













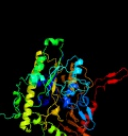




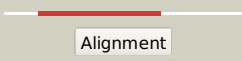

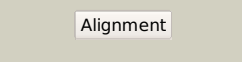
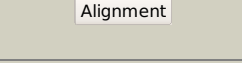
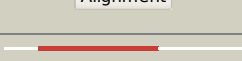
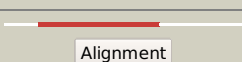
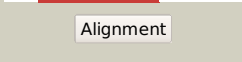
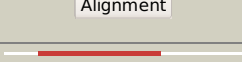
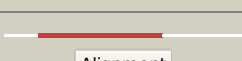
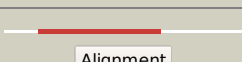
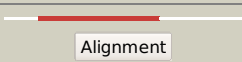

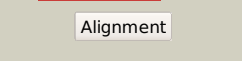
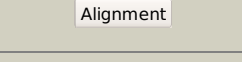
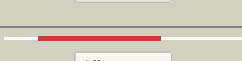
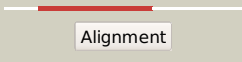
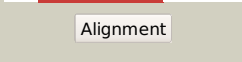
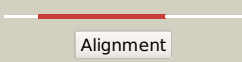
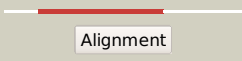
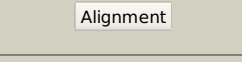

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0711_(atsA)_806338_808701
Date	Fri Jul 26 01:50:28 BST 2019
Unique Job ID	f1b3b8a44cc800c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hdha_	 Alignment		100.0	33	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
2	c4upiA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas1 from silicibacter pomeroyi
3	c4uplC_	 Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
4	c3ed4A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
5	d1p49a_	 Alignment		100.0	23	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
6	c4uphA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: sulfatase (sulfuric ester hydrolase) protein; PDBTitle: crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
7	c4ug4H_	 Alignment		100.0	20	PDB header: hydrolase Chain: H: PDB Molecule: choline sulfatase; PDBTitle: crystal structure of a choline sulfatase from sinorhizobium2 melliloti
8	c4fdiA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a
9	c6b1vB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
10	c4upkC_	 Alignment		100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: phosphonate monoester hydrolase; PDBTitle: phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
11	d1fsua_	 Alignment		100.0	29	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase

12	c2qzuA_	Alignment		100.0	21	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
13	d1auka_	Alignment		100.0	27	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
14	c5fqIA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: iduronate-2-sulfatase; PDBTitle: insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
15	c6j66B_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: chondroitin sulfate/dermatan sulfate 4-o-endosulfatase PDBTitle: chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
16	c4mivB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: n-sulphoglucosamine sulphohydrolase; PDBTitle: crystal structure of sulfamidase, crystal form I
17	c2vqrA_	Alignment		100.0	21	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
18	c3b5qB_	Alignment		100.0	21	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
19	c6hhmA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
20	c5g2vA_	Alignment		100.0	27	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.
21	c6hr5A_	Alignment	not modelled	100.0	24	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
22	c4uopB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
23	c3lxqB_	Alignment	not modelled	100.0	20	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
24	c2w8dB_	Alignment	not modelled	100.0	17	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	c2w5tA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: processed glycerol phosphate lipoteichoic acid PDBTitle: structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
26	c4uorK_	Alignment	not modelled	100.0	15	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
27	c5i5fA_	Alignment	not modelled	100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
28	c2zktB_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii

29	c5k4pA	 Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
30	c6bneA	 Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase; PDBTitle: crystal structure of the intrinsic colistin resistance enzyme icr(m)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
31	c3m8yC	 Alignment	not modelled	100.0	22	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
32	c4kayA	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: yhbxb/yhjw/yjip/yjdb family protein; PDBTitle: structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
33	c5tj3A	 Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase pafa; PDBTitle: crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
34	c6a82A	 Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
35	c3q3qA	 Alignment	not modelled	100.0	16	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
36	c4tn0C	 Alignment	not modelled	100.0	15	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
37	c2i09A	 Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
38	c4lqyA	 Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: bis(5'-adenosyl)-triphosphatase enpp4; PDBTitle: crystal structure of human enpp4 with amp
39	c5udyA	 Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
40	c2gsoB	 Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase-nucleotide pyrophosphatase; PDBTitle: structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
41	d1o98a2	 Alignment	not modelled	100.0	20	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
42	c5vemA	 Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
43	c5egeD	 Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: D: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
44	c5u9zB	 Alignment	not modelled	100.0	15	PDB header: transferase Chain: B: PDB Molecule: phosphoglycerol transferase; PDBTitle: phosphoglycerol transferase gach from streptococcus pyogenes
45	c3szzA	 Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphonoacetate hydrolase; PDBTitle: crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
46	d2i09a1	 Alignment	not modelled	100.0	24	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
47	d1ei6a	 Alignment	not modelled	100.0	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Phosphonoacetate hydrolase
48	c5fgnA	 Alignment	not modelled	100.0	20	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
49	c6c02B	 Alignment	not modelled	100.0	13	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)
50	c5gz5A	Alignment	not modelled	100.0	16	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
51	c5gz4A	Alignment	not modelled	100.0	16	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)
						PDB header: hydrolase

52	c4b56A_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
53	c2xrgA_	Alignment	not modelled	100.0	16	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
54	c2xr9A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
55	c1o98A_	Alignment	not modelled	99.8	25	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
56	c5kgmA_	Alignment	not modelled	99.8	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)
57	c3igzB_	Alignment	not modelled	99.7	22	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
58	c2d1gB_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: B: PDB Molecule: acid phosphatase; PDBTitle: structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
59	c5vpuA_	Alignment	not modelled	99.7	18	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
60	c4my4A_	Alignment	not modelled	99.7	19	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
61	c2iucB_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic bacterium tab5
62	d1k7ha_	Alignment	not modelled	99.3	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
63	d1y6va1	Alignment	not modelled	99.3	22	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
64	c1ew2A_	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
65	d1zeda1	Alignment	not modelled	99.2	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
66	c2w0yB_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
67	c3a52A_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
68	c2x98A_	Alignment	not modelled	99.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
69	c3e2dB_	Alignment	not modelled	98.9	19	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
70	c3wbhB_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
71	c2r1dF_	Alignment	not modelled	98.2	20	PDB header: cell adhesion, splicing Chain: F: PDB Molecule: neurexin-1-beta; PDBTitle: crystal structure of rat neurexin 1beta in the ca2+ containing form
72	c3asiaA_	Alignment	not modelled	98.1	22	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: alpha-neurexin-1 ectodomain fragment; Ins5-egf3-Ins6
73	c3poyA_	Alignment	not modelled	98.1	19	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: crystal structure of the alpha-neurexin-1 ectodomain, Ins 2-6
74	c1okqA_	Alignment	not modelled	98.0	14	PDB header: metal binding protein Chain: A: PDB Molecule: laminin alpha 2 chain; PDBTitle: laminin alpha 2 chain lg4-5 domain pair, ca1 site mutant
75	c2jkbA_	Alignment	not modelled	98.0	16	PDB header: lyase Chain: A: PDB Molecule: sialidase b; PDBTitle: crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac
76	c2jd4B_	Alignment	not modelled	98.0	17	PDB header: metal binding protein Chain: B: PDB Molecule: laminin subunit alpha-1; PDBTitle: mouse laminin alpha1 chain, domains lg4-5

77	c3qcwB_	Alignment	not modelled	98.0	19	PDB header: cell adhesion Chain: B: PDB Molecule: neurexin-1-alpha; PDBTitle: structure of neurexin 1 alpha (domains Ins1-Ins6), no splice inserts
78	d2erfa1	Alignment	not modelled	97.9	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
79	d1dyka1	Alignment	not modelled	97.9	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
80	c3v65A_	Alignment	not modelled	97.9	16	PDB header: protein binding Chain: A: PDB Molecule: agrin; PDBTitle: crystal structure of agrin and Irp4 complex
81	c4yw5A_	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase c; PDBTitle: crystal structure of streptococcus pneumoniae nanc, complex with2 oseltamivir carboxylate
82	c1za4A_	Alignment	not modelled	97.8	16	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin 1; PDBTitle: crystal structure of the thrombospondin-1 n-terminal domain2 in complex with arित्रa
83	c3flpj_	Alignment	not modelled	97.8	13	PDB header: sugar binding protein Chain: J: PDB Molecule: sap-like pentraxin; PDBTitle: crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
84	c2wjsA_	Alignment	not modelled	97.8	15	PDB header: cell adhesion Chain: A: PDB Molecule: laminin subunit alpha-2; PDBTitle: crystal structure of the Ig1-3 region of the laminin alpha22 chain
85	c2v73B_	Alignment	not modelled	97.8	11	PDB header: sugar-binding protein Chain: B: PDB Molecule: putative exo-alpha-sialidase; PDBTitle: the structure of the family 40 cbm from c. perfringens nanj2 in complex with a sialic acid containing molecule
86	d2r1da1	Alignment	not modelled	97.7	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
87	c2h0bC_	Alignment	not modelled	97.7	15	PDB header: cell adhesion Chain: C: PDB Molecule: neurexin-1-alpha; PDBTitle: crystal structure of the second Ins/Ig domain from neurexin 1 alpha
88	c3vkfD_	Alignment	not modelled	97.7	20	PDB header: cell adhesion Chain: D: PDB Molecule: neurexin-1-beta; PDBTitle: crystal structure of neurexin 1beta/neuroigin 1 complex
89	c3vkfC_	Alignment	not modelled	97.7	20	PDB header: cell adhesion Chain: C: PDB Molecule: neurexin-1-beta; PDBTitle: crystal structure of neurexin 1beta/neuroigin 1 complex
90	c5fraD_	Alignment	not modelled	97.6	10	PDB header: sugar binding protein Chain: D: PDB Molecule: sialidase; PDBTitle: cbm40_cpf0721-6'sl
91	c6er3B_	Alignment	not modelled	97.6	17	PDB header: sugar binding protein Chain: B: PDB Molecule: bnr/asp-box repeat protein; PDBTitle: ruminococcus navus it-sialidase cbm40 bound to alpha2,3 sialyllactose
92	c2c5dA_	Alignment	not modelled	97.6	17	PDB header: signaling protein/receptor Chain: A: PDB Molecule: growth-arrest-specific protein 6 precursor; PDBTitle: structure of a minimal gas6-axl complex
93	c3mw3A_	Alignment	not modelled	97.6	17	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-2-beta; PDBTitle: crystal structure of beta-neurexin 2 with the splice insert 4
94	c2r16A_	Alignment	not modelled	97.5	18	PDB header: cell adhesion, splicing Chain: A: PDB Molecule: neurexin-1-alpha; PDBTitle: crystal structure of bovine neurexin 1 alpha Ins/Ig domain 4 (with no2 splice insert)
95	c5mc9A_	Alignment	not modelled	97.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: laminin subunit alpha-1; PDBTitle: crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
96	d1saca_	Alignment	not modelled	97.3	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentaxin)
97	d2slia1	Alignment	not modelled	97.3	14	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Leech intramolecular trans-sialidase, N-terminal domain
98	d1q56a_	Alignment	not modelled	97.2	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
99	c3pveA_	Alignment	not modelled	97.2	18	PDB header: transcription Chain: A: PDB Molecule: agrin, agrin protein; PDBTitle: crystal structure of the g2 domain of agrin from mus musculus
100	c1fv3B_	Alignment	not modelled	97.2	11	PDB header: toxin Chain: B: PDB Molecule: tetanus toxin heavy chain; PDBTitle: the hc fragment of tetanus toxin complexed with an analogue of its2 ganglioside receptor gt1b
101	c5oltA_	Alignment	not modelled	97.2	15	PDB header: transferase Chain: A: PDB Molecule: cellulose biosynthesis protein bcsg; PDBTitle: crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsg from salmonella typhimurium
102	c1yynA_	Alignment	not modelled	97.2	10	PDB header: hydrolase Chain: A: PDB Molecule: tetanus toxin; PDBTitle: a common binding site for disialyllactose and a tri-peptide2 in the c-fragment of tetanus neurotoxin
103	c2sliA_	Alignment	not modelled	97.1	15	PDB header: hydrolase Chain: A: PDB Molecule: intramolecular trans-sialidase;

103	c2shA_	Alignment	not modelled	97.1	19	PDBTitle: leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product PDB header: metal binding protein
104	c1qu0A_	Alignment	not modelled	97.1	20	Chain: A: PDB Molecule: laminin alpha2 chain; PDBTitle: crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
105	c1qu0D_	Alignment	not modelled	97.1	20	PDB header: metal binding protein Chain: D: PDB Molecule: laminin alpha2 chain; PDBTitle: crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
106	d1h30a1	Alignment	not modelled	97.1	23	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
107	c3sh5A_	Alignment	not modelled	97.1	17	PDB header: metal binding protein Chain: A: PDB Molecule: lg3 peptide; PDBTitle: calcium-bound laminin g like domain 3 from human perlecan
108	c4dqaA_	Alignment	not modelled	97.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative carbohydrate binding protein2 (bacova_03559) from bacteroides ovatus atcc 8483 at 1.50 a resolution
109	c2vxrA_	Alignment	not modelled	97.1	8	PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type g; PDBTitle: crystal structure of the botulinum neurotoxin serotype g2 binding domain
110	d1b09a_	Alignment	not modelled	97.0	17	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentaxin)
111	d1pz7a_	Alignment	not modelled	97.0	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
112	c3mppG_	Alignment	not modelled	97.0	9	PDB header: toxin Chain: G: PDB Molecule: botulinum neurotoxin type g; PDBTitle: botulinum neurotoxin type g receptor binding domain
113	c4pboA_	Alignment	not modelled	97.0	16	PDB header: immune system Chain: A: PDB Molecule: c-reactive protein; PDBTitle: crystal structure of zebrafish short-chain pentraxin protein without2 calcium ions
114	d1h30a2	Alignment	not modelled	96.9	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Laminin G-like module
115	c5ho0A_	Alignment	not modelled	96.9	16	PDB header: hydrolase Chain: A: PDB Molecule: extracellular arabinanase; PDBTitle: crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
116	c1qu0C_	Alignment	not modelled	96.8	20	PDB header: metal binding protein Chain: C: PDB Molecule: laminin alpha2 chain; PDBTitle: crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
117	c6hoxA_	Alignment	not modelled	96.7	10	PDB header: toxin Chain: A: PDB Molecule: binding domain (hc) of paraclostridial mosquitocidal PDBTitle: crystal structure of the binding domain of paraclostridial2 mosquitocidal protein 1
118	c4qvsA_	Alignment	not modelled	96.7	13	PDB header: unknown function Chain: A: PDB Molecule: s-layer domain-containing protein; PDBTitle: 2.1 angstrom resolution crystal structure of s-layer domain-containing2 protein (residues 221-444) from clostridium thermocellum atcc 27405
119	c3fuqA_	Alignment	not modelled	96.6	12	PDB header: toxin Chain: A: PDB Molecule: bont/f (neurotoxin type f); PDBTitle: glycosylated sv2 and gangliosides as dual receptors for2 botulinum neurotoxin serotype f
120	c2vu9A_	Alignment	not modelled	96.6	11	PDB header: hydrolase Chain: A: PDB Molecule: botulinum neurotoxin a heavy chain; PDBTitle: crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b