**H9C12WT-HC**

64.8% identity in 122 residues overlap; Score: 369.0; Gap frequency: 4.1%

Reference 1 QVQLKQSGPGLLQPSQRLSITCTVSGFSLGRYGVH---WIRQSPGKGLEWLGVIWRGGTT

Assembly 1 QVQLKQSGPGLLQPSQRLSLTCTVSGFSIGRGGGGSGGFIRQSPGKGLEWIGVIWRRGST

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\* \*\* \* \*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \* \*

Reference 58 DYNAVFMSRLSINKDDSKSQVFFTMNSLRPDDTAIYYCAR--QGSNFPLAYWGQGTLVTV

Assembly 61 CYNPSLKSLVNISLDTSKNQVSLSLSAVQEADLAVYFPQRGQQSGNFPLAYWGQGTLVTV

\*\* \* \* \* \*\* \*\* \* \* \* \* \* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Reference 116 SA

Assembly 121 SA

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**H9C12WT-LC**

67.0% identity in 112 residues overlap; Score: 330.0; Gap frequency: 5.4%

Reference 1 NIVMTQTPKFLLVSIGDSITITCKASQSVTNDAA-----WYQKKPGQSPQLLIYQASTRY

Assembly 2 NLVMTQTPKFLLVTPGEPATITLRSSQSLLNENGYNYKYWYQKKPGQSPQLLIYQASTRA

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Reference 56 TGVPDRFSGSGYGTDFTFTISAVQAEDLAVYFCHQDYSSPLTFGAGTKLELK

Assembly 62 SGVPDRFGSPRYGTGGSDFISRVQAEDLAVPECHQDLQSP-TFGAGTKLEIK

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**Revised parameters**

**H9C12WT-HC**

46.7% identity in 120 residues overlap; Score: 204.0; Gap frequency: 9.2%

Sequence1 1 QVQLKQSGPGLLQPSQRLSITCTVSGFSLGRYGVHW-IRQSPGKGLEWLGVIWRGGTTDY

Sequence2 1 QVQLVLSGNVVQPGASLPLLSCAACAATFSSYGVHVPALQSPGKGLEWLGVIWRMGSVKY

\*\*\*\* \*\* \* \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \* \*

Sequence1 60 NA--VFMSRLSINKDDSKSQVFFTMNSLRPDDTAIYYCARQGSNFPLAYWGQGTLVTVSA

Sequence2 61 TADVVVAGEFTISNDNSKNTLYLQGSNLRPDDTALYY--------PLVNWGQGTLVTVSA

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**H9C12WT-LC**

72.1% identity in 111 residues overlap; Score: 353.0; Gap frequency: 6.3%

Sequence1 3 VMTQTPKFLLVSIGDSITITCKASQSVTND-----AAWYQK-KPGQSPQLLIYQASTRYT

Sequence2 4 VMTQTPKSLPVTPGEPATISLRSSQSLLNENWYNYLDWYQKQKPGQSPQLLIYQASTRAS

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Sequence1 57 GVPDRFSGSGYGTDFTFTISAVQAEDLAVYFCHQDYSSPLTFGAGTKLELK

Sequence2 64 GVPDRFSGSGYGTDFTFTISPVQAEDLAVYYCHQALQSP-TFGAGTKLEIK

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**Umab-HC**

88.2% identity in 119 residues overlap; Score: 519.0; Gap frequency: 2.5%

Reference 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWLGWVRQMPGKGLDWIGIMSPVDSDIRY

Assembly 1 EVQLVQSGAEVKKPGESLKISGHGSGYSFTTYWIGWVRQMPNK-LDWLGIMSPVDSDLRY

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Reference 61 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYCARRRPGQGYFDFWGQGTLVTVSS

Assembly 60 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYHAQRP--QFPFDFWGQGTLVTVSS

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**Umab-LC**

92.5% identity in 107 residues overlap; Score: 506.0; Gap frequency: 0.0%

Reference 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

Assembly 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

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Reference 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNIYPYTFGQGTKLEIK

Assembly 61 RFSGSGSGPDLTLTITLLLPEDFATYYQCQYNLYPYTFGQGTKLEIK

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**Revised parameters**

**Umab-HC**

90.8% identity in 119 residues overlap; Score: 569.0; Gap frequency: 1.7%

Sequence1 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWLGWVRQMPGKGLDWIGIMSPVDSDIRY

Sequence2 1 EVQLVQSGAEVKKPGESLKISGSGSGYSFTTYWIGWVRQMPGGKLDWLGIMSPVDSDLRY

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\* \*\*\* \*\*\*\*\*\*\*\*\* \*\*

Sequence1 61 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYCARRRPGQGYFDFWGQGTLVTVSS

Sequence2 61 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYCARREPGE--FDFWGQGTLVTVSS

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**Umab-LC**

95.3% identity in 107 residues overlap; Score: 525.0; Gap frequency: 0.0%

Sequence1 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

Sequence2 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

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Sequence1 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNIYPYTFGQGTKLEIK

Sequence2 61 RFSGSGSGTDLTLTISTLLPEDFATYYEQQYNLYPYTFGQGTKLEIK

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**PGDM1400-HC**

61.6% identity in 146 residues overlap; Score: 339.0; Gap frequency: 18.5%

Reference 4 LVQSGPEVRKPGTSVKVSCKAPGNTLKTYDLHWVRSVPGQGLQWMGWISHEGDKK----V

Assembly 3 LLQQPEELVKP-SQEKVSCKAPGNTLTTYDIHWVRQVPGQGLQWMGWISHEGDKKKLRKV

\* \* \* \*\* \*\*\*\*\*\*\*\*\*\*\* \*\*\* \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*

Reference 60 IVERFKAKVTIDWD----RSTNTAYLQLSGLTSGDTAVYYCAKGSKHRLRDYALYDDDGA

Assembly 62 LVERFKFTTSTPAAGLGVASTSTAYLQLSLSTSGDTAVYYCAK-------DLADVD----

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Reference 116 LNWAVDVDYLSNLEFWGQGTAVTVSS

Assembly 111 ----VDVDA---LEFWGQGTAVTVSS

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**PGDM1400-LC**

96.4% identity in 112 residues overlap; Score: 571.0; Gap frequency: 0.0%

Reference 1 DFVLTQSPHSLSVTPGESASISCKSSHSLIHGDRNNYLAWYVQKPGRSPQLLIYLASSRA

Assembly 1 DFVLTQSPHSLSVTPGESASISCKSSHSLLHGDRSNYLAWYVQKPGRSPQLLIDLASERA

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\* \*\*

Reference 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

Assembly 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

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**Revised parameters**

**PGDM1400-HC**

58.5% identity in 147 residues overlap; Score: 417.0; Gap frequency: 27.2%

Sequence1 1 QAQLVQSGPEVRKPGTSVKVSCKAPGNTLKTYDLHWVRSVPGQGLQWMGWISHE------

Sequence2 1 QVQLVQSGPEVRKPTGSVKVSCKASGGTLTTYDIHWVRQVPGQGLQWMGWISHETGDKKL

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Sequence1 55 GDKKVIVERFKAKVTIDWDRSTNTAYLQLSGLTSGDTAVYYCAKGSKHRLRDYALYDDDG

Sequence2 61 GDKKVL------RVTITADESTSTPALQLSGLTSEDTAVYYCAKTLQH------------

\*\*\*\*\* \*\*\* \* \*\* \* \*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\* \*

Sequence1 115 ALNWAVDVDYLSNLEFWGQGTAVTVSS

Sequence2 103 ----------------WGQGTLVTVSS

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**PGDM1400-LC**

90.2% identity in 112 residues overlap; Score: 533.0; Gap frequency: 0.0%

Sequence1 1 DFVLTQSPHSLSVTPGESASISCKSSHSLIHGDRNNYLAWYVQKPGRSPQLLIYLASSRA

Sequence2 1 DFVLTQSPHSLSVTPGESASISCKSSHSLLHGDGKTYLYWYVQKPGQPPQLLIDLVSNRN

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\* \*\* \*\*\*\*\*\*\* \*\*\*\*\* \* \* \*

Sequence1 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

Sequence2 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

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