Crystal structures from PDB:

SsIGPS: 2C3Z

TmIGPS: 1I4N chain A

TtIGPS:1VC4 chain A

EcIPGS: 1PII

6xHIS IGPS Protein

>SsΔ1-26, R18S

MSGSHHHHHHSSDIENLYFQGQRPIISLNERILEFNKSNITAIIAEYKRKSPSGLDVERDPIEYSKFMERYAVGLSILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL\*

>TmΔ1-31

MSGSHHHHHHSSDIENLYFQGFLEVLSGKERVKIIAEFKKASPSAGDINADASLEDFIRMYDELADAISILTEKHYFKGDPAFVRAARNLTSRPILAKDFYIDTVQVKLASSVGADAILIIARILTAEQIKEIYEAAEELGMDSLVEVHSREDLEKVFSVIRPKIIGINTRDLDTFEIKKNVLWELLPLVPDDTVVVAESGIKDPRELKDLRGKVNAVLVGTSIMKAENPRRFLEEMRAWSE\*

>TtΔ1-34, C102S

MSGSHHHHHHSSDIENLYFQGPSFKEALLRPGLSVIAEVKRQSPSEGLIREVDPVEAALAYARGGARAVSVLTEPHRFGGSLLDLKRVREAVDLPLLRKDFVVDPFMLEEARAFGASAALLIVALLGELTGAYLEEARRLGLEALVEVHTERELEIALEAGAEVLGINNRDLATLHINLETAPRLGRLARKRGFGGVLVAESGYSRKEELKALEGLFDAVLIGTSLMRAPDLEAALRELVG\*

>EcΔ1-38

MSGSHHHHHHSSDIENLYFQGFYDALQGARTAFILECKKASPSKGVIRDDFDPARIAAIYKHYASAISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIYLARYYQADACLLMLSVLDDDQYRQLAAVAHSLEMGVLTEVSNEEEQERAIALGAKVVGINNRDLRDLSIDLNRTRELAPKLGHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDDLHAAVRRVLLGEN\*\*

DNA

> SsΔ1-26, R18S

ATGTCTGGTTCTCATCATCATCATCATCATAGCAGCGATATCGAAAACTTATACTTCCAAGGTTTTTTGGAAGTACTGAGCGGTAAAGAACGCGTTAAGATTATCGCTGAATTCAAAAAGGCCAGCCCAAGTGCGGGCGATATTAACGCTGACGCATCTCTGGAAGATTTTATCCGCATGTATGATGAATTGGCCGACGCGATTTCAATCCTGACAGAAAAACACTACTTTAAGGGCGATCCAGCTTTCGTTAGAGCTGCACGCAATTTGACATCACGTCCAATTCTGGCTAAAGATTTCTATATCGACACGGTACAAGTTAAGCTGGCATCTTCAGTGGGCGCTGATGCAATTTTAATTATCGCTCGTATCTTGACTGCAGAACAGATTAAAGAAATCTACGAAGCCGCGGAAGAACTGGGTATGGATTCCTTAGTGGAAGTCCATTCGAGAGAAGACCTGGAAAAAGTGTTTTCCGTCATTCGCCCGAAGATTATCGGCATCAATACCCGTGATCTGGACACTTTCGAAATTAAAAAGAACGTGCTGTGGGAACTGTTACCATTAGTCCCGGATGACACCGTTGTGGTCGCCGAATCGGGTATTAAAGATCCGCGTGAATTGAAGGACTTGCGTGGTAAAGTTAATGCCGTATTAGTTGGCACTAGCATTATGAAAGCGGAAAACCCTCGTCGTTTTCTGGAAGAAATGAGAGCGTGGAGTGAATAA

> TmΔ1-31

ATGTCTGGTTCTCATCATCATCATCATCATAGCAGCGATATCGAAAACTTATACTTCCAAGGTTTTTTGGAAGTACTGAGCGGTAAAGAACGCGTTAAGATTATCGCTGAATTCAAAAAGGCCAGCCCAAGTGCGGGCGATATTAACGCTGACGCATCTCTGGAAGATTTTATCCGCATGTATGATGAATTGGCCGACGCGATTTCAATCCTGACAGAAAAACACTACTTTAAGGGCGATCCAGCTTTCGTTAGAGCTGCACGCAATTTGACATCACGTCCAATTCTGGCTAAAGATTTCTATATCGACACGGTACAAGTTAAGCTGGCATCTTCAGTGGGCGCTGATGCAATTTTAATTATCGCTCGTATCTTGACTGCAGAACAGATTAAAGAAATCTACGAAGCCGCGGAAGAACTGGGTATGGATTCCTTAGTGGAAGTCCATTCGAGAGAAGACCTGGAAAAAGTGTTTTCCGTCATTCGCCCGAAGATTATCGGCATCAATACCCGTGATCTGGACACTTTCGAAATTAAAAAGAACGTGCTGTGGGAACTGTTACCATTAGTCCCGGATGACACCGTTGTGGTCGCCGAATCGGGTATTAAAGATCCGCGTGAATTGAAGGACTTGCGTGGTAAAGTTAATGCCGTATTAGTTGGCACTAGCATTATGAAAGCGGAAAACCCTCGTCGTTTTCTGGAAGAAATGAGAGCGTGGAGTGAATAA

> TtΔ1-34, C102S

ATGTCTGGTTCTCATCATCATCATCATCATAGCAGCGATATCGAAAATCTGTACTTCCAAGGCCCTAGTTTTAAAGAAGCCCTGTTACGTCCAGGTTTAAGCGTCATTGCGGAAGTAAAGAGACAATCTCCGTCAGAAGGCTTGATCCGCGAAGTTGATCCTGTGGAAGCTGCACTGGCATACGCACGCGGTGGCGCTCGTGCAGTCTCTGTACTGACCGAACCGCATAGATTTGGTGGCTCATTGCTGGATCTGAAACGCGTTCGTGAAGCCGTGGACTTACCATTATTGCGCAAGGATTTTGTTGTGGACCCGTTCATGCTGGAAGAAGCCCGTGCATTCGGTGCTTCCGCAGCACTGTTAATTGTGGCATTGCTGGGTGAATTGACAGGCGCCTATCTGGAAGAAGCGCGTAGATTAGGCTTGGAAGCTCTGGTTGAAGTGCATACGGAAAGAGAACTGGAAATCGCATTAGAAGCTGGTGCAGAAGTTTTAGGCATTAATAACCGCGATCTGGCCACCTTACACATCAATTTGGAAACTGCTCCTCGTTTGGGTAGACTGGCAAGAAAACGCGGCTTTGGTGGCGTCCTGGTAGCGGAATCCGGTTACTCGCGCAAAGAAGAATTAAAGGCCTTGGAAGGTCTGTTCGATGCGGTCTTAATTGGCACATCTTTGATGCGTGCTCCAGACCTGGAAGCTGCATTAAGAGAATTGGTTGGTTAA

> EcΔ1-38

ATGTCTGGTTCTCATCATCATCATCATCATAGCAGCGATATCGAGAATCTGTATTTTCAAGGTTTTTATGATGCGCTGCAAGGTGCGCGTACCGCGTTTATCCTGGAGTGCAAGAAGGCGAGCCCGAGCAAGGGTGTGATCCGTGACGATTTCGATCCGGCGCGTATCGCGGCGATTTACAAGCACTATGCGAGCGCGATTAGCGTGCTGACCGACGAAAAATACTTCCAGGGCAGCTTCAACTTTCTGCCGATCGTTAGCCAGATTGCGCCGCAACCGATCCTGTGCAAAGATTTTATCATTGACCCGTACCAGATTTATCTGGCGCGTTACTATCAAGCGGATGCGTGCCTGCTGATGCTGAGCGTGCTGGACGATGACCAGTATCGTCAACTGGCGGCGGTTGCGCACAGCCTGGAAATGGGTGTGCTGACCGAGGTTTCTAACGAGGAAGAGCAGGAACGTGCGATCGCGCTGGGTGCGAAGGTGGTTGGCATTAACAACCGTGATCTGCGTGACCTGAGCATCGACCTGAACCGTACCCGTGAGCTGGCGCCGAAACTGGGTCACAACGTGACCGTTATCAGCGAAAGCGGCATTAACACCTACGCGCAAGTTCGTGAGCTGAGCCACTTCGCGAACGGTTTTCTGATTGGCAGCGCGCTGATGGCGCATGATGACCTGCACGCGGCGGTTCGTCGTGTTCTGCTGGGTGAAAACTAATAAGGATCC

Full length protein

Ss

MPRYLKGWLKDVVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAIIAEYKRKSPSGLDVERDPIEYSKFMERYAVGL

SILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLLEYARSYGMEPLIEI

NDENDLDIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNP

EKIKEFIL

Tm

MRRLWEIVEAKKKDILEIDGENLIVQRRNHRFLEVLSGKERVKIIAEFKKASPSAGDINADASLEDFIRMYDELADAISIL

TEKHYFKGDPAFVRAARNLTCRPILAKDFYIDTVQVKLASSVGADAILIIARILTAEQIKEIYEAAEELGMDSLVEVHSR

EDLEKVFSVIRPKIIGINTRDLDTFEIKKNVLWELLPLVPDDTVVVAESGIKDPRELKDLRGKVNAVLVGTSIMKAENPR

RFLEEMRAWSE

Tt

MRPDLSRVPGVLGEIARKRASEVAPYPLPEPPSVPSFKEALLRPGLSVIAEVKRQSPSEGLIREVDPVEAALAYARGGAR

AVSVLTEPHRFGGSLLDLKRVREAVDLPLLRKDFVVDPFMLEEARAFGASAALLIVALLGELTGAYLEEARRLGLEALVE

VHTERELEIALEAGAEVLGINNRDLATLHINLETAPRLGRLARKRGFGGVLVAESGYSRKEELKALEGLFDAVLIGTSLM

RAPDLEAALRELVG