



ScanProsite Results Viewer

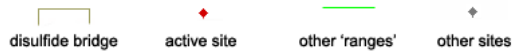
Output format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [\[help\]](#).

[include splice variants \(Swiss-Prot\)](#)

Hits for USERPAT1{[FY]-[NHY]-[VIT]-Y-[GA]-x-[WY]-W-x(1,2)-[SD]-x(2)-[KET]-[LIA]-x-[FIY]-[YF]-[FILY]-[DN]-[GN]-[KER]-x(6)-[PF]} motif on all U

found: 15 hits in 15 sequences

Legend:



Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.

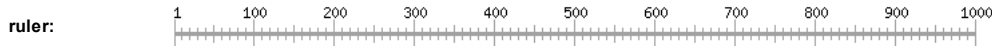
For more information about how these graphical representations are constructed, go to <http://prosite.expasy.org/mydomains/>.

hits by patterns: [15 hits (by 1 pattern) on 15 sequences]

Hits by **USERPAT1** :

Pattern: **[FY]-[NHY]-[VIT]-Y-[GA]-x-[WY]-W-x(1,2)-[SD]-x(2)-[KET]-[LIA]-x-[FIY]-[YF]-[FILY]-[DN]-[GN]-[KER]-x(6)-[PF]**

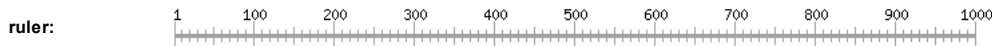
Approximate number of expected random matches [Ref: [PMID 11535175](#)] in ~ 100'000 sequences (50'000'000 residues): 5.406763e-10



D7GXG0
(PORA_ZOBGA) (510 aa) [View all PROSITE motifs hits on sequence](#)

Beta-porphyrinase A. *Zobellia galactanivorans* (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)

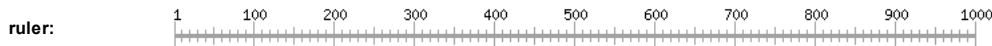
192 - 219: FTYYGfWwk.SpnELlFYFNGKqvmrivP



D7GXF9
(PORB_ZOBGA) (293 aa) [View all PROSITE motifs hits on sequence](#)

Beta-porphyrinase B. *Zobellia galactanivorans* (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)

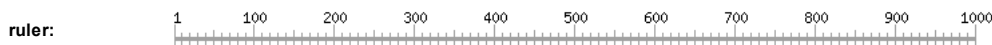
214 - 241: FHVYgVWwk.SkdEiIFFLDGKmqskvtP



D7GXG1
(PORC_ZOBGA) (355 aa) [View all PROSITE motifs hits on sequence](#)

Beta-porphyrinase C. *Zobellia galactanivorans* (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)

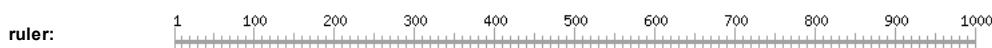
275 - 303: FHIYAaYWhaDgsKIdFYIDGleksitP



D7GXG2
(PORD_ZOBGA) (427 aa) [View all PROSITE motifs hits on sequence](#)

Beta-porphyrinase D. *Zobellia galactanivorans* (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)

225 - 252: FNVYGgWwr.DesTAsYYNNRppkhqkF



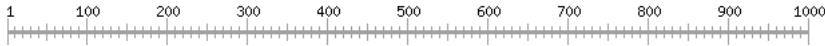
D7GXG3
(279 aa) [View all PROSITE motifs hits on sequence](#)

(PORE_ZOBGA)

**Beta-porphyrinase E.** *Zobellia galactanivorans* (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)

196 - 223: YHVYGeWwV.DanTIkIYLDGEyqftmnP

ruler:



A0M239

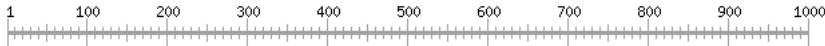


(438 aa)

[View all PROSITE motifs hits on sequence](#)**Secreted glycosyl hydrolase, family 16.** *Gramella forsetii* (strain KT0803)

232 - 259: FHVYGFwWk.DatTLlFYLNGEqvmEitP

ruler:



D5EQS4

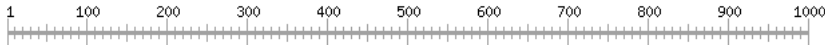


(764 aa)

[View all PROSITE motifs hits on sequence](#)**Ig family protein.** *Coraliomargarita akajimensis* (strain DSM 45221 / IAM 15411 / JCM 23193 / KCTC 12865)

213 - 240: YYVYGLwWk.SetELlFFLDGEhvytinP

ruler:



F0RGA2

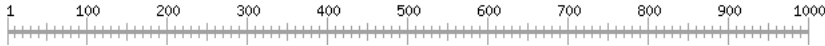


(308 aa)

[View all PROSITE motifs hits on sequence](#)**Glycoside hydrolase family 16.** *Cellulophaga lytica* (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy I20)

231 - 258: YHIYGaWwK.SptEIEFYLDGKkvysitP

ruler:



I3CAX7

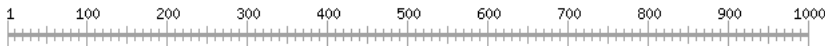


(293 aa)

[View all PROSITE motifs hits on sequence](#)**Beta-glucanase/beta-glucan synthetase.** *Joostella marina* DSM 19592

216 - 243: FHVYGVwWk.SkdEIIFFLDGKkrqstvkP

ruler:



M5TC31

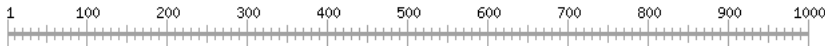


(280 aa)

[View all PROSITE motifs hits on sequence](#)**Glycoside hydrolase family 16.** *Rhodopirellula* sp. SWK7

203 - 230: YYVYGaWwK.SprELrFYLDGKyvysleP

ruler:



M5U6G9

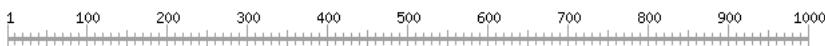


(290 aa)

[View all PROSITE motifs hits on sequence](#)**Glycoside hydrolase family 16.** *Rhodopirellula sallentina* SM41

213 - 240: YYVYGaWwK.SprELrFYLDGKyvyslKp

ruler:



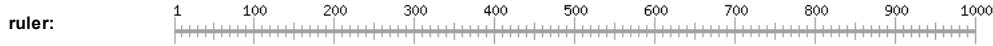
T2KN18



(290 aa)

[View all PROSITE motifs hits on sequence](#)**Beta-porphyrinase B (GH16).** *Formosa agariphila* KMM 3901

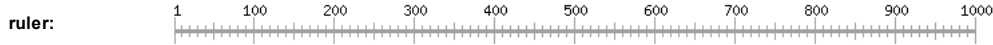
210 - 237: FTYYGcWwK.SptELlFYLNGEyqytlTtP



T2KN47 (278 aa) [View all PROSITE motifs hits on sequence](#)

Beta-porphyrane B (GH16). *Formosa agariphila KMM 3901*

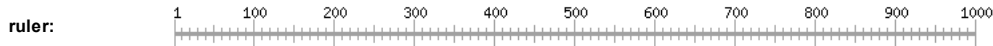
201 - 228: FVVYGAwwk.SptEILFYLDGKyaytlnP



W7QLF1 (308 aa) [View all PROSITE motifs hits on sequence](#)

Glycoside hydrolase family protein. *Cellulophaga geojensis KL-A*

231 - 258: YHIYGaWwK.SptEIEFYLDGKkvysitP



X0Y492 (118 aa) [View all PROSITE motifs hits on sequence](#)

Marine sediment metagenome DNA, contig: S01H1_S42804. *marine sediment metagenome*

41 - 68: FVVYAgWwK.SpeEIqFFLDGKyayslkP

horizontal scaling:

do not show text labels:

do not show sites in hits:

do not show ranges in hits:

[Matched UniProtKB entries](#)

[Taxonomic Distribution of matched entries](#)

[Shaded Alignment of hits](#)