Table 1 Suppl. Sequences of primers used in this study.

| Codes | Sequences | Use |
|---|---|---|
| *EcCATA1*_FLF | 5’-ATGGATCCTACCAAGTTCCG-3’ | for full length |
| *EcCATA1*_FLR | 5’-TCACATGCTTGGCTTGACGTT-3’ | for full length |
| *EcCATB1*_FLF | 5’-ATGGATCCCTACAAGCATCGA-3’ | for full length |
| *EcCATB1*_FLR | 5’-GCTGAAACCGAACATGTAG-3’ | for full length |
| *EcCATA1*_QRF | 5’-ACCCGCCTTTACTACTTTTT-3’ | real time PCR |
| *EcCATA1*_QRR | 5’-CATAGCCGAAAAGCATCCAT-3’ | real-time PCR |
| *EcCATB1*_QFF | 5’-CACAGTTCCCATCATATTATCAT-3’ | real-time PCR |
| *EcCATB1*_QRR | 5’-GGAAGAAGAATGCATAGGTCTT-3’ | real-time PCR |
| EcUbiquitin_QF | 5'-CAAGACTGCGAAGGACTACAA-3' | real-time PCR |
| EcUbiquitin_QR | 5'-ACAGATTGATGACTGCCTCTTTA-3' | real-time PCR |

Table 2 Suppl. Physicochemical parameters of EcCATA1and EcCATB1 analyzed by different softwares.

| Properties | *EcCATA1* | *EcCATB1* |
|---|---|---|
| Number of amino acids | 493 | 472 |
| Formula | $C_{2551}H_{3852}N_{718}O_{724}S_{16}$ | $C_{2450}H_{3724}N_{688}O_{690}S_{20}$ |
| Molecular mass | 56.67 kDa | 54.49 kDa |
| Number of atoms | 7861 | 7572 |
| Aliphatic index | 69.61 | 74.77 |
| Net charge at pH 7 | -3.1 | -0.3 |
| Coefficient of absorption | 69705 $M^{-1}$ $cm^{-1}$ | 65360 $M^{-1}$ $cm^{-1}$ |
| Theoretical pI | 6.54 | 6.91 |
| Localization score | | |
| Cytoplasmic | 5 | - |
| Mitochondrial | 4 | 3.5 |
| Peroxisomal | 4 | 7 |
| Chloroplast | - | 2.5 |
| Final prediction | cytoplasmic | peroxisomal |
| Grand average of hydropathicity (GRAVY) | -0.550 (moderately hydrophilic) | -0.480 (moderately hydrophilic) |
| Instability index | 35.16 (protein is stable) | 27.83 (protein is stable) |
| Estimated half-life | 30 h | 30 h |
| Atomic composition: | | |
| Carbon | 2551 | 2450 |
| Hydrogen | 3852 | 3724 |
| Nitrogen | 718 | 688 |
| Oxygen | 724 | 690 |
| Sulfur | 16 | 20 |

Table 3 Suppl. Validation of the *EcCATA1* and *EcCATB1* model by the *SAVES* server. AAR - additional allowed regions, DAR - disallowed regions, GAR - generously allowed regions, MFR - most favored regions.

| Protein | *PROCHECK* | *Ramachandran plot* | | | | *ERRAT* | *Verify3D* |
|---|---|---|---|---|---|---|---|
| | G-factor | AAR | DAR | GAR | MFR | | |
| *EcCAT*A1 | -0.47 | 19.1 % | 2.1 % | 1.9 % | 76.8 % | 87.47 % | 64.91 % |
| *EcCAT*B1 | -0.44 | 20.3 % | 0.5 % | 1.2 % | 78.0 % | 92.35 % | 69.28 % |

Table 4 Suppl. Structural characteristics and features of *EcCATA1* and *EcCATB1* models from the *VADAR* server. MHBD - mean H-bond distance, MHBE - mean H-bond energy, MHPh - mean helix phi, MHPs - mean helix psi, MCG+ - mean chi gauche+, MCG- - mean chi gauche-, MRV - mean residue volume; TV - total volume (packing).

| Protein | MHBD(Å) | MHBE | MHPh | MHPs | MCG+ | MCG- | MRV(Å3) | TV(Å3) |
|---|---|---|---|---|---|---|---|---|
| *EcCAT*A1 | 2.2 | -1.6 | -65.0 | -37.6 | -68.3 | 67.9 | 141.4 | 69720.1 |
| *EcCAT*B1 | 2.2 | -1.7 | -65.2 | -37.8 | -67.1 | 61.7 | 142.6 | 67307.6 |

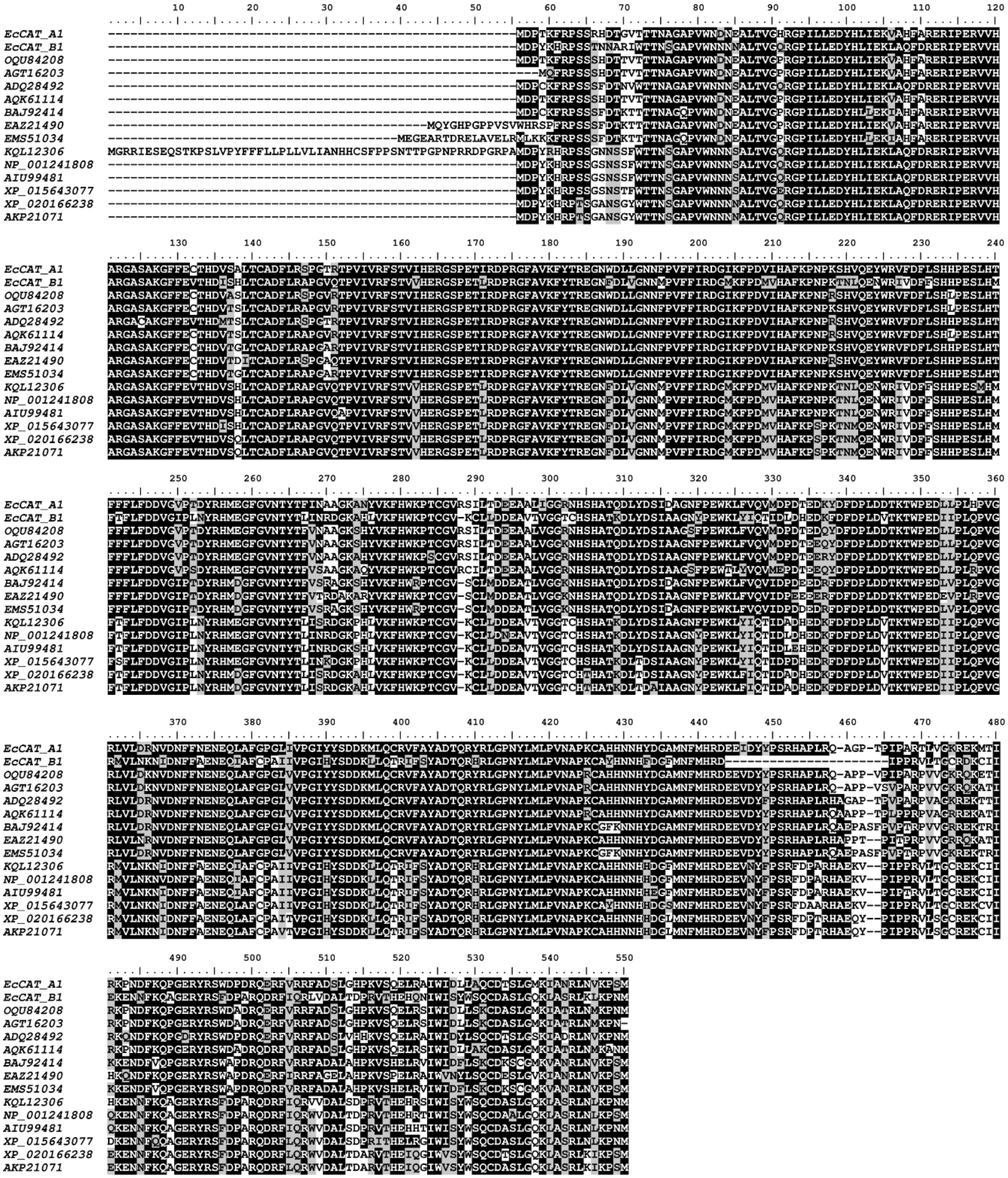

Fig. 1 Suppl. Alignment of *EcCATA1* and *EcCATB1* with homolog proteins. Alignment of the predicted *EcCATA*1 and *EcCATB1* amino acid sequences with 13 catalase proteins from chickpea, soybean, *Arabidopsis*, and rice. Alignment of the predicted polypeptide sequences (residues 1 - 493 and 1 - 473) was performed using the *ClustalX2.1* software. The protein names according to accession numbers are as follows: AlCATa1 (ADQ28492.1) from *Aeluropus littoralis*, SoCAT (AGT16203.1) and SsCAT1 (AIU99481.1) from sugarcane, TaCAT3 (AKP21071.1) and TuCAT2 (EMS51034.1) from wheat, ZmCAT3 (AQK61114.1) and ZmCAT1 (NP_001241808.1) from maize, OsJCAT (EAZ221490.1) and OsJCATB (XP_01564307.1) from rice, HvCAT1 (BAJ92414.1) from barley, SETCAT (KQL12306.1) from foxtail millet, SbCAT(OQU84207.1) from sorghum, and AtCATa1 (XP_020166238.1) from *Aegilops*.

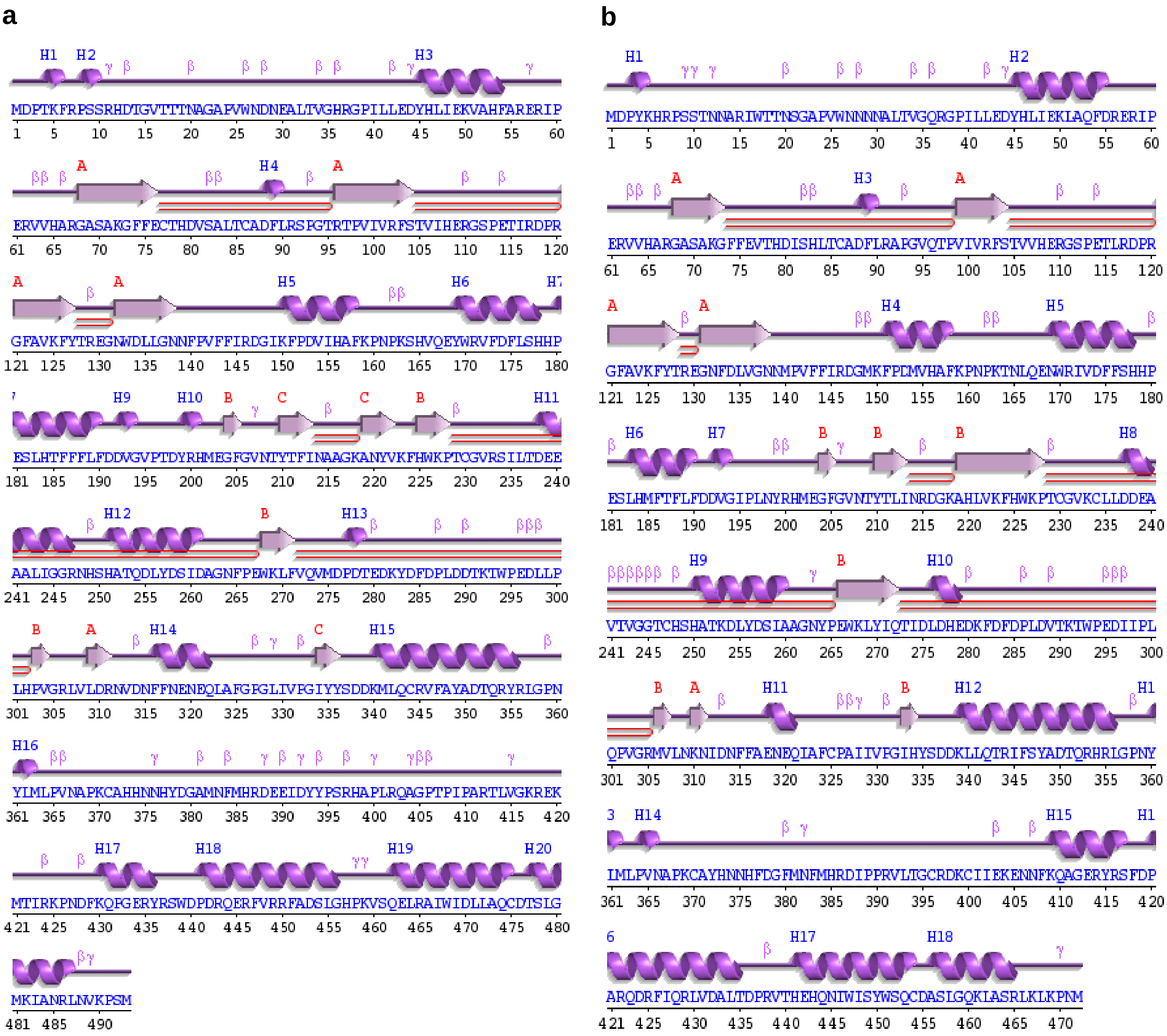

Fig. 2 Suppl. A secondary structure representation for *EcCATA1* (a) and *EcCATB1* (b) models generated via the *ProFunc* server.

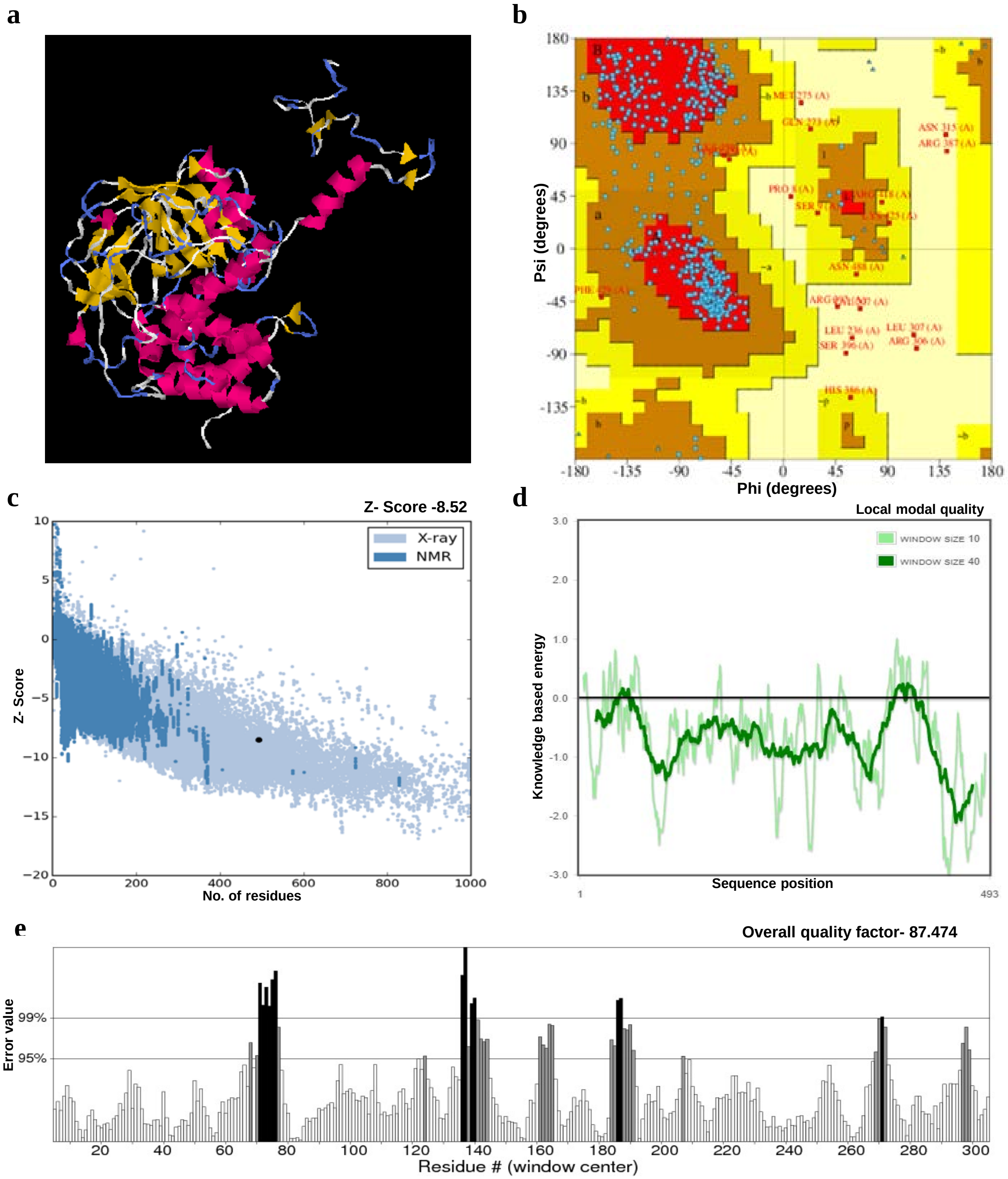

Fig. 3 Suppl. *In silico* modeling of the EcCATA1 protein. *a* - The molecular model of the EcCATA1 protein using *I-TASSER*; *b* - the *Ramachandran plot* of the EcCATA1 model using the *Profunc* server; *c* - structural comparison of residues of EcCATA1 with respective residues of X-ray and NMR structures made using the *PROSA* web server; *d* - energy of the modeled structure in the fraction of window size of 10 (*light green*) and 40 (*dark green*) amino acids using the *PROSA* web server; *e* - model validation by *Errat* using the *SAVES* server.

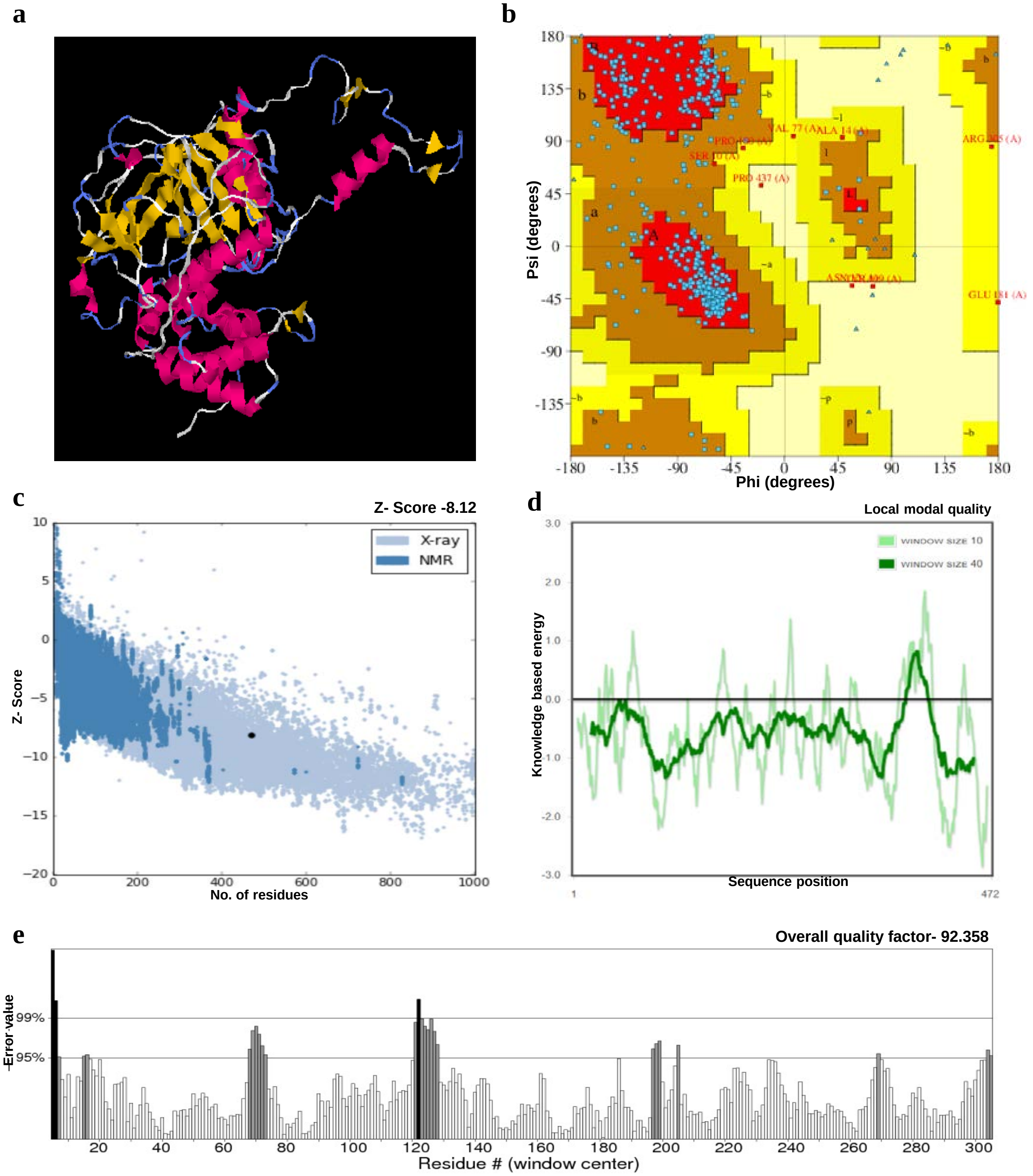

Fig. 4 Suppl. *In silico* modeling of EcCATB1 protein. *a* - The molecular model of the EcCATB1 protein using *I-TASSER*; *b* - the *Ramachandran plot* of the EcCATB1 model using the *Profunc* server; *c* - structural comparison of residues of EcCATB1 with respective residues of X-ray and NMR structures made using the *PROSA* web server; *d* - energy of the modeled structure in the fraction of window size of 10 (*light green*) and 40 (*dark green*) amino acids using the *PROSA* web server; *e* - model validation by *Errat* using the *SAVES* server.