

LanFP1 MP LPA --- THD IHLHGSINGHEFDLVGGGKDPNAGSLVTTAKSTK-GALKFSPYLMIPHLGYGYQYLPYPDG-P
LanFP2 MS LPT --- THDLHIFGSVNGAEFDLVGGGKGNPNDGTLETSVKSTR-GALPCSPLLIGPNLGYGFYQYLPFPGG-A
LanFP3 MP LPA --- THEIHLHGSVNGHEFDLVGSGKDPKAGSLVTEVKSTM-GPLKFSPHLMIPHLGYGYQYLPYPDG-P
LanFP4 MP LPT --- THELHIFGSFNGVEFDLVGRGEGNPKDGSQNLHLKSTK-GPLQFSPWMLIPHIGYGFYQYLPYPDGEM
LanFP5 TPLPT --- THELHIFGSFNGVEFDLMVGRGIGNPNDGYEELNLKSTK-GALKFSPWILVPRQIGYGFHQYLPYPDG-M
LanFP6 MP LPK --- THELHIFGSFNGVKFDMVGEGTGNPNEGSEELKLKSTN-GPLKFSPYILVPHLGYAFNQYLPFPDG-M
LanFP7 MSVPT --- NLDLHIYGSINGMEFDLVGGSGNPNDGSLSVNVKSTK-GALRVSPLLVGPHLGYGHYQYLPFPDG-P
LanFP8 MS LPT --- THDCHMFGSINGHEFDLVGGGNPNNDGTLETKVRSTK-GALPFPSPVILAPNLGYGYHQYLPFPAG-T
LanFP9 MP LPA --- THEIHLHGSINGHEFDLAGGKDPNAGSLVTTAKSTK-GPLKFSPHLMIPHLGYGYQYLPYPDG-P
LanFP10 LPLPK --- THELHIFGSFNGVEFDLVGRGIGNPNEGSEELNAKFTK-GPLKFSPYILVPHLGYAYQYLPFPDG-M
LanFP11 MP LPA --- THEIHIYGSVNGHEFDLVGGGKDPNAGSLVTEVKSTM-GPLKFSPHLMIPHLGYGYQYLPYPDG-P
LanFP12 QPLPT --- THEVHVYGSINGVEFDLVGSGKGNPKDGSSEIQVKSTK-GPLGFSPYIVVPNIGYGFHQYLPFPDG-M
GFP1_Ponme_33243032 MPDM --- KLECHISGTMNGEEFELIGAGDGNTDEGRMTNKMKSIG-GPISFSPYLLSHILGYGYHFATFPAGYE
GFP1_Ponpl_33243026 MPAM --- KIECRISGTLNGVVFEVLVGGGEGIPEQGRMTNKMKSTK-GALTFSPYLLSHVMGYGFYHFGTYPGSYE
GFP_Chipo_85658701 MTTF --- KIESRIHGNNLNGEKFELVGGGVGE-EGRLEIEMKTKD-KPLAFSPFLLSHCMGYGFYHFASFPGKGT
Nemve_156385591 56 YSLSKDAMKHLHFKMEGSVNGHCFEIQVGEGKAFDGEHWSKLCVVKGKHLPF SFDILMPSMSYGTQOF AKYPAGMT
Nemve_156388065 MSLSKDAMKHLHLILEGSVNGHCFEIHGEGEGKAFEGEQWSKFTVKKGGPLPF SFDLIAPCLKYGSKPFVKYPDDMT
Monca_154814320 MSVIKTDMMIKLRMEGAVNGHKFVIEGEGEGKPF DKGQTMDLTVIEGAPLPFAYDILTTVF DYGNRVFAKYPKDIP
Monca_154814322 MSVIKPDMMIKLRMEGAVNGHKFVIEGDGKGKPFEGKGQTMDLTVIEGAPLPFAYDILTTVF DYGNRVFAKYPKDIP
Azami-Green_52839539 MSVIKPEMKIKLCMRGTVNGHNFVIEGEGKGNPYEGTQILD LNVTEGAPLPFAYDILTTVF QYGNRAFTKYPADIQ
Dronpa_56201403 MSVIKPDMMIKLRMEGAVNGHPFAIEGVGLGKPFEGKQSMDLVKEGGPLPFAYDILTTVF CYGNRVFAKYPENIV
EosFP_55667942 MSAIKPDMKINLRMEGAVNGHHFVIDGDGTGKPFEGKQSMDELVEKEGGPLPFAFDILTTAFHYGNRVFAEYPDHIQ
CyanFP_154814310 MSVIKSVMKIKLRMGDNVNGHKFMITGEGEGKPFEGKTHTIILVKEGGPLPFAYDILTTAFQYGNRVFTKYPKDIP
Kaede_23503508 MSLIKPEMKIKLLMEGNVNGHQFVIEGDGKGHPFEGKQSMDLVVKEGAPLPFAYDILTTAFHYGNRVFAKYPDHIP
Photoconvert_125395854 MSVIKSVMNVKLRLEGAVNGHPFVIEGKGNGHHPFEGTQDIKLTVKEGGPLPFAYDILTTVFHYGNRVFVKYPDDIV
YFP_Corca_72256906 4 KQVITQEMKMVYHMDGCVNGHSFTTIEGEGTGKPYEGNQTLKLRLVTKGGPLPFAFDILTATFCYGNRCFCEYPEDMP
NFCP_MONEF_55976263 MSVIATQMTYKVMYMSGTVNGHYFEVEGDGKGRPYEGEQTVKLTVTKGGPLPFAWDILSPQCQYGSIPFTKYPEDIP
RFP_Dissp_85002146 4 KNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLRLVTKGGPLPFAWDILSPQFQYGSKVYVKHPADIP
GFP3_Astla_42521556 4 KQEIKKEMTMDYVMDGCVNGHSFTVKGDGAGKPYEGHQRLSLHVTGGQPLPFAFDILSAAFAYGNRCFTKYPKEIP
GFP_Renmu_12621060 7 NTCLQEVMSYKVNLEGIVNNHVFTMEGCGKGNILFGNQLVQIRLVTKGAPLPFAFDIVSPAFAQYGNRTFTKYPNDIS
YFP_Phial_40365351 4 ALLFHGKIPYVVEMEGNVDGHTFSIRGKGYGDA SVGKVDAQFICTT-GDVPVPWSTLVTTLTGYAQCF AKYGPPELK
GFP_AEQVI_1169893 4 EELFTGVVPILVELDGDVNGHKFSVSGEGEGDATY GKLTLKFICTT-GKLPVPWPTLVTTFSYGVQCF SRYPDHMK
Secondary structure sssssssssssss1ssssssssssssss2ssssssssssss3

LanFP1 --SPFQTSMLEGSGYAVYRVDFDE-DGGKLTTEFKYSYEGS---HIKADMKLMSGFPDDGPVMTSQIVDQDGCVSKKTYLNN
LanFP2 --SPFQTAIT-DGGYQVHRVFKFE-DGGVLSCNFRYTYEGG---KIKGEFQLIGSGFPAGGPVMSGGLTTLDRSVAKLQCSDD
LanFP3 --SPFQTAMLDGSGYKVHRVFNFE-DGGVLSIDYNYAYEGT---HIKSDFKLMGSGFPDDGPVMTSQIVDQDGCVSKKTYLND
LanFP4 --SPYQAAMYGGSGLMHRTMQYE-DGAKISGHYKYTYEGS---HVKGFEQLIGTGFPDGPVMTNQLTAADWCVDKLLYPND
LanFP5 --SPFQAAMQDGSYQVHRTMQFE-DGASLTAHFRYTYEGS---HIKGEFQVIGTGFPADGPVMTNKLTAADWCVVKMVYPND
LanFP6 --SPFQAAMQDESGLYQVHRTLQYE-DGAFVTAANLRYTYEGS---HIKGEFQVIGTGFPDGPVMTNKLTAADWSVVKFVYPND
LanFP7 --SPFQAAVN-NGGYQMHRSFNFE-DGAVLTATYNTSYSGG---KIQGEFHLVGSCEFDDSPVMTNALQLGDRSVAKLMCVSD
LanFP8 --SPYQQAIT-NGGYQKHRTFKFE-DGAVLMTINFRYTYSGN---KIKGEFVVGSGFPDDGPVMTNALQQHDHNVERLVLGD
LanFP9 --SPFQATMLEGSGYTVHRVDFDE-DGGKLSIEFKYSYEGS---HIKADMKFTGTGFPEDGPVMTSQIVDQDGCVSKNTY LND
LanFP10 --SPFQAAMH DGSGLYQVHRTIQYE-DGASVTAHYRYTYEGS---HIKGEFQVIGTGFPDGPVMTNKLTAADWSVTKMLYPND
LanFP11 --SPFQTAMLDGSGYSVHRVDFDE-DGGKLTLEFKYSYEGS---HIKADMKFTGSGFPDDGPVMTSQIVDEDGCVSKNTIHNND
LanFP12 --SPFQAAADDGSGYVVHRTNIQFE-DGASLTGIYRYSYDAG---HIKGEFRVVGSGFPADGPVMTKSLTAADWSVATMLFPND
GFP1_Ponme_33243032 --NIYLHAM-KNGGYSNVRTERYE-DGGIISITFNRYRYEGN---KIIGDFKVVGTGFPNTSLIFTDKIISNPTCENMFPKAD
GFP1_Ponpl_33243026 --NPLFHAA-NNGGYTNTRIEKYE-DGGVLHVSFSYRYEAG---RVIGDFKVVGTGFPEDSVIFTDKIIRS NATVEHLHPMGD
GFP_Chipo_85658701 --NIYLHAM-TNGGYTNTKEIYE-DGGILEVNFRTYEFN---KIIGDVECI GHGFPSPQSPIFKDTIVKSCPTVDLMLPMSG
GFP1_Nemve_156385591 --DFFKAAV-ENGGLSWERTMTFE-DGGYCTIVNTSELKDG---SLHYHTNFHGINLKPDGPVMQKRTMGWLPSVETNIPRRD
GFP2_Nemve_156388065 --DFFKAAV-ENGGLSWERTMSLEQDGGFCSVVNTSKLDKD---GLHYHMTFQGINLDPNGPVMKKMTMGWLPSVETNIPRGN
GFP1_Monca_154814320 --DYFKQTF--PEGYSWERSMTFE-DQGICTVTSDIKLEGD---CFFYEIRFYGVNFPSSGPVMQKKT LKWEPPSTEIMYVRDG
GFP2_Monca_154814322 --DYFKQTF--PEGYSWERSMTYE-DQGICIATNDITMMKGVD DCFVYKIRFDGVNFPANGPVMQKKT LKWEPPSTEKMYVRDG
Azami-Green_52839539 --DYFKQTF--PEGYHWERSMTYE-DQGICTATSNI SMRGD---CFFYDIRFDGVNFPNNGPVMQKKT LKWEPPSTEKMYVRDG
Dronpa_56201403 --DYFKQSF--PEGYSWERSMNYE-DGGICNATNDITLDGD---CYIYEIRFDGVNFPANGPVMQKRTVKWEPPSTEKLYVRDG
EosFP_55667942 --DYFKQSF--PKGYSWERSLTFE-DGGICIANRNDITMEGD---TFYNKVRFHGVNFPANGPVMQKKT LKWEPPSTEKMYVRDG
CyanFP_154814310 --DYFKQSF--PEGYSWERSMTFE-DQGVCTVTSDIKLEGD---CFFYEIRFYGVNFPSSGPVMQKKT LKWEPPSTENMYVRDG
Kaede_23503508 --DYFKQSF--PKGFSWERSLMFE-DGGVCIATNDITLKGD---TFFNKVRFDGVNFPNNGPVMQKKT LKWEASTEKMYLRDG
Photoconvert_125395854 --DYFKLSF--PEGYSWERSMVYE-DGGVCLATSDIKLLKDEENCFHKKIRFDGVNFPANSPVMLKTTQKWEPPSTEKMYARDG
YFP_Corca_72256906 --DYYKQSF--PEGYSFERTMMFE-DGACCTTSVHLSITKN---CFVHNSTFHGVNFPANGPVMQKKT LKWEPPSSEKITPFEG
NFCP_MONEF_55976263 --DYYKQSF--PEGFTWERIMNFE-DGAVCTVSNDSSIQGN---CFTYHVKFSGLNFPPNNGPVMQKKT LKWEPPSERL FARGG
RFP_Dissp_85002146 --DYKKLSF--PEGFKWERVMNFE-DGGVVTVTQDPSLQDG---CFIYKVKFIVGNFPSDGPVMQKKT MGWEASTERLYPRDG
GFP3_Astla_42521556 --DMFKQAF--PGGMSWERTMTFE-DGGVASVSADISIEKD G---CFKHRSKFGVNFPVNGPVMQNKTRGWEPSIEKMTVRDG
GFP_Renmu_12621060 --DYFIQSF--PAGFMYERTLRYE-DGGLVEIRSDINLIED---KFVYRVEYKGSNFPDDGPVMQKTILGIEPSFEAMYMNNG
YFP_Phial_40365351 --DFYKSCM--PEGYVQERTITFE-GDGVFKTRA E VTFENG---SVYNRVKLNQGFKKGHV L GKN-LEFNFTPHCLYI WGD
GFP_AEQVI_1169893 QHDFFKSAM--PEGYVQERTIFFK-DGNYKTRA EVKFEGD---TLVNRIELKGIDFKEDGNILGHK-LEYNYN SHNVYIMAD
Secondary structure sssssssssssss4ssssssssssssssss5 sssssssssss6 sssssssssss7

LanFP1 ---NTIVDSFDWSYNLQN--GKRYRARVSSHYIFDK-PFSADLMKKQPVFVYRKCHVKASK---TEVTLDEREKAFYELA
LanFP2 ---CTITGTNNWSFCTTD--GKRHQADVQTN YTF AK-PLPAGLKEKMPIFLGHQIEVQASK---TEINLSKVKAFIDTV
LanFP3 ---NTIVDSFDWSYNLQN--GKRYRARVTSN YIFGK-PLAADVMKKQPVFVYRKCYVKSTQ---TEITLDEREKAFYEVN
LanFP4 ---KTIIISKFDWSTTTD--GKRYQAKVQTN FFAK-PMAANYLQKQPMFVFRKVELEH SK---TEVKFKWQKAFHDIM
LanFP5 ---KTILSTFDWYTTTE--GKRYQSTVRTNYTF AK-PMAANILQKQPMFVFRKTELQHSK---TELTFKWQKAFSDVM
LanFP6 ---KTILSTFDKTYTTD--GKRYQCTFRENNTFAK-PMAADILQKQPMFIFHKTELQHSNN--AELTFKEKQTA FSDMK
LanFP7 ---DKLAEFVDWYRTSS--GGRYRATVQTN FFAK-PIAAGLKNMMPMFVFRQLEV T GSK---TEISLQEQKAFSTVL
LanFP8 ---KTIGSDNMWTFTEKGGKDKRYKAEVMTNATFAQ-NLQPLKNVMPLFVFRKVDIECSK---TEVSLVEKEKVFQDLI
LanFP9 ---NTIVDNFDWYNLQN--GKRYRARVTSHYIFDK-PFSADLMKKQPVFVYRKCHVKASK---TEINLDEREKAFYELA
LanFP10 ---KTILSTVDCSYTTTE--GKRYQSKMRENNTFAK-PMAADILQKQPMFVFRKTELQHSK---TELTFKWQKAFSDVM
LanFP11 ---NTIVDNFDWTVNLQN--GKRYRAHVTSHYIFGK-PLAADVMKKQPVFVYRKCYVKSTK---TEITLDEREKAFYEVV
LanFP12 ---TTVVSTIDWTCPTTS--GKRYHATVRTNYTF AK-PIAGSILQKQPMFVFRKTEVKASD---SEINLKESQKAFHDLV
GFP1_Ponme_33243032 ---NTLVNAYTRTYLLKD--GGYYS AQVNNHMHFKSAIH TTMLQNGGSMFTYRVVEETH TQ---NEVAIVEYQNVFKTPT
GFP1_Ponpl_33243026 ---NVLVGSFARTFSLRD--GGYYSFVVD SHMHFKSAIHPSILQNGGSMFAFRVEELHSN---TELGIVEYQHAFKTPT
GFP_Chipo_85658701 ---NI I ASSYARAFQLKD--GSFYTA EVKNNIDFKNPIH-ESFSKSGPMFTHRRVEETH TK---ENLAMVEYQQVFNSAP
GFP1_Nemve_156385591 --- - TLLGDINMLLKVN D--GSFLRVQFETVYRFMKVPV PAGFKMPPHHFMAYRLTRVDNDEHC-DTVIQHEWSEAFSCFL
GFP2_Nemve_156388065 --- - TLVG D INMLLKVN D--GSFLRVKFVTVYRFMKVPV PAGFKMPPHHFI AFKLTRVENDADC-NVVL L HEWGKAFSCFL
GFP1_Monca_154814320 --- - VLKGDVNMALLLEG--GGHYRCDFKTTYKAKK---FVQLPDYHFVDHRIEIVSHDKDY-NKVKLYEHAEAHSGLP
GFP2_Monca_154814322 --- - VLKGDVNMALLLEG--GGHYRCDFKTTYKAKK---VVQLPDYHFVDHRIEIVSHDKDY-NKVKLYEHAEAHSGLP
Azami-Green_52839539 --- - VLKGDVNMALLLEG--GGHYRCDFKTTYKAKK---DVRLPDYHFVDHRIEILKHDKDY-NKVKLYENAVARYSML
Dronpa_56201403 --- - VLKGDVNMALSLEG--GGHYRCDFKTTYKAKK---VVQLPDYHFVDHHIEIKSHDKDY-SNVNLHEHAEAHSELP
EosFP_55667942 --- - VLTGDITMALLLEG--NAHYRCDFRTTYKAKE---KGVKLPGYHFVDHCIEILSHDKDY-NKVKLYEHAVAHSGLP
CyanFP_154814310 --- - VLLGDVSRTL LLEG--NKHHR CNFRSTYRAKK---GVVLPEYHFVDHRIEILSHDKDY-NTVEVYENAVARPSML
Kaede_23503508 --- - VLTGDITMALL LKG--DVHYRCDFRTTYKSRQ---EGVKLPGYHFVDHCISILRHDKDY-NEVKLYEHAVAHSGLP
Photoconvert_125395854 --- - VVKGDVNMALL LKG--GGHYRCDFKTTYKAKK---YVPLPDYHFVDHRIEITSHDKDY-NIVNVFEDAVAHSGLT
YFP_Corca_72256906 --- - NLKGDVTMFLKLEG--GQQHRCQFQTTYKAHK---AVKMPPNHIEHRLVRSQDG---DAVQLKEHAVAKCFTA
NFCP_MONEF_55976263 --- - MLIGNNFMAL KLEG--GGHYLCEFKTTYKAKK---PVKMPGYHYVDRKLDVTNHNKDY-TSVEQCEISIARKPVV
RFP_Dissp_85002146 --- - VLKGEIHKALKLD--GGHYLVEFKTIYMAKK---PVQLPGYYYVDSKLDITSHNKDY-TIVEQYERTEGRHHLF
GFP3_Astla_42521556 --- - TLKGHVTMFLKLEG--GGNYRCD FETTYKAKK---AVKMLDSHFIEHRLVTTIRG---NNVELQETA EARN SGL
GFP_Renmu_12621060 --- - LVLGEVILVYKLNS--GKYYSCHMKTLMKSKG---VVKEFPSYHFIEHRL EKTYYVEDG--GFVEQHEDAIAQM TSI
YFP_Phial_40365351 QANHGLKSAFKIMHEITG--SKEDFI VADHTQMNTPIGGGPVHVPEYHHITYHVTLSKDVTDHRDNMSLVETVRAVD CRK
GFP_AEQVI_1169893 KQKNGIKVNFKIRHNIED--GSVQLADHYQQNTPIG--DGPVLLPDNHYLSTQSALSKDPNEKRDMVLL E FVTAAGITH
Secondary structure sssssssssssss8 sssssssssssss9 sssssssssss10 sssssssssss11