

Supplementary data for article:

Ilić Đurđić, K.; Ostafe, R.; Đurđević Đelmaš, A.; Popović, N.; Schillberg, S.; Fischer, R.; Prodanović, R. Saturation Mutagenesis to Improve the Degradation of Azo Dyes by Versatile Peroxidase and Application in Form of VP-Coated Yeast Cell Walls. *Enzyme and Microbial Technology* **2020**, *136*. <https://doi.org/10.1016/j.enzmictec.2020.109509>

Supporting information

Saturation mutagenesis to improve the degradation of azo dyes by versatile peroxidase and application in form of VP-coated yeast cell walls

Karla Ilić Đurđić¹, Raluca Ostafe^{2,3}, Aleksandra Đurđević Đelmaš¹, Nikolina Popović¹, Stefan Schillberg⁴, Rainer Fischer^{3,5}, Radivoje Prodanović^{1*}

¹ University of Belgrade-Faculty of Chemistry, Studentski trg 12-16, 11000 Belgrade, Serbia

²Purdue Institute of Inflammation, Immunology and Infectious Disease; Molecular Evolution, Protein Engineering and Production; Purdue University, 207 S. Martin Jischke Dr., West Lafayette, IN 47907, USA

³Institute of Molecular Biotechnology, RWTH Aachen University Worringerweg 1, 52074 Aachen, Germany

⁴Fraunhofer Institute for Molecular Biology and Applied Ecology IME, Forckenbeckstrasse 6, 52074 Aachen, Germany

⁵Departments of Biological Sciences and Chemistry, Purdue University, 207 S. Martin Jischke Dr., West Lafayette, IN 47907, USA

Correspondence: Prof. Radivoje Prodanović, Faculty of Chemistry, University of Belgrade, Studentski trg 12-16, 11000 Belgrade, Serbia.

E-mail: rprodano@chem.bg.ac.rs

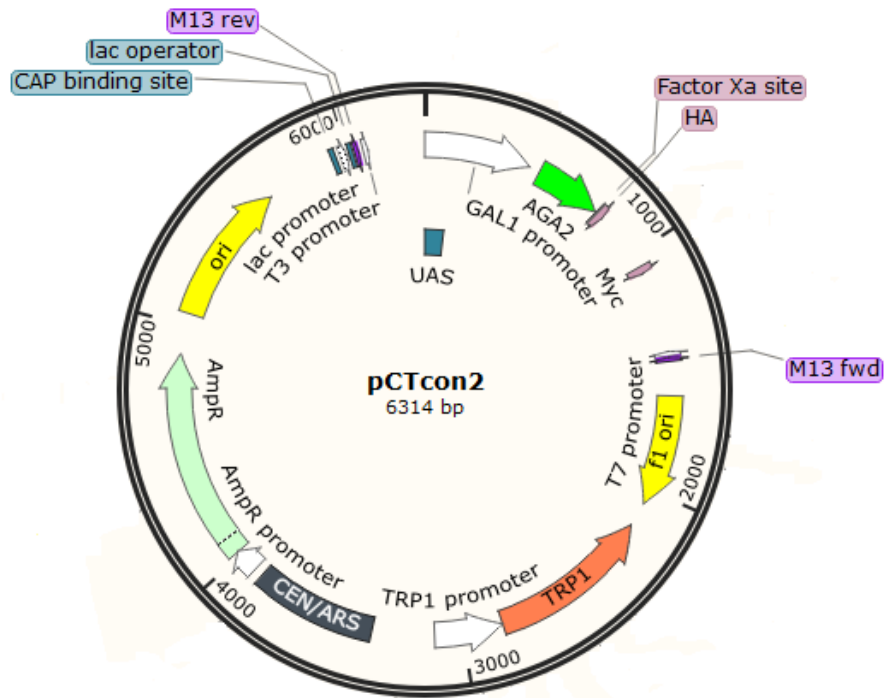


Figure S1. Map of pCTCON2 vector

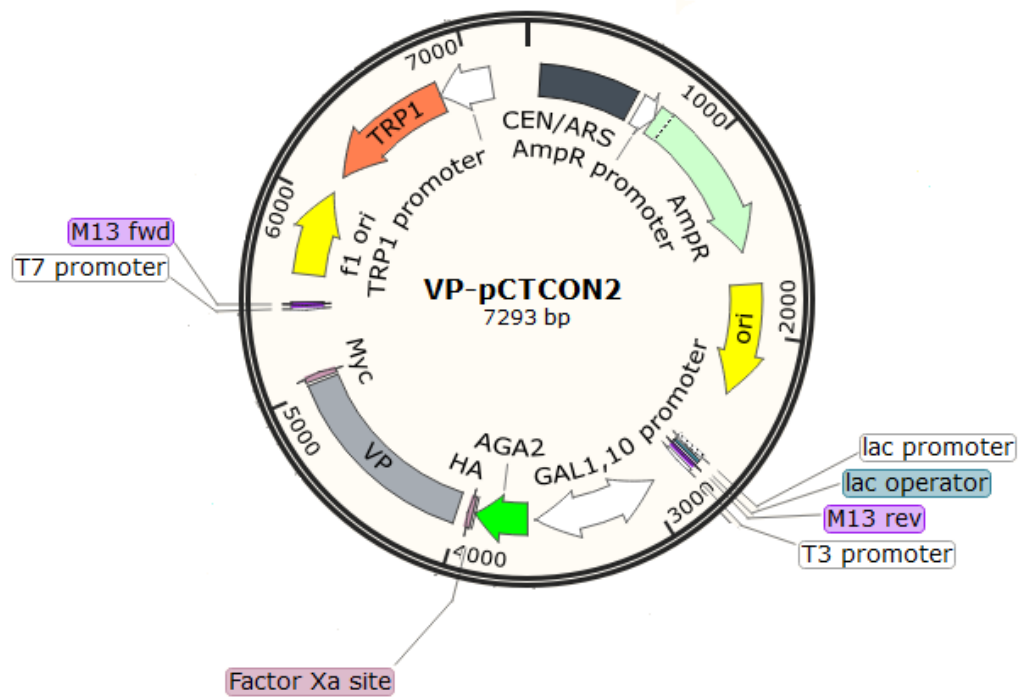


Figure S2. Map of VP-pCTCON2 construct

atggctacttggatgacggtagaacaactgcaaatgccgcatgttgcacatctattccaatcttggacgatattcaggagaactgtttgatggctcaatgcggtgaagag
gttcatgaatccttgcgttgaccttcatgatgccataggattttctccaactttaggtggggggagctgatggtagtatcattgctttgacaccattgaaccaatttccag
caaatgccggtattgatgagatagttcagctcagaaccattcgttgctaaacacaacatttctgctgggtatftatccaattgctggctgtcggagtctcaattgtcctg
gaggagtcagaataccttcttctgggtagaccagatgcagtgccgctagtccagatcatctgttccagaacctttgactcagttgactctatttccagaatgggtgat
gctggttttagctctgtagaagttgatggttacttgcacccattctattgctgcagcagataaagtcgacccctctatacctgtactccattcattcaacacctggttattcg
actcccagttcttattgaaactcagttaaagggtcgtttgtttccaggtacagctgataataagggtgaagctcaatctcctttgcaaggagaaatagggtgcaatctgatca
cttgttagctagagatcctcaaacggcttgaatggcaatctatggtgaacaatcaacctaagatccaaaacagattcgtgcaactatgtcgaaaatggccttgtgggtca
agacaagacgaaactaatcgattgttccgatgtgataccaactcctccagccttagtcgggtcagctcatttccagcaggatttccgctatcagacgtggaacaagcttgtg
ctgctacccatttccagccttaacagctgatcctggctcctgtaacatctgttccaccagttccaggtagtctcgagtaa

Figure S3. Versatile peroxidase sequence

```

CLUSTAL format alignment by MAFFT (v7.452)

Lignin|PDBID|CH AAVIEKRATCSNGKTVGDASCCAWFDVLDLDDIQNLFHGGQCGAEAHESIRLVFHDSIAIS
Versatile|PDBID -----ATCDDGRTTANAACCILFPILDDIQENLFDGANCGEVHESLRLTFHDAIGFS
                ***.:*:*..:*** * :*****:***.:** *.***:*.***:*.:*

Lignin|PDBID|CH PAMEAQGKFGGGGADGSIMIFDDIETAFHPNIGLDEIVKLQKPFVQKHGVTPGDFIAFAG
Versatile|PDBID PTL-----GGGGADGSIIAFDTIETNFPANAGIDEIVSAQKPFVAKHNISAGDFIQFAG
*: : *****: ** ** * .* *:***. ***** **.:***** **

Lignin|PDBID|CH AVALSNCPGAPQMFFFTGRAPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWML
Versatile|PDBID AVGVSNCPGGVRIPFFLGRPDVAASPDHLVPEPFDSVDSILARMGDAG-FSPVEVVWLL
**.:*****. : : ** ** . * . : ** *****.:**.*: *:.*** * . :***:*

Lignin|PDBID|CH SAHSVAAVNDVDPTVQGLPFDSTPGIFDSQFFVETQLRGTAFPGSGGNQGEVESPLPGEI
Versatile|PDBID ASHSIAAADKVDPSIPGTPFDSTPEVFDSQFFIETQLKGRLFPGTADNKGEAQSPLQGEI
:***:***.:***: : * ***** :*****:*****:* ***:..*:***:*** **

Lignin|PDBID|CH RIQSDHTIARDSRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSK
Versatile|PDBID RLQSDHLLARDPQTACEWQSMVNNQPKIQNRFAATMSKMALLGQDKTKLIDCSDVIPTPP
*:*** :***.:*****:***.*: : * : : : *** . : ***** .

Lignin|PDBID|CH PIPGNLPFSFFPAGKTIKDVEQACAETPFPTLTTLPGPETSQVRIPPPPGA
Versatile|PDBID ALVGA---AHLPAAGFSLSDVEQACAATPFPAALTADPGPVTSV---PPVPGS
.: * :.:*** :.:***** *****:***: *** ** ** ***:

```

Figure S4. Multiple alignment of VP form *P. eryngii* and LiP form *P. chrysosporium* performed using MAFFT algorithm.

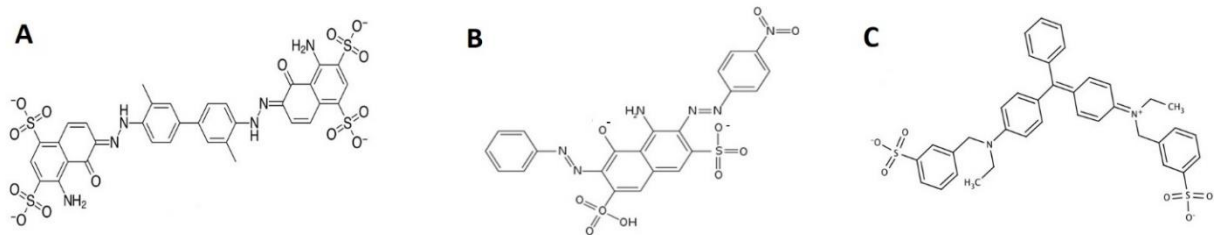


Figure S5. Structures of tested azo-dyes (A) Evans blue (B) Amido black 10B (C) Guinea green

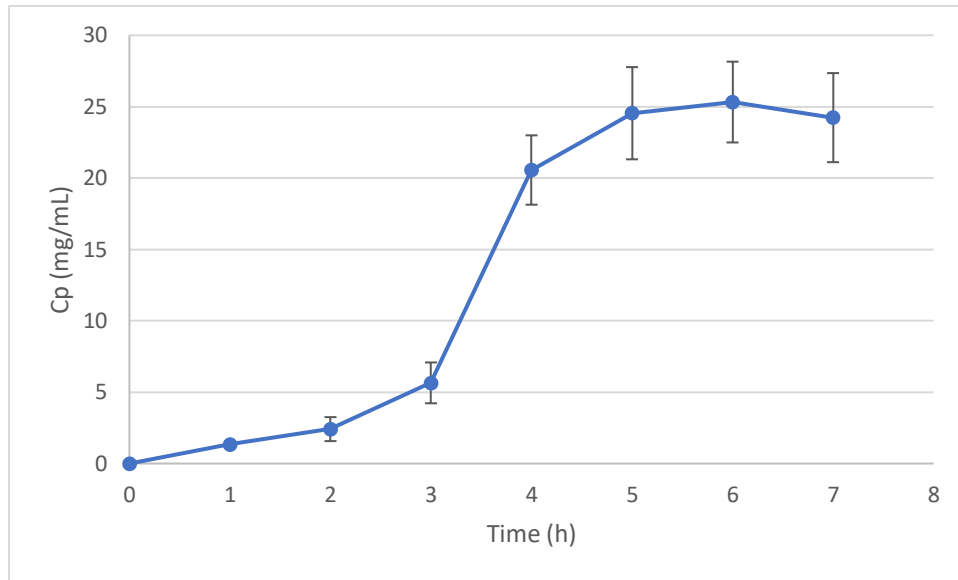


Figure S6. Protein concentration during cell lysis. Before and after every hour of toluene-induced cell lysis process 100 μ L aliquots were taken and centrifuged. Protein concentration was determined in supernatant using Bradford reagent. Data are means of triplicate experiments with error bars indicating standard deviations. Error bars are not visible when smaller than the symbol size.

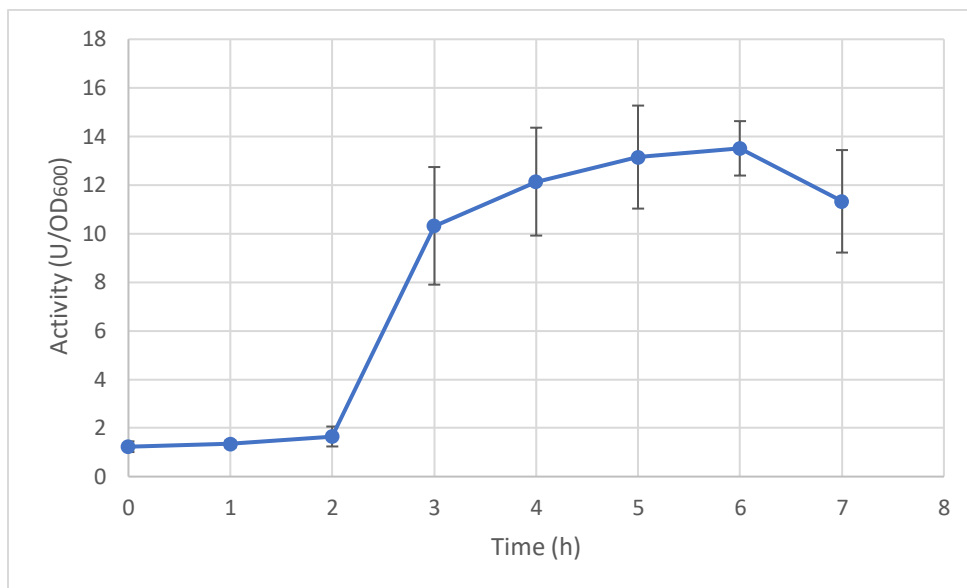


Figure S7. Activity of VP during lysis. Before and after every hour of lysis process 100 μ L aliquots were taken and centrifuged. After 3 washing steps cells/cell walls were resuspended to final OD₆₀₀ = 0.1. Activity of VP was measured with ABTS assay (2 mM ABTS, 0.5 mM H₂O₂ in 100 mM Na-tartrate buffer pH 3.5) by monitoring absorbance at 405 nm. Data are means of triplicate experiments with error bars indicating standard deviations. Error bars are not visible when smaller than the symbol size.

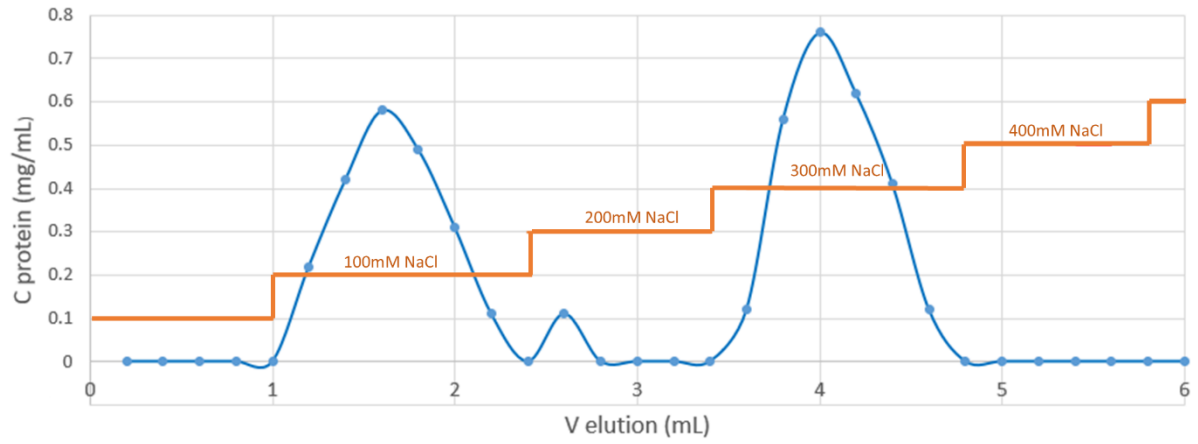


Figure S8. Chromatogram showing the elution of Aga2-wtVP chimera using Vivapure mini spin columns with optimized NaCl step elution.

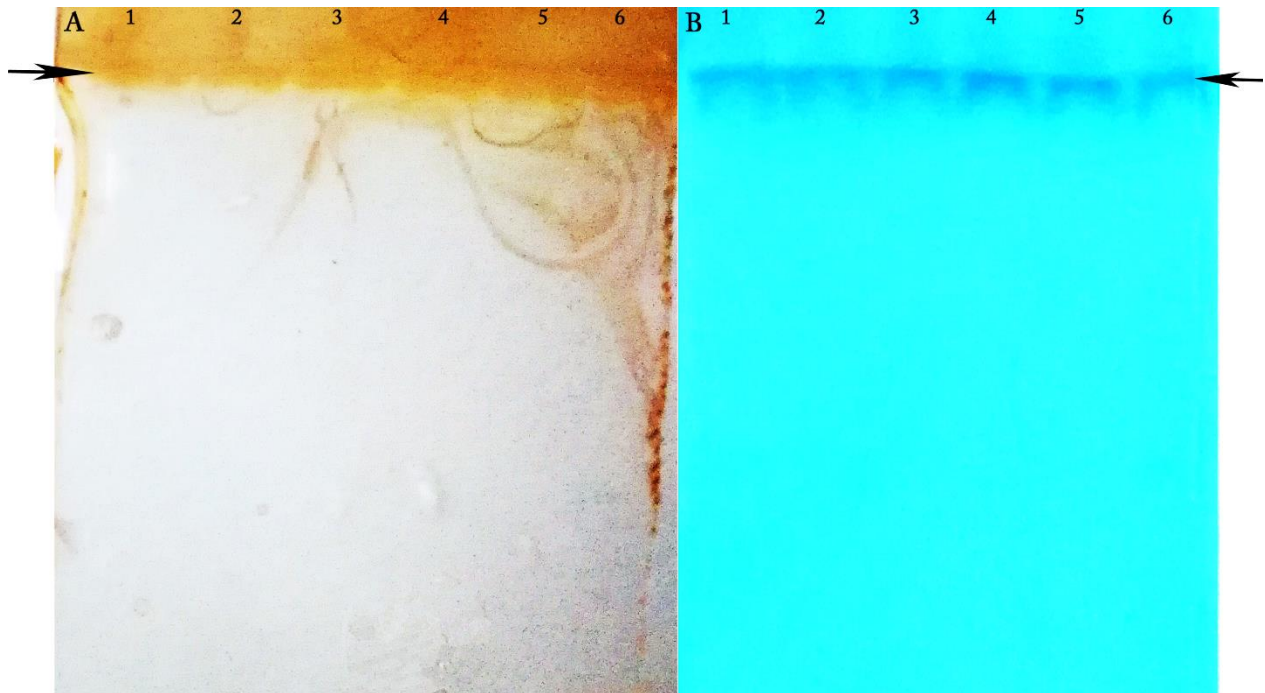


Figure S9. Native 12% polyacrylamide gel electrophoresis. (1) Aga2-wtVP (2) Aga2-MVP1 (3) Aga2-MVP2 (4) Aga2-MVP3 (5) Aga2-MVP4 (6) Aga2-MVP5 A. Activity bands in the gel after incubation with 0.5 mM H₂O₂ and 9 mM guaiacol (arrow pointing at them). B. Protein bands after CBB R250 staining (arrow pointing at them).

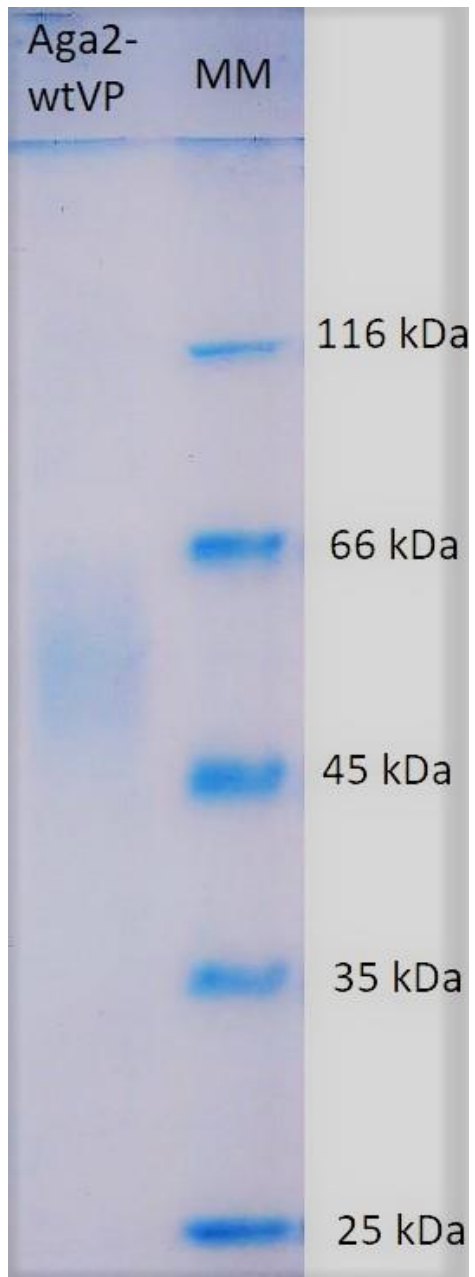


Figure S10. SDS-PAGE of purified aga2-wtVP compared with molecular weight markers (MM)

Table S1. Primers sequences

Application	Sequence
Forward primer for cloning of VP gene	ATCGATGCTAGCATGGCTACTTGTGATGACGGTAGAACAACTGCAAATGCCGC
Reverse primer for cloning of VP gene	TACTAGTGGATCCCTCGAGACTACCTGGAAGTGGTGGGAAGAGATGTTACAGGACC
Forward primer for sequencing	CCCATACGACGTTCCAGACTACGC
Reverse primer for sequencing	GATCTCGAGCTATTACAAGTCCTCTTCAG
Primer for mutation of A160N	CTGGTTTTAGTCCTNNNGAAGTTGTATGG
Primer for mutation of V260N	CAAAACAGATTCNNNGCAACTATGTTCG

Table S2. Kinetic parameters for wtVP and MV1-5 for evans blue, amido black 10B and guinea green determined for Aga2-VP fusion proteins. Data are means of triplicate experiments and error bars indicate standard deviation.

Variant	k_{cat} (s^{-1})	K_{m} (μM)	$k_{\text{cat}}/K_{\text{m}}$ ($\text{mM}^{-1}\text{s}^{-1}$)
Evans blue			
WT VP	1.17±0.23	27.52±2.95	42.51
MV1	1.95±0.19	7.74±0.95	251.94
MV2	2.95±0.09	6.54±0.93	451.07
MV3	2.03±0.64	37.32±7.44	54.39
MV4	1.30±0.23	9.92±1.10	110.89
MV5	1.58±0.05	8.15±0.45	193.86
Amido black 10B			
WT VP	1.05±0.40	15.76±2.73	66.62
MV1	5.14±0.79	6.91±0.94	743.85
MV2	4.64±0.82	17.53±1.44	260.47
MV3	6.34±0.90	5.88±0.94	1078.23
MV4	1.99±0.19	11.23±2.24	177.20
MV5	0.50±0.29	19.43±1.94	25.57
Guinea green			
WT VP	0.81±0.16	31.28±5.42	25.89
MV1	3.24±0.25	19.91±2.23	162.73
MV2	0.33±0.12	40.15±2.32	82.19
MV3	0.53±0.14	38.34±1.94	13.82
MV4	5.14±0.40	8.23±1.02	624.54
MV5	3.96±0.82	11.52±3.12	343.75