

“Remote homology searches identify bacterial homologues of eukaryotic lipid transfer proteins, including Chorein-N domains in TamB and AsmA and Mdm31p”

Also, included for comparison: BPI N vs BPI C (page 16).

DUF4403C [hit #1] &DUF4403N [hit#2] vs. YceB (whole domain MSA)

[illegible]

DUF4403 (whole domain MSA) vs. self [hits #2/3 both = DUF4403N vs. C]

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_Novo_D4403_p3	100.0	3.4E-96	3.4E-96	741.1	72.9	489	1-489		1-489	(489)
2	Q_Novo_D4403_p3	96.6	9.3E-07	9.3E-07	58.5	24.2	205	22-275		278-489	(489)
3	Q_Novo_D4403_p3	96.5	1.4E-06	1.4E-06	57.1	24.2	205	278-489		22-275	(489)

[illegible]

Q ss_pred		ccceeeEEeeecccCCceeeEEEEeeEcceEEEEECEEEEEeeeeEEEEEEccccccceeeEeEEEEEEEEEEEECCC	
Q Novo_D4403_p	81	PSKSVDIGIAKITTPSLKCRIVGDTVRGLRFLFAGKGRIEVLDMPLHAVVRAEDIGGVLKRETATADAVAAHVINLTQAQ	160 (489)
T Consensus	81	+++++ +.++++++ + ++++ +. .+++ +++++++.+.+++++.++++.+++ rgpi-----Pi-----i~d	160 (489)
T Novo_D4403_p	81	PSKSVDIGIAKITTPSLKCRIVGDTVRGLRFLFAGKGRIEVLDMPLHAVVRAEDIGGVLKRETATADAVAAHVINLTQAQ	160 (489)
T ss_pred		ccceeeEEeeecccCCceeeEEEEeeEcceEEEEECEEEEEeeeeEEEEEEccccccceeeEeEEEEEEEEEEEECCC	160 (489)

[illegible][illegible][illegible][illegible]

Q ss_pred		EEeeEEEEc	
Q Q_Novo_D4403_p	481	ADGTASITV	489 (489)
Q Consensus	481	~G~v~v	489 (489)
		++ ++++	
T Consensus	481	~G~v~v	489 (489)
T Q_Novo_D4403_p	481	ADGTASITV	489 (489)
T ss_pred		EEeeEEEEc	

0 ss pred hcCCCCCCCCCCCCCCCCCceEEEEEEEeHHHHHHHHHHhCCccccCCCCCccccceeeEEFeeeCCceeeEE

DUF2140 vs. YceB

[illegible]

Q ss_pred		HHHHHHHHhhcCCCCCEEECC	
Q LactoD2140_p	147	SFVMSYIGHSYKIPSWSLDSKA	169 (205)
Q Consensus	147	~~~VL~~~~~lP~wV~~~~~	169 (205)
		. . . + . + . + - . - . + + ++	
T Consensus	137	~~~~~l~~~~~PVV~L~~~~~	159 (186)
T YceB_p3	137	PYLNQALRNYFNQQPAYVLREDC	159 (186)
T ss_pred		HHHHHHHHHHhcCCCEEECCG	

```
Query          Q_Novo_D4403C_p3
Match_columns  202
No_of_seqs    100 out of 113
Neff          8.36093
Searched_HMMs 1
Date          Sun Oct 28 23:00:27 2018
Command       hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/D4403N_v_D2140.hhr -oa3m
../results/D4403N_v_D2140.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context.data.crf
```

No 1
>Q_LactoD2140_p3
Probab=3.57 E-value=0.058 Score=15.96 Aligned cols=76 Identities=12% Similarity=0.065 Sum probs=0.0 Template Neff=7.500

Q ss_pred		Ee-cCCCCCCCCCeeEE	
Q Q_Novo_D4403C	96	VN-ADNSRRRGTFNFV	111 (202)
Q Consensus	96	~~-D~~~~~l~l~dl~~	111 (202)
		..+..+..l..+..+..	
T Consensus	123	~V~~gnl~L~~~~i~l	139 (205)
T Q_lacto2140_p	123	LVLKNGDVLVLLSKKLNV	139 (205)
T ss_pred		EECCCCCCCCCeeEE	

```
Query Q_LactoD2140_p3
Match_columns 205
No_of_seqs 105 out of 112
Neff 7.36164
Searched_HMMs 1
Date Tue Aug 14 23:56:37 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/LactoD2140_v_NovoD4403.hhr -oa3m
../results/LactoD2140_v_NovoD4403.a3m -p 20 -Z 250 -lcc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres
32000 -context /cluster/toolkit/production/biopros/tools/hh-suite-build/data/context_data.crf
```

No 1
>Q Novo_D4403_p3
Probab=94.15 E-value=4.9e-05 Score=39.16 Aligned cols=183 Identities=8% Similarity=-0.040 Sum probs=0.0 Template Neff=8.500

	Q ss_pred	-----CceEEEECCCEEEEEEeEee--CCEEEEEEeEeEcCc	
	Q _lactoD2140_p	90 --TKYAVTLGNNEAALNGSKFK---LGNNVKFQLTPDFLVLNK	127 (205)
	Q Consensus	90 -----y-v~----d-~-lgv~v~!~l~~P-V~nn +~~~~+.+++.+..t.+.	127 (205)
T	Consensus	81 ~~~~~rpgi-v~~~~~l~~~~Pi~~~~~ ~~~~~+id	160 (489)
T	_Novo_D4403_p	81 PSKSVDIGIAIKTPSLKCRIVGDVTRGLRFGAGRGREI VLDMP LHAVVRADIGGVLKRKETATADAHAHVNITLAQD	160 (489)
T	ss_pred	ccceeEEEEeccccCCEEKEEEEEECcEEEEECCCCccccccccccccccccccEEEEEeeeeEEEEECCCc	

Q_Novo_D4403_p	161	WSPRGTDIRYGTWNRPFLDPLGKRIDFTEQAEELKLAIVIAIRLERELPGLQGLKLEVRQVERAWNSAFTTLLSLNRDNPV	240	(489)
T_ss_pred		ceEEeEEEEeEEcCCCEEEcCEEechHchHHHHHHHHHHHHhhHHHHhhHHHHHHHHHHhhccceECCCCCce		
Q_ss_pred		EEEEeeecCCeEEEEEEcCCCCEEEEEEc		
Q_Q_LactoD2140_p	173	VLKLSQFKLQNGMTLRATKLDPTNDDLEFAVYL	205	(205)
Q_Consensus	173	~i~l~l~~~~~ik~~~idl~d~i~f~l~i	205	(205)
		++.+~+~ - .+ .+ .+ .+ .+ .+ .+		
T_Consensus	241	wL~~~P~-----v~~s~~~~~l~~~l	267	(489)
T_Q_Novo_D4403_p	241	WMRVSP-----RELQYGGYELDGKRLVLRGGV	267	(489)
T_ss_pred		EEEEc-----cEEEEcEEcCEEEEEEE		

T Q_Rv0817c_p3 235 LPFGVVPNTVGARGSDVIEGITRG 259 (270)
T ss pred CCCCccceEEEEcCeEEEEEEec

Rv0817c vs. DUF4403-N

```
Query          Q_Rv0817c_p3
Match_columns 270
No_of_seqs    122 out of 126
Neff          8.86375
Searched_HMMs 1
Date          Sun Oct 28 23:23:55 2018
Command       hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/D4403Nv0816c_v_..hhr -oa3m
              ../results/D4403Nv0816c_v_..a3m -p 0 -Z 1000 -lcc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
              context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context data.crf
```

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_Novo_D4403_p3/1-287	16.8	0.0035	0.0035	25.2	2.4	22	1-22		1-22	(287)
2	Q_Novo_D4403_p3/1-287	2.0	0.058	0.058	17.4	2.4	21	236-256		246-266	(287)

No 1
>Q_Novo_D4403_p3/1-287
Probab=16.84 E-value=0.0035 Score=25.16 Aligned cols=22 Identities=14% Similarity=0.181 Sum probs=0.0 Template Neff=8.900

Q ss_pred		CCCCcchHHHHHHHHHHHHHHHHH	
Q Q_Rv0817c_p3	1	MPMRKVLVGVGTGAATIVAVLVIV	22 (270)
Q ss_conserved	1	m~r~r~r~r~r~r~rvvvvl~v	22 (270)
		+ +. . . +.+++++++.++	
T Consensus		M~~~~~l~C~	22 (287)
Q T_Q_Novo_D4403_p	1	MRTRRYVTAAALTASLLTLPAC	22 (287)
T ss_pred		CcchHHHHHHHHHHHHHHHHhhc	

No 2
>Q_Novo_D4403_p3/1-287
Probab=1.97 E-value=0.058 Score=17.39 Aligned cols=21 Identities=10% Similarity=0.039 Sum probs=0.0 Template Neff=8.900

Q ss_pred		CCGccceEEEEeCcceEEEEEE	
Q Q_Rv0817c_p3	236	PFCCVNTVTVGARGSDVVIIEGI	256 (270)
Q Q_Consensus	236	P-gl~~~~~v~~~~gl~~~~~	256 (270)
		.+.+.+.+.+.+.+.+.+.+	
T Consensus	246	P-v~~~~~v~~~~v~~~~v~~~~~	266 (287)
Q T_Q_Novo_D4403_p	246	PRELQGGYELDGKRLVLRLG	266 (287)
T ss_pred		ceEEEEeCcceEEEEeEEEEEE	

Rv0817c vs. DUF2140

```

Query          Q LactoD2140_p3
Match columns  205
No_of_seqs     105 out of 112
Neff           7.36164
Searched_HMMs 1
Date           Wed Aug 15 00:04:20 2018
Command        hhssearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/LactoD2140_v_Rv0817c.hhr -oa3m
               ../results/LactoD2140_v_Rv0817c.a3m -p 20 -Z 250 -loc z -l -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000
               -context /cluster/toolkit/production/bioprgs/tools/hh-suite-build/data/context data.crf

```

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1 Q Rv0817c p3	95.0	8.9E-06	8.9E-06	40.3	14.7	162	16-177	2-256 (270)

No 1
>Q_Rv0817c_p3
Probab=95.02 E-value=8.9e-06 Score=40.31 Aligned cols=162 Identities=11% Similarity=-0.004 Sum probs=0.0 Template Neff=8.900

	ss_pred	ccCCHHHHHHHHHHHHHHHHHHHHHhhCCC-----	
Q	LactoD2140_p	SMINWWKWAFLILIGLILGSGINFTKTVLAPV----	47 (205)
Q	Consensus	~~~N-WK~aF~~Ll~l~l~~~~~	47 (205)
T	Consensus	.2++++++ + .+++++++ +++++. -....	
T	Rv0817c_p3	..rrr~r~l~vvvvll~l-v-ad-a~ae~ia~l~vv~l~m~p-V~ig~PfL~ql~g~w~v~v~	81 (270)
T	ss_pred	PMRKVLVGVTGAAIIVAVLIVGAVGADFGASIAEYRSLSTTVRKAANLRSDPFVALIRFPFIQAMREHYAELEIKAFPA	81 (270)
T	Consensus	CcechcccccccccccccccccccccccccccccccccccCEEECCcCCCCHhccccCEEEEEeccc	

```

      ss_pred    -----CcCcccccCccCceEEeeCHHHHHHHH-----HHhhcCCCCcEEEEc
Q Q_LactoD2140_p 48 -----SLNTATETKTISNDPVTVKTKSSANIMAH-----YLTYLKDSPIKYAVTLG   97 (205)
Q Consensus     48 -----L~--tk~--v~l~n~m~-----l~n~---y~v~t~       97 (205)
               .....+.++.++|+++|. -.....-.....
T Consensus     82 ~~~~~V~~~~~a~~~~~l~~~~~l~~~~~g~~~~~          161 (270)
T Q_Rv0817c_p3  82 EHAGSGTATLEATHMSIDLSYASHLWRDPAKLVGLEESRIIIDSMLHGYLGYSIDLWVAAPRQSCCATDTGGTSTSGIS   161 (270)
T ss_pred       ecCCCCcEEEEEeccccCHHHhcCCCCCCCcEEEEeEeCHHHHHHchcchhvaccCCcCCCCCCCCCCCCc

```

[illegible]

```

Q ss_pred                ---ECCCEEEEEe
Q Q_lactD2140_p         166 ---DSKAGNVVLKLS      177 (205)
Q Consensus              166 -----Ii~i~l      177 (205)
                           ...+.+.+.+.
T Consensus              242 ~v~v~v~g1~v~v~      256 (270)
Q Q_Rv0817c_p3          242 NTVGARGSDVIEIG      256 (270)
T ss_pred                eEEEECCeEEEEEE

```

```
Query Q_Takeout_p3
Match_columns 249
No_of_seqs 110 out of 115
Neff 9.96623
Searched_HMMs 1
Date Sun Oct 28 23:38:53 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/Takeout_v_YceBa.hhr -oa3m
../results/Takeout_v_YceBa.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seg 1 -dbstrlen 10000 -norealign -maxres 32000 -
cluster /cluster/toolkit/production/bioprogns/tools/hh-suite-build/data/context_data.crf
```

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1 Q_YceB_p3	2.7	0.067	0.067	15.0	7.7	68	109-177		52-119	(186)

No 1
>Q_YceB_p3
Probab=2.72 E-value=0.067 Score=15.04 Aligned cols=68 Identities=9% Similarity=0.067 Sum probs=0.0 Template Neff=8.100

[illegible]

```
Query Q_Novo_D4403C_p3
Match_columns 202
No_of_seqs 100 out of 113
Neff 8.36093
Searched_HMMs 1
Date Wed Aug 15 08:41:35 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/NovoD4403C_v_Takeout.hhr -oa3m
../results/NovoD4403C_v_Takeout.a3m -p 0 -Z 250 -loc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000
-context /cluster/toolkit/production/bioprgs/tools/hh-suite-build/data/context data.crf
```

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_Takeout_p3	30.8	0.0072	0.0072	21.1	6.9	99	50-161		128-226	(249)
2	Q_Takeout_p3	0.1	0.58	0.58	8.9	5.2	36	167-202		111-147	(249)

No 1
>Q Takeout_p3
Probab=30.77 E-value=0.0072 Score=21.12 Aligned cols=99 Identities=13% Similarity=0.233 Sum probs=0.0 Template Neff=10.000

[illegible][illegible]

```
Query          Q_Takeout_p3
Match_columns  249
No_of_seqs    110 out of 115
Neff          9.96623
Searched_HMMs 1
Date          Sun Oct 28 23:33:50 2018
Command       hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/Takeout_v_D4403N.hhr -oa3m
              ../results/Takeout_v_D4403N.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
              ctxt /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf
```

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1 Q Novo D4403 p3/1-287	0.6	0.23	0.23	12.8	22.8	198	2-239	8-227 (287)

No 1
>Q_Novo_D4403_p3/1-287
Probab=0.62 E-value=0.23 Score=12.82 Aligned cols=198 Identities=11% Similarity=-0.003 Sum probs=0.0 Template Neff=8.900

[illegible]

Q ss_pred	ceEEEcCCCCcEEEEEEccEEEEeeEEEEeccccCeeEEEEEEEcCEEEEEEEEEEEEEEEEEeeeeeE		
Q _Takeout_p3	66 RMVISQGESSSPVGITLTFTDNLLYGIDKRIKVKGGRDLTAHHEVKIVTKTFSLVGPYINIQGVLLILPISGTGSNM	145	(249)
Q Consensus	66 ~~~~~~gls~~~~~p~l~-g-g-y-~i~-g-g~~~~~+..+.....+...+..-+..+..+... ..+..+..+	145	(249)
T Consensus	83 ~~~~~~v~~~~~_l~~~~~Pi~~~~~	133	(287)

Takeout vs. DUF2140

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_Takeout_p3	1.6	0.11	0.11	14.4	5.6	35	104-139	142-176	(249)	

Q ss_pred	EEEEEECEEEEEEEEEEECECCCCCEEE		
Q Q_Lactato2140_p	NGSFKPLGNVVKFQLTFDPLVLKNGDVLKSKKLV	139	(205)
Q Consensus	g~~~~~lg~~~~~l~~~~~P~V~nGnl~L~~~~~iv	139	(205)
	.+.....+.+.+.+.+.+.+ +..++++++		
T Consensus	~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~l~~~~~	142	176 (249)
T Q_Takeout_p3	QSNMTMNVNRAIVSFGKPLV-KNGETLYDVLTLKI	176	(249)
T ss_pred	EEEEEEEEEEEEEEEBEECEBEECEEEEEEEEEEE		

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1 Q Takeout p3	0.2	0.44	0.44	10.4	5.0	49	216-264		37-91	(249)

[illegible]

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1 Q AsmA1 180 p3	0.2	0.41	0.41	10.6	3.4	21	361-381		3-23	(180)

Q ss_pred		hhHHHHHHHHHHHHHHHHHHH	
Q Q_Closp47_6EK	361	PGDLISLAVLSVVTHWSIKSI	381 (427)
Q Consensus	361	~+~+~+~+~+~+~+~+~+	381 (427)
		+++.++.+.+.+.+.+.+	
T Consensus	3	~~~~~	23 (180)
T Q_AsmA1_180_p3	3	RFLTTLMLILVLVLVAGLSALV	23 (180)
T ss_pred		HHHHHHHHHHHHHHHHHHHHH	

```
Query Q_YceB_p3
Match_columns 186
No_of_seqs 101 out of 105
Neff 8.13253
Searched_HMMs 1
Date Mon Oct 22 20:22:36 2018
Command hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/YceB_v_AsmA180_p3.hhr -oa3m
../results/YceB_v_AsmA180_p3.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf
```

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_AsmA1_180_p3	91.1	2.8E-05	2.8E-05	32.6	7.9	107	1-119		1-112	(180)
2	O_AsmA1_180_p3	5.7	0.031	0.031	15.8	4.7	65	55-119		103-175	(180)

Q ss_pred	ChhHHHHHHHHHHHHHHhhccccceecC---HHHHHHHHHHHHHCCcCcccccCceeeE---EEEEecCeeeccccCCCEEE	
Q Q_yceB_p3	1 MNKFLFAAALLVSGLLVGCNQLQTYTIT---EQEINQSLAKHHNFSKDIGLPGVADA---HIVLTNLTLSQIGREEPKNVLT	75 (186)
Q Consensus	1 Mkk-----l-----l-gca-----is-e-elg-l-----fP-k-----l-----v-----l-----r-----l	75 (186)
	+...+	
T Consensus	1 mK-----l-----l-----g-v-i-----p-----l-----l-----l-----l-----l-----l	80 (180)
T Q_Asmal_180_p3	1 MRRLFTTLLMILLVAVGLSALLVLLVNPNDFRDYMVKVGAARGSYQLQDLGPFREHVVWFQLSLISGRMSLTAGQASPLV	80 (180)
T ss_pred	ChhHHHHHHHHHHHHHHHHhhccccceecCChhHHHHHHHHHHHCCcCcccccCceeeCpCceEEeeecEEEEeeeccccCCCEEE	

Q	ss_pred		EEEEEEEEEcCCCceeeEEEEEEEEEEEcCCCEeEEecE	
Q	YceB_p3	76	TGDANLDMNSLFSGSKATMKLLKALPVFDKEGAGFLFKEMEVV	119 (186)
Q	Consensus	76	~~~~~1-----gagsgsl-lyl~~~~-	119 (186)
			+++ .+.+.+.+++++..#.+.++ ++.	
T	Consensus	81	~::~:::::::::: ~:: ~:: ~:: ~::v~v~	112 (180)
T	Q_AsmA1_180_p3	81	RAD-----NMRLDVALLPLSHQLSVKQMVLKGAVIQ	112 (180)
T	ss_pred		EEd-----eEEeeeHHHHeEHHEEECEE	

```
Query      Q_AsmA1_180_p3
Match_columns 180
No_of_seqs  184 out of 186
Neff        10.5998
Searched_HMMs 1
Date        Thu Aug 16 13:00:05 2018
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/AsmA_N_v_D4403C.hhr -oa3m
../results/AsmA_N_v_D4403C.a3m -p 20 -Z 250 -lcc -z 1 -b 1 -B 250 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
context /cluster/toolkit/production/bioproqs/tools/hh-suite-build/data/context_data.crf
```

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	O Novo D4403C p3	7.9	0.022	0.022	16.3	4.2	26	154-179	86-116	(202)	

[illegible]

```
Query          Q_Novo_D4403_p3/1-287
Match_columns  287
No_of_seqs     108 out of 114
Neff          8.87215
Searched_HMMs 1
Date          Sun Oct 28 21:30:24 2018
Command        hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/D4403N_v AsmAN.hhr -oa3m
               ../results/D4403N_v AsmAN.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000 -
               context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context_data.crf
```

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q AsmA1 180 p3	7.9	0.014	0.014	19.1	3.0	22	1-22		1-22	(180)

Q ss_pred	CchHHHHHHHHHHHHHHHHHHhC	
Q Q_Novo_D4403_p	1 MRTRRYVTAAALTASLLTLPAC	22 (287)
Q Consensus	1 M~~~~~l~~~~C	22 (287)

AsmA-N vs. DUF4403-C

AsmA-N vs. DUF2140

Rv0817c-N vs. AsmA-N

10

Takeout vs. AsmA-N

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1 Q Takeout p3	3.0	0.038	0.038	15.3	2.1	18	1-18		1-18	(249)

Q ss_pred	CHHHHHHHHHHHHHHHHHH		
Q Q_AsmAl_180_p3	1 MRRFLTTLMLLVVLVVG	18	(180)
Q Consensus	1 mK~::~~::~~::~~::~~	18	(180)
	.++.++.++...+.		
T Consensus	1 M~::~~::~~::~~::~~	18	(249)
T Q_Takeout_p3	1 MFATAFAVLCLLVSVDA	18	(249)
T ss_pred	CHHHHHHHHHHHHHHHHcc		

Figure 4C

AsmA-N vs. Rv0817c-N – as above.

Chorein-N vs. Rv0817c-N

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1 Q_ChorN115_p3	54.6	0.00029	0.00029	24.0	1.8	37	59-100	50-86 (115)
2 Q_ChorN115_p3	6.4	0.022	0.022	14.8	4.6	39	92-130	33-73 (115)

[illegible]

Chorein-N vs. AsmA-N

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_ChorN115_p3	92.7	1E-05	1E-05	30.0	6.4	89	31-122		1-97	(115)
2	Q_ChorN115_p3	0.1	0.47	0.47	7.8	6.3	39	142-180		50-92	(115)

[illegible]

Q ss_pred		EEEEeCCEEEeeeCcccCCC	
Q Q_AsmA1_180_p3	103	QVMLKGAVIQLTPTQTEAVRS	122 (180)
Q Consensus	103	~i~l~~~~v~l~~~~g~~~	122 (180)

Rv0817c-N vs. TamB-N

[illegible]

Q	ss_pred		eecCCCCceeEEEEEEeeeeee		
Q	Rv0817c_p3/1	81	VHAGGSGGTATLEATMHSIDL	101	(130)
Q	Consensus	81	~~~~~g~~~~~g~~~~~g~~~~~	101	(130)
			-+.++...+++..+..+..+		
T	Sensensus	53	G-1---lTl--v-y~~~gv-v-	73	(150)
T	Q_TamB1_150_p1	53	GGWRDLTLSDVRYEQPGVAVK	73	(150)
T	ss_pred		eccccEEEEEeEecCCAAK		

0 ss pred ChHHHHHHHHHHHHHHHHHHHHHHHHHHHHhCChHHHHHHHHHHHHHHHHhCCeEEecCcceEEeccceeEEEEeeeecCCCCCceE

Q ss_pred		c	
Q Q_AsmA1_180_p3	161	H	161 (180)
Q Consensus	161	d	161 (180)
T Consensus	149	d	149 (150)
T Q_TamB1_150_p3	149	D	149 (150)
T ss_pred		C	

Q ss_pred		c	
Q Q_AsmA1_180_p3	161	H	161 (180)
Q Consensus	161	d	161 (180)
T Consensus	149	d	149 (150)
T Q_TamB1_150_p1	149	D	149 (150)
T ss_pred		C	

[illegible]

Chorein-N vs. TamB-N (BLASTx1)

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1 O ChorN115 p3	86.4	6.6E-05	6.6E-05	29.2	6.0	83	33-118	7-101 (115)

Q	ss_pred		eEEEEccccCCCcCCcCCC	
Q	Tambl_150_p1	101	IQVNIVDSKMKPSEQVEE	118 (150)
Q	Consensus	101	~v-1~~~~~p-s~~~~~	118 (150)
			+..+..+...+..+++++	
T	Consensus	84	v-1-1~~~~~	101 (115)
T	Q_ChorN115_p3	84	LHIISQPQTVVFVDAEQY	101 (115)
T	ss_pred		EEEEEEEcCcCccCHHHH	

No Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1 Q Rv0817c p3/30-130	0.2	0.38	0.38	9.1	8.9	39	17-57	10-49 (101)

T ss		HHHHHHHHHhhCccCCcEEeEeCcC-CcccCCCEeeEEEEEE	
Q Q_Mdm31_b3/131	17	LASKHGK1FTKNESLSIVFESA-IPVPMWSGGISPKQVFVS	57 (182)
Q Consensus	17	va---ig---ltn--tGi-V-FesA-I-Pv-WkGd-I-f-NV-V- +..+...+..... .. .+. ..+..+..... .. .	57 (182)
T Consensus	10	vvvvvvvvvvP-Lg-Llgllggllvvvvvvvvvv~	49 (101)
T_Rv0817c_p3/3	10	LSTTVRKAAANLRSPFVAIIIRPFPIQAMRHYH--ABELEIK	49 (101)
T ss		HHHHHHHHCCCCCCCCEEEeEcCcchHHHHHCcccc--ccceEEE	
Confidence		33333332222333345555542 45555565654 4444433	

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	Q_Mdm31_b3/131-312	56.9	0.0019	0.0019	22.4	7.9	63	30-92		43-138	(182)
2	Q_Mdm31_b3/131-312	0.7	0.17	0.17	12.0	4.4	28	16-43		96-129	(182)

0 ss pred EEecEEEEEEeEEECHHHHHh-----CCCCEEEEEEEcEEEEeehhh-ccccCE

```
Q ss_pred --EEEEEEEEEEEEeC
Q Q_Vps13chorN_p 79 --KINTEDVFLFLASP 92 (127)
Q Consensus 79 --i-i-v~v~l~l~ 92 (127)
      .+!|||.++.-+
T Consensus 123 T-d~i-I-GvR-Vdr~ 138 (182)
T Q_Mdm31_b3/131 123 LDEVTINGLRGVDIRT 138 (182)
T ss_pred eeeeeeeceEEEEeC
Confidence 4778887777543
```

Q ss_pred		HHHh-CCCCHHhc-----cEEEEEEEEEEc	
Q Vpsl3chorN_p	16	MVYK--NNPKQLL-KKEWVE---NGKVRLDNLLEQ	43 (127)
Q Consensus		~y-i-l~::~:l~::l~::G-i-l~::+~:	43 (127)
		. . . +++++++ ++!+. !.+..+++!	
T Consensus		n-t-fd-l-I-dvdtLsl-kwI-GKGIL-dv~-I-	129 (182)
T Q_Mdm3l_b3/131	96	NYPQFDLIQDVIGISLNFRKWINGKLIDEVTIN	129 (182)
T ss_pred		CeEEEEEEEEEEEEEEEHhHHCcCCcCeeEEEEe	
Confidence		3443 3444444 44553 587777777765	

```
Query           Q_Mdm31_b3/131-312
Match_columns   182
No_of_seqs      104 out of 136
Neff            6.14424
Searched_HMMs   1
Date            Thu Jul 11 16:26:32 2019
Command          hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/Mdm31cut_v_AsmALLdNr.hhr -oa3m
                  ../results/Mdm31cut_v_AsmALLdNr.a3m -p 0 -Z 1000 -loc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -realn -mact 0.3 -
                  maxres 32000 -context /cluster/toolkit/production/bioprogs/tools/hh-suite-build/data/context data.crf
```

T ss_pred		HHHHHHHHHHHCCCEEECCcCccCcc-CCCEEEeEEEEECccccCcChHHHHHHHHHHhhhhhhhccccccc	
T Q_Mdm31_b3/131	16	YLASKGKIKTINKESLISVFESAIVPDW-SSGKISQKFVFSRRPKVSRGFTKGSSQQDALQRAKLALSERILVNQDFDN	94 (182)
T Consensus		-va--ig--Lt--TG-I-V-FesAivP-W-kdG-I-f-NV-V-----	94 (182)
		.+...++++ +.+.+.+++.+- _-. +.+.+.+.+....	
T Consensus	5	~k~i~v~v~tGr~~I-G~L~~~~P~~~~~-----	50 (98)
T Q_AsmA_p3/26-1		DFRDYVMVKQAARSGYQLQLDGLPLRWHPVQLSILSGRMSLTAAQA	50 (98)
T ss_pred		hHHHHHHHHHHHCCCEEECCcCeEEEEcCcEEEEeeEecCCcC-	
Confidence		345677778888999998875432221 12225666666643110	

T ss_pnd		CCcEeEEEEEEEEEHHCcCccGcEeEEeEeeCEEEEC	
Q Q_Mdm31_b3/131	95	GNYTQFDLTIQVDIVLSNFRKXWGLLDEVTINGLRGVDR	137 (182)
Q Consensus	95	-n-t--fd-l-I-d-ivtLSl-Kw-l-GkGLd--d-T-Gvrg-Vdr	137 (182)
		..+.....+...+...+...+...+...+...+	
T Consensus	51	-----P-Ll-g-v-i-----p-i-l-t-p-	90 (98)
T Q_AsmA p3/26-1	51	--SQPLVRADNMRLDVALLPLLSHQLSVKQVMLKGAVIQLTP	90 (98)
T ss_pnd		-----CCCcEeEEEEEEEcCHHHHCcCcEeEEeEeCEEEe	
Confidence		12327899999999999999999999999998865444333	

```
Query      Q_TamB1_150_p3/27-150
Match_columns 124
No_of_seqs  100 out of 104
Neff        9.57656
Searched_HMMs 1
Date        Thu Jul 11 16:16:02 2019
Command     hhsearch -cpu 8 -i ../results/full.a3m -d ../results/db -o ../results/TamB_delT_v_Mdm3lcut.hhr -oa3m
../results/TamB_delT_v_Mdm3lcut.a3m -p 0 -Z 1000 -lcc -z 1 -b 1 -B 1000 -ssm 2 -sc 1 -seq 1 -dbstrlen 10000 -norealign -maxres 32000
-context /cluster/toolkit/production/bioprogns/tools/hh-suite-build/data/context_data.crf
```

Q ss_pred		CChHHHHHHHHHHhhCC---CcEEEEEEeeec-----c-EEEEEEEcC-----	
Q Q_Tambl_150_p3	1	GTTSGGLHVLVFKAADRVVP---GLDIGKVTGGWR---D-LTLDSDVRVEQP-	42 (124)
Q Consensus		t~g~g~l~l~~~~~l~i~~~G~l~l~~~~~l~v~~~~~	42 (124)
T Consensus		+ -..t+.++...+ . + + ..-+.++ ++ . .+..	
T Consensus		Nt~~~~q~e~va~~~~ig~L~t~G~V~-FesAlvP~Wkd~I~f~NV~V~~~~~	88 (182)
T Q_Mdm31_b3/131	9	NTVFAGQEYLASKIGKFITKNESLIIVFESAIICVDPSWGSKIIFQKVVSRRPKVSRGFTKGSQQDALQRAKLALSERILVN	88 (182)
T ss_pred		hhhhhHHHHHHHHHHCCCCCEEEECCccccCCCCcCCcEEeEeeeeCCCCCCCCccccCHHHHHHHHHHHHHHHHHHH	

