# Score: 629.0

# Align Len: 442

# Identity: 116/442 (26.24%)

# Similarity: 117/442 (26.47%)

# Gap Count: 324/442 (73.30%)

VDJ 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

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PEAKS 1 EVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

VDJ 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

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PEAKS 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

VDJ 101 HGNYFDFWGQGTTLTVSQ-------------------------------- 118

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PEAKS 101 HGNYFDFWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY 150

VDJ 119 -------------------------------------------------- 118

PEAKS 151 FPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTC 200

VDJ 119 -------------------------------------------------- 118

PEAKS 201 NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL 250

VDJ 119 -------------------------------------------------- 118

PEAKS 251 TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVSE 300

VDJ 119 -------------------------------------------------- 118

PEAKS 301 LPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 350

VDJ 119 -------------------------------------------------- 118

PEAKS 351 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYF 400

VDJ 119 ------------------------------------------ 118

PEAKS 401 VYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

# Score: 528.0

# Align Len: 213

# Identity: 100/213 (46.95%)

# Similarity: 101/213 (47.42%)

# Gap Count: 107/213 (50.23%)

VDJ 1 QIVLSQSPTILSASPGEKVTMTCRANSSVGFMHWCQQKPGSSPKPWIYAT 50

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PEAKS 1 DGVLCQNGVILSASPGEKVTMTCRANSSVGFMHWCQQKPGSSPKPWIYAT 50

VDJ 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

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PEAKS 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

VDJ 101 TKLEIK-------------------------------------------- 106

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PEAKS 101 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID 150

VDJ 107 -------------------------------------------------- 106

PEAKS 151 GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS 200

VDJ 107 ------------- 106

PEAKS 201 TSPIVKSFNRNEC 213

# Score: 630.0

# Align Len: 442

# Identity: 117/442 (26.47%)

# Similarity: 117/442 (26.47%)

# Gap Count: 324/442 (73.30%)

VDJ 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

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Fusion 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

VDJ 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

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Fusion 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

VDJ 101 HGNYFDFWGQGTTLTVSQ-------------------------------- 118

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Fusion 101 HGNYFDFWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY 150

VDJ 119 -------------------------------------------------- 118

Fusion 151 FPEPVTVTWNSGSLSSGVHTFPAVLESDLYTLSSSVTVPSSTWPSETVTC 200

VDJ 119 -------------------------------------------------- 118

Fusion 201 NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL 250

VDJ 119 -------------------------------------------------- 118

Fusion 251 TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVSE 300

VDJ 119 -------------------------------------------------- 118

Fusion 301 LPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 350

VDJ 119 -------------------------------------------------- 118

Fusion 351 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYF 400

VDJ 119 ------------------------------------------ 118

Fusion 401 VYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

# Score: 558.0

# Align Len: 213

# Identity: 105/213 (49.30%)

# Similarity: 106/213 (49.77%)

# Gap Count: 107/213 (50.23%)

VDJ 1 QIVLSQSPTILSASPGEKVTMTCRANSSVGFMHWCQQKPGSSPKPWIYAT 50

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Fusion 1 QIVLSQSPTILSASPGEKVTMTCRADSSVGFMHWCQQKPGSSPKPWIYAT 50

VDJ 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

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Fusion 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

VDJ 101 TKLEIK-------------------------------------------- 106

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Fusion 101 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID 150

VDJ 107 -------------------------------------------------- 106

Fusion 151 GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS 200

VDJ 107 ------------- 106

Fusion 201 TSPIVKSFNRNEC 213

# Score: 596.0

# Align Len: 445

# Identity: 113/445 (25.39%)

# Similarity: 114/445 (25.62%)

# Gap Count: 330/445 (74.16%)

VDJ 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

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Stitch 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

VDJ 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

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Stitch 51 IYPGNVKSLYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

VDJ 101 HGNYFDFWGQGTTLTVSQ-------------------------------- 118

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Stitch 101 HGNYF---GQGTTLTVSSAKSAKTTPPSVYPLAPGSAAQTNSMVTLGCLV 147

VDJ 119 -------------------------------------------------- 118

Stitch 148 KGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSET 197

VDJ 119 -------------------------------------------------- 118

Stitch 198 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 247

VDJ 119 -------------------------------------------------- 118

Stitch 248 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRS 297

VDJ 119 -------------------------------------------------- 118

Stitch 298 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 347

VDJ 119 -------------------------------------------------- 118

Stitch 348 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 397

VDJ 119 --------------------------------------------- 118

Stitch 398 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

# Score: 548.0

# Align Len: 214

# Identity: 105/214 (49.07%)

# Similarity: 106/214 (49.53%)

# Gap Count: 108/214 (50.47%)

VDJ 1 QIVLSQSPTILSASPGEKVTMTCRANSSVGFMHWCQQKPGSSPKPWIYAT 50

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Stitch 1 QIVLSQSPTILSASPGEKVTMTCRADSSVGFMHWCQQKPGSSPKPWIYAT 50

VDJ 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPP-TFGS 99

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Stitch 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPFTFGS 100

VDJ 100 GTKLEIK------------------------------------------- 106

|||||||

Stitch 101 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI 150

VDJ 107 -------------------------------------------------- 106

Stitch 151 DGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKT 200

VDJ 107 -------------- 106

Stitch 201 STSPIVKSFNRNEC 214

# Score: 2379.0

# Align Len: 442

# Identity: 441/442 (99.77%)

# Similarity: 442/442 (100.00%)

# Gap Count: 0/442 (0.00%)

Fusion 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

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PEAKS 1 EVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

Fusion 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

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PEAKS 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

Fusion 101 HGNYFDFWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY 150

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PEAKS 101 HGNYFDFWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY 150

Fusion 151 FPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTC 200

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PEAKS 151 FPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTC 200

Fusion 201 NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL 250

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 201 NVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITL 250

Fusion 251 TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVSE 300

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PEAKS 251 TPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVSE 300

Fusion 301 LPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 350

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PEAKS 301 LPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK 350

Fusion 351 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYF 400

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PEAKS 351 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYF 400

Fusion 401 VYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

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PEAKS 401 VYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

# Score: 1093.0

# Align Len: 213

# Identity: 206/213 (96.71%)

# Similarity: 208/213 (97.65%)

# Gap Count: 0/213 (0.00%)

Fusion 1 QIVLSQSPTILSASPGEKVTMTCRADSSVGFMHWCQQKPGSSPKPWIYAT 50

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PEAKS 1 DGVLCQNGVILSASPGEKVTMTCRANSSVGFMHWCQQKPGSSPKPWIYAT 50

Fusion 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

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PEAKS 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPTFGSG 100

Fusion 101 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID 150

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PEAKS 101 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID 150

Fusion 151 GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS 200

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 151 GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTS 200

Fusion 201 TSPIVKSFNRNEC 213

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PEAKS 201 TSPIVKSFNRNEC 213

# Score: 2339.0

# Align Len: 445

# Identity: 438/445 (98.43%)

# Similarity: 439/445 (98.65%)

# Gap Count: 6/445 (1.35%)

Fusion 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

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Stitch 1 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGW 50

Fusion 51 IYPGNVKSIYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

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Stitch 51 IYPGNVKSLYNEKFKGKATLTADKSSNTAYMQLSSLTSEDSAVYFCAGEE 100

Fusion 101 HGNYFDFWGQGTTLTVS---SAKTTPPSVYPLAPGSAAQTNSMVTLGCLV 147

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Stitch 101 HGNYF---GQGTTLTVSSAKSAKTTPPSVYPLAPGSAAQTNSMVTLGCLV 147

Fusion 148 KGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSET 197

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 148 KGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSET 197

Fusion 198 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 247

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 198 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 247

Fusion 248 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRS 297

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 248 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRS 297

Fusion 298 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 347

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 298 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 347

Fusion 348 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 397

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 348 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 397

Fusion 398 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

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Stitch 398 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 442

# Score: 1123.0

# Align Len: 214

# Identity: 213/214 (99.53%)

# Similarity: 213/214 (99.53%)

# Gap Count: 1/214 (0.47%)

Fusion 1 QIVLSQSPTILSASPGEKVTMTCRADSSVGFMHWCQQKPGSSPKPWIYAT 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 1 QIVLSQSPTILSASPGEKVTMTCRADSSVGFMHWCQQKPGSSPKPWIYAT 50

Fusion 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPP-TFGS 99

||||||||||||||||||||||||||||||||||||||||||||| ||||

Stitch 51 SNLASGVPGRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSDPPFTFGS 100

Fusion 100 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI 149

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 101 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI 150

Fusion 150 DGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKT 199

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 151 DGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKT 200

Fusion 200 STSPIVKSFNRNEC 213

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Stitch 201 STSPIVKSFNRNEC 214