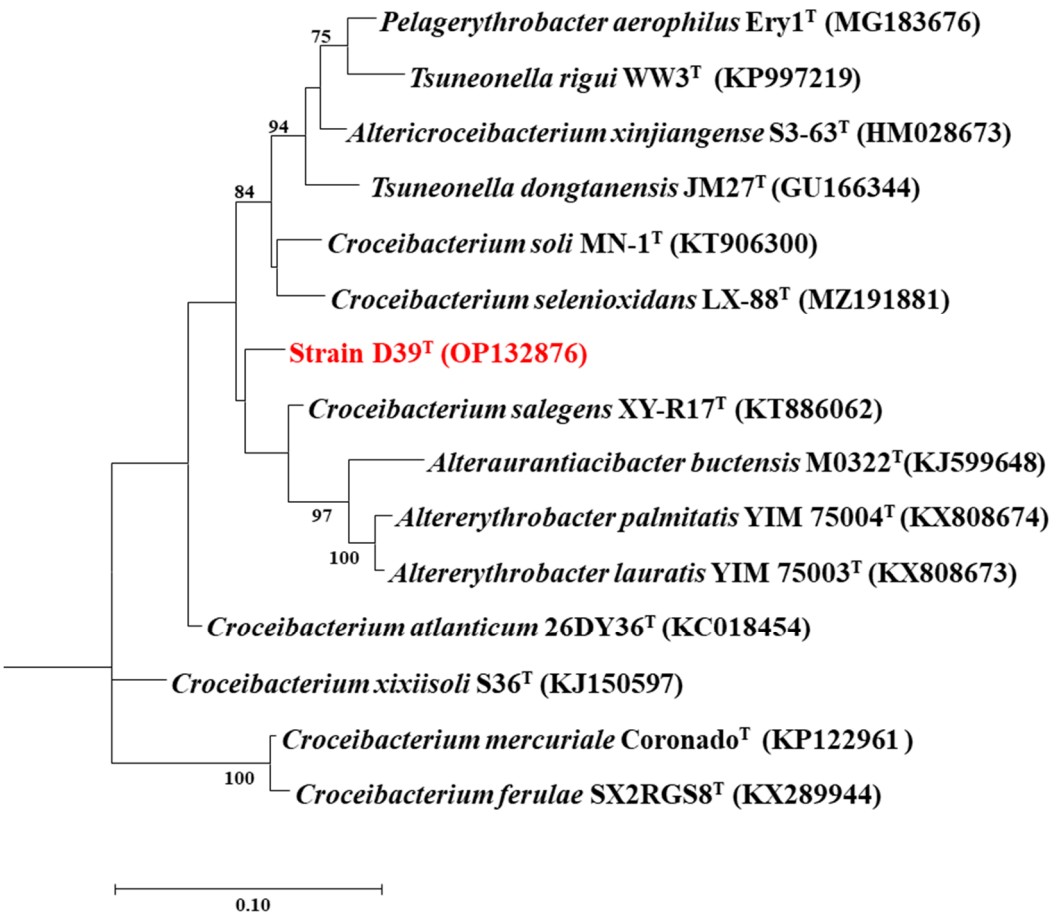
Region	Relative abundance	Reference
China		
Beibu Gulf	39-52%	[1]
Daya Bay	55%	[2]
Hangzhou Bay	28-32%	[3]
Mai Po Wetland	45-60%	[4,5]
Pearl River Estuary	44-55%	[6]
Sheyang	50%	[7]
Yellow River Delta	15-44%	[8]
Germany		
Spiekeroog	26-37%	[9]
Kenya		
Mida Creek and Gazi Bay	41%	[10]
Korea		
Sinduri Beach	55-72%	[11]
Incheon	41-50%	[12]
Taean Coast	65-67%	[13]
New Zealand		
Waiwera River estuary	54-58%	[14]
Oman		
Gulf of Oman	27-46%	[15]
Spain		
Bay of Biscay	21-50%	[16]

Figure S1. Neighbor-joining (A), maximum-likelihood (B) and maximum-parsimony (C) phylogenetic trees based on 16S rRNA gene sequences showing he phylogenetic relationship of strain D39^{T} and its similar type strains. Only bootstrap values higher than 70 % are shown.

(A)



(B)


Pelagerythrobacter aerophilus Ery1T (MG183676)
Tsuneonella rigui WW3T (KP997219)
Altericroceibacterium xinjiangense S3-63T (HM028673)
Tsuneonella dongtanensis JM27T (GU166344)
Croceibacterium soli MN-1T (KT906300)
Croceibacterium selenioxidans LX-88T (MZ191881)
Strain D39T (OP132876)
Croceibacterium salegens XY-R17T (KT886062)
Alteraurantiacibacter buctensis M0322T(KJ599648)
Altererythrobacter palmitatis YIM 75004T (KX808674)
Altererythrobacter lauratis YIM 75003T (KX808673)
Croceibacterium atlanticum 26DY36T (KC018454)
Croceibacterium xixiisoli S36T (KJ150597)
Croceibacterium mercuriale CoronadoT (KP122961)
Croceibacterium ferulae SX2RGS8T (KX289944)
75
94
84
97
100
100
0.10

(C)

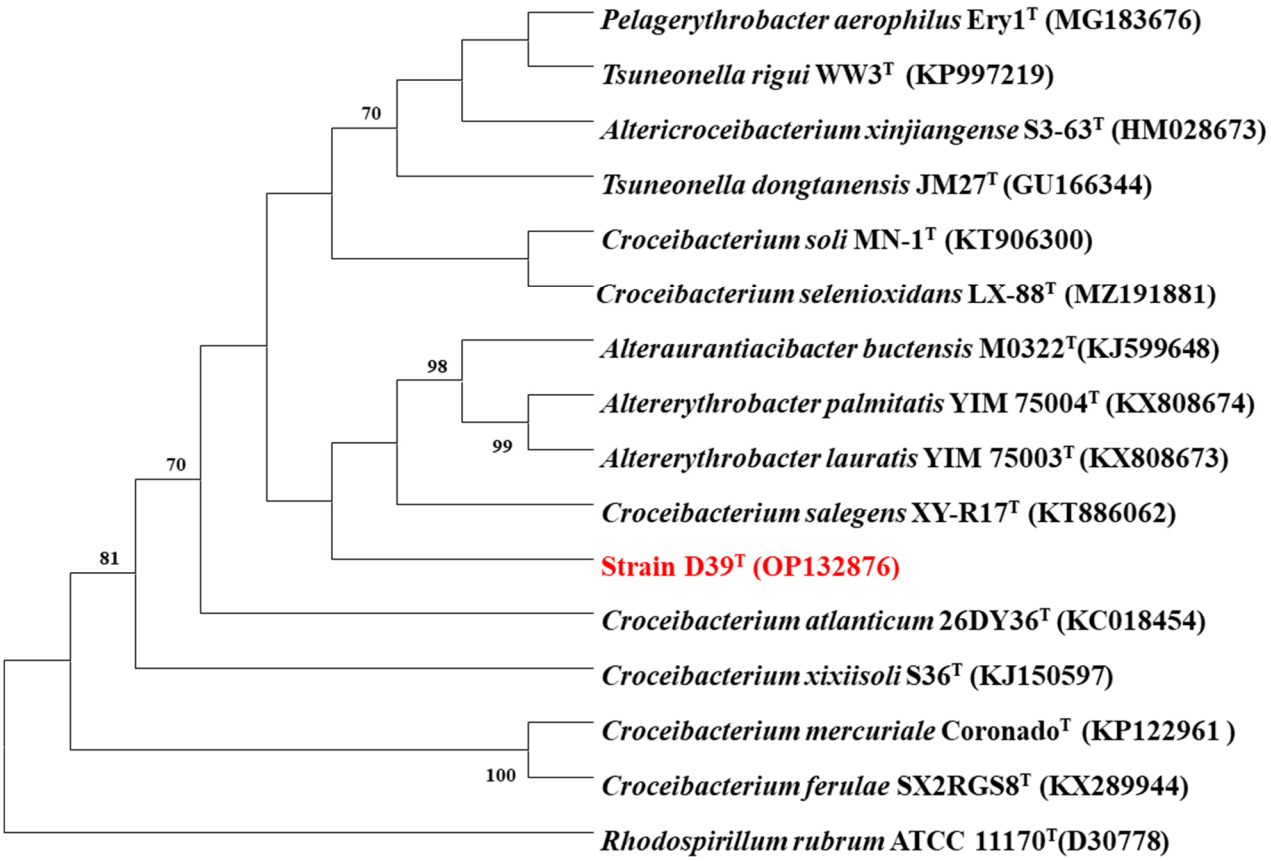
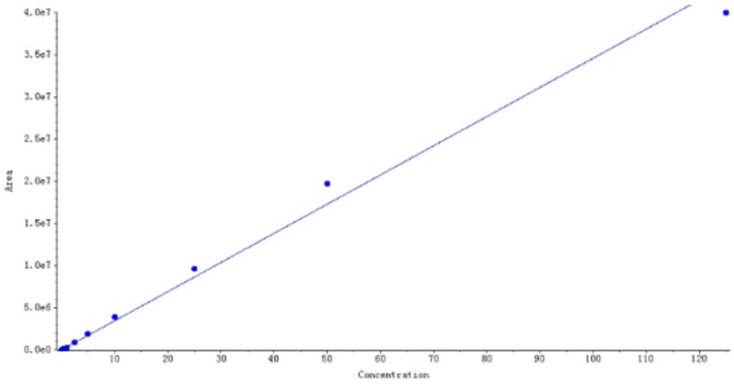

Pelagerythrobacter aerophilus Ery1T (MG183676)
Tsuneonella rigui WW3T (KP997219)
70
Altericroceibacterium xinjiangense S3-63T (HM028673)
Tsuneonella dongtanensis JM27T (GU166344)
Croceibacterium soli MN-1T (KT906300)
Croceibacterium selenioxidans LX-88T (MZ191881)
Alteraurantiacibacter buctensis M0322T(KJ599648)
98
Altererythrobacter palmitatis YIM 75004T (KX808674)
99
Altererythrobacter lauratis YIM 75003T (KX808673)
70
Croceibacterium salegens XY-R17T (KT886062)
81
Strain D39T (OP132876)
Croceibacterium atlanticum 26DY36T (KC018454)
Croceibacterium xixiisoli S36T (KJ150597)
Croceibacterium mercuriale Coronado T (KP122961)
100
Croceibacterium ferulae SX2RGS8T (KX289944)
Rhodospirillum rubrum ATCC 11170T(D30778)

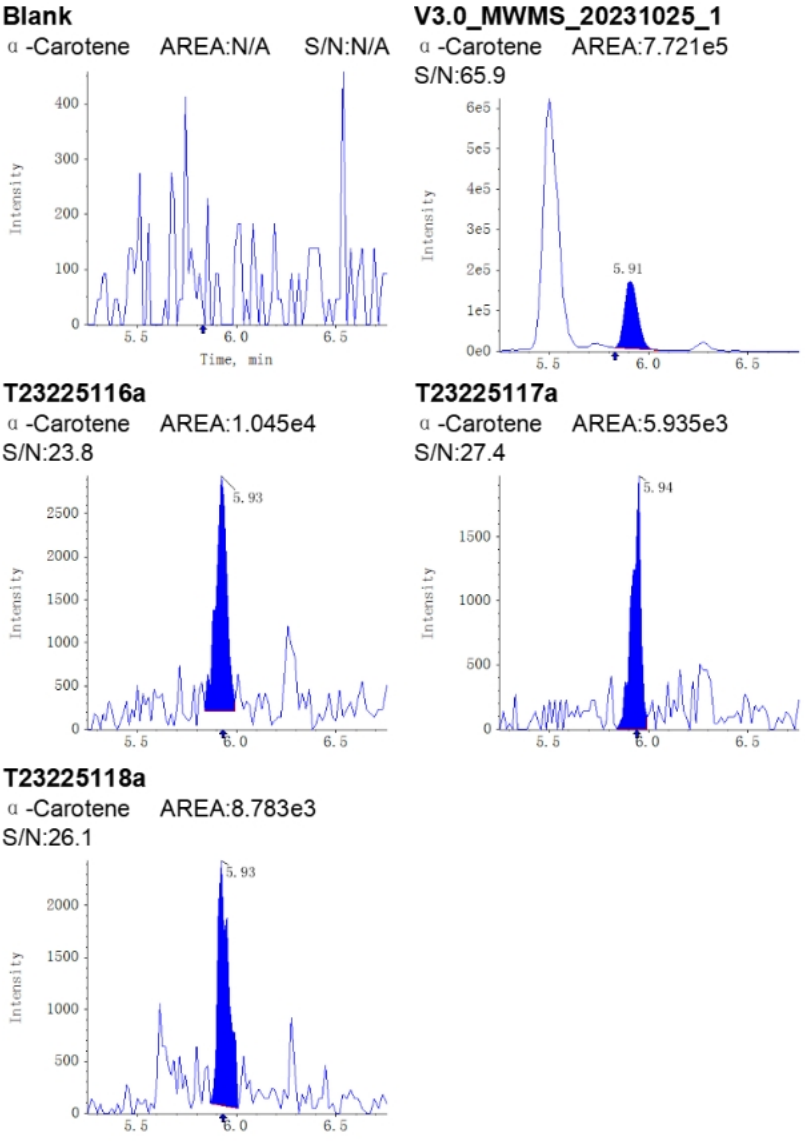
Figure S2. The regression equation and peak review of six major carotenoids content in strain D39^{T} are shown.

Compound name: α-Carotene

Regression Equation: y = 3.46e5 x + 1084.00 (r = 0.99)

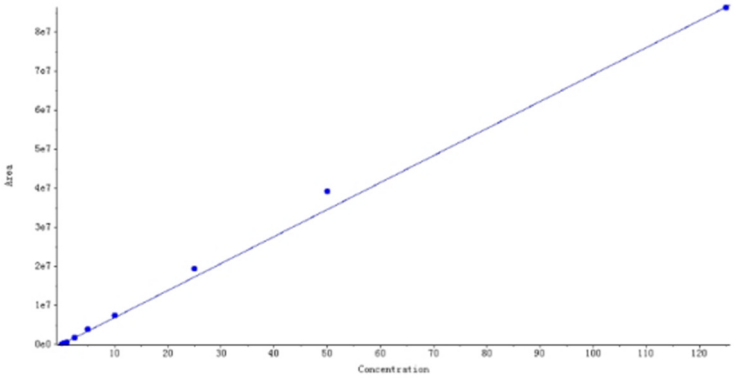


Peak Review



Compound name: *β*-Carotene

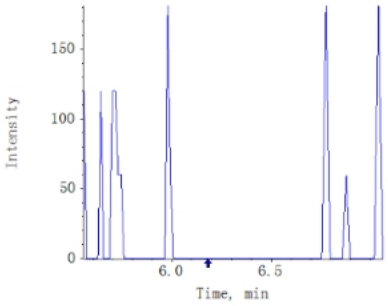
Regression Equation: y = 6.91e5 x + -1853.60 (r = 0.99)



Peak Review

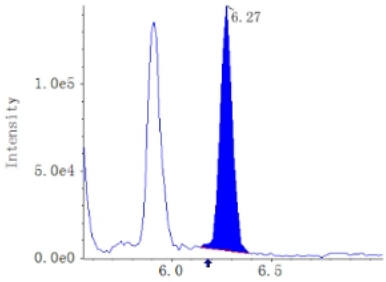
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β -Carotene AREA:N/A S/N:N/A



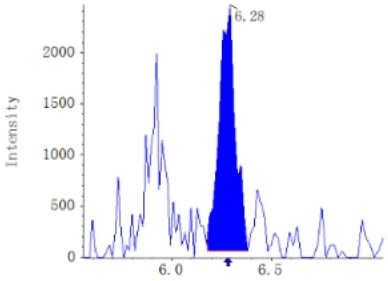
V3.0_MWMS_20231025_1

β -Carotene AREA:5.872e5 S/N:50.3



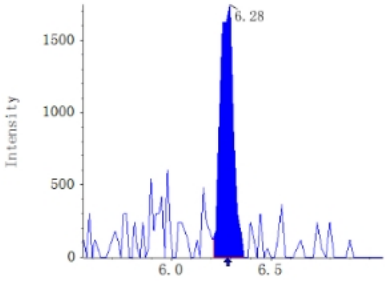
T23225116a

β -Carotene AREA:1.356e4 S/N:13.5



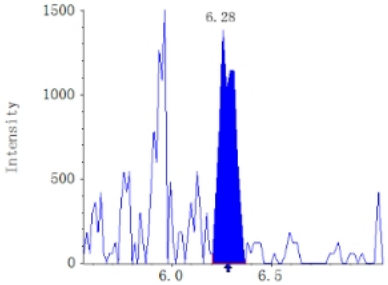
T23225117a

β -Carotene AREA:8.078e3 S/N:13.0



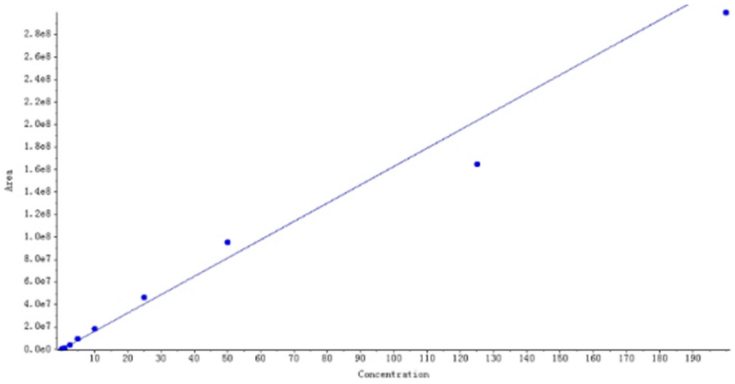
T23225118a

β -Carotene AREA:7.402e3 S/N:9.7



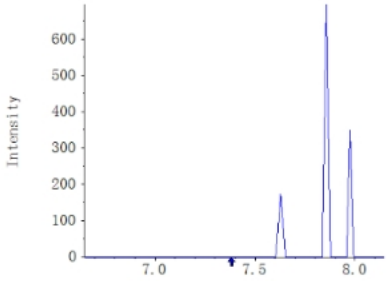
Compound name: lutein-dimyristate

Regression Equation: y = 1.63e6 x + -189.26 (r = 0.99)

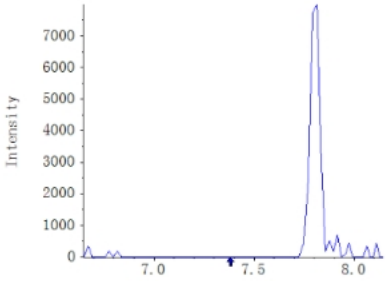


Peak Review

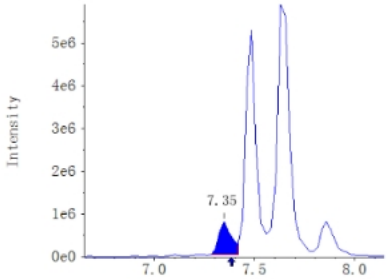
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lutein-dimyristate AREA:N/A
S/N:N/A



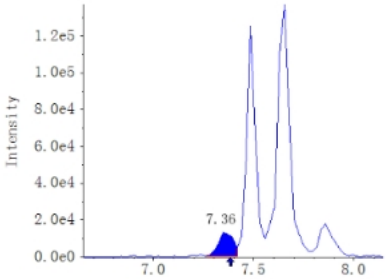
V3.0_MWMS_20231025_1
lutein-dimyristate AREA:N/A
S/N:N/A



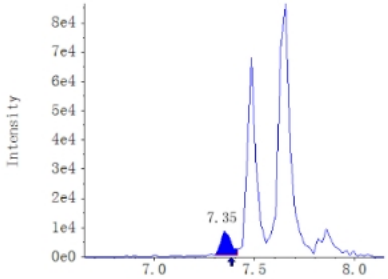
T23225116a
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S/N:15.1



T23225117a
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S/N:17.9

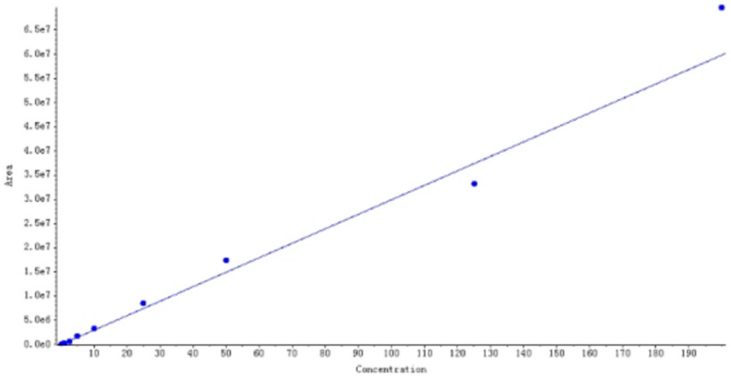


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lutein-dimyristate AREA:2.936e4
S/N:12.9



Compound name: Zeaxanthin

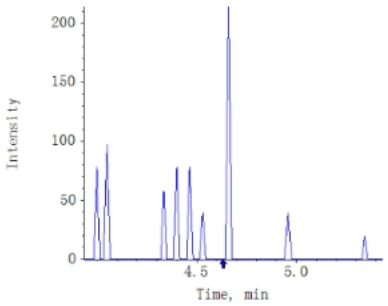
Regression Equation: y = 2.99e5 x + -731.12 (r = 0.99)



Peak Review

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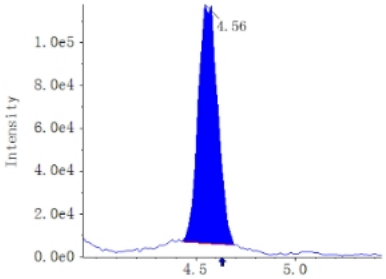
Zeaxanthin AREA:N/A S/N:N/A



V3.0_MWMS_20231025_1

Zeaxanthin AREA:7.567e5

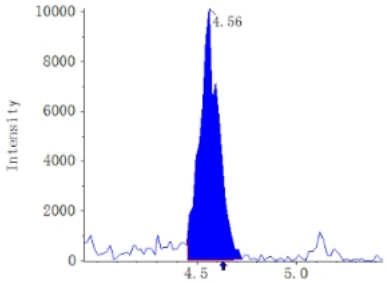
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T23225116a

Zeaxanthin AREA:6.527e4

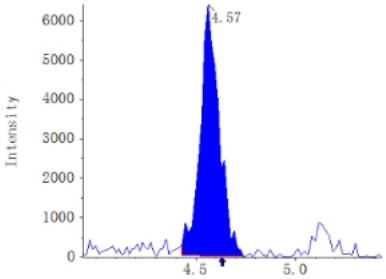
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T23225117a

Zeaxanthin AREA:4.218e4

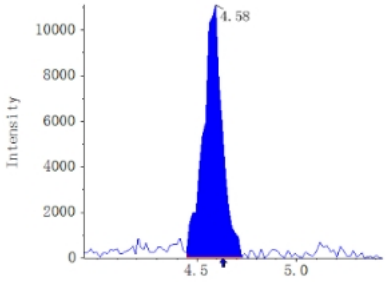
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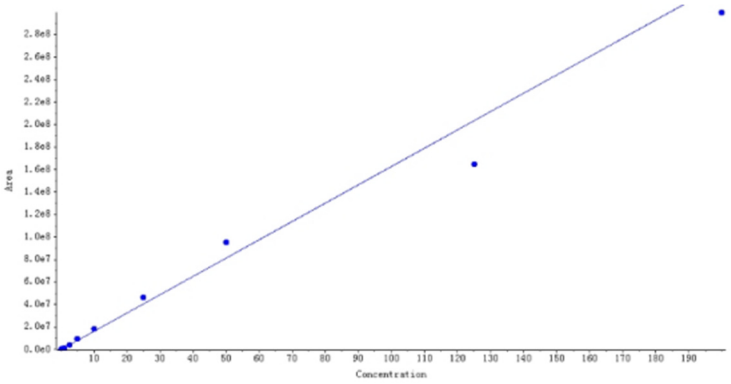
Zeaxanthin AREA:7.361e4

S/N:83.9



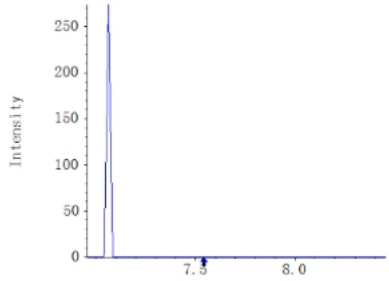
Compound name: zeaxanthin-dimyristate

Regression Equation: y = 1.63e6 x + -189.26 (r = 0.99)

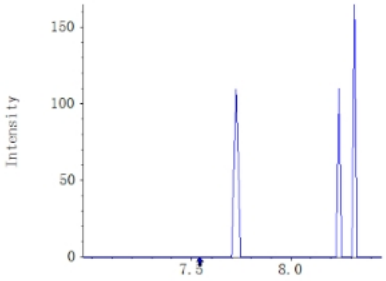


Peak Review

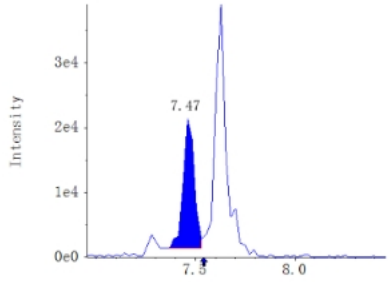
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zeaxanthin-dimyristate AREA:N/A
S/N:N/A



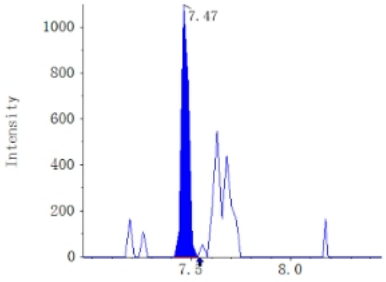
V3.0_MWMS_20231025_1
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S/N:N/A



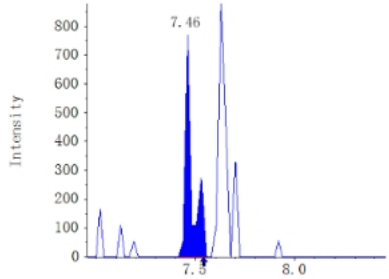
T23225116a
zeaxanthin-dimyristate
AREA:7.637e4 S/N:111.1



T23225117a
zeaxanthin-dimyristate
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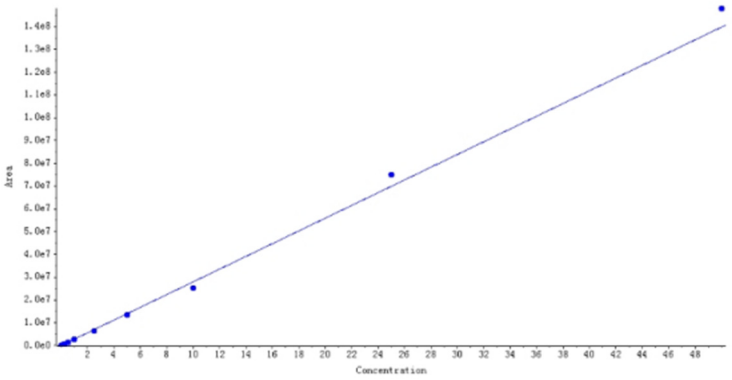


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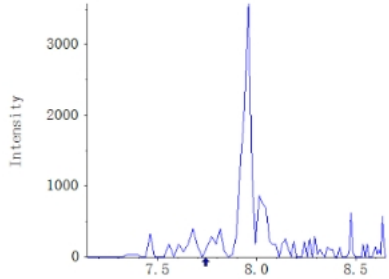
Compound name: zeaxanthin-dipalmitate_2

Regression Equation: y = 2.80e6 x + 4137.54 (r = 0.99)

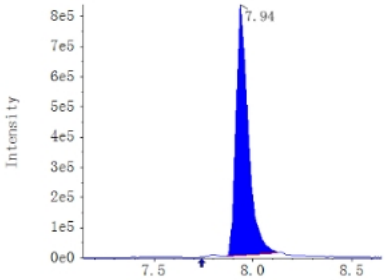


Peak Review

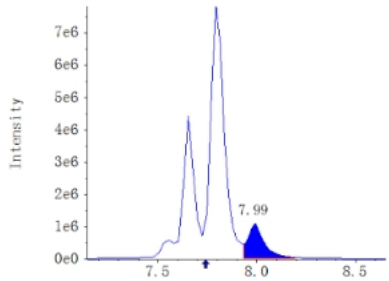
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S/N:N/A



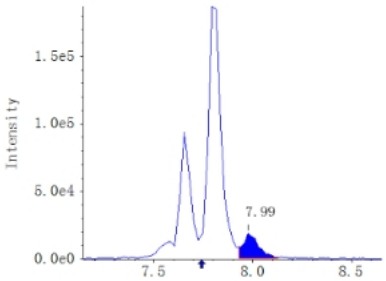
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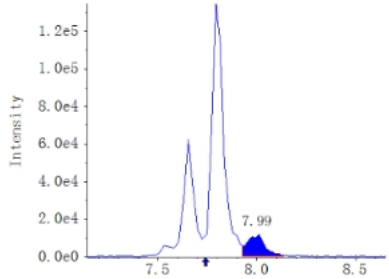
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AREA:9.819e4 S/N:10.7



T23225118a
zeaxanthin-dipalmitate_2
AREA:7.319e4 S/N:11.2



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