



c rNLRP1_{FIIND} monomer

[Sequence]
Ser Pro Met Gly Val

[Estimated Sequence]

	1	2	3	4	5
1st	Ser	Pro	Met	Gly	Val
2nd	Gly	Asp	Thr	Tyr	Leu
3rd	Asp	Phe	Ile	Asn	Ala
4th	His	Glu	Leu	Glu	Tyr
Reliability(%)	20.9	100.0	79.0	72.4	100.0

[Evaluated Value]

	1	2	3	4	5
Asp	5.52	3.19	0.64	0.70	1.12
Glu	0.73	1.08	1.04	1.12	1.11
Asn	0.24	0.52	0.67	1.20	0.78
Gln	3.88	0.44	1.39	0.63	0.96
Ser	18.30	0.11	0.18	0.54	1.00
Thr	2.24	0.47	2.24	0.41	1.25
His	4.59	0.23	0.92	0.00	0.00
Gly	7.23	0.51	0.74	11.65	0.44
Ala	2.61	0.29	1.42	0.38	1.43
Tyr	0.87	0.86	1.04	1.40	1.26
Arg	1.29	0.20	1.23	0.62	0.83
Met	1.25	0.88	19.94	0.21	0.18
Val	0.62	0.98	1.15	0.84	41.15
Pro	0.03	47.23	0.32	0.27	0.47
Trp	1.08	0.45	0.00	0.00	0.00
Phe	0.83	1.19	1.40	0.62	0.91
Lys	1.05	0.73	1.37	0.18	0.39
Ile	0.95	1.06	2.15	0.83	0.94
Leu	0.98	1.00	1.74	0.58	2.33

rNLRP1_{FIIND}rDPP9 complex

[Sequence]
Ser Pro Met Gly Val

[Estimated Sequence]

	1	2	3	4	5
1st	Ser	Pro	Met	Gly	Val
2nd	Leu	Ile	Ile	Asn	Leu
3rd	Gln	Ala	Tyr	Ile	Ala
4th	Gly	Glu	Glu	Glu	Tyr
Reliability(%)	36.9	68.6	81.2	48.8	100.0

[Evaluated Value]

	1	2	3	4	5
Asp	0.20	1.93	0.58	0.78	0.84
Glu	0.69	2.33	1.77	1.32	0.80
Asn	0.05	0.48	0.89	2.78	0.55
Gln	3.18	0.50	0.88	0.78	0.86
Ser	19.37	0.19	0.31	0.83	0.90
Thr	1.09	0.92	1.65	1.07	0.73
His	2.49	0.14	0.84	0.34	1.01
Gly	2.87	0.88	0.60	13.75	0.38
Ala	0.64	2.49	0.73	0.77	2.10
Tyr	0.93	1.09	2.37	1.03	1.87
Arg	0.42	2.09	0.88	0.69	0.73
Met	1.01	0.99	25.91	0.31	0.02
Val	0.86	1.22	1.41	1.26	37.73
Pro	0.06	26.14	0.40	0.45	1.33
Trp	1.82	0.60	0.38	0.00	0.00
Phe	0.57	1.84	0.68	1.27	1.00
Lys	1.14	0.17	1.18	0.25	1.09
Ile	0.43	3.37	3.41	2.13	0.58
Leu	4.71	0.40	1.00	1.13	2.40