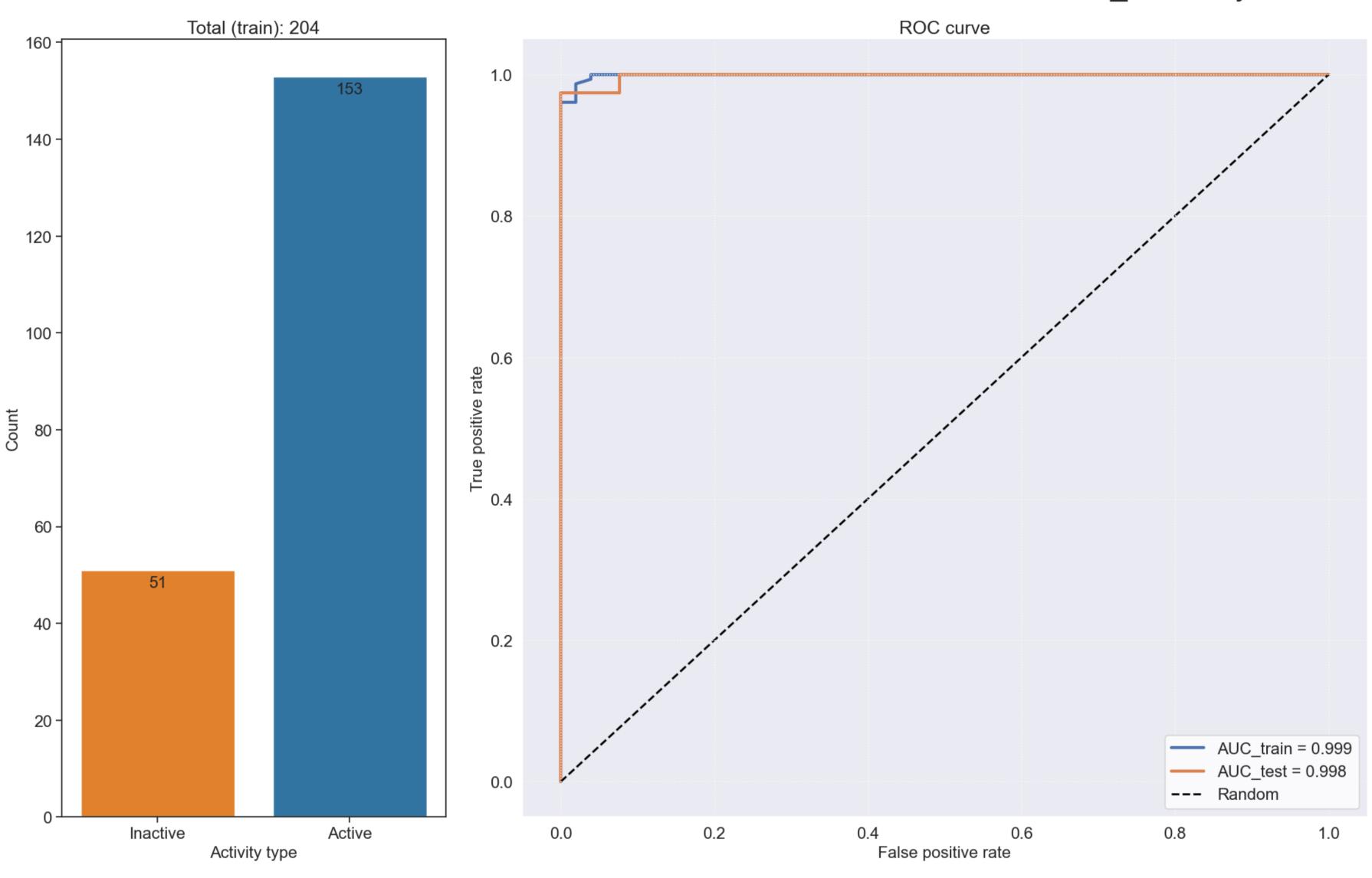
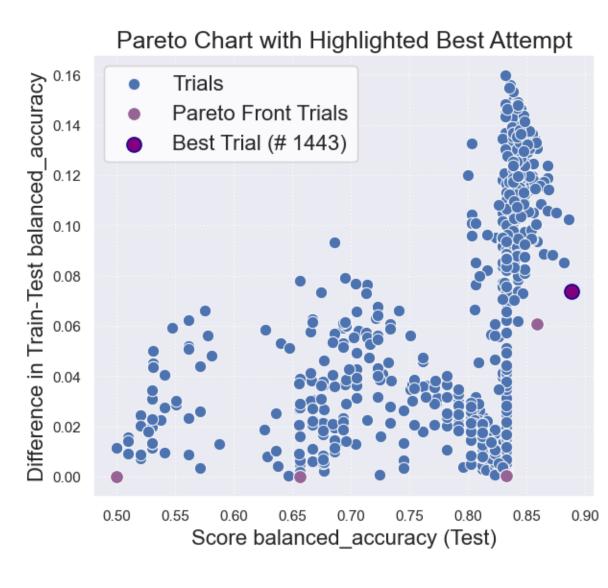
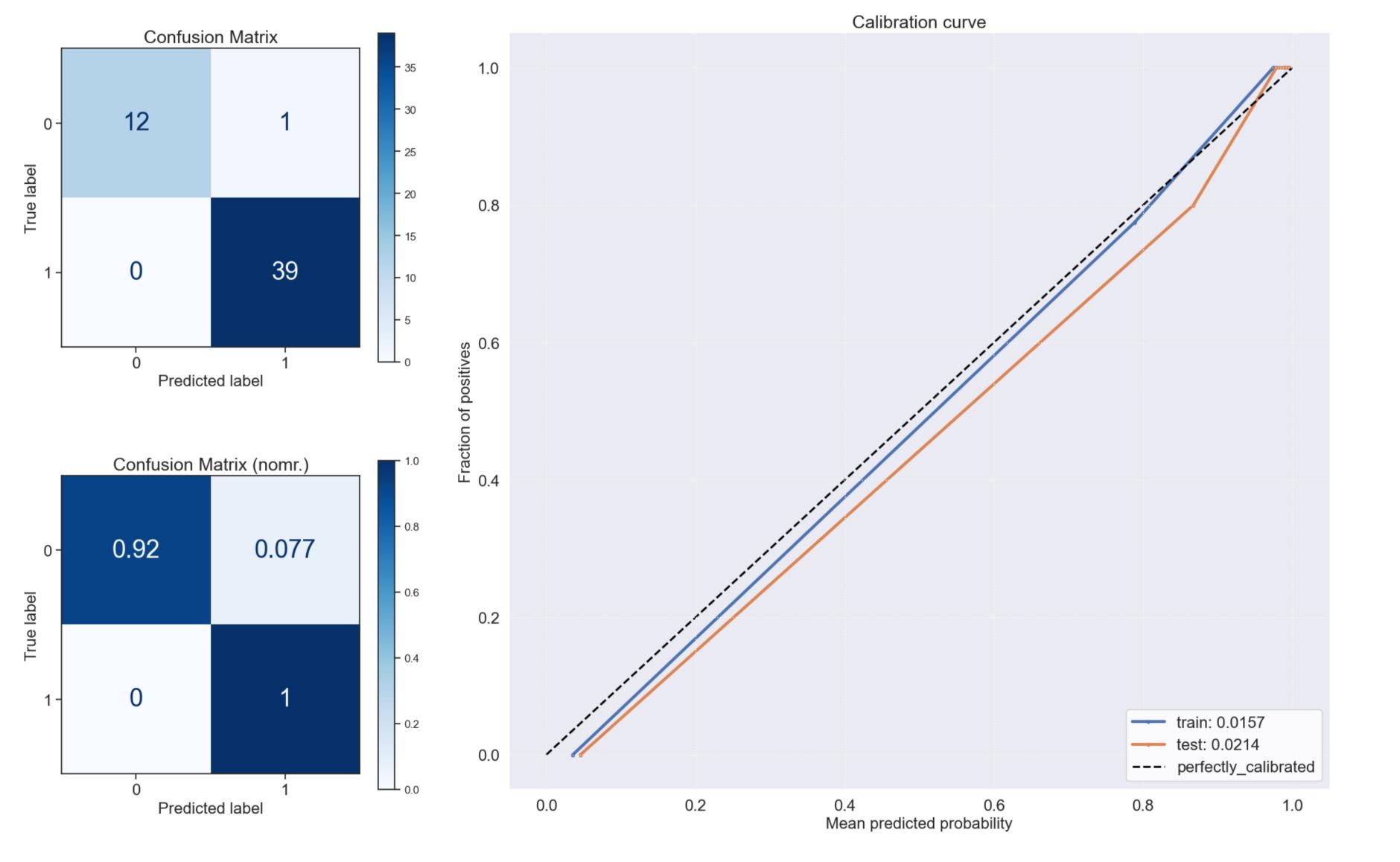
Protein: P29317 - metric: balanced_accuracy





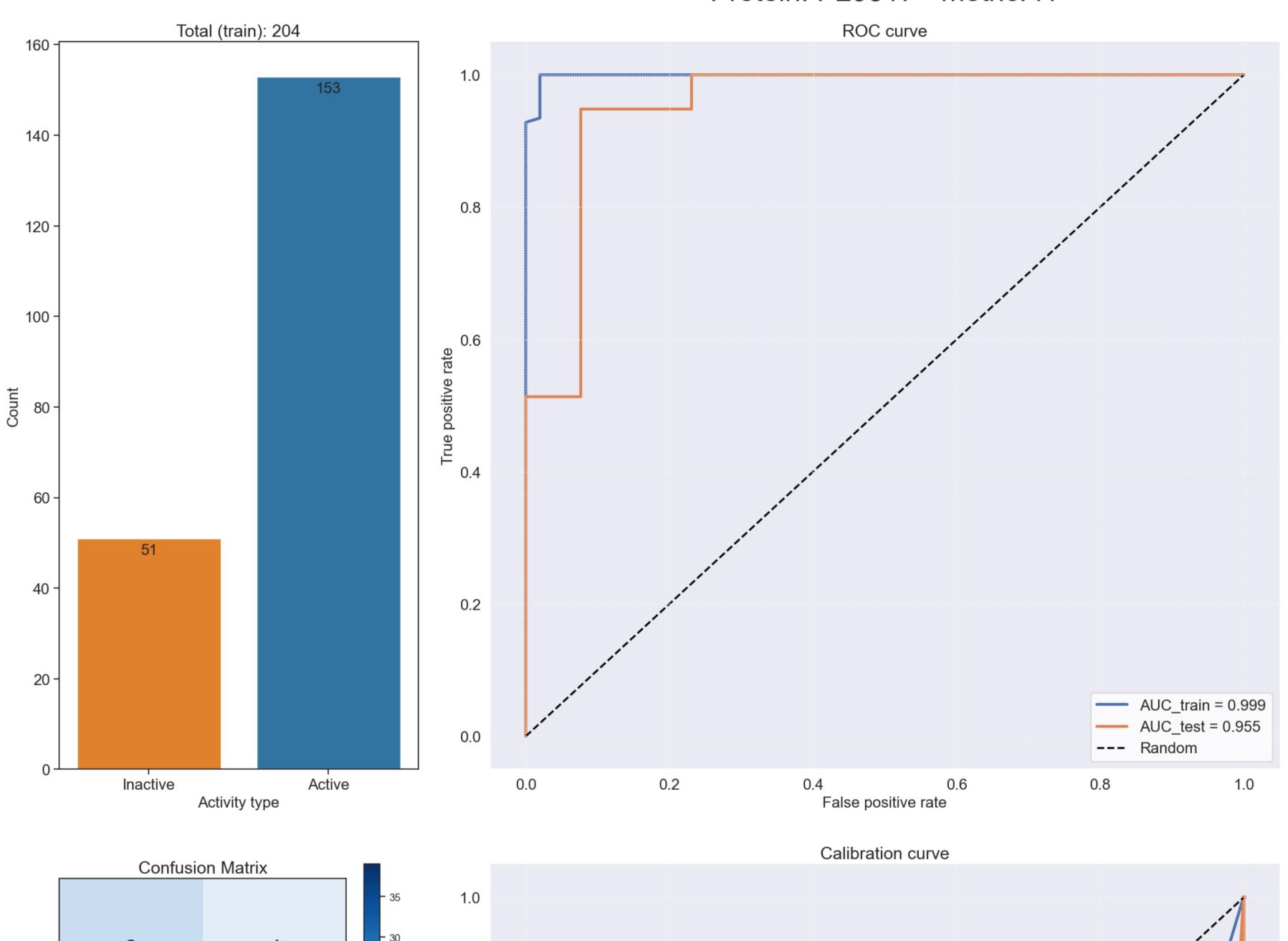
XGBoost Parameters	Value
alpha	2.8189
colsample_bytree	0.592
gamma	0.4424
lambda	1.6954
learning_rate	0.6814
max_depth	6.0
min_child_weight	1.0
n_estimators	111.0
reg_alpha	0.675
reg_lambda	0.3696
scale_pos_weight	1.0198
subsample	0.8813

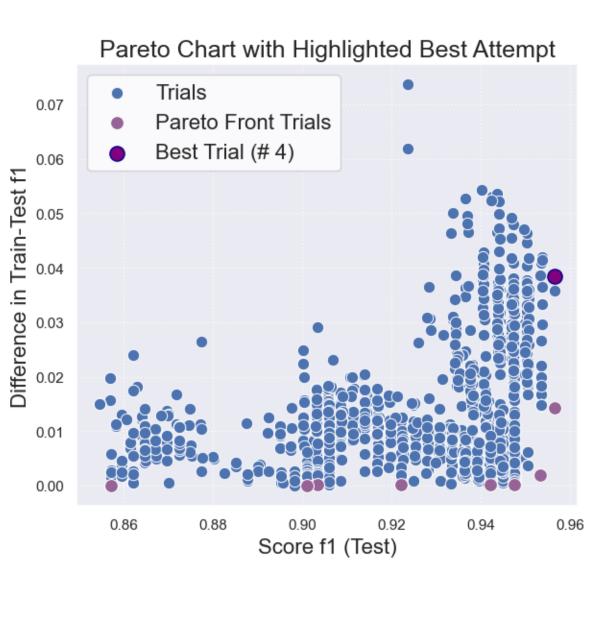


		Active/	Inactive probability		
60	Ina	ctive zone		Active zone	type active (39) inactive (13) decoy (52)
50 -····					
Percent					
20					
0-		.2 0.4	0.6	0.8	10
	0.0	.2 0.4	Probability	0.0	1.0

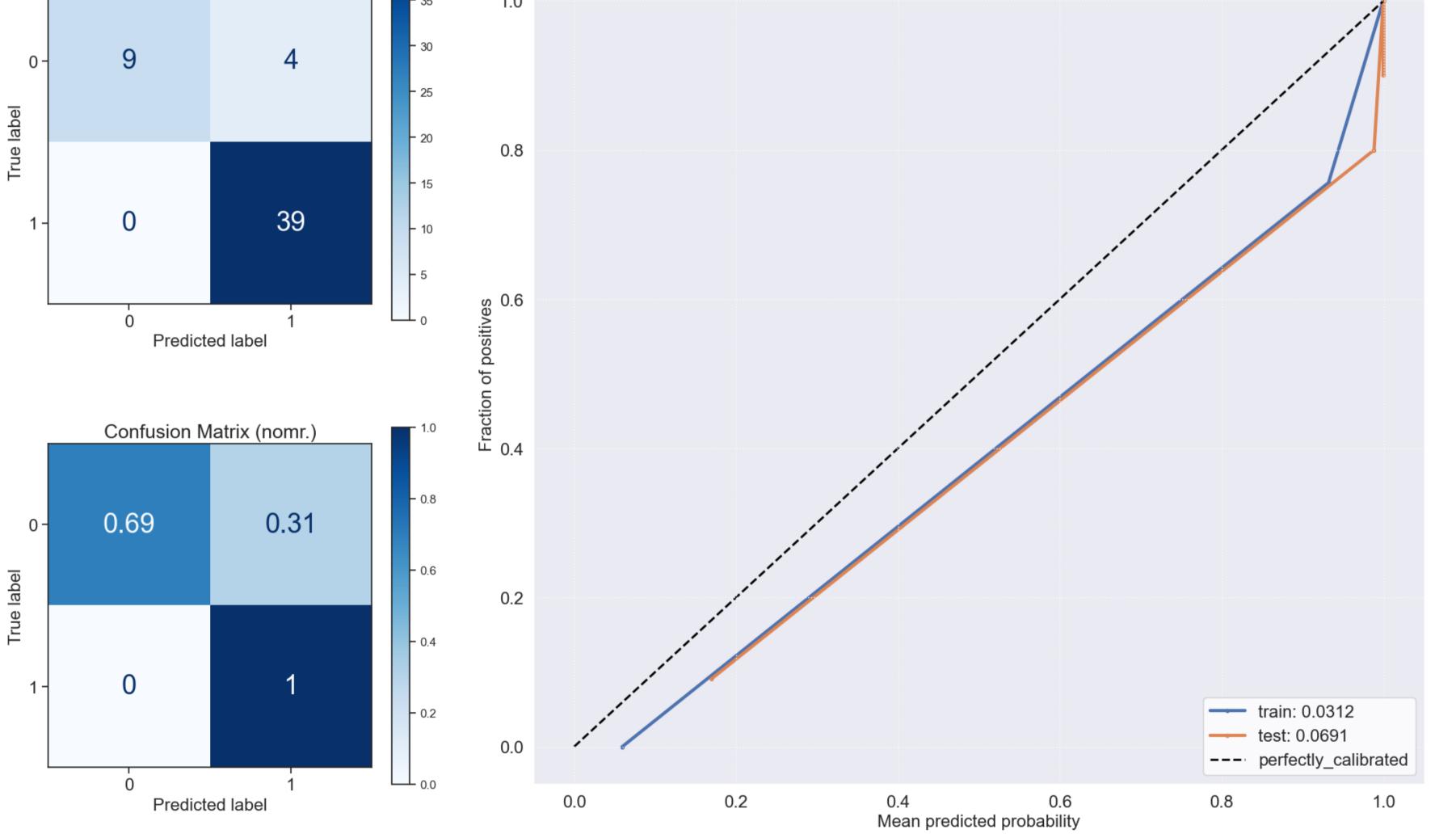
Metric	Train	Test
AUC	0.999	0.998
accuracy	0.9804	0.9808
balanced accuracy	0.9608	0.9615
recall_(sens)	1.0	1.0
specificity	0.9216	0.9231
precision	0.9745	0.975
f1_score	0.9801	0.9805

Protein: P29317 - metric: f1





XGBoost Parameters	Value
alpha	4.1279
colsample_bytree	0.8298
gamma	0.0697
lambda	0.0903
learning_rate	0.2515
max_depth	3.0
min_child_weight	1.0
n_estimators	758.0
reg_alpha	0.5369
reg_lambda	0.498
scale_pos_weight	99.3476
subsample	0.9358

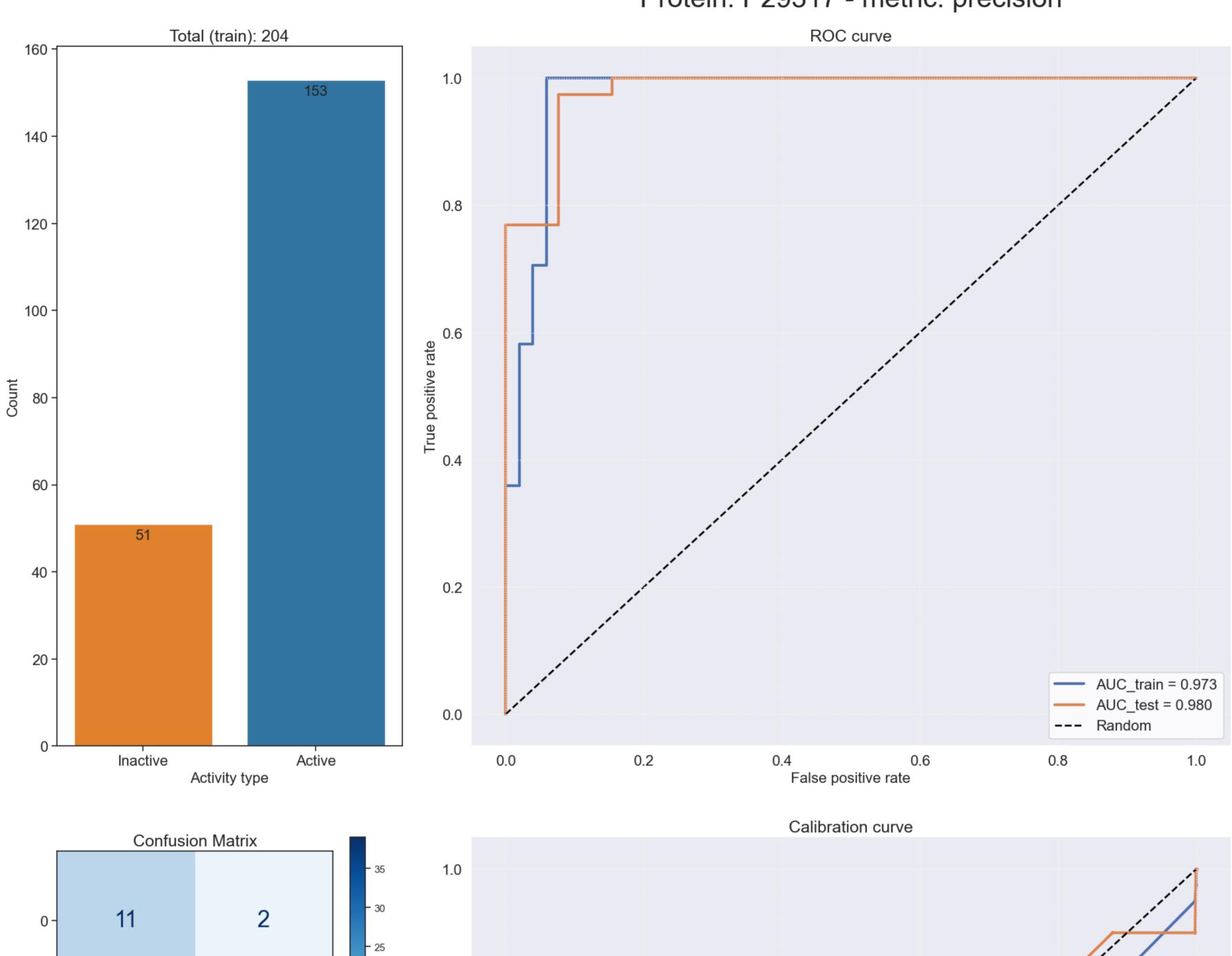


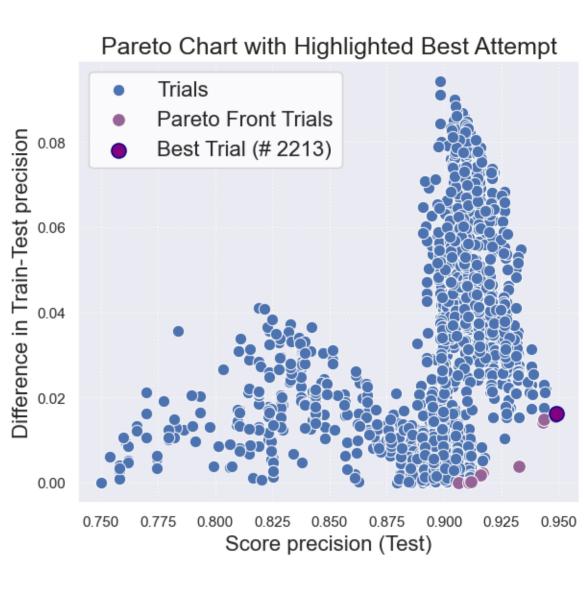
80			active zone		 		ctive zone	type active (39) inactive (13) decoy (52)
Percent					 			
00								
0								
O	0.0	0	.2 0).4 Proba	0 ability).6	0.8	1.0

Active/Inactive probability

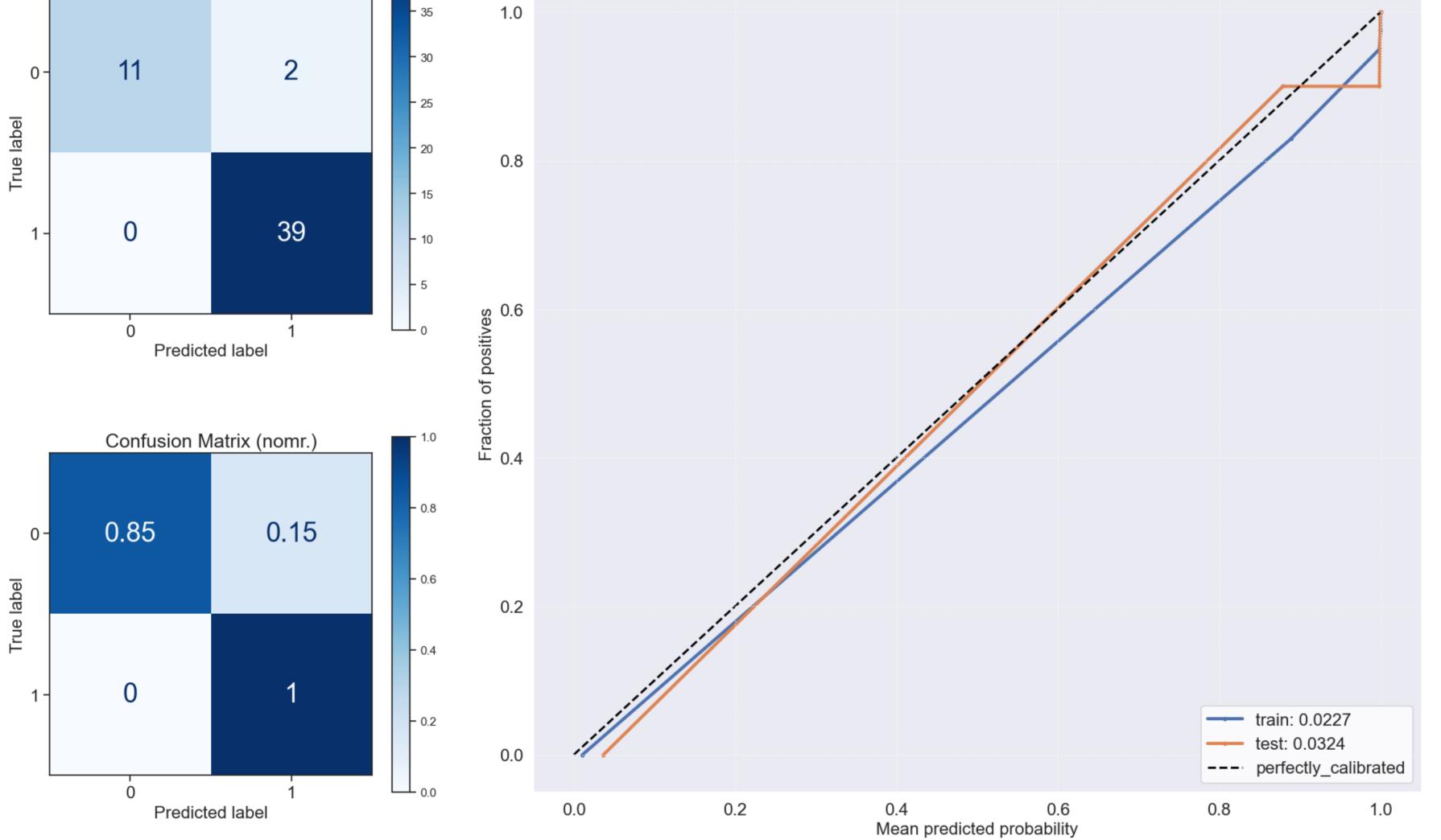
Metric	Train	Test
AUC	0.9987	0.9546
accuracy	0.9559	0.9231
balanced accuracy	0.9118	0.8462
recall_(sens)	1.0	1.0
specificity	0.8235	0.6923
precision	0.9444	0.907
f1_score	0.9544	0.918

Protein: P29317 - metric: precision





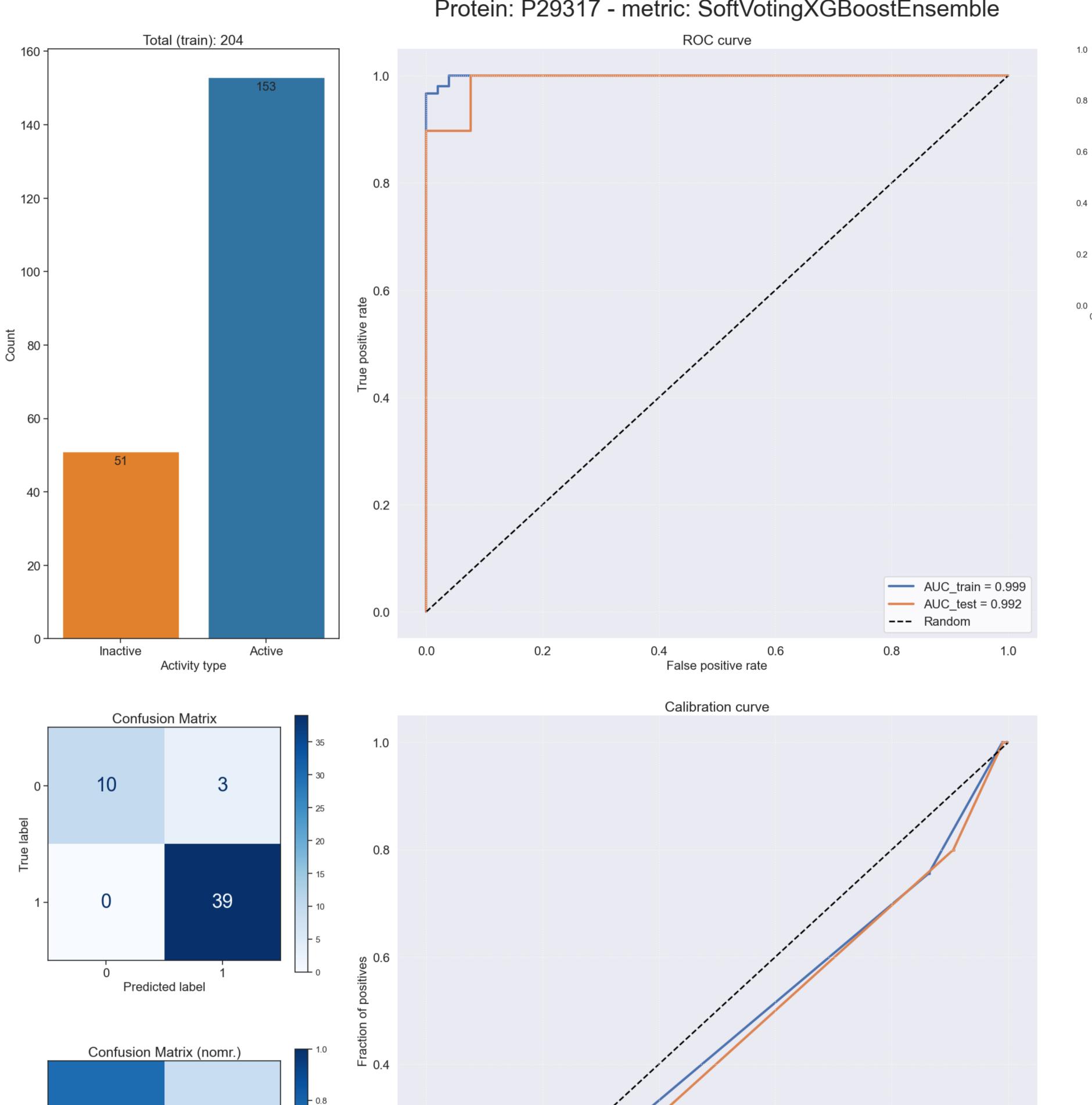
XGBoost Parameters	Value
alpha	1.9388
colsample_bytree	0.6089
gamma	0.9659
lambda	2.2733
learning_rate	0.9659
max_depth	5.0
min_child_weight	3.0
n_estimators	864.0
reg_alpha	0.1189
reg_lambda	0.2629
scale_pos_weight	18.2506
subsample	0.5862

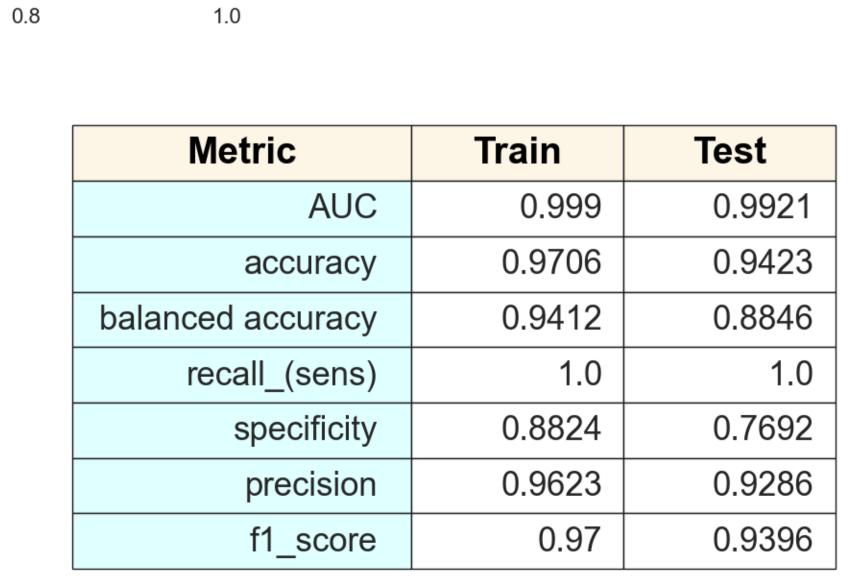


			Active/Inactive	probability		
80		Inactive zone			Active zone	type active (39) inactive (13) decoy (52)
60						
Percent 6	_					
20						
0 —	0.0	0.2	0.4 Probab	0.6	0.8	1.0

Metric	Train	Test
AUC	0.9735	0.9803
accuracy	0.9755	0.9615
balanced accuracy	0.951	0.9231
recall_(sens)	1.0	1.0
specificity	0.902	0.8462
precision	0.9684	0.9512
f1_score	0.9751	0.9604

Protein: P29317 - metric: SoftVotingXGBoostEnsemble





train: 0.0208

- test: 0.0345

0.4 0.6 Mean predicted probability

--- perfectly_calibrated

0.0

0.2

0.6

		Inactive zone				ina dec	ve (39) ctive (13) oy (52)
50							
Percent 05							
30							
40							
0 —	0.0	0.2	0.4	0.6	0.	8	1.0

0.77

0

Predicted label

True label

0.23

- 0.6

0.4

0.2

0.2

0.0

Active/Inactive probability

0.0

0.2