Phyre^2

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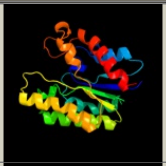
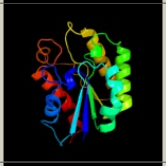
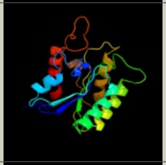
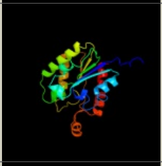
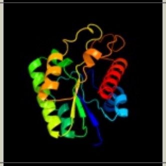
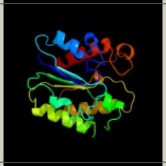
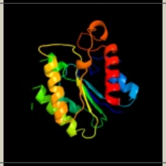
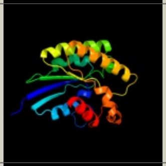
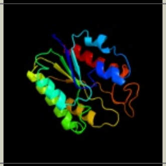
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jrla_	Alignment		100.0	99	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
2	c3hp4A_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-esterase; **PDBTitle:** crystal structure of psychrotrophic esterase esta from2 pseudoalteromonas sp. 643a inhibited by monoethylphosphonate
3	c2o14A_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
4	c3milA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamyl acetate-hydrolyzing esterase; **PDBTitle:** crystal structure of isoamyl acetate-hydrolyzing esterase from2 saccharomyces cerevisiae
5	c3p94A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gdsl-like lipase; **PDBTitle:** crystal structure of a gdsl-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution
6	c3rjtA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic protein g-d-s-l family; **PDBTitle:** crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
7	d1yzfa1	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
8	c2vptA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic enzyme; **PDBTitle:** clostridium thermocellum family 3 carbohydrate esterase
9	d3bzwa1	Alignment		100.0	17	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**BT2961-like
10	c3bzwA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative lipase; **PDBTitle:** crystal structure of a putative lipase from bacteroides2 thetaiotaomicron
11	c2waoA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase e; **PDBTitle:** structure of a family two carbohydrate esterase from2 clostridium thermocellum in complex with cellohexaose

12	d1k7ca_	Alignment		99.9	18	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Rhamnogalacturonan acetylesterase
13	c2waaA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylan esterase, putative, axe2c; **PDBTitle:** structure of a family two carbohydrate esterase from2 cellvibrio japonicus
14	d2o14a2	Alignment		99.9	24	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**YxiM C-terminal domain-like
15	d3dc7a1	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**BT2961-like
16	c3dc7B_	Alignment		99.9	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein lp_3323; **PDBTitle:** crystal structure of the protein q88sr8 from lactobacillus plantarum.2 northeast structural genomics consortium target lpr109.
17	d1vjga_	Alignment		99.9	20	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Hypothetical protein alr1529
18	d1es9a_	Alignment		99.9	20	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
19	d1fxwf_	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
20	c2q0qC_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aryl esterase; **PDBTitle:** structure of the native m. smegmatis aryl esterase
21	c3dciB_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**arylesterase; **PDBTitle:** the structure of a putative arylesterase from agrobacterium2 tumefaciens str. c58
22	d2hsja1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Acetylhydrolase
23	c2w9xA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative acetyl xylan esterase; **PDBTitle:** the active site of a carbohydrate esterase displays2 divergent3 catalytic and non-catalytic binding functions
24	d1esca_	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Esterase
25	c3kvnA_	Alignment	not modelled	98.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
26	d2apja1	Alignment	not modelled	97.6	11	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
27	c3bmaC_	Alignment	not modelled	97.0	9	**PDB header:**ligase **Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
28	c3pt5A_	Alignment	not modelled	96.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nans (yjhs), a 9-o-acetyl n-acetylneuraminic acid esterase; **PDBTitle:** crystal structure of nans
						Fold: Flavodoxin-like

29	d1zmba1	Alignment	not modelled	96.3	14	**Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
30	c3nvbA_	Alignment	not modelled	88.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
31	d1jlja_	Alignment	not modelled	87.7	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
32	d2f7wa1	Alignment	not modelled	85.9	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
33	c2pjkA_	Alignment	not modelled	84.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
34	d1mkza_	Alignment	not modelled	82.9	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
35	c3q9cF_	Alignment	not modelled	81.5	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetylpolyamine amidohydrolase; **PDBTitle:** crystal structure of h159a apah complexed with n8-acetylspermidine
36	c3menC_	Alignment	not modelled	80.4	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**acetylpolyamine aminohydrolase; **PDBTitle:** crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
37	c1vcnA_	Alignment	not modelled	77.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
38	d1uuya_	Alignment	not modelled	77.4	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
39	d1vcoa2	Alignment	not modelled	77.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
40	c2is8A_	Alignment	not modelled	76.6	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
41	d1y5ea1	Alignment	not modelled	72.4	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
42	c3maxB_	Alignment	not modelled	71.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histone deacetylase 2; **PDBTitle:** crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
43	d1t64a_	Alignment	not modelled	70.8	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
44	c3ew8A_	Alignment	not modelled	70.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
45	d2csua1	Alignment	not modelled	69.8	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
46	c3nvaB_	Alignment	not modelled	69.5	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
47	d1c3pa_	Alignment	not modelled	55.9	16	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
48	c3qi7A_	Alignment	not modelled	55.9	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
49	c2bg5C_	Alignment	not modelled	47.2	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
50	c2g4rB_	Alignment	not modelled	44.1	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
51	c1y8aA_	Alignment	not modelled	40.7	45	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1437; **PDBTitle:** structure of gene product af1437 from archaeoglobus fulgidus
52	d2g2ca1	Alignment	not modelled	40.5	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
53	c2hwgA_	Alignment	not modelled	35.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
54	d1iuka_	Alignment	not modelled	35.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: CoA-binding domain
55	c3kbqA_	Alignment	not modelled	34.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
56	c2hroA_	Alignment	not modelled	28.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
57	d2vo1a1	Alignment	not modelled	25.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
58	d3c10a1	Alignment	not modelled	25.8	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
59	c2ohoA_	Alignment	not modelled	25.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
60	c3rfqC_	Alignment	not modelled	24.8	11	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
61	d1xpja_	Alignment	not modelled	24.6	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
62	d1s1ma2	Alignment	not modelled	24.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
63	c3fxtB_	Alignment	not modelled	23.7	16	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the n-terminal domain of human nudt6
64	c2ad5B_	Alignment	not modelled	22.3	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
65	c1hyhA_	Alignment	not modelled	20.2	16	**PDB header:**oxidoreductase (choh(d)-nad+(a)) **Chain:** A: **PDB Molecule:**l-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
66	c2ps3A_	Alignment	not modelled	19.1	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
67	c2olsA_	Alignment	not modelled	17.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
68	d1hyha1	Alignment	not modelled	15.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
69	d1dxea_	Alignment	not modelled	14.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
70	d2bdua1	Alignment	not modelled	14.6	36	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
71	d1y81a1	Alignment	not modelled	14.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
72	c3cyvA_	Alignment	not modelled	14.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
73	c2bs9B_	Alignment	not modelled	14.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-xylosidase; **PDBTitle:** native crystal structure of a gh39 beta-xylosidase xynb12 from geobacillus stearothermophilus
74	d1c7ga_	Alignment	not modelled	14.0	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
75	d2d59a1	Alignment	not modelled	13.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
76	c2csuB_	Alignment	not modelled	13.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
77	d1edta_	Alignment	not modelled	13.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
78	c2vqqA_	Alignment	not modelled	13.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 4; **PDBTitle:** structure of hdac4 catalytic domain (a double cysteine-to-2 alanine mutant) bound to a trifluoromethylketone inhbitor
79	d2v1pa1	Alignment	not modelled	12.7	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases

						Family: Beta-eliminating lyases
80	c3gycB_	Alignment	not modelled	12.3	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
81	d5ldha1	Alignment	not modelled	12.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
82	c2i55C_	Alignment	not modelled	12.0	28	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
83	c2v5jB_	Alignment	not modelled	11.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
84	d1e0ta2	Alignment	not modelled	11.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
85	d1tpla_	Alignment	not modelled	11.2	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
86	c3i5tB_	Alignment	not modelled	11.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
87	c2r47C_	Alignment	not modelled	10.4	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
88	d2tpsa_	Alignment	not modelled	10.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
89	d9ldta1	Alignment	not modelled	10.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
90	d1llda1	Alignment	not modelled	10.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
91	c3fcrA_	Alignment	not modelled	10.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
92	d1ohwa_	Alignment	not modelled	10.1	4	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
93	c2jfqA_	Alignment	not modelled	9.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
94	c1uhvD_	Alignment	not modelled	9.8	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-xylosidase; **PDBTitle:** crystal structure of beta-d-xylosidase from2 thermoanaerobacterium saccharolyticum, a family 393 glycoside hydrolase
95	d1iv0a_	Alignment	not modelled	9.7	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
96	c2e7vA_	Alignment	not modelled	9.3	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transmembrane protease; **PDBTitle:** crystal structure of sea domain of transmembrane protease2 from mus musculus
97	c3jszA_	Alignment	not modelled	9.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
98	c2wvsD_	Alignment	not modelled	9.0	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
99	c2vwtA_	Alignment	not modelled	8.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex