

Article

Representation of the Structure—A Key Point of Building QSAR/QSPR Models for Ionic Liquids

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Table S1. The experimental data of ILs' toxicity towards *Escherichia coli* collected from the literature.

ID	Cation	Cation's Abbreviation	Cation's SMILES	Anion	Anion's Abbreviation	Anion's SMILES	Set	EC50 [mM]	log_EC50 [mM]
1	1-butyl-3-methylpyridinium	C4mpy	<chem>CCCC[N+]1=CC=CC(=C1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	45.12	1.65
2	1-butyl-3-methylpyridinium	C4mpy	<chem>CCCC[N+]1=CC=CC(=C1)C</chem>	thiocyanate	SCN	<chem>C(#N)[S-]</chem>	V	55.47	1.74
3	1-hexyl-3-methylpyridinium	C6mpy	<chem>CCCCC[N+]1=CC=CC(=C1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	9.75	0.99
4	1-hexyl-3-methylpyridinium	C6mpy	<chem>CCCCC[N+]1=CC=CC(=C1)C</chem>	thiocyanate	SCN	<chem>C(#N)[S-]</chem>	T	14.29	1.16
5	1-octyl-3-methylpyridinium	C8mpy	<chem>CCCCCCCC[N+]1=CC=CC(=C1)C</chem>	bromide	Br	<chem>[Br-]</chem>	V	1.09	0.04
6	1-octyl-3-methylpyridinium	C8mpy	<chem>CCCCCCCC[N+]1=CC=CC(=C1)C</chem>	thiocyanate	SCN	<chem>C(#N)[S-]</chem>	V	0.57	−0.24
7	1-decyl-3-methylpyridinium	C10mpy	<chem>CCCCCCCCC[N+]1=CC=CC(=C1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	0.27	−0.57
8	1-decyl-3-methylpyridinium	C10mpy	<chem>CCCCCCCCC[N+]1=CC=CC(=C1)C</chem>	thiocyanate	SCN	<chem>C(#N)[S-]</chem>	T	0.02	−1.70
9	1-ethyl-1-methylpyrrolidinium m	C2mpyrr	<chem>CC[N+]1(CCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	222.19	2.35
10	1-butyl-1-methylpyrrolidinium m	C4mpyrr	<chem>CCCC[N+]1(CCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	108.88	2.04
11	1-octyl-1-methylpyrrolidinium m	C8mpyrr	<chem>CCCCCCCC[N+]1(CCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	V	3.22	0.51
12	1-decyl-1-methylpyrrolidinium m	C10mpyrr	<chem>CCCCCCCCC[N+]1(CCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	0.52	−0.28
13	1-butyl-1-methylpiperidinium	C4mpip	<chem>CCCC[N+]1(CCCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	80.4	1.91
14	1-hexyl-1-methylpiperidinium m	C6mpip	<chem>CCCCC[N+]1(CCCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	V	10.83	1.03
15	1-octyl-1-methylpiperidinium	C8mpip	<chem>CCCCCCCC[N+]1(CCCCC1)C</chem>	bromide	Br	<chem>[Br-]</chem>	T	1.91	0.28

16	1-octyl-3-methylimidazolium	C8mim	CCCCCCCCN1C=C[N+](=C1)C	thiocyanate	SCN	C(#N)[S-]	T	2.53	0.40
17	1-butyl-3-methylimidazolium	C4mim	CCCCN1C=C[N+](=C1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	1.64	0.21
18	1-butylpyridinium	C4py	CCCC[N+]1=CC=CC=C1	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	2.3	0.36
19	1-butyl-1-methylpyrrolidinium	C4mpyrr	CCCC[N+]1(CCCC1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	3.29	0.52
20	1-butyl-1-methylpiperidinium	C4mpip	CCCC[N+]1(CCCCC1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	V	2.05	0.31
21	1-octyl-3-methylimidazolium	C8mim	CCCCCCCCN1C=C[N+](=C1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	V	0.35	-0.46
22	1-octylpyridinium	C8py	CCCCCCCC[N+]1=CC=CC=C1	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	0.47	-0.33
23	1-octyl-1-methylpyrrolidinium	C8mpyrr	CCCCCCCC[N+]1(CCCC1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	0.64	-0.19
24	1-octyl-1-methylpiperidinium	C8mpip	CCCCCCCC[N+]1(CCCCC1)C	bis(trifluoromethylsulfonyl)amide	NTf2	C(F)(F)(F)S(=O)(=O)[N-]S(=O)(=O)C(F)(F)F	T	0.9	-0.05

T – training set, V – validation set

Table S2. Details of the model based on 2D descriptors calculated for each of the cations and anions separately (M1).

Variable	Coeff.	Std. Error
Intercept	2.49	0.18
Psi_i_0 ^A	-0.14	0.02
SMTIV ^C	-0.001	0.0001

Quality Parameters:

<i>Fitting criteria</i>	<i>Internal validation criteria</i>	<i>External validation criteria</i>
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R ²	0.91	Q ² loo	0.86	R ² ext/Q ² –F1	0.83		
RMSE _c	0.30	RMSE _{cv}	0.38	RMSE _{EXT}	0.30		
R ² adj	0.90	R ² –Q ² loo	0.05	Q ² –F2	0.83		
R ² –R ² adj	0.01	MAE _{cv}	0.31	MAE _{EXT}	0.28		
MAE _c	0.25			r ² m aver.	0.76		
RSS _c	1.53			r ² m delta	0.11		
				r ²	0.85		
				r0 ²	0.84		
				reverse r0 ²	0.82		
Golbraikh and Tropsha Acceptable Model Criteria's:							
1. Q ²		0.86		Q ² > 0.5	Passed		
2. r ²		0.85		r ² > 0.6	Passed		
3. r0 ² –r' ²		0.03		r0 ² –r'0 ² < 0.3	Passed		
4. k		0.89		[0.85 < k < 1.15 and ((r ² –r0 ²)/r ² < 0.1)]	Passed		
[(r ² –r0 ²)/r ²]		0.01					
OR*							
k'		1.00		[0.85 < k' < 1.15 and ((r ² –r'0 ²)/ r ²) < 0.1)]	Passed		
[(r ² –r'0 ²)/r ²]		0.04					
ID	Set	Psi_i_0 ^A	SMTIV ^c	Exp. Endpoint	Pred. by Model eq.	Pred.Mod.Eq.Res.	Outlier or out of AD? (StdAD)
1	T	0	900	1.65	1.58	0.08	No
3	T	0	1480	0.99	0.99	0.00	No
4	T	1.56	1480	1.16	0.76	0.39	No
7	T	0	3370	–0.57	–0.93	0.36	No
8	T	1.56	3370	–1.70	–1.15	–0.55	No
9	T	0	262	2.35	2.22	0.12	No
10	T	0	518	2.04	1.96	0.07	No

12	T	0	2370	−0.28	0.08	−0.37	No
13	T	0	669	1.91	1.81	0.10	No
15	T	0	1840	0.28	0.62	−0.34	No
16	T	1.56	1960	0.40	0.28	0.13	No
17	T	8.09	721	0.22	0.60	−0.38	No
18	T	8.09	740	0.36	0.58	−0.22	No
19	T	8.09	518	0.52	0.80	−0.29	No
22	T	8.09	1990	−0.33	−0.69	0.36	No
23	T	8.09	1540	−0.19	−0.23	0.04	No
24	T	8.09	1840	−0.05	−0.54	0.49	No
2	V	1.56	900	1.74	1.35	0.39	No
5	V	0	2300	0.04	0.16	−0.12	No
6	V	1.56	2300	−0.24	−0.07	−0.18	No
11	V	0	1540	0.51	0.93	−0.42	No
14	V	0	1150	1.04	1.32	−0.29	No
20	V	8.09	669	0.31	0.65	−0.34	No
21	V	8.09	1960	−0.46	−0.66	0.20	No

Table S3. Details of the model based on 3D descriptors calculated for each of the cations and anions separately (M2).

Variable	Coef.	Std. Error
Intercept	2.52	0.20
L1m ^c	−0.12	0.01
L1i ^A	−0.19	0.03

Quality Parameters:					
Fitting criteria		Internal validation criteria		External validation criteria	
R ²	0.90	Q ² loo	0.85	R ² ext/Q ² –F1	0.85

RMSE _c	0.33	RMSE _{cv}	0.40	RMSE _{EXT}	0.27
R ² _{adj}	0.89	R ² –Q ² _{loo}	0.05	Q ² –F2	0.85
R ² –R ² _{adj}	0.01	MAE _{cv}	0.33	MAE _{EXT}	0.25
MAE _c	0.27			r ² _{m aver.}	0.80
RSS _c	1.80			r ² _{m delta}	0.10
				r ²	0.86
				r ⁰²	0.86
				reverse r ⁰²	0.85
Golbraikh and Tropsha Acceptable Model Criteria's:					
1. Q ²	0.85		Q ² > 0.5		Passed
2. r ²	0.86		r ² > 0.6		Passed
3. r ⁰² –r' ⁰²	0.01		r ⁰² –r' ⁰² < 0.3		Passed
4. k	0.93				
[(r ² –r' ⁰²)/r ²]	0.002		[0.85 < k < 1.15 and ((r ² –r' ⁰²)/r ²) < 0.1]		Passed
OR*					
k'	0.96				
[(r ² –r' ⁰²)/r ²]	0.02		[0.85 < k' < 1.15 and ((r ² –r' ⁰²)/r ²) < 0.1])		Passed

ID	Set	L1m ^c	L1i ^A	Exp. Endpoint	Pred. by Model eq.	Pred.Mod.Eq.Res.	Outlier or out of AD? (StdAD)
1	T	6.779	0	1.65	1.68	–0.03	No
3	T	11.763	0	0.99	1.07	–0.08	No

4	T	11.763	1.378	1.16	0.81	0.35	No
7	T	26.051	0	−0.57	−0.69	0.12	No
8	T	26.051	1.378	−1.70	−0.95	−0.75	No
9	T	2.543	0	2.35	2.20	0.15	No
10	T	4.483	0	2.04	1.96	0.08	No
12	T	22.202	0	−0.28	−0.22	−0.06	No
13	T	6.231	0	1.91	1.75	0.16	No
15	T	15.419	0	0.28	0.62	−0.34	No
16	T	18.4	1.378	0.40	−0.01	0.41	No
17	T	6.996	5.665	0.22	0.59	−0.38	No
18	T	6.482	5.665	0.36	0.65	−0.29	No
19	T	4.483	5.665	0.52	0.90	−0.38	No
22	T	17.744	5.665	−0.33	−0.73	0.40	No
23	T	15.31	5.665	−0.19	−0.43	0.24	No
24	T	15.419	5.665	−0.05	−0.45	0.40	No
2	V	6.779	1.378	1.74	1.42	0.32	No
5	V	18.237	0	0.04	0.27	−0.23	No
6	V	18.237	1.378	−0.24	0.01	−0.26	No
11	V	15.31	0	0.51	0.63	−0.12	No
14	V	11.166	0	1.04	1.14	−0.11	No
20	V	6.231	5.665	0.31	0.68	−0.37	No
21	V	18.4	5.665	−0.46	−0.81	0.36	No

Table 4. Details of the model based on 2D and 3D descriptors calculated for each of the cations and anions separately (M3).

Variable	Coeff.	Std. Error			
Intercept	2.304	0.1653			
Psi_i_0 ^A	−0.142	0.0217			
QZZm ^C	−0.006	0.0005			
Quality Parameters:					
Fitting criteria		Internal validation criteria		External validation criteria	
R ²	0.92	Q ² loo	0.87	R ² ext/Q ² −F1	0.86
RMSE _c	0.30	RMSE _{cv}	0.38	RMSE _{EXT}	0.27
R ² adj	0.905	R ² −Q ² loo	0.05	Q ² −F2	0.86
R ² −R ² adj	0.012	MAE _{cv}	0.32	MAE _{EXT}	0.26
MAE _c	0.25			r ² m aver.	0.75
RSS _c	1.50			r ² m delta	0.10
				r ²	0.89
				r0 ²	0.87
				reverse r0 ²	0.84
Golbraikh and Tropsha acceptable model criteria's:					
1. Q ²		0.86	Q ² > 0.5		Passed
2. r ²		0.89	r ² > 0.6		Passed
3. r0 ² −r'0 ²		0.03	r0 ² −r'0 ² < 0.3		Passed
4. k		0.91	[0.85 < k < 1.15 and ((r ² −r0 ²)/r ²) < 0.1]		Passed
[(r ² −r0 ²)/r ²]		0.02			
OR*					
k'		0.99	[0.85 < k' < 1.15 and ((r ² −r'0 ²)/r ²) < 0.1])		Passed

		[(r ² −r' ⁰²)/r ²]		0.06			
ID	Set	Psi_i_0 ^A	QZZm ^C	Exp. Endpoint	Pred. by Model eq.	Pred.Mod.Eq.R es.	Outlier or out of AD? (StdAD)
1	T	0	99	1.65	1.71	−0.06	No
3	T	0	190.258	0.99	1.17	−0.18	No
4	T	1.56	190.258	1.16	0.95	0.21	No
7	T	0	525.383	−0.57	−0.83	0.26	No
8	T	1.56	525.383	−1.70	−1.05	−0.65	No
9	T	0	30.861	2.35	2.12	0.23	No
10	T	0	67.211	2.04	1.90	0.13	No
12	T	0	436.357	−0.28	−0.29	0.01	No
13	T	0	91.447	1.91	1.76	0.15	No
15	T	0	290.62	0.28	0.57	−0.29	No
16	T	1.56	307.266	0.40	0.25	0.15	No
17	T	8.09	87.871	0.22	0.63	−0.42	No
18	T	8.09	81.203	0.36	0.67	−0.31	No
19	T	8.09	67.211	0.52	0.76	−0.24	No
22	T	8.09	292.369	−0.33	−0.59	0.26	No
23	T	8.09	266.49	−0.19	−0.43	0.24	No
24	T	8.09	290.62	−0.05	−0.57	0.53	No
2	V	1.56	99	1.74	1.49	0.25	No
5	V	0	329.776	0.04	0.34	−0.30	No
6	V	1.56	329.776	−0.24	0.12	−0.36	No
11	V	0	266.49	0.51	0.72	−0.21	No
14	V	0	182.483	1.04	1.22	−0.18	No
20	V	8.09	91.447	0.31	0.61	−0.30	No

21	V	8.09	307.266	−0.46	−0.67	0.22	No
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Table S5. Details of the model based on 2D descriptors calculated for whole ionic pairs (M4).

Variable		Coeff.	Std. Error		
Intercept		4.15	0.40		
GMTI		−0.001	0.0001		
MDDD		−0.09	0.02		
AMW		−0.16	0.04		
Quality Parameters:					
Fitting criteria		Internal validation criteria		External validation criteria	
R ²	0.97	Q ² loo	0.94	R ² ext/Q ² −F1	0.91
RMSE _C	0.18	RMSE _{CV}	0.25	RMSE _{EXT}	0.21
R ² adj	0.96	R ² −Q ² loo	0.03	Q ² −F2	0.91
R ² −R ² adj	0.01	MAE _{CV}	0.19	MAE _{EXT}	0.21
MAE _C	0.14			r ² m aver.	0.74
RSS _C	0.52			r ² m delta	0.07
				r ²	0.97
				r0 ²	0.92
				reverse r0 ²	0.89
Golbraikh and Tropsha acceptable model criteria's:					

1. Q ²	0.94	Q ² > 0.5		Passed				
2. r ²	0.97	r ² > 0.6		Passed				
3. r ⁰² −r' ⁰²	0.03	r ⁰² −r' ⁰² < 0.3		Passed				
4. k	0.93	[0.85 < k < 1.15 and ((r ² −r ⁰²)/r ² < 0.1)]		Passed				
[(r ² −r ⁰²)/r ²]	0.06							
OR*								
k'	1.01	[0.85 < k' < 1.15 and ((r ² −r' ⁰²)/r ²) < 0.1]		Passed				
[(r ² −r' ⁰²)/r ²]	0.09							
ID	Set	GMTI	MDDD	AMW	Exp. Endpoint	Pred. by Model eq.	Pred.Mod.E q.Res.	Outlier or out of AD? (StdAD)
1	T	609	7.17	8.22	1.65	1.66	−0.01	No
3	T	1080	10.3	7.59	0.99	1.07	−0.08	No
4	T	1090	14.1	6.57	1.16	0.87	0.29	No
7	T	2690	17.9	6.83	−0.57	−0.90	0.33	No
8	T	2690	24	6.09	−1.70	−1.34	−0.36	No
9	T	201	3.65	7.77	2.35	2.41	−0.06	No
10	T	435	5.95	7.17	2.04	2.09	−0.05	No
12	T	2230	16	6.25	−0.28	−0.23	−0.05	No
13	T	577	7	6.95	1.91	1.91	0.00	No
15	T	1700	13.5	6.36	0.28	0.43	−0.15	No
16	T	1490	17.3	6.34	0.40	0.27	0.13	No
17	T	1420	10.4	10.5	0.22	0.31	−0.10	No
18	T	1440	10.3	10.7	0.36	0.27	0.09	No
19	T	1390	10.9	9.39	0.52	0.46	0.06	No
22	T	2460	8.73	9.27	−0.33	−0.23	−0.10	No

23	T	2370	8.28	8.4	−0.19	0.02	−0.21	No
24	T	2660	9.65	8.21	−0.05	−0.32	0.27	No
2	V	615	9.92	6.95	1.74	1.60	0.14	No
5	V	1770	14	7.16	0.04	0.20	−0.17	No
6	V	1770	18.9	6.3	−0.24	−0.12	−0.13	No
11	V	1420	12.1	6.47	0.51	0.79	−0.28	No
14	V	1040	10	6.61	1.04	1.29	−0.25	No
20	V	1530	9.54	9.09	0.31	0.52	−0.21	No
21	V	2430	8.66	9.15	−0.46	−0.18	−0.27	No

Table S6. Details of the model based on 3D descriptors calculated from the optimized geometries of whole ionic pairs (M5).

Variable	Coeff.	Std. Error			
Intercept	6.91	0.34			
L/Bw	−0.24	0.02			
RTv	−1.05	0.07			
L3u	0.53	0.18			
Quality Parameters:					
Fitting criteria		Internal validation criteria		External validation criteria	
R ²	0.97	Q ² loo	0.94	R ² ext/Q ² –F1	0.84
RMSE _c	0.18	RMSE _{cv}	0.26	RMSE _{EXT}	0.28
R ² adj	0.96	R ² –Q ² loo	0.04	Q ² –F2	0.85
R ² –R ² adj	0.01	MAE _{cv}	0.20	MAE _{EXT}	0.25
MAE _c	0.14			r ² m aver.	0.77
RSS _c	0.52			r ² m delta	0.09
				r ²	0.89
				r0 ²	0.88
				reverse r0 ²	0.89
Golbraikh and Tropsha Acceptable Model Criteria’s:					
1. Q ²	0.94	Q ² > 0.5		Passed	
2. r ²	0.89	r ² > 0.6		Passed	
3. r0 ² –r’0 ²	0.01	r0 ² –r’0 ² < 0.3		Passed	
4. k	0.86	[0.85 < k < 1.15 and ((r ² –r0 ²)/r ² < 0.1)]		Passed	
[(r ² –r0 ²)/r ²]	0.02				
OR*				Passed	
k’	1.06	[0.85 < k’ < 1.15 and ((r ² –r’0 ²)/r ²) < 0.1)]		Passed	
[(r ² –r’0 ²)/r ²]	0.01				

ID	Set	L/Bw	RTv	L3u	Exp. Endpoint	Pred. by model eq.	Pred.Mod.Eq .Res.	Outlier or out of AD? (StdAD)
1	T	1.6	4.874	0.746	1.65	1.81	−0.16	No
3	T	4.37	5.002	0.903	0.99	1.08	−0.09	No
4	T	4.18	5.474	1.454	1.16	0.92	0.24	No
7	T	9.44	5.509	0.905	−0.57	−0.69	0.12	No
8	T	10.52	6.068	0.941	−1.70	−1.52	−0.18	No
9	T	3.76	4.232	1.147	2.35	2.17	0.18	No
10	T	1.59	4.725	1.094	2.04	2.15	−0.11	No
12	T	7.66	5.532	0.992	−0.28	−0.23	−0.05	No
13	T	1.29	5.175	1.284	1.91	1.85	0.06	No
15	T	4.61	5.671	1.151	0.28	0.45	−0.17	No
16	T	6.58	5.298	0.941	0.40	0.25	0.15	No
17	T	1.96	6.685	2.292	0.22	0.64	−0.43	No
18	T	1.68	6.651	1.392	0.36	0.27	0.09	No
19	T	2.3	6.749	2.127	0.52	0.40	0.12	No
22	T	2.2	7.163	1.557	−0.33	−0.31	−0.02	No
23	T	2.05	6.929	1.277	−0.19	−0.18	−0.01	No
24	T	2.23	7.341	1.896	−0.05	−0.32	0.27	No
2	V	2.8	4.732	1.003	1.74	1.80	−0.06	No
5	V	8.96	5.498	1.127	0.04	−0.44	0.48	No
6	V	7.86	5.778	1.185	−0.24	−0.43	0.19	No
11	V	4.56	5.3	1.018	0.51	0.78	−0.27	No
14	V	2.41	5.458	1.22	1.04	1.25	−0.21	No
20	V	2.03	6.818	1.391	0.31	0.01	0.31	No

21	V	2.85	7.201	2.126	−0.46	−0.21	−0.25	No
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Table S7. Details of the model based on 2D and 3D descriptors from the optimized geometries of whole ionic pairs (M6).

Variable	Coeff.	Std. Error
Intercept	3.49	0.53
GMTI	−0.001	0.00
E1e	−3.21	0.81
DISPm	0.04	0.02

Quality Parameters:					
Fitting criteria		Internal validation criteria		External validation criteria	
R ²	0.96	Q ² loo	0.91	R ² ext/Q ² −F1	0.90
RMSE _c	0.20	RMSE _{cv}	0.30	RMSE _{EXT}	0.23
R ² adj	0.95	R ² −Q ² loo	0.05	Q ² −F2	0.90
R ² −R ² adj	0.01	MAE _{cv}	0.22	MAE _{EXT}	0.21
MAE _c	0.16			r ² m aver.	0.65
RSS _c	0.68			r ² m delta	0.11
				r ²	0.98
				r0 ²	0.90
				reverse r0 ²	0.85

Golbraikh and Tropsha Acceptable Model Criteria's:			
1. Q ²	0.91	Q ² > 0.5	Passed
2. r ²	0.98	r ² > 0.6	Passed
3. r0 ² −r'0 ²	0.05	r0 ² −r'0 ² < 0.3	Passed
4. k	1.03	[0.85 < k < 1.15 and ((r ² −r0 ²)/r ² < 0.1]	Passed
[(r ² −r0 ²)/r ²]	0.08		Passed
OR*			Passed

					k' $[(r^2-r'^0^2)/r^2]$	0.90 0.13	$[0.85 < k' < 1.15 \text{ and } ((r^2-r'^0^2)/r^2) < 0.1]$	Passed
ID	Set	GMTI	E1e	DISPm	Exp. Endpoint	Pred. by Model eq.	Pred.Mod.Eq.Res.	Outlier or out of AD? (StdAD)
1	T	609	0.528	11.096	1.65	1.49	0.16	No
3	T	1080	0.562	17.687	0.99	1.06	−0.07	No
4	T	1090	0.546	11.082	1.16	0.80	0.36	No
7	T	2690	0.568	23.257	−0.57	−0.83	0.26	No
8	T	2690	0.547	13.135	−1.70	−1.21	−0.49	No
9	T	201	0.446	16.767	2.35	2.55	−0.20	No
10	T	435	0.464	14.929	2.04	2.10	−0.06	No
12	T	2230	0.557	17.057	−0.28	−0.47	0.19	No
13	T	577	0.452	13.776	1.91	1.90	0.01	No
15	T	1700	0.52	14.36	0.28	0.23	0.05	No
16	T	1490	0.537	12.694	0.40	0.38	0.02	No
17	T	1420	0.622	15.915	0.21	0.34	−0.13	No
18	T	1440	0.616	17.52	0.36	0.40	−0.04	No
19	T	1390	0.616	19.885	0.52	0.57	−0.05	No
22	T	2460	0.454	21.417	−0.33	−0.24	−0.09	No
23	T	2370	0.41	21.32	−0.19	0.01	−0.20	No
24	T	2660	0.385	20.641	−0.05	−0.32	0.27	No
2	V	615	0.545	11.476	1.74	1.45	0.30	No
5	V	1770	0.579	23.399	0.04	0.35	−0.31	No
6	V	1770	0.553	14.124	−0.24	0.02	−0.26	No
11	V	1420	0.536	15.651	0.51	0.60	−0.10	No

14	V	1040	0.488	13.477	1.04	1.16	−0.13	No
20	V	1530	0.613	20.523	0.31	0.43	−0.12	No
21	V	2430	0.446	20.942	−0.46	−0.20	−0.26	No



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