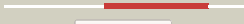



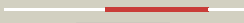



















Phyre2


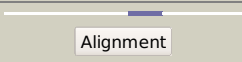
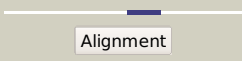
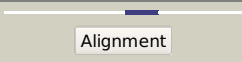
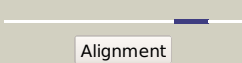
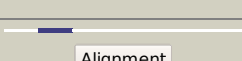
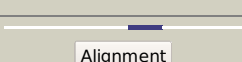
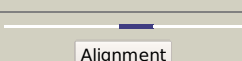
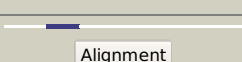
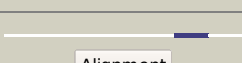

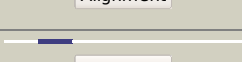

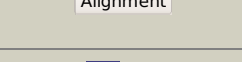
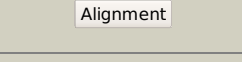
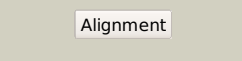
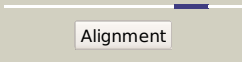
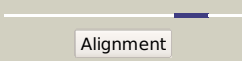
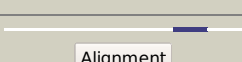

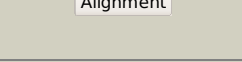
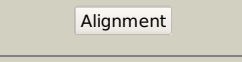
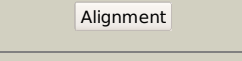
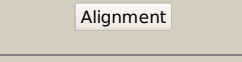
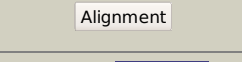
Email	mdejesus@rockefeller.edu
Description	RVBD2313c_(-)_2585062_2585916
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	22dd3582ff691707

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gmya1	 Alignment		100.0	22	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
2	c6ohiA_	 Alignment		100.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
3	d2o4da1	 Alignment		100.0	26	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
4	c3c1lB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
5	d2pfxa1	 Alignment		100.0	16	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
6	d2oyoal	 Alignment		100.0	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
7	d2prra1	 Alignment		100.0	14	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
8	c3lvvB_	 Alignment		100.0	14	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
9	d2ouwa1	 Alignment		99.1	20	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
10	d1knca_	 Alignment		99.1	19	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
11	d1vkea_	 Alignment		99.1	23	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like

12	c1p8cD_	Alignment		99.0	22	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
13	c3beyC_	Alignment		98.9	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
14	c5djpB_	Alignment		98.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
15	d1vkeb_	Alignment		98.8	23	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
16	c5dj4D_	Alignment		98.6	11	PDB header: signaling protein Chain: D: PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens
17	c2qeuA_	Alignment		98.6	11	PDB header: lyase Chain: A: PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
18	c3d7iB_	Alignment		98.5	16	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
19	d2cwqa1	Alignment		98.3	19	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
20	d2q0ta1	Alignment		97.8	17	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
21	c4g9qA_	Alignment	not modelled	96.9	18	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
22	d2af7a1	Alignment	not modelled	96.9	22	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
23	c5gzxD_	Alignment	not modelled	91.9	20	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
24	d1a9xa1	Alignment	not modelled	89.0	17	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
25	c5dotA_	Alignment	not modelled	63.9	12	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
26	c5douC_	Alignment	not modelled	57.1	12	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
27	c5nwuA_	Alignment	not modelled	44.6	30	PDB header: viral protein Chain: A: PDB Molecule: wtfp-tag,gp41; PDBTitle: nmr assignment and structure of a peptide derived from the fusion2 peptide of hiv-1 gp41 in the presence of hexafluoroisopropanol

28	c1m6vE_	Alignment	not modelled	33.6	17	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of 2 carbamoyl phosphate synthetase
29	c1erfA_	Alignment	not modelled	28.7	55	PDB header: viral protein Chain: A: PDB Molecule: transmembrane glycoprotein; PDBTitle: conformational mapping of the n-terminal fusion peptide of 2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
30	c2kniA_	Alignment	not modelled	27.0	13	PDB header: antimicrobial protein Chain: A: PDB Molecule: microplusin preprotein; PDBTitle: nmr structure of microplusin a antimicrobial peptide from 2 rhipicephalus (boophilus) microplu
31	c2pivA_	Alignment	not modelled	26.7	55	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: solution structure of hiv-1 gp41 fusion domain bound to dpc micelle
32	c3kdvB_	Alignment	not modelled	22.3	36	PDB header: dna binding protein Chain: B: PDB Molecule: dna damage response b protein; PDBTitle: crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
33	c2hm2Q_	Alignment	not modelled	20.8	20	PDB header: apoptosis Chain: Q: PDB Molecule: pyrin-only protein 1; PDBTitle: solution structure of asc2
34	d1fc2c_	Alignment	not modelled	20.7	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
35	d1deeg_	Alignment	not modelled	20.2	24	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
36	d1lp1b_	Alignment	not modelled	20.1	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
37	d2jwda1	Alignment	not modelled	18.8	29	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
38	d1lucpa_	Alignment	not modelled	17.0	20	Fold: DEATH domain Superfamily: DEATH domain Family: Pyrin domain, PYD
39	c2do9A_	Alignment	not modelled	17.0	28	PDB header: signaling protein Chain: A: PDB Molecule: nacht-, lrr- and pyd-containing protein 10; PDBTitle: solution structure of the pyrin/paad-dapin domain in mouse2 nalp10 (nacht, leucine rich repeat and pyd containing 10)
40	c2km6A_	Alignment	not modelled	16.6	19	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: nacht, lrr and pyd domains-containing protein 7; PDBTitle: nmr structure of the nlrp7 pyrin domain
41	c3ermD_	Alignment	not modelled	16.0	4	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein with unknown function2 from pseudomonas syringae pv. tomato str. dc3000
42	d1pn5a1	Alignment	not modelled	15.3	16	Fold: DEATH domain Superfamily: DEATH domain Family: Pyrin domain, PYD
43	c1pn5A_	Alignment	not modelled	15.3	16	PDB header: apoptosis Chain: A: PDB Molecule: nacht-, lrr- and pyd-containing protein 2; PDBTitle: nmr structure of the nalp1 pyrin domain (pyd)
44	c2a7uA_	Alignment	not modelled	14.5	38	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase alpha chain; PDBTitle: nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
45	c3deeA_	Alignment	not modelled	14.4	9	PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in 2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
46	c2ariA_	Alignment	not modelled	12.5	55	PDB header: viral protein Chain: A: PDB Molecule: envelope polyprotein gp160; PDBTitle: solution structure of micelle-bound fusion domain of hiv-12 gp41
47	c4ewiA_	Alignment	not modelled	12.2	16	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: nacht, lrr and pyd domains-containing protein 4; PDBTitle: crystal structure of the nlrp4 pyrin domain
48	c2qjxA_	Alignment	not modelled	11.6	9	PDB header: protein binding Chain: A: PDB Molecule: protein bim1; PDBTitle: structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1
49	c1a6bB_	Alignment	not modelled	11.6	33	PDB header: viral protein/dna Chain: B: PDB Molecule: zinc finger protein ncp10; PDBTitle: nmr structure of the complex between the zinc finger2 protein ncp10 of moloney murine leukemia virus and a3 sequence of the psi-packaging domain of hiv-1, 204 structures
50	c6ncvE_	Alignment	not modelled	11.5	16	PDB header: signaling protein, protein fibril Chain: E: PDB Molecule: nacht, lrr and pyd domains-containing protein 6; PDBTitle: cryo-em structure of nlrp6 pyd filament
51	c1hwcA_	Alignment	not modelled	11.2	40	PDB header: growth response protein Chain: A: PDB Molecule: bba1; PDBTitle: 23-residue designed metal-free peptide based on the zinc2 finger domains, nmr, 35 structures
52	c4pwoA_	Alignment	not modelled	10.7	22	PDB header: structural genomics Chain: A: PDB Molecule: dsba; PDBTitle: crystal structure of dsba from the gram positive bacterium2 corynebacterium diphtheriae

53	c1p5aA	 Alignment	not modelled	10.5	55	PDB header: viral protein Chain: A: PDB Molecule: envelope polyprotein gp160; PDBTitle: conformational mapping of the n-terminal peptide of hiv-12 gp41 in lipid detergent and aqueous environments using 13c-3 enhanced fourier transform infrared spectroscopy
54	d2qja1	 Alignment	not modelled	10.4	9	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
55	c4fybA	 Alignment	not modelled	9.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide interchange protein (dsbc); PDBTitle: structural and functional characterizations of a thioredoxin-fold2 protein from helicobacter pylori
56	d1u6pa	 Alignment	not modelled	9.7	33	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
57	c2l6aA	 Alignment	not modelled	9.6	24	PDB header: signaling protein Chain: A: PDB Molecule: nacht, Irr and pyd domains-containing protein 12; PDBTitle: three-dimensional structure of the n-terminal effector pyrin domain of2 nlrp12
58	d1dt0a1	 Alignment	not modelled	9.1	30	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
59	c1t3bA	 Alignment	not modelled	8.9	33	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
60	c5il0B	 Alignment	not modelled	8.8	31	PDB header: rna binding protein Chain: B: PDB Molecule: mettl14; PDBTitle: crystal structural of the mettl3-mettl14 complex for n6-adenosine2 methylation
61	c4wwrD	 Alignment	not modelled	8.7	18	PDB header: transport protein Chain: D: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
62	c2m5vA	 Alignment	not modelled	8.7	28	PDB header: immune system Chain: A: PDB Molecule: nacht, Irr and pyd domains-containing protein 10; PDBTitle: three-dimensional structure of human nlrp10/pynod pyrin domain
63	d1khia2	 Alignment	not modelled	8.5	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
64	d1y67a1	 Alignment	not modelled	8.3	35	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
65	c1wyoA	 Alignment	not modelled	8.3	9	PDB header: structural protein Chain: A: PDB Molecule: microtubule-associated protein rp/eb family PDBTitle: solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
66	c3w20B	 Alignment	not modelled	8.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a novel n-substituted l-amino acid dioxygenase2 from burkholderia ambifaria ammd
67	c4odaC	 Alignment	not modelled	8.1	19	PDB header: hydrolase/replication Chain: C: PDB Molecule: dna polymerase processivity factor component a20; PDBTitle: crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
68	c2ob9A	 Alignment	not modelled	8.0	40	PDB header: chaperone Chain: A: PDB Molecule: tail assembly chaperone; PDBTitle: structure of bacteriophage hk97 tail assembly chaperone
69	c2kn6A	 Alignment	not modelled	7.6	20	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis-associated speck-like protein containing a card; PDBTitle: structure of full-length human asc (apoptosis-associated speck-like2 protein containing a card)
70	c4fc8B	 Alignment	not modelled	7.5	10	PDB header: transcription Chain: B: PDB Molecule: transcription protein rtr1; PDBTitle: crystal structure of transcription regulator protein rtr1 from2 kluveromyces lactis
71	c5ctdA	 Alignment	not modelled	7.3	32	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
72	c1s5lu	 Alignment	not modelled	7.2	22	PDB header: photosynthesis Chain: U: PDB Molecule: photosystem ii 12 kda extrinsic protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
73	c5lutK	 Alignment	not modelled	7.1	47	PDB header: transferase Chain: K: PDB Molecule: blm helicase; PDBTitle: structures of dhn domain of gallus gallus blm helicase
74	c5givD	 Alignment	not modelled	7.0	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxypeptidase 1; PDBTitle: crystal structure of m32 carboxypeptidase from deinococcus radiodurans2 r1
75	c4wwrB	 Alignment	not modelled	6.9	17	PDB header: transport protein Chain: B: PDB Molecule: ubiquitin-like protein 4a; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
76	c3hq2A	 Alignment	not modelled	6.8	13	PDB header: hydrolase Chain: A: PDB Molecule: bacillus subtilis m32 carboxypeptidase; PDBTitle: bsucp crystal structure
77	c5oarC	 Alignment	not modelled	6.8	23	PDB header: hydrolase Chain: C: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase

						isolated from2 aspergillus oryzae
78	c4npbA_	Alignment	not modelled	6.7	33	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
79	c3pt8B_	Alignment	not modelled	6.7	16	PDB header: oxygen transport Chain: B: PDB Molecule: hemoglobin iii; PDBTitle: structure of hbii-iii-cn from lucina pectinata at ph 5.0
80	d1vz0a2	Alignment	not modelled	6.7	30	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: ParB-like nuclease domain
81	c1v57A_	Alignment	not modelled	6.7	38	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
82	c6os5A_	Alignment	not modelled	6.6	15	PDB header: transferase Chain: A: PDB Molecule: cymd prenyltransferase; PDBTitle: crystal structure of cymd prenyltransferase complexed with l-2 tryptophan
83	c3gv1A_	Alignment	not modelled	6.6	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
84	c2jnrB_	Alignment	not modelled	6.4	55	PDB header: viral protein Chain: B: PDB Molecule: env polyprotein; PDBTitle: discovery and optimization of a natural hiv-1 entry2 inhibitor targeting the gp41 fusion peptide
85	d1mc0a1	Alignment	not modelled	6.3	11	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
86	c1hyuA_	Alignment	not modelled	6.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
87	d2nyba1	Alignment	not modelled	6.2	30	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
88	c4kmgA_	Alignment	not modelled	6.2	15	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c6 (soluble cytochrome f) (cytochrome c553); PDBTitle: crystal structure of cytochrome c6b from synechococcus sp. wh8102
89	c4aezB_	Alignment	not modelled	6.1	33	PDB header: cell cycle Chain: B: PDB Molecule: mitotic spindle checkpoint component mad2; PDBTitle: crystal structure of mitotic checkpoint complex
90	c2j2sA_	Alignment	not modelled	6.0	25	PDB header: transcription regulation Chain: A: PDB Molecule: zinc finger protein hrx; PDBTitle: solution structure of the nonmethyl-cpg-binding cxxc domain of the2 leukaemia-associated mll histone methyltransferase
91	c2jviA_	Alignment	not modelled	5.9	25	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein hrx; PDBTitle: solution structure of mll cxxc domain
92	d1eeja1	Alignment	not modelled	5.8	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
93	c3dvwA_	Alignment	not modelled	5.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis
94	c5tdyD_	Alignment	not modelled	5.7	19	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
95	c3ol4B_	Alignment	not modelled	5.7	19	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
96	c2ki8A_	Alignment	not modelled	5.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
97	c3iraA_	Alignment	not modelled	5.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
98	d1wpga4	Alignment	not modelled	5.7	19	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
99	c1jzdA_	Alignment	not modelled	5.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex