

Respiratory Burst Oxidase Homolog (RBOH)

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Respiratory Burst Oxidase Homolog

-Les RBOHs sont une sous-famille des NADPH oxidase chez les **végétaux**.

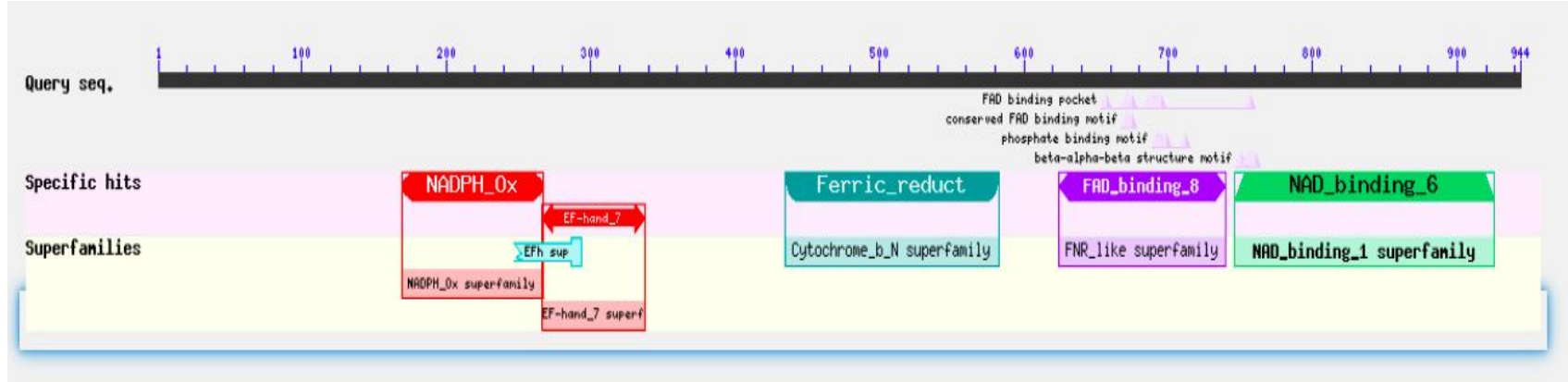
- Protéines présentes dans différents processus biologiques tels que : *la morphogenèse, le développement* et *les réponses au stress*.

- Rôles :

NADP → produit des molécules ROS (espèces réactive d'oxygène)

RBOH → même rôle que les NADPH oxidase.

Respiratory Burst Oxidase Homolog



5 domaines spécifiques identifiés chez les RBOH.

Objectifs

- ① Identifier les résidus caractéristiques de cette famille.
- ② Connaître la répartition taxonomique de la famille protéique.
- ③ Établir une signature et une HMM spécifique aux RBOH

Exploitation de la base de données : Pfam

RBOH sous famille des NADPH oxydases

PF08022 : FAD_binding_8 : domaine caractéristique des NADPH oxydases

Pfam PF08022 FAD-binding domain
Pfam entry ⓘ

Overview

Proteins 35k

Domain Architectures 603

Taxonomy 13k

Proteomes 3k

Structures 9

Signature

AlphaFold 25k

Alignment

Curation

This entry matches these proteins:

Filter By

UniProt Curation


- All 35k
- Reviewed 81
- Unreviewed 35k

1 - 16 of 16 proteins

RBOH

Export

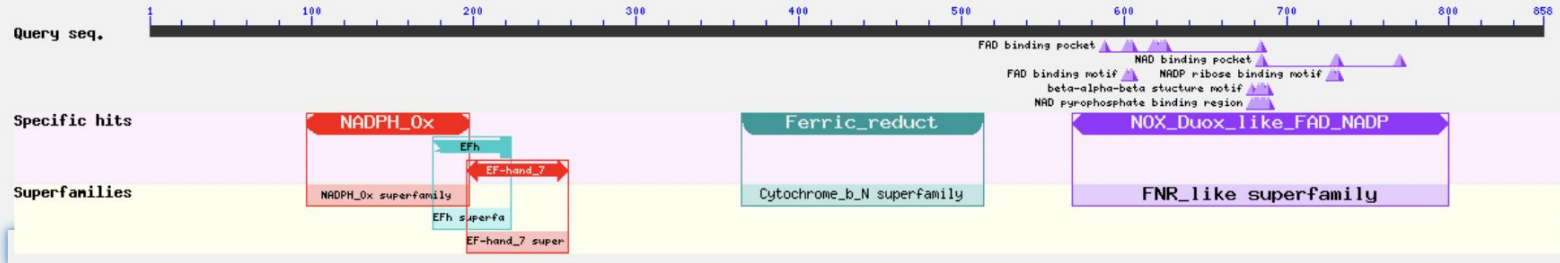
ACCESSION	NAME	SPECIES	MATCHES
048538 ✓	Respiratory burst oxidase homolog protein F	Arabidopsis thaliana (Mouse-ear cress)	200 400 600 800
081209 ✓	Respiratory burst oxidase homolog protein A	Arabidopsis thaliana (Mouse-ear cress)	200 400 600 800
081210 ✓	Respiratory burst oxidase homolog protein C	Arabidopsis thaliana (Mouse-ear cress)	200 400 600 800
081211 ✓	Respiratory burst oxidase homolog protein E	Arabidopsis thaliana (Mouse-ear cress)	500
Q2HXK9 ✓	Respiratory burst oxidase homolog protein D	Solanum tuberosum (Potato)	200 400 600 800



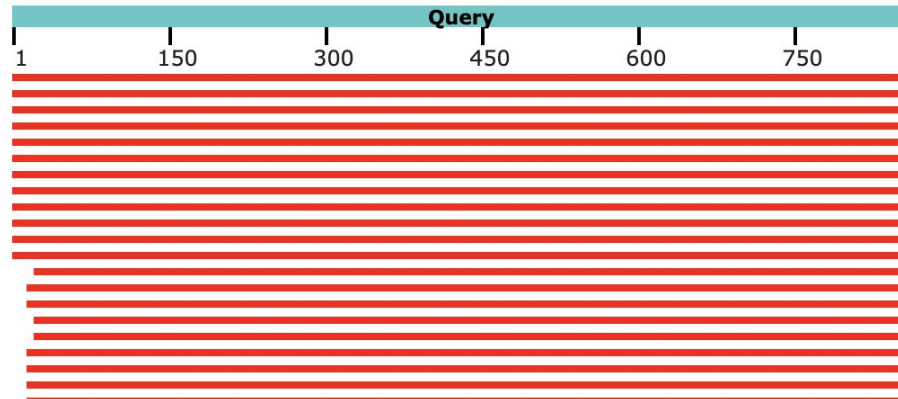
Blastp d'un RBOH et identification de ses domaines spécifique



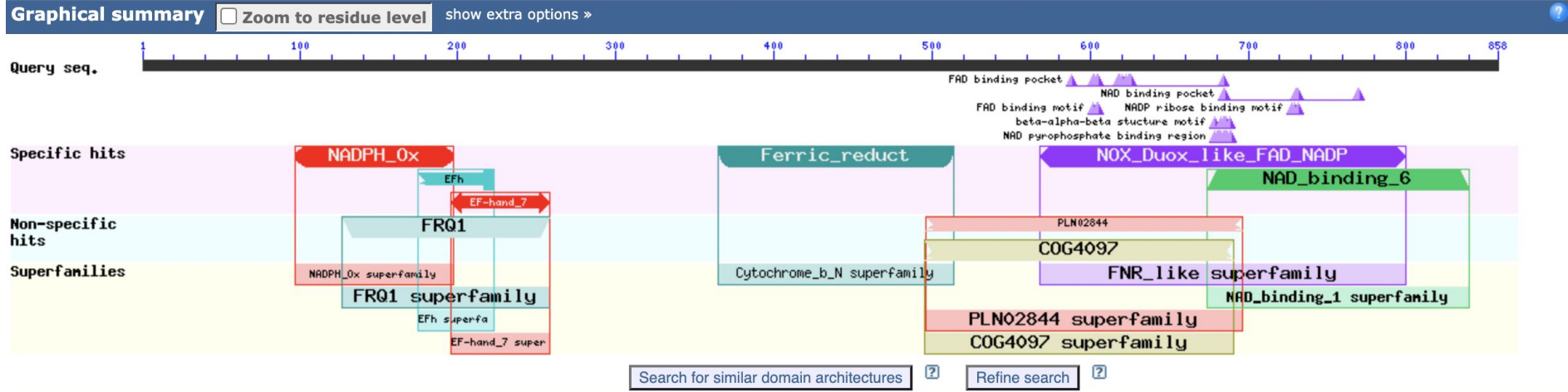
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 70 Blast Hits on 70 subject sequences



Etude de 3 séquences spécifique des RBOH pour en extraire un pattern commun aux RBOH



List of domain hits					
	Name	Accession	Description	Interval	E-value
[+]	NADPH_Ox	pfam08414	Respiratory burst NADPH oxidase; This domain is found in plant proteins such as respiratory ...	97-197	1.92e-51
[+]	NOX_Duox_like_FAD_NADP	cd06186	NADPH oxidase (NOX) catalyzes the generation of reactive oxygen species (ROS) such as ...	568-800	2.13e-49
[+]	NAD_binding_6	pfam08030	Ferric reductase NAD binding domain;	674-840	1.06e-46
[+]	PLN02844	PLN02844	oxidoreductase/ferric-chelate reductase	496-696	2.27e-25
[+]	Ferric_reduct	pfam01794	Ferric reductase like transmembrane component; This family includes a common region in the ...	365-514	3.31e-11
[+]	COG4097	COG4097	Predicted ferric reductase [Inorganic ion transport and metabolism];	495-691	5.50e-11
[+]	EFh	cd00051	EF-hand, calcium binding motif; A diverse superfamily of calcium sensors and calcium signal ...	175-223	3.75e-06
[+]	EF-hand_7	pfam13499	EF-hand domain pair;	196-258	7.54e-05
[+]	FRQ1	COG5126	Ca2+-binding protein, EF-hand superfamily [Signal transduction mechanisms];	127-258	4.47e-03

Domaine étudiés : NADPH_Ox, NAD_Binding_6 et Ferric_reduct

Analyse des domaines, un à un, par Blastp (ici NADPH_ox)

select all 100 sequences selected

[GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D [Solanum tuberosum]	Solanum tuberosum	237	237	100%	2e-72	100.00%	858	NP_001305507.1
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D [Solanum verrucosum]	Solanum verrucosum	234	234	100%	4e-71	98.18%	859	XP_049363780.1
<input checked="" type="checkbox"/>	hypothetical.protein H5410_033511 [Solanum commersonii]	Solanum commersonii	227	227	100%	3e-70	96.36%	616	KAG5602141.1
<input checked="" type="checkbox"/>	hypothetical.protein KY285_029314 [Solanum tuberosum]	Solanum tuberosum	231	231	100%	6e-70	97.27%	859	KAH0668108.1
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D [Solanum stenotomum]	Solanum stenotomum	229	229	100%	2e-69	96.36%	859	XP_049408970.1
<input checked="" type="checkbox"/>	hypothetical.protein MTR67_028596 [Solanum verrucosum]	Solanum verrucosum	232	232	100%	2e-69	98.18%	1396	WMV35211.1
<input checked="" type="checkbox"/>	PREDICTED: respiratory_burst oxidase homolog.protein D [Solanum tuberosum]	Solanum tuberosum	228	228	99%	7e-69	95.41%	902	XP_015160290.1
<input checked="" type="checkbox"/>	hypothetical.protein KY290_028775 [Solanum tuberosum]	Solanum tuberosum	226	226	99%	2e-68	95.41%	859	KAH0749543.1
<input checked="" type="checkbox"/>	hypothetical.protein KY284_029234 [Solanum tuberosum]	Solanum tuberosum	226	226	100%	2e-67	96.36%	1462	KAH0664303.1
<input checked="" type="checkbox"/>	hypothetical.protein KY289_029453 [Solanum tuberosum]	Solanum tuberosum	226	226	99%	4e-67	95.41%	1462	KAH0660705.1
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D isoform X2 [Solanum pennellii]	Solanum pennellii	219	219	100%	1e-66	90.91%	662	XP_015077626.1
<input checked="" type="checkbox"/>	hypothetical.protein EJD97_019311 [Solanum chilense]	Solanum chilense	221	221	100%	3e-66	90.91%	861	TMW87888.1
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D isoform X1 [Solanum pennellii]	Solanum pennellii	219	219	100%	8e-66	90.91%	856	XP_015077625.1
<input checked="" type="checkbox"/>	respiratory_burst oxidase homolog.protein D [Solanum lycopersicum]	Solanum lycopersicum	217	217	100%	6e-65	89.09%	857	XP_004241641.1



Alignement multiple : MAFFT

Alignement multiple : MAFFT



Mise en place d'un pattern spécifique du domaine NADPH_ox

STEP 1 - Enter a set of PROTEIN sequences or an alignment

Examples

```
YPGNVLTLHMSKPQG
FKYKSGQYIFVNCAAVSPFEWHPFSITSAPRDDYVSVHIRTLDGWTRQLKVVVFSEVCQPPP
NGKSGLLRADYLQGENNPN
FPKVLIDGPYGAPTQDYKDYDVLLVGLGIGATPMISVVKDIVNNMKAVEDEANAVEEGALA
PAPNASPVSMMSKQRKG
ASSGSGRQASFRTRRAYFYWVTREQGSFDWFKGVMNEVAEMDNKGVIEMHNYCTSVYEE
GDARSALITMLQSLNHAKNGV
DVVSGTRVKSHFAKPNWRTVYKRIALNHPNSRVGVFYCGAPPPVKELRQLASDFSHKTNT
KFEFHKENF
```

Supported input:

- Sequences in [FASTA](#) or [UniProtKB/Swiss-Prot](#) format
- Alignment of sequences in FASTA format

Your input is a set of sequences an alignment [?](#)

STEP 1 - Enter a MOTIF or a combination of MOTIFS [Examples](#) [\[help \]](#)

```
F-A-x-E-L-[FY]-[DN]-[AS]-L-[AGST]-R-R-[HR]-x-[IM]-x(3)-[CNST]-[IV]-[NST]-[KR]-x(2)-[LV]-x-E-[FY]-W-
[DE]-Q-[IV]-[AS]-[DN]-Q-[CDS]-F-D-[ACST]-R-L-[QR]-T-F-F-D-M-[IV]-D-K
```

Pattern pour le NADPH_ox

Supported input:

On fait la même chose pour les autres domaines spécifique des RBOH

Recherche PROSITE : Chercher les séquences protéiques qui correspondent à ce motif spécifique possédant les 3 domaines

STEP 1 - Enter a MOTIF or a combination of MOTIFS [Examples](#) [[help](#)]

```
S-x(1,2)-F-A-x-E-L-[FY]-[ADNS]-[AST]-L-[AGST]-R-[KR]-[HR]-x-[IM]-x(4)-[IV]-[NST]-[KR]-x(2)-L-x-[DE]-F-W-[DE]-[QR]-[IV]-x-[DNT]-x-[CDS]-x-[DS]-[ACNST]-[NR]-x(2)-[ST]-x-[FI]-[DEQ] and M-G-x(0,1)-C-V-[CS]-[FLMV]-[AD]-K-G-[AG]-[AG]-[DE]-x(2)-K-[FL]-N-M-A-[IL]-I-L-[FL]-P-V-C-R-[NS]-T-[IV]-x-W-L-R-
```

Supported input:

- A PROSITE accession e.g. [PS50240](#) or identifier e.g. [TRYPSIN_DOM](#)
- Your own pattern e.g. [P-x\(2\)-G-E-S-G\(2\)-\[AS\]](#)

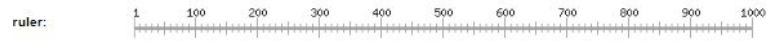
Recherche dans la base de données Swiss-Prot et TrEMBL

STEP2 - Select a PROTEIN sequence database [[help](#)]

- UniProtKB
 - Swiss-Prot Include isoforms
 - TrEMBL (sequences belonging to reference proteomes only)
- PDB
- Your protein database
- Randomized UniProtKB/Swiss-Prot
- Exclude fragments (concerns UniProtKB only)

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function. For more information about how these graphical representations are constructed, go to <https://prosite.expasy.org/mydomains/>.

hits by patterns: [117 hits (by 3 distinct patterns) on 39 sequences]



Q2HXL0 (RBOHC_SOLTU) (938 aa) View all PROSITE motifs hits on sequence

Respiratory burst oxidase homolog protein C (EC 1.11.1.-) (EC 1.6.3.-) (NADPH oxidase RBOHC) (StRBOHC). *Solanum tuberosum* (Potato)

USERPAT1 : Pattern: S-x(1,2)-F-A-x-E-L-[FY]-[ADNS]-[AST]-L-[AGST]-R-[KR]-[HR]-x-[IM]-x(4)-[IV]-[NST]-[KR]-x(2)-L-x-[DE]-F-W-[DE]-[QR]-[IV]-x-[DNT]-x-[CDS]-x-[DS]-[ACNST]-[NR]-x(2)-[ST]-x-[FI]-[DEQ] Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 9.124234e-25

207 - 255: SKeFAgELYDALARRRnIttdsINKaqLkEFwDQVaDqSFDTRlqTFFD

USERPAT2 : Pattern: M-G-x(0,1)-C-V-[CS]-[FLMV]-[AD]-K-G-[AG]-[AG]-[DE]-x(2)-K-[FL]-N-M-A-[IL]-I-L-[FL]-P-V-C-R-[NS]-T-[IV]-x-W-L-R-[NS]-[KR]-T-[KR]-L-[AGS]-x-[ASV]-[ILV]-P-F-D-D-N Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 7.904859e-43

400 - 448: MSpCVCLAKGAAEtIKLNMAIILLPVCRTIITLWRNKTRLGSAVPPDDN

USERPAT3 : Pattern: I-E-[LM]-H-N-[FY]-C-T-S-V-Y-E-[DE]-G-D-A-R-[SV]-A-L-I-x-M-L-Q-[ADS]-[IL]-x-H-A-K-x-G-V-D-[IV]-V-S-G-T-x-V-x-[ST]-H-F-A-[KR]-P-[DN] Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 5.380320e-47

836 - 885: IEM#NYCTSVYEEGDARSALITMLQSLHHAksGVDIVSGTpvkSHFAKPN

39 séquences possédant ce pattern : 20 sont des RBOH

Pas 100 % spécifique des RBOH



Faire un pattern avec TOUS les domaines des RBOH?

Utilisation de la Modélisation HMM pour Détecter les RBOH

```
# output directed to file: RBOH.search
# -----
Query: RBOH [M=911]
Scores for complete sequences (score includes all domains):
--- full sequence --- --- best 1 domain --- -#dom-
E-value score bias E-value score bias exp N Sequence
Description
-----
0 1884.9 0.0 0 1884.7 0.0 1.0 1 sp|Q2HXL0|RBOHC_SOLTU
Respiratory burst oxidase homolog
0 1794.8 0.1 0 1794.5 0.1 1.0 1 sp|Q2HXX9|RBOHD_SOLTU
Respiratory burst oxidase homolog
0 1579.4 0.0 0 1579.1 0.0 1.0 1 sp|Q9FIJ0|RBOHD_ARATH
Respiratory burst oxidase homolog
0 1570.4 0.0 0 1570.1 0.0 1.0 1 sp|081210|RBOHC_ARATH
Respiratory burst oxidase homolog
0 1446.7 0.2 0 1446.4 0.2 1.0 1 sp|Q948T9|RBOHB_SOLTU
Respiratory burst oxidase homolog
0 1436.4 0.0 0 1436.2 0.0 1.0 1 sp|081209|RBOHA_ARATH
Respiratory burst oxidase homolog
0 1361.2 1.5 0 1360.9 1.5 1.0 1 sp|Q9SW17|RBOHG_ARATH
Putative respiratory burst oxidase
0 1319.8 0.0 0 1319.5 0.0 1.0 1 sp|Q5ZAJ0|RBOHB_ORYSJ
Respiratory burst oxidase homolog
0 1319.8 0.0 0 1319.5 0.0 1.0 1 sp|Q6J2K5|RBOHB_ORYSI
Respiratory burst oxidase homolog
0 1292.5 9.7 0 1285.5 5.4 2.0 2 sp|Q9SBI0|RBOHB_ARATH
Respiratory burst oxidase homolog
0 1238.9 4.7 0 1227.8 1.4 2.0 2 sp|Q948U0|RBOHA_SOLTU
Respiratory burst oxidase homolog
0 1235.0 6.8 0 1217.3 1.6 2.0 2 sp|Q48538|RBOHF_ARATH
Respiratory burst oxidase homolog
0 1088.8 3.0 0 1086.4 3.0 1.8 1 sp|081211|RBOHE_ARATH
Respiratory burst oxidase homolog
0 1079.5 1.5 0 1079.2 1.5 1.0 1 sp|Q9SUT8|RBOHI_ARATH
Probable respiratory burst oxidase
2.2e-288 964.1 0.0 2.6e-288 963.9 0.0 1.0 1 sp|Q9FJD6|RBOHH_ARATH
Putative respiratory burst oxidase
1.5e-287 961.4 0.0 1.8e-287 961.1 0.0 1.0 1 sp|09LZU9|RBOHJ_ARATH
Putative respiratory burst oxidase
7e-98 333.7 11.5 5.7e-96 327.4 11.5 2.1 1 sp|Q9XYS3|NOXA_DICDI
Superoxide-generating NADPH oxidas
2.9e-90 308.5 13.2 6.8e-90 307.3 13.2 1.6 1 sp|Q86GL4|NOXB_DICDI
Superoxide-generating NADPH oxidas
5.9e-83 284.3 11.5 6.6e-82 280.9 6.3 2.9 2 sp|Q9NRD9|DUOX1_HUMAN
Dual oxidase 1 OS=Homo sapiens OX=
1.3e-82 283.2 14.9 8.3e-56 194.5 0.6 3.3 2 sp|Q95L74|CY24B_BISBI
Cytochrome b-245 heavy chain OS=Bi
```

score élevé = la séquence analysée a des caractéristiques similaires aux séquences qui ont été utilisées pour construire le modèle (ici NADPH_{ox}).

RBOH avec des scores > 960

Seuil de 960 : bon indicateur pour distinguer les RBOH

Arabidopsis thaliana



BLASTp

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Select columns

Show

100



select all 26 sequences selected

GenPept

Graphics

Distance tree of results

Multiple alignment

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	respiratory burst oxidase protein F [Arabidopsis thaliana]	Arabidopsis thali...	1966	1966	100%	0.0	100.00%	944	NP_564821.1
<input type="checkbox"/>	Atrboh F [Arabidopsis thaliana]	Arabidopsis thali...	1965	1965	100%	0.0	99.89%	944	BAA28953.1
<input type="checkbox"/>	Ferric reductase NAD binding domain [Arabidopsis thaliana x Arabidopsis arenosa]	Arabidopsis thali...	1962	1962	100%	0.0	99.79%	944	KAG7650492.1
<input type="checkbox"/>	Ferric reductase NAD binding domain [Arabidopsis suecica]	Arabidopsis sue...	1960	1960	100%	0.0	99.68%	944	KAG7658358.1
<input type="checkbox"/>	F22C12.18 [Arabidopsis thaliana]	Arabidopsis thali...	1948	1948	100%	0.0	96.62%	977	AAF24574.1
<input checked="" type="checkbox"/>	respiratory burst oxydase [Solanum tuberosum]	Solanum tubero...	1936	1936	100%	0.0	99.05%	1013	BAC06825.1
<input type="checkbox"/>	Riboflavin synthase-like beta-barrel [Arabidopsis thaliana x Arabidopsis arenosa]	Arabidopsis thali...	1929	1929	100%	0.0	98.62%	940	KAG7584684.1
<input checked="" type="checkbox"/>	respiratory burst oxidase [Arabidopsis lyrata subsp. lyrata]	Arabidopsis lyrat...	1928	1928	100%	0.0	98.31%	941	EFH64182.1
<input type="checkbox"/>	unnamed protein product [Arabidopsis arenosa]	Arabidopsis aren...	1926	1926	100%	0.0	98.41%	940	CAE5962231.1
<input type="checkbox"/>	Ferric reductase NAD binding domain [Arabidopsis thaliana x Arabidopsis arenosa]	Arabidopsis thali...	1887	1887	96%	0.0	99.78%	912	KAG7650493.1
<input type="checkbox"/>	hypothetical protein CARUB_v10021686mg.[Capsella rubella]	Capsella rubella	1865	1865	100%	0.0	95.45%	938	EOA34183.1
<input type="checkbox"/>	FAD-binding_8 [Arabidopsis suecica]	Arabidopsis sue...	1858	1858	100%	0.0	95.66%	914	KAG7587703.1
<input type="checkbox"/>	unnamed protein product [Brassica rapa]	Brassica rapa	1823	1823	100%	0.0	92.46%	948	CAG7861149.1
<input checked="" type="checkbox"/>	Respiratory burst oxidase-like protein F [Raphanus sativus]	Raphanus sativus	1822	1822	100%	0.0	92.55%	944	KAJ4877247.1
<input type="checkbox"/>	hypothetical protein BRARA_I01360 [Brassica rapa]	Brassica rapa	1821	1821	100%	0.0	92.46%	948	RID44576.1
<input type="checkbox"/>	hypothetical protein N665_2228s0003 [Sinapis alba]	Sinapis alba	1819	1819	100%	0.0	92.36%	949	KAF8049358.1
<input type="checkbox"/>	hypothetical protein Bca52824_059996 [Brassica carinata]	Brassica carinata	1818	1818	100%	0.0	92.53%	944	KAG2277441.1
<input checked="" type="checkbox"/>	respiratory burst oxidase protein F [Solanum tuberosum]	Solanum tubero...	1816	1816	100%	0.0	93.54%	944	BAB84124.1
<input type="checkbox"/>	hypothetical protein Bca52824_031429 [Brassica carinata]	Brassica carinata	1816	1816	100%	0.0	91.84%	947	KAG2302778.1
<input type="checkbox"/>	unnamed protein product [Brassica napus]	Brassica napus	1815	1815	100%	0.0	92.43%	944	CAF1721677.1
<input checked="" type="checkbox"/>	Respiratory burst oxidase protein F [Hirschfeldia incana]	Hirschfeldia incana	1813	1813	100%	0.0	92.33%	945	KAJ0265691.1

Résumé graphique

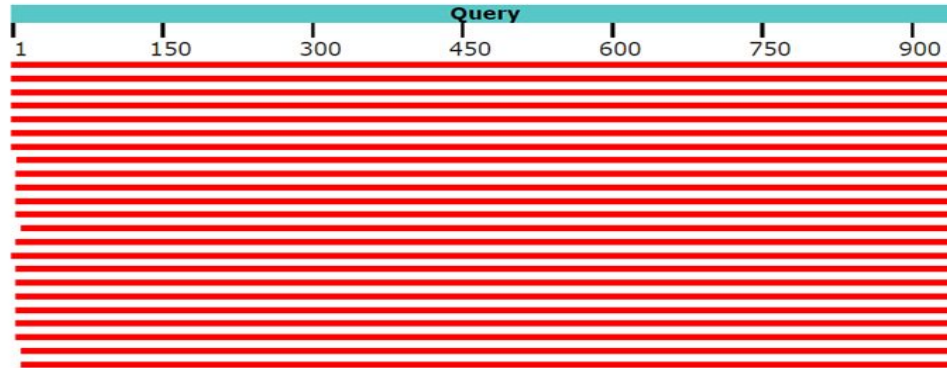
26 sequences selected



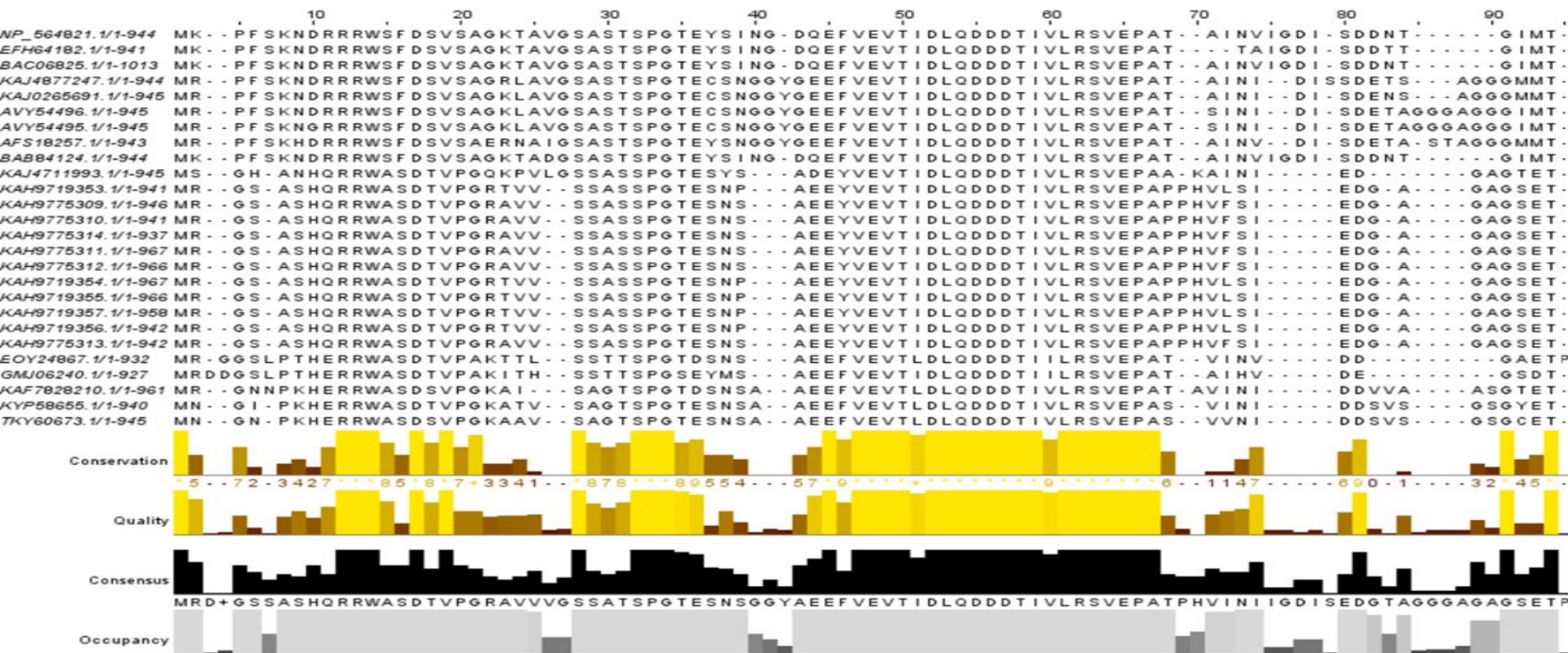
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 23 Blast Hits on 26 subject sequences



Alignement multiple: MAFFT



Pattern:

prosite

Home ScanProsite Browse ProRule Documentation Downloads About Contact

ScanProsite Results Viewer

Output format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [\[help\]](#).

[exclude splice variants \(UniProtKB/Swiss-Prot\)](#)

Hits for USERPAT1 "E-Q-G-S-F-D-W-F-K-G-V-M-N-E-V-A-E-L-D-Q-R-G-V-I-E-M-H-N-Y-L-T-S-V-Y-E-E-G-D-A-R-S-A-L-I-T-M-V-Q-A-L" on UniProtKB/Swiss-Prot and UniProtKB/TrEMBL (Release 2023_04 of 13-Sep-23) contains 570157 entries.

UniProtKB/TrEMBL (Release 2023_04 of 13-Sep-23) contains 0 entries.

found: [120 hits in 120 sequences](#)

Legend:

- disulfide bridge
- active site
- other 'ranges'
- other sites

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function. For more information about how these graphical representations are constructed, go to <https://prosite.expasy.org/mydomains/>.

hits by patterns: [120 hits (by 1 pattern) on 120 sequences]

ruler: 1 100 200 300 400 500 600 700 800 900 1000

Q948U0 (RBOHA_SOLTU) (963 aa) [View all PROSITE motifs hits on sequence](#)

Respiratory burst oxidase homolog protein A (EC 1.11.1.-) (EC 1.6.3.-) (NADPH oxidase RBOHA) (StRBOHA). *Solanum tuberosum* (Potato)

Sur 120 hits: 17 sont des RBOH

pas très spécifique

HMM

HMM	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R
S	T	V	W	Y											
COMPO	2.51852	4.28251	2.97226	2.76175	3.16681	2.90034	3.74976	2.79534	2.69934	2.37684	3.67150	3.13386	3.43493	3.15517	2.88788
2.61370	2.87229	2.62082	4.30109	3.38958											
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801
2.37887	2.77519	2.98518	4.58477	3.61503											
	0.03256	3.83663	4.55898	0.61958	0.77255	0.00000	*								
1	2.94176	4.49641	4.01124	3.60246	3.19321	3.80738	4.34592	2.36528	3.37231	1.79372	1.44839	3.88423	4.26819	3.75681	3.58175
3.28691	3.24658	2.36712	5.02898	3.78732	1 m	- - -									
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801
2.37887	2.77519	2.98518	4.58477	3.61503											
	0.03256	3.83663	4.55898	0.61958	0.77255	0.48576	0.95510								
2	2.83123	4.96288	3.13787	2.59815	4.35323	3.49037	3.56816	3.73620	1.80068	3.24784	4.10069	2.84489	3.89783	2.71405	1.65626
2.76675	3.03616	3.41126	5.35671	4.12761	2 r	- - -									
	2.68618	4.42225	2.77513	2.73124	3.46354	2.40511	3.72495	3.29354	2.67741	2.69355	4.24690	2.90347	2.73740	3.18147	2.89801
2.37887	2.77520	2.98519	4.58477	3.61504											
	0.06617	2.92703	4.55898	0.57929	0.82165	0.48576	0.95510								

--More--(0%)

Hmm.search pour comparer notre profil à la banque de données uniprot

```
2. genologin.toulouse.inra.fr (per... X
# hmmsearch :: search profile(s) against a sequence database
# HMMER 3.2.1 (June 2018); http://hmmmer.org/
# Copyright (C) 2018 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
#
# query HMM file:          RBOH.hmm
# target sequence database: /bank/ebi/uniprot/current/fasta/uniprot_sprot.fasta
# output directed to file: RBOH.search
#
Query:          RBOH [M=945]
Scores for complete sequences (score includes all domains):
--- full sequence ---          --- best 1 domain ---          -#dom-
E-value  score  bias  E-value  score  bias  exp  N  Sequence          Description
-----
0 2074.6  2.7  0 2074.5  2.7  1.0  1  sp|O48538|RBOHF_ARATH  Respiratory burst oxidase homolog
0 1911.3  0.6  0 1911.1  0.6  1.0  1  sp|O948U0|RBOHA_SOLTU  Respiratory burst oxidase homolog
0 1354.3  0.1  0 1354.1  0.1  1.0  1  sp|O9SUT8|RBOHI_ARATH  Probable respiratory burst oxidase
0 1204.1  3.3  0 1202.7  3.3  1.6  1  sp|O81211|RBOHE_ARATH  Respiratory burst oxidase homolog
0 1202.7  1.7  0 1176.3  0.1  2.0  2  sp|Q2HXL0|RBOHC_SOLTU  Respiratory burst oxidase homolog
0 1164.6  8.7  0 1159.6  4.4  2.9  2  sp|O948T9|RBOHB_SOLTU  Respiratory burst oxidase homolog
0 1149.9  7.9  0 1139.4  4.0  2.6  2  sp|O9FIJ0|RBOHD_ARATH  Respiratory burst oxidase homolog
0 1136.3  7.5  0 1132.4  3.8  2.5  2  sp|Q5ZAJ0|RBOHB_ORYSJ  Respiratory burst oxidase homolog
0 1136.3  7.5  0 1132.4  3.8  2.5  2  sp|Q6J2K5|RBOHB_ORYSJ  Respiratory burst oxidase homolog
0 1127.4  6.5  0 1116.7  1.7  2.4  2  sp|Q2HXX9|RBOHD_SOLTU  Respiratory burst oxidase homolog
0 1126.6  0.7  0 1126.6  0.7  1.8  2  sp|O81210|RBOHC_ARATH  Respiratory burst oxidase homolog
0 1117.0  15.5  0 1107.4  12.0  2.7  2  sp|O9SII0|RBOHB_ARATH  Respiratory burst oxidase homolog
0 1095.3  1.5  0 1090.2  0.3  2.9  2  sp|O81209|RBOHA_ARATH  Respiratory burst oxidase homolog
0 1053.1  2.3  0 1052.7  2.3  1.0  1  sp|Q9SW17|RBOHG_ARATH  Putative respiratory burst oxidase
8.1e-295 985.5  0.1  9.9e-295 985.2  0.1  1.0  1  sp|O9FJD6|RBOHH_ARATH  Putative respiratory burst oxidase
2.6e-289 967.2  0.0  3.3e-289 966.9  0.0  1.0  1  sp|Q9LZU9|RBOHJ_ARATH  Putative respiratory burst oxidase
2.8e-88 301.9  12.6  4.3e-71 245.0  9.0  2.1  2  sp|Q9YYS3|NOXA_DICDI  Superoxide-generating NADPH oxidas
1.7e-85 292.7  21.3  3.7e-66 228.7  13.5  2.3  2  sp|Q86GL4|NOXB_DICDI  Superoxide-generating NADPH oxidas
4.1e-82 281.5  11.2  3.7e-61 212.1  8.6  2.4  2  sp|Q8HZK3|DUOX1_PIG  Dual oxidase 1 OS=Sus scrofa OX=98
7.7e-81 277.3  10.3  7.1e-61 211.2  7.9  2.4  2  sp|Q9MZFA|DUOX1_CANLF  Dual oxidase 1 OS=Canis lupus fami
2.1e-80 275.9  11.3  2.4e-59 206.2  8.6  2.4  2  sp|Q8CIY2|DUOX1_RAT  Dual oxidase 1 OS=Rattus norvegicu
4.2e-80 274.9  17.7  1.2e-37 134.4  0.5  4.0  3  sp|Q8CIZ9|NOX1_MOUSE  NADPH oxidase 1 OS=Mus musculus OX
8.6e-80 273.8  11.5  2.2e-59 206.3  8.9  2.7  2  sp|Q9NRD9|DUOX1_HUMAN  Dual oxidase 1 OS=Homo sapiens OX=
1e-79 273.6  19.5  4.7e-39 139.0  0.3  4.1  3  sp|Q9YSS8|NOX1_HUMAN  NADPH oxidase 1 OS=Homo sapiens OX
1.4e-79 273.1  14.0  1.4e-58 203.6  11.3  2.5  2  sp|Q8HZK2|DUOX2_PIG  Dual oxidase 2 OS=Sus scrofa OX=98
2.7e-79 272.2  17.1  1.7e-35 127.2  0.3  4.0  3  sp|Q9VWB7|NOX1_RAT  NADPH oxidase 1 OS=Rattus norvegic
1.1e-78 270.1  18.0  3.4e-61 212.3  10.1  2.6  2  sp|O9ES45|DUOX2_RAT  Dual oxidase 2 OS=Rattus norvegicu
2.9e-78 268.8  18.7  2.2e-60 209.6  10.1  2.7  3  sp|Q9NRD8|DUOX2_HUMAN  Dual oxidase 2 OS=Homo sapiens OX=
2.8e-75 258.9  16.4  1.2e-38 137.7  0.2  3.2  3  sp|Q9JL74|CY24B_BISBI  Cytochrome b-245 heavy chain OS=Bi
4.1e-75 258.3  14.0  1.9e-38 137.0  0.1  3.2  3  sp|P04839|CY24B_HUMAN  Cytochrome b-245 heavy chain OS=Ho
7.5e-75 257.5  16.0  1.2e-38 137.7  0.2  3.2  3  sp|O46522|CY24B_BOVIN  Cytochrome b-245 heavy chain OS=Bo
1.8e-74 256.2  13.2  1.7e-37 133.8  0.1  3.2  3  sp|Q672J9|NOX3_MOUSE  NADPH oxidase 3 OS=Mus musculus OX
1.3e-72 247.1  13.1  1.9e-47 132.6  12.1  2.5  2  sp|O54F44|NOXC_DICDI  Superoxide-generating NADPH oxidas
5.8e-72 247.9  13.2  2.1e-38 136.8  0.1  3.3  3  sp|Q61093|CY24B_MOUSE  Cytochrome b-245 heavy chain OS=Mu
1.3e-71 246.7  13.7  4.5e-36 129.1  0.1  3.2  3  sp|Q672K1|NOX3_RAT  NADPH oxidase 3 OS=Rattus norvegic
1.2e-70 243.6  14.7  2.8e-57 199.3  7.9  2.7  2  sp|Q9VQH2|DUOX_DROME  Dual oxidase OS=Drosophila melanog
3.8e-70 241.9  12.1  7.1e-35 125.2  0.1  3.4  3  sp|Q9HBY0|NOX3_HUMAN  NADPH oxidase 3 OS=Homo sapiens OX
2.2e-62 216.2  9.8  3.7e-38 136.0  0.2  3.3  3  sp|P52649|CY24B_PIG  Cytochrome b-245 heavy chain (Frag
1.4e-61 213.6  2.3  1.3e-60 210.4  2.3  2.2  1  sp|Q96PH1|NOX5_HUMAN  NADPH oxidase 5 OS=Homo sapiens OX
6.4e-59 204.8  22.5  4.2e-43 152.4  15.6  3.1  2  sp|O61213|DUOX1_CAEL  Dual oxidase 1 OS=Caenorhabditis e
3.9e-53 185.6  15.2  3.1e-30 109.8  0.0  4.1  3  sp|Q5RSC5|NOX4_PONAB  NADPH oxidase 4 OS=Pongo abelii OX
1.2e-52 184.0  15.6  3.2e-30 109.8  0.0  4.1  3  sp|Q9NP5H|NOX4_HUMAN  NADPH oxidase 4 OS=Homo sapiens OX
1.1e-50 177.5  16.5  1.5e-29 107.5  0.0  4.1  3  sp|Q9JH18|NOX4_MOUSE  NADPH oxidase 4 OS=Mus musculus OX
pervenche@node122 ~/work $
```

Conclusion

Taxonomie des RBOH.

<i>Solanum tuberosum</i> (Potato)	<i>Capsicum baccatum</i> (Peruvian pepper)	<i>Abrus precatorius</i> (Indian licorice)
<i>Arabidopsis thaliana</i> (Mouse-ear cress)	<i>Juglans regia</i> (English walnut)	<i>Rhodamnia argentea</i>
<i>Cicer arietinum</i> (Chickpea)	<i>Striga asiatica</i> (Asiatic witchweed)	<i>Olea europaea</i> subsp. <i>europaea</i>
<i>Vigna radiata</i> var. <i>radiata</i> (Mung bean)	<i>Sesamum indicum</i> (Oriental sesame)	<i>Arachis duranensis</i> (Wild peanut)
<i>Vigna radiata</i> var. <i>radiata</i> (Mung bean)	<i>Raphanus sativus</i> (Radish)	<i>Solanum tuberosum</i> (Potato)
<i>Nicotiana tabacum</i> (Common tobacco)	<i>Ziziphus jujuba</i> (Chinese jujube)	
<i>Nicotiana glauca</i> (Wood tobacco)	<i>Durio zibethinus</i> (Durian)	
<i>Gossypium hirsutum</i> (Upland cotton)	<i>Phtheirospermum japonicum</i>	

Sx(1,2)-FAXEL-[FY]-[ADNS]-[AST]-L-[AGST]-R-[KR]-[HR]-x-[IM]-x(4)-[IV]-[NST]-[KR]-x(2)-Lx-[DE]-FW-[DE]-[QR]-[IV]-x-[DNT]-x-[CDS]-x-[DS]-[ACNST]-[NR]-x(2)-[ST]-x-[FI]-[DEQ] and
MGx(0,1)-CV-[CS]-[FLMV]-[AD]-KG-[AG]-[AG]-[DE]-x(2)-K-[FL]-NMA-[IL]-IL-[FL]-PVCR-[NS]-T-[IV]-xWLR-[NS]-[KR]-T-[KR]-L-[AGS]-x-[ASV]-[ILV]-PFDDN and
IE-[LM]-HN-[FY]-CTSVYE-[DE]-GDAR-[SV]-ALixMLQ-[ADS]-[IL]-xHAKxGVD-[IV]-VSGTxVx-[ST]-HFA- [KR]-P-[DN]

E-Q-G-S-F-D-W-F-K-G-V-M-N-E-V-A-E-L-D-Q-R-G-V-I-E-M-H-N-Y-L-T-S-V-Y-E-E-G-D-A-R-S-A-L-I-T-M-V-Q-A-L

On obtient des HMM spécifiques similaires pour les 2 méthodes cependant faut établir un seuil score >960.

Merci de votre écoute !