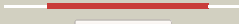



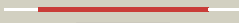



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0876c (- )_974294_975940
Date	Fri Jul 26 01:50:46 BST 2019
Unique Job ID	80a7037c2859f858

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5aynA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
2	<a href="#">c5aymA_</a>	 Alignment		99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
3	<a href="#">d1pw4a_</a>	 Alignment		99.9	14	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
4	<a href="#">c3wdoA_</a>	 Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
5	<a href="#">c4zp0A_</a>	 Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
6	<a href="#">c6e9oA_</a>	 Alignment		99.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
7	<a href="#">c1pv7B_</a>	 Alignment		99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tgd
8	<a href="#">d1pv7a_</a>	 Alignment		99.8	11	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
9	<a href="#">c4cl5B_</a>	 Alignment		99.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
10	<a href="#">c2gfpA_</a>	 Alignment		99.8	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
11	<a href="#">c4ldsB_</a>	 Alignment		99.8	11	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcb; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis

12	<a href="#">c6g9xB_</a>	Alignment		99.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
13	<a href="#">c4j05A_</a>	Alignment		99.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
14	<a href="#">c3o7pA_</a>	Alignment		99.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
15	<a href="#">c4ikyA_</a>	Alignment		99.7	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
16	<a href="#">c6h7dA_</a>	Alignment		99.7	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
17	<a href="#">c4apsB_</a>	Alignment		99.7	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di-or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.
18	<a href="#">c6gs7A_</a>	Alignment		99.7	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
19	<a href="#">c4ybaB_</a>	Alignment		99.7	11	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
20	<a href="#">c6exsA_</a>	Alignment		99.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
21	<a href="#">c4w6vA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-/tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
22	<a href="#">c4q65A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
23	<a href="#">c5c65A_</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
24	<a href="#">c6ei3A_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
25	<a href="#">c4pypA_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1
26	<a href="#">c4gbzA_</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose
27	<a href="#">c4iu8A_</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
28	<a href="#">c4lepB_</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> membrane protein, tranport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters

29	<a href="#">c2xutC</a>	Alignment	not modelled	99.5	7	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
30	<a href="#">c4iu9A</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
31	<a href="#">c6ob7A</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
32	<a href="#">c4m64D</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
33	<a href="#">c3b9yA</a>	Alignment	not modelled	32.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein
34	<a href="#">c3eccA</a>	Alignment	not modelled	21.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
35	<a href="#">c6bwaB</a>	Alignment	not modelled	21.2	57	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein w; <b>PDBTitle:</b> hendra virus w protein c-terminus in complex with importin alpha 32 crystal form 2
36	<a href="#">c6bwbB</a>	Alignment	not modelled	21.2	57	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein w; <b>PDBTitle:</b> hendra virus w protein c-terminus in complex with importin alpha 32 crystal form 3
37	<a href="#">c2zxaA</a>	Alignment	not modelled	21.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
38	<a href="#">c6nbxG</a>	Alignment	not modelled	16.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
39	<a href="#">c5sxpF</a>	Alignment	not modelled	14.7	44	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> F: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
40	<a href="#">c4m0mA</a>	Alignment	not modelled	13.6	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein lpg2422 from2 legionella pneumophila subsp. pneumophila str. philadelphia 1
41	<a href="#">c2rqra</a>	Alignment	not modelled	13.5	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> engulfment and cell motility protein 1, linker, dedicator <b>PDBTitle:</b> the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
42	<a href="#">c2f6aF</a>	Alignment	not modelled	12.9	59	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
43	<a href="#">c2f6aG</a>	Alignment	not modelled	12.9	59	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
44	<a href="#">c2f6aH</a>	Alignment	not modelled	12.9	59	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
45	<a href="#">c2f6aE</a>	Alignment	not modelled	12.9	59	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
46	<a href="#">c2f6aI</a>	Alignment	not modelled	12.9	59	<b>PDB header:</b> cell adhesion/structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> collagen; <b>PDBTitle:</b> collagen adhesin and collagen complex structure
47	<a href="#">c3kikE</a>	Alignment	not modelled	12.6	23	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
48	<a href="#">c3kikF</a>	Alignment	not modelled	12.6	23	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
49	<a href="#">c3kikH</a>	Alignment	not modelled	12.5	23	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
50	<a href="#">c3kikG</a>	Alignment	not modelled	12.4	23	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
51	<a href="#">c2i5nH</a>	Alignment	not modelled	12.2	20	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> reaction center protein h chain; <b>PDBTitle:</b> 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
52	<a href="#">c3kijF</a>	Alignment	not modelled	12.1	23	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
53	<a href="#">c2kr6A</a>	Alignment	not modelled	11.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> presenilin-1; <b>PDBTitle:</b> solution structure of presenilin-1 ctf subunit
54	<a href="#">c3kijH</a>	Alignment	not modelled	11.4	23	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex

55	<a href="#">c3kjlE_</a>	Alignment	not modelled	11.4	23	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
56	<a href="#">c5sxpG_</a>	Alignment	not modelled	11.2	35	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
57	<a href="#">c5wufA_</a>	Alignment	not modelled	11.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> structural basis for conductance through tric cation channels
58	<a href="#">c1wlpA_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> oxidoreductase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b-245 light chain; <b>PDBTitle:</b> solution structure of the p22phox-p47phox complex
59	<a href="#">c4auoF_</a>	Alignment	not modelled	11.0	36	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> F: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
60	<a href="#">c4auoG_</a>	Alignment	not modelled	11.0	36	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> G: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
61	<a href="#">c4auoD_</a>	Alignment	not modelled	11.0	36	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> D: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
62	<a href="#">d1b8xa1</a>	Alignment	not modelled	10.8	24	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
63	<a href="#">c6fhsH_</a>	Alignment	not modelled	10.8	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> les2; <b>PDBTitle:</b> cryoem structure of ino80core
64	<a href="#">c3kjlG_</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> sgf11:sus1 complex
65	<a href="#">c4auoC_</a>	Alignment	not modelled	10.7	33	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
66	<a href="#">c5khnB_</a>	Alignment	not modelled	10.6	10	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
67	<a href="#">c4uk2H_</a>	Alignment	not modelled	10.4	33	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> suppressor protein stm1; <b>PDBTitle:</b> crystal structure of anisomycin bound to the yeast 80s ribosome
68	<a href="#">c6bvvB_</a>	Alignment	not modelled	10.2	36	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein w; <b>PDBTitle:</b> nipah virus w protein c-terminus in complex with importin alpha 3
69	<a href="#">d1jvra_</a>	Alignment	not modelled	10.2	29	<b>Fold:</b> Retroviral matrix proteins <b>Superfamily:</b> Retroviral matrix proteins <b>Family:</b> HTLV-II matrix protein
70	<a href="#">c1eysH_</a>	Alignment	not modelled	10.0	19	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
71	<a href="#">d1mhyd_</a>	Alignment	not modelled	10.0	17	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Ferritin-like <b>Family:</b> Ribonucleotide reductase-like
72	<a href="#">c4k0eC_</a>	Alignment	not modelled	9.8	8	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> heavy metal cation tricomponent efflux pump znea(czca- <b>PDBTitle:</b> x-ray crystal structure of a heavy metal efflux pump, crystal form ii
73	<a href="#">c3j0gO_</a>	Alignment	not modelled	9.7	25	<b>PDB header:</b> virus <b>Chain:</b> O: <b>PDB Molecule:</b> e3 protein; <b>PDBTitle:</b> homology model of e3 protein of venezuelan equine encephalitis virus2 tc-83 strain fitted with a cryo-em map
74	<a href="#">c1z1IA_</a>	Alignment	not modelled	9.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent 3',5'-cyclic phosphodiesterase; <b>PDBTitle:</b> the crystal structure of the phosphodiesterase 2a catalytic2 domain
75	<a href="#">c3u5gh_</a>	Alignment	not modelled	9.7	33	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 40s ribosomal protein s7-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
76	<a href="#">c3v94F_</a>	Alignment	not modelled	9.6	36	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> F: <b>PDB Molecule:</b> cyclic nucleotide specific phosphodiesterase; <b>PDBTitle:</b> tcrpdec1 catalytic domain in complex with inhibitor wyq16
77	<a href="#">c4nl6C_</a>	Alignment	not modelled	9.6	10	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> structure of the full-length form of the protein smn found in healthy2 patients
78	<a href="#">d2h44a1</a>	Alignment	not modelled	9.6	27	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> PDEase
79	<a href="#">c2n24A_</a>	Alignment	not modelled	9.6	45	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> o2_contryphan_vc1; <b>PDBTitle:</b> solution nmr structure of contryphan-vc1
80	<a href="#">c2y5tF_</a>	Alignment	not modelled	9.6	35	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> c1; <b>PDBTitle:</b> crystal structure of the pathogenic autoantibody ciic1 in

						complex with2 the triple-helical c1 peptide
81	<a href="#">c4auoH_</a>	Alignment	not modelled	9.6	40	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> H: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
82	<a href="#">c4auoE_</a>	Alignment	not modelled	9.6	40	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> E: <b>PDB Molecule:</b> triple-helical collagen peptide; <b>PDBTitle:</b> crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
83	<a href="#">c6a0cB_</a>	Alignment	not modelled	9.6	48	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
84	<a href="#">c3hd6A_</a>	Alignment	not modelled	9.5	11	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
85	<a href="#">c2y94C_</a>	Alignment	not modelled	9.4	56	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 5'-amp-activated protein kinase catalytic subunit alpha-1; <b>PDBTitle:</b> structure of an active form of mammalian ampk
86	<a href="#">c3qi4A_</a>	Alignment	not modelled	9.4	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> high affinity cgmp-specific 3',5'-cyclic phosphodiesterase <b>PDBTitle:</b> crystal structure of pde9a(q453e) in complex with ibmx
87	<a href="#">c1ciiA_</a>	Alignment	not modelled	9.4	24	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
88	<a href="#">d3dy8a1</a>	Alignment	not modelled	9.3	36	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> PDEase
89	<a href="#">c5vydB_</a>	Alignment	not modelled	9.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase; <b>PDBTitle:</b> crystal structure of phosphodiesterase domain of rhopde fusion protein2 from the choanoflagellate salpingoeca rosetta
90	<a href="#">c6immi_</a>	Alignment	not modelled	9.2	0	<b>PDB header:</b> virus <b>Chain:</b> I: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of an alphavirus, sindbis virus
91	<a href="#">c2l2iB_</a>	Alignment	not modelled	9.2	36	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> krueppel-like factor 1; <b>PDBTitle:</b> nmr structure of the complex between the tfb1 subunit of tfiih and the2 activation domain of ekf
92	<a href="#">c4dveA_</a>	Alignment	not modelled	9.2	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biotin transporter bio; <b>PDBTitle:</b> crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
93	<a href="#">c4x0fA_</a>	Alignment	not modelled	9.2	40	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> camp-specific 3',5'-cyclic phosphodiesterase 4b; <b>PDBTitle:</b> crystal structure of crosslink stabilized long-form pde4b in complex2 with (r)-(-)-rolipram
94	<a href="#">c6a0cC_</a>	Alignment	not modelled	9.1	48	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
95	<a href="#">c6a0cA_</a>	Alignment	not modelled	9.1	48	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
96	<a href="#">c5nf2A_</a>	Alignment	not modelled	9.1	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> minor fimbrium subunit mfa1; <b>PDBTitle:</b> the fimbrial shaft protein mfa1 from porphyromonas gingivalis
97	<a href="#">c1zkIA_</a>	Alignment	not modelled	9.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> high-affinity camp-specific 3',5'-cyclic nucleotide phosphodiesterases <b>PDBTitle:</b> multiple determinants for inhibitor selectivity of cyclic2
98	<a href="#">c2kdcC_</a>	Alignment	not modelled	8.9	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> diacylglycerol kinase; <b>PDBTitle:</b> nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
99	<a href="#">c6cpuA_</a>	Alignment	not modelled	8.9	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphodiesterase; <b>PDBTitle:</b> crystal structure of yeast capde2