

## Gal\_Lectin[[pfam02140](#)], Galactose binding lectin domain

**Cd Length:** 79 **Bit Score:** 85.81 **E-value:** 4.95e-19

```
lcl|local_MKAALLVLL 392 INCGSRFV-DILSAVYGRNSKENCPHYRMKSTNCAASKSLEVVGLQCQGHQCRLTVNNGVFGNPCCGTFKYLHAKYRC 469
Cdd:pfam02140      1  LSCPSGVIiSIKFAASYGRPDGTTCPFSQGSNTNCHAPNSLAVVSKACLKQKSCSVPASNSVFGDPCPGTYKYLEVQYIC 79
```

## VWD[[smart00216](#)], von Willebrand factor (vWF) type D domain

**Cd Length:** 163 **Bit Score:** 87.07 **E-value:** 1.12e-18

```
lcl|local_MKAALLVLL 523 CRAWGDPHYTGFNGRNFYDQGMCKYTLATPCVDNKDF--LFRVVGVNKVASWNNRVSynrgmeLKIGGSDIVLAQ-GKQV 599
Cdd:smart00216      12  CSVSGDPHYTTFDGVAYTFPGNCYYVLAQDCSSEPTFsvLLKNVPCGGGATCLKSVK-----VELNGDEIELKDdNGKV 85
```

```
lcl|local_MKAALLVLL 600 QIDGALVNAPCGVKDTKIDLD--GKFLVVTNERLGKVMWDGSEVFKIFAEkGIYGDNMCLCGSIRAQKDDPFVMSNG 676
Cdd:smart00216      86  TVNGQQVSLPYKTSDGSIQIRssGGYLVVITSLGLIQVTFDGLTLLSVQLP-SKYRGKTCGLCGNFDGEPEDDFRTPDG 163
```

```
lcl|local_MKAALLVLL 523 CRAWGDPHYTGFNGRNFYDQGMCKYTLATPCVDNKDF--LFRVVGVNKVASWNNRVSynrgmeLKIGGSDIVLAQ-GKQV 599
Cdd:smart00216      12  CSVSGDPHYTTFDGVAYTFPGNCYYVLAQDCSSEPTFsvLLKNVPCGGGATCLKSVK-----VELNGDEIELKDdNGKV 85
```

```
lcl|local_MKAALLVLL 600 QIDGALVNAPCGVKDTKIDLD--GKFLVVTNERLGKVMWDGSEVFKIFAEkGIYGDNMCLCGSIRAQKDDPFVMSNG 676
Cdd:smart00216      86  TVNGQQVSLPYKTSDGSIQIRssGGYLVVITSLGLIQVTFDGLTLLSVQLP-SKYRGKTCGLCGNFDGEPEDDFRTPDG 163
```

## FA58C[[cd00057](#)], Coagulation factor 5/8 C-terminal domain, discoidin domain

**Cd Length:** 143 **Bit Score:** 98.96 **E-value:** 6.79e-23

```
lcl|local_MKAALLVLL 1097 LGVQSGEILDSSMTASTERGDFK-AFRGRIdNSDGActWTANINNQDQWLQVDLFEVKLVIGVVTOGHCGMVDDDAdhlf 1175
Cdd:cd00057        3  LGMESGLA-DDQITASSSYSSGWEASRARL-NSDNA--WTPAVNDPPQWLQVDLQVLDLTKTRRVVTGIQTQGRKGGSSSEW---- 74
```

```
lcl|local_MKAALLVLL 1176 gcVKKFHVQVSDGNDFEYITDEDGrDELF----DSKCSFHahnkNFFKEAVNVRYVRFIPTVWVTSISMRVEIIG 1247
Cdd:cd00057        75  --VTSYKVQYSLDGETWTTYKDKGE-EKVFtgnSDGSTPVT----NDFPPPIVARYIRILPTTWNGNISLRLELYG 143
```

## FA58C[[cd00057](#)], Coagulation factor 5/8 C-terminal domain, discoidin domain

**Cd Length:** 143 **Bit Score:** 94.34 **E-value:** 2.71e-21

```
lcl|local_MKAALLVLL 1415 TNMGLQDGLiTSEQITSNIGICDSNGKADRVRLG1kdqqgMLGGWCGRQIDQSAYIQIDFKKRPCCGVTTQGLSSPTRKW 1494
Cdd:cd00057        1  EPLGMESGL-ADDQITASSSYSSGWEASRARLN-----SDNAWTPAVNDPPQWLQVDLQVLDLTKTRRVVTGIQTQGRKGGSSSE 73
```

```
lcl|local_MKAALLVLL 1495 FVQKFIARHSVDLQVTDVADEGGNtIMFGGNYDQETQVKNFPTLLITQSIRIQPMKWtGNfPSMRMDVLG 1566
Cdd:cd00057        74  WVTSYKVQYSLDGETWTTYKDKGEE-KVFTGNSDGS TPVTNDFPPPIVARYIRILPTTWNGN-ISLRLELYG 143
```

## FA58C[[cd00057](#)], Coagulation factor 5/8 C-terminal domain, discoidin domain

**Cd Length:** 143 **Bit Score:** 129.39 **E-value:** 2.48e-33

```
lcl|local_MKAALLVLL 1743 NPVGLANGiLVDTsITVSSYVHEGdshsfGPRSARLrhvgmheNLGGAWVADQKDESPWLQVDFRVEGTVTGLITQGRH 1822
Cdd:cd00057        1  EPLGMESG-LADDQITASSSYSSGW-----EASRARL-----NSDNAWTPAVNDPPQWLQVDLQVLDLTKTRRVVTGIQTQGRK 67
```

```
lcl|local_MKAALLVLL 1823 AKVNW-WVTRYAVYYSVNCEDWMPVEDaNGDEMVFEGNVSDTEVERYFPNAVKAQCIRVYPRGFFGRAAMRLEVLG 1898
Cdd:cd00057        68  GGGSSeWVTSYKVQYSLDGETWTTYKD-KGEEKVFTGNSDGS TPVTNDFPPPIVARYIRILPTTWNGNISLRLELYG 143
```

FA58C[cd00057], Coagulation factor 5/8 C-terminal domain, discoidin domain

Cd Length: 143 Bit Score: 134.40 E-value: 4.52e-35

lcl|local\_MKAALLVLL 2071 LGMEDGLiPDQSiEASSLFGSQYTYSQARLNSRSSaalkgeWAPATDETDQYVQVDLKGKPTIVTGVSVQGCNDEER--WV 2148  
Cdd:cd00057 3 LGMESGL-ADDQITASSYSSGWEASRARLNSDNA-----WTPAVNDPPQWLQVDLKGKTRRVGTGIQTQGRKGGGSseWV 75

lcl|local\_MKAALLVLL 2149 SKLRVQLSLDGSNWEDALGTDGSKIIFYGNTDSDSVSMFFNEEAKVQFVRIIVQEWSNQIGLRFVEMG 2216  
Cdd:cd00057 76 TSYKVQYSLDGETWTTTKDKGEEKVFTGNSDGSTPVTFNDFPPPIVARYIRILPTTWNGNISLRLELYG 143

FA58C[cd00057], Coagulation factor 5/8 C-terminal domain, discoidin domain

Cd Length: 143 Bit Score: 103.59 E-value: 1.58e-24

lcl|local\_MKAALLVLL 2404 IGMESGRiPDDFiFSSSSNDPiKLGPGQARLNNDLAWQASPTDENIYLQVDIGYIAMLGTGIVTQG--DPVNSCWVTSYSV 2481  
Cdd:cd00057 3 LGMESGL-ADDQITASSYSS-GWEASRARLNSDNAWTPAVNDPPQWLQVDLKGKTRRVGTGIQTQGRKGGGSSEWVTSYKV 80

lcl|local\_MKAALLVLL 2482 EYTASH---DYRNPLEPtkfawvaetnaikEIFAGNSDQNGMKTNFKKALEARVIRIAINDFKGCPAMRMEVLG 2553  
Cdd:cd00057 81 QYSLDGetwtTYKDKGEE-----KVFTGNSDGSTPVTFNDFPPPIVARYIRILPTTWNGNISLRLELYG 143

EGF\_CA[cd00054], Calcium-binding EGF-like domain

Cd Length: 38 Bit Score: 37.62 E-value: 6.49e-03

lcl|local\_MKAALLVLL 2556 DPDTc-SPNPCKQGAMCRkaqNSDG-YTCNCPAEWGGKNCE 2594  
Cdd:cd00054 1 DIDEcASGNPCQNGGTCV---NTVGSYRCSPPGYTGRNCE 38

VWD[pfam00094], von Willebrand factor type D domain

Cd Length: 159 Bit Score: 104.45 E-value: 1.24e-24

lcl|local\_MKAALLVLL 2600 CFGWGDPHYGQFDGAKYFMGACTY--VLTRTVAGSTKDAFEVTAkNEKSlRQPSVSTREVVYIRINKRFYEFKQNR-- 2675  
Cdd:pfam00094 1 CSVSGDPHYTTFDGVSYTFPGNCSYv1VLAQDCSSSEPSFKFVSLNKNVND-GAEGVTCLKSvTVILGNLEIELVPGNqvk 79

lcl|local\_MKAALLVLL 2676 VFVDNEKIRSPYEKDG--VTIIDGCNSRVILMTDFGLRVVWDGRSKVEVYLTEDYKHEVEGLCGNYDGQQGPDYFMRSGE 2753  
Cdd:pfam00094 80 VLVNGQEVSLPYSSDNglIEILGSGFVLVTLRLGVTLQFDGDGRTQLFVSLSPMYRGKTCGLCGNFDGEPADDFRTPDGS 159

C8[smart00832]

Cd Length: 76 Bit Score: 73.14 E-value: 1.17e-14

lcl|local\_MKAALLVLL 2790 EEAQKACHVLINHPGPFsmCHGIISVDAYYKECTFDfCKLYPNMENLCEDIQVYADDCNDKKIQIGIWRTPGFC 2863  
Cdd:smart00832 2 YYACSQCgILLSPRGPFaACHSVVDPEPFENCvYDTCACGGDCECLCDALAAyAAACAeAGVCISPWRTPFC 75

Gal\_Lectin[pfam02140], Galactose binding lectin domain

Cd Length: 79 Bit Score: 66.55 E-value: 1.83e-12

lcl|local\_MKAALLVLL 3104 ISCEGNTldldcgflKISVIRASyGRGQDfVCTetgddtSTTPLTEDCfKSAFRLISEACHGKQCTTITSdTGLFGtD 3183  
Cdd:pfam02140 1 LSCPSGV-----IISKfASyGRPDGT-TCP-----FSQGSNTNChAPNSLAVVSKACLGRKQCSVPASNSVFG-D 64

lcl|local\_MKAALLVLL 3184 SCPTVSKYAKVQYQC 3198  
Cdd:pfam02140 65 PCPGTYKYLEVQYIC 79

## VWD[[pfam00094](#)], von Willebrand factor type D domain

**Cd Length:** 159 **Bit Score:** 109.45 **E-value:** 2.78e-26

lc1|local\_MKAALLVLL 3251 CKALGDPHYITFD<sup>1</sup>DVRYDFMGPCVYTLVKNADK-EVKDFEVRVTNEKARRN-PSMSSTVAVDFTIYENHVIKL---RKM<sup>3225</sup>GV 3325  
Cdd:pfam00094 1 CSVSGDPHYITFDGVS<sup>1</sup>YTFPGNCSYV<sup>1</sup>LVLAQDCsSEPSFKFSVLNKNVNDG<sup>1</sup>aEGVTCLKSVTVILGNLEIELvp<sup>1</sup>gNQVKV 80

lc1|local\_MKAALLVLL 3326 TYIDDVITNGYTTAGLTVS<sup>1</sup>IDTP-NVVVTDSGIVIR--WDGRYLVEVDVTGDYFNHVEGLCGNYNSDQEDEF<sup>1</sup>TTRMGM 3401  
Cdd:pfam00094 81 LVNGQEVSLPYSSDNG<sup>1</sup>LIEILGSgFVLVTLRLGVTLQfdGDGR<sup>1</sup>TQLFVSLSPMYR<sup>1</sup>GKTCGLCGNFDGEPADDFRTPDGS 159

## C8[[smart00832](#)]

**Cd Length:** 76 **Bit Score:** 68.91 **E-value:** 3.47e-13

lc1|local\_MKAALLVLL 3448 AQEVCSQLIDASGPFQE<sup>1</sup>CHGTVDPATAYKNCMTDMCTMPEGLAY-CEDYQFYAEECLDKQITIS-WRRADFC 3517  
Cdd:smart00832 4 ACSQCGILLSPRG<sup>1</sup>PFACHSVVDEPEFFENC<sup>1</sup>VYDTCACGGDCELCDALAA<sup>1</sup>YAAACAEGVCISpWRTPTFC 75

## Gal\_Lectin[[pfam02140](#)], Galactose binding lectin domain

**Cd Length:** 79 **Bit Score:** 62.70 **E-value:** 4.06e-11

lc1|local\_MKAALLVLL 3665 IECQDERFINILD<sup>1</sup>AHFGNPkQAEICLEVSG-DQSCNAESSISRMKALCQNKHSCIPQALIKQFGDPCFEDFKYLHVEFSC 3743  
Cdd:pfam02140 1 LSCPSGVIISIKFAS<sup>1</sup>YGRP-DGTTCPFSQsNTNCHAPNSLAVVSKACLGKQSCSVPASNSVFGDPCPGTYKYLEVQYIC 79

Dataset S1: Conserved domains in Sfp1. Alignments between the sequence of Sfp1 (lc1) and domains from the Conserved Domain Database (Cdd). Conserved amino acids are highlighted in red.