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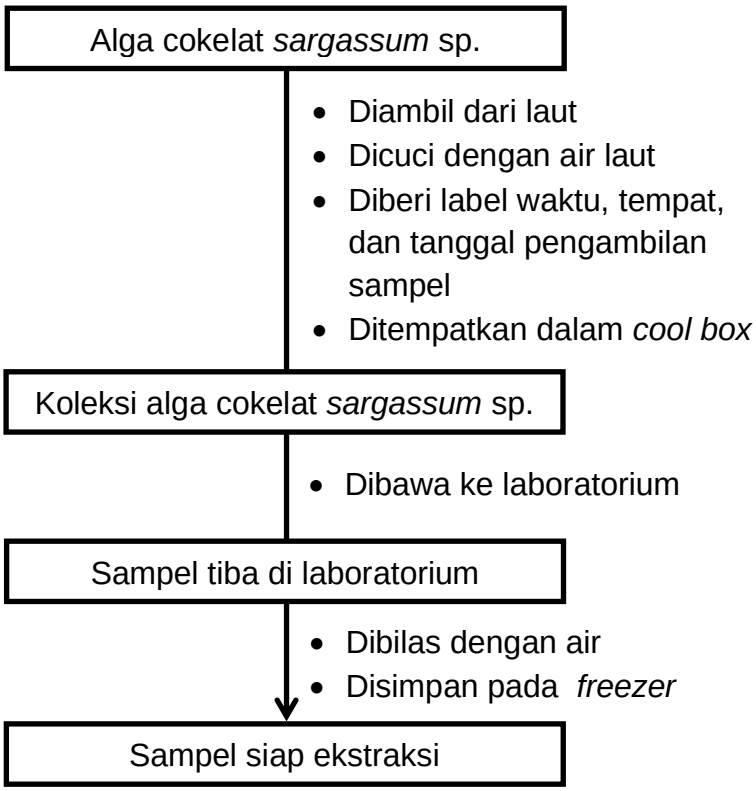
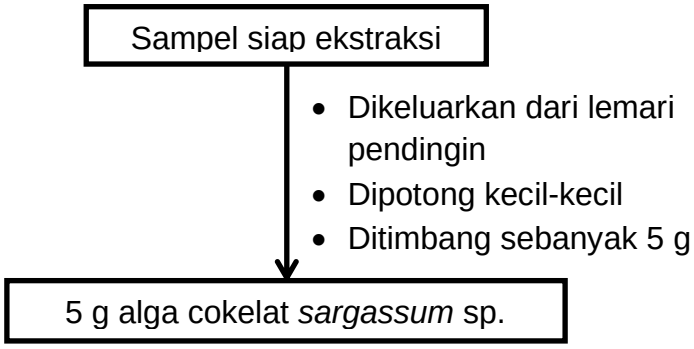
LAMPIRAN-LAMPIRAN

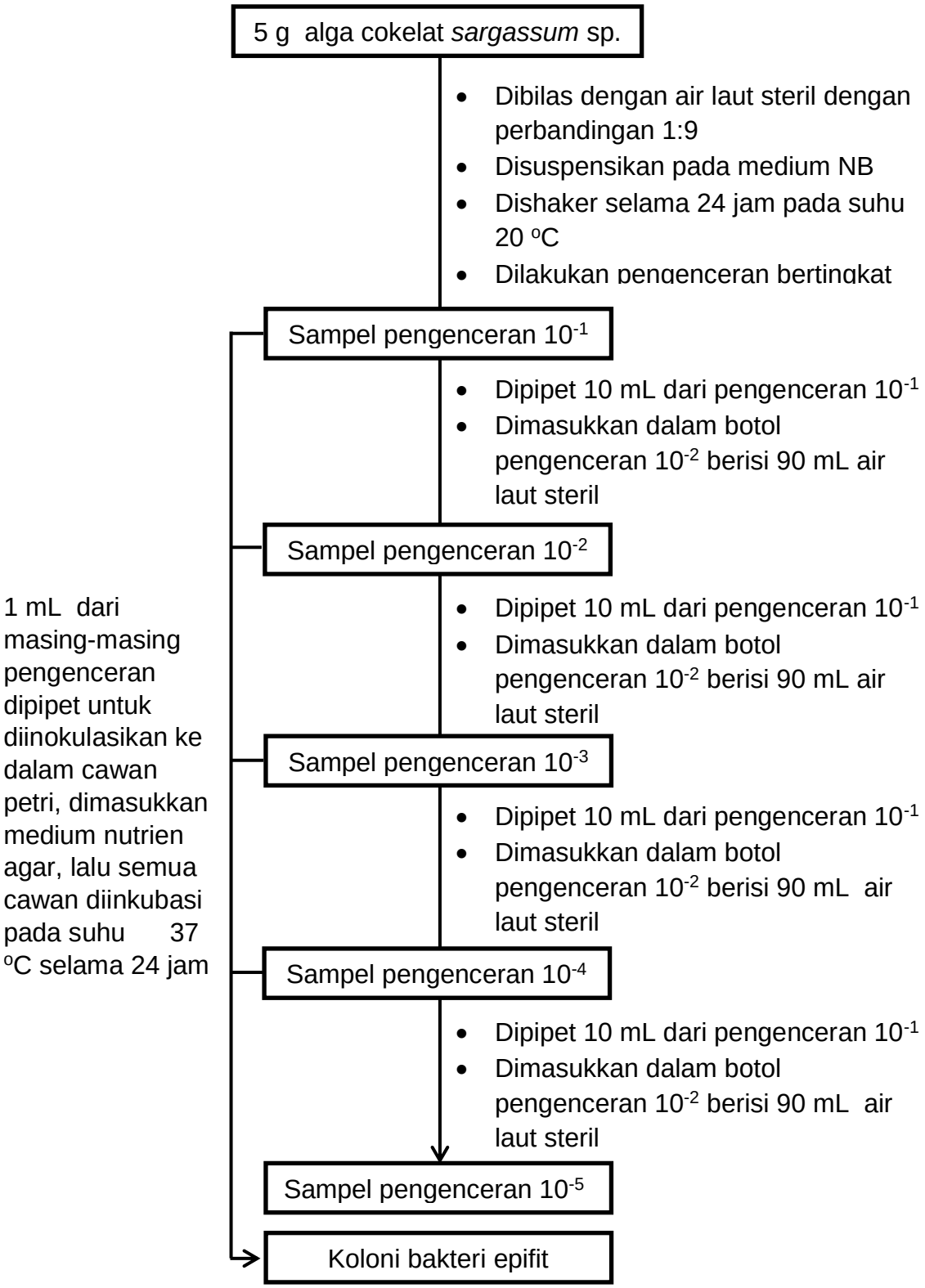
Lampiran 1. Skema kerja pengambilan sampel



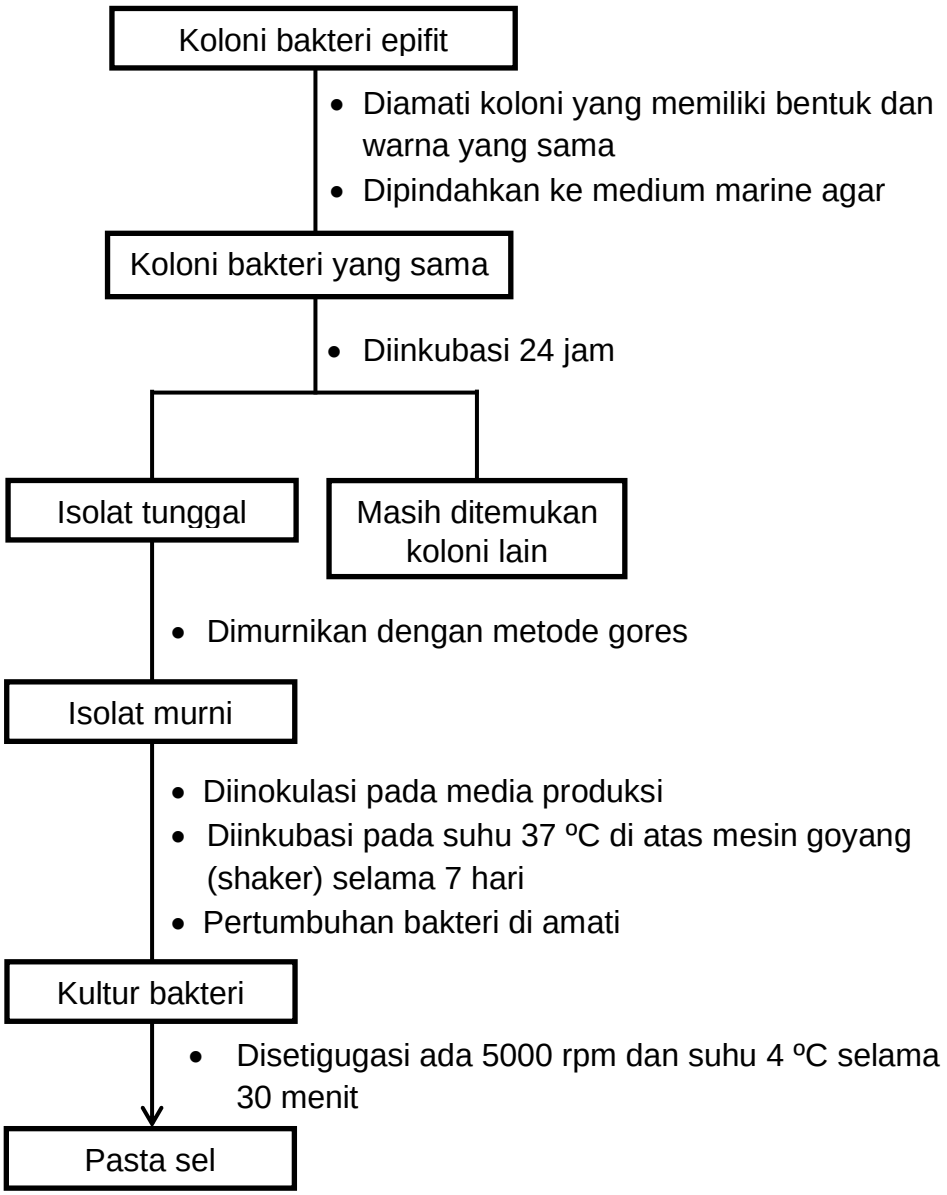
Lampiran 2. Skema kerja preprasi sampel



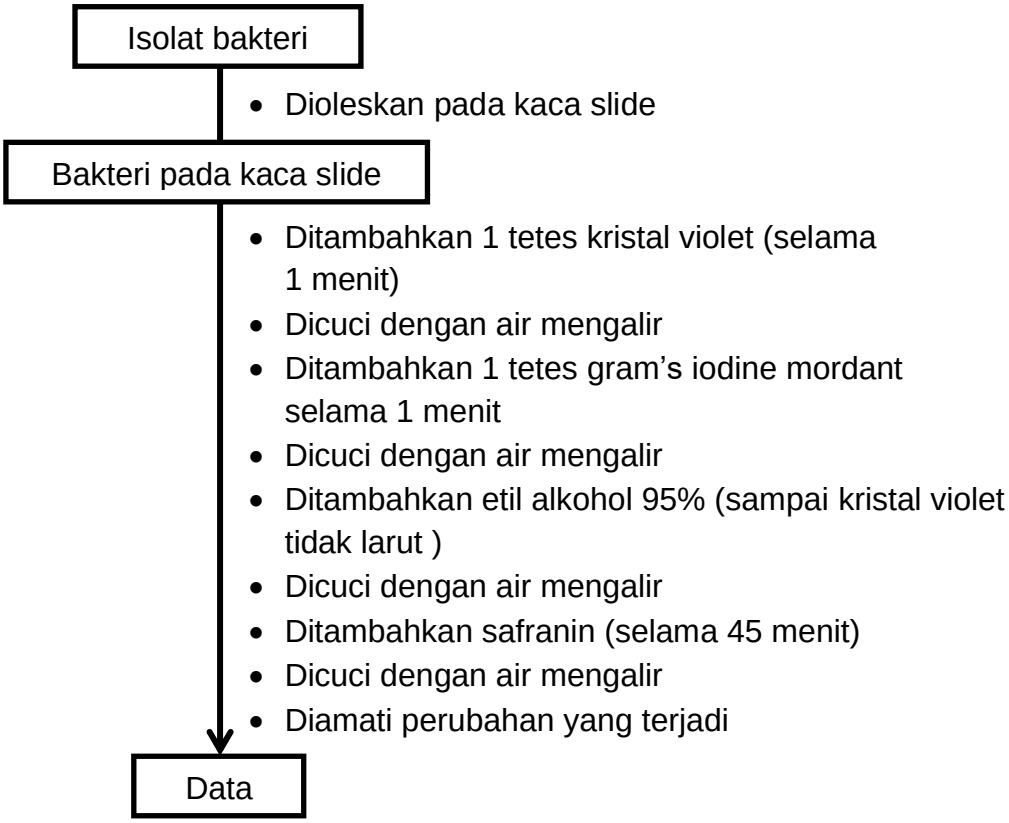
Lampiran 3. Skema kerja isolasi bakteri epifit simbion alga cokelat (*Phaeophyceae*)



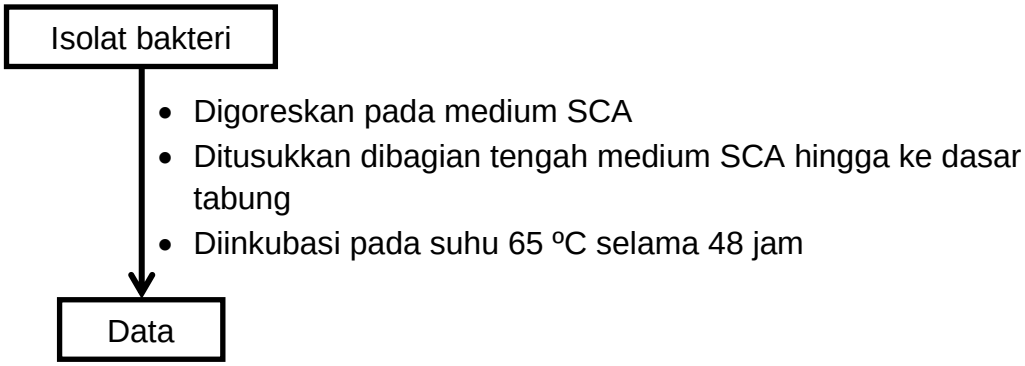
Lampiran 4. Skema kerja purifikasi bakteri



Lampiran 5. Skema kerja uji morfologi bakteri

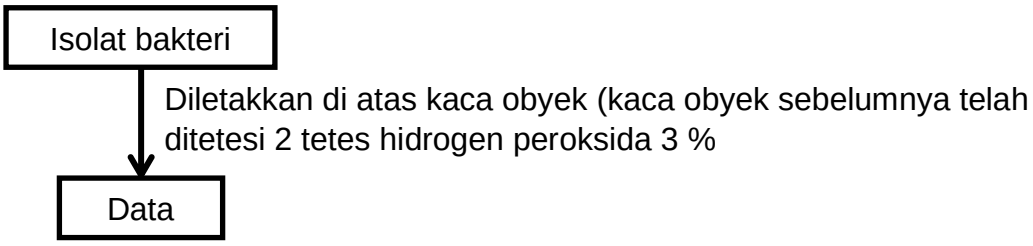


Lampiran 6. Skema kerja uji SCA (Simon Citrat Agar)



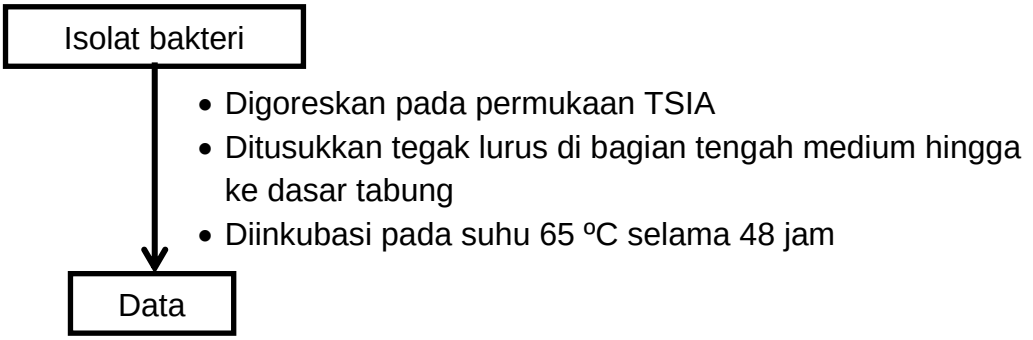
Catatan:
Uji positif jika medium berubah warna dari hijau menjadi warna biru

Lampiran 7. Skema kerja uji katalase



Catatan:
Uji positif ditandai dengan terbentuknya gelembug udara

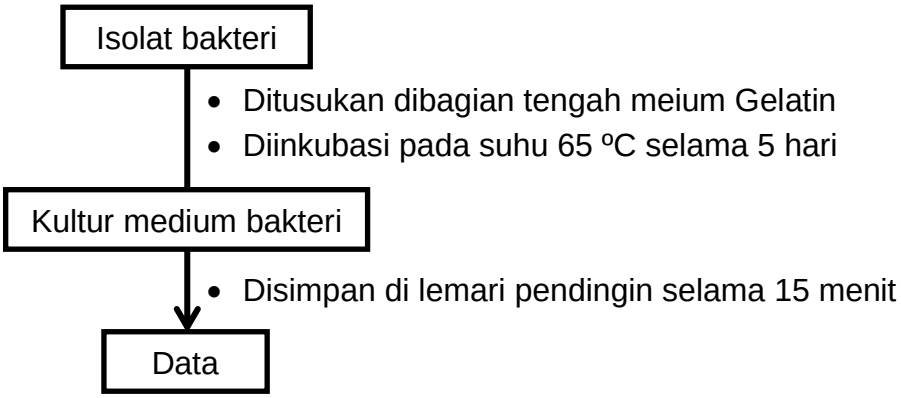
Lampiran 8. Skema kerja uji TSIA (Triple Sugar Ion Agar)



Catatan:

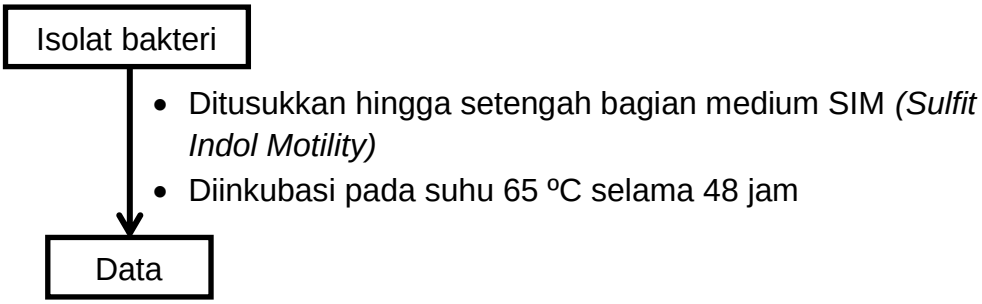
1. Uji positif jika medium berubah warna dari cokelat tua mejadi warna orange
2. Terbentuknya H_2S jika terbentuk warna kehitaman pada bekas goresan
3. Pembentukan gas diamati dengan terbentuknya rongga pada bagian bawah

Lampiran 9. Skema kerja uji gelatinase



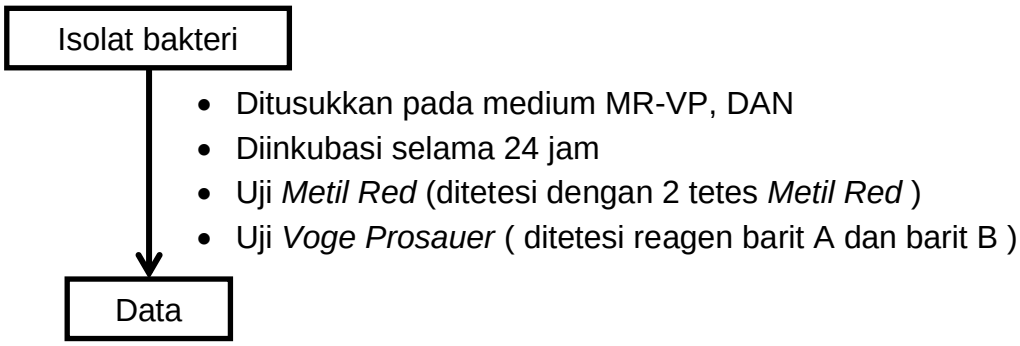
Catatan :
Uji positif ditandai dengan medium tetap cair meskipun disimpan pada lemari pendingin

Lampiran 10. Skema kerja uji motilitas



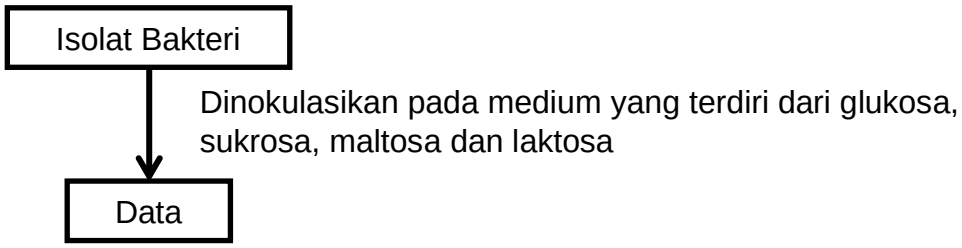
Catatan:
Uji positi ditujukkan dengan adanya jejak pergerakan bakteri

Lampiran 11. Skema kerja uji MR-VP (*Metil Red- Voge Prosauer*)



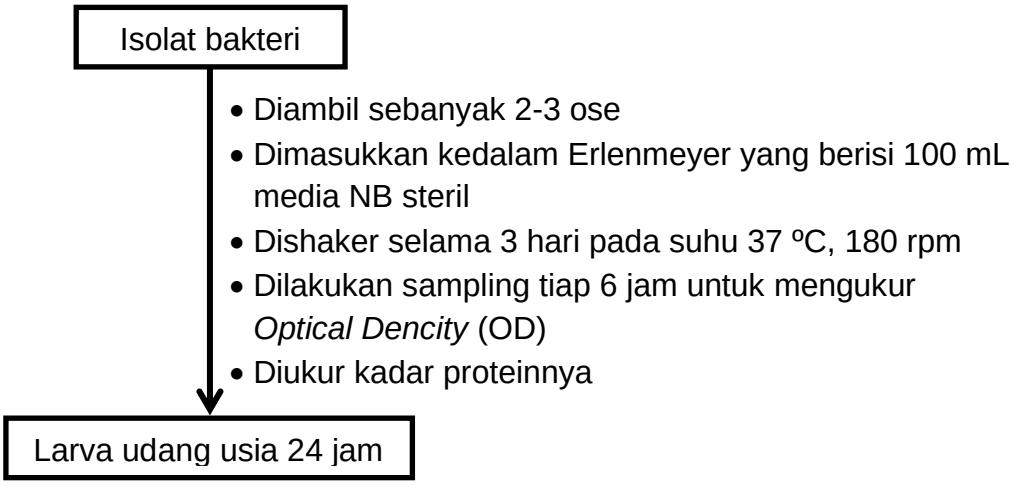
Catatan:
Uji positif jika terbentuk cincin ungu

Lampiran 12. Skema kerja uji fermentasi karbohidrat

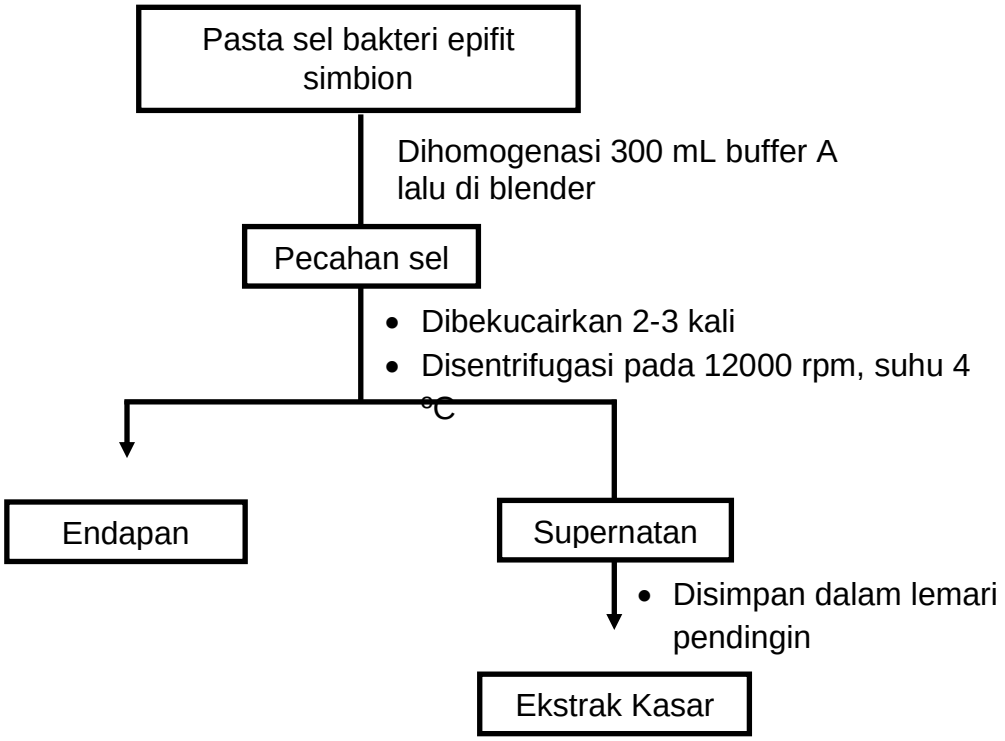


Catatan: Uji positif ditandai dengan perubahan medium menjadi warna kuning

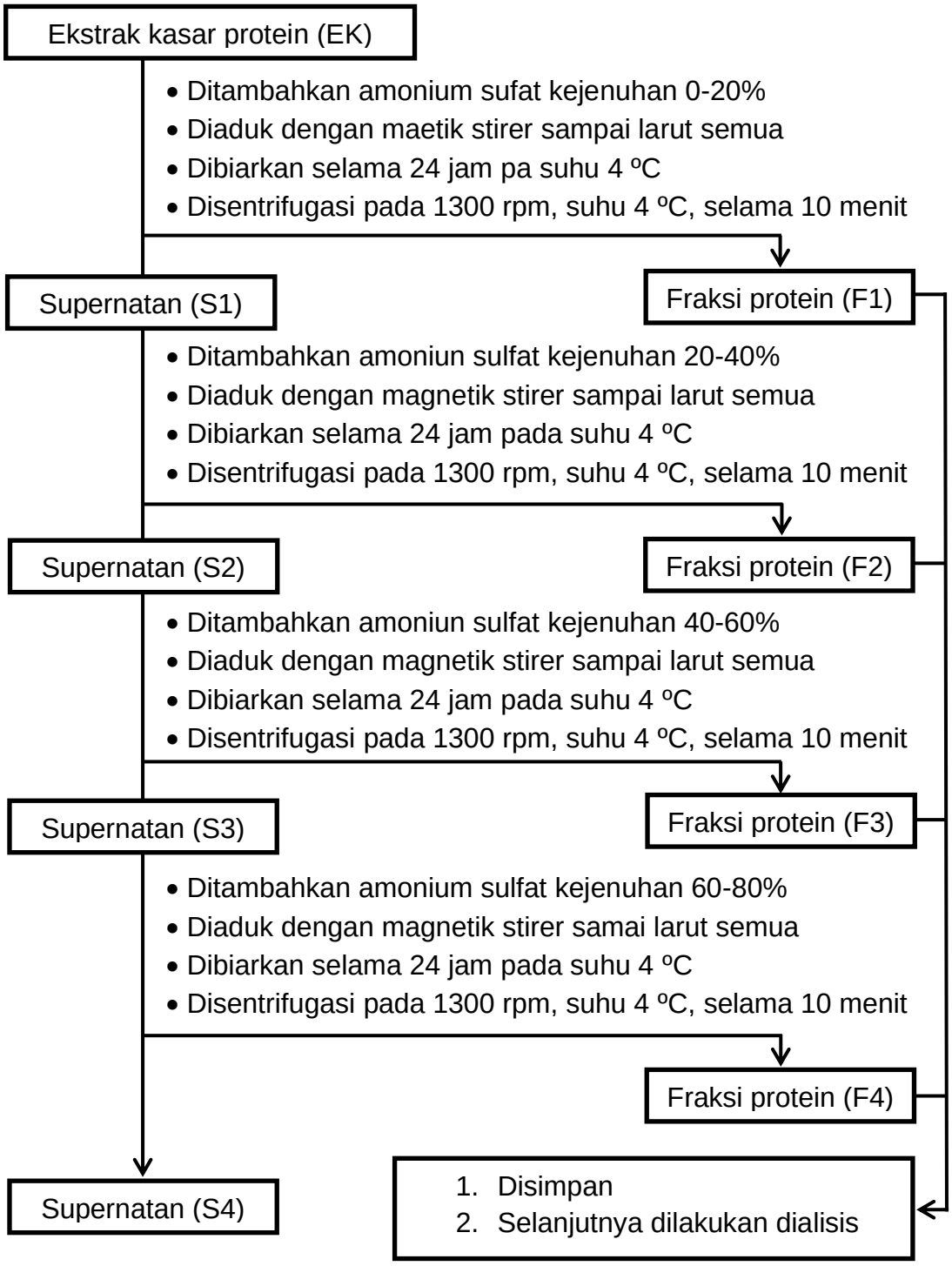
Lampiran 13. Skema kerja penentuan waktu produksi optimum protein



Lampiran 14. Skema kerja isolasi protein



Lampiran 15. Skema kerja fraksinasi protein dengan ammonium sulfat

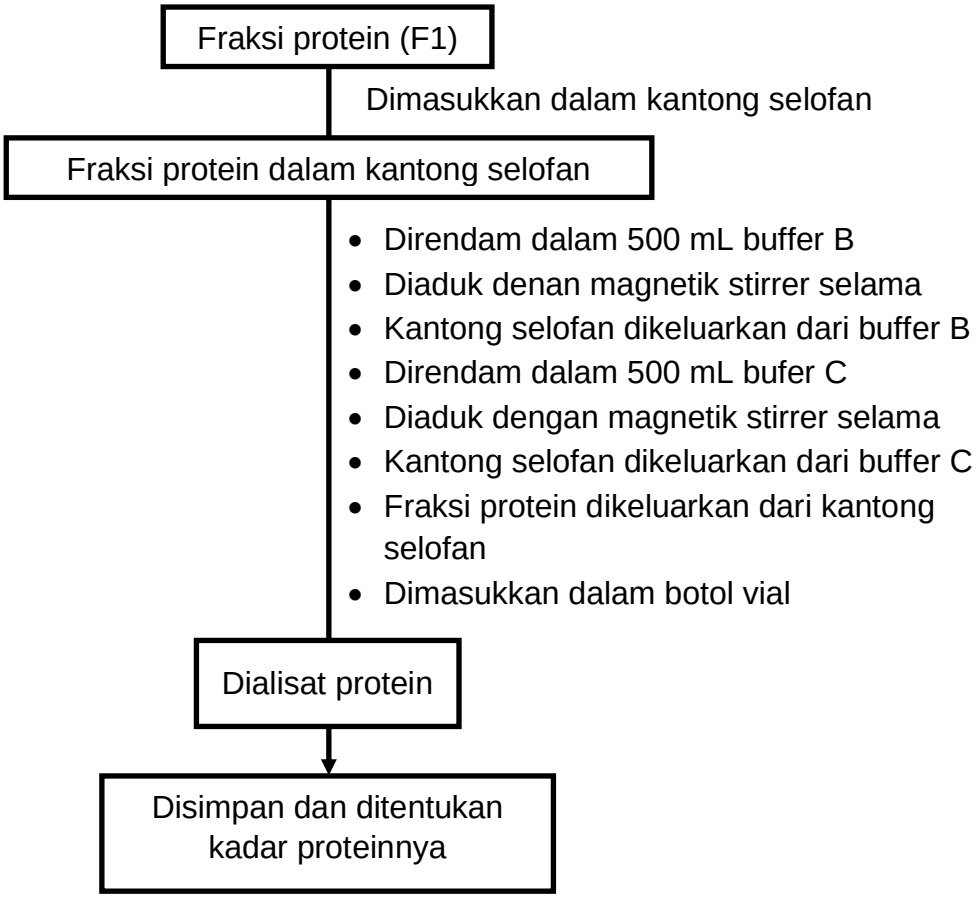


Lampiran 16. Penambahan Ammonium Sulfat Fraksionasi Protein

Kejenuhan Awal dari Amonium Sulfat (% pada 0-4°C)	%Kejenuhan pada 0-4°C																
	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100
	Penambahan Amonium sulfat kristal (gram) untuk satu liter larutan																
0	106	134	164	194	226	258	291	326	361	398	436	474	516	559	603	650	697
5	79	108	137	166	197	229	262	296	331	368	405	444	484	526	570	615	662
10	53	81	109	139	169	200	233	266	301	337	374	412	452	493	536	581	627
15	26	54	82	111	141	172	204	237	271	306	343	381	420	460	503	547	592
20	0	27	55	83	113	143	175	207	241	276	312	349	387	427	469	512	557
25		0	27	56	84	115	146	179	211	245	280	317	355	395	436	478	522
30			0	28	56	86	117	148	181	214	249	285	323	362	402	445	488
35				0	28	57	87	118	151	184	218	254	291	329	369	410	453
40					0	29	58	89	120	153	187	222	258	296	335	376	418
45						0	29	59	89	123	156	190	226	263	302	342	383
50							0	30	59	92	125	159	194	230	268	308	348
55								0	30	61	93	127	161	197	235	273	313
60									0	31	62	95	129	164	201	239	279
65										0	31	63	97	132	168	205	244
70											0	32	65	99	134	171	209
75												0	32	66	101	137	174
80													0	33	67	103	139
85														0	34	68	105
90															0	34	70
95																0	35
100																	0

Juga bisa dengan menggunakan “Ammonium Sulphate Calkulator” http://www.encorbio.com/protocols/AM-SO4.htm

Lampiran 17. Skema kerja dialisis protein



Catatan:

Perlakuan yang sama untuk fraksi F2, F3, F4, dan EK

Lampiran 18. Skema kerja penentuan kadar protein

4 mL fraksi protein (F1)

- Ditambahkan 5,5 mL reagen lowry B
- Dikocok dan dibiarkan pada suhu kamar selama 10 menit
- Ditambahkan 1 mL reagen lowry A
- Dikocok dengan cepat
- Didiamkanpada suhu kamar selama 30 menit
- Diukur absorbannya pada panjang gelombang maksimum

Data

Catatan :
Hal yang sama dilakukan untuk fraksi protein (F2, F3, F4, EK), larutan baku, larutan blanko

Lampiran 19. Skema kerja hidrolisis protein dengan enzim pepsin

Fraksi protein

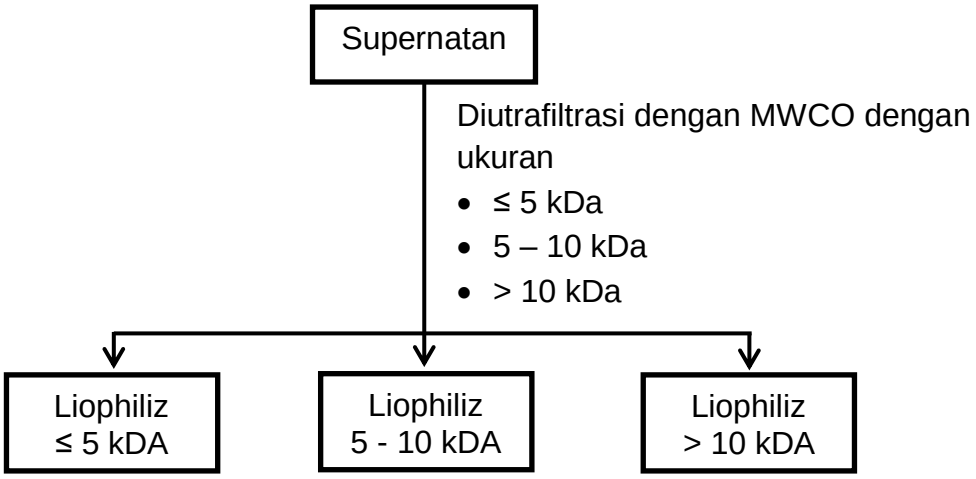
- Diencerkan menjadi larutan 3%

Larutan protein 3%

- Dihidrolisis dengan enzim pepsin
- Perbandingan enzim dan substrat 6:100
- Suhu 37 ºC
- pH 2
- reaksi dibiarkan 2 jam
- Reaksi dihentikan (pemanasan pada air 95 ºC

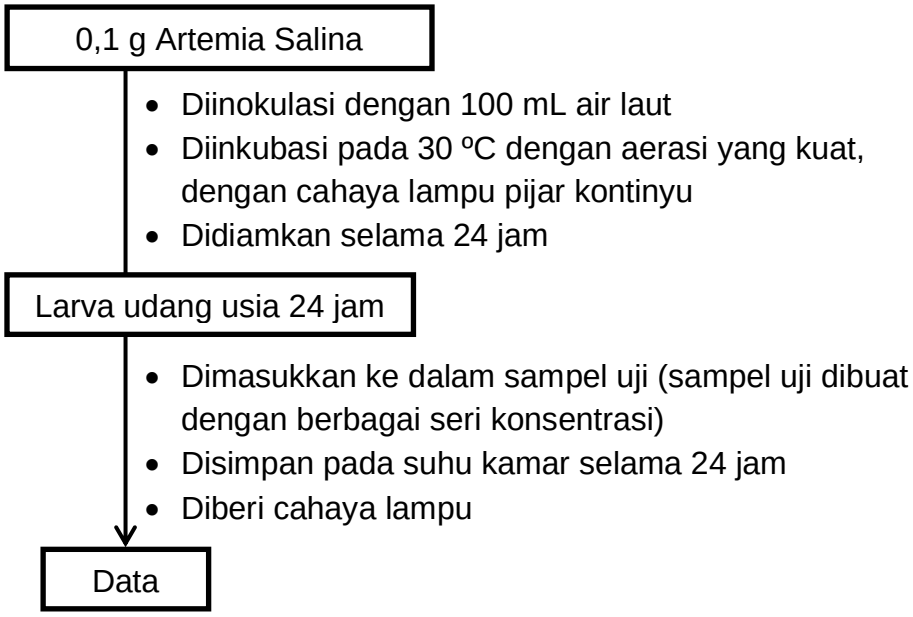
Hidrolisat protein

Lampiran 20. Skema kerja ultrafiltrasi hidrolisat protein



Liophyiz yang didapatkan dikumpulkan dan disimpan pada suhu -20 ºC

Lampiran 21. Skema kerja uji toksisitas BSLT



Lampiran 22. Uji antiproliferasi

Sel kanker (LK-2) & Sel normal (M5S)

- Didistribusikan kedalam sumuran 96-well plate sebanyak 180 µL
- Diinkubasi pada suhu suhu 37 ºC, 5% CO_2, 24 jam

Sel dalam sumuran

- Dimasukkan 20 µL larutan uji (0,1; 1; 10; 100 µg/mL kedalam tiap sumuran (replika 4 kali)
- Diinkubasi pada suhu suhu 37 ºC, 5% CO_2, 24 jam
- Diamati perubahan yang terjadi pada sel selama inkubasi

Sel + Larutan uji

- Ditambahkan 20 µL reagen MTT mg/mL kedalam tiap sumuran
- Diinkubasi 3-4 jam sampai terbentukendavan Kristal ungu formazon
- Medium yang mengandung reagen MTT dibuang

Kristal ungu formazon

- Dilarutkan dengan 100 µL DMSO tiap sumuran
- Diukur absorbansinya dengan ELISA Reader pada 550 nm kemudian dihitung % viabilitasnya

% Viabilitas

- Dilakukan perhitungan nilai penghambatan

Nilai IC_{50}

Lampiran 23. Pembuatan larutan buffer Tris-HCl

a. Pembuatan larutan buffer A (Tris-HCl 0,1 M pH 8,3; NaCl 2 M; $CaCl_2$ 0,01 M, β-mercaptoetanol 1 %, Triton X-100 0,5 %)

Prosedur pembuatan larutan:

1. Ditimbang 6,05 gram Tris (Hidroksimetil) aminometana ($NH_2C(CH_2OH)_3$) lalu dilarutkan dengan akuades sampai 125 mL.
2. Ke dalam 125 mL larutan Tris (Hidroksimetil) aminometana 0,4 M ditambahkan HCl 2 M sedikit demi sedikit sambil diatur pHnya sampai mencapai 8,3.
3. Selanjutnya ditambahkan NaCl sebanyak 58,5 gram dan 0,555 gram $CaCl_2$, β-mercaptoetanol 5 mL dan triton X-100 2,5 mL dan dicukupkan volumenya sampai 500 mL dengan akuades.

b. Pembuatan larutan buffer B (Tris-HCl 0,1 M pH 8,3; NaCl 0,2 M; $CaCl_2$ 0,01 M)

Prosedur pembuatan larutan:

1. Ditimbang 6,05 gram Tris (Hidroksimetil) aminometana ($NH_2C(CH_2OH)_3$) lalu dilarutkan dengan akuades sampai 125 mL.
2. Ke dalam 125 mL larutan Tris (Hidroksimetil) aminometana 0,4 M ditambahkan HCl 0,2 M sedikit demi sedikit sambil diatur pHnya sampai mencapai 8,3.

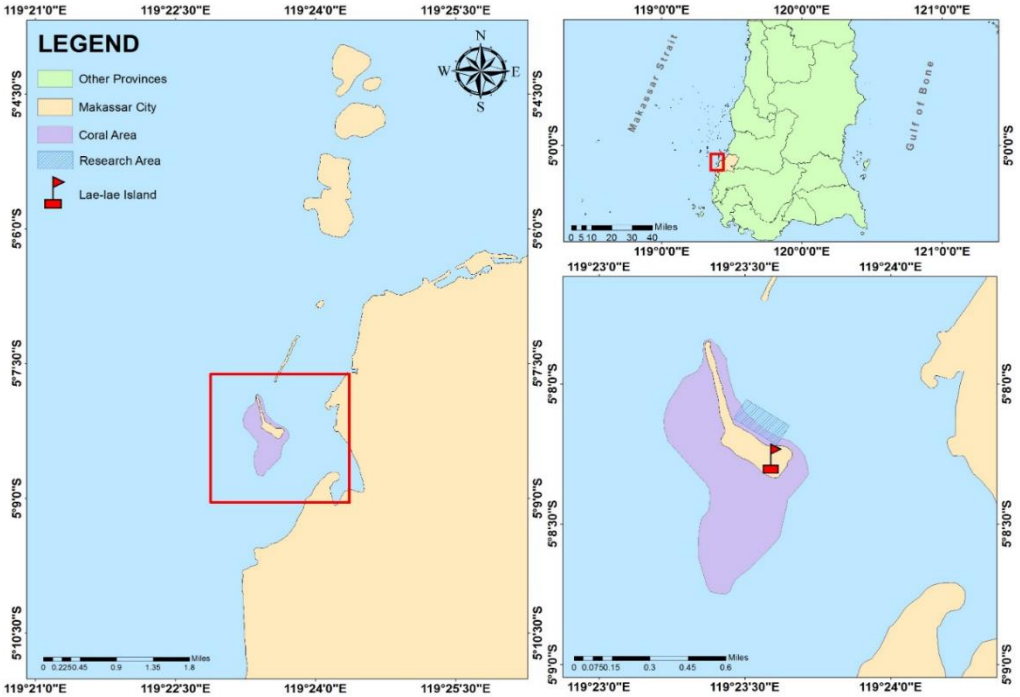
3. Selanjutnya ditambahkan NaCl sebanyak 5,85 gram dan 0,555 gram $CaCl_2$ dan dicukupkan volumenya sampai 500 mL dengan akuades.

c. Pembuatan Larutan Buffer C (Tris-HCl 0,01 M pH 8,3; NaCl 0,2 M; $CaCl_2$ 0,01 M)

Prosedur pembuatan larutan:

1. Ditimbang 0,605 gram Tris (Hidroksimetil) aminometana ($NH_2C(CH_2OH)_3$) lalu dilarutkan dengan akuades sampai 125 mL.
2. Ke dalam 125 mL larutan Tris (Hidroksimetil) aminometana 0,04 M ditambahkan HCl 2 M sedikit demi sedikit sambil diatur pHnya sampai mencapai 8,3.
3. Selanjutnya ditambahkan NaCl sebanyak 5,85 gram dan 0,555 gram $CaCl_2$ dan dicukupkan volumenya sampai 500 mL dengan akuades.

Lampiran 24. Lokasi pengambilan sampel alga cokelat *Sargassum* sp. di Pulau Lae-lae, Makassar, Sulawesi selatan

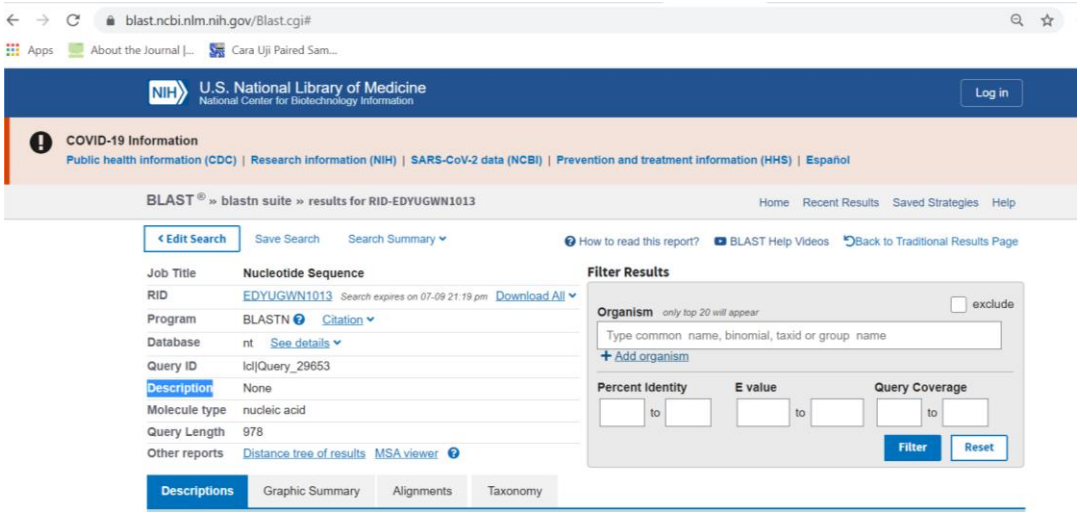


Lampiran 25. Sekuen 16S rRNA dan hasil BLAST bakteri epifit strain SG-A1 dan SG-A2, hasil BLAST dan rekontruksi pohon filogenik

StrainA1_63F_Sargassum>GCTTGCTCTCGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTG
GGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCA
AGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCAGATGTGCCCAGATGGGATTAGCTAGT
AGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACA
CTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG
CGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAG
CGGGGAGGAAGGTGTTGTGGTTAATAACCACAGCAATTGACGTTACCCGCAGAAGAAGCACCG
GCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGG
CGTAAAGCGCACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAAC
TGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGA
AATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGC
TCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGA
TGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCC
TGGGGAGTACGGCCGCAAGGTTAAGACTCACATGAATTGACGGGGGCCCGCACAAGCGGTGG
AGCATGTGGTTTAATTCGATGCAACGCGAAGAAACCTTACCTACTCTTGACATCCAGAGAACTTT
CCAGAGATGGATTGGTGCCTTCGGGAACTCTGAAA

StrainA2_63F_Sargassum>CTTCGGGATGCCGGCGAGCGGCGGACGGGTGAGTAATGCCTAG
GAATCTGCCTGGTAGTGGGGGATAACTCGGGGAAACTCGAGCTAATACCGCATACGTCCTACG
GGAGAAAGCGGGGGATCTTCGGACCTCGCGCTACCAGATGAGCCTAGGTCGGATTAGCTAGTT
GGTGAGGTAAAGGCTCACCAAGGCGACGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACAC
TGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGG
CGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAG
TTGGGAGGAAGGGCAGTAAGCTAATACCTTGCTGTTTTGACGTTACCGACAGAATAAGCACCG
GCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGG
CGTAAAGCGCGCGTAGGTGGTTTGATAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAAT
TGCATCCAAAACTGTCTGACTAGAGTATGGCAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGA
AATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGGCTAATACTGACACT
GAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGAT
GTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCGCAGCTAACGCATTAAGTCGACCGCCT
GGGGAGTACGGCCGCAAGGTTAAAACTCACATGAATTGACGGGGGCCCGCACAAGCGGTGGA
GCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATGCAGAGAACTTTC
CAGAGATGGATTGGTGCCTTCGGGAGCTCTGACACAGGTGCTGCATGGCTGTCGTCAGCTCGT
GTCCTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGTCCTTAGTTACCAGCACGTCA
TGGTGGG

Hasil BLAST isolat strain SG-A1



Sequences producing significant alignments

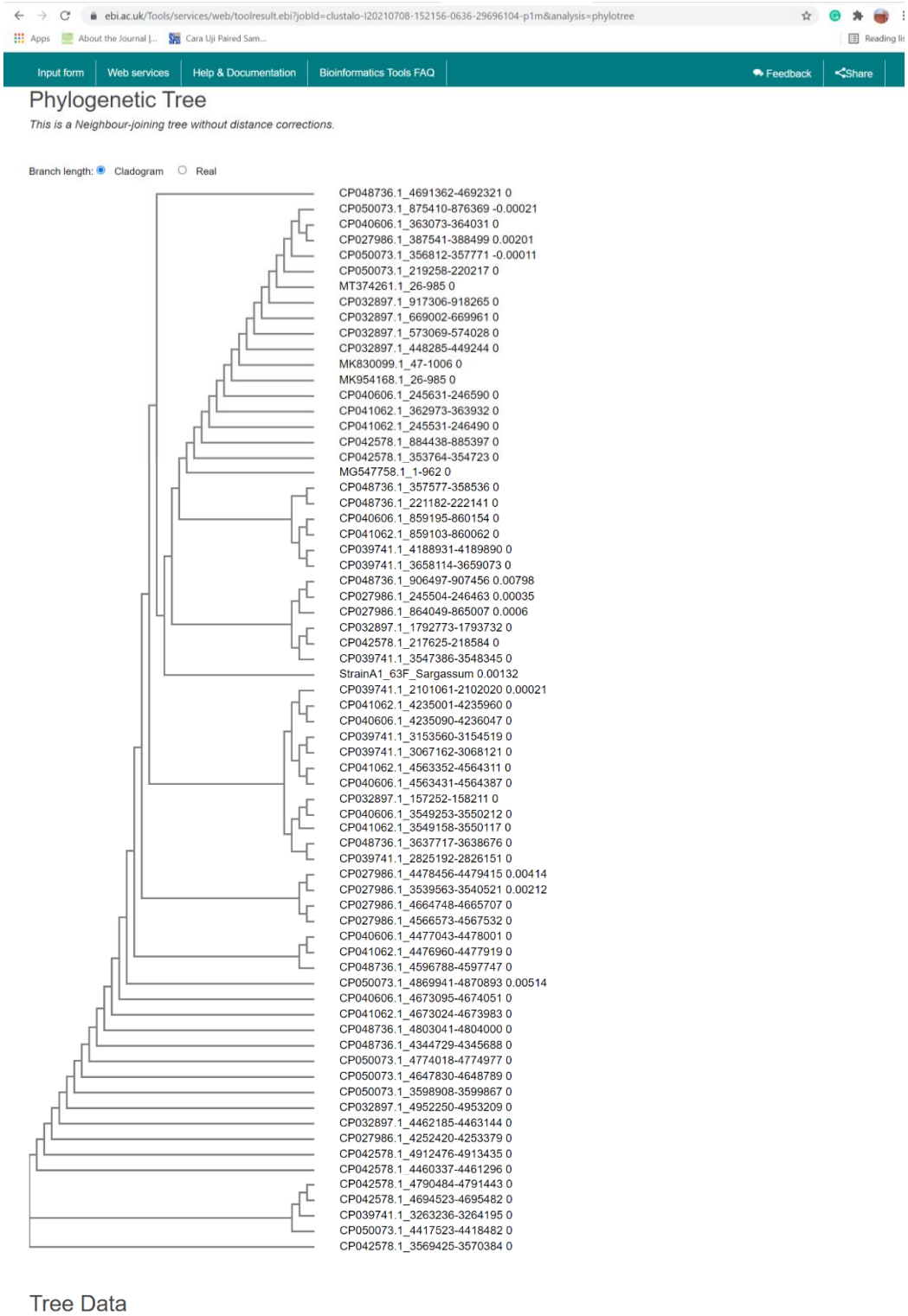
Download | New Select columns | Show 100

select all 100 sequences selected

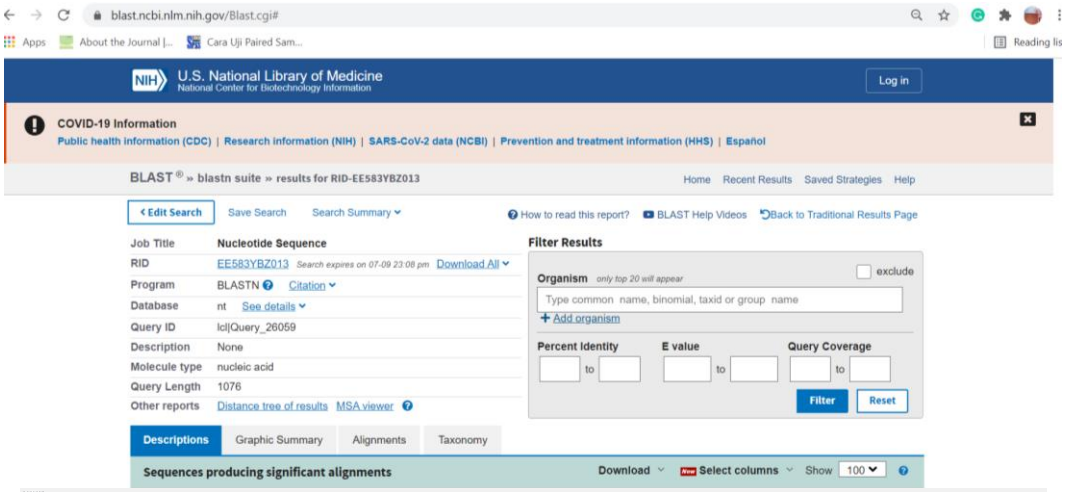
GenBank | Graphics | Distance tree of results | New MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Enterobacter sp. strain E23 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1760	1760	98%	0.0	99.69%	1014	MG547758.1
Bacterium strain Ma02 16S ribosomal RNA gene, partial sequence	bacterium	1757	1757	98%	0.0	99.69%	1413	MT436801.1
Enterobacter ludwigii strain D8 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1413	MT374261.1
Enterobacter kobei strain 070 chromosome, complete genome	Enterobacter kobei	1757	13991	98%	0.0	99.69%	4921999	CP050073.1
Enterobacter ludwigii strain CEB04 chromosome	Enterobacter ludwigii	1757	13919	98%	0.0	99.69%	4892475	CP039741.1
Pantoea agglomerans strain TY171-21 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	1757	1757	98%	0.0	99.69%	1415	MT083951.1
Pantoea agglomerans strain BB7 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	1757	1757	98%	0.0	99.69%	1386	MT071499.1
Enterobacter sp. T2 chromosome, complete genome	Enterobacter sp. T2	1757	13903	98%	0.0	99.69%	4854376	CP048736.1
Enterobacter kobei strain MR4 16S ribosomal RNA gene, partial sequence	Enterobacter kobei	1757	1757	98%	0.0	99.69%	1432	MN847594.1
Enterobacter kobei strain NPKC1_2_4 16S ribosomal RNA gene, partial sequence	Enterobacter kobei	1757	1757	98%	0.0	99.69%	1044	MN691794.1
Enterobacter kobei strain NPKC1_2_3 16S ribosomal RNA gene, partial sequence	Enterobacter kobei	1757	1757	98%	0.0	99.69%	1035	MN691793.1
Enterobacter kobei strain NPKC1_2_1 16S ribosomal RNA gene, partial sequence	Enterobacter kobei	1757	1757	98%	0.0	99.69%	1023	MN691791.1
Enterobacter sichuanensis strain SGAir0282 chromosome, complete genome	Enterobacter sichuanensis	1757	13869	98%	0.0	99.69%	4711389	CP027986.1
Enterobacter kobei strain C16 chromosome, complete genome	Enterobacter kobei	1757	14025	98%	0.0	99.69%	4964300	CP042578.1
Leclercia sp. FSFGR62 gene for 16S ribosomal RNA, partial sequence	Leclercia sp.	1757	1757	98%	0.0	99.69%	1436	LC484695.1
Enterobacter ludwigii strain ESK17 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1406	MN173452.1
Pantoea sp. strain PA-4 16S ribosomal RNA gene, partial sequence	Pantoea sp.	1757	1757	98%	0.0	99.69%	1435	MK188869.1
Enterobacter cloacae strain EC-3 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1757	1757	98%	0.0	99.69%	1416	MK188868.1
Enterobacter sp. strain EC-2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1757	1757	98%	0.0	99.69%	1431	MK188867.1
Enterobacter ludwigii strain I140 chromosome, complete genome	Enterobacter ludwigii	1757	13947	98%	0.0	99.69%	4719401	CP041062.1
Pantoea sp. strain PA-4 16S ribosomal RNA gene, partial sequence	Pantoea sp.	1757	1757	98%	0.0	99.69%	1435	MK188869.1
Enterobacter cloacae strain EC-3 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1757	1757	98%	0.0	99.69%	1416	MK188868.1
Enterobacter sp. strain EC-2 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1757	1757	98%	0.0	99.69%	1431	MK188867.1
Enterobacter ludwigii strain I140 chromosome, complete genome	Enterobacter ludwigii	1757	13947	98%	0.0	99.69%	4719401	CP041062.1
Enterobacter ludwigii strain I42 chromosome, complete genome	Enterobacter ludwigii	1757	13886	98%	0.0	99.69%	4719369	CP040606.1
Enterobacter sp. strain E4 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1757	1757	98%	0.0	99.69%	1410	MK954168.1
Enterobacter ludwigii strain LY6 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1433	MK830099.1
Bacterium strain BS0438 16S ribosomal RNA gene, partial sequence	bacterium	1757	1757	98%	0.0	99.69%	1430	MK823626.1
Bacterium strain BS0423 16S ribosomal RNA gene, partial sequence	bacterium	1757	1757	98%	0.0	99.69%	1429	MK823611.1
Bacterium strain BS0419 16S ribosomal RNA gene, partial sequence	bacterium	1757	1757	98%	0.0	99.69%	1426	MK823607.1
Uncultured bacterium clone GS_2 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1757	1757	98%	0.0	99.69%	1466	MK185477.1
Uncultured bacterium clone GS_12 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1757	1757	98%	0.0	99.69%	1466	MK185476.1
Uncultured bacterium clone GS_1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1757	1757	98%	0.0	99.69%	1466	MK185473.1
Enterobacter kobei strain WCHEK045523 chromosome, complete genome	Enterobacter kobei	1757	14013	98%	0.0	99.69%	4953590	CP032897.1
Enterobacter ludwigii strain I140 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1413	MH244328.1
Enterobacter ludwigii strain PgBe217 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1338	MH211306.1
Enterobacter cloacae strain NP07 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1757	1757	98%	0.0	99.69%	1528	MH169128.1
Enterobacter sp. strain L 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1757	1757	98%	0.0	99.69%	1381	MF000792.1
Pantoea agglomerans strain 30ft5a 16S ribosomal RNA gene, partial sequence	Pantoea agglomerans	1757	1757	98%	0.0	99.69%	1359	MG639901.1
Enterobacter ludwigii strain 30ft1b 16S ribosomal RNA gene, partial sequence	Enterobacter ludwigii	1757	1757	98%	0.0	99.69%	1475	MG602668.1
Enterobacter cloacae strain MF01 16S ribosomal RNA gene, partial sequence	Enterobacter cloacae	1757	1757	98%	0.0	99.69%	1394	MG461635.1
Enterobacter ludwigii strain AA4 chromosome, complete genome	Enterobacter ludwigii	1757	13947	98%	0.0	99.69%	4799256	CP018785.1
Gamma proteobacterium BIWA50 gene for 16S ribosomal RNA, partial sequence	gamma proteobacterium BIWA50	1757	1757	98%	0.0	99.69%	1470	LC217437.1
Enterobacter sp. strain P18 16S ribosomal RNA gene, partial sequence	Enterobacter sp.	1757	1757	98%	0.0	99.69%	1404	KY084459.1
Enterobacter ludwigii strain EN-119 plasmid pEN-119, complete sequence	Enterobacter ludwigii	1757	3472	98%	0.0	99.69%	95331	CP017280.1

Pohon filogenik isolat strain SG-A1

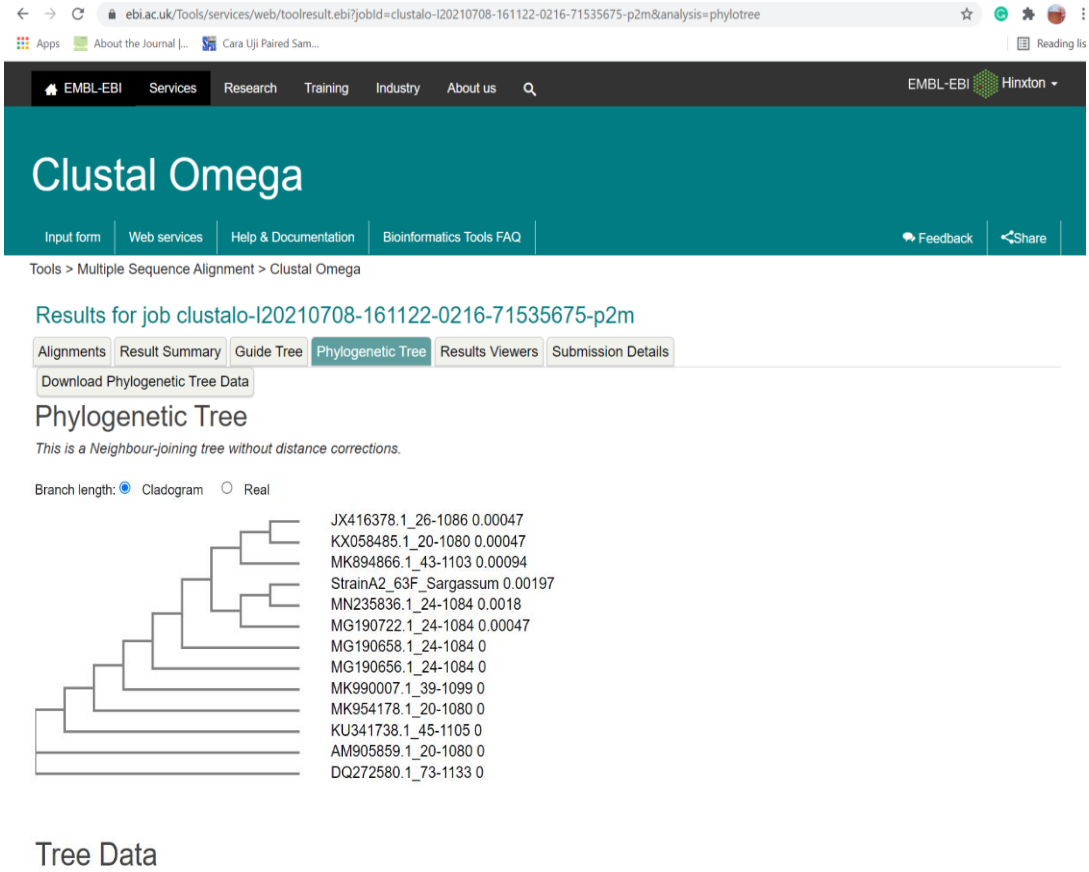


Hasil BLAST isolat strain SG-A2



Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Pseudomonas balearica strain IMB16-093 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1943	1943	98%	0.0	99.72%	1410	MG190658.1
Pseudomonas balearica strain IMB16-091 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1943	1943	98%	0.0	99.72%	1410	MG190656.1
Bacterium strain ZH1 16S ribosomal RNA gene, partial sequence	bacterium	1943	1943	98%	0.0	99.72%	1435	MK990007.1
Pseudomonas sp. strain P4 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1943	1943	98%	0.0	99.72%	1383	MK954178.1
Pseudomonas sp. SA03 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. SA03	1943	1943	98%	0.0	99.72%	1320	KU341738.1
Pseudomonas balearica partial 16S rRNA gene, isolate st101	Pseudomonas balearica	1943	1943	98%	0.0	99.72%	1383	AM905859.1
Pseudomonas sp. LB-2 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. LB-2	1943	1943	98%	0.0	99.72%	1498	DQ272580.1
Pseudomonas balearica strain FU-130 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1938	1938	98%	0.0	99.62%	1203	MN235836.1
Pseudomonas balearica strain IMB16-119 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1938	1938	98%	0.0	99.62%	1437	MG190722.1
Bacterium strain ZH2 16S ribosomal RNA gene, partial sequence	bacterium	1938	1938	98%	0.0	99.62%	1424	MK990008.1
Pseudomonas balearica strain ST8 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1938	1938	98%	0.0	99.62%	1437	MK894866.1
Pseudomonas balearica strain 58 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1938	1938	98%	0.0	99.62%	1279	KX058485.1
Pseudomonas sp. a-2-3 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. a-2-3	1938	1938	98%	0.0	99.62%	1408	JX416378.1
Pseudomonas balearica strain IMB16-106 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1934	1934	98%	0.0	99.62%	1394	MG190684.1
Pseudomonas balearica strain EC28 chromosome, complete genome	Pseudomonas balearica	1932	7692	98%	0.0	99.53%	4642566	CP045858.1
Pseudomonas sp. strain HC16 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1932	1932	98%	0.0	99.53%	1395	MH398515.1
Pseudomonas sp. strain HC13 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1932	1932	98%	0.0	99.53%	1382	MH398124.1
Pseudomonas sp. strain PrPc079 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1932	1932	98%	0.0	99.53%	1446	MF948937.1
Pseudomonas balearica strain 56 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1473	KX713145.1
Pseudomonas balearica strain Y91 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1390	KU601285.1
Pseudomonas balearica strain Y70 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1394	KU601277.1
Pseudomonas balearica strain Y60 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1396	KU601274.1
Pseudomonas sp. SinB10 partial 16S rRNA gene, strain SinB10	Pseudomonas sp. SinB10	1932	1932	98%	0.0	99.53%	1468	LT594955.1
Pseudomonas balearica strain RMR34 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1473	KT731542.1
Pseudomonas sp. MSSRF DN521 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. MSSRF DN521	1932	1932	98%	0.0	99.53%	1390	KU131272.1
Pseudomonas sp. QND9 gene for 16S ribosomal RNA, partial sequence	Pseudomonas sp. QND9	1932	1932	98%	0.0	99.53%	1426	LC037157.1
Pseudomonas sp. 38M1 FL01 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. 38M1 FL01	1932	1932	98%	0.0	99.53%	1500	KM357381.1
Pseudomonas balearica DSM 6083 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica DSM 6083	1932	1932	98%	0.0	99.53%	1435	MZ276325.1
Pseudomonas balearica strain LT0504 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1402	MW663930.1
Pseudomonas sp. JNU-SGY009 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. JNU-SGY009	1932	1932	98%	0.0	99.53%	1421	KC337110.1
Pseudomonas balearica strain FDAARGOS_1013 chromosome, complete genome	Pseudomonas balearica	1932	7725	98%	0.0	99.53%	4411233	CP067013.1
Pseudomonas balearica strain MR4 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1932	1932	98%	0.0	99.53%	1397	MT995050.1
Pseudomonas sp. strain YP08 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1932	1932	98%	0.0	99.53%	1422	MT914227.1
Pseudomonas sp. BC044 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. BC044	1932	1932	98%	0.0	99.53%	1421	HQ105012.1
Pseudomonas sp. XM-1 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. XM-1	1932	1932	98%	0.0	99.53%	1396	HM242290.1
Uncultured Pseudomonas sp. clone F5 16S ribosomal RNA gene, partial sequence	uncultured Pseudomonas sp.	1932	1932	98%	0.0	99.53%	1421	FJ863108.1
Pseudomonas sp. Y5C 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. Y5C	1932	1932	98%	0.0	99.53%	1391	EU301685.1
Pseudomonas sp. N9-5 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. N9-5	1932	1932	98%	0.0	99.53%	1412	EU107175.1
Pseudomonas sp. YP-A-4-1 16S ribosomal RNA gene, partial sequence	Pseudomonas sp. YP-A-4-1	1930	1930	98%	0.0	99.53%	1432	KF052582.1
Uncultured Pseudomonas sp. clone TJ-4 16S ribosomal RNA gene, partial sequence	uncultured Pseudomonas sp.	1929	1929	98%	0.0	99.43%	1413	JQ858219.1
Pseudomonas sp. strain Can-25 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1927	1927	98%	0.0	99.43%	1401	MK503531.1
Pseudomonas balearica strain RAD-17 16S ribosomal RNA gene, partial sequence	Pseudomonas balearica	1927	1927	98%	0.0	99.43%	1428	MK881511.1
Pseudomonas sp. strain L1 16S ribosomal RNA gene, partial sequence	Pseudomonas sp.	1927	1927	98%	0.0	99.43%	1398	MN410633.1

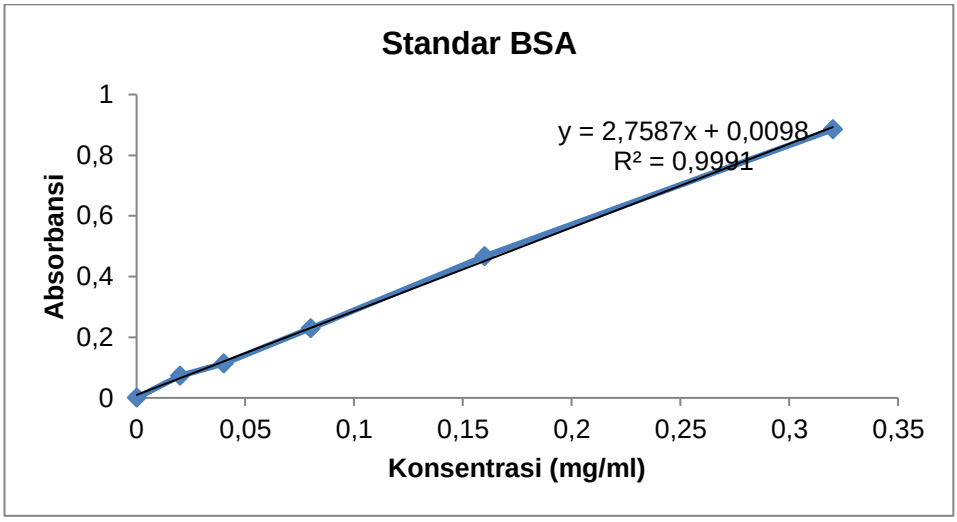
Pohon filogenik isolat strain SG-A2



Lampiran 26. Perhitungan Kadar/Konsentrasi Prote in, Hidrolisat Protein dan Peptida

A. Perhitungan kadar/konsentrasi protein ekstrak kasar dan fraksi protein bakteri epifit isolat strain SG-A1

Konsentrasi BSA (mg/ml)	Absorbansi (λ=660)
0	0
0,02	0,073
0,04	0,114
0,08	0,23
0,16	0,467
0,32	0,885



Sampel	Absorbansi	Fp	Konsentrasi (mg/ml)
Ekp	1,16	50	20,8468
F1p	0,84	50	15,0469
F2p	0,59	50	10,5158
F3p	1,005	50	18,0375
F4p	0,95	50	17,0406

- Perhitungan konsentrasi protein dihitung menggunakan persamaan
  $y = 2{,}7587x + 0{,}0098$

Contoh untuk Ekp:

$x = \frac{y-0,0098}{2,7587}$ x Fp

y=absorban; x= konsentrasi protein

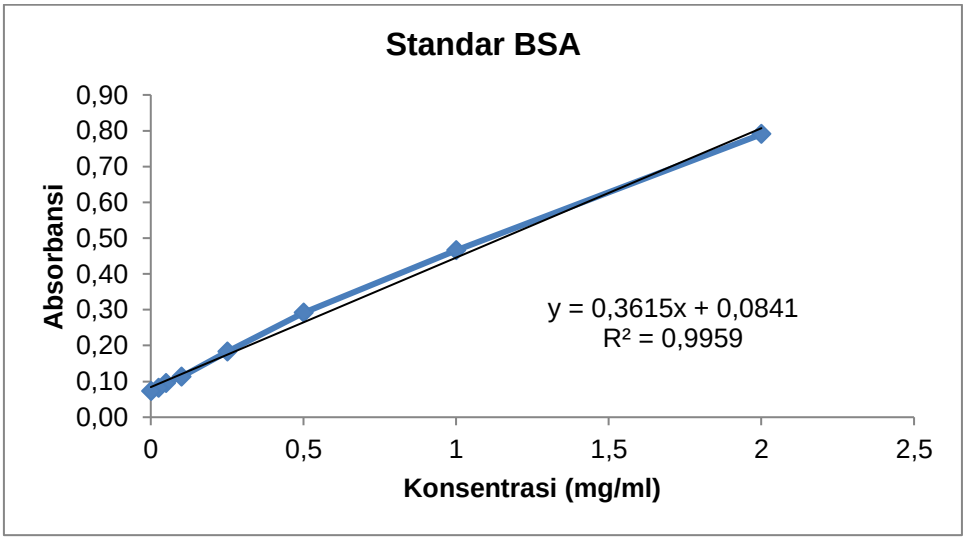
$x = \frac{1,16-0,0098}{2,7587}$ x 50

$x = 20,8468$

- Hal yang sama dilakukan untuk F1p, F2p, F3p dan F4p.

B. Perhitungan kadar/konsentrasi hidrolisat protein bakteri epifit isolat strain SG-A1

Konsetrasi BSA (mg/ml)	Absorbansi (λ=660)
2	0,7901
1	0,4654
0,5	0,2909
0,25	0,1831
0,1	0,1129
0,05	0,0944
0,025	0,0816
0	0,0728



Sampel	Absorbansi	Fp	Konsentrasi (mg/ml)
Ekh	0,5401	10	12,61
F1h	0,6501	10	15,66
F2h	0,7307	10	17,89
F3h	0,6479	10	15,60
F4h	0,6546	10	15,78

- Perhitungan konsentrasi protein dihitung menggunakan persamaan
  $y = 0{,}3615x + 0{,}0841$

  Contoh untuk Ekh:

  $x = \frac{y-0{,}0841}{0{,}3615}$ x Fp

  y=absorban; x= konsentrasi protein

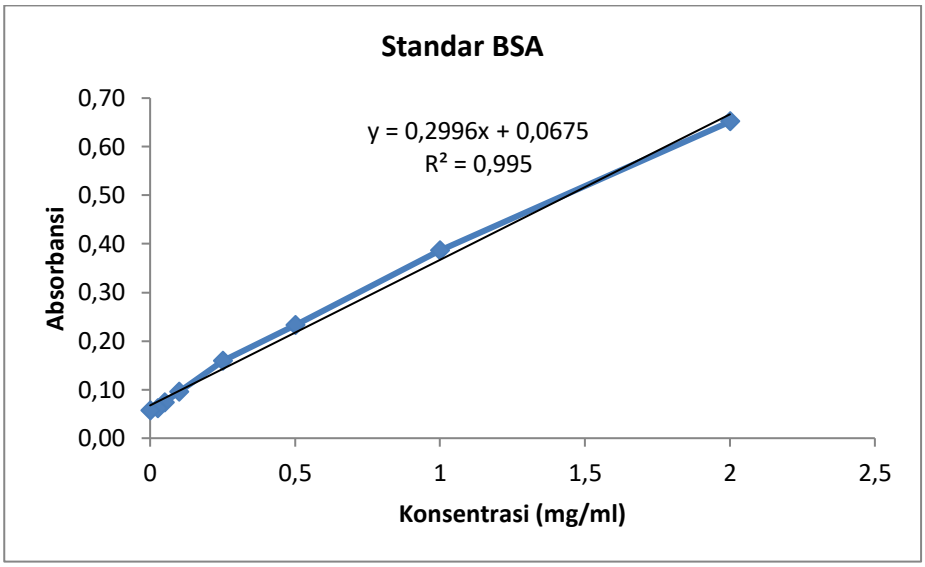
  $x = \frac{0{,}5401-0{,}0815}{0{,}3615}$ x 10

  $x = 12{,}61$

- Hal yang sama dilakukan untuk F1h, F2h, F3h dan F4h.

C. Perhitungan kadar/konsentrasi peptida bakteri epifit isolat strain SG-A1

Konsetrasi BSA (mg/ml)	Absorbansi (λ=660)
2	0,6515
1	0,3865
0,5	0,2325
0,25	0,1593
0,1	0,0947
0,05	0,0738
0,025	0,0609
0	0,0565



Sampel	Absorbansi	Fp	Konsentrasi (mg/ml)
F4h1	0,28	1	0,71
F4h2	0,43	1	1,21
F4h3	0,55	1	1,60

- Perhitungan konsentrasi protein dihitung menggunakan persamaan:
  $y = 0{,}2996x + 0{,}0675$

  Contoh untuk F4h1:

  $x = \frac{y-0{,}0675}{0{,}2996}$ x Fp

  y=absorban; x= konsentrasi protein

  $x = \frac{0{,}28-0{,}0675}{0{,}2996}$ x 1

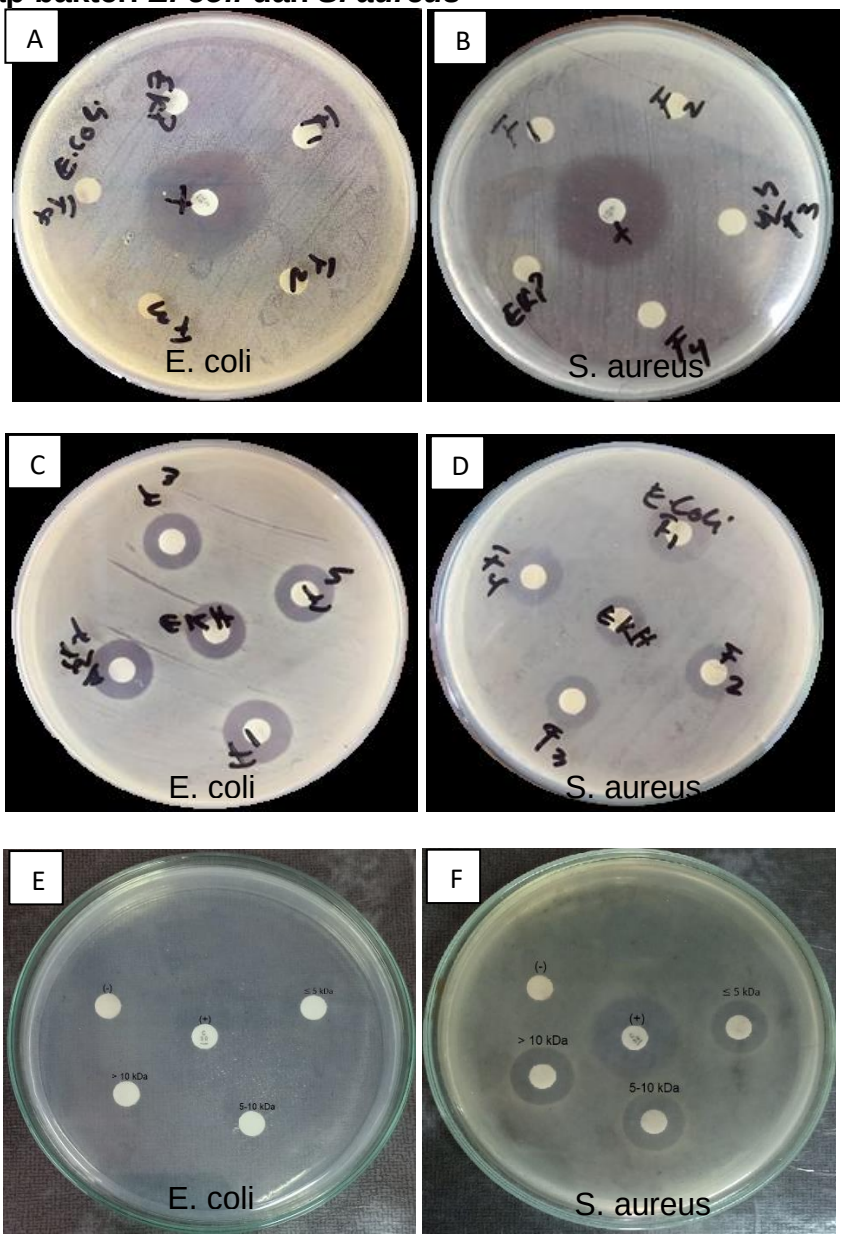
  $x = 0{,}71$

- Hal yang sama dilakukan untuk F4h2 dan F4h3

Lampiran 27. Perhitungan derajat hidrolisis protein dari bakteri epifit isolat strain SG-A1.

Sampel	Waktu (menit)	Protein total	Protein terlarut 10 % TCA	Derajat Hidrolisis (%)
EK	0	0,056	0	0
	30	0,560	0,225	40,2
	60	0,584	0,236	40,4
	90	0,608	0,282	46,4
	120	0,599	0,261	43,6
	150	0,597	0,253	42,4
	180	0,681	0,287	42,1
F1	0	0,036	0	0
	30	0,538	0,195	36,2
	60	0,562	0,217	38,6
	90	0,599	0,235	39,2
	120	0,556	0,216	38,8
	150	0,566	0,219	38,7
	180	0,650	0,249	38,3
F2	0	0,017	0	0
	30	0,585	0,198	33,8
	60	0,556	0,204	36,7
	90	0,609	0,255	41,9
	120	0,589	0,240	40,7
	150	0,593	0,243	41,0
	180	0,647	0,265	41,0
F3	0	0,003	0	0
	30	0,562	0,215	38,3
	60	0,599	0,268	44,7
	90	0,625	0,285	45,6
	120	0,600	0,252	42,0
	150	0,599	0,242	40,4
	180	0,681	0,276	40,5
F4	0	0,004	0	0
	30	0,574	0,228	39,7
	60	0,599	0,240	40,1
	90	0,637	0,259	40,7
	120	0,621	0,250	40,3
	150	0,601	0,243	40,4
	180	0,660	0,267	40,5

Lampiran 28. Hasil uji aktivitas antibakteri fraksi protein, hidrolisat protein dan fragmen peptida dari bakteri epifit isolat strain SG-A1 terhadap bakteri *E. coli* dan *S. aureus*



*Visualisasi diameter zona hambat fraksi protein (**A**), hidrolisat protein (**C**), fragmen peptide (**E**) terhadap pertumbuhan Escherichia coli dan visualisasi diameter zona hambat fraksi protein (**B**), hidrolisat protein (**D**), fragmen peptide (**F**) terhadap Staphylococcus aureus.*
(Catatan: EKp: ekstrak kasar protein, F1p-F4p: fraksi protein, EKh: hidrolisat protein ekstrak kasar, F1h-F4h: fraksi hidrolisat protein, ≤5 kDa, 5-10 kDa, > 10 kDa: fragmen peptide, (-): Kontrol Negatif, (+): Kontrol Positif).

Tabel diameter zona hambatan fraksi protein, hidrolisat protein dan fragmen peptida

No	Purification steps	* Diameter Inhibition Zone (mm)					
		E. coli			*S. aureus*		
		24 h	48 h	72 h	24 h	48 h	72 h
1	Crude extract	6.3 ± 0.06	6.6 ± 0.10	6.8 ± 0.10	7.0 ± 0.03	7.2 ± 0.03	7.2 ± 0.04
2	F1p	6.1 ± 0.06	6.1 ± 0.10	6.1 ± 0.10	6.6 ± 0.05	6.6 ± 0.01	6.7 ± 0.10
3	F2p	6.1 ± 0.10	6.1 ± 0.06	6.5 ± 0.21	6.2 ± 0.02	6.4 ± 0.02	6.5 ± 0.02
4	F3p	6.1 ± 0.12	6.2 ± 0.10	6.2 ± 0.15	6.3 ± 0.03	6.7 ± 0.01	6.9 ± 0.03
5	F4p	6.4 ± 0.10	6.6 ± 0.06	7.0 ± 0.06	6.9 ± 0.02	7.4 ± 0.02	7.4 ± 0.01
6	Control (-)	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
7	Control (+)	22.0 ± 0.06	22.5 ± 0.12	22.7 ± 0.06	26.6 ± 0.05	27.1 ± 0.18	27.7 ± 0.12

No	Purification steps	* Diameter Inhibition Zone (mm)					
		E. coli			*S. aureus*		
		24 h	48 h	72 h	24 h	48 h	72 h
1	Crude extract	12.5 ± 0.10	13.0 ± 0.03	14.3 ± 0.02	13.9 ± 0.03	14.1 ± 0.09	14.2 ± 0.04
2	F1h	15.3 ± 0.01	16.1 ± 0.02	16.3 ± 0.03	15.8 ± 0.03	16.4 ± 0.02	16.7 ± 0.03
3	F2h	13.6 ± 0.02	13.8 ± 0.05	14.2 ± 0.05	14.0 ± 0.01	14.6 ± 0.03	14.8 ± 0.05
4	F3h	12.5 ± 0.04	13.1 ± 0.04	13.6 ± 0.04	13.6 ± 0.07	14.3 ± 0.04	15.0 ± 0.06
5	F4h	14.7 ± 0.03	15.7 ± 0.01	16.0 ± 0.01	14.8 ± 0.06	15.8 ± 0.06	16.3 ± 0.01
6	Control (-)	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
7	Control (+)	22.0 ± 0.06	22.5 ± 0.12	22.7 ± 0.06	26.6 ± 0.06	27.2 ± 0.18	27.7 ± 0.12

No	Purification steps	* Diameter Inhibition Zone (mm)					
		E. coli			*S. aureus*		
		24 h	48 h	72 h	24 h	48 h	72 h
1	≤ 5 kDa	6.83 ± 0.11	6.96 ± 0.06	6.97 ± 0.06	13.63 ± 0.06	13.73 ± 0.06	13.87 ± 0.06
2	5-10 kDa	7.17 ± 0.06	7.67 ± 0.06	7.73 ± 0.06	13.80 ± 0.10	15.03 ± 0.06	15.27 ± 0.12
3	>10 kDa	7.37 ± 0.06	8.66 ± 0.06	8.80 ± 0.10	14.23 ± 0.12	15.07 ± 0.06	15.40 ± 0.06
4	kontrol (-)	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
5	kontrol (+)	27.53 ± 0.11	27.73 ± 0.15	29.37 ± 0.21	20.23 ± 0.21	22.23 ± 0.15	22.37 ± 0.06

Lampiran 29. Perhitungan LC_{50} hasil kultivasi Isolat strain SG-A1

Kode Fraksi	K (µg/ ml)	Larva Mati			RLM	M (%)	Nilai Probit	Persamaan Regresi	LC50 (ppm)	Kategori Toksisitas
6	1	0	1	2	1	7	3,52	y = 1,68x + 3,7	5,94	Sangat toksik
	10	8	8	8	8	77	5,74			
	100	10	10	10	10	97	6,88			
12	1	2	2	2	2	17	4,05	y = 1,415x + 3,92	5,78	Sangat toksik
	10	5	6	6	5,67	53	5,08			
	100	10	10	10	10	97	6,88			
18	1	4	4	4	4	37	4,07	y = 1,405x + 4,02	4,97	Sangat toksik
	10	6	7	7	6,67	63	5,33			
	100	10	10	10	10	97	6,88			
24	1	5	5	5	5	47	4,92	y = 0,98 + 4,77	1,73	Sangat toksik
	10	7	7	7	7	67	5,44			
	100	10	10	10	10	97	6,88			
30	1	2	2	4	2,67	23	4,26	y = 1,31x + 4,22	3,94	Sangat toksik
	10	7	7	7	7	67	5,44			
	100	10	10	10	10	97	6,88			
36	1	3	3	4	3,33	30	4,48	y = 1,2x + 4,57	2,28	Sangat toksik
	10	8	8	10	8,67	83	5,95			
	100	10	10	10	10,00	97	6,88			
Kontrol	1	0	0	1	0,33	Rata-rata Kontrol mati (RKM) = 0,33			Total Larva awal (TL) = 10	
	10	0	0	1	0,33					
	100	0	0	1	0,33					

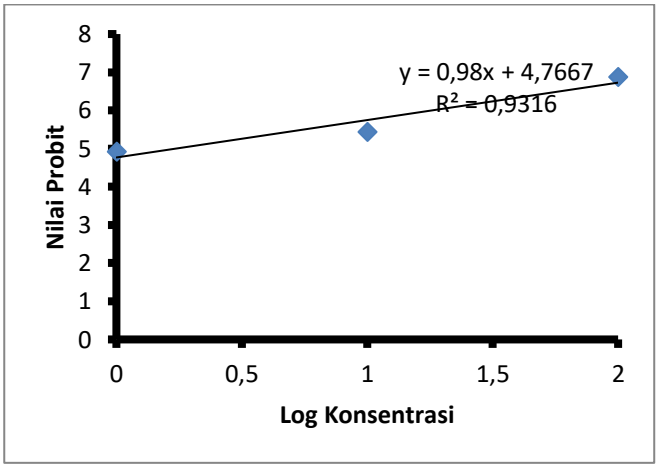
Keterangan:
K = Konsentrasi
RLM = Rata-rata larva mati
RKM = Rata-rata Kontrol mati
TL = Total Larva awal
M = Persen Kematian
LC_{50} = Konsentrasi yang dibutuhkan untuk menimbulkan kematian 50%

Cara perhitungan

- $\% M = \frac{\sum RLM - \sum RKH}{\sum TL} x100\%$
- Nilai probit diperoleh dari Tabel probit berdasarkan % kematian (M)
- Persamaan regresi diperoleh dengan menghubungkan nilai probit dengan log K

Contoh Untuk 24 jam

Log Konsentrasi (X)	% Kematian	Nilai Probit (Y)
1	47	4,92
2	67	5,44
3	97	6,88



- LC_{50} diperoleh dari perhitungan menggunakan nilai regresi dengan mengganti Y=5, karena untuk mendapatkan kematian 50% diperoleh nilai probit = 5

  Contoh untuk F4h

  Persamaan regresinya

  $$y = 0{,}98x + 4{,}77$$

  $$x = \frac{y - 4{,}77}{0{,}98}$$

  untuk memperoleh kematian 50% maka nilai probitnya (y) = 5

  $$x = \frac{5 - 4{,}77}{0{,}98}$$

  $$x = 0{,}238$$

  $$\text{Log } LC_{50} = 0{,}238$$

  $$LC_{50} = 1{,}73\ \mu g/ml$$

- Hal yang sama dilakukan untuk hasil kultivasi pada jam yang berbeda.

Lampiran 30. Perhitungan LC_{50} ekstrak kasar dan fraksi protein isolat strain SG-A1

Kode Fraksi	K (µg/ml)	Larva Mati			RLM	M (%)	Nilai Probit	Persamaan Regresi	LC50 (ppm)	Kategori Toksisitas
Ekp	1	4	4	3	3,67	33	4,56	y = 1,16x + 4,74	1,675	Sangat toksik
	10	10	10	8	9,33	90	6,28			
	100	10	10	10	10	97	6,88			
F1p	1	1	0	1	0,67	3	3,12	y = 1,88x + 3,74	4,68	Sangat toksik
	10	10	10	10	10	97	6,88			
	100	10	10	10	10	97	6,88			
F2p	1	2	1	2	1,67	13	3,87	y = 1,505x + 4,17	3,56	Sangat toksik
	10	10	10	8	9,33	90	6,28			
	100	10	10	10	10	97	6,88			
F3p	1	0	3	1	1,33	10	3,72	y = 1,58x + 4,25	3,00	Sangat toksik
	10	10	10	10	10	97	6,88			
	100	10	10	10	10	97	6,88			
F4p	1	3	5	1	3	27	4,39	y = 1,245x + 4,81	1,43	Sangat toksik
	10	10	10	10	10	97	6,88			
	100	10	10	10	10	97	6,88			
Kontrol	1	1	0	0	0,33	Rata-rata Kontrol mati (RKM) = 0,33			Total Larva awal (TL) = 10	
	10	1	0	0	0,33					
	100	1	0	0	0,33					

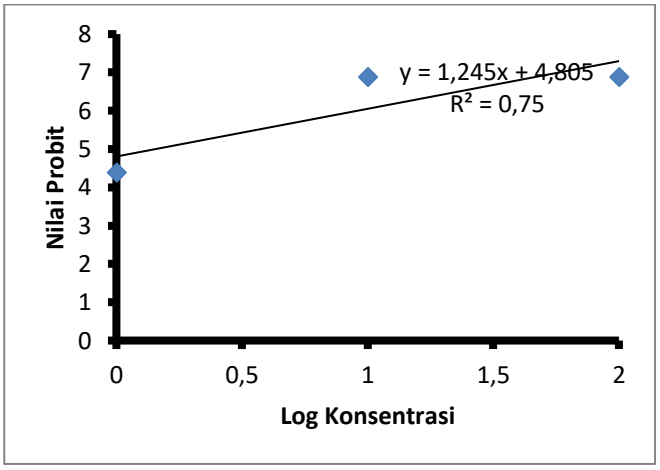
Keterangan:
K = Konsentrasi
RLM = Rata-rata larva mati
RKM = Rata-rata Kontrol mati
TL = Total Larva awal
M = Persen Kematian
LC_{50} = Konsentrasi yang dibutuhkan untuk menimbulkan kematian 50%

Cara perhitungan

- $\% M = \frac{\sum RLM - \sum RKH}{\sum TL} x100\%$
- Nilai probit diperoleh dari Tabel probit berdasarkan % kematian (M)
- Persamaan regresi diperoleh dengan menghubungkan nilai probit dengan log K

  Contoh Untuk F4p

Log Konsentrasi (X)	% Kematian	Nilai Probit (Y)
1	**27**	**4,39**
2	**97**	**6,88**
3	**97**	**6,88**



- LC_{50} diperoleh dari perhitungan menggunakan nilai regresi dengan mengganti Y=5, karena untuk mendapatkan kematian 50% diperoleh nilai probit = 5
  Contoh untuk F4h
  Persamaan regresinya

  $$y = 1{,}245x + 4{,}81$$

  $$x = \frac{y - 4{,}81}{1{,}245}$$

  untuk memperoleh kematian 50% maka nilai probitnya (y) = 5

  $$x = \frac{5 - 4{,}81}{1{,}245}$$

  $$x = 0{,}157$$

  $$\text{Log } LC_{50} = 0{,}157$$

  $$LC_{50} = 1{,}43\ \mu g/ml$$
- Hal yang sama dilakukan untuk EKp, F1p, F2p, dan F3p.

Lampiran 31. Perhitungan LC_{50} hidrolisat protein Isolat strain SG-A1

Kode Fraksi	K (µg/ml)	Larva Mati			RLM	M (%)	Nilai Probit	Persamaan Regresi	LC50 (ppm)	Kategori Toksisitas
Ekh	1	0	2	6	2,67	23	4,26	y = 1,31x + 4,69	1,704	Sangat toksik
	10	10	10	10	10	97	6,88			
	100	10	10	10	10	97	6,88			
F1h	1	3	4	2	3,00	27	4,39	y = 1,245x + 4,81	1,434	Sangat toksik
	10	10	10	10	10,00	97	6,88			
	100	10	10	10	10,00	97	6,88			
F2h	1	4	7	3	4,67	43	4,82	y = 1,03x + 5,16	0.69	Sangat toksik
	10	10	10	10	10,00	97	6,88			
	100	10	10	10	10,00	97	6,88			
F3h	1	2	3	4	3,00	27	4,39	y = 1,245 + 4,81	1,43	Sangat toksik
	10	10	10	10	10,00	97	6,88			
	100	10	10	10	10,00	97	6,88			
F4h	1	5	7	8	6,67	63	5,33	y = 0,775x + 5,59	0,17	Sangat toksik
	10	10	10	10	10,00	97	6,88			
	100	10	10	10	10,00	97	6,88			
Kontrol	1	0	1	0	0,33	Rata-rata Kontrol mati (RKM) = 0,33			Total Larva awal (TL) = 10	
	10	0	1	0	0,33					
	100	0	1	0	0,33					

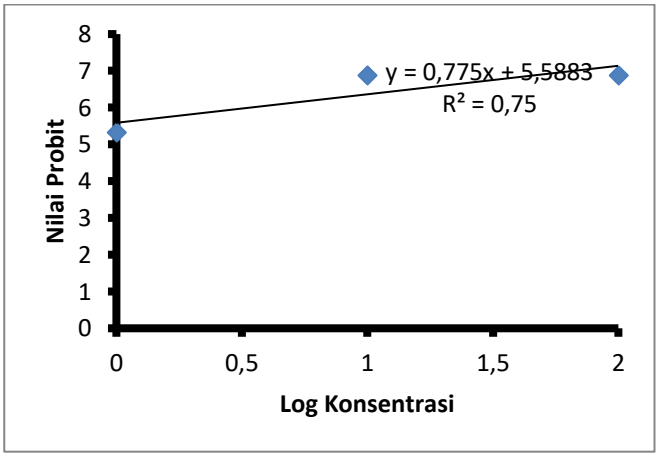
Keterangan:
K = Konsentrasi
RLM = Rata-rata larva mati
RKM = Rata-rata Kontrol mati
TL = Total Larva awal
M = Persen Kematian
LC_{50} = Konsentrasi yang dibutuhkan untuk menimbulkan kematian 50%

Cara perhitungan

- $\% M = \frac{\sum RLM - \sum RKH}{\sum TL} x100\%$
- Nilai probit diperoleh dari Tabel probit berdasarkan % kematian (M)
- Persamaan regresi diperoleh dengan menghubungkan nilai probit dengan log K

  Contoh Untuk F4h

Log Konsentrasi (X)	% Kematian	Nilai Probit (Y)
1	**63**	**5,33**
2	**97**	**6,88**
3	**97**	**6,88**



- LC_{50} diperoleh dari perhitungan menggunakan nilai regresi dengan mengganti Y=5, karena untuk mendapatkan kematian 50% diperoleh nilai probit = 5
  Contoh untuk F4h
  Persamaan regresinya

  $$y = 0{,}775x + 5{,}59$$

  $$x = \frac{y - 5{,}59}{0{,}775}$$

  untuk memperoleh kematian 50% maka nilai probitnya (y) = 5

  $$x = \frac{5 - 5{,}59}{0{,}775}$$

  $$x = -0{,}759$$

  $$\text{Log } LC_{50} = -0{,}759$$

  $$LC_{50} = 0{,}174\ \mu g/ml$$
- Hal yang sama dilakukan untuk EKh, F1h, F2h, dan F3h.

Lampiran 32. Perhitungan LC_{50} fragmen peptida Isolat strain SG-A1

Kode Fraksi	K (µg/ml)	Larva Mati			RLM	M (%)	Nilai Probit	Persamaan Regresi	LC50 (ppm)	Kategori Toksisitas
F4h1	0,01	2	1	1	1,33	13	3,87	y = 1,73x + 3,42	8,15	Sangat toksik
	0,1	4	2	1	2,33	23	4,26			
	1	10	10	10	10	100	7,33			
F4h2	0,01	2	1	1	1,33	13	3,87	y = 0,985x + 3,64	24,12	Toksik
	0,1	1	3	2	2	20	4,16			
	1	5	9	10	8	80	5,84			
F4h3	0,01	1	2	2	1,67	17	4,05	y = 0,95x + 3,77	19,71	Sangat toksik
	0,1	1	2	3	2	20	4,16			
	1	8	8	9	8,33	83	5,95			
Kontrol	0,01	0	0	0	0	Rata-rata Kontrol mati (RKM) = 0			Total Larva awal (TL) = 10	
	0,1	0	0	0	0					
	1	0	0	0	0					

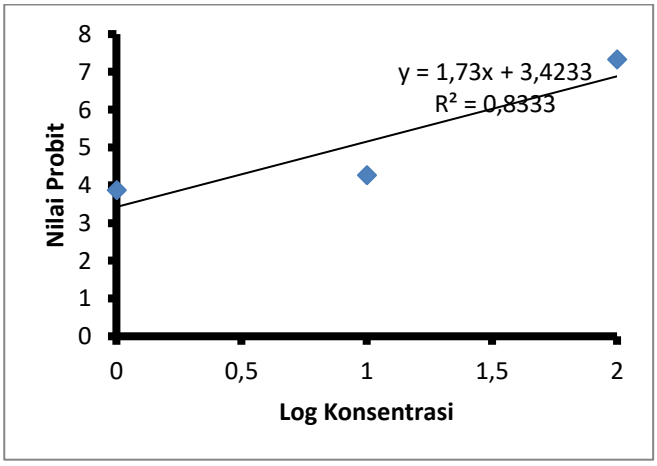
Keterangan:
K = Konsentrasi
RLM = Rata-rata larva mati
RKM = Rata-rata Kontrol mati
TL = Total Larva awal
M = Persen Kematian
LC_{50} = Konsentrasi yang dibutuhkan untuk menimbulkan kematian 50%

Cara perhitungan

- $\% M = \frac{\sum RLM - \sum RKH}{\sum TL} x100\%$
- Nilai probit diperoleh dari Tabel probit berdasarkan % kematian (M)
- Persamaan regresi diperoleh dengan menghubungkan nilai probit dengan log K

  Contoh Untuk F4h1

Log Konsentrasi (X)	% Kematian	Nilai Probit (Y)
1	**13**	**3,87**
2	**23**	**4,26**
3	**100**	**7,33**



- LC_{50} diperoleh dari perhitungan menggunakan nilai regresi dengan mengganti Y=5, karena untuk mendapatkan kematian 50% diperoleh nilai probit = 5

  Contoh untuk F4h

  Persamaan regresinya

  $$y = 1{,}73x + 3{,}42$$

  $$x = \frac{y - 3{,}42}{1{,}73}$$

  untuk memperoleh kematian 50% maka nilai probitnya (y) = 5

  $$x = \frac{5 - 3{,}42}{1{,}73}$$

  $$x = 0{,}911$$

  $$\text{Log } LC_{50} = 0{,}911$$

  $$LC_{50} = 8{,}15 \text{ ppm}$$

- Hal yang sama dilakukan untuk EKh, F1h, F2h, dan F3h.

Lampiran 33. Hasil perhitungan IC_{50} ekstrak kasar,fraksi protein potensial, fraksi hidrolisat potensial, dan fragmen peptide terhadap sel kanker LK-2

Sample	C (µg/mL)	n=1	n=2	n=3	Average	s.d	Viable cells (%)	IC_{50} (µg/mL)
Crude extract	0	0,5030	0,5111	0,4906	0,5016	0,01	100,00	1116,84
	5	0,7234	0,6770	0,6896	0,6967	0,02	142,83	
	10	0,6337	0,6337	0,6233	0,6302	0,01	100,00	
	20	0,6482	0,5946	0,6124	0,6184	0,03	95,20	
	40	0,6117	0,5901	0,6137	0,6052	0,01	89,83	
	80	0,5403	0,5700	0,6103	0,5735	0,04	77,00	
	160	0,5548	0,5717	0,5467	0,5577	0,01	113,72	
	Blank	0,0444	0,0449	0,0488	0,0460	0,00		
F4p	0	0,4955	0,5001	0,4701	0,4886	0,02	100,00	33,27
	5	0,3975	0,4027	0,3508	0,3837	0,03	76,30	
	10	0,2814	0,2912	0,2784	0,2837	0,01	53,70	
	20	0,2535	0,2325	0,2325	0,2395	0,01	43,72	
	40	0,0782	0,0782	0,0745	0,0770	0,00	6,99	
	80	0,1084	0,1084	0,1010	0,1059	0,00	13,54	
	160	0,1649	0,1790	0,1538	0,1659	0,01	27,09	
	Blank	0,0444	0,0449	0,0488	0,0460	0,00		
F4h	0	0,2434	0,2434	0,2434	0,2434	0,00	100,00	62,16
	5	0,3183	0,2173	0,4268	0,3208	0,10	138,87	
	10	0,3235	0,2231	0,3416	0,2961	0,06	126,45	
	20	0,2533	0,1794	0,2572	0,2300	0,04	93,25	
	40	0,0405	0,0393	0,0428	0,0409	0,00	-1,72	
	80	0,0398	0,0428	0,0403	0,0410	0,00	-1,67	
	160	0,0398	0,0398	0,0405	0,0400	0,00	-2,14	
	Blank	0,0443	0,0443	0,0443	0,0443	0,00		
F4h1	0	0,2434	0,2434	0,2434	0,2434	0,00	100,00	35,66
	1,5	0,3124	0,2678	0,2811	0,2871	0,02	121,95	
	3	0,3002	0,2708	0,2691	0,2800	0,02	118,40	
	6	0,2922	0,2971	0,2641	0,2845	0,02	120,63	
	12	0,2566	0,2307	0,1857	0,2243	0,04	90,42	
	25	0,1984	0,1486	0,1510	0,1660	0,03	61,13	
	50	0,0969	0,0943	0,0976	0,0963	0,00	26,10	
	Blank	0,0443	0,0443	0,0443	0,0443	0,00		

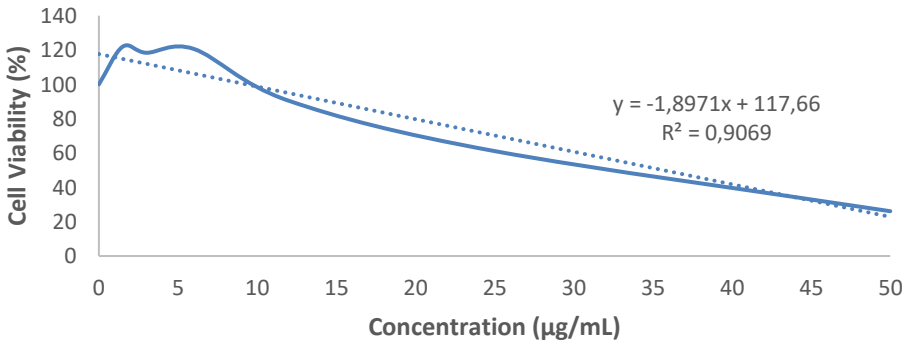
Sample		n=1	n=2	n=3	Average	s.d	Viable cells (%)	IC50 (µg/mL)
F4h2	0	0,2434	0,2434	0,2434	0,2434	0,00	100,00	60,54
	3	0,2784	0,2838	0,2756	0,2793	0,00	118,01	
	6	0,2735	0,3134	0,2894	0,2921	0,02	124,46	
	12	0,2643	0,3000	0,2595	0,2746	0,02	115,67	
	25	0,2485	0,2946	0,2795	0,2742	0,02	115,47	
	50	0,1380	0,1771	0,1483	0,1545	0,02	55,33	
	100	0,0430	0,0423	0,0411	0,0421	0,00	-1,09	
	Blank	0,0443	0,0443	0,0443	0,0443	0,00		
F4h3	0	0,2434	0,2434	0,2434	0,2434	0,00	100,00	71,56
	3	0,2842	0,2802	0,2861	0,2835	0,00	120,14	
	6	0,2814	0,2356	0,2297	0,2489	0,03	102,76	
	12	0,3399	0,3007	0,2414	0,2940	0,05	125,41	
	25	0,2340	0,2316	0,2134	0,2263	0,01	91,43	
	50	0,2061	0,1930	0,2135	0,2042	0,01	80,31	
	100	0,0793	0,0842	0,0702	0,0779	0,01	16,88	
	Blank	0,0443	0,0443	0,0443	0,0443	0,00		

Rumus untuk menghitung persen viabilitas

$$\%viabilitas\ sel = \frac{Absorbansi\ sel\ uji - Absorbansi\ blanko}{Absorbansi\ kontrol - Absorbansi\ blanko} \times 100\%$$

Contoh untuk F4h1

Grafik hubungan persen viabilitas dengan konsentrasi



Perhitungan IC_{50} =

$$y = -1{,}8971x + 117{,}66$$

$$x = \frac{y - 117{,}66}{-1{,}8971}$$

Untuk memperoleh viabilitas 50%, maka nilai y=50

$$x = \frac{50 - 117{,}66}{-1{,}8971}$$

$$x = 35{,}66$$

IC_{50} = 35,66 µg/mL

Lampiran 34. Hasil perhitungan IC_{50} ekstrak kasar,fraksi protein potensial, fraksi hidrolisat potensial, dan fragmen peptide terhadap sel normal fibroblast M5S

Sample	C (µg/mL)	n=1	n=2	n=3	Average	s.d	Viable cells (%)	IC_{50} (µg/mL)
Crude Extract	0	0,6238	0,6094	0,5954	0,6095	0,01	100,00	110,93
	5	0,5823	0,5859	0,5633	0,5772	0,01	94,28	
	10	0,5785	0,5830	0,5718	0,5778	0,01	94,39	
	20	0,5687	0,6129	0,5758	0,5858	0,02	95,81	
	40	0,5529	0,6182	0,5798	0,5836	0,03	95,43	
	80	0,5676	0,5782	0,5880	0,5779	0,01	94,42	
	160	0,0952	0,0829	0,1075	0,0952	0,01	9,16	
	Blank	0,0428	0,0440	0,0433	0,0434	0,00		
F4p	0	0,5868	0,5812	0,5855	0,5845	0,00	100,00	56,51
	5	0,5269	0,5301	0,5408	0,5326	0,01	90,43	
	10	0,5114	0,5325	0,5277	0,5239	0,01	88,82	
	20	0,5213	0,4656	0,4686	0,4852	0,03	81,68	
	40	0,0704	0,0721	0,0668	0,0698	0,00	5,07	
	80	0,0954	0,0879	0,0827	0,0887	0,01	8,56	
	160	0,1453	0,1576	0,1341	0,1457	0,01	19,07	
	Blank	0,0429	0,0428	0,0411	0,0423	0,00		
F4h	0	0,6196	0,5544	0,5691	0,5810	0,03	100,00	50,06
	5	0,5896	0,5747	0,5306	0,5650	0,03	97,02	
	10	0,5501	0,5454	0,5343	0,5433	0,01	93,00	
	20	0,5068	0,4872	0,4693	0,4878	0,02	82,71	
	40	0,0466	0,0477	0,0456	0,0466	0,00	0,93	
	80	0,0423	0,0445	0,0441	0,0436	0,00	0,38	
	160	0,0414	0,0418	0,0455	0,0429	0,00	0,24	
	Blank	0,0441	0,0411	0,0396	0,0416	0,00		
F4h1	0	0,6198	0,6168	0,6292	0,6219	0,01	100,00	105,14
	1,5	0,5953	0,6055	0,5874	0,5961	0,01	95,54	
	3	0,5644	0,5759	0,5784	0,5729	0,01	91,54	
	6	0,5534	0,6036	0,6103	0,5891	0,03	94,34	
	12	0,5724	0,5616	0,6063	0,5801	0,02	92,78	
	25	0,4939	0,5307	0,5374	0,5207	0,02	82,53	
	50	0,4507	0,4802	0,5111	0,4807	0,03	75,63	
	Blank	0,0428	0,0421	0,0421	0,0423	0,00		

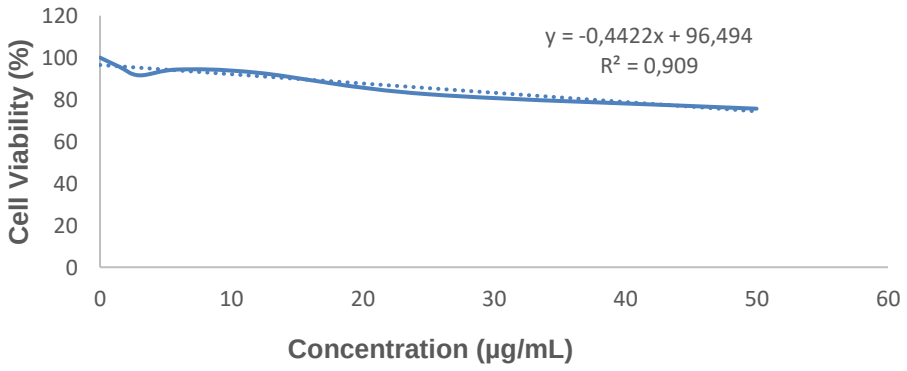
Sample		n=1	n=2	n=3	Average	s.d	Viable cells (%)	IC_{50} (µg/mL)
F4h2	0	0,6194	0,6070	0,6057	0,6107	0,01	100,00	164,64
	3	0,5968	0,5523	0,5524	0,5672	0,03	92,34	
	6	0,5756	0,5437	0,5619	0,5604	0,02	91,15	
	12	0,5715	0,5778	0,5669	0,5721	0,01	93,20	
	25	0,5599	0,5285	0,5571	0,5485	0,02	89,05	
	50	0,5434	0,5206	0,5264	0,5301	0,01	85,82	
	100	0,4278	0,4091	0,4247	0,4205	0,01	66,54	
	Blank	0,0460	0,0399	0,0414	0,0424	0,00		
F4h3	0	0,5792	0,6198	0,5816	0,5935	0,02	100,00	116,86
	3	0,5270	0,5595	0,5172	0,5346	0,02	89,00	
	6	0,5191	0,5206	0,5097	0,5165	0,01	85,62	
	12	0,5201	0,5268	0,4923	0,5131	0,02	84,99	
	25	0,5006	0,4903	0,5087	0,4999	0,01	82,53	
	50	0,4752	0,4862	0,4298	0,4637	0,03	75,79	
	100	0,3611	0,3662	0,3455	0,3576	0,01	55,99	
	Blank	0,0441	0,0852	0,0431	0,0575	0,02		

Rumus untuk menghitung persen viabilitas

$$\%viabilitas\ sel = \frac{Absorbansi\ sel\ uji - Absorbansi\ blanko}{Absorbansi\ kontrol - Absorbansi\ blanko} \times 100\%$$

Contoh untuk F4h1

Grafik hubungan persen viabilitas dengan konsentrasi



Perhitungan IC_{50} =

$$y = -0{,}4422x + 96{,}494$$

$$x = \frac{y - 96{,}494}{-0{,}4422}$$

Untuk memperoleh viabilitas 50%, maka nilai y=50

$$x = \frac{50 - 96{,}494}{-0{,}4422}$$

$$x = 105{,}14$$

IC_{50} = 105,14 µg/mL

Lampiran 35. Proliferasi sel fragmen peptida, ekstrak kasar, fraksi protein potensial dan hidrolisat protein potensial terhadap sel kanker LK-2 pada berbagai variasi waktu yang berbeda

Fraction	Time	n1	n2	n3	n4	Average	Viability (%)	sda
	Blank	0,0413	0,4081	0,3898	0,3990	0,3096		0,18
F4h1	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,5172	0,4863	0,4882	0,4746	0,4916	85,36	0,02
	12	0,4846	0,5032	0,4823	0,4871	0,4893	84,29	0,01
	16	0,3124	0,3124	0,3124	0,3124	0,3124	1,34	0,00
F4h2	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,3749	0,3784	0,3685	0,3835	0,3763	31,31	0,02
	12	0,3590	0,3718	0,3966	0,3714	0,3747	30,55	0,00
	16	0,3134	0,3134	0,3134	0,3134	0,3134	1,81	0,01
F4h3	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,3780	0,3651	0,3672	0,3472	0,3644	25,71	0,02
	12	0,3577	0,3615	0,3116	0,3542	0,3463	17,21	0,00
	16	0,3399	0,3399	0,3399	0,3399	0,3399	14,23	0,01
Crude extract	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,4594	0,4847	0,4928	0,5619	0,4997	89,17	0,04
	12	0,4326	0,4163	0,3587	0,4072	0,4037	44,15	0,03
	16	0,3932	0,3630	0,3538	0,3317	0,3604	23,86	0,03
F4p	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,1803	0,1802	0,2673	0,1980	0,2065	-48,35	0,04
	12	0,2286	0,2244	0,2353	0,2056	0,2235	-40,36	0,01
	16	0,1649	0,1790	0,1538	0,1659	0,1659	-67,36	0,01
F4h	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,3719	0,3708	0,3860	0,3745	0,3758	31,07	0,01
	12	0,3574	0,3626	0,3287	0,3581	0,3517	19,77	0,02
	16	0,3235	0,3416	0,3235	0,3416	0,3326	10,79	0,01
Control	0	0,5147	0,5391	0,4994	0,5380	0,5228	100,00	0,02
	6	0,5688	0,5469	0,5192	0,5412	0,5440	109,95	0,02
	12	0,5570	0,5705	0,5701	0,5585	0,5640	119,33	0,01
	16	0,5030	0,5111	0,4906	0,5016	0,5016	90,05	0,01

Lampiran 36. Proliferasi sel fragmen peptida, ekstrak kasar, fraksi protein potensial dan hidrolisat protein potensial terhadap sel normal fibroblast M5S pada berbagai variasi waktu yang berbeda

Fraction	Time	n1	n2	n3	n4	Average	Viabilit (%)	sda
	blank	0,0534	0,0432	0,0436	0,0503	0,0476		0,01
F4h1	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,3526	0,3660	0,3099	0,3504	0,3447	98,75	0,02
	12	0,6159	0,6365	0,5807	0,5710	0,6010	183,93	0,03
	16	0,5953	0,6055	0,5874	0,5961	0,5961	182,29	0,01
F4h2	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,3338	0,3354	0,2552	0,3044	0,3072	86,27	0,04
	12	0,5661	0,5411	0,5313	0,4971	0,5339	161,62	0,03
	16	0,5599	0,5285	0,5571	0,5485	0,5485	166,47	0,01
F4h3	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,2874	0,3168	0,2839	0,2781	0,2916	81,07	0,02
	12	0,4058	0,4239	0,4670	0,4749	0,4429	131,38	0,03
	16	0,4752	0,4862	0,4298	0,4637	0,4637	138,30	0,02
Crude Extract	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,3761	0,4078	0,2585	0,2098	0,3131	88,22	0,09
	12	0,6522	0,6412	0,6169	0,5756	0,6215	190,73	0,03
	16	0,5676	0,5782	0,5580	0,5579	0,5654	172,10	0,01
F4p	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,1273	0,1137	0,0875	0,0878	0,1041	18,76	0,02
	12	0,1072	0,0899	0,0856	0,0903	0,0933	15,16	0,01
	16	0,1453	0,1576	0,1341	0,1457	0,1457	32,59	0,01
F4h	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,2719	0,3063	0,2478	0,2592	0,2713	74,34	0,03
	12	0,5141	0,4899	0,4971	0,4614	0,4906	147,24	0,02
	16	0,5068	0,4872	0,4693	0,4878	0,4878	146,29	0,02
Control	0	0,3478	0,3441	0,3592	0,3429	0,3485	100,00	0,01
	6	0,3853	0,3702	0,3663	0,4255	0,3868	112,74	0,03
	12	0,6888	0,6754	0,6310	0,6139	0,6523	200,96	0,04
	16	0,6541	0,6351	0,6314	0,6412	0,6405	197,03	0,01

Lampiran 37. Output uji statistik SPSS untuk independent samples T Test pengujian sitotoksik

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\Crude Extract independen t test - Copy.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.597614	.0615938	.0232803
	M5S	7	.515286	.1855844	.0701443

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	2.035	.179	1.114	12
	Equal variances not assumed			1.114	7.306

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.287	.0823286	.0739067
	Equal variances not assumed	.301	.0823286	.0739067

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.0787002	.2433574
	Equal variances not assumed	-.0909601	.2556173

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\F4P independen t test - Copy.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.249186	.1493394	.0564450
	M5S	7	.347200	.2328542	.0880106

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	6.988	.021	-.937	12
	Equal variances not assumed			-.937	10.222

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.367	-.0980143	.1045558
	Equal variances not assumed	.370	-.0980143	.1045558

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.3258217	.1297932
	Equal variances not assumed	-.3302962	.1342677

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\F4h independen t test - Copy.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.173171	.1276498	.0482471
	M5S	7	.330029	.2687403	.1015743

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	34.202	.000	-1.395	12
	Equal variances not assumed			-1.395	8.576

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.188	-.1568571	.1124505
	Equal variances not assumed	.198	-.1568571	.1124505

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.4018657	.0881514
	Equal variances not assumed	-.4131666	.0994523

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\5kDA Independent.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.225943	.0716559	.0270834
	M5S	7	.565919	.0485617	.0183546

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	.882	.366	-10.391	12
	Equal variances not assumed			-10.391	10.551

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.000	-.3399762	.0327170
	Equal variances not assumed	.000	-.3399762	.0327170

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.4112604	-.2686920
	Equal variances not assumed	-.4123611	-.2675913

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\10 kDa independen t test.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.222881	.0922410	.0348638
	M5S	7	.544214	.0598589	.0226245

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	1.622	.227	-7.732	12
	Equal variances not assumed			-7.732	10.292

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.000	-.3213333	.0415615
	Equal variances not assumed	.000	-.3213333	.0415615

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.4118880	-.2307787
	Equal variances not assumed	-.4135828	-.2290839

[DataSet1] D:\~ PENELITIAN\SPSS ANTIKANKER\lebih 10 kDa independen t test.sav

Group Statistics

	sampel	N	Mean	Std. Deviation	Std. Error Mean
absorbansi	LK-2	7	.225462	.0720698	.0272398
	M5S	7	.496976	.0729318	.0275656

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
absorbansi	Equal variances assumed	.002	.968	-7.006	12
	Equal variances not assumed			-7.006	11.998

Independent Samples Test

		t-test for Equality of Means		
		Sig. (2-tailed)	Mean Difference	Std. Error Difference
absorbansi	Equal variances assumed	.000	-.2715143	.0387540
	Equal variances not assumed	.000	-.2715143	.0387540

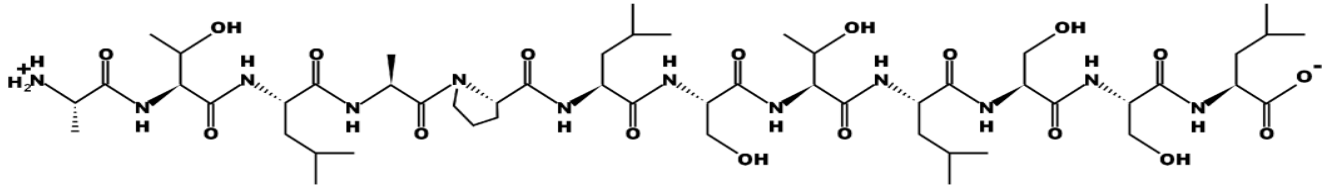
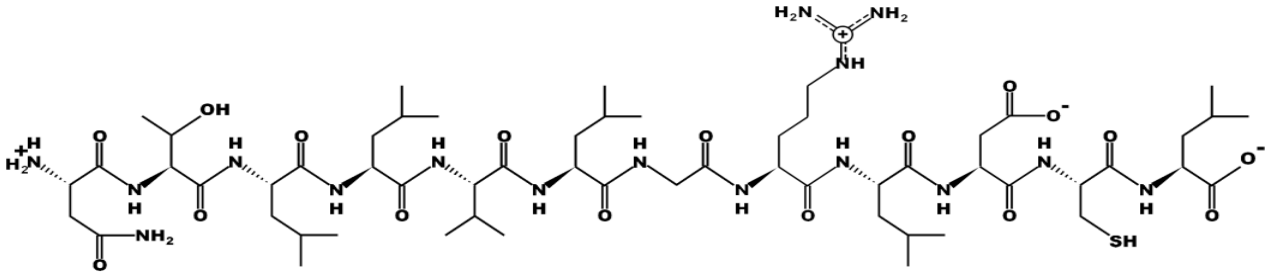
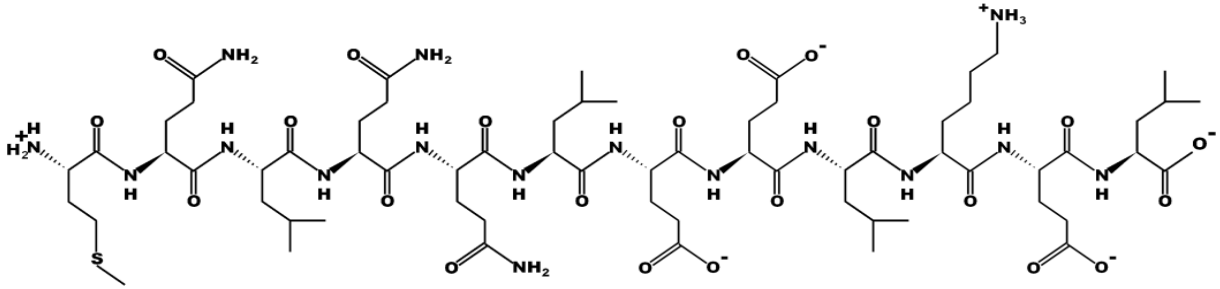
Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
absorbansi	Equal variances assumed	-.3559520	-.1870766
	Equal variances not assumed	-.3559533	-.1870753

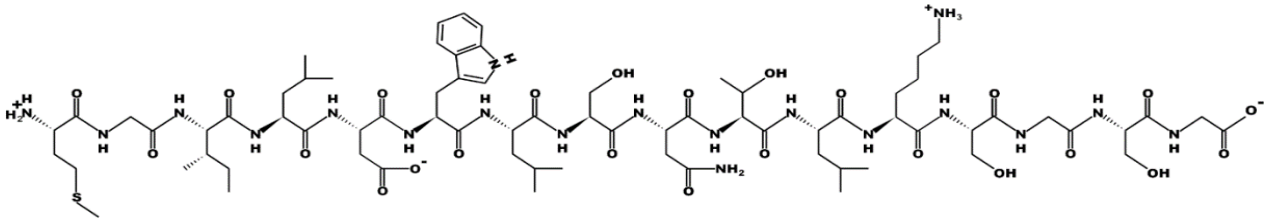
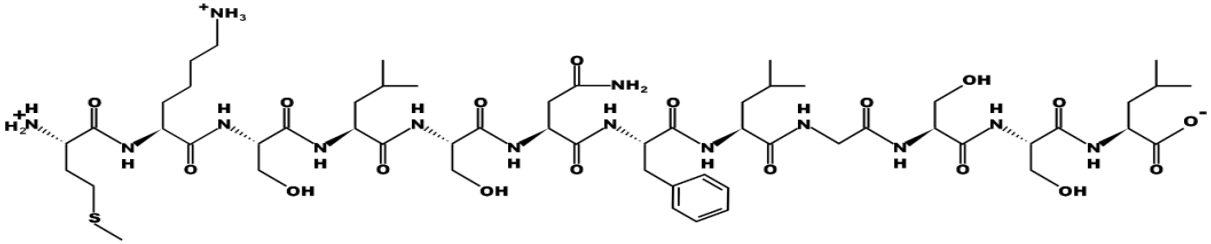
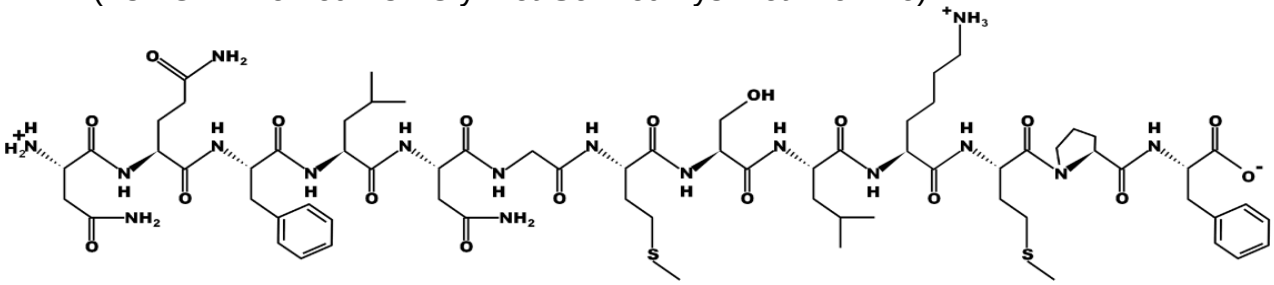
Lampiran 38. Hasil identifikasi peptida ≤ 5 kDa dari isolat strain SG-A1 dengan program MASCOT

Puncak LC (menit)	Kode	Prediksi Urutan Peptida	BM (Da)	Jumlah asam amino	Skor	Protein coverage (%)	Taksonomi ID Protein (NCBIprot)	Nama Organisme Asal
2,02	F4h1a	FPG	n.d	3	29	7	1736779	Californiconus californicus
3,54	F4h1b	P	n.d	1	17	20	31087	Pardachirus marmoratus
4,08	F4h1c	ATLAPLSTLSSL	1173.37	12	31	2	877550	Aspergillus sp. MF297-2
4,19	F4h1d	H	n.d	1	15	16	7385	Sarcophaga bullata
4,55	F4h1e	NTLLVLGRLDCL	1329.62	12	42	10	6687	Penaeus monodon
5,09	F4h1f	MQLQQLEELKEL	1501.76	12	46	10	243232	Methanocaldococcus jannaschii
5,67	F4h1g	MGILDWLSNTLKSGSG	1678.92	16	43	8	52351	Brassica rapa subsp. pekinensis
6,14	F4h1h	MKSLSNFLGSSL	1283.51	12	42	12	293813	Agelena orientalis
6,54	F4h1i	NQFLNGMSLKMPF	1526.83	13	42	12	315456	Rickettsia felis URRWXCal2
6,88	F4h1j	LERFTARAFVVLHV	1657.98	14	39	11	234826	Anaplasma marginale str. St. Maries
7,17	F4h1k	SYLDLAFGCVLKPARH	1790.11	16	40	25	12165	Chrysanthemum virus B
7,44	F4h1l	NKYDLRLPGVLHGLITL PKLGEL	2560.08	23	36	7	393305	Yersinia enterocolitica subsp. enterocolitica 8081
8,29	F4h1m	RKHKLVDCAGAFGAEY ELEVVKGF	2667.08	24	38	6	4081	Solanum lycopersicum

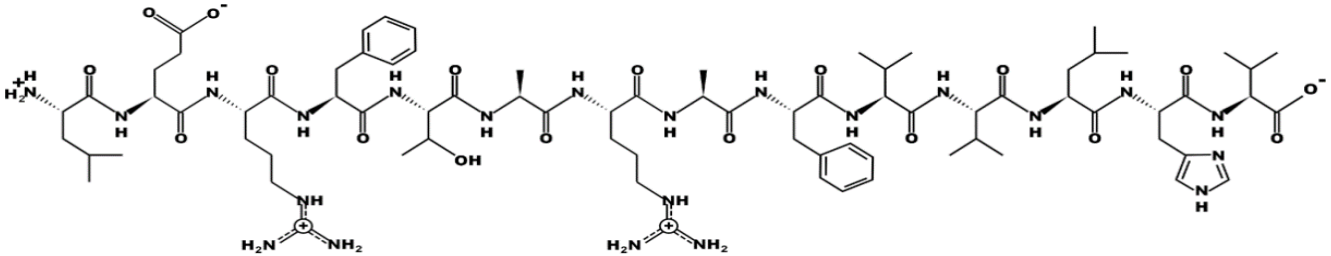
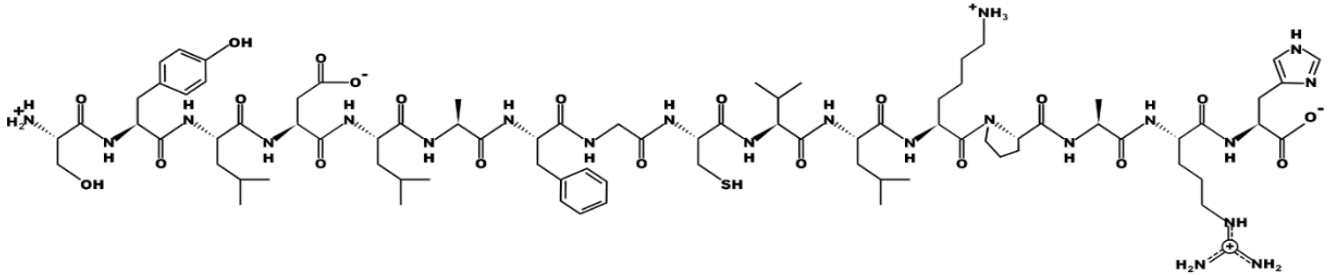
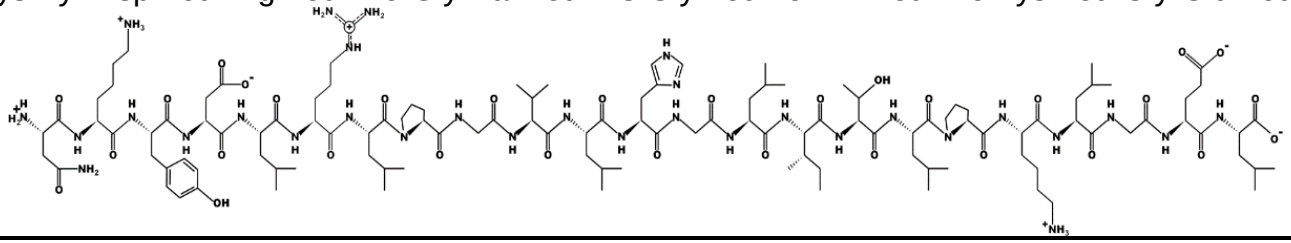
Lampiran 39. Struktur kimia peptida ≤ 5 kDa dari isolat strain SG-A1

Kode, Sekuen Asam Amino, dan Struktur Kimia
F4h1c (Ala-Thr-Leu-Ala-Pro-Leu-Ser-Thr-Leu-Ser-Ser-Leu) 
F4h1e (Asn-Thr-Leu-Leu-Val-Leu-Gly-Arg-Leu-Asp-Cys-Leu) 
F4h1f (Met-Gln-Leu-Gln-Gln-Leu-Glu-Glu-Leu-Lys-Glu-Leu) 

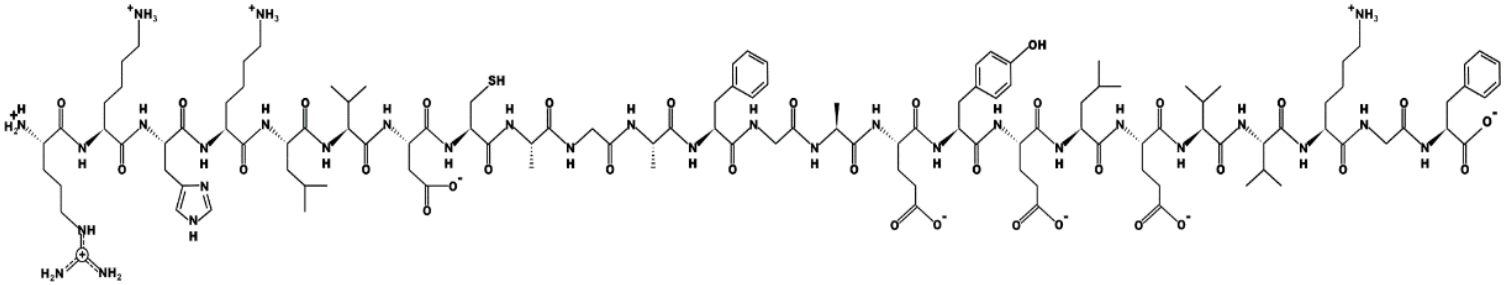
Lampiran 39. (Lanjutan)

Kode, Sekuen Asam Amino, dan Struktur Kimia
F4h1g (Met-Gly-Ile-Leu-Asp-Trp-Leu-Ser-Asn-Thr-Leu-Lys-Ser-Gly-Ser-Gly) 
F4h1h (Met-Lys-Ser-Leu-Ser-Asn-Phe-Leu-Gly-Ser-Ser-Leu) 
F4h1i (Asn-Gln-Phe-Leu-Asn-Gly-Met-Ser-Leu-Lys-Met-Pro-Phe) 

Lampiran 39. (Lanjutan)

Kode, Sekuen Asam Amino, dan Struktur Kimia
F4h1j (Leu-Glu-Arg-Phe-Thr-Ala-Arg-Phe-Val-Val-Leu-His-Val) 
F4h1k (Ser-Tyr-Leu-Asp-Leu-Ala-Phe-Gly-Cys-Val-Leu-Lys-Pro-Ala-Arg-His) 
F4h1l (Asn-Lys-Tyr-Asp-Leu-Arg-Leu-Pro-Gly-Val-Leu-His-Gly-Leu-Ile-Thr-Leu-Pro-Lys-Leu-Gly-Glu-Leu) 

Lampiran 39. (Lanjutan)

Kode, Sekuen Asam Amino, dan Struktur Kimia
F4h1m (Arg-Lys-His-Lys-Leu-Val-Asp-Cys-Ala-Gly-Ala-Phe-Gly-Ala-Glu-Tyr-Glu-Leu-Glu-Val-Val-Lys-Gly-Phe)


Lampiran 40. Interaksi ikatan peptida dengan ATPase

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
ATLAPLSTLSSL-ATPase	-364.7	:ALA1:HT2 - A:GLU54:OE2	2,60	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ALA1:HT2	H-Donor; Positive	A:GLU54:OE2	H-Acceptor; Negative
		:LEU3:HN - :ALA1:O	2,33	Hydrogen Bond	Conventional Hydrogen Bond	:LEU3:HN	H-Donor	:ALA1:O	H-Acceptor
		:THR8:HN - :PRO5:O	2,80	Hydrogen Bond	Conventional Hydrogen Bond	:THR8:HN	H-Donor	:PRO5:O	H-Acceptor
		:THR8:HN - :SER7:OG	2,36	Hydrogen Bond	Conventional Hydrogen Bond	:THR8:HN	H-Donor	:SER7:OG	H-Acceptor
		:THR8:HG1 - :THR2:O	1,65	Hydrogen Bond	Conventional Hydrogen Bond	:THR8:HG1	H-Donor	:THR2:O	H-Acceptor
		:LEU9:HN - :LEU3:O	2,78	Hydrogen Bond	Conventional Hydrogen Bond	:LEU9:HN	H-Donor	:LEU3:O	H-Acceptor
		:LEU9:HN - :PRO5:O	1,94	Hydrogen Bond	Conventional Hydrogen Bond	:LEU9:HN	H-Donor	:PRO5:O	H-Acceptor
		:SER10:HN - :LEU6:O	1,85	Hydrogen Bond	Conventional Hydrogen Bond	:SER10:HN	H-Donor	:LEU6:O	H-Acceptor
		:SER11:HN - :SER7:O	2,21	Hydrogen Bond	Conventional Hydrogen Bond	:SER11:HN	H-Donor	:SER7:O	H-Acceptor
		:SER11:HG - :SER7:O	1,64	Hydrogen Bond	Conventional Hydrogen Bond	:SER11:HG	H-Donor	:SER7:O	H-Acceptor
		:LEU12:HN - :THR8:O	2,70	Hydrogen Bond	Conventional Hydrogen Bond	:LEU12:HN	H-Donor	:THR8:O	H-Acceptor
		:LEU12:HN - :LEU9:O	2,06	Hydrogen Bond	Conventional Hydrogen Bond	:LEU12:HN	H-Donor	:LEU9:O	H-Acceptor
		A:GLY22:CA - :SER11:O	2,84	Hydrogen Bond	Carbon Hydrogen Bond	A:GLY22:CA	H-Donor	:SER11:O	H-Acceptor
		:PRO5:CD - :THR2:O	3,19	Hydrogen Bond	Carbon Hydrogen Bond	:PRO5:CD	H-Donor	:THR2:O	H-Acceptor
		:SER11:CB - A:GLY18:O	2,70	Hydrogen Bond	Carbon Hydrogen Bond	:SER11:CB	H-Donor	A:GLY18:O	H-Acceptor
		A:ALA14 - :PRO5	4,83	Hydrophobic	Alkyl	A:ALA14	Alkyl	:PRO5	Alkyl
		A:ALA17 - :ALA1	2,73	Hydrophobic	Alkyl	A:ALA17	Alkyl	:ALA1	Alkyl
		A:VAL25 - :LEU12	5,35	Hydrophobic	Alkyl	A:VAL25	Alkyl	:LEU12	Alkyl
		:ALA1 - A:PRO57	3,27	Hydrophobic	Alkyl	:ALA1	Alkyl	A:PRO57	Alkyl

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		:LEU3 - :LEU12	4,90	Hydrophobic	Alkyl	:LEU3	Alkyl	:LEU12	Alkyl
MGILDWLSNTLKSGSG-ATPase	-475.2	:LYS12:HZ1 - :ASP5:OD2	2,46	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:LYS12:HZ1	H-Donor; Positive	:ASP5:OD2	H-Acceptor; Negative
		A:ARG34:HH11 - :SER13:O	2,74	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG34:HH11	H-Donor	:SER13:O	H-Acceptor
		:GLY2:HN - :MET1:SD	2,60	Hydrogen Bond	Conventional Hydrogen Bond	:GLY2:HN	H-Donor	:MET1:SD	H-Acceptor
		:LEU4:HN - :MET1:O	2,08	Hydrogen Bond	Conventional Hydrogen Bond	:LEU4:HN	H-Donor	:MET1:O	H-Acceptor
		:ASP5:HN - :GLY2:O	2,98	Hydrogen Bond	Conventional Hydrogen Bond	:ASP5:HN	H-Donor	:GLY2:O	H-Acceptor
		:TRP6:HN - :GLY2:O	1,90	Hydrogen Bond	Conventional Hydrogen Bond	:TRP6:HN	H-Donor	:GLY2:O	H-Acceptor
		:LEU7:HN - :ILE3:O	1,82	Hydrogen Bond	Conventional Hydrogen Bond	:LEU7:HN	H-Donor	:ILE3:O	H-Acceptor
		:LEU7:HN - :LEU4:O	3,00	Hydrogen Bond	Conventional Hydrogen Bond	:LEU7:HN	H-Donor	:LEU4:O	H-Acceptor
		:SER8:HN - :LEU4:O	1,94	Hydrogen Bond	Conventional Hydrogen Bond	:SER8:HN	H-Donor	:LEU4:O	H-Acceptor
		:ASN9:HN - :ASP5:O	1,64	Hydrogen Bond	Conventional Hydrogen Bond	:ASN9:HN	H-Donor	:ASP5:O	H-Acceptor
		:ASN9:HD21 - :ASP5:O	2,90	Hydrogen Bond	Conventional Hydrogen Bond	:ASN9:HD21	H-Donor	:ASP5:O	H-Acceptor
		:ASN9:HD22 - :ASP5:OD1	1,81	Hydrogen Bond	Conventional Hydrogen Bond	:ASN9:HD22	H-Donor	:ASP5:OD1	H-Acceptor
		:THR10:HN - :TRP6:O	1,98	Hydrogen Bond	Conventional Hydrogen Bond	:THR10:HN	H-Donor	:TRP6:O	H-Acceptor
		:THR10:HG1 - :TRP6:O	1,89	Hydrogen Bond	Conventional Hydrogen Bond	:THR10:HG1	H-Donor	:TRP6:O	H-Acceptor
		:LEU11:HN - :LEU7:O	1,96	Hydrogen Bond	Conventional Hydrogen Bond	:LEU11:HN	H-Donor	:LEU7:O	H-Acceptor
		:LEU11:HN - :THR10:OG1	2,68	Hydrogen Bond	Conventional Hydrogen Bond	:LEU11:HN	H-Donor	:THR10:OG1	H-Acceptor
		:LYS12:HN - :SER8:O	1,72	Hydrogen Bond	Conventional Hydrogen Bond	:LYS12:HN	H-Donor	:SER8:O	H-Acceptor
		:LYS12:HZ2 - :SER8:OG	1,86	Hydrogen Bond	Conventional Hydrogen Bond	:LYS12:HZ2	H-Donor	:SER8:OG	H-Acceptor

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		:LYS12:HZ3 - :ASN9:OD1	1,76	Hydrogen Bond	Conventional Hydrogen Bond	:LYS12:HZ3	H-Donor	:ASN9:OD1	H-Acceptor
		:SER13:HN - :ASN9:O	2,14	Hydrogen Bond	Conventional Hydrogen Bond	:SER13:HN	H-Donor	:ASN9:O	H-Acceptor
		:SER13:HN - :THR10:O	3,04	Hydrogen Bond	Conventional Hydrogen Bond	:SER13:HN	H-Donor	:THR10:O	H-Acceptor
		:SER13:HG - :ASN9:O	1,72	Hydrogen Bond	Conventional Hydrogen Bond	:SER13:HG	H-Donor	:ASN9:O	H-Acceptor
		:GLY14:HN - :THR10:O	1,87	Hydrogen Bond	Conventional Hydrogen Bond	:GLY14:HN	H-Donor	:THR10:O	H-Acceptor
		:GLY14:HN - :LEU11:O	2,97	Hydrogen Bond	Conventional Hydrogen Bond	:GLY14:HN	H-Donor	:LEU11:O	H-Acceptor
		:GLY14:HN - :SER13:OG	2,57	Hydrogen Bond	Conventional Hydrogen Bond	:GLY14:HN	H-Donor	:SER13:OG	H-Acceptor
		:SER15:HN - :LEU11:O	1,78	Hydrogen Bond	Conventional Hydrogen Bond	:SER15:HN	H-Donor	:LEU11:O	H-Acceptor
		:GLY2:CA - A:ALA17:O	2,91	Hydrogen Bond	Carbon Hydrogen Bond	:GLY2:CA	H-Donor	A:ALA17:O	H-Acceptor
		:SER8:CB - :ASP5:OD2	3,32	Hydrogen Bond	Carbon Hydrogen Bond	:SER8:CB	H-Donor	:ASP5:OD2	H-Acceptor
		A:LEU23:CD1 - :TRP6	3,31	Hydrophobic	Pi-Sigma	A:LEU23:CD1	C-H	:TRP6	Pi-Orbitals
		A:LEU23:CD1 - :TRP6	3,68	Hydrophobic	Pi-Sigma	A:LEU23:CD1	C-H	:TRP6	Pi-Orbitals
		A:ALA17 - :MET1	4,10	Hydrophobic	Alkyl	A:ALA17	Alkyl	:MET1	Alkyl
		:MET1 - :ILE3	4,80	Hydrophobic	Alkyl	:MET1	Alkyl	:ILE3	Alkyl
MKSLSNFLGSSL-ATPase	-422.5	A:ASN21:HD21 - :LYS2:O	2,50	Hydrogen Bond	Conventional Hydrogen Bond	A:ASN21:HD21	H-Donor	:LYS2:O	H-Acceptor
		:LYS2:HZ3 - A:ASN21:OD1	2,82	Hydrogen Bond	Conventional Hydrogen Bond	:LYS2:HZ3	H-Donor	A:ASN21:OD1	H-Acceptor
		:LEU4:HN - :MET1:O	2,67	Hydrogen Bond	Conventional Hydrogen Bond	:LEU4:HN	H-Donor	:MET1:O	H-Acceptor
		:LEU4:HN - :SER3:OG	2,26	Hydrogen Bond	Conventional Hydrogen Bond	:LEU4:HN	H-Donor	:SER3:OG	H-Acceptor
		:SER5:HN - :MET1:O	1,90	Hydrogen Bond	Conventional Hydrogen Bond	:SER5:HN	H-Donor	:MET1:O	H-Acceptor
		:SER5:HG - A:ALA14:O	3,08	Hydrogen Bond	Conventional Hydrogen Bond	:SER5:HG	H-Donor	A:ALA14:O	H-Acceptor

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		:ASN6:HN - :LYS2:O	1,81	Hydrogen Bond	Conventional Hydrogen Bond	:ASN6:HN	H-Donor	:LYS2:O	H-Acceptor
		:ASN6:HN - :SER3:O	2,93	Hydrogen Bond	Conventional Hydrogen Bond	:ASN6:HN	H-Donor	:SER3:O	H-Acceptor
		:ASN6:HD21 - :ASN6:O	1,89	Hydrogen Bond	Conventional Hydrogen Bond	:ASN6:HD21	H-Donor	:ASN6:O	H-Acceptor
		:PHE7:HN - :SER3:O	1,91	Hydrogen Bond	Conventional Hydrogen Bond	:PHE7:HN	H-Donor	:SER3:O	H-Acceptor
		:PHE7:HN - :LEU4:O	3,04	Hydrogen Bond	Conventional Hydrogen Bond	:PHE7:HN	H-Donor	:LEU4:O	H-Acceptor
		:LEU8:HN - :LEU4:O	1,81	Hydrogen Bond	Conventional Hydrogen Bond	:LEU8:HN	H-Donor	:LEU4:O	H-Acceptor
		:GLY9:HN - :SER5:O	1,83	Hydrogen Bond	Conventional Hydrogen Bond	:GLY9:HN	H-Donor	:SER5:O	H-Acceptor
		:SER10:HN - :PHE7:O	1,84	Hydrogen Bond	Conventional Hydrogen Bond	:SER10:HN	H-Donor	:PHE7:O	H-Acceptor
		:SER10:HG - :ASN6:O	1,77	Hydrogen Bond	Conventional Hydrogen Bond	:SER10:HG	H-Donor	:ASN6:O	H-Acceptor
		:SER10:HG - :PHE7:O	2,52	Hydrogen Bond	Conventional Hydrogen Bond	:SER10:HG	H-Donor	:PHE7:O	H-Acceptor
		:SER11:HN - :PHE7:O	1,91	Hydrogen Bond	Conventional Hydrogen Bond	:SER11:HN	H-Donor	:PHE7:O	H-Acceptor
		:SER11:HN - :SER10:OG	2,59	Hydrogen Bond	Conventional Hydrogen Bond	:SER11:HN	H-Donor	:SER10:OG	H-Acceptor
		:LEU12:HN - :LEU8:O	2,01	Hydrogen Bond	Conventional Hydrogen Bond	:LEU12:HN	H-Donor	:LEU8:O	H-Acceptor
		:SER5:CA - A:ALA14:O	2,71	Hydrogen Bond	Carbon Hydrogen Bond	:SER5:CA	H-Donor	A:ALA14:O	H-Acceptor
		:ASN6:CA - A:GLY18:O	3,00	Hydrogen Bond	Carbon Hydrogen Bond	:ASN6:CA	H-Donor	A:GLY18:O	H-Acceptor
		:GLY9:CA - A:LEU15:O	2,51	Hydrogen Bond	Carbon Hydrogen Bond	:GLY9:CA	H-Donor	A:LEU15:O	H-Acceptor
		:SER11:HG - :PHE7	2,11	Hydrogen Bond	Pi-Donor Hydrogen Bond	:SER11:HG	H-Donor	:PHE7	Pi-Orbitals
		A:ALA14 - :LEU8	3,91	Hydrophobic	Alkyl	A:ALA14	Alkyl	:LEU8	Alkyl
		A:LEU15 - :LEU12	4,12	Hydrophobic	Alkyl	A:LEU15	Alkyl	:LEU12	Alkyl
		A:VAL50 - :LYS2	5,31	Hydrophobic	Alkyl	A:VAL50	Alkyl	:LYS2	Alkyl

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		A:VAL53 - :LYS2	5,40	Hydrophobic	Alkyl	A:VAL53	Alkyl	:LYS2	Alkyl
		A:PRO57 - :MET1	3,70	Hydrophobic	Alkyl	A:PRO57	Alkyl	:MET1	Alkyl
		A:ILE58 - :MET1	4,80	Hydrophobic	Alkyl	A:ILE58	Alkyl	:MET1	Alkyl
NTLLVLGRLDCL-ATPase	-399.6	:ARG8:HH22 - :ASP10:OD1	1,99	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ARG8:HH22	H-Donor; Positive	:ASP10:OD1	H-Acceptor; Negative
		:ASN1:N - A:GLU30:OE1	3,76	Electrostatic	Attractive Charge	:ASN1:N	Positive	A:GLU30:OE1	Negative
		:ARG8:NH1 - :ASP10:OD2	3,54	Electrostatic	Attractive Charge	:ARG8:NH1	Positive	:ASP10:OD2	Negative
		:ASN1:HD22 - :LEU12:OT	1,71	Hydrogen Bond	Conventional Hydrogen Bond	:ASN1:HD22	H-Donor	:LEU12:OT	H-Acceptor
		:LEU3:HN - :ASN1:OD1	1,99	Hydrogen Bond	Conventional Hydrogen Bond	:LEU3:HN	H-Donor	:ASN1:OD1	H-Acceptor
		:LEU3:HN - :THR2:OG1	2,95	Hydrogen Bond	Conventional Hydrogen Bond	:LEU3:HN	H-Donor	:THR2:OG1	H-Acceptor
		:LEU4:HN - :THR2:O	2,66	Hydrogen Bond	Conventional Hydrogen Bond	:LEU4:HN	H-Donor	:THR2:O	H-Acceptor
		:VAL5:HN - :LEU3:O	2,30	Hydrogen Bond	Conventional Hydrogen Bond	:VAL5:HN	H-Donor	:LEU3:O	H-Acceptor
		:LEU6:HN - :LEU4:O	1,85	Hydrogen Bond	Conventional Hydrogen Bond	:LEU6:HN	H-Donor	:LEU4:O	H-Acceptor
		:GLY7:HN - :VAL5:O	1,89	Hydrogen Bond	Conventional Hydrogen Bond	:GLY7:HN	H-Donor	:VAL5:O	H-Acceptor
		:ARG8:HN - :LEU6:O	2,05	Hydrogen Bond	Conventional Hydrogen Bond	:ARG8:HN	H-Donor	:LEU6:O	H-Acceptor
		:ARG8:HH11 - :ARG8:O	2,09	Hydrogen Bond	Conventional Hydrogen Bond	:ARG8:HH11	H-Donor	:ARG8:O	H-Acceptor
		:LEU9:HN - :GLY7:O	2,24	Hydrogen Bond	Conventional Hydrogen Bond	:LEU9:HN	H-Donor	:GLY7:O	H-Acceptor
		:ASP10:HN - :ASP10:OD2	2,12	Hydrogen Bond	Conventional Hydrogen Bond	:ASP10:HN	H-Donor	:ASP10:OD2	H-Acceptor
		:CYS11:HN - :ASP10:OD2	1,75	Hydrogen Bond	Conventional Hydrogen Bond	:CYS11:HN	H-Donor	:ASP10:OD2	H-Acceptor
		:CYS11:HG - :ASP10:OD2	1,51	Hydrogen Bond	Conventional Hydrogen Bond	:CYS11:HG	H-Donor	:ASP10:OD2	H-Acceptor
		:LEU12:HN - :ASP10:O	2,22	Hydrogen Bond	Conventional Hydrogen Bond	:LEU12:HN	H-Donor	:ASP10:O	H-Acceptor

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		A:GLY49:CA - :LEU6:O	3,25	Hydrogen Bond	Carbon Hydrogen Bond	A:GLY49:CA	H-Donor	:LEU6:O	H-Acceptor
		A:LEU23 - :LEU12	3,88	Hydrophobic	Alkyl	A:LEU23	Alkyl	:LEU12	Alkyl
		A:ARG27 - :LEU12	5,49	Hydrophobic	Alkyl	A:ARG27	Alkyl	:LEU12	Alkyl
		A:ILE45 - :LEU4	4,41	Hydrophobic	Alkyl	A:ILE45	Alkyl	:LEU4	Alkyl
		A:ILE48 - :LEU6	4,16	Hydrophobic	Alkyl	A:ILE48	Alkyl	:LEU6	Alkyl
		:ARG8 - A:VAL53	5,15	Hydrophobic	Alkyl	:ARG8	Alkyl	A:VAL53	Alkyl
		:CYS11 - :LEU3	4,96	Hydrophobic	Alkyl	:CYS11	Alkyl	:LEU3	Alkyl
SYLDLAFGCVLKPARH-ATPase	-440.9	:ARG15:HH21 - :ASP4:OD1	2,85	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ARG15:HH21	H-Donor; Positive	:ASP4:OD1	H-Acceptor; Negative
		:ARG15:NH1 - :ASP4:OD2	5,41	Electrostatic	Attractive Charge	:ARG15:NH1	Positive	:ASP4:OD2	Negative
		:TYR2:HN - :SER1:OG	2,65	Hydrogen Bond	Conventional Hydrogen Bond	:TYR2:HN	H-Donor	:SER1:OG	H-Acceptor
		:TYR2:HN - :LEU11:O	2,11	Hydrogen Bond	Conventional Hydrogen Bond	:TYR2:HN	H-Donor	:LEU11:O	H-Acceptor
		:TYR2:HH - :LEU11:O	2,83	Hydrogen Bond	Conventional Hydrogen Bond	:TYR2:HH	H-Donor	:LEU11:O	H-Acceptor
		:TYR2:HH - :LYS12:O	2,31	Hydrogen Bond	Conventional Hydrogen Bond	:TYR2:HH	H-Donor	:LYS12:O	H-Acceptor
		:ASP4:HN - :TYR2:O	2,80	Hydrogen Bond	Conventional Hydrogen Bond	:ASP4:HN	H-Donor	:TYR2:O	H-Acceptor
		:ASP4:HN - :CYS9:O	2,05	Hydrogen Bond	Conventional Hydrogen Bond	:ASP4:HN	H-Donor	:CYS9:O	H-Acceptor
		:LEU5:HN - :LEU3:O	2,03	Hydrogen Bond	Conventional Hydrogen Bond	:LEU5:HN	H-Donor	:LEU3:O	H-Acceptor
		:PHE7:HN - :ASP4:O	2,14	Hydrogen Bond	Conventional Hydrogen Bond	:PHE7:HN	H-Donor	:ASP4:O	H-Acceptor
		:GLY8:HN - :LEU5:O	1,99	Hydrogen Bond	Conventional Hydrogen Bond	:GLY8:HN	H-Donor	:LEU5:O	H-Acceptor
		:CYS9:HN - :ASP4:O	2,19	Hydrogen Bond	Conventional Hydrogen Bond	:CYS9:HN	H-Donor	:ASP4:O	H-Acceptor
		:CYS9:HG - :PHE7:O	1,57	Hydrogen Bond	Conventional Hydrogen Bond	:CYS9:HG	H-Donor	:PHE7:O	H-Acceptor

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		:VAL10:HN - A:ILE24:O	1,77	Hydrogen Bond	Conventional Hydrogen Bond	:VAL10:HN	H-Donor	A:ILE24:O	H-Acceptor
		:VAL10:HN - A:THR28:OG1	2,43	Hydrogen Bond	Conventional Hydrogen Bond	:VAL10:HN	H-Donor	A:THR28:OG1	H-Acceptor
		:LEU11:HN - :TYR2:O	1,81	Hydrogen Bond	Conventional Hydrogen Bond	:LEU11:HN	H-Donor	:TYR2:O	H-Acceptor
		:LYS12:HN - A:GLY20:O	2,58	Hydrogen Bond	Conventional Hydrogen Bond	:LYS12:HN	H-Donor	A:GLY20:O	H-Acceptor
		:LYS12:HZ3 - :PRO13:O	1,83	Hydrogen Bond	Conventional Hydrogen Bond	:LYS12:HZ3	H-Donor	:PRO13:O	H-Acceptor
		:ALA14:HN - :TYR2:OH	1,81	Hydrogen Bond	Conventional Hydrogen Bond	:ALA14:HN	H-Donor	:TYR2:OH	H-Acceptor
		:ALA14:HN - :LYS12:O	2,67	Hydrogen Bond	Conventional Hydrogen Bond	:ALA14:HN	H-Donor	:LYS12:O	H-Acceptor
		:ARG15:HN - :TYR2:OH	1,83	Hydrogen Bond	Conventional Hydrogen Bond	:ARG15:HN	H-Donor	:TYR2:OH	H-Acceptor
		:ARG15:HE - :ASP4:OD1	2,07	Hydrogen Bond	Conventional Hydrogen Bond	:ARG15:HE	H-Donor	:ASP4:OD1	H-Acceptor
		:ARG15:HH11 - :ARG15:O	1,91	Hydrogen Bond	Conventional Hydrogen Bond	:ARG15:HH11	H-Donor	:ARG15:O	H-Acceptor
		:HIS16:HN - :ALA14:O	2,32	Hydrogen Bond	Conventional Hydrogen Bond	:HIS16:HN	H-Donor	:ALA14:O	H-Acceptor
		:HIS16:HE2 - :ASP4:OD2	1,84	Hydrogen Bond	Conventional Hydrogen Bond	:HIS16:HE2	H-Donor	:ASP4:OD2	H-Acceptor
		:HIS16:HE1 - :ASP4:OD1	2,89	Hydrogen Bond	Carbon Hydrogen Bond	:HIS16:HE1	H-Donor	:ASP4:OD1	H-Acceptor
		:ARG15:NH1 - :HIS16	3,80	Electrostatic	Pi-Cation	:ARG15:NH1	Positive	:HIS16	Pi-Orbitals
		:ARG15:NH2 - :PHE7	3,94	Hydrogen Bond; Electrostatic	Pi-Cation; Pi-Donor Hydrogen Bond	:ARG15:NH2	Positive; H-Donor	:PHE7	Pi-Orbitals; Pi-Orbitals
		:ALA6:CB - :PHE7	4,00	Hydrophobic	Pi-Sigma	:ALA6:CB	C-H	:PHE7	Pi-Orbitals
		:HIS16 - :TYR2	4,70	Hydrophobic	Pi-Pi T-shaped	:HIS16	Pi-Orbitals	:TYR2	Pi-Orbitals
		A:ALA17 - :LYS12	4,51	Hydrophobic	Alkyl	A:ALA17	Alkyl	:LYS12	Alkyl
		A:ILE24 - :LEU11	3,97	Hydrophobic	Alkyl	A:ILE24	Alkyl	:LEU11	Alkyl
		A:ARG27 - :VAL10	4,42	Hydrophobic	Alkyl	A:ARG27	Alkyl	:VAL10	Alkyl

peptide-protein complex	ΔGi (kj/mol)	residues	Distance (A)	Category	Types	From	From Chemistry	To	To Chemistry
		A:VAL53 - :LYS12	4,41	Hydrophobic	Alkyl	A:VAL53	Alkyl	:LYS12	Alkyl
		:CYS9 - :LEU11	4,26	Hydrophobic	Alkyl	:CYS9	Alkyl	:LEU11	Alkyl
		:VAL10 - A:LEU23	5,49	Hydrophobic	Alkyl	:VAL10	Alkyl	A:LEU23	Alkyl
		:VAL10 - :LEU3	5,25	Hydrophobic	Alkyl	:VAL10	Alkyl	:LEU3	Alkyl
		:ALA14 - A:VAL53	4,16	Hydrophobic	Alkyl	:ALA14	Alkyl	A:VAL53	Alkyl
		:ALA14 - A:LEU56	4,33	Hydrophobic	Alkyl	:ALA14	Alkyl	A:LEU56	Alkyl
		:ARG15 - A:LEU52	4,71	Hydrophobic	Alkyl	:ARG15	Alkyl	A:LEU52	Alkyl
		:ARG15 - :LEU11	4,85	Hydrophobic	Alkyl	:ARG15	Alkyl	:LEU11	Alkyl
		:PHE7 - A:ILE45	4,00	Hydrophobic	Pi-Alkyl	:PHE7	Pi-Orbitals	A:ILE45	Alkyl
		:PHE7 - A:ILE48	5,26	Hydrophobic	Pi-Alkyl	:PHE7	Pi-Orbitals	A:ILE48	Alkyl

Lampiran 41. Interaksi ikatan peptida dengan Caspase-8

Protein	Ligand	name	distance	category	types	from	from chemistry	to	to chemistry
Caspase 8	F4h1c	A:ARG258:HH12 - :LEU9:O	282,577	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH12	H-Donor	:LEU9:O	H-Acceptor
		A:ARG258:HH21 - :LEU3:O	166,421	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH21	H-Donor	:LEU3:O	H-Acceptor
		A:ARG258:HH22 - :THR2:O	258,616	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH22	H-Donor	:THR2:O	H-Acceptor
		A:ASN261:HN - :SER11:OG	298,575	Hydrogen Bond	Conventional Hydrogen Bond	A:ASN261:HN	H-Donor	:SER11:OG	H-Acceptor
		A:ASN261:HD21 - :SER11:O	241,294	Hydrogen Bond	Conventional Hydrogen Bond	A:ASN261:HD21	H-Donor	:SER11:O	H-Acceptor
		B:ARG413:HH11 - :SER7:O	257,171	Hydrogen Bond	Conventional Hydrogen Bond	B:ARG413:HH11	H-Donor	:SER7:O	H-Acceptor
		:SER7:CA - B:ARG413:O	290,687	Hydrogen Bond	Carbon Hydrogen Bond	:SER7:CA	H-Donor	B:ARG413:O	H-Acceptor
		:LEU6:CD1 - B:TYR412	377,018	Hydrophobic	Pi-Sigma	:LEU6:CD1	C-H	B:TYR412	Pi-Orbitals
		B:VAL410 - :PRO5	425,364	Hydrophobic	Alkyl	B:VAL410	Alkyl	:PRO5	Alkyl
		B:LYS457 - :LEU9	532,965	Hydrophobic	Alkyl	B:LYS457	Alkyl	:LEU9	Alkyl
		:ALA1 - A:ILE257	363,233	Hydrophobic	Alkyl	:ALA1	Alkyl	A:ILE257	Alkyl
		A:TYR365 - :ALA4	466,933	Hydrophobic	Pi-Alkyl	A:TYR365	Pi-Orbitals	:ALA4	Alkyl
		A:TYR365 - :PRO5	522,213	Hydrophobic	Pi-Alkyl	A:TYR365	Pi-Orbitals	:PRO5	Alkyl
		A:SER256:C -	200,521	Unfavorable	Unfavorable	A:SER256:C	Steric	:ALA1:N	Steric

		:ALA1:N			Bump				
		A:SER256:C - :ALA1:HT1	164,739	Unfavorable	Unfavorable Bump	A:SER256:C	Steric	:ALA1:HT1	Steric
		A:SER256:C - :ALA1:HT2	165,129	Unfavorable	Unfavorable Bump	A:SER256:C	Steric	:ALA1:HT2	Steric
		A:SER256:O - :ALA1:N	157,038	Unfavorable	Unfavorable Bump	A:SER256:O	Steric	:ALA1:N	Steric
		A:SER256:O - :ALA1:HT1	181,134	Unfavorable	Unfavorable Bump	A:SER256:O	Steric	:ALA1:HT1	Steric
		A:ILE257:N - :ALA1:N	215,943	Unfavorable	Unfavorable Bump	A:ILE257:N	Steric	:ALA1:N	Steric
		A:ILE257:N - :ALA1:HT1	125,596	Unfavorable	Unfavorable Bump	A:ILE257:N	Steric	:ALA1:HT1	Steric
		A:ILE257:CA - :ALA1:N	203,461	Unfavorable	Unfavorable Bump	A:ILE257:CA	Steric	:ALA1:N	Steric
		A:ILE257:CA - :ALA1:HT1	11,714	Unfavorable	Unfavorable Bump	A:ILE257:CA	Steric	:ALA1:HT1	Steric
		A:ARG258:CZ - :THR8:C	202,214	Unfavorable	Unfavorable Bump	A:ARG258:CZ	Steric	:THR8:C	Steric
		A:ARG258:CZ - :THR8:O	194,152	Unfavorable	Unfavorable Bump	A:ARG258:CZ	Steric	:THR8:O	Steric
		A:ARG258:NH1 - :THR8:C	180,773	Unfavorable	Unfavorable Bump	A:ARG258:NH1	Steric	:THR8:C	Steric
		A:ARG258:NH1 - :THR8:O	133,147	Unfavorable	Unfavorable Bump	A:ARG258:NH1	Steric	:THR8:O	Steric
		A:ARG258:NH2 - :THR8:CB	224,598	Unfavorable	Unfavorable Bump	A:ARG258:NH2	Steric	:THR8:CB	Steric
		A:ARG258:HH12 -	129,301	Unfavorable	Unfavorable	A:ARG258:HH12	Steric	:THR8:O	Steric

		:THR8:O			Bump				
		A:TYR365:OH - :ALA4:CB	192,646	Unfavorable	Unfavorable Bump	A:TYR365:OH	Steric	:ALA4:CB	Steric
		A:TYR365:HH - :ALA4:CB	178,626	Unfavorable	Unfavorable Bump	A:TYR365:HH	Steric	:ALA4:CB	Steric
		B:ARG413:HH11 - :SER11:HG	136,546	Unfavorable	Unfavorable Bump	B:ARG413:HH11	Steric	:SER11:HG	Steric
		:ALA1:HT2 - A:SER256:O	0,878212	Unfavorable	Unfavorable Bump; Conventional Hydrogen Bond	:ALA1:HT2	Steric; H-Donor	A:SER256:O	Steric; H-Acceptor
Caspase 8	F4h1h	:LYS2:HZ1 - B:GLU445:OE1	25,177	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:LYS2:HZ1	H-Donor; Positive	B:GLU445:OE1	H-Acceptor; Negative
		:MET1:N - A:ASP374:OD1	404,947	Electrostatic	Attractive Charge	:MET1:N	Positive	A:ASP374:OD1	Negative
		:LYS2:NZ - B:GLU449:OE2	501,325	Electrostatic	Attractive Charge	:LYS2:NZ	Positive	B:GLU449:OE2	Negative
		:SER5:CB - B:THR444:O	333,412	Hydrogen Bond	Carbon Hydrogen Bond	:SER5:CB	H-Donor	B:THR444:O	H-Acceptor
		:LEU12:O - B:PHE468	384,721	Electrostatic	Pi-Cation	:LEU12:O	Positive	B:PHE468	Pi-Orbitals
		:LYS2:CG - B:TYR448	313,038	Hydrophobic	Pi-Sigma	:LYS2:CG	C-H	B:TYR448	Pi-Orbitals
		B:THR444:CG2 - :ASN6:CB	229,591	Unfavorable	Unfavorable Bump	B:THR444:CG2	Steric	:ASN6:CB	Steric
Caspase 8	F4h1e	:ARG8:HH22 - :ASP10:OD1	198,761	Hydrogen Bond;	Salt Bridge; Attractive	:ARG8:HH22	H-Donor; Positive	:ASP10:OD1	H-Acceptor; Negative

				Electrostatic	Charge				
		A:ARG258:NH1 - :ASP10:OD2	386,265	Electrostatic	Attractive Charge	A:ARG258:NH1	Positive	:ASP10:OD2	Negative
		:ASN1:N - A:ASP319:OD2	55,931	Electrostatic	Attractive Charge	:ASN1:N	Positive	A:ASP319:OD2	Negative
		:ASN1:N - A:ASP363:OD2	363,886	Electrostatic	Attractive Charge	:ASN1:N	Positive	A:ASP363:OD2	Negative
		A:ARG258:HH22 - :CYS11:O	275,332	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH22	H-Donor	:CYS11:O	H-Acceptor
		:GLY7:HN - B:ASP455:OD2	300,249	Hydrogen Bond	Conventional Hydrogen Bond	:GLY7:HN	H-Donor	B:ASP455:OD2	H-Acceptor
		:THR2:CA - A:GLY318:O	312,593	Hydrogen Bond	Carbon Hydrogen Bond	:THR2:CA	H-Donor	A:GLY318:O	H-Acceptor
		:GLY7:CA - B:ASN458:OD1	347,511	Hydrogen Bond	Carbon Hydrogen Bond	:GLY7:CA	H-Donor	B:ASN458:OD1	H-Acceptor
		A:ILE257 - :LEU3	490,825	Hydrophobic	Alkyl	A:ILE257	Alkyl	:LEU3	Alkyl
		A:ARG258 - :LEU3	500,165	Hydrophobic	Alkyl	A:ARG258	Alkyl	:LEU3	Alkyl
		A:ARG258 - :CYS11	358,878	Hydrophobic	Alkyl	A:ARG258	Alkyl	:CYS11	Alkyl
		B:VAL410 - :VAL5	370,431	Hydrophobic	Alkyl	B:VAL410	Alkyl	:VAL5	Alkyl
		B:ARG413 - :LEU4	457,325	Hydrophobic	Alkyl	B:ARG413	Alkyl	:LEU4	Alkyl
		:ARG8 - B:LYS457	506,026	Hydrophobic	Alkyl	:ARG8	Alkyl	B:LYS457	Alkyl
		A:HIS317 - :LEU3	539,351	Hydrophobic	Pi-Alkyl	A:HIS317	Pi-Orbitals	:LEU3	Alkyl
		A:TYR365 - :VAL5	412,866	Hydrophobic	Pi-Alkyl	A:TYR365	Pi-Orbitals	:VAL5	Alkyl
		A:ARG258:CD -	213,174	Unfavorable	Unfavorable	A:ARG258:CD	Steric	:CYS11:SG	Steric

		:CYS11:SG			Bump				
		A:ARG258:NE - :CYS11:SG	187,017	Unfavorable	Unfavorable Bump	A:ARG258:NE	Steric	:CYS11:SG	Steric
		A:ARG258:NH2 - :LEU9:CD2	156,739	Unfavorable	Unfavorable Bump	A:ARG258:NH2	Steric	:LEU9:CD2	Steric
		A:ARG258:HE - :CYS11:SG	201,173	Unfavorable	Unfavorable Bump	A:ARG258:HE	Steric	:CYS11:SG	Steric
		A:ARG258:HH21 - :LEU9:CD2	103,997	Unfavorable	Unfavorable Bump	A:ARG258:HH21	Steric	:LEU9:CD2	Steric
		A:ARG258:HH22 - :LEU9:CD2	18,197	Unfavorable	Unfavorable Bump	A:ARG258:HH22	Steric	:LEU9:CD2	Steric
		A:HIS317:HD1 - :THR2:O	149,531	Unfavorable	Unfavorable Bump; Conventional Hydrogen Bond	A:HIS317:HD1	Steric;H-Donor	:THR2:O	Steric; H-Acceptor
		A:TYR324:CD2 - :THR2:CG2	23,682	Unfavorable	Unfavorable Bump	A:TYR324:CD2	Steric	:THR2:CG2	Steric
		A:TYR324:CE2 - :THR2:CG2	174,917	Unfavorable	Unfavorable Bump	A:TYR324:CE2	Steric	:THR2:CG2	Steric
		A:TYR324:HE2 - :THR2:CG2	100,681	Unfavorable	Unfavorable Bump	A:TYR324:HE2	Steric	:THR2:CG2	Steric
		A:ASP363:CB - :ASN1:N	183,365	Unfavorable	Unfavorable Bump	A:ASP363:CB	Steric	:ASN1:N	Steric
		A:ASP363:CB - :ASN1:HT1	191,589	Unfavorable	Unfavorable Bump	A:ASP363:CB	Steric	:ASN1:HT1	Steric
		B:SER411:C - :LEU4:CD1	236,061	Unfavorable	Unfavorable Bump	B:SER411:C	Steric	:LEU4:CD1	Steric
		B:SER411:O -	141,011	Unfavorable	Unfavorable	B:SER411:O	Steric	:LEU4:CD1	Steric

		:LEU4:CD1			Bump				
Caspase 8	F4h1i	A:ARG258:NH2 - :PHE13:OT	550,763	Electrostatic	Attractive Charge	A:ARG258:NH2	Positive	:PHE13:OT	Negative
		:LYS10:NZ - A:ASP319:OD2	422,362	Electrostatic	Attractive Charge	:LYS10:NZ	Positive	A:ASP319:OD2	Negative
		A:ARG258:HH21 - :GLY6:O	246,473	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH21	H-Donor	:GLY6:O	H-Acceptor
		A:ARG258:HH22 - :MET11:O	243,848	Hydrogen Bond	Conventional Hydrogen Bond	A:ARG258:HH22	H-Donor	:MET11:O	H-Acceptor
		B:ARG413:HH21 - :MET7:O	250,676	Hydrogen Bond	Conventional Hydrogen Bond	B:ARG413:HH21	H-Donor	:MET7:O	H-Acceptor
		B:ARG413:HH22 - :SER8:O	224,289	Hydrogen Bond	Conventional Hydrogen Bond	B:ARG413:HH22	H-Donor	:SER8:O	H-Acceptor
		B:TRP420:HE1 - :ASN5:OD1	291,367	Hydrogen Bond	Conventional Hydrogen Bond	B:TRP420:HE1	H-Donor	:ASN5:OD1	H-Acceptor
		:ASN5:HD22 - B:ASP454:O	307,125	Hydrogen Bond	Conventional Hydrogen Bond	:ASN5:HD22	H-Donor	B:ASP454:O	H-Acceptor
		:SER8:HN - B:ARG413:O	289,738	Hydrogen Bond	Conventional Hydrogen Bond	:SER8:HN	H-Donor	B:ARG413:O	H-Acceptor
		:LYS10:HN - A:CYS360:SG	24,935	Hydrogen Bond	Conventional Hydrogen Bond	:LYS10:HN	H-Donor	A:CYS360:SG	H-Acceptor
		A:HIS317:CE1 - :LEU9:O	34,643	Hydrogen Bond	Carbon Hydrogen Bond	A:HIS317:CE1	H-Donor	:LEU9:O	H-Acceptor
		B:PRO415:CD - :LEU4:O	372,568	Hydrogen Bond	Carbon Hydrogen Bond	B:PRO415:CD	H-Donor	:LEU4:O	H-Acceptor
		A:CYS360 - :LYS10	327,529	Hydrophobic	Alkyl	A:CYS360	Alkyl	:LYS10	Alkyl
		B:VAL410 - :LEU9	411,667	Hydrophobic	Alkyl	B:VAL410	Alkyl	:LEU9	Alkyl
		B:PRO415 - :LEU4	452,758	Hydrophobic	Alkyl	B:PRO415	Alkyl	:LEU4	Alkyl

		A:HIS317 - :LYS10	495,265	Hydrophobic	Pi-Alkyl	A:HIS317	Pi-Orbitals	:LYS10	Alkyl
		B:TYR412 - :LEU9	520,367	Hydrophobic	Pi-Alkyl	B:TYR412	Pi-Orbitals	:LEU9	Alkyl
		A:GLY318:O - :LYS10:CD	143,848	Unfavorable	Unfavorable Bump	A:GLY318:O	Steric	:LYS10:CD	Steric
		A:GLY318:O - :LYS10:CE	189,205	Unfavorable	Unfavorable Bump	A:GLY318:O	Steric	:LYS10:CE	Steric
		B:ARG413:CA - :SER8:HG	164,915	Unfavorable	Unfavorable Bump	B:ARG413:CA	Steric	:SER8:HG	Steric
		B:ARG413:C - :SER8:OG	174,354	Unfavorable	Unfavorable Bump	B:ARG413:C	Steric	:SER8:OG	Steric
		B:ARG413:C - :SER8:HG	0,786555	Unfavorable	Unfavorable Bump	B:ARG413:C	Steric	:SER8:HG	Steric
		B:ARG413:O - :SER8:CB	225,111	Unfavorable	Unfavorable Bump	B:ARG413:O	Steric	:SER8:CB	Steric
		B:ARG413:O - :SER8:OG	110,794	Unfavorable	Unfavorable Bump	B:ARG413:O	Steric	:SER8:OG	Steric
		B:ARG413:O - :SER8:HG	0,781709	Unfavorable	Unfavorable Bump	B:ARG413:O	Steric	:SER8:HG	Steric
		B:TRP420:CZ2 - :ASN5:ND2	203,682	Unfavorable	Unfavorable Bump	B:TRP420:CZ2	Steric	:ASN5:ND2	Steric
		B:TRP420:CZ2 - :ASN5:HD22	143,798	Unfavorable	Unfavorable Bump	B:TRP420:CZ2	Steric	:ASN5:HD22	Steric
		B:LYS456:C - :GLN2:OE1	206,088	Unfavorable	Unfavorable Bump	B:LYS456:C	Steric	:GLN2:OE1	Steric
		B:LYS456:O - :GLN2:OE1	208,686	Unfavorable	Unfavorable Bump	B:LYS456:O	Steric	:GLN2:OE1	Steric

		B:LYS457:N - :GLN2:CB	213,395	Unfavorable	Unfavorable Bump	B:LYS457:N	Steric	:GLN2:CB	Steric
		B:LYS457:N - :GLN2:CG	175,679	Unfavorable	Unfavorable Bump	B:LYS457:N	Steric	:GLN2:CG	Steric
		B:LYS457:N - :GLN2:CD	168,065	Unfavorable	Unfavorable Bump	B:LYS457:N	Steric	:GLN2:CD	Steric
		B:LYS457:N - :GLN2:OE1	165,409	Unfavorable	Unfavorable Bump	B:LYS457:N	Steric	:GLN2:OE1	Steric
		B:LYS457:CA - :GLN2:CG	165,267	Unfavorable	Unfavorable Bump	B:LYS457:CA	Steric	:GLN2:CG	Steric
		B:LYS457:CA - :GLN2:CD	0,485016	Unfavorable	Unfavorable Bump	B:LYS457:CA	Steric	:GLN2:CD	Steric
		B:LYS457:CA - :GLN2:OE1	1,257	Unfavorable	Unfavorable Bump	B:LYS457:CA	Steric	:GLN2:OE1	Steric
		B:LYS457:CA - :GLN2:NE2	140,605	Unfavorable	Unfavorable Bump	B:LYS457:CA	Steric	:GLN2:NE2	Steric
		B:LYS457:C - :GLN2:CD	192,403	Unfavorable	Unfavorable Bump	B:LYS457:C	Steric	:GLN2:CD	Steric
		B:LYS457:C - :GLN2:NE2	17,243	Unfavorable	Unfavorable Bump	B:LYS457:C	Steric	:GLN2:NE2	Steric
		B:LYS457:C - :GLN2:HE22	191,897	Unfavorable	Unfavorable Bump	B:LYS457:C	Steric	:GLN2:HE22	Steric
		B:LYS457:O - :GLN2:NE2	200,314	Unfavorable	Unfavorable Bump	B:LYS457:O	Steric	:GLN2:NE2	Steric
		B:LYS457:O - :GLN2:HE22	157,423	Unfavorable	Unfavorable Bump	B:LYS457:O	Steric	:GLN2:HE22	Steric
		B:LYS457:CB - :GLN2:CG	113,792	Unfavorable	Unfavorable Bump	B:LYS457:CB	Steric	:GLN2:CG	Steric

		B:LYS457:CB - :GLN2:CD	130,299	Unfavorable	Unfavorable Bump	B:LYS457:CB	Steric	:GLN2:CD	Steric
		B:LYS457:CB - :GLN2:NE2	153,166	Unfavorable	Unfavorable Bump	B:LYS457:CB	Steric	:GLN2:NE2	Steric
		B:LYS457:CB - :GLN2:HE21	149,936	Unfavorable	Unfavorable Bump	B:LYS457:CB	Steric	:GLN2:HE21	Steric
		B:LYS457:CG - :GLN2:CD	234,588	Unfavorable	Unfavorable Bump	B:LYS457:CG	Steric	:GLN2:CD	Steric
		B:LYS457:CG - :GLN2:NE2	155,832	Unfavorable	Unfavorable Bump	B:LYS457:CG	Steric	:GLN2:NE2	Steric
		B:LYS457:CG - :GLN2:HE21	0,907315	Unfavorable	Unfavorable Bump	B:LYS457:CG	Steric	:GLN2:HE21	Steric
		B:LYS457:CD - :GLN2:NE2	223,013	Unfavorable	Unfavorable Bump	B:LYS457:CD	Steric	:GLN2:NE2	Steric
		B:LYS457:HN - :GLN2:CB	15,694	Unfavorable	Unfavorable Bump	B:LYS457:HN	Steric	:GLN2:CB	Steric
		B:LYS457:HN - :GLN2:CG	153,857	Unfavorable	Unfavorable Bump	B:LYS457:HN	Steric	:GLN2:CG	Steric
		B:LYS457:HB1 - :GLN2:CG	115,599	Unfavorable	Unfavorable Bump	B:LYS457:HB1	Steric	:GLN2:CG	Steric
		B:LYS457:HB1 - :GLN2:CD	176,529	Unfavorable	Unfavorable Bump	B:LYS457:HB1	Steric	:GLN2:CD	Steric
		B:LYS456:NZ - :ASN1:N	490,037	Unfavorable	Unfavorable Positive-Positive	B:LYS456:NZ	Positive	:ASN1:N	Positive
		B:ARG413:O - :LEU4:O	270,583	Unfavorable	Unfavorable Acceptor-Acceptor	B:ARG413:O	H-Acceptor	:LEU4:O	H-Acceptor
Caspase	F4h1m	B:ASN407:HD21 -	268,361	Hydrogen Bond	Conventional	B:ASN407:HD21	H-Donor	:HIS3:O	H-Acceptor

8		:HIS3:O			Hydrogen Bond				
		:LYS2 - A:ILE333	441,977	Hydrophobic	Alkyl	:LYS2	Alkyl	A:ILE333	Alkyl
		:LYS2 - B:MET403	50,182	Hydrophobic	Alkyl	:LYS2	Alkyl	B:MET403	Alkyl
		:CYS8 - :VAL20	544,934	Hydrophobic	Alkyl	:CYS8	Alkyl	:VAL20	Alkyl
		A:TYR334 - :ARG1	53,141	Hydrophobic	Pi-Alkyl	A:TYR334	Pi-Orbitals	:ARG1	Alkyl
		A:TYR334 - :VAL21	528,881	Hydrophobic	Pi-Alkyl	A:TYR334	Pi-Orbitals	:VAL21	Alkyl
		:HIS3 - A:LYS320	358,862	Hydrophobic	Pi-Alkyl	:HIS3	Pi-Orbitals	A:LYS320	Alkyl
		A:TYR334:CE2 - :LEU5:CD1	200,443	Unfavorable	Unfavorable Bump	A:TYR334:CE2	Steric	:LEU5:CD1	Steric
		B:ASN407:CB - :VAL6:CG2	224,859	Unfavorable	Unfavorable Bump	B:ASN407:CB	Steric	:VAL6:CG2	Steric
		B:ASN407:HB1 - :VAL6:CB	195,239	Unfavorable	Unfavorable Bump	B:ASN407:HB1	Steric	:VAL6:CB	Steric
		B:ASN408:OD1 - :HIS3:CE1	198,882	Unfavorable	Unfavorable Bump	B:ASN408:OD1	Steric	:HIS3:CE1	Steric
		B:THR467:CG2 - :GLU17:N	201,007	Unfavorable	Unfavorable Bump	B:THR467:CG2	Steric	:GLU17:N	Steric
		B:THR467:CG2 - :LEU18:N	216,834	Unfavorable	Unfavorable Bump	B:THR467:CG2	Steric	:LEU18:N	Steric
		B:THR467:CG2 - :LEU18:HN	126,551	Unfavorable	Unfavorable Bump	B:THR467:CG2	Steric	:LEU18:HN	Steric
		B:THR467:CG2:B - :GLU17:N	205,645	Unfavorable	Unfavorable Bump	B:THR467:CG2:B	Steric	:GLU17:N	Steric
		B:THR467:CG2:B - :GLU17:HN	131,832	Unfavorable	Unfavorable Bump	B:THR467:CG2:B	Steric	:GLU17:HN	Steric

		B:THR467:HG23:B - :GLU17:HN	13,209	Unfavorable	Unfavorable Bump	B:THR467:HG23:B	Steric	:GLU17:HN	Steric
		B:PHE468:CD1 - :TYR16:CE2	214,543	Unfavorable	Unfavorable Bump	B:PHE468:CD1	Steric	:TYR16:CE2	Steric
		:HIS3:HE1 - B:ASN408:OD1	100,078	Unfavorable	Unfavorable Bump; Carbon Hydrogen Bond	:HIS3:HE1	Steric; H-Donor	B:ASN408:OD1	Steric; H-Acceptor
		B:PHE468:O - :GLU19:OE2	235,847	Unfavorable	Unfavorable Acceptor-Acceptor	B:PHE468:O	H-Acceptor	:GLU19:OE2	H-Acceptor
Caspase 8	F4h1k	:LEU3:HN - B:ASN447:O	262,436	Hydrogen Bond	Conventional Hydrogen Bond	:LEU3:HN	H-Donor	B:ASN447:O	H-Acceptor
		:LEU5:HN - B:MET463:SD	215,232	Hydrogen Bond	Conventional Hydrogen Bond	:LEU5:HN	H-Donor	B:MET463:SD	H-Acceptor
		:ARG15:HH22 - B:GLN465:OE1	277,018	Hydrogen Bond	Conventional Hydrogen Bond	:ARG15:HH22	H-Donor	B:GLN465:OE1	H-Acceptor
		B:GLN465:CA - :HIS16:ND1	2,914	Hydrogen Bond	Carbon Hydrogen Bond	B:GLN465:CA	H-Donor	:HIS16:ND1	H-Acceptor
		:HIS16:HD2 - B:ASN447:OD1	17,671	Hydrogen Bond	Carbon Hydrogen Bond	:HIS16:HD2	H-Donor	B:ASN447:OD1	H-Acceptor
		B:MET463:SD - :LEU5:N	285,646	Other	Sulfur-X	B:MET463:SD	Sulfur	:LEU5:N	O,N,S
		B:GLN465:CA - :HIS16	35,037	Hydrophobic	Pi-Sigma	B:GLN465:CA	C-H	:HIS16	Pi-Orbitals
		B:MET463:SD - :HIS16	58,487	Other	Pi-Sulfur	B:MET463:SD	Sulfur	:HIS16	Pi-Orbitals
		A:VAL371 - :VAL10	529,376	Hydrophobic	Alkyl	A:VAL371	Alkyl	:VAL10	Alkyl

		B:LYS461 - :LEU5	382,792	Hydrophobic	Alkyl	B:LYS461	Alkyl	:LEU5	Alkyl
		B:MET463 - :LEU5	503,874	Hydrophobic	Alkyl	B:MET463	Alkyl	:LEU5	Alkyl
		:ALA6 - B:VAL406	369,001	Hydrophobic	Alkyl	:ALA6	Alkyl	B:VAL406	Alkyl
		:PHE7 - B:VAL406	541,262	Hydrophobic	Pi-Alkyl	:PHE7	Pi-Orbitals	B:VAL406	Alkyl
		:HIS16 - B:PRO466	455,945	Hydrophobic	Pi-Alkyl	:HIS16	Pi-Orbitals	B:PRO466	Alkyl
		A:GLN366:NE2 - :LEU5:C	202,959	Unfavorable	Unfavorable Bump	A:GLN366:NE2	Steric	:LEU5:C	Steric
		A:GLN366:NE2 - :ALA6:N	148,516	Unfavorable	Unfavorable Bump	A:GLN366:NE2	Steric	:ALA6:N	Steric
		A:GLN366:NE2 - :ALA6:CA	190,879	Unfavorable	Unfavorable Bump	A:GLN366:NE2	Steric	:ALA6:CA	Steric
		A:GLN366:HE21 - :LEU5:C	140,373	Unfavorable	Unfavorable Bump	A:GLN366:HE21	Steric	:LEU5:C	Steric
		A:GLN366:HE21 - :ALA6:N	150,599	Unfavorable	Unfavorable Bump	A:GLN366:HE21	Steric	:ALA6:N	Steric
		A:GLN366:HE22 - :ALA6:N	123,014	Unfavorable	Unfavorable Bump	A:GLN366:HE22	Steric	:ALA6:N	Steric
		A:GLN366:HE22 - :ALA6:CA	0,920603	Unfavorable	Unfavorable Bump	A:GLN366:HE22	Steric	:ALA6:CA	Steric
		A:ILE369:CD1 - :GLY8:CA	236,819	Unfavorable	Unfavorable Bump	A:ILE369:CD1	Steric	:GLY8:CA	Steric
		A:ILE369:CD1 - :GLY8:C	227,605	Unfavorable	Unfavorable Bump	A:ILE369:CD1	Steric	:GLY8:C	Steric
		A:ILE369:CD1 - :GLY8:O	207,382	Unfavorable	Unfavorable Bump	A:ILE369:CD1	Steric	:GLY8:O	Steric
		B:ASN447:CB -	216,288	Unfavorable	Unfavorable	B:ASN447:CB	Steric	:TYR2:CB	Steric

		:TYR2:CB			Bump				
		B:SER451:CB - :LEU3:CB	206,694	Unfavorable	Unfavorable Bump	B:SER451:CB	Steric	:LEU3:CB	Steric
		B:SER451:OG - :LEU3:CB	218,814	Unfavorable	Unfavorable Bump	B:SER451:OG	Steric	:LEU3:CB	Steric
		B:SER451:OG - :LEU3:O	20,555	Unfavorable	Unfavorable Bump	B:SER451:OG	Steric	:LEU3:O	Steric
		B:SER451:HG - :LEU3:CB	174,589	Unfavorable	Unfavorable Bump	B:SER451:HG	Steric	:LEU3:CB	Steric
		B:MET463:SD - :LEU3:O	183,095	Unfavorable	Unfavorable Bump; Sulfur-X	B:MET463:SD	Steric; Sulfur	:LEU3:O	Steric;O,N,S
		B:MET463:SD - :ASP4:CA	235,532	Unfavorable	Unfavorable Bump	B:MET463:SD	Steric	:ASP4:CA	Steric
		B:PRO466:O - :HIS16:OT	19,811	Unfavorable	Unfavorable Bump	B:PRO466:O	Steric	:HIS16:OT	Steric
		B:PRO466:CD - :HIS16:CB	228,792	Unfavorable	Unfavorable Bump	B:PRO466:CD	Steric	:HIS16:CB	Steric
Caspase8	F4h1j	:ARG3:NH2 - A:ASP374:OD1	323,895	Electrostatic	Attractive Charge	:ARG3:NH2	Positive	A:ASP374:OD1	Negative
		B:PHE468:HN - :HIS13:O	281,756	Hydrogen Bond	Conventional Hydrogen Bond	B:PHE468:HN	H-Donor	:HIS13:O	H-Acceptor
		B:THR467:CA - :HIS13:O	264,001	Hydrogen Bond	Carbon Hydrogen Bond	B:THR467:CA	H-Donor	:HIS13:O	H-Acceptor
		B:THR467:CA:B - :HIS13:O	259,331	Hydrogen Bond	Carbon Hydrogen Bond	B:THR467:CA:B	H-Donor	:HIS13:O	H-Acceptor
		:VAL14:CA - B:THR467:OG1	353,656	Hydrogen Bond	Carbon Hydrogen Bond	:VAL14:CA	H-Donor	B:THR467:OG1	H-Acceptor

		B:GLN465:CG - :PHE9	351,511	Hydrophobic	Pi-Sigma	B:GLN465:CG	C-H	:PHE9	Pi-Orbitals
		:HIS13 - B:PHE468	468,125	Hydrophobic	Pi-Pi T-shaped	:HIS13	Pi-Orbitals	B:PHE468	Pi-Orbitals
		A:ILE369 - :LEU1	409,655	Hydrophobic	Alkyl	A:ILE369	Alkyl	:LEU1	Alkyl
		:VAL10 - B:LEU440	456,963	Hydrophobic	Alkyl	:VAL10	Alkyl	B:LEU440	Alkyl
		B:TYR448 - :ARG3	529,594	Hydrophobic	Pi-Alkyl	B:TYR448	Pi-Orbitals	:ARG3	Alkyl
		A:ASP374:CG - :ARG3:NH1	201,326	Unfavorable	Unfavorable Bump	A:ASP374:CG	Steric	:ARG3:NH1	Steric
		B:SER451:CB - :GLU2:CB	173,257	Unfavorable	Unfavorable Bump	B:SER451:CB	Steric	:GLU2:CB	Steric
		B:SER451:CB - :GLU2:CG	225,145	Unfavorable	Unfavorable Bump	B:SER451:CB	Steric	:GLU2:CG	Steric
		B:SER451:OG - :GLU2:CB	205,029	Unfavorable	Unfavorable Bump	B:SER451:OG	Steric	:GLU2:CB	Steric
		B:SER451:HG - :GLU2:CB	162,763	Unfavorable	Unfavorable Bump	B:SER451:HG	Steric	:GLU2:CB	Steric
		:ARG3:HH11 - A:ASP374:OD2	138,771	Unfavorable	Unfavorable Bump; Salt Bridge; Attractive Charge	:ARG3:HH11	Steric; H-Donor; Positive	A:ASP374:OD2	Steric; H-Acceptor; Negative
Caspase 8	F4h1f	:LYS10:HZ1 - :GLU11:OE1	20,042	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:LYS10:HZ1	H-Donor; Positive	:GLU11:OE1	H-Acceptor; Negative
		B:LYS472:NZ -	516,021	Electrostatic	Attractive	B:LYS472:NZ	Positive	:GLU11:OE2	Negative

		:GLU11:OE2			Charge				
		B:LYS472:NZ - :LEU12:OT	536,594	Electrostatic	Attractive Charge	B:LYS472:NZ	Positive	:LEU12:OT	Negative
		:LYS10:NZ - A:ASP308:OD1	470,816	Electrostatic	Attractive Charge	:LYS10:NZ	Positive	A:ASP308:OD1	Negative
		B:ILE393:HN - :GLU8:OE2	280,956	Hydrogen Bond	Conventional Hydrogen Bond	B:ILE393:HN	H-Donor	:GLU8:OE2	H-Acceptor
		B:LYS472:HZ3 - :GLU11:O	188,956	Hydrogen Bond	Conventional Hydrogen Bond	B:LYS472:HZ3	H-Donor	:GLU11:O	H-Acceptor
		A:PRO352:CD - :GLU11:OE2	371,504	Hydrogen Bond	Carbon Hydrogen Bond	A:PRO352:CD	H-Donor	:GLU11:OE2	H-Acceptor
		B:TYR392:CA - :GLU8:OE2	34,078	Hydrogen Bond	Carbon Hydrogen Bond	B:TYR392:CA	H-Donor	:GLU8:OE2	H-Acceptor
		:MET1:SD - B:TYR392	599,875	Other	Pi-Sulfur	:MET1:SD	Sulfur	B:TYR392	Pi-Orbitals
		A:PRO346 - :LEU3	505,436	Hydrophobic	Alkyl	A:PRO346	Alkyl	:LEU3	Alkyl
		B:ARG391 - :LEU9	511,015	Hydrophobic	Alkyl	B:ARG391	Alkyl	:LEU9	Alkyl
		A:LYS351:CE - :GLU7:OE1	148,657	Unfavorable	Unfavorable Bump	A:LYS351:CE	Steric	:GLU7:OE1	Steric
		A:LYS351:NZ - :GLU7:OE1	155,214	Unfavorable	Unfavorable Bump; Attractive Charge	A:LYS351:NZ	Steric; Positive	:GLU7:OE1	Steric; Negative
		A:LYS351:HZ1 - :GLU7:OE1	125,146	Unfavorable	Unfavorable Bump	A:LYS351:HZ1	Steric	:GLU7:OE1	Steric
		A:LYS224:NZ - :LEU12:O	496,264	Unfavorable	Unfavorable Positive-Positive	A:LYS224:NZ	Positive	:LEU12:O	Positive
		B:LYS472:NZ -	402,919	Unfavorable	Unfavorable	B:LYS472:NZ	Positive	:LEU12:O	Positive

		:LEU12:O			Positive-Positive				
		B:ARG391:O - :GLU8:OE2	254,271	Unfavorable	Unfavorable Acceptor-Acceptor	B:ARG391:O	H-Acceptor	:GLU8:OE2	H-Acceptor
Caspase 8	F4h1l	:ASN1:HT1 - B:GLU431:OE1	207,557	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ASN1:HT1	H-Donor; Positive	B:GLU431:OE1	H-Acceptor; Negative
		:ASN1:HT2 - B:GLU431:OE1	188,632	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ASN1:HT2	H-Donor; Positive	B:GLU431:OE1	H-Acceptor; Negative
		:ARG6:HH22 - B:GLU417:OE2	270,656	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:ARG6:HH22	H-Donor; Positive	B:GLU417:OE2	H-Acceptor; Negative
		:LYS2:HZ1 - B:SER424:OG:B	286,329	Hydrogen Bond	Conventional Hydrogen Bond	:LYS2:HZ1	H-Donor	B:SER424:OG:B	H-Acceptor
		:THR16:HG1 - A:HIS264:O	18,525	Hydrogen Bond	Conventional Hydrogen Bond	:THR16:HG1	H-Donor	A:HIS264:O	H-Acceptor
		A:ALA269 - :LYS19	457,522	Hydrophobic	Alkyl	A:ALA269	Alkyl	:LYS19	Alkyl
		B:ALA416 - :LEU14	498,764	Hydrophobic	Alkyl	B:ALA416	Alkyl	:LEU14	Alkyl
		B:CYS426 - :LYS19	369,304	Hydrophobic	Alkyl	B:CYS426	Alkyl	:LYS19	Alkyl
		B:ARG430 - :LEU20	521,976	Hydrophobic	Alkyl	B:ARG430	Alkyl	:LEU20	Alkyl
		A:LEU265:O - :THR16:CG2	189,463	Unfavorable	Unfavorable Bump	A:LEU265:O	Steric	:THR16:CG2	Steric
		B:GLN423:OE1 - :LYS19:CE	15,875	Unfavorable	Unfavorable Bump	B:GLN423:OE1	Steric	:LYS19:CE	Steric

		B:GLN423:OE1 - :LYS19:NZ	132,234	Unfavorable	Unfavorable Bump	B:GLN423:OE1	Steric	:LYS19:NZ	Steric
		B:GLN423:OE1 - :LYS19:HZ1	102,307	Unfavorable	Unfavorable Bump	B:GLN423:OE1	Steric	:LYS19:HZ1	Steric
		B:GLN427:CA - :LYS19:O	213,388	Unfavorable	Unfavorable Bump; Carbon Hydrogen Bond	B:GLN427:CA	Steric; H-Donor	:LYS19:O	Steric; H-Acceptor
		B:GLN427:CD - :LYS2:CG	181,455	Unfavorable	Unfavorable Bump	B:GLN427:CD	Steric	:LYS2:CG	Steric
		B:GLN427:OE1 - :LYS2:CG	152,398	Unfavorable	Unfavorable Bump	B:GLN427:OE1	Steric	:LYS2:CG	Steric
		B:GLN427:OE1 - :LYS2:CD	200,862	Unfavorable	Unfavorable Bump	B:GLN427:OE1	Steric	:LYS2:CD	Steric
		B:GLN427:OE1 - :LYS2:CE	212,903	Unfavorable	Unfavorable Bump	B:GLN427:OE1	Steric	:LYS2:CE	Steric
		B:GLN427:NE2 - :LYS2:CG	178,278	Unfavorable	Unfavorable Bump	B:GLN427:NE2	Steric	:LYS2:CG	Steric
		B:GLN427:HE22 - :LYS2:CG	138,221	Unfavorable	Unfavorable Bump	B:GLN427:HE22	Steric	:LYS2:CG	Steric
	F4h1g	B:ARG471:HH21 - :GLY16:OT	319,449	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	B:ARG471:HH21	H-Donor; Positive	:GLY16:OT	H-Acceptor; Negative
		B:LYS473:HZ1 - :ASP5:OD1	281,948	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	B:LYS473:HZ1	H-Donor; Positive	:ASP5:OD1	H-Acceptor; Negative
		B:LYS473:HZ3 - :ASP5:OD2	314,698	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	B:LYS473:HZ3	H-Donor; Positive	:ASP5:OD2	H-Acceptor; Negative

		:LYS12:HZ1 - :ASP5:OD2	24,606	Hydrogen Bond; Electrostatic	Salt Bridge; Attractive Charge	:LYS12:HZ1	H-Donor; Positive	:ASP5:OD2	H-Acceptor; Negative
		B:LYS472:NZ - :GLY16:OT	396,754	Electrostatic	Attractive Charge	B:LYS472:NZ	Positive	:GLY16:OT	Negative
		:LYS12:NZ - A:ASP223:OD2	462,192	Electrostatic	Attractive Charge	:LYS12:NZ	Positive	A:ASP223:OD2	Negative
		B:LYS472:CE - :GLY16:OT	302,624	Hydrogen Bond	Carbon Hydrogen Bond	B:LYS472:CE	H-Donor	:GLY16:OT	H-Acceptor
		:GLY16:CA - B:ARG471:O	373,745	Hydrogen Bond	Carbon Hydrogen Bond	:GLY16:CA	H-Donor	B:ARG471:O	H-Acceptor
		B:ARG471 - :LEU11	384,756	Hydrophobic	Alkyl	B:ARG471	Alkyl	:LEU11	Alkyl
		B:LYS473 - :LYS12	526,098	Hydrophobic	Alkyl	B:LYS473	Alkyl	:LYS12	Alkyl
		B:PHE468 - :LEU7	495,833	Hydrophobic	Pi-Alkyl	B:PHE468	Pi-Orbitals	:LEU7	Alkyl
		B:LEU470:O - :LEU11:CD2	169,852	Unfavorable	Unfavorable Bump	B:LEU470:O	Steric	:LEU11:CD2	Steric
		B:ARG471:HH11 - :GLY16:OT	149,074	Unfavorable	Unfavorable Bump; Salt Bridge; Attractive Charge	B:ARG471:HH11	Steric; H-Donor; Positive	:GLY16:OT	Steric; H-Acceptor; Negative
		B:ARG471:NH1 - :GLY16:O	327,162	Unfavorable	Unfavorable Positive-Positive	B:ARG471:NH1	Positive	:GLY16:O	Positive
		B:LYS472:NZ - :GLY16:O	551,022	Unfavorable	Unfavorable Positive-Positive	B:LYS472:NZ	Positive	:GLY16:O	Positive

Lampiran 42. Daftar nama perangkat lunak yang digunakan untuk analisis bioinformatik

NO	NAMA	APLIKASI/WEBSITE	FUNGSI
1	BioEdit	Software	Membaca dan mengolah file sequence DNA
2	BLAST	https://blast.ncbi.nlm.nih.gov/Blast.cgi	Sekuensing bakteri
3	Masslynx V4.1	Software	Analisis LC-MS/MS
4	Mascot	Software	Identifikasi Peptida
5	ProtParam	http://web.expasy.org/protparam/	Analisis fisikokimia peptida
6	APD3	http://aps.unmc.edu/AP/prediction/prediction_main.php	Untuk analisis fisikokimia peptida
7	AntiCP	https://webs.iiitd.edu.in/raghava/anticp/	Analisis prediksi Aktivitas antikanker
8	DBAASP	https://dbaasp.org/prediction	Analisis prediksi Aktivitas antibakteri
9	iAMP-2L	http://cabgrid.res.in:8080/amppred/	Analisis prediksi Aktivitas antibakteri
10	AMP Scanner Vr.2	https://www.dveltri.com/ascan/v2/	Analisis prediksi Aktivitas antibakteri
11	PEP-FOLD3	https://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD3/	Prediksi struktur 3D