Supplemental figures: Consurf results for ascomyceteous orthologs of *nop-1*, *orp*-1 and *carO*.

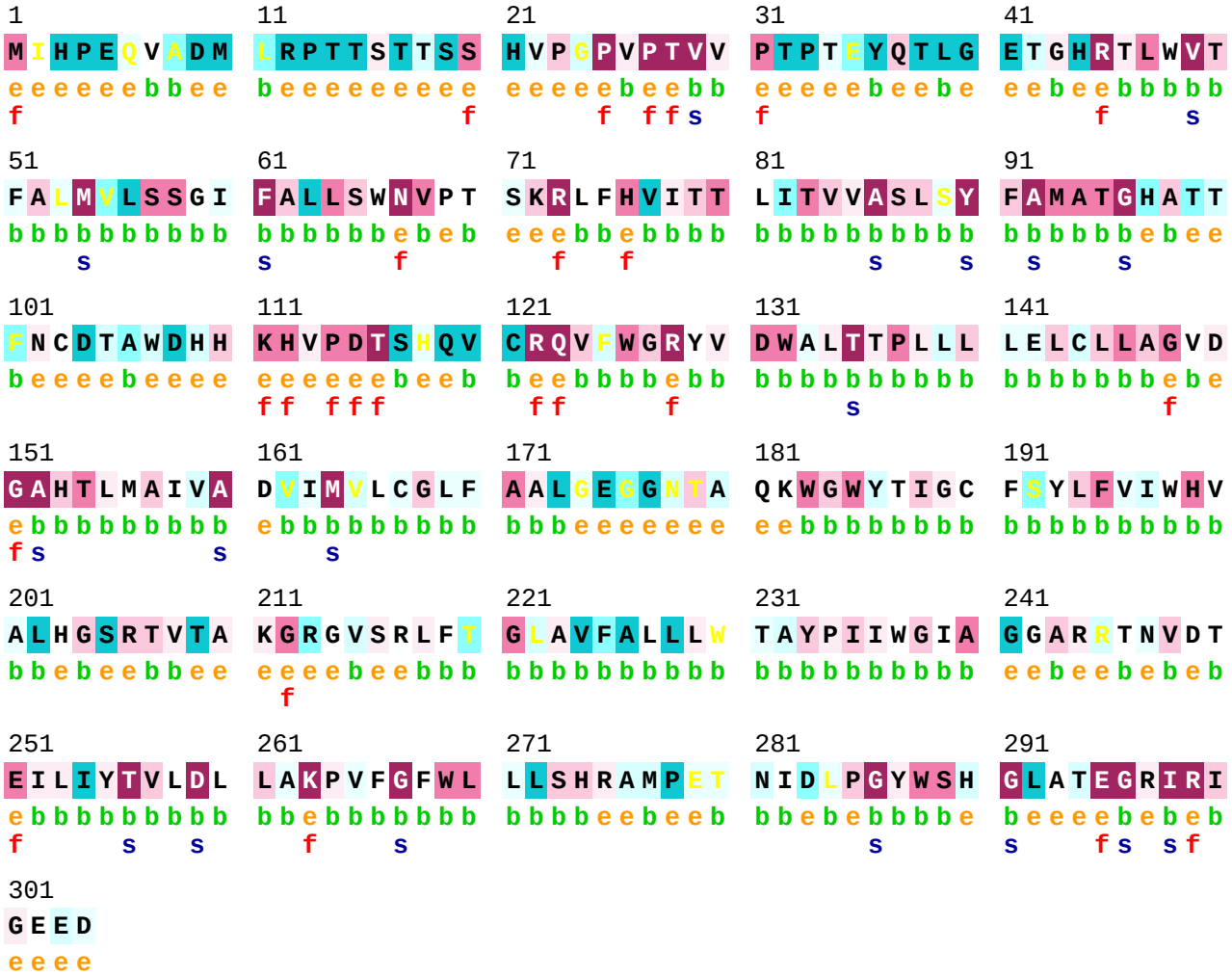
Page 1: Consurf results for *nop-1* mapped on *N. crassa nop-1* protein sequence.

Page 2: Consurf results for *nop-1* mapped on *G. zeae nop-1* protein sequence.

Page 3: Consurf results for *orp-1* mapped on *G. zeae orp-1* protein sequence.

Page 4: Consurf results for *carO* mapped on G. zeae *carO* protein sequence.

ConSurf Results



The conservation scale:

1 2 3 4 5 6 7 8 9

Variable — Average — Conserved

e - An exposed residue according to the neural-network algorithm.

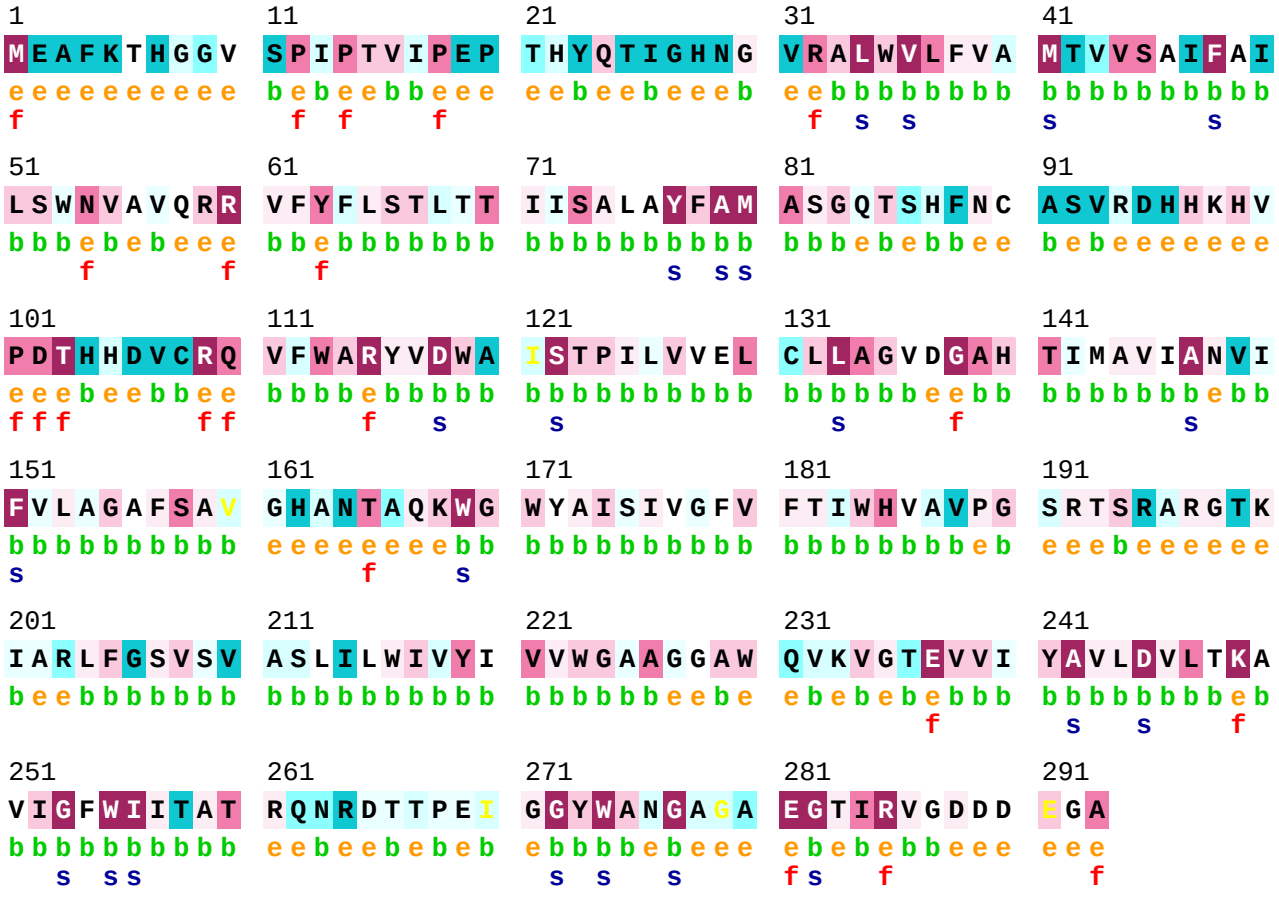
b - A buried residue according to the neural-network algorithm.

f - A predicted functional residue (highly conserved and exposed).

s - A predicted structural residue (highly conserved and buried).

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

ConSurf Results



The conservation scale:

1 2 3 4 5 6 7 8 9

Variable **Average** **Conserved**

e - An exposed residue according to the neural-network algorithm.

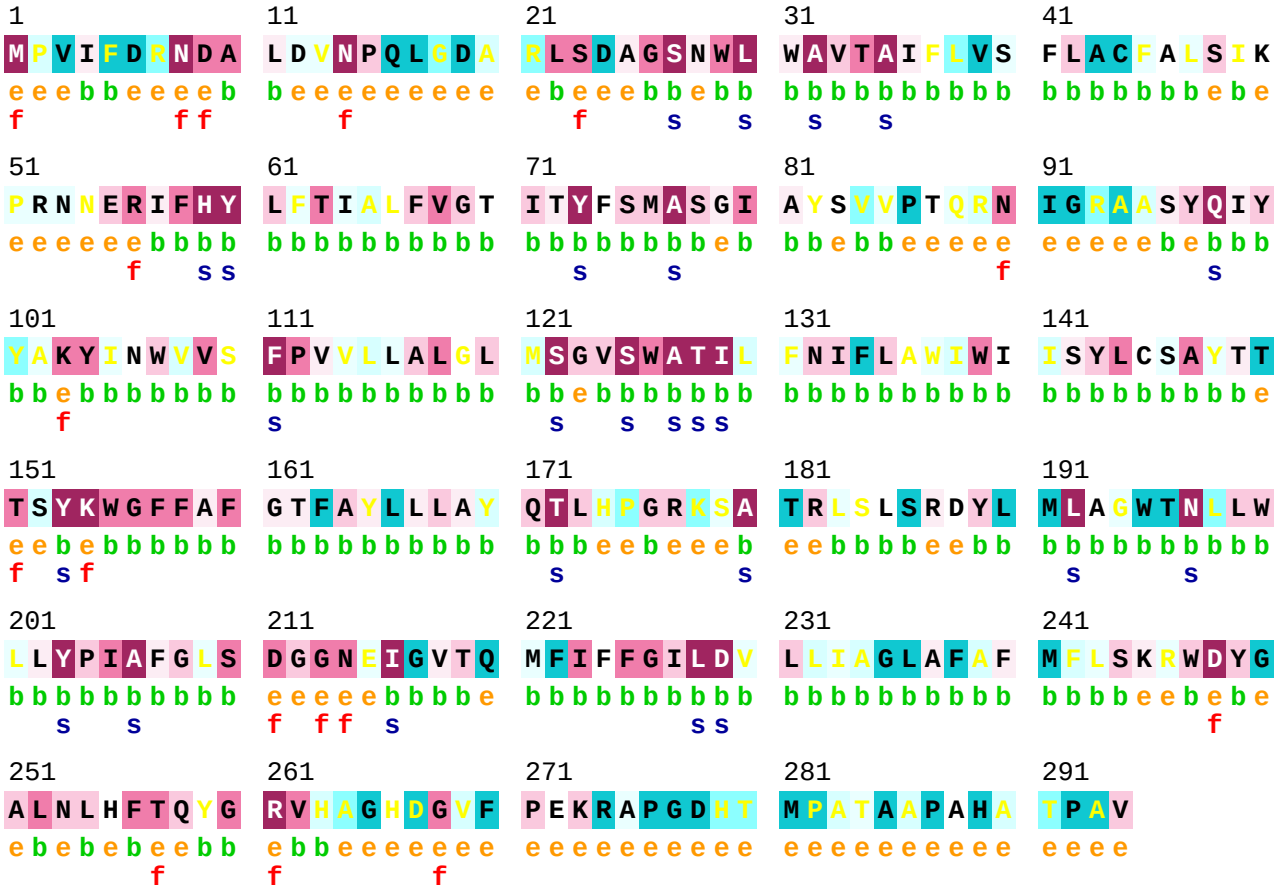
b - A buried residue according to the neural-network algorithm.

f - A predicted functional residue (highly conserved and exposed).

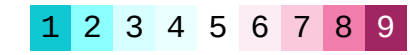
s - A predicted structural residue (highly conserved and buried).

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

ConSurf Results



The conservation scale:



e - An exposed residue according to the neural-network algorithm.

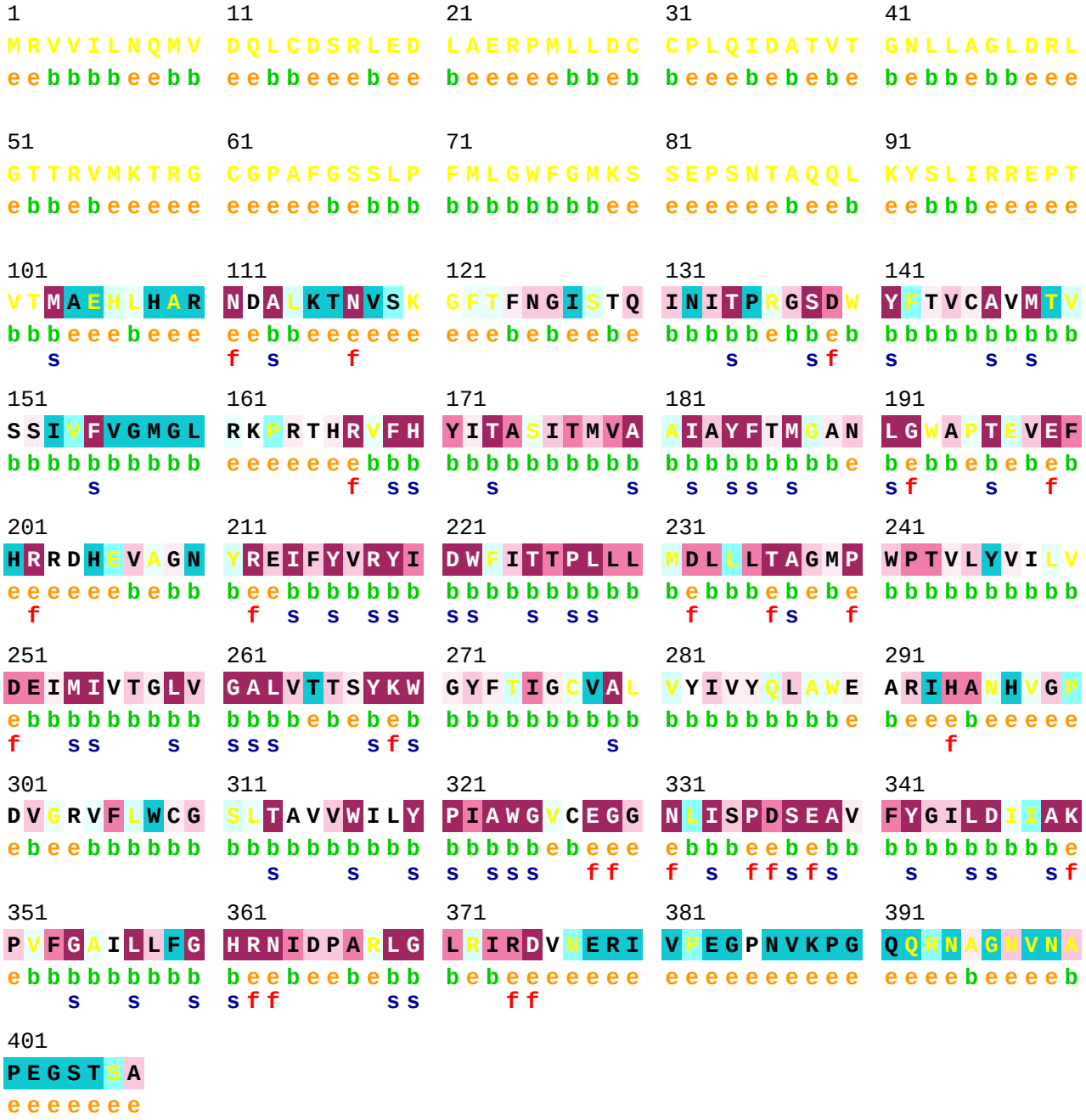
b - A buried residue according to the neural-network algorithm.

f - A predicted functional residue (highly conserved and exposed).

s - A predicted structural residue (highly conserved and buried).

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

ConSurf Results



The conservation scale:

1	2	3	4	5	6	7	8	9

Variable **Average** **Conserved**

e - An exposed residue according to the neural-network algorithm.

b - A buried residue according to the neural-network algorithm.

f - A predicted functional residue (highly conserved and exposed).

s - A predicted structural residue (highly conserved and buried).

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.