Comparison of:

(A) 4FVT 275 bp - 275 aa

(B) 2H4F 246 bp - 246 aa

 38.6% identity in 207 aa overlap (19-222:16-212); score: 371

 20 30 40 50 60 70

4FVT VVVMVGAGISTPSGIPDFRSPGSGLYSNLQQYDLPYPEAIFELPFFFHNPKPFFTLAKE-

 .:...::::::::::::::.: .:.:.. : . .:.. ::. .:. :. .:::

2H4F TVTLTGAGISTPSGIPDFRGP-NGIYKK-------YSQNVFDIDFFYSHPEEFYRFAKEG

 20 30 40 50 60

 80 90 100 110 120 130

4FVT LYPG-NYKPNVTHYFLRLLHDKGLLLRLYTQNIDGLERVSGIPASKLVEAHGTFASATXT

 ..: . :::..: .: :..:::. . ::::: :.. .: ..:..: ::. :.

2H4F IFPMLQAKPNLAHVLLAKLEEKGLIEAVITQNIDRLHQRAG--SKKVIELHGNVEEYYXV

 70 80 90 100 110 120

 140 150 160 170 180 190

4FVT VXQRPFPGEDIRADVMADRVPRXPVXTGVVKPDIVFFGEPLPQRFLLHVVDFPM-ADLLL

 :.. . ::. . .. :: : :.....:.:::::: ::: : ... . :.:..

2H4F RXEKKYTVEDVIKKLESSDVPLXDDXNSLIRPNIVFFGENLPQDALREAIGLSSRASLMI

 130 140 150 160 170 180

 200 210 220

4FVT ILGTSLEVEPFASLTEAVRSSVPRLLI

 .::.:: : : : : . : .:.:

2H4F VLGSSLVVYPAAELPLITVRSGGKLVI

 190 200 210

Structural alignment:

 ..........+.........+.........+.........+.........+

4FVT:SSA 122 -CCCHHHHHHHHHHCCCCCEEEEECHHHHHHCCCCCCC-C-CCCHHHHHHH

2H4F:SSA 1 C--CHHHHHHHH-H-HHCEEEEEECHHHHHHHCCCCCCCCCCCC--CC-C-

4FVT 122 -KLSLQDVAELIRARACQRVVVMVGAGISTPSGIPDFR-S-PGSGLYSNLQ

2H4F 1 M--KMKEFLDLL-N-ESRLTVTLTGAGISTPSGIPDFRGPNGIY--KK-Y-

 ..........+.........+.........+.........+.........+

4FVT:SSA 170 HHCCCCHHHHHCHHHHHHCHHHHHHHHH-HHH-HCCCCCCHHHHHHHHHHH

2H4F:SSA 44 ---C--CC-CECHHHHHHCHHHHHHHHHHHCHHHHHHCCHHHHHHHHHHHH

4FVT 170 QYDLPYPEAIFELPFFFHNPKPFFTLAK-ELY-PGNYKPNVTHYFLRLLHD

2H4F 44 ---S--QN-VFDIDFFYSHPEEFYRFAKEGIFPMLQAKPNLAHVLLAKLEE

 ..........+.........+.........+.........+.........+

4FVT:SSA 219 HCCCCEEEECCCCCHHHHHCCCCCEEECCCCCCCCECCCCCCECHH-HHHC

2H4F:SSA 89 HCCCCEEEECCCCCHHHHHCCC--EEECCCCCCEEECC-CCCCECHHHHHH

4FVT 219 KGLLLRLYTQNIDGLERVSGIPASKLVEAHGTFASATTVQRPFPGE-DIRA

2H4F 89 KGLIEAVITQNIDRLHQRAGSK--KVIELHGNVEEYYV-REKKYTVEDVIK

 ..........+.........+.........+.........+.........+

4FVT:SSA 271 -CCCCC-CCCCCCCCCCCCCCCCCCCCCCH-HHHHHHHHHHHHCEEEEECC

2H4F:SSA 139 HH--HHCCCCCCCCCCCCCCCCCCCCCECHHHHHHHHHHHHHHEEEEEECC

4FVT 271 -DVMAD-RVPRPVTGVVKPDIVFFGEPLPQ-RFLLHVVDFPMADLLLILGT

2H4F 139 KL--ESSDVPLDDNSLIRPNIVFFGENLPQDALREAIGLSSRASLMIVLGS

 ..........+.........+.........+.........+.........+

4FVT:SSA 321 CCCCEHHHHHHHHH--CCCCEEEEEECCCCCCCCCCCCCCCEEECCCHHHH

2H4F:SSA 190 CCCCEHHHHHHHHHHHHC-CEEEEEECCCCCCCC--CC--CEEEEECHHHH

4FVT 321 SLEVEPFASLTEAV--RSSVPRLLINRDLVGPLAWHPRSRDVAQLGDVVHG

2H4F 190 SLVVYPAAELPLITVRSG-GKLVIVNLGETPFDD--IA--TLKYNMDVVEF

 ..........+.........+.........+.........+.........+

4FVT:SSA 370 HHHHHHHHCCHHHHHHHHHHHHHHHH-C-CCEC-

2H4F:SSA 236 HHHHHHHHCCC---------------CCEEEECC

4FVT 370 VESLVELLGWTEEMRDLVQRETGKLD-S-GKVL-

2H4F 236 ARRVMEEGGIS---------------SRHKKLMF

Alignment Score: 0.185 (smaller is better)

 RMSD: 2.140 Angstrom

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Comparison of:

(A) 4I5I 272 bp - 272 aa

(B) 2H4F 246 bp - 246 aa

 37.3% identity in 212 aa overlap (3-212:3-200); score: 368 E(10000): 4.7e-30

 10 20 30 40 50 60

4I5I IEDAVKLLQECKKIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFPDLPDPQAMFDIEYF

 ... . ::.: . ..:::::.:. ::::::. .::: . . : .:::..:

2H4F MKEFLDLLNESRLTVTLTGAGISTPSGIPDFRGPNGIYKKYS---------QNVFDIDFF

 10 20 30 40 50

 70 80 90 100 110 120

4I5I RKDPRPFFKFAKE-IYPG-QFQPSLCHKFIALSDKEGKLLRNYTQNIDTLEQVAGIQRII

 . :. :..:::: :.: : .:.: : ..: ...: . ::::: :.: :: ...:

2H4F YSHPEEFYRFAKEGIFPMLQAKPNLAHVLLAKLEEKGLIEAVITQNIDRLHQRAGSKKVI

 60 70 80 90 100 110

 130 140 150 160 170 180

4I5I QCHGSFATASXLIXKYKVDCEAVRGDIFNQVVPRXPRXPADEPLAIMKPEIVFFGENLPE

 . ::. :. :. : : : . .. :: :. ....:.:::::::::.

2H4F ELHGNVEEYYXVRXEKKYTVEDVIKKLESSDVPL-----XDDXNSLIRPNIVFFGENLPQ

 120 130 140 150 160

 190 200 210

4I5I QFHRAMKYDKDEVDLLIVIGSSLKVRPVALIP

 . : .....:.::.:::: : :.: .:

2H4F DALREAIGLSSRASLMIVLGSSLVVYPAAELP

 170 180 190 200

Structural alignment:

 ..........+.........+.........+.........+.........+

2H4F:SSA 1 --CCHHHHHHHHHHHCEEEEEECHHHHHHHCCCCCCCCCCCCC----CCC-

4I5I:SSA 241 CC-H-HHHHHHHHHHCCEEEEECCCCCCCCCCCCCCCC-C---HHHHHHHH

2H4F 1 --MKMKEFLDLLNESRLTVTLTGAGISTPSGIPDFRGPNGIYK----KYS-

4I5I 241 NT-I-EDAVKLLQECKKIIVLTGAGVSVSCGIPDFRSR-D---GIYARLAV

 ..........+.........+.........+.........+.........+

2H4F:SSA 45 -------CC-CECHHHHHHCHHHHHHHHHHHCHHHHHHCCHHHHHHHHHHH

4I5I:SSA 286 HCCCCCCCCCCCCHHHHHHCHHHHHHHHCC-CC-CCCCCCHHHHHHHHHHH

2H4F 45 -------QN-VFDIDFFYSHPEEFYRFAKEGIFPMLQAKPNLAHVLLAKLE

4I5I 286 DFPDLPDPQAMFDIEYFRKDPRPFFKFAKE-IY-PGQFQPSLCHKFIALSD

 ..........+.........+.........+.........+.........+

2H4F:SSA 88 HHCCCCEEEECCCCCHHHHHCCCEEECCCCCCEEEC-CC-CCCECH-HHHH

4I5I:SSA 335 HHCCCCEEEECCCCCHHHHHCCCEEECCCCC-CEEECCCCCCECCCCCH--

2H4F 88 EKGLIEAVITQNIDRLHQRAGSKKVIELHGNVEEYY-VR-EKKYTV-EDVI

4I5I 335 KEGKLLRNYTQNIDTLEQVAGIQRIIQCHGS-FATASLIKYKVDCEAVR--

 ..........+.........+.........+.........+.........+

2H4F:SSA 138 HHH-HHCCCCCCC--C----CCCCCCCCCCCCCECHHHHHHHHHHHHHHEE

4I5I:SSA 385 HHHHHCC-CCC-CCCCCCCCCCCCCCCCCECCCCCHHHHHHHHHHHCCCCE

2H4F 138 KKL-ESSDVPLDD--N----SLIRPNIVFFGENLPQDALREAIGLSSRASL

4I5I 385 GDIFNQV-VPR-PRPADEPLAIMKPEIVFFGENLPEQFHRAMKYDKDEVDL

 ..........+.........+.........+.........+.........+

2H4F:SSA 184 EEEECCCCCCEHHHHHHHHHHHH-CCEEEEEECCCCC-CCCCCCEEEEECH

4I5I:SSA 436 EEEECCCCCCCHHHHHHCCC--CCCCEEEEEECCCCCCC--CCCEEECCCH

2H4F 184 MIVLGSSLVVYPAAELPLITVRS-GGKLVIVNLGETP-FDDIATLKYNMDV

4I5I 436 LIVIGSSLKVRPVALIPSSI--PHEVPQILINREPLPHL--HFDVELLGDC

 ..........+.........+.........+.........+.........+

2H4F:SSA 233 HHHHHHHHHHH-CC--CCCEEEECC-------------

4I5I:SSA 483 HHHHHHHHHHHCCHHHH--------HHCCCCCCCCCCC

2H4F 233 VEFARRVMEEG-GI--SSRHKKLMF-------------

4I5I 483 DVIINELCHRLGGEYAK--------LCCNPVKLSEITE

Alignment Score: 0.146 (smaller is better)

 RMSD: 1.884 Angstrom

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Comparison of:

(A) 4I5I 272 bp - 272 aa

(B) 4FVT 274 bp - 274 aa

 using matrix file: BL50 (15/-5), gap-open/ext: -14/-4 E(limit) 0.05

 42.0% identity in 231 aa overlap (2-227:3-225); score: 562 E(10000): 1.5e-49

 10 20 30 40 50

4I5I TIEDAVKLLQE--CKKIIVLTGAGVSVSCGIPDFRSR-DGIYARLAVDFPDLPDPQAMFD

 ...:...:.. :....:..:::.:. ::::::: .:.:. : ::: :.:.:.

4FVT SLQDVAELIRARACQRVVVMVGAGISTPSGIPDFRSPGSGLYSNLQQY--DLPYPEAIFE

 10 20 30 40 50 60

 60 70 80 90 100 110

4I5I IEYFRKDPRPFFKFAKEIYPGQFQPSLCHKFIALSDKEGKLLRNYTQNIDTLEQVAGI--

 . .: ..:.::: .:::.:::...:.. : :. : .: ::: :::::: ::.:.::

4FVT LPFFFHNPKPFFTLAKELYPGNYKPNVTHYFLRLLHDKGLLLRLYTQNIDGLERVSGIPA

 70 80 90 100 110 120

 120 130 140 150 160 170

4I5I QRIIQCHGSFATASXLIXKYKVDCEAVRGDIFNQVVPRXPRXPADEPLAIMKPEIVFFGE

 ..... ::.::.:.: .:. : .:.:.. . ::::: : ...::.::::::

4FVT SKLVEAHGTFASATXTVXQRPFPGEDIRADVMADRVPRXPVX-----TGVVKPDIVFFGE

 130 140 150 160 170

 180 190 200 210 220

4I5I NLPEQFHRAMKYDKDEVDLLIVIGSSLKVRPVALIPSSIPHEVPQILINRE

 ::..: . : .:::...:.::.:.: : . .. ::..::::.

4FVT PLPQRFLLHV-VDFPMADLLLILGTSLEVEPFASLTEAVRSSVPRLLINRD

 180 190 200 210 220

Structural alignment:

 ..........+.........+.........+.........+.........+

4FVT:SSA 122 CCCHHHHHHHHHHCCCCCEEEEECHHHHHHCCCCC-----C-CCCCCHHHH

4I5I:SSA 241 -CCHHHHHHHHH--HHCCEEEEECCCCCCCCCCCCCCCCCHHHHH---HHH

4FVT 122 KLSLQDVAELIRARACQRVVVMVGAGISTPSGIPD-----F-RSPGSGLYS

 90766 241 -NTIEDAVKLLQ--ECKKIIVLTGAGVSVSCGIPDFRSRDGIYAR---LAV

 ..........+.........+.........+.........+.........+

4FVT:SSA 167 HHHHHCCCCHHHHHCHHHHH-HCHHHHHHHHHHHHHCCCCCCHHHHHHHHH

4I5I:SSA 286 --HCCCCCCCCCCCCHHHHHHC-HHHHHHHHCCCCCCCCCCHHHHHHHHHH

4FVT 167 NLQQYDLPYPEAIFELPFFF-HNPKPFFTLAKELYPGNYKPNVTHYFLRLL

 90766 286 --DFPDLPDPQAMFDIEYFRKD-PRPFFKFAKEIYPGQFQPSLCHKFIALS

 ..........+.........+.........+.........+.........+

4FVT:SSA 217 HHHCCCCEEEECCCCCHHHHHCCCCCEEECCCCCCCCECCCCCCECHHHHH

4I5I:SSA 334 HHHCCCCEEEECCCCCHHHHHCCC--EEECCCCCCEEECCCCCCECCCCCH

4FVT 217 HDKGLLLRLYTQNIDGLERVSGIPASKLVEAHGTFASATTVQRPFPGEDIR

 90766 334 DKEGKLLRNYTQNIDTLEQVAGIQ--RIIQCHGSFATASLIKYKVDCEAVR

 ..........+.........+.........+.........+.........+

4FVT:SSA 270 CCCCCCCCCCCC-C----CCCCCCCCCCCCCCCHHHH-HHHHHHHHHCEEE

4I5I:SSA 385 HHHHHCCCCCCCCCCCCCCCCCCCCCCECCCCCHHHHHHHHHHHCCCCEEE

4FVT 270 ADVMADRVPRPV-T----GVVKPDIVFFGEPLPQRFL-LHVVDFPMADLLL

 90766 385 GDIFNQVVPRPRPADEPLAIMKPEIVFFGENLPEQFHRAMKYDKDEVDLLI

 ..........+.........+.........+.........+.........+

4FVT:SSA 317 EECCCCCCEHHHHHHHHHCCCCEEEEEECCCC-CCCCCCCCCCCEEECCCH

4I5I:SSA 438 EECCCCCCCHHHHHHCCCCCCCEEEEEECCCCCCC----CC--CEEECCCH

4FVT 317 ILGTSLEVEPFASLTEAVRSSVPRLLINRDLV-GPLAWHPRSRDVAQLGDV

 90766 438 VIGSSLKVRPVALIPSSIPHEVPQILINREPLPHL----HF--DVELLGDC

 ..........+.........+.........+.........+.........+

4FVT:SSA 367 HHHHHHHHHHHC--CHHHHHHHHHHHHHHHHCCCEC----------

4I5I:SSA 483 HHHHHHHHHHHCCHHHH-HH--C-------------CCCCCCCCCC

4FVT 367 VHGVESLVELLG--WTEEMRDLVQRETGKLDSGKVL----------

 90766 483 DVIINELCHRLGGEYAK-LC--C-------------NPVKLSEITE

Alignment Score: 0.144 (smaller is better)

 RMSD: 1.888 Angstrom