

遺伝性乳癌や卵巣癌に関わると言われるBRCA1についてVaProSで調べてみましょう。

まず、BRCA1のアミノ酸配列をSequenceのQueryとして入力し、Searchをクリック

HISTORY

VaProS

Platform for Drug Discovery, Informatics, and Structural Life Science

HOMEABOUTSTATISTICSMANUALTUTORIAL

KeywordSequenceID List

Query: DNA/protein sequence (FASTA format). example

DLRNPEQSTSEKAVLTSSQSSSEYPISONPEGLSANKFEVSADSSISKKEPGVERSSPSK
CPSLDDRWMHSCSGSLQNRNYPSEELIKVVDVEEQLEESGPHDLTETSYLPRODLEG
TPYLESGISLFSDDPESDPSEDRAPE SARVGNIPSSISALKVPOLKVAESAQSPAAHTT
DTAGYNAMEE SVSREKPELTASTERNKRMVMVSGLTPEEFMLVYKFARKHHITLNL
TEETHVMKTDAEFFVCERTLK YFLGIAGGKVVVS YFWVTQSIKERKMLNEHDFEVRGDV
VNGRNHOGPKRARESDRKIFRGL EICCYGPFINMPTDQLEMMVOLCGASVVKELSSFTL
GTGVHPVVVQPDAWTEDNGFHAIGOMCEAPVVIREWVLDSVALYQCQELDTYLIQIPH
SHY

Space and numerical/control characters are automatically neglected.

SearchClear

Questionnaire

あなたはの所属は以下のいずれですか？
☐ 企業
☐ アカデミア
☐ その他
VaProSの利用ははじめてですか？
☐ はじめて
☐ 2回目以降
VaProSの更新やアンケートなどの最新情報を
受け取りたい方は、以下にメールアドレスを記載ください。

SubmitReset

VaProS: VARIation effect on PROtein Structure and function

VaProS, VARIation effect on PROtein Structure and function, is a new data cloud for Structural Life Science and is the core technology to lead the collaboration between the discipline in Structural Biology and the whole Life Sciences. Led by the initiative of National Institute of Genetics, VaProS has been developed around the Integrated Structural Biology Database at Institute for Protein Research in Osaka

20件の結果が表示されますが、その中で情報量の多い1番を選んでチェックを入れ、Details(go)をクリック。

VaProS | Home - Mozilla Firefox

ファイル(E) 編集(E) 表示(V) 履歴(S) ブックマーク(B) ScrapBook(Q) ツール(T) ヘルプ(H)

VaProS | Home

検索

HISTORY

VaProS Variation effect on PROtein Structure and function

Platform for Drug Discovery, Informatics, and Structural Life Science

HOME ABOUT STATISTICS MANUAL TUTORIAL

Sequence results - hits:20

Details (Go)

	UniProtKB	Organism	Name	Gene ID	Variant Position	Sequence	Molecular Interactions #	PPi	3D Interaction ?	NLDB ?	hGloP ?	GNP Expression ?	COXPRESdb ?	Pathway DB	Phenotype	S-VAR ?
1	☒ P38398	Homo sapiens	breast cancer 1, early onset	672	show	show	16461	674	1	0	1	1	0	32	4	link
2	☐ P38398	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
3	☐ P38398	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
4	☐ B7ZA83	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
5	☐ E7ENB7	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
6	☐ C9IZW4	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
7	☐ E7EQW4	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
8	☐ E9PH68	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
9	☐ K7EPC7	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
10	☐ H0Y850	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
11	☐ E7EWN5	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link

最初にMolecular Interactions とTag Cloudが表示されます。
BRCA1は多くのタンパク質とInteractionを持つのでリストとして示されます。

VaProS | Home x VaProS | Detail x
p4d-info.nig.ac.jp/vapros/detail/detail.html?ac=P38398&varpos=P38398@G1038E&dna=0&mmi=16461

Molecular Interactions (Powered by Cytoscape.js)

Molecular Interactions: 16461

Download

	Query: Type	Query: Name	Query: Organism	Target: Type	Target: Name	Target
1	protein	BRCA1	Homo sapiens	ligand	SID17434062	-
2	protein	BRCA1	Homo sapiens	ligand	SID57257558	-
3	protein	BRCA1	Homo sapiens	protein	ORC2	Homo
4	protein	BRCA1	Homo sapiens	ligand	SID56317210	-
5	protein	BRCA1	Homo sapiens	ligand	SID3716944	-
6	protein	BRCA1	Homo sapiens	ligand	GNF-Pf-2718	-
7	protein	BRCA1	Homo sapiens	ligand	SID17431444	-
8	protein	BRCA1	Homo sapiens	ligand	SID24813212	-
9	protein	BRCA1	Homo sapiens	ligand	SID17403180	-
10	protein	BRCA1	Homo sapiens	ligand	SID26728881	-
11	protein	BRCA1	Homo sapiens	ligand	SID850628	-
12	protein	BRCA1	Homo sapiens	ligand	SID26659571	-
13	protein	BRCA1	Homo sapiens	ligand	SID24822091	-
14	protein	BRCA1	Homo sapiens	ligand	5-(3-Azido-4-chloro-phenyl)-6-ethyl-pyrimidine-2,4-diamine	-
15	protein	BRCA1	Homo sapiens	ligand	SID49824534	-
16	protein	BRCA1	Homo sapiens	ligand	SID24816355	-
17	protein	BRCA1	Homo sapiens	ligand	SID14737177	-
18	protein	BRCA1	Homo sapiens	ligand	SID22405572	-
19	protein	BRCA1	Homo sapiens	ligand	SID56323463	-
20	protein	BRCA1	Homo sapiens	ligand	SID22413990	-
21	protein	BRCA1	Homo sapiens	ligand	SID103051160	-
22	protein	BRCA1	Homo sapiens	ligand	SID103074795	-
23	protein	BRCA1	Homo sapiens	ligand	SID49731064	-
24	protein	BRCA1	Homo sapiens	ligand	SID17508694	-
25	protein	BRCA1	Homo sapiens	ligand	SID51086638	-

ここをクリックすると

prev next 1 2 10 100 600 650 659

Powered by d3-cloud)

Export image(PNG)



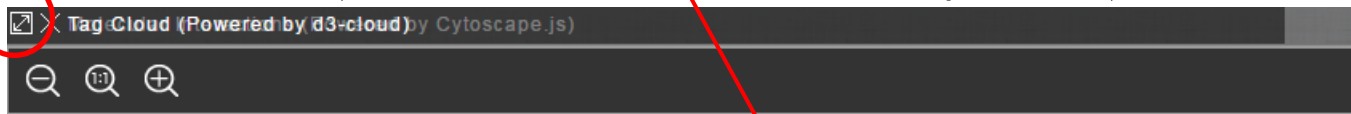
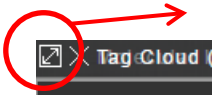
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	Query: Type	Query: Name	Query: Organism	Target: Type	Target: Name	Target: Organism	Target: EntrezGene ID	Target: RefSeq
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16453	protein	BRCA1	Homo sapiens	ligand	SID57258376	-	-	-
16454	protein	BRCA1	Homo sapiens	protein	MAP3K3	Homo sapiens	4215	Q96J14
16455	protein	BRCA1	Homo sapiens	ligand	SID24797339	-	-	-
16456	protein	BRCA1	Homo sapiens	ligand	SID24830013	-	-	-
16457	protein	BRCA1	Homo sapiens	ligand	SID24793084	-	-	-
16458	protein	BRCA1	Homo sapiens	ligand	SID124895165	-	-	-
16459	protein	BRCA1	Homo sapiens	protein	KPNA2	Homo sapiens	3838	P51588
16460	protein	BRCA1	Homo sapiens	ligand	SID22400861	-	-	-
16461	protein	BRCA1	Homo sapiens	ligand	SID49644597	-	-	-

あまりに多いのでとりあえずTag Cloudの方を見てみましょう。



全画面表示にしてみると BRCA1が一番大きく表示されています。



BRCA1

BRCA1をクリック



- References

文献が表示されます。

タイトルから、癌抑制遺伝子産物で癌の抑制に関わっているようです。

Word: **BRCA1**

ID

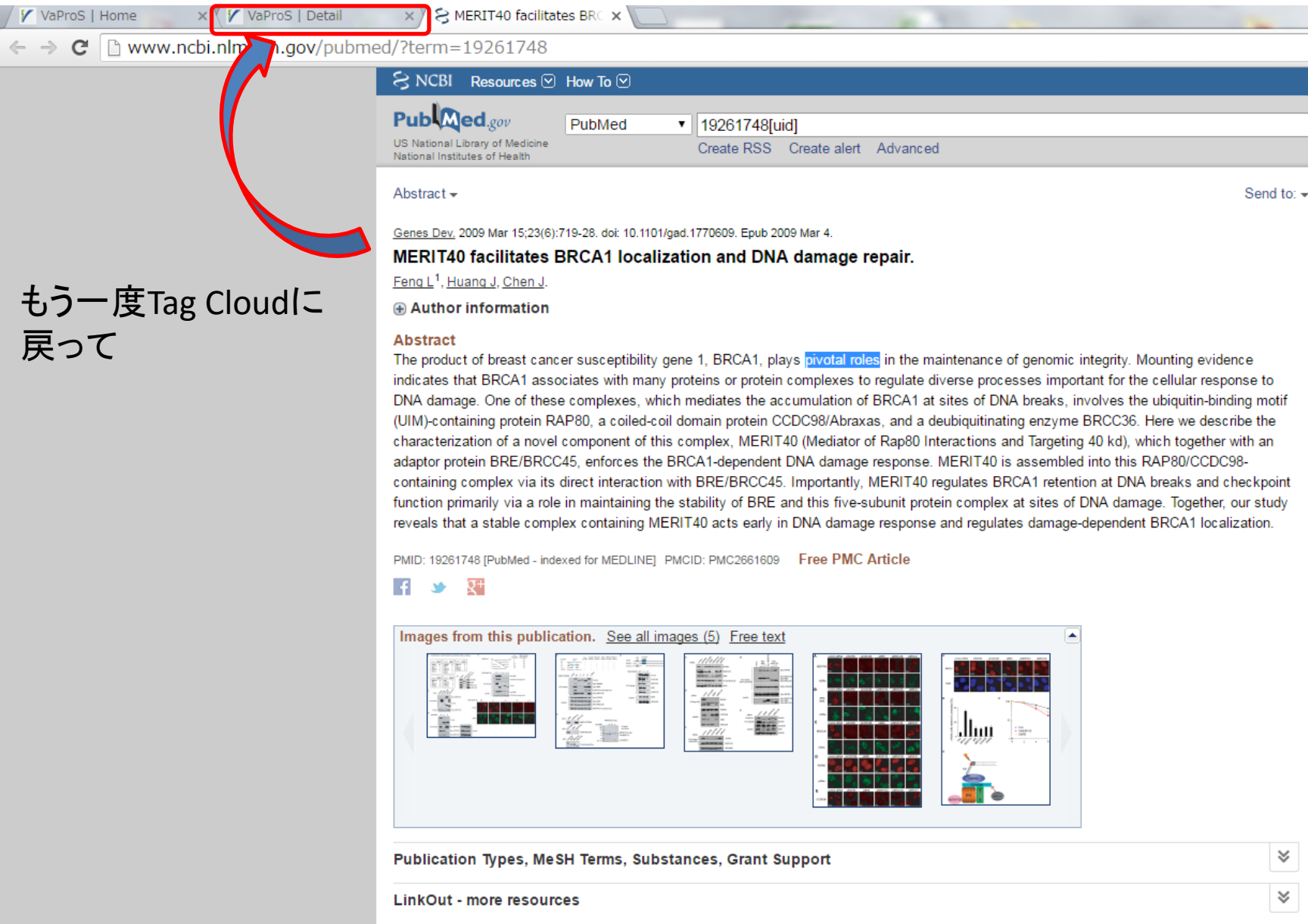
Title

- [PMID:23867111](#) A high-throughput functional complementation assay for classification of BRCA1 missense variants.
Bouwman P., van der Gulden H., van der Heijden I., Drost R., Klijn C.N., Prasetyanti P., Pieterse M., Wientjens E., Seibler J., Hogervorst F.B., Jonkers J.
Cancer Discov. 3:1142-1155(2013).
- [PMID:21673012](#) KIAA0101 interacts with **BRCA1** and regulates centrosome number.
Kais Z., Barsky S.H., Mathsyaraja H., Zha A., Ransburgh D.J., He G., Pilarski R.T., Shapiro C.L., Huang K., Parvin J.D.
Mol. Cancer Res. 9:1091-1099(2011).
- [PMID:20513136](#) Detection of splicing aberrations caused by **BRCA1** and BRCA2 sequence variants encoding missense substitutions: implications for prediction of pathogenicity.
Walker L.C., Whiley P.J., Couch F.J., Farrugia D.J., Healey S., Eccles D.M., Lin F., Butler S.A., Goff S.A., Thompson B.A., Lakhani S.R., Da Silva L.M., Tavtigian S.V., Goldgar D.E., Brown M.A., Spurdle A.B.
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Stolz A., Ertlych N., Kienitz A., Vogel C., Schneider V., Fritz B., Jacob R., Dittmar G., Weichert W., Petersen I., Bastians H.
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- [PMID:20351172](#) The UBXN1 protein associates with autoubiquitinated forms of the BRCA1 tumor suppressor and inhibits its enzymatic function.
Wu-Baer F., Ludwig T., Baer R.
Mol. Cell. Biol. 30:2787-2798(2010).
- [PMID:20160719](#) Identification of DBC1 as a transcriptional repressor for **BRCA1**.
Hiraie H
Br J Cancer
- [PMID:20159462](#) Comparison of the structures and peptide binding specificities of the BRCT domains of MDC1 and **BRCA1**.
Campbell S.J., Edwards R.A., Glover J.N.
Structure 18:167-176(2010).
- [PMID:19261748](#) MERIT40 facilitates **BRCA1** localization and DNA damage repair.
Feng L., Huang J., Chen J.
Genes Dev. 23:719-728(2009).
- [PMID:19261748](#) MERIT40 controls **BRCA1**-Rap80 complex integrity and recruitment to DNA double-strand breaks.
Feng L., Patterson-Fortin J., Messick T., Feng D., Shanbhag N., Wang Y., Greenberg R.A.
Genes Dev. 23:740-754(2009).

気になる文献があればPMIDをクリック

文献を参照することができます

もう一度Tag Cloudに戻って



Abstract

Genes Dev. 2009 Mar 15;23(6):719-28. doi: 10.1101/gad.1770609. Epub 2009 Mar 4.

MERIT40 facilitates BRCA1 localization and DNA damage repair.

Feng L¹, Huang J, Chen J.

Author information

Abstract

The product of breast cancer susceptibility gene 1, BRCA1, plays **pivotal roles** in the maintenance of genomic integrity. Mounting evidence indicates that BRCA1 associates with many proteins or protein complexes to regulate diverse processes important for the cellular response to DNA damage. One of these complexes, which mediates the accumulation of BRCA1 at sites of DNA breaks, involves the ubiquitin-binding motif (UIM)-containing protein RAP80, a coiled-coil domain protein CCDC98/Abraxas, and a deubiquitinating enzyme BRCC36. Here we describe the characterization of a novel component of this complex, MERIT40 (Mediator of Rap80 Interactions and Targeting 40 kd), which together with an adaptor protein BRE/BRCC45, enforces the BRCA1-dependent DNA damage response. MERIT40 is assembled into this RAP80/CCDC98-containing complex via its direct interaction with BRE/BRCC45. Importantly, MERIT40 regulates BRCA1 retention at DNA breaks and checkpoint function primarily via a role in maintaining the stability of BRE and this five-subunit protein complex at sites of DNA damage. Together, our study reveals that a stable complex containing MERIT40 acts early in DNA damage response and regulates damage-dependent BRCA1 localization.

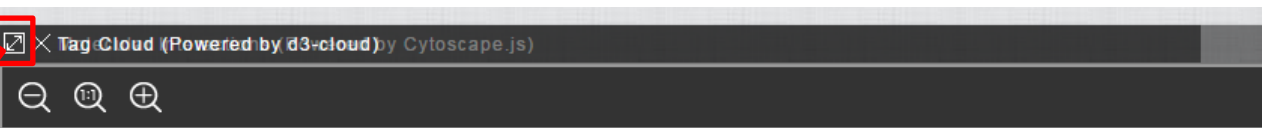
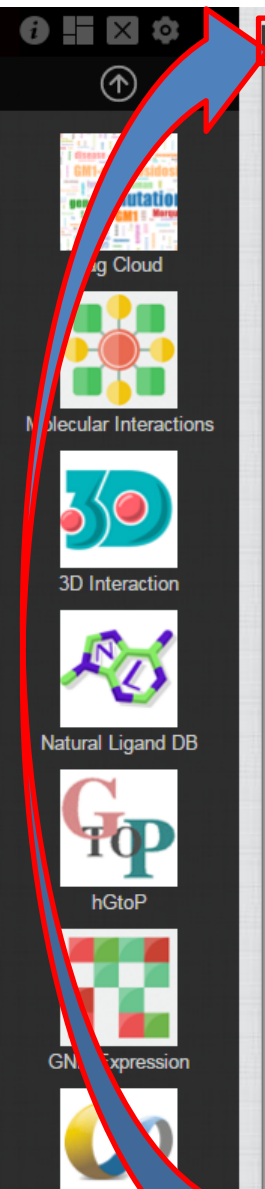
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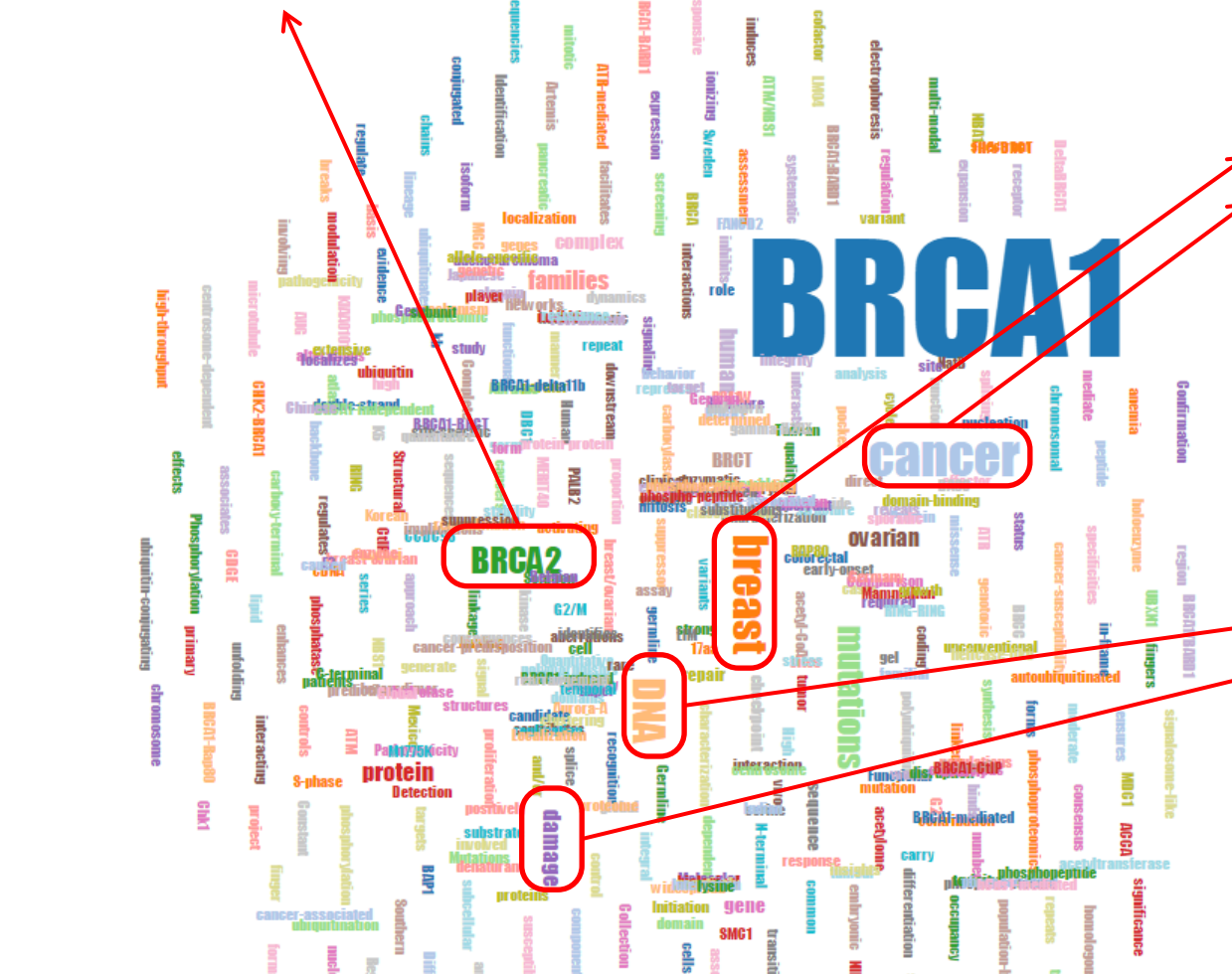
Publication Types, MeSH Terms, Substances, Grant Support

LinkOut - more resources

画面を小さくしてもう一度Molecular Interactionsを見てみましょう。



更にBRCA2もあるようです。



癌やbreastという言葉が見えます。

DNAの損傷と癌化も関係があるようです。

たくさんの単語が挙げられているのはMolecular Interactionsの結果からもわかるように相互作用を持つタンパク質の種類が多いことを表しているようです。

そのためにTarget: Typeをクリック

Tag Cloud

Molecular Interactions

3D Interaction

Natural Ligand DB

hGtoP

GNP Expression

COXPRESdb

Molecular Interactions: 16461 Download

	Query: Type	Query: Name	Query: Organism	Target: Type	Target: Name	Target: Organism
1	protein	BRCA1	Homo sapiens	ligand	SID17434062	-
2	protein	BRCA1	Homo sapiens	ligand	SID57257558	-
3	protein	BRCA1	Homo sapiens	protein	ORC2	Homo sapiens
4	protein	BRCA1	Homo sapiens	ligand	SID56317210	-
5	protein	BRCA1	Homo sapiens	ligand	SID3716944	-
6	protein	BRCA1	Homo sapiens	ligand	GNF-Pf-2718	-
7	protein	BRCA1	Homo sapiens	ligand	SID17431444	-
8	protein	BRCA1	Homo sapiens	ligand	SID24813212	-
9	protein	BRCA1	Homo sapiens	ligand	SID17403180	-
10	protein	BRCA1	Homo sapiens	ligand	SID26728881	-
11	protein	BRCA1	Homo sapiens	ligand	SID850628	-
12	protein	BRCA1	Homo sapiens	ligand	SID26659571	-
13	protein	BRCA1	Homo sapiens	ligand	SID24822091	-
14	protein	BRCA1	Homo sapiens	ligand	5-(3-Azido-4-chloro-phenyl)-6-ethyl-pyrimidine-2,4-diamine	-
15	protein	BRCA1	Homo sapiens	ligand	SID49824534	-
16	protein	BRCA1	Homo sapiens	ligand	SID24816355	-
17	protein	BRCA1	Homo sapiens	ligand	SID14737177	-
18	protein	BRCA1	Homo sapiens	ligand	SID22405572	-
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21	protein	BRCA1	Homo sapiens	ligand	SID103051160	-
22	protein	BRCA1	Homo sapiens	ligand	SID103074795	-
23	protein	BRCA1	Homo sapiens	ligand	SID49731064	-
24	protein	BRCA1	Homo sapiens	ligand	SID17508694	-
25	protein	BRCA1	Homo sapiens	ligand	SID51086638	-

prev next 1 2 10 100 800 850 850

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Export image(PNG)

Molecular Interactions: 16461

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	Query: Type ▲	Query: Name	Query: Organism	Target: Type	Target: Name	Target: Organism	T ▲
1	protein	BRCA1	Homo sapiens	complex	SUMO1:C93-UBE2I	-	-
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3	protein	BRCA1	Homo sapiens	complex	SUMO1:BRCA1	-	-
4	protein	BRCA1	Homo sapiens	complex	SUMO1:BRCA1	-	-
5	protein	BRCA1	Homo sapiens	complex	RPA heterotrimer	-	-
6	protein	BRCA1	Homo sapiens	complex	Meiotic single-stranded DNA complex	-	-
7	protein	BRCA1	Homo sapiens	complex	ATF2/BRCA1/Oct-1/Neurofibromin	-	-
8	protein	BRCA1	Homo sapiens	complex	BARD1/CSTF1/BRCA1	-	-
9	protein	BRCA1	Homo sapiens	complex	Aurora A/BRCA1	-	-
10	protein	BRCA1	Homo sapiens	complex	E2F6/DP	-	-
11	protein	BRCA1	Homo sapiens	complex	H2AFX-Nucleosome	-	-
12	protein	BRCA1	Homo sapiens	complex	BRCA1/BARD1	-	-
13	protein	BRCA1	Homo sapiens	complex	BRCA1:BARD1	-	-
14	protein	BRCA1	Homo sapiens	complex	H2AFX-Nucleosome	-	-
15	protein	BRCA1	Homo sapiens	complex	Meiotic single-stranded DNA complex	-	-
16	protein	BRCA1	Homo sapiens	complex	SUMO1:C93-UBE2I	-	-
17	protein	BRCA1	Homo sapiens	complex	E2F6/DP	-	-

Complexが並びます。

更に下へスクロールしていくと

Molecular Interactions: 16461

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	Query: Type ▲	Query: Name	Query: Organism	Target: Type	Target: Name	Target: Organism	T ▲
9	protein	BRCA1	Homo sapiens	complex	Aurora A/BRCA1	-	-
10	protein	BRCA1	Homo sapiens	complex	E2F6/DP	-	-
11	protein	BRCA1	Homo sapiens	complex	H2AFX-Nucleosome	-	-
12	protein	BRCA1	Homo sapiens	complex	BRCA1/BARD1	-	-
13	protein	BRCA1	Homo sapiens	complex	BRCA1:BARD1	-	-
14	protein	BRCA1	Homo sapiens	complex	H2AFX-Nucleosome	-	-
15	protein	BRCA1	Homo sapiens	complex	Meiotic single-stranded DNA complex	-	-
16	protein	BRCA1	Homo sapiens	complex	SUMO1:C93-UBE2I	-	-
17	protein	BRCA1	Homo sapiens	complex	E2/ERA (dimer)/BRCA1	-	-
18	protein	BRCA1	Homo sapiens	complex	FANCD2/FANCI/H2AX	-	-
19	protein	BRCA1	Homo sapiens	complex	UBE2I:SUMO2,UBE2I:SUMO3	-	-
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22	protein	BRCA1	Homo sapiens	complex	BRCA1/BACH1	-	-
23	protein	BRCA1	Homo sapiens	complex	UBE2I:SUMO2,UBE2I:SUMO3	-	-
24	protein	BRCA1	Homo sapiens	complex	UBE2I:SUMO2,UBE2I:SUMO3	-	-
25	protein	BRCA1	Homo sapiens	ligand	SID17434062	-	-

リガンドが現れました。

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Molecular Interactions 16461

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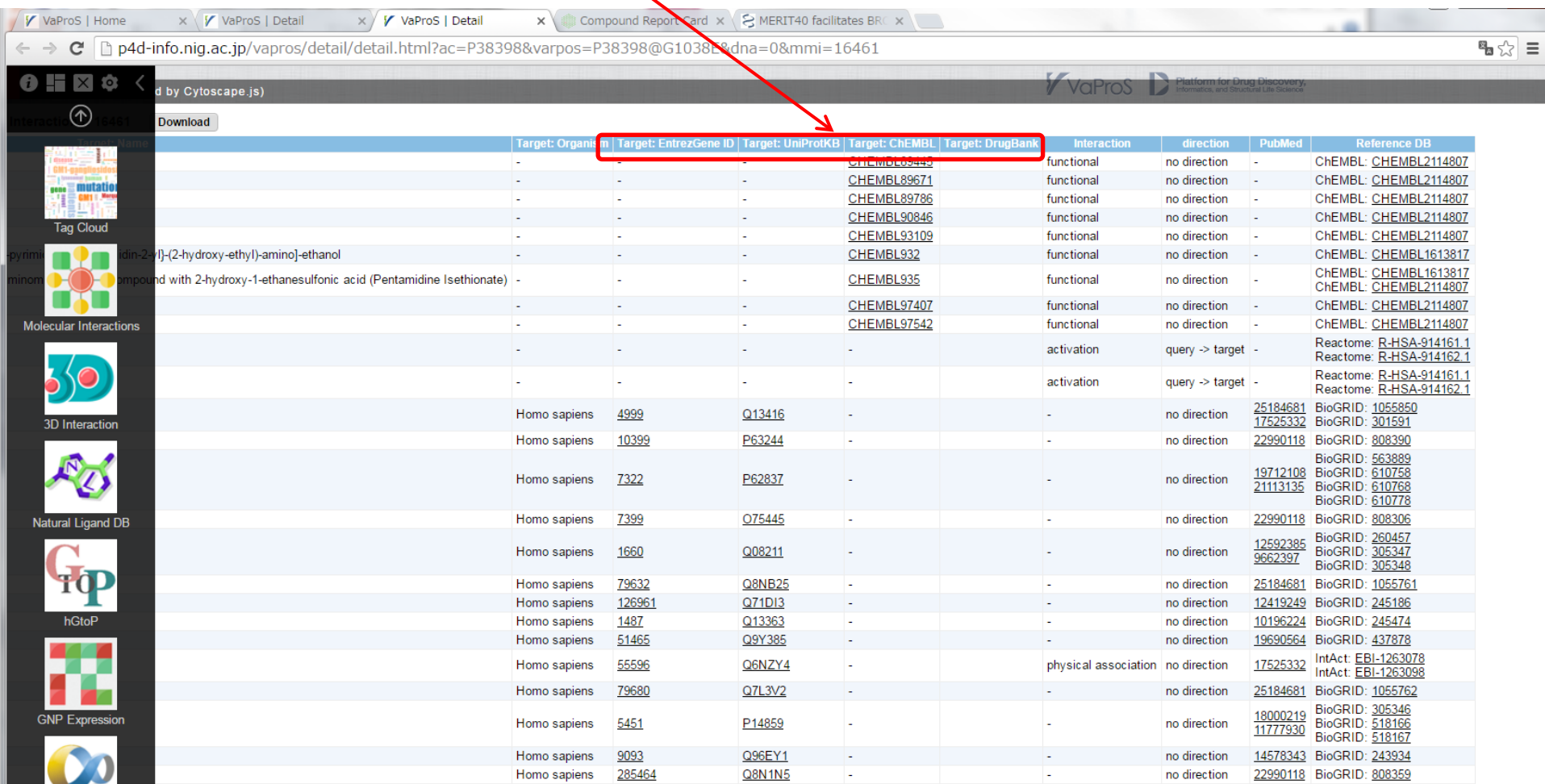
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15813	protein	BRCA1	Homo sapiens	protein	PRKAG3	Homo s
15814	protein	BRCA1	Homo sapiens	protein	PPP2CA	Homo s
15815	protein	BRCA1	Homo sapiens	protein	GNB2L1	Homo s
15816	protein	BRCA1	Homo sapiens	protein	CDK4	Homo s
15817	protein	BRCA1	Homo sapiens	protein	KIF22	Homo s
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15819	protein	BRCA1	Homo sapiens	protein	CCND1	Homo s
15820	protein	BRCA1	Homo sapiens	protein	USH2A	Homo s
15821	protein	BRCA1	Homo sapiens	protein	DHX9	Homo s
15822	protein	BRCA1	Homo sapiens	protein	FAM184A	Homo s
15823	protein	BRCA1	Homo sapiens	protein	HIST2H3D	Homo s

全画面表示にして

633番目の画面でproteinが現れました。

更に右側をみていくと

Targetに関してUniProtKB, ChEMBLなどで更に詳しい情報を得ることができます。



Target: Organism	Target: EntrezGene ID	Target: UniProtKB	Target: ChEMBL	Target: DrugBank	Interaction	direction	PubMed	Reference DB
-	-	-	CHEMBL89449	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL89671	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL89786	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL90846	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL93109	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL932	-	functional	no direction	-	ChEMBL: CHEMBL1613817
-	-	-	CHEMBL935	-	functional	no direction	-	ChEMBL: CHEMBL1613817 ChEMBL: CHEMBL2114807
-	-	-	CHEMBL97407	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL97542	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	-	-	activation	query -> target	-	Reactome: R-HSA-914161.1 Reactome: R-HSA-914162.1
-	-	-	-	-	activation	query -> target	-	Reactome: R-HSA-914161.1 Reactome: R-HSA-914162.1
Homo sapiens	4999	Q13416	-	-	-	no direction	25184681 17525332	BioGRID: 1055850 BioGRID: 301591
Homo sapiens	10399	P63244	-	-	-	no direction	22990118	BioGRID: 808390
Homo sapiens	7322	P62837	-	-	-	no direction	19712108 21113135	BioGRID: 563889 BioGRID: 610758 BioGRID: 610768 BioGRID: 610778
Homo sapiens	7399	Q75445	-	-	-	no direction	22990118	BioGRID: 808306
Homo sapiens	1660	Q08211	-	-	-	no direction	12592385 9662397	BioGRID: 260457 BioGRID: 305347 BioGRID: 305348
Homo sapiens	79632	Q8NB25	-	-	-	no direction	25184681	BioGRID: 1055761
Homo sapiens	126961	Q71D13	-	-	-	no direction	12419249	BioGRID: 245186
Homo sapiens	1487	Q13363	-	-	-	no direction	10196224	BioGRID: 245474
Homo sapiens	51465	Q9Y385	-	-	-	no direction	19690564	BioGRID: 437878
Homo sapiens	55596	Q6NZY4	-	-	physical association	no direction	17525332	IntAct: EBI-1263078 IntAct: EBI-1263098
Homo sapiens	79680	Q7L3V2	-	-	-	no direction	25184681	BioGRID: 1055762
Homo sapiens	5451	P14859	-	-	-	no direction	18000219 11777930	BioGRID: 305346 BioGRID: 518166 BioGRID: 518167
Homo sapiens	9093	Q96EY1	-	-	-	no direction	14578343	BioGRID: 243934
Homo sapiens	285464	Q8N1N5	-	-	-	no direction	22990118	BioGRID: 808359

ここで一度VaProSのHomeに戻りましょう。

Homeをクリック

Browser tabs: VaProS | Home, VaProS | Detail, VaProS | Detail, Compound Report Card, MERIT40 facilitates BR...

URL: ig.ac.jp/vaproS/detail/detail.html?ac=P38398&varpos=P38398@G1038E&dna=0&mmi=16461

VaProS Platform for Drug Discovery, Informatics, and Structural Life Science

Download

Target: Organism	Target: EntrezGene ID	Target: UniProtKB	Target: ChEMBL	Target: DrugBank	Interaction	direction	PubMed	Reference DB
-	-	-	CHEMBL89445	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL89671	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL89786	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL90846	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL93109	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL932	-	functional	no direction	-	ChEMBL: CHEMBL1613817
-	-	-	CHEMBL935	-	functional	no direction	-	ChEMBL: CHEMBL1613817 ChEMBL: CHEMBL2114807
-	-	-	CHEMBL97407	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	CHEMBL97542	-	functional	no direction	-	ChEMBL: CHEMBL2114807
-	-	-	-	-	activation	query -> target	-	Reactome: R-HSA-914161.1 Reactome: R-HSA-914162.1
-	-	-	-	-	activation	query -> target	-	Reactome: R-HSA-914161.1 Reactome: R-HSA-914162.1
Homo sapiens	4999	Q13416	-	-	-	no direction	25184681 17525332	BioGRID: 1055850 BioGRID: 301591
Homo sapiens	10399	P63244	-	-	-	no direction	22990118	BioGRID: 808390
Homo sapiens	7322	P62837	-	-	-	no direction	19712108 21113135	BioGRID: 563889 BioGRID: 610758 BioGRID: 610768 BioGRID: 610778
Homo sapiens	7399	Q75445	-	-	-	no direction	22990118	BioGRID: 808306
Homo sapiens	1660	Q08211	-	-	-	no direction	12592385 9662397	BioGRID: 260457 BioGRID: 305347 BioGRID: 305348
Homo sapiens	79632	Q8NB25	-	-	-	no direction	25184681	BioGRID: 1055761
Homo sapiens	126961	Q71DI3	-	-	-	no direction	12419249	BioGRID: 245186
Homo sapiens	1487	Q13363	-	-	-	no direction	10196224	BioGRID: 245474

Left sidebar icons: Tag Cloud, Molecular Interactions, 3D Interaction, Natural Ligand DB, hGtoP

ここでPPIをクリック

VaProS | Home x VaProS | Detail x VaProS | Detail x Compound Report Card x MERIT40 facilitates BR x

← → ↻ p4d-info.nig.ac.jp/vaproS/

HISTORY

VaProS Variation effect on PROtein Structure and function

Platform for Drug Discovery, Informatics, and Structural Life Science

HOME ABOUT STATISTICS MANUAL TUTORIAL

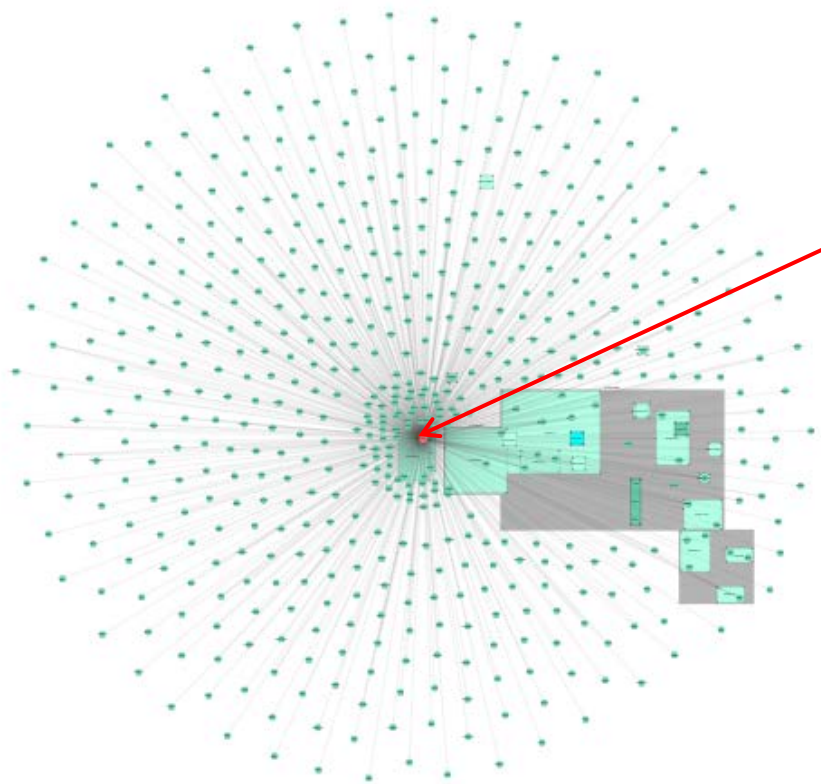
Keyword Sequence ID List Questionnaire

Sequence results - hits:20

Details (Go)

	UniProtKB	Organism	Name	Gene ID	Variant Position	Sequence	Molecular Interactions	PPI	3D Interaction	NLDB	hGtoP	GNP Expression	COXPRESdb	Pathway DB	Phenotype	S-VAR
1	☒ P38398	Homo sapiens	breast cancer 1, early onset	672	show	show	16461	674		0	1	1	0	32	4	link
2	☐ C6YB45	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
3	☐ Q3B891	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
4	☐ B7ZA85	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
5	☐ E7ENB7	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
6	☐ C9IZW4	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
7	☐ E7EQW4	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
8	☐ E9PH68	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
9	☐ K7EPC7	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
10	☐ H0Y850	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
11	☐ E7EWN5	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link
12	☐ E9PC22	Homo sapiens	breast cancer 1, early onset		show	show	0	0	0	0	1	0	0	0	0	link

こうするとMolecular Interactionsを図として
見ることができます。



SELECT

SEARCH

FILTER

Nodes

- ☐ all phenotype
- ☐ LEUKEMIA,
CHRONIC
MYELOID
- ☐ ACETYL-CoA
CARBOXYLASE
DEFICIENCY
- ☐ DEAFNESS,
AUTOSOMAL
DOMINANT 20

Edges

- ☐ physical association
- ☐ Formation of Early
Recombination
Nodule
- ☐ colocalization
- ☐ Conjugation of
SUMO2,3 to
BRCA1
- ☐ association
- ☐ direct interaction

ここに詳細
なデータが
現れます

中央のBRCA1を
クリックすると

UniProtの
Accession IDをクリック

BRCA1

type : protein

UniProt : **P38398**

EntrezGene : 672

DrugBank : -

InterPro : IPR017907 IPR031099

IPR013083 IPR018957

IPR001841 IPR001357

IPR011364 IPR025994

ChEMBL : ChEMBL5990

UniProtに移動します。

UniProtのFunctionの記述の数行からからBRCA1は

- ①ユビキチンリガーゼで E3 ubiquitin-protein ligase
- ②DNA損傷の修復に重要、更に plays a central role in DNA repair by facilitating cellular responses to DNA damage
- ③癌抑制にも重要な働きをしていることがわかります。
The E3 ubiquitin-protein ligase activity is required for its tumor suppressor function.

UniProtKB

Advanced Search

BLAST Align Retrieve/ID mapping Help Contact

UniProtKB - P38398 (BRCA1_HUMAN)

Display

Entry Feature viewer Feature table

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequences (8)

Cross-references

Publications

Protein

Gene

Organism

Status

Function

Enzyme regulation

Pathway

Protein

Gene

Organism

Status

Function

Enzyme regulation

Pathway

Pathology & Biotechをクリック

1アミノ酸の変異によってさまざまな癌が引き起こされることがわかります。

乳癌患者 (Breast cancer (BC))

Pathology & Biotechⁱ

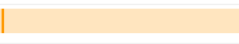
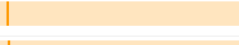
Involvement in diseaseⁱ

Breast cancer (BC)ⁱ 15 Publications ▼

Disease susceptibility is associated with variations affecting the gene represented in this entry. Mutations in BRCA1 are thought to be responsible for 45% of inherited breast cancer. Moreover, BRCA1 carriers have a 4-fold increased risk of colon cancer, whereas male carriers face a 3-fold increased risk of prostate cancer. Cells lacking BRCA1 show defects in DNA repair by homologous recombination.

Disease description: A common malignancy originating from breast epithelial tissue. Breast neoplasms can be distinguished by their histologic pattern. Invasive ductal carcinoma is by far the most common type. Breast cancer is etiologically and genetically heterogeneous. Important genetic factors have been indicated by familial occurrence and bilateral involvement. Mutations at more than one locus can be involved in different families or even in the same case.

See also OMIM:114480

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Natural variant ⁱ	4 – 4		1 S → F in BC; unknown pathological significance. 🔍 1 Publication ▼		VAR_070458	
Natural variant ⁱ	10 – 10		1 E → K in BC and BROVCA1. 🔍 1 Publication ▼		VAR_020679	
Natural variant ⁱ	18 – 18		1 M → T in BC; unknown pathological significance. 🔍 2 Publications ▼		VAR_063899	
Natural variant ⁱ	22 – 22		1 L → S in BC. 🔍 1 Publication ▼		VAR_007756	
Natural variant ⁱ	23 – 23		1 E → K in BC and BROVCA1. 🔍 1 Publication ▼		VAR_020680	
Natural variant ⁱ	45 – 45		1 K → Q in BC; unknown pathological significance; functionally neutral in vitro. 🔍 1 Publication ▼		VAR_070459	
Natural variant ⁱ	61 – 61		1 C → G in BC and ovarian cancer; no interaction with BAP1. 🔍 7 Publications ▼ Corresponds to variant rs28897672 [dbSNP Ensembl].		VAR_007757	
Natural variant ⁱ	64 – 64		1 C → G in BC; no interaction with BAP1. 🔍 4 Publications ▼		VAR_007758	
Natural variant ⁱ	67 – 67		1 D → Y in BC; unknown pathological significance; functionally neutral in vitro. 🔍 1 Publication ▼		VAR_070460	
Natural variant ⁱ	71 – 71		1 R → K in BC; unknown pathological significance. 🔍 1 Publication ▼		VAR_020681	
Natural variant ⁱ	132 – 132		1 N → K in BC; unknown pathological significance; functionally neutral in vitro. 🔍 1 Publication ▼		VAR_070462	
Natural variant ⁱ	142 – 142		1 P → H in BC; unknown pathological significance; functionally		VAR_070463	



更に下を見ていくと

乳癌子宮癌家系 (Breast-ovarian cancer, familial, 1 (BROVCA1))

Breast-ovarian cancer, familial, 1 (BROVCA1) 3 Publications

Disease susceptibility is associated with variations affecting the gene represented in this entry. Mutations in BRCA1 are thought to be responsible for more than 80% of inherited breast-ovarian cancer.

Disease description: A condition associated with familial predisposition to cancer of the breast and ovaries. Characteristic features in affected families are an early age of onset of breast cancer (often before age 50), increased chance of bilateral cancers (cancer that develop in both breasts, or both ovaries, independently), frequent occurrence of breast cancer among men, increased incidence of tumors of other specific organs, such as the prostate.

See also OMIM:604370

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Natural variant ⁱ	10 - 10		1 E → K in BC and BROVCA1. 1 Publication		VAR_020679	
Natural variant ⁱ	23 - 23		1 E → K in BC and BROVCA1. 1 Publication		VAR_020680	
Natural variant ⁱ	835 - 835		1 H → Y in BROVCA1; unknown pathological significance. 1 Publication		VAR_020684	
Natural variant ⁱ	841 - 841		1 R → W in BROVCA1; unknown pathological significance. 2 Publications Corresponds to variant rs1800709 [dbSNP Ensembl].		VAR_007773	
Natural variant ⁱ	1187 - 1187		1 S → I in BC and BROVCA1. 1 Publication		VAR_020690	
Natural variant ⁱ	1200 - 1200		1 Q → H in BC and BROVCA1. 1 Publication Corresponds to variant rs56214134 [dbSNP Ensembl].		VAR_020691	
Natural variant ⁱ	1217 - 1217		1 S → Y in BC and BROVCA1. 1 Publication		VAR_020695	
Natural variant ⁱ	1226 - 1226		1 F → L in BROVCA1. 1 Publication		VAR_020696	
Natural variant ⁱ	1243 - 1243		1 R → G in BROVCA1. 1 Publication		VAR_020697	
Natural variant ⁱ	1786 - 1786		1 L → P in BROVCA1; unknown pathological significance. 1 Publication		VAR_020704	

子宮癌患者 (Ovarian cancer(OC))

Ovarian cancer (OC) 3 Publications

Disease susceptibility is associated with variations affecting the gene represented in this entry.

Disease description: The term ovarian cancer defines malignancies originating from ovarian tissue. Although many histologic types of ovarian tumors have been described, epithelial ovarian carcinoma is the most common form. Ovarian cancers are often asymptomatic and the recognized signs and symptoms, even of late-stage disease, are vague. Consequently, most patients are diagnosed with advanced disease.

See also OMIM:167000

Pancreatic cancer 4 (PNCA4) 1 Publication

Disease susceptibility is associated with variations affecting the gene represented in this entry.

Disease description: A malignant neoplasm of the pancreas. Tumors can arise from both the exocrine and endocrine portions of the pancreas, but 95% of them develop from the exocrine portion, including the ductal epithelium.

膵臓癌患者 (Pancreatic cancer 4 (PNCA4))

BRCA1遺伝子のミスセンス変異によりさまざまな癌が発症することがわかります。

Display

Entry

Feature viewer

Feature table

None

☒ Function

☒ Names & Taxonomy

☒ Subcellular location

☒ Pathology & Biotech

☒ PTM / Processing

☒ Expression

☒ Interaction

☒ Structure

☒ Family & Domains

☒ Sequences (8)

☒ Cross-references

☒ Publications

☒ Entry information

☒ Miscellaneous

☒ Similar proteins

▲ Top

Pathology & Biotechⁱ

Involvement in diseaseⁱ

Breast cancer (BC) 15 Publications ▼

Disease susceptibility is associated with variations affecting the gene represented in this entry. Mutations in BRCA1 are thought to be responsible for increased risk of colon cancer, whereas male carriers face a 3-fold increased risk of prostate cancer. Cells lacking BRCA1 show defects in DNA repair. Disease description: A common malignancy originating from breast epithelial tissue. Breast neoplasms can be distinguished by their histologic, etiologically and genetically heterogeneous. Important genetic factors have been indicated by familial occurrence and bilateral involvement. MIM:114480

See also OMIM:114480

Feature key	Position(s)	Length	Description
Natural variant ⁱ	4 - 4		1 S → F in BC; unknown pathological significance. 1 Publication ▼
Natural variant ⁱ	10 - 10		1 E → K in BC and BROVCA1. 1 Publication ▼
Natural variant ⁱ	18 - 18		1 M → T in BC; unknown pathological significance. 2 Publications ▼
Natural variant ⁱ	22 - 22		1 L → S in BC. 1 Publication ▼
Natural variant ⁱ	23 - 23		1 E → K in BC and BROVCA1. 1 Publication ▼
Natural variant ⁱ	45 - 45		1 K → Q in BC; unknown pathological significance; functionally neutral in vitro. 1 Publication ▼
Natural variant ⁱ	61 - 61		1 C → G in BC and ovarian cancer; no interaction with BAP1. 7 Publications ▼ Corresponds to variant rs28897672 [dbSNP Ensembl].
Natural variant ⁱ	64 - 64		1 C → G in BC; no interaction with BAP1. 4 Publications ▼
Natural variant ⁱ	67 - 67		1 D → Y in BC; unknown pathological significance; functionally neutral in vitro. 1 Publication ▼
Natural variant ⁱ	71 - 71		1 R → K in BC; unknown pathological significance. 1 Publication ▼
Natural variant ⁱ	132 - 132		1 N → K in BC; unknown pathological significance; functionally neutral in vitro. 1 Publication ▼

Structureをクリックしてみると

たくさんの立体構造の報告があるようです。

Structureⁱ

Secondary structure



strand



1863

Legend: Helix Turn Beta

[Show more details](#)

3D structure databases

Select the link destinations:

- ☒ PDBeⁱ
- ☐ RCSB PDBⁱ
- ☐ PDBjⁱ

Entry	Method	Resolution (Å)	Chain	Positions	PDBsum
1JM7	NMR	-	A	1-110	[»]
1JNX	X-ray	2.50	X	1646-1859	[»]
1N50	X-ray	2.80	X	1646-1859	[»]
1OQA	NMR	-	A	1755-1863	[»]
1T15	X-ray	1.85	A	1646-1859	[»]
1T29	X-ray	2.30	A	1646-1859	[»]
1T2U	X-ray	2.80	A	1646-1859	[»]
1T2V	X-ray	3.30	A/B/C/D/E	1646-1859	[»]
1Y98	X-ray	2.50	A	1646-1859	[»]
2ING	X-ray	3.60	X	1649-1859	[»]
3COJ	X-ray	3.21	A/B/C/D/E/F/G/X	1646-1859	[»]
3K0H	X-ray	2.70	A	1646-1859	[»]
3K0K	X-ray	2.70	A	1646-1859	[»]
3K15	X-ray	2.80	A	1646-1859	[»]
3K16	X-ray	3.00	A	1646-1859	[»]
3PXA	X-ray	2.55	A	1646-1859	[»]
3PXB	X-ray	2.50	A	1646-1859	[»]
3PXC	X-ray	2.80	X	1646-1859	[»]
3PXD	X-ray	2.80	A	1646-1859	[»]
3PXE	X-ray	2.85	A/B/C/D	1646-1859	[»]
4IFI	X-ray	2.20	A	1646-1859	[»]



アイコンをクリック

でも構造が解かれている部位には偏りがあるようです。

VaProSにある3D Interactionに戻ってみましょう。

拡大して下方を
見てみましょう。


3D Interaction: Contact Bar(summary)[0.0 %]



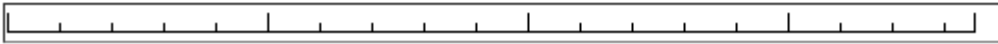
seq.id(%): [0] [30] [40] [50] [60] [70] [80] [90] [95] [100]

[\[bars:full\]](#) [\[SiteTable\]](#)
[\[show\]](#) [\[download\]](#) [\[help\]](#)

PID	QueryLength	Homolous Sequence in PDB	UniProt Query	TITLE
37968	1863	96	BRCA1 HUMAN(P38398)	RecName: Full=RING finger
QUERYSEQ	MDLSALRVEEVQNVINAMQKILECPICLELIKPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSSQ SLSVQLSNLGTVRTLRKQRIQPKTSVYIELGSDSSDVTNKATYCSVQDQELLQITPQGRDEISLDSAKKAACEFSET KAEFCNKSQKQGLARSOHNRWAGSKETCNDRTPTSTEKKVDLNADPLCERKEWNKQKLPCESENPRDTEVPWI TLNSSIQ SVESNIEDKIFGKTYRKKASLPNLSHVTENLII GAFVTEPQII GERPLTNKLRKRRTSGLHPEDF IKKADLAVGKTPM HNSKAPKKNRLRRKSSSTRHIALELVSRNLSPPNCTELQIDSCSSSEEIKKKKYNQMPVRHSRNLQLMGKEPATGAKKS MLSGERVLQTERSVESSISLVPGTDYGTQESI SLLEVSTLGAKTEPNKCVSQCAA FENPKGLIHGCSKDNRNDTEGFKY FECEQKEENQGNESNIKPQTVNI TAGFPVVGQDKPVDNAKCSIKGGSRFCLSSQFRGNETGLITPNKHQLQNPYRIP TNEVGSSINEIGSSDENIQAE LGRNRGPKLNAMLRLGVLOPEVYKQSLPGSNCKHPEIKKQEEYEEVQTVNTDFSPYLI SD GYRRGAKKLESSEENLSSDEELPCFQHLFGKVNNI PSQSTRHSTVATECLSKNTEENLLSLKNSLNDCSNOVILAKASQ LEENNGEEQSMDSNLGEAASGCESETSVSEDCSLSSGSDILTTQGRDTMOHNLIKLOQEMAELEAVLEQHGSQPSNSYPS QPSLDRLWYMHSCSGSLQNRNYPQQEELIKVVDVEEQGLEESGPHDLTETSYLPRQDLEGTPLYESGISLFSDDPESDPSE SMVVSGLTPEEFMLVYKFARKHHITLTNLITETTHVVMKTD AEFVCERTLKYFLGI AGGKVVVSYFVWVTSIKERKMLNE GTGVHPIVVQPDATDNGFHAIGQMCEAPVVTREWVLDVALYQCGELDTYLIPIPHSHY			

[BLAST file for PDB] [\(plain\)](#) [\(bar\)](#) [BLAST for UniProt: [\(plain\)](#) [\(bar\)](#) [\(multiple alignment\)](#) [\(PSSM file\)](#)]

UniProt Feature Tables [\[P38398\(BRCA1 HUMAN\)\]](#)

1863		region	name
		1-1863	CHAIN

BRCA1は1863残基からなる高分子で、C末端に2つのBRCTドメインを連続して有すること、N末端にRINGドメイン(Znフィンガー様ドメイン)を有することが分かります。

3D Interactions (Powered by Cytoscape.js)

VaProS Platform for Drug Discovery

UniProt Feature Tables [P38398(BRCA1 HUMAN)]

1863

region	name	description
1-1863	CHAIN	Breast cancer type 1 susceptibility protein. /FTId=PRO_0000055830.
1642-1736	DOMAIN	BRCT 1.
1756-1855	DOMAIN	BRCT 2.
24-65	ZN_FING	RING-type.
1397-1424	REGION	Interaction with PALB2.
651-654	COMPBIAS	Poly-Lys.

MONOMER

1863

pdb_id	asym_id	identity	description
4u4a	B	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1jm7	A	100.0	BRCA1 HUMAN BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN

HETERO

1863

contact mol	homologue			
asym_id	description	asym_id	SqID(%)	description
4ofb[1]	nonphosphopeptide inhibitor[14 aa]	A	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
4v18[4]	F175A HUMAN BRCA1-A complex subunit Abraxas[7 aa]	H	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
4v18[3]	F175A HUMAN BRCA1-A complex subunit Abraxas[7 aa]	G	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1t2v[2]	BRCTide-7PS[11 aa]	D	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1t2v[1]	BRCTide-7PS[11 aa]	A	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1t2v[2]	BRCTide-7PS[12 aa]	E	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1t2v[3]	BRCTide-7PS[14 aa]	B	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
1t2v[1]	BRCTide-7PS[14 aa]	D	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
3coj[1]	ACACA HUMAN Acetyl-CoA carboxylase 1[13 aa]	D	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein
4ilu[1]	F175A HUMAN BRCA1-A complex subunit Abraxas[11 aa]	A	100.0	BRCA1 HUMAN Breast cancer type 1 susceptibility protein

これまでに報告されたBRCA1タンパク質の立体構造は、C末端の2個連続したBRCTドメイン (pdb id: 4u4a)とN末端のRingドメイン (pdb id: 1jm7) のみのようです。

pdb idをクリックすると

構造を見ることができます。

ipproo.protein.osaka-u.ac.jp/homcos/cgi-bin/model3D.cgi?VER=&PID=37968&pdb_id=4u4a&asym0=B&oper0=1&que0=A&sbjidA

 Protein Model on 4u4a_B_1 (TEMPLATE: [PDBj](#)4u4a)



JSmol

DOWNLOAD:

 [sequence-replaced 3D model]

 [3D template]

MODELLER [Modeller script]

ALL MOLECULES IN THE BIOLOGICAL UNIT:

ALL3D [assembly id:2]

sequence-replaced 3D model ▾ CurrentView: HTML5 Change to: [JAVA (faster than HTML5)]

model	mark	query	asym_id oper (auth_asym_id)	type	description	contact site
1 	a	A(BRCA1 HUMAN)	B 1 (B)	polymer(polypeptide(L)) [214 aa]	Breast cancer type 1 susceptibility protein :BRCA1 HUMAN	

MODEL[1] Protein A "quervA" TEMPLATE:4u4a_B.1 SeqID=100.0%

[illegible]

構造は先ほどの UniProtのStructureに戻って



下方にある同じIDをクリック

3D structure databases

Select the link destinations:
☒ PDB*e*
☐ RCSB PDB
☐ PDB*j*

Entry	Method	Resolution (Å)	Chain	Positions	PDBsum
1JM7	NMR	-	A	1-110	[>]
1JNX	X-ray	2.50	X	1646-1859	[>]
1N50	X-ray	2.80	X	1646-1859	[>]
1OQA	NMR	-	A	1755-1863	[>]
1T15	X-ray	1.85	A	1646-1859	[>]
1T29	X-ray	2.30	A	1646-1859	[>]
1T2U	X-ray	2.80	A	1646-1859	[>]
1T2V	X-ray	3.30	A/B/C/D/E	1646-1859	[>]
1Y98	X-ray	2.50	A	1646-1859	[>]
2ING	X-ray	3.60	X	1649-1859	[>]
3COJ	X-ray	3.21	A/B/C/D/E/F/G/X	1646-1859	[>]
3K0H	X-ray	2.70	A	1646-1859	[>]
3K0K	X-ray	2.70	A	1646-1859	[>]
3K15	X-ray	2.80	A	1646-1859	[>]
3K16	X-ray	3.00	A	1646-1859	[>]
3PXA	X-ray	2.55	A	1646-1859	[>]
3PXB	X-ray	2.50	A	1646-1859	[>]
3PXC	X-ray	2.80	X	1646-1859	[>]
3PXD	X-ray	2.80	A	1646-1859	[>]
3PXE	X-ray	2.85	A/B/C/D	1646-1859	[>]
4IFI	X-ray	2.20	A	1646-1859	[>]
4IGK	X-ray	1.75	A/B	1646-1859	[>]
4JLU	X-ray	3.50	A	1649-1859	[>]
4OFB	X-ray	3.05	A	1646-1859	[>]
4U4A	X-ray	3.51	A/B/C	1646-1859	[>]
4Y18	X-ray	3.50	A/B/C/D/E/F/G/H	1646-1859	[>]
4Y2G	X-ray	2.50	A	1646-1859	[>]

PDBから見ることもできます。

Browser tabs: VaProS | Home, VaProS | Detail, Protein Model on 4u4a, PDB 4u4a structure sur, VaProS | Detail, Compound Report Card, MERIT40 facilitates BR

Address bar: www.ebi.ac.uk/pdbe/entry/pdb/4U4A

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Examples: [hemoglobin](#), [BRCA1_HUMAN](#) [Search EMBL](#)

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PDBe > 4u4a

Complex Structure of BRCA1 BRCT with singly phospho Abraxas

Source organism: *Homo sapiens*

X-ray diffraction
3.51Å resolution

Released: 26 Aug 2015

Model geometry 

Quick links

[4u4a overview](#)

[Citations](#)

もう一度VaProSに戻って今度はhGTOPをクリックしてみると

hGTOP

SEARCH

Homo sapiens(Human)

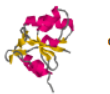
Recname:Breast cancer type 1 susceptibility protein

AccessionID:[P38398](#)

Gene:BRCA1_HUMAN

Organism	HUM	PRI	ROD	MAM	VRT	INV	PLN	BCT	ARC
Hits	27	30	3	4	12	12	11	0	0

SCOP Domains

c.15.1.3

c.15.1.4

g.44.1.1

Database	Range	Top-Hit	Cross-Reference	Evalue	SeqID
1862 amino acids					
SECSTR					
PSIPRED					
DISOPRED					
BLT:PDB	1->103	1jm7A	PDBj	2e-66	100.0%
BLT:PDB	1649->1859	1t15A	PDBj	4e-141	93.4%
RPS:PDB	1->103	1jm7A	PDBj	5e-49	100.0%
RPS:PDB	349->475	3v0aB	PDBj	6e-07	18.3%
RPS:PDB	1649->1859	1t15A	PDBj	3e-83	100.0%
RPS:SCOP	1->103	1jm7A	g.44.1.1	3e-20	100.0%
RPS:SCOP	1083->1204	2btvA	e.28.1.1	2e-04	13.2%
RPS:SCOP	1649->1757	1jnxX1	c.15.1.3	3e-46	100.0%
RPS:SCOP	1758->1859	1jnxX2	c.15.1.3	2e-19	99.0%
HMM:SCOP	1608->1753	1kzyC1	BRCT domain	3.6e-30	0.0%
HMM:SCOP	1759->1857	1jnxX2	BRCT domain	2.4e-25	0.0%
HMM:SCOP	1->103	1jm7A	RING/U-box	1.3e-40	0.0%

Tag Cloud

Molecular Interactions

3D Interaction

Natural Ligand DB

hGTOP

GNP Expression

COXPRESdb

Pathway DB

BRCA1タンパク質とアミノ酸配列相同性のあるタンパク質が脊椎動物、無脊椎動物、そして植物にも存在することがわかります。細菌や古細菌にはありません。

“PSIPRED”と“DISOPRED”の出力から、N末端RingドメインとC末端BRCTドメイン1・2以外の大部分は特定の高次構造を有しない領域であると予測されていることがわかります。

今度はS-VARをクリックしてみましょう。

S-VAR is a tool that predicts and assesses functional impact of sequence variations on phenotype.

UniProt	Variations	Sequence	S-VAR
P38398	E1038G View	MDLSALRVVEEVQNVINAMQKILECPICL...	Start

スタートをクリック

早速始めてみましょう

“S-VAR”解析では、点変異がタンパク質の機能にどの程度有害な影響を与えるかを評価します。

“E1038G”という変異がすでに記入されていますのでこれを調べてみましょう。

S-VAR is a tool that predicts and assesses functional impact of sequence variations on phenotype.

Enter your sequence variations * Mandatory fields

Amino acid sequence(FASTA format) *

```
>BRCA1_HUMAN
MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLC
KNDITKRSLQESTRFSQLVEELLKIICAFQLDTGLEANSYNFAKKENNSPEHLKDEVSIIQSM
GYRNRARLLQSEPENPSLQETSLSVQLSNLGTVRTLRKQRIQPQKTSVYIELGSDSSEDTV
NKATYCSVGDQELLQITPQGTREISLDSAKKAACEFSETDVTNTEHHQPSNNDLNTTEKRA
AERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSLLLLTKDRMNVEKAIEFCNKSQPGLA
```

[\[Sample\]](#)

Variations *

E1038G [\[Sample1\]](#) [\[Sample2\]](#)

Prediction tools *

☒ PolyPhen2 ☒ SIFT ☒ PROVEAN ☒ PANTHER

E-mail Optional, but strongly recommended.

結果をメールで送ってもらうことが勧められています。 [Clear](#) [Submit](#)

Submitをクリック

解析は無事終わったようです。

S-VAR is a tool that predicts and assesses functional impact of sequence variations on phenotype.

Your job has been successfully submitted.

JobID:160722180351852_vh

The results will be available at

http://pford.info/s-var/jobresult?jobId=160722180351852_vh

This page is autoloading checking calculation process every one minute.

It will automatically jump to the result page if the analysis is finished.

結果はこのURLをクリック

(この解析には時間がかかるようです。)

[Back to Top page](#)

Prediction results

[About score](#)

JobID: 160722180351852_vh

[Download Results](#)

Variations	Prediction tools			
	PolyPhen2	SIFT	PROVEAN	PANTHER
E1038G	possibly damaging (0.936)	TOLERATED (0.07)	Deleterious (-5.08)	neutral (-2.4878)

Your query sequence

>BRCA1_HUMAN

MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSQLVEELLKIIC
AFQLDTGLEAYNSYNFAKKENNSPEHLKDEVSIQSMGYRNRARLLQSEPENPSLQETSLSVQLSNLGTVRTLRKQRIQPQKTSVYI
ELGSDSSEDTVNKATYCSVGDQELLQITPQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNNDLNTTEKRAAERHPEKYQGSSVS
NLHVEPCGTNTHASSLQHENSLLLTKDRMNVEKAIEFCNKSQKQPLARSQHNRWAGSKETCNDRRTPSTEEKVDLNADPLCERKEW
NKQKLPCSENPRDTEVPWITLNSSIQKVNEWFSRDELLGSDDSHDGESESNKQVADVLDVLNEVDEYSGSSEKIDLLASDPHEALI

[Back to Top page](#)

解析結果はPolyPhen2では“possibly damaging”、SIFTでは“TOLERATED”、PROVEANでは“Deleterious”、PANTHERでは“neutral”と評価が分かれました。
このように複数のツールを同時並行で走らせて、結果も横並びで比較できます。

今度は変異をクリックしてみましょう。

別の窓でMutation@A Glanceが開きます。

↓
ここで変異を探してS-VARにも戻ることができます。

Mutation @ A Glance | Gene: BRCA1 - Mozilla Firefox

harrier.nagahama-i-bio.ac.jp/mutation/at_a_glance/BRCA1/

Mutation@A Glance BETA Home Tools About Search for...

BRCA1 breast cancer 1

Selected: NM_007300.3 - NP_009231.2 DNA Protein Table External resources Disease

chr17:43044195

DNA Sequence Show Peptide

5' Gene flanking [chr17:43125483-43125583, complement]

TTCCGTCCTCTTCCTTTTACGTCATCCGGGGGCGAGCTGGGTGGCCAATCCAGAGCCCCGAGAGAGCTTGGCTCTTTCTGTCCCTCCCATCC

Exon 1 [chr17:43125271-43125483, complement]

GTACCTTGATTTCGTATTCTGAGAGGCTGCTGCTTAGCGGAGCCCCCTTGGTTTCCGTGGCAACGGAAAAGCGCGGAATTACAGATAAATTA

GACTGCGCGGCGTGAGCTCGCTGAGACTTCTGGAACGGGACAGGCTGTGGGGTTTCTCAGATAACTGGCCCTGCGCTCAGGAGGCCCTTC

GCTTGGGTAAAGtagtagagtccgggaaaggaca

Exon 2 [chr17:43124017-43124115, complement]

tatatgtttttctaagtgttbaagTTCATTGGAAACAGAAAGAAATGATTATATGCTCTTCGCGTTGAAGAAGTACAAATGTCATTAAATG

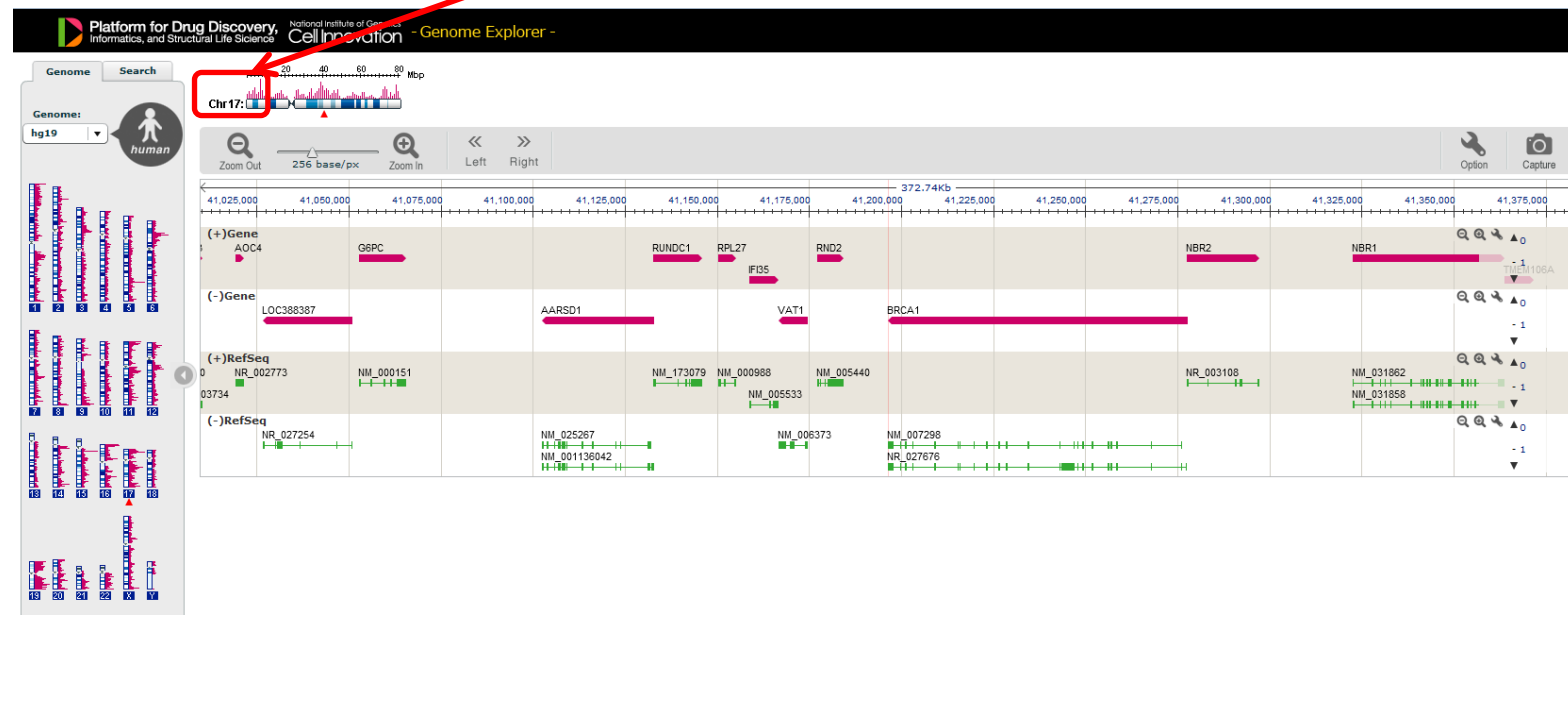
次にGenome Explorerをクリックしてみましょう。



Symbol	EntrezGene ID	UniProtKB AC	GNP Genome Explorer	CellInnovation Genome Explorer
BRCA1	672	P38398	Open	Open

BRCA1遺伝子が17番染色体上にあることが分かります。

ここをクリックすると



このようにVaProSを利用してBRCA1を検索すると、VaProSからリンクが張られているデータベースも使ってBRCA1タンパク質の構造・機能・疾患との関連について様々な知識を得ることができます。