Full wwPDB NMR Structure Validation Report ⓘ

Jun 3, 2023 – 08:26 AM EDT

PDB ID	:	6CTB
BMRB ID	:	27530
Title	:	Apo-Calmodulin Bound to Calcium Voltage Gated Channel 1.2 IQ-Motif
Authors	:	Turner, M.L.; Anderson, D.E.; Ames, J.B.
Deposited on	:	2018-03-22

The following versions of software and data (see references ⓘ) were used in the production of this report:

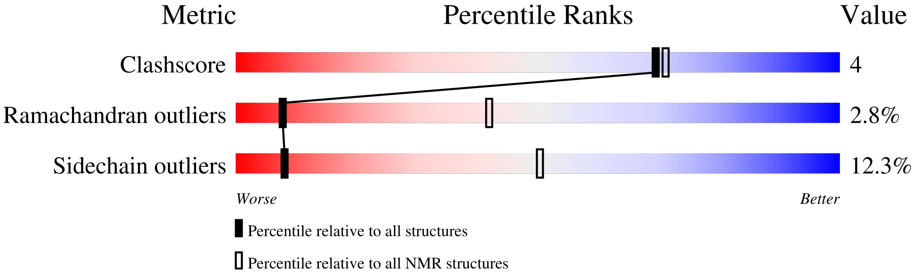
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
SOLUTION NMR

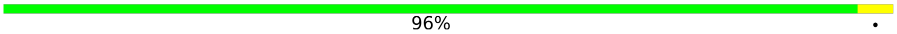
The overall completeness of chemical shifts assignment is 10%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	147	
2	B	25	

2 Ensemble composition and analysis (i)

This entry contains 4 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:82-A:148, B:1644-B:1668 (92)	0.70	3

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 1 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4

3 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 1479 atoms, of which 722 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	67	1029	327	493	88	117	4	0

- Molecule 2 is a protein called Voltage-dependent L-type calcium channel subunit alpha-1C.

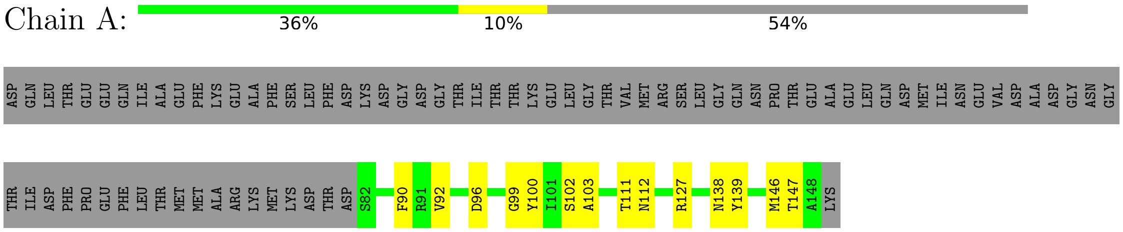
Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	25	450	148	229	38	35	0

4 Residue-property plots ⓘ

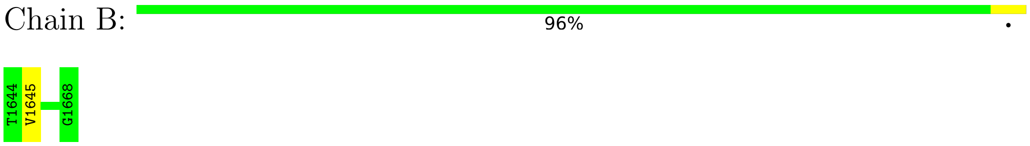
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Calmodulin-1



- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

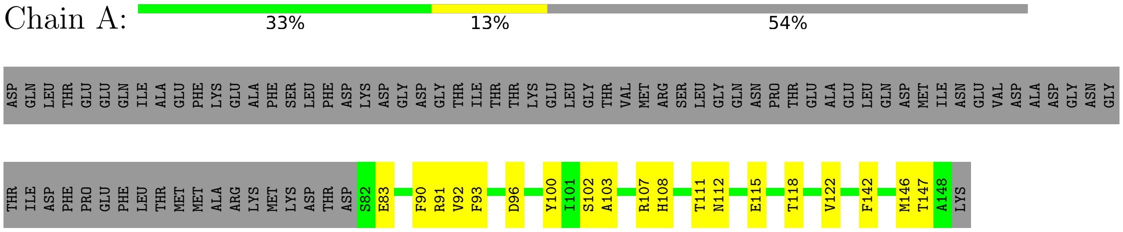


4.2 Scores per residue for each member of the ensemble

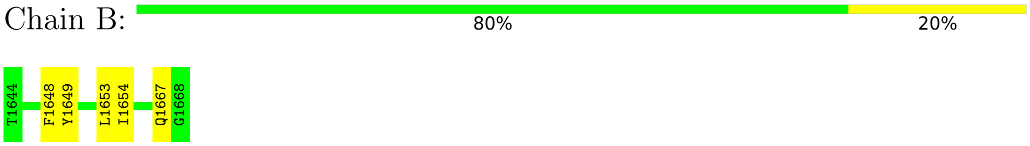
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Calmodulin-1

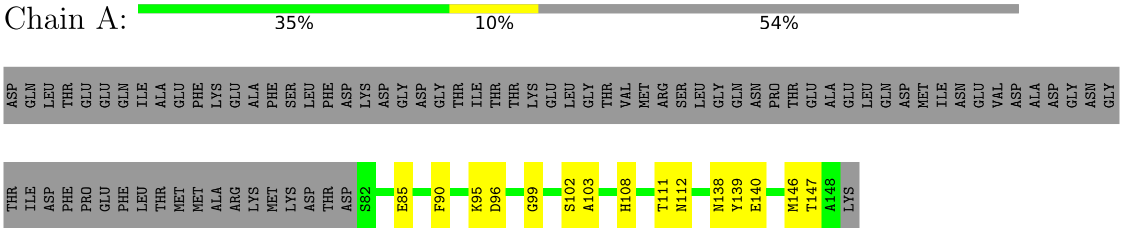


- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

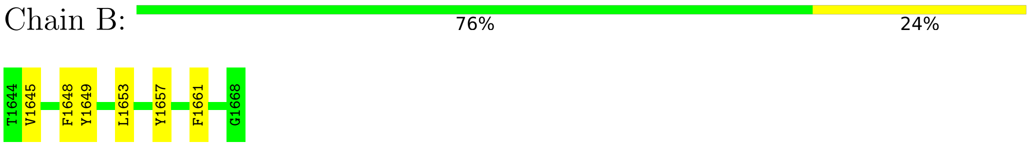


4.2.2 Score per residue for model 2

- Molecule 1: Calmodulin-1

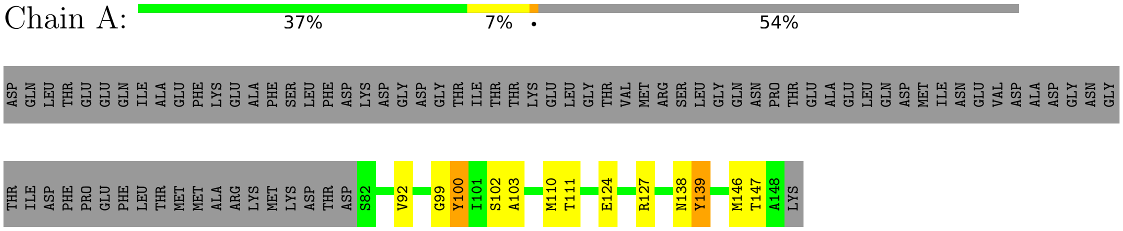


- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

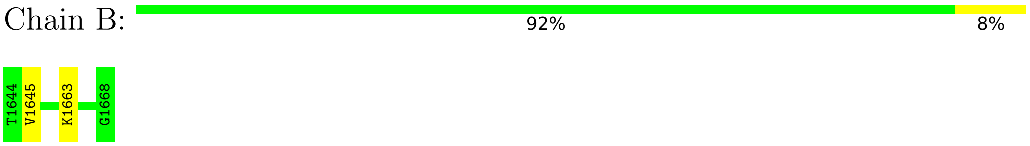


4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Calmodulin-1



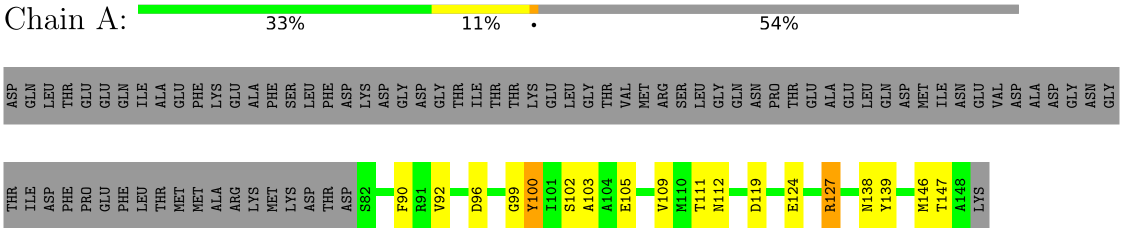
- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C



4.2.4 Score per residue for model 4

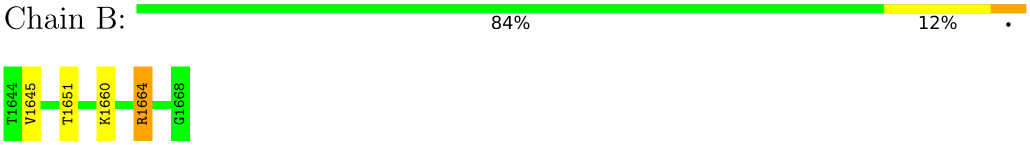
- Molecule 1: Calmodulin-1

Chain A:



- Molecule 2: Voltage-dependent L-type calcium channel subunit alpha-1C

Chain B:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 4 were deposited, based on the following criterion: *l*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	**Classification**	**Version**
HADDOCK	structure calculation	
PALES	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	290
Number of shifts mapped to atoms	134
Number of unparsed shifts	0
Number of shifts with mapping errors	156
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	10%

6 Model quality (i)

6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	536	493	492	4±0
2	B	221	229	228	2±1
All	All	3028	2888	2880	22

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1660:LYS:O	2:B:1664:ARG:HB2	0.62	1.95	4	1
1:A:108:HIS:O	1:A:112:ASN:HB2	0.59	1.98	2	2
1:A:99:GLY:HA2	1:A:139:TYR:CZ	0.55	2.35	3	2
1:A:99:GLY:HA2	1:A:139:TYR:CE1	0.52	2.40	4	1
2:B:1649:TYR:O	2:B:1653:LEU:HG	0.49	2.06	2	2
1:A:146:MET:HA	2:B:1648:PHE:CE2	0.49	2.42	2	1
1:A:100:TYR:CE2	1:A:138:ASN:HB2	0.48	2.43	4	1
1:A:107:ARG:HG3	1:A:122:VAL:HG11	0.48	1.85	1	1
1:A:124:GLU:OE1	1:A:127:ARG:HD3	0.47	2.08	3	1
1:A:99:GLY:O	1:A:138:ASN:HA	0.47	2.09	3	2
1:A:146:MET:HA	2:B:1648:PHE:CE1	0.46	2.46	1	1
1:A:124:GLU:OE2	1:A:127:ARG:HD2	0.45	2.11	4	1
1:A:105:GLU:O	1:A:109:VAL:HG23	0.45	2.12	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:TYR:CD1	1:A:100:TYR:N	0.42	2.87	4	2
2:B:1657:TYR:O	2:B:1661:PHE:HB2	0.42	2.14	2	1
1:A:91:ARG:C	1:A:93:PHE:H	0.41	2.18	1	1
1:A:118:THR:O	1:A:122:VAL:HG23	0.41	2.16	1	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	65/147 (44%)	56±1 (86±1%)	8±1 (12±2%)	2±0 (3±1%)	8	43
2	B	23/25 (92%)	21±0 (92±2%)	1±1 (4±3%)	1±0 (3±2%)	6	37
All	All	352/688 (51%)	308 (88%)	34 (10%)	10 (3%)	8	42

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	103	ALA	4
1	A	92	VAL	3
2	B	1645	VAL	3

6.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	57/126 (45%)	48±1 (85±2%)	8±1 (15±2%)	6	44
2	B	22/22 (100%)	21±1 (94±4%)	1±1 (6±4%)	24	73
All	All	316/592 (53%)	277 (88%)	39 (12%)	8	50

All 23 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	102	SER	4
1	A	111	THR	4
1	A	147	THR	4
1	A	90	PHE	3
1	A	96	ASP	3
1	A	100	TYR	3
1	A	146	MET	2
1	A	83	GLU	1
1	A	115	GLU	1
1	A	142	PHE	1
2	B	1654	ILE	1
2	B	1667	GLN	1
1	A	85	GLU	1
1	A	95	LYS	1
1	A	140	GLU	1
1	A	110	MET	1
1	A	139	TYR	1
2	B	1663	LYS	1
1	A	112	ASN	1
1	A	119	ASP	1
1	A	127	ARG	1
2	B	1651	THR	1
2	B	1664	ARG	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation ⓘ

The completeness of assignment taking into account all chemical shift lists is 10% for the well-defined parts and 10% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *apocammitzunmrstarfix_ V9mMuzS.txt*

7.1.1 Bookkeeping ⓘ

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	290
Number of shifts mapped to atoms	134
Number of unparsed shifts	0
Number of shifts with mapping errors	156
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. All 10 occurrences are reported below.

List ID	**Chain**	**Res**	**Type**	**Atom**	**Shift Data**		
					Value	Uncertainty	Ambiguity
1	A	83	GLU	H	8.2	.	1
1	A	83	GLU	N	119.12	.	1
1	A	103	ALA	H	8.29	.	1
1	A	103	ALA	N	119.43	.	1
1	A	120	GLU	H	7.82	.	1
1	A	120	GLU	N	121.19	.	1
1	A	140	GLU	H	7.84	.	1
1	A	140	GLU	N	117.96	.	1
1	A	145	MET	H	8.01	.	1
1	A	145	MET	N	116.88	.	1

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 156 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	3	ASP	H	8.72	.	1
1	A	3	ASP	N	120.85	.	1
1	A	4	GLN	H	8.23	.	1
1	A	4	GLN	N	119.18	.	1
1	A	5	LEU	H	8.32	.	1
1	A	5	LEU	N	122.52	.	1
1	A	6	THR	H	8.78	.	1
1	A	6	THR	N	113.55	.	1
1	A	7	GLU	H	9.04	.	1
1	A	7	GLU	N	120.82	.	1
1	A	8	GLU	H	8.71	.	1
1	A	8	GLU	N	119.94	.	1
1	A	9	GLN	H	7.76	.	1
1	A	9	GLN	N	120.99	.	1
1	A	10	ILE	H	8.26	.	1
1	A	10	ILE	N	118.99	.	1
1	A	11	ALA	H	7.95	.	1
1	A	11	ALA	N	121.03	.	1
1	A	12	GLU	H	7.85	.	1
1	A	12	GLU	N	120.65	.	1
1	A	13	PHE	H	8.89	.	1
1	A	13	PHE	N	121.14	.	1
1	A	14	LYS	H	9.25	.	1
1	A	14	LYS	N	122.17	.	1
1	A	15	GLU	H	8.08	.	1
1	A	15	GLU	N	121.02	.	1
1	A	16	ALA	H	7.69	.	1
1	A	16	ALA	N	121.48	.	1
1	A	17	PHE	H	8.57	.	1
1	A	17	PHE	N	118.43	.	1
1	A	18	SER	H	8.44	.	1
1	A	18	SER	N	111.64	.	1
1	A	19	LEU	H	7.39	.	1
1	A	19	LEU	N	121.79	.	1
1	A	20	PHE	H	7.47	.	1
1	A	20	PHE	N	115.22	.	1
1	A	21	ASP	H	7.86	.	1
1	A	21	ASP	N	122.07	.	1
1	A	22	LYS	H	8.4	.	1
1	A	22	LYS	N	124.98	.	1
1	A	23	ASP	H	8.65	.	1
1	A	23	ASP	N	116.72	.	1

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List ID	**Chain**	**Res**	**Type**	**Atom**	**Shift Data**		
					Value	Uncertainty	Ambiguity
1	A	24	GLY	H	8.04	.	1
1	A	24	GLY	N	110.82	.	1
1	A	25	ASP	H	8.79	.	1
1	A	25	ASP	N	121.31	.	1
1	A	26	GLY	H	10.21	.	1
1	A	26	GLY	N	112.62	.	1
1	A	27	THR	H	7.68	.	1
1	A	27	THR	N	110.33	.	1
1	A	28	ILE	H	8.32	.	1
1	A	28	ILE	N	111.0	.	1
1	A	29	THR	H	8.35	.	1
1	A	29	THR	N	111.23	.	1
1	A	30	THR	H	8.34	.	1
1	A	30	THR	N	113.04	.	1
1	A	31	LYS	H	7.67	.	1
1	A	31	LYS	N	119.6	.	1
1	A	32	GLU	H	7.55	.	1
1	A	32	GLU	N	118.09	.	1
1	A	33	LEU	H	7.41	.	1
1	A	33	LEU	N	121.52	.	1
1	A	34	GLY	H	8.81	.	1
1	A	34	GLY	N	106.06	.	1
1	A	35	THR	H	7.55	.	1
1	A	35	THR	N	119.02	.	1
1	A	36	VAL	H	8.0	.	1
1	A	36	VAL	N	123.37	.	1
1	A	37	MET	H	8.48	.	1
1	A	37	MET	N	119.24	.	1
1	A	38	ARG	H	8.54	.	1
1	A	38	ARG	N	120.12	.	1
1	A	39	SER	H	8.15	.	1
1	A	39	SER	N	119.66	.	1
1	A	40	LEU	H	7.39	.	1
1	A	40	LEU	N	121.79	.	1
1	A	41	GLY	H	7.95	.	1
1	A	41	GLY	N	107.85	.	1
1	A	42	GLN	H	7.81	.	1
1	A	42	GLN	N	118.45	.	1
1	A	43	ASN	H	8.69	.	1
1	A	43	ASN	N	117.28	.	1
1	A	45	THR	H	8.77	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	45	THR	N	113.76	.	1
1	A	46	GLU	H	8.89	.	1
1	A	46	GLU	N	121.14	.	1
1	A	47	ALA	H	8.36	.	1
1	A	47	ALA	N	121.63	.	1
1	A	48	GLU	H	7.77	.	1
1	A	48	GLU	N	119.57	.	1
1	A	49	LEU	H	8.36	.	1
1	A	49	LEU	N	120.72	.	1
1	A	50	GLN	H	8.1	.	1
1	A	50	GLN	N	118.12	.	1
1	A	51	ASP	H	7.89	.	1
1	A	51	ASP	N	119.59	.	1
1	A	52	MET	H	8.02	.	1
1	A	52	MET	N	119.75	.	1
1	A	53	ILE	H	8.36	.	1
1	A	53	ILE	N	119.74	.	1
1	A	54	ASN	H	8.32	.	1
1	A	54	ASN	N	118.07	.	1
1	A	55	GLU	H	7.64	.	1
1	A	55	GLU	N	117.97	.	1
1	A	56	VAL	H	7.64	.	1
1	A	56	VAL	N	112.69	.	1
1	A	57	ASP	H	8.46	.	1
1	A	57	ASP	N	122.43	.	1
1	A	58	ALA	H	8.15	.	1
1	A	58	ALA	N	125.61	.	1
1	A	59	ASP	H	8.43	.	1
1	A	59	ASP	N	115.67	.	1
1	A	60	GLY	H	7.96	.	1
1	A	60	GLY	N	109.49	.	1
1	A	61	ASN	H	9.17	.	1
1	A	61	ASN	N	120.18	.	1
1	A	62	GLY	H	9.85	.	1
1	A	62	GLY	N	110.53	.	1
1	A	63	THR	H	7.63	.	1
1	A	63	THR	N	111.5	.	1
1	A	64	ILE	H	8.97	.	1
1	A	64	ILE	N	119.79	.	1
1	A	65	ASP	H	8.29	.	1
1	A	65	ASP	N	124.57	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	66	PHE	H	8.72	.	1
1	A	66	PHE	N	119.19	.	1
1	A	68	GLU	H	8.14	.	1
1	A	68	GLU	N	118.08	.	1
1	A	69	PHE	H	8.54	.	1
1	A	69	PHE	N	123.16	.	1
1	A	70	LEU	H	8.5	.	1
1	A	70	LEU	N	119.19	.	1
1	A	71	THR	H	7.75	.	1
1	A	71	THR	N	116.19	.	1
1	A	72	MET	H	7.77	.	1
1	A	72	MET	N	121.96	.	1
1	A	73	MET	H	8.1	.	1
1	A	73	MET	N	118.12	.	1
1	A	74	ALA	H	8.33	.	1
1	A	74	ALA	N	121.81	.	1
1	A	75	ARG	H	7.5	.	1
1	A	75	ARG	N	117.45	.	1
1	A	76	LYS	H	7.76	.	1
1	A	76	LYS	N	119.01	.	1
1	A	77	MET	H	8.02	.	1
1	A	77	MET	N	118.53	.	1
1	A	78	LYS	H	7.77	.	1
1	A	78	LYS	N	121.16	.	1
1	A	79	ASP	H	8.33	.	1
1	A	79	ASP	N	122.33	.	1
1	A	80	THR	H	8.17	.	1
1	A	80	THR	N	115.51	.	1
1	A	81	ASP	H	8.47	.	1
1	A	81	ASP	N	123.66	.	1
1	A	149	LYS	H	7.73	.	1
1	A	149	LYS	N	126.09	.	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	None (insufficient data)
$^{13}C_{\beta}$	0	—	None (insufficient data)
$^{13}C'$	0	—	None (insufficient data)

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Nucleus	**# values**	**Correction ± precision, *ppm***	**Suggested action**
^{15}N	140	-0.14 ± 0.22	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 10%, i.e. 124 atoms were assigned a chemical shift out of a possible 1279. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	**^{1}H**	**^{13}C**	**^{15}N**
Backbone	124/467 (27%)	62/191 (32%)	0/184 (0%)	62/92 (67%)
Sidechain	0/699 (0%)	0/445 (0%)	0/222 (0%)	0/32 (0%)
Aromatic	0/113 (0%)	0/55 (0%)	0/57 (0%)	0/1 (0%)
Overall	124/1279 (10%)	62/691 (9%)	0/463 (0%)	62/125 (50%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 124 atoms were assigned a chemical shift out of a possible 1279. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	**^{1}H**	**^{13}C**	**^{15}N**
Backbone	124/467 (27%)	62/191 (32%)	0/184 (0%)	62/92 (67%)
Sidechain	0/699 (0%)	0/445 (0%)	0/222 (0%)	0/32 (0%)
Aromatic	0/113 (0%)	0/55 (0%)	0/57 (0%)	0/1 (0%)
Overall	124/1279 (10%)	62/691 (9%)	0/463 (0%)	62/125 (50%)

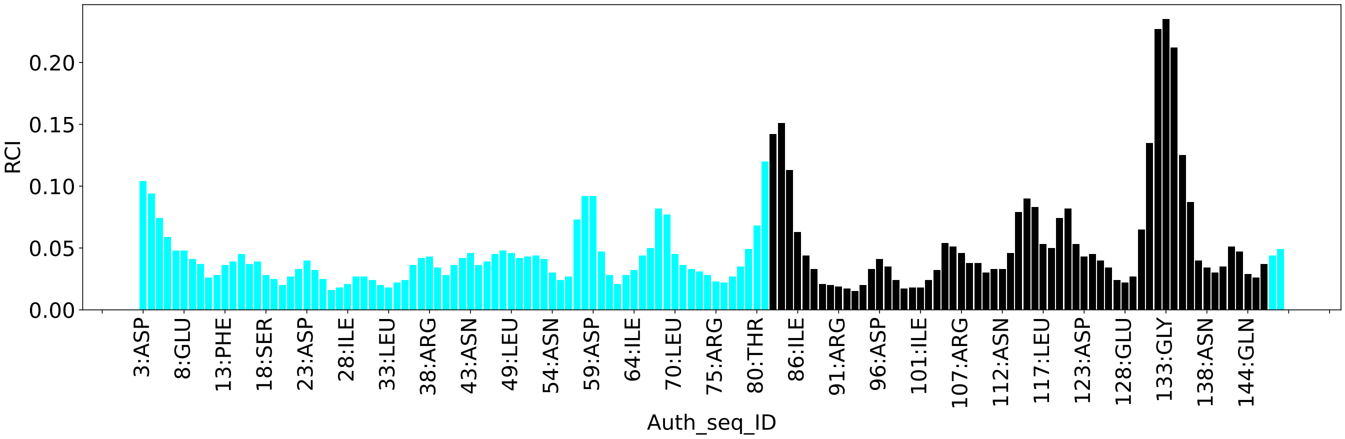
7.1.4 Statistically unusual chemical shifts

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:


RCI
0.20
0.15
0.10
0.05
0.00
3:ASP
8:GLU
13:PHE
18:SER
23:ASP
28:ILE
33:LEU
38:ARG
43:ASN
49:LEU
54:ASN
59:ASP
64:ILE
70:LEU
75:ARG
80:THR
86:ILE
91:ARG
96:ASP
101:ILE
107:ARG
112:ASN
117:LEU
123:ASP
128:GLU
133:GLY
138:ASN
144:GLN
Auth_seq_ID

8 NMR restraints analysis ⓘ

8.1 Conformationally restricting restraints ⓘ

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	31
Intra-residue (|i-j|=0)	0
Sequential (|i-j|=1)	0
Medium range (|i-j|>1 and |i-j|<5)	0
Long range (|i-j|≥5)	0
Inter-chain	7
Hydrogen bond restraints	24
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	0.2
Number of long range restraints per residue[1]	0.0

[1] Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations ⓘ

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model ⓘ

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	0.2	0.14
0.2-0.5 (Medium)	None	None
>0.5 (Large)	1.0	2.4

8.2.2 Average number of dihedral-angle violations per model ⓘ

Dihedral-angle violations less than 1° are not included in the calculation.There are no dihedral-angle violations

9 Distance violation analysis

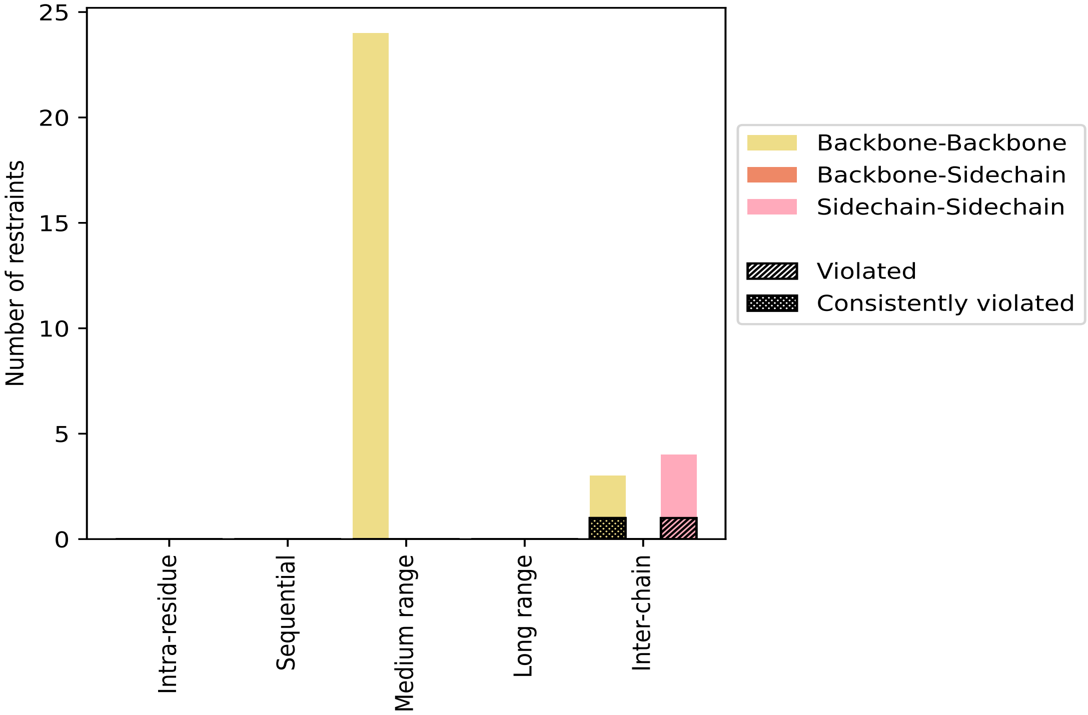
9.1 Summary of distance violations

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restraints type	Count	%^{1}	Violated^{3}			Consistently Violated^{4}		
			Count	%^{2}	%^{1}	Count	%^{2}	%^{1}
Intra-residue (|i-j|=0)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range (|i-j|≥5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	7	22.6	2	28.6	6.5	1	14.3	3.2
Backbone-Backbone	3	9.7	1	33.3	3.2	1	33.3	3.2
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	4	12.9	1	25.0	3.2	0	0.0	0.0
Hydrogen bond	24	77.4	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	31	100.0	2	6.5	6.5	1	3.2	3.2
Backbone-Backbone	27	87.1	1	3.7	3.2	1	3.7	3.2
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	4	12.9	1	25.0	3.2	0	0.0	0.0

[1] percentage calculated with respect to the total number of distance restraints, [2] percentage calculated with respect to the number of restraints in a particular restraint category, [3] violated in at least one model, [4] violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations ⓘ



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

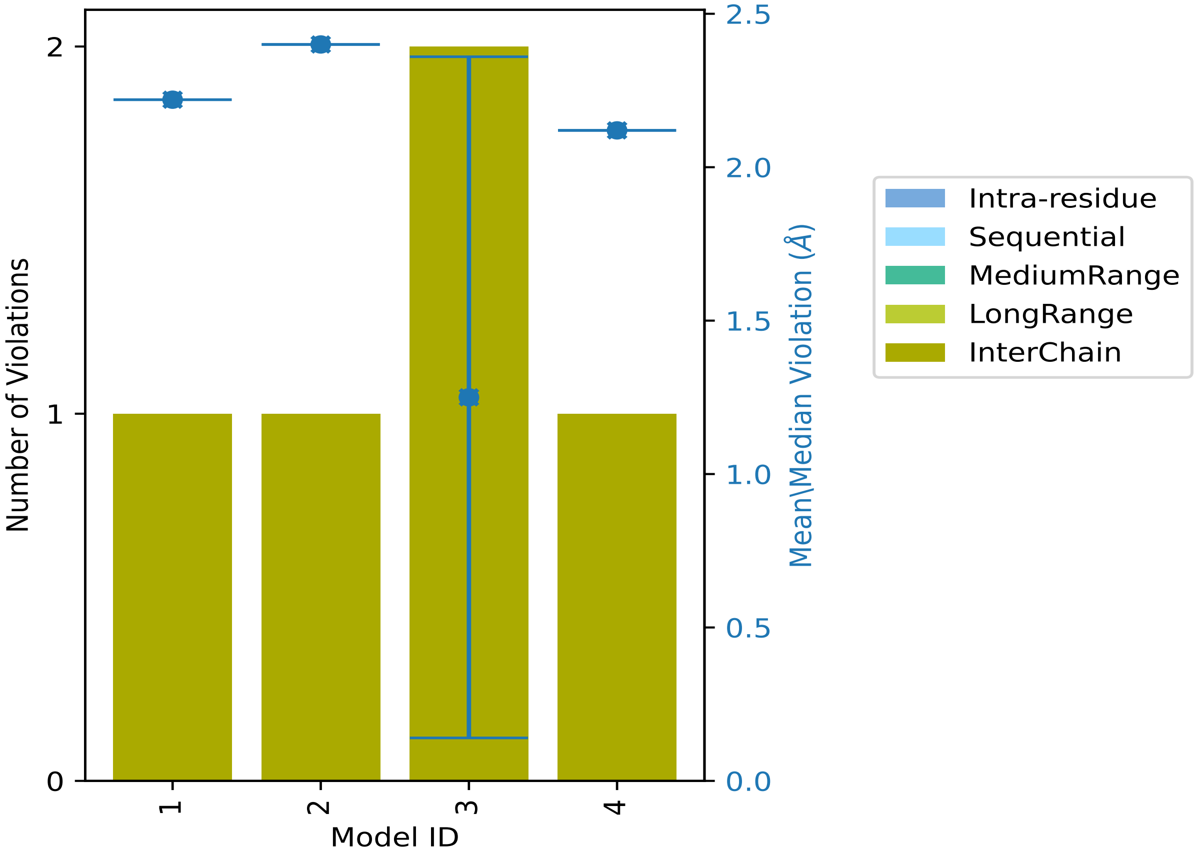
9.2 Distance violation statistics for each model ⓘ

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	0	0	0	0	1	1	2.22	2.22	0.0	2.22
2	0	0	0	0	1	1	2.4	2.4	0.0	2.4
3	0	0	0	0	2	2	1.25	2.36	1.11	1.25
4	0	0	0	0	1	1	2.12	2.12	0.0	2.12

[1] Intra-residue restraints, [2] Sequential restraints, [3] Medium range restraints, [4] Long range restraints, [5] Inter-chain restraints, [6] Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

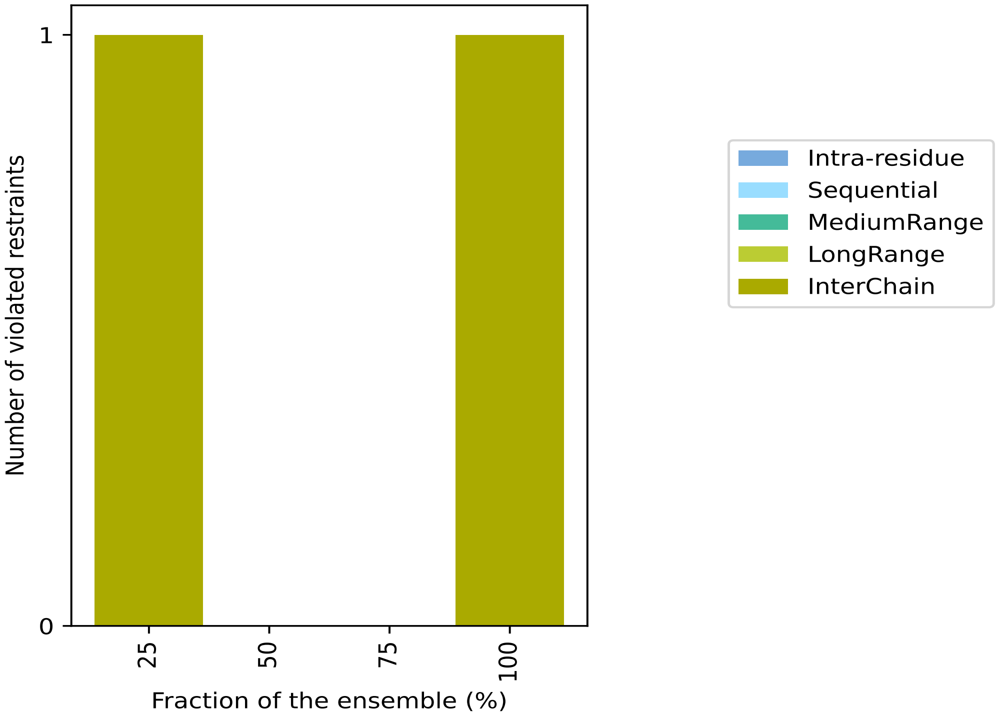
9.3 Distance violation statistics for the ensemble ⓘ

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 5(IR:0, SQ:0, MR:0, LR:0, IC:5) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
0	0	0	0	1	1	1	25.0
0	0	0	0	0	0	2	50.0
0	0	0	0	0	0	3	75.0
0	0	0	0	1	1	4	100.0

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints, [5]Inter-chain restraints, [6] Number of models with violations

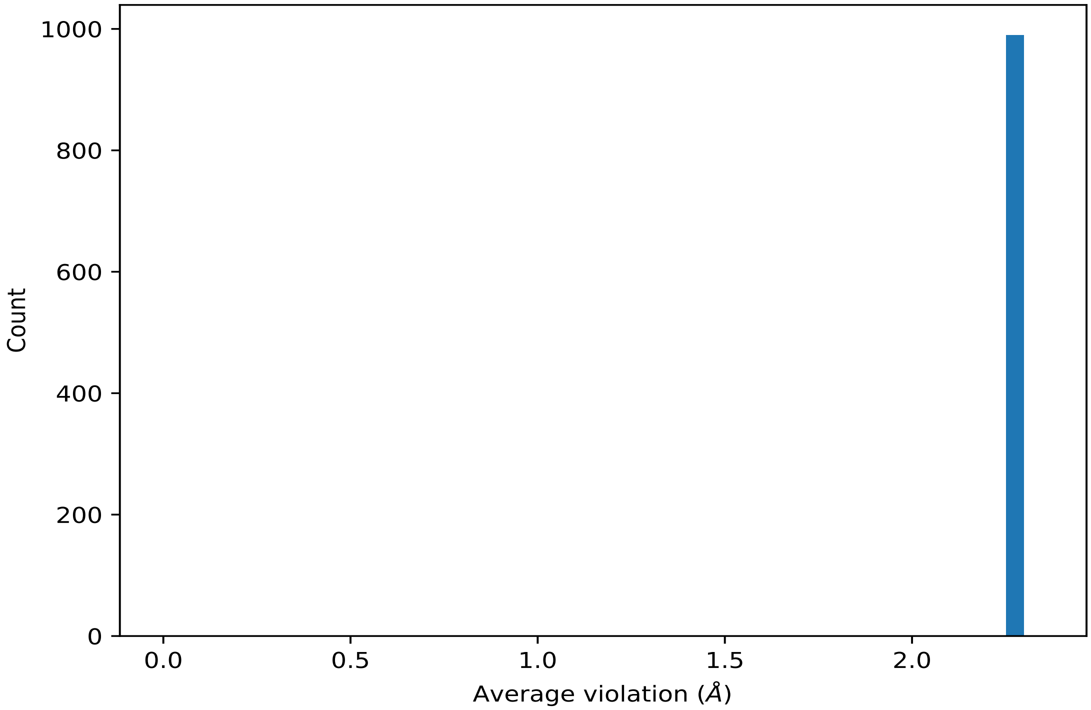
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



9.4.2 Table: Most violated distance restraints

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:C	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:O	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG2	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HA	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CD	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:C	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:O	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG2	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HA	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CD	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:C	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:O	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG2	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HA	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CD	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:C	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:O	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG2	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models^1	Mean (Å)	SD^1 (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HA	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CD	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:C	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:O	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG2	4	2.28	0.11	2.29

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:C	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CA	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CB	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CD	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CG	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:H	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HA	4	2.28	0.11	2.29

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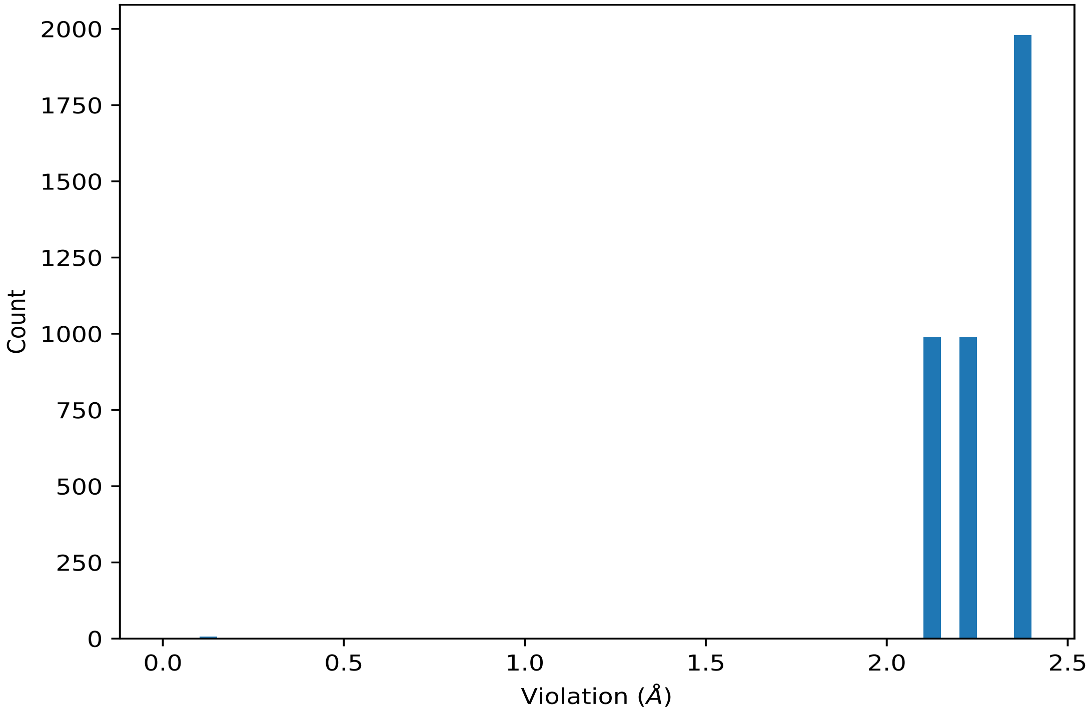
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG2	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG3	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:N	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:O	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE1	4	2.28	0.11	2.29
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE2	4	2.28	0.11	2.29

[1]Number of violated models, [2]Standard deviation

9.5 All violated distance restraints ⓘ

9.5.1 Histogram : Distribution of distance violations ⓘ

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



9.5.2 Table : All distance violations ⓘ

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG3	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB2	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CG	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CA	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE1	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG3	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB2	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CG	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CA	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE1	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG3	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB2	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CG	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CA	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE1	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG3	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB2	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CG	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CA	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE1	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG3	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB2	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CG	2	2.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:C	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CB	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CD	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CG	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:H	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HA	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG2	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG3	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:N	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:O	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE1	2	2.4
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE2	2	2.4
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CA	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE1	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG3	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB2	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CG	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CA	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE1	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG3	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB2	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CG	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CA	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE1	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG3	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB2	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CG	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CA	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE1	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG3	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB2	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CG	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CA	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE1	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG3	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:C	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CB	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CD	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CG	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:H	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HA	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB2	3	2.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG2	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG3	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:N	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:O	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE1	3	2.36
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE2	3	2.36
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CG	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CA	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE1	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG3	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB2	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CG	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CA	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE1	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG3	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB2	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CG	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CA	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE1	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG3	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB2	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CG	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CA	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE1	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG3	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB2	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CG	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CA	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE1	1	2.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:C	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CB	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CD	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CG	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:H	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HA	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG2	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG3	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:N	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:O	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE1	1	2.22
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE2	1	2.22
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:HG3	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:C	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB2	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CA	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:CG	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CB	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CA	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE1	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CD	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:HG3	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CE	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB2	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:CG	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:CG	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:H	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CA	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HA	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE1	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB2	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HB2	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:HG3	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HB3	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB2	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD2	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:CG	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HD3	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CA	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HE2	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE1	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HE3	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HE3	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:HG3	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG2	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB2	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HG3	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:CG	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ1	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CA	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE1	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ2	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:HG3	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:HZ3	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB2	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:N	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:CG	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:NZ	1:A:128:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:121:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CA	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:124:GLU:OE2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:C	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CA	4	2.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CB	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CD	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:CG	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:H	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HA	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HB3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG2	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:HG3	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:N	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:O	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE1	4	2.12
(3,1)	2:B:1662:LYS:O	1:A:128:GLU:OE2	4	2.12
(1,3)	1:A:90:PHE:HD1	2:B:1654:ILE:HD11	3	0.14
(1,3)	1:A:90:PHE:HD1	2:B:1654:ILE:HD12	3	0.14
(1,3)	1:A:90:PHE:HD1	2:B:1654:ILE:HD13	3	0.14
(1,3)	1:A:90:PHE:HD2	2:B:1654:ILE:HD11	3	0.14
(1,3)	1:A:90:PHE:HD2	2:B:1654:ILE:HD12	3	0.14
(1,3)	1:A:90:PHE:HD2	2:B:1654:ILE:HD13	3	0.14

10 Dihedral-angle violation analysis (i)

No dihedral-angle restraints found