

## Hitlist

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Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
<input type="checkbox"/> 1	<a href="#">PF10874.8</a>	; DUF2746 ; Protein of unknown function (DUF2746)	100	7.4e-32	13.1	96	101
<input type="checkbox"/> 2	<a href="#">PF10805.8</a>	; DUF2730 ; Protein of unknown function (DUF2730)	92.47	3.4	11.4	87	95
<input type="checkbox"/> 3	<a href="#">2N64_B</a>	SH3 domain-containing kinase-binding protein 1; Signaling Protein, Adaptor Protein, Coiled-Coil; NMR {Homo sapiens}	90.83	2.5	6.4	40	75
<input type="checkbox"/> 4	<a href="#">5ABS_A</a>	SH3 DOMAIN-CONTAINING KINASE-BINDING PROTEIN 1; SIGNALING PROTEIN, CBL-INTERACTING PROTEIN OF; HET: MSE; 1.74A {HOMO SAPIENS}	90.83	2.7	6.4	40	66
<input type="checkbox"/> 5	<a href="#">PF06120.11</a>	; Phage_HK97_TLTM ; Tail length tape measure protein	90.22	11	10.9	88	295
<input type="checkbox"/> 6	<a href="#">PF02326.15</a>	; YMF19 ; Plant ATP synthase F0	87.98	12	8.6	81	92
<input type="checkbox"/> 7	<a href="#">PF13314.6</a>	; DUF4083 ; Domain of unknown function (DUF4083)	85.54	14	6.4	53	59
<input type="checkbox"/> 8	<a href="#">PF06295.12</a>	; DUF1043 ; Protein of unknown function (DUF1043)	83.12	31	9.3	74	121
<input type="checkbox"/> 9	<a href="#">6GPZ_A</a>	Cell cycle protein GpsB, PBP1A; Bacterial cell division regulator, peptidoglycan; 1.6A { Bacillus subtilis subsp. subtilis str. 168}	82.56	17	5.8	35	63
<input type="checkbox"/> 10	<a href="#">PF12732.7</a>	; YtxH ; YtxH-like protein	82.16	24	8.7	80	82
<input type="checkbox"/> 11	<a href="#">6GQN_B</a>	Cell cycle protein GpsB, PBP1A; Bacterial cell division regulator, peptidoglycan; HET: SO4; 1.8A {Streptococcus pneumoniae R6}	81.76	20	5.8	35	62
<input type="checkbox"/> 12	<a href="#">PF07798.11</a>	; DUF1640 ; Protein of unknown function (DUF1640)	81.72	16	6.1	53	175
<input type="checkbox"/> 13	<a href="#">2WUJ_A</a>	SEPTUM SITE-DETERMINING PROTEIN DIVIVA; BACTERIAL CELL DIVISION, SEPTATION, CELL; 1.4A {BACILLUS SUBTILIS}	81.57	20	5.6	35	57
<input type="checkbox"/> 14	<a href="#">PF16082.5</a>	; Phage_holin_2_4 ; Bacteriophage holin family, superfamily II-like	81.4	18	5.7	60	76
<input type="checkbox"/> 15	<a href="#">4UG3_B</a>	CELL CYCLE PROTEIN GPSB; CELL CYCLE, BACTERIAL GROWTH REGULATION; 2.8A {BACILLUS SUBTILIS}	81.16	20	5.8	35	71
<input type="checkbox"/> 16	<a href="#">4UG1_A</a>	CELL CYCLE PROTEIN GPSB; CELL CYCLE, PEPTIDOGLYCAN SYNTHESIS, BACTERIAL; HET: IMD; 1.6A {LISTERIA MONOCYTOGENES}	80.95	20	5.8	35	76
<input type="checkbox"/> 17	<a href="#">PF16959.5</a>	; Collectrin ; Renal amino acid transporter	73.9	12	3.2	41	154
<input type="checkbox"/> 18	<a href="#">PF06103.11</a>	; DUF948 ; Bacterial protein of unknown function (DUF948)	73.75	52	11	78	87