
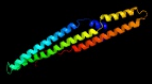
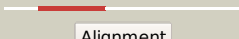
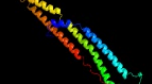
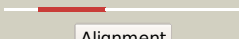
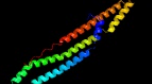



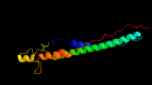














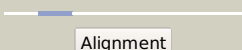
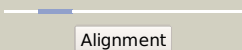
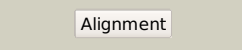
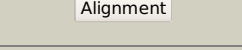
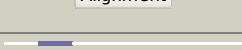
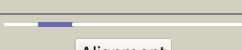
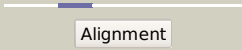
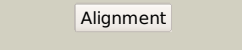
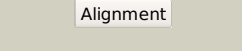

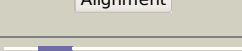


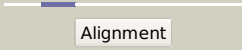
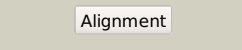
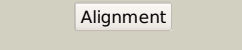

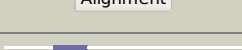
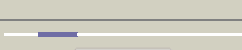


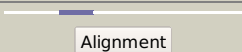


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3558_(PPE64)_3998159_399817
Date	Fri Aug 9 18:20:23 BST 2019
Unique Job ID	aa55ee00dabec1a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	53	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	17	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		98.8	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		98.1	8	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.9	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.8	13	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		97.8	13	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.4	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.7	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.5	10	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.3	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		93.6	19	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	Alignment		77.4	17	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	Alignment		77.4	26	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	d1xkna_	Alignment		51.6	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
19	c3h6pB_	Alignment		27.8	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
20	c3r5zB_	Alignment		27.2	11	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
21	c2kg7A_	Alignment	not modelled	27.0	39	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
22	c2iu1A_	Alignment	not modelled	26.6	22	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
23	c4y9iA_	Alignment	not modelled	26.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
24	c4n91A_	Alignment	not modelled	23.6	13	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
25	c5frgA_	Alignment	not modelled	23.2	75	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
26	c2lyyB_	Alignment	not modelled	23.1	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
27	c3r5wO_	Alignment	not modelled	21.3	23	PDB header: oxidoreductase Chain: O: PDB Molecule: deazaflavin-dependent nitroreductase; PDBTitle: structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420

28	c3jywF_	 Alignment	not modelled	20.4	46	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
29	c3zfsA_	 Alignment	not modelled	20.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
30	c1bkvA_	 Alignment	not modelled	20.0	38	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
31	c2fulE_	 Alignment	not modelled	19.9	39	PDB header: translation Chain: E; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
32	c2ahmG_	 Alignment	not modelled	19.0	12	PDB header: viral protein, replication Chain: G; PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
33	c1bkvC_	 Alignment	not modelled	18.7	38	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
34	c1bkvB_	 Alignment	not modelled	18.7	38	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
35	c3h96B_	 Alignment	not modelled	17.6	11	PDB header: flavoprotein Chain: B; PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
36	c2l5bA_	 Alignment	not modelled	17.5	41	PDB header: apoptosis Chain: A; PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
37	c2l5aA_	 Alignment	not modelled	17.2	22	PDB header: nuclear protein Chain: A; PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
38	c2ke4A_	 Alignment	not modelled	16.0	75	PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
39	c1paqA_	 Alignment	not modelled	16.0	15	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
40	d1paqa_	 Alignment	not modelled	16.0	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
41	c4mnpA_	 Alignment	not modelled	16.0	16	PDB header: sugar binding protein Chain: A; PDB Molecule: n-acetylneuraminat-binding protein; PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
42	c3r5yC_	 Alignment	not modelled	15.0	17	PDB header: unknown function Chain: C; PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
43	c3ub0D_	 Alignment	not modelled	13.5	15	PDB header: replication Chain: D; PDB Molecule: non-structural protein 6, nsp6;; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of2 feline coronavirus
44	c2kp7A_	 Alignment	not modelled	13.4	20	PDB header: hydrolase Chain: A; PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
45	c3juia_	 Alignment	not modelled	13.3	15	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
46	c3trhl_	 Alignment	not modelled	13.2	19	PDB header: lyase Chain: I; PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
47	d2ewoa1	 Alignment	not modelled	12.6	24	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
48	c5lzkB_	 Alignment	not modelled	12.2	4	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
49	c3qthA_	 Alignment	not modelled	11.6	9	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
50	c2hzbB_	 Alignment	not modelled	11.1	15	PDB header: ligand binding, transport protein Chain: B; PDB Molecule: trap-t family sorbitol/mannitol transporter, periplasmic PDBTitle: crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
51	c2jerG_	 Alignment	not modelled	10.6	28	PDB header: hydrolase Chain: G; PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
52	c4el8A_	Alignment	not modelled	10.2	31	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
						PDB header: photosynthesis

53	c2o01H_	Alignment	not modelled	9.7	22	Chain: H: PDB Molecule: photosystem i reaction center subunit vi, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
54	c6b2wB_	Alignment	not modelled	9.7	13	PDB header: hydrolase Chain: B: PDB Molecule: putative peptidyl-arginine deiminase family protein; PDBTitle: c. jejuni c315s agmatine deiminase with substrate bound
55	d2jera1	Alignment	not modelled	9.5	28	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
56	d1vkpa_	Alignment	not modelled	9.5	31	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
57	c3j3bF_	Alignment	not modelled	9.1	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
58	c5ec0A_	Alignment	not modelled	9.1	33	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
59	c3n6xA_	Alignment	not modelled	9.1	13	PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mf1a_0391) from methylobacillus flagellatus kt at 2.35 a resolution
60	c3j21Y_	Alignment	not modelled	9.0	25	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
61	c5h18B_	Alignment	not modelled	9.0	18	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein l; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspL3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
62	c4kkkA_	Alignment	not modelled	8.8	19	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
63	c3b50A_	Alignment	not modelled	8.7	14	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
64	c5i4rA_	Alignment	not modelled	8.6	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
65	c1l2aD_	Alignment	not modelled	8.5	19	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
66	d1l1ya_	Alignment	not modelled	8.5	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
67	c4fusA_	Alignment	not modelled	8.2	31	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
68	c2np3A_	Alignment	not modelled	8.2	10	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
69	d2apla1	Alignment	not modelled	8.2	9	Fold: PG0816-like Superfamily: PG0816-like Family: PG0816-like
70	c2nvjA_	Alignment	not modelled	8.0	30	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
71	c4i6jB_	Alignment	not modelled	7.8	22	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
72	c3j39F_	Alignment	not modelled	7.7	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
73	c4jijA_	Alignment	not modelled	7.7	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
74	c2kwuA_	Alignment	not modelled	7.7	38	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
75	c6o9l6_	Alignment	not modelled	7.5	40	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
76	c3fy6A_	Alignment	not modelled	7.5	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of v. cholerae. integron cassette2 protein vch_cass3
77	c5vmoB_	Alignment	not modelled	7.5	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66:bim complex

78	d2fpga1	Alignment	not modelled	7.2	40	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
79	c2jtwA	Alignment	not modelled	7.2	38	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
80	c1bzgA	Alignment	not modelled	7.2	0	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
81	c6epiC	Alignment	not modelled	7.2	20	PDB header: toxin Chain: C: PDB Molecule: epsilon_1 antitoxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae in complex with unam-4p.
82	c3izce	Alignment	not modelled	7.1	19	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein rpl11 (l5p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
83	c4c5eG	Alignment	not modelled	7.0	22	PDB header: transcription Chain: G: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
84	c4c5eH	Alignment	not modelled	7.0	22	PDB header: transcription Chain: H: PDB Molecule: polycomb protein pho; PDBTitle: crystal structure of the minimal pho-sfmbt complex (p21 spacegroup)
85	c4xb6D	Alignment	not modelled	6.9	11	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
86	c1d0rA	Alignment	not modelled	6.9	30	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in2 trifluoroethanol/water
87	c6igzH	Alignment	not modelled	6.9	12	PDB header: plant protein Chain: H: PDB Molecule: psah; PDBTitle: structure of psi-lhci
88	d1kx5a	Alignment	not modelled	6.8	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
89	c2yfwC	Alignment	not modelled	6.7	22	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
90	c6hu9u	Alignment	not modelled	6.7	27	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
91	c3a9rA	Alignment	not modelled	6.6	14	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
92	c4wpyA	Alignment	not modelled	6.5	20	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
93	c3zf7w	Alignment	not modelled	6.5	25	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
94	c2zdjA	Alignment	not modelled	6.4	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tma177; PDBTitle: crystal structure of tma177, a hypothetical protein from2 thermus thermophilus phage tma
95	d1g9ga	Alignment	not modelled	6.3	21	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
96	c4u0zH	Alignment	not modelled	6.3	12	PDB header: transferase Chain: H: PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
97	d1vqow1	Alignment	not modelled	6.3	25	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
98	c3ggyC	Alignment	not modelled	6.2	13	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
99	d1uadc	Alignment	not modelled	6.1	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Other IPT/TIG domains