

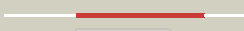




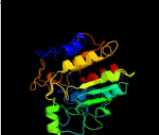



















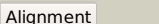
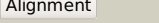
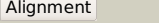
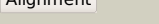
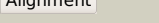
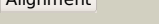
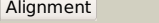
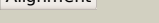
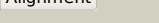
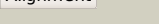
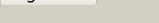
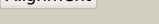








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2351c_(plcA)_2630547_2632085
Date	Mon Aug 5 13:25:50 BST 2019
Unique Job ID	b3f98decd9b199e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d1gB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B; PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
2	c6hr5A_	 Alignment		99.4	15	PDB header: hydrolase Chain: A; PDB Molecule: alpha-l-rhamnosidase/sulfatase (gh78); PDBTitle: structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
3	d1auka_	 Alignment		99.4	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
4	c6b1vB_	 Alignment		99.3	16	PDB header: hydrolase Chain: B; PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
5	c4fdiA_	 Alignment		99.3	18	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
6	c3lxqB_	 Alignment		99.3	11	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
7	c6j66B_	 Alignment		99.3	19	PDB header: hydrolase Chain: B; PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
8	d1p49a_	 Alignment		99.2	21	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
9	c3ed4A_	 Alignment		99.2	12	PDB header: transferase Chain: A; PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
10	c4mivB_	 Alignment		99.2	20	PDB header: hydrolase Chain: B; PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
11	d1fsua_	 Alignment		99.2	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase

12	c5fqIA_	Alignment		99.1	16	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
13	c6hhmA_	Alignment		99.1	15	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
14	c2qzuA_	Alignment		99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
15	c4upkC_	Alignment		99.0	17	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
16	c4uopB_	Alignment		99.0	10	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
17	c4ug4H_	Alignment		99.0	12	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
18	c5g2vA_	Alignment		99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosamine-6-sulfatase; PDBTitle: structure of bt4656 in complex with its substrate d-glucosamine-2-n,2 6-o-disulfate.
19	c2vqrA_	Alignment		99.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative sulfatase; PDBTitle: crystal structure of a phosphonate monoester hydrolase from rhizobium2 leguminosarum: a new member of the alkaline phosphatase superfamily
20	c4uorK_	Alignment		99.0	13	PDB header: transferase Chain: K: PDB Molecule: lipoteichoic acid synthase; PDBTitle: structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
21	c4uplC_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
22	c3b5qB_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
23	c4uphA_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
24	c2w8dB_	Alignment	not modelled	98.9	11	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
25	d1hdha_	Alignment	not modelled	98.9	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
26	c4upiA_	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
27	c5i5fA_	Alignment	not modelled	98.8	12	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
28	c6a82A_	Alignment	not modelled	98.7	12	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli

29	c5k4pA	 Alignment	not modelled	98.7	16	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
30	c2w5tA	 Alignment	not modelled	98.6	13	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
31	c4kayA	 Alignment	not modelled	98.6	12	PDB header: transferase Chain: A: PDB Molecule: yhbxb/yjhwy/yjpb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
32	c6bneA	 Alignment	not modelled	98.5	11	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase; PDBTitle: crystal structure of the intrinsic colistin resistance enzyme icr(mc)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
33	c5vemA	 Alignment	not modelled	98.5	11	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
34	c4tn0C	 Alignment	not modelled	98.4	13	PDB header: transferase Chain: C: PDB Molecule: upf0141 protein yjdb; PDBTitle: crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
35	d1o98a2	 Alignment	not modelled	98.2	12	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
36	c5egeD	 Alignment	not modelled	98.1	12	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
37	c4lqyA	 Alignment	not modelled	97.9	12	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
38	c5fgnA	 Alignment	not modelled	97.8	15	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
39	c5u9zB	 Alignment	not modelled	97.8	9	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
40	c5udyA	 Alignment	not modelled	97.7	14	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
41	d2i09a1	 Alignment	not modelled	97.7	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
42	c2gsoB	 Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
43	c3m8yC	 Alignment	not modelled	97.4	22	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
44	c5gz4A	 Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
45	c3q3qA	 Alignment	not modelled	97.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
46	c5gz5A	 Alignment	not modelled	96.9	12	PDB header: hydrolase Chain: A: PDB Molecule: snake venom phosphodiesterase (pde); PDBTitle: crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
47	c4b56A	 Alignment	not modelled	96.8	12	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
48	c2i09A	 Alignment	not modelled	96.4	16	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
49	c2zktB	 Alignment	not modelled	96.3	12	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
50	c6c02B	 Alignment	not modelled	96.2	10	PDB header: hydrolase Chain: B: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c), inactive (t205a), n594s, with alpha,beta-methylene-atp3 (ampcpp)
51	c2xr9A	 Alignment	not modelled	94.8	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family

						PDBTitle: crystal structure of autotaxin (enpp2)
52	c2xrgA_	Alignment	not modelled	94.4	14	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
53	c5kgmA_	Alignment	not modelled	93.4	25	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
54	c2e76D_	Alignment	not modelled	92.7	15	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
55	c3igzB_	Alignment	not modelled	90.5	14	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
56	c5tj3A_	Alignment	not modelled	88.0	10	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
57	c1o98A_	Alignment	not modelled	86.7	20	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
58	c2fynO_	Alignment	not modelled	85.3	22	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
59	d1ei6a_	Alignment	not modelled	78.7	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
60	c2pq4B_	Alignment	not modelled	75.4	33	PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
61	c2fyuE_	Alignment	not modelled	74.5	12	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
62	c5vpuA_	Alignment	not modelled	73.4	15	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
63	c1p84E_	Alignment	not modelled	73.1	14	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
64	c4my4A_	Alignment	not modelled	72.4	22	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
65	d1y6va1	Alignment	not modelled	69.8	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
66	c6fo2R_	Alignment	not modelled	65.5	14	PDB header: membrane protein Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound
67	c3szzA_	Alignment	not modelled	63.0	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
68	c2w0yB_	Alignment	not modelled	61.3	31	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
69	c3couA_	Alignment	not modelled	41.8	27	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
70	d1k0ma2	Alignment	not modelled	40.1	23	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
71	d1okta2	Alignment	not modelled	38.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
72	c3e2dB_	Alignment	not modelled	28.9	27	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: the 1.4 a crystal structure of the large and cold-active vibrio sp.2 alkaline phosphatase
73	c2iucB_	Alignment	not modelled	28.2	14	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5
74	c2x98A_	Alignment	not modelled	27.1	30	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
						Fold: Thioredoxin fold

75	d2gsra2	Alignment	not modelled	25.4	21	Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
76	c3wbbB_	Alignment	not modelled	25.2	21	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
77	c4ke3D_	Alignment	not modelled	24.5	26	PDB header: transferase Chain: D: PDB Molecule: glutathione s-transferase domain; PDBTitle: crystal structure of a glutathione transferase family member from2 burkholderia graminis, target efi-507264, no gsh, disordered domains,3 space group p21, form(2)
78	d1g57a_	Alignment	not modelled	24.0	29	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
79	c3kvhA_	Alignment	not modelled	23.6	31	PDB header: rna binding protein Chain: A: PDB Molecule: protein syndesmos; PDBTitle: crystal structure of human protein syndesmos (nudt16-like protein)
80	c5jx6C_	Alignment	not modelled	23.4	14	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme
81	d2e74d2	Alignment	not modelled	22.5	22	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
82	d1dysa_	Alignment	not modelled	22.0	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
83	c6jcnB_	Alignment	not modelled	21.9	11	PDB header: transferase Chain: B: PDB Molecule: dehydrodolichyl diphosphate synthase complex subunit nus1; PDBTitle: yeast dehydrodolichyl diphosphate synthase complex subunit nus1
84	c6acsA_	Alignment	not modelled	20.5	27	PDB header: transferase Chain: A: PDB Molecule: ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- PDBTitle: poly-cis-prenyltransferase
85	c1x5eA_	Alignment	not modelled	19.7	13	PDB header: electron transport Chain: A: PDB Molecule: thioredoxin domain containing protein 1; PDBTitle: the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
86	d1qjwa_	Alignment	not modelled	19.5	23	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
87	c5j43F_	Alignment	not modelled	19.1	56	PDB header: toxin Chain: F: PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct from uropathogenic escherichia coli in complex with cysk
88	d1v2aa2	Alignment	not modelled	18.7	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
89	d1b5ea_	Alignment	not modelled	18.5	17	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
90	d1m0ua2	Alignment	not modelled	17.8	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
91	c3a64A_	Alignment	not modelled	17.4	14	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: crystal structure of cccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
92	d1uoza_	Alignment	not modelled	17.2	9	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
93	c4yn5A_	Alignment	not modelled	16.9	11	PDB header: hydrolase Chain: A: PDB Molecule: mannan endo-1,4-beta-mannosidase; PDBTitle: catalytic domain of bacillus sp. jamb-750 gh26 endo-beta-1,4-mannanase
94	c4nv4A_	Alignment	not modelled	16.3	33	PDB header: hydrolase Chain: A: PDB Molecule: signal peptidase i; PDBTitle: 1.8 angstrom crystal structure of signal peptidase i from bacillus2 anthracis.
95	c5xczA_	Alignment	not modelled	15.9	17	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: structure of the cellobiohydrolase cel6a from phanerochaete2 chrysosporium in complex with cellobiose at 2.1 angstrom
96	c6hwhB_	Alignment	not modelled	15.3	26	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
97	c1q7tA_	Alignment	not modelled	15.2	27	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
98	d2gsqa2	Alignment	not modelled	15.1	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
99	d1txka2	Alignment	not modelled	14.8	36	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: MdoG-like