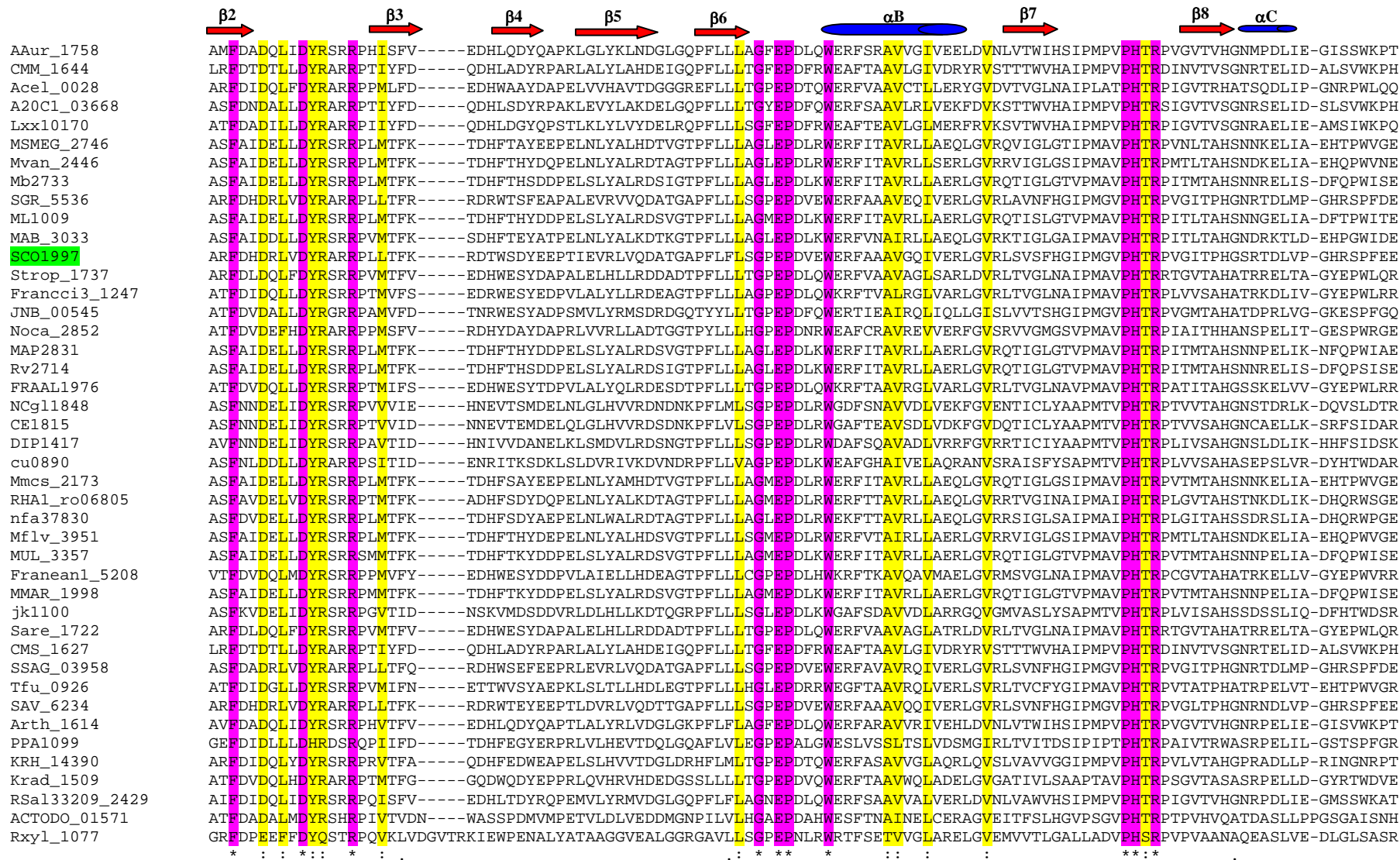


Additional file 3. Alignment of all available ASP1 homologues from actinobacterial species.

		$\beta 1$ →	← αA →	→ $\beta 2$
AAur_1758	MPSDVMSPGVMCWVPEPPRTLSLRKEHAVFERISGSLDDPES---	LYARNIETFH--SP-----	ELRGLNVMVGFT-----	GFADAGHVVRQINAEILLDELGAEVV
CMM_1644	-----MADADG---	LYEIDTDIGE--VP-----	TGLPLVAGLT-----	GFSDAGSGVSVQSEYLLSTLSHRDV
Acel_0028	-----MLDPTD---	LYTISGTPPAR--AP-----	DAPL-ILVHALS-----	GYVDAGDAVRLTARHLDTLDHREI
A20Cl_03668	-----MRDPAG---	LYDIATDVAG--VP-----	RGLPLVAGLT-----	GFADAGGAVSQFSQYLLDTLERSV
Lxx10170	-----MRDPGE---	LFELTS-ALE--VP-----	DGLPLVAGLT-----	GFADAGSGVSQLGTYLLATLHSEVV
MSMEG_2746	-----MADN-ENPQQRYQPDSG---	MYLEFPAPQLSSD-----	GRGP-VLIHALE-----	GFSDAGHAIRLAAEHLKSLDTEL
Mvan_2446	-----MADDVHDPGHEYQPEQTG---	MYELEFPGPQLSSPD-----	GRGP-VLIHALE-----	GFSDAGHAIRLSAQHLKDTLDTEL
Mb2733	-----MARDQGADAEAREYEPGQPG---	MYELEFPAPQLSSD-----	GRGP-VLVHALE-----	GFSDAGHAIRLAAHLKAALDTEL
SGR_5536	-----MPDPQS---	LYEWEPKGL-----	AVVDMALAQESAGLVMLYHFDGYIDAGETGEQIVDGLLETLPHQVV	
ML1009	-----MSHSHYQDPDDEQHYQPQPG---	MYVLEFPAPQLLASD-----	GRGP-VLIHALE-----	GFSDAGHAIRLAAHLKAALDTEL
MAB_3033	-----MTSNEGVEPQPYKPDQSG---	MYELEFPGPQLASAD-----	GRGP-VLVHALQ-----	GFSDSGHAVKLAAHLRQTLESEL
SCO1997	-----MLDPQD---	LYTWEPKGL-----	AVVDMALAQESAGLVMLYHFDGYIDAGETGQIVDQVLDLSLPHQVV	
Strop_1737	-----MLDPHE---	LYELTDDL-----	DLGQPLIQALS-----	GFVDAGNATRLAREQLTSLDARPV
Franci3_1247	-----MLDPDA---	LYDLAEDLAGG--SI-----	DLGRPVMLEAMT-----	GVVDAGSAVSLAGEHLKSLDHRLL
JNB_00545	-----MQNPSD---	LYRFEDGPA--PT-----	R-EPGALIVLLG-----	AFIDAGNIQRILGTHLVDTSEAEVV
Noca_2852	-----MPER---	LVHIVDEVPELDDAR-----	SRGALTMVLVLD-----	GFLDAGNAAGRAAHLVDLSEGPVV
MAP2831	-----MTHRQDAGD--QYQPGQAG---	MYEELPAPQLSTSD-----	GRGP-VLVHALE-----	GFSDAGHAIRLAAHLKAALDSEL
Rv2714	-----MARDQGADAEAREYEPGQPG---	MYELEFPAPQLSSD-----	GRGP-VLIHALE-----	GFSDAGHAIRLAAHLKAALDTEL
FRAAL1976	-----MLDPQE---	LYSLTEDASDD--PI-----	DAHRPIMLEALT-----	GVVDAGNAVSLAGEHLTALDHRIV
NCg11848	-----MSDNND---	RMYELEYPSPEVSGQT-----	AGGPTLIVALQ-----	GYADAGHAVESSSHLMDALDHRLLI
CE1815	-----MSDNKE---	SMYELEYPSPEVNGGG-----	SEGPTLIVALQ-----	GYADAGHAVEASASHLMAALDHRLLI
DIP1417	-----MNEREA---	KMYELEFPAPDVASDG-----	VDGPTLIAMQ-----	GYADAGLAVASADHLLSALEHRPV
cu0890	-----MPQ-----	DNSFGRRRPNA--MYEMEYPVLEADSP-----	DEGIPMLIALQ-----	GYADAGQAIASVGNHLEALESSVV
Mmcs_2173	-----MADHPDIPEQQYQPEQTG---	MYELEFPAPQLSAAD-----	GRGP-VLLHALE-----	GFSDAGHVVRLATAHLKNSLDTEL
RHA1_ro06805	-----MDEQSK---	MYELEFPAPQLSSAD-----	GQGP-VLIHGLE-----	GFSDAGHAVKLATTHRESLESEL
nfa37830	-----MDYESR---	MYELEFPAPQLSSAD-----	GSGP-VLVHGLE-----	GFSDAGHAVRLATTHRESLESEL
Mflv_3951	-----MADDAHDSGSRYQPEQTG---	MYELEFPGPQLSTPD-----	GRGP-VLIHALE-----	GFSDAGHAIKLAAHLKNSLDTEL
MUL_3357	-----MAHDQDPGEAQDYQPQSG---	MYELEFPAPQLSTSD-----	GRGP-VLVHALE-----	GFSDAGHAIRLAAHLKDGLDTEL
Franean1_5208	-----MLDPRE---	LYEIRSDLD-----	DLGRPVLIEAMT-----	GVVDAGGAVGLASEHLTTALQHERI
MMAR_1998	-----MAHDQDPGEAQDYQPQSG---	MYELEFPAPQLSTSD-----	GRGP-VLVHALE-----	GFSDAGHAIRLAAHLKDGLDTEL
jk1100	-----MHQHFNNGDEHNGRHERKAAGRMYEMEYPAPIQFDRPSIADATGLGSAVGESEELPMLVALQ-----			GYADAGQAVSSASSHLAALAEHSPV
Sare_1722	-----MLDPHE---	LYELADDLP-----	DLGQPLIQALS-----	GFVDAGNATRLAREQLTSLDARPV
CMS_1627	-----			MSQVSEYLLSTLSHRDV
SSAG_03958	-----MLDPQG---	LYEWDKGL-----	AVADLALAQDSAGLVMLYHFEGYIDAGEAGEQIVERLLDTPHLQV	
Tfu_0926	-----MRDPAD---	LYELRSDL-----	ELSEPMLVSLD-----	GFVDAGAAGKQAVATLLDGLQHTEL
SAV_6234	-----MLDPQG---	LYAWEPKGL-----	AVVDMALAQESAGLVMLYHFDGYIDAGETGQIVDRLLDLSLPHQVV	
Arth_1614	-----MLERISGSLDDPDA---	LYVSNAELFD--NP-----	ELRGLNLMVGFT-----	GFADAGHVVKQITAEILLDTLESEVV
PPA1099	-----MDRQSN---	RFSWHPGIVG--PD-----	Q-EVSALITLVQ-----	SFSDTGLVQARVRDALLSQLPHHEL
KRH_14390	-----MLDPTA---	LYLGNPALLG--DP-----	RLRGLPLVVALS-----	GYVDEGLAAQIEAVVLDSSMPSETV
Krad_1509	-----MLDPGS---	LYSYGERP-----	ALVEPPLVVALS-----	GFIDAGNAVRLSVEHLLATCRHEVV
RSa133209_2429	-----MTDRCGRIR---	MKEIKYVPLRDPDT---	LYATNGAMLQ--DE-----	GLRGLNLLMGFT-----
ACTODO_01571	-----MSINATD---	LYADGPAAG--DE-----		AKAKILLIHFD-----
Rxyl_1077	-----MDERYLDLEWRPELERP-----			VLVSAFT-----
				GWNDAAEAASMAALSALGNWGVRRF



AAur_1758 VDVPAAIIGHILELRLTEAERNVAGYVIHVPHYLSEAEYPPAAVAGLEYLGAATSLMLP--TDRLEAGREVGRQIAEQIEA-SEEVQAVVTNLETRYD---EKSEGIVRRSLLAD-EN-D
CMM_1644 TQVPANALHLVEHRLHDAGHPVAGFVLLVPHYLADTEFPPLAAVAALLESISAATGLIFP--TDRLEEGRDFVGRIDEQVAG-NQELARLVTTLEERYD---SYMEDTPLKSPLTD-ED-G
Acel_0028 VHVPSAAHLLLEFRLGEGQRKAMGIAVHVPHYVAQSEFPAAALRLIDELRERTGLDLP--REPIATAAAATLAEIDRQVGE-STDAMAMVSTLEQQYD---AFLHARSGESPLGGG-T-D
A20C1_03668 TQVPANAMHLLIEYRLQELGHPTAGFVLLIIPHYLADTEWPTAAVTALESVSAATGLIFP--TDRLEDRGREFVAKIDSQVES-NQELARLVGTLEERHD---NYMENPMRSPPLTD-ED-G
Lxx10170 TQVPANALHLLLEFRLQPLSYPIAGFVLLIIPHYLADAEYPAAAITGLESISAATGLIFP--TDRLEDDRQFVANINEQVAG-NAELGRLVGTLENRHD---SYMEDNQPRSPLTD-RD-G
MSMEG_2746 VQVPASVSNLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTAYPPAAEALLAEVARTGSLLELP--LAALSEAGAEVYTKINEQVEA-SPEVAQVVSALERQYD---AFIAAQENRS-LLARD--E
Mvan_2446 VQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTDYPSAAETLLSEVARNGSLEIP--TTKLTQAAAQVFDKINEQVAG-SAEVAQVVEALERQYD---AFVAAQENRS-LLARD--E
Mb2733 IQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LAALAEAAAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
SGR_5536 AQVPGSAEALVEYRLMESGHGHDVVGTVHVPHYVARSAYPDAALTALEAITAATGLVLPALAHTRTEAHRQTQTEIDRQIQGDEELVSLVEGLEHQYD---AVAGSETRGNLVAEP---V
ML1009 IQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LSALAEAAAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
MAB_3033 VQVPGSASNLLEFRMAQHGHGHDVVGFAVHVPHYLQTDYPEASQRLLLEEVARTGDLTDL--LQELSEAAAQVNRQINEQVEG-SEVAQVVAALERQYD---AFVAAQENRS-LLARD--E
SCO1997 AQVPGSAEALVEYRLAQAGHDVVGFAVHVPHYVARSAYPDAALTVLEAITAATGLVLPPIAHSRTDAHRQTQTEIDRQIQEGDEELIALVQGLEHQYD---AAAGAEITRGNMLAEP---V
Strop_1737 VQVPGSIGHLLLEFRMAQHGHGHDVVGFAVHVPHYVARSAYPDAALTVLEAITAATGLVLPPIAHSRTDAHRQTQTEIDRQIQEGDEELIALVQGLEHQYD---AAAGAEITRGNMLAEP---V
Francci3_1247 LQVPGSAGHLLLEFELGREGRDAMGFAAHVPHYLQTTYPAAETVLLTSVSKATGLLLP--LDGLRSAAVAQDEVDQIAR-GGEEAAALVSALEEQYD---AYQRGRGSPSLPAADDV-Q
JNB_00545 IQVPAFPPALLELRLGEGRDALGFIAHVPHYLQQAQAEWAGALALNAITDATTGLNLP--NDLLAKAGINNREIASELND-NADAGQIVSALEEQYD---AFVQGERPS-LLATEA-E
Noca_2852 LRIPSSAQALLEVRLGEWGDAMGFVAHVPHYLQMDYPRASAALLEQVEIAGRLTVD--LSGLRAEAEDREAEIARYLAA-NEEVAEVVAALERQYD---AFERAESGTSLLARD--Q
MAP2831 LQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LAVLAEAAAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
Rv2714 IQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LAVLAEAAAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
FRAAL1976 LQVPGSAGHLLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTTYPAAETVLLTSVSKATGMLLP--LDGLRSAAVAVQDEVDNSQIAR-GGEEAAALVHALLEEQYD---AYQRGRGSPSLPTIDAE-Q
NCg11848 MTVPGSASLMLEKLLKDKGNVSGYTVHVPHYVSASPYPAATLKLKQSIADSLNLP--LLALERDAEKVHRQLMEQTEE-SSEIQRVVGALEEQYD---SELERYRNRHPQAVMPGE-S
I1815 ISIPGSAHLLLEFRMAQHGHGHEVVGFVTVHVPHYVAASPYPAATLKLKQSAVETAGLNL--LLSGLRAEAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
DIP1417 VTIIPGASLHIERLLNKNNDVAGYTAHVPHYLSASAYPLATLKLLEAITTSTNLDFF--LKTLEADAQKTAQVEEQVAG-SQIEESVVKILEEQYD---EELEKYRERNPKALEIAE-D
cu0890 LVVPGAAALETEMQLSAAGFDAIGLTAHVPHYIAGSEYPEASYALLKAFADLADREL--LKTLEKDMRVQQLAQQTQD-SHEIATVVGALVEEQYD---KEVRLQKKK-SSLEPG-Q
Mmcs_2173 VQVPASVSNLLEFRMAQHGHGHEVVGFVTVHVPHYLSQTAYPPAAESLLAEVAKTAALQIP--LTALEAGAEVYTKINEQVEA-SPEVAQVVTALERQYD---AFVAAQENRS-LLAHD--E
RHA1_ro06805 LQVPGSASSLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTDYPSAAETLLLENVSDVTDLDP--LAALGEAAARVREQVDEHIAG-NEEVQTVVHALERQYD---AYVTAQEQSTLLASE--E
nfa37830 LQVPGSASSLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTTYPAAEQTLLEHVADNAGLELP--LAALGEAAARVREQVNEHIAG-NPEVETVVAALERQYD---SFVTAQERQSSLLAAD--G
Mflv_3951 VQVPGSASNLLEFRMAQHGHGHEVVGFVTVHVPHYLAQTDYPSAAETLLAEVARTASLDIP--TAEITAAAVVFDKINEQVTA-SAEVAQVVDALERQYD---AFVAAQENRS-LLARD--E
MUL_3357 IQVPAASASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LAALTDASAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
Franean1_5208 LSVPGSAGHLLLEFRMAQHGHGHEVVGFVTVHVPHYLAQATYPAAETALLSSVSKSTGLLPP--LDGLRSAALEVVRGEVDSQIAR-GGEEAADVVKAIIEQYD---AFHRTGEGEHLPVVDDS-E
MMAR_1998 IQVPAASASNLLEFRMAQHGHGHEVVGFVTVHVPHYLTQTDYPAQAALLEQVAKTGSLLQLP--LAALTDASAQVQAKIDEQVQA-SAEVAQVVAALERQYD---AFIDAQENRS-LLTRD--E
jk1100 MIVPGAAALETEKLLNRHGFFETVGLTAHVPHYIAASDYPEAPLRLQAFGKVANREL--LKALEKELERVQHQLQDQVED-SQIEIATVVSALVEHQYD---AEMERMRRKRENNLLKPG-Q
Sare_1722 VQVPGSVGYLLEFRMAQHGHGHEVVGFVTVHVPHYVAQTEYPAAAEVLLSSVSRSTGLLLP--CDELRAATEAVRTEIDRQVAG-TEDAALVQALEEQYD---AFTRGRGQPNLLNTG-A-G
CMS_1627 TQVPANALHLLLEHRLHDAGHPVAGFVLLVPHYLADTEFPPLAAVAALLESISAATGLIFP--TDRLEEGRDFVGRIDEQVAG-NQELARLVTTLEERYD---SYMEDTPLKSPLTD-ED-G
SSAG_03958 AQVPGSAESLVEFRLGQAGHDVVGFAVHVPHYVARSPYDAALTALEAITAATGLVLPVAHAHRTEAHRQTQTEIDRQIREGDEELVSLVQGLEHQYD---AAAGAEITRGNMLAEP---A
Tfu_0926 IQVPGNIMSLLEFRMAQHGHGHEVVGFVTVHVPHYLAQSEYPRAGLAVLEIARVTVGLVLP--TEKLAEEATRVGDENRQVEA-SEEVQRVVRLNLEAQYDNFMAVHNGLDVLDALLAGD-E-S
SAV_6234 AQVPGSAESLVEYRLMEAGHDVVGFAVHVPHYIARSPYDAALTVLEAITAATGLVLPGLAHSRTEAHRQTQTEIDRQIQEGDEELVALVQGLEHQYD---AAAGAEITRGNMLAEP---V
Arth_1614 VEVPAAVGHILLELRLSEAGRNIAGYAVHVPHYLADAEYPAAAVAGLEYLGAATSLMLP--TDRLEAGREVGRQIAEQLEA-SEEVQVVSRLLETRYD---EKABGTTPVRSLLAD-EN-D
PPA1099 LQVPAFPPVVLGQRLGETNHAVIGLASHVPHYLADLDYPEARALVEALRGATGLALP--INSLAVAANTVRAEIDTQVNN-SEELKAMLHLEEQYD---SRVAQRE-----LGTTQ-V
KRH_14390 FEVSASVSHLLELRLQENGIDHVGLSVHVPHYLAEVSYLPAQAAVAALVEYLAVTGRTP--TDELREASRDVIRQIDEQAGS-SPEVQAVIENMERRYD---DVVDASARRSILAGPDD-A
Krad_1509 AQVPGHASALLHLRGSQQGRDVLVSLAVHVPHYLAGNDYDPAAAVIVRTLSGATGVGIP--VQSLQEASRTRVEVDRQITE-SPEAASVVEALERQYD---AIG-EEGRG-TGAAS---A
RSa133209_2429 VQIPSAIGHILLELRLSAGRNIAGYAVHVPHYLADAEYPAAAVAGLEYLGAATSLMLP--TDRLEAGREVGRQIAEQLEA-SEEVQVVSRLLETRYD---EKABGTTPVRSLLAD-EN-D
ACTODO_01571 MQFPSPSTFMQIRMQRGIGGLVLLGAVPYMADTGYPAASSALLTSFAKFAFADLSLP--VGDLEQGAQDQENIAKLVEG-NPDISHTVSNLEHFDWATGGEGAIPLPGLGQRPASAGG
Rxyl_1077 YEGPTGITVGLHTLCAEAGLPAVSLWASMPHYLPAVPSAPGALALVESLAGLGTVEVE--TGDLEBGAERYQEQVSAAVAR-DPDLSSYVKMLLEERYD-----ASQEEGGGQIR

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The Gene ID of each sequence corresponds to the following genomes:

AAur_1758	ELPNAEDI GA AVEAYLARKDSAQ-----	AAur_1758: <i>Arthrobacter aurescens</i> TC1;
CMM_1644	ALPTADEI AAELEKFLARRRPGDGDA-----	CMM_1644: <i>Clavibacter michiganensis</i> NCPPB 382;
Acel_0028	NLPSADEL AAELEKFLAEQA--RRHRDDRQ-----	Acel_0028: <i>Acidothermus cellulolyticus</i> 11B;
A20C1_03668	ELPSADEI AAELEKFLAIRRAGDDDDSTTGLPL-----	A20C1_03668: marine actinobacterium PHSC20C1;
Lxx10170	ELPSADEI AAELENFLAFRRHGDEDNSRGR-----	Lxx10170: <i>Leifsonia xyli</i> subsp. <i>xyli</i> str. CTCB07;
MSMEG_2746	DLPSGDEL GA EFERFLAQQAGEKFKDDKYKDGHGEGFGGRIRGTVTTTDDVDPDQG-----	MSMEG_2746: <i>Mycobacterium smegmatis</i> str. MC2 155;
Mvan_2446	DLPSGEEL GA EFERFLAQQAGEKKRKKD-GDD-PREGL-----	Mvan_2446: <i>Mycobacterium vanbaalenii</i> PYR-1;
Mb2733	DLPSGDEL GA EFERFLAQQAEKKSDDDPT-----	Mb2733: <i>Mycobacterium bovis</i> AF2122/97;
SGR_5536	DLPSADEI GREFERFLAERE----GEG-----	SGR_5536: <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350;
ML1009	DLPSGDEL GA EFERFLAQQAEKKRDDDLT-----	ML1009: <i>Mycobacterium leprae</i> TN;
MAB_3033	ELPSGDEL AGEFERFLAEQA--KFGDDPSGSPSPEGPIL-----	MAB_3033: <i>Mycobacterium abscessus</i> ;
SCO1997	EIPSADEI GREFERFLAERE----GDG-----	SCO1997: <i>Streptomyces coelicolor</i> A3(2);
Strop_1737	ALPTADEL GA ELERFLAEQT-RPND-NPGG-----	Strop_1737: <i>Salinispora tropica</i> CNB-440;
Francci3_1247	PLPTADEL GDALERFLAEQT-EPDGPTPNP-----	Francci3_1247: <i>Frankia</i> sp. CcI3;
JNB_00545	DLPSADEL GA D I E E F L R N V S D D-----	JNB_00545: <i>Janibacter</i> sp. HTCC2649;
Noca_2852	RLPTGEEI GKEFERFLAGLDRPGDDEPQG-----	Noca_2852: <i>Nocardioides</i> sp. JS614;
MAP2831	DLPSGDEL GA EFERFLAQQAEKKFDDDDQA-----	MAP2831: <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> K-10;
Rv2714	DLPSGDEL GA EFERFLAQQAEKKSDDDPT-----	Rv2714: <i>Mycobacterium tuberculosis</i> H37Rv;
FRAAL1976	KLPTADEL GA ELERFLAEQS-EPGGPNPLS-----	FRAAL1976: <i>Frankia alni</i> ACN14a;
NCg11848	ELPSGDEI GA EFKFLADLDDQGGSDHKETPEA-----	NCg11848: <i>Corynebacterium glutamicum</i> ATCC 13032;
CE1815	PVPSGDEI GA EFERFLANLDDSGDPDGPEDNGQ-----	CE1815: <i>Corynebacterium efficiens</i> YS-314;
DIP1417	DLPDADDEL GEEFERFLANLDEENGSD-----	DIP1417: <i>Corynebacterium diphtheriae</i> NCTC 13129;
cu0890	DIPTGEEL GA EFAELARMNDAADTDEADGEDPKKPGDSNDPHDDGEGDTQ-----	cu0890: <i>Corynebacterium urealyticum</i> DSM 7109;
Mmcs_2173	DLPSGDEL GA EFERFLAQQAGEKDKEDRYRDFSDGE-----DRS-----	Mmcs_2173: <i>Mycobacterium</i> sp. MCS;
RHA1_ro06805	DLPSGDEL GA EFERFLAEQALQDGGSDDEGGSPGGA-----	RHA1_ro06805: <i>Rhodococcus</i> sp. RHA1;
nfa37830	DLPSGEEL GA EFERFLAEQGGYDG---DKD-----	nfa37830: <i>Nocardia farcinica</i> IFM 10152;
Mflv_3951	DLPSGEEL GA EFERFLAQQAGEKKRKKD-GDDQPREGL-----	Mflv_3951: <i>Mycobacterium gilvum</i> PYR-GCK;
MUL_3357	DLPSGDEL GA EFERFLAQQAEKKFDDDDQP-----	MUL_3357: <i>Mycobacterium ulcerans</i> Agy99;
Franean1_5208	PLPTGEEL GA ALERFLAEQS-EPGGQPPT-----	Franean1_5208: <i>Frankia</i> sp. EAN1pec;
MMAR_1998	DLPSGDEL GA EFERFLAQQAEKKFDDDDQP-----	MMAR_1998: <i>Mycobacterium marinum</i> M;
jk1100	DIPTGEEL GA EFAELQNMSDGDLSD--ENGADN--SADSDEQEEN-----	jk1100: <i>Corynebacterium jeikeium</i> K411;
Sare_1722	SLPTADEL GA ELERFLAEQT-RPND-NPGG-----	Sare_1722: <i>Salinispora arenicola</i> CNS-205;
CMS_1627	ALPTADEI AAELEKFLARRRPGDGDA-----	CMS_1627: <i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i> ;
SSAG_03958	EIPSADEI GREFERFLAERE----GEG-----	SSAG_03958: <i>Streptomyces</i> sp. Mg1;
Tfu_0926	RLPTADEL GA ELERFLAEHGRGSAEHDRGSEG-----	Tfu_0926: <i>Thermobifida fusca</i> YX;
SAV_6234	EIPSADEI GQEFERFLAERE----GEG-----	SAV_6234: <i>Streptomyces avermitilis</i> MA-4680;
Arth_1614	ELPNADAL GA AVEAYLAREEPRQ-----	Arth_1614: <i>Arthrobacter</i> sp. FB24;
PPA1099	AVPDAEDI GA EVDLRS IDEDDGSPNDDPDTQSGPRRSSDDTSDDDKPDYHPRRGDDL-----	PPA1099: <i>Propionibacterium acnes</i> KPA171202;
KRH_14390	DLPDADDL GAAA E A F L A A Q S D P D A H E D-----	KRH_14390: <i>Kocuria rhizophila</i> DC2201;
Krad_1509	FLPTADEL GEEFERFLAGQEDEPDGDGPPGDRPGAG-----	Krad_1509: <i>Kineococcus radiotolerans</i> SRS30216;
RSa133209_2429	ELPDADDEL GAAI EAYLAERDDTAERDDTTG-----	RSa133209_2429: <i>Renibacterium salmoninarum</i> ATCC 33209;
ACTODO_01571	EKTPKDI GDVI EAYLAQVSRAQDEEIESVQRAPRTEESEEPSKPDITIEDVLARIEARRN-----	ACTODO_01571: <i>Actinomyces odontolyticus</i> ATCC 17982;
Rxy1_1077	HLPSGDEL LAREL E D F L R R Q R G E D E Q-----	Rxy1_1077: <i>Rubrobacter xylanophilus</i> DSM 9941.
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Notes: Conserved residues are colored as such: purple, absolutely conserved residues; yellow, highly conserved. β strands and α helices are labeled in red and blue, corresponding to the ribbon diagram in Figure 2.