

Dataset-Level Metadata for *VISIT_R*

Variable	Value
DESCRIPTION	
KEYFIELDS	
STRUCTURE	
INPUT_NOTES	<ol style="list-style-type: none">1. For all data sets with "Raw." libnames, the library location is: "S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive"2. For all data sets with "Der." libnames, the library location is: "S:\RhoFED\CSCC\Protocol Committees\Arginine2\data\derive"3. Merge Der.Add_Pt with: RAW.VISIT,, by CSCC_ID --> DER.VISIT_R
OUTPUT_NOTES	

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
1	ABECHDT	999	N8	Date of most recent abnormal ECHO	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:08	No
2	ABEFRAC	999	N8	Ejection Fraction -Abnormal	Notes: #Imported from CSCC Arginine	2.		Yes
3	ABENOT	999	C1	Ejection Fraction, Not reported -Abnormal	Notes: #Imported from CSCC Arginine	\$1.		Yes
4	ABJETUN	999	N8	TR Jet Undetectable -Abnormal	Notes: #Imported from CSCC Arginine	1.		Yes
5	ABLVH	999	C3	LVH -Abnormal	Notes: #Imported from CSCC Arginine	\$3.		Yes
6	ABRVH	999	C3	RVH -Abnormal	Notes: #Imported from CSCC Arginine	\$3.		Yes
7	ABSFRAC	999	N8	Shortening Fraction -Abnormal	Notes: #Imported from CSCC Arginine	2.		Yes
8	ABSRETICCN T	999	N8	Absolute Retic Count	Notes: #Imported from CSCC Arginine	3.		Yes
9	ABSRETICCN THIGH	999	N8	Absolute Retic Count upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
10	ABSRETICCN TLOW	999	N8	Absolute Retic Count lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
11	ABSRETICCN T_NA	999	C8	Absolute Retic Count - Normal or Abnormal	= ' ' if (AbsReticCnt or AbsReticCntLow or AbsReticCntHigh)=. ~= 'Normal' if AbsReticCntLow LE AbsReticCnt LE AbsReticCntHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
12	ABSTNOT	999	C1	Shortening Fraction, Not reported -Abnormal	Notes: #Imported from CSCC Arginine	\$1.		Yes
13	ABTRJET	999	N8	TR Jet- Abnormal	Notes: #Imported from CSCC Arginine	8.2		Yes
14	AB_ECHO_ DAY	999	N8	Day (relative to 1st day of Study drug) of most recent abnormal ECHO	=Der.Visit_R.abechdt-Der.ADD_PT.PT_Start_date+1 Notes: New Variable	8.	12JUN09:16:50	Yes
15	AE_CYS_ INT_STD_ _	999	N8	AE_Cys__int_std_ (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
16	AGE	999	N3	Age	Notes: #Imported from CSCC Arginine	3.	12JUN09:16:17	No
17	AGE_GROUP	2	C5	Age Group	Notes: #Imported from CSCC Arginine	\$5.	26JUN09:10:33	Yes
18	AGE_TRUNC	3	N3	All ages >45 years are recoded to 45.0	if Der.Visit_R.age>45.0 then Der.visit_R.Age_trunc=45; Else Der.visit_R.Age_trunc=Der.Visit_R.age; Notes: New Variable	3.	26JUN09:10:33	Yes
19	ALANINE	999	N8	Alanine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
20	ALBUMIN	999	N8	Albumin (g/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62); Notes: #Imported from CSCC Arginine	8.1		Yes
21	ALBUMINHIG H	999	N8	Albumin (g/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
22	ALBUMINLO W	999	N8	Albumin (g/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
23	ALBUMIN_NA	999	C8	Albumin (g/dL) - Normal or Abnormal	= ' ' if (Albumin or AlbuminLow or AlbuminHigh)=. -= 'Normal' if AlbuminLow LE Albumin LE AlbuminHigh -= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
24	ALKPHOSPH	999	N8	Alk Phosphatase (IU/L)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1(HC62); Notes: #Imported from CSCC Arginine	8.		Yes
25	ALKPHOSPH HIGH	999	N8	Alk Phosphatase (IU/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
26	ALKPHOSPH LOW	999	N8	Alk Phosphatase (IU/L) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
27	ALKPHOSPH _NA	999	C8	Alk Phosphatase (IU/L) - Normal or Abnormal	= ' ' if (AlkPhosph or AlkPhosphLow or AlkPhosphHigh)=. -= 'Normal' if AlkPhosphLow LE AlkPhosph LE AlkPhosphHigh -= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
28	ALKPHOSPH_NORM1	999	N8	Norm ALKPHOSPH - LS Bakerman	<p>=30+(ALKPHOSPH-ALKPHOSPHLOW)*((35-30)/(ALKPHOSPHHIGH-ALKPHOSPHLOW)), IF ALKPHOSPH_NORM1<0 THEN ALKPHOSPH_NORM1=0</p> <p>Description: Normalized ALKPHOSPH Values Using Location-Scale Model and Bakerman's Limits</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
29	ALKPHOSPH_NORM2	999	N8	Norm ALKPHOSPH - S Bakerman	<p>=ALKPHOSPH*(35/ALKPHOSPHHIGH)</p> <p>Description: Normalized ALKPHOSPH Values Using Scale Model and Bakerman's Upper Limits</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
30	ALKPHOSPH_NORM3	999	N8	Norm ALKPHOSPH - LS Phantom Lab	<p>=20+(ALKPHOSPH-ALKPHOSPHLOW)*((530-20)/(ALKPHOSPHHIGH-ALKPHOSPHLOW)), IF ALKPHOSPH_NORM3<0 THEN ALKPHOSPH_NORM3=0</p> <p>Description: Normalized ALKPHOSPH Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
31	ALKPHOSPH_NORM4	999	N8	Norm ALKPHOSPH - ECDF	<p>Take all ALKPHOSPH values and separate by site. Rank and find percentiles by dividing by (number of records+1) and multiply by 100. Then use the following code:</p> <p>a/ alkphosph_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/alkphosph_oak is the data we are transforming the oakland data to. c/alkphosph_duk is the data that is being transformed. Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need values and percentile ranks</p> <p>proc iml;</p> <p>use alkphosph_duk_base; read all var {alkphosph_a perca} into aam;</p> <p>use alkphosph_oak; read all var {alkphosph_b perc} into</p>	8.2		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
31	ALKPHOSPH_NORM4				<pre> bbm; use alkphosph_duk; read all var {alkphosph_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the following] do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm [i,1]-aam[j,1])+aam[j,2]; end; end; [end] do i=1 to nc; if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob [i,2]-bbm[j,2])+bbm[j,1]; end; end; </pre>			

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
31	ALKPHOSPH_NORM4				<p>names={result percent}; create naam from aam [colname=names]; append from aam; create nbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob;</p> <p>quit;</p> <p>Description: Normalized ALKPHOSPH Values Using ECDF</p> <p>Notes: #Imported from CSCC Arginine</p>			
32	ALT	999	N8	ALT (IU/L)	<p>=. if CSCC_ID = '1000021' and VISIT_NUM = 1(HC62);</p> <p>Notes: #Imported from CSCC Arginine</p>	8.		Yes
33	ALTHIGH	999	N8	ALT (IU/L) upper limit of normal range	<p>Description: copy to all observations for that subject</p> <p>Notes: #Imported from CSCC Arginine</p>	8.		Yes
34	ALTLow	999	N8	ALT (IU/L) lower limit of normal range	<p>Description: copy to all observations for that subject</p> <p>Notes: #Imported from CSCC Arginine</p>	8.		Yes
35	ALT_LLOD	999	N8	ALT - Value below Limit of Detection (10 IU/L)	<p>=1 if (CSCC_ID=0000011 and PHASE=2000) or (CSCC_ID=0000022 and PHASE in (2200)) or (CSCC_ID=0000097 and PHASE=2200) or (CSCC_ID=0000104 and PHASE=2000) or (CSCC_ID=0000132 and PHASE in(2000 2100 2200 2500)) or (CSCC_ID=0000033 and PHASE=2700) (HC24, HC27, HC30, HC31, HC32-35, HC28); ~=0 otherwise</p> <p>Notes: #Imported from CSCC Arginine</p>	1.		Yes
36	ALT_NA	999	C8	ALT (IU/L) - Normal or Abnormal	<p>= ' ' if (ALT or ALTLow or ALTHigh)=. ~= 'Normal' if ALTLow LE ALT LE ALTHigh ~= 'Abnormal' otherwise</p> <p>Notes: #Imported from CSCC Arginine</p>	\$8.		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
37	AMMONIA	999	N8	Ammonia (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
38	APNOT	999	C1	Right Venticular to Right Atrial Difference, Not Reported -Abnormal	Notes: #Imported from CSCC Arginine	\$1.		Yes
39	ARGINASE	999	N8	Arginase (ng/mL)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
40	ARGINASE_ADJ	999	N8	Arginase (ng/mL) - adjusted values when above LOD	=2560 if ARGINASE_UDL=1 ~=ARGINASE otherwise Notes: #Imported from CSCC Arginine	8.1		Yes
41	ARGINASE_UDL	999	N8	Arginase measure above Limit of Detection (>2560)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	1.		Yes
42	ARGININE	999	N8	Arginine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
43	ARG_CIT	999	N8	Arginine to Citruline Ratio	=ARGINE / CITRULLINE Notes: #Imported from CSCC Arginine	8.3		Yes
44	ARG_ORN	999	N8	Arginine to Ornithine Ratio	=ARGININE / ORNITHINE Notes: #Imported from CSCC Arginine	8.3		Yes
45	ARVTRAD	999	N8	Right Venticular to Right Atrial Difference -Abnormal	Notes: #Imported from CSCC Arginine	3.		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
46	ASPARAGINE	999	N8	Asparagine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
47	ASPARTIC_ACID	999	N8	Aspartic_Acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
48	A_AMINOADIPIC_ACID	999	N8	a_Amino adipic acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
49	A_AMINO_N_BUTYRIC_ACID	999	N8	a_Amino_n_butyric acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
50	A_ARETICCNT	999	N8	Advia - Absolute Reticulocyte Count (x10^9 cells/L)	=ADVIA.ABSRETICCNT; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.3		Yes
51	A_CH	999	N8	Advia - Cellular Hemoglobin (pg)	=ADVIA.CH; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
52	A_CHCM	999	N8	Advia - Cellular Hemoglobin Concentration Mean (g/dL)	=ADVIA.CHCM; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes

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53	A_GARDOS	999	N8	Advia - Gardos Channel Activity (mmol/10 ¹³ cells x min)	=ADVIA.GARDOS; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.3		Yes
54	A_HCT	999	N8	Advia - Hematocrit (%)	=ADVIA.HCT; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
55	A_HGB	999	N8	Advia - Hemoglobin (g/dL)	=ADVIA.HGB; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
56	A_HGB_HIGH	999	N8	Advia - Hemoglobin (g/dL) >=13	=1 if ADVIA.HGB ge 13; Notes: #Imported from CSCC Arginine	1.		Yes
57	A_HGB_ORIGINAL	999	N8	Advia - Hemoglobin (g/dL)	=ADVIA.HGB; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
58	A_MCH	999	N8	Advia - Mean Corpuscular Hemoglobin (pg)	=ADVIA.MCH; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
59	A_MCHC	999	N8	Advia - Mean Corpuscular Hemoglobin Concentration (g/dL)	=ADVIA.MCHC; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
60	A_MCV	999	N8	Advia - Mean Corpuscular Volume (fL)	=ADVIA.MCV; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
61	A_M_CHCM	999	N8	Advia - Cellular Hemoglobin Concentration Mean - Mature (g/dL)	=ADVIA.M_CHCM; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
62	A_M_MCV	999	N8	Advia - Mean Corpuscular Volume - Mature (fL)	=ADVIA.M_MCV; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
63	A_PERCBA	999	N8	Advia - Percent Hemoglobin A (%)	=ADVIA.PERCBA; ~= ' ' if ADVIA.HGB ge 13; Notes: #Imported from CSCC Arginine	8.1		Yes
64	A_PF	999	N8	Advia - Percent HbF (%)	=ADVIA.PERCF; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.5		Yes
65	A_PHYPER	999	N8	Advia - Percent of RBCs with density (CHCM) greater than 41 g/dl (%)	=ADVIA.PERCHYPER; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
66	A_PRETIC	999	N8	Advia - Reticulocyte Percentage (%)	=ADVIA.PERCRETIC; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes

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67	A_RBC	999	N8	Advia - Red Blood Cell Count (x10 ⁶ cells/uL)	=ADVIA.RBC; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.2		Yes
68	A_WBC	999	N8	Advia - White Blood Cell Count (x10 ³ cells/uL)	=ADVIA.WBC; ~= ' ' if ADVIA.HGB ge 13; Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ADVIA - merge ADVIA data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.2		Yes
69	BASEABSRE TICCNT	999	N8	Baseline: Absolute Retic Count	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ABSRETICCNT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
70	BASEABSRE TICCNT_NA	999	C8	Baseline: Absolute Retic Count- Normal or Abnormal	= ' ' if (BASEABSRETICCNT or ABSRETICCNTLOW or ABSRETICCNTHIGH)=. ~= 'Normal' if ABSRETICCNTLOW LE BASEABSRETICCNT LE ABSRETICCNTHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
71	BASEALANIN E	999	N8	Baseline: Alanine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Alanine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
72	BASEALBUMI N	999	N8	Baseline: Albumin (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ALBUMIN Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
73	BASEALBUMI N_NA	999	C8	Baseline: Albumin (g/dL) - Normal or Abnormal	= ' ' if (BASEALBUMIN or ALBUMINLOW or ALBUMINHIGH)=. ~= 'Normal' if ALBUMINLOW LE BASEALBUMIN LE ALBUMINHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
74	BASEALKPH OSPH	999	N8	Baseline: Alk Phosphatase (IU/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ALKPHOSPH Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
75	BASEALKPH OSPH_NA	999	C8	Baseline: Alk Phosphatase (IU/L) - Normal or Abnormal	= ' ' if (BASEALKPHOSPH or ALKPHOSPHLOW or ALKPHOSPHHIGH)=. ~= 'Normal' if ALKPHOSPHLOW LE BASEALKPHOSPH LE ALKPHOSPHHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
76	BASEALT	999	N8	Baseline: ALT (IU/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ALT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
77	BASEALT_NA	999	C8	Baseline: ALT (IU/L) - Normal or Abnormal	= ' ' if (BASEALT or ALTLOW or ALTHIGH)=. ~= 'Normal' if ALTLOW LE BASEALT LE ALTHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
78	BASEAMMON IA	999	N8	Baseline: Ammonia (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Ammonia Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
79	BASEARGINASE	999	N8	Baseline: Arginase (ng/mL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ARGINASE Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
80	BASEARGINASE SE_ADJ	999	N8	Baseline: Arginase (ng/mL) - adjusted values when above LOD	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ARGINASE_ADJ Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
81	BASEARGININE	999	N8	Baseline: Arginine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Arginine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
82	BASEARGININE_TERTILES	999	C6	Baseline arginine: tertile group	= 'Low' lowest baseline arginine (BASEARGININE) tertile group (0-33.3 percentile); ~='Medium' for middle baseline arginine levels (BASEARGININE) (33.3 - 67.7 percentile); ~='High' for highest baseline arginine levels (BASEARGININE) (67.7 - 100 percentile); Programming notes: proc rank data=x out=y groups=3; var basearginine; ranks basearginine_tertiles; run; ~=' then name group=0 'Low', group=1 'Medium' and group=2 'High' Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$6.		Yes
83	BASEARG_CIT	999	N8	Baseline: ARG_CIT	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ARG_CIT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
84	BASEARG_ORN	999	N8	Baseline: ARG_ORN	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ARG_ORN Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
85	BASEASPARAGINE	999	N8	Baseline: Asparagine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Asparagine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
86	BASEASPARTIC_ACID	999	N8	Baseline: Aspartic_Acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Aspartic_Acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
87	BASEA_AMINOADIPIC_ACID	999	N8	Baseline: a_Amino adipic acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable a_Amino adipic acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
88	BASEA_AMINO_N_BUTYRIC_ACID	999	N8	Baseline: a_Amino_n_butyric acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable a_Amino_n_butyric acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
89	BASEA_ARETICCNT	999	N8	Baseline: Absolute Reticulocyte Count (x10^9 cells/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_ARETICCNT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
90	BASEA_CH	999	N8	Baseline: Cellular Hemoglobin (pg)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_CH Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
91	BASEA_CHCM	999	N8	Baseline: Cellular Hemoglobin Concentration Mean (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_CHCM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
92	BASEA_GARDOS	999	N8	Baseline: Gardos Channel Activity (mmol/10 ¹³ cells x min)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_GARDOS Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
93	BASEA_HCT	999	N8	Baseline: Hematocrit (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_HCT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
94	BASEA_HGB	999	N8	Baseline: Hemoglobin (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_HGB Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
95	BASEA_MCH	999	N8	Baseline: Mean Corpuscular Hemoglobin (pg)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_MCH Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
96	BASEA_MCHC	999	N8	Baseline: Mean Corpuscular Hemoglobin Concentration (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_MCHC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
97	BASEA_MCV	999	N8	Baseline: Mean Corpuscular Volume (fL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_MCV Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
98	BASEA_M_CHCM	999	N8	Baseline: Cellular Hemoglobin Concentration Mean - Mature (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_M_CHCM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
99	BASEA_M_MCV	999	N8	Baseline: Mean Corpuscular Volume - Mature (fL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_M_MCV Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
100	BASEA_PF	999	N8	Baseline: Percent HbF (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_PH Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.5		Yes
101	BASEA_PHYPER	999	N8	Baseline: Percent of RBCs with density (CHCM) greater than 41 g/dl (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_PHYPER Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
102	BASEA_PRETIC	999	N8	Baseline: Reticulocyte Percentage (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_PRETIC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
103	BASEA_RBC	999	N8	Baseline: Red Blood Cell Count (x10 ⁶ cells/uL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_RBC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
104	BASEA_WBC	999	N8	Baseline: White Blood Cell Count (x10 ³ cells/uL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable A_WBC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
105	BASEBUN	999	N8	Baseline: BUN (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable BUN Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
106	BASEBUN_NA	999	C8	Baseline: BUN (mg/dL) - Normal or Abnormal	= ' ' if (BASEBUN or BUNLOW or BUNHIGH)=. ~= 'Normal' if BUNLOW LE BASEBUN LE BUNHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
107	BASEB_ALANINE	999	N8	Baseline: b_Alanine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable b_Alanine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
108	BASEB_AMINOISOBUTYRIC_ACID	999	N8	Baseline: b_Aminoisobutyric_acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable b_Aminoisobutyric_acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
109	BASECALCIUM	999	N8	Baseline: Calcium (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable CALCIUM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
110	BASECALCIUM_NA	999	C8	Baseline: Calcium (mg/dL) - Normal or Abnormal	= ' ' if (BASECALCIUM or CALCIUMLOW or CALCIUMHIGH)=. ~= 'Normal' if CALCIUMLOW LE BASECALCIUM LE CALCIUMHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
111	BASECHLORIDE	999	N8	Baseline: Cl (mEq/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable CHLORIDE Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
112	BASECHLORIDE_NA	999	C8	Baseline: Cl (mEq/L) - Normal or Abnormal	= ' ' if (BASECHLORIDE or CHLORIDELOW or CHLORIDEHIGH)=. ~= 'Normal' if CHLORIDELOW LE BASECHLORIDE LE CHLORIDEHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
113	BASECITRULLINE	999	N8	Baseline: Citrulline (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Citrulline Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
114	BASECO2	999	N8	Baseline: CO2 (mEq/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable CO2 <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
115	BASECO2_NA	999	C8	Baseline: CO2 (mEq/L) - Normal or Abnormal	= ' ' if (BASECO2 or CO2LOW or CO2HIGH)=. ~= 'Normal' if CO2LOW LE BASECO2 LE CO2HIGH ~= 'Abnormal' otherwise <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	\$8.		Yes
116	BASECREATININE	999	N8	Baseline: Creatinine (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable CREATININE <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
117	BASECREATININE_NA	999	C8	Baseline: Creatinine (mg/dL) - Normal or Abnormal	= ' ' if (BASECREATININE or CREATININELOW or CREATININEHIGH)=. ~= 'Normal' if CREATININELOW LE BASECREATININE LE CREATININEHIGH ~= 'Abnormal' otherwise <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	\$8.		Yes
118	BASECYSTAT HIONINE	999	N8	Baseline: Cystathionine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Cystathionine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
119	BASECYSTIN E	999	N8	Baseline: Cystine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Cystine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
120	BASEC_LD H	999	N8	Baseline LDH (IU/L), Central lab	= Mean of C_LD H where Visits 1, 2 and 3 and EXCLUDE ne 'Yes' <i>Description:</i> Baseline LDH, Central lab <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
121	BASEDIMAX	999	N8	Baseline: Dimax	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable DIMAX <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
122	BASEEJFRAC T	999	N8	Baseline: Ejection Fraction (%)	=EJFRAC from Visit 3 where EXCLUDE ne 'Yes' Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	2.		Yes
123	BASEENDO1	999	N8	Baseline: ET-1 (pg/mL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ENDO1 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
124	BASEENDO1 _ADJ	999	N8	Baseline: Endo1 (ng/mL) - adjusted values when below LOD	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable ENDO1_ADJ Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
125	BASEETHAN OLAMINE	999	N8	Baseline: Ethanolamine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Ethanolamine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
126	BASEGLUCO SE	999	N8	Baseline: Glucose (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable GLUCOSE Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
127	BASEGLUCO SE_NA	999	C8	Baseline: Glucose (mg/dL) - Normal or Abnormal	= ' ' if (BASEGLUCOSE or GLUCOSELOW or GLUCOSEHIGH)=. ~='Normal' if GLUCOSELOW LE BASEGLUCOSE LE GLUCOSEHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
128	BASEGLUTA MIC_ACID	999	N8	Baseline: Glutamic_acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Glutamic_acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
129	BASEGLUTA MINE	999	N8	Baseline: Glutamine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Glutamine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
130	BASEGLYCINE	999	N8	Baseline: Glycine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Glycine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
131	BASEG_AMINO BUTYRIC_ACID	999	N8	Baseline: g_Aminobutyric_acid (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable g_Aminobutyric_acid Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
132	BASEHEMATOCRIT	999	N8	Baseline: Hematocrit (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable HEMATOCRIT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
133	BASEHEMATOCRIT_NA	999	C8	Baseline: Hematocrit (%) - Normal or Abnormal	= ' ' if (BASEHEMATOCRIT or HEMATOCRITLOW or HEMATOCRITHIGH)=. ~='Normal' if HEMATOCRITLOW LE BASEHEMATOCRIT LE HEMATOCRITHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
134	BASEHEMOGLOBIN	999	N8	Baseline: Hemoglobin (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable HEMOGLOBIN Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
135	BASEHEMOGLOBIN_NA	999	C8	Baseline: Hemoglobin (mg/dL) - Normal or Abnormal	= ' ' if (BASEHEMOGLOBIN or HEMOGLOBINLOW or HEMOGLOBINHIGH)=. ~='Normal' if HEMOGLOBINLOW LE BASEHEMOGLOBIN LE HEMOGLOBINHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
136	BASEHISTIDINE	999	N8	Baseline: Histidine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Histidine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
137	BASEHOMOCYSTINE	999	N8	Baseline: Homocystine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Homocystine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
138	BASEHYDROXYLYSINE	999	N8	Baseline: Hydroxylysine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Hydroxylysine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
139	BASEHYDROXYPROLINE	999	N8	Baseline: Hydroxyproline (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Hydroxyproline <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
140	BASEHYPRO	999	N8	Baseline: Hypro (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Hypro <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		No
141	BASEISOLEUCINE	999	N8	Baseline: Isoleucine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Isoleucine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
142	BASELDH	999	N8	Baseline: LDH (u/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable LDH <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
143	BASELDH_NA	999	C8	Baseline: LDH (u/L) - Normal or Abnormal	= ' ' if (BASELDH or LDHLOW or LDHHIGH)=. ~='Normal' if LDHLOW LE BASELDH LE LDHHIGH ~='Abnormal' otherwise <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	\$8.		Yes
144	BASELEUCINE	999	N8	Baseline: Leucine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Leucine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
145	BASELYSINE	999	N8	Baseline: Lysine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Lysine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
146	BASEMCHC	999	N8	Baseline: MCHC (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable MCHC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
147	BASEMCHC_NA	999	C8	Baseline: MCHC (g/dL)- Normal or Abnormal	= ' ' if (BASEMCHC or MCHCLOW or MCHCHIGH)=. ~= 'Normal' if MCHCLOW LE BASEMCHC LE MCHCHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
148	BASEMCV	999	N8	Baseline: MCV (fl)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable MCV Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
149	BASEMCV_NA	999	C8	Baseline: MCV (fl)- Normal or Abnormal	= ' ' if (BASEMCV or MCVLOW or MCVHIGH)=. ~= 'Normal' if MCVLOW LE BASEMCV LE MCVHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
150	BASEMETHB	999	N8	Baseline: Met Hb (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable METHB Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
151	BASEMETHB_NA	999	C8	Baseline: Met Hb (%) - Normal or Abnormal	= ' ' if (BASEMETHB or METHBLOW or METHBHIGH)=. ~= 'Normal' if METHBLOW LE BASEMETHB LE METHBHIGH ~= 'Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
152	BASEMETHIO NINE	999	N8	Baseline: Methionine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Methionine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
153	BASENOX	999	N8	Baseline: Nitric Oxide (NOx) in uM	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Nox Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
154	BASEOHYP	999	N8	Baseline: Ohyp	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable OHYP Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	Best12.		Yes
155	BASEOPRE	999	N8	Baseline: Opre	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable OPRE Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	Best12.		Yes
156	BASEORNITHINE	999	N8	Baseline: Ornithine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Ornithine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
157	BASEO_PHOSPHOETHANOLAMINE	999	N8	Baseline: O_phosphoethanolamine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable O_phosphoethanolamine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
158	BASEO_PHOSPHOSERINE	999	N8	Baseline: O_phosphoserine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable O_phosphoserine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
159	BASEPERCRETIC	999	N8	Baseline: Percent Retic (%)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable PERCRETIC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
160	BASEPERCRETIC_NA	999	C8	Baseline: Percent Retic (%) - Normal or Abnormal	= ' ' if (BASEPERCRETIC or PERCRETICLOW or PERCRETICHIGH)=. ~='Normal' if PERCRETICLOW LE BASEPERCRETIC LE PERCRETICHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
161	BASEPGF2	999	N8	Baseline: PGF2 (pg/mL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable PGF2 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
162	BASEPGF2_ADJ	999	N8	Baseline: PGF2 (ng/mL) - adjusted values when below LOD	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable PGF2_ADJ Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
163	BASEPHENY LALANINE	999	N8	Baseline: Phenylalanine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Phenylalanine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
164	BASEPLATEL ETCNT	999	N8	Baseline: Platelet Count (Xe3/mm3)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable PLATELETCNT Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
165	BASEPLATEL ETCNT_NA	999	C8	Baseline: Platelet Count (Xe3/mm3)- Normal or Abnormal	= ' ' if (BASEPLATELETCNT or PLATELETCNTLOW or PLATELETCNTHIGH)=. ~='Normal' if PLATELETCNTLOW LE BASEPLATELETCNT LE PLATELETCNTHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
166	BASEPOTAS SIUM	999	N8	Baseline: K (mEq/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable POTASSIUM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
167	BASEPOTAS SIUM_NA	999	C8	Baseline: K (mEq/L) - Normal or Abnormal	= ' ' if (BASEPOTASSIUM or POTASSIUMLOW or POTASSIUMHIGH)=. ~='Normal' if POTASSIUMLOW LE BASEPOTASSIUM LE POTASSIUMHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
168	BASEPROLIN E	999	N8	Baseline: Proline (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Proline Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
169	BASERBC	999	N8	Baseline: RBC (Xe3/mm3)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable RBC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
170	BASERBC_ NA	999	C8	Baseline: RBC (Xe3/mm3)- Normal or Abnormal	= ' ' if (BASERBC or RBCLOW or RBCHIGH)=. ~= 'Normal' if RBCLOW LE BASERBC LE RBCHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
171	BASERVTRA D	999	N8	Baseline: Right Ventricular to Right Atrial difference (mm Hg)	=RVTRAD from Visit 3 where EXCLUDE ne 'Yes' Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
172	BASESARCO SINE	999	N8	Baseline: Sarcosine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Sarcosine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
173	BASESERINE	999	N8	Baseline: Serine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Serine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
174	BASESODIU M	999	N8	Baseline: Na (mEq/L)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable SODIUM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
175	BASESODIU M_NA	999	C8	Baseline: Na (mEq/L) - Normal or Abnormal	= ' ' if (BASESODIUM or SODIUMLOW or SODIUMHIGH)=. ~= 'Normal' if SODIUMLOW LE BASESODIUM LE SODIUMHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
176	BASESTFRA CT	999	N8	Baseline: Shortening Fraction (%)	=STFRACT from Visit 3 where EXCLUDE ne 'Yes' Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
177	BASETAURIN E	999	N8	Baseline: Taurine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Taurine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
178	BASETHREONINE	999	N8	Baseline: Threonine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Threonine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
179	BASETOTBILIRUBIN	999	N8	Baseline: Total Bilirubin (mg/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable TOTBILIRUBIN <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
180	BASETOTBILIRUBIN_NA	999	C8	Baseline: Total Bilirubin (mg/dL) - Normal or Abnormal	= ' ' if (BASETOTBILIRUBIN or TOTBILIRUBINLOW or TOTBILIRUBINHIGH)=. ~='Normal' if TOTBILIRUBINLOW LE BASETOTBILIRUBIN LE TOTBILIRUBINHIGH ~='Abnormal' otherwise <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	\$8.		Yes
181	BASETOTPROTEIN	999	N8	Baseline: Total Protein (g/dL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable TOTPROTEIN <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
182	BASETOTPROTEIN_NA	999	C8	Baseline: Total Protein (g/dL) - Normal or Abnormal	= ' ' if (BASETOTPROTEIN or TOTPROTEINLOW or TOTPROTEINHIGH)=. ~='Normal' if TOTPROTEINLOW LE BASETOTPROTEIN LE TOTPROTEINHIGH ~='Abnormal' otherwise <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	\$8.		Yes
183	BASETRJET	999	N8	Baseline: TR Jet result	=TRJET from Visit 3 where EXCLUDE ne 'Yes' <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
184	BASETRYPTOPHAN	999	N8	Baseline: Tryptophan (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Tryptophan <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
185	BASETYROSINE	999	N8	Baseline: Tyrosine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Tyrosine <i>Description:</i> copy to all observations for that subject <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
186	BASEVALINE	999	N8	Baseline: Valine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Valine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
187	BASEVCAM	999	N8	Baseline: VCAM (ug/mL)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable VCAM Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
188	BASEWBC	999	N8	Baseline: WBC (Xe3/mm3)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable WBC Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
189	BASEWBC_NA	999	C8	Baseline: WBC (Xe3/mm3)- Normal or Abnormal	= ' ' if (BASEWBC or WBCLOW or WBCHIGH)=. ~='Normal' if WBCLOW LE BASEWBC LE WBCHIGH ~='Abnormal' otherwise Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
190	BASEWIDTH	999	N8	Baseline: Width	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable Width Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	Best12.		Yes
191	BASE_1_METHYLHISTIDINE	999	N8	Baseline: _1_Methylhistidine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable _1_Methylhistidine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
192	BASE_3_METHYLHISTIDINE	999	N8	Baseline: _3_Methylhistidine (uM)	=Average of Visits 1, 2 and 3 where EXCLUDE ne 'Yes' - variable _3_Methylhistidine Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
193	BIRTHDATE	999	N8	Birth Date	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:16	No
194	BUN	999	N8	BUN (mg/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62) Notes: #Imported from CSCC Arginine	8.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
195	BUNHIGH	999	N8	BUN (mg/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
196	BUNLOW	999	N8	BUN (mg/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
197	BUN_LLOD	999	N8	BUN - Value below Limit of Detection (3 mg/dL)	=1 if (CSCC_ID=0500307 and PHASE=2200) (HC63); ~=0 otherwise Notes: #Imported from CSCC Arginine	1.		Yes
198	BUN_NA	999	C8	BUN (mg/dL) - Normal or Abnormal	= ' ' if (BUN or BUNLow or BUNHigh)=. ~= 'Normal' if BUNLow LE BUN LE BUNHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
199	B_ALANINE	999	N8	b_Alanine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
200	B_ AMINOISOBUTYRIC_ACID	999	N8	b_Aminoisobutyric_ acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
201	CALCIUM	999	N8	Calcium (mg/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62); Notes: #Imported from CSCC Arginine	8.1		Yes
202	CALCIUMHIGH	999	N8	Calcium (mg/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
203	CALCIUMLOW	999	N8	Calcium (mg/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
204	CALCIUM_NA	999	C8	Calcium (mg/dL) - Normal or Abnormal	= ' ' if (Calcium or CalciumLow or CalciumHigh)=. ~= 'Normal' if CalciumLow LE Calcium LE CalciumHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
205	CENTER	999	C3	Center	Notes: #Imported from CSCC Arginine	\$3.	12JUN09:16:15	No

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
206	CF_HGB	999	N8	Cell-free Hemoglobin, mg/dL	=CF_HGB from S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\HGB <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
207	CHANGEBAS EABSRETICCNT	999	N8	Change from Baseline: Absolute Retic Count	=AbsReticCnt - BaseAbsReticCnt <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
208	CHANGEBAS EALBUMIN	999	N8	Change from Baseline: Albumin (g/dL)	=Albumin - BaseAlbumin <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
209	CHANGEBAS EALKPHOSPH H	999	N8	Change from Baseline: Alk Phosphatase (IU/L)	=AlkPhosph - BaseAlkPhosph <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
210	CHANGEBAS EALT	999	N8	Change from Baseline: ALT (IU/L)	=ALT - BaseALT <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
211	CHANGEBAS EARGINASE	999	N8	Change from Baseline: Arginase (ng/mL)	=ARGINASE - BASEARGINASE <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
212	CHANGEBAS EARGINASE_ ADJ	999	N8	Change from Baseline: Arginase (ng/mL) - adjusted values when above LOD	=ARGINASE_ADJ - BaseARGINASE_ADJ <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
213	CHANGEBAS EA_ ARETICCNT	999	N8	Change from Baseline: Absolute Reticulocyte Count (x10 ⁹ cells/L)	=A_ARETICCNT - BASEA_ARETICCNT <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes
214	CHANGEBAS EA_ CH	999	N8	Change from Baseline: Cellular Hemoglobin (pg)	=A_CH - BASEA_CH <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
215	CHANGEBAS EA_ CHCM	999	N8	Change from Baseline: Cellular Hemoglobin Concentration Mean (g/dL)	=A_CHCM - BASEA_CHCM <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
216	CHANGEBAS EA_ GARDOS	999	N8	Change from Baseline: Gardos Channel Activity (mmol/10 ¹³ cells x min)	=A_GARDOS - BASEA_GARDOS <i>Notes:</i> #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
217	CHANGEBAS EA_HCT	999	N8	Change from Baseline: Hematocrit (%)	=A_HCT - BASEA_HCT Notes: #Imported from CSCC Arginine	8.1		Yes
218	CHANGEBAS EA_HGB	999	N8	Change from Baseline: Hemoglobin (g/dL)	=A_HGB - BASEA_HGB Notes: #Imported from CSCC Arginine	8.1		Yes
219	CHANGEBAS EA_MCH	999	N8	Change from Baseline: Mean Corpuscular Hemoglobin (pg)	=A_MCH - BASEA_MCH Notes: #Imported from CSCC Arginine	8.1		Yes
220	CHANGEBAS EA_MCHC	999	N8	Change from Baseline: Mean Corpuscular Hemoglobin Concentration (g/dL)	=A_MCHC - BASEA_MCHC Notes: #Imported from CSCC Arginine	8.1		Yes
221	CHANGEBAS EA_MCV	999	N8	Change from Baseline: Mean Corpuscular Volume (fL)	=A_MCV - BASEA_MCV Notes: #Imported from CSCC Arginine	8.1		Yes
222	CHANGEBAS EA_M_CHCM	999	N8	Change from Baseline: Cellular Hemoglobin Concentration Mean - Mature (g/dL)	=A_M_CHCM - BASEA_M_CHCM Notes: #Imported from CSCC Arginine	8.1		Yes
223	CHANGEBAS EA_M_MCV	999	N8	Change from Baseline: Mean Corpuscular Volume - Mature (fL)	=A_M_MCV - BASEA_M_MCV Notes: #Imported from CSCC Arginine	8.1		Yes
224	CHANGEBAS EA_PF	999	N8	Change from Baseline: Percent HbF (%)	=A_PH - BASEA_PH Notes: #Imported from CSCC Arginine	8.5		Yes
225	CHANGEBAS EA_PHYPER	999	N8	Change from Baseline: Percent of RBCs with density (CHCM) greater than 41 g/dl (%)	=A_PHYPER - BASEA_PHYPER Notes: #Imported from CSCC Arginine	8.1		Yes
226	CHANGEBAS EA_PRETIC	999	N8	Change from Baseline: Reticulocyte Percentage (%)	=A_PRETIC - BASEA_PRETIC Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
227	CHANGEBAS EA_RBC	999	N8	Change from Baseline: Red Blood Cell Count (x10 ⁶ cells/uL)	=A_RBC - BASEA_RBC <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
228	CHANGEBAS EA_WBC	999	N8	Change from Baseline: White Blood Cell Count (x10 ³ cells/uL)	=A_WBC - BASEA_WBC <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
229	CHANGEBAS EBUN	999	N8	Change from Baseline: BUN (mg/dL)	=BUN - BaseBUN <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
230	CHANGEBAS ECALCIUM	999	N8	Change from Baseline: Calcium (mg/dL)	=Calcium - BaseCalcium <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
231	CHANGEBAS ECHLORIDE	999	N8	Change from Baseline: Cl (mEq/L)	=Chloride - BaseChloride <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
232	CHANGEBAS ECO2	999	N8	Change from Baseline: CO2 (mEq/L)	=CO2 - BaseCO2 <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
233	CHANGEBAS ECREATININ E	999	N8	Change from Baseline: Creatinine (mg/dL)	=Creatinine - BaseCreatinine <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes
234	CHANGEBAS EDIMAX	999	N8	Change from Baseline: Dimax	=DIMAX - BASEDIMAX <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
235	CHANGEBAS EEJFRACT	999	N8	Change from Baseline: Ejection Fraction (%)	=EJFRACT - BASEEJFRACT <i>Notes:</i> #Imported from CSCC Arginine	8.		Yes
236	CHANGEBAS EENDO1	999	N8	Change from Baseline: ET-1 (pg/mL)	=ENDO1 - BASEENDO1 <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
237	CHANGEBAS EENDO1_ADJ	999	N8	Change from Baseline: Endo1 (ng/mL) - adjusted values when below LOD	=ENDO1_ADJ - BaseENDO1_ADJ <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
238	CHANGEBAS EGLUCOSE	999	N8	Change from Baseline: Glucose (mg/dL)	=Glucose - BaseGlucose <i>Notes:</i> #Imported from CSCC Arginine	8.1		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
239	CHANGEBAS EHEMATOCRIT	999	N8	Change from Baseline: Hematocrit (%)	=Hematocrit - BaseHematocrit Notes: #Imported from CSCC Arginine	8.1		Yes
240	CHANGEBAS EHEMOGLOBIN	999	N8	Change from Baseline: Hemoglobin (mg/dL)	=Hemoglobin - BaseHemoglobin Notes: #Imported from CSCC Arginine	8.1		Yes
241	CHANGEBAS ELDH	999	N8	Change from Baseline: LDH (u/L)	=LDH - BaseLDH Notes: #Imported from CSCC Arginine	8.1		Yes
242	CHANGEBAS EMCHC	999	N8	Change from Baseline: MCHC (g/dL)	=MCHC - BaseMCHC Notes: #Imported from CSCC Arginine	8.1		Yes
243	CHANGEBAS EMCV	999	N8	Change from Baseline: MCV (fl)	=MCV - BaseMCV Notes: #Imported from CSCC Arginine	8.1		Yes
244	CHANGEBAS EMETHB	999	N8	Change from Baseline: Met Hb (%)	=Methb - BaseMethb Notes: #Imported from CSCC Arginine	8.1		Yes
245	CHANGEBAS ENOX	999	N8	Change from Baseline: Nitric Oxide (NOx) in uM	=NOX - BASENOX Notes: #Imported from CSCC Arginine	8.1		Yes
246	CHANGEBAS EOHYP	999	N8	Change from Baseline: Ohyp	=OHYP - BASEOHYP Notes: #Imported from CSCC Arginine	Best12.		Yes
247	CHANGEBAS EOPRE	999	N8	Change from Baseline: Opre	=OPRE - BASEOPRE Notes: #Imported from CSCC Arginine	Best12.		Yes
248	CHANGEBAS EPERCRETIC	999	N8	Change from Baseline: Percent Retic (%)	=PercRetic - BasePercRetic Notes: #Imported from CSCC Arginine	8.1		Yes
249	CHANGEBAS EPGF2	999	N8	Change from Baseline: PGF2 (pg/mL)	=PGF2 - BASEPGF2 Notes: #Imported from CSCC Arginine	8.1		Yes
250	CHANGEBAS EPGF2_ADJ	999	N8	Change from Baseline: PGF2 (ng/mL) - adjusted values when below LOD	=PGF2_ADJ - BasePGF2_ADJ Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
251	CHANGEBAS EPLATELETC NT	999	N8	Change from Baseline: Platelet Count (Xe3/mm3)	=PlateletCnt - BasePlateletCnt Notes: #Imported from CSCC Arginine	8.1		Yes
252	CHANGEBAS EPOTASSIUM	999	N8	Change from Baseline: K (mEq/L)	=Potassium - BasePotassium Notes: #Imported from CSCC Arginine	8.1		Yes
253	CHANGEBAS ERBC	999	N8	Change from Baseline: RBC (Xe3/mm3)	=RBC - BaseRBC Notes: #Imported from CSCC Arginine	8.1		Yes
254	CHANGEBAS ERVTRAD	999	N8	Change from Baseline: Right Ventricular to Right Atrial difference (mm Hg)	=RVTRAD - BASERVTRAD Notes: #Imported from CSCC Arginine	8.		Yes
255	CHANGEBAS ESODIUM	999	N8	Change from Baseline: Na (mEq/L)	=Sodium - BaseSodium Notes: #Imported from CSCC Arginine	8.1		Yes
256	CHANGEBAS ESTFRACT	999	N8	Change from Baseline: Shortening Fraction (%)	=STFRACT - BASESTFRACT Notes: #Imported from CSCC Arginine	8.		Yes
257	CHANGEBAS ETOTBILIRUB IN	999	N8	Change from Baseline: Total Bilirubin (mg/dL)	=TotBilirubin - BaseTotBilirubin Notes: #Imported from CSCC Arginine	8.1		Yes
258	CHANGEBAS ETOTPROTEI N	999	N8	Change from Baseline: Total Protein (gm/dL)	=TotProtein - BaseTotProtein Notes: #Imported from CSCC Arginine	8.1		Yes
259	CHANGEBAS ETRJET	999	N8	Change from Baseline: TR Jet result	=TRJET - BASETRJET Notes: #Imported from CSCC Arginine	8.2		Yes
260	CHANGEBAS EVCAM	999	N8	Change from Baseline: VCAM (ug/mL)	=VCAM - BASEVCAM Notes: #Imported from CSCC Arginine	8.2		Yes
261	CHANGEBAS EWBC	999	N8	Change from Baseline: WBC (Xe3/mm3)	=WBC - BaseWBC Notes: #Imported from CSCC Arginine	8.1		Yes
262	CHANGEBAS EWIDTH	999	N8	Change from Baseline: Width	=WIDTH - BASEWIDTH Notes: #Imported from CSCC Arginine	Best12.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
263	CHBASEALANINE	999	N8	Change from Baseline: Alanine (uM)	=Alanine - BASEAlanine Notes: #Imported from CSCC Arginine	8.3		Yes
264	CHBASEAMMONIA	999	N8	Change from Baseline: Ammonia (uM)	=Ammonia - BASEAmmonia Notes: #Imported from CSCC Arginine	8.3		Yes
265	CHBASEARGININE	999	N8	Change from Baseline: Arginine (uM)	=Arginine - BASEArginine Notes: #Imported from CSCC Arginine	8.3		Yes
266	CHBASEARG_CIT	999	N8	Change from Baseline: ARG_CIT	=ARG_CIT -basearg_cit Notes: #Imported from CSCC Arginine	8.3		Yes
267	CHBASEARG_ORN	999	N8	Change from Baseline: ARG_ORN	= ARG_ORN - basearg_orn Notes: #Imported from CSCC Arginine	8.3		Yes
268	CHBASEASPARAGINE	999	N8	Change from Baseline: Asparagine (uM)	=Asparagine - BASEAsparagine Notes: #Imported from CSCC Arginine	8.3		Yes
269	CHBASEASPARTIC_ACID	999	N8	Change from Baseline: Aspartic_Acid (uM)	=Aspartic_Acid - BASEAspartic_Acid Notes: #Imported from CSCC Arginine	8.3		Yes
270	CHBASEA_AMINOADIPIC_ACID	999	N8	Change from Baseline: a_Aminoadipic_acid (uM)	= a_Aminoadipic_acid - BASE a_Aminoadipic_acid Notes: #Imported from CSCC Arginine	8.3		Yes
271	CHBASEA_AMINO_N_BUTYRIC_ACID	999	N8	Change from Baseline: a_Amino_n_butyric_acid (uM)	=a_Amino_n_butyric_acid - BASEa_Amino_n_butyric_acid Notes: #Imported from CSCC Arginine	8.3		Yes
272	CHBASEA_GARDOS_TERT6	999	N8	Change from Baseline A_GARDOS at Visit 6: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEA_GARDOS, VISIT_NUM = 6) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
273	CHBASEA_GARDOS_TERT8	999	N8	Change from Baseline A_GARDOS at Visit 8: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEA_GARDOS, VISIT_NUM = 8) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
274	CHBASEA_PHYPER_TERT6	999	N8	Change from Baseline A_PHYPER at Visit 6: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEA_PHYPER, VISIT_NUM = 6) ~-0 if lowest tertile group (>= 0 to <= 33.3) ~-1 if middle tertile group (>33.3 to <= 66.7) ~-2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
275	CHBASEA_PHYPER_TERT8	999	N8	Change from Baseline A_PHYPER at Visit 8: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEA_PHYPER, VISIT_NUM = 8) ~-0 if lowest tertile group (>= 0 to <= 33.3) ~-1 if middle tertile group (>33.3 to <= 66.7) ~-2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
276	CHBASEB_ALANINE	999	N8	Change from Baseline: b_Alanine (uM)	=b_Alanine - BASEb_Alanine Notes: #Imported from CSCC Arginine	8.3		Yes
277	CHBASEB_AMINOISOBUTYRIC_ACID	999	N8	Change from Baseline: b_Aminoisobutyric_acid (uM)	=b_Aminoisobutyric_acid - BASEb_Aminoisobutyric_acid Notes: #Imported from CSCC Arginine	8.3		Yes
278	CHBASECITRULLINE	999	N8	Change from Baseline: Citrulline (uM)	=Citrulline - BASECitrulline Notes: #Imported from CSCC Arginine	8.3		Yes
279	CHBASECYSATHIONINE	999	N8	Change from Baseline: Cystathionine (uM)	=Cystathionine - BASECystathionine Notes: #Imported from CSCC Arginine	8.3		Yes
280	CHBASECYS-TINE	999	N8	Change from Baseline: Cystine (uM)	=Cystine - BASECystine Notes: #Imported from CSCC Arginine	8.3		Yes
281	CHBASEC_LDH	999	N8	LDH (IU/L), Central lab, Change from baseline	=C_LDH - BASEC_LDH if VISIT_NUM >=4 Description: LDH (IU/L), Central lab, Change from baseline Notes: #Imported from CSCC Arginine	8.1		Yes
282	CHBASEETHANOLAMINE	999	N8	Change from Baseline: Ethanolamine (uM)	=Ethanolamine - BASEEthanolamine Notes: #Imported from CSCC Arginine	8.3		Yes
283	CHBASEGLUTAMIC_ACID	999	N8	Change from Baseline: Glutamic_acid (uM)	=Glutamic_acid - BASEGlutamic_acid Notes: #Imported from CSCC Arginine	8.3		Yes
284	CHBASEGLUTAMINE	999	N8	Change from Baseline: Glutamine (uM)	=Glutamine - BASEGlutamine Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
285	CHBASEGLYCINE	999	N8	Change from Baseline: Glycine (uM)	=Glycine - BASEGlycine Notes: #Imported from CSCC Arginine	8.3		Yes
286	CHBASEG_AMINO BUTYRIC_ACID	999	N8	Change from Baseline: g_Aminobutyric_acid (uM)	=g_Aminobutyric_acid - BASEg_Aminobutyric_acid Notes: #Imported from CSCC Arginine	8.3		Yes
287	CHBASEHISTIDINE	999	N8	Change from Baseline: Histidine (uM)	=Histidine - BASEHistidine Notes: #Imported from CSCC Arginine	8.3		Yes
288	CHBASEHOMOCYSTINE	999	N8	Change from Baseline: Homocystine (uM)	=Homocystin - BASEHomocystin Notes: #Imported from CSCC Arginine	8.3		Yes
289	CHBASEHYDROXYLYSINE	999	N8	Change from Baseline: Hydroxylysine (uM)	=Hydroxylysine - BASEHydroxylysine Notes: #Imported from CSCC Arginine	8.3		Yes
290	CHBASEHYDROXYPROLINE	999	N8	Change from Baseline: Hydroxyproline (uM)	=Hydroxyproline - BASEHydroxyproline Notes: #Imported from CSCC Arginine	8.3		Yes
291	CHBASEHYPRO	999	N8	Change from Baseline: Hypro (uM)	=Hypro - BASEHypro Notes: #Imported from CSCC Arginine	8.3		No
292	CHBASEISOLEUCINE	999	N8	Change from Baseline: Isoleucine (uM)	=Isoleucine - BASEIsoleucine Notes: #Imported from CSCC Arginine	8.3		Yes
293	CHBASELEUCINE	999	N8	Change from Baseline: Leucine (uM)	= Leucine - BASELeucine Notes: #Imported from CSCC Arginine	8.3		Yes
294	CHBASELYSINE	999	N8	Change from Baseline: Lysine (uM)	=Lysine - BASELysine Notes: #Imported from CSCC Arginine	8.3		Yes
295	CHBASEMETHIONINE	999	N8	Change from Baseline: Methionine (uM)	=Methionine - BASEMethionine Notes: #Imported from CSCC Arginine	8.3		Yes
296	CHBASENOX_TERT6	999	N8	Change from Baseline NOX at Visit 6: tertile group	Use PROC RANK (groups = 3, var CHANGEBASENOX, VISIT_NUM = 6) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
297	CHBASENOX_TERT8	999	N8	Change from Baseline NOX at Visit 8: tertile group	Use PROC RANK (groups = 3, var CHANGEBASENOX, VISIT_NUM = 8) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
298	CHBASEORNITHINE	999	N8	Change from Baseline: Ornithine (uM)	=Ornithine - BASEOrnithine Notes: #Imported from CSCC Arginine	8.3		Yes
299	CHBASEO_PHOSPHOETHANOLAMINE	999	N8	Change from Baseline: O_phosphoethanolamine (uM)	=O_phosphoethanolamine - BASEO_phosphoethanolamine Notes: #Imported from CSCC Arginine	8.3		Yes
300	CHBASEO_PHOSPHOSERINE	999	N8	Change from Baseline: O_phosphoserine (uM)	=O_phosphoserine - BASEO_phosphoserine Notes: #Imported from CSCC Arginine	8.3		Yes
301	CHBASEPGF2_TERT6	999	N8	Change from Baseline PGF2 at Visit 6: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEPGF2, VISIT_NUM = 6) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
302	CHBASEPGF2_TERT8	999	N8	Change from Baseline PGF2 at Visit 8: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEPGF2, VISIT_NUM = 8) ~ =0 if lowest tertile group (>= 0 to <= 33.3) ~ =1 if middle tertile group (>33.3 to <= 66.7) ~ =2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
303	CHBASEPHENYLALANINE	999	N8	Change from Baseline: Phenylalanine (uM)	=Phenylalanine - BASEPhenylalanine Notes: #Imported from CSCC Arginine	8.3		Yes
304	CHBASEPROLINE	999	N8	Change from Baseline: Proline (uM)	=Proline - BASEProline Notes: #Imported from CSCC Arginine	8.3		Yes
305	CHBASESARCOSINE	999	N8	Change from Baseline: Sarcosine (uM)	=Sarcosine - BASESarcosine Notes: #Imported from CSCC Arginine	8.3		Yes
306	CHBASESERINE	999	N8	Change from Baseline: Serine (uM)	=Serine - BASESerine Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
307	CHBASETAURINE	999	N8	Change from Baseline: Taurine (uM)	=Taurine - BASETaurine Notes: #Imported from CSCC Arginine	8.3		Yes
308	CHBASETHREONINE	999	N8	Change from Baseline: Threonine (uM)	=Threonine - BASEThreonine Notes: #Imported from CSCC Arginine	8.3		Yes
309	CHBASETRYPTOPHAN	999	N8	Change from Baseline: Tryptophan (uM)	=Tryptophan - BASETryptophan Notes: #Imported from CSCC Arginine	8.3		Yes
310	CHBASETYROSINE	999	N8	Change from Baseline: Tyrosine (uM)	=Tyrosine - BASETyrosine Notes: #Imported from CSCC Arginine	8.3		Yes
311	CHBASEVALINE	999	N8	Change from Baseline: Valine (uM)	=Valine - BASEValine Notes: #Imported from CSCC Arginine	8.3		Yes
312	CHBASEVCAM_TERT6	999	N8	Change from Baseline VCAM at Visit 6: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEVCAM, VISIT_NUM = 6) ~-0 if lowest tertile group (>= 0 to <= 33.3) ~-1 if middle tertile group (>33.3 to <= 66.7) ~-2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
313	CHBASEVCAM_TERT8	999	N8	Change from Baseline VCAM at Visit 8: tertile group	Use PROC RANK (groups = 3, var CHANGEBASEVCAM, VISIT_NUM = 8) ~-0 if lowest tertile group (>= 0 to <= 33.3) ~-1 if middle tertile group (>33.3 to <= 66.7) ~-2 if highest tertile group (>66.7 to <=100) Notes: #Imported from CSCC Arginine	1.		Yes
314	CHBASE_1_METHYLHISTIDINE	999	N8	Change from Baseline: _1_Methylhistidine (uM)	=_1_Methylhistidine - BASE_1_Methylhistidine Notes: #Imported from CSCC Arginine	8.3		Yes
315	CHBASE_3_METHYLHISTIDINE	999	N8	Change from Baseline: _3_Methylhistidine (uM)	=_3_Methylhistidine - BASE_3_Methylhistidine Notes: #Imported from CSCC Arginine	8.3		Yes
316	CHEMLABDATE	999	N8	Date of Chemistry Labs Collection	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:34	No
317	CHEMLABDAY	999	N8	Day (relative to 1st day on study drug) of Chemistry Lab Collection	=Der.Visit_R.chemlabdate-Der.ADD_PT.PT_Start_date+1; Notes: New variable	8.	08JUL09:09:10	Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
318	CHEM_TIME	999	N8	Time in days from enrollment to chemistry lab	=chemlabdate-enrollment_date; Notes: #Imported from CSCC Arginine	8.0		Yes
319	CHLORIDE	999	N8	Cl (mEq/L)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62); Notes: #Imported from CSCC Arginine	8.		Yes
320	CHLORIDEHIGH	999	N8	Cl (mEq/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
321	CHLORIDELOW	999	N8	Cl (mEq/L) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	3.		Yes
322	CHLORIDE_NA	999	C8	Cl (mEq/L) - Normal or Abnormal	= ' ' if (Chloride or ChlorideLow or ChlorideHigh)=. ~= 'Normal' if ChlorideLow LE Chloride LE ChlorideHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
323	CITRULLINE	999	N8	Citrulline (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE = 2.5 / (AAA_DATA.AE_Cys__int_std_) * (AAA_DATA.Citrulline) * 50 Notes: #Imported from CSCC Arginine	8.3		Yes
324	CO2	999	N8	CO2 (mEq/L)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62); Notes: #Imported from CSCC Arginine	8.1		Yes
325	CO2HIGH	999	N8	CO2 (mEq/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
326	CO2LOW	999	N8	CO2 (mEq/L) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
327	CO2_NA	999	C8	CO2 (mEq/L) - Normal or Abnormal	= ' ' if (CO2 or CO2Low or CO2High)=. ~= 'Normal' if CO2Low LE CO2 LE CO2High ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
328	COMPLETED	999	C3	Has patient completed study	Notes: #Imported from CSCC Arginine	\$3.		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
329	CREATININE	999	N8	Creatinine (mg/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62); Notes: #Imported from CSCC Arginine	8.1		Yes
330	CREATININE HIGH	999	N8	Creatinine (mg/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
331	CREATININELOW	999	N8	Creatinine (mg/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
332	CREATININE_NA	999	C8	Creatinine (mg/dL) - Normal or Abnormal	= ' ' if (Creatinine or CreatinineLow or CreatinineHigh)=. ~='Normal' if CreatinineLow LE Creatinine LE CreatinineHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
333	CREATININE_NORM1	999	N8	Norm Creatinine - LS Bakerman	=0.6+(Creatinine-CreatinineLOW)*((1.3-0.6)/(Creatinine HIGH-CreatinineLOW)) if gender = Male, =0.5+(Creatinine-CreatinineLOW)*((1.2-0.5)/(Creatinine HIGH-CreatinineLOW)) if gender=Female; IF CREATININE_NORM1<0 THEN CREATININE_NORM1=0 Description: Normalized Creatinine Values Using Location-Scale Model and Bakerman's Limits Notes: #Imported from CSCC Arginine	8.2		Yes
334	CREATININE_NORM2	999	N8	Norm Creatinine - S Bakerman	=Creatinine*(1.3/CreatinineHIGH) if gender=Male, =Creatinine*(1.2/CreatinineHIGH) if gender=Female Description: Normalized Creatinine Values Using Scale Model and Bakerman's Upper Limits Notes: #Imported from CSCC Arginine	8.2		Yes
335	CREATININE_NORM3	999	N8	Norm Creatinine - LS Phantom Lab	=0.3+(Creatinine-CreatinineLOW)*((1.4-0.3)/(Creatinine HIGH-CreatinineLOW)), IF CREATININE_NORM3<0 THEN CREATININE_NORM3=0 Description: Normalized Creatinine Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH Notes: #Imported from CSCC Arginine	8.2		Yes
336	CREATININE_NORM4	999	N8	Norm Creatinine - ECDF	Take all CREATININE values and separate by site. Rank and find percentiles by dividing by (number of records+1)	8.2		Yes

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Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
336	CREATININE_NORM4				<p>and multiply by 100. Then use the following code:</p> <p>a/ CREATININE_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/CREATININE_oak is the data we are transforming the oakland data to.</p> <p>c/CREATININE_duk is the data that is being transformed. Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need values and percentile ranks</p> <pre> proc iml; use CREATININE_duk_base; read all var {CREATININE_a perca} into aam; use CREATININE_oak; read all var {CREATININE_b percb} into bbm; use CREATININE_duk; read all var {CREATININE_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the following] do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm[i,1]-aam[j,1])+aam[j,2]; </pre>			

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
336	CREATININE_NORM4				<pre> end; end; [end] do i=1 to nc; if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob [i,2]-bbm[j,2])+bbm[j,1]; end; end; names={result percent}; create naam from aam [colname=names]; append from aam; create nbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob; quit; </pre> <p>Description: Normalized Creatinine Values Using ECDF</p> <p>Notes: #Imported from CSCC Arginine</p>			
337	CSCC_ID	999	C7	CSCC ID number	Notes: #Imported from CSCC Arginine	\$7.	12JUN09:16:19	No

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
338	CYSTATHIONINE	999	N8	Cystathionine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
339	CYSTINE	999	N8	Cystine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
340	C_LDH	999	N8	LDH (IU/L), Central lab	=LDH.LDH_IU_L_ (S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\LDH) Description: LDH from central lab Notes: #Imported from CSCC Arginine	8.1		Yes
341	DIAGNOSIS	999	C3	Diagnosis	Notes: #Imported from CSCC Arginine	\$3.		Yes
342	DIMAX	999	N8	Maximum EI of the smoothed curve	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\EKTA xy data -Merge EKTAMAX with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE then merge by ID PHASE Notes: #Imported from CSCC Arginine	Best12.		Yes
343	DISCONTINUED	999	C3	Did the patient discontinue from the study	Notes: #Imported from CSCC Arginine	\$3.		Yes
344	DISCONTIN_REASON	999	C17	Reason for study discontinuation	Notes: #Imported from CSCC Arginine	\$17.		Yes
345	ECHOABN	999	C3	Echo ever been abnormal?	Notes: #Imported from CSCC Arginine	\$3.		Yes
346	ECHO_ABNORM	999	C3	Abnormal echocardiogram	= ' ' if TRJET=. And RVTRAD=. ~='Yes' if TRJET > 2.5 OR RVTRAD >= 25 ~='No' otherwise Notes: #Imported from CSCC Arginine	\$3.		Yes
347	EJFRACT	999	N8	Ejection Fraction (%)	Notes: #Imported from CSCC Arginine	8.		Yes
348	EJNOT	999	C1	Ejection Fraction - Not Reported	Notes: #Imported from CSCC Arginine	\$1.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
349	ENDO1	999	N8	ET-1 (pg/mL)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.2		Yes
350	ENDO1_ADJ	999	N8	ET-1 (pg/mL) - adjusted values when below LOD	=0.1 if endo_idl=1 ~=ENDO1 otherwise Notes: #Imported from CSCC Arginine	8.2		Yes
351	ENDO1_LDL	999	N8	ENDO1 measurement below Limit of Detection (<0.20)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	1.		Yes
352	ENROLLED	999	C3	Has patient enrolled in the study?	Notes: #Imported from CSCC Arginine	\$3.		Yes
353	ENROLLMENT_DATE	999	N8	Enrollment Date	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:24	No
354	ENROLLMENT_DAY	999	N8	Day of Enrollment (relative to 1st day on study drug)	=Der.Visit_R.enrollment_date-Der.ADD_PT.PT_Start_date+1; Notes: New variable	8.	12JUN09:16:23	Yes
355	ETHANOLAMINE	999	N8	Ethanolamine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
356	EXCLUDE	6	C3	Exclude this record	= 'Yes' if HOSPMSTR.VOC ne missing OR EMRGMSTR.VOC ne missing OR INHHMSTR.CLINYN= 'Yes' and the visit occurs within the 7 days prior to 14 days after the event; ~= 'Yes' if A_PERCBA > 15 (exclude all labs for just the visit this has been reported at) ; ~= 'Yes' if EXCL.EXCL8= 'Yes' (It should be copied to all visits for the subject); ~If INHH.TRANSYN = 'Yes' for a certain phase (called TRANS_PHASE and TRANSDT, for example) then EXCLUDE = 'Yes' for that phase and all subsequent phases for that subject. ~If (TRANS_PHASE = '4000' or PHASE = '4000') then compare transfusion date and lab dates and if (.<TRANSDT =< CHEMLABDATE) or (.<TRANSDT =< HEMALABDATE) or (.<TRANSDT=< METHLABDATE) then EXCLUDE = 'Yes' ~= 'No' otherwise; Notes: #Imported from CSCC Arginine	\$3.	26JUN09:10:33	Yes
357	GENDER	4	C6	Gender	Notes: #Imported from CSCC Arginine	\$6.	26JUN09:10:33	Yes
358	GLUCOSE	999	N8	Glucose (mg/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62) Notes: #Imported from CSCC Arginine	8.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
359	GLUCOSEHI GH	999	N8	Glucose (mg/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
360	GLUCOSELO W	999	N8	Glucose (mg/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
361	GLUCOSE_ NA	999	C8	Glucose (mg/dL) - Normal or Abnormal	= ' ' if (Glucose or GlucoseLow or GlucoseHigh)=. ~= 'Normal' if GlucoseLow LE Glucose LE GlucoseHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
362	GLUTAMIC_ ACID	999	N8	Glutamic_acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
363	GLUTAMINE	999	N8	Glutamine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
364	GLYCINE	999	N8	Glycine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
365	G_ AMINOBU TYRIC_ ACID	999	N8	g_Aminobutyric_acid (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
366	HEMALABDA TE	999	N8	Date of Hematology Labs Collection	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:30	No
367	HEMATOCRIT	999	N8	Hematocrit (%)	Notes: #Imported from CSCC Arginine	8.		Yes
368	HEMATOCRIT HIGH	999	N8	Hematocrit (%) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
369	HEMATOCRIT LOW	999	N8	Hematocrit (%) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
370	HEMATOCRIT _NA	999	C8	Hematocrit (%) - Normal or Abnormal	= ' ' if (Hematocrit or HematocritLow or HematocritHigh)=. ~= 'Normal' if HematocritLow LE Hematocrit LE HematocritHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
371	HEMATOCRIT _NORM1	999	N8	Norm HEMATOCRIT - LS Bakerman	=42+(HEMATOCRIT-HEMATOCRITLOW)*((52-42)/(HEMATOCRITHIGH-HEMATOCRITLOW)) if gender = M, =37+(HEMATOCRIT-HEMATOCRITLOW)*((47-37)/(HEMATOCRITHIGH-HEMATOCRITLOW)) if gender=F; IF HEMATOCRIT _NORM1<0 THEN HEMATOCRIT _NORM1=0 Description: Normalized HEMATOCRIT Values Using Location-Scale Model and Bakerman's Limits Notes: #Imported from CSCC Arginine	8.2		Yes
372	HEMATOCRIT _NORM2	999	N8	Norm HEMATOCRIT - S Bakerman	=HEMATOCRIT*(52/HEMATOCRITHIGH) if gender=M, =HEMATOCRIT*(47/HEMATOCRITHIGH) if gender=F Description: Normalized HEMATOCRIT Values Using Scale Model and Bakerman's Upper Limits Notes: #Imported from CSCC Arginine	8.2		Yes
373	HEMATOCRIT _NORM3	999	N8	Norm HEMATOCRIT - LS Phantom Lab	=34+(HEMATOCRIT-HEMATOCRITLOW)*((52-34)/(HEMATOCRITHIGH-HEMATOCRITLOW)), IF HEMATOCRIT _NORM3<0 THEN HEMATOCRIT _NORM3=0 Description: Normalized HEMATOCRIT Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH Notes: #Imported from CSCC Arginine	8.2		Yes
374	HEMATOCRIT _NORM4	999	N8	Norm HEMATOCRIT - ECDF	Take all HEMATOCRIT values and separate by site. Rank and find percentiles by dividing by (number of records+1) and multiply by 100. Then use the following code: a/ HEMATOCRIT_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/HEMATOCRIT_oak is the data we are transforming the oakland data to.	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
374	HEMATOCRIT_NORM4				<p>c/HEMATOCRIT_duk is the data that is being transformed. Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need values and percentile ranks</p> <pre> proc iml; use HEMATOCRIT_duk_base; read all var {HEMATOCRIT_a perca} into aam; use HEMATOCRIT_oak; read all var {HEMATOCRIT_b percb} into bbm; use HEMATOCRIT_duk; read all var {HEMATOCRIT_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the following] do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm[i,1]-aam[j,1])+aam[j,2]; end; end; [end] do i=1 to nc; </pre>			

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
374	HEMATOCRIT_NORM4				<pre> if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob [i,2]-bbm[j,2])+bbm[j,1]; end; end; names={result percent}; create naam from aam [colname=names]; append from aam; create nbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob; quit; </pre> <p>Description: Normalized HEMATOCRIT Values Using ECDF</p> <p>Notes: #Imported from CSCC Arginine</p>			
375	HEMA_LAB_DAY	999	N8	Day of hematology lab collection (relative to 1st day on study drug)	<pre> =Der.Visit_R.hemalabdate-Der.ADD_PT.PT_Start_date+1; </pre> <p>Notes: New variable</p>	8.	12JUN09:16:31	Yes
376	HEMA_TIME	999	N8	Time in days from enrollment to hematology lab	<pre> =hemalabdate-enrollment_date; </pre> <p>Notes: #Imported from CSCC Arginine</p>	8.0		Yes
377	HEMOGLOBIN	999	N8	Hemoglobin (mg/dL)	<p>Notes: #Imported from CSCC Arginine</p>	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
378	HEMOGLOBI NHIGH	999	N8	Hemoglobin (mg/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
379	HEMOGLOBI NLOW	999	N8	Hemoglobin (mg/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
380	HEMOGLOBI N_NA	999	C8	Hemoglobin (mg/dL) - Normal or Abnormal	= ' ' if (Hemoglobin or HemoglobinLow or HemoglobinHigh)=. ~= 'Normal' if HemoglobinLow LE Hemoglobin LE HemoglobinHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
381	HH_FORMDT	999	N8	Baseline and Interim Health History Formdt	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:27	No
382	HH_FORM_ DAY	999	N8	Day of baseline and interim health history form (relative to 1st day on study drug)	=Der.Visit_R.HH_formdt-Der.ADD_PT.PT_Start_date+1; Notes: New variable	8.	12JUN09:16:26	Yes
383	HISTIDINE	999	N8	Histidine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
384	HOMOCYSTI NE	999	N8	Homocystine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
385	HYDROXYLY SINE	999	N8	Hydroxylysine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
386	HYDROXYPR OLINE	999	N8	Hydroxyproline (uM)	=AAA_DATA.Hypro Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
387	HYPRO	999	N8	Hypro (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		No
388	IHX_AES	999	C3	Has the patient had any Adverse Events since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
389	IHX_BLDURINE	999	C3	Has the patient had blood in the urine since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
390	IHX_BREATH	999	C3	Has the patient had any problems breathing, including asthma, since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
391	IHX_FEVER	999	C3	Has the patient had a fever 101 (F) or higher since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
392	IHX_HEADACHE	999	C3	Has the patient had any unusual headaches since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
393	IHX_HEAD_FREQ	999	C21	How often subject had headache since last visit?	Notes: #Imported from CSCC Arginine	\$21.		Yes
394	IHX_LEGULCERS	999	C3	Has the patient had any leg ulcers since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
395	IHX_NEWMEDS	999	C3	Has the patient taken any new medications since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
396	IHX_PAINERC	999	C3	Has the patient had any increased problems with priapism since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
397	IHX_PHIPS	999	C3	Has the patient had chronic pain in the hips or shoulders?	Notes: #Imported from CSCC Arginine	\$3.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
398	IHX_POTH	999	C3	Has the patient had chronic pain in other locations?	Notes: #Imported from CSCC Arginine	\$3.		Yes
399	IHX_TIRED	999	C8	Has the patient been unusually tired, or more tired than usually since last visit?	Notes: #Imported from CSCC Arginine	\$8.		Yes
400	IHX_VISION	999	C3	Has the patient had vision problems since last visit?	Notes: #Imported from CSCC Arginine	\$3.		Yes
401	ISOLEUCINE	999	N8	Isoleucine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
402	ITT	999	C3	Intent-To-Treat Population	Notes: #Imported from CSCC Arginine	\$3.		Yes
403	LDH	999	N8	LDH (u/L)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1(HC62) Notes: #Imported from CSCC Arginine	8.		Yes
404	LDHHIGH	999	N8	LDH (u/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
405	LDHLOW	999	N8	LDH (u/L) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
406	LDH_NA	999	C8	LDH (u/L) - Normal or Abnormal	= ' ' if (LDH or LDHLow or LDHHigh)=. ~= 'Normal' if LDHLow LE LDH LE LDHHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
407	LDH_NORM1	999	N8	Norm LDH - LS Bakerman	=118+(LDH-LDHLOW)*((273-118)/(LDHHIGH-LDHLOW)) if gender = M, =122+(LDH-LDHLOW)*((220-122)/(LDHHIGH-LDHLOW)) if gender=F; IF LDH_NORM1<0 THEN LDH_NORM1=0 Description: Normalized LDH Values Using Location-Scale Model and Bakerman's Limits Notes: #Imported from CSCC Arginine	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
408	LDH_NORM2	999	N8	Norm LDH - S Bakerman	<p>=LDH*(273/LDHHIGH) if gender=M, =LDH*(220/LDHHIGH) if gender=F</p> <p>Description: Normalized LDH Values Using Scale Model and Bakerman's Upper Limits</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
409	LDH_NORM3	999	N8	Norm LDH - LS Phantom Lab	<p>=98+(LDH-LDHLOW)*((750-98)/(LDHHIGH-LDHLOW)), IF LDH_NORM3<0 THEN LDH_NORM3=0</p> <p>Description: Normalized LDH Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
410	LDH_NORM4	999	N8	Norm LDH - ECDF	<p>Take all LDH values and separate by site. Rank and find percentiles by dividing by (number of records+1) and multiply by 100. Then use the following code:</p> <p>a/LDH_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/LDH_oak is the data we are transforming the oakland data to. c/LDH_duk is the data that is being transformed. Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need values and percentile ranks</p> <pre> proc iml; use LDH_duk_base; read all var {LDH_a perca} into aam; use LDH_oak; read all var {LDH_b percb} into bbm; use LDH_duk; read all var {LDH_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the </pre>	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
410	LDH_NORM4				<pre> following] do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm [i,1]-aam[j,1])+aam[j,2]; end; end; [end] do i=1 to nc; if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob [i,2]-bbm[j,2])+bbm[j,1]; end; end; names={result percent}; create naam from aam [colname=names]; append from aam; create nbbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob; </pre>			

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
410	LDH_NORM4				<p>quit;</p> <p>Description: Normalized LDH Values Using ECDF</p> <p>Notes: #Imported from CSCC Arginine</p>			
411	LEUCINE	999	N8	Leucine (uM)	<p>Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE</p> <p>Notes: #Imported from CSCC Arginine</p>	8.3		Yes
412	LYSINE	999	N8	Lysine (uM)	<p>Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE</p> <p>Notes: #Imported from CSCC Arginine</p>	8.3		Yes
413	MCHC	999	N8	MCHC (g/dL)	<p>Notes: #Imported from CSCC Arginine</p>	8.1		Yes
414	MCHCHIGH	999	N8	MCHC (g/dL) upper limit of normal range	<p>Description: copy to all observations for that subject</p> <p>Notes: #Imported from CSCC Arginine</p>	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
415	MCHCLOW	999	N8	MCHC (g/dL) lower limit of normal range	if cscs_id='0800135' then mchclow=31.4 (do this before normalization coding) Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
416	MCHC_NA	999	C8	MCHC (g/dL) - Normal or Abnormal	= ' ' if (MCHC or MCHCLow or MCHCHigh)=. ~='Normal' if MCHCLow LE MCHC LE MCHCHigh ~='Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
417	MCHC_NORM1	999	N8	Norm MCHC - LS Bakerman	=30+(MCHC-MCHCLOW)*((35-30)/(MCHCHIGH-MCHCLOW)), IF MCHC_NORM1<0 THEN MCHC_NORM1=0 Description: Normalized MCHC Values Using Location-Scale Model and Bakerman's Limits Notes: #Imported from CSCC Arginine	8.2		Yes
418	MCHC_NORM2	999	N8	Norm MCHC - S Bakerman	=MCHC*(35/MCHCHIGH) Description: Normalized MCHC Values Using Scale Model and Bakerman's Upper Limits Notes: #Imported from CSCC Arginine	8.2		Yes
419	MCHC_NORM3	999	N8	Norm MCHC - LS Phantom Lab	=27+(MCHC-MCHCLOW)*((37-27)/(MCHCHIGH-MCHCLOW)), IF MCHC_NORM3<0 THEN MCHC_NORM3=0 Description: Normalized MCHC Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH Notes: #Imported from CSCC Arginine	8.2		Yes
420	MCHC_NORM4	999	N8	Norm MCHC - ECDF	Take all MCHC values and separate by site. Rank and find percentiles by dividing by (number of records+1) and multiply by 100. Then use the following code: a/MCHC_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/MCHC_oak is the data we are transforming the oakland data to. c/MCHC_duk is the data that is being transformed. Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
420	MCHC_NORM4				<p>values and percentile ranks</p> <pre> proc iml; use MCHC_duk_base; read all var {MCHC_a perca} into aam; use MCHC_oak; read all var {MCHC_b percb} into bbm; use MCHC_duk; read all var {MCHC_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the following] do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm[i,1]-aam[j,1])+aam[j,2]; end; end; [end] do i=1 to nc; if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob[i,2]-bbm[j,2])+bbm[j,1]; </pre>			

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
420	MCHC_NORM4				<p>end; end;</p> <p>names={result percent}; create naam from aam [colname=names]; append from aam; create nbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob;</p> <p>quit;</p> <p>Description: Normalized MCHC Values Using ECDF</p> <p>Notes: #Imported from CSCC Arginine</p>			
421	MCV	999	N8	MCV (fl)	Notes: #Imported from CSCC Arginine	8.1		Yes
422	MCVHIGH	999	N8	MCV (fl) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
423	MCVLOW	999	N8	MCV (fl) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
424	MCV_NA	999	C8	MCV (fl) - Normal or Abnormal	= ' ' if (MCV or MCVLow or MCVHigh)=. ~='Normal' if MCVLow LE MCV LE MCVHigh ~='Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
425	MCV_NORM1	999	N8	Norm MCV - LS Bakerman	=30+(MCV-MCVLOW)*((35-30)/(MCVHIGH-MCVLOW)), IF MCV_NORM1<0 THEN MCV_NORM1=0 Description: Normalized MCV Values Using Location-Scale Model and Bakerman's Limits Notes: #Imported from CSCC Arginine	8.2		Yes

Variable-Level Metadata for 637 Variables in Table *VISIT_R*

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
426	MCV_NORM2	999	N8	Norm MCV - S Bakerman	<p>=MCV*(35/MCVHIGH)</p> <p>Description: Normalized MCV Values Using Scale Model and Bakerman's Upper Limits</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
427	MCV_NORM3	999	N8	Norm MCV - LS Phantom Lab	<p>=75+(MCV-MCVLOW)*((100-75)/(MCVHIGH-MCVLOW)), IF MCV_NORM3<0 THEN MCV_NORM3=0</p> <p>Description: Normalized MCV Values Using Location-Scale Transformation and 5th and 95th percentile upper and lower limits of normal for LDH</p> <p>Notes: #Imported from CSCC Arginine</p>	8.2		Yes
428	MCV_NORM4	999	N8	Norm MCV - ECDF	<p>Take all MCV values and separate by site. Rank and find percentiles by dividing by (number of records+1) and multiply by 100. Then use the following code:</p> <p>a/MCV_duk_base is the baseline values (visits 1,2, or 3) for the oakland site. b/MCV_oak is the data we are transforming the oakland data to. c/MCV_duk is the data that is being transformed (example site duke). Do this for all sites (except oakland, keep the oakland values as is), all sites should be transformed to the oakland data. All three datasets need values and percentile ranks</p> <pre> proc iml; use MCV_duk_base; read all var {MCV_a perca} into aam; use MCV_oak; read all var {MCV_b percb} into bbm; use MCV_duk; read all var {MCV_c percc} into ccm; na=nrow(aam); nb=nrow(bbm); nc=nrow(ccm); ctob=ccm; [if the number of baseline values>=10 then do the following] </pre>	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
428	MCV_NORM4				<pre> do i=1 to nc; if ccm[i,1]<aam[1,1] then ctob[i,2]=aam[1,2]; if ccm[i,1]>=aam[na,1] then ctob[i,2]=aam[na,2]; do j=1 to na-1; if ccm[i,1]>=aam[j,1] & ccm[i,1]<aam[j+1,1] then ctob[i,2]=(aam[j+1,2]-aam[j,2])/(aam[j+1,1]-aam[j,1])*(ccm [i,1]-aam[j,1])+aam[j,2]; end; end; [end] do i=1 to nc; if ctob[i,2]<bbm[1,2] then ctob[i,1]=bbm[1,1]; if ctob[i,2]>=bbm[nb,2] then ctob[i,1]=bbm[nb,1]; do j=1 to nb-1; if ctob[i,2]>=bbm[j,2] & ctob[i,2]<bbm[j+1,2] then ctob[i,1]=(bbm[j+1,1]-bbm[j,1])/(bbm[j+1,2]-bbm[j,2])*(ctob [i,2]-bbm[j,2])+bbm[j,1]; end; end; names={result percent}; create naam from aam [colname=names]; append from aam; create nbbm from bbm [colname=names]; append from bbm; create nccm from ccm [colname=names]; append from ccm; create nctob from ctob [colname=names]; append from ctob; </pre>			

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
428	MCV_NORM4				quit; Description: Normalized MCV Values Using ECDF Notes: #Imported from CSCC Arginine			
429	METHB	999	N8	Met Hb (%)	Notes: #Imported from CSCC Arginine	8.1		Yes
430	METHBDATE	999	N8	Date of Met Hb Collection	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:39	No
431	METHBHIGH	999	N8	Met Hb (%) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
432	METHBLOW	999	N8	Met Hb (%) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
433	METHB_DAY	999	N8	Day of Met-Hb collection (relative to 1st day on study drug)	=Der.Visit_R.methbdate-Der.ADD_PT.PT_Start_date+1; Notes: New Variable	8.	12JUN09:16:47	Yes
434	METHB_LLOD	999	N8	METHB - Value below Limit of Detection (0.5 %)	=1 if (CSCC_ID=0700106 and PHASE=2100) (HC22); ~=0 otherwise Notes: #Imported from CSCC Arginine	1.		Yes
435	METHB_NA	999	C8	Met Hb (%) - Normal or Abnormal	= ' ' if (MethHb or MethHbLow or MethHbHigh)=. ~= 'Normal' if MethHbLow LE MetHb LE MethHbHigh ~='Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
436	METHIONINE	999	N8	Methionine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
437	NOX	999	N8	Nitric Oxide (NOx) in uM	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
438	OHYP	999	N8	OSM of the half maximum after dimax	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\EKTA xy data -Merge EKTAMAX with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE then merge by ID PHASE Notes: #Imported from CSCC Arginine	Best12.		Yes
439	OPRE	999	N8	OSM of the half maximum before dimax	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\EKTA xy data -Merge EKTAMAX with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE then merge by ID PHASE Notes: #Imported from CSCC Arginine	Best12.		Yes
440	ORNITHINE	999	N8	Ornithine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
441	O_PHOSPHOETHANOLAMINE	999	N8	O_phosphoethanolamine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
442	O_PHOSPHOSERINE	999	N8	O_phosphoserine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
443	PANOT	999	C1	Right Ventricular to Right Atrial difference - Not Reported	Notes: #Imported from CSCC Arginine	\$1.		Yes
444	PCHANGEBASEARGINASE	999	N8	Percent Change from Baseline: Arginase (ng/mL)	=100 * (CHANGEBASEARGINASE / BASEARGINASE) Notes: #Imported from CSCC Arginine	8.2		Yes
445	PCHANGEBASEARGINASE_ADJ	999	N8	Percent Change from Baseline: Arginase (ng/mL) - adjusted values when above LOD	=100 * (CHANGEBASEARGINASE_ADJ / BASEARGINASE_ADJ) Notes: #Imported from CSCC Arginine	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
446	PCHANGEBA SEA_ ARETICCNT	999	N8	Percent Change from Baseline: Absolute Reticulocyte Count (x10 ⁹ cells/L)	=100 * (CHANGEBASEA_ARETICCNT / BASEA_ARETICCNT) Notes: #Imported from CSCC Arginine	8.2		Yes
447	PCHANGEBA SEA_CH	999	N8	Percent Change from Baseline: Cellular Hemoglobin (pg)	=100 * (CHANGEBASEA_CH / BASEA_CH) Notes: #Imported from CSCC Arginine	8.2		Yes
448	PCHANGEBA SEA_CHCM	999	N8	Percent Change from Baseline: Cellular Hemoglobin Concentration Mean (g/dL)	=100 * (CHANGEBASEA_CHCM / BASEA_CHCM) Notes: #Imported from CSCC Arginine	8.2		Yes
449	PCHANGEBA SEA_ GARDOS	999	N8	Percent Change from Baseline: Gardos Channel Activity (mmol/10 ¹³ cells x min)	=100 * (CHANGEBASEA_GARDOS / BASEA_GARDOS) Notes: #Imported from CSCC Arginine	8.2		Yes
450	PCHANGEBA SEA_HCT	999	N8	Percent Change from Baseline: Hematocrit (%)	=100 * (CHANGEBASEA_HCT / BASEA_HCT) Notes: #Imported from CSCC Arginine	8.2		Yes
451	PCHANGEBA SEA_HGB	999	N8	Percent Change from Baseline: Hemoglobin (g/dL)	=100 * (CHANGEBASEA_HGB / BASEA_HGB) Notes: #Imported from CSCC Arginine	8.2		Yes
452	PCHANGEBA SEA_MCH	999	N8	Percent Change from Baseline: Mean Corpuscular Hemoglobin (pg)	=100 * (CHANGEBASEA_MCH / BASEA_MCH) Notes: #Imported from CSCC Arginine	8.2		Yes
453	PCHANGEBA SEA_MCHC	999	N8	Percent Change from Baseline: Mean Corpuscular Hemoglobin Concentration (g/dL)	=100 * (CHANGEBASEA_MCHC / BASEA_MCHC) Notes: #Imported from CSCC Arginine	8.2		Yes
454	PCHANGEBA SEA_MCV	999	N8	Percent Change from Baseline: Mean Corpuscular Volume (fL)	=100 * (CHANGEBASEA_MCV / BASEA_MCV) Notes: #Imported from CSCC Arginine	8.2		Yes
455	PCHANGEBA SEA_M_ CHCM	999	N8	Percent Change from Baseline: Cellular Hemoglobin Concentration Mean - Mature (g/dL)	=100 * (CHANGEBASEA_M_CHCM / BASEA_M_CHCM) Notes: #Imported from CSCC Arginine	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
456	PCHANGEBA SEA_M_MCV	999	N8	Percent Change from Baseline: Mean Corpuscular Volume - Mature (fL)	=100 * (CHANGEBASEA_M_MCV / BASEA_M_MCV) Notes: #Imported from CSCC Arginine	8.2		Yes
457	PCHANGEBA SEA_PF	999	N8	Percent Change from Baseline: Percent HbF (%)	=100 * (CHANGEBASEA_PH / BASEA_PH) Notes: #Imported from CSCC Arginine	8.2		Yes
458	PCHANGEBA SEA_ PHYPER	999	N8	Percent Change from Baseline: Percent of RBCs with density (CHCM) greater than 41 g/dl (%)	=100 * (CHANGEBASEA_PHYPER / BASEA_PHYPER) Notes: #Imported from CSCC Arginine	8.2		Yes
459	PCHANGEBA SEA_PRETIC	999	N8	Percent Change from Baseline: Reticulocyte Percentage (%)	=100 * (CHANGEBASEA_PRETIC / BASEA_PRETIC) Notes: #Imported from CSCC Arginine	8.2		Yes
460	PCHANGEBA SEA_RBC	999	N8	Percent Change from Baseline: Red Blood Cell Count (x10 ⁶ cells/uL)	=100 * (CHANGEBASEA_RBC / BASEA_RBC) Notes: #Imported from CSCC Arginine	8.2		Yes
461	PCHANGEBA SEA_WBC	999	N8	Percent Change from Baseline: White Blood Cell Count (x10 ³ cells/uL)	=100 * (CHANGEBASEA_WBC / BASEA_WBC) Notes: #Imported from CSCC Arginine	8.2		Yes
462	PCHANGEBA SEDIMAX	999	N8	Percent Change from Baseline: Dimax	=100 * (CHANGEBASEDIMAX / BASEDIMAX) Notes: #Imported from CSCC Arginine	8.2		Yes
463	PCHANGEBA SEEJFRACT	999	N8	Percent Change from Baseline: Ejection Fraction (%)	=100 * (CHANGEBASEEJFRACT / BASEEJFRACT) Notes: #Imported from CSCC Arginine	8.2		Yes
464	PCHANGEBA SEENDO1	999	N8	Percent Change from Baseline: ET-1 (pg/mL)	=100 * (CHANGEBASEENDO1 / BASEENDO1) Notes: #Imported from CSCC Arginine	8.2		Yes
465	PCHANGEBA SEENDO1_ ADJ	999	N8	Percent Change from Baseline: Endo1 (ng/mL) - adjusted values when below LOD	=100 * (CHANGEBASEENDO1_ADJ / BASEENDO1_ADJ) Notes: #Imported from CSCC Arginine	8.2		Yes
466	PCHANGEBA SENOX	999	N8	Percent Change from Baseline: Nitric Oxide (NOx) in uM	=100 * (CHANGEBASENOX / BASENOX) Notes: #Imported from CSCC Arginine	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
467	PCHANGEBA SEOHYP	999	N8	Percent Change from Baseline: Ohyp	=100 * (CHANGEBASEOHYP / BASEOHYP) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
468	PCHANGEBA SEOPRE	999	N8	Percent Change from Baseline: Opre	=100 * (CHANGEBASEOPRE / BASEOPRE) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
469	PCHANGEBA SEPGF2	999	N8	Percent Change from Baseline: PGF2 (pg/mL)	=100 * (CHANGEBASEPGF2 / BASEPGF2) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
470	PCHANGEBA SEPGF2_ADJ	999	N8	Percent Change from Baseline: PGF2 (ng/mL) - adjusted values when below LOD	=100 * (CHANGEBASEPGF2_ADJ / BASEPGF2_ADJ) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
471	PCHANGEBA SERVTRAD	999	N8	Percent Change from Baseline: Right Ventricular to Right Atrial difference (mm Hg)	=100 * (CHANGEBASERVTRAD / BASERVTRAD) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
472	PCHANGEBA SESTFRACT	999	N8	Percent Change from Baseline: Shortening Fraction (%)	=100 * (CHANGEBASESTFRACT / BASESTFRACT) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
473	PCHANGEBA SETRJET	999	N8	Percent Change from Baseline: TR Jet result	=100 * (CHANGEBASETRJET / BASETRJET) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
474	PCHANGEBA SEVCAM	999	N8	Percent Change from Baseline: VCAM (ug/mL)	=100 * (CHANGEBASEVCAM / BASEVCAM) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
475	PCHANGEBA SEWIDTH	999	N8	Percent Change from Baseline: Width	=100 * (CHANGEBASEWIDTH / BASEWIDTH) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
476	PCHBASEAL ANINE	999	N8	Percent Change from Baseline: Alanine (uM)	=100 * (ChBaseAlanine / BaseAlanine) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
477	PCHBASEAM MONIA	999	N8	Percent Change from Baseline: Ammonia (uM)	=100 * (ChBaseAmmonia / BaseAmmonia) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes
478	PCHBASEAR GININE	999	N8	Percent Change from Baseline: Arginine (uM)	=100 * (ChBaseArginine / BaseArginine) <i>Notes: #Imported from CSCC Arginine</i>	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
479	PCHBASEARG_CIT	999	N8	Percent Change from Baseline: ARG_CIT	= (ARG_CIT - basearg_cit) / basearg_cit * 100 Notes: #Imported from CSCC Arginine	8.3		Yes
480	PCHBASEARG_ORN	999	N8	Percent Change from Baseline: ARG_ORN	= (ARG_ORN - basearg_orn) / basearg_orn * 100 Notes: #Imported from CSCC Arginine	8.3		Yes
481	PCHBASEASPARAGINE	999	N8	Percent Change from Baseline: Asparagine (uM)	= 100 * (ChBaseAsparagine / BaseAsparagine) Notes: #Imported from CSCC Arginine	8.2		Yes
482	PCHBASEASPARTIC_ACID	999	N8	Percent Change from Baseline: Aspartic Acid (uM)	= 100 * (ChBaseAspartic_Acid / BaseAspartic_Acid) Notes: #Imported from CSCC Arginine	8.2		Yes
483	PCHBASEAAMINOADIPIC_ACID	999	N8	Percent Change from Baseline: a_Amino adipic acid (uM)	= 100 * (ChBasea_Amino adipic_acid / Basea_Amino adipic_acid) Notes: #Imported from CSCC Arginine	8.2		Yes
484	PCHBASEAAMINO_N_BUTYRIC_ACID	999	N8	Percent Change from Baseline: a_Amino_n_butyric acid (uM)	= 100 * (ChBasea_Amino_n_butyric_acid / Basea_Amino_n_butyric_acid) Notes: #Imported from CSCC Arginine	8.2		Yes
485	PCHBASEBALANINE	999	N8	Percent Change from Baseline: b_Alanine (uM)	= 100 * (ChBaseb_Alanine / Baseb_Alanine) Notes: #Imported from CSCC Arginine	8.2		Yes
486	PCHBASEBAMINOISOBUTYRIC_ACID	999	N8	Percent Change from Baseline: b_Amino isobutyric acid (uM)	= 100 * (ChBaseb_Amino isobutyric_acid / Baseb_Amino isobutyric_acid) Notes: #Imported from CSCC Arginine	8.2		Yes
487	PCHBASECITRULLINE	999	N8	Percent Change from Baseline: Citrulline (uM)	= 100 * (ChBaseCitrulline / BaseCitrulline) Notes: #Imported from CSCC Arginine	8.2		Yes
488	PCHBASECYSTATHIONINE	999	N8	Percent Change from Baseline: Cystathionine (uM)	= 100 * (ChBaseCystathionine / BaseCystathionine) Notes: #Imported from CSCC Arginine	8.2		Yes
489	PCHBASECYSTINE	999	N8	Percent Change from Baseline: Cystine (uM)	= 100 * (ChBaseCystine / BaseCystine) Notes: #Imported from CSCC Arginine	8.2		Yes
490	PCHBASECALDH	999	N8	LDH (IU/L), Central lab, % Change from baseline	= CHBASECALDH / BASECALDH * 100 if VISIT_NUM >= 4 Description: LDH (IU/L), Central lab, % Change from baseline Notes: #Imported from CSCC Arginine	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
491	PCHBASEETHANOLAMINE	999	N8	Percent Change from Baseline: Ethanolamine (uM)	=100 * (ChBaseEthanolamine / BaseEthanolamine) Notes: #Imported from CSCC Arginine	8.2		Yes
492	PCHBASEGLUTAMIC_ACID	999	N8	Percent Change from Baseline: Glutamic_acid (uM)	=100 * (ChBaseGlutamic_acid / BaseGlutamic_acid) Notes: #Imported from CSCC Arginine	8.2		Yes
493	PCHBASEGLUTAMINE	999	N8	Percent Change from Baseline: Glutamine (uM)	=100 * (ChBaseGlutamine / BaseGlutamine) Notes: #Imported from CSCC Arginine	8.2		Yes
494	PCHBASEGLYCINE	999	N8	Percent Change from Baseline: Glycine (uM)	=100 * (ChBaseGlycine / BaseGlycine) Notes: #Imported from CSCC Arginine	8.2		Yes
495	PCHBASEGAMINOBUTYRIC_ACID	999	N8	Percent Change from Baseline: g_Aminobutyric_acid (uM)	=100 * (ChBaseg_Aminobutyric_acid / Baseg_Aminobutyric_acid) Notes: #Imported from CSCC Arginine	8.2		Yes
496	PCHBASEHISTIDINE	999	N8	Percent Change from Baseline: Histidine (uM)	=100 * (ChBaseHistidine / BaseHistidine) Notes: #Imported from CSCC Arginine	8.2		Yes
497	PCHBASEHOMOCYSTINE	999	N8	Percent Change from Baseline: Homocystine (uM)	=100 * (ChBaseHomocystine / BaseHomocystine) Notes: #Imported from CSCC Arginine	8.2		Yes
498	PCHBASEHYDROXYLYSINE	999	N8	Percent Change from Baseline: Hydroxylysine (uM)	=100 * (ChBaseHydroxylysine / BaseHydroxylysine) Notes: #Imported from CSCC Arginine	8.2		Yes
499	PCHBASEHYDROXYPROLINE	999	N8	Percent Change from Baseline: Hydroxyproline (uM)	=100 * (ChBaseHydroxyproline / BaseHydroxyproline) Notes: #Imported from CSCC Arginine	8.2		Yes
500	PCHBASEHYPRO	999	N8	Percent Change from Baseline: Hypro (uM)	=100 * (ChBaseHypro / BaseHypro) Notes: #Imported from CSCC Arginine	8.2		No

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
501	PCHBASEISO LEUCINE	999	N8	Percent Change from Baseline: Isoleucine (uM)	=100 * (ChBaselsoleucine / Baselsoleucine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
502	PCHBASELE UCINE	999	N8	Percent Change from Baseline: Leucine (uM)	=100 * (ChBaseLeucine / BaseLeucine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
503	PCHBASELY SINE	999	N8	Percent Change from Baseline: Lysine (uM)	=100 * (ChBaseLysine / BaseLysine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
504	PCHBASEME THIONINE	999	N8	Percent Change from Baseline: Methionine (uM)	=100 * (ChBaseMethionine / BaseMethionine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
505	PCHBASEOR NITHINE	999	N8	Percent Change from Baseline: Ornithine (uM)	=100 * (ChBaseOrnithine / BaseOrnithine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
506	PCHBASEO_ PHOSPHOET HANOLAMINE	999	N8	Percent Change from Baseline: O_ phosphoethanolamin e (uM)	=100 * (ChBaseO_phosphoethanolamine / BaseO_phosphoethanolamine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
507	PCHBASEO_ PHOSPHOSE RINE	999	N8	Percent Change from Baseline: O_phosphoserine (uM)	=100 * (ChBaseO_phosphoserine / BaseO_phosphoserine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
508	PCHBASEPH ENYLALANIN E	999	N8	Percent Change from Baseline: Phenylalanine (uM)	=100 * (ChBasePhenylalanine / BasePhenylalanine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
509	PCHBASEPR OLINE	999	N8	Percent Change from Baseline: Proline (uM)	=100 * (ChBaseProline / BaseProline) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
510	PCHBASESA RCOSINE	999	N8	Percent Change from Baseline: Sarcosine (uM)	=100 * (ChBaseSarcosine / BaseSarcosine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
511	PCHBASESE RINE	999	N8	Percent Change from Baseline: Serine (uM)	=100 * (ChBaseSerine / BaseSerine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes
512	PCHBASETA URINE	999	N8	Percent Change from Baseline: Taurine (uM)	=100 * (ChBaseTaurine / BaseTaurine) <i>Notes:</i> #Imported from CSCC Arginine	8.2		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
513	PCHBASETHREONINE	999	N8	Percent Change from Baseline: Threonine (uM)	=100 * (ChBaseThreonine / BaseThreonine) Notes: #Imported from CSCC Arginine	8.2		Yes
514	PCHBASETRYPTOPHAN	999	N8	Percent Change from Baseline: Tryptophan (uM)	=100 * (ChBaseTryptophan / BaseTryptophan) Notes: #Imported from CSCC Arginine	8.2		Yes
515	PCHBASETYROSINE	999	N8	Percent Change from Baseline: Tyrosine (uM)	=100 * (ChBaseTyrosine / BaseTyrosine) Notes: #Imported from CSCC Arginine	8.2		Yes
516	PCHBASEVALINE	999	N8	Percent Change from Baseline: Valine (uM)	=100 * (ChBaseValine / BaseValine) Notes: #Imported from CSCC Arginine	8.2		Yes
517	PCHBASE_1_METHYLHISTIDINE	999	N8	Percent Change from Baseline: _1_Methylhistidine (uM)	=100 * (ChBase_1_Methylhistidine / Base_1_Methylhistidine) Notes: #Imported from CSCC Arginine	8.2		Yes
518	PCHBASE_3_METHYLHISTIDINE	999	N8	Percent Change from Baseline: _3_Methylhistidine (uM)	=100 * (ChBase_3_Methylhistidine / Base_3_Methylhistidine) Notes: #Imported from CSCC Arginine	8.2		Yes
519	PERCRETIC	999	N8	Percent Retic (%)	= . If CSCC_ID="0700051" and phase="1000" (HC74); ~=HEMAMSTR.RETIC otherwise Notes: #Imported from CSCC Arginine	8.3		Yes
520	PERCRETICHIGH	999	N8	Percent Retic (%) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
521	PERCRETICLOW	999	N8	Percent Retic (%) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.3		Yes
522	PERCRETIC_NA	999	C8	Percent Retic (%) - Normal or Abnormal	= ' ' if (PercRetic or PercReticLow or PercReticHigh)=. ~= 'Normal' if PercReticLow LE PercRetic LE PercReticHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
523	PGF2	999	N8	PGF2 (pg/mL)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.1		Yes
524	PGF2_ADJ	999	N8	PGF2 (pg/mL) - adjusted values when below LOD	=2.5 if PGF2_LDL=1 ~=PGF2 otherwise Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
525	PGF2_LDL	999	N8	PGF-2 measure below Limit of Detection (< 5)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	1.		Yes
526	PHASE	999	C8	Study Phase	=Phase from MSTR datasets. ~If CSCC_ID = '0900229' and PHASE='1000' in MEHBMSTR, then delete record (HC43); ~If CSCC_ID = '0900229' and PHASE='4000' in MHB2MSTR, then re-code to PHASE='1000' (HC43); Notes: #Imported from CSCC Arginine	\$8.		Yes
527	PHENYLALANINE	999	N8	Phenylalanine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
528	PLATELETCT	999	N8	Platelet Count (Xe3/mm3)	= 1064 if CSCC_ID=0900048 and PHASE=2000 (HC42); ~=1264 if CSCC_ID=0000022 and PHASE=2000 (HC25); ~=1015 if CSCC_ID=0000022 and PHASE=2100 (HC26) ~=HEMAMSTR.PLAT otherwise Notes: #Imported from CSCC Arginine	8.		Yes
529	PLATELETCTHIGH	999	N8	Platelet Count (Xe3/mm3) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
530	PLATELETCTLOW	999	N8	Platelet Count (Xe3/mm3) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
531	PLATELETCT_NA	999	C8	Platelet Count (Xe3/mm3) - Normal or Abnormal	= ' ' if (PlateletCnt or PlateletCntLow or PlateletCntHigh)=. ~= 'Normal' if PlateletCntLow LE PlateletCnt LE PlateletCntHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
532	POTASSIUM	999	N8	K (mEq/L)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1(HC62); Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
533	POTASSIUMHIGH	999	N8	K (mEq/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
534	POTASSIUMLOW	999	N8	K (mEq/L) lower limit of normal range	Notes: #Imported from CSCC Arginine	8.1		Yes

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26 variable(s) with changes

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535	POTASSIUM_NA	999	C8	K (mEq/L) - Normal or Abnormal	= ' ' if (Potassium or PotassiumLow or PotassiumHigh)=. ~= 'Normal' if PotassiumLow LE Potassium LE PotassiumHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
536	PROLINE	999	N8	Proline (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
537	PT_ID	1	C7	New Patient ID	=Der.Add_PT.PT_ID Notes: New Variable	\$7.	26JUN09:10:40	Yes
538	RANDOMIZE D	5	C3	Was patient randomized?	Notes: #Imported from CSCC Arginine	\$3.	26JUN09:10:34	Yes
539	RBC	999	N8	RBC (Xe3/mm3)	Notes: #Imported from CSCC Arginine	8.2		Yes
540	RBCHIGH	999	N8	RBC (Xe3/mm3) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
541	RBCLOW	999	N8	RBC (Xe3/mm3) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.2		Yes
542	RBC_NA	999	C8	RBC (Xe3/mm3) - Normal or Abnormal	= ' ' if (RBC or RBCLow or RBCHigh)=. ~= 'Normal' if RBCLow LE RBC LE RBCHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
543	RVTRAD	999	N8	Right Ventricular to Right Atrial difference (mm Hg)	Notes: #Imported from CSCC Arginine	8.		Yes
544	SARCOSINE	999	N8	Sarcosine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
545	SERINE	999	N8	Serine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
546	SHIFABSRE TICCNT	999	C20	Shift of Absolute Retic Count form baseline to worst value	=BaseAbsReticCnt_NA "->" WorstAbsReticCnt_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseAbsReticCnt_NA or WorstAbsReticCnt_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
547	SHIFALBUMI N	999	C20	Shift of Albumin (g/dL) form baseline to worst value	=BaseAlbumin_NA "->" WorstAlbumin_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseLDH_NA or WorstLDH_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
548	SHIFALKPH OSPH	999	C20	Shift of Alk Phosphatase (IU/L) form baseline to worst value	=BaseAlkPhosph_NA "->" WorstAlkPhosph_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseTotBilirubin_NA or WorstTotBilirubin_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
549	SHIFTALT	999	C20	Shift of ALT (IU/L) form baseline to worst value	=BaseALT_NA "->" WorstALT_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseAlkPhosph_NA or WorstAlkPhosph_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
550	SHIFTBUN	999	C20	Shift of BUN (mg/dL) form baseline to worst value	=BaseBUN_NA "->" WorstBUN_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseALT_NA or WorstALT_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
551	SHIFTCALCIU M	999	C20	Shift of Calcium (mg/dL) form baseline to worst value	=BaseCalcium_NA "->" WorstCalcium_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseCreatinine_NA or WorstCreatinine_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
552	SHIFTCHELO RIDE	999	C20	Shift of Cl form baseline to worst value	=BaseChloride_NA "->" WorstChloride_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseCO2_NA or WorstCO2_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
553	SHIFTCO2	999	C20	Shift of CO2 form baseline to worst value	=BaseCO2_NA "->" WorstCO2_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseCalcium_NA or WorstCalcium_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes

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554	SHIFTCREATI NINE	999	C20	Shift of Creatinine (mg/dL) form baseline to worst value	=BaseCreatinine_NA "->" WorstCreatinine_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseGlucose_NA or WorstGlucose_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
555	SHIFTGLUCO SE	999	C20	Shift of Glucose (mg/dL) form baseline to worst value	=BaseGlucose_NA "->" WorstGlucose_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseBUN_NA or WorstBUN_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
556	SHIFTHEMAT OCRIT	999	C20	Shift of Hematocrit (%) form baseline to worst value	=BaseHematocrit_NA "->" WorstHematocrit_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseHematocrit_NA or WorstHematocrit_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
557	SHIFTHEMO GLOBIN	999	C20	Shift of Hemoglobin (mg/dL) form baseline to worst value	=BaseHemoglobin_NA "->" WorstHemoglobin_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseSodium_NA or WorstSodium_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
558	SHIFTLDH	999	C20	Shift of LDH (u/L) form baseline to worst value	=BaseLDH_NA "->" WorstLDH_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseHemoglobin_NA or WorstHemoglobin_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
559	SHIFTMCHC	999	C20	Shift of MCHC (g/dL) form baseline to worst value	=BaseMCHC_NA "->" WorstMCHC_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseMCHC_NA or WorstMCHC_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
560	SHIFTMCV	999	C20	Shift of MCV (fl) form baseline to worst value	=BaseMCV_NA "->" WorstMCV_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseMCV_NA or WorstMCV_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
561	SHIFTMETHB	999	C20	Shift of Met Hb (%) form baseline to worst value	=BaseMetHb_NA "->" WorstMetHb_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseMetHb_NA or WorstMetHb_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes

Variable-Level Metadata for 637 Variables in Table *VISIT_R*

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
562	SHIFTPERCRETIC	999	C20	Shift of Percent Retic (%) form baseline to worst value	=BasePercRetic_NA "->" WorstPercRetic_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BasePercRetic_NA or WorstPercRetic_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
563	SHIFTPATELET CNT	999	C20	Shift of Platelet Count (Xe3/mm3) form baseline to worst value	=BasePlateletCnt_NA "->" WorstPlateletCnt_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BasePlatelet_NA or WorstPlatelet_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
564	SHIFTPOTASSIUM	999	C20	Shift of K form baseline to worst value	=BasePotassium_NA "->" WorstPotassium_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BasePotassium_NA or WorstPotassium_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
565	SHIFTRBC	999	C20	Shift of RBC (Xe3/mm3) form baseline to worst value	=BaseRBC_NA "->" WorstRBC_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseRBC_NA or WorstRBC_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
566	SHIFTSODIUM	999	C20	Shift of Na form baseline to worst value	=BaseSodium_NA "->" WorstSodium_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseSodium_NA or WorstSodium_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
567	SHIFTTOTBILIRUBIN	999	C20	Shift of Total Bilirubin (mg/dL) form baseline to worst value	=BaseTotBilirubin_NA "->" WorstTotBilirubin_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseTotProtein_NA or WorstTotProtein_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
568	SHIFTTOTPROTEIN	999	C20	Shift of Total Protein (g/dL) form baseline to worst value	=BaseTotProtein_NA "->" WorstTotProtein_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseAlbumin_NA or WorstAlbumin_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
569	SHIFTWBC	999	C20	Shift of WBC (Xe3/mm3) form baseline to worst value	=BaseWBC_NA "->" WorstWBC_NA ~This should be copied onto all records for a given patient. Description: This variable will be missing if BaseWBC_NA or WorstWBC_NA is missing Notes: #Imported from CSCC Arginine	\$20.		Yes
570	SITE	999	C3	Site	Notes: #Imported from CSCC Arginine	\$3.	12JUN09:16:31	No
571	SODIUM	999	N8	Na (mEq/L)	=CHEMMSTR.SOD ~=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62) Notes: #Imported from CSCC Arginine	8.		Yes
572	SODIUMHIGH	999	N8	Na (mEq/L) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
573	SODIUMLOW	999	N8	Na (mEq/L) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.		Yes
574	SODIUM_NA	999	C8	Na (mEq/L) - Normal or Abnormal	= ' ' if (Sodium or SodiumLow or SodiumHigh)=. ~= 'Normal' if SodiumLow LE Sodium LE SodiumHigh ~='Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
575	STFRACT	999	N8	Shortening Fraction (%)	Notes: #Imported from CSCC Arginine	8.		Yes
576	STNOT	999	C1	Shortening Fraction - Not Reported	Notes: #Imported from CSCC Arginine	\$1.		Yes
577	STUDY_DRUG_STARTDT	999	N8	Date of Start of Study Drug	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:40	No
578	TAURINE	999	N8	Taurine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
579	THREONINE	999	N8	Threonine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
580	TOTBILIRUBIN	999	N8	Total Bilirubin (mg/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62) Notes: #Imported from CSCC Arginine	8.2		Yes
581	TOTBILIRUBINHIGH	999	N8	Total Bilirubin (mg/dL) upper limit of normal range	=1.2 if (CSCC_ID=0000299 and PHASE ge 2200) or (CSCC_ID=0000423 and PHASE ge 2000) (HC75, HC76); ~=CHEMMSTR.TBILIUL otherwise Description: copy to all observations for that subject (watch out that phases these two subjects have different limits depending on phase!) Notes: #Imported from CSCC Arginine	8.2		Yes
582	TOTBILIRUBINLOW	999	N8	Total Bilirubin (mg/dL) lower limit of normal range	=0.3 if (CSCC_ID=0000299 and PHASE ge 2200) or (CSCC_ID=0000423 and PHASE ge 2000) (HC75, HC76); ~=CHEMMSTR.TBILILL otherwise Description: copy to all observations for that subject (watch out that phases these two subjects have different limits depending on phase!) Notes: #Imported from CSCC Arginine	8.2		Yes
583	TOTBILIRUBIN_NA	999	C8	Total Bilirubin (mg/dL) - Normal or Abnormal	= ' ' if (TotBilirubin or TotBilirubinLow or TotBilirubinHigh)=. ~= 'Normal' if TotBilirubinLow LE TotBilirubin LE TotBilirubinHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
584	TOTPROTEIN	999	N8	Total Protein (g/dL)	=. if CSCC_ID = '1000021' and VISIT_NUM = 1 (HC62) Notes: #Imported from CSCC Arginine	8.1		Yes
585	TOTPROTEINHIGH	999	N8	Total Protein (g/dL) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
586	TOTPROTEINLOW	999	N8	Total Protein (g/dL) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
587	TOTPROTEIN_NA	999	C8	Total Protein (g/dL) - Normal or Abnormal	= ' ' if (TotProtein or TotProteinLow or TotProteinHigh)=. ~= 'Normal' if TotProteinLow LE TotProtein LE TotProteinHigh ~= 'Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
588	TRANSYN	999	C3	Transfused?	=BLHHmstr.TRANSYN (for phase=1000); =INHHMSTR.TRANSYN(for subsequent phases) Notes: #Imported from CSCC Arginine	\$3.		Yes
589	TREATGRP	7	C9	Treatment Group, Actual	=Patient.TREATGRP Notes: #Imported from CSCC Arginine	\$9.	26JUN09:10:33	Yes
590	TREATMENT	8	C1	Treatment Group	Notes: #Imported from CSCC Arginine	\$1.	26JUN09:10:33	Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
591	TRJET	999	N8	TR Jet result	Notes: #Imported from CSCC Arginine	8.2		Yes
592	TRJETUN	999	N8	TR Jet undetectable	Notes: #Imported from CSCC Arginine	1.		Yes
593	TRYPTOPHAN	999	N8	Tryptophan (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
594	TYROSINE	999	N8	Tyrosine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
595	URINALYSIS_DAY	999	N8	Day of urinalysis (relative to 1st day on study drug)	=Der.Visit_R.urin_formdt-Der.ADD_PT.PT_Start_date+1 Notes: New Variable	8.	12JUN09:16:46	Yes
596	URIN_FORMMDT	999	N8	Urinalysis	Notes: #Imported from CSCC Arginine	Date9.	12JUN09:16:41	No
597	URIN_MCRORBC	999	C5	Microscopic RBC (#/mm ³) -Urinalysis	Notes: #Imported from CSCC Arginine	\$5.		Yes
598	URIN_PH	999	N8	pH -Urinalysis	Notes: #Imported from CSCC Arginine	8.1		Yes
599	URIN_PROT	999	C8	Protein -Urinalysis	Notes: #Imported from CSCC Arginine	\$8.		Yes
600	URIN_SPGRA	999	N8	Specific gravity -Urinalysis	Notes: #Imported from CSCC Arginine	8.3		Yes
601	URIN_WBC	999	C5	WBC (#/mm ³) -Urinalysis	Notes: #Imported from CSCC Arginine	\$5.		Yes
602	VALINE	999	N8	Valine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
603	VCAM	999	N8	VCAM (ug/mL)	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH - merge ANNABETH data with VISIT on CSCC_ID and PHASE. Notes: #Imported from CSCC Arginine	8.2		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

Metadata last updated [08JUL2009:09:10:24] Most recent change made [08JUL09:09:10]

Display order [Alphabetical] Filtering [] Key Fields [unknown]

26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
604	VISIT	9	C18	Study Visit	if phase='4000' then visit="Unscheduled"; ~else if phase='1000' then visit="Visit 1, Week -4";~else if phase='1100' then visit="Visit 2, Week -2";~else if phase='2000' then visit="Visit 3, Week 0";~else if phase='2100' then visit="Visit 4, Week 1";~else if phase='2200' then visit="Visit 5, Week 2";~else if phase='2300' then visit="Visit 6, Week 4";~else if phase='2400' then visit="Visit 7, Week 8";~else if phase='2500' then visit="Visit 8, Week 12";~else if phase='2600' then visit="Visit 9, Week 14";~else if phase='2700' then visit="Visit 10, Week 16"; Notes: #Imported from CSCC Arginine	\$18.	26JUN09:10:33	Yes
605	VISIT_NUM	10	N8	Visit - Numeric	=1 if phase = 1000 ~2 if phase = 1100 ~3 if phase = 2000 ~4 if phase = 2100 ~5 if phase = 2200 ~6 if phase = 2300 ~7 if phase = 2400 ~8 if phase = 2500 ~9 if phase = 2600 ~10 if phase = 2700 ~99 if phase = 4000 Notes: #Imported from CSCC Arginine	2.	26JUN09:10:33	Yes
606	WBC	999	N8	WBC (Xe3/mm3)	Notes: #Imported from CSCC Arginine	8.1		Yes
607	WBCHIGH	999	N8	WBC (Xe3/mm3) upper limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
608	WBCLOW	999	N8	WBC (Xe3/mm3) lower limit of normal range	Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	8.1		Yes
609	WBC_NA	999	C8	WBC (Xe3/mm3) - Normal or Abnormal	= ' ' if (WBC or WBCLow or WBCHigh)=. ~='Normal' if WBCLow LE WBC LE WBCHigh ~='Abnormal' otherwise Notes: #Imported from CSCC Arginine	\$8.		Yes
610	WEEK	999	N8	Week number	=-4 if phase='1000'; ~=-2 if phase='1100'; ~0 if phase='2000';~1 if phase='2100'; ~2 if phase='2200'; ~4 if phase='2300'; ~8 if phase='2400'; ~12 if phase='2500'; ~14 if phase='2600'; ~16 if phase='2700' Notes: #Imported from CSCC Arginine	8.0		Yes
611	WIDTH	999	N8	Width between OPRE and OHYP	Description: S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\EKTA xy data -Merge EKTAMAX with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE then merge by ID PHASE Notes: #Imported from CSCC Arginine	Best12.		Yes
612	WORSTABSR ETICCNT_NA	999	C8	Worst Absolute Retic Count- Normal or Abnormal	= 'Abnormal' if and any AbsReticCnt_NA='Abnormal' where phase >=2100 ~='Normal' if all AbsReticCnt_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
613	WORSTALBU MIN_NA	999	C8	Worst Albumin (g/dL) - Normal or Abnormal	= 'Abnormal' if and any Albumin_NA='Abnormal' where phase >=2100 ~='Normal' if all Albumin_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
614	WORSTALKP HOSPH_NA	999	C8	Worst Alk Phosphatase (IU/L) - Normal or Abnormal	= 'Abnormal' if and any AlkPhosph_NA='Abnormal' where phase >=2100 ~='Normal' if all AlkPhosph_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
615	WORSTALT_ NA	999	C8	Worst ALT (IU/L) - Normal or Abnormal	= 'Abnormal' if and any ALT_NA='Abnormal' where phase >=2100 ~='Normal' if all ALT_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
616	WORSTBUN_ NA	999	C8	Worst BUN (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any BUN_NA='Abnormal' where phase >=2100 ~='Normal' if all BUN_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
617	WORSTCALC IUM_NA	999	C8	Worst Calcium (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any Calcium_NA='Abnormal' where phase >=2100 ~='Normal' if all Calcium_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
618	WORSTCHLO RIDE_NA	999	C8	Worst Cl (mEq/L) - Normal or Abnormal	= 'Abnormal' if and any Chloride_NA='Abnormal' where phase >=2100 ~='Normal' if all Chloride_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
619	WORSTCO2_ NA	999	C8	Worst CO2 (mEq/L) - Normal or Abnormal	= 'Abnormal' if and any CO2_NA='Abnormal' where phase >=2100 ~='Normal' if all CO2_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
620	WORSTCREA TININE_NA	999	C8	Worst Creatinine (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any Creatinine_NA='Abnormal' where phase >=2100 ~='Normal' if all Creatinine_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
621	WORSTGLUC OSE_NA	999	C8	Worst Glucose (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any Glucose_NA='Abnormal' where phase >=2100 ~='Normal' if all Glucose_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
622	WORSTHEMA TOCRIT_NA	999	C8	Worst Hematocrit (%) - Normal or Abnormal	= 'Abnormal' if and any Hematocrit_NA='Abnormal' where phase >=2100 ~='Normal' if all Hematocrit_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
623	WORSTHEM OGLOBIN_NA	999	C8	Worst Hemoglobin (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any Hemoglobin_NA='Abnormal' where phase >=2100 ~='Normal' if all Hemoglobin_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
624	WORSTLDH_ NA	999	C8	Worst LDH (u/L) - Normal or Abnormal	= 'Abnormal' if and any LDH_NA='Abnormal' where phase >=2100 ~='Normal' if all LDH_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
625	WORSTMCH C_NA	999	C8	Worst MCHC (g/dL)- Normal or Abnormal	= 'Abnormal' if and any MCHC_NA='Abnormal' where phase >=2100 ~='Normal' if all MCHC_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
626	WORSTMCV_ NA	999	C8	Worst MCV (fl)- Normal or Abnormal	= 'Abnormal' if and any MCV_NA='Abnormal' where phase >=2100 ~='Normal' if all MCV_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes

Variable-Level Metadata for 637 Variables in Table VISIT_R

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
627	WORSTMETH B_NA	999	C8	Worst Met Hb (%) - Normal or Abnormal	= 'Abnormal' if and any MetHb_NA='Abnormal' where phase >=2100 ~='Normal' if all MetHb_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
628	WORSTPERC RETIC_NA	999	C8	Worst Percent Retic (%) - Normal or Abnormal	= 'Abnormal' if and any PercRetic_NA='Abnormal' where phase >=2100 ~='Normal' if all PercRetic_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
629	WORSTPLAT ELETcnt_NA	999	C8	Worst Platelet Count (Xe3/mm3) - Normal or Abnormal	= 'Abnormal' if and any PlateletCnt_NA='Abnormal' where phase >=2100 ~='Normal' if all PlateletCnt_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
630	WORSTPOTA SSIUM_NA	999	C8	Worst K (mEq/L) - Normal or Abnormal	= 'Abnormal' if and any Potassium_NA='Abnormal' where phase >=2100 ~='Normal' if all Potassium_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
631	WORSTRBC_ NA	999	C8	Worst RBC (Xe3/mm3) - Normal or Abnormal	= 'Abnormal' if and any RBC_NA='Abnormal' where phase >=2100 ~='Normal' if all RBC_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
632	WORSTSODI UM_NA	999	C8	Worst Na (mEq/L) - Normal or Abnormal	= 'Abnormal' if and any Sodium_NA='Abnormal' where phase >=2100 ~='Normal' if all Sodium_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
633	WORSTTOTB ILIRUBIN_NA	999	C8	Worst Total Bilirubin (mg/dL) - Normal or Abnormal	= 'Abnormal' if and any TotBilirubin_NA='Abnormal' where phase >=2100 ~='Normal' if all TotBilirubin_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes

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26 variable(s) with changes

Var #	name8 [1]	Order	Type/ Len	Label	Definition, Notes, et al.	Format	Latest Update	Use
634	WORSTTOTP ROTEIN_NA	999	C8	Worst Total Protein (g/dL) - Normal or Abnormal	= 'Abnormal' if and any TotProtein_NA='Abnormal' where phase >=2100 ~='Normal' if all TotProtein_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
635	WORSTWBC_ NA	999	C8	Worst WBC (Xe3/mm3)- Normal or Abnormal	= 'Abnormal' if and any WBC_NA='Abnormal' where phase >=2100 ~='Normal' if all WBC_NA='Normal' where phase >=2100 ~=' ' if there are no records where phase >=2100 Description: copy to all observations for that subject Notes: #Imported from CSCC Arginine	\$8.		Yes
636	_1_ METHYLHISTI DINE	999	N8	_1_Methylhistidine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes
637	_3_ METHYLHISTI DINE	999	N8	_3_Methylhistidine (uM)	Description: Merge S:\RhoFED\CSCC\Protocol Committees\Arginine\data\fromspon\ANNABETH\AAA\AAA_DATA with S:\RhoFED\CSCC\Protocol Committees\Arginine\data\derive\RhoLab\Rholab_clean by id sampleid to get PHASE. Then merge this dataset with VISIT by ID PHASE Notes: #Imported from CSCC Arginine	8.3		Yes

[1] Shaded variable names indicate a variable identified in DATASETS.KEYFIELDS