

バイオサイエンスデータベースセンター統合化推進プログラム
「ゲノム・疾患・医薬品のネットワークデータベース」

ネットワークによる
ゲノム・疾患・医薬品の統合

京都大学化学研究所

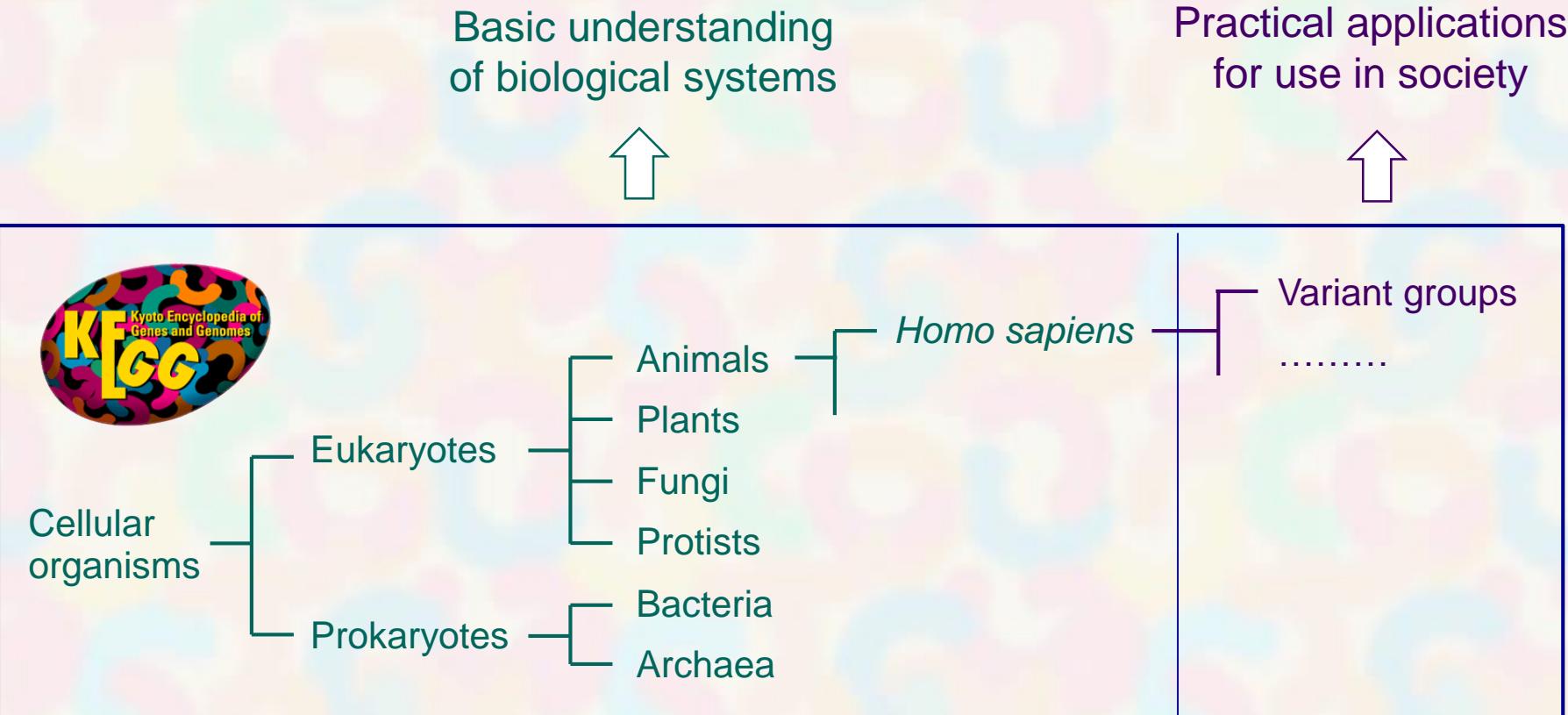
金久 實

2018年10月5日 トーゴーの日シンポジウム



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KEGG: Kyoto Encyclopedia of Genes and Genomes



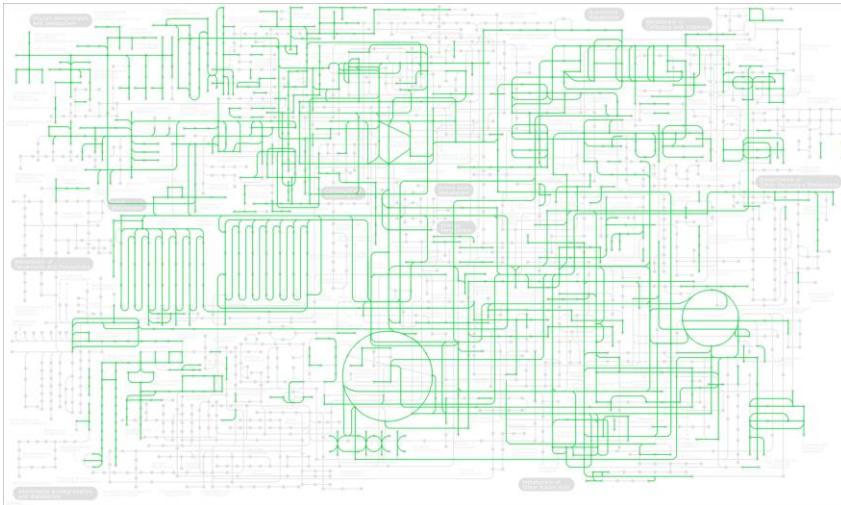
Genome, Metagenome, Metabolome,
Transcriptome, Proteome

Personal genome
Pathogen genome

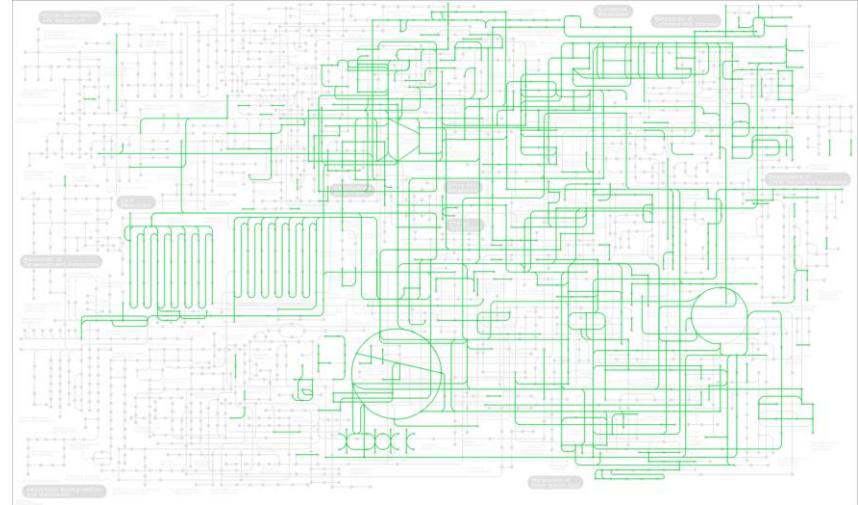
Blueprints of life

- Genetic blueprint – molecules (parts) encoded in the genome
- Chemical blueprint – molecular networks (wiring diagrams) encoded in the cell

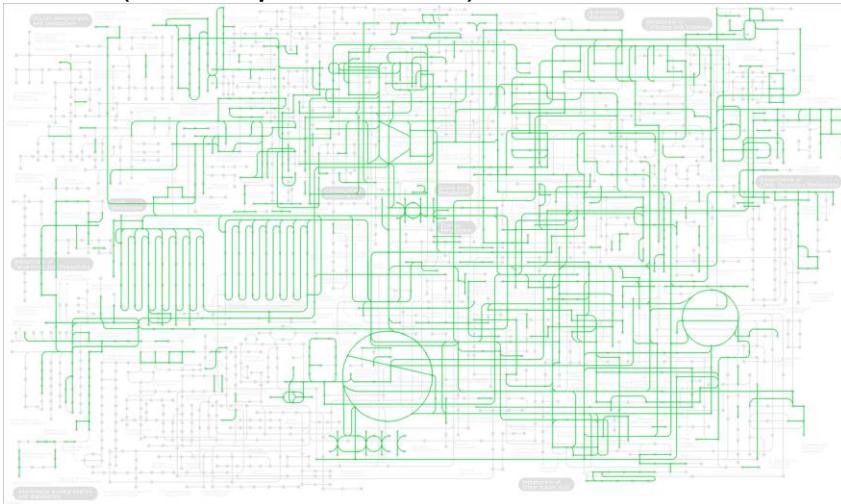
Animal (*Homo sapiens*)



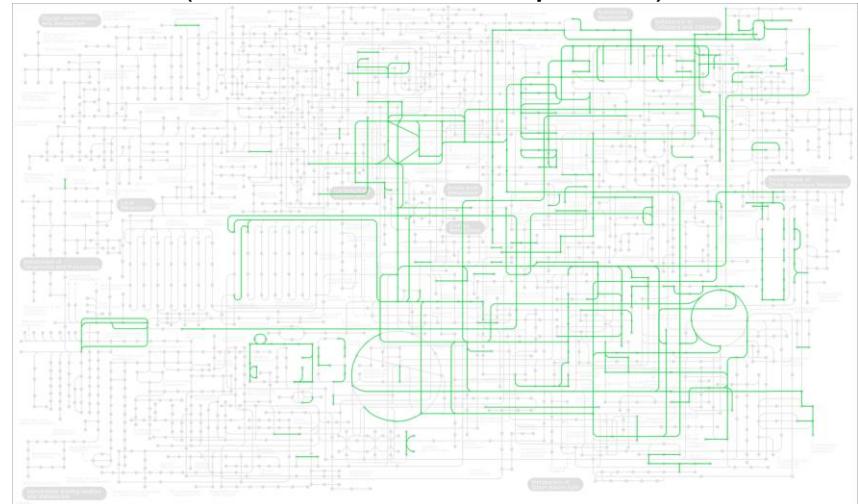
Bacteria (*Escherichia coli*)



Plant (*Arabidopsis thaliana*)



Archaea (*Methanococcus maripaludis*)



KEGG PATHWAY: Database of molecular networks

Basic network

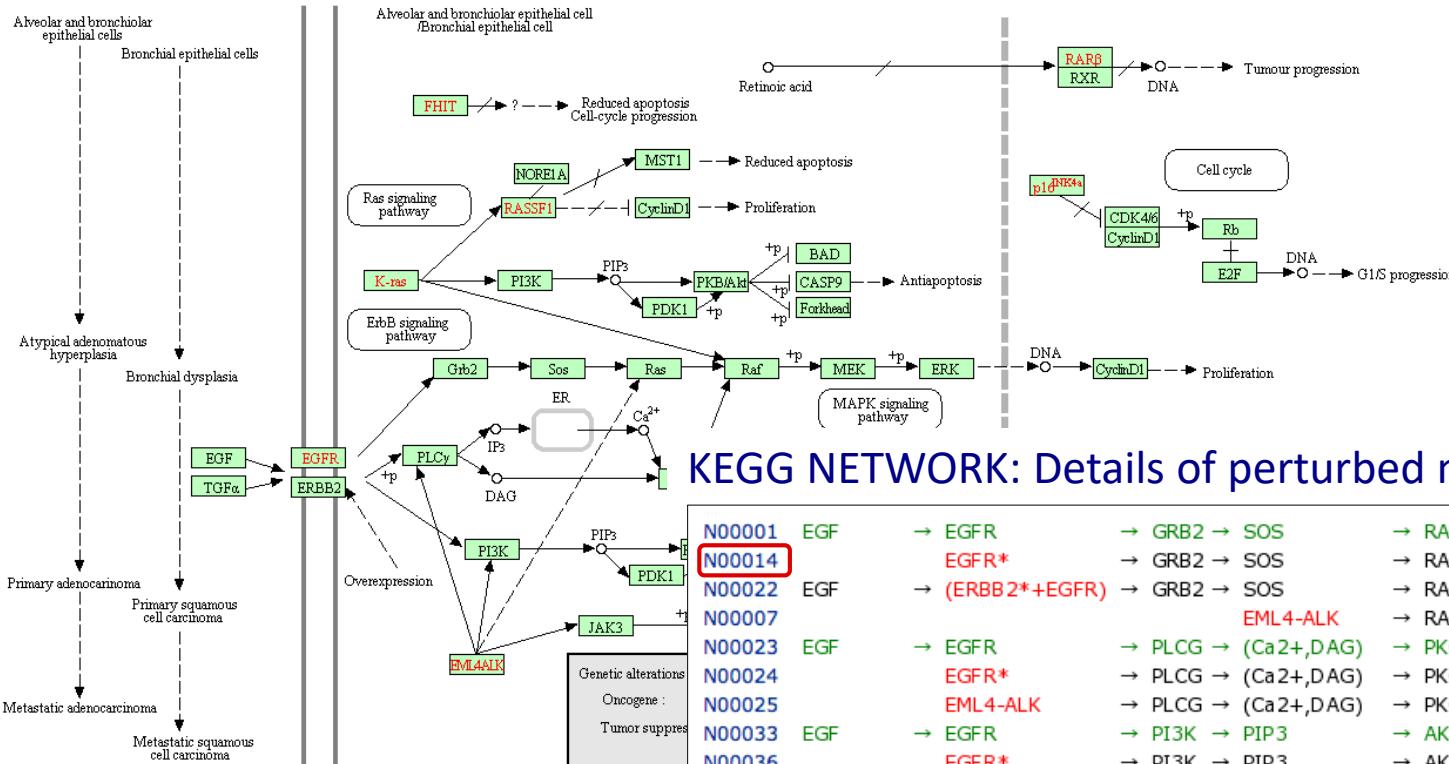
1. Metabolism
2. Genetic information processing
3. Environmental information processing
4. Cellular processes
5. Organismal systems
6. Human diseases

Cell-level network

Organism-level network

Perturbed network

NON-SMALL CELL LUNG CANCER



hsa05223 Non-small cell lung cancer

KEGG NETWORK: Details of perturbed molecular networks

N00001	EGF	\rightarrow EGFR	\rightarrow RAS	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK	\rightarrow CCND1
N00014		\rightarrow EGFR*	\rightarrow GRB2 \rightarrow SOS	\rightarrow RAS	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK
N00022	EGF	\rightarrow (ERBB2*+EGFR)	\rightarrow GRB2 \rightarrow SOS	\rightarrow RAS	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK
N00007				\rightarrow EML4-ALK	\rightarrow RAS	\rightarrow RAF	\rightarrow MEK
N00023	EGF	\rightarrow EGFR	\rightarrow PLCG \rightarrow (Ca ²⁺ ,DAG)	\rightarrow PKC	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK
N00024		\rightarrow EGFR*	\rightarrow PLCG \rightarrow (Ca ²⁺ ,DAG)	\rightarrow PKC	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK
N00025		\rightarrow EML4-ALK	\rightarrow PLCG \rightarrow (Ca ²⁺ ,DAG)	\rightarrow PKC	\rightarrow RAF	\rightarrow MEK	\rightarrow ERK
N00033	EGF	\rightarrow EGFR	\rightarrow PI3K \rightarrow PIP3	\rightarrow AKT	\rightarrow BAD		
N00036		\rightarrow EGFR*	\rightarrow PI3K \rightarrow PIP3	\rightarrow AKT	\rightarrow BAD		
N00047		\rightarrow EML4-ALK	\rightarrow PI3K \rightarrow PIP3	\rightarrow AKT	\rightarrow BAD		
N00053	Cytokine	\rightarrow Receptor	\rightarrow JAK \rightarrow STAT	\rightarrow PIM1			
N00105		\rightarrow EML4-ALK	\rightarrow JAK3 \rightarrow STAT3,STAT5				

Network Element Entry



NETWORK: N00014

Help

Entry	N00014	Network
Name	Mutation-activated EGFR to RAS-ERK signaling pathway	
Definition	EGFR* -> GRB2 -> SOS -> RAS -> RAF -> MEK -> ERK -> CCND1	
Expanded	(1956v2,1956v3) -> 2885 -> (6654,6655) -> (3265,3845,4893) -> (369,673,5894) -> (5604,5605) -> (5594,5595) -> 595	
Class	Cancer network; Signaling network; 06210 MAPK (ERK) signaling	
Type	Variant	
Pathway	hsa05223 Non-small cell lung cancer	
Disease	H00014 Non-small cell lung cancer	
Gene	1956 EGFR; epidermal growth factor receptor 2885 GRB2; growth factor receptor bound protein 2 6654 SOS1; SOS Ras/Rac guanine nucleotide exchange factor 1 6655 SOS2; SOS Ras/Rho guanine nucleotide exchange factor 2 3265 HRAS; HRas proto-oncogene, GTPase 3845 KRAS; KRAS proto-oncogene, GTPase 4893 NRAS; NRAS proto-oncogene, GTPase 369 ARAF; A-Raf proto-oncogene, serine/threonine kinase 673 BRAF; B-Raf proto-oncogene, serine/threonine kinase 5894 RAF1; Raf-1 proto-oncogene, serine/threonine kinase 5604 MAP2K1; mitogen-activated protein kinase kinase 1 5605 MAP2K2; mitogen-activated protein kinase kinase 2 5594 MAPK1; mitogen-activated protein kinase 1 5595 MAPK3; mitogen-activated protein kinase 3 595 CCND1; cyclin D1	
Variant	1956v2 EGFR mutation 1956v3 First generation TKI-resistant EGFR mutation	
Reference		
Authors	Osada H, Takahashi T.	
Title	Genetic alterations of multiple tumor suppressors and carcinogenesis and progression of lung cancer.	
Journal	Oncogene 21:7421-34 (2002) DOI: 10.1038/sj.onc.1205802	
Reference		
Authors	Hirsch FR, Scagliotti GV, Langer CJ, Varella-Garcia M	
Title	Epidermal growth factor family of receptors in preneoplastic and neoplastic lung tissue: perspectives for targeted therapies.	
Journal	Lung Cancer 41 Suppl 1:S29-42 (2003) DOI: 10.1016/S0169-5002(03)00137-5	
LinkDB	All DBs	

Variant Entry

VARIANT: 1956v2

Help

Entry	1956v2	Variant
Name	EGFR mutation	
Gene	EGFR; epidermal growth factor receptor [KO: K04361]	
Organism	hsa_var Human gene variants (Homo sapiens)	
Variation	exon 19 deletion	
Variation	mutation L858R ClinVar: 16609 376282 376280 dbSNP: 121434568 1057519848 1057519847	
Network	N00014 Mutation-activated EGFR to RAS-ERK signaling pathway N00024 Mutation-activated EGFR to PLCG-ERK signaling pathway N00036 Mutation-activated EGFR to PI3K signaling pathway N10005 First/second-generation tyrosine kinase inhibitor to EGFR mutation	
Reference		
Authors	Toyooka S, Mitsudomi T, Soh J, Aokage K, Yamane M, Oto T, Kiura K, Miyoshi S	
Title	Molecular oncology of lung cancer.	
Journal	Gen Thorac Cardiovasc Surg 59:527-37 (2011) DOI: 10.1007/s11748-010-0743-3	
Reference		
Authors	Lee DH	
Title	Treatments for EGFR-mutant non-small cell lung cancer (NSCLC): The road to a success, paved with failures.	
Journal	Pharmacol Ther 174:1-21 (2017) DOI: 10.1016/j.pharmthera.2017.02.001	
LinkDB	All DBs	

KEGG NETWORK database

Collection of network elements + Network variation maps

Nodes and edges of network elements

Node	Identifier	Coloring
Human reference gene/protein	hsa ID	None
Human gene variant	variant ID	Red
Viral or other pathogen gene/protein	K number	Purple
Metabolite and other chemical compound	C number	None
Drug	D number	Blue

Signaling network	Metabolic network	Text	Symbol
Activation (single- or multi-step)	Enzymatic reaction	->	→
Inhibition (single- or multi-step)		-	⊣
Complex formation	Substrate binding	--	—
Missing interaction	Missing reaction	//	/
Expression (single-step)	Enhanced reaction	=>	⇒
Repression (single-step)		=	⊐

Coloring of nodes and symbol representation of edges are used in network variation maps

KEGG NETWORK: Cancer Network

N00001		EGF → EGFR → GRB2 → SOS → RAS → RAF → MEK → ERK → CCND 1
N00276	■	EGF* → EGFR → GRB2 → SOS → RAS → RAF → MEK → ERK
N10005		(Gefitinib,Erlotinib,Afatinib) ⊥
N10006		Osimertinib ⊥
N00014	■	EGFR* → GRB2 → SOS → RAS → RAF → MEK → ERK → CCND 1
N00021		EGF → (ERBB 2+EGFR) → GRB2 → SOS → RAS → RAF → MEK → ERK
N10009		(Trastuzumab,Trastuzumab_emtansine,Pertuzumab,Lapatinib,Neratinib) ⊥
N00022	■■ ■	EGF → (ERBB 2*+EGFR) → GRB2 → SOS → RAS → RAF → MEK → ERK
N00015		PDGF → PDGFR → GRB2 → SOS → RAS → RAF → MEK → ERK
N00016	■	PDGF* → PDGFR → GRB2 → SOS → RAS → RAF → MEK → ERK
N00018	■	PDGFR* → GRB2 → SOS → RAS → RAF → MEK → ERK
N00215		KITLG → KIT → GRB2 → SOS → RAS → RAF → MEK → ERK
N00003	■	KIT* → GRB2 → SOS → RAS → RAF → MEK → ERK
N10001		Imatinib ⊥
N10002		(Dasatinib,Nilotinib,Bosutinib,Ponatinib) ⊥
N00002	■	BCR-ABL → GRB2 → SOS → RAS → RAF → MEK → ERK
N10003		Crizotinib ⊥
N10004		(Alectinib,Ceritinib,Brigatinib) ⊥
N00007	■	EML4-ALK → RAS → RAF → MEK → ERK → CCND 1
N00160	■	kshvK1 → RAS → RAF → MEK → ERK
N00012	■■ ■ ■ ■ ■	(KRAS*,NRAS*) → RAS → RAF → MEK → ERK → CCND 1
N10007		(Vemurafenib,Dabrafenib,Encorafenib) ⊥
N10008		(Trametinib,Cobimetinib,Binimatinib) ⊥
N00013	■ ■	BRAF* → MEK → ERK

Cancer types

Reference network

Perturbations: gene variants, viral proteins, drugs

KEGG NETWORK: Virus Network (1)

Viral Oncoprotein

KSHV (Kaposi sarcoma-associated herpesvirus) K1 protein
in comparison with
EML4-ALK fusion gene in non-small cell lung cancer

N00001	EGF	→ EGFR	→ GRB2	→ SOS	→ RAS	→ RAF	→ MEK	→ ERK	→ CCND 1
N00007				EML4-ALK	→ RAS	→ RAF	→ MEK	→ ERK	→ CCND 1
N00160				kshvK1	→ RAS	→ RAF	→ MEK	→ ERK	
N00023	EGF	→ EGFR	→ PLCG	→ (Ca2+,DAG)	→ PKC	→ RAF	→ MEK	→ ERK	→ CCND 1
N00025		EML4-ALK	→ PLCG	→ (Ca2+,DAG)	→ PKC	→ RAF	→ MEK	→ ERK	→ CCND 1
N00147	EGF	→ EGFR	→ PLCG	→ IP3	→ Ca2+	→ CALM	→ CN	→ NFAT	
N00180		kshvK1	→ PLCG2	→ IP3	→ Ca2+	→ CALM	→ CN	→ NFAT	
N00033	EGF	→ EGFR	→ PI3K	→ PIP3	→ AKT	→ BAD			
N00047		EML4-ALK	→ PI3K	→ PIP3	→ AKT	→ BAD			
N00159		kshvK1	→ PI3K	→ PIP3	→ AKT	→ MTOR			
N00053	Cytokine	→ Receptor	→ JAK	→ STAT	⇒ PIM1				
N00105		EML4-ALK	→ JAK3	→ STAT3,STAT5					

KEGG NETWORK: Virus Network (2)

Viral Mimicry

Chemokines and chemokine receptors

KSHV vCCL1, vCCL2, vCCL3 KSHV vGPCR

N00401	CXCL12	→ CXCR4	→ GNAQ	→ (PLCB,PLCG..	→ IP3	→ Ca2+	→ CALM	- CN	→ NFAT
N00432	hivEnv	→ (CXCR4,CCR..	→ GNAQ	→ PLCG	→ IP3	→ Ca2+	→ CALM	- CN	→ NFAT
N00402		hcmvUS28	→ GNAQ	→ PLCB	→ IP3	→ Ca2+	→ CALM	- CN	→ NFAT
N00407		hcmvUL33	→ (GNAQ,GNA1..	→ PLCB					⇒ (CXCL8,PTG..
N00410	DA	→ DRD1	→ GNAS	→ ADCY5	→ cAMP	→ PKA	→ CREB		
N00411		hcmvUL33	→ GNAS	→ ADCY	→ cAMP	→ PKA	→ CREB		
N00403	CX3CL1	→ CX3CR1	→ GNAI	→ ADCY	→ cAMP	→ PKA			
N00404		hcmvUS28	→ (GNAI,GNAO..	→ ADCY	→ cAMP	→ PKA			
N00412		hcmvUL33	→ (GNAI,GNAO..	→ ADCY	→ cAMP	→ PKA	→ CREB		
N00430	CXCL12	→ CXCR4	→ GNAI	→ PI3K	→ PIP3	→ AKT	→ BAD		
N00431	hivEnv	→ (CXCR4,CCR..	→ GNAI	→ PI3K	→ PIP3	→ AKT	→ BAD		
N00405	CXCL12	→ CXCR4	→ GNA12/13	→ (ARHGEF12,..	→ RHOA	→ ROCK1/2			
N00406	(CCL2,CCL3..	→ hcmvUS28	→ GNA12/13	→ (ARHGEF12,..	→ RHOA	→ ROCK1/2	→ CTNNB1		
N00408	LPA	→ LPAR	→ GNB/G	→ RHOA					
N00409		hcmvUL33	→ GNB/G	→ RHOA	→ MAP2K6	→ p38	→ CREB		
N00152	CXCL8	→ CXCR2	→ GNB/G	→ RAS	→ RAF1	→ MEK	→ ERK		
N00157		kshvGPCR	→ GNB/G	→ RAS	→ RAF1	→ MEK	→ ERK	→ (HIF1A,FOS..	⇒ (VEGFA,PDG..
N00433	CXCL12	→ CXCR4	→ GNB/G	→ RAC	→ PAK	→ LIMK1	→ CFL		
N00434	hivEnv	→ (CXCR4,CCR..	→ GNB/G	→ RAC	→ PAK	→ LIMK1	→ CFL		
N00399	CCL2	→ CCR2	→ GNB/G	→ PI3K	→ PIP3	→ AKT	→ IKK	→ NFKBIA	→ NFKB
N00400		hcmvUS28	→ GNB/G	→ PI3K	→ PIP3	→ AKT	→ IKK	→ NFKBIA	→ NFKB
N00153	(CC,CXC)	→ (CCR,CXCR)	→ GNB/G	→ PI3Kgamma	→ PREX1	→ RAC1			⇒ (IL6,CXCL8..
N00462	(kshvCCL1,..	→ (CCR3,CCR4..							
N00212	kshvCCL2	→ (CCR1,CCR5..							
N00178		kshvGPCR	→ GNB/G	→ PI3Kgamma	→ PREX1	→ RAC1	→ JNK	→ (NFKB1+REL..	⇒ (IL6,CXCL8..
N00154	CXCL8	→ CXCR2	→ GNB/G	→ PI3Kgamma	→ PIP3	→ AKT	→ MTOR		
N00427	hcmvCXCL1	→ CXCR2							
N00158		kshvGPCR	→ GNB/G	→ PI3Kgamma	→ PIP3	→ AKT	→ MTOR		
N00413	CXCL12	→ CXCR4	→ GNB/G	→ PLCB	→ (Ca2+,DAG)	→ PKC	→ PTK2B	→ (PTK2+BCAR..	
N00414				hcmvUS27	→ Ca2+	→ PKC	→ PTK2B	→ (PTK2+BCAR..	
N00428	CCL5	→ CCR5	→ GNB/G	→ PLCB	→ (Ca2+,DAG)	→ PKC			
N00429	hcmvUL22A	→ CCL5							

KEGG NETWORK: Endocrine Network

CRH-ACTH-Cortisol network

N00297	ACTH	\rightarrow (MC2R+MRAP) \rightarrow GNAS	\rightarrow ADCY	\rightarrow cAMP	\rightarrow PKA	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow (STAR,CYP11B1) \rightarrow Cortisol
N00299	ACTH	$\not\rightarrow$ (MC2R*+MRAP) $\not\rightarrow$ GNAS				
N00300	ACTH	$\not\rightarrow$ (MC2R+MRAP*) $\not\rightarrow$ GNAS				
N00321		GNAS*	\rightarrow ADCY	\rightarrow cAMP	\rightarrow PKA	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow (STAR,CYP11B1) \rightarrow Cortisol
N00323			(PDE11A*,PDE8B*)	$\not\rightarrow$ cAMP	\rightarrow (PRKAR1A+PRKACA)	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow (STAR,CYP11B1) \rightarrow Cortisol
N00320					PRKACA*	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow (STAR,CYP11B1) \rightarrow Cortisol
N00322					(PRKAR1A*+PRKACA)	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow (STAR,CYP11B1) \rightarrow Cortisol
N00298	ACTH	\rightarrow (MC2R+MRAP) \rightarrow GNAS	\rightarrow ADCY	\rightarrow cAMP	\rightarrow PKA	\rightarrow (NR5A1,NR4A1,SP1,P.. \Rightarrow CYP11B2* \rightarrow Aldosterone
N00324	CRH	\rightarrow CRHR	\rightarrow GNAS	\rightarrow ADCY	\rightarrow cAMP	\rightarrow CREB \rightarrow ACTH
N00325		RASD1*	$\not\rightarrow$ GNAI	$\not\rightarrow$ ADCY	\rightarrow cAMP	\rightarrow PKA \rightarrow ACTH
N00326			GNAS*	\rightarrow ADCY	\rightarrow cAMP	\rightarrow CREB \rightarrow ACTH
N00327	CRH	\rightarrow CRHR	\rightarrow GNAS	\rightarrow ADCY	\rightarrow cAMP	\rightarrow (PRKAR1A*+PRKACA) \rightarrow CREB \rightarrow ACTH
N00318					EGFR	\rightarrow ERK1/2 \rightarrow ACTH
N00319			USP8*	\rightarrow EGFR	\rightarrow ERK1/2	\rightarrow ACTH
N00306				NR0B1	\rightarrow NR5A1	\Rightarrow (CYP11B1,CYP17A1)
N00307				NR0B1*	$\not\rightarrow$ NR5A1	\Rightarrow (CYP11B1,CYP17A1)
N00308				NR0B1	$\not\rightarrow$ NR5A1*	$\not\rightarrow$ (CYP11B1,CYP17A1)
N00339	Cholesterol	\dashv CYP11A1	\rightarrow Pregnenolone	\dashv (HSD 3B+CYP21A2+CYP.. \rightarrow Aldosterone		
N00338	Cholesterol	\dashv CYP11A1	\rightarrow Pregnenolone	\dashv (HSD 3B+CYP17A1+CYP.. \rightarrow Cortisone	\dashv HSD11B	\rightarrow Cortisol
N00309				(Cortisone+NADPH)	\dashv HSD11B	\rightarrow (Cortisol+NADP+)
N00310				Cortisone	$\not\rightarrow$ HSD11B 1*	$\not\rightarrow$ Cortisol
N00311		NADP	\dashv H6PD	\rightarrow NADPH		
N00312		NADP	$\not\rightarrow$ H6PD*	$\not\rightarrow$ NADPH	SERPINA6	\dashv Cortisol
N00313					SERPINA6*	$\not\rightarrow$ Cortisol
N00314						

視床下部 CRH (Corticotropin releasing hormone)

↓
下垂体 ACTH (Corticotropin)

↓
副腎 Cortisol

過剰分泌 ACTH 依存性
ACTH 非依存性

PRKACA

[Brite menu | Download htext | Download json]

ICD-11 による疾患分類

Go

One-click mode

- ▼ 01 Certain infectious or parasitic diseases
 - ▼ Gastroenteritis or colitis of infectious origin
 - ▼ Bacterial intestinal infections
 - ▼ 1A00 Cholera
 - H00110 コレラ
 - ▼ 1A01 Intestinal infection due to other Vibrio
 - H00307 腸炎ビブリオ感染症
 - H00308 ビブリオ・バルニフィカス感染症
 - ▼ 1A02 Intestinal infections due to Shigella
 - H00299 細菌性赤痢
 - ▼ 1A03 Intestinal infections due to Escherichia coli
 - H00278 腸管病原性大腸菌感染症
 - H00280 腸管毒素原性大腸菌感染症
 - H01311 腸管組織侵襲性大腸菌感染症
 - H00277 腸管出血性大腸菌感染症
 - H01312 腸管凝集性大腸菌感染症
 - ▼ 1A04 Enterocolitis due to Clostridium difficile
 - H00338 偽膜性大腸炎
 - ▼ 1A05 Intestinal infections due to Yersinia enterocolitica
 - H00298 エルシニア感染症
 - ▼ 1A06 Gastroenteritis due to Campylobacter
 - H00321 カンピロバクター感染症
 - ▼ 1A07 Typhoid fever
 - H00111 腸チフス
 - ▼ 1A08 Paratyphoid Fever
 - H00112 パラチフス
 - ▼ 1A09 Infections due to other Salmonella
 - H00113 サルモネラ感染症
 - ▼ 1A0Y Other specified bacterial intestinal infections
 - H01454 結腸スピロヘータ症
 - 1A0Z Bacterial intestinal infections, unspecified
 - ▼ Bacterial foodborne intoxications
 - ▼ 1A10 Foodborne staphylococcal intoxication
 - H01175 ブドウ球菌感染症
 - ▼ 1A11 Botulism
 - H00339 ポツリヌス中毒症
 - ▼ 1A12 Foodborne Clostridium perfringens intoxication
 - H00335 ウエルシュ菌食中毒
 - ▼ 1A13 Foodborne Bacillus cereus intoxication
 - H00329 セレウス菌食中毒
 - ▼ 1A1Y Other specified bacterial foodborne intoxications
 - H00300 エンテロバクター感染症
 - 1A1Z Bacterial foodborne intoxications, unspecified

jp08403



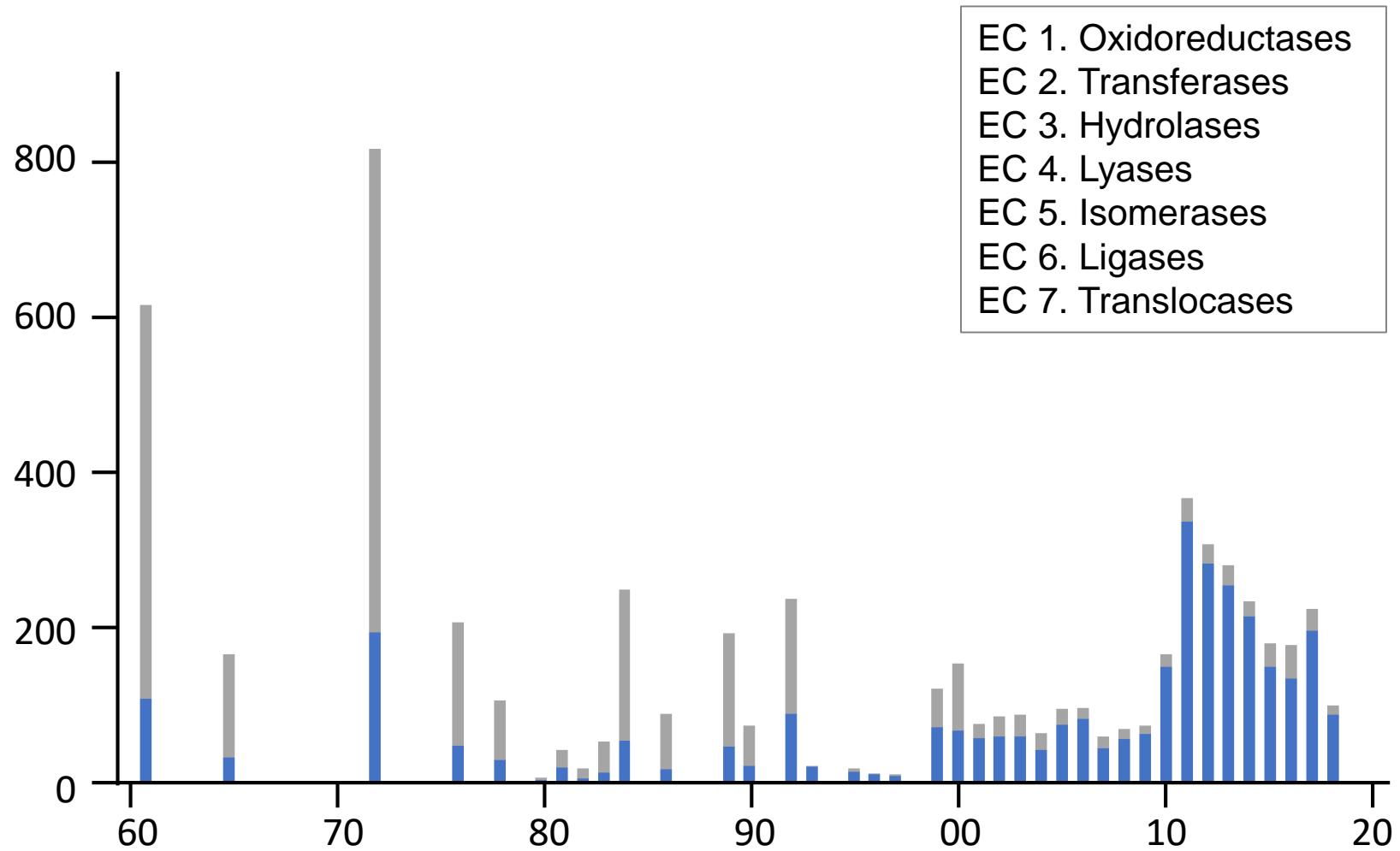
DISEASE: コレラ

Help

エントリ	H00110
名称	コレラ
概要	コレラはコレラ菌 (<i>vibrio cholerae</i>) を病原体とする腸管感染症である。コレラ毒素を产生するコレラ菌のほとんどはO1血清型であるが、O139血清型も知られている。1817年以来これまでに7回コレラの世界的な流行があり、6回目まではインドから、1961年の7回目はインドネシアから広がった。最後の流行はEl Torと名づけられたO1血清型の新しいバリエントによるもので、これは現在も続いている。O139血清型は1992年にインドで見いだされたが、世界的な流行には至っていない。
カテゴリ	感染症
階層分類	<p>感染症疾患 [BR:jp08401] 細菌感染症 その他のガムマプロテオバクテリアによる感染症 H00110 コレラ</p> <p>ICD-11 による疾患分類 [BR:jp08403] 01 Certain infectious or parasitic diseases Gastroenteritis or colitis of infectious origin Bacterial intestinal infections 1A00 Cholera H00110 コレラ</p> <p>感染症法による感染症分類 [jp08406.html] H00110</p> <p>BRITE hierarchy</p>
パスウェイ	hsa05110 コレラ菌感染
病原体	<i>Vibrio cholerae</i> O1 [GN:vch vcf vcs vce vcq vcj vci vco vcr vcm]
モジュール	M00852 <i>Vibrio cholerae</i> pathogenicity signature, toxin coregulated pilus M00850 <i>Vibrio cholerae</i> pathogenicity signature, cholera toxins
治療薬	レボフロキサシン水和物 [DR:D00588] ドキシサイクリン塩酸塩水和物 [DR:D02129]
リンク	ICD-11: 1A00 ICD-10: A00 MeSH: D002771 MedlinePlus: 000303
文献	PMID:7704895
著者	Kaper JB, Morris JG Jr, Levine MM
タイトル	Cholera.
雑誌	Clin Microbiol Rev 8:48-86 (1995)

H00110

EC番号について



引用文献より実験を行った酵素のアミノ酸配列が判明したものの割合を青で示した