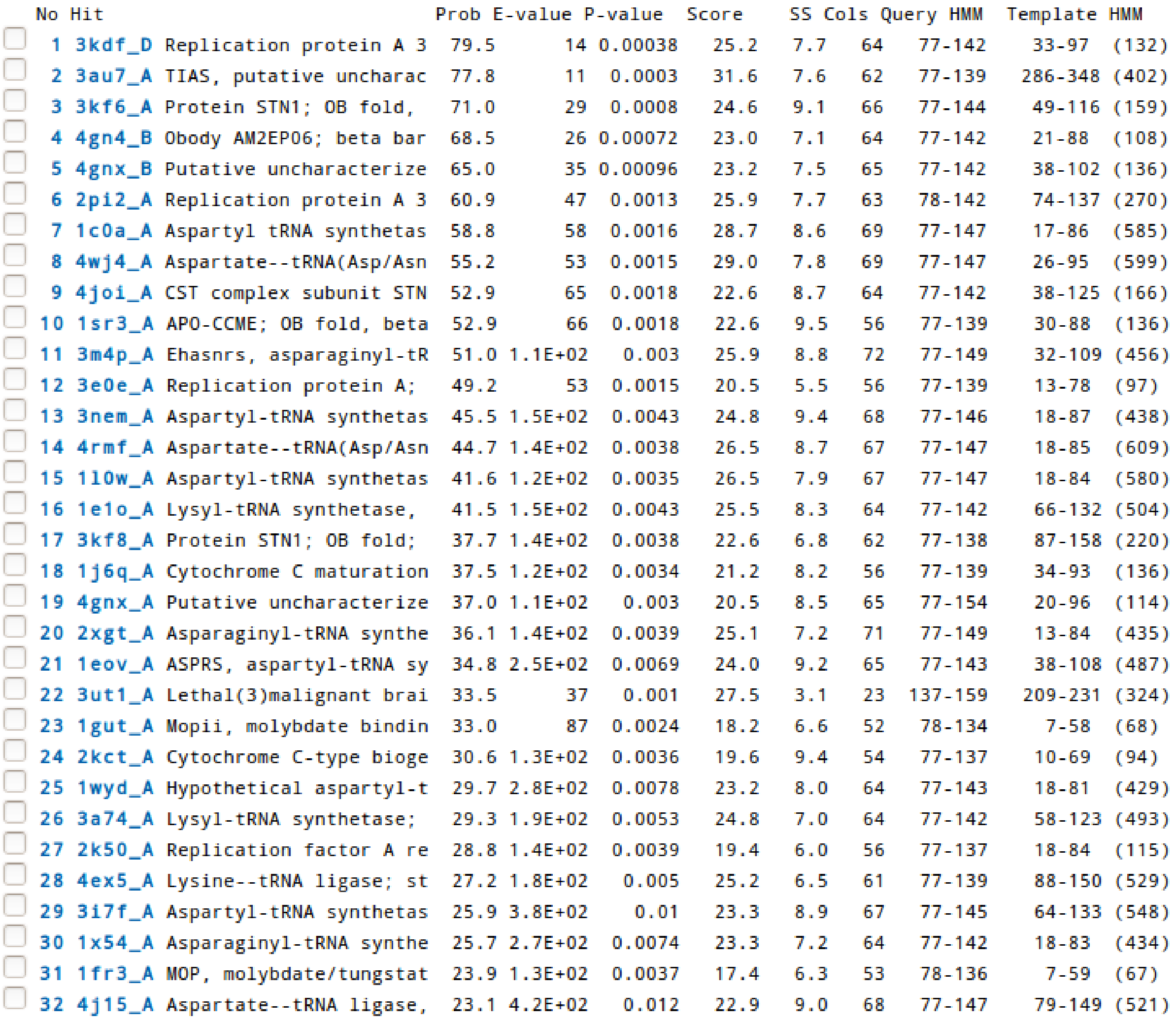
Supplementary Figures

Fig 1. Raw HHpred server output for a) residues 1-191 containing the OB fold and b) residues 479-776, containing the β-lactamase-like nuclease domain, of *B. subtilis* ComEC.

a)



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   No Hit                             Prob E-value P-value  Score    SS Cols Query HMM  Template HMM
☐   1 3kdf_D Replication protein A 3  79.5      14 0.00038   25.2   7.7   64   77-142    33-97   (132)
☐   2 3au7_A TIAS, putative uncharac  77.8      11  0.0003   31.6   7.6   62   77-139   286-348 (402)
☐   3 3kf6_A Protein STN1; OB fold,   71.0      29  0.0008   24.6   9.1   66   77-144    49-116 (159)
☐   4 4gn4_B Obody AM2EP06; beta bar  68.5      26 0.00072   23.0   7.1   64   77-142    21-88  (108)
☐   5 4gnx_B Putative uncharacterize  65.0      35 0.00096   23.2   7.5   65   77-142    38-102 (136)
☐   6 2pi2_A Replication protein A 3  60.9      47  0.0013   25.9   7.7   63   78-142    74-137 (270)
☐   7 1c0a_A Aspartyl tRNA synthetas  58.8      58  0.0016   28.7   8.6   69   77-147    17-86  (585)
☐   8 4wj4_A Aspartate--tRNA(Asp/Asn  55.2      53  0.0015   29.0   7.8   69   77-147    26-95  (599)
☐   9 4joi_A CST complex subunit STN  52.9      65  0.0018   22.6   8.7   64   77-142    38-125 (166)
☐  10 1sr3_A APO-CCME; OB fold, beta  52.9      66  0.0018   22.6   9.5   56   77-139    30-88  (136)
☐  11 3m4p_A Ehasnrs, asparaginyl-tR  51.0 1.1E+02   0.003   25.9   8.8   72   77-149    32-109 (456)
☐  12 3e0e_A Replication protein A;   49.2      53  0.0015   20.5   5.5   56   77-139    13-78  (97)
☐  13 3nem_A Aspartyl-tRNA synthetas  45.5 1.5E+02  0.0043   24.8   9.4   68   77-146    18-87  (438)
☐  14 4rmf_A Aspartate--tRNA(Asp/Asn  44.7 1.4E+02  0.0038   26.5   8.7   67   77-147    18-85  (609)
☐  15 110w_A Aspartyl-tRNA synthetas  41.6 1.2E+02  0.0035   26.5   7.9   67   77-147    18-84  (580)
☐  16 1e1o_A Lysyl-tRNA synthetase,   41.5 1.5E+02  0.0043   25.5   8.3   64   77-142    66-132 (504)
☐  17 3kf8_A Protein STN1; OB fold;   37.7 1.4E+02  0.0038   22.6   6.8   62   77-138    87-158 (220)
☐  18 1j6q_A Cytochrome C maturation  37.5 1.2E+02  0.0034   21.2   8.2   56   77-139    34-93  (136)
☐  19 4gnx_A Putative uncharacterize  37.0 1.1E+02   0.003   20.5   8.5   65   77-154    20-96  (114)
☐  20 2xgt_A Asparaginyl-tRNA synthe  36.1 1.4E+02  0.0039   25.1   7.2   71   77-149    13-84  (435)
☐  21 1eov_A ASPRS, aspartyl-tRNA sy  34.8 2.5E+02  0.0069   24.0   9.2   65   77-143    38-108 (487)
☐  22 3ut1_A Lethal(3)malignant brai  33.5      37   0.001   27.5   3.1   23  137-159   209-231 (324)
☐  23 1gut_A Mopii, molybdate bindin  33.0      87  0.0024   18.2   6.6   52   78-134     7-58  (68)
☐  24 2kct_A Cytochrome C-type bioge  30.6 1.3E+02  0.0036   19.6   9.4   54   77-137    10-69  (94)
☐  25 1wyd_A Hypothetical aspartyl-t  29.7 2.8E+02  0.0078   23.2   8.0   64   77-143    18-81  (429)
☐  26 3a74_A Lysyl-tRNA synthetase;   29.3 1.9E+02  0.0053   24.8   7.0   64   77-142    58-123 (493)
☐  27 2k50_A Replication factor A re  28.8 1.4E+02  0.0039   19.4   6.0   56   77-137    18-84  (115)
☐  28 4ex5_A Lysine--tRNA ligase; st  27.2 1.8E+02   0.005   25.2   6.5   61   77-139    88-150 (529)
☐  29 3i7f_A Aspartyl-tRNA synthetas  25.9 3.8E+02    0.01   23.3   8.9   67   77-145    64-133 (548)
☐  30 1x54_A Asparaginyl-tRNA synthe  25.7 2.7E+02  0.0074   23.3   7.2   64   77-142    18-83  (434)
☐  31 1fr3_A MOP, molybdate/tungstat  23.9 1.3E+02  0.0037   17.4   6.3   53   78-136     7-59  (67)
☐  32 4j15_A Aspartate--tRNA ligase,  23.1 4.2E+02   0.012   22.9   9.0   68   77-147    79-149 (521)
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b)

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☐  1 2bib_A CBPE, teichoic acid pho 100.0 4.2E-33 1.2E-37  264.4  28.0  245   16-281     1-297 (547)
☐  2 3bv6_A Metal-dependent hydrola  99.9 4.7E-25 1.3E-29  200.0  18.3  241   17-298    58-372 (379)
☐  3 2gcu_A Putative hydroxyacylglu  99.9   1E-26 2.8E-31  198.6   6.6  216   19-272     1-244 (245)
☐  4 2wyl_A L-ascorbate-6-phosphate  99.9 5.1E-25 1.4E-29  198.4  17.7  248   17-298    34-347 (360)
☐  5 1xm8_A Glyoxalase II; structur  99.9 9.7E-25 2.7E-29  187.3  11.5  196   21-266     1-209 (254)
☐  6 3adr_A Putative uncharacterize  99.9 2.1E-25   6E-30  191.8   6.1  214   19-268     2-258 (261)
☐  7 1qh5_A Glyoxalase II, protein   99.9 4.6E-23 1.3E-27  177.5  15.7  170   21-233     1-189 (260)
☐  8 4ysb_A Metallo-beta-lactamase   99.9 2.4E-24 6.7E-29  182.6   7.6  201   19-262     1-222 (233)
☐  9 2qed_A Hydroxyacylglutathione   99.9   4E-23 1.1E-27  177.7  13.3  196   19-259     6-237 (258)
☐ 10 4chl_A Persulfide dioxygenase   99.9 3.7E-24   1E-28  182.0   5.6  210   13-262     1-230 (238)
☐ 11 2p18_A Glyoxalase II; metallop  99.9 8.5E-22 2.4E-26  173.9  17.3  174   21-233    29-242 (311)
☐ 12 1zkp_A Hypothetical protein BA  99.9 3.2E-21 8.9E-26  166.5  19.7  216   17-273    21-266 (268)
☐ 13 3md7_A Beta-lactamase-like; ss  99.9 3.7E-22   1E-26  174.7  12.6  218   15-283    23-291 (293)
☐ 14 2xf4_A Hydroxyacylglutathione   99.9 9.3E-22 2.6E-26  163.6  13.5  177   21-225     1-201 (210)
☐ 15 1k07_A FEZ-1 beta-lactamase; m  99.8 2.4E-20 6.6E-25  160.4  16.1  177   23-233    17-232 (263)
☐ 16 3g1p_A Protein PHNP; C-P lyase  99.8   3E-20 8.2E-25  159.7  16.4  208   19-283     1-251 (258)
☐ 17 3kl7_A Putative metal-dependen  99.8 1.2E-19 3.4E-24  153.7  17.1  199   15-269    24-235 (235)
☐ 18 1sml_A Protein (penicillinase)  99.8 1.8E-19 4.9E-24  155.4  18.3  165   23-220    30-230 (269)
☐ 19 4jo0_A CMLA; nonheme oxygenase  99.8 2.6E-20 7.3E-25  174.9  13.3  232   18-274   250-534 (534)
☐ 20 2cbn_A Ribonuclease Z; phospho  99.8 1.6E-19 4.4E-24  158.7  17.5  212   21-273     2-304 (306)
☐ 21 1y44_A Ribonuclease Z; zinc-de  99.8 2.8E-19 7.8E-24  158.3  18.0  213   21-273     1-302 (320)
☐ 22 4ax1_B Metallo-beta-lactamase   99.8 1.7E-19 4.7E-24  158.2  16.4  210    2-258     6-279 (303)
☐ 23 2vw8_A PA1000, PQSE; quinolone  99.8 6.8E-22 1.9E-26  173.6   1.0  229   10-263     1-278 (303)
☐ 24 2zwr_A Metallo-beta-lactamase   99.8 8.4E-20 2.3E-24  151.5  13.4  170   21-225     1-193 (207)
☐ 25 3m8t_A 'BLR6230 protein; subcl  99.8 2.9E-19 8.1E-24  156.2  15.8  171   23-227    47-253 (294)
☐ 26 3vpe_A Metallo-beta-lactamase;  99.8 8.7E-19 2.4E-23  150.5  16.0  194   23-258    18-251 (262)
☐ 27 5aeb_A LRA-12; hydrolase, carb  99.8 3.2E-19 8.8E-24  154.2  13.3  169   23-225    30-236 (272)
☐ 28 3tp9_A Beta-lactamase and rhod  99.8 1.9E-19 5.4E-24  167.8  12.0  182   18-232     1-225 (474)
☐ 29 2i7t_A Cleavage and polyadenyl  99.8 1.8E-18 5.1E-23  160.6  16.4  216   18-265     9-270 (459)
☐ 30 4efz_A Metallo-beta-lactamase   99.8 1.6E-18 4.5E-23  152.0  14.4  175   18-218     2-218 (298)
☐ 31 2e7y_A TRNAse Z; tRNA maturati  99.8 2.9E-18 7.9E-23  148.9  15.5  211   21-273     1-278 (280)
☐ 32 3zq4_A Ribonuclease J 1, RNAse  99.8 2.1E-17 5.9E-22  156.7  20.7  212   16-267     4-256 (555)
☐ 33 4ysl_A Beta-lactamase domain p  99.8 4.1E-18 1.1E-22  149.2  14.7  170   24-219    11-215 (294)
☐ 34 2ohh_A Type A flavoprotein FPR  99.8 2.2E-18   6E-23  157.1  13.0  207   30-263    34-288 (404)
☐ 35 1e5d_A Rubredoxin\:oxygen oxid  99.8 1.1E-18 3.1E-23  159.1  10.4  201   31-263    35-284 (402)
☐ 36 2zo4_A Metallo-beta-lactamase   99.8   3E-17 8.3E-22  145.0  19.0  182   23-230     8-247 (317)
☐ 37 3r2u_A Metallo-beta-lactamase   99.8 2.8E-18 7.8E-23  159.6  12.9  180   14-232    20-245 (466)
☐ 38 3jxp_A Coenzyme PQQ synthesis   99.8 4.4E-18 1.2E-22  150.7  13.3  220   21-273     3-303 (321)
☐ 39 3iek_A Ribonuclease TTHA0252;   99.8 5.1E-18 1.4E-22  156.4  13.9  214   21-265     1-249 (431)
☐ 40 3bk2_A RNAse J, metal dependen  99.8 3.7E-17   1E-21  155.2  20.1  211   15-267    11-272 (562)
☐ 41 1ycg_A Nitric oxide reductase;  99.8 3.5E-18 9.6E-23  155.6  12.5  202   31-263    36-283 (398)
☐ 42 4ojv_A 3',5'-cyclic-nucleotide  99.8   5E-18 1.4E-22  153.0  12.1  217   21-273     4-367 (369)
☐ 43 4ad9_A Lactb2, beta-lactamase-  99.7   2E-17 5.4E-22  144.4  13.4  171   28-229    29-213 (289)
☐ 44 4qn9_A N-acyl-phosphatidyletha  99.7 2.6E-16 7.2E-21  143.0  18.8  230   18-273   122-384 (393)
☐ 45 4c1d_A Beta-lactamase class B   99.7 9.9E-17 2.7E-21  136.2  14.0  167   31-236    45-241 (242)
☐ 46 5a0t_A Ribonuclease J; hydrola  99.7 8.3E-16 2.3E-20  146.0  21.8  209   18-267    16-266 (561)
☐ 47 2az4_A Hypothetical protein EF  99.7 1.8E-16   5E-21  146.0  16.7  210   16-266     2-282 (429)
☐ 48 4eyb_A Beta-lactamase NDM-1; m  99.7 2.6E-17 7.3E-22  142.0  10.0  181    2-219    15-253 (270)
☐ 49 2i7x_A Protein CFT2; polyadeny  99.7   4E-17 1.1E-21  158.6  11.8  215   21-277     1-249 (717)
☐ 50 1vjn_A Zn-dependent hydrolase   99.7 6.2E-17 1.7E-21  135.7  11.3  173   18-258    10-195 (220)
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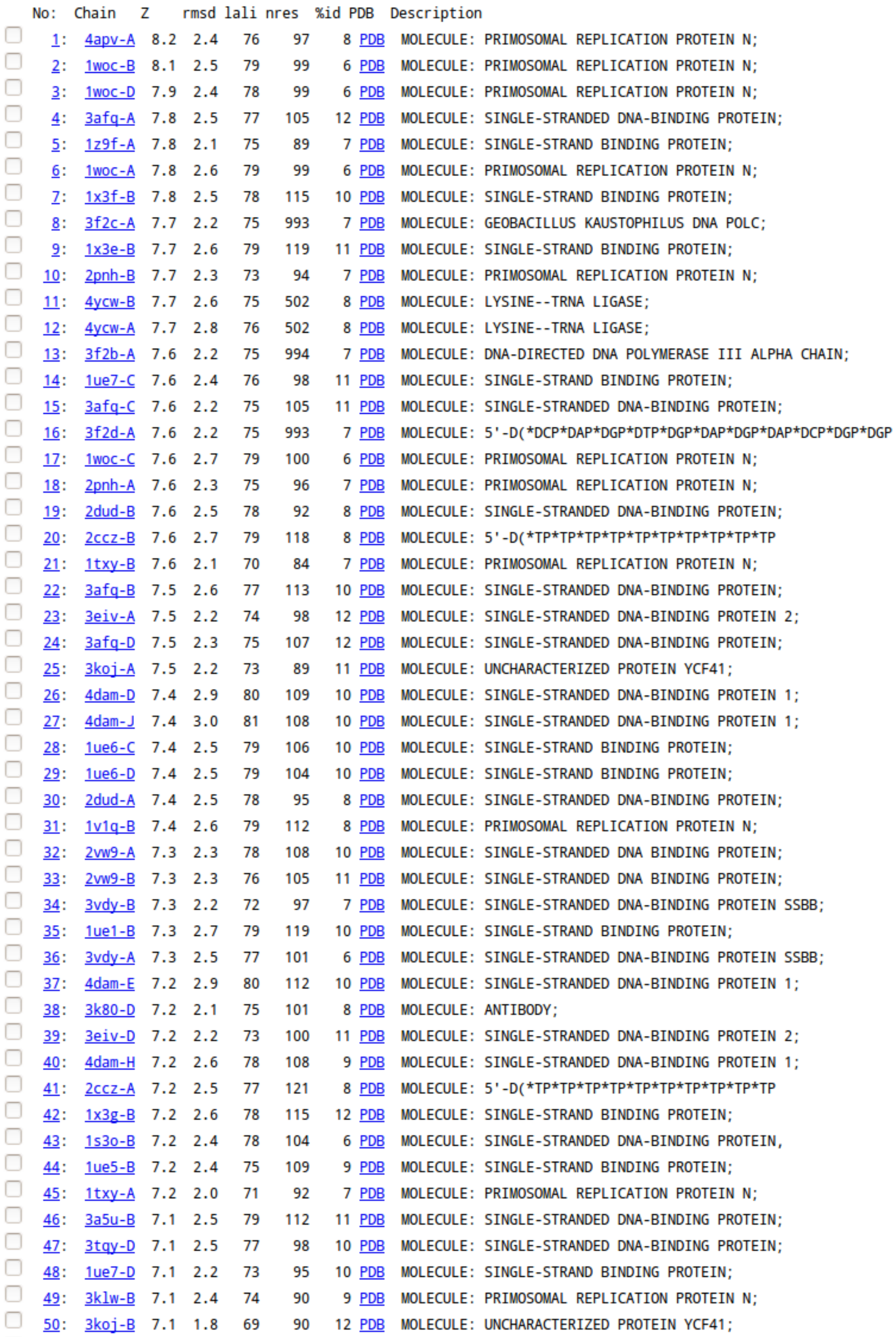
Fig 2. Raw DALI scores for a) the chosen final model, encompassing residues 72-167 of *B. subtilis* ComEC (see Fig 3B) and b) the top cluster centroid model for residues 72-172. Each is the top cluster centroid resulting from contact-assisted (PconsC2/bbcontacts predictions) *ab initio* Rosetta modelling.

a)



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     No:  Chain   Z    rmsd lali nres  %id PDB  Description
☐     1:  4apv-A  8.2  2.4   76   97    8 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐     2:  1woc-B  8.1  2.5   79   99    6 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐     3:  1woc-D  7.9  2.4   78   99    6 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐     4:  3afq-A  7.8  2.5   77  105   12 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐     5:  1z9f-A  7.8  2.1   75   89    7 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐     6:  1woc-A  7.8  2.6   79   99    6 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐     7:  1x3f-B  7.8  2.5   78  115   10 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐     8:  3f2c-A  7.7  2.2   75  993    7 PDB  MOLECULE: GEOBACILLUS KAUSTOPHILUS DNA POLC;
☐     9:  1x3e-B  7.7  2.6   79  119   11 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    10:  2pnh-B  7.7  2.3   73   94    7 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    11:  4ycw-B  7.7  2.6   75  502    8 PDB  MOLECULE: LYSINE--TRNA LIGASE;
☐    12:  4ycw-A  7.7  2.8   76  502    8 PDB  MOLECULE: LYSINE--TRNA LIGASE;
☐    13:  3f2b-A  7.6  2.2   75  994    7 PDB  MOLECULE: DNA-DIRECTED DNA POLYMERASE III ALPHA CHAIN;
☐    14:  1ue7-C  7.6  2.4   76   98   11 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    15:  3afq-C  7.6  2.2   75  105   11 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    16:  3f2d-A  7.6  2.2   75  993    7 PDB  MOLECULE: 5'-D(*DCP*DAP*DGP*DTP*DGP*DAP*DGP*DAP*DCP*DGP*DGP
☐    17:  1woc-C  7.6  2.7   79  100    6 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    18:  2pnh-A  7.6  2.3   75   96    7 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    19:  2dud-B  7.6  2.5   78   92    8 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    20:  2ccz-B  7.6  2.7   79  118    8 PDB  MOLECULE: 5'-D(*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP
☐    21:  1txy-B  7.6  2.1   70   84    7 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    22:  3afq-B  7.5  2.6   77  113   10 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    23:  3eiv-A  7.5  2.2   74   98   12 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 2;
☐    24:  3afq-D  7.5  2.3   75  107   12 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    25:  3koj-A  7.5  2.2   73   89   11 PDB  MOLECULE: UNCHARACTERIZED PROTEIN YCF41;
☐    26:  4dam-D  7.4  2.9   80  109   10 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 1;
☐    27:  4dam-J  7.4  3.0   81  108   10 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 1;
☐    28:  1ue6-C  7.4  2.5   79  106   10 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    29:  1ue6-D  7.4  2.5   79  104   10 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    30:  2dud-A  7.4  2.5   78   95    8 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    31:  1v1q-B  7.4  2.6   79  112    8 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    32:  2vw9-A  7.3  2.3   78  108   10 PDB  MOLECULE: SINGLE-STRANDED DNA BINDING PROTEIN;
☐    33:  2vw9-B  7.3  2.3   76  105   11 PDB  MOLECULE: SINGLE-STRANDED DNA BINDING PROTEIN;
☐    34:  3vdy-B  7.3  2.2   72   97    7 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN SSBB;
☐    35:  1ue1-B  7.3  2.7   79  119   10 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    36:  3vdy-A  7.3  2.5   77  101    6 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN SSBB;
☐    37:  4dam-E  7.2  2.9   80  112   10 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 1;
☐    38:  3k80-D  7.2  2.1   75  101    8 PDB  MOLECULE: ANTIBODY;
☐    39:  3eiv-D  7.2  2.2   73  100   11 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 2;
☐    40:  4dam-H  7.2  2.6   78  108    9 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN 1;
☐    41:  2ccz-A  7.2  2.5   77  121    8 PDB  MOLECULE: 5'-D(*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP
☐    42:  1x3g-B  7.2  2.6   78  115   12 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    43:  1s3o-B  7.2  2.4   78  104    6 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN,
☐    44:  1ue5-B  7.2  2.4   75  109    9 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    45:  1txy-A  7.2  2.0   71   92    7 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    46:  3a5u-B  7.1  2.5   79  112   11 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    47:  3tqy-D  7.1  2.5   77   98   10 PDB  MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐    48:  1ue7-D  7.1  2.2   73   95   10 PDB  MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐    49:  3klw-B  7.1  2.4   74   90    9 PDB  MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐    50:  3koj-B  7.1  1.8   69   90   12 PDB  MOLECULE: UNCHARACTERIZED PROTEIN YCF41;
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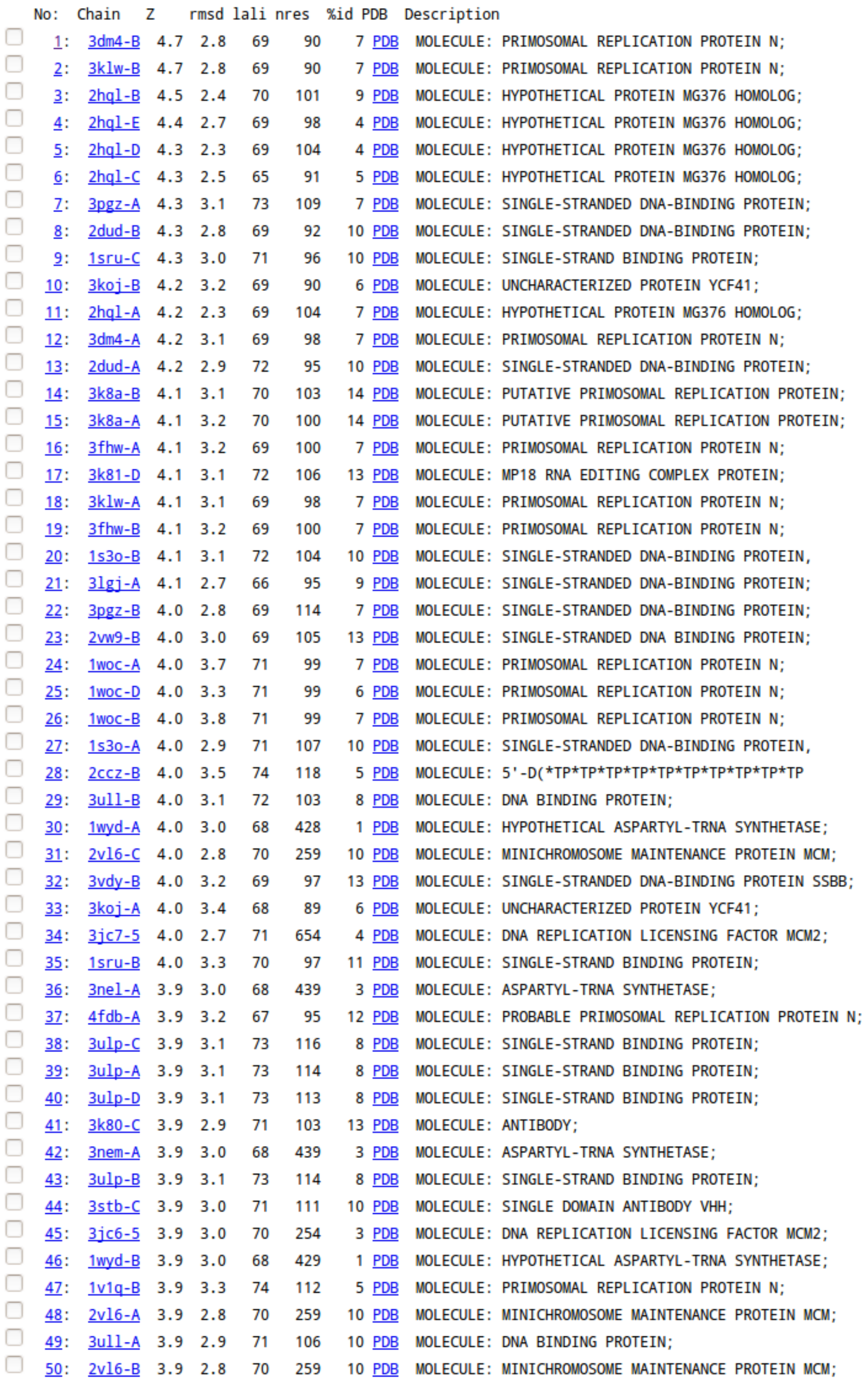
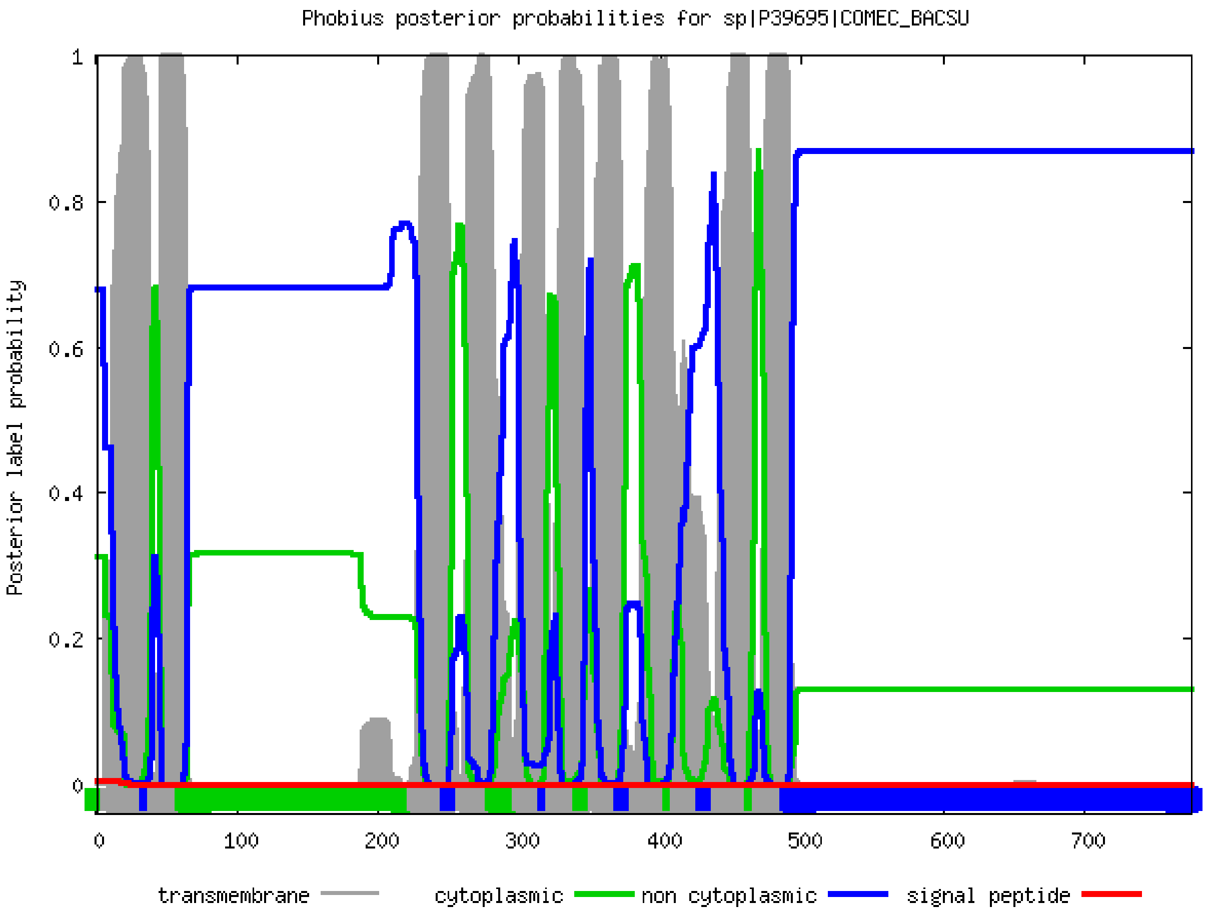
b)



	No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
☐	1:	3dm4-B	4.7	2.8	69	90	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	2:	3klw-B	4.7	2.8	69	90	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	3:	2hql-B	4.5	2.4	70	101	9	PDB	MOLECULE: HYPOTHETICAL PROTEIN MG376 HOMOLOG;
☐	4:	2hql-E	4.4	2.7	69	98	4	PDB	MOLECULE: HYPOTHETICAL PROTEIN MG376 HOMOLOG;
☐	5:	2hql-D	4.3	2.3	69	104	4	PDB	MOLECULE: HYPOTHETICAL PROTEIN MG376 HOMOLOG;
☐	6:	2hql-C	4.3	2.5	65	91	5	PDB	MOLECULE: HYPOTHETICAL PROTEIN MG376 HOMOLOG;
☐	7:	3pgz-A	4.3	3.1	73	109	7	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐	8:	2dud-B	4.3	2.8	69	92	10	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐	9:	1sru-C	4.3	3.0	71	96	10	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	10:	3koj-B	4.2	3.2	69	90	6	PDB	MOLECULE: UNCHARACTERIZED PROTEIN YCF41;
☐	11:	2hql-A	4.2	2.3	69	104	7	PDB	MOLECULE: HYPOTHETICAL PROTEIN MG376 HOMOLOG;
☐	12:	3dm4-A	4.2	3.1	69	98	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	13:	2dud-A	4.2	2.9	72	95	10	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐	14:	3k8a-B	4.1	3.1	70	103	14	PDB	MOLECULE: PUTATIVE PRIMOSOMAL REPLICATION PROTEIN;
☐	15:	3k8a-A	4.1	3.2	70	100	14	PDB	MOLECULE: PUTATIVE PRIMOSOMAL REPLICATION PROTEIN;
☐	16:	3fhw-A	4.1	3.2	69	100	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	17:	3k81-D	4.1	3.1	72	106	13	PDB	MOLECULE: MP18 RNA EDITING COMPLEX PROTEIN;
☐	18:	3klw-A	4.1	3.1	69	98	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	19:	3fhw-B	4.1	3.2	69	100	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	20:	1s3o-B	4.1	3.1	72	104	10	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN,
☐	21:	3lgj-A	4.1	2.7	66	95	9	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐	22:	3pgz-B	4.0	2.8	69	114	7	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN;
☐	23:	2vw9-B	4.0	3.0	69	105	13	PDB	MOLECULE: SINGLE-STRANDED DNA BINDING PROTEIN;
☐	24:	1woc-A	4.0	3.7	71	99	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	25:	1woc-D	4.0	3.3	71	99	6	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	26:	1woc-B	4.0	3.8	71	99	7	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	27:	1s3o-A	4.0	2.9	71	107	10	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN,
☐	28:	2ccz-B	4.0	3.5	74	118	5	PDB	MOLECULE: 5'-D(*TP*TP*TP*TP*TP*TP*TP*TP*TP*TP
☐	29:	3ull-B	4.0	3.1	72	103	8	PDB	MOLECULE: DNA BINDING PROTEIN;
☐	30:	1wyd-A	4.0	3.0	68	428	1	PDB	MOLECULE: HYPOTHETICAL ASPARTYL-TRNA SYNTHETASE;
☐	31:	2vl6-C	4.0	2.8	70	259	10	PDB	MOLECULE: MINICHROMOSOME MAINTENANCE PROTEIN MCM;
☐	32:	3vdy-B	4.0	3.2	69	97	13	PDB	MOLECULE: SINGLE-STRANDED DNA-BINDING PROTEIN SSBB;
☐	33:	3koj-A	4.0	3.4	68	89	6	PDB	MOLECULE: UNCHARACTERIZED PROTEIN YCF41;
☐	34:	3jc7-5	4.0	2.7	71	654	4	PDB	MOLECULE: DNA REPLICATION LICENSING FACTOR MCM2;
☐	35:	1sru-B	4.0	3.3	70	97	11	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	36:	3nel-A	3.9	3.0	68	439	3	PDB	MOLECULE: ASPARTYL-TRNA SYNTHETASE;
☐	37:	4fdb-A	3.9	3.2	67	95	12	PDB	MOLECULE: PROBABLE PRIMOSOMAL REPLICATION PROTEIN N;
☐	38:	3ulp-C	3.9	3.1	73	116	8	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	39:	3ulp-A	3.9	3.1	73	114	8	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	40:	3ulp-D	3.9	3.1	73	113	8	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	41:	3k80-C	3.9	2.9	71	103	13	PDB	MOLECULE: ANTIBODY;
☐	42:	3nem-A	3.9	3.0	68	439	3	PDB	MOLECULE: ASPARTYL-TRNA SYNTHETASE;
☐	43:	3ulp-B	3.9	3.1	73	114	8	PDB	MOLECULE: SINGLE-STRAND BINDING PROTEIN;
☐	44:	3stb-C	3.9	3.0	71	111	10	PDB	MOLECULE: SINGLE DOMAIN ANTIBODY VHH;
☐	45:	3jc6-5	3.9	3.0	70	254	3	PDB	MOLECULE: DNA REPLICATION LICENSING FACTOR MCM2;
☐	46:	1wyd-B	3.9	3.0	68	429	1	PDB	MOLECULE: HYPOTHETICAL ASPARTYL-TRNA SYNTHETASE;
☐	47:	1v1q-B	3.9	3.3	74	112	5	PDB	MOLECULE: PRIMOSOMAL REPLICATION PROTEIN N;
☐	48:	2vl6-A	3.9	2.8	70	259	10	PDB	MOLECULE: MINICHROMOSOME MAINTENANCE PROTEIN MCM;
☐	49:	3ull-A	3.9	2.9	71	106	10	PDB	MOLECULE: DNA BINDING PROTEIN;
☐	50:	2vl6-B	3.9	2.8	70	259	10	PDB	MOLECULE: MINICHROMOSOME MAINTENANCE PROTEIN MCM;

Fig.3 Phobius transmembrane helix prediction for *B. subtilis* ComEC



Supplementary Table 1: Numbers of sequences in alignments used by the metapredictor PconsC2 to predict contacts for DUF4131 region of *B. subtilis* ComEC. Figures exclude the query sequence.

E-value	Number of sequences in alignment (HHblits)	Number of sequences in alignment (Jackhmmer)
1	4478	11621
1e-4	2180	11039
1e-10	1262	3028
1e-40	0	93