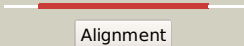

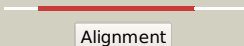

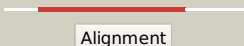







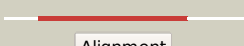









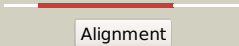

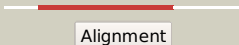

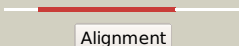



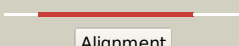

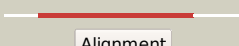

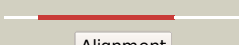





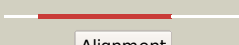
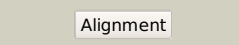

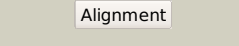
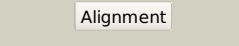
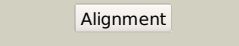
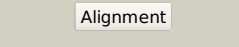


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2690c_(-)_3007246_3009219
Date	Wed Aug 7 12:50:34 BST 2019
Unique Job ID	df7d54aa3a037f96

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6nplA_	 Alignment		100.0	13	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 12 (sodium/potassium/chloride) PDBTitle: cryo-em structure of nkcc1
2	c4djiA_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
3	c6f2wA_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: putative amino acid/polyamine transport protein; PDBTitle: bacterial asc transporter crystal structure in open to in conformation
4	c3giaA_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
5	c5oqtA_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
6	c6irtB_	 Alignment		100.0	12	PDB header: membrane protein Chain: B: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
7	c3lrcC_	 Alignment		100.0	13	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
8	c6jmqA_	 Alignment		100.0	12	PDB header: membrane protein/immune system Chain: A: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: lat1-cd98hc complex bound to mem-108 fab
9	c6csfC_	 Alignment		99.9	13	PDB header: membrane protein Chain: C: PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
10	c2jlnA_	 Alignment		99.9	11	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
11	c5m87A_	 Alignment		99.2	10	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter

12	c4wgvC_	 Alignment		99.1	8	PDB header: transport protein Chain: C: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
13	c4wgvA_	 Alignment		99.1	8	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
14	c6c08F_	 Alignment		99.0	9	PDB header: membrane protein Chain: F: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
15	c5nvaA_	 Alignment		98.8	11	PDB header: membrane protein Chain: A: PDB Molecule: putative sodium:solute symporter; PDBTitle: substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
16	c2xq2A_	 Alignment		98.3	11	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsglt
17	c3dh4A_	 Alignment		97.9	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
18	c6c08C_	 Alignment		97.8	11	PDB header: membrane protein Chain: C: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
19	c4m48A_	 Alignment		96.0	11	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
20	c5i6xA_	 Alignment		93.1	9	PDB header: membrane protein Chain: A: PDB Molecule: sodium-dependent serotonin transporter; PDBTitle: x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
21	c2w8aC_	 Alignment	not modelled	92.9	12	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
22	c3n0vD_	 Alignment	not modelled	91.2	12	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
23	c3o1bB_	 Alignment	not modelled	89.7	11	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
24	c3obiC_	 Alignment	not modelled	89.5	7	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
25	c3w7bB_	 Alignment	not modelled	85.4	17	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
26	c3louB_	 Alignment	not modelled	84.9	11	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
27	c4ainB_	 Alignment	not modelled	82.3	13	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
						PDB header: transport protein/immune system

28	c5kteA	Alignment	not modelled	81.2	14	Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
29	c3nrbd	Alignment	not modelled	78.7	13	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
30	c5z1fa	Alignment	not modelled	71.0	13	PDB header: metal transport Chain: A: PDB Molecule: cscl1-like protein erd4; PDBTitle: structure of atosca3.1 channel
31	c3hfxA	Alignment	not modelled	66.8	10	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
32	c5yd1B	Alignment	not modelled	65.5	13	PDB header: metal transport Chain: B: PDB Molecule: protein osca1; PDBTitle: structure of atosca1.1 channel
33	c2l69A	Alignment	not modelled	64.0	13	PDB header: de novo protein Chain: A: PDB Molecule: rossmann 2x3 fold protein; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
34	d1tq8a	Alignment	not modelled	56.0	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
35	c3dloC	Alignment	not modelled	45.7	14	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
36	c3loqA	Alignment	not modelled	43.7	18	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
37	c5b6aA	Alignment	not modelled	42.7	13	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase pdxy; PDBTitle: structure of pyridoxal kinasefrom pseudomonas aeruginosa
38	c6nt5B	Alignment	not modelled	41.2	14	PDB header: immune system Chain: B: PDB Molecule: stimulator of interferon protein; PDBTitle: cryo-em structure of full-length human sting in the apo state
39	c4j29A	Alignment	not modelled	40.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: engineered protein or258; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or258.
40	c1o94D	Alignment	not modelled	40.4	16	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
41	c3foqA	Alignment	not modelled	38.5	13	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of n-acetylglucosamine-1-phosphate2 uridylyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
42	d2lela1	Alignment	not modelled	36.4	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
43	d2cl5a1	Alignment	not modelled	34.6	8	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: COMT-like
44	c4hkrB	Alignment	not modelled	34.0	10	PDB header: transport protein Chain: B: PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
45	c3kl7A	Alignment	not modelled	33.8	22	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent hydrolase; PDBTitle: crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distansonis atcc 8503 at 2.30 a3 resolution
46	c5c2gD	Alignment	not modelled	31.5	16	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
47	c2hu7A	Alignment	not modelled	30.5	8	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
48	c4us3A	Alignment	not modelled	29.3	9	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
49	d1vi9a	Alignment	not modelled	28.1	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
50	d2ajta2	Alignment	not modelled	27.8	16	Fold: FucI/AraA N-terminal and middle domains Superfamily: FucI/AraA N-terminal and middle domains Family: AraA N-terminal and middle domain-like
51	c5lhmA	Alignment	not modelled	27.4	17	PDB header: transferase Chain: A: PDB Molecule: putative o-methyltransferase; PDBTitle: crystal structure of safc from myxococcus xanthus apo-form
52	c3mt0A	Alignment	not modelled	27.1	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1 PDB header: transferase

53	c2qkxA	Alignment	not modelled	26.8	12	Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridylyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
54	d5ruba1	Alignment	not modelled	26.8	23	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
55	c2hncC	Alignment	not modelled	26.7	15	PDB header: transferase Chain: C: PDB Molecule: sam-dependent o-methyltransferase; PDBTitle: crystal structure of sam-dependent o-methyltransferase from pathogenic2 bacterium leptospira interrogans
56	c3r3hA	Alignment	not modelled	26.7	16	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase, sam-dependent; PDBTitle: crystal structure of o-methyltransferase from legionella pneumophila
57	c2j89A	Alignment	not modelled	26.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
58	c3av3A	Alignment	not modelled	25.7	6	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of glycinamide ribonucleotide transformylase 1 from2 geobacillus kaustophilus
59	c3d8vA	Alignment	not modelled	25.1	9	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
60	d1susa1	Alignment	not modelled	24.4	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: COMT-like
61	c5ghaC	Alignment	not modelled	24.3	10	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
62	c9rubB	Alignment	not modelled	23.9	23	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribose-1,5-bisphosphate
63	c4r2IB	Alignment	not modelled	23.8	15	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
64	c5h7pB	Alignment	not modelled	23.5	28	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 46; PDBTitle: nmr structure of the vta1ntd-did2(176-204) complex
65	c3tr6A	Alignment	not modelled	22.8	14	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: structure of a o-methyltransferase from coxiella burnetii
66	d3clsd1	Alignment	not modelled	21.3	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
67	c6rtfA	Alignment	not modelled	20.6	13	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
68	d2z3va1	Alignment	not modelled	20.3	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
69	d1amua	Alignment	not modelled	20.2	12	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
70	c5wb4H	Alignment	not modelled	19.6	7	PDB header: transferase Chain: H: PDB Molecule: n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
71	d2gm3a1	Alignment	not modelled	19.4	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
72	c5f9yB	Alignment	not modelled	19.1	16	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp
73	d1jkxA	Alignment	not modelled	18.7	13	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
74	c3g74B	Alignment	not modelled	18.5	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of unknown function; PDBTitle: crystal structure of a functionally unknown protein from eubacterium2 ventriosum atcc 27560
75	d1hyua4	Alignment	not modelled	18.2	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
76	c3p3dA	Alignment	not modelled	18.0	20	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
77	c4zrsA	Alignment	not modelled	17.6	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library PDB header: metal binding protein

78	c2xvzA_	Alignment	not modelled	17.2	12	Chain: A: PDB Molecule: chelataase, putative; PDBTitle: cobalt chelatase cbik (periplasmatic) from desulfovibrio2 vulgaris hildenborough (co-crystallized with cobalt)
79	c1keeH_	Alignment	not modelled	16.0	35	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
80	d1u11a_	Alignment	not modelled	15.7	13	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
81	c6ajjA_	Alignment	not modelled	15.7	14	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
82	c3b4uB_	Alignment	not modelled	15.7	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
83	c5n5dA_	Alignment	not modelled	15.4	18	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of the o-methyltransferase tomg from streptomyces2 achromogenes involved in tomaymycin synthesis in complex with sam
84	c4ds3A_	Alignment	not modelled	15.3	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
85	d2v0ea1	Alignment	not modelled	15.1	26	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
86	c2fw9A_	Alignment	not modelled	15.0	13	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
87	c4n7wA_	Alignment	not modelled	14.9	8	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
88	c3pilA_	Alignment	not modelled	14.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
89	d1w7pd2	Alignment	not modelled	14.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
90	c5fa9B_	Alignment	not modelled	14.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
91	c3tqkA_	Alignment	not modelled	14.3	19	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
92	c2pfsA_	Alignment	not modelled	14.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
93	c1qcrD_	Alignment	not modelled	14.1	18	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
94	c3d98A_	Alignment	not modelled	14.1	12	PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
95	d1k47a2	Alignment	not modelled	14.1	22	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
96	c3ecsD_	Alignment	not modelled	14.1	20	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
97	c5jipC_	Alignment	not modelled	14.0	21	PDB header: ligase Chain: C: PDB Molecule: nonribosomal peptide synthase; PDBTitle: crystal structure of cmis6
98	c5ahkB_	Alignment	not modelled	13.9	16	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
99	c3bchA_	Alignment	not modelled	13.8	17	PDB header: cell adhesion, ribosomal protein Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: crystal structure of the human laminin receptor precursor