Phyre^2

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Description	P0AG63
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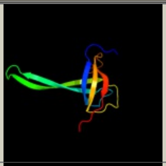
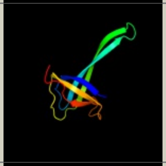
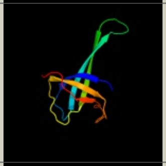
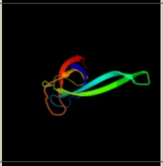
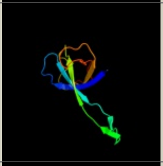
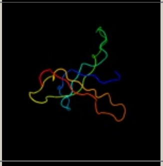
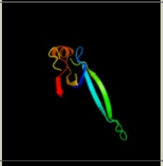
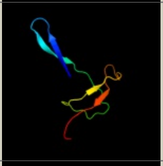
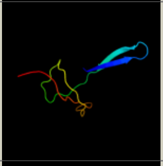
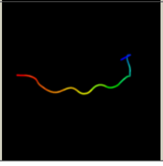
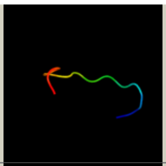
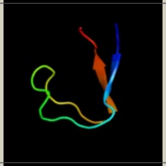
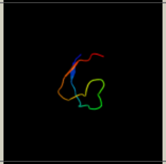
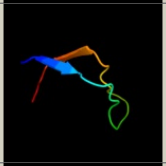
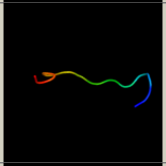
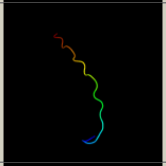
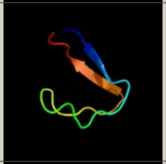
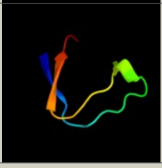
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xznQ_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
2	d2gy9q1	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	c3bbnQ_	Alignment		100.0	37	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
4	d2uubq1	Alignment		100.0	49	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	d1i94q_	Alignment		100.0	49	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
6	c1s1hQ_	Alignment		100.0	35	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
7	d1ripa_	Alignment		100.0	54	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
8	c2zkqq_	Alignment		100.0	36	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
9	c3izbP_	Alignment		99.8	31	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein rps11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
10	c3iz6P_	Alignment		99.8	24	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein s11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	d1e32a1	Alignment		26.8	38	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like

12	c2xzm1_	Alignment		26.0	50	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein s28e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
13	c1negA_	Alignment		23.6	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** crystal structure analysis of n-and c-terminal labeled sh3-2 domain of alpha-chicken spectrin
14	d1nega_	Alignment		23.6	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
15	d1ue9a_	Alignment		22.4	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
16	d1uuea_	Alignment		21.7	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
17	d1ny4a_	Alignment		21.6	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
18	d1ne3a_	Alignment		20.5	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
19	c2pqhA_	Alignment		19.9	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal
20	c2rqrA_	Alignment		19.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**engulfment and cell motility protein 1, linker, dedicator **PDBTitle:** the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
21	d1h8ka_	Alignment	not modelled	19.8	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
22	c2jvvA_	Alignment	not modelled	19.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
23	c2kvqG_	Alignment	not modelled	19.6	12	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
24	d1utia_	Alignment	not modelled	19.4	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
25	d1e6ga_	Alignment	not modelled	19.3	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
26	c2d8jA_	Alignment	not modelled	19.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fyn-related kinase; **PDBTitle:** solution structure of the sh3 domain of fyn-related kinase
27	c3d3rA_	Alignment	not modelled	18.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
28	d1nz9a_	Alignment	not modelled	18.9	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain

29	c3nmzD_	Alignment	not modelled	18.6	25	**PDB header:**cell adhesion/cell cycle **Chain:** D: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crytal structure of apc complexed with asef
30	d3d3ra1	Alignment	not modelled	18.4	24	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
31	c2dl3A_	Alignment	not modelled	18.3	16	**PDB header:**cell adhesion, signaling protein **Chain:** A: **PDB Molecule:**sorbin and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the first sh3 domain of human sorbin2 and sh3 domain-containing protein 1
32	c2dmoA_	Alignment	not modelled	18.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 2; **PDBTitle:** refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2)
33	d2ot2a1	Alignment	not modelled	17.9	27	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
34	d1arka_	Alignment	not modelled	17.6	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
35	c2nwmA_	Alignment	not modelled	17.6	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the first sh3 domain of human vinexin2 and its interaction with the peptides from vinculin
36	d1nppa2	Alignment	not modelled	17.5	36	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
37	d1gria2	Alignment	not modelled	17.3	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
38	d1k4us_	Alignment	not modelled	17.3	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
39	d1dzfa2	Alignment	not modelled	17.3	18	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
40	d1u0la1	Alignment	not modelled	17.1	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
41	d1uj0a_	Alignment	not modelled	17.1	6	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
42	d1udxa3	Alignment	not modelled	16.9	36	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
43	c2jteA_	Alignment	not modelled	16.9	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cd2-associated protein; **PDBTitle:** third sh3 domain of cd2ap
44	d1i07a_	Alignment	not modelled	16.6	21	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
45	c2yupA_	Alignment	not modelled	16.5	7	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the second sh3 domain of human vinexin
46	d2z1ca1	Alignment	not modelled	16.5	22	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
47	c1zx6A_	Alignment	not modelled	16.4	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ypr154wp; **PDBTitle:** high-resolution crystal structure of yeast pin3 sh3 domain
48	c1x2pA_	Alignment	not modelled	16.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 2; **PDBTitle:** solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2
49	c3cqtA_	Alignment	not modelled	15.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase fyn; **PDBTitle:** n53i v55l mutant of fyn sh3 domain
50	d1hmja_	Alignment	not modelled	15.7	24	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
51	c2ct3A_	Alignment	not modelled	15.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the sh3 domain of the vinexin protein
52	d1pwta_	Alignment	not modelled	15.4	6	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
53	c2e5kA_	Alignment	not modelled	15.3	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**suppressor of t-cell receptor signaling 1; **PDBTitle:** solution structure of sh3 domain in suppressor of t-cell2 receptor signaling 1
54	c2xmfA_	Alignment	not modelled	15.2	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**myosin 1e sh3; **PDBTitle:** myosin 1e sh3
55	c2crvA_	Alignment	not modelled	14.7	31	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of

						mitochondrial2 translational initiationfactor 2
56	c3p8bB_	Alignment	not modelled	14.6	25	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
57	d1ppya_	Alignment	not modelled	14.2	36	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
58	d1e6ha_	Alignment	not modelled	14.2	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
59	c2dl8A_	Alignment	not modelled	14.1	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**slit-robo rho gtpase-activating protein 2; **PDBTitle:** solution structure of the sh3 domain of human slit-robo rho2 gtpase-activating protein 2
60	d1t9ha1	Alignment	not modelled	14.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
61	c3iz6Y_	Alignment	not modelled	13.9	21	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s28 (s28e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
62	c2dlpA_	Alignment	not modelled	13.8	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kiaa1783 protein; **PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein
63	c2d8hA_	Alignment	not modelled	13.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sh3yl1 protein; **PDBTitle:** solution structure of the sh3 domain of hypothetical2 protein sh3yl1
64	c2c45F_	Alignment	not modelled	13.6	27	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
65	c3ougA_	Alignment	not modelled	13.5	45	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
66	c1pt1B_	Alignment	not modelled	13.4	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
67	c2krnA_	Alignment	not modelled	13.3	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cd2-associated protein; **PDBTitle:** high resolution structure of the second sh3 domain of cd2ap
68	c2dbkA_	Alignment	not modelled	13.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2 protein
69	c1wxbA_	Alignment	not modelled	13.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**epidermal growth factor receptor pathway **PDBTitle:** solution structure of the sh3 domain from human epidermal2 growth factor receptor pathway substrate 8-like protein
70	d1oeba_	Alignment	not modelled	13.0	18	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
71	d1opka1	Alignment	not modelled	13.0	10	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
72	d1wpga1	Alignment	not modelled	12.9	25	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
73	d2uubd1	Alignment	not modelled	12.9	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
74	c3plxB_	Alignment	not modelled	12.7	36	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
75	d2f4la1	Alignment	not modelled	12.4	18	**Fold:**CUB-like **Superfamily:**Acetamidase/Formamidase-like **Family:**Acetamidase/Formamidase-like
76	c1vc3B_	Alignment	not modelled	12.4	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
77	c1uheA_	Alignment	not modelled	12.4	55	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
78	c2rf0D_	Alignment	not modelled	12.3	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mitogen-activated protein kinase kinase kinase 10; **PDBTitle:** crystal structure of human mixed lineage kinase map3k10 sh3 domain
79	c2eyxA_	Alignment	not modelled	12.1	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** c-terminal sh3 domain of ct10-regulated kinase
80	c2dilA_	Alignment	not modelled	12.1	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**proline-serine-threonine phosphatase-interacting **PDBTitle:** solution structure of the sh3 domain of the human proline-2 serine-threonine phosphatase-interacting protein 1

81	d1g31a_	Alignment	not modelled	12.1	18	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
82	c2ct4A_	Alignment	not modelled	11.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** solution strutcure of the sh3 domain of the cdc42-2 interacting protein 4
83	d1c06a_	Alignment	not modelled	11.8	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
84	c1pyuD_	Alignment	not modelled	11.7	36	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
85	c2yuoA_	Alignment	not modelled	11.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**run and tbc1 domain containing 3; **PDBTitle:** solution structure of the sh3 domain of mouse run and tbc12 domain containing 3
86	c2i0nA_	Alignment	not modelled	11.6	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**class vii unconventional myosin; **PDBTitle:** structure of dictyostelium discoideum myosin vii sh3 domain2 with adjacent proline rich region
87	d1ov3a1	Alignment	not modelled	11.5	22	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
88	c1z9zA_	Alignment	not modelled	11.5	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** crystal structure of yeast sla1 sh3 domain 3
89	c2k6dA_	Alignment	not modelled	11.5	14	**PDB header:**sh3 domain/ubiquitin **Chain:** A: **PDB Molecule:**sh3 domain-containing kinase-binding protein 1; **PDBTitle:** cin85 sh3-c domain in complex with ubiquitin
90	c1yn8E_	Alignment	not modelled	11.4	21	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**nap1-binding protein 2; **PDBTitle:** sh3 domain of yeast nbp2
91	d1j3ta_	Alignment	not modelled	11.3	15	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
92	c2djqA_	Alignment	not modelled	11.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain containing ring finger 2; **PDBTitle:** the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2
93	c2creA_	Alignment	not modelled	11.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hef-like protein; **PDBTitle:** solution structure of rsgi ruh-036, an sh3 domain from2 human cdna
94	c1w70A_	Alignment	not modelled	11.1	10	**PDB header:**sh3 domain **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** sh3 domain of p40phox complexed with c-terminal polyproline2 region of p47phox
95	c1wi7A_	Alignment	not modelled	11.0	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sh3-domain kinase binding protein 1; **PDBTitle:** solution structure of the sh3 domain of sh3-domain kinase2 binding protein 1
96	d2fo0a1	Alignment	not modelled	11.0	10	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
97	c2cucA_	Alignment	not modelled	11.0	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 domain containing ring finger 2; **PDBTitle:** solution structure of the sh3 domain of the mouse2 hypothetical protein sh3rf2
98	c1zukA_	Alignment	not modelled	10.9	6	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin tail region-interacting protein mti1; **PDBTitle:** yeast bbc1 sh3 domain complexed with a peptide from las17
99	c3mmlD_	Alignment	not modelled	10.9	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436