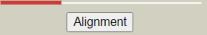
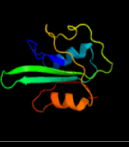
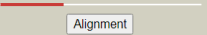

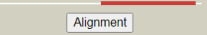

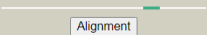
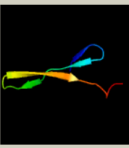
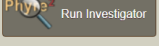
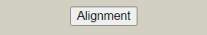
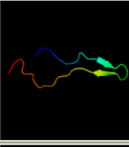
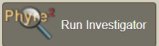
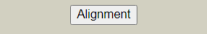
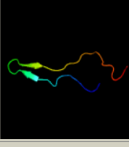
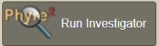
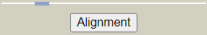
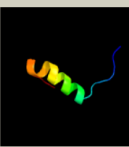
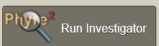
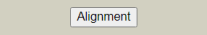
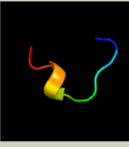
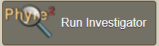
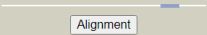

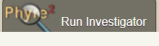


Sample	Phyre2 Results						
DNA-A BcssDV1	#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
	1	c6g1mA	 Alignment		99.9	28	PDB header: replication Chain: A; PDB Molecule: replication-associated protein; PDBTitle: crystal structure of the wheat dwarf virus rep domain PDB Entry: PDBe RCSB PDBj
	2	d115ia	 Alignment		99.9	26	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: DNA-binding domain of REP protein PDB entry: PDBe RCSB PDBj
	3	c7om0C	 Alignment		98.8	17	PDB header: replication Chain: C; PDB Molecule: dna primase; PDBTitle: structure of primase-helicase in sapi5 PDB Entry: PDBe RCSB PDBj
DNA-B BcssDV1	#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
	1	c2mx4A	 Alignment		40.6	52	PDB header: translation,protein binding Chain: A; PDB Molecule: eukaryotic translation initiation factor 4e-binding protein PDBTitle: nmr structure of phosphorylated 4e-bp2 PDB Entry: PDBe RCSB PDBj 
	2	c1v0eB	 Alignment		32.7	33	PDB header: hydrolase Chain: B; PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f PDB Entry: PDBe RCSB PDBj 
	3	d1v0ea1	 Alignment		29.0	33	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Endo-alpha-sialidase PDB entry: PDBe RCSB PDBj 
	4	c6wxoB	 Alignment		27.1	46	PDB header: de novo protein Chain: B; PDB Molecule: tfd-he; PDBTitle: de novo tim barrel-ferredoxin fold fusion homodimer with 2-histidine 2-glutamate centre tfd-he PDB Entry: PDBe RCSB PDBj 
	5	c4hceA	 Alignment		26.5	42	PDB header: cell cycle Chain: A; PDB Molecule: cell division control protein 13; PDBTitle: crystal structure of the telomeric saccharomyces cerevisiae cdc13 ob22 domain PDB Entry: PDBe RCSB PDBj 
	6	c4hizA	 Alignment		25.3	33	PDB header: hydrolase,viral protein Chain: A; PDB Molecule: endosialidase; PDBTitle: phage phi92 endosialidase PDB Entry: PDBe RCSB PDBj 

DNA-B
FgGV1

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ofda3			61.1	23	<p>Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases PDB entry: PDBe RCSB PDBj</p>
2	d1ea0a3			57.4	28	<p>Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases PDB entry: PDBe RCSB PDBj</p>
3	c2lrqA			35.8	24	<p>PDB header:transcription Chain: A; PDB Molecule:nua4 complex subunit eaf3 homolog; PDBTitle: chemical shift assignment and solution structure of fr822a from2 drosophila melanogaster. northeast structural genomics consortium3 target fr822a PDB Entry: PDBe RCSB PDBj</p>
4	d3byqa1			25.7	38	<p>Fold: Bacillus chorismate mutase-like Superfamily: BB2672-like Family: BB2672-like PDB entry: PDBe RCSB PDBj</p>
5	c2cw1A			23.6	53	<p>PDB header:de novo protein Chain: A; PDB Molecule:sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold protein PDB Entry: PDBe RCSB PDBj</p>
6	d2d0ta1			22.1	18	<p>Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like PDB entry: PDBe RCSB PDBj</p>

DNA-C
BcssDV1

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8xA			89.3	27	<p>PDB header:transferase Chain: A; PDB Molecule:ephrin type-a receptor 2; PDBTitle: crystal structure of the ligand binding domain of human ephrin a22 (epha2) receptor protein kinase PDB Entry: PDBe RCSB PDBj</p>
2	d1shwb			82.9	37	<p>Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Ephrin receptor ligand binding domain PDB entry: PDBe RCSB PDBj</p>
3	c3p1c			74.3	32	<p>PDB header:transferase;signaling protein Chain: C; PDB Molecule:ephrin type-b receptor 3; PDBTitle: ligand binding domain of human ephrin type-b receptor 3 PDB Entry: PDBe RCSB PDBj</p>
4	c2qbxB			73.6	31	<p>PDB header:signaling protein Chain: B; PDB Molecule:ephrin type-b receptor 2; PDBTitle: ephb2/snew antagonistic peptide complex PDB Entry: PDBe RCSB PDBj</p>
5	c7k7jA			66.8	33	<p>PDB header:transferase Chain: A; PDB Molecule:ephrin type-b receptor 6; PDBTitle: ephb6 receptor ectodomain PDB Entry: PDBe RCSB PDBj</p>
6	c3mbwA			62.4	34	<p>PDB header:transferase/signaling protein Chain: A; PDB Molecule:ephrin type-a receptor 2; PDBTitle: crystal structure of the human ephrin a2 lbd and crd domains in2 complex with ephrin a1 PDB Entry: PDBe RCSB PDBj</p>

DNA-C
FgGV1

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2v7fa1			56.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rps19E-like PDB entry: PDBe RCSB PDBJ
2	c5xauD			52.0	13	PDB header: cell adhesion Chain: D; PDB Molecule: laminin subunit alpha-5; PDBTitle: crystal structure of integrin binding fragment of laminin-511 PDB Entry: PDBe RCSB PDBJ
3	c5xyIT			50.9	25	PDB header: ribosome Chain: T; PDB Molecule: ribosomal protein s19e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome PDB Entry: PDBe RCSB PDBJ
4	c3j38T			47.5	45	PDB header: ribosome Chain: T; PDB Molecule: 40s ribosomal protein s19a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins PDB Entry: PDBe RCSB PDBJ
5	c3j3aT			47.2	40	PDB header: ribosome Chain: T; PDB Molecule: 40s ribosomal protein s19; PDBTitle: structure of the human 40s ribosomal proteins PDB Entry: PDBe RCSB PDBJ
6	c3zeyO			46.9	30	PDB header: ribosome Chain: O; PDB Molecule: ribosomal protein s19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome PDB Entry: PDBe RCSB PDBJ

DNA-D
BcssDV1

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zxdD			71.2	43	PDB header: cell cycle Chain: D; PDB Molecule: ctf19; PDBTitle: crystal structure of the ctf19-mcm21 kinetochore heterodimer from 2 yeast PDB Entry: PDBe RCSB PDBJ
2	c5w65P			62.4	18	PDB header: transcription Chain: P; PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: rna polymerase i initial transcribing complex state 2 PDB Entry: PDBe RCSB PDBJ
3	c5n5xN			60.2	18	PDB header: transcription Chain: N; PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: crystal structure of s. cerevisiae core factor at 3.2a resolution PDB Entry: PDBe RCSB PDBJ
4	c6ohzA			37.6	32	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of an uncharacterized protein from leptospira borgpeterseni2 serovar hardjo-bovis (strain jb197) PDB Entry: PDBe RCSB PDBJ
5	c3mi6A			36.8	23	PDB header: hydrolase Chain: A; PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11. PDB Entry: PDBe RCSB PDBJ

Additional file 4a. Results of structural homologies modelled by Phyre 2 in proteins of BcssDV1 and FgGV1.

Sample	DALI Results							
DNA-A BcssDV1	No:	Chain	Z	rmsd	lali	nres	%id PDB	Description
	<input type="checkbox"/>	1: 6q1m-A	12.5	2.3	97	119	24 PDB	MOLECULE: REPLICATION-ASSOCIATED PROTEIN;
	<input type="checkbox"/>	2: 4gdf-A	9.2	12.5	251	497	12 PDB	MOLECULE: LARGE T ANTIGEN;
	<input type="checkbox"/>	3: 3bos-B	9.2	3.9	141	231	10 PDB	MOLECULE: PUTATIVE DNA REPLICATION FACTOR;
	<input type="checkbox"/>	4: 5zr1-A	9.1	5.8	142	494	11 PDB	MOLECULE: ORIGIN RECOGNITION COMPLEX SUBUNIT 1;
	<input type="checkbox"/>	5: 2hw0-A	9.1	3.6	96	115	18 PDB	MOLECULE: REPLICASE;
	<input type="checkbox"/>	6: 6pxk-K	8.8	3.6	135	429	13 PDB	MOLECULE: ATP-DEPENDENT PROTEASE ATPASE SUBUNIT HSLU;
	<input type="checkbox"/>	7: 6h8o-A	8.8	2.6	82	95	15 PDB	MOLECULE: REPLICATION-ASSOCIATED PROTEIN;
	<input type="checkbox"/>	8: 7jsf-A	8.8	6.9	171	276	15 PDB	MOLECULE: PROTEIN REP68;
	<input type="checkbox"/>	9: 7tts-D	8.7	6.3	145	463	12 PDB	MOLECULE: CASEINOLYTIC PEPTIDASE B PROTEIN HOMOLOG;
	<input type="checkbox"/>	10: 5v8f-D	8.5	3.5	125	456	10 PDB	MOLECULE: DNA REPLICATION LICENSING FACTOR MCM2;
	<input type="checkbox"/>	11: 7jgr-D	8.5	3.2	125	441	14 PDB	MOLECULE: ORIGIN RECOGNITION COMPLEX SUBUNIT 2;
	<input type="checkbox"/>	12: 1l8q-A	8.4	3.4	126	321	14 PDB	MOLECULE: CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA;
	<input type="checkbox"/>	13: 1ixs-B	8.4	3.3	131	315	12 PDB	MOLECULE: HOLLIDAY JUNCTION DNA HELICASE RUVA;
	<input type="checkbox"/>	14: 7uqj-A	8.3	3.9	138	585	12 PDB	MOLECULE: ATPASE HISTONE CHAPERONE YTA7;
	<input type="checkbox"/>	15: 5j1s-A	8.3	3.5	133	277	15 PDB	MOLECULE: TORSIN-1A;
	<input type="checkbox"/>	16: 1g4a-E	8.3	3.5	133	356	14 PDB	MOLECULE: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT
	<input type="checkbox"/>	17: 3pvs-D	8.1	3.1	122	424	11 PDB	MOLECULE: REPLICATION-ASSOCIATED RECOMBINATION PROTEIN A;
	<input type="checkbox"/>	18: 6iy8-A	8.1	18.1	144	469	13 PDB	MOLECULE: POSITIVE REGULATOR CAPR;
	<input type="checkbox"/>	19: 6l1q-A	8.1	3.9	138	267	14 PDB	MOLECULE: CBBQ PROTEIN;
	<input type="checkbox"/>	20: 7mi1-A	8.0	6.5	151	2628	10 PDB	MOLECULE: CHIMERA PROTEIN OF DYNEIN AND ENDOLYSIN;
	<input type="checkbox"/>	21: 7mi8-A	8.0	3.5	141	868	13 PDB	MOLECULE: FUSION PROTEIN OF DYNEIN AND ENDOLYSIN;
	<input type="checkbox"/>	22: 7jpp-E	8.0	3.0	123	406	15 PDB	MOLECULE: ORIGIN RECOGNITION COMPLEX SUBUNIT 1;
	<input type="checkbox"/>	23: 5e7p-A	7.9	6.0	134	719	10 PDB	MOLECULE: CELL DIVISION CONTROL PROTEIN CDC48;
	<input type="checkbox"/>	24: 7apd-B	7.9	6.2	152	289	14 PDB	MOLECULE: REPLICATION PROTEIN E1;
	<input type="checkbox"/>	25: 7vcs-A	7.8	10.1	154	766	10 PDB	MOLECULE: TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE;
	<input type="checkbox"/>	26: 2qby-B	7.8	3.1	130	368	17 PDB	MOLECULE: CELL DIVISION CONTROL PROTEIN 6 HOMOLOG 1;
	<input type="checkbox"/>	27: 7w42-B	7.7	4.3	154	402	9 PDB	MOLECULE: UNCHARACTERIZED ATPASE YJOB;
	<input type="checkbox"/>	28: 8dr5-A	7.7	7.2	136	646	12 PDB	MOLECULE: REPLICATION FACTOR C SUBUNIT 1;
	<input type="checkbox"/>	29: 7mi6-A	7.6	12.0	167	2419	10 PDB	MOLECULE: FUSION PROTEIN OF DYNEIN AND ENDOLYSIN;
	<input type="checkbox"/>	30: 6z1f-3	7.6	4.2	134	284	13 PDB	MOLECULE: RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIV
	<input type="checkbox"/>	31: 7qo4-M	7.6	12.8	189	421	12 PDB	MOLECULE: 26S PROTEASOME REGULATORY SUBUNIT RPN1;
	<input type="checkbox"/>	32: 6mdm-D	7.6	11.7	179	713	9 PDB	MOLECULE: VESICLE-FUSING ATPASE;
	<input type="checkbox"/>	33: 7tjj-I	7.5	3.2	116	380	10 PDB	MOLECULE: ORIGIN RECOGNITION COMPLEX SUBUNIT 1;
	<input type="checkbox"/>	34: 6dgd-A	7.5	4.6	126	704	10 PDB	MOLECULE: PRIMOSOMAL PROTEIN N';
	<input type="checkbox"/>	35: 1w5s-B	7.5	3.3	133	396	14 PDB	MOLECULE: ORIGIN RECOGNITION COMPLEX SUBUNIT 2 ORC2;

DNA-B
BcssDV1

No:	Chain	Z	rmsd	lali	nres	%id PDB	Description
<input type="checkbox"/> 1:	6f2s-H	9.5	3.3	152	218	9 PDB	MOLECULE: CAPSID PROTEIN;
<input type="checkbox"/> 2:	6s44-A	8.8	3.6	123	146	12 PDB	MOLECULE: CAPSID PROTEIN;
<input type="checkbox"/> 3:	1r64-A	8.7	10.4	132	481	4 PDB	MOLECULE: KEXIN;
<input type="checkbox"/> 4:	4bcu-A	8.4	4.1	149	188	11 PDB	MOLECULE: COAT PROTEIN;
<input type="checkbox"/> 5:	6qfo-A	8.2	5.7	113	1348	10 PDB	MOLECULE: PEGA DOMAIN-CONTAINING PROTEIN, PEGA DOMAIN-CONTAI
<input type="checkbox"/> 6:	2wq4-A	8.0	2.9	109	134	8 PDB	MOLECULE: LECTIN;
<input type="checkbox"/> 7:	2xom-A	8.0	2.7	104	145	5 PDB	MOLECULE: ARABINOGALACTAN ENDO-1,4-BETA-GALACTOSIDASE;
<input type="checkbox"/> 8:	5azx-A	7.9	2.8	92	100	8 PDB	MOLECULE: TRANSMEMBRANE EMP24 DOMAIN-CONTAINING PROTEIN 10;
<input type="checkbox"/> 9:	3afg-B	7.6	5.7	130	507	5 PDB	MOLECULE: SUBTILISIN-LIKE SERINE PROTEASE;
<input type="checkbox"/> 10:	3wso-A	7.6	3.1	122	252	8 PDB	MOLECULE: F-BOX ONLY PROTEIN 44;
<input type="checkbox"/> 11:	2gsy-E	7.4	3.4	121	433	5 PDB	MOLECULE: POLYPROTEIN;
<input type="checkbox"/> 12:	5gu5-A	7.3	2.8	93	108	9 PDB	MOLECULE: TRANSMEMBRANE EMP24 DOMAIN-CONTAINING PROTEIN 5;
<input type="checkbox"/> 13:	4qx1-A	7.2	3.5	103	115	15 PDB	MOLECULE: FLAGELLAR PROTEIN FLHE;
<input type="checkbox"/> 14:	6yrf-A	7.2	10.0	108	777	5 PDB	MOLECULE: VEGETATIVE INSECTICIDAL PROTEIN;
<input type="checkbox"/> 15:	6vls-D	7.1	11.6	106	963	7 PDB	MOLECULE: MALTOSSE/MALTODEXTRIN-BINDING PERIPLASMIC PROTEIN,
<input type="checkbox"/> 16:	4z11-A	7.0	4.8	116	513	6 PDB	MOLECULE: AURONE SYNTHASE;
<input type="checkbox"/> 17:	6wpx-B	6.9	5.8	120	451	5 PDB	MOLECULE: BLEST2;
<input type="checkbox"/> 18:	4gwm-A	6.9	6.0	126	561	9 PDB	MOLECULE: MEPRIN A SUBUNIT BETA;
<input type="checkbox"/> 19:	5gka-A	6.9	3.4	123	253	7 PDB	MOLECULE: CAPSID PROTEIN VP1;
<input type="checkbox"/> 20:	8e2f-A	6.6	3.0	106	771	8 PDB	MOLECULE: BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 6;
<input type="checkbox"/> 21:	4jdm-C	6.6	3.1	108	269	10 PDB	MOLECULE: VIRULENCE PLASMID PROTEIN PGP3-D;
<input type="checkbox"/> 22:	3iii-A	6.5	7.6	129	556	7 PDB	MOLECULE: COCE/NOND FAMILY HYDROLASE;
<input type="checkbox"/> 23:	6yfe-A	6.5	6.6	108	140	8 PDB	MOLECULE: GALACTOSE-BINDING LECTIN;
<input type="checkbox"/> 24:	2c26-A	6.5	7.9	117	250	9 PDB	MOLECULE: ENDOGLUCANASE;
<input type="checkbox"/> 25:	6e5c-A	6.5	2.6	76	78	9 PDB	MOLECULE: DE NOVO BETA PROTEIN;
<input type="checkbox"/> 26:	4k6b-B	6.4	3.5	108	157	10 PDB	MOLECULE: HS1 KNOB DOMAIN;
<input type="checkbox"/> 27:	6bqm-A	6.4	14.0	107	460	11 PDB	MOLECULE: SERINE PROTEASE VESC;
<input type="checkbox"/> 28:	5ta1-A	6.4	11.4	135	627	5 PDB	MOLECULE: GLYCOSIDE HYDROLASE;
<input type="checkbox"/> 29:	6za2-B	6.4	11.1	115	1083	3 PDB	MOLECULE: POR SECRETION SYSTEM PROTEIN PORU;
<input type="checkbox"/> 30:	1auy-B	6.4	4.1	123	189	8 PDB	MOLECULE: TURNIP YELLOW MOSAIC VIRUS;
<input type="checkbox"/> 31:	1stm-A	6.4	3.2	112	141	7 PDB	MOLECULE: SATELLITE PANICUM MOSAIC VIRUS;
<input type="checkbox"/> 32:	5yvl-D	6.4	3.2	106	206	9 PDB	MOLECULE: CYCLASE;
<input type="checkbox"/> 33:	7l2z-F	6.4	3.2	114	664	9 PDB	MOLECULE: CYCLIC DI-GMP-BINDING PROTEIN;
<input type="checkbox"/> 34:	6uwr-A	6.4	13.5	117	660	6 PDB	MOLECULE: ADP-RIBOSYLTRANSFERASE BINDING COMPONENT;
<input type="checkbox"/> 35:	3pvm-B	6.3	4.7	126	1225	8 PDB	MOLECULE: COMPLEMENT C5;
<input type="checkbox"/> 36:	4agg-A	6.3	3.1	86	144	9 PDB	MOLECULE: GALECTIN;
<input type="checkbox"/> 37:	8des-A	6.3	4.7	150	475	8 PDB	MOLECULE: MAJOR CAPSID PROTEIN;
<input type="checkbox"/> 38:	6tku-A	6.3	4.0	116	545	8 PDB	MOLECULE: DEPOLYMERASE KP32GP38;
<input type="checkbox"/> 39:	6mkb-B	6.3	3.1	114	165	6 PDB	MOLECULE: TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 9
<input type="checkbox"/> 40:	6i56-A	6.3	11.9	104	279	6 PDB	MOLECULE: PHAGE-LIKE ELEMENT PBSX PROTEIN XEPA;

DNA-C
BcssDV1

No:	Chain	Z	rmsd	lali	nres	%id PDB	Description
<input type="checkbox"/> 1:	7zel-A	2.3	12.4	106	827	5 PDB	MOLECULE: SCHLAFEN FAMILY MEMBER 11;
<input type="checkbox"/> 2:	3ajv-A	2.3	3.3	73	168	12 PDB	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
<input type="checkbox"/> 3:	5yh1-A	2.3	9.4	75	439	7 PDB	MOLECULE: MEMBER OF S1P FAMILY OF RIBOSOMAL PROTEINS;
<input type="checkbox"/> 4:	7or1-A	2.2	4.1	65	2183	8 PDB	MOLECULE: RNA (5'-D(*(GTG))-R(P*AP*AP*UP*AP*CP*UP*AP*UP*AP*
<input type="checkbox"/> 5:	6qfj-A	2.2	3.4	52	84	6 PDB	MOLECULE: MAGNETOSOME MEMBRANE PROTEIN MAMB, PUTATIVE CO/ZN
<input type="checkbox"/> 6:	3fov-A	2.2	3.4	60	102	5 PDB	MOLECULE: UPF0102 PROTEIN RPA0323;
<input type="checkbox"/> 7:	5cet-A	2.1	10.3	84	328	6 PDB	MOLECULE: BIFUNCTIONAL OLIGORIBONUCLEASE AND PAP PHOSPHATAS
<input type="checkbox"/> 8:	1u6z-B	2.1	7.2	86	500	5 PDB	MOLECULE: EXOPOLYPHOSPHATASE;
<input type="checkbox"/> 9:	6gzb-A	2.1	5.0	70	287	1 PDB	MOLECULE: SPORE GERMINATION PROTEIN GERM;
<input type="checkbox"/> 10:	1n63-B	2.1	4.1	63	805	2 PDB	MOLECULE: CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN;

DNA-D
BcssDV1

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
<input type="checkbox"/> 1:	6ya7-A	4.2	4.5	90	350	7	PDB	MOLECULE: CELL DIVISION CYCLE 7-RELATED PROTEIN KINASE,CELL
<input type="checkbox"/> 2:	3u1w-C	3.6	8.1	86	250	6	PDB	MOLECULE: HYPOTHETICAL PERIPLASMIC PROTEIN;
<input type="checkbox"/> 3:	3w0s-A	3.5	5.5	83	298	12	PDB	MOLECULE: HYGROMYCIN-B 4-O-KINASE;
<input type="checkbox"/> 4:	7vnx-A	3.5	4.4	89	216	11	PDB	MOLECULE: TKARKI;
<input type="checkbox"/> 5:	6sum-A	3.4	6.0	82	335	2	PDB	MOLECULE: AMICOUMACIN KINASE;
<input type="checkbox"/> 6:	7s3l-A	3.2	4.8	72	254	11	PDB	MOLECULE: AMINOGLYCOSIDE PHOSPHOTRANSFERASE FAMILY PROTEIN;
<input type="checkbox"/> 7:	2xgl-A	3.2	3.1	61	90	5	PDB	MOLECULE: COLICIN-M IMMUNITY PROTEIN;
<input type="checkbox"/> 8:	6c9j-A	3.2	4.5	82	386	12	PDB	MOLECULE: 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT
<input type="checkbox"/> 9:	3i0o-A	3.1	6.7	87	329	9	PDB	MOLECULE: SPECTINOMYCIN PHOSPHOTRANSFERASE;
<input type="checkbox"/> 10:	5xzw-B	3.1	6.8	101	379	6	PDB	MOLECULE: SERINE/THREONINE-PROTEIN KINASE RAD53;
<input type="checkbox"/> 11:	3ats-A	3.1	5.5	80	352	5	PDB	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
<input type="checkbox"/> 12:	2q83-A	3.1	7.4	88	332	5	PDB	MOLECULE: YTAA PROTEIN;
<input type="checkbox"/> 13:	5iqc-A	3.1	6.5	88	301	5	PDB	MOLECULE: BIFUNCTIONAL AAC/APH;
<input type="checkbox"/> 14:	4ocu-A	3.0	5.8	90	356	8	PDB	MOLECULE: N-ACETYLHEXOSAMINE 1-PHOSPHATE KINASE;
<input type="checkbox"/> 15:	8gwe-A	3.0	4.7	87	931	8	PDB	MOLECULE: RNA-DIRECTED RNA POLYMERASE;
<input type="checkbox"/> 16:	5dzt-A	3.0	12.1	114	886	5	PDB	MOLECULE: CYLM;
<input type="checkbox"/> 17:	2nyk-A	3.0	8.2	90	237	7	PDB	MOLECULE: M157;
<input type="checkbox"/> 18:	3pgb-A	2.9	6.3	98	740	4	PDB	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
<input type="checkbox"/> 19:	7s9w-B	2.9	14.4	107	529	3	PDB	MOLECULE: DRMA;
<input type="checkbox"/> 20:	4hbr-A	2.9	4.3	73	140	7	PDB	MOLECULE: PUTATIVE PERIPLASMIC PROTEIN;
<input type="checkbox"/> 21:	5dzc-A	2.9	17.5	95	816	4	PDB	MOLECULE: CGMP-DEPENDENT PROTEIN KINASE, PUTATIVE;
<input type="checkbox"/> 22:	6rkw-B	2.9	21.6	75	781	3	PDB	MOLECULE: DNA GYRASE SUBUNIT A;
<input type="checkbox"/> 23:	3bb9-B	2.9	2.9	58	125	7	PDB	MOLECULE: PUTATIVE ORPHAN PROTEIN;
<input type="checkbox"/> 24:	4lv8-A	2.9	4.8	91	360	13	PDB	MOLECULE: RHOPTRY PROTEIN 5 C;
<input type="checkbox"/> 25:	3dyp-A	2.8	5.3	79	329	9	PDB	MOLECULE: PUTATIVE ACYL-COA DEHYDROGENASE;
<input type="checkbox"/> 26:	4gki-A	2.8	5.6	76	272	1	PDB	MOLECULE: AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE APHA1-IAB;
<input type="checkbox"/> 27:	4ped-A	2.8	6.2	100	387	8	PDB	MOLECULE: CHAPERONE ACTIVITY OF BC1 COMPLEX-LIKE, MITOCHOND
<input type="checkbox"/> 28:	5ncl-A	2.8	19.8	79	418	5	PDB	MOLECULE: SERINE/THREONINE-PROTEIN KINASE CBK1;
<input type="checkbox"/> 29:	7wb4-f	2.8	7.2	78	321	6	PDB	MOLECULE: OUTER NUP133;
<input type="checkbox"/> 30:	5hl8-A	2.8	2.8	49	81	8	PDB	MOLECULE: TYPE II SECRETION SYSTEM PROTEIN L;
<input type="checkbox"/> 31:	6dzk-Y	2.8	3.1	60	103	8	PDB	MOLECULE: 16S RRNA;
<input type="checkbox"/> 32:	7zgr-A	2.8	8.2	102	1253	3	PDB	MOLECULE: PROTEIN CFT1;

Additional file 4b. Results of structural homologies modelled by DALI in proteins of BcssDV1.