

Operator: manfred
Date/time: 2017-09-09/11:43:46am
Title/Comment:

Reference series: gly2

hdx_kin-File: c:\massmap\web_site\reports\hdx\hdx_kin version_sept_17\gly2.hdx_kin

Experiment series: degly2

hdx_kin-File: c:\massmap\web_site\reports\hdx\hdx_kin version_sept_17\degly2.hdx_kin

lis-File:

C:\massmap\web_site\reports\hdx\lis_etc\MAB_Demo.lis

Total number lis-entries: 239

Number entries molecule HC: 143

Number entries molecule LC: 96

Standards:

C:\massmap\web_site\reports\hdx\standards\series1_1101_t2.mmp

C:\massmap\web_site\reports\hdx\standards\series1_1201_t2.mmp

C:\massmap\web_site\reports\hdx\standards\series1_1301_t2.mmp

Data sets of reference series:

Exchange Time	Path
0.0 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1101_t2.mmp
0.5 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1201_t2.mmp
1.0 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1301_t2.mmp
10.0 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1401_t2.mmp
60.0 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1501_t2.mmp
240.0 min	C:\massmap\web_site\reports\hdx\gly_2\series3_1601_t2.mmp

Data sets of experiment series:

Exchange Time	Path
0.0 min	C:\massmap\web_site\reports\hdx\degly_2\series3_1701_t2.mmp
0.5 min	C:\massmap\web_site\reports\hdx\degly_2\series3_1801_t2.mmp
1.0 min	C:\massmap\web_site\reports\hdx\degly_2\series3_1901_t2.mmp
10.0 min	C:\massmap\web_site\reports\hdx\degly_2\series3_2001_t2.mmp
60.0 min	C:\massmap\web_site\reports\hdx\degly_2\series3_2101_t2.mmp
240.0 min	C:\massmap\web_site\reports\hdx\degly_2\series3_2201_t2.mmp

Printout of HDX plots restricted to peptides with significant differences or problems

No printout of DU overview plot(s)

Printout of kinetics difference plot(s) for all peptides with sufficient HDX data

Molecule HC: Peptides with sufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC001-017	1	0.0 min	7.059	7.061	0.00	0.00	0.00	0.00
		0.5 min	7.048	7.053	36.48	34.94	5.47	5.24
		1.0 min	7.062	7.054	38.36	36.80	5.75	5.52
		10.0 min	7.051	7.047	45.36	44.15	6.80	6.62
		60.0 min	7.047	7.046	46.48	46.52	6.97	6.98
		240.0 min	7.051	7.045	46.96	47.45	7.04	7.12
		Score1: 0.99	DU sum difference: -0.57 u					
Score2: 1.03								
HC001-018	1	0.0 min	9.006	9.015	0.00	0.00	0.00	0.00
		0.5 min	9.002	9.003	30.53	27.89	4.89	4.46
		1.0 min	9.001	9.008	30.88	29.37	4.94	4.70
		10.0 min	8.998	9.001	36.93	36.28	5.91	5.80
		60.0 min	8.995	8.997	40.80	40.84	6.53	6.53
		240.0 min	8.996	9.009	42.54	42.31	6.81	6.77
		Score1: 1.30	DU sum difference: -0.80 u					
Score2: 1.08								
HC001-020	1	0.0 min	9.593	9.594	0.00	0.00	0.00	0.00
		0.5 min	9.603	9.596	27.88	25.28	5.02	4.55
		1.0 min	9.621	9.596	29.46	26.95	5.30	4.85
		10.0 min	9.597	9.607	32.47	32.47	5.84	5.84
		60.0 min	9.585	9.598	36.27	36.01	6.53	6.48
		240.0 min	9.591	9.606	37.53	37.53	6.75	6.75
		Score1: 1.40	DU sum difference: -0.97 u					
Score2: 1.14								
HC001-022	1	0.0 min	9.454	9.440	0.00	0.00	0.00	0.00
		0.5 min	9.448	9.452	27.90	25.86	5.58	5.17
		1.0 min	9.467	9.452	29.62	27.88	5.92	5.58
		10.0 min	9.450	9.453	38.80	35.92	7.76	7.18
		60.0 min	9.439	9.457	41.34	41.34	8.27	8.27
		240.0 min	9.457	9.461	43.95	43.75	8.79	8.75
		Score1: 0.98	DU sum difference: -0.92 u					
Score2: 0.98								
HC001-023	1	0.0 min	9.384	9.395	0.00	0.00	0.00	0.00
		0.5 min	9.393	9.389	28.67	26.49	6.02	5.56
		1.0 min	9.407	9.392	31.09	28.29	6.53	5.94
		10.0 min	9.387	9.386	37.73	35.76	7.92	7.51
		60.0 min	9.382	9.393	40.13	40.13	8.43	8.43
		240.0 min	9.405	9.403	42.33	42.34	8.89	8.89
		Score1: 1.42	DU sum difference: -1.25 u					
Score2: 1.28								
HC002-044	1	0.0 min	9.813	9.802	0.45	0.40	0.18	0.16
		0.5 min	9.806	9.785	21.84	20.65	8.74	8.26
		1.0 min	9.824	9.789	22.65	21.49	9.06	8.60
		10.0 min	9.806	9.781	26.70	25.77	10.68	10.31
		60.0 min	9.782	9.794	27.14	26.95	10.86	10.78
		240.0 min	9.795	9.794	27.24	27.18	10.90	10.87
		Score1: 0.93	DU sum difference: -1.43 u					
Score2: 0.76								
HC012-043	1	0.0 min	12.932	12.937	0.00	0.00	0.00	0.00
		0.5 min	12.940	12.944	6.71	6.22	1.95	1.80
		1.0 min	12.964	12.934	6.99	7.25	2.03	2.10
		10.0 min	12.963	12.934	9.41	8.95	2.73	2.60
		60.0 min	12.936	12.935	10.86	11.04	3.15	3.20
		240.0 min	12.936	12.932	13.82	14.61	4.01	4.24
		Score1: 0.07	DU sum difference: 0.08 u					
Score2: 0.46								

Molecule HC: Peptides with sufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC019-037	1	0.0 min	7.994	7.995	0.00	0.00	0.00	0.00
		0.5 min	7.997	7.995	0.00	0.00	0.00	0.00
		1.0 min	8.006	7.996	0.00	0.00	0.00	0.00
		10.0 min	7.999	7.994	0.00	0.00	0.00	0.00
		60.0 min	7.995	7.988	0.66	0.65	0.12	0.12
		240.0 min	7.999	7.987	2.26	1.97	0.41	0.35
		Score1: 0.08	DU sum difference:-0.05 u					
Score2: 0.06								
HC024-032	1	0.0 min	12.456	12.470	0.00	0.00	0.00	0.00
		0.5 min	12.466	12.481	33.07	31.51	2.65	2.52
		1.0 min	12.473	12.482	32.11	32.11	2.57	2.57
		10.0 min	12.467	12.474	34.20	33.42	2.74	2.67
		60.0 min	12.469	12.479	36.32	36.32	2.91	2.91
		240.0 min	12.477	12.481	38.33	38.91	3.07	3.11
		Score1: 0.46	DU sum difference:-0.14 u					
Score2: 0.62								
HC026-057	1	0.0 min	12.793	12.801	0.17	0.00	0.05	0.00
		0.5 min	12.797	12.801	4.84	4.41	1.45	1.32
		1.0 min	12.807	12.791	5.00	5.22	1.50	1.57
		10.0 min	12.793	12.783	6.89	7.02	2.07	2.11
		60.0 min	12.792	12.795	10.37	10.03	3.11	3.01
		240.0 min	12.798	12.802	14.05	13.44	4.21	4.03
		Score1: 0.31	DU sum difference:-0.35 u					
Score2: 0.40								
HC027-031	1	0.0 min	10.171	10.172	0.60	0.00	0.02	0.00
		0.5 min	10.178	10.183	38.53	33.31	1.54	1.33
		1.0 min	10.189	10.169	41.54	34.02	1.66	1.36
		10.0 min	10.183	10.183	44.55	38.53	1.78	1.54
		60.0 min	10.175	10.178	41.74	40.13	1.67	1.61
		240.0 min	10.188	10.177	39.73	41.54	1.59	1.66
		Score1: 3.75	DU sum difference:-0.63 u					
Score2: 4.28								
HC027-032	1	0.0 min	12.120	12.135	0.00	0.00	0.00	0.00
		0.5 min	12.126	12.137	19.47	18.46	0.97	0.92
		1.0 min	12.134	12.120	20.67	20.67	1.03	1.03
		10.0 min	12.121	12.129	20.17	20.17	1.01	1.01
		60.0 min	12.123	12.137	25.00	25.84	1.25	1.29
		240.0 min	12.135	12.134	29.70	29.70	1.48	1.48
		Score1: 0.04	DU sum difference:-0.01 u					
Score2: 0.39								
HC035-047	1	0.0 min	9.666	9.670	0.00	0.00	0.00	0.00
		0.5 min	9.673	9.672	5.59	5.16	0.62	0.57
		1.0 min	9.689	9.674	6.30	5.54	0.69	0.61
		10.0 min	9.674	9.672	10.77	9.16	1.18	1.01
		60.0 min	9.661	9.670	16.89	16.85	1.86	1.85
		240.0 min	9.672	9.672	22.47	22.26	2.47	2.45
		Score1: 0.80	DU sum difference:-0.34 u					
Score2: 0.65								
HC035-050	1	0.0 min	8.994	8.985	0.00	0.00	0.00	0.00
		0.5 min	8.999	8.989	5.80	5.47	0.81	0.77
		1.0 min	9.003	8.996	6.37	5.81	0.89	0.81
		10.0 min	8.995	8.989	10.58	9.14	1.48	1.28
		60.0 min	8.987	8.991	16.25	15.85	2.28	2.22
		240.0 min	8.993	9.003	20.47	21.15	2.87	2.96
		Score1: 0.53	DU sum difference:-0.29 u					
Score2: 0.73								

Molecule HC: Peptides with sufficient kinetics data, part 3

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC036-047	1	0.0 min	8.826	8.841	0.14	0.09	0.01	0.01
		0.5 min	8.829	8.826	6.90	6.45	0.69	0.65
		1.0 min	8.836	8.829	7.43	6.69	0.74	0.67
		10.0 min	8.834	8.840	12.77	11.42	1.28	1.14
		60.0 min	8.834	8.835	20.94	19.99	2.09	2.00
		240.0 min	8.839	8.847	26.39	25.98	2.64	2.60
Score1:		1.03	DU sum difference:-0.40 u					
Score2:		0.84						
HC036-049	1	0.0 min	9.248	9.243	0.02	0.02	0.00	0.00
		0.5 min	9.251	9.246	5.85	5.22	0.70	0.63
		1.0 min	9.266	9.246	6.04	5.42	0.72	0.65
		10.0 min	9.253	9.246	10.64	8.83	1.28	1.06
		60.0 min	9.264	9.259	19.06	17.26	2.29	2.07
		240.0 min	9.250	9.262	22.27	23.48	2.67	2.82
Score1:		0.96	DU sum difference:-0.44 u					
Score2:		1.29						
HC037-050	1	0.0 min	7.936	7.939	0.00	0.00	0.00	0.00
		0.5 min	7.936	7.936	8.38	8.01	1.01	0.96
		1.0 min	7.956	7.935	8.61	8.60	1.03	1.03
		10.0 min	7.939	7.937	14.05	12.81	1.69	1.54
		60.0 min	7.930	7.926	21.87	21.67	2.62	2.60
		240.0 min	7.934	7.912	27.48	28.09	3.30	3.37
Score1:		0.31	DU sum difference:-0.14 u					
Score2:		0.51						
HC051-068	1	0.0 min	9.696	9.720	0.00	0.00	0.00	0.00
		0.5 min	9.712	9.713	16.14	15.08	2.58	2.41
		1.0 min	9.730	9.702	18.46	16.79	2.95	2.69
		10.0 min	9.715	9.714	28.87	25.74	4.62	4.12
		60.0 min	9.697	9.702	34.13	32.52	5.46	5.20
		240.0 min	9.704	9.719	36.30	36.40	5.81	5.82
Score1:		1.21	DU sum difference:-0.81 u					
Score2:		1.13						
HC051-079	1	0.0 min	9.292	9.276	0.07	0.07	0.02	0.02
		0.5 min	9.276	9.281	13.34	12.41	3.60	3.35
		1.0 min	9.293	9.278	15.17	14.09	4.09	3.80
		10.0 min	9.266	9.265	23.19	21.45	6.26	5.79
		60.0 min	9.257	9.260	29.50	29.50	7.96	7.96
		240.0 min	9.259	9.263	32.45	32.44	8.76	8.76
Score1:		0.30	DU sum difference:-0.38 u					
Score2:		0.30						
HC057-068	1	0.0 min	9.025	9.029	0.00	0.00	0.00	0.00
		0.5 min	9.031	9.032	9.14	8.37	0.91	0.84
		1.0 min	9.038	9.034	11.28	10.29	1.13	1.03
		10.0 min	9.035	9.031	25.96	23.13	2.60	2.31
		60.0 min	9.026	9.028	35.92	36.12	3.59	3.61
		240.0 min	9.040	9.043	39.33	39.13	3.93	3.91
Score1:		0.91	DU sum difference:-0.43 u					
Score2:		1.03						
HC057-079	1	0.0 min	8.737	8.741	0.00	0.00	0.00	0.00
		0.5 min	8.733	8.739	10.55	9.93	2.22	2.08
		1.0 min	8.749	8.747	12.35	11.36	2.59	2.39
		10.0 min	8.740	8.732	21.44	18.93	4.50	3.98
		60.0 min	8.729	8.728	29.26	28.93	6.15	6.08
		240.0 min	8.739	8.828	32.28	33.03	6.78	6.94
Score1:		0.67	DU sum difference:-0.66 u					
Score2:		1.11p						

Molecule HC: Peptides with sufficient kinetics data, part 4

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC058-079	1	0.0 min	8.245	8.231	0.00	0.00	0.00	0.00
		0.5 min	8.248	8.238	11.76	10.39	2.35	2.08
		1.0 min	8.244	8.235	13.67	12.36	2.73	2.47
		10.0 min	8.224	8.222	22.46	20.84	4.49	4.17
		60.0 min	8.221	8.215	31.30	31.29	6.26	6.26
		240.0 min	8.229	8.219	34.97	34.11	6.99	6.82
		Score1:	0.72	DU sum difference:-0.67 u				
Score2:	0.72							
HC065-101	1	0.0 min	13.434	13.450	0.00	0.00	0.00	0.00
		0.5 min	13.437	13.459	4.09	4.30	1.47	1.55
		1.0 min	13.447	13.451	4.74	4.64	1.71	1.67
		10.0 min	13.429	13.466	6.43	5.47	2.31	1.97
		60.0 min	13.450	13.459	8.63	8.82	3.11	3.17
		240.0 min	13.443	13.440	11.64	11.69	4.19	4.21
		Score1:	0.16	DU sum difference:-0.22 u				
Score2:	0.32							
HC069-079	1	0.0 min	4.824	4.826	0.00	0.00	0.00	0.00
		0.5 min	4.811	4.817	27.09	26.28	2.71	2.63
		1.0 min	4.827	4.807	29.71	29.10	2.97	2.91
		10.0 min	4.805	4.809	34.14	33.52	3.41	3.35
		60.0 min	4.804	4.804	41.55	41.33	4.16	4.13
		240.0 min	4.814	4.811	44.74	44.95	4.47	4.50
		Score1:	0.53	DU sum difference:-0.21 u				
Score2:	0.53							
HC069-080	1	0.0 min	6.160	6.162	0.00	0.00	0.00	0.00
		0.5 min	6.164	6.164	23.88	21.41	2.63	2.36
		1.0 min	6.176	6.157	23.88	23.88	2.63	2.63
		10.0 min	6.162	6.157	29.10	27.29	3.20	3.00
		60.0 min	6.152	6.154	34.92	34.11	3.84	3.75
		240.0 min	6.160	6.171	38.73	37.73	4.26	4.15
		Score1:	1.03	DU sum difference:-0.48 u				
Score2:	0.92							
HC080-083	1	0.0 min	9.815	9.822	0.00	0.00	0.00	0.00
		0.5 min	9.825	9.833	0.00	0.60	0.00	0.02
		1.0 min	9.825	9.825	0.00	1.00	0.00	0.03
		10.0 min	9.822	9.829	1.00	0.40	0.03	0.01
		60.0 min	9.822	9.822	1.61	1.20	0.05	0.04
		240.0 min	9.825	9.836	4.41	4.01	0.13	0.12
		Score1:	0.05	DU sum difference: 0.01 u				
Score2:	0.64							
HC084-093	1	0.0 min	5.962	5.981	0.00	0.00	0.00	0.00
		0.5 min	5.960	5.961	13.44	12.83	1.21	1.16
		1.0 min	5.966	5.951	13.44	13.00	1.21	1.17
		10.0 min	5.961	5.957	13.78	13.25	1.24	1.19
		60.0 min	5.952	5.958	15.24	14.84	1.37	1.34
		240.0 min	5.962	5.960	18.00	17.26	1.62	1.55
		Score1:	0.71	DU sum difference:-0.24 u				
Score2:	0.58							
HC087-093	1	0.0 min	4.255	4.255	0.00	0.00	0.00	0.00
		0.5 min	4.261	4.262	8.18	7.90	0.49	0.47
		1.0 min	4.266	4.253	7.99	8.22	0.48	0.49
		10.0 min	4.250	4.259	8.16	7.29	0.49	0.44
		60.0 min	4.259	4.255	8.35	7.70	0.50	0.46
		240.0 min	4.264	4.262	8.34	8.70	0.50	0.52
		Score1:	0.31	DU sum difference:-0.07 u				
Score2:	0.51							

Molecule HC: Peptides with sufficient kinetics data, part 5

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC089-127	1	0.0 min	7.548	7.550	0.00	0.00	0.00	0.00
		0.5 min	7.539	7.538	6.62	6.18	2.51	2.35
		1.0 min	7.550	7.543	7.49	7.29	2.85	2.77
		10.0 min	7.534	7.538	10.14	9.34	3.85	3.55
		60.0 min	7.528	7.527	11.31	11.16	4.30	4.24
		240.0 min	7.534	7.558	13.58	13.14	5.16	4.99
		Score1:	0.53	DU sum difference:-0.77 u				
Score2:	0.43							
HC094-109	1	0.0 min	7.854	7.867	0.00	0.00	0.00	0.00
		0.5 min	7.855	7.859	33.34	31.70	5.00	4.75
		1.0 min	7.861	7.858	34.12	33.65	5.12	5.05
		10.0 min	7.858	7.855	35.90	34.69	5.39	5.20
		60.0 min	7.851	7.856	35.25	36.31	5.29	5.45
		240.0 min	7.855	7.866	37.27	36.64	5.59	5.50
		Score1:	0.76	DU sum difference:-0.44 u				
Score2:	1.07							
HC094-110	1	0.0 min	8.905	8.912	0.00	0.00	0.00	0.00
		0.5 min	8.925	8.938	31.10	29.81	4.98	4.77
		1.0 min	8.922	8.914	30.90	30.90	4.94	4.94
		10.0 min	8.913	8.913	36.32	34.52	5.81	5.52
		60.0 min	8.903	8.894	36.12	36.12	5.78	5.78
		240.0 min	8.901	8.894	37.12	37.12	5.94	5.94
		Score1:	0.81	DU sum difference:-0.50 u				
Score2:	0.66							
HC094-137	1	0.0 min	9.703	9.689	0.00	0.00	0.00	0.00
		0.5 min	9.695	9.697	20.14	18.26	7.86	7.12
		1.0 min	9.706	9.688	21.32	20.25	8.32	7.90
		10.0 min	9.695	9.688	25.52	25.49	9.95	9.94
		60.0 min	9.680	9.684	28.24	27.79	11.01	10.84
		240.0 min	9.693	9.694	26.86	29.54	10.48	11.52
		Score1:	0.20	DU sum difference:-0.30 u				
Score2:	1.30							
HC095-112	1	0.0 min	8.680	8.680	0.00	0.00	0.00	0.00
		0.5 min	8.689	8.677	29.50	27.91	5.02	4.74
		1.0 min	8.691	8.683	30.77	29.28	5.23	4.98
		10.0 min	8.680	8.676	34.92	32.87	5.94	5.59
		60.0 min	8.690	8.677	34.93	34.92	5.94	5.94
		240.0 min	8.680	8.664	36.93	36.92	6.28	6.28
		Score1:	1.35	DU sum difference:-0.88 u				
Score2:	1.10							
HC105-143	1	0.0 min	13.174	13.173	0.00	0.12	0.00	0.04
		0.5 min	13.176	13.180	5.45	5.51	1.85	1.87
		1.0 min	13.193	13.172	6.06	5.95	2.06	2.02
		10.0 min	13.169	13.179	7.12	7.07	2.42	2.40
		60.0 min	13.173	13.173	9.64	9.68	3.28	3.29
		240.0 min	13.171	13.168	12.48	12.42	4.24	4.22
		Score1:	0.00	DU sum difference: 0.00 u				
Score2:	0.09							
HC111-120	1	0.0 min	10.274	10.283	0.00	0.00	0.00	0.00
		0.5 min	10.274	10.286	20.51	18.51	1.85	1.67
		1.0 min	10.288	10.289	21.50	17.96	1.94	1.62
		10.0 min	10.269	10.282	29.31	27.01	2.64	2.43
		60.0 min	10.269	10.284	35.68	35.77	3.21	3.22
		240.0 min	10.288	10.288	38.66	38.73	3.48	3.49
		Score1:	1.62	DU sum difference:-0.61 u				
Score2:	1.53							

Molecule HC: Peptides with sufficient kinetics data, part 6

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC111-139	1	0.0 min	11.330	11.345	0.00	0.00	0.00	0.00
		0.5 min	11.335	11.346	15.17	14.66	3.64	3.52
		1.0 min	11.347	11.337	16.72	15.47	4.01	3.71
		10.0 min	11.332	11.339	23.28	21.88	5.59	5.25
		60.0 min	11.332	11.340	28.27	28.09	6.79	6.74
		240.0 min	11.332	11.341	32.71	32.84	7.85	7.88
		Score1:	0.90	DU sum difference:-1.02 u				
Score2:	0.90							
HC111-145	1	0.0 min	11.467	11.474	0.60	0.89	0.18	0.27
		0.5 min	11.465	11.474	19.03	18.38	5.71	5.51
		1.0 min	11.469	11.443	20.98	17.60	6.30	5.28
		10.0 min	11.462	11.466	25.27	24.09	7.58	7.23
		60.0 min	11.455	11.475	28.45	28.48	8.53	8.54
		240.0 min	11.455	11.465	31.94	31.88	9.58	9.57
		Score1:	0.44	DU sum difference:-0.56 u				
Score2:	0.56							
HC112-120	1	0.0 min	9.782	9.784	0.00	0.00	0.00	0.00
		0.5 min	9.774	9.778	23.95	21.53	1.92	1.72
		1.0 min	9.786	9.788	24.98	22.37	2.00	1.79
		10.0 min	9.772	9.779	28.67	26.65	2.29	2.13
		60.0 min	9.776	9.783	34.04	33.68	2.72	2.69
		240.0 min	9.785	9.790	38.25	37.90	3.06	3.03
		Score1:	2.02	DU sum difference:-0.62 u				
Score2:	1.65							
HC112-139	1	0.0 min	11.048	11.063	0.00	0.00	0.00	0.00
		0.5 min	11.063	11.073	16.65	15.64	3.83	3.60
		1.0 min	11.079	11.060	18.46	17.00	4.25	3.91
		10.0 min	11.059	11.066	22.88	21.07	5.26	4.85
		60.0 min	11.061	11.062	26.11	26.07	6.01	6.00
		240.0 min	11.057	11.069	30.30	31.30	6.97	7.20
		Score1:	0.86	DU sum difference:-0.76 u				
Score2:	1.13							
HC113-120	1	0.0 min	7.633	7.626	0.00	0.00	0.00	0.00
		0.5 min	7.611	7.626	19.70	18.93	1.38	1.33
		1.0 min	7.632	7.618	19.87	19.40	1.39	1.36
		10.0 min	7.623	7.608	25.31	23.88	1.77	1.67
		60.0 min	7.606	7.611	32.51	32.11	2.28	2.25
		240.0 min	7.627	7.637	37.93	39.98	2.65	2.80
		Score1:	0.12	DU sum difference: 0.04 u				
Score2:	0.94							
HC113-139	1	0.0 min	10.233	10.244	0.00	0.00	0.00	0.00
		0.5 min	10.227	10.237	13.28	12.89	2.92	2.84
		1.0 min	10.256	10.206	14.05	64.42	3.09	14.17
		10.0 min	10.240	10.237	20.66	18.86	4.55	4.15
		60.0 min	10.218	10.226	24.86	25.28	5.47	5.56
		240.0 min	10.232	10.239	30.82	30.65	6.78	6.74
		Score1:	0.05	DU sum difference:-0.05 u				
Score2:	0.31							
HC115-140	1	0.0 min	10.579	10.590	0.00	0.00	0.00	0.00
		0.5 min	10.623	10.616	21.37	20.23	4.49	4.25
		1.0 min	10.645	10.611	22.73	21.46	4.77	4.51
		10.0 min	10.611	10.603	29.57	27.24	6.21	5.72
		60.0 min	10.599	10.609	31.89	31.72	6.70	6.66
		240.0 min	10.615	10.615	33.93	34.11	7.12	7.16
		Score1:	1.02	DU sum difference:-0.90 u				
Score2:	1.01							

Molecule HC: Peptides with sufficient kinetics data, part 7

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC118-156	1	0.0 min	10.818	10.821	0.22	0.20	0.08	0.07
		0.5 min	10.830	10.831	4.11	3.73	1.40	1.27
		1.0 min	10.840	10.825	4.00	4.29	1.36	1.46
		10.0 min	10.825	10.825	6.92	5.62	2.35	1.91
		60.0 min	10.832	10.835	8.27	8.70	2.81	2.96
		240.0 min	10.831	10.823	10.18	14.67	3.46	4.99
Score1:	0.92	DU sum difference: 1.20 u						
Score2:	1.47							
HC119-139	1	0.0 min	9.128	9.126	0.00	0.34	0.00	0.05
		0.5 min	9.122	9.121	16.94	15.83	2.71	2.53
		1.0 min	9.135	9.118	19.44	17.88	3.11	2.86
		10.0 min	9.131	9.114	23.74	22.13	3.80	3.54
		60.0 min	9.103	9.112	25.57	25.06	4.09	4.01
		240.0 min	9.113	9.093	28.24	28.34	4.52	4.53
Score1:	0.78	DU sum difference: -0.53 u						
Score2:	0.93							
HC119-145	1	0.0 min	9.559	9.559	0.60	0.60	0.13	0.13
		0.5 min	9.557	9.557	25.41	24.28	5.59	5.34
		1.0 min	9.563	9.551	25.08	25.28	5.52	5.56
		10.0 min	9.548	9.553	30.50	27.89	6.71	6.14
		60.0 min	9.543	9.550	30.70	30.50	6.75	6.71
		240.0 min	9.553	9.556	33.51	33.71	7.37	7.42
Score1:	0.26	DU sum difference: -0.24 u						
Score2:	0.44							
HC121-139	1	0.0 min	8.896	8.890	0.00	0.00	0.00	0.00
		0.5 min	8.902	8.895	18.92	17.51	2.65	2.45
		1.0 min	8.901	8.899	21.35	19.63	2.99	2.75
		10.0 min	8.903	8.897	25.36	23.73	3.55	3.32
		60.0 min	8.890	8.886	25.85	25.51	3.62	3.57
		240.0 min	8.898	8.905	28.46	28.34	3.98	3.97
Score1:	0.60	DU sum difference: -0.39 u						
Score2:	0.60							
HC121-142	1	0.0 min	8.591	8.587	0.00	0.00	0.00	0.00
		0.5 min	8.596	8.595	27.29	26.49	4.64	4.50
		1.0 min	8.598	8.601	29.70	27.89	5.05	4.74
		10.0 min	8.595	8.578	32.27	31.30	5.49	5.32
		60.0 min	8.583	8.581	32.51	32.51	5.53	5.53
		240.0 min	8.583	8.586	35.52	35.32	6.04	6.00
Score1:	0.56	DU sum difference: -0.40 u						
Score2:	0.50							
HC121-145	1	0.0 min	9.406	9.389	1.84	1.62	0.37	0.32
		0.5 min	9.383	9.387	29.56	27.94	5.91	5.59
		1.0 min	9.389	9.373	31.44	28.83	6.29	5.77
		10.0 min	9.378	9.391	33.79	31.71	6.76	6.34
		60.0 min	9.380	9.387	33.07	32.79	6.61	6.56
		240.0 min	9.396	9.393	35.06	35.02	7.01	7.00
Score1:	1.79p	DU sum difference: -1.37 u						
Score2:	1.46p							
HC132-184	1	0.0 min	11.644	11.594	0.00	0.00	0.00	0.00
		0.5 min	11.625	11.576	3.41	3.81	1.60	1.79
		1.0 min	11.583	11.577	4.01	4.62	1.89	2.17
		10.0 min	11.581	11.565	6.42	7.42	3.02	3.49
		60.0 min	11.622	11.581	9.23	11.04	4.34	5.19
		240.0 min	11.571	11.579	13.44	13.65	6.32	6.41
Score1:	1.05	DU sum difference: 1.89 u						
Score2:	0.85							

Molecule HC: Peptides with sufficient kinetics data, part 8

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC146-151	1	0.0 min	11.846	11.847	0.00	0.00	0.00	0.00
		0.5 min	11.846	11.861	0.80	1.00	0.04	0.05
		1.0 min	11.846	11.861	0.60	1.40	0.03	0.07
		10.0 min	11.840	11.854	1.00	0.80	0.05	0.04
		60.0 min	11.847	11.860	1.20	0.60	0.06	0.03
		240.0 min	11.847	11.832	0.60	2.41	0.03	0.12
		Score1: 0.52	DU sum difference: 0.10 u					
Score2: 0.77								
HC151-161	1	0.0 min	10.012	10.010	0.00	0.00	0.00	0.00
		0.5 min	10.018	10.021	2.83	3.21	0.23	0.26
		1.0 min	10.024	10.018	3.65	3.89	0.29	0.31
		10.0 min	10.013	10.013	11.51	10.75	0.92	0.86
		60.0 min	10.004	10.008	22.88	22.07	1.83	1.77
		240.0 min	10.008	10.018	24.48	24.08	1.96	1.93
		Score1: 0.35	DU sum difference: -0.11 u					
Score2: 0.55								
HC152-161	1	0.0 min	9.407	9.405	0.00	0.00	0.00	0.00
		0.5 min	9.405	9.407	2.27	2.21	0.16	0.15
		1.0 min	9.413	9.413	3.14	3.23	0.22	0.23
		10.0 min	9.403	9.406	12.43	11.43	0.87	0.80
		60.0 min	9.397	9.402	24.69	24.46	1.73	1.71
		240.0 min	9.406	9.402	26.69	26.68	1.87	1.87
		Score1: 0.31	DU sum difference: -0.08 u					
Score2: 0.29								
HC152-164	1	0.0 min	13.031	13.032	0.00	0.00	0.00	0.00
		0.5 min	13.034	13.045	9.23	9.43	0.92	0.94
		1.0 min	13.045	13.040	11.84	11.64	1.18	1.16
		10.0 min	13.029	13.052	21.75	21.27	2.18	2.13
		60.0 min	13.034	13.043	28.09	28.29	2.81	2.83
		240.0 min	13.031	13.040	29.10	29.10	2.91	2.91
		Score1: 0.06	DU sum difference: 0.02 u					
Score2: 0.15								
HC160-195	1	0.0 min	12.445	12.447	0.00	0.00	0.00	0.00
		0.5 min	12.453	12.461	5.15	5.44	1.70	1.80
		1.0 min	12.465	12.450	5.57	5.42	1.84	1.79
		10.0 min	12.455	12.454	7.31	6.75	2.41	2.23
		60.0 min	12.440	12.459	9.83	9.80	3.24	3.23
		240.0 min	12.458	12.450	13.07	13.44	4.31	4.44
		Score1: 0.02	DU sum difference: -0.03 u					
Score2: 0.30								
HC161-183	1	0.0 min	14.813	14.820	0.03	0.29	0.01	0.06
		0.5 min	14.803	14.831	7.00	7.32	1.47	1.54
		1.0 min	14.827	14.828	7.32	7.22	1.54	1.52
		10.0 min	14.814	14.821	8.15	7.83	1.71	1.64
		60.0 min	14.821	14.832	10.63	10.64	2.23	2.23
		240.0 min	14.825	14.826	14.45	14.84	3.03	3.12
		Score1: 0.14	DU sum difference: 0.12 u					
Score2: 0.30								
HC162-169	1	0.0 min	10.825	10.838	0.00	0.00	0.00	0.00
		0.5 min	10.812	10.831	24.90	23.49	1.74	1.64
		1.0 min	10.820	10.825	31.22	29.31	2.19	2.05
		10.0 min	10.817	10.825	40.46	37.27	2.83	2.61
		60.0 min	10.818	10.827	41.37	41.40	2.90	2.90
		240.0 min	10.826	10.832	44.09	44.28	3.09	3.10
		Score1: 0.38	DU sum difference: -0.13 u					
Score2: 0.52								

Molecule HC: Peptides with sufficient kinetics data, part 9

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)		
			Ref	Exp	Ref	Exp	Ref	Exp	
HC162-180	1	0.0 min	12.934	12.941	0.00	0.00	0.00	0.00	
		0.5 min	12.924	12.938	13.96	14.53	2.37	2.47	
		1.0 min	12.940	12.924	18.06	16.14	3.07	2.74	
		10.0 min	12.919	12.919	22.02	21.97	3.74	3.73	
		60.0 min	12.918	12.934	21.83	21.84	3.71	3.71	
		240.0 min	12.932	12.948	23.24	23.20	3.95	3.94	
	Score1:	0.40	DU sum difference:-0.28 u						
	Score2:	0.65							
	=====								
	HC162-180	2	0.0 min	13.150	13.151	0.00	0.00	0.00	0.00
0.5 min			13.154	13.158	14.05	12.84	2.39	2.18	
1.0 min			13.166	13.158	17.62	15.60	3.00	2.65	
10.0 min			13.147	13.153	20.44	20.44	3.47	3.47	
60.0 min			13.153	13.155	21.67	21.67	3.68	3.68	
240.0 min			13.155	13.157	23.32	23.07	3.96	3.92	
Score1:		0.99	DU sum difference:-0.71 u						
Score2:		0.89							
=====									
HC163-180		1	0.0 min	12.702	12.717	0.00	0.00	0.00	0.00
	0.5 min		12.712	12.723	15.23	13.64	2.44	2.18	
	1.0 min		12.722	12.703	17.73	16.37	2.84	2.62	
	10.0 min		12.706	12.701	20.33	19.06	3.25	3.05	
	60.0 min		12.704	12.722	20.17	19.84	3.23	3.17	
	240.0 min		12.719	12.715	21.37	21.67	3.42	3.47	
	Score1:	1.10	DU sum difference:-0.68 u						
	Score2:	1.03							
	=====								
	HC164-180	1	0.0 min	12.602	12.615	0.00	0.00	0.00	0.00
0.5 min			12.600	12.609	16.40	14.85	2.46	2.23	
1.0 min			12.603	12.605	19.87	17.86	2.98	2.68	
10.0 min			12.583	12.598	22.68	21.27	3.40	3.19	
60.0 min			12.592	12.620	21.67	21.67	3.25	3.25	
240.0 min			12.603	12.615	23.08	23.03	3.46	3.45	
Score1:		1.31	DU sum difference:-0.75 u						
Score2:		1.07							
=====									
HC165-180		1	0.0 min	11.511	11.513	0.00	0.00	0.00	0.00
	0.5 min		11.516	11.513	14.45	12.36	2.02	1.73	
	1.0 min		11.518	11.567	15.84	15.84	2.22	2.22	
	10.0 min		11.515	11.511	21.27	19.06	2.98	2.67	
	60.0 min		11.512	11.519	18.46	18.46	2.58	2.58	
	240.0 min		11.506	11.515	20.47	19.26	2.87	2.70	
	Score1:	0.94	DU sum difference:-0.55 u						
	Score2:	0.84							
	=====								
	HC170-180	1	0.0 min	10.853	10.855	0.00	0.00	0.00	0.00
0.5 min			10.856	10.856	12.52	11.11	1.13	1.00	
1.0 min			10.860	10.856	16.22	15.08	1.46	1.36	
10.0 min			10.847	10.858	21.50	19.87	1.94	1.79	
60.0 min			10.846	10.862	20.26	20.07	1.82	1.81	
240.0 min			10.860	10.863	22.70	22.37	2.04	2.01	
Score1:		1.23	DU sum difference:-0.42 u						
Score2:		1.00							
=====									
HC170-180		2	0.0 min	11.028	11.034	0.00	0.00	0.00	0.00
	0.5 min		11.036	11.040	12.47	11.58	1.12	1.04	
	1.0 min		n.d.	11.039	n.d.	15.29	n.d.	1.38	
	10.0 min		11.026	11.032	22.07	21.67	1.99	1.95	
	60.0 min		11.023	11.037	20.78	20.24	1.87	1.82	
	240.0 min		11.038	11.039	22.92	22.33	2.06	2.01	
	Score1:	0.69	DU sum difference:-0.26 u						
	Score2:	0.62							
	=====								

Molecule HC: Peptides with sufficient kinetics data, part 10

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC175-182	1	0.0 min	11.909	11.895	0.20	0.00	0.01	0.00
		0.5 min	11.879	11.890	5.47	5.44	0.33	0.33
		1.0 min	11.874	11.903	6.44	7.81	0.39	0.47
		10.0 min	11.892	11.897	19.43	17.75	1.17	1.06
		60.0 min	11.894	11.885	19.93	20.98	1.20	1.26
		240.0 min	11.888	11.911	20.76	21.51	1.25	1.29
		Score1:	0.03	DU sum difference:-0.01 u				
Score2:	0.95							
HC185-189	1	0.0 min	6.813	6.821	0.00	0.00	0.00	0.00
		0.5 min	6.827	6.820	2.72	2.75	0.11	0.11
		1.0 min	6.838	6.831	2.81	3.21	0.11	0.13
		10.0 min	6.817	6.840	2.81	2.49	0.11	0.10
		60.0 min	6.824	6.829	3.21	2.93	0.13	0.12
		240.0 min	6.840	6.821	2.97	2.61	0.12	0.10
		Score1:	0.27	DU sum difference:-0.04 u				
Score2:	0.25							
HC185-190	1	0.0 min	6.571	6.586	0.00	0.00	0.00	0.00
		0.5 min	6.578	6.581	3.21	3.41	0.16	0.17
		1.0 min	6.583	6.578	3.41	3.81	0.17	0.19
		10.0 min	6.581	6.581	3.65	3.01	0.18	0.15
		60.0 min	6.581	6.575	3.70	3.21	0.18	0.16
		240.0 min	6.600	6.552	3.81	5.22	0.19	0.26
		Score1:	0.23	DU sum difference: 0.04 u				
Score2:	0.67							
HC185-201	1	0.0 min	11.642	11.648	0.54	0.00	0.08	0.00
		0.5 min	11.628	11.656	6.82	6.22	0.96	0.87
		1.0 min	11.641	11.635	8.51	7.02	1.19	0.98
		10.0 min	11.623	11.644	11.24	10.23	1.57	1.43
		60.0 min	11.645	11.602	13.85	14.68	1.94	2.06
		240.0 min	11.635	11.644	16.86	16.86	2.36	2.36
		Score1:	0.73	DU sum difference:-0.39 u				
Score2:	0.95							
HC185-202	1	0.0 min	11.484	11.495	0.00	0.00	0.00	0.00
		0.5 min	11.496	11.513	6.46	5.95	0.97	0.89
		1.0 min	11.492	11.434	7.90	9.83	1.18	1.47
		10.0 min	11.487	11.498	10.99	10.43	1.65	1.57
		60.0 min	11.503	11.503	13.65	13.54	2.05	2.03
		240.0 min	11.499	11.502	15.80	16.61	2.37	2.49
		Score1:	0.41	DU sum difference: 0.24 u				
Score2:	0.83							
HC191-201	1	0.0 min	9.963	9.972	0.00	0.00	0.00	0.00
		0.5 min	9.960	9.966	20.55	18.74	1.64	1.50
		1.0 min	9.968	9.962	23.78	23.49	1.90	1.88
		10.0 min	9.957	9.965	30.17	29.75	2.41	2.38
		60.0 min	9.958	9.965	36.73	35.35	2.94	2.83
		240.0 min	9.972	9.974	38.13	37.27	3.05	2.98
		Score1:	1.24	DU sum difference:-0.38 u				
Score2:	1.01							
HC191-202	1	0.0 min	9.838	9.849	0.40	0.00	0.04	0.00
		0.5 min	9.853	9.840	17.98	17.98	1.62	1.62
		1.0 min	9.859	9.846	24.48	22.45	2.20	2.02
		10.0 min	9.851	9.859	30.89	30.89	2.78	2.78
		60.0 min	9.858	9.860	35.12	35.08	3.16	3.16
		240.0 min	9.858	9.866	36.12	36.12	3.25	3.25
		Score1:	0.64	DU sum difference:-0.22 u				
Score2:	0.52							

Molecule HC: Peptides with sufficient kinetics data, part 11

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC212-229	1	0.0 min	9.151	9.137	0.00	0.00	0.00	0.00
		0.5 min	9.153	9.153	3.41	2.80	0.51	0.42
		1.0 min	9.168	9.164	2.61	2.61	0.39	0.39
		10.0 min	9.162	9.148	6.42	5.82	0.96	0.87
		60.0 min	9.141	9.155	13.65	12.64	2.05	1.90
		240.0 min	9.170	9.155	17.06	17.26	2.56	2.59
Score1:	0.53	DU sum difference: -0.30 u						
Score2:	0.51							
HC214-225	1	0.0 min	9.822	9.822	0.00	0.00	0.00	0.00
		0.5 min	9.822	9.826	4.62	4.62	0.46	0.46
		1.0 min	9.836	9.834	7.83	7.63	0.78	0.76
		10.0 min	9.823	9.825	16.46	16.46	1.65	1.65
		60.0 min	9.813	9.823	22.68	22.68	2.27	2.27
		240.0 min	9.820	9.829	23.28	31.51	2.33	3.15
Score1:	2.09	DU sum difference: 0.80 u						
Score2:	1.79							
HC219-253	1	0.0 min	10.723	10.722	0.00	0.00	0.00	0.00
		0.5 min	10.729	10.739	4.31	4.19	1.21	1.17
		1.0 min	10.747	10.733	4.51	5.05	1.26	1.41
		10.0 min	10.730	10.721	6.90	7.12	1.93	1.99
		60.0 min	10.730	10.734	10.35	11.55	2.90	3.23
		240.0 min	10.732	10.736	15.22	16.37	4.26	4.58
Score1:	0.78	DU sum difference: 0.84 u						
Score2:	0.69							
HC240-252	1	0.0 min	10.388	10.389	0.00	0.00	0.00	0.00
		0.5 min	10.393	10.398	5.82	6.42	0.52	0.58
		1.0 min	10.402	10.433	7.63	7.63	0.69	0.69
		10.0 min	10.386	10.391	17.46	19.67	1.57	1.77
		60.0 min	10.381	10.391	21.47	28.70	1.93	2.58
		240.0 min	10.389	10.396	30.50	41.94	2.75	3.77
Score1:	5.60p	DU sum difference: 1.93 u						
Score2:	4.57p							
HC241-251	1	0.0 min	10.416	10.423	0.00	0.00	0.00	0.00
		0.5 min	10.440	10.436	7.02	6.22	0.49	0.44
		1.0 min	10.451	10.443	9.83	9.83	0.69	0.69
		10.0 min	10.433	10.428	20.47	20.87	1.43	1.46
		60.0 min	10.420	10.442	21.67	25.28	1.52	1.77
		240.0 min	10.433	10.442	24.88	34.11	1.74	2.39
Score1:	3.24	DU sum difference: 0.87 u						
Score2:	2.99							
HC241-252	1	0.0 min	9.822	9.824	0.00	0.00	0.00	0.00
		0.5 min	9.822	9.828	6.42	5.84	0.51	0.47
		1.0 min	9.836	9.835	9.85	9.25	0.79	0.74
		10.0 min	9.823	9.823	18.35	20.09	1.47	1.61
		60.0 min	9.813	9.823	23.22	28.07	1.86	2.25
		240.0 min	9.825	9.828	28.90	39.13	2.31	3.13
Score1:	4.08	DU sum difference: 1.25 u						
Score2:	3.83							
HC242-252	1	0.0 min	7.826	7.829	0.00	0.00	0.00	0.00
		0.5 min	7.823	7.820	8.23	8.23	0.58	0.58
		1.0 min	7.830	7.825	13.65	12.04	0.96	0.84
		10.0 min	7.823	7.823	23.68	25.08	1.66	1.76
		60.0 min	7.814	7.811	27.89	36.32	1.95	2.54
		240.0 min	7.826	7.826	35.52	49.77	2.49	3.48
Score1:	5.86	DU sum difference: 1.57 u						
Score2:	5.47							

Molecule HC: Peptides with sufficient kinetics data, part 12

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC243-251	1	0.0 min	10.424	10.433	0.00	0.00	0.00	0.00
		0.5 min	10.440	10.440	8.79	8.36	0.44	0.42
		1.0 min	10.451	10.451	13.24	13.65	0.66	0.68
		10.0 min	10.440	10.426	28.09	28.09	1.40	1.40
		60.0 min	10.426	10.440	29.10	34.31	1.45	1.72
		240.0 min	10.438	10.440	33.31	43.75	1.67	2.19
		Score1: 4.07	DU sum difference: 0.78 u	Score2: 3.51				
HC243-252	1	0.0 min	9.822	9.822	0.00	0.00	0.00	0.00
		0.5 min	9.822	9.833	8.03	7.39	0.48	0.44
		1.0 min	9.836	9.836	12.44	11.84	0.75	0.71
		10.0 min	9.825	9.828	23.28	24.48	1.40	1.47
		60.0 min	9.822	9.822	27.29	33.51	1.64	2.01
		240.0 min	9.825	9.829	34.72	47.16	2.08	2.83
		Score1: 4.85	DU sum difference: 1.12 u	Score2: 4.49				
HC252-261	1	0.0 min	8.828	8.817	0.40	0.00	0.03	0.00
		0.5 min	8.821	8.819	18.96	19.06	1.52	1.53
		1.0 min	8.821	8.824	19.97	19.69	1.60	1.58
		10.0 min	8.817	8.821	24.23	25.17	1.94	2.01
		60.0 min	8.807	8.808	32.51	33.91	2.60	2.71
		240.0 min	8.819	8.828	37.08	32.71	2.97	2.62
		Score1: 0.68	DU sum difference: -0.21 u	Score2: 1.60				
HC253-261	1	0.0 min	8.432	8.435	0.00	0.00	0.00	0.00
		0.5 min	8.439	8.434	8.83	11.84	0.62	0.83
		1.0 min	8.447	8.434	9.83	9.83	0.69	0.69
		10.0 min	8.441	8.445	16.66	18.87	1.17	1.32
		60.0 min	8.438	8.435	25.69	27.49	1.80	1.92
		240.0 min	8.448	8.456	30.40	33.19	2.13	2.32
		Score1: 1.94	DU sum difference: 0.57 u	Score2: 1.74				
HC263-274	1	0.0 min	7.305	7.313	0.00	0.00	0.00	0.00
		0.5 min	7.306	7.308	18.46	17.86	1.85	1.79
		1.0 min	7.311	7.302	21.87	21.87	2.19	2.19
		10.0 min	7.298	7.292	27.29	33.51	2.73	3.35
		60.0 min	7.294	7.286	31.10	37.53	3.11	3.75
		240.0 min	7.300	7.300	35.83	38.73	3.58	3.87
		Score1: 3.89p	DU sum difference: 1.49 u	Score2: 3.43p				
HC263-275	1	0.0 min	10.573	10.570	0.20	0.60	0.02	0.07
		0.5 min	10.570	10.576	15.25	14.45	1.68	1.59
		1.0 min	10.581	10.586	19.06	19.06	2.10	2.10
		10.0 min	10.571	10.577	29.10	31.91	3.20	3.51
		60.0 min	10.569	10.567	32.60	34.92	3.59	3.84
		240.0 min	10.560	10.569	35.23	37.53	3.88	4.13
		Score1: 1.83p	DU sum difference: 0.77 u	Score2: 1.83p				
HC266-274	1	0.0 min	4.679	4.694	0.00	0.00	0.00	0.00
		0.5 min	4.684	4.688	25.73	23.85	1.80	1.67
		1.0 min	4.688	4.678	28.29	27.05	1.98	1.89
		10.0 min	4.676	4.681	34.72	34.72	2.43	2.43
		60.0 min	4.679	4.678	36.32	35.32	2.54	2.47
		240.0 min	4.686	4.683	37.45	37.45	2.62	2.62
		Score1: 0.82	DU sum difference: -0.24 u	Score2: 0.74				

Molecule HC: Peptides with sufficient kinetics data, part 13

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC266-275	1	0.0 min	9.298	9.289	0.00	0.00	0.00	0.00
		0.5 min	9.293	9.293	17.46	14.45	1.40	1.16
		1.0 min	9.301	9.298	18.86	18.86	1.51	1.51
		10.0 min	9.294	9.289	31.91	29.70	2.55	2.38
		60.0 min	9.279	9.279	30.70	30.70	2.46	2.46
		240.0 min	9.292	9.297	32.51	33.31	2.60	2.66
		Score1:	0.63	DU sum difference:-0.21 u				
Score2:	0.97							
HC272-294	1	0.0 min	11.500	11.507	0.60	0.52	0.13	0.11
		0.5 min	11.520	11.506	11.14	11.20	2.34	2.35
		1.0 min	11.519	11.530	12.10	12.14	2.54	2.55
		10.0 min	11.513	11.501	12.72	12.14	2.67	2.55
		60.0 min	11.506	11.507	13.81	13.65	2.90	2.87
		240.0 min	11.504	11.507	17.66	17.06	3.71	3.58
		Score1:	0.35	DU sum difference:-0.28 u				
Score2:	0.32							
HC278-281	1	0.0 min	5.721	5.721	0.00	0.00	0.00	0.00
		0.5 min	5.721	5.721	5.62	6.02	0.17	0.18
		1.0 min	5.721	5.721	6.22	6.62	0.19	0.20
		10.0 min	5.707	5.721	12.04	12.04	0.36	0.36
		60.0 min	5.714	5.713	17.86	19.06	0.54	0.57
		240.0 min	5.721	5.721	19.47	20.07	0.58	0.60
		Score1:	0.68	DU sum difference: 0.08 u				
Score2:	0.56							
HC291-315	1	0.0 min	11.419	11.407	0.00	0.20	0.00	0.04
		0.5 min	11.427	11.456	5.18	4.90	1.14	1.08
		1.0 min	11.432	11.410	6.83	6.04	1.50	1.33
		10.0 min	11.456	11.435	10.55	9.98	2.32	2.20
		60.0 min	11.431	11.452	13.81	13.44	3.04	2.96
		240.0 min	11.467	11.458	15.47	15.45	3.40	3.40
		Score1:	0.47	DU sum difference:-0.40 u				
Score2:	0.47							
HC297-350	1	0.0 min	10.064	10.051	0.22	0.25	0.11	0.12
		0.5 min	10.076	10.067	4.81	5.26	2.31	2.52
		1.0 min	10.089	10.075	5.39	5.93	2.59	2.85
		10.0 min	10.062	10.059	8.45	8.56	4.06	4.11
		60.0 min	10.058	10.063	10.65	11.24	5.11	5.39
		240.0 min	10.055	10.067	14.62	14.02	7.02	6.73
		Score1:	0.29	DU sum difference: 0.53 u				
Score2:	0.49							
HC301-306	1	0.0 min	6.287	6.297	0.00	0.00	0.00	0.00
		0.5 min	6.284	6.308	1.38	2.57	0.07	0.13
		1.0 min	6.304	6.283	1.71	2.79	0.09	0.14
		10.0 min	6.285	6.305	2.97	3.46	0.15	0.17
		60.0 min	6.287	6.291	9.60	9.26	0.48	0.46
		240.0 min	6.289	6.297	20.97	19.82	1.05	0.99
		Score1:	0.33	DU sum difference: 0.06 u				
Score2:	0.90							
HC301-318	1	0.0 min	11.118	11.091	0.00	0.00	0.00	0.00
		0.5 min	11.101	11.110	1.15	0.99	0.18	0.16
		1.0 min	11.108	11.107	2.01	2.56	0.32	0.41
		10.0 min	11.147	11.103	2.04	3.76	0.33	0.60
		60.0 min	11.099	11.120	8.03	8.23	1.28	1.32
		240.0 min	11.093	11.118	11.73	11.62	1.88	1.86
		Score1:	0.57	DU sum difference: 0.35 u				
Score2:	0.58							

Molecule HC: Peptides with sufficient kinetics data, part 14

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC307-333	1	0.0 min	11.166	11.176	0.18	0.00	0.04	0.00
		0.5 min	11.204	11.194	3.03	4.02	0.70	0.92
		1.0 min	11.203	11.167	4.65	5.62	1.07	1.29
		10.0 min	11.222	11.194	8.86	7.32	2.04	1.68
		60.0 min	11.189	11.194	11.32	12.56	2.60	2.89
		240.0 min	11.218	11.203	14.58	16.45	3.35	3.78
		Score1:	0.87	DU sum difference: 0.77 u				
Score2:	1.45							
HC308-340	1	0.0 min	10.963	10.991	0.24	0.43	0.07	0.13
		0.5 min	10.973	10.971	2.93	2.69	0.88	0.81
		1.0 min	10.983	10.992	3.22	3.35	0.97	1.00
		10.0 min	10.998	10.968	5.53	5.74	1.66	1.72
		60.0 min	10.995	10.981	9.21	10.16	2.76	3.05
		240.0 min	10.971	10.967	13.47	14.70	4.04	4.41
		Score1:	0.64	DU sum difference: 0.74 u				
Score2:	0.63							
HC318-359	1	0.0 min	8.732	8.738	0.00	0.00	0.00	0.00
		0.5 min	8.724	8.712	8.16	7.95	2.77	2.70
		1.0 min	8.729	8.725	9.22	9.26	3.13	3.15
		10.0 min	8.722	8.705	13.96	13.36	4.75	4.54
		60.0 min	8.700	8.704	15.03	16.02	5.11	5.45
		240.0 min	8.706	8.685	18.01	19.60	6.12	6.66
		Score1:	0.47	DU sum difference: 0.62 u				
Score2:	0.73							
HC319-333	1	0.0 min	9.403	9.409	0.00	0.00	0.00	0.00
		0.5 min	9.411	9.403	7.42	8.19	0.89	0.98
		1.0 min	9.421	9.411	8.85	9.94	1.06	1.19
		10.0 min	9.413	9.408	16.76	17.15	2.01	2.06
		60.0 min	9.402	9.407	20.19	21.73	2.42	2.61
		240.0 min	9.408	9.415	23.89	24.81	2.87	2.98
		Score1:	1.12	DU sum difference: 0.57 u				
Score2:	1.00p							
HC326-348	1	0.0 min	7.484	7.482	0.00	0.00	0.00	0.00
		0.5 min	7.477	7.476	16.25	15.05	2.92	2.71
		1.0 min	7.498	7.467	18.86	18.06	3.40	3.25
		10.0 min	7.468	7.453	26.29	25.28	4.73	4.55
		60.0 min	7.448	7.440	28.50	28.70	5.13	5.17
		240.0 min	7.449	7.439	30.90	32.06	5.56	5.77
		Score1:	0.18	DU sum difference: -0.14 u				
Score2:	0.86							
HC334-348	1	0.0 min	3.587	3.593	0.00	0.00	0.00	0.00
		0.5 min	3.593	3.596	22.01	21.27	2.64	2.55
		1.0 min	3.601	3.587	24.28	23.62	2.91	2.83
		10.0 min	3.588	3.589	27.56	27.03	3.31	3.24
		60.0 min	3.589	3.587	27.75	27.46	3.33	3.30
		240.0 min	3.600	3.596	28.50	28.43	3.42	3.41
		Score1:	0.60	DU sum difference: -0.28 u				
Score2:	0.49							
HC334-361	1	0.0 min	5.387	5.387	0.00	0.00	0.00	0.00
		0.5 min	5.386	5.388	27.40	26.99	6.03	5.94
		1.0 min	5.390	5.376	29.70	28.75	6.53	6.32
		10.0 min	5.382	5.375	31.60	31.30	6.95	6.89
		60.0 min	5.377	5.377	31.77	31.44	6.99	6.92
		240.0 min	5.382	5.384	31.90	31.82	7.02	7.00
		Score1:	0.54	DU sum difference: -0.46 u				
Score2:	0.44							

Molecule HC: Peptides with sufficient kinetics data, part 15

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC334-365	1	0.0 min	6.767	6.778	0.00	0.00	0.00	0.00
		0.5 min	6.762	6.762	22.27	21.14	5.79	5.50
		1.0 min	6.778	6.759	24.24	22.96	6.30	5.97
		10.0 min	6.775	6.754	26.53	25.44	6.90	6.61
		60.0 min	6.761	6.752	25.82	25.89	6.71	6.73
		240.0 min	6.760	6.781	28.07	27.32	7.30	7.10
Score1:		1.09	DU sum difference: -1.09 u					
Score2:		0.92						
HC334-368	1	0.0 min	7.758	7.741	0.00	0.00	0.00	0.00
		0.5 min	7.746	7.732	18.16	17.70	5.27	5.13
		1.0 min	7.748	7.739	19.90	19.87	5.77	5.76
		10.0 min	7.746	7.733	23.06	21.28	6.69	6.17
		60.0 min	7.725	7.723	24.63	25.67	7.14	7.44
		240.0 min	7.728	7.726	28.04	26.36	8.13	7.65
Score1:		0.76	DU sum difference: -0.85 u					
Score2:		1.06						
HC336-348	1	0.0 min	3.708	3.710	0.00	0.00	0.00	0.00
		0.5 min	3.706	3.707	25.58	24.34	2.56	2.43
		1.0 min	3.708	3.703	28.50	28.48	2.85	2.85
		10.0 min	3.702	3.703	32.47	31.60	3.25	3.16
		60.0 min	3.710	3.702	31.64	31.84	3.16	3.18
		240.0 min	3.709	3.707	32.65	31.54	3.26	3.15
Score1:		0.79	DU sum difference: -0.30 u					
Score2:		0.73						
HC342-366	1	0.0 min	10.650	10.646	0.00	0.00	0.00	0.00
		0.5 min	10.658	10.675	7.67	7.82	1.46	1.49
		1.0 min	10.668	10.674	8.64	9.03	1.64	1.72
		10.0 min	10.653	10.664	14.65	13.65	2.78	2.59
		60.0 min	10.675	10.676	18.29	20.58	3.48	3.91
		240.0 min	10.699	10.697	24.24	25.34	4.61	4.82
Score1:		0.77	DU sum difference: 0.56 u					
Score2:		1.05						
HC345-374	1	0.0 min	12.947	12.939	0.00	0.00	0.00	0.00
		0.5 min	12.947	12.953	9.83	11.02	2.36	2.64
		1.0 min	12.963	12.940	12.39	11.26	2.97	2.70
		10.0 min	12.937	12.937	16.83	45.20	4.04	10.85
		60.0 min	12.943	12.944	19.05	19.57	4.57	4.70
		240.0 min	12.918	12.943	21.94	22.13	5.26	5.31
Score1:		0.22	DU sum difference: 0.22 u					
Score2:		0.77						
HC349-365	1	0.0 min	8.019	8.019	0.00	0.00	0.00	0.00
		0.5 min	8.008	8.000	30.10	27.89	3.91	3.63
		1.0 min	8.016	8.011	29.30	29.30	3.81	3.81
		10.0 min	8.016	8.011	31.71	29.72	4.12	3.86
		60.0 min	8.001	8.001	30.50	30.50	3.97	3.97
		240.0 min	8.010	8.063	33.63	32.31	4.37	4.20
Score1:		1.44p	DU sum difference: -0.72 u					
Score2:		1.17p						
HC357-385	1	0.0 min	7.173	7.170	0.00	0.00	0.00	0.00
		0.5 min	7.176	7.175	2.19	2.16	0.59	0.58
		1.0 min	7.185	7.170	2.17	1.93	0.59	0.52
		10.0 min	7.175	7.168	2.61	2.45	0.71	0.66
		60.0 min	7.166	7.166	3.30	3.28	0.89	0.88
		240.0 min	7.172	7.191	4.55	5.15	1.23	1.39
Score1:		0.04	DU sum difference: 0.04 u					
Score2:		0.22						

Molecule HC: Peptides with sufficient kinetics data, part 16

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC364-393	1	0.0 min	6.360	6.358	0.00	0.00	0.00	0.00
		0.5 min	6.363	6.359	5.42	5.02	1.46	1.35
		1.0 min	6.363	6.354	6.59	6.13	1.78	1.65
		10.0 min	6.368	6.356	9.23	8.63	2.49	2.33
		60.0 min	6.350	6.352	11.13	10.98	3.00	2.96
		240.0 min	6.358	6.355	13.28	13.06	3.59	3.53
		Score1: 0.48	DU sum difference: -0.49 u					
Score2: 0.39								
HC367-390	1	0.0 min	8.263	8.262	0.13	0.32	0.03	0.07
		0.5 min	8.264	8.256	23.42	21.87	4.92	4.59
		1.0 min	8.265	8.256	24.69	23.03	5.18	4.84
		10.0 min	8.260	8.259	28.88	27.50	6.07	5.78
		60.0 min	8.251	8.252	29.21	28.96	6.14	6.08
		240.0 min	8.256	8.255	30.25	30.20	6.35	6.34
		Score1: 1.23	DU sum difference: -0.99 u					
Score2: 1.08								
HC368-387	1	0.0 min	8.315	8.314	0.00	0.00	0.00	0.00
		0.5 min	8.318	8.312	2.58	2.37	0.44	0.40
		1.0 min	8.320	8.312	3.70	3.31	0.63	0.56
		10.0 min	8.317	8.310	5.17	4.38	0.88	0.75
		60.0 min	8.302	8.307	5.61	5.32	0.95	0.90
		240.0 min	8.313	8.305	7.78	7.77	1.32	1.32
		Score1: 0.44	DU sum difference: -0.29 u					
Score2: 0.36								
HC369-372	1	0.0 min	9.064	9.064	0.00	0.00	0.00	0.00
		0.5 min	9.085	9.070	2.21	2.21	0.07	0.07
		1.0 min	9.076	9.075	2.21	2.61	0.07	0.08
		10.0 min	9.072	9.069	3.01	2.81	0.09	0.08
		60.0 min	9.065	9.064	5.62	4.62	0.17	0.14
		240.0 min	9.089	9.090	10.21	9.63	0.31	0.29
		Score1: 0.36	DU sum difference: -0.04 u					
Score2: 0.47								
HC369-380	1	0.0 min	14.001	14.016	0.00	0.00	0.00	0.00
		0.5 min	13.996	14.019	6.21	5.23	0.62	0.52
		1.0 min	14.013	14.011	8.60	7.42	0.86	0.74
		10.0 min	13.998	14.008	11.41	11.02	1.14	1.10
		60.0 min	14.009	14.009	13.45	12.64	1.35	1.26
		240.0 min	14.004	14.009	16.64	15.64	1.66	1.56
		Score1: 1.14	DU sum difference: -0.44 u					
Score2: 0.93								
HC372-397	1	0.0 min	12.782	12.804	0.34	0.40	0.07	0.09
		0.5 min	12.804	12.815	5.82	5.82	1.28	1.28
		1.0 min	12.822	12.809	6.49	6.22	1.43	1.37
		10.0 min	12.810	12.797	7.34	6.62	1.61	1.46
		60.0 min	12.816	12.813	9.55	9.43	2.10	2.07
		240.0 min	12.818	12.814	13.10	12.84	2.88	2.83
		Score1: 0.34	DU sum difference: -0.28 u					
Score2: 0.30								
HC373-376	1	0.0 min	6.353	6.363	0.00	0.00	0.00	0.00
		0.5 min	6.357	6.367	15.45	15.45	0.31	0.31
		1.0 min	6.367	6.353	22.48	19.67	0.45	0.39
		10.0 min	6.357	6.357	37.53	37.12	0.75	0.74
		60.0 min	6.353	6.353	40.94	40.33	0.82	0.81
		240.0 min	6.367	6.356	45.15	45.35	0.90	0.91
		Score1: 0.23	DU sum difference: -0.02 u					
Score2: 0.31								

Molecule HC: Peptides with sufficient kinetics data, part 17

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC377-380	1	0.0 min	5.857	5.872	0.00	0.00	0.00	0.00
		0.5 min	5.857	5.872	19.06	17.52	0.57	0.53
		1.0 min	5.872	5.868	40.94	33.31	1.23	1.00
		10.0 min	5.858	5.872	35.12	34.53	1.05	1.04
		60.0 min	5.858	5.868	35.52	35.52	1.07	1.07
		240.0 min	5.886	5.845	35.52	36.32	1.07	1.09
		Score1:	0.07	DU sum difference: 0.01 u				
Score2:	0.44							
HC379-390	1	0.0 min	11.331	11.344	0.20	0.00	0.02	0.00
		0.5 min	11.336	11.346	27.69	26.69	2.77	2.67
		1.0 min	11.342	11.330	29.90	28.70	2.99	2.87
		10.0 min	11.328	11.339	37.93	36.12	3.79	3.61
		60.0 min	11.328	11.330	37.91	37.91	3.79	3.79
		240.0 min	11.334	11.346	38.41	38.89	3.84	3.89
		Score1:	0.72	DU sum difference:-0.30 u				
Score2:	0.89							
HC381-390	1	0.0 min	10.622	10.622	0.00	0.00	0.00	0.00
		0.5 min	10.624	10.646	35.11	32.84	2.81	2.63
		1.0 min	10.641	10.637	36.88	35.70	2.95	2.86
		10.0 min	10.625	10.631	47.48	44.43	3.80	3.55
		60.0 min	10.619	10.644	47.20	47.37	3.78	3.79
		240.0 min	10.646	10.654	48.40	47.18	3.87	3.77
		Score1:	1.65	DU sum difference:-0.62 u				
Score2:	1.68p							
HC381-398	1	0.0 min	11.475	11.479	0.00	0.00	0.00	0.00
		0.5 min	11.483	11.489	19.68	18.06	2.95	2.71
		1.0 min	11.497	11.466	20.45	20.45	3.07	3.07
		10.0 min	11.489	11.484	34.74	32.23	5.21	4.83
		60.0 min	11.473	11.491	35.46	35.46	5.32	5.32
		240.0 min	11.476	11.491	38.30	38.53	5.75	5.78
		Score1:	0.07	DU sum difference: 0.05 u				
Score2:	0.07							
HC390-398	1	0.0 min	7.305	7.296	0.00	0.00	0.00	0.00
		0.5 min	7.302	7.312	8.55	7.02	0.60	0.49
		1.0 min	7.327	7.304	12.44	10.41	0.87	0.73
		10.0 min	7.316	7.304	24.87	22.88	1.74	1.60
		60.0 min	7.303	7.310	31.71	30.62	2.22	2.14
		240.0 min	7.311	7.316	39.13	35.92	2.74	2.51
		Score1:	2.57	DU sum difference:-0.69 u				
Score2:	2.10							
HC391-398	1	0.0 min	7.049	7.056	0.00	0.00	0.00	0.00
		0.5 min	7.050	7.049	7.76	6.33	0.47	0.38
		1.0 min	7.067	7.049	12.39	9.63	0.74	0.58
		10.0 min	7.056	7.051	26.49	24.50	1.59	1.47
		60.0 min	7.048	7.045	33.39	30.66	2.00	1.84
		240.0 min	7.054	7.044	37.42	36.81	2.25	2.21
		Score1:	2.48	DU sum difference:-0.57 u				
Score2:	2.03							
HC391-404	1	0.0 min	8.544	8.540	0.01	0.00	0.00	0.00
		0.5 min	8.544	8.529	12.52	11.24	1.50	1.35
		1.0 min	8.559	8.523	14.27	13.27	1.71	1.59
		10.0 min	8.531	8.534	22.64	20.66	2.72	2.48
		60.0 min	8.529	8.518	24.45	23.59	2.93	2.83
		240.0 min	8.554	8.512	28.90	27.09	3.47	3.25
		Score1:	1.69	DU sum difference:-0.85 u				
Score2:	1.47p							

Molecule HC: Peptides with sufficient kinetics data, part 18

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC395-426	1	0.0 min	11.122	11.125	0.60	0.40	0.18	0.12
		0.5 min	11.151	11.127	16.18	15.24	4.85	4.57
		1.0 min	11.159	11.130	17.07	17.76	5.12	5.33
		10.0 min	11.140	11.122	18.84	17.65	5.65	5.30
		60.0 min	11.134	11.145	19.29	19.66	5.79	5.90
		240.0 min	11.141	11.130	20.15	20.27	6.05	6.08
		Score1: 0.30	DU sum difference:-0.34 u					
Score2: 0.74								
HC399-404	1	0.0 min	5.253	5.284	0.00	0.00	0.00	0.00
		0.5 min	5.262	5.287	14.65	14.25	0.73	0.71
		1.0 min	5.265	5.273	16.66	16.46	0.83	0.82
		10.0 min	5.254	5.276	18.66	18.66	0.93	0.93
		60.0 min	5.239	5.271	25.28	22.88	1.26	1.14
		240.0 min	5.267	5.271	28.09	27.89	1.40	1.39
		Score1: 0.84	DU sum difference:-0.16 u					
Score2: 0.68								
HC405-410	1	0.0 min	9.193	9.176	0.00	0.00	0.00	0.00
		0.5 min	9.190	9.177	1.29	1.30	0.06	0.06
		1.0 min	9.195	9.198	1.40	1.53	0.07	0.08
		10.0 min	9.177	9.177	1.63	1.23	0.08	0.06
		60.0 min	9.180	9.175	1.62	1.18	0.08	0.06
		240.0 min	9.191	9.195	1.90	1.65	0.10	0.08
		Score1: 0.25	DU sum difference:-0.05 u					
Score2: 0.26								
HC407-418	1	0.0 min	9.023	9.024	0.00	0.06	0.00	0.01
		0.5 min	9.031	9.036	9.00	7.93	0.99	0.87
		1.0 min	9.040	9.034	10.96	9.62	1.21	1.06
		10.0 min	9.035	9.030	23.92	22.31	2.63	2.45
		60.0 min	9.020	9.027	33.35	33.35	3.67	3.67
		240.0 min	9.040	9.042	36.16	36.16	3.98	3.98
		Score1: 0.33	DU sum difference:-0.17 u					
Score2: 0.36								
HC411-417	1	0.0 min	6.877	6.877	0.00	0.00	0.00	0.00
		0.5 min	6.885	6.878	31.51	31.09	1.89	1.87
		1.0 min	6.895	6.877	35.52	34.30	2.13	2.06
		10.0 min	6.888	6.877	39.75	38.57	2.39	2.31
		60.0 min	6.887	6.870	40.74	40.13	2.44	2.41
		240.0 min	6.891	6.887	44.15	45.35	2.65	2.72
		Score1: 0.30	DU sum difference:-0.07 u					
Score2: 0.88								
HC411-422	1	0.0 min	6.353	6.351	0.00	0.00	0.00	0.00
		0.5 min	6.345	6.354	36.94	36.13	4.06	3.97
		1.0 min	6.357	6.341	39.35	38.35	4.33	4.22
		10.0 min	6.350	6.346	42.13	40.93	4.63	4.50
		60.0 min	6.344	6.345	44.55	44.15	4.90	4.86
		240.0 min	6.351	6.347	48.77	48.76	5.36	5.36
		Score1: 0.89	DU sum difference:-0.38 u					
Score2: 0.73								
HC411-447	1	0.0 min	8.631	8.623	0.10	0.00	0.04	0.00
		0.5 min	8.628	8.601	9.30	9.19	3.26	3.22
		1.0 min	8.631	8.615	10.58	10.50	3.70	3.68
		10.0 min	8.602	8.609	11.64	10.88	4.07	3.81
		60.0 min	8.621	8.588	13.32	13.20	4.66	4.62
		240.0 min	8.611	8.615	16.34	n.d.	5.72	n.d.
		Score1: 0.33	DU sum difference:-0.49 u					
Score2: 0.30								

Molecule HC: Peptides with sufficient kinetics data, part 19

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC426-446	1	0.0 min	4.254	4.252	0.01	0.00	0.00	0.00
		0.5 min	4.247	4.252	6.01	5.90	1.14	1.12
		1.0 min	4.258	4.240	6.24	6.02	1.19	1.14
		10.0 min	4.248	4.242	7.42	7.42	1.41	1.41
		60.0 min	4.244	4.242	10.43	9.41	1.98	1.79
		240.0 min	4.251	4.248	11.24	11.24	2.14	2.14
	Score1:	0.36	DU sum difference:-0.26 u					
	Score2:	0.29						
=====								
HC429-446	1	0.0 min	3.555	3.554	0.00	0.00	0.00	0.00
		0.5 min	3.555	3.558	8.23	8.23	1.32	1.32
		1.0 min	3.560	3.552	8.57	8.43	1.37	1.35
		10.0 min	3.549	3.551	9.48	9.43	1.52	1.51
		60.0 min	3.550	3.550	11.91	11.64	1.91	1.86
		240.0 min	3.558	3.556	13.77	13.70	2.20	2.19
	Score1:	0.14	DU sum difference:-0.09 u					
	Score2:	0.12						
=====								

Molecule HC: Peptides/Ranges with insufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

Bold typing: problematic DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC016-027	1	0.0 min	9.228	9.218	n.d.	n.d.	n.d.	n.d.
		0.5 min	9.226	9.221	n.d.	n.d.	n.d.	n.d.
		1.0 min	9.232	9.220	n.d.	n.d.	n.d.	n.d.
		10.0 min	9.209	9.213	n.d.	n.d.	n.d.	n.d.
		60.0 min	9.201	9.210	n.d.	n.d.	n.d.	n.d.
		240.0 min	9.208	9.213	n.d.	n.d.	n.d.	n.d.
=====								
HC070-078	1	0.0 min	4.800	4.808	n.d.	n.d.	n.d.	n.d.
		0.5 min	4.805	4.806	n.d.	n.d.	n.d.	n.d.
		1.0 min	4.818	4.797	n.d.	n.d.	n.d.	n.d.
		10.0 min	4.798	4.797	n.d.	n.d.	n.d.	n.d.
		60.0 min	4.792	4.797	n.d.	n.d.	n.d.	n.d.
		240.0 min	4.805	4.805	n.d.	n.d.	n.d.	n.d.
=====								
HC112-145	1	0.0 min	11.162	11.172	6.58	1.13	1.91	0.33
		0.5 min	11.169	11.173	27.18	30.70	7.88	8.90
		1.0 min	11.184	11.166	27.52	30.50	7.98	8.85
		10.0 min	11.160	11.178	37.32	24.20	10.82	7.02
		60.0 min	11.153	11.165	35.43	34.79	10.27	10.09
		240.0 min	11.163	11.163	36.16	35.43	10.49	10.27
=====								
HC119-142	1	0.0 min	8.818	8.823	n.d.	n.d.	n.d.	n.d.
		0.5 min	8.822	8.812	n.d.	n.d.	n.d.	n.d.
		1.0 min	8.802	8.825	n.d.	n.d.	n.d.	n.d.
		10.0 min	8.796	8.836	n.d.	n.d.	n.d.	n.d.
		60.0 min	8.805	8.819	n.d.	n.d.	n.d.	n.d.
		240.0 min	8.833	8.811	n.d.	n.d.	n.d.	n.d.
=====								
HC138-177	1	0.0 min	11.243	11.225	0.20	0.00	0.07	0.00
		0.5 min	11.256	11.248	4.01	4.01	1.44	1.44
		1.0 min	11.265	11.246	4.62	n.d.	1.66	n.d.
		10.0 min	11.233	11.238	7.42	n.d.	2.67	n.d.
		60.0 min	11.237	11.235	n.d.	n.d.	n.d.	n.d.
		240.0 min	11.253	11.232	n.d.	n.d.	n.d.	n.d.
=====								

Molecule HC: Peptides/Ranges with insufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

Bold typing: problematic DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC146-161	1	0.0 min	13.377	13.388	n.d.	n.d.	n.d.	n.d.
		0.5 min	13.382	13.397	n.d.	n.d.	n.d.	n.d.
		1.0 min	13.403	13.390	n.d.	n.d.	n.d.	n.d.
		10.0 min	13.380	13.430	n.d.	n.d.	n.d.	n.d.
		60.0 min	13.384	13.392	n.d.	n.d.	n.d.	n.d.
		240.0 min	13.389	13.397	n.d.	n.d.	n.d.	n.d.
HC210-239	1	0.0 min	12.420	12.431	0.00	0.00	0.00	0.00
		0.5 min	12.416	12.437	28.70	n.d.	7.17	n.d.
		1.0 min	12.427	12.427	30.70	n.d.	7.68	n.d.
		10.0 min	12.399	12.432	36.92	n.d.	9.23	n.d.
		60.0 min	12.407	12.443	n.d.	n.d.	n.d.	n.d.
		240.0 min	12.423	12.423	n.d.	n.d.	n.d.	n.d.
HC240-251	1	0.0 min	10.994	10.991	n.d.	n.d.	n.d.	n.d.
		0.5 min	11.002	11.000	8.23	8.23	0.66	0.66
		1.0 min	11.019	11.001	10.43	8.63	0.83	0.69
		10.0 min	10.994	10.991	20.07	21.67	1.61	1.73
		60.0 min	10.999	11.004	24.08	25.69	1.93	2.05
		240.0 min	10.990	10.996	28.09	37.32	2.25	2.99
HC280-292	1	0.0 min	9.425	9.359	n.d.	0.00	n.d.	0.00
		0.5 min	9.312	9.308	8.83	9.23	0.97	1.02
		1.0 min	9.326	9.319	11.47	10.23	1.26	1.13
		10.0 min	9.312	9.312	n.d.	19.55	n.d.	2.15
		60.0 min	9.305	9.309	32.11	25.80	3.53	2.84
		240.0 min	9.326	9.312	n.d.	n.d.	n.d.	n.d.
HC334-358	1	0.0 min	6.147	6.140	5.52	10.88	1.05	2.07
		0.5 min	6.140	6.141	23.53	28.73	4.47	5.46
		1.0 min	6.166	6.132	33.71	28.49	6.40	5.41
		10.0 min	6.150	6.132	30.10	28.52	5.72	5.42
		60.0 min	6.141	6.129	27.03	27.75	5.14	5.27
		240.0 min	6.151	6.135	26.44	27.89	5.02	5.30
HC347-370	1	0.0 min	10.484	10.490	0.66	0.22	0.13	0.04
		0.5 min	10.435	10.431	2.69	7.04	0.54	1.41
		1.0 min	10.444	10.495	4.19	2.77	0.84	0.55
		10.0 min	10.496	10.449	9.86	7.99	1.97	1.60
		60.0 min	10.427	10.413	15.94	7.22	3.19	1.44
		240.0 min	10.429	10.428	17.60	17.29	3.52	3.46
HC377-390	1	0.0 min	12.360	12.403	0.00	0.01	0.00	0.00
		0.5 min	12.345	12.432	21.67	n.d.	2.60	n.d.
		1.0 min	12.361	12.439	22.66	n.d.	2.72	n.d.
		10.0 min	12.335	12.422	33.51	n.d.	4.02	n.d.
		60.0 min	12.401	n.d.	32.11	n.d.	3.85	n.d.
		240.0 min	12.411	12.399	n.d.	n.d.	n.d.	n.d.
HC411-446	1	0.0 min	9.139	9.140	n.d.	n.d.	n.d.	n.d.
		0.5 min	9.140	9.140	n.d.	n.d.	n.d.	n.d.
		1.0 min	9.152	9.161	n.d.	n.d.	n.d.	n.d.
		10.0 min	9.121	n.d.	n.d.	n.d.	n.d.	n.d.
		60.0 min	9.133	9.126	n.d.	n.d.	n.d.	n.d.
		240.0 min	9.147	9.161	n.d.	n.d.	n.d.	n.d.

(Experiment series: degly2, reference series: gly2)

Molecule HC: Peptides lacking equivalent range, part 1

Peptide	Peptide	Peptide
HC279-300_p1444.53	HC282-306_p1216.42	HC293-312_p1095.4

Molecule HC: no peptides lacking HDX data in experiment series available

Molecule HC: no peptides lacking HDX data in reference series available

Molecule HC: Peptides lacking HDX data in both series, part 1

Peptide	Peptide	Peptide
HC133-159		

Molecule LC: Peptides with sufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC001-004	1	0.0 min	10.740	10.765	0.00	0.00	0.00	0.00
		0.5 min	10.735	10.771	22.88	21.87	0.69	0.66
		1.0 min	10.752	10.761	33.91	32.91	1.02	0.99
		10.0 min	10.736	10.756	54.58	53.98	1.64	1.62
		60.0 min	10.752	10.766	53.18	53.18	1.60	1.60
		240.0 min	10.771	10.773	53.38	53.18	1.60	1.60
		Score1:	0.73	DU sum difference:-0.08 u				
Score2:	0.60							
LC001-042	1	0.0 min	11.589	11.598	0.40	0.20	0.16	0.08
		0.5 min	11.613	11.609	4.68	4.72	1.83	1.84
		1.0 min	11.613	11.577	5.46	5.80	2.13	2.26
		10.0 min	11.595	11.598	7.73	7.53	3.01	2.94
		60.0 min	11.595	11.557	11.28	12.20	4.40	4.76
		240.0 min	11.594	11.561	14.69	16.42	5.73	6.40
		Score1:	0.68	DU sum difference: 1.02 u				
Score2:	0.73							
LC001-042	2	0.0 min	11.724	11.725	0.46	0.53	0.18	0.21
		0.5 min	11.719	11.697	4.22	4.58	1.64	1.79
		1.0 min	11.747	11.707	4.70	5.17	1.83	2.02
		10.0 min	11.735	11.689	6.98	7.26	2.72	2.83
		60.0 min	11.721	11.708	10.08	12.02	3.93	4.69
		240.0 min	11.721	11.701	15.32	17.49	5.98	6.82
		Score1:	1.38	DU sum difference: 2.07 u				
Score2:	1.13							
LC003-018	1	0.0 min	11.509	11.513	0.20	0.00	0.03	0.00
		0.5 min	11.515	11.513	15.65	13.65	2.03	1.77
		1.0 min	11.518	11.567	19.06	16.66	2.48	2.17
		10.0 min	11.518	11.509	20.27	20.27	2.63	2.63
		60.0 min	11.511	11.526	20.43	20.27	2.66	2.63
		240.0 min	11.506	11.518	21.94	21.07	2.85	2.74
		Score1:	1.47	DU sum difference:-0.73 u				
Score2:	1.20							
LC005-011	1	0.0 min	7.070	7.074	0.00	0.00	0.00	0.00
		0.5 min	7.061	7.070	42.74	41.74	2.14	2.09
		1.0 min	7.073	7.064	41.34	40.33	2.07	2.02
		10.0 min	7.063	7.068	42.74	42.54	2.14	2.13
		60.0 min	7.067	7.062	44.71	45.13	2.24	2.26
		240.0 min	7.072	7.065	49.77	48.76	2.49	2.44
		Score1:	0.73	DU sum difference:-0.14 u				
Score2:	0.77							
LC005-018	1	0.0 min	7.882	7.887	0.00	0.00	0.00	0.00
		0.5 min	7.868	7.864	26.29	26.49	2.89	2.91
		1.0 min	7.868	7.871	29.50	27.09	3.24	2.98
		10.0 min	7.848	7.875	31.91	29.70	3.51	3.27
		60.0 min	7.861	7.878	35.22	34.11	3.87	3.75
		240.0 min	7.882	7.878	39.80	39.53	4.38	4.35
		Score1:	1.51	DU sum difference:-0.64 u				
Score2:	1.32							
LC005-039	1	0.0 min	6.759	6.765	0.04	0.12	0.01	0.04
		0.5 min	6.767	6.761	6.02	5.55	1.93	1.78
		1.0 min	6.774	6.759	7.39	6.75	2.36	2.16
		10.0 min	6.772	6.758	10.60	9.65	3.39	3.09
		60.0 min	6.758	6.753	11.95	11.81	3.82	3.78
		240.0 min	6.756	6.772	14.44	14.37	4.62	4.60
		Score1:	0.57	DU sum difference:-0.70 u				
Score2:	0.50							

Molecule LC: Peptides with sufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC10-043	1	0.0 min	6.946	6.953	0.12	0.19	0.04	0.06
		0.5 min	6.956	6.949	3.57	3.29	1.14	1.05
		1.0 min	6.972	6.949	3.83	3.41	1.23	1.09
		10.0 min	6.962	6.950	3.89	3.84	1.25	1.23
		60.0 min	6.948	6.941	4.86	4.90	1.56	1.57
		240.0 min	6.945	6.947	6.81	7.03	2.18	2.25
		Score1: 0.11	DU sum difference: -0.13 u					
Score2: 0.23								
LC012-018	1	0.0 min	4.097	4.097	0.00	0.00	0.00	0.00
		0.5 min	4.097	4.108	12.44	12.04	0.62	0.60
		1.0 min	4.106	4.097	15.45	15.85	0.77	0.79
		10.0 min	4.094	4.097	21.27	21.00	1.06	1.05
		60.0 min	4.092	4.097	32.51	32.51	1.63	1.63
		240.0 min	4.104	4.099	41.94	42.34	2.10	2.12
		Score1: 0.03	DU sum difference: 0.01 u					
Score2: 0.31								
LC012-020	1	0.0 min	5.260	5.266	0.00	0.00	0.00	0.00
		0.5 min	5.260	5.262	17.82	17.83	1.25	1.25
		1.0 min	5.265	5.254	19.88	19.77	1.39	1.38
		10.0 min	5.251	5.260	24.10	23.22	1.69	1.63
		60.0 min	5.239	5.260	33.11	31.30	2.32	2.19
		240.0 min	5.259	5.258	38.97	38.98	2.73	2.73
		Score1: 0.73	DU sum difference: -0.20 u					
Score2: 0.60								
LC021-032	1	0.0 min	7.533	7.538	0.00	0.00	0.00	0.00
		0.5 min	7.519	7.519	18.86	18.26	2.07	2.01
		1.0 min	7.521	7.519	21.47	21.47	2.36	2.36
		10.0 min	7.512	7.509	28.70	27.49	3.16	3.02
		60.0 min	7.502	7.491	34.31	34.31	3.77	3.77
		240.0 min	7.504	7.495	39.93	n.d.	4.39	n.d.
		Score1: 0.19	DU sum difference: -0.10 u					
Score2: 0.19								
LC022-035	1	0.0 min	9.994	9.986	0.49	0.49	0.06	0.06
		0.5 min	9.980	9.982	14.86	13.01	1.93	1.69
		1.0 min	9.998	9.976	16.95	16.28	2.20	2.12
		10.0 min	9.980	10.019	21.08	19.67	2.74	2.56
		60.0 min	9.986	9.985	25.86	25.04	3.36	3.26
		240.0 min	9.975	9.984	30.36	28.35	3.95	3.69
		Score1: 1.76	DU sum difference: -0.88 u					
Score2: 1.44								
LC022-046	1	0.0 min	8.828	8.819	0.00	0.00	0.00	0.00
		0.5 min	8.823	8.815	9.92	9.23	2.28	2.12
		1.0 min	8.832	8.818	11.62	10.76	2.67	2.48
		10.0 min	8.819	8.814	15.98	14.85	3.68	3.42
		60.0 min	8.805	8.806	18.49	18.32	4.25	4.21
		240.0 min	8.810	8.828	20.07	19.46	4.62	4.48
		Score1: 0.90	DU sum difference: -0.79 u					
Score2: 0.73								
LC024-033	1	0.0 min	6.858	6.863	0.00	0.00	0.00	0.00
		0.5 min	6.860	6.854	19.06	18.66	1.72	1.68
		1.0 min	6.860	6.886	21.67	23.68	1.95	2.13
		10.0 min	6.852	6.849	30.10	26.89	2.71	2.42
		60.0 min	6.849	6.873	37.42	36.92	3.37	3.32
		240.0 min	6.863	6.856	39.53	37.93	3.56	3.41
		Score1: 0.97	DU sum difference: -0.33 u					
Score2: 1.64								

Molecule LC: Peptides with sufficient kinetics data, part 3

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC024-035	1	0.0 min	9.652	9.643	0.24	0.19	0.03	0.02
		0.5 min	9.656	9.657	10.83	10.82	1.19	1.19
		1.0 min	9.669	9.647	13.63	14.89	1.50	1.64
		10.0 min	9.647	9.648	18.33	17.13	2.02	1.88
		60.0 min	9.650	9.652	21.65	21.70	2.38	2.39
		240.0 min	9.659	9.664	23.65	23.76	2.60	2.61
		Score1: 0.04	DU sum difference: 0.02 u					
Score2: 0.57								
LC024-046	1	0.0 min	8.266	8.262	0.00	0.00	0.00	0.00
		0.5 min	8.258	8.256	7.59	6.84	1.59	1.44
		1.0 min	8.263	8.256	8.89	7.95	1.87	1.67
		10.0 min	8.258	8.252	12.79	11.17	2.69	2.35
		60.0 min	8.244	8.241	14.02	14.06	2.94	2.95
		240.0 min	8.252	8.257	14.85	16.19	3.12	3.40
		Score1: 0.50	DU sum difference: -0.41 u					
Score2: 1.00								
LC027-042	1	0.0 min	6.394	6.405	0.20	0.80	0.03	0.12
		0.5 min	6.403	6.397	19.65	18.32	2.95	2.75
		1.0 min	6.412	6.389	20.99	19.78	3.15	2.97
		10.0 min	6.403	6.390	26.64	25.10	4.00	3.76
		60.0 min	6.393	6.389	27.01	26.68	4.05	4.00
		240.0 min	6.398	6.386	29.36	29.71	4.40	4.46
		Score1: 0.55	DU sum difference: -0.35 u					
Score2: 0.98								
LC027-084	1	0.0 min	8.995	8.996	0.46	0.63	0.25	0.35
		0.5 min	8.991	8.983	9.85	9.37	5.42	5.15
		1.0 min	8.997	8.988	10.06	9.45	5.53	5.20
		10.0 min	8.986	8.981	10.91	10.00	6.00	5.50
		60.0 min	8.977	8.978	11.84	11.96	6.51	6.58
		240.0 min	8.985	8.991	14.15	14.38	7.78	7.91
		Score1: 0.38	DU sum difference: -0.81 u					
Score2: 0.54								
LC028-047	1	0.0 min	9.493	9.491	0.65	0.34	0.12	0.06
		0.5 min	9.478	9.479	22.60	20.86	4.07	3.76
		1.0 min	9.494	9.482	24.28	21.77	4.37	3.92
		10.0 min	9.474	9.473	35.87	31.14	6.46	5.60
		60.0 min	9.465	9.472	40.19	39.04	7.23	7.03
		240.0 min	9.467	9.482	43.16	42.10	7.77	7.58
		Score1: 1.36	DU sum difference: -1.15 u					
Score2: 1.36								
LC028-084	1	0.0 min	9.212	9.196	0.79	0.47	0.43	0.26
		0.5 min	9.208	9.191	9.33	8.70	5.04	4.70
		1.0 min	9.211	9.194	9.69	9.23	5.23	4.98
		10.0 min	9.194	9.185	10.34	9.98	5.58	5.39
		60.0 min	9.177	9.185	11.66	11.68	6.30	6.31
		240.0 min	9.182	9.188	13.46	13.80	7.27	7.45
		Score1: 0.37	DU sum difference: -0.76 u					
Score2: 0.45								
LC030-046	1	0.0 min	8.251	8.248	0.13	0.00	0.02	0.00
		0.5 min	8.244	8.247	7.22	6.62	1.08	0.99
		1.0 min	8.250	8.250	8.38	7.71	1.26	1.16
		10.0 min	8.253	8.249	13.04	11.24	1.96	1.69
		60.0 min	8.242	8.249	12.04	13.85	1.81	2.08
		240.0 min	8.255	8.232	12.24	n.d.	1.84	n.d.
		Score1: 0.40	DU sum difference: -0.25 u					
Score2: 1.28								

Molecule LC: Peptides with sufficient kinetics data, part 4

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC033-046	1	0.0 min	7.438	7.440	0.00	0.00	0.00	0.00
		0.5 min	7.439	7.443	3.59	2.73	0.43	0.33
		1.0 min	7.469	7.437	4.14	4.16	0.50	0.50
		10.0 min	7.459	7.442	8.23	7.24	0.99	0.87
		60.0 min	7.437	7.430	8.96	8.78	1.07	1.05
		240.0 min	7.447	7.434	8.42	8.83	1.01	1.06
		Score1: Score2:	0.42 0.52	DU sum difference:-0.19 u				
LC034-046	1	0.0 min	6.216	6.222	0.00	0.00	0.00	0.00
		0.5 min	6.219	6.219	5.56	5.09	0.61	0.56
		1.0 min	6.233	6.214	6.63	6.32	0.73	0.70
		10.0 min	6.225	6.213	10.91	9.94	1.20	1.09
		60.0 min	6.213	6.214	12.48	11.68	1.37	1.28
		240.0 min	6.225	6.220	12.31	12.67	1.35	1.39
		Score1: Score2:	0.57 0.62	DU sum difference:-0.24 u				
LC036-046	1	0.0 min	4.518	4.522	0.00	0.00	0.00	0.00
		0.5 min	4.522	4.522	9.55	8.82	0.86	0.79
		1.0 min	4.536	4.517	11.04	10.43	0.99	0.94
		10.0 min	4.520	4.522	16.46	15.65	1.48	1.41
		60.0 min	4.518	4.519	18.77	17.86	1.69	1.61
		240.0 min	4.526	4.522	18.46	18.26	1.66	1.64
		Score1: Score2:	0.85 0.69	DU sum difference:-0.29 u				
LC041-078	1	0.0 min	15.672	15.677	0.20	0.20	0.07	0.07
		0.5 min	15.665	15.688	0.00	0.38	0.00	0.13
		1.0 min	15.688	15.671	0.20	0.60	0.07	0.21
		10.0 min	15.674	15.674	0.20	0.55	0.07	0.19
		60.0 min	15.669	15.674	0.00	0.40	0.00	0.14
		240.0 min	15.677	15.671	0.37	0.40	0.13	0.14
		Score1: Score2:	0.41 0.33	DU sum difference: 0.55 u				
LC047-053	1	0.0 min	5.612	5.625	0.00	0.00	0.00	0.00
		0.5 min	5.616	5.625	5.16	5.39	0.31	0.32
		1.0 min	5.626	5.614	6.59	6.88	0.40	0.41
		10.0 min	5.614	5.614	23.43	22.87	1.41	1.37
		60.0 min	5.609	5.613	47.87	47.31	2.87	2.84
		240.0 min	5.615	5.616	54.18	54.40	3.25	3.26
		Score1: Score2:	0.10 0.39	DU sum difference:-0.02 u				
LC047-062	1	0.0 min	10.323	10.330	0.32	0.60	0.04	0.08
		0.5 min	10.315	10.303	20.62	19.76	2.89	2.77
		1.0 min	10.320	10.310	22.62	20.59	3.17	2.88
		10.0 min	10.301	10.297	32.65	31.40	4.57	4.40
		60.0 min	10.297	10.296	41.26	41.46	5.78	5.80
		240.0 min	10.291	10.304	44.69	45.03	6.26	6.30
		Score1: Score2:	0.38 0.91	DU sum difference:-0.25 u				
LC047-071	1	0.0 min	10.703	10.708	0.00	0.00	0.00	0.00
		0.5 min	10.712	10.714	14.96	13.53	3.44	3.11
		1.0 min	10.720	10.708	16.54	15.14	3.80	3.48
		10.0 min	10.704	10.696	22.37	20.66	5.15	4.75
		60.0 min	10.695	10.704	25.44	25.69	5.85	5.91
		240.0 min	10.701	10.699	27.70	27.89	6.37	6.41
		Score1: Score2:	0.68 0.83	DU sum difference:-0.66 u				

Molecule LC: Peptides with sufficient kinetics data, part 5

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC054-062	1	0.0 min	9.878	9.879	0.00	0.00	0.00	0.00
		0.5 min	9.881	9.879	28.90	27.09	2.02	1.90
		1.0 min	9.893	9.878	27.86	27.86	1.95	1.95
		10.0 min	9.876	9.871	35.52	35.52	2.49	2.49
		60.0 min	9.865	9.874	41.94	41.34	2.94	2.89
		240.0 min	9.872	9.883	45.75	45.75	3.20	3.20
		Score1: Score2:	0.19 0.19	DU sum difference:-0.06 u				
LC054-070	1	0.0 min	8.619	8.618	0.00	0.00	0.00	0.00
		0.5 min	8.605	8.612	23.30	23.30	3.49	3.49
		1.0 min	8.605	8.614	24.45	24.45	3.67	3.67
		10.0 min	8.606	8.611	33.00	30.59	4.95	4.59
		60.0 min	8.593	8.602	34.22	34.35	5.13	5.15
		240.0 min	8.604	8.634	36.32	36.32	5.45	5.45
		Score1: Score2:	0.59 0.54	DU sum difference:-0.34 u				
LC054-071	1	0.0 min	10.540	10.541	0.20	0.53	0.03	0.08
		0.5 min	10.555	10.557	13.24	13.24	2.12	2.12
		1.0 min	10.556	10.532	14.60	14.12	2.34	2.26
		10.0 min	10.543	10.541	16.84	16.84	2.69	2.69
		60.0 min	10.526	10.560	19.70	19.19	3.15	3.07
		240.0 min	10.546	10.554	22.07	22.07	3.53	3.53
		Score1: Score2:	0.17 0.28	DU sum difference:-0.11 u				
LC054-095	1	0.0 min	8.952	8.938	0.05	0.15	0.02	0.06
		0.5 min	8.945	8.927	21.54	21.02	8.40	8.20
		1.0 min	8.954	8.932	23.19	21.07	9.05	8.22
		10.0 min	8.947	8.928	27.46	25.66	10.71	10.01
		60.0 min	8.923	8.918	27.75	28.10	10.82	10.96
		240.0 min	8.928	8.919	29.27	29.36	11.42	11.45
		Score1: Score2:	1.02 1.06	DU sum difference:-1.52 u				
LC055-070	1	0.0 min	8.297	8.272	0.00	0.00	0.00	0.00
		0.5 min	8.275	8.287	25.69	22.90	3.60	3.21
		1.0 min	8.282	8.297	25.79	25.79	3.61	3.61
		10.0 min	8.264	8.297	31.00	31.00	4.34	4.34
		60.0 min	8.258	8.261	34.72	34.54	4.86	4.84
		240.0 min	8.263	8.259	38.22	38.33	5.35	5.37
		Score1: Score2:	0.02 0.09	DU sum difference:-0.01 u				
LC055-085	1	0.0 min	12.587	12.586	0.17	0.26	0.05	0.08
		0.5 min	12.591	12.597	7.28	5.79	2.11	1.68
		1.0 min	12.610	12.594	7.25	7.01	2.10	2.03
		10.0 min	12.594	12.603	8.41	8.01	2.44	2.32
		60.0 min	12.597	12.601	10.38	10.23	3.01	2.97
		240.0 min	12.597	12.610	13.00	13.14	3.77	3.81
		Score1: Score2:	0.53 0.54	DU sum difference:-0.59 u				
LC059-100	1	0.0 min	9.947	9.936	0.62	0.50	0.24	0.19
		0.5 min	9.948	9.939	17.97	17.21	7.01	6.71
		1.0 min	9.957	9.930	20.26	19.38	7.90	7.56
		10.0 min	9.945	9.937	23.02	22.44	8.98	8.75
		60.0 min	9.929	9.934	23.85	24.57	9.30	9.58
		240.0 min	9.955	9.949	24.61	24.81	9.60	9.67
		Score1: Score2:	0.37 0.69	DU sum difference:-0.55 u				

Molecule LC: Peptides with sufficient kinetics data, part 6

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC071-076	1	0.0 min	11.113	11.120	0.00	0.00	0.00	0.00
		0.5 min	11.154	11.136	4.62	4.21	0.23	0.21
		1.0 min	11.124	11.130	5.82	6.02	0.29	0.30
		10.0 min	11.137	11.127	19.67	18.26	0.98	0.91
		60.0 min	11.116	11.127	19.06	19.06	0.95	0.95
		240.0 min	11.134	11.127	18.06	19.06	0.90	0.95
		Score1: 0.23	DU sum difference: 0.05 u					
Score2: 0.41								
LC071-077	1	0.0 min	10.836	10.848	0.00	0.00	0.00	0.00
		0.5 min	10.812	10.830	6.55	6.56	0.39	0.39
		1.0 min	10.819	10.813	8.38	8.77	0.50	0.53
		10.0 min	10.804	10.830	23.28	22.27	1.40	1.34
		60.0 min	10.816	10.827	26.49	26.09	1.59	1.57
		240.0 min	10.823	10.814	26.29	26.09	1.58	1.57
		Score1: 0.07	DU sum difference: -0.02 u					
Score2: 0.32								
LC071-079	1	0.0 min	11.891	11.911	0.00	0.00	0.00	0.00
		0.5 min	11.888	11.910	5.30	5.28	0.42	0.42
		1.0 min	11.894	11.892	6.73	6.93	0.54	0.55
		10.0 min	11.874	11.896	17.48	16.59	1.40	1.33
		60.0 min	11.898	11.903	18.93	18.72	1.51	1.50
		240.0 min	11.899	11.909	18.92	19.04	1.51	1.52
		Score1: 0.21	DU sum difference: -0.06 u					
Score2: 0.30								
LC072-079	1	0.0 min	9.221	9.228	0.00	0.20	0.00	0.01
		0.5 min	9.218	9.228	4.01	4.01	0.28	0.28
		1.0 min	9.224	9.227	6.02	6.82	0.42	0.48
		10.0 min	9.217	9.226	17.46	17.46	1.22	1.22
		60.0 min	9.216	9.217	19.87	19.87	1.39	1.39
		240.0 min	9.231	9.229	19.47	19.67	1.36	1.38
		Score1: 0.31	DU sum difference: 0.08 u					
Score2: 0.26								
LC074-079	1	0.0 min	5.588	5.598	0.00	0.00	0.00	0.00
		0.5 min	5.588	5.598	5.96	6.02	0.30	0.30
		1.0 min	5.598	5.588	8.57	7.93	0.43	0.40
		10.0 min	5.584	5.591	23.88	23.68	1.19	1.18
		60.0 min	5.587	5.591	27.49	27.49	1.37	1.37
		240.0 min	5.594	5.591	26.49	27.09	1.32	1.35
		Score1: 0.07	DU sum difference: -0.01 u					
Score2: 0.37								
LC078-085	1	0.0 min	10.908	10.919	0.00	0.00	0.00	0.00
		0.5 min	10.921	10.934	18.47	16.16	1.29	1.13
		1.0 min	10.942	10.936	19.31	17.60	1.35	1.23
		10.0 min	10.920	10.928	23.38	22.85	1.64	1.60
		60.0 min	10.925	10.936	23.92	24.69	1.67	1.73
		240.0 min	10.936	10.949	29.70	28.37	2.08	1.99
		Score1: 0.72	DU sum difference: -0.24 u					
Score2: 1.22								
LC080-086	1	0.0 min	11.393	11.414	0.00	0.00	0.00	0.00
		0.5 min	11.393	11.408	6.08	5.80	0.36	0.35
		1.0 min	11.408	11.393	9.57	6.06	0.57	0.36
		10.0 min	11.391	11.408	11.79	10.74	0.71	0.64
		60.0 min	11.399	11.411	14.53	13.65	0.87	0.82
		240.0 min	11.404	11.416	19.24	21.27	1.15	1.28
		Score1: 0.98	DU sum difference: -0.25 u					
Score2: 1.65p								

Molecule LC: Peptides with sufficient kinetics data, part 7

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC086-101	1	0.0 min	14.560	14.604	0.59	0.07	0.08	0.01
		0.5 min	14.546	14.605	7.23	8.03	1.01	1.12
		1.0 min	14.574	14.609	8.53	7.83	1.19	1.10
		10.0 min	14.562	14.679	10.64	9.43	1.49	1.32
		60.0 min	14.610	14.612	13.44	13.44	1.88	1.88
		240.0 min	14.599	14.594	17.86	18.06	2.50	2.53
Score1:	0.37	DU sum difference:-0.20 u						
Score2:	0.73							
LC086-106	1	0.0 min	14.813	14.823	0.00	0.00	0.00	0.00
		0.5 min	14.804	14.831	7.18	7.40	1.36	1.41
		1.0 min	14.825	14.828	7.53	7.42	1.43	1.41
		10.0 min	14.814	14.817	8.51	8.22	1.62	1.56
		60.0 min	14.823	14.832	11.14	11.15	2.12	2.12
		240.0 min	14.825	14.826	15.25	15.79	2.90	3.00
Score1:	0.09	DU sum difference: 0.07 u						
Score2:	0.25							
LC087-104	1	0.0 min	13.332	13.337	0.20	0.20	0.03	0.03
		0.5 min	13.331	13.339	8.23	8.23	1.32	1.32
		1.0 min	13.320	13.333	8.63	8.63	1.38	1.38
		10.0 min	13.324	13.296	9.43	9.43	1.51	1.51
		60.0 min	13.324	13.340	13.24	13.44	2.12	2.15
		240.0 min	13.320	13.326	17.66	17.86	2.83	2.86
Score1:	0.10	DU sum difference: 0.06 u						
Score2:	0.09							
LC087-106	1	0.0 min	14.349	14.358	0.00	0.00	0.00	0.00
		0.5 min	14.345	14.367	8.23	8.16	1.48	1.47
		1.0 min	14.363	14.360	8.54	8.26	1.54	1.49
		10.0 min	14.352	14.377	9.64	9.00	1.74	1.62
		60.0 min	14.364	14.360	12.43	12.40	2.24	2.23
		240.0 min	14.356	14.364	17.07	17.20	3.07	3.10
Score1:	0.23	DU sum difference:-0.16 u						
Score2:	0.24							
LC098-106	1	0.0 min	10.483	10.481	0.00	0.00	0.00	0.00
		0.5 min	10.468	10.465	5.22	3.81	0.42	0.31
		1.0 min	10.475	10.468	4.62	4.62	0.37	0.37
		10.0 min	10.455	10.469	7.22	5.62	0.58	0.45
		60.0 min	10.457	10.468	8.43	8.43	0.67	0.67
		240.0 min	10.469	10.469	11.64	11.44	0.93	0.92
Score1:	0.84	DU sum difference:-0.26 u						
Score2:	0.68							
LC102-106	1	0.0 min	8.543	8.543	0.00	0.00	0.00	0.00
		0.5 min	8.543	8.545	1.61	2.01	0.06	0.08
		1.0 min	8.552	8.553	2.21	2.33	0.09	0.09
		10.0 min	8.550	8.545	2.81	2.21	0.11	0.09
		60.0 min	8.550	8.546	3.53	3.40	0.14	0.14
		240.0 min	8.557	8.557	4.96	5.62	0.20	0.22
Score1:	0.12	DU sum difference: 0.02 u						
Score2:	0.41							
LC104-124	1	0.0 min	11.576	11.573	0.40	0.00	0.07	0.00
		0.5 min	11.577	11.593	15.80	15.80	2.69	2.69
		1.0 min	11.598	11.576	17.66	16.75	3.00	2.85
		10.0 min	11.571	11.583	23.08	23.08	3.92	3.92
		60.0 min	11.573	11.579	27.89	27.69	4.74	4.71
		240.0 min	11.586	11.579	29.50	29.50	5.01	5.01
Score1:	0.39	DU sum difference:-0.26 u						
Score2:	0.32							

Molecule LC: Peptides with sufficient kinetics data, part 8

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC105-123	2	0.0 min	10.037	10.034	0.00	0.00	0.00	0.00
		0.5 min	10.036	10.033	18.26	17.26	2.74	2.59
		1.0 min	10.050	10.018	19.26	18.86	2.89	2.83
		10.0 min	10.033	10.028	22.88	21.27	3.43	3.19
		60.0 min	10.025	10.032	24.48	24.28	3.67	3.64
		240.0 min	10.039	10.031	26.49	25.49	3.97	3.82
Score1:		1.10	DU sum difference:-0.63 u					
Score2:		0.90						
LC105-124	1	0.0 min	9.699	9.692	0.20	0.00	0.03	0.00
		0.5 min	9.686	9.681	18.72	17.61	3.00	2.82
		1.0 min	9.692	9.680	19.67	18.79	3.15	3.01
		10.0 min	9.679	9.684	24.48	22.52	3.92	3.60
		60.0 min	9.673	9.681	26.43	26.58	4.23	4.25
		240.0 min	9.681	9.686	28.20	28.34	4.51	4.54
Score1:		1.00	DU sum difference:-0.62 u					
Score2:		0.95						
LC105-125	1	0.0 min	11.134	11.131	0.10	0.20	0.02	0.03
		0.5 min	11.138	11.144	17.04	16.01	2.90	2.72
		1.0 min	11.151	11.132	18.01	16.83	3.06	2.86
		10.0 min	11.141	11.141	25.04	23.24	4.26	3.95
		60.0 min	11.130	11.142	27.46	27.49	4.67	4.67
		240.0 min	11.131	11.141	28.90	28.71	4.91	4.88
Score1:		1.06	DU sum difference:-0.69 u					
Score2:		0.92						
LC105-131	1	0.0 min	10.323	10.331	0.00	0.00	0.00	0.00
		0.5 min	10.311	10.307	21.86	20.65	5.03	4.75
		1.0 min	10.316	10.304	23.27	21.50	5.35	4.94
		10.0 min	10.300	10.313	28.88	26.68	6.64	6.14
		60.0 min	10.303	10.317	31.03	30.98	7.14	7.12
		240.0 min	10.308	10.316	33.30	33.29	7.66	7.66
Score1:		1.15	DU sum difference:-1.11 u					
Score2:		1.03						
LC107-122	1	0.0 min	9.416	9.419	0.00	0.53	0.00	0.06
		0.5 min	9.425	9.418	23.28	21.27	2.79	2.55
		1.0 min	9.428	9.418	22.27	22.27	2.67	2.67
		10.0 min	9.419	9.418	27.29	25.08	3.27	3.01
		60.0 min	9.409	9.418	30.50	30.10	3.66	3.61
		240.0 min	9.423	9.428	33.31	33.31	4.00	4.00
Score1:		1.06p	DU sum difference:-0.49 u					
Score2:		1.09p						
LC107-123	1	0.0 min	9.569	9.569	0.00	0.00	0.00	0.00
		0.5 min	9.572	9.566	21.26	20.21	2.76	2.63
		1.0 min	9.588	9.565	21.91	20.83	2.85	2.71
		10.0 min	9.564	9.566	25.05	23.15	3.26	3.01
		60.0 min	9.559	9.564	27.59	27.03	3.59	3.51
		240.0 min	9.571	9.574	28.41	30.29	3.69	3.94
Score1:		0.71	DU sum difference:-0.35 u					
Score2:		1.38						
LC107-124	1	0.0 min	9.370	9.366	0.06	0.00	0.01	0.00
		0.5 min	9.369	9.368	19.49	18.51	2.73	2.59
		1.0 min	9.372	9.370	21.01	19.18	2.94	2.69
		10.0 min	9.367	9.368	26.14	24.21	3.66	3.39
		60.0 min	9.362	9.371	28.85	28.33	4.04	3.97
		240.0 min	9.371	9.379	30.30	30.05	4.24	4.21
Score1:		1.45	DU sum difference:-0.78 u					
Score2:		1.19						

Molecule LC: Peptides with sufficient kinetics data, part 9

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC107-125	1	0.0 min	10.891	10.892	0.00	0.09	0.00	0.01
		0.5 min	10.907	10.907	17.95	16.88	2.69	2.53
		1.0 min	10.920	10.900	19.67	18.06	2.95	2.71
		10.0 min	10.901	10.899	27.53	25.51	4.13	3.83
		60.0 min	10.895	10.906	30.58	30.26	4.59	4.54
		240.0 min	10.897	10.901	32.16	32.08	4.82	4.81
		Score1:	1.12	DU sum difference:-0.71 u				
Score2:	1.05							
LC107-131	1	0.0 min	10.079	10.086	0.00	0.00	0.00	0.00
		0.5 min	10.091	10.088	22.73	21.29	4.77	4.47
		1.0 min	10.112	10.089	24.34	22.73	5.11	4.77
		10.0 min	10.090	10.086	30.62	28.30	6.43	5.94
		60.0 min	10.081	10.089	33.21	32.76	6.97	6.88
		240.0 min	10.084	10.101	35.58	35.16	7.47	7.38
		Score1:	1.37	DU sum difference:-1.21 u				
Score2:	1.23							
	2	0.0 min	10.580	10.577	0.01	0.00	0.00	0.00
		0.5 min	10.617	10.617	20.27	20.27	4.26	4.26
		1.0 min	10.633	10.598	22.68	21.47	4.76	4.51
		10.0 min	10.615	10.602	27.09	27.09	5.69	5.69
		60.0 min	10.603	10.614	32.11	31.91	6.74	6.70
		240.0 min	10.618	10.596	33.93	34.52	7.13	7.25
		Score1:	0.24	DU sum difference:-0.21 u				
Score2:	0.51							
LC110-120	1	0.0 min	10.854	10.855	0.00	0.00	0.00	0.00
		0.5 min	10.863	10.860	15.65	14.25	1.10	1.00
		1.0 min	10.864	10.860	19.47	19.47	1.36	1.36
		10.0 min	10.855	10.866	26.89	25.08	1.88	1.76
		60.0 min	10.849	10.868	25.89	25.89	1.81	1.81
		240.0 min	10.864	10.870	28.29	28.29	1.98	1.98
		Score1:	0.40	DU sum difference:-0.12 u				
Score2:	0.36							
	2	0.0 min	11.030	11.034	0.04	0.03	0.00	0.00
		0.5 min	11.038	11.038	15.76	14.59	1.10	1.02
		1.0 min	n.d.	11.037	n.d.	19.37	n.d.	1.36
		10.0 min	11.027	11.034	25.72	25.19	1.80	1.76
		60.0 min	11.023	11.035	26.50	26.13	1.85	1.83
		240.0 min	11.039	11.040	29.21	28.91	2.04	2.02
		Score1:	0.68	DU sum difference:-0.20 u				
Score2:	0.61							
LC111-153	1	0.0 min	11.586	11.586	0.23	0.00	0.09	0.00
		0.5 min	11.616	11.612	3.91	4.24	1.49	1.61
		1.0 min	11.611	11.597	5.03	4.98	1.91	1.89
		10.0 min	11.601	11.605	7.78	7.91	2.96	3.01
		60.0 min	11.599	11.577	11.22	12.03	4.26	4.57
		240.0 min	11.593	11.587	14.87	16.23	5.65	6.17
		Score1:	0.62	DU sum difference: 0.90 u				
Score2:	0.62							
	2	0.0 min	11.730	11.729	0.59	0.20	0.23	0.08
		0.5 min	11.725	11.701	4.21	4.64	1.60	1.76
		1.0 min	11.741	11.725	4.70	4.74	1.79	1.80
		10.0 min	11.728	11.690	7.20	7.23	2.73	2.75
		60.0 min	11.689	11.712	10.28	12.17	3.91	4.63
		240.0 min	11.708	11.711	15.37	17.20	5.84	6.54
		Score1:	1.00	DU sum difference: 1.45 u				
Score2:	0.98							

Molecule LC: Peptides with sufficient kinetics data, part 10

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC124-131	1	0.0 min	4.139	4.140	0.00	0.00	0.00	0.00
		0.5 min	4.137	4.144	37.32	36.52	2.61	2.56
		1.0 min	4.144	4.134	38.93	38.53	2.73	2.70
		10.0 min	4.131	4.137	42.34	42.14	2.96	2.95
		60.0 min	4.133	4.132	46.36	46.15	3.24	3.23
		240.0 min	4.137	4.137	50.47	50.37	3.53	3.53
		Score1:	0.45	DU sum difference:-0.12 u				
Score2:	0.36							
LC132-145	1	0.0 min	13.796	13.803	0.00	0.00	0.00	0.00
		0.5 min	13.800	13.813	8.43	8.73	1.01	1.05
		1.0 min	13.815	13.800	9.90	10.06	1.19	1.21
		10.0 min	13.798	13.807	16.12	16.12	1.93	1.93
		60.0 min	13.801	13.802	17.38	17.65	2.09	2.12
		240.0 min	13.801	13.807	19.26	19.19	2.31	2.30
		Score1:	0.14	DU sum difference: 0.07 u				
Score2:	0.16							
LC136-146	1	0.0 min	10.521	10.529	0.60	0.20	0.05	0.02
		0.5 min	10.529	10.533	19.47	19.26	1.75	1.73
		1.0 min	10.539	10.531	22.88	22.07	2.06	1.99
		10.0 min	10.527	10.527	31.91	30.70	2.87	2.76
		60.0 min	10.521	10.527	33.31	33.91	3.00	3.05
		240.0 min	10.529	10.531	34.31	34.31	3.09	3.09
		Score1:	0.38	DU sum difference:-0.16 u				
Score2:	0.77							
LC136-154	1	0.0 min	10.569	10.563	0.00	0.00	0.00	0.00
		0.5 min	10.570	10.567	14.45	13.84	2.46	2.35
		1.0 min	10.581	10.569	16.23	15.33	2.76	2.61
		10.0 min	10.567	10.561	22.28	21.47	3.79	3.65
		60.0 min	10.556	10.572	24.59	24.00	4.18	4.08
		240.0 min	10.565	10.565	27.37	27.33	4.65	4.65
		Score1:	0.61	DU sum difference:-0.44 u				
Score2:	0.55							
LC137-161	1	0.0 min	10.749	10.749	0.00	0.00	0.00	0.00
		0.5 min	10.761	10.757	12.79	12.53	2.94	2.88
		1.0 min	10.778	10.747	14.85	14.91	3.42	3.43
		10.0 min	10.754	10.741	19.73	19.00	4.54	4.37
		60.0 min	10.751	10.761	23.49	23.77	5.40	5.47
		240.0 min	10.745	10.767	25.90	25.30	5.96	5.82
		Score1:	0.33	DU sum difference:-0.29 u				
Score2:	0.41							
LC140-161	1	0.0 min	10.667	10.675	0.00	0.00	0.00	0.00
		0.5 min	10.662	10.676	25.75	22.86	5.15	4.57
		1.0 min	10.683	10.668	25.19	24.40	5.04	4.88
		10.0 min	10.676	10.669	32.31	30.65	6.46	6.13
		60.0 min	10.669	10.674	34.92	34.92	6.98	6.98
		240.0 min	10.678	10.686	37.32	37.32	7.46	7.46
		Score1:	0.70	DU sum difference:-0.59 u				
Score2:	0.63							
LC146-160	1	0.0 min	8.629	8.625	0.00	0.00	0.00	0.00
		0.5 min	8.643	8.629	17.74	15.23	2.48	2.13
		1.0 min	8.652	8.647	18.86	17.10	2.64	2.39
		10.0 min	8.640	8.633	23.97	22.55	3.36	3.16
		60.0 min	8.626	8.630	26.73	26.30	3.74	3.68
		240.0 min	8.629	8.643	29.50	29.50	4.13	4.13
		Score1:	1.34	DU sum difference:-0.79 u				
Score2:	1.20							

Molecule LC: Peptides with sufficient kinetics data, part 11

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC147-160	1	0.0 min	8.187	8.185	0.00	0.00	0.00	0.00
		0.5 min	8.187	8.189	16.59	15.58	2.16	2.03
		1.0 min	8.193	8.189	18.73	17.05	2.44	2.22
		10.0 min	8.194	8.193	23.80	21.83	3.09	2.84
		60.0 min	8.178	8.182	25.07	24.15	3.26	3.14
		240.0 min	8.194	8.180	27.15	26.49	3.53	3.44
		Score1: 1.15	DU sum difference: -0.70 u	Score2: 1.15				
LC155-160	1	0.0 min	5.914	5.914	0.00	0.00	0.00	0.00
		0.5 min	5.906	5.914	24.68	24.08	1.23	1.20
		1.0 min	5.914	5.911	27.29	27.29	1.36	1.36
		10.0 min	5.909	5.914	33.51	32.91	1.68	1.65
		60.0 min	5.911	5.914	34.31	34.31	1.72	1.72
		240.0 min	5.914	5.917	36.72	36.72	1.84	1.84
		Score1: 0.17	DU sum difference: -0.04 u	Score2: 0.15				
LC161-172	1	0.0 min	6.271	6.273	0.00	0.00	0.00	0.00
		0.5 min	6.269	6.265	22.89	22.07	2.52	2.43
		1.0 min	6.272	6.261	24.10	23.38	2.65	2.57
		10.0 min	6.259	6.263	30.86	29.49	3.39	3.24
		60.0 min	6.260	6.258	36.93	36.52	4.06	4.02
		240.0 min	6.265	6.262	40.33	40.30	4.44	4.43
		Score1: 0.40	DU sum difference: -0.21 u	Score2: 0.40				
LC161-175	1	0.0 min	9.345	9.345	0.01	0.00	0.00	0.00
		0.5 min	9.349	9.348	10.65	10.23	1.49	1.43
		1.0 min	9.354	9.345	11.52	11.59	1.61	1.62
		10.0 min	9.343	9.344	16.48	14.25	2.31	2.00
		60.0 min	9.343	9.347	17.59	17.76	2.46	2.49
		240.0 min	9.352	9.353	20.42	20.11	2.86	2.82
		Score1: 0.14	DU sum difference: -0.08 u	Score2: 0.25				
LC161-179	1	0.0 min	10.572	10.581	0.00	0.00	0.00	0.00
		0.5 min	10.582	10.580	7.08	6.02	1.28	1.08
		1.0 min	10.594	10.583	7.55	6.79	1.36	1.22
		10.0 min	10.575	10.579	9.77	8.08	1.76	1.45
		60.0 min	10.569	10.579	10.96	10.84	1.97	1.95
		240.0 min	10.577	10.582	12.61	12.59	2.27	2.27
		Score1: 0.96	DU sum difference: -0.66 u	Score2: 0.78				
LC164-189	1	0.0 min	12.733	12.753	0.20	0.20	0.05	0.05
		0.5 min	12.753	12.757	5.82	5.82	1.45	1.45
		1.0 min	12.771	12.749	6.42	6.42	1.61	1.61
		10.0 min	12.753	12.747	6.75	7.42	1.69	1.86
		60.0 min	12.741	12.757	8.96	8.63	2.24	2.16
		240.0 min	12.752	12.753	12.64	12.24	3.16	3.06
		Score1: 0.02	DU sum difference: -0.01 u	Score2: 0.30				
LC173-179	1	0.0 min	9.812	9.808	0.00	0.00	0.00	0.00
		0.5 min	9.811	9.811	1.00	1.81	0.06	0.11
		1.0 min	9.817	9.812	2.01	1.40	0.12	0.08
		10.0 min	9.808	9.808	2.21	1.20	0.13	0.07
		60.0 min	9.808	9.808	2.21	1.61	0.13	0.10
		240.0 min	9.808	9.815	2.96	2.41	0.18	0.14
		Score1: 0.51	DU sum difference: -0.12 u	Score2: 0.76				

Molecule LC: Peptides with sufficient kinetics data, part 12

Ref: reference series, Exp: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sums)

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC173-199	1	0.0 min	12.587	12.586	0.00	0.09	0.00	0.02
		0.5 min	12.586	12.602	7.01	6.99	1.82	1.82
		1.0 min	12.611	12.596	7.80	7.36	2.03	1.91
		10.0 min	12.597	12.602	9.21	8.71	2.39	2.26
		60.0 min	12.595	12.600	11.31	11.20	2.94	2.91
		240.0 min	12.583	12.612	13.84	15.20	3.60	3.95
		Score1:	0.10	DU sum difference: 0.10 u				
Score2:	0.54							
LC174-199	1	0.0 min	12.388	12.396	0.02	0.00	0.00	0.00
		0.5 min	12.397	12.399	7.80	7.22	1.95	1.81
		1.0 min	12.410	12.372	8.43	7.83	2.11	1.96
		10.0 min	12.391	12.389	10.14	8.63	2.53	2.16
		60.0 min	12.390	12.394	12.64	n.d.	3.16	n.d.
		240.0 min	12.387	12.385	n.d.	17.86	n.d.	4.46
		Score1:	0.86	DU sum difference:-1.01 u				
Score2:	0.86							
LC179-195	1	0.0 min	7.237	7.222	0.00	0.00	0.00	0.00
		0.5 min	7.227	7.227	5.95	5.57	0.95	0.89
		1.0 min	7.242	7.224	7.34	6.59	1.18	1.05
		10.0 min	7.231	7.222	10.24	8.92	1.64	1.43
		60.0 min	7.222	7.226	11.02	11.53	1.76	1.84
		240.0 min	7.228	7.228	14.92	15.84	2.39	2.53
		Score1:	0.27	DU sum difference:-0.17 u				
Score2:	0.83							
LC180-195	1	0.0 min	6.072	6.074	0.06	0.00	0.01	0.00
		0.5 min	6.079	6.074	5.94	5.69	0.89	0.85
		1.0 min	6.079	6.061	7.84	7.34	1.18	1.10
		10.0 min	6.072	6.067	10.03	9.60	1.50	1.44
		60.0 min	6.063	6.068	11.49	11.32	1.72	1.70
		240.0 min	6.072	6.063	14.83	14.54	2.22	2.18
		Score1:	0.44	DU sum difference:-0.25 u				
Score2:	0.36							
LC180-214	1	0.0 min	6.958	6.973	0.00	0.00	0.00	0.00
		0.5 min	6.955	6.946	9.62	9.19	3.18	3.03
		1.0 min	6.968	6.943	11.92	11.48	3.93	3.79
		10.0 min	6.950	6.937	15.09	14.33	4.98	4.73
		60.0 min	6.933	6.931	17.08	17.11	5.64	5.65
		240.0 min	6.934	6.937	20.29	19.94	6.70	6.58
		Score1:	0.51	DU sum difference:-0.64 u				
Score2:	0.43							
LC182-195	1	0.0 min	5.205	5.211	0.00	0.00	0.00	0.00
		0.5 min	5.211	5.211	2.33	2.68	0.30	0.35
		1.0 min	5.216	5.197	2.59	2.75	0.34	0.36
		10.0 min	5.207	5.206	3.20	2.81	0.42	0.37
		60.0 min	5.197	5.205	3.93	4.13	0.51	0.54
		240.0 min	5.211	5.210	7.88	7.60	1.02	0.99
		Score1:	0.01	DU sum difference: 0.01 u				
Score2:	0.29							
LC196-214	1	0.0 min	6.162	6.163	0.00	0.00	0.00	0.00
		0.5 min	6.160	6.161	17.19	15.95	2.92	2.71
		1.0 min	6.172	6.147	19.26	18.63	3.27	3.17
		10.0 min	6.155	6.149	24.69	23.87	4.20	4.06
		60.0 min	6.133	6.140	27.50	27.29	4.67	4.64
		240.0 min	6.146	6.146	30.31	30.30	5.15	5.15
		Score1:	0.65	DU sum difference:-0.46 u				
Score2:	0.58							

Molecule LC: Peptides/Ranges with insufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

Bold typing: problematic DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC004-021	1	0.0 min	9.984	9.985	n.d.	n.d.	n.d.	n.d.
		0.5 min	9.984	9.981	n.d.	n.d.	n.d.	n.d.
		1.0 min	9.992	9.991	n.d.	n.d.	n.d.	n.d.
		10.0 min	9.988	9.984	n.d.	n.d.	n.d.	n.d.
		60.0 min	9.986	9.987	n.d.	n.d.	n.d.	n.d.
		240.0 min	9.989	9.981	n.d.	n.d.	n.d.	n.d.
LC019-023	1	0.0 min	7.896	7.901	n.d.	n.d.	n.d.	n.d.
		0.5 min	7.889	7.893	n.d.	n.d.	n.d.	n.d.
		1.0 min	7.896	7.896	n.d.	n.d.	n.d.	n.d.
		10.0 min	7.893	7.896	n.d.	n.d.	n.d.	n.d.
		60.0 min	7.889	7.900	n.d.	n.d.	n.d.	n.d.
		240.0 min	7.900	7.899	n.d.	n.d.	n.d.	n.d.
LC019-046	1	0.0 min	11.611	11.570	70.38	0.00	18.30	0.00
		0.5 min	11.620	11.571	77.46	89.10	20.14	23.17
		1.0 min	11.568	11.562	68.83	86.89	17.90	22.59
		10.0 min	11.558	11.596	88.54	88.44	23.02	22.99
		60.0 min	11.560	11.565	84.48	87.87	21.97	22.85
		240.0 min	11.552	11.564	81.72	90.10	21.25	23.43
LC029-046	1	0.0 min	8.010	8.021	n.d.	n.d.	n.d.	n.d.
		0.5 min	8.018	8.037	n.d.	n.d.	n.d.	n.d.
		1.0 min	8.036	8.023	n.d.	n.d.	n.d.	n.d.
		10.0 min	8.015	8.024	n.d.	n.d.	n.d.	n.d.
		60.0 min	8.017	8.012	n.d.	n.d.	n.d.	n.d.
		240.0 min	8.042	8.003	n.d.	n.d.	n.d.	n.d.
LC051-070	1	0.0 min	8.732	8.744	0.08	0.87	0.02	0.16
		0.5 min	8.751	8.751	22.85	21.15	4.11	3.81
		1.0 min	8.744	8.759	23.76	25.04	4.28	4.51
		10.0 min	8.741	8.745	28.26	22.21	5.09	4.00
		60.0 min	8.734	8.739	26.67	39.13	4.80	7.04
		240.0 min	8.728	8.750	40.44	n.d.	7.28	n.d.
LC051-093	1	0.0 min	9.476	9.424	0.00	n.d.	0.00	n.d.
		0.5 min	9.466	9.444	11.14	n.d.	4.57	n.d.
		1.0 min	9.475	9.450	11.64	n.d.	4.77	n.d.
		10.0 min	9.449	9.418	13.68	n.d.	5.61	n.d.
		60.0 min	9.441	9.399	15.29	n.d.	6.27	n.d.
		240.0 min	9.428	9.431	19.07	n.d.	7.82	n.d.
LC087-101	1	0.0 min	13.860	13.881	1.00	1.20	0.13	0.16
		0.5 min	13.866	13.886	8.43	9.14	1.10	1.19
		1.0 min	13.880	13.869	9.01	11.98	1.17	1.56
		10.0 min	13.857	13.899	13.09	11.04	1.70	1.43
		60.0 min	13.883	13.886	15.97	15.69	2.08	2.04
		240.0 min	13.890	13.896	20.07	20.78	2.61	2.70
LC105-123	1	0.0 min	9.857	9.855	n.d.	n.d.	n.d.	n.d.
		0.5 min	9.865	9.850	n.d.	n.d.	n.d.	n.d.
		1.0 min	9.865	9.867	n.d.	n.d.	n.d.	n.d.
		10.0 min	9.849	9.846	n.d.	n.d.	n.d.	n.d.
		60.0 min	9.847	9.856	n.d.	n.d.	n.d.	n.d.
		240.0 min	9.865	9.845	n.d.	n.d.	n.d.	n.d.
LC105-131	2	0.0 min	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		0.5 min	10.578	10.583	n.d.	n.d.	n.d.	n.d.
		1.0 min	10.600	10.574	n.d.	n.d.	n.d.	n.d.
		10.0 min	10.589	10.567	n.d.	n.d.	n.d.	n.d.
		60.0 min	10.569	10.577	n.d.	n.d.	n.d.	n.d.
		240.0 min	10.584	10.584	n.d.	n.d.	n.d.	n.d.

Molecule LC: Peptides/Ranges with insufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

Bold typing: problematic DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC105-132	1	0.0 min	10.857	10.864	n.d.	n.d.	n.d.	n.d.
		0.5 min	10.876	10.866	n.d.	n.d.	n.d.	n.d.
		1.0 min	10.874	10.869	n.d.	n.d.	n.d.	n.d.
		10.0 min	10.862	10.849	n.d.	n.d.	n.d.	n.d.
		60.0 min	10.878	10.850	n.d.	n.d.	n.d.	n.d.
		240.0 min	10.866	10.856	n.d.	n.d.	n.d.	n.d.
LC136-143	1	0.0 min	7.889	7.911	n.d.	n.d.	n.d.	n.d.
		0.5 min	7.915	7.915	n.d.	n.d.	n.d.	n.d.
		1.0 min	7.915	7.908	n.d.	n.d.	n.d.	n.d.
		10.0 min	7.917	7.911	n.d.	n.d.	n.d.	n.d.
		60.0 min	7.909	7.912	n.d.	n.d.	n.d.	n.d.
		240.0 min	7.919	7.915	n.d.	n.d.	n.d.	n.d.
LC136-145	1	0.0 min	8.428	8.439	0.00	0.00	0.00	0.00
		0.5 min	8.441	8.441	12.68	12.92	1.01	1.03
		1.0 min	8.443	8.429	15.56	13.99	1.24	1.12
		10.0 min	8.441	8.437	26.10	25.16	2.09	2.01
		60.0 min	n.d.	8.434	n.d.	28.18	n.d.	2.25
	240.0 min	n.d.	8.444	n.d.	29.76	n.d.	2.38	
	2	0.0 min	8.975	8.975	0.09	0.00	0.01	0.00
		0.5 min	8.971	8.961	12.46	10.92	1.00	0.87
		1.0 min	8.972	8.977	15.61	13.85	1.25	1.11
		10.0 min	8.975	8.965	27.69	24.08	2.22	1.93
60.0 min		8.957	8.991	n.d.	28.29	n.d.	2.26	
240.0 min	8.987	9.029	34.06	29.10	2.73	2.33		
LC140-160	1	0.0 min	9.341	9.358	16.86	16.46	3.20	3.13
		0.5 min	9.361	9.361	26.58	45.15	5.05	8.58
		1.0 min	9.369	9.357	49.23	46.35	9.35	8.81
		10.0 min	9.354	9.371	34.49	49.59	6.55	9.42
		60.0 min	9.350	9.359	50.37	47.41	9.57	9.01
		240.0 min	9.366	9.374	52.98	48.00	10.07	9.12
LC152-162	1	0.0 min	11.943	11.944	n.d.	n.d.	n.d.	n.d.
		0.5 min	11.943	11.960	n.d.	n.d.	n.d.	n.d.
		1.0 min	11.941	11.941	n.d.	n.d.	n.d.	n.d.
		10.0 min	11.941	11.955	n.d.	n.d.	n.d.	n.d.
		60.0 min	11.944	11.955	n.d.	n.d.	n.d.	n.d.
		240.0 min	11.955	11.955	n.d.	n.d.	n.d.	n.d.
LC161-178	1	0.0 min	8.626	8.630	0.00	1.09	0.00	0.18
		0.5 min	8.617	8.621	11.83	8.95	2.01	1.52
		1.0 min	8.620	8.621	12.46	9.76	2.12	1.66
		10.0 min	8.618	8.630	14.72	12.73	2.50	2.16
		60.0 min	8.609	8.616	16.25	16.03	2.76	2.73
		240.0 min	8.624	8.642	18.85	17.89	3.20	3.04
LC173-178	1	0.0 min	6.339	6.335	0.00	0.00	0.00	0.00
		0.5 min	6.339	6.350	15.45	14.73	0.77	0.74
		1.0 min	6.339	6.335	12.15	8.83	0.61	0.44
		10.0 min	6.339	6.350	19.42	22.07	0.97	1.10
		60.0 min	6.325	6.339	18.28	21.13	0.91	1.06
		240.0 min	6.332	6.348	11.94	13.20	0.60	0.66
LC179-206	1	0.0 min	11.035	11.035	0.00	0.00	0.00	0.00
		0.5 min	11.037	11.043	20.07	18.86	5.22	4.90
		1.0 min	11.043	11.031	20.47	20.87	5.32	5.43
		10.0 min	11.024	11.035	26.29	n.d.	6.83	n.d.
		60.0 min	11.035	11.038	30.50	n.d.	7.93	n.d.
		240.0 min	11.040	11.040	n.d.	n.d.	n.d.	n.d.

Molecule LC: no peptides lacking equivalent range available

Molecule LC: no peptides lacking HDX data in experiment series available

Molecule LC: no peptides lacking HDX data in reference series available

Molecule LC: no peptides lacking HDX data in both series available

Molecule: **HC**
 Peptide: **HC001-017**
 Exchangeable protons: 15
 Index lis-file: 88
 Sequence: EVQGVESGGGLVKPGGS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

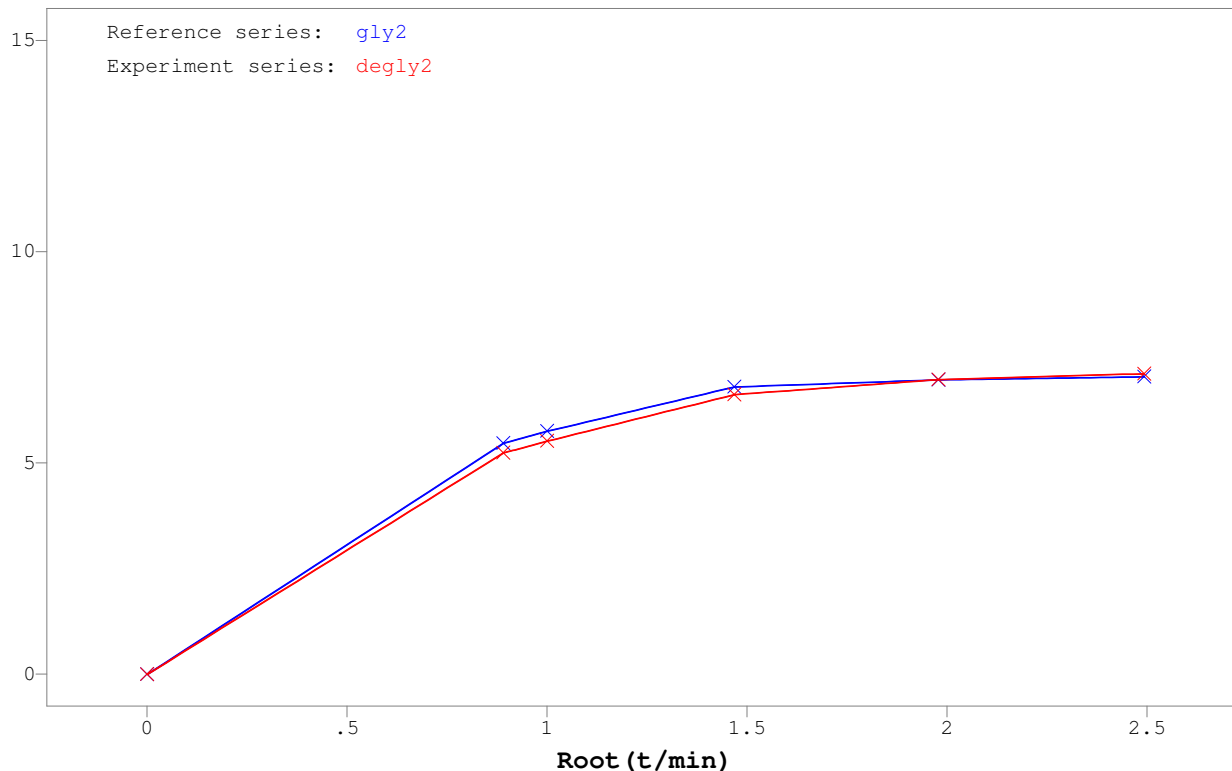
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.059	7.061	0.00	0.00	0.00	0.00
0.5	7.048	7.053	36.48	34.94	5.47	5.24
1.0	7.062	7.054	38.36	36.80	5.75	5.52
10.0	7.051	7.047	45.36	44.15	6.80	6.62
60.0	7.047	7.046	46.48	46.52	6.97	6.98
240.0	7.051	7.045	46.96	47.45	7.04	7.12

Score1 (DU sum): 0.99
 Score2 (DU Profile): **1.03**
 DU sum difference (u): -0.57

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC001-018**
 Exchangeable protons: 16
 Index lis-file: 89
 Sequence: EVQGVESGGGLVKPGGSL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

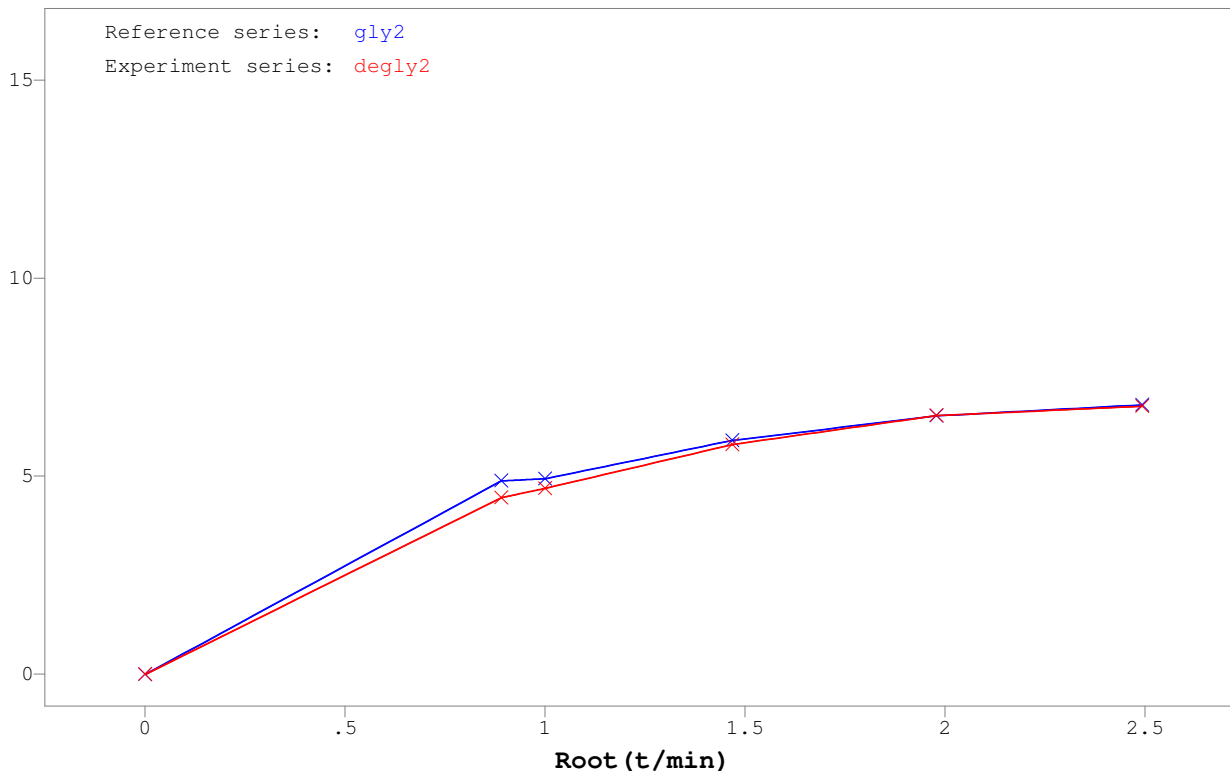
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.006	9.015	0.00	0.00	0.00	0.00
0.5	9.002	9.003	30.53	27.89	4.89	4.46
1.0	9.001	9.008	30.88	29.37	4.94	4.70
10.0	8.998	9.001	36.93	36.28	5.91	5.80
60.0	8.995	8.997	40.80	40.84	6.53	6.53
240.0	8.996	9.009	42.54	42.31	6.81	6.77

Score1 (DU sum): **1.30**
 Score2 (DU Profile): 1.08
DU sum difference (u): -0.80

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC001-020**
 Exchangeable protons: 18
 Index lis-file: 90
 Sequence: EVQGVESGGGLVKPGGSLKL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

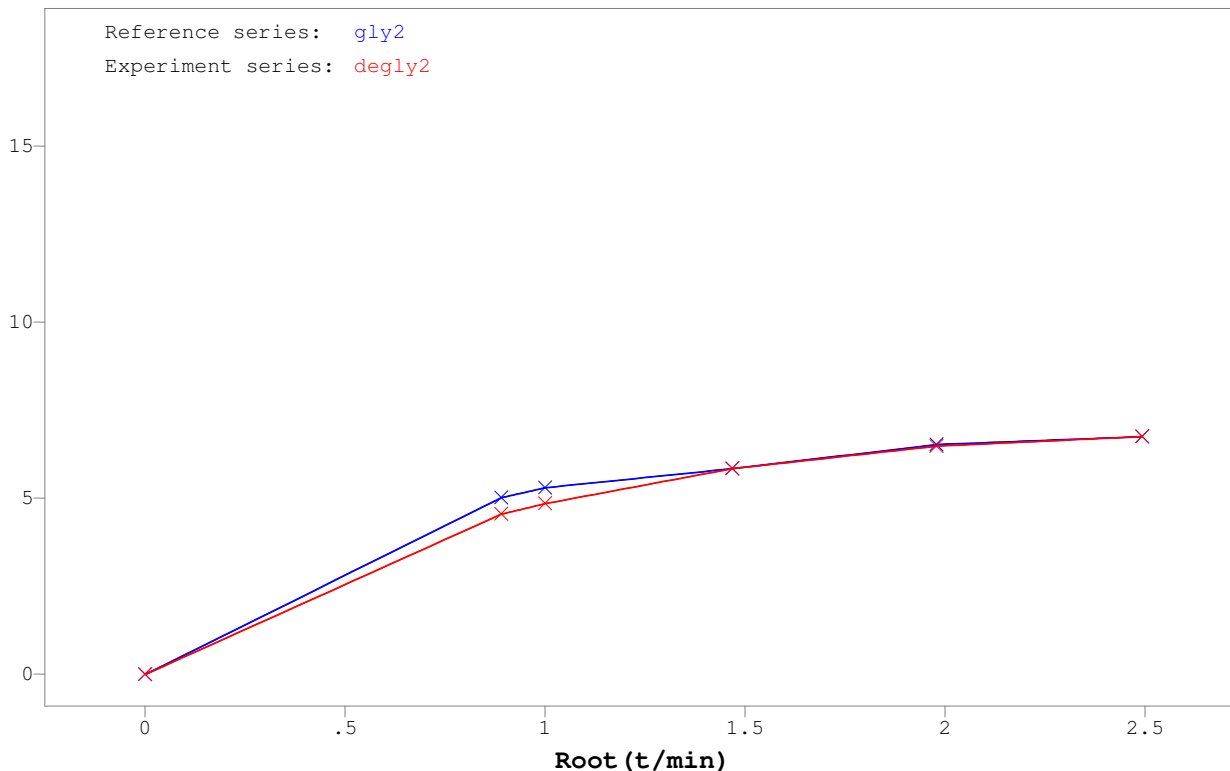
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.593	9.594	0.00	0.00	0.00	0.00
0.5	9.603	9.596	27.88	25.28	5.02	4.55
1.0	9.621	9.596	29.46	26.95	5.30	4.85
10.0	9.597	9.607	32.47	32.47	5.84	5.84
60.0	9.585	9.598	36.27	36.01	6.53	6.48
240.0	9.591	9.606	37.53	37.53	6.75	6.75

Score1 (DU sum): **1.40**

Score2 (DU Profile): 1.14

DU sum difference (u): -0.97

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC001-023**
 Exchangeable protons: 21
 Index lis-file: 91
 Sequence: EVQGVESGGGLVKPGGSLKLSKA
 Range: 1 / 1

Reference: reference series, experiment: experiment series

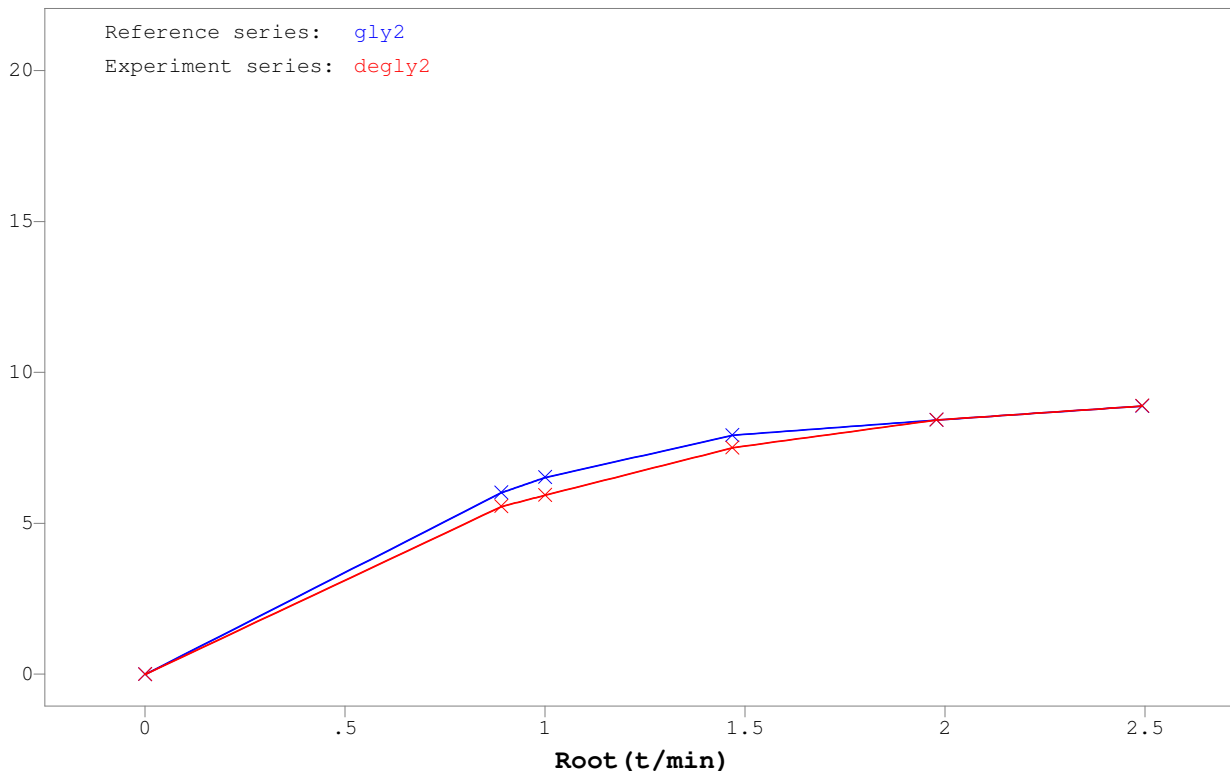
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.384	9.395	0.00	0.00	0.00	0.00
0.5	9.393	9.389	28.67	26.49	6.02	5.56
1.0	9.407	9.392	31.09	28.29	6.53	5.94
10.0	9.387	9.386	37.73	35.76	7.92	7.51
60.0	9.382	9.393	40.13	40.13	8.43	8.43
240.0	9.405	9.403	42.33	42.34	8.89	8.89

Score1 (DU sum): **1.42**
 Score2 (DU Profile): 1.28
DU sum difference (u): -1.25

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC027-031**
 Exchangeable protons: 4
 Index lis-file: 96
 Sequence: FTFS D
 Range: 1 / 1

Reference: reference series, experiment: experiment series

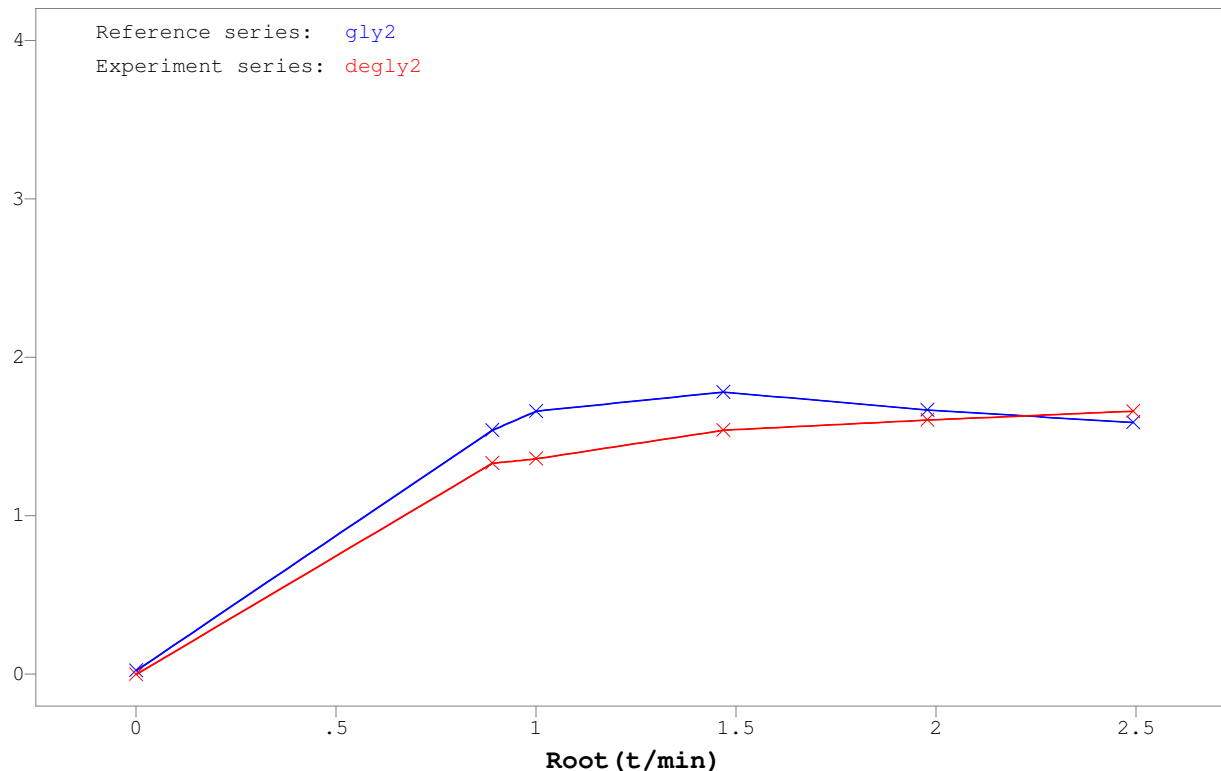
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.171	10.172	0.60	0.00	0.02	0.00
0.5	10.178	10.183	38.53	33.31	1.54	1.33
1.0	10.189	10.169	41.54	34.02	1.66	1.36
10.0	10.183	10.183	44.55	38.53	1.78	1.54
60.0	10.175	10.178	41.74	40.13	1.67	1.61
240.0	10.188	10.177	39.73	41.54	1.59	1.66

Score1 (DU sum): **3.75**
 Score2 (DU Profile): 4.28
DU sum difference (u): -0.63

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC036-047**
 Exchangeable protons: 10
 Index lis-file: 99
 Sequence: WVRQIPEKRLEW
 Range: 1 / 1

Reference: reference series, experiment: experiment series

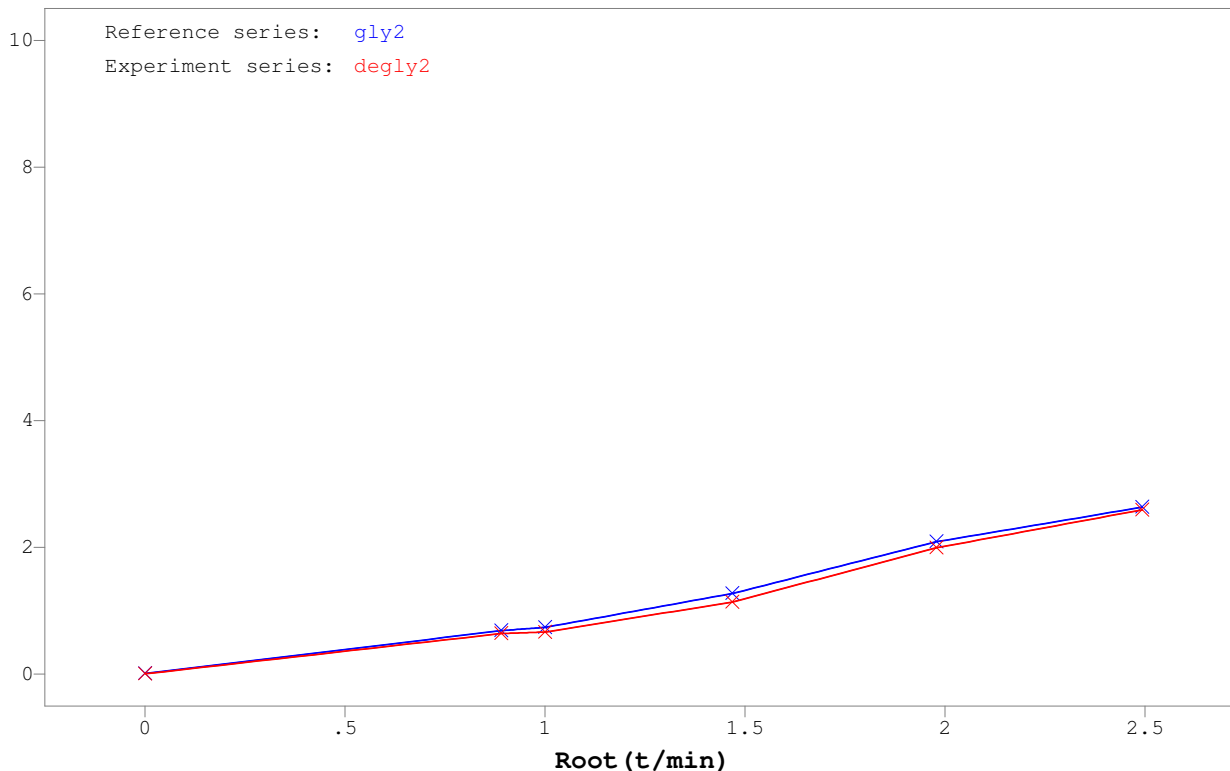
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.826	8.841	0.14	0.09	0.01	0.01
0.5	8.829	8.826	6.90	6.45	0.69	0.65
1.0	8.836	8.829	7.43	6.69	0.74	0.67
10.0	8.834	8.840	12.77	11.42	1.28	1.14
60.0	8.834	8.835	20.94	19.99	2.09	2.00
240.0	8.839	8.847	26.39	25.98	2.64	2.60

Score1 (DU sum): **1.03**
 Score2 (DU Profile): 0.84
DU sum difference (u): -0.40

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC036-049**
 Exchangeable protons: 12
 Index lis-file: 100
 Sequence: WVRQIPEKRLEWVA
 Range: 1 / 1

Reference: reference series, experiment: experiment series

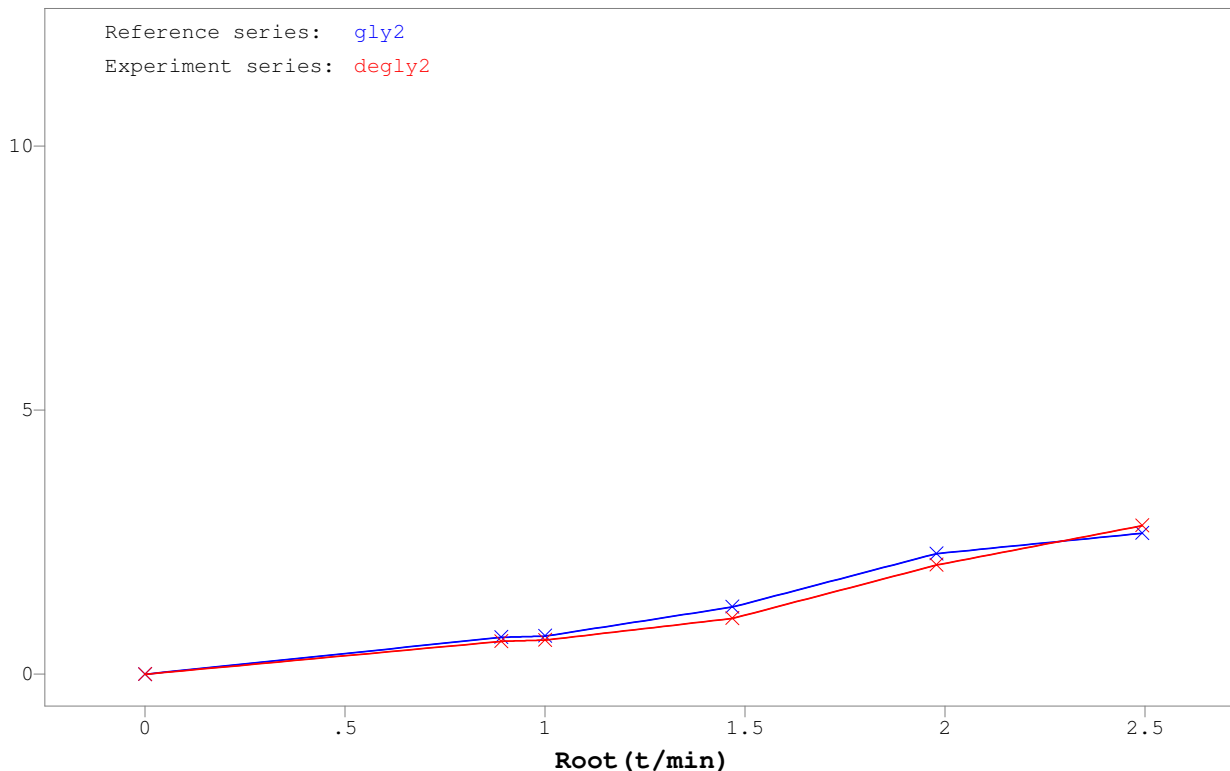
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.248	9.243	0.02	0.02	0.00	0.00
0.5	9.251	9.246	5.85	5.22	0.70	0.63
1.0	9.266	9.246	6.04	5.42	0.72	0.65
10.0	9.253	9.246	10.64	8.83	1.28	1.06
60.0	9.264	9.259	19.06	17.26	2.29	2.07
240.0	9.250	9.262	22.27	23.48	2.67	2.82

Score1 (DU sum): 0.96
 Score2 (DU Profile): **1.29**
 DU sum difference (u): -0.44

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC051-068**
 Exchangeable protons: 16
 Index lis-file: 102
 Sequence: ISDGGSYTYYPDSVKGRF
 Range: 1 / 1

Reference: reference series, experiment: experiment series

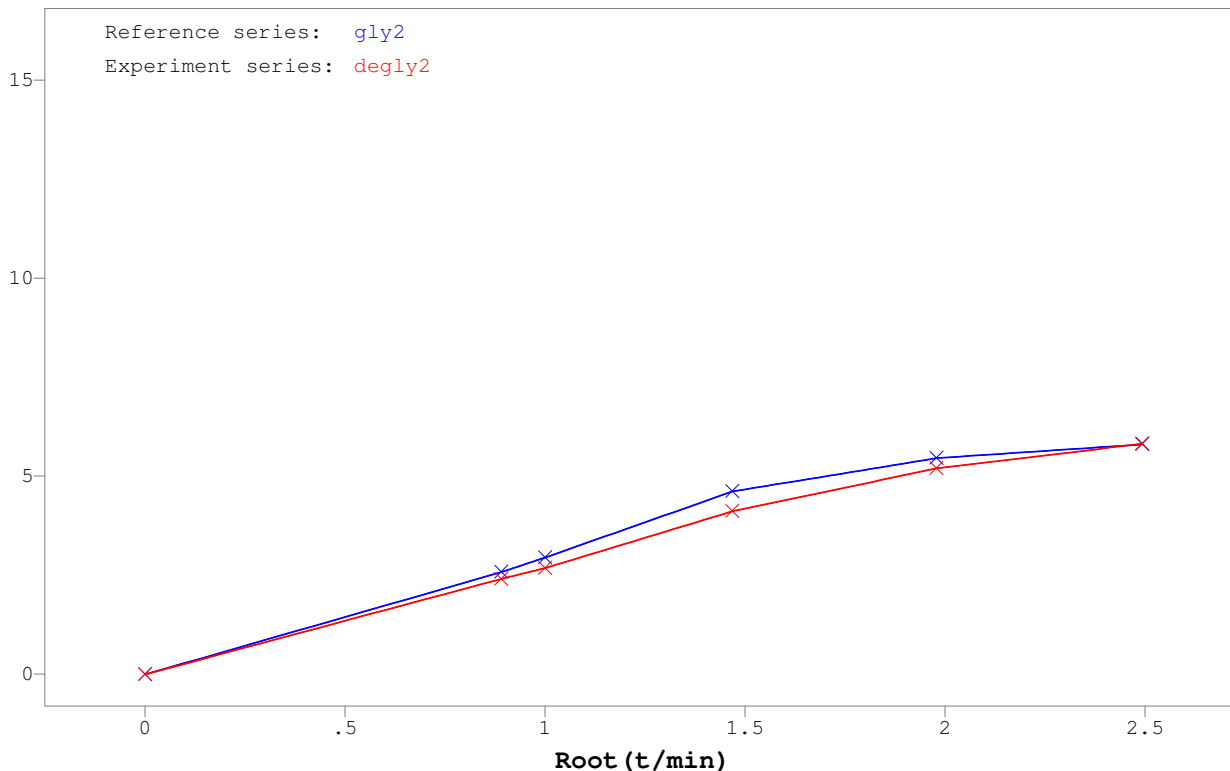
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.696	9.720	0.00	0.00	0.00	0.00
0.5	9.712	9.713	16.14	15.08	2.58	2.41
1.0	9.730	9.702	18.46	16.79	2.95	2.69
10.0	9.715	9.714	28.87	25.74	4.62	4.12
60.0	9.697	9.702	34.13	32.52	5.46	5.20
240.0	9.704	9.719	36.30	36.40	5.81	5.82

Score1 (DU sum): **1.21**
 Score2 (DU Profile): 1.13
DU sum difference (u): -0.81

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC057-068**
 Exchangeable protons: 10
 Index lis-file: 104
 Sequence: YTYYPDSVKGRF
 Range: 1 / 1

Reference: reference series, experiment: experiment series

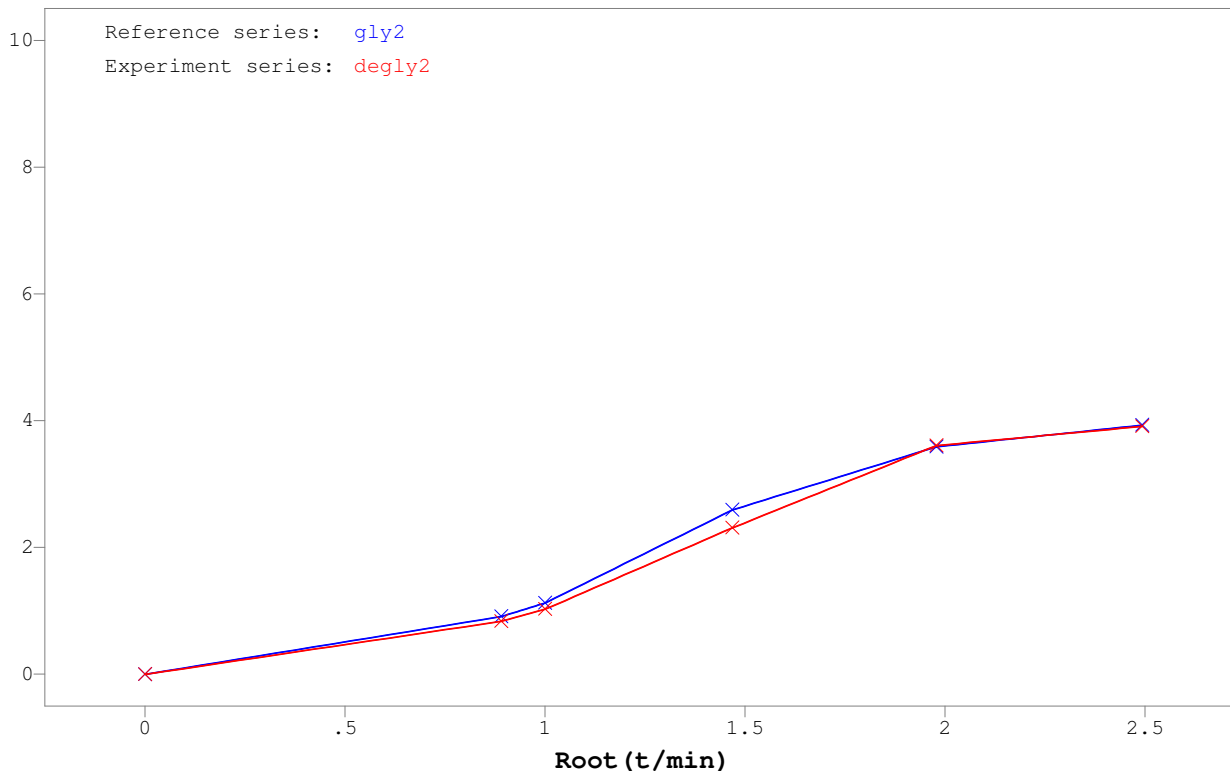
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.025	9.029	0.00	0.00	0.00	0.00
0.5	9.031	9.032	9.14	8.37	0.91	0.84
1.0	9.038	9.034	11.28	10.29	1.13	1.03
10.0	9.035	9.031	25.96	23.13	2.60	2.31
60.0	9.026	9.028	35.92	36.12	3.59	3.61
240.0	9.040	9.043	39.33	39.13	3.93	3.91

Score1 (DU sum): 0.91
 Score2 (DU Profile): **1.03**
 DU sum difference (u): -0.43

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC057-079**
 Exchangeable protons: 21
 Index lis-file: 105
 Sequence: YTYYPDSVKGRFTISRDNAKNNL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

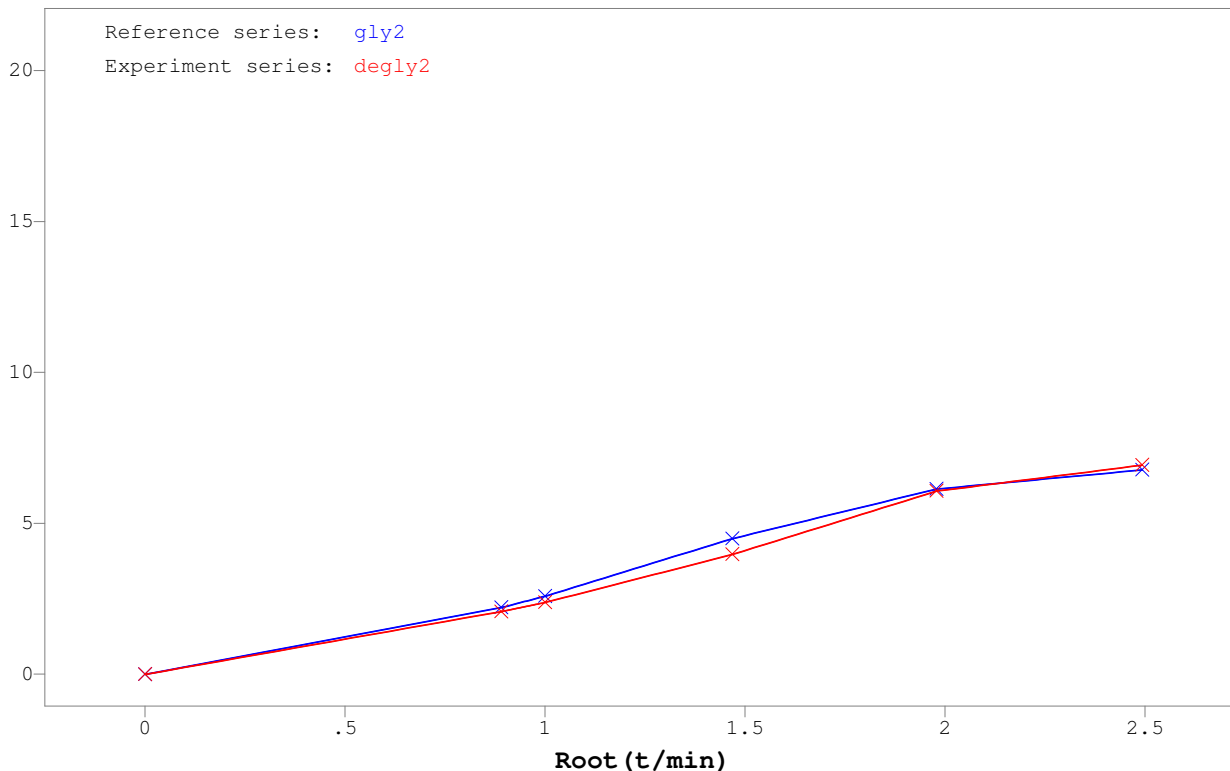
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.737	8.741	0.00	0.00	0.00	0.00
0.5	8.733	8.739	10.55	9.93	2.22	2.08
1.0	8.749	8.747	12.35	11.36	2.59	2.39
10.0	8.740	8.732	21.44	18.93	4.50	3.98
60.0	8.729	8.728	29.26	28.93	6.15	6.08
240.0	8.739	8.828	32.28	33.03	6.78	6.94

Score1 (DU sum): 0.67
 Score2 (DU Profile): **1.11p**
 DU sum difference (u): -0.66

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC069-080**
 Exchangeable protons: 11
 Index lis-file: 108
 Sequence: TISRDNAKNNLY
 Range: 1 / 1

Reference: reference series, experiment: experiment series

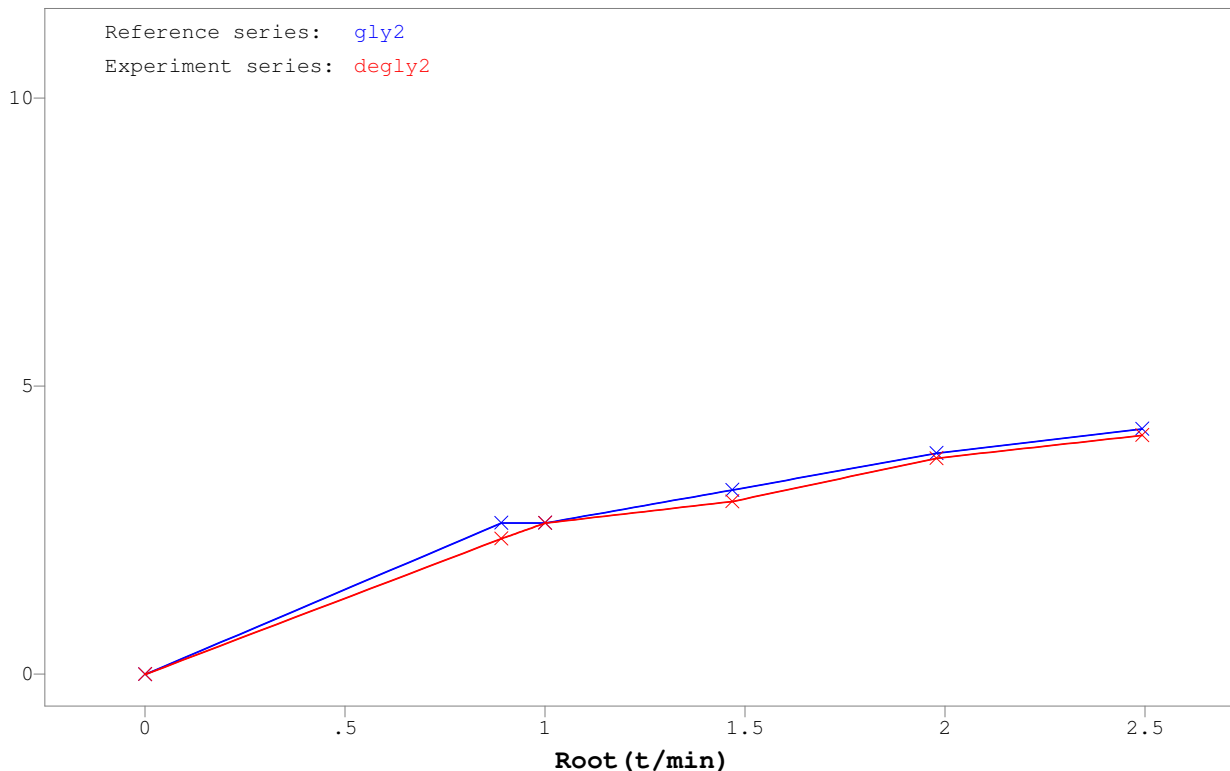
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.160	6.162	0.00	0.00	0.00	0.00
0.5	6.164	6.164	23.88	21.41	2.63	2.36
1.0	6.176	6.157	23.88	23.88	2.63	2.63
10.0	6.162	6.157	29.10	27.29	3.20	3.00
60.0	6.152	6.154	34.92	34.11	3.84	3.75
240.0	6.160	6.171	38.73	37.73	4.26	4.15

Score1 (DU sum): **1.03**
 Score2 (DU Profile): 0.92
DU sum difference (u): -0.48

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC094-109**
 Exchangeable protons: 15
 Index lis-file: 114
 Sequence: YYCARDKAYYGNYGDA
 Range: 1 / 1

Reference: reference series, experiment: experiment series

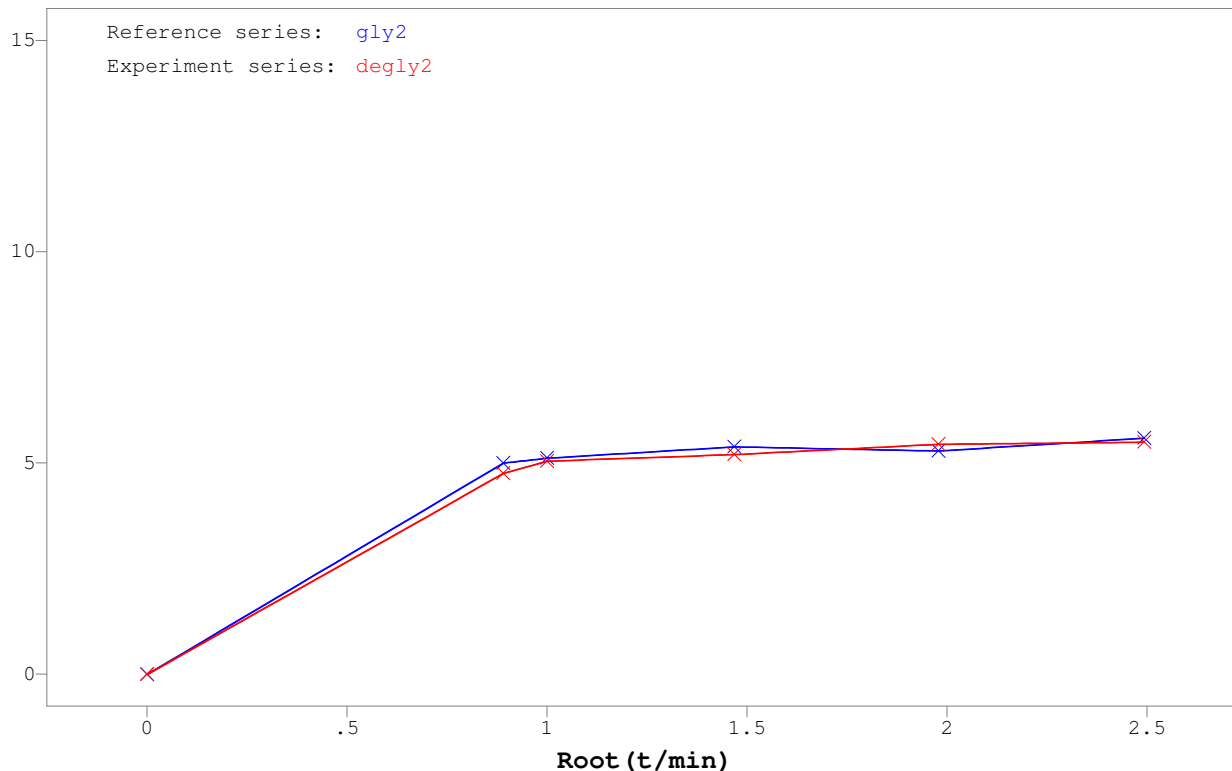
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.854	7.867	0.00	0.00	0.00	0.00
0.5	7.855	7.859	33.34	31.70	5.00	4.75
1.0	7.861	7.858	34.12	33.65	5.12	5.05
10.0	7.858	7.855	35.90	34.69	5.39	5.20
60.0	7.851	7.856	35.25	36.31	5.29	5.45
240.0	7.855	7.866	37.27	36.64	5.59	5.50

Score1 (DU sum): 0.76
 Score2 (DU Profile): **1.07**
 DU sum difference (u): -0.44

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC094-137**
 Exchangeable protons: 39
 Index lis-file: 116
 Sequence: YYCARDKAYYGNYGDAMDYWGQTSVTVSSAKTTPPSVYPLAPG
 Range: 1 / 1

Reference: reference series, experiment: experiment series

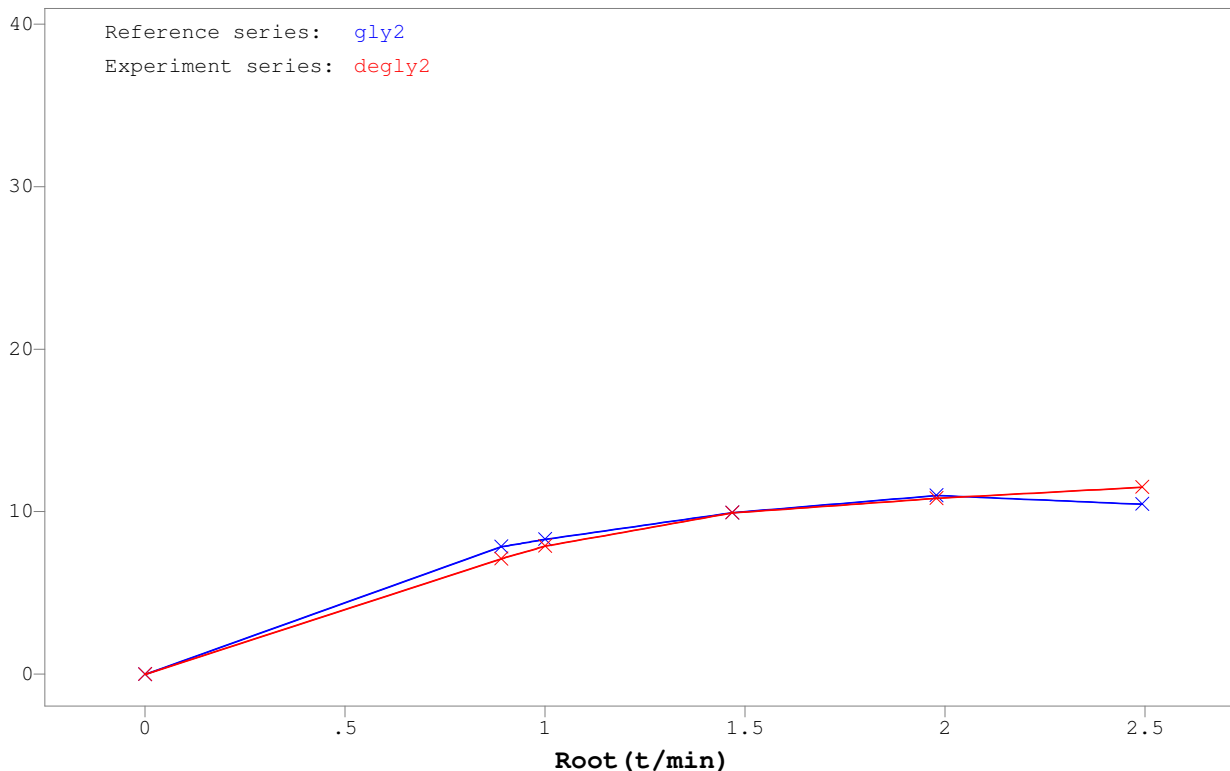
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.703	9.689	0.00	0.00	0.00	0.00
0.5	9.695	9.697	20.14	18.26	7.86	7.12
1.0	9.706	9.688	21.32	20.25	8.32	7.90
10.0	9.695	9.688	25.52	25.49	9.95	9.94
60.0	9.680	9.684	28.24	27.79	11.01	10.84
240.0	9.693	9.694	26.86	29.54	10.48	11.52

Score1 (DU sum): 0.20
 Score2 (DU Profile): **1.30**
 DU sum difference (u): -0.30

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC095-112**
 Exchangeable protons: 17
 Index lis-file: 210
 Sequence: YCARDKAYYGNYGDAMDY
 Range: 1 / 1

Reference: reference series, experiment: experiment series

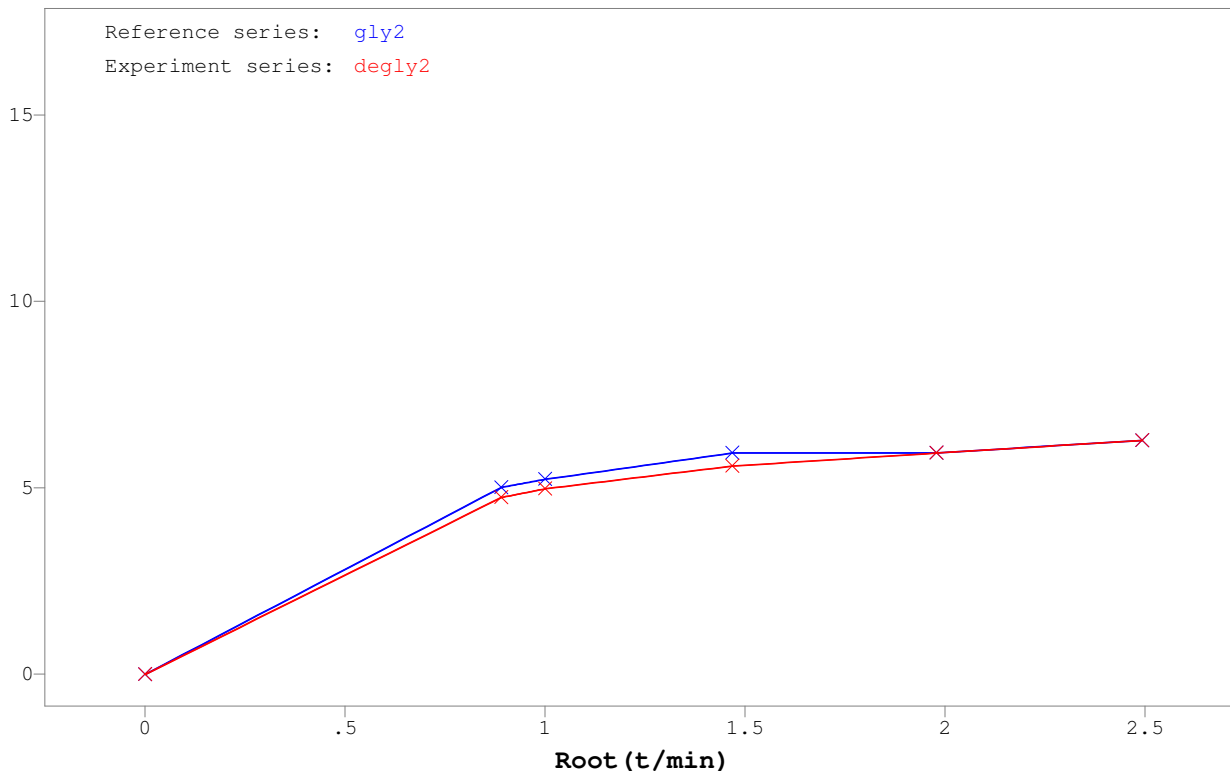
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.680	8.680	0.00	0.00	0.00	0.00
0.5	8.689	8.677	29.50	27.91	5.02	4.74
1.0	8.691	8.683	30.77	29.28	5.23	4.98
10.0	8.680	8.676	34.92	32.87	5.94	5.59
60.0	8.690	8.677	34.92	34.92	5.94	5.94
240.0	8.680	8.664	36.93	36.92	6.28	6.28

Score1 (DU sum): **1.35**
 Score2 (DU Profile): 1.10
DU sum difference (u): -0.88

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC111-120**
 Exchangeable protons: 9
 Index lis-file: 118
 Sequence: DYWGQGTSTV
 Range: 1 / 1

Reference: reference series, experiment: experiment series

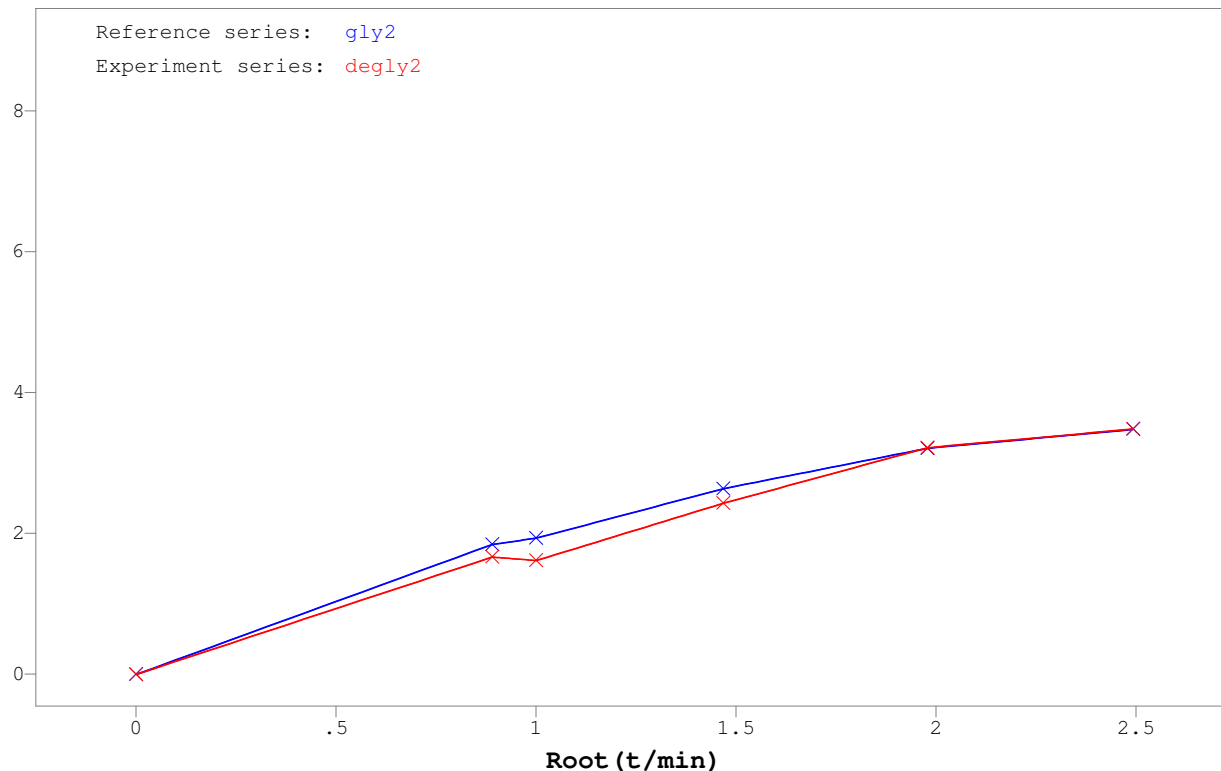
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.274	10.283	0.00	0.00	0.00	0.00
0.5	10.274	10.286	20.51	18.51	1.85	1.67
1.0	10.288	10.289	21.50	17.96	1.94	1.62
10.0	10.269	10.282	29.31	27.01	2.64	2.43
60.0	10.269	10.284	35.68	35.77	3.21	3.22
240.0	10.288	10.288	38.66	38.73	3.48	3.49

Score1 (DU sum): **1.62**
 Score2 (DU Profile): 1.53
DU sum difference (u): -0.61

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC112-120**
 Exchangeable protons: 8
 Index lis-file: 120
 Sequence: YWGQGSVT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

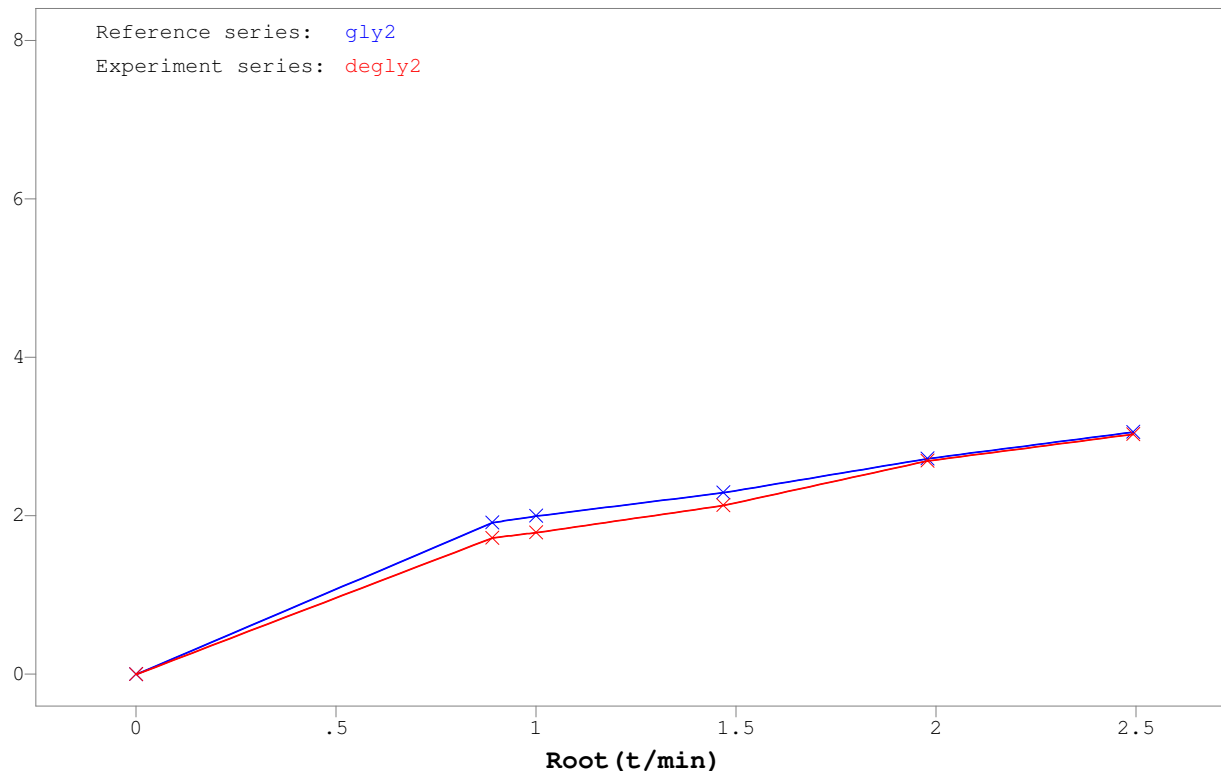
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.782	9.784	0.00	0.00	0.00	0.00
0.5	9.774	9.778	23.95	21.53	1.92	1.72
1.0	9.786	9.788	24.98	22.37	2.00	1.79
10.0	9.772	9.779	28.67	26.65	2.29	2.13
60.0	9.776	9.783	34.04	33.68	2.72	2.69
240.0	9.785	9.790	38.25	37.90	3.06	3.03

Score1 (DU sum): **2.02**
 Score2 (DU Profile): 1.65
DU sum difference (u): -0.62

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC112-139**
 Exchangeable protons: 23
 Index lis-file: 121
 Sequence: YWGQGSVTVSSAKTTPPSVYPLAPGSA
 Range: 1 / 1

Reference: reference series, experiment: experiment series

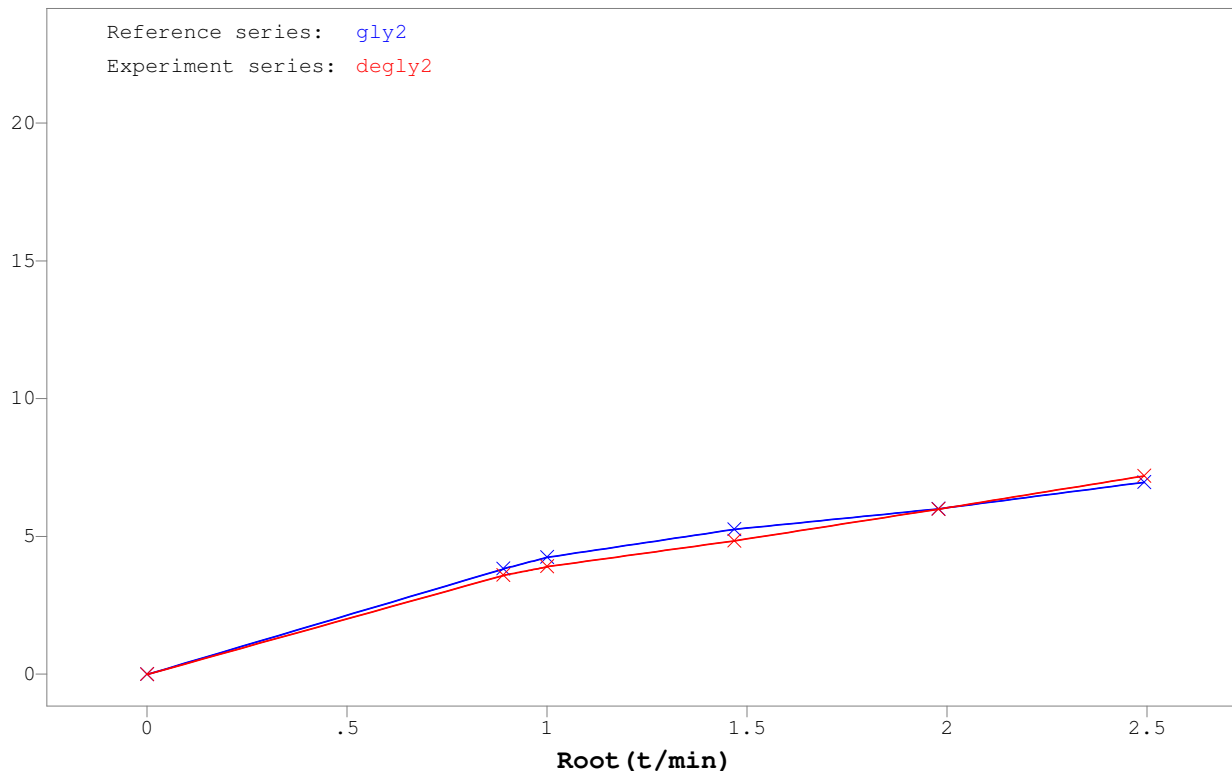
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.048	11.063	0.00	0.00	0.00	0.00
0.5	11.063	11.073	16.65	15.64	3.83	3.60
1.0	11.079	11.060	18.46	17.00	4.25	3.91
10.0	11.059	11.066	22.88	21.07	5.26	4.85
60.0	11.061	11.062	26.11	26.07	6.01	6.00
240.0	11.057	11.069	30.30	31.30	6.97	7.20

Score1 (DU sum): 0.86
 Score2 (DU Profile): **1.13**
 DU sum difference (u): -0.76

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC115-140**
 Exchangeable protons: 21
 Index lis-file: 212
 Sequence: QGTSVTVSSAKITPPSVYPLAPGSAA
 Range: 1 / 1

Reference: reference series, experiment: experiment series

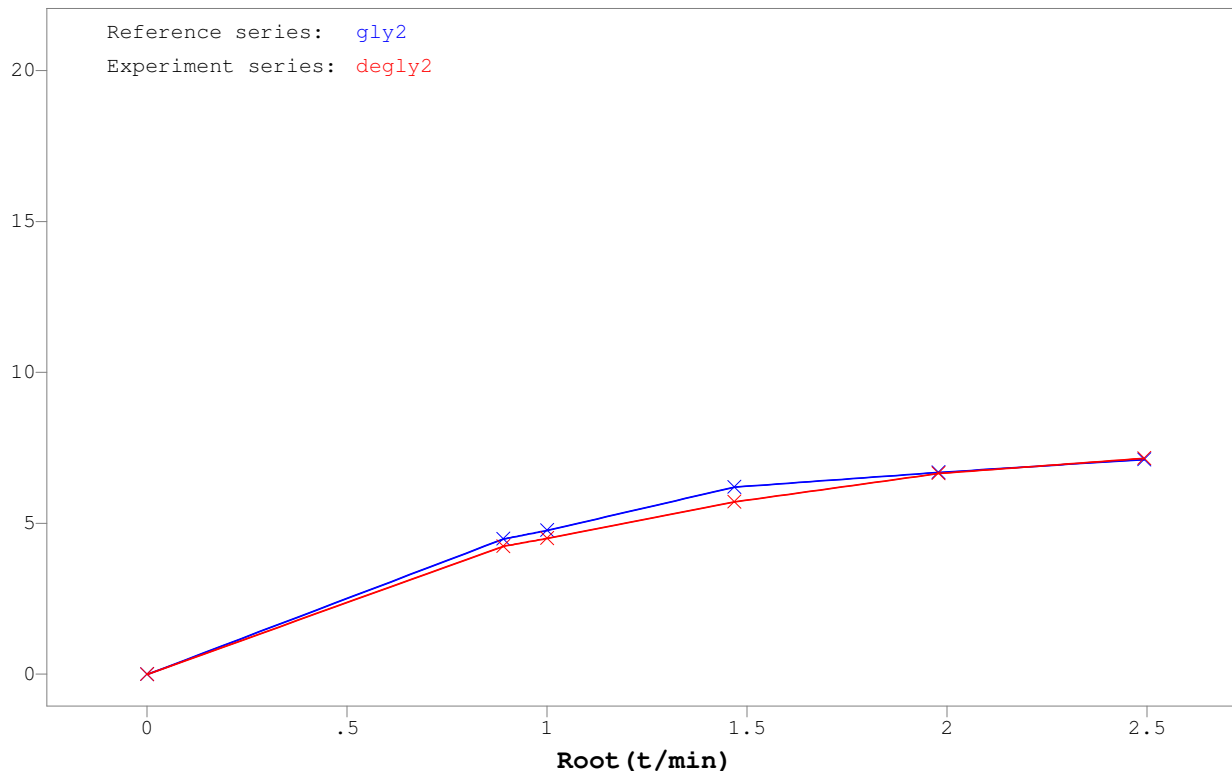
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.579	10.590	0.00	0.00	0.00	0.00
0.5	10.623	10.616	21.37	20.23	4.49	4.25
1.0	10.645	10.611	22.73	21.46	4.77	4.51
10.0	10.611	10.603	29.57	27.24	6.21	5.72
60.0	10.599	10.609	31.89	31.72	6.70	6.66
240.0	10.615	10.615	33.93	34.11	7.12	7.16

Score1 (DU sum): **1.02**
 Score2 (DU Profile): 1.01
DU sum difference (u): -0.90

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC118-156**
 Exchangeable protons: 34
 Index lis-file: 125
 Sequence: SVTVSSAKTTPPSVYPLAPGSAAQNSMVTLGCLVKGYF
 Range: 1 / 1

Reference: reference series, experiment: experiment series

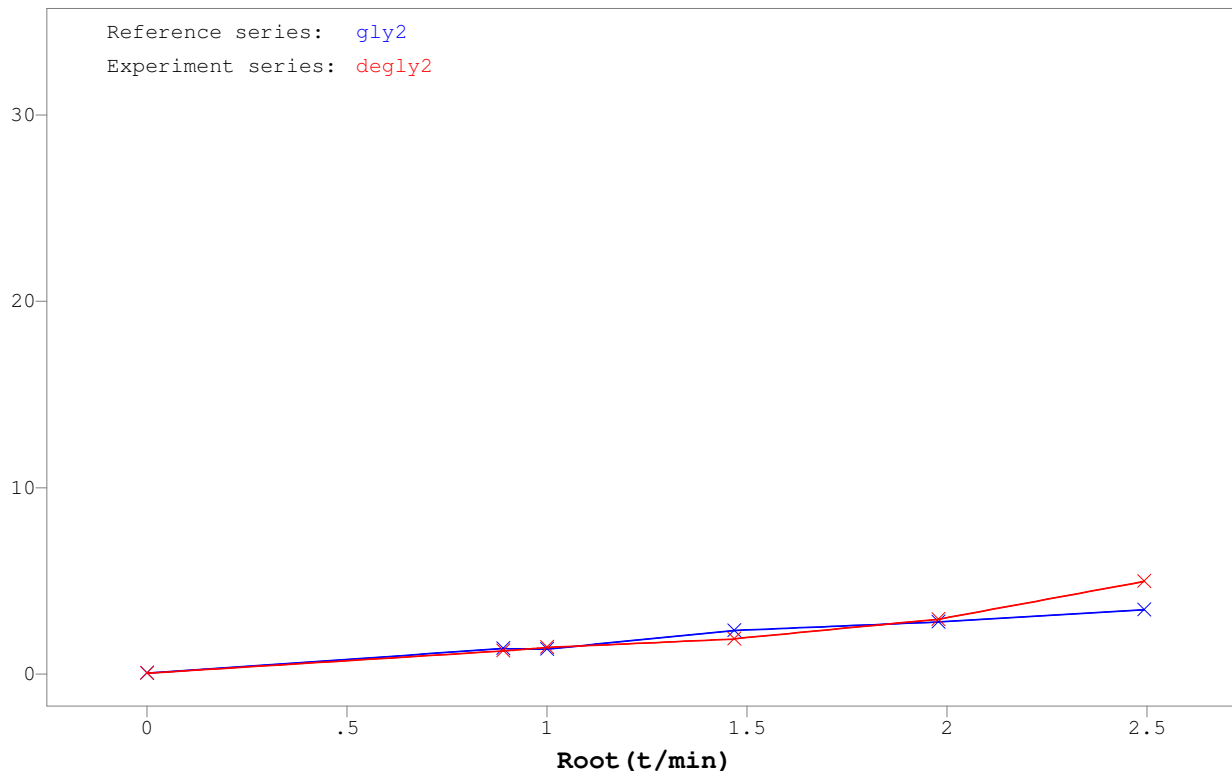
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.818	10.821	0.22	0.20	0.08	0.07
0.5	10.830	10.831	4.11	3.73	1.40	1.27
1.0	10.840	10.825	4.00	4.29	1.36	1.46
10.0	10.825	10.825	6.92	5.62	2.35	1.91
60.0	10.832	10.835	8.27	8.70	2.81	2.96
240.0	10.831	10.823	10.18	14.67	3.46	4.99

Score1 (DU sum): 0.92
 Score2 (DU Profile): **1.47**
 DU sum difference (u): 1.20

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC121-145**
 Exchangeable protons: 20
 Index lis-file: 131
 Sequence: VSSAKTTPPSVYPLAPGSAAQTNSM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

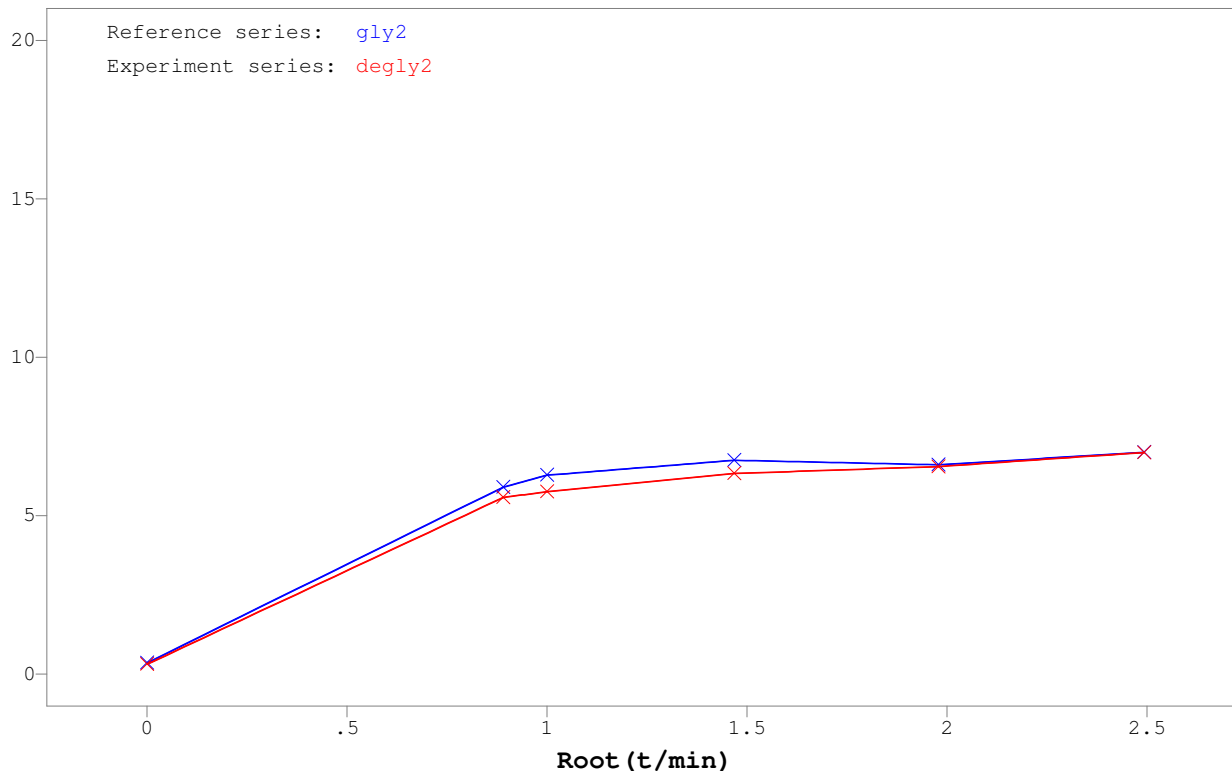
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.406	9.389	1.84	1.62	0.37	0.32
0.5	9.383	9.387	29.56	27.94	5.91	5.59
1.0	9.389	9.373	31.44	28.83	6.29	5.77
10.0	9.378	9.391	33.79	31.71	6.76	6.34
60.0	9.380	9.387	33.07	32.79	6.61	6.56
240.0	9.396	9.393	35.06	35.02	7.01	7.00

Score1 (DU sum): **1.79p**

Score2 (DU Profile): 1.46p

DU sum difference (u): **-1.37**

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC132-184**
 Exchangeable protons: 47
 Index lis-file: 213
 Sequence: YPLAPGSAAQTNSMVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFFPAVLQSDL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

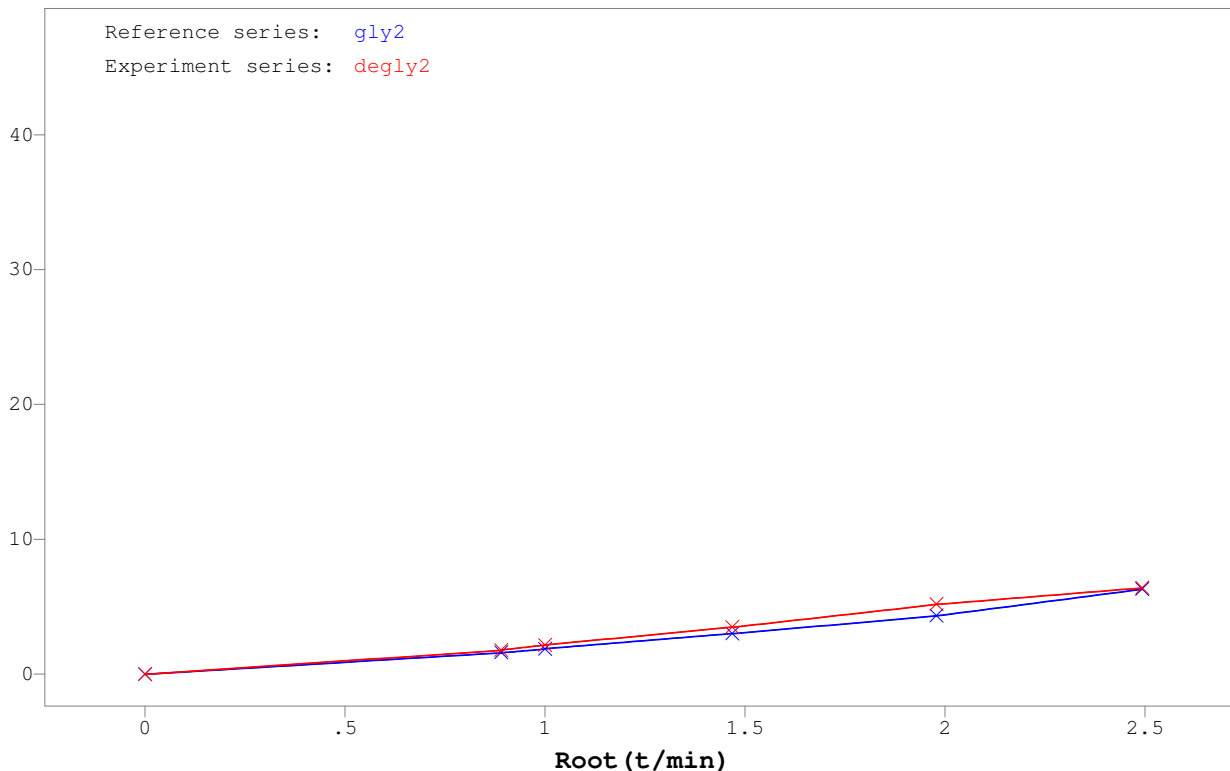
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.644	11.594	0.00	0.00	0.00	0.00
0.5	11.625	11.576	3.41	3.81	1.60	1.79
1.0	11.583	11.577	4.01	4.62	1.89	2.17
10.0	11.581	11.565	6.42	7.42	3.02	3.49
60.0	11.622	11.581	9.23	11.04	4.34	5.19
240.0	11.571	11.579	13.44	13.65	6.32	6.41

Score1 (DU sum): **1.05**
 Score2 (DU Profile): 0.85
DU sum difference (u): 1.89

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC163-180**
 Exchangeable protons: 16
 Index lis-file: 218
 Sequence: TWNSGSLSSGVHTFPAVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

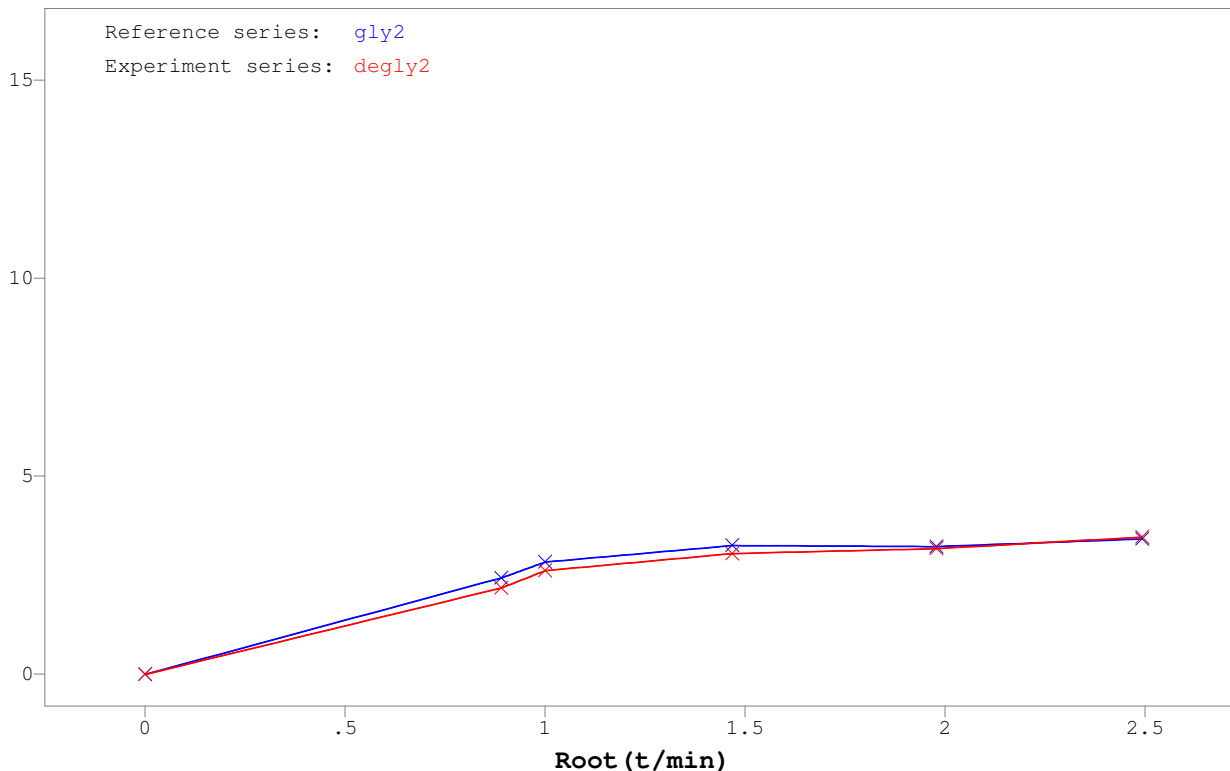
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.702	12.717	0.00	0.00	0.00	0.00
0.5	12.712	12.723	15.23	13.64	2.44	2.18
1.0	12.722	12.703	17.73	16.37	2.84	2.62
10.0	12.706	12.701	20.33	19.06	3.25	3.05
60.0	12.704	12.722	20.17	19.84	3.23	3.17
240.0	12.719	12.715	21.37	21.67	3.42	3.47

Score1 (DU sum): **1.10**
 Score2 (DU Profile): 1.03
DU sum difference (u): -0.68

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC164-180**
 Exchangeable protons: 15
 Index lis-file: 219
 Sequence: WNSGSLSSGVHTFPAVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

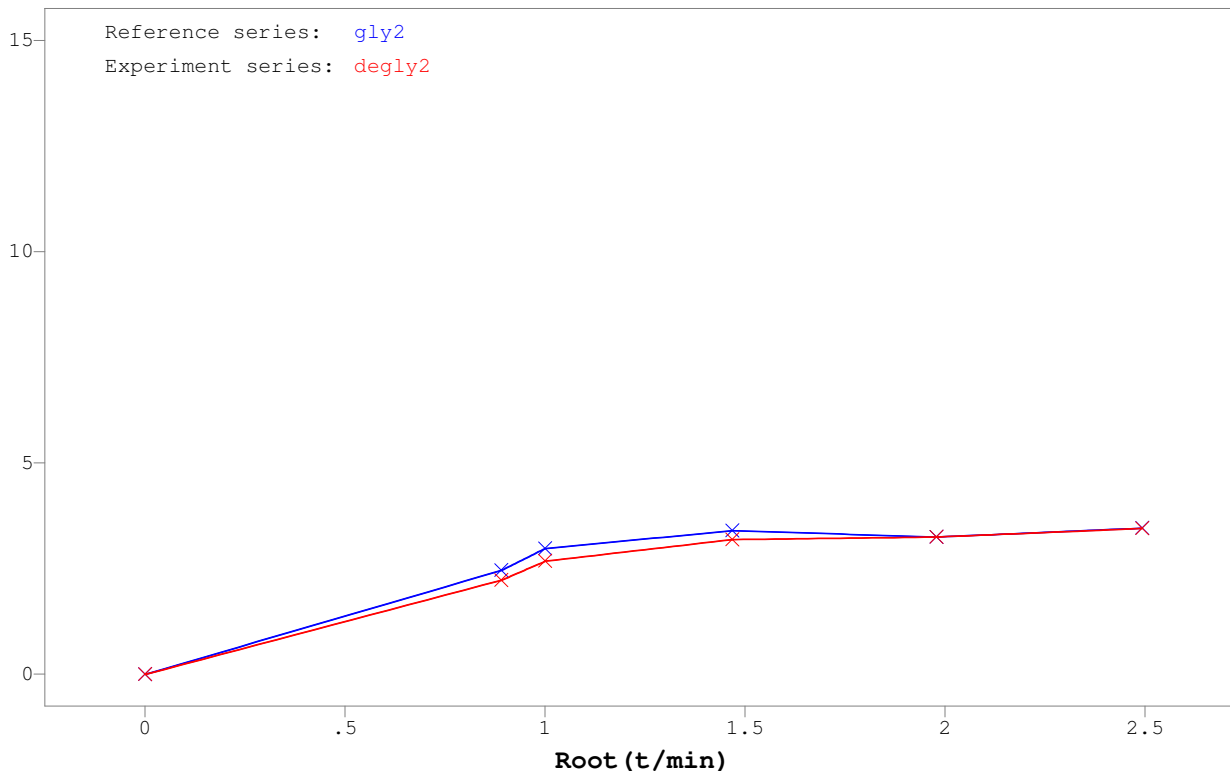
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.602	12.615	0.00	0.00	0.00	0.00
0.5	12.600	12.609	16.40	14.85	2.46	2.23
1.0	12.603	12.605	19.87	17.86	2.98	2.68
10.0	12.583	12.598	22.68	21.27	3.40	3.19
60.0	12.592	12.620	21.67	21.67	3.25	3.25
240.0	12.603	12.615	23.08	23.03	3.46	3.45

Score1 (DU sum): **1.31**
 Score2 (DU Profile): 1.07
DU sum difference (u): -0.75

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC170-180**
 Exchangeable protons: 9
 Index lis-file: 140
 Sequence: SSGVHTFPAVL
 Range: 1 / 2

Reference: reference series, experiment: experiment series

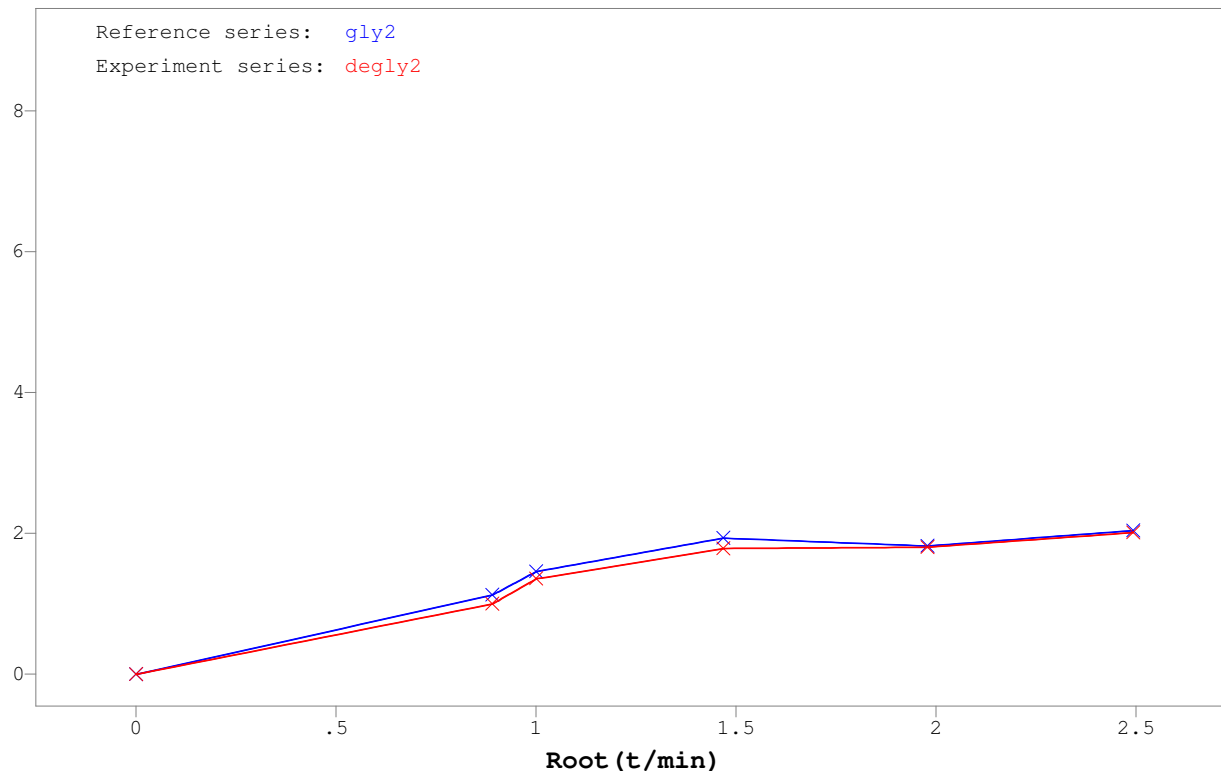
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.853	10.855	0.00	0.00	0.00	0.00
0.5	10.856	10.856	12.52	11.11	1.13	1.00
1.0	10.860	10.856	16.22	15.08	1.46	1.36
10.0	10.847	10.858	21.50	19.87	1.94	1.79
60.0	10.846	10.862	20.26	20.07	1.82	1.81
240.0	10.860	10.863	22.70	22.37	2.04	2.01

Score1 (DU sum): **1.23**
 Score2 (DU Profile): 1.00
DU sum difference (u): -0.42

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC191-201**
 Exchangeable protons: 8
 Index lis-file: 145
 Sequence: VIVPSSTWPSE
 Range: 1 / 1

Reference: reference series, experiment: experiment series

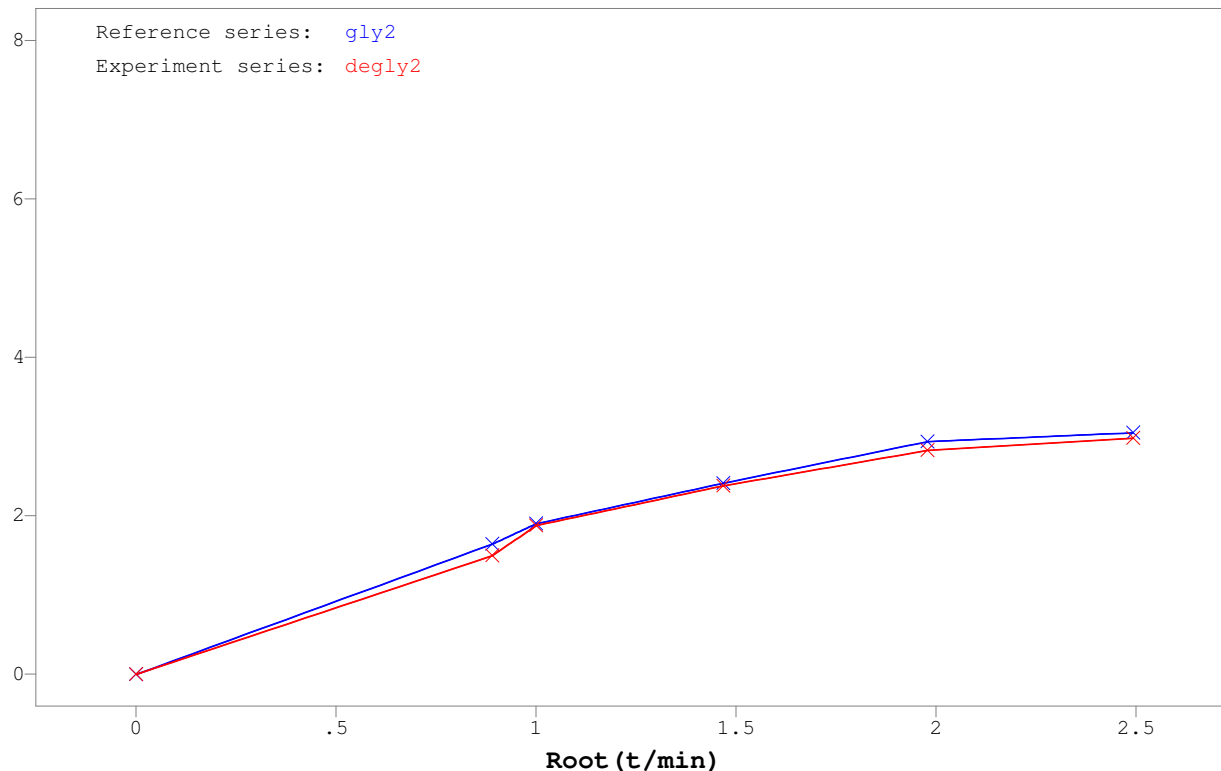
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.963	9.972	0.00	0.00	0.00	0.00
0.5	9.960	9.966	20.55	18.74	1.64	1.50
1.0	9.968	9.962	23.78	23.49	1.90	1.88
10.0	9.957	9.965	30.17	29.75	2.41	2.38
60.0	9.958	9.965	36.73	35.35	2.94	2.83
240.0	9.972	9.974	38.13	37.27	3.05	2.98

Score1 (DU sum): **1.24**
 Score2 (DU Profile): 1.01
DU sum difference (u): -0.38

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC214-225**
 Exchangeable protons: 10
 Index lis-file: 147
 Sequence: TKVDKKIVPRDC
 Range: 1 / 1

Reference: reference series, experiment: experiment series

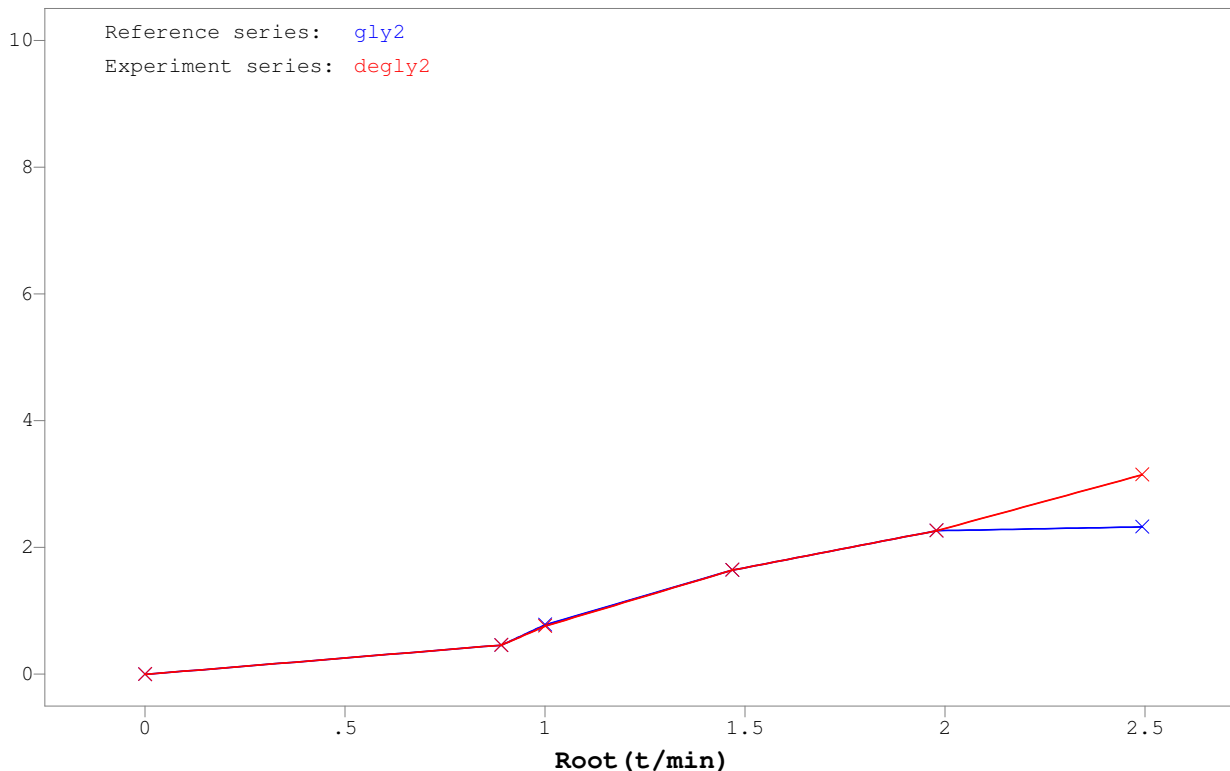
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.822	9.822	0.00	0.00	0.00	0.00
0.5	9.822	9.826	4.62	4.62	0.46	0.46
1.0	9.836	9.834	7.83	7.63	0.78	0.76
10.0	9.823	9.825	16.46	16.46	1.65	1.65
60.0	9.813	9.823	22.68	22.68	2.27	2.27
240.0	9.820	9.829	23.28	31.51	2.33	3.15

Score1 (DU sum): **2.09**
 Score2 (DU Profile): 1.79
DU sum difference (u): 0.80

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC240-252**
 Exchangeable protons: 9
 Index lis-file: 223
 Sequence: VFIFPPKPKDVLV
 Range: 1 / 1

Reference: reference series, experiment: experiment series

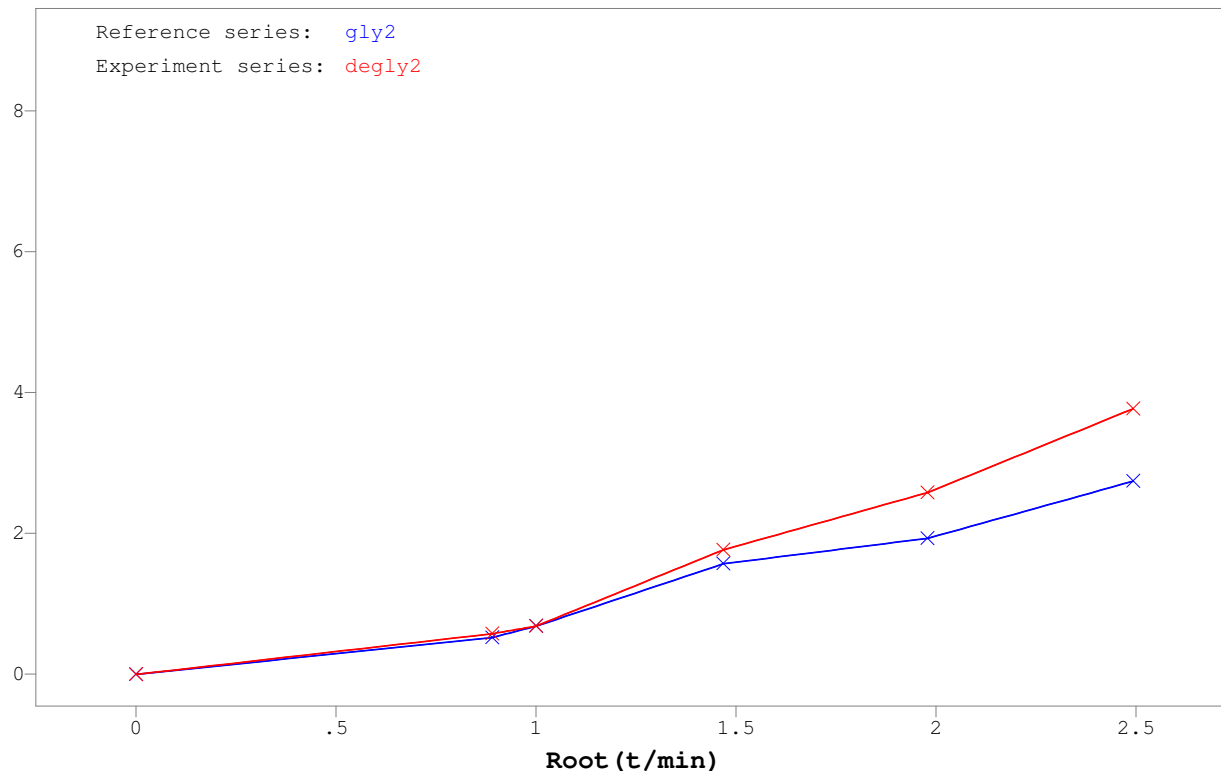
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.388	10.389	0.00	0.00	0.00	0.00
0.5	10.393	10.398	5.82	6.42	0.52	0.58
1.0	10.402	10.433	7.63	7.63	0.69	0.69
10.0	10.386	10.391	17.46	19.67	1.57	1.77
60.0	10.381	10.391	21.47	28.70	1.93	2.58
240.0	10.389	10.396	30.50	41.94	2.75	3.77

Score1 (DU sum): **5.60p**
 Score2 (DU Profile): 4.57p
DU sum difference (u): 1.93

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC241-251**
 Exchangeable protons: 7
 Index lis-file: 150
 Sequence: FIFPPKPKDVL
 Range: 1 / 2

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

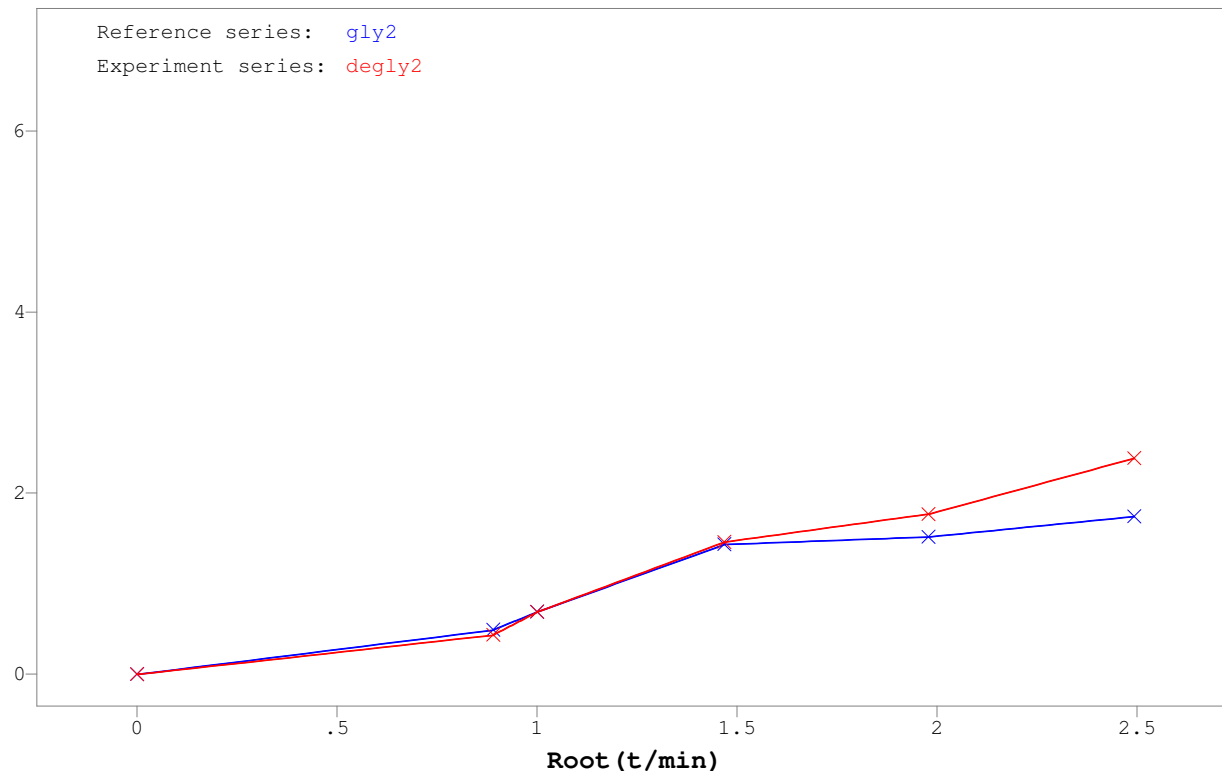
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.416	10.423	0.00	0.00	0.00	0.00
0.5	10.440	10.436	7.02	6.22	0.49	0.44
1.0	10.451	10.443	9.83	9.83	0.69	0.69
10.0	10.433	10.428	20.47	20.87	1.43	1.46
60.0	10.420	10.442	21.67	25.28	1.52	1.77
240.0	10.433	10.442	24.88	34.11	1.74	2.39

Score1 (DU sum): **3.24**

Score2 (DU Profile): 2.99

DU sum difference (u): 0.87

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC241-252**
 Exchangeable protons: 8
 Index lis-file: 224
 Sequence: FIFPPKPKDVLT
 Range: 1 / 2

Reference: reference series, experiment: experiment series

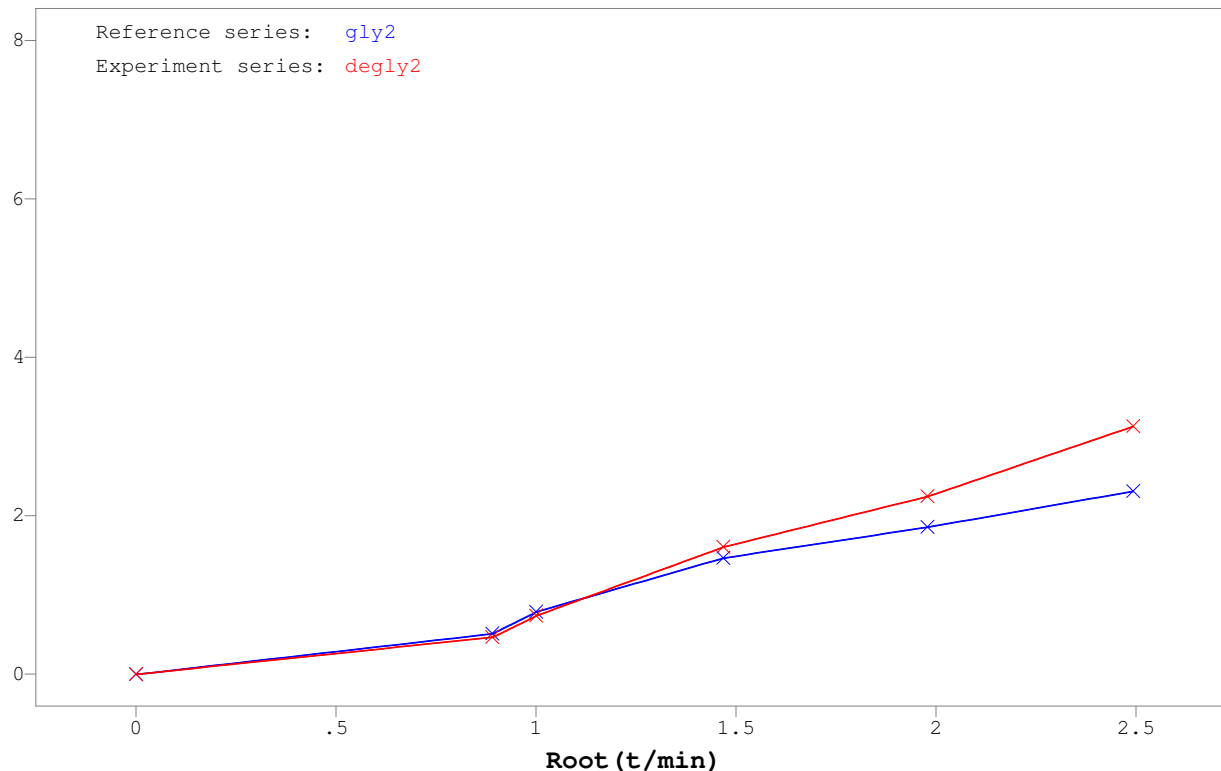
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.822	9.824	0.00	0.00	0.00	0.00
0.5	9.822	9.828	6.42	5.84	0.51	0.47
1.0	9.836	9.835	9.85	9.25	0.79	0.74
10.0	9.823	9.823	18.35	20.09	1.47	1.61
60.0	9.813	9.823	23.22	28.07	1.86	2.25
240.0	9.825	9.828	28.90	39.13	2.31	3.13

Score1 (DU sum): **4.08**
 Score2 (DU Profile): 3.83
DU sum difference (u): 1.25

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC242-252**
 Exchangeable protons: 7
 Index lis-file: 151
 Sequence: IFPPKPKDVLVLT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

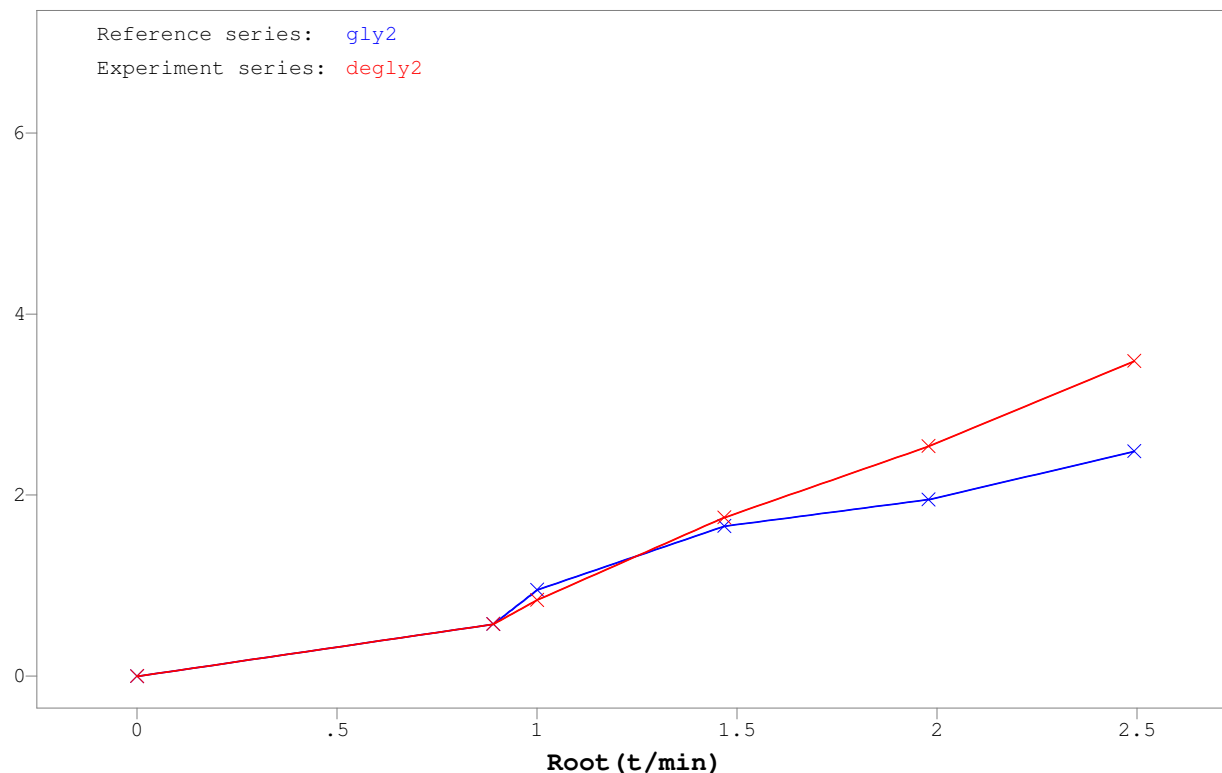
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.826	7.829	0.00	0.00	0.00	0.00
0.5	7.823	7.820	8.23	8.23	0.58	0.58
1.0	7.830	7.825	13.65	12.04	0.96	0.84
10.0	7.823	7.823	23.68	25.08	1.66	1.76
60.0	7.814	7.811	27.89	36.32	1.95	2.54
240.0	7.826	7.826	35.52	49.77	2.49	3.48

Score1 (DU sum): **5.86**
 Score2 (DU Profile): 5.47
DU sum difference (u): 1.57

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC243-251**
 Exchangeable protons: 5
 Index lis-file: 225
 Sequence: FPPKPKDVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

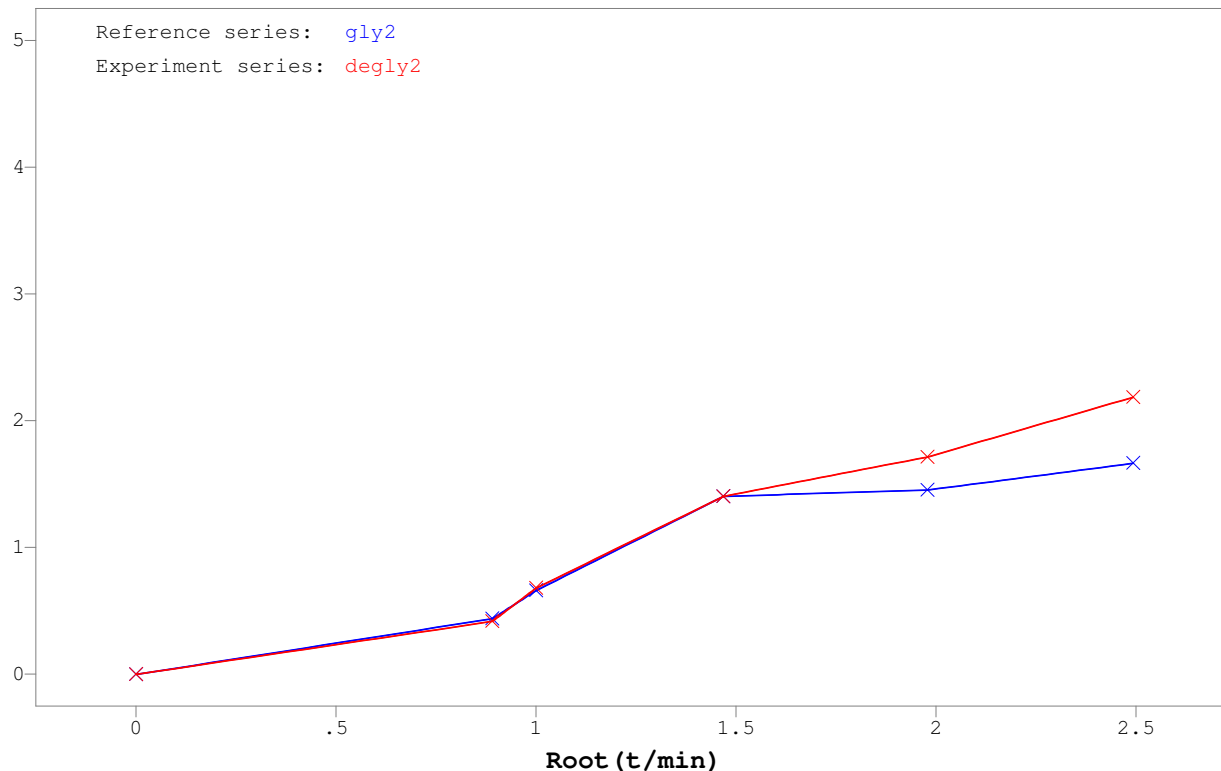
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.424	10.433	0.00	0.00	0.00	0.00
0.5	10.440	10.440	8.79	8.36	0.44	0.42
1.0	10.451	10.451	13.24	13.65	0.66	0.68
10.0	10.440	10.426	28.09	28.09	1.40	1.40
60.0	10.426	10.440	29.10	34.31	1.45	1.72
240.0	10.438	10.440	33.31	43.75	1.67	2.19

Score1 (DU sum): **4.07**
 Score2 (DU Profile): 3.51
DU sum difference (u): 0.78

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC243-252**
 Exchangeable protons: 6
 Index lis-file: 152
 Sequence: FPPKPKDVLV
 Range: 1 / 1

Reference: reference series, experiment: experiment series

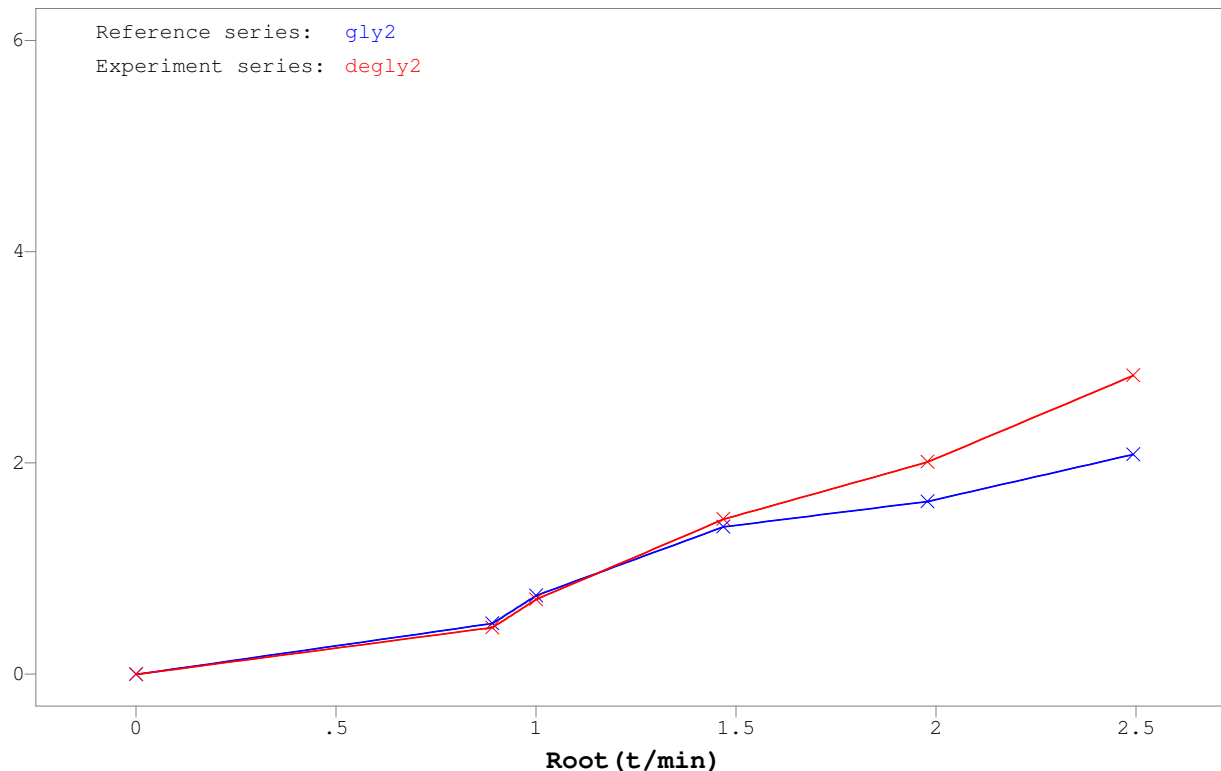
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.822	9.822	0.00	0.00	0.00	0.00
0.5	9.822	9.833	8.03	7.39	0.48	0.44
1.0	9.836	9.836	12.44	11.84	0.75	0.71
10.0	9.825	9.828	23.28	24.48	1.40	1.47
60.0	9.822	9.822	27.29	33.51	1.64	2.01
240.0	9.825	9.829	34.72	47.16	2.08	2.83

Score1 (DU sum): **4.85**
 Score2 (DU Profile): 4.49
DU sum difference (u): 1.12

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC252-261**
 Exchangeable protons: 8
 Index lis-file: 153
 Sequence: TITLTPKVTC
 Range: 1 / 1

Reference: reference series, experiment: experiment series

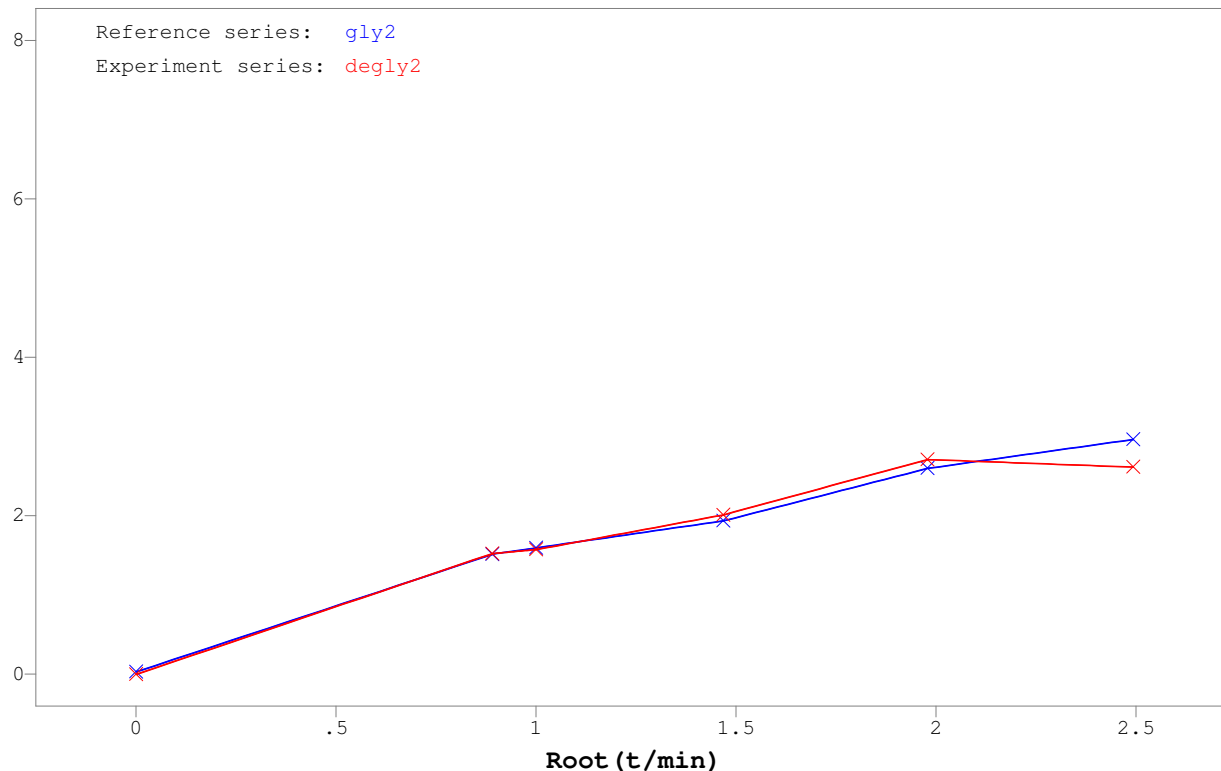
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.828	8.817	0.40	0.00	0.03	0.00
0.5	8.821	8.819	18.96	19.06	1.52	1.53
1.0	8.821	8.824	19.97	19.69	1.60	1.58
10.0	8.817	8.821	24.23	25.17	1.94	2.01
60.0	8.807	8.808	32.51	33.91	2.60	2.71
240.0	8.819	8.828	37.08	32.71	2.97	2.62

Score1 (DU sum): 0.68
 Score2 (DU Profile): **1.60**
 DU sum difference (u): -0.21

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC253-261**
 Exchangeable protons: 7
 Index lis-file: 154
 Sequence: ITLTPKVTC
 Range: 1 / 1

Reference: reference series, experiment: experiment series

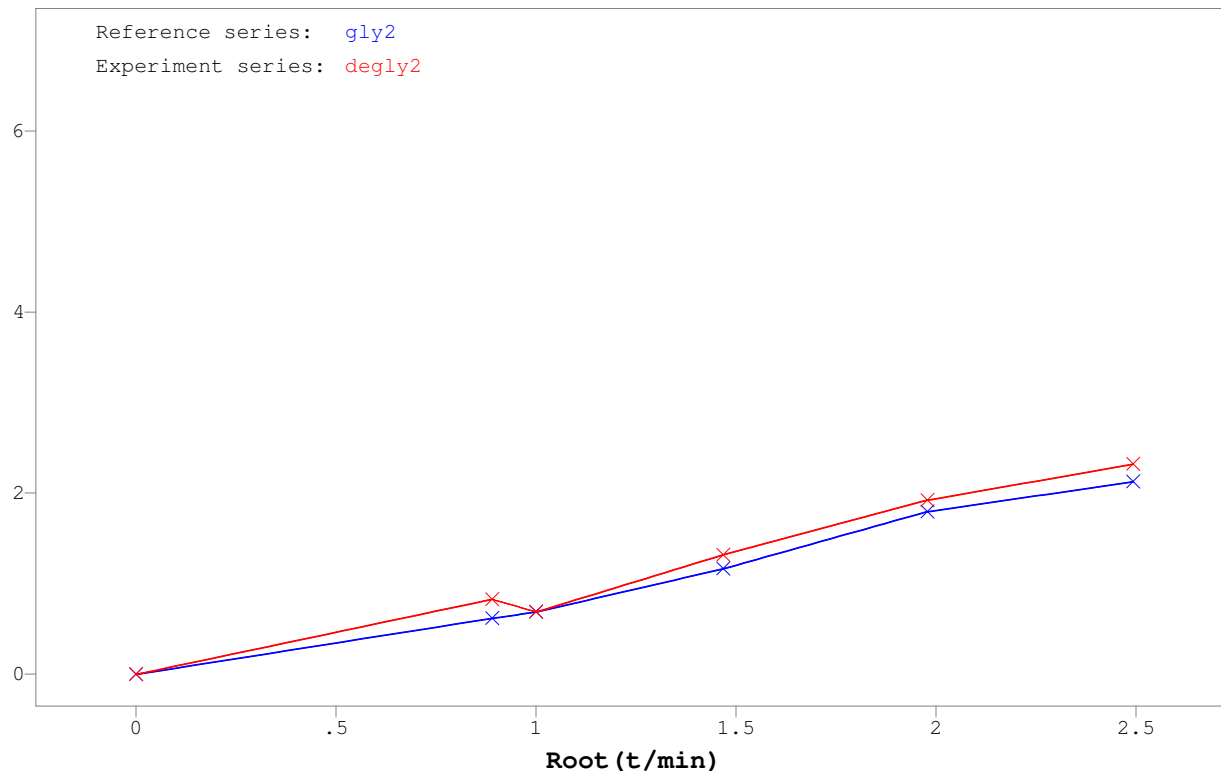
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.432	8.435	0.00	0.00	0.00	0.00
0.5	8.439	8.434	8.83	11.84	0.62	0.83
1.0	8.447	8.434	9.83	9.83	0.69	0.69
10.0	8.441	8.445	16.66	18.87	1.17	1.32
60.0	8.438	8.435	25.69	27.49	1.80	1.92
240.0	8.448	8.456	30.40	33.19	2.13	2.32

Score1 (DU sum): **1.94**
 Score2 (DU Profile): 1.74
DU sum difference (u): 0.57

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC263-274**
 Exchangeable protons: 10
 Index lis-file: 155
 Sequence: VVDISKDDPEVQ
 Range: 1 / 1

Reference: reference series, experiment: experiment series

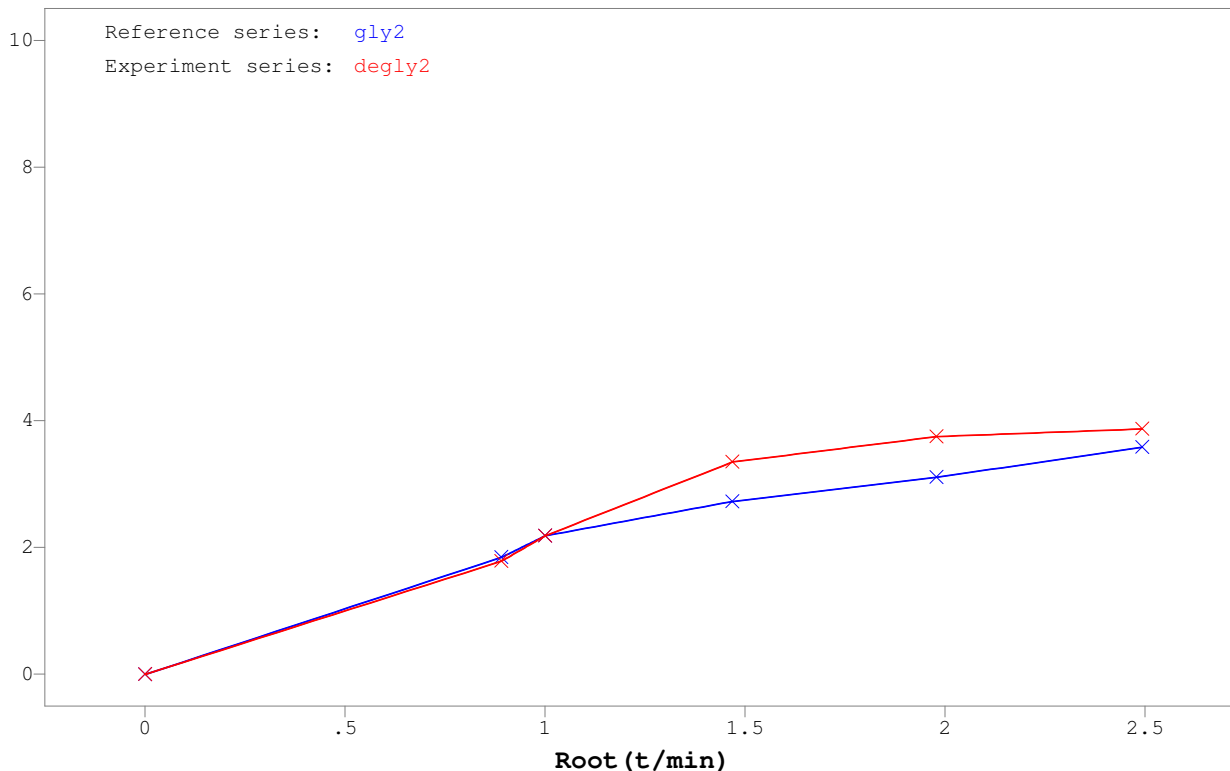
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.305	7.313	0.00	0.00	0.00	0.00
0.5	7.306	7.308	18.46	17.86	1.85	1.79
1.0	7.311	7.302	21.87	21.87	2.19	2.19
10.0	7.298	7.292	27.29	33.51	2.73	3.35
60.0	7.294	7.286	31.10	37.53	3.11	3.75
240.0	7.300	7.300	35.83	38.73	3.58	3.87

Score1 (DU sum): **3.89p**
 Score2 (DU Profile): 3.43p
DU sum difference (u): 1.49

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC263-275**
 Exchangeable protons: 11
 Index lis-file: 156
 Sequence: VVDISKDDPEVQF
 Range: 1 / 1

Reference: reference series, experiment: experiment series

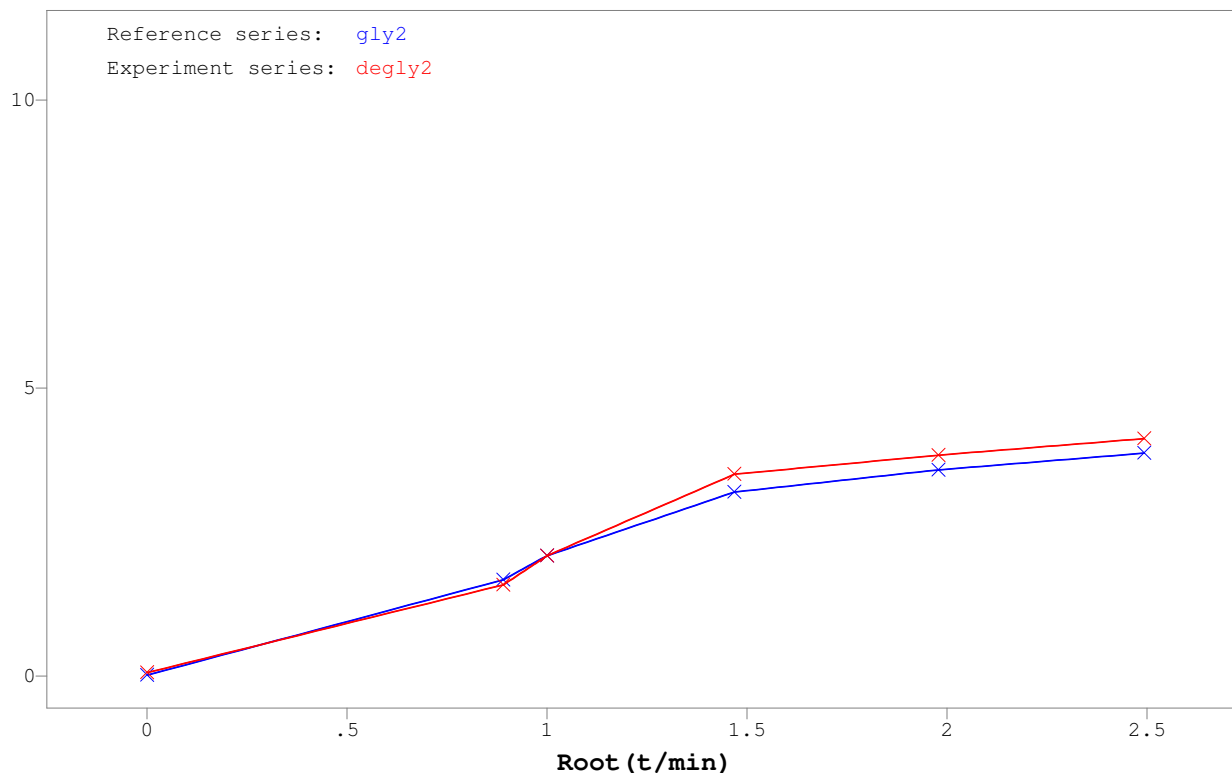
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.573	10.570	0.20	0.60	0.02	0.07
0.5	10.570	10.576	15.25	14.45	1.68	1.59
1.0	10.581	10.586	19.06	19.06	2.10	2.10
10.0	10.571	10.577	29.10	31.91	3.20	3.51
60.0	10.569	10.567	32.60	34.92	3.59	3.84
240.0	10.560	10.569	35.23	37.53	3.88	4.13

Score1 (DU sum): **1.83p**
 Score2 (DU Profile): 1.83p
DU sum difference (u): 0.77

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC307-333**
 Exchangeable protons: 23
 Index lis-file: 232
 Sequence: PIMHQDWLNGKEFKCRVNSAAFPAPIE
 Range: 1 / 1

Reference: reference series, experiment: experiment series

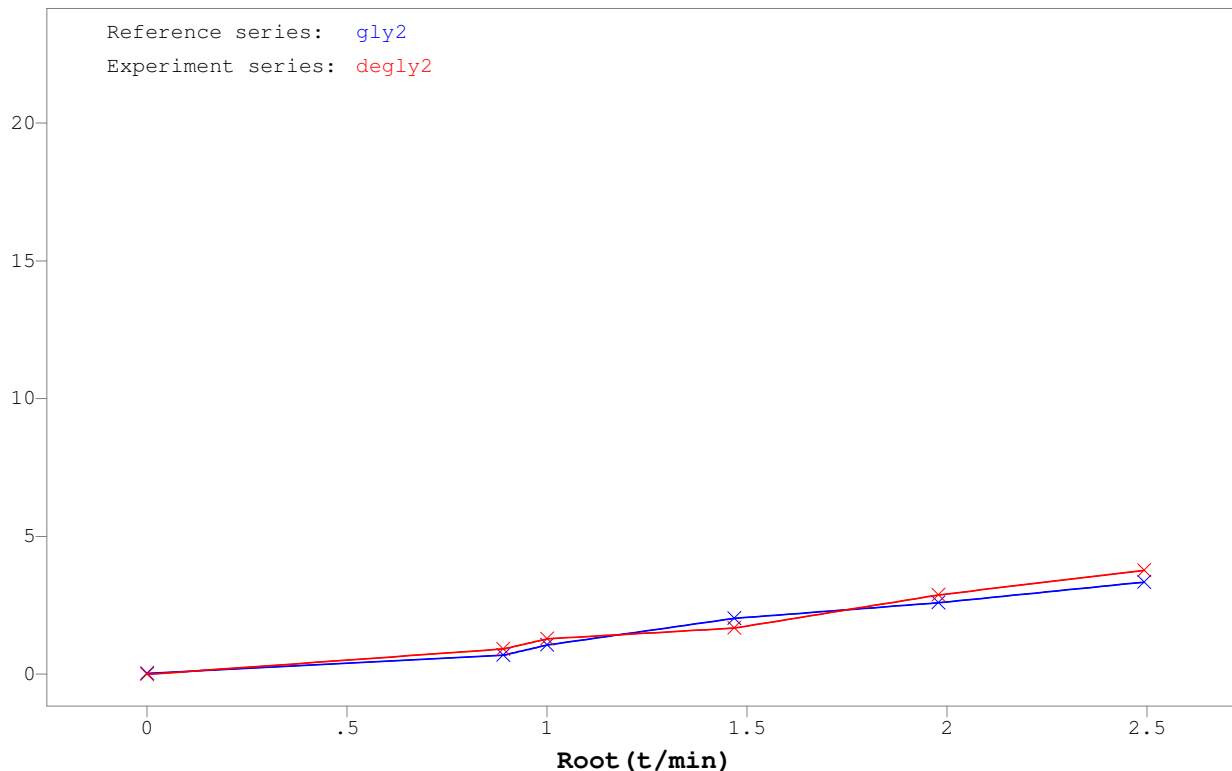
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.166	11.176	0.18	0.00	0.04	0.00
0.5	11.204	11.194	3.03	4.02	0.70	0.92
1.0	11.203	11.167	4.65	5.62	1.07	1.29
10.0	11.222	11.194	8.86	7.32	2.04	1.68
60.0	11.189	11.194	11.32	12.56	2.60	2.89
240.0	11.218	11.203	14.58	16.45	3.35	3.78

Score1 (DU sum): 0.87
 Score2 (DU Profile): **1.45**
 DU sum difference (u): 0.77

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC319-333**
 Exchangeable protons: 12
 Index lis-file: 164
 Sequence: FKCRVNSAAFPAPIE
 Range: 1 / 1

Reference: reference series, experiment: experiment series

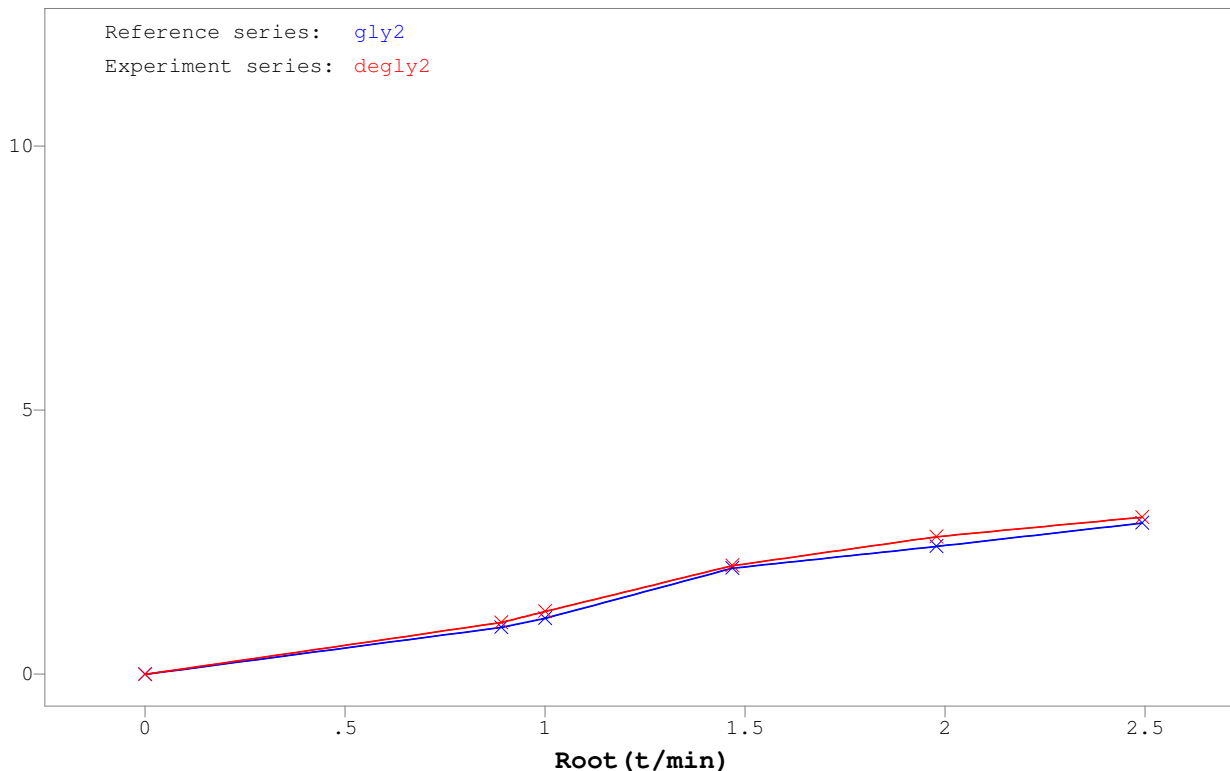
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.403	9.409	0.00	0.00	0.00	0.00
0.5	9.411	9.403	7.42	8.19	0.89	0.98
1.0	9.421	9.411	8.85	9.94	1.06	1.19
10.0	9.413	9.408	16.76	17.15	2.01	2.06
60.0	9.402	9.407	20.19	21.73	2.42	2.61
240.0	9.408	9.415	23.89	24.81	2.87	2.98

Score1 (DU sum): **1.12**
 Score2 (DU Profile): 1.00p
DU sum difference (u): 0.57

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC334-365**
 Exchangeable protons: 26
 Index lis-file: 169
 Sequence: KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

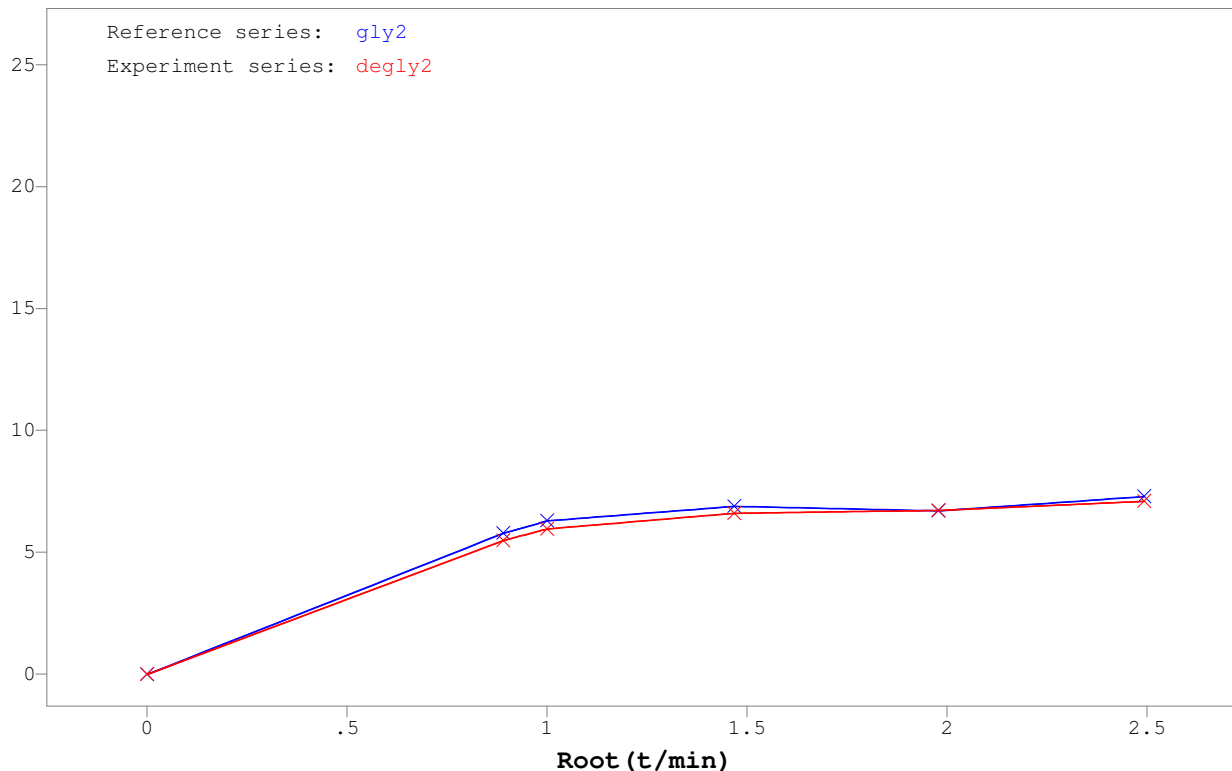
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.767	6.778	0.00	0.00	0.00	0.00
0.5	6.762	6.762	22.27	21.14	5.79	5.50
1.0	6.778	6.759	24.24	22.96	6.30	5.97
10.0	6.775	6.754	26.53	25.44	6.90	6.61
60.0	6.761	6.752	25.82	25.89	6.71	6.73
240.0	6.760	6.781	28.07	27.32	7.30	7.10

Score1 (DU sum): **1.09**
 Score2 (DU Profile): 0.92
DU sum difference (u): -1.09

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC334-368**
 Exchangeable protons: 29
 Index lis-file: 170
 Sequence: KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

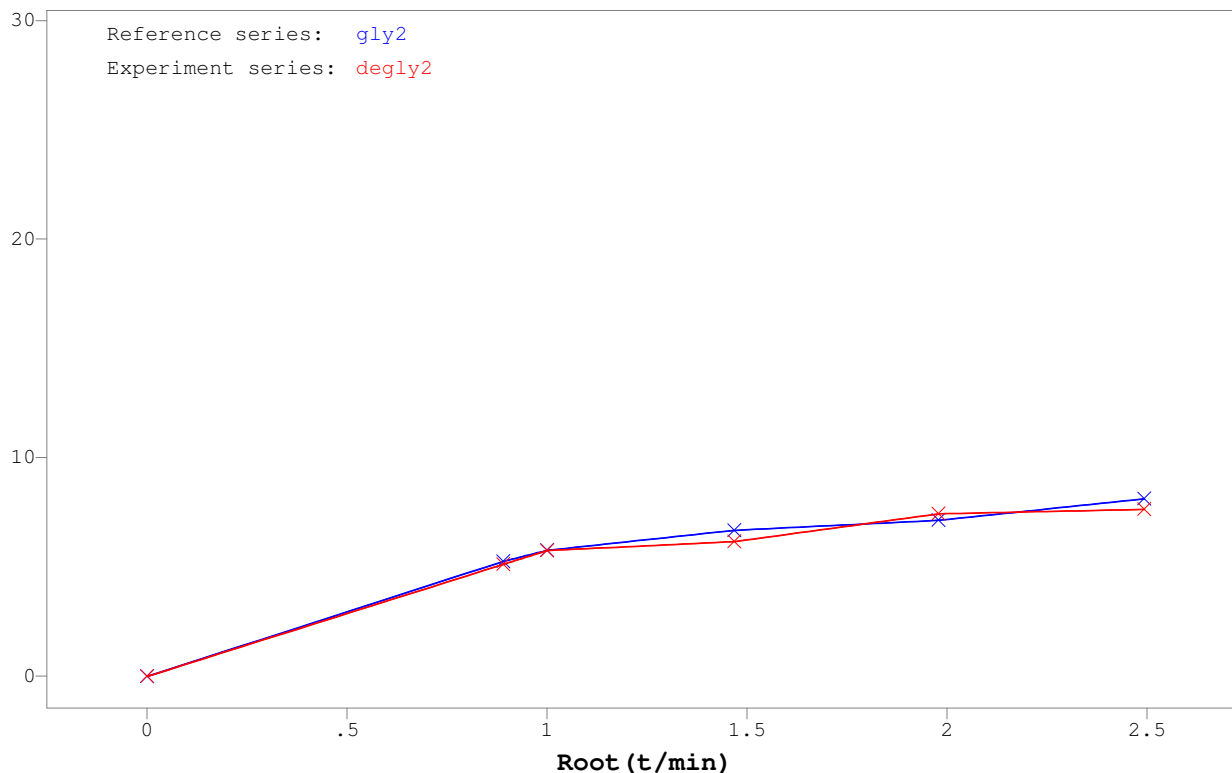
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.758	7.741	0.00	0.00	0.00	0.00
0.5	7.746	7.732	18.16	17.70	5.27	5.13
1.0	7.748	7.739	19.90	19.87	5.77	5.76
10.0	7.746	7.733	23.06	21.28	6.69	6.17
60.0	7.725	7.723	24.63	25.67	7.14	7.44
240.0	7.728	7.726	28.04	26.36	8.13	7.65

Score1 (DU sum): 0.76
 Score2 (DU Profile): **1.06**
 DU sum difference (u): -0.85

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC342-366**
 Exchangeable protons: 19
 Index lis-file: 234
 Sequence: RPKAPQVYTIPPPKQMAKDKVSLT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

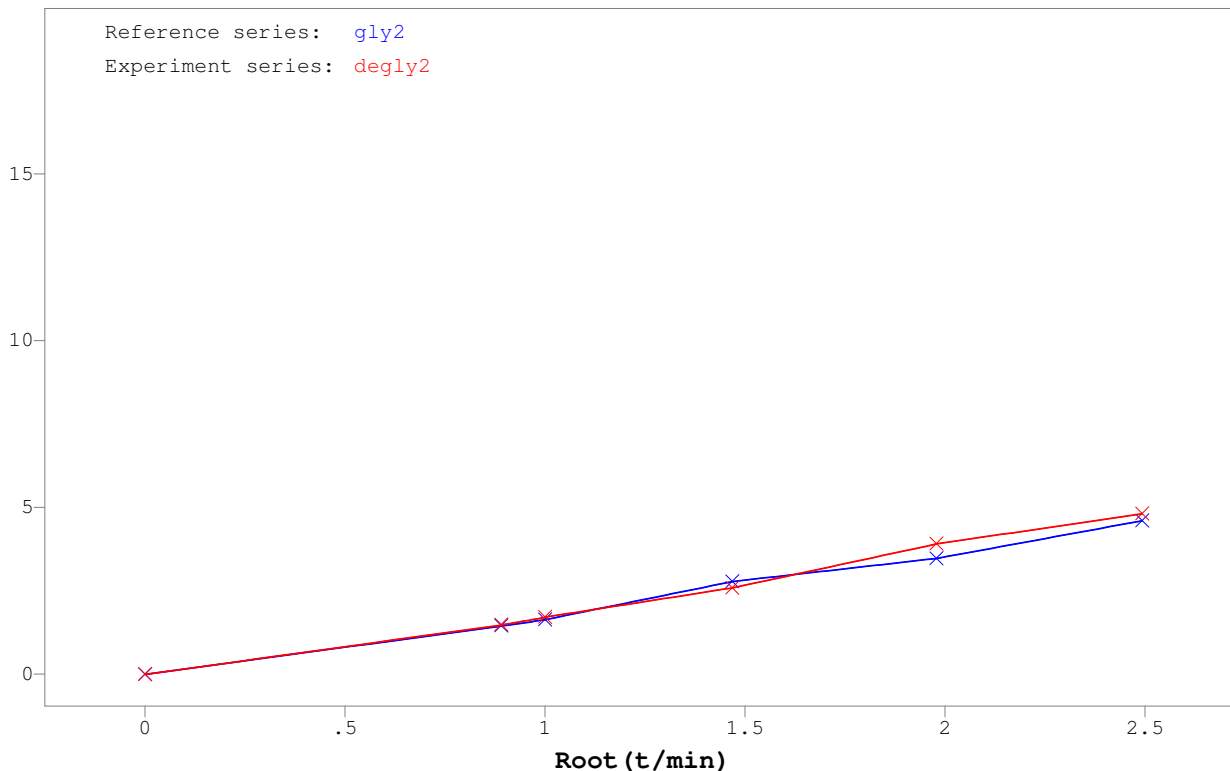
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.650	10.646	0.00	0.00	0.00	0.00
0.5	10.658	10.675	7.67	7.82	1.46	1.49
1.0	10.668	10.674	8.64	9.03	1.64	1.72
10.0	10.653	10.664	14.65	13.65	2.78	2.59
60.0	10.675	10.676	18.29	20.58	3.48	3.91
240.0	10.699	10.697	24.24	25.34	4.61	4.82

Score1 (DU sum): 0.77
 Score2 (DU Profile): **1.05**
 DU sum difference (u): 0.56

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC349-365**
 Exchangeable protons: 13
 Index lis-file: 174
 Sequence: YTIPPPKEQMAKDKVSL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

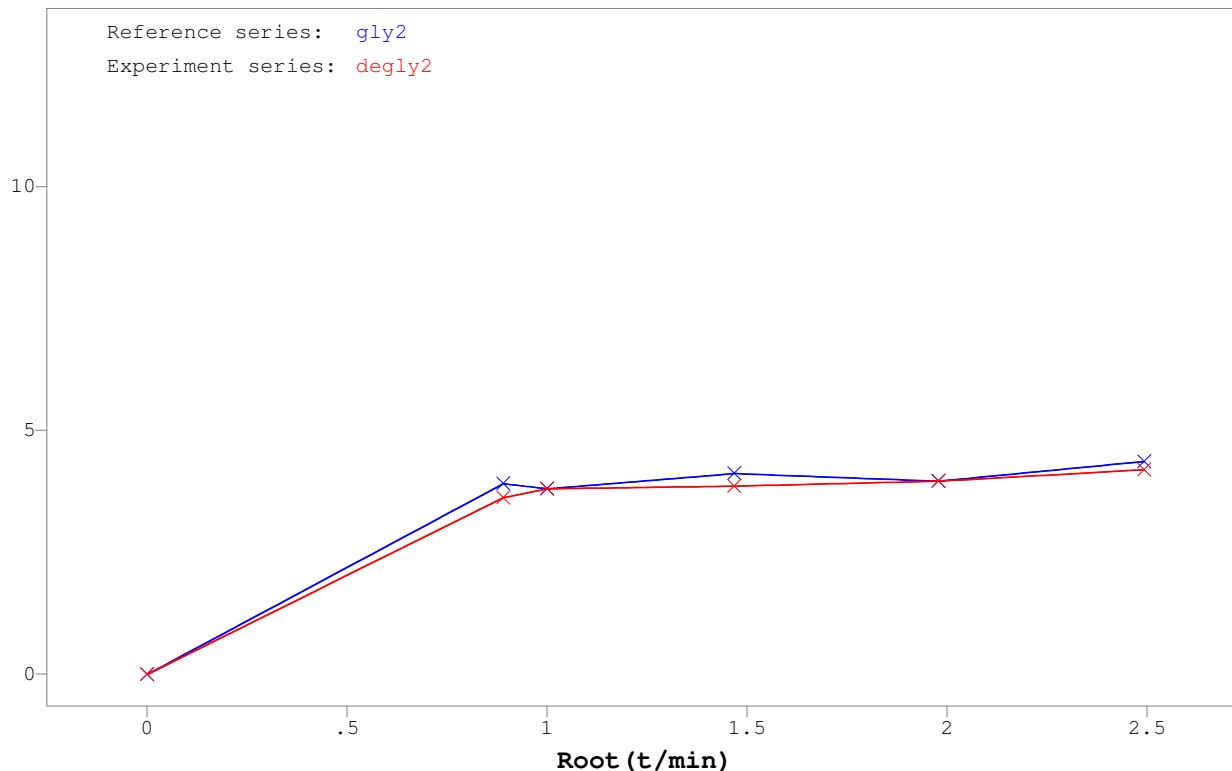
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.019	8.019	0.00	0.00	0.00	0.00
0.5	8.008	8.000	30.10	27.89	3.91	3.63
1.0	8.016	8.011	29.30	29.30	3.81	3.81
10.0	8.016	8.011	31.71	29.72	4.12	3.86
60.0	8.001	8.001	30.50	30.50	3.97	3.97
240.0	8.010	8.063	33.63	32.31	4.37	4.20

Score1 (DU sum): **1.44p**
 Score2 (DU Profile): 1.17p
DU sum difference (u): -0.72

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC367-390**
 Exchangeable protons: 21
 Index lis-file: 177
 Sequence: CMITDFFPEDITVEWQWNGQPAEN
 Range: 1 / 1

Reference: reference series, experiment: experiment series

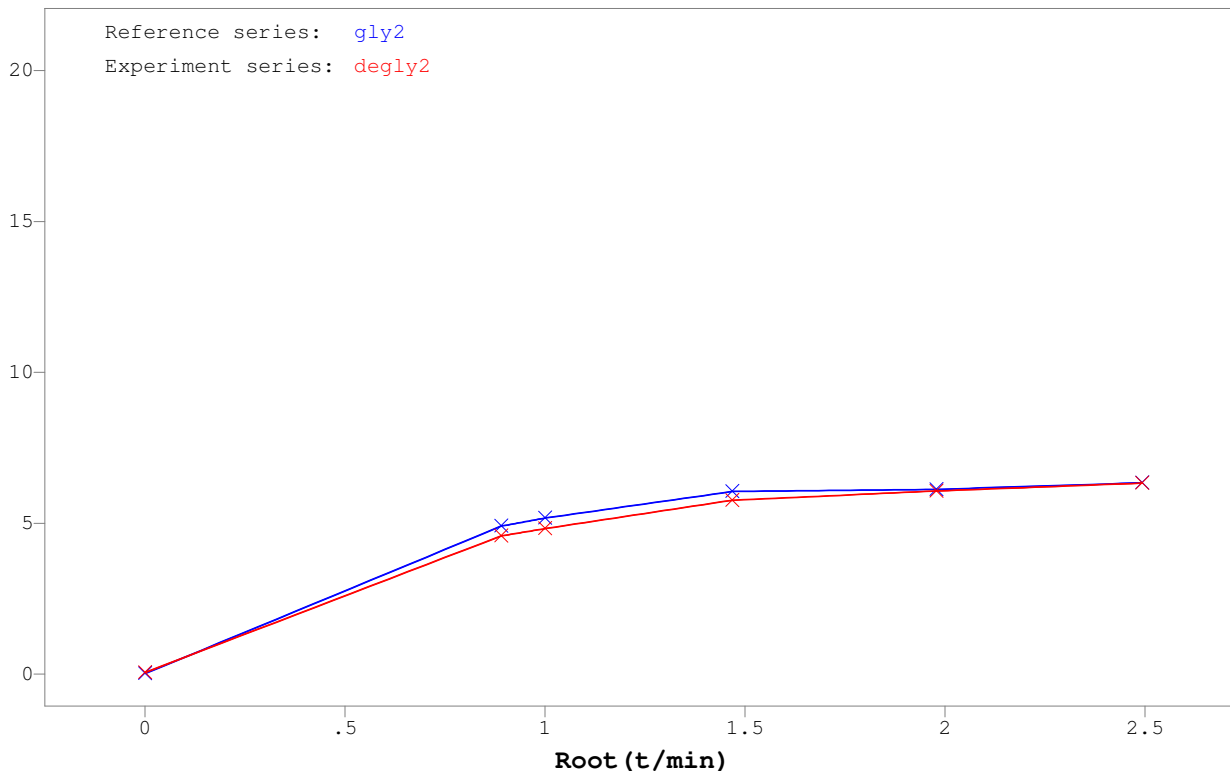
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.263	8.262	0.13	0.32	0.03	0.07
0.5	8.264	8.256	23.42	21.87	4.92	4.59
1.0	8.265	8.256	24.69	23.03	5.18	4.84
10.0	8.260	8.259	28.88	27.50	6.07	5.78
60.0	8.251	8.252	29.21	28.96	6.14	6.08
240.0	8.256	8.255	30.25	30.20	6.35	6.34

Score1 (DU sum): **1.23**
 Score2 (DU Profile): 1.08
DU sum difference (u): -0.99

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC369-380**
 Exchangeable protons: 10
 Index lis-file: 180
 Sequence: ITDFFPEDITVE
 Range: 1 / 1

Reference: reference series, experiment: experiment series

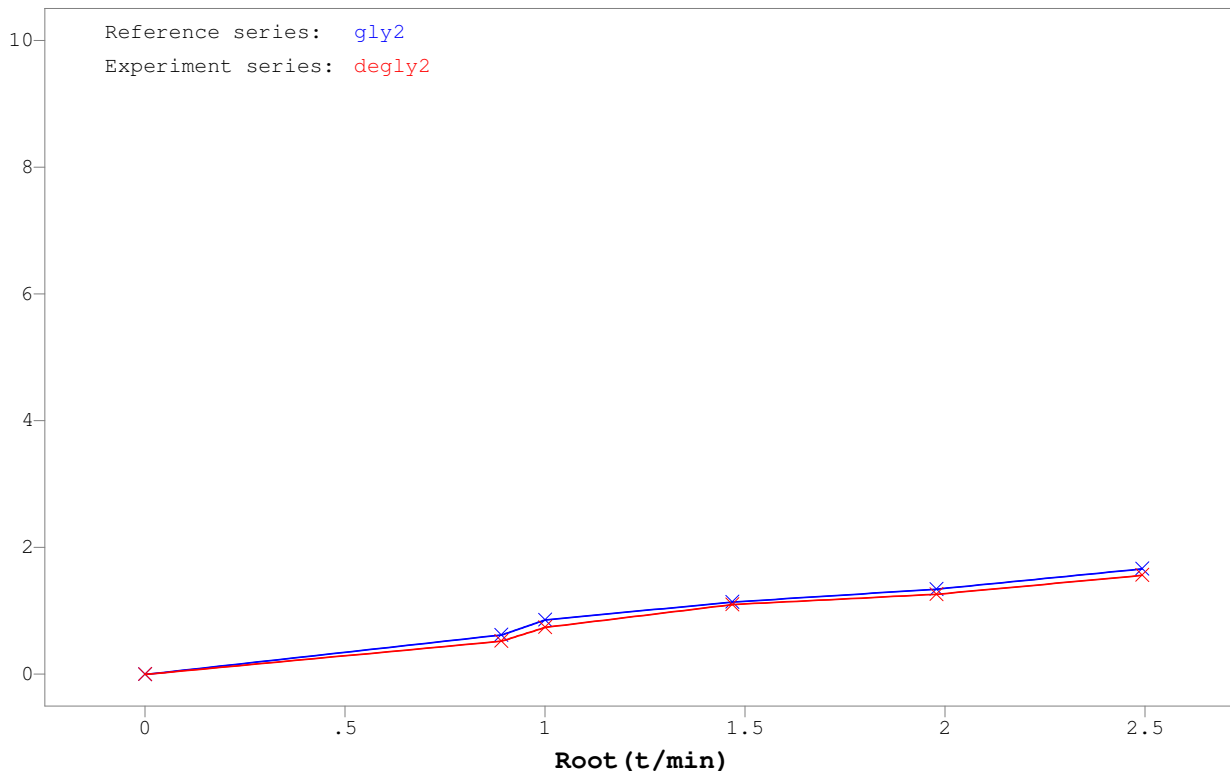
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	14.001	14.016	0.00	0.00	0.00	0.00
0.5	13.996	14.019	6.21	5.23	0.62	0.52
1.0	14.013	14.011	8.60	7.42	0.86	0.74
10.0	13.998	14.008	11.41	11.02	1.14	1.10
60.0	14.009	14.009	13.45	12.64	1.35	1.26
240.0	14.004	14.009	16.64	15.64	1.66	1.56

Score1 (DU sum): **1.14**
 Score2 (DU Profile): 0.93
DU sum difference (u): -0.44

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC381-390**
 Exchangeable protons: 8
 Index lis-file: 183
 Sequence: WQWNGQPAEN
 Range: 1 / 1

Reference: reference series, experiment: experiment series

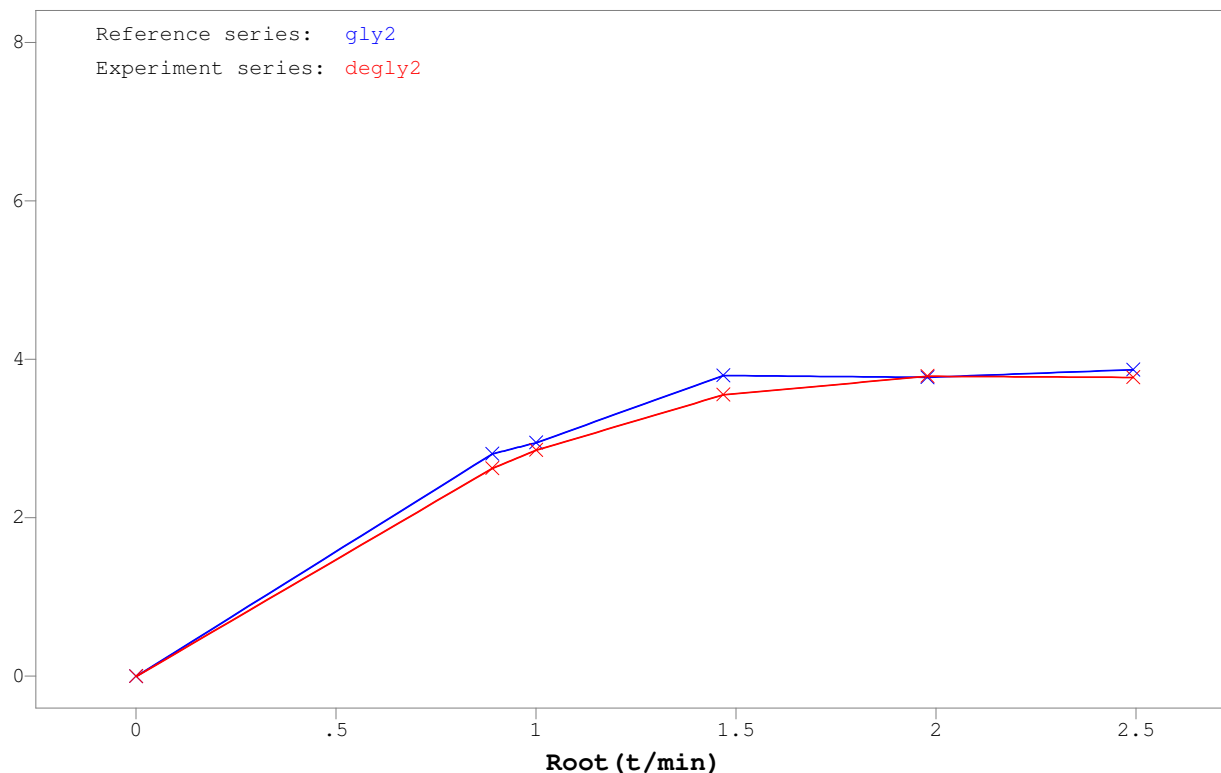
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.622	10.622	0.00	0.00	0.00	0.00
0.5	10.624	10.646	35.11	32.84	2.81	2.63
1.0	10.641	10.637	36.88	35.70	2.95	2.86
10.0	10.625	10.631	47.48	44.43	3.80	3.55
60.0	10.619	10.644	47.20	47.37	3.78	3.79
240.0	10.646	10.654	48.40	47.18	3.87	3.77

Score1 (DU sum): **1.65**
 Score2 (DU Profile): 1.68p
DU sum difference (u): -0.62

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC390-398**
 Exchangeable protons: 7
 Index lis-file: 185
 Sequence: NYKNTQPIM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

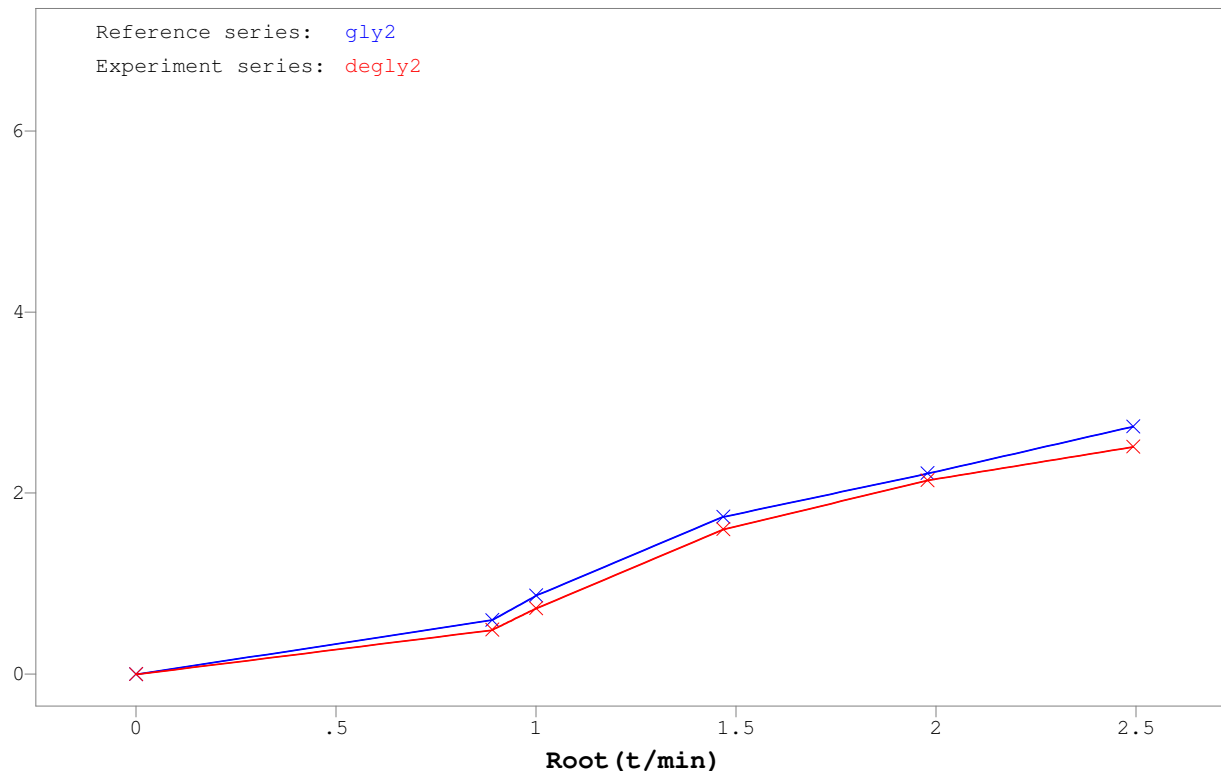
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.305	7.296	0.00	0.00	0.00	0.00
0.5	7.302	7.312	8.55	7.02	0.60	0.49
1.0	7.327	7.304	12.44	10.41	0.87	0.73
10.0	7.316	7.304	24.87	22.88	1.74	1.60
60.0	7.303	7.310	31.71	30.62	2.22	2.14
240.0	7.311	7.316	39.13	35.92	2.74	2.51

Score1 (DU sum): **2.57**
 Score2 (DU Profile): 2.10
DU sum difference (u): -0.69

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC391-398**
 Exchangeable protons: 6
 Index lis-file: 238
 Sequence: YKNTQPIM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

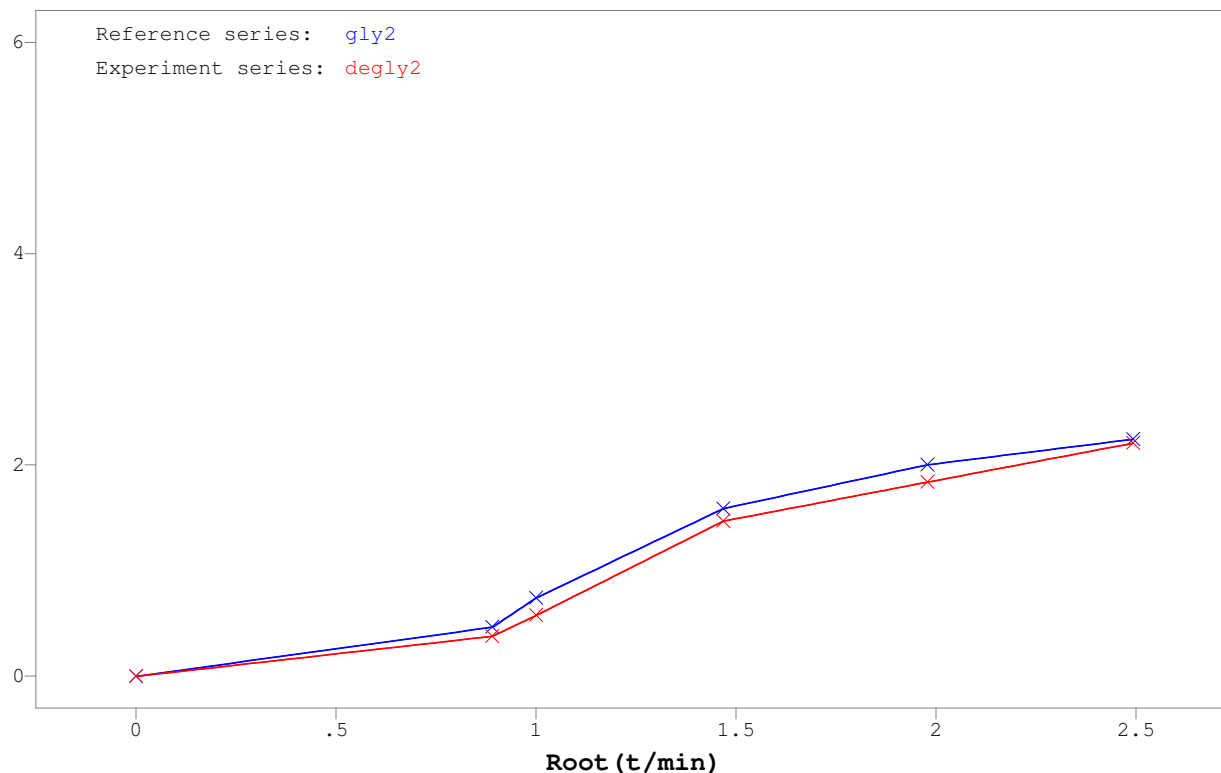
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.049	7.056	0.00	0.00	0.00	0.00
0.5	7.050	7.049	7.76	6.33	0.47	0.38
1.0	7.067	7.049	12.39	9.63	0.74	0.58
10.0	7.056	7.051	26.49	24.50	1.59	1.47
60.0	7.048	7.045	33.39	30.66	2.00	1.84
240.0	7.054	7.044	37.42	36.81	2.25	2.21

Score1 (DU sum): **2.48**
 Score2 (DU Profile): 2.03
DU sum difference (u): -0.57

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**
 Peptide: **HC391-404**
 Exchangeable protons: 12
 Index lis-file: 186
 Sequence: YKNTQPIMDTDGSY
 Range: 1 / 1

Reference: reference series, experiment: experiment series

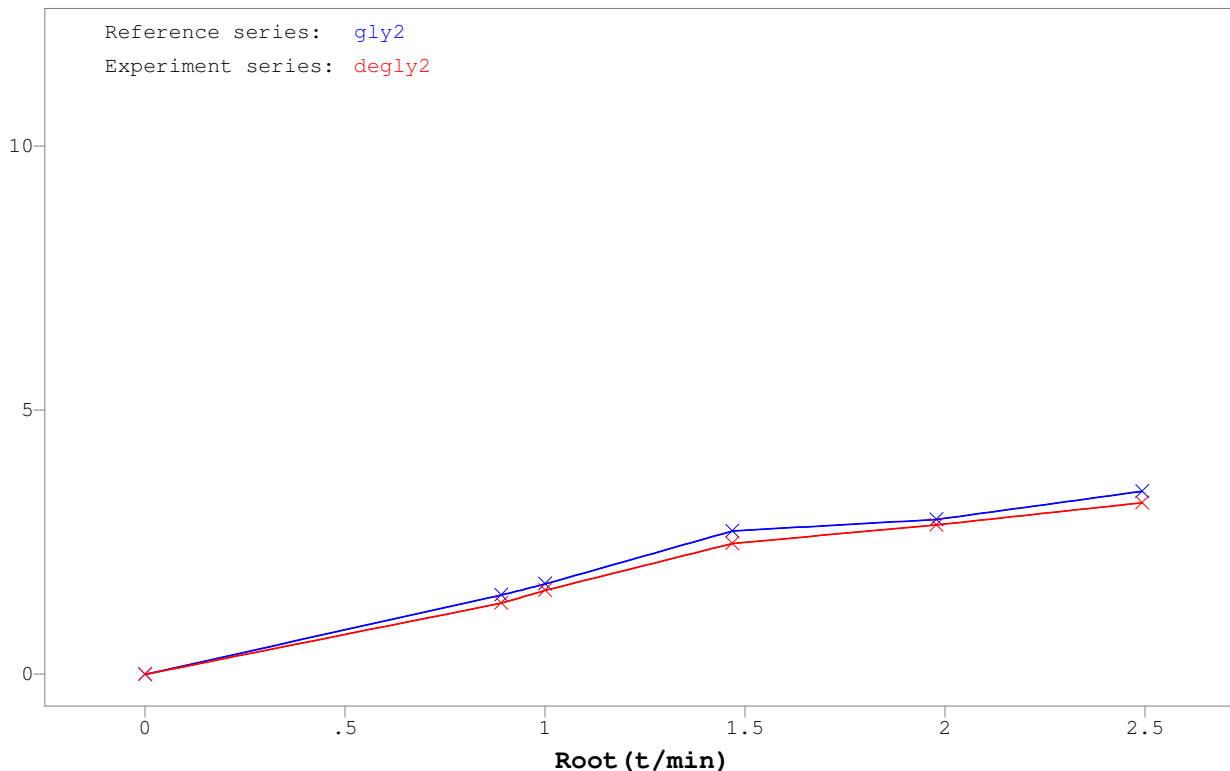
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.544	8.540	0.01	0.00	0.00	0.00
0.5	8.544	8.529	12.52	11.24	1.50	1.35
1.0	8.559	8.523	14.27	13.27	1.71	1.59
10.0	8.531	8.534	22.64	20.66	2.72	2.48
60.0	8.529	8.518	24.45	23.59	2.93	2.83
240.0	8.554	8.512	28.90	27.09	3.47	3.25

Score1 (DU sum): **1.69**
 Score2 (DU Profile): 1.47p
DU sum difference (u): -0.85

DU Value



Root(t/min): 6th roots of exchange times

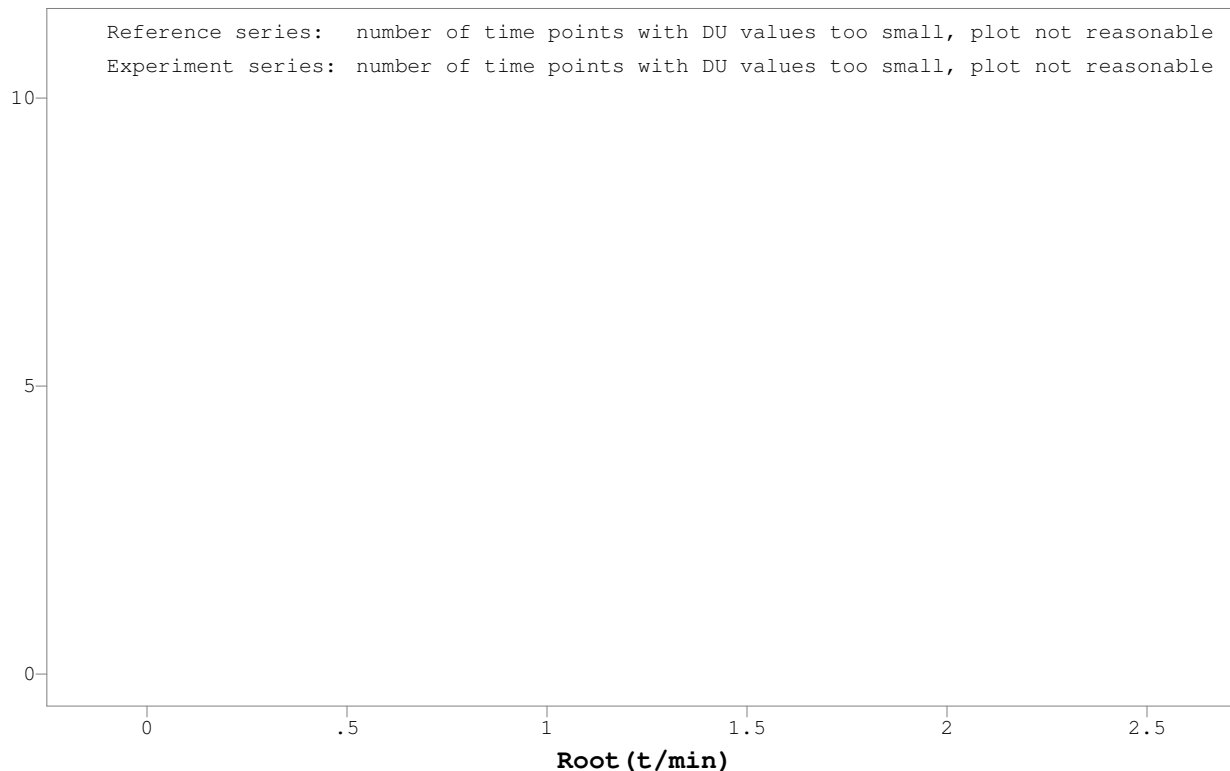
Molecule: **HC**
 Peptide: **HC016-027**
 Exchangeable protons: 11
 Index lis-file: 93
 Sequence: GSLKLSCAASGF
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.228	9.218	n.d.	n.d.	n.d.	n.d.
0.5	9.226	9.221	n.d.	n.d.	n.d.	n.d.
1.0	9.232	9.220	n.d.	n.d.	n.d.	n.d.
10.0	9.209	9.213	n.d.	n.d.	n.d.	n.d.
60.0	9.201	9.210	n.d.	n.d.	n.d.	n.d.
240.0	9.208	9.213	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

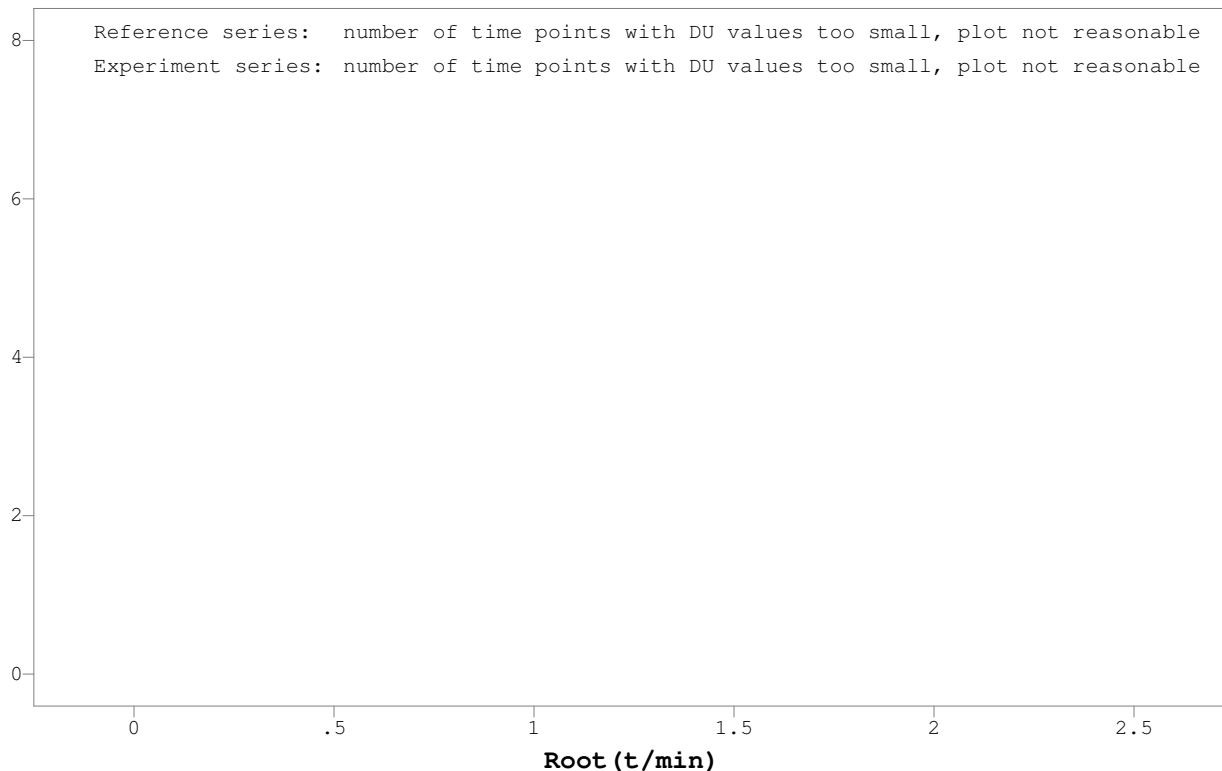
Molecule: **HC**
 Peptide: **HC070-078**
 Exchangeable protons: 8
 Index lis-file: 109
 Sequence: ISRDNAKNN
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	4.800	4.808	n.d.	n.d.	n.d.	n.d.
0.5	4.805	4.806	n.d.	n.d.	n.d.	n.d.
1.0	4.818	4.797	n.d.	n.d.	n.d.	n.d.
10.0	4.798	4.797	n.d.	n.d.	n.d.	n.d.
60.0	4.792	4.797	n.d.	n.d.	n.d.	n.d.
240.0	4.805	4.805	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

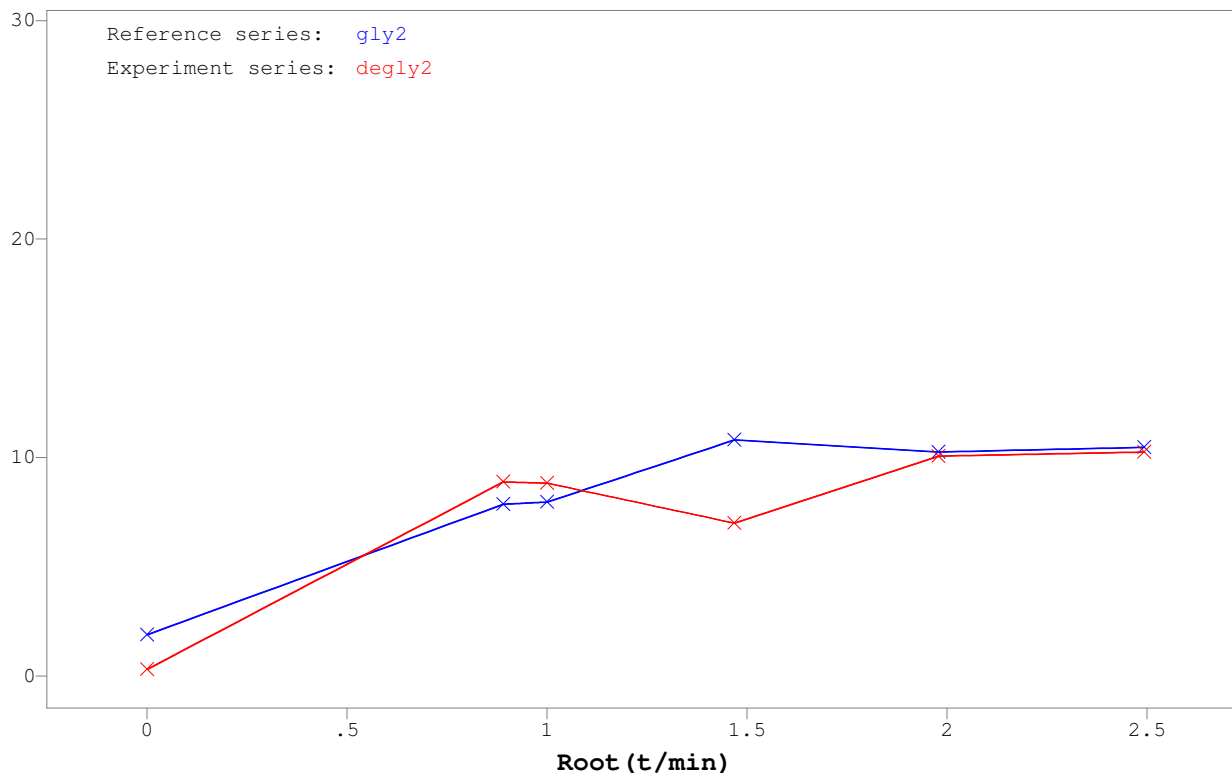
Molecule: **HC**
 Peptide: **HC112-145**
 Exchangeable protons: 29
 Index lis-file: 122
 Sequence: YWGQGSVTVSSAKTTPPSVYPLAPGSAAQTNSM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.162	11.172	6.58	1.13	1.91	0.33
0.5	11.169	11.173	27.18	30.70	7.88	8.90
1.0	11.184	11.166	27.52	30.50	7.98	8.85
10.0	11.160	11.178	37.32	24.20	10.82	7.02
60.0	11.153	11.165	35.43	34.79	10.27	10.09
240.0	11.163	11.163	36.16	35.43	10.49	10.27

DU Value



Root(t/min): 6th roots of exchange times

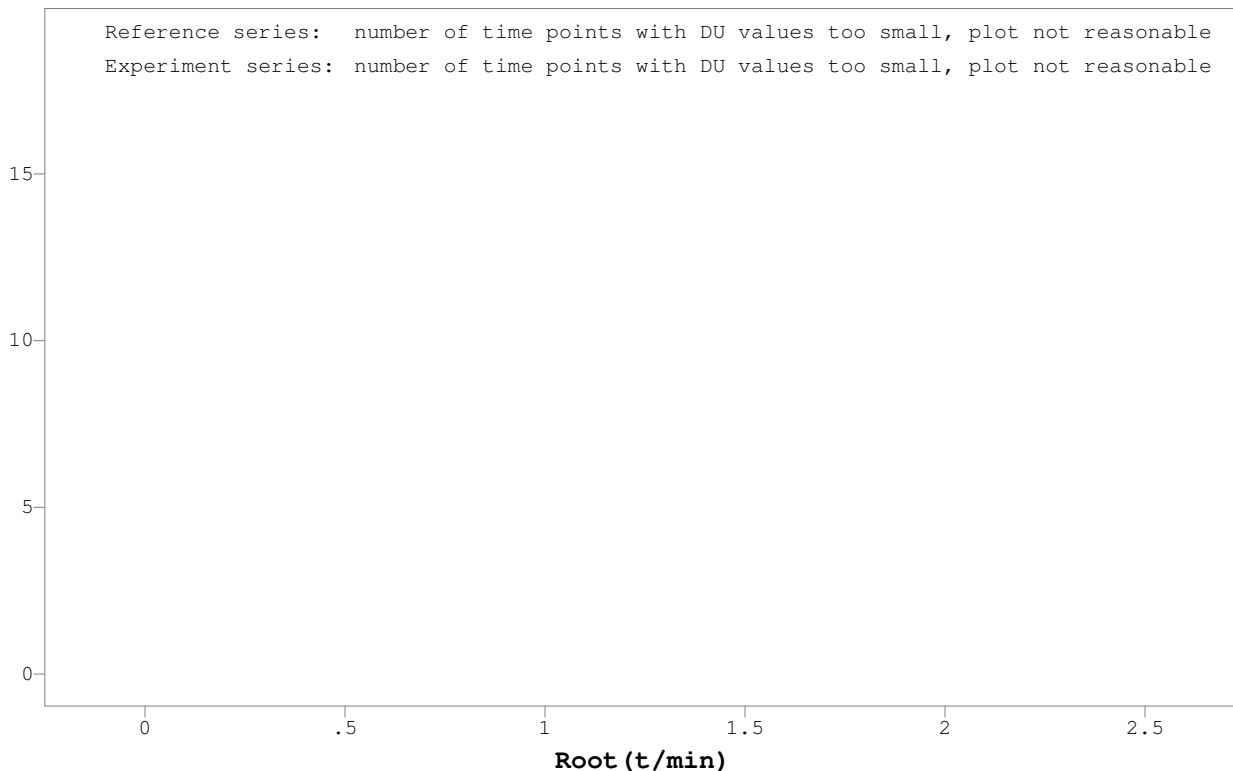
Molecule: **HC**
 Peptide: **HC119-142**
 Exchangeable protons: 19
 Index lis-file: 127
 Sequence: VTVSSAKTTPPSVYPLAPGSAAQT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.818	8.823	n.d.	n.d.	n.d.	n.d.
0.5	8.822	8.812	n.d.	n.d.	n.d.	n.d.
1.0	8.802	8.825	n.d.	n.d.	n.d.	n.d.
10.0	8.796	8.836	n.d.	n.d.	n.d.	n.d.
60.0	8.805	8.819	n.d.	n.d.	n.d.	n.d.
240.0	8.833	8.811	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

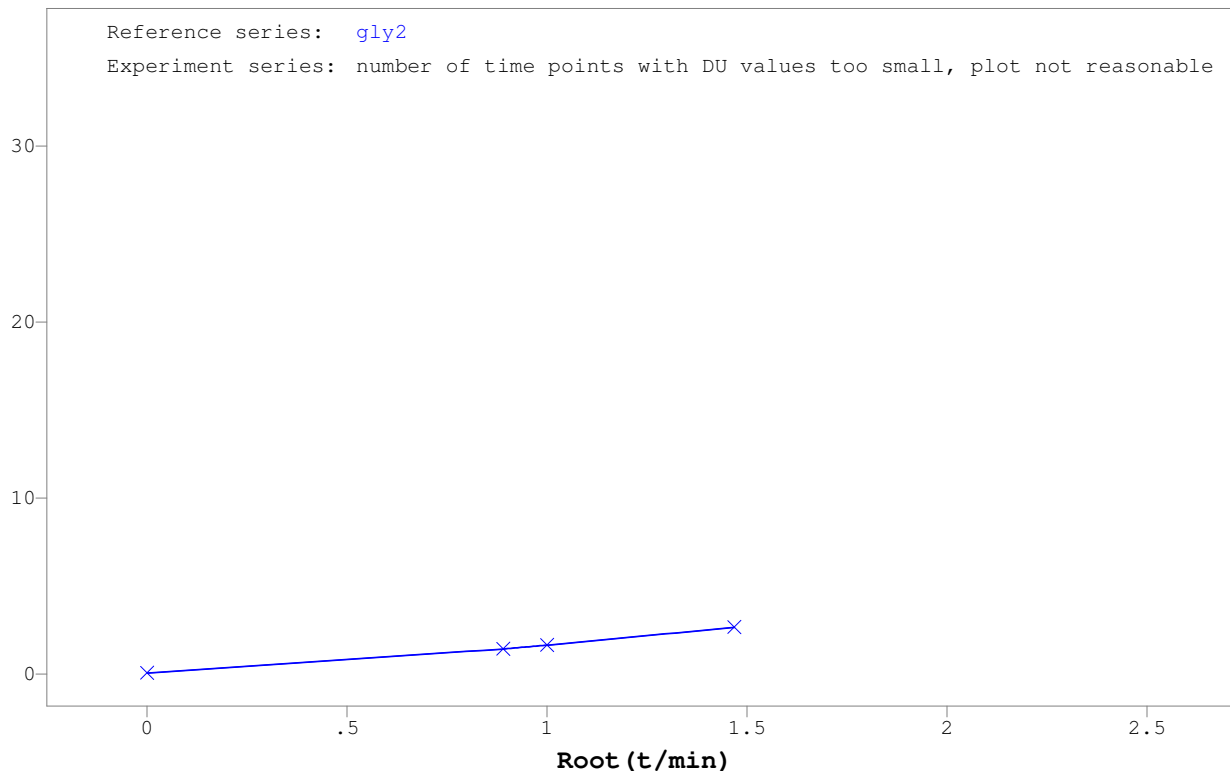
Molecule: **HC**
 Peptide: **HC138-177**
 Exchangeable protons: 36
 Index lis-file: 133
 Sequence: SAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFP
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.243	11.225	0.20	0.00	0.07	0.00
0.5	11.256	11.248	4.01	4.01	1.44	1.44
1.0	11.265	11.246	4.62	n.d.	1.66	n.d.
10.0	11.233	11.238	7.42	n.d.	2.67	n.d.
60.0	11.237	11.235	n.d.	n.d.	n.d.	n.d.
240.0	11.253	11.232	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

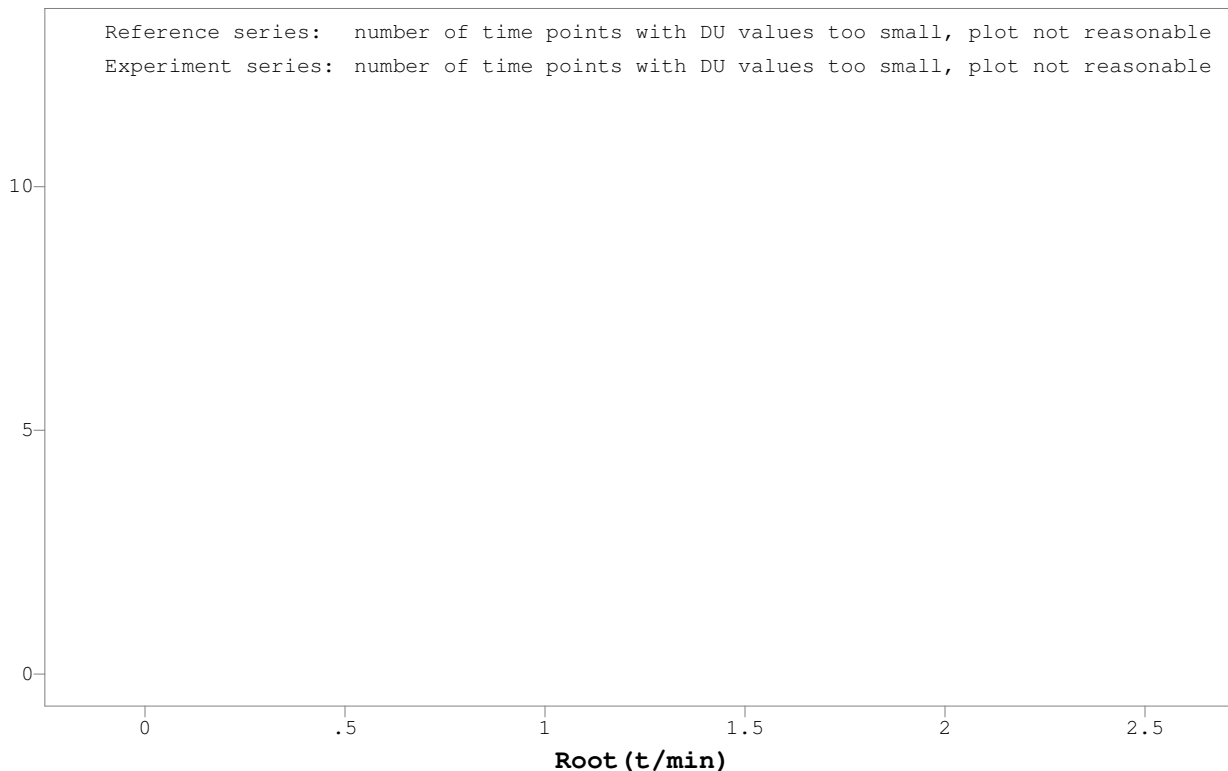
Molecule: **HC**
 Peptide: **HC146-161**
 Exchangeable protons: 13
 Index lis-file: 214
 Sequence: VTLGCLVKGYFPEPVT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	13.377	13.388	n.d.	n.d.	n.d.	n.d.
0.5	13.382	13.397	n.d.	n.d.	n.d.	n.d.
1.0	13.403	13.390	n.d.	n.d.	n.d.	n.d.
10.0	13.380	13.430	n.d.	n.d.	n.d.	n.d.
60.0	13.384	13.392	n.d.	n.d.	n.d.	n.d.
240.0	13.389	13.397	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

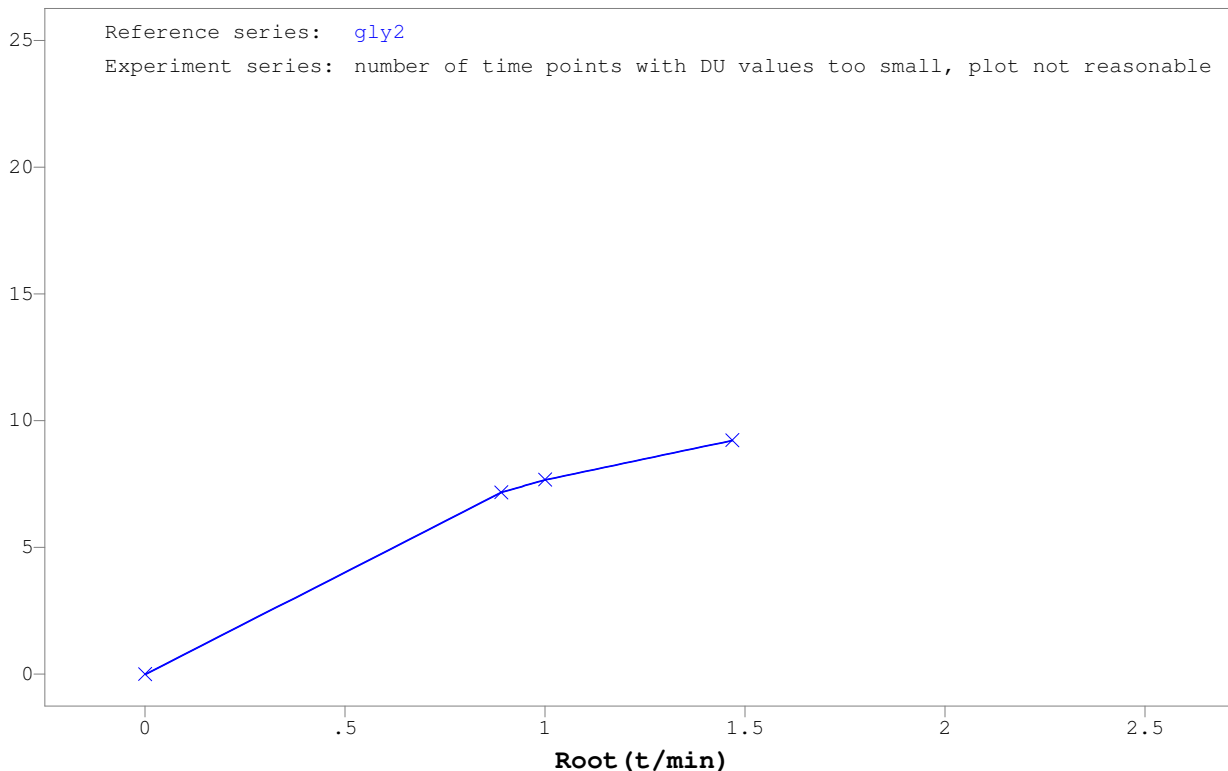
Molecule: **HC**
 Peptide: **HC210-239**
 Exchangeable protons: 25
 Index lis-file: 221
 Sequence: PASSTKVDDKKIVPRDCGCKPCICTVPEVSS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.420	12.431	0.00	0.00	0.00	0.00
0.5	12.416	12.437	28.70	n.d.	7.17	n.d.
1.0	12.427	12.427	30.70	n.d.	7.68	n.d.
10.0	12.399	12.432	36.92	n.d.	9.23	n.d.
60.0	12.407	12.443	n.d.	n.d.	n.d.	n.d.
240.0	12.423	12.423	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

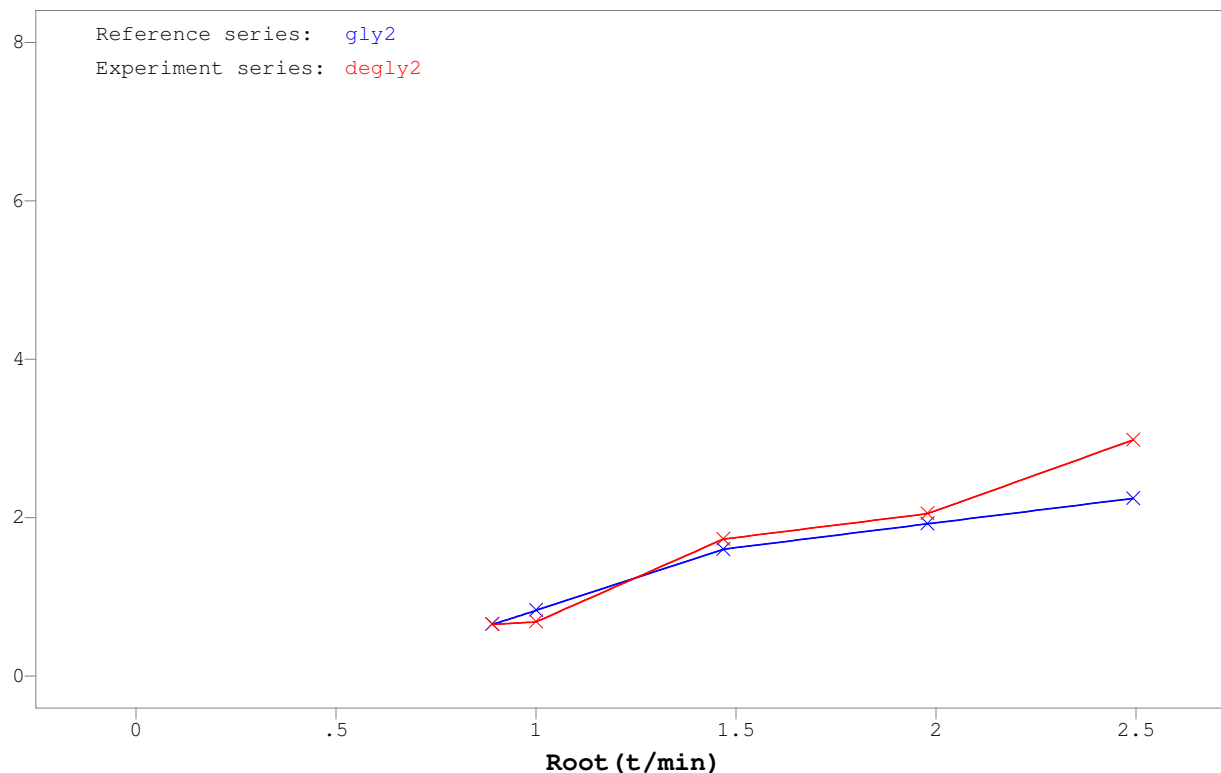
Molecule: **HC**
 Peptide: **HC240-251**
 Exchangeable protons: 8
 Index lis-file: 149
 Sequence: VFIFPPKPKDVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.994	10.991	n.d.	n.d.	n.d.	n.d.
0.5	11.002	11.000	8.23	8.23	0.66	0.66
1.0	11.019	11.001	10.43	8.63	0.83	0.69
10.0	10.994	10.991	20.07	21.67	1.61	1.73
60.0	10.999	11.004	24.08	25.69	1.93	2.05
240.0	10.990	10.996	28.09	37.32	2.25	2.99

DU Value



Root(t/min): 6th roots of exchange times

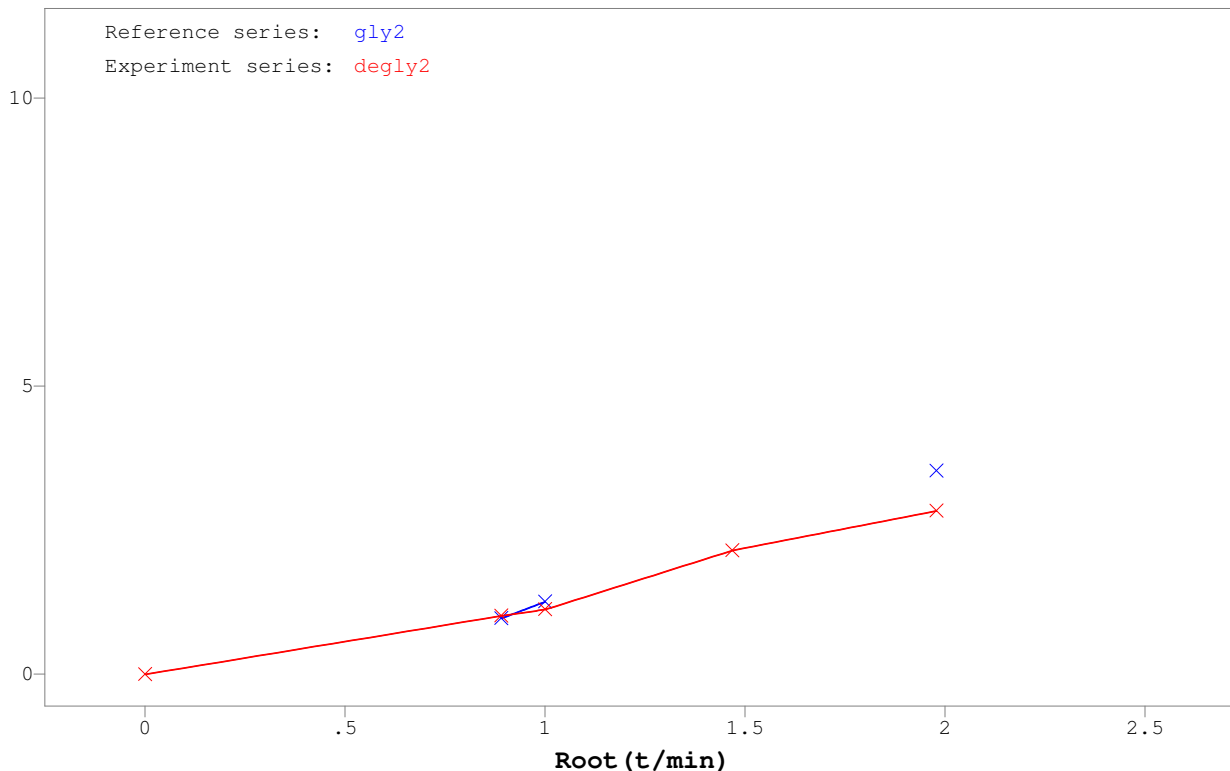
Molecule: **HC**
 Peptide: **HC280-292**
 Exchangeable protons: 11
 Index lis-file: 227
 Sequence: DDVEVHTAQTQPR
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.425	9.359	n.d.	0.00	n.d.	0.00
0.5	9.312	9.308	8.83	9.23	0.97	1.02
1.0	9.326	9.319	11.47	10.23	1.26	1.13
10.0	9.312	9.312	n.d.	19.55	n.d.	2.15
60.0	9.305	9.309	32.11	25.80	3.53	2.84
240.0	9.326	9.312	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

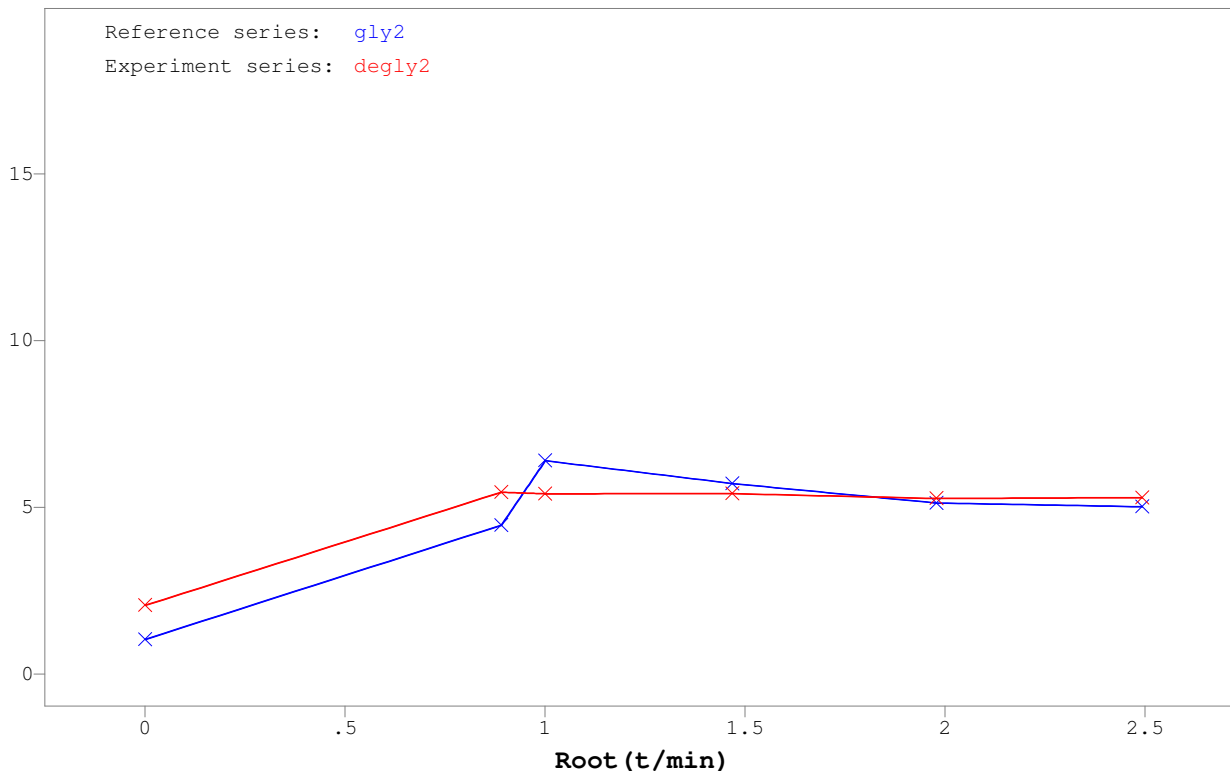
Molecule: **HC**
 Peptide: **HC334-358**
 Exchangeable protons: 19
 Index lis-file: 167
 Sequence: KTISKTKGRPKAPQVYTIPPPKEQM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.147	6.140	5.52	10.88	1.05	2.07
0.5	6.140	6.141	23.53	28.73	4.47	5.46
1.0	6.166	6.132	33.71	28.49	6.40	5.41
10.0	6.150	6.132	30.10	28.52	5.72	5.42
60.0	6.141	6.129	27.03	27.75	5.14	5.27
240.0	6.151	6.135	26.44	27.89	5.02	5.30

DU Value



Root(t/min): 6th roots of exchange times

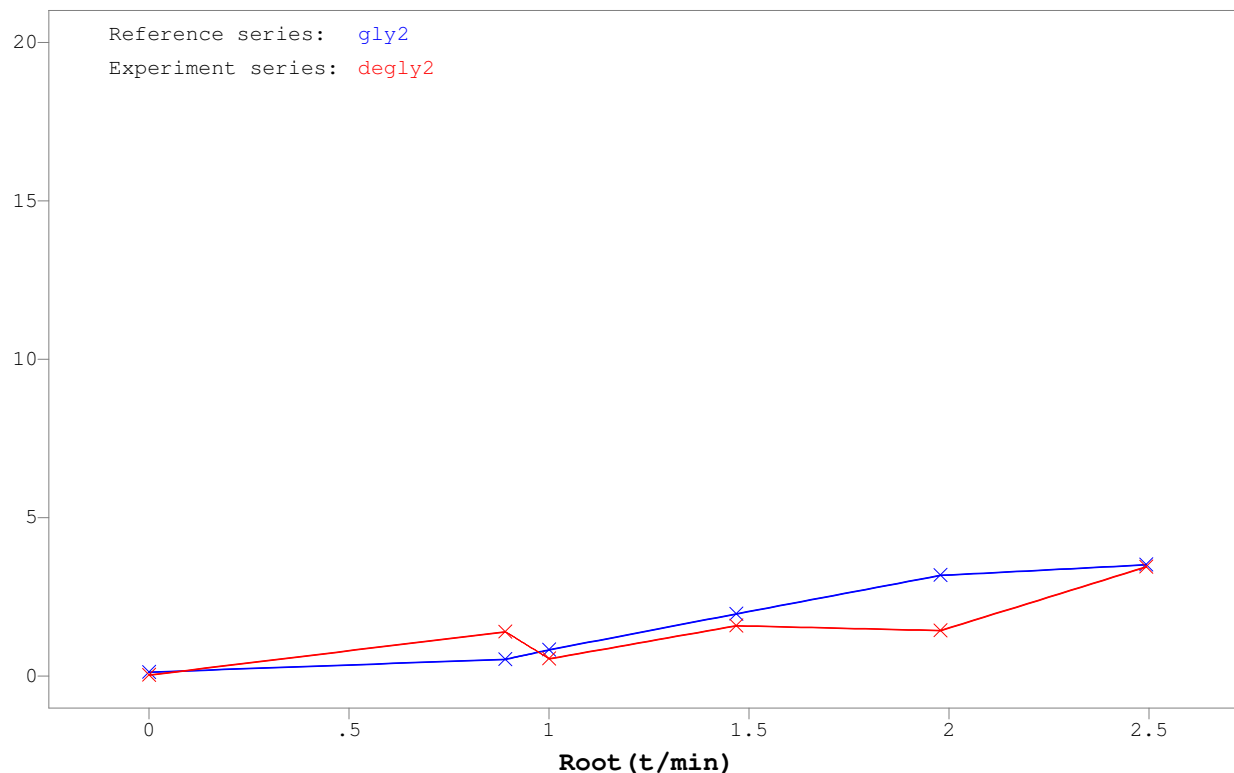
Molecule: **HC**
 Peptide: **HC347-370**
 Exchangeable protons: 20
 Index lis-file: 173
 Sequence: QVYTIPPPKEQMAKDKVSLTCMIT
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.484	10.490	0.66	0.22	0.13	0.04
0.5	10.435	10.431	2.69	7.04	0.54	1.41
1.0	10.444	10.495	4.19	2.77	0.84	0.55
10.0	10.496	10.449	9.86	7.99	1.97	1.60
60.0	10.427	10.413	15.94	7.22	3.19	1.44
240.0	10.429	10.428	17.60	17.29	3.52	3.46

DU Value



Root(t/min): 6th roots of exchange times

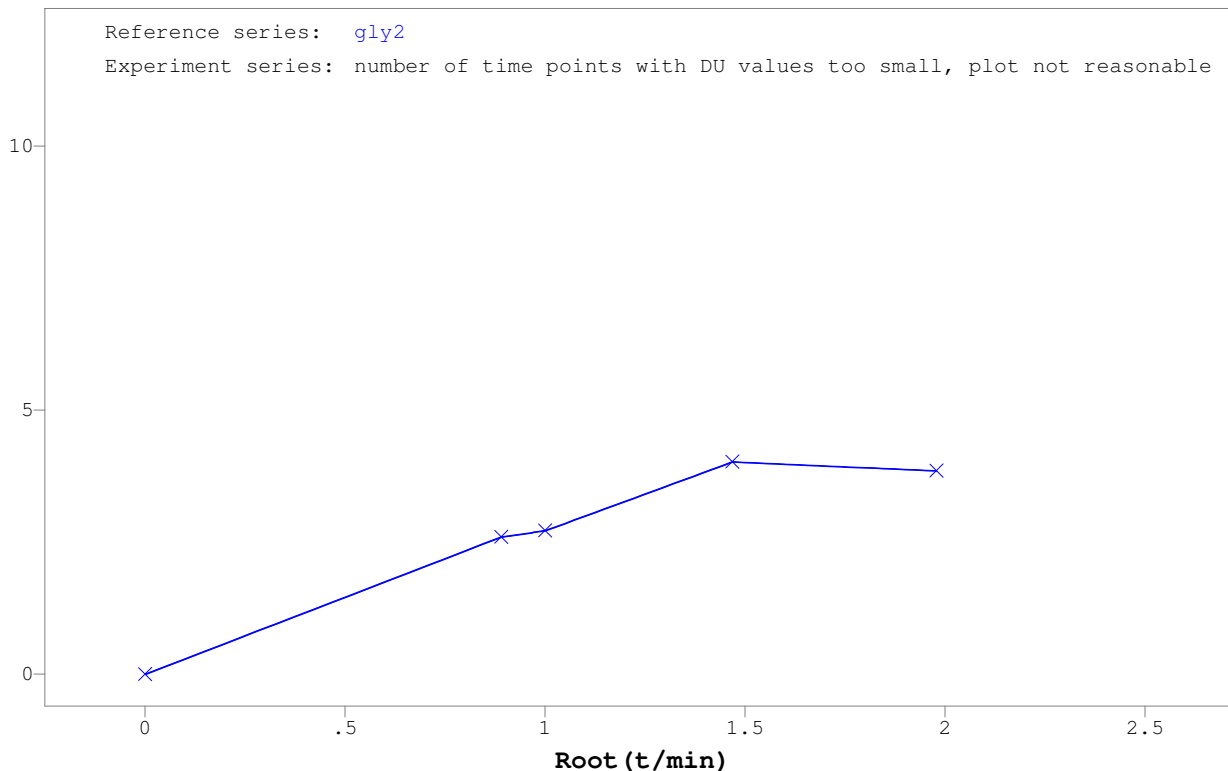
Molecule: **HC**
 Peptide: **HC377-390**
 Exchangeable protons: 12
 Index lis-file: 236
 Sequence: ITVEWQWNGQPAEN
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.360	12.403	0.00	0.01	0.00	0.00
0.5	12.345	12.432	21.67	n.d.	2.60	n.d.
1.0	12.361	12.439	22.66	n.d.	2.72	n.d.
10.0	12.335	12.422	33.51	n.d.	4.02	n.d.
60.0	12.401	n.d.	32.11	n.d.	3.85	n.d.
240.0	12.411	12.399	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

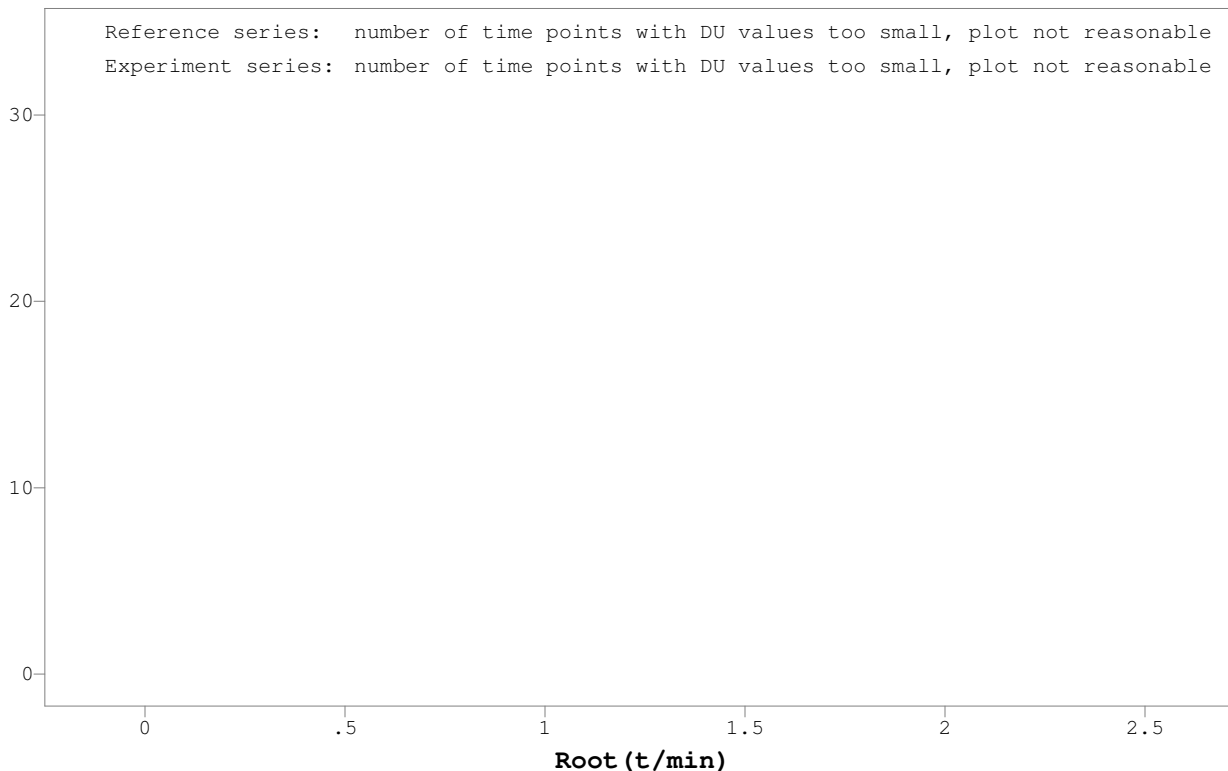
Molecule: **HC**
 Peptide: **HC411-446**
 Exchangeable protons: 34
 Index lis-file: 193
 Sequence: NVQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.139	9.140	n.d.	n.d.	n.d.	n.d.
0.5	9.140	9.140	n.d.	n.d.	n.d.	n.d.
1.0	9.152	9.161	n.d.	n.d.	n.d.	n.d.
10.0	9.121	n.d.	n.d.	n.d.	n.d.	n.d.
60.0	9.133	9.126	n.d.	n.d.	n.d.	n.d.
240.0	9.147	9.161	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC001-042**
 Exchangeable protons: 39
 Index lis-file: 1
 Sequence: DIVLTQSPATLSVTPGDSVLSLSCRASQSISSNNLHWYQKKSHE
 Range: 2 / 2

Reference: reference series, experiment: experiment series

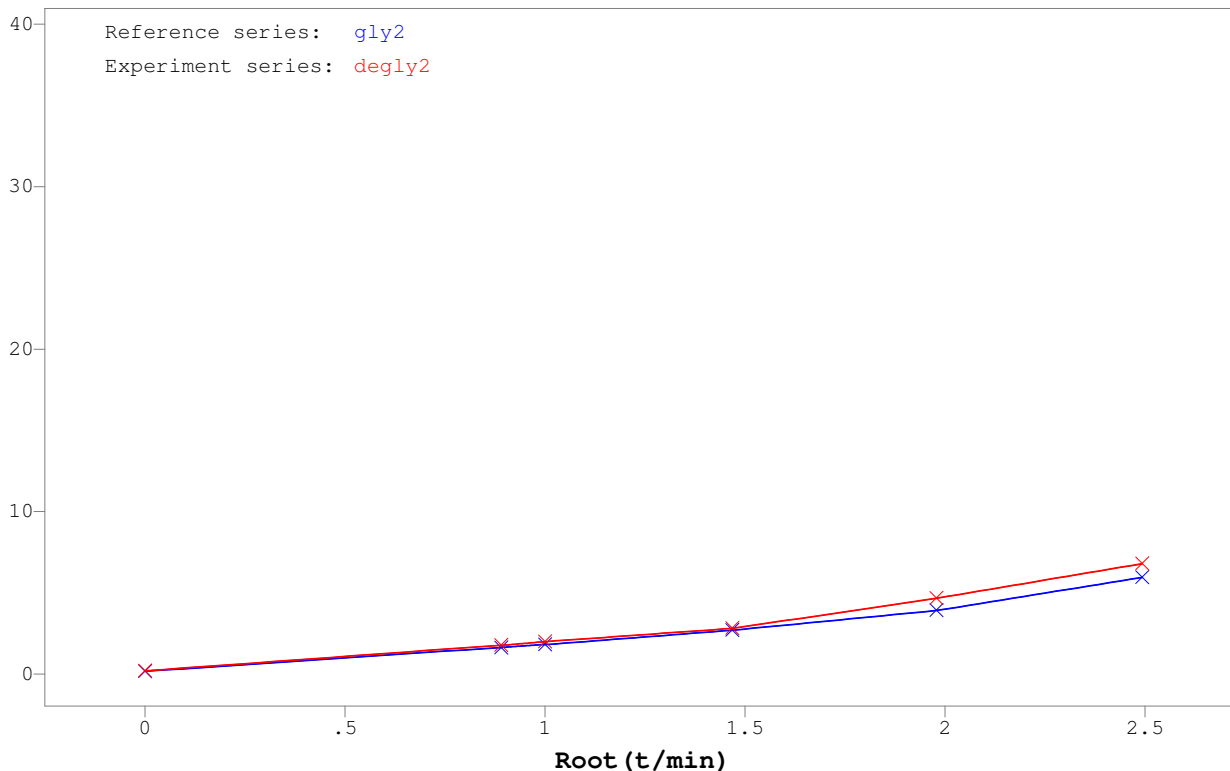
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.724	11.725	0.46	0.53	0.18	0.21
0.5	11.719	11.697	4.22	4.58	1.64	1.79
1.0	11.747	11.707	4.70	5.17	1.83	2.02
10.0	11.735	11.689	6.98	7.26	2.72	2.83
60.0	11.721	11.708	10.08	12.02	3.93	4.69
240.0	11.721	11.701	15.32	17.49	5.98	6.82

Score1 (DU sum): **1.38**
 Score2 (DU Profile): 1.13
DU sum difference (u): 2.07

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC003-018**
 Exchangeable protons: 13
 Index lis-file: 197
 Sequence: VLTQSPATLSVTPGDS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

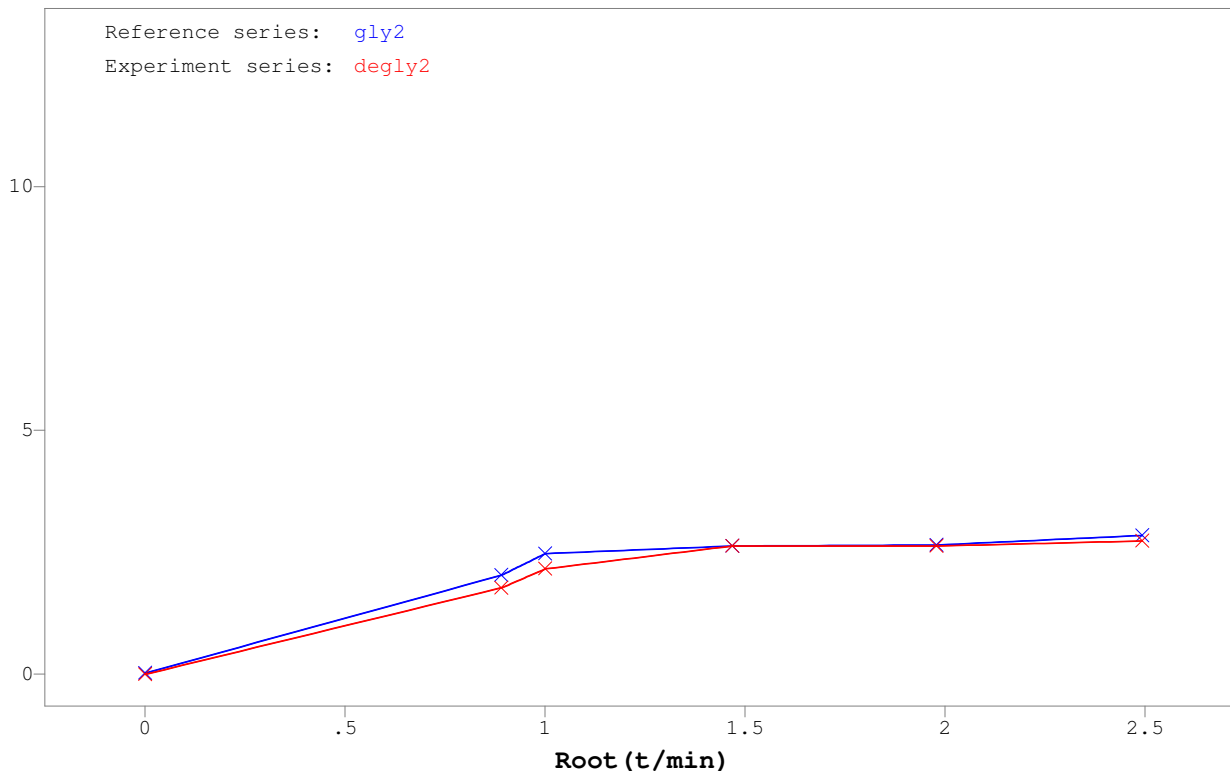
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.509	11.513	0.20	0.00	0.03	0.00
0.5	11.515	11.513	15.65	13.65	2.03	1.77
1.0	11.518	11.567	19.06	16.66	2.48	2.17
10.0	11.518	11.509	20.27	20.27	2.63	2.63
60.0	11.511	11.526	20.43	20.27	2.66	2.63
240.0	11.506	11.518	21.94	21.07	2.85	2.74

Score1 (DU sum): **1.47**

Score2 (DU Profile): 1.20

DU sum difference (u): -0.73

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC005-018**
 Exchangeable protons: 11
 Index lis-file: 198
 Sequence: TQSPATLSVIPGDS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

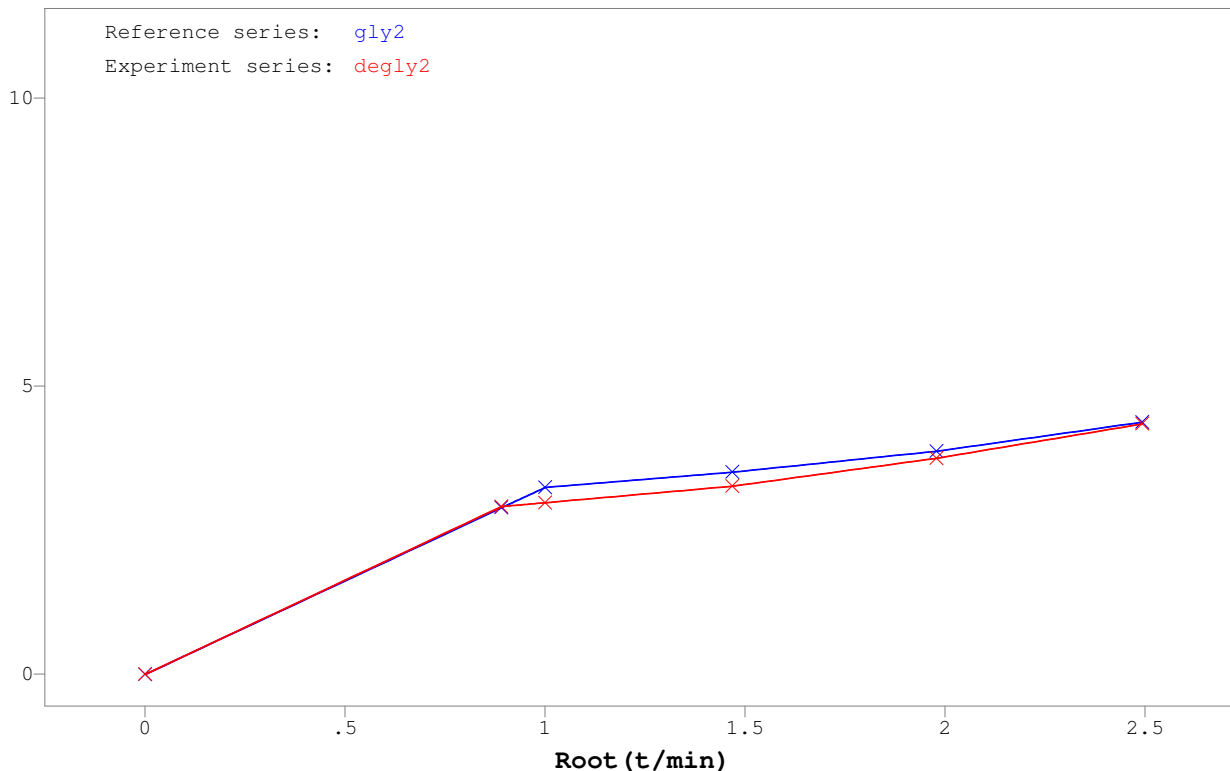
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.882	7.887	0.00	0.00	0.00	0.00
0.5	7.868	7.864	26.29	26.49	2.89	2.91
1.0	7.868	7.871	29.50	27.09	3.24	2.98
10.0	7.848	7.875	31.91	29.70	3.51	3.27
60.0	7.861	7.878	35.22	34.11	3.87	3.75
240.0	7.882	7.878	39.80	39.53	4.38	4.35

Score1 (DU sum): **1.51**
 Score2 (DU Profile): 1.32
DU sum difference (u): -0.64

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC022-035**
 Exchangeable protons: 13
 Index lis-file: 10
 Sequence: SCRASQISISNNLHW
 Range: 1 / 1

Reference: reference series, experiment: experiment series

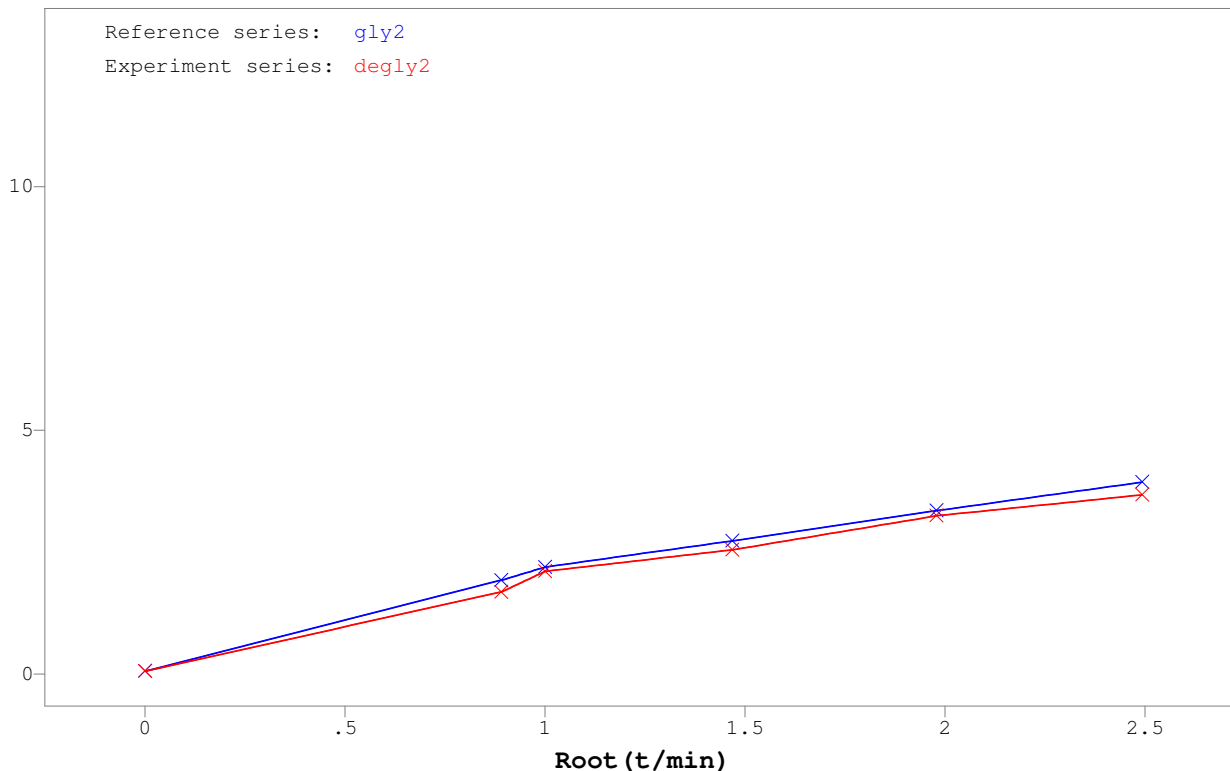
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.994	9.986	0.49	0.49	0.06	0.06
0.5	9.980	9.982	14.86	13.01	1.93	1.69
1.0	9.998	9.976	16.95	16.28	2.20	2.12
10.0	9.980	10.019	21.08	19.67	2.74	2.56
60.0	9.986	9.985	25.86	25.04	3.36	3.26
240.0	9.975	9.984	30.36	28.35	3.95	3.69

Score1 (DU sum): **1.76**
 Score2 (DU Profile): 1.44
DU sum difference (u): -0.88

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC024-033**
 Exchangeable protons: 9
 Index lis-file: 12
 Sequence: RASQSISSNNL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

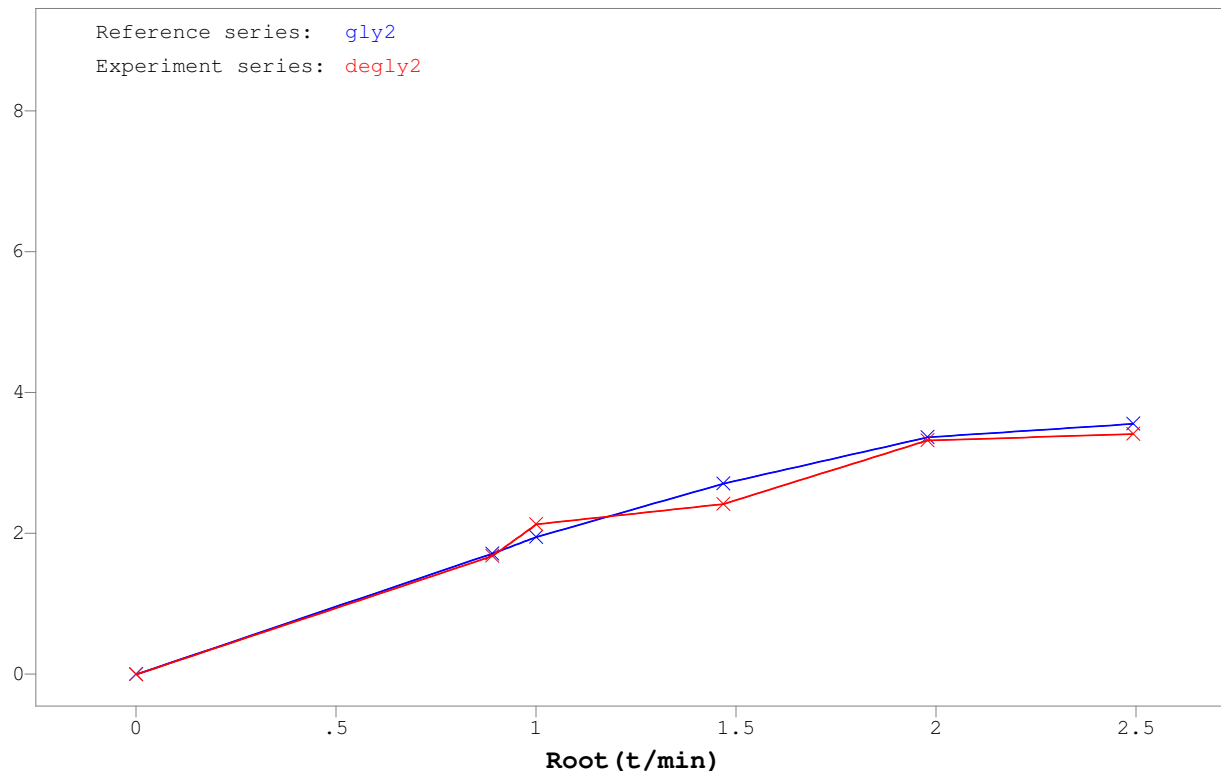
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.858	6.863	0.00	0.00	0.00	0.00
0.5	6.860	6.854	19.06	18.66	1.72	1.68
1.0	6.860	6.886	21.67	23.68	1.95	2.13
10.0	6.852	6.849	30.10	26.89	2.71	2.42
60.0	6.849	6.873	37.42	36.92	3.37	3.32
240.0	6.863	6.856	39.53	37.93	3.56	3.41

Score1 (DU sum): 0.97
 Score2 (DU Profile): **1.64**
 DU sum difference (u): -0.33

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC028-047**
 Exchangeable protons: 18
 Index lis-file: 17
 Sequence: SISNNLHWYQQKSHESPRLL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

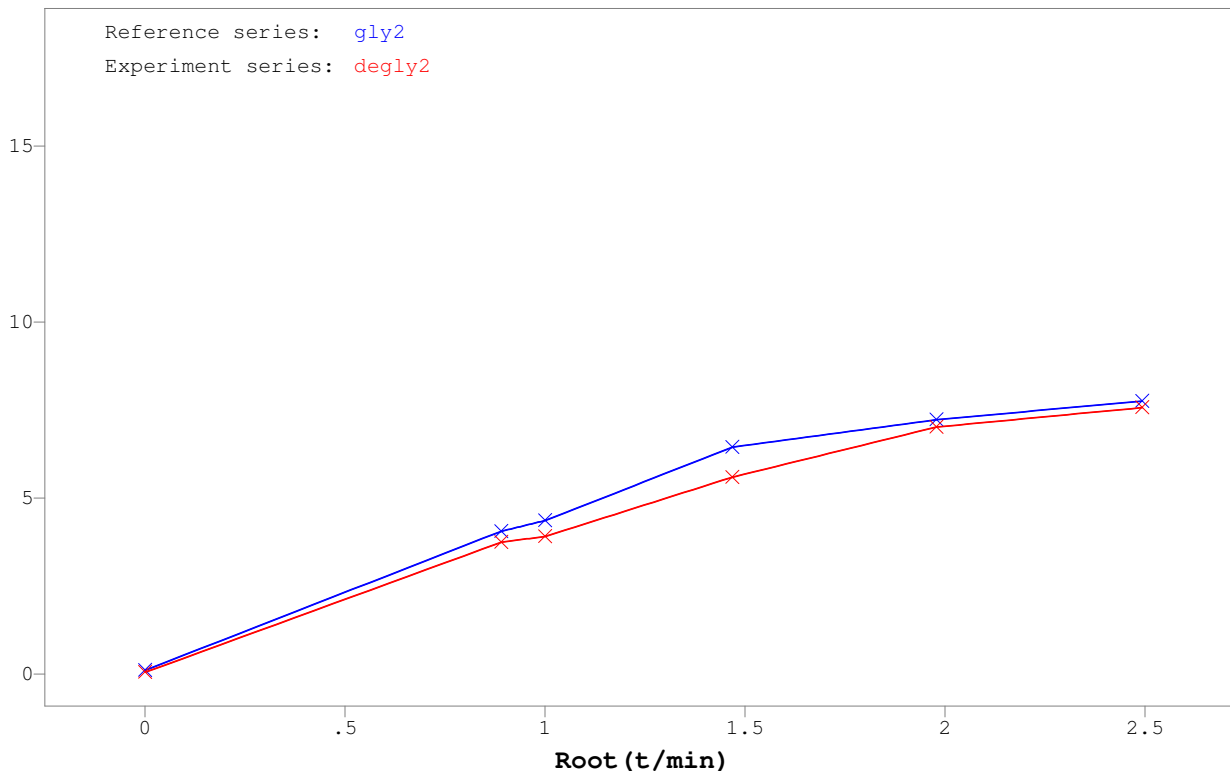
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.493	9.491	0.65	0.34	0.12	0.06
0.5	9.478	9.479	22.60	20.86	4.07	3.76
1.0	9.494	9.482	24.28	21.77	4.37	3.92
10.0	9.474	9.473	35.87	31.14	6.46	5.60
60.0	9.465	9.472	40.19	39.04	7.23	7.03
240.0	9.467	9.482	43.16	42.10	7.77	7.58

Score1 (DU sum): **1.36**
 Score2 (DU Profile): 1.36
DU sum difference (u): -1.15

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC030-046**
 Exchangeable protons: 15
 Index lis-file: 20
 Sequence: SNNLHWYQQKSHESPRL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

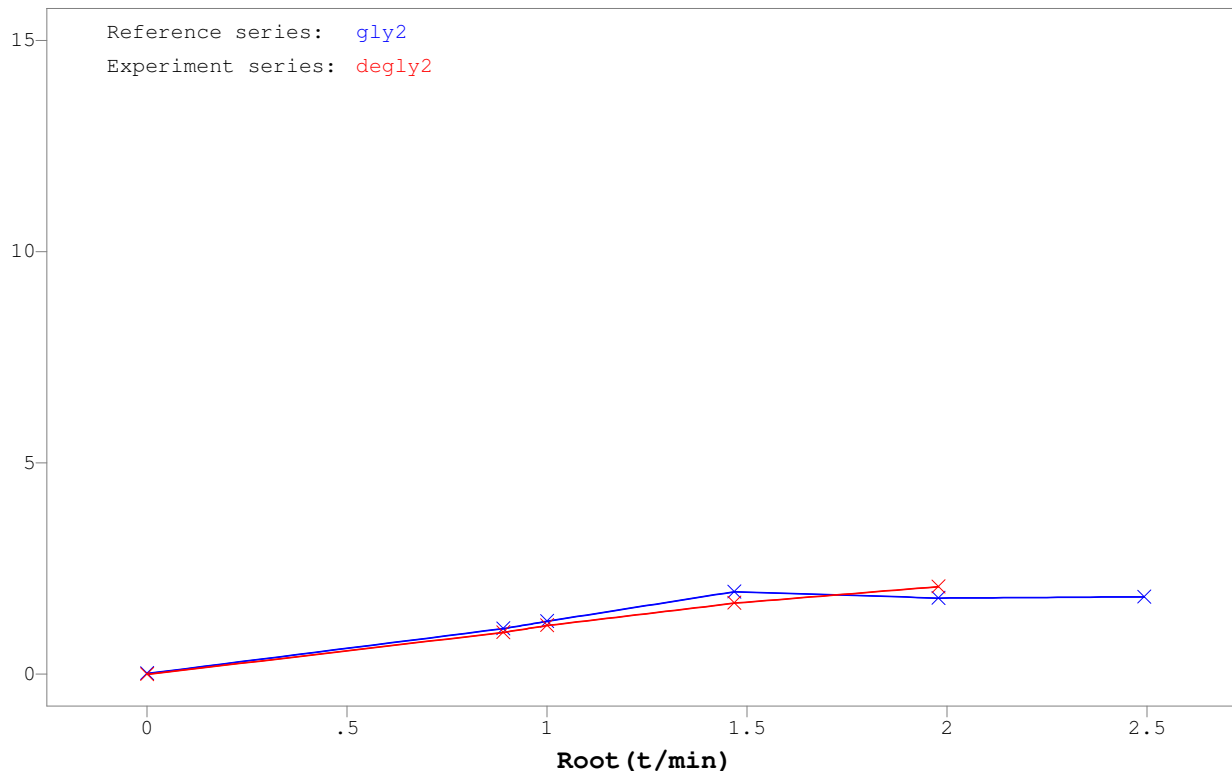
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.251	8.248	0.13	0.00	0.02	0.00
0.5	8.244	8.247	7.22	6.62	1.08	0.99
1.0	8.250	8.250	8.38	7.71	1.26	1.16
10.0	8.253	8.249	13.04	11.24	1.96	1.69
60.0	8.242	8.249	12.04	13.85	1.81	2.08
240.0	8.255	8.232	12.24	n.d.	1.84	n.d.

Score1 (DU sum): 0.40
 Score2 (DU Profile): **1.28**
 DU sum difference (u): -0.25

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC054-095**
 Exchangeable protons: 39
 Index lis-file: 32
 Sequence: SISGIPSRFSGSGSGTDFTLINSVETEDFGMYFCQSNNSWP
 Range: 1 / 1

Reference: reference series, experiment: experiment series

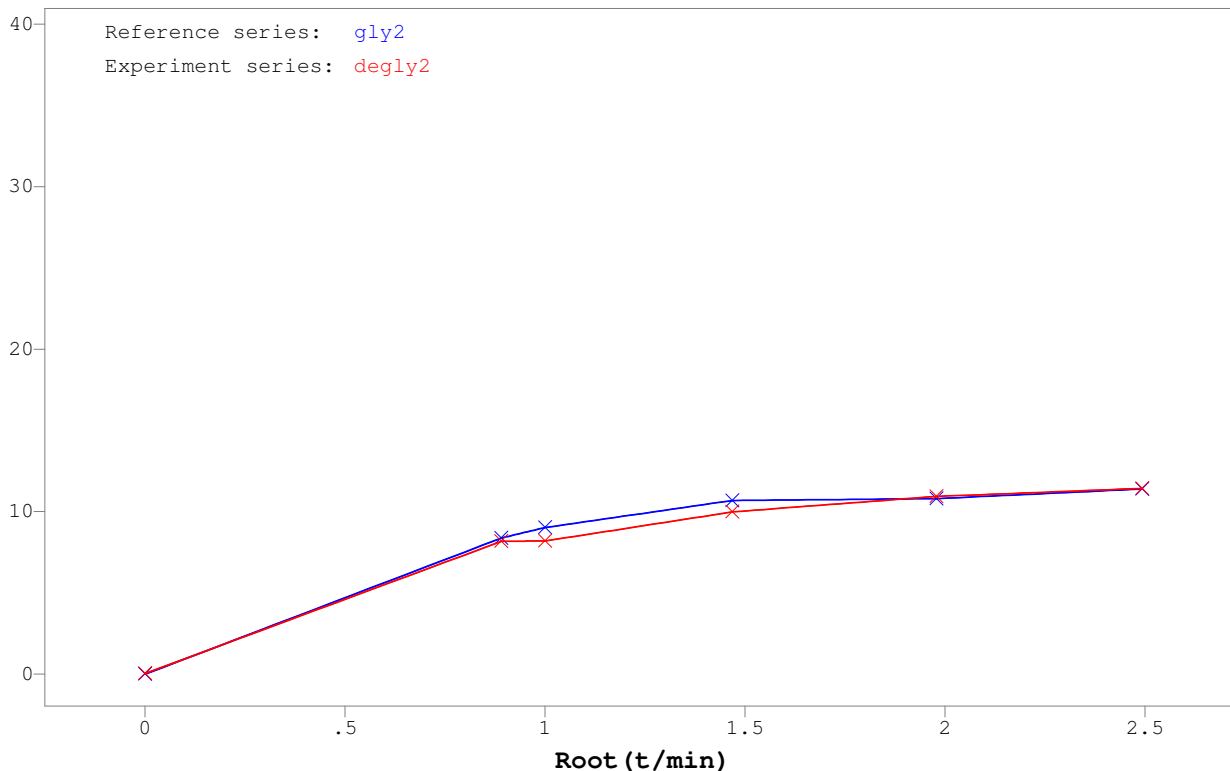
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.952	8.938	0.05	0.15	0.02	0.06
0.5	8.945	8.927	21.54	21.02	8.40	8.20
1.0	8.954	8.932	23.19	21.07	9.05	8.22
10.0	8.947	8.928	27.46	25.66	10.71	10.01
60.0	8.923	8.918	27.75	28.10	10.82	10.96
240.0	8.928	8.919	29.27	29.36	11.42	11.45

Score1 (DU sum): **1.02**
 Score2 (DU Profile): 1.06
DU sum difference (u): -1.52

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC078-085**
 Exchangeable protons: 7
 Index lis-file: 41
 Sequence: VETEDFGM
 Range: 1 / 1

Reference: reference series, experiment: experiment series

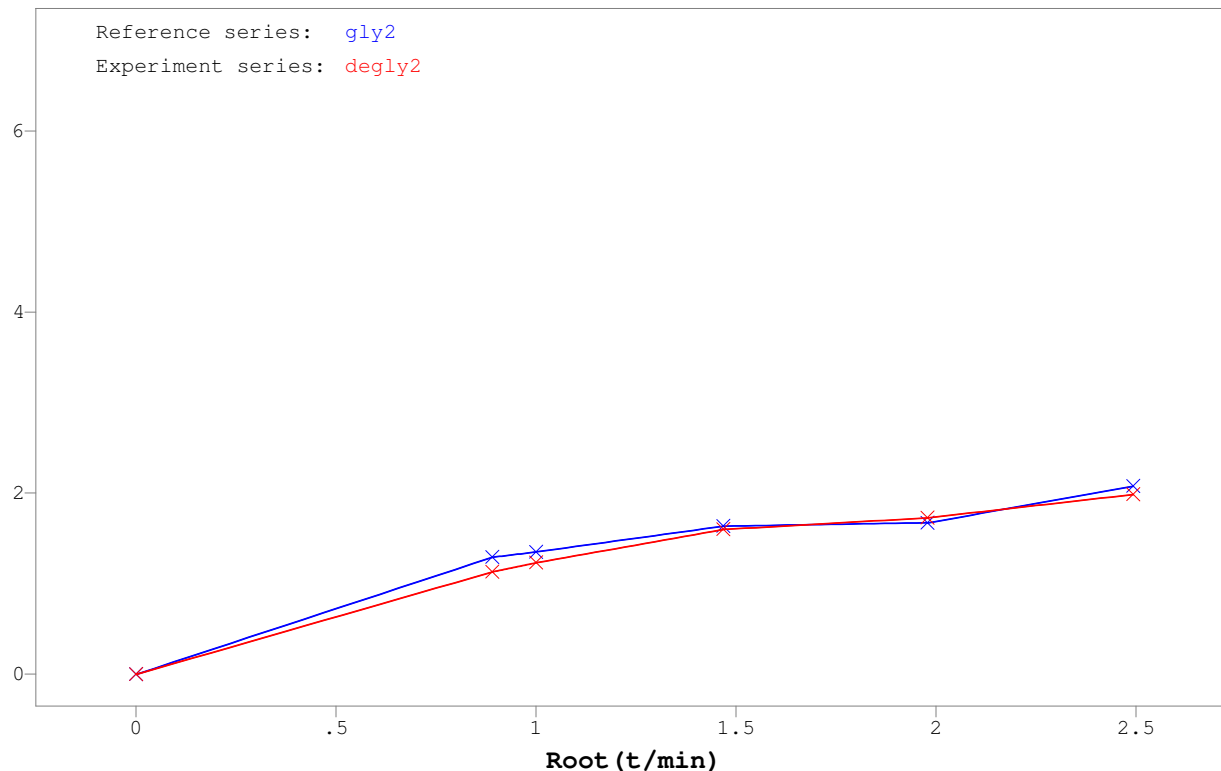
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.908	10.919	0.00	0.00	0.00	0.00
0.5	10.921	10.934	18.47	16.16	1.29	1.13
1.0	10.942	10.936	19.31	17.60	1.35	1.23
10.0	10.920	10.928	23.38	22.85	1.64	1.60
60.0	10.925	10.936	23.92	24.69	1.67	1.73
240.0	10.936	10.949	29.70	28.37	2.08	1.99

Score1 (DU sum): 0.72
 Score2 (DU Profile): **1.22**
 DU sum difference (u): -0.24

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC080-086**
 Exchangeable protons: 6
 Index lis-file: 42
 Sequence: TEDFGMY
 Range: 1 / 1

Reference: reference series, experiment: experiment series

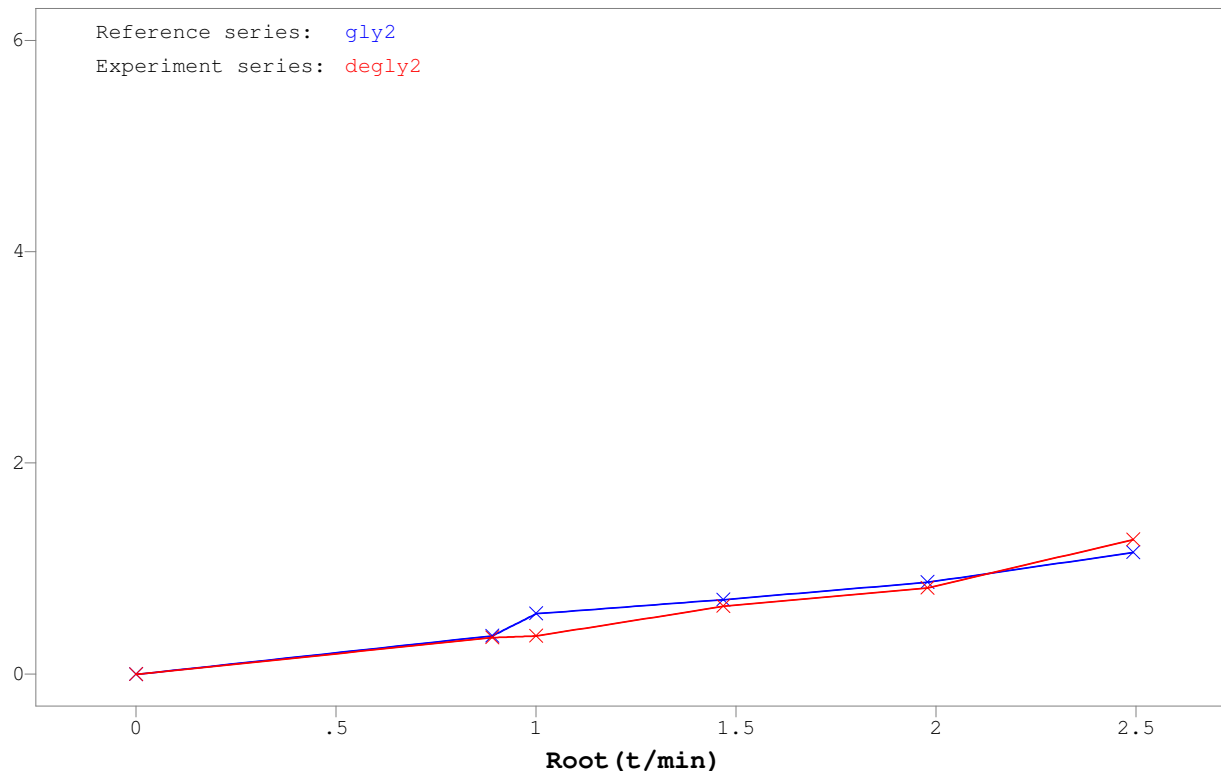
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.393	11.414	0.00	0.00	0.00	0.00
0.5	11.393	11.408	6.08	5.80	0.36	0.35
1.0	11.408	11.393	9.57	6.06	0.57	0.36
10.0	11.391	11.408	11.79	10.74	0.71	0.64
60.0	11.399	11.411	14.53	13.65	0.87	0.82
240.0	11.404	11.416	19.24	21.27	1.15	1.28

Score1 (DU sum): 0.98
 Score2 (DU Profile): **1.65p**
 DU sum difference (u): -0.25

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC105-123**
 Exchangeable protons: 15
 Index lis-file: 50
 Sequence: ELKRADAAPTVSIFPPSSE
 Range: 2 / 2

Reference: reference series, experiment: experiment series

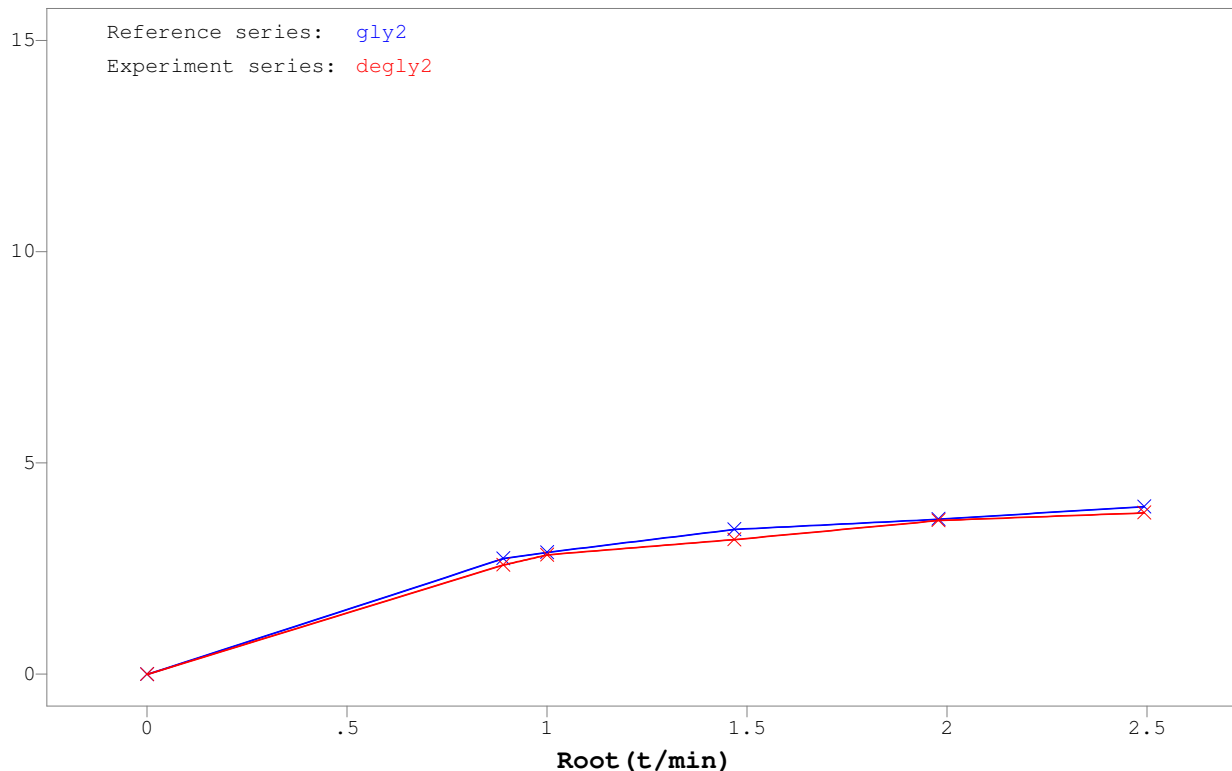
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.037	10.034	0.00	0.00	0.00	0.00
0.5	10.036	10.033	18.26	17.26	2.74	2.59
1.0	10.050	10.018	19.26	18.86	2.89	2.83
10.0	10.033	10.028	22.88	21.27	3.43	3.19
60.0	10.025	10.032	24.48	24.28	3.67	3.64
240.0	10.039	10.031	26.49	25.49	3.97	3.82

Score1 (DU sum): **1.10**
 Score2 (DU Profile): 0.90
DU sum difference (u): -0.63

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC105-124**
 Exchangeable protons: 16
 Index lis-file: 51
 Sequence: ELKRADAAPTVSIFPPSSEQ
 Range: 1 / 1

Reference: reference series, experiment: experiment series

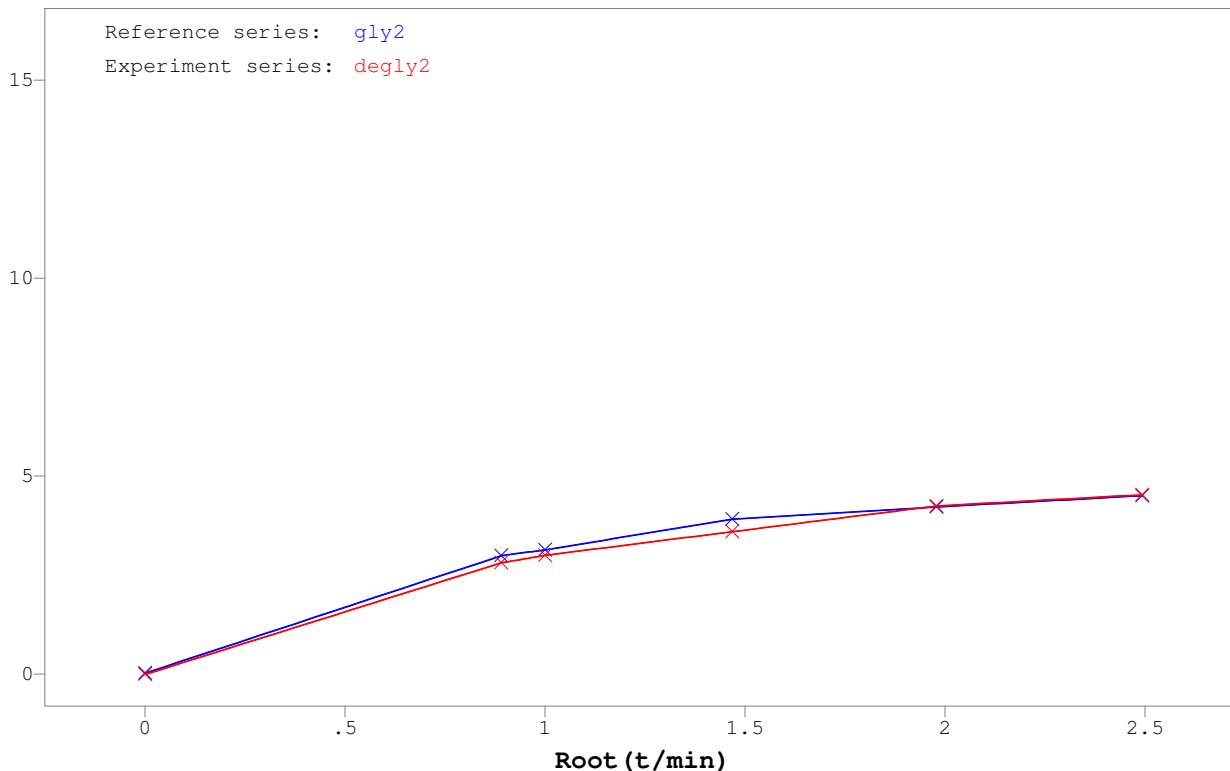
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.699	9.692	0.20	0.00	0.03	0.00
0.5	9.686	9.681	18.72	17.61	3.00	2.82
1.0	9.692	9.680	19.67	18.79	3.15	3.01
10.0	9.679	9.684	24.48	22.52	3.92	3.60
60.0	9.673	9.681	26.43	26.58	4.23	4.25
240.0	9.681	9.686	28.20	28.34	4.51	4.54

Score1 (DU sum): **1.00**
 Score2 (DU Profile): 0.95
DU sum difference (u): -0.62

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC105-125**
 Exchangeable protons: 17
 Index lis-file: 52
 Sequence: ELKRADAAPTVSIFPPSSEQL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

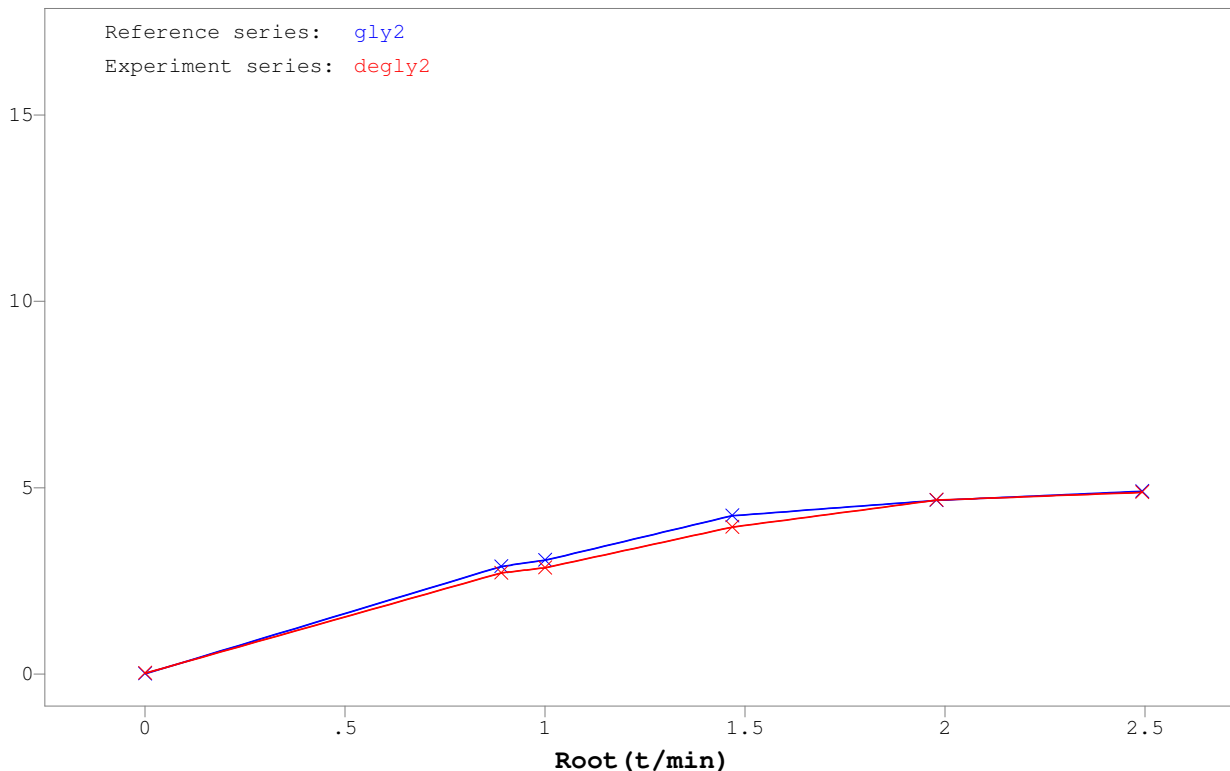
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.134	11.131	0.10	0.20	0.02	0.03
0.5	11.138	11.144	17.04	16.01	2.90	2.72
1.0	11.151	11.132	18.01	16.83	3.06	2.86
10.0	11.141	11.141	25.04	23.24	4.26	3.95
60.0	11.130	11.142	27.46	27.49	4.67	4.67
240.0	11.131	11.141	28.90	28.71	4.91	4.88

Score1 (DU sum): **1.06**

Score2 (DU Profile): 0.92

DU sum difference (u): -0.69

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC105-131**
 Exchangeable protons: 23
 Index lis-file: 53
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGAS
 Range: 1 / 2

Reference: reference series, experiment: experiment series

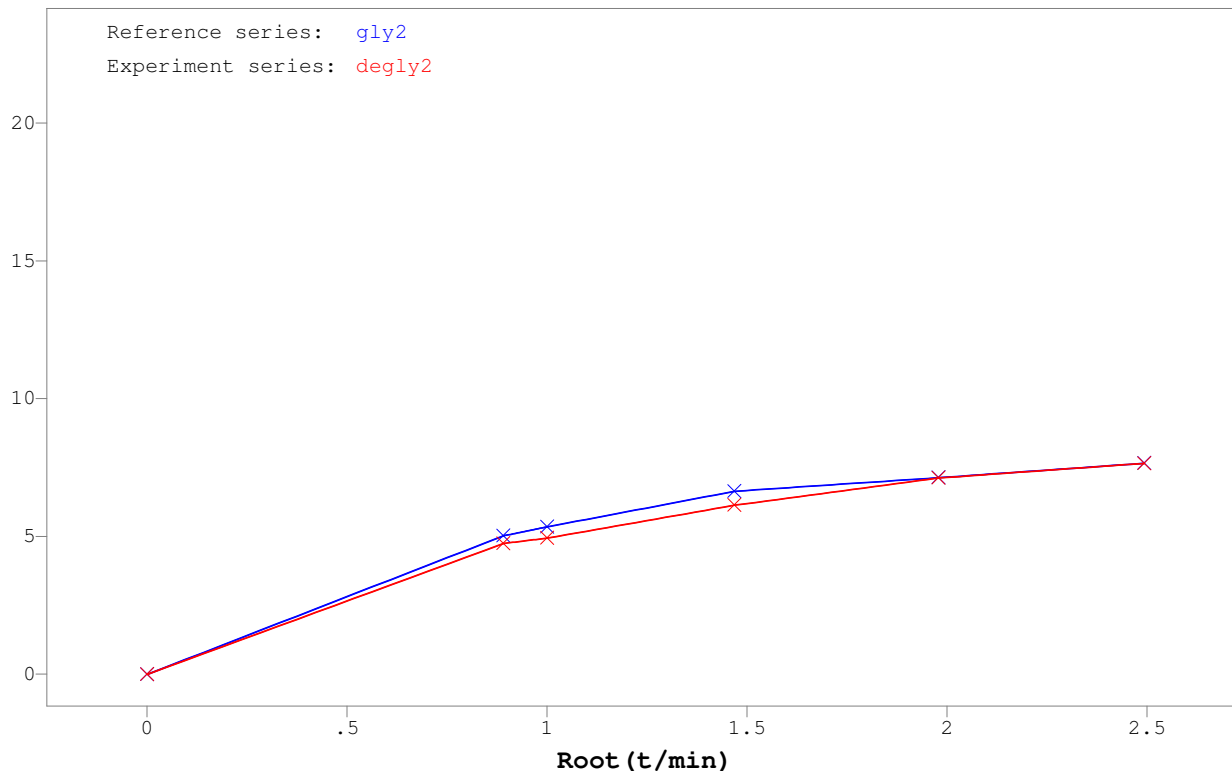
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.323	10.331	0.00	0.00	0.00	0.00
0.5	10.311	10.307	21.86	20.65	5.03	4.75
1.0	10.316	10.304	23.27	21.50	5.35	4.94
10.0	10.300	10.313	28.88	26.68	6.64	6.14
60.0	10.303	10.317	31.03	30.98	7.14	7.12
240.0	10.308	10.316	33.30	33.29	7.66	7.66

Score1 (DU sum): **1.15**
 Score2 (DU Profile): 1.03
DU sum difference (u): -1.11

DU Value



Root(t/min): 6th roots of exchange times

Molecule: LC
 Peptide: LC107-122
 Exchangeable protons: 12
 Index lis-file: 203
 Sequence: KRADAAPTVSIFPPSS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

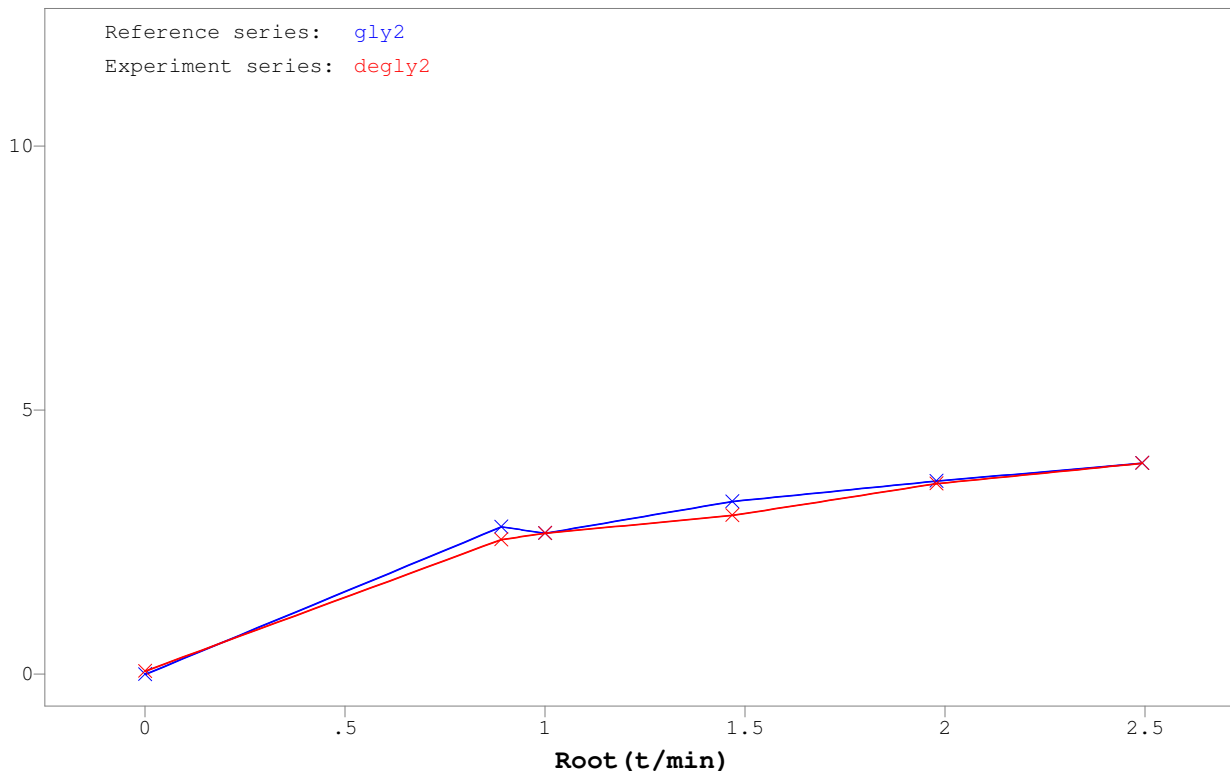
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.416	9.419	0.00	0.53	0.00	0.06
0.5	9.425	9.418	23.28	21.27	2.79	2.55
1.0	9.428	9.418	22.27	22.27	2.67	2.67
10.0	9.419	9.418	27.29	25.08	3.27	3.01
60.0	9.409	9.418	30.50	30.10	3.66	3.61
240.0	9.423	9.428	33.31	33.31	4.00	4.00

Score1 (DU sum): **1.06p**
 Score2 (DU Profile): 1.09p
DU sum difference (u): -0.49

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC107-123**
 Exchangeable protons: 13
 Index lis-file: 55
 Sequence: KRADAAPTVSIFPPSSE
 Range: 1 / 1

Reference: reference series, experiment: experiment series

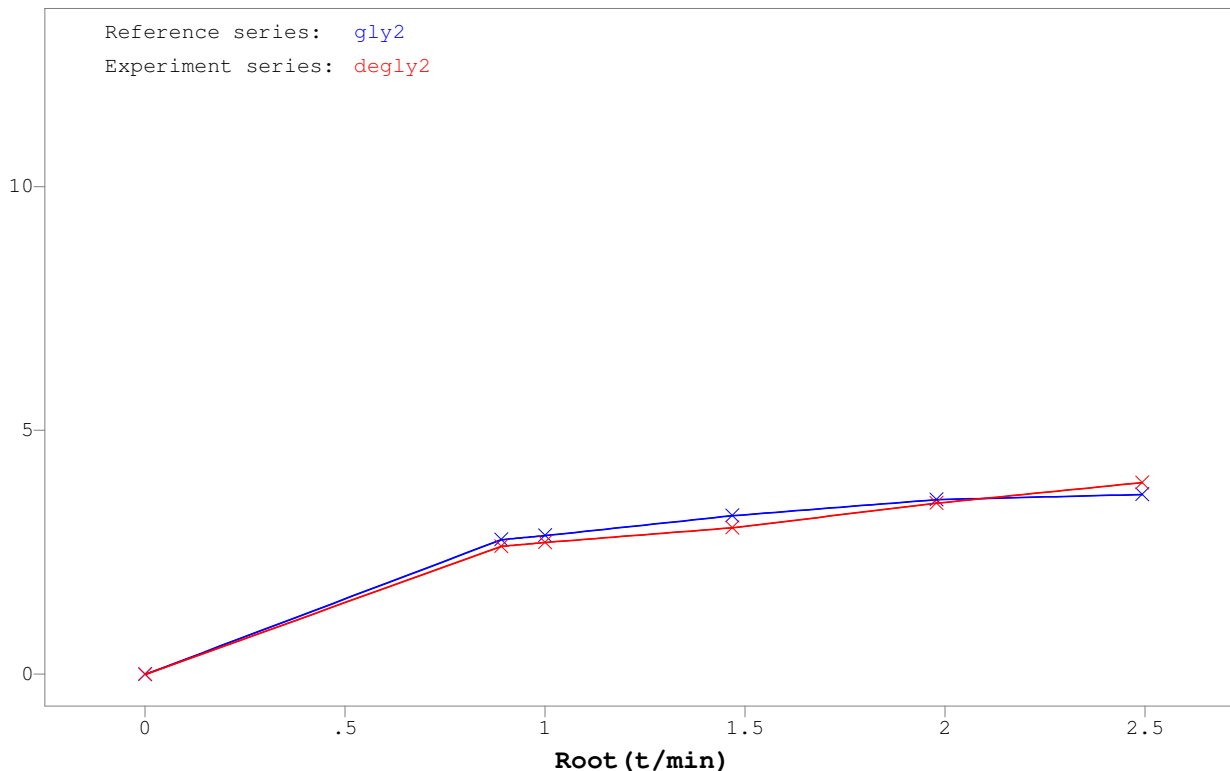
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.569	9.569	0.00	0.00	0.00	0.00
0.5	9.572	9.566	21.26	20.21	2.76	2.63
1.0	9.588	9.565	21.91	20.83	2.85	2.71
10.0	9.564	9.566	25.05	23.15	3.26	3.01
60.0	9.559	9.564	27.59	27.03	3.59	3.51
240.0	9.571	9.574	28.41	30.29	3.69	3.94

Score1 (DU sum): 0.71
 Score2 (DU Profile): **1.38**
 DU sum difference (u): -0.35

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC107-124**
 Exchangeable protons: 14
 Index lis-file: 56
 Sequence: KRADAAPTVSIFPPSSEQ
 Range: 1 / 1

Reference: reference series, experiment: experiment series

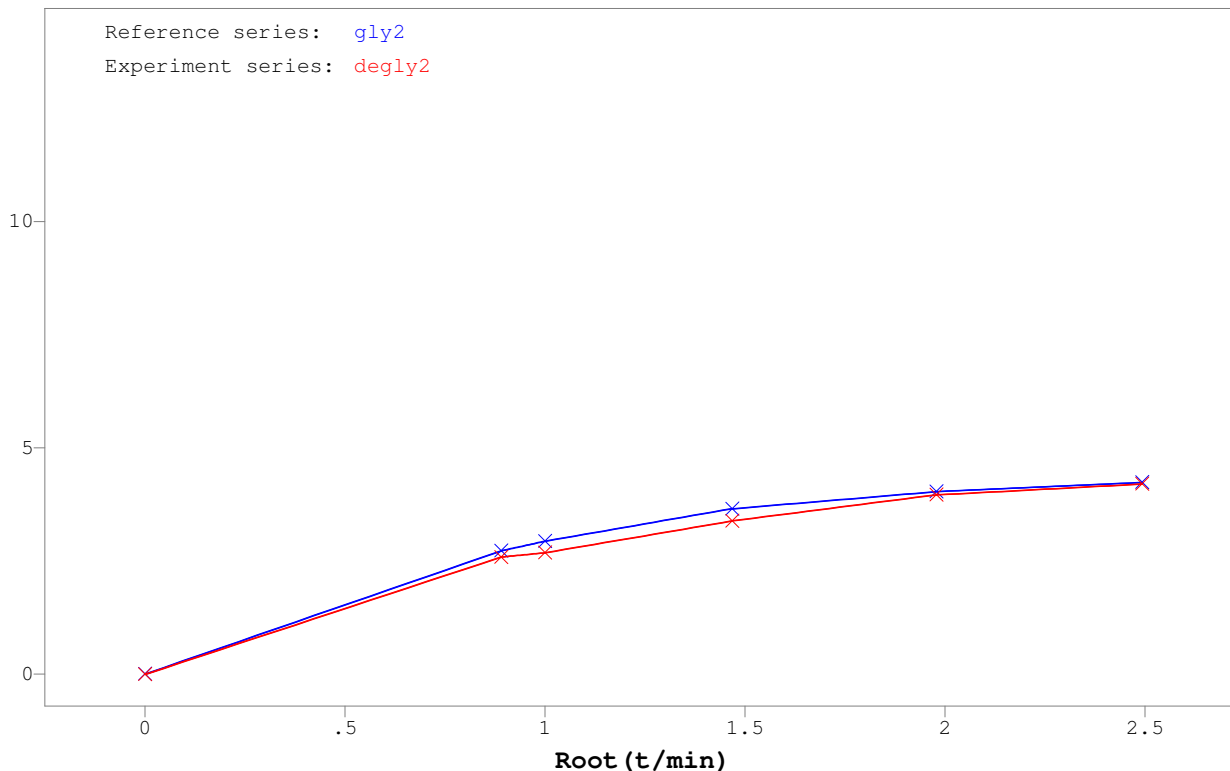
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.370	9.366	0.06	0.00	0.01	0.00
0.5	9.369	9.368	19.49	18.51	2.73	2.59
1.0	9.372	9.370	21.01	19.18	2.94	2.69
10.0	9.367	9.368	26.14	24.21	3.66	3.39
60.0	9.362	9.371	28.85	28.33	4.04	3.97
240.0	9.371	9.379	30.30	30.05	4.24	4.21

Score1 (DU sum): **1.45**
 Score2 (DU Profile): 1.19
DU sum difference (u): -0.78

DU Value



Root(t/min): 6th roots of exchange times

Molecule: LC
 Peptide: LC107-125
 Exchangeable protons: 15
 Index lis-file: 204
 Sequence: KRADAAPTVSIFPPSSEQL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

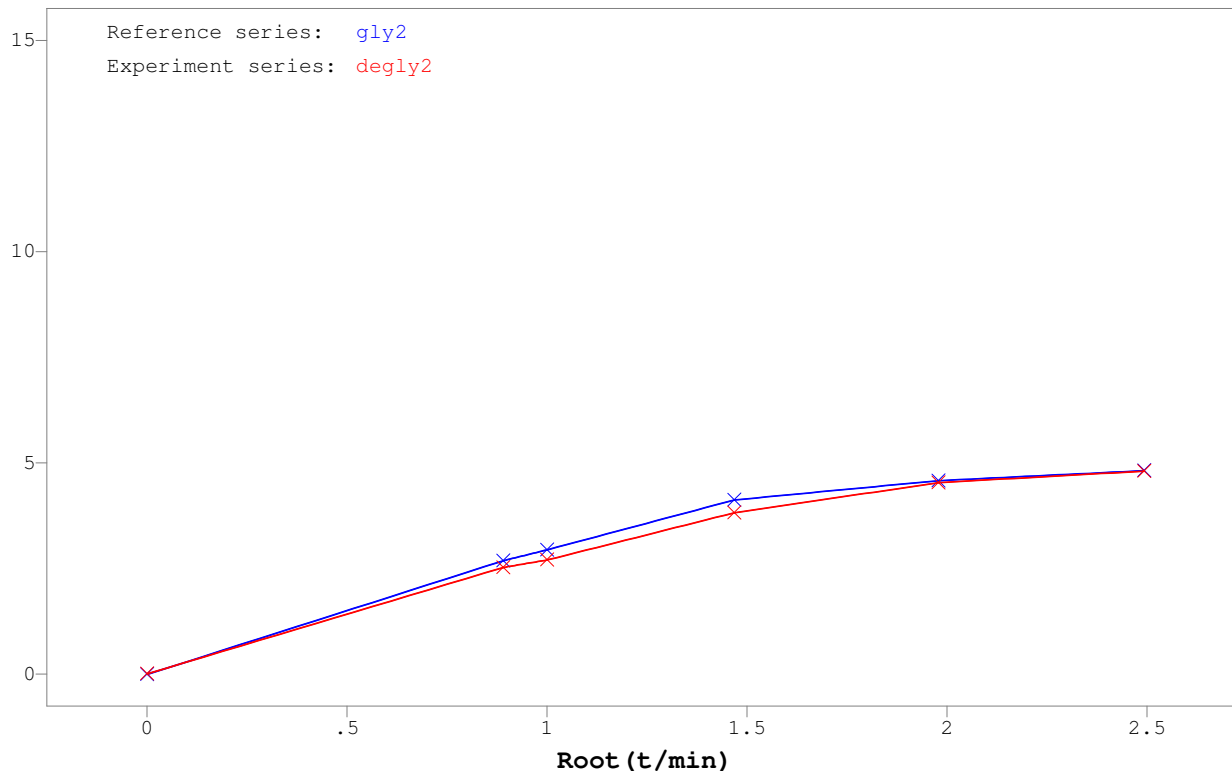
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.891	10.892	0.00	0.09	0.00	0.01
0.5	10.907	10.907	17.95	16.88	2.69	2.53
1.0	10.920	10.900	19.67	18.06	2.95	2.71
10.0	10.901	10.899	27.53	25.51	4.13	3.83
60.0	10.895	10.906	30.58	30.26	4.59	4.54
240.0	10.897	10.901	32.16	32.08	4.82	4.81

Score1 (DU sum): **1.12**

Score2 (DU Profile): 1.05

DU sum difference (u): **-0.71**

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC107-131**
 Exchangeable protons: 21
 Index lis-file: 57
 Sequence: KRADAAPTVSIFPPSSEQLTSGGAS
 Range: 1 / 2

Reference: reference series, experiment: experiment series

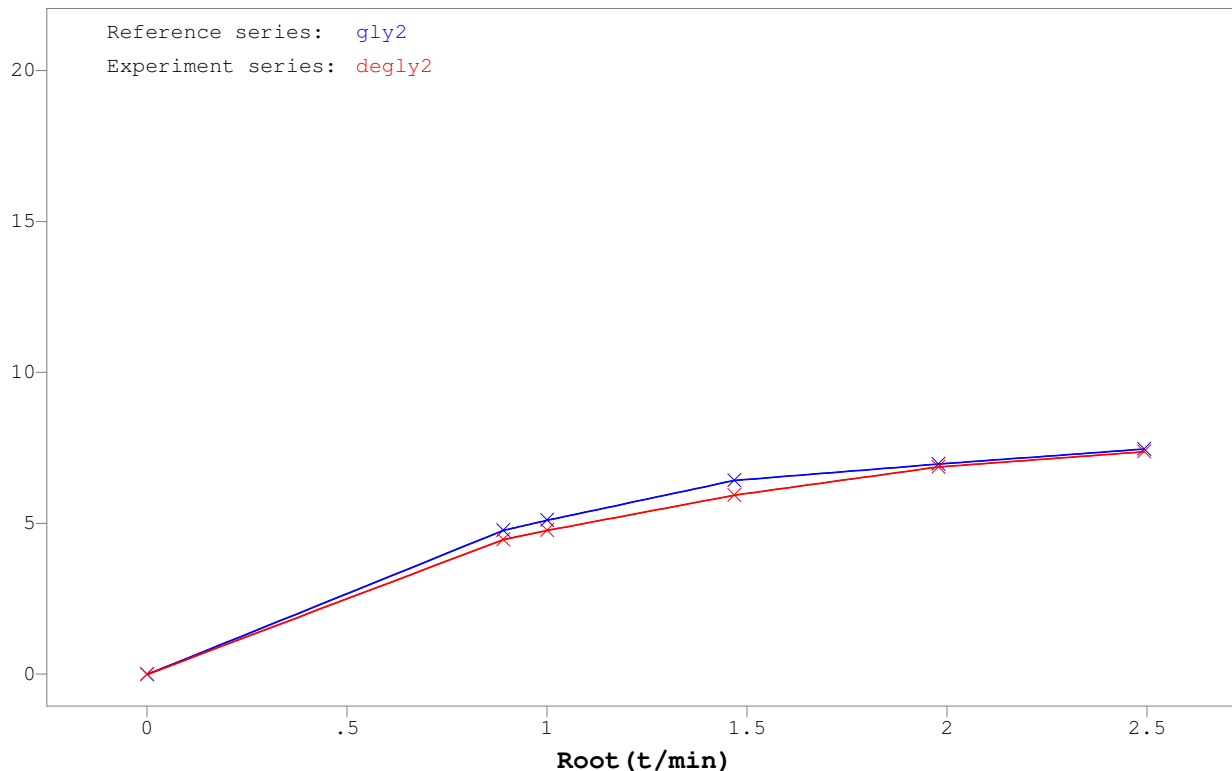
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.079	10.086	0.00	0.00	0.00	0.00
0.5	10.091	10.088	22.73	21.29	4.77	4.47
1.0	10.112	10.089	24.34	22.73	5.11	4.77
10.0	10.090	10.086	30.62	28.30	6.43	5.94
60.0	10.081	10.089	33.21	32.76	6.97	6.88
240.0	10.084	10.101	35.58	35.16	7.47	7.38

Score1 (DU sum): **1.37**
 Score2 (DU Profile): 1.23
DU sum difference (u): -1.21

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC146-160**
 Exchangeable protons: 14
 Index lis-file: 69
 Sequence: VKWKIDGSERQNGVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

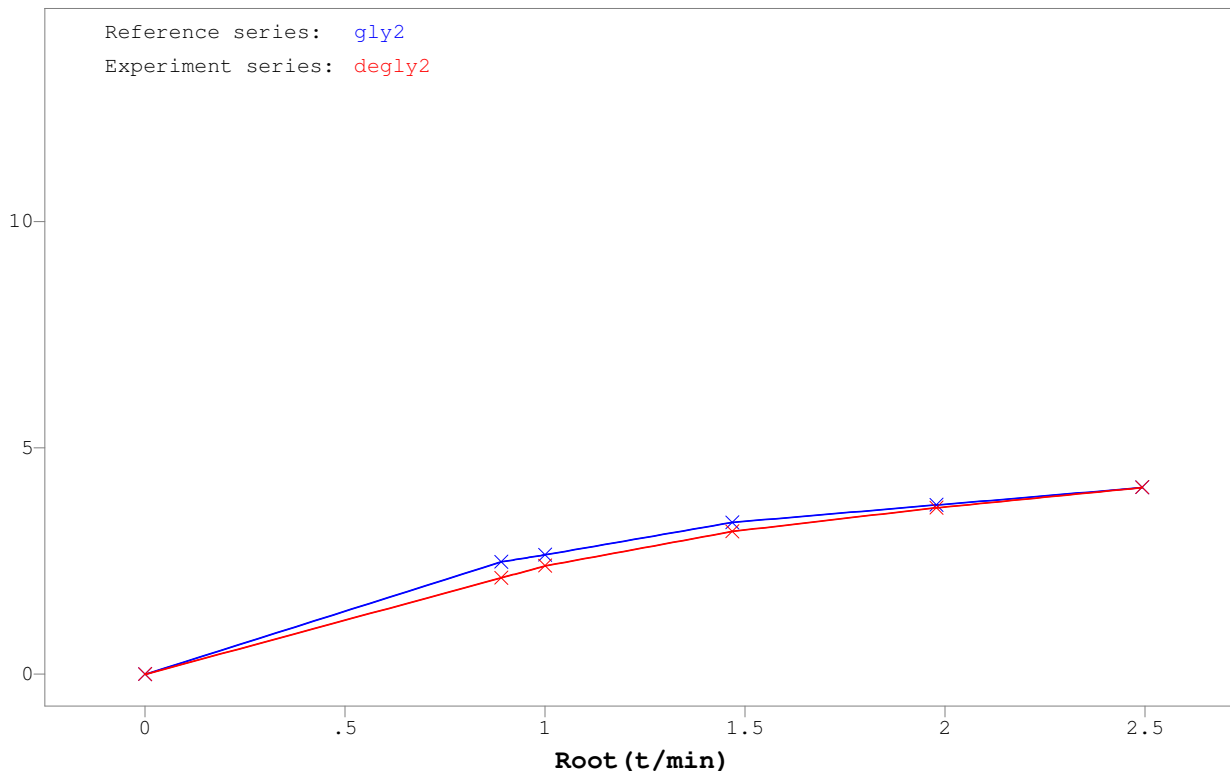
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.629	8.625	0.00	0.00	0.00	0.00
0.5	8.643	8.629	17.74	15.23	2.48	2.13
1.0	8.652	8.647	18.86	17.10	2.64	2.39
10.0	8.640	8.633	23.97	22.55	3.36	3.16
60.0	8.626	8.630	26.73	26.30	3.74	3.68
240.0	8.629	8.643	29.50	29.50	4.13	4.13

Score1 (DU sum): **1.34**
 Score2 (DU Profile): 1.20
DU sum difference (u): -0.79

DU Value



Root(t/min): 6th roots of exchange times

Molecule: **LC**
 Peptide: **LC147-160**
 Exchangeable protons: 13
 Index lis-file: 70
 Sequence: KWKIDGSERQNGVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

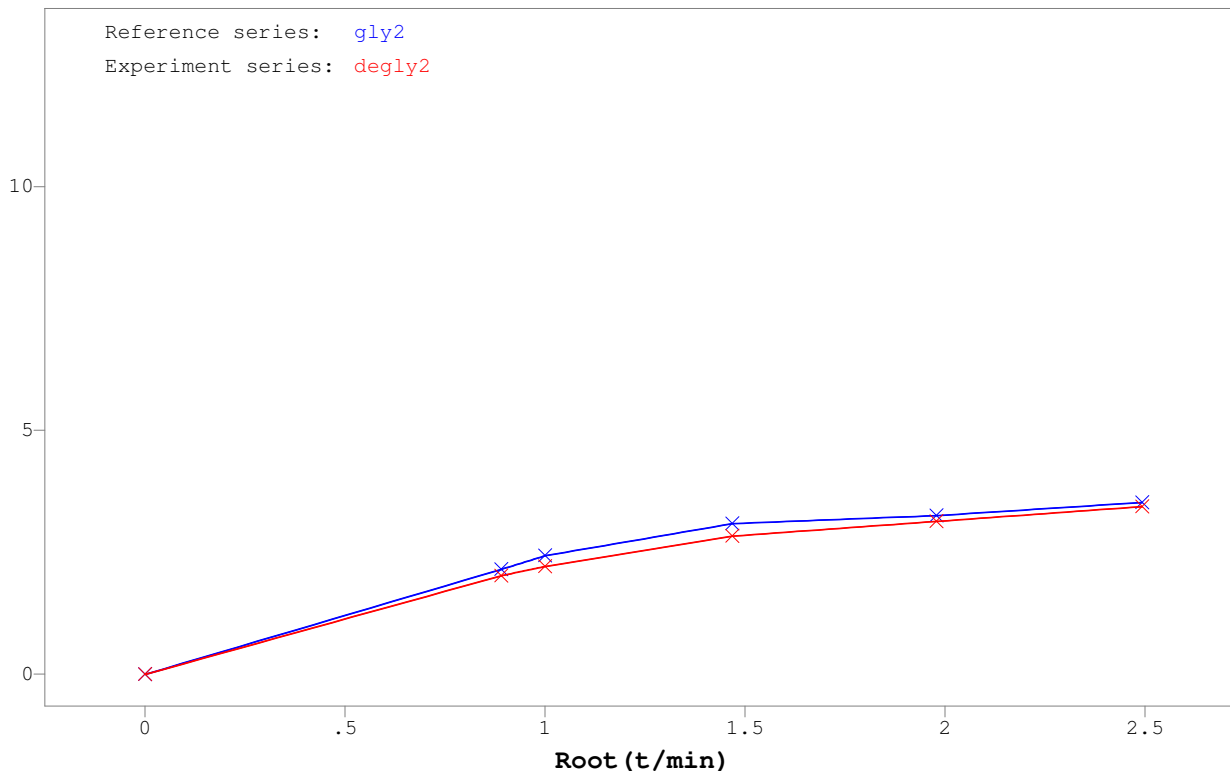
Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.187	8.185	0.00	0.00	0.00	0.00
0.5	8.187	8.189	16.59	15.58	2.16	2.03
1.0	8.193	8.189	18.73	17.05	2.44	2.22
10.0	8.194	8.193	23.80	21.83	3.09	2.84
60.0	8.178	8.182	25.07	24.15	3.26	3.14
240.0	8.194	8.180	27.15	26.49	3.53	3.44

Score1 (DU sum): **1.15**
 Score2 (DU Profile): 1.15
DU sum difference (u): -0.70

DU Value



Root(t/min): 6th roots of exchange times

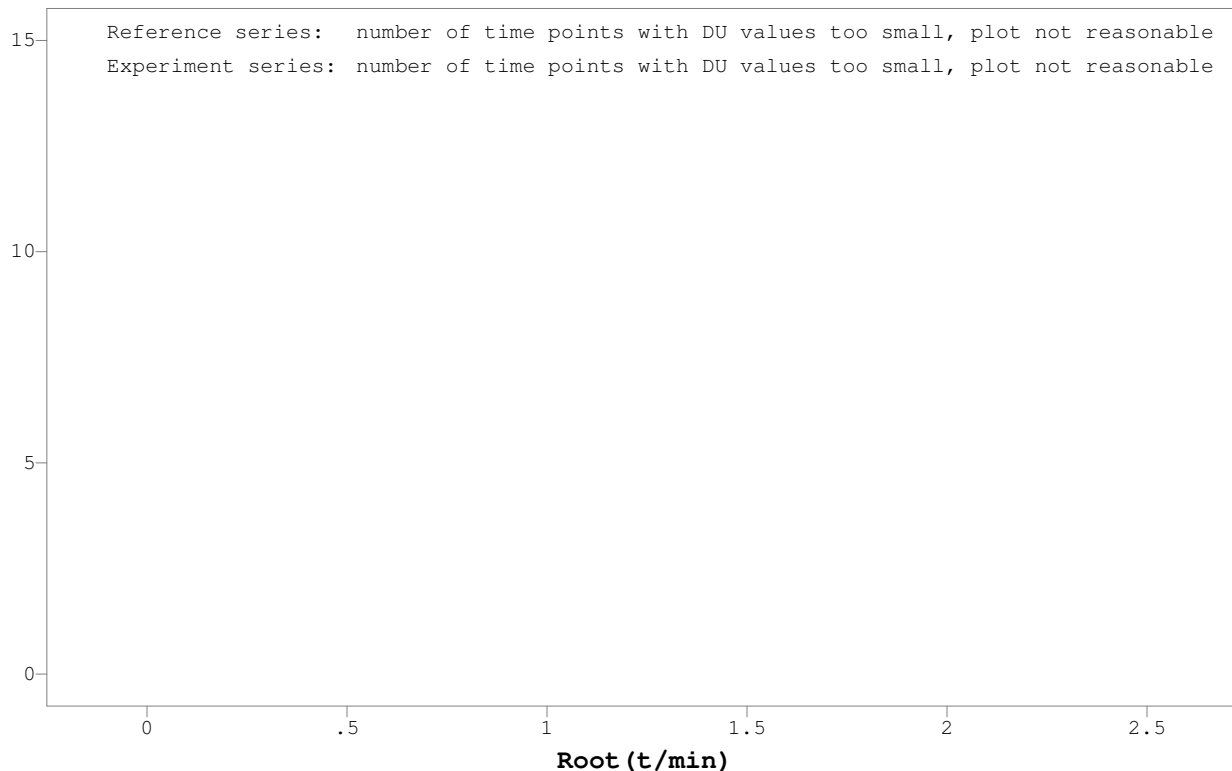
Molecule: **LC**
 Peptide: **LC004-021**
 Exchangeable protons: 15
 Index lis-file: 2
 Sequence: LTQSPATLSVTPGDSVSL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.984	9.985	n.d.	n.d.	n.d.	n.d.
0.5	9.984	9.981	n.d.	n.d.	n.d.	n.d.
1.0	9.992	9.991	n.d.	n.d.	n.d.	n.d.
10.0	9.988	9.984	n.d.	n.d.	n.d.	n.d.
60.0	9.986	9.987	n.d.	n.d.	n.d.	n.d.
240.0	9.989	9.981	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

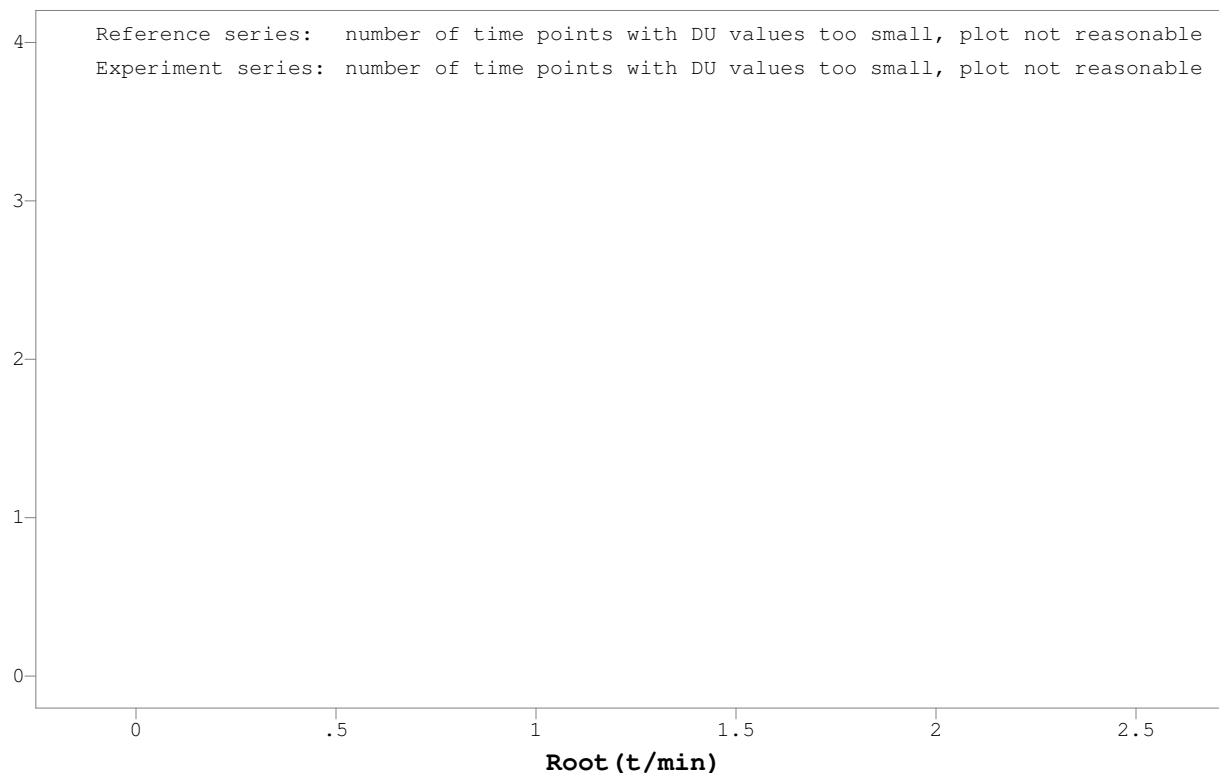
Molecule: **LC**
 Peptide: **LC019-023**
 Exchangeable protons: 4
 Index lis-file: 7
 Sequence: VSLSC
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.896	7.901	n.d.	n.d.	n.d.	n.d.
0.5	7.889	7.893	n.d.	n.d.	n.d.	n.d.
1.0	7.896	7.896	n.d.	n.d.	n.d.	n.d.
10.0	7.893	7.896	n.d.	n.d.	n.d.	n.d.
60.0	7.889	7.900	n.d.	n.d.	n.d.	n.d.
240.0	7.900	7.899	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

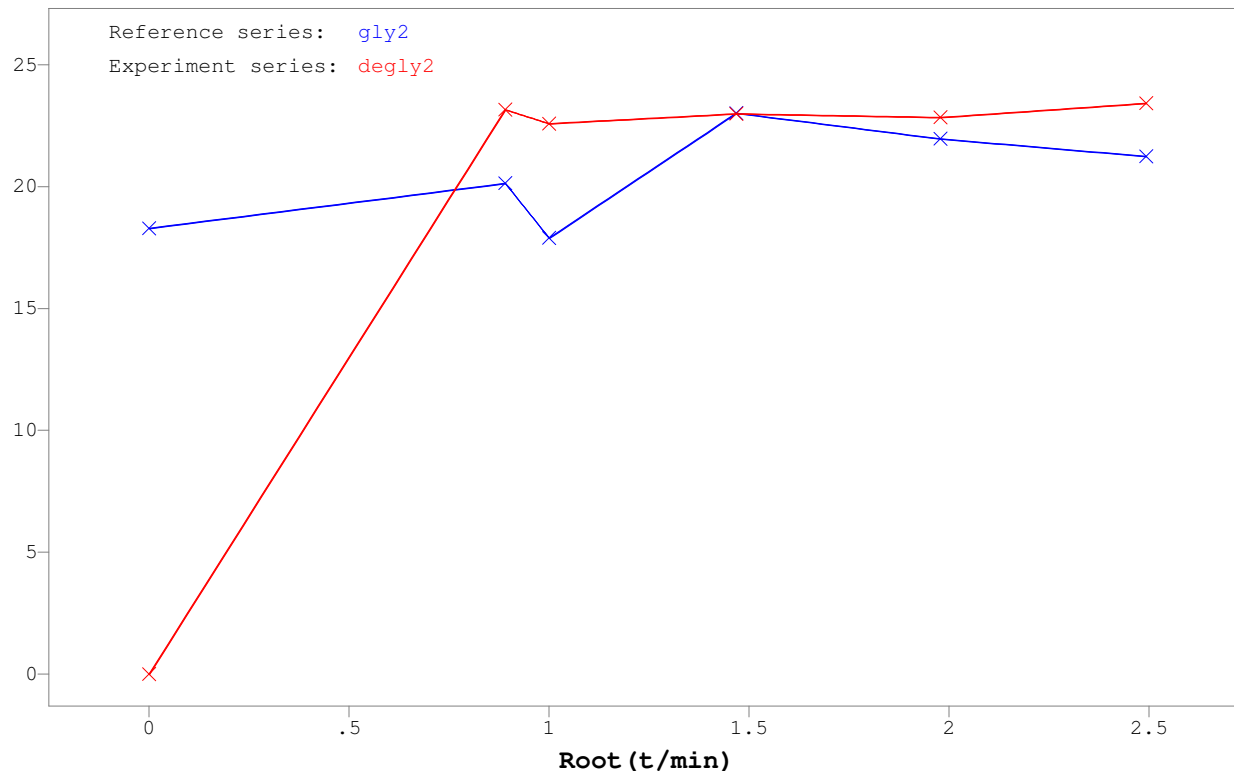
Molecule: **LC**
 Peptide: **LC019-046**
 Exchangeable protons: 26
 Index lis-file: 8
 Sequence: VLSLCRASQSISSNNLHWYQQKSHESPRL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.611	11.570	70.38	0.00	18.30	0.00
0.5	11.620	11.571	77.46	89.10	20.14	23.17
1.0	11.568	11.562	68.83	86.89	17.90	22.59
10.0	11.558	11.596	88.54	88.44	23.02	22.99
60.0	11.560	11.565	84.48	87.87	21.97	22.85
240.0	11.552	11.564	81.72	90.10	21.25	23.43

DU Value



Root(t/min): 6th roots of exchange times

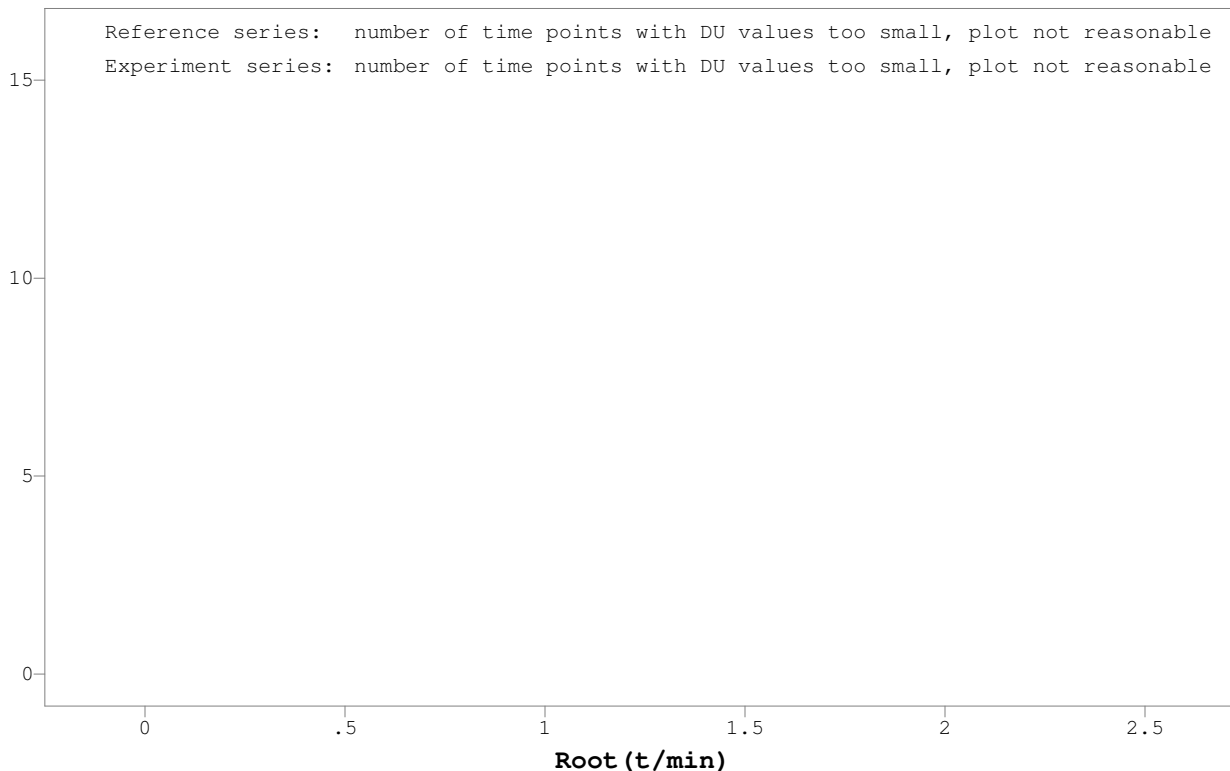
Molecule: **LC**
 Peptide: **LC029-046**
 Exchangeable protons: 16
 Index lis-file: 19
 Sequence: ISNNLHWYQQKSHESPRL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.010	8.021	n.d.	n.d.	n.d.	n.d.
0.5	8.018	8.037	n.d.	n.d.	n.d.	n.d.
1.0	8.036	8.023	n.d.	n.d.	n.d.	n.d.
10.0	8.015	8.024	n.d.	n.d.	n.d.	n.d.
60.0	8.017	8.012	n.d.	n.d.	n.d.	n.d.
240.0	8.042	8.003	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

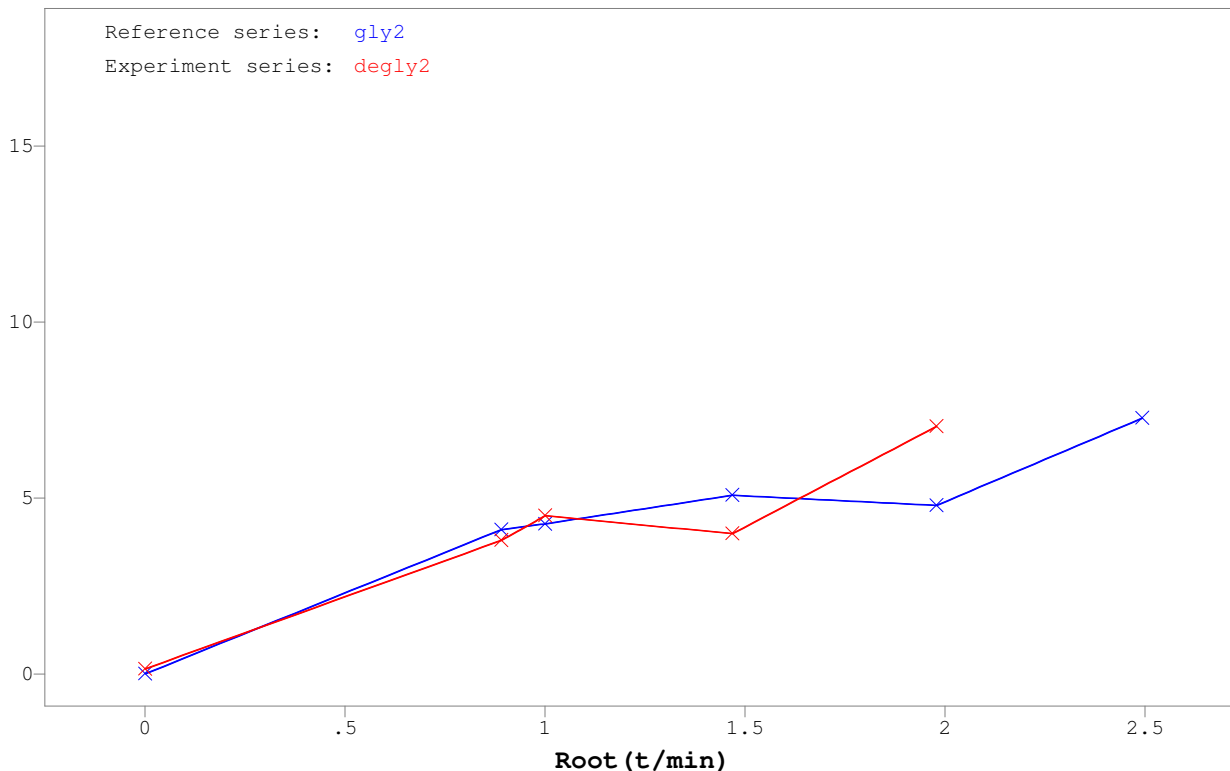
Molecule: **LC**
 Peptide: **LC051-070**
 Exchangeable protons: 18
 Index lis-file: 27
 Sequence: ASQSISGIPSRFSGSGSGTD
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.732	8.744	0.08	0.87	0.02	0.16
0.5	8.751	8.751	22.85	21.15	4.11	3.81
1.0	8.744	8.759	23.76	25.04	4.28	4.51
10.0	8.741	8.745	28.26	22.21	5.09	4.00
60.0	8.734	8.739	26.67	39.13	4.80	7.04
240.0	8.728	8.750	40.44	n.d.	7.28	n.d.

DU Value



Root(t/min): 6th roots of exchange times

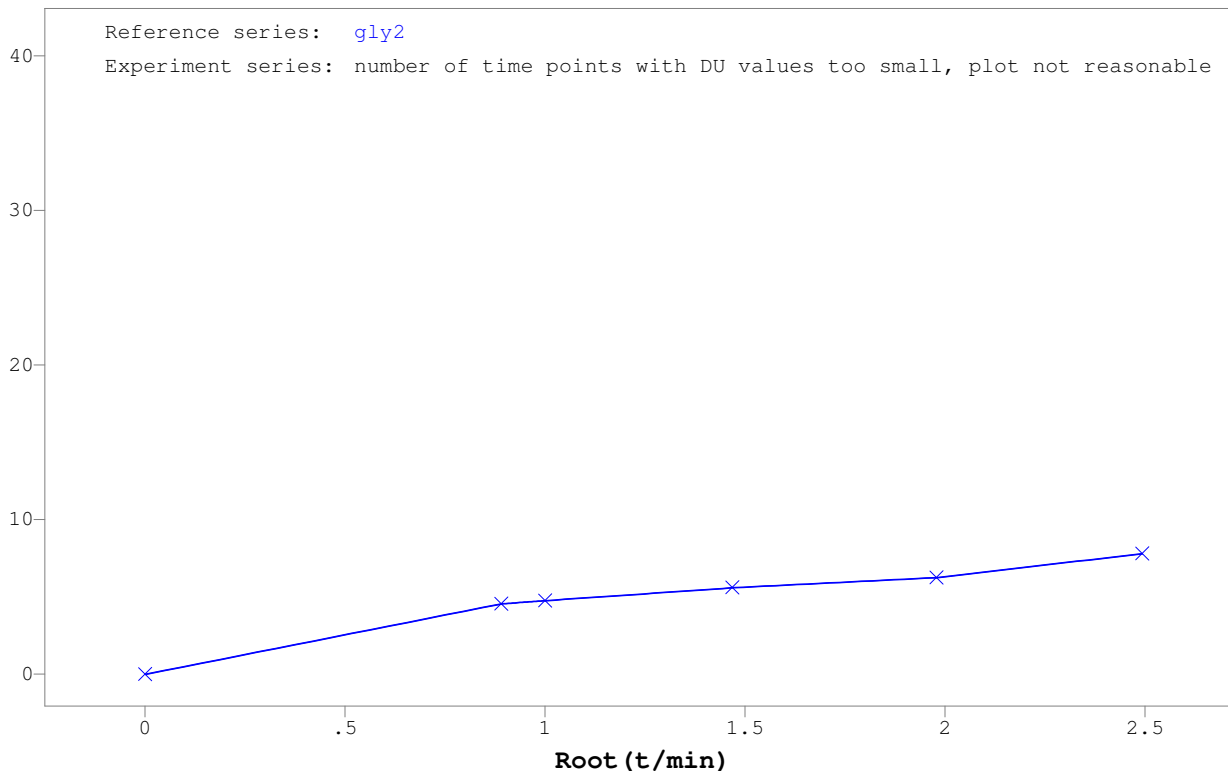
Molecule: **LC**
 Peptide: **LC051-093**
 Exchangeable protons: 41
 Index lis-file: 28
 Sequence: ASQSISGIPSRFSGSGSGTDFTLINSVETEDFGMYFCQQSNS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.476	9.424	0.00	n.d.	0.00	n.d.
0.5	9.466	9.444	11.14	n.d.	4.57	n.d.
1.0	9.475	9.450	11.64	n.d.	4.77	n.d.
10.0	9.449	9.418	13.68	n.d.	5.61	n.d.
60.0	9.441	9.399	15.29	n.d.	6.27	n.d.
240.0	9.428	9.431	19.07	n.d.	7.82	n.d.

DU Value



Root(t/min): 6th roots of exchange times

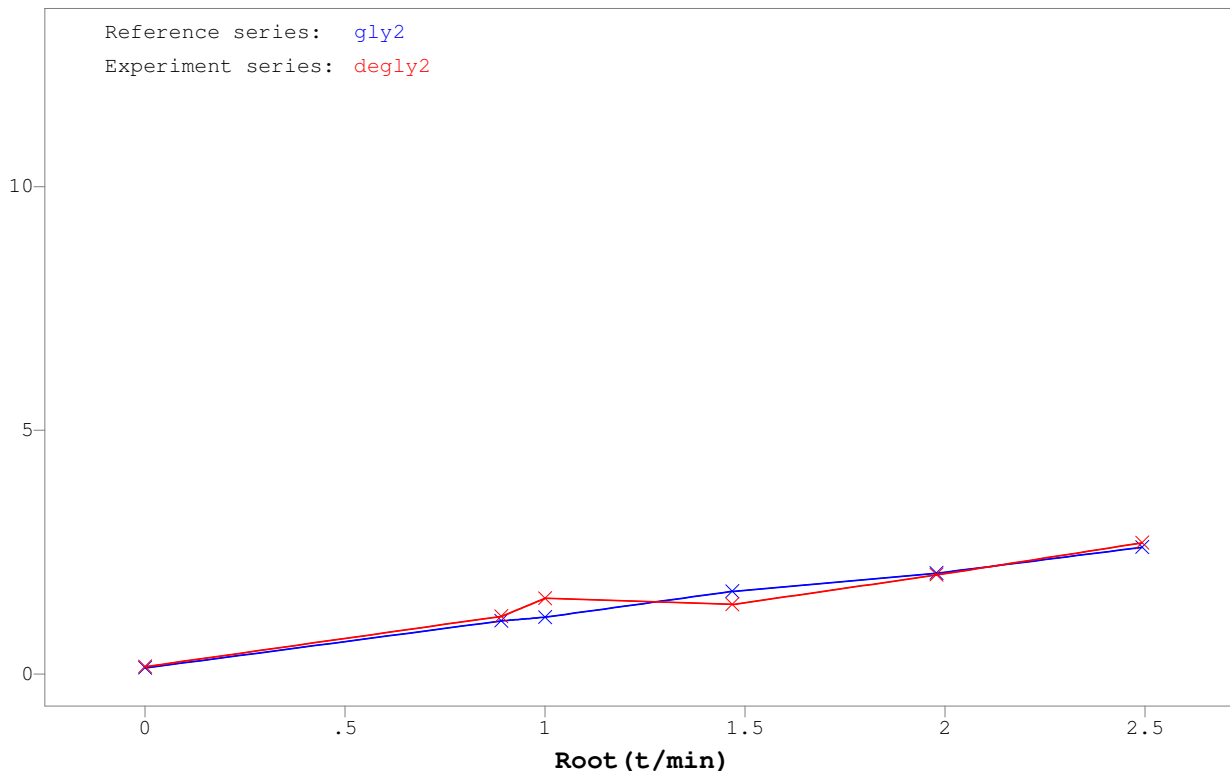
Molecule: **LC**
 Peptide: **LC087-101**
 Exchangeable protons: 13
 Index lis-file: 45
 Sequence: FCQQSNSWPLTFGAG
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	13.860	13.881	1.00	1.20	0.13	0.16
0.5	13.866	13.886	8.43	9.14	1.10	1.19
1.0	13.880	13.869	9.01	11.98	1.17	1.56
10.0	13.857	13.899	13.09	11.04	1.70	1.43
60.0	13.883	13.886	15.97	15.69	2.08	2.04
240.0	13.890	13.896	20.07	20.78	2.61	2.70

DU Value



Root(t/min): 6th roots of exchange times

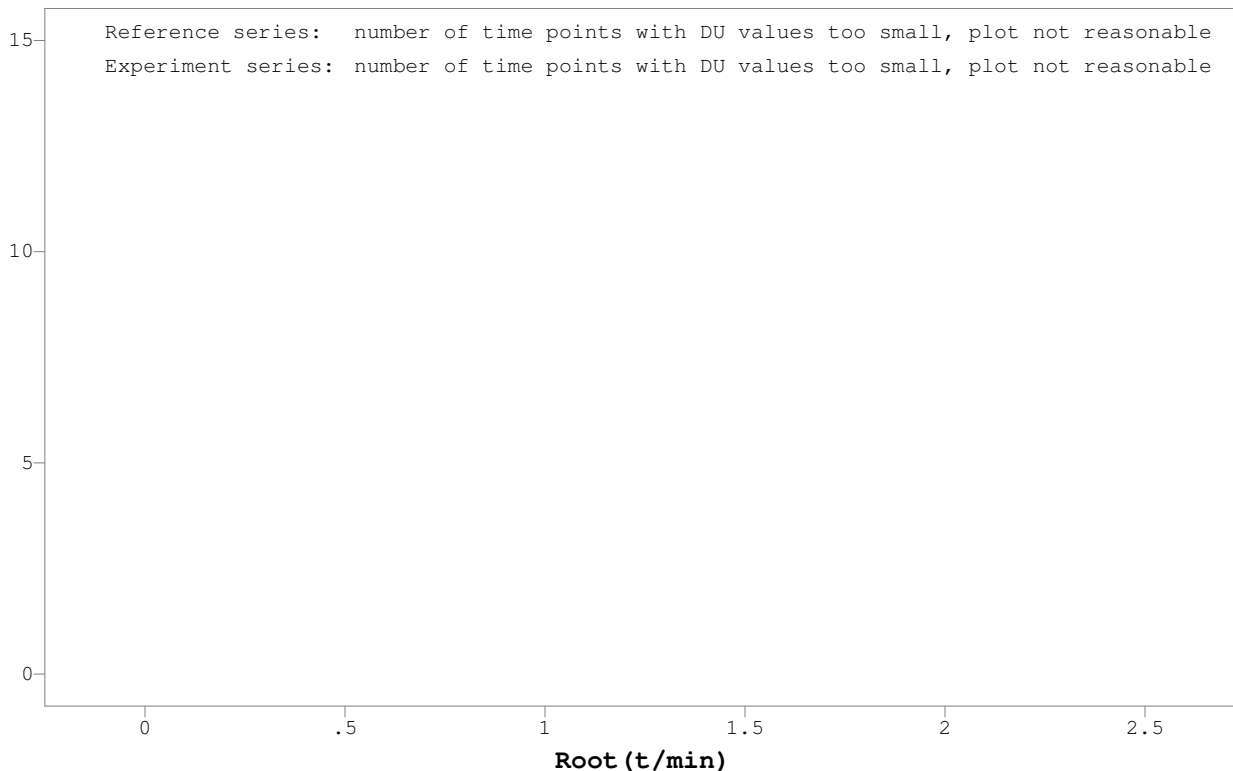
Molecule: **LC**
 Peptide: **LC105-123**
 Exchangeable protons: 15
 Index lis-file: 50
 Sequence: ELKRADAAPTVSIFPPSSE
 Range: 1 / 2

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.857	9.855	n.d.	n.d.	n.d.	n.d.
0.5	9.865	9.850	n.d.	n.d.	n.d.	n.d.
1.0	9.865	9.867	n.d.	n.d.	n.d.	n.d.
10.0	9.849	9.846	n.d.	n.d.	n.d.	n.d.
60.0	9.847	9.856	n.d.	n.d.	n.d.	n.d.
240.0	9.865	9.845	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

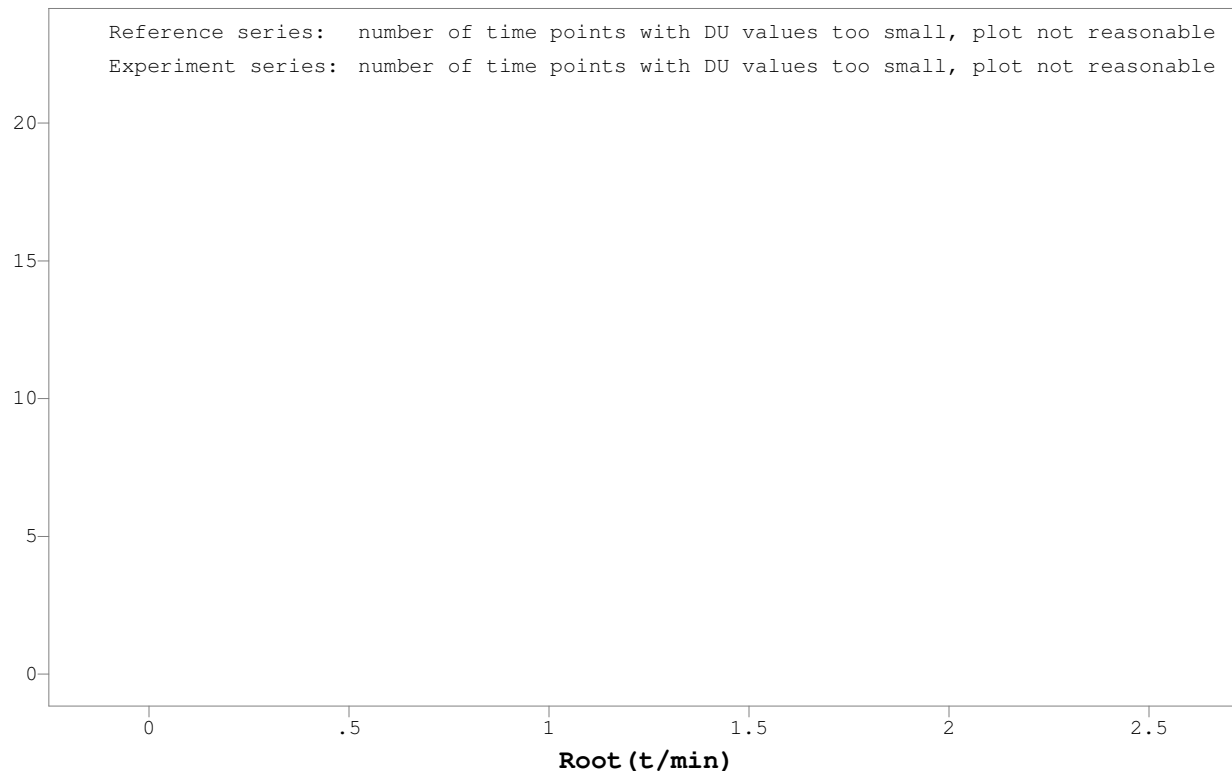
Molecule: **LC**
 Peptide: **LC105-131**
 Exchangeable protons: 23
 Index lis-file: 53
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGAS
 Range: 2 / 2

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
0.5	10.578	10.583	n.d.	n.d.	n.d.	n.d.
1.0	10.600	10.574	n.d.	n.d.	n.d.	n.d.
10.0	10.589	10.567	n.d.	n.d.	n.d.	n.d.
60.0	10.569	10.577	n.d.	n.d.	n.d.	n.d.
240.0	10.584	10.584	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

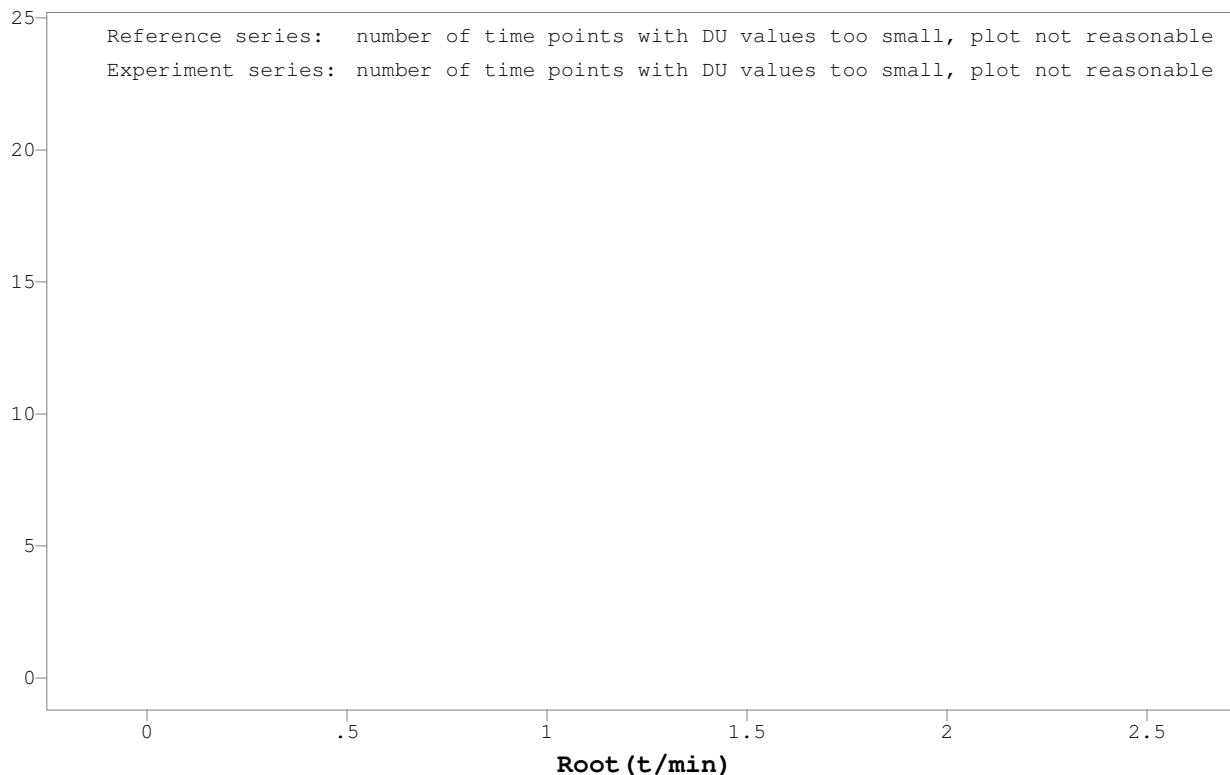
Molecule: **LC**
 Peptide: **LC105-132**
 Exchangeable protons: 24
 Index lis-file: 54
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGASV
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.857	10.864	n.d.	n.d.	n.d.	n.d.
0.5	10.876	10.866	n.d.	n.d.	n.d.	n.d.
1.0	10.874	10.869	n.d.	n.d.	n.d.	n.d.
10.0	10.862	10.849	n.d.	n.d.	n.d.	n.d.
60.0	10.878	10.850	n.d.	n.d.	n.d.	n.d.
240.0	10.866	10.856	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

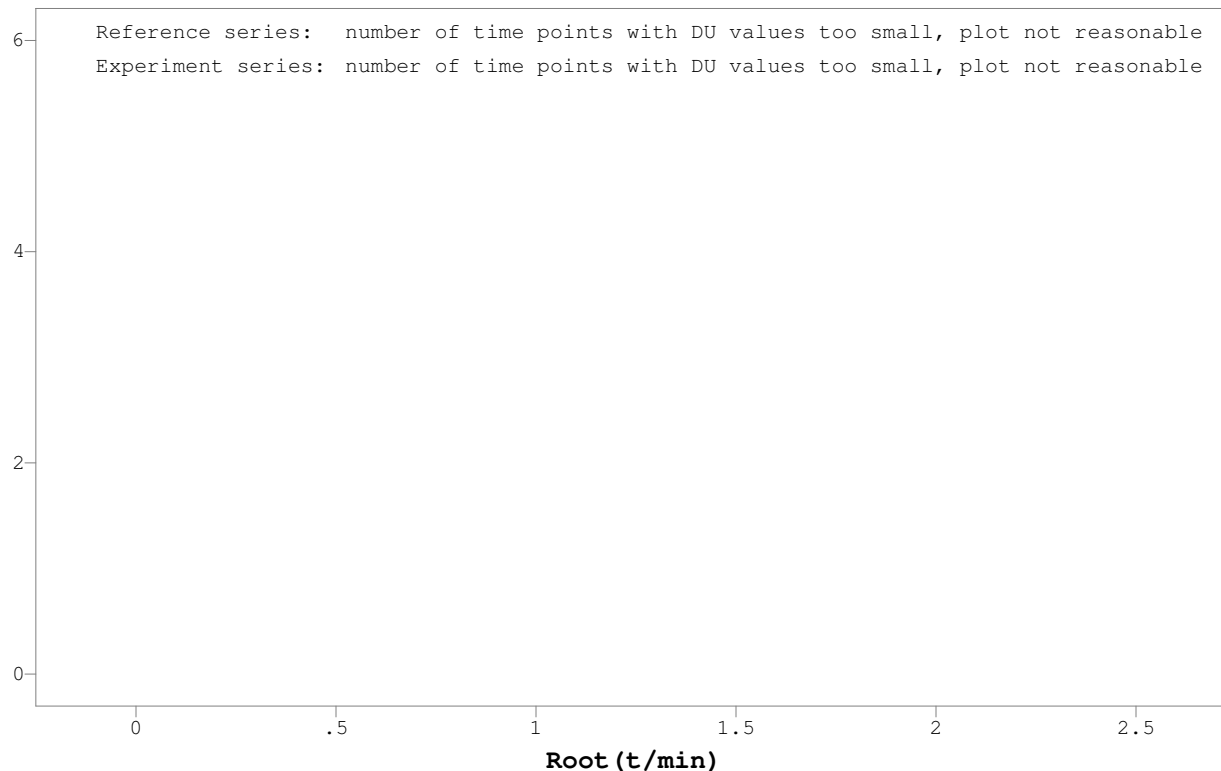
Molecule: **LC**
 Peptide: **LC136-143**
 Exchangeable protons: 6
 Index lis-file: 62
 Sequence: LNNFYPKD
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.889	7.911	n.d.	n.d.	n.d.	n.d.
0.5	7.915	7.915	n.d.	n.d.	n.d.	n.d.
1.0	7.915	7.908	n.d.	n.d.	n.d.	n.d.
10.0	7.917	7.911	n.d.	n.d.	n.d.	n.d.
60.0	7.909	7.912	n.d.	n.d.	n.d.	n.d.
240.0	7.919	7.915	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

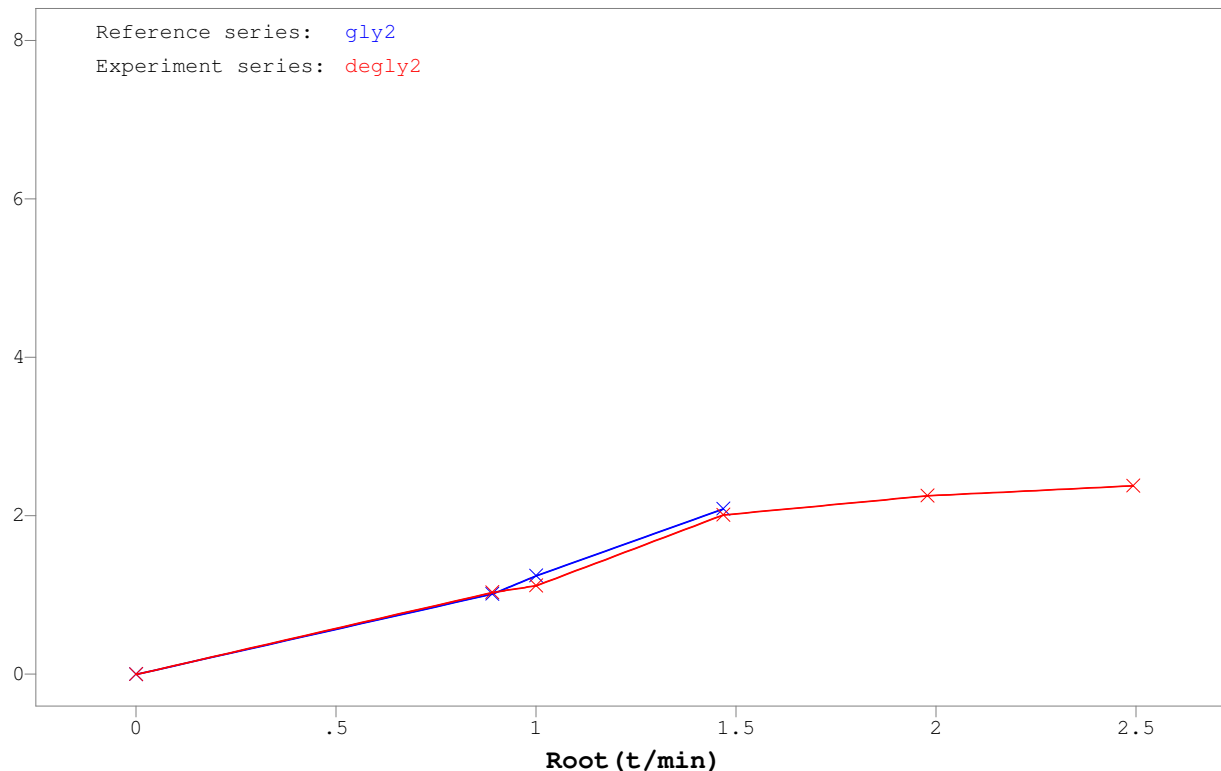
Molecule: **LC**
 Peptide: **LC136-145**
 Exchangeable protons: 8
 Index lis-file: 63
 Sequence: LNNFYPKDIN
 Range: 1 / 3

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.428	8.439	0.00	0.00	0.00	0.00
0.5	8.441	8.441	12.68	12.92	1.01	1.03
1.0	8.443	8.429	15.56	13.99	1.24	1.12
10.0	8.441	8.437	26.10	25.16	2.09	2.01
60.0	n.d.	8.434	n.d.	28.18	n.d.	2.25
240.0	n.d.	8.444	n.d.	29.76	n.d.	2.38

DU Value



Root(t/min): 6th roots of exchange times

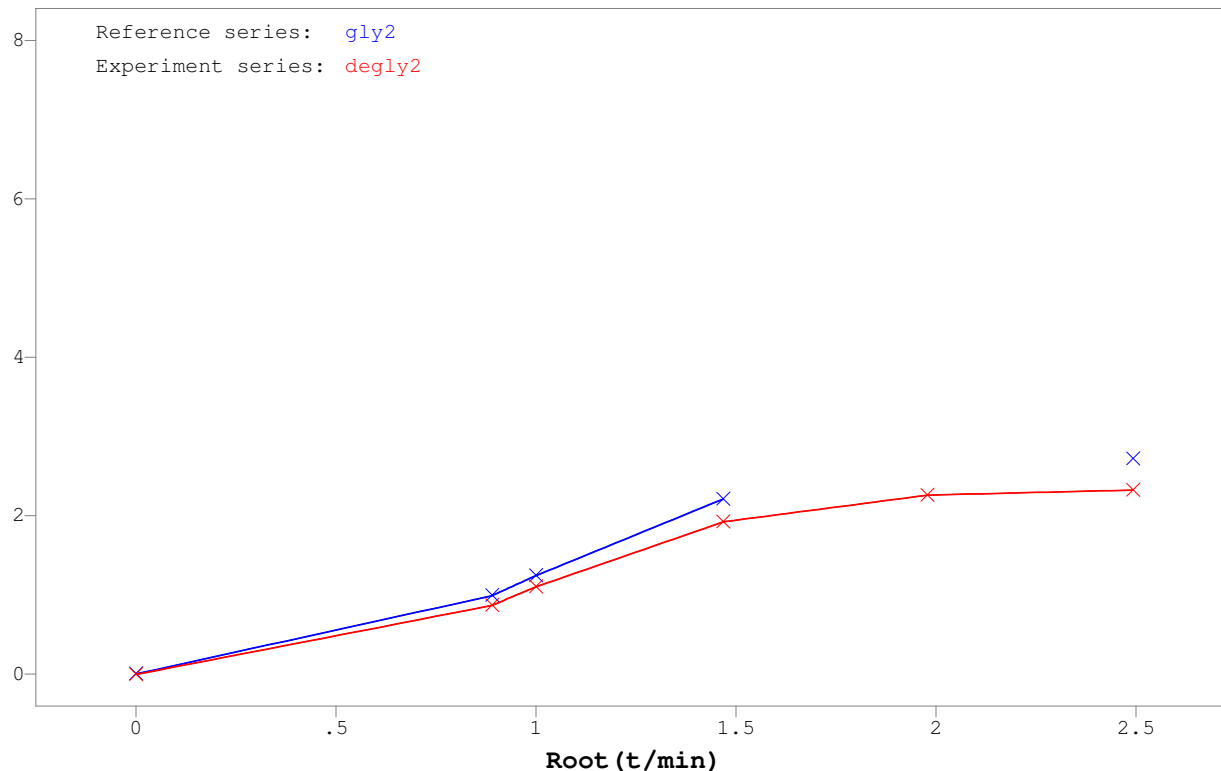
Molecule: **LC**
 Peptide: **LC136-145**
 Exchangeable protons: 8
 Index lis-file: 63
 Sequence: LNNFYPKDIN
 Range: 2 / 3

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.975	8.975	0.09	0.00	0.01	0.00
0.5	8.971	8.961	12.46	10.92	1.00	0.87
1.0	8.972	8.977	15.61	13.85	1.25	1.11
10.0	8.975	8.965	27.69	24.08	2.22	1.93
60.0	8.957	8.991	n.d.	28.29	n.d.	2.26
240.0	8.987	9.029	34.06	29.10	2.73	2.33

DU Value



Root(t/min): 6th roots of exchange times

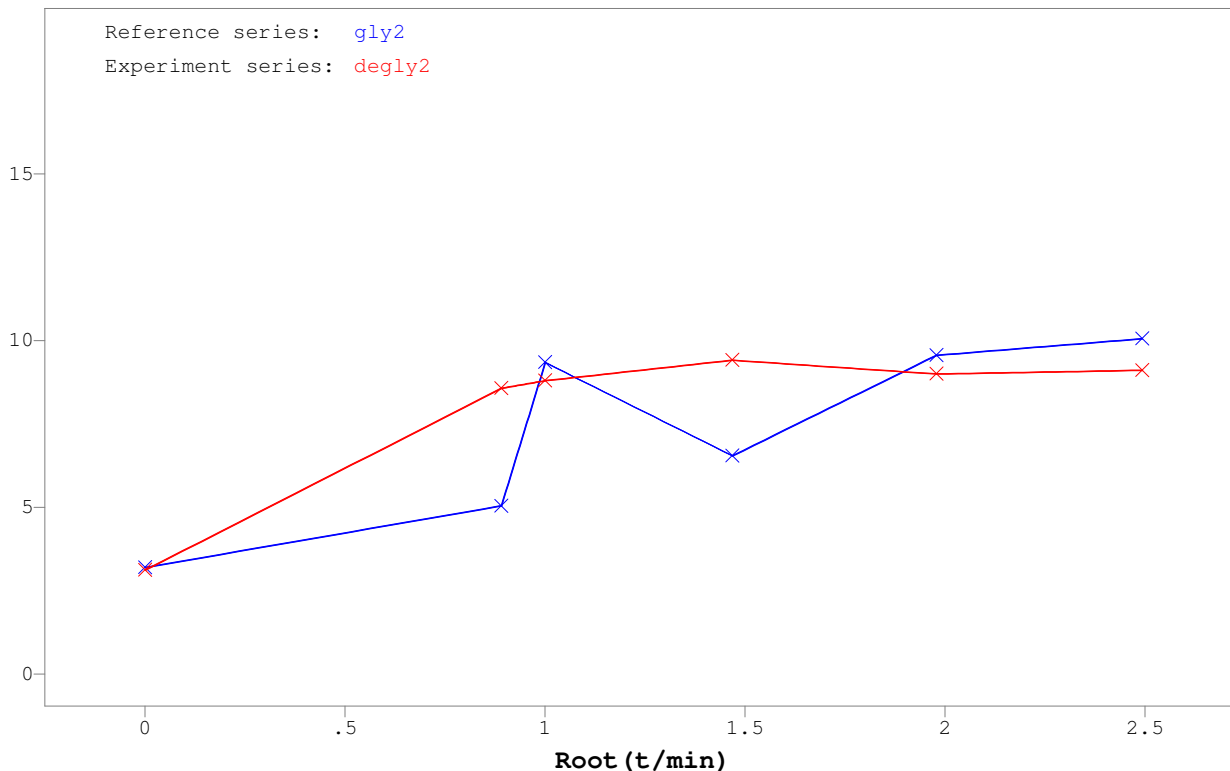
Molecule: **LC**
 Peptide: **LC140-160**
 Exchangeable protons: 19
 Index lis-file: 67
 Sequence: YPKDINVKWKIDGSERQNGVL
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.341	9.358	16.86	16.46	3.20	3.13
0.5	9.361	9.361	26.58	45.15	5.05	8.58
1.0	9.369	9.357	49.23	46.35	9.35	8.81
10.0	9.354	9.371	34.49	49.59	6.55	9.42
60.0	9.350	9.359	50.37	47.41	9.57	9.01
240.0	9.366	9.374	52.98	48.00	10.07	9.12

DU Value



Root(t/min): 6th roots of exchange times

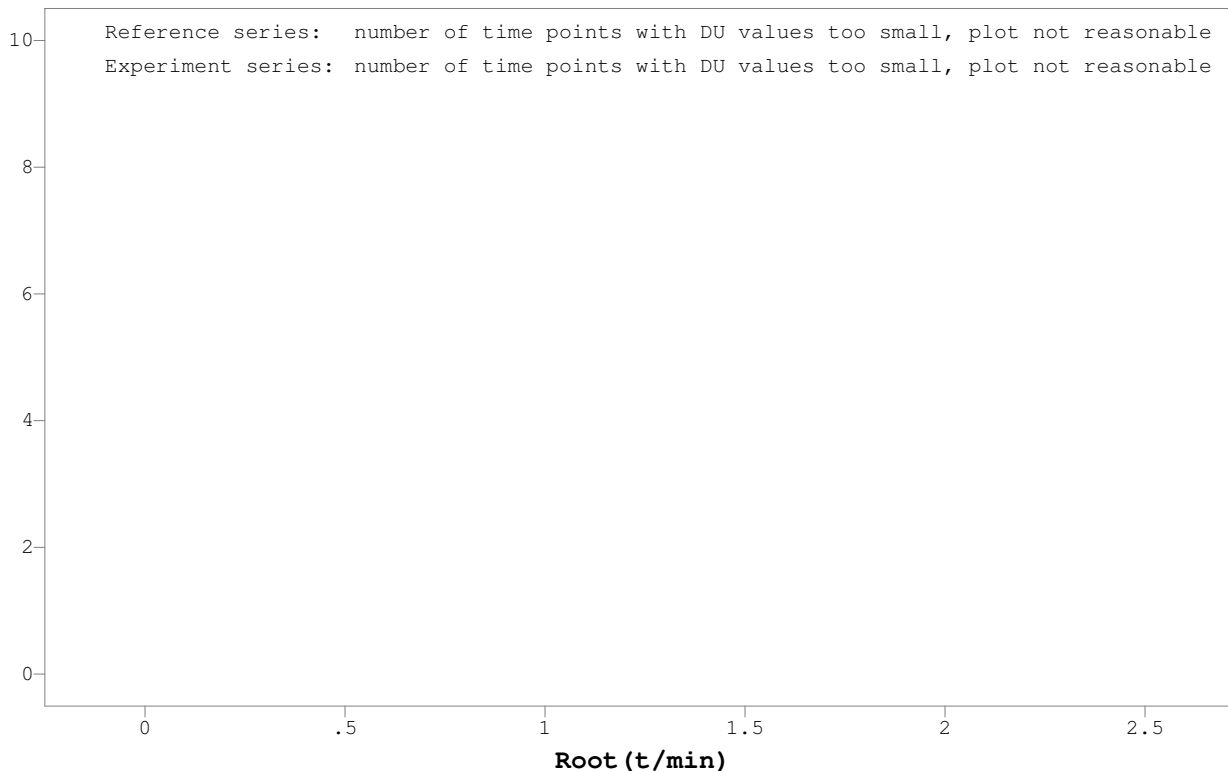
Molecule: **LC**
 Peptide: **LC152-162**
 Exchangeable protons: 10
 Index lis-file: 71
 Sequence: GSERQNGVLNS
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.943	11.944	n.d.	n.d.	n.d.	n.d.
0.5	11.943	11.960	n.d.	n.d.	n.d.	n.d.
1.0	11.941	11.941	n.d.	n.d.	n.d.	n.d.
10.0	11.941	11.955	n.d.	n.d.	n.d.	n.d.
60.0	11.944	11.955	n.d.	n.d.	n.d.	n.d.
240.0	11.955	11.955	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

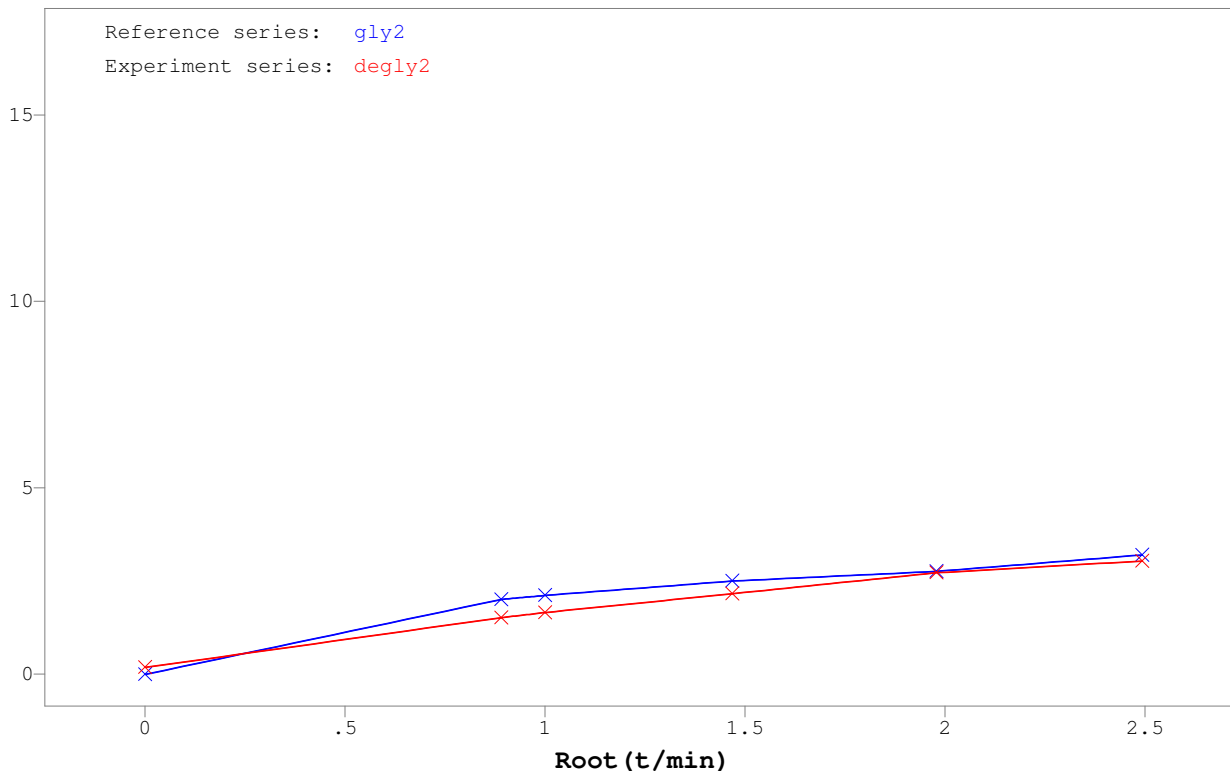
Molecule: **LC**
 Peptide: **LC161-178**
 Exchangeable protons: 17
 Index lis-file: 75
 Sequence: NSWTDQDSKDYMSST
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.626	8.630	0.00	1.09	0.00	0.18
0.5	8.617	8.621	11.83	8.95	2.01	1.52
1.0	8.620	8.621	12.46	9.76	2.12	1.66
10.0	8.618	8.630	14.72	12.73	2.50	2.16
60.0	8.609	8.616	16.25	16.03	2.76	2.73
240.0	8.624	8.642	18.85	17.89	3.20	3.04

DU Value



Root(t/min): 6th roots of exchange times

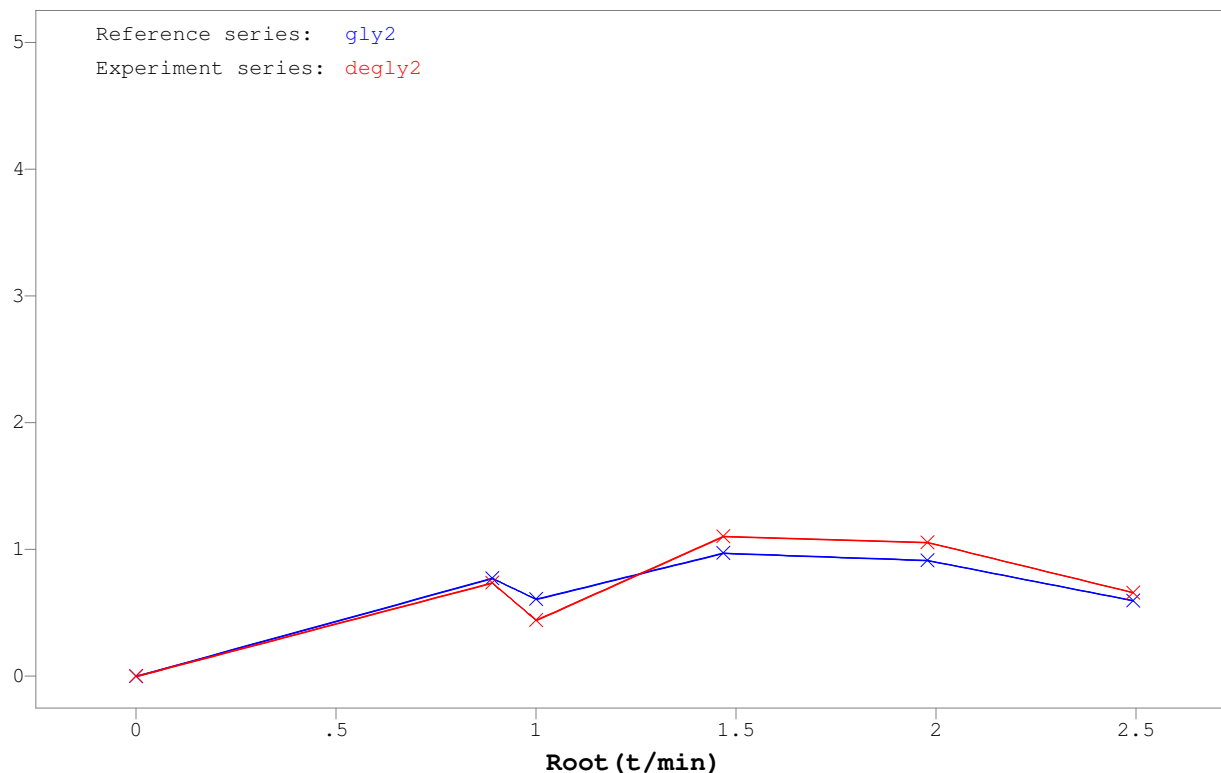
Molecule: LC
 Peptide: LC173-178
 Exchangeable protons: 5
 Index lis-file: 78
 Sequence: YSMSST
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.339	6.335	0.00	0.00	0.00	0.00
0.5	6.339	6.350	15.45	14.73	0.77	0.74
1.0	6.339	6.335	12.15	8.83	0.61	0.44
10.0	6.339	6.350	19.42	22.07	0.97	1.10
60.0	6.325	6.339	18.28	21.13	0.91	1.06
240.0	6.332	6.348	11.94	13.20	0.60	0.66

DU Value



Root(t/min): 6th roots of exchange times

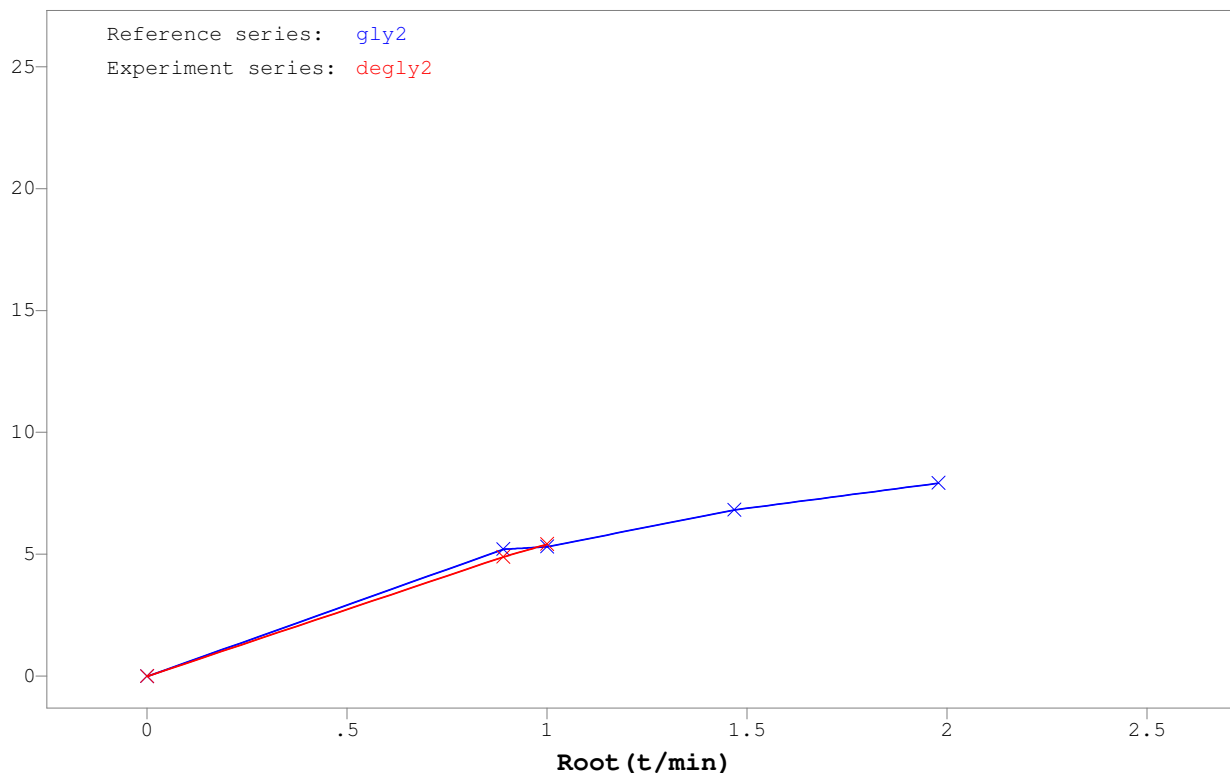
Molecule: **LC**
 Peptide: **LC179-206**
 Exchangeable protons: 26
 Index lis-file: 83
 Sequence: LTLTKDEYERHNSYTCEATHKTSTSPIV
 Range: 1 / 1

Reference: reference series, experiment: experiment series

Bold typing: problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.035	11.035	0.00	0.00	0.00	0.00
0.5	11.037	11.043	20.07	18.86	5.22	4.90
1.0	11.043	11.031	20.47	20.87	5.32	5.43
10.0	11.024	11.035	26.29	n.d.	6.83	n.d.
60.0	11.035	11.038	30.50	n.d.	7.93	n.d.
240.0	11.040	11.040	n.d.	n.d.	n.d.	n.d.

DU Value



Root(t/min): 6th roots of exchange times

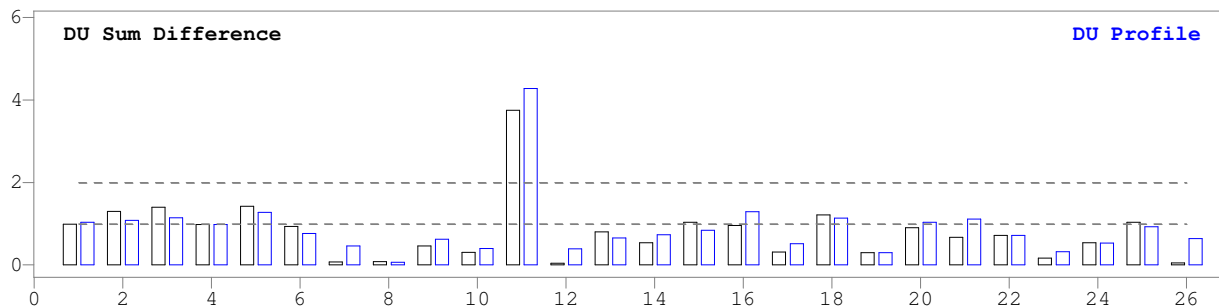
Molecule HC: Peptides with sufficient kinetics data, part 1

No.	Peptide/Range	Sequence
1	HC001-017/1	EVQGVESGGGLVKPGGS
2	HC001-018/1	EVQGVESGGGLVKPGGSL
3	HC001-020/1	EVQGVESGGGLVKPGGSLKL
4	HC001-022/1	EVQGVESGGGLVKPGGSLKLSC
5	HC001-023/1	EVQGVESGGGLVKPGGSLKLSCA
6	HC002-044/1	VQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKR
7	HC012-043/1	VKPGGSLKLSCAASGFTFSDYYMYWVRQTPEK
8	HC019-037/1	KLSCAASGFTFSDYYMYW
9	HC024-032/1	ASGFTFSDY
10	HC026-057/1	GFTFSDYYMYWVRQTPEKRLEWVATISDGGSY
11	HC027-031/1	FTFSD
12	HC027-032/1	FTFSDY

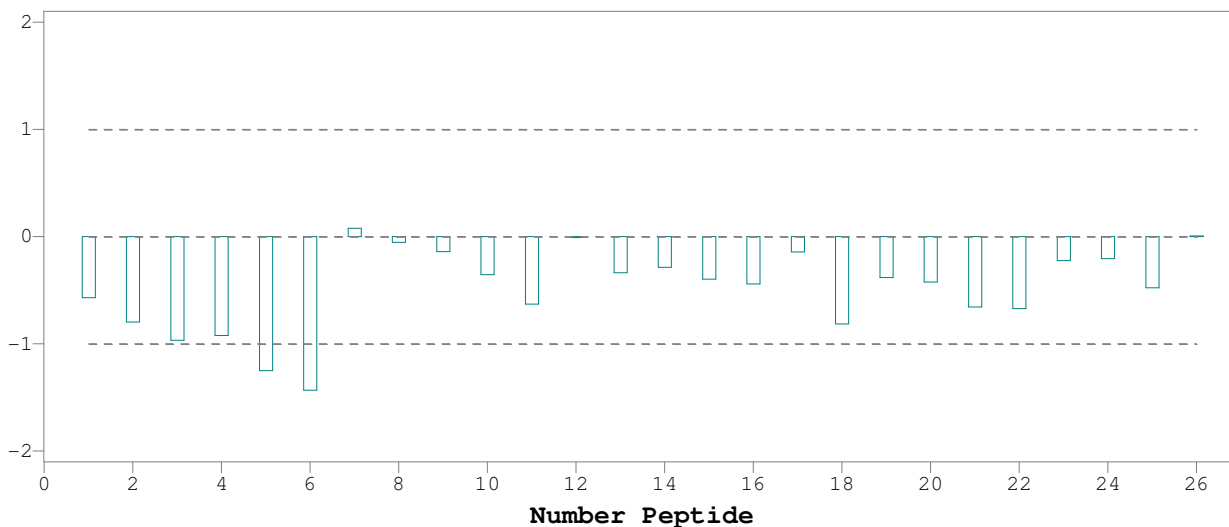
13	HC035-047/1	YWVRQTPEKRLEW
14	HC035-050/1	YWVRQTPEKRLEWVAT
15	HC036-047/1	WVRQTPEKRLEW
16	HC036-049/1	WVRQTPEKRLEWVA
17	HC037-050/1	VRQTPEKRLEWVAT

18	HC051-068/1	ISDGGSYTYYPDSVKGRF
19	HC051-079/1	ISDGGSYTYYPDSVKGRFTISRDNAKNNL
20	HC057-068/1	YTYYPDSVKGRF
21	HC057-079/1	YTYYPDSVKGRFTISRDNAKNNL
22	HC058-079/1	TYYPDSVKGRFTISRDNAKNNL
23	HC065-101/1	KGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKA
24	HC069-079/1	TISRDNAKNNL
25	HC069-080/1	TISRDNAKNNLY
26	HC080-083/1	YLQM

Score



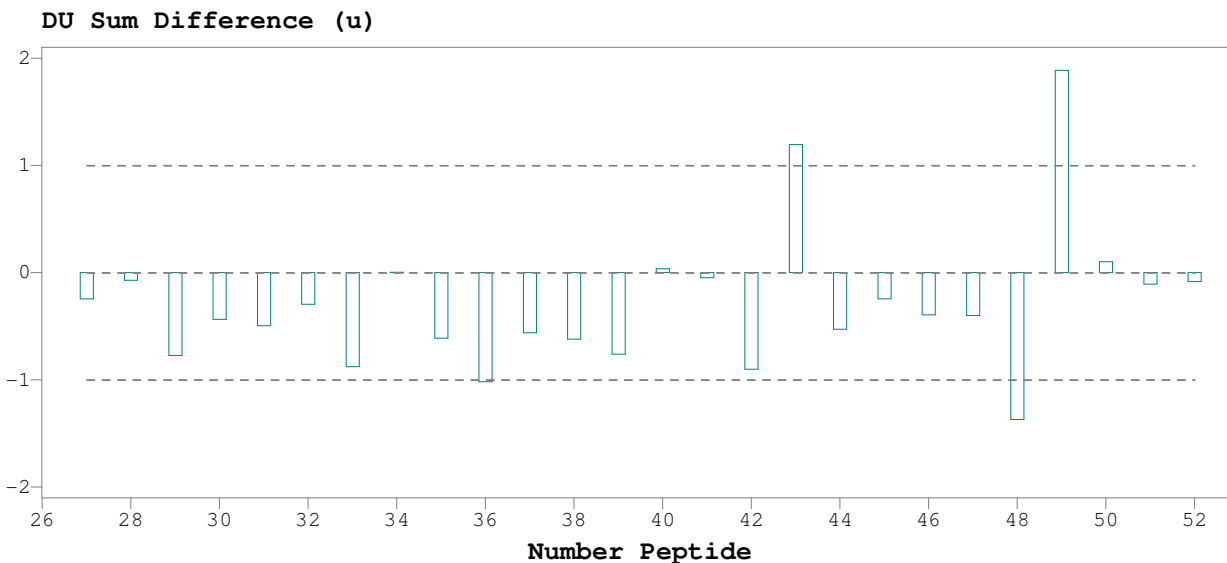
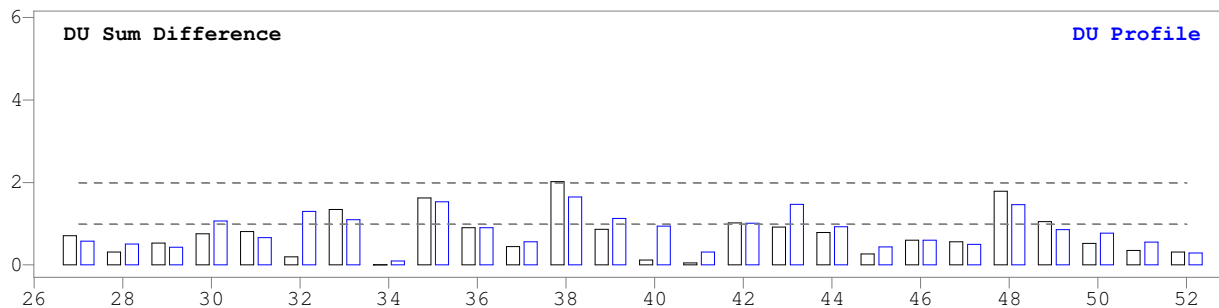
DU Sum Difference (u)



Molecule HC: Peptides with sufficient kinetics data, part 2

No.	Peptide/Range	Sequence
27	HC084-093/1	SSLKSED TAM
28	HC087-093/1	KSED TAM
29	HC089-127/1	EDTAMYICARDKAYYGNYGDAMDYWGQGT SVTVSSAKTT
30	HC094-109/1	YICARDKAYYGNYGDA
31	HC094-110/1	YICARDKAYYGNYGDAM
32	HC094-137/1	YICARDKAYYGNYGDAMDYWGQGT SVTVSSAKTTPPSVYPLAPG
33	HC095-112/1	YICARDKAYYGNYGDAMDY
34	HC105-143/1	NYGDAMDYWGQGT SVTVSSAKTTPPSVYPLAPGSAAQT N
35	HC111-120/1	DYWGQGT SVT
36	HC111-139/1	DYWGQGT SVTVSSAKTTPPSVYPLAPGSA
37	HC111-145/1	DYWGQGT SVTVSSAKTTPPSVYPLAPGSAAQTNSM
38	HC112-120/1	YWGQGT SVT
39	HC112-139/1	YWGQGT SVTVSSAKTTPPSVYPLAPGSA
40	HC113-120/1	WGQGT SVT
41	HC113-139/1	WGQGT SVTVSSAKTTPPSVYPLAPGSA
42	HC115-140/1	QGTSVTVSSAKTTPPSVYPLAPGSAA
43	HC118-156/1	SVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYF
44	HC119-139/1	VTVSSAKTTPPSVYPLAPGSA
45	HC119-145/1	VTVSSAKTTPPSVYPLAPGSAAQTNSM
46	HC121-139/1	VSSAKTTPPSVYPLAPGSA
47	HC121-142/1	VSSAKTTPPSVYPLAPGSAAQT
48	HC121-145/1	VSSAKTTPPSVYPLAPGSAAQTNSM
49	HC132-184/1	YPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDL
50	HC146-151/1	VTLGCL
51	HC151-161/1	LVKGYFPEPVT
52	HC152-161/1	VKGYFPEPVT

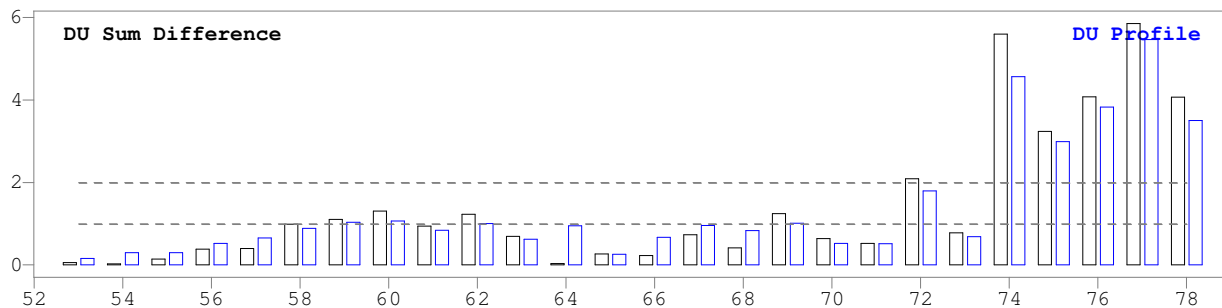
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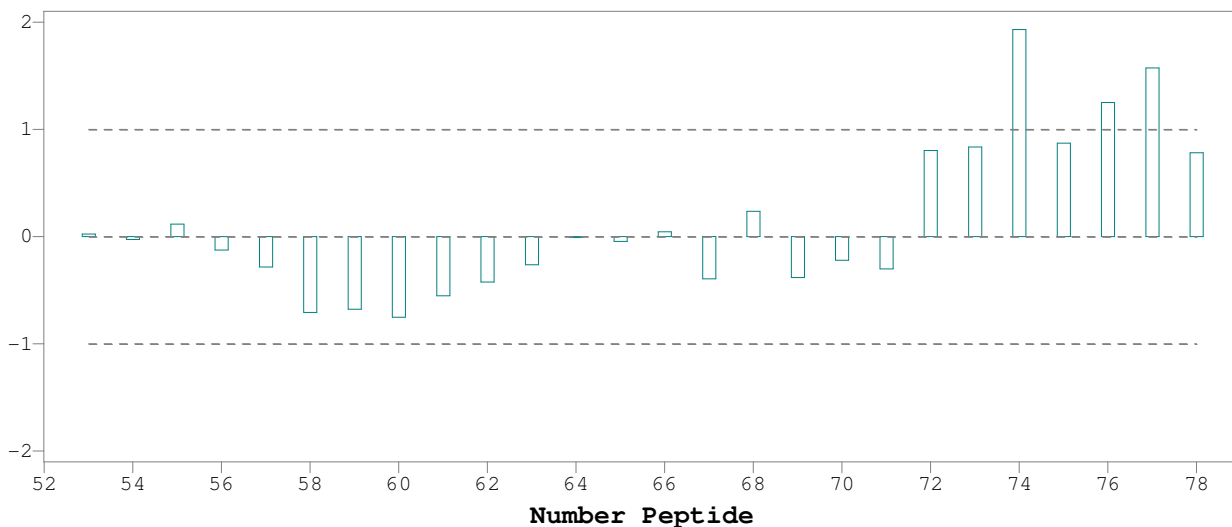
Molecule HC: Peptides with sufficient kinetics data, part 3

No.	Peptide/Range	Sequence
53	HC152-164/1	VKGYFPEPVTVTW
54	HC160-195/1	VTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPS
55	HC161-183/1	TVTWNNSGSLSSGVHTFPAVLQSD
56	HC162-169/1	VTWNSGSL
57	HC162-180/1	VTWNSGSLSSGVHTFPAVL
58	HC162-180/2	VTWNSGSLSSGVHTFPAVL
59	HC163-180/1	TWNSGSLSSGVHTFPAVL
60	HC164-180/1	WNSGSLSSGVHTFPAVL
61	HC165-180/1	NSGSLSSGVHTFPAVL
62	HC170-180/1	SSGVHTFPAVL
63	HC170-180/2	SSGVHTFPAVL
64	HC175-182/1	TFPAVLQS
65	HC185-189/1	YTLSS
66	HC185-190/1	YTLSSS
67	HC185-201/1	YTLSSSVTVPSSTWPSE
68	HC185-202/1	YTLSSSVTVPSSTWPSET
69	HC191-201/1	VTVPSSSTWPSE
70	HC191-202/1	VIVPSSSTWPSET
71	HC212-229/1	SSTKVDKKIVPRDCGCKP
72	HC214-225/1	TKVDKKIVPRDC
73	HC219-253/1	KIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI
74	HC240-252/1	VFIFPPKPKDVLTI
75	HC241-251/1	FIFPPKPKDVL
76	HC241-252/1	FIFPPKPKDVL
77	HC242-252/1	IFPPKPKDVL
78	HC243-251/1	FPPKPKDVL

Score



DU Sum Difference (u)



Molecule HC: Peptides with sufficient kinetics data, part 4

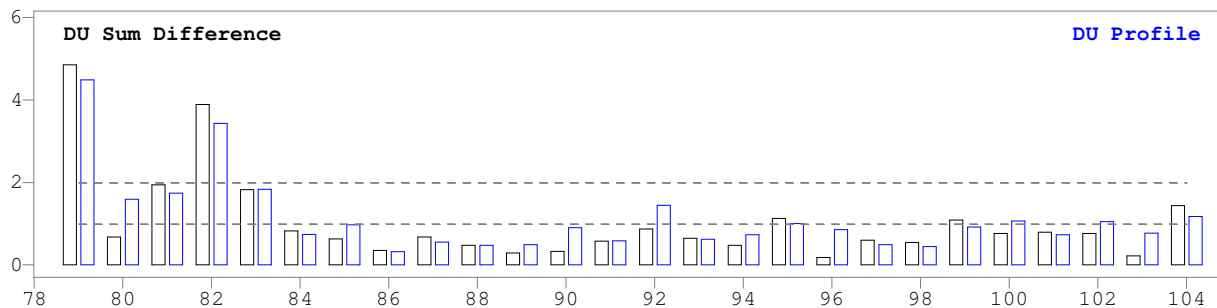
No.	Peptide/Range	Sequence
79	HC243-252/1	FPPKPKDVLT
80	HC252-261/1	TITLTPKVTC
81	HC253-261/1	ITLTPKVTC

82	HC263-274/1	VVDISKDDPEVQ
83	HC263-275/1	VVDISKDDPEVQF
84	HC266-274/1	ISKDDPEVQ
85	HC266-275/1	ISKDDPEVQF
86	HC272-294/1	EVQFSWFVDDVEVHTAQTQPREE
87	HC278-281/1	FVDD

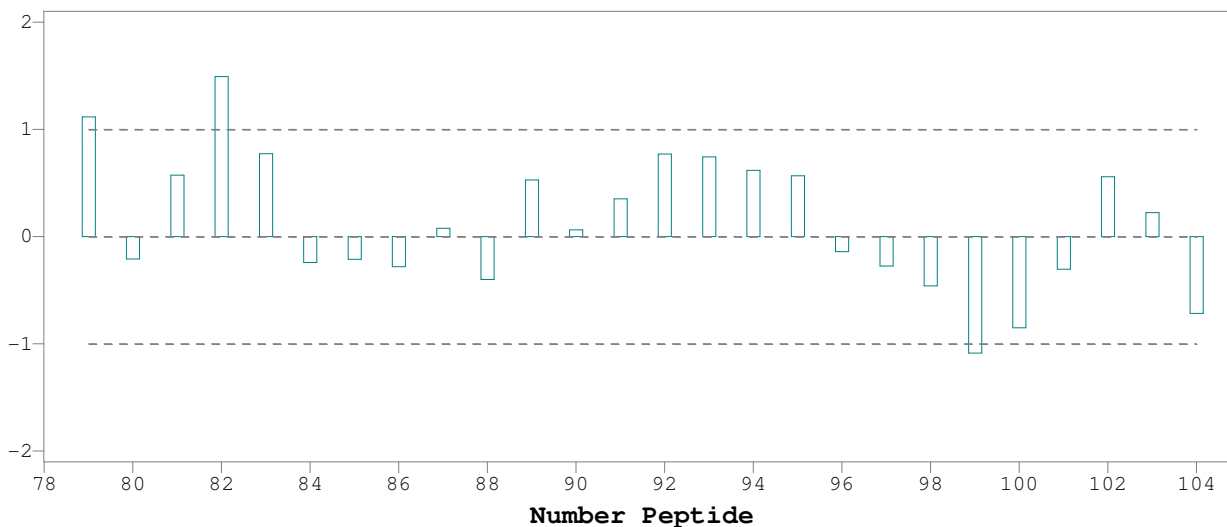
88	HC291-315/1	PREEQFNSTFRSVSELPIMHQDWLN
89	HC297-350/1	NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT
90	HC301-306/1	RSVSEL
91	HC301-318/1	RSVSELPIMHQDWLNGKE
92	HC307-333/1	PIMHQDWLNGKEFKCRVNSAAFPAPIE
93	HC308-340/1	IMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK

94	HC318-359/1	EFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMA
95	HC319-333/1	FKCRVNSAAFPAPIE
96	HC326-348/1	AAFPAPIEKTISKTKGRPKAPQV
97	HC334-348/1	KTISKTKGRPKAPQV
98	HC334-361/1	KTISKTKGRPKAPQVYTIPPPKEQMAKD
99	HC334-365/1	KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSL
100	HC334-368/1	KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCM
101	HC336-348/1	ISKTKGRPKAPQV
102	HC342-366/1	RPKAPQVYTIPPPKEQMAKDKVSLT
103	HC345-374/1	APQVYTIPPPKEQMAKDKVSLTCMITDFFP
104	HC349-365/1	YTIPPPKEQMAKDKVSL

Score

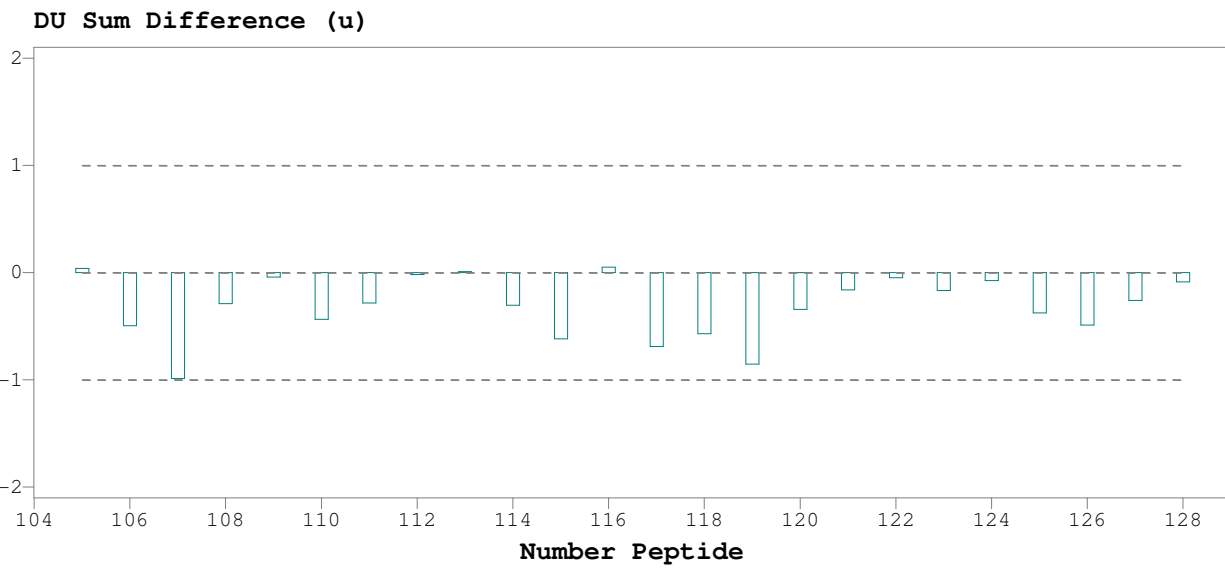
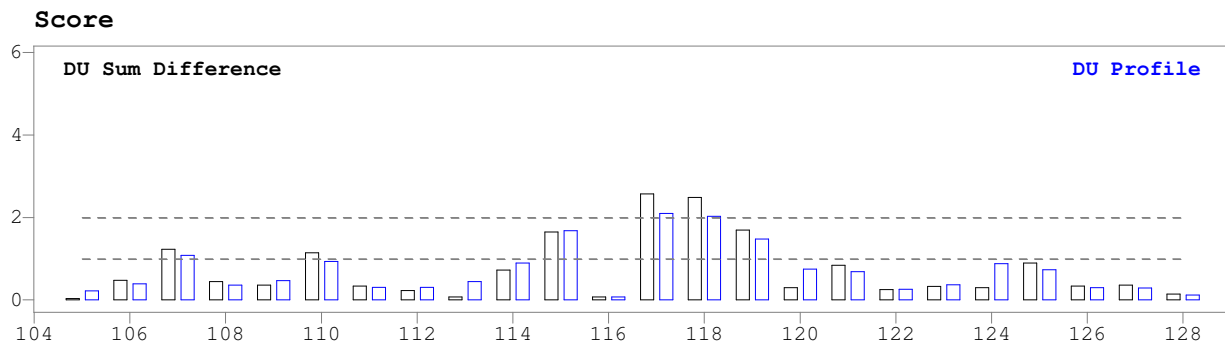


DU Sum Difference (u)



Molecule HC: Peptides with sufficient kinetics data, part 5

No.	Peptide/Range	Sequence
105	HC357-385/1	QMAKDKVSLTCMITDFFPEDITVEWQWNG
106	HC364-393/1	SLTCMITDFFPEDITVEWQWNGQPAENYKN
107	HC367-390/1	CMITDFFPEDITVEWQWNGQPAEN
108	HC368-387/1	MITDFFPEDITVEWQWNGQP
109	HC369-372/1	ITDF
110	HC369-380/1	ITDFFPEDITVE
111	HC372-397/1	FFPEDITVEWQWNGQPAENYKNTQPI
112	HC373-376/1	FPED
113	HC377-380/1	ITVE
114	HC379-390/1	VEWQWNGQPAEN
115	HC381-390/1	WQWNGQPAEN
116	HC381-398/1	WQWNGQPAENYKNTQPI
117	HC390-398/1	NYKNTQPI
118	HC391-398/1	YKNTQPI
119	HC391-404/1	YKNTQPI
120	HC395-426/1	QPI
121	HC399-404/1	DTDGSY
122	HC405-410/1	FVYSKL
123	HC407-418/1	YSKLVQKSNWE
124	HC411-417/1	NVQKSNW
125	HC411-422/1	NVQKSNWEAGNT
126	HC411-447/1	NVQKSNWEAGNTFTCSVLHEGLHNNHTEKSLSHSPGK
127	HC426-446/1	SVLHEGLHNNHTEKSLSHSPG
128	HC429-446/1	HEGLHNNHTEKSLSHSPG

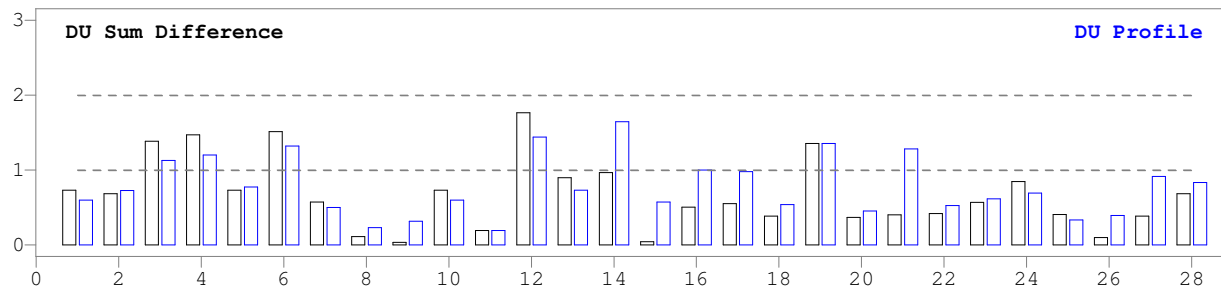


Molecule LC: Peptides with sufficient kinetics data, part 1

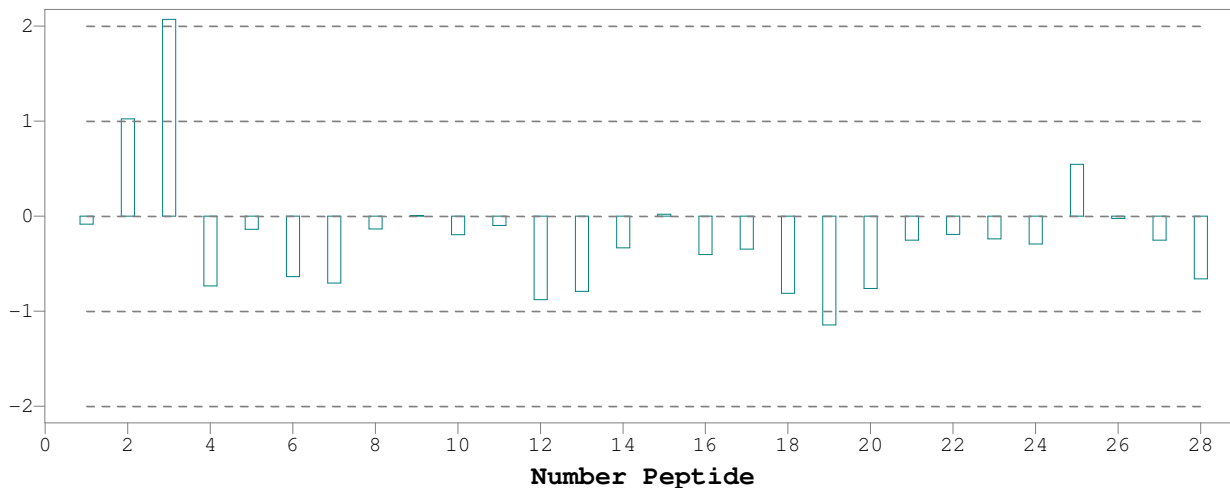
No.	Peptide/Range	Sequence
1	LC001-004/1	DIVL
2	LC001-042/1	DIVLTQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHE
3	LC001-042/2	DIVLTQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHE
4	LC003-018/1	VLTQSPATLSVTPGDS
5	LC005-011/1	TQSPATL
6	LC005-018/1	TQSPATLSVTPGDS
7	LC005-039/1	TQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQK
8	LC10-043/1	TLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHE
9	LC012-018/1	SVTPGDS
10	LC012-020/1	SVTPGDSVS

11	LC021-032/1	LSCRASQSIENN
12	LC022-035/1	SCRASQSIENNHLW
13	LC022-046/1	SCRASQSIENNHLHWYQQKSHEPRL
14	LC024-033/1	RASQSIENN
15	LC024-035/1	RASQSIENNHLW
16	LC024-046/1	RASQSIENNHLHWYQQKSHEPRL
17	LC027-042/1	QSIENNHLHWYQQKSHE
18	LC027-084/1	QSIENNHLHWYQQKSHEPRLLIKIASQISGIPSRFSGSGSGTDFTLINSVETEDFG
19	LC028-047/1	SISNNHLHWYQQKSHEPRL
20	LC028-084/1	SISNNHLHWYQQKSHEPRLLIKIASQISGIPSRFSGSGSGTDFTLINSVETEDFG
21	LC030-046/1	SNNHLHWYQQKSHEPRL
22	LC033-046/1	LHWYQQKSHEPRL
23	LC034-046/1	HWYQQKSHEPRL
24	LC036-046/1	YQQKSHEPRL
25	LC041-078/1	HESPRLLIKIASQISGIPSRFSGSGSGTDFTLINSV
26	LC047-053/1	LIKIASQ
27	LC047-062/1	LIKIASQISGIPSRF
28	LC047-071/1	LIKIASQISGIPSRFSGSGSGTDF

Score



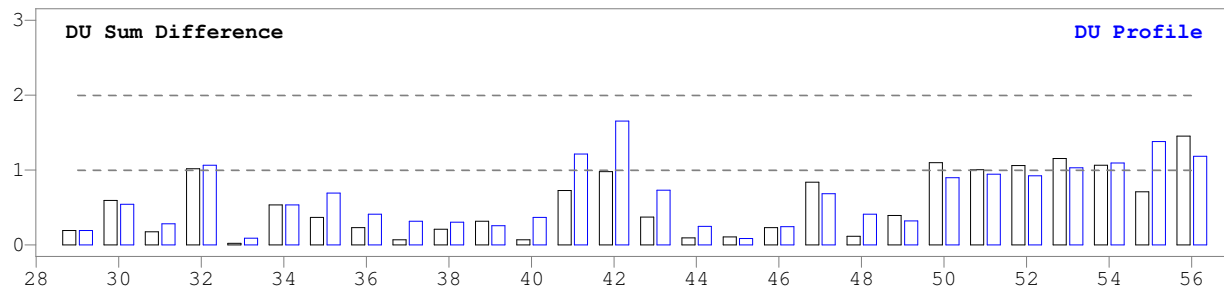
DU Sum Difference (u)



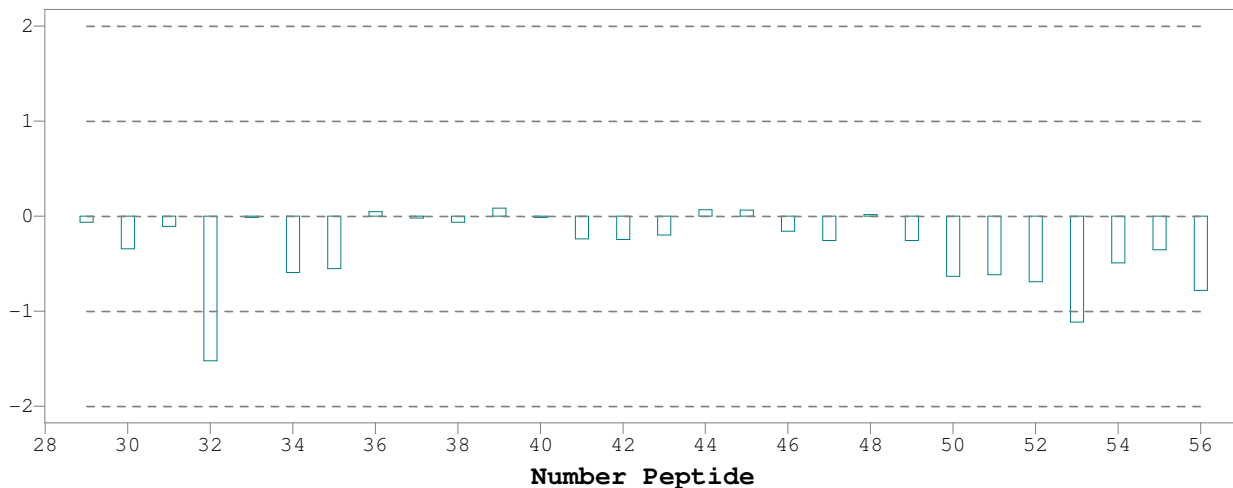
Molecule LC: Peptides with sufficient kinetics data, part 2

No.	Peptide/Range	Sequence
29	LC054-062/1	SISGIPSRF
30	LC054-070/1	SISGIPSRFSGSGGTD
31	LC054-071/1	SISGIPSRFSGSGGTD
32	LC054-095/1	SISGIPSRFSGSGGTDFTLSINSVETEDFGMYFCQQSNSWP
33	LC055-070/1	ISGIPSRFSGSGGTD
34	LC055-085/1	ISGIPSRFSGSGGTDFTLSINSVETEDFGM
35	LC059-100/1	PSRFSGSGGTDFTLSINSVETEDFGMYFCQQSNSWPLTFGA
36	LC071-076/1	FTLSIN
37	LC071-077/1	FTLSINS
38	LC071-079/1	FTLSINSVE
39	LC072-079/1	TLINSVE
40	LC074-079/1	SINSVE
41	LC078-085/1	VETEDFGM
42	LC080-086/1	TEDFGMY
43	LC086-101/1	YFCQQSNSWPLTFGAG
44	LC086-106/1	YFCQQSNSWPLTFGAGTKLEL
45	LC087-104/1	FCQQSNSWPLTFGAGTKL
46	LC087-106/1	FCQQSNSWPLTFGAGTKLEL
47	LC098-106/1	FGAGTKLEL
48	LC102-106/1	TKLEL
49	LC104-124/1	LELKRADAAPTIVSIFPPSSEQ
50	LC105-123/2	ELKRADAAPTIVSIFPPSSE
51	LC105-124/1	ELKRADAAPTIVSIFPPSSEQ
52	LC105-125/1	ELKRADAAPTIVSIFPPSSEQL
53	LC105-131/1	ELKRADAAPTIVSIFPPSSEQLTSGGAS
54	LC107-122/1	KRADAAPTIVSIFPPSS
55	LC107-123/1	KRADAAPTIVSIFPPSSE
56	LC107-124/1	KRADAAPTIVSIFPPSSEQ

Score



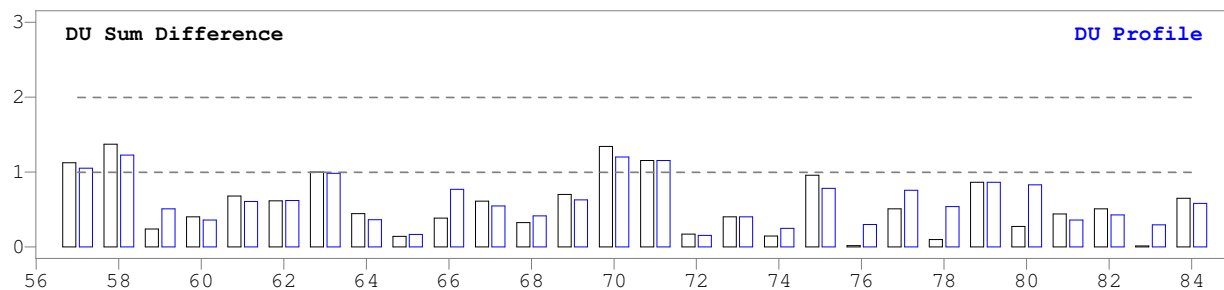
DU Sum Difference (u)



Molecule LC: Peptides with sufficient kinetics data, part 3

No.	Peptide/Range	Sequence
57	LC107-125/1	KRADAAPTVSIFPPSSEQL
58	LC107-131/1	KRADAAPTVSIFPPSSEQLTSGGAS
59	LC107-131/2	KRADAAPTVSIFPPSSEQLTSGGAS
60	LC110-120/1	DAAPTVSIFPP
61	LC110-120/2	DAAPTVSIFPP
62	LC111-153/1	AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS
63	LC111-153/2	AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS
64	LC124-131/1	QLTSGGAS
65	LC132-145/1	VVCFLNNFYPKDIN
66	LC136-146/1	LNNFYPKDINV
67	LC136-154/1	LNNFYPKDINVKWKIDGSE
68	LC137-161/1	NNFYPKDINVKWKIDGSRQNGVLN
69	LC140-161/1	YPKDINVKWKIDGSRQNGVLN
70	LC146-160/1	VKWKIDGSRQNGVL
71	LC147-160/1	KWKIDGSRQNGVL
72	LC155-160/1	RQNGVL
73	LC161-172/1	NSWTDQDSKDST
74	LC161-175/1	NSWTDQDSKDYISM
75	LC161-179/1	NSWTDQDSKDYISMSSL
76	LC164-189/1	TDQDSKDYISMSSLTLTKDEYERH
77	LC173-179/1	YSMSSL
78	LC173-199/1	YSMSSLTLTKDEYERHNSYTCEATHK
79	LC174-199/1	SMSSLTLTKDEYERHNSYTCEATHK
80	LC179-195/1	LTLTKDEYERHNSYTCE
81	LC180-195/1	TLTKDEYERHNSYTCE
82	LC180-214/1	TLTKDEYERHNSYTCEATHKTSTSPIVKSFNREC
83	LC182-195/1	TKDEYERHNSYTCE
84	LC196-214/1	ATHKTSTSPIVKSFNREC

Score



DU Sum Difference (u)

