

EXHIBIT T

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 3 (Query) and BHA (Sbjct)

NW Score	Identities	Positives	Gaps
2204	416/447(93%)	421/447(94%)	16/447(3%)
Query 1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct 1	--.....	58	
Query 61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct 59		118	
Query 121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct 119		178	
Query 181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct 179		238	
Query 241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct 239		298	
Query 301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct 299	SWENT.TKE..QAIKE..D.T.....	358	
Query 361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct 359		418	
Query 421	DVCIADGVCIDAF LKPPMETEEPQIFY	447	
Sbjct 419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 32 (Query) and BHA (Sbjct)

NW Score	Identities	Positives	Gaps
2199	413/433(95%)	418/433(96%)	5/433(1%)
Query 1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct 1	--.....	58	
Query 61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct 59		118	
Query 121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct 119		178	
Query 181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct 179		238	
Query 241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct 239		298	
Query 301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct 299	SWENT.TKE..QAIKE..D.T.....	358	
Query 361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct 359		418	
Query 421	DVCIADGVC I---	430	
Sbjct 419	DAF	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 33 (Query) and BHA (Sbjt)

NW Score	Identities	Positives	Gaps
2206	414/433(96%)	419/433(96%)	4/433(0%)
Query 1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR	60	
Sbjct 1	--.....	58	
Query 61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct 59		118	
Query 121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct 119		178	
Query 181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct 179		238	
Query 241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct 239		298	
Query 301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct 299	SWENT.TKE..QAIKE..D.T.....	358	
Query 361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct 359		418	
Query 421	DVCIADGVCID--	431	
Sbjct 419	AF	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 34 (Query) and BHA (Sbjt)

NW Score	Identities	Positives	Gaps
2211	415/433(96%)	420/433(96%)	3/433(0%)
Query 1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR	60	
Sbjct 1	--.....	58	
Query 61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct 59		118	
Query 121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct 119		178	
Query 181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct 179		238	
Query 241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct 239		298	
Query 301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct 299	SWENT.TKE..QAIKE..D.T.....	358	
Query 361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct 359		418	
Query 421	DVCIADGVCIDA-	432	
Sbjct 419	F	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 35 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2229		416/433(96%)	421/433(97%)	2/433(0%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF	433	
Sbjct	419		431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 36 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2217		416/434(96%)	421/434(97%)	3/434(0%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF	434	
Sbjct	419	-	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 37 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2216		416/435(96%)	421/435(96%)	4/435(0%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFLEK	435	
Sbjct	419	--	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 38 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2215		416/436(95%)	421/436(96%)	5/436(1%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFLEK	436	
Sbjct	419	---	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 39 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2214		416/437(95%)	421/437(96%)	6/437(1%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	 SWENT.TKE..QAIKE..D.T		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAFKPP	437	
Sbjct	419	----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 40 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2213		416/438(95%)	421/438(96%)	7/438(1%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	 SWENT.TKE..QAIKE..D.T		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAFKPPM	438	
Sbjct	419	----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 41 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2212		416/439(95%)	421/439(95%)	8/439(1%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKDTPDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAFKPPME	439	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 42 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2211		416/440(95%)	421/440(95%)	9/440(2%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKDTPDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAFKPPMET	440	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 43 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2210		416/441(94%)	421/441(95%)	10/441(2%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETE	441	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 44 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2209		416/442(94%)	421/442(95%)	11/442(2%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEE	442	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 45 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2208		416/443(94%)	421/443(95%)	12/443(2%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEP	443	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 46 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2207		416/444(94%)	421/444(94%)	13/444(2%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQ	444	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 47 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2206		416/445(93%)	421/445(94%)	14/445(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYPPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE..QAIKE..D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQI	445	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 48 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2205		416/446(93%)	421/446(94%)	15/446(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYPPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE..QAIKE..D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQIF	446	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 49 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2203		416/448(93%)	421/448(93%)	17/448(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGGQVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYN	448	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 50 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2202		416/449(93%)	421/449(93%)	18/449(4%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGGQVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYNA	449	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 51 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2201		416/450(92%)	421/450(93%)	19/450(4%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYNAS	450	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 52 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2200		416/451(92%)	421/451(93%)	20/451(4%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYNASP	451	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 53 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2199		416/452(92%)	421/452(93%)	21/452(4%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE.QAIKE.D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYNASPS	452	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 54 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2198		416/453(92%)	421/453(92%)	22/453(4%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE.QAIKE.D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFYNASPST	453	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 55 (Query) and BHA (Sbjt).

NW Score		Identities	Positives	Gaps
2197		416/454(92%)	421/454(92%)	23/454(5%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFYNASPSTL	454	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 56 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2196		416/455(91%)	421/455(92%)	24/455(5%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFYNASPSTLS	455	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 57 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2195		416/456(91%)	421/456(92%)	25/456(5%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFYNASPSTLSA	456	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 58 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2194		416/457(91%)	421/457(92%)	26/457(5%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR		60
Sbjct	1	--.....		58
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA		120
Sbjct	59			118
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL		180
Sbjct	119			178
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT		240
Sbjct	179			238
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG		300
Sbjct	239			298
Query	301	IVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS		360
Sbjct	299	SWENT.TKE..QAIKE..D.T.....		358
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV		420
Sbjct	359			418
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFYNASPSTLSAT	457	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 591 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2204		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 592 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2203		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSGKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFYCSYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 593 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2204		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSHKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.TKE..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCYSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 594 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2210		417/447(93%)	422/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVTIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSKKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	SWENT.T.E..QAIKE..D.T.....	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCYSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 595 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2204		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDL SWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTL SIMRSPKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 596 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2207		416/447(93%)	422/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDL SWLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTL SIMSRKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAF LKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 597 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2204		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSTKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFY	447	
Sbjct	419	-----	431	

Needleman-Wunsch Global Sequence Alignment Between SEQ ID NO: 598 (Query) and BHA (Sbjt)

NW Score		Identities	Positives	Gaps
2203		416/447(93%)	421/447(94%)	16/447(3%)
Query	1	LNFRAPPVIPNPVFLWAWNAPSEFCLGKFDEPLDMSLFSFIGSPRINATGQGVITIFYVDR	60	
Sbjct	1	--.....	58	
Query	61	LGYYPYIDSITGVTVNGGIPQKISLQDHLDAKAKDITFYMPVDNLGMAVIDWEEWRPTWA	120	
Sbjct	59		118	
Query	121	RNWKPKDVYKNRSIELVQQNVQLSLTEATEKAKQEFKAGKDFLVETIKLGKLLRPNHL	180	
Sbjct	119		178	
Query	181	WGYYLFPDCYNHHYKPGYNGSCFNVEIKRNDLSQLWNESTALYPSIYLNTQQSPVAAT	240	
Sbjct	179		238	
Query	241	LYVRNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVLKFLSQDELVYTFGETVALGASG	300	
Sbjct	239		298	
Query	301	IVIWGTLSIMRSYKSCLLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCIRKNWNSS	360	
Sbjct	299	 SWENT.TKE.QAIKE.D.T	358	
Query	361	DYLHLNPDNFAIQLEKGGKFTVRGKPTLEDLEQFSEKFCSCYSTLSCKEKADVKTDAV	420	
Sbjct	359		418	
Query	421	DVCIADGVCIDAFKPPMETEEPQIFY	447	
Sbjct	419	-----	431	