

例題 3.3

シロイヌナズナのホウ素トランスporter (NP_850469.1, BOR1_ARATH) のアミノ酸配列をクエリとして、NCBI のサイトで、DB として「UniProtKB/Swiss-Prot(swissprot)」を指定し、blastp を用いて検索せよ。パラメータはとくに変更する必要はない。検索でヒットした配列のうち、シロイヌナズナ以外のホウ素トランスporterとして最初にヒットしたものは何か。また、その E-value、配列一致度を求めよ。

解答例

NCBI BLAST の検索結果は例えば次のようになる。

Descriptions		Graphic Summary	Alignments	Taxonomy				
Sequences producing significant alignments								
Download Select columns Show 100								
select all 51 sequences selected								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
RecName: Full=Boron transporter 1 [Arabidopsis thaliana]	Arabidopsis thali...	1333	1333	100%	0.0	100.00%	704	Q8VYR7.1
RecName: Full=Probable boron transporter 2 [Arabidopsis thaliana]	Arabidopsis thali...	1190	1190	97%	0.0	91.12%	703	Q9M1P7.1
RecName: Full=Probable boron transporter 3 [Arabidopsis thaliana]	Arabidopsis thali...	946	946	91%	0.0	73.60%	732	Q93713.1
RecName: Full=Boron transporter 4 [Arabidopsis thaliana]	Arabidopsis thali...	760	760	90%	0.0	60.81%	683	Q9X123.1
RecName: Full=Putative boron transporter 5 [Arabidopsis thaliana]	Arabidopsis thali...	739	739	91%	0.0	58.23%	683	Q9SSG5.1
RecName: Full=Probable boron transporter 6 [Arabidopsis thaliana]	Arabidopsis thali...	707	707	90%	0.0	56.88%	671	Q3E954.2
RecName: Full=Probable boron transporter 7 [Arabidopsis thaliana]	Arabidopsis thali...	695	695	91%	0.0	54.93%	673	Q9SUU1.3
RecName: Full=Boron transporter 1 [Saccharomyces cerevisiae S288C]	Saccharomyces...	150	150	50%	3e-37	30.60%	576	P53838.1
RecName: Full=Putative transporter C543.05c [Schizosaccharomyces pombe 972h-]	Schizosaccharo...	143	143	83%	3e-35	22.75%	517	Q9HGM6.1
RecName: Full=Band 3 anion transport protein; AllName: Full=Anion exchange protein 1; Short=AE 1; Short=Anion...	Mus musculus	100	100	46%	1e-20	23.68%	929	P04919.1
RecName: Full=Anion exchange protein 2; Short=AE 2; Short=Anion exchanger 2; AllName: Full=Band 3-related or...	Mus musculus	97.8	97.8	47%	1e-19	23.39%	1237	P13808.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Solute carrier fam...	Pongo abelii	96.7	176	66%	2e-19	25.83%	1232	Q5R85.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Anion exchanger...	Oryzias latipes	96.3	179	66%	4e-19	26.63%	1233	Q18971.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Anion exchanger...	Rattus norvegicus	95.1	181	67%	8e-19	26.68%	1227	P23348.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Band 3-related or...	Rattus norvegicus	95.1	181	67%	8e-19	26.68%	1227	P23348.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Band 3-related or...	Rattus norvegicus	95.1	181	67%	8e-19	26.68%	1227	P23348.1
RecName: Full=Anion exchange protein 1; Short=AE 1; Short=Anion...	Homo sapiens	94.7	94.7	47%	1e-18	24.14%	911	P02730.3
RecName: Full=Anion exchange protein 2; Short=AE 2; Short=Anion exchanger 2; AllName: Full=Band 3-related or...	Rattus norvegicus	94.7	94.7	47%	1e-18	24.14%	911	P02730.3
RecName: Full=Band 3 anion transport protein; AllName: Full=Anion exchange protein 1; Short=AE 1; Short=Anion...	Homo sapiens	94.7	94.7	47%	1e-18	24.14%	911	P02730.3
RecName: Full=Anion exchange protein 2; Short=AE 2; Short=Anion exchanger 2; AllName: Full=Band 3-related or...	Rattus norvegicus	93.6	93.6	46%	2e-18	24.26%	927	P23562.3
RecName: Full=Band 3 anion transport protein; AllName: Full=Anion exchange protein 1; Short=AE 1; Short=Anion...	Rattus norvegicus	93.6	93.6	46%	2e-18	24.26%	927	P23562.3
RecName: Full=Anion exchange protein 2; Short=AE 2; Short=Anion exchanger 2; AllName: Full=Non-erythroid ba...	Cavia porcellus	93.6	93.6	47%	2e-18	24.19%	1238	Q9Z0S8.1
RecName: Full=Anion exchange protein 3; Short=AE 3; Short=Anion exchanger 3; AllName: Full=Solute carrier fam...	Plecturocebus m...	91.3	173	66%	1e-17	25.00%	1232	B1MTL0.1
RecName: Full=Solute carrier family 4 member 11; AllName: Full=Sodium borate cotransporter 1; Short=NaBC1 (H...	Homo sapiens	90.1	152	45%	2e-17	30.22%	875	Q9NBS3.3
RecName: Full=Band 3 anion transport protein; AllName: Full=Solute carrier family 4 member 1 [Gallus gallus]	Gallus gallus	88.2	169	67%	9e-17	23.96%	922	P15575.1
RecName: Full=Band 3 anion exchange protein; AllName: Full=Anion exchange protein 1; Short=AE 1; Short=Anio...	Oncorhynchus m...	88.2	169	79%	1e-16	22.66%	918	P32847.2

出芽酵母のホウ素

トランスポーター

シロイヌナズナのホウ素トランスポーター1~7の後に、出芽酵母のホウ素トランスポーターがヒットする。これは、高濃度のホウ素に対する耐性付与に機能していることが知られている。また、さらに下位の方では、ヒトの炭酸水素イオン共輸送体が配列一致度 22%で検索結果に表れていることがわかる。

クエリ配列とのアラインメントは以下の通り。

GenPept (GenBank の塩基配列を自動翻訳し

Download

GenPept Graphics

で得られるデータベース)のエントリ

RecName: **FliH=Boron transporter 1 [Saccharomyces cerevisiae S288C]**

Sequence ID: **P53838.1** Length: **576** Number of Matches: **1**

ビットスコア raw スコア E-Value 置換スコアが正の割合 配列一致度 ギャップの割合

Range 1: 61 to 404 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
179 bits(454)	3e-47	Compositional matrix adjust.	118/367(32%)	190/367(51%)	31/367(8%)
Query 10	GIKNDLKGRLMCMYKQDWTGGFKAGFRILAPTTYIFFASAIIPVISFGEQLERSTDGVLTA	69			
Sbjct 61	GI DLK R+ YK DW F +R++ +F + +P I+F + + TD	118			
Query 70	QTLASTAICGMIHSIIGGQPLLLILGVAEPTVIMYTFMFNFAKARPELGRDLFLAWSG---	126			
Sbjct 119	+ L S+A+ G++ ++GGQPL I+GV P I FN+ E+ + L ++ G	171			
Query 127	EVLLSSAMAGIVFGVLGGQPLCIVGVTGPISI-----FNYSYVY--EIIKPLNTSYFGFMF	171			
Query 127	WVCVWTALMLFVLAICGACSIINRFTRVAGELFGLLIAMLFMQQAIKGLVDEFRIPIREN	186			
Sbjct 172	W+C+W+ + VLA A ++ T ++FGL I ++++Q+ I+ L +F E	231			
Query 187	WICMWSMIFHLVLAFTNAVCLLQYVTTTFPCDIFGLFINVVYIQKGIQILTRQFSAKSGEK	231			
Query 187	QKLKEFLPSWRPANGMFALVLS-FGLLLTGLRSRKARSWRYGTGWLRSIADYGVPLMVL	245			
Sbjct 232	F A+ + ALV++ FGL S R +R+ I+DY L VL	280			
	SVQDGF-----ASVVVALVMTAFGLFFKLFHYYPFLFSHR-----IRTFISDYSTALS	280			