

Paraclique 1 (29 members)

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P07948		
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P12830		
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P22223		
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Q12959		
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Q15700		
Q562R1		
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Q96QZ7		
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014514	P78352	known
014514	Q12959	novel
014514	Q156A1	novel
014514	Q15700	novel
014514	Q92796	novel
014514	Q96QZ7	known
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Q15700	Q92796	novel
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Q562R1	Q92796	novel
Q562R1	Q9BYD9	novel
Q562R1	Q9BYX7	novel
Q92796	Q9BYX7	novel
Q9BYD9	Q9BYX7	novel
(MF)	adherens junction organization	4.84664511e-10 17.2414% (5/29) 0.1421% (32/22513)
(MF)	cell junction assembly	4.98227744e-10 20.6897% (6/29) 0.3331% (75/22513)
(MF)	cell-cell junction organization	9.85577767e-09 17.2414% (5/29) 0.2532% (57/22513)
(BP)	ATP binding	1.12495587e-08 44.8276% (13/29) 6.6273% (1492/22513)
(BP)	integrin binding	4.27579274e-08 17.2414% (5/29) 0.3376% (76/22513)
(MF)	platelet degranulation	5.54402301e-08 17.2414% (5/29) 0.3554% (80/22513)
(MF)	axon guidance	9.66504979e-08 24.1379% (7/29) 1.3592% (306/22513)
(MF)	muscle filament sliding	1.58962300e-07 13.7931% (4/29) 0.1688% (38/22513)

(BP)	guanylate kinase activity	3.14884047e-07	10.3448% (3/29)	0.0489% (11/22513)
(BP)	nucleotide binding	7.36072775e-07	44.8276% (13/29)	9.4523% (2128/22513)
(BP)	protein binding	8.43379830e-07	62.0690% (18/29)	19.9307% (4487/22513)

Paraclique 2 (29 members)

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P06731		
P07947		
P09769		
P11464		
P11465		
P12931		
P13688		
P29350		
P29353		
P31997		
P40199		
P49023		
P84022		
Q00887		
Q00888		
Q00889		
Q05209		
Q06124		
Q13046		
Q14002		
Q15235		
Q15238		
Q16557		
Q96A09		
Q9UQ72		
Q9UQ74		
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A6NMY6	P07947	novel
A6NMY6	P09769	novel
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A6NMY6	P11465	novel
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Q06124	Q15235	novel
Q06124	Q15238	novel
Q06124	Q16557	novel
Q06124	Q9UQ72	novel
Q06124	Q9UQ74	novel
Q13046	Q14002	novel
Q13046	Q15235	novel
Q13046	Q96A09	novel
Q13046	Q9UQ72	novel
Q14002	Q15235	novel
Q14002	Q15238	novel
Q14002	Q16557	novel
Q14002	Q9UQ72	novel
Q14002	Q9UQ74	novel
Q15238	Q96A09	novel
Q16557	Q96A09	novel
(MF)	female pregnancy	1.73638231e-16 31.0345% (9/29) 0.3154% (71/22513)
(BP)	protein tyrosine kinase activity	3.45198727e-09 20.6897% (6/29) 0.4575% (103/22513)
(MF)	peptidyl-tyrosine phosphorylation	5.55890051e-09 17.2414% (5/29) 0.2265% (51/22513)
(MF)	leukocyte migration	2.39344352e-07 17.2414% (5/29) 0.4753% (107/22513)
(MF)	epidermal growth factor receptor signaling pathway	6.07648267e-07 17.2414% (5/29) 0.5730% (129/22513)

Paraclique 3 (29 members)

000506
000743
043815
060285
P02811
P17844
P23508
P30153

P30154
P36873
P60510
P62714
P63151
P67775
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Q13033
Q14BN4
Q156A1
Q5VSL9
Q66LE6
Q8WZ74
Q9BUL8
Q9NRL3
Q9NVK5
Q9P289
Q9ULQ0
Q9Y2T4
Q9Y3A3
Q9Y6E0
000506 000743 novel
000506 043815 known
000506 P02811 novel
000506 P17844 novel
000506 P23508 novel
000506 P30153 known
000506 P30154 known
000506 P36873 novel
000506 P60510 novel
000506 P62714 novel
000506 P67775 known
000506 Q13033 known
000506 Q14BN4 known
000506 Q5VSL9 known
000506 Q8WZ74 novel
000506 Q9BUL8 known
000506 Q9NRL3 known
000506 Q9NVK5 known
000506 Q9P289 novel
000506 Q9ULQ0 known
000506 Q9Y3A3 known
000506 Q9Y6E0 known
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000743 Q66LE6 novel
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000743 Q9BUL8 novel
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000743 Q9Y2T4 novel
000743 Q9Y3A3 novel
000743 Q9Y6E0 novel
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043815 P60510 novel
043815 P62714 known
043815 P63151 novel

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043815	Q14BN4	known
043815	Q5VSL9	known
043815	Q66LE6	novel
043815	Q8WZ74	known
043815	Q9BUL8	known
043815	Q9NRL3	known
043815	Q9NVK5	known
043815	Q9P289	novel
043815	Q9ULQ0	known
043815	Q9Y3A3	known
043815	Q9Y6E0	known
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060285	P30154	known
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060285	P62714	novel
060285	P63151	known
060285	P67775	known
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060285	Q66LE6	novel
060285	Q9Y2T4	novel
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P02811	Q9NRL3	novel
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P02811	Q9Y3A3	novel
P02811	Q9Y6E0	novel
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P17844	Q9P289	novel
P17844	Q9Y6E0	known
P23508	P30153	known
P23508	P30154	novel
P23508	Q13033	known
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P23508	Q9BUL8	known
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P23508	Q9P289	novel
P23508	Q9ULQ0	novel
P23508	Q9Y6E0	known
P30153	P30154	known
P30153	P60510	known
P30153	P62714	known
P30153	P63151	known
P30153	P67775	known
P30153	Q00005	novel
P30153	Q13033	known
P30153	Q156A1	novel
P30153	Q5VSL9	known
P30153	Q66LE6	known
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P30153	Q9BUL8	known
P30153	Q9NRL3	known
P30153	Q9P289	novel
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P30153	Q9Y3A3	known
P30153	Q9Y6E0	known
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P30154	P62714	known
P30154	P63151	known

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P30154	Q156A1	novel
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P60510	Q5VSL9	novel
P60510	Q66LE6	novel
P60510	Q8WZ74	novel
P60510	Q9BUL8	novel
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P60510	Q9Y6E0	novel
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P62714	Q13033	known
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P62714	Q66LE6	novel
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P62714	Q9BUL8	novel
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P62714	Q9Y3A3	known
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P67775	Q13033	known
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Q00005	Q156A1	novel
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Q13033	Q9BUL8	known			
Q13033	Q9NRL3	known			
Q13033	Q9NVK5	known			
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Q14BN4	Q9Y6E0	known			
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Q156A1	Q9NRL3	novel			
Q156A1	Q9Y2T4	novel			
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Q5VSL9	Q9BUL8	known			
Q5VSL9	Q9NRL3	known			
Q5VSL9	Q9NVK5	known			
Q5VSL9	Q9P289	novel			
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Q5VSL9	Q9Y3A3	known			
Q5VSL9	Q9Y6E0	known			
Q8WZ74	Q9BUL8	known			
Q8WZ74	Q9NRL3	known			
Q8WZ74	Q9P289	novel			
Q8WZ74	Q9ULQ0	known			
Q8WZ74	Q9Y3A3	known			
Q8WZ74	Q9Y6E0	known			
Q9BUL8	Q9NRL3	known			
Q9BUL8	Q9NVK5	known			
Q9BUL8	Q9P289	novel			
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Q9BUL8	Q9Y3A3	known			
Q9BUL8	Q9Y6E0	known			
Q9NRL3	Q9P289	novel			
Q9NRL3	Q9ULQ0	novel			
Q9NRL3	Q9Y3A3	known			
Q9NRL3	Q9Y6E0	known			
Q9NVK5	Q9P289	novel			
Q9NVK5	Q9ULQ0	novel			
Q9NVK5	Q9Y3A3	known			
Q9NVK5	Q9Y6E0	known			
Q9P289	Q9ULQ0	novel			
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Q9ULQ0	Q9Y3A3	known			
Q9ULQ0	Q9Y6E0	known			
Q9Y3A3	Q9Y6E0	known			
(BP)	protein serine/threonine phosphatase activity	4.98718557e-12	20.6897% (6/29)	0.1599% (36/22513)	
(BP)	protein phosphatase type 2A regulator activity	2.83112314e-11	17.2414% (5/29)	0.0844% (19/22513)	
(BP)	protein binding	1.50499303e-09	72.4138% (21/29)	19.9307% (4487/22513)	
(MF)	protein dephosphorylation	3.45198727e-09	20.6897% (6/29)	0.4575% (103/22513)	
(BP)	armadillo repeat domain binding	2.29205105e-07	10.3448% (3/29)	0.0444% (10/22513)	
(BP)	protein phosphatase 2A binding	8.65312332e-07	10.3448% (3/29)	0.0666% (15/22513)	

Paraclique 4 (29 members)

043707
 P00533
 P02811
 P07948
 P12814
 P12830
 P15311
 P17252

P28223
P35609
P42025
P60709
P61163
P62736
P63261
P63267
P68032
P68133
P78352
P78559
Q08043
Q12959
Q156A1
Q15700
Q562R1
Q92796
Q9BYD9
Q9BYX7
Q9C0D5
043707 P02811 novel
043707 P12814 novel
043707 P12830 novel
043707 P35609 novel
043707 P42025 novel
043707 P60709 novel
043707 P61163 novel
043707 P62736 novel
043707 P63261 novel
043707 P63267 novel
043707 P68032 known
043707 P68133 novel
043707 P78352 novel
043707 Q08043 known
043707 Q12959 novel
043707 Q156A1 novel
043707 Q15700 novel
043707 Q562R1 novel
043707 Q92796 novel
043707 Q9BYD9 novel
043707 Q9BYX7 novel
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P00533 P07948 known
P00533 P12830 known
P00533 P15311 known
P00533 P17252 known
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P00533 P60709 novel
P00533 P61163 novel
P00533 P62736 novel
P00533 P63261 novel
P00533 P63267 novel
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P00533 P68133 known
P00533 P78352 novel
P00533 Q12959 novel
P00533 Q156A1 novel
P00533 Q15700 novel
P00533 Q562R1 novel
P00533 Q92796 novel
P00533 Q9BYD9 novel
P00533 Q9BYX7 novel
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P02811 P12814 novel
P02811 P12830 novel
P02811 P17252 novel
P02811 P35609 novel
P02811 P42025 novel
P02811 P60709 novel

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P02811	P62736	novel
P02811	P63261	novel
P02811	P63267	novel
P02811	P68032	novel
P02811	P68133	novel
P02811	P78352	novel
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P02811	Q9BYX7	novel
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P07948	P42025	novel
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P07948	Q15700	novel
P07948	Q562R1	novel
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P07948	Q9BYD9	novel
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P42025	Q9BYX7	novel
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P60709	P62736	novel
P60709	P63261	known
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P78352	Q12959	known
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P78559	Q562R1	novel
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Q08043	Q9BYX7	novel
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Q12959	Q562R1	novel
Q12959	Q92796	known
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Q12959	Q9BYX7	novel
Q12959	Q9C0D5	known
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Q156A1	Q562R1	novel
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Q562R1	Q9C0D5	novel
Q92796	Q9BYX7	novel
Q92796	Q9C0D5	novel
Q9BYD9	Q9BYX7	novel
Q9BYD9	Q9C0D5	novel
Q9BYX7	Q9C0D5	novel

(BP)	ATP binding	1.12495587e-08	44.8276% (13/29)	6.6273% (1492/22513)
(BP)	integrin binding	4.27579274e-08	17.2414% (5/29)	0.3376% (76/22513)
(MF)	platelet degranulation	5.54402301e-08	17.2414% (5/29)	0.3554% (80/22513)
(MF)	blood coagulation	8.00650746e-08	27.5862% (8/29)	2.0299% (457/22513)
(MF)	axon guidance	9.66504979e-08	24.1379% (7/29)	1.3592% (306/22513)
(MF)	muscle filament sliding	1.58962300e-07	13.7931% (4/29)	0.1688% (38/22513)
(MF)	platelet activation	2.05330328e-07	20.6897% (6/29)	0.9061% (204/22513)
(BP)	guanylate kinase activity	3.14884047e-07	10.3448% (3/29)	0.0489% (11/22513)
(MF)	synaptic transmission	4.98447848e-07	24.1379% (7/29)	1.7323% (390/22513)
(BP)	nucleotide binding	7.36072775e-07	44.8276% (13/29)	9.4523% (2128/22513)
(BP)	protein binding	8.43379830e-07	62.0690% (18/29)	19.9307% (4487/22513)

Paraclique 5 (29 members)

P04637		
P06493		
P08107		
P11021		
P11142		
P17066		
P24941		
P27348		
P31946		
P31947		
P34931		
P36873		
P48741		
P54652		
P61981		
P62136		
P62140		
P62258		
P62877		
P62988		
P63104		
Q00526		
Q04917		
Q13618		
Q13619		
Q13620		
Q156A1		
Q15843		
Q99459		
P04637	P06493	known
P04637	P08107	novel
P04637	P11021	novel
P04637	P11142	known
P04637	P17066	novel
P04637	P24941	known
P04637	P27348	novel
P04637	P31946	novel
P04637	P31947	known
P04637	P34931	novel
P04637	P36873	novel
P04637	P48741	novel
P04637	P54652	novel
P04637	P61981	known
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P04637	P62258	novel
P04637	P62988	novel
P04637	P63104	known
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P04637	Q04917	novel
P04637	Q156A1	novel
P04637	Q15843	known
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P06493	P11021	novel
P06493	P11142	novel
P06493	P17066	novel

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P06493	P31947	known
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Q04917	Q99459	novel
Q13618	Q15843	known
Q13619	Q15843	known
Q13620	Q15843	known
Q156A1	Q15843	novel

Q156A1 Q99459 novel

(BP)	protein domain specific binding	2.75142304e-13	31.0345%	(9/29)	0.6974%	(157/22513)
(MF)	response to unfolded protein	5.14002573e-11	20.6897%	(6/29)	0.2310%	(52/22513)
(BP)	ubiquitin protein ligase binding	7.82601760e-11	24.1379%	(7/29)	0.4886%	(110/22513)
(BP)	protein binding	1.33533847e-10	75.8621%	(22/29)	19.9307%	(4487/22513)
(MF)	protein targeting	5.94384882e-08	13.7931%	(4/29)	0.1333%	(30/22513)
(MF)	induction of apoptosis by intracellular signals	2.90787833e-07	13.7931%	(4/29)	0.1954%	(44/22513)
(BP)	cyclin binding	5.44853972e-07	10.3448%	(3/29)	0.0577%	(13/22513)
(MF)	G1/S transition of mitotic cell cycle	9.77846624e-07	17.2414%	(5/29)	0.6307%	(142/22513)

... (continued)