LAMPIRAN 2. Perhitungan Hasil Analisa Kadar Air

Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
Summary (detailed tables shown below)					
Linear	0,1212	0,0272	0,2132	-0,3982	
2FI	0,1640	0,0314	0,3035	-0,8832	Suggested
Quadratic	0,9874	0,0144	0,1077	-2,4444	
Cubic	0,0219	0,0747	0,7293	-3,3259	Aliased

Ket : tabel summary diatas diperoleh dari aplikasi design expert

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Sequential Model Sum of Squares [Type I]						
Mean vs Total	35213,39	1	35213,39			Suggested
Linear vs Mean	34,89	2	17,44	2,63		
2FI vs Linear	13,51	1	13,51	2,30		Suggested
Quadratic vs 2FI	0,19	2	0,096	0,013	0,1212	
Cubic vs Quadratic	41,32	2	20,66	9,04	0,1640	Aliased
Residual	11,43	5	2,29		0,9874	
Total	35314,72	13	2716,52		0,0219	

Ket : tabel sequntial model sum of squares diperoleh dari aplikasi design expert

ANOVA UNTUK RESPONSE SURFACE 2FI MODEL

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Analysis of variance table [Partial sum of squares - Type III]						
Model	48,40	3	16,13	2,74	0,1051	not significant
A-curd protein	24,07	1	24,07	4,09	0,0737	
B-pati modofikasi	10,82	1	10,82	1,84	0,2081	
AB	13,51	1	13,51	2,30	0,1640	
Residual	52,94	9	5,88			
Lack of Fit	48,24	5	9,65	8,22	0,0314	significant
Pure Error	4,69	4	1,17			
Cor Total	101,33	12				

Ket : tabel anova diperoleh dari aplikasi design expert

The Model F-value of 2,74 implies the model is not significant relative to the noise. There is a10,51 % chance that a F-value this large could occur due to noise. Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case there are no significant model terms.Values greater than 0.1000 indicate the model terms are not significant.If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 8,22 implies the Lack of Fit

is significant. There is only a3,14% chance that a "Lack of Fit F-value" this large could occur due to noise.Significant lack of fit is bad -- we want the model to fit.

Std. Dev.	2,43	R-Squared	0,4776
Mean	52,05	Adj R-Squared	0,3035
C.V. %	4,66	Pred R-Squared	-0,8832
PRESS	190,82	Adeq Precision	5,343
-2 Log Likelihood	55,15	BIC	65,41
		AICc	68,15

A negative "Pred R-Squared" implies that the overall mean may be a better predictor of yourresponse than the current model."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Yourratio of 5,343 indicates an adequate signal. This model can be used to navigate the design space.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High	VIF
Intercept	52,05	1	0,67	50,52	53,57	
A-curd protein	-1,73	1	0,86	-3,67	0,20	1,00
B-pati modofikasi	1,16	1	0,86	-0,78	3,10	1,00
AB	1,84	1	1,21	-0,91	4,58	1,00

Final Equation in Terms of Coded Factors:

kadar air =
+52,05
-1,73 * A
+1,16 * B
+1,84 * AB

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficient

Final Equation in Terms of Actual Factors:

kadar air =
+100,84278
-2,18444 * curd protein
-1,60495 * pati modofikasi
+0,073500 * curd protein * pati modofikasi

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of

residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model

Graphs icon.

LAMPIRAN 3. Perhitungan Hasil Analisa Kadar Abu

Summary (detailed tables shown below)				
Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared
Linear	0,1502	0,0707	0,1786	-0,4258	
2FI	0,0560	0,1179	0,4052	-0,4772	Suggested
Quadratic	0,9728	0,0583	0,2412	-1,7003	
Cubic	0,1217	0,0797	0,5425	-6,1674	Aliased

Ket : tabel summary diperoleh dari aplikasi design expert

Sequential Model Sum of Squares [Type I]					
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F
Mean vs Total	101,47	1	101,47			Suggested
Linear vs Mean	5,54	2	2,77	2,31	0,1502	
2FI vs Linear	4,18	1	4,18	4,81	0,0560	Suggested
Quadratic vs 2FI	0,062	2	0,031	0,028	0,9728	
Cubic vs Quadratic	4,42	2	2,21	3,30	0,1217	Aliased
Residual	3,35	5	0,67			
Total	119,02	13	9,16			

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE 2F1 MODEL					
Analysis of variance table [Partial sum of squares - Type III]					
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F
Model	9,72	3	3,24	3,72	0,0545	not significant
A-curd protein	4,04	1	4,04	4,65	0,0595	
B-pati modifikasi	1,49	1	1,49	1,72	0,2225	
AB	4,18	1	4,18	4,81	0,0560	
Residual	7,83	9	0,87			
Lack of Fit	6,41	5	1,28	3,63	0,1179	not significant
Pure Error	1,41	4	0,35			
Cor Total	17,55	12				

Ket : tabel anova diperoleh dari aplikasi design expert

The Model F-value of 3,72 implies there is a 5,45% chance that an F-valuethis large could occur due to noise.Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case there are no significant model terms.Values greater than 0.1000 indicate the model terms are not significant.If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 3,63 implies the Lack of Fit is not significant relative to the pureerror. There is a

11,79% chance that a "Lack of Fit F-value" this large could occur dueto noise. Non-significant lack of fit is good -- we want the model to fit.

Std. Dev.	0,93	R-Squared	0,5539
Mean	2,79	Adj R-Squared	0,4052
C.V. %	33,38	Pred R-Squared	-0,4772
PRESS	25,92	Adeq Precision	6,701
-2 Log Likelihood	30,30	BIC	40,56
		AICc	43,30

A negative "Pred R-Squared" implies that the overall mean may be a better predictor of yourresponse than the current model."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Yourratio of 6,701 indicates an adequate signal. This model can be used to navigate the design space.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High	VIF
Intercept	2,79	1	0,26	2,21	3,38	
A-curd protein	-0,71	1	0,33	-1,46	0,035	1,00
B-pati modifikasi	0,43	1	0,33	-0,31	1,18	1,00
AB	-1,02	1	0,47	-2,08	0,032	1,00

Final Equation in Terms of Coded Factors:

kadar abu	=
+2,79	
-0,71	* A
+0,43	* B
-1,02	* AB

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:

kadar abu	=
-21,37478	
+0,88032	* curd protein
+1,10893	* pati modifikasi
-0,040900	* curd protein * pati modifikasi

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of

residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 4. Perhitungan Hasil Analisa Kadar Lemak

	Summary (detailed tables shown below)				
Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
Linear	0,0003	0,9757	0,7657	0,7405	Suggested
2FI	0,9539	0,9513	0,7397	0,6968	
Quadratic	0,5664	0,9734	0,7155	0,6953	
Cubic	0,9943	0,6794	0,6026	0,2540	Aliased

Ket : tabel summary diperoleh dari aplikasi design expert

	Sequential Model Sum of Squares [Type I]				
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F
Mean vs Total	86,95	1	86,95		
Linear vs Mean	12,89	2	6,44	20,60	0,0003	Suggested
2FI vs Linear	1,225E-003	1	1,225E-003	3,527E-003	0,9539
Quadratic vs 2FI	0,47	2	0,23	0,62	0,5664
Cubic vs Quadratic	6,103E-003	2	3,052E-003	5,754E-003	0,9943	Aliased
Residual	2,65	5	0,53		
Total	102,96	13	7,92		

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE LINEAR MODEL

	Analysis of variance table [Partial sum of squares - Type III]					
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Model	12,89	2	6,44	20,60	0,0003	Significant
A-curd protein	0,10	1	0,10	0,32	0,5823	
B-pati modifikasi	12,79	1	12,79	40,88	< 0.0001	
Residual	3,13	10	0,31			
Lack of Fit	0,60	6	0,10	0,16	0,9757	not significant
Pure Error	2,53	4	0,63			
Cor Total	16,01	12				

Ket : tabel anova diperoleh dari aplikasi design expert

The Model F-value of 20,60 implies the model is significant. There is onlya 0,03% chance that an F-value this large could occur due to noise.Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case B is a significant model term.Values greater than 0.1000 indicate the model terms are not significant. If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 0,16 implies the Lack of Fit is not significant relative to the pureerror. There is a 97,57% chance that a "Lack of Fit F-value" this large could occur dueto noise. Non-significant lack of fit is good -- we want the model to fit.

Std. Dev.	0,56	R-Squared	0,8047
Mean	2,59	Adj R-Squared	0,7657
C.V. %	21,62	Pred R-Squared	0,7405
PRESS	4,16	Adeq Precision	13,310
-2 Log Likelihood	18,37	BIC	26,07
		AICc	27,04

The "Pred R-Squared" of 0,7405 is in reasonable agreement with the "Adj R-Squared" of 0,7657;i.e. the difference is less than 0.2."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Yourratio of 13,310 indicates an adequate signal. This model can be used to navigate the design space.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High	VIF
Intercept	2,59	1	0,16	2,24	2,93	
A-curd protein	0,11	1	0,20	-0,33	0,55	1,00
B-pati modifikasi	1,26	1	0,20	0,82	1,70	1,00

Final Equation in Terms of Coded Factors:
lemak =
+2,59
+0,11 * A
+1,26 * B

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:
lemak =
-4,29698
+0,022478 * curd protein
+0,25285 * pati modifikasi

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 5. Perhitungan Hasil Analisa Kadar Protein

Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
	Summary (detailed tables shown below)				
Linear	< 0.0001	0,7667	0,9532	0,9456	Suggested
2FI	0,9672	0,6865	0,9480	0,9282	
Quadratic	0,1680	0,9520	0,9598	0,9538	
Cubic	0,8627	0,8026	0,9470	0,9413	Aliased

Ket : tabel summary diperoleh dari aplikasi design expert

Source	Sum ofSquares	df	MeanSquare	FValue	p-valueProb > F	
	Sequential Model Sum of Squares [Type I]					
Mean vs Total	4335,65	1	4335,65			
Linear vs Mean	3,11	2	1,55	123,16	< 0.0001	Suggested
2FI vs Linear	2,500E-005	1	2,500E-005	1,785E-003	0,9672	
Quadratic vs 2FI	0,050	2	0,025	2,33	0,1680	
Cubic vs Quadratic	4,342E-003	2	2,171E-003	0,15	0,8627	Aliased
Residual	0,071	5	0,014			
Total	4338,89	13	333,76			

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE LINEAR MODEL

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
	Analysis of variance table [Partial sum of squares - Type III]					
Model	3,11	2	1,55	123,16	< 0.0001	significant
A-curd protein	3,08	1	3,08	244,30	< 0.0001	
B-pati modofikasi	0,025	1	0,025	2,01	0,1865	
Residual	0,13	10	0,013			
Lack of Fit	0,056	6	9,325E-003	0,53	0,7667	not significant
Pure Error	0,070	4	0,018			
Cor Total	3,23	12				

The Model F-value of 123,16 implies the model is significant. There is onlya 0,01% chance that an F-value this large could occur due to noise.Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case A is a significant model term. Values greater than 0.1000 indicate the model terms are not significant. If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 0,53 implies the Lack of Fit is not significant relative to the pureerror. There is a 76,67% chance that a "Lack of Fit F-value" this large could occur dueto noise. Non-significant lack of fit is good -- we want the model to fit.

Std. Dev.	0,11	R-Squared	0,9610
Mean	18,26	Adj R-Squared	0,9532
C.V. %	0,61	Pred R-Squared	0,9456
PRESS	0,18	Adeq Precision	32,537
-2 Log Likelihood	-23,37	BIC	-15,68
		AICc	-14,71

The "Pred R-Squared" of 0,9456 is in reasonable agreement with the "Adj R-Squared" of 0,9532;i.e. the difference is less than 0.2."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Yourratio of 32,537 indicates an adequate signal. This model can be used to navigate the design space.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High	VIF
Intercept	18,26	1	0,031	18,19	18,33	
A-curd protein	0,62	1	0,040	0,53	0,71	1,00
B-pati modofikasi	0,056	1	0,040	-0,032	0,14	1,00

Final Equation in Terms of Coded Factors:

protein	=
+18,26	
+0,62	* A
+0,056	* B

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:

protein	=
+14,87838	
+0,12410	* curd protein
+0,011260	* pati modofikasi

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 6. Perhitungan Hasil Analisa Kadar Karbohidrat

Summary (detailed tables shown below)					
Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
Linear	0,0416	0,0022	0,3647	-0,1477	Suggested
2FI	0,1437	0,0027	0,4507	-0,4744	
Quadratic	0,8381	0,0013	0,3285	-1,7279	
Cubic	0,0179	0,0069	0,8119	-3,3671	Aliased

Ket : tabel summary diperoleh dari aplikasi design expert

Sequential Model Sum of Squares [Type I]						
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Mean vs Total	7830,71	1	7830,71			Suggested
Linear vs Mean	56,21	2	28,11	4,44	0,0416	Suggested
2FI vs Linear	14,03	1	14,03	2,56	0,1437	
Quadratic vs 2FI	2,42	2	1,21	0,18	0,8381	
Cubic vs Quadratic	37,43	2	18,71	10,00	0,0179	Aliased
Residual	9,36	5	1,87			
Total	7950,16	13	611,55			

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE LINEAR MODEL

Analysis of variance table [Partial sum of squares - Type III]						
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Model	56,21	2	28,11	4,44	0,0416	significant
A-curd protein	11,03	1	11,03	1,74	0,2161	
B-pati modifikasi	45,19	1	45,19	7,15	0,0234	
Residual	63,24	10	6,32			
Lack of Fit	62,00	6	10,33	33,32	0,0022	significant
Pure Error	1,24	4	0,31			
Cor Total	119,45	12				

The Model F-value of 4,44 implies the model is significant. There is onlya 4,16% chance that an F-value this large could occur due to noise.Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case B is a significant model term.Values greater than 0.1000 indicate the model terms are not significant. If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 33,32 implies the Lack of Fit is significant. There is only a0,22% chance that a "Lack of Fit F-value" this large could occur due to noise.Significant lack of fit is bad -- we want the model to fit.

Std. Dev.	2,51	R-Squared	0,4706
Mean	24,54	Adj R-Squared	0,3647
C.V. %	10,25	Pred R-Squared	-0,1477
PRESS	137,10	Adeq Precision	5,878
-2 Log Likelihood	57,46	BIC	65,15
		AICc	66,12

A negative "Pred R-Squared" implies that the overall mean may be a better predictor of yourresponse than the current model."Adeq Precision" measures the signal to noise ratio. A ratio greater than 4 is desirable. Yourratio of 5,878 indicates an adequate signal. This model can be used to navigate the design space.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High	VIF
Intercept	24,54	1	0,70	22,99	26,10	
A-curd protein	1,17	1	0,89	-0,81	3,15	1,00
B-pati modifikasi	-2,38	1	0,89	-4,36	-0,40	1,00

Final Equation in Terms of Coded Factors:

karbohidrat   =
+24,54
+1,17   * A
-2,38   * B

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:

karbohidrat   =
+30,55637
+0,23480   * curd protein
-0,47533   * pati modifikasi

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 7. Perhitungan Hasil Analisa Nilai Tekstur

Summary (detailed tables shown below)

Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
Mean	< 0.0001				Suggested
Linear	0,7251	0,5347	-0,1253	-0,6757	
2FI	0,9321	0,4522	-0,2492	-1,2036	
Quadratic	0,3864	0,4256	-0,2241	-1,9663	
Cubic	0,6431	0,2047	-0,4363	-13,5427	Aliased

Ket : tabel summary diperoleh dari aplikasi design expert

Sequential Model Sum of Squares [Type I]						
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Mean vs Total	0,068	1	0,068			Suggested
Linear vs Mean	7,790E-005	2	3,895E-005	0,33	0,7251	
2FI vs Linear	1,000E-006	1	1,000E-006	7,679E-003	0,9321	
Quadratic vs 2FI	2,788E-004	2	1,394E-004	1,09	0,3864	
Cubic vs Quadratic	1,446E-004	2	7,229E-005	0,48	0,6431	Aliased
Residual	7,486E-004	5	1,497E-004			
Total	0,069	13	5,315E-003			

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE MEAN MODEL

Analysis of variance table [Partial sum of squares - Type III]						
Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Model	0,000	0				
Residual	1,251E-003	12	1,042E-004			
Lack of Fit	*7,749E-004*	*8*	*9,686E-005*	*0,81*	*0,6285*	*not significant*
Pure Error	*4,759E-004*	*4*	*1,190E-004*			
Cor Total	1,251E-003	12				

Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case there are no significant model terms.Values greater than 0.1000 indicate the model terms are not significant.If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 0,81 implies the Lack of Fit is not significant relative to the pureerror. There is a 62,85% chance that a "Lack of Fit F-value" this large could occur dueto noise. Non-significant lack of fit is good -- we want the model to fit.

Std. Dev.	0,010	R-Squared	0,0000
Mean	0,072	Adj R-Squared	0,0000
C.V. %	14,13	Pred R-Squared	-0,1736
PRESS	1,468E-003	Adeq Precision	
-2 Log Likelihood	-83,34	BIC	-80,78
		AICc	-80,98

A negative "Pred R-Squared" implies that the overall mean may be a better predictor of yourresponse than the current model.

Factor	Coefficient Estimate	df	Standard Error	95% CI Low	95% CI High
Intercept	0,072	1	2,832E-003	0,066	0,078

Final Equation in Terms of Coded Factors:

tekstur =
+0,072

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:

tekstur =
+0,072238

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 8. Perhitungan Hasil Analisa nilai warna

Source	Sequential p-value	Lack of Fit p-value	Adjusted R-Squared	Predicted R-Squared	
Summary (detailed tables shown below)					
Mean	< 0.0001				Suggested
Linear	0,7749	0,5467	-0,1403	-0,5910	
2FI	0,5991	0,4851	-0,2266	-1,5435	
Quadratic	0,4999	0,4078	-0,2936	-2,1897	

Ket : tabel summary diperoleh dari aplikasi design expert

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Sequential Model Sum of Squares [Type I]						
Mean vs Total	12023,81	1	12023,81			Suggested
Linear vs Mean	22,92	2	11,46	0,26	0,7749	
2FI vs Linear	13,99	1	13,99	0,30	0,5991	
Quadratic vs 2FI	76,23	2	38,11	0,77	0,4999	
Residual	241,79	5	48,36			
Total	12484,87	13	960,37			

Ket : tabel sequential model sum of squares diperoleh dari aplikasi design expert

ANOVA FOR RESPONSE SURFACE MEAN MODEL

Source	Sum of Squares	df	Mean Square	F Value	p-value Prob > F	
Analysis of variance table [Partial sum of squares - Type III]						
Model	0,000	0				
Residual	461,06	12	38,42			
Lack of Fit	*280,21*	*8*	*35,03*	*0,77*	*0,6495*	*not significant*
Pure Error	*180,85*	*4*	*45,21*			
Cor Total	461,06	12				

Ket : tabel anova diperoleh dari aplikasi design expert

Values of "Prob > F" less than 0,0500 indicate model terms are significant.In this case there are no significant model terms.Values greater than 0.1000 indicate the model terms are not significant.If there are many insignificant model terms (not counting those required to support hierarchy),model reduction may improve your model.The "Lack of Fit F-value" of 0,77 implies the Lack of Fit is not significant relative to the pureerror. There is a 64,95% chance that a "Lack of Fit F-value" this large could occur dueto noise. Non-significant lack of fit is good -- we want the model to fit.

Std. Dev.	6,20	R-Squared	0,0000
Mean	30,41	Adj R-Squared	0,0000
C.V. %	20,38	Pred R-Squared	-0,1736
PRESS	541,11	Adeq Precision	
-2 Log Likelihood	83,28	BIC	85,85
		AICc	85,65

A negative "Pred R-Squared" implies that the overall mean may be a better predictor of yourresponse than the current model.

Factor	Coefficient Estimate	Df	Standard Error	95% CI Low	95% CI High
Intercept	30,41	1	1,72	26,67	34,16

Final Equation in Terms of Coded Factors:

$$warna = +30,41$$

The equation in terms of coded factors can be used to make predictions about the response forgiven levels of each factor. By default, the high levels of the factors are coded as +1 and thelow levels of the factors are coded as -1. The coded equation is useful for identifying therelative impact of the factors by comparing the factor coefficients.

Final Equation in Terms of Actual Factors:

$$warna = +30,41231$$

The equation in terms of actual factors can be used to make predictions about the response forgiven levels of each factor. Here, the levels should be specified in the original units foreach factor. This equation should not be used to determine the relative impact of each factorbecause the coefficients are scaled to accommodate the units of each factor and the interceptis not at the center of the design space.

Proceed to Diagnostic Plots (the next icon in progression). Be sure to look at the:

1) Normal probability plot of the studentized residuals to check for normality of residuals.

2) Studentized residuals versus predicted values to check for constant error.

3) Externally Studentized Residuals to look for outliers, i.e., influential values.

4) Box-Cox plot for power transformations.

If all the model statistics and diagnostic plots are OK, finish up with the Model Graphs icon.

Lampiran 9. Hasil Optimum

No	c. protein	p. modifikasi	air	Abu	protein	lemak	karbo hidrat	warna	tekstur	Desirability	
1	30,000	30,000	53,311	1,493	18,939	3,963	23,340	30,412	0,072	0,931	Selected
2	29,998	29,960	53,287	1,498	18,938	3,953	23,359	30,412	0,072	0,931	
3	30,000	21,578	48,257	2,487	18,844	1,833	27,344	30,412	0,072	0,834	
4	30,000	21,020	47,923	2,553	18,838	1,692	27,609	30,412	0,072	0,825	

Number of Starting Points: 105	
curd protein	**pati modifikasi**
25	25
30	30
20	20
20	30
30	20
29,1968	27,673
27,2991	26,1923
20,3646	27,498
27,6654	28,396
22,4295	28,722
20,3217	22,161
20,7382	28,6125
27,9134	23,2708
21,3144	22,7414
21,2838	22,4181
20,2859	20,7342
21,9593	20,859
24,7049	26,5498
21,0862	26,7127
20,3624	26,3603
22,3333	23,5984
28,9515	28,8216
29,4594	25,9941
28,3372	25,1621
23,8747	24,9466
26,9649	20,2877
28,8204	24,8299
28,756	24,3118
27,5383	24,1219
28,5787	24,8369
27,6948	22,4233

28,1448	23,3052
27,9867	20,9165
21,5231	25,8606
26,1688	21,1064
21,2037	26,397
27,1195	23,8704
29,6121	29,3331
28,0143	24,3744
29,9845	24,3527
23,4241	28,0839
22,8096	23,8608
21,6645	28,5326
29,1609	28,6177
26,3096	20,4338
23,5325	29,4377
25,7321	28,3365
26,3335	29,7694
22,7613	28,7707
24,1899	28,6701
28,2303	29,1373
22,4387	21,5692
20,2302	21,2658
29,7038	28,7645
24,0791	23,298
27,3939	24,614
25,7534	24,4539
26,9426	27,9384
24,7103	27,1533
23,4852	27,5968
21,4387	28,7804
20,2032	20,7519
21,481	23,6487
22,0835	22,2727
28,0849	20,607
28,9434	29,201
26,5225	25,8364
27,2358	28,1165
23,903	20,2969
24,7526	29,0357
26,5069	26,0046
24,0526	22,47

20,1039	26,6405
26,4075	21,0177
23,3401	27,0864
21,1451	26,3263
24,9778	24,8459
25,033	27,0664
27,7336	23,9509
22,2562	26,4108
26,3382	23,39
21,4261	22,35
23,7807	23,7904
22,5342	29,1993
22,5146	28,6399
25,899	22,2664
29,7001	28,8024
27,3856	24,8269
20,2133	25,1615
25,0878	26,6484
28,3654	25,2845
20,4188	22,3147
20,3613	23,375
20,2707	29,3988
20,0579	27,574
29,2808	27,4489
27,6046	22,2241
26,8852	27,934
25,1363	28,6822
27,2819	21,2105
26,6758	23,1104
23,6166	28,7737
28,0371	21,6871
23,8367	25,8536
27,2149	21,6648