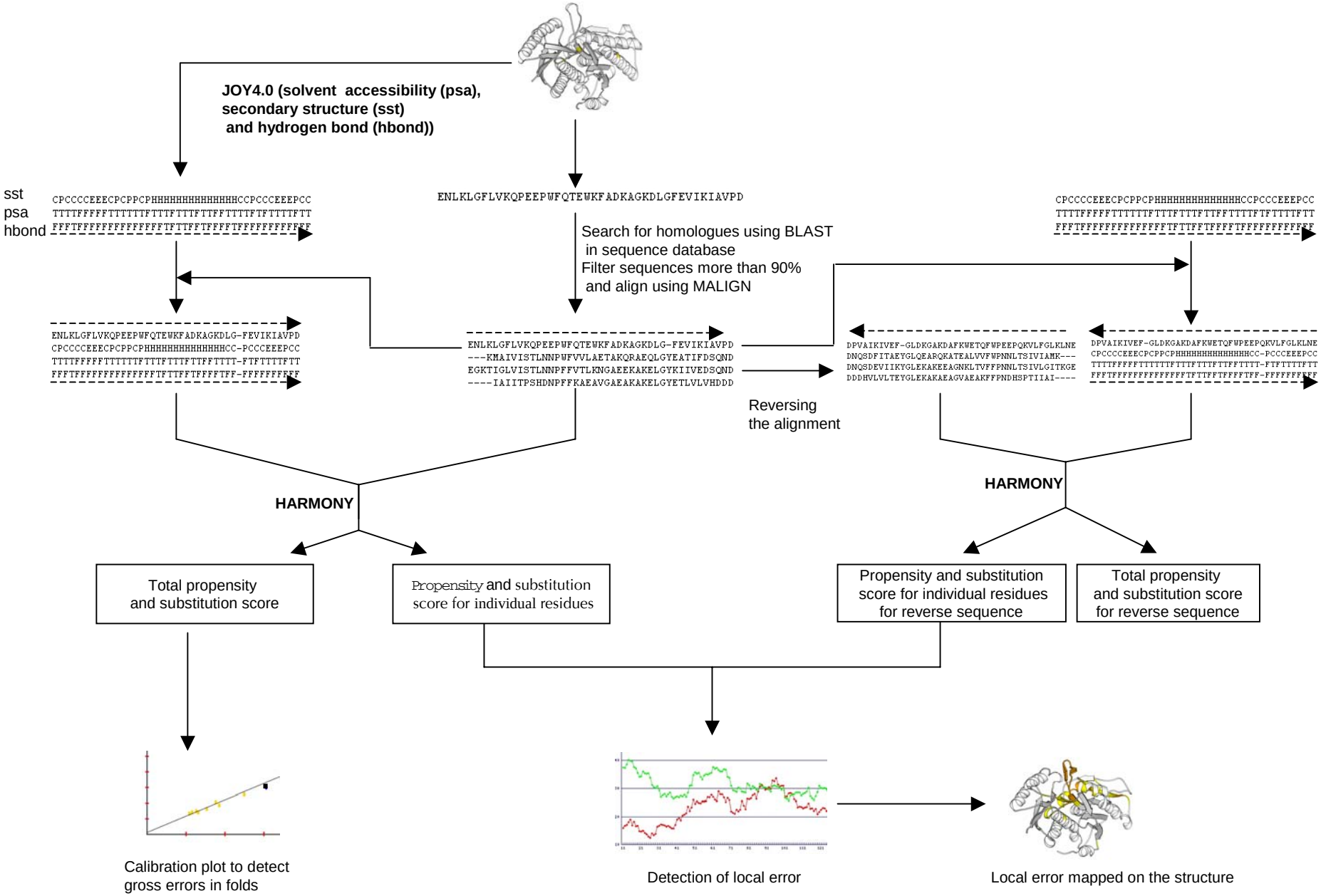
JOY4.0 (solvent accessibility (psa), secondary structure (sst) and hydrogen bond (hbond))
sst
psa
hbond
CPCCCCEEECPCPPCPHHHHHHHHHHHHHHCCPCCCEEEPCC
TTTTFFFFFTTTTTTFTTTFTTTFTTFFTTTTFTFTTTTFTT
FFFTFFFFFFFFFFFFFFTFTTFFTFFFFTFFFFFFFFFFFF
ENLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPD
Search for homologues using BLAST in sequence database
Filter sequences more than 90% and align using MALIGN
ENLKLGFLVKQPEEPWFQTEWKFADKAGKDLG-FEVIKIAVPD
CPCCCCEEECPCPPCPHHHHHHHHHHHHHHCC-PCCCEEEPCC
TTTTFFFFFTTTTTTFTTTFTTTFTTFFTTTT-FTFTTTTFTT
FFFTFFFFFFFFFFFFFFTFTTFFTFFFFTFF-FFFFFFFFFF
ENLKLGFLVKQPEEPWFQTEWKFADKAGKDLG-FEVIKIAVPD
---KMAIVISTLNNPWFVVLAETAKQRAEQLGYEATIFDSQND
EGKTIGLVISTLNNPFFVTLKNGAEEKAKELGYKIIVEDSQND
----IAIITPSHDNPFFKAEAVGAEAKAKELGYETLVLVHDDD
Reversing the alignment
DPVAIKIVEF-GLDKGAKDAFKWETQFWPEEPQKVLFGLKLNE
DNQSDFITAEYGLQEARQKATEALVVFWPNNLTSIVIAMK---
DNQSDEVIIKYGLEKAKEEAGNKLTVFFPNNLTSIVLGITKGE
DDDHVLVLTEYGLEKAKAEAGVAEAKFFPNDHSPTIIAI----
CPCCCCEEECPCPPCPHHHHHHHHHHHHHHCCPCCCEEEPCC
TTTTFFFFFTTTTTTFTTTFTTTFTTFFTTTTFTFTTTTFTT
FFFTFFFFFFFFFFFFFFTFTTFFTFFFFTFFFFFFFFFFFF
CPCCCCEEECPCPPCPHHHHHHHHHHHHHHCC-PCCCEEEPCC
TTTTFFFFFTTTTTTFTTTFTTTFTTFFTTTT-FTFTTTTFTT
FFFTFFFFFFFFFFFFFFTFTTFFTFFFFTFF-FFFFFFFFFF
HARMONY
HARMONY
Total propensity and substitution score
Propensity and substitution score for individual residues
Propensity and substitution score for individual residues for reverse sequence
Total propensity and substitution score for reverse sequence
Calibration plot to detect gross errors in folds
Detection of local error
Local error mapped on the structure