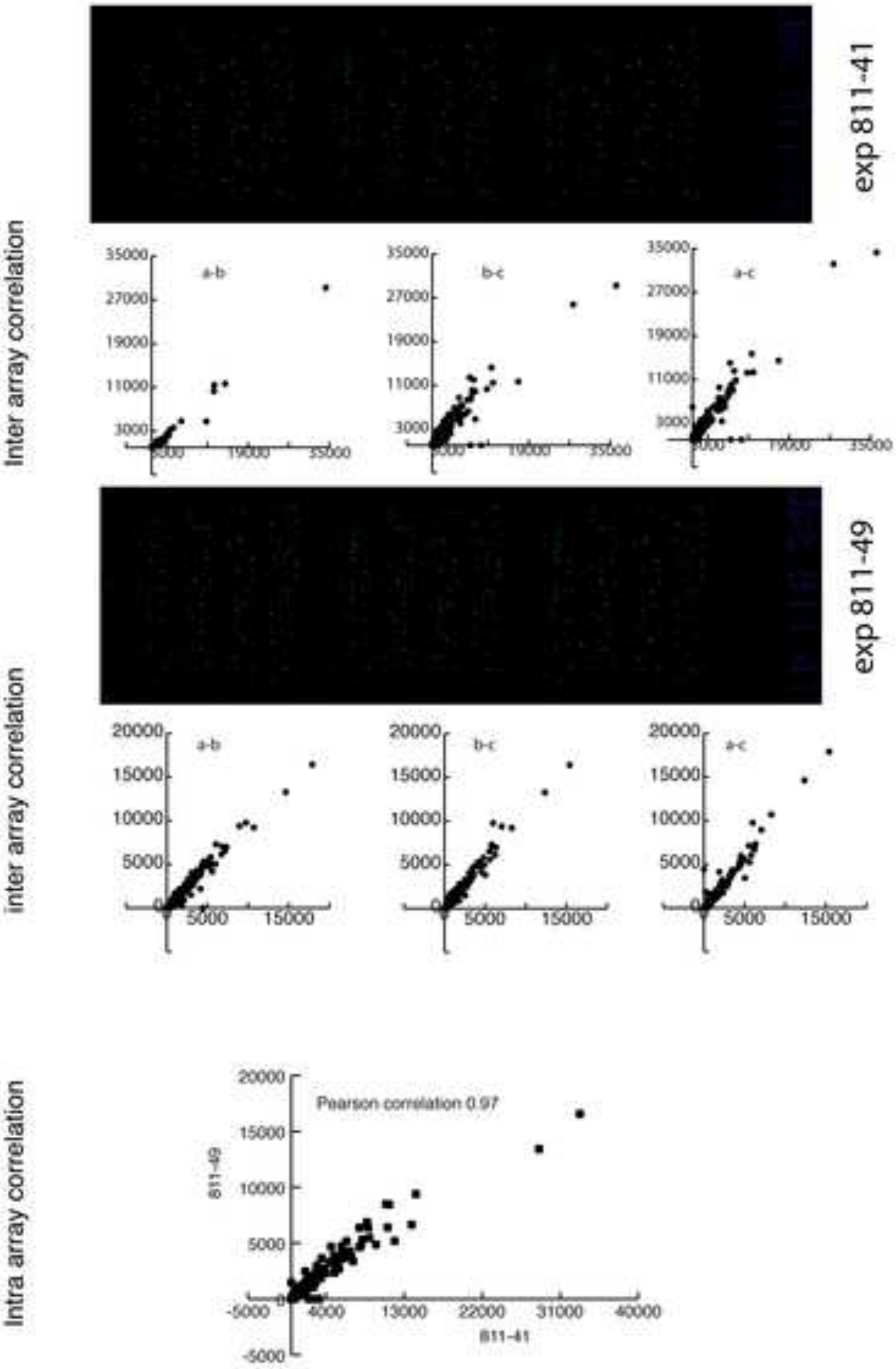
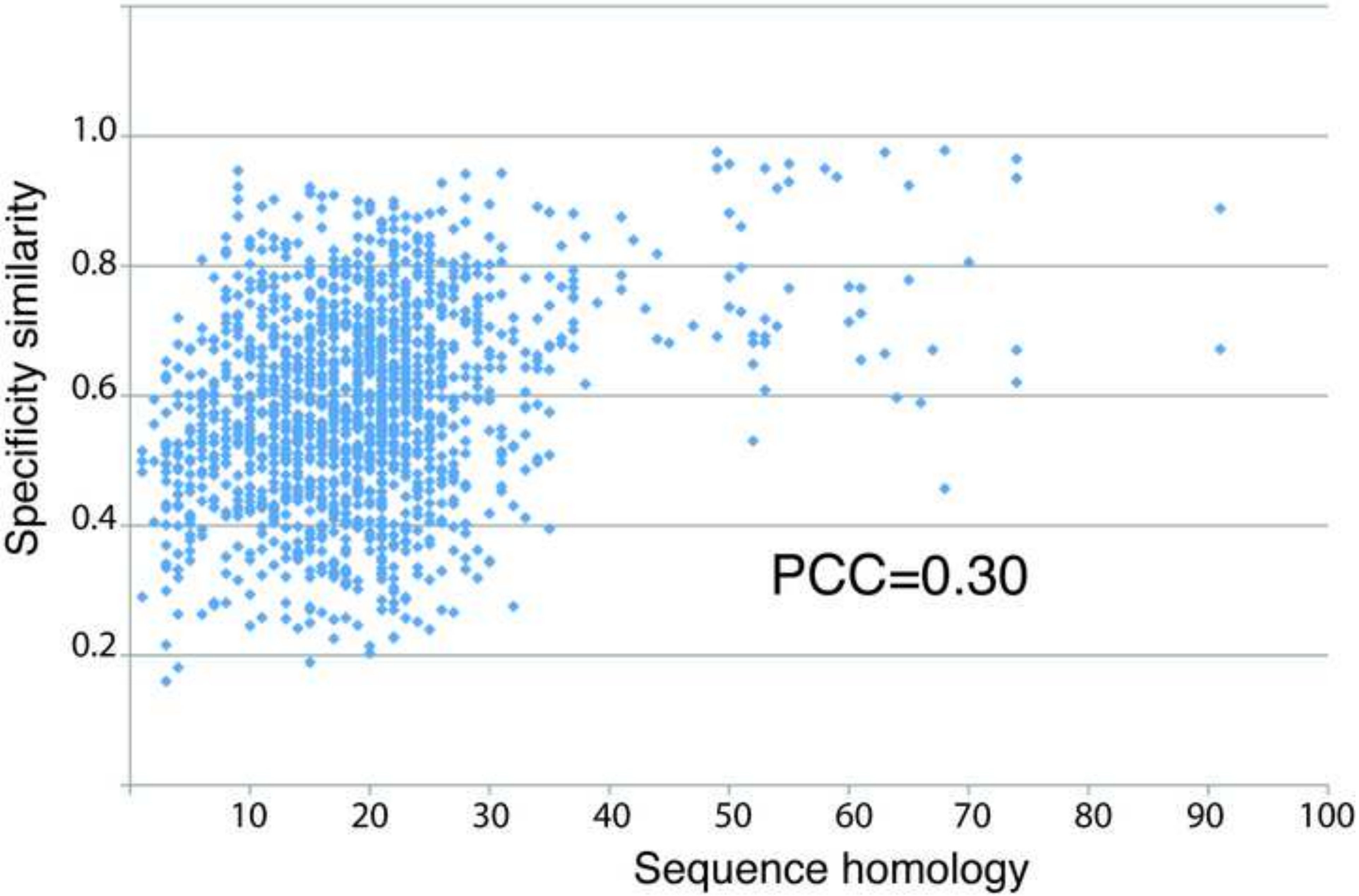
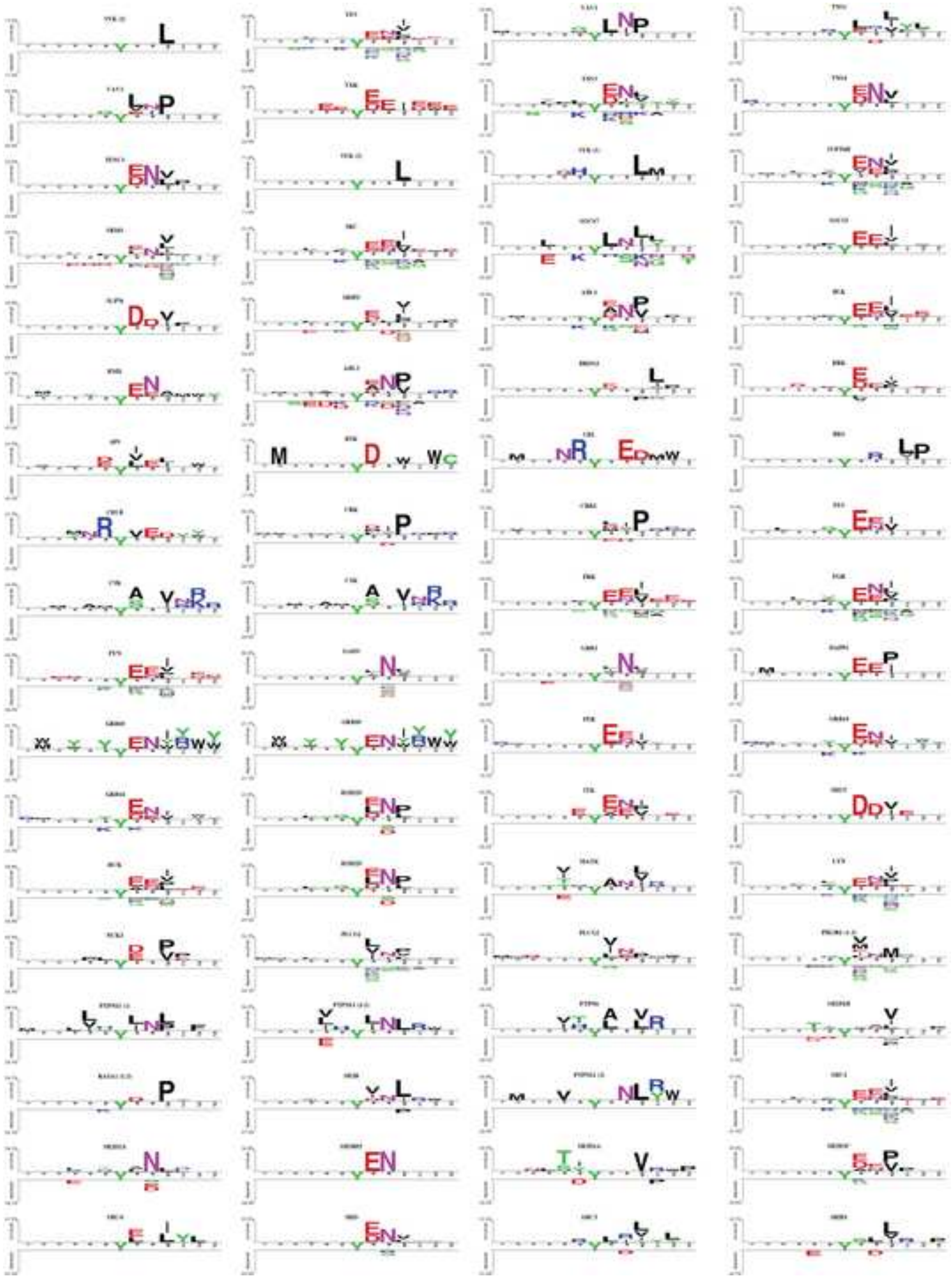
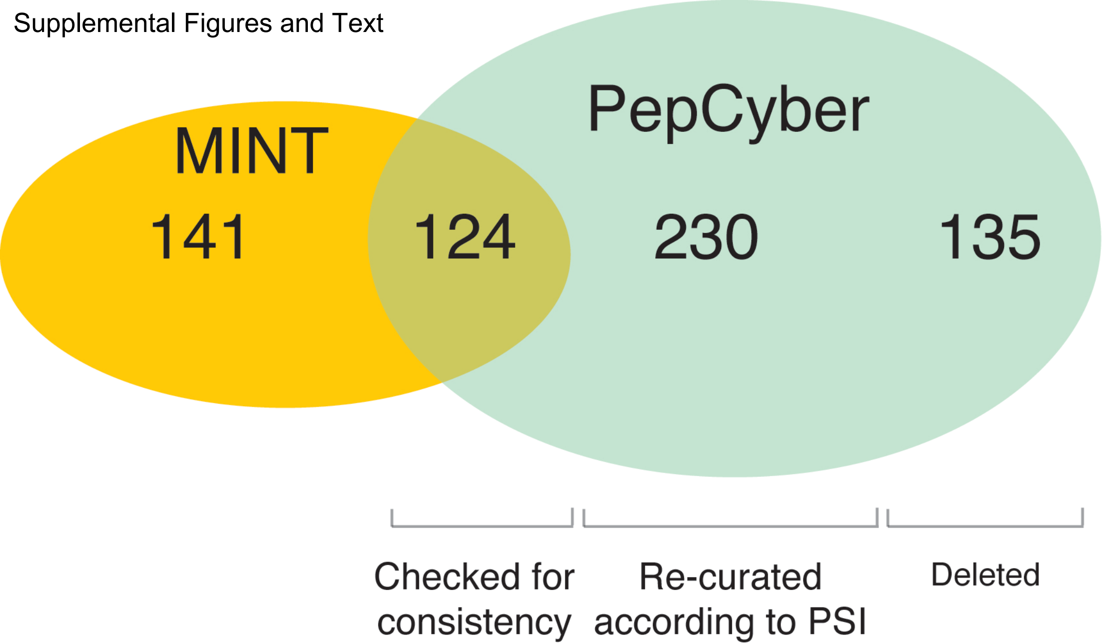
Inter experiments correlation (VAV2)

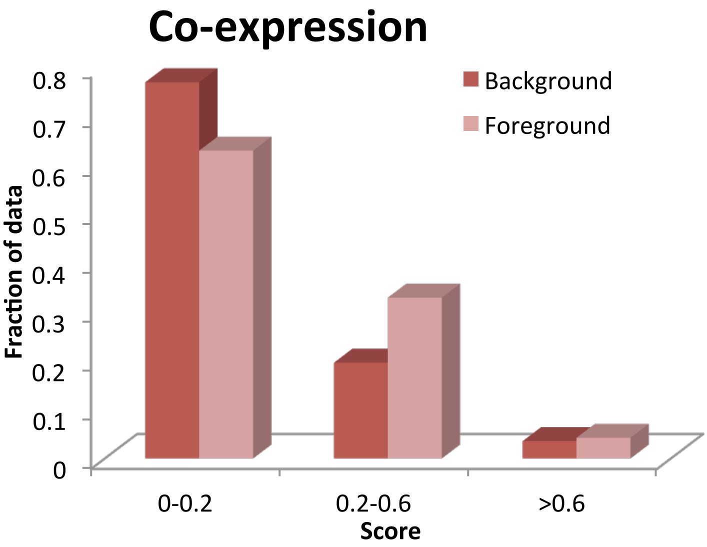


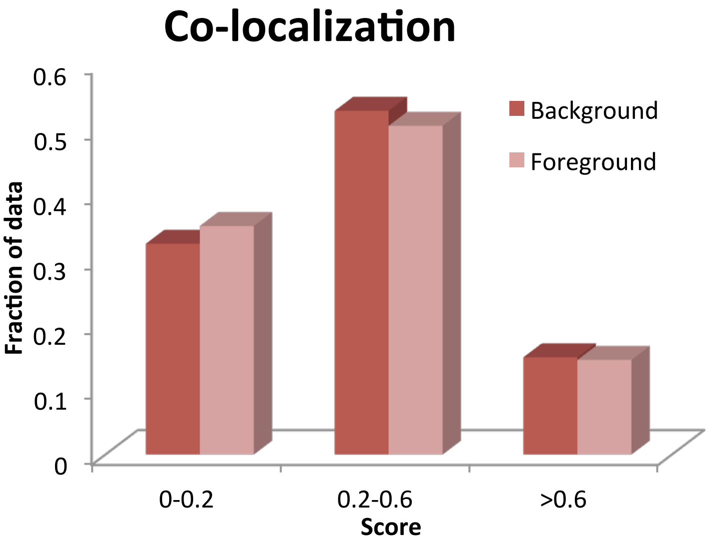

1.0
0.8
0.6
0.4
0.2
Specificity similarity
10
20
30
40
50
60
70
80
90
100
Sequence homology
PCC=0.30

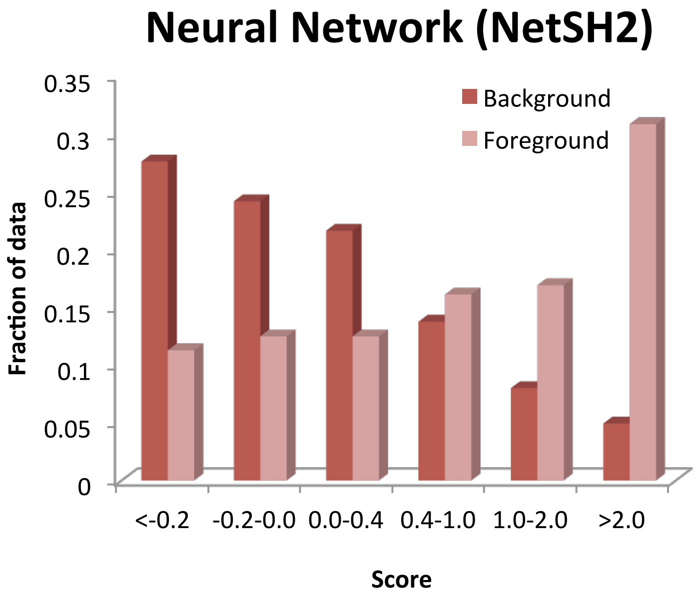


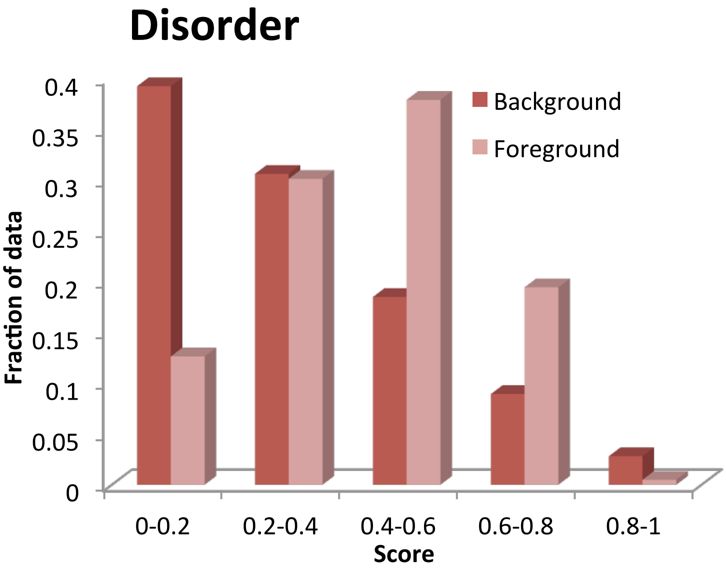
Supplemental Figures and Text

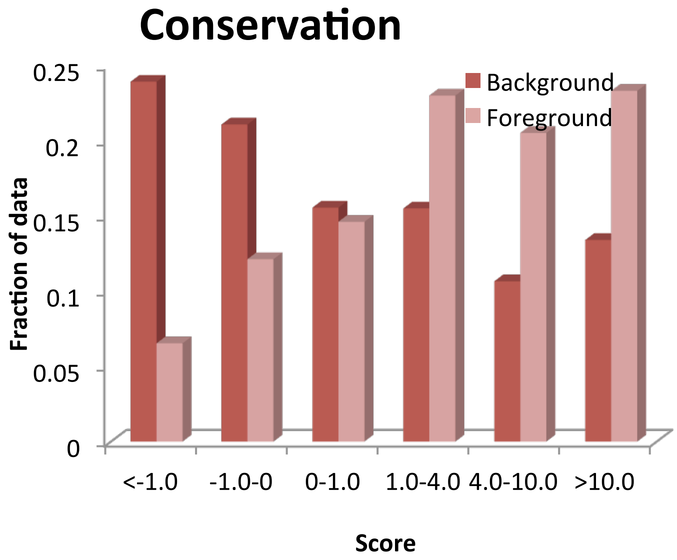


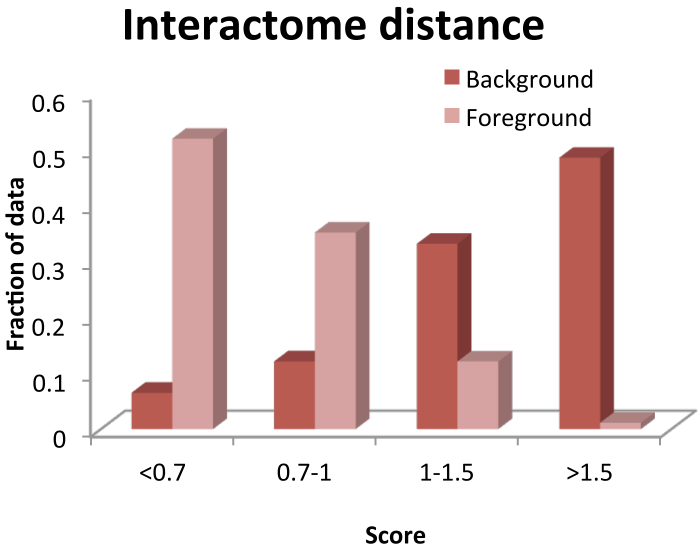

Co-expression
Background
Foreground
Fraction of data
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0-0.2
0.2-0.6
>0.6
Score

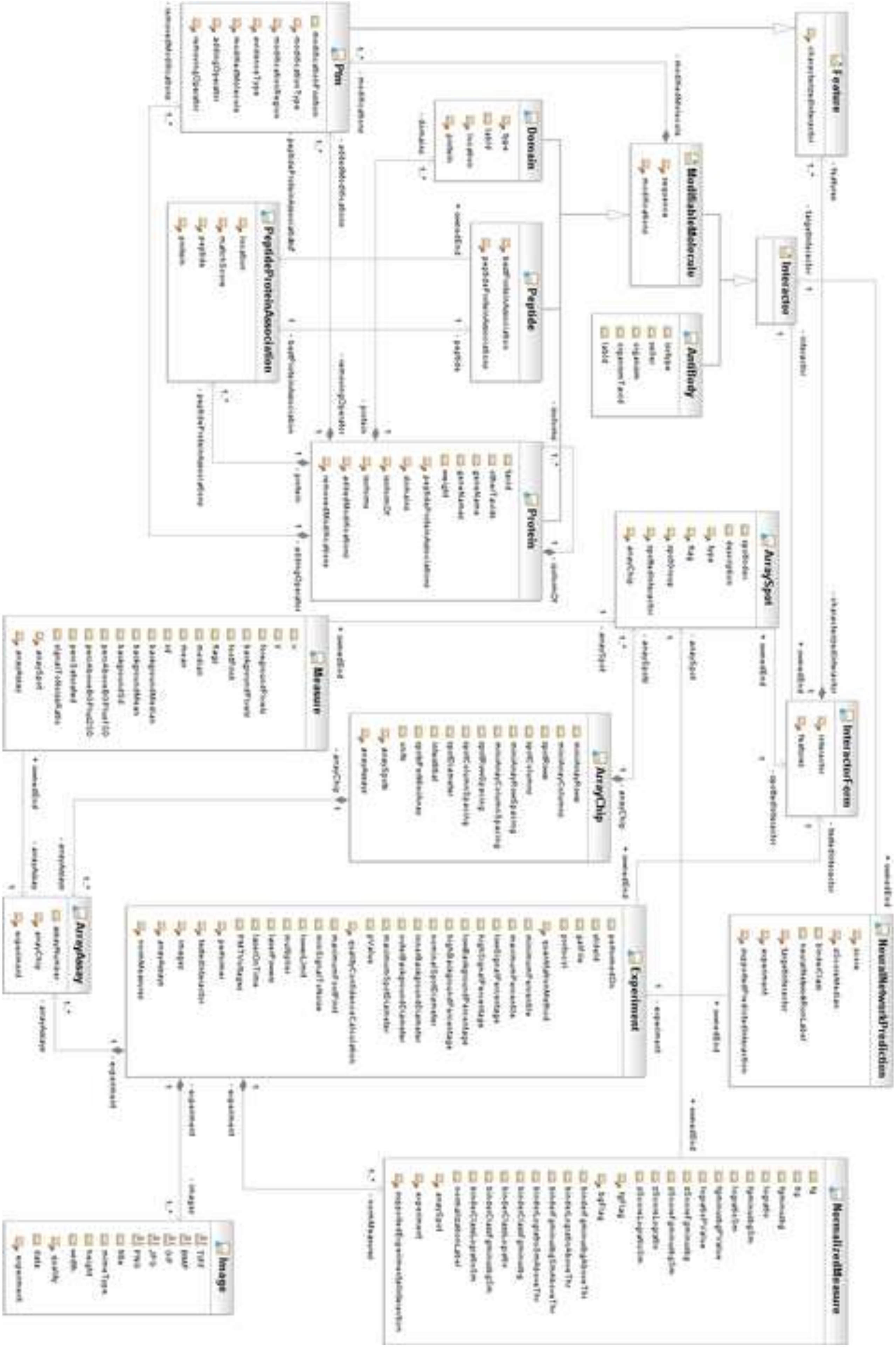

Co-localization
Background
Foreground
Fraction of data
0.6
0.5
0.4
0.3
0.2
0.1
0
0-0.2
0.2-0.6
>0.6
Score


Neural Network (NetSH2)
Background
Foreground
Fraction of data
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
<-0.2
-0.2-0.0
0.0-0.4
0.4-1.0
1.0-2.0
>2.0
Score


Disorder
Background
Foreground
Fraction of data
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0-0.2
0.2-0.4
0.4-0.6
0.6-0.8
0.8-1
Score


Conservation
Background
Foreground
Fraction of data
0.25
0.2
0.15
0.1
0.05
0
<-1.0
-1.0-0
0-1.0
1.0-4.0
4.0-10.0
>10.0
Score


Interactome distance
Background
Foreground
Fraction of data
0.6
0.5
0.4
0.3
0.2
0.1
0
<0.7
0.7-1
1-1.5
>1.5
Score


Ptm
Feature
Domain
ModifiableMolecule
Interactor
Peptide
PeptideProteinAssociation
Antibody
Protein
ArraySpot
Measure
ArrayChip
InteractorForm
NeuralNetworkPrediction
ArrayAssay
Experiment
NormalizedMeasure
Image

PEP_ID	PEP_SEQ	PEP_REF	phosphoELM_REF
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2	NLSQGGYEELERV	gi|13124040|sp|O14649|	NA
3	ALAAEGYYDIRRV	gi|17368942|sp|Q9H254|	NA
4	QHDEPCYWRLTRV	gi|24212369|sp|P82930|	NA
5	EAGKPIYSRYGSV	gi|74738536|sp|Q7L1V2|	NA
6	IVTESEYTSGHSV	gi|23397016|sp|Q9Y462|	NA
7	FTTMDLYKSSLCW	gi|74762106|sp|O43897|	NA
8	GYTYEDYQSTAEW	gi|108935929|sp|P00491	NA
9	KYLPDEYASVQAW	gi|148709183|gb|EDL411	NA
10	LRRGTKYQRFPDW	gi|146325737|sp|Q658P	NA
11	PPCFDEYKMSKEW	gi|56757653|sp|Q13029|	NA
12	IGANPLYCDCNMQ	gi|33112440|sp|O94813|	NA
13	AFFNPKYQHEGFY	gi|62901456|sp|Q8NET8	NA
14	ALVDLDYEDRPEY	gi|22095550|sp|Q9HCU4	NA
15	IIEEGKYSLVMEY	gi|60393639|sp|Q13546|	NA
16	QFSKGVYAIFGFY	gi|116242505|sp|P42261	NA
17	YLNNSNYEEGDEY	gi|27151690|sp|Q9UHW	NA
18	FPFNFSYSDYDMP	gi|33112428|sp|Q8TCW	NA
19	TRFDDWYLWVQMY	gi|17368685|sp|Q9BV94|	NA
20	GDSWEKYVHGVRY	gi|2506872|sp|P02751|F	NA
21	AKLKDYYIFNKYL	gi|97045403|sp|Q96M95|	NA
22	ALNDSKYIGMSVY	gi|12643641|sp|O75899|	NA
23	GQMKDLYHYITSY	gi|108935880|sp|Q16557	NA
24	STPKVLYEIPDTY	gi|74733187|sp|Q9BU68|	NA
25	IENMGLYEDLSSA	gi|147744560|sp|O1536	NA
26	LKDKEGYTSFWND	gi|119573912|gb|EAW53	NA
27	WMYNEQYTFVSND	gi|13123945|sp|O95477|	NA
28	DEVELSYAKNGQD	gi|126302554|sp|Q0083	NA
29	ECYDGSYAGNPQD	gi|116242808|sp|Q1502	NA
30	SYIEEPYMDIDRD	gi|25091357|sp|Q8TEL6|	NA
31	YKSEVVYFDGQSA	gi|21263499|sp|Q9BZ76|	NA
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35	IKAEELYEKDIEE	gi|119621961|gb|EAX01	NA
36	LSPSDKYPGFGFE	gi|13124629|sp|O15353|	NA
37	KIDAFHYVQLGTA	gi|74733765|sp|Q9H857|	NA
38	SGYKEYYSIPVME	gi|147742922|sp|Q7Z5J	NA
39	ICFNTSYKNGDPE	gi|117283|sp|P05093|CP	NA
40	LLPNSHYEQVMTA	gi|20455027|sp|Q9UJ83|	NA
41	FTFSPIYDKSAQE	gi|51338734|sp|O00462|	NA
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43	<<Marker>>	contol_spot	NA
44	QGFAPHYDDIEAF	gi|74733619|sp|Q9H6W	NA
45	AGVKEKYLSEYCF	gi|1705710|sp|P49961|E	NA
46	KRSSSDYAQREDF	gi|28201859|sp|Q9BZV7|	NA
47	RIYESKYWKEECF	gi|74760086|sp|Q8NAV1	NA
48	YPREGKYGHAACF	gi|1708983|sp|P52888|M	NA
49	EHEGEYYMTPRDF	gi|115502157|sp|Q8IYU	NA
50	IHLNDIYSVVGIP	gi|61248558|sp|Q9BTF0|	NA
51	SAKDGDYWRLLIP	gi|115892|sp|P16870|CB	NA

<table>
<tr><td>52</td><td>LKEANGYVLFGKP</td><td>gi|50949388|emb|CAB70</td><td>NA</td></tr>
<tr><td>53</td><td>RASAEFYVQCSLT</td><td>gi|74732914|sp|Q9BRQ3</td><td>NA</td></tr>
<tr><td>54</td><td>EGPEKEYISCQNT</td><td>gi|74721007|sp|Q9UKL3|</td><td>NA</td></tr>
<tr><td>55</td><td>HPSKPYYAPGAPT</td><td>gi|150383499|sp|O15054</td><td>NA</td></tr>
<tr><td>56</td><td>VISPEKYDIKCAV</td><td>gi|119631194|gb|EAX10</td><td>NA</td></tr>
<tr><td>57</td><td>FKTEIQYEKLADA</td><td>gi|109896161|sp|Q8IZQ1</td><td>NA</td></tr>
<tr><td>58</td><td>DGDFTVYECPGLA</td><td>gi|22261810|sp|Q9NQX5</td><td>NA</td></tr>
<tr><td>59</td><td>REKEDKYLFTILA</td><td>gi|74762719|sp|Q9BZA8|</td><td>NA</td></tr>
<tr><td>60</td><td>DEKCDYYFSVDAD</td><td>gi|62906878|sp|O00469|</td><td>NA</td></tr>
<tr><td>61</td><td>HSYNESYHCKDAD</td><td>gi|152112423|sp|Q2KHM</td><td>NA</td></tr>
<tr><td>62</td><td>KVEDPFYWVSPGV</td><td>gi|2497312|sp|Q16653|M</td><td>NA</td></tr>
<tr><td>63</td><td>QMSKFSYPTVPGV</td><td>gi|150421532|sp|Q5JPB</td><td>NA</td></tr>
<tr><td>64</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>65</td><td>HFGENGYVEATKQ</td><td>gi|37999486|sp|O95470|</td><td>NA</td></tr>
<tr><td>66</td><td>HTFKGDYSTKKHV</td><td>gi|18202503|sp|Q15223|</td><td>NA</td></tr>
<tr><td>67</td><td>MWPERIYQSPYGV</td><td>gi|74756797|sp|Q5VTH9</td><td>NA</td></tr>
<tr><td>68</td><td>REDNLYYGNLGIV</td><td>gi|147734568|sp|Q86XM</td><td>NA</td></tr>
<tr><td>69</td><td>YATLDVYNPFETR</td><td>gi|119573478|gb|EAW53</td><td>NA</td></tr>
<tr><td>70</td><td>RKEIADYLAAGKD</td><td>gi|1723119|sp|P53990|K</td><td>NA</td></tr>
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<tr><td>72</td><td>HTSNDPYCFVEFY</td><td>gi|267131|sp|Q01085|TI</td><td>NA</td></tr>
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<tr><td>75</td><td>LFHEAPYISNHPF</td><td>gi|114593095|ref|XP_001</td><td>NA</td></tr>
<tr><td>76</td><td>QAVERQYVIPGMF</td><td>gi|3123225|sp|P21399|IR</td><td>NA</td></tr>
<tr><td>77</td><td>DGLETKYMEILRF</td><td>gi|27734865|ref|NP_775</td><td>NA</td></tr>
<tr><td>78</td><td>PDDENKYFHNMQF</td><td>gi|74749827|sp|Q75V66|</td><td>NA</td></tr>
<tr><td>79</td><td>HAFDLEYHDTCSF</td><td>gi|72384339|ref|NP_963</td><td>NA</td></tr>
<tr><td>80</td><td>ASEPISYVNFTIA</td><td>gi|20454827|sp|Q9BXC9</td><td>NA</td></tr>
<tr><td>81</td><td>SDPKSRYDITGLH</td><td>gi|81175198|sp|Q9UQP3</td><td>NA</td></tr>
<tr><td>82</td><td>EFRECGYCNINPH</td><td>gi|74732358|sp|Q96MF0</td><td>NA</td></tr>
<tr><td>83</td><td>RRFEYKYSFKGPH</td><td>gi|22261801|sp|P49257|</td><td>NA</td></tr>
<tr><td>84</td><td>DFQWDYYDRMYSH</td><td>gi|108935845|sp|P07910</td><td>NA</td></tr>
<tr><td>85</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>86</td><td>QREAEVYDSSQSH</td><td>gi|14194461|sp|Q99996|</td><td>NA</td></tr>
<tr><td>87</td><td>MGYWPTYVPMEVH</td><td>gi|55977850|sp|Q13620|</td><td>NA</td></tr>
<tr><td>88</td><td>QSTDDEYALDGKI</td><td>gi|46397678|sp|Q13017|</td><td>NA</td></tr>
<tr><td>89</td><td>AWCMEVYASEKEQ</td><td>gi|33112668|sp|Q13615|</td><td>NA</td></tr>
<tr><td>90</td><td>WLDETTYEWGYKI</td><td>gi|119616435|gb|EAW96</td><td>NA</td></tr>
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<tr><td>94</td><td>WSRDPLYRDDPCK</td><td>gi|51315869|sp|Q6PJ61|</td><td>NA</td></tr>
<tr><td>95</td><td>GFERPKYFVPPDK</td><td>gi|119579560|gb|EAW59</td><td>NA</td></tr>
<tr><td>96</td><td>IRHEVIYINLKDK</td><td>gi|119599627|gb|EAW79</td><td>NA</td></tr>
<tr><td>97</td><td>FREKLAYAIAPEK</td><td>gi|266667|sp|Q01959|SC</td><td>NA</td></tr>
<tr><td>98</td><td>ALAEQVYMDWYEK</td><td>gi|56405304|sp|O75643|</td><td>NA</td></tr>
<tr><td>99</td><td>PYRKEAYLEMEFK</td><td>gi|71153483|sp|Q14966|</td><td>NA</td></tr>
<tr><td>100</td><td>CRDDPTYFAQQQK</td><td>gi|119620267|gb|EAW99</td><td>NA</td></tr>
<tr><td>101</td><td>RFNMELYKLSGRK</td><td>gi|25090820|sp|O95631|</td><td>NA</td></tr>
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108	VPNSEEYHSHLFM	gi|121948761|sp|Q14CX	NA
109	ASKKLPYKNPTHL	gi|56204806|emb|CAI22	NA
110	TRDETNYGIPQRA	gi|54037168|sp|P63244|	NA
111	STEDTWYKMVKIQ	gi|146345452|sp|Q9BS4	NA
112	FESENYYEFDVRA	gi|37999827|sp|Q9Y5F7|	NA
113	IEEDGDYKVTFHM	gi|50400545|sp|Q8IZF2|	NA
114	SAAVTSYANSASL	gi|143811424|sp|Q8WY	NA
115	CTSPFSYKNVLSL	gi|119606362|gb|EAW85	NA
116	KVSAPYYSSWGTL	gi|147744602|sp|Q8N5A	NA
117	KISKGEYGNAGIM	gi|109659849|ref|NP_05	NA
118	MILNTIYEKVAIM	gi|116242820|sp|Q4KM	NA
119	PLTTGVYVKMPPT	gi|27735177|sp|P16410|	[PLTTGVYVKMPPT|Y|2
120	PTGNHTYQEIAVP	gi|27735219|sp|P49023|	[PTGNHTYQEIAVP|Y|40
121	QLGQRIYQYIQSR	gi|3219996|sp|Q13627|D	[QLGQRIYQYIQSR|Y|27
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123	RIEEGTYGVVYRA	gi|145559452|sp|Q9UQ8	NA
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125	DIYSTDYYRVGGR	gi|94730402|sp|P04629|	[DIYSTDYYRVGGR|Y|6
126	DPSDPTYTSSLGG	gi|76803655|sp|P54753|	NA
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129	EDADENYFINEED	gi|12643788|sp|Q92569|	[EDADENYFINEED|Y|34
130	EELDENYVPMNPN	gi|90180201|sp|Q13480|	[EELDENYVPMNPN|Y|4
131	EPDEILYVNMDEG	gi|48429194|sp|P30530|	[EPDEILYVNMDEG|Y|81
132	KNVVPVYDLLLEM	gi|6166154|sp|Q92731|E	[KNVVPVYDLLLEM|Y|4
133	KIGEGTYGVVYKG	gi|115922|sp|P06493|CD	[KIGEGTYGVVYKG|Y|1
134	SVQNPVYHNQPLN	gi|2811086|sp|P00533|E	[SVQNPVYHNQPLN|Y|1
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136	LTTNEEYLDLSQP	gi|120049|sp|P21802|FG	[LTTNEEYLDLSQP|Y|76
137	FLRCINYVFFPSL	gi|90110827|sp|P17181|	[FLRCINYVFFPSL|Y|46
138	GTAEPDYGALYEG	gi|130225|sp|P19174|PL	[GTAEPDYGALYEG|Y|7
139	DKMAEAYSEIGMK	gi|23830999|sp|P20963|	[DKMAEAYSEIGMK|Y|1
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141	NEGVATYAAAVLF	gi|461854|sp|P35222|CT	[NEGVATYAAAVLF|Y|65
142	AKAVDGYVKPQIK	gi|1174462|sp|P42229|S	[AKAVDGYVKPQIK|Y|69
143	SVYESPYSDPEEL	gi|1177044|sp|P43403|Z	[SVYESPYSDPEEL|Y|31
144	AAPEARYTDIILY	gi|13432140|sp|P22455|	NA
145	VLEDNDYGRAVDW	gi|12643943|sp|Q9Y243|	[VLEDNDYGRAVDW|Y|
146	FSRPVKYEDVEHK	gi|2499640|sp|Q99759|M	NA
147	LEYDYEYDENGDR	gi|6685617|sp|Q99683|M	NA
148	<<Marker>>	contol_spot	NA
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150	NDMDDLYHNGRCG	gi|586313|sp|P38128|SM	NA
151	NNPAGLYSSENIS	gi|20178312|sp|O00151|	[NNPAGLYSSENIS|Y|15
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154	PQIQDLYGKVDFT	gi|1170586|sp|P46940|I	[PQIQDLYGKVDFT|Y|17
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158	EAPSNIYVEVEDE	gi|143811460|sp|Q9NP3	[EAPSNIYVEVEDE|Y|30
159	LNLGRTYASGYAH	gi|51702204|sp|Q9Y3S2|	[LNLGRTYASGYAH|Y|3
160	HTGEKPYKCEECG	gi|110825754|sp|Q9NZL	NA
161	LAMEATYINHNFS	gi|6685526|sp|O15371|I	NA
162	HTGEKPYECVQCG	gi|10720410|sp|P17028|	[HTGEKPYECVQCG|Y|3
163	KDPDQLYTTLKNL	gi|13431548|sp|Q92830|	[KDPDQLYTTLKNL|Y|73
164	RFHTSTYDLPGPE	gi|51338794|sp|P78559|	NA
165	CHNQDGYSYPSRQ	gi|126073|sp|P01130|LD	[CHNQDGYSYPSRQ|Y|
166	KSKQPLYSSIVTV	gi|17433153|sp|O60245|	[KSKQPLYSSIVTV|Y|94
167	STIMTDYNPNYCF	gi|146328566|sp|Q9UM7	[STIMTDYNPNYCF|Y|10
168	GMARDIYRASYYR	gi|146328566|sp|Q9UM7	[GMARDIYRASYYR|Y|1
169	<<Marker>>	contol_spot	NA
170	LAQQGEYSEAIPI	gi|6225321|sp|Q14318|F	[LAQQGEYSEAIPI|Y|265
171	SKLSDSYSNTLPV	gi|73917636|sp|Q9UQB8	[SKLSDSYSNTLPV|Y|33
172	TQPEPIYAESTKR	gi|118573870|sp|Q86YV	[TQPEPIYAESTKR|Y|41
173	NIGEDTYDIVIPV	gi|84029319|sp|Q86T24|	[NIGEDTYDIVIPV|Y|442|
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175	QPLCKPYTVVDVS	gi|118572719|sp|Q9H79	[QPLCKPYTVVDVS|Y|4
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177	QILESSYNNSNHT	gi|114814|sp|P14164|BA	NA
178	SISSPEYTFGQFS	gi|462626|sp|P33749|MS	NA
179	QSKQPAYVNKQPQ	gi|131653|sp|P25502|PU	NA
180	PISASLYVTTNNT	gi|9910692|sp|Q07928|G	NA
181	HCEVESYPQVPPV	gi|113022|sp|P21192|AC	NA
182	QCCEDAYLILRRH	gi|1171955|sp|P42338|P	NA
183	GMVCSAYDNVNKV	gi|119554|sp|P28482|MK	NA
184	INFDPVYKVKPNP	gi|729833|sp|P40189|IL6	NA
185	TPSSPMYVDLLKH	gi|1170596|sp|P45985|M	NA
186	IQFTDGYEVKEDI	gi|1730070|sp|P51812|K	NA
187	EKDETEYEYSGSE	gi|29427585|sp|O95819|	NA
188	HYWDDKYWFENTM	gi|119596609|gb|EAW76	NA
189	LWEIPPYETKGVM	gi|12230553|sp|Q92545|	NA
190	<<Marker>>	contol_spot	NA
191	WRRSGKYVYKPVM	gi|22002033|sp|O95260|	NA
192	DCSMTSYSGNQCN	gi|124106290|sp|Q9Y4C	NA
193	FPADELYGIVGAN	gi|20138731|sp|Q9HCC0	NA
194	HLQSTDYGNFLAN	gi|47606646|sp|P61421|	NA
195	FYKEGLYLVKAIN	gi|119622470|gb|EAX02	NA
196	ISSSPIYTAWNGN	gi|113430889|ref|XP_00	NA
197	RVNKPPYPKLGGN	gi|1346733|sp|P13796|P	NA
198	VNKESQYGFTPGN	gi|71153252|sp|Q9H5U8	NA
199	DGWEGAYCETNIN	gi|20455033|sp|P78504|	NA
200	HLDSGDYICQAKN	gi|37081671|sp|Q9P2V4|	NA
201	KFSETYYTRILPN	gi|119628642|gb|EAX08	NA
202	VNCRNEYAMIGNN	gi|23396597|sp|Q9BXR6	NA
203	DNEDWWYGSIGKG	gi|73921659|sp|Q8N157|	NA
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205	GGSDQNYDIVTIG	gi|73920059|sp|Q96PE3|	[GGSDQNYDIVTIG|Y|35
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214	QLERDAYVQALAR	gi|146329988|sp|Q9Y6D	NA
215	TISFEEYIRVKAR	gi|121941773|sp|Q2TAL	NA
216	VGNQPPYSRINAR	gi|134798|sp|P11277|SP	NA
217	ASFNMSYANPALG	gi|1708274|sp|P55317|H	NA
218	DVVKTRYMNSALG	gi|2497981|sp|P55851|U	NA
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220	ELEFVDYVFHGER	gi|119581049|gb|EAW60	NA
221	LLKDDVYCELAER	gi|74712933|sp|Q76M96|	NA
222	QVYMDWYEKFQDR	gi|56405304|sp|O75643|	NA
223	TGEKIAYVYPDER	gi|25091217|sp|Q8WTS	NA
224	CWDSFIYESSAFR	gi|119619483|gb|EAW99	NA
225	EPSVDDYMGMIKR	gi|6016308|sp|Q02556|IF	NA
226	GLDPEGYGNPDFC	gi|22095552|sp|Q9NYQ7	NA
227	INCERYYVPEGEC	gi|67460590|sp|Q9NZV1	NA
228	KRMKSEYKNCAEC	gi|143811449|sp|Q96EQ	NA
229	NTNFEDYESSHFC	gi|68053324|sp|Q9P0V9|	NA
230	RQENLRYNNMLKR	gi|34534829|dbj|BAC871	NA
231	AKSVTQYVFLAQR	gi|126215700|sp|Q8IZU8	NA
232	FRCPPDYPIHPPR	gi|134035344|sp|Q9H83	NA
233	LNCFTDYKDQGPR	gi|32470620|sp|Q9Y6K5|	NA
234	TNARDTYVSSFPR	gi|1174652|sp|P23193|T	NA
235	DLANDIYNINLQR	gi|913523|gb|AAB34231.	NA
236	LVSNSTYRKPPTL	gi|32472704|ref|NP_865	NA
237	VDEYEHYERVENG	gi|55976620|sp|Q9UNH5	NA
238	DGSPGKYMSHLAS	gi|51315898|sp|Q76MJ5|	NA
239	FLVKSGYAFVDCP	gi|74761835|sp|Q9NZI8|	NA
240	KCSMCKYASVEAS	gi|30172878|sp|Q8NI51|	NA
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244	SLWKWKYEELKES	gi|71153214|sp|Q68D86|	NA
245	YWMEDIYTPGYDS	gi|32699623|sp|Q9UPX6	NA
246	EAVELCYKNVNES	gi|38258635|sp|Q96RI9|	NA
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248	RTSETSYLNEAFS	gi|73620041|sp|Q8N9R8	NA
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250	SGRETIYPNASLL	gi|3172147|gb|AAC1843	NA
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253	ETTKNVYEEIAAP	gi|399227|sp|Q02224|CE	NA
254	MGYWPTYVPMEVH	gi|55977850|sp|Q13620|	NA
255	FLASPEYVNLPIN	gi|121746|sp|P09211|GS	NA
256	RTSLDLYANVIHC	gi|1708404|sp|P51553|ID	NA
257	CWCSYKYLNAGAG	gi|3913982|sp|Q16719|K	NA
258	LNSSRHYLNIRYT	gi|21431783|sp|O43451|	NA
259	RADLGAYLNPRPP	gi|17369917|sp|Q9Y3R4|	NA

260	LGHPKVYINLDKE	gi|6093600|sp|O75380|N	NA
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262	SAGCAAYMAPERI	gi|6831583|sp|O14733|M	NA
263	TSMSPDYPNPMFE	gi|38258929|sp|P78527|	NA
264	AIAVDRYLRVKLT	gi|1351831|sp|P33765|A	NA
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268	LEGRHIYIYVPDP	gi|129892|sp|P16234|PG	NA
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270	WSKEGFYAVVIFL	gi|134039192|sp|Q1525	NA
271	GVPDSDYINASFI	gi|126467|sp|P18433|PT	NA
272	LQESTGYMAPTLR	gi|18202506|sp|Q15413|	NA
273	EVQKDTYVMAVNC	gi|41017504|sp|Q9HC56	NA
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275	LRGMDYYASGAPC	gi|55958905|emb|CAI15	NA
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278	PTFGPCYINLYGS	gi|20137708|sp|O75923|	NA
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280	LKAMDGYFNLTMS	gi|1730136|sp|P51993|F	NA
281	APPGEEYGDGSPS	gi|119576126|gb|EAW55	NA
282	GDDSEIYEILSPS	gi|119605696|gb|EAW85	NA
283	LGPSDIYLDDLPS	gi|71153524|sp|Q9BQK8	NA
284	ASLSPQYVSYNQS	gi|1705571|sp|P32004|L	NA
285	PASKTGYSFTATS	gi|116256100|sp|Q5T2D	NA
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288	ACEEIAYQVAGVS	gi|12643896|sp|Q9UL36|	NA
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305	ETDKEYYTVKDDR	gi|125060|sp|P23458|JA	[ETDKEYYTVKDDR|Y|1
306	RAKIQDYHILTRK	gi|12643404|sp|O60674|	[RAKIQDYHILTRK|Y|221
307	SEDIKSYYTVRQL	gi|131467|sp|P18031|PT	[SEDIKSYYTVRQL|Y|15
308	APTSFGYDKPHVL	gi|124474|sp|P15260|IN	[APTSFGYDKPHVL|Y|45
309	KMNEVTYSTLNFE	gi|3172147|gb|AAC1843	[KMNEVTYSTLNFE|Y|4
310	LGRREEYDVLDKR	gi|23830999|sp|P20963|	[LGRREEYDVLDKR|Y|8
311	SKPKKSYIATQGC	gi|84028248|sp|Q06124|	[SKPKKSYIATQGC|Y|32

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<tr><td>326</td><td>PAEDSTYDEYEND</td><td>gi|2498954|sp|Q14247|S</td><td>[PAEDSTYDEYEND|Y|4</td></tr>
<tr><td>327</td><td>FITC</td><td>contol_spot</td><td>NA</td></tr>
<tr><td>328</td><td>IgG</td><td>contol_spot</td><td>NA</td></tr>
<tr><td>329</td><td>pY</td><td>contol_spot</td><td>NA</td></tr>
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<tr><td>333</td><td>HELGQDYEHVTML</td><td>gi|116242799|sp|Q0108</td><td>NA</td></tr>
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<tr><td>335</td><td>YEYPSRYQKDVYD</td><td>gi|8134360|sp|Q14511|C</td><td>NA</td></tr>
<tr><td>336</td><td>DREDDQYSHLQGN</td><td>gi|115993|sp|P09693|CD</td><td>[DREDDQYSHLQGN|Y|1</td></tr>
<tr><td>337</td><td>VTVVSQYDNLEDY</td><td>gi|131573277|gb|ABO33</td><td>NA</td></tr>
<tr><td>338</td><td>KGRARQYTSPEEI</td><td>gi|2498464|sp|Q13442|H</td><td>NA</td></tr>
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<tr><td>344</td><td>GSISNMYAVNLAR</td><td>gi|116241317|sp|Q9Y60</td><td>NA</td></tr>
<tr><td>345</td><td>IKRKIPYILKRQL</td><td>gi|2828196|sp|P30990|N</td><td>NA</td></tr>
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367	MHATSQYMWGVQD	gi|112894|sp|P21580|TN	NA
368	PRAPSGYSQPPSV	gi|120659962|gb|AAI306	NA
369	LPFYEVYGELIRP	gi|56405390|sp|Q9Y6X2|	NA
370	PYIAWGYPNLKSV	gi|133021|sp|P18124|RL	NA
371	RREFEVYGPIKRI	gi|13635663|sp|P08621|	NA
372	ACRVAPYVNVGAL	gi|145559528|sp|O6090	NA
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374	CHIDALYPNVENM	gi|30316344|sp|O15457|	NA
375	CIYNTTYLNVQRE	gi|112877|sp|P02763|A1	NA
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377	IRAHTPYINIYNC	gi|115968|sp|P11836|CD	NA
378	ESRSEIYGLVQRC	gi|34395525|sp|Q9NZN5	NA
379	CQELDTYLIPQIP	gi|728984|sp|P38398|BR	NA
380	SDRSAWYMGPVSR	gi|1169094|sp|P46109|C	NA
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382	LQMAQIYINALSE	gi|3913115|sp|Q92858|A	NA
383	QLRRAAYLNLSQE	gi|88911273|sp|Q12873|	NA
384	PPVIIKYIIINRF	gi|143811385|sp|O6067	NA
385	RIEIATYLNLSEK	gi|27923786|sp|Q9H4S2|	NA
386	LPAGELYGWAVET	gi|116242593|sp|Q9298	NA
387	TETRTNYPNIFRI	gi|119370323|sp|Q1628	NA
388	DTKFRNYLIPKGT	gi|117225|sp|P10632|CP	NA
389	QVKKKLYEEIDQN	gi|117283|sp|P05093|CP	NA
390	RPEGAEYINPGER	gi|76803797|sp|Q99698|	NA
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392	THNWTVYLNPRRS	gi|90110050|sp|Q04671|	NA
393	KICANHYITPMME	gi|1172837|sp|P43487|R	NA
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410	EEEEDGYRAVLMQ	gi|1008842|gb|AAC4191	NA
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416	FVKCERYKETSCY	gi|59803114|sp|Q9NVE5	NA
417	KTPHGDYIEFPCY	gi|126407|sp|P09917|LO	NA
418	LTTKPDYAGHQLQ	gi|74735576|sp|O95149|	NA
419	VINKDEYYSRPLQ	gi|118186|sp|P28325|CY	NA
420	EDKSPEYFYVGLY	gi|23503099|sp|O60636|	NA
421	KPECEGYDPNALY	gi|116241332|sp|Q9BTC	NA
422	RMRAPDYTTPEMY	gi|9087218|sp|P35968|V	NA
423	YRNEGFYADPYLY	gi|147733121|sp|Q5T5P	[YRNEGFYADPYLY|Y|3
424	IVYEDPYQVSLQY	gi|74732294|sp|Q96M34|	NA
425	IVIDKSYMNPGDQ	gi|12643310|sp|Q92754|	NA
426	GLPVTSYVSINSA	gi|13878435|sp|Q9Y5I4|	NA
427	HVSDWTYSEGALD	gi|116241278|sp|P23280	NA
428	VTTKELYPEFGLD	gi|119608174|gb|EAW87	NA
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431	CGTEVRYVIDYYD	gi|1705694|sp|P53701|C	NA
432	FGAVDLYVSTSYD	gi|46395756|sp|Q7Z7M0	NA
433	MSELPSYGEMAAE	gi|146286138|sp|Q8NDI1	NA
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435	HQVEEDYLFEKAE	gi|119620706|gb|EAX00	NA
436	CSSELKYSMELDE	gi|71151883|sp|Q5JRC9|	NA
437	LKYNNVYVYPPWG	gi|1352525|sp|P48065|S	NA
438	AGEATAYASKDLE	gi|1718154|sp|P49767|VI	NA
439	IMPADYYCNTLTA	gi|23822260|sp|Q9BYX2	NA
440	FNAMGKYVDKRLE	gi|2851393|sp|P16435|N	NA
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447	YQEAEDYPYGPVE	gi|114152779|sp|Q1283	NA
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459	VWKENKYMKRDWL	gi|33604031|gb|AAH562	NA
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<tr><td>469</td><td>LDSKLNYKPPPQK</td><td>gi|1707893|sp|P52566|G</td><td>[LDSKLNYKPPPQK|Y|2</td></tr>
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<tr><td>474</td><td>SCQNLGYTAASPQ</td><td>gi|143811460|sp|Q9NP3</td><td>[SCQNLGYTAASPQ|Y|3</td></tr>
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<tr><td>477</td><td>TKRDIYYTDSQLF</td><td>gi|7674367|sp|Q9Y5K1|</td><td>NA</td></tr>
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<tr><td>481</td><td>LYWKSIYISMTGH</td><td>gi|11467315|ref|NP_043</td><td>NA</td></tr>
<tr><td>482</td><td>VTPAEPYARVLFH</td><td>gi|121940967|sp|Q24JP</td><td>NA</td></tr>
<tr><td>483</td><td>GNDCDLYAHHSTA</td><td>gi|416926|sp|P32249|EB</td><td>NA</td></tr>
<tr><td>484</td><td>FFDGDCYIILAIH</td><td>gi|138529|sp|P09327|VIL</td><td>NA</td></tr>
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<tr><td>487</td><td>KVSFPKYRINKLH</td><td>gi|4206388|gb|AAD1162</td><td>NA</td></tr>
<tr><td>488</td><td>YGDMDIYITASGI</td><td>gi|74750586|sp|Q86Z14|</td><td>NA</td></tr>
<tr><td>489</td><td>LLESTLYESSVVP</td><td>gi|62901470|sp|Q9HBA0</td><td>NA</td></tr>
<tr><td>490</td><td>VCNEHRYGYMNVP</td><td>gi|119608194|gb|EAW87</td><td>NA</td></tr>
<tr><td>491</td><td>KKLGPDYVDLFII</td><td>gi|74744643|sp|Q5T2L2|</td><td>NA</td></tr>
<tr><td>492</td><td>VKDMVEYKDRCMA</td><td>gi|1168366|sp|P43652|A</td><td>NA</td></tr>
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<tr><td>495</td><td>VRSKWEYDESHVI</td><td>gi|29840801|sp|Q9Y6J8|</td><td>NA</td></tr>
<tr><td>496</td><td>GHEFDLYENKDYI</td><td>gi|123116|sp|P14210|HG</td><td>NA</td></tr>
<tr><td>497</td><td>LTHPPLYESVTWI</td><td>gi|115449|sp|P00915|CA</td><td>NA</td></tr>
<tr><td>498</td><td>PSYEDLYTQNVVI</td><td>gi|116242812|sp|P29083</td><td>NA</td></tr>
<tr><td>499</td><td>GWSEDSYYEALAK</td><td>gi|74761958|sp|Q9UHR5</td><td>NA</td></tr>
<tr><td>500</td><td>QDNEWNYTRAGQA</td><td>gi|20978536|sp|Q9GZY0</td><td>NA</td></tr>
<tr><td>501</td><td>LKSALAYVDGKCC</td><td>gi|2494289|sp|Q99435|N</td><td>NA</td></tr>
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<tr><td>503</td><td>ARPCPDYCRNVLK</td><td>gi|462190|sp|P35052|GP</td><td>NA</td></tr>
<tr><td>504</td><td>STVFEEYEKIANK</td><td>gi|126302519|sp|P13928</td><td>NA</td></tr>
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<tr><td>509</td><td>RFREVPYAYIREG</td><td>gi|60392771|sp|P50281|</td><td>NA</td></tr>
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<tr><td>512</td><td>HFDMTTYLASGGL</td><td>gi|148744318|gb|AAI426</td><td>NA</td></tr>
<tr><td>513</td><td>KVAMDDYLKNVML</td><td>gi|74708170|sp|Q5S007|</td><td>NA</td></tr>
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<tr><td>515</td><td>LWSNTAYPSLKPL</td><td>gi|119619961|gb|EAW99</td><td>NA</td></tr>
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651	RHVKDLYLIPLSA	gi|116241332|sp|Q9BTC	NA
652	KLSGEAYGFVARI	gi|401413|sp|P04275|V	NA
653	KKLAELYGEIESE	gi|3023435|sp|Q13634|C	NA
654	PNEDCLYLNVYVP	gi|31076855|sp|Q9NZ94|	NA
655	DIHVGDYIIPKNT	gi|3182968|sp|O15528|C	NA
656	PPERIIYANPCKQ	gi|118377|sp|P11926|DC	NA
657	DLRTAAYVNAIEK	gi|118541|sp|P00367|DH	NA
658	AAFQFSYTAVFGA	gi|13431529|sp|Q9Y256|	NA
659	AVCFFSYLRVSRD	gi|121137|sp|P21217|FU	NA
660	LKQIPRYLIPCYF	gi|116242491|sp|P35573	NA
661	FLMHSVYQPQPSA	gi|34222653|sp|Q9NSY1	NA
662	CKVESIYLNVEAV	gi|2507178|sp|P16118|F	NA
663	FSSSEIYGLIKTG	gi|12230076|sp|Q14410|	NA
664	VLRKEAYGKPVDI	gi|12643413|sp|Q13554|	NA
665	NLLGELYGKAGLN	gi|1170685|sp|P46019|K	NA
666	TLGTAAYMAPEVI	gi|6685621|sp|Q9Y6R4|	NA
667	SQCIHLYTAVLRG	gi|126302596|sp|P08922	NA
668	VHVNATYVNVKCV	gi|125484|sp|P08581|ME	[VHVNATYVNVKCV|Y|1
669	APLCSSYLIPKEI	gi|1709020|sp|P41594|M	NA
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671	GSAIVMYMAPKSR	gi|85692724|sp|Q96R48|	NA
672	SFQKSFYINAHIR	gi|2495042|sp|Q99677|P	NA
673	LVYVTRYLDNGLC	gi|92090608|sp|P35475|	NA
674	PTKCDCYTASPKC	gi|145559531|sp|Q8WW	NA
675	SPTNPGYVVPCNC	gi|6831689|sp|O95416|S	NA

676	NRNEPEYNISQPG	gi|12643957|sp|Q9Y618|	NA
677	SSFCVHYVNLLPG	gi|13623347|gb|AAH062	NA
678	AGSYSSYVQVRGS	gi|2497367|sp|Q92562|S	NA
679	LGAEMDYVEDKLS	gi|119605300|gb|EAW84	NA
680	PTQEETYPSNILS	gi|62899891|sp|Q9HC77	NA
681	SEPSIDYLDSKLS	gi|143458429|sp|Q9P2F	NA
682	CESCPLYKKLRLS	gi|83300977|sp|P42575|	NA
683	MLDKLRYVFSQMS	gi|13626370|sp|O60941|	NA
684	WPHEGLYEKPSLS	gi|14329506|emb|CAC4	NA
685	RRYFTGYVINGGP	gi|61212254|sp|Q9Y5Z6|	NA
686	GGDKETYNNIIRS	gi|46397621|sp|P98088|	NA
687	CHSTVDYATFYRS	gi|116241270|sp|Q8N8U	NA
688	LETEEHYKSRWRS	gi|119625598|gb|EAX05	NA
689	MQKNGGYIWIQSS	gi|38604888|sp|Q8IXF0|	NA
690	VWRMEIYLSLGVL	gi|146325737|sp|Q658P	NA
691	DPSEFEYLFSKDT	gi|119612677|gb|EAW92	NA
692	GMKKLSYIRIADT	gi|129951|sp|P07585|PG	NA
693	LRSMSLYLSNKDT	gi|85701302|sp|Q96JB2|	NA
694	TFNKCDYDSMGDT	gi|119578213|gb|EAW57	NA
695	EKGEEQYGADGET	gi|116242672|sp|Q1468	NA
696	VCEELTYEEIRDT	gi|3023733|sp|Q16875|F	NA
697	SVDSSLYNLPRSY	gi|90180201|sp|Q13480|	[SVDSSLYNLPRSY|Y|25
698	YATEAVYESAEAP	gi|2498954|sp|Q14247|S	[YATEAVYESAEAP|Y|47
699	SDGMMDYSGPPSG	gi|127624|sp|P15172|MY	[SDGMMDYSGPPSG|Y|
700	EANYHLYGSRMDR	gi|60393639|sp|Q13546|	[EANYHLYGSRMDR|Y|3
701	GPLGPLYASSNPE	gi|33112647|sp|P06213|	[GPLGPLYASSNPE|Y|9
702	NSSDSDYDLHGAQ	gi|116024|sp|P06127|CD	[NSSDSDYDLHGAQ|Y|4
703	GQYGEVYEGVWKK	gi|85681908|sp|P00519|	[GQYGEVYEGVWKK|Y|
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705	RWDDLHYRLTDLG	gi|13124441|sp|O14939|	NA
706	SPGHTIYAKVDNE	gi|56404432|sp|O14639|	[SPGHTIYAKVDNE|Y|37
707	TAGLSTYLYNRQR	gi|68067956|sp|P05362|	[TAGLSTYLYNRQR|Y|5
708	AASKQKYLENYLN	gi|13124441|sp|O14939|	NA
709	RGKSTYYWPRPRR	gi|3023873|sp|Q13067|G	NA
710	TPSPKSYENLWFQ	gi|729564|sp|Q99062|CS	[TPSPKSYENLWFQ|Y|7
711	FREDEGYIKEEER	gi|1345813|sp|P16389|K	[FREDEGYIKEEER|Y|13
712	QDNSGTYGKIWEG	gi|547803|sp|Q05655|KP	NA
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716	LPSSPVYEDAASF	gi|2498954|sp|Q14247|S	[LPSSPVYEDAASF|Y|42
717	PSFSTIYQELQSI	gi|115502390|sp|P07332	[PSFSTIYQELQSI|Y|811
718	RPPGLEYCYNPSH	gi|120046|sp|P11362|FG	[RPPGLEYCYNPSH|Y|5
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721	TANVVYYVGENVV	gi|2499575|sp|Q15139|K	[TANVVYYVGENVV|Y|5
722	AAQDEFYRSGWAL	gi|729887|sp|P41240|CS	[AAQDEFYRSGWAL|Y|1
723	DFREYEYDLKWEF	gi|544320|sp|P36888|FL	[DFREYEYDLKWEF|Y|5
724	EFMCKVYSDPQPH	gi|120046|sp|P11362|FG	[EFMCKVYSDPQPH|Y|2
725	KSGFEGYVELPPI	gi|1345923|sp|P32927|IL	[KSGFEGYVELPPI|Y|76
726	LQQVGDYCFLPGL	gi|1345923|sp|P32927|IL	[LQQVGDYCFLPGL|Y|8
727	EDDLPVYLARPGT	gi|50417352|gb|AAH770	NA

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<tr><td>730</td><td>SPTSPTYSPTTPK</td><td>gi|133326|sp|P24928|RP</td><td>NA</td></tr>
<tr><td>731</td><td>TSSGQRYFLNHID</td><td>gi|1175423|sp|P46937|Y</td><td>NA</td></tr>
<tr><td>732</td><td>DGSVIDYELIDQD</td><td>gi|113950|sp|P07355|AN</td><td>NA</td></tr>
<tr><td>733</td><td>LKIDEDYKEKTVI</td><td>gi|62903511|sp|Q07617|</td><td>NA</td></tr>
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<tr><td>752</td><td>REELTRYLFVLQL</td><td>gi|14916925|sp|Q9HCM</td><td>NA</td></tr>
<tr><td>753</td><td>DYYDRMYSYPARV</td><td>gi|108935845|sp|P07910</td><td>NA</td></tr>
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<tr><td>759</td><td>IPLQETYDVCEQP</td><td>gi|2495730|sp|Q92558|</td><td>[IPLQETYDVCEQP|Y|12</td></tr>
<tr><td>760</td><td>DSWEQNYSPGEGF</td><td>gi|30913162|sp|Q8TEW</td><td>NA</td></tr>
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<tr><td>772</td><td>FCGTIEYMAPEII</td><td>gi|37999483|sp|O75676|</td><td>NA</td></tr>
<tr><td>773</td><td>EIDEETYEEIYKS</td><td>gi|61227725|sp|P62310|</td><td>NA</td></tr>
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<tr><td>775</td><td>GFTGLTYANPQGC</td><td>gi|2497600|sp|Q13751|L</td><td>NA</td></tr>
<tr><td>776</td><td>FVPSNNYIIPNKS</td><td>gi|48429157|sp|P61812|</td><td>NA</td></tr>
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783	TAAMQKYPNPMNP	gi|26392626|sp|Q9Y3B1|	NA
784	PDPTTVYVDMRAL	gi|32700084|sp|Q14689|	NA
785	REIQGGYMDMYRR	gi|145559499|sp|O1504	NA
786	KQLQLSYVEMYQR	gi|6136547|sp|O60299|K	NA
787	EALDKVYEEIEKD	gi|8134317|sp|O43520|A	NA
788	QRTPENYPNAGLT	gi|114062|sp|P08519|AP	NA
789	PYLMEAYGPIPAY	gi|12585187|sp|P82251|	NA
790	SIFFIIYIIIVAF	gi|116241275|sp|Q0166	NA
791	SSYYVFYIYVGVA	gi|147744553|sp|P13569	NA
792	IFFFVSYIIISFL	gi|119631737|gb|EAX11	NA
793	SRDYNPYNYSDSI	gi|77416392|sp|O75122|	NA
794	FLGNLPYDVTEES	gi|124219|sp|P23588|IF4	NA
795	GLARDIYKNPDYV	gi|143811474|sp|P17948	NA
796	SRASISYGSNMRP	gi|71151982|sp|Q7Z406|	NA
797	AILDHTYSKHVKS	gi|23396462|sp|O94805|	NA
798	GVAKETYKSLPKL	gi|17369704|sp|Q9ULB1|	NA
799	G1:17	contol_spot	NA
800	G5:17	contol_spot	NA
801	LVGAPTYDDVSKV	gi|126302583|sp|P80108	NA
802	YPHKTLYVPNRKV	gi|74760061|sp|Q8NA75|	NA
803	PPDWTDYNDFELQ	gi|126469|sp|P23467|PT	NA
804	QDELDHYINHLLQ	gi|1170685|sp|P46019|K	NA
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806	HFFAPEYGEVTNV	gi|74761962|sp|Q9UHY1	NA
807	YVPRTYYANPAVV	gi|1705606|sp|P07498|C	NA
808	FMIQEEYVDTVSG	gi|18201966|sp|O15399|	NA
809	DISWDPYQPNRVV	gi|119620540|gb|EAX00	NA
810	LYLMEDYVGSPVV	gi|128581|sp|P20783|NT	NA
811	AWNDQGYEHTAED	gi|73621409|sp|Q8WZA1	NA
812	LKKEPLYVGVDDD	gi|20532388|sp|Q9NVP1	NA
813	KEFKNDYKKLSMQ	gi|6686048|sp|Q9Y210|T	NA
814	ERFEGPYTDFTPW	gi|146328628|sp|Q9954	NA
815	LATETVYVDDASW	gi|118572728|sp|Q1278	NA
816	RKSFDEYWAHTRW	gi|31652312|emb|CAD9	NA
817	TLSNEEYMYAYRW	gi|1350587|sp|P48382|R	NA
818	WLSCQEYEEEGPW	gi|10720024|sp|Q9UBN7	NA
819	YDDMDYYFGPPPP	gi|62089074|dbj|BAD929	NA
820	FESEVRYQCNPGY	gi|148886654|ref|NP_69	NA
821	LEQMPDYSIFRGY	gi|145559531|sp|Q8WW	NA
822	NGSGAPYVYHAIY	gi|74719655|sp|Q9NZI7|	NA
823	SDYELKYCFVDKY	gi|74759693|sp|Q8IY67|	NA
824	VVLENYYKDFTIY	gi|38258809|sp|Q8TAA9|	NA
825	ESDGDEYAMASSA	gi|74762140|sp|Q15020|	NA
826	ADMEAKYEEILHD	gi|119587879|gb|EAW67	NA
827	DVFPDSYVSTWHD	gi|45477325|sp|Q96K62|	NA
828	KNEKGQYISPFHD	gi|8247940|sp|Q15181|I	NA
829	AVRENRYIVLAKD	gi|20532409|sp|P43686|	NA
830	KKSKLRYTEEGKD	gi|1706179|sp|P49711|C	NA
831	ELEGDTYDRVLVD	gi|152125805|sp|Q96CB	NA

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<tr><td>837</td><td>VELGPYYVEIGHE</td><td>gi|23821932|sp|Q8TDX9</td><td>NA</td></tr>
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<tr><td>839</td><td>ELPQDVYTIKALE</td><td>gi|7387495|sp|Q14738|</td><td>NA</td></tr>
<tr><td>840</td><td>ILFCSTYRNMALE</td><td>gi|2829667|sp|P78333|G</td><td>NA</td></tr>
<tr><td>841</td><td>TIDAEAYAIGKKE</td><td>gi|74762440|sp|Q7Z6E9|</td><td>NA</td></tr>
<tr><td>842</td><td>CISNDFYSHMPVG</td><td>gi|154350236|ref|NP_06</td><td>NA</td></tr>
<tr><td>843</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>844</td><td>GEHMDVYVPVACH</td><td>gi|152031705|sp|Q8NHU</td><td>NA</td></tr>
<tr><td>845</td><td>GTEKPKYLQHSCH</td><td>gi|119584213|gb|EAW63</td><td>NA</td></tr>
<tr><td>846</td><td>TNNGNMYTSSLYG</td><td>gi|61252474|sp|P54869|</td><td>NA</td></tr>
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<tr><td>850</td><td>DMSKYLYADSSKT</td><td>gi|146286138|sp|Q8NDI</td><td>NA</td></tr>
<tr><td>851</td><td>HLEAGGYHSLALT</td><td>gi|30580361|sp|Q96Q42|</td><td>NA</td></tr>
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<tr><td>860</td><td>ASTEDHYLSIVTT</td><td>gi|119497911|ref|XP_00</td><td>NA</td></tr>
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<tr><td>862</td><td>RFAVDEYSDMVAV</td><td>gi|49036087|sp|Q86VI3|</td><td>NA</td></tr>
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<tr><td>864</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>865</td><td>ICFEAKYVGSLDV</td><td>gi|57012635|sp|O75052|</td><td>NA</td></tr>
<tr><td>866</td><td>PNVEESYLPSPDV</td><td>gi|148880116|sp|Q9UPR</td><td>NA</td></tr>
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<tr><td>868</td><td>FYESLKYARVKEV</td><td>gi|13878337|sp|Q13315|</td><td>NA</td></tr>
<tr><td>869</td><td>LHNKGVYVRVGLQ</td><td>gi|1708624|sp|P52824|D</td><td>NA</td></tr>
<tr><td>870</td><td>HEPKGYYANFCSG</td><td>gi|135684|sp|P10600|TG</td><td>NA</td></tr>
<tr><td>871</td><td>KGDEEEYWNSSKF</td><td>gi|41016926|sp|Q9H9C1</td><td>[KGDEEEYWNSSKF|Y|1</td></tr>
<tr><td>872</td><td>CDYCDTYLTHDSP</td><td>gi|134093|sp|P09234|RU</td><td>[CDYCDTYLTHDSP|Y|1</td></tr>
<tr><td>873</td><td>DSEGHLYTVPIRE</td><td>gi|13637934|sp|Q03135|</td><td>[DSEGHLYTVPIRE|Y|14</td></tr>
<tr><td>874</td><td>GTYGVVYKAKNRE</td><td>gi|231726|sp|Q00526|CD</td><td>NA</td></tr>
<tr><td>875</td><td>DCETDGYLSSSGF</td><td>gi|41688789|sp|Q96J92|</td><td>NA</td></tr>
<tr><td>876</td><td>DALKEKYDSAAAM</td><td>gi|731157|sp|P41221|W</td><td>NA</td></tr>
<tr><td>877</td><td>RRKKEPYGASPGF</td><td>gi|14589937|ref|NP_116</td><td>NA</td></tr>
<tr><td>878</td><td>DKNSEVYQEVQAM</td><td>gi|74735811|sp|Q52LJ0|</td><td>NA</td></tr>
<tr><td>879</td><td>GFEKYSYEIIQKF</td><td>gi|113414409|ref|XP_49</td><td>NA</td></tr>
<tr><td>880</td><td>LFWSLKYVIMAKF</td><td>gi|113418228|ref|XP_00</td><td>NA</td></tr>
<tr><td>881</td><td>MGSESTYSECETF</td><td>gi|14424221|sp|O75154|</td><td>NA</td></tr>
<tr><td>882</td><td>GYSEVIYGRKRWF</td><td>gi|67848436|gb|AAY822</td><td>NA</td></tr>
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1114	QLNLKEYNLV	gi|38258883|sp|P50148|	[QLNLKEYNLV|Y|356|P2
1115	GRYYEGYYAAGPG	gi|74751663|sp|Q93052|I	[GRYYEGYYAAGPG|Y|3
1116	KELEEIYMLPRMR	gi|3182949|sp|O14646|C	[KELEEIYMLPRMR|Y|10
1117	QNTDLIYQTGPKS	gi|32469749|sp|Q8TBA6|	[QNTDLIYQTGPKS|Y|54
1118	TVRQGGYMPQ	gi|729833|sp|P40189|IL6	[TVRQGGYMPQ|Y|915|
1119	DKQRLSYGAFTNQ	gi|119370361|sp|Q9ULH	[DKQRLSYGAFTNQ|Y|7
1120	EKDLPNYNWNSFG	gi|6016439|sp|Q15726|K	[EKDLPNYNWNSFG|Y|1
1121	DERSWVYSPLHYS	gi|78099088|sp|O60331|I	[DERSWVYSPLHYS|Y|6
1122	EFRDSTYDLPRSL	gi|46396035|sp|Q9UQC	[EFRDSTYDLPRSL|Y|26
1123	FGQQKLYQVPNPQ	gi|8134360|sp|Q14511|C	NA
1124	LPTTVDYSSVPKQ	gi|8928283|sp|O00559|R	[LPTTVDYSSVPKQ|Y|4
1125	QEQYELYCEMGST	gi|88911265|sp|Q13191|	[QEQYELYCEMGST|Y|3
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1127	NGGPGPYVGQAGT	gi|14916543|sp|O60716|	NA
1128	SLDNGGYYISPRI	gi|125480|sp|P07948|LY	[SLDNGGYYISPRI|Y|19
1129	DEAISDYFRKQYS	gi|23831360|sp|P31939|	NA
1130	QAGMTGYGMPRQI	gi|586000|sp|P37802|TA	NA
1131	KEDQTEYLEERRV	gi|17865718|sp|P08238|	NA
1132	SGKIEKYNVPLNR	gi|20138067|sp|Q9UHB6	NA
1133	MVEDCLYETVKEI	gi|84029384|sp|Q9NWQ	[MVEDCLYETVKEI|Y|18
1134	DLSDRVYLKTQLE	gi|51316025|sp|Q8N4A0|	NA
1135	LLEAADYLERRER	gi|729978|sp|Q05195|M	NA
1136	HEGETSYIRVYPE	gi|3929377|sp|Q13242|S	NA
1137	CRNATRYVVLHAS	gi|11387208|sp|Q9UKU6	NA
1138	AHPLSPYGETLTE	gi|143811460|sp|Q9NP3	NA
1139	DDYPGSYSPQDPS	gi|23813907|sp|Q9NQG	NA
1140	LNTLAHYKIPEGA	gi|51701868|sp|Q9Y4D7|	NA
1141	GSYRDSYDSYATH	gi|5921786|sp|Q14011|C	NA
1142	AQGEMLYLATRIE	gi|27734215|sp|Q9H9E1|	NA
1143	PSRNKPYISWPSS	gi|92090617|sp|Q9Y5S2|	NA

1144	KLNCRLYRKANKS	gi|113936|sp|P01008|AN	NA
1145	YGGFDDYGGYNNY	gi|23503095|sp|P31942|	NA
1146	AAAWKGYADIVQL	gi|108885279|sp|Q92882	NA
1147	EFVNQYYGSFKEA	gi|1352513|sp|P35228|N	NA
1148	KEALKFYTDPSYF	gi|59800456|sp|Q9Y6W5	[KEALKFYTDPSYF|Y|15
1149	EEQKKYYNAMKKL	gi|150417969|ref|NP_00	[EEQKKYYNAMKKL|Y|1
1150	IQAEEWYFGKLGR	gi|125370|sp|P06241|FY	NA
1151	ELEEPVYEEPVYE	gi|73619965|sp|Q8WWN	NA
1152	YSSEDDYVGYSDV	gi|29337242|sp|Q9UH99	NA
1153	DDISSSYTTTTTI	gi|21431730|sp|O00767|	NA
1154	TRFTDDYQLFEEL	gi|62512173|sp|Q13555|	NA
1155	KLAPITYPQGLAL	gi|131806|sp|P15153|RA	NA
1156	LQGKSLYSYAGLA	gi|131573277|gb|ABO33	NA
1157	INEASNYNVTSDY	gi|48474955|sp|Q9HAU0	NA
1158	LRPQANYSQIHHP	gi|116242614|sp|Q96RT	NA
1159	CLDRPIYPCRWLC	gi|61216811|sp|Q8N474|	NA
1160	TAPNDLYLKLEDV	gi|50401072|sp|Q8NFU5	NA
1161	TTPDEDYEYMNRQ	gi|119534|sp|P21860|ER	NA
1162	PNRVEIYEKTVEV	gi|134034199|sp|Q96F07	NA
1163	LKSKMIYASSKDA	gi|6831517|sp|Q9Y281|C	NA
1164	GSVGGTYRQKSMP	gi|115502447|sp|O43166	NA
1165	QLEEDLYDGQVLQ	gi|20139178|sp|Q9HBI1|	NA
1166	SDVNKEYYTQNME	gi|74762758|sp|Q9NW64	NA
1167	IRELVPYDIFTEK	gi|119621883|gb|EAX014	NA
1168	EEADENYNSVNTR	gi|3041737|sp|Q12846|S	NA
1169	QEKQELYGKLRST	gi|145559478|sp|Q14789	NA
1170	SEHENAYENVPEE	gi|6225642|sp|Q13113|P	NA
1171	WMFSLGYINPKNS	gi|32171483|sp|Q8NFP9	NA
1172	DTTEPGYINIMEL	gi|34098663|sp|Q92613|	NA
1173	YGPQGGYQPDYGQ	gi|135162|sp|P08247|SY	NA
1174	ILDEDLYINANDQ	gi|1705486|sp|P54132|B	NA
1175	SGEGTDYINASYI	gi|400199|sp|P23471|PT	NA
1176	SFTILSYLNATDL	gi|13124142|sp|Q9NRD0	NA
1177	LSGFELYGTVNGV	gi|85682779|sp|Q9ULT8|	NA
1178	LPQLLAYPNPIDP	gi|51338683|sp|P62256|	NA
1179	CLKMVYYANVVGG	gi|6648106|sp|Q05086|U	NA
1180	EPDYQVYLNASKV	gi|28201801|sp|Q9P2B2|	NA
1181	TGKSADYVNLSLK	gi|17369343|sp|Q9P2S2|	NA
1182	RYAGEVYGMIRFS	gi|38258919|sp|P42356|	NA
1183	VPRCTSYLNPGLP	gi|13632586|sp|O75747|	NA
1184	VDGKEIYNTIRRK	gi|121743|sp|P20936|RA	[VDGKEIYNTIRRK|Y|46
1185	MLVTHDYTAVKED	gi|8928460|sp|O75962|T	NA
1186	AVALQDYMAPDCR	gi|2498559|sp|Q16674|M	NA
1187	RKQLVIYEEISDP	gi|115502458|sp|O60225	NA
1188	PSPMPEYLNVHYI	gi|1351190|sp|P49116|T	NA
1189	FYKCEAYGRAFNW	gi|152031765|sp|Q03924	NA
1190	DTVQESYENVDSL	gi|24418868|sp|O14978|	NA
1191	ASFSWTYEEIKEV	gi|76803797|sp|Q99698|	NA
1192	LYKNVCYVNLLFW	gi|30316350|sp|O94823|	NA
1193	EFYKIHYWDTTTL	gi|1169096|sp|P46108|C	NA
1194	QGPPEIYSNTQFP	gi|119599582|gb|EAW79	NA
1195	TTMKKAYYLACGF	gi|62900106|sp|Q9UJW	NA

1196	AFIPFSYLVDQWR	gi|113041|sp|P22966|AC	NA
1197	VQVSSAYVKTSEK	gi|20141658|sp|O43399|	NA
1198	RYESSSYTDQFSR	gi|85700443|sp|Q07157|	NA
1199	FQYEGTYKWVNPH	gi|116242483|sp|P11413	[FQYEGTYKWVNPH|Y|
1200	F5:17	contol_spot	NA
1201	pY	contol_spot	NA
1202	pY	contol_spot	NA
1203	Triple Flaq	contol_spot	NA
1204	pY	contol_spot	NA
1205	pY	contol_spot	NA
1206	Triple Flaq	contol_spot	NA
1207	VDEREKYMIGNSV	gi|116242614|sp|Q96RT	NA
1208	KEEMGDYIRSYSV	gi|97046413|sp|Q567U6|	NA
1209	SKADEYYPEHTSV	gi|46397678|sp|Q13017|	NA
1210	IISKMMYENTTTV	gi|30172802|sp|Q15021|	NA
1211	PNEQNIYIVVGVV	gi|6624134|gb|AAF1926	NA
1212	SHSRELYTSKWTV	gi|134035045|sp|O9488	NA
1213	DGYQDGYWDGPHW	gi|124219|sp|P23588|IF4	NA
1214	GIENIHYLNDGLW	gi|119632280|gb|EAX11	NA
1215	KFSKAIYKYVNHW	gi|154240671|ref|NP_77	NA
1216	MFSRSKYASAEKW	gi|57162167|emb|CAI39	NA
1217	ITENYKYEEGSLQ	gi|20532415|sp|O43548|	NA
1218	QQMLEGYSDPGIW	gi|133777266|gb|AAI010	NA
1219	LLECLDYLTAPNP	gi|22653810|sp|O15344|	NA
1220	QKAGEGYEQTLLQ	gi|10834694|gb|AAG237	NA
1221	EGICDSYTDFSTG	gi|126366|sp|P07942|LA	NA
1222	RNEKFNYVVMQLQ	gi|97203020|sp|Q5TCY1	NA
1223	ENSCTYYECHYPP	gi|46397255|sp|Q96E35|	NA
1224	MSSNLEYAKGYPP	gi|119611661|gb|EAW91	NA
1225	EDHKSYYAINTVY	gi|108860796|sp|Q8IXI2|	NA
1226	KHTRTHYVDKPYY	gi|74762721|sp|Q9BZE0|	NA
1227	QDEEYLYLVMDYY	gi|74762299|sp|Q6DT37|	NA
1228	EMDDERYFNEMSA	gi|2498281|sp|Q16204|C	NA
1229	IKEWPGYGSTLFD	gi|17433142|sp|Q9HD67	NA
1230	LVENVKYEDIYED	gi|152031557|sp|Q92481	NA
1231	LEASGDYKYSGRD	gi|125729|sp|P12956|KU	NA
1232	TPAKSHYVFNLRD	gi|119619959|gb|EAW99	NA
1233	IPDAEIYKITATD	gi|60416428|sp|O15056|	NA
1234	RFKKCIYVGMATD	gi|586092|sp|P10828|TH	NA
1235	LMCQESYACSGTD	gi|34098716|sp|Q9HBF4	NA
1236	TRTKEKYRVVYTD	gi|3023467|sp|O14627|C	NA
1237	AMQKWYYKDPQGE	gi|74710467|sp|Q6Y7W	NA
1238	DWMEEEYRHIPGE	gi|1730125|sp|Q10981|F	NA
1239	EKTEQGYSNTETA	gi|115502355|sp|O95671	NA
1240	EYSCTPYNSLGTA	gi|119573141|gb|EAW52	NA
1241	DMETDHYSNGVGE	gi|61215334|sp|Q96S59|	NA
1242	PEERDGYGRWNHE	gi|37999812|sp|Q9UL42|	NA
1243	<<Marker>>	contol_spot	NA
1244	APKLPPYVWVASE	gi|34535146|dbj|BAC872	NA
1245	LWYDQDYARFESP	gi|5870276|gb|AAD5450	NA
1246	DPESSDYGHVQSP	gi|32699509|sp|Q14241|	NA
1247	NKFVDEYIISPSP	gi|119590881|gb|EAW70	NA

1248	EDVDLGYVEDGTP	gi|14423634|sp|Q9P0K1|	NA
1249	SFCFLEYEDHKTA	gi|23397427|ref|NP_006	NA
1250	ETASSGYASVQGT	gi|74751443|sp|Q8TEB7|	NA
1251	LEFYADYSDNPWL	gi|119370373|sp|P51530	NA
1252	GAIKDLYGDFKIT	gi|2506889|sp|P51674|G	NA
1253	ISPNCGYINSHIT	gi|585912|sp|Q04912|R	NA
1254	RGQELIYAGMPIT	gi|116241237|sp|P53396	NA
1255	VDASDDYIFFNIT	gi|152031605|sp|Q5H8C	NA
1256	RSAKIEYVIPNNT	gi|51094947|gb|EAL241	NA
1257	VFRSLKYAESDPT	gi|17368466|sp|Q14703|	NA
1258	LEERTRYASPGPT	gi|88997880|ref|XP_938	NA
1259	AGRLGSYVINGRT	gi|32129513|sp|Q96KS0|	NA
1260	KPSSPSYTVVGRT	gi|125888011|sp|Q3SX6	NA
1261	TCYADGYEQVYQT	gi|62510692|sp|Q8N475|	NA
1262	PRFSEIYHNINAD	gi|114163|sp|P27540|AR	NA
1263	VAEWEKYIISLAD	gi|126469|sp|P23467|PT	NA
1264	<<Marker>>	contol_spot	NA
1265	LPRVSAYVDTTAD	gi|72533478|gb|AAI0095	NA
1266	RYSNEKYQKFKAV	gi|74757585|sp|Q6GMR	NA
1267	FTPKPEYEGPFCV	gi|116241339|sp|Q07864	NA
1268	LLPKTKYVACVCV	gi|37081671|sp|Q9P2V4|	NA
1269	KFHAEIYFDHDLQ	gi|45477317|sp|Q8N302|	NA
1270	IYVSDGYCNSRIV	gi|23503036|sp|P19021|	NA
1271	MDSEFRYTLFPIV	gi|129557|sp|P25105|PT	NA
1272	PILEPKYAVEKIV	gi|119607188|gb|EAW86	NA
1273	SMEKGVYVCIIKV	gi|74747057|sp|Q5VU65|	NA
1274	GVADGAYVSPWKP	gi|4063508|gb|AAC9831	NA
1275	KQCKDIYCDYLDF	gi|12229836|sp|Q99665|	NA
1276	PWSENKYDISKDF	gi|74708278|sp|Q5XXA6	NA
1277	GRPGDGYMGMAGF	gi|48429103|sp|P61978|	NA
1278	IQLKDTYETNTFF	gi|2833281|sp|Q16816|P	NA
1279	LDDGPAYEDCSEF	gi|108757328|ref|YP_63	NA
1280	QKTERDYVGTLEF	gi|74758897|sp|Q70Z35|	NA
1281	SCFTKDYEEHDKA	gi|117558|sp|P09603|CS	NA
1282	GKDDHGYKQSKDM	gi|109825713|sp|Q68D5	NA
1283	GPDAEHYWSLAAM	gi|152061018|gb|AAI505	NA
1284	AASTAIYVYMYSF	gi|13878808|sp|Q9HD45	NA
1285	<<Marker>>	contol_spot	NA
1286	DPSEQRYGMIRTF	gi|148886707|ref|NP_00	NA
1287	LASALDYETLYTF	gi|62287160|sp|Q9BYE9	NA
1288	SEHDFAYQDPKVH	gi|51701722|sp|O43157|	NA
1289	LPSKDDYFQVLCM	gi|119631984|gb|EAX11	NA
1290	MEAKNSYVRDDAI	gi|23503103|sp|Q12933|	NA
1291	EKIKSLYVNMIDI	gi|4895029|gb|AAD3270	NA
1292	MEPSDSYEVLSCI	gi|13124090|sp|Q9UBF2	NA
1293	SDAEEKYSQKEDI	gi|51094986|gb|EAL242	NA
1294	WGEETDYTPVWCM	gi|2507533|sp|P06132|D	NA
1295	GWEELVYYTVPLI	gi|17380133|sp|O75323|	NA
1296	YSSWSDYIHICNI	gi|37538034|sp|Q8TEB1|	NA
1297	PCCKEDYNGCPNI	gi|32469734|sp|Q8IZD9|	NA
1298	FASSNIYSDSERI	gi|74751127|sp|Q8N9S7|	NA
1299	LIIDEYYDNTGRI	gi|20532415|sp|O43548|	NA

1300	PPRVPKYVLTDHK	gi|74735426|sp|O60284|	NA
1301	VSEWTEYKTADGK	gi|52783427|sp|O14776|	NA
1302	EVEAESYEGSRIK	gi|114762|sp|P06748|NP	NA
1303	TKEKEFYDEWPIK	gi|90111861|sp|P51160|	NA
1304	ADRKDGYVWSGKK	gi|20178106|sp|Q8WXH	NA
1305	ESEESLYKPGAKK	gi|77416856|sp|P35663|	NA
1306	<<Marker>>	contol_spot	NA
1307	NIRNDKYAGEEGM	gi|73921624|sp|Q86U86|	NA
1308	DKAKDKYVRSLWK	gi|115502390|sp|P07332	NA
1309	NYECLVYVQLPFM	gi|125731|sp|P13010|KU	NA
1310	DMSCAKYEFTDAL	gi|94536836|ref|NP_060	NA
1311	HDFRPDYLRLGAL	gi|22654276|sp|O94762|	NA
1312	ALSHSGYVSFQAL	gi|118568027|sp|Q6ZRQ	NA
1313	NFFVDDYARFTIL	gi|68053323|sp|Q9NYU2	NA
1314	ELDPQKYHDLAKL	gi|10720321|sp|Q9UL62|	NA
1315	ALRKDWYSDCSKL	gi|76803799|sp|O15151|	NA
1316	IDAEGKYMAEALL	gi|14285643|sp|O94826|	NA
1317	NIEADTYWCMSKL	gi|25008319|sp|Q8WUA	NA
1318	VSPAEYYHQMALL	gi|116242494|sp|P10071	NA
1319	RARGDEYLSWQHM	gi|21264427|sp|P30711|	NA
1320	IEKNIEYVSSSAA	gi|152031673|sp|Q92766	NA
1321	VITEPIYPEVVHM	gi|116241235|sp|Q13362	NA
1322	YSKNQKYTQVEIM	gi|42538984|ref|NP_973	NA
1323	AHERTLYTDIAIG	gi|20137971|sp|Q9H5Z1|	NA
1324	CLGAGGYADNDIG	gi|119594421|gb|EAW74	NA
1325	RVDPNGYMMMSPS	gi|547738|sp|P35568|IRS	[RVDPNGYMMMSPS|Y|
1326	SEDLSAYASISFQ	gi|547738|sp|P35568|IRS	NA
1327	<<Marker>>	contol_spot	NA
1328	SFLDSGYRILGAV	gi|21903479|sp|P18206|	NA
1329	SIRMKRYILHFHS	gi|47117832|sp|P21709|	NA
1330	SQESEDYSQPSTS	gi|266516|sp|Q00987|M	[SQESEDYSQPSTS|Y|3
1331	TATKDTYDALHMQ	gi|23830999|sp|P20963|	[TATKDTYDALHMQ|Y|1
1332	AIKMERYKDNFTA	gi|146345416|sp|Q15375	NA
1333	AIKMGRYEESFAA	gi|19860819|sp|P54760|	NA
1334	FDERQPYAHMNGG	gi|124240|sp|P08069|IG	[FDERQPYAHMNGG|Y|
1335	FQNGLKYIAIDVR	gi|2809059|dbj|BAA2450	NA
1336	FVLDDQYTSSTGT	gi|585361|sp|Q08881|IT	[FVLDDQYTSSTGT|Y|51
1337	GEEQSQYMHVGSC	gi|1168948|sp|P22001|K	[GEEQSQYMHVGSC|Y|
1338	SQGVDTYVEMRPV	gi|547770|sp|P07333|CS	[SQGVDTYVEMRPV|Y|7
1339	KKGNFNYVEFTRI	gi|20141521|sp|P24844|	[KKGNFNYVEFTRI|Y|15
1340	GVCAERYSQEVFE	gi|31077008|sp|O15304|	[GVCAERYSQEVFE|Y|3
1341	EDCYGNYDNLLSQ	gi|17380162|sp|O15530|	[EDCYGNYDNLLSQ|Y|3
1342	EEEEEAYGWMDFG	gi|120952|sp|P01350|GA	[EEEEEAYGWMDFG|Y|
1343	EELQDDYEDMMEE	gi|114787|sp|P02730|B3	[EELQDDYEDMMEE|Y|
1344	GALSPLYGVPETN	gi|27735219|sp|P49023|	[GALSPLYGVPETN|Y|1
1345	FMDDDSYSHHSGL	gi|5915890|sp|P51636|C	[FMDDDSYSHHSGL|Y|1
1346	KKFKVEYHAGGST	gi|6840802|sp|P55263|A	NA
1347	SSDGHEYIYVDPM	gi|129890|sp|P09619|PG	[SSDGHEYIYVDPM|Y|5
1348	<<Marker>>	contol_spot	NA
1349	KDESVDYVPMLDM	gi|129890|sp|P09619|PG	[KDESVDYVPMLDM|Y|7
1350	MAPYDNYVPSAPE	gi|129890|sp|P09619|PG	[MAPYDNYVPSAPE|Y|7
1351	VSRLTLYDIAHTP	gi|6648067|sp|P40926|M	[VSRLTLYDIAHTP|Y|56|

1352	SSPGGVYATRSSA	gi|55977767|sp|P08670|	[SSPGGVYATRSSA|Y|6
1353	QPDSAGYTALHYA	gi|74740664|sp|Q53RE8|	[QPDSAGYTALHYA|Y|6
1354	LQRTLHYECIVLV	gi|20455192|sp|Q9UKK9	[LQRTLHYECIVLV|Y|74|
1355	NLDPLVYLLSKLT	gi|21450889|sp|Q9BSJ2|	[NLDPLVYLLSKLT|Y|83|
1356	TPQGREYGMIYLG	gi|60415926|sp|Q7KZF4|	NA
1357	QGPPEIYSDTQFP	gi|119599582|gb|EAW79	[QGPPEIYSDTQFP|Y|19
1358	EQYNEQYGAVRTP	gi|62511129|sp|Q9BQ04	[EQYNEQYGAVRTP|Y|1
1359	APDKRIYQFTAAS	gi|74735515|sp|O75563|	[APDKRIYQFTAAS|Y|19
1360	ANVLARYASICQQ	gi|134254704|gb|ABO65	NA
1361	RDEESPYATSLYH	gi|74728034|sp|Q8IV50|	[RDEESPYATSLYH|Y|2
1362	SAVGFEYQGKTEK	gi|2498954|sp|Q14247|S	[SAVGFEYQGKTEK|Y|2
1363	KAVCSTYLQSRYY	gi|21431782|sp|Q9H2X6|	[KAVCSTYLQSRYY|Y|3
1364	GGSDQNYDIVTIG	gi|73920059|sp|Q96PE3|	[GGSDQNYDIVTIG|Y|35
1365	FNHTEDYVLLPDE	gi|461848|sp|Q05048|CS	[FNHTEDYVLLPDE|Y|36
1366	TSRESNYFGLSPE	gi|118572680|sp|Q01804	NA
1367	PPHPLTYSQLPRV	gi|61213006|sp|Q8WXE	[PPHPLTYSQLPRV|Y|3
1368	KGETGKYLRLPQL	gi|125711|sp|P12931|SR	NA
1369	<<Marker>>	contol_spot	NA
1370	SSTETCYSAIPKA	gi|38257363|sp|O75369|	[SSTETCYSAIPKA|Y|25
1371	SDMHRGYADSPSK	gi|116241280|sp|Q0151	NA
1372	PASTPTYSPAPTQ	gi|74737148|sp|Q6P1N0|	[PASTPTYSPAPTQ|Y|2
1373	KDPVGVYCRVRPL	gi|118572664|sp|Q02241	NA
1374	AEDGEEYDDPFAG	gi|74735515|sp|O75563|	NA
1375	DEVEDLYELLKLV	gi|143955280|sp|Q7L8W	[DEVEDLYELLKLV|Y|97|
1376	DSLEPPYVMKKYH	gi|417110|sp|P25364|HC	NA
1377	EKWEPKYLITPNL	gi|11133517|sp|Q03125|	NA
1378	YAIEGEYKTLATD	gi|135077|sp|P08153|S	NA
1379	TTVNDSYQNIWLM	gi|56757368|sp|P07248|	NA
1380	TTLTEKYVNSLEY	gi|1711597|sp|P46676|S	NA
1381	NESNEDYLGNEKF	gi|50400296|sp|Q04052|	NA
1382	LENDDDYERRNLV	gi|74644956|sp|Q06266|	NA
1383	VRYDEEYVVHEDM	gi|1351976|sp|P05085|A	NA
1384	ATDATKYENSFSG	gi|417456|sp|P19880|YA	NA
1385	TSQSTEYENGAQI	gi|1708907|sp|P35192|M	NA
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1403	CEEEFKYAMLALN	gi|119611661|gb|EAW91	NA

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1457	RECMSHYLRVFNF	gi|21362575|sp|Q96CW	NA
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<tr><td>1509</td><td>KVSSTHYYLLPER</td><td>gi|27923810|sp|Q9UJM3</td><td>[KVSSTHYYLLPER|Y|85</td></tr>
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<tr><td>1516</td><td>PRDFAAYRS</td><td>gi|115973|sp|P10747|CD</td><td>[PRDFAAYRS|Y|218|P1</td></tr>
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<tr><td>1525</td><td>TVVHSGYRHQVPS</td><td>gi|729833|sp|P40189|IL6</td><td>[TVVHSGYRHQVPS|Y|7</td></tr>
<tr><td>1526</td><td>APGAGHYEDTILK</td><td>gi|146328566|sp|Q9UM7</td><td>[APGAGHYEDTILK|Y|16</td></tr>
<tr><td>1527</td><td>LNPKQDYCSICLQ</td><td>gi|126253822|sp|Q8N3P</td><td>NA</td></tr>
<tr><td>1528</td><td>SFFEGGYPAYASG</td><td>gi|38348376|ref|NP_940</td><td>NA</td></tr>
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<tr><td>1531</td><td>LSDAQIYVDKVKQ</td><td>gi|6831570|sp|O14879|I</td><td>NA</td></tr>
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<tr><td>1535</td><td>RELNKLYPTHACR</td><td>gi|136120|sp|P17532|TP</td><td>NA</td></tr>
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1613	AHSKVTYEAHKEY	gi|32171483|sp|Q8NFP9	NA
1614	EKRTDGYAAFQEY	gi|34098413|sp|Q15311|	NA
1615	KRERDEYKRRCFY	gi|32425493|gb|AAH1043	NA
1616	SDNEYFYVDFREY	gi|544320|sp|P36888|FL	[SDNEYFYVDFREY|Y|5
1617	CPENSHYEVCGPP	gi|117949403|sp|Q9Y6R	NA
1618	GGAADDYGKAGPP	gi|109892840|sp|Q9ULL5	NA
1619	VEKGDYYEAHQMY	gi|74738593|sp|Q7L5D6|	NA
1620	GNQDSGYGRSGSY	gi|119623229|gb|EAX028	NA
1621	RPGKVKYMSKPSY	gi|119576355|gb|EAW55	NA
1622	CRPSDPYSMNSVY	gi|118572660|sp|O43151	NA
1623	IGFFTDYEIGPVY	gi|74721310|sp|Q9Y238|	NA
1624	AKDERIYVTNYYY	gi|119611102|gb|EAW90	NA
1625	GAWENPYTALAFA	gi|77416517|sp|Q9UEF7	NA
1626	IGSESAYESFLSA	gi|1170875|sp|P46821|M	NA
1627	LCNNFSYVVMLSA	gi|2498243|sp|Q13286|C	NA
1628	DHYDPDYEFLQQD	gi|143811452|sp|Q13905	NA
1629	GAMNDQYHRAARD	gi|81175048|sp|Q495M9|	NA
1630	YASMLPYNNKDRD	gi|729978|sp|Q05195|M	NA
1631	KEEADRYQRLKDE	gi|29336622|sp|Q14683|	NA
1632	RVCDSCYDSIKDE	gi|51316866|sp|Q8IWB7|	NA
1633	FTDFDKYMTISDE	gi|3123230|sp|P55884|IF	NA
1634	YKNRPDYVSEEEE	gi|83305554|sp|P49792|	NA
1635	VDHIDIYADVGEE	gi|88909266|sp|Q16630|	NA
1636	NDEDKVYHDVNFE	gi|113414409|ref|XP_497	NA
1637	GYRDPPYHNWMHA	gi|3182954|sp|O00408|P	NA
1638	ADEVVKYIDTKNE	gi|41018471|sp|Q8NEG5	NA
1639	ILDTDEYVLKYME	gi|74762202|sp|Q5JVL4|	NA
1640	ARSEAGYGPFGQE	gi|19860819|sp|P54760|	NA
1641	LCCCESYGKINPE	gi|13959538|sp|O15105|	NA
1642	MGGFDGYVRLNTA	gi|52783044|sp|Q6JEL2|	NA
1643	<<Marker>>	contol_spot	NA
1644	QQLEPLYLNLHAF	gi|113045|sp|P12821|AC	NA
1645	YKEAQEYGSFGTA	gi|34223721|sp|P29144|	NA
1646	LGEGESYSMPTAF	gi|127819|sp|P22736|NR	NA
1647	RNEQDFYAAVDDF	gi|18202948|sp|Q9H8V3|	NA
1648	ANYMPGYHSKKDF	gi|32172451|sp|Q12913|	NA
1649	IIECLKYICTGDF	gi|60392986|sp|Q92878|	NA
1650	LAEKYKYRSIAIP	gi|110815960|sp|Q460N5	NA
1651	VGSCSSYEDKTIP	gi|155369266|ref|NP_001	NA
1652	MGRMDTYFEDPLT	gi|12585217|sp|Q9Y6A2|	NA
1653	SFDMLRYVETLLT	gi|68565328|sp|Q9NXX6	NA
1654	EQSCEAYKHRGNT	gi|17433039|sp|Q9C0A0|	NA
1655	IDFAQEYEDVLNT	gi|119605464|gb|EAW85	NA
1656	VVSEPPYYATDYT	gi|74737318|sp|Q6P4A8|	NA
1657	MYANFGYSINGDA	gi|109127525|ref|XP_001	NA
1658	LEEEVHYGSSPLA	gi|30913318|sp|Q8TDD2	NA
1659	TRQEGLYAMGPLA	gi|48429264|sp|Q9UJX0|	NA
1660	DKEKREYVLVGAD	gi|121957949|sp|O15090	NA
1661	LVDCGIYEIVPVC	gi|148677790|gb|EDL097	NA
1662	KYEDNIYMYIYFV	gi|34098756|sp|Q9UQD0	NA
1663	TLANNTYVQKYFV	gi|119603447|gb|EAW83	NA

1664	<<Marker>>	contol_spot	NA
1665	DMDEEDYAWLEIV	gi|12229697|sp|O95696|	NA
1666	KHGDEIYIAPSGV	gi|74731866|sp|Q96GX9	NA
1667	PQFEAKYYKMEIV	gi|41018366|sp|Q9BYT9|	NA
1668	TFLEPAYPTPGHV	gi|126302563|sp|O1523	NA
1669	RIPYDDYPVVFLP	gi|73621365|sp|Q5EBL8|	[RIPYDDYPVVFLP|Y|10|
1670	GASTGIYEALELR	gi|134254702|gb|ABO65	[GASTGIYEALELR|Y|44|
1671	GPARLEYYENEKK	gi|547738|sp|P35568|IR	[GPARLEYYENEKK|Y|4
1672	RISGLIYEETRGV	gi|124504316|gb|AAI281	[RISGLIYEETRGV|Y|52|
1673	TRRSLGYAYVNFQ	gi|119627671|gb|EAX07	[TRRSLGYAYVNFQ|Y|5
1674	PSHARTYSSNTTL	gi|27734865|ref|NP_775	NA
1675	LPHSEGYMPVPNF	gi|23831069|sp|Q9NRM1	NA
1676	QLENDSYAKEKPF	gi|119576348|gb|EAW55	NA
1677	FVPSPSYFDVVYL	gi|74762141|sp|Q15198|	NA
1678	YCRYDNYADSLRF	gi|74750447|sp|Q86V42|	NA
1679	HPQYTAYNEAWRF	gi|2506538|sp|Q02962|P	NA
1680	CPCSDCYLDSAKA	gi|5915798|sp|O75936|B	NA
1681	TLCSDEYFAGGLH	gi|47605903|sp|Q8NEM	NA
1682	HLREITYKEKKPH	gi|20141039|sp|Q9HBT8	NA
1683	SKSSESYGIIIQH	gi|21757251|dbj|BAC050	NA
1684	DISNNEYLEYGSH	gi|145559462|sp|O1493	NA
1685	<<Marker>>	contol_spot	NA
1686	RDMDDAYDRLTRH	gi|123081|sp|P07686|HE	NA
1687	QRGDPIYVTELTH	gi|7023332|dbj|BAA9192	NA
1688	VWEIDEYIDFEKI	gi|17380163|sp|O60313|	NA
1689	CCSNISYERDGEQ	gi|32171848|sp|Q8IV20|	NA
1690	ALSPPTYLQGGYA	gi|13626838|sp|P58012|	NA
1691	NEWFTKYTEMDYA	gi|51316541|sp|Q9UKD2	NA
1692	NWMESSYWDGRYA	gi|61252474|sp|P54869|	NA
1693	LRQMEDYHYAHLI	gi|32469678|sp|Q14185|	NA
1694	ARQEKDYSSLCDK	gi|119602885|gb|EAW82	NA
1695	EVNETQYNEMFGM	gi|143811429|sp|Q04721	NA
1696	YIPKDAYFSMMDK	gi|119591292|gb|EAW70	NA
1697	GLEECNYECKGEK	gi|14602977|gb|AAH099	NA
1698	CLKDVVYKNNDFK	gi|17369343|sp|Q9P2S2|	NA
1699	ESSEILYRNKLGK	gi|73621383|sp|Q8NEN9	NA
1700	ELSSPEYPRPYPK	gi|117949604|sp|O0018	NA
1701	GDCQEPYAINDSK	gi|114626350|ref|XP_00	NA
1702	HPKEGPYVEDLSK	gi|50403793|sp|Q96L93|	NA
1703	SAFSERYLGMPSK	gi|67460566|sp|Q8N608|	NA
1704	LKEMLKYSRNCEG	gi|148887400|sp|O1506	NA
1705	EFYKDTYNKLKTK	gi|231724|sp|P21926|CD	NA
1706	<<Marker>>	contol_spot	NA
1707	KLKNQEYETLDHL	gi|73921624|sp|Q86U86|	NA
1708	TAGQEKYHSVCHL	gi|37999892|sp|Q9H0T7|	NA
1709	GLSAEKYSVATHL	gi|119619965|gb|EAW99	NA
1710	AASEYKYVVKHKM	gi|32172451|sp|Q12913|	NA
1711	AHEDIKYEQACIL	gi|68053318|sp|Q9H3S7|	NA
1712	SLANSPYATLASA	gi|20532299|sp|O75132|	NA
1713	KEAEESYMMAKSL	gi|134035047|sp|Q6ZXV	NA
1714	TACEILYERMKSL	gi|3023637|sp|Q14562|D	NA
1715	QKEYEDYEVASSL	gi|82802803|gb|ABB924	NA

1716	LRVQDTYLDCGTL	gi|74705745|sp|O60486|	NA
1717	KPRDSKYPCSDKM	gi|73620045|sp|Q8IYX7|	NA
1718	NQSEAGYHILQGM	gi|553586|gb|AAA66955.	NA
1719	PQDKEYYKVKEPG	gi|12643404|sp|O60674|	[PQDKEYYKVKEPG|Y|1
1720	QDSNPLYKSAITT	gi|124973|sp|P26010|IT	NA
1721	QQDGKDYIPINAI	gi|143811474|sp|P17948	[QQDGKDYIPINAI|Y|116
1722	REGSKRYCIQTKH	gi|125987789|sp|Q0707	NA
1723	RIIDSEYTAQEGA	gi|1705485|sp|P51451|B	NA
1724	RQPFVKYATLISN	gi|116242617|sp|P48357	NA
1725	DKPKQEYLNPVEE	gi|3913590|sp|Q15303|E	NA
1726	DTSDPTYTSALGG	gi|76803654|sp|P29323|	[DTSDPTYTSALGG|Y|7
1727	<<Marker>>	contol_spot	NA
1728	DVYSTDYYRVGGH	gi|2497560|sp|Q16620|N	[DVYSTDYYRVGGH|Y|7
1729	EEADGVYAASGGS	gi|46241292|gb|AAS828	NA
1730	EIGEGAYGKVFKA	gi|266423|sp|Q00534|CD	[EIGEGAYGKVFKA|Y|24
1731	AIKMDRYKDNFTA	gi|1711371|sp|P54764|E	[AIKMDRYKDNFTA|Y|92
1732	KPDLERYEAQAHG	gi|84028176|sp|P35670|	NA
1733	PPEPGPYAQPSVN	gi|1169096|sp|P46108|C	[PPEPGPYAQPSVN|Y|2
1734	SLDNPDYQQDFFP	gi|2811086|sp|P00533|E	[SLDNPDYQQDFFP|Y|1
1735	CSPQPEYVNQPDV	gi|119533|sp|P04626|ER	[CSPQPEYVNQPDV|Y|1
1736	VTSTDEYLDLSAP	gi|120050|sp|P22607|FG	[VTSTDEYLDLSAP|Y|76
1737	SSSIDEYFSEQPL	gi|90110827|sp|P17181|	[SSSIDEYFSEQPL|Y|48
1738	GRNPGFYVEANPM	gi|130225|sp|P19174|PL	[GRNPGFYVEANPM|Y|
1739	GEEDTEYMTPSSR	gi|115855|sp|P22681|CB	[GEEDTEYMTPSSR|Y|7
1740	TGFLTEYVATRWY	gi|232066|sp|P27361|MK	[TGFLTEYVATRWY|Y|1
1741	ADIDGQYAMTRAQ	gi|461854|sp|P35222|CT	[ADIDGQYAMTRAQ|Y|8
1742	DFGMTRYVLDDEY	gi|116242835|sp|P42681	NA
1743	SFMMTPYVVTRYY	gi|2507195|sp|P45983|M	[SFMMTPYVVTRYY|Y|1
1744	TQEGPLYVIVECA	gi|13432140|sp|P22455|	NA
1745	HQEFSDYDNPIFE	gi|97536681|sp|Q9Y2U5|	NA
1746	QKIGDKYISFARK	gi|6685621|sp|Q9Y6R4|	NA
1747	PCYTPYYVAPEVL	gi|1346538|sp|P49137|M	NA
1748	<<Marker>>	contol_spot	NA
1749	QHEKLSYINTHNS	gi|1710804|sp|P38165|R	NA
1750	GRCGSTYVNNKTF	gi|586313|sp|P38128|SM	NA
1751	PDYPPNYILFLNN	gi|134095|sp|P08579|RU	NA
1752	SRGDNVYVVTEVL	gi|13124058|sp|P57764|	[SRGDNVYVVTEVL|Y|1
1753	VSIYEGYTLPHAI	gi|62420975|gb|AAX822	NA
1754	VSLEEIYSGCTKR	gi|8928155|sp|Q9UDY4|	[VSLEEIYSGCTKR|Y|17
1755	ETEVELYNEFPEP	gi|1709999|sp|P51149|R	[ETEVELYNEFPEP|Y|18
1756	NLDGLEYKLHDFG	gi|1172027|sp|P43490|N	[NLDGLEYKLHDFG|Y|1
1757	EDFLKDYIHINIG	gi|129383|sp|P17844|DD	NA
1758	VVGGEDYEEVDRY	gi|74727495|sp|Q86UK7|	[VVGGEDYEEVDRY|Y|3
1759	LTAEFLYDEVHPK	gi|94730596|sp|Q6IBS0|	[LTAEFLYDEVHPK|Y|30
1760	ASGYAHYEEQEN	gi|51702204|sp|Q9Y3S2|	[ASGYAHYEEQEN|Y|31
1761	NDQDGEYCPEVKL	gi|68566065|sp|P78362|	[NDQDGEYCPEVKL|Y|3
1762	LKKEDIYAVEIVG	gi|6226869|sp|P34932|H	[LKKEDIYAVEIVG|Y|336
1763	GKQKLQYEGIFIK	gi|2498882|sp|Q15459|S	[GKQKLQYEGIFIK|Y|75
1764	PDYGALYEGRNPG	gi|130225|sp|P19174|PL	[PDYGALYEGRNPG|Y|7
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1766	QSAPQIYGPPQYN	gi|116242614|sp|Q96RT	[QSAPQIYGPPQYN|Y|9
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1773	REVDAEYEARSRL	gi|74729129|sp|Q8N6H7	NA
1774	REYDQLYEEYTRT	gi|4558641|gb|AAD2267	[REYDQLYEEYTRT|Y|4
1775	HTGEKPYECVECG	gi|147742906|sp|Q08ER	NA
1776	KYWENLYLKNGGI	gi|1177049|sp|P46974|Z	NA
1777	KKKMGEYNDLQPS	gi|114814|sp|P14164|BA	NA
1778	RETPNAYANVAQL	gi|549671|sp|P36093|PH	NA
1779	PLSFTDYTISTAL	gi|131653|sp|P25502|PU	NA
1780	KRYSTTYVEALQS	gi|1168927|sp|P43634|C	NA
1781	NVVDPWYINPSGF	gi|113022|sp|P21192|AC	NA
1782	DLNMPAYVKFNYM	gi|127962|sp|P16333|NC	NA
1783	KSPDTNYLFMGDY	gi|50402236|sp|P62714|	NA
1784	EASGITYEDRPSK	gi|729833|sp|P40189|IL6	NA
1785	RQEEAEYVRALFD	gi|1169096|sp|P46108|C	NA
1786	VYDDGKYVYVVTE	gi|1730070|sp|P51812|K	NA
1787	VEREQEYIRRQLE	gi|29427585|sp|O95819|	NA
1788	CWSKATYIYMKAA	gi|74743633|sp|Q5SRH9	NA
1789	NSSFEVYCDMETM	gi|12230074|sp|Q14314|	NA
1790	<<Marker>>	contol_spot	NA
1791	YYSKIEYQNHLSM	gi|62296764|sp|Q13129|	NA
1792	RIKNEPYQVVECA	gi|52783467|sp|Q96AE7|	NA
1793	FRAESKYTFERWM	gi|93204574|sp|O94887|	NA
1794	IFSKVKYYNVEYM	gi|119615516|gb|EAW95	NA
1795	GKQEGVYAWIGIN	gi|74752912|sp|Q9NQZ7	NA
1796	KACENLYFTLGIN	gi|34223733|sp|P59046|	NA
1797	RYSSSGYSSAEIN	gi|55958101|emb|CAI13	NA
1798	ALKGIDYETVPIN	gi|119601687|gb|EAW81	NA
1799	DWREKGYVTPVKN	gi|115741|sp|P07711|CA	NA
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1801	LLSEQKYGALVNN	gi|152125805|sp|Q96CB	NA
1802	AKDNSIYVVANIG	gi|88952267|sp|Q9NY84|	NA
1803	ELSCDHYCHNYIG	gi|19860140|sp|P48740|	NA
1804	DREMKDYEPAKGG	gi|121949057|sp|Q3SYE	NA
1805	GTKVDDYWEPGKG	gi|119585619|gb|EAW65	NA
1806	KRYMDDYIFTYIG	gi|23821872|sp|Q12965|	NA
1807	CAPPTAYIDFARQ	gi|39932641|sp|P60174|	NA
1808	FVSSDYYNENDWN	gi|146345530|sp|P20061	NA
1809	GLCDPNYKDVDWN	gi|119624708|gb|EAX04	NA
1810	IFGDLEYVTVEGG	gi|113412849|ref|XP_00	NA
1811	PFPELRYLSLAYN	gi|150378449|ref|NP_89	NA
1812	TISKGGYLQGNVN	gi|12585385|sp|Q9UPY5	NA
1813	MLIEELYAFMPAR	gi|119629151|gb|EAX08	NA
1814	SGPKGPYVSWGAR	gi|119587448|gb|EAW67	NA
1815	QQRKNDYIITGGG	gi|110815960|sp|Q460N	NA
1816	YGVCPVYEDVPAR	gi|134034147|sp|Q86XL	NA
1817	CECDQGYIMVRKG	gi|41017299|sp|Q14767|	NA
1818	FAFKDKYKQFFLG	gi|113463|sp|P12236|AD	NA
1819	AFEKNHYVVGAER	gi|57015304|sp|Q04741|	NA

1820	EWRELRYDSTCER	gi|729167|sp|P07357|CO	NA
1821	PREEGLYFAARDR	gi|119613520|gb|EAW93	NA
1822	RVSPKGYESVGER	gi|92117045|ref|YP_576	NA
1823	VDYEIEYVCRGER	gi|12643873|sp|Q9UBS5	NA
1824	DFEGSGYTDLQER	gi|33112396|sp|Q9NQ76	NA
1825	FHENRKYYNKTEC	gi|149047690|gb|EDM00	NA
1826	GRNETGYLSSVEC	gi|81175180|sp|Q9P2G3	NA
1827	INESENYEALLEC	gi|74727834|sp|Q86XI2|	NA
1828	LNKKSIYSRVPEC	gi|113421409|ref|XP_00	NA
1829	PSPCGKYISCAEC	gi|124056465|sp|P05107	NA
1830	GEYSTGYIDNVTL	gi|90185107|sp|Q13753|	NA
1831	CMPKEKYEPPDPR	gi|6330365|dbj|BAA8650	NA
1832	LADQTPYPNTPPR	gi|149271283|ref|XP_91	NA
1833	LYSTFTYMNPAQR	gi|1351096|sp|P48436|S	NA
1834	VDYEEKYGRMFPR	gi|74746777|sp|Q5VIR6|	NA
1835	EATEEIYLTPVQR	gi|17433093|sp|Q9UQF2	NA
1836	SQCNEMYINSSQR	gi|14194461|sp|Q99996|	NA
1837	YGRDLDYSDHPNG	gi|23503093|sp|P38159|	NA
1838	DKFNSKYNPVGAS	gi|399033|sp|Q01432|A	NA
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1840	KLCKLDYACKLAS	gi|61675704|ref|NP_001	NA
1841	SPCQSYYVQAPAS	gi|56205464|emb|CAI20	NA
1842	ARQGEQYMNTRCP	gi|3122245|sp|Q14642|I5	NA
1843	GIQDEKYYQICES	gi|29839394|sp|Q9BY41|	NA
1844	VGDDKKYTSMKES	gi|116242695|sp|Q9HC1	NA
1845	ALSTAKYKNWPES	gi|83288393|sp|Q92954|	NA
1846	EEKCQAYESNRES	gi|1168366|sp|P43652|A	NA
1847	NGIEACYCNMGFS	gi|42559012|sp|Q9HBW	NA
1848	VGDEGRYQCVAFS	gi|114627229|ref|XP_52	NA
1849	WYRNCHYANLNGL	gi|9087217|sp|P22105|T	NA
1850	SGREIIYPNASLL	gi|115940|sp|P06731|CE	NA
1851	ISALLQYINLSLT	gi|37537862|sp|Q9UJX5|	NA
1852	KIGEGTYGVVYKG	gi|115922|sp|P06493|CD	[KIGEGTYGVVYKG|Y|1
1853	MLLASKYEEIYPP	gi|8134359|sp|P78396|C	NA
1854	VRMLDDYEEISAG	gi|57015409|sp|Q8IWT3|	NA
1855	FGLPPRYQPDVKF	gi|20455027|sp|Q9UJ83|	NA
1856	MNPLSPYLNVDPR	gi|18201964|sp|O14925|	NA
1857	LGWYPPYANPPPE	gi|13629029|sp|Q08397|	NA
1858	HGGLRGYLRVFFR	gi|12229870|sp|Q9UI09|	NA
1859	LGTVMRYEEIELR	gi|30580486|sp|Q9BZQ4	NA
1860	RWLAVDYENVRPD	gi|129018|sp|P04181|OA	NA
1861	DAGCRPYMAPERI	gi|1170596|sp|P45985|M	NA
1862	PLAAYCYLRVVGK	gi|1709347|sp|P51957|N	NA
1863	NGGTLYYMAPEHL	gi|60393639|sp|Q13546|	NA
1864	IRRHKNYLRVVGN	gi|34922250|sp|Q9UKV5	NA
1865	VPQVKFYEEIKEY	gi|116241253|sp|P35626	NA
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1868	FENNGDYMDMKQA	gi|129892|sp|P16234|PG	[FENNGDYMDMKQA|Y|
1869	GVEGSDYINASFL	gi|125978|sp|P10586|PT	NA
1870	TDSLSTYINANYI	gi|134039192|sp|Q1525	NA
1871	YPNDSVYANWMLS	gi|547807|sp|P07949|RE	[YPNDSVYANWMLS|Y|1

<table>
<tr><td>1872</td><td>PAVILFYVNACFF</td><td>gi|6226142|sp|Q99835|S</td><td>NA</td></tr>
<tr><td>1873</td><td>FMPPPTYTEVDPC</td><td>gi|74752618|sp|Q9H3M7</td><td>NA</td></tr>
<tr><td>1874</td><td>LGRNLDYVCEGPC</td><td>gi|81905882|sp|Q9DA19|</td><td>NA</td></tr>
<tr><td>1875</td><td>THATDKYSDYHPC</td><td>gi|74758686|sp|Q6ZMW</td><td>NA</td></tr>
<tr><td>1876</td><td>AYVETKYSPPAIS</td><td>gi|2501458|sp|Q14694|U</td><td>NA</td></tr>
<tr><td>1877</td><td>NIDKSLYVAEYHS</td><td>gi|116241327|sp|P26196</td><td>NA</td></tr>
<tr><td>1878</td><td>QKRSDSYVLLEHS</td><td>gi|37537861|sp|Q9UJX4|</td><td>NA</td></tr>
<tr><td>1879</td><td>GKIKEWYEKHGNS</td><td>gi|147744568|sp|P13645</td><td>NA</td></tr>
<tr><td>1880</td><td>PGHGDIYASFYNS</td><td>gi|59803098|sp|Q16851|</td><td>NA</td></tr>
<tr><td>1881</td><td>DLPEETYETKLPS</td><td>gi|73619948|sp|Q6UY09|</td><td>NA</td></tr>
<tr><td>1882</td><td>GLVPTDYVEILPS</td><td>gi|12643956|sp|Q9Y5X1|</td><td>NA</td></tr>
<tr><td>1883</td><td>PAEEPEYAYHIPS</td><td>gi|143811399|sp|Q86SQ</td><td>NA</td></tr>
<tr><td>1884</td><td>DDNEDEYAPVIQS</td><td>gi|462334|sp|Q03933|HS</td><td>NA</td></tr>
<tr><td>1885</td><td>PSWGEKYQYPDTS</td><td>gi|90652851|ref|NP_054</td><td>NA</td></tr>
<tr><td>1886</td><td>TFTATGYVVVTSS</td><td>gi|116242740|sp|Q1526</td><td>NA</td></tr>
<tr><td>1887</td><td>KKKCDEYIPGTTS</td><td>gi|117168275|ref|NP_10</td><td>NA</td></tr>
<tr><td>1888</td><td>ADTQEAYSSVPVS</td><td>gi|1708274|sp|P55317|H</td><td>NA</td></tr>
<tr><td>1889</td><td>FLSEDKYPLIIVS</td><td>gi|74753323|sp|Q9UH65</td><td>NA</td></tr>
<tr><td>1890</td><td>TWEYEYYEIGPVS</td><td>gi|68565259|sp|Q96G30|</td><td>NA</td></tr>
<tr><td>1891</td><td>IGLMEVYKNTPET</td><td>gi|17368720|sp|Q9C0E2|</td><td>NA</td></tr>
<tr><td>1892</td><td>RATKPPYECPVET</td><td>gi|116241271|sp|P55201</td><td>NA</td></tr>
<tr><td>1893</td><td>CNYNLPYVCKKGT</td><td>gi|3288885|gb|AAC2558</td><td>NA</td></tr>
<tr><td>1894</td><td>GADFTKYAIMLFT</td><td>gi|119574493|gb|EAW54</td><td>NA</td></tr>
<tr><td>1895</td><td>RKWDDDYVRYWFT</td><td>gi|6581091|gb|AAF1845</td><td>NA</td></tr>
<tr><td>1896</td><td>DDSLDGYVFGTGT</td><td>gi|126549|sp|P06887|LV</td><td>NA</td></tr>
<tr><td>1897</td><td>RTDDLVYLNVMEL</td><td>gi|3183003|sp|Q14289|F</td><td>[RTDDLVYLNVMEL|Y|8</td></tr>
<tr><td>1898</td><td>VFPCSVYVPDEWE</td><td>gi|33112647|sp|P06213|</td><td>[VFPCSVYVPDEWE|Y|1</td></tr>
<tr><td>1899</td><td>APVYSVYSKLHPP</td><td>gi|71153548|sp|O75886|</td><td>[APVYSVYSKLHPP|Y|37</td></tr>
<tr><td>1900</td><td>DSFLQRYSSDPTG</td><td>gi|2811086|sp|P00533|E</td><td>[DSFLQRYSSDPTG|Y|1</td></tr>
<tr><td>1901</td><td>EEISAMYSSVNKP</td><td>gi|84029384|sp|Q9NWQ</td><td>[EEISAMYSSVNKP|Y|31</td></tr>
<tr><td>1902</td><td>GGWMEDYDYVHLQ</td><td>gi|8134339|sp|P56945|B</td><td>[GGWMEDYDYVHLQ|Y|</td></tr>
<tr><td>1903</td><td>SYLPLSYWQQP</td><td>gi|730980|sp|P40238|TP</td><td>[SYLPLSYWQQP|Y|631|</td></tr>
<tr><td>1904</td><td>EDDQEVYDDVAEQ</td><td>gi|6166197|sp|O15117|F</td><td>[EDDQEVYDDVAEQ|Y|5</td></tr>
<tr><td>1905</td><td>LLTIDRYLAIVHA</td><td>gi|31542354|ref|NP_034</td><td>[LLTIDRYLAIVHA|Y|139|</td></tr>
<tr><td>1906</td><td>RCKRQFYLYKGKC</td><td>gi|97189858|sp|Q2I0M5|</td><td>[RCKRQFYLYKGKC|Y|1</td></tr>
<tr><td>1907</td><td>YSKNTDYTELHQQ</td><td>gi|32469749|sp|Q8TBA6|</td><td>[YSKNTDYTELHQQ|Y|4</td></tr>
<tr><td>1908</td><td>DLVSCAYQVARGM</td><td>gi|119602968|gb|EAW82</td><td>[DLVSCAYQVARGM|Y|6</td></tr>
<tr><td>1909</td><td>KTPAILYTYSGLR</td><td>gi|74759932|sp|Q8N684|</td><td>[KTPAILYTYSGLR|Y|72|</td></tr>
<tr><td>1910</td><td>LMARALYDNVPEC</td><td>gi|8134360|sp|Q14511|C</td><td>[LMARALYDNVPEC|Y|1</td></tr>
<tr><td>1911</td><td>SLETLLYKPVDRV</td><td>gi|143811366|sp|P11274</td><td>[SLETLLYKPVDRV|Y|64</td></tr>
<tr><td>1912</td><td>TSSTVQYSTVVHS</td><td>gi|729833|sp|P40189|IL6</td><td>[TSSTVQYSTVVHS|Y|7</td></tr>
<tr><td>1913</td><td>GGYGYGYGRSRDY</td><td>gi|1710620|sp|P98179|R</td><td>[GGYGYGYGRSRDY|Y|</td></tr>
<tr><td>1914</td><td>LLREETYDVPPAF</td><td>gi|8134339|sp|P56945|B</td><td>[LLREETYDVPPAF|Y|32</td></tr>
<tr><td>1915</td><td>EEGYQDYEPEA</td><td>gi|586067|sp|P37840|SY</td><td>[EEGYQDYEPEA|Y|136|</td></tr>
<tr><td>1916</td><td>FVGTLQYLAPELL</td><td>gi|14285497|sp|O14920|</td><td>NA</td></tr>
<tr><td>1917</td><td>HTTQGVYDIPPSS</td><td>gi|8134360|sp|Q14511|C</td><td>NA</td></tr>
<tr><td>1918</td><td>KQPYTEYISTRWY</td><td>gi|41017258|sp|Q9UQ07</td><td>[KQPYTEYISTRWY|Y|1</td></tr>
<tr><td>1919</td><td>CSPQPEYVNQPDV</td><td>gi|119533|sp|P04626|ER</td><td>[CSPQPEYVNQPDV|Y|1</td></tr>
<tr><td>1920</td><td>RGLQGTYQDVGSL</td><td>gi|547896|sp|P11912|CD</td><td>[RGLQGTYQDVGSL|Y|2</td></tr>
<tr><td>1921</td><td>SVQNPVYHNQPLN</td><td>gi|2811086|sp|P00533|E</td><td>[SVQNPVYHNQPLN|Y|1</td></tr>
<tr><td>1922</td><td>TLGGNPYPGIPPE</td><td>gi|547807|sp|P07949|RE</td><td>NA</td></tr>
<tr><td>1923</td><td>YDQTNPYTDVRRR</td><td>gi|85681902|sp|Q9UPU5</td><td>[YDQTNPYTDVRRR|Y|1</td></tr>
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1924	EKVSGDYGHPVYI	gi|2494367|sp|Q15768|E	[EKVSGDYGHPVYI|Y|31
1925	IEDEDYYKASVTR	gi|3183003|sp|Q14289|F	[IEDEDYYKASVTR|Y|58
1926	PGGSDNYGSLSRV	gi|14916543|sp|O60716|	[PGGSDNYGSLSRV|Y|2
1927	TAMRA	contol_spot	NA
1928	IgM	contol_spot	NA
1929	pY	contol_spot	NA
1930	TAMRA	contol_spot	NA
1931	IgM	contol_spot	NA
1932	pY	contol_spot	NA
1933	DEGGEVYEDLMKA	gi|12643372|sp|Q9UKW	NA
1934	ARVSSGYVPPPVA	gi|2497677|sp|Q15942|Z	NA
1935	RYEGRVYHYRINT	gi|1168268|sp|P42684|A	NA
1936	TVEFMHYIIAARA	gi|21542165|sp|O00541|	NA
1937	IWKKEIYEESSTW	gi|20138899|sp|O96007|	NA
1938	KQERISYTPPESP	gi|730927|sp|P41212|ET	NA
1939	HPATAEYEFANPS	gi|6016268|sp|Q16082|H	NA
1940	GADPNPYVKTYLL	gi|152031652|sp|O0044	NA
1941	KPPYTDYVSTRWY	gi|48428273|sp|Q9UPZ9	[KPPYTDYVSTRWY|Y|1
1942	KCDPAGYYCGFKA	gi|46397659|sp|P60900|	NA
1943	SRNAAEYLLSSGI	gi|85681908|sp|P00519|	NA
1944	PTPRSQYLSAEEN	gi|47117044|sp|O75581|	NA
1945	RQLREQYDEKRSQ	gi|60390262|sp|O95453|	NA
1946	SYHPSAYSPFHFQ	gi|17380231|sp|Q9UKK3	NA
1947	AYADSYYYEDGGM	gi|73619722|sp|Q8IVM0|	NA
1948	RGFGFVYFQNHDA	gi|8134660|sp|Q13151|R	NA
1949	RAYADSYYYEDGG	gi|73619722|sp|Q8IVM0|	NA
1950	LFQPVQYGQKPEG	gi|55976571|sp|Q96L91|	NA
1951	YDEQSNYDQQHDS	gi|8928305|sp|Q92804|R	NA
1952	YAVQAKYGDYNKE	gi|464541|sp|P35241|RA	NA
1953	IVRSNHYDPEEDE	gi|85700443|sp|Q07157|	NA
1954	KEKKYDYDNLPRT	gi|84028209|sp|Q8IXK2|	NA
1955	DQDINYYIPAEDF	gi|85396869|gb|AAI0478	NA
1956	GSFIGQYTVKKDK	gi|83304988|sp|O94856|	NA
1957	FGGLVNYFKSKPV	gi|6685982|sp|O95721|S	NA
1958	GSHISGYATLRRG	gi|82581557|sp|Q70E73|	NA
1959	RNDSGTYLCGAIS	gi|145559515|sp|Q1511	NA
1960	MGATAVYELDTEK	gi|3123165|sp|O15541|R	NA
1961	AVRRACYGVLRFI	gi|417719|sp|P23396|RS	NA
1962	NSYPWPYGRQTAP	gi|27805737|sp|Q96GD4	[NSYPWPYGRQTAP|Y|
1963	GCTPLHYAASKNR	gi|20532206|sp|O75832|	NA
1964	LLITGRYVEARNI	gi|116242491|sp|P35573	NA
1965	KHINEVYYAKKKR	gi|3219996|sp|Q13627|D	NA
1966	DKNADGYIDLDEL	gi|54042075|sp|P63316|	NA
1967	SINTVTYEWAPPV	gi|17380320|sp|Q9UGI8|	NA
1968	ANSVASYENEEPA	gi|119572412|gb|EAW52	NA
1969	IEWWDSYIIPNGF	gi|37082334|sp|O43395|	NA
1970	GNRFEPYANPTKR	gi|55977747|sp|P52272|	NA
1971	FLKAIGYLIPLMD	gi|15214275|sp|O75533|	NA
1972	DKLKELYGQVLYR	gi|6094347|sp|O76094|S	NA
1973	ARFCNRYPNIELS	gi|56405304|sp|O75643|	NA
1974	AKREKEYVNIQTF	gi|67477390|sp|Q01968|	NA
1975	CFYNSSYLNVQRE	gi|231458|sp|P19652|A1	NA

1976	YASLRHYLNLVTR	gi|1172796|sp|P10082|P	NA
1977	GLQEHVYEEIGDA	gi|116241250|sp|Q02410	NA
1978	PMLPNTYQPQPDS	gi|8134339|sp|P56945|B	NA
1979	VVALYDYMPMNAN	gi|547759|sp|Q06187|BT	NA
1980	VVKREPYGKPVDV	gi|145559462|sp|O14936	NA
1981	LAGEIVYQPDGSA	gi|108935822|sp|Q15911	NA
1982	KLSSGQYPNLETF	gi|22653668|sp|Q9UIF8|	NA
1983	LQAQSDYEEIKTE	gi|67476941|sp|O14529|	NA
1984	DTESDFYEEIEVS	gi|1352398|sp|P49640|E	NA
1985	MRLTISYLRVRKL	gi|2498017|sp|Q16665|H	NA
1986	APEAPVYANLSSY	gi|135308|sp|P17535|JU	NA
1987	GTDSWVYPNISIP	gi|13959682|sp|Q16281|	NA
1988	DVKFKNYLIPKGM	gi|306327|gb|AAA02630.	NA
1989	ILLLVIYTAVFTP	gi|26006810|sp|Q9H252|	NA
1990	FFAPSLYIIPLGI	gi|6225708|sp|O15403|M	NA
1991	MRDVDMYINLFHD	gi|1709292|sp|P55011|S	NA
1992	MARFYTYINPAEI	gi|1172435|sp|P46059|S	NA
1993	EDAANNYARGHYT	gi|119591124|gb|EAW70	NA
1994	SVKDIQYLKDSLA	gi|1171955|sp|P42338|P	NA
1995	STENQSYAKHSAN	gi|116242614|sp|Q96RT	NA
1996	PCLQGYYTAAELK	gi|51315841|sp|Q14435|	NA
1997	TFPNLDYSECCLF	gi|134047802|sp|Q9BYX	NA
1998	LEHLICYSFQVAK	gi|9087218|sp|P35968|V	[LEHLICYSFQVAK|Y|10
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2000	H6:17	contol_spot	NA
2001	NFSWRGYAQMAPV	gi|126302563|sp|O15230	NA
2002	TDSCDPYFMLNNV	gi|27151691|sp|Q9UP95|	NA
2003	ERRESLYAHHAQV	gi|122890477|emb|CAM1	NA
2004	LQPCTAYVPVYPV	gi|23821870|sp|Q99946|	NA
2005	VIYCDQYASLIPV	gi|38503353|sp|Q8NFU1	NA
2006	SAAKTYYMSGGLQ	gi|134044259|sp|P11177	NA
2007	RFVEFYYWDSYWV	gi|3287921|sp|O43280|T	NA
2008	YRCELLYEGPPDD	gi|119172|sp|P13639|EF	NA
2009	IASPSKYVYILYV	gi|119623143|gb|EAX02	NA
2010	LRSDCFYEQPDED	gi|90185249|sp|Q9BYK8	NA
2011	YFSRDAYWEKLYV	gi|547807|sp|P07949|RE	NA
2012	EPEEVQYKKSTAW	gi|150456451|ref|NP_06	NA
2013	LSFGESYDNSKSW	gi|119608751|gb|EAW88	NA
2014	LILECKYVKKPLQ	gi|68565242|sp|Q8WW1	NA
2015	LLKKTKYGDRGNQ	gi|17366458|sp|Q14573|	NA
2016	LPDELLYGRAGYL	gi|47116933|sp|Q9NS86|	NA
2017	LRSDDIYNQVSAY	gi|2495719|sp|Q12768|S	NA
2018	RGLQEGYENSRCY	gi|134035341|sp|Q9C0C	NA
2019	DIDENAYAKVCLY	gi|6174930|sp|Q13200|P	NA
2020	EFQDELYKNTPKY	gi|119585105|gb|EAW64	NA
2021	QADMTKYLEGSLY	gi|147668009|sp|Q8N6K	NA
2022	VLQWSDYEIVRLQ	gi|13633364|sp|O14966|	NA
2023	AQSGEDYDSFLMY	gi|13638154|sp|P16144|	NA
2024	KLGYDPYANPPNY	gi|6686059|sp|O60507|T	NA
2025	TCTEGKYGIHCDQ	gi|145559531|sp|Q8WW	NA
2026	FCQRELYEDSLLD	gi|143811449|sp|Q96EQ	NA
2027	KKHFDSYIETALD	gi|119576332|gb|EAW55	NA

2028	AAAEWKYVAMVMD	gi|113071|sp|P02708|AC	NA
2029	KTSMSGYIPSYLD	gi|135705|sp|P10827|TH	NA
2030	HLECARYMDVREA	gi|7020152|dbj|BAA9101	NA
2031	DFSKQPYIVSAAE	gi|109896166|sp|Q3MJ1	NA
2032	FGRSEQYRQVASP	gi|20178334|sp|O95409|	NA
2033	NPLEYKYKNGASP	gi|56404632|sp|Q8TAT5|	NA
2034	YEAFEGYDSIDSP	gi|20978543|sp|O00231|	NA
2035	LSCEGRYERGRAE	gi|68565596|sp|Q8IZL2|	NA
2036	EQSGTIYLQHADE	gi|134047855|sp|P37198	NA
2037	SYGDSLYYNNAYG	gi|62511089|sp|Q9BWF	NA
2038	ILSDEIYCPPETA	gi|125987826|sp|P15311	NA
2039	LDRMAKYEISALE	gi|81170632|sp|Q6NV75|	NA
2040	IPGATGYEENTYL	gi|21753422|dbj|BAC043	NA
2041	KALDTSYVILPTA	gi|10719900|sp|O14514|	NA
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2043	<<Marker>>	contol_spot	NA
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2045	ASDMSPYVRKTAA	gi|18202497|sp|Q13367|	NA
2046	MLGKALYENMLVE	gi|67462009|sp|Q15386|	NA
2047	YYADTIYTSAGVE	gi|134053883|ref|NP_99	NA
2048	GREATKYVRWIAF	gi|122063373|sp|Q8NHV	NA
2049	LDDNFYYQSMRYE	gi|116242735|sp|Q8IV42	NA
2050	LQHEYPYEDHLWL	gi|119575395|gb|EAW55	NA
2051	FHFEGSYDSISKA	gi|145617724|ref|ZP_01	NA
2052	IAEELLYLRVVRG	gi|32364694|gb|AAP803	NA
2053	SDWDSPYLDMELA	gi|51702148|sp|Q9H987|	NA
2054	CIYEWFYSNIDKP	gi|74708186|sp|Q5TKA1|	NA
2055	EHCGAAYEDFNIP	gi|3192971|gb|AAC1916	NA
2056	GPPEPPYSFHQVT	gi|5921785|sp|O43525|K	NA
2057	KEFDPKYAHIQVT	gi|32469767|sp|Q96BY6|	NA
2058	DPDESSYFVIGAV	gi|10719903|sp|O60241|	NA
2059	FSKDPDYIVVPYT	gi|332129|gb|AAA46542.	NA
2060	MDEKTLYLALGAV	gi|2833247|sp|Q13797|IT	NA
2061	QVSSPIYDINYYT	gi|1705896|sp|P51681|C	NA
2062	RGSRTGYVHIYDV	gi|109892504|sp|Q53GT	NA
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2066	VGAWGDYDDSAFV	gi|113413200|ref|XP_93	NA
2067	ALPPTDYDRSPFV	gi|7676156|sp|O00482|N	NA
2068	GFSGEQYVLEKGV	gi|74750904|sp|Q8N1P7|	NA
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2070	TVEVDLYTAKGLF	gi|20981682|sp|P09104|	[TVEVDLYTAKGLF|Y|25
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2073	TGAKNLYIISVKG	gi|51338639|sp|P62829|	NA
2074	GPYSKQYAGYDYS	gi|74760683|sp|Q969M3|	[GPYSKQYAGYDYS|Y|3
2075	HFIKDEYKENPLF	gi|55976292|sp|Q08683|	NA
2076	LRMKGDYVLGGLF	gi|62299063|sp|Q7RTX0	NA
2077	VESKNAYGITPLF	gi|20531999|sp|Q96Q27|	NA
2078	GRESSGYLRLAFH	gi|114607680|ref|XP_51	NA
2079	DSHMDTYEQGVLF	gi|115311843|sp|Q5JRX	NA

2080	IQSDFIYFRKGPF	gi|71891697|dbj|BAA864	NA
2081	NTSSYEYTDVPFH	gi|67477354|sp|O95897|	NA
2082	YCKWPEYQRGGFH	gi|6686252|sp|Q99765|	NA
2083	ILEHLEYADEAEA	gi|74761513|sp|Q9H7X2|	NA
2084	GRRKVDYILVYHH	gi|74708278|sp|Q5XXA6	NA
2085	<<Marker>>	contol_spot	NA
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2087	KLPDDHYQEKTAM	gi|74750502|sp|Q86WG	NA
2088	QIKSLQYSNTGDM	gi|119576364|gb|EAW55	NA
2089	NDEHTSYGETGVP	gi|125991837|sp|Q9NZJ	NA
2090	SEELTKYKIVTYL	gi|20137579|sp|Q9Y239|	NA
2091	KWEEIPYVQAFMA	gi|21751026|dbj|BAC038	NA
2092	VPSKEAYCAYAII	gi|2499523|sp|Q13183|S	NA
2093	LNEEGGYHQIGPA	gi|119569260|gb|EAW48	NA
2094	QGSEATYESGFVI	gi|119572311|gb|EAW51	NA
2095	DGRSQDYINDAAK	gi|115556|sp|P21941|MA	NA
2096	GLEKTHYNSTSWI	gi|30315933|sp|Q8TF62|	NA
2097	LWRKDKYDCLIWI	gi|729367|sp|P40879|S2	NA
2098	QSNKEAYVISLYI	gi|20455347|sp|O95922|	NA
2099	HVGESLYAIVLCK	gi|71152986|sp|Q8TBM7	NA
2100	CRSFSLYVSCNCC	gi|24370915|emb|CAC8	NA
2101	NIGKGSYAIPGDC	gi|3024670|sp|Q15831|S	NA
2102	NGREAEYSDKHGQ	gi|19860819|sp|P54760|	NA
2103	LFFDDSYGFYPGQ	gi|134035341|sp|Q9C0C	NA
2104	VFSMVLYCQIGNK	gi|116589|sp|P19075|TS	NA
2105	KVAKVEYVRKKPK	gi|129719|sp|P04085|PD	NA
2106	<<Marker>>	contol_spot	NA
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2108	TRPNTDYSCGGFL	gi|85687556|sp|Q9UGM	NA
2109	TRVAPAYAKMGEM	gi|27735161|sp|P17342|	NA
2110	CSFKCSYVVTNGL	gi|1172027|sp|P43490|N	NA
2111	GGENTAYMSNGGL	gi|12643949|sp|Q9Y2T1|	NA
2112	HLEEVVYNQLNGL	gi|143811393|sp|Q9HCQ	NA
2113	RQSKELYGTWEML	gi|22256935|sp|Q96TA1|	NA
2114	VTVKETYCSVTNL	gi|119582843|gb|EAW62	NA
2115	QPPGGDYQQPPPL	gi|88909269|sp|Q86UL8|	NA
2116	MLEEEDYPGAIQL	gi|119597226|gb|EAW76	NA
2117	HKPDEIYGMIERL	gi|33301371|sp|Q86U44|	NA
2118	EESDADYDYQNRL	gi|60416383|sp|P12259|	NA
2119	AYKESTYAKGKNM	gi|113422349|ref|XP_93	NA
2120	ENGCEEYGIMCPM	gi|74762527|sp|Q8N573|	NA
2121	AGYGDIYLNAGPM	gi|66774048|sp|Q14004|	NA
2122	NVMMGPYRQDLLA	gi|21903479|sp|P18206|	NA
2123	PDVLEYYKNDHAK	gi|90180201|sp|Q13480|	NA
2124	PIQEANYVPMTPG	gi|90180201|sp|Q13480|	[PIQEANYVPMTPG|Y|4
2125	DEVYSKYYTPVPC	gi|41019536|sp|P51692|	NA
2126	WGLAEFYHPGQEY	gi|55977123|sp|P68400|	NA
2127	<<Marker>>	contol_spot	NA
2128	YFLDDQYTSSSGA	gi|1174630|sp|P42680|T	NA
2129	YIEDEDYYKASVT	gi|3183003|sp|Q14289|F	[YIEDEDYYKASVT|Y|57
2130	YVDPHTYEDPNQA	gi|125333|sp|P29317|EP	[YVDPHTYEDPNQA|Y|5
2131	YVLDDQYVSSVGT	gi|1705489|sp|P51813|B	[YVLDDQYVSSVGT|Y|5

2132	IKLMEKYHVEAEE	gi|9626575|ref|NP_0408	NA
2133	INNIDYYKKTTNG	gi|119569729|gb|EAW49	NA
2134	IYKDPDYVRKGSA	gi|1718189|sp|P35916|V	NA
2135	APGMKVYIDPFTY	gi|76803655|sp|P54753|	[APGMKVYIDPFTY|Y|60
2136	KAYGNGYSSNGNT	gi|114765|sp|P07550|AD	NA
2137	KKTFASYMPQFQT	gi|116242617|sp|P48357	[KKTFASYMPQFQT|Y|1
2138	VHVNATYVNVKCV	gi|125484|sp|P08581|ME	[VHVNATYVNVKCV|Y|1
2139	NGNNYVVYIDPTQL	gi|125472|sp|P10721|KIT	[NGNNYVVYIDPTQL|Y|56
2140	ESTNHIYSNLANC	gi|125472|sp|P10721|KIT	[ESTNHIYSNLANC|Y|93
2141	PTAGALYSGSEGD	gi|134876|sp|P11831|SR	NA
2142	VEEEPVYEAEPEP	gi|123557|sp|P14317|HC	[VEEEPVYEAEPEP|Y|3
2143	MLRLQDYEEKTKK	gi|125987826|sp|P15311	[MLRLQDYEEKTKK|Y|3
2144	TLSEESYKDSTLI	gi|51702210|sp|P62258|	NA
2145	EEAEEPYEEATER	gi|112927|sp|P05067|A4_	NA
2146	IFKSSCYIDVRWF	gi|91208254|sp|Q494W8	NA
2147	KNPKNPYEESSRD	gi|119226|sp|P01133|EG	NA
2148	<<Marker>>	contol_spot	NA
2149	GVESEFYLAMNKE	gi|122756|sp|P21781|FG	NA
2150	TQDGPLYVIVEYA	gi|119583714|gb|EAW63	NA
2151	TLQQAEYEFLSFV	gi|116242694|sp|Q9Y3B	NA
2152	HTGEKPYACLECG	gi|74757437|sp|Q6DD87	[HTGEKPYACLECG|Y|1
2153	ATREGDYVLFHHE	gi|116241237|sp|P53396	NA
2154	MKNLTQYEQLKAH	gi|60389833|sp|Q8IZD4|	NA
2155	EHALLAYTLGVKQ	gi|156056334|ref|XP_00	[EHALLAYTLGVKQ|Y|14
2156	KRLTHVYDLCKGK	gi|133326|sp|P24928|RP	[KRLTHVYDLCKGK|Y|1
2157	ERYTEFYHVPTHS	gi|47605572|sp|Q96HC4	[ERYTEFYHVPTHS|Y|2
2158	KIVDNGYGYVSNG	gi|20141641|sp|P49589|	NA
2159	HFPLATYAPVISA	gi|119591124|gb|EAW70	[HFPLATYAPVISA|Y|27
2160	SKFDTIYQILLKK	gi|12585547|sp|Q14258|	[SKFDTIYQILLKK|Y|278|
2161	HTGEKPYECIKCG	gi|91208389|sp|Q2M3W	[HTGEKPYECIKCG|Y|2
2162	IDDESDYFASDSN	gi|116242828|sp|Q1565	[IDDESDYFASDSN|Y|28
2163	ARIQRAYNHYFDL	gi|42560556|sp|Q9NZW	[ARIQRAYNHYFDL|Y|50
2164	HSGEKPYECVECG	gi|14548338|sp|O43296|	[HSGEKPYECVECG|Y|5
2165	GGEDPLYVARRLV	gi|73622085|sp|Q96S55|	NA
2166	ENTEDQYSLVEDD	gi|118572681|sp|P27986	[ENTEDQYSLVEDD|Y|6
2167	YTTDFIYQLYSEE	gi|1346355|sp|Q01813|K	[YTTDFIYQLYSEE|Y|651
2168	DPGAAPYLKTKFI	gi|21618338|ref|NP_003	NA
2169	<<Marker>>	contol_spot	NA
2170	YGGGGQYFAKPRN	gi|133254|sp|P09651|RO	[YGGGGQYFAKPRN|Y|
2171	TPDHVVYARSKTA	gi|56749614|sp|Q6NZI2|	[TPDHVVYARSKTA|Y|31
2172	PSQDSLYSDPLDS	gi|17366642|sp|Q99704|	[PSQDSLYSDPLDS|Y|31
2173	HVPAGLYRIRKGV	gi|45645212|sp|Q9Y2X7|	[HVPAGLYRIRKGV|Y|55
2174	QRKKPLYWDLYEH	gi|17366642|sp|Q99704|	[QRKKPLYWDLYEH|Y|3
2175	PLPNCTYATRQAI	gi|74742134|sp|Q5JTD0|	NA
2176	LTPENLYDVHGPG	gi|1708905|sp|P53338|M	NA
2177	ILENNEYPDIVTW	gi|730744|sp|P38889|SK	NA
2178	MKNFEDYSNRLPS	gi|729290|sp|P21657|DA	NA
2179	EFEEFDYSINRVL	gi|731945|sp|P39529|YJ	NA
2180	TSSKKKYLDHIIL	gi|1173439|sp|P46954|S	NA
2181	YNEEQNYSEARKK	gi|88984071|sp|P17106|	NA
2182	VMSVSSYMDNHNV	gi|1169823|sp|P04386|G	NA
2183	YKSAPIYEIINKE	gi|1169136|sp|P41817|C	NA

2184	NNSNNSYYSNNED	gi|3024551|sp|Q12224|R	NA
2185	KRVNDSYDSPLSG	gi|41016991|sp|Q03063|	NA
2186	KIYQPSYLSINNE	gi|6685617|sp|Q99683|M	NA
2187	KPSNILYVDESGD	gi|147906429|ref|NP_001	NA
2188	MLEGVKYLCIPAA	gi|74752929|sp|Q9NRW4	NA
2189	ETEARKYVRNSRM	gi|23831505|sp|O43709|	NA
2190	<<Marker>>	contol_spot	NA
2191	LGRWPGYLNGGRM	gi|74758793|sp|Q6ZS27|	NA
2192	RICMWKYLDVHSM	gi|118764281|gb|AAI2813	NA
2193	SSRNEDYPRTCRM	gi|146345419|sp|Q5XUX	NA
2194	AKSEEAYAEDSVM	gi|52783206|sp|Q8NC51	NA
2195	DYPDNTYVSSSEN	gi|74714811|sp|Q8N3A8|	NA
2196	FCRKPIYLMNNFN	gi|119581094|gb|EAW60	NA
2197	KRFIGDYERNAGN	gi|61563659|gb|AAX4679	NA
2198	LMEKTGYNMVQEN	gi|119625308|gb|EAX049	NA
2199	QEFVDAYVDYIFN	gi|74707832|sp|Q5GLZ8|	NA
2200	AECKTSYESRSGN	gi|34364940|emb|CAE46	NA
2201	ASVMQEYTQSGGV	gi|130850|sp|P25787|PSA	NA
2202	NMLMERYRVESDL	gi|149395322|gb|ABR275	NA
2203	LLVAEDYMIVYLN	gi|38257451|sp|Q86WG3	NA
2204	RRCNIEYSSTGLN	gi|74733564|sp|Q9H2Q1	NA
2205	VKKCTRYIDCDLN	gi|1168340|sp|P45381|A	NA
2206	CGKEGKYIHFTPN	gi|5729769|ref|NP_00652	NA
2207	NGGDHRYVNNYTN	gi|116242825|sp|Q14134	NA
2208	VVHLDDYNDHAPQ	gi|2493422|sp|Q08554|D	NA
2209	DVCSIDYISGNPQ	gi|152031705|sp|Q8NHU	NA
2210	GLGESLYILVGQQ	gi|143811416|sp|P29376	NA
2211	LRENGTYPDAEQQ	gi|21748502|dbj|BAC033	NA
2212	RHSGPPYVGPPQQ	gi|48428276|sp|O43432|	NA
2213	IGVKSAYVSYDVQ	gi|109895058|sp|Q9NUM	NA
2214	LYLEDFYVTQAYQ	gi|143583359|sp|Q86VE3	NA
2215	RIKKPDYKVAYVQ	gi|68566020|sp|Q16540|	NA
2216	CLDDDTYMKDLYQ	gi|74723724|sp|Q8N392|	NA
2217	FGSKDYYWTHQAR	gi|74706096|sp|O96028|	NA
2218	LDDSPEYGLHGYQ	gi|51316029|sp|Q8NCQ5	NA
2219	GYACPYYHNSKDR	gi|47117622|sp|Q9C0B0|	NA
2220	IPEMEGYMKAEVA	gi|119591469|gb|EAW71	NA
2221	RDKWDQYKGVGVA	gi|119226260|ref|NP_006	NA
2222	AKNKDGYTPLLVA	gi|22653655|sp|Q92527|A	NA
2223	EAPEVLYWAVPVA	gi|119620941|gb|EAX005	NA
2224	TLETEHYPHPGGG	gi|119624572|gb|EAX041	NA
2225	DRRDDAYWPEGKR	gi|38372432|sp|Q14151|S	NA
2226	GAAMAEYVKAGKR	gi|74728990|sp|Q8N5F7|	NA
2227	ISNAAEYENIPIR	gi|56405304|sp|O75643|U	NA
2228	LLFENQYYPNGIR	gi|74748429|sp|Q6DN90	NA
2229	VESEQQYFEIEKR	gi|1730009|sp|P12270|TF	NA
2230	ECKEGRYLEIEFC	gi|21264084|sp|O00300|T	NA
2231	LFACEEYAQNALR	gi|124020999|sp|Q6NXG	NA
2232	RVAESTYQHHPKR	gi|41017505|sp|Q9HCL0	NA
2233	SWSMGAYKSSTIC	gi|81175180|sp|Q9P2G3	NA
2234	NLPLPDYVHPQLR	gi|74745673|sp|Q5T9G4|	NA
2235	DAHDDSYTCECPR	gi|119591638|gb|EAW71	NA

2236	PIYGTYYVDHINR	gi|88909269|sp|Q86UL8|	NA
2237	LVPESDYTNNVVR	gi|417269|sp|P28300|LY	NA
2238	AGFTTIYKWNGNG	gi|32469669|sp|O95970|	NA
2239	EARQDGYGDRTLG	gi|18202503|sp|Q15223|	NA
2240	GIPEGPYSEGGNG	gi|110808200|sp|Q6Y2X	NA
2241	LLFDDGYECDVLG	gi|8928568|sp|Q12888|T	NA
2242	QYVKELYEQECNG	gi|15214192|sp|Q9UKL6|	NA
2243	LPSDTSYSEQEDS	gi|150383497|sp|Q9UGL	NA
2244	SLVGEEYKSIPCS	gi|74753030|sp|Q9NWU	NA
2245	ASGAEPYIKNPDS	gi|32469767|sp|Q96BY6|	NA
2246	GAVEECYVSELDS	gi|32129530|sp|Q14315|	NA
2247	LLYKTDYSNDFDS	gi|119591469|gb|EAW71	NA
2248	TKDSDIYCTLNDS	gi|116256077|sp|Q9BYW	NA
2249	HRQGHIYMEMNFT	gi|51702211|sp|P63010|	NA
2250	IIQAEFYLNPDQS	gi|122206|sp|P01903|2D	NA
2251	TSADHLYVNVSEL	gi|1345957|sp|P48023|T	NA
2252	DKDLRHYLNLRFQ	gi|88909269|sp|Q86UL8|	NA
2253	IFPQPNYVDMLIS	gi|37999836|sp|Q9Y5G6	NA
2254	AAAAETYANISWE	gi|33112413|sp|Q92823|	NA
2255	RLSGELYGRATAW	gi|22001556|sp|Q99999|	NA
2256	IAANCIYLNIPNK	gi|6831528|sp|O94760|D	NA
2257	KHATGNYIIIMDA	gi|20137697|sp|O60762|	NA
2258	NFHSFLYQPDWRF	gi|585126|sp|P37268|FD	NA
2259	AVCFFSYLRVSQD	gi|1730136|sp|P51993|F	NA
2260	KVLGLKYEEIDCL	gi|62901521|sp|O94923|	NA
2261	CTLWEAYANLHTA	gi|1705489|sp|P51813|B	NA
2262	VCEELTYEEIRDT	gi|3023733|sp|Q16875|F	NA
2263	RVGTVGYMAPEVV	gi|143811400|sp|P32298	NA
2264	LQMFMWYLNPRQV	gi|12643642|sp|O75912|	NA
2265	DFEGFSYVNPQFV	gi|125549|sp|P17252|KP	[DFEGFSYVNPQFV|Y|6
2266	FTGTLQYMAPEII	gi|116248533|sp|Q6ZN1	NA
2267	FWGCDSYANLNTE	gi|21542119|sp|Q9BXB1	NA
2268	FLGATNYIYVLNE	gi|125484|sp|P08581|ME	NA
2269	GKDYFDYINVGSW	gi|1709020|sp|P41594|M	NA
2270	HNGVSYYINLCQK	gi|60416403|sp|P11717|	NA
2271	IMSKAAYMPMAAS	gi|14423818|sp|Q9NQN1	NA
2272	GESDGGYMDMSKD	gi|129890|sp|P09619|PG	[GESDGGYMDMSKD|Y|
2273	MTGEDGYYFTNLC	gi|56405102|sp|Q9UJ41|	NA
2274	QARGSAYTDPHLC	gi|119622563|gb|EAX02	NA
2275	YRMDDVYKEPLKC	gi|24211441|sp|Q13443|	NA
2276	PLPAEGYNKVGPG	gi|9087156|sp|Q14934|N	NA
2277	GTFGTEYVFPEVL	gi|134047954|sp|O95498	NA
2278	CEFETLYKAFSNC	gi|74757726|sp|Q6ICH7|	NA
2279	LSEADPYVILQLS	gi|74750540|sp|Q86XP0|	NA
2280	QAKAEIYEMRPLS	gi|20141419|sp|Q12887|	NA
2281	SFCNPVYQFINLS	gi|134254443|ref|NP_05	NA
2282	GEAEEEYVGPRLS	gi|108884834|sp|Q1389	NA
2283	QGSCLVYQNSAMS	gi|27734555|sp|Q96BD0|	NA
2284	AKTKEKYVLGQNS	gi|110816415|sp|Q15464	NA
2285	SLREGLYFNPYFP	gi|117759|sp|P08574|CY	NA
2286	GTEDESYEYRPRS	gi|125991860|sp|O9491	NA
2287	GMSDHRYGDGGSS	gi|2500576|sp|P55795|H	NA

2288	RNSEVKYTEACSS	gi|114593243|ref|XP_001	NA
2289	PCSRVEYVSSLSS	gi|131573277|gb|ABO33	NA
2290	GTPEGYYMFIETS	gi|46396459|sp|Q8NFP4	NA
2291	EFYMTIYEDSVAT	gi|74762463|sp|Q86XP1|	NA
2292	HHKKECYLNFDDT	gi|116242623|sp|Q9NS1	NA
2293	GACGDSYAAQGWL	gi|116242837|sp|Q9Y2K	NA
2294	TTFMCEYADETAT	gi|45593462|sp|P60568|	NA
2295	GFYEVDYASFHET	gi|125987834|sp|Q9280	NA
2296	AEPFEGYLEPNET	gi|67477390|sp|Q01968|	NA
2297	VCPQAHYNMYPQN	gi|41019536|sp|P51692|	[VCPQAHYNMYPQN|Y|7
2298	YQSITHYRPVSAS	gi|1706639|sp|P50402|E	[YQSITHYRPVSAS|Y|16
2299	SKDKDAYSSFGSR	gi|73620957|sp|O15523|	[SKDKDAYSSFGSR|Y|6
2300	EDEEYEYMNRRRR	gi|119534|sp|P21860|ER	[EDEEYEYMNRRRR|Y|1
2301	LNNGKFYVGVCAF	gi|1172823|sp|P43351|R	[LNNGKFYVGVCAF|Y|1
2302	PGVASGYVSSADL	gi|1345923|sp|P32927|IL	[PGVASGYVSSADL|Y|7
2303	GTGGSVYTEDNDD	gi|6094447|sp|P55072|T	[GTGGSVYTEDNDD|Y|7
2304	GGPGGDYAAMGAC	gi|119534|sp|P21860|ER	[GGPGGDYAAMGAC|Y|
2305	RYYEGYYAAGPGY	gi|74751663|sp|Q93052|	[RYYEGYYAAGPGY|Y|3
2306	SSNGHVYEKLSSI	gi|14548162|sp|Q13224|	[SSNGHVYEKLSSI|Y|14
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2308	DDEDDSYLEPDSP	gi|3023207|sp|P78314|3	[DDEDDSYLEPDSP|Y|1
2309	SSQRRSYAFETQA	gi|134035020|sp|Q7Z6I6	[SSQRRSYAFETQA|Y|1
2310	VNEAPVYSVYSKL	gi|71153548|sp|O75886|	[VNEAPVYSVYSKL|Y|37
2311	KQVEELYHSLLEL	gi|94730425|sp|Q13813|	NA
2312	VQEAEKYKAEDEV	gi|147744565|sp|P08107	[VQEAEKYKAEDEV|Y|5
2313	ASLESLYSACSMQ	gi|6166186|sp|Q13322|G	[ASLESLYSACSMQ|Y|6
2314	FANFSAYPSEEDM	gi|67476728|sp|P42566|	[FANFSAYPSEEDM|Y|8
2315	KKSWEVYQGVCQK	gi|2506481|sp|P30411|B	[KKSWEVYQGVCQK|Y|
2316	LSADSGYIIPLPD	gi|129892|sp|P16234|PG	[LSADSGYIIPLPD|Y|101
2317	QRKIKKYRLQQAQ	gi|68067956|sp|P05362|	[QRKIKKYRLQQAQ|Y|5
2318	RTALLNYENLPSL	gi|71152057|sp|Q8WU2	NA
2319	VDSDNAYIGVTYK	gi|129892|sp|P16234|PG	[VDSDNAYIGVTYK|Y|98
2320	DDFDSDYENPDEH	gi|82592659|sp|Q8WV2	[DDFDSDYENPDEH|Y|7
2321	TKDGWVYYANHTE	gi|74725363|sp|Q9NZC7	[TKDGWVYYANHTE|Y|
2322	ADERVDYVVVDQQ	gi|90180201|sp|Q13480|	[ADERVDYVVVDQQ|Y|6
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2324	AVENPEYLTPQGG	gi|119533|sp|P04626|ER	[AVENPEYLTPQGG|Y|1
2325	LDVLKFYDSNTVK	gi|143811432|sp|Q13177	[LDVLKFYDSNTVK|Y|13
2326	YVNEPLYLNTFAN	gi|3913590|sp|Q15303|E	NA
2327	LIESELYFLIARY	gi|97535778|sp|Q9NSI6|	NA
2328	VTIDSSYDIAKIS	gi|84028186|sp|P36222|	NA
2329	PKGVLLYGPPGTG	gi|148702336|gb|EDL34	NA
2330	DKHNCPYDYKAEA	gi|25091738|sp|O76080|	NA
2331	TPGDFSYAYQKPE	gi|1170875|sp|P46821|M	NA
2332	ACGTPGYVAPEVL	gi|3122301|sp|Q14012|K	NA
2333	TVSEENYMCRRFL	gi|47116568|sp|Q96EK6|	NA
2334	AECLDEYEDDEAG	gi|66773935|sp|Q96IZ0|	NA
2335	NANSGYYEAHPVT	gi|116242482|sp|Q9UN8	NA
2336	ITTNRFYGPQVNN	gi|62291053|sp|O00401|	NA
2337	DKEGDDYEVIPNS	gi|30173386|sp|Q9NTJ3|	NA
2338	KIVLQKYHTINGH	gi|133257|sp|P22626|RO	NA
2339	YDLSSKYYQTIGN	gi|20978558|sp|Q9UNM	NA

2340	GADGGLYQIPLPS	gi|17433253|sp|Q9NZQ3	NA
2341	FKKHGVYNPNKIF	gi|6648067|sp|P40926|M	NA
2342	LQVKTWYQNRRMK	gi|13431329|sp|Q9UMQ	NA
2343	ILDDSGYVSAYKN	gi|28380040|sp|Q9BW3	NA
2344	RSEPDLYCDPRGT	gi|20138951|sp|Q13835|	NA
2345	ERRDLQYITVSKE	gi|12644018|sp|P55196|	NA
2346	VGSRLGYLPGKGT	gi|1710032|sp|P29375|J	NA
2347	ITLSAIYKWITDN	gi|12644465|sp|Q92949|	NA
2348	QAQPRQYYLKGLS	gi|119575831|gb|EAW55	NA
2349	SEWKQKYEETQAE	gi|3041707|sp|P13535|M	NA
2350	SLEYSEYMTGKKL	gi|74760971|sp|Q96MM	NA
2351	AQWKTKYETDAIQ	gi|13431717|sp|Q9UKX3	NA
2352	YRLYVIYKVPQVR	gi|31077165|sp|P09661|	NA
2353	RHMDGMYGPPAKR	gi|73921720|sp|Q8NFD5	NA
2354	YRKEPLYAAFPGS	gi|42559872|sp|Q9C0H9	NA
2355	IRLKLVYDKCDRS	gi|3041727|sp|Q07869|P	NA
2356	LKELEKYEQLPED	gi|8928460|sp|O75962|T	NA
2357	TAYEVCYGLVNDD	gi|13638154|sp|P16144|	[TAYEVCYGLVNDD|Y|1
2358	REIQDNYLLIVKG	gi|148886692|ref|NP_00	NA
2359	DDLDPNYVLSSRV	gi|125305|sp|P06732|KC	NA
2360	HMYHSLYLKVKGN	gi|51338661|sp|P84098|	NA
2361	RGGARRYACRGGG	gi|1709254|sp|P55055|N	NA
2362	SLEELGYEYMDVG	gi|119534|sp|P21860|ER	NA
2363	DMKYGIYAVENEH	gi|126302613|sp|Q9UEU	NA
2364	HSYEDPYFDDRVH	gi|20139104|sp|Q99569|	NA
2365	PADDHRYKFADNK	gi|12644474|sp|Q99593|	NA
2366	DEEDTYYTKDLPI	gi|17380291|sp|Q92900|	NA
2367	FEDKSAYALCTFA	gi|30173120|sp|Q9BY32|	NA
2368	FIRVVMYEGKKIM	gi|117949802|sp|P07996	NA
2369	IFVERRYTAVVLN	gi|24418367|sp|Q9UPY3	NA
2370	TFNVDMYEEIHRK	gi|20981690|sp|Q13098|	NA
2371	EGIKQFYINVERE	gi|45645183|sp|Q14240|	NA
2372	FCGTIEYMAPDIV	gi|37999482|sp|O75582|	NA
2373	PCGSAEYMAPEVV	gi|90102033|sp|Q9HBH9	NA
2374	SCLNISYANVAGP	gi|33516944|sp|Q9UNW	NA
2375	HPYLEPYGLVYCV	gi|27805644|sp|Q9BU40|	NA
2376	DGFYYLYANICFR	gi|12643360|sp|O14788|	NA
2377	RLDPEAYGAPCAR	gi|3914477|sp|O43240|K	NA
2378	TGETCVYPNPANV	gi|124056489|sp|P02458	NA
2379	RLLHSDYMNMTPR	gi|115973|sp|P10747|CD	[RLLHSDYMNMTPR|Y|1
2380	RSAWLPYPNPNPH	gi|109939725|sp|Q13591	NA
2381	PFIKITYEEIPLP	gi|5921793|sp|O75503|C	NA
2382	NLQMLTYLNLSRN	gi|49066056|sp|Q9Y2L9|	NA
2383	MVRKEYPNLSTS	gi|76803550|sp|Q9BTX7|	NA
2384	ILPRSDYIIIPKS	gi|2495717|sp|Q12766|S	NA
2385	GLVDVLYTAVLDL	gi|3024887|sp|O15063|K	NA
2386	HKPSQSYLRVRNK	gi|20140756|sp|Q9BVV6	NA
2387	NRTTENYPNAGLI	gi|114062|sp|P08519|AP	NA
2388	QKIEEAYGDVSGL	gi|116241261|sp|Q1672	NA
2389	PVEILNYIIPSGD	gi|145559458|sp|Q9NYL	NA
2390	YELALKYLNIAFT	gi|146345380|sp|Q1587	NA
2391	IFFFVSYIIISFL	gi|119631737|gb|EAX11	NA

2392	ITAIIAYPNPYTR	gi|20141247|sp|P51793|	NA
2393	DPGERLYDLNMPA	gi|127962|sp|P16333|NC	NA
2394	IIDKEYYYTKEEQ	gi|55976470|sp|Q7L5N1|	NA
2395	KWLHNEYVRDLPV	gi|51316565|sp|O14795|	NA
2396	VRANTAYHLHQRL	gi|116242614|sp|Q96RT	NA
2397	VVACNLYPFVKTV	gi|23831360|sp|P31939|	NA
2398	LCKSADYMNLHFK	gi|71153185|sp|Q9UPW	NA
2399	G2:17	contol_spot	NA
2400	G6:17	contol_spot	NA
2401	NWDMTGYGSHSKV	gi|21431782|sp|Q9H2X6|	NA
2402	AAATDAYSQMQLV	gi|14602658|gb|AAH098	NA
2403	ILKKNYYKSPNLV	gi|11493437|gb|AAG354	NA
2404	NSTDLGYANGNLV	gi|119611339|gb|EAW90	NA
2405	AAFEPVYWLVDNV	gi|37999852|sp|Q969W1	NA
2406	ISFDGIYANMRMV	gi|52000732|sp|Q99700|	NA
2407	AAFKAHYSSNPSG	gi|91207142|sp|Q9NT99|	NA
2408	PWGEVKYSTYGTG	gi|119600767|gb|EAW80	NA
2409	ENCKDKYYNCNVV	gi|119598279|gb|EAW77	NA
2410	PNYKWGYCSNTVV	gi|48474987|sp|Q9P2L0|	NA
2411	DSDAEGYVEGLDD	gi|730318|sp|P39687|AN	NA
2412	MNYKGRYEITAED	gi|74752718|sp|Q9H814|	NA
2413	DPRNEIYILFNPW	gi|57015359|sp|P22735|	NA
2414	FNPECLYVFPCQW	gi|152125899|sp|A0PJZ	NA
2415	KLREEGYLAYYLQ	gi|3913541|sp|Q99956|D	NA
2416	KNEVQDYVSVEYL	gi|67461057|sp|Q8NHP6	NA
2417	TTMNLSYVFIPLW	gi|47605551|sp|Q9H2L4|	NA
2418	KRSEYIYGENQLQ	gi|119607215|gb|EAW86	NA
2419	CTVEQIYEILKIY	gi|2493531|sp|Q14790|C	NA
2420	FNMEPSYDFLHIY	gi|38604975|sp|Q96PZ7|	NA
2421	LFEMNGYLDSAIY	gi|74751569|sp|Q8WW2	NA
2422	PYNMETYDQRAIY	gi|61813357|ref|XP_598	NA
2423	SQADLDYVVPQIY	gi|61252289|sp|Q8TEQ8	NA
2424	AAWMAYYINHPLY	gi|20177939|sp|Q9NZ01|	NA
2425	SDIEGEYVPVEGD	gi|32129852|sp|Q9Y534|	NA
2426	ATGNEEYLINLID	gi|119619494|gb|EAW99	NA
2427	EASKVIYTNGCID	gi|74727485|sp|Q86UF1|	NA
2428	KSQRSSYVSMRID	gi|120940|sp|P24046|GB	NA
2429	FLSWPDYGVPSSA	gi|1172724|sp|P43378|P	NA
2430	SGMNHMYEDNDKD	gi|85542144|sp|Q562F6|	NA
2431	FYSASDYISDCWD	gi|108936027|sp|Q9Y2G	NA
2432	SEYAEGYESVSVD	gi|119580509|gb|EAW60	NA
2433	CAPCDIYWCWPRP	gi|28316330|dbj|BAC569	NA
2434	PACLPIYQDMTQP	gi|119591033|gb|EAW70	NA
2435	AINAEEYMSIIVG	gi|115502124|sp|Q6ZS8	NA
2436	WADPGKYALMGAA	gi|12644301|sp|P51798|	NA
2437	DFGSEVYVWHGKE	gi|57013034|sp|O95425|	NA
2438	YSCEPSYDLRGAA	gi|117310|sp|P17927|CR	NA
2439	EPFPTIYVDSQKE	gi|3915059|sp|O43776|S	NA
2440	LTSSIDYSRLNKE	gi|148612801|ref|NP_05	NA
2441	ACKSGGYKSKDYG	gi|31559829|ref|NP_853	NA
2442	CMEDLIYEIYTVG	gi|133021|sp|P18124|RL	NA
2443	<<Marker>>	contol_spot	NA

2444	GGDFNLYENMRCH	gi|20137929|sp|Q9BPU6	NA
2445	LREATEYEIELYG	gi|3915888|sp|P24821|T	NA
2446	VTYKPKYIEQQYG	gi|27734564|sp|Q9NYB5	NA
2447	ASFAPAYADLLSE	gi|123271|sp|P14653|HX	NA
2448	NGIEDAYILEATE	gi|74732251|sp|Q96LW4	NA
2449	DIFEEEYLEQDVE	gi|119614736|gb|EAW94	NA
2450	LLDKEAYWTPVVL	gi|145559500|sp|Q86W2	NA
2451	LNTNLYYTSNALT	gi|62906890|sp|Q92485|	NA
2452	SHPAEQYVSKLKT	gi|154089852|emb|CAO	NA
2453	IIIEPDYLGNHHP	gi|42518115|ref|NP_964	NA
2454	LGPTADYVFPDLT	gi|74734719|sp|Q9NZ53|	NA
2455	PQFDGKYIHWNHP	gi|74743637|sp|Q5SRI9|	NA
2456	EIEDHIYQELKST	gi|28380172|sp|O75764|	NA
2457	TICNDLYIYDTRT	gi|119573049|gb|EAW52	NA
2458	HSNPAKYVSINST	gi|119606839|gb|EAW86	NA
2459	PYYPPEYTCTPST	gi|8134810|sp|O60320|	NA
2460	CFEKDKYILQGVT	gi|130316|sp|P00747|PL	NA
2461	KDKVTIYENLDVT	gi|85542144|sp|Q562F6|	NA
2462	TICKVSYASLADV	gi|119618163|gb|EAW97	NA
2463	FFSMVDYDEGTDV	gi|6166601|sp|Q13454|T	NA
2464	<<Marker>>	contol_spot	NA
2465	KSFEEKYEVFMDV	gi|13878337|sp|Q13315|	NA
2466	EDMENLYVQLKLQ	gi|74729997|sp|Q8NAS9	NA
2467	YLSMSYYFDRDDV	gi|120516|sp|P02794|FR	NA
2468	GSDGEFYENHCEV	gi|62510692|sp|Q8N475|	NA
2469	EDEEGPYYSALSG	gi|116242809|sp|Q8WX	NA
2470	IARGPCYSDNGSG	gi|74750770|sp|Q8IYR6|	NA
2471	EDLPKSYDYDLII	gi|50403780|sp|Q16881|	[EDLPKSYDYDLII|Y|11|
2472	CRADQQYECVAEI	gi|266423|sp|Q00534|CD	[CRADQQYECVAEI|Y|1
2473	NEIKVVYLRCTGG	gi|266921|sp|P30050|RL	NA
2474	GSWAAIYQDIRHE	gi|131467|sp|P18031|PT	[GSWAAIYQDIRHE|Y|2
2475	FEWEKGYSDRYGF	gi|77416521|sp|Q6UWM	NA
2476	MGHEDLYKRYGGF	gi|127976|sp|P01213|PD	NA
2477	DISDTIYPRNPAM	gi|12643387|sp|P98170|	NA
2478	DDFETFYEIWEKF	gi|34098756|sp|Q9UQD	NA
2479	GTSTPEYNVKGIF	gi|28376972|sp|O15484|	NA
2480	PYKNELYHWFPIF	gi|17366354|sp|P58397|	NA
2481	SGNEIEYMEPHVF	gi|146330009|sp|Q86UE	NA
2482	LKESGSYMWIYVF	gi|12643959|sp|Q9Y6L6|	NA
2483	SVEGWDYVDSLYF	gi|24636285|sp|Q9HB15|	NA
2484	CTRGDKYPNDTGH	gi|74738220|sp|Q6UXH8	NA
2485	<<Marker>>	contol_spot	NA
2486	FKKEPVYQLPCGH	gi|21363047|sp|O94941|	NA
2487	GWEGGVYVQTCGH	gi|74762410|sp|Q6ZT12|	NA
2488	YDCSDSYDKAPEI	gi|113418951|ref|XP_94	NA
2489	CFSKLDYAVAWFI	gi|2498228|sp|Q16739|C	NA
2490	RSPKLFYADHPFI	gi|20141241|sp|P50454|	NA
2491	AEEMGGYFIINGI	gi|92090637|sp|Q9H9Y6|	NA
2492	FLTCDEYEKKQHI	gi|2833252|sp|Q14571|IT	NA
2493	PFENGQYLDIYGI	gi|88984537|sp|Q7Z3B1|	NA
2494	RAFEQQYSPIPRI	gi|8134597|sp|Q9Y5S8|	NA
2495	VTKEGEYIPLDQI	gi|119569494|gb|EAW49	NA

2496	SSSESSYHGPSRI	gi|61213482|sp|Q6ZNL6|	NA
2497	FFEMESYSVTQAG	gi|728834|sp|P39191|AL	NA
2498	FILSPNYVNGPSI	gi|74762124|sp|O95256|	NA
2499	YGYESIYAALRSI	gi|74751821|sp|Q96DW6	NA
2500	YDIKDDYTLRIKK	gi|49036496|sp|Q9HCK4	NA
2501	GNGEQQYVYLKDG	gi|62896957|dbj|BAD964	NA
2502	PCNEDGYMSCKDG	gi|131086|sp|P07225|PR	NA
2503	SSDEIRYGVVALK	gi|5921193|sp|P12111|C	NA
2504	DPMEDPYELKLLK	gi|41019528|sp|Q9Y6V0|	NA
2505	SEGNVGYVQMRLK	gi|27151474|sp|Q14692|	NA
2506	<<Marker>>	contol_spot	NA
2507	LQYSPDYRNYLAL	gi|68566054|sp|Q8N5J4|	NA
2508	CALESKYVKTVCL	gi|73919921|sp|Q14520|	NA
2509	PHSKGDYYSHNCL	gi|11643585|gb|AAG396	NA
2510	DFVDDSYLMKNDL	gi|6581091|gb|AAF1845	NA
2511	LYFVLDYVNGGEL	gi|28558166|sp|Q9HBY8	NA
2512	IISMNLYSSICFL	gi|2506481|sp|P30411|B	NA
2513	GDSNDDYDSAGLL	gi|119568243|gb|EAW47	NA
2514	PSDKEGYSGVGLL	gi|113984|sp|P27695|AP	NA
2515	GDYEILYWDVAGG	gi|121945710|sp|Q32P4	NA
2516	TVTDDDYAGFIFG	gi|2623750|gb|AAB8650	NA
2517	RQKSGRYVCVQLL	gi|125950459|sp|Q2KHT	NA
2518	EYYFPTYENDTLL	gi|12230860|sp|Q9NRM	NA
2519	EFEDGMYANLGIG	gi|48428678|sp|Q9BYC2	NA
2520	GFRNSSYPETGHG	gi|59803097|sp|Q00537|	NA
2521	HPYPEDYGDIEIG	gi|62298062|sp|Q9Y4H2|	NA
2522	NASDSSYRTPGIG	gi|116241363|sp|Q96M9	NA
2523	PKKSPIYVILVGG	gi|55977754|sp|O14524|	NA
2524	TAFDGPYCNHDIG	gi|17433016|sp|P78357|	NA
2525	TSAEPQYQPGDQT	gi|125358|sp|P09769|FG	[TSAEPQYQPGDQT|Y|5
2526	VAENPEYLSEFSL	gi|3913590|sp|Q15303|E	[VAENPEYLSEFSL|Y|12
2527	<<Marker>>	contol_spot	NA
2528	VDNEDIYESRHEI	gi|1169745|sp|P42685|F	NA
2529	VHNLDYYKKTTNG	gi|120050|sp|P22607|FG	[VHNLDYYKKTTNG|Y|6
2530	VKDPTEYTGPESY	gi|2833252|sp|Q14571|IT	NA
2531	VPTHSPYAQPSST	gi|8928244|sp|O15350|P	[VPTHSPYAQPSST|Y|9
2532	GKDGRGYVPATIK	gi|1174459|sp|P42226|S	[GKDGRGYVPATIK|Y|6
2533	GMSRDVYSTDYYR	gi|134035335|sp|Q1628	[GMSRDVYSTDYYR|Y|7
2534	GQRIYQYIQSRFY	gi|3219996|sp|Q13627|D	[GQRIYQYIQSRFY|Y|27
2535	HDSEENYVPMNPN	gi|90180201|sp|Q13480|	[HDSEENYVPMNPN|Y|5
2536	HMEKHNYESAAEA	gi|548377|sp|Q05586|N	NA
2537	IHHIDYYKKTTNG	gi|120046|sp|P11362|FG	[IHHIDYYKKTTNG|Y|65
2538	TANNPLYKEATST	gi|125987835|sp|P05106	[TANNPLYKEATST|Y|77
2539	LGFKRSYEEHIPY	gi|33112647|sp|P06213|	[LGFKRSYEEHIPY|Y|13
2540	DGLGLSYLSSHIA	gi|121116|sp|P06396|GE	NA
2541	PVPTNLYGDFFTG	gi|121116|sp|P06396|GE	NA
2542	MVKRRDYLDLAAS	gi|547807|sp|P07949|RE	[MVKRRDYLDLAAS|Y|1
2543	QAFPVSYSSSGAR	gi|547807|sp|P07949|RE	[QAFPVSYSSSGAR|Y|6
2544	IGNQHIYQPVGKP	gi|3183518|sp|Q05397|F	[IGNQHIYQPVGKP|Y|86
2545	VMLGASYWYRARL	gi|29337230|sp|Q13444|	[VMLGASYWYRARL|Y|
2546	AQEENLYAAVKHT	gi|37537910|sp|Q8NHL6	NA
2547	PKEDPIYDEPEGL	gi|17366642|sp|Q99704|	[PKEDPIYDEPEGL|Y|36

2548	<<Marker>>	contol_spot	NA
2549	LFDDPSYVNVQNL	gi|17380299|sp|P29353|	[LFDDPSYVNVQNL|Y|4
2550	QAEENTYDEYENE	gi|45382633|ref|NP_990	[QAEENTYDEYENE|Y|4
2551	EKSNLAYDIVQLP	gi|6226869|sp|P34932|H	[EKSNLAYDIVQLP|Y|89|
2552	LYGNLHYLQTGRL	gi|74753488|sp|Q9Y3P8|	[LYGNLHYLQTGRL|Y|9
2553	DYYEESYFTTRTY	gi|1706639|sp|P50402|E	[DYYEESYFTTRTY|Y|99
2554	LGASGDYADFQYL	gi|116242733|sp|P28070	[LGASGDYADFQYL|Y|1
2555	LYTLVTYVPVTTF	gi|51702807|sp|P62899|	[LYTLVTYVPVTTF|Y|10
2556	NSHDPSYFACLIK	gi|116242816|sp|Q86TI0	NA
2557	IKEKLCYVALDFE	gi|89276723|gb|ABD665	[IKEKLCYVALDFE|Y|21
2558	LSDSYNYSGTENL	gi|50401753|sp|Q7Z3T8|	[LSDSYNYSGTENL|Y|22
2559	INQEGEYIKMFMR	gi|18202954|sp|Q9HC35	[INQEGEYIKMFMR|Y|22
2560	LSLANCYEVLSAA	gi|14286002|sp|O94819|	[LSLANCYEVLSAA|Y|23
2561	MVVESAYEVIKLK	gi|126041|sp|P07195|LD	[MVVESAYEVIKLK|Y|24
2562	KADGLIYCLKEAC	gi|1177044|sp|P43403|Z	[KADGLIYCLKEAC|Y|24
2563	TEAPGEYFFSDGI	gi|124419|sp|P12268|IM	NA
2564	ITYEPFYTSGYDD	gi|56404432|sp|O14639|	[ITYEPFYTSGYDD|Y|41
2565	LINRMDYVEINID	gi|2498434|sp|Q00341|V	[LINRMDYVEINID|Y|437
2566	VYDELFYTLSPIN	gi|18202935|sp|Q9H223|	[VYDELFYTLSPIN|Y|45
2567	HTGEKPYECVECG	gi|147742906|sp|Q08ER	NA
2568	LGADDSYYTARSA	gi|1177044|sp|P43403|Z	[LGADDSYYTARSA|Y|4
2569	<<Marker>>	contol_spot	NA
2570	GEEEHVYSFPNKQ	gi|27735219|sp|P49023|	[GEEEHVYSFPNKQ|Y|1
2571	PPPDSVYSGVQPG	gi|12230547|sp|O43390|	NA
2572	YDEDSPYQNIKIL	gi|8247960|sp|P52788|S	NA
2573	RVCEPCYEQLNRK	gi|71152119|sp|O14964|	[RVCEPCYEQLNRK|Y|2
2574	TYVSSFYHAFSGA	gi|13123943|sp|O43707|	[TYVSSFYHAFSGA|Y|2
2575	ELQSPEYKLSKLR	gi|146328566|sp|Q9UM7	[ELQSPEYKLSKLR|Y|10
2576	SMSMISYSDAALE	gi|73921276|sp|Q04116|	NA
2577	EVNESQYLHSNQP	gi|730855|sp|P25302|S	NA
2578	EQFEDFYAYCKAI	gi|731532|sp|P39956|RP	NA
2579	NDDELEYASPSNA	gi|1168370|sp|P22149|A	NA
2580	TAKETIYIMLRFF	gi|129733|sp|P12383|PD	NA
2581	LYHDNLYVIWPLL	gi|1708905|sp|P53338|M	NA
2582	ILENSRYVNDKQK	gi|2507068|sp|P22148|M	NA
2583	LNRKSSYKSLDFE	gi|74645031|sp|Q12180|	NA
2584	RQRREKYIKNLEE	gi|729140|sp|P40917|YA	NA
2585	RLSELGYMDRLND	gi|1708201|sp|P32480|H	NA
2586	EYFASIYKNSNRG	gi|1168610|sp|P41696|A	NA
2587	DEDDEEYDVFRNV	gi|2493550|sp|Q02516|H	NA
2588	LMSEGLYKALEAA	gi|10720303|sp|Q15750|	NA
2589	FQTQDTYEIIPLM	gi|119572439|gb|EAW52	NA
2590	<<Marker>>	contol_spot	NA
2591	IRKKTKYTILDNM	gi|74747200|sp|Q5VV43|	NA
2592	PFKDDRYYRLAPM	gi|108935999|sp|Q9P2C	NA
2593	SFDEQEYPQSELM	gi|6606080|gb|AAF1905	NA
2594	VYDNISYEDLKLM	gi|62288848|sp|Q9ULL1|	NA
2595	HMFSDQYLDKEEN	gi|116242524|sp|Q9Y36	NA
2596	KPVQDEYEYVSDN	gi|119628606|gb|EAX08	NA
2597	NEPGTSYMSVQDN	gi|51316191|sp|O14990|	NA
2598	VLDELGYTVHPAA	gi|7019233|gb|AAF3525	NA
2599	TDNPPLYCNPKDN	gi|45709009|gb|AAH675	NA

2600	ADLCPQYTNSPFN	gi|57284115|emb|CAI43	NA
2601	LLEDESYDGGAGA	gi|90110048|sp|P06401|	NA
2602	LPGLRTYVDPHTY	gi|116241351|sp|P29320	[LPGLRTYVDPHTY|Y|5
2603	LQERRKYLKHRLI	gi|1711552|sp|P52630|S	[LQERRKYLKHRLI|Y|69
2604	LYAGDYYRVQGRA	gi|729008|sp|Q08345|DD	NA
2605	MESIDDYVNVPES	gi|14194891|sp|O43561|	NA
2606	MTCAELYEKLPQG	gi|464868|sp|Q02763|TI	[MTCAELYEKLPQG|Y|1
2607	SRPPPDYKDQRRN	gi|68565596|sp|Q8IZL2|	NA
2608	EKQMPKYSSENSN	gi|55976445|sp|Q6S8J3|	NA
2609	SNPDESYGCLSSN	gi|143811435|sp|Q1337	NA
2610	APNYDSYASYDVN	gi|129542|sp|P29122|PC	NA
2611	FAGHESYQNMGPQ	gi|71153483|sp|Q14966|	NA
2612	LNRTDCYIMNDPQ	gi|73920194|sp|Q8TD26|	NA
2613	FLHNDRYIEFHSQ	gi|73921231|sp|Q9BSC4	NA
2614	GVPNQDYEFQASQ	gi|17511840|gb|AAH187	NA
2615	LFPEDWYQFVLRQ	gi|116243177|sp|Q63HM	NA
2616	VMEKLQYASLLSQ	gi|119598865|gb|EAW78	NA
2617	GTPDPEYPDDYSQ	gi|145559564|sp|P10696	NA
2618	SKEDGQYGEVVSQ	gi|94730684|sp|Q96BR6|	NA
2619	LDFFDSYSITACR	gi|83286904|sp|P78348|	NA
2620	NVEAGSYVSFHCR	gi|74761421|sp|Q9H3W	NA
2621	QEQETSYTILRAR	gi|116241351|sp|P29320	NA
2622	SMPSSSYRDMPGG	gi|48474599|sp|Q96S82|	NA
2623	ACKESEYHYEYTA	gi|147647000|sp|Q6UXG	NA
2624	ELDMEPYTVAGVA	gi|81175100|sp|Q93008|	NA
2625	PEEEDQYWLSMGR	gi|20140440|sp|O75140|	NA
2626	YRPKAIYLDIDGR	gi|6166014|sp|O76083|P	NA
2627	DSDDSDYASSKHR	gi|12643892|sp|Q9UKJ3|	NA
2628	HLVTAGYVDMAIR	gi|21928245|dbj|BAC057	NA
2629	QGEEPDYETYLHR	gi|61222937|sp|Q9UHL0	NA
2630	VLCADGYILNAHR	gi|4884120|emb|CAB432	NA
2631	SYEEAVYGSSGHC	gi|2495723|sp|Q92537|K	NA
2632	AQRVEAYETHGLG	gi|143811399|sp|Q86SQ	NA
2633	KAPLPKYEESNLG	gi|74750394|sp|Q86TU7|	NA
2634	LSPDNQYVKVLLG	gi|6831570|sp|O14879|I	NA
2635	ELAKVNYVKNNIC	gi|74762615|sp|Q8TD20|	NA
2636	FLPDEPYIKVRIC	gi|6685318|sp|Q9Y5I7|C	NA
2637	WVSSEAYTSPVSR	gi|9297048|sp|Q15491|S	NA
2638	ESAPPGYVIALVR	gi|73620979|sp|Q8TAB3|	NA
2639	QASKPKYYFAWTL	gi|74749574|sp|Q6ZNC8	NA
2640	QNPYPIYTSVNVR	gi|110815895|sp|Q68DD	NA
2641	QTVENGYHDNPTL	gi|17865536|sp|O00592|	NA
2642	IHFGSDYEDRYYR	gi|130912|sp|P04156|PR	NA
2643	LGWEALYEQRAEP	gi|154937324|ref|NP_93	NA
2644	TESPEGYYEEAEP	gi|68052360|sp|Q8N4X5|	NA
2645	DGSDEGYLCDECS	gi|57015418|sp|Q9NZR2	NA
2646	EGMNPSYDEYADS	gi|730840|sp|Q08945|SS	NA
2647	FYFLSQYVSPADS	gi|20140912|sp|Q9UP52|	NA
2648	GSYSDLYPDSDDS	gi|74723109|sp|Q70CQ2	NA
2649	RTYDETYQRYRPV	gi|41017262|sp|O14974|	NA
2650	QPGDETYQDIFRD	gi|39932727|sp|Q15057|	[QPGDETYQDIFRD|Y|7
2651	LRENPYYDSRVVG	gi|1705916|sp|Q00610|C	[LRENPYYDSRVVG|Y|9

2652	STGSEQYSDYSYR	gi|24212077|sp|Q08174|	[STGSEQYSDYSYR|Y|9
2653	AQGNENYAGIAAR	gi|81175200|sp|Q9Y490|	[AQGNENYAGIAAR|Y|1
2654	SHRLSIYEDWDPF	gi|152031709|sp|Q13009	NA
2655	QMKTAGYPNVNIH	gi|116242799|sp|Q01082	NA
2656	GDRVAIYMPMIPE	gi|20137525|sp|Q9NR19	NA
2657	YQLTEAYGVPDAS	gi|62906890|sp|Q92485|	NA
2658	RRFANEYPNITRL	gi|115502368|sp|O75976	NA
2659	DTGSNAYLNVDYV	gi|37999771|sp|Q9BZP6|	NA
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2662	EGDPPLYVNVNMF	gi|17368550|sp|Q92611|	NA
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2664	LVSPASYENVRAK	gi|131806|sp|P15153|RA	NA
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2669	VQVNEVYGLVDGL	gi|123120|sp|P25021|HR	NA
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2672	RVGTKRYMAPEVL	gi|119631843|gb|EAX11	NA
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<tr><td>2923</td><td>AKDTGEYACVTGG</td><td>gi|97180266|sp|Q5VST9|</td><td>NA</td></tr>
<tr><td>2924</td><td>DGNKWLYKNKDHG</td><td>gi|6174930|sp|Q13200|P</td><td>NA</td></tr>
<tr><td>2925</td><td>RYQPGKYPMPNQS</td><td>gi|14548196|sp|Q9NRQ2</td><td>[RYQPGKYPMPNQS|Y|</td></tr>
<tr><td>2926</td><td>SEEIRFYQLGEEA</td><td>gi|1168948|sp|P22001|K</td><td>[SEEIRFYQLGEEA|Y|13</td></tr>
<tr><td>2927</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>2928</td><td>CSPPPDYNSVVLY</td><td>gi|143811474|sp|P17948</td><td>[CSPPPDYNSVVLY|Y|1</td></tr>
<tr><td>2929</td><td>SKNFDDYMKSLGV</td><td>gi|119802|sp|P05413|FA</td><td>[SKNFDDYMKSLGV|Y|2</td></tr>
<tr><td>2930</td><td>SRGEEVYVKKTMG</td><td>gi|549081|sp|P35590|TIE</td><td>NA</td></tr>
<tr><td>2931</td><td>TGENPIYKSAVTT</td><td>gi|124963|sp|P05556|ITB</td><td>[TGENPIYKSAVTT|Y|78</td></tr>
<tr><td>2932</td><td>ERGDKGYVPSVFI</td><td>gi|6226158|sp|Q14765|S</td><td>[ERGDKGYVPSVFI|Y|69</td></tr>
<tr><td>2933</td><td>ETQFNQYKTEAAS</td><td>gi|547937|sp|P15941|MU</td><td>NA</td></tr>
<tr><td>2934</td><td>AIKMVQYRDSFLT</td><td>gi|1706663|sp|P54762|E</td><td>NA</td></tr>
<tr><td>2935</td><td>FQQQMIYDSPPSR</td><td>gi|90180201|sp|Q13480|</td><td>[FQQQMIYDSPPSR|Y|2</td></tr>
<tr><td>2936</td><td>GCPPAVYEVMKNC</td><td>gi|729887|sp|P41240|CS</td><td>NA</td></tr>
<tr><td>2937</td><td>GGGGEFYGYMTMD</td><td>gi|62298062|sp|Q9Y4H2|</td><td>NA</td></tr>
<tr><td>2938</td><td>IMNDSNYIVKGNA</td><td>gi|547770|sp|P07333|CS</td><td>[IMNDSNYIVKGNA|Y|80</td></tr>
<tr><td>2939</td><td>VPNQPVYNQPVYN</td><td>gi|14548191|sp|O15162|</td><td>[VPNQPVYNQPVYN|Y|6</td></tr>
<tr><td>2940</td><td>LMEKDSYPRFLKS</td><td>gi|3914624|sp|O15492|R</td><td>[LMEKDSYPRFLKS|Y|16</td></tr>
<tr><td>2941</td><td>RTTSQLYDAVPIQ</td><td>gi|17380162|sp|O15530|</td><td>[RTTSQLYDAVPIQ|Y|9|</td></tr>
<tr><td>2942</td><td>GGKGGSYSQAACS</td><td>gi|231404|sp|P30481|1B</td><td>[GGKGGSYSQAACS|Y|</td></tr>
<tr><td>2943</td><td>EEGRDEYDEVAMP</td><td>gi|114787|sp|P02730|B3</td><td>[EEGRDEYDEVAMP|Y|9</td></tr>
<tr><td>2944</td><td>LSEETPYSYPTGN</td><td>gi|27735219|sp|P49023|</td><td>[LSEETPYSYPTGN|Y|31</td></tr>
<tr><td>2945</td><td>ENDDDVYRSLEEL</td><td>gi|1718101|sp|P52735|V</td><td>[ENDDDVYRSLEEL|Y|1</td></tr>
<tr><td>2946</td><td>ENTEDQYSLVEDD</td><td>gi|118572681|sp|P27986</td><td>[ENTEDQYSLVEDD|Y|6</td></tr>
<tr><td>2947</td><td>DGHEYIYVDPMQL</td><td>gi|129892|sp|P16234|PG</td><td>[DGHEYIYVDPMQL|Y|5</td></tr>
<tr><td>2948</td><td><<Marker>></td><td>contol_spot</td><td>NA</td></tr>
<tr><td>2949</td><td>MKGDVKYADIESS</td><td>gi|129890|sp|P09619|PG</td><td>[MKGDVKYADIESS|Y|76</td></tr>
<tr><td>2950</td><td>IMRDSNYISKGST</td><td>gi|129890|sp|P09619|PG</td><td>[IMRDSNYISKGST|Y|85</td></tr>
<tr><td>2951</td><td>TGQHQGYGFVEFL</td><td>gi|2500587|sp|Q15427|S</td><td>[TGQHQGYGFVEFL|Y|5</td></tr>
<tr><td>2952</td><td>IQNTGDYYDLYGG</td><td>gi|84028248|sp|Q06124|</td><td>[IQNTGDYYDLYGG|Y|6</td></tr>
<tr><td>2953</td><td>AKKEGPYDVVVLP</td><td>gi|56404943|sp|Q99497|</td><td>[AKKEGPYDVVVLP|Y|6</td></tr>
<tr><td>2954</td><td>AVVEEDYNENAKN</td><td>gi|23396771|sp|P82970|</td><td>[AVVEEDYNENAKN|Y|7</td></tr>
<tr><td>2955</td><td>EELESQYQQSMDS</td><td>gi|74735316|sp|O00193|</td><td>[EELESQYQQSMDS|Y|8</td></tr>
<tr><td>2956</td><td>KEDALLYQSKGYN</td><td>gi|1706639|sp|P50402|E</td><td>[KEDALLYQSKGYN|Y|8</td></tr>
<tr><td>2957</td><td>ADLTEQYNEQYGA</td><td>gi|62511089|sp|Q9BWF</td><td>[ADLTEQYNEQYGA|Y|1</td></tr>
<tr><td>2958</td><td>EFGGSIYQKVNKK</td><td>gi|130683|sp|P21796|VD</td><td>NA</td></tr>
<tr><td>2959</td><td>EKSDAEYTNSPLV</td><td>gi|73620123|sp|Q8IX90|</td><td>[EKSDAEYTNSPLV|Y|2</td></tr>
<tr><td>2960</td><td>PHLSKGYAYVEFE</td><td>gi|74754492|sp|Q15287|</td><td>[PHLSKGYAYVEFE|Y|2</td></tr>
<tr><td>2961</td><td>SKDQPDYAMYSRI</td><td>gi|32469765|sp|Q92608|</td><td>[SKDQPDYAMYSRI|Y|2</td></tr>
<tr><td>2962</td><td>GEPNVSYICSRYY</td><td>gi|20455502|sp|P49841|</td><td>[GEPNVSYICSRYY|Y|27</td></tr>
<tr><td>2963</td><td>SARAFPYGNVAFP</td><td>gi|74749365|sp|Q6UN15</td><td>[SARAFPYGNVAFP|Y|4</td></tr>
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2967	QNGQTIYLRGTGD	gi|18203627|sp|Q9Y227|	NA
2968	GQGPYPYSLSEPA	gi|13431358|sp|Q9NZB2	[GQGPYPYSLSEPA|Y|3
2969	<<Marker>>	contol_spot	NA
2970	QRAQENYEGSEEV	gi|81175100|sp|Q93008|	[QRAQENYEGSEEV|Y|2
2971	PAQDPLYDVPNAS	gi|116242760|sp|Q13671	[PAQDPLYDVPNAS|Y|3
2972	KENEEDYGTCSSS	gi|119611684|gb|EAW91	[KENEEDYGTCSSS|Y|3
2973	CSSSVQYTPVYKL	gi|119611684|gb|EAW91	[CSSSVQYTPVYKL|Y|4
2974	RFPLDYYSIPFPT	gi|109940042|sp|Q14157	[RFPLDYYSIPFPT|Y|835
2975	DRGRSDYDGIGSR	gi|3023628|sp|O00571|D	[DRGRSDYDGIGSR|Y|1
2976	HLFEDLYCSPLFR	gi|417110|sp|P25364|HC	NA
2977	IDFETAYQMLSSN	gi|124503|sp|P26798|IN	NA
2978	LRRERSYDGNGTG	gi|135077|sp|P08153|S	NA
2979	RQRKEKYIKNLEQ	gi|45477263|sp|Q03935|	NA
2980	DSTNTLYENTADM	gi|50400296|sp|Q04052|	NA
2981	IAYETIYCEKNKR	gi|50400296|sp|Q04052|	NA
2982	SVSNPPYHRGYSI	gi|417770|sp|P32432|SF	NA
2983	SSIPEKYKDVLTA	gi|1351976|sp|P05085|A	NA
2984	DMSANHYVVNDNS	gi|417456|sp|P19880|YA	NA
2985	SMSSIQYVENNNP	gi|462625|sp|P33748|MS	NA
2986	ATSNGIYTQAQYS	gi|417039|sp|Q01722|G	NA
2987	ANFVDSYKSSNAY	gi|1169692|sp|P41813|F	NA
2988	KPSNILYVDESGN	gi|1730070|sp|P51812|K	NA
2989	IARQGSYTSINSE	gi|2499640|sp|Q99759|M	NA
2990	<<Marker>>	contol_spot	NA
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2993	ERDEPAYPRGDSS	gi|6685621|sp|Q9Y6R4|	NA
2994	PMWGSDYVQLSRT	gi|6685621|sp|Q9Y6R4|	NA
2995	LKPNDDYLLKTAN	gi|1345616|sp|P48595|S	NA
2996	SLNELTYNNLPAN	gi|74727919|sp|Q86YC2|	NA
2997	VYTELLYTNKCYM	gi|74762741|sp|Q9H6R0	NA
2998	YVRDLGYVVEGYM	gi|8928460|sp|O75962|T	NA
2999	EGLEENYCRNPDN	gi|130316|sp|P00747|PL	NA
3000	TKSKGPYICALCA	gi|3024110|sp|P56270|M	NA
3001	PGEEEEYRCEAKN	gi|120660202|gb|AAI304	NA
3002	QTNKRDYVSKYIN	gi|47116944|sp|Q9UII4|	NA
3003	CGVDGDYEDAELN	gi|143811366|sp|P11274	[CGVDGDYEDAELN|Y|2
3004	GKGMFKYSDHPLN	gi|147734568|sp|Q86XM	NA
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3009	EFQCDAYTCSNGG	gi|116242598|sp|Q9Y21	NA
3010	HGRPDHYEEAPRN	gi|74723955|sp|Q8TEB9|	NA
3011	KSVEEDYVTNIRN	gi|74751385|sp|Q8TBM8	NA
3012	PNSELHYSLSGRN	gi|119625608|gb|EAX05	NA
3013	DMADEAYSIGPAP	gi|108861983|sp|Q96RQ	NA
3014	GGGNSEYVRCDAP	gi|20137548|sp|Q9R160|	NA
3015	KFENELYVTMHYN	gi|13124361|sp|Q9UKN7	NA

3016	PDRECIYIIEAAP	gi|59798466|sp|Q8TDF5|	NA
3017	TTAWEDYIWFQAP	gi|3123048|sp|Q15013|M	NA
3018	YLGDTHYKEIPAP	gi|116241261|sp|Q16720	NA
3019	KLFKEAYQIACLG	gi|20140806|sp|Q9HBG6	NA
3020	LIRDTMYKIFPKG	gi|2598719|dbj|BAA2330	NA
3021	PETNQIYENDNKG	gi|85542144|sp|Q562F6|	NA
3022	RLGEDPYYTENGG	gi|3183511|sp|P28906|C	[RLGEDPYYTENGG|Y|3
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3024	GHNGETYSSVCAA	gi|20178043|sp|O95980|	NA
3025	YSYSNSYNSPGGG	gi|62512150|sp|Q12906|	NA
3026	AEETPPYSNYNTL	gi|152031709|sp|Q13009	NA
3027	RGHEGSYVGKHFR	gi|153792764|ref|NP_065	NA
3028	AAKELDYEISHGR	gi|17366834|sp|Q9H251|	NA
3029	FAFKVPYVELGGR	gi|32700066|sp|O00445|	NA
3030	HFGERDYDILAGR	gi|118573058|sp|Q9P273	NA
3031	AFQEVLYVDPSFC	gi|6136154|sp|O15550|U	NA
3032	GFSEFYYCTEDVL	gi|18203627|sp|Q9Y227|	NA
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3035	LDREGNYLRPRGC	gi|27437034|ref|NP_7584	NA
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3037	NLPHSGYSDSAVL	gi|12643409|sp|P43243|	NA
3038	MFASDSYICFASR	gi|37538010|sp|O95759|	NA
3039	EMPKTLYVGNLSR	gi|6094480|sp|P31483|TI	NA
3040	SARNVPYGNIQSR	gi|51315838|sp|Q10471|	NA
3041	GIIDGEYVVNPTR	gi|115502437|sp|Q8TCS	NA
3042	SLNEEWYVSYITR	gi|10720065|sp|Q13094|	NA
3043	VKDKFIYVAQPTL	gi|62510692|sp|Q8N475|	NA
3044	HRVKEDYTRVVCP	gi|51316071|sp|Q96FL9|	NA
3045	IRSLPPYSDIHDP	gi|119568598|gb|EAW48	NA
3046	MGRKPGYFSFLDP	gi|3287848|sp|Q16099|G	NA
3047	QHRGERYKNMIDP	gi|17380317|sp|Q9Y345|	NA
3048	HPSDEKYSGLTAS	gi|114149931|sp|Q96AT1	NA
3049	YHPADGYAFSSNI	gi|2833239|sp|Q12929|E	NA
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3057	AEVRTQYEEIAQR	gi|547752|sp|Q01546|K2	NA
3058	LDAETAYPNLIFS	gi|8928170|sp|O15553|M	NA
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3064	HWVYKKYPNVFKK	gi|92090640|sp|O43865|	NA
3065	RGEGMRYIIILDP	gi|267050|sp|P14410|SU	NA
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3074	NVSENIYFLIDGS	gi|113414409|ref|XP_49	NA
3075	TSLMNQYVNKKFS	gi|1709999|sp|P51149|R	NA
3076	DRKKDQYKVGEVL	gi|85681919|sp|P08603|	NA
3077	GCGETIYVIGQGS	gi|152031617|sp|O0017	NA
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3079	CSNNPSYIDRLIS	gi|116242829|sp|Q9Y4A	NA
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3097	GQPASKYLRVNPN	gi|24418671|sp|Q8TAG9	NA
3098	SRLGNQYVNVMNM	gi|67472674|sp|Q07837|	NA
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3107	TRICKIYDSPCLP	gi|548663|sp|Q06609|RA	[TRICKIYDSPCLP|Y|315
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3109	LAEGSAYEEVPTS	gi|130225|sp|P19174|PL	[LAEGSAYEEVPTS|Y|47
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3111	STGSVDYLALDFQ	gi|46396035|sp|Q9UQC	[STGSVDYLALDFQ|Y|61
3112	ASREGKYIPLPQR	gi|52000729|sp|Q8WW	[ASREGKYIPLPQR|Y|34
3113	DMGDEVYDDVDTS	gi|6166197|sp|O15117|F	[DMGDEVYDDVDTS|Y|
3114	PLDSTFYRSLLED	gi|119533|sp|P04626|ER	NA
3115	PALAKGYLKQDPL	gi|3024000|sp|Q13651|I1	[PALAKGYLKQDPL|Y|49
3116	PRPDHIYDKPEGV	gi|3043919|gb|AAC1326	NA
3117	RGLPSDYGRPLSF	gi|119595261|gb|EAW74	[RGLPSDYGRPLSF|Y|1
3118	SSRAVLYADYRAP	gi|54036152|sp|Q96J84|	[SSRAVLYADYRAP|Y|62
3119	VPPQGLYDLPREP	gi|17366642|sp|Q99704|	[VPPQGLYDLPREP|Y|3

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3122	SSANAIYSLAARP	gi|115855|sp|P22681|CB	[SSANAIYSLAARP|Y|67
3123	TFIGEHYVHVNAT	gi|125484|sp|P08581|ME	[TFIGEHYVHVNAT|Y|13
3124	TSAGDRYDSLLGR	gi|41017262|sp|O14974|	[TSAGDRYDSLLGR|Y|9
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3128	LPDNDPYDNLCYL	gi|23396800|sp|Q9NTG1	NA
3129	AVSTPDYGEKKLP	gi|61214417|sp|Q9Y661|	NA
3130	LNTGPPYCDPTLP	gi|4033376|sp|Q14524|S	NA
3131	VESNGRYISVLKV	gi|74756617|sp|Q5THJ4|	NA
3132	KFPKGDYTCCDLV	gi|143377520|sp|Q96M0	NA
3133	AQSNPYYNGPHLN	gi|45477156|sp|Q8WWI1	NA
3134	KVKELTYQTEEDR	gi|13638390|sp|P12882|	NA
3135	YSSPGLYSKTMTP	gi|38258220|sp|Q96AC1|	NA
3136	LDCTNPYYLAAGS	gi|62751417|ref|NP_776	NA
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3138	WGSSPTYGPRSTP	gi|5870130|gb|AAD5448	[WGSSPTYGPRSTP|Y|1
3139	GPLSPAYTGQVPY	gi|112382252|ref|NP_84	NA
3140	STDNIKYQPKGGQ	gi|51338754|sp|P11137|	NA
3141	TMSVDRYIAVCHP	gi|2851402|sp|P35372|O	NA
3142	EGRLSFYSGHSSF	gi|45477007|sp|O14494|	NA
3143	NSLSTSYKTVSLP	gi|119582458|gb|EAW62	NA
3144	KIVIQKYHTVNGH	gi|133254|sp|P09651|RO	NA
3145	ITDNFCYFRHADP	gi|12644465|sp|Q92949|	NA
3146	NFKVMIYQDEVKL	gi|56749614|sp|Q6NZI2|	NA
3147	KTFVEKYEKQIKH	gi|21542000|sp|Q16543|	NA
3148	HASQKDYSSGFGG	gi|2498954|sp|Q14247|S	NA
3149	DDLMPVYCGNEVT	gi|118573679|sp|Q96DV	NA
3150	TVLKIFYQTCRAV	gi|17375734|sp|O14976|	NA
3151	RSNPQVYMDIKIG	gi|13124097|sp|Q9UNP9	NA
3152	PKEEADYEDDFLE	gi|24418367|sp|Q9UPY3	NA
3153	VMSVDRYLAVVHP	gi|12644225|sp|P35346|	NA
3154	SRGLFYYYANEKS	gi|122070147|sp|Q86WV	NA
3155	KEKSHSYRTDNCS	gi|71152386|sp|Q96NH3	NA
3156	VYEEPVYEEVGAF	gi|73619965|sp|Q8WWN	NA
3157	EMRRLNYQTPGMR	gi|125978|sp|P10586|PT	NA
3158	LKTKSQYHDLQAP	gi|74725117|sp|Q9H788|	NA
3159	RKNLDPYEQWSDQ	gi|147744553|sp|P13569	NA
3160	GRGTAQYSSQKSV	gi|20139105|sp|Q99959|	NA
3161	REQLIDYLMLKVA	gi|116242614|sp|Q96RT	NA
3162	WGIDEIYLESCCQ	gi|24418855|sp|Q92953|	[WGIDEIYLESCCQ|Y|12
3163	QGNQLNYYKQEIP	gi|24418367|sp|Q9UPY3	NA
3164	AGTTATYEGRWGR	gi|20139105|sp|Q99959|	NA
3165	DPIAMEYYNWGRF	gi|74752543|sp|Q9GZY6	NA
3166	EHSKRGYYGQSAR	gi|13634076|sp|Q9UDY2	NA
3167	DSFSDPYAIVSFL	gi|20137708|sp|O75923|	NA
3168	LDPTVEYVKFSKE	gi|74739634|sp|O75815|	NA
3169	QVGTARYMAPEVL	gi|116242818|sp|P37173	[QVGTARYMAPEVL|Y|4
3170	RNMELTYLNPMGL	gi|22095552|sp|Q9NYQ7	NA
3171	LDCSIGYIYVDHL	gi|124945|sp|P13612|IT	NA

3172	QERTVAYINVDIS	gi|20139287|sp|Q9UQQ1	NA
3173	LATSGDYLRVWRV	gi|48428729|sp|P61962|	NA
3174	SRAGILYINPADL	gi|12643822|sp|Q9NYC9	NA
3175	KLKEIVYPNIEET	gi|12644410|sp|Q13614|	NA
3176	LKGNEDYINANYI	gi|131531|sp|P29074|PT	NA
3177	PSQDSDYINANFI	gi|50403764|sp|Q05209|	NA
3178	DDPCSDYINASYI	gi|126469|sp|P23467|PT	NA
3179	GQEYTDYINASFI	gi|126471|sp|P23469|PT	NA
3180	NKHKNRYINIVAY	gi|400199|sp|P23471|PT	NA
3181	VSETDDYAEIIDE	gi|3183518|sp|Q05397|F	[VSETDDYAEIIDE|Y|397
3182	SLGASPYPNLSNQ	gi|115502390|sp|P07332	NA
3183	DHKNGHYIIPQMA	gi|45645212|sp|Q9Y2X7|	NA
3184	EEELSNYICMGGK	gi|547738|sp|P35568|IR	[EEELSNYICMGGK|Y|4
3185	PSSRGDYMTMQMS	gi|547738|sp|P35568|IR	NA
3186	YVAIKAYTAVEGD	gi|127946|sp|P14598|NC	NA
3187	DYITAAYVEMRRE	gi|20981696|sp|P33993|	NA
3188	DYARRSYANIKEK	gi|12644536|sp|Q99551|	NA
3189	QLLSENYTAVAQT	gi|38372376|sp|Q8IXH7|	NA
3190	GGLPMPYPNLAPD	gi|19863082|sp|Q12972|	NA
3191	SLPLEYYLIPFLI	gi|21362880|sp|O43567|	NA
3192	WYLQDPYPNPSKK	gi|115502450|sp|O9547	NA
3193	DEDLAAYCRRRDI	gi|1705945|sp|P09543|C	NA
3194	QKNLEGYVGFANL	gi|67472677|sp|Q16181|	NA
3195	EDAPVVYLGSFRG	gi|118573870|sp|Q86YV	NA
3196	QARERDYAEIQDF	gi|30913162|sp|Q8TEW	NA
3197	VRIGSGYDNVDIK	gi|3182976|sp|P56545|C	NA
3198	IRGSTPYRHGDSV	gi|117315|sp|P20023|CR	NA
3199	EKNPLMYLTGVQT	gi|124942|sp|P17301|IT	NA
3200	VSKKVSYSHIQSK	gi|20455500|sp|P27816|	NA
3201	KPREEQYNSTFRV	gi|34364807|emb|CAE45	NA
3202	SLHKGDYNDSVQV	gi|46576868|sp|O95490|	NA
3203	FCQESGYDTILRV	gi|399328|sp|Q02153|G	NA
3204	VKMKDSYFWIALQ	gi|62988664|gb|AAY240	NA
3205	GVSENCYRAVPSV	gi|12856007|dbj|BAB305	NA
3206	MVSTVDYEDYQSV	gi|62286460|sp|Q13535|	NA
3207	GDDTNEYVSAVCW	gi|55976539|sp|Q8NHY2	NA
3208	KTRSSSYLDNLAW	gi|2499596|sp|Q16659|M	NA
3209	LPDLEFYVNLGDW	gi|110810398|sp|Q7Z4H	NA
3210	LTVEEKYPYMVEW	gi|117949804|sp|Q9H0P	NA
3211	SLDEEHYNRQEEW	gi|42558898|sp|Q7Z7G8|	NA
3212	CLFMESYKVVSGW	gi|8247951|sp|P23759|P	NA
3213	ALAETSYVKVLEY	gi|1170855|sp|P43355|M	NA
3214	FLEEDHYLAPDFY	gi|1708004|sp|Q10469|M	NA
3215	LKKKPEYHCMNFY	gi|18996327|emb|CAD24	NA
3216	TWREFHYIQGGEY	gi|51095023|gb|EAL242	NA
3217	CSSWYYYVTMPMP	gi|61211648|sp|Q8N6M6	NA
3218	PVQKELYKTVTLQ	gi|20141038|sp|Q9HBT7	NA
3219	AENDEFYANNMYL	gi|23396937|sp|Q9NRW	NA
3220	LCSCPPYKYKLRY	gi|150383497|sp|Q9UGL	NA
3221	SRHCPFYVSIQSY	gi|48428180|sp|Q9UJ42|	NA
3222	DVNSDDYKGDKVY	gi|67462100|sp|Q5VYS8	NA
3223	IQYNGTYDDTLVY	gi|116242620|sp|Q96NI6	NA

3224	CQNQGKYEEVEYY	gi|585363|sp|Q07866|KL	NA
3225	HDQDPGYMHHKFA	gi|119576122|gb|EAW55	NA
3226	LVGAPEYECYAPD	gi|146334837|sp|Q8N0V	NA
3227	APPDDLYLFPTPD	gi|3073775|dbj|BAA2576	NA
3228	DRSNYEYSEVTQD	gi|21755273|dbj|BAC046	NA
3229	LWEEAAYDQSLPD	gi|54035724|sp|Q8WZ55	NA
3230	AANYEPYVVVPRD	gi|146345450|sp|Q8N3Y	NA
3231	LSWELLYATNDDE	gi|116243177|sp|Q63HM	NA
3232	DVFEFRYAKMPDE	gi|12230989|sp|P25440|	NA
3233	LTFCLEYEQHPDE	gi|47117837|sp|P26374|	NA
3234	FGCRPEYDNGLEE	gi|120660054|gb|AAI304	NA
3235	VQKRPNYKNVGEE	gi|125950459|sp|Q2KHT	NA
3236	PWVESEYLDYLFE	gi|55976528|sp|Q8IU57|	NA
3237	PRNCERYLNWAHA	gi|7706095|ref|NP_0576	NA
3238	ASRKGLYLCVGNE	gi|26006900|sp|Q8WU6	NA
3239	KFRKVKYKAVYNE	gi|149273101|ref|XP_001	NA
3240	ELPCDDYGYAPPE	gi|116242783|sp|Q1277	NA
3241	LRSEKSYSQETYL	gi|149193321|ref|NP_00	NA
3242	PSSSVPYMSPNQE	gi|56404909|sp|Q8NF64|	NA
3243	<<Marker>>	contol_spot	NA
3244	QVPDDIYHSPSWE	gi|109079698|ref|XP_001	NA
3245	GRSWESYSSCGDF	gi|27805716|sp|Q15414|	NA
3246	LKSVEQYHEHNAF	gi|18202258|sp|O94892|	NA
3247	VESFSDYPSLGCF	gi|927065|gb|AAC09385	NA
3248	AYGEIYYDSNPDF	gi|117949793|sp|Q9NT6	NA
3249	KFEVEKYIVHKEF	gi|137119|sp|P00750|TP	NA
3250	NECKDIYQKSTVL	gi|1171882|sp|P46721|S	NA
3251	IFDNGLYDEKPLT	gi|34098715|sp|Q9H7Z3|	NA
3252	PGAEPFYIRANLT	gi|116241281|sp|Q9BWT	NA
3253	AYYESGYNTTAPT	gi|18204355|gb|AAH217	NA
3254	FTESSSYVEKYNT	gi|76789660|sp|Q9ULL0|	NA
3255	IDTREEYEMKDPT	gi|54036152|sp|Q96J84|	NA
3256	ADCNFSYTSSRDA	gi|119576383|gb|EAW55	NA
3257	VTDEEIYYVAKDA	gi|152031686|sp|Q8TF0	NA
3258	LHEFPQYVKTHLA	gi|62299063|sp|Q7RTX0	NA
3259	TVSSLDYSRDGLA	gi|119576383|gb|EAW55	NA
3260	GRASPLYASYKAD	gi|62511244|sp|Q9BUH8	NA
3261	LYCKYEYFDLAAD	gi|145309317|ref|NP_68	NA
3262	NLSMERYALVFGV	gi|12643426|sp|O60779|	NA
3263	AESEDLYDFVFIV	gi|150421588|sp|Q1534	NA
3264	<<Marker>>	contol_spot	NA
3265	EVEFIDYGNSAIV	gi|118572727|sp|O6052	NA
3266	LDSKYAYIQVTHV	gi|24212635|sp|Q9BZ29|	NA
3267	PRSVDSYSSTQHV	gi|66774203|sp|P18850|	NA
3268	APDFSDYSEMAKV	gi|17369290|sp|Q9NQC	NA
3269	SKQYAGYDYSQQG	gi|74760683|sp|Q969M3|	[SKQYAGYDYSQQG|Y|
3270	ASSQETYGKSPFW	gi|74723330|sp|Q7Z4G4|	[ASSQETYGKSPFW|Y|
3271	NLNTITYETLKYI	gi|20532033|sp|O75575|	NA
3272	REPPPAYEPPAPA	gi|21542431|sp|O14828|	[REPPPAYEPPAPA|Y|5
3273	DIDEGLYSRQLYV	gi|24418865|sp|P22314|	[DIDEGLYSRQLYV|Y|55
3274	LDNGGYYISPRIT	gi|125480|sp|P07948|LY	NA
3275	NREKNRYRDILPF	gi|55959180|emb|CAI14	NA

3276	SGINDDYGQLKNF	gi|74762960|sp|O60934|	NA
3277	ISCSPGYHNGVPF	gi|10834698|gb|AAG237	NA
3278	ASANNSYCIVGIA	gi|129542|sp|P29122|PC	NA
3279	RCPNGDYCSNRRF	gi|116256077|sp|Q9BYW	NA
3280	FDNSPDYCVLDKA	gi|14424481|sp|Q93097|	NA
3281	CTHEHDYEVVFPH	gi|74741766|sp|Q5JQS6|	NA
3282	HLYSDHYSPSGRH	gi|74762456|sp|Q86WS	NA
3283	TPTDNEYGAWKRH	gi|119568293|gb|EAW47	NA
3284	HYEHGGYERPPSH	gi|20978536|sp|Q9GZY0	NA
3285	<<Marker>>	contol_spot	NA
3286	TPCELTYKVPTRH	gi|148841209|sp|Q6ZU6	NA
3287	RRPQGSYEEAGTH	gi|115311311|sp|Q6ZMM	NA
3288	WTRENTYVEYSII	gi|119625348|gb|EAX04	NA
3289	FYQNEDYNERPKI	gi|119616245|gb|EAW95	NA
3290	GNSMVIYVILRYA	gi|401124|sp|P30872|SS	NA
3291	NGSFDMYVCWDYA	gi|1346133|sp|P48546|G	NA
3292	VKPSHLYVTIPYA	gi|50401058|sp|Q8IU89|	NA
3293	LYWGGSYTSMGLI	gi|115964|sp|P15813|CD	NA
3294	ESEKEWYFGNADK	gi|83302113|sp|O75165|	NA
3295	GRNCYEYVDGKDK	gi|17369297|sp|Q9NQV7	NA
3296	AVDEVDYKTAEEK	gi|152032608|sp|Q2TAK	NA
3297	NFNMGEYDSNMEK	gi|56404449|sp|P78316|	NA
3298	CNSDDPYNPLNFK	gi|119611917|gb|EAW91	NA
3299	GFNYEIYVAPDHK	gi|25090493|sp|O43424|	NA
3300	GLSKNPYLSVKQK	gi|93186129|sp|Q92665|	NA
3301	IVSEEAYILFVRK	gi|73620993|sp|Q9Y2L1|	NA
3302	IGEMPSYDLVLSK	gi|33860178|sp|O15226|	NA
3303	CHIGDLYVDLRDG	gi|17368942|sp|Q9H254|	NA
3304	RRGDFIYVDIFEG	gi|74710277|sp|Q6UVK1	NA
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3306	<<Marker>>	contol_spot	NA
3307	LIKEFKYALVWGL	gi|6685390|sp|Q9Y295|D	NA
3308	YLSDIAYKSTEHL	gi|6136393|sp|Q14191|W	NA
3309	WGEWDEYSATCGM	gi|22760486|dbj|BAC112	NA
3310	KCNESLYGRKYIQ	gi|8489005|sp|Q13643|F	NA
3311	CGFEATYLELASA	gi|74732925|sp|Q9BRT3	NA
3312	TVVELKYTGNASA	gi|112874|sp|P01011|AA	NA
3313	LLSAELYCRAGSL	gi|115528764|gb|AAI252	NA
3314	TLYEINYKAVGSL	gi|117949771|sp|O14522	NA
3315	KELEAKYENSIIM	gi|74710067|sp|Q6R2W	NA
3316	RRFTEIYEFHKTL	gi|127946|sp|P14598|NC	NA
3317	LLQETLYMCVGIM	gi|5921731|sp|O95067|C	NA
3318	PIHCPDYLRSAKM	gi|149274624|ref|NP_11	NA
3319	PSDKFIYATVKQS	gi|548377|sp|Q05586|NM	NA
3320	QEDGGVYSSSGLK	gi|97536202|sp|P16591|	[QEDGGVYSSSGLK|Y|7
3321	QRDSSYYWEIEAS	gi|125651|sp|P04049|RA	[QRDSSYYWEIEAS|Y|3
3322	RGPEENYSRPEAP	gi|3334210|sp|O15379|H	NA
3323	RKDRMSYHVRSHD	gi|3024110|sp|P56270|M	NA
3324	RSPLSDYMNLDFS	gi|62298062|sp|Q9Y4H2|	NA
3325	DLEFTIYDDDDVS	gi|130848|sp|P25786|PS	NA
3326	DTSDPTYTSSLGG	gi|1706663|sp|P54762|E	[DTSDPTYTSSLGG|Y|7
3327	<<Marker>>	contol_spot	NA

3328	EAPEDLYKDFLTL	gi|9087218|sp|P35968|V	[EAPEDLYKDFLTL|Y|99
3329	EEELSNYICMGGK	gi|547738|sp|P35568|IR	[EEELSNYICMGGK|Y|46
3330	EIGVGAYGTVYKA	gi|1168867|sp|P11802|C	NA
3331	EPKDDAYPLYSDF	gi|90110048|sp|P06401|	NA
3332	KVDEVLYEDSSTA	gi|1706921|sp|P49914|M	NA
3333	VVDADEYLIPQQG	gi|2811086|sp|P00533|E	[VVDADEYLIPQQG|Y|10
3334	TAENAEYLRVAPQ	gi|2811086|sp|P00533|E	[TAENAEYLRVAPQ|Y|11
3335	AFDNLYYWDQDPP	gi|119533|sp|P04626|ER	[AFDNLYYWDQDPP|Y|1
3336	LAVSEEYLDLRLT	gi|13432140|sp|P22455|	[LAVSEEYLDLRLT|Y|75
3337	PEGGVDYKNIHLE	gi|547770|sp|P07333|CS	[PEGGVDYKNIHLE|Y|69
3338	VDGKEIYNTIRRK	gi|121743|sp|P20936|RA	[VDGKEIYNTIRRK|Y|46
3339	ENEDDGYDVPKPP	gi|115855|sp|P22681|CB	[ENEDDGYDVPKPP|Y|7
3340	HQLRIQYGTSKGK	gi|115311627|sp|P28370	NA
3341	RVGTKRYMAPEVL	gi|119631843|gb|EAX11	NA
3342	ETSKLIYDFIEDQ	gi|1722836|sp|P42768|W	[ETSKLIYDFIEDQ|Y|291
3343	NFMMTPYVVTRYY	gi|85700366|sp|P45984|	[NFMMTPYVVTRYY|Y|1
3344	FCRESRYMDQWVP	gi|120751|sp|P24522|GA	NA
3345	SIFTPEYDDSRIR	gi|97536681|sp|Q9Y2U5|	NA
3346	LHREEMYIFMEYC	gi|6685621|sp|Q9Y6R4|	NA
3347	RIRMGQYEFPNPE	gi|1346538|sp|P49137|M	NA
3348	<<Marker>>	contol_spot	NA
3349	FSPDGKYLASGSD	gi|110282967|sp|P32479	NA
3350	PSDYGDYVKKPRV	gi|586313|sp|P38128|SM	NA
3351	DQENCVYETVVLP	gi|74725796|sp|Q53EL6|	NA
3352	SGVSYGYWGCAIG	gi|130859|sp|P25788|PS	NA
3353	THTVPIYEGYALP	gi|117167827|gb|AAI130	[THTVPIYEGYALP|Y|16
3354	EGDNVNYDWIHWD	gi|67465046|sp|Q04446|	[EGDNVNYDWIHWD|Y|
3355	RWYPEEYEFAPKK	gi|116242694|sp|Q9Y3B	[RWYPEEYEFAPKK|Y|1
3356	EVTICNYEASANP	gi|74752536|sp|Q9GZP4	[EVTICNYEASANP|Y|18
3357	LDPVEVYESLPEE	gi|21542000|sp|Q16543|	[LDPVEVYESLPEE|Y|29
3358	ATENDIYNFFSPL	gi|1710632|sp|P31943|H	[ATENDIYNFFSPL|Y|30
3359	LKVLYQYKEKQYM	gi|45476775|sp|O95373|	NA
3360	PMDTSVYESPYSD	gi|1177044|sp|P43403|Z	[PMDTSVYESPYSD|Y|3
3361	SVYESPYSDPEEL	gi|1177044|sp|P43403|Z	[SVYESPYSDPEEL|Y|31
3362	HSGENPYECLECG	gi|14548338|sp|O43296|	[HSGENPYECLECG|Y|3
3363	GPEQEEYSTFVID	gi|13959562|sp|Q14644|	[GPEQEEYSTFVID|Y|76
3364	DNDDDLYG	gi|6094447|sp|P55072|T	[DNDDDLYG|Y|805|P55
3365	PASVTDYQNVSFS	gi|20138768|sp|Q9NZM3	NA
3366	PQYNIQYSSSAAV	gi|116242614|sp|Q96RT	[PQYNIQYSSSAAV|Y|98
3367	EGDYLSYREFHSA	gi|116242614|sp|Q96RT	[EGDYLSYREFHSA|Y|1
3368	ESLESLYFTPIPA	gi|145559510|sp|Q1498	[ESLESLYFTPIPA|Y|177
3369	<<Marker>>	contol_spot	NA
3370	PPAEDVYDVPPPA	gi|8134339|sp|P56945|B	NA
3371	PPAPDLYDVPPGL	gi|8134339|sp|P56945|B	[PPAPDLYDVPPGL|Y|37
3372	RVKEEGYELPYNP	gi|17366642|sp|Q99704|	[RVKEEGYELPYNP|Y|3
3373	TQDSGFY	gi|41019126|sp|P60228|	[TQDSGFY|Y|445|P6022
3374	EVGTGQYATTKGI	gi|17433099|sp|Q9Y2J2|	[EVGTGQYATTKGI|Y|47
3375	PLDGSPYAQVQRP	gi|150416153|sp|Q63HR	NA
3376	QLKEPSYSDPISH	gi|1177049|sp|P46974|Z	NA
3377	SISSPSYSSPSFS	gi|544474|sp|P14064|HA	NA
3378	DQKKPFYEEFRTN	gi|547746|sp|P33417|IX	NA
3379	SAKELGYENGLED	gi|114834|sp|P22035|BA	NA

3380	DTQDEEYVQHHDN	gi|113022|sp|P21192|AC	NA
3381	IHCNSVYECIKFL	gi|3123263|sp|P48743|R	NA
3382	LKWDYTYANMTFQ	gi|90110827|sp|P17181|	NA
3383	YLFMGDYVDRGYY	gi|54038809|sp|P67775|	NA
3384	MVRMAAYTDEGGK	gi|729833|sp|P40189|IL6	NA
3385	AEDNLEYVRTLYD	gi|1169094|sp|P46109|C	NA
3386	AENDDTYKDDVNH	gi|148887396|sp|Q1323	NA
3387	GAEEGIYTLNLHE	gi|45593475|sp|Q12851|	NA
3388	PLRNEKYLASVAA	gi|62901464|sp|Q92547|	NA
3389	QTVFPDYTNPNCA	gi|21431783|sp|O43451|	NA
3390	<<Marker>>	contol_spot	NA
3391	ADDESDYYCVLYM	gi|119579897|gb|EAW59	NA
3392	DQCKDGYIGPNCN	gi|116242627|sp|Q9H1U	NA
3393	GSSCNKYERLKAN	gi|57015325|sp|Q9Y6U3|	NA
3394	IQDMTGYKNFSCN	gi|74760489|sp|Q8TDW	NA
3395	GQRECDYSIDGIN	gi|26400725|sp|Q9Y4G6	NA
3396	LDKEEQYMQWKIN	gi|119600046|gb|EAW79	NA
3397	TVEGNTYVTNVHN	gi|114646051|ref|XP_00	NA
3398	CLGEDLYNSSLKN	gi|23821932|sp|Q8TDX9	NA
3399	FSSMEYYSSCHKN	gi|44887883|sp|Q14264|	NA
3400	LLSMNLYELIKKN	gi|148887370|sp|Q9263	NA
3401	RWRKPTYSDKAQN	gi|133777742|gb|AAI104	NA
3402	AYYDVDYEKNAKG	gi|2507461|sp|P30101|P	NA
3403	ERFWESYIYNGKG	gi|20140421|sp|O14669|	NA
3404	GEFEDYYEGLSIG	gi|124297121|gb|AAI317	NA
3405	HSCKEGYVKDLKG	gi|24638219|sp|Q96KP1|	NA
3406	LEDSDCYEKEAKG	gi|119569941|gb|EAW49	NA
3407	IDWGEEYSNSGGG	gi|22256935|sp|Q96TA1|	NA
3408	FWDEFGYLSANWN	gi|114152840|sp|Q9Y6X	NA
3409	GSSQDTYVLHLVN	gi|23397655|ref|NP_115	NA
3410	MEVSSKYVKLNWN	gi|146345397|sp|Q9971	NA
3411	PRGTPEYVKFARQ	gi|148877240|sp|P20648	NA
3412	IVTVDGYVDPSGG	gi|13959561|sp|Q13485|	NA
3413	PMDENCYEQMKAR	gi|74749223|sp|Q6PIZ9|	NA
3414	SLEEEKYDMSGAR	gi|12231007|sp|P31944|	NA
3415	TTKHPDYAILAAR	gi|132608|sp|P23921|RI	NA
3416	AEEWGQYVDLPKG	gi|119371160|sp|Q96CN	NA
3417	QWYKPHYQNSGGG	gi|143811435|sp|Q1337	NA
3418	FLLDSDYERIELG	gi|26454656|sp|O95248|	NA
3419	CGSSDSYVGYNDR	gi|119587532|gb|EAW67	NA
3420	HMSEFAYTRNYDR	gi|3954897|emb|CAA101	NA
3421	VPKEDIYSGGGGG	gi|8134660|sp|Q13151|R	[VPKEDIYSGGGGG|Y|1
3422	SLSDPCYYNKVDR	gi|12644413|sp|Q14202|	NA
3423	VMDELGYMYFRDR	gi|74749156|sp|Q6PCB7	NA
3424	EADEKTYNDALFR	gi|20532022|sp|Q9NY35|	NA
3425	FEVEDGYDLEAVL	gi|12643252|sp|Q9UIV8|	NA
3426	GSYSPGYAKINKR	gi|17433089|sp|Q9UHC6	NA
3427	IQVEEPYYDCHEC	gi|74762724|sp|Q9GZU2	NA
3428	LQCPDGYAIGSEC	gi|56405374|sp|Q13219|	NA
3429	PVMEFDYVICEEC	gi|139816|sp|P23025|XP	NA
3430	RSFSSDYTHLPEC	gi|59803113|sp|Q9HCF6	NA
3431	CRKNGLYTRSPPR	gi|90183175|sp|Q58EX2|	NA

3432	LHSHPAYVAHCVL	gi|115502131|sp|Q8WW	NA
3433	NNFYEYYVDDPPR	gi|2506906|sp|P30047|G	NA
3434	VPSEGAYDIILPR	gi|46396014|sp|Q9NQ84	NA
3435	LACGEKYQVLARR	gi|119607881|gb|EAW87	NA
3436	YLSQEEYEAWSQR	gi|20137932|sp|Q9BXL6|	NA
3437	CEDCSQYHDSECP	gi|118572696|sp|P57071	NA
3438	VGFEDSYGQEPTL	gi|46397079|sp|P60852|	NA
3439	HDCCLKYINLKAS	gi|17380310|sp|Q12874|	NA
3440	LLLELDYADFGCP	gi|74748436|sp|Q6EMK4	NA
3441	VPVEFHYENMHAS	gi|20455187|sp|Q9H4D5	NA
3442	CTEGTTYVCSVCP	gi|17380345|sp|Q9HC78	NA
3443	QLFNVLYEKKGES	gi|13632817|sp|Q9UQ80	NA
3444	WKRSIGYDDTDES	gi|21264409|sp|Q99541|	NA
3445	CWKNPLYPFPGFS	gi|143811435|sp|Q1337	NA
3446	FWEQSDYVPVEFS	gi|71151936|sp|Q9BYG8	NA
3447	PLRVDKYEIPQES	gi|113430861|ref|XP_94	NA
3448	ANDSLAYSDSAGS	gi|114150022|sp|Q7Z3D	NA
3449	WKDAPYYINLVEM	gi|17366834|sp|Q9H251|	NA
3450	SNRETIYPNASLL	gi|6166048|sp|P31997|C	NA
3451	IYTLIHYINQRPS	gi|13878337|sp|Q13315|	NA
3452	KIGEGTYGVVYKA	gi|119609759|gb|EAW89	[KIGEGTYGVVYKA|Y|15
3453	NAYRQLYLNPKGD	gi|30172802|sp|Q15021|	NA
3454	KLNTEEYLRVIGK	gi|1723117|sp|P50748|K	NA
3455	GSDANTYANLCQL	gi|18202620|sp|Q92743|	NA
3456	KYIKDKYPNLQVI	gi|124419|sp|P12268|IM	NA
3457	NPPPEAYGPPRAL	gi|13629029|sp|Q08397|	NA
3458	DPLTETYGIPFYL	gi|47606438|sp|P61599|	NA
3459	LTPSFEYQPDPWN	gi|1709333|sp|P29475|N	NA
3460	STSLVGYLRVQGV	gi|48429265|sp|Q9UKG9	NA
3461	YVGTNAYMAPERI	gi|118572669|sp|Q1316	NA
3462	EISEDVYTAVEHS	gi|25453223|sp|Q9ULU4	NA
3463	EDNQETYLNISQV	gi|14423909|sp|O94768|	NA
3464	EAGTQRYMAPELL	gi|9087133|sp|Q16671|A	NA
3465	QVGTRRYMAPEVL	gi|97535735|sp|Q13705|	NA
3466	LCFLVFYIIPLSI	gi|416726|sp|P32247|BR	NA
3467	DGHEYIYVDPMQL	gi|129892|sp|P16234|PG	[DGHEYIYVDPMQL|Y|5
3468	QADTTQYVPMLER	gi|129892|sp|P16234|PG	[QADTTQYVPMLER|Y|7
3469	DYPLAFYINPWSK	gi|33112422|sp|Q16827|	NA
3470	DGESSNYINAALM	gi|117949771|sp|O14522	NA
3471	VCMLFEYINQGDL	gi|118572711|sp|Q0197	NA
3472	RQEEPEYENVVPI	gi|20140022|sp|Q14162|	NA
3473	FVCSGAYVITRGS	gi|119630463|gb|EAX10	NA
3474	LLCKISYVDTYPC	gi|74733473|sp|Q9BYG0	NA
3475	HTEDDIYKLSLVL	gi|34395670|sp|Q8IV61|	NA
3476	CLPGTDYVLKDHS	gi|37089988|sp|Q9UI38|	NA
3477	PEHEGCYLSVGHS	gi|22001808|sp|Q9Y5X9|	NA
3478	VVTREDYEENGHS	gi|27923737|sp|Q9GZN1	NA
3479	HNVKPEYLDAYNS	gi|17380144|sp|Q9BPW	NA
3480	RYREVHYVLLDPS	gi|118573083|sp|Q3KNT	NA
3481	FYADPNYASEKPS	gi|74760694|sp|Q96A28|	NA
3482	GMKNTSYVLKHPS	gi|74751215|sp|Q8ND82	NA
3483	QTIDDYYTDASPS	gi|134035377|sp|Q8WU	NA

3484	DIEEPIYTMDKQS	gi|145503430|ref|XP_00	NA
3485	QEESTKYFNFATS	gi|12643717|sp|Q13349|	NA
3486	FHYEFSYQIGNTS	gi|23821932|sp|Q8TDX9	NA
3487	LVLKGSYEDTQTS	gi|74750540|sp|Q86XP0|	NA
3488	LNAELSYFITGAA	gi|123123257|emb|CAI1	NA
3489	GFFKDGYMVVNVS	gi|68565572|sp|Q5VW3	NA
3490	VTVNTAYGSNGVS	gi|62089210|dbj|BAD930	NA
3491	ISESDKYDLKTET	gi|20139281|sp|Q9UBK8	NA
3492	TTSDGGYSFKYET	gi|124274|sp|P05111|IN	NA
3493	DDCKAAYIDILGT	gi|108935991|sp|Q6UXV	NA
3494	LLHDEPYTDFDGT	gi|20139243|sp|Q9P1W	NA
3495	YIECTAYPDKNFT	gi|74759634|sp|Q8IWG1	NA
3496	DPSSLHYINPMGT	gi|33860150|sp|Q96FN4|	NA
3497	STDNDDYDDISAA	gi|13637684|sp|P30203|	[STDNDDYDDISAA|Y|66
3498	YNSVVLYSTPPI	gi|143811474|sp|P17948	[YNSVVLYSTPPI|Y|133
3499	DDDANSYENVLIC	gi|74752543|sp|Q9GZY6	[DDDANSYENVLIC|Y|13
3500	DVEDPVYQYIVFE	gi|150421536|sp|O7555	[DVEDPVYQYIVFE|Y|19
3501	ENADDSYEPPPVE	gi|82592659|sp|Q8WV2	[ENADDSYEPPPVE|Y|9
3502	GTPEGLYL	gi|49065817|sp|P62191|	[GTPEGLYL|Y|439|P621
3503	TVEAVAYAPKKEL	gi|548663|sp|Q06609|RA	[TVEAVAYAPKKEL|Y|54
3504	EESRLLYEIQNRD	gi|118572680|sp|Q0180	NA
3505	PEPAHAYAQPQTT	gi|1169094|sp|P46109|C	[PEPAHAYAQPQTT|Y|2
3506	REFLDQYDAPL	gi|20178094|sp|O14543|	[REFLDQYDAPL|Y|221|
3507	PKAEDEYVNEPLY	gi|3913590|sp|Q15303|E	NA
3508	EGWMVHYTSKDTL	gi|2499575|sp|Q15139|K	[EGWMVHYTSKDTL|Y|
3509	LDNGGFYISPRIT	gi|125474|sp|P06239|LC	[LDNGGFYISPRIT|Y|192
3510	QSSGYRYGTDPTP	gi|125370|sp|P06241|FY	[QSSGYRYGTDPTP|Y|3
3511	SLFTPDYELLTEN	gi|12643404|sp|O60674|	[SLFTPDYELLTEN|Y|81
3512	VKCVAPYPSLLSS	gi|125484|sp|P08581|ME	[VKCVAPYPSLLSS|Y|13
3513	GLGVKYYIDPSTY	gi|6919882|sp|O15197|E	NA
3514	LNSDVQYTEVQVS	gi|129747|sp|P16284|PE	[LNSDVQYTEVQVS|Y|6
3515	ETTVELYSLAERC	gi|20141582|sp|Q04759|	[ETTVELYSLAERC|Y|90
3516	GFNPLIYCRSPDF	gi|114765|sp|P07550|AD	[GFNPLIYCRSPDF|Y|32
3517	KAQQGLYQVPGPS	gi|8134339|sp|P56945|B	[KAQQGLYQVPGPS|Y|1
3518	KSATLLYDQPLQV	gi|116242614|sp|Q96RT	[KSATLLYDQPLQV|Y|92
3519	LSPSSGYMPMNQG	gi|119534|sp|P21860|ER	NA
3520	RIGDELYLEPLED	gi|74717382|sp|Q99638|	[RIGDELYLEPLED|Y|28|
3521	RREVGDYGQLHET	gi|12643404|sp|O60674|	[RREVGDYGQLHET|Y|5
3522	TRRTPDYFL	gi|50402236|sp|P62714|	[TRRTPDYFL|Y|307|P67
3523	YGVSPNYDKWEME	gi|85681908|sp|P00519|	[YGVSPNYDKWEME|Y|
3524	ETADGGYMTLNPR	gi|399478|sp|P31995|FC	[ETADGGYMTLNPR|Y|2
3525	LLRRGEYPDYQQW	gi|117464|sp|P07315|CR	[LLRRGEYPDYQQW|Y|
3526	PTDNEDYEHDDED	gi|3023207|sp|P78314|3	[PTDNEDYEHDDED|Y|1
3527	GST	contol_spot	[IMRDSNYISKGST|Y|85
3528	pY	contol_spot	NA
3529	pY	contol_spot	NA
3530	GST	contol_spot	[IMRDSNYISKGST|Y|85
3531	pY	contol_spot	NA
3532	pY	contol_spot	NA
3533	PNSNSMYIDRPPS	gi|10720065|sp|Q13094|	[PNSNSMYIDRPPS|Y|1
3534	DLDDEDYEEDTPK	gi|2842711|sp|Q92785|R	NA
3535	LSENVPYKFKVQA	gi|13638154|sp|P16144|	NA

3536	GGGYAPYGRPGRG	gi|20454955|sp|Q14526|	NA
3537	MEKGEPYMSIQPA	gi|61247587|sp|Q969G3|	NA
3538	FWVGQPYPTLSTP	gi|1705545|sp|P55285|C	NA
3539	YLHRKEYSQNLTS	gi|108864727|sp|Q8TE67	NA
3540	QVLQLVYKDGSPC	gi|60416403|sp|P11717|	NA
3541	DYKNICYVITHGD	gi|74760696|sp|Q96A32|	NA
3542	GAGQLDYGSKGIP	gi|131573277|gb|ABO33	NA
3543	TASLAKYADPVAD	gi|51704233|sp|O15194|	NA
3544	DEVETTYSRFQDL	gi|1177024|sp|P42694|H	NA
3545	QGGYDRYSGGNYR	gi|1710620|sp|P98179|R	NA
3546	HTVQLKYYNKPLL	gi|22095550|sp|Q9HCU4	NA
3547	ANSSMAYPSLVAM	gi|14285501|sp|P78318|	NA
3548	AGCGKFYEGTADE	gi|2494849|sp|Q16775|G	NA
3549	PVDILTYVAWKIS	gi|126047|sp|P00338|LD	NA
3550	PKVLQDYRKLKNT	gi|60392197|sp|P09884|	NA
3551	RQHHDEYEDEIRM	gi|115502368|sp|O75976	NA
3552	YNVTSDYAVHPMS	gi|48474955|sp|Q9HAU0	NA
3553	FRNGIPYLNQEEE	gi|60390262|sp|O95453|	NA
3554	KVVQDTYQIMKVE	gi|71152119|sp|O14964|	NA
3555	EYVRTLYDFPGND	gi|1169094|sp|P46109|C	NA
3556	YCPDSLYQVMQQC	gi|585912|sp|Q04912|RC	NA
3557	GRGHTRYYPQYRD	gi|119611307|gb|EAW90	NA
3558	QNQDDGYLALSSR	gi|119372014|sp|Q8IVL1	NA
3559	YHPMSEYPTYHTH	gi|547937|sp|P15941|MU	NA
3560	VSRALEYNSKRTP	gi|66268793|gb|AAY4312	NA
3561	NGLLSYYRSKAEM	gi|129308|sp|P22059|OS	NA
3562	VARGMEYLAEQKF	gi|585912|sp|Q04912|RC	NA
3563	FTVLEHYRRTHCV	gi|116242668|sp|Q14896	NA
3564	KITRLTYEIEDEK	gi|115502381|sp|P15924	NA
3565	TLKDFQYVDRDGK	gi|41017059|sp|Q9Y6I3|	NA
3566	GMLGASYAAVPLY	gi|60416378|sp|Q9Y6N1|	NA
3567	GYSDEIYVVPDDS	gi|46397678|sp|Q13017|	NA
3568	SGADRIYDLNIPA	gi|20532395|sp|O43639|	NA
3569	LSHTDFYEEIQEF	gi|51704228|sp|P55786|	NA
3570	NLKKKSYLNIRTH	gi|21759409|sp|Q96B26|	NA
3571	YGPPPSYPNLKIP	gi|2498883|sp|Q13435|S	NA
3572	VISTLQYLNLINY	gi|30923328|sp|Q92993|	NA
3573	LKLAEPYGKIKNY	gi|12643409|sp|P43243|	NA
3574	NALAKWYVNAKGY	gi|2499703|sp|Q13393|P	NA
3575	NLKDINYVNPVIK	gi|116607|sp|P01031|CO	NA
3576	VFYVETYGVIEKL	gi|14548113|sp|O15232|	NA
3577	ELLTEAYGEVHIK	gi|6226953|sp|O96018|A	NA
3578	EWSKDQYVNPNSQ	gi|116241267|sp|Q9Y6D	NA
3579	QQSCGTYLRVRQP	gi|547896|sp|P11912|CD	NA
3580	TDADYEYEEITLE	gi|2497504|sp|Q12959|D	NA
3581	LASEEIYINQLEA	gi|5915668|sp|Q12979|A	NA
3582	PFCLPFYLIPPSA	gi|20137254|sp|O14503|	NA
3583	LDVGAMYPNIILT	gi|116241339|sp|Q07864	NA
3584	SPTGGIYPNPNVP	gi|399496|sp|Q01543|FL	NA
3585	MSSSYYVNALFS	gi|3915721|sp|P31268|H	NA
3586	SSSLDSYTAVNQA	gi|6136122|sp|O75840|K	NA
3587	LLYDLRYLNIVLT	gi|22653695|sp|Q8WTW	NA

3588	DTIFRGYLIPKGT	gi|117250|sp|P05181|CP	NA
3589	INFRTTYVNANEE	gi|7531135|sp|Q12809|K	NA
3590	VILGLSYANLQTG	gi|6093462|sp|O75694|N	NA
3591	LCQSGIYINVLDI	gi|3024212|sp|O00476|N	NA
3592	VTDQESYANVKQW	gi|23396834|sp|Q9H0U4	NA
3593	GAYLLPYLILLMV	gi|18202939|sp|Q9H2J7|	NA
3594	ASLLARYPPEKLF	gi|56404535|sp|Q6XZF7|	NA
3595	RTILSRYEGKMET	gi|115855|sp|P22681|CB	NA
3596	WDTTGLYSFSEQT	gi|13633914|sp|Q15796|	NA
3597	HLQDVPYVMVRER	gi|148876773|sp|Q1412	NA
3598	LLGLPSYMLQSEE	gi|56404535|sp|Q6XZF7|	NA
3599	H3:17	contol_spot	NA
3600	H7:17	contol_spot	NA
3601	QVDKSDYDMVDYL	gi|20981701|sp|Q14974|	NA
3602	TQVVDHYENPRNV	gi|24307953|ref|NP_055	NA
3603	FGTKTRYEDVNPV	gi|68565617|sp|Q9UNW	NA
3604	LTRQEKYTSEKPV	gi|119585370|gb|EAW64	NA
3605	YTWEYEYYEIGPV	gi|68565259|sp|Q96G30|	NA
3606	DFVKEKYLEYQQV	gi|123271938|emb|CAM	NA
3607	SGSAHEYSSSPDD	gi|115892|sp|P16870|CB	NA
3608	AFMEPRYHVRGED	gi|55976445|sp|Q6S8J3|	NA
3609	IRDFQEYVEPGED	gi|134047749|sp|Q9Y6G	NA
3610	LVEKGEYCQTRYV	gi|90110053|sp|Q06587|	NA
3611	AFSCPAYWMPGEW	gi|76800647|sp|Q8TE60|	NA
3612	SADCLDYKEPGAA	gi|417425|sp|P32242|OT	NA
3613	NDHFDTYADALWW	gi|14285389|sp|O43526|	NA
3614	TLNLSKYQNVNTW	gi|74761446|sp|Q9H5K3|	NA
3615	EVLSDIYIIPPAY	gi|74751163|sp|Q8NB91|	NA
3616	GCKHNSYEDAKAY	gi|73920089|sp|Q5JUK3|	NA
3617	MTSQGYYKRTPAY	gi|119605027|gb|EAW84	NA
3618	WNPNKEYEDLLDY	gi|62899863|sp|Q76N32|	NA
3619	DKSDTAYQWNLKY	gi|129122|sp|P23515|OM	NA
3620	VIVMSKYMENGMQ	gi|12585199|sp|O00257|	NA
3621	QENDPAYILNDLY	gi|119585925|gb|EAW65	NA
3622	SWYNHFYVSVCLY	gi|117949602|sp|Q7Z2K	NA
3623	CPASDGYKQIMPY	gi|67462180|sp|Q8N6G6	NA
3624	NISDLKYCELPPY	gi|115502208|sp|Q8N9F	NA
3625	TLRCNEYENCLCQ	gi|401413|sp|P04275|VW	NA
3626	GLCGEDYVFFHLD	gi|113912|sp|P16066|AN	NA
3627	GPAQDIYQVPPSA	gi|8134339|sp|P56945|B	NA
3628	AKSKFEYVRDFEA	gi|146325755|sp|Q9NW	NA
3629	LFTDDKYNDFIEA	gi|134035014|sp|Q9P22	NA
3630	LGDKETYHFDPEA	gi|3123244|sp|P49641|M	NA
3631	DNSTEGYWKYGYD	gi|2497915|sp|Q30201|H	NA
3632	GRRRDSYYDRGYD	gi|4033480|sp|Q13595|T	NA
3633	QKYKSLYGDVDSP	gi|134048492|sp|Q9Y4B	NA
3634	FFYDGGYINASAE	gi|1709662|sp|P55058|P	NA
3635	WAENQTYMDCRAE	gi|126302546|sp|Q5JY7	NA
3636	ESEYEEYTDSEDE	gi|1709012|sp|P55081|M	NA
3637	VEFMFSYGNFGYG	gi|74726955|sp|Q53TS8|	NA
3638	GIPPPLYTETGLE	gi|68565213|sp|Q8N6L7|	NA
3639	DDHDEKYGVPSLE	gi|74735764|sp|Q16526|	NA

3640	CRECNSYVYFQGA	gi|119589959|gb|EAW69	NA
3641	RDEKGRYKRFHGA	gi|74732921|sp|Q9BRR8	NA
3642	CPSEFDYNATDHA	gi|30923161|sp|O75487|	NA
3643	<<Marker>>	contol_spot	NA
3644	TDKSDKYDARDVE	gi|67461057|sp|Q8NHP6	NA
3645	FTSSSSYFDEPVE	gi|21263420|sp|Q9NP61|	NA
3646	NPYKEVYTDMWVE	gi|20532391|sp|Q9Y6K1|	NA
3647	AAAAETYANISWE	gi|33112413|sp|Q92823|	NA
3648	GTADDRYLRPHAF	gi|9087155|sp|Q12968|N	NA
3649	NRGKEGYIERKAF	gi|74734998|sp|Q9UEE9	NA
3650	VWEEQAYSNCSGP	gi|113015|sp|P28330|AC	NA
3651	GPAFESYESMELA	gi|28380093|sp|Q9Y2U9|	NA
3652	IETDSGYNSMDLA	gi|27734215|sp|Q9H9E1|	NA
3653	SWNCDGYVVMRKA	gi|119593844|gb|EAW73	NA
3654	DTWRTEYVPVPIP	gi|17369677|sp|Q9UBW	NA
3655	EKGKTKYVIFKIP	gi|41688803|sp|Q9HAY6	NA
3656	HWQDSGYLIVYVT	gi|118595707|sp|O00562	NA
3657	VLPCLEYHNNTWT	gi|114149325|sp|Q14667	NA
3658	DTSALSYDSVKYT	gi|17433093|sp|Q9UQF2	NA
3659	FSSNDPYPYPRYT	gi|13124785|sp|P16519|	NA
3660	NSRCEYYCSPGYT	gi|2498958|sp|P78539|S	NA
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3662	ELQEGRYESEKLQ	gi|119586105|gb|EAW65	NA
3663	KARSKTYINMREV	gi|1345664|sp|P20807|C	NA
3664	<<Marker>>	contol_spot	NA
3665	FIRVGYYVNNEYL	gi|74734533|sp|Q9NVP2	NA
3666	VITDVYYVDGTEV	gi|8928568|sp|Q12888|T	NA
3667	DNAENVYVWKQGV	gi|121531|sp|P07359|GP	NA
3668	IVSGTRYKGNGGV	gi|20137697|sp|O60762|	NA
3669	IQLLDDYPKCFIV	gi|133041|sp|P05388|RL	[IQLLDDYPKCFIV|Y|24|
3670	LKGSNLYSQLERQ	gi|59798964|sp|Q8N5T2|	[LKGSNLYSQLERQ|Y|2
3671	TDFPGNYSGYDDA	gi|3914807|sp|O15160|R	[TDFPGNYSGYDDA|Y|3
3672	DDDFEPYLSPQAR	gi|41019527|sp|Q9Y5A9|	[DDDFEPYLSPQAR|Y|3
3673	DVKEQIYKLAKKG	gi|50403608|sp|P62277|	NA
3674	NGAEPNYHSLPSA	gi|125863645|sp|Q6IAA8	[NGAEPNYHSLPSA|Y|4
3675	IGNKERYDFHKLF	gi|55957529|emb|CAI17	NA
3676	MAFSPNYMSMLLF	gi|119567991|gb|EAW47	NA
3677	YQYMETYMGPALF	gi|20981701|sp|Q14974|	NA
3678	FFSEKIYKLNEDM	gi|130861|sp|P25789|PS	NA
3679	GHKNEKYCIFANF	gi|74762455|sp|Q86VZ2|	NA
3680	KNSEGKYHCPVLF	gi|23813917|sp|Q13356|	NA
3681	PVWEFKYGDLLGH	gi|5921793|sp|O75503|C	NA
3682	YLTMDIYAFPAGH	gi|74751178|sp|Q8NBV4	NA
3683	IRAPPTYVKVEVP	gi|24212387|sp|Q9UJQ4	NA
3684	HIEVKGYEDGGIH	gi|59799178|sp|O00478|	NA
3685	<<Marker>>	contol_spot	NA
3686	CVKNSSYVHSSLH	gi|265484|gb|AAB25346.	NA
3687	LKQADLYISEGLH	gi|22654293|sp|Q92526|	NA
3688	EQPETYYKWDNWP	gi|97052424|sp|Q8N201|	NA
3689	PEVSEKYEIGSVP	gi|37087933|sp|O76003|	NA
3690	DEGESRYKITDII	gi|118601083|sp|Q1308	NA
3691	LLCCGEYQDVLII	gi|109896166|sp|Q3MJ1	NA

3692	CDINGKYENNYNA	gi|90101756|sp|Q8IYR2|	NA
3693	VYSKLIYVCSFPA	gi|11387048|sp|O14901|	NA
3694	SDPAEEYELVQVI	gi|14548230|sp|Q9NZL6|	NA
3695	FNVEEMYEAHAWI	gi|48474734|sp|Q8IXQ6|	NA
3696	HYRESRYRRSPYI	gi|89024885|ref|XP_935	NA
3697	MASLEVYVRRGYI	gi|134047740|sp|O0076	NA
3698	AEYCEQYVSYFCK	gi|17433089|sp|Q9UHC6	NA
3699	KTDTDLYEFAKCK	gi|74760739|sp|Q96BP3|	NA
3700	KFIEQSYSSVAEM	gi|23830899|sp|Q13733|	NA
3701	QMYNSPYHRVTDC	gi|74751734|sp|Q96A46|	NA
3702	SPCSRGYCDHGGQ	gi|125987841|sp|Q9910	NA
3703	PPDNSFYVRTCNK	gi|74751754|sp|Q96B02|	NA
3704	AEMEGKYVINMPK	gi|74729722|sp|Q8N9M1	NA
3705	VRRNNIYELNPNK	gi|97535778|sp|Q9NSI6|	NA
3706	<<Marker>>	contol_spot	NA
3707	EVSMSRYIPHPFL	gi|66347356|emb|CAI95	NA
3708	VEASNPYVEPRFL	gi|1705545|sp|P55285|C	NA
3709	AAYNPSYYSGPGL	gi|34364899|emb|CAE45	NA
3710	DMYNTPYTYNAGL	gi|119625041|gb|EAX04	NA
3711	GQQEEYYRKLAGL	gi|125993|sp|P04180|LC	NA
3712	SGSEVWYSNGPGL	gi|94717653|sp|Q38SD2|	NA
3713	ACMWGEYVDNTNL	gi|123079|sp|P06865|HE	NA
3714	YPDKIDYASLDPL	gi|146286137|sp|Q8N3D	NA
3715	CYSDGKYYEPKQL	gi|48428570|sp|O75443|	NA
3716	EQPAPGYDTHGRL	gi|85700443|sp|Q07157|	NA
3717	PARKGLYEGTGRL	gi|17375667|sp|Q9UBC3	NA
3718	KGNEEGYFGTRRL	gi|1169653|sp|P98095|F	NA
3719	CVSWSLYHDLGPM	gi|119613484|gb|EAW93	NA
3720	AELVNNYGKGWSL	gi|145559521|sp|Q1370	NA
3721	NQGVRTYVDPFTY	gi|1711371|sp|P54764|E	[NQGVRTYVDPFTY|Y|5
3722	PAAPVSYADMRTG	gi|547738|sp|P35568|IR	NA
3723	PEDKAKYDAIFDS	gi|67476728|sp|P42566|	NA
3724	PKSPGEYINIDFG	gi|62298062|sp|Q9Y4H2|	NA
3725	VYEEDSYVKRSQG	gi|547807|sp|P07949|RE	[VYEEDSYVKRSQG|Y|9
3726	YAEPHTYEEPGRA	gi|19857975|sp|P29322|	[YAEPHTYEEPGRA|Y|6
3727	<<Marker>>	contol_spot	NA
3728	YIDPETYEDPNRA	gi|146345416|sp|Q1537	NA
3729	YMEDSTYYKASKG	gi|3183518|sp|Q05397|F	[YMEDSTYYKASKG|Y|6
3730	YVDPHTYEDPTQA	gi|116241351|sp|P29320	[YVDPHTYEDPTQA|Y|6
3731	DIYKNDYYRKRGE	gi|126302596|sp|P08922	[DIYKNDYYRKRGE|Y|21
3732	ILEEVRYIANRFR	gi|91208254|sp|Q494W8	[ILEEVRYIANRFR|Y|442
3733	ISKAEEYFLLKSR	gi|543759|sp|Q07001|AC	NA
3734	IYKNDYYRKRGEG	gi|126302596|sp|P08922	[IYKNDYYRKRGEG|Y|21
3735	IYSGDYYRQGCAS	gi|1717829|sp|Q06418|T	NA
3736	KDTETVYSEVRKA	gi|129747|sp|P16284|PE	[KDTETVYSEVRKA|Y|71
3737	KKVVALYDYMPMN	gi|547759|sp|Q06187|BT	[KKVVALYDYMPMN|Y|2
3738	VIEDNEYTAREGA	gi|20141296|sp|P08631|	[VIEDNEYTAREGA|Y|39
3739	HAEAALYKNLLHS	gi|125472|sp|P10721|KIT	[HAEAALYKNLLHS|Y|70
3740	LDGENIYIRHSNL	gi|90101808|sp|P11171|	[LDGENIYIRHSNL|Y|66
3741	SQQTNDYMQPEED	gi|46397817|sp|P12814|	[SQQTNDYMQPEED|Y|
3742	PEPENDYEDVEEM	gi|123557|sp|P14317|HC	[PEPENDYEDVEEM|Y|3
3743	RDINSLYDVSRMY	gi|143811440|sp|P16885	[RDINSLYDVSRMY|Y|75

3744	AEQAERYDDMATC	gi|112690|sp|P27348|143	NA
3745	PDAVDKYLETPGD	gi|112927|sp|P05067|A4_	NA
3746	ECCKEPYPDVTFT	gi|91208254|sp|Q494W8	NA
3747	INTEGGYVCRCSE	gi|119226|sp|P01133|EG	NA
3748	<<Marker>>	contol_spot	NA
3749	SGSDTTYFSVNVS	gi|120046|sp|P11362|FG	NA
3750	NCTNELYMMMRDC	gi|119583708|gb|EAW63	[NCTNELYMMMRDC|Y|
3751	SSDNSLYTNAKGS	gi|47117704|sp|P61244|	[SSDNSLYTNAKGS|Y|12
3752	QRLGLDYEERVLP	gi|74752151|sp|Q99623|	NA
3753	VTCTRIYEKVE	gi|232081|sp|Q01469|FA	NA
3754	RPTQPVYQIQNRG	gi|74733529|sp|Q9H0W8	[RPTQPVYQIQNRG|Y|14
3755	LRIVEPYIAWGYP	gi|133021|sp|P18124|RL	[LRIVEPYIAWGYP|Y|139
3756	KKNLQYYDISAKS	gi|51338598|sp|P62826|	[KKNLQYYDISAKS|Y|147
3757	KRVPCAYDKTALA	gi|1169094|sp|P46109|C	[KRVPCAYDKTALA|Y|25
3758	NKEVLDYSTPTTN	gi|20455516|sp|P08240|	[NKEVLDYSTPTTN|Y|26
3759	GQRIYQYIQSRFY	gi|3219996|sp|Q13627|D	[GQRIYQYIQSRFY|Y|27
3760	SCRNLVYDQSPNR	gi|108860813|sp|Q9NXR	[SCRNLVYDQSPNR|Y|2
3761	RLFQQIYSDGSDE	gi|62512186|sp|Q9Y2Z0|	[RLFQQIYSDGSDE|Y|31
3762	ETSKLIYDFIEDQ	gi|1722836|sp|P42768|W	[ETSKLIYDFIEDQ|Y|291
3763	TATEGQYQPQP	gi|125474|sp|P06239|LC	[TATEGQYQPQP|Y|505|
3764	WQKNGDYLCVKVD	gi|3123230|sp|P55884|IF	NA
3765	TQAVAAYQGCHFM	gi|14349166|dbj|BAB607	NA
3766	KHFTNPYCNIYLN	gi|121743|sp|P20936|RA	[KHFTNPYCNIYLN|Y|61
3767	LPDGTFYSTLYLP	gi|24418367|sp|Q9UPY3	[LPDGTFYSTLYLP|Y|65
3768	PGSAAPYLKTKFI	gi|48429227|sp|P40763|	[PGSAAPYLKTKFI|Y|705
3769	<<Marker>>	contol_spot	NA
3770	NLANNPYSGDVTK	gi|7688705|gb|AAF6749	[NLANNPYSGDVTK|Y|8
3771	VKLISWYDNEFGY	gi|120649|sp|P04406|G3	NA
3772	KLAAVTYNGVDNN	gi|67472677|sp|Q16181|	[KLAAVTYNGVDNN|Y|3
3773	RLGEDPYYTENGG	gi|3183511|sp|P28906|C	[RLGEDPYYTENGG|Y|3
3774	EVKRNVYDLTSIP	gi|20454906|sp|Q9UNN5	NA
3775	LTADFLYEEVHPK	gi|41688753|sp|Q12792|	[LTADFLYEEVHPK|Y|32
3776	PPLEESYINNDQY	gi|731631|sp|P38704|ST	NA
3777	MSKMESYATKVEL	gi|730744|sp|P38889|SK	NA
3778	IALETFYARVGRP	gi|729290|sp|P21657|DA	NA
3779	NSYECKYDRPPRN	gi|731945|sp|P39529|YJ	NA
3780	NPSLTKYNDTATY	gi|1352985|sp|P47043|Z	NA
3781	RKEGIEYEDMHTH	gi|88984071|sp|P17106|	NA
3782	IQTCEKYIQVLEE	gi|1169823|sp|P04386|G	NA
3783	KIFSDYYTLVNSI	gi|1169136|sp|P41817|C	NA
3784	NSNNSYYSNNEDA	gi|3024551|sp|Q12224|R	NA
3785	PTADAIYTDVHKL	gi|729486|sp|P39521|FH	NA
3786	KPENILYADDTPG	gi|37999483|sp|O75676|	NA
3787	FNYPDQYVREYAV	gi|1171955|sp|P42338|P	NA
3788	CSEGLDYKSMGRM	gi|119610537|gb|EAW90	NA
3789	GLREKDYDFPPPM	gi|8134360|sp|Q14511|C	NA
3790	<<Marker>>	contol_spot	NA
3791	MDNQGGYGSVGRM	gi|23503095|sp|P31942|	[MDNQGGYGSVGRM|Y
3792	SIHNDLYVIGGQM	gi|148664248|ref|NP_99	NA
3793	SYFEPRYILVVPM	gi|85397400|gb|AAI0489	NA
3794	FLTENGYAHNVSM	gi|74735330|sp|O14777|	NA
3795	EIKKEDYVLTKFN	gi|134035019|sp|Q9P2N	NA

3796	GQNEKKYDCVIFN	gi|109458219|ref|XP_001	NA
3797	KSDGDSYFTIDGN	gi|1705551|sp|P55289|C	NA
3798	LNIPDAYADPRFN	gi|7993747|sp|Q9Y233|P	NA
3799	SSRFGKYIDIYFN	gi|119615728|gb|EAW95	NA
3800	CDNCDAYLQMKGN	gi|54039624|sp|P63272|	NA
3801	NLEQEEYEDPDIP	gi|114787|sp|P02730|B3	[NLEQEEYEDPDIP|Y|21
3802	HKRCPDYIIQKLN	gi|33112650|sp|P08575|	NA
3803	NTHKDRYKFIHLN	gi|24212102|sp|P59045|	NA
3804	RVGELEYAVIDLN	gi|148806872|ref|NP_05	NA
3805	YCTCISYVNSCLN	gi|543823|sp|P35414|AP	NA
3806	DGEVTPYANTNNN	gi|14286105|sp|P23634|	[DGEVTPYANTNNN|Y|1
3807	SVNCELYFMVGVN	gi|147647000|sp|Q6UXG	NA
3808	YPSPPGYIFDNTN	gi|60223083|ref|NP_001	NA
3809	ETNEWRYVSSLPQ	gi|81175180|sp|Q9P2G3	NA
3810	GQGPPPYVFMYPQ	gi|61213006|sp|Q8WXE	NA
3811	NNSMENYLSKMQQ	gi|109940217|sp|Q9UPS	NA
3812	SDTESGYLQSHPQ	gi|17380345|sp|Q9HC78	NA
3813	NRDSYSYGSRRGG	gi|20981728|sp|Q13247|	NA
3814	NPTEFDYLNPNVQ	gi|119584881|gb|EAW64	NA
3815	YCKEDYYRRFSVQ	gi|8247936|sp|P50458|L	NA
3816	DADQDIYAVVTYQ	gi|17366834|sp|Q9H251|	NA
3817	GYASFDYEDAGYQ	gi|74728811|sp|Q8N442|	NA
3818	LGSKVGYLDVEAR	gi|22028344|gb|AAH349	NA
3819	SRFREGYEIPPGG	gi|119606058|gb|EAW85	NA
3820	LAFERGYEFLGVA	gi|146286173|sp|P0C2W	NA
3821	SYGGSDYGNGFGG	gi|8134660|sp|Q13151|R	NA
3822	CLHKEYYETKKVA	gi|63995543|gb|AAY410	NA
3823	ESSKSSYELIVVA	gi|73620979|sp|Q8TAB3|	NA
3824	VPMPDKYSSEPVA	gi|52788229|sp|P00558|	NA
3825	EAEKRPYIDEAKR	gi|6831689|sp|O95416|	NA
3826	GHQETKYRSGRIR	gi|62899891|sp|Q9HC77	NA
3827	KEDEFGYSWKNIR	gi|68052394|sp|O75970|	NA
3828	RKRDRKYDTPGKR	gi|74761976|sp|Q9UJL9|	NA
3829	YKIKQGYVIYGIR	gi|114664783|ref|XP_001	NA
3830	EDEEDFYQGSMEC	gi|50400556|sp|Q8N9N2	NA
3831	LKVEPGYPKSALR	gi|60392771|sp|P50281|	NA
3832	SFESKDYLQVCLR	gi|124015168|sp|Q96Q8	NA
3833	YMEEDVYQLQELR	gi|122889217|emb|CAI1	NA
3834	PQRKSLYESDRLR	gi|123263697|emb|CAM	NA
3835	DQFMNDYVEEANR	gi|74746271|sp|Q5TEA3|	NA
3836	YEEELLYEIKLNR	gi|20137479|sp|Q9H2U9	NA
3837	QLFREPYIRTGYR	gi|51316493|sp|Q8TEZ7|	NA
3838	RIVDTDYSSFAVL	gi|71296898|gb|AAH351	NA
3839	EISFSYYVRPGNG	gi|119609013|gb|EAW88	NA
3840	GLQNDDYETWLNG	gi|62988803|gb|AAY241	NA
3841	LRHLPDYHDLPNG	gi|88943851|ref|XP_372	NA
3842	RVRKDMYNDTLNG	gi|74761039|sp|Q96PU8|	NA
3843	MNSSGVYASPTCS	gi|55957964|emb|CAI14	NA
3844	SSSNLSYQSHDCS	gi|143811459|sp|Q96T6	NA
3845	CPEGTVYDDIGDS	gi|2506877|sp|Q02817|M	NA
3846	GPSNPSYCYGNDS	gi|46397621|sp|P98088|	NA
3847	LVAEEYYADAFDS	gi|74715639|sp|Q8NG66	NA

3848	WTCMEYYERDSDS	gi|62287833|sp|O75157|	NA
3849	RRYGDRYINLRGP	gi|113045|sp|P12821|AC	NA
3850	EETREAYANIAEL	gi|416732|sp|P33076|C2	NA
3851	EVTFHLYLIPSDC	gi|17380146|sp|Q9C000|	NA
3852	ENPIDLYIYVIDM	gi|81175161|sp|P55283|	NA
3853	ARTGILYVNASLD	gi|22095683|sp|Q9NYQ8	NA
3854	LEVGAPYLRVDGK	gi|24212077|sp|Q08174|	NA
3855	RIYIHRYENVSIL	gi|729242|sp|P40145|AD	NA
3856	QRLDCIYLNAGIM	gi|8134404|sp|P56937|D	NA
3857	TFPPISYLNAISW	gi|1706681|sp|P53602|E	NA
3858	EAALNEYLRVKTV	gi|59802911|sp|O75891|	NA
3859	GDVAACYANPSLA	gi|68056598|sp|Q14376|	NA
3860	ASTSELYGKVQEI	gi|9087147|sp|O60547|G	NA
3861	DSTAETYGKIVHY	gi|1706450|sp|Q09013|D	NA
3862	VCEEMTYEEIQDN	gi|6226609|sp|Q16877|F	NA
3863	AVQKYAYLNVVGM	gi|1346355|sp|Q01813|K	NA
3864	EKKDEVYLNLVLD	gi|20455502|sp|P49841|	NA
3865	TMKFNGYLRVRIG	gi|1346393|sp|P24723|K	NA
3866	ENIAELYGAVLWG	gi|50403742|sp|P41279|	NA
3867	NDINCGYPNAFIC	gi|126730|sp|P22897|MR	NA
3868	NSGLHSYMEMPLE	gi|125484|sp|P08581|ME	NA
3869	LYMPKVYIIIFHP	gi|12644040|sp|O00222|	NA
3870	IFFLLPYINPDLY	gi|128359|sp|P25103|NK	NA
3871	CFFLVTYMAPLCL	gi|6225810|sp|O43614|O	NA
3872	KDESVDYVPMLDM	gi|129890|sp|P09619|PG	[KDESVDYVPMLDM|Y|7
3873	PEVKVQYEEIANC	gi|12314174|emb|CAC0	NA
3874	QGSDLSYVTIFLC	gi|14549162|sp|Q12967|	NA
3875	GQRAEPYCSVLPG	gi|90101344|sp|Q9BUJ2|	NA
3876	KSSKAYYVLSDAA	gi|109826957|sp|Q3B7T	NA
3877	YKRNNFYIKIRPG	gi|17433099|sp|Q9Y2J2|	NA
3878	DTEKEKYEITEQC	gi|89025433|ref|XP_940	NA
3879	NVSSLPYAVPPLS	gi|124951|sp|P08514|IT	NA
3880	QPKAPGYICHGLS	gi|119581630|gb|EAW61	NA
3881	LGSGPAYDFPGVL	gi|17378648|sp|Q9GZZ0	NA
3882	GIECPDYRGNRLS	gi|74749905|sp|Q7L8L6|	NA
3883	VIFNNTYIYSGMS	gi|50400302|sp|Q13564|	NA
3884	ARRDSPYAEINNS	gi|119582811|gb|EAW62	NA
3885	TSFDETYIKKHGP	gi|153792764|ref|NP_06	NA
3886	NGESPIYMYLQRS	gi|119575454|gb|EAW55	NA
3887	IKAEDHYWGQDSS	gi|20178228|sp|Q9H4T2|	NA
3888	SGAGEPYDIIDSS	gi|121940655|sp|Q1AE9	NA
3889	TGGWNDYKNNNSS	gi|38258268|sp|Q9UPQ9	NA
3890	KHPGDFYVQLYSS	gi|119569861|gb|EAW49	NA
3891	EPDADGYESDDCT	gi|51701386|sp|Q14184|	NA
3892	IQNQESYEDGPCT	gi|20178178|sp|Q9Y2L5|	NA
3893	SLCAGPYQNTADT	gi|119606839|gb|EAW86	NA
3894	VKVEPLYELVTAT	gi|20141201|sp|P07358|	NA
3895	HYSEVPYGDPRDT	gi|66912176|ref|NP_001	NA
3896	EVCEPLYVLALET	gi|12644525|sp|P57678|	NA
3897	VQQQEVYGMMPRD	gi|94730425|sp|Q13813|	[VQQQEVYGMMPRD|Y|
3898	EKQFQPYFIPIN	gi|27735177|sp|P16410|	[EKQFQPYFIPIN|Y|218|
3899	VIAVDRYFAITSP	gi|114765|sp|P07550|AD	[VIAVDRYFAITSP|Y|132

3900	EGMPKSYLPQTVR	gi|729833|sp|P40189|IL6	[EGMPKSYLPQTVR|Y|9
3901	LVDAEEYLVPQQG	gi|119533|sp|P04626|ER	NA
3902	PSPLQRYSEDPTV	gi|119533|sp|P04626|ER	[PSPLQRYSEDPTV|Y|11
3903	ILPRQQYFKQNCS	gi|729833|sp|P40189|IL6	[ILPRQQYFKQNCS|Y|81
3904	PGTPVKYSEVVLD	gi|74753488|sp|Q9Y3P8|	[PGTPVKYSEVVLD|Y|14
3905	SINSPVYSRHSYT	gi|56404432|sp|O14639|	[SINSPVYSRHSYT|Y|46
3906	SSQEVTYAQLDHW	gi|74736490|sp|Q6GTX8	[SSQEVTYAQLDHW|Y|2
3907	TSDQVLYGQLLGS	gi|729564|sp|Q99062|CS	[TSDQVLYGQLLGS|Y|7
3908	EEDADSYENMDNP	gi|110282942|sp|P15391	[EEDADSYENMDNP|Y|5
3909	TATEIIYSEVKKQ	gi|3172147|gb|AAC1843	[TATEIIYSEVKKQ|Y|520
3910	YDRPASYKKKSML	gi|129892|sp|P16234|PG	[YDRPASYKKKSML|Y|7
3911	LAGVSEYELPEDP	gi|119583714|gb|EAW63	[LAGVSEYELPEDP|Y|46
3912	VSTFEQYQFLYDV	gi|33112650|sp|P08575|	[VSTFEQYQFLYDV|Y|12
3913	DKKSIYYLGVTSI	gi|116242617|sp|P48357	NA
3914	HIGHTGYLNTVTV	gi|54037168|sp|P63244|	[HIGHTGYLNTVTV|Y|19
3915	LERGQEYLILEKN	gi|1174630|sp|P42680|T	[LERGQEYLILEKN|Y|20
3916	LSSFTSYENPT	gi|8928302|sp|Q13882|P	[LSSFTSYENPT|Y|447|
3917	REDKFMYFEFPQP	gi|42560209|sp|P60484|	[REDKFMYFEFPQP|Y|2
3918	SADAPAYQQGQNQ	gi|23830999|sp|P20963|	[SADAPAYQQGQNQ|Y|
3919	VTPPEGYEVVTVF	gi|20178312|sp|O00151|	[VTPPEGYEVVTVF|Y|32
3920	DIQRSLYDRPASY	gi|129892|sp|P16234|PG	[DIQRSLYDRPASY|Y|76
3921	TVVNPKYEGK	gi|124963|sp|P05556|IT	[TVVNPKYEGK|Y|795|P
3922	AHHGGLYHTNAEV	gi|74751027|sp|Q8N5H7	[AHHGGLYHTNAEV|Y|7
3923	DTGAGGYSGNSGS	gi|50897492|sp|Q92738|	[DTGAGGYSGNSGS|Y|
3924	AVGNPEYLNTVQP	gi|2811086|sp|P00533|E	NA
3925	LGTEDLYDYIDKY	gi|55977123|sp|P68400|	[LGTEDLYDYIDKY|Y|25
3926	NGHLDSYEKVTQL	gi|20178094|sp|O14543|	[NGHLDSYEKVTQL|Y|2
3927	DYDYESYEKTTRT	gi|1170875|sp|P46821|M	NA
3928	TKKVIQYLAYVAS	gi|6166599|sp|P35579|M	NA
3929	DEEDYDYESYEKT	gi|1170875|sp|P46821|M	NA
3930	KLDGKVYAVKVLQ	gi|17402861|gb|AAF270	NA
3931	QEAVITYQPYLIQ	gi|84028176|sp|P35670|	NA
3932	QNRYSFYSTCSGQ	gi|20138951|sp|Q13835|	NA
3933	QDLGIQYKALKPE	gi|461853|sp|P35221|CT	NA
3934	LRISVVYKIWIPE	gi|5052123|gb|AAD3842	NA
3935	KLAPAQYIRYTPS	gi|2500813|sp|Q13573|S	NA
3936	DYPKFKYALLAVM	gi|17368701|sp|Q9BY50|	NA
3937	SSVSNNYIQTLGR	gi|14916543|sp|O60716|	NA
3938	EGRVYHYRINTAS	gi|85681908|sp|P00519|	NA
3939	LAAKLAYLQILSE	gi|125527|sp|P19525|E2	[LAAKLAYLQILSE|Y|162
3940	GADGGLYQIPPQP	gi|119585319|gb|EAW64	NA
3941	KVLNELYSVMKTY	gi|48427907|sp|O75044|	NA
3942	DNHDGTYTVAYVP	gi|116241365|sp|P21333	NA
3943	RSSGGSYRDSYDS	gi|5921786|sp|Q14011|C	NA
3944	TIAVDRYVVLVHP	gi|20141395|sp|P49683|	NA
3945	HEVGWKYQAVTAT	gi|730451|sp|P40429|RL	NA
3946	LQDDDFYAYDEDG	gi|12643721|sp|Q13507|	NA
3947	ANWRSKYISLSEK	gi|38258919|sp|P42356|	NA
3948	WPHSAPYSRFSIS	gi|145559492|sp|Q8IWU	NA
3949	TVQLKYYNKPLLG	gi|22095550|sp|Q9HCU4	NA
3950	YFDENPYFENKVL	gi|46397790|sp|Q01105|	NA
3951	FQMYVTYCKNKPD	gi|8928460|sp|O75962|T	NA

3952	YIFDSSYGEHPKR	gi|67461014|sp|Q6NYC1	NA
3953	FYMVSYYERNHRI	gi|73920974|sp|Q9Y4E6|	NA
3954	IFHVNLYGSILFL	gi|1352692|sp|P47900|P	NA
3955	SQPPEDYSFGAGE	gi|20178305|sp|Q13568|	NA
3956	FKVKEMYLTKLLS	gi|74705745|sp|O60486|	NA
3957	AGHGHLYSRIPGL	gi|67476453|sp|P49327|	NA
3958	LISLDRYLLILSP	gi|1703010|sp|P50406|5	[LISLDRYLLILSP|Y|125|
3959	GSGKMQYFQPTIQ	gi|74714582|sp|Q8IZH2|	NA
3960	GSGSYEYPVAEKA	gi|8928556|sp|P36382|C	NA
3961	PRPPVEYDSDFML	gi|93141229|sp|Q6UB98|	NA
3962	VKTKFGYHIIMVE	gi|20139299|sp|Q9Y237|	NA
3963	GSRRSGYAFSHQE	gi|30316371|sp|P98198|	NA
3964	TLGENEYFRVFME	gi|115855|sp|P22681|CB	NA
3965	IKSHLPYRFLPSD	gi|22096149|sp|Q9BR01|	NA
3966	PLSARTYSIDGPN	gi|116242614|sp|Q96RT	[PLSARTYSIDGPN|Y|11
3967	KVELFHYQDGAFH	gi|2501208|sp|Q14554|P	NA
3968	PARLEYYENARKF	gi|4504733|ref|NP_0035	NA
3969	PYSQKRYEEIVKE	gi|55665593|emb|CAH7	NA
3970	RVGTVGYMAPEVL	gi|462203|sp|P34947|GR	NA
3971	FCGTIEYMAPEVV	gi|90110031|sp|Q15349|	NA
3972	FCGTIEYMAPEIL	gi|12643872|sp|Q9UBS0	NA
3973	TQGVIKYMGPAGA	gi|1171032|sp|P43246|M	NA
3974	GHNLRTYIIPRSV	gi|22256943|sp|Q9ULW	NA
3975	DFLLESYLNLARS	gi|145559521|sp|Q1370	NA
3976	SNPLEVYLIPTPP	gi|2499839|sp|Q14669|T	NA
3977	NLEKECYEEICVY	gi|131092|sp|P22891|PR	NA
3978	RGTCNYYANAYSF	gi|125987809|sp|P02462	NA
3979	DDGEITYENVQVP	gi|116029|sp|P21854|CD	NA
3980	QRVKIAYEEIFVK	gi|125932|sp|P10646|TF	NA
3981	NWELALYIIISGI	gi|12230553|sp|Q92545|	NA
3982	CADDVAYINVETK	gi|34582343|sp|Q9P0R6|	NA
3983	MPYNSQYLNPVYS	gi|32699623|sp|Q9UPX6	NA
3984	MCVEDIYANIFII	gi|18202619|sp|Q92508|	NA
3985	GMTWEVYGAAVDP	gi|15079708|gb|AAH116	NA
3986	RPYQDVYVNVVDP	gi|20140440|sp|O75140|	NA
3987	SRTPAYYPNAGLI	gi|114062|sp|P08519|AP	NA
3988	VRIGEKYVDMSVK	gi|1352049|sp|P48047|A	NA
3989	SIFFIIYIIIIAF	gi|6165981|sp|Q13936|C	NA
3990	SVFFIVYIIIIAF	gi|6165989|sp|O60840|C	NA
3991	ICFFCSYIIISFL	gi|44889019|sp|P35499|	NA
3992	ERRYTPYPNLYPD	gi|1705910|sp|P51797|C	NA
3993	YFTTRTYGEPESA	gi|1706639|sp|P50402|E	[YFTTRTYGEPESA|Y|1
3994	WGRRRPYILTLGV	gi|145572854|sp|Q9UM	NA
3995	LAKLEKYYLKNSP	gi|41688714|sp|Q8TB72|	NA
3996	VDLIKTYKHINEV	gi|3219996|sp|Q13627|D	NA
3997	NEPAVLYNLKDRY	gi|3043372|sp|P11055|M	NA
3998	YSPHTAYDAAPQG	gi|20978527|sp|Q9GZT8	NA
3999	G3:17	contol_spot	NA
4000	G7:17	contol_spot	NA
4001	YACAGGYVDVVKV	gi|119626061|gb|EAX05	NA
4002	DAENSPYLNPQLV	gi|50402102|sp|P62508|	NA
4003	LAHFEDYKSVEMV	gi|74747057|sp|Q5VU65|	NA

4004	PEQETFYEQPPLV	gi|51316115|sp|Q9UJU6|	[PEQETFYEQPPLV|Y|3
4005	CHVEGDYIGSQNV	gi|23821958|sp|Q8TCZ9|	NA
4006	LAKEGNYAIVANV	gi|24418674|sp|Q96A65|	NA
4007	DGDGDFYIEPTSG	gi|22095551|sp|Q9NYQ6	NA
4008	TSSNDWYWNGSSG	gi|1655422|dbj|BAA1143	NA
4009	GQNEVDYRQKQVV	gi|20455356|sp|Q9BZX2|	NA
4010	PPDFPYYHDEGWV	gi|17433016|sp|P78357|	NA
4011	DSSFGKYGRNAYV	gi|6685306|sp|P56746|C	NA
4012	NSSDLLYDDLYDD	gi|74749761|sp|Q712K3|	NA
4013	EEEFNDYEANDPW	gi|48429262|sp|Q9H9E3|	NA
4014	FPEDASYSVPAPW	gi|74717666|sp|Q9BY79|	NA
4015	PFEGPNYHIAPRW	gi|119593162|gb|EAW72	NA
4016	SCEDSTYTQLWNW	gi|21264534|sp|P20333|	NA
4017	VEMKEIYTSNHMW	gi|17366467|sp|Q14643|	NA
4018	EANRYDYVHVGTW	gi|62297775|sp|Q13255|	NA
4019	TDDEYTYLNWYLQ	gi|119578133|gb|EAW57	NA
4020	ITASPDYLEIAIY	gi|120049|sp|P21802|FG	NA
4021	LQKGQKYFDSGHY	gi|113416910|ref|XP_93	NA
4022	QVPKTLYKDKGHY	gi|134048661|sp|P23352	NA
4023	SSVKSEYTDPWGY	gi|119568301|gb|EAW47	NA
4024	CGSDVGYIRYTLY	gi|37537905|sp|P59901|	NA
4025	SLFSEPYKTNKGD	gi|126302515|sp|P51826	NA
4026	EYKNFYYAAVPSA	gi|51315838|sp|Q10471|	NA
4027	EGYEGYYSQSQGD	gi|62511098|sp|Q07666|	NA
4028	VFEGRIYVSGGHD	gi|30179881|sp|O94889|	NA
4029	FPEDPSYDANVID	gi|20178276|sp|P54646|	NA
4030	VADMLEYVPVKKD	gi|29429215|sp|Q12769|	NA
4031	IQNERTYEVPDQP	gi|24211557|sp|Q9NZA1	NA
4032	VPPVDGYVMVLQP	gi|23396490|sp|O94985|	NA
4033	HKQKGGYTESQRP	gi|119601418|gb|EAW81	NA
4034	QVSGTEYEVAQRP	gi|145559527|sp|Q8IWY	NA
4035	QVWEECYSQVLYL	gi|73619933|sp|Q99459|	NA
4036	YAEEAPYDAIHVG	gi|2507187|sp|P22061|P	NA
4037	GGNMPGYLRPETA	gi|21264523|sp|P41250|	NA
4038	AWEMKPYAVMALE	gi|141795194|gb|AAI250	NA
4039	FISESQYTYALKE	gi|85681919|sp|P08603|	NA
4040	RIANEKYLRTHKE	gi|119573802|gb|EAW53	NA
4041	AGMQTKYLDVGWG	gi|85681909|sp|P19801|	NA
4042	DGSVTGYKDAYVG	gi|74753330|sp|Q9UHN6	NA
4043	<<Marker>>	contol_spot	NA
4044	GRIEHLYKNPQAH	gi|9087147|sp|O60547|G	NA
4045	NCEEKDYTIWLAH	gi|84028263|sp|Q99523|	NA
4046	SVEDLLYVRDNTA	gi|55665746|emb|CAH71	NA
4047	IACEQDYVATLSE	gi|148753299|gb|AAI426	NA
4048	QVGKEKYATSVSE	gi|67472130|sp|Q6WKZ	NA
4049	IISERKYSRKKTE	gi|134035376|sp|Q5TYW	NA
4050	EDLKDTYASLGKT	gi|400266|sp|Q02045|ML	NA
4051	NTWNEKYSSLQKT	gi|74708186|sp|Q5TKA1|	NA
4052	YKEMVDYSNTYKT	gi|20532121|sp|Q969F9|	NA
4053	LNGEPGYTIGTVL	gi|154816130|dbj|BAF75	NA
4054	LPSCFDYVMHFLT	gi|152012479|gb|AAI501	NA
4055	PSEGDDYIFHCHP	gi|116241283|sp|Q9279	NA

4056	FSEEFDYELAMST	gi|74728477|sp|Q8N0Z2|	NA
4057	TIQKGSYTFVPWL	gi|13124573|sp|Q9Y275|	NA
4058	IQWNGDYQVAGTT	gi|11131377|sp|Q9UKP4	NA
4059	SDYVERYMNSDTT	gi|37999759|sp|Q96ST3|	NA
4060	EAWELGYTGKGVT	gi|13124785|sp|P16519|	NA
4061	KSSGCAYQDVGVT	gi|129825|sp|P05164|PE	NA
4062	TLSDPLYVLDQAV	gi|82581628|sp|Q5K4L6|	NA
4063	FKCNSGYVVQDDV	gi|67462103|sp|Q9UNQ	NA
4064	<<Marker>>	contol_spot	NA
4065	MAEESIYICGQDV	gi|119603141|gb|EAW82	NA
4066	RSRAEGYEKTDDV	gi|8134331|sp|Q9Y2Q0|	NA
4067	AYGKEGYGSLEEV	gi|23396602|sp|Q9Y680|	NA
4068	LKNPQDYINCAEV	gi|119570675|gb|EAW50	NA
4069	FQISDIYISGESG	gi|56405387|sp|Q9UPN3	NA
4070	TEKGEVYFIDHNT	gi|88909269|sp|Q86UL8|	NA
4071	TYDDRAYSSFGGG	gi|18276665|sp|Q15056|	[TYDDRAYSSFGGG|Y|1
4072	LPKSYDYDLIIIG	gi|50403780|sp|Q16881|	[LPKSYDYDLIIIG|Y|13|Q
4073	IDLGTTYSCVGVF	gi|147744565|sp|P08107	[IDLGTTYSCVGVF|Y|15
4074	GGEPLSYTRFSLA	gi|108935939|sp|P02786	[GGEPLSYTRFSLA|Y|2
4075	FMREKEYLQVMHF	gi|20178315|sp|O95340|	NA
4076	MVEVDIYESGKHF	gi|119575831|gb|EAW55	NA
4077	WYFGLHYVDNKGF	gi|125987826|sp|P15311	NA
4078	DLNAVKYVSNIKF	gi|24657779|gb|AAH392	NA
4079	HTISGDYVIMTIF	gi|27820121|sp|Q8N1C3	NA
4080	DQSQPPYYNVTAM	gi|126306|sp|P07098|LIP	NA
4081	VSYDPLYAVFAVF	gi|118572729|sp|Q9BZW	NA
4082	LQYSTDYTFKAYF	gi|33112650|sp|P08575|	NA
4083	HYTCDQYGNKACM	gi|116242598|sp|Q9Y21	NA
4084	DHREDVYLYISGH	gi|71152375|sp|Q5T5N4|	NA
4085	<<Marker>>	contol_spot	NA
4086	FLHNEGYSSMCGH	gi|74731582|sp|Q96EM0	NA
4087	HMNEYEYACIKHH	gi|21757891|dbj|BAC052	NA
4088	ATEKSSYFQTTEI	gi|55977888|sp|Q9UDV6	NA
4089	DTTSDEYLRSYFI	gi|1352692|sp|P47900|P	NA
4090	SGRELSYVLLAGI	gi|2495077|sp|Q14833|M	NA
4091	AESSQEYVTLQGI	gi|74736252|sp|Q5XKL5|	NA
4092	GILNGKYKRNGHI	gi|2501506|sp|Q16880|C	NA
4093	PSAEAEYWRIRAM	gi|147742985|sp|Q5TH6	NA
4094	SSRTPGYKSVLRI	gi|117949795|sp|Q6N02	NA
4095	AVNTSKYAESYRI	gi|60390262|sp|O95453|	NA
4096	YLNEPNYEALISI	gi|119569993|gb|EAW49	NA
4097	MKKNEVYETFSYP	gi|47117336|sp|Q9UN30	NA
4098	GVFKHGYEKYNTI	gi|94707511|sp|Q3L8U1|	NA
4099	EAVNFSYSDNAVI	gi|119616159|gb|EAW95	NA
4100	ADGMEDYEQELCG	gi|13623635|gb|AAH064	NA
4101	LFHETLYQKADDG	gi|113606|sp|P04075|ALI	NA
4102	WDSSGCYVEEGDG	gi|50400545|sp|Q8IZF2|	NA
4103	WEYDESYCDAVKK	gi|34921397|sp|O75063|	NA
4104	GLSDDYYGAKNLK	gi|2497506|sp|Q92796|D	NA
4105	VSCTPLYVEIRLK	gi|74754109|sp|Q4W4Y	NA
4106	<<Marker>>	contol_spot	NA
4107	RGSDDDYSFCRAL	gi|20138528|sp|Q9Y6Y9|	NA

4108	HSMKKKYECNKCL	gi|23397010|sp|Q9NR11	NA
4109	RREEGIYSILVAL	gi|1351993|sp|Q04656|A	NA
4110	RGEERPYCEICEM	gi|266902|sp|P30622|CL	NA
4111	SNEADIYSFLKGM	gi|131756|sp|P20742|PZ	NA
4112	LQSEAAYCCVSEL	gi|59803038|sp|Q93050|	NA
4113	IAIKNKYASSKLL	gi|5921731|sp|O95067|C	NA
4114	TSYHHSYEDTGLL	gi|29840846|sp|Q10713|	NA
4115	HTGEKPYVCPYEG	gi|74762721|sp|Q9BZE0|	NA
4116	EHCWVLYVDVLLL	gi|21362903|sp|Q15024|	NA
4117	YYGEDDYPIVRLL	gi|46397079|sp|P60852|	NA
4118	HDGKDNYHWNYLL	gi|119625348|gb|EAX04	NA
4119	EVQRDPYSNYGHG	gi|59797947|sp|Q8IUH3|	NA
4120	GGSMEDYCDSPHG	gi|48427907|sp|O75044|	NA
4121	ILKESKYKRSSGG	gi|67460301|sp|Q6V1X1|	NA
4122	KMKKDIYWDDSAA	gi|38503351|sp|Q8N1M1	NA
4123	PKSTDKYPFSSGG	gi|150036319|emb|CAM	NA
4124	TGYNDHYMYLNHG	gi|119615886|gb|EAW95	NA
4125	TSMFDDYQGDSST	gi|143811474|sp|P17948	[TSMFDDYQGDSST|Y|1
4126	VAMHVAYRRHEKK	gi|77416855|sp|P29033|	NA
4127	<<Marker>>	contol_spot	NA
4128	DDPEAVYTTTGGK	gi|146345416|sp|Q1537	NA
4129	DEDEDDYHNPGYL	gi|14194891|sp|O43561|	NA
4130	VMLGAGYWYRARL	gi|1235674|gb|AAC5040	NA
4131	VQLPATYMNLGPS	gi|585912|sp|Q04912|RC	[VQLPATYMNLGPS|Y|1
4132	GLARDIYKNDYYR	gi|126302596|sp|P08922	NA
4133	GMSRNLYAGDYYR	gi|729008|sp|Q08345|DD	NA
4134	GRGTDEYFIRKPP	gi|21903373|sp|P11230|	NA
4135	HDTEMKYYIVHLK	gi|3219996|sp|Q13627|D	NA
4136	AMLMEKYHVDHDE	gi|9626638|ref|NP_0409	NA
4137	IHKPGSYIFRLSC	gi|115855|sp|P22681|CB	NA
4138	GMTRDIYETDYYR	gi|33112647|sp|P06213|	[GMTRDIYETDYYR|Y|11
4139	YEEHIPYTHMNGG	gi|33112647|sp|P06213|	[YEEHIPYTHMNGG|Y|1
4140	PVDPATYGQFYGG	gi|121116|sp|P06396|GE	[PVDPATYGQFYGG|Y|4
4141	GASTGIYEALELR	gi|134254702|gb|ABO65	[GASTGIYEALELR|Y|44|
4142	PSDSLIYDDGLSE	gi|547807|sp|P07949|RE	[PSDSLIYDDGLSE|Y|10
4143	RKVGPGYLGSGGS	gi|547807|sp|P07949|RE	[RKVGPGYLGSGGS|Y|
4144	RSNDKVYENVTGL	gi|3183518|sp|Q05397|F	[RSNDKVYENVTGL|Y|9
4145	KGPTCQYRAAQSG	gi|29337230|sp|Q13444|	[KGPTCQYRAAQSG|Y|
4146	APQDVTYAQLHSL	gi|37537904|sp|O75023|	NA
4147	RVKEEGYELPYNP	gi|17366642|sp|Q99704|	[RVKEEGYELPYNP|Y|3
4148	<<Marker>>	contol_spot	NA
4149	TPSSPVYQDAVSY	gi|45382633|ref|NP_990	[TPSSPVYQDAVSY|Y|4
4150	SRGQEVYVKKTMG	gi|464868|sp|Q02763|TI	[SRGQEVYVKKTMG|Y|
4151	KGPNGVYDFSQAH	gi|62906893|sp|Q9Y5V3|	[KGPNGVYDFSQAH|Y|
4152	GYNDDYYEESYFT	gi|1706639|sp|P50402|E	[GYNDDYYEESYFT|Y|9
4153	APQWEGYDELQTD	gi|2493285|sp|P55957|B	[APQWEGYDELQTD|Y|
4154	DSPNKLYTLVTYV	gi|51702807|sp|P62899|	[DSPNKLYTLVTYV|Y|10
4155	NARLSIYGIWFYD	gi|60389833|sp|Q8IZD4|	[NARLSIYGIWFYD|Y|11
4156	TISQEAYDQRQDT	gi|3023518|sp|Q99426|T	[TISQEAYDQRQDT|Y|11
4157	TTLSDSYNYSGTE	gi|50401753|sp|Q7Z3T8|	[TTLSDSYNYSGTE|Y|21
4158	RHYEDGYPGGSDN	gi|14916543|sp|O60716|	[RHYEDGYPGGSDN|Y|
4159	RGYISPYFINTSK	gi|129379|sp|P10809|CH	[RGYISPYFINTSK|Y|227

4160	AHDGGIYAISWSP	gi|12643636|sp|O75083|	[AHDGGIYAISWSP|Y|23
4161	YGGYDDYNGYNDG	gi|1710632|sp|P31943|H	[YGGYDDYNGYNDG|Y|
4162	LVVEEYYEVLDHC	gi|6226814|sp|O00170|A	[LVVEEYYEVLDHC|Y|24
4163	QPNEAVYTKMMTK	gi|116242483|sp|P11413	[QPNEAVYTKMMTK|Y|4
4164	CEICGNYTYRGPK	gi|17380310|sp|Q12874|	[CEICGNYTYRGPK|Y|41
4165	AKDKPVYDELFYT	gi|18202935|sp|Q9H223|	[AKDKPVYDELFYT|Y|45
4166	ARQAHLYRGIFPV	gi|20178296|sp|P14618|	NA
4167	QATTNVYQVQTGS	gi|17376322|sp|Q14161|	[QATTNVYQVQTGS|Y|4
4168	VQTGSEYTDTSNH	gi|17376322|sp|Q14161|	[VQTGSEYTDTSNH|Y|
4169	<<Marker>>	contol_spot	NA
4170	YYAKKDYNEAYNY	gi|46397879|sp|Q99615|	NA
4171	RADFDHYTGRDSE	gi|84029396|sp|Q86SQ0	NA
4172	QGPPEIYSDTQFP	gi|119599582|gb|EAW79	[QGPPEIYSDTQFP|Y|19
4173	YKSYSPYDMLESI	gi|113950|sp|P07355|AN	[YKSYSPYDMLESI|Y|23
4174	ERYTEFYHVPTHS	gi|47605572|sp|Q96HC4	[ERYTEFYHVPTHS|Y|2
4175	WKLQMIYGNGAES	gi|149944486|ref|NP_00	[WKLQMIYGNGAES|Y|2
4176	PLEDEYYYDVEND	gi|74583475|sp|Q04383|	NA
4177	PVFKPTYEQFEDF	gi|731532|sp|P39956|RP	NA
4178	LSRMKDYSNIVEP	gi|731532|sp|P39956|RP	NA
4179	NPDSEEYKKFKEK	gi|1168370|sp|P22149|A	NA
4180	CASCEIYSCECTF	gi|129733|sp|P12383|PD	NA
4181	KLLEEKYNDNYVY	gi|1708905|sp|P53338|M	NA
4182	KKQEGKYKEKNNL	gi|74645031|sp|Q12180|	NA
4183	DFFRDYYGNSGSN	gi|2506885|sp|P32607|R	NA
4184	TLEEPGYESRTGS	gi|729140|sp|P40917|YA	NA
4185	PSSGGAYSNLPRL	gi|1168610|sp|P41696|A	NA
4186	NNSIPEYFNNSHV	gi|2506540|sp|P20134|S	NA
4187	ENKQDIYGSSPTT	gi|74583758|sp|Q08887|	NA
4188	DGRVEPYVDFAEF	gi|10720303|sp|Q15750|	NA
4189	GSYMWIYVFMGNM	gi|12643959|sp|Q9Y6L6|	NA
4190	<<Marker>>	contol_spot	NA
4191	IVFETAYNTNENM	gi|50400552|sp|Q8N3C0	NA
4192	QPEENPYWWNANM	gi|119610135|gb|EAW89	NA
4193	TDFESGYSEIFLM	gi|23396772|sp|Q13822|	NA
4194	WPNKNTYKSIQMM	gi|20141712|sp|P29508|	NA
4195	IRCEEPYLRISDN	gi|12643876|sp|Q9UBX5	NA
4196	KQDEVVYYDPCEN	gi|152112352|sp|Q8TF3	NA
4197	PGWHLSYVDVKDN	gi|119621884|gb|EAX01	NA
4198	RSNYDQYGDAGEN	gi|108936027|sp|Q9Y2G	NA
4199	TLPCQAYVNQGEN	gi|119572941|gb|EAW52	NA
4200	AEFDDKYLITGFN	gi|118572727|sp|O60522	NA
4201	LLSNPAYRLLLAT	gi|729008|sp|Q08345|DD	[LLSNPAYRLLLAT|Y|51
4202	LPGVRTYIDPHTY	gi|1706628|sp|P54756|E	NA
4203	ACEHRGYLYLAIE	gi|464868|sp|Q02763|TI	[ACEHRGYLYLAIE|Y|89
4204	LYEKFTYAGIDCS	gi|464868|sp|Q02763|TI	[LYEKFTYAGIDCS|Y|11
4205	MLNSKGYTKSIDI	gi|232066|sp|P27361|MK	[MLNSKGYTKSIDI|Y|20
4206	MVLKHPYPRKVEE	gi|51317293|sp|Q9UN19	NA
4207	VALDDPYENYRRN	gi|119226260|ref|NP_00	NA
4208	GEKEEVYIVQASN	gi|92087039|sp|P10911|	NA
4209	TMKEKIYTMIYRN	gi|17483726|gb|AAL401	NA
4210	CSRRNMYVNIAVN	gi|119578974|gb|EAW58	NA
4211	FVKKKGYVRLHTN	gi|23813917|sp|Q13356|	NA

4212	LNSGSEYVPAGPQ	gi|13629029|sp|Q08397|	NA
4213	FQGKDIYEMNLSQ	gi|6686181|sp|Q9Y2G7|	NA
4214	GYGEESYPAKDSQ	gi|2493260|sp|Q16825|P	NA
4215	RPSMEGYRAPSRQ	gi|14916543|sp|O60716|	NA
4216	EEGKPGYLDCLTQ	gi|116242736|sp|Q1330	NA
4217	ISSDPRYWYGKTQ	gi|11182425|sp|P56524|	NA
4218	SSEENYYSTSYSQ	gi|47117238|sp|Q8IWW	NA
4219	RYRADEYQPPDGG	gi|38258175|sp|Q8NBP7	NA
4220	SEAKERYQQGNGG	gi|34783880|gb|AAH096	NA
4221	QLSPGIYDDTSAR	gi|47117817|sp|O75376|	NA
4222	SLNSGNYLNPACR	gi|47117338|sp|Q9UQR	NA
4223	SPCEDFYQFSCGG	gi|20178279|sp|O60344|	NA
4224	EVVEIEYVEKYTA	gi|20140802|sp|Q9GZL7|	NA
4225	QTYNVDYVDAEGR	gi|51316029|sp|Q8NCQ	NA
4226	AKVEGRYEVTDHR	gi|2138330|gb|AAB5838	NA
4227	DVEKFKYKTPQHR	gi|23396536|sp|Q9NX36|	NA
4228	KKWCDDYFFIAHR	gi|67476671|sp|P36551|	NA
4229	RSTRPLYISVGHR	gi|119610015|gb|EAW89	NA
4230	WLKDNDYLLHGHR	gi|38372248|sp|Q96A54|	NA
4231	TSDKPYYCKIRGC	gi|30173473|sp|Q96T25|	NA
4232	CVSSGRYAVFGLG	gi|143678193|sp|Q9NV6	NA
4233	IPVDNLYAEPAVL	gi|46397477|sp|P60891|	NA
4234	MEDGSPYVNGSLG	gi|74758950|sp|Q76FK4|	NA
4235	FDRNADYVQEVKR	gi|52783098|sp|Q9HCJ6|	NA
4236	GLPENGYQILYKR	gi|22002000|sp|Q9BYH1	NA
4237	AAAEGGYQRYGVR	gi|74750784|sp|Q8IZ57|	NA
4238	GDPVNYYVDTAVR	gi|417719|sp|P23396|RS	NA
4239	LPSEVLYMLKNVR	gi|152032658|sp|Q6ZV2	NA
4240	RCNNLGYEINKVR	gi|126314|sp|P06858|LIP	NA
4241	CASLDHYSRLGWR	gi|148841196|sp|A2VEC	NA
4242	IVSGLKYVQHTYR	gi|1707893|sp|P52566|G	NA
4243	LPPNWKYESSTAS	gi|50403608|sp|P62277|	NA
4244	WGSNQNYICNTDP	gi|45477011|sp|O75113|	NA
4245	AMCTPSYLSTAAA	gi|143458429|sp|Q9P2F	NA
4246	FCFYLKYVNMYAS	gi|21263618|sp|Q9BXC1	NA
4247	GCSNPLYPGVYAS	gi|120660130|gb|AAI304	NA
4248	ISGDSGYTNYADS	gi|32899|emb|CAA78209	NA
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4250	CSVEELYAIPPDA	gi|118572719|sp|Q9H79	NA
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4254	HVAYGGYSTPEDR	gi|55976600|sp|Q9HBL0|	NA
4255	DPAETDYTAVGCA	gi|81175200|sp|Q9Y490|	NA
4256	YYAYYMYANIMVL	gi|113697|sp|P23109|AM	NA
4257	YRARETYGLPNTL	gi|19856545|sp|P17405|	NA
4258	KKLLGKYPNVDAR	gi|2498228|sp|Q16739|C	NA
4259	LSEDCLYLNVWIP	gi|116353|sp|P06276|CH	NA
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4261	LAQEVTYANLRPF	gi|84028279|sp|P38435|	NA
4262	VKDTCSYVNVLSD	gi|13432151|sp|P46976|	NA
4263	GDFPYYYANLGLK	gi|20141422|sp|Q16394|	NA

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4267	GNLGSVYIYVLLI	gi|121509|sp|P15509|CS	NA
4268	AVALDRYLRVVHP	gi|60416427|sp|O00270|	NA
4269	FFNLSIYLNIQRR	gi|17367264|sp|Q9Y5N1|	NA
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4275	DFWGDDYKNHVKC	gi|71153817|sp|Q9NX58|	NA
4276	FPEENIYKVYKKC	gi|116242504|sp|Q8TE8	NA
4277	KDCKDPYCPPSLC	gi|55742730|ref|NP_064	NA
4278	LQRWDKYSNKMLC	gi|113421409|ref|XP_001	NA
4279	KLQELYYEIVHVL	gi|29470284|gb|AAO130	NA
4280	DDDDDPYYYYYKS	gi|146325723|sp|Q149N	NA
4281	GPSMDTYGETFLS	gi|88974674|ref|XP_932	NA
4282	PLRCLIYIEVALS	gi|114559150|ref|XP_001	NA
4283	ALKKSGYNNKHLS	gi|120953300|ref|NP_00	NA
4284	KIMEKKYHNVGLS	gi|13124489|sp|Q14103|	NA
4285	EGDEELYFHFKFP	gi|146345416|sp|Q1537	NA
4286	FTNMLGYTDHQFP	gi|57015285|sp|O75390|	NA
4287	PNSNLDYMFFKFP	gi|24212102|sp|P59045|	NA
4288	AGEELLYDYGDRS	gi|25091219|sp|Q9NQR1	NA
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4290	GPRESSYMEMKGP	gi|119573284|gb|EAW52	NA
4291	ADSEVLYPNYQSC	gi|68052821|sp|Q9NPH0	NA
4292	LGEDTDYLIYDTC	gi|24308334|ref|NP_115	NA
4293	TDSGIFYEDSGYS	gi|74749781|sp|Q71RS6|	NA
4294	GLEKKKYERGSAT	gi|21542165|sp|O00541|	NA
4295	PLFKLKYPSSPYS	gi|71153522|sp|Q96AY4|	NA
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4303	AFDNPDYWHSRLF	gi|119534|sp|P21860|ER	[AFDNPDYWHSRLF|Y|1
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4306	TATEGQYQPQP	gi|125474|sp|P06239|LC	[TATEGQYQPQP|Y|505|
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4308	GELKTGYLSIVMD	gi|9087218|sp|P35968|V	[GELKTGYLSIVMD|Y|80
4309	FITEEDYQALRTS	gi|1705916|sp|Q00610|C	[FITEEDYQALRTS|Y|14
4310	GTRERLYEWISID	gi|119595261|gb|EAW74	[GTRERLYEWISID|Y|88
4311	LRNDQVYQPLRDR	gi|115985|sp|P04234|CD	[LRNDQVYQPLRDR|Y|1
4312	PLDKDYYVVREPG	gi|50403745|sp|P52333|	[PLDKDYYVVREPG|Y|9
4313	PTLVQTYVLQGDP	gi|729564|sp|Q99062|CS	[PTLVQTYVLQGDP|Y|7
4314	RKTRDQYLMWLTQ	gi|118572681|sp|P27986	[RKTRDQYLMWLTQ|Y|
4315	HRPSRQYATRDVY	gi|21542431|sp|O14828|	[HRPSRQYATRDVY|Y|3

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<tr><td>4317</td><td>SPRHALYPPSPRK</td><td>gi|50897492|sp|Q92738|</td><td>[SPRHALYPPSPRK|Y|5</td></tr>
<tr><td>4318</td><td>ADNDKEYLVLTLT</td><td>gi|42560209|sp|P60484|</td><td>[ADNDKEYLVLTLT|Y|31</td></tr>
<tr><td>4319</td><td>DRDDAQYSHLGGN</td><td>gi|115985|sp|P04234|CD</td><td>[DRDDAQYSHLGGN|Y|</td></tr>
<tr><td>4320</td><td>FMDGSPYAHMFEM</td><td>gi|14548162|sp|Q13224|</td><td>[FMDGSPYAHMFEM|Y|</td></tr>
<tr><td>4321</td><td>PTDSNFYARLMDE</td><td>gi|2811086|sp|P00533|E</td><td>NA</td></tr>
<tr><td>4322</td><td>FCGTPDYIAPEIL</td><td>gi|400135|sp|Q02156|KP</td><td>NA</td></tr>
<tr><td>4323</td><td>GSSDNEYFYVDFR</td><td>gi|544320|sp|P36888|FL</td><td>[GSSDNEYFYVDFR|Y|5</td></tr>
<tr><td>4324</td><td>LYHKKSY</td><td>gi|74762751|sp|Q9HD26</td><td>[DDLHTLYHKKSY|Y|457</td></tr>
<tr><td>4325</td><td>RKHYQPYAPPRDF</td><td>gi|115973|sp|P10747|CD</td><td>[RKHYQPYAPPRDF|Y|2</td></tr>
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<tr><td>4327</td><td>SDSGYSYETIGKT</td><td>gi|1170875|sp|P46821|M</td><td>NA</td></tr>
<tr><td>4328</td><td>PLGPQNYGGAMRP</td><td>gi|27734570|sp|P81877|</td><td>NA</td></tr>
<tr><td>4329</td><td>VIQYLAYVASSHK</td><td>gi|6166599|sp|P35579|M</td><td>NA</td></tr>
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<tr><td>4336</td><td>EQIGLLYQEYRDK</td><td>gi|114152090|sp|Q8N5V</td><td>NA</td></tr>
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<tr><td>4338</td><td>SALQLLYTAKEAG</td><td>gi|81175200|sp|Q9Y490|</td><td>NA</td></tr>
<tr><td>4339</td><td>EPEVRYYLRQILS</td><td>gi|51338822|sp|Q9H4B4|</td><td>NA</td></tr>
<tr><td>4340</td><td>SLDGPEYEEEEVA</td><td>gi|121743|sp|P20936|RA</td><td>NA</td></tr>
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<tr><td>4342</td><td>HERMPWYHSSLTR</td><td>gi|1177044|sp|P43403|Z</td><td>NA</td></tr>
<tr><td>4343</td><td>SDSLLDYSCMQRL</td><td>gi|10720350|sp|Q9Y487|</td><td>NA</td></tr>
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<tr><td>4345</td><td>KGKEKIYSAESFL</td><td>gi|37542493|gb|AAL154</td><td>NA</td></tr>
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<tr><td>4351</td><td>VKTPGNYESKRQR</td><td>gi|32469769|sp|Q96L73|</td><td>NA</td></tr>
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<tr><td>4353</td><td>PITIARYGRSRNK</td><td>gi|74762638|sp|Q92519|</td><td>NA</td></tr>
<tr><td>4354</td><td>MEENELYSSAVTV</td><td>gi|143220234|sp|O6049</td><td>[MEENELYSSAVTV|Y|1</td></tr>
<tr><td>4355</td><td>PKDTAIYQKDEAL</td><td>gi|51338794|sp|P78559|</td><td>NA</td></tr>
<tr><td>4356</td><td>CRLQTMYEMEMSG</td><td>gi|38372886|sp|Q9BXI2|</td><td>NA</td></tr>
<tr><td>4357</td><td>VFGLSLYTTERDL</td><td>gi|51703330|sp|P62995|</td><td>NA</td></tr>
<tr><td>4358</td><td>GEARALYNIGNVY</td><td>gi|74759541|sp|Q86YR5|</td><td>NA</td></tr>
<tr><td>4359</td><td>EADRDTYRRSAVP</td><td>gi|1173177|sp|P46783|R</td><td>NA</td></tr>
<tr><td>4360</td><td>PDYLQEYSTKYFY</td><td>gi|3913590|sp|Q15303|E</td><td>NA</td></tr>
<tr><td>4361</td><td>MPTSVAYICSNQI</td><td>gi|29427834|sp|Q8N4C8</td><td>NA</td></tr>
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<tr><td>4364</td><td>HSKGRDYRDNTEL</td><td>gi|119591435|gb|EAW71</td><td>NA</td></tr>
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4372	YGSTQDYLNPIIL	gi|122066060|sp|Q9NZJ	NA
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4374	LLVLPIYANLPSD	gi|26006959|sp|O60231|	NA
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4378	NKGNWCYINATLQ	gi|2501458|sp|Q14694|U	NA
4379	SDICTIYLNLGDE	gi|71164791|sp|Q14139|	NA
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4434	IEFEVVYVAPEVD	gi|74762751|sp|Q9HD26	NA
4435	QHSPSTYIDLAVD	gi|50400889|sp|Q6UWY	NA
4436	DFEENAYSYASVD	gi|94730692|sp|Q8N1W	NA
4437	CGEDIIYMNENGE	gi|76803797|sp|Q99698|	NA
4438	EYFQPIYVYNPGE	gi|22261808|sp|Q13508|	NA
4439	LQPKDIYPYSDGE	gi|71153524|sp|Q9BQK8	NA
4440	TVVESGYVRLLGE	gi|129890|sp|P09619|PG	NA
4441	ITKEELYRMLAHE	gi|34922029|sp|Q96KC2|	NA
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4447	RLIYEDYVSILSP	gi|1730186|sp|P49795|R	NA
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4454	SRKEDFYTVETIT	gi|119611102|gb|EAW90	NA
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4456	TCCFPSYVYPDPT	gi|62899891|sp|Q9HC77	NA
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4462	RGSTSAYTKSGYC	gi|74735576|sp|O95149|	NA
4463	KESEYHYEYTACD	gi|147647000|sp|Q6UXG	NA
4464	<<Marker>>	contol_spot	NA
4465	RRKEDNYDTHNCD	gi|74743566|sp|Q5SQS8	NA
4466	DGAQDYYSDYAYL	gi|74727495|sp|Q86UK7|	NA
4467	GWRQDTYCPMADV	gi|74731207|sp|Q96B77|	NA
4468	QEYKDAYSFAADV	gi|2554915|gb|AAB8786	NA
4469	DPWEPFYVAGGKV	gi|23396461|sp|O43505|	NA
4470	KTEPVDYEFKPIV	gi|6166575|sp|P37275|Z	NA
4471	NSAGDPYGNCGKV	gi|20141191|sp|O43184|	NA

4472	RPESPEYSGGNIV	gi|38258257|sp|Q9NZV8	NA
4473	DAKECIYWQPGLP	gi|152969420|ref|YP_001	NA
4474	PPSDFYYINEYKP	gi|25091325|sp|Q9H5I1|	NA
4475	LEFSDYYLDSPDF	gi|21759325|sp|O60890|	NA
4476	VFANGDYEKAAEF	gi|18202494|sp|Q13099|	NA
4477	HVENDGYKTIYFF	gi|3024413|sp|O15305|P	NA
4478	KAFKPKYPICYFF	gi|8573114|gb|AAF7722	NA
4479	PFSSADYWSNYEF	gi|146286062|sp|O6029	NA
4480	VFGEPHYHTFDGF	gi|48428570|sp|O75443|	NA
4481	AYSPVDYMSITSF	gi|152031612|sp|Q9UJ1	NA
4482	GNEWLGYDNTKSF	gi|109013506|ref|XP_001	NA
4483	VFSSSIYGMTGSF	gi|47606207|sp|Q9BZD2	NA
4484	AGNNSLYRDTAVF	gi|543826|sp|P02749|AP	NA
4485	<<Marker>>	contol_spot	NA
4486	HISEFLYDKALTF	gi|94710252|sp|Q6P158|	NA
4487	LPPEPDYSLLLTF	gi|266392|sp|Q00978|IR	NA
4488	CVKHIIYVDNKAI	gi|13432172|sp|O60488|	NA
4489	LMTDEEYIINRAI	gi|60549585|gb|AAX241	NA
4490	VKIKETYGDTEAI	gi|14286115|sp|Q01814|	NA
4491	FPKNSKYEYDPDI	gi|74732865|sp|Q9BRD0	NA
4492	QLRCGPYLSSGDI	gi|14549162|sp|Q12967|	NA
4493	FSQELDYWGIDEI	gi|24418854|sp|Q14721|	NA
4494	FQGKSLYINSGNI	gi|20138032|sp|Q9NPP4	NA
4495	MERDDIYVFEINI	gi|28381406|sp|Q9Y4E8|	NA
4496	FKEHSDYVRCGCA	gi|73920292|sp|Q8TED0	NA
4497	YEEMPAYTHASPI	gi|74762083|sp|Q9Y6R6|	NA
4498	GYSNEWYLNRLRI	gi|38372640|sp|Q8N127|	NA
4499	CSCNAGYEERGFM	gi|116241351|sp|P29320	NA
4500	SVNELIYKSGYGK	gi|4176369|gb|AAD0884	NA
4501	YKGGDEYDNHCGK	gi|127293|sp|P20645|MP	NA
4502	IFENNIYYQPDIK	gi|67460566|sp|Q8N608|	NA
4503	YFGKGTYTDCAIK	gi|125987811|sp|P12109	NA
4504	DKELDEYMHGGKK	gi|74752718|sp|Q9H814|	NA
4505	KKEDCKYIVVEKK	gi|131436|sp|P08118|MS	NA
4506	<<Marker>>	contol_spot	NA
4507	SVPEDVYDKGCVK	gi|134047740|sp|O0076	NA
4508	KSSNFGYITSCYK	gi|134034989|sp|Q58A4	NA
4509	VPSCFVYEAVGYK	gi|24212024|sp|Q9WVC	NA
4510	EDQEDIYFMKGAL	gi|19924283|sp|O75185|	NA
4511	LRKKPCYGTVAAL	gi|10439953|dbj|BAB156	NA
4512	DLDNVRYTSLPAL	gi|119608269|gb|EAW87	NA
4513	ALKENLYYEAGKM	gi|74738611|sp|Q7L622|	NA
4514	RMENPAYCLSAKL	gi|24418475|sp|Q9BQ31	NA
4515	CCRQEMYIDLQGM	gi|13124811|sp|O00292|	NA
4516	LCTDDFYCTVNKL	gi|108935991|sp|Q6UXV	NA
4517	VKKEPRYWLLALL	gi|74749674|sp|Q6ZUK4	NA
4518	CFSHPTYQSPDLL	gi|109940217|sp|Q9UPS	NA
4519	RSSEGFYPSPQHM	gi|3183518|sp|Q05397|F	NA
4520	VAKDPRYARYLKM	gi|6831732|sp|Q9Y3C0|	NA
4521	IEPPTSYVSDGCA	gi|150403921|sp|Q8IY17	NA
4522	AARKEDYLRHEIG	gi|8134736|sp|P82094|T	NA
4523	ANYELVYKDGEHG	gi|1709906|sp|P23468|P	NA

4524	DNDWPIYVESEIG	gi|46577502|sp|Q8NAP8	NA
4525	SCRSDDYMPMSPA	gi|62298062|sp|Q9Y4H2|	[SCRSDDYMPMSPA|Y|
4526	SENFDDYMKALGV	gi|127725|sp|P02689|MY	NA
4527	<<Marker>>	contol_spot	NA
4528	SIKMQQYTEHFMA	gi|125333|sp|P29317|EP	[SIKMQQYTEHFMA|Y|9
4529	CYLLIRYCSGKSK	gi|77416855|sp|P29033|	NA
4530	SSDDVRYVNAFKF	gi|143811474|sp|P17948	[SSDDVRYVNAFKF|Y|1
4531	TLQHPDYLQEYST	gi|3913590|sp|Q15303|E	NA
4532	AIKMGQYKESFAN	gi|76803654|sp|P29323|	[AIKMGQYKESFAN|Y|9
4533	AIKMGRYKESFVS	gi|76803655|sp|P54753|	NA
4534	FLYHEKYKVVELF	gi|62512174|sp|Q15546|	NA
4535	FRHDSGYEVHHQK	gi|112927|sp|P05067|A4_	NA
4536	GDKQVEYLDLDLD	gi|90180201|sp|Q13480|	[GDKQVEYLDLDLD|Y|6
4537	GHGTKVYIDPFTY	gi|19860819|sp|P54760|	NA
4538	GLNKQGYKCRQCN	gi|547803|sp|Q05655|KP	[GLNKQGYKCRQCN|Y|
4539	VYNQPVYNQPVGA	gi|14548191|sp|O15162|	[VYNQPVYNQPVGA|Y|7
4540	FLKSPAYRDLAAQ	gi|3914624|sp|O15492|R	[FLKSPAYRDLAAQ|Y|17
4541	LLAKKGYQERDLE	gi|3914240|sp|O15547|P	NA
4542	DKDGNGYISAAEL	gi|119609501|gb|EAW89	[DKDGNGYISAAEL|Y|10
4543	KNVVPLYDLLLEM	gi|544257|sp|P03372|ES	[KNVVPLYDLLLEM|Y|53
4544	GEPNVSYICSRYY	gi|20455502|sp|P49841|	[GEPNVSYICSRYY|Y|27
4545	DGGDDIYEDIIKV	gi|1718101|sp|P52735|V	[DGGDDIYEDIIKV|Y|172
4546	DTSSVLYTAVQPN	gi|129890|sp|P09619|PG	[DTSSVLYTAVQPN|Y|1
4547	PPSAELYSNALPV	gi|129890|sp|P09619|PG	[PPSAELYSNALPV|Y|71
4548	<<Marker>>	contol_spot	NA
4549	DIESSNYMAPYDN	gi|129890|sp|P09619|PG	[DIESSNYMAPYDN|Y|7
4550	DSEGHLYTVPIRE	gi|13637934|sp|Q03135|	[DSEGHLYTVPIRE|Y|14
4551	SLNSNDYGYGGQK	gi|116241370|sp|Q96AE	[SLNSNDYGYGGQK|Y|5
4552	SSGEIVYCGQVFE	gi|730538|sp|Q02543|RL	[SSGEIVYCGQVFE|Y|6
4553	AGKALDYYMLRNG	gi|81175200|sp|Q9Y490|	NA
4554	GSLAADYGFPDVG	gi|24212077|sp|Q08174|	NA
4555	DDGRVSYPLCFIF	gi|6831548|sp|O60234|G	[DDGRVSYPLCFIF|Y|84
4556	FNVCNRYLVVLYY	gi|12585536|sp|Q9Y3B4|	NA
4557	TSSSAIYDNPNLI	gi|60389833|sp|Q8IZD4|	[TSSSAIYDNPNLI|Y|191
4558	EFGGSIYQKVNEK	gi|12643945|sp|Q9Y277|	NA
4559	DLIHEIYTVGKRF	gi|133021|sp|P18124|RL	[DLIHEIYTVGKRF|Y|195
4560	LKYENDYPSVILR	gi|119641|sp|P14921|ET	[LKYENDYPSVILR|Y|20
4561	QPDYAMYSRISSS	gi|32469765|sp|Q92608|	[QPDYAMYSRISSS|Y|21
4562	RVCEPCYEQLNRK	gi|71152119|sp|O14964|	[RVCEPCYEQLNRK|Y|2
4563	EQERLAYINPDLA	gi|400042|sp|P31948|ST	[EQERLAYINPDLA|Y|35
4564	KTVCSTYLQSRYY	gi|61213741|sp|Q9H422|	[KTVCSTYLQSRYY|Y|3
4565	ADGGAEYATYQTK	gi|27502427|ref|NP_758	NA
4566	PPSQGDYHGCPFR	gi|51338777|sp|P49643|	[PPSQGDYHGCPFR|Y|
4567	LMTGDTYTAHAGA	gi|1168268|sp|P42684|A	[LMTGDTYTAHAGA|Y|3
4568	PKVKAIYDIERPD	gi|56404432|sp|O14639|	[PKVKAIYDIERPD|Y|396
4569	<<Marker>>	contol_spot	NA
4570	STPPSAYGSVKAY	gi|113950|sp|P07355|AN	[STPPSAYGSVKAY|Y|2
4571	RIPYDDYPVVFLP	gi|73621365|sp|Q5EBL8|	[RIPYDDYPVVFLP|Y|10|
4572	MGQKDSYVGDKAQ	gi|126337369|ref|XP_001	NA
4573	FSRVQIYHNPTAN	gi|1718079|sp|P50552|V	[FSRVQIYHNPTAN|Y|39
4574	NKLDTKYPYVCHA	gi|23503055|sp|P32321|	NA
4575	ASDPILYRPVAVA	gi|20178296|sp|P14618|	[ASDPILYRPVAVA|Y|10

4576	PVSPSDYITYPSQ	gi|729995|sp|P39678|MB	NA
4577	ENVEDVYANSLSP	gi|135077|sp|P08153|SW	NA
4578	YTNEDGYDDAENA	gi|56757368|sp|P07248|	NA
4579	TKENAEYERKTPG	gi|1711597|sp|P46676|S	NA
4580	KIDDFDYIGPDSL	gi|50400296|sp|Q04052|	NA
4581	GLEALDYDIHNYF	gi|416737|sp|P24813|YA	NA
4582	IGCEKTYKNQNGL	gi|417770|sp|P32432|SF	NA
4583	SEEDDNYKPLDTS	gi|1351976|sp|P05085|A	NA
4584	ITTHPKYSDIDVD	gi|417456|sp|P19880|YA	NA
4585	DSMLDDYVSSDLL	gi|462625|sp|P33748|MS	NA
4586	NITVPDYSIIPTS	gi|88984445|sp|P32389|	NA
4587	VPSLEEYSANPPN	gi|2507068|sp|P22148|M	NA
4588	HQEFTDYDNPIFE	gi|62297871|sp|Q61083|	NA
4589	VISGEGYGRKADV	gi|2499640|sp|Q99759|M	NA
4590	<<Marker>>	contol_spot	NA
4591	AESDDTYKDDVNH	gi|2499638|sp|Q62925|M	NA
4592	TSSSSEYGSVSPD	gi|6685617|sp|Q99683|M	NA
4593	NVEEYSYKQEKKI	gi|6685621|sp|Q9Y6R4|	NA
4594	TNTENLYGTSPPS	gi|6685621|sp|Q9Y6R4|	NA
4595	MVEENPYRQLPCN	gi|55957234|emb|CAI17	NA
4596	TAKESQYVMKIAN	gi|3183087|sp|Q99574|N	NA
4597	YFDRLDYVSMMCN	gi|20178314|sp|O75306|	NA
4598	AHEDPMYDIIRDN	gi|38372427|sp|Q8TA86|	NA
4599	EISCDFYAWTSDN	gi|126302607|sp|P01266	NA
4600	GHDSSYYARIGDN	gi|91207950|sp|Q9BZF9|	NA
4601	QGFQVEYKDFPKN	gi|90185286|sp|O95793|	NA
4602	CFDETRYEYLEGG	gi|547643|sp|Q04756|H	NA
4603	DSKEGPYVSVPLN	gi|74753102|sp|Q9P0V3|	NA
4604	LDGSREYVNVSQE	gi|14194891|sp|O43561|	[LDGSREYVNVSQE|Y|2
4605	LGADDSYYTARSA	gi|1177044|sp|P43403|Z	[LGADDSYYTARSA|Y|4
4606	LIKEDVYLSHDHN	gi|8928302|sp|Q13882|P	[LIKEDVYLSHDHN|Y|34
4607	RGKSDPYAKVSIG	gi|119599471|gb|EAW79	NA
4608	TDNDDIYGAAWIG	gi|6226907|sp|O75841|U	NA
4609	FPNSGKYATTARN	gi|12643337|sp|Q9UPC5	NA
4610	IKSNEGYGYSNRN	gi|51094655|gb|EAL239	NA
4611	LSEMVEYITHNRN	gi|116241235|sp|Q1336	NA
4612	QGRKLGYTFNNQN	gi|12643822|sp|Q9NYC9	NA
4613	ERENKSYISSLAP	gi|118572671|sp|O6023	NA
4614	IPSELGYGERGAP	gi|23503054|sp|P26885|	NA
4615	KHDCVGYVMKKAP	gi|38258924|sp|P51784|	NA
4616	RQSPLTYEDHGAP	gi|12643957|sp|Q9Y618|	NA
4617	TTNGEIYIIAGAP	gi|117949792|sp|Q9UKZ	NA
4618	AYNPEPYLNNESQ	gi|109940053|sp|O1501	NA
4619	KTCKLIYDSMALG	gi|32172457|sp|Q8TB24|	NA
4620	LRCDPDYLRGALG	gi|34921813|sp|Q8IZR5|	NA
4621	QVRGDSYESGCLG	gi|12643476|sp|P56557|	NA
4622	WKSWDSYYSKALG	gi|37090037|sp|Q9Y4X1|	NA
4623	GAEEIYYKHVHCR	gi|38258636|sp|Q96RJ0|	NA
4624	IFEELEYHEPVCR	gi|125950975|sp|Q9Y4F	NA
4625	GGRERDYIAPWER	gi|74733529|sp|Q9H0W	NA
4626	NFRSVYYEKVGFR	gi|37538019|sp|Q9P0N9|	NA
4627	RRYEVEYLQFAFR	gi|47117913|sp|Q9NU19	NA

4628	AVCSGGYPDPPFR	gi|119619130|gb|EAW98	NA
4629	FPHCEDYVASLGR	gi|119622317|gb|EAX01	NA
4630	HVKEPRYLLMGGR	gi|23821814|sp|Q9P2E3|	NA
4631	APEDHRYITVSGC	gi|74747583|sp|Q5VXU1	NA
4632	FSSEMEYNDFAIC	gi|61211648|sp|Q8N6M6	NA
4633	HCWEESYEMNIGC	gi|62740001|gb|AAH938	NA
4634	GKEWEEYVQIRTL	gi|74750394|sp|Q86TU7|	NA
4635	LIEKTLYHHVHGC	gi|109940166|sp|P81133	NA
4636	SGRAEYYQWVGIC	gi|74752693|sp|Q9H6D3	NA
4637	GGAELGYGCKASR	gi|74752228|sp|Q9BPX1	NA
4638	AGPNFEYAEAPSR	gi|126314|sp|P06858|LIP	NA
4639	ERGRSYYVDHNSR	gi|32172435|sp|P46934|	NA
4640	SLREGHYAQRLSR	gi|55977069|sp|P98176|	NA
4641	ITRSERYVCAVTR	gi|74735248|sp|Q9Y314|	NA
4642	TKEMEPYMPLYTR	gi|74749827|sp|Q75V66|	NA
4643	DVSALIYASVGDP	gi|30046564|gb|AAH504	NA
4644	HVFKEAYLGPADP	gi|119595124|gb|EAW74	NA
4645	KLEEGKYLILKDP	gi|6685526|sp|O15371|IF	NA
4646	PFLKDVYVDSKDP	gi|30912745|sp|Q9P032|	NA
4647	VAATYKYVNMQDP	gi|2499325|sp|O00217|N	NA
4648	KMDGPGYGDEEEP	gi|119612288|gb|EAW91	NA
4649	DPDSNPYSLLDTS	gi|90177782|sp|P51116|	[DPDSNPYSLLDTS|Y|52
4650	HRSLEQYDQVLDG	gi|61223942|sp|Q9UBC2	NA
4651	GMARDIYRASYYR	gi|146328566|sp|Q9UM7	[GMARDIYRASYYR|Y|12
4652	VINPNAYDNLAIY	gi|118572719|sp|Q9H79	[VINPNAYDNLAIY|Y|632
4653	LGETASYSLFLPT	gi|84029267|sp|Q86SP6|	[LGETASYSLFLPT|Y|67
4654	SKDSNPYATLPRA	gi|147644956|sp|Q3V6T	[SKDSNPYATLPRA|Y|1
4655	LNTPNTYLRVNVA	gi|543774|sp|P35612|AD	NA
4656	ICHDAEYVNVTAE	gi|148876773|sp|Q1412	NA
4657	AEVRAQYEEIAQR	gi|82654947|sp|P19013|	NA
4658	LDPATRYPNLNLR	gi|45593495|sp|Q8TDZ2|	NA
4659	LEANKDYIIISWK	gi|1709202|sp|P52179|M	NA
4660	HADWKEYLNLLIC	gi|14195005|sp|O60437|	NA
4661	DRGLSKYPNLLNQ	gi|1346694|sp|P49354|P	NA
4662	SRISGGYENVPTD	gi|62906878|sp|O00469|	NA
4663	SIKIDPYINIDAG	gi|20981706|sp|P17812|	NA
4664	ESFTEKYVNATPS	gi|17433306|sp|Q9NY91|	NA
4665	LHLRGGYIIPIQE	gi|267050|sp|P14410|SU	NA
4666	LFNLSTYLIPRHW	gi|1351188|sp|P48775|T	NA
4667	KGHDGLYQGLSTA	gi|23830999|sp|P20963|	[KGHDGLYQGLSTA|Y|1
4668	PTCDEKYANITVD	gi|33112650|sp|P08575|	NA
4669	AISIDRYTAVAMP	gi|118206|sp|P14416|DR	NA
4670	CLRVELYGCLWRD	gi|729008|sp|Q08345|DD	NA
4671	VREITGYLNIQSW	gi|119534|sp|P21860|ER	NA
4672	TVTTISYLNLAVA	gi|120427|sp|P21462|FP	NA
4673	HKEGPNYQWMPFS	gi|8134696|sp|Q13275|S	NA
4674	PKPGDDYSYNQFS	gi|2498802|sp|Q92733|P	NA
4675	VLCTEEYSRWAGS	gi|34922606|sp|Q96CW	NA
4676	CQSEDWYKNQLGS	gi|116242861|sp|Q96ND	NA
4677	DSPDDDYHALFVL	gi|125950459|sp|Q2KHT	NA
4678	IAPQTKYIIPGGS	gi|148226485|ref|NP_96	NA
4679	DKEEIKYLNNIIS	gi|116241294|sp|O1507	NA

4680	HFFCDLYALMKIS	gi|85681882|sp|Q15612|	NA
4681	PADDELYQRTRIS	gi|74733183|sp|Q9BU61|	NA
4682	SLQGVRYVDGGIS	gi|74731110|sp|Q96AD5|	NA
4683	DGEETSYCFKEKS	gi|2495290|sp|Q15475|S	NA
4684	LLCMEEYVIEPKS	gi|74751888|sp|Q96GM8	NA
4685	GTHEVRYVSAGQS	gi|27734555|sp|Q96BD0|	NA
4686	PWVEPGYWESWPS	gi|74761282|sp|Q9BV99|	NA
4687	LFQEFDYQPIAAA	gi|121958055|sp|Q3MIX3	NA
4688	GMNMEPYGFHARG	gi|94730396|sp|Q10571|	NA
4689	SWAETTYWISPQG	gi|2494720|sp|Q14627|I1	NA
4690	CKEMSCYSDFPFP	gi|399505|sp|Q01740|FM	NA
4691	FVKNTHYYDKRWS	gi|74752540|sp|Q9GZU3	NA
4692	DHCEALYKEVQRC	gi|38372396|sp|Q9UG22	NA
4693	FCSSVIYVIFGSC	gi|119624269|gb|EAX038	NA
4694	LTEKKEYDEKNSC	gi|128485546|ref|NP_001	NA
4695	VNPMESYQNRQSC	gi|23396507|sp|Q9BQT9	NA
4696	KHSMLVYVAKGRG	gi|148685156|gb|EDL171	NA
4697	CRSCRTYINPFVS	gi|13124510|sp|O95487|	NA
4698	EWYRFHYINILSR	gi|585966|sp|P37088|SC	NA
4699	QLSDPDYINQYVI	gi|24418867|sp|Q9Y5W8	NA
4700	IGVRESYVNLCSN	gi|14917099|sp|Q93034|	NA
4701	WIEDTLYANVDFF	gi|6707663|sp|P78363|A	NA
4702	BMADPKYADLPGI	gi|22096346|sp|Q13561|	NA
4703	ILQGLKYTFSVDW	gi|547803|sp|Q05655|KP	NA
4704	MDEELHYASLNFH	gi|116241290|sp|P20138	[MDEELHYASLNFH|Y|34
4705	QFEYAAYIIHAYK	gi|20140422|sp|O15455|	[QFEYAAYIIHAYK|Y|759
4706	SQEELHYATLNFP	gi|118572721|sp|Q96LC7	[SQEELHYATLNFP|Y|66
4707	TVVIALYDYQTND	gi|585361|sp|Q08881|ITK	[TVVIALYDYQTND|Y|18
4708	YSTKYFYKQNGRI	gi|3913590|sp|Q15303|E	NA
4709	LDSGGFYITSRTQ	gi|125711|sp|P12931|SR	[LDSGGFYITSRTQ|Y|21
4710	RLQNFSYDQREMI	gi|30173387|sp|Q9NTZ6|	[RLQNFSYDQREMI|Y|52
4711	TLSEVDYAPAGPA	gi|119595261|gb|EAW74	[TLSEVDYAPAGPA|Y|11
4712	AYGERPYWNMTNR	gi|19857975|sp|P29322|	[AYGERPYWNMTNR|Y|
4713	SLDNPDYQQDFFP	gi|2811086|sp|P00533|E	[SLDNPDYQQDFFP|Y|1
4714	EELGYEYMDVGSD	gi|119534|sp|P21860|ER	NA
4715	PGLEYCYNPSHNP	gi|120046|sp|P11362|FG	[PGLEYCYNPSHNP|Y|5
4716	QAHYNMYPQNPDS	gi|41019536|sp|P51692|	[QAHYNMYPQNPDS|Y|
4717	RGQEGEYAVPFDA	gi|143220234|sp|O60496	[RGQEGEYAVPFDA|Y|2
4718	SVNKLVYENINGL	gi|71152057|sp|Q8WU20	NA
4719	YRSPPPYVPP	gi|2498284|sp|Q14118|D	[YRSPPPYVPP|Y|892|Q
4720	DPPPELYFVKVDV	gi|6226780|sp|O14746|T	[DPPPELYFVKVDV|Y|70
4721	SEPVGIYQGFEKK	gi|547803|sp|Q05655|KP	[SEPVGIYQGFEKK|Y|31
4722	STDRSPYEKVSAG	gi|547937|sp|P15941|MU	[STDRSPYEKVSAG|Y|1
4723	TFTNITYRGT	gi|125987835|sp|P05106	[TFTNITYRGT|Y|785|P0
4724	TSSGEWYQNFQPP	gi|13637684|sp|P30203|	[TSSGEWYQNFQPP|Y|
4725	VGDEDIYSGLSDQ	gi|13124807|sp|P15498|	[VGDEDIYSGLSDQ|Y|14
4726	ATYAEPYRPIQYR	gi|20139104|sp|Q99569|	[ATYAEPYRPIQYR|Y|48
4727	RLYAESYERDPSG	gi|152031655|sp|Q15124	NA
4728	TEEKFRYMCILSG	gi|85700954|sp|Q9UQ84	NA
4729	DGRKNLYTAMPLP	gi|38372888|sp|Q9UKV8	NA
4730	LTYGNRYKNVKLP	gi|116242483|sp|P11413	NA
4731	ACEDLKYGDQSKV	gi|8475983|sp|O75916|R	NA

4732	KLSEDPYGIFCLV	gi|74753527|sp|Q9Y6V7|	NA
4733	SHSEQEYGKAGGS	gi|41016969|sp|O95208|	NA
4734	QCEQAVYQTILEE	gi|150421536|sp|O75553	NA
4735	PQQPLAYPKLQRQ	gi|50400978|sp|Q7Z5J4|	NA
4736	LAVMGAYVLLKRE	gi|17368701|sp|Q9BY50|	NA
4737	PNEFDKYRMFIGD	gi|74716122|sp|Q8TF72|	NA
4738	WEHGDGYPFDGKD	gi|116856|sp|P08253|MM	NA
4739	ALEQDTYWRELSC	gi|51338794|sp|P78559|	NA
4740	IQSHCSYTYGRKG	gi|14548118|sp|Q13459|	NA
4741	TRDLAQYDAAHHE	gi|90110780|sp|Q02818|	NA
4742	PEEESAYVAGEKR	gi|41017512|sp|Q9UNZ2	NA
4743	HYTHSDYQYSQRS	gi|20139105|sp|Q99959|	NA
4744	KNETSKYAEYSFT	gi|68565701|sp|Q5UIP0|	NA
4745	RQETFVYEMESHA	gi|8134719|sp|Q92966|S	NA
4746	RIGAFGYMECSAK	gi|47606458|sp|P61586|	NA
4747	LKRHGKYCHLRGG	gi|20454955|sp|Q14526|	NA
4748	DYINANYIRGYDG	gi|20141721|sp|P35236|	NA
4749	GPGLSSYGVPASL	gi|38257363|sp|O75369|	NA
4750	KLGEGTYATVFKG	gi|116242704|sp|Q07002	NA
4751	EQTQKIYNCHVLL	gi|51704324|sp|Q86X76|	NA
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4753	SDFETVYQQCVRC	gi|1709543|sp|P24666|P	NA
4754	ERRKSRYSDLDFE	gi|12643618|sp|O60242|	NA
4755	SREQTVYYAKAFS	gi|29840827|sp|O75439|	NA
4756	SENEDIYYKSMPN	gi|46576868|sp|O95490|	NA
4757	SEGPSNYDSYKKV	gi|30913162|sp|Q8TEW	NA
4758	RRTLMRYVNLTSL	gi|38503351|sp|Q8N1M1	NA
4759	VAHQPPYTQPHCS	gi|116242614|sp|Q96RT	NA
4760	GDSKVIYMARNPK	gi|22096149|sp|Q9BR01|	NA
4761	YTLLFAYFSSRKR	gi|34098662|sp|Q92576|	NA
4762	KVSYQDYEIEISD	gi|127566|sp|P20591|MX	NA
4763	PIAMEYYNWGRFS	gi|74752543|sp|Q9GZY6	NA
4764	SNGLLSYYRSKAE	gi|129308|sp|P22059|OS	NA
4765	YQNQGIYQVPTGH	gi|8134360|sp|Q14511|C	NA
4766	KTVHEKYQGQAPS	gi|56405328|sp|P29597|	NA
4767	YKSNEDYVYVRGR	gi|83305815|sp|P31629|	NA
4768	GYGSGRYYDSRPG	gi|1710620|sp|P98179|R	NA
4769	NLTQLRYLNLSST	gi|20140873|sp|Q9NR97	NA
4770	RWDPADYENVTSI	gi|1351848|sp|P43681|A	NA
4771	LPHGFCYIIPSNL	gi|2833247|sp|Q13797|IT	NA
4772	AYKIFLYPNAGQL	gi|119628734|gb|EAX08	NA
4773	SQFNTLYLRVRGD	gi|21542405|sp|Q9Y375|	NA
4774	ALPRLIYLNLSNN	gi|2498405|sp|Q14392|L	NA
4775	LDLTYIYPNIIAM	gi|42560209|sp|P60484|	NA
4776	NIPGSDYINANYI	gi|131469|sp|P29350|PT	NA
4777	LGDEGGYINASFI	gi|12643716|sp|Q12923|	NA
4778	ENIKGYYIIIVPL	gi|1709906|sp|P23468|P	NA
4779	DSKHSDYINANYV	gi|143811444|sp|P23470	NA
4780	DGKLTDYINANYV	gi|400199|sp|P23471|PT	NA
4781	IDEEDTYTMPSTR	gi|3183518|sp|Q05397|F	[IDEEDTYTMPSTR|Y|40
4782	EMLEGFYEEISKG	gi|62512187|sp|Q9Y613|	NA
4783	PEPENDYEDVEEM	gi|123557|sp|P14317|HC	[PEPENDYEDVEEM|Y|3

4784	VASIEEYTEMMPA	gi|547738|sp|P35568|IRS	NA
4785	PAAPVSYADMRTG	gi|547738|sp|P35568|IRS	NA
4786	MADDEDYEEVVEY	gi|19856971|sp|P20929|	NA
4787	REKDEIYGHPLFP	gi|59803105|sp|Q99687|	NA
4788	SSQARKYVNAFSA	gi|2815504|sp|P10242|M	NA
4789	KKEYPLYINQTCH	gi|116242679|sp|Q13287	NA
4790	LKGIGEYVNIRTG	gi|85700389|sp|Q92620|	NA
4791	KEETLAYLNIVSP	gi|17380293|sp|Q9UBS8	NA
4792	RKQLVIYEEISDP	gi|115502458|sp|O60225	NA
4793	GAKEITYGNNKPV	gi|115502349|sp|P10323	NA
4794	PNQTRTYDPEGFK	gi|68565913|sp|Q8NFP7	NA
4795	AEPEDHYFLLTEP	gi|47117647|sp|P61158|	NA
4796	QREQRSYVDLLVK	gi|116283438|gb|AAH209	NA
4797	QQGDFGYCPRVYC	gi|54037520|sp|P67870|	NA
4798	SVAGVRYFQCEPL	gi|266902|sp|P30622|CL	NA
4799	IVGNEYYFRVYTE	gi|6093456|sp|Q14324|M	NA
4800	DHLEGLYAKVNKP	gi|30913163|sp|Q8TEW8	NA
4801	LSVMPQYEDILQV	gi|134035014|sp|Q9P227	NA
4802	VKDWDKYGLMPQV	gi|145559531|sp|Q8WW	NA
4803	ILSKVAYVLMASV	gi|37081373|sp|Q8NGS6	NA
4804	DLEPDTYCRYDSV	gi|6919941|sp|Q15113|P	NA
4805	ILPNPLYHCLGSV	gi|156151445|ref|NP_079	NA
4806	SAPEWPYMLVGSV	gi|12643301|sp|O95342|	NA
4807	FPPCEEYLQGGYL	gi|20141491|sp|P09016|	NA
4808	KTSDAPYDSADDW	gi|117949358|sp|Q9BTA9	NA
4809	GTTSTSYKSLANQ	gi|28202103|sp|Q9C0B5|	NA
4810	HLRKDPYANLMLQ	gi|119594256|gb|EAW73	NA
4811	VVFLPAYENPPAW	gi|73621365|sp|Q5EBL8|	[VVFLPAYENPPAW|Y|18
4812	DCAENMYIDMMLW	gi|66347357|emb|CAI950	NA
4813	NQDNCPYISNANQ	gi|549136|sp|P35442|TS	NA
4814	GYDDLDYGMMSDY	gi|14916543|sp|O60716|	NA
4815	PFCAEDYTESLLQ	gi|74735407|sp|O43663|	NA
4816	VKEDVCYVSQDFY	gi|27923737|sp|Q9GZN1	NA
4817	FLNLDYYVAVYLP	gi|148612805|ref|NP_059	NA
4818	LHNVELYEDNHMP	gi|116241243|sp|Q13023	NA
4819	AGPSPVYVKVKSA	gi|55665713|emb|CAH71	NA
4820	NYETVKYFNNERY	gi|8928549|sp|O75027|A	NA
4821	VRTDVQYKNNKSY	gi|34534113|dbj|BAC869	NA
4822	EEEEVAYISLYSY	gi|116241332|sp|Q9BTC	NA
4823	CSSKEEYQKESSA	gi|50401059|sp|Q8IZK6|	NA
4824	DGCPPKYAKTLYL	gi|25091548|sp|Q9HCS7	NA
4825	HYGKDAYRSGGPD	gi|67550215|gb|AAY6848	NA
4826	SDTKKSYVNGGFA	gi|1352332|sp|P43005|E	NA
4827	ARMREDYDSVEQD	gi|10720244|sp|Q9Y5S9|	NA
4828	ECSEEDYRPSQQD	gi|125987835|sp|P05106	NA
4829	PAGDDGYSGANQD	gi|74762240|sp|Q5T619|	NA
4830	HLTEKAYSDTPRD	gi|119583324|gb|EAW62	NA
4831	RESEGLYGQPGDE	gi|39932727|sp|Q15057|	[RESEGLYGQPGDE|Y|7
4832	EGYKKKYQQVDEE	gi|129890|sp|P09619|PG	NA
4833	NLKMEAYVPSEEE	gi|87299628|ref|NP_6836	NA
4834	GGDMFDYIMKHEE	gi|90185235|sp|Q9NRH2	NA
4835	LAAMEGYIGVDFE	gi|12643641|sp|O75899|	NA

4836	QKAETLYTMGDFE	gi|145572736|sp|Q96NG	NA
4837	QAAEVTYGAMAHA	gi|89039216|ref|XP_942	NA
4838	DDYDLMYVNLDNE	gi|1346908|sp|P26022|P	NA
4839	LSRAELYKEPTNE	gi|62900709|sp|Q9H6R4	NA
4840	FLTDQSYIDVLPE	gi|125484|sp|P08581|ME	NA
4841	EDSSSLYEEGNQE	gi|74728222|sp|Q8IXQ4|	NA
4842	RRLCDDYDEAARE	gi|24418474|sp|Q96KK3|	NA
4843	<<Marker>>	contol_spot	NA
4844	SQESGYYDRMDYE	gi|12643409|sp|P43243|	NA
4845	YRDGEEYEWKETA	gi|74721539|sp|Q9Y6M7	NA
4846	RGKEVCYERLGCF	gi|121948240|sp|Q17RR	NA
4847	YAEEEMYRPHPAF	gi|51702249|sp|P62955|	NA
4848	CVDNSEYMRNGDF	gi|1709796|sp|P55036|P	NA
4849	KGPVEGYEENEEF	gi|47606219|sp|Q9UI30|	NA
4850	NWRDDQYLDDCKP	gi|28558814|sp|Q93074|	NA
4851	PEDMPSYGVYPWL	gi|2499917|sp|P78562|P	NA
4852	PIYEGDYHPEPLT	gi|148664213|ref|NP_00	NA
4853	DLNTTEYVVGAPT	gi|124951|sp|P08514|IT	NA
4854	GARKPHYDIWGNT	gi|118572618|sp|O6026	NA
4855	LHSDIRYESMINT	gi|147742985|sp|Q5TH6	NA
4856	ATPELQYKDKLDA	gi|47116570|sp|Q96RP7|	NA
4857	DDSEIAYKYAQLA	gi|77540235|gb|ABA869	NA
4858	PDWKDFYVVEPLA	gi|123079|sp|P06865|HE	NA
4859	ASVKDGYAVRAAD	gi|13431554|sp|Q9NQX3	NA
4860	GRPGACYVDIPAD	gi|20455027|sp|Q9UJ83|	NA
4861	ATSPGQYVLSGLQ	gi|44680159|ref|NP_976	NA
4862	PRNNSPYEIENGV	gi|1706799|sp|P02671|F	NA
4863	ATERADYVALAIV	gi|114152771|sp|O0046	NA
4864	<<Marker>>	contol_spot	NA
4865	HSVETVYKDLCLQ	gi|118573898|sp|Q6PIF2	NA
4866	LNSPDPYEKIPHV	gi|23503045|sp|O95180|	NA
4867	QNSVPHYAEADIV	gi|729008|sp|Q08345|DD	NA
4868	PDFIDGYINLAAA	gi|68067509|sp|O15294|	NA
4869	PFIDLNYMVYMFQ	gi|120649|sp|P04406|G3	NA
4870	QYAGYDYSQQGRF	gi|74760683|sp|Q969M3|	[QYAGYDYSQQGRF|Y|
4871	SLPNPEYYTLRYA	gi|30913107|sp|Q96JJ3|	[SLPNPEYYTLRYA|Y|48
4872	DADDAVYELNGKD	gi|20981726|sp|Q08170|	[DADDAVYELNGKD|Y|5
4873	NIVFGDYTWTEFD	gi|85541056|sp|Q15645|	[NIVFGDYTWTEFD|Y|5
4874	GWPSSAYGVTKIG	gi|118519|sp|P16152|DH	NA
4875	PSKSTVYVSNLPF	gi|74760425|sp|Q8TBF4|	NA
4876	DAYKDKYVCFDQF	gi|128997|sp|P25929|NP	NA
4877	LLSKGSYQTSHQF	gi|114520607|ref|NP_94	NA
4878	FISSFQYLIVAIA	gi|30316388|sp|Q9H7F0|	NA
4879	SSNLPKYCDNCSF	gi|119628762|gb|EAX08	NA
4880	FEPMELYGEHAKA	gi|148699332|gb|EDL31	NA
4881	LGEDSDYDKLSDM	gi|89026785|ref|XP_940	NA
4882	KGFTPYYARLGPH	gi|20141580|sp|Q02978|	NA
4883	AGREWYYGNVTRH	gi|20532395|sp|O43639|	NA
4884	LCEWTDYGNTFSH	gi|74758336|sp|Q6PG37	NA
4885	<<Marker>>	contol_spot	NA
4886	CRNKDHYGIMMYH	gi|108935853|sp|Q1414	NA
4887	LPEKVEYVIKCDM	gi|116242792|sp|P51532	NA

4888	YLAEAGYTSRGKI	gi|3023637|sp|Q14562|D	NA
4889	LTTELIYVRKLKI	gi|119609213|gb|EAW88	NA
4890	IGKGEGYADLEYA	gi|119615827|gb|EAW95	NA
4891	VLEEGHYPCLSAM	gi|76800646|sp|Q9Y4K1|	NA
4892	DQEGSTYEQIPAC	gi|89039180|ref|XP_9421	NA
4893	TPSPVEYHSPGLI	gi|32469743|sp|Q8N1I0|	NA
4894	FPSEDFYRCGYCK	gi|22002033|sp|O95260|	NA
4895	HTSMFIYKWPADK	gi|18203633|sp|Q9Y5L3|	NA
4896	CFDATLYIQMNEK	gi|20138891|sp|O75925|	NA
4897	QTSEKKYHFGCEK	gi|2501464|sp|O00507|U	NA
4898	GDSPGRYEIMNFK	gi|1709020|sp|P41594|M	NA
4899	LGSASDYIQSVFK	gi|119620108|gb|EAW99	NA
4900	HVFEDSYRELHRK	gi|73915353|sp|Q7Z6Z7|	NA
4901	KTADPRYELPSRK	gi|41018380|sp|O96006|	NA
4902	LFHNPEYNKNTSK	gi|6166019|sp|P20273|C	NA
4903	DNRAFGYVCGGEG	gi|145559465|sp|P98082	NA
4904	SRVNSDYETDGEG	gi|12230848|sp|O95049|	NA
4905	LNHKNSYVIKTTK	gi|55662050|emb|CAH7	NA
4906	<<Marker>>	contol_spot	NA
4907	LLLKELYVENAHL	gi|118601093|sp|Q9Y2I6	NA
4908	ADENHLYEDLFRA	gi|746415|gb|AAA85819.	NA
4909	VTQKADYPNIQHL	gi|6226957|sp|Q13635|P	NA
4910	LLCESRYNESDKQ	gi|73921624|sp|Q86U86|	NA
4911	FACKLDYDEDASA	gi|74762570|sp|Q8NFI4|	NA
4912	ECKQDEYAKSMIL	gi|74745673|sp|Q5T9G4|	NA
4913	QCSVDVYKKVGSL	gi|17375490|sp|Q14203|	NA
4914	AVPEEIYRYSRSL	gi|50400856|sp|Q14160|	NA
4915	HKKRPSYVVPTSL	gi|116242837|sp|Q9Y2K	NA
4916	KESSGKYTFSAHM	gi|3914237|sp|Q15363|T	NA
4917	LSASTDYEQSTGM	gi|74732111|sp|Q96IW7|	NA
4918	QNQWPNYEEKPHM	gi|12644018|sp|P55196|	NA
4919	PSSRGDYMTMQMS	gi|547738|sp|P35568|IR	NA
4920	QGDLKLYSLEGYG	gi|3183117|sp|Q15118|P	NA
4921	QYFMTEYVATRWY	gi|2499599|sp|Q13164|M	[QYFMTEYVATRWY|Y|2
4922	RHVSISYDIPPTP	gi|90180201|sp|Q13480|	[RHVSISYDIPPTP|Y|307
4923	RKFGDDYQVVTTS	gi|1352482|sp|P48549|IR	NA
4924	RSSLKAYGNGYSS	gi|114765|sp|P07550|AD	NA
4925	DLFPMDYHCLGDN	gi|1710811|sp|P34925|R	NA
4926	DVYETDYYRKGGK	gi|12644000|sp|P14616|	NA
4927	<<Marker>>	contol_spot	NA
4928	EATATDYHTTSHP	gi|114787|sp|P02730|B3	[EATATDYHTTSHP|Y|4
4929	EEKGGLYIVTEYM	gi|729887|sp|P41240|CS	NA
4930	EIYSADYYRVQSK	gi|118572711|sp|Q0197	NA
4931	EPKKKKYAKEAWP	gi|19863082|sp|Q12972|	[EPKKKKYAKEAWP|Y|3
4932	DRKGGSYSQAASS	gi|147744695|gb|ABQ51	[DRKGGSYSQAASS|Y|3
4933	FLPVPEYINQSVP	gi|2811086|sp|P00533|E	[FLPVPEYINQSVP|Y|10
4934	EHAQDTYLVLDKW	gi|119524|sp|P19235|EP	[EHAQDTYLVLDKW|Y|3
4935	TAENPEYLGLDVP	gi|119533|sp|P04626|ER	[TAENPEYLGLDVP|Y|12
4936	LIEDNEYTARQGA	gi|125870|sp|P07947|YE	[LIEDNEYTARQGA|Y|41
4937	IHLEKKYVRRDSG	gi|547770|sp|P07333|CS	[IHLEKKYVRRDSG|Y|70
4938	NPQEGLYNELQKD	gi|23830999|sp|P20963|	[NPQEGLYNELQKD|Y|1
4939	KIGEGTYGVVYKA	gi|119609759|gb|EAW89	[KIGEGTYGVVYKA|Y|15

4940	HFPQFSYSASSTA	gi|18027298|gb|AAL557	NA
4941	GPKGTGYIKTELI	gi|2507413|sp|P42224|S	[GPKGTGYIKTELI|Y|701
4942	PMDTSVYESPYSD	gi|1177044|sp|P43403|Z	[PMDTSVYESPYSD|Y|3
4943	GEEEHVYSFPNKQ	gi|27735219|sp|P49023|	[GEEEHVYSFPNKQ|Y|1
4944	TWDNEAYVHDAPV	gi|62906858|sp|P01584|	NA
4945	RHRMPGYETMKNK	gi|2499640|sp|Q99759|M	NA
4946	KGNEPEYEGDDTE	gi|6685621|sp|Q9Y6R4|	NA
4947	NWEPPLYDSVGNH	gi|1710804|sp|P38165|R	NA
4948	<<Marker>>	contol_spot	NA
4949	NFYPSPYENLPKP	gi|586313|sp|P38128|SM	NA
4950	KGENRGYEFVKDS	gi|417110|sp|P25364|HC	NA
4951	HTGEKPYTCPDCG	gi|74757437|sp|Q6DD87	NA
4952	APVGSVYQKTNAV	gi|51316115|sp|Q9UJU6|	[APVGSVYQKTNAV|Y|1
4953	NYDGKEYDPVEAR	gi|60390165|sp|Q15555|	[NYDGKEYDPVEAR|Y|1
4954	VPKEDIYSGGGGG	gi|8134660|sp|Q13151|R	[VPKEDIYSGGGGG|Y|1
4955	TGFLTEYVATRWY	gi|232066|sp|P27361|MK	[TGFLTEYVATRWY|Y|1
4956	HEGETAYIRVKVD	gi|730773|sp|Q07955|SF	NA
4957	ITDESPYVHYLNT	gi|12643898|sp|Q9ULV4|	NA
4958	DEEEDEYSGGLC	gi|3024632|sp|Q99747|S	[DEEEDEYSGGLC|Y|30
4959	NMSGSLYEMVSRV	gi|730840|sp|Q08945|SS	NA
4960	NDSDPTYGQQGHP	gi|74751663|sp|Q93052|	[NDSDPTYGQQGHP|Y|
4961	NRKSDIYVCMISY	gi|1707886|sp|P31150|G	NA
4962	KGYPGDYTKGVEI	gi|131616|sp|P22102|PU	NA
4963	GTAEPDYGALYEG	gi|130225|sp|P19174|PL	[GTAEPDYGALYEG|Y|7
4964	TKHLSPYATLTVG	gi|74733019|sp|Q9BSJ8|	[TKHLSPYATLTVG|Y|82
4965	DADEFGYSR	gi|60415926|sp|Q7KZF4|	[DADEFGYSR|Y|908|Q7
4966	RDPPDPYVSLLLL	gi|74733019|sp|Q9BSJ8|	[RDPPDPYVSLLLL|Y|10
4967	PDTEEIYKLTGTG	gi|122889176|emb|CAI3	NA
4968	RGADSAYYQVGQT	gi|47117931|sp|Q9Y2I7|	[RGADSAYYQVGQT|Y|1
4969	<<Marker>>	contol_spot	NA
4970	VATKPLYVALAQR	gi|3183544|sp|P11940|P	[VATKPLYVALAQR|Y|36
4971	HTGENLYKCKVCA	gi|20141959|sp|Q14586|	[HTGENLYKCKVCA|Y|5
4972	IPSAPLYEEITYS	gi|110810435|sp|O60291	[IPSAPLYEEITYS|Y|389|
4973	LYEEITYSGISDG	gi|110810435|sp|O60291	[LYEEITYSGISDG|Y|394
4974	FPIPEEYTFIQNV	gi|126302554|sp|Q0083	[FPIPEEYTFIQNV|Y|472
4975	ETQKSIYYITGES	gi|17865718|sp|P08238|	NA
4976	SHANSSYYDNLLL	gi|465688|sp|P34233|AS	NA
4977	AGTDDDYTKVLKS	gi|544474|sp|P14064|HA	NA
4978	PAKKAEYTETYKK	gi|547746|sp|P33417|IXF	NA
4979	TLCHPEYKRISVE	gi|9910692|sp|Q07928|G	NA
4980	KSRDDRYAAGTFT	gi|113022|sp|P21192|AC	NA
4981	SLNAPKYSSQPPP	gi|3123263|sp|P48743|R	NA
4982	VTFSFDYQKTGMD	gi|90110827|sp|P17181|	NA
4983	AEQAERYDDMAAC	gi|52000887|sp|P63104|	NA
4984	TIPKEQYTIINRT	gi|729833|sp|P40189|IL6	NA
4985	RPEDTFYFDPEFT	gi|1730070|sp|P51812|K	NA
4986	YEDEGVYVNTYGR	gi|119622212|gb|EAX01	NA
4987	IHFTDGYEIKEDI	gi|90110031|sp|Q15349|	NA
4988	LAVSFHYVDSTTM	gi|74719147|sp|Q9NS00|	NA
4989	SEKQDTYLSNSSM	gi|14424438|sp|P51587|	NA
4990	<<Marker>>	contol_spot	NA
4991	ANFSEFYVELEAN	gi|118572619|sp|O95622	NA

4992	FFCEEDYKNYKAN	gi|148540038|ref|NP_00	NA
4993	GTHCELYKDPCAN	gi|74730301|sp|Q8NFT8|	NA
4994	ISSHEGYTQIIAN	gi|119572981|gb|EAW52	NA
4995	GVSKGAYAGITGN	gi|119627361|gb|EAX06	NA
4996	LKSSDAYKKAWGN	gi|46397726|sp|P60880|	NA
4997	VCEQDIYEWTKIN	gi|132533|sp|P25791|RB	NA
4998	CQGEVYYAKMNKN	gi|34532689|dbj|BAC865	NA
4999	GLHVTEYEDNLKN	gi|2498342|sp|Q16134|E	NA
5000	LVSKGEYDWNIKN	gi|74752809|sp|Q9HCR9	NA
5001	TISEYIYHCNAQN	gi|74762601|sp|Q8TB40|	NA
5002	DNWEELYNRYQGG	gi|51704228|sp|P55786|	NA
5003	FNKSELYEIPVIG	gi|74751727|sp|Q969S0|	NA
5004	GGRASDYKSAHKG	gi|17378805|sp|P02686|	NA
5005	INAEIIYAFINIG	gi|37999831|sp|Q9Y5G1	NA
5006	LSGDEFYSDVAKG	gi|126253808|sp|Q8TB2	NA
5007	EEDDSLYCISAWN	gi|73621409|sp|Q8WZA1	NA
5008	IEEVPNYENQDGG	gi|148886692|ref|NP_00	NA
5009	IFHKGSYLRNGWN	gi|146345380|sp|Q1587	NA
5010	NGFKIHYESVTVN	gi|38604740|sp|Q7Z407|	NA
5011	RGAELEYESLKRQ	gi|13431722|sp|Q9Y4I1|	NA
5012	WSEQRDYIDTTWN	gi|12644052|sp|O15260|	NA
5013	QASSGKYTQHGGG	gi|119578137|gb|EAW57	NA
5014	SYNFELYVDVVYQ	gi|130321|sp|P16471|PR	NA
5015	VFSGPAYAAEAAR	gi|18201966|sp|O15399|	NA
5016	ANSSYPYVEIALG	gi|13124361|sp|Q9UKN7	NA
5017	DLFENAYGSSMKG	gi|55665657|emb|CAH72	NA
5018	GEEDVIYTWKALG	gi|66774034|sp|Q9NQ25	NA
5019	ECAQDFYHNVAER	gi|56405102|sp|Q9UJ41|	NA
5020	KHSNGSYSAFGER	gi|119609013|gb|EAW88	NA
5021	QPSLTYYVCPTDR	gi|42516574|ref|NP_963	NA
5022	WDFEEKYSFEIGG	gi|21759444|sp|Q9NSC7	NA
5023	WNKKLLYEKMKGG	gi|23830842|sp|P05408|	NA
5024	EATDSLYVFGGFR	gi|46395756|sp|Q7Z7M0	NA
5025	GGYETFYSEYPEC	gi|2499746|sp|Q16690|D	NA
5026	FFEKPDYEYLRTL	gi|18202957|sp|Q9HCP0	NA
5027	KACGVDYEVKAFC	gi|20141238|sp|P49407|	NA
5028	LSIADHYVEVLEC	gi|17372894|sp|O75718|	NA
5029	RLENNYYWAASEC	gi|12230989|sp|P25440|	NA
5030	VKSMDGYESYGEC	gi|119595261|gb|EAW74	NA
5031	DLEEDPYLPGNPR	gi|124174|sp|P22304|ID	NA
5032	LDKDPIYVGGLPR	gi|126363|sp|P25391|LA	NA
5033	REREVDYDSDMPR	gi|74752415|sp|Q9BX10|	NA
5034	CRRRDYYDDFLQR	gi|74751721|sp|Q969K4|	NA
5035	LICDPGYYYTGQR	gi|116241318|sp|Q7Z40	NA
5036	YNPMCTYVNRGRR	gi|8134696|sp|Q13275|S	NA
5037	DESETGYWITCCP	gi|2498830|sp|P55895|R	NA
5038	EIAIDDYDSSGAS	gi|17366467|sp|Q14643|	NA
5039	IFSFPDYFCCPAS	gi|14250804|gb|AAH088	NA
5040	QVNFTGYVDEHAS	gi|62287160|sp|Q9BYE9	NA
5041	AFQENPYTFSPDP	gi|116268127|ref|NP_68	NA
5042	DLIEERYKASQDP	gi|83305809|sp|Q96KB5|	NA
5043	RKSKGKYAYLLES	gi|116242505|sp|P42261	NA

5044	KGSSGGYGSGGAA	gi|60390855|sp|Q8TF74|	NA
5045	DYEIDQYEEFCFS	gi|544320|sp|P36888|FL	NA
5046	HGNKTGYIFVDFS	gi|73620990|sp|Q9Y4C8|	NA
5047	PPGEKPYESHDFS	gi|74762546|sp|Q8NB42|	NA
5048	EQKELHYASLSFS	gi|25009254|sp|O15389|	NA
5049	KRQVGDYENVIPD	gi|6166019|sp|P20273|C	[KRQVGDYENVIPD|Y|8
5050	VESITVYEEILRQ	gi|23396507|sp|Q9BQT9	NA
5051	TLMGHEYMEMKNT	gi|37537859|sp|Q9UJX2|	NA
5052	RIEEGTYGVVYRA	gi|145559452|sp|Q9UQ8	NA
5053	RAETEHYEEIEDY	gi|18848311|gb|AAH242	NA
5054	DSKFEDYLNAESR	gi|67472677|sp|Q16181|	NA
5055	YENILKYVNLDAW	gi|1708322|sp|P52848|N	NA
5056	VTTDSPYIIPQHR	gi|21903442|sp|P55073|	NA
5057	FCGLLFYINLADH	gi|93195043|sp|Q9UKM	NA
5058	LYEANDYEEIVFL	gi|17369917|sp|Q9Y3R4|	NA
5059	LSPAFRYQPDPWK	gi|266648|sp|P29474|NO	NA
5060	LKEVQKYPNAELA	gi|1352618|sp|Q02218|O	NA
5061	DAGCKPYMAPERI	gi|24638466|sp|P46734|	NA
5062	QWFREAYGAVTQT	gi|3024422|sp|Q15126|P	NA
5063	AIAVDRYLRVKIP	gi|231473|sp|P30542|AA	NA
5064	RPLVEFYEEIKKY	gi|126302521|sp|P25098	NA
5065	CIMAFVYLRVFRE	gi|48429211|sp|P08588|	NA
5066	SHLKGIYLNLAAN	gi|20137430|sp|Q99467|	NA
5067	LSADSGYIIPLPD	gi|129892|sp|P16234|PG	[LSADSGYIIPLPD|Y|101
5068	GIMGSDYINANYV	gi|50403770|sp|Q13332|	NA
5069	EEEGADYINANYI	gi|33112422|sp|Q16827|	NA
5070	DGDSNNYINAALT	gi|2499758|sp|Q92729|P	NA
5071	LMMKNEYIIPITS	gi|18202506|sp|Q15413|	NA
5072	GAVFIIYTAVLGF	gi|12644225|sp|P35346|	NA
5073	GSSRPAYEEFYNC	gi|74730301|sp|Q8NFT8|	NA
5074	LQPETSYDIKMQC	gi|74761309|sp|Q9BWV	NA
5075	YKDEELYDFPAPC	gi|50949350|emb|CAB66	NA
5076	LLYSGKYVWPSHS	gi|31981922|ref|NP_666	NA
5077	PSYCPAYGRVPHS	gi|150416153|sp|Q63HR	NA
5078	YEEKFQYDIVGHS	gi|126361953|gb|AAI318	NA
5079	LEKAGKYVDEENS	gi|145580615|ref|NP_07	NA
5080	VDPQGIYVISAPS	gi|12229810|sp|Q9NYJ7|	NA
5081	GAEGDVYKAPTPS	gi|119621454|gb|EAX01	NA
5082	IVHETGYFSALPS	gi|7387592|sp|Q99612|K	NA
5083	MLYMDHYHINPVL	gi|119579245|gb|EAW58	NA
5084	EEDEDCYILNVQS	gi|119625689|gb|EAX05	NA
5085	QHPEGGYAIASSS	gi|62286592|sp|O95352|	NA
5086	GLDKSGYFELPTS	gi|119610057|gb|EAW89	NA
5087	WPAKDSYTKQYTS	gi|1054776|emb|CAA625	NA
5088	CHSDGSYCQWPVS	gi|93204600|sp|Q6P1M3	NA
5089	GVETSEYAQGGVS	gi|119593736|gb|EAW73	NA
5090	YSETGDYGNVKVS	gi|33301662|sp|Q8TDW	NA
5091	LASSENYKCPGFT	gi|12644377|sp|Q01954|	NA
5092	IISEGLYAIAVVL	gi|6686048|sp|Q9Y210|T	NA
5093	MCVDDAYVRRMAA	gi|68566065|sp|P78362|	NA
5094	MQANPHYARVIGT	gi|74733568|sp|Q9H336|	NA
5095	KMLDDLYEDIHWL	gi|17368720|sp|Q9C0E2|	NA

5096	DSCRENYVRMEHT	gi|51094680|gb|EAL2393	NA
5097	TAGQEDYDRLRPL	gi|119613432|gb|EAW93	[TAGQEDYDRLRPL|Y|6
5098	AEGDEIYEDLMRS	gi|13124807|sp|P15498|	[AEGDEIYEDLMRS|Y|17
5099	DEESEDYQNSASI	gi|74752543|sp|Q9GZY6	[DEESEDYQNSASI|Y|19
5100	EDGEPDYVNGEVA	gi|74752543|sp|Q9GZY6	[EDGEPDYVNGEVA|Y|2
5101	EPPDHQYYNDFPG	gi|17380299|sp|P29353|	[EPPDHQYYNDFPG|Y|3
5102	HAPAEMYDIMKTC	gi|125472|sp|P10721|KIT	[HAPAEMYDIMKTC|Y|9
5103	WKKYDIYEKQTKE	gi|2494718|sp|P78552|I1	NA
5104	ERRCKHYVELLVA	gi|62901470|sp|Q9HBA0	[ERRCKHYVELLVA|Y|25
5105	PTSAPVYQQPQQQ	gi|3122342|sp|Q14847|L	[PTSAPVYQQPQQQ|Y|1
5106	RVDTPHYPRWITK	gi|547803|sp|Q05655|KP	[RVDTPHYPRWITK|Y|5
5107	ALEVAEYLTPVLK	gi|61212142|sp|Q9NT62|	[ALEVAEYLTPVLK|Y|18|
5108	GAMAATYSALNRN	gi|1730070|sp|P51812|K	[GAMAATYSALNRN|Y|7
5109	LDPMHNYVNTENV	gi|71152057|sp|Q8WU2	[LDPMHNYVNTENV|Y|3
5110	SFNNPAYYVLEGV	gi|119595261|gb|EAW74	[SFNNPAYYVLEGV|Y|9
5111	SLISSDYELLSDP	gi|50403745|sp|P52333|	[SLISSDYELLSDP|Y|785
5112	EETNNDYETADGG	gi|399478|sp|P31995|FC	[EETNNDYETADGG|Y|2
5113	GPTRKHYQPYAPP	gi|115973|sp|P10747|CD	[GPTRKHYQPYAPP|Y|2
5114	MAESITYAAVAR	gi|74736490|sp|Q6GTX8	[MAESITYAAVARH|Y|28
5115	FASDPKYATPQVI	gi|37999491|sp|Q07912|	[FASDPKYATPQVI|Y|82
5116	GVGGTTYEISV	gi|57015419|sp|Q9ULC8	NA
5117	KDTSTEYSEVRTQ	gi|116241290|sp|P20138	[KDTSTEYSEVRTQ|Y|35
5118	LNQSSGYRYGTDP	gi|125370|sp|P06241|FY	[LNQSSGYRYGTDP|Y|2
5119	PTLVIAYLMMRQK	gi|1718191|sp|P51452|D	[PTLVIAYLMMRQK|Y|13
5120	RLLHSDYMNMTPR	gi|115973|sp|P10747|CD	[RLLHSDYMNMTPR|Y|1
5121	SNESVDYRATFPE	gi|125484|sp|P08581|ME	[SNESVDYRATFPE|Y|1
5122	VKAGESYTHIQYL	gi|74751027|sp|Q8N5H7	NA
5123	ASVNPEYFSAADV	gi|124240|sp|P08069|IG	[ASVNPEYFSAADV|Y|9
5124	FLRRGEYPDYQQW	gi|117461|sp|P07316|CR	[FLRRGEYPDYQQW|Y|
5125	NPATDDYAVPPPR	gi|17366642|sp|Q99704|	[NPATDDYAVPPPR|Y|4
5126	RARVANYQRDGPM	gi|115702|sp|P04040|CA	[RARVANYQRDGPM|Y|
5127	Triple Flaq	contol_spot	NA
5128	pY	contol_spot	NA
5129	pY	contol_spot	NA
5130	Triple Flaq	contol_spot	NA
5131	pY	contol_spot	NA
5132	pY	contol_spot	NA
5133	EEEGENYQKGERG	gi|134461|sp|P05060|SC	NA
5134	IGNHASYYKDALR	gi|20978558|sp|Q9UNM	NA
5135	YDNLEDYHSLPQH	gi|131573277|gb|ABO33	NA
5136	ATREPPYRVPRDD	gi|12643409|sp|P43243|	NA
5137	EAAYDPYAYPSDY	gi|23396631|sp|Q9Y262|	NA
5138	TDEYQLYEDIGKG	gi|12643413|sp|Q13554|	NA
5139	LLPNHSYVFRVRA	gi|13638154|sp|P16144|	NA
5140	KPGMFGYGRVPFA	gi|118573317|sp|Q6UY1	NA
5141	SGQNNRYSPKKEK	gi|50403806|sp|Q9ULJ8|	NA
5142	PKQTSAYNISNSS	gi|93140549|sp|Q9UIW2	NA
5143	RGPPRNYQQNYQN	gi|54040031|sp|P67809|	NA
5144	GPTPASYTTASTP	gi|20981729|sp|Q15654|	NA
5145	QMPEPRYVVSMGS	gi|90110040|sp|O75251|	NA
5146	FQKFSAYQKSEQQ	gi|23822155|sp|Q9BX26|	NA
5147	ADGEDAYAMKRDL	gi|728880|sp|P41227|AR	NA

5148	KAFSRGYQLSQHQ	gi|34925661|sp|Q9NQX6	NA
5149	LQKLPFYDLLDEL	gi|20138891|sp|O75925|	NA
5150	GRNQGGYDRYSGG	gi|1710620|sp|P98179|R	NA
5151	PEEDEEYYRKQLS	gi|85700443|sp|Q07157|	NA
5152	GLKLGIYADVGNK	gi|113499|sp|P06280|AG	NA
5153	QADSCPYGTMYLS	gi|68565585|sp|Q6UUV9	NA
5154	IVHLINYQDDAEL	gi|130257|sp|P14923|PL	NA
5155	TSTRQTYFLPVIG	gi|20532406|sp|P17980|	NA
5156	SVSPTRYELIVDK	gi|90110033|sp|Q16363|	NA
5157	HPEIVGYSVPGRN	gi|56404535|sp|Q6XZF7|	NA
5158	VYENKKYLYLVLE	gi|116241272|sp|Q8IWQ	NA
5159	AQGEGPYSSLVSC	gi|13638154|sp|P16144|	[AQGEGPYSSLVSC|Y|1
5160	NRRFSSYSQMENW	gi|20138951|sp|Q13835|	NA
5161	QSWFDEYNDFDFG	gi|1706135|sp|P54108|	NA
5162	EDEDEEYEYMNRR	gi|119534|sp|P21860|ER	NA
5163	QKHPDIYAVPIKT	gi|13634076|sp|Q9UDY2	[QKHPDIYAVPIKT|Y|111
5164	LQHQQLYYSQDDS	gi|20139104|sp|Q99569|	NA
5165	APARLEYYENARK	gi|4504733|ref|NP_0035	NA
5166	KVYLTGYNFTLAD	gi|17378996|sp|O43324|	NA
5167	IKGERGYTGSAGE	gi|143811380|sp|Q07092	NA
5168	HGSEEAYIDPIAM	gi|74752543|sp|Q9GZY6	NA
5169	HNFRPCYLRVCKV	gi|18206225|sp|O94761|	NA
5170	PLTEASYVNLPTI	gi|125969|sp|P08865|RS	[PLTEASYVNLPTI|Y|139
5171	FLRFDHYLNPYYK	gi|3929376|sp|Q12872|S	NA
5172	LSNSPNYEEITKW	gi|22096235|sp|Q9UBB9	NA
5173	YLTESGYVNLQRV	gi|30173484|sp|Q9H0D6	NA
5174	ISPDDKYIYVADI	gi|6174935|sp|Q15165|	NA
5175	VLGRDLYPNLAEE	gi|117424|sp|P23508|CR	NA
5176	RRGERVYVNISHP	gi|549088|sp|Q06643|TN	NA
5177	SLKLSEYPNVEEL	gi|34395525|sp|Q9NZN5	NA
5178	EYLSSIYEEIEGK	gi|146329988|sp|Q9Y6D	NA
5179	TQEQEVYQVPPSV	gi|8134360|sp|Q14511|C	NA
5180	SDGMFKYEEIVLE	gi|2497506|sp|Q92796|D	NA
5181	GDVLGFYINLPED	gi|32141382|sp|Q9UBL3|	NA
5182	SKKHHPYQPDPKM	gi|12585199|sp|O00257|	NA
5183	STLEEVYGSVAKV	gi|116241339|sp|Q07864	NA
5184	FSPPHPYINPYMD	gi|116242494|sp|P10071	NA
5185	MSSLYYANALFS	gi|123255|sp|P09629|HX	NA
5186	QSVPVVYTAVRSP	gi|91771555|sp|Q9Y4X4|	NA
5187	HTSFRGYIIPKDT	gi|117205|sp|P20813|CP	NA
5188	RDRATFYLNVLQQ	gi|13124090|sp|Q9UBF2	NA
5189	AYMLEVYGSLPAF	gi|12643412|sp|Q01650|	NA
5190	VPSGSPYPNPSFL	gi|6093462|sp|O75694|N	NA
5191	FSITASYANLLIG	gi|6226404|sp|O94956|	NA
5192	MEKVKVYLRVRPL	gi|6225915|sp|O95235|K	NA
5193	AIESLNYSVYTTK	gi|549081|sp|P35590|TIE	NA
5194	RVKCVRYWPDDTE	gi|117949771|sp|O14522	NA
5195	LPPPPEYELAPSK	gi|55977848|sp|Q12849|	NA
5196	GCVAQLYISLALG	gi|38372794|sp|Q8NGZ4	NA
5197	GLSMGNYIGLINR	gi|125527|sp|P19525|E2	[GLSMGNYIGLINR|Y|10
5198	LFTIARYMELRGY	gi|41018482|sp|Q9P217|	NA
5199	H4:17	contol_spot	NA

5200	H8:17	contol_spot	NA
5201	QVDETKYPSTCNV	gi|18202928|sp|Q9GZN6	NA
5202	DGEDEYYKSLSPV	gi|126302572|sp|Q8WX	NA
5203	FRENLIYTYIGPV	gi|13431674|sp|O00159|	NA
5204	SCSTPLYDQGGPV	gi|1346900|sp|P28562|D	NA
5205	AEAEKQYEDSCRV	gi|12643392|sp|O75110|	NA
5206	GFYRTTYTENGRV	gi|125987789|sp|Q0707	NA
5207	VVKSDDYALPAYV	gi|176657|gb|AAA35408.	NA
5208	CPVKPSYLNILED	gi|450277|gb|AAA60120.	NA
5209	LDEEVEYDMDEED	gi|116241271|sp|P55201	NA
5210	ERENTSYDVTTLQ	gi|126723390|ref|NP_59	NA
5211	ESEDPNYYQYNMQ	gi|45709285|gb|AAH678	NA
5212	FERDEEYLMDCDW	gi|148806872|ref|NP_05	NA
5213	PPDSPGYFDGHVW	gi|50401180|sp|Q9NWW	NA
5214	VFIDEAYVEVAAY	gi|145559533|sp|Q6P1X	NA
5215	FADDLGYGDLGCY	gi|114221|sp|P15289|AR	NA
5216	HVDFNSYVQSPAY	gi|33516903|sp|Q9NP62|	NA
5217	PMMNSSYHSNPAY	gi|3024154|sp|Q92794|M	NA
5218	YIEEVDYLGKKAY	gi|126031792|gb|AAI314	NA
5219	DPANVDYEDLFLY	gi|74732160|sp|Q96JZ2|	NA
5220	IAWEETYRTIGLY	gi|20140763|sp|Q9BZW	NA
5221	RANKSDYCNLPLY	gi|73620825|sp|Q8TD84|	NA
5222	TNESGYYLDISLY	gi|118601083|sp|Q1308	NA
5223	FGRSGSYNDFGNY	gi|133254|sp|P09651|RO	NA
5224	SRYMELYTHVYNY	gi|19863257|sp|Q13616|	NA
5225	WDFNDKYHSQWCQ	gi|81901863|sp|Q8VCI0|	NA
5226	HFVEATYKNPELD	gi|150421594|sp|Q8IWA	NA
5227	VSRIPDYLWMGLD	gi|1352387|sp|P48449|E	NA
5228	CYLKDAYDNVTLD	gi|119364639|sp|O4327	NA
5229	LKIKPEYVSGLMD	gi|88911290|sp|P49917|	NA
5230	SDELPAYVGINEA	gi|74734682|sp|Q9NWY	NA
5231	RRSKDMYHASKSA	gi|147744602|sp|Q8N5A	NA
5232	LFRLEPYADPYYD	gi|28273142|dbj|BAC569	NA
5233	REVEVEYSTVASP	gi|126302534|sp|Q9UGN	NA
5234	GEYADEYVYTRAE	gi|94730407|sp|Q9QYX7	NA
5235	CIPCEPYEYLADE	gi|76803803|sp|Q14832|	NA
5236	HWSVESYSDFWAE	gi|119618879|gb|EAW98	NA
5237	VIFWSLYVDGEWG	gi|73620825|sp|Q8TD84|	NA
5238	GLFKGTYGSHGLE	gi|146345419|sp|Q5XUX	NA
5239	DWDDDKYYGTSLE	gi|123829|sp|P04438|HV	NA
5240	DPANCDYVIVSGA	gi|134037158|sp|P13994	NA
5241	SKSCCIYVNNSGA	gi|134048550|gb|AAI040	NA
5242	EEGEVIYTDWKME	gi|74759634|sp|Q8IWG1	NA
5243	<<Marker>>	contol_spot	NA
5244	VCEPEDYVVVSTE	gi|23831360|sp|P31939|	NA
5245	GKEDDIYLMVIWE	gi|119590507|gb|EAW70	NA
5246	SHVDDEYRWAGVE	gi|73621060|sp|Q96G21|	NA
5247	DGKNGFYINGGYE	gi|119598482|gb|EAW78	NA
5248	HHEAEYYVAAVYE	gi|1168695|sp|P43251|B	NA
5249	PIGEFTYKSSCAF	gi|126180|sp|P16581|LY	NA
5250	AREKEHYCLADLA	gi|20140092|sp|Q92552|	NA
5251	GTCGPRYSNLTKA	gi|6226213|sp|O75949|T	NA

5252	LDEEGLYCNSCLA	gi|34098678|sp|Q96NE9|	NA
5253	MKTYDTYVGIGWL	gi|85681942|sp|O95302|	NA
5254	EFYESAYFIVLIP	gi|34098465|sp|Q86UP2|	NA
5255	IHDETSYKGKKIP	gi|14424438|sp|P51587|	NA
5256	ILDSDNYSPIPVT	gi|24418685|sp|Q9Y2D4|	NA
5257	VYESFLYKQVYWT	gi|119605860|gb|EAW85	NA
5258	FKRELLYEDVFAV	gi|145566943|sp|O43147	NA
5259	HNAMDNYECNLYT	gi|7657265|ref|NP_0561	NA
5260	PVEVDKYGNIDAV	gi|121082|sp|P23378|GC	NA
5261	RRDCKDYVSIFVC	gi|17380347|sp|Q9P2S5|	NA
5262	AESSFKYESGLFV	gi|71152412|sp|Q96LT7|	NA
5263	KMRAYDYMCMGFV	gi|119592606|gb|EAW72	NA
5264	<<Marker>>	contol_spot	NA
5265	SFCANVYVDTGFV	gi|1171882|sp|P46721|S	NA
5266	WTDGSHYDNTGFV	gi|50401129|sp|Q96NW7	NA
5267	EDEFDAYIIVSFV	gi|116242787|sp|Q1539	NA
5268	KGQETYYTAAQFV	gi|119599761|gb|EAW79	NA
5269	EIGEGAYGKVFKA	gi|266423|sp|Q00534|CD	[EIGEGAYGKVFKA|Y|24
5270	NRFSGWYDADLSP	gi|130348|sp|P18669|PG	[NRFSGWYDADLSP|Y|2
5271	PARNLTYFGVVHG	gi|74761551|sp|Q9H977|	[PARNLTYFGVVHG|Y|3
5272	STGFQPYCLVVRK	gi|13124058|sp|P57764|	[STGFQPYCLVVRK|Y|3
5273	AADSAPYDWFGDF	gi|153945761|ref|NP_05	[AADSAPYDWFGDF|Y|3
5274	ERTINLYPLTNYT	gi|74735411|sp|O43809|	NA
5275	ISYEGQYIWNMLF	gi|24212102|sp|P59045|	NA
5276	SPEELTYLIEALF	gi|124894|sp|P10745|IR	NA
5277	EMVESGYVCEGDH	gi|41688795|sp|Q9H4A3|	NA
5278	AENEKQYVVEPNF	gi|74739159|sp|Q6UXI7|	NA
5279	FLSCQDYGDCEDM	gi|113418117|ref|XP_00	NA
5280	LDHKTLYYDTDPF	gi|30923328|sp|Q92993|	NA
5281	RPCAEDYFNFMGH	gi|74756634|sp|Q5THR3	NA
5282	IHDSDLYAESVYL	gi|129874|sp|P02775|SC	NA
5283	AQSRNSYVEAEIH	gi|90185285|sp|Q9Y3M8	NA
5284	LLAFEHYVNHRKH	gi|135705|sp|P10827|TH	NA
5285	<<Marker>>	contol_spot	NA
5286	IIFHENYSSPGLH	gi|119625974|gb|EAX05	NA
5287	PTYKDDYRAWDLH	gi|119619491|gb|EAW99	NA
5288	GHSWDKYGFTSVP	gi|27151703|sp|Q9UPU3	NA
5289	SIMDTIYICITVP	gi|38258180|sp|Q8NGX2	NA
5290	SHCCSRYLCMGAM	gi|47117811|sp|O43609|	NA
5291	TKTEEPYFAPCII	gi|56204404|emb|CAI20	NA
5292	GKRKVQYESSEPA	gi|116241277|sp|P19022	NA
5293	CDEVSKYEKLAKI	gi|68067660|sp|P50750|	NA
5294	EIREKYYYAVYDM	gi|126366|sp|P07942|LA	NA
5295	EKSFPTYKDLDFM	gi|78099088|sp|O60331|	NA
5296	INETINYEDPCAK	gi|90110720|sp|O60518|	NA
5297	NDEEMSYDNNPYI	gi|85687376|sp|P20908|	NA
5298	GQPDFSYKRSNCK	gi|61216828|sp|Q96HF1|	NA
5299	EVESTEYVNRQFM	gi|2498733|sp|Q14444|C	NA
5300	HLMNPEYVPKPCC	gi|115076|sp|P22004|BM	NA
5301	SWHNIDYIDNTCC	gi|119598285|gb|EAW77	NA
5302	TTYNTLYEILTEQ	gi|32171483|sp|Q8NFP9	NA
5303	RGNSDGYIIPINK	gi|46576868|sp|O95490|	NA

5304	CGEGFSYVKIPNK	gi|57013082|sp|Q8IZX4|	NA
5305	AGEPGKYDSMARK	gi|68840003|sp|Q14993|	NA
5306	<<Marker>>	contol_spot	NA
5307	GKAMELYHTAPFL	gi|119606705|gb|EAW86	NA
5308	TPRDLDYSRVSFM	gi|119579320|gb|EAW58	NA
5309	ATPMDAYLRKLGL	gi|118572680|sp|Q01804	NA
5310	ELFNEKYGEALGL	gi|21263630|sp|Q9UHL9	NA
5311	GSCNPGYVLAQGL	gi|85700961|sp|Q9C0B6|	NA
5312	YEIEFIYAISPGL	gi|74705746|sp|O60502|	NA
5313	GGYSFKYETVPNL	gi|124274|sp|P05111|IN	NA
5314	HHHSKGYIDINPL	gi|119580040|gb|EAW59	NA
5315	FESFVDYVAVEQL	gi|2501460|sp|Q93009|U	NA
5316	ERNNLSYDCIGRL	gi|1708239|sp|Q01581|H	NA
5317	SPYPEEYARLGRL	gi|68565854|sp|O95251|	NA
5318	RKWREQYSDPTRL	gi|1731427|sp|Q03172|Z	NA
5319	DAEDVIYVNWLNM	gi|20532389|sp|Q9NY33|	NA
5320	DIDETEYHADGGK	gi|119533|sp|P04626|ER	[DIDETEYHADGGK|Y|87
5321	NSSDPTYTSSLGG	gi|19860819|sp|P54760|	NA
5322	PAFDNLYYWDQDP	gi|119533|sp|P04626|ER	[PAFDNLYYWDQDP|Y|1
5323	AVLMERYRLDNDL	gi|70907264|gb|AAZ152	NA
5324	PKSPGEYVNIEFG	gi|547738|sp|P35568|IR	[PKSPGEYVNIEFG|Y|89
5325	VYSTDYYRLFNPS	gi|134035335|sp|Q1628	NA
5326	YEDENLYEGLNLD	gi|547896|sp|P11912|CD	[YEDENLYEGLNLD|Y|1
5327	<<Marker>>	contol_spot	NA
5328	YIDPFTYEDPNEA	gi|119615430|gb|EAW95	[YIDPFTYEDPNEA|Y|61
5329	YVDLQAYEDPAQG	gi|47117832|sp|P21709|	NA
5330	YVLDDEYTSSVGS	gi|547759|sp|Q06187|BT	[YVLDDEYTSSVGS|Y|5
5331	DIYRASYYRRGDR	gi|143811416|sp|P29376	NA
5332	IMHDSNYVSKGST	gi|129892|sp|P16234|PG	NA
5333	APESLAYNKFSIK	gi|85681908|sp|P00519|	NA
5334	IYKNPDYVRKGDT	gi|143811474|sp|P17948	NA
5335	IYSGDYYRQGRIA	gi|10720097|sp|Q12866|	[IYSGDYYRQGRIA|Y|75
5336	KIGEGTYGTVFKA	gi|4033704|sp|Q00535|C	[KIGEGTYGTVFKA|Y|15
5337	KLWLKPYVDLQAY	gi|47117832|sp|P21709|	NA
5338	SGDRSGYSSPGSP	gi|13124806|sp|P10636|	NA
5339	SDSTNEYMDMKPG	gi|125472|sp|P10721|KIT	[SDSTNEYMDMKPG|Y|
5340	LTSNQEYLDLSMP	gi|120046|sp|P11362|FG	[LTSNQEYLDLSMP|Y|76
5341	TSTEPQYQPGENL	gi|125711|sp|P12931|SR	[TSTEPQYQPGENL|Y|5
5342	DEPEGDYEEVLEP	gi|123557|sp|P14317|HC	[DEPEGDYEEVLEP|Y|3
5343	YDVSRMYVDPSEI	gi|143811440|sp|P16885	[YDVSRMYVDPSEI|Y|75
5344	TLNEDSYKDSTLI	gi|1345593|sp|Q04917|1	NA
5345	KMQQNGYENPTYK	gi|112927|sp|P05067|A4_	[KMQQNGYENPTYK|Y|
5346	LLNWIGYVNSGFN	gi|114765|sp|P07550|AD	NA
5347	TNTEGGYTCMCAGXX	gi|119226|sp|P01133|EG	NA
5348	<<Marker>>	contol_spot	NA
5349	CIVENEYGSINHT	gi|120046|sp|P11362|FG	NA
5350	GPDGTPYVTVLKT	gi|120050|sp|P22607|FG	NA
5351	NYDGKDYDPVAAR	gi|20138589|sp|Q15691|	[NYDGKDYDPVAAR|Y|1
5352	LINKKCYEMASHL	gi|130979|sp|P07737|PR	[LINKKCYEMASHL|Y|12
5353	IKWSNIYEDNGDD	gi|74751065|sp|Q8N6N3	[IKWSNIYEDNGDD|Y|13
5354	ELQANCYEEVKDR	gi|116848|sp|P23528|CO	[ELQANCYEEVKDR|Y|1
5355	RVITNQYNNPAGL	gi|20178312|sp|O00151|	[RVITNQYNNPAGL|Y|14

5356	CSVCPDYDLCSVC	gi|74735628|sp|Q13501|	[CSVCPDYDLCSVC|Y|1
5357	VERADGYEPPVQE	gi|47117764|sp|P61247|	[VERADGYEPPVQE|Y|2
5358	LYPNTPYAYTFWT	gi|113984|sp|P27695|AP	NA
5359	YSNTRAYYFVKFK	gi|68565218|sp|Q8N884|	NA
5360	HSGEKPYGCVECG	gi|10720410|sp|P17028|	NA
5361	FKQAEEYLSFAFE	gi|85681034|sp|Q5JVF3|	NA
5362	DIRKDLYANTVLS	gi|89276723|gb|ABD665	[DIRKDLYANTVLS|Y|29
5363	DTYLGKYWAIKLA	gi|9988062|sp|P50990|T	NA
5364	TATEPQYQPGENL	gi|125870|sp|P07947|YE	[TATEPQYQPGENL|Y|5
5365	YMEDSTYYKASKG	gi|3183518|sp|Q05397|F	[YMEDSTYYKASKG|Y|6
5366	APPPVFYNKPPEI	gi|2498313|sp|Q16643|D	[APPPVFYNKPPEI|Y|62
5367	RTTDGVYEGVAIG	gi|116241237|sp|P53396	[RTTDGVYEGVAIG|Y|6
5368	KDTETVYSEVRKA	gi|129747|sp|P16284|PE	[KDTETVYSEVRKA|Y|71
5369	<<Marker>>	contol_spot	NA
5370	KLVDGCYSFWQAG	gi|1346696|sp|P49356|P	[KLVDGCYSFWQAG|Y|
5371	GAFGEVYEGQVSG	gi|146328566|sp|Q9UM7	[GAFGEVYEGQVSG|Y|1
5372	SGGEDGYVRIHYF	gi|2494895|sp|Q13347|IF	NA
5373	EVPSDQYYWAPLA	gi|14916543|sp|O60716|	NA
5374	PLYWDLYEHAQQQ	gi|17366642|sp|Q99704|	[PLYWDLYEHAQQQ|Y|
5375	DDSDDSYFTSSSS	gi|21263420|sp|Q9NP61|	[DDSDDSYFTSSSS|Y|3
5376	SSDKPLYDQLLQH	gi|134937|sp|P13574|ST	NA
5377	DEEDENYTRGGIR	gi|731873|sp|P40466|FK	NA
5378	LNFNDNYTTILQH	gi|729290|sp|P21657|DA	NA
5379	ILNMGLYINPKNL	gi|1173439|sp|P46954|S	NA
5380	PGSDDCYCTPKIL	gi|1352985|sp|P47043|Z	NA
5381	CYKEELYQCRNSD	gi|1177049|sp|P46974|Z	NA
5382	NNISVKYVSPGSV	gi|1169823|sp|P04386|G	NA
5383	STCSTDYELSKRF	gi|1169136|sp|P41817|C	NA
5384	KPIMTPYVSYPYP	gi|41016991|sp|Q03063|	NA
5385	GKFEDVYQLTSEL	gi|30315972|sp|O08605|	NA
5386	HSEPPVYANLSNF	gi|135298|sp|P05412|JU	[HSEPPVYANLSNF|Y|1
5387	YVEKCKYMDSKMK	gi|1171955|sp|P42338|P	NA
5388	DKVEFLYCDLASM	gi|32469744|sp|Q8N5I4|	NA
5389	GLYKDRYAYRDSM	gi|20140806|sp|Q9HBG6	NA
5390	<<Marker>>	contol_spot	NA
5391	NEECTSYSTINPM	gi|40067493|gb|AAR385	NA
5392	PAAEDNYGYDACA	gi|25008854|sp|Q99567|	NA
5393	WDWKDPYEVGHSM	gi|62286903|sp|O15033|	NA
5394	GGKKPKYPPNKVM	gi|85542094|sp|Q5MNZ6	NA
5395	ETADGKYAQKLFN	gi|13626094|sp|Q9UGM1	NA
5396	IGPEEDYDPGYFN	gi|34395516|sp|O15085|	NA
5397	KVNKDPYVADMEN	gi|116241243|sp|Q1302	NA
5398	NCKKLKYIDAQEN	gi|120953300|ref|NP_00	NA
5399	SYRNSSYENAREN	gi|68566212|sp|Q8NAP3	NA
5400	FAEEPIYCYTPHN	gi|20139072|sp|Q96RD6	NA
5401	NLYAGDYYRVQGR	gi|729008|sp|Q08345|D	NA
5402	IKDRDKYIPKQLN	gi|119120884|ref|NP_00	NA
5403	NWPEEHYATVELN	gi|148675937|gb|EDL07	NA
5404	SPSMLDYDTENLN	gi|74723323|sp|Q7Z460|	NA
5405	YVAPPKYKSSLLN	gi|74762494|sp|Q8IYA7|	NA
5406	HTGEEPYEYKGMN	gi|119604454|gb|EAW84	NA
5407	TWFPESYVIYPTN	gi|47117358|sp|Q8NG68	NA

5408	AASEVHYSTRNPQ	gi|119591472|gb|EAW71	NA
5409	FSAKPLYTALPPQ	gi|13124503|sp|O60315|	NA
5410	IINKEGYLEDSPQ	gi|23397010|sp|Q9NR11	NA
5411	NWYNDTYPLSPPQ	gi|66774052|sp|Q8WVQ	NA
5412	YRNEIAYLNKLQQ	gi|464971|sp|P33981|TT	NA
5413	IHKMDGYSCDGVQ	gi|14423634|sp|Q9P0K1|	NA
5414	PACDPGYQPTPGG	gi|119577388|gb|EAW56	NA
5415	PCKDDEYCMEEGG	gi|48428570|sp|O75443|	NA
5416	DLIEKDYADREAR	gi|13959371|sp|Q9H479|	NA
5417	IMRECWYANGAAR	gi|547777|sp|P36897|TG	NA
5418	LYREAVYNSVAAR	gi|119569633|gb|EAW49	NA
5419	HGEWAKYSNFDVA	gi|124174|sp|P22304|ID	NA
5420	SSSPGTYVGPPGG	gi|27734581|sp|Q9BWW	NA
5421	VYDDETYMMQDVA	gi|68052029|sp|Q15723|	NA
5422	DEELPDYIMVMVA	gi|50233812|ref|NP_997	NA
5423	MNNIENYVDSKVA	gi|12230074|sp|Q14314|	NA
5424	AARETSYQWKAER	gi|68067946|sp|O75182|	NA
5425	EKFSGAYVNNRIR	gi|29337239|sp|Q9P241|	NA
5426	HAPDNKYKMDGIR	gi|17433288|sp|Q9Y264|	NA
5427	LAADSAYDQKNIR	gi|8039810|sp|Q14188|T	NA
5428	EECNKDYGSSQTL	gi|119605325|gb|EAW84	NA
5429	CSHENPYLCSNEC	gi|34922606|sp|Q96CW	NA
5430	EGRCGYYVEKKKR	gi|108885172|sp|Q9NUP	NA
5431	LRELERYVTSCLR	gi|20141192|sp|O60885|	NA
5432	SRTASKYTDRALR	gi|27805463|sp|Q96DF8|	NA
5433	FFSGDKYYRVNLR	gi|139653|sp|P04004|VT	NA
5434	YTFDGKYEAKQLR	gi|94730583|sp|Q9NSE4	NA
5435	MQKGIDYVKNKMR	gi|25014054|sp|Q9NY46|	NA
5436	YQEKIRYARVYLR	gi|110278938|sp|Q7Z47	NA
5437	VDCMEVYEYPGYR	gi|1717814|sp|P49746|T	NA
5438	DNDSWDYTKPYLG	gi|62286941|sp|Q8WVV	NA
5439	ERSGECYHQVAMG	gi|119587445|gb|EAW67	NA
5440	IFESCGYEANYLG	gi|62511243|sp|Q92625|	NA
5441	MGNEPAYVWLWLG	gi|3183202|sp|O14975|S	NA
5442	SFFPELYFNVDNG	gi|47606646|sp|P61421|	NA
5443	PRFDTEYRSRGCS	gi|61211870|sp|Q96L58|	NA
5444	VMQEPGYIMGICS	gi|17380293|sp|Q9UBS8	NA
5445	DVPHDPYVKISDS	gi|74732954|sp|Q9BS16|	NA
5446	GTFFDKYSAAPDS	gi|94730396|sp|Q10571|	NA
5447	PKPQELYVCFHDS	gi|73621379|sp|Q9ULD6	NA
5448	ARPAEHYSRMKES	gi|50949921|emb|CAH1	NA
5449	AYQNTIYLNLWDH	gi|143811362|sp|P15144	NA
5450	EDNVKSYMDMQRR	gi|109940027|sp|Q1307	NA
5451	QGEDQYYLRVTTV	gi|116533|sp|P10909|CL	NA
5452	TLPPCIYMAPMNQ	gi|13432121|sp|P55286|	NA
5453	DVRAAVYQPQPHP	gi|2506872|sp|P02751|F	NA
5454	EENWSFYPNAVRT	gi|20139420|sp|P78509|	NA
5455	LKMKEKYLNVSAC	gi|14916977|sp|O75343|	NA
5456	MVIPDLYLNAGGV	gi|118541|sp|P00367|DH	NA
5457	LSEDCLYLNIYTP	gi|119576|sp|P23141|ES	NA
5458	GECSIDYVEMAVN	gi|59802911|sp|O75891|	NA
5459	EPPPPGYENVSDI	gi|548615|sp|Q04609|FO	NA

5460	AKAWELYGSPNAL	gi|1346191|sp|P48637|G	NA
5461	VCEEMTYEEIQEH	gi|2507178|sp|P16118|F	NA
5462	PAPPEEYVPMVKE	gi|3183518|sp|Q05397|F	NA
5463	LGTEELYGYLKKY	gi|125266|sp|P19784|CS	[LGTEELYGYLKKY|Y|25
5464	ELLTELYGKVGEI	gi|110282976|sp|P46020	NA
5465	NTVWVDYPNIVRV	gi|8247933|sp|P30613|K	NA
5466	DALQHPYINVWYD	gi|2507196|sp|P53779|M	NA
5467	RTGSISYINIIMP	gi|33860175|sp|Q99705|	NA
5468	MFTPKMYIIIAKP	gi|62297775|sp|Q13255|	NA
5469	GKEYLFYLNVCGE	gi|60416403|sp|P11717|	NA
5470	AVITVMYTAVTPM	gi|14423819|sp|Q9P1Q5	NA
5471	LVRFLFYANLHGS	gi|2495018|sp|Q15077|P	NA
5472	DTSSVLYTAVQPN	gi|129890|sp|P09619|PG	[DTSSVLYTAVQPN|Y|1
5473	PREGPPYEGKKNC	gi|152032205|sp|Q8N9Y	NA
5474	FKFEENYTSQNVL	gi|113422894|ref|XP_00	NA
5475	LQRKEAYIFYPPG	gi|119599990|gb|EAW79	NA
5476	PNDDRDYCDCDPG	gi|118572677|sp|P46531	NA
5477	AGSNTKYRRLCPC	gi|152040009|sp|Q3V5L	NA
5478	ELRSTKYISDGQC	gi|62287504|sp|Q6X4U4|	NA
5479	LGQEERYELLNVL	gi|8134331|sp|Q9Y2Q0|	NA
5480	RMDDSSYTSKLLS	gi|122065126|sp|Q9Y2D	NA
5481	VNECEIYSGTPLS	gi|88911282|sp|O60494|	NA
5482	IIWATSYEDFYLS	gi|73920246|sp|O00750|	NA
5483	VVKDPFYVIESLS	gi|23396800|sp|Q9NTG1	NA
5484	ESAPDSYIGIGNS	gi|74731046|sp|Q969I6|	NA
5485	FYGEDFYCEIPRS	gi|13959562|sp|Q14644|	NA
5486	SVSNVEYPDMPRS	gi|74756617|sp|Q5THJ4|	NA
5487	IMKRPKYCSSDSS	gi|73920151|sp|Q6ZT98|	NA
5488	ETECDVYMLPKSS	gi|13937007|gb|AAK500	NA
5489	TLPEHKYPSLHSS	gi|2506535|sp|Q01851|P	NA
5490	LQSELQYRRGATS	gi|115502505|sp|Q86VF	NA
5491	FLRQPIYMEVRVL	gi|466206|sp|Q05996|ZP	NA
5492	LGSEDYYSHERCT	gi|114223|sp|P15848|AR	NA
5493	TALESDYAGPGDT	gi|51316104|sp|Q9NQC7	NA
5494	APQEGSYLDFWDT	gi|5902808|ref|NP_0061	NA
5495	SFSTDVYIVMWDT	gi|119585869|gb|EAW65	NA
5496	FGKEHFYVIDGFT	gi|109896161|sp|Q8IZQ1	NA
5497	VVNLINYQDDAEL	gi|461854|sp|P35222|CT	[VVNLINYQDDAEL|Y|14
5498	KKAGNLYDISEDN	gi|14548162|sp|Q13224|	[KKAGNLYDISEDN|Y|12
5499	DYHNPGYLVVLPD	gi|14194891|sp|O43561|	NA
5500	GEDDGDYESPNEE	gi|10720065|sp|Q13094|	[GEDDGDYESPNEE|Y|1
5501	NCSEEMYRLMLQC	gi|547807|sp|P07949|RE	[NCSEEMYRLMLQC|Y|9
5502	PTIEDSYTKICSV	gi|133486|sp|P10301|RR	[PTIEDSYTKICSV|Y|66|
5503	KAEFAEYASVDRN	gi|84029384|sp|Q9NWQ	[KAEFAEYASVDRN|Y|2
5504	RPDSPVYANLQEL	gi|47117238|sp|Q8IWW	[RPDSPVYANLQEL|Y|2
5505	SNQEEAYVTMSSF	gi|124351|sp|P16871|IL7	[SNQEEAYVTMSSF|Y|4
5506	SYKVILYELENFQ	gi|13124690|sp|P26998|	[SYKVILYELENFQ|Y|29|
5507	VVDSGVYAVPPPA	gi|8134339|sp|P56945|B	[VVDSGVYAVPPPA|Y|4
5508	KLGGGQYGEVYEG	gi|85681908|sp|P00519|	[KLGGGQYGEVYEG|Y|
5509	TIICLCYLFIIIK	gi|401126|sp|P30874|SS	[TIICLCYLFIIIK|Y|228|P3
5510	MMDAEEYLVPQAF	gi|3913590|sp|Q15303|E	NA
5511	LVSIDRYLALVKT	gi|2506481|sp|P30411|B	[LVSIDRYLALVKT|Y|161

5512	ANGEAVYCKFHYK	gi|115702|sp|P04040|CA	[ANGEAVYCKFHYK|Y|2
5513	DTGSRYYKEIPLS	gi|2499575|sp|Q15139|K	[DTGSRYYKEIPLS|Y|46
5514	HPDYEEYINLEGT	gi|46397678|sp|Q13017|	[HPDYEEYINLEGT|Y|30
5515	LGNGVLYASVNPE	gi|124240|sp|P08069|IG	[LGNGVLYASVNPE|Y|9
5516	NSRLSAYPALEGV	gi|116024|sp|P06127|CD	[NSRLSAYPALEGV|Y|4
5517	RGEYPDYQQWMGL	gi|117461|sp|P07316|CR	[RGEYPDYQQWMGL|Y|
5518	TGHGYVYEYPSRY	gi|8134360|sp|Q14511|C	[TGHGYVYEYPSRY|Y|1
5519	CANPILYAFLSDN	gi|401126|sp|P30874|SS	[CANPILYAFLSDN|Y|31
5520	ECQRYVYSILCCK	gi|20178318|sp|P25116|	[ECQRYVYSILCCK|Y|38
5521	YVNTTLYEKFTYA	gi|464868|sp|Q02763|TI	[YVNTTLYEKFTYA|Y|11
5522	VVDADEYLIPQQG	gi|2811086|sp|P00533|E	[VVDADEYLIPQQG|Y|10
5523	EEDEDLYDCVENE	gi|13124807|sp|P15498|	[EEDEDLYDCVENE|Y|1
5524	IPDPSKYCGPYKP	gi|114276|sp|P20933|AS	[IPDPSKYCGPYKP|Y|17
5525	LGTEELYGYLKKY	gi|125266|sp|P19784|CS	[LGTEELYGYLKKY|Y|25
5526	PEGHEYYRVREDG	gi|56405328|sp|P29597|	[PEGHEYYRVREDG|Y|1
5527	TPDGTCYPPPPVP	gi|50403731|sp|P27708|	NA
5528	AMSTDAYPKNPHL	gi|6685982|sp|O95721|S	NA
5529	SPDEEDYDYESYE	gi|1170875|sp|P46821|M	NA
5530	VKDAGFYVCRVNN	gi|20455075|sp|Q9UDY8	NA
5531	LDEGGYYISPRIT	gi|1705485|sp|P51451|B	NA
5532	REELAPYPKSKKA	gi|74735456|sp|O60828|	NA
5533	DQAVTEYVATRWY	gi|74760462|sp|Q8TD08|	NA
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5622	RLKCDFYLMNAIY	gi|114676760|ref|XP_001	NA
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5768	SERDELYAQWGKG	gi|74732865|sp|Q9BRD0	[SERDELYAQWGKG|Y|
5769	<<Marker>>	contol_spot	NA
5770	YGRSRDYNGRNQG	gi|1710620|sp|P98179|R	NA
5771	QQWQQLYDTLNAW	gi|62896687|dbj|BAD962	NA

5772	MDPSDIYAVIQIP	gi|23396534|sp|Q9NUD5	[MDPSDIYAVIQIP|Y|202
5773	PIIVGDYGPMWVY	gi|12643956|sp|Q9Y5X1|	NA
5774	KLVQTTYECLMQA	gi|33302602|sp|P53582|	NA
5775	QIIQEIYSQIQSK	gi|1729976|sp|P29401|T	[QIIQEIYSQIQSK|Y|275|
5776	STPMFEYENLEDN	gi|121066|sp|P03069|GC	NA
5777	PGVNDSYLYAGLW	gi|731532|sp|P39956|RP	NA
5778	IAEQPFYVNAKQY	gi|122217|sp|P06774|HA	NA
5779	PKSASEYVVNHNE	gi|1168370|sp|P22149|A	NA
5780	DMINPDYAQPTNG	gi|129733|sp|P12383|PD	NA
5781	LHREETYGSLTFE	gi|1708905|sp|P53338|M	NA
5782	DLAEKYYSESGEK	gi|74645031|sp|Q12180|	NA
5783	APFESSYTTASTF	gi|729140|sp|P40917|YA	NA
5784	YSATDQYSDSSFP	gi|74655046|sp|Q12398|	NA
5785	LNDEDNYSSAISR	gi|1168610|sp|P41696|A	NA
5786	NNSHVTYENANHA	gi|2506540|sp|P20134|S	NA
5787	VMSEFKYNFNSPL	gi|74583758|sp|Q08887|	NA
5788	CTTPNKYVVVDAA	gi|67461085|sp|Q9UJG1	NA
5789	IGEENKYAEQIMM	gi|38505226|ref|NP_078	NA
5790	<<Marker>>	contol_spot	NA
5791	LIPKWLYEDIPNM	gi|119371147|sp|Q5VW	NA
5792	RESSSIYISKYLM	gi|6175086|sp|O60701|U	NA
5793	TEFNAAYVPPGLM	gi|119621086|gb|EAX00	NA
5794	AEDPDDYDDGFSM	gi|61247587|sp|Q969G3|	NA
5795	KAQCDEYCIQGDN	gi|12643419|sp|P22079|	NA
5796	LFSASKYSFINDN	gi|50541963|ref|NP_001	NA
5797	RHYEDGYPGGSDN	gi|14916543|sp|O60716|	[RHYEDGYPGGSDN|Y|
5798	SFSNVKYVMLEEN	gi|6226957|sp|Q13635|P	NA
5799	VISWSHYKSVAEN	gi|88943889|sp|Q70EK8|	NA
5800	AVSGDYYPIIYFN	gi|74735596|sp|O96005|	NA
5801	LMTGDTYTAHAGA	gi|1168268|sp|P42684|A	[LMTGDTYTAHAGA|Y|3
5802	LPLDKDYYVVREP	gi|50403745|sp|P52333|	[LPLDKDYYVVREP|Y|98
5803	LRADENYYKAQTH	gi|1174527|sp|P43405|K	[LRADENYYKAQTH|Y|5
5804	MEDSTYYKASKGK	gi|3183518|sp|Q05397|F	[MEDSTYYKASKGK|Y|6
5805	MPSTRDYEIQRER	gi|3183518|sp|Q05397|F	NA
5806	NANYTEYVATRWY	gi|6175070|sp|O76039|C	NA
5807	YIWEFKYLFVQRN	gi|149588695|ref|NP_00	NA
5808	IGVRESYVNLCSN	gi|14917099|sp|Q93034|	NA
5809	TYSSDTYYYPGSN	gi|114677592|ref|XP_52	NA
5810	DDMSCDYDNMAVN	gi|74738165|sp|Q6UX15|	NA
5811	KAEVEKYKDCDPQ	gi|14149769|ref|NP_115	NA
5812	LPVNPEYSSTRNQ	gi|17376322|sp|Q14161|	NA
5813	LQEEDFYILDQGG	gi|61252134|sp|O15195|	NA
5814	KFGCSQYECVPRQ	gi|20178043|sp|O95980|	NA
5815	VALEESYPDLKSQ	gi|119630592|gb|EAX10	NA
5816	EFDNPIYETGGTQ	gi|4456459|emb|CAB374	NA
5817	KEEKCTYADKYTQ	gi|119600756|gb|EAW80	NA
5818	YSSGSRYQSAPSQ	gi|148746220|ref|NP_07	NA
5819	LRPGPIYAEDGDR	gi|45477168|sp|Q9HBB8	NA
5820	PPQRDSYSRSGCR	gi|74754395|sp|O75526|	NA
5821	SARIPEYLDVTAR	gi|119621930|gb|EAX01	NA
5822	SPIKVKYGDVYCR	gi|2498958|sp|P78539|S	NA
5823	DGPAVDYENQDVA	gi|62511238|sp|Q9UGK	NA

5824	FSSTESYLQALDR	gi|119588453|gb|EAW68	NA
5825	RCSSSIYSSICGR	gi|119569481|gb|EAW49	NA
5826	AMMETLYSDPHHR	gi|74737212|sp|Q6P2H3|	NA
5827	EGADVSYTNHRGR	gi|68565531|sp|Q96AX9|	NA
5828	LHSDSEYIKLMHR	gi|114520607|ref|NP_94	NA
5829	SLLETQYQNVRGR	gi|25008833|sp|Q93015|	NA
5830	AFPEHLYQRVKIR	gi|3122031|sp|Q14194|D	NA
5831	VGDVDDYSLHGGC	gi|32129516|sp|Q9NXG6	NA
5832	FAVDTAYVAKKLG	gi|94730680|sp|O95070|	NA
5833	LNVKVNYDNVGLG	gi|44889019|sp|P35499|	NA
5834	PAPEECYVYSPLG	gi|119575321|gb|EAW54	NA
5835	KCSSEMYESSRTL	gi|26006702|sp|Q96A23|	NA
5836	IEEFDNYAEWDLR	gi|13431275|sp|O75478|	NA
5837	DPNKYRYIDDGVR	gi|89060481|ref|XP_2921	NA
5838	KEAPTEYASICVR	gi|71152346|sp|Q7Z6A9|	NA
5839	MKSTESYFIPEVR	gi|129747|sp|P16284|PE	NA
5840	RGRKGTYWEGGVR	gi|74722581|sp|Q5FYB1|	NA
5841	FASPEEYAEFQYR	gi|146325086|sp|Q9P2G	NA
5842	KPAEPWYKETTYR	gi|74743878|sp|Q5SVJ3|	NA
5843	PKVPESYVETSAS	gi|108935982|sp|Q96RQ	NA
5844	CSPDTIYEDCDCS	gi|51315819|sp|O94989|	NA
5845	DHHENKYCDLECS	gi|2499596|sp|Q16659|M	NA
5846	FHDVQDYADSSCS	gi|10834712|gb|AAG2378	NA
5847	GIPPDDYLCSLCS	gi|20306246|gb|AAH2858	NA
5848	KAREEMYEKYVAS	gi|73920251|sp|Q8WXW	NA
5849	GTAEPDYGALYEG	gi|130225|sp|P19174|PL	[GTAEPDYGALYEG|Y|7
5850	RSTSSPYHAGNLL	gi|118572719|sp|Q9H79	NA
5851	VICSDCYDNANIY	gi|54036167|sp|O94898|	NA
5852	YEVEVTYDGVPVP	gi|116241365|sp|P21333	[YEVEVTYDGVPVP|Y|1
5853	SKGEPQYSSHSSS	gi|92058729|sp|O60292|	NA
5854	VKLQQTYAALNSK	gi|1170586|sp|P46940|IQ	NA
5855	SNLAASYLNPVKS	gi|23396625|sp|Q9NQT8	NA
5856	RRGEEIYGTISMK	gi|88983969|sp|Q9NR22	NA
5857	KTDDDVYVNVPEL	gi|23813679|sp|O96024|	NA
5858	GDEDCLYLNIWVP	gi|231629|sp|P19835|CE	NA
5859	EDRFIQYANPAFE	gi|23503044|sp|O60658|	NA
5860	GPNNNNYANVELI	gi|118601083|sp|Q13085	NA
5861	DDTAKMYVPMTED	gi|3183202|sp|O14975|S	NA
5862	VHLRAGYIIPLQG	gi|126590|sp|P10253|LY	NA
5863	IAKHLTYENVERW	gi|50402542|sp|P62491|	NA
5864	KVNENKYENVDLL	gi|78099770|sp|Q9NSV4	NA
5865	ESLVLTYVNAISS	gi|417031|sp|P32455|GB	NA
5866	SGGLELYGEPRHT	gi|14194461|sp|Q99996|	NA
5867	SLILMAYIIIFLT	gi|3122160|sp|O15552|F	NA
5868	RVGTVGYMAPEVV	gi|143811400|sp|P32298	NA
5869	DKLVVEYANAICQ	gi|123504|sp|P08910|AB	NA
5870	ASSNPEYLSASDV	gi|33112647|sp|P06213|	[ASSNPEYLSASDV|Y|9
5871	SQGVDTYVEMRPV	gi|547770|sp|P07333|CS	[SQGVDTYVEMRPV|Y|7
5872	HAEAALYKNLLHS	gi|125472|sp|P10721|KIT	[HAEAALYKNLLHS|Y|70
5873	LEFNDVYQEVKGS	gi|730840|sp|Q08945|SS	NA
5874	PQYYDEYVTFNGS	gi|93141229|sp|Q6UB98|	NA
5875	DSMEEKYCGCNKC	gi|10720377|sp|Q9UL59|	NA

5876	FPSSWDYKRASLC	gi|488364|emb|CAA5478	NA
5877	KKPWTEYVDMTLC	gi|145566894|sp|Q9UHE	NA
5878	LVLEGGYENWLLC	gi|731046|sp|P40818|UB	NA
5879	VVESSKYAACPKS	gi|148667492|gb|EDK99	NA
5880	ESSTSPYVTSYKS	gi|74749380|sp|Q6UW4	NA
5881	KKVEDEYKAFYKS	gi|119360|sp|P14625|EN	NA
5882	VKKELTYQNTDLS	gi|114149995|sp|Q32MZ	NA
5883	CGKKRRYVRLGLS	gi|94730574|sp|Q5MJ70|	NA
5884	KISEIHYGDTLLS	gi|74728160|sp|Q8IWA6|	NA
5885	ESPGIDYVQIGFP	gi|6094289|sp|O14893|G	NA
5886	IAKMDSYARIFFP	gi|116242488|sp|P18507	NA
5887	RSVNDLYIQKQFP	gi|123055|sp|P05546|HE	NA
5888	AHRDSLYVVRNGP	gi|41205052|ref|XP_372	NA
5889	SICLERYKNPKVL	gi|21363034|sp|Q9C040|	NA
5890	TTEELKYSPEGVL	gi|119590617|gb|EAW70	NA
5891	GWVEQAYVDKCVC	gi|4140704|gb|AAD041	NA
5892	EKDNNTYENRRVL	gi|93004094|ref|NP_005	NA
5893	VEKPLDYMNHYTC	gi|91208389|sp|Q2M3W	NA
5894	FCFSEDYPNGTWL	gi|109698609|ref|NP_52	NA
5895	FDSKKAYRDVAWL	gi|38258608|sp|Q8IXJ6|	NA
5896	DEDMLKYMKMTAT	gi|147668009|sp|Q8N6K	NA
5897	EPLPPSYVACS	gi|119524|sp|P19235|EP	[EPLPPSYVACS|Y|504|
5898	IRNTNEYTEGPTV	gi|13124551|sp|O43597|	[IRNTNEYTEGPTV|Y|55
5899	PGPQDIYDVPPVR	gi|8134339|sp|P56945|B	[PGPQDIYDVPPVR|Y|24
5900	QIPEGDYLSYREF	gi|116242614|sp|Q96RT	[QIPEGDYLSYREF|Y|11
5901	RNPLQGYYQVRRP	gi|46576866|sp|O94910|	[RNPLQGYYQVRRP|Y|1
5902	SHVDNEYSQPPRN	gi|116024|sp|P06127|CD	[SHVDNEYSQPPRN|Y|4
5903	AFDNPDYWNHSLP	gi|3913590|sp|Q15303|E	[AFDNPDYWNHSLP|Y|1
5904	GLARDMYDKEYYS	gi|125484|sp|P08581|ME	[GLARDMYDKEYYS|Y|1
5905	KPEIQVYENIHLA	gi|56206384|emb|CAI18	[KPEIQVYENIHLA|Y|281
5906	TEDELPYDDCVFG	gi|126682|sp|P25963|IK	[TEDELPYDDCVFG|Y|3
5907	DDSDEDYEKVPLP	gi|3023207|sp|P78314|3	NA
5908	GNYRDNYDN	gi|1710620|sp|P98179|R	[GNYRDNYDN|Y|155|P9
5909	GADDSYYTARSAG	gi|1177044|sp|P43403|Z	[GADDSYYTARSAG|Y|4
5910	HQEDNDYINASLI	gi|131467|sp|P18031|PT	[HQEDNDYINASLI|Y|66|
5911	NEGKHLYTLDGGD	gi|54037168|sp|P63244|	[NEGKHLYTLDGGD|Y|2
5912	PMDTEVYESPYAD	gi|1174527|sp|P43405|K	[PMDTEVYESPYAD|Y|3
5913	FLPVPEYINQSVP	gi|2811086|sp|P00533|E	[FLPVPEYINQSVP|Y|10
5914	RNMKSQYEVFRSS	gi|73917693|sp|Q63HQ0	NA
5915	ISQGMQYLAEMKL	gi|547807|sp|P07949|RE	NA
5916	QIDSCTYEAMYNI	gi|115855|sp|P22681|CB	[QIDSCTYEAMYNI|Y|73
5917	SRLPVDYYGIPFA	gi|74745207|sp|Q5T6F2|	[SRLPVDYYGIPFA|Y|83
5918	AVLYADYRAPGPA	gi|54036152|sp|Q96J84|	[AVLYADYRAPGPA|Y|6
5919	EEPEALYAAVNKK	gi|20138768|sp|Q9NZM3	[EEPEALYAAVNKK|Y|96
5920	HSTILDYINVVPT	gi|118572721|sp|Q96LC	[HSTILDYINVVPT|Y|597
5921	EADGELYVFNTPS	gi|90180201|sp|Q13480|	[EADGELYVFNTPS|Y|2
5922	FCGTPEYLAPEVL	gi|57210108|emb|CAI42	[FCGTPEYLAPEVL|Y|31
5923	HIANHSYLPLSYW	gi|730980|sp|P40238|TP	[HIANHSYLPLSYW|Y|62
5924	PDEDYEYMNRQRD	gi|119534|sp|P21860|ER	[PDEDYEYMNRQRD|Y|
5925	RPPEPVYSTVNKL	gi|73920200|sp|Q15700|	[RPPEPVYSTVNKL|Y|34
5926	SPGPGHYLRCDST	gi|729564|sp|Q99062|CS	[SPGPGHYLRCDST|Y|7
5927	SPSDSGYSYETIG	gi|1170875|sp|P46821|M	NA

5928	LNKTKEYTACELM	gi|12643818|sp|Q9NSD9	NA
5929	KPSSAAYQKAPTK	gi|464745|sp|P34741|SD	NA
5930	NEELPTYEEAKAQ	gi|74728292|sp|Q8IY63|	NA
5931	SDVGGYYYEKIER	gi|1170875|sp|P46821|M	NA
5932	AEQAERYEDMAAF	gi|398953|sp|P31947|14	[AEQAERYEDMAAF|Y|1
5933	DRKNPAYIPRKGL	gi|18266743|sp|O15234|	NA
5934	IEWPGAYPKLMEI	gi|30923321|sp|Q92556|	NA
5935	DFTPSPYDTDSLK	gi|145559526|sp|O9488	NA
5936	LLTMSFYRNYHAM	gi|13124441|sp|O14939|	NA
5937	LGLALNYSVFYYE	gi|48428721|sp|P61981|	NA
5938	VRWAKLYSLVIWG	gi|2506481|sp|P30411|B	[VRWAKLYSLVIWG|Y|1
5939	DEIRKKYGLFKEE	gi|1711387|sp|P53801|P	NA
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5941	SDKELQYIDAISN	gi|73917636|sp|Q9UQB8	NA
5942	RRQEEGYYSRLEA	gi|12644018|sp|P55196|	NA
5943	DLSSKYYQTIGNH	gi|20978558|sp|Q9UNM	NA
5944	EDSDRKYEEVARK	gi|136090|sp|P07951|TP	NA
5945	CKAANLYASSPHS	gi|119607309|gb|EAW86	NA
5946	LLSNPDYINQMLL	gi|119613823|gb|EAW93	NA
5947	ATSYIAYLMDLLA	gi|47117699|sp|P61296|	NA
5948	LVGEGSYGMVMKC	gi|74762639|sp|Q92772|	NA
5949	VEFEPTYEEFPSL	gi|10720350|sp|Q9Y487|	NA
5950	RPGYGAYDAFKHA	gi|124200|sp|P05198|IF2	NA
5951	SAVGFDYKGEVEK	gi|123557|sp|P14317|HC	NA
5952	RNVNAPYRDRIPL	gi|13633994|sp|Q9UBN4	NA
5953	TRFTDEYQLYEDI	gi|12643413|sp|Q13554|	NA
5954	GEARALYNLGNVY	gi|38258887|sp|P81274|	NA
5955	RCPSDPYKHSLPS	gi|14285603|sp|Q12879|	NA
5956	PKSENIYDYLDSS	gi|125987727|sp|Q58A6	NA
5957	DGASPDYVLVEAE	gi|416959|sp|Q03468|ER	NA
5958	GSLSGDYLYIFDG	gi|73920246|sp|O00750|	NA
5959	LRNQPIYIQYSNH	gi|74761983|sp|Q9UKA9	NA
5960	TLESAQYPGILPS	gi|1169233|sp|P43146|D	NA
5961	LCEFRPYSCPCPG	gi|46577493|sp|Q8IUQ4|	NA
5962	IPNVVKYSPNCKL	gi|126047|sp|P00338|LD	NA
5963	SYSGVLYITETDE	gi|118573058|sp|Q9P27	NA
5964	IDNKALYDTFSAF	gi|3183544|sp|P11940|P	NA
5965	VKMKMKYYIEYME	gi|67461014|sp|Q6NYC1	NA
5966	RYHLRCYMYQARD	gi|20137708|sp|O75923|	NA
5967	ELDEEGYMTPMRD	gi|3913590|sp|Q15303|E	NA
5968	EPKGEKYECALKR	gi|93141033|ref|NP_031	NA
5969	RMNDLHYLNLDTW	gi|90110030|sp|Q8N7A1|	NA
5970	FDEVEIYGEPQTV	gi|20139241|sp|Q9NZM1	NA
5971	RLTGITYLRVRSL	gi|3914299|sp|O60683|P	NA
5972	QTDFVQYQPDLDT	gi|21362912|sp|O15079|	NA
5973	RDVARGYENVPIP	gi|116241348|sp|Q96KQ	NA
5974	QLIELDYLNPGSI	gi|12643886|sp|Q9UHI6|	NA
5975	THTIPFYPNPLHP	gi|13124249|sp|Q9Y3I1|	NA
5976	YCSKLRYLNARGC	gi|37537858|sp|Q9UJT9|	NA
5977	YQVPASYQPDEEE	gi|17865680|sp|Q9BYM8	NA
5978	YSRDPNYLNLFII	gi|6648106|sp|Q05086|U	NA
5979	NITENVYINLTCS	gi|1168851|sp|P42081|C	NA

5980	HSVNGEYLNVHMK	gi|90110033|sp|Q16363|	NA
5981	YKLLPPYLRVIQG	gi|1172027|sp|P43490|N	NA
5982	FHPNKGYIYVVKV	gi|73920246|sp|O00750|	NA
5983	VDDFQNYLRVAFQ	gi|28201876|sp|Q8WYP	NA
5984	YENDLGYTAVALY	gi|2498954|sp|Q14247|S	NA
5985	DAEKPFYVNVEFH	gi|143811366|sp|P11274	[DAEKPFYVNVEFH|Y|1
5986	TDGYTTYINASTC	gi|3023214|sp|Q15777|M	NA
5987	VKGFRSYVDMYLK	gi|13959709|sp|P11388|	NA
5988	IVNSTYYANVSAT	gi|13634020|sp|Q9UPW	NA
5989	ILFVKEYVNASEV	gi|14286186|sp|O15231|	NA
5990	DNSPKRYLIPKGD	gi|83305815|sp|P31629|	NA
5991	GVEAKNYEEIAKV	gi|3915893|sp|P49755|T	NA
5992	KFTSKEYEEIDKR	gi|30316395|sp|Q9Y2G3	NA
5993	MGFIGHYLDQKRL	gi|116241237|sp|P53396	NA
5994	PHVVKVYSEDGAC	gi|116242503|sp|Q14451	NA
5995	DSPVFWYAPECLK	gi|56405328|sp|P29597|	NA
5996	APRDTIYQVPPSY	gi|8134360|sp|Q14511|C	NA
5997	NWAKGHYTEGAEL	gi|146424310|gb|AAI419	NA
5998	EERLLRYLIHLRF	gi|154350236|ref|NP_06	NA
5999	F4:17	contol_spot	NA
6000	F8:17	contol_spot	NA
6001	pY	contol_spot	NA
6002	IgG	contol_spot	NA
6003	FITC	contol_spot	NA
6004	pY	contol_spot	NA
6005	IgG	contol_spot	NA
6006	FITC	contol_spot	NA
6007	GICEEAYSWNLTV	gi|11136143|sp|Q9Y2L8|	NA
6008	MMEEIDYDHDGTV	gi|12643960|sp|Q9Y6T7|	NA
6009	IAECLTYLDNGVV	gi|12643730|sp|Q16531|	NA
6010	WKPEREYWESGLQ	gi|119619475|gb|EAW99	NA
6011	RHLEGAYADWDVV	gi|5915798|sp|O75936|B	NA
6012	VVLEEHYLVVGVV	gi|32700084|sp|Q14689|	NA
6013	GARGDHYARNLLW	gi|47116570|sp|Q96RP7|	NA
6014	IQPSTVYVCNENQ	gi|82654940|sp|Q9Y5Y3|	NA
6015	KQKYDLYISIAGW	gi|21263618|sp|Q9BXC1	NA
6016	NLLEEDYFGLAIW	gi|90101808|sp|P11171|	NA
6017	QPSKQKYIFLLLW	gi|74762064|sp|Q9Y546|	NA
6018	CKPKSVYENFRLW	gi|74747838|sp|Q5VZR2	NA
6019	QRTDFPYVSAAMP	gi|123283730|emb|CAM	NA
6020	DNEEGVYDYENTG	gi|84028206|sp|P20930|	NA
6021	SANWTEYQDPRTG	gi|2506380|sp|Q08431|M	NA
6022	RNPDHDYTGNKNQ	gi|29611340|gb|AAO918	NA
6023	SPAEEFYTRHVLQ	gi|400630|sp|P31645|SC	NA
6024	RGSAGAYADFLPP	gi|113428577|ref|XP_94	NA
6025	ISSEFTYAWSVED	gi|730891|sp|P40200|TA	NA
6026	MYYNDAYGALDYY	gi|62511129|sp|Q9BQ04	NA
6027	FDVRDHYKDFGGD	gi|59802987|sp|O75153|	NA
6028	IFEKDRYSGENGD	gi|20138033|sp|Q9NQI0|	NA
6029	IPASGDYVARPGD	gi|74731608|sp|Q96ES7|	NA
6030	VRYSFRYVDDKAA	gi|37999478|sp|O60330|	NA
6031	SSWDEHYSRGYRD	gi|27805715|sp|Q15380|	NA

6032	DKRSPLYDISATD	gi|2493600|sp|Q15842|IF	NA
6033	NNVEEGYPRPVSD	gi|21264469|sp|Q9ULZ9|	NA
6034	ILFKEWYSMSAVD	gi|145558936|sp|Q0D2K	NA
6035	QNSKFSYEQLETD	gi|145559478|sp|Q1478	NA
6036	EFGKLKYVHVTVD	gi|332129|gb|AAA46542.	NA
6037	CQASPRYLQPGGE	gi|74752049|sp|Q96N96|	NA
6038	GKDEIVYPRMPGE	gi|118918431|ref|NP_00	NA
6039	MWDFDIYGDLYFE	gi|20140440|sp|O75140|	NA
6040	FHYETKYVVLSYL	gi|23396740|sp|Q9BXK5	NA
6041	KKRMDYYDSEHHE	gi|23831324|sp|O43252|	NA
6042	TRRTELYAVIDIE	gi|71152057|sp|Q8WU2	NA
6043	<<Marker>>	contol_spot	NA
6044	IKAMTYYGNLDSE	gi|89365949|gb|AAI1447	NA
6045	YKFMDLYPCSASE	gi|71153231|sp|Q12996|	NA
6046	LSSMTAYVSGGSP	gi|150421552|sp|Q12951	NA
6047	CHEADGYDYTVSP	gi|74738627|sp|Q7LC44|	NA
6048	NKCSTGYEKNMTP	gi|1709214|sp|P49790|N	NA
6049	DRDKDMYAGNCAH	gi|67462124|sp|O95841|	NA
6050	RGDTDKYLKKLHT	gi|17390940|gb|AAH183	NA
6051	FISVTSYQNHKIT	gi|51338786|sp|P57082|	NA
6052	GPCGWKYENIYIT	gi|71153342|sp|Q9H295|	NA
6053	PLPMDSYMHLEIT	gi|47606649|sp|Q8NFA0	NA
6054	STPEEIYPPYNIT	gi|91207975|sp|O75445|	NA
6055	CYDDSVYWKVPKT	gi|548729|sp|Q02094|RH	NA
6056	TGDMPTYQIRAPT	gi|146345406|sp|Q0306	NA
6057	KPPEITYMSQGPT	gi|74730279|sp|Q8NEP4	NA
6058	WLEEAVYEDFPQT	gi|119370527|sp|Q9BQF	NA
6059	RPQEEKYPVGPWL	gi|74751068|sp|Q8N6R1	NA
6060	QVENDAYPGTDRT	gi|45477317|sp|Q8N302|	NA
6061	CNGTDIYKDKEST	gi|115985|sp|P04234|CD	NA
6062	RITEDYYVHLIAD	gi|13878804|sp|Q92544|	NA
6063	KISKVKYVIWSAD	gi|1705996|sp|P53621|C	NA
6064	<<Marker>>	contol_spot	NA
6065	RRSVEKYNSARAD	gi|122063473|sp|O1452	NA
6066	FCSSSGYIQEKCV	gi|118574152|sp|Q9C0I4	NA
6067	HDPNGEYMFMRAV	gi|50400701|sp|Q9Y6W	NA
6068	QKSLPIYIQMACV	gi|11094327|gb|AAG295	NA
6069	DVMLENYENVAKV	gi|97219157|sp|Q96MR9	NA
6070	KLSKLDYRDITKQ	gi|71153483|sp|Q14966|	NA
6071	PIEESFYIFFAKV	gi|119585682|gb|EAW65	NA
6072	SAKPLDYVEIHKV	gi|130321|sp|P16471|PR	NA
6073	GQSEGSYLLHHLP	gi|74749590|sp|Q6ZP29|	NA
6074	YGGSDDYIGLALP	gi|119576383|gb|EAW55	NA
6075	LKLEDIYGCPYDF	gi|119569691|gb|EAW49	NA
6076	YCKEKIYAGVGEF	gi|143811368|sp|O6056	NA
6077	ILVNEPYYNEAGF	gi|134035341|sp|Q9C0C	NA
6078	KLTALDYHNPAGF	gi|20138086|sp|Q9Y224|	NA
6079	PVSSEEYDRTDGF	gi|116248529|sp|Q5VUJ	NA
6080	YQEEKCYEDGIFF	gi|46395756|sp|Q7Z7M0	NA
6081	FETNNKYEIKNSF	gi|14548191|sp|O15162|	NA
6082	LDLEEDYNVMTSF	gi|74738329|sp|Q6ZUJ4|	NA
6083	YQRTPYYACPQSF	gi|114152782|sp|Q9BXF	NA

6084	AGSSDKYFFVETF	gi|154089854|emb|CAO	NA
6085	<<Marker>>	contol_spot	NA
6086	ILKDHGYIENLTF	gi|12229715|sp|Q9NVD3	NA
6087	MENNLPYDDNGTF	gi|113413918|ref|XP_94	NA
6088	DGEMAKYVQGDAI	gi|1170636|sp|P23743|D	NA
6089	LTFKDQYIGRGDM	gi|20140440|sp|O75140|	NA
6090	AIPGLDYVSHEDI	gi|50401206|sp|Q9Y2S7|	NA
6091	ITFSWKYKNNSDI	gi|148717943|gb|AAV40	NA
6092	RTPDELYFEEGDI	gi|108885279|sp|Q9288	NA
6093	GERNQIYIQLPEI	gi|82802803|gb|ABB924	NA
6094	GDWMIDYVSNRLI	gi|116242491|sp|P35573	NA
6095	YCIKEGYADKNLI	gi|23831082|sp|P41223|	NA
6096	ISSIPLYVQVLNI	gi|17366818|sp|Q9H159|	NA
6097	DLDHPGYNNTYQI	gi|6166014|sp|O76083|P	NA
6098	IAEELGYDLLGQI	gi|116242674|sp|P29120	NA
6099	NNDEKFYLSNGRI	gi|110611231|ref|NP_00	NA
6100	VENLEKYVVKDGK	gi|1703012|sp|P49902|5	NA
6101	AQEMFTYICNHIK	gi|266648|sp|P29474|NO	NA
6102	IWDCEEYNMIKIK	gi|126215680|sp|Q96MC	NA
6103	YIHEHEYVHGDIK	gi|45593726|sp|Q99986|	NA
6104	DYEFIDYECLAKK	gi|51094632|gb|EAL238	NA
6105	SDEDQGYVDLVIK	gi|74761957|sp|Q9UHQ	NA
6106	<<Marker>>	contol_spot	NA
6107	AYLNVDYVMNYWK	gi|37999771|sp|Q9BZP6|	NA
6108	PRSATTYITVLVK	gi|22095551|sp|Q9NYQ6	NA
6109	PADGENYVTMVEM	gi|119610537|gb|EAW90	NA
6110	FVWMHYYVSMDAL	gi|401235|sp|P14679|TY	NA
6111	PHKERPYTIAAAL	gi|116268127|ref|NP_68	NA
6112	DWYHFHYVDILAL	gi|116242784|sp|P51172	NA
6113	CVSCLDYDEHYIL	gi|20139075|sp|Q96SU4|	NA
6114	YTSKDRYFYFGKL	gi|152031723|sp|Q96DA	NA
6115	HVCNVKYKRWALL	gi|119604152|gb|EAW83	NA
6116	LFSPGTYERLALL	gi|17380172|sp|Q9H1Y3|	NA
6117	DGSEVMYDAVSIM	gi|61563951|sp|Q6PI25|	NA
6118	EKFCDLYWDEKLL	gi|119581720|gb|EAW61	NA
6119	SFSDPLYLTMFKM	gi|38258919|sp|P42356|	NA
6120	VDHRGDYVSHEIM	gi|32363141|sp|Q8TE57|	NA
6121	VSREAGYDSTYGM	gi|116242695|sp|Q9HC1	NA
6122	ISEAEDYKMFICA	gi|74761374|sp|Q9H069|	NA
6123	CDNFPYYKNAGIG	gi|13626933|sp|Q9P0K8|	NA
6124	DQEEKKYLMGEHG	gi|10720176|sp|O15297|	NA
6125	SDTDSSYCIPTAG	gi|90180201|sp|Q13480|	[SDTDSSYCIPTAG|Y|37
6126	SENFDDYMKEVGV	gi|119781|sp|P15090|FA	[SENFDDYMKEVGV|Y|2
6127	<<Marker>>	contol_spot	NA
6128	SIRMGRYRDHFAA	gi|19857975|sp|P29322|	NA
6129	SPGMKIYIDPFTY	gi|1706663|sp|P54762|E	[SPGMKIYIDPFTY|Y|59
6130	DCLDGLYALMSRC	gi|48429194|sp|P30530|	[DCLDGLYALMSRC|Y|7
6131	DDFDGTYETQGGK	gi|47117832|sp|P21709|	[DDFDGTYETQGGK|Y|7
6132	ETGTEEYMKMDLG	gi|547738|sp|P35568|IR	NA
6133	AIKMGRYTEIFME	gi|1706628|sp|P54756|E	NA
6134	FPGTKTYIDPETY	gi|146345416|sp|Q1537	NA
6135	FRQGKDYVGAIPV	gi|9087218|sp|P35968|V	[FRQGKDYVGAIPV|Y|9

6136	GEEEEEYLDKINP	gi|12643789|sp|Q92692|	NA
6137	GIDDQSYKHLFQP	gi|3334210|sp|O15379|H	NA
6138	EEVDEMYREAPVD	gi|188586|gb|AAA59852.	NA
6139	DAEMTGYVVTRWY	gi|6685642|sp|O15264|M	NA
6140	EDDEDCYGNYDNL	gi|17380162|sp|O15530|	[EDDEDCYGNYDNL|Y|3
6141	VKKLKDYAFIHFD	gi|92090361|sp|O60506|	[VKKLKDYAFIHFD|Y|37
6142	KPDSSFYKGLDLN	gi|114787|sp|P02730|B3	[KPDSSFYKGLDLN|Y|3
6143	ENEEQEYVQTVKS	gi|113944|sp|P04083|AN	[ENEEQEYVQTVKS|Y|2
6144	YREGPTYQRRGSL	gi|12643411|sp|P50549|	NA
6145	DSEMTGYVVTRWY	gi|2851522|sp|P53778|M	[DSEMTGYVVTRWY|Y|
6146	NEGDNDYIIPLPD	gi|129890|sp|P09619|PG	[NEGDNDYIIPLPD|Y|10
6147	GESDGGYMDMSKD	gi|129890|sp|P09619|PG	[GESDGGYMDMSKD|Y|
6148	<<Marker>>	contol_spot	NA
6149	SNYMAPYDNYVPS	gi|129890|sp|P09619|PG	[SNYMAPYDNYVPS|Y|7
6150	VSETDDYAEIIDE	gi|3183518|sp|Q05397|F	[VSETDDYAEIIDE|Y|397
6151	LSFEELYRNAYTM	gi|12643396|sp|Q13618|	[LSFEELYRNAYTM|Y|5
6152	SKCCCIYEKPRAF	gi|74739598|sp|O60927|	[SKCCCIYEKPRAF|Y|64
6153	NAEDCLYELPENI	gi|74753081|sp|Q9NZ63|	[NAEDCLYELPENI|Y|14
6154	SHGTHEYHAETIK	gi|20178296|sp|P14618|	[SHGTHEYHAETIK|Y|83
6155	VSVPKGYVAKSPD	gi|94730427|sp|Q9P2R7|	NA
6156	VQRISTYGLPAGG	gi|30172980|sp|Q9Y5K6|	[VQRISTYGLPAGG|Y|8
6157	VQKSKEYFSKQK	gi|548453|sp|Q06830|PR	[VQKSKEYFSKQK|Y|19
6158	MKKELNYFAKALE	gi|52788229|sp|P00558|	[MKKELNYFAKALE|Y|1
6159	HTSNNIYEAVKYS	gi|145558902|sp|Q9H9T	[HTSNNIYEAVKYS|Y|20
6160	SDARALYEAGERR	gi|113944|sp|P04083|AN	NA
6161	PYATSLYHS	gi|74728034|sp|Q8IV50|	[PYATSLYHS|Y|213|Q8I
6162	QDPNPQYSPIIKQ	gi|143811460|sp|Q9NP3	[QDPNPQYSPIIKQ|Y|21
6163	GDQIDTYELSGGA	gi|461976|sp|Q05193|DY	[GDQIDTYELSGGA|Y|3
6164	PKEDPIYDEPEGL	gi|17366642|sp|Q99704|	[PKEDPIYDEPEGL|Y|36
6165	GAEYATYQTKSTT	gi|27502427|ref|NP_758	NA
6166	HTGEKPYQCGQCG	gi|3123173|sp|Q15697|Z	NA
6167	APGQGPYPYSLSE	gi|13431358|sp|Q9NZB2	[APGQGPYPYSLSE|Y|3
6168	QPGEQKYEYKSDQ	gi|41019505|sp|Q04637|	[QPGEQKYEYKSDQ|Y|
6169	<<Marker>>	contol_spot	NA
6170	PAGTEDYIHIRIQ	gi|1174483|sp|P41567|E	[PAGTEDYIHIRIQ|Y|30|
6171	EPPYTAYVGNLPF	gi|18276665|sp|Q15056|	[EPPYTAYVGNLPF|Y|45
6172	STSRSLYASSPGG	gi|55977767|sp|P08670|	[STSRSLYASSPGG|Y|5
6173	AGAVASYDYLVIG	gi|14916998|sp|P00390|	[AGAVASYDYLVIG|Y|65
6174	DHSHLLYSTIPRM	gi|14916543|sp|O60716|	NA
6175	GVEDPEYAVTQLA	gi|60415944|sp|Q9UJZ1|	[GVEDPEYAVTQLA|Y|1
6176	IVSNDAYNKMANS	gi|11133517|sp|Q03125|	NA
6177	EDQESEYSEKPLG	gi|135077|sp|P08153|SW	NA
6178	TDKEYDYEHYQIL	gi|56757368|sp|P07248|	NA
6179	SINEEDYAAKSKH	gi|1711597|sp|P46676|S	NA
6180	HYKWSDYANDPEL	gi|50400296|sp|Q04052|	NA
6181	ISSLPKYSSLDID	gi|416737|sp|P24813|YA	NA
6182	NIYEGSYSIMELD	gi|126217|sp|P08638|LE	NA
6183	SVDEPQYQRRNID	gi|1351976|sp|P05085|A	NA
6184	GVSDQQYDSMAKT	gi|1711459|sp|P53438|S	NA
6185	NISASDYTVANNS	gi|1708268|sp|P54785|M	NA
6186	DNEDDEYDDADLH	gi|88984445|sp|P32389|	NA
6187	GQSQGLYISSNSS	gi|2507068|sp|P22148|M	NA

6188	SVFTPEYDDSRIR	gi|62297871|sp|Q61083|	NA
6189	TDSLSTYINANYI	gi|134039192|sp|Q1525	NA
6190	<<Marker>>	contol_spot	NA
6191	SIQEGKYEFPDKD	gi|90102033|sp|Q9HBH9	NA
6192	QIDENWYEGMLHG	gi|10720276|sp|Q99962|	NA
6193	LTFKVDYGSFAFV	gi|6685621|sp|Q9Y6R4|	NA
6194	DTSDDNYGERSEA	gi|67477383|sp|P49796|	NA
6195	NGPREKYGIVDYM	gi|119530|sp|P13667|PD	NA
6196	TSMEPGYFDNLAN	gi|73621176|sp|Q6UXM1	NA
6197	YMWEVYYPNLGWM	gi|56757653|sp|Q13029|	NA
6198	CTYKDDYMISKDN	gi|134035407|sp|Q9NW	NA
6199	EKSKGHYHTIPDN	gi|19856971|sp|P20929|	NA
6200	GPEKSMYVVTKEN	gi|1170784|sp|P42702|LI	NA
6201	QLPPEGYVVVVKN	gi|3183003|sp|Q14289|F	NA
6202	AFPSDKYEQDDLN	gi|130484567|ref|NP_00	NA
6203	DSYKSGYVYSELN	gi|120660202|gb|AAI304	NA
6204	LEERKTYVNTTLY	gi|464868|sp|Q02763|TIE	[LEERKTYVNTTLY|Y|11
6205	LHTDDGYMPMSPG	gi|547738|sp|P35568|IRS	[LHTDDGYMPMSPG|Y|
6206	ARVTVKYDRRELQ	gi|55583974|sp|Q96A00|	NA
6207	SCSKQSYYNKEKG	gi|33112447|sp|Q8IWU6	NA
6208	WAGETNYISVFKG	gi|55977853|sp|Q16820|	NA
6209	GESSHRYEVSGQN	gi|150378520|ref|NP_11	NA
6210	IPEEADYVGIERN	gi|48429232|sp|P53708|	NA
6211	NASREMYERENRN	gi|73920251|sp|Q8WXW	NA
6212	RYTKEVYVPHPRN	gi|20139806|sp|Q9P0M9	NA
6213	FHCHEGYILHGAP	gi|148886654|ref|NP_69	NA
6214	IREHLSYEDWNYN	gi|119600085|gb|EAW79	NA
6215	LFKTDIYMYVCAP	gi|85700269|sp|P51811|	NA
6216	SAFELSYDQKKAP	gi|31747511|gb|AAP576	NA
6217	VFYEKDYEGTVYN	gi|52782976|sp|Q9BQS7	NA
6218	DEEAPDYGSGVRQ	gi|119364606|sp|Q1275	NA
6219	KTFSGGYVHVLKG	gi|20379566|gb|AAH276	NA
6220	NEYKQDYNEWYKG	gi|19856971|sp|P20929|	NA
6221	RPFSDPYCEGPKG	gi|51701298|sp|O94812|	NA
6222	ALKMFLYADNEDR	gi|30580379|sp|Q9NP79|	NA
6223	HHSSPGYDSSPCR	gi|83305815|sp|P31629|	NA
6224	ITFNPLYWNVVAR	gi|148887406|sp|Q9UBM	NA
6225	LSSKPEYVKPDFR	gi|119621930|gb|EAX01	NA
6226	PPSMLRYEEMTER	gi|84028217|sp|Q9P2K6|	NA
6227	AQEVDDYHAFQTL	gi|68053323|sp|Q9NYU2	NA
6228	AVSMETYHVTLTL	gi|46577674|sp|O14523|	NA
6229	FVSERKYDEDLGR	gi|148746220|ref|NP_07	NA
6230	IETELIYKYSPFR	gi|114152840|sp|Q9Y6X	NA
6231	ATEGPAYSQSAIC	gi|116242721|sp|P78424	NA
6232	FTNESSYHRRGGC	gi|141795194|gb|AAI250	NA
6233	IEYTSDYEFSNGC	gi|74744660|sp|Q5T2S8|	NA
6234	KGANPNYQDISGC	gi|134034136|sp|Q8IYU2	NA
6235	NFPEPPYPDQIIC	gi|74731809|sp|Q96GC9	NA
6236	HQSEREYIRYHAA	gi|74756617|sp|Q5THJ4|	NA
6237	NVSETRYVSELTL	gi|129890|sp|P09619|PG	NA
6238	DKCEPKYFVFNSR	gi|74731046|sp|Q969I6|	NA
6239	GERDLIYAFHGSR	gi|116248565|sp|Q8N5Y	NA

6240	FDDEAYYAALGTR	gi|83305809|sp|Q96KB5|	NA
6241	PVCSEAYIDARTL	gi|51316944|sp|O95625|	NA
6242	VECDLTYHNVYSR	gi|6648106|sp|Q05086|U	NA
6243	ELHVDRYDNHPDP	gi|118575127|sp|Q6ZTA	NA
6244	IKRNLSYGDNSDP	gi|116241334|sp|Q9Y2H	NA
6245	KRSSETYRVTPDP	gi|12230074|sp|Q14314|	NA
6246	WAHMEKYLSFPTL	gi|152013421|sp|Q5VYM	NA
6247	CTHHTGYCDIAEP	gi|119605306|gb|EAW84	NA
6248	WWNRDKYLGPAVL	gi|114589581|ref|XP_001	NA
6249	GFKQRPYSVAVPA	gi|73917636|sp|Q9UQB8	NA
6250	REDAVLYLLEIPK	gi|13634076|sp|Q9UDY2	[REDAVLYLLEIPK|Y|554
6251	YEPVSPYSCKEAP	gi|135104|sp|P07814|SY	NA
6252	YDNLAIYKSFLGT	gi|118572719|sp|Q9H79	[YDNLAIYKSFLGT|Y|63
6253	RTTDGVYEGVAIG	gi|116241237|sp|P53396	[RTTDGVYEGVAIG|Y|6
6254	IKRNRYYDEDEDE	gi|20138067|sp|Q9UHB6	[IKRNRYYDEDEDE|Y|74
6255	PQITSPYENVPSQ	gi|1703310|sp|Q01484|A	NA
6256	YSYTVKYTAVQQG	gi|32129530|sp|Q14315|	NA
6257	AEVKAQYEEIANR	gi|143811411|sp|P13647	NA
6258	KKGNFNYVEFTRI	gi|20141521|sp|P24844|	[KKGNFNYVEFTRI|Y|15
6259	FTWCKSYEEISDD	gi|1709093|sp|P54296|M	NA
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6261	AELEELYGDIDAL	gi|129899|sp|P23219|PG	NA
6262	SRLAGGYENVPTV	gi|6093731|sp|O60568|P	NA
6263	YEGNFHYINLIKT	gi|132326|sp|P00797|RE	NA
6264	TLQHRRYPNVFGI	gi|27151704|sp|Q9Y6N5|	NA
6265	PGPACAYVNLNIC	gi|730870|sp|P41252|SY	NA
6266	VIPVHYYLIPPPT	gi|34223721|sp|P29144|	NA
6267	NPQEGLYNELQKD	gi|23830999|sp|P20963|	[NPQEGLYNELQKD|Y|1
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6269	AISIDRYTAVVMP	gi|1169206|sp|P35462|D	NA
6270	CMRVELYGCVWLD	gi|2497564|sp|Q16832|D	NA
6271	LSPSSGYMPMNQG	gi|119534|sp|P21860|ER	NA
6272	KANNLLYINPEAF	gi|544350|sp|P23945|FS	NA
6273	ILADEIYGDMVFS	gi|114713|sp|P17735|AT	NA
6274	RGKKFSYVDADGS	gi|34223720|sp|P25940|	NA
6275	ASRVSIYDNVPGS	gi|90185285|sp|Q9Y3M8	NA
6276	DKSYGGYEVVGGS	gi|67476890|sp|Q15517|	NA
6277	GPNNGGYDDDQGS	gi|148887370|sp|Q9263	NA
6278	IGEEILYCELKGS	gi|41019474|sp|P15529|	NA
6279	DVLKDDYDYVLIS	gi|74751081|sp|Q8N766|	NA
6280	IHRSNPYIQLGIS	gi|29840784|sp|Q8N448|	NA
6281	QERTVAYINVDIS	gi|20139287|sp|Q9UQQ1	NA
6282	THSKEHYHFYEIS	gi|119591033|gb|EAW70	NA
6283	GWEKGAYKKWGKS	gi|118572659|sp|Q9262	NA
6284	RERDGHYSNSHKS	gi|74760546|sp|Q8WUA	NA
6285	LEPDSTYFDLPQS	gi|8928244|sp|O15350|P	NA
6286	SCVKDIYKHLARS	gi|119611154|gb|EAW90	NA
6287	YAKCNPYMDSPQS	gi|2507187|sp|P22061|P	NA
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6289	VDSEFQYTYEYQG	gi|119587444|gb|EAW67	NA
6290	DNEKCKYLTKPEP	gi|29336810|sp|Q8TE59|	NA
6291	INFMLTYVAVDYS	gi|119599806|gb|EAW79	NA

6292	DIDMTDYDDVRRC	gi|1346792|sp|P49642|P	NA
6293	CDSCEKYITGRVL	gi|56404514|sp|Q6H8Q1	NA
6294	MAKMEKYLHSSRC	gi|6136393|sp|Q14191|	NA
6295	DFENSAYVVFVVL	gi|1346190|sp|P48506|G	NA
6296	LGCMDDYTTDSRG	gi|74733154|sp|Q9BTW	NA
6297	AHLNVYYIIILAW	gi|1352531|sp|P48066|S	NA
6298	GIICTFYTAVGGM	gi|12643359|sp|Q92911|	NA
6299	DCAHFHYENVDFG	gi|68846537|sp|O14559|	NA
6300	SVTSSAYPNPSIL	gi|62906845|sp|P27352|	NA
6301	ASKKTIYTYIMAS	gi|74762772|sp|Q9UIB8|	NA
6302	EEQVHTYVNTTGV	gi|71152057|sp|Q8WU2	[EEQVHTYVNTTGV|Y|1
6303	LEKIQDYEKMPES	gi|124308|sp|P14778|IL1	[LEKIQDYEKMPES|Y|49
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6305	RGSRDTYAWHKQK	gi|119595261|gb|EAW74	[RGSRDTYAWHKQK|Y|
6306	SYEGNSYTFIDPT	gi|547770|sp|P07333|CS	[SYEGNSYTFIDPT|Y|56
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['VIM|phospho|Y60|P086	NA
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['GCP2|phospho|Y83|Q9	NA
['SND1|phospho|Y84|Q1	NA
['CDV-3|phospho|Y190|Q	NA
['RBM30|phospho|Y194|	NA
['RA70|phospho|Y197|Q	NA
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['Shc1 iso2|phospho|Y23	NA
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['Dok1|phospho|Y449|Q9	NA
['Bcr|phospho|Y591|P11	NA
['PIST|phospho|Y457|Q9	NA
['Dok1|phospho|Y296|Q9	NA
['SHP-2|phospho|Y304|P	NA
['CD28|phospho|Y218|P1	NA
['PXN|phospho|Y88|P49	NA
['P130Cas|phospho|Y30	NA
['SLP76|phospho|Y145|	NA
['CD22|phospho|Y842|P	NA
['UBAP2|phospho|Y839|	NA
['PL10|phospho|Y67|P16	NA
['PKCD|phospho|Y64|Q0	NA
['Gab2|phospho|Y452|Q	NA
['gp130|phospho|Y767|P	NA
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['TPM4|phospho|Y184|P	NA
['calponin 1|phospho|Y1	NA
['KPNA5|phospho|Y17|Q	NA
['PLD2|phospho|Y169|O1	NA
['Plakophilin 2|phospho|	NA
['HIC1|phospho|Y168|Q1	NA
['KIF1A|phospho|Y1666|	NA
['CMPK|phospho|Y166|P	NA
['CXCR4|phospho|Y157|	NA
['PSMD13|phospho|Y15	NA
['Ran|phospho|Y155|P62	NA
['CMPK|phospho|Y155|P	NA
['MOGAT2|phospho|Y15	NA
['PSMA7|phospho|Y153|	NA
['SUN2|phospho|Y143|Q	NA
['NRBF2|phospho|Y143|	NA
['CIRBP|phospho|Y141|Q	NA
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['RICS|phospho|Y1315|O	NA
['TRIP6|phospho|Y131|Q	NA
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['HDJ2|phospho|Y119|P	NA
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['PABP 1|phospho|Y54|P	NA
['UNC5CL|phospho|Y194	NA
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['EGFR|phospho|Y1171|	PREDICTED
['HER2|phospho|Y1139|	PREDICTED
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['Rab7|phospho|Y183|P5	NA
['PBEF|phospho|Y188|P4	NA
['DDX5|phospho|Y297|P1	NA
['ZFP 598|phospho|Y306	NA
['A6r|phospho|Y309|Q6I	NA
['ZNF330|phospho|Y315|	NA
['SRPK2|phospho|Y318|	NA
['HSP70RY|phospho|Y33	NA
['SF3A1|phospho|Y759|Q	NA
['PLCG1|phospho|Y775|	NA
['PRP4|phospho|Y849|Q	NA
['Erbin|phospho|Y972|Q9	NA
['GRF-1|phospho|Y1105|	NA

['HYD|phospho|Y1746|O	NA
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['EGFR|phospho|Y1069|P	NA
['PAG|phospho|Y314|Q9J	NA
['P130Cas|phospho|Y668	NA
['Mpl|phospho|Y621|Q083	NA
['SLAP-130|phospho|Y59	NA
['CCR2|phospho|Y139|P4	NA
['R-spondin|phospho|Y11	NA
['Golgin-84|phospho|Y42	NA
['FGFR3|phospho|Y599|P	NA
['CPSF7|phospho|Y72|Q8	NA
['Cas-L|phospho|Y12|Q14	NA
['Bcr|phospho|Y644|P112	NA
['gp130|phospho|Y759|P4	NA
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['SNCA|phospho|Y133|P3	NA
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['MOK|phospho|Y161|Q9	NA
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['USP24|phospho|Y1274|	NA

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['Tel|phospho|Y17|P4121	NA
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['ICK|phospho|Y159|Q9U	NA
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['Abl iso1|phospho|Y139|	NA
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['radixin|phospho|Y134|P	NA
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['GALNT12|phospho|Y13	NA
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['SNAP29|phospho|Y122	NA
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['ZNF183|phospho|Y120|	NA
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['GDE|phospho|Y1117|P3	NA
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['HER3|phospho|Y1328|P	NA
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['A2LP|phospho|Y264|Q8	NA
['Lck|phospho|Y505|P06	NA
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['VEGFR-2|phospho|Y80	NA
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['Jak3|phospho|Y980|P5	NA
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['PIK3R1|phospho|Y580|	NA
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['PKCD|phospho|Y512|P	NA
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['CD28|phospho|Y209|P1	NA
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['MYH9|phospho|Y192|P	NA
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['BCS1L|phospho|Y181|	NA
['tau iso9|phospho|Y18|N	NA
['syndecan-2|phospho|Y1	NA
['ephexin1|phospho|Y87|	NA
['cortactin|phospho|Y178	NA
['talin 1|phospho|Y1777|	NA
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['MYH9|phospho|Y150|P	NA
['PABPC5|phospho|Y15|	NA
['ITGB4 iso2|phospho|Y1	NA
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['NSD1|phospho|Y1400|	NA
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['Trb2|phospho|Y14|Q92	NA
['Dok2|phospho|Y139|O6	NA
['MAP1A|phospho|Y1388	NA
['SLC25A2|phospho|Y13	NA
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['RPL18a|phospho|Y63|Q	NA
['talin 1|phospho|Y70|Q9Y	NA
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['SF3B14|phospho|Y86|Q	NA
['Dcp1b|phospho|Y191|Q	NA
['VDAC-3|phospho|Y195|	NA
['RPL7|phospho|Y195|P1	NA
['Ets-1|phospho|Y205|P14	NA
['DOCK2|phospho|Y224|	NA
['Hrs|phospho|Y216|O149	NA
['STI1|phospho|Y354|P31	NA
['HIPK3|phospho|Y359|Q	NA
['CD46 iso4|phospho|Y35	NA
['PRI2|phospho|Y381|P49	NA
['Abl iso1|phospho|Y393|	PREDICTED
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['PKM2|phospho|Y104|P	NA

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['NSFL1C|phospho|Y167	NA
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['FLNB|phospho|Y1530|	NA
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['NIT1|phospho|Y143|Q	NA
['ZO1|phospho|Y1423|Q	NA
['ACP1|phospho|Y142|P	NA
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['PMPCB|phospho|Y141|	NA
['latrophilin 2|phospho|Y1	NA
['PARD3|phospho|Y1310	NA
['VMD2L3|phospho|Y131	NA
['Erbin|phospho|Y1304|Q	NA
['SULT4A1|phospho|Y13	NA
['PHF3|phospho|Y1291|Q	NA
['Mx1|phospho|Y128|P20	NA
['LAB|phospho|Y118|Q9	NA
['OSBP|phospho|Y119|P	NA
['Cas-L|phospho|Y118|Q	NA
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['HIVEP2|phospho|Y117	NA
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['CK2-B|phospho|Y108|P	NA
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['PAR3-beta|phospho|Y1	NA
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['SNCA|phospho|Y133|P	NA
['SHIP-2|phospho|Y671|	NA
['CSFR|phospho|Y561|P	NA
['Pim1|phospho|Y218|P0	NA
['PIK3R1|phospho|Y688|	NA
['RIPK1|phospho|Y384|Q	NA
['Abl|phospho|Y245|P00	NA
['MIG-6|phospho|Y394|Q	NA
['RACK1|phospho|Y246|	NA
['HER4|phospho|Y1188|	PREDICTED
['FcRII-A|phospho|Y281|	NA
['CSF2RB|phospho|Y628	NA
['ephrin-B2|phospho|Y33	NA
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['abLIM|phospho|Y439|O	NA
['DBNL|phospho|Y335|Q	NA
NA	NA
['SLP76|phospho|Y113|	NA
['Abi-1|phospho|Y332|Q8	NA
['PIK3R1|phospho|Y368|	NA
['Syk|phospho|Y323|P43	NA
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['PPAP2A|phospho|Y185	NA
['CASD1|phospho|Y184|	NA
['calponin 2|phospho|Y1	NA
['DOCK1|phospho|Y1811	NA
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['TOM1L2|phospho|Y168	NA
['TAS2R40|phospho|Y16	NA
['ATRX|phospho|Y1667|	NA
['Nice-3|phospho|Y166|Q	NA

['P130Cas|phospho|Y165	NA
['ITGB4|phospho|Y1564|	NA
['PKCD|phospho|Y155|P	NA
['MEKK3|phospho|Y155|	NA
['MRLC2|phospho|Y154|	NA
['Casp9|phospho|Y153|P	NA
['ZNF183|phospho|Y153|	NA
['NEDD4|phospho|Y143|	NA
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['MYO7A|phospho|Y142|	NA
['SPTAN1|phospho|Y141	NA
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['ACP1|phospho|Y131|P	NA
['HYAL4|phospho|Y131|	NA
['ZDHHC7|phospho|Y130	NA
['GRK2|phospho|Y13|P25	NA
['USP34|phospho|Y1288|	NA
['DYX1C1|phospho|Y128	NA
['LOC390998|phospho|Y	NA
['A6|phospho|Y119|Q127	NA
['HSPA9B|phospho|Y118	NA
['PCM-1|phospho|Y1176|	NA
['KIAA0372|phospho|Y11	NA
['Sec24B|phospho|Y117|	NA
['TrkC|phospho|Y800|Q1	NA
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['PTP1B|phospho|Y66|P1	NA
['HePTP|phospho|Y149|	NA
['PTPRB|phospho|Y1981	NA
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['NAALADL2|phospho|Y1	NA
['XDH|phospho|Y1091|P	NA
['GRF-1|phospho|Y1087|	NA

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SH2_id	slide_id	sprot_id	sprot_name	sh2_range	expressior	Gene_name
3	714-34	O14492	APS_HUMAN	417 – 515	yes	SH2B2
68	none	O14508	SOCS2_HUMAN	48 – 156	insoluble	SOCS2
39	811-24	O14512	SOCS7_HUMAN	400 – 509	yes	SOCS7
69	none	O14543	SOCS3_HUMAN	46 – 142	insoluble	SOCS3
70	none	O14544	SOCS6_HUMAN	384 – 491	insoluble	SOCS6
19	714-29	O14796	SH21B_HUMAN	5 – 101	yes	SH2D1B
62	811-65	O15357	SHIP2_HUMAN	21 – 117	yes	INPPL1
67	none	O15524	SOCS1_HUMAN	79 – 174	insoluble	SOCS1
41	714-48	O43639	NCK2_HUMAN	285 – 380	yes	NCK2
55	714-31	O60880	SH21A_HUMAN	6 – 104	yes	SH2D1A
71	none	O75159	SOCS5_HUMAN	381 – 476	insoluble	SOCS5
27	714-74	O75791	GRAP2_HUMAN	58 – 149	yes	GRAP2
43	811-35	O75815	BCAR3_HUMAN	154 – 253	yes	BCAR3
1	714-59	P00519	ABL1_HUMAN	127 – 217	yes	ABL1
73	811-30	P00523	SRC_CHICK	148 – 245	yes	SRC
36	none	P06239	LCK_HUMAN	439 – 544	degraded	LCK
25	714-56	P06241	FYN_HUMAN	149 – 246	yes	FYN
21	811-55	P07332	FES_HUMAN	460 – 549	yes	FES
90	811-37	P07947	YES_HUMAN	158 – 255	yes	YES1
38	811-22	P07948	LYN_HUMAN	129 – 226	yes	LYN
32	714-53	P08631	HCK_HUMAN	144 – 241	yes	HCK
22	811-53	P09769	FGR_HUMAN	77 – 138	yes	FGR
47	816-39	P10686	PLCG1_RAT	550 – 657,	yes	Plcg1
86	714-61	P15498	VAV_HUMAN	671 – 765	yes	VAV1
13	none	P15882	CHIN_HUMAN	49 – 135	insoluble	CHN1
40	none	P16333	NCK1_HUMAN	282 – 376	degraded	NCK1
20	811-54	P16591	FER_HUMAN	460 – 550	yes	FER
48	811-29	P16885	PLCG2_HUMAN	532 – 635,	yes	PLCG2
49	714-70	P20936	RASA1_HUMAN	181 – 272,	yes	RASA1
10	816-10	P22681	CBL_HUMAN	267 – 341	yes	CBL
34	none	P23458	JAK1_HUMAN	127 – 224	degraded	JAK1
45	811-18	P27986	P85A_HUMAN	333 – 428,	yes	PIK3R1
63	811-20	P29350	PTN6_HUMAN	4 – 100, 1	yes	PTPN6
57	811-23	P29353	SHC1_HUMAN	488 – 579	yes	SHC1
85	none	P29597	TYK2_HUMAN	450 – 529	none	TYK2
201	816-15	P35235	PTN11_MOUSE	6 – 102	yes	Ptpn11
202	816-16	P35235	PTN11_MOUSE	112 – 216	yes	Ptpn11
76	none	P40763	STAT3_HUMAN	580 – 670	insoluble	STAT3
17	714-51	P41241	CSK_MOUSE	82 – 171	yes	Csk
74	none	P42224	STAT1_HUMAN	573 – 670	insoluble	STAT1
77	none	P42229	STAT5A_HUMAN	589 – 686	insoluble	STAT5A
81	none	P42680	TEC_HUMAN	247 – 345	none	TEC
93	811-42	P42681	TXK_HUMAN	150 – 246	yes	TXK
2	714-58	P42684	ABL2_HUMAN	173 – 263	yes	ABL2
23	714-27	P42685	FRK_HUMAN	116 – 208	yes	FRK
91	811-47	P43403	ZAP70_HUMAN	10 – 102,	yes	ZAP70
15	714-68	P46108	CRK_HUMAN	13 – 118	yes	CRK
16	714-66	P46109	CRKL_HUMAN	14 – 102	yes	CRKL
104	714-38	P48025	KSYK_MOUSE	167 – 25	yes	Syk
102	714-36	P48025	KSYK_MOUSE	14 – 106	yes	Syk
5	714-49	P51451	BLK_HUMAN	124 – 220	yes	BLK

78	none	P51692	STA5B_HUMAN	589 – 686	insoluble	STAT5B
100	811-63	P51813	BMX_HUMAN	296 – 392	yes	BMX
35	none	P52333	JAK3_HUMAN	375 – 475	degraded	JAK3
75	none	P52630	STAT2_HUMAN	572 – 667	insoluble	STAT2
87	811-41	P52735	VAV2_HUMAN	673 – 767	yes	VAV2
30	811-51	P62993	GRB2_HUMAN	60 – 152	yes	GRB2
56	811-59	P78314	3BP2_HUMAN	457 – 555	yes	SH3BP2
9	714-50	Q06187	BTK_HUMAN	281 – 377	yes	BTK
33	714-52	Q08881	ITK_HUMAN	239 – 338	yes	ITK
66	714-65	Q13094	LCP2_HUMAN	422 – 530	yes	LCP2
11	811-11	Q13191	CBLB_HUMAN	259 – 333	yes	CBLB
107	714-40	Q13191	CBLB_HUMAN	259 – 333	yes	CBLB
65	none	Q13239	SLAP1_HUMAN	84 – 175	insoluble	SLA
28	714-55	Q13322	GRB10_HUMAN	493 – 574	yes	GRB10
50	none	Q13671	RIN1_HUMAN	69 – 163	degraded	RIN1
8	714-67	Q13882	PTK6_HUMAN	78 – 170	yes	PTK6
29	714-54	Q14449	GRB14_HUMAN	439 – 535	yes	GRB14
31	none	Q14451	GRB7_HUMAN	431 – 527	degraded	GRB7
37	811-60	Q16176	Q16176_HUMAN	79 - 161	yes	lsk
83	811-25	Q63HR2	TENC1_HUMAN	1140 – 124	yes	TENC1
82	811-48	Q68CZ2	TENS3_HUMAN	1172 – 128	yes	TNS3
59	714-64	Q6S5L8	SHC4_HUMAN	526 – 617	yes	SHC4
79	811-52	Q7KZ85	SPT6H_HUMAN	1325 – 143	yes	SUPT6H
4	none	Q7M4L6	SHF_HUMAN	380 – 475	insoluble	SHF
96	714-41	Q7Z7G1	CLNK_HUMAN	309 – 419	yes	CLNK
99	811-38	Q8IZW8	TENS4_HUMAN	449 – 556	yes	TNS4
44	811-39	Q8N5H7	SH2D3_HUMAN	220 – 319	yes	SH2D3C
52	none	Q8TB24	RIN3_HUMAN	63 – 158	degraded	RIN3
6	none	Q8WV28	BLNK_HUMAN	346 – 453	insoluble	BLNK
72	none	Q8WXH5	SOCS4_HUMAN	286 – 381	insoluble	SOCS4
51	none	Q8WYP3	RIN2_HUMAN	97 – 190	degraded	RIN2
58	811-69	Q92529	SHC3_HUMAN	499 – 590	yes	SHC3
46	811-19	Q92569	P55G_HUMAN	65 – 160, 3	yes	PIK3R3
61	811-66	Q92835	SHIP1_HUMAN	5 – 101	yes	INPP5D
60	714-60	Q96IW2	SHD_HUMAN	240 – 335	yes	SHD
94	811-46	Q96JZ2	HSH2D_HUMAN	34 – 125	yes	HSH2D
42	811-34	Q9BRG2	SH23A_HUMAN	15 – 114	yes	SH2D3A
95	811-62	Q9H3Y6	SRMS_HUMAN	120 – 212	yes	SRMS
53	none	Q9H788	SH24A_HUMAN	347 – 440	insoluble	SH2D4A
84	714-62	Q9HBL0	TENS1_HUMAN	1463 – 157	yes	TNS1
89	811-44	Q9NP31	SH22A_HUMAN	95 – 186	yes	SH2D2A
54	714-73	Q9NRF2	SH2B1_HUMAN	527 – 625	yes	SH2B1
14	none	Q9NSE2	CISH_HUMAN	82 – 163	insoluble	CISH
101	714-35	Q9UGK3	STAP2_HUMAN	133 – 248	yes	STAP2
88	none	Q9UKW4	VAV3_HUMAN	672 – 766	insoluble	VAV3
12	none	Q9ULV8	CBLC_HUMAN	235 - 332	insoluble	CBLC
7	714-75	Q9ULZ2	STAP1_HUMAN	177 – 280	yes	STAP1
18	714-28	Q9UN19	DAPP1_HUMAN	35 – 129	yes	DAPP1

Correlations between the results of probing three different replica array on a single glass chip.

a-b	a-c	b-c	SH2
0.99194	0.979747	0.980817	ITK
0.9915	0.970316	0.969368	YES
0.991378	0.990506	0.993484	PTPN11 (1)
0.988643	0.987636	0.989362	SH2D3C
0.988095	0.978131	0.983175	LYN
0.986866	0.967952	0.980126	SRMS
0.986808	0.951581	0.960863	VAV2
0.985855	0.979009	0.976557	SRC
0.985789	0.976538	0.984389	ABL2
0.985691	0.985899	0.987661	PTPN11 (1-2)
0.984729	0.977608	0.983574	TXK
0.984556	0.98332	0.989567	SYK (2)
0.984311	0.987109	0.984505	VAV2
0.984176	0.978171	0.980091	TNS4
0.983623	0.970853	0.985646	SHC1
0.983149	0.971702	0.989767	MATK
0.982249	0.900358	0.910242	PIK3R1 (1-2)
0.98073	0.976571	0.968514	NCK2
0.980589	0.970094	0.968852	FYN
0.978566	0.973105	0.988984	PLCG1
0.977663	0.951676	0.951555	PIK3R3 (1-2)
0.975798	0.954761	0.958432	SYK (1)
0.974336	0.973988	0.989016	SHC1
0.973581	0.962673	0.962834	HCK
0.972913	0.972464	0.986435	SH2D1B
0.971682	0.6948	0.708777	PTPN6
0.970835	0.942722	0.952076	GRB14
0.970696	0.953177	0.980344	SUPT6H
0.97029	0.950847	0.976134	CBLB
0.969105	0.875674	0.907289	SOCS5
0.967759	0.981703	0.969613	SHIP1
0.965321	0.962414	0.968183	SH2D2A
0.965171	0.913722	0.913329	PTPN11 (2)
0.964933	0.947802	0.975969	APS
0.964795	0.941817	0.982894	FGR
0.963368	0.963922	0.967851	ABL1
0.961872	0.859325	0.922882	CRK
0.956653	0.921144	0.948954	BTK
0.954952	0.927293	0.97885	BKS
0.953751	0.917518	0.919393	CRKL
0.952318	0.970063	0.972416	TNS1
0.949748	0.931126	0.941072	GADS
0.948802	0.924193	0.972202	TNS3
0.947647	0.904806	0.957132	GRB2
0.941619	0.908747	0.955065	SHIP2
0.939934	0.922709	0.970346	BLK

For four domains the profiling experi was repeated twice. Below are repor Pearson correlation coefficients amo two experiments.

DOMAIN	PCC
FYN	0.95
GADS	0.96
NCK2	0.95
SHC1	0.9
VAV2	0.98

0.937779	0.93338	0.970997	FES
0.933764	0.880788	0.902211	NCK2
0.932958	0.740925	0.774856	SHC3
0.931854	0.793439	0.813826	BRK
0.930263	0.890118	0.940094	BMX
0.928161	0.881169	0.92699	FER
0.924988	0.90033	0.904372	SHD
0.920134	0.93048	0.969113	SOCS7
0.919566	0.921647	0.892553	FRK
0.915614	0.96226	0.914874	HSH2D
0.913085	0.889983	0.976309	CSK
0.908422	0.928755	0.88452	PLCG2
0.907833	0.913724	0.959472	FYN
0.900977	0.871108	0.862867	CBL
0.900796	0.945205	0.925392	TENC1
0.900571	0.889163	0.87943	SH2D1A
0.897288	0.880378	0.984053	SH2D3A
0.89603	0.832932	0.886903	BCAR3
0.879208	0.765469	0.860921	VAV1
0.877635	0.89453	0.816364	SH3BP2
0.876256	0.922348	0.892637	BRDG1
0.871556	0.839902	0.878097	SLP76
0.869127	0.862699	0.888412	RASA1 (1-2)
0.859044	0.899826	0.940927	GADS
0.836069	0.866174	0.948066	SH2B
0.820522	0.799402	0.822885	ZAP70 (1-2)
0.800041	0.765792	0.861451	SHC4
0.788028	0.807225	0.882372	MIST
0.62765	0.447228	0.379438	DAPP1
0.284759	0.827822	0.281346	GRB10

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PMID	sprot_SH2	name_SH2	sprot_bi	name_binder	method	Y_site
8226808	P27986	P85A_HUMAN	P04629	NTRK1_HUMAN	coimmunopr	Y757
8226808	P27986	P85A_HUMAN	P04629	NTRK1_HUMAN	competitio	Y757
11323411	Q06124	PTN11_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y659
12855672	Q06124	PTN11_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y659
14679216	P24604	TEC_MOUSE	Q61152	PTN18_MOUSE	pull down	Y381
17050525	P27986	P85A_HUMAN	P15498	VAV_HUMAN	pull down	Y174
17050525	Q62077	PLCG1_HUMAN	P15498	VAV_HUMAN	pull down	Y174
17050525	P06239	LCK_HUMAN	P15498	VAV_HUMAN	pull down	Y174
8577729	P29350	PTN6_HUMAN	P31994	FCG2B_HUMAN	proteinchi	Y292
9603468	P29350	PTN6_HUMAN	P31994	FCG2B_HUMAN	pull down	Y292
9973396	Q9ES52	SHIP1_MOUSE	P08101	FCGR2_MOUSE	pull down	Y309
10382761	P07948	LYN_HUMAN	P31994	FCG2B_HUMAN	pull down	Y292
10382761	P29353	SHC1_HUMAN	P31994	FCG2B_HUMAN	pull down	Y292
10382761	Q06124	PTN11_HUMAN	P31994	FCG2B_HUMAN	pull down	Y292
10382761	O00145	SHIP1_HUMAN	P31994	FCG2B_HUMAN	pull down	Y292
10976913	Q06124	PTN11_HUMAN	P16310	GHR_RAT	pull down	Y594
11337495	P27986	P85A_HUMAN	P27986	P85A_HUMAN	coimmunopr	Y688
11940572	P40763	STAT3_HUMAN	P04626	ERBB2_HUMAN	coimmunopr	Y1222
8798570	Q60631	GRB2_MOUSE	P54762	EPHB1_HUMAN	two hybrid	Y928
8798570	Q60760	GRB10_MOUSE	P54762	EPHB1_HUMAN	two hybrid	Y928
12223469	Q14451	GRB7_HUMAN	P54762	EPHB1_HUMAN	two hybrid	Y928
12223469	Q14451	GRB7_HUMAN	P54762	EPHB1_HUMAN	pull down	Y928
9837784	P46109	CRKL_HUMAN	P42229	STA5A_HUMAN	pull down	Y694
9837784	P46109	CRKL_HUMAN	P42229	STA5A_HUMAN	far wester	Y694
11494128	Q4JIM5	ABL2_MOUSE	P54754	EPHB3_MOUSE	pull down	Y603
11494128	Q4JIM5	ABL2_MOUSE	P54754	EPHB3_MOUSE	lex-a dime	Y603
8156998	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	coimmunopr	Y457
8156998	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	competitio	Y457
8662591	P42227	STAT3_MOUSE	P15260	INGR1_HUMAN	electropho	Y457
8662591	P42227	STAT3_MOUSE	P15260	INGR1_HUMAN	competitio	Y457
8662591	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	electropho	Y457
8662591	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	competitio	Y457
8662795	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	inferred b	Y457
15780933	P42224	STAT1_HUMAN	P15260	INGR1_HUMAN	x-ray crys	Y457
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	pull down	Y794
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	two hybrid	Y794
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	coimmunopr	Y794
8384556	P19174	PLCG1_HUMAN	P04629	NTRK1_HUMAN	coimmunopr	Y791
8384556	P19174	PLCG1_HUMAN	P04629	NTRK1_HUMAN	competitio	Y791
9890995	P29351	PTN6_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y857
11551923	P29351	PTN6_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y857
12070153	P42224	STAT1_HUMAN	P00533	EGFR_HUMAN	electropho	Y978
12070153	P42224	STAT1_HUMAN	P00533	EGFR_HUMAN	competitio	Y978
11432792	Q06124	PTN11_HUMAN	O43559	FRS3_HUMAN	two hybrid	Y455
12928397	O14796	SH21B_HUMAN	Q9UIB8	SLAF5_HUMAN	coimmunopr	Y279
12928397	O60880	SH21A_HUMAN	Q9UIB8	SLAF5_HUMAN	coimmunopr	Y279
9428692	P51692	STA5B_HUMAN	P06213	INSR_HUMAN	two hybrid	Y999
7642582	P20936	RASA1_HUMAN	P08069	IGF1R_HUMAN	pull down	Y980
9480911	Q64010	CRK_MOUSE	P08069	IGF1R_HUMAN	coimmunopr	Y980
9480911	Q64010	CRK_MOUSE	P08069	IGF1R_HUMAN	pull down	Y980
12023952	P12931	SRC_HUMAN	P35918	VGFR2_MOUSE	pull down	Y1212
16966330	P16333	NCK1_HUMAN	P35968	VGFR2_HUMAN	anti bait	Y1214

11786908	P29350	PTN6_HUMAN	P19438	TNR1A_HUMAN	pull down	Y401
11786908	Q06124	PTN11_HUMAN	P19438	TNR1A_HUMAN	pull down	Y401
11786908	O00145	SHIP1_HUMAN	P19438	TNR1A_HUMAN	pull down	Y401
15128762	P41499	PTN11_RAT	Q8K558	TRML1_MOUSE	coimmunopr	Y286
9079677	Q14451	GRB7_HUMAN	P04626	ERBB2_HUMAN	competitio	Y1139
11940572	P12931	SRC_HUMAN	P04626	ERBB2_HUMAN	coimmunopr	Y1139
11940572	P40763	STAT3_HUMAN	P04626	ERBB2_HUMAN	coimmunopr	Y1139
12061724	Q14451	GRB7_HUMAN	P04626	ERBB2_HUMAN	nuclear ma	Y1139
12975581	Q14451	GRB7_HUMAN	P04626	ERBB2_HUMAN	x-ray crys	Y1139
14665640	P29353	SHC1_HUMAN	Q02763	TIE2_HUMAN	coimmunopr	Y1080
14665640	P29353	SHC1_HUMAN	Q02763	TIE2_HUMAN	pull down	Y1080
7529874	P62994	GRB2_RAT	P11274	BCR_HUMAN	coimmunopr	Y177
8112292	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	coimmunopr	Y177
8112292	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	pull down	Y177
8955135	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	pull down	Y177
8995379	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	pull down	Y177
8995379	Q13588	GRAP_HUMAN	P11274	BCR_HUMAN	pull down	Y177
9174058	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	pull down	Y177
9178913	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	pull down	Y177
10887132	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	coimmunopr	Y177
11726515	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	anti bait	Y177
11726515	P62993	GRB2_HUMAN	P11274	BCR_HUMAN	coimmunopr	Y177
15861137	P41241	CSK_MOUSE	P55284	CADH5_MOUSE	pull down	Y685
15861137	P41241	CSK_MOUSE	P55284	CADH5_MOUSE	anti bait	Y685
16909109	P12931	SRC_HUMAN	P33151	CADH5_HUMAN	pull down	Y685
9278444	P05480	SRC_MOUSE	P08050	CXA1_RAT	pull down	Y264
11035005	P12931	SRC_CHICK	P17302	CXA1_HUMAN	pull down	Y265
9178760	P62993	GRB2_HUMAN	P30530	UFO_HUMAN	far wester	Y779
7487883	P43405	KSYK_HUMAN	P12318	FCG2A_HUMAN	pull down	Y304
11390470	P15498	VAV_HUMAN	P78314	3BP2_HUMAN	pull down	Y183
11390470	P16885	PLCG2_HUMAN	P78314	3BP2_HUMAN	pull down	Y183
11390470	P19174	PLCG1_HUMAN	P78314	3BP2_HUMAN	pull down	Y183
11390470	P52735	VAV2_HUMAN	P78314	3BP2_HUMAN	pull down	Y183
12709437	P07948	LYN_HUMAN	Q06649	3BP2_MOUSE	pull down	Y446
15751964	P06239	LCK_HUMAN	P78314	3BP2_HUMAN	pull down	Y448
9183008	Q63206	Q63206_RAT	P14317	HCLS1_HUMAN	enzymatic	Y397
15795233	P07948	LYN_HUMAN	P14317	HCLS1_HUMAN	pull down	Y397
10837138	Q15464	SHB_HUMAN	P26618	PGFRA_MOUSE	pull down	Y720
10837138	Q6PD21	SHB_MOUSE	P26618	PGFRA_MOUSE	coimmunopr	Y720
9182757	Q60631	GRB2_MOUSE	Q8C180	FRS2_MOUSE	pull down	Y196
7685273	P07947	YES_HUMAN	P09619	PGFRB_HUMAN	pull down	Y581
7685273	P12931	SRC_HUMAN	P09619	PGFRB_HUMAN	pull down	Y581
9742401	Q13239	SLAP1_HUMAN	P09619	PGFRB_HUMAN	pull down	Y581
9742401	Q13239	SLAP1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y581
12706723	P25020	SRC_RSVH1	P09619	PGFRB_HUMAN	isothermal	Y581
12706723	P25020	SRC_RSVH1	P09619	PGFRB_HUMAN	x-ray crys	Y581
1314164	P20936	RASA1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y771
1375321	P20936	RASA1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y771
8382774	P20936	RASA1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y771
10454568	Q13322	GRB10_HUMAN	P09619	PGFRB_HUMAN	pull down	Y771
10733900	P46108	CRK_HUMAN	P09619	PGFRB_HUMAN	pull down	Y771
9546424	P46108	CRK_HUMAN	P16234	PGFRA_HUMAN	coimmunopr	Y762
9546424	P46108	CRK_HUMAN	P16234	PGFRA_HUMAN	enzymatic	Y762

9546424	P46109	CRKL_HUMAN	P16234	PGFRA_HUMAN	coimmunopr	Y762
9546424	P46109	CRKL_HUMAN	P16234	PGFRA_HUMAN	enzymatic	Y762
10733900	P46108	CRK_HUMAN	P16234	PGFRA_HUMAN	pull down	Y762
9506989	Q13322	GRB10_HUMAN	P06213	INSR_HUMAN	protein tr	Y1189
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	coimmunopr	Y1189
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	two hybrid	Y1189
7528772	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y123
10752619	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	isothermal	Y123
14993273	O00145	SHIP1_HUMAN	Q9QZK7	DOK3_MOUSE	pull down	Y325
14993273	P41240	CSK_HUMAN	Q9QZK7	DOK3_MOUSE	pull down	Y325
10570256	Q13094	LCP2_HUMAN	O15117	FYB_HUMAN	coimmunopr	Y651
15477347	Q60787	LCP2_MOUSE	O35601	FYB_MOUSE	pull down	Y687
15647376	P00523	SRC_CHICK	P15311	EZRI_HUMAN	pull down	Y191
15752563	Q9NP31	SH22A_HUMAN	P55072	TERA_HUMAN	pull down	Y805
9774102	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	two hybrid	Y307
11477403	P39688	FYN_MOUSE	Q9QUM4	SLAF1_MOUSE	pull down	Y315
11477403	Q9ES52	SHIP1_MOUSE	Q9QUM4	SLAF1_MOUSE	pull down	Y315
9655255	P00523	SRC_CHICK	Q90738	AFAP1_CHICK	coimmunopr	Y451
15474475	P41240	CSK_HUMAN	Q8NHL6	LIRB1_HUMAN	coimmunopr	Y562
15474475	P41240	CSK_HUMAN	Q8NHL6	LIRB1_HUMAN	protein tr	Y562
8574854	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y303
8648092	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y303
8648092	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	surface pl	Y303
8648092	Q06124	PTN11_HUMAN	P43628	KI2L3_HUMAN	pull down	Y303
8648092	Q06124	PTN11_HUMAN	P43628	KI2L3_HUMAN	surface pl	Y303
8691154	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	coimmunopr	Y303
8691154	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y303
9148918	P29351	PTN6_MOUSE	P43628	KI2L3_HUMAN	affinity c	Y303
8691146	P29350	PTN6_HUMAN	P43626	KI2L1_HUMAN	coimmunopr	Y302
8691146	P29350	PTN6_HUMAN	P43626	KI2L1_HUMAN	pull down	Y302
9751747	P27986	P85A_HUMAN	P43626	KI2L1_HUMAN	two hybrid	Y302
9751747	P27986	P85A_HUMAN	P43626	KI2L1_HUMAN	lex-a dime	Y302
9751747	Q06124	PTN11_HUMAN	P43626	KI2L1_HUMAN	two hybrid	Y302
9751747	Q06124	PTN11_HUMAN	P43626	KI2L1_HUMAN	lex-a dime	Y302
18258597	P62993	GRB2_HUMAN	Q6X936	KIRR1_RAT	coimmunopr	Y637
9380408	P62993	GRB2_HUMAN	P09581	CSF1R_MOUSE	two hybrid	Y921
11075810	Q03160	GRB7_MOUSE	Q03135	CAV1_HUMAN	pull down	Y14
11075810	Q03160	GRB7_MOUSE	Q03135	CAV1_HUMAN	coimmunopr	Y14
11075810	Q03160	GRB7_MOUSE	Q03135	CAV1_HUMAN	competitio	Y14
11805080	P41241	CSK_MOUSE	P49817	CAV1_MOUSE	pull down	Y14
11805080	P41241	CSK_MOUSE	P49817	CAV1_MOUSE	coimmunopr	Y14
16678999	P41240	CSK_HUMAN	Q03135	CAV1_HUMAN	coimmunopr	Y14
1396585	P19174	PLCG1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y1009
7530043	Q06124	PTN11_HUMAN	P09619	PGFRB_HUMAN	surface pl	Y1009
7678051	XP_542998	PLCG1 DOG	P09619	PGFRB_HUMAN	coimmunopr	Y1009
7688466	Q06124	PTN11_HUMAN	P09619	PGFRB_HUMAN	unspecifie	Y1009
7691811	XP_534686	PTN11	P09619	PGFRB_HUMAN	coimmunopr	Y1009
8041791	Q06124	PTN11_HUMAN	P05622	PGFRB_MOUSE	coimmunopr	Y1008
8183548	Q06124	PTN11_HUMAN	P09619	PGFRB_HUMAN	experiment	Y1009
8538796	Q06124	PTN11_HUMAN	P09619	PGFRB_HUMAN	x-ray crys	Y1009
11027258	O43639	NCK2_HUMAN	P09619	PGFRB_HUMAN	unspecifie	Y1009
12606549	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	circular d	Y316
12606549	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	nuclear ma	Y316

15764601	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	nuclear ma	Y316
10811803	P19174	PLCG1_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y161
10811803	P19174	PLCG1_HUMAN	O43561	LAT_HUMAN	pull down	Y161
9655255	P00523	SRC_CHICK	Q90738	AFAP1_CHICK	coimmunopr	Y453
12387735	P43405	KSYK_HUMAN	P26038	MOES_HUMAN	pull down	Y191
10570256	Q13094	LCP2_HUMAN	O15117	FYB_HUMAN	coimmunopr	Y595
15477347	Q60787	LCP2_MOUSE	O35601	FYB_MOUSE	pull down	Y584
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	pull down	Y700
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	coimmunopr	Y700
15751964	P15498	VAV_HUMAN	Q06649	3BP2_MOUSE	coimmunopr	Y183
9516479	Q14451	GRB7_HUMAN	P21860	ERBB3_HUMAN	competitio	Y1199
9890995	P29351	PTN6_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y837
8622870	Q14451	GRB7_HUMAN	P35235	PTN11_MOUSE	two hybrid	Y584
8959326	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	coimmunopr	Y584
11432792	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	two hybrid	Y584
12531430	P62994	GRB2_RAT	P35235	PTN11_MOUSE	coimmunopr	Y584
15751964	P06239	LCK_HUMAN	Q06649	3BP2_MOUSE	pull down	Y446
15751964	P15498	VAV_HUMAN	Q06649	3BP2_MOUSE	coimmunopr	Y446
7687763	P07332	FES_HUMAN	Q6GTU5	FES_HUMAN	pull down	Y713
7684160	P27986	P85A_HUMAN	P15391	CD19_HUMAN	coimmunopr	Y531
10022120	P46109	CRKL_HUMAN	Q13191	CBLB_HUMAN	coimmunopr	Y709
17050525	P27986	P85A_HUMAN	P15498	VAV_HUMAN	pull down	Y160
17050525	Q62077	PLCG1_HUMAN	P15498	VAV_HUMAN	pull down	Y160
17050525	P06239	LCK_HUMAN	P15498	VAV_HUMAN	pull down	Y160
1382595	P26450	P85A_MOUSE	P03076	MT_POVM3	coimmunopr	Y315
8065326	Q63787	P85A_RAT	P03076	MT_POVM3	competitio	Y315
11123912	P27986	P85A_HUMAN	P03076	MT_POVM3	nuclear ma	Y315
7680435	P06239	LCK_HUMAN	P03079	MT_POVHA	nuclear ma	Y324
10790433	P41240	CSK_HUMAN	Q9NWQ8	PAG1_HUMAN	pull down	Y317
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	pull down	Y447
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y447
9182757	Q60631	GRB2_MOUSE	Q8C180	FRS2_MOUSE	pull down	Y392
9182757	Q60631	GRB2_MOUSE	Q8C180	FRS2_MOUSE	pull down	Y349
8662591	P42227	STAT3_MOUSE	P40189	IL6RB_HUMAN	electropho	Y905
8662591	P42227	STAT3_MOUSE	P40189	IL6RB_HUMAN	competitio	Y905
8662591	P42224	STAT1_HUMAN	P40189	IL6RB_HUMAN	electropho	Y905
8662591	P42224	STAT1_HUMAN	P40189	IL6RB_HUMAN	competitio	Y905
15953601	Q62077	PLCG1_HUMAN	P14753	EPOR_MOUSE	phage disp	Y367
9632781	Q06124	PTN11_HUMAN	Q8WU20	FRS2_HUMAN	far wester	Y436
9632781	Q06124	PTN11_HUMAN	Q8WU20	FRS2_HUMAN	coimmunopr	Y436
9528781	P29350	PTN6_HUMAN	P05532	KIT_MOUSE	coimmunopr	Y567
9712716	P39688	FYN_MOUSE	P09793	CTLA4_MOUSE	coimmunopr	Y218
7623809	P43405	KSYK_HUMAN	P20411	FCERG_RAT	coimmunopr	Y65
8810294	P43405	KSYK_HUMAN	P30273	FCERG_HUMAN	kinase sc	Y65
16675548	O14508	SOCS2_HUMAN	P10912	GHR_HUMAN	isothermal	Y595
17666591	O35717	SOCS2_MOUSE	P19941	GHR_RABIT	two hybrid	Y595
17666591	Q62225	CISH_MOUSE	P19941	GHR_RABIT	two hybrid	Y595
12387735	P43405	KSYK_HUMAN	P26038	MOES_HUMAN	pull down	Y205
8524328	P46108	CRK_HUMAN	P22681	CBL_HUMAN	pull down	Y774
8626543	P46108	CRK_HUMAN	P22681	CBL_HUMAN	coimmunopr	Y774
8626543	P46109	CRKL_HUMAN	P22681	CBL_HUMAN	pull down	Y774
15556646	P27986	P85A_HUMAN	P22681	CBL_HUMAN	far wester	Y774
15556646	P46109	CRKL_HUMAN	P22681	CBL_HUMAN	far wester	Y774

10930415	P39688	FYN_MOUSE	Q9NZA1	CLIC5_HUMAN	pull down	Y33
9178760	P19174	PLCG1_HUMAN	P30530	UFO_HUMAN	far western	Y821
9178760	P19174	PLCG1_HUMAN	P30530	UFO_HUMAN	coimmunopre	Y821
9178760	P27986	P85A_HUMAN	P30530	UFO_HUMAN	far western	Y821
9178760	P27986	P85A_HUMAN	P30530	UFO_HUMAN	coimmunopre	Y821
9178760	P62993	GRB2_HUMAN	P30530	UFO_HUMAN	far western	Y821
9178760	P62993	GRB2_HUMAN	P30530	UFO_HUMAN	coimmunopre	Y821
7559499	P26450	P85A_MOUSE	P19235	EPOR_HUMAN	coimmunopre	Y504
7559499	P23727	P85A_BOVIN	P19235	EPOR_HUMAN	pull down	Y504
9573010	P25911	LYN_MOUSE	P14753	EPOR_MOUSE	pull down	Y503
15953601	Q62077	PLCG1_HUMAN	P14753	EPOR_MOUSE	phage displ	Y503
8939605	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	pull down	Y349
9872323	O89100	GRAP2_MOUSE	P29353	SHC1_HUMAN	pull down	Y349
9535915	Q06124	PTN11_HUMAN	P97710	SHPS1_RAT	pull down	Y501
12928397	O14796	SH21B_HUMAN	Q9UIB8	SLAF5_HUMAN	coimmunopre	Y316
11514608	Q9QUN3	BLNK_MOUSE	P70218	M4K1_MOUSE	pull down	Y379
7537096	P19174	PLCG1_HUMAN	P10721	KIT_HUMAN	coimmunopre	Y936
10377264	P62993	GRB2_HUMAN	P10721	KIT_HUMAN	pull down	Y936
10377264	Q14451	GRB7_HUMAN	P10721	KIT_HUMAN	pull down	Y936
7487883	P43405	KSYK_HUMAN	P12318	FCG2A_HUMAN	pull down	Y288
15062102	P47941	CRKL_MOUSE	P97318	DAB1_MOUSE	pull down	Y220
11403293	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	enzymatic s	Y941
14632132	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	two hybrid	Y941
8657103	P19174	PLCG1_HUMAN	P43405	KSYK_HUMAN	coimmunopre	Y352
8657103	P19174	PLCG1_HUMAN	P43405	KSYK_HUMAN	pull down	Y352
16410013	P08487	PLCG1_BOVIN	P48025	KSYK_MOUSE	nuclear mag	Y346
16410013	P08487	PLCG1_BOVIN	P48025	KSYK_MOUSE	electrophor	Y346
7589433	P27986	P85A_HUMAN	P08069	IGF1R_HUMAN	coimmunopre	Y1346
7642582	P27986	P85A_HUMAN	P08069	IGF1R_HUMAN	pull down	Y1346
7642582	Q06124	PTN11_HUMAN	P08069	IGF1R_HUMAN	pull down	Y1346
8603569	P27986	P85A_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y1346
8895367	Q06124	PTN11_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y1346
8895367	Q06124	PTN11_HUMAN	P08069	IGF1R_HUMAN	beta galact	Y1346
9415396	Q64143	P55G_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y1346
9415396	Q64143	P55G_MOUSE	P08069	IGF1R_HUMAN	pull down	Y1346
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y1346
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	coimmunopre	Y1346
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y1346
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	pull down	Y743
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	coimmunopre	Y743
17666591	P42230	STA5A_MOUSE	P19941	GHR_RABIT	two hybrid	Y534
17666591	P42232	STA5B_HUMAN	P19941	GHR_RABIT	two hybrid	Y534
17666591	P42232	STA5B_MOUSE	P19941	GHR_RABIT	electrophor	Y534
7527043	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopre	Y1092
8940013	Q60631	GRB2_MOUSE	P00533	EGFR_HUMAN	surface pla	Y1092
7518560	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopre	Y1092
7993895	P19174	PLCG1_HUMAN	P00533	EGFR_HUMAN	cross-linki	Y1092
9153411	P06240	LCK_MOUSE	P00533	EGFR_HUMAN	pull down	Y1092
10229072	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopre	Y1092
10229072	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	pull down	Y1092
10229072	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	competition	Y1092
11896612	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopre	Y1092
12577067	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	pull down	Y1092

14966128	P40763	STAT3_HUMAN	P00533	EGFR_HUMAN	pull down	Y1092
9516477	P19174	PLCG1_HUMAN	P30556	AGTR1_HUMAN	pull down	Y319
9814969	Q62689	JAK2_RAT	P25095	AGTRA_RAT	pull down	Y319
9814969	Q06124	PTN11_HUMAN	P25095	AGTRA_RAT	pull down	Y319
8605876	P52630	STAT2_HUMAN	P17181	INAR1_HUMAN	pull down	Y466
9121453	P52630	STAT2_HUMAN	P17181	INAR1_HUMAN	inferred b	Y466
9677371	P52630	STAT2_HUMAN	P17181	INAR1_HUMAN	anti bait	Y466
12220192	P52630	STAT2_HUMAN	P17181	INAR1_HUMAN	pull down	Y466
12220192	P52630	STAT2_HUMAN	P17181	INAR1_HUMAN	surface pl	Y466
17666591	P42230	STA5A_MOUSE	P19941	GHR_RABIT	two hybrid	Y627
17666591	P42232	STA5B_MOUSE	P19941	GHR_RABIT	two hybrid	Y627
17666591	P42232	STA5B_MOUSE	P19941	GHR_RABIT	electropho	Y627
9223670	P27986	P85A_HUMAN	P29376	LTK_HUMAN	coimmunopr	Y753
11323411	Q06124	PTN11_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y627
11453982	Q06124	PTN11_HUMAN	Q13480	GAB1_HUMAN	surface pl	Y627
12855672	Q06124	PTN11_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y627
8673706	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	coimmunopr	Y128
8673706	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y128
9047237	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y128
10229072	P16333	NCK1_HUMAN	Q13094	LCP2_HUMAN	coimmunopr	Y128
10347175	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y128
8524328	P46108	CRK_HUMAN	P22681	CBL_HUMAN	pull down	Y700
9200440	P15498	VAV_HUMAN	P22681	CBL_HUMAN	pull down	Y700
15556646	P27986	P85A_HUMAN	P22681	CBL_HUMAN	far wester	Y700
15556646	P46109	CRKL_HUMAN	P22681	CBL_HUMAN	far wester	Y700
7493940	P46109	CRKL_HUMAN	P49023	PAXI_HUMAN	pull down	Y118
7537852	Q04929	CRK_CHICK	P49024	PAXI_CHICK	experiment	Y118
1314164	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y740
1330535	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	biophysica	Y740
7683666	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	surface pl	Y740
7730365	P39688	FYN_MOUSE	P05622	PGFRB_MOUSE	pull down	Y739
7876130	Q63787	P85A_RAT	P09619	PGFRB_HUMAN	pull down	Y740
8382612	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	nuclear ma	Y740
8382774	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	coimmunopr	Y740
8670861	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	nuclear ma	Y740
9512716	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	competitio	Y740
10644978	Q91ZM2	SH2B1_MOUSE	P05622	PGFRB_MOUSE	competitio	Y739
10644978	Q91ZM2	SH2B1_MOUSE	P05622	PGFRB_MOUSE	coimmunopr	Y739
10752619	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	isothermal	Y740
11710529	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	two hybrid	Y740
11896612	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y740
8524328	P46108	CRK_HUMAN	P22681	CBL_HUMAN	pull down	Y337
16888623	P00519	ABL1_HUMAN	P15941	MUC1_HUMAN	coimmunopr	Y1243
9360983	P06241	FYN_HUMAN	P56945	BCAR1_HUMAN	coimmunopr	Y664
9360983	P06241	FYN_HUMAN	P56945	BCAR1_HUMAN	pull down	Y664
10542110	P12931	SRC_HUMAN	P56945	BCAR1_HUMAN	fluorescen	Y664
16245368	P06239	LCK_HUMAN	Q63767	BCAR1_RAT	surface pl	Y762
16245368	P06239	LCK_HUMAN	Q63767	BCAR1_RAT	pull down	Y762
16245368	P06239	LCK_HUMAN	Q63767	BCAR1_RAT	x-ray crys	Y762
7493946	Q06124	PTN11_HUMAN	P06213	INSR_HUMAN	pull down	Y1185
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	coimmunopr	Y1185
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	two hybrid	Y1185
8194526	P46108	CRK_HUMAN	Q64010	CRK_MOUSE	pull down	Y221

8605877	P42224	STAT1_HUMAN	P42224	STAT1_HUMAN	coimmunopr	Y701
8605877	P42224	STAT1_HUMAN	P42224	STAT1_HUMAN	competitio	Y701
8605877	P42224	STAT1_HUMAN	P42224	STAT1_HUMAN	pull down	Y701
8605877	P52630	STAT2_HUMAN	P42224	STAT1_HUMAN	coimmunopr	Y701
8605877	P52630	STAT2_HUMAN	P42224	STAT1_HUMAN	competitio	Y701
8605877	P52630	STAT2_HUMAN	P42224	STAT1_HUMAN	pull down	Y701
9630226	P42224	STAT1_HUMAN	P42224	STAT1_HUMAN	x-ray crys	Y701
9573010	P25911	LYN_MOUSE	P14753	EPOR_MOUSE	pull down	Y488
9281317	P62994	GRB2_RAT	P10686	PLCG1_RAT	coimmunopr	Y783
9281317	P62994	GRB2_RAT	P08487	PLCG1_BOVIN	pull down	Y783
15764700	P10686	PLCG1_RAT	P10686	PLCG1_RAT	coimmunopr	Y783
16684964	Q06124	PTN11_HUMAN	P36888	FLT3_HUMAN	competitio	Y589
16684964	Q06124	PTN11_HUMAN	P36888	FLT3_HUMAN	coimmunopr	Y589
9281317	P62994	GRB2_RAT	P10686	PLCG1_RAT	coimmunopr	Y771
9281317	P62994	GRB2_RAT	P08487	PLCG1_BOVIN	pull down	Y771
10377264	P62993	GRB2_HUMAN	P10721	KIT_HUMAN	pull down	Y703
14679216	P24604	TEC_MOUSE	Q61152	PTN18_MOUSE	pull down	Y354
12878163	P46108	CRK_HUMAN	P10721	KIT_HUMAN	pull down	Y900
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	pull down	Y589
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y589
11786908	O00145	SHIP1_HUMAN	P25445	TNR6_HUMAN	pull down	Y291
15536091	P62993	GRB2_HUMAN	P11137	MAP2_HUMAN	pull down	Y67
15536091	P62993	GRB2_HUMAN	P11137	MAP2_HUMAN	far wester	Y67
15536091	P62993	GRB2_HUMAN	P11137	MAP2_HUMAN	enzyme lin	Y67
10022120	P46109	CRKL_HUMAN	Q13191	CBLB_HUMAN	coimmunopr	Y665
15143214	P43404	ZAP70_MOUSE	Q8R4V1	NFAM1_MOUSE	pull down	Y215
15143214	P43405	KSYK_HUMAN	Q8R4V1	NFAM1_MOUSE	pull down	Y215
10681522	Q06124	PTN11_HUMAN	O95297	MPZL1_HUMAN	coimmunopr	Y241
7797556	P27986	P85A_HUMAN	P00533	EGFR_HUMAN	competitio	Y944
7518772	P62993	GRB2_HUMAN	P18433	PTPRA_HUMAN	pull down	Y798
10698938	P12931	SRC_HUMAN	P18433	PTPRA_HUMAN	coimmunopr	Y798
10698938	P00523	SRC_CHICK	P18433	PTPRA_HUMAN	pull down	Y798
12834342	P00523	SRC_CHICK	P18052	PTPRA_MOUSE	fluorescen	Y825
17440088	P29353	SHC1_HUMAN	P37173	TGFR2_HUMAN	coimmunopr	Y284
8226808	P29353	SHC1_HUMAN	P04629	NTRK1_HUMAN	coimmunopr	Y496
8226808	P29353	SHC1_HUMAN	P04629	NTRK1_HUMAN	competitio	Y496
8662591	P42227	STAT3_MOUSE	P40189	IL6RB_HUMAN	electropho	Y814
8662591	P42227	STAT3_MOUSE	P40189	IL6RB_HUMAN	competitio	Y814
8662795	P42224	STAT1_HUMAN	P40189	IL6RB_HUMAN	inferred b	Y814
7681396	P06241	FYN_HUMAN	P07333	CSF1R_HUMAN	pull down	Y809
1661130	P06241	FYN_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y857
12815057	P22681	CBL_HUMAN	O43597	SPY2_HUMAN	coimmunopr	Y55
9506989	Q13322	GRB10_HUMAN	P06213	INSR_HUMAN	protein tr	Y1190
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	coimmunopr	Y1190
9742218	Q9NRF1	SH2B1_HUMAN	P06213	INSR_HUMAN	two hybrid	Y1190
17998938	Q9UKW4	VAV3_HUMAN	Q9UM73	ALK_HUMAN	coimmunopr	Y1283
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	pull down	Y684
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	two hybrid	Y684
10748052	P62994	GRB2_RAT	P35739	NTRK1_RAT	coimmunopr	Y684
16917505	P27986	P85A_HUMAN	P30875	SSR2_MOUSE	coimmunopr	Y71
16917505	P27986	P85A_HUMAN	P30875	SSR2_MOUSE	surface pl	Y71
10660620	P29350	PTN6_HUMAN	Q9UKJ1	PILRA_HUMAN	surface pl	Y269
1314164	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y751

1330535	O00459	P85B_HUMAN	P09619	PGFRB_HUMAN	biophysica	Y751
1330535	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	circular d	Y751
1330535	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	classical	Y751
7536927	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	surface pl	Y751
7680644	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	cross-link	Y751
7683666	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	surface pl	Y751
7692233	P16333	NCK1_HUMAN	P09619	PGFRB_HUMAN	pull down	Y751
7692233	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	pull down	Y751
7730365	P39688	FYN_MOUSE	P05622	PGFRB_MOUSE	pull down	Y750
7876130	Q63787	P85A_RAT	P09619	PGFRB_HUMAN	pull down	Y751
8382774	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	coimmunopr	Y751
8564419	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	pull down	Y751
8670861	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	nuclear ma	Y751
9153411	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	pull down	Y751
10336465	P23727	P85A_BOVIN	P09619	PGFRB_HUMAN	surface pl	Y751
10752619	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	isothermal	Y751
11027258	P16333	NCK1_HUMAN	P09619	PGFRB_HUMAN	unspecifie	Y751
11710529	P27986	P85A_HUMAN	P09619	PGFRB_HUMAN	two hybrid	Y751
16569213	P27986	P85A_HUMAN	Q05030	PGFRB_RAT	pull down	Y750
15557335	P12931	SRC_HUMAN	Q8WUM4	PDC6I_HUMAN	pull down	Y319
15557335	P12931	SRC_HUMAN	Q8WUM4	PDC6I_HUMAN	coimmunopr	Y319
18258597	P62993	GRB2_HUMAN	Q6X936	KIRR1_RAT	coimmunopr	Y637
9162084	P12931	SRC_HUMAN	P16284	PECA1_HUMAN	pull down	Y713
9774457	P29350	PTN6_HUMAN	P16284	PECA1_HUMAN	pull down	Y713
9774457	P29350	PTN6_HUMAN	P16284	PECA1_HUMAN	surface pl	Y713
9774457	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	pull down	Y713
9774457	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	surface pl	Y713
10704309	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	lambda pha	Y713
12535670	P41499	PTN11_RAT	P16284	PECA1_HUMAN	pull down	Y713
10556798	P29350	PTN6_HUMAN	P20138	CD33_HUMAN	coimmunopr	Y358
14652006	P29350	PTN6_HUMAN	Q7Z6A9	BTLA_HUMAN	coimmunopr	Y282
14652006	Q06124	PTN11_HUMAN	Q7Z6A9	BTLA_HUMAN	coimmunopr	Y282
12171928	P06241	FYN_HUMAN	O15268	SKAP1_HUMAN	coimmunopr	Y271
12171928	P62993	GRB2_HUMAN	O15268	SKAP1_HUMAN	coimmunopr	Y271
7509083	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	coimmunopr	Y142
7528772	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y142
7544002	P29353	SHC1_HUMAN	P20963	CD3Z_HUMAN	nuclear ma	Y142
8901551	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y142
7761456	P43403	ZAP70_HUMAN	P07766	CD3E_HUMAN	surface pl	Y199
7761456	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	surface pl	Y199
7761456	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	pull down	Y199
9698567	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	x-ray crys	Y199
11855827	P43403	ZAP70_HUMAN	P07766	CD3E_HUMAN	pull down	Y199
10488096	P27986	P85A_HUMAN	P29350	PTN6_HUMAN	pull down	Y564
10488096	P27986	P85A_HUMAN	P29350	PTN6_HUMAN	coimmunopr	Y564
16649996	P78314	3BP2_HUMAN	P29350	PTN6_HUMAN	pull down	Y564
16649996	P78314	3BP2_HUMAN	P29350	PTN6_HUMAN	surface pl	Y564
17094949	P22681	CBL_HUMAN	Q7Z698	SPRE2_HUMAN	coimmunopr	Y228
9774102	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	two hybrid	Y281
10549287	O14796	SH21B_HUMAN	Q13291	SLAF1_HUMAN	pull down	Y281
10549287	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	pull down	Y281
10607564	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	fluorescen	Y281
11313386	O00145	SHIP1_HUMAN	Q13291	SLAF1_HUMAN	pull down	Y281

11313386	O00145	SHIP1_HUMAN	Q13291	SLAF1_HUMAN	coimmunopr	Y281
11313386	Q06124	PTN11_HUMAN	Q13291	SLAF1_HUMAN	pull down	Y281
11313386	Q06124	PTN11_HUMAN	Q13291	SLAF1_HUMAN	coimmunopr	Y281
11389028	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	two hybrid	Y281
11477068	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	fluorescen	Y281
11477068	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	coimmunopr	Y281
11477403	P39688	FYN_MOUSE	Q9QUM4	SLAF1_MOUSE	pull down	Y288
11689425	O35324	SH21B_MOUSE	Q9QUM4	SLAF1_MOUSE	fluorescen	Y288
11689425	O35324	SH21B_MOUSE	Q9QUM4	SLAF1_MOUSE	two hybrid	Y288
11806999	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	coimmunopr	Y281
11823424	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	nuclear ma	Y281
12225753	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	nuclear ma	Y281
12545174	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	x-ray crys	Y281
14674764	O60880	SH21A_HUMAN	Q13291	SLAF1_HUMAN	fluorescen	Y281
12225753	O60880	SH21A_HUMAN	Q9UIB8	SLAF5_HUMAN	nuclear ma	Y281
9867848	P35235	PTN11_MOUSE	P31809	CEAM1_MOUSE	pull down	Y488
11694516	P29353	SHC1_HUMAN	P13688	CEAM1_HUMAN	pull down	Y493
11279131	P00519	ABL1_HUMAN	P05067	A4_HUMAN	pull down	Y757
11032808	P00523	SRC_CHICK	P03372	ESR1_HUMAN	pull down	Y537
14963108	P12931	SRC_HUMAN	P03372	ESR1_HUMAN	pull down	Y537
12070037	Q06124	PTN11_HUMAN	P02730	B3AT_HUMAN	coimmunopr	Y359
12852788	P62993	GRB2_HUMAN	O95869	LY66F_HUMAN	pull down	Y281
12852788	P62993	GRB2_HUMAN	O95869	LY66F_HUMAN	coimmunopr	Y281
12852788	Q14451	GRB7_HUMAN	O95869	LY66F_HUMAN	pull down	Y281
12852788	Q14451	GRB7_HUMAN	O95869	LY66F_HUMAN	coimmunopr	Y281
7522233	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	coimmunopr	Y546
11432792	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	two hybrid	Y546
11684012	P35235	PTN11_MOUSE	P35235	PTN11_MOUSE	pull down	Y546
11684012	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	pull down	Y546
12403768	O35718	SOCS3_MOUSE	P35235	PTN11_MOUSE	pull down	Y546
12403768	O35718	SOCS3_MOUSE	P35235	PTN11_MOUSE	surface pl	Y546
12531430	P62994	GRB2_RAT	P35235	PTN11_MOUSE	coimmunopr	Y546
11551923	Q60631	GRB2_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y822
10681522	Q06124	PTN11_HUMAN	O95297	MPZL1_HUMAN	coimmunopr	Y263
11877430	P29320	EPHA3_HUMAN	Q96T51	RUFY1_HUMAN	coimmunopr	Y389
10464310	P46108	CRK_HUMAN	P11362	FGFR1_HUMAN	xxx(Affi-G	Y463
9489702	P19174	PLCG1_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y220
9489702	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y220
10811803	P27986	P85A_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y220
10811803	P27986	P85A_HUMAN	O43561	LAT_HUMAN	pull down	Y220
10811803	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y220
10811803	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	pull down	Y220
15029250	O89100	GRAP2_MOUSE	O43561	LAT_HUMAN	x-ray crys	Y220
9182757	Q60631	GRB2_MOUSE	Q8C180	FRS2_MOUSE	pull down	Y306
15121872	Q91ZM2	O55033_MOUSE	Q62137	JAK3_MOUSE	coimmunopr	Y781
9632797	P27986	P85A_HUMAN	Q02858	TIE2_MOUSE	two hybrid	Y1100
9632797	P26450	P85A_MOUSE	Q02858	TIE2_MOUSE	pull down	Y1100
10521483	Q60631	GRB2_MOUSE	Q02858	TIE2_MOUSE	two hybrid	Y1100
10521483	Q60631	GRB2_MOUSE	Q02858	TIE2_MOUSE	surface pl	Y1100
10521483	Q60631	GRB2_MOUSE	Q02858	TIE2_MOUSE	pull down	Y1100
10521483	P62993	GRB2_HUMAN	Q02858	TIE2_MOUSE	coimmunopr	Y1100
10521483	Q03160	GRB7_MOUSE	Q02858	TIE2_MOUSE	two hybrid	Y1100
10521483	Q03160	GRB7_MOUSE	Q02858	TIE2_MOUSE	surface pl	Y1100

10521483	Q03160	GRB7_MOUSE	Q02858	TIE2_MOUSE	pull down	Y1100
10521483	Q14451	GRB7_HUMAN	Q02858	TIE2_MOUSE	coimmunopr	Y1100
15549731	P29350	PTN6_HUMAN	Q8TDQ1	CLM1_HUMAN	coimmunopr	Y205
12598525	P19174	PLCG1_HUMAN	P35968	VGFR2_HUMAN	pull down	Y1008
7504175	Q06124	PTN11_HUMAN	P35570	IRS1_RAT	pull down	Y1172
7513703	Q06124	PTN11_HUMAN	P35568	IRS1_HUMAN	surface pl	Y1179
8631859	P39688	FYN_MOUSE	P35570	IRS1_RAT	pull down	Y1172
8631859	P39688	FYN_MOUSE	P35570	IRS1_RAT	anti bait	Y1172
11602579	Q06124	PTN11_HUMAN	P16581	LYAM2_HUMAN	coimmunopr	Y603
7529871	Q60631	GRB2_MOUSE	P98083	SHC1_MOUSE	coimmunopr	Y423
8084588	P62994	GRB2_RAT	P29353	SHC1_HUMAN	pull down	Y427
8663178	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	surface pl	Y427
8940013	Q60631	GRB2_MOUSE	P29353	SHC1_HUMAN	surface pl	Y427
8995379	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	pull down	Y427
8995379	Q13588	GRAP_HUMAN	P29353	SHC1_HUMAN	pull down	Y427
9083103	P62994	GRB2_RAT	P29353	SHC1_HUMAN	coimmunopr	Y427
9175774	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	pull down	Y427
9254595	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	isothermal	Y427
9872323	O89100	GRAP2_MOUSE	P29353	SHC1_HUMAN	pull down	Y427
9973396	Q9ES52	SHIP1_MOUSE	P29353	SHC1_HUMAN	surface pl	Y427
11827484	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	x-ray crys	Y427
12213123	P62993	GRB2_HUMAN	P29353	SHC1_HUMAN	surface pl	Y427
18056706	P06241	FYN_HUMAN	Q9NWQ8	PAG1_HUMAN	coimmunopr	Y163
18056706	P06241	FYN_HUMAN	Q9NWQ8	PAG1_HUMAN	peptide ar	Y163
9480911	Q64010	CRK_MOUSE	P08069	IGF1R_HUMAN	pull down	Y973
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y973
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	coimmunopr	Y973
10026153	P41240	CSK_HUMAN	P08069	IGF1R_HUMAN	two hybrid	Y973
7528772	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y83
8648092	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	surface pl	Y83
8648092	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y83
8901551	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y83
9185620	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	surface pl	Y83
10704231	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y83
15832366	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	peptide ar	Y83
11714803	O00145	SHIP1_HUMAN	P24394	IL4RA_HUMAN	pull down	Y713
11714803	P29350	PTN6_HUMAN	P24394	IL4RA_HUMAN	pull down	Y713
11416002	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	coimmunopr	Y612
16230374	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	pull down	Y612
8631775	P32577	CSK_RAT	P06239	LCK_HUMAN	surface pl	Y394
8631775	P32577	CSK_RAT	P06239	LCK_HUMAN	two hybrid	Y394
7524477	P41240	CSK_HUMAN	P06241	FYN_HUMAN	pull down	Y420
11536047	P40763	STAT3_HUMAN	P07949	RET_HUMAN	coimmunopr	Y752
16407827	P62993	GRB2_HUMAN	O14939	PLD2_HUMAN	pull down	Y179
17666591	P42230	STA5A_MOUSE	P19941	GHR_RABIT	two hybrid	Y566
17666591	P42232	STA5B_MOUSE	P19941	GHR_RABIT	two hybrid	Y566
17666591	P42232	STA5B_MOUSE	P19941	GHR_RABIT	electropho	Y566
9162084	P12931	SRC_HUMAN	P16284	PECA1_HUMAN	pull down	Y690
9312087	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	pull down	Y690
9774457	P29350	PTN6_HUMAN	P16284	PECA1_HUMAN	pull down	Y690
9774457	P29350	PTN6_HUMAN	P16284	PECA1_HUMAN	surface pl	Y690
9774457	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	pull down	Y690
9774457	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	surface pl	Y690

10704309	Q06124	PTN11_HUMAN	P16284	PECA1_HUMAN	lambda pha	Y690
12535670	P41499	PTN11_RAT	P16284	PECA1_HUMAN	pull down	Y690
7680095	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	surface pl	Y732
17700527	P12931	SRC_HUMAN	P23743	DGKA_HUMAN	coimmunopr	Y335
17700527	P12931	SRC_HUMAN	P23743	DGKA_HUMAN	pull down	Y335
10064597	O35716	SOCS1_MOUSE	Q62120	JAK2_MOUSE	two hybrid	Y1007
10064597	O35716	SOCS1_MOUSE	Q62120	JAK2_MOUSE	coimmunopr	Y1007
10421843	O14543	SOCS3_HUMAN	O60674	JAK2_HUMAN	pull down	Y1007
10421843	O15524	SOCS1_HUMAN	O60674	JAK2_HUMAN	two hybrid	Y1007
9890938	Q14765	STAT4_HUMAN	Q99665	I12R2_HUMAN	fluorescen	Y800
10415122	Q14765	STAT4_HUMAN	Q99665	I12R2_HUMAN	pull down	Y800
14559241	O14543	SOCS3_HUMAN	Q99665	I12R2_HUMAN	pull down	Y800
8605877	P42224	STAT1_HUMAN	P52630	STAT2_HUMAN	coimmunopr	Y690
8605877	P42224	STAT1_HUMAN	P52630	STAT2_HUMAN	competitio	Y690
8605877	P42224	STAT1_HUMAN	P52630	STAT2_HUMAN	pull down	Y690
8605877	P52630	STAT2_HUMAN	P52630	STAT2_HUMAN	coimmunopr	Y690
8605877	P52630	STAT2_HUMAN	P52630	STAT2_HUMAN	competitio	Y690
8605877	P52630	STAT2_HUMAN	P52630	STAT2_HUMAN	pull down	Y690
8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	two hybrid	Y525
8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	pull down	Y525
8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	coimmunopr	Y525
7535778	P19174	PLCG1_HUMAN	P16234	PGFRA_HUMAN	experiment	Y1018
7493940	P46109	CRKL_HUMAN	P49023	PAXI_HUMAN	pull down	Y31
7537852	Q04929	CRK_CHICK	P49024	PAXI_CHICK	experiment	Y31
17666591	O35717	SOCS2_MOUSE	P19941	GHR_RABIT	two hybrid	Y487
17666591	Q62225	CISH_MOUSE	P19941	GHR_RABIT	coimmunopr	Y487
15056653	Q13882	PTK6_HUMAN	Q13882	PTK6_HUMAN	surface pl	Y447
10704446	P46108	CRK_HUMAN	P49024	PAXI_CHICK	pull down	Y31
1656221	P19174	PLCG1_HUMAN	P11362	FGFR1_HUMAN	pull down	Y766
8321198	P19174	PLCG1_HUMAN	P11362	FGFR1_HUMAN	anti bait	Y766
12181353	Q6PD21	SHB_MOUSE	P11362	FGFR1_HUMAN	experiment	Y766
18412956	P27986	P85A_HUMAN	P11362	FGFR1_HUMAN	pull down	Y766
18412956	P27986	P85A_HUMAN	P11362	FGFR1_HUMAN	coimmunopr	Y766
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	pull down	Y717
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	coimmunopr	Y717
16380958	P41240	CSK_HUMAN	Q6GTX8	LAIR1_HUMAN	3 hybrid m	Y281
10764762	P29350	PTN6_HUMAN	Q6GTX8	LAIR1_HUMAN	coimmunopr	Y281
10764762	P29350	PTN6_HUMAN	Q6GTX8	LAIR1_HUMAN	pull down	Y281
10206955	P29350	PTN6_HUMAN	P20138	CD33_HUMAN	pull down	Y340
10206955	Q06124	PTN11_HUMAN	P20138	CD33_HUMAN	pull down	Y340
10206955	P29350	PTN6_HUMAN	P20138	CD33_HUMAN	coimmunopr	Y340
10206955	Q06124	PTN11_HUMAN	P20138	CD33_HUMAN	coimmunopr	Y340
10556798	P29350	PTN6_HUMAN	P20138	CD33_HUMAN	coimmunopr	Y340
10556798	P29350	PTN6_HUMAN	P20138	CD33_HUMAN	enzymatic	Y340
9890995	P29351	PTN6_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y777
9489702	P19174	PLCG1_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y200
9489702	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y200
10811803	P27986	P85A_HUMAN	O43561	LAT_HUMAN	pull down	Y200
10811803	P27986	P85A_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y200
10811803	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	coimmunopr	Y200
10811803	P62993	GRB2_HUMAN	O43561	LAT_HUMAN	pull down	Y200
15029250	O89100	GRAP2_MOUSE	O43561	LAT_HUMAN	x-ray crys	Y200
10377409	P27986	P85A_HUMAN	P15311	EZRI_HUMAN	pull down	Y354

11123912	P27986	P85A_HUMAN	P03076	MT_POVM3	nuclear ma	Y322
17094949	P22681	CBL_HUMAN	Q7Z698	SPRE2_HUMAN	coimmunopr	Y231
18056706	P06241	FYN_HUMAN	Q9NWQ8	PAG1_HUMAN	coimmunopr	Y181
18056706	P06241	FYN_HUMAN	Q9NWQ8	PAG1_HUMAN	peptide ar	Y181
8628282	P19174	PLCG1_HUMAN	P07949	RET_HUMAN	competitio	Y1015
8662982	Q62077	PLCG1_MOUSE	P07949	RET_HUMAN	two hybrid	Y1015
8662982	Q62077	PLCG1_MOUSE	P07949	RET_HUMAN	pull down	Y1015
9047383	P08487	PLCG1_BOVIN	P07949	RET_HUMAN	pull down	Y1015
16569669	Q62985	SH2B1_RAT	P07949	RET_HUMAN	two hybrid	Y981
17471236	Q62985	SH2B1_RAT	P07949	RET_HUMAN	two hybrid	Y981
17471236	Q62985	SH2B1_RAT	P07949	RET_HUMAN	pull down	Y981
11827956	Q9JID9	SH2B2_MOUSE	Q61851	FGFR3_MOUSE	lex-a dime	Y719
11827956	Q9JID9	SH2B2_MOUSE	Q61851	FGFR3_MOUSE	coimmunopr	Y719
11827956	Q9JID9	SH2B2_MOUSE	Q61851	FGFR3_MOUSE	two hybrid	Y719
18412956	P27986	P85A_HUMAN	P11362	FGFR1_HUMAN	pull down	Y730
18412956	P27986	P85A_HUMAN	P11362	FGFR1_HUMAN	coimmunopr	Y730
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	pull down	Y779
11316748	P46108	CRK_HUMAN	O14654	IRS4_HUMAN	coimmunopr	Y779
1396585	P19174	PLCG1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y1021
7678051	XP_542998	PLCG1 DOG	P09619	PGFRB_HUMAN	coimmunopr	Y1021
7876130	P08487	PLCG1_BOVIN	P09619	PGFRB_HUMAN	pull down	Y1021
8119896	Q06124	PTN11_HUMAN	P09619	PGFRB_HUMAN	enzymatic	Y1021
8181064	P08487	PLCG1_BOVIN	P09619	PGFRB_HUMAN	nuclear ma	Y1021
8555205	P08487	PLCG1_BOVIN	P09619	PGFRB_HUMAN	nuclear ma	Y1021
9989826	O14492	SH2B2_HUMAN	P09619	PGFRB_HUMAN	pull down	Y1021
10373546	P10686	PLCG1_RAT	P09619	PGFRB_HUMAN	surface pl	Y1021
11896612	P19174	PLCG1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y1021
15641795	P19174	PLCG1_HUMAN	P09619	PGFRB_HUMAN	nuclear ma	Y1021
17620338	P22681	CBL_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y1021
7522233	P62993	GRB2_HUMAN	P35235	PTN11_MOUSE	coimmunopr	Y304
9528781	Q06124	PTN11_HUMAN	P05532	KIT_MOUSE	coimmunopr	Y569
14652006	P29350	PTN6_HUMAN	Q7Z6A9	BTLA_HUMAN	coimmunopr	Y257
14652006	Q06124	PTN11_HUMAN	Q7Z6A9	BTLA_HUMAN	coimmunopr	Y257
7528772	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y111
8901551	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y111
10752619	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	isothermal	Y111
11266449	P29350	PTN6_HUMAN	Q78DX7	ROS_MOUSE	two hybrid	Y2267
16765915	P39688	FYN_MOUSE	Q9QYB8	ADDB_MOUSE	pull down	Y489
11266449	P29350	PTN6_HUMAN	P08922	ROS_HUMAN	pull down	Y2274
11266449	P29350	PTN6_HUMAN	P08922	ROS_HUMAN	coimmunopr	Y2274
9079809	P27986	P85A_HUMAN	P06127	CD5_HUMAN	surface pl	Y487
9079809	P27986	P85A_HUMAN	P06127	CD5_HUMAN	pull down	Y487
15886098	P00519	ABL1_HUMAN	Q13671	RIN1_HUMAN	coimmunopr	Y36
15886098	P42684	ABL2_HUMAN	Q13671	RIN1_HUMAN	coimmunopr	Y36
9516479	Q14451	GRB7_HUMAN	P21860	ERBB3_HUMAN	competitio	Y1262
11551923	P29351	PTN6_MOUSE	P35329	CD22_MOUSE	coimmunopr	Y837
9380408	P62993	GRB2_HUMAN	P09581	CSF1R_MOUSE	two hybrid	Y697
9857184	O89100	GRAP2_MOUSE	P09581	CSF1R_MOUSE	two hybrid	Y697
9857184	O89100	GRAP2_MOUSE	P09581	CSF1R_MOUSE	pull down	Y697
16407264	O15524	SOCS1_HUMAN	Q99683	M3K5_HUMAN	pull down	Y718
14993273	O00145	SHIP1_HUMAN	Q9QZK7	DOK3_MOUSE	pull down	Y343
16436051	P62993	GRB2_HUMAN	Q7L591	DOK3_HUMAN	coimmunopr	Y398
7510216	P40763	STAT3_HUMAN	P40763	STAT3_HUMAN	coimmunopr	Y705

8662591	P42227	STAT3_MOUSE	P40763	STAT3_HUMAN	electropho	Y705
8662591	P42227	STAT3_MOUSE	P40763	STAT3_HUMAN	competitio	Y705
8662591	P42224	STAT1_HUMAN	P40763	STAT3_HUMAN	electropho	Y705
8662591	P42224	STAT1_HUMAN	P40763	STAT3_HUMAN	competitio	Y705
10209036	Q06124	PTN11_HUMAN	Q9Y3P8	SIT1_HUMAN	coimmunopr	Y148
10209036	Q06124	PTN11_HUMAN	Q9Y3P8	SIT1_HUMAN	competitio	Y148
15953601	Q62077	PLCG1_HUMAN	P14753	EPOR_MOUSE	phage disp	Y455
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	pull down	Y472
10978177	P27986	P85A_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y472
11445578	P26450	P85A_MOUSE	Q9QYY0	GAB1_MOUSE	competitio	Y473
11445578	P26450	P85A_MOUSE	Q9QYY0	GAB1_MOUSE	pull down	Y473
7504175	P62993	GRB2_HUMAN	P35570	IRS1_RAT	pull down	Y895
7513703	Q06124	PTN11_HUMAN	P35568	IRS1_HUMAN	surface pl	Y896
8491186	P62993	GRB2_HUMAN	P35570	IRS1_RAT	coimmunopr	Y895
8491186	P62993	GRB2_HUMAN	P35570	IRS1_RAT	pull down	Y895
8491186	P62993	GRB2_HUMAN	P35570	IRS1_RAT	competitio	Y895
8631859	P39688	FYN_MOUSE	P35570	IRS1_RAT	pull down	Y895
8631859	P39688	FYN_MOUSE	P35570	IRS1_RAT	anti bait	Y895
10602027	P42229	STA5A_HUMAN	P14784	IL2RB_HUMAN	pull down	Y536
10602027	P51692	STA5B_HUMAN	P14784	IL2RB_HUMAN	pull down	Y536
12200137	Q15464	SHB_HUMAN	P14784	IL2RB_HUMAN	pull down	Y536
7807015	P27986	P85A_HUMAN	P16410	CTLA4_HUMAN	coimmunopr	Y201
9398332	P27986	P85A_HUMAN	P16410	CTLA4_HUMAN	pull down	Y201
9712716	P39688	FYN_MOUSE	P09793	CTLA4_MOUSE	coimmunopr	Y201
9813138	P27986	P85A_HUMAN	P16410	CTLA4_HUMAN	coimmunopr	Y201
8657103	P19174	PLCG1_HUMAN	P43405	KSYK_HUMAN	coimmunopr	Y348
8657103	P19174	PLCG1_HUMAN	P43405	KSYK_HUMAN	pull down	Y348
8986718	P15498	VAV_HUMAN	Q00655	KSYK_PIG	coimmunopr	Y341
11672534	P14234	FGR_MOUSE	P48025	KSYK_MOUSE	pull down	Y342
16410013	P08487	PLCG1_BOVIN	P48025	KSYK_MOUSE	nuclear ma	Y342
16410013	P08487	PLCG1_BOVIN	P48025	KSYK_MOUSE	electropho	Y342
9151714	P15498	VAV_HUMAN	P43403	ZAP70_HUMAN	coimmunopr	Y315
16339550	P46108	CRK_HUMAN	P43403	ZAP70_HUMAN	pull down	Y315
10409671	P06241	FYN_HUMAN	O15117	FYB_HUMAN	pull down	Y625
9392697	P42226	STAT6_HUMAN	P24394	IL4RA_HUMAN	pull down	Y603
7528537	P29350	PTN6_HUMAN	P32927	IL3RB_HUMAN	experiment	Y628
9162089	P29350	PTN6_HUMAN	P32927	IL3RB_HUMAN	pull down	Y628
9162089	Q06124	PTN11_HUMAN	P32927	IL3RB_HUMAN	pull down	Y628
9973406	Q06124	PTN11_HUMAN	P32927	IL3RB_HUMAN	pull down	Y628
10704825	P29353	SHC1_HUMAN	P32927	IL3RB_HUMAN	coimmunopr	Y628
18046454	P07332	FES_HUMAN	P15311	EZRI_HUMAN	coimmunopr	Y478
18046454	P07332	FES_HUMAN	P15311	EZRI_HUMAN	pull down	Y478
11432792	Q06124	PTN11_HUMAN	O43559	FRS3_HUMAN	two hybrid	Y417
7935391	P62993	GRB2_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y716
7935391	P62993	GRB2_HUMAN	P09619	PGFRB_HUMAN	competitio	Y716
8940081	Q14451	GRB7_HUMAN	P09619	PGFRB_HUMAN	pull down	Y716
8940081	Q14451	GRB7_HUMAN	P09619	PGFRB_HUMAN	competitio	Y716
10660620	P29350	PTN6_HUMAN	Q9UKJ1	PILRA_HUMAN	surface pl	Y298
11689432	P16333	NCK1_HUMAN	O70469	DOK2_MOUSE	coimmunopr	Y351
10428862	P16333	NCK1_HUMAN	O60496	DOK2_HUMAN	pull down	Y345
8574854	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y333
8648092	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y333
8648092	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	surface pl	Y333

8648092	Q06124	PTN11_HUMAN	P43628	KI2L3_HUMAN	pull down	Y333
8648092	Q06124	PTN11_HUMAN	P43628	KI2L3_HUMAN	surface pl	Y333
8691146	P29350	PTN6_HUMAN	P43626	KI2L1_HUMAN	coimmunopr	Y332
8691146	P29350	PTN6_HUMAN	P43626	KI2L1_HUMAN	pull down	Y332
8691154	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	coimmunopr	Y333
8691154	P29350	PTN6_HUMAN	P43628	KI2L3_HUMAN	pull down	Y333
9864141	P40763	STAT3_HUMAN	Q99062	CSF3R_HUMAN	coimmunopr	Y727
9864141	P40763	STAT3_HUMAN	Q99062	CSF3R_HUMAN	pull down	Y727
15574420	P20936	RASA1_HUMAN	Q13480	GAB1_HUMAN	coimmunopr	Y317
16436051	P62993	GRB2_HUMAN	Q7L591	DOK3_HUMAN	coimmunopr	Y432
15240681	P29350	PTN6_HUMAN	Q15116	PDCD1_HUMAN	coimmunopr	Y223
15240681	Q06124	PTN11_HUMAN	Q15116	PDCD1_HUMAN	coimmunopr	Y223
7761456	P43403	ZAP70_HUMAN	P07766	CD3E_HUMAN	surface pl	Y188
7761456	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	surface pl	Y188
7761456	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	pull down	Y188
9698567	P43405	KSYK_HUMAN	P07766	CD3E_HUMAN	x-ray crys	Y188
11855827	P06239	LCK_HUMAN	P07766	CD3E_HUMAN	pull down	Y188
11855827	P29353	SHC1_HUMAN	P07766	CD3E_HUMAN	pull down	Y188
12024011	Q5M824	SHC1_RAT	Q05655	KPCD_HUMAN	coimmunopr	Y334
11544253	P29350	PTN6_HUMAN	O95866	G6B_HUMAN	coimmunopr	Y211
11544253	Q06124	PTN11_HUMAN	O95866	G6B_HUMAN	coimmunopr	Y211
11877430	P29320	EPHA3_HUMAN	Q96T51	RUFY1_HUMAN	coimmunopr	Y400
16337946	Q06124	PTN11_HUMAN	Q08345	DDR1_HUMAN	coimmunopr	Y740
7528772	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y72
8648092	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	surface pl	Y72
8648092	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	pull down	Y72
8901551	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y72
9185620	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	surface pl	Y72
10704231	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	enzymatic	Y72
15832366	P43403	ZAP70_HUMAN	P20963	CD3Z_HUMAN	peptide ar	Y72
9160881	P27986	P85A_HUMAN	P22681	CBL_HUMAN	two hybrid	Y731
9414268	P26450	P85A_MOUSE	P22681	CBL_HUMAN	coimmunopr	Y731
9414268	P26450	P85A_MOUSE	P22681	CBL_HUMAN	enzymatic	Y731
9890970	P39688	FYN_MOUSE	P22681	CBL_HUMAN	pull down	Y731
15556646	P27986	P85A_HUMAN	P22681	CBL_HUMAN	far wester	Y731
15556646	P46109	CRKL_HUMAN	P22681	CBL_HUMAN	far wester	Y731
15062102	P47941	CRKL_MOUSE	P97318	DAB1_MOUSE	pull down	Y232
9692543	Q07014	LYN_RAT	P28867	KPCD_MOUSE	coimmunopr	Y52
16407827	P62993	GRB2_HUMAN	O14939	PLD2_HUMAN	pull down	Y169
14679216	P24604	TEC_MOUSE	Q61152	PTN18_MOUSE	pull down	Y303
10749680	P29353	SHC1_HUMAN	P35968	VGFR2_HUMAN	beta galac	Y1175
10749680	P29353	SHC1_HUMAN	P35968	VGFR2_HUMAN	two hybrid	Y1175
10749680	P29353	SHC1_HUMAN	P35968	VGFR2_HUMAN	pull down	Y1175
10749680	P98077	SHC2_HUMAN	P35968	VGFR2_HUMAN	pull down	Y1175
10749680	P98077	SHC2_HUMAN	P35968	VGFR2_HUMAN	two hybrid	Y1175
11387210	Q62077	PLCG1_MOUSE	P35918	VGFR2_MOUSE	coimmunopr	Y1173
11387210	Q62077	PLCG1_MOUSE	P35918	VGFR2_MOUSE	pull down	Y1173
12214271	P29353	SHC1_HUMAN	P35968	VGFR2_HUMAN	coimmunopr	Y1175
15026417	Q15464	SHB_HUMAN	P35968	VGFR2_HUMAN	coimmunopr	Y1175
15546884	Q06124	PTN11_HUMAN	Q99704	DOK1_HUMAN	coimmunopr	Y337
15764601	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	nuclear ma	Y330
17027227	P35235	PTN11_MOUSE	Q62120	JAK2_MOUSE	pull down	Y201
8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	two hybrid	Y526

8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	pull down	Y526
8798676	P06239	LCK_HUMAN	P43405	KSYK_HUMAN	coimmunopre	Y526
15737992	P22681	CBL_HUMAN	O14492	SH2B2_HUMAN	pull down	Y629
11331873	P20936	RASA1_HUMAN	O14543	SOCS3_HUMAN	pull down	Y221
11331873	P20936	RASA1_HUMAN	O14543	SOCS3_HUMAN	coimmunopre	Y221
15504032	P20936	RASA1_HUMAN	Q03135	CAV1_HUMAN	pull down	Y25
18070987	P07948	LYN_HUMAN	Q9NWQ8	PAG1_HUMAN	structure	Y299
1380456	P27986	P85A_HUMAN	P35570	IRS1_RAT	coimmunopre	Y628
7680095	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	surface pla	Y632
7680644	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	cross-link	Y632
8382612	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	nuclear ma	Y632
11416002	P27986	P85A_HUMAN	P35568	IRS1_HUMAN	coimmunopre	Y632
7568038	P27986	P85A_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
7584133	P27986	P85A_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
7584133	P62993	GRB2_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
7807015	P27986	P85A_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
8146197	P27986	P85A_HUMAN	P10747	CD28_HUMAN	competitio	Y191
8183372	P27986	P85A_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
8621607	P26450	P85A_MOUSE	P10747	CD28_HUMAN	coimmunopre	Y191
8621607	P23727	P85A_BOVIN	P10747	CD28_HUMAN	pull down	Y191
9417079	P27986	P55G_MOUSE	P10747	CD28_HUMAN	coimmunopre	Y191
10820259	P27986	P85A_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
10820259	P27986	P85A_HUMAN	P10747	CD28_HUMAN	pull down	Y191
10820259	O75791	GRAP2_HUMAN	P10747	CD28_HUMAN	coimmunopre	Y191
10820259	O75791	GRAP2_HUMAN	P10747	CD28_HUMAN	pull down	Y191
12384576	P46108	CRK_HUMAN	P00519	ABL1_HUMAN	nuclear ma	Y226
9600917	Q06124	PTN11_HUMAN	P48357	LEPR_HUMAN	anti tag c	Y986
11342028	Q06124	PTN11_HUMAN	P48357	LEPR_HUMAN	surface pla	Y986
15143214	P43404	ZAP70_MOUSE	Q8R4V1	NFAM1_MOUSE	pull down	Y226
15143214	P43405	KSYK_HUMAN	Q8R4V1	NFAM1_MOUSE	pull down	Y226
7597091	P62993	GRB2_HUMAN	Q05397	FAK1_HUMAN	pull down	Y925
7997267	Q60631	GRB2_MOUSE	P34152	FAK1_MOUSE	experimenta	Y963
8816475	P62993	GRB2_HUMAN	P34152	FAK1_MOUSE	coimmunopre	Y963
8816475	P62993	GRB2_HUMAN	P34152	FAK1_MOUSE	pull down	Y963
9148935	P12931	SRC_HUMAN	P34152	FAK1_MOUSE	coimmunopre	Y963
9148935	P62993	GRB2_HUMAN	P34152	FAK1_MOUSE	coimmunopre	Y963
9830057	P62993	GRB2_HUMAN	P07550	ADRB2_HUMAN	coimmunopre	Y350
12881490	Q60631	GRB2_MOUSE	P20444	KPCA_MOUSE	coimmunopre	Y657
10671560	Q13094	LCP2_HUMAN	O15117	FYB_HUMAN	coimmunopre	Y559
10671560	Q13094	LCP2_HUMAN	O15117	FYB_HUMAN	pull down	Y559
8695788	P62993	GRB2_HUMAN	Q14289	FAK2_HUMAN	pull down	Y881
8918688	P27986	P85A_HUMAN	P09564	CD7_HUMAN	competitio	Y222
8918688	P23727	P85A_BOVIN	P09564	CD7_HUMAN	pull down	Y222
7528537	P29350	PTN6_HUMAN	P19235	EPOR_HUMAN	experimenta	Y426
8639815	Q06124	PTN11_HUMAN	P14753	EPOR_MOUSE	pull down	Y425
9774439	Q9NSE2	CISH_HUMAN	P14753	EPOR_MOUSE	coimmunopre	Y425
10660611	O00145	SHIP1_HUMAN	P19235	EPOR_HUMAN	pull down	Y426
10882725	O14543	SOCS3_HUMAN	P19235	EPOR_HUMAN	pull down	Y426
11781573	O14508	SOCS2_HUMAN	P19235	EPOR_HUMAN	two hybrid	Y426
15953601	Q62077	PLCG1_HUMAN	P14753	EPOR_MOUSE	phage disp	Y425
10498895	P06241	FYN_HUMAN	O09127	EPHA8_MOUSE	anti bait	Y615
9392697	P29350	PTN6_HUMAN	P24394	IL4RA_HUMAN	pull down	Y575
9392697	P42226	STAT6_HUMAN	P24394	IL4RA_HUMAN	pull down	Y575

15170389	Q06124	PTN11_HUMAN	Q9UQC2	GAB2_HUMAN	pull down	Y643
1382595	P27986	P85A_HUMAN	P10721	KIT_HUMAN	coimmunopr	Y721
7509796	P27986	P85A_HUMAN	P05532	KIT_MOUSE	coimmunopr	Y719
7537096	O00459	P85B_HUMAN	P10721	KIT_HUMAN	coimmunopr	Y721
7537096	P27986	P85A_HUMAN	P10721	KIT_HUMAN	coimmunopr	Y721
7513703	Q06124	PTN11_HUMAN	P35568	IRS1_HUMAN	surface pl	Y1229
9535915	Q06124	PTN11_HUMAN	P97710	SHPS1_RAT	pull down	Y477
10704446	P46108	CRK_HUMAN	P49024	PAXI_CHICK	pull down	Y118
8673706	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	coimmunopr	Y113
8673706	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y113
9047237	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y113
10229072	P16333	NCK1_HUMAN	Q13094	LCP2_HUMAN	coimmunopr	Y113
10347175	P15498	VAV_HUMAN	Q13094	LCP2_HUMAN	pull down	Y113
16177062	P78314	3BP2_HUMAN	Q9BZW8	CD244_HUMAN	3 hybrid m	Y342
10852966	O60880	SH21A_HUMAN	Q99704	DOK1_HUMAN	pull down	Y449
10852966	O60880	SH21A_HUMAN	Q99704	DOK1_HUMAN	coimmunopr	Y449
9603468	P20936	RASA1_HUMAN	P06127	CD5_HUMAN	pull down	Y453
8849729	P12931	SRC_HUMAN	Q14289	FAK2_HUMAN	pull down	Y402
10521452	P12931	SRC_HUMAN	Q14289	FAK2_HUMAN	pull down	Y402
10867021	P06241	FYN_HUMAN	Q14289	FAK2_HUMAN	pull down	Y402
10867021	P06241	FYN_HUMAN	Q14289	FAK2_HUMAN	coimmunopr	Y402
11149930	P12931	SRC_HUMAN	Q14289	FAK2_HUMAN	coimmunopr	Y402
12063569	P42679	MATK_HUMAN	Q14289	FAK2_HUMAN	pull down	Y402
12063569	P42679	MATK_HUMAN	Q14289	FAK2_HUMAN	coimmunopr	Y402
12454019	P52735	VAV2_HUMAN	P00533	EGFR_HUMAN	pull down	Y1172
11536047	P40763	STAT3_HUMAN	P07949	RET_HUMAN	coimmunopr	Y928
15121872	Q91ZM2	O55033_MOUSE	Q62120	JAK2_MOUSE	coimmunopr	Y813
15767667	O14492	SH2B2_HUMAN	O60674	JAK2_HUMAN	pull down	Y813
15767667	Q9NRF1	SH2B1_HUMAN	O60674	JAK2_HUMAN	pull down	Y813
16914724	Q9Z200	SH2B2_RAT	Q62120	JAK2_MOUSE	pull down	Y813
16914724	Q62985	SH2B1_RAT	Q62120	JAK2_MOUSE	pull down	Y813
17565041	Q9NRF1	SH2B1_HUMAN	O60674	JAK2_HUMAN	coimmunopr	Y813
7684160	P27986	P85A_HUMAN	P15391	CD19_HUMAN	coimmunopr	Y500
12881490	Q60631	GRB2_MOUSE	P6840	KPCB_RAT	coimmunopr	Y656
15196926	P10686	PLCG1_RAT	P32239	GASR_HUMAN	surface pl	Y438
16963136	P35235	PTN11_MOUSE	P32239	GASR_HUMAN	surface pl	Y438
16963136	Q06124	PTN11_HUMAN	P32239	GASR_HUMAN	pull down	Y438
16899217	P62993	GRB2_HUMAN	Q9H204	MED28_HUMAN	coimmunopr	Y64
9892650	P27986	P85A_HUMAN	P25963	IKBA_HUMAN	coimmunopr	Y42
9892650	P27986	P85A_HUMAN	P25963	IKBA_HUMAN	competitio	Y42
7537362	Q15464	SHB_HUMAN	P11362	FGFR1_HUMAN	peptide ar	Y776
8940081	Q14451	GRB7_HUMAN	P09619	PGFRB_HUMAN	pull down	Y775
8940081	Q14451	GRB7_HUMAN	P09619	PGFRB_HUMAN	competitio	Y775
18301737	P06241	FYN_HUMAN	P89654	P89654_MHV68	pull down	Y127
18301737	P15498	VAV_HUMAN	P89654	P89654_MHV68	pull down	Y127
9430661	P16333	NCK1_HUMAN	P54762	EPHB1_HUMAN	anti bait	Y594
9430661	Q9Z279	Q9Z279_MOUSE	P54762	EPHB1_HUMAN	two hybrid	Y594
9864141	P40763	STAT3_HUMAN	Q99062	CSF3R_HUMAN	coimmunopr	Y767
9864141	P40763	STAT3_HUMAN	Q99062	CSF3R_HUMAN	pull down	Y767
12163025	P29350	PTN6_HUMAN	Q96LC7	SIG10_HUMAN	biochemica	Y667
1314163	P23727	P85A_BOVIN	P09581	CSF1R_MOUSE	pull down	Y721
9312046	Q8CIH5	PLCG2_MOUSE	P07333	CSF1R_HUMAN	two hybrid	Y723
9312046	Q8CIH5	PLCG2_MOUSE	P07333	CSF1R_HUMAN	pull down	Y723

7657594	P27986	P85A_HUMAN	P17948	VGFR1_HUMAN	coimmunopr	Y1213
7685273	P06241	FYN_HUMAN	P09619	PGFRB_HUMAN	pull down	Y579
7685273	P07947	YES_HUMAN	P09619	PGFRB_HUMAN	pull down	Y579
7685273	P12931	SRC_HUMAN	P09619	PGFRB_HUMAN	pull down	Y579
7687537	P06241	FYN_HUMAN	P09619	PGFRB_HUMAN	pull down	Y579
7730365	P39688	FYN_MOUSE	P05622	PGFRB_MOUSE	pull down	Y578
9742401	Q13239	SLAP1_HUMAN	P09619	PGFRB_HUMAN	pull down	Y579
9742401	Q13239	SLAP1_HUMAN	P09619	PGFRB_HUMAN	coimmunopr	Y579
12706723	P25020	SRC_RSVH1	P09619	PGFRB_HUMAN	isothermal	Y579
12706723	P25020	SRC_RSVH1	P09619	PGFRB_HUMAN	x-ray crys	Y579
8816495	P42226	STAT6_HUMAN	P24394	IL4RA_HUMAN	fluorescen	Y631
9651359	P42226	STAT6_HUMAN	P24394	IL4RA_HUMAN	pull down	Y631
10764762	P29350	PTN6_HUMAN	Q6GTX8	LAIR1_HUMAN	coimmunopr	Y251
10764762	P29350	PTN6_HUMAN	Q6GTX8	LAIR1_HUMAN	pull down	Y251
11152665	P12931	SRC_HUMAN	P15941	MUC1_HUMAN	pull down	Y1229
11152665	P12931	SRC_HUMAN	P15941	MUC1_HUMAN	coimmunopr	Y1229
11483589	P12931	SRC_HUMAN	P15941	MUC1_HUMAN	pull down	Y1229
11572860	Q06124	PTN11_HUMAN	Q9Z1S8	GAB2_MOUSE	coimmunopr	Y603
15170389	Q06124	PTN11_HUMAN	Q9UQC2	GAB2_HUMAN	pull down	Y614
12606549	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	circular d	Y304
12606549	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	nuclear ma	Y304
15096211	O55033	O55033_MOUSE	P52800	EFNB2_MOUSE	pull down	Y307
15096211	O55033	O55033_MOUSE	P52800	EFNB2_MOUSE	peptide ar	Y307
15764601	O43639	NCK2_HUMAN	P52799	EFNB2_HUMAN	nuclear ma	Y304
11865050	P26450	P85A_MOUSE	Q06806	TIE1_MOUSE	pull down	Y1113
7518560	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopr	Y1110
7527043	P62993	GRB2_HUMAN	P00533	EGFR_HUMAN	coimmunopr	Y1110
14966128	P40763	STAT3_HUMAN	P00533	EGFR_HUMAN	pull down	Y1110
10318843	P06239	LCK_HUMAN	P43403	ZAP70_HUMAN	anti tag c	Y319
10500481	P27986	P85A_HUMAN	P06213	INSR_HUMAN	fluorescen	Y941
7730365	P39688	FYN_MOUSE	P07333	CSF1R_HUMAN	pull down	Y561
7730365	Q04736	YES_MOUSE	P07333	CSF1R_HUMAN	coimmunopr	Y561
7730365	P05480	SRC_MOUSE	P07333	CSF1R_HUMAN	coimmunopr	Y561
7518560	P29353	SHC1_HUMAN	P00533	EGFR_HUMAN	coimmunopr	Y1197
7542744	P29353	SHC1_HUMAN	P00533	EGFR_HUMAN	coimmunopr	Y1197
7693694	P19174	PLCG1_HUMAN	P00533	EGFR_HUMAN	pull down	Y1197
8034616	P29353	SHC1_HUMAN	P00533	EGFR_HUMAN	coimmunopr	Y1197
8034616	P29353	SHC1_HUMAN	P00533	EGFR_HUMAN	competitio	Y1197
9544989	P29353	SHC1_HUMAN	P00533	EGFR_HUMAN	experiment	Y1197
9733788	P29350	PTN6_HUMAN	P00533	EGFR_HUMAN	pull down	Y1197
9461599	P41240	CSK_HUMAN	P04626	ERBB2_HUMAN	competitio	Y1248
12122014	P42679	MATK_HUMAN	P04626	ERBB2_HUMAN	pull down	Y1248
12791772	Q06124	PTN11_HUMAN	P05106	ITB3_HUMAN	coimmunopr	Y773

start|end	peptide_binder
750|763	ACPPEVYAIMRGC
750|763	ACPPEVYAIMRGC
652|665	ADERVDYVVVDQQ
652|665	ADERVDYVVVDQQ
374|387	STDTPIYSQVAPR
167|180	AEGDEIYEDLMRS
167|180	AEGDEIYEDLMRS
167|180	AEGDEIYEDLMRS
285|298	AENTITYSLLMHP
285|298	AENTITYSLLMHP
302|315	AENTITYSLLKHP
285|298	AENTITYSLLMHP
285|298	AENTITYSLLMHP
285|298	AENTITYSLLMHP
285|298	AENTITYSLLMHP
587|600	AEPVPDYTTVHTV
681|694	AEPYNLYSSLKEL
1215|1228	AFDNLYYWDQDPP
921|934	AIKMVQYRDSFLT
921|934	AIKMVQYRDSFLT
921|934	AIKMVQYRDSFLT
921|934	AIKMVQYRDSFLT
687|700	AKAVDGYVKPQIK
687|700	AKAVDGYVKPQIK
596|609	APGMKVYIDPFTY
596|609	APGMKVYIDPFTY
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
450|463	APTSFGYDKPHVL
787|799	AQAPPSYLDVLG
787|799	AQAPPSYLDVLG
787|799	AQAPPSYLDVLG
784|796	AQAPPVYLDVLG
784|796	AQAPPVYLDVLG
850|862	AKEDVDYVTLKH
850|862	AKEDVDYVTLKH
971|984	ARDPQRYLVIQGD
971|984	ARDPQRYLVIQGD
448|461	ARSSDSYAVIDLK
272|285	ASKKTIYTYIMAS
272|285	ASKKTIYTYIMAS
992|1005	ASSNPEYLSASDV
973|986	ASVNPEYFSAADV
973|986	ASVNPEYFSAADV
973|986	ASVNPEYFSAADV
1205|1218	CDPKFHYDNTAGI
1207|1220	CDPKFHYDNTAGI

394|407	CLREAQYSMLATW
394|407	CLREAQYSMLATW
394|407	CLREAQYSMLATW
279|292	SSKSVTYATVVFP
1132|1145	CSPQPEYVNQPDV
1132|1145	CSPQPEYVNQPDV
1132|1145	CSPQPEYVNQPDV
1132|1145	CSPQPEYVNQPDV
1132|1145	CSPQPEYVNQPDV
1073|1086	CWREKPYERPSFA
1073|1086	CWREKPYERPSFA
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
170|183	DAEKPFYVNVEFH
678|691	DARPAVYTQVQKP
678|691	DARPAVYTQVQKP
678|691	DARPSLYAQVQKP
258|270	DCGSPKYAYFNGC
258|271	DCGSQKYAYFNGC
772|785	DCLDGLYALMSRC
297|310	DDDKNIYLTLPPN
176|189	DDEDDSYLEPDSP
176|189	DDEDDSYLEPDSP
176|189	DDEDDSYLEPDSP
176|189	DDEDDSYLEPDSP
439|452	EDSDEDYEKVPLP
441|454	DDSDEDYEKVPLP
390|403	DEPEGDYEEVLEP
390|403	DEPEGDYEEVLEP
713|726	DESTRSYVILSFE
713|726	DESTRSYVILSFE
190|202	EEQVHTYVNTTGV
574|587	DGHEYIYVDPMQL
574|587	DGHEYIYVDPMQL
574|587	DGHEYIYVDPMQL
574|587	DGHEYIYVDPMQL
574|587	DGHEYIYVDPMQL
574|587	DGHEYIYVDPMQL
764|777	DIESSNYMAPYDN
764|777	DIESSNYMAPYDN
764|777	DIESSNYMAPYDN
764|777	DIESSNYMAPYDN
764|777	DIESSNYMAPYDN
755|768	DIQRSLYDRPASY
755|768	DIQRSLYDRPASY

755|768	DIQRSLYDRPASY
755|768	DIQRSLYDRPASY
755|768	DIQRSLYDRPASY
1182|1195	DIYETDYYRKGGK
1182|1195	DIYETDYYRKGGK
1182|1195	DIYETDYYRKGGK
116|129	DKMAEAYSEIGMK
116|129	DKMAEAYSEIGMK
318|331	GPASGLYASVCKQ
318|331	GPASGLYASVCKQ
644|657	DMGDEVYDDVDTS
680|693	DVGEEVYDDVDAS
184|197	DNAMLEYLKIAQD
798|806	DNDDDLYG
300|313	DPCTTIYVAATEP
308|321	DPCTTIYVAATEP
308|321	DPCTTIYVAATEP
444|457	DPGALHYDYIDVE
555|568	DPQAVTYAEVKHS
555|568	DPQAVTYAEVKHS
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
296|309	DPQEVTYAQLNHC
295|308	DPQEVTYTQLNHC
295|308	DPQEVTYTQLNHC
295|308	DPQEVTYTQLNHC
295|308	DPQEVTYTQLNHC
295|308	DPQEVTYTQLNHC
295|308	DPQEVTYTQLNHC
630|643	KDPTNGYYNVRAH
914|927	ERRDQDYANLPSS
7|20	DSEGHLYTVPIRE
7|20	DSEGHLYTVPIRE
7|20	DSEGHLYTVPIRE
7|20	DSEGHLYTVPIRE
7|20	DSEGHLYTVPIRE
7|20	DSEGHLYTVPIRE
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1001|1014	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
1002|1015	DTSSVLYTAVQPN
309|322	DYGHPVYIVQEMP
309|322	DYGHPVYIVQEMP

309|322	DYGHPVYIVQEMP
154|167	DYHNPGYLVVLPD
154|167	DYHNPGYLVVLPD
446|459	GALHYDYIDVEMT
184|197	EDAVLEYLKIAQD
588|601	EDDQEVYDDVAEQ
577|590	EDDQDVYDDVAEQ
693|706	EDEDDPYVPMRPG
693|706	EDEDDPYVPMRPG
176|189	EDEDDSYLEPDSP
1192|1205	EDEEYEYMNRRRR
830|843	EDESIHYSELVQF
577|590	EDSARVYENVGLM
577|590	EDSARVYENVGLM
577|590	EDSARVYENVGLM
577|590	EDSARVYENVGLM
439|452	EDSDEDYEKVPLP
439|452	EDSDEDYEKVPLP
706|719	EEADGVYAASGGL
524|537	EEDADSYENMDNP
702|715	EEDDDEYKIPSSH
153|166	EEDEDLYDCVENE
153|166	EEDEDLYDCVENE
153|166	EEDEDLYDCVENE
308|321	EEEEEEYMPMEDL
308|321	EEEEEEYMPMEDL
308|321	EEEEEEYMPMEDL
317|330	EEEEPQYEEIPIY
310|323	EEISAMYSSVNKP
440|453	EELDENYVPMNPN
440|453	EELDENYVPMNPN
386|398	LDPMHNYVNTENV
343|355	RPALLNYENLPSL
898|911	EGMPKSYLPQTVR
898|911	EGMPKSYLPQTVR
898|911	EGMPKSYLPQTVR
898|911	EGMPKSYLPQTVR
360|373	EHAQDTYLVLDKW
429|442	EHRQLNYIQVDLE
429|442	EHRQLNYIQVDLE
560|573	EINGNNYVYIDPT
211|223	EKQFQPYFIPIN
58|71	EKSDAVYTGLNTR
58|71	EKSDGVYTGLSTR
588|601	EMPVPDYTSIHIV
588|601	EMPVPDYTSIHLV
588|601	EMPVPDYTSIHLV
198|211	EMYGVNYFSIKNK
767|780	ENEDDGYDVPKPP
767|780	ENEDDGYDVPKPP
767|780	ENEDDGYDVPKPP
767|780	ENEDDGYDVPKPP
767|780	ENEDDGYDVPKPP

26|39	ENESPHYDDVHEY
814|827	EPDEILYVNMDEG
814|827	EPDEILYVNMDEG
814|827	EPDEILYVNMDEG
814|827	EPDEILYVNMDEG
814|827	EPDEILYVNMDEG
814|827	EPDEILYVNMDEG
497|508	EPLPPSYVACS
497|508	EPLPPSYVACS
496|507	EPLHPGYVACS
496|507	EPLHPGYVACS
342|355	EPPDHQYYNDFPG
342|355	EPPDHQYYNDFPG
494|507	EPSFSEYASVQVQ
309|322	EPVNTVYSEVQFA
372|385	SDSDDDYDDVDIP
929|942	ESTNHIYSNLANC
929|942	ESTNHIYSNLANC
929|942	ESTNHIYSNLANC
281|294	ETADGGYMTLNPR
213|226	ETEENIYQVPTSQ
934|947	ETGTEEYMKMDLG
934|947	ETGTEEYMKMDLG
345|358	EVYESPYADPEEI
345|358	EVYESPYADPEEI
339|352	EVYESPYADPEEI
339|352	EVYESPYADPEEI
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
1339|1352	FDERQPYAHMNGG
736|749	FEDSRGYMMMFPR
736|749	FEDSRGYMMMFPR
527|540	FIMDNAYFCEADA
527|540	FIMDNAYFCEADA
527|540	FIMDNAYFCEADA
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP
1085|1098	FLPVPEYINQSVP

1085|1098	FLPVPEYINQSVP
312|325	FLQLLKYIPPKAK
312|325	FLQLLKYIPPKAK
312|325	FLQLLKYIPPKAK
459|472	FLRCINYVFFPSL
459|472	FLRCINYVFFPSL
459|472	FLRCINYVFFPSL
459|472	FLRCINYVFFPSL
459|472	FLRCINYVFFPSL
620|633	FLSSCGYVSTDQL
620|633	FLSSCGYVSTDQL
620|633	FLSSCGYVSTDQL
746|759	GCPGPVYRIMTQC
620|633	GDKQVEYLDLDLD
620|633	GDKQVEYLDLDLD
620|633	GDKQVEYLDLDLD
121|134	GEDDGDYESPNEE
121|134	GEDDGDYESPNEE
121|134	GEDDGDYESPNEE
121|134	GEDDGDYESPNEE
121|134	GEDDGDYESPNEE
693|706	GEEDTEYMTPSSR
693|706	GEEDTEYMTPSSR
693|706	GEEDTEYMTPSSR
693|706	GEEDTEYMTPSSR
111|124	GEEEHVYSFPNKQ
111|124	SEEEHVYSFPNKQ
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
732|745	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
732|745	GESDGGYMDMSKD
732|745	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
733|746	GESDGGYMDMSKD
330|343	GFREGFYLFPDGR
1236|1249	GGSSLSYTNPAVA
657|670	GGWMEDYDYVHLQ
657|670	GGWMEDYDYVHLQ
657|670	GGWMEDYDYVHLQ
755|768	GGWMEDYDYVHLQ
755|768	GGWMEDYDYVHLQ
755|768	GGWMEDYDYVHLQ
1178|1191	GMTRDIYETDYYR
1178|1191	GMTRDIYETDYYR
1178|1191	GMTRDIYETDYYR
214|227	GPEPGPYAQPSVN

694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
694|707	GPKGTGYIKTELI
481|494	GPYSHPYENSLVP
776|789	GRNPGFYVEANPM
776|789	GRNPGFYVEANPM
776|789	GRNPGFYVEANPM
582|595	GSSDNEYFYVDFR
582|595	GSSDNEYFYVDFR
764|777	GTAEPDYGALYEG
764|777	GTAEPDYGALYEG
696|709	HAEAALYKNLLHS
347|360	LPMADTYAVVQKR
893|906	HAPAEMYDIMKTC
582|595	HDSEENYVPMNPN
582|595	HDSEENYVPMNPN
284|297	HGKKEAYDTLIKD
60|73	HGSQGTYSNTKEN
60|73	HGSQGTYSNTKEN
60|73	HGSQGTYSNTKEN
658|671	HLGSEEYDVPPRL
208|221	PPAESVYTSLQRR
208|221	PPAESVYTSLQRR
234|247	HQGPVIYAQLDHS
937|950	ICTIDVYMIMVKC
791|802	IDAFSDYANFK
791|802	IDAFSDYANFK
791|802	IDAFSDYANFK
818|829	IDAFSDYANFK
277|290	IFPYEEYASWKTE
489|502	IIENPQYFSDACV
489|502	IIENPQYFSDACV
807|820	ILPRQQYFKQNCS
807|820	ILPRQQYFKQNCS
807|820	ILPRQQYFKQNCS
802|815	IMNDSNYIVKGNA
850|863	IMRDSNYISKGST
48|61	IRNTNEYTEGPTV
1183|1196	IYETDYYRKGGKG
1183|1196	IYETDYYRKGGKG
1183|1196	IYETDYYRKGGKG
1276|1289	IYRASYYRKGGCA
677|690	IYSTDYYRVGGRT
677|690	IYSTDYYRVGGRT
677|690	IYSTDYYRVGGRT
64|77	IYVILRYAKMKTI
64|77	IYVILRYAKMKTI
262|275	KDDGIVYASLALS
744|757	KDESVDYVPMLDM

744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
743|756	KDESIDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
744|757	KDESVDYVPMLDM
743|756	KDESVDYVPMLDM
312|325	KDNDFIYHDRVPD
312|325	KDNDFIYHDRVPD
630|643	KDPTNGYYNVRAH
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
706|719	KDTETVYSEVRKA
351|364	KDTSTEYSEVRTQ
275|288	KEAPTEYASICVR
275|288	KEAPTEYASICVR
264|277	KEEEDIYEVLPDE
264|277	KEEEDIYEVLPDE
135|148	KGHDGLYQGLSTA
135|148	KGHDGLYQGLSTA
135|148	KGHDGLYQGLSTA
135|148	KGHDGLYQGLSTA
192|205	KGQRDLYSGLNQR
192|205	KGQRDLYSGLNQR
192|205	KGQRDLYSGLNQR
192|205	KGQRDLYSGLNQR
192|205	KGQRDLYSGLNQR
557|570	KHKEDVYENLHTK
557|570	KHKEDVYENLHTK
557|570	KHKEDVYENLHTK
557|570	KHKEDVYENLHTK
221|234	KIWMTGYEDYRHA
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP

274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
281|294	EKSLTIYAQVQKS
281|294	EKSLTIYAQVQKS
281|294	EKSLTIYAQVQKS
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKSLTIYAQVQKP
274|287	KKTIYTYIMASRN
481|494	KVDDVAYTVLNFN
486|499	KMNEVTYSTLNFE
750|763	KMQQNGYENPTYK
530|543	KNVVPLYDLLLEM
530|543	KNVVPLYDLLLEM
352|365	KPDSSFYKGLDLN
274|287	KPEIQVYENIHLA
274|287	KPEIQVYENIHLA
274|287	KPEIQVYENIHLA
274|287	KPEIQVYENIHLA
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
539|552	KRKGHEYTNIKYS
815|828	KRPMGDYENVNPS
256|269	KSESVVYADIRKN
382|395	KVELETYKQTRQG
456|469	LAGVSEYELPEDP
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
213|226	LDGSREYVNVSQE
300|312	PVNKLVYENINGL
781|787	GLITSDYELLQTP
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY

1093|1106	LEERKTYVNTTLY
1093|1106	LEERKTYVNTTLY
198|211	LEGDLCYADLTLQ
1001|1014	LEHLICYSFQVAK
1165|1178	LEKSLNYIDLDLV
1172|1185	LENGLNYIDLDLV
1165|1178	LEKSLNYIDLDLV
1165|1178	LEKSLNYIDLDLV
596|609	LESDGSYQKPSYI
416|429	LFDDPSYVNIQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
420|433	LFDDPSYVNVQNL
156|169	LGMEGPYEVLKDS
156|169	LGMEGPYEVLKDS
966|979	LGNGVLYASVNPE
966|979	LGNGVLYASVNPE
966|979	LGNGVLYASVNPE
966|979	LGNGVLYASVNPE
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
76|89	LGRREEYDVLDKR
706|719	LGSGIVYSALTCH
706|719	LGSGIVYSALTCH
605|618	LHTDDGYMPMSPG
605|618	LHTDDGYMPMSPG
387|400	LIEDNEYTAREGA
387|400	LIEDNEYTAREGA
413|426	LIEDNEYTARQGA
745|758	LKGRAGYTTVAVK
172|185	LLTMSFYRNYHAM
559|572	FNQEDIYITTESL
559|572	FNQEDIYITTESL
559|572	FNQEDIYITTESL
683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS

683|696	LNSDVQYTEVQVS
683|696	LNSDVQYTEVQVS
725|738	LPCTGDYMNMSPV
328|341	LPPSSIYPSVLAS
328|341	LPPSSIYPSVLAS
1000|1013	LPQDKEYYKVKEP
1000|1013	LPQDKEYYKVKEP
1000|1013	LPQDKEYYKVKEP
1000|1013	LPQDKEYYKVKEP
793|806	LPTHDGYLPSNID
793|806	LPTHDGYLPSNID
793|806	LPTHDGYLPSNID
683|696	LQERRKYLKHRLI
683|696	LQERRKYLKHRLI
683|696	LQERRKYLKHRLI
683|696	LQERRKYLKHRLI
683|696	LQERRKYLKHRLI
683|696	LQERRKYLKHRLI
518|531	LRADENYYKAQTH
518|531	LRADENYYKAQTH
518|531	LRADENYYKAQTH
1011|1024	LSADSGYIIPLPD
24|37	LSEETPYSYPTGN
24|37	LTEETPYSYPTGN
480|493	LANIDFYAQVSDI
480|493	LANIDFYAQVSDI
440|451	LSSFTSYENPT
24|37	LTEETPYSYPTGN
759|772	LTSNQEYLDLSMP
759|772	LTSNQEYLDLSMP
759|772	LTSNQEYLDLSMP
759|772	LTSNQEYLDLSMP
759|772	LTSNQEYLDLSMP
710|723	LVSSSDYMPMAPQ
710|723	LVSSSDYMPMAPQ
274|287	MAESITYAAVARH
274|287	MAESITYAAVARH
274|287	MAESITYAAVARH
333|346	MDEELHYASLNFH
333|346	MDEELHYASLNFH
333|346	MDEELHYASLNFH
333|346	MDEELHYASLNFH
333|346	MDEELHYASLNFH
333|346	MDEELHYASLNFH
770|783	MDDTVSYAILRFP
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
193|206	MESIDDYVNVPES
347|360	MLRLQDYEEKTKK

315|328	MPMEDLYLDILPE
224|237	MTGYEDYRHAPVR
174|187	MVEDCLYETVKEI
174|187	MVEDCLYETVKEI
1008|1021	MVKRRDYLDLAAS
1008|1021	MVKRRDYLDLAAS
1008|1021	MVKRRDYLDLAAS
1008|1021	MVKRRDYLDLAAS
974|987	NCSEEMYRLMLQC
974|987	NCSEEMYRLMLQC
974|987	NCSEEMYRLMLQC
712|725	SCTHDLYMIMREC
712|725	SCTHDLYMIMREC
712|725	SCTHDLYMIMREC
723|736	NCTNELYMMMRDC
723|736	NCTNELYMMMRDC
772|785	NDSESDYMFMAPG
772|785	NDSESDYMFMAPG
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
1014|1027	NEGDNDYIIPLPD
297|310	NEPVSDYINANII
562|575	NGNNYVYIDPTQL
250|263	NKPGIVYASLNHS
250|263	NKPGIVYASLNHS
104|117	NPQEGLYNELQKD
104|117	NPQEGLYNELQKD
104|117	NPQEGLYNELQKD
2260|2273	NQEGLNYMVLATK
482|495	NQFVPLYTDPQEV
2267|2280	NREGLNYMVLATE
2267|2280	NREGLNYMVLATE
480|493	NSSDSDYDLHGAQ
480|493	NSSDSDYDLHGAQ
29|42	PAQDPLYDVPNAS
29|42	PAQDPLYDVPNAS
1255|1268	PDEDYEYMNRQRD
830|843	EDESIHYSELVQF
690|703	SEGDSSYKNIHLE
690|703	SEGDSSYKNIHLE
690|703	SEGDSSYKNIHLE
711|724	PERDSRYSQPLHE
336|349	GTAEHLYENVCML
391|404	PGNEHLYENLCVL
698|711	PGSAAPYLKTKFI

698|711	PGSAAPYLKTKFI
698|711	PGSAAPYLKTKFI
698|711	PGSAAPYLKTKFI
698|711	PGSAAPYLKTKFI
141|154	PGTPVKYSEVVLD
141|154	PGTPVKYSEVVLD
448|461	PHLKYLYLVVSDS
465|478	PIQEANYVPMTPG
465|478	PIQEANYVPMTPG
466|479	PIQEPNYVPMTPG
466|479	PIQEPNYVPMTPG
888|901	PKSPGEYVNIEFG
889|902	PKSPGEYVNIEFG
888|901	PKSPGEYVNIEFG
888|901	PKSPGEYVNIEFG
888|901	PKSPGEYVNIEFG
888|901	PKSPGEYVNIEFG
888|901	PKSPGEYVNIEFG
529|542	PLNTDAYLSLQEL
529|542	PLNTDAYLSLQEL
529|542	PLNTDAYLSLQEL
194|207	PLTTGVYVKMPPT
194|207	PLTTGVYVKMPPT
194|207	PLTTGVYVKMPPT
194|207	PLTTGVYVKMPPT
341|354	PMDTEVYESPYAD
341|354	PMDTEVYESPYAD
334|347	PMDTEVYESPYAD
335|348	PMDTEVYESPYAD
335|348	PMDTEVYESPYAD
335|348	PMDTEVYESPYAD
308|321	PMDTSVYESPYSD
308|321	PMDTSVYESPYSD
618|631	PPDDDIYDGIEEE
596|609	PPGEAGYKAFSSL
621|634	PPGSLEYLCLPAG
621|634	PPGSLEYLCLPAG
621|634	PPGSLEYLCLPAG
621|634	PPGSLEYLCLPAG
621|634	PPGSLEYLCLPAG
471|484	PPPPPVYEPVSYH
471|484	PPPPPVYEPVSYH
410|423	PPRQLNYIQVELK
709|722	PPSAELYSNALPV
709|722	PPSAELYSNALPV
709|722	PPSAELYSNALPV
709|722	PPSAELYSNALPV
291|303	PQNETLYSVLKA
344|357	PLPDHIYDEPEGV
338|351	PRPDHIYDEPEGV
326|339	PTDIIVYTELPNA
326|339	PTDIIVYTELPNA
326|339	PTDIIVYTELPNA

326|339	PTDIIVYTELPNA
326|339	PTDIIVYTELPNA
325|338	PTDIIVYTELPNA
325|338	PTDIIVYTELPNA
326|339	PTDIIVYTELPNA
326|339	PTDIIVYTELPNA
720|733	PTLVQTYVLQGDP
720|733	PTLVQTYVLQGDP
310|323	PTPGNTYQIPRTF
425|438	PTTSPIYHNGQDL
216|229	PVFSVDYGELDFQ
216|229	PVFSVDYGELDFQ
181|194	PVPNPDYEPIRKG
181|194	PVPNPDYEPIRKG
181|194	PVPNPDYEPIRKG
181|194	PVPNPDYEPIRKG
181|194	PVPNPDYEPIRKG
181|194	PVPNPDYEPIRKG
327|340	QDNSGTYGKIWEG
204|217	QEPSLLYADLDHL
204|217	QEPSLLYADLDHL
393|406	QGLDEMYSDVWKQ
733|746	QGPTISYPMLLHV
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
65|78	QGQNQLYNELNLG
724|737	QIDSCTYEAMYNI
724|737	QIDSCTYEAMYNI
724|737	QIDSCTYEAMYNI
724|737	QIDSCTYEAMYNI
724|737	QIDSCTYEAMYNI
724|737	QIDSCTYEAMYNI
225|238	QKKEGVYDVPKSQ
45|58	QKKPTMYPEWKTT
162|175	QKYLENYLNRLLT
296|309	QDTSPHYQNLKEN
1168|1181	QQDGKDYIVLPIS
1168|1181	QQDGKDYIVLPIS
1168|1181	QQDGKDYIVLPIS
1168|1181	QQDGKDYIVLPIS
1168|1181	QQDGKDYIVLPIS
1166|1179	QQDGKDYIVLPMS
1166|1179	QQDGKDYIVLPMS
1168|1181	QQDGKDYIVLPIS
1168|1181	QQDGKDYIVLPIS
330|343	QRKKPLYWDLYEH
323|333	QSPANIYYKV
194|207	QTPLAVYNSVSYK
519|532	RADENYYKAQTHG

519|532	RADENYYKAQTHG
519|532	RADENYYKAQTHG
622|632	RAVENQYSFY
214|225	REFLDQYDAPL
214|225	REFLDQYDAPL
18|31	REQGNIYKPNNKA
292|305	RFSSLSYKSREED
621|634	RKGNGDYMPMSPK
625|638	RKGSGDYMPMSPK
625|638	RKGSGDYMPMSPK
625|638	RKGSGDYMPMSPK
625|638	RKGSGDYMPMSPK
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
184|197	RLLHSDYMNMTPR
219|232	RNKPTVYGVSPNY
979|992	RQPFVKYATLISN
979|992	RQPFVKYATLISN
219|232	RRETEVYACMKEE
219|232	RRETEVYACMKEE
918|931	RSNDKVYENVTGL
956|969	RSNDKVYENVTGL
956|969	RSNDKVYENVTGL
956|969	RSNDKVYENVTGL
956|969	RSNDKVYENVTGL
956|969	RSNDKVYENVTGL
343|356	RSSLKAYGNGYSS
651|663	DFEGFSYVNPQFV
552|565	RTARGSYGYIKTT
552|565	RTARGSYGYIKTT
874|887	RTDDLVYLNVMEL
215|228	SAACVVYEDMSHS
215|228	SAACVVYEDMSHS
419|432	SAASFEYTILDPS
418|431	SPSSFEYTILDPS
418|431	SPSSFEYTILDPS
419|432	SAASFEYTILDPS
419|432	SAASFEYTILDPS
419|432	SAASFEYTILDPS
418|431	SPSSFEYTILDPS
608|621	SAEPHTYEEPGRA
568|581	SAPTSGYQEFVHA
568|581	SAPTSGYQEFVHA

636|649	SDEKVDYVQVDKE
714|727	SDSTNEYMDMKPG
712|725	CDSSNEYMDMKPG
714|727	SDSTNEYMDMKPG
714|727	SDSTNEYMDMKPG
1222|1235	SEDLSAYASISFQ
470|483	PEDTLTYADLDMV
111|124	SEEEHVYSFPNKQ
106|119	SFEEDDYESPNDD
106|119	SFEEDDYESPNDD
106|119	SFEEDDYESPNDD
106|119	SFEEDDYESPNDD
106|119	SFEEDDYESPNDD
335|348	SFNSTIYEVIGKS
442|455	SHNSALYSQVQKS
442|455	SHNSALYSQVQKS
446|459	SHVDNEYSQPPRN
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
395|408	SIESDIYAEIPDE
1165|1178	SLDNPDYQQDFFP
921|934	SLFDHIYTTQSDV
806|819	SLFTPDYELLTEN
806|819	SLFTPDYELLTEN
806|819	SLFTPDYELLTEN
806|819	SLFTPDYELLTEN
806|819	SLFTPDYELLTEN
806|819	SLFTPDYELLTEN
493|506	SLGSQSYEDMRGI
623|668	EFAGFSYTNPEFV
431|444	SLSRLSYTTISTL
431|444	SLSRLSYTTISTL
431|444	SLSRLSYTTISTL
57|70	SLVSQDYVNGTDQ
35|48	SMKDEEYEQMVKE
35|48	SMKDEEYEQMVKE
769|782	SMPLDQYSPSFPD
768|781	SNYMAPYDNYVPS
768|781	SNYMAPYDNYVPS
120|133	SPEENIYETANSE
120|133	SPEENIYETANSE
587|600	SPGMKIYIDPFTY
587|600	SPGMKIYIDPFTY
760|773	SPGPGHYLRCDST
760|773	SPGPGHYLRCDST
660|673	SQEELHYATLNFP
714|727	SQGVDTYVEMRPV
716|729	SQGVDTYVEMRPV
716|729	SQGVDTYVEMRPV

1206|1219	SSDDVRYVNAFKF
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
571|584	SSDGHEYIYVDPV
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
572|585	SSDGHEYIYVDPM
624|637	SSGEEGYKPFQDL
624|637	SSGEEGYKPFQDL
244|257	SSQEVTYAQLDHW
244|257	SSQEVTYAQLDHW
1222|1235	STDRSPYEKVSAG
1222|1235	STDRSPYEKVSAG
1222|1235	STDRSPYEKVSAG
596|609	STGSVDYLALDFQ
607|620	STGSVDYLALDFQ
297|310	SVFCPHYEKVSGD
297|310	SVFCPHYEKVSGD
300|313	SVFCPHYEKVSGD
300|313	SVFCPHYEKVSGD
297|310	SVFCPHYEKVSGD
1107|1119	LEARKAYVNMSLF
1103|1116	SVQNPVYHNQPLN
1103|1116	SVQNPVYHNQPLN
1103|1116	SVQNPVYHNQPLN
312|325	SVYESPYSDPEEL
934|947	SWTEPTYFYVTDY
554|567	SYEGNSYTFIDPT
554|567	SYEGNSYTFIDPT
554|567	SYEGNSYTFIDPT
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1190|1203	TAENAEYLRVAPQ
1241|1254	TAENPEYLGLDVP
1241|1254	TAENPEYLGLDVP
766|779	TANNPLYKEATST

Pull down peptides	Thirteenmer	Target pr	prot name	Tyr resid
ETSKVIYDFIEKT	ETSKVIYDFIEKT	O00401	WASL	256
ETSKVIYDFIEKT	ETSKVIYDFIEKT	O00401	WASL	256
NETEDQYALMEDE	NETEDQYALMEDE	O00459	PIK3R2	605
EADSSSDpYVNMDFTKR	ADSSSDYVNMDFT	O14654	IRS4	921
EADSSSDpYVNMDFTKR	ADSSSDYVNMDFT	O14654	IRS4	921
EADSSSDpYVNMDFTKR	ADSSSDYVNMDFT	O14654	IRS4	921
EADSSSDpYVNMDFTKR	ADSSSDYVNMDFT	O14654	IRS4	921
PPASSLYSSPVNS	PPASSLYSSPVNS	O14964	HGS	308
PPASSLYSSPVNS	PPASSLYSSPVNS	O14964	HGS	308
KSKQPLYSSIVTV	KSKQPLYSSIVTV	O60245	PCDH7	948
KSKQPLYSSIVTV	KSKQPLYSSIVTV	O60245	PCDH7	948
DHNHLLYSTIPRM	DHNHLLYSTIPRM	O60716	CTNND1	96
QRKEVKYEAPQAT	QRKEVKYEAPQAT	O60784	TOM1	386
QRKEVKYEAPQAT	QRKEVKYEAPQAT	O60784	TOM1	386
TETKSLYPSSEIQ	TETKSLYPSSEIQ	O75886	STAM2	192
AFGTVYKGLWI	GAFGTVYKGLWIP	P00533	EGFR	727
RDPQRYLVIQG	ARDPQRYLVIQGD	P00533	EGFR	978
RDPQRYLVIQG	ARDPQRYLVIQGD	P00533	EGFR	978
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
TDSNFYRALMD	PTDSNFYRALMDE	P00533	EGFR	998
VDADEYLIPQQ	VVDADEYLIPQQG	P00533	EGFR	1016
SFLQRYSSDPT	DSFLQRYSSDPTG	P00533	EGFR	1069
LPVPEYINQSV	FLPVPEYINQSVP	P00533	EGFR	1092
VQNPVYHNQPL	SVQNPVYHNQPLN	P00533	EGFR	1110
VGNPEYLNTVQ	AVGNPEYLNTVQP	P00533	EGFR	1138
SVQNPVYHNQPLN	SVQNPVYHNQPLN	P00533	EGFR	1110
FIENEEQEpYVQTVK	ENEEQEYVQTVKS	P04083	ANXA1	20
AFGTVYKGIWI	GAFGTVYKGIWIP	P04626	ERBB2	735
FGAKPYDGIPA	TFGAKPYDGIPAR	P04626	ERBB2	923
LDSTFYRSLLE	PLDSTFYRSLLED	P04626	ERBB2	1005
SPQPEYVNQPD	CSPQPEYVNQPDV	P04626	ERBB2	1139
SPSSGYMPMNQ	SSPSSGYMPMNQG	P21860	ERBB3	1054
DEDEEYEYMNRRR	EDEDEEYEYMNRR	P21860	ERBB3	1197
DEEYEYMNRRRRH	DEEYEYMNRRRRH	P21860	ERBB3	1199
DEEYEYMNRRRRH	DEEYEYMNRRRRH	P21860	ERBB3	1199
LEELGYEYMDVGS	SLEELGYEYMDVG	P21860	ERBB3	1222
TPDEDYEYMNRQR	TTPDEDYEYMNRQ	P21860	ERBB3	1260
TPDEDYEYMNRQR	PDEDYEYMNRQRD	P21860	ERBB3	1262
GPGGDYAAMGA	GGPGGDYAAMGAC	P21860	ERBB3	1276
ASEQGYEEMRA	PASEQGYEEMRAF	P21860	ERBB3	1289

LFDDPSYVNVQNL	LFDDPSYVNVQNL	P29353	SHC1	427
LFDDPSYVNVQNL	LFDDPSYVNVQNL	P29353	SHC1	427
LFDDPSYVNIQNL	LFDDPSYVNIQNL	P29353	SHC1	427
LHTDDGYMPMSPG	LHTDDGYMPMSPG	P35568	IRS1	612
RVDPNGYMMMSPS	RVDPNGYMMMSPS	P35568	IRS1	662
RVDPNGYMMMSPS	RVDPNGYMMMSPS	P35568	IRS1	662
ETSKLIYDFIEDQ	ETSKLIYDFIEDQ	P42768	WAS	291
ETSKLIYDFIEDQ	ETSKLIYDFIEDQ	P42768	WAS	291
GEEEHVYSFPNKQ	GEEEHVYSFPNKQ	P49023	PXN	118
GYNDDYYEESYFT	GYNDDYYEESYFT	P50402	EMD	95
YDEDSPYQNIKIL	YDEDSPYQNIKIL	P52788	SMS	147
YDEDSPYQNIKIL	YDEDSPYQNIKIL	P52788	SMS	147
VVDSGVYAVPPPA	VVDSGVYAVPPPA	P56945	BCAR1	410
IKEKLCYVALDFE	IKEKLCYVALDFE	P60709	ACTB	218
GNYRDNYDN	GNYRDNYDN	P98179	RBM3	155
LINRMDYVEINID	LINRMDYVEINID	Q00341	VGL	437
VSSTHYYLLPERP	VSSTHYYLLPERP	Q07912	ACK1	858
VSSTHYYLLPERP	VSSTHYYLLPERP	Q07912	ACK1	858
SEELDENpYVPMNPNS	EELDENYVPMNPN	Q13480	GAB1	447
PSTDPLYDTPDTR	PSTDPLYDTPDTR	Q13671	RIN1	36
PSTDPLYDTPDTR	PSTDPLYDTPDTR	Q13671	RIN1	36
AFGTVYKGIWV	GAFGTVYKGIWVP	Q15303	ERBB4	733
RDPQRYLVIQG	ARDPQRYLVIQGD	Q15303	ERBB4	984
MDAEEYLVPQA	MMDAEEYLVPQAF	Q15303	ERBB4	1022
SPPPAYTPMSG	HSPPPAYTPMSGN	Q15303	ERBB4	1056
KPKQEYLNPVE	DKPKQEYLNPVEE	Q15303	ERBB4	1162
LDNPEYHNASN	ALDNPEYHNASNG	Q15303	ERBB4	1188
KAEDEYVNEPL	PKAEDEYVNEPLY	Q15303	ERBB4	1202
VNEPLYLNTFA	YVNEPLYLNTFAN	Q15303	ERBB4	1208
LGKAEYLKNNI	TLGKAEYLKNNIL	Q15303	ERBB4	1221
LFDDPSYVNVQNL	LFDDPSYVNVQNL	Q15303	ERBB4	427
KLSLGQYDNDAGG	KLSLGQYDNDAGG	Q68CZ2	TNS	780
LTAEFLYDEVHPK	LTAEFLYDEVHPK	Q6IBS0	TWF2	309
TQPEPIYAESTKR	TQPEPIYAESTKR	Q86YV5	SGK223	390
AYADSYpYYEDGG	AYADSYYYEDGGM	Q8IVM0	CCDC50	145
GEDADpYTHFTNQQS	DGEDADYTHFTNQ	Q8IVM0	CCDC50	279
PKEDPIYDEPEGL	PKEDPIYDEPEGL	Q99704	DOK1	362
PKEDPIYDEPEGL	PKEDPIYDEPEGL	Q99704	DOK1	362
EKVTSPYWEERI	EKVTSPYWEERI	Q9NQC7	CYLD	15
PASVTDYQNVSFS	PASVTDYQNVSFS	Q9NZM3	ITSN	858

SH2 protei	SH2 prot name	operator
P16333	NCK2	Martin
O15357	SHIP2	Martin
P23726	PIK3R2	Jesper*
P27986	PIK3R1	Jesper*
P62993	GRB2	Jesper
Q06124	PTPN11	Jesper
P16885	PLCG2	Jesper
P20936	RASA1	Jesper
P27986	PIK3R1	Jesper
O15357	SHIP2	Martin
Q06124	PTPN11	Martin
O15357	SHIP2	Martin
P20936	RASA1	Jesper
Q06124	PTPN11	Jesper
P52735	VAV2	Jesper
P29353	SHC1	Schultze
Q06124	PTPN11	Schultze
P51692	STAT5B	Schultze*
P46109	CRKL	Schultze
P41240	CSK	Schultze
Q06124	PTPN11	Schultze
P29353	SHC1	Schultze
P51692	STAT5B	Schultze*
P29353	SHC1	Schultze
Q06124	PTPN11	Schultze
P22681	CBL	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Jesper
Q06124	PTPN11	Jesper
P29353	SHC1	Schultze
P27986	PIK3R1	Schultze
P29353	SHC1	Schultze
P62993	GRB2	Schultze
P27986	PIK3R1	Schultze
P27986	PIK3R1	Schultze
P41240	CSK	Schultze
P62993	GRB2	Schultze
P27986	PIK3R1	Schultze
P27986	PIK3R1	Schultze
P62993	GRB2	Schultze
P27986	PIK3R1	Schultze
P27986	PIK3R1	Schultze

P20936	RASA1	Jesper
P62993	GRB2	Jesper
P62993	GRB2	Martin
P27986	PIK3R1	Martin
P27986	PIK3R1	Martin
P27986	PIK3R1	Martin
P16333	NCK2	Martin*
O15357	SHIP2	Martin
P46109	CRKL	Jesper
P29353	SHC1	Jesper
P62993	GRB2	Martin
P20936	RASA1	Martin
P20936	RASA1	Martin
Q06124	PTPN11	Martin
P62993	GRB2	Jesper
Q06124	PTPN11	Martin
P16885	PLCG2	Jesper
Q06124	PTPN11	Jesper
P23726	PIK3R2	Jesper*
P16333	NCK2	Martin*
P20936	RASA1	Martin
P29353	SHC1	Schultze
Q06124	PTPN11	Schultze
P46109	CRKL	Schultze
O00459	PIK3R2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Schultze
P62993	GRB2	Jesper
P62993	GRB2	Jesper
P20936	RASA1	Martin
P41240	CSK	Jesper
P20936	RASA1	Jesper
P52735	VAV2	Jesper
P16333	NCK2	Jesper*
P20936	RASA1	Jesper
P27986	PIK3R1	Jesper*
P62993	GRB2	Martin

SH2-domain containing p	Observed by LC-MS in HeLa?	Uniprot ID	Predictor
ABL1	YES	P00519	YES
ABL2	YES	P42684	YES
BLK	YES	P51451	YES
CRK	YES	P46108	YES
CRKL	YES	P46109	YES
CSK	YES	P41240	YES
FER	YES	P16591	YES
FRK	YES	P42685	YES
FYN	YES	P06241	YES
GRB10	YES	Q13322	YES
GRB2	YES	P62993	YES
HCK	YES	P08631	YES
LYN	YES	P07948	YES
P55G	YES	Q92569	YES
P85A	YES	P27986	YES
P85B	YES	O00459	YES
PLCG1	YES	P19174	YES
PTK6	YES	Q13882	YES
PTN11	YES	Q06124	YES
RASA1	YES	P20936	YES
SH23A	YES	Q9BRG2	YES
SHC1	YES	P29353	YES
SHIP2	YES	O15357	YES
SRC	YES	P12931	YES
TENS1	YES	Q9HBL0	YES
TENS3	YES	Q68CZ2	YES
VAV2	YES	P52735	YES
YES	YES	P07947	YES
BCAR3	YES	O75815	NO
JAK1	YES	P23458	NO
LCK	YES	P06239	NO
NCK1	YES	P16333	NO
RIN1	YES	Q13671	NO
SH24A	YES	Q9H788	NO
SHB	YES	Q15464	NO
SPT6H	YES	Q7KZ85	NO
STA5A	YES	P42229	NO
STA5B	YES	P51692	NO
STAT1	YES	P42224	NO
STAT2	YES	P52630	NO
STAT3	YES	P40763	NO
STAT6	YES	P42226	NO
TENS4	YES	Q8IZW8	NO

TYK2	YES	P29597	NO
VAV3	YES	Q9UKW4	NO
3BP2	NO	P78314	
AFAP1	NO	Q8N556	
BCR	NO	P11274	
BLNK	NO	Q8WV28	
BMX	NO	P51813	
BTK	NO	Q06187	
CBL	NO	P22681	
CBLB	NO	Q13191	
CBLC	NO	Q9ULV8	
CHIN	NO	P15882	
CHIO	NO	P52757	
CISH	NO	Q9NSE2	
DAPP1	NO	Q9UN19	
FES	NO	P07332	
FGR	NO	P09769	
FYB	NO	O15117	
GRAP	NO	Q13588	
GRAP2	NO	O75791	
GRB14	NO	Q14449	
GRB7	NO	Q14451	
HSH2D	NO	Q96JZ2	
ITBP2	NO	Q9UKP3	
ITK	NO	Q08881	
JAK2	NO	O60674	
JAK3	NO	P52333	
KSYK	NO	P43405	
LCP2	NO	Q13094	
LRP2	NO	P98164	
MATK	NO	P42679	
MIST	NO	Q7Z7G1	
NCK2	NO	O43639	
PLCG2	NO	P16885	
PTN6	NO	P29350	
RIN2	NO	Q8WYP3	
RIN3	NO	Q8TB24	
S18L1	NO	O75177	
S18L2	NO	Q9UHA2	
SH21A	NO	O60880	
SH21B	NO	O14796	
SH22A	NO	Q9NP31	
SH24B	NO	Q5SQS7	
SH2B1	NO	Q9NRF2	

SH2B2	NO	O14492
SH2B3	NO	Q9UQQ2
SH2D3	NO	Q8N5H7
SH2D5	NO	Q6ZV89
SH2D6	NO	Q7Z4S9
SHC2	NO	P98077
SHC3	NO	Q92529
SHC4	NO	Q6S5L8
SHCBP	NO	Q8NEM2
SHD	NO	Q96IW2
SHE	NO	Q5VZ18
SHF	NO	Q7M4L6
SHIP1	NO	Q92835
SHPS1	NO	P78324
SLAF1	NO	Q13291
SLAF5	NO	Q9UIB8
SLAP1	NO	Q13239
SLAP2	NO	Q9H6Q3
SOCS1	NO	O15524
SOCS2	NO	O14508
SOCS3	NO	O14543
SOCS4	NO	Q8WXH5
SOCS5	NO	O75159
SOCS6	NO	O14544
SOCS7	NO	O14512
SRMS	NO	Q9H3Y6
SSXT	NO	Q15532
STAP1	NO	Q9ULZ2
STAP2	NO	Q9UGK3
STAT4	NO	Q14765
TEC	NO	P42680
TENC1	NO	Q63HR2
TM1L1	NO	O75674
TXK	NO	P42681
VAV	NO	P15498
YO025	NO	A6NKC9
YQ012	NO	Q8TC17
ZAP70	NO	P43403

Supplemental Information

Extended Results

Reproducibility of chip experiments

The correlation coefficient of the results of the triplicate arrays represents a good measure of the quality of the experiment. In Suppl_Table 2 we have reported the Pearson correlation coefficients between the results of triplicate arrays or between independent experiments carried out at different times with different preparation of the same domain. Typical correlation graphs are reported in Suppl Figure S1.

PepspotDB: Motivation and Brief Description

PepspotDB is a new database, specifically designed to store in a single integrated resource the results of experiments exploiting molecular array technology. We decided to develop a brand new database, because readily available alternative solutions were either too broad (Ceol et al., 2010; Ceol et al., 2007), or too narrow (Gong et al., 2008) in scope.

Although PepspotDB has been developed primarily to support research activities within our group, we have opened it to the community as a key reference for the storage and retrieval of peptide chip data.

PepspotDB contains five main data types:

(a) Experimental evidence supporting SH2 peptide interaction

(b) Computational predictions

(c) Binary interactions

(d) Bayesian integration of contextual evidence

(e) Phosphorylation sites

Among all domain-peptide pairs that have either experimental or computational support, only those with signal intensity or prediction score above a certain threshold are considered. These candidate binary interactions are singled out and stored in the database in a separate table for easy visualization and retrieval. The Bayesian integration of experimental data with orthogonal contextual evidence provides a Bayesian score for each tested domain-peptide pair.

Since SH2 domains bind to phospho-tyrosine containing peptides, and since other families of interaction domains also recognize phosphorylated residues, we imported into the database information on experimentally determined phosphorylation sites, as annotated in the two most comprehensive publicly available databases hosting phosphorylation data, PhosphoSite (Hornbeck et al., 2012) and PhosphoELM (Diella et al., 2008). Information on protein sequences was also imported from an external database, UniProtKB (The UniProt Consortium 2009), the reference repository for protein records. Furthermore, PepspotDB is tightly integrated with the MINT protein interaction database (Chatr-aryamontri et al., 2007).

PepspotDB: Requirements and Guidelines

The key requirement for PepspotDB was flexibility to ensure the database could grow smoothly, with no need for major redesign steps, as the number and diversity of projects increased.

The integration of external data sources was another issue. The two most common alternative integration strategies are “deep” and “shallow” integration. Deep integration basically consists in replicating the information stored in an external data source into the in-house database; it requires the translation or mapping of the external database data model to the data model of the destination database and periodic updates to bring the local copy of the data in line with the original source. Shallow integration is much easier to accomplish: the data remain in the primary data source (no replication occurs) and some sort of hyperlink pointing to them is created in the secondary data source. The advantage of the first solution lies in the superior performance achievable in terms of response times since no additional network traffic is generated. On the other hand, deep integration involves a considerable design effort to work out a more complex unified schema and comes with major maintenance issues. Shallow integration imposes a much lighter burden on the database design, often involving nothing more than the storage of a Unified Resource Locator (URL) in the proper table column. However, this second solution presents serious drawbacks in terms of performance, due to network latency and possibly failure. Maintenance issues are also not completely absent (URLs should be updated once in a while as broken links may occur).

Our design choices were oriented towards the achievement of the most suitable trade-off between flexibility and performance. PepspotDB is not yet another protein interaction database but focuses on experiments based on peptide array technology. As for integration of external data sources, we did not fully commit ourselves to either to a deep or a shallow strategy, but we decided on a case by case basis which one was most appropriate to gain performance without losing too much flexibility. Hence, for instance, we chose deep integration to import protein data from UniProtKB (UniProt,

2009) and phosphorylation data from Phospho.ELM and PhosphoSite (Diella et al., 2008; Hornbeck et al., 2004), whereas shallow integration seemed to us more effective for linking binary interactions stored in PepspotDB with relevant records in the general purpose Molecular INTeraction database.

PepspotDB: Data Model

Although the database was originally conceived as a repository of experiments employing peptide arrays to detect domain-peptide interactions, we aimed at making the database structure as general as possible, to be able to accommodate virtually any kind of interaction assay based on array technology. Figure 1 shows a class diagram portraying a subset of classes, extracted from the larger PepspotDB data model, capturing the concept of experiment and the concepts related to it.

First of all, it should be noted that PepspotDB assumes that any experiment involves the probing of one or more arrays of some kind with a potential interactor. In other words, PepspotDB assumes experiments are based on array technology. This, of course, imposes a strict constraint to the number of different types of experiments that can be stored in the database, but, on the other hand, it paves the way for a database structure specifically tailored for these kinds of experiment, thus allowing PepspotDB to organize the data more effectively and with a greater level of detail than other more general purpose databases of molecular interactions, such as MINT. More specifically, an Experiment is composed of one or more ArrayAssays, each one referring to a specific ArrayChip and identifying a group of Measures, each of which is related to a single ArraySpot (see Fig. 1). ArrayChips are composed of ArraySpots and represent a particular array layout. ArraySpots correspond to positions in the array and can be either control spots, marker spots (used by the scanner software to align the quantization grid), blank spots or spots containing an Interactor. A Measure object encapsulates most of the data produced by the scanner software upon quantization of a particular array spot. Experiments are often performed in duplicate or in triplicate: different replicates of the same array layout within the same experiment are modeled by different ArrayAssay objects, one for each replicate, referring to the same ArrayChip and Experiment. Thus, in an experiment performed in triplicate, three Measures for each ArraySpot will be associated to the respective ArrayAssay object representing one replicate of the same ArrayChip. The Interactor class conveys the general idea of a molecule that can interact with some other molecule, abstracting from the actual type of molecule we are talking about (e.g. a protein, a region of a protein, a nucleic acid, etc...). ModifiableMolecule is a particular class of Interactor provided with a sequence to which one or more PTM (Post-Translational Modification) objects can be attached. ModifiableMolecule is further specialized into Peptide, Domain and Protein. A Peptide can be associated to many proteins through PeptideProteinAssociation entities (most often a peptide matches the sequence of several homologous proteins); a Protein in turn can be composed of many domains. These layers of abstraction allow PepspotDB to deal with experiments of different nature exactly in the same manner: since experiments are modeled as interaction assays testing, in one-versus-all fashion, a generic Interactor against one or more arrays composed of ArraySpots containing also generic Interactors, domain-peptide, domain-domain, antibody-antigen or protein-protein interaction assays are viewed as perfectly equal.

Furthermore, PepspotDB foresees the possibility that an Interactor may participate in different experiments in modified forms, e.g. it could be mutated in one experiment and phosphorylated in another: InteractorForm objects signify the particular configurations assumed by Interactors in the context of a specific experiment and are used to create experiment-wise variants of an Interactor by associating to it one or more Features (the only implemented one so far being PTM, Post-Translational Modification). This is the reason why the ArraySpot class is associated to the Interactor class through the InteractorForm class and not immediately. The same is true for the Experiment class. To illustrate this concept with an example: let's suppose we wanted to capture the fact that protein A participates in experiment X in its canonical form and in experiment Y in a phosphorylated form and no InteractorForm class was present; we would have to create two distinct Protein objects, one representing A in its canonical form and another representing A in its phosphorylated form and link them to the respective experiments, thus unnecessarily duplicating information. With the introduction of the InteractorForm class, we can now create two InteractorForms, associate one of them to the proper post-translational modification (PTM), and link both forms to the same Protein object corresponding to protein A.

Besides raw data, i.e. the figures output by the laser scanner, encapsulated by the Measure object, PepspotDB's data model allows the storage also of experimental data after processing, a procedure during which filters are applied to the data to attenuate noise and the redundant information contained in the two or more replicates is collapsed into one figure. In a typical triplicated experiment, the three Measures associated to a particular spot undergo processing and are merged into a single NormalizedMeasure instance relative to the spot. As was mentioned earlier, PepspotDB encompasses not only experimental observations, but also computational predictions obtained from Neural Network predictors. The NeuralNetworkPrediction class models such computational predictions, linking the target Interactor for which the prediction was made to the Experiment whose data were used to train the Neural Network predictor.

Finally, scanned images (Image class) of the chip may be stored in the database and linked to their respective experiment.

PepspotDB: Web Interface

On top of the relational database, we have built a user friendly web interface, with the aim of facilitating data access and retrieval to non computer experts (http://mint.bio.uniroma2.it/PepspotDB). Access to the web site is open to anyone using the “guest” account, which comes with reading privileges only. Authenticated users are granted different privileges in accordance with their assigned role(s): Reader, Writer, Curator or SuperUser. Since the PepspotDB short term goal was to support the research projects carried out in our lab, an entire section of the web site is dedicated to presenting these projects: the aim of each project is briefly described and its final results can be browsed through direct links. The SH2 specificity data can be explored from an interactive homology tree obtained by hierarchical clustering of the human SH2 domains according to sequence homology. Node color reflects the domain target recognition specificity, as established from the results of our experimental and computational analysis. Domains similarly colored have similar consensus sequences, as apparent from the logos popping up upon mouse hovering, whereas white nodes indicate a SH2 domain that we have not profiled yet. A click on a tree leaf forwards the user to the search page, where the candidate domain targets we have identified for that particular SH2 domain are listed.

The Search page allows quick retrieval of domain-peptide interactions. After the protein containing the domain (let us call it protein A) and the protein containing the peptide (let us call it protein B) have been selected, interactions involving any of the domains belonging to protein A and/or (depending on user selection) any of the peptides belonging to protein B are looked up and are displayed on the page. It is also possible to specify a range within the sequence of the peptide containing protein, to narrow the result set to certain peptides only. An interaction may be supported by experimental evidence, if it has been observed in at least one peptide chip experiment, by computational evidence, if it has received a sufficiently high score from a Neural Network predictor, or both. Which is the case can be easily grasped by looking at the search result: experimentally verified interactions are associated with an "experimental score", calculated as the logarithmic ratio between the foreground and background signals quantified by the scanner, whereas predicted interactions come with a "NeuralNetwork score", that is the output of the Neural Network predictor. On the bottom of the page there is a panel displaying several buttons controlling the set of operations that can be performed on the result set, such as filtering out records based on their content, sorting and exporting the query result in a textual format with comma-separated columns. Each retrieved interaction is also assigned a "global score", as calculated by the Bayesian classifier integrating orthogonal sources of information. In addition to the score itself, it is also possible to inspect the pieces of contextual evidence that were combined in the Bayesian framework to obtain the final value. A simple click on "Details" opens up a new panel containing such information. Another valuable piece of information provided by the query result table regards the status of our previous knowledge of an interaction stored in PepspotDB. Given a domain-peptide interaction between a domain of protein A and a peptide of protein B, if one or more protein interactions between A and B are annotated in MINT, regardless of whether the binding regions correspond or not, cross-references to the relevant MINT records appear on the corresponding row of the result table. Furthermore, if PepspotDB contains one or more interactions, that have been manually curated from the literature, for which both the proteins and the binding regions (e.g. domain and peptide) match, a little gold bar icon shows up next to the cross-references. After clicking on the icon, a list of these “golden standard” interactions is produced, complete with links to the original papers they were taken from.

The search page that we have just described is very powerful for mining domain-peptide interactions, but PepspotDB allows the user to browse in great detail also proteins, domains, domain targets (e.g. peptides) and experiments. The “Advanced Search” page is the entry point to start digging into the available data. From there, we can move on to the “Protein View”, the “Domain View” or the “Peptide View”, depending on the object of our quest. The “Protein View” provides us with a basic description of the selected protein, which is essentially a short version of the UniProtKB description of the protein. Moreover, we can find a list of post-translational modifications the protein may undergo carrying out its activity in the cell. The original source of the information is reported as well. At the bottom of the page, two panels display respectively a list of the peptides matching the sequence of the protein and a list of the domains the protein is composed of. It is important to note that, in order to be listed here, a peptide or domain must have been tested in at least one experiment, or, in the case of a peptide, with at least one binding predictor.

The “Domain View” and the “Peptide View” have similar structure, with a general description at the top of the page and further details as we scroll down. The most relevant pieces of information the “Domain View” gives us are: 1) what experiments involving this domain are available; 2) what predictors have been trained for this domain. By clicking on the relevant link, we are taken either to the “Experiment View” or to the “Neural Network Predictor View”, where the outcome of the experiment or of the predictor can be carefully scrutinized, manipulated through filtering and sorting, and finally exported. There is also the possibility to draw a sequence logo of the peptides currently selected and displayed in the table.

The “Peptide View” collects four pieces of data about the selected peptide: 1) what protein sequences are matched by the peptide sequence (a range identifying the location of the match in the protein sequence is specified); 2) what modifications were effected on the peptide upon synthesis; 3) what experiments the peptide participated in and what was the outcome (observed to bind or not); 4) what predictors produced a score for the peptide and what these scores indicated (predicted to bind or not).

PepspotDB: Technical Details

The realization of PepspotDB required the development and the concerted operation of multiple pieces of software employing different technologies: 1) a relational database; 2) an object-oriented API implementing PepspotDB's data model and providing a low-level interface to populate the database tables, as well as to retrieve the data; 3) a web application providing a user-friendly, universally accessible, high-level interface to the data; 4) a collection of scripts to process experimental results and computational predictions; 5) a tool to draw sequence logos.

The objected-oriented API is written in the Java language and is built on top of the Java Enterprise platform version 5. The Enterprise Edition of the Java platform was chosen because technologies like Enterprise Java Beans (EJB) 3.0, Java Persistence, Java Transaction and Java Architecture for XML Binding (JAXB) 2.0 greatly facilitate the task of developing the server-side part of distributed, transactional and data-oriented applications. Thanks to the Java Persistence API, a Plain Old Java Object (POJO) model, implementing PepspotDB's data model, could be readily employed to generate a relational database schema. The underlying engine actually providing object-relational mapping (i.e. providing automatic conversion from Java objects to records in a relational database and viceversa) and querying services is Hibernate.

The web application has been developed with JavaServer Faces (JSF) 1.2, a technology designed to simplify the building of user interfaces for JavaServer applications by providing a ready-to-use library of UI components with server-side event handling capabilities. To further reduce the complexity originating from the simultaneous employment of multiple advanced technologies, we exploited a powerful open source platform for building rich Internet applications in Java, called Seam. The Seam framework effectively glues together technologies such as Asynchronous JavaScript and XML (AJAX), JSF, Java Persistence and EJB 3.0: its unifying role is fundamental to simplify the development of web applications.

The tool for drawing sequence logos, dubbed rXLogo, has also been developed on the Java 5 platform; the Standard edition of the platform was used. The tool allows to draw a logo according to information content or relative entropy, to correct for sampling error, to calculate a frequency matrix from the alignment, to align the input sequences according to a user-defined regular expression and to produce multiple logos in a single run. Its source code has been integrated in PepspotDB's web application, though only a limited set of features are available in the online version.

The scripts used to process experimental results and computational predictions have been developed with R.

PepspotDB database runs on PostgreSQL 8.1, an open source Relational Database Management System (RDBMS), while PepspotDB web application runs on JBoss AS 4.2, a Java application server implementing the full J2EE 1.4 specification, plus some features of J2EE 5, such as EJB 3.0. Both server programs run on a dual-processor Intel Xeon 3.4 GHz machine, with 4GB RAM and two SATA 250GB Hard Drives configured in a RAID1 array.

PepspotDB: Content

PepspotDB so far contains close to 80 experiments, from which we could successfully profile 70 human SH2 domains. Both the raw and processed experimental data have been stored in the database. Besides the amino acid sequences spotted on the chips used for the experiments (~6,000), PepspotDB also contains all human peptides (13-mers) with a phosphorylated tyrosine residue in the central position, as reported by the PhosphoSite and Phospho.ELM repositories of experimentally observed phosphorylation sites. For each of the profiled SH2 domains, a Neural Network predictor has been trained and applied to the full set of peptides collected in the database (~13,600 sequences); after processing, all the binding predictions were stored in the database as well. From the whole experimental and computational datasets, all binary domain-peptide interactions with strong support from either dataset (or both datasets) have been extracted: two sets of 10,580 experimentally determined and 49,175 computationally predicted binary interactions, with an overlap of 4,207 interactions, have thus been produced and stored in PepspotDB. Finally, Bayesian integrated confidence scores have been generated (one for each possible domain-peptide pair) and have been stored in the database.

Extended Experimental Procedures

Spatial smoothing of array signal

Initial inspection of the array scans revealed the presence of spatial signal bias across the surface of the physical array. Spatial signal bias may arise from hybridization dynamics or array manufacturing affects related to washing steps or differences in print tip performance. Such affects should be removed before further analysis. The spatial signal bias was observed to similarly affect both the foreground (FG) and background (BG) spot intensity estimates. Two-dimensional effects of this type can be considered as background signal and can be removed when the FG is adjusted to remove the BG.

The shape and extent of spatial bias was observed to vary dramatically from array to array. Due to this, conditional steps were performed to best correct the specific bias depending on the array. The reduction of bias was assessed by the reduction in variance for replicated spots that were located across the array. Three BG estimation methods were considered: un-adjusted BG, 2D median smoothed (median of 7x7 feature window), or using a low-pass filter (LPF) (lowpass function from the rimage package). The BG that resulted in the lowest sum of squared replicate error (SSE) was selected on an array-by-array basis. The image analysis based LPF method was much faster but gave poorer results than the simple median 2D windowing approach.

The relative signal, log(FG/BG), often retained some spatial bias. The remaining spatial bias was removed by subtracting median smoothed estimates of log(FG/BG) using an iterative method, decreasing the smoothing window at each step and stopping when no improvement in SSE was achieved. No adjustment was made if the first iteration increased the SSE. With this smoothed BG and log(FG/BG) adjustment method, 43% of the replicate error was removed as assessed by SSE.

Data processing pipeline

In order to identify possible flawed spots, a sample of glass slides for each chip batch was probed against a collection of three different anti-pY antibodies. The chips were tested separately with a preparation containing each single antibody and with a mixture of all three antibodies as probe. The spots that did not light up in any of the experiments were flagged 'BAD' and were not taken into account in further data processing steps.

The glass chips were incubated with purified GST-SH2 fusions (1 μg/ml) for 3 hours in blocking buffer (BSA 5% in PBS) at room temperature. Spot bound GST fusion proteins were revealed by incubating with a fluorescently labelled anti-GST antibody. A control slide was probed with GST to identify false positive peptides that either bind to the tag or to the antibodies used in the assay. Since each slide contains three replica arrays the foreground and background intensity values for each spot were computed by taking the median of the three replicated measures.

The log-ratio of foreground versus background intensity, which is obtained by subtracting the intensity values in logarithmic rather than linear scale (i.e. log(FG) – log(BG) was taken as a measure of signal strength. Measuring intensities as log ratios between foreground and background can be prone to artifacts when background values are very low. To prevent log-ratios from increasing indefinitely when background intensity is close to zero, we added a small fixed amount (delta) to all foreground and background intensity values. The value of delta is defined on a per experiment basis and it is equal to the median background intensity of the experiment.

In a few cases, due to a wrong positioning of the grid delimiting spot areas by the software of the array reader, one obtains an excessively high background intensity which results in a low log ratio value. In such cases, there is a risk of missing good binding candidates, that is spots with considerably high foreground intensity that would also have high FG-BG or log (FG/BG) values, if such an artifactually high background estimate had not occurred. To detect likely instances of this problem, we introduced a couple of flags, 'high foreground' (fg_flag) and 'low background' (bg_flag): spots whose foreground intensity value is greater than twice the median foreground intensity of the experiment have their fg_flag set to 'GOOD'; conversely, spots whose background intensity value is greater than twice the median background intensity of the experiment have their bg_flag set to 'BAD'. Thus, problematic spots may be identified by looking for spots with fg_flag set to 'GOOD and bg_flag set to 'BAD'.

When the signal intensity of a spot exceeds a certain threshold, we consider that a successful binding reaction between the peptide spotted on that position in the chip and the tested domain. For each experiment, the threshold was set to the median signal intensity of the experiment plus twice the standard deviation from the median.

We distinguish between three classes of binders: true binders, potential binders and non-binders, identified with 2, 1 and 0 respectively in the data files. True binders are defined as spots with signal intensity above the binding threshold and having their fg_flag set to 'GOOD'. Spots with either signal intensity lower that the binding threshold or fg_flag set to 'BAD' are classified as potential binders. Finally, non-binders are those spots with both low signal and low foreground intensity (fg_flag = 'BAD').

A few peptides are spotted more than once in each array the spot with the highest smoothed log-ratio value was chosen and the others were not considered further. If different replicas of a domain profiling experiment were carried out, the highest normalized measure was considered. For all interactions that are stored in the database we keep track of the experimental evidence supporting it.

Supplementary Tables

Suppl Table S1: Phosphotyrosine peptide list, related to Figure 1The first column is the reference position in the peptide chip. The second column is the sequence of the thirteenmer centered on the phosphotyrosine residue. The third column contains the gi and UNIPROT id of the human protein containing the phosphopeptide. The fourth and fifth column contain the PhosphoELM and PhosphoSite annotation. The last column labels the peptides whose phosphorylation in the tyrosine at position 7 was predicted.

Suppl. Table S2: List of SH2 domains used in this work, related to Figure 2. The different columns contain the identifier of the domain, the identifier of the experiment, the UniprotKB id and entry name of the protein, the nucleotide range defining the SH2 domain, a comment on the result of the expression experiment and the protein gene name respectively

Suppl Table S3: Result reproducibility, related to Figure 2. The table reports the correlation coefficients (Pearson) of the different replicas arrays on a single glass chip (columns A, B, C, D) and of two independent experiments performed with two different preparations of the same domain.

Suppl. Table S4: Literature curated interactions between SH2 domains and phospho-tyrosine peptides, related to Figure 5. The table columns contain: the PubMed identifiers of the article reporting the evidence of the interaction, UniprotKB id and entry names of the SH2 domain containing protein and the interacting partner, the method used to identify the interaction, the phosphorylated tyrosine supporting SH2 binding, the amino acid range of the interacting peptide and the sequence of the interacting phosphotyrosine peptide centered on the phosphotyrosine.

Suppl. Table S5: Results of the pull down experiments, related to Figure 5. The different columns contain A) aminoacid sequence of the phospho-peptide used in the pull down experiment. B) Thirteenmer peptide centered on the phosphotyrosine C) UniprotKB id of the phospho protein D) gene name E) position of the phosphotyrosine F) UniprotKB id of the affinity purified protein G) Gene name of the affinity purified protein H) name of the operator

Suppl. Table S6: List of SH2 containing proteins that have ever been identified in HeLa cells, related to Figure 5.

Supplementary figure Legends

Supplementary Figure S1: Intra- and inter-experiment correlation, related to Figure 1. Two replica arrays were probed, at different times, with two different preparations of the domain VAV2. A Pearson correlation coefficient of 0.97 was calculated between the results of the two experiments. The correlation between the results of different replicas in the same chip experiment was also calculated and found to range from 0.8 to 0.98 in different experiments (Table S2).

Supplementary Figure S2: Correlation between peptide target and domain sequence similarity, related to Figure 3. The same matrix used to draw the specificity tree in Figure 1 was given as input to the EPCLUST program (http://www.bioinf.ebc.ee/EP/EP/EPCLUST/) to obtain a specificity distance by using the algorithm “linear coefficient based distance, Pearson centered”. The complement to 1 of the domain-domain distances output were then plotted against and equivalent the distance based on sequence homology distance retrieved with ClustalW.

Supplementary Figure S3: Two sample Logos representation of the motifs recognized by SH2 domains, related to Figure 3. Peptides with binding intensity higher than the chip median intensity plus one standard deviation were considered "binders" (positive data set), whereas the peptides with a fluorescence signal lower than the median signal are the negative data set. The peptides sequences were aligned on their phosphotyrosine residues and used as input for the Two Sample Logo software (Vacic et al., 2006) to generate a sequence Logo representing the specificity profile of each SH2 domain.The two Sample Logo visualization represents the amino acids enrichment at each position of the aligned sequences. The phosphorylated tyrosine, shared by both interacting and non interacting peptides, is shown in the central position. The upper part of the Logo shows the over-represented amino acids in the positive data set, while the lower section displays the under-represented residues in the positive data set, as compared to the negative data set.

Supplementary Figure S4: Summary of literature curation, related to Figure 5. The numbers in the Venn diagram represent curated articles. The details of the curation strategy are described in Methods

Supplementary Figure S5: Estimate of the parameters of the Bayesian model, related to Figure 5. The bar graph represents the distribution of the posterior probabilities of the evidence given interaction (foreground) and the probability of the evidence given non-interaction (background). These parameters, which were used in the Bayesian model, are determined from a set of known SH2 interactions that was collected and curated manually, deemed 'the foreground set', as well as the full range of possible combinations of SH2 domain containing protein and peptides ('the background set'), assuming that most of these combinations are non-interacting *in vivo*. Scores were binned for each predictor optimizing separation between the foreground set and the background set using a cross-validation approach. The contribution to the overall prediction varies greatly as can be inspected in the different graphs, where the bins and distributions for the foreground and the background set are shown."

Supplementary Figure S6: UML class diagram portraying the entities in PepspotDB data model.

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