



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:05 am BST

PDB ID : 2AAZ  
Title : *Cryptococcus neoformans* thymidylate synthase complexed with substrate and an antifolate  
Authors : Finer-Moore, J.S.; Anderson, A.C.; O'Neil, R.H.; Costi, M.P.; Ferrari, S.; Krucinski, J.; Stroud, R.M.  
Deposited on : 2005-07-14  
Resolution : 2.08 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

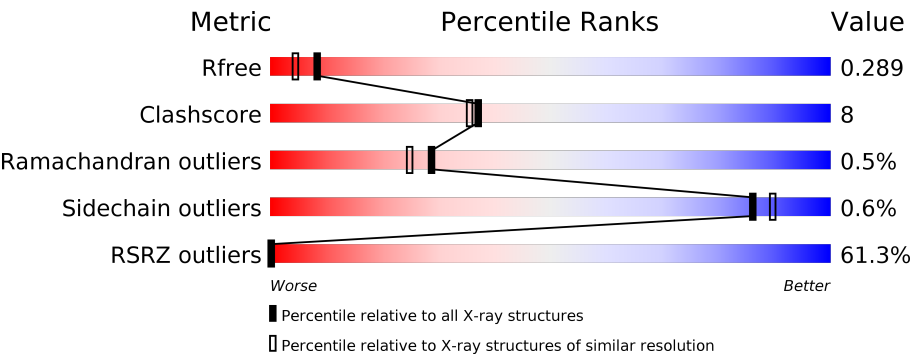
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.08 Å.

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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	317	<div><div>25%</div><div><div></div><div></div><div></div><div></div></div><div>77%</div><div>18%</div><div>• •</div></div>
1	1-B	317	<div><div>25%</div><div><div></div><div></div><div></div><div></div></div><div>81%</div><div>15%</div><div>• •</div></div>
1	1-C	317	<div><div>23%</div><div><div></div><div></div><div></div><div></div></div><div>79%</div><div>17%</div><div>• •</div></div>
1	1-D	317	<div><div>23%</div><div><div></div><div></div><div></div><div></div></div><div>79%</div><div>15%</div><div>• •</div></div>
1	1-E	317	<div><div>25%</div><div><div></div><div></div><div></div><div></div></div><div>81%</div><div>14%</div><div>• •</div></div>
1	1-F	317	<div><div>22%</div><div><div></div><div></div><div></div><div></div></div><div>78%</div><div>16%</div><div>• •</div></div>

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Mol	Chain	Length	Quality of chain
1	1-G	317	<div> <div>25%</div> <div>83%</div> <div>12%</div> <div>• •</div> </div>
1	1-H	317	<div> <div>21%</div> <div>79%</div> <div>16%</div> <div>• •</div> </div>
1	1-I	317	<div> <div>92%</div> <div>80%</div> <div>14%</div> <div>• 6%</div> </div>
1	1-J	317	<div> <div>93%</div> <div>78%</div> <div>15%</div> <div>• 6%</div> </div>
1	1-K	317	<div> <div>93%</div> <div>78%</div> <div>15%</div> <div>• 6%</div> </div>
1	1-L	317	<div> <div>92%</div> <div>78%</div> <div>15%</div> <div>• 6%</div> </div>
1	1-M	317	<div> <div>93%</div> <div>79%</div> <div>15%</div> <div>• 6%</div> </div>
1	1-N	317	<div> <div>93%</div> <div>78%</div> <div>16%</div> <div>• 6%</div> </div>
1	1-O	317	<div> <div>92%</div> <div>80%</div> <div>14%</div> <div>• 6%</div> </div>
1	1-P	317	<div> <div>92%</div> <div>79%</div> <div>15%</div> <div>• 6%</div> </div>
1	2-A	317	<div> <div>25%</div> <div>78%</div> <div>17%</div> <div>• •</div> </div>
1	2-B	317	<div> <div>25%</div> <div>82%</div> <div>15%</div> <div>•</div> </div>
1	2-C	317	<div> <div>23%</div> <div>80%</div> <div>16%</div> <div>•</div> </div>
1	2-D	317	<div> <div>23%</div> <div>80%</div> <div>15%</div> <div>•</div> </div>
1	2-E	317	<div> <div>25%</div> <div>82%</div> <div>14%</div> <div>•</div> </div>
1	2-F	317	<div> <div>22%</div> <div>78%</div> <div>18%</div> <div>•</div> </div>
1	2-G	317	<div> <div>25%</div> <div>85%</div> <div>12%</div> <div>•</div> </div>
1	2-H	317	<div> <div>21%</div> <div>80%</div> <div>16%</div> <div>• •</div> </div>
1	2-I	317	<div> <div>92%</div> <div>79%</div> <div>16%</div> <div>6%</div> </div>
1	2-J	317	<div> <div>93%</div> <div>78%</div> <div>17%</div> <div>6%</div> </div>
1	2-K	317	<div> <div>93%</div> <div>77%</div> <div>18%</div> <div>6%</div> </div>
1	2-L	317	<div> <div>92%</div> <div>78%</div> <div>16%</div> <div>6%</div> </div>
1	2-M	317	<div> <div>93%</div> <div>78%</div> <div>16%</div> <div>6%</div> </div>
1	2-N	317	<div> <div>93%</div> <div>76%</div> <div>18%</div> <div>6%</div> </div>
1	2-O	317	<div> <div>92%</div> <div>77%</div> <div>17%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
1	2-P	317	
1	3-A	317	
1	3-B	317	
1	3-C	317	
1	3-D	317	
1	3-E	317	
1	3-F	317	
1	3-G	317	
1	3-H	317	
1	3-I	317	
1	3-J	317	
1	3-K	317	
1	3-L	317	
1	3-M	317	
1	3-N	317	
1	3-O	317	
1	3-P	317	
1	4-A	317	
1	4-B	317	
1	4-C	317	
1	4-D	317	
1	4-E	317	
1	4-F	317	
1	4-G	317	
1	4-H	317	

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Mol	Chain	Length	Quality of chain
1	4-I	317	
1	4-J	317	
1	4-K	317	
1	4-L	317	
1	4-M	317	
1	4-N	317	
1	4-O	317	
1	4-P	317	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UMP	1-I	350[A]	-	-	-	X
2	UMP	1-J	400[A]	-	-	-	X
2	UMP	1-K	450[A]	-	-	-	X
2	UMP	1-L	500[A]	-	-	-	X
2	UMP	1-M	550[A]	-	-	-	X
2	UMP	1-N	600[A]	-	-	-	X
2	UMP	1-P	700[A]	-	-	-	X
2	UMP	2-I	350[B]	-	-	-	X
2	UMP	2-J	400[B]	-	-	-	X
2	UMP	2-K	450[B]	-	-	-	X
2	UMP	2-L	500[B]	-	-	-	X
2	UMP	2-M	550[B]	-	-	-	X
2	UMP	2-N	600[B]	-	-	-	X
2	UMP	2-P	700[B]	-	-	-	X
2	UMP	3-I	350[C]	-	-	-	X
2	UMP	3-J	400[C]	-	-	-	X
2	UMP	3-K	450[C]	-	-	-	X
2	UMP	3-L	500[C]	-	-	-	X
2	UMP	3-M	550[C]	-	-	-	X
2	UMP	3-N	600[C]	-	-	-	X
2	UMP	3-P	700[C]	-	-	-	X
2	UMP	4-I	350[D]	-	-	-	X
2	UMP	4-J	400[D]	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UMP	4-K	450[D]	-	-	-	X
2	UMP	4-L	500[D]	-	-	-	X
2	UMP	4-M	550[D]	-	-	-	X
2	UMP	4-N	600[D]	-	-	-	X
2	UMP	4-P	700[D]	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 161392 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	2-A	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	3-A	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	4-A	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	1-B	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-B	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-B	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-B	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	1-C	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	2-C	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	3-C	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	4-C	305	Total	C	N	O	S	0	305	0
			2427	1553	419	442	13			
1	1-D	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-D	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-D	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-D	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-E	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-E	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-E	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-E	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	1-F	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-F	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-F	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-F	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	1-G	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-G	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-G	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-G	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	1-H	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	2-H	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	3-H	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	4-H	305	Total	C	N	O	S	0	305	0
			2431	1555	419	444	13			
1	1-I	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	2-I	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	3-I	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	4-I	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	1-J	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			

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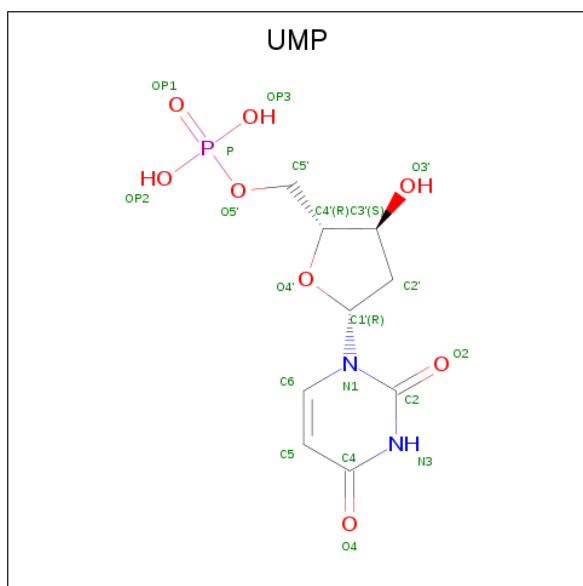
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	2-J	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	3-J	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	4-J	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	1-K	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	2-K	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	3-K	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	4-K	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	1-L	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	2-L	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	3-L	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	4-L	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	1-M	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	2-M	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	3-M	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	4-M	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	1-N	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	2-N	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	3-N	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	4-N	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	1-O	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0
1	2-O	299	Total 2387	C 1532	N 409	O 433	S 13	0	299	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	3-O	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	4-O	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	1-P	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	2-P	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	3-P	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			
1	4-P	299	Total	C	N	O	S	0	299	0
			2387	1532	409	433	13			

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula:  $C_9H_{13}N_2O_8P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	1-A	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	2-A	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	3-A	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	4-A	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	1-B	1	Total	C	N	O	P	0	1
			20	9	2	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	2-B	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-B	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-B	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-C	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-C	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-C	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-C	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-D	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-D	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-D	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-D	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-E	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-E	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-E	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-E	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-F	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-F	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-F	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-F	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-G	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-G	1	Total 20	C 9	N 2	O 8	P 1	0	1

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	3-G	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-G	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-H	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-H	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-H	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-H	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-I	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-I	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-I	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-I	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-J	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-J	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-J	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-J	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-K	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-K	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-K	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	4-K	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	1-L	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	2-L	1	Total 20	C 9	N 2	O 8	P 1	0	1
2	3-L	1	Total 20	C 9	N 2	O 8	P 1	0	1

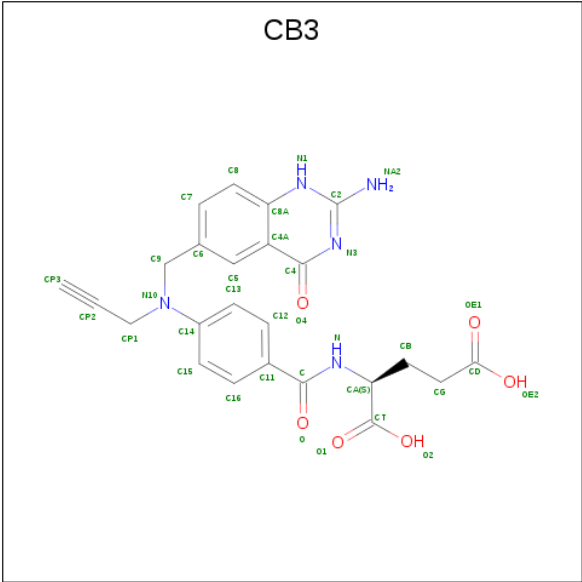
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	4-L	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	1-M	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	2-M	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	3-M	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	4-M	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	1-N	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	2-N	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	3-N	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	4-N	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	1-O	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	2-O	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	3-O	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	4-O	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	1-P	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	2-P	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	3-P	1	Total	C	N	O	P	0	1
			20	9	2	8	1		
2	4-P	1	Total	C	N	O	P	0	1
			20	9	2	8	1		

- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLIC ACID (three-letter code: CB3) (formula: C<sub>24</sub>H<sub>23</sub>N<sub>5</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	1-A	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-A	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-A	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-A	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-B	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-B	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-B	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-B	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-C	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-C	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-C	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-C	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-D	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-D	1	Total	C	N	O	0	1
			35	24	5	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	3-D	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-D	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-E	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-E	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-E	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-E	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-F	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-F	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-F	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-F	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-G	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-G	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-G	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-G	1	Total	C	N	O	0	1
			35	24	5	6		
3	1-H	1	Total	C	N	O	0	1
			35	24	5	6		
3	2-H	1	Total	C	N	O	0	1
			35	24	5	6		
3	3-H	1	Total	C	N	O	0	1
			35	24	5	6		
3	4-H	1	Total	C	N	O	0	1
			35	24	5	6		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	1-A	185	Total	O	0	185
			185	185		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	2-A	185	Total O 185 185	0	185
4	3-A	185	Total O 185 185	0	185
4	4-A	185	Total O 185 185	0	185
4	1-B	143	Total O 143 143	0	143
4	2-B	143	Total O 143 143	0	143
4	3-B	143	Total O 143 143	0	143
4	4-B	143	Total O 143 143	0	143
4	1-C	151	Total O 151 151	0	151
4	2-C	151	Total O 151 151	0	151
4	3-C	151	Total O 151 151	0	151
4	4-C	151	Total O 151 151	0	151
4	1-D	148	Total O 148 148	0	148
4	2-D	148	Total O 148 148	0	148
4	3-D	148	Total O 148 148	0	148
4	4-D	148	Total O 148 148	0	148
4	1-E	155	Total O 155 155	0	155
4	2-E	155	Total O 155 155	0	155
4	3-E	155	Total O 155 155	0	155
4	4-E	155	Total O 155 155	0	155
4	1-F	138	Total O 138 138	0	138
4	2-F	138	Total O 138 138	0	138

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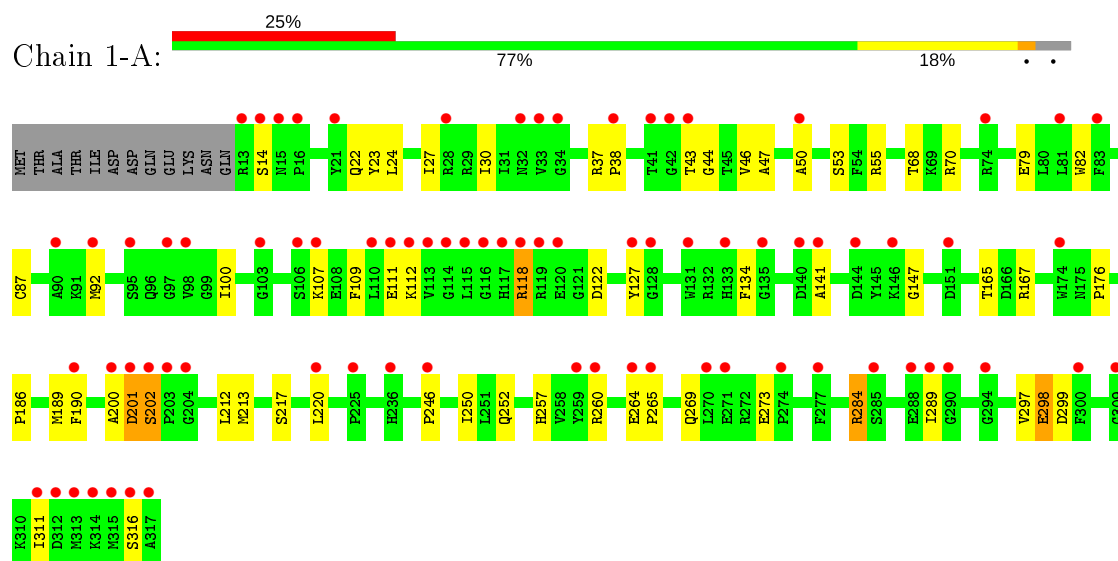
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	3-F	138	Total 138	O 138	0	138
4	4-F	138	Total 138	O 138	0	138
4	1-G	153	Total 153	O 153	0	153
4	2-G	153	Total 153	O 153	0	153
4	3-G	153	Total 153	O 153	0	153
4	4-G	153	Total 153	O 153	0	153
4	1-H	139	Total 139	O 139	0	139
4	2-H	139	Total 139	O 139	0	139
4	3-H	139	Total 139	O 139	0	139
4	4-H	139	Total 139	O 139	0	139

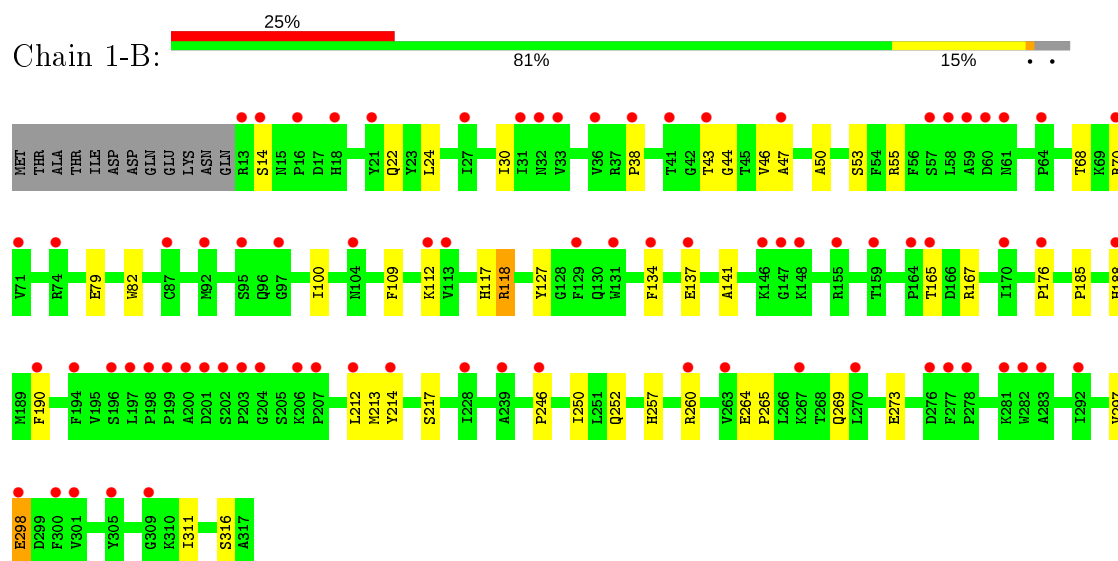
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.


#### • Molecule 1: Thymidylate synthase

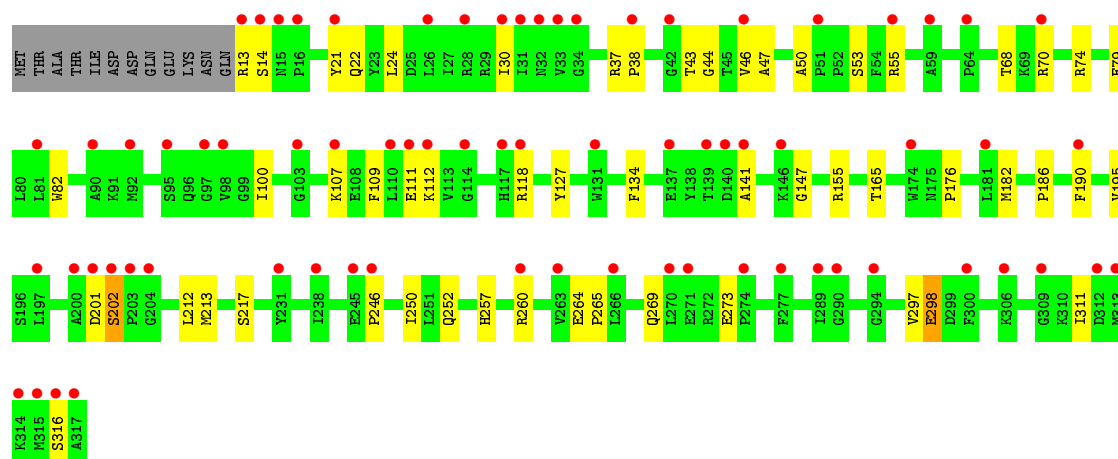


#### • Molecule 1: Thymidylate synthase




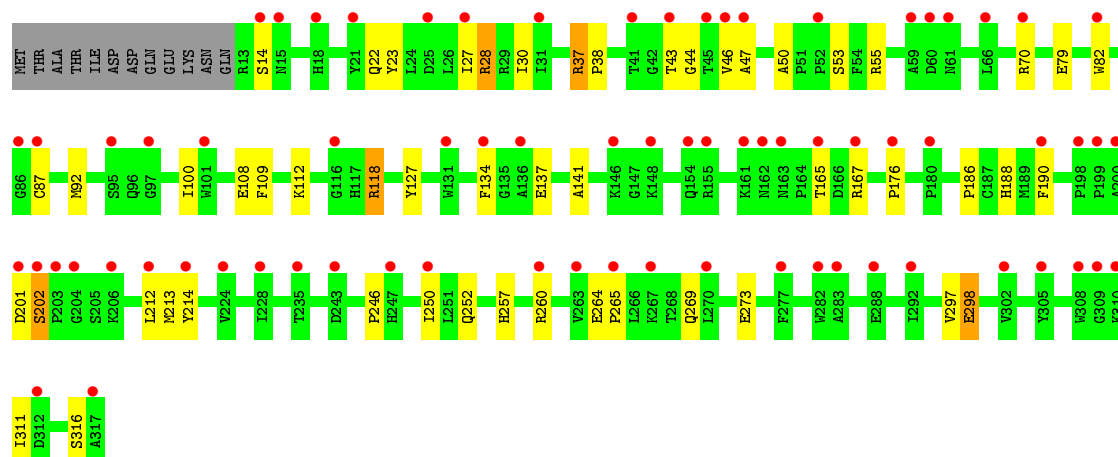
#### • Molecule 1: Thymidylate synthase

Chain 1-C: 




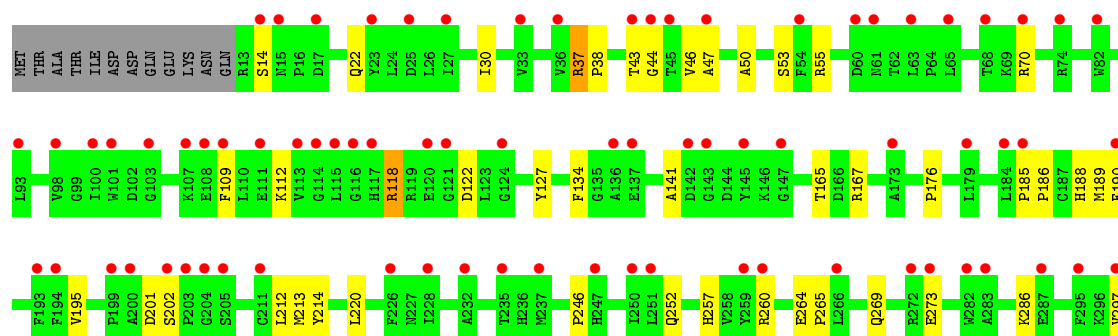
• Molecule 1: Thymidylate synthase

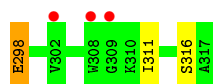
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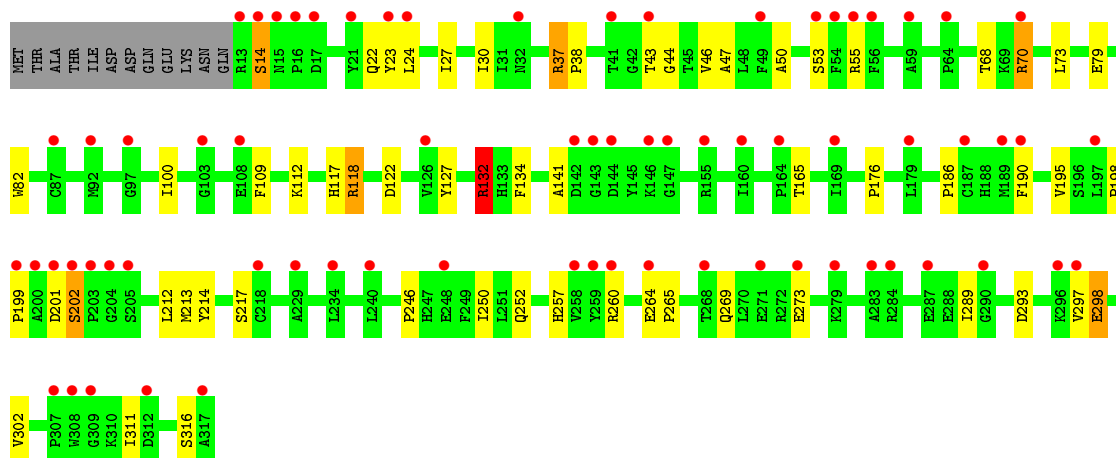
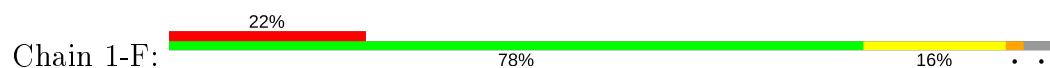
• Molecule 1: Thymidylate synthase

Chain 1-E: 

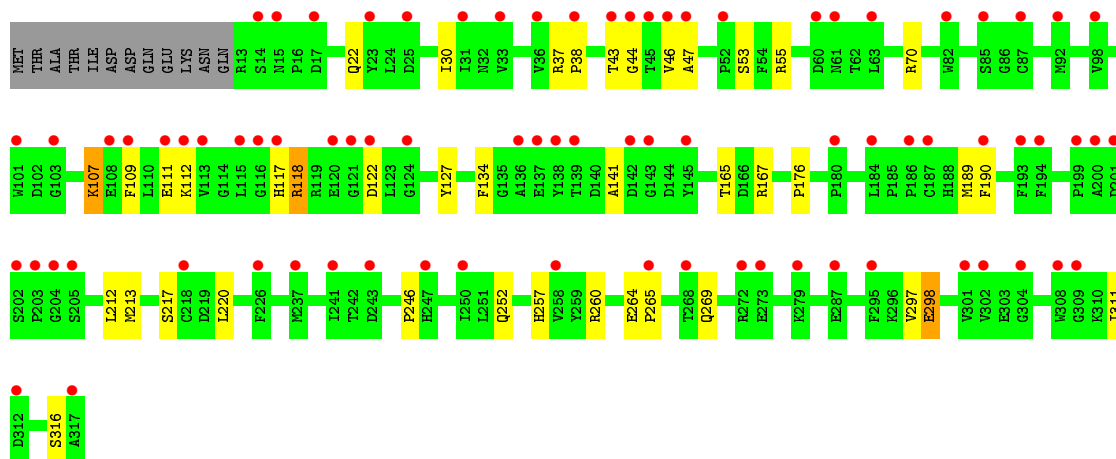
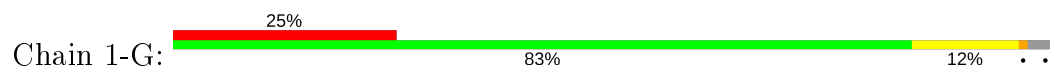




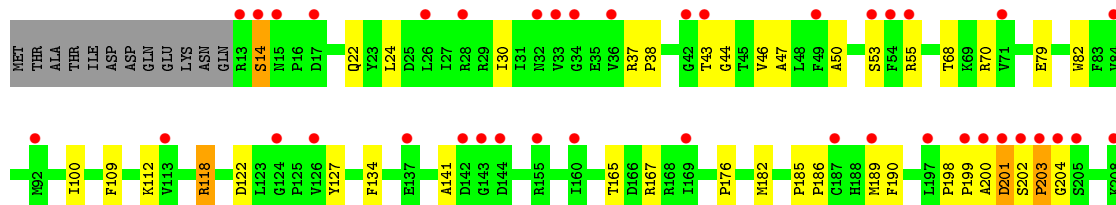
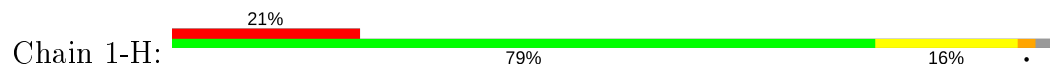
• Molecule 1: Thymidylate synthase



• Molecule 1: Thymidylate synthase



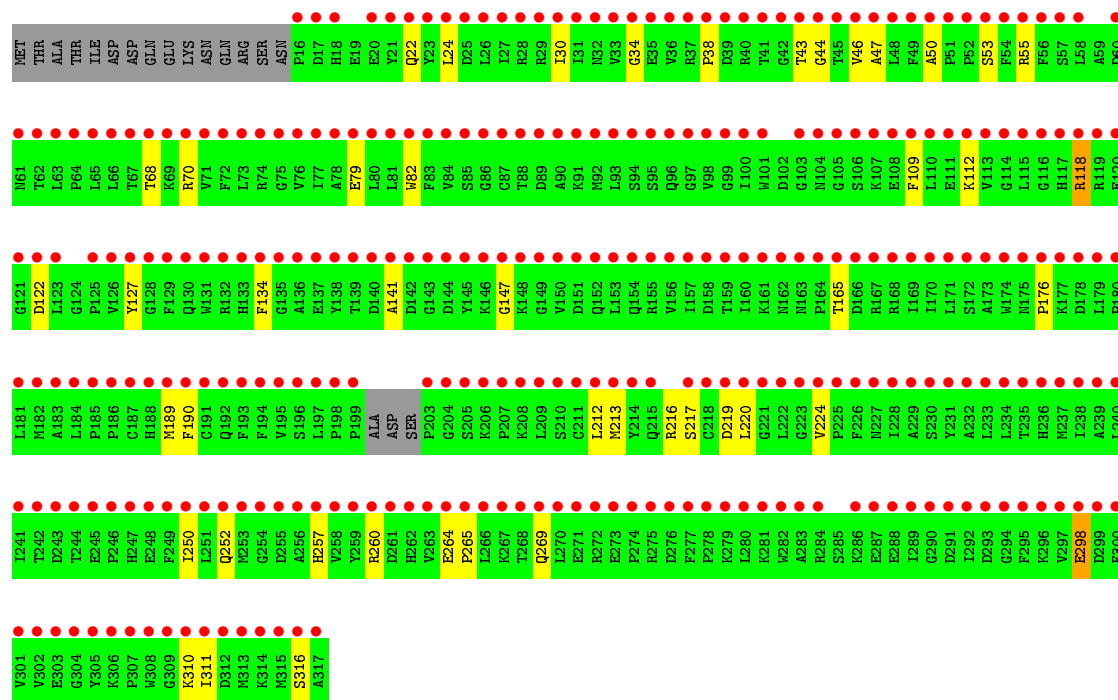
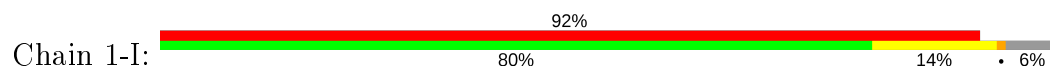
• Molecule 1: Thymidylate synthase



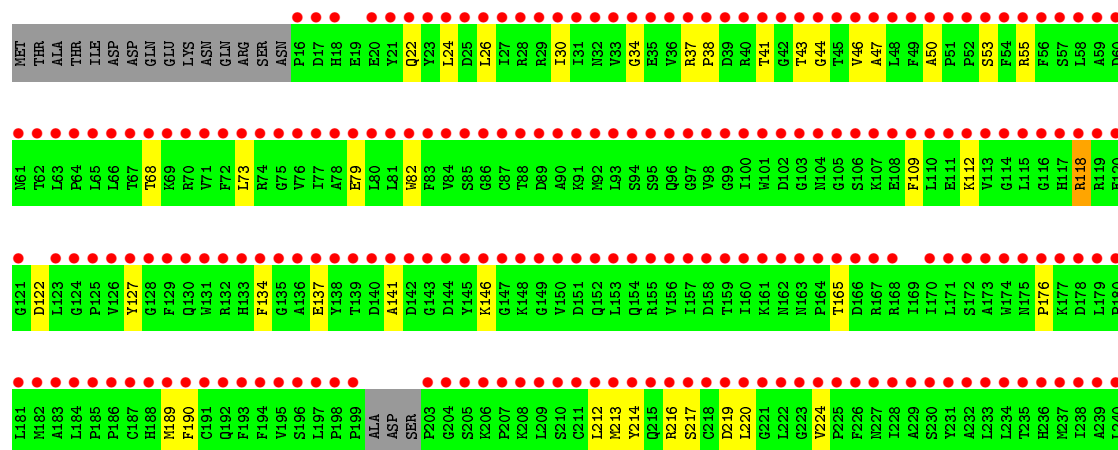
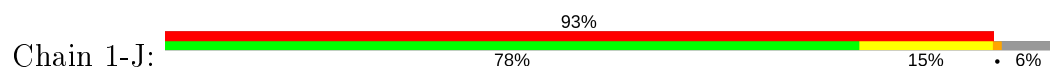


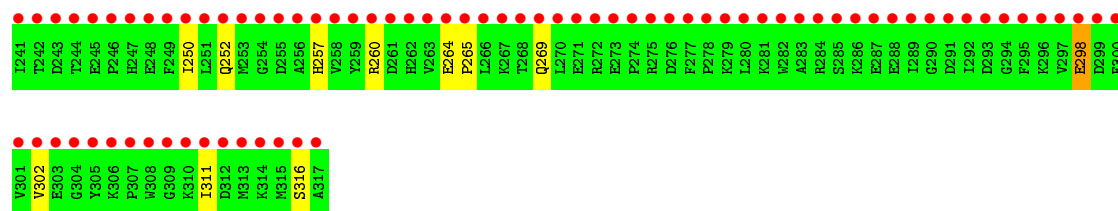


• Molecule 1: Thymidylate synthase

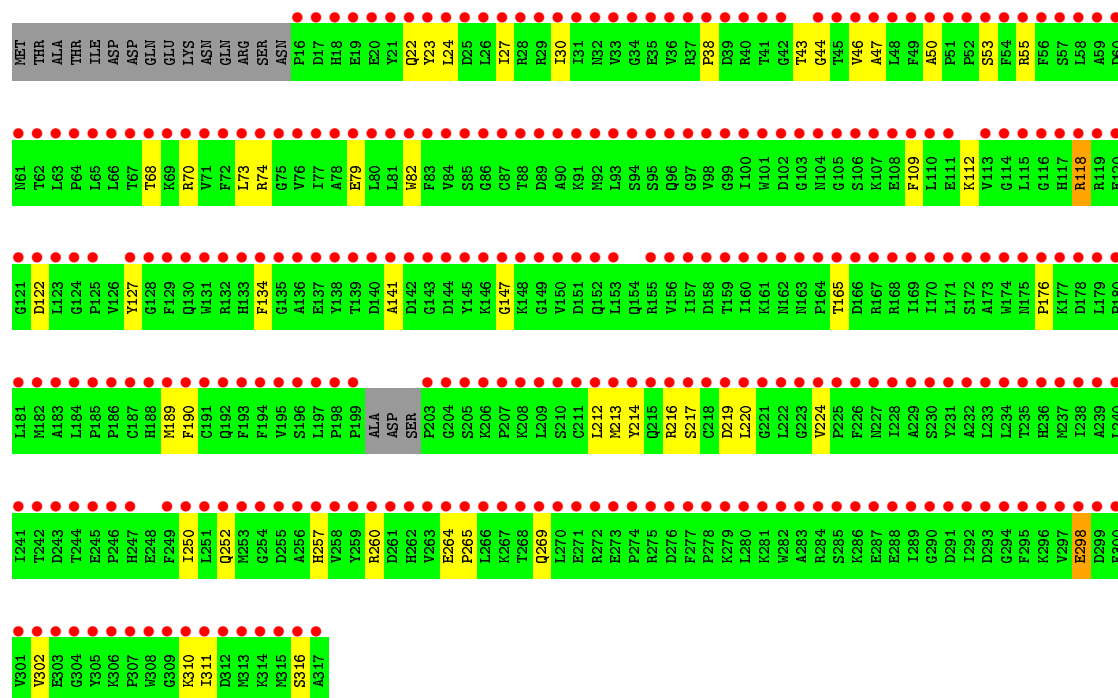
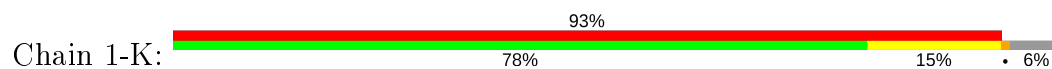


• Molecule 1: Thymidylate synthase

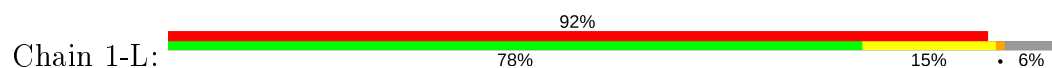


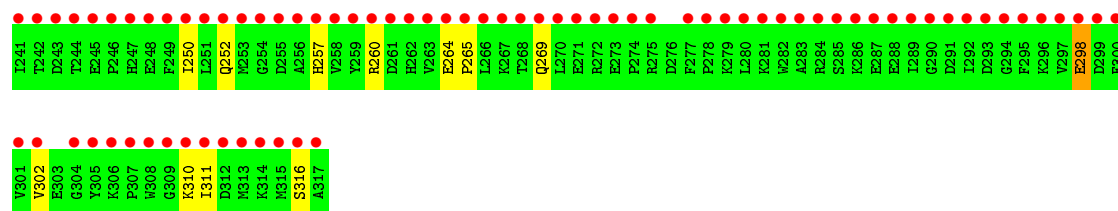


• Molecule 1: Thymidylate synthase



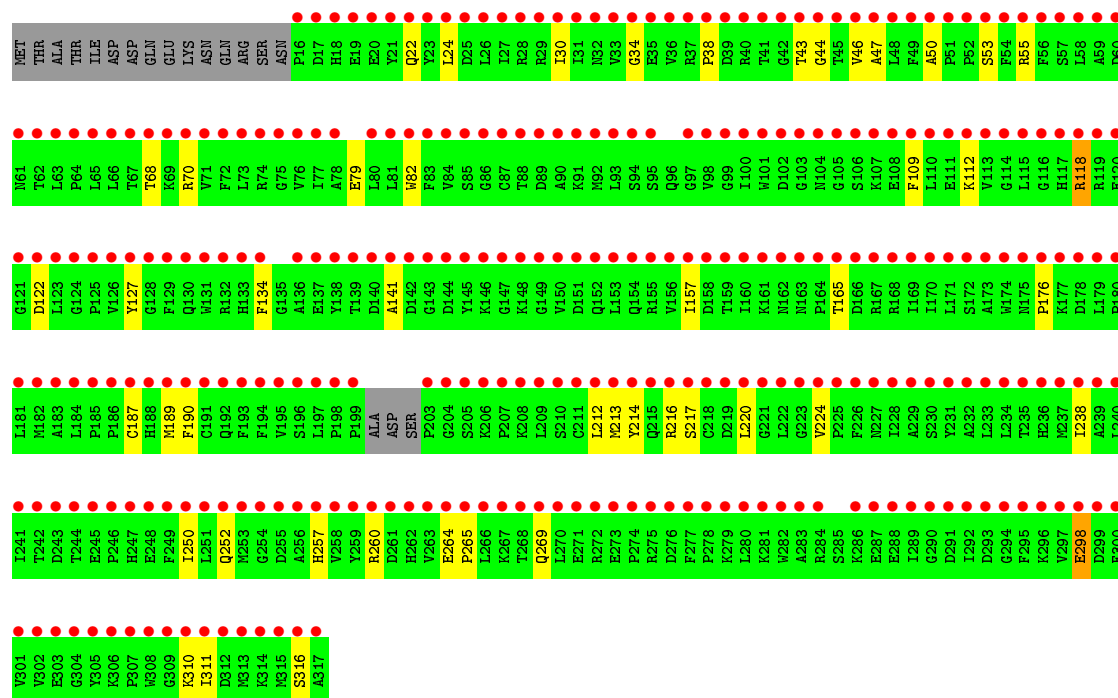
• Molecule 1: Thymidylate synthase





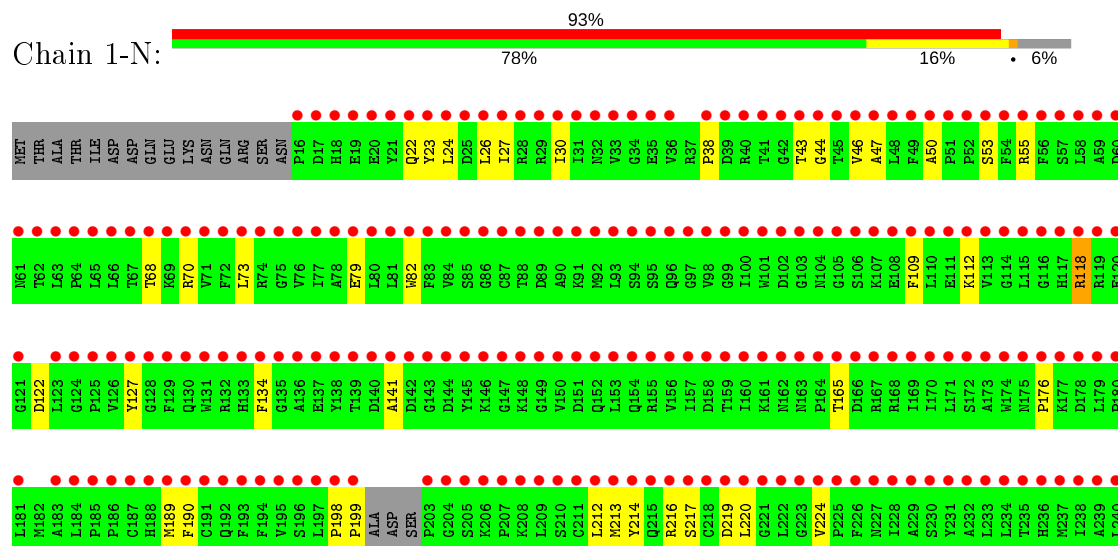
• Molecule 1: Thymidylate synthase

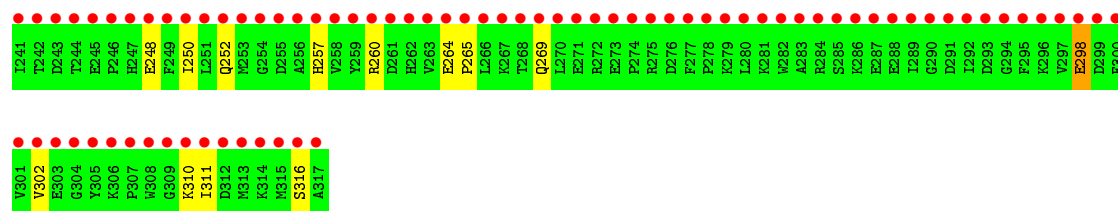
Chain 1-M:



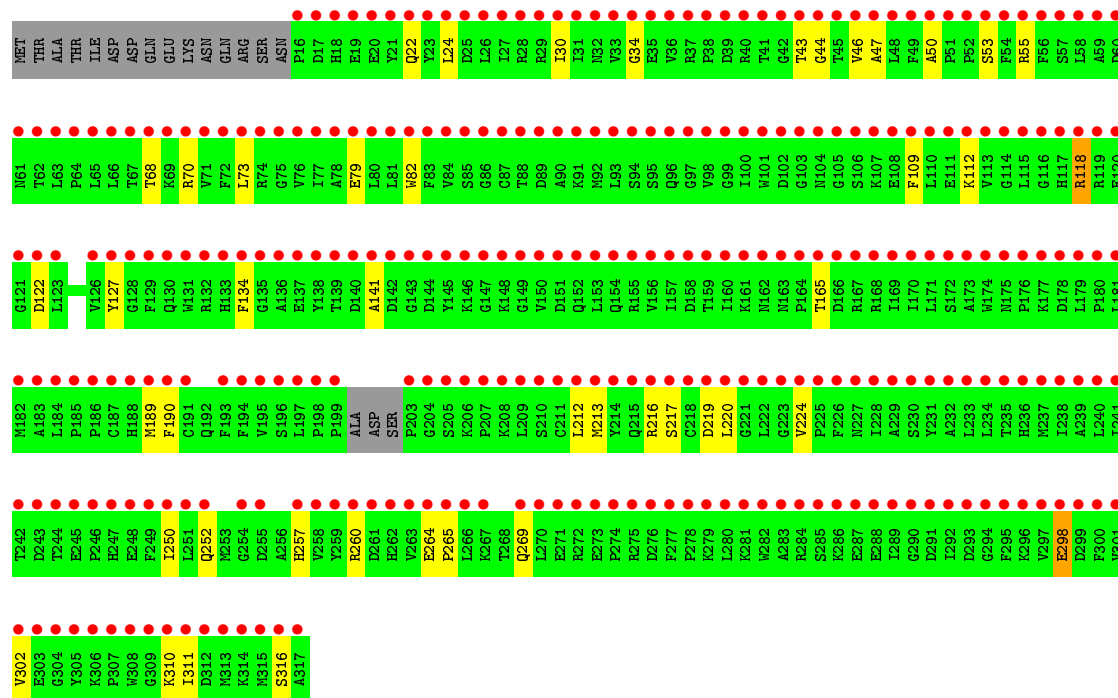
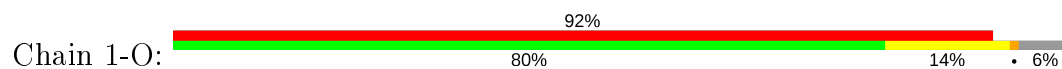
• Molecule 1: Thymidylate synthase

Chain 1-N:

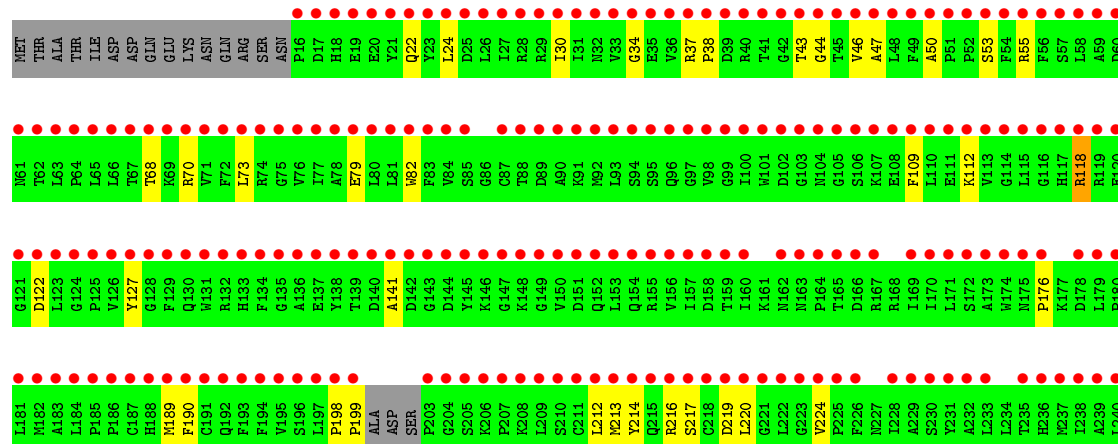
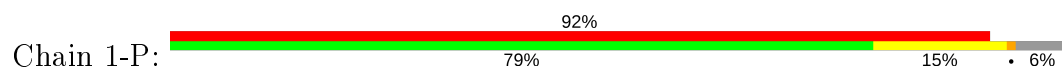


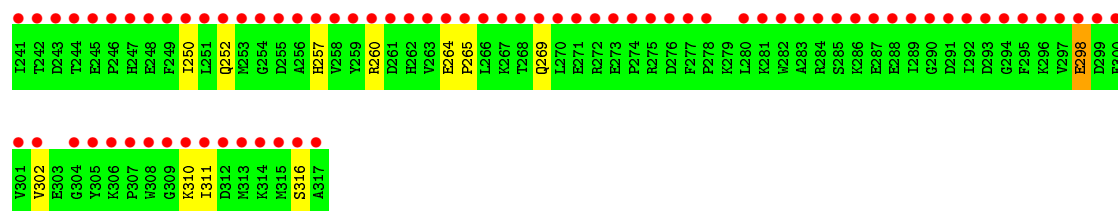


• Molecule 1: Thymidylate synthase



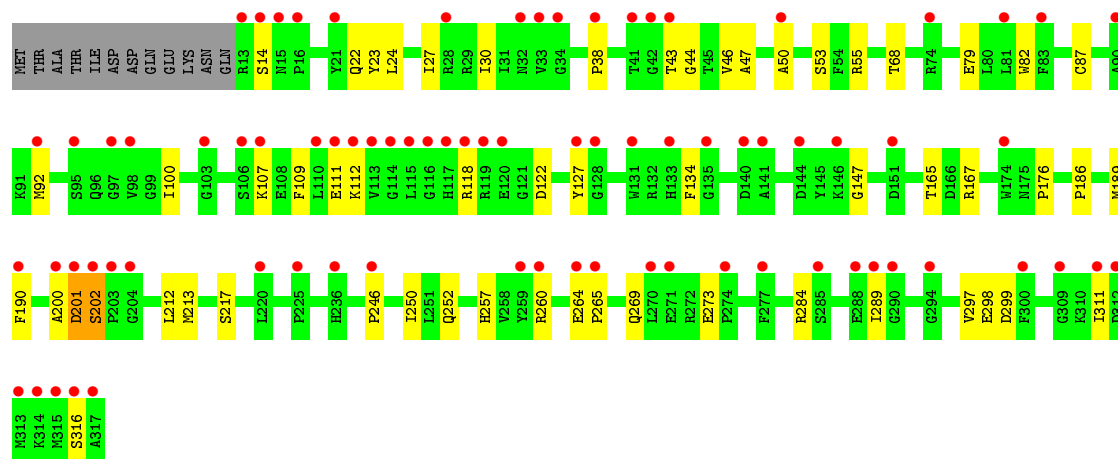
• Molecule 1: Thymidylate synthase





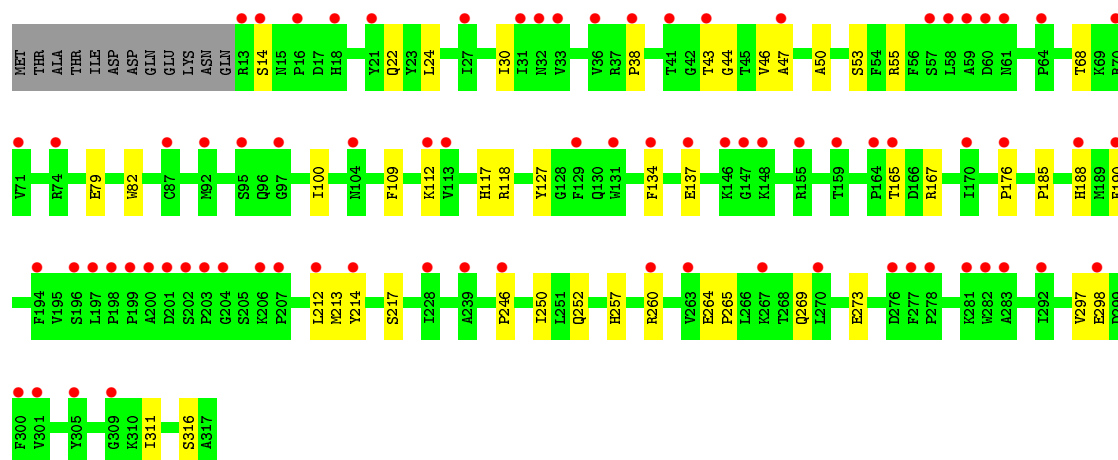
• Molecule 1: Thymidylate synthase

Chain 2-A:



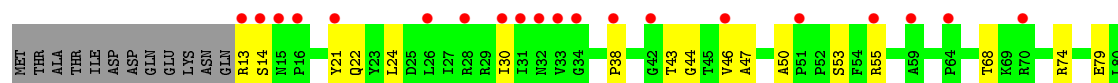
• Molecule 1: Thymidylate synthase

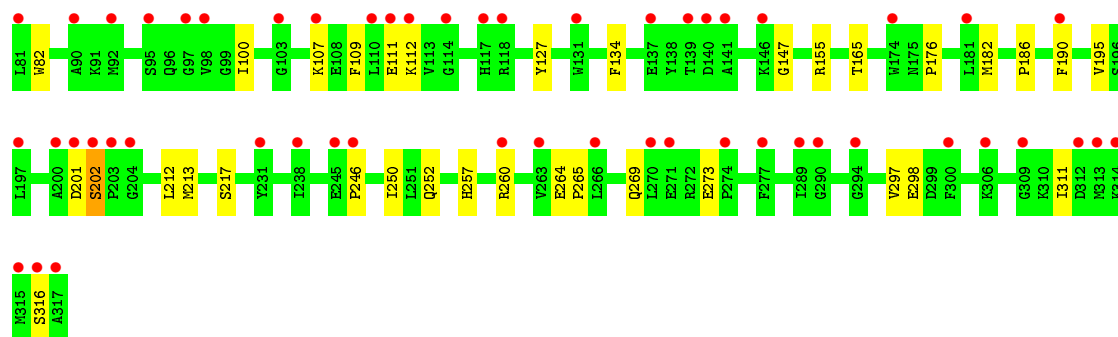
Chain 2-B:



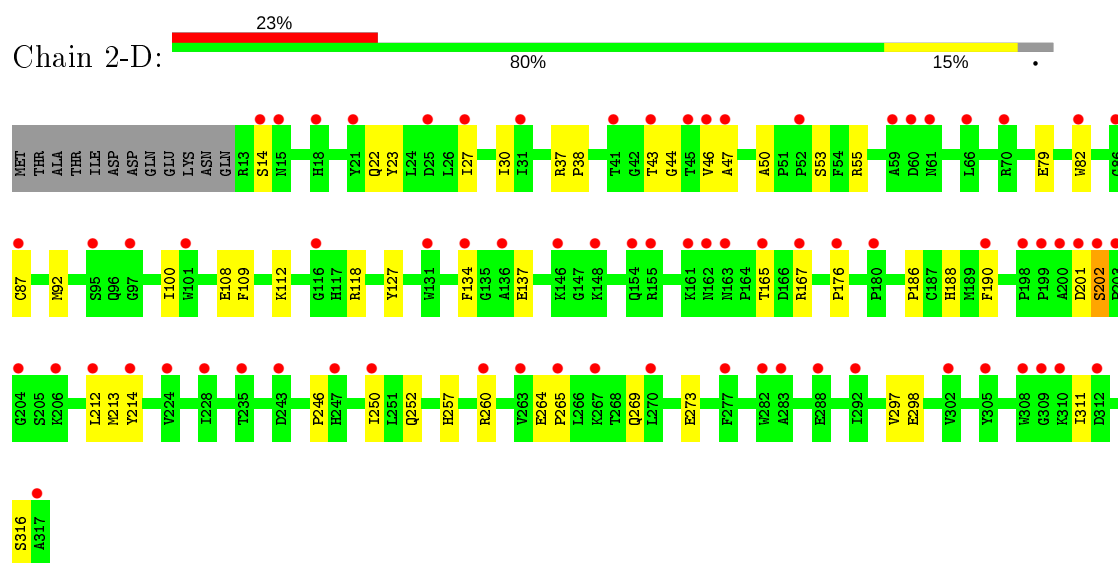
• Molecule 1: Thymidylate synthase

Chain 2-C:

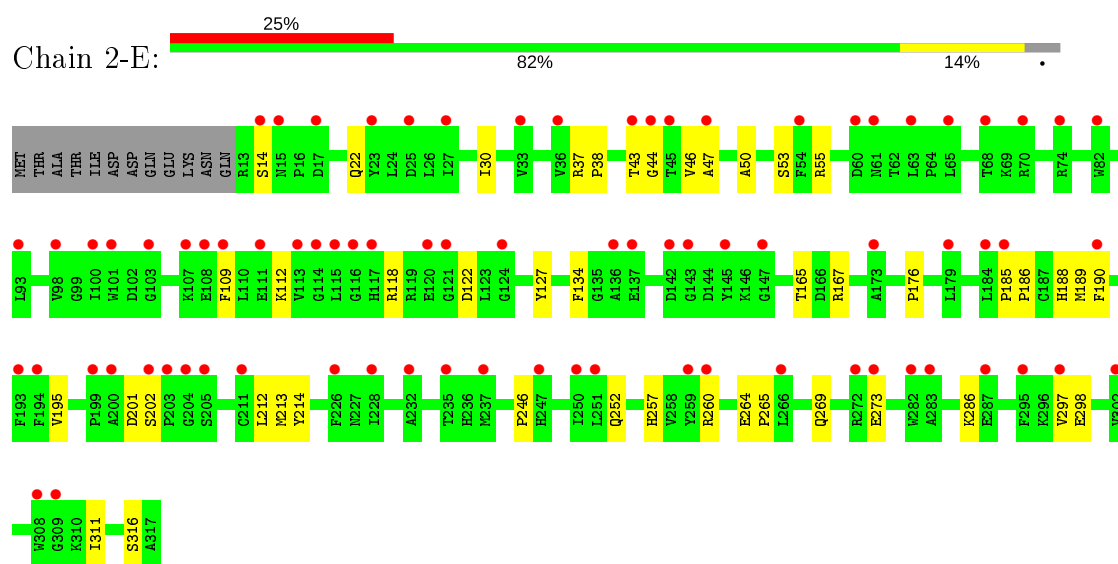




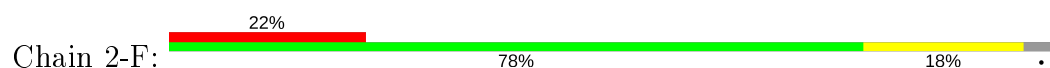
- Molecule 1: Thymidylate synthase

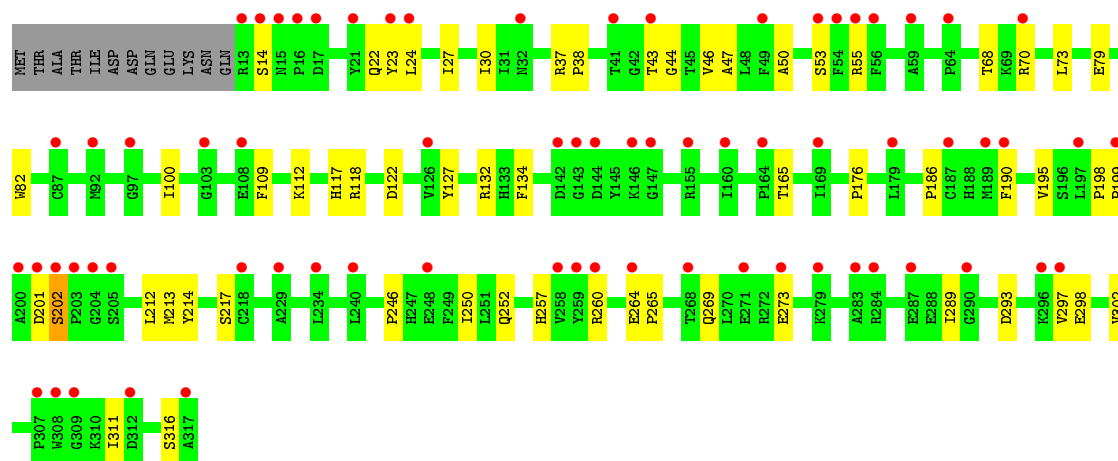


- Molecule 1: Thymidylate synthase

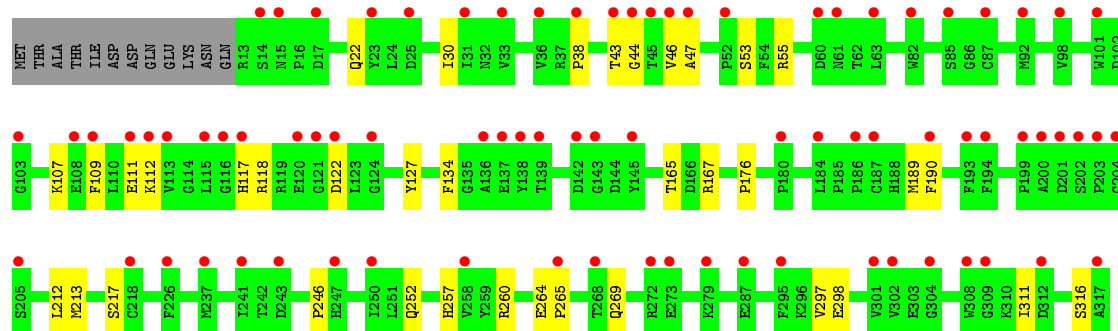
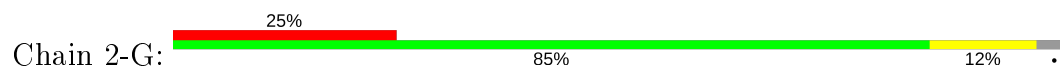


- Molecule 1: Thymidylate synthase

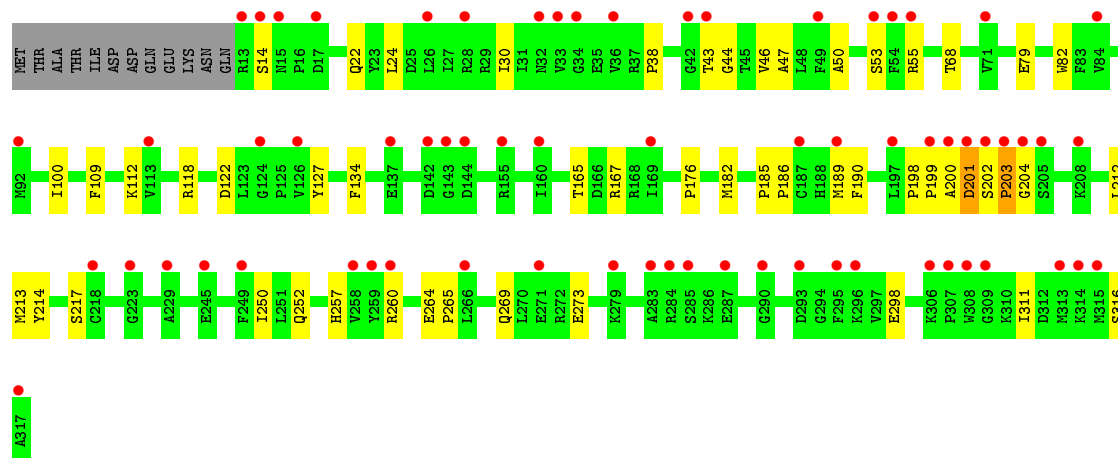
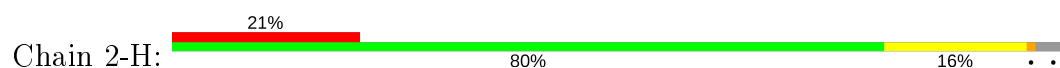




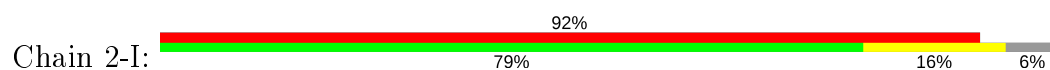
- Molecule 1: Thymidylate synthase

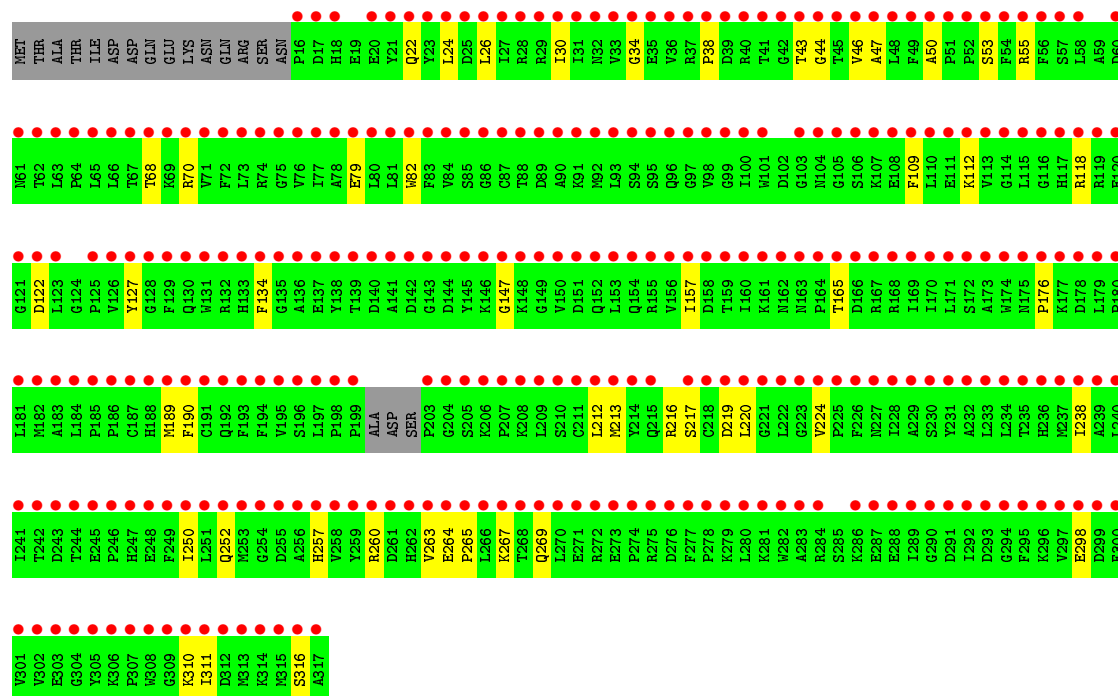


- Molecule 1: Thymidylate synthase

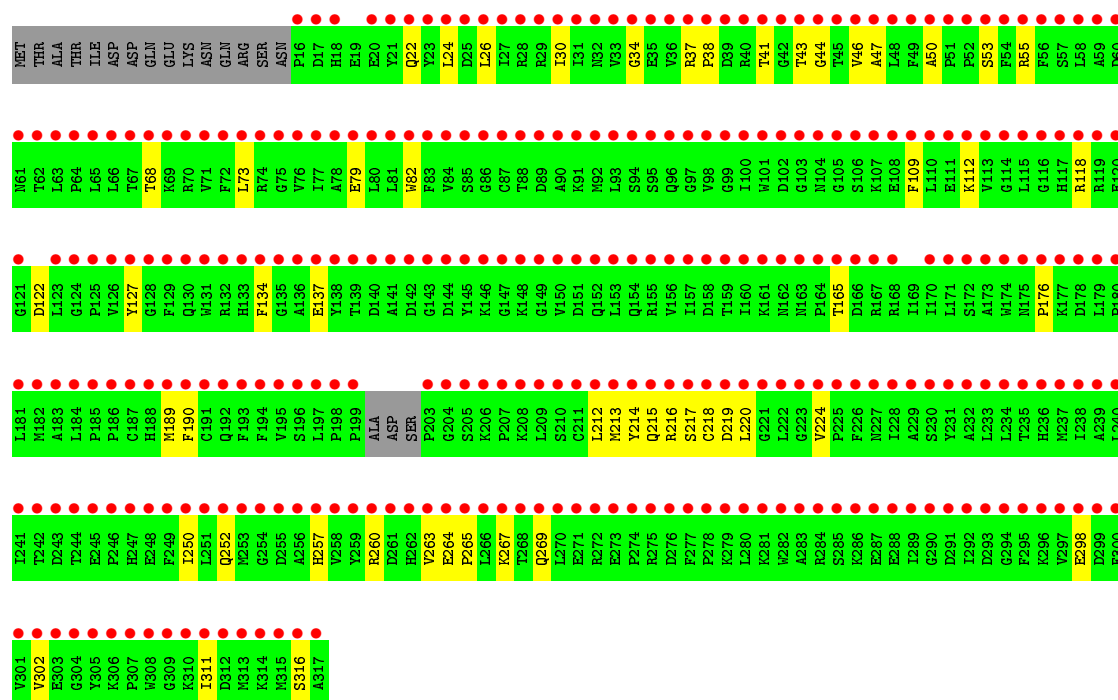
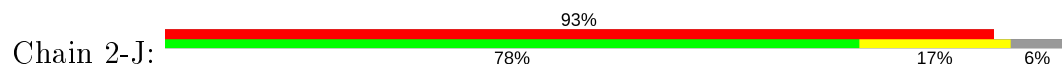


- Molecule 1: Thymidylate synthase

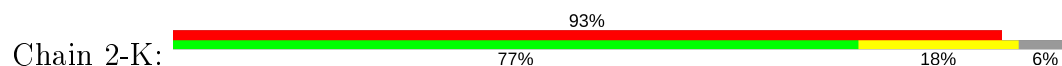




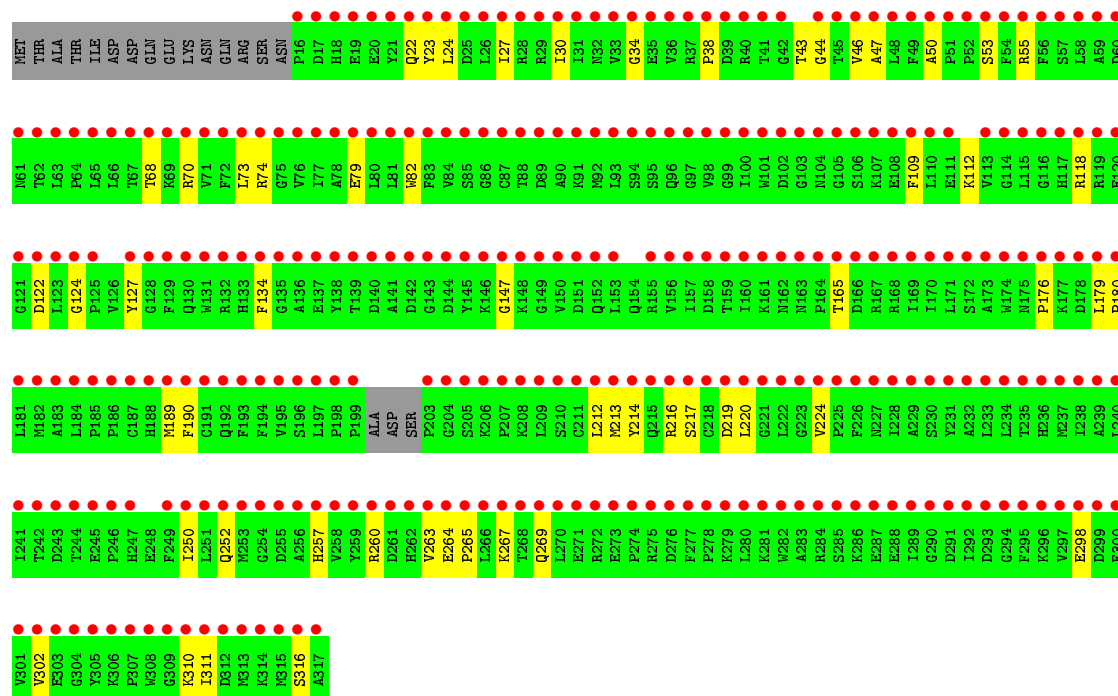
- Molecule 1: Thymidylate synthase



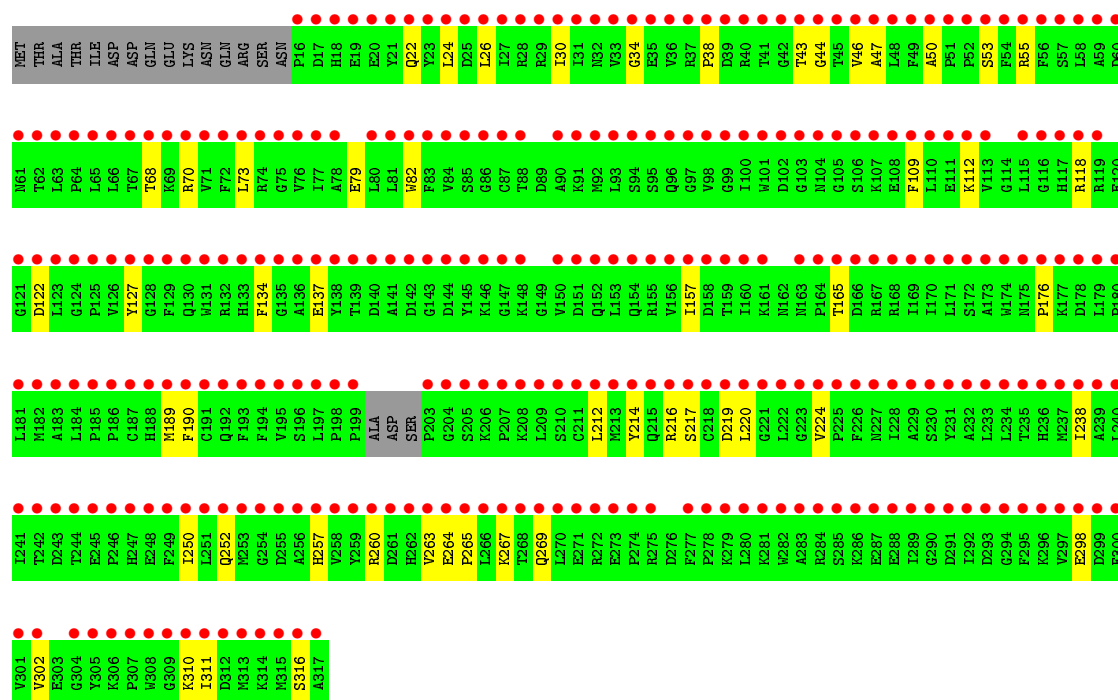
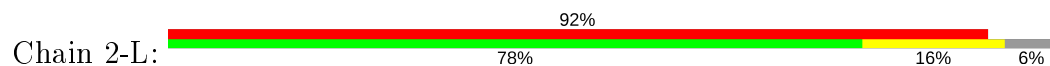
- Molecule 1: Thymidylate synthase



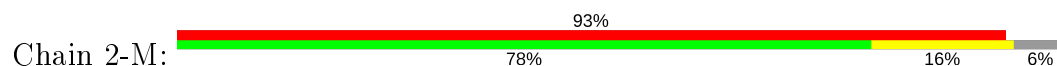


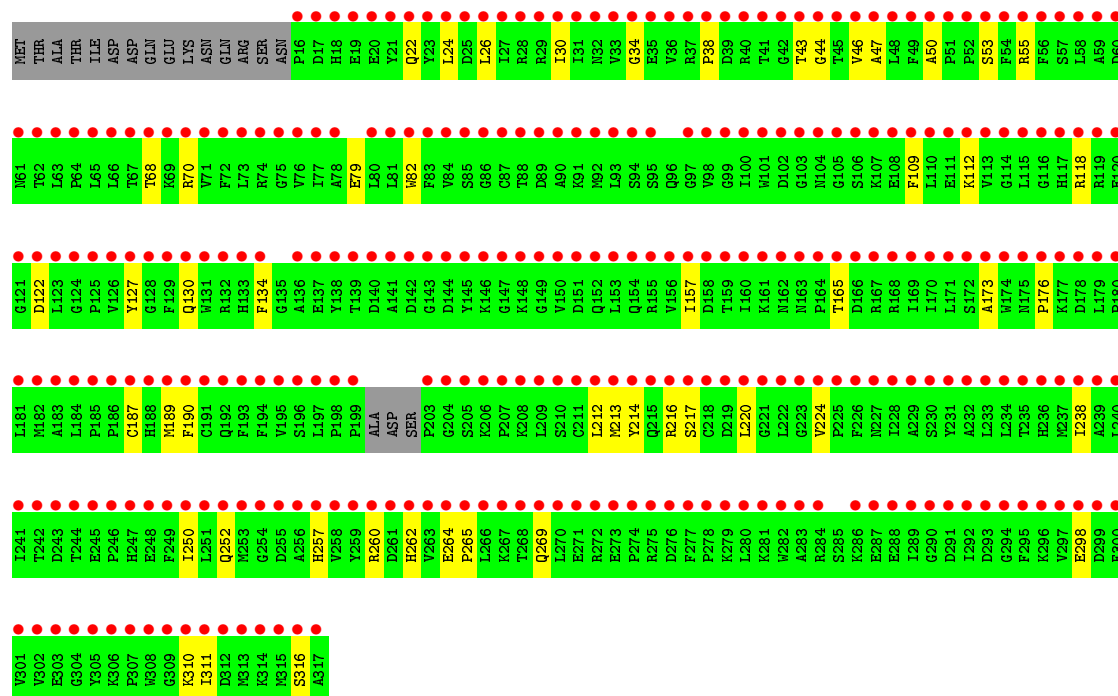


• Molecule 1: Thymidylate synthase

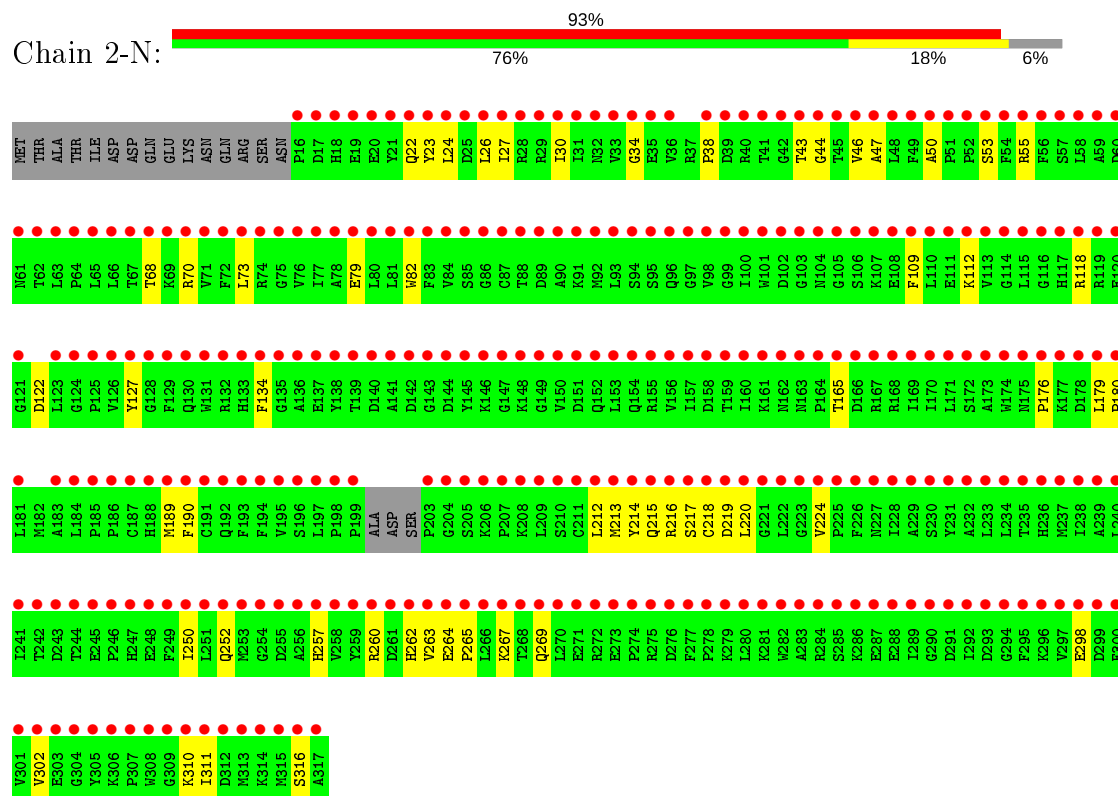


• Molecule 1: Thymidylate synthase

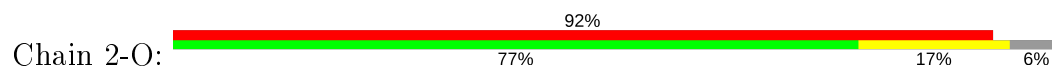


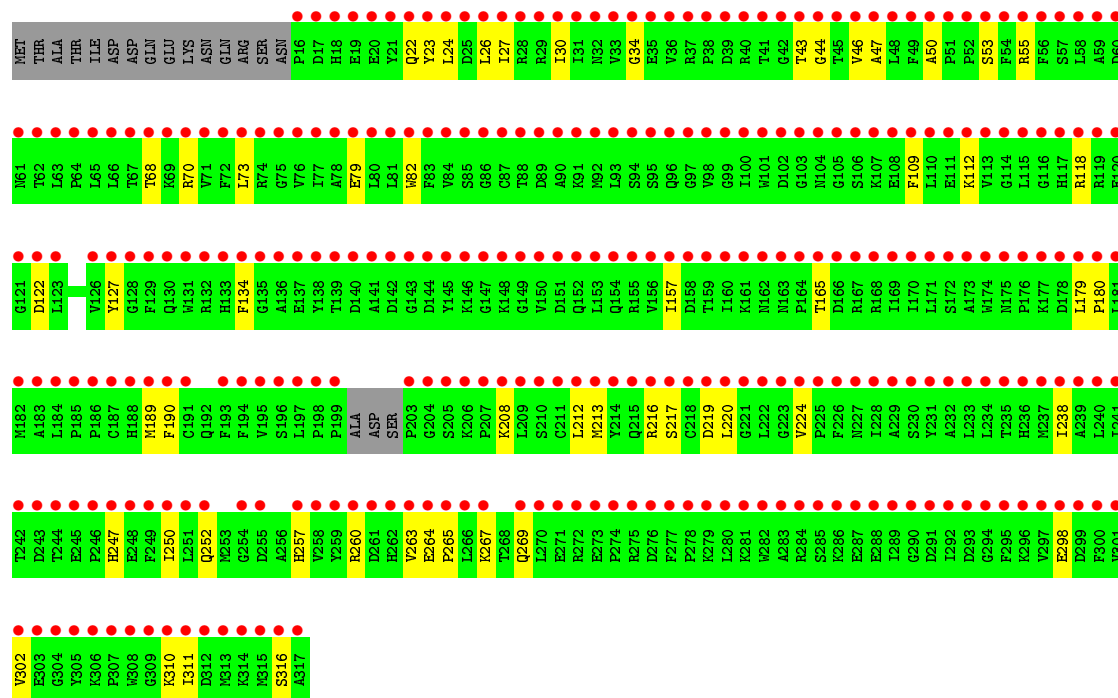


- Molecule 1: Thymidylate synthase

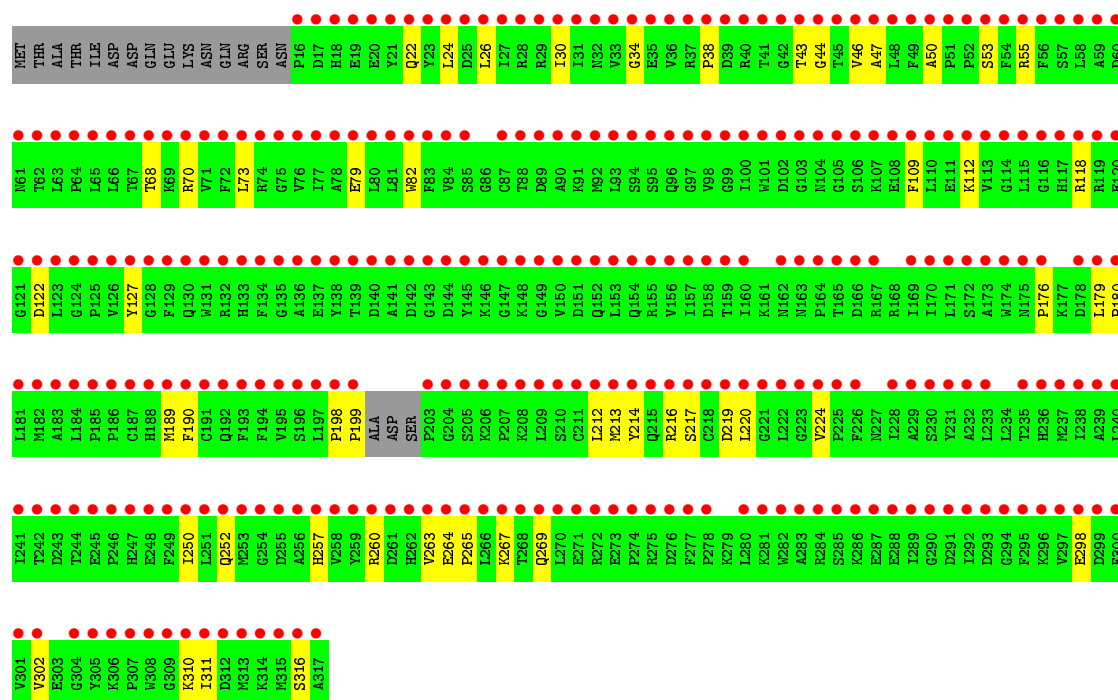
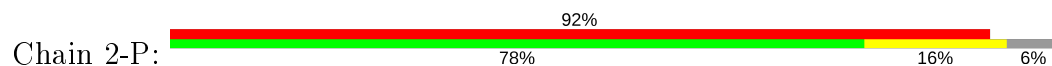


- Molecule 1: Thymidylate synthase

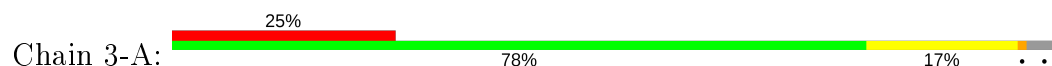


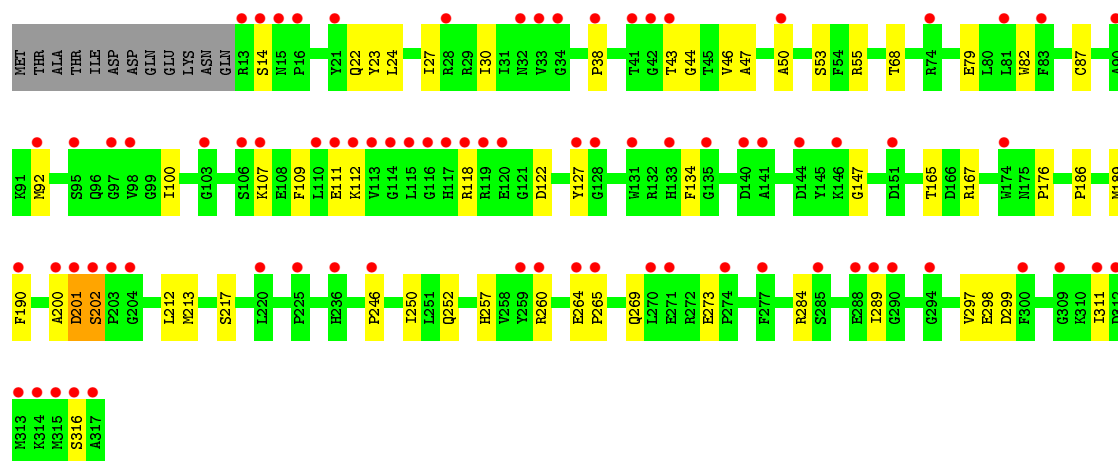


• Molecule 1: Thymidylate synthase

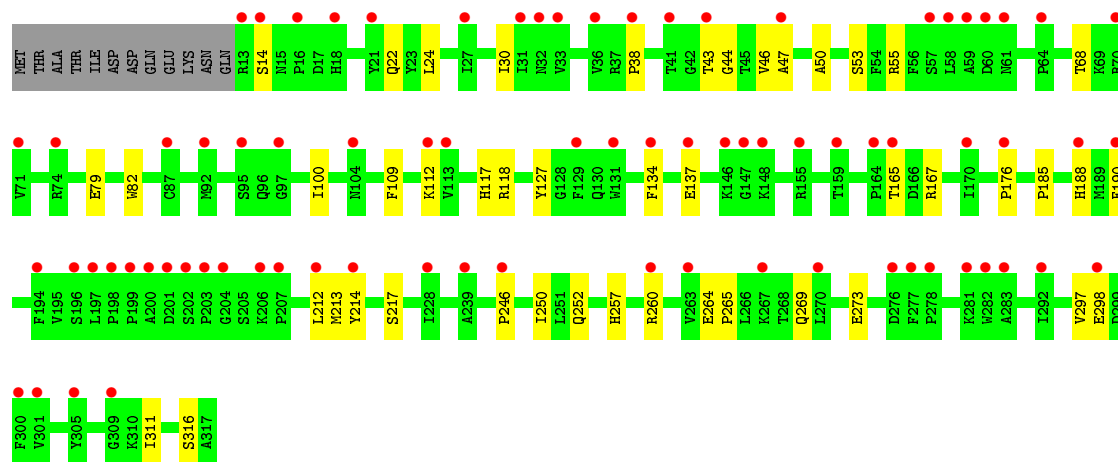
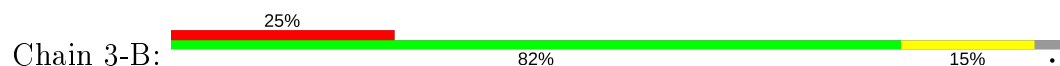


• Molecule 1: Thymidylate synthase

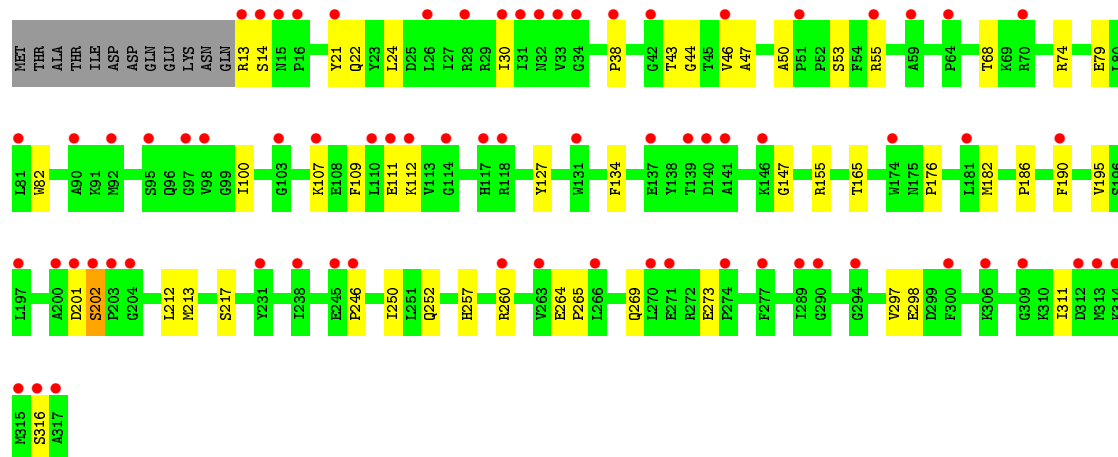
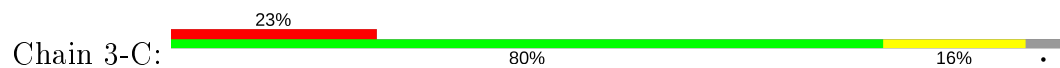




• Molecule 1: Thymidylate synthase

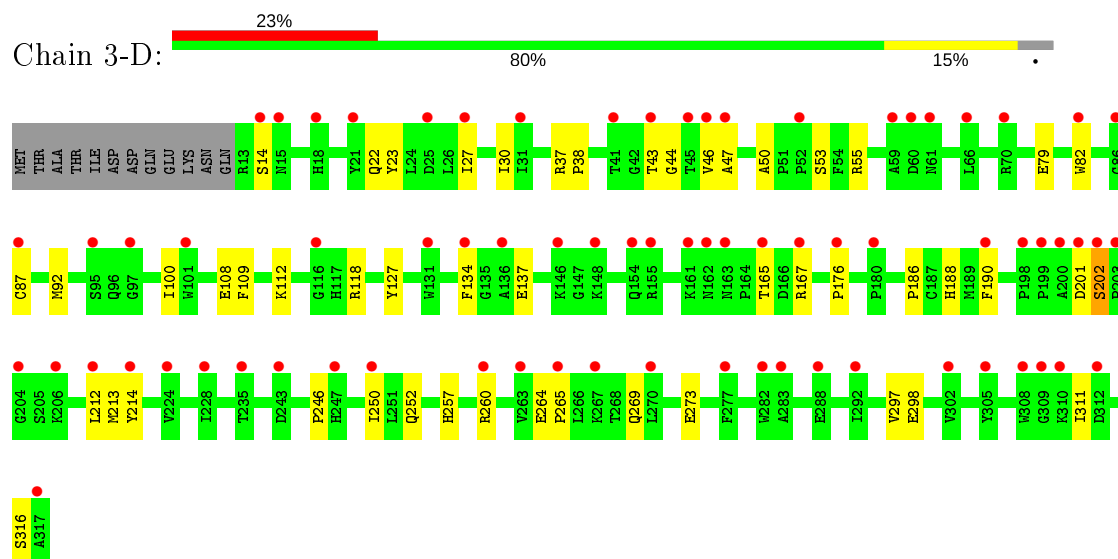


• Molecule 1: Thymidylate synthase



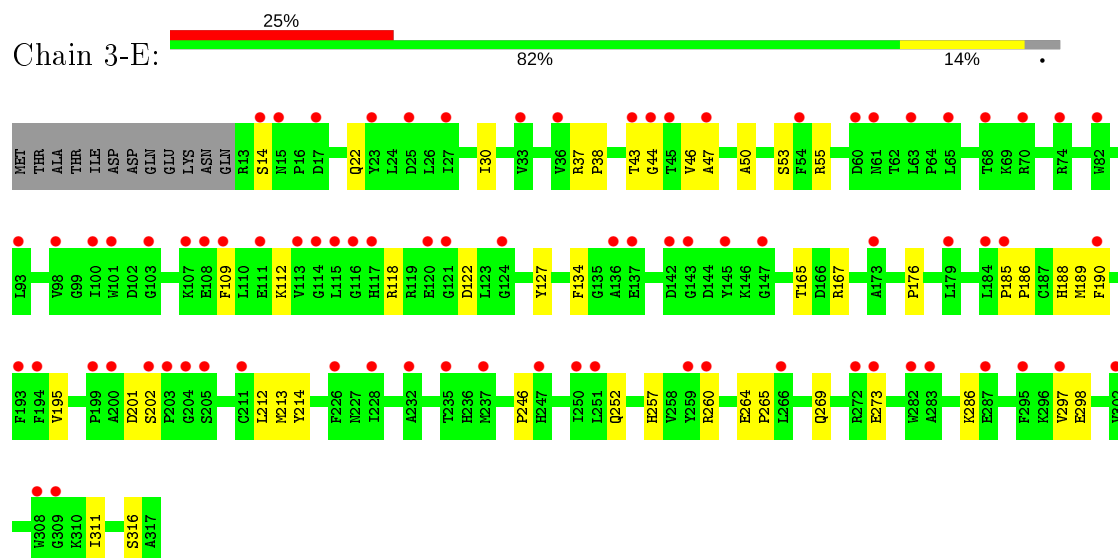
- Molecule 1: Thymidylate synthase

Chain 3-D:



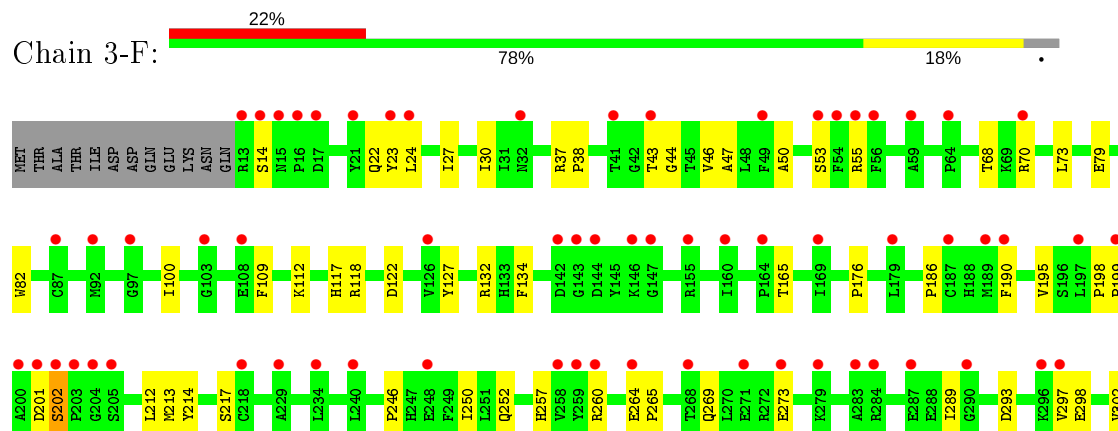
- Molecule 1: Thymidylate synthase

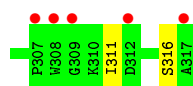
Chain 3-E:



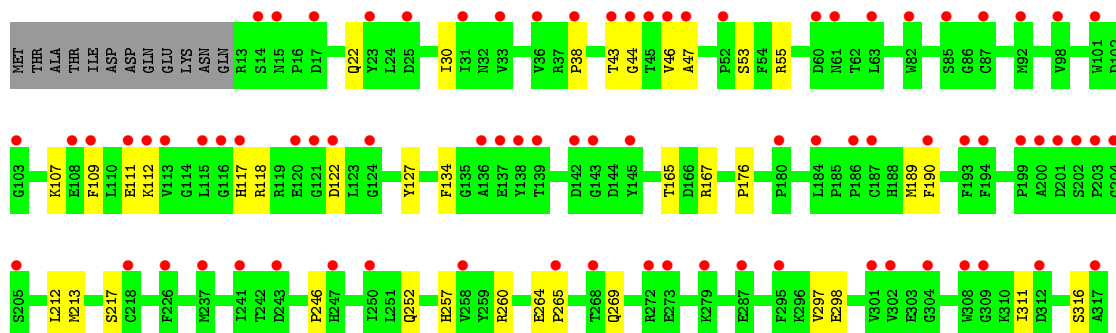
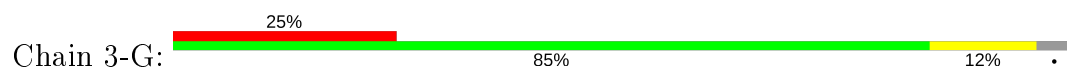
- Molecule 1: Thymidylate synthase

Chain 3-F:

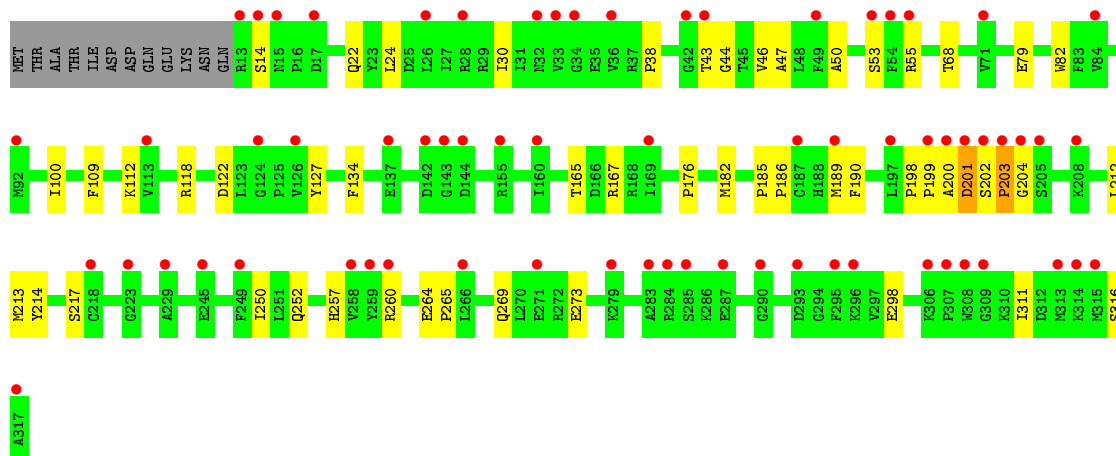
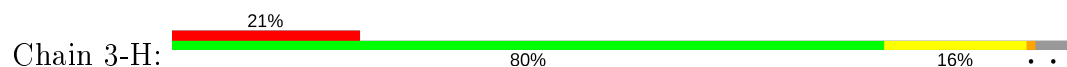




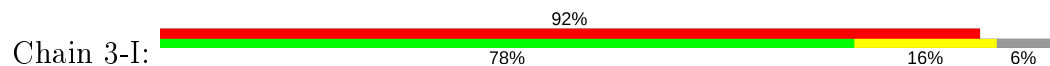
• Molecule 1: Thymidylate synthase

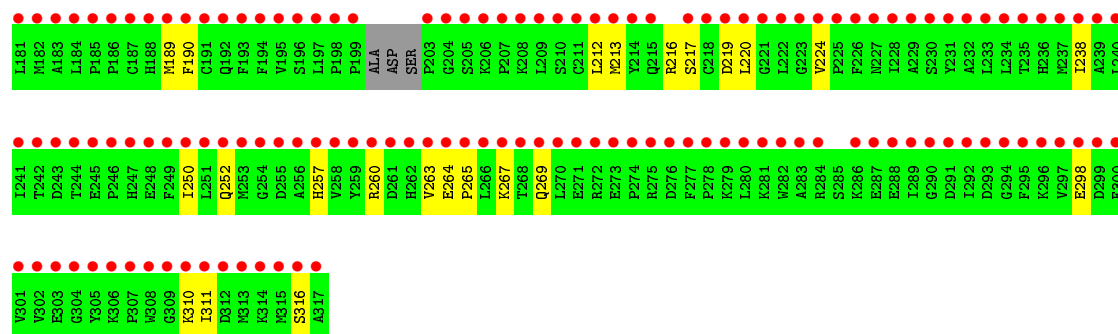


• Molecule 1: Thymidylate synthase

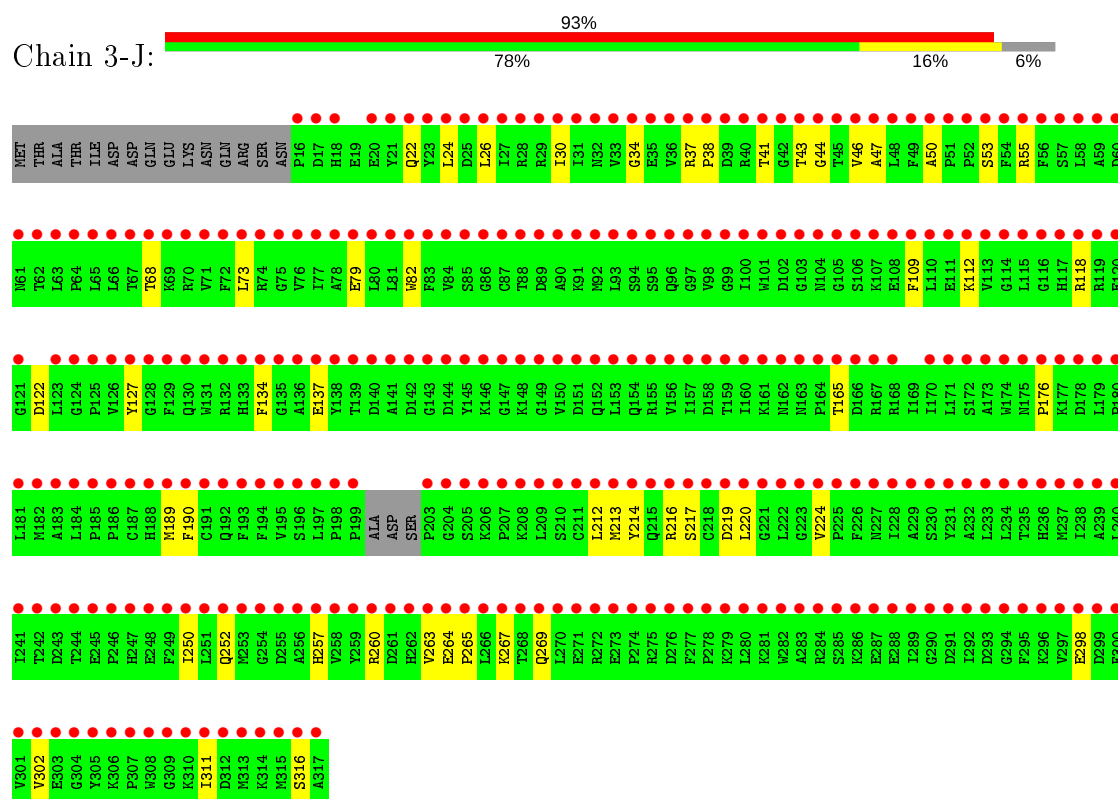


• Molecule 1: Thymidylate synthase

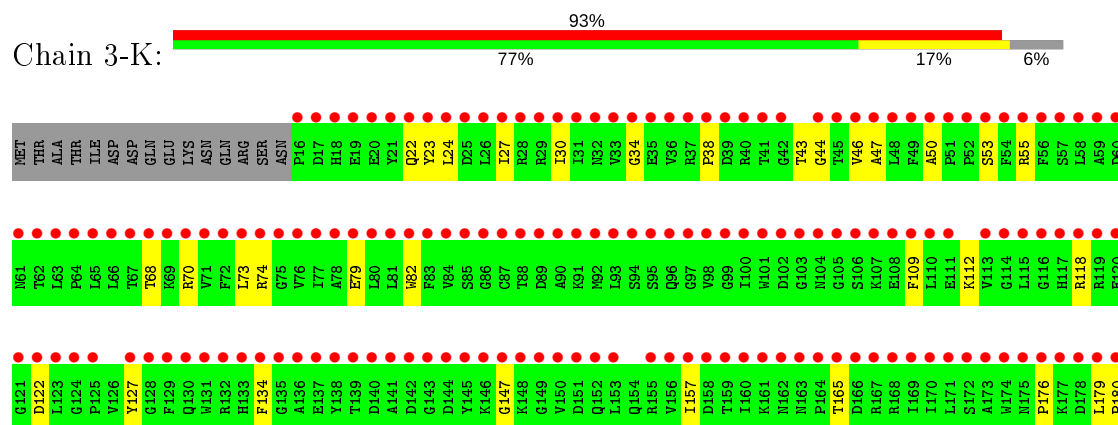


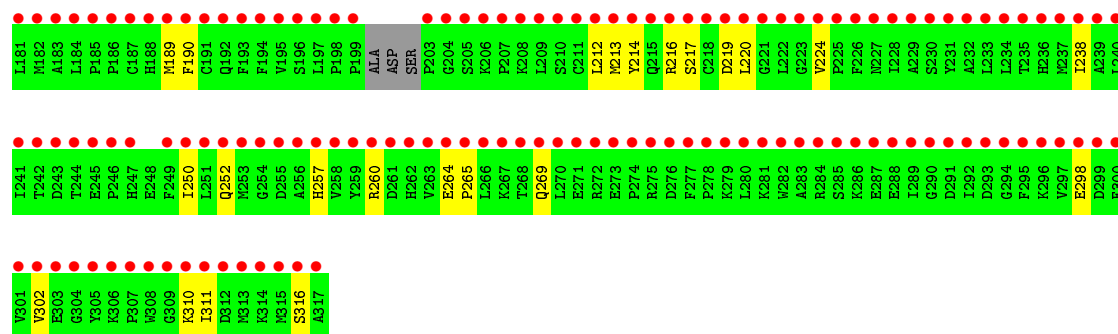


• Molecule 1: Thymidylate synthase

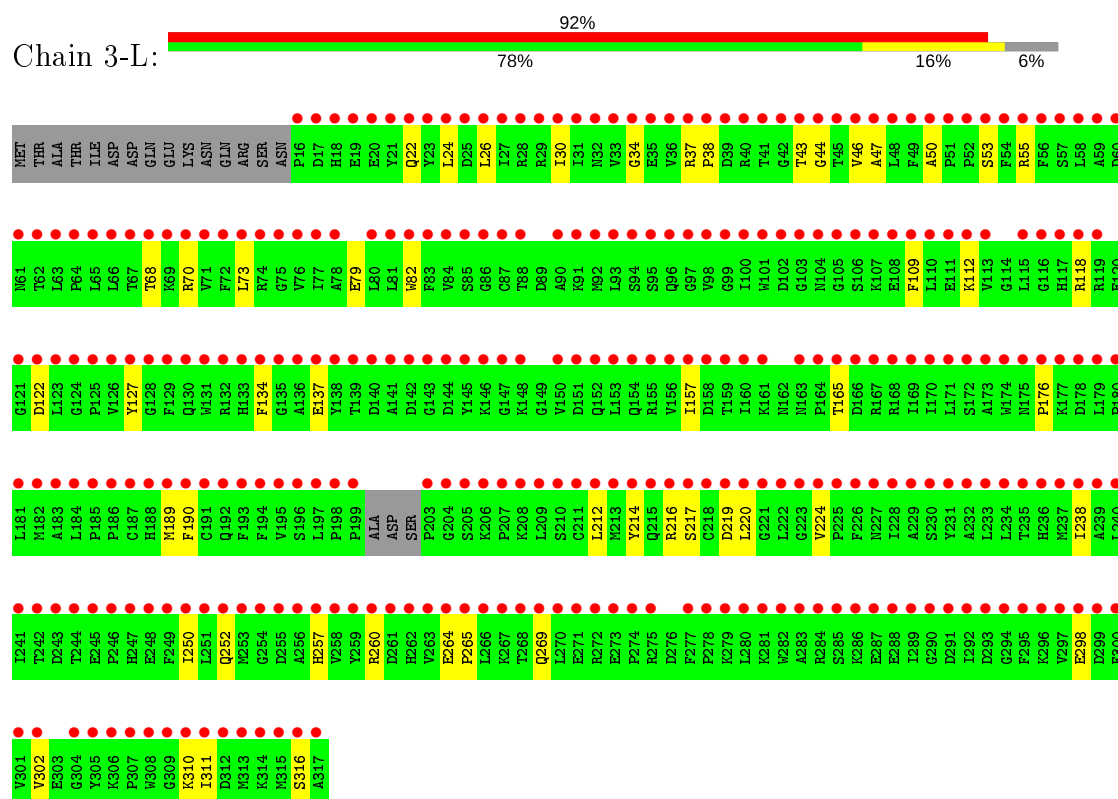


• Molecule 1: Thymidylate synthase

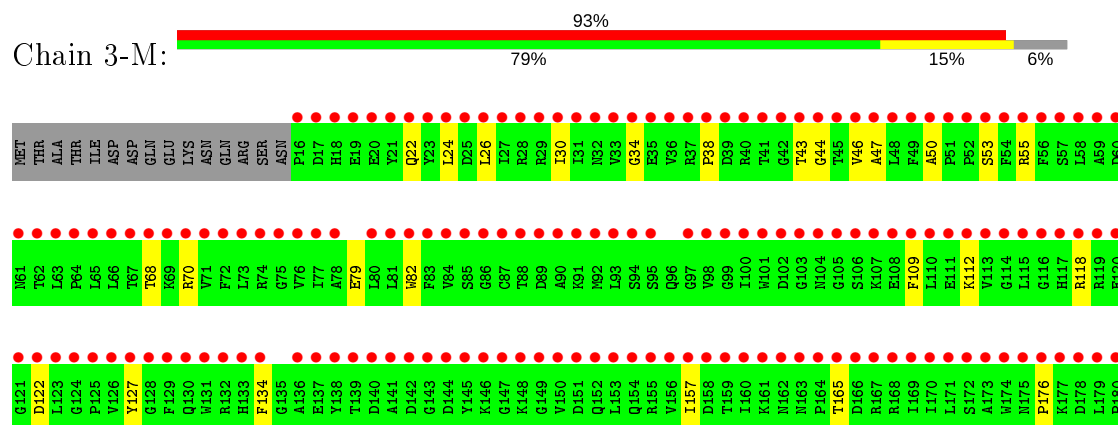




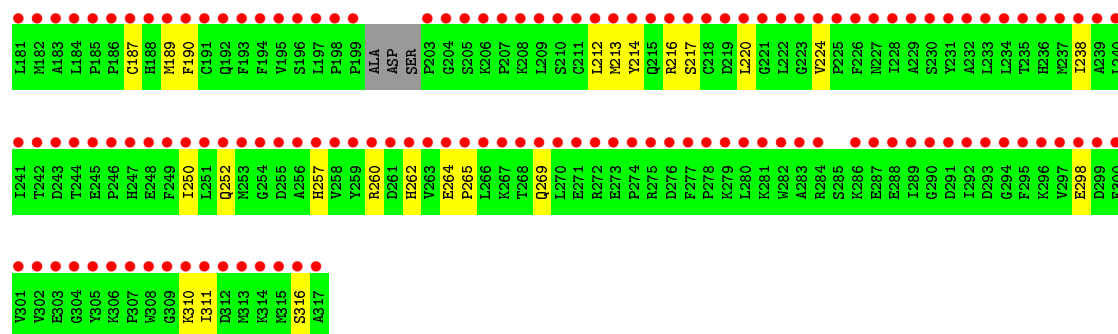
• Molecule 1: Thymidylate synthase



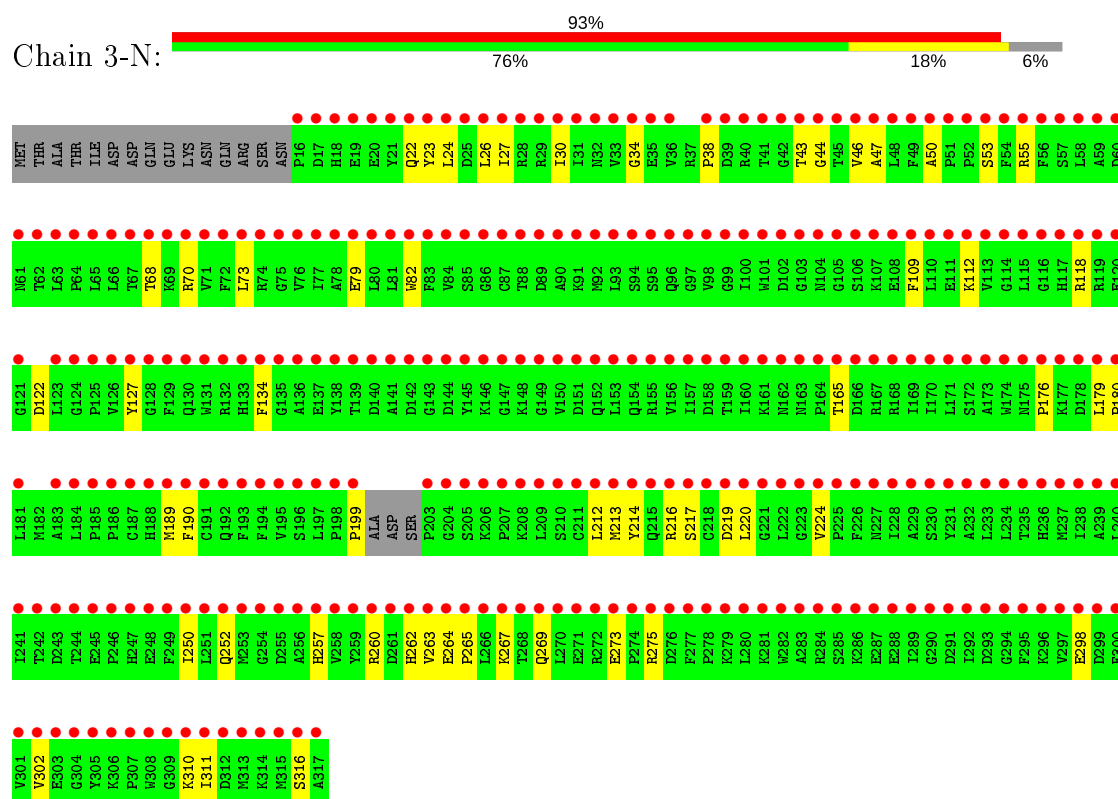
• Molecule 1: Thymidylate synthase



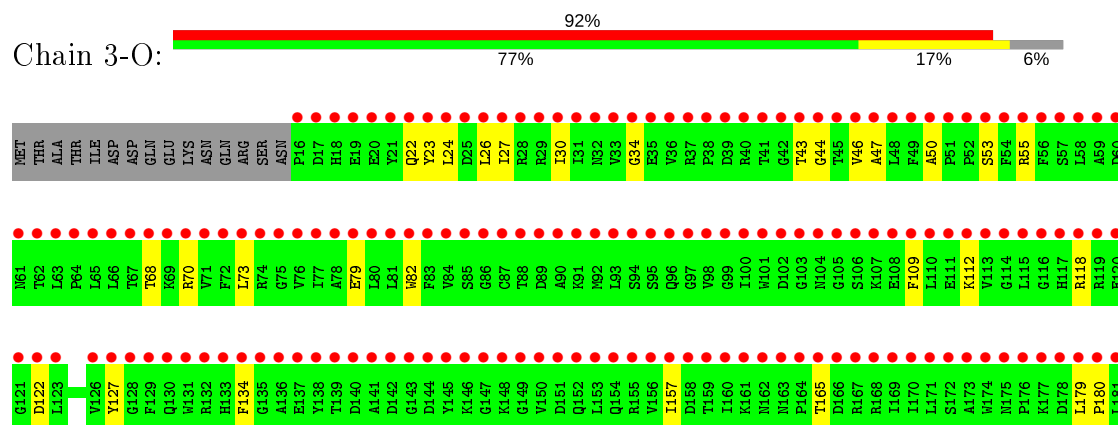


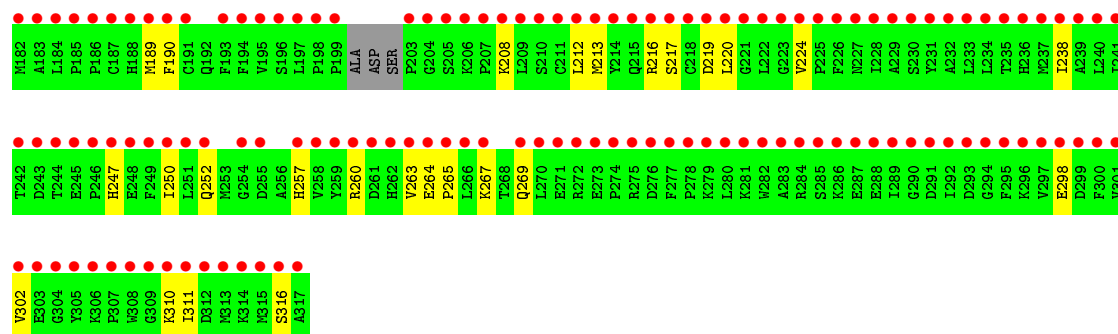


• Molecule 1: Thymidylate synthase

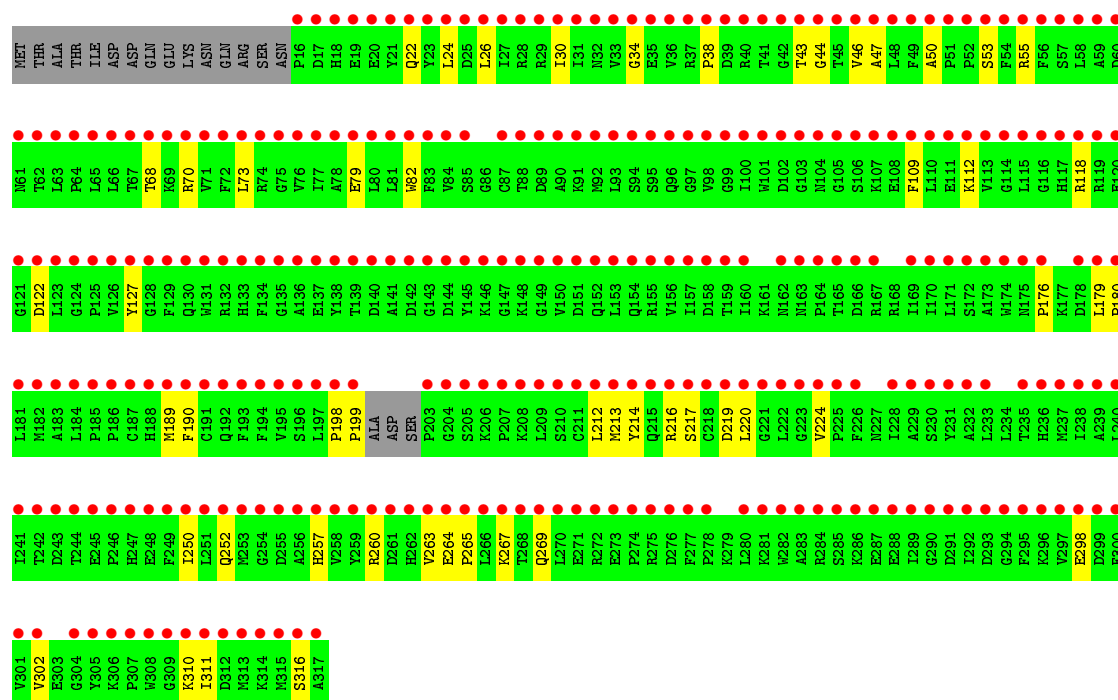
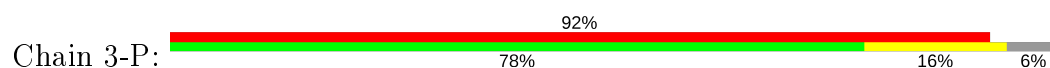


• Molecule 1: Thymidylate synthase

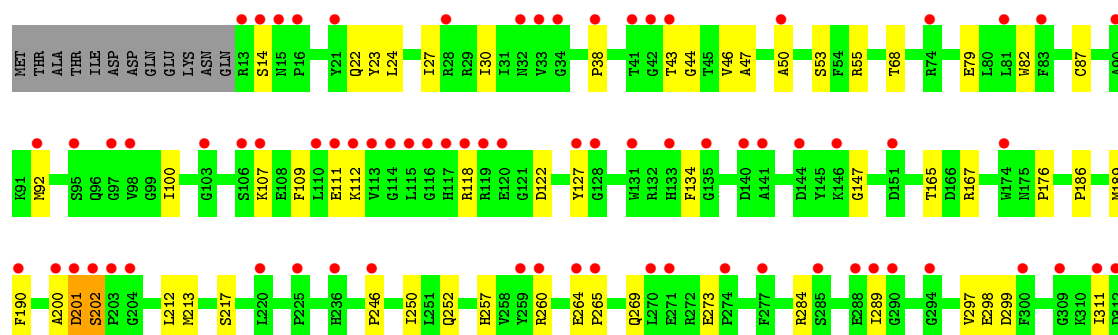
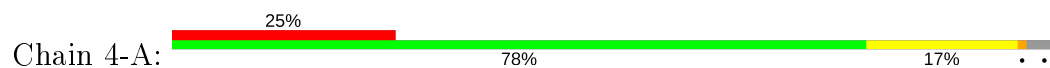


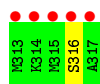


• Molecule 1: Thymidylate synthase

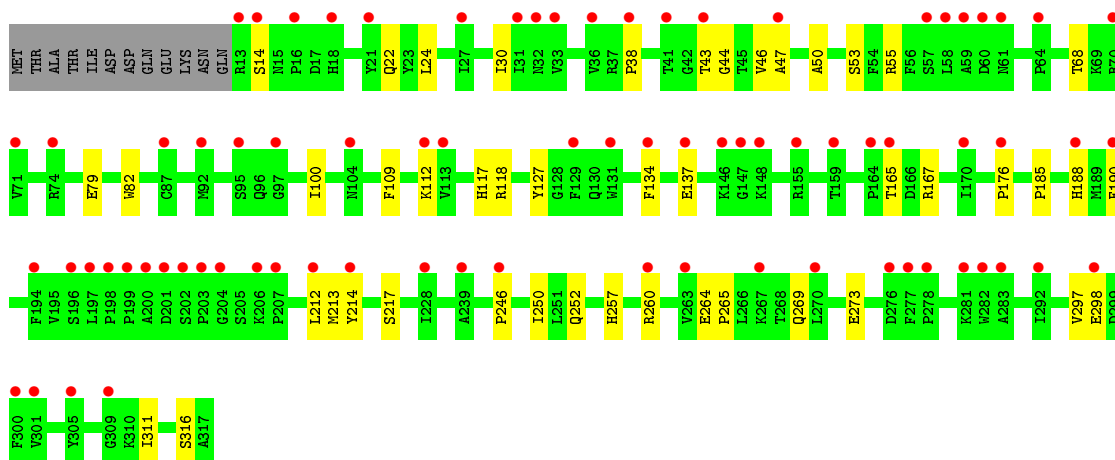
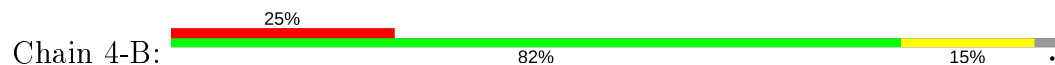


• Molecule 1: Thymidylate synthase

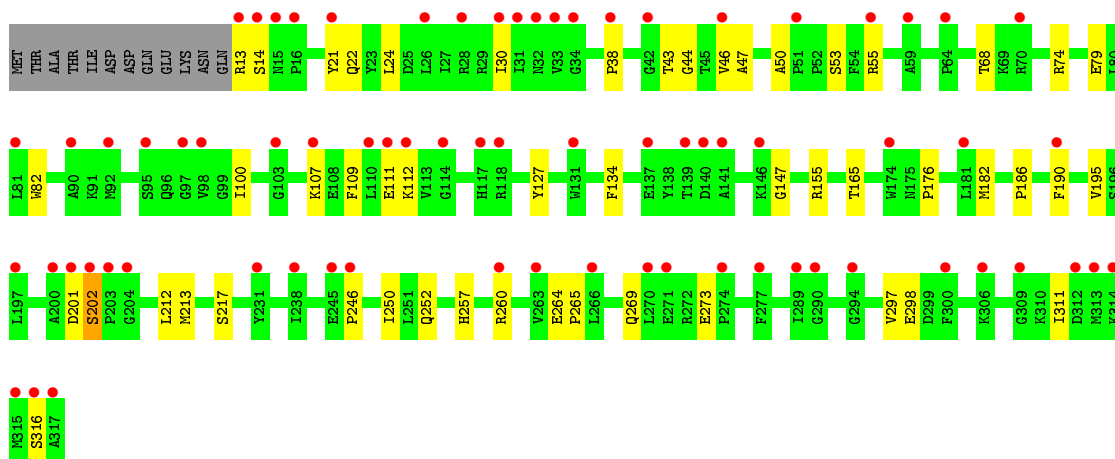
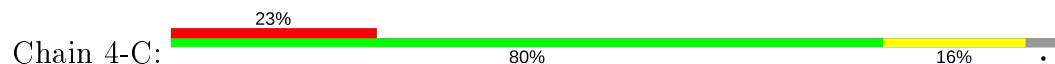




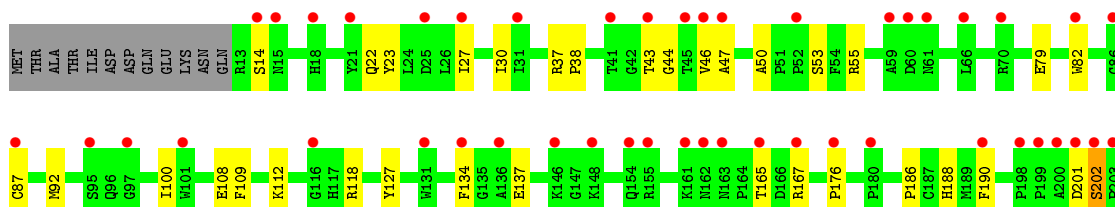
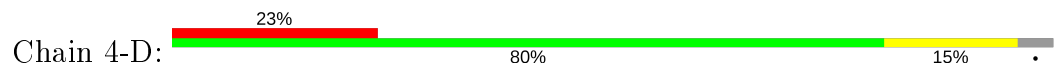
• Molecule 1: Thymidylate synthase

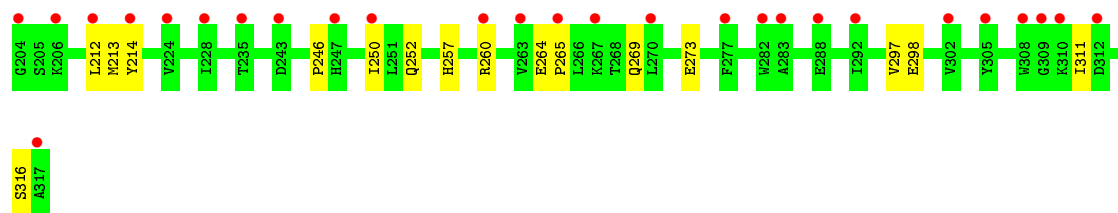


• Molecule 1: Thymidylate synthase

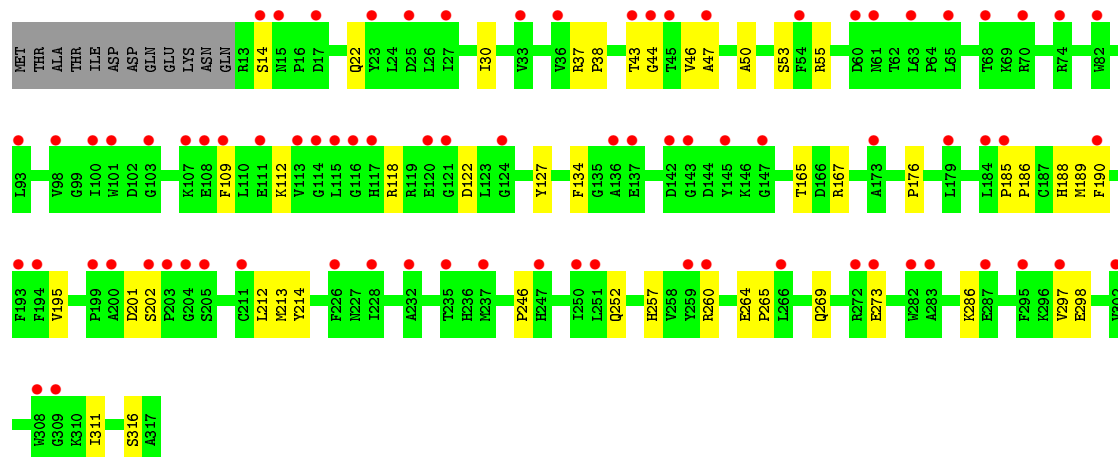
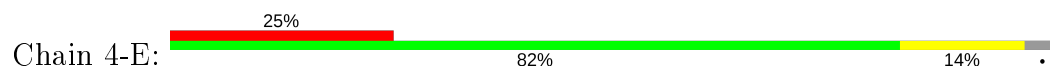


• Molecule 1: Thymidylate synthase

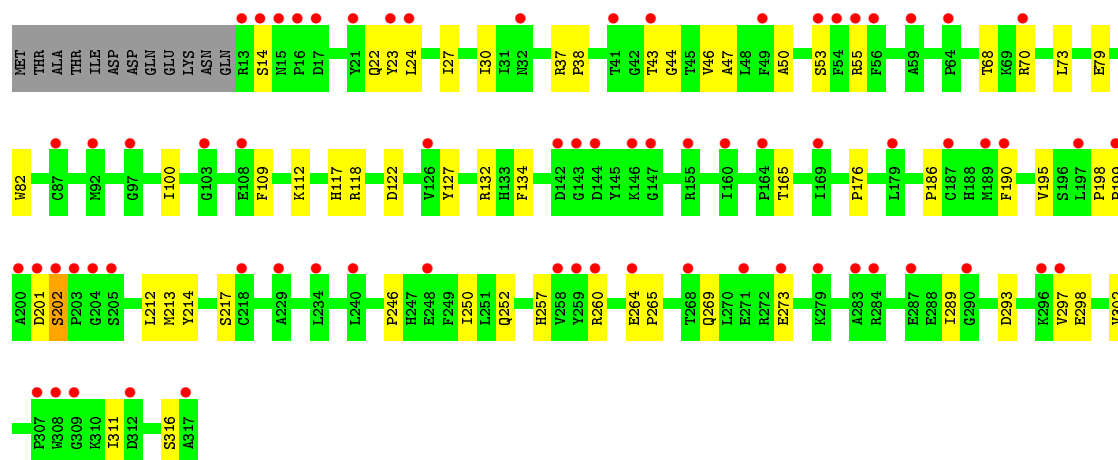
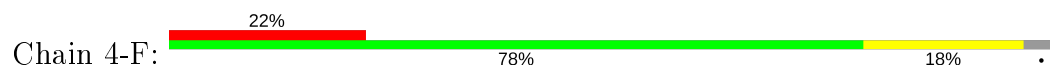




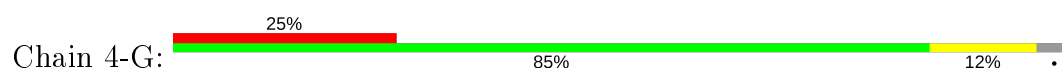
• Molecule 1: Thymidylate synthase

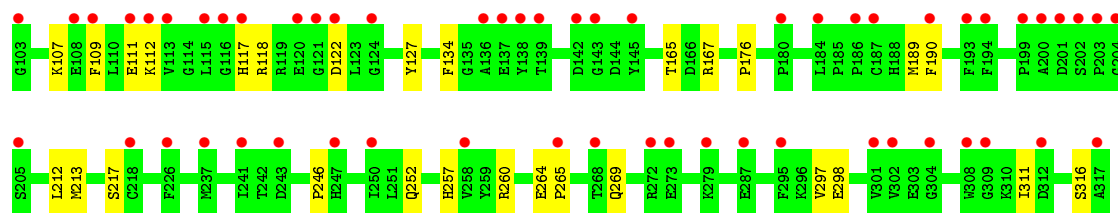


• Molecule 1: Thymidylate synthase

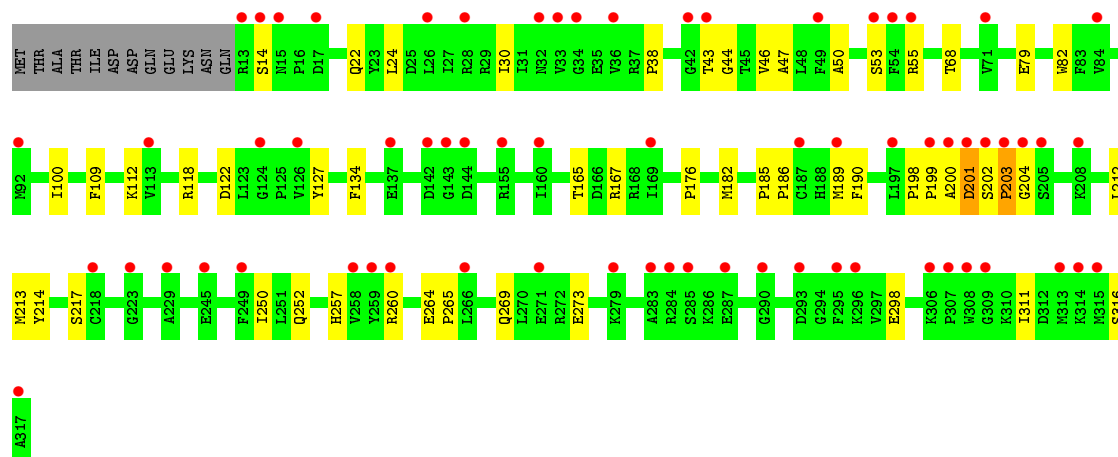
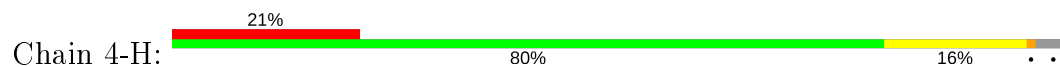


• Molecule 1: Thymidylate synthase

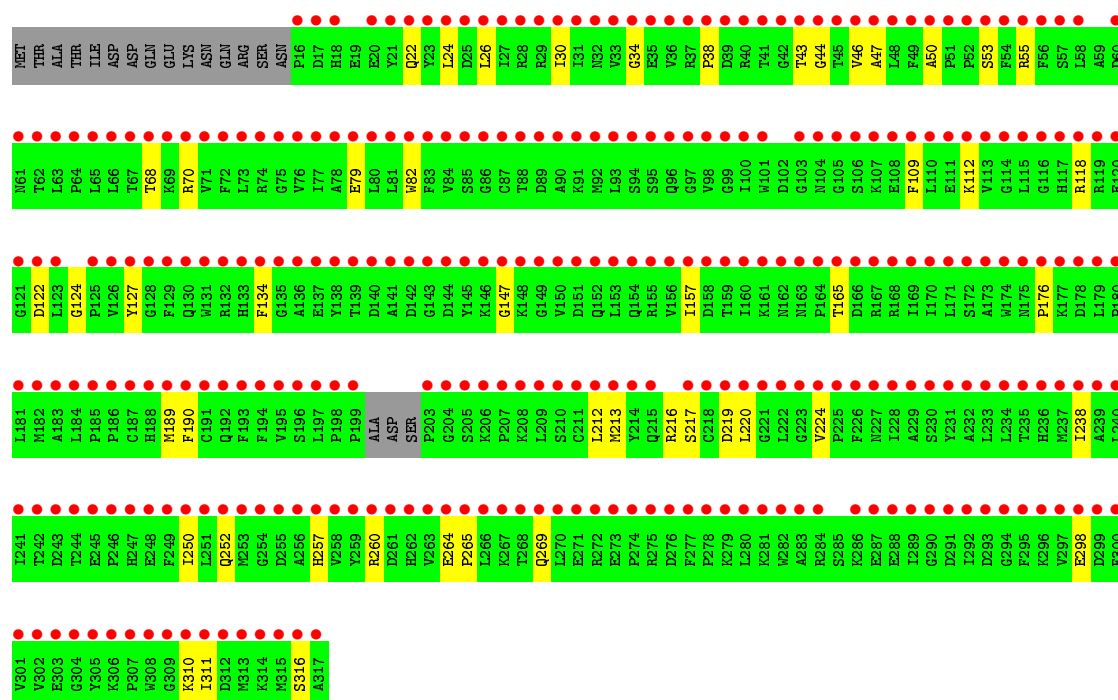
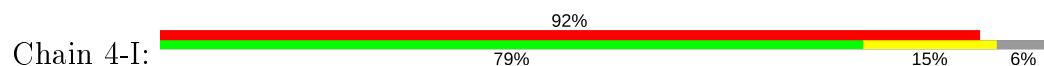




• Molecule 1: Thymidylate synthase

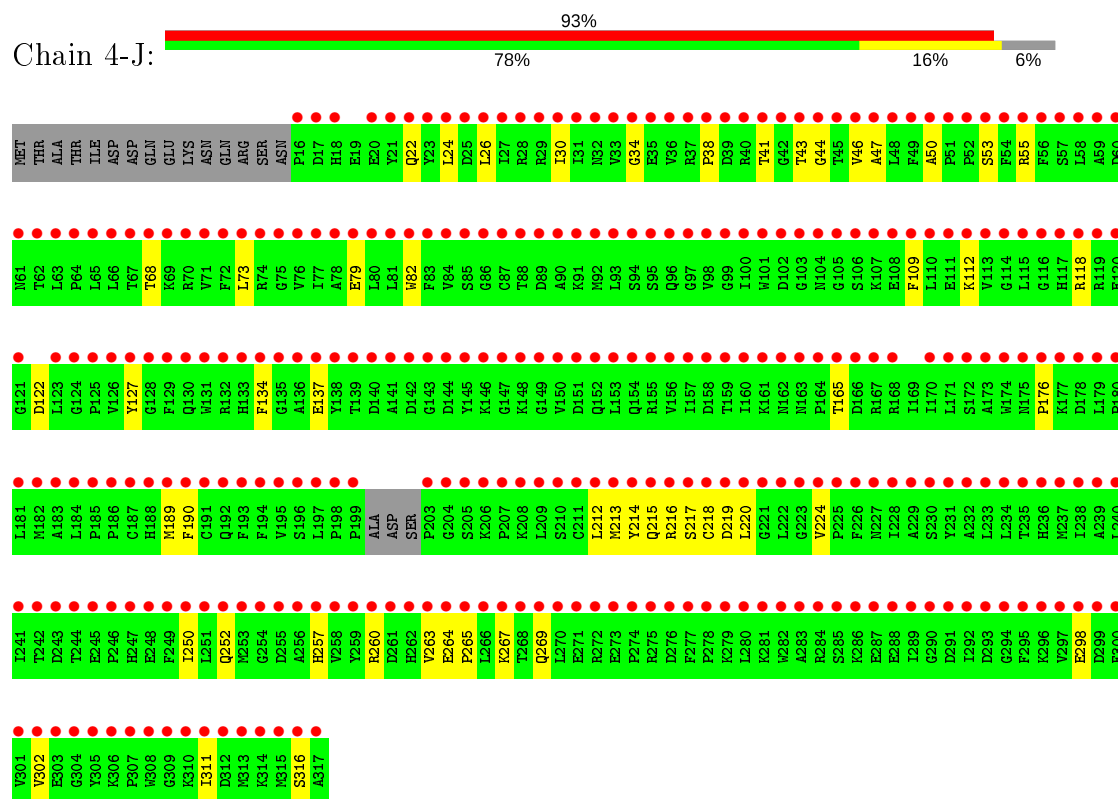


• Molecule 1: Thymidylate synthase



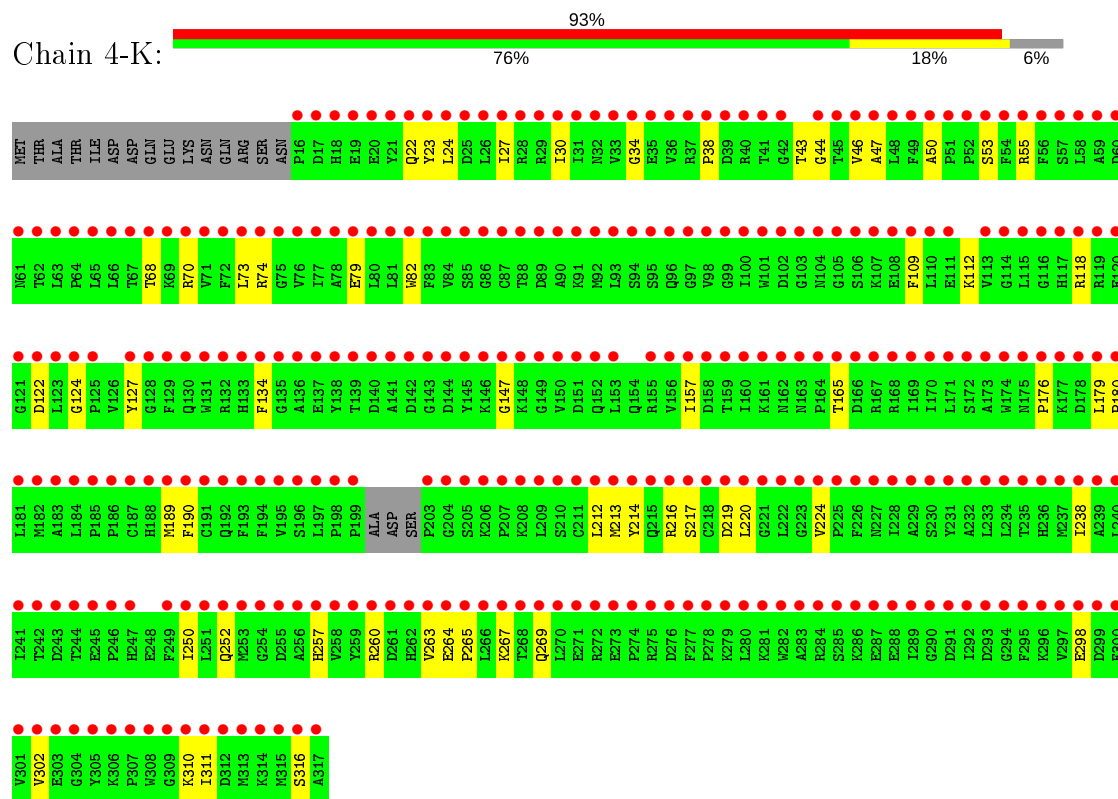
- Molecule 1: Thymidylate synthase

Chain 4-J:

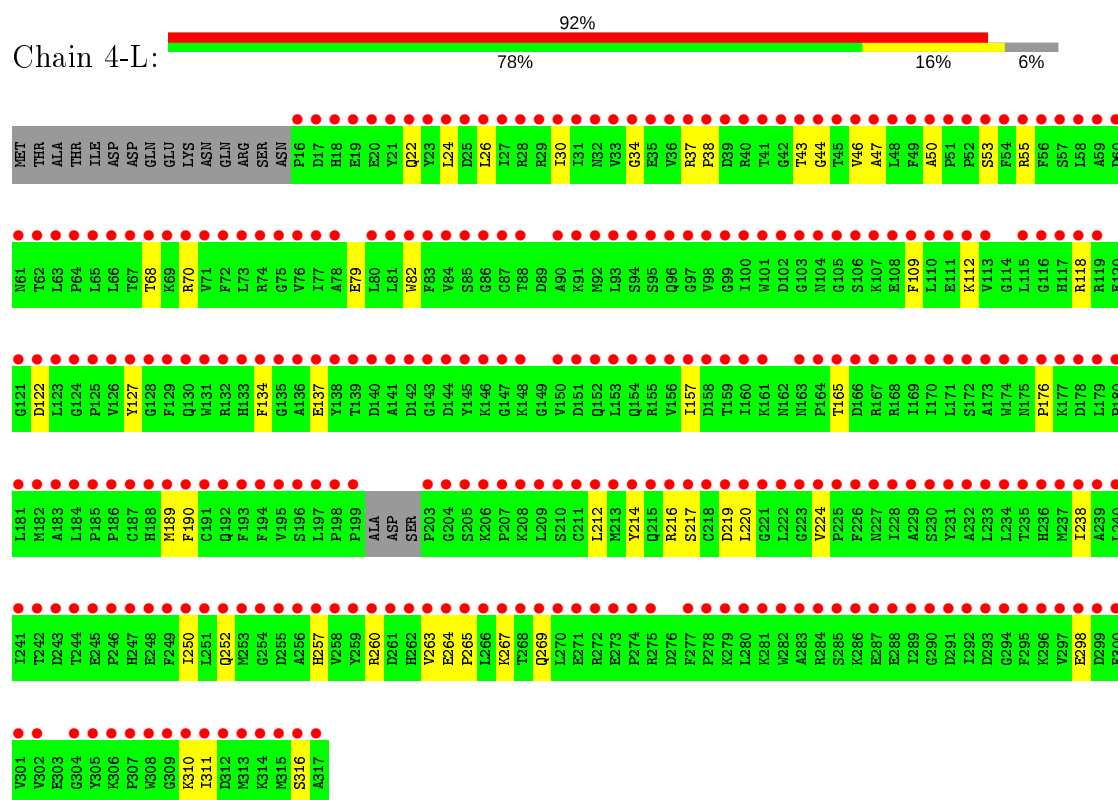


- Molecule 1: Thymidylate synthase

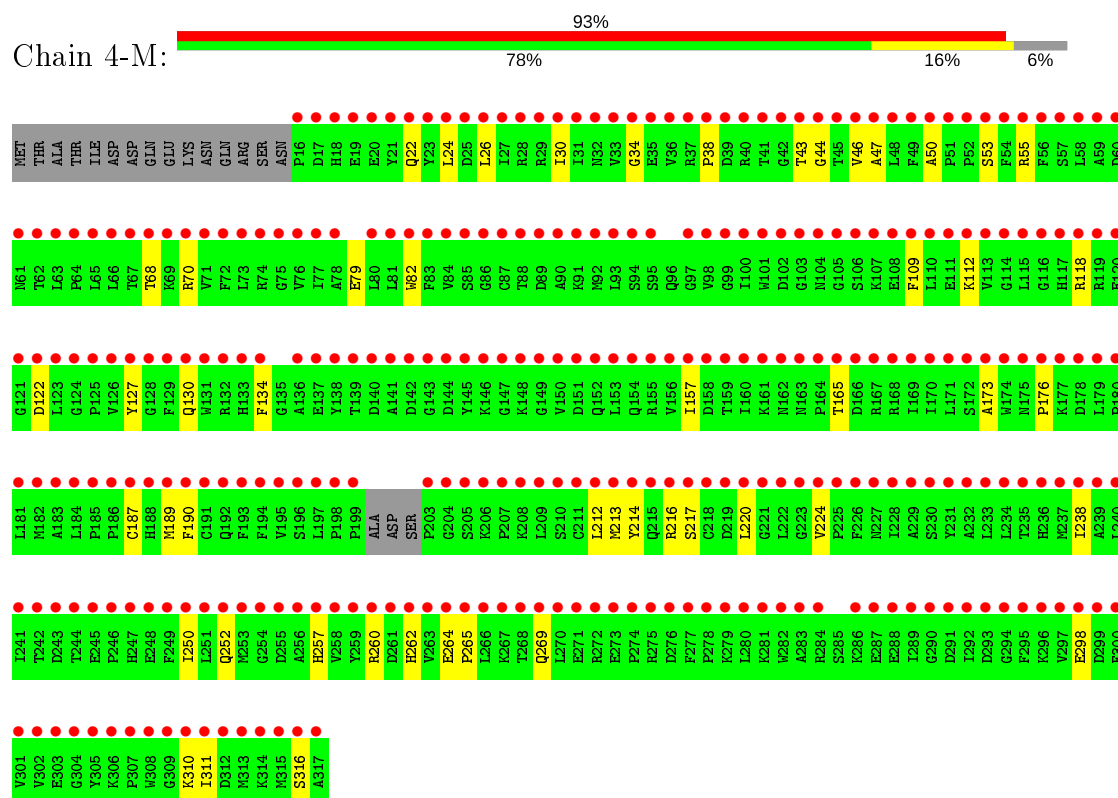
Chain 4-K:

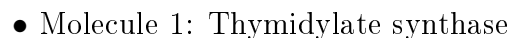


- Molecule 1: Thymidylate synthase



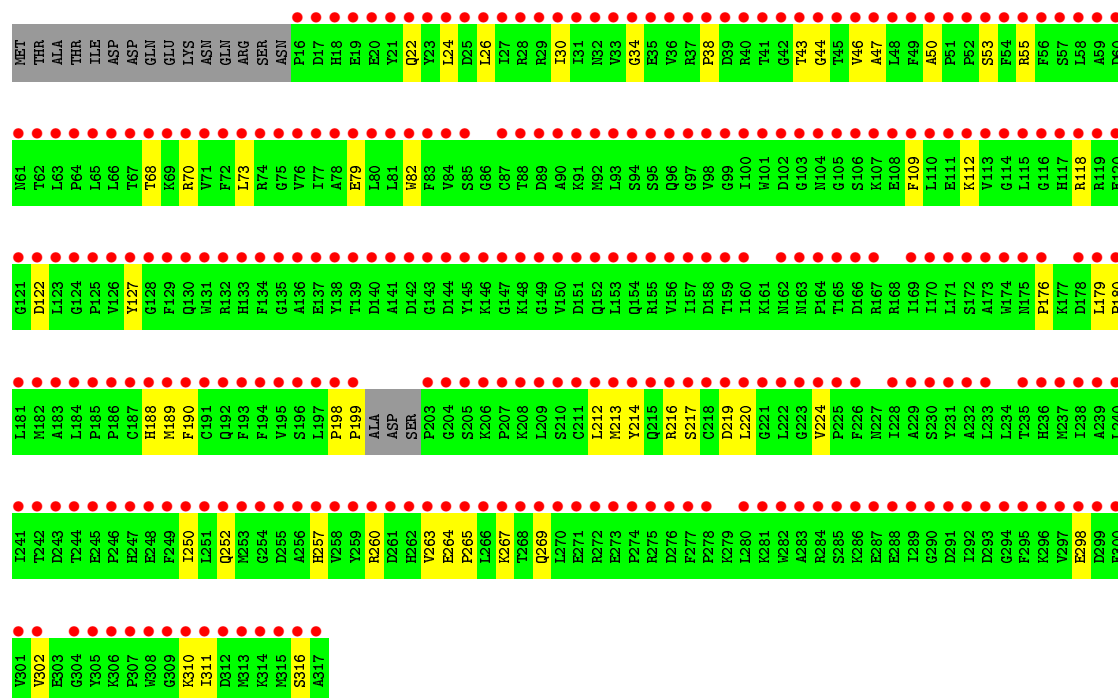
• Molecule 1: Thymidylate synthase







Response	Percentage
Yes	92%
No	78%
Don't know	17%
No answer	6%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	179.40Å 179.50Å 209.10Å 90.00° 89.80° 90.00°	Depositor
Resolution (Å)	49.91 – 2.08 89.75 – 2.07	Depositor EDS
% Data completeness (in resolution range)	88.1 (49.91-2.08) 87.3 (89.75-2.07)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.39 (at 2.07Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.290 , 0.305 0.273 , 0.289	Depositor DCC
$R_{free}$ test set	37242 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.4	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 29.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.206 for k,h,-l 0.198 for -k,-h,-l 0.349 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	161392	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CB3, UMP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1-A	0.50	0/2492	1.21	11/3375 (0.3%)
1	1-B	0.47	0/2496	0.71	4/3380 (0.1%)
1	1-C	0.48	0/2492	1.03	8/3375 (0.2%)
1	1-D	0.51	0/2496	1.39	13/3380 (0.4%)
1	1-E	0.49	0/2496	1.01	8/3380 (0.2%)
1	1-F	0.50	1/2496 (0.0%)	1.28	12/3380 (0.4%)
1	1-G	0.49	0/2496	0.86	8/3380 (0.2%)
1	1-H	0.49	0/2496	0.85	7/3380 (0.2%)
1	1-I	0.28	0/2451	0.59	2/3316 (0.1%)
1	1-J	0.28	0/2451	0.59	3/3316 (0.1%)
1	1-K	0.28	0/2451	0.59	3/3316 (0.1%)
1	1-L	0.28	0/2451	0.59	2/3316 (0.1%)
1	1-M	0.28	0/2451	0.59	2/3316 (0.1%)
1	1-N	0.28	0/2451	0.59	2/3316 (0.1%)
1	1-O	0.28	0/2451	0.59	2/3316 (0.1%)
1	1-P	0.28	0/2451	0.59	3/3316 (0.1%)
All	All	0.40	1/39568 (0.0%)	0.86	90/53558 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-F	132[A]	ARG	CD-NE	-5.44	1.37	1.46

All (90) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-D	37[A]	ARG	NE-CZ-NH1	-31.12	104.74	120.30
1	1-F	132[A]	ARG	NE-CZ-NH1	-30.91	104.84	120.30
1	1-F	132[A]	ARG	NE-CZ-NH2	30.10	135.35	120.30
1	1-E	37[A]	ARG	NE-CZ-NH1	-29.08	105.76	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-F	37[A]	ARG	NE-CZ-NH1	-28.95	105.82	120.30
1	1-D	28[A]	ARG	NE-CZ-NH1	-28.34	106.13	120.30
1	1-D	37[A]	ARG	NE-CZ-NH2	27.90	134.25	120.30
1	1-E	37[A]	ARG	NE-CZ-NH2	26.39	133.50	120.30
1	1-F	37[A]	ARG	NE-CZ-NH2	25.99	133.29	120.30
1	1-D	28[A]	ARG	NE-CZ-NH2	25.82	133.21	120.30
1	1-D	70[A]	ARG	NE-CZ-NH2	-24.85	107.87	120.30
1	1-A	284[A]	ARG	NE-CZ-NH2	-24.67	107.97	120.30
1	1-A	284[A]	ARG	NE-CZ-NH1	24.53	132.57	120.30
1	1-A	70[A]	ARG	NE-CZ-NH2	-24.42	108.09	120.30
1	1-C	70[A]	ARG	NE-CZ-NH2	-23.57	108.52	120.30
1	1-A	118[A]	ARG	NE-CZ-NH2	-23.39	108.61	120.30
1	1-G	118[A]	ARG	NE-CZ-NH2	-22.73	108.93	120.30
1	1-C	118[A]	ARG	NE-CZ-NH2	-22.58	109.01	120.30
1	1-D	70[A]	ARG	NE-CZ-NH1	22.51	131.55	120.30
1	1-H	118[A]	ARG	NE-CZ-NH2	-22.04	109.28	120.30
1	1-A	70[A]	ARG	NE-CZ-NH1	21.89	131.25	120.30
1	1-C	70[A]	ARG	NE-CZ-NH1	21.63	131.12	120.30
1	1-C	118[A]	ARG	NE-CZ-NH1	19.52	130.06	120.30
1	1-G	118[A]	ARG	NE-CZ-NH1	19.23	129.92	120.30
1	1-A	118[A]	ARG	NE-CZ-NH1	19.04	129.82	120.30
1	1-H	118[A]	ARG	NE-CZ-NH1	18.39	129.50	120.30
1	1-F	132[A]	ARG	CD-NE-CZ	15.17	144.84	123.60
1	1-D	37[A]	ARG	CD-NE-CZ	14.76	144.27	123.60
1	1-F	37[A]	ARG	CD-NE-CZ	13.96	143.15	123.60
1	1-E	37[A]	ARG	CD-NE-CZ	13.95	143.13	123.60
1	1-D	28[A]	ARG	CD-NE-CZ	13.21	142.09	123.60
1	1-F	118[A]	ARG	NE-CZ-NH1	-11.03	114.78	120.30
1	1-A	70[A]	ARG	CD-NE-CZ	11.01	139.01	123.60
1	1-C	70[A]	ARG	CD-NE-CZ	10.98	138.97	123.60
1	1-B	118[A]	ARG	NE-CZ-NH1	-10.82	114.89	120.30
1	1-D	70[A]	ARG	CD-NE-CZ	10.73	138.63	123.60
1	1-A	284[A]	ARG	CD-NE-CZ	10.57	138.40	123.60
1	1-D	118[A]	ARG	NE-CZ-NH1	-10.54	115.03	120.30
1	1-E	118[A]	ARG	NE-CZ-NH1	-9.80	115.40	120.30
1	1-C	118[A]	ARG	CD-NE-CZ	9.25	136.55	123.60
1	1-A	118[A]	ARG	CD-NE-CZ	9.24	136.54	123.60
1	1-G	118[A]	ARG	CD-NE-CZ	8.99	136.19	123.60
1	1-H	118[A]	ARG	CD-NE-CZ	8.94	136.11	123.60
1	1-F	118[A]	ARG	NE-CZ-NH2	8.78	124.69	120.30
1	1-D	37[A]	ARG	CG-CD-NE	-7.95	95.10	111.80
1	1-F	37[A]	ARG	CG-CD-NE	-7.90	95.22	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-D	118[A]	ARG	NE-CZ-NH2	7.84	124.22	120.30
1	1-E	37[A]	ARG	CG-CD-NE	-7.77	95.48	111.80
1	1-B	118[A]	ARG	NE-CZ-NH2	7.59	124.10	120.30
1	1-E	118[A]	ARG	NE-CZ-NH2	7.01	123.81	120.30
1	1-F	132[A]	ARG	CG-CD-NE	-6.98	97.13	111.80
1	1-P	118[A]	ARG	NE-CZ-NH1	-6.19	117.21	120.30
1	1-E	70[A]	ARG	NE-CZ-NH1	-6.17	117.21	120.30
1	1-M	118[A]	ARG	NE-CZ-NH1	-6.05	117.27	120.30
1	1-K	118[A]	ARG	NE-CZ-NH1	-6.00	117.30	120.30
1	1-L	118[A]	ARG	NE-CZ-NH1	-5.97	117.31	120.30
1	1-N	118[A]	ARG	NE-CZ-NH1	-5.96	117.32	120.30
1	1-I	118[A]	ARG	NE-CZ-NH1	-5.84	117.38	120.30
1	1-J	118[A]	ARG	NE-CZ-NH1	-5.79	117.41	120.30
1	1-O	118[A]	ARG	NE-CZ-NH1	-5.74	117.43	120.30
1	1-G	70[A]	ARG	NE-CZ-NH1	-5.70	117.45	120.30
1	1-B	70[A]	ARG	NE-CZ-NH1	-5.57	117.52	120.30
1	1-H	37[A]	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	1-G	70[A]	ARG	NE-CZ-NH2	5.51	123.05	120.30
1	1-O	141[A]	ALA	N-CA-CB	-5.50	102.40	110.10
1	1-I	141[A]	ALA	N-CA-CB	-5.47	102.44	110.10
1	1-N	141[A]	ALA	N-CA-CB	-5.47	102.44	110.10
1	1-P	141[A]	ALA	N-CA-CB	-5.45	102.47	110.10
1	1-L	141[A]	ALA	N-CA-CB	-5.44	102.49	110.10
1	1-M	141[A]	ALA	N-CA-CB	-5.42	102.52	110.10
1	1-K	141[A]	ALA	N-CA-CB	-5.40	102.54	110.10
1	1-J	141[A]	ALA	N-CA-CB	-5.40	102.54	110.10
1	1-F	141[A]	ALA	N-CA-CB	-5.34	102.62	110.10
1	1-H	141[A]	ALA	N-CA-CB	-5.30	102.67	110.10
1	1-A	37[A]	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	1-E	141[A]	ALA	N-CA-CB	-5.28	102.70	110.10
1	1-B	141[A]	ALA	N-CA-CB	-5.22	102.78	110.10
1	1-H	37[A]	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	1-G	37[A]	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	1-D	141[A]	ALA	N-CA-CB	-5.17	102.87	110.10
1	1-G	141[A]	ALA	N-CA-CB	-5.15	102.89	110.10
1	1-A	141[A]	ALA	N-CA-CB	-5.14	102.90	110.10
1	1-C	141[A]	ALA	N-CA-CB	-5.13	102.91	110.10
1	1-H	70[A]	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	1-P	118[A]	ARG	NE-CZ-NH2	5.10	122.85	120.30
1	1-F	70[A]	ARG	NE-CZ-NH1	-5.07	117.76	120.30
1	1-G	37[A]	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	1-J	118[A]	ARG	NE-CZ-NH2	5.04	122.82	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-C	37[A]	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	1-K	118[A]	ARG	NE-CZ-NH2	5.00	122.80	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	2427	0	2393	50	0
1	1-B	2431	0	2397	45	0
1	1-C	2427	0	2393	49	0
1	1-D	2431	0	2397	48	0
1	1-E	2431	0	2397	43	0
1	1-F	2431	0	2397	53	0
1	1-G	2431	0	2397	35	0
1	1-H	2431	0	2397	51	0
1	1-I	2387	0	2360	40	0
1	1-J	2387	0	2360	47	0
1	1-K	2387	0	2360	47	0
1	1-L	2387	0	2360	46	0
1	1-M	2387	0	2360	41	0
1	1-N	2387	0	2360	46	0
1	1-O	2387	0	2360	37	0
1	1-P	2387	0	2360	38	0
1	2-A	2427	0	2393	50	0
1	2-B	2431	0	2397	45	0
1	2-C	2427	0	2393	49	0
1	2-D	2431	0	2397	48	0
1	2-E	2431	0	2397	43	0
1	2-F	2431	0	2397	53	0
1	2-G	2431	0	2397	35	0
1	2-H	2431	0	2397	47	0
1	2-I	2387	0	2360	45	0
1	2-J	2387	0	2360	46	0
1	2-K	2387	0	2360	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2-L	2387	0	2360	46	0
1	2-M	2387	0	2360	46	0
1	2-N	2387	0	2360	49	0
1	2-O	2387	0	2360	45	0
1	2-P	2387	0	2360	45	0
1	3-A	2427	0	2393	50	0
1	3-B	2431	0	2397	45	0
1	3-C	2427	0	2393	49	0
1	3-D	2431	0	2397	48	0
1	3-E	2431	0	2397	43	0
1	3-F	2431	0	2397	53	0
1	3-G	2431	0	2397	35	0
1	3-H	2431	0	2397	61	0
1	3-I	2387	0	2360	46	0
1	3-J	2387	0	2360	45	0
1	3-K	2387	0	2360	49	0
1	3-L	2387	0	2360	45	0
1	3-M	2387	0	2360	44	0
1	3-N	2387	0	2360	62	0
1	3-O	2387	0	2360	46	0
1	3-P	2387	0	2360	45	0
1	4-A	2427	0	2393	50	0
1	4-B	2431	0	2397	45	0
1	4-C	2427	0	2393	49	0
1	4-D	2431	0	2397	48	0
1	4-E	2431	0	2397	43	0
1	4-F	2431	0	2397	53	0
1	4-G	2431	0	2397	35	0
1	4-H	2431	0	2397	47	0
1	4-I	2387	0	2360	45	0
1	4-J	2387	0	2360	44	0
1	4-K	2387	0	2360	52	0
1	4-L	2387	0	2360	46	0
1	4-M	2387	0	2360	44	0
1	4-N	2387	0	2360	46	0
1	4-O	2387	0	2360	45	0
1	4-P	2387	0	2360	45	0
2	1-A	20	0	10	0	0
2	1-B	20	0	10	0	0
2	1-C	20	0	10	0	0
2	1-D	20	0	10	0	0
2	1-E	20	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1-F	20	0	10	0	0
2	1-G	20	0	10	0	0
2	1-H	20	0	10	0	0
2	1-I	20	0	10	1	0
2	1-J	20	0	10	1	0
2	1-K	20	0	10	1	0
2	1-L	20	0	10	1	0
2	1-M	20	0	10	1	0
2	1-N	20	0	10	1	0
2	1-O	20	0	10	1	0
2	1-P	20	0	10	1	0
2	2-A	20	0	10	0	0
2	2-B	20	0	10	0	0
2	2-C	20	0	10	0	0
2	2-D	20	0	10	0	0
2	2-E	20	0	10	0	0
2	2-F	20	0	10	0	0
2	2-G	20	0	10	0	0
2	2-H	20	0	10	0	0
2	2-I	20	0	10	1	0
2	2-J	20	0	10	1	0
2	2-K	20	0	10	1	0
2	2-L	20	0	10	1	0
2	2-M	20	0	10	1	0
2	2-N	20	0	10	1	0
2	2-O	20	0	10	1	0
2	2-P	20	0	10	1	0
2	3-A	20	0	10	0	0
2	3-B	20	0	10	0	0
2	3-C	20	0	10	0	0
2	3-D	20	0	10	0	0
2	3-E	20	0	10	0	0
2	3-F	20	0	10	0	0
2	3-G	20	0	10	0	0
2	3-H	20	0	10	0	0
2	3-I	20	0	10	1	0
2	3-J	20	0	10	1	0
2	3-K	20	0	10	1	0
2	3-L	20	0	10	1	0
2	3-M	20	0	10	1	0
2	3-N	20	0	10	1	0
2	3-O	20	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	3-P	20	0	10	1	0
2	4-A	20	0	10	0	0
2	4-B	20	0	10	0	0
2	4-C	20	0	10	0	0
2	4-D	20	0	10	0	0
2	4-E	20	0	10	0	0
2	4-F	20	0	10	0	0
2	4-G	20	0	10	0	0
2	4-H	20	0	10	0	0
2	4-I	20	0	10	1	0
2	4-J	20	0	10	1	0
2	4-K	20	0	10	1	0
2	4-L	20	0	10	1	0
2	4-M	20	0	10	1	0
2	4-N	20	0	10	1	0
2	4-O	20	0	10	1	0
2	4-P	20	0	10	1	0
3	1-A	35	0	21	1	0
3	1-B	35	0	21	1	0
3	1-C	35	0	21	1	0
3	1-D	35	0	21	1	0
3	1-E	35	0	21	0	0
3	1-F	35	0	21	1	0
3	1-G	35	0	21	0	0
3	1-H	35	0	21	1	0
3	2-A	35	0	21	1	0
3	2-B	35	0	21	1	0
3	2-C	35	0	21	1	0
3	2-D	35	0	21	1	0
3	2-E	35	0	21	0	0
3	2-F	35	0	21	1	0
3	2-G	35	0	21	0	0
3	2-H	35	0	21	1	0
3	3-A	35	0	21	1	0
3	3-B	35	0	21	1	0
3	3-C	35	0	21	1	0
3	3-D	35	0	21	1	0
3	3-E	35	0	21	0	0
3	3-F	35	0	21	1	0
3	3-G	35	0	21	0	0
3	3-H	35	0	21	1	0
3	4-A	35	0	21	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	4-B	35	0	21	1	0
3	4-C	35	0	21	1	0
3	4-D	35	0	21	1	0
3	4-E	35	0	21	0	0
3	4-F	35	0	21	1	0
3	4-G	35	0	21	0	0
3	4-H	35	0	21	1	0
4	1-A	185	0	0	4	0
4	1-B	143	0	0	7	0
4	1-C	151	0	0	4	0
4	1-D	148	0	0	5	0
4	1-E	155	0	0	6	0
4	1-F	138	0	0	6	0
4	1-G	153	0	0	3	0
4	1-H	139	0	0	2	0
4	2-A	185	0	0	4	0
4	2-B	143	0	0	7	0
4	2-C	151	0	0	4	0
4	2-D	148	0	0	5	0
4	2-E	155	0	0	6	0
4	2-F	138	0	0	6	0
4	2-G	153	0	0	3	0
4	2-H	139	0	0	2	0
4	3-A	185	0	0	4	0
4	3-B	143	0	0	7	0
4	3-C	151	0	0	4	0
4	3-D	148	0	0	5	0
4	3-E	155	0	0	6	0
4	3-F	138	0	0	6	0
4	3-G	153	0	0	3	0
4	3-H	139	0	0	2	0
4	4-A	185	0	0	4	0
4	4-B	143	0	0	7	0
4	4-C	151	0	0	4	0
4	4-D	148	0	0	5	0
4	4-E	155	0	0	6	0
4	4-F	138	0	0	6	0
4	4-G	153	0	0	3	0
4	4-H	139	0	0	2	0
All	All	161392	0	153504	2427	0

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 8.

All (2427) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:201[C]:ASP:HB3	1:N:273[C]:GLU:CG	1.82	1.08
1:H:287[A]:GLU:HG2	1:J:146[A]:LYS:HZ3	1.25	0.99
1:H:287[A]:GLU:HG2	1:J:146[A]:LYS:NZ	1.78	0.98
1:H:201[C]:ASP:HB3	1:N:273[C]:GLU:HG2	1.45	0.93
1:H:202[C]:SER:HB3	1:N:275[C]:ARG:HG3	1.54	0.89
1:A:284[A]:ARG:HD3	1:A:299[A]:ASP:OD1	1.75	0.86
1:A:284[B]:ARG:HD3	1:A:299[B]:ASP:OD1	1.75	0.86
1:A:284[C]:ARG:HD3	1:A:299[C]:ASP:OD1	1.75	0.86
1:A:284[D]:ARG:HD3	1:A:299[D]:ASP:OD1	1.75	0.86
1:H:14[C]:SER:OG	1:N:199[C]:PRO:HB3	1.76	0.85
1:H:201[A]:ASP:CG	1:H:202[A]:SER:H	1.81	0.82
1:H:201[B]:ASP:CG	1:H:202[B]:SER:H	1.81	0.82
1:H:201[C]:ASP:CG	1:H:202[C]:SER:H	1.81	0.82
1:H:201[D]:ASP:CG	1:H:202[D]:SER:H	1.81	0.82
1:E:22[A]:GLN:HE22	1:E:55[A]:ARG:H	1.28	0.82
1:E:22[B]:GLN:HE22	1:E:55[B]:ARG:H	1.28	0.82
1:E:22[C]:GLN:HE22	1:E:55[C]:ARG:H	1.28	0.82
1:E:22[D]:GLN:HE22	1:E:55[D]:ARG:H	1.28	0.82
1:B:22[A]:GLN:HE22	1:B:55[A]:ARG:H	1.27	0.81
1:B:22[B]:GLN:HE22	1:B:55[B]:ARG:H	1.27	0.81
1:B:22[C]:GLN:HE22	1:B:55[C]:ARG:H	1.27	0.81
1:B:22[D]:GLN:HE22	1:B:55[D]:ARG:H	1.27	0.81
1:D:22[A]:GLN:HE22	1:D:55[A]:ARG:H	1.27	0.81
1:D:22[B]:GLN:HE22	1:D:55[B]:ARG:H	1.27	0.81
1:D:22[C]:GLN:HE22	1:D:55[C]:ARG:H	1.27	0.81
1:D:22[D]:GLN:HE22	1:D:55[D]:ARG:H	1.27	0.81
1:H:202[A]:SER:C	1:H:204[A]:GLY:H	1.82	0.80
1:H:202[B]:SER:C	1:H:204[B]:GLY:H	1.82	0.80
1:H:202[C]:SER:C	1:H:204[C]:GLY:H	1.82	0.80
1:H:202[D]:SER:C	1:H:204[D]:GLY:H	1.82	0.80
1:C:22[A]:GLN:HE22	1:C:55[A]:ARG:H	1.28	0.80
1:H:202[A]:SER:O	1:H:204[A]:GLY:N	2.15	0.80
1:C:22[B]:GLN:HE22	1:C:55[B]:ARG:H	1.28	0.80
1:H:202[B]:SER:O	1:H:204[B]:GLY:N	2.15	0.80
1:C:22[C]:GLN:HE22	1:C:55[C]:ARG:H	1.28	0.80
1:H:202[C]:SER:O	1:H:204[C]:GLY:N	2.15	0.80
1:C:22[D]:GLN:HE22	1:C:55[D]:ARG:H	1.28	0.80
1:H:202[D]:SER:O	1:H:204[D]:GLY:N	2.15	0.80
1:A:22[A]:GLN:HE22	1:A:55[A]:ARG:H	1.28	0.80
1:A:22[B]:GLN:HE22	1:A:55[B]:ARG:H	1.28	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22[C]:GLN:HE22	1:A:55[C]:ARG:H	1.28	0.80
1:A:22[D]:GLN:HE22	1:A:55[D]:ARG:H	1.28	0.80
1:H:185[A]:PRO:HG3	4:H:1363[A]:HOH:O	1.80	0.79
1:H:185[B]:PRO:HG3	4:H:1363[B]:HOH:O	1.80	0.79
1:H:185[C]:PRO:HG3	4:H:1363[C]:HOH:O	1.80	0.79
1:H:185[D]:PRO:HG3	4:H:1363[D]:HOH:O	1.80	0.79
1:A:190[A]:PHE:HE2	1:B:190[A]:PHE:HE2	1.30	0.79
1:G:190[A]:PHE:HE2	1:H:190[A]:PHE:HE2	1.29	0.79
1:A:190[B]:PHE:HE2	1:B:190[B]:PHE:HE2	1.30	0.79
1:G:190[B]:PHE:HE2	1:H:190[B]:PHE:HE2	1.29	0.79
1:A:190[C]:PHE:HE2	1:B:190[C]:PHE:HE2	1.30	0.79
1:G:190[C]:PHE:HE2	1:H:190[C]:PHE:HE2	1.29	0.79
1:A:190[D]:PHE:HE2	1:B:190[D]:PHE:HE2	1.30	0.79
1:G:190[D]:PHE:HE2	1:H:190[D]:PHE:HE2	1.29	0.79
1:B:55[A]:ARG:NH2	4:B:975[A]:HOH:O	2.15	0.79
1:B:55[B]:ARG:NH2	4:B:975[B]:HOH:O	2.15	0.79
1:B:55[C]:ARG:NH2	4:B:975[C]:HOH:O	2.15	0.79
1:B:55[D]:ARG:NH2	4:B:975[D]:HOH:O	2.15	0.79
1:C:190[A]:PHE:HE2	1:D:190[A]:PHE:HE2	1.30	0.79
1:E:190[A]:PHE:HE2	1:F:190[A]:PHE:HE2	1.30	0.79
1:C:190[B]:PHE:HE2	1:D:190[B]:PHE:HE2	1.30	0.79
1:E:190[B]:PHE:HE2	1:F:190[B]:PHE:HE2	1.30	0.79
1:C:190[C]:PHE:HE2	1:D:190[C]:PHE:HE2	1.30	0.79
1:E:190[C]:PHE:HE2	1:F:190[C]:PHE:HE2	1.30	0.79
1:C:190[D]:PHE:HE2	1:D:190[D]:PHE:HE2	1.30	0.79
1:E:190[D]:PHE:HE2	1:F:190[D]:PHE:HE2	1.30	0.79
1:G:190[A]:PHE:CE2	1:H:190[A]:PHE:HE2	2.03	0.77
1:H:22[A]:GLN:HE22	1:H:55[A]:ARG:H	1.30	0.77
1:G:190[B]:PHE:CE2	1:H:190[B]:PHE:HE2	2.03	0.77
1:H:22[B]:GLN:HE22	1:H:55[B]:ARG:H	1.30	0.77
1:G:190[C]:PHE:CE2	1:H:190[C]:PHE:HE2	2.03	0.77
1:H:22[C]:GLN:HE22	1:H:55[C]:ARG:H	1.30	0.77
1:G:190[D]:PHE:CE2	1:H:190[D]:PHE:HE2	2.03	0.77
1:H:22[D]:GLN:HE22	1:H:55[D]:ARG:H	1.30	0.77
1:G:22[A]:GLN:HE22	1:G:55[A]:ARG:H	1.33	0.77
1:G:22[B]:GLN:HE22	1:G:55[B]:ARG:H	1.33	0.77
1:G:22[C]:GLN:HE22	1:G:55[C]:ARG:H	1.33	0.77
1:G:22[D]:GLN:HE22	1:G:55[D]:ARG:H	1.33	0.77
1:G:190[A]:PHE:HE2	1:H:190[A]:PHE:CE2	2.03	0.77
1:G:190[B]:PHE:HE2	1:H:190[B]:PHE:CE2	2.03	0.77
1:G:190[C]:PHE:HE2	1:H:190[C]:PHE:CE2	2.03	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:190[D]:PHE:HE2	1:H:190[D]:PHE:CE2	2.03	0.77
1:L:22[D]:GLN:HE22	1:L:55[D]:ARG:H	1.31	0.77
1:F:22[A]:GLN:HE22	1:F:55[A]:ARG:H	1.32	0.76
1:F:22[B]:GLN:HE22	1:F:55[B]:ARG:H	1.32	0.76
1:F:22[C]:GLN:HE22	1:F:55[C]:ARG:H	1.32	0.76
1:F:22[D]:GLN:HE22	1:F:55[D]:ARG:H	1.32	0.76
1:L:22[B]:GLN:HE22	1:L:55[B]:ARG:H	1.34	0.75
1:L:22[C]:GLN:HE22	1:L:55[C]:ARG:H	1.34	0.74
1:L:22[A]:GLN:HE22	1:L:55[A]:ARG:H	1.34	0.74
1:A:190[A]:PHE:CE2	1:B:190[A]:PHE:HE2	2.04	0.74
1:A:190[B]:PHE:CE2	1:B:190[B]:PHE:HE2	2.04	0.74
1:A:190[C]:PHE:CE2	1:B:190[C]:PHE:HE2	2.04	0.74
1:A:190[D]:PHE:CE2	1:B:190[D]:PHE:HE2	2.04	0.74
1:E:44[A]:GLY:O	1:E:260[A]:ARG:HG2	1.88	0.74
1:E:44[B]:GLY:O	1:E:260[B]:ARG:HG2	1.88	0.74
1:E:44[C]:GLY:O	1:E:260[C]:ARG:HG2	1.88	0.74
1:E:44[D]:GLY:O	1:E:260[D]:ARG:HG2	1.88	0.74
1:E:190[A]:PHE:HE2	1:F:190[A]:PHE:CE2	2.06	0.74
1:E:190[B]:PHE:HE2	1:F:190[B]:PHE:CE2	2.06	0.74
1:E:190[C]:PHE:HE2	1:F:190[C]:PHE:CE2	2.06	0.74
1:E:190[D]:PHE:HE2	1:F:190[D]:PHE:CE2	2.06	0.74
1:A:190[A]:PHE:HE2	1:B:190[A]:PHE:CE2	2.06	0.73
1:A:190[B]:PHE:HE2	1:B:190[B]:PHE:CE2	2.06	0.73
1:A:190[C]:PHE:HE2	1:B:190[C]:PHE:CE2	2.06	0.73
1:A:190[D]:PHE:HE2	1:B:190[D]:PHE:CE2	2.06	0.73
1:C:190[A]:PHE:HE2	1:D:190[A]:PHE:CE2	2.06	0.73
1:C:190[B]:PHE:HE2	1:D:190[B]:PHE:CE2	2.06	0.73
1:C:190[C]:PHE:HE2	1:D:190[C]:PHE:CE2	2.06	0.73
1:C:190[D]:PHE:HE2	1:D:190[D]:PHE:CE2	2.06	0.73
1:C:190[A]:PHE:CE2	1:D:190[A]:PHE:HE2	2.05	0.73
1:C:190[B]:PHE:CE2	1:D:190[B]:PHE:HE2	2.05	0.73
1:C:190[C]:PHE:CE2	1:D:190[C]:PHE:HE2	2.05	0.73
1:C:190[D]:PHE:CE2	1:D:190[D]:PHE:HE2	2.05	0.73
1:K:22[A]:GLN:HE22	1:K:55[A]:ARG:H	1.37	0.72
1:I:22[A]:GLN:HE22	1:I:55[A]:ARG:H	1.38	0.72
1:N:22[B]:GLN:HE22	1:N:55[B]:ARG:H	1.37	0.72
1:N:22[D]:GLN:HE22	1:N:55[D]:ARG:H	1.36	0.72
1:H:201[C]:ASP:HB3	1:N:273[C]:GLU:CB	2.20	0.71
1:N:22[A]:GLN:HE22	1:N:55[A]:ARG:H	1.35	0.71
1:N:22[C]:GLN:HE22	1:N:55[C]:ARG:H	1.37	0.71
1:E:190[A]:PHE:CE2	1:F:190[A]:PHE:HE2	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:190[A]:PHE:CE2	1:H:190[A]:PHE:CE2	2.78	0.71
1:E:190[B]:PHE:CE2	1:F:190[B]:PHE:HE2	2.07	0.71
1:G:190[B]:PHE:CE2	1:H:190[B]:PHE:CE2	2.78	0.71
1:E:190[C]:PHE:CE2	1:F:190[C]:PHE:HE2	2.07	0.71
1:G:190[C]:PHE:CE2	1:H:190[C]:PHE:CE2	2.78	0.71
1:E:190[D]:PHE:CE2	1:F:190[D]:PHE:HE2	2.07	0.71
1:G:190[D]:PHE:CE2	1:H:190[D]:PHE:CE2	2.78	0.71
1:K:22[D]:GLN:HE22	1:K:55[D]:ARG:H	1.39	0.71
1:H:202[A]:SER:C	1:H:204[A]:GLY:N	2.42	0.71
1:H:202[B]:SER:C	1:H:204[B]:GLY:N	2.42	0.71
1:H:202[C]:SER:C	1:H:204[C]:GLY:N	2.42	0.71
1:H:202[D]:SER:C	1:H:204[D]:GLY:N	2.42	0.71
1:D:108[A]:GLU:HG3	4:D:1117[A]:HOH:O	1.89	0.71
1:G:107[A]:LYS:HD2	1:G:111[A]:GLU:HG3	1.73	0.71
1:D:108[B]:GLU:HG3	4:D:1117[B]:HOH:O	1.89	0.71
1:G:107[B]:LYS:HD2	1:G:111[B]:GLU:HG3	1.73	0.71
1:D:108[C]:GLU:HG3	4:D:1117[C]:HOH:O	1.89	0.71
1:G:107[C]:LYS:HD2	1:G:111[C]:GLU:HG3	1.73	0.71
1:D:108[D]:GLU:HG3	4:D:1117[D]:HOH:O	1.89	0.71
1:G:107[D]:LYS:HD2	1:G:111[D]:GLU:HG3	1.73	0.71
1:D:44[A]:GLY:O	1:D:260[A]:ARG:HG2	1.92	0.70
1:D:44[B]:GLY:O	1:D:260[B]:ARG:HG2	1.92	0.70
1:D:44[C]:GLY:O	1:D:260[C]:ARG:HG2	1.92	0.70
1:D:44[D]:GLY:O	1:D:260[D]:ARG:HG2	1.92	0.70
1:P:22[A]:GLN:HE22	1:P:55[A]:ARG:H	1.37	0.70
1:O:22[A]:GLN:HE22	1:O:55[A]:ARG:H	1.39	0.69
1:I:22[D]:GLN:HE22	1:I:55[D]:ARG:H	1.40	0.69
1:A:107[A]:LYS:HG3	1:A:111[A]:GLU:OE2	1.92	0.69
1:A:107[B]:LYS:HG3	1:A:111[B]:GLU:OE2	1.92	0.69
1:A:107[C]:LYS:HG3	1:A:111[C]:GLU:OE2	1.92	0.69
1:A:107[D]:LYS:HG3	1:A:111[D]:GLU:OE2	1.92	0.69
1:M:22[A]:GLN:HE22	1:M:55[A]:ARG:H	1.39	0.69
1:A:14[A]:SER:HB3	1:A:273[A]:GLU:OE1	1.91	0.69
1:J:22[A]:GLN:HE22	1:J:55[A]:ARG:H	1.38	0.69
1:A:14[B]:SER:HB3	1:A:273[B]:GLU:OE1	1.91	0.69
1:A:14[C]:SER:HB3	1:A:273[C]:GLU:OE1	1.91	0.69
1:A:14[D]:SER:HB3	1:A:273[D]:GLU:OE1	1.91	0.69
1:B:44[A]:GLY:O	1:B:260[A]:ARG:HG2	1.93	0.69
1:B:44[B]:GLY:O	1:B:260[B]:ARG:HG2	1.93	0.69
1:B:44[C]:GLY:O	1:B:260[C]:ARG:HG2	1.93	0.69
1:K:22[C]:GLN:HE22	1:K:55[C]:ARG:H	1.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44[D]:GLY:O	1:B:260[D]:ARG:HG2	1.93	0.69
1:K:22[B]:GLN:HE22	1:K:55[B]:ARG:H	1.41	0.69
1:I:22[C]:GLN:HE22	1:I:55[C]:ARG:H	1.41	0.68
1:I:22[B]:GLN:HE22	1:I:55[B]:ARG:H	1.41	0.68
1:F:44[A]:GLY:O	1:F:260[A]:ARG:HG2	1.94	0.68
1:F:44[B]:GLY:O	1:F:260[B]:ARG:HG2	1.94	0.68
1:F:44[C]:GLY:O	1:F:260[C]:ARG:HG2	1.94	0.68
1:F:44[D]:GLY:O	1:F:260[D]:ARG:HG2	1.94	0.68
1:F:14[A]:SER:HB3	1:F:273[A]:GLU:OE1	1.94	0.68
1:H:44[A]:GLY:O	1:H:260[A]:ARG:HG2	1.94	0.68
1:F:14[B]:SER:HB3	1:F:273[B]:GLU:OE1	1.94	0.68
1:H:44[B]:GLY:O	1:H:260[B]:ARG:HG2	1.94	0.68
1:F:14[C]:SER:HB3	1:F:273[C]:GLU:OE1	1.94	0.68
1:H:44[C]:GLY:O	1:H:260[C]:ARG:HG2	1.94	0.68
1:F:14[D]:SER:HB3	1:F:273[D]:GLU:OE1	1.94	0.68
1:H:44[D]:GLY:O	1:H:260[D]:ARG:HG2	1.94	0.68
1:J:47[D]:ALA:HB2	1:J:257[D]:HIS:HB3	1.76	0.68
1:J:47[C]:ALA:HB2	1:J:257[C]:HIS:HB3	1.76	0.68
1:E:286[A]:LYS:HA	4:E:529[A]:HOH:O	1.93	0.67
1:O:190[A]:PHE:CE2	1:P:190[A]:PHE:HE2	2.12	0.67
1:E:286[B]:LYS:HA	4:E:529[B]:HOH:O	1.93	0.67
1:E:286[C]:LYS:HA	4:E:529[C]:HOH:O	1.93	0.67
1:P:22[C]:GLN:HE22	1:P:55[C]:ARG:H	1.39	0.67
1:E:286[D]:LYS:HA	4:E:529[D]:HOH:O	1.93	0.67
1:A:190[A]:PHE:CE2	1:B:190[A]:PHE:CE2	2.80	0.67
1:A:190[B]:PHE:CE2	1:B:190[B]:PHE:CE2	2.80	0.67
1:A:190[C]:PHE:CE2	1:B:190[C]:PHE:CE2	2.80	0.67
1:A:190[D]:PHE:CE2	1:B:190[D]:PHE:CE2	2.80	0.67
1:J:47[B]:ALA:HB2	1:J:257[B]:HIS:HB3	1.76	0.67
1:O:47[B]:ALA:HB2	1:O:257[B]:HIS:HB3	1.77	0.67
1:C:190[A]:PHE:CE2	1:D:190[A]:PHE:CE2	2.81	0.67
1:E:190[A]:PHE:CE2	1:F:190[A]:PHE:CE2	2.83	0.67
1:C:190[B]:PHE:CE2	1:D:190[B]:PHE:CE2	2.81	0.67
1:E:190[B]:PHE:CE2	1:F:190[B]:PHE:CE2	2.83	0.67
1:P:22[B]:GLN:HE22	1:P:55[B]:ARG:H	1.40	0.67
1:C:190[C]:PHE:CE2	1:D:190[C]:PHE:CE2	2.81	0.67
1:E:190[C]:PHE:CE2	1:F:190[C]:PHE:CE2	2.83	0.67
1:C:190[D]:PHE:CE2	1:D:190[D]:PHE:CE2	2.81	0.67
1:E:190[D]:PHE:CE2	1:F:190[D]:PHE:CE2	2.83	0.67
1:O:47[C]:ALA:HB2	1:O:257[C]:HIS:HB3	1.78	0.66
1:M:22[D]:GLN:HE22	1:M:55[D]:ARG:H	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:118[A]:ARG:HD3	4:D:901[A]:HOH:O	1.96	0.66
1:D:118[B]:ARG:HD3	4:D:901[B]:HOH:O	1.96	0.66
1:D:118[C]:ARG:HD3	4:D:901[C]:HOH:O	1.96	0.66
1:D:118[D]:ARG:HD3	4:D:901[D]:HOH:O	1.96	0.66
1:O:47[D]:ALA:HB2	1:O:257[D]:HIS:HB3	1.78	0.66
1:M:22[B]:GLN:HE22	1:M:55[B]:ARG:H	1.42	0.66
1:P:22[D]:GLN:HE22	1:P:55[D]:ARG:H	1.41	0.66
1:H:200[C]:ALA:HB3	1:N:273[C]:GLU:OE2	1.96	0.66
1:B:118[A]:ARG:HD3	4:B:1013[A]:HOH:O	1.96	0.65
1:B:118[B]:ARG:HD3	4:B:1013[B]:HOH:O	1.96	0.65
1:B:118[C]:ARG:HD3	4:B:1013[C]:HOH:O	1.96	0.65
1:B:118[D]:ARG:HD3	4:B:1013[D]:HOH:O	1.96	0.65
1:M:47[D]:ALA:HB2	1:M:257[D]:HIS:HB3	1.78	0.65
1:H:201[A]:ASP:CG	1:H:202[A]:SER:N	2.50	0.65
1:H:201[B]:ASP:CG	1:H:202[B]:SER:N	2.50	0.65
1:H:201[C]:ASP:CG	1:H:202[C]:SER:N	2.50	0.65
1:H:201[D]:ASP:CG	1:H:202[D]:SER:N	2.50	0.65
1:G:44[A]:GLY:O	1:G:260[A]:ARG:HG2	1.97	0.65
1:H:14[A]:SER:HB3	1:H:273[A]:GLU:OE1	1.96	0.65
1:G:44[B]:GLY:O	1:G:260[B]:ARG:HG2	1.97	0.65
1:H:14[B]:SER:HB3	1:H:273[B]:GLU:OE1	1.96	0.65
1:G:44[C]:GLY:O	1:G:260[C]:ARG:HG2	1.97	0.65
1:H:14[C]:SER:HB3	1:H:273[C]:GLU:OE1	1.96	0.65
1:M:47[C]:ALA:HB2	1:M:257[C]:HIS:HB3	1.79	0.65
1:G:44[D]:GLY:O	1:G:260[D]:ARG:HG2	1.97	0.65
1:H:14[D]:SER:HB3	1:H:273[D]:GLU:OE1	1.96	0.65
1:A:44[A]:GLY:O	1:A:260[A]:ARG:HG2	1.96	0.65
1:K:190[A]:PHE:HE2	1:L:190[A]:PHE:HE2	1.44	0.65
1:A:44[B]:GLY:O	1:A:260[B]:ARG:HG2	1.96	0.65
1:A:44[C]:GLY:O	1:A:260[C]:ARG:HG2	1.96	0.65
1:M:22[C]:GLN:HE22	1:M:55[C]:ARG:H	1.43	0.65
1:A:44[D]:GLY:O	1:A:260[D]:ARG:HG2	1.96	0.65
1:C:107[A]:LYS:HG3	1:C:111[A]:GLU:OE2	1.97	0.65
1:C:107[B]:LYS:HG3	1:C:111[B]:GLU:OE2	1.97	0.65
1:C:107[C]:LYS:HG3	1:C:111[C]:GLU:OE2	1.97	0.65
1:C:107[D]:LYS:HG3	1:C:111[D]:GLU:OE2	1.97	0.65
1:D:43[A]:THR:HG21	1:D:316[A]:SER:OG	1.96	0.65
1:H:43[A]:THR:HG21	1:H:316[A]:SER:OG	1.97	0.65
1:O:190[A]:PHE:HE2	1:P:190[A]:PHE:CE2	2.15	0.65
1:D:43[B]:THR:HG21	1:D:316[B]:SER:OG	1.96	0.65
1:H:43[B]:THR:HG21	1:H:316[B]:SER:OG	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:47[B]:ALA:HB2	1:N:257[B]:HIS:HB3	1.78	0.65
1:D:43[C]:THR:HG21	1:D:316[C]:SER:OG	1.96	0.65
1:H:43[C]:THR:HG21	1:H:316[C]:SER:OG	1.97	0.65
1:N:47[C]:ALA:HB2	1:N:257[C]:HIS:HB3	1.77	0.65
1:D:43[D]:THR:HG21	1:D:316[D]:SER:OG	1.96	0.65
1:H:43[D]:THR:HG21	1:H:316[D]:SER:OG	1.97	0.65
1:I:50[C]:ALA:HB2	1:J:212[C]:LEU:HD12	1.79	0.65
1:I:50[D]:ALA:HB2	1:J:212[D]:LEU:HD12	1.79	0.65
1:N:47[D]:ALA:HB2	1:N:257[D]:HIS:HB3	1.78	0.64
1:B:14[A]:SER:HB3	1:B:273[A]:GLU:OE1	1.97	0.64
1:B:14[B]:SER:HB3	1:B:273[B]:GLU:OE1	1.97	0.64
1:M:47[B]:ALA:HB2	1:M:257[B]:HIS:HB3	1.79	0.64
1:B:14[C]:SER:HB3	1:B:273[C]:GLU:OE1	1.97	0.64
1:B:14[D]:SER:HB3	1:B:273[D]:GLU:OE1	1.97	0.64
1:N:269[B]:GLN:HB2	1:N:311[B]:ILE:CD1	2.28	0.64
1:J:22[C]:GLN:HE22	1:J:55[C]:ARG:H	1.43	0.64
1:J:22[B]:GLN:HE22	1:J:55[B]:ARG:H	1.43	0.64
1:H:201[C]:ASP:H	1:N:273[C]:GLU:CD	2.01	0.64
1:J:47[A]:ALA:HB2	1:J:257[A]:HIS:HB3	1.80	0.64
1:O:53[D]:SER:HB3	1:O:252[D]:GLN:NE2	2.12	0.64
1:O:190[A]:PHE:CE2	1:P:190[A]:PHE:CE2	2.86	0.64
1:F:43[A]:THR:HG21	1:F:316[A]:SER:OG	1.98	0.64
1:F:43[B]:THR:HG21	1:F:316[B]:SER:OG	1.98	0.64
1:F:43[C]:THR:HG21	1:F:316[C]:SER:OG	1.98	0.64
1:F:43[D]:THR:HG21	1:F:316[D]:SER:OG	1.98	0.64
1:N:269[D]:GLN:HB2	1:N:311[D]:ILE:CD1	2.28	0.64
1:B:43[A]:THR:HG21	1:B:316[A]:SER:OG	1.98	0.64
1:B:43[B]:THR:HG21	1:B:316[B]:SER:OG	1.98	0.64
1:B:43[C]:THR:HG21	1:B:316[C]:SER:OG	1.98	0.64
1:B:43[D]:THR:HG21	1:B:316[D]:SER:OG	1.98	0.64
1:H:269[A]:GLN:HB2	1:H:311[A]:ILE:CD1	2.28	0.63
1:H:269[B]:GLN:HB2	1:H:311[B]:ILE:CD1	2.28	0.63
1:L:47[B]:ALA:HB2	1:L:257[B]:HIS:HB3	1.80	0.63
1:H:269[C]:GLN:HB2	1:H:311[C]:ILE:CD1	2.28	0.63
1:I:269[C]:GLN:HB2	1:I:311[C]:ILE:CD1	2.28	0.63
1:H:269[D]:GLN:HB2	1:H:311[D]:ILE:CD1	2.28	0.63
1:K:53[D]:SER:HB3	1:K:252[D]:GLN:NE2	2.13	0.63
1:A:269[A]:GLN:HB2	1:A:311[A]:ILE:CD1	2.28	0.63
1:A:269[B]:GLN:HB2	1:A:311[B]:ILE:CD1	2.28	0.63
1:A:269[C]:GLN:HB2	1:A:311[C]:ILE:CD1	2.28	0.63
1:L:47[C]:ALA:HB2	1:L:257[C]:HIS:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269[D]:GLN:HB2	1:A:311[D]:ILE:CD1	2.28	0.63
1:I:269[D]:GLN:HB2	1:I:311[D]:ILE:CD1	2.28	0.63
1:I:50[B]:ALA:HB2	1:J:212[B]:LEU:HD12	1.80	0.63
1:K:53[B]:SER:HB3	1:K:252[B]:GLN:NE2	2.14	0.63
1:O:53[B]:SER:HB3	1:O:252[B]:GLN:NE2	2.13	0.63
1:I:47[C]:ALA:HB2	1:I:257[C]:HIS:HB3	1.81	0.63
1:F:289[A]:ILE:HB	4:F:534[A]:HOH:O	1.98	0.63
1:F:289[B]:ILE:HB	4:F:534[B]:HOH:O	1.98	0.63
1:F:289[C]:ILE:HB	4:F:534[C]:HOH:O	1.98	0.63
1:O:53[C]:SER:HB3	1:O:252[C]:GLN:NE2	2.13	0.63
1:F:289[D]:ILE:HB	4:F:534[D]:HOH:O	1.98	0.63
1:A:297[A]:VAL:HG23	4:A:546[A]:HOH:O	1.99	0.63
1:J:44[A]:GLY:O	1:J:260[A]:ARG:HG2	1.98	0.63
1:A:297[B]:VAL:HG23	4:A:546[B]:HOH:O	1.99	0.63
1:A:297[C]:VAL:HG23	4:A:546[C]:HOH:O	1.99	0.63
1:N:269[C]:GLN:HB2	1:N:311[C]:ILE:CD1	2.29	0.63
1:A:297[D]:VAL:HG23	4:A:546[D]:HOH:O	1.99	0.63
1:L:47[D]:ALA:HB2	1:L:257[D]:HIS:HB3	1.81	0.63
1:C:269[A]:GLN:HB2	1:C:311[A]:ILE:CD1	2.28	0.63
1:C:44[A]:GLY:O	1:C:260[A]:ARG:HG2	1.99	0.63
1:N:269[A]:GLN:HB2	1:N:311[A]:ILE:CD1	2.29	0.63
1:C:269[B]:GLN:HB2	1:C:311[B]:ILE:CD1	2.28	0.63
1:C:44[B]:GLY:O	1:C:260[B]:ARG:HG2	1.99	0.63
1:I:269[B]:GLN:HB2	1:I:311[B]:ILE:CD1	2.28	0.63
1:C:44[C]:GLY:O	1:C:260[C]:ARG:HG2	1.99	0.63
1:C:269[C]:GLN:HB2	1:C:311[C]:ILE:CD1	2.28	0.63
1:C:269[D]:GLN:HB2	1:C:311[D]:ILE:CD1	2.28	0.63
1:C:44[D]:GLY:O	1:C:260[D]:ARG:HG2	1.99	0.63
1:H:201[C]:ASP:HB3	1:N:273[C]:GLU:CD	2.18	0.63
1:I:47[D]:ALA:HB2	1:I:257[D]:HIS:HB3	1.81	0.63
1:J:22[D]:GLN:HE22	1:J:55[D]:ARG:H	1.45	0.62
1:M:44[A]:GLY:O	1:M:260[A]:ARG:HG2	1.99	0.62
1:P:44[A]:GLY:O	1:P:260[A]:ARG:HG2	1.99	0.62
1:I:47[B]:ALA:HB2	1:I:257[B]:HIS:HB3	1.81	0.62
1:K:190[A]:PHE:HE2	1:L:190[A]:PHE:CE2	2.18	0.62
1:M:190[A]:PHE:HE2	1:N:190[A]:PHE:HE2	1.46	0.62
1:O:22[B]:GLN:HE22	1:O:55[B]:ARG:H	1.45	0.62
1:L:53[C]:SER:HB3	1:L:252[C]:GLN:NE2	2.15	0.62
1:I:190[A]:PHE:HE2	1:J:190[A]:PHE:HE2	1.46	0.62
1:O:190[B]:PHE:CE2	1:P:190[B]:PHE:HE2	2.18	0.62
1:P:47[B]:ALA:HB2	1:P:257[B]:HIS:HB3	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:212[C]:LEU:HD12	1:L:50[C]:ALA:HB2	1.80	0.62
1:I:269[A]:GLN:HB2	1:I:311[A]:ILE:CD1	2.29	0.62
1:M:44[D]:GLY:O	1:M:260[D]:ARG:HG2	1.99	0.62
1:N:44[A]:GLY:O	1:N:260[A]:ARG:HG2	2.00	0.62
1:L:53[B]:SER:HB3	1:L:252[B]:GLN:NE2	2.15	0.62
1:P:47[C]:ALA:HB2	1:P:257[C]:HIS:HB3	1.80	0.62
1:O:190[D]:PHE:CE2	1:P:190[D]:PHE:HE2	2.18	0.62
1:I:50[A]:ALA:HB2	1:J:212[A]:LEU:HD12	1.82	0.62
1:L:44[A]:GLY:O	1:L:260[A]:ARG:HG2	2.00	0.62
1:K:212[B]:LEU:HD12	1:L:50[B]:ALA:HB2	1.80	0.62
1:M:212[C]:LEU:HD12	1:N:50[C]:ALA:HB2	1.81	0.62
1:M:44[C]:GLY:O	1:M:260[C]:ARG:HG2	1.99	0.62
1:O:269[C]:GLN:HB2	1:O:311[C]:ILE:CD1	2.29	0.62
1:O:269[D]:GLN:HB2	1:O:311[D]:ILE:CD1	2.29	0.62
1:O:22[D]:GLN:HE22	1:O:55[D]:ARG:H	1.45	0.62
1:G:117[A]:HIS:HD2	4:G:1338[A]:HOH:O	1.83	0.62
1:O:190[A]:PHE:HE2	1:P:190[A]:PHE:HE2	1.44	0.62
1:G:117[B]:HIS:HD2	4:G:1338[B]:HOH:O	1.83	0.62
1:G:117[C]:HIS:HD2	4:G:1338[C]:HOH:O	1.83	0.62
1:O:22[C]:GLN:HE22	1:O:55[C]:ARG:H	1.45	0.62
1:G:117[D]:HIS:HD2	4:G:1338[D]:HOH:O	1.83	0.62
1:C:201[A]:ASP:O	1:C:202[A]:SER:HB3	2.00	0.61
1:I:190[A]:PHE:HE2	1:J:190[A]:PHE:CE2	2.18	0.61
1:M:190[A]:PHE:HE2	1:N:190[A]:PHE:CE2	2.18	0.61
1:C:201[B]:ASP:O	1:C:202[B]:SER:HB3	2.00	0.61
1:C:201[C]:ASP:O	1:C:202[C]:SER:HB3	2.00	0.61
1:O:190[C]:PHE:CE2	1:P:190[C]:PHE:HE2	2.18	0.61
1:C:201[D]:ASP:O	1:C:202[D]:SER:HB3	2.00	0.61
1:M:190[A]:PHE:CE2	1:N:190[A]:PHE:HE2	2.19	0.61
1:O:269[A]:GLN:HB2	1:O:311[A]:ILE:CD1	2.30	0.61
1:J:44[B]:GLY:O	1:J:260[B]:ARG:HG2	2.00	0.61
1:J:53[B]:SER:HB3	1:J:252[B]:GLN:NE2	2.15	0.61
1:D:269[A]:GLN:HB2	1:D:311[A]:ILE:CD1	2.30	0.61
1:G:269[A]:GLN:HB2	1:G:311[A]:ILE:CD1	2.29	0.61
1:K:190[A]:PHE:CE2	1:L:190[A]:PHE:HE2	2.16	0.61
1:K:44[A]:GLY:O	1:K:260[A]:ARG:HG2	2.00	0.61
1:D:269[B]:GLN:HB2	1:D:311[B]:ILE:CD1	2.30	0.61
1:G:269[B]:GLN:HB2	1:G:311[B]:ILE:CD1	2.29	0.61
1:D:269[C]:GLN:HB2	1:D:311[C]:ILE:CD1	2.30	0.61
1:G:269[C]:GLN:HB2	1:G:311[C]:ILE:CD1	2.29	0.61
1:J:44[C]:GLY:O	1:J:260[C]:ARG:HG2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:53[C]:SER:HB3	1:K:252[C]:GLN:NE2	2.15	0.61
1:D:269[D]:GLN:HB2	1:D:311[D]:ILE:CD1	2.30	0.61
1:G:269[D]:GLN:HB2	1:G:311[D]:ILE:CD1	2.29	0.61
1:I:190[A]:PHE:CE2	1:J:190[A]:PHE:HE2	2.17	0.61
1:O:47[A]:ALA:HB2	1:O:257[A]:HIS:HB3	1.83	0.61
1:L:53[D]:SER:HB3	1:L:252[D]:GLN:NE2	2.16	0.61
1:M:212[D]:LEU:HD12	1:N:50[D]:ALA:HB2	1.81	0.61
1:P:269[A]:GLN:HB2	1:P:311[A]:ILE:CD1	2.31	0.61
1:O:269[B]:GLN:HB2	1:O:311[B]:ILE:CD1	2.30	0.61
1:K:212[D]:LEU:HD12	1:L:50[D]:ALA:HB2	1.81	0.61
1:K:269[A]:GLN:HB2	1:K:311[A]:ILE:CD1	2.30	0.61
1:N:44[B]:GLY:O	1:N:260[B]:ARG:HG2	2.01	0.61
1:J:44[D]:GLY:O	1:J:260[D]:ARG:HG2	2.00	0.61
1:P:47[D]:ALA:HB2	1:P:257[D]:HIS:HB3	1.81	0.61
1:L:269[A]:GLN:HB2	1:L:311[A]:ILE:CD1	2.31	0.61
1:M:269[B]:GLN:HB2	1:M:311[B]:ILE:CD1	2.30	0.61
1:P:269[C]:GLN:HB2	1:P:311[C]:ILE:CD1	2.31	0.61
1:L:219[D]:ASP:HB2	2:L:500[D]:UMP:O3'	2.01	0.61
1:P:269[B]:GLN:HB2	1:P:311[B]:ILE:CD1	2.31	0.61
1:I:118[C]:ARG:HD2	1:I:122[C]:ASP:OD2	2.00	0.61
1:N:44[C]:GLY:O	1:N:260[C]:ARG:HG2	2.01	0.61
1:J:269[A]:GLN:HB2	1:J:311[A]:ILE:CD1	2.31	0.60
1:M:269[A]:GLN:HB2	1:M:311[A]:ILE:CD1	2.30	0.60
1:I:118[B]:ARG:HD2	1:I:122[B]:ASP:OD2	2.00	0.60
1:K:212[A]:LEU:HD12	1:L:50[A]:ALA:HB2	1.82	0.60
1:L:44[B]:GLY:O	1:L:260[B]:ARG:HG2	2.01	0.60
1:J:53[C]:SER:HB3	1:J:252[C]:GLN:NE2	2.16	0.60
1:M:269[C]:GLN:HB2	1:M:311[C]:ILE:CD1	2.31	0.60
1:P:269[D]:GLN:HB2	1:P:311[D]:ILE:CD1	2.32	0.60
1:L:219[A]:ASP:HB2	2:L:500[A]:UMP:O3'	2.01	0.60
1:I:118[D]:ARG:HD2	1:I:122[D]:ASP:OD2	2.00	0.60
1:J:53[D]:SER:HB3	1:J:252[D]:GLN:NE2	2.16	0.60
1:M:44[B]:GLY:O	1:M:260[B]:ARG:HG2	2.01	0.60
1:F:118[A]:ARG:HD3	4:F:1070[A]:HOH:O	2.01	0.60
1:F:118[B]:ARG:HD3	4:F:1070[B]:HOH:O	2.01	0.60
1:F:118[C]:ARG:HD3	4:F:1070[C]:HOH:O	2.01	0.60
1:F:118[D]:ARG:HD3	4:F:1070[D]:HOH:O	2.01	0.60
1:O:190[D]:PHE:HE2	1:P:190[D]:PHE:CE2	2.20	0.60
1:L:269[B]:GLN:HB2	1:L:311[B]:ILE:CD1	2.31	0.60
1:L:219[B]:ASP:HB2	2:L:500[B]:UMP:O3'	2.01	0.60
1:J:269[C]:GLN:HB2	1:J:311[C]:ILE:CD1	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:44[C]:GLY:O	1:L:260[C]:ARG:HG2	2.02	0.60
1:M:269[D]:GLN:HB2	1:M:311[D]:ILE:CD1	2.31	0.60
1:M:212[A]:LEU:HD12	1:N:50[A]:ALA:HB2	1.83	0.60
1:O:44[A]:GLY:O	1:O:260[A]:ARG:HG2	2.01	0.60
1:J:269[B]:GLN:HB2	1:J:311[B]:ILE:CD1	2.31	0.60
1:L:269[C]:GLN:HB2	1:L:311[C]:ILE:CD1	2.32	0.60
1:K:269[D]:GLN:HB2	1:K:311[D]:ILE:CD1	2.31	0.60
1:L:44[D]:GLY:O	1:L:260[D]:ARG:HG2	2.02	0.60
1:K:53[A]:SER:HB3	1:K:252[A]:GLN:NE2	2.17	0.60
1:M:47[A]:ALA:HB2	1:M:257[A]:HIS:HB3	1.84	0.60
1:P:44[B]:GLY:O	1:P:260[B]:ARG:HG2	2.02	0.60
1:J:219[D]:ASP:HB2	2:J:400[D]:UMP:O3'	2.02	0.60
1:J:269[D]:GLN:HB2	1:J:311[D]:ILE:CD1	2.32	0.60
1:C:14[A]:SER:HB3	1:C:273[A]:GLU:OE1	2.02	0.60
1:E:269[A]:GLN:HB2	1:E:311[A]:ILE:CD1	2.31	0.60
1:C:14[B]:SER:HB3	1:C:273[B]:GLU:OE1	2.02	0.60
1:E:269[B]:GLN:HB2	1:E:311[B]:ILE:CD1	2.31	0.60
1:K:269[B]:GLN:HB2	1:K:311[B]:ILE:CD1	2.32	0.60
1:M:212[B]:LEU:HD12	1:N:50[B]:ALA:HB2	1.83	0.60
1:M:50[B]:ALA:HB2	1:N:212[B]:LEU:HD12	1.83	0.60
1:C:14[C]:SER:HB3	1:C:273[C]:GLU:OE1	2.02	0.60
1:E:269[C]:GLN:HB2	1:E:311[C]:ILE:CD1	2.31	0.60
1:C:14[D]:SER:HB3	1:C:273[D]:GLU:OE1	2.02	0.60
1:E:269[D]:GLN:HB2	1:E:311[D]:ILE:CD1	2.31	0.60
1:F:212[A]:LEU:C	1:F:212[A]:LEU:HD23	2.22	0.59
1:O:53[A]:SER:HB3	1:O:252[A]:GLN:NE2	2.17	0.59
1:F:212[B]:LEU:HD23	1:F:212[B]:LEU:C	2.22	0.59
1:I:44[B]:GLY:O	1:I:260[B]:ARG:HG2	2.02	0.59
1:J:219[B]:ASP:HB2	2:J:400[B]:UMP:O3'	2.02	0.59
1:F:212[C]:LEU:C	1:F:212[C]:LEU:HD23	2.22	0.59
1:H:201[C]:ASP:N	1:N:273[C]:GLU:OE2	2.35	0.59
1:F:212[D]:LEU:C	1:F:212[D]:LEU:HD23	2.22	0.59
1:F:269[A]:GLN:HB2	1:F:311[A]:ILE:CD1	2.32	0.59
1:F:30[A]:ILE:HG22	1:F:46[A]:VAL:HG13	1.84	0.59
1:L:47[A]:ALA:HB2	1:L:257[A]:HIS:HB3	1.85	0.59
1:F:269[B]:GLN:HB2	1:F:311[B]:ILE:CD1	2.32	0.59
1:F:30[B]:ILE:HG22	1:F:46[B]:VAL:HG13	1.84	0.59
1:F:269[C]:GLN:HB2	1:F:311[C]:ILE:CD1	2.32	0.59
1:F:30[C]:ILE:HG22	1:F:46[C]:VAL:HG13	1.84	0.59
1:F:269[D]:GLN:HB2	1:F:311[D]:ILE:CD1	2.32	0.59
1:F:30[D]:ILE:HG22	1:F:46[D]:VAL:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246[A]:PRO:HG2	4:B:864[A]:HOH:O	2.03	0.59
1:I:190[A]:PHE:CE2	1:J:190[A]:PHE:CE2	2.90	0.59
1:K:190[A]:PHE:CE2	1:L:190[A]:PHE:CE2	2.90	0.59
1:B:246[B]:PRO:HG2	4:B:864[B]:HOH:O	2.03	0.59
1:O:190[B]:PHE:CE2	1:P:190[B]:PHE:CE2	2.90	0.59
1:B:246[C]:PRO:HG2	4:B:864[C]:HOH:O	2.03	0.59
1:L:219[C]:ASP:HB2	2:L:500[C]:UMP:O3'	2.02	0.59
1:B:246[D]:PRO:HG2	4:B:864[D]:HOH:O	2.03	0.59
1:O:190[D]:PHE:CE2	1:P:190[D]:PHE:CE2	2.90	0.59
1:O:190[B]:PHE:HE2	1:P:190[B]:PHE:CE2	2.21	0.59
1:N:44[D]:GLY:O	1:N:260[D]:ARG:HG2	2.03	0.59
1:D:246[A]:PRO:HG2	4:D:936[A]:HOH:O	2.02	0.59
1:N:47[A]:ALA:HB2	1:N:257[A]:HIS:HB3	1.83	0.59
1:P:47[A]:ALA:HB2	1:P:257[A]:HIS:HB3	1.84	0.59
1:D:246[B]:PRO:HG2	4:D:936[B]:HOH:O	2.02	0.59
1:D:246[C]:PRO:HG2	4:D:936[C]:HOH:O	2.02	0.59
1:K:190[C]:PHE:HE2	1:L:190[C]:PHE:HE2	1.50	0.59
1:K:269[C]:GLN:HB2	1:K:311[C]:ILE:CD1	2.32	0.59
1:K:44[C]:GLY:O	1:K:260[C]:ARG:HG2	2.02	0.59
1:D:246[D]:PRO:HG2	4:D:936[D]:HOH:O	2.02	0.59
1:F:246[A]:PRO:HG2	4:F:1320[A]:HOH:O	2.02	0.59
1:J:219[A]:ASP:HB2	2:J:400[A]:UMP:O3'	2.03	0.59
1:F:246[B]:PRO:HG2	4:F:1320[B]:HOH:O	2.02	0.59
1:K:190[B]:PHE:HE2	1:L:190[B]:PHE:HE2	1.50	0.59
1:F:246[C]:PRO:HG2	4:F:1320[C]:HOH:O	2.02	0.59
1:M:190[C]:PHE:HE2	1:N:190[C]:PHE:CE2	2.21	0.59
1:F:246[D]:PRO:HG2	4:F:1320[D]:HOH:O	2.02	0.59
1:I:47[A]:ALA:HB2	1:I:257[A]:HIS:HB3	1.85	0.59
1:I:44[A]:GLY:O	1:I:260[A]:ARG:HG2	2.02	0.59
1:O:190[C]:PHE:CE2	1:P:190[C]:PHE:CE2	2.91	0.59
1:M:50[D]:ALA:HB2	1:N:212[D]:LEU:HD12	1.84	0.59
1:P:44[D]:GLY:O	1:P:260[D]:ARG:HG2	2.03	0.59
1:L:53[A]:SER:HB3	1:L:252[A]:GLN:NE2	2.18	0.59
1:I:53[B]:SER:HB3	1:I:252[B]:GLN:NE2	2.17	0.59
1:O:190[C]:PHE:HE2	1:P:190[C]:PHE:CE2	2.21	0.59
1:C:43[A]:THR:HG21	1:C:316[A]:SER:OG	2.02	0.59
1:F:117[A]:HIS:HD2	4:F:1306[A]:HOH:O	1.84	0.59
1:C:43[B]:THR:HG21	1:C:316[B]:SER:OG	2.02	0.59
1:F:117[B]:HIS:HD2	4:F:1306[B]:HOH:O	1.84	0.59
1:C:43[C]:THR:HG21	1:C:316[C]:SER:OG	2.02	0.59
1:F:117[C]:HIS:HD2	4:F:1306[C]:HOH:O	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43[D]:THR:HG21	1:C:316[D]:SER:OG	2.02	0.59
1:F:117[D]:HIS:HD2	4:F:1306[D]:HOH:O	1.84	0.59
1:A:289[A]:ILE:HB	4:A:551[A]:HOH:O	2.02	0.59
1:A:289[B]:ILE:HB	4:A:551[B]:HOH:O	2.02	0.59
1:K:44[B]:GLY:O	1:K:260[B]:ARG:HG2	2.03	0.59
1:A:289[C]:ILE:HB	4:A:551[C]:HOH:O	2.02	0.59
1:M:190[C]:PHE:HE2	1:N:190[C]:PHE:HE2	1.49	0.59
1:M:50[C]:ALA:HB2	1:N:212[C]:LEU:HD12	1.84	0.59
1:N:118[C]:ARG:HD2	1:N:122[C]:ASP:OD2	2.02	0.59
1:A:289[D]:ILE:HB	4:A:551[D]:HOH:O	2.02	0.59
1:M:190[D]:PHE:HE2	1:N:190[D]:PHE:CE2	2.21	0.59
1:J:219[C]:ASP:HB2	2:J:400[C]:UMP:O3'	2.03	0.58
1:O:219[D]:ASP:HB2	2:O:650[D]:UMP:O3'	2.03	0.58
1:B:269[A]:GLN:HB2	1:B:311[A]:ILE:CD1	2.33	0.58
1:B:269[B]:GLN:HB2	1:B:311[B]:ILE:CD1	2.33	0.58
1:B:269[C]:GLN:HB2	1:B:311[C]:ILE:CD1	2.33	0.58
1:B:269[D]:GLN:HB2	1:B:311[D]:ILE:CD1	2.33	0.58
1:K:190[D]:PHE:HE2	1:L:190[D]:PHE:HE2	1.51	0.58
1:N:43[A]:THR:HG21	1:N:316[A]:SER:OG	2.03	0.58
1:O:118[B]:ARG:HD2	1:O:122[B]:ASP:OD2	2.03	0.58
1:I:53[C]:SER:HB3	1:I:252[C]:GLN:NE2	2.17	0.58
1:K:44[D]:GLY:O	1:K:260[D]:ARG:HG2	2.03	0.58
1:O:44[B]:GLY:O	1:O:260[B]:ARG:HG2	2.03	0.58
1:M:190[C]:PHE:CE2	1:N:190[C]:PHE:HE2	2.22	0.58
1:O:219[C]:ASP:HB2	2:O:650[C]:UMP:O3'	2.03	0.58
1:I:44[D]:GLY:O	1:I:260[D]:ARG:HG2	2.03	0.58
1:M:190[D]:PHE:CE2	1:N:190[D]:PHE:HE2	2.22	0.58
1:M:190[D]:PHE:HE2	1:N:190[D]:PHE:HE2	1.50	0.58
1:K:50[B]:ALA:HB2	1:L:212[B]:LEU:HD12	1.85	0.58
1:I:250[C]:ILE:HD12	1:I:250[C]:ILE:N	2.19	0.58
1:K:118[C]:ARG:HD2	1:K:122[C]:ASP:OD2	2.03	0.58
1:L:269[D]:GLN:HB2	1:L:311[D]:ILE:CD1	2.33	0.58
1:O:219[B]:ASP:HB2	2:O:650[B]:UMP:O3'	2.04	0.58
1:A:43[A]:THR:HG21	1:A:316[A]:SER:OG	2.03	0.58
1:A:43[B]:THR:HG21	1:A:316[B]:SER:OG	2.03	0.58
1:A:43[C]:THR:HG21	1:A:316[C]:SER:OG	2.03	0.58
1:O:44[C]:GLY:O	1:O:260[C]:ARG:HG2	2.02	0.58
1:A:43[D]:THR:HG21	1:A:316[D]:SER:OG	2.03	0.58
1:N:118[D]:ARG:HD2	1:N:122[D]:ASP:OD2	2.03	0.58
1:M:190[B]:PHE:HE2	1:N:190[B]:PHE:CE2	2.22	0.58
1:N:118[B]:ARG:HD2	1:N:122[B]:ASP:OD2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:201[C]:ASP:HB3	1:N:273[C]:GLU:HB3	1.84	0.58
1:O:118[C]:ARG:HD2	1:O:122[C]:ASP:OD2	2.03	0.58
1:I:250[D]:ILE:HD12	1:I:250[D]:ILE:N	2.19	0.58
1:M:118[B]:ARG:HD2	1:M:122[B]:ASP:OD2	2.04	0.58
1:M:190[B]:PHE:CE2	1:N:190[B]:PHE:HE2	2.22	0.58
1:J:53[A]:SER:HB3	1:J:252[A]:GLN:NE2	2.19	0.57
1:O:219[A]:ASP:HB2	2:O:650[A]:UMP:O3'	2.04	0.57
1:K:118[D]:ARG:HD2	1:K:122[D]:ASP:OD2	2.04	0.57
1:I:190[B]:PHE:CE2	1:J:190[B]:PHE:HE2	2.21	0.57
1:I:250[B]:ILE:HD12	1:I:250[B]:ILE:N	2.20	0.57
1:M:118[C]:ARG:HD2	1:M:122[C]:ASP:OD2	2.04	0.57
1:K:50[D]:ALA:HB2	1:L:212[D]:LEU:HD12	1.86	0.57
1:K:47[B]:ALA:HB2	1:K:257[B]:HIS:HB3	1.87	0.57
1:I:44[C]:GLY:O	1:I:260[C]:ARG:HG2	2.04	0.57
1:O:220[C]:LEU:HG	1:O:224[C]:VAL:HG21	1.86	0.57
1:I:53[D]:SER:HB3	1:I:252[D]:GLN:NE2	2.18	0.57
1:F:297[A]:VAL:HG23	4:F:740[A]:HOH:O	2.03	0.57
1:F:297[B]:VAL:HG23	4:F:740[B]:HOH:O	2.03	0.57
1:F:297[C]:VAL:HG23	4:F:740[C]:HOH:O	2.03	0.57
1:K:50[C]:ALA:HB2	1:L:212[C]:LEU:HD12	1.86	0.57
1:F:297[D]:VAL:HG23	4:F:740[D]:HOH:O	2.03	0.57
1:I:190[D]:PHE:CE2	1:J:190[D]:PHE:HE2	2.21	0.57
1:M:118[D]:ARG:HD2	1:M:122[D]:ASP:OD2	2.04	0.57
1:M:190[B]:PHE:HE2	1:N:190[B]:PHE:HE2	1.51	0.57
1:I:190[C]:PHE:CE2	1:J:190[C]:PHE:HE2	2.21	0.57
1:K:190[C]:PHE:HE2	1:L:190[C]:PHE:CE2	2.23	0.57
1:M:190[A]:PHE:CE2	1:N:190[A]:PHE:CE2	2.92	0.57
1:F:132[A]:ARG:NH1	1:F:293[A]:ASP:OD1	2.38	0.57
1:G:246[A]:PRO:HG2	4:G:412[A]:HOH:O	2.05	0.57
1:F:132[B]:ARG:NH1	1:F:293[B]:ASP:OD1	2.38	0.57
1:G:246[B]:PRO:HG2	4:G:412[B]:HOH:O	2.05	0.57
1:I:190[B]:PHE:HE2	1:J:190[B]:PHE:HE2	1.52	0.57
1:F:132[C]:ARG:NH1	1:F:293[C]:ASP:OD1	2.38	0.57
1:G:246[C]:PRO:HG2	4:G:412[C]:HOH:O	2.05	0.57
1:P:44[C]:GLY:O	1:P:260[C]:ARG:HG2	2.05	0.57
1:F:132[D]:ARG:NH1	1:F:293[D]:ASP:OD1	2.38	0.57
1:G:246[D]:PRO:HG2	4:G:412[D]:HOH:O	2.05	0.57
1:H:212[A]:LEU:HD23	1:H:212[A]:LEU:C	2.25	0.57
1:H:212[B]:LEU:C	1:H:212[B]:LEU:HD23	2.25	0.57
1:K:118[B]:ARG:HD2	1:K:122[B]:ASP:OD2	2.05	0.57
1:H:212[C]:LEU:HD23	1:H:212[C]:LEU:C	2.25	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:212[D]:LEU:C	1:H:212[D]:LEU:HD23	2.25	0.57
1:N:43[D]:THR:HG21	1:N:316[D]:SER:OG	2.05	0.57
1:P:53[B]:SER:HB3	1:P:252[B]:GLN:NE2	2.19	0.57
1:P:53[C]:SER:HB3	1:P:252[C]:GLN:NE2	2.19	0.57
1:O:44[D]:GLY:O	1:O:260[D]:ARG:HG2	2.04	0.57
1:K:190[B]:PHE:HE2	1:L:190[B]:PHE:CE2	2.23	0.56
1:K:190[C]:PHE:CE2	1:L:190[C]:PHE:HE2	2.21	0.56
1:K:47[C]:ALA:HB2	1:K:257[C]:HIS:HB3	1.87	0.56
1:K:250[D]:ILE:HD12	1:K:250[D]:ILE:N	2.20	0.56
1:O:190[D]:PHE:HE2	1:P:190[D]:PHE:HE2	1.50	0.56
1:J:43[A]:THR:HG21	1:J:316[A]:SER:OG	2.06	0.56
1:L:43[A]:THR:HG21	1:L:316[A]:SER:OG	2.05	0.56
1:K:190[B]:PHE:CE2	1:L:190[B]:PHE:HE2	2.21	0.56
1:L:250[B]:ILE:N	1:L:250[B]:ILE:HD12	2.20	0.56
1:N:43[B]:THR:HG21	1:N:316[B]:SER:OG	2.05	0.56
1:N:219[C]:ASP:HB2	2:N:600[C]:UMP:O3'	2.05	0.56
1:K:190[D]:PHE:HE2	1:L:190[D]:PHE:CE2	2.23	0.56
1:D:30[A]:ILE:HG22	1:D:46[A]:VAL:HG13	1.86	0.56
1:E:53[A]:SER:HB3	1:E:252[A]:GLN:NE2	2.20	0.56
1:C:165[A]:THR:HG21	1:D:38[A]:PRO:HD2	1.88	0.56
1:D:30[B]:ILE:HG22	1:D:46[B]:VAL:HG13	1.86	0.56
1:E:53[B]:SER:HB3	1:E:252[B]:GLN:NE2	2.20	0.56
1:C:165[B]:THR:HG21	1:D:38[B]:PRO:HD2	1.88	0.56
1:K:250[B]:ILE:N	1:K:250[B]:ILE:HD12	2.21	0.56
1:D:30[C]:ILE:HG22	1:D:46[C]:VAL:HG13	1.86	0.56
1:E:53[C]:SER:HB3	1:E:252[C]:GLN:NE2	2.20	0.56
1:C:165[C]:THR:HG21	1:D:38[C]:PRO:HD2	1.88	0.56
1:J:118[C]:ARG:HD2	1:J:122[C]:ASP:OD2	2.05	0.56
1:D:30[D]:ILE:HG22	1:D:46[D]:VAL:HG13	1.86	0.56
1:E:53[D]:SER:HB3	1:E:252[D]:GLN:NE2	2.20	0.56
1:O:118[D]:ARG:HD2	1:O:122[D]:ASP:OD2	2.05	0.56
1:C:165[D]:THR:HG21	1:D:38[D]:PRO:HD2	1.88	0.56
1:I:190[D]:PHE:HE2	1:J:190[D]:PHE:HE2	1.52	0.56
1:P:53[D]:SER:HB3	1:P:252[D]:GLN:NE2	2.19	0.56
1:H:30[A]:ILE:HG22	1:H:46[A]:VAL:HG13	1.87	0.56
1:H:30[B]:ILE:HG22	1:H:46[B]:VAL:HG13	1.87	0.56
1:I:190[B]:PHE:HE2	1:J:190[B]:PHE:CE2	2.24	0.56
1:H:30[C]:ILE:HG22	1:H:46[C]:VAL:HG13	1.87	0.56
1:H:30[D]:ILE:HG22	1:H:46[D]:VAL:HG13	1.87	0.56
1:K:47[D]:ALA:HB2	1:K:257[D]:HIS:HB3	1.88	0.56
1:K:190[D]:PHE:CE2	1:L:190[D]:PHE:HE2	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165[A]:THR:HG21	1:F:38[A]:PRO:HD2	1.87	0.56
1:E:165[B]:THR:HG21	1:F:38[B]:PRO:HD2	1.87	0.56
1:O:250[B]:ILE:N	1:O:250[B]:ILE:HD12	2.21	0.56
1:E:165[C]:THR:HG21	1:F:38[C]:PRO:HD2	1.87	0.56
1:I:190[C]:PHE:HE2	1:J:190[C]:PHE:HE2	1.53	0.56
1:M:250[C]:ILE:N	1:M:250[C]:ILE:HD12	2.21	0.56
1:E:165[D]:THR:HG21	1:F:38[D]:PRO:HD2	1.87	0.56
1:I:190[D]:PHE:HE2	1:J:190[D]:PHE:CE2	2.24	0.56
1:N:219[B]:ASP:HB2	2:N:600[B]:UMP:O3'	2.06	0.56
1:O:190[B]:PHE:HE2	1:P:190[B]:PHE:HE2	1.51	0.56
1:K:50[A]:ALA:HB2	1:L:212[A]:LEU:HD12	1.88	0.56
1:L:250[C]:ILE:HD12	1:L:250[C]:ILE:N	2.21	0.56
1:O:250[C]:ILE:N	1:O:250[C]:ILE:HD12	2.21	0.56
1:L:109[D]:PHE:O	1:L:112[D]:LYS:HB3	2.06	0.56
1:I:53[A]:SER:HB3	1:I:252[A]:GLN:NE2	2.20	0.56
1:J:118[B]:ARG:HD2	1:J:122[B]:ASP:OD2	2.06	0.56
1:I:190[C]:PHE:HE2	1:J:190[C]:PHE:CE2	2.24	0.56
1:K:47[A]:ALA:HB2	1:K:257[A]:HIS:HB3	1.88	0.56
1:O:220[B]:LEU:HG	1:O:224[B]:VAL:HG21	1.88	0.56
1:K:250[C]:ILE:HD12	1:K:250[C]:ILE:N	2.21	0.56
1:N:250[C]:ILE:HD12	1:N:250[C]:ILE:N	2.21	0.56
1:K:190[C]:PHE:CE2	1:L:190[C]:PHE:CE2	2.94	0.55
1:K:134[D]:PHE:CZ	1:L:176[D]:PRO:HD2	2.42	0.55
1:O:250[D]:ILE:HD12	1:O:250[D]:ILE:N	2.21	0.55
1:K:134[C]:PHE:CZ	1:L:176[C]:PRO:HD2	2.41	0.55
1:O:212[C]:LEU:HD12	1:P:50[C]:ALA:HB2	1.88	0.55
1:O:190[C]:PHE:HE2	1:P:190[C]:PHE:HE2	1.51	0.55
1:L:118[D]:ARG:HD2	1:L:122[D]:ASP:OD2	2.06	0.55
1:L:250[D]:ILE:HD12	1:L:250[D]:ILE:N	2.21	0.55
1:O:220[D]:LEU:HG	1:O:224[D]:VAL:HG21	1.89	0.55
1:A:246[A]:PRO:HG2	4:A:790[A]:HOH:O	2.06	0.55
1:A:246[B]:PRO:HG2	4:A:790[B]:HOH:O	2.06	0.55
1:K:43[B]:THR:HG21	1:K:316[B]:SER:OG	2.07	0.55
1:A:246[C]:PRO:HG2	4:A:790[C]:HOH:O	2.06	0.55
1:J:250[C]:ILE:N	1:J:250[C]:ILE:HD12	2.21	0.55
1:A:246[D]:PRO:HG2	4:A:790[D]:HOH:O	2.06	0.55
1:N:219[D]:ASP:HB2	2:N:600[D]:UMP:O3'	2.06	0.55
1:E:118[A]:ARG:HD3	4:E:1098[A]:HOH:O	2.06	0.55
1:E:118[B]:ARG:HD3	4:E:1098[B]:HOH:O	2.06	0.55
1:K:134[B]:PHE:CZ	1:L:176[B]:PRO:HD2	2.42	0.55
1:E:118[C]:ARG:HD3	4:E:1098[C]:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118[D]:ARG:HD3	4:E:1098[D]:HOH:O	2.06	0.55
1:I:50[D]:ALA:CB	1:J:212[D]:LEU:HD12	2.35	0.55
1:B:117[A]:HIS:HD2	4:B:928[A]:HOH:O	1.90	0.55
1:F:44[A]:GLY:C	1:F:260[A]:ARG:HG2	2.27	0.55
1:B:117[B]:HIS:HD2	4:B:928[B]:HOH:O	1.90	0.55
1:F:44[B]:GLY:C	1:F:260[B]:ARG:HG2	2.27	0.55
1:I:190[B]:PHE:CE2	1:J:190[B]:PHE:CE2	2.94	0.55
1:L:118[B]:ARG:HD2	1:L:122[B]:ASP:OD2	2.06	0.55
1:K:212[B]:LEU:HD12	1:L:50[B]:ALA:CB	2.37	0.55
1:B:117[C]:HIS:HD2	4:B:928[C]:HOH:O	1.90	0.55
1:F:44[C]:GLY:C	1:F:260[C]:ARG:HG2	2.27	0.55
1:L:109[C]:PHE:O	1:L:112[C]:LYS:HB3	2.06	0.55
1:K:212[C]:LEU:HD12	1:L:50[C]:ALA:CB	2.37	0.55
1:B:117[D]:HIS:HD2	4:B:928[D]:HOH:O	1.90	0.55
1:F:44[D]:GLY:C	1:F:260[D]:ARG:HG2	2.27	0.55
1:D:14[A]:SER:HB3	1:D:273[A]:GLU:OE1	2.06	0.55
1:D:14[B]:SER:HB3	1:D:273[B]:GLU:OE1	2.06	0.55
1:I:212[B]:LEU:HD12	1:J:50[B]:ALA:HB2	1.88	0.55
1:M:250[B]:ILE:HD12	1:M:250[B]:ILE:N	2.22	0.55
1:N:250[B]:ILE:N	1:N:250[B]:ILE:HD12	2.21	0.55
1:P:250[B]:ILE:N	1:P:250[B]:ILE:HD12	2.21	0.55
1:D:14[C]:SER:HB3	1:D:273[C]:GLU:OE1	2.06	0.55
1:I:190[C]:PHE:CE2	1:J:190[C]:PHE:CE2	2.95	0.55
1:D:14[D]:SER:HB3	1:D:273[D]:GLU:OE1	2.06	0.55
1:I:190[D]:PHE:CE2	1:J:190[D]:PHE:CE2	2.95	0.55
1:B:30[A]:ILE:HG22	1:B:46[A]:VAL:HG13	1.88	0.55
1:H:44[A]:GLY:C	1:H:260[A]:ARG:HG2	2.27	0.55
1:B:30[B]:ILE:HG22	1:B:46[B]:VAL:HG13	1.88	0.55
1:H:44[B]:GLY:C	1:H:260[B]:ARG:HG2	2.27	0.55
1:B:30[C]:ILE:HG22	1:B:46[C]:VAL:HG13	1.88	0.55
1:H:44[C]:GLY:C	1:H:260[C]:ARG:HG2	2.27	0.55
1:I:70[C]:ARG:NH1	1:I:310[C]:LYS:HD3	2.22	0.55
1:M:212[C]:LEU:HD12	1:N:50[C]:ALA:CB	2.37	0.55
1:B:30[D]:ILE:HG22	1:B:46[D]:VAL:HG13	1.88	0.55
1:H:44[D]:GLY:C	1:H:260[D]:ARG:HG2	2.27	0.55
1:K:190[D]:PHE:CE2	1:L:190[D]:PHE:CE2	2.95	0.55
1:E:195[A]:VAL:O	1:F:37[A]:ARG:NH1	2.36	0.55
1:M:50[A]:ALA:HB2	1:N:212[A]:LEU:HD12	1.88	0.55
1:E:195[B]:VAL:O	1:F:37[B]:ARG:NH1	2.36	0.55
1:I:70[B]:ARG:NH1	1:I:310[B]:LYS:HD3	2.22	0.55
1:E:195[C]:VAL:O	1:F:37[C]:ARG:NH1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:190[C]:PHE:CE2	1:N:190[C]:PHE:CE2	2.94	0.55
1:E:195[D]:VAL:O	1:F:37[D]:ARG:NH1	2.36	0.55
1:J:250[D]:ILE:N	1:J:250[D]:ILE:HD12	2.22	0.55
1:K:212[D]:LEU:HD12	1:L:50[D]:ALA:CB	2.37	0.55
1:G:47[A]:ALA:HB2	1:G:257[A]:HIS:HB3	1.89	0.55
1:G:47[B]:ALA:HB2	1:G:257[B]:HIS:HB3	1.89	0.55
1:J:250[B]:ILE:HD12	1:J:250[B]:ILE:N	2.22	0.55
1:K:190[B]:PHE:CE2	1:L:190[B]:PHE:CE2	2.95	0.55
1:L:109[B]:PHE:O	1:L:112[B]:LYS:HB3	2.07	0.55
1:G:47[C]:ALA:HB2	1:G:257[C]:HIS:HB3	1.89	0.55
1:P:118[C]:ARG:HD2	1:P:122[C]:ASP:OD2	2.07	0.55
1:G:47[D]:ALA:HB2	1:G:257[D]:HIS:HB3	1.89	0.55
1:O:43[A]:THR:HG21	1:O:316[A]:SER:OG	2.07	0.55
1:I:50[C]:ALA:CB	1:J:212[C]:LEU:HD12	2.36	0.55
1:M:190[D]:PHE:CE2	1:N:190[D]:PHE:CE2	2.94	0.55
1:D:44[A]:GLY:C	1:D:260[A]:ARG:HG2	2.27	0.54
1:P:53[A]:SER:HB3	1:P:252[A]:GLN:NE2	2.21	0.54
1:D:44[B]:GLY:C	1:D:260[B]:ARG:HG2	2.27	0.54
1:D:44[C]:GLY:C	1:D:260[C]:ARG:HG2	2.27	0.54
1:L:43[C]:THR:HG21	1:L:316[C]:SER:OG	2.07	0.54
1:N:43[C]:THR:HG21	1:N:316[C]:SER:OG	2.07	0.54
1:D:44[D]:GLY:C	1:D:260[D]:ARG:HG2	2.27	0.54
1:I:70[D]:ARG:NH1	1:I:310[D]:LYS:HD3	2.22	0.54
1:M:250[D]:ILE:HD12	1:M:250[D]:ILE:N	2.22	0.54
1:M:53[D]:SER:HB3	1:M:252[D]:GLN:NE2	2.21	0.54
1:A:212[A]:LEU:HD12	1:B:50[A]:ALA:HB2	1.89	0.54
1:A:212[B]:LEU:HD12	1:B:50[B]:ALA:HB2	1.89	0.54
1:O:212[B]:LEU:HD12	1:P:50[B]:ALA:HB2	1.89	0.54
1:A:212[C]:LEU:HD12	1:B:50[C]:ALA:HB2	1.89	0.54
1:A:212[D]:LEU:HD12	1:B:50[D]:ALA:HB2	1.89	0.54
1:E:30[A]:ILE:HG22	1:E:46[A]:VAL:HG13	1.89	0.54
1:N:219[A]:ASP:HB2	2:N:600[A]:UMP:O3'	2.07	0.54
1:E:30[B]:ILE:HG22	1:E:46[B]:VAL:HG13	1.89	0.54
1:M:53[B]:SER:HB3	1:M:252[B]:GLN:NE2	2.22	0.54
1:E:30[C]:ILE:HG22	1:E:46[C]:VAL:HG13	1.89	0.54
1:E:30[D]:ILE:HG22	1:E:46[D]:VAL:HG13	1.89	0.54
1:M:212[D]:LEU:HD12	1:N:50[D]:ALA:CB	2.38	0.54
1:K:212[A]:LEU:HD12	1:L:50[A]:ALA:CB	2.38	0.54
1:P:118[B]:ARG:HD2	1:P:122[B]:ASP:OD2	2.07	0.54
1:I:212[C]:LEU:HD12	1:J:50[C]:ALA:HB2	1.88	0.54
1:I:212[D]:LEU:HD12	1:J:50[D]:ALA:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30[A]:ILE:HG22	1:A:46[A]:VAL:HG13	1.89	0.54
1:A:30[B]:ILE:HG22	1:A:46[B]:VAL:HG13	1.89	0.54
1:M:190[B]:PHE:CE2	1:N:190[B]:PHE:CE2	2.95	0.54
1:A:30[C]:ILE:HG22	1:A:46[C]:VAL:HG13	1.89	0.54
1:J:43[C]:THR:HG21	1:J:316[C]:SER:OG	2.08	0.54
1:A:30[D]:ILE:HG22	1:A:46[D]:VAL:HG13	1.89	0.54
1:I:50[B]:ALA:CB	1:J:212[B]:LEU:HD12	2.37	0.54
1:P:109[C]:PHE:O	1:P:112[C]:LYS:HB3	2.08	0.54
1:P:250[C]:ILE:HD12	1:P:250[C]:ILE:N	2.22	0.54
1:K:43[D]:THR:HG21	1:K:316[D]:SER:OG	2.08	0.54
1:L:43[D]:THR:HG21	1:L:316[D]:SER:OG	2.08	0.54
1:J:118[D]:ARG:HD2	1:J:122[D]:ASP:OD2	2.08	0.54
1:N:250[D]:ILE:N	1:N:250[D]:ILE:HD12	2.22	0.54
1:P:109[D]:PHE:O	1:P:112[D]:LYS:HB3	2.08	0.54
1:G:165[A]:THR:HG21	1:H:38[A]:PRO:HD2	1.88	0.54
1:G:165[B]:THR:HG21	1:H:38[B]:PRO:HD2	1.88	0.54
1:G:165[C]:THR:HG21	1:H:38[C]:PRO:HD2	1.88	0.54
1:K:264[C]:GLU:HB2	1:K:265[C]:PRO:HD3	1.90	0.54
1:G:165[D]:THR:HG21	1:H:38[D]:PRO:HD2	1.88	0.54
1:K:43[A]:THR:HG21	1:K:316[A]:SER:OG	2.08	0.54
1:M:264[B]:GLU:HB2	1:M:265[B]:PRO:HD3	1.90	0.54
1:K:43[C]:THR:HG21	1:K:316[C]:SER:OG	2.08	0.54
1:O:212[D]:LEU:HD12	1:P:50[D]:ALA:HB2	1.90	0.54
1:A:165[A]:THR:HG21	1:B:38[A]:PRO:HD2	1.90	0.53
1:C:53[A]:SER:HB3	1:C:252[A]:GLN:NE2	2.23	0.53
1:C:30[A]:ILE:HG22	1:C:46[A]:VAL:HG13	1.89	0.53
1:M:212[A]:LEU:HD12	1:N:50[A]:ALA:CB	2.38	0.53
1:A:165[B]:THR:HG21	1:B:38[B]:PRO:HD2	1.90	0.53
1:C:30[B]:ILE:HG22	1:C:46[B]:VAL:HG13	1.89	0.53
1:C:53[B]:SER:HB3	1:C:252[B]:GLN:NE2	2.23	0.53
1:A:165[C]:THR:HG21	1:B:38[C]:PRO:HD2	1.90	0.53
1:C:30[C]:ILE:HG22	1:C:46[C]:VAL:HG13	1.89	0.53
1:C:53[C]:SER:HB3	1:C:252[C]:GLN:NE2	2.23	0.53
1:A:165[D]:THR:HG21	1:B:38[D]:PRO:HD2	1.90	0.53
1:C:53[D]:SER:HB3	1:C:252[D]:GLN:NE2	2.23	0.53
1:C:30[D]:ILE:HG22	1:C:46[D]:VAL:HG13	1.89	0.53
1:N:79[D]:GLU:O	1:N:82[D]:TRP:HB3	2.09	0.53
1:B:185[A]:PRO:HG3	4:B:908[A]:HOH:O	2.09	0.53
1:E:44[A]:GLY:C	1:E:260[A]:ARG:HG2	2.28	0.53
1:B:185[B]:PRO:HG3	4:B:908[B]:HOH:O	2.09	0.53
1:E:44[B]:GLY:C	1:E:260[B]:ARG:HG2	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185[C]:PRO:HG3	4:B:908[C]:HOH:O	2.09	0.53
1:E:44[C]:GLY:C	1:E:260[C]:ARG:HG2	2.28	0.53
1:B:185[D]:PRO:HG3	4:B:908[D]:HOH:O	2.09	0.53
1:E:44[D]:GLY:C	1:E:260[D]:ARG:HG2	2.28	0.53
1:M:264[D]:GLU:HB2	1:M:265[D]:PRO:HD3	1.90	0.53
1:E:43[A]:THR:HG21	1:E:316[A]:SER:OG	2.08	0.53
1:J:44[A]:GLY:C	1:J:260[A]:ARG:HG2	2.28	0.53
1:E:43[B]:THR:HG21	1:E:316[B]:SER:OG	2.08	0.53
1:E:43[C]:THR:HG21	1:E:316[C]:SER:OG	2.08	0.53
1:O:298[C]:GLU:H	1:O:298[C]:GLU:CD	2.11	0.53
1:E:43[D]:THR:HG21	1:E:316[D]:SER:OG	2.08	0.53
1:I:220[D]:LEU:HG	1:I:224[D]:VAL:HG21	1.91	0.53
1:K:70[D]:ARG:NH1	1:K:310[D]:LYS:HD3	2.24	0.53
1:P:250[D]:ILE:HD12	1:P:250[D]:ILE:N	2.23	0.53
1:C:212[A]:LEU:HD12	1:D:50[A]:ALA:HB2	1.91	0.53
1:I:250[A]:ILE:N	1:I:250[A]:ILE:HD12	2.24	0.53
1:C:212[B]:LEU:HD12	1:D:50[B]:ALA:HB2	1.91	0.53
1:M:212[B]:LEU:HD12	1:N:50[B]:ALA:CB	2.39	0.53
1:O:298[B]:GLU:CD	1:O:298[B]:GLU:H	2.12	0.53
1:C:212[C]:LEU:HD12	1:D:50[C]:ALA:HB2	1.91	0.53
1:C:212[D]:LEU:HD12	1:D:50[D]:ALA:HB2	1.91	0.53
1:A:147[A]:GLY:CA	1:D:137[A]:GLU:OE1	2.56	0.53
1:I:50[A]:ALA:CB	1:J:212[A]:LEU:HD12	2.38	0.53
1:A:147[B]:GLY:CA	1:D:137[B]:GLU:OE1	2.56	0.53
1:L:43[B]:THR:HG21	1:L:316[B]:SER:OG	2.09	0.53
1:A:147[C]:GLY:CA	1:D:137[C]:GLU:OE1	2.56	0.53
1:A:147[D]:GLY:CA	1:D:137[D]:GLU:OE1	2.56	0.53
1:M:53[A]:SER:HB3	1:M:252[A]:GLN:NE2	2.23	0.53
1:P:109[B]:PHE:O	1:P:112[B]:LYS:HB3	2.09	0.53
1:K:70[C]:ARG:NH1	1:K:310[C]:LYS:HD3	2.24	0.53
1:P:212[D]:LEU:HD23	1:P:212[D]:LEU:C	2.29	0.53
1:G:43[A]:THR:HG21	1:G:316[A]:SER:OG	2.09	0.53
1:G:30[A]:ILE:HG22	1:G:46[A]:VAL:HG13	1.90	0.53
1:G:30[B]:ILE:HG22	1:G:46[B]:VAL:HG13	1.90	0.53
1:G:43[B]:THR:HG21	1:G:316[B]:SER:OG	2.09	0.53
1:G:43[C]:THR:HG21	1:G:316[C]:SER:OG	2.09	0.53
1:G:30[C]:ILE:HG22	1:G:46[C]:VAL:HG13	1.90	0.53
1:M:53[C]:SER:HB3	1:M:252[C]:GLN:NE2	2.23	0.53
1:G:43[D]:THR:HG21	1:G:316[D]:SER:OG	2.09	0.53
1:G:30[D]:ILE:HG22	1:G:46[D]:VAL:HG13	1.90	0.53
1:K:264[D]:GLU:HB2	1:K:265[D]:PRO:HD3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297[A]:VAL:HG23	4:B:980[A]:HOH:O	2.07	0.53
1:N:250[A]:ILE:N	1:N:250[A]:ILE:HD12	2.23	0.53
1:P:43[A]:THR:HG21	1:P:316[A]:SER:OG	2.09	0.53
1:B:297[B]:VAL:HG23	4:B:980[B]:HOH:O	2.07	0.53
1:K:70[B]:ARG:NH1	1:K:310[B]:LYS:HD3	2.24	0.53
1:B:297[C]:VAL:HG23	4:B:980[C]:HOH:O	2.07	0.53
1:B:297[D]:VAL:HG23	4:B:980[D]:HOH:O	2.07	0.53
1:O:298[D]:GLU:H	1:O:298[D]:GLU:CD	2.12	0.53
1:I:118[A]:ARG:HD2	1:I:122[A]:ASP:OD2	2.08	0.53
1:K:250[A]:ILE:HD12	1:K:250[A]:ILE:N	2.24	0.53
1:M:250[A]:ILE:N	1:M:250[A]:ILE:HD12	2.24	0.53
1:J:109[D]:PHE:O	1:J:112[D]:LYS:HB3	2.09	0.53
1:P:118[D]:ARG:HD2	1:P:122[D]:ASP:OD2	2.09	0.53
1:A:38[A]:PRO:HD2	1:B:165[A]:THR:HG21	1.91	0.53
1:B:44[A]:GLY:C	1:B:260[A]:ARG:HG2	2.28	0.53
1:B:260[A]:ARG:NH1	4:B:851[A]:HOH:O	2.39	0.53
1:C:50[A]:ALA:HB2	1:D:212[A]:LEU:HD12	1.91	0.53
1:E:297[A]:VAL:HG23	4:E:682[A]:HOH:O	2.09	0.53
1:H:47[A]:ALA:HB2	1:H:257[A]:HIS:HB3	1.91	0.53
1:P:212[A]:LEU:C	1:P:212[A]:LEU:HD23	2.30	0.53
1:A:38[B]:PRO:HD2	1:B:165[B]:THR:HG21	1.91	0.53
1:B:44[B]:GLY:C	1:B:260[B]:ARG:HG2	2.28	0.53
1:B:260[B]:ARG:NH1	4:B:851[B]:HOH:O	2.39	0.53
1:C:50[B]:ALA:HB2	1:D:212[B]:LEU:HD12	1.91	0.53
1:E:297[B]:VAL:HG23	4:E:682[B]:HOH:O	2.09	0.53
1:H:47[B]:ALA:HB2	1:H:257[B]:HIS:HB3	1.91	0.53
1:A:38[C]:PRO:HD2	1:B:165[C]:THR:HG21	1.91	0.53
1:B:44[C]:GLY:C	1:B:260[C]:ARG:HG2	2.28	0.53
1:B:260[C]:ARG:NH1	4:B:851[C]:HOH:O	2.39	0.53
1:C:50[C]:ALA:HB2	1:D:212[C]:LEU:HD12	1.91	0.53
1:E:297[C]:VAL:HG23	4:E:682[C]:HOH:O	2.09	0.53
1:H:47[C]:ALA:HB2	1:H:257[C]:HIS:HB3	1.91	0.53
1:J:44[C]:GLY:C	1:J:260[C]:ARG:HG2	2.28	0.53
1:J:30[C]:ILE:HG22	1:J:46[C]:VAL:HG13	1.89	0.53
1:K:38[C]:PRO:HD2	1:L:165[C]:THR:HG21	1.91	0.53
1:A:38[D]:PRO:HD2	1:B:165[D]:THR:HG21	1.91	0.53
1:B:44[D]:GLY:C	1:B:260[D]:ARG:HG2	2.28	0.53
1:B:260[D]:ARG:NH1	4:B:851[D]:HOH:O	2.39	0.53
1:C:50[D]:ALA:HB2	1:D:212[D]:LEU:HD12	1.91	0.53
1:E:297[D]:VAL:HG23	4:E:682[D]:HOH:O	2.09	0.53
1:H:47[D]:ALA:HB2	1:H:257[D]:HIS:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:44[D]:GLY:C	1:J:260[D]:ARG:HG2	2.28	0.53
1:H:199[A]:PRO:HB2	1:H:201[A]:ASP:OD1	2.09	0.52
1:L:250[A]:ILE:N	1:L:250[A]:ILE:HD12	2.24	0.52
1:H:199[B]:PRO:HB2	1:H:201[B]:ASP:OD1	2.09	0.52
1:I:220[B]:LEU:HG	1:I:224[B]:VAL:HG21	1.92	0.52
1:J:44[B]:GLY:C	1:J:260[B]:ARG:HG2	2.28	0.52
1:K:264[B]:GLU:HB2	1:K:265[B]:PRO:HD3	1.91	0.52
1:H:199[C]:PRO:HB2	1:H:201[C]:ASP:OD1	2.09	0.52
1:I:264[C]:GLU:HB2	1:I:265[C]:PRO:HD3	1.90	0.52
1:H:199[D]:PRO:HB2	1:H:201[D]:ASP:OD1	2.09	0.52
1:G:217[A]:SER:OG	1:H:167[A]:ARG:HD3	2.10	0.52
1:I:43[A]:THR:HG21	1:I:316[A]:SER:OG	2.09	0.52
1:J:250[A]:ILE:HD12	1:J:250[A]:ILE:N	2.24	0.52
1:K:134[A]:PHE:CZ	1:L:176[A]:PRO:HD2	2.45	0.52
1:O:250[A]:ILE:HD12	1:O:250[A]:ILE:N	2.24	0.52
1:O:298[A]:GLU:H	1:O:298[A]:GLU:CD	2.13	0.52
1:G:217[B]:SER:OG	1:H:167[B]:ARG:HD3	2.10	0.52
1:N:79[B]:GLU:O	1:N:82[B]:TRP:HB3	2.10	0.52
1:G:217[C]:SER:OG	1:H:167[C]:ARG:HD3	2.10	0.52
1:J:109[C]:PHE:O	1:J:112[C]:LYS:HB3	2.10	0.52
1:L:30[C]:ILE:HG22	1:L:46[C]:VAL:HG13	1.90	0.52
1:N:79[C]:GLU:O	1:N:82[C]:TRP:HB3	2.10	0.52
1:G:217[D]:SER:OG	1:H:167[D]:ARG:HD3	2.10	0.52
1:O:212[A]:LEU:HD12	1:P:50[A]:ALA:HB2	1.91	0.52
1:J:298[B]:GLU:CD	1:J:298[B]:GLU:H	2.12	0.52
1:N:30[B]:ILE:HG22	1:N:46[B]:VAL:HG13	1.90	0.52
1:M:264[C]:GLU:HB2	1:M:265[C]:PRO:HD3	1.91	0.52
1:J:298[D]:GLU:CD	1:J:298[D]:GLU:H	2.12	0.52
1:J:30[D]:ILE:HG22	1:J:46[D]:VAL:HG13	1.89	0.52
1:N:30[D]:ILE:HG22	1:N:46[D]:VAL:HG13	1.90	0.52
1:E:212[A]:LEU:C	1:E:212[A]:LEU:HD23	2.29	0.52
1:E:38[A]:PRO:HD2	1:F:165[A]:THR:HG21	1.91	0.52
1:E:47[A]:ALA:HB2	1:E:257[A]:HIS:HB3	1.92	0.52
1:N:30[A]:ILE:HG22	1:N:46[A]:VAL:HG13	1.90	0.52
1:E:212[B]:LEU:C	1:E:212[B]:LEU:HD23	2.29	0.52
1:E:47[B]:ALA:HB2	1:E:257[B]:HIS:HB3	1.92	0.52
1:E:38[B]:PRO:HD2	1:F:165[B]:THR:HG21	1.91	0.52
1:L:30[B]:ILE:HG22	1:L:46[B]:VAL:HG13	1.90	0.52
1:E:212[C]:LEU:C	1:E:212[C]:LEU:HD23	2.29	0.52
1:E:47[C]:ALA:HB2	1:E:257[C]:HIS:HB3	1.92	0.52
1:E:38[C]:PRO:HD2	1:F:165[C]:THR:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:212[D]:LEU:HD23	1:E:212[D]:LEU:C	2.29	0.52
1:E:47[D]:ALA:HB2	1:E:257[D]:HIS:HB3	1.92	0.52
1:E:38[D]:PRO:HD2	1:F:165[D]:THR:HG21	1.91	0.52
1:I:264[D]:GLU:HB2	1:I:265[D]:PRO:HD3	1.91	0.52
1:J:43[D]:THR:HG21	1:J:316[D]:SER:OG	2.10	0.52
1:A:44[A]:GLY:C	1:A:260[A]:ARG:HG2	2.29	0.52
1:A:44[B]:GLY:C	1:A:260[B]:ARG:HG2	2.29	0.52
1:M:70[B]:ARG:NH1	1:M:310[B]:LYS:HD3	2.25	0.52
1:A:44[C]:GLY:C	1:A:260[C]:ARG:HG2	2.29	0.52
1:O:43[C]:THR:HG21	1:O:316[C]:SER:OG	2.10	0.52
1:A:44[D]:GLY:C	1:A:260[D]:ARG:HG2	2.29	0.52
1:J:43[B]:THR:HG21	1:J:316[B]:SER:OG	2.10	0.52
1:K:38[B]:PRO:HD2	1:L:165[B]:THR:HG21	1.91	0.52
1:O:43[D]:THR:HG21	1:O:316[D]:SER:OG	2.10	0.52
1:C:298[A]:GLU:H	1:C:298[A]:GLU:CD	2.12	0.52
1:E:212[A]:LEU:HD12	1:F:50[A]:ALA:HB2	1.92	0.52
1:C:298[B]:GLU:H	1:C:298[B]:GLU:CD	2.12	0.52
1:E:212[B]:LEU:HD12	1:F:50[B]:ALA:HB2	1.92	0.52
1:P:212[B]:LEU:C	1:P:212[B]:LEU:HD23	2.30	0.52
1:C:298[C]:GLU:CD	1:C:298[C]:GLU:H	2.12	0.52
1:E:212[C]:LEU:HD12	1:F:50[C]:ALA:HB2	1.92	0.52
1:I:109[C]:PHE:O	1:I:112[C]:LYS:HB3	2.10	0.52
1:C:298[D]:GLU:H	1:C:298[D]:GLU:CD	2.12	0.52
1:E:212[D]:LEU:HD12	1:F:50[D]:ALA:HB2	1.92	0.52
1:B:212[A]:LEU:HD23	1:B:212[A]:LEU:C	2.30	0.52
1:E:176[A]:PRO:HD2	1:F:134[A]:PHE:CZ	2.44	0.52
1:B:212[B]:LEU:HD23	1:B:212[B]:LEU:C	2.30	0.52
1:E:176[B]:PRO:HD2	1:F:134[B]:PHE:CZ	2.44	0.52
1:I:264[B]:GLU:HB2	1:I:265[B]:PRO:HD3	1.91	0.52
1:K:298[B]:GLU:H	1:K:298[B]:GLU:CD	2.12	0.52
1:B:212[C]:LEU:C	1:B:212[C]:LEU:HD23	2.30	0.52
1:E:176[C]:PRO:HD2	1:F:134[C]:PHE:CZ	2.44	0.52
1:J:298[C]:GLU:CD	1:J:298[C]:GLU:H	2.12	0.52
1:M:70[C]:ARG:NH1	1:M:310[C]:LYS:HD3	2.25	0.52
1:P:264[C]:GLU:HB2	1:P:265[C]:PRO:HD3	1.91	0.52
1:B:212[D]:LEU:C	1:B:212[D]:LEU:HD23	2.30	0.52
1:E:176[D]:PRO:HD2	1:F:134[D]:PHE:CZ	2.44	0.52
1:I:30[D]:ILE:HG22	1:I:46[D]:VAL:HG13	1.91	0.52
1:K:298[D]:GLU:H	1:K:298[D]:GLU:CD	2.12	0.52
1:J:212[A]:LEU:C	1:J:212[A]:LEU:HD23	2.30	0.52
1:N:212[A]:LEU:C	1:N:212[A]:LEU:HD23	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:109[B]:PHE:O	1:J:112[B]:LYS:HB3	2.10	0.52
1:N:109[D]:PHE:O	1:N:112[D]:LYS:HB3	2.10	0.52
1:N:212[D]:LEU:C	1:N:212[D]:LEU:HD23	2.30	0.52
1:C:38[A]:PRO:HD2	1:D:165[A]:THR:HG21	1.92	0.52
1:F:186[A]:PRO:HG3	4:F:800[A]:HOH:O	2.10	0.52
1:I:212[A]:LEU:HD12	1:J:50[A]:ALA:HB2	1.92	0.52
1:M:38[A]:PRO:HD2	1:N:165[A]:THR:HG21	1.92	0.52
1:P:30[A]:ILE:HG22	1:P:46[A]:VAL:HG13	1.91	0.52
1:C:38[B]:PRO:HD2	1:D:165[B]:THR:HG21	1.92	0.52
1:F:186[B]:PRO:HG3	4:F:800[B]:HOH:O	2.10	0.52
1:I:109[B]:PHE:O	1:I:112[B]:LYS:HB3	2.10	0.52
1:I:30[B]:ILE:HG22	1:I:46[B]:VAL:HG13	1.91	0.52
1:J:212[B]:LEU:C	1:J:212[B]:LEU:HD23	2.30	0.52
1:L:298[B]:GLU:H	1:L:298[B]:GLU:CD	2.13	0.52
1:C:38[C]:PRO:HD2	1:D:165[C]:THR:HG21	1.92	0.52
1:F:186[C]:PRO:HG3	4:F:800[C]:HOH:O	2.10	0.52
1:L:118[C]:ARG:HD2	1:L:122[C]:ASP:OD2	2.09	0.52
1:L:298[C]:GLU:CD	1:L:298[C]:GLU:H	2.12	0.52
1:N:109[C]:PHE:O	1:N:112[C]:LYS:HB3	2.10	0.52
1:C:38[D]:PRO:HD2	1:D:165[D]:THR:HG21	1.92	0.52
1:F:186[D]:PRO:HG3	4:F:800[D]:HOH:O	2.10	0.52
1:L:298[D]:GLU:H	1:L:298[D]:GLU:CD	2.12	0.52
1:P:298[D]:GLU:H	1:P:298[D]:GLU:CD	2.12	0.52
1:A:47[A]:ALA:HB2	1:A:257[A]:HIS:HB3	1.92	0.51
1:H:298[A]:GLU:H	1:H:298[A]:GLU:CD	2.13	0.51
1:J:30[A]:ILE:HG22	1:J:46[A]:VAL:HG13	1.90	0.51
1:L:109[A]:PHE:O	1:L:112[A]:LYS:HB3	2.10	0.51
1:A:47[B]:ALA:HB2	1:A:257[B]:HIS:HB3	1.92	0.51
1:H:298[B]:GLU:CD	1:H:298[B]:GLU:H	2.13	0.51
1:N:212[B]:LEU:HD23	1:N:212[B]:LEU:C	2.31	0.51
1:A:47[C]:ALA:HB2	1:A:257[C]:HIS:HB3	1.92	0.51
1:H:298[C]:GLU:H	1:H:298[C]:GLU:CD	2.13	0.51
1:J:264[C]:GLU:HB2	1:J:265[C]:PRO:HD3	1.91	0.51
1:K:298[C]:GLU:CD	1:K:298[C]:GLU:H	2.12	0.51
1:P:212[C]:LEU:C	1:P:212[C]:LEU:HD23	2.30	0.51
1:A:47[D]:ALA:HB2	1:A:257[D]:HIS:HB3	1.92	0.51
1:H:298[D]:GLU:CD	1:H:298[D]:GLU:H	2.13	0.51
1:K:38[D]:PRO:HD2	1:L:165[D]:THR:HG21	1.92	0.51
1:D:47[A]:ALA:HB2	1:D:257[A]:HIS:HB3	1.92	0.51
1:H:100[A]:ILE:HB	3:H:2701[A]:CB3:C13	2.40	0.51
1:I:30[A]:ILE:HG22	1:I:46[A]:VAL:HG13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:287[A]:GLU:CG	1:J:146[A]:LYS:NZ	2.63	0.51
1:D:47[B]:ALA:HB2	1:D:257[B]:HIS:HB3	1.92	0.51
1:H:100[B]:ILE:HB	3:H:2701[B]:CB3:C13	2.40	0.51
1:J:264[B]:GLU:HB2	1:J:265[B]:PRO:HD3	1.91	0.51
1:K:109[B]:PHE:O	1:K:112[B]:LYS:HB3	2.10	0.51
1:D:47[C]:ALA:HB2	1:D:257[C]:HIS:HB3	1.92	0.51
1:H:100[C]:ILE:HB	3:H:2701[C]:CB3:C13	2.40	0.51
1:O:264[C]:GLU:HB2	1:O:265[C]:PRO:HD3	1.92	0.51
1:P:298[C]:GLU:CD	1:P:298[C]:GLU:H	2.12	0.51
1:D:47[D]:ALA:HB2	1:D:257[D]:HIS:HB3	1.92	0.51
1:H:100[D]:ILE:HB	3:H:2701[D]:CB3:C13	2.40	0.51
1:M:70[D]:ARG:NH1	1:M:310[D]:LYS:HD3	2.25	0.51
1:C:190[A]:PHE:HZ	1:D:214[A]:TYR:CD2	2.28	0.51
1:J:298[A]:GLU:H	1:J:298[A]:GLU:CD	2.12	0.51
1:K:264[A]:GLU:HB2	1:K:265[A]:PRO:HD3	1.92	0.51
1:L:298[A]:GLU:CD	1:L:298[A]:GLU:H	2.12	0.51
1:M:264[A]:GLU:HB2	1:M:265[A]:PRO:HD3	1.92	0.51
1:C:190[B]:PHE:HZ	1:D:214[B]:TYR:CD2	2.28	0.51
1:K:79[B]:GLU:O	1:K:82[B]:TRP:HB3	2.10	0.51
1:M:50[B]:ALA:CB	1:N:212[B]:LEU:HD12	2.40	0.51
1:O:264[B]:GLU:HB2	1:O:265[B]:PRO:HD3	1.92	0.51
1:P:298[B]:GLU:H	1:P:298[B]:GLU:CD	2.12	0.51
1:C:190[C]:PHE:HZ	1:D:214[C]:TYR:CD2	2.28	0.51
1:I:220[C]:LEU:HG	1:I:224[C]:VAL:HG21	1.93	0.51
1:I:30[C]:ILE:HG22	1:I:46[C]:VAL:HG13	1.91	0.51
1:J:212[C]:LEU:C	1:J:212[C]:LEU:HD23	2.30	0.51
1:L:220[C]:LEU:HG	1:L:224[C]:VAL:HG21	1.91	0.51
1:C:190[D]:PHE:HZ	1:D:214[D]:TYR:CD2	2.28	0.51
1:F:298[A]:GLU:CD	1:F:298[A]:GLU:H	2.13	0.51
1:K:38[A]:PRO:HD2	1:L:165[A]:THR:HG21	1.92	0.51
1:K:30[A]:ILE:HG22	1:K:46[A]:VAL:HG13	1.91	0.51
1:P:250[A]:ILE:N	1:P:250[A]:ILE:HD12	2.25	0.51
1:F:298[B]:GLU:CD	1:F:298[B]:GLU:H	2.13	0.51
1:O:43[B]:THR:HG21	1:O:316[B]:SER:OG	2.11	0.51
1:F:298[C]:GLU:CD	1:F:298[C]:GLU:H	2.13	0.51
1:F:298[D]:GLU:CD	1:F:298[D]:GLU:H	2.13	0.51
1:J:264[D]:GLU:HB2	1:J:265[D]:PRO:HD3	1.91	0.51
1:M:50[D]:ALA:CB	1:N:212[D]:LEU:HD12	2.40	0.51
1:O:212[D]:LEU:C	1:O:212[D]:LEU:HD23	2.30	0.51
1:E:246[A]:PRO:HG2	4:E:639[A]:HOH:O	2.10	0.51
1:E:246[B]:PRO:HG2	4:E:639[B]:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:30[B]:ILE:HG22	1:J:46[B]:VAL:HG13	1.90	0.51
1:N:109[B]:PHE:O	1:N:112[B]:LYS:HB3	2.11	0.51
1:E:246[C]:PRO:HG2	4:E:639[C]:HOH:O	2.10	0.51
1:N:298[C]:GLU:H	1:N:298[C]:GLU:CD	2.12	0.51
1:E:246[D]:PRO:HG2	4:E:639[D]:HOH:O	2.10	0.51
1:H:186[A]:PRO:HG3	4:H:1050[A]:HOH:O	2.10	0.51
1:I:70[A]:ARG:NH1	1:I:310[A]:LYS:HD3	2.26	0.51
1:L:30[A]:ILE:HG22	1:L:46[A]:VAL:HG13	1.90	0.51
1:H:186[B]:PRO:HG3	4:H:1050[B]:HOH:O	2.10	0.51
1:K:30[B]:ILE:HG22	1:K:46[B]:VAL:HG13	1.92	0.51
1:H:186[C]:PRO:HG3	4:H:1050[C]:HOH:O	2.10	0.51
1:M:50[C]:ALA:CB	1:N:212[C]:LEU:HD12	2.41	0.51
1:H:186[D]:PRO:HG3	4:H:1050[D]:HOH:O	2.10	0.51
1:I:298[D]:GLU:H	1:I:298[D]:GLU:CD	2.13	0.51
1:I:43[D]:THR:HG21	1:I:316[D]:SER:OG	2.11	0.51
1:O:264[D]:GLU:HB2	1:O:265[D]:PRO:HD3	1.92	0.51
1:O:79[D]:GLU:O	1:O:82[D]:TRP:HB3	2.11	0.51
1:K:118[A]:ARG:HD2	1:K:122[A]:ASP:OD2	2.11	0.51
1:K:298[A]:GLU:H	1:K:298[A]:GLU:CD	2.13	0.51
1:N:118[A]:ARG:HD2	1:N:122[A]:ASP:OD2	2.10	0.51
1:N:298[A]:GLU:H	1:N:298[A]:GLU:CD	2.13	0.51
1:O:220[A]:LEU:HG	1:O:224[A]:VAL:HG21	1.93	0.51
1:I:109[D]:PHE:O	1:I:112[D]:LYS:HB3	2.11	0.51
1:L:30[D]:ILE:HG22	1:L:46[D]:VAL:HG13	1.91	0.51
1:N:298[D]:GLU:H	1:N:298[D]:GLU:CD	2.13	0.51
1:P:30[D]:ILE:HG22	1:P:46[D]:VAL:HG13	1.91	0.51
1:F:201[A]:ASP:O	1:F:202[A]:SER:HB3	2.11	0.51
1:M:118[A]:ARG:HD2	1:M:122[A]:ASP:OD2	2.10	0.51
1:P:298[A]:GLU:H	1:P:298[A]:GLU:CD	2.13	0.51
1:F:201[B]:ASP:O	1:F:202[B]:SER:HB3	2.11	0.51
1:F:201[C]:ASP:O	1:F:202[C]:SER:HB3	2.11	0.51
1:N:212[C]:LEU:C	1:N:212[C]:LEU:HD23	2.31	0.51
1:P:30[C]:ILE:HG22	1:P:46[C]:VAL:HG13	1.92	0.51
1:F:201[D]:ASP:O	1:F:202[D]:SER:HB3	2.11	0.51
1:K:109[D]:PHE:O	1:K:112[D]:LYS:HB3	2.11	0.51
1:A:190[A]:PHE:HZ	1:B:214[A]:TYR:CD2	2.29	0.51
1:G:212[A]:LEU:C	1:G:212[A]:LEU:HD23	2.30	0.51
1:G:298[A]:GLU:CD	1:G:298[A]:GLU:H	2.14	0.51
1:H:201[A]:ASP:O	1:H:203[A]:PRO:HD2	2.11	0.51
1:L:212[A]:LEU:HD23	1:L:212[A]:LEU:C	2.31	0.51
1:M:298[A]:GLU:CD	1:M:298[A]:GLU:H	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190[B]:PHE:HZ	1:B:214[B]:TYR:CD2	2.29	0.51
1:G:212[B]:LEU:HD23	1:G:212[B]:LEU:C	2.30	0.51
1:G:298[B]:GLU:CD	1:G:298[B]:GLU:H	2.14	0.51
1:H:201[B]:ASP:O	1:H:203[B]:PRO:HD2	2.11	0.51
1:A:190[C]:PHE:HZ	1:B:214[C]:TYR:CD2	2.29	0.51
1:G:212[C]:LEU:HD23	1:G:212[C]:LEU:C	2.30	0.51
1:G:298[C]:GLU:CD	1:G:298[C]:GLU:H	2.14	0.51
1:H:201[C]:ASP:O	1:H:203[C]:PRO:HD2	2.11	0.51
1:O:212[C]:LEU:HD12	1:P:50[C]:ALA:CB	2.41	0.51
1:A:190[D]:PHE:HZ	1:B:214[D]:TYR:CD2	2.29	0.51
1:G:212[D]:LEU:HD23	1:G:212[D]:LEU:C	2.30	0.51
1:G:298[D]:GLU:H	1:G:298[D]:GLU:CD	2.14	0.51
1:H:201[D]:ASP:O	1:H:203[D]:PRO:HD2	2.11	0.51
1:K:30[D]:ILE:HG22	1:K:46[D]:VAL:HG13	1.92	0.51
1:E:298[A]:GLU:CD	1:E:298[A]:GLU:H	2.14	0.51
1:O:264[A]:GLU:HB2	1:O:265[A]:PRO:HD3	1.93	0.51
1:P:44[A]:GLY:C	1:P:260[A]:ARG:HG2	2.31	0.51
1:E:298[B]:GLU:H	1:E:298[B]:GLU:CD	2.14	0.51
1:I:298[B]:GLU:CD	1:I:298[B]:GLU:H	2.13	0.51
1:E:298[C]:GLU:H	1:E:298[C]:GLU:CD	2.14	0.51
1:K:109[C]:PHE:O	1:K:112[C]:LYS:HB3	2.11	0.51
1:E:298[D]:GLU:CD	1:E:298[D]:GLU:H	2.14	0.51
1:J:212[D]:LEU:HD23	1:J:212[D]:LEU:C	2.31	0.51
1:I:264[A]:GLU:HB2	1:I:265[A]:PRO:HD3	1.92	0.50
1:J:109[A]:PHE:O	1:J:112[A]:LYS:HB3	2.11	0.50
1:M:212[A]:LEU:C	1:M:212[A]:LEU:HD23	2.31	0.50
1:P:109[A]:PHE:O	1:P:112[A]:LYS:HB3	2.11	0.50
1:I:43[B]:THR:HG21	1:I:316[B]:SER:OG	2.11	0.50
1:P:79[D]:GLU:O	1:P:82[D]:TRP:HB3	2.12	0.50
1:I:298[A]:GLU:CD	1:I:298[A]:GLU:H	2.13	0.50
1:M:30[A]:ILE:HG22	1:M:46[A]:VAL:HG13	1.92	0.50
1:N:298[B]:GLU:H	1:N:298[B]:GLU:CD	2.13	0.50
1:P:264[B]:GLU:HB2	1:P:265[B]:PRO:HD3	1.92	0.50
1:P:264[D]:GLU:HB2	1:P:265[D]:PRO:HD3	1.92	0.50
1:B:298[A]:GLU:CD	1:B:298[A]:GLU:H	2.13	0.50
1:B:47[A]:ALA:HB2	1:B:257[A]:HIS:HB3	1.93	0.50
1:G:53[A]:SER:HB3	1:G:252[A]:GLN:NE2	2.26	0.50
1:M:165[A]:THR:HG21	1:N:38[A]:PRO:HD2	1.93	0.50
1:M:43[A]:THR:HG21	1:M:316[A]:SER:OG	2.11	0.50
1:O:212[A]:LEU:HD23	1:O:212[A]:LEU:C	2.31	0.50
1:O:44[A]:GLY:C	1:O:260[A]:ARG:HG2	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298[B]:GLU:H	1:B:298[B]:GLU:CD	2.13	0.50
1:B:47[B]:ALA:HB2	1:B:257[B]:HIS:HB3	1.93	0.50
1:G:53[B]:SER:HB3	1:G:252[B]:GLN:NE2	2.26	0.50
1:B:47[C]:ALA:HB2	1:B:257[C]:HIS:HB3	1.93	0.50
1:B:298[C]:GLU:CD	1:B:298[C]:GLU:H	2.13	0.50
1:G:53[C]:SER:HB3	1:G:252[C]:GLN:NE2	2.26	0.50
1:M:38[C]:PRO:HD2	1:N:165[C]:THR:HG21	1.93	0.50
1:N:30[C]:ILE:HG22	1:N:46[C]:VAL:HG13	1.92	0.50
1:P:79[C]:GLU:O	1:P:82[C]:TRP:HB3	2.12	0.50
1:B:298[D]:GLU:CD	1:B:298[D]:GLU:H	2.13	0.50
1:B:47[D]:ALA:HB2	1:B:257[D]:HIS:HB3	1.93	0.50
1:G:53[D]:SER:HB3	1:G:252[D]:GLN:NE2	2.26	0.50
1:C:212[A]:LEU:HD12	1:D:50[A]:ALA:CB	2.42	0.50
1:K:212[A]:LEU:C	1:K:212[A]:LEU:HD23	2.31	0.50
1:L:118[A]:ARG:HD2	1:L:122[A]:ASP:OD2	2.11	0.50
1:C:212[B]:LEU:HD12	1:D:50[B]:ALA:CB	2.42	0.50
1:K:165[B]:THR:HG21	1:L:38[B]:PRO:HD2	1.94	0.50
1:P:30[B]:ILE:HG22	1:P:46[B]:VAL:HG13	1.92	0.50
1:O:212[B]:LEU:HD12	1:P:50[B]:ALA:CB	2.42	0.50
1:C:212[C]:LEU:HD12	1:D:50[C]:ALA:CB	2.42	0.50
1:P:220[C]:LEU:HG	1:P:224[C]:VAL:HG21	1.92	0.50
1:C:212[D]:LEU:HD12	1:D:50[D]:ALA:CB	2.42	0.50
1:M:38[D]:PRO:HD2	1:N:165[D]:THR:HG21	1.93	0.50
1:O:109[D]:PHE:O	1:O:112[D]:LYS:HB3	2.11	0.50
1:C:13[A]:ARG:HD3	1:C:21[A]:TYR:CZ	2.46	0.50
1:I:109[A]:PHE:O	1:I:112[A]:LYS:HB3	2.12	0.50
1:O:30[A]:ILE:HG22	1:O:46[A]:VAL:HG13	1.93	0.50
1:C:13[B]:ARG:HD3	1:C:21[B]:TYR:CZ	2.46	0.50
1:C:13[C]:ARG:HD3	1:C:21[C]:TYR:CZ	2.46	0.50
1:K:189[C]:MET:O	1:K:190[C]:PHE:HB3	2.11	0.50
1:C:13[D]:ARG:HD3	1:C:21[D]:TYR:CZ	2.46	0.50
1:M:79[D]:GLU:O	1:M:82[D]:TRP:HB3	2.12	0.50
1:P:220[D]:LEU:HG	1:P:224[D]:VAL:HG21	1.92	0.50
1:O:109[B]:PHE:O	1:O:112[B]:LYS:HB3	2.11	0.50
1:O:212[B]:LEU:C	1:O:212[B]:LEU:HD23	2.31	0.50
1:H:201[C]:ASP:CB	1:N:273[C]:GLU:HB3	2.42	0.50
1:I:43[C]:THR:HG21	1:I:316[C]:SER:OG	2.11	0.50
1:O:109[C]:PHE:O	1:O:112[C]:LYS:HB3	2.11	0.50
1:M:298[D]:GLU:CD	1:M:298[D]:GLU:H	2.15	0.50
1:A:134[A]:PHE:CZ	1:B:176[A]:PRO:HD2	2.47	0.50
1:J:118[A]:ARG:HD2	1:J:122[A]:ASP:OD2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:44[A]:GLY:C	1:N:260[A]:ARG:HG2	2.32	0.50
1:A:134[B]:PHE:CZ	1:B:176[B]:PRO:HD2	2.47	0.50
1:L:212[B]:LEU:C	1:L:212[B]:LEU:HD23	2.31	0.50
1:A:134[C]:PHE:CZ	1:B:176[C]:PRO:HD2	2.47	0.50
1:I:298[C]:GLU:H	1:I:298[C]:GLU:CD	2.14	0.50
1:A:134[D]:PHE:CZ	1:B:176[D]:PRO:HD2	2.47	0.50
1:N:264[D]:GLU:HB2	1:N:265[D]:PRO:HD3	1.92	0.50
1:C:47[A]:ALA:HB2	1:C:257[A]:HIS:HB3	1.94	0.50
1:K:165[A]:THR:HG21	1:L:38[A]:PRO:HD2	1.94	0.50
1:N:109[A]:PHE:O	1:N:112[A]:LYS:HB3	2.12	0.50
1:P:264[A]:GLU:HB2	1:P:265[A]:PRO:HD3	1.93	0.50
1:C:47[B]:ALA:HB2	1:C:257[B]:HIS:HB3	1.94	0.50
1:I:79[B]:GLU:O	1:I:82[B]:TRP:HB3	2.12	0.50
1:M:109[B]:PHE:O	1:M:112[B]:LYS:HB3	2.12	0.50
1:C:47[C]:ALA:HB2	1:C:257[C]:HIS:HB3	1.94	0.50
1:K:30[C]:ILE:HG22	1:K:46[C]:VAL:HG13	1.93	0.50
1:C:47[D]:ALA:HB2	1:C:257[D]:HIS:HB3	1.94	0.50
1:I:38[D]:PRO:HD2	1:J:165[D]:THR:HG21	1.94	0.50
1:L:212[D]:LEU:C	1:L:212[D]:LEU:HD23	2.31	0.50
1:A:100[A]:ILE:HB	3:A:2351[A]:CB3:C13	2.42	0.50
1:I:212[A]:LEU:HD23	1:I:212[A]:LEU:C	2.31	0.50
1:O:118[A]:ARG:HD2	1:O:122[A]:ASP:OD2	2.11	0.50
1:A:100[B]:ILE:HB	3:A:2351[B]:CB3:C13	2.42	0.50
1:L:220[B]:LEU:HG	1:L:224[B]:VAL:HG21	1.92	0.50
1:L:79[B]:GLU:O	1:L:82[B]:TRP:HB3	2.11	0.50
1:M:38[B]:PRO:HD2	1:N:165[B]:THR:HG21	1.93	0.50
1:A:100[C]:ILE:HB	3:A:2351[C]:CB3:C13	2.42	0.50
1:K:165[C]:THR:HG21	1:L:38[C]:PRO:HD2	1.94	0.50
1:A:100[D]:ILE:HB	3:A:2351[D]:CB3:C13	2.42	0.50
1:O:212[D]:LEU:HD12	1:P:50[D]:ALA:CB	2.42	0.50
1:K:109[A]:PHE:O	1:K:112[A]:LYS:HB3	2.12	0.49
1:M:79[B]:GLU:O	1:M:82[B]:TRP:HB3	2.12	0.49
1:O:79[B]:GLU:O	1:O:82[B]:TRP:HB3	2.12	0.49
1:I:79[C]:GLU:O	1:I:82[C]:TRP:HB3	2.12	0.49
1:K:79[C]:GLU:O	1:K:82[C]:TRP:HB3	2.12	0.49
1:L:212[C]:LEU:C	1:L:212[C]:LEU:HD23	2.32	0.49
1:L:264[D]:GLU:HB2	1:L:265[D]:PRO:HD3	1.93	0.49
1:A:53[A]:SER:HB3	1:A:252[A]:GLN:NE2	2.26	0.49
1:H:212[A]:LEU:HD23	1:H:213[A]:MET:N	2.26	0.49
1:A:53[B]:SER:HB3	1:A:252[B]:GLN:NE2	2.26	0.49
1:H:212[B]:LEU:HD23	1:H:213[B]:MET:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:212[B]:LEU:HD23	1:M:212[B]:LEU:C	2.32	0.49
1:M:298[B]:GLU:H	1:M:298[B]:GLU:CD	2.15	0.49
1:A:53[C]:SER:HB3	1:A:252[C]:GLN:NE2	2.26	0.49
1:H:212[C]:LEU:HD23	1:H:213[C]:MET:N	2.26	0.49
1:M:165[C]:THR:HG21	1:N:38[C]:PRO:HD2	1.94	0.49
1:O:44[C]:GLY:C	1:O:260[C]:ARG:HG2	2.32	0.49
1:A:53[D]:SER:HB3	1:A:252[D]:GLN:NE2	2.26	0.49
1:H:212[D]:LEU:HD23	1:H:213[D]:MET:N	2.26	0.49
1:K:79[D]:GLU:O	1:K:82[D]:TRP:HB3	2.12	0.49
1:O:44[D]:GLY:C	1:O:260[D]:ARG:HG2	2.32	0.49
1:A:298[A]:GLU:H	1:A:298[A]:GLU:CD	2.14	0.49
1:A:298[B]:GLU:H	1:A:298[B]:GLU:CD	2.14	0.49
1:O:44[B]:GLY:C	1:O:260[B]:ARG:HG2	2.32	0.49
1:P:220[B]:LEU:HG	1:P:224[B]:VAL:HG21	1.93	0.49
1:A:298[C]:GLU:H	1:A:298[C]:GLU:CD	2.14	0.49
1:M:43[C]:THR:HG21	1:M:316[C]:SER:OG	2.12	0.49
1:M:79[C]:GLU:O	1:M:82[C]:TRP:HB3	2.13	0.49
1:N:264[C]:GLU:HB2	1:N:265[C]:PRO:HD3	1.93	0.49
1:A:298[D]:GLU:CD	1:A:298[D]:GLU:H	2.14	0.49
1:I:79[D]:GLU:O	1:I:82[D]:TRP:HB3	2.12	0.49
1:L:79[D]:GLU:O	1:L:82[D]:TRP:HB3	2.12	0.49
1:M:187[D]:CYS:HB2	2:M:550[D]:UMP:C4	2.47	0.49
1:B:137[A]:GLU:OE1	1:C:147[A]:GLY:CA	2.60	0.49
1:N:264[A]:GLU:HB2	1:N:265[A]:PRO:HD3	1.93	0.49
1:B:137[B]:GLU:OE1	1:C:147[B]:GLY:CA	2.60	0.49
1:K:189[B]:MET:O	1:K:190[B]:PHE:HB3	2.12	0.49
1:B:137[C]:GLU:OE1	1:C:147[C]:GLY:CA	2.60	0.49
1:O:79[C]:GLU:O	1:O:82[C]:TRP:HB3	2.13	0.49
1:B:137[D]:GLU:OE1	1:C:147[D]:GLY:CA	2.60	0.49
1:K:189[D]:MET:O	1:K:190[D]:PHE:HB3	2.11	0.49
1:K:212[D]:LEU:HD23	1:K:212[D]:LEU:C	2.32	0.49
1:L:220[D]:LEU:HG	1:L:224[D]:VAL:HG21	1.93	0.49
1:M:109[D]:PHE:O	1:M:112[D]:LYS:HB3	2.12	0.49
1:P:70[D]:ARG:NH1	1:P:310[D]:LYS:HD3	2.27	0.49
1:M:70[A]:ARG:NH1	1:M:310[A]:LYS:HD3	2.28	0.49
1:O:212[A]:LEU:HD12	1:P:50[A]:ALA:CB	2.42	0.49
1:N:264[B]:GLU:HB2	1:N:265[B]:PRO:HD3	1.93	0.49
1:M:298[C]:GLU:H	1:M:298[C]:GLU:CD	2.16	0.49
1:P:44[C]:GLY:C	1:P:260[C]:ARG:HG2	2.33	0.49
1:M:30[D]:ILE:HG22	1:M:46[D]:VAL:HG13	1.93	0.49
1:A:212[A]:LEU:HD12	1:B:50[A]:ALA:CB	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:264[A]:GLU:HB2	1:G:265[A]:PRO:HD3	1.95	0.49
1:G:38[A]:PRO:HD2	1:H:165[A]:THR:HG21	1.94	0.49
1:G:176[A]:PRO:HD2	1:H:134[A]:PHE:CZ	2.47	0.49
1:J:264[A]:GLU:HB2	1:J:265[A]:PRO:HD3	1.93	0.49
1:A:212[B]:LEU:HD12	1:B:50[B]:ALA:CB	2.43	0.49
1:G:264[B]:GLU:HB2	1:G:265[B]:PRO:HD3	1.95	0.49
1:G:176[B]:PRO:HD2	1:H:134[B]:PHE:CZ	2.47	0.49
1:G:38[B]:PRO:HD2	1:H:165[B]:THR:HG21	1.94	0.49
1:I:212[B]:LEU:HD23	1:I:212[B]:LEU:C	2.32	0.49
1:K:50[B]:ALA:CB	1:L:212[B]:LEU:HD12	2.42	0.49
1:M:187[B]:CYS:HB2	2:M:550[B]:UMP:C4	2.47	0.49
1:N:44[B]:GLY:C	1:N:260[B]:ARG:HG2	2.33	0.49
1:P:44[B]:GLY:C	1:P:260[B]:ARG:HG2	2.33	0.49
1:A:212[C]:LEU:HD12	1:B:50[C]:ALA:CB	2.43	0.49
1:G:176[C]:PRO:HD2	1:H:134[C]:PHE:CZ	2.47	0.49
1:G:264[C]:GLU:HB2	1:G:265[C]:PRO:HD3	1.95	0.49
1:G:38[C]:PRO:HD2	1:H:165[C]:THR:HG21	1.94	0.49
1:I:212[C]:LEU:C	1:I:212[C]:LEU:HD23	2.32	0.49
1:M:212[C]:LEU:C	1:M:212[C]:LEU:HD23	2.32	0.49
1:P:70[C]:ARG:NH1	1:P:310[C]:LYS:HD3	2.27	0.49
1:A:212[D]:LEU:HD12	1:B:50[D]:ALA:CB	2.43	0.49
1:G:264[D]:GLU:HB2	1:G:265[D]:PRO:HD3	1.95	0.49
1:G:38[D]:PRO:HD2	1:H:165[D]:THR:HG21	1.94	0.49
1:G:176[D]:PRO:HD2	1:H:134[D]:PHE:CZ	2.47	0.49
1:D:201[A]:ASP:O	1:D:202[A]:SER:HB3	2.12	0.49
1:F:269[A]:GLN:HB2	1:F:311[A]:ILE:HD13	1.95	0.49
1:G:44[A]:GLY:C	1:G:260[A]:ARG:HG2	2.32	0.49
1:I:38[A]:PRO:HD2	1:J:165[A]:THR:HG21	1.95	0.49
1:N:79[A]:GLU:O	1:N:82[A]:TRP:HB3	2.13	0.49
1:D:201[B]:ASP:O	1:D:202[B]:SER:HB3	2.12	0.49
1:F:269[B]:GLN:HB2	1:F:311[B]:ILE:HD13	1.95	0.49
1:G:44[B]:GLY:C	1:G:260[B]:ARG:HG2	2.32	0.49
1:D:201[C]:ASP:O	1:D:202[C]:SER:HB3	2.12	0.49
1:F:269[C]:GLN:HB2	1:F:311[C]:ILE:HD13	1.95	0.49
1:G:44[C]:GLY:C	1:G:260[C]:ARG:HG2	2.32	0.49
1:M:109[C]:PHE:O	1:M:112[C]:LYS:HB3	2.12	0.49
1:D:201[D]:ASP:O	1:D:202[D]:SER:HB3	2.12	0.49
1:F:269[D]:GLN:HB2	1:F:311[D]:ILE:HD13	1.95	0.49
1:G:44[D]:GLY:C	1:G:260[D]:ARG:HG2	2.32	0.49
1:P:44[D]:GLY:C	1:P:260[D]:ARG:HG2	2.33	0.49
1:C:190[A]:PHE:HA	4:C:1021[A]:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:264[A]:GLU:HB2	1:F:265[A]:PRO:HD3	1.94	0.49
1:C:190[B]:PHE:HA	4:C:1021[B]:HOH:O	2.12	0.49
1:F:264[B]:GLU:HB2	1:F:265[B]:PRO:HD3	1.94	0.49
1:C:190[C]:PHE:HA	4:C:1021[C]:HOH:O	2.12	0.49
1:F:264[C]:GLU:HB2	1:F:265[C]:PRO:HD3	1.94	0.49
1:L:264[C]:GLU:HB2	1:L:265[C]:PRO:HD3	1.94	0.49
1:M:30[C]:ILE:HG22	1:M:46[C]:VAL:HG13	1.94	0.49
1:M:187[C]:CYS:HB2	2:M:550[C]:UMP:C4	2.47	0.49
1:N:44[C]:GLY:C	1:N:260[C]:ARG:HG2	2.33	0.49
1:H:202[C]:SER:CB	1:N:275[C]:ARG:HG3	2.36	0.49
1:C:190[D]:PHE:HA	4:C:1021[D]:HOH:O	2.12	0.49
1:F:264[D]:GLU:HB2	1:F:265[D]:PRO:HD3	1.94	0.49
1:N:44[D]:GLY:C	1:N:260[D]:ARG:HG2	2.33	0.49
1:C:297[A]:VAL:HG23	4:C:629[A]:HOH:O	2.12	0.49
1:E:134[A]:PHE:CZ	1:F:176[A]:PRO:HD2	2.48	0.49
1:C:297[B]:VAL:HG23	4:C:629[B]:HOH:O	2.12	0.49
1:E:134[B]:PHE:CZ	1:F:176[B]:PRO:HD2	2.48	0.49
1:L:264[B]:GLU:HB2	1:L:265[B]:PRO:HD3	1.94	0.49
1:C:297[C]:VAL:HG23	4:C:629[C]:HOH:O	2.12	0.49
1:E:134[C]:PHE:CZ	1:F:176[C]:PRO:HD2	2.48	0.49
1:K:212[C]:LEU:HD23	1:K:212[C]:LEU:C	2.33	0.49
1:N:73[C]:LEU:HD21	1:N:302[C]:VAL:HG21	1.95	0.49
1:C:297[D]:VAL:HG23	4:C:629[D]:HOH:O	2.12	0.49
1:E:134[D]:PHE:CZ	1:F:176[D]:PRO:HD2	2.48	0.49
1:M:212[D]:LEU:HD23	1:M:212[D]:LEU:C	2.32	0.49
1:C:212[A]:LEU:HD23	1:C:212[A]:LEU:C	2.33	0.49
1:C:44[A]:GLY:C	1:C:260[A]:ARG:HG2	2.32	0.49
1:H:287[A]:GLU:HG2	1:J:146[A]:LYS:HZ1	1.74	0.49
1:I:220[A]:LEU:HG	1:I:224[A]:VAL:HG21	1.95	0.49
1:C:212[B]:LEU:C	1:C:212[B]:LEU:HD23	2.33	0.49
1:C:44[B]:GLY:C	1:C:260[B]:ARG:HG2	2.32	0.49
1:P:79[B]:GLU:O	1:P:82[B]:TRP:HB3	2.13	0.49
1:C:212[C]:LEU:HD23	1:C:212[C]:LEU:C	2.33	0.49
1:C:44[C]:GLY:C	1:C:260[C]:ARG:HG2	2.32	0.49
1:C:212[D]:LEU:C	1:C:212[D]:LEU:HD23	2.33	0.49
1:C:44[D]:GLY:C	1:C:260[D]:ARG:HG2	2.32	0.49
1:K:165[D]:THR:HG21	1:L:38[D]:PRO:HD2	1.95	0.49
1:A:212[A]:LEU:HD23	1:A:212[A]:LEU:C	2.33	0.48
1:H:269[A]:GLN:HB2	1:H:311[A]:ILE:HD13	1.96	0.48
1:L:264[A]:GLU:HB2	1:L:265[A]:PRO:HD3	1.94	0.48
1:M:187[A]:CYS:HB2	2:M:550[A]:UMP:C4	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:74[A]:ARG:NH2	1:N:70[A]:ARG:HD3	2.28	0.48
1:O:109[A]:PHE:O	1:O:112[A]:LYS:HB3	2.13	0.48
1:A:212[B]:LEU:HD23	1:A:212[B]:LEU:C	2.33	0.48
1:H:269[B]:GLN:HB2	1:H:311[B]:ILE:HD13	1.96	0.48
1:K:212[B]:LEU:C	1:K:212[B]:LEU:HD23	2.33	0.48
1:A:212[C]:LEU:HD23	1:A:212[C]:LEU:C	2.33	0.48
1:H:269[C]:GLN:HB2	1:H:311[C]:ILE:HD13	1.96	0.48
1:P:43[C]:THR:HG21	1:P:316[C]:SER:OG	2.13	0.48
1:A:212[D]:LEU:HD23	1:A:212[D]:LEU:C	2.33	0.48
1:H:269[D]:GLN:HB2	1:H:311[D]:ILE:HD13	1.96	0.48
1:F:212[A]:LEU:HD23	1:F:213[A]:MET:N	2.27	0.48
1:L:44[A]:GLY:C	1:L:260[A]:ARG:HG2	2.32	0.48
1:F:212[B]:LEU:HD23	1:F:213[B]:MET:N	2.27	0.48
1:F:212[C]:LEU:HD23	1:F:213[C]:MET:N	2.27	0.48
1:L:79[C]:GLU:O	1:L:82[C]:TRP:HB3	2.13	0.48
1:F:212[D]:LEU:HD23	1:F:213[D]:MET:N	2.27	0.48
1:I:212[D]:LEU:C	1:I:212[D]:LEU:HD23	2.33	0.48
1:M:165[D]:THR:HG21	1:N:38[D]:PRO:HD2	1.95	0.48
1:P:118[A]:ARG:HD2	1:P:122[A]:ASP:OD2	2.13	0.48
1:I:38[B]:PRO:HD2	1:J:165[B]:THR:HG21	1.95	0.48
1:P:70[B]:ARG:NH1	1:P:310[B]:LYS:HD3	2.28	0.48
1:K:50[D]:ALA:CB	1:L:212[D]:LEU:HD12	2.43	0.48
1:O:50[D]:ALA:HB2	1:P:212[D]:LEU:HD12	1.95	0.48
1:A:176[A]:PRO:HD2	1:B:134[A]:PHE:CZ	2.48	0.48
1:M:109[A]:PHE:O	1:M:112[A]:LYS:HB3	2.13	0.48
1:A:176[B]:PRO:HD2	1:B:134[B]:PHE:CZ	2.48	0.48
1:A:176[C]:PRO:HD2	1:B:134[C]:PHE:CZ	2.48	0.48
1:J:220[C]:LEU:HG	1:J:224[C]:VAL:HG21	1.94	0.48
1:A:176[D]:PRO:HD2	1:B:134[D]:PHE:CZ	2.48	0.48
1:M:220[B]:LEU:HG	1:M:224[B]:VAL:HG21	1.96	0.48
1:M:30[B]:ILE:HG22	1:M:46[B]:VAL:HG13	1.94	0.48
1:I:38[C]:PRO:HD2	1:J:165[C]:THR:HG21	1.95	0.48
1:O:53[D]:SER:HB3	1:O:252[D]:GLN:HE21	1.77	0.48
1:K:70[A]:ARG:NH1	1:K:310[A]:LYS:HD3	2.29	0.48
1:N:53[B]:SER:HB3	1:N:252[B]:GLN:NE2	2.28	0.48
1:C:176[A]:PRO:HD2	1:D:134[A]:PHE:CZ	2.48	0.48
1:D:269[A]:GLN:HB2	1:D:311[A]:ILE:HD13	1.95	0.48
1:C:176[B]:PRO:HD2	1:D:134[B]:PHE:CZ	2.48	0.48
1:D:269[B]:GLN:HB2	1:D:311[B]:ILE:HD13	1.95	0.48
1:M:165[B]:THR:HG21	1:N:38[B]:PRO:HD2	1.96	0.48
1:C:176[C]:PRO:HD2	1:D:134[C]:PHE:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269[C]:GLN:HB2	1:D:311[C]:ILE:HD13	1.95	0.48
1:O:53[C]:SER:HB3	1:O:252[C]:GLN:HE21	1.77	0.48
1:C:176[D]:PRO:HD2	1:D:134[D]:PHE:CZ	2.48	0.48
1:D:269[D]:GLN:HB2	1:D:311[D]:ILE:HD13	1.95	0.48
1:D:298[A]:GLU:CD	1:D:298[A]:GLU:H	2.16	0.48
1:F:47[A]:ALA:HB2	1:F:257[A]:HIS:HB3	1.96	0.48
1:N:53[A]:SER:HB3	1:N:252[A]:GLN:NE2	2.28	0.48
1:D:298[B]:GLU:H	1:D:298[B]:GLU:CD	2.16	0.48
1:F:47[B]:ALA:HB2	1:F:257[B]:HIS:HB3	1.96	0.48
1:D:298[C]:GLU:CD	1:D:298[C]:GLU:H	2.16	0.48
1:F:47[C]:ALA:HB2	1:F:257[C]:HIS:HB3	1.96	0.48
1:K:50[C]:ALA:CB	1:L:212[C]:LEU:HD12	2.43	0.48
1:D:298[D]:GLU:H	1:D:298[D]:GLU:CD	2.16	0.48
1:F:47[D]:ALA:HB2	1:F:257[D]:HIS:HB3	1.96	0.48
1:M:43[D]:THR:HG21	1:M:316[D]:SER:OG	2.13	0.48
1:O:30[D]:ILE:HG22	1:O:46[D]:VAL:HG13	1.95	0.48
1:K:190[A]:PHE:HZ	1:L:214[A]:TYR:CD2	2.31	0.48
1:N:220[C]:LEU:HG	1:N:224[C]:VAL:HG21	1.95	0.48
1:O:212[C]:LEU:HD23	1:O:212[C]:LEU:C	2.33	0.48
1:B:212[A]:LEU:HD23	1:B:213[A]:MET:N	2.29	0.48
1:D:100[A]:ILE:HB	3:D:2501[A]:CB3:C13	2.43	0.48
1:J:137[A]:GLU:OE1	1:K:147[A]:GLY:CA	2.62	0.48
1:B:212[B]:LEU:HD23	1:B:213[B]:MET:N	2.29	0.48
1:D:100[B]:ILE:HB	3:D:2501[B]:CB3:C13	2.43	0.48
1:O:30[B]:ILE:HG22	1:O:46[B]:VAL:HG13	1.95	0.48
1:B:212[C]:LEU:HD23	1:B:213[C]:MET:N	2.29	0.48
1:D:100[C]:ILE:HB	3:D:2501[C]:CB3:C13	2.43	0.48
1:O:46[C]:VAL:HG13	1:O:46[C]:VAL:O	2.13	0.48
1:B:212[D]:LEU:HD23	1:B:213[D]:MET:N	2.29	0.48
1:D:100[D]:ILE:HB	3:D:2501[D]:CB3:C13	2.43	0.48
1:D:53[A]:SER:HB3	1:D:252[A]:GLN:NE2	2.29	0.47
1:E:264[A]:GLU:HB2	1:E:265[A]:PRO:HD3	1.96	0.47
1:G:269[A]:GLN:HB2	1:G:311[A]:ILE:HD13	1.97	0.47
1:M:79[A]:GLU:O	1:M:82[A]:TRP:HB3	2.14	0.47
1:D:53[B]:SER:HB3	1:D:252[B]:GLN:NE2	2.29	0.47
1:E:264[B]:GLU:HB2	1:E:265[B]:PRO:HD3	1.96	0.47
1:G:269[B]:GLN:HB2	1:G:311[B]:ILE:HD13	1.97	0.47
1:N:220[B]:LEU:HG	1:N:224[B]:VAL:HG21	1.95	0.47
1:O:50[B]:ALA:HB2	1:P:212[B]:LEU:HD12	1.96	0.47
1:P:43[B]:THR:HG21	1:P:316[B]:SER:OG	2.14	0.47
1:D:53[C]:SER:HB3	1:D:252[C]:GLN:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:264[C]:GLU:HB2	1:E:265[C]:PRO:HD3	1.96	0.47
1:G:269[C]:GLN:HB2	1:G:311[C]:ILE:HD13	1.97	0.47
1:O:70[C]:ARG:NH1	1:O:310[C]:LYS:HD3	2.29	0.47
1:D:53[D]:SER:HB3	1:D:252[D]:GLN:NE2	2.29	0.47
1:E:264[D]:GLU:HB2	1:E:265[D]:PRO:HD3	1.96	0.47
1:G:269[D]:GLN:HB2	1:G:311[D]:ILE:HD13	1.97	0.47
1:M:220[D]:LEU:HG	1:M:224[D]:VAL:HG21	1.96	0.47
1:N:220[D]:LEU:HG	1:N:224[D]:VAL:HG21	1.95	0.47
1:B:53[A]:SER:HB3	1:B:252[A]:GLN:NE2	2.29	0.47
1:E:186[A]:PRO:HG3	4:E:1092[A]:HOH:O	2.14	0.47
1:E:269[A]:GLN:HB2	1:E:311[A]:ILE:HD13	1.97	0.47
1:P:79[A]:GLU:O	1:P:82[A]:TRP:HB3	2.15	0.47
1:B:53[B]:SER:HB3	1:B:252[B]:GLN:NE2	2.29	0.47
1:E:186[B]:PRO:HG3	4:E:1092[B]:HOH:O	2.14	0.47
1:E:269[B]:GLN:HB2	1:E:311[B]:ILE:HD13	1.97	0.47
1:I:212[B]:LEU:HD12	1:J:50[B]:ALA:CB	2.44	0.47
1:M:43[B]:THR:HG21	1:M:316[B]:SER:OG	2.14	0.47
1:O:53[B]:SER:HB3	1:O:252[B]:GLN:HE21	1.77	0.47
1:B:53[C]:SER:HB3	1:B:252[C]:GLN:NE2	2.29	0.47
1:E:186[C]:PRO:HG3	4:E:1092[C]:HOH:O	2.14	0.47
1:E:269[C]:GLN:HB2	1:E:311[C]:ILE:HD13	1.97	0.47
1:J:46[C]:VAL:HG13	1:J:46[C]:VAL:O	2.14	0.47
1:O:30[C]:ILE:HG22	1:O:46[C]:VAL:HG13	1.96	0.47
1:B:53[D]:SER:HB3	1:B:252[D]:GLN:NE2	2.29	0.47
1:E:186[D]:PRO:HG3	4:E:1092[D]:HOH:O	2.14	0.47
1:E:269[D]:GLN:HB2	1:E:311[D]:ILE:HD13	1.97	0.47
1:P:43[D]:THR:HG21	1:P:316[D]:SER:OG	2.14	0.47
1:L:53[C]:SER:HB3	1:L:252[C]:GLN:HE21	1.79	0.47
1:L:44[C]:GLY:C	1:L:260[C]:ARG:HG2	2.33	0.47
1:J:46[D]:VAL:O	1:J:46[D]:VAL:HG13	2.15	0.47
1:N:53[D]:SER:HB3	1:N:252[D]:GLN:NE2	2.29	0.47
1:H:264[A]:GLU:HB2	1:H:265[A]:PRO:HD3	1.95	0.47
1:I:147[A]:GLY:CA	1:L:137[A]:GLU:OE1	2.62	0.47
1:H:264[B]:GLU:HB2	1:H:265[B]:PRO:HD3	1.95	0.47
1:N:73[B]:LEU:HD21	1:N:302[B]:VAL:HG21	1.96	0.47
1:H:264[C]:GLU:HB2	1:H:265[C]:PRO:HD3	1.95	0.47
1:H:264[D]:GLU:HB2	1:H:265[D]:PRO:HD3	1.95	0.47
1:B:264[A]:GLU:HB2	1:B:265[A]:PRO:HD3	1.95	0.47
1:C:134[A]:PHE:CZ	1:D:176[A]:PRO:HD2	2.50	0.47
1:C:50[A]:ALA:CB	1:D:212[A]:LEU:HD12	2.45	0.47
1:M:50[A]:ALA:CB	1:N:212[A]:LEU:HD12	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264[B]:GLU:HB2	1:B:265[B]:PRO:HD3	1.95	0.47
1:C:134[B]:PHE:CZ	1:D:176[B]:PRO:HD2	2.50	0.47
1:C:50[B]:ALA:CB	1:D:212[B]:LEU:HD12	2.45	0.47
1:L:44[B]:GLY:C	1:L:260[B]:ARG:HG2	2.34	0.47
1:B:264[C]:GLU:HB2	1:B:265[C]:PRO:HD3	1.95	0.47
1:C:134[C]:PHE:CZ	1:D:176[C]:PRO:HD2	2.50	0.47
1:C:50[C]:ALA:CB	1:D:212[C]:LEU:HD12	2.45	0.47
1:B:264[D]:GLU:HB2	1:B:265[D]:PRO:HD3	1.95	0.47
1:C:50[D]:ALA:CB	1:D:212[D]:LEU:HD12	2.45	0.47
1:C:134[D]:PHE:CZ	1:D:176[D]:PRO:HD2	2.50	0.47
1:I:79[A]:GLU:O	1:I:82[A]:TRP:HB3	2.14	0.47
1:J:220[B]:LEU:HG	1:J:224[B]:VAL:HG21	1.95	0.47
1:L:53[B]:SER:HB3	1:L:252[B]:GLN:HE21	1.80	0.47
1:N:269[B]:GLN:HB2	1:N:311[B]:ILE:HD13	1.97	0.47
1:J:220[D]:LEU:HG	1:J:224[D]:VAL:HG21	1.95	0.47
1:L:44[D]:GLY:C	1:L:260[D]:ARG:HG2	2.34	0.47
1:C:74[A]:ARG:HH21	1:F:70[A]:ARG:HD2	1.79	0.47
1:G:118[A]:ARG:HD3	1:G:122[A]:ASP:OD2	2.14	0.47
1:K:44[A]:GLY:C	1:K:260[A]:ARG:HG2	2.34	0.47
1:E:212[A]:LEU:HD12	1:F:50[A]:ALA:CB	2.45	0.47
1:M:44[A]:GLY:C	1:M:260[A]:ARG:HG2	2.35	0.47
1:C:74[B]:ARG:HH21	1:F:70[B]:ARG:HD2	1.79	0.47
1:G:118[B]:ARG:HD3	1:G:122[B]:ASP:OD2	2.14	0.47
1:K:190[B]:PHE:HZ	1:L:214[B]:TYR:CD2	2.32	0.47
1:E:212[B]:LEU:HD12	1:F:50[B]:ALA:CB	2.45	0.47
1:C:74[C]:ARG:HH21	1:F:70[C]:ARG:HD2	1.79	0.47
1:G:118[C]:ARG:HD3	1:G:122[C]:ASP:OD2	2.14	0.47
1:E:212[C]:LEU:HD12	1:F:50[C]:ALA:CB	2.45	0.47
1:C:74[D]:ARG:HH21	1:F:70[D]:ARG:HD2	1.79	0.47
1:G:118[D]:ARG:HD3	1:G:122[D]:ASP:OD2	2.14	0.47
1:E:212[D]:LEU:HD12	1:F:50[D]:ALA:CB	2.45	0.47
1:E:190[A]:PHE:HZ	1:F:214[A]:TYR:CD2	2.33	0.47
1:G:190[A]:PHE:HZ	1:H:214[A]:TYR:CD2	2.33	0.47
1:E:190[B]:PHE:HZ	1:F:214[B]:TYR:CD2	2.33	0.47
1:G:190[B]:PHE:HZ	1:H:214[B]:TYR:CD2	2.33	0.47
1:E:190[C]:PHE:HZ	1:F:214[C]:TYR:CD2	2.33	0.47
1:G:190[C]:PHE:HZ	1:H:214[C]:TYR:CD2	2.33	0.47
1:K:220[C]:LEU:HG	1:K:224[C]:VAL:HG21	1.97	0.47
1:M:220[C]:LEU:HG	1:M:224[C]:VAL:HG21	1.97	0.47
1:M:134[C]:PHE:CZ	1:N:176[C]:PRO:HD2	2.50	0.47
1:E:190[D]:PHE:HZ	1:F:214[D]:TYR:CD2	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:190[D]:PHE:HZ	1:H:214[D]:TYR:CD2	2.33	0.47
1:O:70[D]:ARG:NH1	1:O:310[D]:LYS:HD3	2.30	0.47
1:F:24[A]:LEU:HD11	1:F:68[A]:THR:HG21	1.97	0.47
1:K:50[A]:ALA:CB	1:L:212[A]:LEU:HD12	2.44	0.47
1:K:79[A]:GLU:O	1:K:82[A]:TRP:HB3	2.15	0.47
1:O:79[A]:GLU:O	1:O:82[A]:TRP:HB3	2.15	0.47
1:F:24[B]:LEU:HD11	1:F:68[B]:THR:HG21	1.97	0.47
1:F:24[C]:LEU:HD11	1:F:68[C]:THR:HG21	1.97	0.47
1:O:189[C]:MET:O	1:O:190[C]:PHE:HB3	2.14	0.47
1:F:24[D]:LEU:HD11	1:F:68[D]:THR:HG21	1.97	0.47
1:C:269[A]:GLN:HB2	1:C:311[A]:ILE:HD13	1.97	0.47
1:I:219[A]:ASP:HB2	2:I:350[A]:UMP:O3'	2.14	0.47
1:C:269[B]:GLN:HB2	1:C:311[B]:ILE:HD13	1.97	0.47
1:C:269[C]:GLN:HB2	1:C:311[C]:ILE:HD13	1.97	0.47
1:C:269[D]:GLN:HB2	1:C:311[D]:ILE:HD13	1.97	0.47
1:K:220[D]:LEU:HG	1:K:224[D]:VAL:HG21	1.97	0.47
1:L:26[D]:LEU:O	1:L:30[D]:ILE:HG13	2.15	0.47
1:O:46[D]:VAL:HG13	1:O:46[D]:VAL:O	2.14	0.47
1:D:212[A]:LEU:HD23	1:D:212[A]:LEU:C	2.35	0.46
1:D:212[B]:LEU:C	1:D:212[B]:LEU:HD23	2.35	0.46
1:M:134[B]:PHE:CZ	1:N:176[B]:PRO:HD2	2.51	0.46
1:D:212[C]:LEU:HD23	1:D:212[C]:LEU:C	2.35	0.46
1:K:190[C]:PHE:HZ	1:L:214[C]:TYR:CD2	2.33	0.46
1:N:53[C]:SER:HB3	1:N:252[C]:GLN:NE2	2.29	0.46
1:D:212[D]:LEU:HD23	1:D:212[D]:LEU:C	2.35	0.46
1:A:250[A]:ILE:N	1:A:250[A]:ILE:HD12	2.30	0.46
1:A:264[A]:GLU:HB2	1:A:265[A]:PRO:HD3	1.96	0.46
1:A:250[B]:ILE:HD12	1:A:250[B]:ILE:N	2.30	0.46
1:A:264[B]:GLU:HB2	1:A:265[B]:PRO:HD3	1.96	0.46
1:K:44[B]:GLY:C	1:K:260[B]:ARG:HG2	2.35	0.46
1:O:189[B]:MET:O	1:O:190[B]:PHE:HB3	2.15	0.46
1:A:250[C]:ILE:HD12	1:A:250[C]:ILE:N	2.30	0.46
1:A:264[C]:GLU:HB2	1:A:265[C]:PRO:HD3	1.96	0.46
1:I:212[C]:LEU:HD12	1:J:50[C]:ALA:CB	2.46	0.46
1:O:50[C]:ALA:HB2	1:P:212[C]:LEU:HD12	1.97	0.46
1:A:250[D]:ILE:HD12	1:A:250[D]:ILE:N	2.30	0.46
1:A:264[D]:GLU:HB2	1:A:265[D]:PRO:HD3	1.96	0.46
1:I:212[D]:LEU:HD12	1:J:50[D]:ALA:CB	2.46	0.46
1:L:53[D]:SER:HB3	1:L:252[D]:GLN:HE21	1.80	0.46
1:N:73[D]:LEU:HD21	1:N:302[D]:VAL:HG21	1.97	0.46
1:O:189[D]:MET:O	1:O:190[D]:PHE:HB3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201[A]:ASP:O	1:A:202[A]:SER:HB3	2.16	0.46
1:E:50[A]:ALA:HB2	1:F:212[A]:LEU:HD12	1.98	0.46
1:G:217[A]:SER:HG	1:H:167[A]:ARG:HD3	1.80	0.46
1:N:269[A]:GLN:HB2	1:N:311[A]:ILE:HD13	1.98	0.46
1:A:201[B]:ASP:O	1:A:202[B]:SER:HB3	2.16	0.46
1:E:50[B]:ALA:HB2	1:F:212[B]:LEU:HD12	1.98	0.46
1:G:217[B]:SER:HG	1:H:167[B]:ARG:HD3	1.80	0.46
1:J:46[B]:VAL:O	1:J:46[B]:VAL:HG13	2.16	0.46
1:O:70[B]:ARG:NH1	1:O:310[B]:LYS:HD3	2.30	0.46
1:A:201[C]:ASP:O	1:A:202[C]:SER:HB3	2.16	0.46
1:E:50[C]:ALA:HB2	1:F:212[C]:LEU:HD12	1.98	0.46
1:G:217[C]:SER:HG	1:H:167[C]:ARG:HD3	1.80	0.46
1:J:189[C]:MET:O	1:J:190[C]:PHE:HB3	2.15	0.46
1:N:26[C]:LEU:O	1:N:30[C]:ILE:HG13	2.15	0.46
1:A:201[D]:ASP:O	1:A:202[D]:SER:HB3	2.16	0.46
1:E:50[D]:ALA:HB2	1:F:212[D]:LEU:HD12	1.98	0.46
1:G:217[D]:SER:HG	1:H:167[D]:ARG:HD3	1.80	0.46
1:L:79[A]:GLU:O	1:L:82[A]:TRP:HB3	2.15	0.46
1:M:134[A]:PHE:CZ	1:N:176[A]:PRO:HD2	2.51	0.46
1:M:220[A]:LEU:HG	1:M:224[A]:VAL:HG21	1.98	0.46
1:I:134[B]:PHE:CZ	1:J:176[B]:PRO:HD2	2.51	0.46
1:O:46[B]:VAL:HG13	1:O:46[B]:VAL:O	2.14	0.46
1:N:269[D]:GLN:HB2	1:N:311[D]:ILE:HD13	1.98	0.46
1:A:269[A]:GLN:HB2	1:A:311[A]:ILE:HD13	1.97	0.46
1:C:100[A]:ILE:HB	3:C:2451[A]:CB3:C13	2.45	0.46
1:L:220[A]:LEU:HG	1:L:224[A]:VAL:HG21	1.96	0.46
1:A:269[B]:GLN:HB2	1:A:311[B]:ILE:HD13	1.97	0.46
1:C:100[B]:ILE:HB	3:C:2451[B]:CB3:C13	2.45	0.46
1:A:269[C]:GLN:HB2	1:A:311[C]:ILE:HD13	1.97	0.46
1:C:100[C]:ILE:HB	3:C:2451[C]:CB3:C13	2.45	0.46
1:J:79[C]:GLU:O	1:J:82[C]:TRP:HB3	2.15	0.46
1:A:269[D]:GLN:HB2	1:A:311[D]:ILE:HD13	1.97	0.46
1:C:100[D]:ILE:HB	3:C:2451[D]:CB3:C13	2.45	0.46
1:I:134[D]:PHE:CZ	1:J:176[D]:PRO:HD2	2.51	0.46
1:M:134[D]:PHE:CZ	1:N:176[D]:PRO:HD2	2.51	0.46
1:K:44[C]:GLY:C	1:K:260[C]:ARG:HG2	2.35	0.46
1:N:269[C]:GLN:HB2	1:N:311[C]:ILE:HD13	1.98	0.46
1:F:250[A]:ILE:N	1:F:250[A]:ILE:HD12	2.30	0.46
1:P:220[A]:LEU:HG	1:P:224[A]:VAL:HG21	1.96	0.46
1:F:250[B]:ILE:HD12	1:F:250[B]:ILE:N	2.30	0.46
1:I:219[B]:ASP:HB2	2:I:350[B]:UMP:O3'	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:189[B]:MET:O	1:J:190[B]:PHE:HB3	2.16	0.46
1:F:250[C]:ILE:N	1:F:250[C]:ILE:HD12	2.30	0.46
1:M:157[C]:ILE:HD13	1:M:238[C]:ILE:HG23	1.98	0.46
1:F:250[D]:ILE:N	1:F:250[D]:ILE:HD12	2.30	0.46
1:K:44[D]:GLY:C	1:K:260[D]:ARG:HG2	2.35	0.46
1:M:44[D]:GLY:C	1:M:260[D]:ARG:HG2	2.36	0.46
1:J:220[A]:LEU:HG	1:J:224[A]:VAL:HG21	1.97	0.46
1:N:26[B]:LEU:O	1:N:30[B]:ILE:HG13	2.16	0.46
1:L:70[C]:ARG:NH1	1:L:310[C]:LYS:HD3	2.31	0.46
1:M:44[C]:GLY:C	1:M:260[C]:ARG:HG2	2.36	0.46
1:M:176[A]:PRO:HD2	1:N:134[A]:PHE:CZ	2.50	0.46
1:J:79[B]:GLU:O	1:J:82[B]:TRP:HB3	2.15	0.46
1:M:157[B]:ILE:HD13	1:M:238[B]:ILE:HG23	1.98	0.46
1:I:134[C]:PHE:CZ	1:J:176[C]:PRO:HD2	2.51	0.46
1:I:46[D]:VAL:HG13	1:I:46[D]:VAL:O	2.16	0.46
1:O:73[D]:LEU:HD21	1:O:302[D]:VAL:HG21	1.98	0.46
1:J:79[A]:GLU:O	1:J:82[A]:TRP:HB3	2.16	0.46
1:J:26[B]:LEU:O	1:J:30[B]:ILE:HG13	2.17	0.46
1:M:44[B]:GLY:C	1:M:260[B]:ARG:HG2	2.36	0.46
1:N:70[C]:ARG:NH1	1:N:310[C]:LYS:HD3	2.30	0.46
1:J:79[D]:GLU:O	1:J:82[D]:TRP:HB3	2.16	0.46
1:C:250[A]:ILE:N	1:C:250[A]:ILE:HD12	2.31	0.45
1:I:165[A]:THR:HG21	1:J:38[A]:PRO:HD2	1.98	0.45
1:I:190[A]:PHE:HZ	1:J:214[A]:TYR:CD2	2.34	0.45
1:I:212[A]:LEU:HD12	1:J:50[A]:ALA:CB	2.47	0.45
1:C:250[B]:ILE:N	1:C:250[B]:ILE:HD12	2.31	0.45
1:K:220[B]:LEU:HG	1:K:224[B]:VAL:HG21	1.98	0.45
1:C:250[C]:ILE:N	1:C:250[C]:ILE:HD12	2.31	0.45
1:I:165[C]:THR:HG21	1:J:38[C]:PRO:HD2	1.98	0.45
1:C:250[D]:ILE:N	1:C:250[D]:ILE:HD12	2.31	0.45
1:O:269[A]:GLN:HB2	1:O:311[A]:ILE:HD13	1.99	0.45
1:I:46[B]:VAL:O	1:I:46[B]:VAL:HG13	2.17	0.45
1:I:46[C]:VAL:O	1:I:46[C]:VAL:HG13	2.17	0.45
1:O:269[C]:GLN:HB2	1:O:311[C]:ILE:HD13	1.99	0.45
1:N:26[D]:LEU:O	1:N:30[D]:ILE:HG13	2.16	0.45
1:K:189[A]:MET:O	1:K:190[A]:PHE:HB3	2.15	0.45
1:I:165[B]:THR:HG21	1:J:38[B]:PRO:HD2	1.98	0.45
1:L:46[B]:VAL:HG13	1:L:46[B]:VAL:O	2.16	0.45
1:N:70[B]:ARG:NH1	1:N:310[B]:LYS:HD3	2.30	0.45
1:P:219[B]:ASP:HB2	2:P:700[B]:UMP:O3'	2.17	0.45
1:J:26[D]:LEU:O	1:J:30[D]:ILE:HG13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264[A]:GLU:HB2	1:C:265[A]:PRO:HD3	1.97	0.45
1:E:212[A]:LEU:HD23	1:E:213[A]:MET:N	2.32	0.45
1:H:118[A]:ARG:HD3	1:H:122[A]:ASP:OD2	2.16	0.45
1:C:264[B]:GLU:HB2	1:C:265[B]:PRO:HD3	1.97	0.45
1:E:212[B]:LEU:HD23	1:E:213[B]:MET:N	2.32	0.45
1:H:118[B]:ARG:HD3	1:H:122[B]:ASP:OD2	2.16	0.45
1:C:264[C]:GLU:HB2	1:C:265[C]:PRO:HD3	1.97	0.45
1:E:212[C]:LEU:HD23	1:E:213[C]:MET:N	2.32	0.45
1:H:118[C]:ARG:HD3	1:H:122[C]:ASP:OD2	2.16	0.45
1:O:73[C]:LEU:HD21	1:O:302[C]:VAL:HG21	1.98	0.45
1:C:264[D]:GLU:HB2	1:C:265[D]:PRO:HD3	1.97	0.45
1:E:212[D]:LEU:HD23	1:E:213[D]:MET:N	2.32	0.45
1:H:118[D]:ARG:HD3	1:H:122[D]:ASP:OD2	2.16	0.45
1:K:190[D]:PHE:HZ	1:L:214[D]:TYR:CD2	2.34	0.45
1:O:269[D]:GLN:HB2	1:O:311[D]:ILE:HD13	1.99	0.45
1:P:269[B]:GLN:HB2	1:P:311[B]:ILE:HD13	1.99	0.45
1:I:219[C]:ASP:HB2	2:I:350[C]:UMP:O3'	2.15	0.45
1:I:165[D]:THR:HG21	1:J:38[D]:PRO:HD2	1.99	0.45
1:P:26[D]:LEU:HD23	1:P:220[D]:LEU:HD21	1.98	0.45
1:P:269[D]:GLN:HB2	1:P:311[D]:ILE:HD13	1.99	0.45
1:L:26[C]:LEU:O	1:L:30[C]:ILE:HG13	2.17	0.45
1:J:189[D]:MET:O	1:J:190[D]:PHE:HB3	2.17	0.45
1:P:219[D]:ASP:HB2	2:P:700[D]:UMP:O3'	2.17	0.45
1:I:134[A]:PHE:CZ	1:J:176[A]:PRO:HD2	2.52	0.45
1:M:269[A]:GLN:HB2	1:M:311[A]:ILE:HD13	1.99	0.45
1:I:53[B]:SER:HB3	1:I:252[B]:GLN:HE21	1.80	0.45
1:M:176[B]:PRO:HD2	1:N:134[B]:PHE:CZ	2.51	0.45
1:I:53[C]:SER:HB3	1:I:252[C]:GLN:HE21	1.81	0.45
1:J:26[C]:LEU:O	1:J:30[C]:ILE:HG13	2.17	0.45
1:K:269[A]:GLN:HB2	1:K:311[A]:ILE:HD13	1.99	0.45
1:J:53[B]:SER:HB3	1:J:252[B]:GLN:HE21	1.80	0.45
1:M:269[C]:GLN:HB2	1:M:311[C]:ILE:HD13	1.99	0.45
1:M:157[D]:ILE:HD13	1:M:238[D]:ILE:HG23	1.99	0.45
1:A:212[A]:LEU:HD23	1:A:213[A]:MET:N	2.32	0.45
1:D:264[A]:GLU:HB2	1:D:265[A]:PRO:HD3	1.98	0.45
1:J:212[A]:LEU:HD23	1:J:213[A]:MET:N	2.32	0.45
1:K:220[A]:LEU:HG	1:K:224[A]:VAL:HG21	1.99	0.45
1:N:220[A]:LEU:HG	1:N:224[A]:VAL:HG21	1.97	0.45
1:P:269[A]:GLN:HB2	1:P:311[A]:ILE:HD13	1.99	0.45
1:A:212[B]:LEU:HD23	1:A:213[B]:MET:N	2.32	0.45
1:D:264[B]:GLU:HB2	1:D:265[B]:PRO:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:216[B]:ARG:HG3	1:I:217[B]:SER:N	2.31	0.45
1:L:26[B]:LEU:O	1:L:30[B]:ILE:HG13	2.17	0.45
1:L:70[B]:ARG:NH1	1:L:310[B]:LYS:HD3	2.32	0.45
1:O:269[B]:GLN:HB2	1:O:311[B]:ILE:HD13	1.99	0.45
1:A:212[C]:LEU:HD23	1:A:213[C]:MET:N	2.32	0.45
1:D:264[C]:GLU:HB2	1:D:265[C]:PRO:HD3	1.98	0.45
1:K:74[C]:ARG:NH2	1:N:70[C]:ARG:HD3	2.31	0.45
1:P:24[C]:LEU:HD11	1:P:68[C]:THR:HG21	1.98	0.45
1:A:212[D]:LEU:HD23	1:A:213[D]:MET:N	2.32	0.45
1:D:264[D]:GLU:HB2	1:D:265[D]:PRO:HD3	1.98	0.45
1:L:46[D]:VAL:O	1:L:46[D]:VAL:HG13	2.17	0.45
1:N:70[D]:ARG:NH1	1:N:310[D]:LYS:HD3	2.31	0.45
1:K:74[B]:ARG:NH2	1:N:70[B]:ARG:HD3	2.32	0.45
1:J:212[C]:LEU:HD23	1:J:213[C]:MET:N	2.32	0.45
1:K:216[D]:ARG:HG3	1:K:217[D]:SER:N	2.32	0.45
1:K:74[D]:ARG:NH2	1:N:70[D]:ARG:HD3	2.32	0.45
1:B:250[A]:ILE:N	1:B:250[A]:ILE:HD12	2.31	0.44
1:C:212[A]:LEU:HD23	1:C:213[A]:MET:N	2.32	0.44
1:K:176[A]:PRO:HD2	1:L:134[A]:PHE:CZ	2.52	0.44
1:B:250[B]:ILE:N	1:B:250[B]:ILE:HD12	2.31	0.44
1:C:212[B]:LEU:HD23	1:C:213[B]:MET:N	2.32	0.44
1:K:46[B]:VAL:HG13	1:K:46[B]:VAL:O	2.17	0.44
1:K:176[B]:PRO:HD2	1:L:134[B]:PHE:CZ	2.51	0.44
1:K:134[B]:PHE:CE1	1:L:176[B]:PRO:HD2	2.52	0.44
1:M:269[B]:GLN:HB2	1:M:311[B]:ILE:HD13	2.00	0.44
1:O:134[B]:PHE:CZ	1:P:176[B]:PRO:HD2	2.52	0.44
1:P:26[B]:LEU:HD23	1:P:220[B]:LEU:HD21	1.99	0.44
1:P:24[B]:LEU:HD11	1:P:68[B]:THR:HG21	1.98	0.44
1:B:250[C]:ILE:HD12	1:B:250[C]:ILE:N	2.31	0.44
1:C:212[C]:LEU:HD23	1:C:213[C]:MET:N	2.32	0.44
1:M:46[C]:VAL:HG13	1:M:46[C]:VAL:O	2.17	0.44
1:N:189[C]:MET:O	1:N:190[C]:PHE:HB3	2.17	0.44
1:O:216[C]:ARG:HG3	1:O:217[C]:SER:N	2.31	0.44
1:B:250[D]:ILE:HD12	1:B:250[D]:ILE:N	2.31	0.44
1:C:212[D]:LEU:HD23	1:C:213[D]:MET:N	2.32	0.44
1:K:46[D]:VAL:O	1:K:46[D]:VAL:HG13	2.17	0.44
1:L:70[D]:ARG:NH1	1:L:310[D]:LYS:HD3	2.32	0.44
1:D:212[A]:LEU:HD23	1:D:213[A]:MET:N	2.32	0.44
1:L:269[A]:GLN:HB2	1:L:311[A]:ILE:HD13	1.99	0.44
1:D:212[B]:LEU:HD23	1:D:213[B]:MET:N	2.32	0.44
1:D:212[C]:LEU:HD23	1:D:213[C]:MET:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:26[C]:LEU:HD23	1:O:220[C]:LEU:HD21	1.99	0.44
1:P:219[C]:ASP:HB2	2:P:700[C]:UMP:O3'	2.17	0.44
1:D:212[D]:LEU:HD23	1:D:213[D]:MET:N	2.32	0.44
1:I:53[D]:SER:HB3	1:I:252[D]:GLN:HE21	1.82	0.44
1:A:217[A]:SER:OG	1:B:167[A]:ARG:HD3	2.17	0.44
1:B:109[A]:PHE:O	1:B:112[A]:LYS:HB3	2.18	0.44
1:C:217[A]:SER:OG	1:D:167[A]:ARG:HD3	2.17	0.44
1:D:79[A]:GLU:O	1:D:82[A]:TRP:HB3	2.17	0.44
1:G:212[A]:LEU:HD12	1:H:50[A]:ALA:HB2	1.99	0.44
1:G:134[A]:PHE:CZ	1:H:176[A]:PRO:HD2	2.52	0.44
1:B:109[B]:PHE:O	1:B:112[B]:LYS:HB3	2.18	0.44
1:A:217[B]:SER:OG	1:B:167[B]:ARG:HD3	2.17	0.44
1:C:217[B]:SER:OG	1:D:167[B]:ARG:HD3	2.17	0.44
1:D:79[B]:GLU:O	1:D:82[B]:TRP:HB3	2.17	0.44
1:G:212[B]:LEU:HD12	1:H:50[B]:ALA:HB2	1.99	0.44
1:G:134[B]:PHE:CZ	1:H:176[B]:PRO:HD2	2.52	0.44
1:J:73[B]:LEU:HD21	1:J:302[B]:VAL:HG21	1.99	0.44
1:K:269[B]:GLN:HB2	1:K:311[B]:ILE:HD13	1.99	0.44
1:N:189[B]:MET:O	1:N:190[B]:PHE:HB3	2.17	0.44
1:B:109[C]:PHE:O	1:B:112[C]:LYS:HB3	2.18	0.44
1:A:217[C]:SER:OG	1:B:167[C]:ARG:HD3	2.17	0.44
1:C:217[C]:SER:OG	1:D:167[C]:ARG:HD3	2.17	0.44
1:D:79[C]:GLU:O	1:D:82[C]:TRP:HB3	2.17	0.44
1:G:134[C]:PHE:CZ	1:H:176[C]:PRO:HD2	2.52	0.44
1:G:212[C]:LEU:HD12	1:H:50[C]:ALA:HB2	1.99	0.44
1:K:134[C]:PHE:CE1	1:L:176[C]:PRO:HD2	2.52	0.44
1:A:217[D]:SER:OG	1:B:167[D]:ARG:HD3	2.17	0.44
1:B:109[D]:PHE:O	1:B:112[D]:LYS:HB3	2.18	0.44
1:C:217[D]:SER:OG	1:D:167[D]:ARG:HD3	2.17	0.44
1:D:79[D]:GLU:O	1:D:82[D]:TRP:HB3	2.17	0.44
1:G:212[D]:LEU:HD12	1:H:50[D]:ALA:HB2	1.99	0.44
1:G:134[D]:PHE:CZ	1:H:176[D]:PRO:HD2	2.52	0.44
1:J:34[D]:GLY:HA3	1:J:46[D]:VAL:HG22	1.99	0.44
1:K:269[D]:GLN:HB2	1:K:311[D]:ILE:HD13	1.99	0.44
1:I:189[B]:MET:O	1:I:190[B]:PHE:HB3	2.17	0.44
1:J:212[B]:LEU:HD23	1:J:213[B]:MET:N	2.33	0.44
1:O:216[B]:ARG:HG3	1:O:217[B]:SER:N	2.31	0.44
1:J:216[D]:ARG:HG3	1:J:217[D]:SER:N	2.32	0.44
1:M:189[D]:MET:O	1:M:190[D]:PHE:HB3	2.17	0.44
1:P:216[D]:ARG:HG3	1:P:217[D]:SER:N	2.31	0.44
1:C:195[A]:VAL:O	1:D:37[A]:ARG:NH1	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:269[A]:GLN:HB2	1:I:311[A]:ILE:HD13	2.00	0.44
1:J:269[A]:GLN:HB2	1:J:311[A]:ILE:HD13	1.99	0.44
1:C:195[B]:VAL:O	1:D:37[B]:ARG:NH1	2.42	0.44
1:P:46[B]:VAL:HG13	1:P:46[B]:VAL:O	2.16	0.44
1:C:195[C]:VAL:O	1:D:37[C]:ARG:NH1	2.42	0.44
1:O:24[C]:LEU:HD11	1:O:68[C]:THR:HG21	1.99	0.44
1:P:46[C]:VAL:HG13	1:P:46[C]:VAL:O	2.17	0.44
1:C:195[D]:VAL:O	1:D:37[D]:ARG:NH1	2.42	0.44
1:I:190[D]:PHE:HZ	1:J:214[D]:TYR:CD2	2.35	0.44
1:J:53[D]:SER:HB3	1:J:252[D]:GLN:HE21	1.81	0.44
1:L:34[D]:GLY:HA3	1:L:46[D]:VAL:HG22	2.00	0.44
1:O:134[D]:PHE:CZ	1:P:176[D]:PRO:HD2	2.53	0.44
1:A:23[A]:TYR:CZ	1:A:27[A]:ILE:HD11	2.53	0.44
1:D:250[A]:ILE:N	1:D:250[A]:ILE:HD12	2.32	0.44
1:G:212[A]:LEU:HD23	1:G:213[A]:MET:N	2.33	0.44
1:O:212[A]:LEU:HD23	1:O:213[A]:MET:N	2.33	0.44
1:A:23[B]:TYR:CZ	1:A:27[B]:ILE:HD11	2.53	0.44
1:D:250[B]:ILE:HD12	1:D:250[B]:ILE:N	2.32	0.44
1:G:212[B]:LEU:HD23	1:G:213[B]:MET:N	2.33	0.44
1:I:44[B]:GLY:C	1:I:260[B]:ARG:HG2	2.37	0.44
1:I:190[B]:PHE:HZ	1:J:214[B]:TYR:CD2	2.35	0.44
1:L:34[B]:GLY:HA3	1:L:46[B]:VAL:HG22	2.00	0.44
1:A:23[C]:TYR:CZ	1:A:27[C]:ILE:HD11	2.53	0.44
1:D:250[C]:ILE:HD12	1:D:250[C]:ILE:N	2.32	0.44
1:G:212[C]:LEU:HD23	1:G:213[C]:MET:N	2.33	0.44
1:I:34[C]:GLY:HA3	1:I:46[C]:VAL:HG22	1.99	0.44
1:K:216[C]:ARG:HG3	1:K:217[C]:SER:N	2.32	0.44
1:K:24[C]:LEU:HD11	1:K:68[C]:THR:HG21	1.98	0.44
1:L:34[C]:GLY:HA3	1:L:46[C]:VAL:HG22	2.00	0.44
1:L:46[C]:VAL:HG13	1:L:46[C]:VAL:O	2.18	0.44
1:O:134[C]:PHE:CZ	1:P:176[C]:PRO:HD2	2.53	0.44
1:A:23[D]:TYR:CZ	1:A:27[D]:ILE:HD11	2.53	0.44
1:D:250[D]:ILE:HD12	1:D:250[D]:ILE:N	2.32	0.44
1:G:212[D]:LEU:HD23	1:G:213[D]:MET:N	2.33	0.44
1:I:189[D]:MET:O	1:I:190[D]:PHE:HB3	2.17	0.44
1:K:176[D]:PRO:HD2	1:L:134[D]:PHE:CZ	2.52	0.44
1:P:73[D]:LEU:HD21	1:P:302[D]:VAL:HG21	1.99	0.44
1:A:118[A]:ARG:HD3	1:A:122[A]:ASP:OD2	2.18	0.44
1:B:269[A]:GLN:HB2	1:B:311[A]:ILE:HD13	1.99	0.44
1:D:109[A]:PHE:O	1:D:112[A]:LYS:HB3	2.18	0.44
1:P:219[A]:ASP:HB2	2:P:700[A]:UMP:O3'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118[B]:ARG:HD3	1:A:122[B]:ASP:OD2	2.18	0.44
1:B:269[B]:GLN:HB2	1:B:311[B]:ILE:HD13	1.99	0.44
1:D:109[B]:PHE:O	1:D:112[B]:LYS:HB3	2.18	0.44
1:K:73[B]:LEU:HD21	1:K:302[B]:VAL:HG21	2.00	0.44
1:O:26[B]:LEU:HD23	1:O:220[B]:LEU:HD21	1.99	0.44
1:A:118[C]:ARG:HD3	1:A:122[C]:ASP:OD2	2.18	0.44
1:B:269[C]:GLN:HB2	1:B:311[C]:ILE:HD13	1.99	0.44
1:D:109[C]:PHE:O	1:D:112[C]:LYS:HB3	2.18	0.44
1:J:269[C]:GLN:HB2	1:J:311[C]:ILE:HD13	2.00	0.44
1:J:53[C]:SER:HB3	1:J:252[C]:GLN:HE21	1.82	0.44
1:K:73[C]:LEU:HD21	1:K:302[C]:VAL:HG21	2.00	0.44
1:M:176[C]:PRO:HD2	1:N:134[C]:PHE:CZ	2.52	0.44
1:A:118[D]:ARG:HD3	1:A:122[D]:ASP:OD2	2.18	0.44
1:B:269[D]:GLN:HB2	1:B:311[D]:ILE:HD13	1.99	0.44
1:D:109[D]:PHE:O	1:D:112[D]:LYS:HB3	2.18	0.44
1:I:219[D]:ASP:HB2	2:I:350[D]:UMP:O3'	2.17	0.44
1:K:73[D]:LEU:HD21	1:K:302[D]:VAL:HG21	2.00	0.44
1:M:176[D]:PRO:HD2	1:N:134[D]:PHE:CZ	2.52	0.44
1:O:26[D]:LEU:HD23	1:O:220[D]:LEU:HD21	1.99	0.44
1:C:190[A]:PHE:CZ	1:D:214[A]:TYR:CD2	3.05	0.44
1:E:50[A]:ALA:CB	1:F:212[A]:LEU:HD12	2.48	0.44
1:F:100[A]:ILE:HB	3:F:2601[A]:CB3:C13	2.47	0.44
1:O:46[A]:VAL:O	1:O:46[A]:VAL:HG13	2.17	0.44
1:O:50[A]:ALA:HB2	1:P:212[A]:LEU:HD12	1.99	0.44
1:C:190[B]:PHE:CZ	1:D:214[B]:TYR:CD2	3.05	0.44
1:E:50[B]:ALA:CB	1:F:212[B]:LEU:HD12	2.48	0.44
1:F:100[B]:ILE:HB	3:F:2601[B]:CB3:C13	2.47	0.44
1:J:269[B]:GLN:HB2	1:J:311[B]:ILE:HD13	2.00	0.44
1:K:216[B]:ARG:HG3	1:K:217[B]:SER:N	2.32	0.44
1:C:190[C]:PHE:CZ	1:D:214[C]:TYR:CD2	3.05	0.44
1:E:50[C]:ALA:CB	1:F:212[C]:LEU:HD12	2.48	0.44
1:F:100[C]:ILE:HB	3:F:2601[C]:CB3:C13	2.47	0.44
1:J:73[C]:LEU:HD21	1:J:302[C]:VAL:HG21	1.99	0.44
1:C:190[D]:PHE:CZ	1:D:214[D]:TYR:CD2	3.05	0.44
1:F:100[D]:ILE:HB	3:F:2601[D]:CB3:C13	2.47	0.44
1:E:50[D]:ALA:CB	1:F:212[D]:LEU:HD12	2.48	0.44
1:C:246[A]:PRO:HG2	4:C:999[A]:HOH:O	2.17	0.44
1:E:118[A]:ARG:HD2	1:E:122[A]:ASP:OD2	2.18	0.44
1:F:79[A]:GLU:O	1:F:82[A]:TRP:HB3	2.18	0.44
1:I:46[A]:VAL:O	1:I:46[A]:VAL:HG13	2.18	0.44
1:C:246[B]:PRO:HG2	4:C:999[B]:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118[B]:ARG:HD2	1:E:122[B]:ASP:OD2	2.18	0.44
1:F:79[B]:GLU:O	1:F:82[B]:TRP:HB3	2.18	0.44
1:L:269[B]:GLN:HB2	1:L:311[B]:ILE:HD13	2.00	0.44
1:O:73[B]:LEU:HD21	1:O:302[B]:VAL:HG21	2.00	0.44
1:C:246[C]:PRO:HG2	4:C:999[C]:HOH:O	2.17	0.44
1:E:118[C]:ARG:HD2	1:E:122[C]:ASP:OD2	2.18	0.44
1:F:79[C]:GLU:O	1:F:82[C]:TRP:HB3	2.18	0.44
1:J:34[C]:GLY:HA3	1:J:46[C]:VAL:HG22	2.00	0.44
1:P:269[C]:GLN:HB2	1:P:311[C]:ILE:HD13	2.00	0.44
1:C:246[D]:PRO:HG2	4:C:999[D]:HOH:O	2.17	0.44
1:E:118[D]:ARG:HD2	1:E:122[D]:ASP:OD2	2.18	0.44
1:F:79[D]:GLU:O	1:F:82[D]:TRP:HB3	2.18	0.44
1:I:216[D]:ARG:HG3	1:I:217[D]:SER:N	2.32	0.44
1:I:44[D]:GLY:C	1:I:260[D]:ARG:HG2	2.37	0.44
1:P:46[D]:VAL:O	1:P:46[D]:VAL:HG13	2.17	0.44
1:F:118[A]:ARG:HD2	1:F:122[A]:ASP:OD2	2.17	0.43
1:M:212[A]:LEU:HD23	1:M:213[A]:MET:N	2.33	0.43
1:P:70[A]:ARG:NH1	1:P:310[A]:LYS:HD3	2.33	0.43
1:F:118[B]:ARG:HD2	1:F:122[B]:ASP:OD2	2.17	0.43
1:P:216[B]:ARG:HG3	1:P:217[B]:SER:N	2.32	0.43
1:F:118[C]:ARG:HD2	1:F:122[C]:ASP:OD2	2.17	0.43
1:K:176[C]:PRO:HD2	1:L:134[C]:PHE:CZ	2.52	0.43
1:L:269[C]:GLN:HB2	1:L:311[C]:ILE:HD13	2.00	0.43
1:F:118[D]:ARG:HD2	1:F:122[D]:ASP:OD2	2.17	0.43
1:J:269[D]:GLN:HB2	1:J:311[D]:ILE:HD13	2.00	0.43
1:M:269[D]:GLN:HB2	1:M:311[D]:ILE:HD13	2.00	0.43
1:O:212[D]:LEU:HD23	1:O:213[D]:MET:N	2.33	0.43
1:O:24[D]:LEU:HD11	1:O:68[D]:THR:HG21	1.99	0.43
1:B:100[A]:ILE:HB	3:B:2401[A]:CB3:C13	2.47	0.43
1:E:109[A]:PHE:O	1:E:112[A]:LYS:HB3	2.17	0.43
1:N:189[A]:MET:O	1:N:190[A]:PHE:HB3	2.18	0.43
1:O:189[A]:MET:O	1:O:190[A]:PHE:HB3	2.17	0.43
1:O:73[A]:LEU:HD21	1:O:302[A]:VAL:HG21	2.00	0.43
1:B:100[B]:ILE:HB	3:B:2401[B]:CB3:C13	2.47	0.43
1:E:109[B]:PHE:O	1:E:112[B]:LYS:HB3	2.17	0.43
1:B:100[C]:ILE:HB	3:B:2401[C]:CB3:C13	2.47	0.43
1:E:109[C]:PHE:O	1:E:112[C]:LYS:HB3	2.17	0.43
1:I:44[C]:GLY:C	1:I:260[C]:ARG:HG2	2.37	0.43
1:P:216[C]:ARG:HG3	1:P:217[C]:SER:N	2.32	0.43
1:B:100[D]:ILE:HB	3:B:2401[D]:CB3:C13	2.47	0.43
1:E:109[D]:PHE:O	1:E:112[D]:LYS:HB3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:220[D]:LEU:HA	1:I:224[D]:VAL:CG2	2.48	0.43
1:J:212[D]:LEU:HD23	1:J:213[D]:MET:N	2.33	0.43
1:N:189[D]:MET:O	1:N:190[D]:PHE:HB3	2.18	0.43
1:E:22[A]:GLN:NE2	1:E:55[A]:ARG:H	2.07	0.43
1:H:24[A]:LEU:HD11	1:H:68[A]:THR:HG21	2.01	0.43
1:J:189[A]:MET:O	1:J:190[A]:PHE:HB3	2.18	0.43
1:K:212[A]:LEU:HD23	1:K:213[A]:MET:N	2.34	0.43
1:N:73[A]:LEU:HD21	1:N:302[A]:VAL:HG21	2.00	0.43
1:P:212[A]:LEU:HD23	1:P:213[A]:MET:N	2.33	0.43
1:E:22[B]:GLN:NE2	1:E:55[B]:ARG:H	2.07	0.43
1:H:24[B]:LEU:HD11	1:H:68[B]:THR:HG21	2.01	0.43
1:M:189[B]:MET:O	1:M:190[B]:PHE:HB3	2.18	0.43
1:M:46[B]:VAL:O	1:M:46[B]:VAL:HG13	2.18	0.43
1:O:212[B]:LEU:HD23	1:O:213[B]:MET:N	2.33	0.43
1:O:24[B]:LEU:HD11	1:O:68[B]:THR:HG21	1.99	0.43
1:E:22[C]:GLN:NE2	1:E:55[C]:ARG:H	2.07	0.43
1:H:24[C]:LEU:HD11	1:H:68[C]:THR:HG21	2.01	0.43
1:I:190[C]:PHE:HZ	1:J:214[C]:TYR:CD2	2.36	0.43
1:N:212[C]:LEU:HD23	1:N:213[C]:MET:N	2.33	0.43
1:P:26[C]:LEU:HD23	1:P:220[C]:LEU:HD21	2.00	0.43
1:E:22[D]:GLN:NE2	1:E:55[D]:ARG:H	2.07	0.43
1:H:24[D]:LEU:HD11	1:H:68[D]:THR:HG21	2.01	0.43
1:J:73[D]:LEU:HD21	1:J:302[D]:VAL:HG21	2.00	0.43
1:O:165[D]:THR:HG21	1:P:38[D]:PRO:HD2	2.00	0.43
1:K:74[A]:ARG:HH21	1:N:70[A]:ARG:HD2	1.83	0.43
1:I:216[C]:ARG:HG3	1:I:217[C]:SER:N	2.33	0.43
1:K:269[C]:GLN:HB2	1:K:311[C]:ILE:HD13	2.00	0.43
1:K:74[D]:ARG:HH21	1:N:70[D]:ARG:HD2	1.83	0.43
1:P:189[D]:MET:O	1:P:190[D]:PHE:HB3	2.19	0.43
1:A:50[A]:ALA:HB2	1:B:212[A]:LEU:HD12	2.01	0.43
1:C:201[A]:ASP:O	1:C:202[A]:SER:CB	2.66	0.43
1:F:109[A]:PHE:O	1:F:112[A]:LYS:HB3	2.19	0.43
1:E:37[A]:ARG:NH1	1:F:195[A]:VAL:O	2.45	0.43
1:L:46[A]:VAL:O	1:L:46[A]:VAL:HG13	2.19	0.43
1:A:50[B]:ALA:HB2	1:B:212[B]:LEU:HD12	2.01	0.43
1:C:201[B]:ASP:O	1:C:202[B]:SER:CB	2.66	0.43
1:F:109[B]:PHE:O	1:F:112[B]:LYS:HB3	2.19	0.43
1:E:37[B]:ARG:NH1	1:F:195[B]:VAL:O	2.45	0.43
1:I:34[B]:GLY:HA3	1:I:46[B]:VAL:HG22	1.99	0.43
1:A:50[C]:ALA:HB2	1:B:212[C]:LEU:HD12	2.01	0.43
1:C:201[C]:ASP:O	1:C:202[C]:SER:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:109[C]:PHE:O	1:F:112[C]:LYS:HB3	2.19	0.43
1:E:37[C]:ARG:NH1	1:F:195[C]:VAL:O	2.45	0.43
1:I:269[C]:GLN:HB2	1:I:311[C]:ILE:HD13	2.01	0.43
1:A:50[D]:ALA:HB2	1:B:212[D]:LEU:HD12	2.01	0.43
1:C:201[D]:ASP:O	1:C:202[D]:SER:CB	2.66	0.43
1:F:109[D]:PHE:O	1:F:112[D]:LYS:HB3	2.19	0.43
1:E:37[D]:ARG:NH1	1:F:195[D]:VAL:O	2.45	0.43
1:N:212[A]:LEU:HD23	1:N:213[A]:MET:N	2.33	0.43
1:M:46[D]:VAL:O	1:M:46[D]:VAL:HG13	2.18	0.43
1:M:190[D]:PHE:HZ	1:N:214[D]:TYR:CD2	2.36	0.43
1:P:24[D]:LEU:HD11	1:P:68[D]:THR:HG21	1.99	0.43
1:G:297[A]:VAL:HG23	4:G:429[A]:HOH:O	2.19	0.43
1:H:109[A]:PHE:O	1:H:112[A]:LYS:HB3	2.19	0.43
1:H:79[A]:GLU:O	1:H:82[A]:TRP:HB3	2.19	0.43
1:I:44[A]:GLY:C	1:I:260[A]:ARG:HG2	2.38	0.43
1:M:24[A]:LEU:HD11	1:M:68[A]:THR:HG21	2.00	0.43
1:P:189[A]:MET:O	1:P:190[A]:PHE:HB3	2.19	0.43
1:G:297[B]:VAL:HG23	4:G:429[B]:HOH:O	2.19	0.43
1:H:109[B]:PHE:O	1:H:112[B]:LYS:HB3	2.19	0.43
1:H:79[B]:GLU:O	1:H:82[B]:TRP:HB3	2.19	0.43
1:G:297[C]:VAL:HG23	4:G:429[C]:HOH:O	2.19	0.43
1:H:109[C]:PHE:O	1:H:112[C]:LYS:HB3	2.19	0.43
1:H:79[C]:GLU:O	1:H:82[C]:TRP:HB3	2.19	0.43
1:L:24[C]:LEU:HD11	1:L:68[C]:THR:HG21	2.00	0.43
1:M:216[C]:ARG:HG3	1:M:217[C]:SER:N	2.32	0.43
1:N:216[C]:ARG:HG3	1:N:217[C]:SER:N	2.33	0.43
1:P:189[C]:MET:O	1:P:190[C]:PHE:HB3	2.19	0.43
1:G:297[D]:VAL:HG23	4:G:429[D]:HOH:O	2.19	0.43
1:H:109[D]:PHE:O	1:H:112[D]:LYS:HB3	2.19	0.43
1:H:79[D]:GLU:O	1:H:82[D]:TRP:HB3	2.19	0.43
1:M:216[D]:ARG:HG3	1:M:217[D]:SER:N	2.32	0.43
1:A:147[A]:GLY:HA2	1:D:137[A]:GLU:OE1	2.18	0.43
1:K:219[A]:ASP:HB2	2:K:450[A]:UMP:O3'	2.18	0.43
1:A:147[B]:GLY:HA2	1:D:137[B]:GLU:OE1	2.18	0.43
1:K:53[B]:SER:HB3	1:K:252[B]:GLN:HE21	1.81	0.43
1:L:216[B]:ARG:HG3	1:L:217[B]:SER:N	2.33	0.43
1:M:216[B]:ARG:HG3	1:M:217[B]:SER:N	2.32	0.43
1:K:74[B]:ARG:HH21	1:N:70[B]:ARG:HD2	1.84	0.43
1:A:147[C]:GLY:HA2	1:D:137[C]:GLU:OE1	2.18	0.43
1:I:157[C]:ILE:HD13	1:I:238[C]:ILE:HG23	2.00	0.43
1:M:189[C]:MET:O	1:M:190[C]:PHE:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:212[C]:LEU:HD23	1:O:213[C]:MET:N	2.34	0.43
1:A:147[D]:GLY:HA2	1:D:137[D]:GLU:OE1	2.18	0.43
1:M:24[D]:LEU:HD11	1:M:68[D]:THR:HG21	2.00	0.43
1:O:216[D]:ARG:HG3	1:O:217[D]:SER:N	2.33	0.43
1:P:70[D]:ARG:HH12	1:P:310[D]:LYS:HD3	1.83	0.43
1:C:74[A]:ARG:NH2	1:F:70[A]:ARG:HD3	2.34	0.43
1:G:189[A]:MET:O	1:G:190[A]:PHE:HB3	2.18	0.43
1:H:200[A]:ALA:O	1:H:203[A]:PRO:HD3	2.19	0.43
1:I:176[A]:PRO:HD2	1:J:134[A]:PHE:CZ	2.53	0.43
1:M:157[A]:ILE:HD13	1:M:238[A]:ILE:HG23	2.01	0.43
1:C:74[B]:ARG:NH2	1:F:70[B]:ARG:HD3	2.34	0.43
1:G:189[B]:MET:O	1:G:190[B]:PHE:HB3	2.18	0.43
1:H:200[B]:ALA:O	1:H:203[B]:PRO:HD3	2.19	0.43
1:J:216[B]:ARG:HG3	1:J:217[B]:SER:N	2.34	0.43
1:N:212[B]:LEU:HD23	1:N:213[B]:MET:N	2.34	0.43
1:N:216[B]:ARG:HG3	1:N:217[B]:SER:N	2.33	0.43
1:P:73[B]:LEU:HD21	1:P:302[B]:VAL:HG21	2.00	0.43
1:C:74[C]:ARG:NH2	1:F:70[C]:ARG:HD3	2.34	0.43
1:G:189[C]:MET:O	1:G:190[C]:PHE:HB3	2.18	0.43
1:H:200[C]:ALA:O	1:H:203[C]:PRO:HD3	2.19	0.43
1:I:189[C]:MET:O	1:I:190[C]:PHE:HB3	2.19	0.43
1:P:73[C]:LEU:HD21	1:P:302[C]:VAL:HG21	2.01	0.43
1:C:74[D]:ARG:NH2	1:F:70[D]:ARG:HD3	2.34	0.43
1:G:189[D]:MET:O	1:G:190[D]:PHE:HB3	2.18	0.43
1:H:200[D]:ALA:O	1:H:203[D]:PRO:HD3	2.19	0.43
1:I:24[D]:LEU:HD11	1:I:68[D]:THR:HG21	1.99	0.43
1:K:70[D]:ARG:HH12	1:K:310[D]:LYS:HD3	1.81	0.43
1:N:212[D]:LEU:HD23	1:N:213[D]:MET:N	2.33	0.43
1:P:34[D]:GLY:HA3	1:P:46[D]:VAL:HG22	2.01	0.43
1:A:186[A]:PRO:HG3	4:A:1157[A]:HOH:O	2.17	0.43
1:D:297[A]:VAL:HG23	4:D:973[A]:HOH:O	2.19	0.43
1:E:167[A]:ARG:HD3	1:F:217[A]:SER:OG	2.19	0.43
1:I:212[A]:LEU:HD23	1:I:213[A]:MET:N	2.34	0.43
1:A:186[B]:PRO:HG3	4:A:1157[B]:HOH:O	2.17	0.43
1:D:297[B]:VAL:HG23	4:D:973[B]:HOH:O	2.19	0.43
1:E:167[B]:ARG:HD3	1:F:217[B]:SER:OG	2.19	0.43
1:I:269[B]:GLN:HB2	1:I:311[B]:ILE:HD13	2.01	0.43
1:J:34[B]:GLY:HA3	1:J:46[B]:VAL:HG22	2.01	0.43
1:M:24[B]:LEU:HD11	1:M:68[B]:THR:HG21	2.00	0.43
1:N:46[B]:VAL:O	1:N:46[B]:VAL:HG13	2.18	0.43
1:A:186[C]:PRO:HG3	4:A:1157[C]:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:297[C]:VAL:HG23	4:D:973[C]:HOH:O	2.19	0.43
1:E:167[C]:ARG:HD3	1:F:217[C]:SER:OG	2.19	0.43
1:L:189[C]:MET:O	1:L:190[C]:PHE:HB3	2.19	0.43
1:M:70[C]:ARG:HH12	1:M:310[C]:LYS:HD3	1.82	0.43
1:M:190[C]:PHE:HZ	1:N:214[C]:TYR:CD2	2.37	0.43
1:A:186[D]:PRO:HG3	4:A:1157[D]:HOH:O	2.17	0.43
1:D:297[D]:VAL:HG23	4:D:973[D]:HOH:O	2.19	0.43
1:E:167[D]:ARG:HD3	1:F:217[D]:SER:OG	2.19	0.43
1:I:34[D]:GLY:HA3	1:I:46[D]:VAL:HG22	2.00	0.43
1:K:134[D]:PHE:CE1	1:L:176[D]:PRO:HD2	2.54	0.43
1:K:24[D]:LEU:HD11	1:K:68[D]:THR:HG21	1.99	0.43
1:E:189[A]:MET:O	1:E:190[A]:PHE:HB3	2.18	0.42
1:I:189[A]:MET:O	1:I:190[A]:PHE:HB3	2.19	0.42
1:I:216[A]:ARG:HG3	1:I:217[A]:SER:N	2.34	0.42
1:E:189[B]:MET:O	1:E:190[B]:PHE:HB3	2.18	0.42
1:K:24[B]:LEU:HD11	1:K:68[B]:THR:HG21	1.99	0.42
1:M:70[B]:ARG:HH12	1:M:310[B]:LYS:HD3	1.81	0.42
1:M:190[B]:PHE:HZ	1:N:214[B]:TYR:CD2	2.37	0.42
1:E:189[C]:MET:O	1:E:190[C]:PHE:HB3	2.18	0.42
1:K:23[C]:TYR:CZ	1:K:27[C]:ILE:HD11	2.54	0.42
1:E:189[D]:MET:O	1:E:190[D]:PHE:HB3	2.18	0.42
1:I:269[D]:GLN:HB2	1:I:311[D]:ILE:HD13	2.01	0.42
1:L:189[D]:MET:O	1:L:190[D]:PHE:HB3	2.19	0.42
1:H:250[A]:ILE:N	1:H:250[A]:ILE:HD12	2.33	0.42
1:I:70[A]:ARG:HH12	1:I:310[A]:LYS:HD3	1.83	0.42
1:K:216[A]:ARG:HG3	1:K:217[A]:SER:N	2.34	0.42
1:H:250[B]:ILE:N	1:H:250[B]:ILE:HD12	2.33	0.42
1:I:70[B]:ARG:HH12	1:I:310[B]:LYS:HD3	1.81	0.42
1:L:24[B]:LEU:HD11	1:L:68[B]:THR:HG21	2.00	0.42
1:H:250[C]:ILE:N	1:H:250[C]:ILE:HD12	2.33	0.42
1:I:147[C]:GLY:CA	1:L:137[C]:GLU:OE1	2.67	0.42
1:H:250[D]:ILE:N	1:H:250[D]:ILE:HD12	2.33	0.42
1:N:46[D]:VAL:HG13	1:N:46[D]:VAL:O	2.18	0.42
1:A:167[A]:ARG:HD3	1:B:217[A]:SER:HG	1.83	0.42
1:A:189[A]:MET:O	1:A:190[A]:PHE:HB3	2.19	0.42
1:B:79[A]:GLU:O	1:B:82[A]:TRP:HB3	2.19	0.42
1:D:201[A]:ASP:O	1:D:202[A]:SER:CB	2.67	0.42
1:A:189[B]:MET:O	1:A:190[B]:PHE:HB3	2.19	0.42
1:A:167[B]:ARG:HD3	1:B:217[B]:SER:HG	1.83	0.42
1:B:79[B]:GLU:O	1:B:82[B]:TRP:HB3	2.19	0.42
1:D:201[B]:ASP:O	1:D:202[B]:SER:CB	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:176[B]:PRO:HD2	1:J:134[B]:PHE:CZ	2.54	0.42
1:K:23[B]:TYR:CZ	1:K:27[B]:ILE:HD11	2.54	0.42
1:O:165[B]:THR:HG21	1:P:38[B]:PRO:HD2	2.01	0.42
1:A:189[C]:MET:O	1:A:190[C]:PHE:HB3	2.19	0.42
1:A:167[C]:ARG:HD3	1:B:217[C]:SER:HG	1.83	0.42
1:B:79[C]:GLU:O	1:B:82[C]:TRP:HB3	2.19	0.42
1:D:201[C]:ASP:O	1:D:202[C]:SER:CB	2.67	0.42
1:O:165[C]:THR:HG21	1:P:38[C]:PRO:HD2	2.01	0.42
1:O:157[C]:ILE:HD13	1:O:238[C]:ILE:HG23	2.00	0.42
1:A:189[D]:MET:O	1:A:190[D]:PHE:HB3	2.19	0.42
1:A:167[D]:ARG:HD3	1:B:217[D]:SER:HG	1.83	0.42
1:B:79[D]:GLU:O	1:B:82[D]:TRP:HB3	2.19	0.42
1:D:201[D]:ASP:O	1:D:202[D]:SER:CB	2.67	0.42
1:K:263[D]:VAL:HG12	1:K:267[D]:LYS:HE3	2.00	0.42
1:J:46[A]:VAL:O	1:J:46[A]:VAL:HG13	2.20	0.42
1:L:24[A]:LEU:HD11	1:L:68[A]:THR:HG21	2.01	0.42
1:O:134[A]:PHE:CZ	1:P:176[A]:PRO:HD2	2.55	0.42
1:O:165[A]:THR:HG21	1:P:38[A]:PRO:HD2	2.01	0.42
1:O:24[A]:LEU:HD11	1:O:68[A]:THR:HG21	2.01	0.42
1:P:24[A]:LEU:HD11	1:P:68[A]:THR:HG21	2.01	0.42
1:I:24[B]:LEU:HD11	1:I:68[B]:THR:HG21	2.00	0.42
1:O:157[B]:ILE:HD13	1:O:238[B]:ILE:HG23	2.00	0.42
1:O:263[B]:VAL:HG12	1:O:267[B]:LYS:HE3	2.01	0.42
1:I:24[C]:LEU:HD11	1:I:68[C]:THR:HG21	1.99	0.42
1:K:46[C]:VAL:O	1:K:46[C]:VAL:HG13	2.20	0.42
1:N:46[C]:VAL:O	1:N:46[C]:VAL:HG13	2.18	0.42
1:I:176[D]:PRO:HD2	1:J:134[D]:PHE:CZ	2.54	0.42
1:K:53[D]:SER:HB3	1:K:252[D]:GLN:HE21	1.82	0.42
1:M:26[D]:LEU:O	1:M:30[D]:ILE:HG13	2.19	0.42
1:K:134[A]:PHE:CE1	1:L:176[A]:PRO:HD2	2.54	0.42
1:K:24[A]:LEU:HD11	1:K:68[A]:THR:HG21	2.00	0.42
1:M:190[A]:PHE:HZ	1:N:214[A]:TYR:CD2	2.37	0.42
1:J:41[C]:THR:HB	1:J:316[C]:SER:HB3	2.01	0.42
1:K:212[C]:LEU:HD23	1:K:213[C]:MET:N	2.35	0.42
1:M:24[C]:LEU:HD11	1:M:68[C]:THR:HG21	2.01	0.42
1:H:14[C]:SER:CB	1:N:199[C]:PRO:HB3	2.48	0.42
1:O:220[C]:LEU:HA	1:O:224[C]:VAL:CG2	2.49	0.42
1:P:34[C]:GLY:HA3	1:P:46[C]:VAL:HG22	2.01	0.42
1:J:137[D]:GLU:OE1	1:K:147[D]:GLY:CA	2.67	0.42
1:B:188[A]:HIS:CD2	1:B:188[A]:HIS:H	2.37	0.42
1:L:189[A]:MET:O	1:L:190[A]:PHE:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:34[A]:GLY:HA3	1:L:46[A]:VAL:HG22	2.02	0.42
1:L:53[A]:SER:HB3	1:L:252[A]:GLN:HE21	1.84	0.42
1:B:188[B]:HIS:H	1:B:188[B]:HIS:CD2	2.37	0.42
1:N:34[B]:GLY:HA3	1:N:46[B]:VAL:HG22	2.01	0.42
1:B:188[C]:HIS:CD2	1:B:188[C]:HIS:H	2.37	0.42
1:K:74[C]:ARG:HH21	1:N:70[C]:ARG:HD2	1.85	0.42
1:B:188[D]:HIS:CD2	1:B:188[D]:HIS:H	2.37	0.42
1:K:23[D]:TYR:CZ	1:K:27[D]:ILE:HD11	2.55	0.42
1:L:24[D]:LEU:HD11	1:L:68[D]:THR:HG21	2.01	0.42
1:A:109[A]:PHE:O	1:A:112[A]:LYS:HB3	2.20	0.42
1:L:212[A]:LEU:HD23	1:L:213[A]:MET:N	2.35	0.42
1:L:73[A]:LEU:HD21	1:L:302[A]:VAL:HG21	2.01	0.42
1:A:109[B]:PHE:O	1:A:112[B]:LYS:HB3	2.20	0.42
1:I:220[B]:LEU:HA	1:I:224[B]:VAL:CG2	2.49	0.42
1:J:215[B]:GLN:HB3	1:J:218[B]:CYS:SG	2.60	0.42
1:M:34[B]:GLY:HA3	1:M:46[B]:VAL:HG22	2.00	0.42
1:A:109[C]:PHE:O	1:A:112[C]:LYS:HB3	2.20	0.42
1:H:202[C]:SER:HB3	1:N:275[C]:ARG:CG	2.37	0.42
1:L:216[C]:ARG:HG3	1:L:217[C]:SER:N	2.34	0.42
1:M:34[C]:GLY:HA3	1:M:46[C]:VAL:HG22	2.01	0.42
1:A:109[D]:PHE:O	1:A:112[D]:LYS:HB3	2.20	0.42
1:L:269[D]:GLN:HB2	1:L:311[D]:ILE:HD13	2.02	0.42
1:M:70[D]:ARG:HH12	1:M:310[D]:LYS:HD3	1.82	0.42
1:O:157[D]:ILE:HD13	1:O:238[D]:ILE:HG23	2.01	0.42
1:A:87[A]:CYS:SG	1:A:92[A]:MET:HG3	2.60	0.42
1:J:24[A]:LEU:HD11	1:J:68[A]:THR:HG21	2.02	0.42
1:K:46[A]:VAL:HG13	1:K:46[A]:VAL:O	2.20	0.42
1:O:216[A]:ARG:HG3	1:O:217[A]:SER:N	2.34	0.42
1:O:53[A]:SER:HB3	1:O:252[A]:GLN:HE21	1.82	0.42
1:P:216[A]:ARG:HG3	1:P:217[A]:SER:N	2.34	0.42
1:A:87[B]:CYS:SG	1:A:92[B]:MET:HG3	2.60	0.42
1:K:70[B]:ARG:HH12	1:K:310[B]:LYS:HD3	1.82	0.42
1:P:189[B]:MET:O	1:P:190[B]:PHE:HB3	2.20	0.42
1:A:87[C]:CYS:SG	1:A:92[C]:MET:HG3	2.60	0.42
1:J:24[C]:LEU:HD11	1:J:68[C]:THR:HG21	2.02	0.42
1:N:220[C]:LEU:HA	1:N:224[C]:VAL:CG2	2.50	0.42
1:A:87[D]:CYS:SG	1:A:92[D]:MET:HG3	2.60	0.42
1:L:216[D]:ARG:HG3	1:L:217[D]:SER:N	2.34	0.42
1:O:50[D]:ALA:CB	1:P:212[D]:LEU:HD12	2.50	0.42
1:A:167[A]:ARG:HD3	1:B:217[A]:SER:OG	2.20	0.42
1:C:74[A]:ARG:NH2	1:F:70[A]:ARG:CD	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:189[A]:MET:O	1:M:190[A]:PHE:HB3	2.19	0.42
1:A:167[B]:ARG:HD3	1:B:217[B]:SER:OG	2.20	0.42
1:C:74[B]:ARG:NH2	1:F:70[B]:ARG:CD	2.82	0.42
1:J:137[B]:GLU:OE1	1:K:147[B]:GLY:CA	2.68	0.42
1:N:263[B]:VAL:HG12	1:N:267[B]:LYS:HE3	2.02	0.42
1:P:34[B]:GLY:HA3	1:P:46[B]:VAL:HG22	2.02	0.42
1:A:167[C]:ARG:HD3	1:B:217[C]:SER:OG	2.20	0.42
1:C:74[C]:ARG:NH2	1:F:70[C]:ARG:CD	2.82	0.42
1:I:176[C]:PRO:HD2	1:J:134[C]:PHE:CZ	2.54	0.42
1:I:70[C]:ARG:HH12	1:I:310[C]:LYS:HD3	1.82	0.42
1:K:70[C]:ARG:HH12	1:K:310[C]:LYS:HD3	1.82	0.42
1:A:167[D]:ARG:HD3	1:B:217[D]:SER:OG	2.20	0.42
1:C:74[D]:ARG:NH2	1:F:70[D]:ARG:CD	2.82	0.42
1:C:109[A]:PHE:O	1:C:112[A]:LYS:HB3	2.20	0.42
1:C:217[A]:SER:HG	1:D:167[A]:ARG:HD3	1.84	0.42
1:H:53[A]:SER:HB3	1:H:252[A]:GLN:NE2	2.34	0.42
1:K:74[A]:ARG:NH2	1:N:70[A]:ARG:CD	2.83	0.42
1:M:216[A]:ARG:HG3	1:M:217[A]:SER:N	2.34	0.42
1:C:109[B]:PHE:O	1:C:112[B]:LYS:HB3	2.20	0.42
1:C:217[B]:SER:HG	1:D:167[B]:ARG:HD3	1.84	0.42
1:H:53[B]:SER:HB3	1:H:252[B]:GLN:NE2	2.34	0.42
1:J:41[B]:THR:HB	1:J:316[B]:SER:HB3	2.02	0.42
1:M:26[B]:LEU:HD23	1:M:220[B]:LEU:HD21	2.02	0.42
1:C:109[C]:PHE:O	1:C:112[C]:LYS:HB3	2.20	0.42
1:C:217[C]:SER:HG	1:D:167[C]:ARG:HD3	1.84	0.42
1:H:53[C]:SER:HB3	1:H:252[C]:GLN:NE2	2.34	0.42
1:J:216[C]:ARG:HG3	1:J:217[C]:SER:N	2.35	0.42
1:J:137[C]:GLU:OE1	1:K:147[C]:GLY:CA	2.68	0.42
1:P:70[C]:ARG:HH12	1:P:310[C]:LYS:HD3	1.84	0.42
1:C:109[D]:PHE:O	1:C:112[D]:LYS:HB3	2.20	0.42
1:C:217[D]:SER:HG	1:D:167[D]:ARG:HD3	1.84	0.42
1:H:53[D]:SER:HB3	1:H:252[D]:GLN:NE2	2.34	0.42
1:J:215[D]:GLN:HB3	1:J:218[D]:CYS:SG	2.60	0.42
1:J:24[D]:LEU:HD11	1:J:68[D]:THR:HG21	2.02	0.42
1:I:147[D]:GLY:CA	1:L:137[D]:GLU:OE1	2.68	0.42
1:O:34[D]:GLY:HA3	1:O:46[D]:VAL:HG22	2.02	0.42
1:P:212[D]:LEU:HD23	1:P:213[D]:MET:N	2.34	0.42
1:F:198[A]:PRO:HA	1:F:199[A]:PRO:HD3	1.95	0.41
1:I:24[A]:LEU:HD11	1:I:68[A]:THR:HG21	2.01	0.41
1:M:46[A]:VAL:HG13	1:M:46[A]:VAL:O	2.20	0.41
1:O:70[A]:ARG:NH1	1:O:310[A]:LYS:HD3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:198[B]:PRO:HA	1:F:199[B]:PRO:HD3	1.95	0.41
1:M:212[B]:LEU:HD23	1:M:213[B]:MET:N	2.35	0.41
1:F:198[C]:PRO:HA	1:F:199[C]:PRO:HD3	1.95	0.41
1:M:26[C]:LEU:O	1:M:30[C]:ILE:HG13	2.20	0.41
1:N:263[C]:VAL:HG12	1:N:267[C]:LYS:HE3	2.02	0.41
1:F:198[D]:PRO:HA	1:F:199[D]:PRO:HD3	1.95	0.41
1:K:214[D]:TYR:CD2	1:L:190[D]:PHE:HZ	2.37	0.41
1:M:130[D]:GLN:HG3	1:M:173[D]:ALA:O	2.20	0.41
1:N:34[D]:GLY:HA3	1:N:46[D]:VAL:HG22	2.01	0.41
1:A:134[A]:PHE:CE1	1:B:176[A]:PRO:HD2	2.55	0.41
1:A:190[A]:PHE:CZ	1:B:214[A]:TYR:CD2	3.06	0.41
1:A:134[B]:PHE:CE1	1:B:176[B]:PRO:HD2	2.55	0.41
1:A:190[B]:PHE:CZ	1:B:214[B]:TYR:CD2	3.06	0.41
1:I:147[B]:GLY:CA	1:L:137[B]:GLU:OE1	2.68	0.41
1:I:157[B]:ILE:HD13	1:I:238[B]:ILE:HG23	2.01	0.41
1:J:24[B]:LEU:HD11	1:J:68[B]:THR:HG21	2.02	0.41
1:K:212[B]:LEU:HD23	1:K:213[B]:MET:N	2.35	0.41
1:A:134[C]:PHE:CE1	1:B:176[C]:PRO:HD2	2.55	0.41
1:A:190[C]:PHE:CZ	1:B:214[C]:TYR:CD2	3.06	0.41
1:M:212[C]:LEU:HD23	1:M:213[C]:MET:N	2.35	0.41
1:M:26[C]:LEU:HD23	1:M:220[C]:LEU:HD21	2.02	0.41
1:P:212[C]:LEU:HD23	1:P:213[C]:MET:N	2.35	0.41
1:A:134[D]:PHE:CE1	1:B:176[D]:PRO:HD2	2.55	0.41
1:A:190[D]:PHE:CZ	1:B:214[D]:TYR:CD2	3.06	0.41
1:I:157[D]:ILE:HD13	1:I:238[D]:ILE:HG23	2.01	0.41
1:I:26[D]:LEU:O	1:I:30[D]:ILE:HG13	2.20	0.41
1:J:41[D]:THR:HB	1:J:316[D]:SER:HB3	2.02	0.41
1:K:179[D]:LEU:N	1:K:180[D]:PRO:HD2	2.34	0.41
1:M:34[D]:GLY:HA3	1:M:46[D]:VAL:HG22	2.01	0.41
1:O:23[D]:TYR:CZ	1:O:27[D]:ILE:HD11	2.55	0.41
1:G:109[A]:PHE:O	1:G:112[A]:LYS:HB3	2.19	0.41
1:J:73[A]:LEU:HD21	1:J:302[A]:VAL:HG21	2.02	0.41
1:L:37[A]:ARG:HA	1:L:38[A]:PRO:HD3	1.89	0.41
1:G:109[B]:PHE:O	1:G:112[B]:LYS:HB3	2.19	0.41
1:K:179[B]:LEU:N	1:K:180[B]:PRO:HD2	2.35	0.41
1:K:263[B]:VAL:HG12	1:K:267[B]:LYS:HE3	2.01	0.41
1:N:24[B]:LEU:HD11	1:N:68[B]:THR:HG21	2.01	0.41
1:O:34[B]:GLY:HA3	1:O:46[B]:VAL:HG22	2.02	0.41
1:G:109[C]:PHE:O	1:G:112[C]:LYS:HB3	2.19	0.41
1:I:26[C]:LEU:O	1:I:30[C]:ILE:HG13	2.20	0.41
1:K:179[C]:LEU:N	1:K:180[C]:PRO:HD2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:34[C]:GLY:HA3	1:O:46[C]:VAL:HG22	2.02	0.41
1:G:109[D]:PHE:O	1:G:112[D]:LYS:HB3	2.19	0.41
1:I:70[D]:ARG:HH12	1:I:310[D]:LYS:HD3	1.82	0.41
1:N:263[D]:VAL:HG12	1:N:267[D]:LYS:HE3	2.03	0.41
1:P:263[D]:VAL:HG12	1:P:267[D]:LYS:HE3	2.02	0.41
1:A:79[A]:GLU:O	1:A:82[A]:TRP:HB3	2.20	0.41
1:D:186[A]:PRO:HG3	4:D:1122[A]:HOH:O	2.19	0.41
1:D:188[A]:HIS:CD2	1:D:188[A]:HIS:H	2.38	0.41
1:G:107[A]:LYS:HD2	1:G:111[A]:GLU:OE2	2.20	0.41
1:G:212[A]:LEU:HD12	1:H:50[A]:ALA:CB	2.50	0.41
1:L:216[A]:ARG:HG3	1:L:217[A]:SER:N	2.35	0.41
1:A:79[B]:GLU:O	1:A:82[B]:TRP:HB3	2.20	0.41
1:D:186[B]:PRO:HG3	4:D:1122[B]:HOH:O	2.19	0.41
1:D:188[B]:HIS:CD2	1:D:188[B]:HIS:H	2.38	0.41
1:G:107[B]:LYS:HD2	1:G:111[B]:GLU:OE2	2.20	0.41
1:G:212[B]:LEU:HD12	1:H:50[B]:ALA:CB	2.50	0.41
1:M:26[B]:LEU:O	1:M:30[B]:ILE:HG13	2.20	0.41
1:N:220[B]:LEU:HA	1:N:224[B]:VAL:CG2	2.51	0.41
1:P:263[B]:VAL:HG12	1:P:267[B]:LYS:HE3	2.02	0.41
1:A:79[C]:GLU:O	1:A:82[C]:TRP:HB3	2.20	0.41
1:D:186[C]:PRO:HG3	4:D:1122[C]:HOH:O	2.19	0.41
1:D:188[C]:HIS:CD2	1:D:188[C]:HIS:H	2.38	0.41
1:G:107[C]:LYS:HD2	1:G:111[C]:GLU:OE2	2.20	0.41
1:G:212[C]:LEU:HD12	1:H:50[C]:ALA:CB	2.50	0.41
1:I:212[C]:LEU:HD23	1:I:213[C]:MET:N	2.36	0.41
1:K:214[C]:TYR:CD2	1:L:190[C]:PHE:HZ	2.37	0.41
1:A:79[D]:GLU:O	1:A:82[D]:TRP:HB3	2.20	0.41
1:D:186[D]:PRO:HG3	4:D:1122[D]:HOH:O	2.19	0.41
1:D:188[D]:HIS:H	1:D:188[D]:HIS:CD2	2.38	0.41
1:G:107[D]:LYS:HD2	1:G:111[D]:GLU:OE2	2.20	0.41
1:G:212[D]:LEU:HD12	1:H:50[D]:ALA:CB	2.50	0.41
1:M:214[D]:TYR:CD2	1:N:190[D]:PHE:HZ	2.38	0.41
1:N:23[D]:TYR:CZ	1:N:27[D]:ILE:HD11	2.56	0.41
1:O:263[D]:VAL:HG12	1:O:267[D]:LYS:HE3	2.02	0.41
1:O:190[D]:PHE:HZ	1:P:214[D]:TYR:CD2	2.38	0.41
1:F:53[A]:SER:HB3	1:F:252[A]:GLN:NE2	2.35	0.41
1:H:198[A]:PRO:HA	1:H:199[A]:PRO:HD3	1.95	0.41
1:J:216[A]:ARG:HG3	1:J:217[A]:SER:N	2.35	0.41
1:J:34[A]:GLY:HA3	1:J:46[A]:VAL:HG22	2.03	0.41
1:K:73[A]:LEU:HD21	1:K:302[A]:VAL:HG21	2.02	0.41
1:N:46[A]:VAL:HG13	1:N:46[A]:VAL:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:53[B]:SER:HB3	1:F:252[B]:GLN:NE2	2.35	0.41
1:H:198[B]:PRO:HA	1:H:199[B]:PRO:HD3	1.95	0.41
1:L:73[B]:LEU:HD21	1:L:302[B]:VAL:HG21	2.02	0.41
1:F:53[C]:SER:HB3	1:F:252[C]:GLN:NE2	2.35	0.41
1:H:198[C]:PRO:HA	1:H:199[C]:PRO:HD3	1.95	0.41
1:O:23[C]:TYR:CZ	1:O:27[C]:ILE:HD11	2.55	0.41
1:F:53[D]:SER:HB3	1:F:252[D]:GLN:NE2	2.35	0.41
1:H:198[D]:PRO:HA	1:H:199[D]:PRO:HD3	1.95	0.41
1:P:220[D]:LEU:HA	1:P:224[D]:VAL:CG2	2.51	0.41
1:C:182[A]:MET:SD	1:C:186[A]:PRO:HD3	2.59	0.41
1:E:167[A]:ARG:HD3	1:F:217[A]:SER:HG	1.86	0.41
1:J:37[A]:ARG:HA	1:J:38[A]:PRO:HD3	1.89	0.41
1:M:70[A]:ARG:HH12	1:M:310[A]:LYS:HD3	1.84	0.41
1:C:182[B]:MET:SD	1:C:186[B]:PRO:HD3	2.59	0.41
1:E:167[B]:ARG:HD3	1:F:217[B]:SER:HG	1.86	0.41
1:I:26[B]:LEU:O	1:I:30[B]:ILE:HG13	2.21	0.41
1:K:219[B]:ASP:HB2	2:K:450[B]:UMP:O3'	2.20	0.41
1:N:23[B]:TYR:CZ	1:N:27[B]:ILE:HD11	2.56	0.41
1:C:182[C]:MET:SD	1:C:186[C]:PRO:HD3	2.59	0.41
1:E:167[C]:ARG:HD3	1:F:217[C]:SER:HG	1.86	0.41
1:M:262[C]:HIS:C	1:M:265[C]:PRO:HD2	2.41	0.41
1:N:34[C]:GLY:HA3	1:N:46[C]:VAL:HG22	2.02	0.41
1:O:263[C]:VAL:HG12	1:O:267[C]:LYS:HE3	2.02	0.41
1:O:190[C]:PHE:HZ	1:P:214[C]:TYR:CD2	2.38	0.41
1:P:220[C]:LEU:HA	1:P:224[C]:VAL:CG2	2.51	0.41
1:C:182[D]:MET:SD	1:C:186[D]:PRO:HD3	2.59	0.41
1:E:167[D]:ARG:HD3	1:F:217[D]:SER:HG	1.86	0.41
1:P:198[D]:PRO:HA	1:P:199[D]:PRO:HD3	1.95	0.41
1:K:214[A]:TYR:CD2	1:L:190[A]:PHE:HZ	2.37	0.41
1:P:26[B]:LEU:O	1:P:30[B]:ILE:HG13	2.21	0.41
1:P:70[B]:ARG:HH12	1:P:310[B]:LYS:HD3	1.84	0.41
1:I:220[C]:LEU:HA	1:I:224[C]:VAL:CG2	2.51	0.41
1:K:34[C]:GLY:HA3	1:K:46[C]:VAL:HG22	2.02	0.41
1:N:179[C]:LEU:N	1:N:180[C]:PRO:HD2	2.35	0.41
1:N:215[D]:GLN:HB3	1:N:218[D]:CYS:SG	2.60	0.41
1:F:73[A]:LEU:HD21	1:F:302[A]:VAL:HG21	2.02	0.41
1:L:26[A]:LEU:O	1:L:30[A]:ILE:HG13	2.21	0.41
1:M:214[A]:TYR:CD2	1:N:190[A]:PHE:HZ	2.38	0.41
1:N:70[A]:ARG:NH1	1:N:310[A]:LYS:HD3	2.35	0.41
1:P:46[A]:VAL:O	1:P:46[A]:VAL:HG13	2.20	0.41
1:F:73[B]:LEU:HD21	1:F:302[B]:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:212[B]:LEU:HD23	1:I:213[B]:MET:N	2.36	0.41
1:J:263[B]:VAL:HG12	1:J:267[B]:LYS:HE3	2.03	0.41
1:O:220[B]:LEU:HA	1:O:224[B]:VAL:CG2	2.50	0.41
1:P:198[B]:PRO:HA	1:P:199[B]:PRO:HD3	1.95	0.41
1:P:212[B]:LEU:HD23	1:P:213[B]:MET:N	2.35	0.41
1:F:73[C]:LEU:HD21	1:F:302[C]:VAL:HG21	2.02	0.41
1:J:220[C]:LEU:HA	1:J:224[C]:VAL:CG2	2.51	0.41
1:N:23[C]:TYR:CZ	1:N:27[C]:ILE:HD11	2.56	0.41
1:O:70[C]:ARG:HH12	1:O:310[C]:LYS:HD3	1.84	0.41
1:F:73[D]:LEU:HD21	1:F:302[D]:VAL:HG21	2.02	0.41
1:C:24[A]:LEU:HD11	1:C:68[A]:THR:HG21	2.03	0.41
1:C:79[A]:GLU:O	1:C:82[A]:TRP:HB3	2.21	0.41
1:E:14[A]:SER:HB3	1:E:273[A]:GLU:OE1	2.20	0.41
1:H:182[A]:MET:SD	1:H:186[A]:PRO:HD3	2.61	0.41
1:H:189[A]:MET:O	1:H:190[A]:PHE:HB3	2.21	0.41
1:I:34[A]:GLY:HA3	1:I:46[A]:VAL:HG22	2.02	0.41
1:K:23[A]:TYR:CZ	1:K:27[A]:ILE:HD11	2.56	0.41
1:P:198[A]:PRO:HA	1:P:199[A]:PRO:HD3	1.95	0.41
1:A:200[A]:ALA:C	1:A:202[A]:SER:H	2.24	0.41
1:A:24[A]:LEU:HD11	1:A:68[A]:THR:HG21	2.03	0.41
1:N:216[A]:ARG:HG3	1:N:217[A]:SER:N	2.35	0.41
1:P:34[A]:GLY:HA3	1:P:46[A]:VAL:HG22	2.03	0.41
1:C:24[B]:LEU:HD11	1:C:68[B]:THR:HG21	2.03	0.41
1:C:79[B]:GLU:O	1:C:82[B]:TRP:HB3	2.21	0.41
1:E:14[B]:SER:HB3	1:E:273[B]:GLU:OE1	2.20	0.41
1:H:182[B]:MET:SD	1:H:186[B]:PRO:HD3	2.61	0.41
1:H:189[B]:MET:O	1:H:190[B]:PHE:HB3	2.21	0.41
1:L:157[B]:ILE:HD13	1:L:238[B]:ILE:HG23	2.03	0.41
1:L:189[B]:MET:O	1:L:190[B]:PHE:HB3	2.21	0.41
1:O:179[B]:LEU:N	1:O:180[B]:PRO:HD2	2.35	0.41
1:O:50[B]:ALA:CB	1:P:212[B]:LEU:HD12	2.51	0.41
1:A:200[B]:ALA:C	1:A:202[B]:SER:H	2.24	0.41
1:A:24[B]:LEU:HD11	1:A:68[B]:THR:HG21	2.03	0.41
1:M:214[B]:TYR:CD2	1:N:190[B]:PHE:HZ	2.38	0.41
1:C:24[C]:LEU:HD11	1:C:68[C]:THR:HG21	2.03	0.41
1:C:79[C]:GLU:O	1:C:82[C]:TRP:HB3	2.21	0.41
1:E:14[C]:SER:HB3	1:E:273[C]:GLU:OE1	2.20	0.41
1:H:182[C]:MET:SD	1:H:186[C]:PRO:HD3	2.61	0.41
1:H:189[C]:MET:O	1:H:190[C]:PHE:HB3	2.21	0.41
1:P:263[C]:VAL:HG12	1:P:267[C]:LYS:HE3	2.03	0.41
1:A:200[C]:ALA:C	1:A:202[C]:SER:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24[C]:LEU:HD11	1:A:68[C]:THR:HG21	2.03	0.41
1:J:263[C]:VAL:HG12	1:J:267[C]:LYS:HE3	2.03	0.41
1:K:220[C]:LEU:HA	1:K:224[C]:VAL:CG2	2.51	0.41
1:C:24[D]:LEU:HD11	1:C:68[D]:THR:HG21	2.03	0.41
1:C:79[D]:GLU:O	1:C:82[D]:TRP:HB3	2.21	0.41
1:E:14[D]:SER:HB3	1:E:273[D]:GLU:OE1	2.20	0.41
1:H:182[D]:MET:SD	1:H:186[D]:PRO:HD3	2.61	0.41
1:H:189[D]:MET:O	1:H:190[D]:PHE:HB3	2.21	0.41
1:K:219[D]:ASP:HB2	2:K:450[D]:UMP:O3'	2.20	0.41
1:K:34[D]:GLY:HA3	1:K:46[D]:VAL:HG22	2.02	0.41
1:L:263[D]:VAL:HG12	1:L:267[D]:LYS:HE3	2.03	0.41
1:A:200[D]:ALA:C	1:A:202[D]:SER:H	2.24	0.41
1:A:24[D]:LEU:HD11	1:A:68[D]:THR:HG21	2.03	0.41
1:I:212[D]:LEU:HD23	1:I:213[D]:MET:N	2.36	0.41
1:J:263[D]:VAL:HG12	1:J:267[D]:LYS:HE3	2.03	0.41
1:O:179[D]:LEU:N	1:O:180[D]:PRO:HD2	2.35	0.41
1:O:220[D]:LEU:HA	1:O:224[D]:VAL:CG2	2.50	0.41
1:D:87[A]:CYS:SG	1:D:92[A]:MET:HG3	2.61	0.41
1:E:185[A]:PRO:HG3	4:E:1428[A]:HOH:O	2.21	0.41
1:F:23[A]:TYR:CZ	1:F:27[A]:ILE:HD11	2.56	0.41
1:J:26[A]:LEU:O	1:J:30[A]:ILE:HG13	2.21	0.41
1:K:70[A]:ARG:HH12	1:K:310[A]:LYS:HD3	1.85	0.41
1:D:87[B]:CYS:SG	1:D:92[B]:MET:HG3	2.61	0.41
1:E:185[B]:PRO:HG3	4:E:1428[B]:HOH:O	2.21	0.41
1:F:23[B]:TYR:CZ	1:F:27[B]:ILE:HD11	2.56	0.41
1:I:263[B]:VAL:HG12	1:I:267[B]:LYS:HE3	2.02	0.41
1:O:190[B]:PHE:HZ	1:P:214[B]:TYR:CD2	2.39	0.41
1:D:87[C]:CYS:SG	1:D:92[C]:MET:HG3	2.61	0.41
1:E:185[C]:PRO:HG3	4:E:1428[C]:HOH:O	2.21	0.41
1:F:23[C]:TYR:CZ	1:F:27[C]:ILE:HD11	2.56	0.41
1:M:214[C]:TYR:CD2	1:N:190[C]:PHE:HZ	2.39	0.41
1:P:179[C]:LEU:N	1:P:180[C]:PRO:HD2	2.36	0.41
1:P:26[C]:LEU:O	1:P:30[C]:ILE:HG13	2.21	0.41
1:D:87[D]:CYS:SG	1:D:92[D]:MET:HG3	2.61	0.41
1:E:185[D]:PRO:HG3	4:E:1428[D]:HOH:O	2.21	0.41
1:F:23[D]:TYR:CZ	1:F:27[D]:ILE:HD11	2.56	0.41
1:L:157[D]:ILE:HD13	1:L:238[D]:ILE:HG23	2.03	0.41
1:M:212[D]:LEU:HD23	1:M:213[D]:MET:N	2.36	0.41
1:F:37[A]:ARG:HA	1:F:38[A]:PRO:HD3	1.90	0.40
1:K:190[A]:PHE:CZ	1:L:214[A]:TYR:CD2	3.09	0.40
1:N:24[A]:LEU:HD11	1:N:68[A]:THR:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:190[A]:PHE:HZ	1:P:214[A]:TYR:CD2	2.39	0.40
1:F:37[B]:ARG:HA	1:F:38[B]:PRO:HD3	1.90	0.40
1:K:34[B]:GLY:HA3	1:K:46[B]:VAL:HG22	2.03	0.40
1:F:37[C]:ARG:HA	1:F:38[C]:PRO:HD3	1.90	0.40
1:L:157[C]:ILE:HD13	1:L:238[C]:ILE:HG23	2.03	0.40
1:F:37[D]:ARG:HA	1:F:38[D]:PRO:HD3	1.90	0.40
1:K:157[D]:ILE:HD13	1:K:238[D]:ILE:HG23	2.03	0.40
1:K:212[D]:LEU:HD23	1:K:213[D]:MET:N	2.36	0.40
1:L:37[D]:ARG:HA	1:L:38[D]:PRO:HD3	1.88	0.40
1:L:70[A]:ARG:NH1	1:L:310[A]:LYS:HD3	2.36	0.40
1:M:34[A]:GLY:HA3	1:M:46[A]:VAL:HG22	2.03	0.40
1:N:26[A]:LEU:O	1:N:30[A]:ILE:HG13	2.21	0.40
1:P:37[A]:ARG:HA	1:P:38[A]:PRO:HD3	1.89	0.40
1:J:37[B]:ARG:HA	1:J:38[B]:PRO:HD3	1.89	0.40
1:N:179[B]:LEU:N	1:N:180[B]:PRO:HD2	2.35	0.40
1:O:23[B]:TYR:CZ	1:O:27[B]:ILE:HD11	2.56	0.40
1:P:53[B]:SER:HB3	1:P:252[B]:GLN:HE21	1.85	0.40
1:I:263[C]:VAL:HG12	1:I:267[C]:LYS:HE3	2.02	0.40
1:L:73[C]:LEU:HD21	1:L:302[C]:VAL:HG21	2.02	0.40
1:N:262[C]:HIS:C	1:N:265[C]:PRO:HD2	2.41	0.40
1:O:179[C]:LEU:N	1:O:180[C]:PRO:HD2	2.36	0.40
1:P:198[C]:PRO:HA	1:P:199[C]:PRO:HD3	1.95	0.40
1:P:53[C]:SER:HB3	1:P:252[C]:GLN:HE21	1.85	0.40
1:N:198[D]:PRO:HA	1:N:199[D]:PRO:HD3	1.95	0.40
1:N:220[D]:LEU:HA	1:N:224[D]:VAL:CG2	2.52	0.40
1:P:179[D]:LEU:N	1:P:180[D]:PRO:HD2	2.36	0.40
1:D:37[A]:ARG:HA	1:D:38[A]:PRO:HD3	1.94	0.40
1:J:41[A]:THR:HB	1:J:316[A]:SER:HB3	2.04	0.40
1:N:23[A]:TYR:CZ	1:N:27[A]:ILE:HD11	2.57	0.40
1:D:37[B]:ARG:HA	1:D:38[B]:PRO:HD3	1.94	0.40
1:K:214[B]:TYR:CD2	1:L:190[B]:PHE:HZ	2.38	0.40
1:P:179[B]:LEU:N	1:P:180[B]:PRO:HD2	2.36	0.40
1:D:37[C]:ARG:HA	1:D:38[C]:PRO:HD3	1.94	0.40
1:L:37[C]:ARG:HA	1:L:38[C]:PRO:HD3	1.89	0.40
1:O:50[C]:ALA:CB	1:P:212[C]:LEU:HD12	2.51	0.40
1:D:37[D]:ARG:HA	1:D:38[D]:PRO:HD3	1.94	0.40
1:K:118[D]:ARG:NH1	1:K:124[D]:GLY:HA3	2.37	0.40
1:B:24[A]:LEU:HD11	1:B:68[A]:THR:HG21	2.04	0.40
1:C:155[A]:ARG:NH2	4:C:1568[A]:HOH:O	2.51	0.40
1:D:23[A]:TYR:CZ	1:D:27[A]:ILE:HD11	2.56	0.40
1:E:214[A]:TYR:CD2	1:F:190[A]:PHE:HZ	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:73[A]:LEU:HD21	1:P:302[A]:VAL:HG21	2.03	0.40
1:B:24[B]:LEU:HD11	1:B:68[B]:THR:HG21	2.04	0.40
1:C:155[B]:ARG:NH2	4:C:1568[B]:HOH:O	2.51	0.40
1:D:23[B]:TYR:CZ	1:D:27[B]:ILE:HD11	2.56	0.40
1:E:214[B]:TYR:CD2	1:F:190[B]:PHE:HZ	2.39	0.40
1:J:220[B]:LEU:HA	1:J:224[B]:VAL:CG2	2.52	0.40
1:M:262[B]:HIS:C	1:M:265[B]:PRO:HD2	2.42	0.40
1:N:215[B]:GLN:HB3	1:N:218[B]:CYS:SG	2.61	0.40
1:N:262[B]:HIS:C	1:N:265[B]:PRO:HD2	2.41	0.40
1:O:208[B]:LYS:HB3	1:O:247[B]:HIS:HB2	2.04	0.40
1:P:220[B]:LEU:HA	1:P:224[B]:VAL:CG2	2.52	0.40
1:B:24[C]:LEU:HD11	1:B:68[C]:THR:HG21	2.04	0.40
1:C:155[C]:ARG:NH2	4:C:1568[C]:HOH:O	2.51	0.40
1:D:23[C]:TYR:CZ	1:D:27[C]:ILE:HD11	2.56	0.40
1:E:214[C]:TYR:CD2	1:F:190[C]:PHE:HZ	2.39	0.40
1:I:179[C]:LEU:N	1:I:180[C]:PRO:HD2	2.36	0.40
1:J:37[C]:ARG:HA	1:J:38[C]:PRO:HD3	1.89	0.40
1:K:157[C]:ILE:HD13	1:K:238[C]:ILE:HG23	2.03	0.40
1:K:219[C]:ASP:HB2	2:K:450[C]:UMP:O3'	2.21	0.40
1:N:24[C]:LEU:HD11	1:N:68[C]:THR:HG21	2.03	0.40
1:O:208[C]:LYS:HB3	1:O:247[C]:HIS:HB2	2.04	0.40
1:B:24[D]:LEU:HD11	1:B:68[D]:THR:HG21	2.04	0.40
1:C:155[D]:ARG:NH2	4:C:1568[D]:HOH:O	2.51	0.40
1:D:23[D]:TYR:CZ	1:D:27[D]:ILE:HD11	2.56	0.40
1:E:214[D]:TYR:CD2	1:F:190[D]:PHE:HZ	2.39	0.40
1:M:262[D]:HIS:C	1:M:265[D]:PRO:HD2	2.42	0.40
1:P:188[D]:HIS:CD2	1:P:188[D]:HIS:H	2.39	0.40
1:E:188[A]:HIS:H	1:E:188[A]:HIS:CD2	2.39	0.40
1:G:167[A]:ARG:HD3	1:H:217[A]:SER:OG	2.22	0.40
1:J:26[A]:LEU:HD23	1:J:220[A]:LEU:HD21	2.03	0.40
1:N:198[A]:PRO:HA	1:N:199[A]:PRO:HD3	1.96	0.40
1:N:55[A]:ARG:NE	1:N:248[A]:GLU:OE1	2.55	0.40
1:O:34[A]:GLY:HA3	1:O:46[A]:VAL:HG22	2.03	0.40
1:E:188[B]:HIS:CD2	1:E:188[B]:HIS:H	2.39	0.40
1:G:167[B]:ARG:HD3	1:H:217[B]:SER:OG	2.22	0.40
1:K:118[B]:ARG:NH1	1:K:124[B]:GLY:HA3	2.37	0.40
1:K:263[B]:VAL:O	1:K:267[B]:LYS:HG3	2.22	0.40
1:L:220[B]:LEU:HA	1:L:224[B]:VAL:CG2	2.52	0.40
1:L:263[B]:VAL:HG12	1:L:267[B]:LYS:HE3	2.04	0.40
1:M:130[B]:GLN:HG3	1:M:173[B]:ALA:O	2.22	0.40
1:M:44[B]:GLY:HA3	1:M:260[B]:ARG:HH11	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:188[C]:HIS:CD2	1:E:188[C]:HIS:H	2.39	0.40
1:G:167[C]:ARG:HD3	1:H:217[C]:SER:OG	2.22	0.40
1:E:188[D]:HIS:CD2	1:E:188[D]:HIS:H	2.39	0.40
1:G:167[D]:ARG:HD3	1:H:217[D]:SER:OG	2.22	0.40
1:I:118[D]:ARG:NH1	1:I:124[D]:GLY:HA3	2.37	0.40
1:K:220[D]:LEU:HA	1:K:224[D]:VAL:CG2	2.51	0.40
1:L:220[D]:LEU:HA	1:L:224[D]:VAL:CG2	2.52	0.40
1:O:198[D]:PRO:HA	1:O:199[D]:PRO:HD3	1.95	0.40
1:P:26[D]:LEU:O	1:P:30[D]:ILE:HG13	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	1-A	303/317 (96%)	293 (97%)	7 (2%)	3 (1%)	15	10
1	1-B	303/317 (96%)	293 (97%)	9 (3%)	1 (0%)	41	39
1	1-C	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	1-D	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	1-E	303/317 (96%)	292 (96%)	8 (3%)	3 (1%)	15	10
1	1-F	303/317 (96%)	292 (96%)	9 (3%)	2 (1%)	22	17
1	1-G	303/317 (96%)	294 (97%)	8 (3%)	1 (0%)	41	39
1	1-H	303/317 (96%)	291 (96%)	9 (3%)	3 (1%)	15	10
1	1-I	295/317 (93%)	287 (97%)	7 (2%)	1 (0%)	41	39
1	1-J	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	1-K	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	1-L	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	1-M	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-N	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	1-O	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	1-P	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	2-A	303/317 (96%)	293 (97%)	7 (2%)	3 (1%)	15	10
1	2-B	303/317 (96%)	293 (97%)	9 (3%)	1 (0%)	41	39
1	2-C	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	2-D	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	2-E	303/317 (96%)	292 (96%)	8 (3%)	3 (1%)	15	10
1	2-F	303/317 (96%)	292 (96%)	9 (3%)	2 (1%)	22	17
1	2-G	303/317 (96%)	294 (97%)	8 (3%)	1 (0%)	41	39
1	2-H	303/317 (96%)	291 (96%)	9 (3%)	3 (1%)	15	10
1	2-I	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	2-J	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	2-K	295/317 (93%)	287 (97%)	7 (2%)	1 (0%)	41	39
1	2-L	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	2-M	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	2-N	295/317 (93%)	284 (96%)	10 (3%)	1 (0%)	41	39
1	2-O	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	2-P	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	3-A	303/317 (96%)	293 (97%)	7 (2%)	3 (1%)	15	10
1	3-B	303/317 (96%)	293 (97%)	9 (3%)	1 (0%)	41	39
1	3-C	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	3-D	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	3-E	303/317 (96%)	292 (96%)	8 (3%)	3 (1%)	15	10
1	3-F	303/317 (96%)	292 (96%)	9 (3%)	2 (1%)	22	17
1	3-G	303/317 (96%)	294 (97%)	8 (3%)	1 (0%)	41	39
1	3-H	303/317 (96%)	291 (96%)	9 (3%)	3 (1%)	15	10
1	3-I	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	3-J	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	3-K	295/317 (93%)	287 (97%)	7 (2%)	1 (0%)	41	39
1	3-L	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3-M	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	3-N	295/317 (93%)	283 (96%)	11 (4%)	1 (0%)	41	39
1	3-O	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	3-P	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	4-A	303/317 (96%)	293 (97%)	7 (2%)	3 (1%)	15	10
1	4-B	303/317 (96%)	293 (97%)	9 (3%)	1 (0%)	41	39
1	4-C	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	4-D	303/317 (96%)	293 (97%)	8 (3%)	2 (1%)	22	17
1	4-E	303/317 (96%)	292 (96%)	8 (3%)	3 (1%)	15	10
1	4-F	303/317 (96%)	292 (96%)	9 (3%)	2 (1%)	22	17
1	4-G	303/317 (96%)	294 (97%)	8 (3%)	1 (0%)	41	39
1	4-H	303/317 (96%)	291 (96%)	9 (3%)	3 (1%)	15	10
1	4-I	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	4-J	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	4-K	295/317 (93%)	287 (97%)	7 (2%)	1 (0%)	41	39
1	4-L	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	4-M	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
1	4-N	295/317 (93%)	283 (96%)	11 (4%)	1 (0%)	41	39
1	4-O	295/317 (93%)	285 (97%)	9 (3%)	1 (0%)	41	39
1	4-P	295/317 (93%)	286 (97%)	8 (3%)	1 (0%)	41	39
All	All	19136/20288 (94%)	18505 (97%)	531 (3%)	100 (0%)	29	25

All (100) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	127[A]	TYR
1	1-B	127[A]	TYR
1	1-C	127[A]	TYR
1	1-C	202[A]	SER
1	1-D	127[A]	TYR
1	1-D	202[A]	SER
1	1-E	127[A]	TYR
1	1-E	202[A]	SER
1	1-F	202[A]	SER
1	1-G	127[A]	TYR

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Mol	Chain	Res	Type
1	1-I	127[A]	TYR
1	1-J	127[A]	TYR
1	1-K	127[A]	TYR
1	1-L	127[A]	TYR
1	1-M	127[A]	TYR
1	1-N	127[A]	TYR
1	1-O	127[A]	TYR
1	1-P	127[A]	TYR
1	2-A	127[B]	TYR
1	2-B	127[B]	TYR
1	2-C	127[B]	TYR
1	2-C	202[B]	SER
1	2-D	127[B]	TYR
1	2-D	202[B]	SER
1	2-E	127[B]	TYR
1	2-E	202[B]	SER
1	2-F	202[B]	SER
1	2-G	127[B]	TYR
1	2-I	127[B]	TYR
1	2-J	127[B]	TYR
1	2-K	127[B]	TYR
1	2-L	127[B]	TYR
1	2-M	127[B]	TYR
1	2-N	127[B]	TYR
1	2-O	127[B]	TYR
1	2-P	127[B]	TYR
1	3-A	127[C]	TYR
1	3-B	127[C]	TYR
1	3-C	127[C]	TYR
1	3-C	202[C]	SER
1	3-D	127[C]	TYR
1	3-D	202[C]	SER
1	3-E	127[C]	TYR
1	3-E	202[C]	SER
1	3-F	202[C]	SER
1	3-G	127[C]	TYR
1	3-I	127[C]	TYR
1	3-J	127[C]	TYR
1	3-K	127[C]	TYR
1	3-L	127[C]	TYR
1	3-M	127[C]	TYR
1	3-N	127[C]	TYR

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Mol	Chain	Res	Type
1	3-O	127[C]	TYR
1	3-P	127[C]	TYR
1	4-A	127[D]	TYR
1	4-B	127[D]	TYR
1	4-C	127[D]	TYR
1	4-C	202[D]	SER
1	4-D	127[D]	TYR
1	4-D	202[D]	SER
1	4-E	127[D]	TYR
1	4-E	202[D]	SER
1	4-F	202[D]	SER
1	4-G	127[D]	TYR
1	4-I	127[D]	TYR
1	4-J	127[D]	TYR
1	4-K	127[D]	TYR
1	4-L	127[D]	TYR
1	4-M	127[D]	TYR
1	4-N	127[D]	TYR
1	4-O	127[D]	TYR
1	4-P	127[D]	TYR
1	1-A	201[A]	ASP
1	1-A	202[A]	SER
1	1-F	127[A]	TYR
1	1-H	127[A]	TYR
1	1-H	201[A]	ASP
1	1-H	203[A]	PRO
1	2-A	201[B]	ASP
1	2-A	202[B]	SER
1	2-F	127[B]	TYR
1	2-H	127[B]	TYR
1	2-H	201[B]	ASP
1	2-H	203[B]	PRO
1	3-A	201[C]	ASP
1	3-A	202[C]	SER
1	3-F	127[C]	TYR
1	3-H	127[C]	TYR
1	3-H	201[C]	ASP
1	3-H	203[C]	PRO
1	4-A	201[D]	ASP
1	4-A	202[D]	SER
1	4-F	127[D]	TYR
1	4-H	127[D]	TYR

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Mol	Chain	Res	Type
1	4-H	201[D]	ASP
1	4-H	203[D]	PRO
1	1-E	201[A]	ASP
1	2-E	201[B]	ASP
1	3-E	201[C]	ASP
1	4-E	201[D]	ASP

### 5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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	1-A	262/274 (96%)	260 (99%)	2 (1%)	81	85
1	1-B	263/274 (96%)	262 (100%)	1 (0%)	91	93
1	1-C	262/274 (96%)	261 (100%)	1 (0%)	91	93
1	1-D	263/274 (96%)	261 (99%)	2 (1%)	81	85
1	1-E	263/274 (96%)	261 (99%)	2 (1%)	81	85
1	1-F	263/274 (96%)	260 (99%)	3 (1%)	73	78
1	1-G	263/274 (96%)	260 (99%)	3 (1%)	73	78
1	1-H	263/274 (96%)	261 (99%)	2 (1%)	81	85
1	1-I	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-J	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-K	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-L	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-M	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-N	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-O	258/274 (94%)	257 (100%)	1 (0%)	91	93
1	1-P	258/274 (94%)	257 (100%)	1 (0%)	91	93
All	All	4166/4384 (95%)	4142 (99%)	24 (1%)	86	89

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	220[A]	LEU
1	1-A	298[A]	GLU
1	1-B	298[A]	GLU
1	1-C	298[A]	GLU
1	1-D	28[A]	ARG
1	1-D	298[A]	GLU
1	1-E	220[A]	LEU
1	1-E	298[A]	GLU
1	1-F	14[A]	SER
1	1-F	132[A]	ARG
1	1-F	298[A]	GLU
1	1-G	107[A]	LYS
1	1-G	220[A]	LEU
1	1-G	298[A]	GLU
1	1-H	14[A]	SER
1	1-H	298[A]	GLU
1	1-I	298[A]	GLU
1	1-J	298[A]	GLU
1	1-K	298[A]	GLU
1	1-L	298[A]	GLU
1	1-M	298[A]	GLU
1	1-N	298[A]	GLU
1	1-O	298[A]	GLU
1	1-P	298[A]	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	22[A]	GLN
1	1-A	32[A]	ASN
1	1-A	96[A]	GLN
1	1-A	154[A]	GLN
1	1-A	252[A]	GLN
1	1-A	269[A]	GLN
1	1-B	22[A]	GLN
1	1-B	32[A]	ASN
1	1-B	96[A]	GLN
1	1-B	154[A]	GLN
1	1-B	252[A]	GLN
1	1-B	269[A]	GLN
1	1-C	22[A]	GLN
1	1-C	32[A]	ASN
1	1-C	96[A]	GLN

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Mol	Chain	Res	Type
1	1-C	252[A]	GLN
1	1-C	269[A]	GLN
1	1-D	22[A]	GLN
1	1-D	32[A]	ASN
1	1-D	96[A]	GLN
1	1-D	252[A]	GLN
1	1-D	269[A]	GLN
1	1-E	22[A]	GLN
1	1-E	32[A]	ASN
1	1-E	96[A]	GLN
1	1-E	154[A]	GLN
1	1-E	252[A]	GLN
1	1-E	269[A]	GLN
1	1-F	22[A]	GLN
1	1-F	32[A]	ASN
1	1-F	96[A]	GLN
1	1-F	154[A]	GLN
1	1-F	252[A]	GLN
1	1-F	269[A]	GLN
1	1-G	22[A]	GLN
1	1-G	32[A]	ASN
1	1-G	96[A]	GLN
1	1-G	154[A]	GLN
1	1-G	252[A]	GLN
1	1-G	269[A]	GLN
1	1-H	22[A]	GLN
1	1-H	32[A]	ASN
1	1-H	96[A]	GLN
1	1-H	154[A]	GLN
1	1-H	252[A]	GLN
1	1-H	269[A]	GLN
1	1-I	22[A]	GLN
1	1-I	32[A]	ASN
1	1-I	96[A]	GLN
1	1-I	154[A]	GLN
1	1-I	252[A]	GLN
1	1-I	269[A]	GLN
1	1-J	22[A]	GLN
1	1-J	32[A]	ASN
1	1-J	96[A]	GLN
1	1-J	154[A]	GLN
1	1-J	252[A]	GLN

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Mol	Chain	Res	Type
1	1-J	269[A]	GLN
1	1-K	22[A]	GLN
1	1-K	32[A]	ASN
1	1-K	96[A]	GLN
1	1-K	154[A]	GLN
1	1-K	252[A]	GLN
1	1-K	269[A]	GLN
1	1-L	22[A]	GLN
1	1-L	32[A]	ASN
1	1-L	96[A]	GLN
1	1-L	154[A]	GLN
1	1-L	252[A]	GLN
1	1-L	269[A]	GLN
1	1-M	22[A]	GLN
1	1-M	32[A]	ASN
1	1-M	96[A]	GLN
1	1-M	154[A]	GLN
1	1-M	252[A]	GLN
1	1-M	269[A]	GLN
1	1-N	22[A]	GLN
1	1-N	32[A]	ASN
1	1-N	96[A]	GLN
1	1-N	154[A]	GLN
1	1-N	252[A]	GLN
1	1-N	269[A]	GLN
1	1-O	22[A]	GLN
1	1-O	32[A]	ASN
1	1-O	96[A]	GLN
1	1-O	154[A]	GLN
1	1-O	252[A]	GLN
1	1-O	269[A]	GLN
1	1-P	22[A]	GLN
1	1-P	32[A]	ASN
1	1-P	96[A]	GLN
1	1-P	154[A]	GLN
1	1-P	252[A]	GLN
1	1-P	269[A]	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

96 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	UMP	4-O	650[D]	-	18,21,21	3.29	5 (27%)	21,31,31	1.27	2 (9%)
3	CB3	1-A	2351[A]	-	30,37,37	2.79	14 (46%)	38,51,51	2.87	11 (28%)
2	UMP	2-F	600[B]	-	18,21,21	3.02	3 (16%)	21,31,31	1.55	5 (23%)
3	CB3	2-B	2401[B]	-	30,37,37	2.54	15 (50%)	38,51,51	2.76	18 (47%)
2	UMP	3-P	700[C]	-	18,21,21	3.32	5 (27%)	21,31,31	1.34	2 (9%)
2	UMP	2-G	650[B]	-	18,21,21	3.05	2 (11%)	21,31,31	1.82	4 (19%)
2	UMP	4-J	400[D]	-	18,21,21	3.28	5 (27%)	21,31,31	1.31	2 (9%)
2	UMP	4-C	450[D]	-	18,21,21	3.26	4 (22%)	21,31,31	1.85	5 (23%)
2	UMP	2-A	350[B]	-	18,21,21	3.42	4 (22%)	21,31,31	1.61	1 (4%)
2	UMP	3-D	500[C]	-	18,21,21	2.87	5 (27%)	21,31,31	1.52	2 (9%)
3	CB3	3-G	2651[C]	-	30,37,37	2.63	14 (46%)	38,51,51	2.79	16 (42%)
3	CB3	4-G	2651[D]	-	30,37,37	2.63	14 (46%)	38,51,51	2.79	16 (42%)
2	UMP	3-K	450[C]	-	18,21,21	3.32	5 (27%)	21,31,31	1.34	2 (9%)
2	UMP	2-B	400[B]	-	18,21,21	3.18	3 (16%)	21,31,31	1.48	3 (14%)
2	UMP	2-L	500[B]	-	18,21,21	3.31	5 (27%)	21,31,31	1.35	2 (9%)
2	UMP	3-F	600[C]	-	18,21,21	3.02	3 (16%)	21,31,31	1.55	5 (23%)
2	UMP	1-M	550[A]	1	18,21,21	3.19	5 (27%)	21,31,31	1.36	2 (9%)
3	CB3	2-C	2451[B]	-	30,37,37	2.41	13 (43%)	38,51,51	2.80	10 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UMP	2-D	500[B]	-	18,21,21	2.87	5 (27%)	21,31,31	1.52	2 (9%)
2	UMP	3-H	700[C]	-	18,21,21	3.84	7 (38%)	21,31,31	1.61	4 (19%)
2	UMP	4-A	350[D]	-	18,21,21	3.42	4 (22%)	21,31,31	1.61	1 (4%)
2	UMP	4-K	450[D]	-	18,21,21	3.28	5 (27%)	21,31,31	1.35	3 (14%)
2	UMP	4-E	550[D]	-	18,21,21	2.95	2 (11%)	21,31,31	1.77	5 (23%)
2	UMP	4-B	400[D]	-	18,21,21	3.18	3 (16%)	21,31,31	1.48	3 (14%)
2	UMP	1-B	400[A]	1	18,21,21	3.18	3 (16%)	21,31,31	1.48	3 (14%)
2	UMP	1-L	500[A]	1	18,21,21	3.32	5 (27%)	21,31,31	1.38	2 (9%)
2	UMP	1-F	600[A]	1	18,21,21	3.02	3 (16%)	21,31,31	1.55	5 (23%)
2	UMP	4-P	700[D]	-	18,21,21	3.30	5 (27%)	21,31,31	1.33	2 (9%)
2	UMP	4-D	500[D]	-	18,21,21	2.87	5 (27%)	21,31,31	1.52	2 (9%)
2	UMP	1-J	400[A]	1	18,21,21	3.27	5 (27%)	21,31,31	1.36	3 (14%)
2	UMP	1-P	700[A]	1	18,21,21	3.32	5 (27%)	21,31,31	1.35	3 (14%)
2	UMP	2-E	550[B]	-	18,21,21	2.95	2 (11%)	21,31,31	1.77	5 (23%)
3	CB3	3-H	2701[C]	-	30,37,37	2.11	12 (40%)	38,51,51	3.11	17 (44%)
3	CB3	3-B	2401[C]	-	30,37,37	2.54	15 (50%)	38,51,51	2.76	18 (47%)
2	UMP	2-M	550[B]	-	18,21,21	3.23	5 (27%)	21,31,31	1.37	2 (9%)
2	UMP	1-K	450[A]	1	18,21,21	3.27	5 (27%)	21,31,31	1.35	3 (14%)
2	UMP	1-E	550[A]	1	18,21,21	2.95	2 (11%)	21,31,31	1.77	5 (23%)
3	CB3	1-B	2401[A]	-	30,37,37	2.54	15 (50%)	38,51,51	2.76	18 (47%)
2	UMP	3-A	350[C]	-	18,21,21	3.42	4 (22%)	21,31,31	1.61	1 (4%)
2	UMP	3-O	650[C]	-	18,21,21	3.23	5 (27%)	21,31,31	1.30	2 (9%)
3	CB3	2-A	2351[B]	-	30,37,37	2.79	14 (46%)	38,51,51	2.87	11 (28%)
2	UMP	2-K	450[B]	-	18,21,21	3.26	5 (27%)	21,31,31	1.36	3 (14%)
2	UMP	3-M	550[C]	-	18,21,21	3.23	5 (27%)	21,31,31	1.38	2 (9%)
3	CB3	2-H	2701[B]	-	30,37,37	2.11	12 (40%)	38,51,51	3.11	17 (44%)
3	CB3	3-C	2451[C]	-	30,37,37	2.41	13 (43%)	38,51,51	2.80	10 (26%)
3	CB3	4-H	2701[D]	-	30,37,37	2.11	12 (40%)	38,51,51	3.11	17 (44%)
3	CB3	3-A	2351[C]	-	30,37,37	2.79	14 (46%)	38,51,51	2.87	11 (28%)
3	CB3	4-B	2401[D]	-	30,37,37	2.54	15 (50%)	38,51,51	2.76	18 (47%)
2	UMP	2-I	350[B]	-	18,21,21	3.20	5 (27%)	21,31,31	1.30	2 (9%)
3	CB3	1-F	2601[A]	-	30,37,37	2.62	14 (46%)	38,51,51	2.74	15 (39%)
3	CB3	3-F	2601[C]	-	30,37,37	2.62	14 (46%)	38,51,51	2.74	15 (39%)
2	UMP	4-H	700[D]	-	18,21,21	3.84	7 (38%)	21,31,31	1.61	4 (19%)
2	UMP	3-L	500[C]	-	18,21,21	3.31	5 (27%)	21,31,31	1.37	2 (9%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UMP	1-H	700[A]	1	18,21,21	3.84	7 (38%)	21,31,31	1.61	4 (19%)
2	UMP	3-J	400[C]	-	18,21,21	3.27	5 (27%)	21,31,31	1.35	2 (9%)
2	UMP	2-J	400[B]	-	18,21,21	3.27	5 (27%)	21,31,31	1.32	2 (9%)
3	CB3	1-H	2701[A]	-	30,37,37	2.11	12 (40%)	38,51,51	3.11	17 (44%)
2	UMP	1-I	350[A]	1	18,21,21	3.29	5 (27%)	21,31,31	1.34	2 (9%)
3	CB3	1-C	2451[A]	-	30,37,37	2.41	13 (43%)	38,51,51	2.80	10 (26%)
3	CB3	4-A	2351[D]	-	30,37,37	2.79	14 (46%)	38,51,51	2.87	11 (28%)
2	UMP	4-F	600[D]	-	18,21,21	3.02	3 (16%)	21,31,31	1.55	5 (23%)
2	UMP	4-L	500[D]	-	18,21,21	3.32	5 (27%)	21,31,31	1.36	2 (9%)
2	UMP	3-I	350[C]	-	18,21,21	3.26	5 (27%)	21,31,31	1.31	2 (9%)
2	UMP	2-C	450[B]	-	18,21,21	3.26	4 (22%)	21,31,31	1.85	5 (23%)
2	UMP	1-O	650[A]	1	18,21,21	3.22	5 (27%)	21,31,31	1.32	2 (9%)
3	CB3	4-F	2601[D]	-	30,37,37	2.62	14 (46%)	38,51,51	2.74	15 (39%)
2	UMP	1-G	650[A]	1	18,21,21	3.05	2 (11%)	21,31,31	1.82	4 (19%)
2	UMP	3-G	650[C]	-	18,21,21	3.05	2 (11%)	21,31,31	1.82	4 (19%)
3	CB3	3-D	2501[C]	-	30,37,37	2.45	14 (46%)	38,51,51	2.63	16 (42%)
2	UMP	3-E	550[C]	-	18,21,21	2.95	2 (11%)	21,31,31	1.77	5 (23%)
2	UMP	2-O	650[B]	-	18,21,21	3.27	4 (22%)	21,31,31	1.32	2 (9%)
3	CB3	1-G	2651[A]	-	30,37,37	2.63	14 (46%)	38,51,51	2.79	16 (42%)
3	CB3	2-E	2551[B]	-	30,37,37	2.60	15 (50%)	38,51,51	3.18	13 (34%)
2	UMP	1-D	500[A]	1	18,21,21	2.87	5 (27%)	21,31,31	1.52	2 (9%)
2	UMP	1-C	450[A]	1	18,21,21	3.26	4 (22%)	21,31,31	1.85	5 (23%)
3	CB3	4-C	2451[D]	-	30,37,37	2.41	13 (43%)	38,51,51	2.80	10 (26%)
2	UMP	1-N	600[A]	1	18,21,21	3.30	5 (27%)	21,31,31	1.37	2 (9%)
2	UMP	4-M	550[D]	-	18,21,21	3.17	5 (27%)	21,31,31	1.37	2 (9%)
3	CB3	1-D	2501[A]	-	30,37,37	2.45	14 (46%)	38,51,51	2.63	16 (42%)
2	UMP	3-B	400[C]	-	18,21,21	3.18	3 (16%)	21,31,31	1.48	3 (14%)
3	CB3	2-G	2651[B]	-	30,37,37	2.63	14 (46%)	38,51,51	2.79	16 (42%)
3	CB3	4-D	2501[D]	-	30,37,37	2.45	14 (46%)	38,51,51	2.63	16 (42%)
2	UMP	3-C	450[C]	-	18,21,21	3.26	4 (22%)	21,31,31	1.85	5 (23%)
2	UMP	2-H	700[B]	-	18,21,21	3.84	7 (38%)	21,31,31	1.61	4 (19%)
3	CB3	1-E	2551[A]	-	30,37,37	2.60	15 (50%)	38,51,51	3.18	13 (34%)
2	UMP	3-N	600[C]	-	18,21,21	3.34	5 (27%)	21,31,31	1.38	2 (9%)
3	CB3	2-F	2601[B]	-	30,37,37	2.62	14 (46%)	38,51,51	2.74	15 (39%)
2	UMP	2-P	700[B]	-	18,21,21	3.25	5 (27%)	21,31,31	1.33	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UMP	1-A	350[A]	1	18,21,21	3.42	4 (22%)	21,31,31	1.61	1 (4%)
2	UMP	4-G	650[D]	-	18,21,21	3.05	2 (11%)	21,31,31	1.82	4 (19%)
2	UMP	2-N	600[B]	-	18,21,21	3.31	5 (27%)	21,31,31	1.36	2 (9%)
2	UMP	4-I	350[D]	-	18,21,21	3.24	5 (27%)	21,31,31	1.32	3 (14%)
2	UMP	4-N	600[D]	-	18,21,21	3.33	5 (27%)	21,31,31	1.37	2 (9%)
3	CB3	4-E	2551[D]	-	30,37,37	2.60	15 (50%)	38,51,51	3.18	13 (34%)
3	CB3	2-D	2501[B]	-	30,37,37	2.45	14 (46%)	38,51,51	2.63	16 (42%)
3	CB3	3-E	2551[C]	-	30,37,37	2.60	15 (50%)	38,51,51	3.18	13 (34%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UMP	4-O	650[D]	-	-	4/7/22/22	0/2/2/2
3	CB3	1-A	2351[A]	-	-	1/21/28/28	0/3/3/3
2	UMP	2-F	600[B]	-	-	1/7/22/22	0/2/2/2
3	CB3	2-B	2401[B]	-	-	0/21/28/28	0/3/3/3
2	UMP	3-P	700[C]	-	-	4/7/22/22	0/2/2/2
2	UMP	2-G	650[B]	-	-	2/7/22/22	0/2/2/2
2	UMP	4-J	400[D]	-	-	4/7/22/22	0/2/2/2
2	UMP	4-C	450[D]	-	-	2/7/22/22	0/2/2/2
2	UMP	2-A	350[B]	-	-	2/7/22/22	0/2/2/2
2	UMP	3-D	500[C]	-	-	2/7/22/22	0/2/2/2
3	CB3	3-G	2651[C]	-	-	1/21/28/28	0/3/3/3
3	CB3	4-G	2651[D]	-	-	1/21/28/28	0/3/3/3
2	UMP	3-K	450[C]	-	-	4/7/22/22	0/2/2/2
2	UMP	2-B	400[B]	-	-	1/7/22/22	0/2/2/2
2	UMP	2-L	500[B]	-	-	4/7/22/22	0/2/2/2
2	UMP	3-F	600[C]	-	-	1/7/22/22	0/2/2/2
2	UMP	1-M	550[A]	1	-	3/7/22/22	0/2/2/2
3	CB3	2-C	2451[B]	-	-	1/21/28/28	0/3/3/3
2	UMP	2-D	500[B]	-	-	2/7/22/22	0/2/2/2
2	UMP	3-H	700[C]	-	-	1/7/22/22	0/2/2/2
2	UMP	4-A	350[D]	-	-	2/7/22/22	0/2/2/2
2	UMP	4-K	450[D]	-	-	4/7/22/22	0/2/2/2
2	UMP	4-E	550[D]	-	-	2/7/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UMP	4-B	400[D]	-	-	1/7/22/22	0/2/2/2
2	UMP	1-B	400[A]	1	-	1/7/22/22	0/2/2/2
2	UMP	1-L	500[A]	1	-	4/7/22/22	0/2/2/2
2	UMP	1-F	600[A]	1	-	1/7/22/22	0/2/2/2
2	UMP	4-P	700[D]	-	-	4/7/22/22	0/2/2/2
2	UMP	4-D	500[D]	-	-	2/7/22/22	0/2/2/2
2	UMP	1-J	400[A]	1	-	4/7/22/22	0/2/2/2
2	UMP	1-P	700[A]	1	-	4/7/22/22	0/2/2/2
2	UMP	2-E	550[B]	-	-	2/7/22/22	0/2/2/2
3	CB3	3-H	2701[C]	-	-	1/21/28/28	0/3/3/3
3	CB3	3-B	2401[C]	-	-	0/21/28/28	0/3/3/3
2	UMP	2-M	550[B]	-	-	3/7/22/22	0/2/2/2
2	UMP	1-K	450[A]	1	-	4/7/22/22	0/2/2/2
2	UMP	1-E	550[A]	1	-	2/7/22/22	0/2/2/2
3	CB3	1-B	2401[A]	-	-	0/21/28/28	0/3/3/3
2	UMP	3-A	350[C]	-	-	2/7/22/22	0/2/2/2
2	UMP	3-O	650[C]	-	-	4/7/22/22	0/2/2/2
3	CB3	2-A	2351[B]	-	-	1/21/28/28	0/3/3/3
2	UMP	2-K	450[B]	-	-	4/7/22/22	0/2/2/2
2	UMP	3-M	550[C]	-	-	3/7/22/22	0/2/2/2
3	CB3	2-H	2701[B]	-	-	1/21/28/28	0/3/3/3
3	CB3	3-C	2451[C]	-	-	1/21/28/28	0/3/3/3
3	CB3	4-H	2701[D]	-	-	1/21/28/28	0/3/3/3
3	CB3	3-A	2351[C]	-	-	1/21/28/28	0/3/3/3
3	CB3	4-B	2401[D]	-	-	0/21/28/28	0/3/3/3
2	UMP	2-I	350[B]	-	-	2/7/22/22	0/2/2/2
3	CB3	1-F	2601[A]	-	-	1/21/28/28	0/3/3/3
3	CB3	3-F	2601[C]	-	-	1/21/28/28	0/3/3/3
2	UMP	4-H	700[D]	-	-	1/7/22/22	0/2/2/2
2	UMP	3-L	500[C]	-	-	4/7/22/22	0/2/2/2
2	UMP	1-H	700[A]	1	-	1/7/22/22	0/2/2/2
2	UMP	3-J	400[C]	-	-	4/7/22/22	0/2/2/2
2	UMP	2-J	400[B]	-	-	4/7/22/22	0/2/2/2
3	CB3	1-H	2701[A]	-	-	1/21/28/28	0/3/3/3
2	UMP	1-I	350[A]	1	-	2/7/22/22	0/2/2/2
3	CB3	1-C	2451[A]	-	-	1/21/28/28	0/3/3/3
3	CB3	4-A	2351[D]	-	-	1/21/28/28	0/3/3/3
2	UMP	4-F	600[D]	-	-	1/7/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UMP	4-L	500[D]	-	-	4/7/22/22	0/2/2/2
2	UMP	3-I	350[C]	-	-	2/7/22/22	0/2/2/2
2	UMP	2-C	450[B]	-	-	2/7/22/22	0/2/2/2
2	UMP	1-O	650[A]	1	-	4/7/22/22	0/2/2/2
3	CB3	4-F	2601[D]	-	-	1/21/28/28	0/3/3/3
2	UMP	1-G	650[A]	1	-	2/7/22/22	0/2/2/2
2	UMP	3-G	650[C]	-	-	2/7/22/22	0/2/2/2
3	CB3	3-D	2501[C]	-	-	1/21/28/28	0/3/3/3
2	UMP	3-E	550[C]	-	-	2/7/22/22	0/2/2/2
2	UMP	2-O	650[B]	-	-	4/7/22/22	0/2/2/2
3	CB3	1-G	2651[A]	-	-	1/21/28/28	0/3/3/3
3	CB3	2-E	2551[B]	-	-	5/21/28/28	0/3/3/3
2	UMP	1-D	500[A]	1	-	2/7/22/22	0/2/2/2
2	UMP	1-C	450[A]	1	-	2/7/22/22	0/2/2/2
3	CB3	4-C	2451[D]	-	-	1/21/28/28	0/3/3/3
2	UMP	1-N	600[A]	1	-	3/7/22/22	0/2/2/2
2	UMP	4-M	550[D]	-	-	3/7/22/22	0/2/2/2
3	CB3	1-D	2501[A]	-	-	1/21/28/28	0/3/3/3
2	UMP	3-B	400[C]	-	-	1/7/22/22	0/2/2/2
3	CB3	2-G	2651[B]	-	-	1/21/28/28	0/3/3/3
3	CB3	4-D	2501[D]	-	-	1/21/28/28	0/3/3/3
2	UMP	3-C	450[C]	-	-	2/7/22/22	0/2/2/2
2	UMP	2-H	700[B]	-	-	1/7/22/22	0/2/2/2
3	CB3	1-E	2551[A]	-	-	5/21/28/28	0/3/3/3
2	UMP	3-N	600[C]	-	-	3/7/22/22	0/2/2/2
3	CB3	2-F	2601[B]	-	-	1/21/28/28	0/3/3/3
2	UMP	2-P	700[B]	-	-	4/7/22/22	0/2/2/2
2	UMP	1-A	350[A]	1	-	2/7/22/22	0/2/2/2
2	UMP	4-G	650[D]	-	-	2/7/22/22	0/2/2/2
2	UMP	2-N	600[B]	-	-	3/7/22/22	0/2/2/2
2	UMP	4-I	350[D]	-	-	2/7/22/22	0/2/2/2
2	UMP	4-N	600[D]	-	-	3/7/22/22	0/2/2/2
3	CB3	4-E	2551[D]	-	-	5/21/28/28	0/3/3/3
3	CB3	2-D	2501[B]	-	-	1/21/28/28	0/3/3/3
3	CB3	3-E	2551[C]	-	-	5/21/28/28	0/3/3/3

All (723) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3-H	700[C]	UMP	C6-N1	11.93	1.50	1.35
2	4-H	700[D]	UMP	C6-N1	11.93	1.50	1.35
2	1-H	700[A]	UMP	C6-N1	11.93	1.50	1.35
2	2-H	700[B]	UMP	C6-N1	11.93	1.50	1.35
2	2-A	350[B]	UMP	C6-N1	11.30	1.49	1.35
2	4-A	350[D]	UMP	C6-N1	11.30	1.49	1.35
2	3-A	350[C]	UMP	C6-N1	11.30	1.49	1.35
2	1-A	350[A]	UMP	C6-N1	11.30	1.49	1.35
2	3-N	600[C]	UMP	C6-N1	10.42	1.48	1.35
2	4-C	450[D]	UMP	C6-N1	10.41	1.48	1.35
2	2-C	450[B]	UMP	C6-N1	10.41	1.48	1.35
2	1-C	450[A]	UMP	C6-N1	10.41	1.48	1.35
2	3-C	450[C]	UMP	C6-N1	10.41	1.48	1.35
2	4-O	650[D]	UMP	C6-N1	10.39	1.48	1.35
2	4-N	600[D]	UMP	C6-N1	10.37	1.48	1.35
2	1-N	600[A]	UMP	C6-N1	10.27	1.48	1.35
2	3-P	700[C]	UMP	C6-N1	10.25	1.48	1.35
2	2-L	500[B]	UMP	C6-N1	10.23	1.48	1.35
2	2-N	600[B]	UMP	C6-N1	10.23	1.48	1.35
2	4-L	500[D]	UMP	C6-N1	10.23	1.48	1.35
2	3-K	450[C]	UMP	C6-N1	10.19	1.48	1.35
2	1-P	700[A]	UMP	C6-N1	10.18	1.48	1.35
2	1-I	350[A]	UMP	C6-N1	10.16	1.48	1.35
2	4-B	400[D]	UMP	C6-N1	10.15	1.48	1.35
2	1-B	400[A]	UMP	C6-N1	10.15	1.48	1.35
2	2-B	400[B]	UMP	C6-N1	10.15	1.48	1.35
2	3-B	400[C]	UMP	C6-N1	10.15	1.48	1.35
2	4-P	700[D]	UMP	C6-N1	10.15	1.48	1.35
2	3-L	500[C]	UMP	C6-N1	10.14	1.48	1.35
2	2-O	650[B]	UMP	C6-N1	10.12	1.48	1.35
2	2-G	650[B]	UMP	C6-N1	10.10	1.48	1.35
2	1-G	650[A]	UMP	C6-N1	10.10	1.48	1.35
2	3-G	650[C]	UMP	C6-N1	10.10	1.48	1.35
2	4-G	650[D]	UMP	C6-N1	10.10	1.48	1.35
2	1-L	500[A]	UMP	C6-N1	10.09	1.48	1.35
2	2-F	600[B]	UMP	C6-N1	9.99	1.48	1.35
2	3-F	600[C]	UMP	C6-N1	9.99	1.48	1.35
2	1-F	600[A]	UMP	C6-N1	9.99	1.48	1.35
2	4-F	600[D]	UMP	C6-N1	9.99	1.48	1.35
2	3-I	350[C]	UMP	C6-N1	9.99	1.48	1.35
2	4-K	450[D]	UMP	C6-N1	9.99	1.48	1.35
2	1-O	650[A]	UMP	C6-N1	9.95	1.48	1.35
2	1-K	450[A]	UMP	C6-N1	9.93	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-J	400[A]	UMP	C6-N1	9.91	1.48	1.35
2	4-J	400[D]	UMP	C6-N1	9.91	1.48	1.35
2	2-K	450[B]	UMP	C6-N1	9.90	1.48	1.35
2	3-J	400[C]	UMP	C6-N1	9.90	1.48	1.35
2	2-J	400[B]	UMP	C6-N1	9.86	1.48	1.35
2	4-I	350[D]	UMP	C6-N1	9.84	1.48	1.35
2	2-P	700[B]	UMP	C6-N1	9.80	1.47	1.35
2	3-O	650[C]	UMP	C6-N1	9.72	1.47	1.35
2	2-M	550[B]	UMP	C6-N1	9.61	1.47	1.35
2	3-M	550[C]	UMP	C6-N1	9.60	1.47	1.35
2	2-I	350[B]	UMP	C6-N1	9.58	1.47	1.35
2	1-M	550[A]	UMP	C6-N1	9.45	1.47	1.35
2	4-M	550[D]	UMP	C6-N1	9.38	1.47	1.35
2	4-E	550[D]	UMP	C6-N1	9.21	1.47	1.35
2	2-E	550[B]	UMP	C6-N1	9.21	1.47	1.35
2	1-E	550[A]	UMP	C6-N1	9.21	1.47	1.35
2	3-E	550[C]	UMP	C6-N1	9.21	1.47	1.35
2	3-D	500[C]	UMP	C6-N1	8.42	1.46	1.35
2	2-D	500[B]	UMP	C6-N1	8.42	1.46	1.35
2	4-D	500[D]	UMP	C6-N1	8.42	1.46	1.35
2	1-D	500[A]	UMP	C6-N1	8.42	1.46	1.35
3	1-A	2351[A]	CB3	CP1-N10	7.59	1.53	1.46
3	2-A	2351[B]	CB3	CP1-N10	7.59	1.53	1.46
3	3-A	2351[C]	CB3	CP1-N10	7.59	1.53	1.46
3	4-A	2351[D]	CB3	CP1-N10	7.59	1.53	1.46
2	1-L	500[A]	UMP	C6-C5	7.41	1.54	1.38
2	1-P	700[A]	UMP	C6-C5	7.41	1.54	1.38
2	1-I	350[A]	UMP	C6-C5	7.41	1.54	1.38
2	4-K	450[D]	UMP	C6-C5	7.40	1.54	1.38
2	3-J	400[C]	UMP	C6-C5	7.40	1.54	1.38
2	1-J	400[A]	UMP	C6-C5	7.39	1.54	1.38
2	4-P	700[D]	UMP	C6-C5	7.39	1.54	1.38
2	3-K	450[C]	UMP	C6-C5	7.39	1.54	1.38
2	2-J	400[B]	UMP	C6-C5	7.38	1.54	1.38
2	1-K	450[A]	UMP	C6-C5	7.37	1.54	1.38
2	3-I	350[C]	UMP	C6-C5	7.37	1.54	1.38
2	4-J	400[D]	UMP	C6-C5	7.37	1.54	1.38
2	2-K	450[B]	UMP	C6-C5	7.36	1.54	1.38
2	4-I	350[D]	UMP	C6-C5	7.35	1.54	1.38
2	3-P	700[C]	UMP	C6-C5	7.34	1.54	1.38
2	2-P	700[B]	UMP	C6-C5	7.34	1.54	1.38
2	2-I	350[B]	UMP	C6-C5	7.33	1.54	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	4-B	400[D]	UMP	C6-C5	7.33	1.54	1.38
2	1-B	400[A]	UMP	C6-C5	7.33	1.54	1.38
2	2-B	400[B]	UMP	C6-C5	7.33	1.54	1.38
2	3-B	400[C]	UMP	C6-C5	7.33	1.54	1.38
2	3-O	650[C]	UMP	C6-C5	7.33	1.54	1.38
2	2-M	550[B]	UMP	C6-C5	7.32	1.54	1.38
2	4-L	500[D]	UMP	C6-C5	7.31	1.54	1.38
2	3-L	500[C]	UMP	C6-C5	7.30	1.54	1.38
2	1-O	650[A]	UMP	C6-C5	7.30	1.54	1.38
2	2-O	650[B]	UMP	C6-C5	7.30	1.54	1.38
2	3-M	550[C]	UMP	C6-C5	7.29	1.54	1.38
2	1-M	550[A]	UMP	C6-C5	7.28	1.54	1.38
2	3-N	600[C]	UMP	C6-C5	7.28	1.54	1.38
2	4-M	550[D]	UMP	C6-C5	7.27	1.54	1.38
2	2-L	500[B]	UMP	C6-C5	7.24	1.54	1.38
2	2-N	600[B]	UMP	C6-C5	7.24	1.54	1.38
2	1-N	600[A]	UMP	C6-C5	7.24	1.54	1.38
2	4-O	650[D]	UMP	C6-C5	7.22	1.54	1.38
2	4-N	600[D]	UMP	C6-C5	7.19	1.53	1.38
2	4-C	450[D]	UMP	C6-C5	7.16	1.53	1.38
2	2-C	450[B]	UMP	C6-C5	7.16	1.53	1.38
2	1-C	450[A]	UMP	C6-C5	7.16	1.53	1.38
2	3-C	450[C]	UMP	C6-C5	7.16	1.53	1.38
2	4-E	550[D]	UMP	C6-C5	7.12	1.53	1.38
2	2-E	550[B]	UMP	C6-C5	7.12	1.53	1.38
2	1-E	550[A]	UMP	C6-C5	7.12	1.53	1.38
2	3-E	550[C]	UMP	C6-C5	7.12	1.53	1.38
2	2-A	350[B]	UMP	C6-C5	7.11	1.53	1.38
2	4-A	350[D]	UMP	C6-C5	7.11	1.53	1.38
2	3-A	350[C]	UMP	C6-C5	7.11	1.53	1.38
2	1-A	350[A]	UMP	C6-C5	7.11	1.53	1.38
2	3-H	700[C]	UMP	C6-C5	6.99	1.53	1.38
2	4-H	700[D]	UMP	C6-C5	6.99	1.53	1.38
2	1-H	700[A]	UMP	C6-C5	6.99	1.53	1.38
2	2-H	700[B]	UMP	C6-C5	6.99	1.53	1.38
2	2-G	650[B]	UMP	C6-C5	6.90	1.53	1.38
2	1-G	650[A]	UMP	C6-C5	6.90	1.53	1.38
2	3-G	650[C]	UMP	C6-C5	6.90	1.53	1.38
2	4-G	650[D]	UMP	C6-C5	6.90	1.53	1.38
2	3-D	500[C]	UMP	C6-C5	6.57	1.52	1.38
2	2-D	500[B]	UMP	C6-C5	6.57	1.52	1.38
2	4-D	500[D]	UMP	C6-C5	6.57	1.52	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-D	500[A]	UMP	C6-C5	6.57	1.52	1.38
3	1-F	2601[A]	CB3	CP1-N10	6.56	1.52	1.46
3	3-F	2601[C]	CB3	CP1-N10	6.56	1.52	1.46
3	4-F	2601[D]	CB3	CP1-N10	6.56	1.52	1.46
3	2-F	2601[B]	CB3	CP1-N10	6.56	1.52	1.46
2	2-F	600[B]	UMP	C6-C5	6.21	1.51	1.38
2	3-F	600[C]	UMP	C6-C5	6.21	1.51	1.38
2	1-F	600[A]	UMP	C6-C5	6.21	1.51	1.38
2	4-F	600[D]	UMP	C6-C5	6.21	1.51	1.38
3	2-E	2551[B]	CB3	C9-N10	5.76	1.54	1.46
3	1-E	2551[A]	CB3	C9-N10	5.76	1.54	1.46
3	4-E	2551[D]	CB3	C9-N10	5.76	1.54	1.46
3	3-E	2551[C]	CB3	C9-N10	5.76	1.54	1.46
3	2-B	2401[B]	CB3	C9-N10	5.36	1.53	1.46
3	3-B	2401[C]	CB3	C9-N10	5.36	1.53	1.46
3	1-B	2401[A]	CB3	C9-N10	5.36	1.53	1.46
3	4-B	2401[D]	CB3	C9-N10	5.36	1.53	1.46
3	2-E	2551[B]	CB3	O4-C4	5.35	1.38	1.24
3	1-E	2551[A]	CB3	O4-C4	5.35	1.38	1.24
3	4-E	2551[D]	CB3	O4-C4	5.35	1.38	1.24
3	3-E	2551[C]	CB3	O4-C4	5.35	1.38	1.24
3	2-C	2451[B]	CB3	O4-C4	4.91	1.36	1.24
3	3-C	2451[C]	CB3	O4-C4	4.91	1.36	1.24
3	1-C	2451[A]	CB3	O4-C4	4.91	1.36	1.24
3	4-C	2451[D]	CB3	O4-C4	4.91	1.36	1.24
3	2-B	2401[B]	CB3	C16-C15	4.91	1.47	1.38
3	3-B	2401[C]	CB3	C16-C15	4.91	1.47	1.38
3	1-B	2401[A]	CB3	C16-C15	4.91	1.47	1.38
3	4-B	2401[D]	CB3	C16-C15	4.91	1.47	1.38
3	1-A	2351[A]	CB3	C8-C7	4.80	1.46	1.36
3	2-A	2351[B]	CB3	C8-C7	4.80	1.46	1.36
3	3-A	2351[C]	CB3	C8-C7	4.80	1.46	1.36
3	4-A	2351[D]	CB3	C8-C7	4.80	1.46	1.36
3	2-C	2451[B]	CB3	C5-C6	4.79	1.48	1.37
3	3-C	2451[C]	CB3	C5-C6	4.79	1.48	1.37
3	1-C	2451[A]	CB3	C5-C6	4.79	1.48	1.37
3	4-C	2451[D]	CB3	C5-C6	4.79	1.48	1.37
3	1-A	2351[A]	CB3	O4-C4	4.71	1.36	1.24
3	2-A	2351[B]	CB3	O4-C4	4.71	1.36	1.24
3	3-A	2351[C]	CB3	O4-C4	4.71	1.36	1.24
3	4-A	2351[D]	CB3	O4-C4	4.71	1.36	1.24
3	3-G	2651[C]	CB3	O4-C4	4.67	1.36	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4-G	2651[D]	CB3	O4-C4	4.67	1.36	1.24
3	1-G	2651[A]	CB3	O4-C4	4.67	1.36	1.24
3	2-G	2651[B]	CB3	O4-C4	4.67	1.36	1.24
3	3-D	2501[C]	CB3	CP1-N10	4.63	1.50	1.46
3	1-D	2501[A]	CB3	CP1-N10	4.63	1.50	1.46
3	4-D	2501[D]	CB3	CP1-N10	4.63	1.50	1.46
3	2-D	2501[B]	CB3	CP1-N10	4.63	1.50	1.46
2	3-H	700[C]	UMP	P-OP2	-4.62	1.37	1.54
2	4-H	700[D]	UMP	P-OP2	-4.62	1.37	1.54
2	1-H	700[A]	UMP	P-OP2	-4.62	1.37	1.54
2	2-H	700[B]	UMP	P-OP2	-4.62	1.37	1.54
2	3-O	650[C]	UMP	O4'-C1'	4.52	1.52	1.42
3	3-G	2651[C]	CB3	C8-C7	4.52	1.46	1.36
3	4-G	2651[D]	CB3	C8-C7	4.52	1.46	1.36
3	1-G	2651[A]	CB3	C8-C7	4.52	1.46	1.36
3	2-G	2651[B]	CB3	C8-C7	4.52	1.46	1.36
3	3-D	2501[C]	CB3	C5-C6	4.49	1.48	1.37
3	1-D	2501[A]	CB3	C5-C6	4.49	1.48	1.37
3	4-D	2501[D]	CB3	C5-C6	4.49	1.48	1.37
3	2-D	2501[B]	CB3	C5-C6	4.49	1.48	1.37
3	1-F	2601[A]	CB3	C13-C14	4.49	1.48	1.39
3	3-F	2601[C]	CB3	C13-C14	4.49	1.48	1.39
3	4-F	2601[D]	CB3	C13-C14	4.49	1.48	1.39
3	2-F	2601[B]	CB3	C13-C14	4.49	1.48	1.39
2	3-H	700[C]	UMP	P-OP3	-4.41	1.37	1.54
2	4-H	700[D]	UMP	P-OP3	-4.41	1.37	1.54
2	1-H	700[A]	UMP	P-OP3	-4.41	1.37	1.54
2	2-H	700[B]	UMP	P-OP3	-4.41	1.37	1.54
3	2-B	2401[B]	CB3	O4-C4	4.36	1.35	1.24
3	3-B	2401[C]	CB3	O4-C4	4.36	1.35	1.24
3	1-B	2401[A]	CB3	O4-C4	4.36	1.35	1.24
3	4-B	2401[D]	CB3	O4-C4	4.36	1.35	1.24
2	2-P	700[B]	UMP	O4'-C1'	4.36	1.52	1.42
3	2-C	2451[B]	CB3	C8-C7	4.34	1.45	1.36
3	3-C	2451[C]	CB3	C8-C7	4.34	1.45	1.36
3	1-C	2451[A]	CB3	C8-C7	4.34	1.45	1.36
3	4-C	2451[D]	CB3	C8-C7	4.34	1.45	1.36
2	3-M	550[C]	UMP	O4'-C1'	4.31	1.52	1.42
3	1-F	2601[A]	CB3	C11-C	-4.30	1.41	1.50
3	3-F	2601[C]	CB3	C11-C	-4.30	1.41	1.50
3	4-F	2601[D]	CB3	C11-C	-4.30	1.41	1.50
3	2-F	2601[B]	CB3	C11-C	-4.30	1.41	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	4-C	450[D]	UMP	O4'-C1'	4.28	1.51	1.42
2	2-C	450[B]	UMP	O4'-C1'	4.28	1.51	1.42
2	1-C	450[A]	UMP	O4'-C1'	4.28	1.51	1.42
2	3-C	450[C]	UMP	O4'-C1'	4.28	1.51	1.42
3	2-B	2401[B]	CB3	C8-C7	4.28	1.45	1.36
3	3-B	2401[C]	CB3	C8-C7	4.28	1.45	1.36
3	1-B	2401[A]	CB3	C8-C7	4.28	1.45	1.36
3	4-B	2401[D]	CB3	C8-C7	4.28	1.45	1.36
2	1-P	700[A]	UMP	O4'-C1'	4.26	1.51	1.42
3	4-H	2701[D]	CB3	C11-C	-4.26	1.41	1.50
3	3-H	2701[C]	CB3	C11-C	-4.26	1.41	1.50
3	2-H	2701[B]	CB3	C11-C	-4.26	1.41	1.50
3	1-H	2701[A]	CB3	C11-C	-4.26	1.41	1.50
2	4-M	550[D]	UMP	O4'-C1'	4.26	1.51	1.42
3	2-E	2551[B]	CB3	CP1-N10	4.25	1.50	1.46
3	1-E	2551[A]	CB3	CP1-N10	4.25	1.50	1.46
3	4-E	2551[D]	CB3	CP1-N10	4.25	1.50	1.46
3	3-E	2551[C]	CB3	CP1-N10	4.25	1.50	1.46
3	1-A	2351[A]	CB3	C13-C14	4.24	1.47	1.39
3	2-A	2351[B]	CB3	C13-C14	4.24	1.47	1.39
3	3-A	2351[C]	CB3	C13-C14	4.24	1.47	1.39
3	4-A	2351[D]	CB3	C13-C14	4.24	1.47	1.39
2	1-M	550[A]	UMP	O4'-C1'	4.23	1.51	1.42
3	3-D	2501[C]	CB3	C9-N10	4.23	1.52	1.46
3	1-D	2501[A]	CB3	C9-N10	4.23	1.52	1.46
3	4-D	2501[D]	CB3	C9-N10	4.23	1.52	1.46
3	2-D	2501[B]	CB3	C9-N10	4.23	1.52	1.46
3	4-H	2701[D]	CB3	C13-C14	4.19	1.47	1.39
3	3-H	2701[C]	CB3	C13-C14	4.19	1.47	1.39
3	2-H	2701[B]	CB3	C13-C14	4.19	1.47	1.39
3	1-H	2701[A]	CB3	C13-C14	4.19	1.47	1.39
2	2-M	550[B]	UMP	O4'-C1'	4.19	1.51	1.42
2	4-P	700[D]	UMP	O4'-C1'	4.19	1.51	1.42
3	3-G	2651[C]	CB3	C13-C14	4.17	1.47	1.39
3	4-G	2651[D]	CB3	C13-C14	4.17	1.47	1.39
3	1-G	2651[A]	CB3	C13-C14	4.17	1.47	1.39
3	2-G	2651[B]	CB3	C13-C14	4.17	1.47	1.39
2	4-I	350[D]	UMP	O4'-C1'	4.16	1.51	1.42
2	2-J	400[B]	UMP	O4'-C1'	4.15	1.51	1.42
3	3-G	2651[C]	CB3	C5-C6	4.15	1.47	1.37
3	4-G	2651[D]	CB3	C5-C6	4.15	1.47	1.37
3	1-G	2651[A]	CB3	C5-C6	4.15	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2-G	2651[B]	CB3	C5-C6	4.15	1.47	1.37
2	1-L	500[A]	UMP	O4'-C1'	4.14	1.51	1.42
2	4-N	600[D]	UMP	O4'-C1'	4.13	1.51	1.42
3	3-G	2651[C]	CB3	C7-C6	4.12	1.47	1.38
3	4-G	2651[D]	CB3	C7-C6	4.12	1.47	1.38
3	1-G	2651[A]	CB3	C7-C6	4.12	1.47	1.38
3	2-G	2651[B]	CB3	C7-C6	4.12	1.47	1.38
2	1-J	400[A]	UMP	O4'-C1'	4.12	1.51	1.42
2	1-K	450[A]	UMP	O4'-C1'	4.11	1.51	1.42
2	4-J	400[D]	UMP	O4'-C1'	4.11	1.51	1.42
2	2-L	500[B]	UMP	O4'-C1'	4.10	1.51	1.42
2	3-L	500[C]	UMP	O4'-C1'	4.09	1.51	1.42
2	3-J	400[C]	UMP	O4'-C1'	4.09	1.51	1.42
2	3-P	700[C]	UMP	O4'-C1'	4.08	1.51	1.42
3	2-B	2401[B]	CB3	CA-N	4.06	1.51	1.46
3	3-B	2401[C]	CB3	CA-N	4.06	1.51	1.46
3	1-B	2401[A]	CB3	CA-N	4.06	1.51	1.46
3	4-B	2401[D]	CB3	CA-N	4.06	1.51	1.46
2	2-I	350[B]	UMP	O4'-C1'	4.06	1.51	1.42
2	1-I	350[A]	UMP	O4'-C1'	4.06	1.51	1.42
2	2-N	600[B]	UMP	O4'-C1'	4.06	1.51	1.42
3	1-A	2351[A]	CB3	C16-C15	4.05	1.46	1.38
3	2-A	2351[B]	CB3	C16-C15	4.05	1.46	1.38
3	3-A	2351[C]	CB3	C16-C15	4.05	1.46	1.38
3	4-A	2351[D]	CB3	C16-C15	4.05	1.46	1.38
3	3-G	2651[C]	CB3	C11-C	-4.05	1.41	1.50
3	4-G	2651[D]	CB3	C11-C	-4.05	1.41	1.50
3	1-G	2651[A]	CB3	C11-C	-4.05	1.41	1.50
3	2-G	2651[B]	CB3	C11-C	-4.05	1.41	1.50
2	3-K	450[C]	UMP	O4'-C1'	4.03	1.51	1.42
2	3-N	600[C]	UMP	O4'-C1'	4.02	1.51	1.42
2	4-L	500[D]	UMP	O4'-C1'	4.02	1.51	1.42
3	3-D	2501[C]	CB3	C16-C15	4.02	1.46	1.38
3	1-D	2501[A]	CB3	C16-C15	4.02	1.46	1.38
3	4-D	2501[D]	CB3	C16-C15	4.02	1.46	1.38
3	2-D	2501[B]	CB3	C16-C15	4.02	1.46	1.38
2	4-K	450[D]	UMP	O4'-C1'	4.02	1.51	1.42
3	1-F	2601[A]	CB3	C9-N10	4.00	1.52	1.46
3	3-F	2601[C]	CB3	C9-N10	4.00	1.52	1.46
3	4-F	2601[D]	CB3	C9-N10	4.00	1.52	1.46
3	2-F	2601[B]	CB3	C9-N10	4.00	1.52	1.46
2	3-I	350[C]	UMP	O4'-C1'	4.00	1.51	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2-K	450[B]	UMP	O4'-C1'	4.00	1.51	1.42
3	2-E	2551[B]	CB3	C8-C7	3.98	1.45	1.36
3	1-E	2551[A]	CB3	C8-C7	3.98	1.45	1.36
3	4-E	2551[D]	CB3	C8-C7	3.98	1.45	1.36
3	3-E	2551[C]	CB3	C8-C7	3.98	1.45	1.36
2	2-O	650[B]	UMP	O4'-C1'	3.95	1.51	1.42
3	1-A	2351[A]	CB3	C5-C6	3.94	1.46	1.37
3	2-A	2351[B]	CB3	C5-C6	3.94	1.46	1.37
3	3-A	2351[C]	CB3	C5-C6	3.94	1.46	1.37
3	4-A	2351[D]	CB3	C5-C6	3.94	1.46	1.37
2	1-N	600[A]	UMP	O4'-C1'	3.94	1.51	1.42
3	3-G	2651[C]	CB3	CP1-N10	3.89	1.50	1.46
3	4-G	2651[D]	CB3	CP1-N10	3.89	1.50	1.46
3	1-G	2651[A]	CB3	CP1-N10	3.89	1.50	1.46
3	2-G	2651[B]	CB3	CP1-N10	3.89	1.50	1.46
3	3-G	2651[C]	CB3	C16-C11	3.87	1.45	1.39
3	4-G	2651[D]	CB3	C16-C11	3.87	1.45	1.39
3	1-G	2651[A]	CB3	C16-C11	3.87	1.45	1.39
3	2-G	2651[B]	CB3	C16-C11	3.87	1.45	1.39
3	1-A	2351[A]	CB3	C7-C6	3.78	1.47	1.38
3	2-A	2351[B]	CB3	C7-C6	3.78	1.47	1.38
3	3-A	2351[C]	CB3	C7-C6	3.78	1.47	1.38
3	4-A	2351[D]	CB3	C7-C6	3.78	1.47	1.38
2	4-O	650[D]	UMP	O4'-C1'	3.78	1.50	1.42
3	1-F	2601[A]	CB3	C16-C11	3.77	1.45	1.39
3	3-F	2601[C]	CB3	C16-C11	3.77	1.45	1.39
3	4-F	2601[D]	CB3	C16-C11	3.77	1.45	1.39
3	2-F	2601[B]	CB3	C16-C11	3.77	1.45	1.39
2	4-B	400[D]	UMP	O3'-C3'	3.70	1.51	1.43
2	1-B	400[A]	UMP	O3'-C3'	3.70	1.51	1.43
2	2-B	400[B]	UMP	O3'-C3'	3.70	1.51	1.43
2	3-B	400[C]	UMP	O3'-C3'	3.70	1.51	1.43
2	1-O	650[A]	UMP	O4'-C1'	3.69	1.50	1.42
3	2-C	2451[B]	CB3	C13-C14	3.67	1.46	1.39
3	3-C	2451[C]	CB3	C13-C14	3.67	1.46	1.39
3	1-C	2451[A]	CB3	C13-C14	3.67	1.46	1.39
3	4-C	2451[D]	CB3	C13-C14	3.67	1.46	1.39
3	2-B	2401[B]	CB3	C13-C14	3.66	1.46	1.39
3	3-B	2401[C]	CB3	C13-C14	3.66	1.46	1.39
3	1-B	2401[A]	CB3	C13-C14	3.66	1.46	1.39
3	4-B	2401[D]	CB3	C13-C14	3.66	1.46	1.39
3	1-F	2601[A]	CB3	C5-C6	3.65	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3-F	2601[C]	CB3	C5-C6	3.65	1.46	1.37
3	4-F	2601[D]	CB3	C5-C6	3.65	1.46	1.37
3	2-F	2601[B]	CB3	C5-C6	3.65	1.46	1.37
2	3-H	700[C]	UMP	P-O5'	-3.64	1.48	1.60
2	4-H	700[D]	UMP	P-O5'	-3.64	1.48	1.60
2	1-H	700[A]	UMP	P-O5'	-3.64	1.48	1.60
2	2-H	700[B]	UMP	P-O5'	-3.64	1.48	1.60
2	3-D	500[C]	UMP	O3'-C3'	3.61	1.51	1.43
2	2-D	500[B]	UMP	O3'-C3'	3.61	1.51	1.43
2	4-D	500[D]	UMP	O3'-C3'	3.61	1.51	1.43
2	1-D	500[A]	UMP	O3'-C3'	3.61	1.51	1.43
3	3-D	2501[C]	CB3	C13-C14	3.61	1.46	1.39
3	1-D	2501[A]	CB3	C13-C14	3.61	1.46	1.39
3	4-D	2501[D]	CB3	C13-C14	3.61	1.46	1.39
3	2-D	2501[B]	CB3	C13-C14	3.61	1.46	1.39
3	4-H	2701[D]	CB3	CP1-N10	3.56	1.49	1.46
3	3-H	2701[C]	CB3	CP1-N10	3.56	1.49	1.46
3	2-H	2701[B]	CB3	CP1-N10	3.56	1.49	1.46
3	1-H	2701[A]	CB3	CP1-N10	3.56	1.49	1.46
3	2-C	2451[B]	CB3	C7-C6	3.50	1.46	1.38
3	3-C	2451[C]	CB3	C7-C6	3.50	1.46	1.38
3	1-C	2451[A]	CB3	C7-C6	3.50	1.46	1.38
3	4-C	2451[D]	CB3	C7-C6	3.50	1.46	1.38
3	4-H	2701[D]	CB3	C8-C7	3.43	1.43	1.36
3	3-H	2701[C]	CB3	C8-C7	3.43	1.43	1.36
3	2-H	2701[B]	CB3	C8-C7	3.43	1.43	1.36
3	1-H	2701[A]	CB3	C8-C7	3.43	1.43	1.36
3	3-D	2501[C]	CB3	O4-C4	3.37	1.33	1.24
3	1-D	2501[A]	CB3	O4-C4	3.37	1.33	1.24
3	4-D	2501[D]	CB3	O4-C4	3.37	1.33	1.24
3	2-D	2501[B]	CB3	O4-C4	3.37	1.33	1.24
3	2-E	2551[B]	CB3	C16-C11	3.36	1.45	1.39
3	1-E	2551[A]	CB3	C16-C11	3.36	1.45	1.39
3	4-E	2551[D]	CB3	C16-C11	3.36	1.45	1.39
3	3-E	2551[C]	CB3	C16-C11	3.36	1.45	1.39
3	2-C	2451[B]	CB3	C16-C11	3.32	1.45	1.39
3	3-C	2451[C]	CB3	C16-C11	3.32	1.45	1.39
3	1-C	2451[A]	CB3	C16-C11	3.32	1.45	1.39
3	4-C	2451[D]	CB3	C16-C11	3.32	1.45	1.39
3	3-G	2651[C]	CB3	CP1-CP2	3.29	1.51	1.47
3	4-G	2651[D]	CB3	CP1-CP2	3.29	1.51	1.47
3	1-G	2651[A]	CB3	CP1-CP2	3.29	1.51	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2-G	2651[B]	CB3	CP1-CP2	3.29	1.51	1.47
3	2-E	2551[B]	CB3	C5-C6	3.28	1.45	1.37
3	1-E	2551[A]	CB3	C5-C6	3.28	1.45	1.37
3	4-E	2551[D]	CB3	C5-C6	3.28	1.45	1.37
3	3-E	2551[C]	CB3	C5-C6	3.28	1.45	1.37
3	4-H	2701[D]	CB3	C16-C11	3.27	1.44	1.39
3	3-H	2701[C]	CB3	C16-C11	3.27	1.44	1.39
3	2-H	2701[B]	CB3	C16-C11	3.27	1.44	1.39
3	1-H	2701[A]	CB3	C16-C11	3.27	1.44	1.39
2	3-D	500[C]	UMP	C2-N3	-3.22	1.31	1.38
2	2-D	500[B]	UMP	C2-N3	-3.22	1.31	1.38
2	4-D	500[D]	UMP	C2-N3	-3.22	1.31	1.38
2	1-D	500[A]	UMP	C2-N3	-3.22	1.31	1.38
3	2-B	2401[B]	CB3	C5-C6	3.20	1.44	1.37
3	3-B	2401[C]	CB3	C5-C6	3.20	1.44	1.37
3	1-B	2401[A]	CB3	C5-C6	3.20	1.44	1.37
3	4-B	2401[D]	CB3	C5-C6	3.20	1.44	1.37
3	2-C	2451[B]	CB3	C16-C15	3.20	1.44	1.38
3	3-C	2451[C]	CB3	C16-C15	3.20	1.44	1.38
3	1-C	2451[A]	CB3	C16-C15	3.20	1.44	1.38
3	4-C	2451[D]	CB3	C16-C15	3.20	1.44	1.38
3	2-E	2551[B]	CB3	CP1-CP2	3.17	1.51	1.47
3	1-E	2551[A]	CB3	CP1-CP2	3.17	1.51	1.47
3	4-E	2551[D]	CB3	CP1-CP2	3.17	1.51	1.47
3	3-E	2551[C]	CB3	CP1-CP2	3.17	1.51	1.47
3	4-H	2701[D]	CB3	O4-C4	3.16	1.32	1.24
3	3-H	2701[C]	CB3	O4-C4	3.16	1.32	1.24
3	2-H	2701[B]	CB3	O4-C4	3.16	1.32	1.24
3	1-H	2701[A]	CB3	O4-C4	3.16	1.32	1.24
3	2-C	2451[B]	CB3	C11-C	-3.15	1.43	1.50
3	3-C	2451[C]	CB3	C11-C	-3.15	1.43	1.50
3	1-C	2451[A]	CB3	C11-C	-3.15	1.43	1.50
3	4-C	2451[D]	CB3	C11-C	-3.15	1.43	1.50
3	1-F	2601[A]	CB3	O4-C4	3.12	1.32	1.24
3	3-F	2601[C]	CB3	O4-C4	3.12	1.32	1.24
3	4-F	2601[D]	CB3	O4-C4	3.12	1.32	1.24
3	2-F	2601[B]	CB3	O4-C4	3.12	1.32	1.24
3	1-F	2601[A]	CB3	C15-C14	3.11	1.45	1.39
3	3-F	2601[C]	CB3	C15-C14	3.11	1.45	1.39
3	4-F	2601[D]	CB3	C15-C14	3.11	1.45	1.39
3	2-F	2601[B]	CB3	C15-C14	3.11	1.45	1.39
3	3-D	2501[C]	CB3	C13-C12	3.11	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-D	2501[A]	CB3	C13-C12	3.11	1.44	1.38
3	4-D	2501[D]	CB3	C13-C12	3.11	1.44	1.38
3	2-D	2501[B]	CB3	C13-C12	3.11	1.44	1.38
3	1-A	2351[A]	CB3	C4-N3	3.11	1.38	1.33
3	2-A	2351[B]	CB3	C4-N3	3.11	1.38	1.33
3	3-A	2351[C]	CB3	C4-N3	3.11	1.38	1.33
3	4-A	2351[D]	CB3	C4-N3	3.11	1.38	1.33
3	2-E	2551[B]	CB3	C7-C6	3.08	1.45	1.38
3	1-E	2551[A]	CB3	C7-C6	3.08	1.45	1.38
3	4-E	2551[D]	CB3	C7-C6	3.08	1.45	1.38
3	3-E	2551[C]	CB3	C7-C6	3.08	1.45	1.38
3	1-A	2351[A]	CB3	C11-C	-3.07	1.43	1.50
3	2-A	2351[B]	CB3	C11-C	-3.07	1.43	1.50
3	3-A	2351[C]	CB3	C11-C	-3.07	1.43	1.50
3	4-A	2351[D]	CB3	C11-C	-3.07	1.43	1.50
3	1-F	2601[A]	CB3	C7-C6	3.07	1.45	1.38
3	3-F	2601[C]	CB3	C7-C6	3.07	1.45	1.38
3	4-F	2601[D]	CB3	C7-C6	3.07	1.45	1.38
3	2-F	2601[B]	CB3	C7-C6	3.07	1.45	1.38
3	2-B	2401[B]	CB3	C11-C	-3.05	1.43	1.50
3	3-B	2401[C]	CB3	C11-C	-3.05	1.43	1.50
3	1-B	2401[A]	CB3	C11-C	-3.05	1.43	1.50
3	4-B	2401[D]	CB3	C11-C	-3.05	1.43	1.50
3	3-G	2651[C]	CB3	C15-C14	3.04	1.45	1.39
3	4-G	2651[D]	CB3	C15-C14	3.04	1.45	1.39
3	1-G	2651[A]	CB3	C15-C14	3.04	1.45	1.39
3	2-G	2651[B]	CB3	C15-C14	3.04	1.45	1.39
2	2-A	350[B]	UMP	O4'-C1'	3.04	1.49	1.42
2	4-A	350[D]	UMP	O4'-C1'	3.04	1.49	1.42
2	3-A	350[C]	UMP	O4'-C1'	3.04	1.49	1.42
2	1-A	350[A]	UMP	O4'-C1'	3.04	1.49	1.42
3	1-A	2351[A]	CB3	C13-C12	3.03	1.44	1.38
3	2-A	2351[B]	CB3	C13-C12	3.03	1.44	1.38
3	3-A	2351[C]	CB3	C13-C12	3.03	1.44	1.38
3	4-A	2351[D]	CB3	C13-C12	3.03	1.44	1.38
3	3-D	2501[C]	CB3	C7-C6	3.01	1.45	1.38
3	1-D	2501[A]	CB3	C7-C6	3.01	1.45	1.38
3	4-D	2501[D]	CB3	C7-C6	3.01	1.45	1.38
3	2-D	2501[B]	CB3	C7-C6	3.01	1.45	1.38
3	1-F	2601[A]	CB3	C4-N3	3.00	1.38	1.33
3	3-F	2601[C]	CB3	C4-N3	3.00	1.38	1.33
3	4-F	2601[D]	CB3	C4-N3	3.00	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2-F	2601[B]	CB3	C4-N3	3.00	1.38	1.33
3	3-G	2651[C]	CB3	C4-N3	2.99	1.38	1.33
3	4-G	2651[D]	CB3	C4-N3	2.99	1.38	1.33
3	1-G	2651[A]	CB3	C4-N3	2.99	1.38	1.33
3	2-G	2651[B]	CB3	C4-N3	2.99	1.38	1.33
3	2-E	2551[B]	CB3	C13-C14	2.98	1.45	1.39
3	1-E	2551[A]	CB3	C13-C14	2.98	1.45	1.39
3	4-E	2551[D]	CB3	C13-C14	2.98	1.45	1.39
3	3-E	2551[C]	CB3	C13-C14	2.98	1.45	1.39
3	1-A	2351[A]	CB3	C16-C11	2.95	1.44	1.39
3	2-A	2351[B]	CB3	C16-C11	2.95	1.44	1.39
3	3-A	2351[C]	CB3	C16-C11	2.95	1.44	1.39
3	4-A	2351[D]	CB3	C16-C11	2.95	1.44	1.39
3	4-H	2701[D]	CB3	C8A-N1	-2.93	1.32	1.37
3	3-H	2701[C]	CB3	C8A-N1	-2.93	1.32	1.37
3	2-H	2701[B]	CB3	C8A-N1	-2.93	1.32	1.37
3	1-H	2701[A]	CB3	C8A-N1	-2.93	1.32	1.37
2	3-H	700[C]	UMP	P-OP1	-2.93	1.41	1.50
2	4-H	700[D]	UMP	P-OP1	-2.93	1.41	1.50
2	1-H	700[A]	UMP	P-OP1	-2.93	1.41	1.50
2	2-H	700[B]	UMP	P-OP1	-2.93	1.41	1.50
2	4-K	450[D]	UMP	O4'-C4'	2.91	1.51	1.45
2	4-J	400[D]	UMP	C4-N3	2.90	1.38	1.33
2	4-L	500[D]	UMP	O4'-C4'	2.90	1.51	1.45
2	2-J	400[B]	UMP	C4-N3	2.90	1.38	1.33
2	3-K	450[C]	UMP	C4-N3	2.90	1.38	1.33
2	1-L	500[A]	UMP	C4-N3	2.88	1.38	1.33
2	3-L	500[C]	UMP	C4-N3	2.87	1.38	1.33
2	1-M	550[A]	UMP	O4'-C4'	2.86	1.51	1.45
2	3-N	600[C]	UMP	C4-N3	2.86	1.38	1.33
3	3-D	2501[C]	CB3	C8-C7	2.85	1.42	1.36
3	1-D	2501[A]	CB3	C8-C7	2.85	1.42	1.36
3	4-D	2501[D]	CB3	C8-C7	2.85	1.42	1.36
3	2-D	2501[B]	CB3	C8-C7	2.85	1.42	1.36
2	4-L	500[D]	UMP	C4-N3	2.85	1.38	1.33
2	2-L	500[B]	UMP	C4-N3	2.85	1.38	1.33
2	2-M	550[B]	UMP	O4'-C4'	2.84	1.51	1.45
2	1-N	600[A]	UMP	C4-N3	2.83	1.38	1.33
2	3-M	550[C]	UMP	C4-N3	2.83	1.38	1.33
2	3-J	400[C]	UMP	O4'-C4'	2.82	1.51	1.45
2	3-L	500[C]	UMP	O4'-C4'	2.82	1.51	1.45
2	2-N	600[B]	UMP	C4-N3	2.82	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3-D	2501[C]	CB3	C8-C8A	2.82	1.46	1.41
3	1-D	2501[A]	CB3	C8-C8A	2.82	1.46	1.41
3	4-D	2501[D]	CB3	C8-C8A	2.82	1.46	1.41
3	2-D	2501[B]	CB3	C8-C8A	2.82	1.46	1.41
3	3-D	2501[C]	CB3	CA-N	2.81	1.50	1.46
3	1-D	2501[A]	CB3	CA-N	2.81	1.50	1.46
3	4-D	2501[D]	CB3	CA-N	2.81	1.50	1.46
3	2-D	2501[B]	CB3	CA-N	2.81	1.50	1.46
2	3-K	450[C]	UMP	O4'-C4'	2.81	1.51	1.45
2	3-P	700[C]	UMP	C4-N3	2.81	1.37	1.33
2	4-N	600[D]	UMP	C4-N3	2.81	1.37	1.33
2	2-O	650[B]	UMP	C4-N3	2.80	1.37	1.33
2	1-J	400[A]	UMP	C4-N3	2.80	1.37	1.33
2	1-K	450[A]	UMP	C4-N3	2.80	1.37	1.33
2	1-M	550[A]	UMP	C4-N3	2.80	1.37	1.33
2	1-L	500[A]	UMP	O4'-C4'	2.79	1.51	1.45
2	4-M	550[D]	UMP	O4'-C4'	2.79	1.51	1.45
2	2-K	450[B]	UMP	C4-N3	2.79	1.37	1.33
3	2-B	2401[B]	CB3	CP1-N10	2.79	1.48	1.46
3	3-B	2401[C]	CB3	CP1-N10	2.79	1.48	1.46
3	1-B	2401[A]	CB3	CP1-N10	2.79	1.48	1.46
3	4-B	2401[D]	CB3	CP1-N10	2.79	1.48	1.46
3	3-G	2651[C]	CB3	C12-C11	2.78	1.44	1.39
3	4-G	2651[D]	CB3	C12-C11	2.78	1.44	1.39
3	1-G	2651[A]	CB3	C12-C11	2.78	1.44	1.39
3	2-G	2651[B]	CB3	C12-C11	2.78	1.44	1.39
2	1-P	700[A]	UMP	O4'-C4'	2.78	1.51	1.45
2	1-N	600[A]	UMP	O4'-C4'	2.78	1.51	1.45
2	2-K	450[B]	UMP	O4'-C4'	2.78	1.51	1.45
2	2-J	400[B]	UMP	O4'-C4'	2.78	1.51	1.45
2	2-M	550[B]	UMP	C4-N3	2.77	1.37	1.33
2	2-L	500[B]	UMP	O4'-C4'	2.77	1.51	1.45
2	2-N	600[B]	UMP	O4'-C4'	2.77	1.51	1.45
2	3-M	550[C]	UMP	O4'-C4'	2.77	1.51	1.45
3	2-C	2451[B]	CB3	CA-N	-2.76	1.43	1.46
3	3-C	2451[C]	CB3	CA-N	-2.76	1.43	1.46
3	1-C	2451[A]	CB3	CA-N	-2.76	1.43	1.46
3	4-C	2451[D]	CB3	CA-N	-2.76	1.43	1.46
2	4-J	400[D]	UMP	O4'-C4'	2.74	1.51	1.45
2	1-O	650[A]	UMP	C4-N3	2.74	1.37	1.33
2	1-K	450[A]	UMP	O4'-C4'	2.74	1.51	1.45
3	2-C	2451[B]	CB3	CP1-CP2	2.71	1.50	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3-C	2451[C]	CB3	CP1-CP2	2.71	1.50	1.47
3	1-C	2451[A]	CB3	CP1-CP2	2.71	1.50	1.47
3	4-C	2451[D]	CB3	CP1-CP2	2.71	1.50	1.47
3	1-F	2601[A]	CB3	C8A-N1	-2.70	1.33	1.37
3	3-F	2601[C]	CB3	C8A-N1	-2.70	1.33	1.37
3	4-F	2601[D]	CB3	C8A-N1	-2.70	1.33	1.37
3	2-F	2601[B]	CB3	C8A-N1	-2.70	1.33	1.37
2	1-J	400[A]	UMP	O4'-C4'	2.69	1.51	1.45
2	3-P	700[C]	UMP	O4'-C4'	2.69	1.51	1.45
3	2-E	2551[B]	CB3	C11-C	-2.69	1.44	1.50
3	1-E	2551[A]	CB3	C11-C	-2.69	1.44	1.50
3	4-E	2551[D]	CB3	C11-C	-2.69	1.44	1.50
3	3-E	2551[C]	CB3	C11-C	-2.69	1.44	1.50
2	2-I	350[B]	UMP	O4'-C4'	2.69	1.51	1.45
3	2-E	2551[B]	CB3	C13-C12	2.68	1.43	1.38
3	1-E	2551[A]	CB3	C13-C12	2.68	1.43	1.38
3	4-E	2551[D]	CB3	C13-C12	2.68	1.43	1.38
3	3-E	2551[C]	CB3	C13-C12	2.68	1.43	1.38
2	4-N	600[D]	UMP	O4'-C4'	2.68	1.51	1.45
2	4-I	350[D]	UMP	C4-N3	2.68	1.37	1.33
2	3-N	600[C]	UMP	O4'-C4'	2.68	1.51	1.45
3	2-C	2451[B]	CB3	C4-N3	2.67	1.37	1.33
3	3-C	2451[C]	CB3	C4-N3	2.67	1.37	1.33
3	1-C	2451[A]	CB3	C4-N3	2.67	1.37	1.33
3	4-C	2451[D]	CB3	C4-N3	2.67	1.37	1.33
2	2-P	700[B]	UMP	C4-N3	2.67	1.37	1.33
2	1-I	350[A]	UMP	C4-N3	2.67	1.37	1.33
2	4-M	550[D]	UMP	C4-N3	2.67	1.37	1.33
2	2-I	350[B]	UMP	C4-N3	2.67	1.37	1.33
2	3-I	350[C]	UMP	C4-N3	2.66	1.37	1.33
3	2-B	2401[B]	CB3	C7-C6	2.66	1.44	1.38
3	3-B	2401[C]	CB3	C7-C6	2.66	1.44	1.38
3	1-B	2401[A]	CB3	C7-C6	2.66	1.44	1.38
3	4-B	2401[D]	CB3	C7-C6	2.66	1.44	1.38
2	4-K	450[D]	UMP	C4-N3	2.66	1.37	1.33
2	2-A	350[B]	UMP	C4-N3	2.65	1.37	1.33
2	4-A	350[D]	UMP	C4-N3	2.65	1.37	1.33
2	3-A	350[C]	UMP	C4-N3	2.65	1.37	1.33
2	1-A	350[A]	UMP	C4-N3	2.65	1.37	1.33
2	3-J	400[C]	UMP	C4-N3	2.65	1.37	1.33
2	4-P	700[D]	UMP	O4'-C4'	2.65	1.50	1.45
2	2-P	700[B]	UMP	O4'-C4'	2.64	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3-I	350[C]	UMP	O4'-C4'	2.63	1.50	1.45
2	4-P	700[D]	UMP	C4-N3	2.62	1.37	1.33
3	2-E	2551[B]	CB3	C16-C15	2.60	1.43	1.38
3	1-E	2551[A]	CB3	C16-C15	2.60	1.43	1.38
3	4-E	2551[D]	CB3	C16-C15	2.60	1.43	1.38
3	3-E	2551[C]	CB3	C16-C15	2.60	1.43	1.38
2	4-O	650[D]	UMP	C4-N3	2.59	1.37	1.33
2	4-I	350[D]	UMP	O4'-C4'	2.57	1.50	1.45
3	2-E	2551[B]	CB3	C9-C6	-2.57	1.46	1.51
3	1-E	2551[A]	CB3	C9-C6	-2.57	1.46	1.51
3	4-E	2551[D]	CB3	C9-C6	-2.57	1.46	1.51
3	3-E	2551[C]	CB3	C9-C6	-2.57	1.46	1.51
3	2-C	2451[B]	CB3	C8-C8A	2.56	1.46	1.41
3	3-C	2451[C]	CB3	C8-C8A	2.56	1.46	1.41
3	1-C	2451[A]	CB3	C8-C8A	2.56	1.46	1.41
3	4-C	2451[D]	CB3	C8-C8A	2.56	1.46	1.41
2	1-P	700[A]	UMP	C4-N3	2.56	1.37	1.33
2	3-O	650[C]	UMP	C4-N3	2.56	1.37	1.33
2	3-H	700[C]	UMP	O4'-C4'	2.55	1.50	1.45
2	4-H	700[D]	UMP	O4'-C4'	2.55	1.50	1.45
2	1-H	700[A]	UMP	O4'-C4'	2.55	1.50	1.45
2	2-H	700[B]	UMP	O4'-C4'	2.55	1.50	1.45
3	2-B	2401[B]	CB3	C13-C12	2.54	1.43	1.38
3	3-B	2401[C]	CB3	C13-C12	2.54	1.43	1.38
3	1-B	2401[A]	CB3	C13-C12	2.54	1.43	1.38
3	4-B	2401[D]	CB3	C13-C12	2.54	1.43	1.38
3	3-D	2501[C]	CB3	C16-C11	2.50	1.43	1.39
3	1-D	2501[A]	CB3	C16-C11	2.50	1.43	1.39
3	4-D	2501[D]	CB3	C16-C11	2.50	1.43	1.39
3	2-D	2501[B]	CB3	C16-C11	2.50	1.43	1.39
3	3-D	2501[C]	CB3	C15-C14	2.49	1.44	1.39
3	1-D	2501[A]	CB3	C15-C14	2.49	1.44	1.39
3	4-D	2501[D]	CB3	C15-C14	2.49	1.44	1.39
3	2-D	2501[B]	CB3	C15-C14	2.49	1.44	1.39
3	2-B	2401[B]	CB3	C8-C8A	2.47	1.46	1.41
3	3-B	2401[C]	CB3	C8-C8A	2.47	1.46	1.41
3	1-B	2401[A]	CB3	C8-C8A	2.47	1.46	1.41
3	4-B	2401[D]	CB3	C8-C8A	2.47	1.46	1.41
2	4-O	650[D]	UMP	O4'-C4'	2.47	1.50	1.45
3	2-E	2551[B]	CB3	C15-C14	2.45	1.44	1.39
3	1-E	2551[A]	CB3	C15-C14	2.45	1.44	1.39
3	4-E	2551[D]	CB3	C15-C14	2.45	1.44	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3-E	2551[C]	CB3	C15-C14	2.45	1.44	1.39
3	1-F	2601[A]	CB3	C16-C15	2.45	1.43	1.38
3	3-F	2601[C]	CB3	C16-C15	2.45	1.43	1.38
3	4-F	2601[D]	CB3	C16-C15	2.45	1.43	1.38
3	2-F	2601[B]	CB3	C16-C15	2.45	1.43	1.38
2	1-I	350[A]	UMP	O4'-C4'	2.43	1.50	1.45
3	4-H	2701[D]	CB3	C15-C14	2.42	1.44	1.39
3	3-H	2701[C]	CB3	C15-C14	2.42	1.44	1.39
3	2-H	2701[B]	CB3	C15-C14	2.42	1.44	1.39
3	1-H	2701[A]	CB3	C15-C14	2.42	1.44	1.39
3	1-F	2601[A]	CB3	C8-C8A	2.40	1.46	1.41
3	3-F	2601[C]	CB3	C8-C8A	2.40	1.46	1.41
3	4-F	2601[D]	CB3	C8-C8A	2.40	1.46	1.41
3	2-F	2601[B]	CB3	C8-C8A	2.40	1.46	1.41
3	4-H	2701[D]	CB3	C5-C6	2.36	1.42	1.37
3	3-H	2701[C]	CB3	C5-C6	2.36	1.42	1.37
3	2-H	2701[B]	CB3	C5-C6	2.36	1.42	1.37
3	1-H	2701[A]	CB3	C5-C6	2.36	1.42	1.37
3	1-A	2351[A]	CB3	C12-C11	2.36	1.43	1.39
3	2-A	2351[B]	CB3	C12-C11	2.36	1.43	1.39
3	3-A	2351[C]	CB3	C12-C11	2.36	1.43	1.39
3	4-A	2351[D]	CB3	C12-C11	2.36	1.43	1.39
3	1-A	2351[A]	CB3	C9-N10	2.34	1.49	1.46
3	2-A	2351[B]	CB3	C9-N10	2.34	1.49	1.46
3	3-A	2351[C]	CB3	C9-N10	2.34	1.49	1.46
3	4-A	2351[D]	CB3	C9-N10	2.34	1.49	1.46
3	2-B	2401[B]	CB3	C16-C11	2.32	1.43	1.39
3	3-B	2401[C]	CB3	C16-C11	2.32	1.43	1.39
3	1-B	2401[A]	CB3	C16-C11	2.32	1.43	1.39
3	4-B	2401[D]	CB3	C16-C11	2.32	1.43	1.39
3	2-E	2551[B]	CB3	C8-C8A	2.31	1.45	1.41
3	1-E	2551[A]	CB3	C8-C8A	2.31	1.45	1.41
3	4-E	2551[D]	CB3	C8-C8A	2.31	1.45	1.41
3	3-E	2551[C]	CB3	C8-C8A	2.31	1.45	1.41
3	2-B	2401[B]	CB3	C-N	-2.29	1.29	1.34
3	3-B	2401[C]	CB3	C-N	-2.29	1.29	1.34
3	1-B	2401[A]	CB3	C-N	-2.29	1.29	1.34
3	4-B	2401[D]	CB3	C-N	-2.29	1.29	1.34
3	4-H	2701[D]	CB3	C7-C6	2.29	1.43	1.38
3	3-H	2701[C]	CB3	C7-C6	2.29	1.43	1.38
3	2-H	2701[B]	CB3	C7-C6	2.29	1.43	1.38
3	1-H	2701[A]	CB3	C7-C6	2.29	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	4-C	450[D]	UMP	C4-N3	2.28	1.37	1.33
2	2-C	450[B]	UMP	C4-N3	2.28	1.37	1.33
2	1-C	450[A]	UMP	C4-N3	2.28	1.37	1.33
2	3-C	450[C]	UMP	C4-N3	2.28	1.37	1.33
2	2-F	600[B]	UMP	C4-N3	2.28	1.37	1.33
2	3-F	600[C]	UMP	C4-N3	2.28	1.37	1.33
2	1-F	600[A]	UMP	C4-N3	2.28	1.37	1.33
2	4-F	600[D]	UMP	C4-N3	2.28	1.37	1.33
3	1-F	2601[A]	CB3	C8-C7	2.25	1.41	1.36
3	3-F	2601[C]	CB3	C8-C7	2.25	1.41	1.36
3	4-F	2601[D]	CB3	C8-C7	2.25	1.41	1.36
3	2-F	2601[B]	CB3	C8-C7	2.25	1.41	1.36
3	3-D	2501[C]	CB3	C4-N3	2.25	1.36	1.33
3	1-D	2501[A]	CB3	C4-N3	2.25	1.36	1.33
3	4-D	2501[D]	CB3	C4-N3	2.25	1.36	1.33
3	2-D	2501[B]	CB3	C4-N3	2.25	1.36	1.33
3	3-G	2651[C]	CB3	C9-N10	2.22	1.49	1.46
3	4-G	2651[D]	CB3	C9-N10	2.22	1.49	1.46
3	1-G	2651[A]	CB3	C9-N10	2.22	1.49	1.46
3	2-G	2651[B]	CB3	C9-N10	2.22	1.49	1.46
2	3-O	650[C]	UMP	O4'-C4'	2.21	1.49	1.45
3	2-B	2401[B]	CB3	C4-N3	2.20	1.36	1.33
3	3-B	2401[C]	CB3	C4-N3	2.20	1.36	1.33
3	1-B	2401[A]	CB3	C4-N3	2.20	1.36	1.33
3	4-B	2401[D]	CB3	C4-N3	2.20	1.36	1.33
2	1-O	650[A]	UMP	O4'-C4'	2.13	1.49	1.45
3	1-A	2351[A]	CB3	C8-C8A	2.12	1.45	1.41
3	2-A	2351[B]	CB3	C8-C8A	2.12	1.45	1.41
3	3-A	2351[C]	CB3	C8-C8A	2.12	1.45	1.41
3	4-A	2351[D]	CB3	C8-C8A	2.12	1.45	1.41
3	4-H	2701[D]	CB3	C16-C15	2.11	1.42	1.38
3	3-H	2701[C]	CB3	C16-C15	2.11	1.42	1.38
3	2-H	2701[B]	CB3	C16-C15	2.11	1.42	1.38
3	1-H	2701[A]	CB3	C16-C15	2.11	1.42	1.38
3	3-G	2651[C]	CB3	CA-N	-2.10	1.43	1.46
3	4-G	2651[D]	CB3	CA-N	-2.10	1.43	1.46
3	1-G	2651[A]	CB3	CA-N	-2.10	1.43	1.46
3	2-G	2651[B]	CB3	CA-N	-2.10	1.43	1.46
3	4-H	2701[D]	CB3	C12-C11	2.09	1.42	1.39
3	3-H	2701[C]	CB3	C12-C11	2.09	1.42	1.39
3	2-H	2701[B]	CB3	C12-C11	2.09	1.42	1.39
3	1-H	2701[A]	CB3	C12-C11	2.09	1.42	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3-D	500[C]	UMP	O4'-C1'	2.02	1.46	1.42
2	2-D	500[B]	UMP	O4'-C1'	2.02	1.46	1.42
2	4-D	500[D]	UMP	O4'-C1'	2.02	1.46	1.42
2	1-D	500[A]	UMP	O4'-C1'	2.02	1.46	1.42
3	2-C	2451[B]	CB3	C15-C14	2.00	1.43	1.39
3	3-C	2451[C]	CB3	C15-C14	2.00	1.43	1.39
3	1-C	2451[A]	CB3	C15-C14	2.00	1.43	1.39
3	4-C	2451[D]	CB3	C15-C14	2.00	1.43	1.39

All (651) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-A	2351[A]	CB3	C4A-C8A-N1	-10.75	117.76	123.60
3	2-A	2351[B]	CB3	C4A-C8A-N1	-10.75	117.76	123.60
3	3-A	2351[C]	CB3	C4A-C8A-N1	-10.75	117.76	123.60
3	4-A	2351[D]	CB3	C4A-C8A-N1	-10.75	117.76	123.60
3	3-G	2651[C]	CB3	C4A-C8A-N1	-9.40	118.50	123.60
3	4-G	2651[D]	CB3	C4A-C8A-N1	-9.40	118.50	123.60
3	1-G	2651[A]	CB3	C4A-C8A-N1	-9.40	118.50	123.60
3	2-G	2651[B]	CB3	C4A-C8A-N1	-9.40	118.50	123.60
3	2-C	2451[B]	CB3	C4A-C8A-N1	-9.15	118.63	123.60
3	3-C	2451[C]	CB3	C4A-C8A-N1	-9.15	118.63	123.60
3	1-C	2451[A]	CB3	C4A-C8A-N1	-9.15	118.63	123.60
3	4-C	2451[D]	CB3	C4A-C8A-N1	-9.15	118.63	123.60
3	4-H	2701[D]	CB3	N1-C2-N3	-8.97	115.25	127.22
3	3-H	2701[C]	CB3	N1-C2-N3	-8.97	115.25	127.22
3	2-H	2701[B]	CB3	N1-C2-N3	-8.97	115.25	127.22
3	1-H	2701[A]	CB3	N1-C2-N3	-8.97	115.25	127.22
3	2-E	2551[B]	CB3	C4A-C8A-N1	-8.82	118.81	123.60
3	1-E	2551[A]	CB3	C4A-C8A-N1	-8.82	118.81	123.60
3	4-E	2551[D]	CB3	C4A-C8A-N1	-8.82	118.81	123.60
3	3-E	2551[C]	CB3	C4A-C8A-N1	-8.82	118.81	123.60
3	2-B	2401[B]	CB3	C4A-C8A-N1	-8.45	119.01	123.60
3	3-B	2401[C]	CB3	C4A-C8A-N1	-8.45	119.01	123.60
3	1-B	2401[A]	CB3	C4A-C8A-N1	-8.45	119.01	123.60
3	4-B	2401[D]	CB3	C4A-C8A-N1	-8.45	119.01	123.60
3	3-D	2501[C]	CB3	C4A-C8A-N1	-8.27	119.11	123.60
3	1-D	2501[A]	CB3	C4A-C8A-N1	-8.27	119.11	123.60
3	4-D	2501[D]	CB3	C4A-C8A-N1	-8.27	119.11	123.60
3	2-D	2501[B]	CB3	C4A-C8A-N1	-8.27	119.11	123.60
3	1-F	2601[A]	CB3	N1-C2-N3	-7.92	116.66	127.22
3	3-F	2601[C]	CB3	N1-C2-N3	-7.92	116.66	127.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-F	2601[D]	CB3	N1-C2-N3	-7.92	116.66	127.22
3	2-F	2601[B]	CB3	N1-C2-N3	-7.92	116.66	127.22
3	1-F	2601[A]	CB3	C4A-C8A-N1	-7.72	119.41	123.60
3	3-F	2601[C]	CB3	C4A-C8A-N1	-7.72	119.41	123.60
3	4-F	2601[D]	CB3	C4A-C8A-N1	-7.72	119.41	123.60
3	2-F	2601[B]	CB3	C4A-C8A-N1	-7.72	119.41	123.60
3	2-E	2551[B]	CB3	C4A-C4-N3	-7.65	119.07	124.40
3	1-E	2551[A]	CB3	C4A-C4-N3	-7.65	119.07	124.40
3	4-E	2551[D]	CB3	C4A-C4-N3	-7.65	119.07	124.40
3	3-E	2551[C]	CB3	C4A-C4-N3	-7.65	119.07	124.40
3	3-D	2501[C]	CB3	CP1-N10-C9	-7.53	109.93	117.10
3	1-D	2501[A]	CB3	CP1-N10-C9	-7.53	109.93	117.10
3	4-D	2501[D]	CB3	CP1-N10-C9	-7.53	109.93	117.10
3	2-D	2501[B]	CB3	CP1-N10-C9	-7.53	109.93	117.10
3	2-E	2551[B]	CB3	CB-CA-N	7.52	121.15	110.19
3	1-E	2551[A]	CB3	CB-CA-N	7.52	121.15	110.19
3	4-E	2551[D]	CB3	CB-CA-N	7.52	121.15	110.19
3	3-E	2551[C]	CB3	CB-CA-N	7.52	121.15	110.19
3	2-C	2451[B]	CB3	N1-C2-N3	-7.36	117.41	127.22
3	3-C	2451[C]	CB3	N1-C2-N3	-7.36	117.41	127.22
3	1-C	2451[A]	CB3	N1-C2-N3	-7.36	117.41	127.22
3	4-C	2451[D]	CB3	N1-C2-N3	-7.36	117.41	127.22
3	1-A	2351[A]	CB3	N1-C2-N3	-7.31	117.47	127.22
3	2-A	2351[B]	CB3	N1-C2-N3	-7.31	117.47	127.22
3	3-A	2351[C]	CB3	N1-C2-N3	-7.31	117.47	127.22
3	4-A	2351[D]	CB3	N1-C2-N3	-7.31	117.47	127.22
3	4-H	2701[D]	CB3	C4A-C8A-N1	-7.30	119.64	123.60
3	3-H	2701[C]	CB3	C4A-C8A-N1	-7.30	119.64	123.60
3	2-H	2701[B]	CB3	C4A-C8A-N1	-7.30	119.64	123.60
3	1-H	2701[A]	CB3	C4A-C8A-N1	-7.30	119.64	123.60
3	2-E	2551[B]	CB3	N1-C2-N3	-7.19	117.63	127.22
3	1-E	2551[A]	CB3	N1-C2-N3	-7.19	117.63	127.22
3	4-E	2551[D]	CB3	N1-C2-N3	-7.19	117.63	127.22
3	3-E	2551[C]	CB3	N1-C2-N3	-7.19	117.63	127.22
3	2-B	2401[B]	CB3	N1-C2-N3	-7.03	117.84	127.22
3	3-B	2401[C]	CB3	N1-C2-N3	-7.03	117.84	127.22
3	1-B	2401[A]	CB3	N1-C2-N3	-7.03	117.84	127.22
3	4-B	2401[D]	CB3	N1-C2-N3	-7.03	117.84	127.22
3	4-H	2701[D]	CB3	C4A-C4-N3	-6.45	119.90	124.40
3	3-H	2701[C]	CB3	C4A-C4-N3	-6.45	119.90	124.40
3	2-H	2701[B]	CB3	C4A-C4-N3	-6.45	119.90	124.40
3	1-H	2701[A]	CB3	C4A-C4-N3	-6.45	119.90	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-G	2651[C]	CB3	N1-C2-N3	-6.05	119.16	127.22
3	4-G	2651[D]	CB3	N1-C2-N3	-6.05	119.16	127.22
3	1-G	2651[A]	CB3	N1-C2-N3	-6.05	119.16	127.22
3	2-G	2651[B]	CB3	N1-C2-N3	-6.05	119.16	127.22
3	3-G	2651[C]	CB3	CP1-CP2-CP3	-6.03	167.56	177.67
3	4-G	2651[D]	CB3	CP1-CP2-CP3	-6.03	167.56	177.67
3	1-G	2651[A]	CB3	CP1-CP2-CP3	-6.03	167.56	177.67
3	2-G	2651[B]	CB3	CP1-CP2-CP3	-6.03	167.56	177.67
3	1-A	2351[A]	CB3	CP1-CP2-CP3	-6.00	167.61	177.67
3	2-A	2351[B]	CB3	CP1-CP2-CP3	-6.00	167.61	177.67
3	3-A	2351[C]	CB3	CP1-CP2-CP3	-6.00	167.61	177.67
3	4-A	2351[D]	CB3	CP1-CP2-CP3	-6.00	167.61	177.67
3	1-F	2601[A]	CB3	C4A-C4-N3	-5.91	120.28	124.40
3	3-F	2601[C]	CB3	C4A-C4-N3	-5.91	120.28	124.40
3	4-F	2601[D]	CB3	C4A-C4-N3	-5.91	120.28	124.40
3	2-F	2601[B]	CB3	C4A-C4-N3	-5.91	120.28	124.40
3	4-H	2701[D]	CB3	CA-N-C	-5.66	115.05	122.34
3	3-H	2701[C]	CB3	CA-N-C	-5.66	115.05	122.34
3	2-H	2701[B]	CB3	CA-N-C	-5.66	115.05	122.34
3	1-H	2701[A]	CB3	CA-N-C	-5.66	115.05	122.34
3	2-C	2451[B]	CB3	C4A-C4-N3	-5.53	120.55	124.40
3	3-C	2451[C]	CB3	C4A-C4-N3	-5.53	120.55	124.40
3	1-C	2451[A]	CB3	C4A-C4-N3	-5.53	120.55	124.40
3	4-C	2451[D]	CB3	C4A-C4-N3	-5.53	120.55	124.40
2	2-A	350[B]	UMP	C5-C6-N1	-5.47	108.47	120.68
2	4-A	350[D]	UMP	C5-C6-N1	-5.47	108.47	120.68
2	3-A	350[C]	UMP	C5-C6-N1	-5.47	108.47	120.68
2	1-A	350[A]	UMP	C5-C6-N1	-5.47	108.47	120.68
3	3-D	2501[C]	CB3	N1-C2-N3	-5.45	119.95	127.22
3	1-D	2501[A]	CB3	N1-C2-N3	-5.45	119.95	127.22
3	4-D	2501[D]	CB3	N1-C2-N3	-5.45	119.95	127.22
3	2-D	2501[B]	CB3	N1-C2-N3	-5.45	119.95	127.22
3	2-E	2551[B]	CB3	C4-N3-C2	5.44	124.57	115.93
3	1-E	2551[A]	CB3	C4-N3-C2	5.44	124.57	115.93
3	4-E	2551[D]	CB3	C4-N3-C2	5.44	124.57	115.93
3	3-E	2551[C]	CB3	C4-N3-C2	5.44	124.57	115.93
3	4-H	2701[D]	CB3	CP1-N10-C9	-5.42	111.94	117.10
3	3-H	2701[C]	CB3	CP1-N10-C9	-5.42	111.94	117.10
3	2-H	2701[B]	CB3	CP1-N10-C9	-5.42	111.94	117.10
3	1-H	2701[A]	CB3	CP1-N10-C9	-5.42	111.94	117.10
2	4-C	450[D]	UMP	C5-C6-N1	-5.36	108.72	120.68
2	2-C	450[B]	UMP	C5-C6-N1	-5.36	108.72	120.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1-C	450[A]	UMP	C5-C6-N1	-5.36	108.72	120.68
2	3-C	450[C]	UMP	C5-C6-N1	-5.36	108.72	120.68
3	4-H	2701[D]	CB3	C4-N3-C2	5.35	124.42	115.93
3	3-H	2701[C]	CB3	C4-N3-C2	5.35	124.42	115.93
3	2-H	2701[B]	CB3	C4-N3-C2	5.35	124.42	115.93
3	1-H	2701[A]	CB3	C4-N3-C2	5.35	124.42	115.93
3	2-C	2451[B]	CB3	CP1-N10-C9	-5.23	112.12	117.10
3	3-C	2451[C]	CB3	CP1-N10-C9	-5.23	112.12	117.10
3	1-C	2451[A]	CB3	CP1-N10-C9	-5.23	112.12	117.10
3	4-C	2451[D]	CB3	CP1-N10-C9	-5.23	112.12	117.10
3	2-E	2551[B]	CB3	CP1-N10-C9	-5.08	112.27	117.10
3	1-E	2551[A]	CB3	CP1-N10-C9	-5.08	112.27	117.10
3	4-E	2551[D]	CB3	CP1-N10-C9	-5.08	112.27	117.10
3	3-E	2551[C]	CB3	CP1-N10-C9	-5.08	112.27	117.10
2	2-G	650[B]	UMP	C5-C6-N1	-4.73	110.11	120.68
2	1-G	650[A]	UMP	C5-C6-N1	-4.73	110.11	120.68
2	3-G	650[C]	UMP	C5-C6-N1	-4.73	110.11	120.68
2	4-G	650[D]	UMP	C5-C6-N1	-4.73	110.11	120.68
3	1-F	2601[A]	CB3	CA-N-C	-4.73	116.24	122.34
3	3-F	2601[C]	CB3	CA-N-C	-4.73	116.24	122.34
3	4-F	2601[D]	CB3	CA-N-C	-4.73	116.24	122.34
3	2-F	2601[B]	CB3	CA-N-C	-4.73	116.24	122.34
3	2-C	2451[B]	CB3	C9-N10-C14	4.55	128.60	120.78
3	3-C	2451[C]	CB3	C9-N10-C14	4.55	128.60	120.78
3	1-C	2451[A]	CB3	C9-N10-C14	4.55	128.60	120.78
3	4-C	2451[D]	CB3	C9-N10-C14	4.55	128.60	120.78
3	2-E	2551[B]	CB3	C9-N10-C14	4.45	128.43	120.78
3	1-E	2551[A]	CB3	C9-N10-C14	4.45	128.43	120.78
3	4-E	2551[D]	CB3	C9-N10-C14	4.45	128.43	120.78
3	3-E	2551[C]	CB3	C9-N10-C14	4.45	128.43	120.78
2	3-D	500[C]	UMP	C5-C6-N1	-4.42	110.81	120.68
2	2-D	500[B]	UMP	C5-C6-N1	-4.42	110.81	120.68
2	4-D	500[D]	UMP	C5-C6-N1	-4.42	110.81	120.68
2	1-D	500[A]	UMP	C5-C6-N1	-4.42	110.81	120.68
2	2-G	650[B]	UMP	O5'-C5'-C4'	-4.40	93.85	108.99
2	1-G	650[A]	UMP	O5'-C5'-C4'	-4.40	93.85	108.99
2	3-G	650[C]	UMP	O5'-C5'-C4'	-4.40	93.85	108.99
2	4-G	650[D]	UMP	O5'-C5'-C4'	-4.40	93.85	108.99
2	4-E	550[D]	UMP	C5-C6-N1	-4.28	111.12	120.68
2	2-E	550[B]	UMP	C5-C6-N1	-4.28	111.12	120.68
2	1-E	550[A]	UMP	C5-C6-N1	-4.28	111.12	120.68
2	3-E	550[C]	UMP	C5-C6-N1	-4.28	111.12	120.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-C	2451[B]	CB3	C4-N3-C2	4.27	122.71	115.93
3	3-C	2451[C]	CB3	C4-N3-C2	4.27	122.71	115.93
3	1-C	2451[A]	CB3	C4-N3-C2	4.27	122.71	115.93
3	4-C	2451[D]	CB3	C4-N3-C2	4.27	122.71	115.93
3	2-B	2401[B]	CB3	C12-C13-C14	4.26	125.94	120.32
3	3-B	2401[C]	CB3	C12-C13-C14	4.26	125.94	120.32
3	1-B	2401[A]	CB3	C12-C13-C14	4.26	125.94	120.32
3	4-B	2401[D]	CB3	C12-C13-C14	4.26	125.94	120.32
2	3-H	700[C]	UMP	C5-C6-N1	-4.19	111.33	120.68
2	4-H	700[D]	UMP	C5-C6-N1	-4.19	111.33	120.68
2	1-H	700[A]	UMP	C5-C6-N1	-4.19	111.33	120.68
2	2-H	700[B]	UMP	C5-C6-N1	-4.19	111.33	120.68
3	2-B	2401[B]	CB3	CB-CA-N	-4.08	104.25	110.19
3	3-B	2401[C]	CB3	CB-CA-N	-4.08	104.25	110.19
3	1-B	2401[A]	CB3	CB-CA-N	-4.08	104.25	110.19
3	4-B	2401[D]	CB3	CB-CA-N	-4.08	104.25	110.19
3	4-H	2701[D]	CB3	NA2-C2-N1	4.07	124.42	117.79
3	3-H	2701[C]	CB3	NA2-C2-N1	4.07	124.42	117.79
3	2-H	2701[B]	CB3	NA2-C2-N1	4.07	124.42	117.79
3	1-H	2701[A]	CB3	NA2-C2-N1	4.07	124.42	117.79
3	2-B	2401[B]	CB3	C6-C9-N10	4.06	120.71	114.18
3	3-B	2401[C]	CB3	C6-C9-N10	4.06	120.71	114.18
3	1-B	2401[A]	CB3	C6-C9-N10	4.06	120.71	114.18
3	4-B	2401[D]	CB3	C6-C9-N10	4.06	120.71	114.18
2	4-E	550[D]	UMP	O5'-C5'-C4'	-3.93	95.47	108.99
2	2-E	550[B]	UMP	O5'-C5'-C4'	-3.93	95.47	108.99
2	1-E	550[A]	UMP	O5'-C5'-C4'	-3.93	95.47	108.99
2	3-E	550[C]	UMP	O5'-C5'-C4'	-3.93	95.47	108.99
3	1-F	2601[A]	CB3	C4-N3-C2	3.89	122.11	115.93
3	3-F	2601[C]	CB3	C4-N3-C2	3.89	122.11	115.93
3	4-F	2601[D]	CB3	C4-N3-C2	3.89	122.11	115.93
3	2-F	2601[B]	CB3	C4-N3-C2	3.89	122.11	115.93
3	1-A	2351[A]	CB3	C4A-C4-N3	-3.82	121.74	124.40
3	2-A	2351[B]	CB3	C4A-C4-N3	-3.82	121.74	124.40
3	3-A	2351[C]	CB3	C4A-C4-N3	-3.82	121.74	124.40
3	4-A	2351[D]	CB3	C4A-C4-N3	-3.82	121.74	124.40
3	3-G	2651[C]	CB3	C4A-C4-N3	-3.81	121.75	124.40
3	4-G	2651[D]	CB3	C4A-C4-N3	-3.81	121.75	124.40
3	1-G	2651[A]	CB3	C4A-C4-N3	-3.81	121.75	124.40
3	2-G	2651[B]	CB3	C4A-C4-N3	-3.81	121.75	124.40
3	3-G	2651[C]	CB3	C13-C12-C11	-3.75	116.42	120.78
3	4-G	2651[D]	CB3	C13-C12-C11	-3.75	116.42	120.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-G	2651[A]	CB3	C13-C12-C11	-3.75	116.42	120.78
3	2-G	2651[B]	CB3	C13-C12-C11	-3.75	116.42	120.78
3	3-G	2651[C]	CB3	CP1-N10-C9	-3.67	113.61	117.10
3	4-G	2651[D]	CB3	CP1-N10-C9	-3.67	113.61	117.10
3	1-G	2651[A]	CB3	CP1-N10-C9	-3.67	113.61	117.10
3	2-G	2651[B]	CB3	CP1-N10-C9	-3.67	113.61	117.10
3	1-A	2351[A]	CB3	NA2-C2-N1	3.61	123.68	117.79
3	2-A	2351[B]	CB3	NA2-C2-N1	3.61	123.68	117.79
3	3-A	2351[C]	CB3	NA2-C2-N1	3.61	123.68	117.79
3	4-A	2351[D]	CB3	NA2-C2-N1	3.61	123.68	117.79
3	2-B	2401[B]	CB3	C4A-C4-N3	-3.56	121.92	124.40
3	3-B	2401[C]	CB3	C4A-C4-N3	-3.56	121.92	124.40
3	1-B	2401[A]	CB3	C4A-C4-N3	-3.56	121.92	124.40
3	4-B	2401[D]	CB3	C4A-C4-N3	-3.56	121.92	124.40
2	4-B	400[D]	UMP	C5-C6-N1	-3.48	112.91	120.68
2	1-B	400[A]	UMP	C5-C6-N1	-3.48	112.91	120.68
2	2-B	400[B]	UMP	C5-C6-N1	-3.48	112.91	120.68
2	3-B	400[C]	UMP	C5-C6-N1	-3.48	112.91	120.68
2	1-O	650[A]	UMP	C5-C6-N1	-3.42	113.04	120.68
2	2-O	650[B]	UMP	C5-C6-N1	-3.42	113.05	120.68
3	2-B	2401[B]	CB3	C4-N3-C2	3.41	121.35	115.93
3	3-B	2401[C]	CB3	C4-N3-C2	3.41	121.35	115.93
3	1-B	2401[A]	CB3	C4-N3-C2	3.41	121.35	115.93
3	4-B	2401[D]	CB3	C4-N3-C2	3.41	121.35	115.93
3	2-C	2451[B]	CB3	NA2-C2-N3	3.40	122.54	117.25
3	3-C	2451[C]	CB3	NA2-C2-N3	3.40	122.54	117.25
3	1-C	2451[A]	CB3	NA2-C2-N3	3.40	122.54	117.25
3	4-C	2451[D]	CB3	NA2-C2-N3	3.40	122.54	117.25
2	3-O	650[C]	UMP	C5-C6-N1	-3.31	113.30	120.68
3	3-D	2501[C]	CB3	CP1-N10-C14	3.30	125.28	119.01
3	1-D	2501[A]	CB3	CP1-N10-C14	3.30	125.28	119.01
3	4-D	2501[D]	CB3	CP1-N10-C14	3.30	125.28	119.01
3	2-D	2501[B]	CB3	CP1-N10-C14	3.30	125.28	119.01
2	4-O	650[D]	UMP	C5-C6-N1	-3.29	113.34	120.68
3	1-F	2601[A]	CB3	C2-N1-C8A	3.28	124.45	116.33
3	3-F	2601[C]	CB3	C2-N1-C8A	3.28	124.45	116.33
3	4-F	2601[D]	CB3	C2-N1-C8A	3.28	124.45	116.33
3	2-F	2601[B]	CB3	C2-N1-C8A	3.28	124.45	116.33
3	1-A	2351[A]	CB3	C8-C8A-N1	3.27	123.68	118.69
3	2-A	2351[B]	CB3	C8-C8A-N1	3.27	123.68	118.69
3	3-A	2351[C]	CB3	C8-C8A-N1	3.27	123.68	118.69
3	4-A	2351[D]	CB3	C8-C8A-N1	3.27	123.68	118.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-A	2351[A]	CB3	C4-N3-C2	3.26	121.11	115.93
3	2-A	2351[B]	CB3	C4-N3-C2	3.26	121.11	115.93
3	3-A	2351[C]	CB3	C4-N3-C2	3.26	121.11	115.93
3	4-A	2351[D]	CB3	C4-N3-C2	3.26	121.11	115.93
3	2-E	2551[B]	CB3	NA2-C2-N1	3.26	123.10	117.79
3	1-E	2551[A]	CB3	NA2-C2-N1	3.26	123.10	117.79
3	4-E	2551[D]	CB3	NA2-C2-N1	3.26	123.10	117.79
3	3-E	2551[C]	CB3	NA2-C2-N1	3.26	123.10	117.79
3	3-D	2501[C]	CB3	CA-N-C	-3.25	118.15	122.34
3	1-D	2501[A]	CB3	CA-N-C	-3.25	118.15	122.34
3	4-D	2501[D]	CB3	CA-N-C	-3.25	118.15	122.34
3	2-D	2501[B]	CB3	CA-N-C	-3.25	118.15	122.34
3	4-H	2701[D]	CB3	C7-C8-C8A	-3.23	116.77	120.84
3	3-H	2701[C]	CB3	C7-C8-C8A	-3.23	116.77	120.84
3	2-H	2701[B]	CB3	C7-C8-C8A	-3.23	116.77	120.84
3	1-H	2701[A]	CB3	C7-C8-C8A	-3.23	116.77	120.84
3	3-D	2501[C]	CB3	C13-C12-C11	-3.23	117.02	120.78
3	1-D	2501[A]	CB3	C13-C12-C11	-3.23	117.02	120.78
3	4-D	2501[D]	CB3	C13-C12-C11	-3.23	117.02	120.78
3	2-D	2501[B]	CB3	C13-C12-C11	-3.23	117.02	120.78
2	1-L	500[A]	UMP	C5-C6-N1	-3.21	113.51	120.68
3	4-H	2701[D]	CB3	C2-N1-C8A	3.21	124.28	116.33
3	3-H	2701[C]	CB3	C2-N1-C8A	3.21	124.28	116.33
3	2-H	2701[B]	CB3	C2-N1-C8A	3.21	124.28	116.33
3	1-H	2701[A]	CB3	C2-N1-C8A	3.21	124.28	116.33
3	3-G	2651[C]	CB3	C9-N10-C14	3.21	126.29	120.78
3	4-G	2651[D]	CB3	C9-N10-C14	3.21	126.29	120.78
3	1-G	2651[A]	CB3	C9-N10-C14	3.21	126.29	120.78
3	2-G	2651[B]	CB3	C9-N10-C14	3.21	126.29	120.78
3	3-G	2651[C]	CB3	C4-C4A-C8A	-3.20	115.80	118.59
3	4-G	2651[D]	CB3	C4-C4A-C8A	-3.20	115.80	118.59
3	1-G	2651[A]	CB3	C4-C4A-C8A	-3.20	115.80	118.59
3	2-G	2651[B]	CB3	C4-C4A-C8A	-3.20	115.80	118.59
3	3-G	2651[C]	CB3	C4-N3-C2	3.20	121.01	115.93
3	4-G	2651[D]	CB3	C4-N3-C2	3.20	121.01	115.93
3	1-G	2651[A]	CB3	C4-N3-C2	3.20	121.01	115.93
3	2-G	2651[B]	CB3	C4-N3-C2	3.20	121.01	115.93
3	2-B	2401[B]	CB3	C13-C12-C11	-3.18	117.08	120.78
3	3-B	2401[C]	CB3	C13-C12-C11	-3.18	117.08	120.78
3	1-B	2401[A]	CB3	C13-C12-C11	-3.18	117.08	120.78
3	4-B	2401[D]	CB3	C13-C12-C11	-3.18	117.08	120.78
2	4-C	450[D]	UMP	O4'-C4'-C3'	-3.17	98.27	105.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-C	450[B]	UMP	O4'-C4'-C3'	-3.17	98.27	105.67
2	1-C	450[A]	UMP	O4'-C4'-C3'	-3.17	98.27	105.67
2	3-C	450[C]	UMP	O4'-C4'-C3'	-3.17	98.27	105.67
3	2-B	2401[B]	CB3	CA-N-C	-3.16	118.27	122.34
3	3-B	2401[C]	CB3	CA-N-C	-3.16	118.27	122.34
3	1-B	2401[A]	CB3	CA-N-C	-3.16	118.27	122.34
3	4-B	2401[D]	CB3	CA-N-C	-3.16	118.27	122.34
3	1-F	2601[A]	CB3	C7-C8-C8A	-3.15	116.87	120.84
3	3-F	2601[C]	CB3	C7-C8-C8A	-3.15	116.87	120.84
3	4-F	2601[D]	CB3	C7-C8-C8A	-3.15	116.87	120.84
3	2-F	2601[B]	CB3	C7-C8-C8A	-3.15	116.87	120.84
2	3-M	550[C]	UMP	C5-C6-N1	-3.12	113.71	120.68
2	4-L	500[D]	UMP	C5-C6-N1	-3.10	113.76	120.68
2	1-M	550[A]	UMP	C5-C6-N1	-3.09	113.78	120.68
2	2-M	550[B]	UMP	C5-C6-N1	-3.09	113.79	120.68
2	3-L	500[C]	UMP	C5-C6-N1	-3.08	113.81	120.68
3	3-G	2651[C]	CB3	C16-C11-C12	3.06	122.95	118.59
3	4-G	2651[D]	CB3	C16-C11-C12	3.06	122.95	118.59
3	1-G	2651[A]	CB3	C16-C11-C12	3.06	122.95	118.59
3	2-G	2651[B]	CB3	C16-C11-C12	3.06	122.95	118.59
2	4-L	500[D]	UMP	O4'-C4'-C3'	-3.06	98.54	105.67
2	2-L	500[B]	UMP	C5-C6-N1	-3.05	113.86	120.68
2	4-M	550[D]	UMP	O4'-C4'-C3'	-3.04	98.58	105.67
2	3-N	600[C]	UMP	C5-C6-N1	-3.04	113.91	120.68
2	3-L	500[C]	UMP	O4'-C4'-C3'	-3.03	98.60	105.67
2	1-M	550[A]	UMP	O4'-C4'-C3'	-3.02	98.62	105.67
2	4-M	550[D]	UMP	C5-C6-N1	-3.02	113.94	120.68
2	3-M	550[C]	UMP	O4'-C4'-C3'	-3.02	98.63	105.67
2	2-M	550[B]	UMP	O4'-C4'-C3'	-3.01	98.64	105.67
2	2-K	450[B]	UMP	O4'-C4'-C3'	-3.01	98.64	105.67
3	2-E	2551[B]	CB3	C12-C13-C14	3.00	124.27	120.32
3	1-E	2551[A]	CB3	C12-C13-C14	3.00	124.27	120.32
3	4-E	2551[D]	CB3	C12-C13-C14	3.00	124.27	120.32
3	3-E	2551[C]	CB3	C12-C13-C14	3.00	124.27	120.32
3	3-G	2651[C]	CB3	CA-N-C	-3.00	118.47	122.34
3	4-G	2651[D]	CB3	CA-N-C	-3.00	118.47	122.34
3	1-G	2651[A]	CB3	CA-N-C	-3.00	118.47	122.34
3	2-G	2651[B]	CB3	CA-N-C	-3.00	118.47	122.34
2	2-L	500[B]	UMP	O4'-C4'-C3'	-2.99	98.70	105.67
3	1-A	2351[A]	CB3	C2-N1-C8A	2.98	123.71	116.33
3	2-A	2351[B]	CB3	C2-N1-C8A	2.98	123.71	116.33
3	3-A	2351[C]	CB3	C2-N1-C8A	2.98	123.71	116.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-A	2351[D]	CB3	C2-N1-C8A	2.98	123.71	116.33
2	1-I	350[A]	UMP	O4'-C4'-C3'	-2.98	98.71	105.67
2	1-L	500[A]	UMP	O4'-C4'-C3'	-2.98	98.72	105.67
2	1-K	450[A]	UMP	O4'-C4'-C3'	-2.97	98.74	105.67
2	4-C	450[D]	UMP	O4'-C1'-C2'	-2.97	100.64	106.25
2	2-C	450[B]	UMP	O4'-C1'-C2'	-2.97	100.64	106.25
2	1-C	450[A]	UMP	O4'-C1'-C2'	-2.97	100.64	106.25
2	3-C	450[C]	UMP	O4'-C1'-C2'	-2.97	100.64	106.25
2	4-K	450[D]	UMP	O4'-C4'-C3'	-2.96	98.76	105.67
2	1-N	600[A]	UMP	C5-C6-N1	-2.96	114.08	120.68
2	3-K	450[C]	UMP	O4'-C4'-C3'	-2.96	98.77	105.67
2	4-B	400[D]	UMP	C5-C4-N3	-2.96	116.80	123.31
2	1-B	400[A]	UMP	C5-C4-N3	-2.96	116.80	123.31
2	2-B	400[B]	UMP	C5-C4-N3	-2.96	116.80	123.31
2	3-B	400[C]	UMP	C5-C4-N3	-2.96	116.80	123.31
2	4-N	600[D]	UMP	C5-C6-N1	-2.95	114.09	120.68
2	3-J	400[C]	UMP	O4'-C4'-C3'	-2.95	98.78	105.67
2	3-I	350[C]	UMP	O4'-C4'-C3'	-2.95	98.78	105.67
3	2-B	2401[B]	CB3	C2-N1-C8A	2.94	123.60	116.33
3	3-B	2401[C]	CB3	C2-N1-C8A	2.94	123.60	116.33
3	1-B	2401[A]	CB3	C2-N1-C8A	2.94	123.60	116.33
3	4-B	2401[D]	CB3	C2-N1-C8A	2.94	123.60	116.33
3	1-F	2601[A]	CB3	C16-C11-C12	2.93	122.75	118.59
3	3-F	2601[C]	CB3	C16-C11-C12	2.93	122.75	118.59
3	4-F	2601[D]	CB3	C16-C11-C12	2.93	122.75	118.59
3	2-F	2601[B]	CB3	C16-C11-C12	2.93	122.75	118.59
3	1-F	2601[A]	CB3	NA2-C2-N1	2.93	122.56	117.79
3	3-F	2601[C]	CB3	NA2-C2-N1	2.93	122.56	117.79
3	4-F	2601[D]	CB3	NA2-C2-N1	2.93	122.56	117.79
3	2-F	2601[B]	CB3	NA2-C2-N1	2.93	122.56	117.79
2	1-J	400[A]	UMP	O4'-C4'-C3'	-2.92	98.85	105.67
2	3-P	700[C]	UMP	O4'-C4'-C3'	-2.92	98.86	105.67
2	2-F	600[B]	UMP	C4'-O4'-C1'	2.92	116.50	109.45
2	3-F	600[C]	UMP	C4'-O4'-C1'	2.92	116.50	109.45
2	1-F	600[A]	UMP	C4'-O4'-C1'	2.92	116.50	109.45
2	4-F	600[D]	UMP	C4'-O4'-C1'	2.92	116.50	109.45
2	4-I	350[D]	UMP	O4'-C4'-C3'	-2.92	98.86	105.67
2	2-N	600[B]	UMP	C5-C6-N1	-2.91	114.17	120.68
3	3-D	2501[C]	CB3	C12-C13-C14	2.91	124.16	120.32
3	1-D	2501[A]	CB3	C12-C13-C14	2.91	124.16	120.32
3	4-D	2501[D]	CB3	C12-C13-C14	2.91	124.16	120.32
3	2-D	2501[B]	CB3	C12-C13-C14	2.91	124.16	120.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-H	2701[D]	CB3	C13-C12-C11	-2.91	117.39	120.78
3	3-H	2701[C]	CB3	C13-C12-C11	-2.91	117.39	120.78
3	2-H	2701[B]	CB3	C13-C12-C11	-2.91	117.39	120.78
3	1-H	2701[A]	CB3	C13-C12-C11	-2.91	117.39	120.78
2	1-P	700[A]	UMP	C5-C6-N1	-2.90	114.21	120.68
2	4-P	700[D]	UMP	O4'-C4'-C3'	-2.90	98.91	105.67
2	1-P	700[A]	UMP	O4'-C4'-C3'	-2.89	98.93	105.67
2	2-J	400[B]	UMP	O4'-C4'-C3'	-2.89	98.94	105.67
2	4-K	450[D]	UMP	C5-C6-N1	-2.89	114.24	120.68
2	2-I	350[B]	UMP	O4'-C4'-C3'	-2.88	98.94	105.67
2	1-N	600[A]	UMP	O4'-C4'-C3'	-2.87	98.97	105.67
2	1-O	650[A]	UMP	O4'-C4'-C3'	-2.87	98.97	105.67
3	2-E	2551[B]	CB3	C8-C8A-N1	2.87	123.06	118.69
3	1-E	2551[A]	CB3	C8-C8A-N1	2.87	123.06	118.69
3	4-E	2551[D]	CB3	C8-C8A-N1	2.87	123.06	118.69
3	3-E	2551[C]	CB3	C8-C8A-N1	2.87	123.06	118.69
2	2-N	600[B]	UMP	O4'-C4'-C3'	-2.85	99.01	105.67
2	3-N	600[C]	UMP	O4'-C4'-C3'	-2.85	99.02	105.67
2	4-E	550[D]	UMP	O4'-C4'-C3'	-2.85	99.02	105.67
2	2-E	550[B]	UMP	O4'-C4'-C3'	-2.85	99.02	105.67
2	1-E	550[A]	UMP	O4'-C4'-C3'	-2.85	99.02	105.67
2	3-E	550[C]	UMP	O4'-C4'-C3'	-2.85	99.02	105.67
2	2-F	600[B]	UMP	O4'-C4'-C3'	-2.85	99.03	105.67
2	3-F	600[C]	UMP	O4'-C4'-C3'	-2.85	99.03	105.67
2	1-F	600[A]	UMP	O4'-C4'-C3'	-2.85	99.03	105.67
2	4-F	600[D]	UMP	O4'-C4'-C3'	-2.85	99.03	105.67
2	4-J	400[D]	UMP	O4'-C4'-C3'	-2.84	99.04	105.67
2	2-P	700[B]	UMP	O4'-C4'-C3'	-2.84	99.05	105.67
2	2-F	600[B]	UMP	C5-C6-N1	-2.84	114.35	120.68
2	3-F	600[C]	UMP	C5-C6-N1	-2.84	114.35	120.68
2	1-F	600[A]	UMP	C5-C6-N1	-2.84	114.35	120.68
2	4-F	600[D]	UMP	C5-C6-N1	-2.84	114.35	120.68
2	4-N	600[D]	UMP	O4'-C4'-C3'	-2.83	99.06	105.67
2	1-K	450[A]	UMP	C5-C6-N1	-2.83	114.37	120.68
2	3-K	450[C]	UMP	C5-C6-N1	-2.83	114.37	120.68
2	2-K	450[B]	UMP	C5-C6-N1	-2.83	114.37	120.68
3	2-B	2401[B]	CB3	C4-C4A-C8A	-2.81	116.14	118.59
3	3-B	2401[C]	CB3	C4-C4A-C8A	-2.81	116.14	118.59
3	1-B	2401[A]	CB3	C4-C4A-C8A	-2.81	116.14	118.59
3	4-B	2401[D]	CB3	C4-C4A-C8A	-2.81	116.14	118.59
2	2-O	650[B]	UMP	O4'-C4'-C3'	-2.80	99.13	105.67
2	4-P	700[D]	UMP	C5-C6-N1	-2.80	114.43	120.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-P	700[B]	UMP	C5-C6-N1	-2.77	114.50	120.68
3	3-D	2501[C]	CB3	C4-C4A-C8A	-2.76	116.19	118.59
3	1-D	2501[A]	CB3	C4-C4A-C8A	-2.76	116.19	118.59
3	4-D	2501[D]	CB3	C4-C4A-C8A	-2.76	116.19	118.59
3	2-D	2501[B]	CB3	C4-C4A-C8A	-2.76	116.19	118.59
2	3-P	700[C]	UMP	C5-C6-N1	-2.75	114.53	120.68
3	4-H	2701[D]	CB3	C4-C4A-C8A	-2.75	116.19	118.59
3	3-H	2701[C]	CB3	C4-C4A-C8A	-2.75	116.19	118.59
3	2-H	2701[B]	CB3	C4-C4A-C8A	-2.75	116.19	118.59
3	1-H	2701[A]	CB3	C4-C4A-C8A	-2.75	116.19	118.59
2	1-I	350[A]	UMP	C5-C6-N1	-2.75	114.55	120.68
3	1-A	2351[A]	CB3	C9-N10-C14	2.74	125.48	120.78
3	2-A	2351[B]	CB3	C9-N10-C14	2.74	125.48	120.78
3	3-A	2351[C]	CB3	C9-N10-C14	2.74	125.48	120.78
3	4-A	2351[D]	CB3	C9-N10-C14	2.74	125.48	120.78
2	3-O	650[C]	UMP	O4'-C4'-C3'	-2.71	99.34	105.67
2	4-C	450[D]	UMP	C4'-O4'-C1'	2.71	115.99	109.45
2	2-C	450[B]	UMP	C4'-O4'-C1'	2.71	115.99	109.45
2	1-C	450[A]	UMP	C4'-O4'-C1'	2.71	115.99	109.45
2	3-C	450[C]	UMP	C4'-O4'-C1'	2.71	115.99	109.45
2	4-O	650[D]	UMP	O4'-C4'-C3'	-2.70	99.36	105.67
3	1-F	2601[A]	CB3	C13-C12-C11	-2.70	117.64	120.78
3	3-F	2601[C]	CB3	C13-C12-C11	-2.70	117.64	120.78
3	4-F	2601[D]	CB3	C13-C12-C11	-2.70	117.64	120.78
3	2-F	2601[B]	CB3	C13-C12-C11	-2.70	117.64	120.78
2	1-J	400[A]	UMP	C5-C6-N1	-2.69	114.68	120.68
2	4-I	350[D]	UMP	C5-C6-N1	-2.67	114.72	120.68
2	3-J	400[C]	UMP	C5-C6-N1	-2.66	114.75	120.68
3	2-C	2451[B]	CB3	C2-N1-C8A	2.65	122.89	116.33
3	3-C	2451[C]	CB3	C2-N1-C8A	2.65	122.89	116.33
3	1-C	2451[A]	CB3	C2-N1-C8A	2.65	122.89	116.33
3	4-C	2451[D]	CB3	C2-N1-C8A	2.65	122.89	116.33
2	2-J	400[B]	UMP	C5-C6-N1	-2.61	114.85	120.68
2	2-I	350[B]	UMP	C5-C6-N1	-2.58	114.92	120.68
2	3-I	350[C]	UMP	C5-C6-N1	-2.58	114.93	120.68
3	4-H	2701[D]	CB3	C12-C13-C14	2.56	123.70	120.32
3	3-H	2701[C]	CB3	C12-C13-C14	2.56	123.70	120.32
3	2-H	2701[B]	CB3	C12-C13-C14	2.56	123.70	120.32
3	1-H	2701[A]	CB3	C12-C13-C14	2.56	123.70	120.32
3	3-G	2651[C]	CB3	NA2-C2-N1	2.56	121.97	117.79
3	4-G	2651[D]	CB3	NA2-C2-N1	2.56	121.97	117.79
3	1-G	2651[A]	CB3	NA2-C2-N1	2.56	121.97	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-G	2651[B]	CB3	NA2-C2-N1	2.56	121.97	117.79
2	4-J	400[D]	UMP	C5-C6-N1	-2.55	114.99	120.68
2	2-G	650[B]	UMP	O4'-C4'-C3'	-2.54	99.76	105.67
2	1-G	650[A]	UMP	O4'-C4'-C3'	-2.54	99.76	105.67
2	3-G	650[C]	UMP	O4'-C4'-C3'	-2.54	99.76	105.67
2	4-G	650[D]	UMP	O4'-C4'-C3'	-2.54	99.76	105.67
3	2-C	2451[B]	CB3	CP1-CP2-CP3	-2.53	173.42	177.67
3	3-C	2451[C]	CB3	CP1-CP2-CP3	-2.53	173.42	177.67
3	1-C	2451[A]	CB3	CP1-CP2-CP3	-2.53	173.42	177.67
3	4-C	2451[D]	CB3	CP1-CP2-CP3	-2.53	173.42	177.67
3	3-D	2501[C]	CB3	NA2-C2-N1	2.49	121.85	117.79
3	1-D	2501[A]	CB3	NA2-C2-N1	2.49	121.85	117.79
3	4-D	2501[D]	CB3	NA2-C2-N1	2.49	121.85	117.79
3	2-D	2501[B]	CB3	NA2-C2-N1	2.49	121.85	117.79
3	3-G	2651[C]	CB3	C2-N1-C8A	2.48	122.46	116.33
3	4-G	2651[D]	CB3	C2-N1-C8A	2.48	122.46	116.33
3	1-G	2651[A]	CB3	C2-N1-C8A	2.48	122.46	116.33
3	2-G	2651[B]	CB3	C2-N1-C8A	2.48	122.46	116.33
2	2-G	650[B]	UMP	P-O5'-C5'	-2.48	111.47	118.30
2	1-G	650[A]	UMP	P-O5'-C5'	-2.48	111.47	118.30
2	3-G	650[C]	UMP	P-O5'-C5'	-2.48	111.47	118.30
2	4-G	650[D]	UMP	P-O5'-C5'	-2.48	111.47	118.30
3	1-F	2601[A]	CB3	C6-C9-N10	2.48	118.17	114.18
3	3-F	2601[C]	CB3	C6-C9-N10	2.48	118.17	114.18
3	4-F	2601[D]	CB3	C6-C9-N10	2.48	118.17	114.18
3	2-F	2601[B]	CB3	C6-C9-N10	2.48	118.17	114.18
3	1-F	2601[A]	CB3	C4-C4A-C8A	-2.47	116.44	118.59
3	3-F	2601[C]	CB3	C4-C4A-C8A	-2.47	116.44	118.59
3	4-F	2601[D]	CB3	C4-C4A-C8A	-2.47	116.44	118.59
3	2-F	2601[B]	CB3	C4-C4A-C8A	-2.47	116.44	118.59
2	3-H	700[C]	UMP	O5'-P-OP1	2.45	113.35	106.47
2	4-H	700[D]	UMP	O5'-P-OP1	2.45	113.35	106.47
2	1-H	700[A]	UMP	O5'-P-OP1	2.45	113.35	106.47
2	2-H	700[B]	UMP	O5'-P-OP1	2.45	113.35	106.47
3	2-B	2401[B]	CB3	NA2-C2-N1	2.44	121.77	117.79
3	3-B	2401[C]	CB3	NA2-C2-N1	2.44	121.77	117.79
3	1-B	2401[A]	CB3	NA2-C2-N1	2.44	121.77	117.79
3	4-B	2401[D]	CB3	NA2-C2-N1	2.44	121.77	117.79
2	4-E	550[D]	UMP	O4'-C1'-C2'	-2.43	101.65	106.25
2	2-E	550[B]	UMP	O4'-C1'-C2'	-2.43	101.65	106.25
2	1-E	550[A]	UMP	O4'-C1'-C2'	-2.43	101.65	106.25
2	3-E	550[C]	UMP	O4'-C1'-C2'	-2.43	101.65	106.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-E	2551[B]	CB3	C13-C12-C11	-2.43	117.95	120.78
3	1-E	2551[A]	CB3	C13-C12-C11	-2.43	117.95	120.78
3	4-E	2551[D]	CB3	C13-C12-C11	-2.43	117.95	120.78
3	3-E	2551[C]	CB3	C13-C12-C11	-2.43	117.95	120.78
3	3-D	2501[C]	CB3	C2-N1-C8A	2.43	122.34	116.33
3	1-D	2501[A]	CB3	C2-N1-C8A	2.43	122.34	116.33
3	4-D	2501[D]	CB3	C2-N1-C8A	2.43	122.34	116.33
3	2-D	2501[B]	CB3	C2-N1-C8A	2.43	122.34	116.33
2	3-H	700[C]	UMP	O5'-C5'-C4'	-2.42	100.66	108.99
2	4-H	700[D]	UMP	O5'-C5'-C4'	-2.42	100.66	108.99
2	1-H	700[A]	UMP	O5'-C5'-C4'	-2.42	100.66	108.99
2	2-H	700[B]	UMP	O5'-C5'-C4'	-2.42	100.66	108.99
3	3-D	2501[C]	CB3	C4A-C4-N3	-2.40	122.73	124.40
3	1-D	2501[A]	CB3	C4A-C4-N3	-2.40	122.73	124.40
3	4-D	2501[D]	CB3	C4A-C4-N3	-2.40	122.73	124.40
3	2-D	2501[B]	CB3	C4A-C4-N3	-2.40	122.73	124.40
3	3-G	2651[C]	CB3	C6-C9-N10	2.40	118.04	114.18
3	4-G	2651[D]	CB3	C6-C9-N10	2.40	118.04	114.18
3	1-G	2651[A]	CB3	C6-C9-N10	2.40	118.04	114.18
3	2-G	2651[B]	CB3	C6-C9-N10	2.40	118.04	114.18
3	1-A	2351[A]	CB3	C6-C9-N10	2.38	118.01	114.18
3	2-A	2351[B]	CB3	C6-C9-N10	2.38	118.01	114.18
3	3-A	2351[C]	CB3	C6-C9-N10	2.38	118.01	114.18
3	4-A	2351[D]	CB3	C6-C9-N10	2.38	118.01	114.18
3	2-B	2401[B]	CB3	C15-C14-C13	-2.36	114.36	119.16
3	3-B	2401[C]	CB3	C15-C14-C13	-2.36	114.36	119.16
3	1-B	2401[A]	CB3	C15-C14-C13	-2.36	114.36	119.16
3	4-B	2401[D]	CB3	C15-C14-C13	-2.36	114.36	119.16
3	2-E	2551[B]	CB3	CP1-CP2-CP3	-2.34	173.74	177.67
3	1-E	2551[A]	CB3	CP1-CP2-CP3	-2.34	173.74	177.67
3	4-E	2551[D]	CB3	CP1-CP2-CP3	-2.34	173.74	177.67
3	3-E	2551[C]	CB3	CP1-CP2-CP3	-2.34	173.74	177.67
3	4-H	2701[D]	CB3	C9-N10-C14	2.34	124.80	120.78
3	3-H	2701[C]	CB3	C9-N10-C14	2.34	124.80	120.78
3	2-H	2701[B]	CB3	C9-N10-C14	2.34	124.80	120.78
3	1-H	2701[A]	CB3	C9-N10-C14	2.34	124.80	120.78
3	2-B	2401[B]	CB3	C12-C11-C	-2.34	113.06	120.62
3	3-B	2401[C]	CB3	C12-C11-C	-2.34	113.06	120.62
3	1-B	2401[A]	CB3	C12-C11-C	-2.34	113.06	120.62
3	4-B	2401[D]	CB3	C12-C11-C	-2.34	113.06	120.62
2	4-E	550[D]	UMP	C4'-O4'-C1'	2.33	115.08	109.45
2	2-E	550[B]	UMP	C4'-O4'-C1'	2.33	115.08	109.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1-E	550[A]	UMP	C4'-O4'-C1'	2.33	115.08	109.45
2	3-E	550[C]	UMP	C4'-O4'-C1'	2.33	115.08	109.45
2	2-F	600[B]	UMP	O5'-C5'-C4'	-2.32	101.01	108.99
2	3-F	600[C]	UMP	O5'-C5'-C4'	-2.32	101.01	108.99
2	1-F	600[A]	UMP	O5'-C5'-C4'	-2.32	101.01	108.99
2	4-F	600[D]	UMP	O5'-C5'-C4'	-2.32	101.01	108.99
3	2-C	2451[B]	CB3	C13-C14-N10	-2.29	118.22	121.38
3	3-C	2451[C]	CB3	C13-C14-N10	-2.29	118.22	121.38
3	1-C	2451[A]	CB3	C13-C14-N10	-2.29	118.22	121.38
3	4-C	2451[D]	CB3	C13-C14-N10	-2.29	118.22	121.38
3	3-G	2651[C]	CB3	C12-C13-C14	2.29	123.33	120.32
3	4-G	2651[D]	CB3	C12-C13-C14	2.29	123.33	120.32
3	1-G	2651[A]	CB3	C12-C13-C14	2.29	123.33	120.32
3	2-G	2651[B]	CB3	C12-C13-C14	2.29	123.33	120.32
3	3-D	2501[C]	CB3	C16-C11-C12	2.27	121.83	118.59
3	1-D	2501[A]	CB3	C16-C11-C12	2.27	121.83	118.59
3	4-D	2501[D]	CB3	C16-C11-C12	2.27	121.83	118.59
3	2-D	2501[B]	CB3	C16-C11-C12	2.27	121.83	118.59
3	2-B	2401[B]	CB3	C15-C14-N10	2.27	124.50	121.38
3	3-B	2401[C]	CB3	C15-C14-N10	2.27	124.50	121.38
3	1-B	2401[A]	CB3	C15-C14-N10	2.27	124.50	121.38
3	4-B	2401[D]	CB3	C15-C14-N10	2.27	124.50	121.38
2	3-H	700[C]	UMP	O4'-C4'-C3'	-2.26	100.39	105.67
2	4-H	700[D]	UMP	O4'-C4'-C3'	-2.26	100.39	105.67
2	1-H	700[A]	UMP	O4'-C4'-C3'	-2.26	100.39	105.67
2	2-H	700[B]	UMP	O4'-C4'-C3'	-2.26	100.39	105.67
3	3-D	2501[C]	CB3	C9-N10-C14	2.25	124.65	120.78
3	1-D	2501[A]	CB3	C9-N10-C14	2.25	124.65	120.78
3	4-D	2501[D]	CB3	C9-N10-C14	2.25	124.65	120.78
3	2-D	2501[B]	CB3	C9-N10-C14	2.25	124.65	120.78
3	2-B	2401[B]	CB3	C16-C11-C12	2.25	121.79	118.59
3	3-B	2401[C]	CB3	C16-C11-C12	2.25	121.79	118.59
3	1-B	2401[A]	CB3	C16-C11-C12	2.25	121.79	118.59
3	4-B	2401[D]	CB3	C16-C11-C12	2.25	121.79	118.59
3	1-F	2601[A]	CB3	NA2-C2-N3	2.25	120.74	117.25
3	3-F	2601[C]	CB3	NA2-C2-N3	2.25	120.74	117.25
3	4-F	2601[D]	CB3	NA2-C2-N3	2.25	120.74	117.25
3	2-F	2601[B]	CB3	NA2-C2-N3	2.25	120.74	117.25
3	3-D	2501[C]	CB3	C4-N3-C2	2.24	119.49	115.93
3	1-D	2501[A]	CB3	C4-N3-C2	2.24	119.49	115.93
3	4-D	2501[D]	CB3	C4-N3-C2	2.24	119.49	115.93
3	2-D	2501[B]	CB3	C4-N3-C2	2.24	119.49	115.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-H	2701[D]	CB3	C6-C9-N10	2.24	117.79	114.18
3	3-H	2701[C]	CB3	C6-C9-N10	2.24	117.79	114.18
3	2-H	2701[B]	CB3	C6-C9-N10	2.24	117.79	114.18
3	1-H	2701[A]	CB3	C6-C9-N10	2.24	117.79	114.18
3	4-H	2701[D]	CB3	CP1-N10-C14	2.22	123.23	119.01
3	3-H	2701[C]	CB3	CP1-N10-C14	2.22	123.23	119.01
3	2-H	2701[B]	CB3	CP1-N10-C14	2.22	123.23	119.01
3	1-H	2701[A]	CB3	CP1-N10-C14	2.22	123.23	119.01
3	3-G	2651[C]	CB3	C9-C6-C7	-2.21	116.61	120.77
3	4-G	2651[D]	CB3	C9-C6-C7	-2.21	116.61	120.77
3	1-G	2651[A]	CB3	C9-C6-C7	-2.21	116.61	120.77
3	2-G	2651[B]	CB3	C9-C6-C7	-2.21	116.61	120.77
2	4-B	400[D]	UMP	O4'-C1'-C2'	-2.17	102.16	106.25
2	1-B	400[A]	UMP	O4'-C1'-C2'	-2.17	102.16	106.25
2	2-B	400[B]	UMP	O4'-C1'-C2'	-2.17	102.16	106.25
2	3-B	400[C]	UMP	O4'-C1'-C2'	-2.17	102.16	106.25
3	3-D	2501[C]	CB3	C9-C6-C7	-2.16	116.70	120.77
3	1-D	2501[A]	CB3	C9-C6-C7	-2.16	116.70	120.77
3	4-D	2501[D]	CB3	C9-C6-C7	-2.16	116.70	120.77
3	2-D	2501[B]	CB3	C9-C6-C7	-2.16	116.70	120.77
2	1-J	400[A]	UMP	C6-N1-C2	2.14	124.59	121.20
2	3-D	500[C]	UMP	O4'-C4'-C3'	-2.13	100.71	105.67
2	2-D	500[B]	UMP	O4'-C4'-C3'	-2.13	100.71	105.67
2	4-D	500[D]	UMP	O4'-C4'-C3'	-2.13	100.71	105.67
2	1-D	500[A]	UMP	O4'-C4'-C3'	-2.13	100.71	105.67
3	2-E	2551[B]	CB3	C2-N1-C8A	2.12	121.56	116.33
3	1-E	2551[A]	CB3	C2-N1-C8A	2.12	121.56	116.33
3	4-E	2551[D]	CB3	C2-N1-C8A	2.12	121.56	116.33
3	3-E	2551[C]	CB3	C2-N1-C8A	2.12	121.56	116.33
3	4-H	2701[D]	CB3	C16-C11-C12	2.11	121.60	118.59
3	3-H	2701[C]	CB3	C16-C11-C12	2.11	121.60	118.59
3	2-H	2701[B]	CB3	C16-C11-C12	2.11	121.60	118.59
3	1-H	2701[A]	CB3	C16-C11-C12	2.11	121.60	118.59
3	1-F	2601[A]	CB3	C12-C11-C	-2.11	113.78	120.62
3	3-F	2601[C]	CB3	C12-C11-C	-2.11	113.78	120.62
3	4-F	2601[D]	CB3	C12-C11-C	-2.11	113.78	120.62
3	2-F	2601[B]	CB3	C12-C11-C	-2.11	113.78	120.62
3	4-H	2701[D]	CB3	C6-C5-C4A	-2.10	119.50	122.65
3	3-H	2701[C]	CB3	C6-C5-C4A	-2.10	119.50	122.65
3	2-H	2701[B]	CB3	C6-C5-C4A	-2.10	119.50	122.65
3	1-H	2701[A]	CB3	C6-C5-C4A	-2.10	119.50	122.65
3	1-A	2351[A]	CB3	C13-C12-C11	-2.07	118.37	120.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-A	2351[B]	CB3	C13-C12-C11	-2.07	118.37	120.78
3	3-A	2351[C]	CB3	C13-C12-C11	-2.07	118.37	120.78
3	4-A	2351[D]	CB3	C13-C12-C11	-2.07	118.37	120.78
3	2-B	2401[B]	CB3	C8-C8A-N1	2.07	121.84	118.69
3	3-B	2401[C]	CB3	C8-C8A-N1	2.07	121.84	118.69
3	1-B	2401[A]	CB3	C8-C8A-N1	2.07	121.84	118.69
3	4-B	2401[D]	CB3	C8-C8A-N1	2.07	121.84	118.69
2	2-K	450[B]	UMP	O4'-C1'-C2'	-2.06	102.35	106.25
3	3-D	2501[C]	CB3	C8-C8A-N1	2.06	121.84	118.69
3	1-D	2501[A]	CB3	C8-C8A-N1	2.06	121.84	118.69
3	4-D	2501[D]	CB3	C8-C8A-N1	2.06	121.84	118.69
3	2-D	2501[B]	CB3	C8-C8A-N1	2.06	121.84	118.69
2	1-K	450[A]	UMP	O4'-C1'-C2'	-2.06	102.36	106.25
3	2-B	2401[B]	CB3	CP1-CP2-CP3	-2.06	174.22	177.67
3	3-B	2401[C]	CB3	CP1-CP2-CP3	-2.06	174.22	177.67
3	1-B	2401[A]	CB3	CP1-CP2-CP3	-2.06	174.22	177.67
3	4-B	2401[D]	CB3	CP1-CP2-CP3	-2.06	174.22	177.67
3	1-F	2601[A]	CB3	C9-N10-C14	2.05	124.30	120.78
3	3-F	2601[C]	CB3	C9-N10-C14	2.05	124.30	120.78
3	4-F	2601[D]	CB3	C9-N10-C14	2.05	124.30	120.78
3	2-F	2601[B]	CB3	C9-N10-C14	2.05	124.30	120.78
2	4-K	450[D]	UMP	O4'-C1'-C2'	-2.04	102.39	106.25
2	1-P	700[A]	UMP	C6-N1-C2	2.04	124.43	121.20
2	4-C	450[D]	UMP	O3'-C3'-C4'	-2.02	102.39	110.10
2	2-C	450[B]	UMP	O3'-C3'-C4'	-2.02	102.39	110.10
2	1-C	450[A]	UMP	O3'-C3'-C4'	-2.02	102.39	110.10
2	3-C	450[C]	UMP	O3'-C3'-C4'	-2.02	102.39	110.10
2	2-P	700[B]	UMP	C6-N1-C2	2.01	124.39	121.20
2	2-F	600[B]	UMP	OP2-P-O5'	2.01	112.07	106.73
2	3-F	600[C]	UMP	OP2-P-O5'	2.01	112.07	106.73
2	1-F	600[A]	UMP	OP2-P-O5'	2.01	112.07	106.73
2	4-F	600[D]	UMP	OP2-P-O5'	2.01	112.07	106.73
2	4-I	350[D]	UMP	C6-N1-C2	2.01	124.38	121.20

There are no chirality outliers.

All (208) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	3-P	700[C]	UMP	C5'-O5'-P-OP1
2	4-J	400[D]	UMP	C5'-O5'-P-OP1
2	4-J	400[D]	UMP	C5'-O5'-P-OP3
2	3-K	450[C]	UMP	C5'-O5'-P-OP1

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Mol	Chain	Res	Type	Atoms
2	3-K	450[C]	UMP	C5'-O5'-P-OP3
2	4-O	650[D]	UMP	C5'-O5'-P-OP1
2	4-O	650[D]	UMP	C5'-O5'-P-OP3
2	2-L	500[B]	UMP	C5'-O5'-P-OP1
2	2-L	500[B]	UMP	C5'-O5'-P-OP3
2	1-M	550[A]	UMP	C5'-O5'-P-OP1
2	4-K	450[D]	UMP	C5'-O5'-P-OP1
2	4-K	450[D]	UMP	C5'-O5'-P-OP3
2	1-L	500[A]	UMP	C5'-O5'-P-OP1
2	1-L	500[A]	UMP	C5'-O5'-P-OP3
2	4-P	700[D]	UMP	C5'-O5'-P-OP1
2	1-J	400[A]	UMP	C5'-O5'-P-OP1
2	1-P	700[A]	UMP	C5'-O5'-P-OP1
2	2-M	550[B]	UMP	C5'-O5'-P-OP1
2	1-K	450[A]	UMP	C5'-O5'-P-OP1
2	1-K	450[A]	UMP	C5'-O5'-P-OP3
2	3-O	650[C]	UMP	C5'-O5'-P-OP1
2	3-O	650[C]	UMP	C5'-O5'-P-OP3
2	2-K	450[B]	UMP	C5'-O5'-P-OP1
2	2-K	450[B]	UMP	C5'-O5'-P-OP3
2	3-M	550[C]	UMP	C5'-O5'-P-OP1
2	4-L	500[D]	UMP	C5'-O5'-P-OP1
2	4-L	500[D]	UMP	C5'-O5'-P-OP3
2	3-L	500[C]	UMP	C5'-O5'-P-OP1
2	3-L	500[C]	UMP	C5'-O5'-P-OP3
2	3-J	400[C]	UMP	C5'-O5'-P-OP1
2	3-N	600[C]	UMP	C5'-O5'-P-OP1
2	1-O	650[A]	UMP	C5'-O5'-P-OP1
2	1-O	650[A]	UMP	C5'-O5'-P-OP3
2	2-O	650[B]	UMP	C5'-O5'-P-OP1
2	2-O	650[B]	UMP	C5'-O5'-P-OP3
3	2-E	2551[B]	CB3	CB-CA-N-C
3	2-E	2551[B]	CB3	CT-CA-N-C
2	1-N	600[A]	UMP	C5'-O5'-P-OP1
2	4-M	550[D]	UMP	C5'-O5'-P-OP1
3	1-E	2551[A]	CB3	CB-CA-N-C
3	1-E	2551[A]	CB3	CT-CA-N-C
2	2-J	400[B]	UMP	C5'-O5'-P-OP1
2	2-P	700[B]	UMP	C5'-O5'-P-OP1
2	2-N	600[B]	UMP	C5'-O5'-P-OP1
2	4-N	600[D]	UMP	C5'-O5'-P-OP1
3	4-E	2551[D]	CB3	CB-CA-N-C

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Mol	Chain	Res	Type	Atoms
3	4-E	2551[D]	CB3	CT-CA-N-C
3	3-E	2551[C]	CB3	CB-CA-N-C
3	3-E	2551[C]	CB3	CT-CA-N-C
3	1-F	2601[A]	CB3	N-CA-CB-CG
3	3-F	2601[C]	CB3	N-CA-CB-CG
3	4-F	2601[D]	CB3	N-CA-CB-CG
3	2-F	2601[B]	CB3	N-CA-CB-CG
3	2-C	2451[B]	CB3	CT-CA-N-C
3	3-C	2451[C]	CB3	CT-CA-N-C
3	1-C	2451[A]	CB3	CT-CA-N-C
3	4-C	2451[D]	CB3	CT-CA-N-C
2	2-G	650[B]	UMP	C3'-C4'-C5'-O5'
2	1-G	650[A]	UMP	C3'-C4'-C5'-O5'
2	3-G	650[C]	UMP	C3'-C4'-C5'-O5'
2	4-G	650[D]	UMP	C3'-C4'-C5'-O5'
2	4-C	450[D]	UMP	C3'-C4'-C5'-O5'
2	2-C	450[B]	UMP	C3'-C4'-C5'-O5'
2	1-C	450[A]	UMP	C3'-C4'-C5'-O5'
2	3-C	450[C]	UMP	C3'-C4'-C5'-O5'
2	3-D	500[C]	UMP	C3'-C4'-C5'-O5'
2	2-D	500[B]	UMP	C3'-C4'-C5'-O5'
2	4-D	500[D]	UMP	C3'-C4'-C5'-O5'
2	1-D	500[A]	UMP	C3'-C4'-C5'-O5'
2	3-P	700[C]	UMP	C5'-O5'-P-OP3
2	4-O	650[D]	UMP	C5'-O5'-P-OP2
2	4-P	700[D]	UMP	C5'-O5'-P-OP3
2	1-J	400[A]	UMP	C5'-O5'-P-OP3
2	1-P	700[A]	UMP	C5'-O5'-P-OP3
2	3-O	650[C]	UMP	C5'-O5'-P-OP2
2	3-J	400[C]	UMP	C5'-O5'-P-OP3
2	3-N	600[C]	UMP	C5'-O5'-P-OP3
2	1-O	650[A]	UMP	C5'-O5'-P-OP2
2	2-O	650[B]	UMP	C5'-O5'-P-OP2
2	1-N	600[A]	UMP	C5'-O5'-P-OP3
2	2-J	400[B]	UMP	C5'-O5'-P-OP3
2	2-P	700[B]	UMP	C5'-O5'-P-OP3
2	2-N	600[B]	UMP	C5'-O5'-P-OP3
2	4-N	600[D]	UMP	C5'-O5'-P-OP3
3	2-E	2551[B]	CB3	O-C-N-CA
3	1-E	2551[A]	CB3	O-C-N-CA
3	4-E	2551[D]	CB3	O-C-N-CA
3	3-E	2551[C]	CB3	O-C-N-CA

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Mol	Chain	Res	Type	Atoms
3	2-E	2551[B]	CB3	N-CA-CB-CG
3	1-E	2551[A]	CB3	N-CA-CB-CG
3	4-E	2551[D]	CB3	N-CA-CB-CG
3	3-E	2551[C]	CB3	N-CA-CB-CG
3	2-E	2551[B]	CB3	C11-C-N-CA
3	1-E	2551[A]	CB3	C11-C-N-CA
3	4-E	2551[D]	CB3	C11-C-N-CA
3	3-E	2551[C]	CB3	C11-C-N-CA
2	2-I	350[B]	UMP	C5'-O5'-P-OP1
2	1-I	350[A]	UMP	C5'-O5'-P-OP1
2	3-I	350[C]	UMP	C5'-O5'-P-OP1
2	4-I	350[D]	UMP	C5'-O5'-P-OP1
2	2-G	650[B]	UMP	O4'-C4'-C5'-O5'
2	1-G	650[A]	UMP	O4'-C4'-C5'-O5'
2	3-G	650[C]	UMP	O4'-C4'-C5'-O5'
2	4-G	650[D]	UMP	O4'-C4'-C5'-O5'
2	2-A	350[B]	UMP	C3'-C4'-C5'-O5'
2	3-D	500[C]	UMP	O4'-C4'-C5'-O5'
2	2-D	500[B]	UMP	O4'-C4'-C5'-O5'
2	4-A	350[D]	UMP	C3'-C4'-C5'-O5'
2	4-E	550[D]	UMP	C3'-C4'-C5'-O5'
2	4-D	500[D]	UMP	O4'-C4'-C5'-O5'
2	2-E	550[B]	UMP	C3'-C4'-C5'-O5'
2	1-E	550[A]	UMP	C3'-C4'-C5'-O5'
2	3-A	350[C]	UMP	C3'-C4'-C5'-O5'
2	3-E	550[C]	UMP	C3'-C4'-C5'-O5'
2	1-D	500[A]	UMP	O4'-C4'-C5'-O5'
2	1-A	350[A]	UMP	C3'-C4'-C5'-O5'
2	3-P	700[C]	UMP	C5'-O5'-P-OP2
2	4-J	400[D]	UMP	C5'-O5'-P-OP2
2	3-K	450[C]	UMP	C5'-O5'-P-OP2
2	2-L	500[B]	UMP	C5'-O5'-P-OP2
2	1-M	550[A]	UMP	C5'-O5'-P-OP3
2	4-K	450[D]	UMP	C5'-O5'-P-OP2
2	1-L	500[A]	UMP	C5'-O5'-P-OP2
2	4-P	700[D]	UMP	C5'-O5'-P-OP2
2	1-J	400[A]	UMP	C5'-O5'-P-OP2
2	1-P	700[A]	UMP	C5'-O5'-P-OP2
2	2-M	550[B]	UMP	C5'-O5'-P-OP3
2	1-K	450[A]	UMP	C5'-O5'-P-OP2
2	2-K	450[B]	UMP	C5'-O5'-P-OP2
2	3-M	550[C]	UMP	C5'-O5'-P-OP3

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Mol	Chain	Res	Type	Atoms
2	4-L	500[D]	UMP	C5'-O5'-P-OP2
2	3-L	500[C]	UMP	C5'-O5'-P-OP2
2	3-J	400[C]	UMP	C5'-O5'-P-OP2
2	4-M	550[D]	UMP	C5'-O5'-P-OP3
2	2-J	400[B]	UMP	C5'-O5'-P-OP2
2	2-P	700[B]	UMP	C5'-O5'-P-OP2
3	1-A	2351[A]	CB3	CT-CA-N-C
3	3-G	2651[C]	CB3	CT-CA-N-C
3	4-G	2651[D]	CB3	CT-CA-N-C
3	4-H	2701[D]	CB3	CT-CA-N-C
3	3-H	2701[C]	CB3	CT-CA-N-C
3	2-A	2351[B]	CB3	CT-CA-N-C
3	2-H	2701[B]	CB3	CT-CA-N-C
3	3-A	2351[C]	CB3	CT-CA-N-C
3	1-H	2701[A]	CB3	CT-CA-N-C
3	4-A	2351[D]	CB3	CT-CA-N-C
3	1-G	2651[A]	CB3	CT-CA-N-C
3	2-G	2651[B]	CB3	CT-CA-N-C
2	4-B	400[D]	UMP	O4'-C4'-C5'-O5'
2	1-B	400[A]	UMP	O4'-C4'-C5'-O5'
2	2-B	400[B]	UMP	O4'-C4'-C5'-O5'
2	3-B	400[C]	UMP	O4'-C4'-C5'-O5'
2	2-F	600[B]	UMP	O4'-C4'-C5'-O5'
2	3-P	700[C]	UMP	O4'-C4'-C5'-O5'
2	4-J	400[D]	UMP	O4'-C4'-C5'-O5'
2	4-C	450[D]	UMP	O4'-C4'-C5'-O5'
2	2-A	350[B]	UMP	O4'-C4'-C5'-O5'
2	3-K	450[C]	UMP	O4'-C4'-C5'-O5'
2	4-O	650[D]	UMP	O4'-C4'-C5'-O5'
2	2-L	500[B]	UMP	O4'-C4'-C5'-O5'
2	3-F	600[C]	UMP	O4'-C4'-C5'-O5'
2	1-M	550[A]	UMP	O4'-C4'-C5'-O5'
2	3-H	700[C]	UMP	O4'-C4'-C5'-O5'
2	4-A	350[D]	UMP	O4'-C4'-C5'-O5'
2	4-K	450[D]	UMP	O4'-C4'-C5'-O5'
2	1-L	500[A]	UMP	O4'-C4'-C5'-O5'
2	1-F	600[A]	UMP	O4'-C4'-C5'-O5'
2	4-P	700[D]	UMP	O4'-C4'-C5'-O5'
2	1-J	400[A]	UMP	O4'-C4'-C5'-O5'
2	1-P	700[A]	UMP	O4'-C4'-C5'-O5'
2	2-M	550[B]	UMP	O4'-C4'-C5'-O5'
2	1-K	450[A]	UMP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	3-A	350[C]	UMP	O4'-C4'-C5'-O5'
2	3-O	650[C]	UMP	O4'-C4'-C5'-O5'
2	2-K	450[B]	UMP	O4'-C4'-C5'-O5'
2	3-M	550[C]	UMP	O4'-C4'-C5'-O5'
2	4-L	500[D]	UMP	O4'-C4'-C5'-O5'
2	4-H	700[D]	UMP	O4'-C4'-C5'-O5'
2	3-L	500[C]	UMP	O4'-C4'-C5'-O5'
2	1-H	700[A]	UMP	O4'-C4'-C5'-O5'
2	3-J	400[C]	UMP	O4'-C4'-C5'-O5'
2	3-N	600[C]	UMP	O4'-C4'-C5'-O5'
2	4-F	600[D]	UMP	O4'-C4'-C5'-O5'
2	2-C	450[B]	UMP	O4'-C4'-C5'-O5'
2	1-O	650[A]	UMP	O4'-C4'-C5'-O5'
2	2-O	650[B]	UMP	O4'-C4'-C5'-O5'
2	1-N	600[A]	UMP	O4'-C4'-C5'-O5'
2	1-C	450[A]	UMP	O4'-C4'-C5'-O5'
2	4-M	550[D]	UMP	O4'-C4'-C5'-O5'
2	3-C	450[C]	UMP	O4'-C4'-C5'-O5'
2	2-H	700[B]	UMP	O4'-C4'-C5'-O5'
2	2-J	400[B]	UMP	O4'-C4'-C5'-O5'
2	2-P	700[B]	UMP	O4'-C4'-C5'-O5'
2	1-A	350[A]	UMP	O4'-C4'-C5'-O5'
2	2-N	600[B]	UMP	O4'-C4'-C5'-O5'
2	4-N	600[D]	UMP	O4'-C4'-C5'-O5'
2	4-E	550[D]	UMP	O4'-C4'-C5'-O5'
2	2-E	550[B]	UMP	O4'-C4'-C5'-O5'
2	1-E	550[A]	UMP	O4'-C4'-C5'-O5'
2	2-I	350[B]	UMP	O4'-C4'-C5'-O5'
2	1-I	350[A]	UMP	O4'-C4'-C5'-O5'
2	3-I	350[C]	UMP	O4'-C4'-C5'-O5'
2	3-E	550[C]	UMP	O4'-C4'-C5'-O5'
2	4-I	350[D]	UMP	O4'-C4'-C5'-O5'
3	3-D	2501[C]	CB3	CT-CA-N-C
3	1-D	2501[A]	CB3	CT-CA-N-C
3	4-D	2501[D]	CB3	CT-CA-N-C
3	2-D	2501[B]	CB3	CT-CA-N-C

There are no ring outliers.

56 monomers are involved in 56 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	4-O	650[D]	UMP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	1-A	2351[A]	CB3	1	0
3	2-B	2401[B]	CB3	1	0
2	3-P	700[C]	UMP	1	0
2	4-J	400[D]	UMP	1	0
2	3-K	450[C]	UMP	1	0
2	2-L	500[B]	UMP	1	0
2	1-M	550[A]	UMP	1	0
3	2-C	2451[B]	CB3	1	0
2	4-K	450[D]	UMP	1	0
2	1-L	500[A]	UMP	1	0
2	4-P	700[D]	UMP	1	0
2	1-J	400[A]	UMP	1	0
2	1-P	700[A]	UMP	1	0
3	3-H	2701[C]	CB3	1	0
3	3-B	2401[C]	CB3	1	0
2	2-M	550[B]	UMP	1	0
2	1-K	450[A]	UMP	1	0
3	1-B	2401[A]	CB3	1	0
2	3-O	650[C]	UMP	1	0
3	2-A	2351[B]	CB3	1	0
2	2-K	450[B]	UMP	1	0
2	3-M	550[C]	UMP	1	0
3	2-H	2701[B]	CB3	1	0
3	3-C	2451[C]	CB3	1	0
3	4-H	2701[D]	CB3	1	0
3	3-A	2351[C]	CB3	1	0
3	4-B	2401[D]	CB3	1	0
2	2-I	350[B]	UMP	1	0
3	1-F	2601[A]	CB3	1	0
3	3-F	2601[C]	CB3	1	0
2	3-L	500[C]	UMP	1	0
2	3-J	400[C]	UMP	1	0
2	2-J	400[B]	UMP	1	0
3	1-H	2701[A]	CB3	1	0
2	1-I	350[A]	UMP	1	0
3	1-C	2451[A]	CB3	1	0
3	4-A	2351[D]	CB3	1	0
2	4-L	500[D]	UMP	1	0
2	3-I	350[C]	UMP	1	0
2	1-O	650[A]	UMP	1	0
3	4-F	2601[D]	CB3	1	0
3	3-D	2501[C]	CB3	1	0

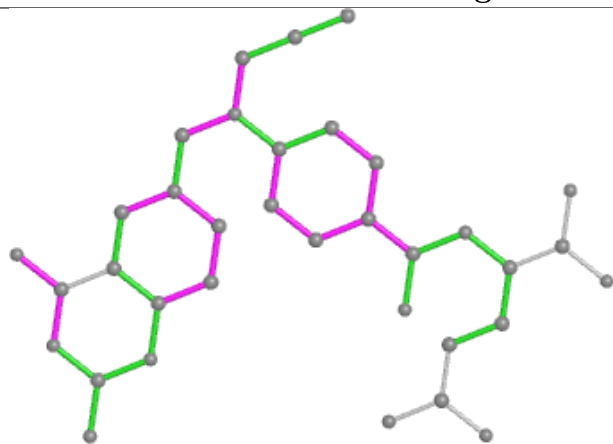
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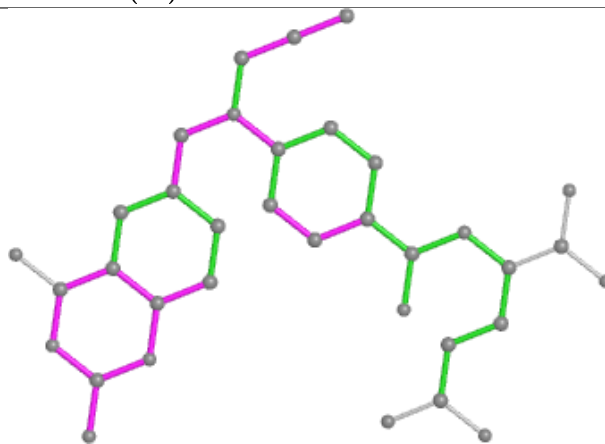
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2-O	650[B]	UMP	1	0
3	4-C	2451[D]	CB3	1	0
2	1-N	600[A]	UMP	1	0
2	4-M	550[D]	UMP	1	0
3	1-D	2501[A]	CB3	1	0
3	4-D	2501[D]	CB3	1	0
2	3-N	600[C]	UMP	1	0
3	2-F	2601[B]	CB3	1	0
2	2-P	700[B]	UMP	1	0
2	2-N	600[B]	UMP	1	0
2	4-I	350[D]	UMP	1	0
2	4-N	600[D]	UMP	1	0
3	2-D	2501[B]	CB3	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

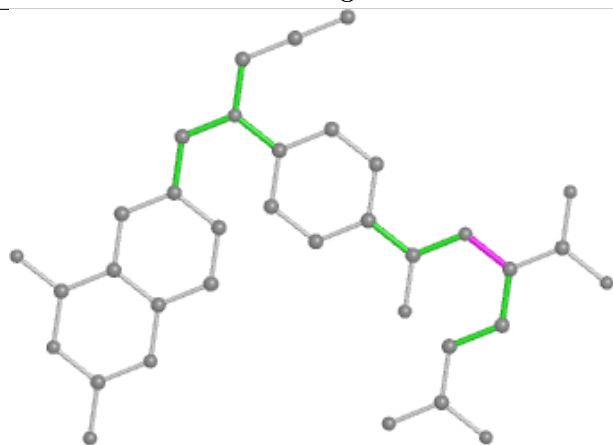
## Ligand CB3 A 2351 (A)



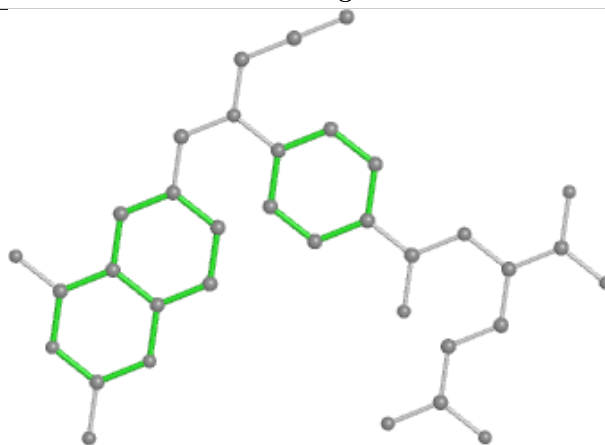
Bond lengths



Bond angles

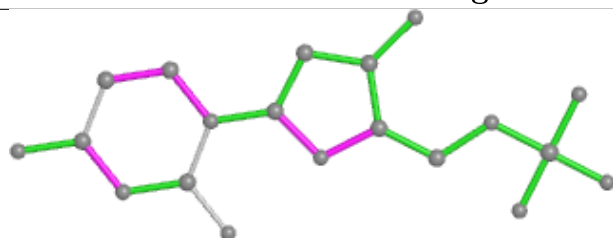


Torsions

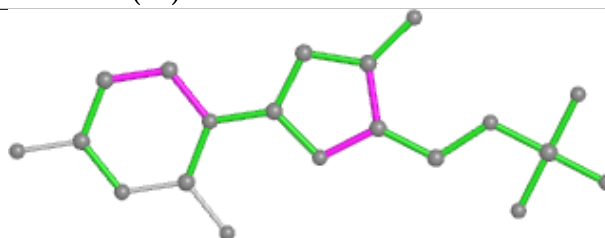


Rings

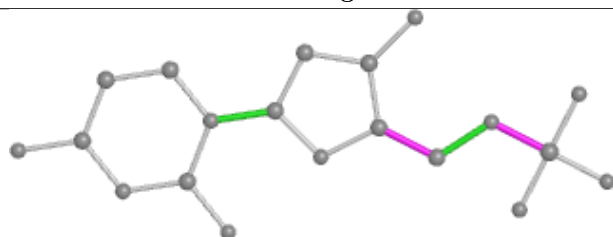
## Ligand UMP M 550 (A)



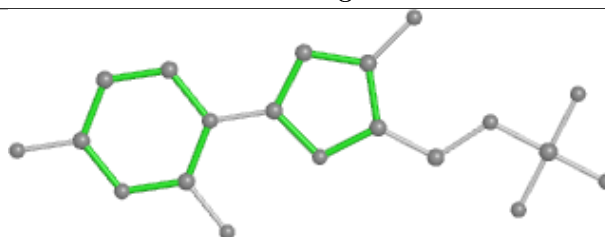
Bond lengths



Bond angles

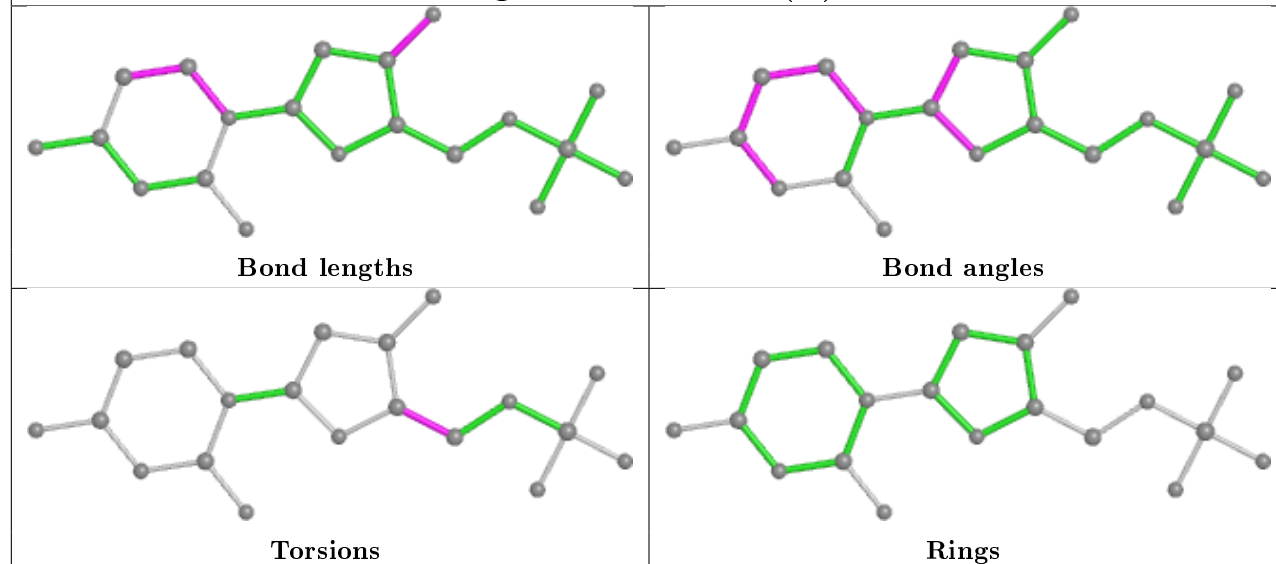


Torsions

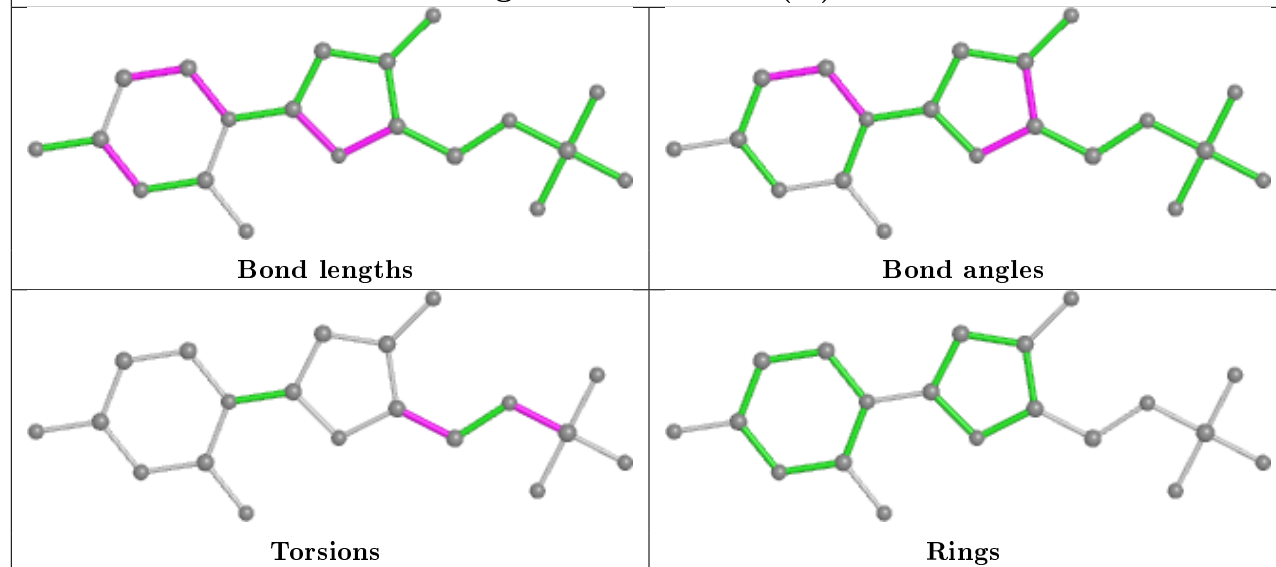


Rings

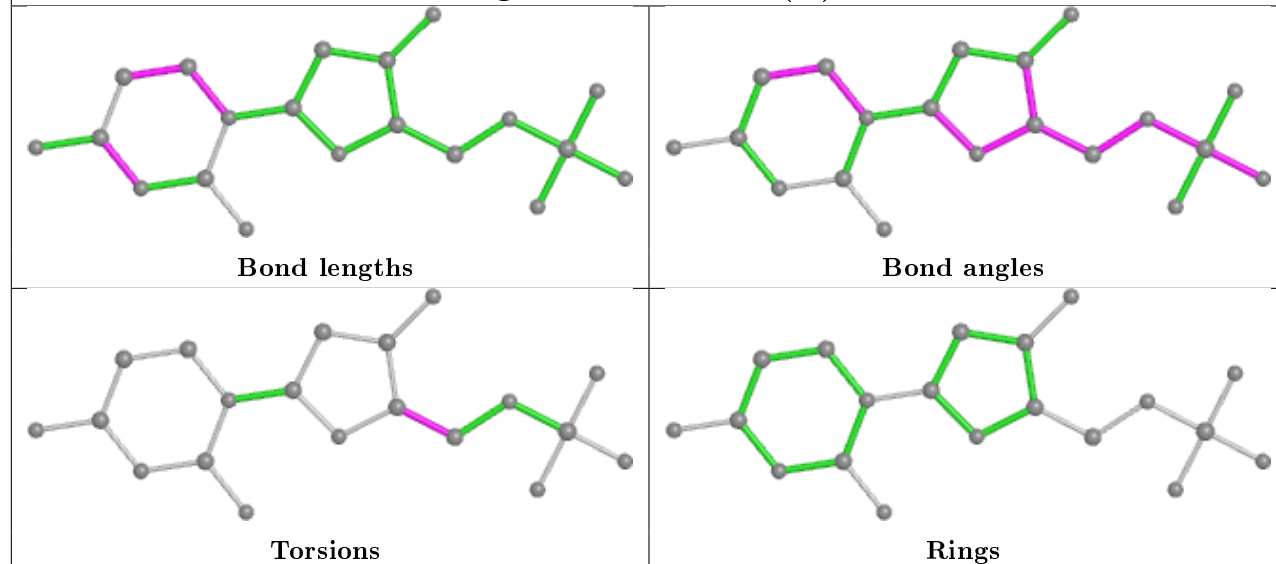
## Ligand UMP B 400 (A)



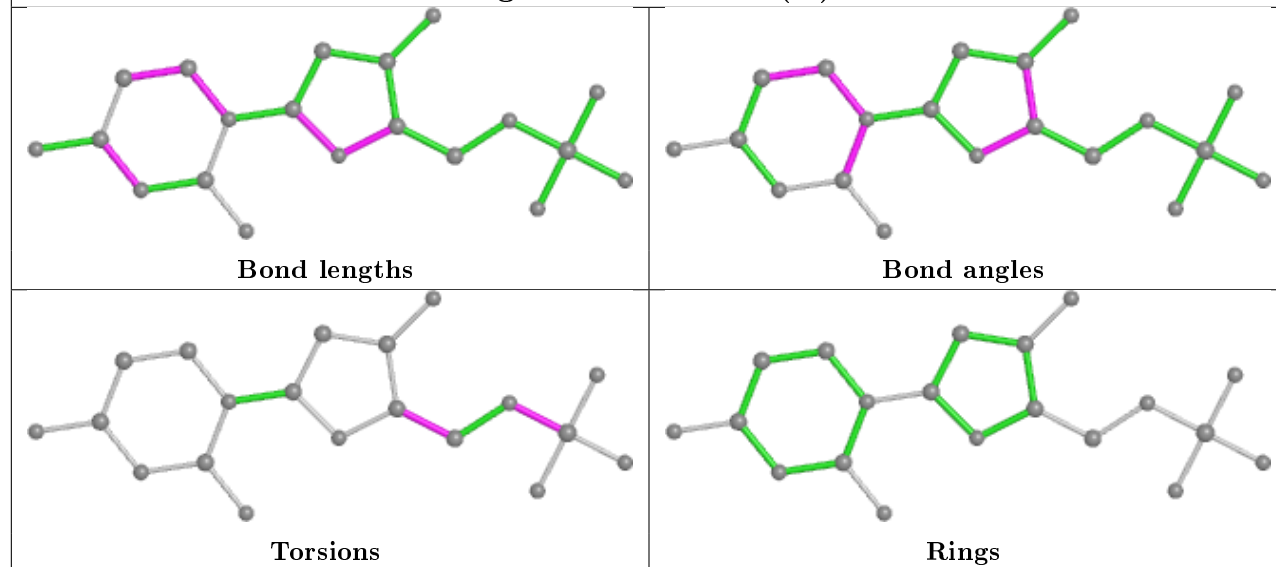
## Ligand UMP L 500 (A)

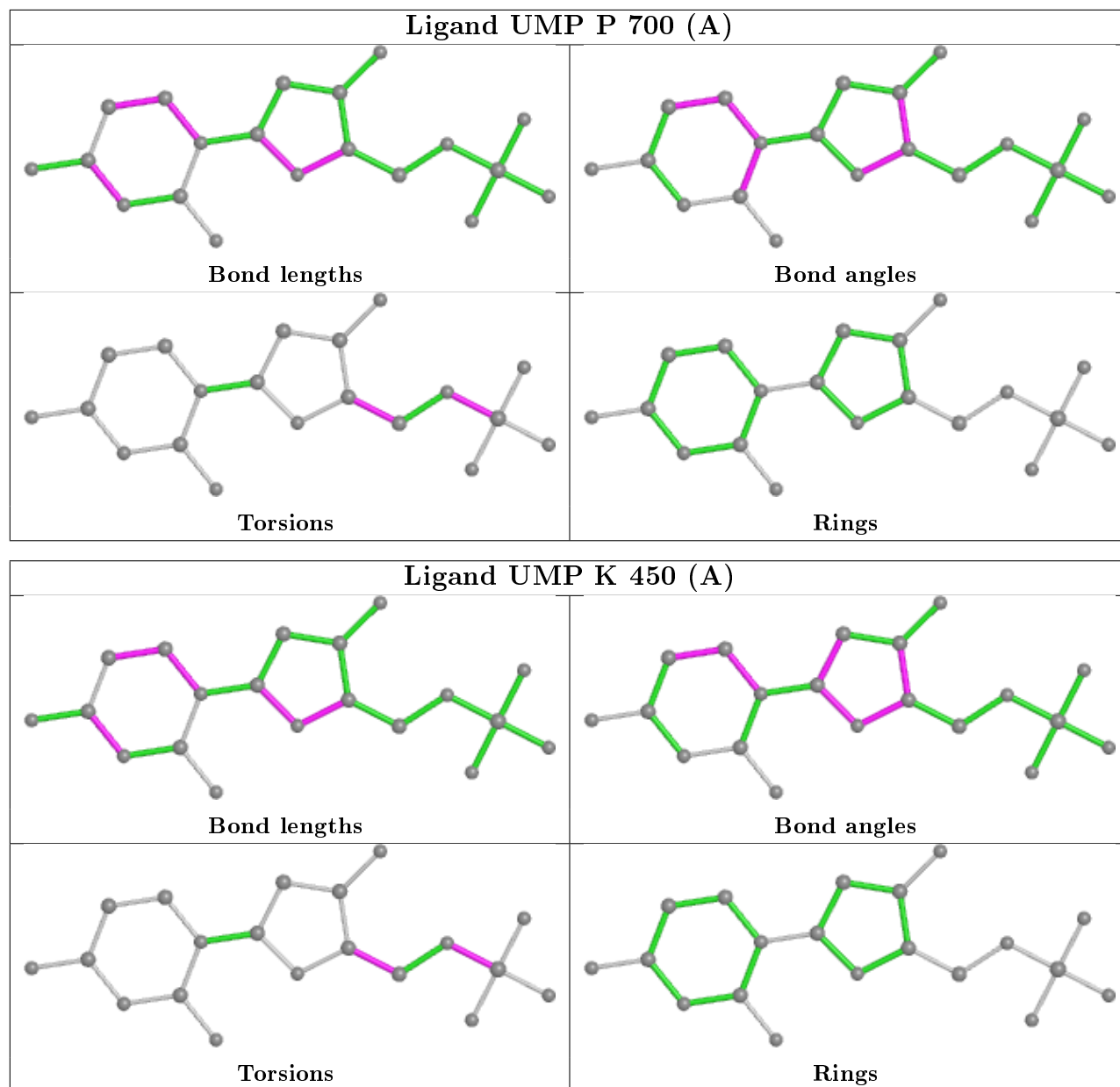


## Ligand UMP F 600 (A)



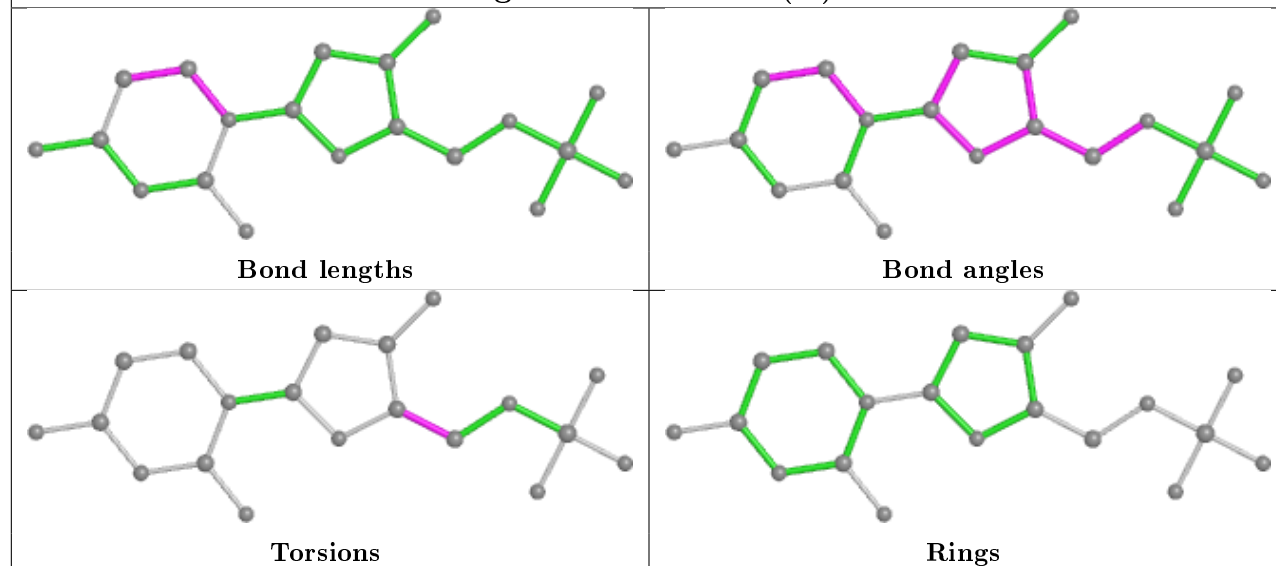
## Ligand UMP J 400 (A)



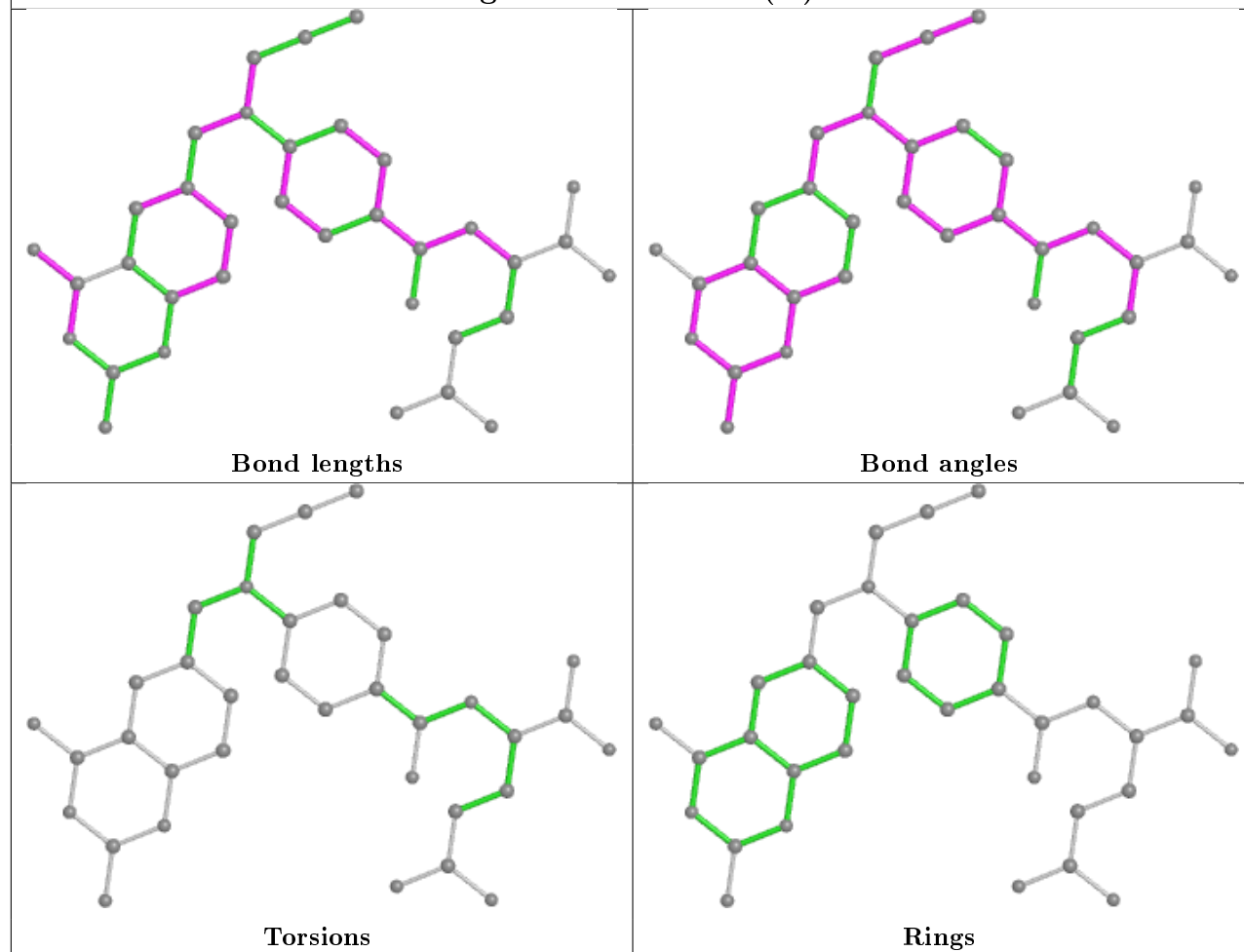




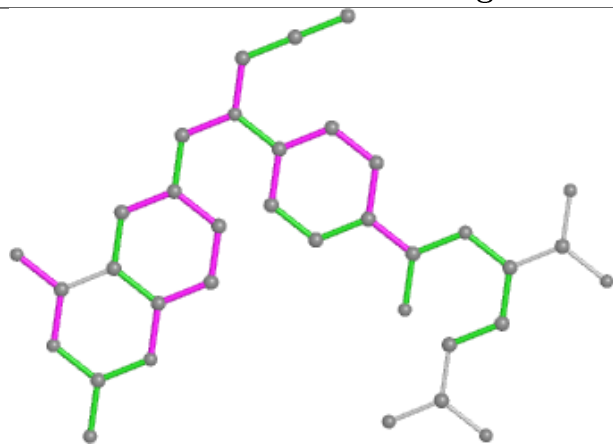
## Ligand UMP E 550 (A)



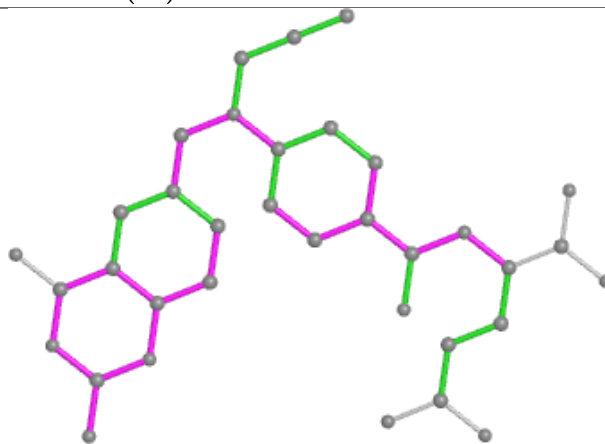
## Ligand CB3 B 2401 (A)



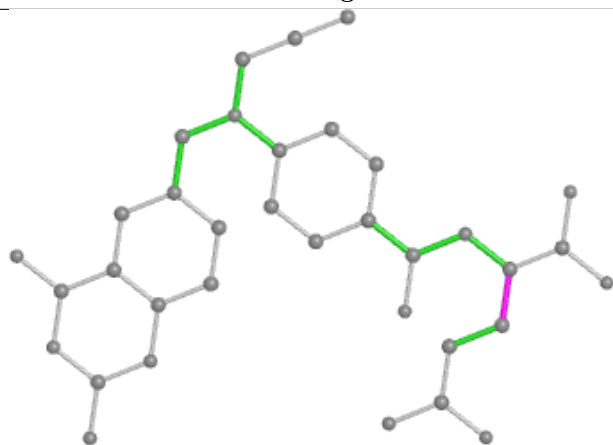
## Ligand CB3 F 2601 (A)



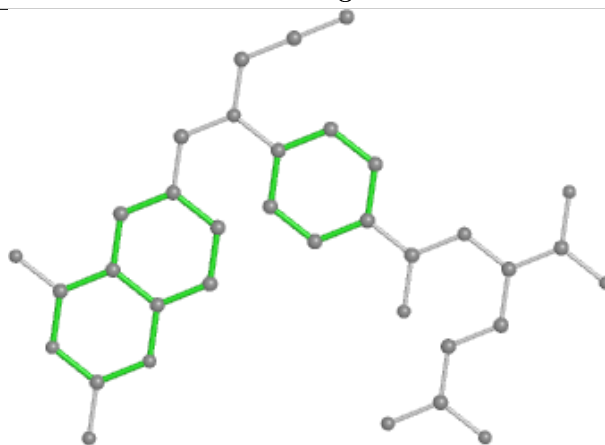
Bond lengths



Bond angles

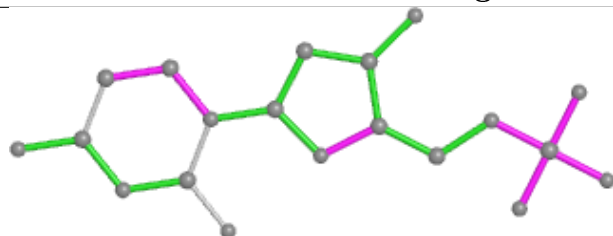


Torsions

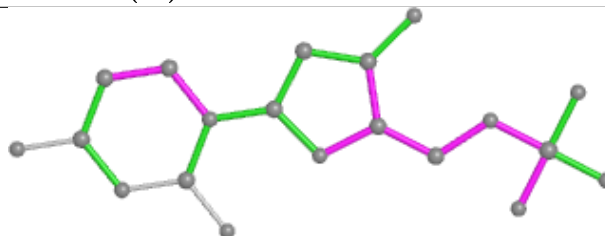


Rings

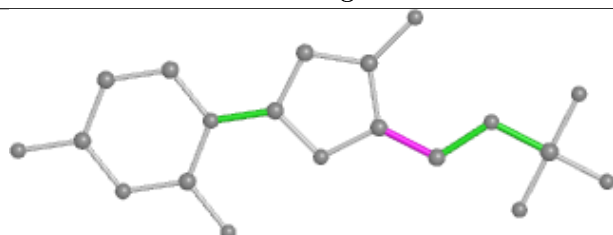
## Ligand UMP H 700 (A)



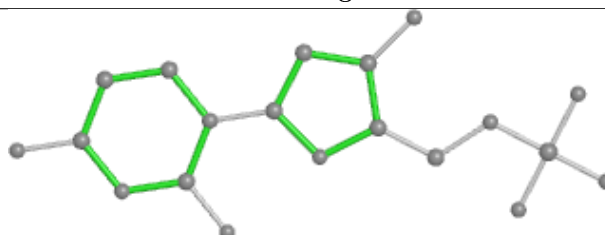
Bond lengths



Bond angles

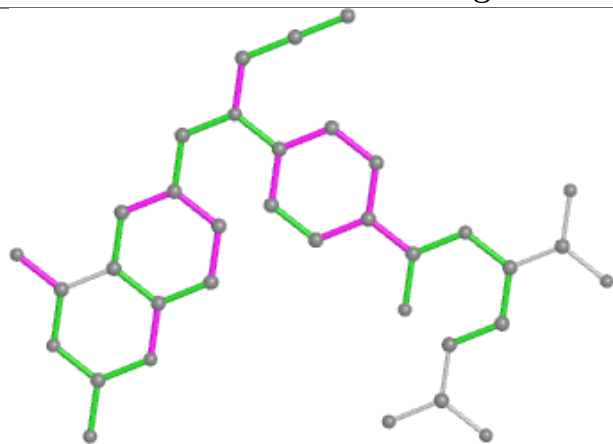


Torsions

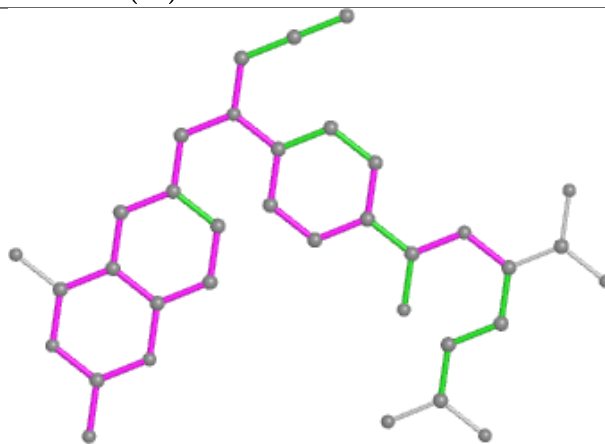


Rings

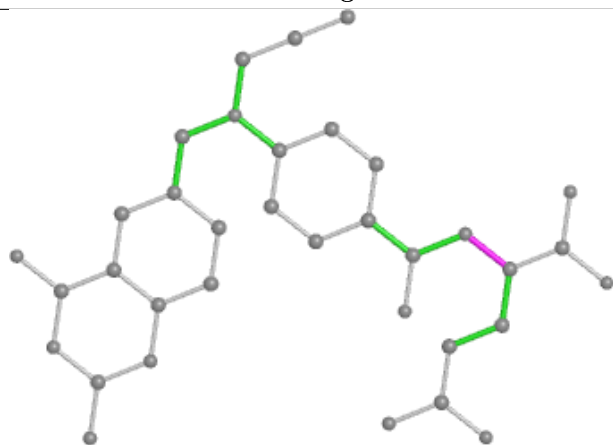
## Ligand CB3 H 2701 (A)



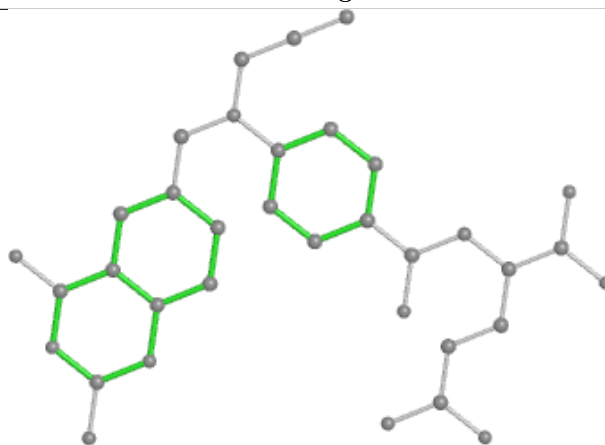
Bond lengths



Bond angles

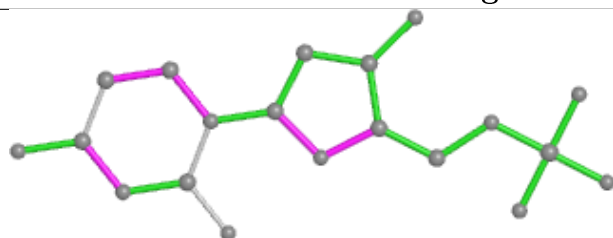


Torsions

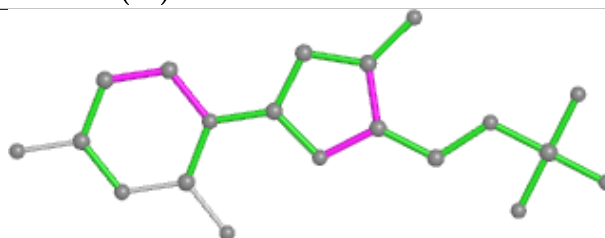


Rings

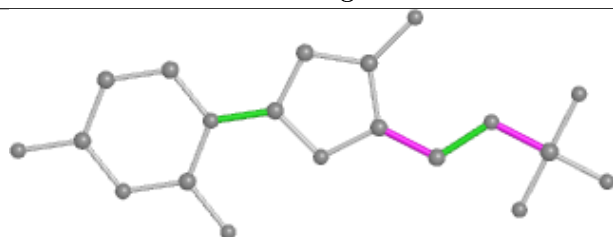
## Ligand UMP I 350 (A)



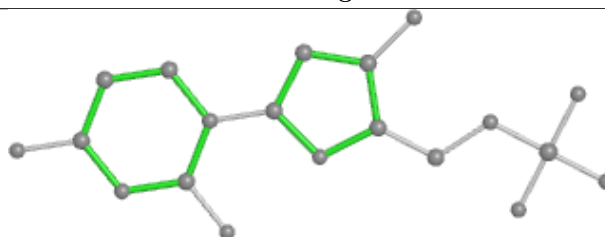
Bond lengths



Bond angles

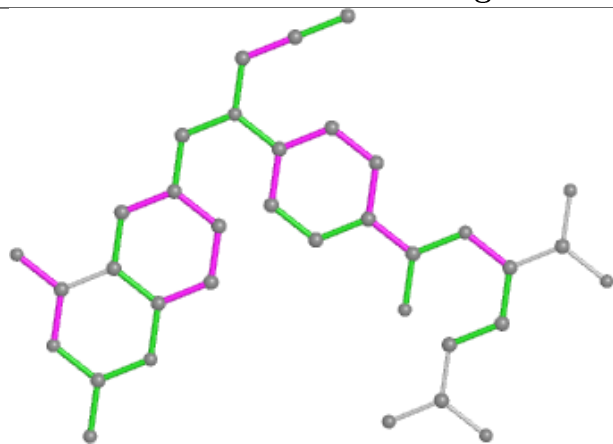


Torsions

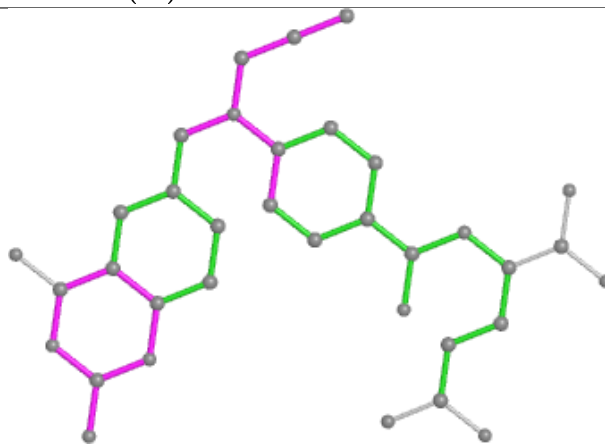


Rings

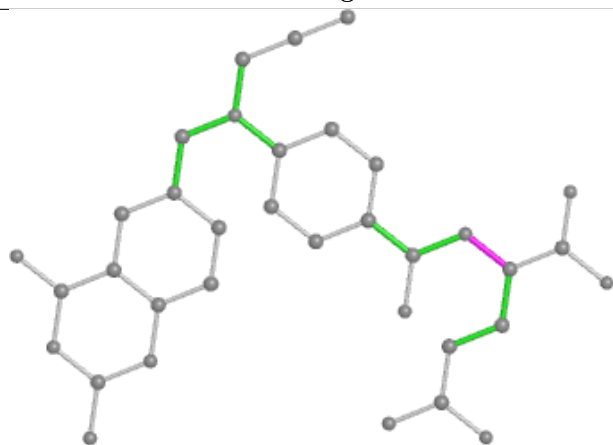
## Ligand CB3 C 2451 (A)



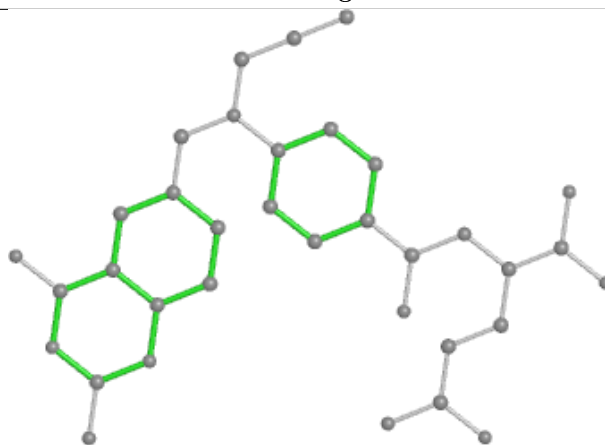
Bond lengths



Bond angles

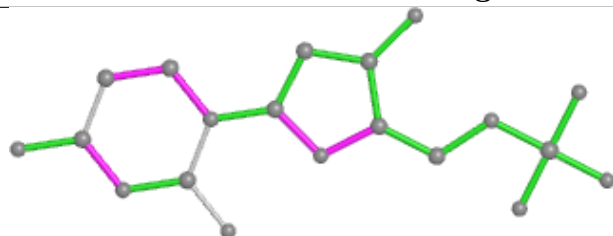


Torsions

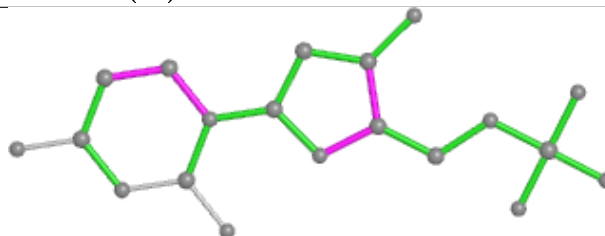


Rings

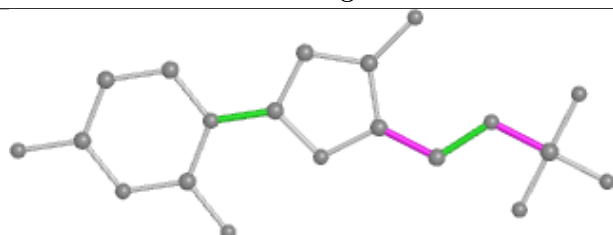
## Ligand UMP O 650 (A)



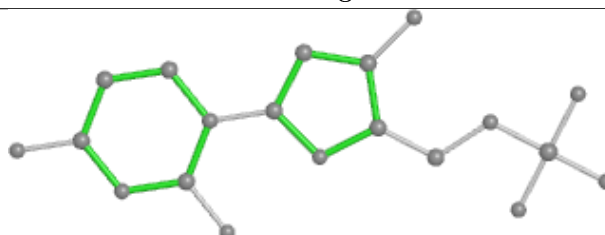
Bond lengths



Bond angles

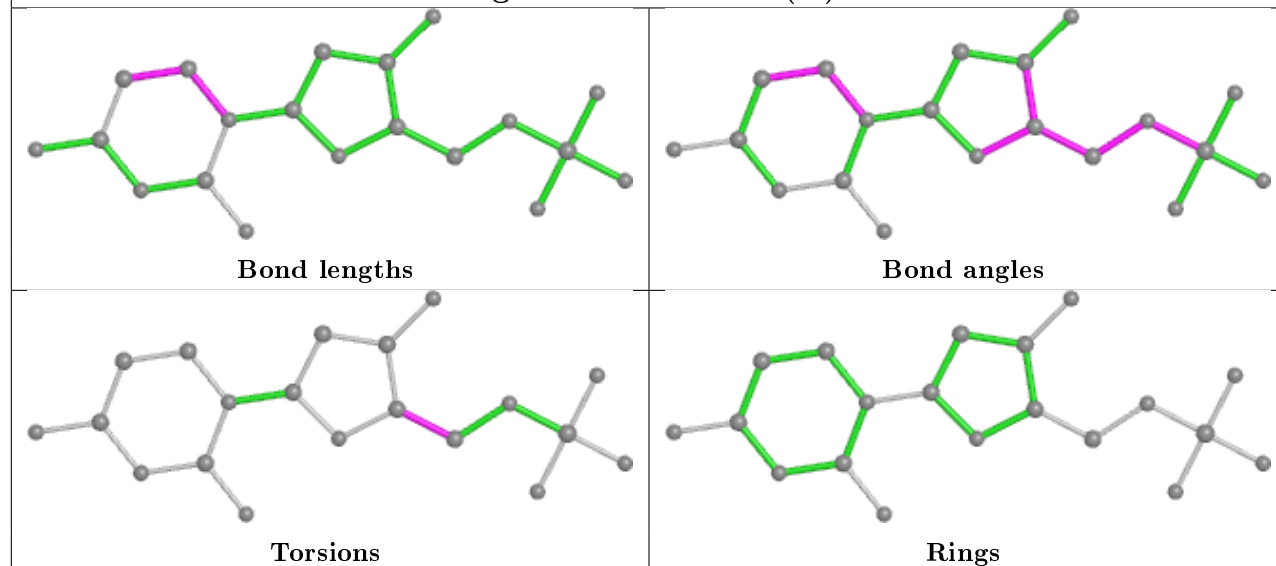


Torsions

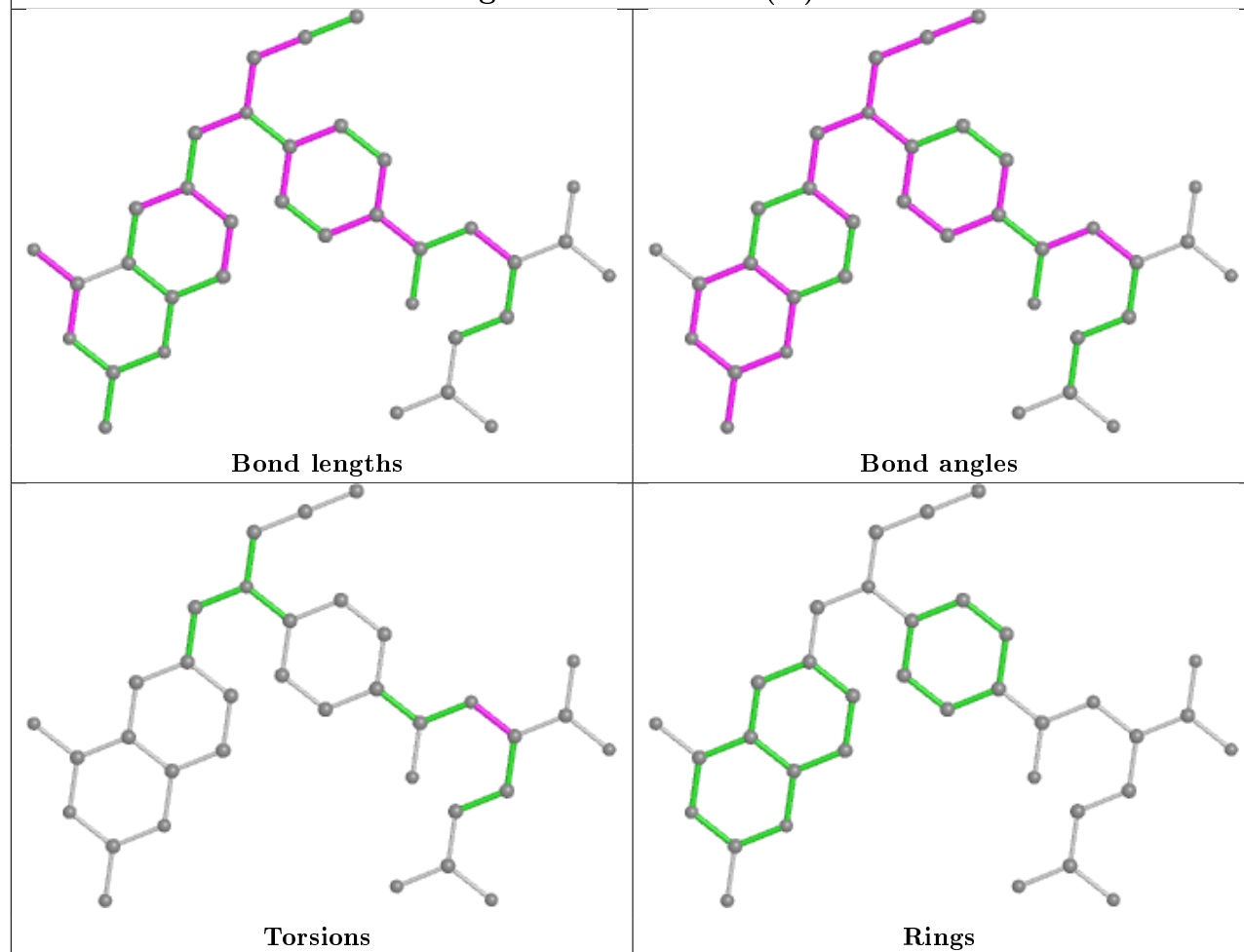


Rings

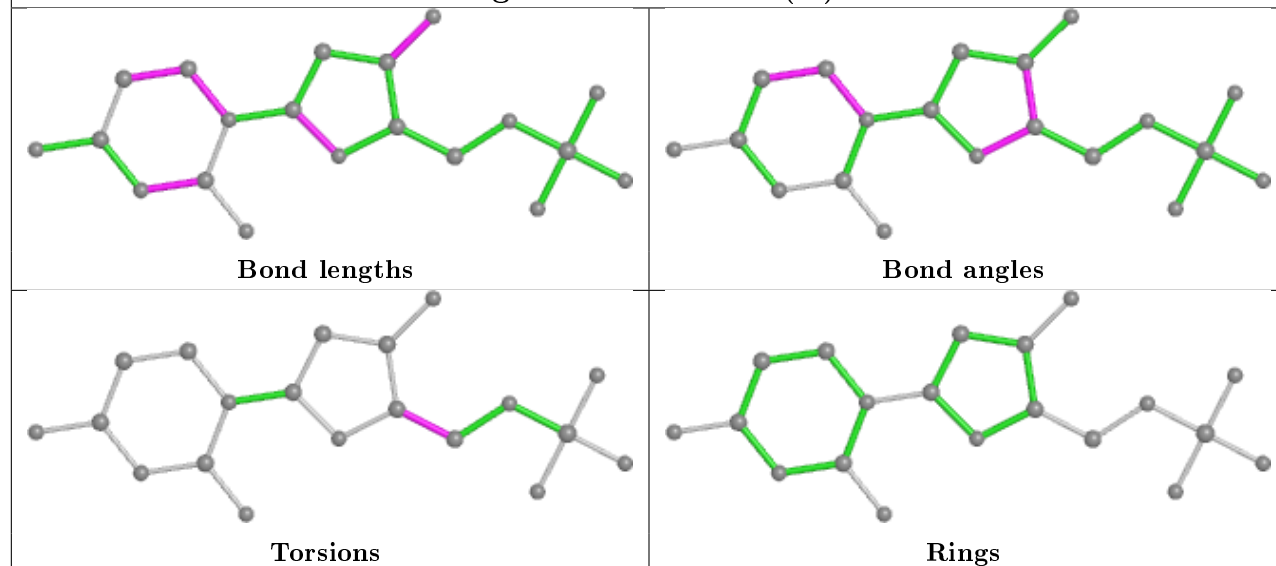
## Ligand UMP G 650 (A)



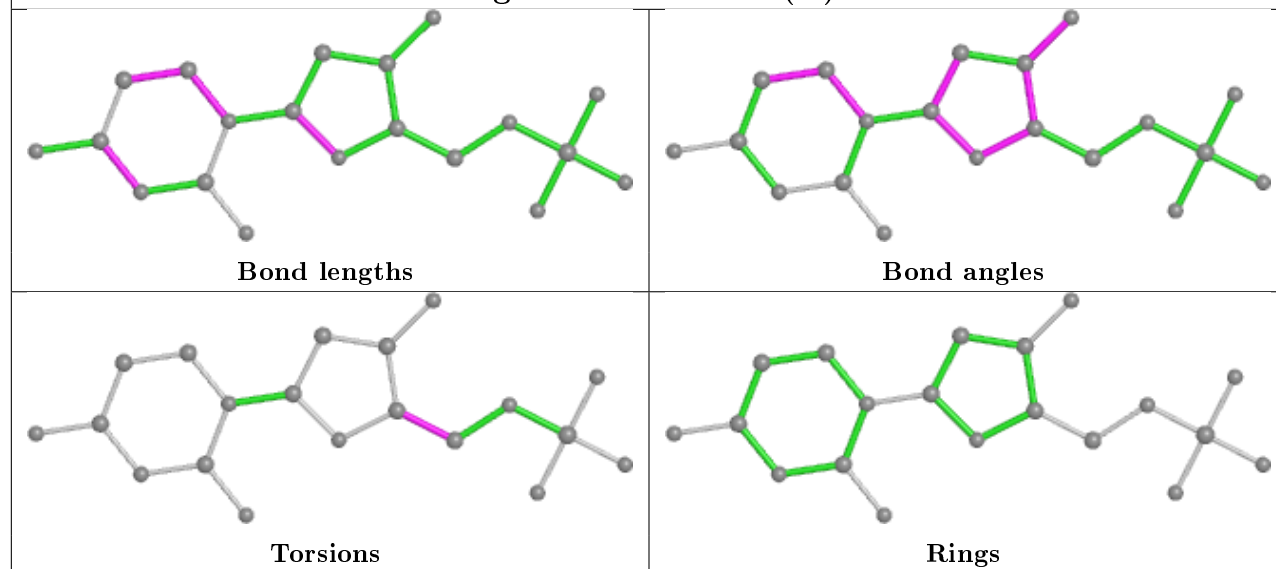
## Ligand CB3 G 2651 (A)



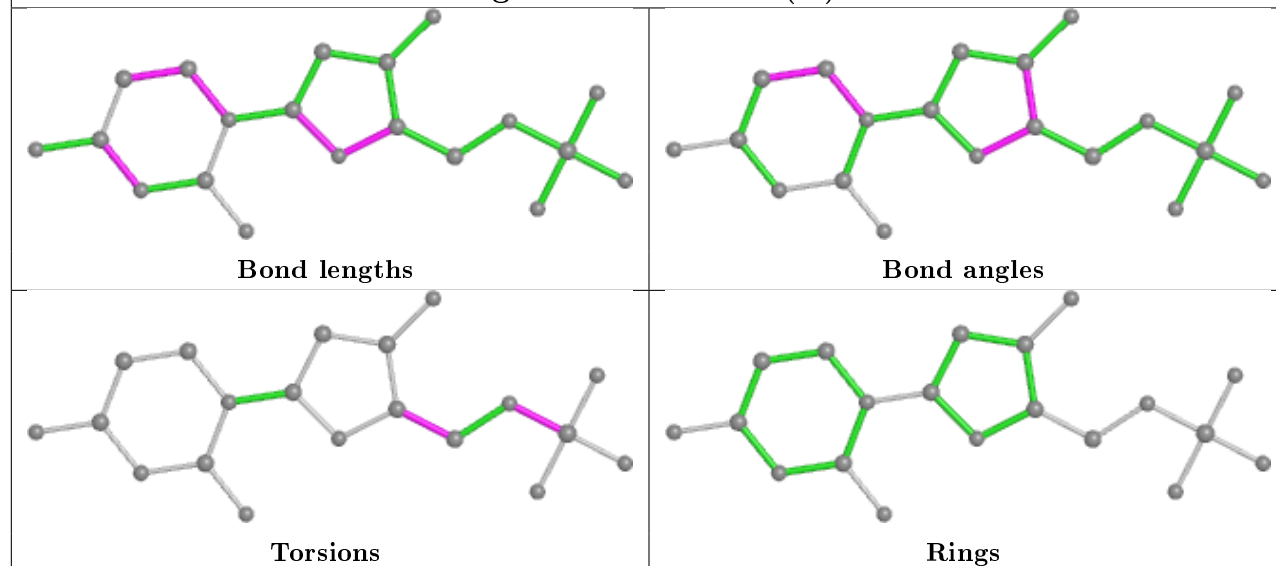
## Ligand UMP D 500 (A)



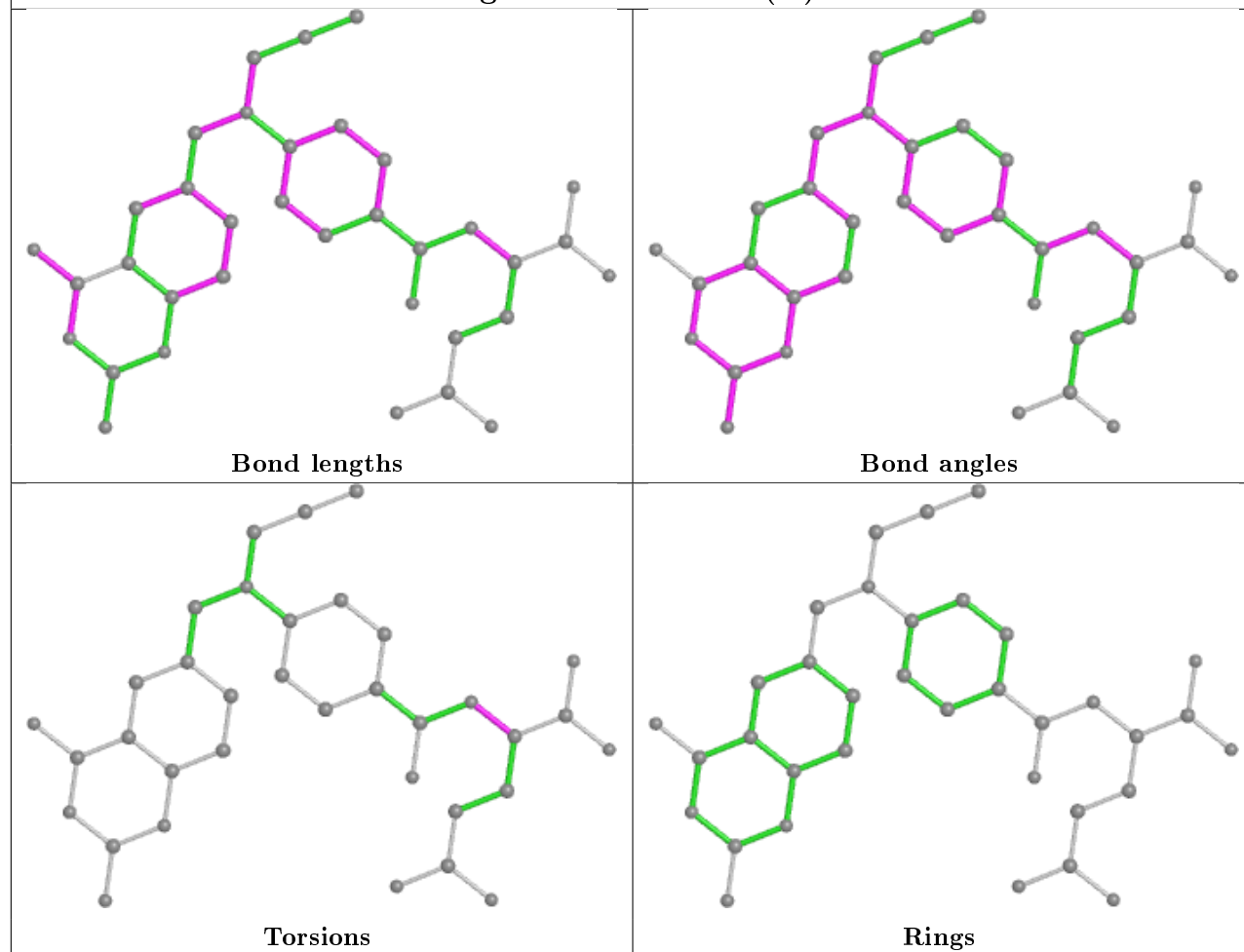
## Ligand UMP C 450 (A)



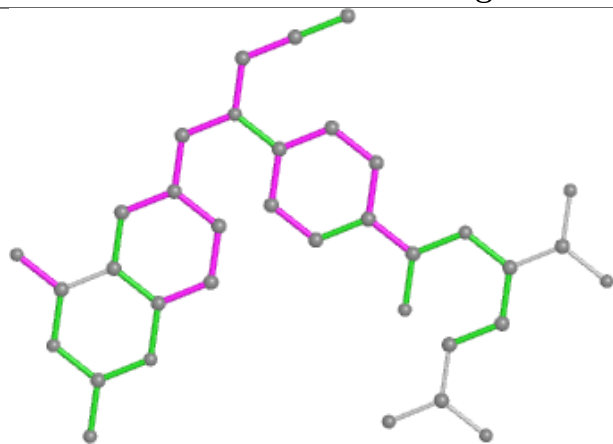
## Ligand UMP N 600 (A)



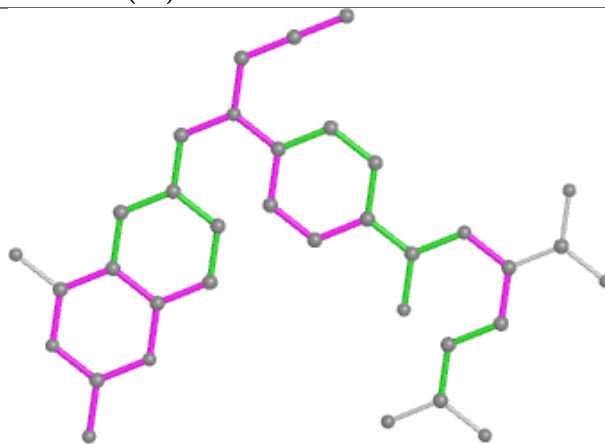
## Ligand CB3 D 2501 (A)



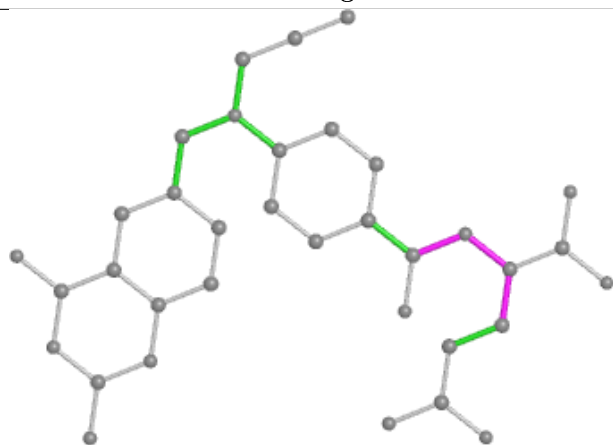
## Ligand CB3 E 2551 (A)



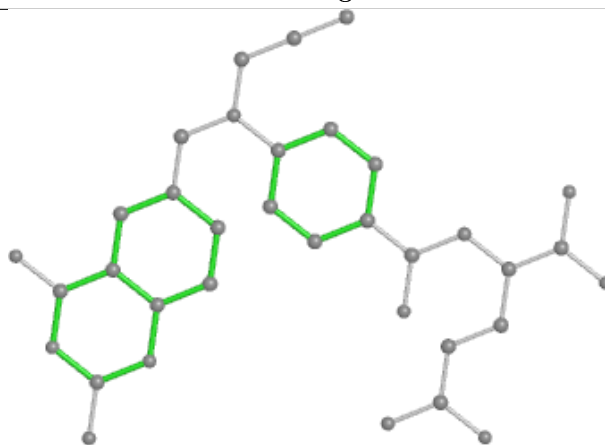
Bond lengths



Bond angles

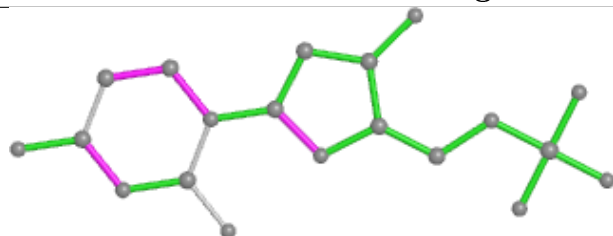


Torsions

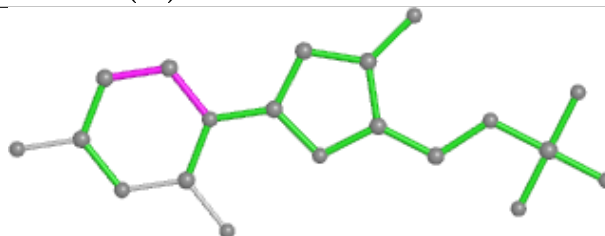


Rings

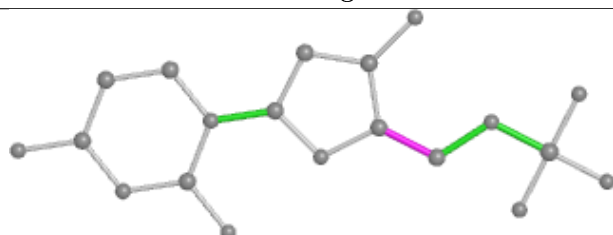
## Ligand UMP A 350 (A)



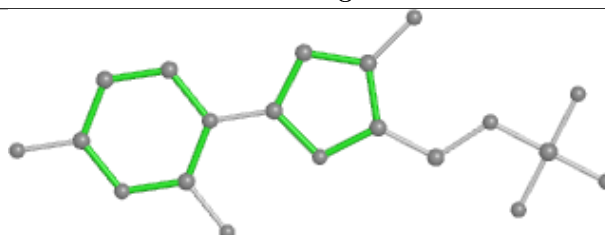
Bond lengths



Bond angles



Torsions



Rings



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	1-A	305/317 (96%)	1.38	79 (25%) 0 0	18, 26, 41, 61	305 (100%)
1	1-B	305/317 (96%)	1.36	78 (25%) 0 0	18, 27, 42, 63	305 (100%)
1	1-C	305/317 (96%)	1.37	72 (23%) 0 0	17, 26, 41, 61	305 (100%)
1	1-D	305/317 (96%)	1.32	73 (23%) 0 0	18, 27, 42, 63	305 (100%)
1	1-E	305/317 (96%)	1.42	79 (25%) 0 0	17, 26, 43, 63	305 (100%)
1	1-F	305/317 (96%)	1.29	70 (22%) 0 0	18, 27, 42, 64	305 (100%)
1	1-G	305/317 (96%)	1.38	80 (26%) 0 0	18, 26, 41, 62	305 (100%)
1	1-H	305/317 (96%)	1.32	67 (21%) 0 0	17, 27, 41, 64	305 (100%)
1	1-I	299/317 (94%)	6.28	293 (97%) 0 0	18, 26, 38, 56	299 (100%)
1	1-J	299/317 (94%)	6.37	296 (98%) 0 0	18, 26, 37, 56	299 (100%)
1	1-K	299/317 (94%)	6.23	294 (98%) 0 0	17, 26, 37, 56	299 (100%)
1	1-L	299/317 (94%)	5.79	291 (97%) 0 0	17, 26, 37, 56	299 (100%)
1	1-M	299/317 (94%)	6.11	295 (98%) 0 0	17, 26, 37, 56	299 (100%)
1	1-N	299/317 (94%)	6.16	296 (98%) 0 0	18, 26, 37, 56	299 (100%)
1	1-O	299/317 (94%)	6.21	293 (97%) 0 0	17, 26, 37, 56	299 (100%)
1	1-P	299/317 (94%)	5.92	291 (97%) 0 0	18, 26, 37, 56	299 (100%)
1	2-A	305/317 (96%)	1.38	79 (25%) 0 0	18, 26, 41, 61	305 (100%)
1	2-B	305/317 (96%)	1.36	78 (25%) 0 0	18, 27, 42, 63	305 (100%)
1	2-C	305/317 (96%)	1.37	72 (23%) 0 0	17, 26, 41, 61	305 (100%)
1	2-D	305/317 (96%)	1.32	73 (23%) 0 0	18, 27, 42, 63	305 (100%)
1	2-E	305/317 (96%)	1.42	79 (25%) 0 0	17, 26, 43, 63	305 (100%)
1	2-F	305/317 (96%)	1.29	70 (22%) 0 0	18, 27, 42, 64	305 (100%)
1	2-G	305/317 (96%)	1.38	80 (26%) 0 0	18, 26, 41, 62	305 (100%)
1	2-H	305/317 (96%)	1.32	67 (21%) 0 0	17, 27, 41, 64	305 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
1	2-I	299/317 (94%)	6.28	293 (97%)	0	0	18, 26, 38, 56	299 (100%)
1	2-J	299/317 (94%)	6.37	296 (98%)	0	0	18, 26, 37, 56	299 (100%)
1	2-K	299/317 (94%)	6.23	294 (98%)	0	0	17, 26, 37, 56	299 (100%)
1	2-L	299/317 (94%)	5.79	291 (97%)	0	0	17, 26, 37, 56	299 (100%)
1	2-M	299/317 (94%)	6.11	295 (98%)	0	0	17, 26, 37, 56	299 (100%)
1	2-N	299/317 (94%)	6.16	296 (98%)	0	0	18, 26, 37, 56	299 (100%)
1	2-O	299/317 (94%)	6.21	293 (97%)	0	0	17, 26, 37, 56	299 (100%)
1	2-P	299/317 (94%)	5.92	291 (97%)	0	0	18, 26, 37, 56	299 (100%)
1	3-A	305/317 (96%)	1.38	79 (25%)	0	0	18, 26, 41, 61	305 (100%)
1	3-B	305/317 (96%)	1.36	78 (25%)	0	0	18, 27, 42, 63	305 (100%)
1	3-C	305/317 (96%)	1.37	72 (23%)	0	0	17, 26, 41, 61	305 (100%)
1	3-D	305/317 (96%)	1.32	73 (23%)	0	0	18, 27, 42, 63	305 (100%)
1	3-E	305/317 (96%)	1.42	79 (25%)	0	0	17, 26, 43, 63	305 (100%)
1	3-F	305/317 (96%)	1.29	70 (22%)	0	0	18, 27, 42, 64	305 (100%)
1	3-G	305/317 (96%)	1.38	80 (26%)	0	0	18, 26, 41, 62	305 (100%)
1	3-H	305/317 (96%)	1.32	67 (21%)	0	0	17, 27, 41, 64	305 (100%)
1	3-I	299/317 (94%)	6.28	293 (97%)	0	0	18, 26, 38, 56	299 (100%)
1	3-J	299/317 (94%)	6.37	296 (98%)	0	0	18, 26, 37, 56	299 (100%)
1	3-K	299/317 (94%)	6.23	294 (98%)	0	0	17, 26, 37, 56	299 (100%)
1	3-L	299/317 (94%)	5.79	291 (97%)	0	0	17, 26, 37, 56	299 (100%)
1	3-M	299/317 (94%)	6.11	295 (98%)	0	0	17, 26, 37, 56	299 (100%)
1	3-N	299/317 (94%)	6.16	296 (98%)	0	0	18, 26, 37, 56	299 (100%)
1	3-O	299/317 (94%)	6.21	293 (97%)	0	0	17, 26, 37, 56	299 (100%)
1	3-P	299/317 (94%)	5.92	291 (97%)	0	0	18, 26, 37, 56	299 (100%)
1	4-A	305/317 (96%)	1.38	79 (25%)	0	0	18, 26, 41, 61	305 (100%)
1	4-B	305/317 (96%)	1.36	78 (25%)	0	0	18, 27, 42, 63	305 (100%)
1	4-C	305/317 (96%)	1.37	72 (23%)	0	0	17, 26, 41, 61	305 (100%)
1	4-D	305/317 (96%)	1.32	73 (23%)	0	0	18, 27, 42, 63	305 (100%)
1	4-E	305/317 (96%)	1.42	79 (25%)	0	0	17, 26, 43, 63	305 (100%)
1	4-F	305/317 (96%)	1.29	70 (22%)	0	0	18, 27, 42, 64	305 (100%)
1	4-G	305/317 (96%)	1.38	80 (26%)	0	0	18, 26, 41, 62	305 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	4-H	305/317 (96%)	1.32	67 (21%) 0 0	17, 27, 41, 64	305 (100%)
1	4-I	299/317 (94%)	6.28	293 (97%) 0 0	18, 26, 38, 56	299 (100%)
1	4-J	299/317 (94%)	6.37	296 (98%) 0 0	18, 26, 37, 56	299 (100%)
1	4-K	299/317 (94%)	6.23	294 (98%) 0 0	17, 26, 37, 56	299 (100%)
1	4-L	299/317 (94%)	5.79	291 (97%) 0 0	17, 26, 37, 56	299 (100%)
1	4-M	299/317 (94%)	6.11	295 (98%) 0 0	17, 26, 37, 56	299 (100%)
1	4-N	299/317 (94%)	6.16	296 (98%) 0 0	18, 26, 37, 56	299 (100%)
1	4-O	299/317 (94%)	6.21	293 (97%) 0 0	17, 26, 37, 56	299 (100%)
1	4-P	299/317 (94%)	5.92	291 (97%) 0 0	18, 26, 37, 56	299 (100%)
All	All	19328/20288 (95%)	3.72	11788 (60%) 0 0	17, 26, 40, 64	19328 (100%)

All (11788) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-J	283[A]	ALA	25.7
1	2-J	283[B]	ALA	25.7
1	3-J	283[C]	ALA	25.7
1	4-J	283[D]	ALA	25.7
1	1-K	283[A]	ALA	25.2
1	2-K	283[B]	ALA	25.2
1	3-K	283[C]	ALA	25.2
1	4-K	283[D]	ALA	25.2
1	1-K	204[A]	GLY	22.7
1	2-K	204[B]	GLY	22.7
1	3-K	204[C]	GLY	22.7
1	4-K	204[D]	GLY	22.7
1	1-J	197[A]	LEU	22.2
1	2-J	197[B]	LEU	22.2
1	3-J	197[C]	LEU	22.2
1	4-J	197[D]	LEU	22.2
1	1-K	153[A]	LEU	21.8
1	2-K	153[B]	LEU	21.8
1	3-K	153[C]	LEU	21.8
1	4-K	153[D]	LEU	21.8
1	1-M	259[A]	TYR	21.5
1	2-M	259[B]	TYR	21.5
1	3-M	259[C]	TYR	21.5
1	4-M	259[D]	TYR	21.5
1	1-K	282[A]	TRP	20.9

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Mol	Chain	Res	Type	RSRZ
1	2-K	282[B]	TRP	20.9
1	3-K	282[C]	TRP	20.9
1	4-K	282[D]	TRP	20.9
1	1-M	204[A]	GLY	19.0
1	2-M	204[B]	GLY	19.0
1	3-M	204[C]	GLY	19.0
1	4-M	204[D]	GLY	19.0
1	1-O	239[A]	ALA	18.3
1	2-O	239[B]	ALA	18.3
1	3-O	239[C]	ALA	18.3
1	4-O	239[D]	ALA	18.3
1	1-N	198[A]	PRO	18.1
1	2-N	198[B]	PRO	18.1
1	3-N	198[C]	PRO	18.1
1	4-N	198[D]	PRO	18.1
1	1-J	289[A]	ILE	18.0
1	2-J	289[B]	ILE	18.0
1	3-J	289[C]	ILE	18.0
1	4-J	289[D]	ILE	18.0
1	1-N	243[A]	ASP	17.9
1	2-N	243[B]	ASP	17.9
1	3-N	243[C]	ASP	17.9
1	4-N	243[D]	ASP	17.9
1	1-N	199[A]	PRO	17.9
1	2-N	199[B]	PRO	17.9
1	3-N	199[C]	PRO	17.9
1	4-N	199[D]	PRO	17.9
1	1-P	211[A]	CYS	17.8
1	2-P	211[B]	CYS	17.8
1	3-P	211[C]	CYS	17.8
1	4-P	211[D]	CYS	17.8
1	1-J	210[A]	SER	17.8
1	2-J	210[B]	SER	17.8
1	3-J	210[C]	SER	17.8
1	4-J	210[D]	SER	17.8
1	1-K	63[A]	LEU	16.8
1	2-K	63[B]	LEU	16.8
1	3-K	63[C]	LEU	16.8
1	4-K	63[D]	LEU	16.8
1	1-O	297[A]	VAL	16.0
1	2-O	297[B]	VAL	16.0
1	3-O	297[C]	VAL	16.0

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Mol	Chain	Res	Type	RSRZ
1	4-O	297[D]	VAL	16.0
1	1-N	36[A]	VAL	15.9
1	2-N	36[B]	VAL	15.9
1	3-N	36[C]	VAL	15.9
1	4-N	36[D]	VAL	15.9
1	1-P	229[A]	ALA	15.8
1	2-P	229[B]	ALA	15.8
1	3-P	229[C]	ALA	15.8
1	4-P	229[D]	ALA	15.8
1	1-I	111[A]	GLU	15.8
1	1-N	194[A]	PHE	15.8
1	2-I	111[B]	GLU	15.8
1	2-N	194[B]	PHE	15.8
1	3-I	111[C]	GLU	15.8
1	3-N	194[C]	PHE	15.8
1	4-I	111[D]	GLU	15.8
1	4-N	194[D]	PHE	15.8
1	1-I	270[A]	LEU	15.5
1	2-I	270[B]	LEU	15.5
1	3-I	270[C]	LEU	15.5
1	4-I	270[D]	LEU	15.5
1	1-O	199[A]	PRO	15.2
1	2-O	199[B]	PRO	15.2
1	3-O	199[C]	PRO	15.2
1	4-O	199[D]	PRO	15.2
1	1-I	232[A]	ALA	15.1
1	2-I	232[B]	ALA	15.1
1	3-I	232[C]	ALA	15.1
1	4-I	232[D]	ALA	15.1
1	1-J	304[A]	GLY	14.7
1	2-J	304[B]	GLY	14.7
1	3-J	304[C]	GLY	14.7
1	4-J	304[D]	GLY	14.7
1	1-P	106[A]	SER	14.6
1	2-P	106[B]	SER	14.6
1	3-P	106[C]	SER	14.6
1	4-P	106[D]	SER	14.6
1	1-J	52[A]	PRO	14.4
1	2-J	52[B]	PRO	14.4
1	3-J	52[C]	PRO	14.4
1	4-J	52[D]	PRO	14.4
1	1-I	33[A]	VAL	14.4

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Mol	Chain	Res	Type	RSRZ
1	2-I	33[B]	VAL	14.4
1	3-I	33[C]	VAL	14.4
1	4-I	33[D]	VAL	14.4
1	1-K	116[A]	GLY	14.3
1	2-K	116[B]	GLY	14.3
1	3-K	116[C]	GLY	14.3
1	4-K	116[D]	GLY	14.3
1	1-L	195[A]	VAL	14.3
1	2-L	195[B]	VAL	14.3
1	3-L	195[C]	VAL	14.3
1	4-L	195[D]	VAL	14.3
1	1-J	100[A]	ILE	14.2
1	2-J	100[B]	ILE	14.2
1	3-J	100[C]	ILE	14.2
1	4-J	100[D]	ILE	14.2
1	1-O	196[A]	SER	14.2
1	2-O	196[B]	SER	14.2
1	3-O	196[C]	SER	14.2
1	4-O	196[D]	SER	14.2
1	1-O	240[A]	LEU	14.1
1	2-O	240[B]	LEU	14.1
1	3-O	240[C]	LEU	14.1
1	4-O	240[D]	LEU	14.1
1	1-J	43[A]	THR	14.0
1	2-J	43[B]	THR	14.0
1	3-J	43[C]	THR	14.0
1	4-J	43[D]	THR	14.0
1	1-J	221[A]	GLY	14.0
1	2-J	221[B]	GLY	14.0
1	3-J	221[C]	GLY	14.0
1	4-J	221[D]	GLY	14.0
1	1-K	97[A]	GLY	13.9
1	2-K	97[B]	GLY	13.9
1	3-K	97[C]	GLY	13.9
1	4-K	97[D]	GLY	13.9
1	1-O	203[A]	PRO	13.8
1	2-O	203[B]	PRO	13.8
1	3-O	203[C]	PRO	13.8
1	4-O	203[D]	PRO	13.8
1	1-I	263[A]	VAL	13.8
1	2-I	263[B]	VAL	13.8
1	3-I	263[C]	VAL	13.8

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Mol	Chain	Res	Type	RSRZ
1	4-I	263[D]	VAL	13.8
1	1-O	54[A]	PHE	13.8
1	2-O	54[B]	PHE	13.8
1	3-O	54[C]	PHE	13.8
1	4-O	54[D]	PHE	13.8
1	1-P	204[A]	GLY	13.7
1	2-P	204[B]	GLY	13.7
1	3-P	204[C]	GLY	13.7
1	4-P	204[D]	GLY	13.7
1	1-J	129[A]	PHE	13.6
1	2-J	129[B]	PHE	13.6
1	3-J	129[C]	PHE	13.6
1	4-J	129[D]	PHE	13.6
1	1-J	256[A]	ALA	13.4
1	2-J	256[B]	ALA	13.4
1	3-J	256[C]	ALA	13.4
1	4-J	256[D]	ALA	13.4
1	1-P	46[A]	VAL	13.4
1	2-P	46[B]	VAL	13.4
1	3-P	46[C]	VAL	13.4
1	4-P	46[D]	VAL	13.4
1	1-M	205[A]	SER	13.3
1	2-M	205[B]	SER	13.3
1	3-M	205[C]	SER	13.3
1	4-M	205[D]	SER	13.3
1	1-I	34[A]	GLY	13.2
1	1-I	309[A]	GLY	13.2
1	2-I	34[B]	GLY	13.2
1	2-I	309[B]	GLY	13.2
1	3-I	34[C]	GLY	13.2
1	3-I	309[C]	GLY	13.2
1	4-I	34[D]	GLY	13.2
1	4-I	309[D]	GLY	13.2
1	1-I	17[A]	ASP	13.1
1	2-I	17[B]	ASP	13.1
1	3-I	17[C]	ASP	13.1
1	4-I	17[D]	ASP	13.1
1	1-P	259[A]	TYR	13.1
1	2-P	259[B]	TYR	13.1
1	3-P	259[C]	TYR	13.1
1	4-P	259[D]	TYR	13.1
1	1-P	311[A]	ILE	13.0

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Mol	Chain	Res	Type	RSRZ
1	2-P	311[B]	ILE	13.0
1	3-P	311[C]	ILE	13.0
1	4-P	311[D]	ILE	13.0
1	1-M	294[A]	GLY	13.0
1	2-M	294[B]	GLY	13.0
1	3-M	294[C]	GLY	13.0
1	4-M	294[D]	GLY	13.0
1	1-O	210[A]	SER	13.0
1	2-O	210[B]	SER	13.0
1	3-O	210[C]	SER	13.0
1	4-O	210[D]	SER	13.0
1	1-L	164[A]	PRO	13.0
1	2-L	164[B]	PRO	13.0
1	3-L	164[C]	PRO	13.0
1	4-L	164[D]	PRO	13.0
1	1-O	113[A]	VAL	12.9
1	2-O	113[B]	VAL	12.9
1	3-O	113[C]	VAL	12.9
1	4-O	113[D]	VAL	12.9
1	1-O	121[A]	GLY	12.8
1	2-O	121[B]	GLY	12.8
1	3-O	121[C]	GLY	12.8
1	4-O	121[D]	GLY	12.8
1	1-N	239[A]	ALA	12.8
1	2-N	239[B]	ALA	12.8
1	3-N	239[C]	ALA	12.8
1	4-N	239[D]	ALA	12.8
1	1-M	290[A]	GLY	12.8
1	2-M	290[B]	GLY	12.8
1	3-M	290[C]	GLY	12.8
1	4-M	290[D]	GLY	12.8
1	1-K	45[A]	THR	12.7
1	2-K	45[B]	THR	12.7
1	3-K	45[C]	THR	12.7
1	4-K	45[D]	THR	12.7
1	1-L	151[A]	ASP	12.7
1	2-L	151[B]	ASP	12.7
1	3-L	151[C]	ASP	12.7
1	4-L	151[D]	ASP	12.7
1	1-I	48[A]	LEU	12.7
1	1-N	203[A]	PRO	12.7
1	2-I	48[B]	LEU	12.7

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Mol	Chain	Res	Type	RSRZ
1	2-N	203[B]	PRO	12.7
1	3-I	48[C]	LEU	12.7
1	3-N	203[C]	PRO	12.7
1	4-I	48[D]	LEU	12.7
1	4-N	203[D]	PRO	12.7
1	1-J	65[A]	LEU	12.6
1	2-J	65[B]	LEU	12.6
1	3-J	65[C]	LEU	12.6
1	4-J	65[D]	LEU	12.6
1	1-M	54[A]	PHE	12.6
1	2-M	54[B]	PHE	12.6
1	3-M	54[C]	PHE	12.6
1	4-M	54[D]	PHE	12.6
1	1-P	181[A]	LEU	12.6
1	2-P	181[B]	LEU	12.6
1	3-P	181[C]	LEU	12.6
1	4-P	181[D]	LEU	12.6
1	1-K	59[A]	ALA	12.5
1	2-K	59[B]	ALA	12.5
1	3-K	59[C]	ALA	12.5
1	4-K	59[D]	ALA	12.5
1	1-P	129[A]	PHE	12.5
1	2-P	129[B]	PHE	12.5
1	3-P	129[C]	PHE	12.5
1	4-P	129[D]	PHE	12.5
1	1-J	238[A]	ILE	12.4
1	2-J	238[B]	ILE	12.4
1	3-J	238[C]	ILE	12.4
1	4-J	238[D]	ILE	12.4
1	1-I	82[A]	TRP	12.4
1	2-I	82[B]	TRP	12.4
1	3-I	82[C]	TRP	12.4
1	4-I	82[D]	TRP	12.4
1	1-L	221[A]	GLY	12.3
1	2-L	221[B]	GLY	12.3
1	3-L	221[C]	GLY	12.3
1	4-L	221[D]	GLY	12.3
1	1-K	108[A]	GLU	12.3
1	1-M	100[A]	ILE	12.3
1	2-K	108[B]	GLU	12.3
1	2-M	100[B]	ILE	12.3
1	3-K	108[C]	GLU	12.3

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Mol	Chain	Res	Type	RSRZ
1	3-M	100[C]	ILE	12.3
1	4-K	108[D]	GLU	12.3
1	4-M	100[D]	ILE	12.3
1	1-J	183[A]	ALA	12.3
1	2-J	183[B]	ALA	12.3
1	3-J	183[C]	ALA	12.3
1	4-J	183[D]	ALA	12.3
1	1-J	66[A]	LEU	12.2
1	2-J	66[B]	LEU	12.2
1	3-J	66[C]	LEU	12.2
1	4-J	66[D]	LEU	12.2
1	1-O	59[A]	ALA	12.2
1	2-O	59[B]	ALA	12.2
1	3-O	59[C]	ALA	12.2
1	4-O	59[D]	ALA	12.2
1	1-O	31[A]	ILE	12.1
1	2-O	31[B]	ILE	12.1
1	3-O	31[C]	ILE	12.1
1	4-O	31[D]	ILE	12.1
1	1-N	27[A]	ILE	12.1
1	2-N	27[B]	ILE	12.1
1	3-N	27[C]	ILE	12.1
1	4-N	27[D]	ILE	12.1
1	1-K	183[A]	ALA	12.1
1	1-N	180[A]	PRO	12.1
1	2-K	183[B]	ALA	12.1
1	2-N	180[B]	PRO	12.1
1	3-K	183[C]	ALA	12.1
1	3-N	180[C]	PRO	12.1
1	4-K	183[D]	ALA	12.1
1	4-N	180[D]	PRO	12.1
1	1-L	263[A]	VAL	12.1
1	2-L	263[B]	VAL	12.1
1	3-L	263[C]	VAL	12.1
1	4-L	263[D]	VAL	12.1
1	1-I	269[A]	GLN	12.1
1	2-I	269[B]	GLN	12.1
1	3-I	269[C]	GLN	12.1
1	4-I	269[D]	GLN	12.1
1	1-O	127[A]	TYR	12.1
1	2-O	127[B]	TYR	12.1
1	3-O	127[C]	TYR	12.1

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Mol	Chain	Res	Type	RSRZ
1	4-O	127[D]	TYR	12.1
1	1-M	308[A]	TRP	12.0
1	2-M	308[B]	TRP	12.0
1	3-M	308[C]	TRP	12.0
1	4-M	308[D]	TRP	12.0
1	1-N	115[A]	LEU	12.0
1	2-N	115[B]	LEU	12.0
1	3-N	115[C]	LEU	12.0
1	4-N	115[D]	LEU	12.0
1	1-M	302[A]	VAL	12.0
1	2-M	302[B]	VAL	12.0
1	3-M	302[C]	VAL	12.0
1	4-M	302[D]	VAL	12.0
1	1-M	268[A]	THR	12.0
1	2-M	268[B]	THR	12.0
1	3-M	268[C]	THR	12.0
1	4-M	268[D]	THR	12.0
1	1-O	73[A]	LEU	12.0
1	2-O	73[B]	LEU	12.0
1	3-O	73[C]	LEU	12.0
1	4-O	73[D]	LEU	12.0
1	1-I	138[A]	TYR	11.9
1	2-I	138[B]	TYR	11.9
1	3-I	138[C]	TYR	11.9
1	4-I	138[D]	TYR	11.9
1	1-L	186[A]	PRO	11.9
1	2-L	186[B]	PRO	11.9
1	3-L	186[C]	PRO	11.9
1	4-L	186[D]	PRO	11.9
1	1-K	218[A]	CYS	11.8
1	2-K	218[B]	CYS	11.8
1	3-K	218[C]	CYS	11.8
1	4-K	218[D]	CYS	11.8
1	1-I	27[A]	ILE	11.8
1	2-I	27[B]	ILE	11.8
1	3-I	27[C]	ILE	11.8
1	4-I	27[D]	ILE	11.8
1	1-J	274[A]	PRO	11.8
1	1-N	51[A]	PRO	11.8
1	2-J	274[B]	PRO	11.8
1	2-N	51[B]	PRO	11.8
1	3-J	274[C]	PRO	11.8

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Mol	Chain	Res	Type	RSRZ
1	3-N	51[C]	PRO	11.8
1	4-J	274[D]	PRO	11.8
1	4-N	51[D]	PRO	11.8
1	1-J	285[A]	SER	11.7
1	2-J	285[B]	SER	11.7
1	3-J	285[C]	SER	11.7
1	4-J	285[D]	SER	11.7
1	1-P	134[A]	PHE	11.7
1	2-P	134[B]	PHE	11.7
1	3-P	134[C]	PHE	11.7
1	4-P	134[D]	PHE	11.7
1	1-K	131[A]	TRP	11.6
1	2-K	131[B]	TRP	11.6
1	3-K	131[C]	TRP	11.6
1	4-K	131[D]	TRP	11.6
1	1-I	160[A]	ILE	11.6
1	2-I	160[B]	ILE	11.6
1	3-I	160[C]	ILE	11.6
1	4-I	160[D]	ILE	11.6
1	1-M	31[A]	ILE	11.5
1	2-M	31[B]	ILE	11.5
1	3-M	31[C]	ILE	11.5
1	4-M	31[D]	ILE	11.5
1	1-I	186[A]	PRO	11.5
1	2-I	186[B]	PRO	11.5
1	3-I	186[C]	PRO	11.5
1	4-I	186[D]	PRO	11.5
1	1-I	30[A]	ILE	11.5
1	2-I	30[B]	ILE	11.5
1	3-I	30[C]	ILE	11.5
1	4-I	30[D]	ILE	11.5
1	1-K	99[A]	GLY	11.4
1	2-K	99[B]	GLY	11.4
1	3-K	99[C]	GLY	11.4
1	4-K	99[D]	GLY	11.4
1	1-L	254[A]	GLY	11.4
1	2-L	254[B]	GLY	11.4
1	3-L	254[C]	GLY	11.4
1	4-L	254[D]	GLY	11.4
1	1-K	229[A]	ALA	11.4
1	2-K	229[B]	ALA	11.4
1	3-K	229[C]	ALA	11.4

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Mol	Chain	Res	Type	RSRZ
1	4-K	229[D]	ALA	11.4
1	1-I	88[A]	THR	11.4
1	2-I	88[B]	THR	11.4
1	3-I	88[C]	THR	11.4
1	4-I	88[D]	THR	11.4
1	1-P	65[A]	LEU	11.3
1	2-P	65[B]	LEU	11.3
1	3-P	65[C]	LEU	11.3
1	4-P	65[D]	LEU	11.3
1	1-N	47[A]	ALA	11.3
1	2-N	47[B]	ALA	11.3
1	3-N	47[C]	ALA	11.3
1	4-N	47[D]	ALA	11.3
1	1-K	300[A]	PHE	11.3
1	2-K	300[B]	PHE	11.3
1	3-K	300[C]	PHE	11.3
1	4-K	300[D]	PHE	11.3
1	1-L	273[A]	GLU	11.3
1	2-L	273[B]	GLU	11.3
1	3-L	273[C]	GLU	11.3
1	4-L	273[D]	GLU	11.3
1	1-O	250[A]	ILE	11.2
1	2-O	250[B]	ILE	11.2
1	3-O	250[C]	ILE	11.2
1	4-O	250[D]	ILE	11.2
1	1-K	317[A]	ALA	11.2
1	2-K	317[B]	ALA	11.2
1	3-K	317[C]	ALA	11.2
1	4-K	317[D]	ALA	11.2
1	1-M	95[A]	SER	11.2
1	2-M	95[B]	SER	11.2
1	3-M	95[C]	SER	11.2
1	4-M	95[D]	SER	11.2
1	1-L	259[A]	TYR	11.2
1	2-L	259[B]	TYR	11.2
1	3-L	259[C]	TYR	11.2
1	4-L	259[D]	TYR	11.2
1	1-J	180[A]	PRO	11.2
1	2-J	180[B]	PRO	11.2
1	3-J	180[C]	PRO	11.2
1	4-J	180[D]	PRO	11.2
1	1-L	199[A]	PRO	11.1

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Mol	Chain	Res	Type	RSRZ
1	2-L	199[B]	PRO	11.1
1	3-L	199[C]	PRO	11.1
1	4-L	199[D]	PRO	11.1
1	1-P	226[A]	PHE	11.1
1	2-P	226[B]	PHE	11.1
1	3-P	226[C]	PHE	11.1
1	4-P	226[D]	PHE	11.1
1	1-I	205[A]	SER	11.1
1	1-K	305[A]	TYR	11.1
1	2-I	205[B]	SER	11.1
1	2-K	305[B]	TYR	11.1
1	3-I	205[C]	SER	11.1
1	3-K	305[C]	TYR	11.1
1	4-I	205[D]	SER	11.1
1	4-K	305[D]	TYR	11.1
1	1-P	199[A]	PRO	11.1
1	2-P	199[B]	PRO	11.1
1	3-P	199[C]	PRO	11.1
1	4-P	199[D]	PRO	11.1
1	1-L	220[A]	LEU	11.1
1	2-L	220[B]	LEU	11.1
1	3-L	220[C]	LEU	11.1
1	4-L	220[D]	LEU	11.1
1	1-N	100[A]	ILE	11.1
1	2-N	100[B]	ILE	11.1
1	3-N	100[C]	ILE	11.1
1	4-N	100[D]	ILE	11.1
1	1-O	96[A]	GLN	11.1
1	2-O	96[B]	GLN	11.1
1	3-O	96[C]	GLN	11.1
1	4-O	96[D]	GLN	11.1
1	1-O	42[A]	GLY	11.1
1	2-O	42[B]	GLY	11.1
1	3-O	42[C]	GLY	11.1
1	4-O	42[D]	GLY	11.1
1	1-M	187[A]	CYS	11.0
1	2-M	187[B]	CYS	11.0
1	3-M	187[C]	CYS	11.0
1	4-M	187[D]	CYS	11.0
1	1-L	46[A]	VAL	11.0
1	2-L	46[B]	VAL	11.0
1	3-L	46[C]	VAL	11.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	4-L	46[D]	VAL	11.0
1	1-P	17[A]	ASP	11.0
1	2-P	17[B]	ASP	11.0
1	3-P	17[C]	ASP	11.0
1	4-P	17[D]	ASP	11.0
1	1-O	99[A]	GLY	11.0
1	2-O	99[B]	GLY	11.0
1	3-O	99[C]	GLY	11.0
1	4-O	99[D]	GLY	11.0
1	1-O	211[A]	CYS	11.0
1	2-O	211[B]	CYS	11.0
1	3-O	211[C]	CYS	11.0
1	4-O	211[D]	CYS	11.0
1	1-L	88[A]	THR	11.0
1	2-L	88[B]	THR	11.0
1	3-L	88[C]	THR	11.0
1	4-L	88[D]	THR	11.0
1	1-M	47[A]	ALA	10.9
1	2-M	47[B]	ALA	10.9
1	3-M	47[C]	ALA	10.9
1	4-M	47[D]	ALA	10.9
1	1-M	77[A]	ILE	10.9
1	2-M	77[B]	ILE	10.9
1	3-M	77[C]	ILE	10.9
1	4-M	77[D]	ILE	10.9
1	1-I	93[A]	LEU	10.9
1	2-I	93[B]	LEU	10.9
1	3-I	93[C]	LEU	10.9
1	4-I	93[D]	LEU	10.9
1	1-M	169[A]	ILE	10.9
1	2-M	169[B]	ILE	10.9
1	3-M	169[C]	ILE	10.9
1	4-M	169[D]	ILE	10.9
1	1-N	139[A]	THR	10.9
1	2-N	139[B]	THR	10.9
1	3-N	139[C]	THR	10.9
1	4-N	139[D]	THR	10.9
1	1-J	54[A]	PHE	10.9
1	2-J	54[B]	PHE	10.9
1	3-J	54[C]	PHE	10.9
1	4-J	54[D]	PHE	10.9
1	1-I	64[A]	PRO	10.8

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Mol	Chain	Res	Type	RSRZ
1	2-I	64[B]	PRO	10.8
1	3-I	64[C]	PRO	10.8
1	4-I	64[D]	PRO	10.8
1	1-O	82[A]	TRP	10.8
1	2-O	82[B]	TRP	10.8
1	3-O	82[C]	TRP	10.8
1	4-O	82[D]	TRP	10.8
1	1-O	205[A]	SER	10.8
1	2-O	205[B]	SER	10.8
1	3-O	205[C]	SER	10.8
1	4-O	205[D]	SER	10.8
1	1-K	16[A]	PRO	10.8
1	2-K	16[B]	PRO	10.8
1	3-K	16[C]	PRO	10.8
1	4-K	16[D]	PRO	10.8
1	1-P	185[A]	PRO	10.7
1	2-P	185[B]	PRO	10.7
1	3-P	185[C]	PRO	10.7
1	4-P	185[D]	PRO	10.7
1	1-J	95[A]	SER	10.7
1	2-J	95[B]	SER	10.7
1	3-J	95[C]	SER	10.7
1	4-J	95[D]	SER	10.7
1	1-K	93[A]	LEU	10.7
1	2-K	93[B]	LEU	10.7
1	3-K	93[C]	LEU	10.7
1	4-K	93[D]	LEU	10.7
1	1-N	211[A]	CYS	10.7
1	2-N	211[B]	CYS	10.7
1	3-N	211[C]	CYS	10.7
1	4-N	211[D]	CYS	10.7
1	1-P	97[A]	GLY	10.7
1	2-P	97[B]	GLY	10.7
1	3-P	97[C]	GLY	10.7
1	4-P	97[D]	GLY	10.7
1	1-P	72[A]	PHE	10.6
1	2-P	72[B]	PHE	10.6
1	3-P	72[C]	PHE	10.6
1	4-P	72[D]	PHE	10.6
1	1-J	225[A]	PRO	10.6
1	2-J	225[B]	PRO	10.6
1	3-J	225[C]	PRO	10.6

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Mol	Chain	Res	Type	RSRZ
1	4-J	225[D]	PRO	10.6
1	1-J	115[A]	LEU	10.6
1	2-J	115[B]	LEU	10.6
1	3-J	115[C]	LEU	10.6
1	4-J	115[D]	LEU	10.6
1	1-K	249[A]	PHE	10.6
1	2-K	249[B]	PHE	10.6
1	3-K	249[C]	PHE	10.6
1	4-K	249[D]	PHE	10.6
1	1-K	115[A]	LEU	10.5
1	2-K	115[B]	LEU	10.5
1	3-K	115[C]	LEU	10.5
1	4-K	115[D]	LEU	10.5
1	1-J	30[A]	ILE	10.5
1	2-J	30[B]	ILE	10.5
1	3-J	30[C]	ILE	10.5
1	4-J	30[D]	ILE	10.5
1	1-O	141[A]	ALA	10.5
1	2-O	141[B]	ALA	10.5
1	3-O	141[C]	ALA	10.5
1	4-O	141[D]	ALA	10.5
1	1-P	230[A]	SER	10.5
1	2-P	230[B]	SER	10.5
1	3-P	230[C]	SER	10.5
1	4-P	230[D]	SER	10.5
1	1-M	190[A]	PHE	10.5
1	2-M	190[B]	PHE	10.5
1	3-M	190[C]	PHE	10.5
1	4-M	190[D]	PHE	10.5
1	1-J	63[A]	LEU	10.5
1	1-K	240[A]	LEU	10.5
1	2-J	63[B]	LEU	10.5
1	2-K	240[B]	LEU	10.5
1	3-J	63[C]	LEU	10.5
1	3-K	240[C]	LEU	10.5
1	4-J	63[D]	LEU	10.5
1	4-K	240[D]	LEU	10.5
1	1-O	136[A]	ALA	10.5
1	2-O	136[B]	ALA	10.5
1	3-O	136[C]	ALA	10.5
1	4-O	136[D]	ALA	10.5
1	1-J	131[A]	TRP	10.5

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Mol	Chain	Res	Type	RSRZ
1	2-J	131[B]	TRP	10.5
1	3-J	131[C]	TRP	10.5
1	4-J	131[D]	TRP	10.5
1	1-J	305[A]	TYR	10.5
1	1-P	127[A]	TYR	10.5
1	2-J	305[B]	TYR	10.5
1	2-P	127[B]	TYR	10.5
1	3-J	305[C]	TYR	10.5
1	3-P	127[C]	TYR	10.5
1	4-J	305[D]	TYR	10.5
1	4-P	127[D]	TYR	10.5
1	1-M	250[A]	ILE	10.4
1	2-M	250[B]	ILE	10.4
1	3-M	250[C]	ILE	10.4
1	4-M	250[D]	ILE	10.4
1	1-O	50[A]	ALA	10.4
1	2-O	50[B]	ALA	10.4
1	3-O	50[C]	ALA	10.4
1	4-O	50[D]	ALA	10.4
1	1-O	285[A]	SER	10.4
1	2-O	285[B]	SER	10.4
1	3-O	285[C]	SER	10.4
1	4-O	285[D]	SER	10.4
1	1-K	103[A]	GLY	10.4
1	1-N	204[A]	GLY	10.4
1	2-K	103[B]	GLY	10.4
1	2-N	204[B]	GLY	10.4
1	3-K	103[C]	GLY	10.4
1	3-N	204[C]	GLY	10.4
1	4-K	103[D]	GLY	10.4
1	4-N	204[D]	GLY	10.4
1	1-P	156[A]	VAL	10.4
1	2-P	156[B]	VAL	10.4
1	3-P	156[C]	VAL	10.4
1	4-P	156[D]	VAL	10.4
1	1-L	134[A]	PHE	10.4
1	2-L	134[B]	PHE	10.4
1	3-L	134[C]	PHE	10.4
1	4-L	134[D]	PHE	10.4
1	1-N	60[A]	ASP	10.4
1	2-N	60[B]	ASP	10.4
1	3-N	60[C]	ASP	10.4

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Mol	Chain	Res	Type	RSRZ
1	4-N	60[D]	ASP	10.4
1	1-J	191[A]	CYS	10.3
1	2-J	191[B]	CYS	10.3
1	3-J	191[C]	CYS	10.3
1	4-J	191[D]	CYS	10.3
1	1-K	238[A]	ILE	10.3
1	2-K	238[B]	ILE	10.3
1	3-K	238[C]	ILE	10.3
1	4-K	238[D]	ILE	10.3
1	1-I	203[A]	PRO	10.2
1	2-I	203[B]	PRO	10.2
1	3-I	203[C]	PRO	10.2
1	4-I	203[D]	PRO	10.2
1	1-P	214[A]	TYR	10.2
1	2-P	214[B]	TYR	10.2
1	3-P	214[C]	TYR	10.2
1	4-P	214[D]	TYR	10.2
1	1-O	16[A]	PRO	10.2
1	2-O	16[B]	PRO	10.2
1	3-O	16[C]	PRO	10.2
1	4-O	16[D]	PRO	10.2
1	1-K	49[A]	PHE	10.2
1	2-K	49[B]	PHE	10.2
1	3-K	49[C]	PHE	10.2
1	4-K	49[D]	PHE	10.2
1	1-K	179[A]	LEU	10.2
1	2-K	179[B]	LEU	10.2
1	3-K	179[C]	LEU	10.2
1	4-K	179[D]	LEU	10.2
1	1-I	293[A]	ASP	10.2
1	2-I	293[B]	ASP	10.2
1	3-I	293[C]	ASP	10.2
1	4-I	293[D]	ASP	10.2
1	1-M	174[A]	TRP	10.2
1	2-M	174[B]	TRP	10.2
1	3-M	174[C]	TRP	10.2
1	4-M	174[D]	TRP	10.2
1	1-O	235[A]	THR	10.1
1	2-O	235[B]	THR	10.1
1	3-O	235[C]	THR	10.1
1	4-O	235[D]	THR	10.1
1	1-O	100[A]	ILE	10.1

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Mol	Chain	Res	Type	RSRZ
1	2-O	100[B]	ILE	10.1
1	3-O	100[C]	ILE	10.1
1	4-O	100[D]	ILE	10.1
1	1-J	246[A]	PRO	10.1
1	2-J	246[B]	PRO	10.1
1	3-J	246[C]	PRO	10.1
1	4-J	246[D]	PRO	10.1
1	1-L	55[A]	ARG	10.1
1	2-L	55[B]	ARG	10.1
1	3-L	55[C]	ARG	10.1
1	4-L	55[D]	ARG	10.1
1	1-K	138[A]	TYR	10.0
1	2-K	138[B]	TYR	10.0
1	3-K	138[C]	TYR	10.0
1	4-K	138[D]	TYR	10.0
1	1-J	300[A]	PHE	10.0
1	2-J	300[B]	PHE	10.0
1	3-J	300[C]	PHE	10.0
1	4-J	300[D]	PHE	10.0
1	1-K	143[A]	GLY	10.0
1	2-K	143[B]	GLY	10.0
1	3-K	143[C]	GLY	10.0
1	4-K	143[D]	GLY	10.0
1	1-L	64[A]	PRO	10.0
1	1-N	109[A]	PHE	10.0
1	2-L	64[B]	PRO	10.0
1	2-N	109[B]	PHE	10.0
1	3-L	64[C]	PRO	10.0
1	3-N	109[C]	PHE	10.0
1	4-L	64[D]	PRO	10.0
1	4-N	109[D]	PHE	10.0
1	1-N	24[A]	LEU	10.0
1	2-N	24[B]	LEU	10.0
1	3-N	24[C]	LEU	10.0
1	4-N	24[D]	LEU	10.0
1	1-I	229[A]	ALA	10.0
1	2-I	229[B]	ALA	10.0
1	3-I	229[C]	ALA	10.0
1	4-I	229[D]	ALA	10.0
1	1-I	134[A]	PHE	10.0
1	2-I	134[B]	PHE	10.0
1	3-I	134[C]	PHE	10.0

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Mol	Chain	Res	Type	RSRZ
1	4-I	134[D]	PHE	10.0
1	1-P	63[A]	LEU	10.0
1	2-P	63[B]	LEU	10.0
1	3-P	63[C]	LEU	10.0
1	4-P	63[D]	LEU	10.0
1	1-M	188[A]	HIS	10.0
1	2-M	188[B]	HIS	10.0
1	3-M	188[C]	HIS	10.0
1	4-M	188[D]	HIS	10.0
1	1-K	270[A]	LEU	10.0
1	1-N	181[A]	LEU	10.0
1	2-K	270[B]	LEU	10.0
1	2-N	181[B]	LEU	10.0
1	3-K	270[C]	LEU	10.0
1	3-N	181[C]	LEU	10.0
1	4-K	270[D]	LEU	10.0
1	4-N	181[D]	LEU	10.0
1	1-I	191[A]	CYS	9.9
1	2-I	191[B]	CYS	9.9
1	3-I	191[C]	CYS	9.9
1	4-I	191[D]	CYS	9.9
1	1-J	119[A]	ARG	9.9
1	2-J	119[B]	ARG	9.9
1	3-J	119[C]	ARG	9.9
1	4-J	119[D]	ARG	9.9
1	1-N	223[A]	GLY	9.9
1	2-N	223[B]	GLY	9.9
1	3-N	223[C]	GLY	9.9
1	4-N	223[D]	GLY	9.9
1	1-M	317[A]	ALA	9.9
1	2-M	317[B]	ALA	9.9
1	3-M	317[C]	ALA	9.9
1	4-M	317[D]	ALA	9.9
1	1-L	145[A]	TYR	9.9
1	2-L	145[B]	TYR	9.9
1	3-L	145[C]	TYR	9.9
1	4-L	145[D]	TYR	9.9
1	1-I	101[A]	TRP	9.9
1	2-I	101[B]	TRP	9.9
1	3-I	101[C]	TRP	9.9
1	4-I	101[D]	TRP	9.9
1	1-M	124[A]	GLY	9.9

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Mol	Chain	Res	Type	RSRZ
1	2-M	124[B]	GLY	9.9
1	3-M	124[C]	GLY	9.9
1	4-M	124[D]	GLY	9.9
1	1-O	115[A]	LEU	9.9
1	2-O	115[B]	LEU	9.9
1	3-O	115[C]	LEU	9.9
1	4-O	115[D]	LEU	9.9
1	1-J	47[A]	ALA	9.9
1	2-J	47[B]	ALA	9.9
1	3-J	47[C]	ALA	9.9
1	4-J	47[D]	ALA	9.9
1	1-I	305[A]	TYR	9.9
1	2-I	305[B]	TYR	9.9
1	3-I	305[C]	TYR	9.9
1	4-I	305[D]	TYR	9.9
1	1-O	173[A]	ALA	9.9
1	2-O	173[B]	ALA	9.9
1	3-O	173[C]	ALA	9.9
1	4-O	173[D]	ALA	9.9
1	1-I	36[A]	VAL	9.9
1	2-I	36[B]	VAL	9.9
1	3-I	36[C]	VAL	9.9
1	4-I	36[D]	VAL	9.9
1	1-J	268[A]	THR	9.9
1	2-J	268[B]	THR	9.9
1	3-J	268[C]	THR	9.9
1	4-J	268[D]	THR	9.9
1	1-N	31[A]	ILE	9.9
1	2-N	31[B]	ILE	9.9
1	3-N	31[C]	ILE	9.9
1	4-N	31[D]	ILE	9.9
1	1-I	214[A]	TYR	9.8
1	2-I	214[B]	TYR	9.8
1	3-I	214[C]	TYR	9.8
1	4-I	214[D]	TYR	9.8
1	1-N	234[A]	LEU	9.8
1	2-N	234[B]	LEU	9.8
1	3-N	234[C]	LEU	9.8
1	4-N	234[D]	LEU	9.8
1	1-L	98[A]	VAL	9.8
1	2-L	98[B]	VAL	9.8
1	3-L	98[C]	VAL	9.8

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Mol	Chain	Res	Type	RSRZ
1	4-L	98[D]	VAL	9.8
1	1-L	212[A]	LEU	9.8
1	2-L	212[B]	LEU	9.8
1	3-L	212[C]	LEU	9.8
1	4-L	212[D]	LEU	9.8
1	1-P	143[A]	GLY	9.8
1	2-P	143[B]	GLY	9.8
1	3-P	143[C]	GLY	9.8
1	4-P	143[D]	GLY	9.8
1	1-P	315[A]	MET	9.8
1	2-P	315[B]	MET	9.8
1	3-P	315[C]	MET	9.8
1	4-P	315[D]	MET	9.8
1	1-K	104[A]	ASN	9.8
1	2-K	104[B]	ASN	9.8
1	3-K	104[C]	ASN	9.8
1	4-K	104[D]	ASN	9.8
1	1-J	281[A]	LYS	9.8
1	2-J	281[B]	LYS	9.8
1	3-J	281[C]	LYS	9.8
1	4-J	281[D]	LYS	9.8
1	1-M	309[A]	GLY	9.7
1	1-O	316[A]	SER	9.7
1	2-M	309[B]	GLY	9.7
1	2-O	316[B]	SER	9.7
1	3-M	309[C]	GLY	9.7
1	3-O	316[C]	SER	9.7
1	4-M	309[D]	GLY	9.7
1	4-O	316[D]	SER	9.7
1	1-L	31[A]	ILE	9.7
1	2-L	31[B]	ILE	9.7
1	3-L	31[C]	ILE	9.7
1	4-L	31[D]	ILE	9.7
1	1-M	98[A]	VAL	9.7
1	2-M	98[B]	VAL	9.7
1	3-M	98[C]	VAL	9.7
1	4-M	98[D]	VAL	9.7
1	1-I	314[A]	LYS	9.7
1	1-L	32[A]	ASN	9.7
1	2-I	314[B]	LYS	9.7
1	2-L	32[B]	ASN	9.7
1	3-I	314[C]	LYS	9.7

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Mol	Chain	Res	Type	RSRZ
1	3-L	32[C]	ASN	9.7
1	4-I	314[D]	LYS	9.7
1	4-L	32[D]	ASN	9.7
1	1-L	187[A]	CYS	9.7
1	1-M	218[A]	CYS	9.7
1	2-L	187[B]	CYS	9.7
1	2-M	218[B]	CYS	9.7
1	3-L	187[C]	CYS	9.7
1	3-M	218[C]	CYS	9.7
1	4-L	187[D]	CYS	9.7
1	4-M	218[D]	CYS	9.7
1	1-P	87[A]	CYS	9.7
1	2-P	87[B]	CYS	9.7
1	3-P	87[C]	CYS	9.7
1	4-P	87[D]	CYS	9.7
1	1-L	167[A]	ARG	9.7
1	2-L	167[B]	ARG	9.7
1	3-L	167[C]	ARG	9.7
1	4-L	167[D]	ARG	9.7
1	1-K	98[A]	VAL	9.6
1	2-K	98[B]	VAL	9.6
1	3-K	98[C]	VAL	9.6
1	4-K	98[D]	VAL	9.6
1	1-P	28[A]	ARG	9.6
1	2-P	28[B]	ARG	9.6
1	3-P	28[C]	ARG	9.6
1	4-P	28[D]	ARG	9.6
1	1-M	91[A]	LYS	9.6
1	2-M	91[B]	LYS	9.6
1	3-M	91[C]	LYS	9.6
1	4-M	91[D]	LYS	9.6
1	1-M	27[A]	ILE	9.6
1	2-M	27[B]	ILE	9.6
1	3-M	27[C]	ILE	9.6
1	4-M	27[D]	ILE	9.6
1	1-K	60[A]	ASP	9.6
1	1-O	26[A]	LEU	9.6
1	2-K	60[B]	ASP	9.6
1	2-O	26[B]	LEU	9.6
1	3-K	60[C]	ASP	9.6
1	3-O	26[C]	LEU	9.6
1	4-K	60[D]	ASP	9.6

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Mol	Chain	Res	Type	RSRZ
1	4-O	26[D]	LEU	9.6
1	1-O	231[A]	TYR	9.6
1	2-O	231[B]	TYR	9.6
1	3-O	231[C]	TYR	9.6
1	4-O	231[D]	TYR	9.6
1	1-K	33[A]	VAL	9.6
1	1-N	195[A]	VAL	9.6
1	2-K	33[B]	VAL	9.6
1	2-N	195[B]	VAL	9.6
1	3-K	33[C]	VAL	9.6
1	3-N	195[C]	VAL	9.6
1	4-K	33[D]	VAL	9.6
1	4-N	195[D]	VAL	9.6
1	1-P	116[A]	GLY	9.6
1	2-P	116[B]	GLY	9.6
1	3-P	116[C]	GLY	9.6
1	4-P	116[D]	GLY	9.6
1	1-M	295[A]	PHE	9.6
1	2-M	295[B]	PHE	9.6
1	3-M	295[C]	PHE	9.6
1	4-M	295[D]	PHE	9.6
1	1-N	142[A]	ASP	9.6
1	2-N	142[B]	ASP	9.6
1	3-N	142[C]	ASP	9.6
1	4-N	142[D]	ASP	9.6
1	1-O	49[A]	PHE	9.6
1	2-O	49[B]	PHE	9.6
1	3-O	49[C]	PHE	9.6
1	4-O	49[D]	PHE	9.6
1	1-L	127[A]	TYR	9.6
1	1-L	138[A]	TYR	9.6
1	2-L	127[B]	TYR	9.6
1	2-L	138[B]	TYR	9.6
1	3-L	127[C]	TYR	9.6
1	3-L	138[C]	TYR	9.6
1	4-L	127[D]	TYR	9.6
1	4-L	138[D]	TYR	9.6
1	1-N	309[A]	GLY	9.6
1	2-N	309[B]	GLY	9.6
1	3-N	309[C]	GLY	9.6
1	4-N	309[D]	GLY	9.6
1	1-N	266[A]	LEU	9.5

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Mol	Chain	Res	Type	RSRZ
1	1-O	197[A]	LEU	9.5
1	2-N	266[B]	LEU	9.5
1	2-O	197[B]	LEU	9.5
1	3-N	266[C]	LEU	9.5
1	3-O	197[C]	LEU	9.5
1	4-N	266[D]	LEU	9.5
1	4-O	197[D]	LEU	9.5
1	1-K	26[A]	LEU	9.5
1	1-N	209[A]	LEU	9.5
1	2-K	26[B]	LEU	9.5
1	2-N	209[B]	LEU	9.5
1	3-K	26[C]	LEU	9.5
1	3-N	209[C]	LEU	9.5
1	4-K	26[D]	LEU	9.5
1	4-N	209[D]	LEU	9.5
1	1-J	103[A]	GLY	9.5
1	2-J	103[B]	GLY	9.5
1	3-J	103[C]	GLY	9.5
1	4-J	103[D]	GLY	9.5
1	1-L	173[A]	ALA	9.5
1	1-O	282[A]	TRP	9.5
1	2-L	173[B]	ALA	9.5
1	2-O	282[B]	TRP	9.5
1	3-L	173[C]	ALA	9.5
1	3-O	282[C]	TRP	9.5
1	4-L	173[D]	ALA	9.5
1	4-O	282[D]	TRP	9.5
1	1-N	17[A]	ASP	9.5
1	2-N	17[B]	ASP	9.5
1	3-N	17[C]	ASP	9.5
1	4-N	17[D]	ASP	9.5
1	1-P	92[A]	MET	9.5
1	2-P	92[B]	MET	9.5
1	3-P	92[C]	MET	9.5
1	4-P	92[D]	MET	9.5
1	1-M	266[A]	LEU	9.5
1	2-M	266[B]	LEU	9.5
1	3-M	266[C]	LEU	9.5
1	4-M	266[D]	LEU	9.5
1	1-L	66[A]	LEU	9.5
1	2-L	66[B]	LEU	9.5
1	3-L	66[C]	LEU	9.5

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Mol	Chain	Res	Type	RSRZ
1	4-L	66[D]	LEU	9.5
1	1-N	46[A]	VAL	9.5
1	2-N	46[B]	VAL	9.5
1	3-N	46[C]	VAL	9.5
1	4-N	46[D]	VAL	9.5
1	1-L	75[A]	GLY	9.5
1	2-L	75[B]	GLY	9.5
1	3-L	75[C]	GLY	9.5
1	4-L	75[D]	GLY	9.5
1	1-J	259[A]	TYR	9.4
1	2-J	259[B]	TYR	9.4
1	3-J	259[C]	TYR	9.4
1	4-J	259[D]	TYR	9.4
1	1-N	63[A]	LEU	9.4
1	1-N	161[A]	LYS	9.4
1	2-N	63[B]	LEU	9.4
1	2-N	161[B]	LYS	9.4
1	3-N	63[C]	LEU	9.4
1	3-N	161[C]	LYS	9.4
1	4-N	63[D]	LEU	9.4
1	4-N	161[D]	LYS	9.4
1	1-P	312[A]	ASP	9.4
1	2-P	312[B]	ASP	9.4
1	3-P	312[C]	ASP	9.4
1	4-P	312[D]	ASP	9.4
1	1-L	204[A]	GLY	9.4
1	1-O	66[A]	LEU	9.4
1	2-L	204[B]	GLY	9.4
1	2-O	66[B]	LEU	9.4
1	3-L	204[C]	GLY	9.4
1	3-O	66[C]	LEU	9.4
1	4-L	204[D]	GLY	9.4
1	4-O	66[D]	LEU	9.4
1	1-M	310[A]	LYS	9.4
1	2-M	310[B]	LYS	9.4
1	3-M	310[C]	LYS	9.4
1	4-M	310[D]	LYS	9.4
1	1-M	23[A]	TYR	9.4
1	2-M	23[B]	TYR	9.4
1	3-M	23[C]	TYR	9.4
1	4-M	23[D]	TYR	9.4
1	1-P	283[A]	ALA	9.4

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Mol	Chain	Res	Type	RSRZ
1	2-P	283[B]	ALA	9.4
1	3-P	283[C]	ALA	9.4
1	4-P	283[D]	ALA	9.4
1	1-J	16[A]	PRO	9.4
1	2-J	16[B]	PRO	9.4
1	3-J	16[C]	PRO	9.4
1	4-J	16[D]	PRO	9.4
1	1-M	300[A]	PHE	9.4
1	2-M	300[B]	PHE	9.4
1	3-M	300[C]	PHE	9.4
1	4-M	300[D]	PHE	9.4
1	1-M	305[A]	TYR	9.4
1	2-M	305[B]	TYR	9.4
1	3-M	305[C]	TYR	9.4
1	4-M	305[D]	TYR	9.4
1	1-O	183[A]	ALA	9.4
1	2-O	183[B]	ALA	9.4
1	3-O	183[C]	ALA	9.4
1	4-O	183[D]	ALA	9.4
1	1-P	93[A]	LEU	9.4
1	2-P	93[B]	LEU	9.4
1	3-P	93[C]	LEU	9.4
1	4-P	93[D]	LEU	9.4
1	1-O	33[A]	VAL	9.4
1	2-O	33[B]	VAL	9.4
1	3-O	33[C]	VAL	9.4
1	4-O	33[D]	VAL	9.4
1	1-K	87[A]	CYS	9.4
1	2-K	87[B]	CYS	9.4
1	3-K	87[C]	CYS	9.4
1	4-K	87[D]	CYS	9.4
1	1-I	206[A]	LYS	9.3
1	2-I	206[B]	LYS	9.3
1	3-I	206[C]	LYS	9.3
1	4-I	206[D]	LYS	9.3
1	1-P	183[A]	ALA	9.3
1	2-P	183[B]	ALA	9.3
1	3-P	183[C]	ALA	9.3
1	4-P	183[D]	ALA	9.3
1	1-I	45[A]	THR	9.3
1	2-I	45[B]	THR	9.3
1	3-I	45[C]	THR	9.3

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Mol	Chain	Res	Type	RSRZ
1	4-I	45[D]	THR	9.3
1	1-I	115[A]	LEU	9.3
1	2-I	115[B]	LEU	9.3
1	3-I	115[C]	LEU	9.3
1	4-I	115[D]	LEU	9.3
1	1-J	46[A]	VAL	9.3
1	2-J	46[B]	VAL	9.3
1	3-J	46[C]	VAL	9.3
1	4-J	46[D]	VAL	9.3
1	1-K	145[A]	TYR	9.3
1	2-K	145[B]	TYR	9.3
1	3-K	145[C]	TYR	9.3
1	4-K	145[D]	TYR	9.3
1	1-I	289[A]	ILE	9.3
1	2-I	289[B]	ILE	9.3
1	3-I	289[C]	ILE	9.3
1	4-I	289[D]	ILE	9.3
1	1-K	239[A]	ALA	9.3
1	2-K	239[B]	ALA	9.3
1	3-K	239[C]	ALA	9.3
1	4-K	239[D]	ALA	9.3
1	1-K	226[A]	PHE	9.3
1	1-L	165[A]	THR	9.3
1	2-K	226[B]	PHE	9.3
1	2-L	165[B]	THR	9.3
1	3-K	226[C]	PHE	9.3
1	3-L	165[C]	THR	9.3
1	4-K	226[D]	PHE	9.3
1	4-L	165[D]	THR	9.3
1	1-I	225[A]	PRO	9.3
1	2-I	225[B]	PRO	9.3
1	3-I	225[C]	PRO	9.3
1	4-I	225[D]	PRO	9.3
1	1-P	173[A]	ALA	9.3
1	2-P	173[B]	ALA	9.3
1	3-P	173[C]	ALA	9.3
1	4-P	173[D]	ALA	9.3
1	1-L	251[A]	LEU	9.2
1	2-L	251[B]	LEU	9.2
1	3-L	251[C]	LEU	9.2
1	4-L	251[D]	LEU	9.2
1	1-J	27[A]	ILE	9.2

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Mol	Chain	Res	Type	RSRZ
1	2-J	27[B]	ILE	9.2
1	3-J	27[C]	ILE	9.2
1	4-J	27[D]	ILE	9.2
1	1-L	256[A]	ALA	9.2
1	1-P	105[A]	GLY	9.2
1	2-L	256[B]	ALA	9.2
1	2-P	105[B]	GLY	9.2
1	3-L	256[C]	ALA	9.2
1	3-P	105[C]	GLY	9.2
1	4-L	256[D]	ALA	9.2
1	4-P	105[D]	GLY	9.2
1	1-O	242[A]	THR	9.2
1	2-O	242[B]	THR	9.2
1	3-O	242[C]	THR	9.2
1	4-O	242[D]	THR	9.2
1	1-P	244[A]	THR	9.2
1	2-P	244[B]	THR	9.2
1	3-P	244[C]	THR	9.2
1	4-P	244[D]	THR	9.2
1	1-N	187[A]	CYS	9.2
1	2-N	187[B]	CYS	9.2
1	3-N	187[C]	CYS	9.2
1	4-N	187[D]	CYS	9.2
1	1-J	139[A]	THR	9.2
1	2-J	139[B]	THR	9.2
1	3-J	139[C]	THR	9.2
1	4-J	139[D]	THR	9.2
1	1-M	171[A]	LEU	9.2
1	2-M	171[B]	LEU	9.2
1	3-M	171[C]	LEU	9.2
1	4-M	171[D]	LEU	9.2
1	1-N	86[A]	GLY	9.2
1	2-N	86[B]	GLY	9.2
1	3-N	86[C]	GLY	9.2
1	4-N	86[D]	GLY	9.2
1	1-P	21[A]	TYR	9.1
1	2-P	21[B]	TYR	9.1
1	3-P	21[C]	TYR	9.1
1	4-P	21[D]	TYR	9.1
1	1-K	24[A]	LEU	9.1
1	1-O	110[A]	LEU	9.1
1	2-K	24[B]	LEU	9.1

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Mol	Chain	Res	Type	RSRZ
1	2-O	110[B]	LEU	9.1
1	3-K	24[C]	LEU	9.1
1	3-O	110[C]	LEU	9.1
1	4-K	24[D]	LEU	9.1
1	4-O	110[D]	LEU	9.1
1	1-K	265[A]	PRO	9.1
1	2-K	265[B]	PRO	9.1
1	3-K	265[C]	PRO	9.1
1	4-K	265[D]	PRO	9.1
1	1-P	302[A]	VAL	9.1
1	2-P	302[B]	VAL	9.1
1	3-P	302[C]	VAL	9.1
1	4-P	302[D]	VAL	9.1
1	1-M	70[A]	ARG	9.1
1	2-M	70[B]	ARG	9.1
1	3-M	70[C]	ARG	9.1
1	4-M	70[D]	ARG	9.1
1	1-M	90[A]	ALA	9.1
1	1-O	109[A]	PHE	9.1
1	1-O	194[A]	PHE	9.1
1	2-M	90[B]	ALA	9.1
1	2-O	109[B]	PHE	9.1
1	2-O	194[B]	PHE	9.1
1	3-M	90[C]	ALA	9.1
1	3-O	109[C]	PHE	9.1
1	3-O	194[C]	PHE	9.1
1	4-M	90[D]	ALA	9.1
1	4-O	109[D]	PHE	9.1
1	4-O	194[D]	PHE	9.1
1	1-I	52[A]	PRO	9.1
1	2-I	52[B]	PRO	9.1
1	3-I	52[C]	PRO	9.1
1	4-I	52[D]	PRO	9.1
1	1-K	128[A]	GLY	9.1
1	2-K	128[B]	GLY	9.1
1	3-K	128[C]	GLY	9.1
1	4-K	128[D]	GLY	9.1
1	1-O	260[A]	ARG	9.1
1	2-O	260[B]	ARG	9.1
1	3-O	260[C]	ARG	9.1
1	4-O	260[D]	ARG	9.1
1	1-I	171[A]	LEU	9.1

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Mol	Chain	Res	Type	RSRZ
1	2-I	171[B]	LEU	9.1
1	3-I	171[C]	LEU	9.1
1	4-I	171[D]	LEU	9.1
1	1-L	189[A]	MET	9.1
1	2-L	189[B]	MET	9.1
1	3-L	189[C]	MET	9.1
1	4-L	189[D]	MET	9.1
1	1-M	203[A]	PRO	9.1
1	2-M	203[B]	PRO	9.1
1	3-M	203[C]	PRO	9.1
1	4-M	203[D]	PRO	9.1
1	1-I	84[A]	VAL	9.1
1	2-I	84[B]	VAL	9.1
1	3-I	84[C]	VAL	9.1
1	4-I	84[D]	VAL	9.1
1	1-M	143[A]	GLY	9.1
1	1-P	47[A]	ALA	9.1
1	2-M	143[B]	GLY	9.1
1	2-P	47[B]	ALA	9.1
1	3-M	143[C]	GLY	9.1
1	3-P	47[C]	ALA	9.1
1	4-M	143[D]	GLY	9.1
1	4-P	47[D]	ALA	9.1
1	1-M	89[A]	ASP	9.0
1	2-M	89[B]	ASP	9.0
1	3-M	89[C]	ASP	9.0
1	4-M	89[D]	ASP	9.0
1	1-J	58[A]	LEU	9.0
1	2-J	58[B]	LEU	9.0
1	3-J	58[C]	LEU	9.0
1	4-J	58[D]	LEU	9.0
1	1-O	289[A]	ILE	9.0
1	2-O	289[B]	ILE	9.0
1	3-O	289[C]	ILE	9.0
1	4-O	289[D]	ILE	9.0
1	1-L	47[A]	ALA	9.0
1	2-L	47[B]	ALA	9.0
1	3-L	47[C]	ALA	9.0
1	4-L	47[D]	ALA	9.0
1	1-O	195[A]	VAL	9.0
1	2-O	195[B]	VAL	9.0
1	3-O	195[C]	VAL	9.0

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Mol	Chain	Res	Type	RSRZ
1	4-O	195[D]	VAL	9.0
1	1-N	250[A]	ILE	9.0
1	2-N	250[B]	ILE	9.0
1	3-N	250[C]	ILE	9.0
1	4-N	250[D]	ILE	9.0
1	1-M	105[A]	GLY	9.0
1	2-M	105[B]	GLY	9.0
1	3-M	105[C]	GLY	9.0
1	4-M	105[D]	GLY	9.0
1	1-O	46[A]	VAL	9.0
1	2-O	46[B]	VAL	9.0
1	3-O	46[C]	VAL	9.0
1	4-O	46[D]	VAL	9.0
1	1-I	311[A]	ILE	9.0
1	1-M	78[A]	ALA	9.0
1	2-I	311[B]	ILE	9.0
1	2-M	78[B]	ALA	9.0
1	3-I	311[C]	ILE	9.0
1	3-M	78[C]	ALA	9.0
1	4-I	311[D]	ILE	9.0
1	4-M	78[D]	ALA	9.0
1	1-N	265[A]	PRO	9.0
1	2-N	265[B]	PRO	9.0
1	3-N	265[C]	PRO	9.0
1	4-N	265[D]	PRO	9.0
1	1-L	136[A]	ALA	9.0
1	2-L	136[B]	ALA	9.0
1	3-L	136[C]	ALA	9.0
1	4-L	136[D]	ALA	9.0
1	1-O	60[A]	ASP	9.0
1	2-O	60[B]	ASP	9.0
1	3-O	60[C]	ASP	9.0
1	4-O	60[D]	ASP	9.0
1	1-J	174[A]	TRP	9.0
1	2-J	174[B]	TRP	9.0
1	3-J	174[C]	TRP	9.0
1	4-J	174[D]	TRP	9.0
1	1-O	38[A]	PRO	9.0
1	2-O	38[B]	PRO	9.0
1	3-O	38[C]	PRO	9.0
1	4-O	38[D]	PRO	9.0
1	1-I	81[A]	LEU	9.0

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Mol	Chain	Res	Type	RSRZ
1	1-K	266[A]	LEU	9.0
1	1-L	249[A]	PHE	9.0
1	2-I	81[B]	LEU	9.0
1	2-K	266[B]	LEU	9.0
1	2-L	249[B]	PHE	9.0
1	3-I	81[C]	LEU	9.0
1	3-K	266[C]	LEU	9.0
1	3-L	249[C]	PHE	9.0
1	4-I	81[D]	LEU	9.0
1	4-K	266[D]	LEU	9.0
1	4-L	249[D]	PHE	9.0
1	1-N	50[A]	ALA	9.0
1	1-P	232[A]	ALA	9.0
1	2-N	50[B]	ALA	9.0
1	2-P	232[B]	ALA	9.0
1	3-N	50[C]	ALA	9.0
1	3-P	232[C]	ALA	9.0
1	4-N	50[D]	ALA	9.0
1	4-P	232[D]	ALA	9.0
1	1-O	291[A]	ASP	8.9
1	2-O	291[B]	ASP	8.9
1	3-O	291[C]	ASP	8.9
1	4-O	291[D]	ASP	8.9
1	1-M	127[A]	TYR	8.9
1	2-M	127[B]	TYR	8.9
1	3-M	127[C]	TYR	8.9
1	4-M	127[D]	TYR	8.9
1	1-N	61[A]	ASN	8.9
1	2-N	61[B]	ASN	8.9
1	3-N	61[C]	ASN	8.9
1	4-N	61[D]	ASN	8.9
1	1-L	65[A]	LEU	8.9
1	2-L	65[B]	LEU	8.9
1	3-L	65[C]	LEU	8.9
1	4-L	65[D]	LEU	8.9
1	1-N	279[A]	LYS	8.9
1	2-N	279[B]	LYS	8.9
1	3-N	279[C]	LYS	8.9
1	4-N	279[D]	LYS	8.9
1	1-P	268[A]	THR	8.9
1	2-P	268[B]	THR	8.9
1	3-P	268[C]	THR	8.9

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Mol	Chain	Res	Type	RSRZ
1	4-P	268[D]	THR	8.9
1	1-O	294[A]	GLY	8.9
1	2-O	294[B]	GLY	8.9
1	3-O	294[C]	GLY	8.9
1	4-O	294[D]	GLY	8.9
1	1-I	197[A]	LEU	8.9
1	2-I	197[B]	LEU	8.9
1	3-I	197[C]	LEU	8.9
1	4-I	197[D]	LEU	8.9
1	1-K	109[A]	PHE	8.9
1	1-L	246[A]	PRO	8.9
1	2-K	109[B]	PHE	8.9
1	2-L	246[B]	PRO	8.9
1	3-K	109[C]	PHE	8.9
1	3-L	246[C]	PRO	8.9
1	4-K	109[D]	PHE	8.9
1	4-L	246[D]	PRO	8.9
1	1-O	22[A]	GLN	8.8
1	2-O	22[B]	GLN	8.8
1	3-O	22[C]	GLN	8.8
1	4-O	22[D]	GLN	8.8
1	1-I	287[A]	GLU	8.8
1	2-I	287[B]	GLU	8.8
1	3-I	287[C]	GLU	8.8
1	4-I	287[D]	GLU	8.8
1	1-I	231[A]	TYR	8.8
1	2-I	231[B]	TYR	8.8
1	3-I	231[C]	TYR	8.8
1	4-I	231[D]	TYR	8.8
1	1-I	170[A]	ILE	8.8
1	2-I	170[B]	ILE	8.8
1	3-I	170[C]	ILE	8.8
1	4-I	170[D]	ILE	8.8
1	1-J	181[A]	LEU	8.8
1	2-J	181[B]	LEU	8.8
1	3-J	181[C]	LEU	8.8
1	4-J	181[D]	LEU	8.8
1	1-I	118[A]	ARG	8.8
1	2-I	118[B]	ARG	8.8
1	3-I	118[C]	ARG	8.8
1	4-I	118[D]	ARG	8.8
1	1-I	258[A]	VAL	8.8

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Mol	Chain	Res	Type	RSRZ
1	2-I	258[B]	VAL	8.8
1	3-I	258[C]	VAL	8.8
1	4-I	258[D]	VAL	8.8
1	1-J	245[A]	GLU	8.8
1	2-J	245[B]	GLU	8.8
1	3-J	245[C]	GLU	8.8
1	4-J	245[D]	GLU	8.8
1	1-N	281[A]	LYS	8.8
1	2-N	281[B]	LYS	8.8
1	3-N	281[C]	LYS	8.8
1	4-N	281[D]	LYS	8.8
1	1-J	135[A]	GLY	8.8
1	2-J	135[B]	GLY	8.8
1	3-J	135[C]	GLY	8.8
1	4-J	135[D]	GLY	8.8
1	1-N	197[A]	LEU	8.8
1	2-N	197[B]	LEU	8.8
1	3-N	197[C]	LEU	8.8
1	4-N	197[D]	LEU	8.8
1	1-J	188[A]	HIS	8.7
1	2-J	188[B]	HIS	8.7
1	3-J	188[C]	HIS	8.7
1	4-J	188[D]	HIS	8.7
1	1-K	251[A]	LEU	8.7
1	2-K	251[B]	LEU	8.7
1	3-K	251[C]	LEU	8.7
1	4-K	251[D]	LEU	8.7
1	1-M	126[A]	VAL	8.7
1	2-M	126[B]	VAL	8.7
1	3-M	126[C]	VAL	8.7
1	4-M	126[D]	VAL	8.7
1	1-I	77[A]	ILE	8.7
1	2-I	77[B]	ILE	8.7
1	3-I	77[C]	ILE	8.7
1	4-I	77[D]	ILE	8.7
1	1-O	198[A]	PRO	8.7
1	2-O	198[B]	PRO	8.7
1	3-O	198[C]	PRO	8.7
1	4-O	198[D]	PRO	8.7
1	1-M	191[A]	CYS	8.7
1	2-M	191[B]	CYS	8.7
1	3-M	191[C]	CYS	8.7

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Mol	Chain	Res	Type	RSRZ
1	4-M	191[D]	CYS	8.7
1	1-J	203[A]	PRO	8.7
1	2-J	203[B]	PRO	8.7
1	3-J	203[C]	PRO	8.7
1	4-J	203[D]	PRO	8.7
1	1-M	177[A]	LYS	8.7
1	2-M	177[B]	LYS	8.7
1	3-M	177[C]	LYS	8.7
1	4-M	177[D]	LYS	8.7
1	1-O	254[A]	GLY	8.7
1	2-O	254[B]	GLY	8.7
1	3-O	254[C]	GLY	8.7
1	4-O	254[D]	GLY	8.7
1	1-I	127[A]	TYR	8.7
1	1-N	138[A]	TYR	8.7
1	2-I	127[B]	TYR	8.7
1	2-N	138[B]	TYR	8.7
1	3-I	127[C]	TYR	8.7
1	3-N	138[C]	TYR	8.7
1	4-I	127[D]	TYR	8.7
1	4-N	138[D]	TYR	8.7
1	1-I	167[A]	ARG	8.6
1	1-K	301[A]	VAL	8.6
1	1-M	195[A]	VAL	8.6
1	2-I	167[B]	ARG	8.6
1	2-K	301[B]	VAL	8.6
1	2-M	195[B]	VAL	8.6
1	3-I	167[C]	ARG	8.6
1	3-K	301[C]	VAL	8.6
1	3-M	195[C]	VAL	8.6
1	4-I	167[D]	ARG	8.6
1	4-K	301[D]	VAL	8.6
1	4-M	195[D]	VAL	8.6
1	1-J	198[A]	PRO	8.6
1	2-J	198[B]	PRO	8.6
1	3-J	198[C]	PRO	8.6
1	4-J	198[D]	PRO	8.6
1	1-N	220[A]	LEU	8.6
1	2-N	220[B]	LEU	8.6
1	3-N	220[C]	LEU	8.6
1	4-N	220[D]	LEU	8.6
1	1-L	155[A]	ARG	8.6

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Mol	Chain	Res	Type	RSRZ
1	2-L	155[B]	ARG	8.6
1	3-L	155[C]	ARG	8.6
1	4-L	155[D]	ARG	8.6
1	1-O	259[A]	TYR	8.6
1	2-O	259[B]	TYR	8.6
1	3-O	259[C]	TYR	8.6
1	4-O	259[D]	TYR	8.6
1	1-M	311[A]	ILE	8.6
1	2-M	311[B]	ILE	8.6
1	3-M	311[C]	ILE	8.6
1	4-M	311[D]	ILE	8.6
1	1-N	126[A]	VAL	8.6
1	1-N	302[A]	VAL	8.6
1	2-N	126[B]	VAL	8.6
1	2-N	302[B]	VAL	8.6
1	3-N	126[C]	VAL	8.6
1	3-N	302[C]	VAL	8.6
1	4-N	126[D]	VAL	8.6
1	4-N	302[D]	VAL	8.6
1	1-L	90[A]	ALA	8.6
1	2-L	90[B]	ALA	8.6
1	3-L	90[C]	ALA	8.6
1	4-L	90[D]	ALA	8.6
1	1-K	142[A]	ASP	8.6
1	1-N	196[A]	SER	8.6
1	2-K	142[B]	ASP	8.6
1	2-N	196[B]	SER	8.6
1	3-K	142[C]	ASP	8.6
1	3-N	196[C]	SER	8.6
1	4-K	142[D]	ASP	8.6
1	4-N	196[D]	SER	8.6
1	1-J	80[A]	LEU	8.6
1	1-O	171[A]	LEU	8.6
1	2-J	80[B]	LEU	8.6
1	2-O	171[B]	LEU	8.6
1	3-J	80[C]	LEU	8.6
1	3-O	171[C]	LEU	8.6
1	4-J	80[D]	LEU	8.6
1	4-O	171[D]	LEU	8.6
1	1-M	101[A]	TRP	8.6
1	2-M	101[B]	TRP	8.6
1	3-M	101[C]	TRP	8.6

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Mol	Chain	Res	Type	RSRZ
1	4-M	101[D]	TRP	8.6
1	1-M	296[A]	LYS	8.5
1	2-M	296[B]	LYS	8.5
1	3-M	296[C]	LYS	8.5
1	4-M	296[D]	LYS	8.5
1	1-O	238[A]	ILE	8.5
1	2-O	238[B]	ILE	8.5
1	3-O	238[C]	ILE	8.5
1	4-O	238[D]	ILE	8.5
1	1-O	48[A]	LEU	8.5
1	2-O	48[B]	LEU	8.5
1	3-O	48[C]	LEU	8.5
1	4-O	48[D]	LEU	8.5
1	1-J	308[A]	TRP	8.5
1	1-N	244[A]	THR	8.5
1	1-O	131[A]	TRP	8.5
1	2-J	308[B]	TRP	8.5
1	2-N	244[B]	THR	8.5
1	2-O	131[B]	TRP	8.5
1	3-J	308[C]	TRP	8.5
1	3-N	244[C]	THR	8.5
1	3-O	131[C]	TRP	8.5
1	4-J	308[D]	TRP	8.5
1	4-N	244[D]	THR	8.5
1	4-O	131[D]	TRP	8.5
1	1-I	212[A]	LEU	8.5
1	1-J	251[A]	LEU	8.5
1	2-I	212[B]	LEU	8.5
1	2-J	251[B]	LEU	8.5
1	3-I	212[C]	LEU	8.5
1	3-J	251[C]	LEU	8.5
1	4-I	212[D]	LEU	8.5
1	4-J	251[D]	LEU	8.5
1	1-J	84[A]	VAL	8.5
1	2-J	84[B]	VAL	8.5
1	3-J	84[C]	VAL	8.5
1	4-J	84[D]	VAL	8.5
1	1-L	253[A]	MET	8.5
1	1-N	145[A]	TYR	8.5
1	2-L	253[B]	MET	8.5
1	2-N	145[B]	TYR	8.5
1	3-L	253[C]	MET	8.5

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Mol	Chain	Res	Type	RSRZ
1	3-N	145[C]	TYR	8.5
1	4-L	253[D]	MET	8.5
1	4-N	145[D]	TYR	8.5
1	1-I	224[A]	VAL	8.5
1	2-I	224[B]	VAL	8.5
1	3-I	224[C]	VAL	8.5
1	4-I	224[D]	VAL	8.5
1	1-N	193[A]	PHE	8.5
1	2-N	193[B]	PHE	8.5
1	3-N	193[C]	PHE	8.5
1	4-N	193[D]	PHE	8.5
1	1-J	311[A]	ILE	8.5
1	2-J	311[B]	ILE	8.5
1	3-J	311[C]	ILE	8.5
1	4-J	311[D]	ILE	8.5
1	1-I	43[A]	THR	8.5
1	1-M	165[A]	THR	8.5
1	2-I	43[B]	THR	8.5
1	2-M	165[B]	THR	8.5
1	3-I	43[C]	THR	8.5
1	3-M	165[C]	THR	8.5
1	4-I	43[D]	THR	8.5
1	4-M	165[D]	THR	8.5
1	1-P	263[A]	VAL	8.5
1	2-P	263[B]	VAL	8.5
1	3-P	263[C]	VAL	8.5
1	4-P	263[D]	VAL	8.5
1	1-L	223[A]	GLY	8.5
1	2-L	223[B]	GLY	8.5
1	3-L	223[C]	GLY	8.5
1	4-L	223[D]	GLY	8.5
1	1-L	181[A]	LEU	8.5
1	2-L	181[B]	LEU	8.5
1	3-L	181[C]	LEU	8.5
1	4-L	181[D]	LEU	8.5
1	1-K	295[A]	PHE	8.4
1	2-K	295[B]	PHE	8.4
1	3-K	295[C]	PHE	8.4
1	4-K	295[D]	PHE	8.4
1	1-H	201[A]	ASP	8.4
1	1-N	30[A]	ILE	8.4
1	2-H	201[B]	ASP	8.4

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Mol	Chain	Res	Type	RSRZ
1	2-N	30[B]	ILE	8.4
1	3-H	201[C]	ASP	8.4
1	3-N	30[C]	ILE	8.4
1	4-H	201[D]	ASP	8.4
1	4-N	30[D]	ILE	8.4
1	1-I	234[A]	LEU	8.4
1	1-J	93[A]	LEU	8.4
1	2-I	234[B]	LEU	8.4
1	2-J	93[B]	LEU	8.4
1	3-I	234[C]	LEU	8.4
1	3-J	93[C]	LEU	8.4
1	4-I	234[D]	LEU	8.4
1	4-J	93[D]	LEU	8.4
1	1-J	187[A]	CYS	8.4
1	2-J	187[B]	CYS	8.4
1	3-J	187[C]	CYS	8.4
1	4-J	187[D]	CYS	8.4
1	1-N	290[A]	GLY	8.4
1	2-N	290[B]	GLY	8.4
1	3-N	290[C]	GLY	8.4
1	4-N	290[D]	GLY	8.4
1	1-P	194[A]	PHE	8.4
1	2-P	194[B]	PHE	8.4
1	3-P	194[C]	PHE	8.4
1	4-P	194[D]	PHE	8.4
1	1-I	169[A]	ILE	8.4
1	1-P	41[A]	THR	8.4
1	2-I	169[B]	ILE	8.4
1	2-P	41[B]	THR	8.4
1	3-I	169[C]	ILE	8.4
1	3-P	41[C]	THR	8.4
1	4-I	169[D]	ILE	8.4
1	4-P	41[D]	THR	8.4
1	1-L	71[A]	VAL	8.4
1	2-L	71[B]	VAL	8.4
1	3-L	71[C]	VAL	8.4
1	4-L	71[D]	VAL	8.4
1	1-P	187[A]	CYS	8.4
1	2-P	187[B]	CYS	8.4
1	3-P	187[C]	CYS	8.4
1	4-P	187[D]	CYS	8.4
1	1-J	109[A]	PHE	8.4

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Mol	Chain	Res	Type	RSRZ
1	1-L	51[A]	PRO	8.4
1	2-J	109[B]	PHE	8.4
1	2-L	51[B]	PRO	8.4
1	3-J	109[C]	PHE	8.4
1	3-L	51[C]	PRO	8.4
1	4-J	109[D]	PHE	8.4
1	4-L	51[D]	PRO	8.4
1	1-K	260[A]	ARG	8.4
1	2-K	260[B]	ARG	8.4
1	3-K	260[C]	ARG	8.4
1	4-K	260[D]	ARG	8.4
1	1-L	76[A]	VAL	8.4
1	2-L	76[B]	VAL	8.4
1	3-L	76[C]	VAL	8.4
1	4-L	76[D]	VAL	8.4
1	1-O	106[A]	SER	8.4
1	2-O	106[B]	SER	8.4
1	3-O	106[C]	SER	8.4
1	4-O	106[D]	SER	8.4
1	1-J	292[A]	ILE	8.4
1	2-J	292[B]	ILE	8.4
1	3-J	292[C]	ILE	8.4
1	4-J	292[D]	ILE	8.4
1	1-J	207[A]	PRO	8.4
1	1-K	203[A]	PRO	8.4
1	2-J	207[B]	PRO	8.4
1	2-K	203[B]	PRO	8.4
1	3-J	207[C]	PRO	8.4
1	3-K	203[C]	PRO	8.4
1	4-J	207[D]	PRO	8.4
1	4-K	203[D]	PRO	8.4
1	1-M	33[A]	VAL	8.4
1	2-M	33[B]	VAL	8.4
1	3-M	33[C]	VAL	8.4
1	4-M	33[D]	VAL	8.4
1	1-P	75[A]	GLY	8.3
1	2-P	75[B]	GLY	8.3
1	3-P	75[C]	GLY	8.3
1	4-P	75[D]	GLY	8.3
1	1-H	202[A]	SER	8.3
1	1-I	53[A]	SER	8.3
1	1-O	300[A]	PHE	8.3

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Mol	Chain	Res	Type	RSRZ
1	2-H	202[B]	SER	8.3
1	2-I	53[B]	SER	8.3
1	2-O	300[B]	PHE	8.3
1	3-H	202[C]	SER	8.3
1	3-I	53[C]	SER	8.3
1	3-O	300[C]	PHE	8.3
1	4-H	202[D]	SER	8.3
1	4-I	53[D]	SER	8.3
1	4-O	300[D]	PHE	8.3
1	1-N	259[A]	TYR	8.3
1	2-N	259[B]	TYR	8.3
1	3-N	259[C]	TYR	8.3
1	4-N	259[D]	TYR	8.3
1	1-O	126[A]	VAL	8.3
1	2-O	126[B]	VAL	8.3
1	3-O	126[C]	VAL	8.3
1	4-O	126[D]	VAL	8.3
1	1-J	121[A]	GLY	8.3
1	1-L	103[A]	GLY	8.3
1	2-J	121[B]	GLY	8.3
1	2-L	103[B]	GLY	8.3
1	3-J	121[C]	GLY	8.3
1	3-L	103[C]	GLY	8.3
1	4-J	121[D]	GLY	8.3
1	4-L	103[D]	GLY	8.3
1	1-L	289[A]	ILE	8.3
1	1-M	299[A]	ASP	8.3
1	2-L	289[B]	ILE	8.3
1	2-M	299[B]	ASP	8.3
1	3-L	289[C]	ILE	8.3
1	3-M	299[C]	ASP	8.3
1	4-L	289[D]	ILE	8.3
1	4-M	299[D]	ASP	8.3
1	1-J	209[A]	LEU	8.3
1	1-O	81[A]	LEU	8.3
1	2-J	209[B]	LEU	8.3
1	2-O	81[B]	LEU	8.3
1	3-J	209[C]	LEU	8.3
1	3-O	81[C]	LEU	8.3
1	4-J	209[D]	LEU	8.3
1	4-O	81[D]	LEU	8.3
1	1-I	21[A]	TYR	8.3

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Mol	Chain	Res	Type	RSRZ
1	1-O	145[A]	TYR	8.3
1	2-I	21[B]	TYR	8.3
1	2-O	145[B]	TYR	8.3
1	3-I	21[C]	TYR	8.3
1	3-O	145[C]	TYR	8.3
1	4-I	21[D]	TYR	8.3
1	4-O	145[D]	TYR	8.3
1	1-K	191[A]	CYS	8.3
1	2-K	191[B]	CYS	8.3
1	3-K	191[C]	CYS	8.3
1	4-K	191[D]	CYS	8.3
1	1-N	65[A]	LEU	8.3
1	2-N	65[B]	LEU	8.3
1	3-N	65[C]	LEU	8.3
1	4-N	65[D]	LEU	8.3
1	1-K	113[A]	VAL	8.3
1	2-K	113[B]	VAL	8.3
1	3-K	113[C]	VAL	8.3
1	4-K	113[D]	VAL	8.3
1	1-J	244[A]	THR	8.3
1	2-J	244[B]	THR	8.3
1	3-J	244[C]	THR	8.3
1	4-J	244[D]	THR	8.3
1	1-J	270[A]	LEU	8.3
1	2-J	270[B]	LEU	8.3
1	3-J	270[C]	LEU	8.3
1	4-J	270[D]	LEU	8.3
1	1-J	98[A]	VAL	8.3
1	1-P	95[A]	SER	8.3
1	2-J	98[B]	VAL	8.3
1	2-P	95[B]	SER	8.3
1	3-J	98[C]	VAL	8.3
1	3-P	95[C]	SER	8.3
1	4-J	98[D]	VAL	8.3
1	4-P	95[D]	SER	8.3
1	1-I	174[A]	TRP	8.3
1	1-K	31[A]	ILE	8.3
1	2-I	174[B]	TRP	8.3
1	2-K	31[B]	ILE	8.3
1	3-I	174[C]	TRP	8.3
1	3-K	31[C]	ILE	8.3
1	4-I	174[D]	TRP	8.3

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Mol	Chain	Res	Type	RSRZ
1	4-K	31[D]	ILE	8.3
1	1-K	134[A]	PHE	8.2
1	2-K	134[B]	PHE	8.2
1	3-K	134[C]	PHE	8.2
1	4-K	134[D]	PHE	8.2
1	1-O	84[A]	VAL	8.2
1	2-O	84[B]	VAL	8.2
1	3-O	84[C]	VAL	8.2
1	4-O	84[D]	VAL	8.2
1	1-K	198[A]	PRO	8.2
1	2-K	198[B]	PRO	8.2
1	3-K	198[C]	PRO	8.2
1	4-K	198[D]	PRO	8.2
1	1-L	257[A]	HIS	8.2
1	2-L	257[B]	HIS	8.2
1	3-L	257[C]	HIS	8.2
1	4-L	257[D]	HIS	8.2
1	1-J	193[A]	PHE	8.2
1	1-J	280[A]	LEU	8.2
1	1-L	43[A]	THR	8.2
1	2-J	193[B]	PHE	8.2
1	2-J	280[B]	LEU	8.2
1	2-L	43[B]	THR	8.2
1	3-J	193[C]	PHE	8.2
1	3-J	280[C]	LEU	8.2
1	3-L	43[C]	THR	8.2
1	4-J	193[D]	PHE	8.2
1	4-J	280[D]	LEU	8.2
1	4-L	43[D]	THR	8.2
1	1-P	301[A]	VAL	8.2
1	2-P	301[B]	VAL	8.2
1	3-P	301[C]	VAL	8.2
1	4-P	301[D]	VAL	8.2
1	1-J	269[A]	GLN	8.2
1	2-J	269[B]	GLN	8.2
1	3-J	269[C]	GLN	8.2
1	4-J	269[D]	GLN	8.2
1	1-N	59[A]	ALA	8.2
1	1-O	181[A]	LEU	8.2
1	1-O	280[A]	LEU	8.2
1	2-N	59[B]	ALA	8.2
1	2-O	181[B]	LEU	8.2

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Mol	Chain	Res	Type	RSRZ
1	2-O	280[B]	LEU	8.2
1	3-N	59[C]	ALA	8.2
1	3-O	181[C]	LEU	8.2
1	3-O	280[C]	LEU	8.2
1	4-N	59[D]	ALA	8.2
1	4-O	181[D]	LEU	8.2
1	4-O	280[D]	LEU	8.2
1	1-O	92[A]	MET	8.2
1	2-O	92[B]	MET	8.2
1	3-O	92[C]	MET	8.2
1	4-O	92[D]	MET	8.2
1	1-L	282[A]	TRP	8.2
1	2-L	282[B]	TRP	8.2
1	3-L	282[C]	TRP	8.2
1	4-L	282[D]	TRP	8.2
1	1-N	112[A]	LYS	8.2
1	2-N	112[B]	LYS	8.2
1	3-N	112[C]	LYS	8.2
1	4-N	112[D]	LYS	8.2
1	1-N	48[A]	LEU	8.2
1	1-P	212[A]	LEU	8.2
1	2-N	48[B]	LEU	8.2
1	2-P	212[B]	LEU	8.2
1	3-N	48[C]	LEU	8.2
1	3-P	212[C]	LEU	8.2
1	4-N	48[D]	LEU	8.2
1	4-P	212[D]	LEU	8.2
1	1-M	97[A]	GLY	8.2
1	2-M	97[B]	GLY	8.2
1	3-M	97[C]	GLY	8.2
1	4-M	97[D]	GLY	8.2
1	1-M	160[A]	ILE	8.2
1	2-M	160[B]	ILE	8.2
1	3-M	160[C]	ILE	8.2
1	4-M	160[D]	ILE	8.2
1	1-N	101[A]	TRP	8.1
1	2-N	101[B]	TRP	8.1
1	3-N	101[C]	TRP	8.1
1	4-N	101[D]	TRP	8.1
1	1-K	149[A]	GLY	8.1
1	2-K	149[B]	GLY	8.1
1	3-K	149[C]	GLY	8.1

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Mol	Chain	Res	Type	RSRZ
1	4-K	149[D]	GLY	8.1
1	1-M	214[A]	TYR	8.1
1	2-M	214[B]	TYR	8.1
1	3-M	214[C]	TYR	8.1
1	4-M	214[D]	TYR	8.1
1	1-M	142[A]	ASP	8.1
1	2-M	142[B]	ASP	8.1
1	3-M	142[C]	ASP	8.1
1	4-M	142[D]	ASP	8.1
1	1-P	131[A]	TRP	8.1
1	2-P	131[B]	TRP	8.1
1	3-P	131[C]	TRP	8.1
1	4-P	131[D]	TRP	8.1
1	1-I	316[A]	SER	8.1
1	2-I	316[B]	SER	8.1
1	3-I	316[C]	SER	8.1
1	4-I	316[D]	SER	8.1
1	1-P	184[A]	LEU	8.1
1	2-P	184[B]	LEU	8.1
1	3-P	184[C]	LEU	8.1
1	4-P	184[D]	LEU	8.1
1	1-M	170[A]	ILE	8.1
1	2-M	170[B]	ILE	8.1
1	3-M	170[C]	ILE	8.1
1	4-M	170[D]	ILE	8.1
1	1-O	166[A]	ASP	8.1
1	2-O	166[B]	ASP	8.1
1	3-O	166[C]	ASP	8.1
1	4-O	166[D]	ASP	8.1
1	1-L	74[A]	ARG	8.1
1	2-L	74[B]	ARG	8.1
1	3-L	74[C]	ARG	8.1
1	4-L	74[D]	ARG	8.1
1	1-G	200[A]	ALA	8.1
1	2-G	200[B]	ALA	8.1
1	3-G	200[C]	ALA	8.1
1	4-G	200[D]	ALA	8.1
1	1-I	250[A]	ILE	8.1
1	1-N	228[A]	ILE	8.1
1	1-P	157[A]	ILE	8.1
1	2-I	250[B]	ILE	8.1
1	2-N	228[B]	ILE	8.1

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Mol	Chain	Res	Type	RSRZ
1	2-P	157[B]	ILE	8.1
1	3-I	250[C]	ILE	8.1
1	3-N	228[C]	ILE	8.1
1	3-P	157[C]	ILE	8.1
1	4-I	250[D]	ILE	8.1
1	4-N	228[D]	ILE	8.1
1	4-P	157[D]	ILE	8.1
1	1-K	50[A]	ALA	8.1
1	2-K	50[B]	ALA	8.1
1	3-K	50[C]	ALA	8.1
1	4-K	50[D]	ALA	8.1
1	1-L	175[A]	ASN	8.1
1	2-L	175[B]	ASN	8.1
1	3-L	175[C]	ASN	8.1
1	4-L	175[D]	ASN	8.1
1	1-N	28[A]	ARG	8.1
1	2-N	28[B]	ARG	8.1
1	3-N	28[C]	ARG	8.1
1	4-N	28[D]	ARG	8.1
1	1-N	159[A]	THR	8.0
1	2-N	159[B]	THR	8.0
1	3-N	159[C]	THR	8.0
1	4-N	159[D]	THR	8.0
1	1-N	99[A]	GLY	8.0
1	2-N	99[B]	GLY	8.0
1	3-N	99[C]	GLY	8.0
1	4-N	99[D]	GLY	8.0
1	1-L	58[A]	LEU	8.0
1	2-L	58[B]	LEU	8.0
1	3-L	58[C]	LEU	8.0
1	4-L	58[D]	LEU	8.0
1	1-I	172[A]	SER	8.0
1	2-I	172[B]	SER	8.0
1	3-I	172[C]	SER	8.0
1	4-I	172[D]	SER	8.0
1	1-J	297[A]	VAL	8.0
1	1-P	70[A]	ARG	8.0
1	2-J	297[B]	VAL	8.0
1	2-P	70[B]	ARG	8.0
1	3-J	297[C]	VAL	8.0
1	3-P	70[C]	ARG	8.0
1	4-J	297[D]	VAL	8.0

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Mol	Chain	Res	Type	RSRZ
1	4-P	70[D]	ARG	8.0
1	1-M	92[A]	MET	8.0
1	2-M	92[B]	MET	8.0
1	3-M	92[C]	MET	8.0
1	4-M	92[D]	MET	8.0
1	1-I	87[A]	CYS	8.0
1	2-I	87[B]	CYS	8.0
1	3-I	87[C]	CYS	8.0
1	4-I	87[D]	CYS	8.0
1	1-O	265[A]	PRO	8.0
1	2-O	265[B]	PRO	8.0
1	3-O	265[C]	PRO	8.0
1	4-O	265[D]	PRO	8.0
1	1-P	275[A]	ARG	8.0
1	2-P	275[B]	ARG	8.0
1	3-P	275[C]	ARG	8.0
1	4-P	275[D]	ARG	8.0
1	1-O	62[A]	THR	8.0
1	2-O	62[B]	THR	8.0
1	3-O	62[C]	THR	8.0
1	4-O	62[D]	THR	8.0
1	1-M	49[A]	PHE	8.0
1	1-O	129[A]	PHE	8.0
1	2-M	49[B]	PHE	8.0
1	2-O	129[B]	PHE	8.0
1	3-M	49[C]	PHE	8.0
1	3-O	129[C]	PHE	8.0
1	4-M	49[D]	PHE	8.0
1	4-O	129[D]	PHE	8.0
1	1-I	114[A]	GLY	8.0
1	1-P	308[A]	TRP	8.0
1	2-I	114[B]	GLY	8.0
1	2-P	308[B]	TRP	8.0
1	3-I	114[C]	GLY	8.0
1	3-P	308[C]	TRP	8.0
1	4-I	114[D]	GLY	8.0
1	4-P	308[D]	TRP	8.0
1	1-J	146[A]	LYS	8.0
1	2-J	146[B]	LYS	8.0
1	3-J	146[C]	LYS	8.0
1	4-J	146[D]	LYS	8.0
1	1-N	207[A]	PRO	8.0

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Mol	Chain	Res	Type	RSRZ
1	2-N	207[B]	PRO	8.0
1	3-N	207[C]	PRO	8.0
1	4-N	207[D]	PRO	8.0
1	1-M	83[A]	PHE	8.0
1	2-M	83[B]	PHE	8.0
1	3-M	83[C]	PHE	8.0
1	4-M	83[D]	PHE	8.0
1	1-L	34[A]	GLY	8.0
1	2-L	34[B]	GLY	8.0
1	3-L	34[C]	GLY	8.0
1	4-L	34[D]	GLY	8.0
1	1-D	14[A]	SER	8.0
1	2-D	14[B]	SER	8.0
1	3-D	14[C]	SER	8.0
1	4-D	14[D]	SER	8.0
1	1-K	268[A]	THR	8.0
1	1-M	43[A]	THR	8.0
1	2-K	268[B]	THR	8.0
1	2-M	43[B]	THR	8.0
1	3-K	268[C]	THR	8.0
1	3-M	43[C]	THR	8.0
1	4-K	268[D]	THR	8.0
1	4-M	43[D]	THR	8.0
1	1-J	78[A]	ALA	8.0
1	2-J	78[B]	ALA	8.0
1	3-J	78[C]	ALA	8.0
1	4-J	78[D]	ALA	8.0
1	1-O	160[A]	ILE	8.0
1	2-O	160[B]	ILE	8.0
1	3-O	160[C]	ILE	8.0
1	4-O	160[D]	ILE	8.0
1	1-J	175[A]	ASN	8.0
1	2-J	175[B]	ASN	8.0
1	3-J	175[C]	ASN	8.0
1	4-J	175[D]	ASN	8.0
1	1-I	181[A]	LEU	8.0
1	1-I	211[A]	CYS	8.0
1	2-I	181[B]	LEU	8.0
1	2-I	211[B]	CYS	8.0
1	3-I	181[C]	LEU	8.0
1	3-I	211[C]	CYS	8.0
1	4-I	181[D]	LEU	8.0

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Mol	Chain	Res	Type	RSRZ
1	4-I	211[D]	CYS	8.0
1	1-M	241[A]	ILE	7.9
1	2-M	241[B]	ILE	7.9
1	3-M	241[C]	ILE	7.9
1	4-M	241[D]	ILE	7.9
1	1-P	94[A]	SER	7.9
1	2-P	94[B]	SER	7.9
1	3-P	94[C]	SER	7.9
1	4-P	94[D]	SER	7.9
1	1-I	315[A]	MET	7.9
1	2-I	315[B]	MET	7.9
1	3-I	315[C]	MET	7.9
1	4-I	315[D]	MET	7.9
1	1-L	126[A]	VAL	7.9
1	2-L	126[B]	VAL	7.9
1	3-L	126[C]	VAL	7.9
1	4-L	126[D]	VAL	7.9
1	1-N	241[A]	ILE	7.9
1	2-N	241[B]	ILE	7.9
1	3-N	241[C]	ILE	7.9
1	4-N	241[D]	ILE	7.9
1	1-J	28[A]	ARG	7.9
1	1-P	74[A]	ARG	7.9
1	2-J	28[B]	ARG	7.9
1	2-P	74[B]	ARG	7.9
1	3-J	28[C]	ARG	7.9
1	3-P	74[C]	ARG	7.9
1	4-J	28[D]	ARG	7.9
1	4-P	74[D]	ARG	7.9
1	1-J	32[A]	ASN	7.9
1	1-J	204[A]	GLY	7.9
1	1-L	124[A]	GLY	7.9
1	1-M	44[A]	GLY	7.9
1	2-J	32[B]	ASN	7.9
1	2-J	204[B]	GLY	7.9
1	2-L	124[B]	GLY	7.9
1	2-M	44[B]	GLY	7.9
1	3-J	32[C]	ASN	7.9
1	3-J	204[C]	GLY	7.9
1	3-L	124[C]	GLY	7.9
1	3-M	44[C]	GLY	7.9
1	4-J	32[D]	ASN	7.9

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Mol	Chain	Res	Type	RSRZ
1	4-J	204[D]	GLY	7.9
1	4-L	124[D]	GLY	7.9
1	4-M	44[D]	GLY	7.9
1	1-M	226[A]	PHE	7.9
1	2-M	226[B]	PHE	7.9
1	3-M	226[C]	PHE	7.9
1	4-M	226[D]	PHE	7.9
1	1-K	247[A]	HIS	7.9
1	2-K	247[B]	HIS	7.9
1	3-K	247[C]	HIS	7.9
1	4-K	247[D]	HIS	7.9
1	1-P	48[A]	LEU	7.9
1	2-P	48[B]	LEU	7.9
1	3-P	48[C]	LEU	7.9
1	4-P	48[D]	LEU	7.9
1	1-J	263[A]	VAL	7.9
1	2-J	263[B]	VAL	7.9
1	3-J	263[C]	VAL	7.9
1	4-J	263[D]	VAL	7.9
1	1-O	41[A]	THR	7.9
1	2-O	41[B]	THR	7.9
1	3-O	41[C]	THR	7.9
1	4-O	41[D]	THR	7.9
1	1-P	50[A]	ALA	7.9
1	2-P	50[B]	ALA	7.9
1	3-P	50[C]	ALA	7.9
1	4-P	50[D]	ALA	7.9
1	1-J	81[A]	LEU	7.9
1	1-J	222[A]	LEU	7.9
1	2-J	81[B]	LEU	7.9
1	2-J	222[B]	LEU	7.9
1	3-J	81[C]	LEU	7.9
1	3-J	222[C]	LEU	7.9
1	4-J	81[D]	LEU	7.9
1	4-J	222[D]	LEU	7.9
1	1-J	277[A]	PHE	7.9
1	1-P	159[A]	THR	7.9
1	2-J	277[B]	PHE	7.9
1	2-P	159[B]	THR	7.9
1	3-J	277[C]	PHE	7.9
1	3-P	159[C]	THR	7.9
1	4-J	277[D]	PHE	7.9

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Mol	Chain	Res	Type	RSRZ
1	4-P	159[D]	THR	7.9
1	1-L	233[A]	LEU	7.9
1	2-L	233[B]	LEU	7.9
1	3-L	233[C]	LEU	7.9
1	4-L	233[D]	LEU	7.9
1	1-O	139[A]	THR	7.8
1	2-O	139[B]	THR	7.8
1	3-O	139[C]	THR	7.8
1	4-O	139[D]	THR	7.8
1	1-M	106[A]	SER	7.8
1	1-N	249[A]	PHE	7.8
1	2-M	106[B]	SER	7.8
1	2-N	249[B]	PHE	7.8
1	3-M	106[C]	SER	7.8
1	3-N	249[C]	PHE	7.8
1	4-M	106[D]	SER	7.8
1	4-N	249[D]	PHE	7.8
1	1-I	239[A]	ALA	7.8
1	2-I	239[B]	ALA	7.8
1	3-I	239[C]	ALA	7.8
1	4-I	239[D]	ALA	7.8
1	1-K	133[A]	HIS	7.8
1	2-K	133[B]	HIS	7.8
1	3-K	133[C]	HIS	7.8
1	4-K	133[D]	HIS	7.8
1	1-I	159[A]	THR	7.8
1	1-M	67[A]	THR	7.8
1	2-I	159[B]	THR	7.8
1	2-M	67[B]	THR	7.8
1	3-I	159[C]	THR	7.8
1	3-M	67[C]	THR	7.8
1	4-I	159[D]	THR	7.8
1	4-M	67[D]	THR	7.8
1	1-O	78[A]	ALA	7.8
1	2-O	78[B]	ALA	7.8
1	3-O	78[C]	ALA	7.8
1	4-O	78[D]	ALA	7.8
1	1-K	285[A]	SER	7.8
1	2-K	285[B]	SER	7.8
1	3-K	285[C]	SER	7.8
1	4-K	285[D]	SER	7.8
1	1-O	315[A]	MET	7.8

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Mol	Chain	Res	Type	RSRZ
1	2-O	315[B]	MET	7.8
1	3-O	315[C]	MET	7.8
1	4-O	315[D]	MET	7.8
1	1-N	155[A]	ARG	7.8
1	1-N	233[A]	LEU	7.8
1	1-O	63[A]	LEU	7.8
1	2-N	155[B]	ARG	7.8
1	2-N	233[B]	LEU	7.8
1	2-O	63[B]	LEU	7.8
1	3-N	155[C]	ARG	7.8
1	3-N	233[C]	LEU	7.8
1	3-O	63[C]	LEU	7.8
1	4-N	155[D]	ARG	7.8
1	4-N	233[D]	LEU	7.8
1	4-O	63[D]	LEU	7.8
1	1-M	30[A]	ILE	7.8
1	2-M	30[B]	ILE	7.8
1	3-M	30[C]	ILE	7.8
1	4-M	30[D]	ILE	7.8
1	1-N	226[A]	PHE	7.8
1	2-N	226[B]	PHE	7.8
1	3-N	226[C]	PHE	7.8
1	4-N	226[D]	PHE	7.8
1	1-M	94[A]	SER	7.8
1	1-O	308[A]	TRP	7.8
1	2-M	94[B]	SER	7.8
1	2-O	308[B]	TRP	7.8
1	3-M	94[C]	SER	7.8
1	3-O	308[C]	TRP	7.8
1	4-M	94[D]	SER	7.8
1	4-O	308[D]	TRP	7.8
1	1-B	200[A]	ALA	7.8
1	2-B	200[B]	ALA	7.8
1	3-B	200[C]	ALA	7.8
1	4-B	200[D]	ALA	7.8
1	1-J	231[A]	TYR	7.8
1	1-M	289[A]	ILE	7.8
1	2-J	231[B]	TYR	7.8
1	2-M	289[B]	ILE	7.8
1	3-J	231[C]	TYR	7.8
1	3-M	289[C]	ILE	7.8
1	4-J	231[D]	TYR	7.8

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Mol	Chain	Res	Type	RSRZ
1	4-M	289[D]	ILE	7.8
1	1-I	92[A]	MET	7.8
1	1-L	174[A]	TRP	7.8
1	1-M	86[A]	GLY	7.8
1	2-I	92[B]	MET	7.8
1	2-L	174[B]	TRP	7.8
1	2-M	86[B]	GLY	7.8
1	3-I	92[C]	MET	7.8
1	3-L	174[C]	TRP	7.8
1	3-M	86[C]	GLY	7.8
1	4-I	92[D]	MET	7.8
1	4-L	174[D]	TRP	7.8
1	4-M	86[D]	GLY	7.8
1	1-I	195[A]	VAL	7.7
1	1-M	301[A]	VAL	7.7
1	2-I	195[B]	VAL	7.7
1	2-M	301[B]	VAL	7.7
1	3-I	195[C]	VAL	7.7
1	3-M	301[C]	VAL	7.7
1	4-I	195[D]	VAL	7.7
1	4-M	301[D]	VAL	7.7
1	1-I	109[A]	PHE	7.7
1	1-N	54[A]	PHE	7.7
1	1-P	190[A]	PHE	7.7
1	2-I	109[B]	PHE	7.7
1	2-N	54[B]	PHE	7.7
1	2-P	190[B]	PHE	7.7
1	3-I	109[C]	PHE	7.7
1	3-N	54[C]	PHE	7.7
1	3-P	190[C]	PHE	7.7
1	4-I	109[D]	PHE	7.7
1	4-N	54[D]	PHE	7.7
1	4-P	190[D]	PHE	7.7
1	1-I	213[A]	MET	7.7
1	2-I	213[B]	MET	7.7
1	3-I	213[C]	MET	7.7
1	4-I	213[D]	MET	7.7
1	1-L	206[A]	LYS	7.7
1	2-L	206[B]	LYS	7.7
1	3-L	206[C]	LYS	7.7
1	4-L	206[D]	LYS	7.7
1	1-J	196[A]	SER	7.7

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Mol	Chain	Res	Type	RSRZ
1	1-P	218[A]	CYS	7.7
1	2-J	196[B]	SER	7.7
1	2-P	218[B]	CYS	7.7
1	3-J	196[C]	SER	7.7
1	3-P	218[C]	CYS	7.7
1	4-J	196[D]	SER	7.7
1	4-P	218[D]	CYS	7.7
1	1-I	86[A]	GLY	7.7
1	2-I	86[B]	GLY	7.7
1	3-I	86[C]	GLY	7.7
1	4-I	86[D]	GLY	7.7
1	1-K	288[A]	GLU	7.7
1	2-K	288[B]	GLU	7.7
1	3-K	288[C]	GLU	7.7
1	4-K	288[D]	GLU	7.7
1	1-L	218[A]	CYS	7.7
1	1-N	157[A]	ILE	7.7
1	2-L	218[B]	CYS	7.7
1	2-N	157[B]	ILE	7.7
1	3-L	218[C]	CYS	7.7
1	3-N	157[C]	ILE	7.7
1	4-L	218[D]	CYS	7.7
1	4-N	157[D]	ILE	7.7
1	1-I	62[A]	THR	7.7
1	1-M	62[A]	THR	7.7
1	2-I	62[B]	THR	7.7
1	2-M	62[B]	THR	7.7
1	3-I	62[C]	THR	7.7
1	3-M	62[C]	THR	7.7
1	4-I	62[D]	THR	7.7
1	4-M	62[D]	THR	7.7
1	1-N	80[A]	LEU	7.7
1	2-N	80[B]	LEU	7.7
1	3-N	80[C]	LEU	7.7
1	4-N	80[D]	LEU	7.7
1	1-P	180[A]	PRO	7.7
1	2-P	180[B]	PRO	7.7
1	3-P	180[C]	PRO	7.7
1	4-P	180[D]	PRO	7.7
1	1-K	214[A]	TYR	7.7
1	1-L	305[A]	TYR	7.7
1	2-K	214[B]	TYR	7.7

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Mol	Chain	Res	Type	RSRZ
1	2-L	305[B]	TYR	7.7
1	3-K	214[C]	TYR	7.7
1	3-L	305[C]	TYR	7.7
1	4-K	214[D]	TYR	7.7
1	4-L	305[D]	TYR	7.7
1	1-K	167[A]	ARG	7.7
1	2-K	167[B]	ARG	7.7
1	3-K	167[C]	ARG	7.7
1	4-K	167[D]	ARG	7.7
1	1-O	311[A]	ILE	7.7
1	2-O	311[B]	ILE	7.7
1	3-O	311[C]	ILE	7.7
1	4-O	311[D]	ILE	7.7
1	1-I	237[A]	MET	7.7
1	1-K	21[A]	TYR	7.7
1	2-I	237[B]	MET	7.7
1	1-K	194[A]	PHE	7.7
1	1-N	295[A]	PHE	7.7
1	2-K	21[B]	TYR	7.7
1	3-I	237[C]	MET	7.7
1	3-K	21[C]	TYR	7.7
1	4-I	237[D]	MET	7.7
1	2-K	194[B]	PHE	7.7
1	2-N	295[B]	PHE	7.7
1	3-K	194[C]	PHE	7.7
1	3-N	295[C]	PHE	7.7
1	4-K	21[D]	TYR	7.7
1	4-K	194[D]	PHE	7.7
1	4-N	295[D]	PHE	7.7
1	1-O	232[A]	ALA	7.7
1	2-O	232[B]	ALA	7.7
1	3-O	232[C]	ALA	7.7
1	4-O	232[D]	ALA	7.7
1	1-J	309[A]	GLY	7.7
1	1-P	251[A]	LEU	7.7
1	2-J	309[B]	GLY	7.7
1	2-P	251[B]	LEU	7.7
1	3-J	309[C]	GLY	7.7
1	3-P	251[C]	LEU	7.7
1	4-J	309[D]	GLY	7.7
1	4-P	251[D]	LEU	7.7
1	1-P	276[A]	ASP	7.6

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Mol	Chain	Res	Type	RSRZ
1	2-P	276[B]	ASP	7.6
1	3-P	276[C]	ASP	7.6
1	4-P	276[D]	ASP	7.6
1	1-I	67[A]	THR	7.6
1	2-I	67[B]	THR	7.6
1	3-I	67[C]	THR	7.6
1	4-I	67[D]	THR	7.6
1	1-I	141[A]	ALA	7.6
1	2-I	141[B]	ALA	7.6
1	3-I	141[C]	ALA	7.6
1	4-I	141[D]	ALA	7.6
1	1-K	61[A]	ASN	7.6
1	1-N	89[A]	ASP	7.6
1	1-O	44[A]	GLY	7.6
1	2-K	61[B]	ASN	7.6
1	2-N	89[B]	ASP	7.6
1	2-O	44[B]	GLY	7.6
1	3-K	61[C]	ASN	7.6
1	3-N	89[C]	ASP	7.6
1	3-O	44[C]	GLY	7.6
1	4-K	61[D]	ASN	7.6
1	4-N	89[D]	ASP	7.6
1	4-O	44[D]	GLY	7.6
1	1-P	265[A]	PRO	7.6
1	2-P	265[B]	PRO	7.6
1	3-P	265[C]	PRO	7.6
1	4-P	265[D]	PRO	7.6
1	1-O	65[A]	LEU	7.6
1	2-O	65[B]	LEU	7.6
1	3-O	65[C]	LEU	7.6
1	4-O	65[D]	LEU	7.6
1	1-I	98[A]	VAL	7.6
1	2-I	98[B]	VAL	7.6
1	3-I	98[C]	VAL	7.6
1	4-I	98[D]	VAL	7.6
1	1-K	197[A]	LEU	7.6
1	2-K	197[B]	LEU	7.6
1	3-K	197[C]	LEU	7.6
1	4-K	197[D]	LEU	7.6
1	1-N	237[A]	MET	7.6
1	2-N	237[B]	MET	7.6
1	3-N	237[C]	MET	7.6

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Mol	Chain	Res	Type	RSRZ
1	4-N	237[D]	MET	7.6
1	1-M	272[A]	ARG	7.6
1	2-M	272[B]	ARG	7.6
1	3-M	272[C]	ARG	7.6
1	4-M	272[D]	ARG	7.6
1	1-K	101[A]	TRP	7.6
1	1-O	79[A]	GLU	7.6
1	2-K	101[B]	TRP	7.6
1	2-O	79[B]	GLU	7.6
1	3-K	101[C]	TRP	7.6
1	3-O	79[C]	GLU	7.6
1	4-K	101[D]	TRP	7.6
1	4-O	79[D]	GLU	7.6
1	1-K	165[A]	THR	7.6
1	2-K	165[B]	THR	7.6
1	3-K	165[C]	THR	7.6
1	4-K	165[D]	THR	7.6
1	1-M	76[A]	VAL	7.6
1	1-M	113[A]	VAL	7.6
1	1-N	18[A]	HIS	7.6
1	1-O	224[A]	VAL	7.6
1	2-M	76[B]	VAL	7.6
1	2-M	113[B]	VAL	7.6
1	2-N	18[B]	HIS	7.6
1	2-O	224[B]	VAL	7.6
1	3-M	76[C]	VAL	7.6
1	3-M	113[C]	VAL	7.6
1	3-N	18[C]	HIS	7.6
1	3-O	224[C]	VAL	7.6
1	4-M	76[D]	VAL	7.6
1	4-M	113[D]	VAL	7.6
1	4-N	18[D]	HIS	7.6
1	4-O	224[D]	VAL	7.6
1	1-I	100[A]	ILE	7.6
1	1-J	250[A]	ILE	7.6
1	2-I	100[B]	ILE	7.6
1	2-J	250[B]	ILE	7.6
1	3-I	100[C]	ILE	7.6
1	3-J	250[C]	ILE	7.6
1	4-I	100[D]	ILE	7.6
1	4-J	250[D]	ILE	7.6
1	1-I	153[A]	LEU	7.6

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Mol	Chain	Res	Type	RSRZ
1	2-I	153[B]	LEU	7.6
1	3-I	153[C]	LEU	7.6
1	4-I	153[D]	LEU	7.6
1	1-M	265[A]	PRO	7.6
1	2-M	265[B]	PRO	7.6
1	3-M	265[C]	PRO	7.6
1	4-M	265[D]	PRO	7.6
1	1-K	80[A]	LEU	7.6
1	2-K	80[B]	LEU	7.6
1	3-K	80[C]	LEU	7.6
1	4-K	80[D]	LEU	7.6
1	1-L	308[A]	TRP	7.5
1	2-L	308[B]	TRP	7.5
1	3-L	308[C]	TRP	7.5
1	4-L	308[D]	TRP	7.5
1	1-P	64[A]	PRO	7.5
1	2-P	64[B]	PRO	7.5
1	3-P	64[C]	PRO	7.5
1	4-P	64[D]	PRO	7.5
1	1-M	56[A]	PHE	7.5
1	1-M	117[A]	HIS	7.5
1	2-M	56[B]	PHE	7.5
1	2-M	117[B]	HIS	7.5
1	3-M	56[C]	PHE	7.5
1	3-M	117[C]	HIS	7.5
1	4-M	56[D]	PHE	7.5
1	4-M	117[D]	HIS	7.5
1	1-J	51[A]	PRO	7.5
1	1-J	195[A]	VAL	7.5
1	1-J	199[A]	PRO	7.5
1	2-J	51[B]	PRO	7.5
1	2-J	195[B]	VAL	7.5
1	2-J	199[B]	PRO	7.5
1	3-J	51[C]	PRO	7.5
1	3-J	195[C]	VAL	7.5
1	3-J	199[C]	PRO	7.5
1	4-J	51[D]	PRO	7.5
1	4-J	195[D]	VAL	7.5
1	4-J	199[D]	PRO	7.5
1	1-J	56[A]	PHE	7.5
1	1-N	268[A]	THR	7.5
1	2-J	56[B]	PHE	7.5

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Mol	Chain	Res	Type	RSRZ
1	2-N	268[B]	THR	7.5
1	3-J	56[C]	PHE	7.5
1	3-N	268[C]	THR	7.5
1	4-J	56[D]	PHE	7.5
1	4-N	268[D]	THR	7.5
1	1-J	284[A]	ARG	7.5
1	2-J	284[B]	ARG	7.5
1	3-J	284[C]	ARG	7.5
1	4-J	284[D]	ARG	7.5
1	1-I	123[A]	LEU	7.5
1	1-O	52[A]	PRO	7.5
1	2-I	123[B]	LEU	7.5
1	2-O	52[B]	PRO	7.5
1	3-I	123[C]	LEU	7.5
1	3-O	52[C]	PRO	7.5
1	4-I	123[D]	LEU	7.5
1	4-O	52[D]	PRO	7.5
1	1-K	141[A]	ALA	7.5
1	2-K	141[B]	ALA	7.5
1	3-K	141[C]	ALA	7.5
1	4-K	141[D]	ALA	7.5
1	1-N	29[A]	ARG	7.5
1	2-N	29[B]	ARG	7.5
1	3-N	29[C]	ARG	7.5
1	4-N	29[D]	ARG	7.5
1	1-I	209[A]	LEU	7.5
1	2-I	209[B]	LEU	7.5
1	3-I	209[C]	LEU	7.5
1	4-I	209[D]	LEU	7.5
1	1-L	258[A]	VAL	7.5
1	2-L	258[B]	VAL	7.5
1	3-L	258[C]	VAL	7.5
1	4-L	258[D]	VAL	7.5
1	1-K	206[A]	LYS	7.5
1	2-K	206[B]	LYS	7.5
1	3-K	206[C]	LYS	7.5
1	4-K	206[D]	LYS	7.5
1	1-K	209[A]	LEU	7.5
1	2-K	209[B]	LEU	7.5
1	3-K	209[C]	LEU	7.5
1	4-K	209[D]	LEU	7.5
1	1-J	61[A]	ASN	7.5

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Mol	Chain	Res	Type	RSRZ
1	2-J	61[B]	ASN	7.5
1	3-J	61[C]	ASN	7.5
1	4-J	61[D]	ASN	7.5
1	1-P	51[A]	PRO	7.5
1	2-P	51[B]	PRO	7.5
1	3-P	51[C]	PRO	7.5
1	4-P	51[D]	PRO	7.5
1	1-N	73[A]	LEU	7.4
1	2-N	73[B]	LEU	7.4
1	3-N	73[C]	LEU	7.4
1	4-N	73[D]	LEU	7.4
1	1-I	126[A]	VAL	7.4
1	2-I	126[B]	VAL	7.4
1	3-I	126[C]	VAL	7.4
1	4-I	126[D]	VAL	7.4
1	1-O	279[A]	LYS	7.4
1	2-O	279[B]	LYS	7.4
1	3-O	279[C]	LYS	7.4
1	4-O	279[D]	LYS	7.4
1	1-O	57[A]	SER	7.4
1	2-O	57[B]	SER	7.4
1	3-O	57[C]	SER	7.4
1	4-O	57[D]	SER	7.4
1	1-K	54[A]	PHE	7.4
1	2-K	54[B]	PHE	7.4
1	3-K	54[C]	PHE	7.4
1	4-K	54[D]	PHE	7.4
1	1-L	270[A]	LEU	7.4
1	2-L	270[B]	LEU	7.4
1	3-L	270[C]	LEU	7.4
1	4-L	270[D]	LEU	7.4
1	1-P	195[A]	VAL	7.4
1	2-P	195[B]	VAL	7.4
1	3-P	195[C]	VAL	7.4
1	4-P	195[D]	VAL	7.4
1	1-L	119[A]	ARG	7.4
1	2-L	119[B]	ARG	7.4
1	3-L	119[C]	ARG	7.4
1	4-L	119[D]	ARG	7.4
1	1-I	38[A]	PRO	7.4
1	1-J	159[A]	THR	7.4
1	1-N	253[A]	MET	7.4

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Mol	Chain	Res	Type	RSRZ
1	2-I	38[B]	PRO	7.4
1	2-J	159[B]	THR	7.4
1	2-N	253[B]	MET	7.4
1	3-I	38[C]	PRO	7.4
1	3-J	159[C]	THR	7.4
1	3-N	253[C]	MET	7.4
1	4-I	38[D]	PRO	7.4
1	4-J	159[D]	THR	7.4
1	4-N	253[D]	MET	7.4
1	1-I	295[A]	PHE	7.4
1	2-I	295[B]	PHE	7.4
1	3-I	295[C]	PHE	7.4
1	4-I	295[D]	PHE	7.4
1	1-I	184[A]	LEU	7.4
1	1-N	81[A]	LEU	7.4
1	2-I	184[B]	LEU	7.4
1	2-N	81[B]	LEU	7.4
1	3-I	184[C]	LEU	7.4
1	3-N	81[C]	LEU	7.4
1	4-I	184[D]	LEU	7.4
1	4-N	81[D]	LEU	7.4
1	1-J	144[A]	ASP	7.4
1	2-J	144[B]	ASP	7.4
1	3-J	144[C]	ASP	7.4
1	4-J	144[D]	ASP	7.4
1	1-P	103[A]	GLY	7.4
1	2-P	103[B]	GLY	7.4
1	3-P	103[C]	GLY	7.4
1	4-P	103[D]	GLY	7.4
1	1-K	169[A]	ILE	7.4
1	1-N	256[A]	ALA	7.4
1	2-K	169[B]	ILE	7.4
1	2-N	256[B]	ALA	7.4
1	3-K	169[C]	ILE	7.4
1	3-N	256[C]	ALA	7.4
1	4-K	169[D]	ILE	7.4
1	4-N	256[D]	ALA	7.4
1	1-J	233[A]	LEU	7.4
1	1-P	73[A]	LEU	7.4
1	2-J	233[B]	LEU	7.4
1	2-P	73[B]	LEU	7.4
1	3-J	233[C]	LEU	7.4

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Mol	Chain	Res	Type	RSRZ
1	3-P	73[C]	LEU	7.4
1	4-J	233[D]	LEU	7.4
1	4-P	73[D]	LEU	7.4
1	1-N	16[A]	PRO	7.4
1	1-P	164[A]	PRO	7.4
1	2-N	16[B]	PRO	7.4
1	2-P	164[B]	PRO	7.4
1	3-N	16[C]	PRO	7.4
1	3-P	164[C]	PRO	7.4
1	4-N	16[D]	PRO	7.4
1	4-P	164[D]	PRO	7.4
1	1-M	217[A]	SER	7.4
1	2-M	217[B]	SER	7.4
1	3-M	217[C]	SER	7.4
1	4-M	217[D]	SER	7.4
1	1-J	105[A]	GLY	7.4
1	1-N	114[A]	GLY	7.4
1	2-J	105[B]	GLY	7.4
1	2-N	114[B]	GLY	7.4
1	3-J	105[C]	GLY	7.4
1	3-N	114[C]	GLY	7.4
1	4-J	105[D]	GLY	7.4
1	4-N	114[D]	GLY	7.4
1	1-K	30[A]	ILE	7.4
1	1-K	289[A]	ILE	7.4
1	2-K	30[B]	ILE	7.4
1	2-K	289[B]	ILE	7.4
1	3-K	30[C]	ILE	7.4
1	3-K	289[C]	ILE	7.4
1	4-K	30[D]	ILE	7.4
1	4-K	289[D]	ILE	7.4
1	1-I	208[A]	LYS	7.4
1	2-I	208[B]	LYS	7.4
1	3-I	208[C]	LYS	7.4
1	4-I	208[D]	LYS	7.4
1	1-M	209[A]	LEU	7.4
1	1-N	280[A]	LEU	7.4
1	2-M	209[B]	LEU	7.4
1	2-N	280[B]	LEU	7.4
1	3-M	209[C]	LEU	7.4
1	3-N	280[C]	LEU	7.4
1	4-M	209[D]	LEU	7.4

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Mol	Chain	Res	Type	RSRZ
1	4-N	280[D]	LEU	7.4
1	1-O	86[A]	GLY	7.4
1	2-O	86[B]	GLY	7.4
1	3-O	86[C]	GLY	7.4
1	4-O	86[D]	GLY	7.4
1	1-O	17[A]	ASP	7.4
1	2-O	17[B]	ASP	7.4
1	3-O	17[C]	ASP	7.4
1	4-O	17[D]	ASP	7.4
1	1-N	225[A]	PRO	7.4
1	2-N	225[B]	PRO	7.4
1	3-N	225[C]	PRO	7.4
1	4-N	225[D]	PRO	7.4
1	1-K	53[A]	SER	7.3
1	2-K	53[B]	SER	7.3
1	3-K	53[C]	SER	7.3
1	4-K	53[D]	SER	7.3
1	1-J	302[A]	VAL	7.3
1	1-M	17[A]	ASP	7.3
1	1-M	71[A]	VAL	7.3
1	1-N	113[A]	VAL	7.3
1	1-O	263[A]	VAL	7.3
1	2-J	302[B]	VAL	7.3
1	2-M	17[B]	ASP	7.3
1	2-M	71[B]	VAL	7.3
1	2-N	113[B]	VAL	7.3
1	2-O	263[B]	VAL	7.3
1	3-J	302[C]	VAL	7.3
1	3-M	17[C]	ASP	7.3
1	3-M	71[C]	VAL	7.3
1	3-N	113[C]	VAL	7.3
1	3-O	263[C]	VAL	7.3
1	4-J	302[D]	VAL	7.3
1	4-M	17[D]	ASP	7.3
1	4-M	71[D]	VAL	7.3
1	4-N	113[D]	VAL	7.3
1	4-O	263[D]	VAL	7.3
1	1-I	103[A]	GLY	7.3
1	2-I	103[B]	GLY	7.3
1	3-I	103[C]	GLY	7.3
1	4-I	103[D]	GLY	7.3
1	1-J	212[A]	LEU	7.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-L	159[A]	THR	7.3
1	2-J	212[B]	LEU	7.3
1	2-L	159[B]	THR	7.3
1	3-J	212[C]	LEU	7.3
1	3-L	159[C]	THR	7.3
1	4-J	212[D]	LEU	7.3
1	4-L	159[D]	THR	7.3
1	1-O	174[A]	TRP	7.3
1	2-O	174[B]	TRP	7.3
1	3-O	174[C]	TRP	7.3
1	4-O	174[D]	TRP	7.3
1	1-N	289[A]	ILE	7.3
1	2-N	289[B]	ILE	7.3
1	3-N	289[C]	ILE	7.3
1	4-N	289[D]	ILE	7.3
1	1-M	93[A]	LEU	7.3
1	1-O	234[A]	LEU	7.3
1	2-M	93[B]	LEU	7.3
1	2-O	234[B]	LEU	7.3
1	3-M	93[C]	LEU	7.3
1	3-O	234[C]	LEU	7.3
1	4-M	93[D]	LEU	7.3
1	4-O	234[D]	LEU	7.3
1	1-I	78[A]	ALA	7.3
1	2-I	78[B]	ALA	7.3
1	3-I	78[C]	ALA	7.3
1	4-I	78[D]	ALA	7.3
1	1-K	18[A]	HIS	7.3
1	2-K	18[B]	HIS	7.3
1	3-K	18[C]	HIS	7.3
1	4-K	18[D]	HIS	7.3
1	1-L	147[A]	GLY	7.3
1	1-O	143[A]	GLY	7.3
1	2-L	147[B]	GLY	7.3
1	2-O	143[B]	GLY	7.3
1	3-L	147[C]	GLY	7.3
1	3-O	143[C]	GLY	7.3
1	4-L	147[D]	GLY	7.3
1	4-O	143[D]	GLY	7.3
1	1-J	206[A]	LYS	7.3
1	1-L	197[A]	LEU	7.3
1	2-J	206[B]	LYS	7.3

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Mol	Chain	Res	Type	RSRZ
1	2-L	197[B]	LEU	7.3
1	3-J	206[C]	LYS	7.3
1	3-L	197[C]	LEU	7.3
1	4-J	206[D]	LYS	7.3
1	4-L	197[D]	LEU	7.3
1	1-J	194[A]	PHE	7.3
1	2-J	194[B]	PHE	7.3
1	3-J	194[C]	PHE	7.3
1	4-J	194[D]	PHE	7.3
1	1-K	263[A]	VAL	7.3
1	2-K	263[B]	VAL	7.3
1	3-K	263[C]	VAL	7.3
1	4-K	263[D]	VAL	7.3
1	1-N	93[A]	LEU	7.3
1	2-N	93[B]	LEU	7.3
1	3-N	93[C]	LEU	7.3
1	4-N	93[D]	LEU	7.3
1	1-D	200[A]	ALA	7.2
1	1-M	274[A]	PRO	7.2
1	1-P	207[A]	PRO	7.2
1	2-D	200[B]	ALA	7.2
1	2-M	274[B]	PRO	7.2
1	2-P	207[B]	PRO	7.2
1	3-D	200[C]	ALA	7.2
1	3-M	274[C]	PRO	7.2
1	3-P	207[C]	PRO	7.2
1	4-D	200[D]	ALA	7.2
1	4-M	274[D]	PRO	7.2
1	4-P	207[D]	PRO	7.2
1	1-M	87[A]	CYS	7.2
1	2-M	87[B]	CYS	7.2
1	3-M	87[C]	CYS	7.2
1	4-M	87[D]	CYS	7.2
1	1-J	287[A]	GLU	7.2
1	2-J	287[B]	GLU	7.2
1	3-J	287[C]	GLU	7.2
1	4-J	287[D]	GLU	7.2
1	1-N	214[A]	TYR	7.2
1	2-N	214[B]	TYR	7.2
1	3-N	214[C]	TYR	7.2
1	4-N	214[D]	TYR	7.2
1	1-J	278[A]	PRO	7.2

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Mol	Chain	Res	Type	RSRZ
1	2-J	278[B]	PRO	7.2
1	3-J	278[C]	PRO	7.2
1	4-J	278[D]	PRO	7.2
1	1-I	65[A]	LEU	7.2
1	1-L	24[A]	LEU	7.2
1	1-M	26[A]	LEU	7.2
1	2-I	65[B]	LEU	7.2
1	2-L	24[B]	LEU	7.2
1	2-M	26[B]	LEU	7.2
1	3-I	65[C]	LEU	7.2
1	3-L	24[C]	LEU	7.2
1	3-M	26[C]	LEU	7.2
1	4-I	65[D]	LEU	7.2
1	4-L	24[D]	LEU	7.2
1	4-M	26[D]	LEU	7.2
1	1-L	193[A]	PHE	7.2
1	2-L	193[B]	PHE	7.2
1	3-L	193[C]	PHE	7.2
1	4-L	193[D]	PHE	7.2
1	1-M	312[A]	ASP	7.2
1	2-M	312[B]	ASP	7.2
1	3-M	312[C]	ASP	7.2
1	4-M	312[D]	ASP	7.2
1	1-N	165[A]	THR	7.2
1	1-P	235[A]	THR	7.2
1	2-N	165[B]	THR	7.2
1	2-P	235[B]	THR	7.2
1	3-N	165[C]	THR	7.2
1	3-P	235[C]	THR	7.2
1	4-N	165[D]	THR	7.2
1	4-P	235[D]	THR	7.2
1	1-N	254[A]	GLY	7.2
1	2-N	254[B]	GLY	7.2
1	3-N	254[C]	GLY	7.2
1	4-N	254[D]	GLY	7.2
1	1-N	311[A]	ILE	7.2
1	2-N	311[B]	ILE	7.2
1	3-N	311[C]	ILE	7.2
1	4-N	311[D]	ILE	7.2
1	1-N	66[A]	LEU	7.2
1	2-N	66[B]	LEU	7.2
1	3-N	66[C]	LEU	7.2

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Mol	Chain	Res	Type	RSRZ
1	4-N	66[D]	LEU	7.2
1	1-K	242[A]	THR	7.2
1	2-K	242[B]	THR	7.2
1	3-K	242[C]	THR	7.2
1	4-K	242[D]	THR	7.2
1	1-I	42[A]	GLY	7.2
1	1-K	196[A]	SER	7.2
1	2-I	42[B]	GLY	7.2
1	2-K	196[B]	SER	7.2
1	3-I	42[C]	GLY	7.2
1	3-K	196[C]	SER	7.2
1	4-I	42[D]	GLY	7.2
1	4-K	196[D]	SER	7.2
1	1-N	222[A]	LEU	7.2
1	2-N	222[B]	LEU	7.2
1	3-N	222[C]	LEU	7.2
1	4-N	222[D]	LEU	7.2
1	1-J	21[A]	TYR	7.2
1	2-J	21[B]	TYR	7.2
1	3-J	21[C]	TYR	7.2
1	4-J	21[D]	TYR	7.2
1	1-I	267[A]	LYS	7.2
1	1-L	182[A]	MET	7.2
1	2-I	267[B]	LYS	7.2
1	2-L	182[B]	MET	7.2
1	3-I	267[C]	LYS	7.2
1	3-L	182[C]	MET	7.2
1	4-I	267[D]	LYS	7.2
1	4-L	182[D]	MET	7.2
1	1-L	67[A]	THR	7.2
1	1-P	84[A]	VAL	7.2
1	1-P	258[A]	VAL	7.2
1	2-L	67[B]	THR	7.2
1	2-P	84[B]	VAL	7.2
1	2-P	258[B]	VAL	7.2
1	3-L	67[C]	THR	7.2
1	3-P	84[C]	VAL	7.2
1	3-P	258[C]	VAL	7.2
1	4-L	67[D]	THR	7.2
1	4-P	84[D]	VAL	7.2
1	4-P	258[D]	VAL	7.2
1	1-L	53[A]	SER	7.2

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Mol	Chain	Res	Type	RSRZ
1	2-L	53[B]	SER	7.2
1	3-L	53[C]	SER	7.2
1	4-L	53[D]	SER	7.2
1	1-J	91[A]	LYS	7.2
1	1-K	107[A]	LYS	7.2
1	1-O	138[A]	TYR	7.2
1	2-J	91[B]	LYS	7.2
1	2-K	107[B]	LYS	7.2
1	2-O	138[B]	TYR	7.2
1	3-J	91[C]	LYS	7.2
1	3-K	107[C]	LYS	7.2
1	3-O	138[C]	TYR	7.2
1	4-J	91[D]	LYS	7.2
1	4-K	107[D]	LYS	7.2
1	4-O	138[D]	TYR	7.2
1	1-L	156[A]	VAL	7.1
1	2-L	156[B]	VAL	7.1
1	3-L	156[C]	VAL	7.1
1	4-L	156[D]	VAL	7.1
1	1-J	186[A]	PRO	7.1
1	2-J	186[B]	PRO	7.1
1	3-J	186[C]	PRO	7.1
1	4-J	186[D]	PRO	7.1
1	1-K	308[A]	TRP	7.1
1	1-N	82[A]	TRP	7.1
1	2-K	308[B]	TRP	7.1
1	2-N	82[B]	TRP	7.1
1	3-K	308[C]	TRP	7.1
1	3-N	82[C]	TRP	7.1
1	4-K	308[D]	TRP	7.1
1	4-N	82[D]	TRP	7.1
1	1-P	34[A]	GLY	7.1
1	1-P	253[A]	MET	7.1
1	2-P	34[B]	GLY	7.1
1	2-P	253[B]	MET	7.1
1	3-P	34[C]	GLY	7.1
1	3-P	253[C]	MET	7.1
1	4-P	34[D]	GLY	7.1
1	4-P	253[D]	MET	7.1
1	1-J	96[A]	GLN	7.1
1	2-J	96[B]	GLN	7.1
1	3-J	96[C]	GLN	7.1

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Mol	Chain	Res	Type	RSRZ
1	4-J	96[D]	GLN	7.1
1	1-O	77[A]	ILE	7.1
1	2-O	77[B]	ILE	7.1
1	3-O	77[C]	ILE	7.1
1	4-O	77[D]	ILE	7.1
1	1-O	28[A]	ARG	7.1
1	2-O	28[B]	ARG	7.1
1	3-O	28[C]	ARG	7.1
1	4-O	28[D]	ARG	7.1
1	1-K	44[A]	GLY	7.1
1	2-K	44[B]	GLY	7.1
1	3-K	44[C]	GLY	7.1
1	4-K	44[D]	GLY	7.1
1	1-K	313[A]	MET	7.1
1	2-K	313[B]	MET	7.1
1	3-K	313[C]	MET	7.1
1	4-K	313[D]	MET	7.1
1	1-K	259[A]	TYR	7.1
1	2-K	259[B]	TYR	7.1
1	3-K	259[C]	TYR	7.1
1	4-K	259[D]	TYR	7.1
1	1-L	48[A]	LEU	7.1
1	2-L	48[B]	LEU	7.1
1	3-L	48[C]	LEU	7.1
1	4-L	48[D]	LEU	7.1
1	1-I	151[A]	ASP	7.1
1	2-I	151[B]	ASP	7.1
1	3-I	151[C]	ASP	7.1
1	4-I	151[D]	ASP	7.1
1	1-M	260[A]	ARG	7.1
1	2-M	260[B]	ARG	7.1
1	3-M	260[C]	ARG	7.1
1	4-M	260[D]	ARG	7.1
1	1-N	33[A]	VAL	7.1
1	2-N	33[B]	VAL	7.1
1	3-N	33[C]	VAL	7.1
1	4-N	33[D]	VAL	7.1
1	1-L	183[A]	ALA	7.1
1	2-L	183[B]	ALA	7.1
1	3-L	183[C]	ALA	7.1
1	4-L	183[D]	ALA	7.1
1	1-N	35[A]	GLU	7.1

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Mol	Chain	Res	Type	RSRZ
1	2-N	35[B]	GLU	7.1
1	3-N	35[C]	GLU	7.1
1	4-N	35[D]	GLU	7.1
1	1-I	243[A]	ASP	7.1
1	2-I	243[B]	ASP	7.1
1	3-I	243[C]	ASP	7.1
1	4-I	243[D]	ASP	7.1
1	1-O	228[A]	ILE	7.1
1	2-O	228[B]	ILE	7.1
1	3-O	228[C]	ILE	7.1
1	4-O	228[D]	ILE	7.1
1	1-M	131[A]	TRP	7.1
1	1-P	197[A]	LEU	7.1
1	2-M	131[B]	TRP	7.1
1	2-P	197[B]	LEU	7.1
1	3-M	131[C]	TRP	7.1
1	3-P	197[C]	LEU	7.1
1	4-M	131[D]	TRP	7.1
1	4-P	197[D]	LEU	7.1
1	1-N	258[A]	VAL	7.1
1	2-N	258[B]	VAL	7.1
1	3-N	258[C]	VAL	7.1
1	4-N	258[D]	VAL	7.1
1	1-K	57[A]	SER	7.1
1	2-K	57[B]	SER	7.1
1	3-K	57[C]	SER	7.1
1	4-K	57[D]	SER	7.1
1	1-M	291[A]	ASP	7.1
1	2-M	291[B]	ASP	7.1
1	3-M	291[C]	ASP	7.1
1	4-M	291[D]	ASP	7.1
1	1-L	80[A]	LEU	7.0
1	1-N	215[A]	GLN	7.0
1	1-O	21[A]	TYR	7.0
1	2-L	80[B]	LEU	7.0
1	2-N	215[B]	GLN	7.0
1	2-O	21[B]	TYR	7.0
1	3-L	80[C]	LEU	7.0
1	3-N	215[C]	GLN	7.0
1	3-O	21[C]	TYR	7.0
1	4-L	80[D]	LEU	7.0
1	4-N	215[D]	GLN	7.0

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Mol	Chain	Res	Type	RSRZ
1	4-O	21[D]	TYR	7.0
1	1-M	132[A]	ARG	7.0
1	1-N	190[A]	PHE	7.0
1	2-M	132[B]	ARG	7.0
1	2-N	190[B]	PHE	7.0
1	3-M	132[C]	ARG	7.0
1	3-N	190[C]	PHE	7.0
1	4-M	132[D]	ARG	7.0
1	4-N	190[D]	PHE	7.0
1	1-M	288[A]	GLU	7.0
1	2-M	288[B]	GLU	7.0
1	3-M	288[C]	GLU	7.0
1	4-M	288[D]	GLU	7.0
1	1-K	262[A]	HIS	7.0
1	1-N	43[A]	THR	7.0
1	2-K	262[B]	HIS	7.0
1	2-N	43[B]	THR	7.0
1	3-K	262[C]	HIS	7.0
1	3-N	43[C]	THR	7.0
1	4-K	262[D]	HIS	7.0
1	4-N	43[D]	THR	7.0
1	1-M	114[A]	GLY	7.0
1	2-M	114[B]	GLY	7.0
1	3-M	114[C]	GLY	7.0
1	4-M	114[D]	GLY	7.0
1	1-I	302[A]	VAL	7.0
1	1-M	84[A]	VAL	7.0
1	2-I	302[B]	VAL	7.0
1	2-M	84[B]	VAL	7.0
1	3-I	302[C]	VAL	7.0
1	3-M	84[C]	VAL	7.0
1	4-I	302[D]	VAL	7.0
1	4-M	84[D]	VAL	7.0
1	1-I	308[A]	TRP	7.0
1	2-I	308[B]	TRP	7.0
1	3-I	308[C]	TRP	7.0
1	4-I	308[D]	TRP	7.0
1	1-M	40[A]	ARG	7.0
1	1-O	135[A]	GLY	7.0
1	1-O	309[A]	GLY	7.0
1	2-M	40[B]	ARG	7.0
1	2-O	135[B]	GLY	7.0

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Mol	Chain	Res	Type	RSRZ
1	2-O	309[B]	GLY	7.0
1	3-M	40[C]	ARG	7.0
1	3-O	135[C]	GLY	7.0
1	3-O	309[C]	GLY	7.0
1	4-M	40[D]	ARG	7.0
1	4-O	135[D]	GLY	7.0
1	4-O	309[D]	GLY	7.0
1	1-C	14[A]	SER	7.0
1	1-I	110[A]	LEU	7.0
1	1-M	85[A]	SER	7.0
1	1-P	205[A]	SER	7.0
1	2-C	14[B]	SER	7.0
1	2-I	110[B]	LEU	7.0
1	2-M	85[B]	SER	7.0
1	2-P	205[B]	SER	7.0
1	3-C	14[C]	SER	7.0
1	3-I	110[C]	LEU	7.0
1	3-M	85[C]	SER	7.0
1	3-P	205[C]	SER	7.0
1	4-C	14[D]	SER	7.0
1	4-I	110[D]	LEU	7.0
1	4-M	85[D]	SER	7.0
1	4-P	205[D]	SER	7.0
1	1-L	50[A]	ALA	7.0
1	2-L	50[B]	ALA	7.0
1	3-L	50[C]	ALA	7.0
1	4-L	50[D]	ALA	7.0
1	1-K	231[A]	TYR	7.0
1	1-N	305[A]	TYR	7.0
1	2-K	231[B]	TYR	7.0
1	2-N	305[B]	TYR	7.0
1	3-K	231[C]	TYR	7.0
1	3-N	305[C]	TYR	7.0
1	4-K	231[D]	TYR	7.0
1	4-N	305[D]	TYR	7.0
1	1-O	277[A]	PHE	7.0
1	2-O	277[B]	PHE	7.0
1	3-O	277[C]	PHE	7.0
1	4-O	277[D]	PHE	7.0
1	1-I	55[A]	ARG	7.0
1	1-L	68[A]	THR	7.0
1	2-I	55[B]	ARG	7.0

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Mol	Chain	Res	Type	RSRZ
1	2-L	68[B]	THR	7.0
1	3-I	55[C]	ARG	7.0
1	3-L	68[C]	THR	7.0
1	4-I	55[D]	ARG	7.0
1	4-L	68[D]	THR	7.0
1	1-J	128[A]	GLY	7.0
1	2-J	128[B]	GLY	7.0
1	3-J	128[C]	GLY	7.0
1	4-J	128[D]	GLY	7.0
1	1-J	234[A]	LEU	7.0
1	1-L	228[A]	ILE	7.0
1	2-J	234[B]	LEU	7.0
1	2-L	228[B]	ILE	7.0
1	3-J	234[C]	LEU	7.0
1	3-L	228[C]	ILE	7.0
1	4-J	234[D]	LEU	7.0
1	4-L	228[D]	ILE	7.0
1	1-N	227[A]	ASN	7.0
1	2-N	227[B]	ASN	7.0
1	3-N	227[C]	ASN	7.0
1	4-N	227[D]	ASN	7.0
1	1-N	147[A]	GLY	7.0
1	2-N	147[B]	GLY	7.0
1	3-N	147[C]	GLY	7.0
1	4-N	147[D]	GLY	7.0
1	1-P	19[A]	GLU	7.0
1	2-P	19[B]	GLU	7.0
1	3-P	19[C]	GLU	7.0
1	4-P	19[D]	GLU	7.0
1	1-L	160[A]	ILE	7.0
1	1-M	153[A]	LEU	7.0
1	2-L	160[B]	ILE	7.0
1	2-M	153[B]	LEU	7.0
1	3-L	160[C]	ILE	7.0
1	3-M	153[C]	LEU	7.0
1	4-L	160[D]	ILE	7.0
1	4-M	153[D]	LEU	7.0
1	1-K	267[A]	LYS	7.0
1	1-N	34[A]	GLY	7.0
1	2-K	267[B]	LYS	7.0
1	2-N	34[B]	GLY	7.0
1	3-K	267[C]	LYS	7.0

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Mol	Chain	Res	Type	RSRZ
1	3-N	34[C]	GLY	7.0
1	4-K	267[D]	LYS	7.0
1	4-N	34[D]	GLY	7.0
1	1-L	129[A]	PHE	7.0
1	2-L	129[B]	PHE	7.0
1	3-L	129[C]	PHE	7.0
1	4-L	129[D]	PHE	7.0
1	1-P	272[A]	ARG	7.0
1	2-P	272[B]	ARG	7.0
1	3-P	272[C]	ARG	7.0
1	4-P	272[D]	ARG	7.0
1	1-I	164[A]	PRO	6.9
1	1-K	312[A]	ASP	6.9
1	2-I	164[B]	PRO	6.9
1	2-K	312[B]	ASP	6.9
1	3-I	164[C]	PRO	6.9
1	3-K	312[C]	ASP	6.9
1	4-I	164[D]	PRO	6.9
1	4-K	312[D]	ASP	6.9
1	1-K	100[A]	ILE	6.9
1	2-K	100[B]	ILE	6.9
1	3-K	100[C]	ILE	6.9
1	4-K	100[D]	ILE	6.9
1	1-I	23[A]	TYR	6.9
1	1-L	242[A]	THR	6.9
1	1-M	108[A]	GLU	6.9
1	1-M	231[A]	TYR	6.9
1	2-I	23[B]	TYR	6.9
1	2-L	242[B]	THR	6.9
1	2-M	108[B]	GLU	6.9
1	2-M	231[B]	TYR	6.9
1	3-I	23[C]	TYR	6.9
1	3-L	242[C]	THR	6.9
1	3-M	108[C]	GLU	6.9
1	3-M	231[C]	TYR	6.9
1	4-I	23[D]	TYR	6.9
1	4-L	242[D]	THR	6.9
1	4-M	108[D]	GLU	6.9
1	4-M	231[D]	TYR	6.9
1	1-I	210[A]	SER	6.9
1	2-I	210[B]	SER	6.9
1	3-I	210[C]	SER	6.9

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Mol	Chain	Res	Type	RSRZ
1	4-I	210[D]	SER	6.9
1	1-J	157[A]	ILE	6.9
1	1-L	250[A]	ILE	6.9
1	1-N	292[A]	ILE	6.9
1	2-J	157[B]	ILE	6.9
1	2-L	250[B]	ILE	6.9
1	2-N	292[B]	ILE	6.9
1	3-J	157[C]	ILE	6.9
1	3-L	250[C]	ILE	6.9
1	3-N	292[C]	ILE	6.9
1	4-J	157[D]	ILE	6.9
1	4-L	250[D]	ILE	6.9
1	4-N	292[D]	ILE	6.9
1	1-M	315[A]	MET	6.9
1	1-O	182[A]	MET	6.9
1	2-M	315[B]	MET	6.9
1	2-O	182[B]	MET	6.9
1	3-M	315[C]	MET	6.9
1	3-O	182[C]	MET	6.9
1	4-M	315[D]	MET	6.9
1	4-O	182[D]	MET	6.9
1	1-J	228[A]	ILE	6.9
1	1-M	172[A]	SER	6.9
1	1-N	68[A]	THR	6.9
1	2-J	228[B]	ILE	6.9
1	2-M	172[B]	SER	6.9
1	2-N	68[B]	THR	6.9
1	3-J	228[C]	ILE	6.9
1	3-M	172[C]	SER	6.9
1	3-N	68[C]	THR	6.9
1	4-J	228[D]	ILE	6.9
1	4-M	172[D]	SER	6.9
1	4-N	68[D]	THR	6.9
1	1-M	293[A]	ASP	6.9
1	2-M	293[B]	ASP	6.9
1	3-M	293[C]	ASP	6.9
1	4-M	293[D]	ASP	6.9
1	1-K	302[A]	VAL	6.9
1	2-K	302[B]	VAL	6.9
1	3-K	302[C]	VAL	6.9
1	4-K	302[D]	VAL	6.9
1	1-K	188[A]	HIS	6.9

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Mol	Chain	Res	Type	RSRZ
1	2-K	188[B]	HIS	6.9
1	3-K	188[C]	HIS	6.9
1	4-K	188[D]	HIS	6.9
1	1-J	167[A]	ARG	6.9
1	1-K	37[A]	ARG	6.9
1	2-J	167[B]	ARG	6.9
1	2-K	37[B]	ARG	6.9
1	3-J	167[C]	ARG	6.9
1	3-K	37[C]	ARG	6.9
1	4-J	167[D]	ARG	6.9
1	4-K	37[D]	ARG	6.9
1	1-L	178[A]	ASP	6.9
1	2-L	178[B]	ASP	6.9
1	3-L	178[C]	ASP	6.9
1	4-L	178[D]	ASP	6.9
1	1-K	245[A]	GLU	6.9
1	1-L	19[A]	GLU	6.9
1	2-K	245[B]	GLU	6.9
1	2-L	19[B]	GLU	6.9
1	3-K	245[C]	GLU	6.9
1	3-L	19[C]	GLU	6.9
1	4-K	245[D]	GLU	6.9
1	4-L	19[D]	GLU	6.9
1	1-O	117[A]	HIS	6.9
1	2-O	117[B]	HIS	6.9
1	3-O	117[C]	HIS	6.9
1	4-O	117[D]	HIS	6.9
1	1-I	249[A]	PHE	6.9
1	2-I	249[B]	PHE	6.9
1	3-I	249[C]	PHE	6.9
1	4-I	249[D]	PHE	6.9
1	1-J	243[A]	ASP	6.9
1	2-J	243[B]	ASP	6.9
1	3-J	243[C]	ASP	6.9
1	4-J	243[D]	ASP	6.9
1	1-N	316[A]	SER	6.9
1	2-N	316[B]	SER	6.9
1	3-N	316[C]	SER	6.9
1	4-N	316[D]	SER	6.9
1	1-K	139[A]	THR	6.9
1	1-K	244[A]	THR	6.9
1	2-K	139[B]	THR	6.9

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Mol	Chain	Res	Type	RSRZ
1	2-K	244[B]	THR	6.9
1	3-K	139[C]	THR	6.9
1	3-K	244[C]	THR	6.9
1	4-K	139[D]	THR	6.9
1	4-K	244[D]	THR	6.9
1	1-O	251[A]	LEU	6.9
1	1-P	233[A]	LEU	6.9
1	2-O	251[B]	LEU	6.9
1	2-P	233[B]	LEU	6.9
1	3-O	251[C]	LEU	6.9
1	3-P	233[C]	LEU	6.9
1	4-O	251[D]	LEU	6.9
1	4-P	233[D]	LEU	6.9
1	1-I	292[A]	ILE	6.9
1	1-N	118[A]	ARG	6.9
1	2-I	292[B]	ILE	6.9
1	1-O	176[A]	PRO	6.9
1	2-N	118[B]	ARG	6.9
1	3-I	292[C]	ILE	6.9
1	3-N	118[C]	ARG	6.9
1	4-I	292[D]	ILE	6.9
1	2-O	176[B]	PRO	6.9
1	3-O	176[C]	PRO	6.9
1	4-N	118[D]	ARG	6.9
1	4-O	176[D]	PRO	6.9
1	1-M	99[A]	GLY	6.9
1	1-N	108[A]	GLU	6.9
1	2-M	99[B]	GLY	6.9
1	2-N	108[B]	GLU	6.9
1	3-M	99[C]	GLY	6.9
1	3-N	108[C]	GLU	6.9
1	4-M	99[D]	GLY	6.9
1	4-N	108[D]	GLU	6.9
1	1-I	283[A]	ALA	6.9
1	2-I	283[B]	ALA	6.9
1	3-I	283[C]	ALA	6.9
1	4-I	283[D]	ALA	6.9
1	1-K	92[A]	MET	6.9
1	2-K	92[B]	MET	6.9
1	3-K	92[C]	MET	6.9
1	4-K	92[D]	MET	6.9
1	1-I	247[A]	HIS	6.8

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Mol	Chain	Res	Type	RSRZ
1	2-I	247[B]	HIS	6.8
1	3-I	247[C]	HIS	6.8
1	4-I	247[D]	HIS	6.8
1	1-J	220[A]	LEU	6.8
1	1-K	220[A]	LEU	6.8
1	2-J	220[B]	LEU	6.8
1	2-K	220[B]	LEU	6.8
1	3-J	220[C]	LEU	6.8
1	3-K	220[C]	LEU	6.8
1	4-J	220[D]	LEU	6.8
1	4-K	220[D]	LEU	6.8
1	1-I	204[A]	GLY	6.8
1	2-I	204[B]	GLY	6.8
1	3-I	204[C]	GLY	6.8
1	4-I	204[D]	GLY	6.8
1	1-K	253[A]	MET	6.8
1	2-K	253[B]	MET	6.8
1	3-K	253[C]	MET	6.8
1	4-K	253[D]	MET	6.8
1	1-L	109[A]	PHE	6.8
1	1-O	74[A]	ARG	6.8
1	2-L	109[B]	PHE	6.8
1	2-O	74[B]	ARG	6.8
1	3-L	109[C]	PHE	6.8
1	3-O	74[C]	ARG	6.8
1	4-L	109[D]	PHE	6.8
1	4-O	74[D]	ARG	6.8
1	1-F	199[A]	PRO	6.8
1	1-O	312[A]	ASP	6.8
1	1-P	176[A]	PRO	6.8
1	2-F	199[B]	PRO	6.8
1	2-O	312[B]	ASP	6.8
1	2-P	176[B]	PRO	6.8
1	3-F	199[C]	PRO	6.8
1	3-O	312[C]	ASP	6.8
1	3-P	176[C]	PRO	6.8
1	4-F	199[D]	PRO	6.8
1	4-O	312[D]	ASP	6.8
1	4-P	176[D]	PRO	6.8
1	1-I	128[A]	GLY	6.8
1	1-L	42[A]	GLY	6.8
1	1-N	240[A]	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
1	2-I	128[B]	GLY	6.8
1	2-L	42[B]	GLY	6.8
1	2-N	240[B]	LEU	6.8
1	3-I	128[C]	GLY	6.8
1	3-L	42[C]	GLY	6.8
1	3-N	240[C]	LEU	6.8
1	4-I	128[D]	GLY	6.8
1	4-L	42[D]	GLY	6.8
1	4-N	240[D]	LEU	6.8
1	1-J	241[A]	ILE	6.8
1	1-L	169[A]	ILE	6.8
1	2-J	241[B]	ILE	6.8
1	2-L	169[B]	ILE	6.8
1	3-J	241[C]	ILE	6.8
1	3-L	169[C]	ILE	6.8
1	4-J	241[D]	ILE	6.8
1	4-L	169[D]	ILE	6.8
1	1-M	145[A]	TYR	6.8
1	2-M	145[B]	TYR	6.8
1	3-M	145[C]	TYR	6.8
1	4-M	145[D]	TYR	6.8
1	1-O	89[A]	ASP	6.8
1	2-O	89[B]	ASP	6.8
1	3-O	89[C]	ASP	6.8
1	4-O	89[D]	ASP	6.8
1	1-I	162[A]	ASN	6.8
1	1-J	176[A]	PRO	6.8
1	1-M	146[A]	LYS	6.8
1	1-O	225[A]	PRO	6.8
1	2-I	162[B]	ASN	6.8
1	2-J	176[B]	PRO	6.8
1	2-M	146[B]	LYS	6.8
1	2-O	225[B]	PRO	6.8
1	3-I	162[C]	ASN	6.8
1	3-J	176[C]	PRO	6.8
1	3-M	146[C]	LYS	6.8
1	3-O	225[C]	PRO	6.8
1	4-I	162[D]	ASN	6.8
1	4-J	176[D]	PRO	6.8
1	4-M	146[D]	LYS	6.8
1	4-O	225[D]	PRO	6.8
1	1-K	124[A]	GLY	6.8

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Mol	Chain	Res	Type	RSRZ
1	2-K	124[B]	GLY	6.8
1	3-K	124[C]	GLY	6.8
1	4-K	124[D]	GLY	6.8
1	1-L	171[A]	LEU	6.8
1	1-M	55[A]	ARG	6.8
1	1-P	115[A]	LEU	6.8
1	2-L	171[B]	LEU	6.8
1	2-M	55[B]	ARG	6.8
1	2-P	115[B]	LEU	6.8
1	3-L	171[C]	LEU	6.8
1	3-M	55[C]	ARG	6.8
1	3-P	115[C]	LEU	6.8
1	4-L	171[D]	LEU	6.8
1	4-M	55[D]	ARG	6.8
1	4-P	115[D]	LEU	6.8
1	1-L	262[A]	HIS	6.8
1	2-L	262[B]	HIS	6.8
1	3-L	262[C]	HIS	6.8
1	4-L	262[D]	HIS	6.8
1	1-I	306[A]	LYS	6.8
1	2-I	306[B]	LYS	6.8
1	3-I	306[C]	LYS	6.8
1	4-I	306[D]	LYS	6.8
1	1-K	290[A]	GLY	6.8
1	1-L	128[A]	GLY	6.8
1	2-K	290[B]	GLY	6.8
1	2-L	128[B]	GLY	6.8
1	3-K	290[C]	GLY	6.8
1	3-L	128[C]	GLY	6.8
1	4-K	290[D]	GLY	6.8
1	4-L	128[D]	GLY	6.8
1	1-P	208[A]	LYS	6.8
1	2-P	208[B]	LYS	6.8
1	3-P	208[C]	LYS	6.8
1	4-P	208[D]	LYS	6.8
1	1-J	142[A]	ASP	6.8
1	2-J	142[B]	ASP	6.8
1	3-J	142[C]	ASP	6.8
1	4-J	142[D]	ASP	6.8
1	1-N	269[A]	GLN	6.8
1	1-P	237[A]	MET	6.8
1	2-N	269[B]	GLN	6.8

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Mol	Chain	Res	Type	RSRZ
1	2-P	237[B]	MET	6.8
1	3-N	269[C]	GLN	6.8
1	3-P	237[C]	MET	6.8
1	4-N	269[D]	GLN	6.8
1	4-P	237[D]	MET	6.8
1	1-O	43[A]	THR	6.8
1	2-O	43[B]	THR	6.8
1	3-O	43[C]	THR	6.8
1	4-O	43[D]	THR	6.8
1	1-O	214[A]	TYR	6.8
1	2-O	214[B]	TYR	6.8
1	3-O	214[C]	TYR	6.8
1	4-O	214[D]	TYR	6.8
1	1-O	249[A]	PHE	6.8
1	2-O	249[B]	PHE	6.8
1	3-O	249[C]	PHE	6.8
1	4-O	249[D]	PHE	6.8
1	1-P	236[A]	HIS	6.8
1	2-P	236[B]	HIS	6.8
1	3-P	236[C]	HIS	6.8
1	4-P	236[D]	HIS	6.8
1	1-K	22[A]	GLN	6.8
1	1-L	283[A]	ALA	6.8
1	2-K	22[B]	GLN	6.8
1	2-L	283[B]	ALA	6.8
1	3-K	22[C]	GLN	6.8
1	3-L	283[C]	ALA	6.8
1	4-K	22[D]	GLN	6.8
1	4-L	283[D]	ALA	6.8
1	1-K	71[A]	VAL	6.8
1	1-N	272[A]	ARG	6.8
1	2-K	71[B]	VAL	6.8
1	2-N	272[B]	ARG	6.8
1	3-K	71[C]	VAL	6.8
1	3-N	272[C]	ARG	6.8
1	4-K	71[D]	VAL	6.8
1	4-N	272[D]	ARG	6.8
1	1-L	38[A]	PRO	6.8
1	2-L	38[B]	PRO	6.8
1	3-L	38[C]	PRO	6.8
1	4-L	38[D]	PRO	6.8
1	1-M	24[A]	LEU	6.7

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Mol	Chain	Res	Type	RSRZ
1	2-M	24[B]	LEU	6.7
1	3-M	24[C]	LEU	6.7
1	4-M	24[D]	LEU	6.7
1	1-K	294[A]	GLY	6.7
1	2-K	294[B]	GLY	6.7
1	3-K	294[C]	GLY	6.7
1	4-K	294[D]	GLY	6.7
1	1-I	180[A]	PRO	6.7
1	1-L	16[A]	PRO	6.7
1	1-M	64[A]	PRO	6.7
1	2-I	180[B]	PRO	6.7
1	2-L	16[B]	PRO	6.7
1	2-M	64[B]	PRO	6.7
1	3-I	180[C]	PRO	6.7
1	3-L	16[C]	PRO	6.7
1	3-M	64[C]	PRO	6.7
1	4-I	180[D]	PRO	6.7
1	4-L	16[D]	PRO	6.7
1	4-M	64[D]	PRO	6.7
1	1-N	67[A]	THR	6.7
1	1-P	88[A]	THR	6.7
1	2-N	67[B]	THR	6.7
1	2-P	88[B]	THR	6.7
1	3-N	67[C]	THR	6.7
1	3-P	88[C]	THR	6.7
1	4-N	67[D]	THR	6.7
1	4-P	88[D]	THR	6.7
1	1-J	316[A]	SER	6.7
1	2-J	316[B]	SER	6.7
1	3-J	316[C]	SER	6.7
1	4-J	316[D]	SER	6.7
1	1-N	111[A]	GLU	6.7
1	2-N	111[B]	GLU	6.7
1	3-N	111[C]	GLU	6.7
1	4-N	111[D]	GLU	6.7
1	1-L	180[A]	PRO	6.7
1	2-L	180[B]	PRO	6.7
1	3-L	180[C]	PRO	6.7
1	4-L	180[D]	PRO	6.7
1	1-N	148[A]	LYS	6.7
1	2-N	148[B]	LYS	6.7
1	3-N	148[C]	LYS	6.7

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Mol	Chain	Res	Type	RSRZ
1	4-N	148[D]	LYS	6.7
1	1-O	120[A]	GLU	6.7
1	2-O	120[B]	GLU	6.7
1	3-O	120[C]	GLU	6.7
1	4-O	120[D]	GLU	6.7
1	1-P	110[A]	LEU	6.7
1	2-P	110[B]	LEU	6.7
1	3-P	110[C]	LEU	6.7
1	4-P	110[D]	LEU	6.7
1	1-L	168[A]	ARG	6.7
1	2-L	168[B]	ARG	6.7
1	3-L	168[C]	ARG	6.7
1	4-L	168[D]	ARG	6.7
1	1-M	102[A]	ASP	6.7
1	2-M	102[B]	ASP	6.7
1	3-M	102[C]	ASP	6.7
1	4-M	102[D]	ASP	6.7
1	1-I	260[A]	ARG	6.7
1	2-I	260[B]	ARG	6.7
1	3-I	260[C]	ARG	6.7
1	4-I	260[D]	ARG	6.7
1	1-I	32[A]	ASN	6.7
1	1-I	244[A]	THR	6.7
1	1-J	88[A]	THR	6.7
1	1-K	287[A]	GLU	6.7
1	1-N	217[A]	SER	6.7
1	2-I	32[B]	ASN	6.7
1	2-I	244[B]	THR	6.7
1	2-J	88[B]	THR	6.7
1	2-K	287[B]	GLU	6.7
1	2-N	217[B]	SER	6.7
1	3-I	32[C]	ASN	6.7
1	3-I	244[C]	THR	6.7
1	3-J	88[C]	THR	6.7
1	3-K	287[C]	GLU	6.7
1	3-N	217[C]	SER	6.7
1	4-I	32[D]	ASN	6.7
1	4-I	244[D]	THR	6.7
1	4-J	88[D]	THR	6.7
1	4-K	287[D]	GLU	6.7
1	4-N	217[D]	SER	6.7
1	1-M	238[A]	ILE	6.7

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Mol	Chain	Res	Type	RSRZ
1	2-M	238[B]	ILE	6.7
1	3-M	238[C]	ILE	6.7
1	4-M	238[D]	ILE	6.7
1	1-L	255[A]	ASP	6.7
1	2-L	255[B]	ASP	6.7
1	3-L	255[C]	ASP	6.7
1	4-L	255[D]	ASP	6.7
1	1-L	54[A]	PHE	6.7
1	2-L	54[B]	PHE	6.7
1	3-L	54[C]	PHE	6.7
1	4-L	54[D]	PHE	6.7
1	1-L	21[A]	TYR	6.7
1	2-L	21[B]	TYR	6.7
1	3-L	21[C]	TYR	6.7
1	4-L	21[D]	TYR	6.7
1	1-M	196[A]	SER	6.7
1	2-M	196[B]	SER	6.7
1	3-M	196[C]	SER	6.7
1	4-M	196[D]	SER	6.7
1	1-J	75[A]	GLY	6.7
1	1-P	128[A]	GLY	6.7
1	2-J	75[B]	GLY	6.7
1	2-P	128[B]	GLY	6.7
1	3-J	75[C]	GLY	6.7
1	3-P	128[C]	GLY	6.7
1	4-J	75[D]	GLY	6.7
1	4-P	128[D]	GLY	6.7
1	1-J	101[A]	TRP	6.7
1	1-N	248[A]	GLU	6.7
1	2-J	101[B]	TRP	6.7
1	2-N	248[B]	GLU	6.7
1	3-J	101[C]	TRP	6.7
1	3-N	248[C]	GLU	6.7
1	4-J	101[D]	TRP	6.7
1	4-N	248[D]	GLU	6.7
1	1-N	64[A]	PRO	6.7
1	2-N	64[B]	PRO	6.7
1	3-N	64[C]	PRO	6.7
1	4-N	64[D]	PRO	6.7
1	1-P	262[A]	HIS	6.6
1	2-P	262[B]	HIS	6.6
1	3-P	262[C]	HIS	6.6

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Mol	Chain	Res	Type	RSRZ
1	4-P	262[D]	HIS	6.6
1	1-I	165[A]	THR	6.6
1	2-I	165[B]	THR	6.6
1	3-I	165[C]	THR	6.6
1	4-I	165[D]	THR	6.6
1	1-N	286[A]	LYS	6.6
1	2-N	286[B]	LYS	6.6
1	3-N	286[C]	LYS	6.6
1	4-N	286[D]	LYS	6.6
1	1-I	70[A]	ARG	6.6
1	1-M	168[A]	ARG	6.6
1	2-I	70[B]	ARG	6.6
1	2-M	168[B]	ARG	6.6
1	3-I	70[C]	ARG	6.6
1	3-M	168[C]	ARG	6.6
1	4-I	70[D]	ARG	6.6
1	4-M	168[D]	ARG	6.6
1	1-M	58[A]	LEU	6.6
1	1-N	184[A]	LEU	6.6
1	2-M	58[B]	LEU	6.6
1	2-N	184[B]	LEU	6.6
1	3-M	58[C]	LEU	6.6
1	3-N	184[C]	LEU	6.6
1	4-M	58[D]	LEU	6.6
1	4-N	184[D]	LEU	6.6
1	1-K	296[A]	LYS	6.6
1	2-K	296[B]	LYS	6.6
1	3-K	296[C]	LYS	6.6
1	4-K	296[D]	LYS	6.6
1	1-J	273[A]	GLU	6.6
1	1-P	188[A]	HIS	6.6
1	2-J	273[B]	GLU	6.6
1	2-P	188[B]	HIS	6.6
1	3-J	273[C]	GLU	6.6
1	3-P	188[C]	HIS	6.6
1	4-J	273[D]	GLU	6.6
1	4-P	188[D]	HIS	6.6
1	1-J	184[A]	LEU	6.6
1	1-K	73[A]	LEU	6.6
1	1-K	163[A]	ASN	6.6
1	2-J	184[B]	LEU	6.6
1	2-K	73[B]	LEU	6.6

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Mol	Chain	Res	Type	RSRZ
1	2-K	163[B]	ASN	6.6
1	3-J	184[C]	LEU	6.6
1	3-K	73[C]	LEU	6.6
1	3-K	163[C]	ASN	6.6
1	4-J	184[D]	LEU	6.6
1	4-K	73[D]	LEU	6.6
1	4-K	163[D]	ASN	6.6
1	1-M	258[A]	VAL	6.6
1	2-M	258[B]	VAL	6.6
1	3-M	258[C]	VAL	6.6
1	4-M	258[D]	VAL	6.6
1	1-J	50[A]	ALA	6.6
1	1-K	241[A]	ILE	6.6
1	1-L	78[A]	ALA	6.6
1	1-N	210[A]	SER	6.6
1	1-O	217[A]	SER	6.6
1	2-J	50[B]	ALA	6.6
1	2-K	241[B]	ILE	6.6
1	2-L	78[B]	ALA	6.6
1	2-N	210[B]	SER	6.6
1	2-O	217[B]	SER	6.6
1	3-J	50[C]	ALA	6.6
1	3-K	241[C]	ILE	6.6
1	3-L	78[C]	ALA	6.6
1	3-N	210[C]	SER	6.6
1	3-O	217[C]	SER	6.6
1	4-J	50[D]	ALA	6.6
1	4-K	241[D]	ILE	6.6
1	4-L	78[D]	ALA	6.6
1	4-N	210[D]	SER	6.6
1	4-O	217[D]	SER	6.6
1	1-L	309[A]	GLY	6.6
1	2-L	309[B]	GLY	6.6
1	3-L	309[C]	GLY	6.6
1	4-L	309[D]	GLY	6.6
1	1-J	252[A]	GLN	6.6
1	2-J	252[B]	GLN	6.6
1	3-J	252[C]	GLN	6.6
1	4-J	252[D]	GLN	6.6
1	1-P	300[A]	PHE	6.6
1	2-P	300[B]	PHE	6.6
1	3-P	300[C]	PHE	6.6

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Mol	Chain	Res	Type	RSRZ
1	4-P	300[D]	PHE	6.6
1	1-A	201[A]	ASP	6.6
1	1-I	24[A]	LEU	6.6
1	2-A	201[B]	ASP	6.6
1	2-I	24[B]	LEU	6.6
1	3-A	201[C]	ASP	6.6
1	3-I	24[C]	LEU	6.6
1	4-A	201[D]	ASP	6.6
1	4-I	24[D]	LEU	6.6
1	1-I	187[A]	CYS	6.6
1	2-I	187[B]	CYS	6.6
1	3-I	187[C]	CYS	6.6
1	4-I	187[D]	CYS	6.6
1	1-O	301[A]	VAL	6.6
1	2-O	301[B]	VAL	6.6
1	3-O	301[C]	VAL	6.6
1	4-O	301[D]	VAL	6.6
1	1-I	262[A]	HIS	6.6
1	1-K	225[A]	PRO	6.6
1	2-I	262[B]	HIS	6.6
1	2-K	225[B]	PRO	6.6
1	3-I	262[C]	HIS	6.6
1	3-K	225[C]	PRO	6.6
1	4-I	262[D]	HIS	6.6
1	4-K	225[D]	PRO	6.6
1	1-L	196[A]	SER	6.6
1	1-L	230[A]	SER	6.6
1	2-L	196[B]	SER	6.6
1	2-L	230[B]	SER	6.6
1	3-L	196[C]	SER	6.6
1	3-L	230[C]	SER	6.6
1	4-L	196[D]	SER	6.6
1	4-L	230[D]	SER	6.6
1	1-I	259[A]	TYR	6.6
1	1-O	283[A]	ALA	6.6
1	2-I	259[B]	TYR	6.6
1	2-O	283[B]	ALA	6.6
1	3-I	259[C]	TYR	6.6
1	3-O	283[C]	ALA	6.6
1	4-I	259[D]	TYR	6.6
1	4-O	283[D]	ALA	6.6
1	1-P	224[A]	VAL	6.6

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Mol	Chain	Res	Type	RSRZ
1	2-P	224[B]	VAL	6.6
1	3-P	224[C]	VAL	6.6
1	4-P	224[D]	VAL	6.6
1	1-N	96[A]	GLN	6.6
1	2-N	96[B]	GLN	6.6
1	3-N	96[C]	GLN	6.6
1	4-N	96[D]	GLN	6.6
1	1-P	241[A]	ILE	6.6
1	2-P	241[B]	ILE	6.6
1	3-P	241[C]	ILE	6.6
1	4-P	241[D]	ILE	6.6
1	1-J	155[A]	ARG	6.6
1	1-O	299[A]	ASP	6.6
1	2-J	155[B]	ARG	6.6
1	2-O	299[B]	ASP	6.6
1	3-J	155[C]	ARG	6.6
1	3-O	299[C]	ASP	6.6
1	4-J	155[D]	ARG	6.6
1	4-O	299[D]	ASP	6.6
1	1-N	117[A]	HIS	6.5
1	2-N	117[B]	HIS	6.5
1	3-N	117[C]	HIS	6.5
1	4-N	117[D]	HIS	6.5
1	1-M	189[A]	MET	6.5
1	2-M	189[B]	MET	6.5
1	3-M	189[C]	MET	6.5
1	4-M	189[D]	MET	6.5
1	1-K	150[A]	VAL	6.5
1	2-K	150[B]	VAL	6.5
1	3-K	150[C]	VAL	6.5
1	4-K	150[D]	VAL	6.5
1	1-K	77[A]	ILE	6.5
1	1-M	112[A]	LYS	6.5
1	2-K	77[B]	ILE	6.5
1	2-M	112[B]	LYS	6.5
1	3-K	77[C]	ILE	6.5
1	3-M	112[C]	LYS	6.5
1	4-K	77[D]	ILE	6.5
1	4-M	112[D]	LYS	6.5
1	1-O	88[A]	THR	6.5
1	2-O	88[B]	THR	6.5
1	3-O	88[C]	THR	6.5

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Mol	Chain	Res	Type	RSRZ
1	4-O	88[D]	THR	6.5
1	1-I	54[A]	PHE	6.5
1	1-I	144[A]	ASP	6.5
1	1-I	255[A]	ASP	6.5
1	1-J	232[A]	ALA	6.5
1	1-L	190[A]	PHE	6.5
1	2-I	54[B]	PHE	6.5
1	2-I	144[B]	ASP	6.5
1	2-I	255[B]	ASP	6.5
1	2-J	232[B]	ALA	6.5
1	2-L	190[B]	PHE	6.5
1	3-I	54[C]	PHE	6.5
1	3-I	144[C]	ASP	6.5
1	3-I	255[C]	ASP	6.5
1	3-J	232[C]	ALA	6.5
1	3-L	190[C]	PHE	6.5
1	4-I	54[D]	PHE	6.5
1	4-I	144[D]	ASP	6.5
1	4-I	255[D]	ASP	6.5
1	4-J	232[D]	ALA	6.5
1	4-L	190[D]	PHE	6.5
1	1-J	242[A]	THR	6.5
1	2-J	242[B]	THR	6.5
1	3-J	242[C]	THR	6.5
1	4-J	242[D]	THR	6.5
1	1-L	311[A]	ILE	6.5
1	2-L	311[B]	ILE	6.5
1	3-L	311[C]	ILE	6.5
1	4-L	311[D]	ILE	6.5
1	1-I	196[A]	SER	6.5
1	2-I	196[B]	SER	6.5
1	3-I	196[C]	SER	6.5
1	4-I	196[D]	SER	6.5
1	1-I	29[A]	ARG	6.5
1	2-I	29[B]	ARG	6.5
1	3-I	29[C]	ARG	6.5
1	4-I	29[D]	ARG	6.5
1	1-M	255[A]	ASP	6.5
1	2-M	255[B]	ASP	6.5
1	3-M	255[C]	ASP	6.5
1	4-M	255[D]	ASP	6.5
1	1-I	49[A]	PHE	6.5

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Mol	Chain	Res	Type	RSRZ
1	1-O	134[A]	PHE	6.5
1	2-I	49[B]	PHE	6.5
1	2-O	134[B]	PHE	6.5
1	3-I	49[C]	PHE	6.5
1	3-O	134[C]	PHE	6.5
1	4-I	49[D]	PHE	6.5
1	4-O	134[D]	PHE	6.5
1	1-I	161[A]	LYS	6.5
1	1-L	101[A]	TRP	6.5
1	1-P	274[A]	PRO	6.5
1	2-I	161[B]	LYS	6.5
1	2-L	101[B]	TRP	6.5
1	2-P	274[B]	PRO	6.5
1	3-I	161[C]	LYS	6.5
1	3-L	101[C]	TRP	6.5
1	3-P	274[C]	PRO	6.5
1	4-I	161[D]	LYS	6.5
1	4-L	101[D]	TRP	6.5
1	4-P	274[D]	PRO	6.5
1	1-N	287[A]	GLU	6.5
1	2-N	287[B]	GLU	6.5
1	3-N	287[C]	GLU	6.5
1	4-N	287[D]	GLU	6.5
1	1-I	97[A]	GLY	6.5
1	2-I	97[B]	GLY	6.5
1	3-I	97[C]	GLY	6.5
1	4-I	97[D]	GLY	6.5
1	1-L	73[A]	LEU	6.5
1	1-O	83[A]	PHE	6.5
1	2-L	73[B]	LEU	6.5
1	2-O	83[B]	PHE	6.5
1	3-L	73[C]	LEU	6.5
1	3-O	83[C]	PHE	6.5
1	4-L	73[D]	LEU	6.5
1	4-O	83[D]	PHE	6.5
1	1-L	268[A]	THR	6.5
1	2-L	268[B]	THR	6.5
1	3-L	268[C]	THR	6.5
1	4-L	268[D]	THR	6.5
1	1-K	307[A]	PRO	6.5
1	2-K	307[B]	PRO	6.5
1	3-K	307[C]	PRO	6.5

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Mol	Chain	Res	Type	RSRZ
1	4-K	307[D]	PRO	6.5
1	1-K	146[A]	LYS	6.5
1	2-K	146[B]	LYS	6.5
1	3-K	146[C]	LYS	6.5
1	4-K	146[D]	LYS	6.5
1	1-L	247[A]	HIS	6.5
1	2-L	247[B]	HIS	6.5
1	3-L	247[C]	HIS	6.5
1	4-L	247[D]	HIS	6.5
1	1-I	222[A]	LEU	6.5
1	2-I	222[B]	LEU	6.5
1	3-I	222[C]	LEU	6.5
1	4-I	222[D]	LEU	6.5
1	1-L	97[A]	GLY	6.5
1	1-I	152[A]	GLN	6.5
1	1-P	77[A]	ILE	6.5
1	2-L	97[B]	GLY	6.5
1	2-I	152[B]	GLN	6.5
1	2-P	77[B]	ILE	6.5
1	3-L	97[C]	GLY	6.5
1	3-I	152[C]	GLN	6.5
1	3-P	77[C]	ILE	6.5
1	4-L	97[D]	GLY	6.5
1	4-I	152[D]	GLN	6.5
1	4-P	77[D]	ILE	6.5
1	1-O	70[A]	ARG	6.4
1	1-P	118[A]	ARG	6.4
1	2-O	70[B]	ARG	6.4
1	2-P	118[B]	ARG	6.4
1	3-O	70[C]	ARG	6.4
1	3-P	118[C]	ARG	6.4
1	4-O	70[D]	ARG	6.4
1	4-P	118[D]	ARG	6.4
1	1-I	176[A]	PRO	6.4
1	1-M	240[A]	LEU	6.4
1	1-P	68[A]	THR	6.4
1	2-I	176[B]	PRO	6.4
1	2-M	240[B]	LEU	6.4
1	2-P	68[B]	THR	6.4
1	3-I	176[C]	PRO	6.4
1	3-M	240[C]	LEU	6.4
1	3-P	68[C]	THR	6.4

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Mol	Chain	Res	Type	RSRZ
1	4-I	176[D]	PRO	6.4
1	4-M	240[D]	LEU	6.4
1	4-P	68[D]	THR	6.4
1	1-P	91[A]	LYS	6.4
1	1-P	193[A]	PHE	6.4
1	2-P	91[B]	LYS	6.4
1	2-P	193[B]	PHE	6.4
1	3-P	91[C]	LYS	6.4
1	3-P	193[C]	PHE	6.4
1	4-P	91[D]	LYS	6.4
1	4-P	193[D]	PHE	6.4
1	1-N	224[A]	VAL	6.4
1	2-N	224[B]	VAL	6.4
1	3-N	224[C]	VAL	6.4
1	4-N	224[D]	VAL	6.4
1	1-K	89[A]	ASP	6.4
1	1-L	293[A]	ASP	6.4
1	1-P	299[A]	ASP	6.4
1	2-K	89[B]	ASP	6.4
1	2-L	293[B]	ASP	6.4
1	2-P	299[B]	ASP	6.4
1	3-K	89[C]	ASP	6.4
1	3-L	293[C]	ASP	6.4
1	3-P	299[C]	ASP	6.4
1	4-K	89[D]	ASP	6.4
1	4-L	293[D]	ASP	6.4
1	4-P	299[D]	ASP	6.4
1	1-O	246[A]	PRO	6.4
1	2-O	246[B]	PRO	6.4
1	3-O	246[C]	PRO	6.4
1	4-O	246[D]	PRO	6.4
1	1-K	48[A]	LEU	6.4
1	2-K	48[B]	LEU	6.4
1	3-K	48[C]	LEU	6.4
1	4-K	48[D]	LEU	6.4
1	1-P	133[A]	HIS	6.4
1	2-P	133[B]	HIS	6.4
1	3-P	133[C]	HIS	6.4
1	4-P	133[D]	HIS	6.4
1	1-I	51[A]	PRO	6.4
1	1-L	203[A]	PRO	6.4
1	2-I	51[B]	PRO	6.4

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Mol	Chain	Res	Type	RSRZ
1	2-L	203[B]	PRO	6.4
1	3-I	51[C]	PRO	6.4
1	3-L	203[C]	PRO	6.4
1	4-I	51[D]	PRO	6.4
1	4-L	203[D]	PRO	6.4
1	1-N	88[A]	THR	6.4
1	2-N	88[B]	THR	6.4
1	3-N	88[C]	THR	6.4
1	4-N	88[D]	THR	6.4
1	1-I	220[A]	LEU	6.4
1	1-J	266[A]	LEU	6.4
1	2-I	220[B]	LEU	6.4
1	2-J	266[B]	LEU	6.4
1	3-I	220[C]	LEU	6.4
1	3-J	266[C]	LEU	6.4
1	4-I	220[D]	LEU	6.4
1	4-J	266[D]	LEU	6.4
1	1-K	190[A]	PHE	6.4
1	1-K	277[A]	PHE	6.4
1	2-K	190[B]	PHE	6.4
1	2-K	277[B]	PHE	6.4
1	3-K	190[C]	PHE	6.4
1	3-K	277[C]	PHE	6.4
1	4-K	190[D]	PHE	6.4
1	4-K	277[D]	PHE	6.4
1	1-I	238[A]	ILE	6.4
1	1-O	94[A]	SER	6.4
1	2-I	238[B]	ILE	6.4
1	2-O	94[B]	SER	6.4
1	3-I	238[C]	ILE	6.4
1	3-O	94[C]	SER	6.4
1	4-I	238[D]	ILE	6.4
1	4-O	94[D]	SER	6.4
1	1-M	167[A]	ARG	6.4
1	2-M	167[B]	ARG	6.4
1	3-M	167[C]	ARG	6.4
1	4-M	167[D]	ARG	6.4
1	1-K	105[A]	GLY	6.4
1	1-K	235[A]	THR	6.4
1	1-P	99[A]	GLY	6.4
1	2-K	105[B]	GLY	6.4
1	2-K	235[B]	THR	6.4

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Mol	Chain	Res	Type	RSRZ
1	2-P	99[B]	GLY	6.4
1	3-K	105[C]	GLY	6.4
1	3-K	235[C]	THR	6.4
1	3-P	99[C]	GLY	6.4
1	4-K	105[D]	GLY	6.4
1	4-K	235[D]	THR	6.4
1	4-P	99[D]	GLY	6.4
1	1-P	248[A]	GLU	6.4
1	2-P	248[B]	GLU	6.4
1	3-P	248[C]	GLU	6.4
1	4-P	248[D]	GLU	6.4
1	1-O	184[A]	LEU	6.4
1	1-P	240[A]	LEU	6.4
1	2-O	184[B]	LEU	6.4
1	2-P	240[B]	LEU	6.4
1	3-O	184[C]	LEU	6.4
1	3-P	240[C]	LEU	6.4
1	4-O	184[D]	LEU	6.4
1	4-P	240[D]	LEU	6.4
1	1-M	184[A]	LEU	6.4
1	2-M	184[B]	LEU	6.4
1	3-M	184[C]	LEU	6.4
1	4-M	184[D]	LEU	6.4
1	1-N	49[A]	PHE	6.4
1	2-N	49[B]	PHE	6.4
1	3-N	49[C]	PHE	6.4
1	4-N	49[D]	PHE	6.4
1	1-I	256[A]	ALA	6.4
1	2-I	256[B]	ALA	6.4
1	3-I	256[C]	ALA	6.4
1	4-I	256[D]	ALA	6.4
1	1-J	130[A]	GLN	6.3
1	1-J	145[A]	TYR	6.3
1	2-J	130[B]	GLN	6.3
1	2-J	145[B]	TYR	6.3
1	3-J	130[C]	GLN	6.3
1	3-J	145[C]	TYR	6.3
1	4-J	130[D]	GLN	6.3
1	4-J	145[D]	TYR	6.3
1	1-M	257[A]	HIS	6.3
1	2-M	257[B]	HIS	6.3
1	3-M	257[C]	HIS	6.3

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Mol	Chain	Res	Type	RSRZ
1	4-M	257[D]	HIS	6.3
1	1-O	281[A]	LYS	6.3
1	2-O	281[B]	LYS	6.3
1	3-O	281[C]	LYS	6.3
1	4-O	281[D]	LYS	6.3
1	1-P	273[A]	GLU	6.3
1	2-P	273[B]	GLU	6.3
1	3-P	273[C]	GLU	6.3
1	4-P	273[D]	GLU	6.3
1	1-L	63[A]	LEU	6.3
1	2-L	63[B]	LEU	6.3
1	3-L	63[C]	LEU	6.3
1	4-L	63[D]	LEU	6.3
1	1-M	313[A]	MET	6.3
1	2-M	313[B]	MET	6.3
1	3-M	313[C]	MET	6.3
1	4-M	313[D]	MET	6.3
1	1-J	190[A]	PHE	6.3
1	1-K	135[A]	GLY	6.3
1	1-M	199[A]	PRO	6.3
1	2-J	190[B]	PHE	6.3
1	2-K	135[B]	GLY	6.3
1	2-M	199[B]	PRO	6.3
1	3-J	190[C]	PHE	6.3
1	3-K	135[C]	GLY	6.3
1	3-M	199[C]	PRO	6.3
1	4-J	190[D]	PHE	6.3
1	4-K	135[D]	GLY	6.3
1	4-M	199[D]	PRO	6.3
1	1-K	68[A]	THR	6.3
1	1-L	292[A]	ILE	6.3
1	1-O	118[A]	ARG	6.3
1	2-K	68[B]	THR	6.3
1	2-L	292[B]	ILE	6.3
1	2-O	118[B]	ARG	6.3
1	3-K	68[C]	THR	6.3
1	3-L	292[C]	ILE	6.3
1	3-O	118[C]	ARG	6.3
1	4-K	68[D]	THR	6.3
1	4-L	292[D]	ILE	6.3
1	4-O	118[D]	ARG	6.3
1	1-J	205[A]	SER	6.3

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Mol	Chain	Res	Type	RSRZ
1	2-J	205[B]	SER	6.3
1	3-J	205[C]	SER	6.3
1	4-J	205[D]	SER	6.3
1	1-J	73[A]	LEU	6.3
1	2-J	73[B]	LEU	6.3
1	3-J	73[C]	LEU	6.3
1	4-J	73[D]	LEU	6.3
1	1-M	103[A]	GLY	6.3
1	2-M	103[B]	GLY	6.3
1	3-M	103[C]	GLY	6.3
1	4-M	103[D]	GLY	6.3
1	1-I	150[A]	VAL	6.3
1	1-O	258[A]	VAL	6.3
1	2-I	150[B]	VAL	6.3
1	2-O	258[B]	VAL	6.3
1	3-I	150[C]	VAL	6.3
1	3-O	258[C]	VAL	6.3
1	4-I	150[D]	VAL	6.3
1	4-O	258[D]	VAL	6.3
1	1-M	41[A]	THR	6.3
1	2-M	41[B]	THR	6.3
1	3-M	41[C]	THR	6.3
1	4-M	41[D]	THR	6.3
1	1-K	316[A]	SER	6.3
1	2-K	316[B]	SER	6.3
1	3-K	316[C]	SER	6.3
1	4-K	316[D]	SER	6.3
1	1-L	271[A]	GLU	6.3
1	2-L	271[B]	GLU	6.3
1	3-L	271[C]	GLU	6.3
1	4-L	271[D]	GLU	6.3
1	1-I	63[A]	LEU	6.3
1	2-I	63[B]	LEU	6.3
1	3-I	63[C]	LEU	6.3
1	4-I	63[D]	LEU	6.3
1	1-F	204[A]	GLY	6.3
1	2-F	204[B]	GLY	6.3
1	3-F	204[C]	GLY	6.3
1	4-F	204[D]	GLY	6.3
1	1-I	257[A]	HIS	6.3
1	2-I	257[B]	HIS	6.3
1	3-I	257[C]	HIS	6.3

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Mol	Chain	Res	Type	RSRZ
1	4-I	257[D]	HIS	6.3
1	1-L	243[A]	ASP	6.3
1	2-L	243[B]	ASP	6.3
1	3-L	243[C]	ASP	6.3
1	4-L	243[D]	ASP	6.3
1	1-I	41[A]	THR	6.3
1	2-I	41[B]	THR	6.3
1	3-I	41[C]	THR	6.3
1	4-I	41[D]	THR	6.3
1	1-L	316[A]	SER	6.3
1	2-L	316[B]	SER	6.3
1	3-L	316[C]	SER	6.3
1	4-L	316[D]	SER	6.3
1	1-M	75[A]	GLY	6.3
1	2-M	75[B]	GLY	6.3
1	3-M	75[C]	GLY	6.3
1	4-M	75[D]	GLY	6.3
1	1-N	278[A]	PRO	6.3
1	2-N	278[B]	PRO	6.3
1	3-N	278[C]	PRO	6.3
1	4-N	278[D]	PRO	6.3
1	1-M	138[A]	TYR	6.3
1	2-M	138[B]	TYR	6.3
1	3-M	138[C]	TYR	6.3
1	4-M	138[D]	TYR	6.3
1	1-P	117[A]	HIS	6.3
1	2-P	117[B]	HIS	6.3
1	3-P	117[C]	HIS	6.3
1	4-P	117[D]	HIS	6.3
1	1-K	234[A]	LEU	6.3
1	2-K	234[B]	LEU	6.3
1	3-K	234[C]	LEU	6.3
1	4-K	234[D]	LEU	6.3
1	1-O	150[A]	VAL	6.3
1	2-O	150[B]	VAL	6.3
1	3-O	150[C]	VAL	6.3
1	4-O	150[D]	VAL	6.3
1	1-M	134[A]	PHE	6.3
1	1-P	49[A]	PHE	6.3
1	2-M	134[B]	PHE	6.3
1	2-P	49[B]	PHE	6.3
1	3-M	134[C]	PHE	6.3

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Mol	Chain	Res	Type	RSRZ
1	3-P	49[C]	PHE	6.3
1	4-M	134[D]	PHE	6.3
1	4-P	49[D]	PHE	6.3
1	1-N	221[A]	GLY	6.3
1	2-N	221[B]	GLY	6.3
1	3-N	221[C]	GLY	6.3
1	4-N	221[D]	GLY	6.3
1	1-K	39[A]	ASP	6.2
1	2-K	39[B]	ASP	6.2
1	3-K	39[C]	ASP	6.2
1	4-K	39[D]	ASP	6.2
1	1-J	229[A]	ALA	6.2
1	2-J	229[B]	ALA	6.2
1	3-J	229[C]	ALA	6.2
1	4-J	229[D]	ALA	6.2
1	1-J	68[A]	THR	6.2
1	2-J	68[B]	THR	6.2
1	3-J	68[C]	THR	6.2
1	4-J	68[D]	THR	6.2
1	1-N	156[A]	VAL	6.2
1	2-N	156[B]	VAL	6.2
1	3-N	156[C]	VAL	6.2
1	4-N	156[D]	VAL	6.2
1	1-M	194[A]	PHE	6.2
1	2-M	194[B]	PHE	6.2
1	3-M	194[C]	PHE	6.2
1	4-M	194[D]	PHE	6.2
1	1-A	260[A]	ARG	6.2
1	1-B	292[A]	ILE	6.2
1	1-N	238[A]	ILE	6.2
1	2-A	260[B]	ARG	6.2
1	2-B	292[B]	ILE	6.2
1	2-N	238[B]	ILE	6.2
1	3-A	260[C]	ARG	6.2
1	3-B	292[C]	ILE	6.2
1	3-N	238[C]	ILE	6.2
1	4-A	260[D]	ARG	6.2
1	4-B	292[D]	ILE	6.2
1	4-N	238[D]	ILE	6.2
1	1-I	240[A]	LEU	6.2
1	1-J	271[A]	GLU	6.2
1	2-I	240[B]	LEU	6.2

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Mol	Chain	Res	Type	RSRZ
1	2-J	271[B]	GLU	6.2
1	3-I	240[C]	LEU	6.2
1	3-J	271[C]	GLU	6.2
1	4-I	240[D]	LEU	6.2
1	4-J	271[D]	GLU	6.2
1	1-P	223[A]	GLY	6.2
1	2-P	223[B]	GLY	6.2
1	3-P	223[C]	GLY	6.2
1	4-P	223[D]	GLY	6.2
1	1-L	302[A]	VAL	6.2
1	1-O	156[A]	VAL	6.2
1	2-L	302[B]	VAL	6.2
1	2-O	156[B]	VAL	6.2
1	3-L	302[C]	VAL	6.2
1	3-O	156[C]	VAL	6.2
1	4-L	302[D]	VAL	6.2
1	4-O	156[D]	VAL	6.2
1	1-P	56[A]	PHE	6.2
1	2-P	56[B]	PHE	6.2
1	3-P	56[C]	PHE	6.2
1	4-P	56[D]	PHE	6.2
1	1-N	163[A]	ASN	6.2
1	2-N	163[B]	ASN	6.2
1	3-N	163[C]	ASN	6.2
1	4-N	163[D]	ASN	6.2
1	1-O	95[A]	SER	6.2
1	1-M	139[A]	THR	6.2
1	1-P	243[A]	ASP	6.2
1	2-O	95[B]	SER	6.2
1	2-M	139[B]	THR	6.2
1	2-P	243[B]	ASP	6.2
1	3-O	95[C]	SER	6.2
1	3-M	139[C]	THR	6.2
1	3-P	243[C]	ASP	6.2
1	4-O	95[D]	SER	6.2
1	4-M	139[D]	THR	6.2
1	4-P	243[D]	ASP	6.2
1	1-L	33[A]	VAL	6.2
1	1-P	38[A]	PRO	6.2
1	1-P	101[A]	TRP	6.2
1	2-L	33[B]	VAL	6.2
1	2-P	38[B]	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
1	2-P	101[B]	TRP	6.2
1	3-L	33[C]	VAL	6.2
1	3-P	38[C]	PRO	6.2
1	3-P	101[C]	TRP	6.2
1	4-P	38[D]	PRO	6.2
1	4-P	101[D]	TRP	6.2
1	4-L	33[D]	VAL	6.2
1	1-I	313[A]	MET	6.2
1	1-P	206[A]	LYS	6.2
1	2-I	313[B]	MET	6.2
1	2-P	206[B]	LYS	6.2
1	3-I	313[C]	MET	6.2
1	3-P	206[C]	LYS	6.2
1	4-I	313[D]	MET	6.2
1	4-P	206[D]	LYS	6.2
1	1-O	190[A]	PHE	6.2
1	2-O	190[B]	PHE	6.2
1	3-O	190[C]	PHE	6.2
1	4-O	190[D]	PHE	6.2
1	1-N	141[A]	ALA	6.2
1	2-N	141[B]	ALA	6.2
1	3-N	141[C]	ALA	6.2
1	4-N	141[D]	ALA	6.2
1	1-L	214[A]	TYR	6.2
1	1-E	203[A]	PRO	6.2
1	1-N	123[A]	LEU	6.2
1	2-L	214[B]	TYR	6.2
1	2-E	203[B]	PRO	6.2
1	2-N	123[B]	LEU	6.2
1	3-L	214[C]	TYR	6.2
1	3-E	203[C]	PRO	6.2
1	3-N	123[C]	LEU	6.2
1	4-L	214[D]	TYR	6.2
1	4-E	203[D]	PRO	6.2
1	4-N	123[D]	LEU	6.2
1	1-L	224[A]	VAL	6.2
1	2-L	224[B]	VAL	6.2
1	3-L	224[C]	VAL	6.2
1	4-L	224[D]	VAL	6.2
1	1-P	59[A]	ALA	6.2
1	2-P	59[B]	ALA	6.2
1	3-P	59[C]	ALA	6.2

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Mol	Chain	Res	Type	RSRZ
1	4-P	59[D]	ALA	6.2
1	1-K	250[A]	ILE	6.2
1	1-M	303[A]	GLU	6.2
1	2-K	250[B]	ILE	6.2
1	2-M	303[B]	GLU	6.2
1	3-K	250[C]	ILE	6.2
1	3-M	303[C]	GLU	6.2
1	4-K	250[D]	ILE	6.2
1	4-M	303[D]	GLU	6.2
1	1-J	64[A]	PRO	6.2
1	2-J	64[B]	PRO	6.2
1	3-J	64[C]	PRO	6.2
1	4-J	64[D]	PRO	6.2
1	1-E	115[A]	LEU	6.2
1	1-I	280[A]	LEU	6.2
1	2-E	115[B]	LEU	6.2
1	2-I	280[B]	LEU	6.2
1	3-E	115[C]	LEU	6.2
1	3-I	280[C]	LEU	6.2
1	4-E	115[D]	LEU	6.2
1	4-I	280[D]	LEU	6.2
1	1-M	140[A]	ASP	6.2
1	2-M	140[B]	ASP	6.2
1	3-M	140[C]	ASP	6.2
1	4-M	140[D]	ASP	6.2
1	1-K	46[A]	VAL	6.2
1	2-K	46[B]	VAL	6.2
1	3-K	46[C]	VAL	6.2
1	4-K	46[D]	VAL	6.2
1	1-I	148[A]	LYS	6.2
1	2-I	148[B]	LYS	6.2
1	3-I	148[C]	LYS	6.2
1	4-I	148[D]	LYS	6.2
1	1-I	193[A]	PHE	6.2
1	1-L	229[A]	ALA	6.2
1	1-M	256[A]	ALA	6.2
1	2-I	193[B]	PHE	6.2
1	2-L	229[B]	ALA	6.2
1	2-M	256[B]	ALA	6.2
1	3-I	193[C]	PHE	6.2
1	3-L	229[C]	ALA	6.2
1	3-M	256[C]	ALA	6.2

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Mol	Chain	Res	Type	RSRZ
1	4-I	193[D]	PHE	6.2
1	4-L	229[D]	ALA	6.2
1	4-M	256[D]	ALA	6.2
1	1-K	261[A]	ASP	6.1
1	2-K	261[B]	ASP	6.1
1	3-K	261[C]	ASP	6.1
1	4-K	261[D]	ASP	6.1
1	1-N	26[A]	LEU	6.1
1	1-O	179[A]	LEU	6.1
1	2-N	26[B]	LEU	6.1
1	2-O	179[B]	LEU	6.1
1	3-N	26[C]	LEU	6.1
1	3-O	179[C]	LEU	6.1
1	4-N	26[D]	LEU	6.1
1	4-O	179[D]	LEU	6.1
1	1-I	85[A]	SER	6.1
1	1-J	36[A]	VAL	6.1
1	2-I	85[B]	SER	6.1
1	2-J	36[B]	VAL	6.1
1	3-I	85[C]	SER	6.1
1	3-J	36[C]	VAL	6.1
1	4-I	85[D]	SER	6.1
1	4-J	36[D]	VAL	6.1
1	1-K	278[A]	PRO	6.1
1	1-L	104[A]	ASN	6.1
1	2-K	278[B]	PRO	6.1
1	2-L	104[B]	ASN	6.1
1	3-K	278[C]	PRO	6.1
1	3-L	104[C]	ASN	6.1
1	4-K	278[D]	PRO	6.1
1	4-L	104[D]	ASN	6.1
1	1-I	107[A]	LYS	6.1
1	2-I	107[B]	LYS	6.1
1	3-I	107[C]	LYS	6.1
1	4-I	107[D]	LYS	6.1
1	1-K	36[A]	VAL	6.1
1	2-K	36[B]	VAL	6.1
1	3-K	36[C]	VAL	6.1
1	4-K	36[D]	VAL	6.1
1	1-J	108[A]	GLU	6.1
1	1-P	267[A]	LYS	6.1
1	2-J	108[B]	GLU	6.1

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Mol	Chain	Res	Type	RSRZ
1	2-P	267[B]	LYS	6.1
1	3-J	108[C]	GLU	6.1
1	3-P	267[C]	LYS	6.1
1	4-J	108[D]	GLU	6.1
1	4-P	267[D]	LYS	6.1
1	1-I	131[A]	TRP	6.1
1	1-P	174[A]	TRP	6.1
1	2-I	131[B]	TRP	6.1
1	2-P	174[B]	TRP	6.1
1	3-I	131[C]	TRP	6.1
1	3-P	174[C]	TRP	6.1
1	4-I	131[D]	TRP	6.1
1	4-P	174[D]	TRP	6.1
1	1-I	221[A]	GLY	6.1
1	1-M	304[A]	GLY	6.1
1	1-I	35[A]	GLU	6.1
1	1-I	266[A]	LEU	6.1
1	2-I	221[B]	GLY	6.1
1	2-M	304[B]	GLY	6.1
1	2-I	35[B]	GLU	6.1
1	2-I	266[B]	LEU	6.1
1	3-I	221[C]	GLY	6.1
1	3-M	304[C]	GLY	6.1
1	3-I	35[C]	GLU	6.1
1	3-I	266[C]	LEU	6.1
1	4-I	221[D]	GLY	6.1
1	4-I	35[D]	GLU	6.1
1	4-I	266[D]	LEU	6.1
1	4-M	304[D]	GLY	6.1
1	1-O	119[A]	ARG	6.1
1	2-O	119[B]	ARG	6.1
1	3-O	119[C]	ARG	6.1
1	4-O	119[D]	ARG	6.1
1	1-O	68[A]	THR	6.1
1	2-O	68[B]	THR	6.1
1	3-O	68[C]	THR	6.1
1	4-O	68[D]	THR	6.1
1	1-K	228[A]	ILE	6.1
1	1-M	287[A]	GLU	6.1
1	2-K	228[B]	ILE	6.1
1	2-M	287[B]	GLU	6.1
1	3-K	228[C]	ILE	6.1

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Mol	Chain	Res	Type	RSRZ
1	3-M	287[C]	GLU	6.1
1	4-K	228[D]	ILE	6.1
1	4-M	287[D]	GLU	6.1
1	1-K	86[A]	GLY	6.1
1	2-K	86[B]	GLY	6.1
1	3-K	86[C]	GLY	6.1
1	4-K	86[D]	GLY	6.1
1	1-J	282[A]	TRP	6.1
1	1-N	308[A]	TRP	6.1
1	2-J	282[B]	TRP	6.1
1	2-N	308[B]	TRP	6.1
1	3-J	282[C]	TRP	6.1
1	3-N	308[C]	TRP	6.1
1	4-J	282[D]	TRP	6.1
1	4-N	308[D]	TRP	6.1
1	1-K	212[A]	LEU	6.1
1	2-K	212[B]	LEU	6.1
1	3-K	212[C]	LEU	6.1
1	4-K	212[D]	LEU	6.1
1	1-M	88[A]	THR	6.1
1	2-M	88[B]	THR	6.1
1	3-M	88[C]	THR	6.1
1	4-M	88[D]	THR	6.1
1	1-N	291[A]	ASP	6.1
1	2-N	291[B]	ASP	6.1
1	3-N	291[C]	ASP	6.1
1	4-N	291[D]	ASP	6.1
1	1-L	194[A]	PHE	6.0
1	1-O	61[A]	ASN	6.0
1	2-L	194[B]	PHE	6.0
1	2-O	61[B]	ASN	6.0
1	3-L	194[C]	PHE	6.0
1	3-O	61[C]	ASN	6.0
1	4-L	194[D]	PHE	6.0
1	4-O	61[D]	ASN	6.0
1	1-N	206[A]	LYS	6.0
1	2-N	206[B]	LYS	6.0
1	3-N	206[C]	LYS	6.0
1	4-N	206[D]	LYS	6.0
1	1-M	233[A]	LEU	6.0
1	1-P	66[A]	LEU	6.0
1	2-M	233[B]	LEU	6.0

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Mol	Chain	Res	Type	RSRZ
1	2-P	66[B]	LEU	6.0
1	3-M	233[C]	LEU	6.0
1	3-P	66[C]	LEU	6.0
1	4-M	233[D]	LEU	6.0
1	4-P	66[D]	LEU	6.0
1	1-N	144[A]	ASP	6.0
1	2-N	144[B]	ASP	6.0
1	3-N	144[C]	ASP	6.0
1	4-N	144[D]	ASP	6.0
1	1-I	175[A]	ASN	6.0
1	2-I	175[B]	ASN	6.0
1	3-I	175[C]	ASN	6.0
1	4-I	175[D]	ASN	6.0
1	1-O	137[A]	GLU	6.0
1	2-O	137[B]	GLU	6.0
1	3-O	137[C]	GLU	6.0
1	4-O	137[D]	GLU	6.0
1	1-I	129[A]	PHE	6.0
1	1-J	134[A]	PHE	6.0
1	2-I	129[B]	PHE	6.0
1	2-J	134[B]	PHE	6.0
1	3-I	129[C]	PHE	6.0
1	3-J	134[C]	PHE	6.0
1	4-I	129[D]	PHE	6.0
1	4-J	134[D]	PHE	6.0
1	1-N	70[A]	ARG	6.0
1	2-N	70[B]	ARG	6.0
1	3-N	70[C]	ARG	6.0
1	4-N	70[D]	ARG	6.0
1	1-P	82[A]	TRP	6.0
1	2-P	82[B]	TRP	6.0
1	3-P	82[C]	TRP	6.0
1	4-P	82[D]	TRP	6.0
1	1-N	130[A]	GLN	6.0
1	2-N	130[B]	GLN	6.0
1	3-N	130[C]	GLN	6.0
1	4-N	130[D]	GLN	6.0
1	1-M	249[A]	PHE	6.0
1	2-M	249[B]	PHE	6.0
1	3-M	249[C]	PHE	6.0
1	4-M	249[D]	PHE	6.0
1	1-P	137[A]	GLU	6.0

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Mol	Chain	Res	Type	RSRZ
1	1-P	239[A]	ALA	6.0
1	2-P	137[B]	GLU	6.0
1	2-P	239[B]	ALA	6.0
1	3-P	137[C]	GLU	6.0
1	3-P	239[C]	ALA	6.0
1	4-P	137[D]	GLU	6.0
1	4-P	239[D]	ALA	6.0
1	1-L	205[A]	SER	6.0
1	1-M	48[A]	LEU	6.0
1	1-O	204[A]	GLY	6.0
1	2-L	205[B]	SER	6.0
1	2-M	48[B]	LEU	6.0
1	2-O	204[B]	GLY	6.0
1	3-L	205[C]	SER	6.0
1	3-M	48[C]	LEU	6.0
1	3-O	204[C]	GLY	6.0
1	4-L	205[D]	SER	6.0
1	4-M	48[D]	LEU	6.0
1	4-O	204[D]	GLY	6.0
1	1-J	82[A]	TRP	6.0
1	1-N	282[A]	TRP	6.0
1	2-J	82[B]	TRP	6.0
1	2-N	282[B]	TRP	6.0
1	3-J	82[C]	TRP	6.0
1	3-N	282[C]	TRP	6.0
1	4-J	82[D]	TRP	6.0
1	4-N	282[D]	TRP	6.0
1	1-J	127[A]	TYR	6.0
1	1-N	120[A]	GLU	6.0
1	1-P	145[A]	TYR	6.0
1	2-J	127[B]	TYR	6.0
1	2-N	120[B]	GLU	6.0
1	2-P	145[B]	TYR	6.0
1	3-J	127[C]	TYR	6.0
1	3-N	120[C]	GLU	6.0
1	3-P	145[C]	TYR	6.0
1	4-J	127[D]	TYR	6.0
1	4-N	120[D]	GLU	6.0
1	4-P	145[D]	TYR	6.0
1	1-I	112[A]	LYS	6.0
1	2-I	112[B]	LYS	6.0
1	3-I	112[C]	LYS	6.0

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Mol	Chain	Res	Type	RSRZ
1	4-I	112[D]	LYS	6.0
1	1-J	136[A]	ALA	6.0
1	2-J	136[B]	ALA	6.0
1	3-J	136[C]	ALA	6.0
1	4-J	136[D]	ALA	6.0
1	1-I	228[A]	ILE	6.0
1	1-N	44[A]	GLY	6.0
1	2-I	228[B]	ILE	6.0
1	2-N	44[B]	GLY	6.0
1	3-I	228[C]	ILE	6.0
1	3-N	44[C]	GLY	6.0
1	4-I	228[D]	ILE	6.0
1	4-N	44[D]	GLY	6.0
1	1-L	146[A]	LYS	6.0
1	2-L	146[B]	LYS	6.0
1	3-L	146[C]	LYS	6.0
1	4-L	146[D]	LYS	6.0
1	1-O	101[A]	TRP	6.0
1	2-O	101[B]	TRP	6.0
1	3-O	101[C]	TRP	6.0
1	4-O	101[D]	TRP	6.0
1	1-F	202[A]	SER	6.0
1	1-N	172[A]	SER	6.0
1	1-P	54[A]	PHE	6.0
1	2-F	202[B]	SER	6.0
1	2-N	172[B]	SER	6.0
1	2-P	54[B]	PHE	6.0
1	3-F	202[C]	SER	6.0
1	3-N	172[C]	SER	6.0
1	3-P	54[C]	PHE	6.0
1	4-F	202[D]	SER	6.0
1	4-N	172[D]	SER	6.0
1	4-P	54[D]	PHE	6.0
1	1-J	79[A]	GLU	6.0
1	1-M	273[A]	GLU	6.0
1	2-J	79[B]	GLU	6.0
1	2-M	273[B]	GLU	6.0
1	3-J	79[C]	GLU	6.0
1	3-M	273[C]	GLU	6.0
1	4-J	79[D]	GLU	6.0
1	4-M	273[D]	GLU	6.0
1	1-P	280[A]	LEU	6.0

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Mol	Chain	Res	Type	RSRZ
1	2-P	280[B]	LEU	6.0
1	3-P	280[C]	LEU	6.0
1	4-P	280[D]	LEU	6.0
1	1-K	182[A]	MET	6.0
1	1-M	237[A]	MET	6.0
1	2-K	182[B]	MET	6.0
1	2-M	237[B]	MET	6.0
1	3-K	182[C]	MET	6.0
1	3-M	237[C]	MET	6.0
1	4-K	182[D]	MET	6.0
1	4-M	237[D]	MET	6.0
1	1-J	53[A]	SER	5.9
1	1-O	105[A]	GLY	5.9
1	1-O	264[A]	GLU	5.9
1	2-J	53[B]	SER	5.9
1	2-O	105[B]	GLY	5.9
1	2-O	264[B]	GLU	5.9
1	3-J	53[C]	SER	5.9
1	3-O	105[C]	GLY	5.9
1	3-O	264[C]	GLU	5.9
1	4-O	105[D]	GLY	5.9
1	4-O	264[D]	GLU	5.9
1	1-K	310[A]	LYS	5.9
1	1-O	168[A]	ARG	5.9
1	2-K	310[B]	LYS	5.9
1	2-O	168[B]	ARG	5.9
1	3-K	310[C]	LYS	5.9
1	3-O	168[C]	ARG	5.9
1	4-J	53[D]	SER	5.9
1	4-K	310[D]	LYS	5.9
1	4-O	168[D]	ARG	5.9
1	1-E	190[A]	PHE	5.9
1	1-I	140[A]	ASP	5.9
1	2-E	190[B]	PHE	5.9
1	2-I	140[B]	ASP	5.9
1	3-E	190[C]	PHE	5.9
1	3-I	140[C]	ASP	5.9
1	4-E	190[D]	PHE	5.9
1	4-I	140[D]	ASP	5.9
1	1-O	191[A]	CYS	5.9
1	2-O	191[B]	CYS	5.9
1	3-O	191[C]	CYS	5.9

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Mol	Chain	Res	Type	RSRZ
1	4-O	191[D]	CYS	5.9
1	1-I	233[A]	LEU	5.9
1	2-I	233[B]	LEU	5.9
1	3-I	233[C]	LEU	5.9
1	4-I	233[D]	LEU	5.9
1	1-P	71[A]	VAL	5.9
1	2-P	71[B]	VAL	5.9
1	3-P	71[C]	VAL	5.9
1	4-P	71[D]	VAL	5.9
1	1-O	85[A]	SER	5.9
1	2-O	85[B]	SER	5.9
1	3-O	85[C]	SER	5.9
1	4-O	85[D]	SER	5.9
1	1-N	232[A]	ALA	5.9
1	2-N	232[B]	ALA	5.9
1	3-N	232[C]	ALA	5.9
1	4-N	232[D]	ALA	5.9
1	1-J	235[A]	THR	5.9
1	2-J	235[B]	THR	5.9
1	3-J	235[C]	THR	5.9
1	4-J	235[D]	THR	5.9
1	1-J	260[A]	ARG	5.9
1	1-N	300[A]	PHE	5.9
1	2-J	260[B]	ARG	5.9
1	2-N	300[B]	PHE	5.9
1	3-J	260[C]	ARG	5.9
1	3-N	300[C]	PHE	5.9
1	4-J	260[D]	ARG	5.9
1	4-N	300[D]	PHE	5.9
1	1-K	95[A]	SER	5.9
1	2-K	95[B]	SER	5.9
1	3-K	95[C]	SER	5.9
1	4-K	95[D]	SER	5.9
1	1-J	71[A]	VAL	5.9
1	2-J	71[B]	VAL	5.9
1	3-J	71[C]	VAL	5.9
1	4-J	71[D]	VAL	5.9
1	1-J	45[A]	THR	5.9
1	1-K	74[A]	ARG	5.9
1	2-J	45[B]	THR	5.9
1	2-K	74[B]	ARG	5.9
1	3-J	45[C]	THR	5.9

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Mol	Chain	Res	Type	RSRZ
1	3-K	74[C]	ARG	5.9
1	4-J	45[D]	THR	5.9
1	4-K	74[D]	ARG	5.9
1	1-P	158[A]	ASP	5.9
1	2-P	158[B]	ASP	5.9
1	3-P	158[C]	ASP	5.9
1	4-P	158[D]	ASP	5.9
1	1-O	169[A]	ILE	5.9
1	2-O	169[B]	ILE	5.9
1	3-O	169[C]	ILE	5.9
1	4-O	169[D]	ILE	5.9
1	1-I	113[A]	VAL	5.9
1	2-I	113[B]	VAL	5.9
1	3-I	113[C]	VAL	5.9
1	4-I	113[D]	VAL	5.9
1	1-L	45[A]	THR	5.9
1	1-P	139[A]	THR	5.9
1	2-L	45[B]	THR	5.9
1	2-P	139[B]	THR	5.9
1	3-L	45[C]	THR	5.9
1	3-P	139[C]	THR	5.9
1	4-L	45[D]	THR	5.9
1	4-P	139[D]	THR	5.9
1	1-K	148[A]	LYS	5.9
1	1-P	186[A]	PRO	5.9
1	2-K	148[B]	LYS	5.9
1	2-P	186[B]	PRO	5.9
1	3-K	148[C]	LYS	5.9
1	3-P	186[C]	PRO	5.9
1	4-K	148[D]	LYS	5.9
1	4-P	186[D]	PRO	5.9
1	1-M	63[A]	LEU	5.9
1	2-M	63[B]	LEU	5.9
1	3-M	63[C]	LEU	5.9
1	4-M	63[D]	LEU	5.9
1	1-I	282[A]	TRP	5.9
1	1-J	303[A]	GLU	5.9
1	2-I	282[B]	TRP	5.9
1	1-K	151[A]	ASP	5.9
1	1-N	166[A]	ASP	5.9
1	1-O	102[A]	ASP	5.9
1	2-J	303[B]	GLU	5.9

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Mol	Chain	Res	Type	RSRZ
1	3-I	282[C]	TRP	5.9
1	3-J	303[C]	GLU	5.9
1	4-I	282[D]	TRP	5.9
1	2-K	151[B]	ASP	5.9
1	2-N	166[B]	ASP	5.9
1	2-O	102[B]	ASP	5.9
1	3-K	151[C]	ASP	5.9
1	3-N	166[C]	ASP	5.9
1	3-O	102[C]	ASP	5.9
1	4-J	303[D]	GLU	5.9
1	4-K	151[D]	ASP	5.9
1	4-N	166[D]	ASP	5.9
1	4-O	102[D]	ASP	5.9
1	1-O	45[A]	THR	5.9
1	2-O	45[B]	THR	5.9
1	3-O	45[C]	THR	5.9
1	4-O	45[D]	THR	5.9
1	1-I	75[A]	GLY	5.8
1	1-K	199[A]	PRO	5.8
1	2-I	75[B]	GLY	5.8
1	2-K	199[B]	PRO	5.8
1	3-I	75[C]	GLY	5.8
1	3-K	199[C]	PRO	5.8
1	4-I	75[D]	GLY	5.8
1	4-K	199[D]	PRO	5.8
1	1-J	55[A]	ARG	5.8
1	1-M	284[A]	ARG	5.8
1	2-J	55[B]	ARG	5.8
1	2-M	284[B]	ARG	5.8
1	3-J	55[C]	ARG	5.8
1	3-M	284[C]	ARG	5.8
1	4-J	55[D]	ARG	5.8
1	4-M	284[D]	ARG	5.8
1	1-K	292[A]	ILE	5.8
1	2-K	292[B]	ILE	5.8
1	3-K	292[C]	ILE	5.8
1	4-K	292[D]	ILE	5.8
1	1-P	26[A]	LEU	5.8
1	2-P	26[B]	LEU	5.8
1	3-P	26[C]	LEU	5.8
1	4-P	26[D]	LEU	5.8
1	1-P	167[A]	ARG	5.8

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Mol	Chain	Res	Type	RSRZ
1	2-P	167[B]	ARG	5.8
1	3-P	167[C]	ARG	5.8
1	4-P	167[D]	ARG	5.8
1	1-L	18[A]	HIS	5.8
1	1-L	188[A]	HIS	5.8
1	2-L	18[B]	HIS	5.8
1	2-L	188[B]	HIS	5.8
1	3-L	18[C]	HIS	5.8
1	3-L	188[C]	HIS	5.8
1	4-L	18[D]	HIS	5.8
1	4-L	188[D]	HIS	5.8
1	1-N	25[A]	ASP	5.8
1	2-N	25[B]	ASP	5.8
1	3-N	25[C]	ASP	5.8
1	4-N	25[D]	ASP	5.8
1	1-I	46[A]	VAL	5.8
1	1-M	20[A]	GLU	5.8
1	2-I	46[B]	VAL	5.8
1	2-M	20[B]	GLU	5.8
1	3-I	46[C]	VAL	5.8
1	3-M	20[C]	GLU	5.8
1	4-I	46[D]	VAL	5.8
1	4-M	20[D]	GLU	5.8
1	1-J	279[A]	LYS	5.8
1	1-L	208[A]	LYS	5.8
1	2-J	279[B]	LYS	5.8
1	2-L	208[B]	LYS	5.8
1	3-J	279[C]	LYS	5.8
1	3-L	208[C]	LYS	5.8
1	4-J	279[D]	LYS	5.8
1	4-L	208[D]	LYS	5.8
1	1-M	122[A]	ASP	5.8
1	2-M	122[B]	ASP	5.8
1	3-M	122[C]	ASP	5.8
1	4-M	122[D]	ASP	5.8
1	1-P	231[A]	TYR	5.8
1	2-P	231[B]	TYR	5.8
1	3-P	231[C]	TYR	5.8
1	4-P	231[D]	TYR	5.8
1	1-I	58[A]	LEU	5.8
1	1-M	222[A]	LEU	5.8
1	1-N	110[A]	LEU	5.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	2-I	58[B]	LEU	5.8
1	2-M	222[B]	LEU	5.8
1	2-N	110[B]	LEU	5.8
1	3-I	58[C]	LEU	5.8
1	3-M	222[C]	LEU	5.8
1	3-N	110[C]	LEU	5.8
1	4-I	58[D]	LEU	5.8
1	4-M	222[D]	LEU	5.8
1	4-N	110[D]	LEU	5.8
1	1-P	246[A]	PRO	5.8
1	2-P	246[B]	PRO	5.8
1	3-P	246[C]	PRO	5.8
1	4-P	246[D]	PRO	5.8
1	1-N	275[A]	ARG	5.8
1	2-N	275[B]	ARG	5.8
1	3-N	275[C]	ARG	5.8
1	4-N	275[D]	ARG	5.8
1	1-N	314[A]	LYS	5.8
1	2-N	314[B]	LYS	5.8
1	3-N	314[C]	LYS	5.8
1	4-N	314[D]	LYS	5.8
1	1-J	290[A]	GLY	5.8
1	1-K	232[A]	ALA	5.8
1	1-O	116[A]	GLY	5.8
1	2-J	290[B]	GLY	5.8
1	2-K	232[B]	ALA	5.8
1	2-O	116[B]	GLY	5.8
1	3-J	290[C]	GLY	5.8
1	3-K	232[C]	ALA	5.8
1	3-O	116[C]	GLY	5.8
1	4-J	290[D]	GLY	5.8
1	4-K	232[D]	ALA	5.8
1	4-O	116[D]	GLY	5.8
1	1-J	165[A]	THR	5.8
1	1-J	230[A]	SER	5.8
1	1-P	125[A]	PRO	5.8
1	2-J	165[B]	THR	5.8
1	2-J	230[B]	SER	5.8
1	2-P	125[B]	PRO	5.8
1	3-J	165[C]	THR	5.8
1	3-J	230[C]	SER	5.8
1	3-P	125[C]	PRO	5.8

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Mol	Chain	Res	Type	RSRZ
1	4-J	165[D]	THR	5.8
1	4-J	230[D]	SER	5.8
1	4-P	125[D]	PRO	5.8
1	1-I	76[A]	VAL	5.8
1	2-I	76[B]	VAL	5.8
1	3-I	76[C]	VAL	5.8
1	4-I	76[D]	VAL	5.8
1	1-I	252[A]	GLN	5.8
1	2-I	252[B]	GLN	5.8
1	3-I	252[C]	GLN	5.8
1	4-I	252[D]	GLN	5.8
1	1-I	16[A]	PRO	5.8
1	2-I	16[B]	PRO	5.8
1	3-I	16[C]	PRO	5.8
1	4-I	16[D]	PRO	5.8
1	1-O	30[A]	ILE	5.8
1	2-O	30[B]	ILE	5.8
1	3-O	30[C]	ILE	5.8
1	4-O	30[D]	ILE	5.8
1	1-O	69[A]	LYS	5.8
1	2-O	69[B]	LYS	5.8
1	3-O	69[C]	LYS	5.8
1	4-O	69[D]	LYS	5.8
1	1-I	236[A]	HIS	5.7
1	2-I	236[B]	HIS	5.7
1	3-I	236[C]	HIS	5.7
1	4-I	236[D]	HIS	5.7
1	1-I	317[A]	ALA	5.7
1	1-I	22[A]	GLN	5.7
1	1-M	215[A]	GLN	5.7
1	1-M	246[A]	PRO	5.7
1	2-I	317[B]	ALA	5.7
1	2-I	22[B]	GLN	5.7
1	2-M	215[B]	GLN	5.7
1	2-M	246[B]	PRO	5.7
1	3-I	317[C]	ALA	5.7
1	3-I	22[C]	GLN	5.7
1	3-M	215[C]	GLN	5.7
1	3-M	246[C]	PRO	5.7
1	4-I	317[D]	ALA	5.7
1	4-I	22[D]	GLN	5.7
1	4-M	215[D]	GLN	5.7

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Mol	Chain	Res	Type	RSRZ
1	4-M	246[D]	PRO	5.7
1	1-K	127[A]	TYR	5.7
1	1-M	251[A]	LEU	5.7
1	2-K	127[B]	TYR	5.7
1	2-M	251[B]	LEU	5.7
1	3-K	127[C]	TYR	5.7
1	3-M	251[C]	LEU	5.7
1	4-K	127[D]	TYR	5.7
1	4-M	251[D]	LEU	5.7
1	1-O	237[A]	MET	5.7
1	2-O	237[B]	MET	5.7
1	3-O	237[C]	MET	5.7
1	4-O	237[D]	MET	5.7
1	1-M	297[A]	VAL	5.7
1	2-M	297[B]	VAL	5.7
1	3-M	297[C]	VAL	5.7
1	4-M	297[D]	VAL	5.7
1	1-K	158[A]	ASP	5.7
1	1-L	227[A]	ASN	5.7
1	1-N	140[A]	ASP	5.7
1	1-N	178[A]	ASP	5.7
1	1-P	32[A]	ASN	5.7
1	2-K	158[B]	ASP	5.7
1	2-L	227[B]	ASN	5.7
1	2-N	140[B]	ASP	5.7
1	2-N	178[B]	ASP	5.7
1	2-P	32[B]	ASN	5.7
1	3-K	158[C]	ASP	5.7
1	3-L	227[C]	ASN	5.7
1	3-N	140[C]	ASP	5.7
1	3-N	178[C]	ASP	5.7
1	3-P	32[C]	ASN	5.7
1	4-K	158[D]	ASP	5.7
1	4-L	227[D]	ASN	5.7
1	4-N	140[D]	ASP	5.7
1	4-N	178[D]	ASP	5.7
1	4-P	32[D]	ASN	5.7
1	1-K	75[A]	GLY	5.7
1	2-K	75[B]	GLY	5.7
1	3-K	75[C]	GLY	5.7
1	4-K	75[D]	GLY	5.7
1	1-J	161[A]	LYS	5.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-P	310[A]	LYS	5.7
1	2-J	161[B]	LYS	5.7
1	2-P	310[B]	LYS	5.7
1	3-J	161[C]	LYS	5.7
1	3-P	310[C]	LYS	5.7
1	4-J	161[D]	LYS	5.7
1	4-P	310[D]	LYS	5.7
1	1-I	94[A]	SER	5.7
1	2-I	94[B]	SER	5.7
1	3-I	94[C]	SER	5.7
1	4-I	94[D]	SER	5.7
1	1-J	307[A]	PRO	5.7
1	2-J	307[B]	PRO	5.7
1	3-J	307[C]	PRO	5.7
1	4-J	307[D]	PRO	5.7
1	1-L	82[A]	TRP	5.7
1	1-L	110[A]	LEU	5.7
1	1-L	170[A]	ILE	5.7
1	1-N	315[A]	MET	5.7
1	1-O	255[A]	ASP	5.7
1	2-L	82[B]	TRP	5.7
1	2-L	110[B]	LEU	5.7
1	2-L	170[B]	ILE	5.7
1	2-N	315[B]	MET	5.7
1	2-O	255[B]	ASP	5.7
1	3-L	82[C]	TRP	5.7
1	3-L	110[C]	LEU	5.7
1	3-L	170[C]	ILE	5.7
1	3-N	315[C]	MET	5.7
1	3-O	255[C]	ASP	5.7
1	4-L	82[D]	TRP	5.7
1	4-L	110[D]	LEU	5.7
1	4-L	170[D]	ILE	5.7
1	4-N	315[D]	MET	5.7
1	4-O	255[D]	ASP	5.7
1	1-L	310[A]	LYS	5.7
1	2-L	310[B]	LYS	5.7
1	3-L	310[C]	LYS	5.7
1	4-L	310[D]	LYS	5.7
1	1-J	211[A]	CYS	5.7
1	1-M	150[A]	VAL	5.7
1	1-N	84[A]	VAL	5.7

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Mol	Chain	Res	Type	RSRZ
1	2-J	211[B]	CYS	5.7
1	2-M	150[B]	VAL	5.7
1	2-N	84[B]	VAL	5.7
1	3-J	211[C]	CYS	5.7
1	3-M	150[C]	VAL	5.7
1	3-N	84[C]	VAL	5.7
1	4-J	211[D]	CYS	5.7
1	4-M	150[D]	VAL	5.7
1	4-N	84[D]	VAL	5.7
1	1-I	37[A]	ARG	5.7
1	2-I	37[B]	ARG	5.7
1	3-I	37[C]	ARG	5.7
1	4-I	37[D]	ARG	5.7
1	1-I	194[A]	PHE	5.7
1	1-K	65[A]	LEU	5.7
1	1-L	240[A]	LEU	5.7
1	2-I	194[B]	PHE	5.7
1	1-M	34[A]	GLY	5.7
1	2-K	65[B]	LEU	5.7
1	2-L	240[B]	LEU	5.7
1	3-I	194[C]	PHE	5.7
1	3-K	65[C]	LEU	5.7
1	3-L	240[C]	LEU	5.7
1	4-I	194[D]	PHE	5.7
1	2-M	34[B]	GLY	5.7
1	3-M	34[C]	GLY	5.7
1	4-K	65[D]	LEU	5.7
1	4-L	240[D]	LEU	5.7
1	4-M	34[D]	GLY	5.7
1	1-J	299[A]	ASP	5.7
1	2-J	299[B]	ASP	5.7
1	3-J	299[C]	ASP	5.7
1	4-J	299[D]	ASP	5.7
1	1-J	62[A]	THR	5.7
1	1-P	45[A]	THR	5.7
1	2-J	62[B]	THR	5.7
1	2-P	45[B]	THR	5.7
1	3-J	62[C]	THR	5.7
1	3-P	45[C]	THR	5.7
1	4-J	62[D]	THR	5.7
1	4-P	45[D]	THR	5.7
1	1-N	119[A]	ARG	5.7

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Mol	Chain	Res	Type	RSRZ
1	2-N	119[B]	ARG	5.7
1	3-N	119[C]	ARG	5.7
1	4-N	119[D]	ARG	5.7
1	1-P	182[A]	MET	5.7
1	2-P	182[B]	MET	5.7
1	3-P	182[C]	MET	5.7
1	4-P	182[D]	MET	5.7
1	1-O	236[A]	HIS	5.7
1	2-O	236[B]	HIS	5.7
1	3-O	236[C]	HIS	5.7
1	4-O	236[D]	HIS	5.7
1	1-O	153[A]	LEU	5.7
1	2-O	153[B]	LEU	5.7
1	3-O	153[C]	LEU	5.7
1	4-O	153[D]	LEU	5.7
1	1-G	203[A]	PRO	5.7
1	1-K	82[A]	TRP	5.7
1	1-L	265[A]	PRO	5.7
1	1-N	274[A]	PRO	5.7
1	2-G	203[B]	PRO	5.7
1	2-K	82[B]	TRP	5.7
1	2-L	265[B]	PRO	5.7
1	2-N	274[B]	PRO	5.7
1	3-G	203[C]	PRO	5.7
1	3-K	82[C]	TRP	5.7
1	3-L	265[C]	PRO	5.7
1	3-N	274[C]	PRO	5.7
1	4-G	203[D]	PRO	5.7
1	4-K	82[D]	TRP	5.7
1	4-L	265[D]	PRO	5.7
1	4-N	274[D]	PRO	5.7
1	1-L	37[A]	ARG	5.7
1	2-L	37[B]	ARG	5.7
1	3-L	37[C]	ARG	5.7
1	4-L	37[D]	ARG	5.7
1	1-N	91[A]	LYS	5.7
1	2-N	91[B]	LYS	5.7
1	3-N	91[C]	LYS	5.7
1	4-N	91[D]	LYS	5.7
1	1-J	85[A]	SER	5.7
1	2-J	85[B]	SER	5.7
1	3-J	85[C]	SER	5.7

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Mol	Chain	Res	Type	RSRZ
1	4-J	85[D]	SER	5.7
1	1-L	277[A]	PHE	5.7
1	1-L	280[A]	LEU	5.7
1	1-M	158[A]	ASP	5.7
1	1-M	234[A]	LEU	5.7
1	1-N	129[A]	PHE	5.7
1	1-N	251[A]	LEU	5.7
1	1-O	226[A]	PHE	5.7
1	2-L	277[B]	PHE	5.7
1	2-L	280[B]	LEU	5.7
1	2-M	158[B]	ASP	5.7
1	2-M	234[B]	LEU	5.7
1	2-N	129[B]	PHE	5.7
1	2-N	251[B]	LEU	5.7
1	2-O	226[B]	PHE	5.7
1	3-L	277[C]	PHE	5.7
1	3-L	280[C]	LEU	5.7
1	3-M	158[C]	ASP	5.7
1	3-M	234[C]	LEU	5.7
1	3-N	129[C]	PHE	5.7
1	3-N	251[C]	LEU	5.7
1	3-O	226[C]	PHE	5.7
1	4-L	277[D]	PHE	5.7
1	4-L	280[D]	LEU	5.7
1	4-M	158[D]	ASP	5.7
1	4-M	234[D]	LEU	5.7
1	4-N	129[D]	PHE	5.7
1	4-N	251[D]	LEU	5.7
1	4-O	226[D]	PHE	5.7
1	1-M	307[A]	PRO	5.7
1	2-M	307[B]	PRO	5.7
1	3-M	307[C]	PRO	5.7
1	4-M	307[D]	PRO	5.7
1	1-P	43[A]	THR	5.6
1	2-P	43[B]	THR	5.6
1	3-P	43[C]	THR	5.6
1	4-P	43[D]	THR	5.6
1	1-N	257[A]	HIS	5.6
1	2-N	257[B]	HIS	5.6
1	3-N	257[C]	HIS	5.6
1	4-N	257[D]	HIS	5.6
1	1-P	196[A]	SER	5.6

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Mol	Chain	Res	Type	RSRZ
1	2-P	196[B]	SER	5.6
1	3-P	196[C]	SER	5.6
1	4-P	196[D]	SER	5.6
1	1-M	252[A]	GLN	5.6
1	2-M	252[B]	GLN	5.6
1	3-M	252[C]	GLN	5.6
1	4-M	252[D]	GLN	5.6
1	1-M	115[A]	LEU	5.6
1	1-N	56[A]	PHE	5.6
1	2-M	115[B]	LEU	5.6
1	2-N	56[B]	PHE	5.6
1	3-M	115[C]	LEU	5.6
1	3-N	56[C]	PHE	5.6
1	4-M	115[D]	LEU	5.6
1	4-N	56[D]	PHE	5.6
1	1-K	297[A]	VAL	5.6
1	2-K	297[B]	VAL	5.6
1	3-K	297[C]	VAL	5.6
1	4-K	297[D]	VAL	5.6
1	1-J	254[A]	GLY	5.6
1	2-J	254[B]	GLY	5.6
1	3-J	254[C]	GLY	5.6
1	4-J	254[D]	GLY	5.6
1	1-O	122[A]	ASP	5.6
1	2-O	122[B]	ASP	5.6
1	3-O	122[C]	ASP	5.6
1	4-O	122[D]	ASP	5.6
1	1-J	94[A]	SER	5.6
1	2-J	94[B]	SER	5.6
1	3-J	94[C]	SER	5.6
1	4-J	94[D]	SER	5.6
1	1-P	104[A]	ASN	5.6
1	2-P	104[B]	ASN	5.6
1	3-P	104[C]	ASN	5.6
1	4-P	104[D]	ASN	5.6
1	1-K	195[A]	VAL	5.6
1	1-L	139[A]	THR	5.6
1	1-O	149[A]	GLY	5.6
1	2-K	195[B]	VAL	5.6
1	2-L	139[B]	THR	5.6
1	2-O	149[B]	GLY	5.6
1	3-K	195[C]	VAL	5.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-L	139[C]	THR	5.6
1	3-O	149[C]	GLY	5.6
1	4-K	195[D]	VAL	5.6
1	4-L	139[D]	THR	5.6
1	4-O	149[D]	GLY	5.6
1	1-I	253[A]	MET	5.6
1	2-I	253[B]	MET	5.6
1	3-I	253[C]	MET	5.6
1	4-I	253[D]	MET	5.6
1	1-O	148[A]	LYS	5.6
1	2-O	148[B]	LYS	5.6
1	3-O	148[C]	LYS	5.6
1	4-O	148[D]	LYS	5.6
1	1-E	199[A]	PRO	5.6
1	1-P	52[A]	PRO	5.6
1	2-E	199[B]	PRO	5.6
1	2-P	52[B]	PRO	5.6
1	3-E	199[C]	PRO	5.6
1	3-P	52[C]	PRO	5.6
1	4-E	199[D]	PRO	5.6
1	4-P	52[D]	PRO	5.6
1	1-M	80[A]	LEU	5.6
1	2-M	80[B]	LEU	5.6
1	3-M	80[C]	LEU	5.6
1	4-M	80[D]	LEU	5.6
1	1-E	200[A]	ALA	5.6
1	1-I	226[A]	PHE	5.6
1	1-J	59[A]	ALA	5.6
1	1-K	173[A]	ALA	5.6
1	2-E	200[B]	ALA	5.6
1	2-I	226[B]	PHE	5.6
1	2-J	59[B]	ALA	5.6
1	2-K	173[B]	ALA	5.6
1	3-E	200[C]	ALA	5.6
1	3-I	226[C]	PHE	5.6
1	3-J	59[C]	ALA	5.6
1	3-K	173[C]	ALA	5.6
1	4-E	200[D]	ALA	5.6
1	4-I	226[D]	PHE	5.6
1	4-J	59[D]	ALA	5.6
1	4-K	173[D]	ALA	5.6
1	1-J	306[A]	LYS	5.6

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Mol	Chain	Res	Type	RSRZ
1	1-L	314[A]	LYS	5.6
1	2-J	306[B]	LYS	5.6
1	2-L	314[B]	LYS	5.6
1	3-J	306[C]	LYS	5.6
1	3-L	314[C]	LYS	5.6
1	4-J	306[D]	LYS	5.6
1	4-L	314[D]	LYS	5.6
1	1-C	15[A]	ASN	5.6
1	1-M	32[A]	ASN	5.6
1	1-M	61[A]	ASN	5.6
1	1-M	210[A]	SER	5.6
1	2-C	15[B]	ASN	5.6
1	2-M	32[B]	ASN	5.6
1	2-M	61[B]	ASN	5.6
1	2-M	210[B]	SER	5.6
1	3-C	15[C]	ASN	5.6
1	3-M	32[C]	ASN	5.6
1	3-M	61[C]	ASN	5.6
1	3-M	210[C]	SER	5.6
1	4-C	15[D]	ASN	5.6
1	4-M	32[D]	ASN	5.6
1	4-M	61[D]	ASN	5.6
1	4-M	210[D]	SER	5.6
1	1-P	298[A]	GLU	5.6
1	2-P	298[B]	GLU	5.6
1	3-P	298[C]	GLU	5.6
1	4-P	298[D]	GLU	5.6
1	1-C	201[A]	ASP	5.6
1	1-M	28[A]	ARG	5.6
1	2-C	201[B]	ASP	5.6
1	2-M	28[B]	ARG	5.6
1	3-C	201[C]	ASP	5.6
1	3-M	28[C]	ARG	5.6
1	4-C	201[D]	ASP	5.6
1	4-M	28[D]	ARG	5.6
1	1-K	47[A]	ALA	5.6
1	2-K	47[B]	ALA	5.6
1	3-K	47[C]	ALA	5.6
1	4-K	47[D]	ALA	5.6
1	1-I	139[A]	THR	5.6
1	2-I	139[B]	THR	5.6
1	3-I	139[C]	THR	5.6

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Mol	Chain	Res	Type	RSRZ
1	4-I	139[D]	THR	5.6
1	1-O	36[A]	VAL	5.6
1	2-O	36[B]	VAL	5.6
1	3-O	36[C]	VAL	5.6
1	4-O	36[D]	VAL	5.6
1	1-P	198[A]	PRO	5.6
1	2-P	198[B]	PRO	5.6
1	3-P	198[C]	PRO	5.6
1	4-P	198[D]	PRO	5.6
1	1-J	239[A]	ALA	5.6
1	2-J	239[B]	ALA	5.6
1	3-J	239[C]	ALA	5.6
1	4-J	239[D]	ALA	5.6
1	1-N	87[A]	CYS	5.6
1	1-P	33[A]	VAL	5.6
1	1-P	100[A]	ILE	5.6
1	2-N	87[B]	CYS	5.6
1	2-P	33[B]	VAL	5.6
1	2-P	100[B]	ILE	5.6
1	3-N	87[C]	CYS	5.6
1	3-P	33[C]	VAL	5.6
1	3-P	100[C]	ILE	5.6
1	4-N	87[D]	CYS	5.6
1	4-P	33[D]	VAL	5.6
1	4-P	100[D]	ILE	5.6
1	1-I	117[A]	HIS	5.5
1	1-J	257[A]	HIS	5.5
1	1-L	294[A]	GLY	5.5
1	2-I	117[B]	HIS	5.5
1	2-J	257[B]	HIS	5.5
1	2-L	294[B]	GLY	5.5
1	3-I	117[C]	HIS	5.5
1	3-J	257[C]	HIS	5.5
1	3-L	294[C]	GLY	5.5
1	4-I	117[D]	HIS	5.5
1	4-J	257[D]	HIS	5.5
1	4-L	294[D]	GLY	5.5
1	1-M	110[A]	LEU	5.5
1	2-M	110[B]	LEU	5.5
1	3-M	110[C]	LEU	5.5
1	4-M	110[D]	LEU	5.5
1	1-K	56[A]	PHE	5.5

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Mol	Chain	Res	Type	RSRZ
1	2-K	56[B]	PHE	5.5
1	3-K	56[C]	PHE	5.5
1	4-K	56[D]	PHE	5.5
1	1-K	243[A]	ASP	5.5
1	1-N	55[A]	ARG	5.5
1	1-P	269[A]	GLN	5.5
1	2-K	243[B]	ASP	5.5
1	2-N	55[B]	ARG	5.5
1	2-P	269[B]	GLN	5.5
1	3-K	243[C]	ASP	5.5
1	3-N	55[C]	ARG	5.5
1	3-P	269[C]	GLN	5.5
1	4-K	243[D]	ASP	5.5
1	4-N	55[D]	ARG	5.5
1	4-P	269[D]	GLN	5.5
1	1-L	81[A]	LEU	5.5
1	1-O	278[A]	PRO	5.5
1	2-L	81[B]	LEU	5.5
1	2-O	278[B]	PRO	5.5
1	3-L	81[C]	LEU	5.5
1	3-O	278[C]	PRO	5.5
1	4-L	81[D]	LEU	5.5
1	4-O	278[D]	PRO	5.5
1	1-J	49[A]	PHE	5.5
1	1-K	72[A]	PHE	5.5
1	2-J	49[B]	PHE	5.5
1	2-K	72[B]	PHE	5.5
1	3-J	49[C]	PHE	5.5
1	3-K	72[C]	PHE	5.5
1	4-J	49[D]	PHE	5.5
1	4-K	72[D]	PHE	5.5
1	1-P	314[A]	LYS	5.5
1	2-P	314[B]	LYS	5.5
1	3-P	314[C]	LYS	5.5
1	4-P	314[D]	LYS	5.5
1	1-J	17[A]	ASP	5.5
1	1-J	217[A]	SER	5.5
1	1-L	102[A]	ASP	5.5
1	1-P	291[A]	ASP	5.5
1	2-J	17[B]	ASP	5.5
1	2-J	217[B]	SER	5.5
1	2-L	102[B]	ASP	5.5

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Mol	Chain	Res	Type	RSRZ
1	2-P	291[B]	ASP	5.5
1	3-J	17[C]	ASP	5.5
1	3-J	217[C]	SER	5.5
1	3-L	102[C]	ASP	5.5
1	3-P	291[C]	ASP	5.5
1	4-J	17[D]	ASP	5.5
1	4-J	217[D]	SER	5.5
1	4-L	102[D]	ASP	5.5
1	4-P	291[D]	ASP	5.5
1	1-I	310[A]	LYS	5.5
1	1-M	213[A]	MET	5.5
1	2-I	310[B]	LYS	5.5
1	2-M	213[B]	MET	5.5
1	3-I	310[C]	LYS	5.5
1	3-M	213[C]	MET	5.5
1	4-I	310[D]	LYS	5.5
1	4-M	213[D]	MET	5.5
1	1-I	304[A]	GLY	5.5
1	2-I	304[B]	GLY	5.5
1	3-I	304[C]	GLY	5.5
1	4-I	304[D]	GLY	5.5
1	1-J	258[A]	VAL	5.5
1	2-J	258[B]	VAL	5.5
1	3-J	258[C]	VAL	5.5
1	4-J	258[D]	VAL	5.5
1	1-M	283[A]	ALA	5.5
1	1-P	90[A]	ALA	5.5
1	2-M	283[B]	ALA	5.5
1	2-P	90[B]	ALA	5.5
1	3-M	283[C]	ALA	5.5
1	3-P	90[C]	ALA	5.5
1	4-M	283[D]	ALA	5.5
1	4-P	90[D]	ALA	5.5
1	1-I	198[A]	PRO	5.5
1	2-I	198[B]	PRO	5.5
1	3-I	198[C]	PRO	5.5
1	4-I	198[D]	PRO	5.5
1	1-N	167[A]	ARG	5.5
1	1-N	137[A]	GLU	5.5
1	1-P	58[A]	LEU	5.5
1	2-N	167[B]	ARG	5.5
1	2-N	137[B]	GLU	5.5

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Mol	Chain	Res	Type	RSRZ
1	2-P	58[B]	LEU	5.5
1	3-N	167[C]	ARG	5.5
1	3-N	137[C]	GLU	5.5
1	3-P	58[C]	LEU	5.5
1	4-N	167[D]	ARG	5.5
1	4-N	137[D]	GLU	5.5
1	4-P	58[D]	LEU	5.5
1	1-J	31[A]	ILE	5.5
1	1-K	224[A]	VAL	5.5
1	2-J	31[B]	ILE	5.5
1	2-K	224[B]	VAL	5.5
1	3-J	31[C]	ILE	5.5
1	3-K	224[C]	VAL	5.5
1	4-J	31[D]	ILE	5.5
1	4-K	224[D]	VAL	5.5
1	1-L	239[A]	ALA	5.5
1	2-L	239[B]	ALA	5.5
1	3-L	239[C]	ALA	5.5
1	4-L	239[D]	ALA	5.5
1	1-M	38[A]	PRO	5.5
1	2-M	38[B]	PRO	5.5
1	3-M	38[C]	PRO	5.5
1	4-M	38[D]	PRO	5.5
1	1-N	262[A]	HIS	5.5
1	1-O	304[A]	GLY	5.5
1	1-O	313[A]	MET	5.5
1	2-N	262[B]	HIS	5.5
1	2-O	304[B]	GLY	5.5
1	2-O	313[B]	MET	5.5
1	3-N	262[C]	HIS	5.5
1	3-O	304[C]	GLY	5.5
1	3-O	313[C]	MET	5.5
1	4-N	262[D]	HIS	5.5
1	4-O	304[D]	GLY	5.5
1	4-O	313[D]	MET	5.5
1	1-I	177[A]	LYS	5.5
1	1-P	81[A]	LEU	5.5
1	2-I	177[B]	LYS	5.5
1	2-P	81[B]	LEU	5.5
1	3-I	177[C]	LYS	5.5
1	3-P	81[C]	LEU	5.5
1	4-I	177[D]	LYS	5.5

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Mol	Chain	Res	Type	RSRZ
1	4-P	81[D]	LEU	5.5
1	1-J	249[A]	PHE	5.4
1	2-J	249[B]	PHE	5.4
1	3-J	249[C]	PHE	5.4
1	4-J	249[D]	PHE	5.4
1	1-N	245[A]	GLU	5.4
1	2-N	245[B]	GLU	5.4
1	3-N	245[C]	GLU	5.4
1	4-N	245[D]	GLU	5.4
1	1-O	207[A]	PRO	5.4
1	2-O	207[B]	PRO	5.4
1	3-O	207[C]	PRO	5.4
1	4-O	207[D]	PRO	5.4
1	1-B	204[A]	GLY	5.4
1	1-M	223[A]	GLY	5.4
1	2-B	204[B]	GLY	5.4
1	2-M	223[B]	GLY	5.4
1	3-B	204[C]	GLY	5.4
1	3-M	223[C]	GLY	5.4
1	4-B	204[D]	GLY	5.4
1	4-M	223[D]	GLY	5.4
1	1-M	19[A]	GLU	5.4
1	2-M	19[B]	GLU	5.4
1	3-M	19[C]	GLU	5.4
1	4-M	19[D]	GLU	5.4
1	1-I	300[A]	PHE	5.4
1	2-I	300[B]	PHE	5.4
1	3-I	300[C]	PHE	5.4
1	4-I	300[D]	PHE	5.4
1	1-N	235[A]	THR	5.4
1	1-P	114[A]	GLY	5.4
1	2-N	235[B]	THR	5.4
1	2-P	114[B]	GLY	5.4
1	3-N	235[C]	THR	5.4
1	3-P	114[C]	GLY	5.4
1	4-N	235[D]	THR	5.4
1	4-P	114[D]	GLY	5.4
1	1-P	305[A]	TYR	5.4
1	2-P	305[B]	TYR	5.4
1	3-P	305[C]	TYR	5.4
1	4-P	305[D]	TYR	5.4
1	1-K	110[A]	LEU	5.4

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Mol	Chain	Res	Type	RSRZ
1	1-P	61[A]	ASN	5.4
1	2-K	110[B]	LEU	5.4
1	2-P	61[B]	ASN	5.4
1	3-K	110[C]	LEU	5.4
1	3-P	61[C]	ASN	5.4
1	4-K	110[D]	LEU	5.4
1	4-P	61[D]	ASN	5.4
1	1-G	36[A]	VAL	5.4
1	1-K	156[A]	VAL	5.4
1	2-G	36[B]	VAL	5.4
1	2-K	156[B]	VAL	5.4
1	3-G	36[C]	VAL	5.4
1	3-K	156[C]	VAL	5.4
1	4-G	36[D]	VAL	5.4
1	4-K	156[D]	VAL	5.4
1	1-J	118[A]	ARG	5.4
1	1-O	155[A]	ARG	5.4
1	2-J	118[B]	ARG	5.4
1	2-O	155[B]	ARG	5.4
1	3-J	118[C]	ARG	5.4
1	3-O	155[C]	ARG	5.4
1	4-J	118[D]	ARG	5.4
1	4-O	155[D]	ARG	5.4
1	1-J	301[A]	VAL	5.4
1	1-L	235[A]	THR	5.4
1	1-M	68[A]	THR	5.4
1	1-M	232[A]	ALA	5.4
1	2-J	301[B]	VAL	5.4
1	2-L	235[B]	THR	5.4
1	2-M	68[B]	THR	5.4
1	2-M	232[B]	ALA	5.4
1	3-J	301[C]	VAL	5.4
1	3-L	235[C]	THR	5.4
1	3-M	68[C]	THR	5.4
1	3-M	232[C]	ALA	5.4
1	4-J	301[D]	VAL	5.4
1	4-L	235[D]	THR	5.4
1	4-M	68[D]	THR	5.4
1	4-M	232[D]	ALA	5.4
1	1-O	56[A]	PHE	5.4
1	2-O	56[B]	PHE	5.4
1	3-O	56[C]	PHE	5.4

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Mol	Chain	Res	Type	RSRZ
1	4-O	56[D]	PHE	5.4
1	1-P	130[A]	GLN	5.4
1	2-P	130[B]	GLN	5.4
1	3-P	130[C]	GLN	5.4
1	4-P	130[D]	GLN	5.4
1	1-L	217[A]	SER	5.4
1	2-L	217[B]	SER	5.4
1	3-L	217[C]	SER	5.4
1	4-L	217[D]	SER	5.4
1	1-K	171[A]	LEU	5.4
1	2-K	171[B]	LEU	5.4
1	3-K	171[C]	LEU	5.4
1	4-K	171[D]	LEU	5.4
1	1-I	272[A]	ARG	5.4
1	2-I	272[B]	ARG	5.4
1	3-I	272[C]	ARG	5.4
1	4-I	272[D]	ARG	5.4
1	1-P	192[A]	GLN	5.4
1	2-P	192[B]	GLN	5.4
1	3-P	192[C]	GLN	5.4
1	4-P	192[D]	GLN	5.4
1	1-J	178[A]	ASP	5.4
1	1-L	95[A]	SER	5.4
1	1-O	172[A]	SER	5.4
1	1-P	316[A]	SER	5.4
1	2-J	178[B]	ASP	5.4
1	2-L	95[B]	SER	5.4
1	2-O	172[B]	SER	5.4
1	2-P	316[B]	SER	5.4
1	3-J	178[C]	ASP	5.4
1	3-L	95[C]	SER	5.4
1	3-O	172[C]	SER	5.4
1	3-P	316[C]	SER	5.4
1	4-J	178[D]	ASP	5.4
1	4-L	95[D]	SER	5.4
1	4-O	172[D]	SER	5.4
1	4-P	316[D]	SER	5.4
1	1-O	290[A]	GLY	5.4
1	2-O	290[B]	GLY	5.4
1	3-O	290[C]	GLY	5.4
1	4-O	290[D]	GLY	5.4
1	1-O	24[A]	LEU	5.4

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Mol	Chain	Res	Type	RSRZ
1	2-O	24[B]	LEU	5.4
1	3-O	24[C]	LEU	5.4
1	4-O	24[D]	LEU	5.4
1	1-D	283[A]	ALA	5.4
1	1-J	141[A]	ALA	5.4
1	2-D	283[B]	ALA	5.4
1	2-J	141[B]	ALA	5.4
1	3-D	283[C]	ALA	5.4
1	3-J	141[C]	ALA	5.4
1	4-D	283[D]	ALA	5.4
1	4-J	141[D]	ALA	5.4
1	1-P	83[A]	PHE	5.3
1	2-P	83[B]	PHE	5.3
1	3-P	83[C]	PHE	5.3
1	4-P	83[D]	PHE	5.3
1	1-J	102[A]	ASP	5.3
1	2-J	102[B]	ASP	5.3
1	3-J	102[C]	ASP	5.3
1	4-J	102[D]	ASP	5.3
1	1-K	227[A]	ASN	5.3
1	2-K	227[B]	ASN	5.3
1	3-K	227[C]	ASN	5.3
1	4-K	227[D]	ASN	5.3
1	1-P	113[A]	VAL	5.3
1	2-P	113[B]	VAL	5.3
1	3-P	113[C]	VAL	5.3
1	4-P	113[D]	VAL	5.3
1	1-J	192[A]	GLN	5.3
1	2-J	192[B]	GLN	5.3
1	3-J	192[C]	GLN	5.3
1	4-J	192[D]	GLN	5.3
1	1-O	218[A]	CYS	5.3
1	2-O	218[B]	CYS	5.3
1	3-O	218[C]	CYS	5.3
1	4-O	218[D]	CYS	5.3
1	1-J	60[A]	ASP	5.3
1	2-J	60[B]	ASP	5.3
1	3-J	60[C]	ASP	5.3
1	4-J	60[D]	ASP	5.3
1	1-P	266[A]	LEU	5.3
1	2-P	266[B]	LEU	5.3
1	3-P	266[C]	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
1	4-P	266[D]	LEU	5.3
1	1-M	82[A]	TRP	5.3
1	1-O	27[A]	ILE	5.3
1	1-O	241[A]	ILE	5.3
1	2-M	82[B]	TRP	5.3
1	2-O	27[B]	ILE	5.3
1	2-O	241[B]	ILE	5.3
1	3-M	82[C]	TRP	5.3
1	3-O	27[C]	ILE	5.3
1	3-O	241[C]	ILE	5.3
1	4-M	82[D]	TRP	5.3
1	4-O	27[D]	ILE	5.3
1	4-O	241[D]	ILE	5.3
1	1-M	137[A]	GLU	5.3
1	2-M	137[B]	GLU	5.3
1	3-M	137[C]	GLU	5.3
1	4-M	137[D]	GLU	5.3
1	1-J	24[A]	LEU	5.3
1	1-O	220[A]	LEU	5.3
1	2-J	24[B]	LEU	5.3
1	2-O	220[B]	LEU	5.3
1	3-J	24[C]	LEU	5.3
1	3-O	220[C]	LEU	5.3
1	4-J	24[D]	LEU	5.3
1	4-O	220[D]	LEU	5.3
1	1-N	116[A]	GLY	5.3
1	2-N	116[B]	GLY	5.3
1	3-N	116[C]	GLY	5.3
1	4-N	116[D]	GLY	5.3
1	1-J	126[A]	VAL	5.3
1	1-K	306[A]	LYS	5.3
1	1-N	208[A]	LYS	5.3
1	2-J	126[B]	VAL	5.3
1	2-K	306[B]	LYS	5.3
1	2-N	208[B]	LYS	5.3
1	3-J	126[C]	VAL	5.3
1	3-K	306[C]	LYS	5.3
1	3-N	208[C]	LYS	5.3
1	4-J	126[D]	VAL	5.3
1	4-K	306[D]	LYS	5.3
1	4-N	208[D]	LYS	5.3
1	1-O	154[A]	GLN	5.3

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Mol	Chain	Res	Type	RSRZ
1	2-O	154[B]	GLN	5.3
1	3-O	154[C]	GLN	5.3
1	4-O	154[D]	GLN	5.3
1	1-P	31[A]	ILE	5.3
1	1-P	292[A]	ILE	5.3
1	2-P	31[B]	ILE	5.3
1	2-P	292[B]	ILE	5.3
1	3-P	31[C]	ILE	5.3
1	3-P	292[C]	ILE	5.3
1	4-P	31[D]	ILE	5.3
1	4-P	292[D]	ILE	5.3
1	1-P	290[A]	GLY	5.3
1	2-P	290[B]	GLY	5.3
1	3-P	290[C]	GLY	5.3
1	4-P	290[D]	GLY	5.3
1	1-L	211[A]	CYS	5.3
1	2-L	211[B]	CYS	5.3
1	3-L	211[C]	CYS	5.3
1	4-L	211[D]	CYS	5.3
1	1-O	80[A]	LEU	5.3
1	2-O	80[B]	LEU	5.3
1	3-O	80[C]	LEU	5.3
1	4-O	80[D]	LEU	5.3
1	1-P	306[A]	LYS	5.2
1	2-P	306[B]	LYS	5.2
1	3-P	306[C]	LYS	5.2
1	4-P	306[D]	LYS	5.2
1	1-K	172[A]	SER	5.2
1	2-K	172[B]	SER	5.2
1	3-K	172[C]	SER	5.2
1	4-K	172[D]	SER	5.2
1	1-I	299[A]	ASP	5.2
1	1-M	157[A]	ILE	5.2
1	2-I	299[B]	ASP	5.2
1	2-M	157[B]	ILE	5.2
1	3-I	299[C]	ASP	5.2
1	3-M	157[C]	ILE	5.2
1	4-I	299[D]	ASP	5.2
1	4-M	157[D]	ILE	5.2
1	1-N	183[A]	ALA	5.2
1	2-N	183[B]	ALA	5.2
1	3-N	183[C]	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	4-N	183[D]	ALA	5.2
1	1-B	198[A]	PRO	5.2
1	1-I	125[A]	PRO	5.2
1	1-L	198[A]	PRO	5.2
1	2-B	198[B]	PRO	5.2
1	2-I	125[B]	PRO	5.2
1	2-L	198[B]	PRO	5.2
1	3-B	198[C]	PRO	5.2
1	3-I	125[C]	PRO	5.2
1	3-L	198[C]	PRO	5.2
1	4-B	198[D]	PRO	5.2
1	4-I	125[D]	PRO	5.2
1	4-L	198[D]	PRO	5.2
1	1-K	76[A]	VAL	5.2
1	1-N	301[A]	VAL	5.2
1	1-P	102[A]	ASP	5.2
1	2-K	76[B]	VAL	5.2
1	2-N	301[B]	VAL	5.2
1	2-P	102[B]	ASP	5.2
1	3-K	76[C]	VAL	5.2
1	3-N	301[C]	VAL	5.2
1	3-P	102[C]	ASP	5.2
1	4-K	76[D]	VAL	5.2
1	4-N	301[D]	VAL	5.2
1	4-P	102[D]	ASP	5.2
1	1-F	160[A]	ILE	5.2
1	1-P	289[A]	ILE	5.2
1	2-F	160[B]	ILE	5.2
1	2-P	289[B]	ILE	5.2
1	3-F	160[C]	ILE	5.2
1	3-P	289[C]	ILE	5.2
1	4-F	160[D]	ILE	5.2
1	4-P	289[D]	ILE	5.2
1	1-O	161[A]	LYS	5.2
1	1-P	189[A]	MET	5.2
1	2-O	161[B]	LYS	5.2
1	2-P	189[B]	MET	5.2
1	3-O	161[C]	LYS	5.2
1	3-P	189[C]	MET	5.2
1	4-O	161[D]	LYS	5.2
1	4-P	189[D]	MET	5.2
1	1-M	16[A]	PRO	5.2

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Mol	Chain	Res	Type	RSRZ
1	2-M	16[B]	PRO	5.2
1	3-M	16[C]	PRO	5.2
1	4-M	16[D]	PRO	5.2
1	1-I	60[A]	ASP	5.2
1	1-J	291[A]	ASP	5.2
1	1-M	276[A]	ASP	5.2
1	2-I	60[B]	ASP	5.2
1	2-J	291[B]	ASP	5.2
1	2-M	276[B]	ASP	5.2
1	3-I	60[C]	ASP	5.2
1	3-J	291[C]	ASP	5.2
1	3-M	276[C]	ASP	5.2
1	4-I	60[D]	ASP	5.2
1	4-J	291[D]	ASP	5.2
1	4-M	276[D]	ASP	5.2
1	1-I	83[A]	PHE	5.2
1	2-I	83[B]	PHE	5.2
1	3-I	83[C]	PHE	5.2
1	4-I	83[D]	PHE	5.2
1	1-I	265[A]	PRO	5.2
1	1-N	186[A]	PRO	5.2
1	1-O	186[A]	PRO	5.2
1	1-P	225[A]	PRO	5.2
1	2-I	265[B]	PRO	5.2
1	2-N	186[B]	PRO	5.2
1	2-O	186[B]	PRO	5.2
1	2-P	225[B]	PRO	5.2
1	3-I	265[C]	PRO	5.2
1	3-N	186[C]	PRO	5.2
1	3-O	186[C]	PRO	5.2
1	3-P	225[C]	PRO	5.2
1	4-I	265[D]	PRO	5.2
1	4-N	186[D]	PRO	5.2
1	4-O	186[D]	PRO	5.2
1	4-P	225[D]	PRO	5.2
1	1-K	70[A]	ARG	5.2
1	1-N	260[A]	ARG	5.2
1	2-K	70[B]	ARG	5.2
1	2-N	260[B]	ARG	5.2
1	3-K	70[C]	ARG	5.2
1	3-N	260[C]	ARG	5.2
1	4-K	70[D]	ARG	5.2

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Mol	Chain	Res	Type	RSRZ
1	4-N	260[D]	ARG	5.2
1	1-I	179[A]	LEU	5.2
1	1-N	153[A]	LEU	5.2
1	1-O	266[A]	LEU	5.2
1	2-I	179[B]	LEU	5.2
1	2-N	153[B]	LEU	5.2
1	2-O	266[B]	LEU	5.2
1	3-I	179[C]	LEU	5.2
1	3-N	153[C]	LEU	5.2
1	3-O	266[C]	LEU	5.2
1	4-I	179[D]	LEU	5.2
1	4-N	153[D]	LEU	5.2
1	4-O	266[D]	LEU	5.2
1	1-M	116[A]	GLY	5.2
1	2-M	116[B]	GLY	5.2
1	3-M	116[C]	GLY	5.2
1	4-M	116[D]	GLY	5.2
1	1-I	157[A]	ILE	5.2
1	1-M	178[A]	ASP	5.2
1	1-N	313[A]	MET	5.2
1	2-I	157[B]	ILE	5.2
1	2-M	178[B]	ASP	5.2
1	2-N	313[B]	MET	5.2
1	3-I	157[C]	ILE	5.2
1	3-M	178[C]	ASP	5.2
1	3-N	313[C]	MET	5.2
1	4-M	178[D]	ASP	5.2
1	4-N	313[D]	MET	5.2
1	1-M	292[A]	ILE	5.2
1	2-M	292[B]	ILE	5.2
1	3-M	292[C]	ILE	5.2
1	4-I	157[D]	ILE	5.2
1	4-M	292[D]	ILE	5.2
1	1-I	190[A]	PHE	5.2
1	2-I	190[B]	PHE	5.2
1	3-I	190[C]	PHE	5.2
1	4-I	190[D]	PHE	5.2
1	1-I	95[A]	SER	5.2
1	1-L	272[A]	ARG	5.2
1	2-I	95[B]	SER	5.2
1	2-L	272[B]	ARG	5.2
1	3-I	95[C]	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	3-L	272[C]	ARG	5.2
1	4-I	95[D]	SER	5.2
1	4-L	272[D]	ARG	5.2
1	1-I	108[A]	GLU	5.2
1	1-L	117[A]	HIS	5.2
1	2-I	108[B]	GLU	5.2
1	2-L	117[B]	HIS	5.2
1	3-I	108[C]	GLU	5.2
1	3-L	117[C]	HIS	5.2
1	4-I	108[D]	GLU	5.2
1	4-L	117[D]	HIS	5.2
1	1-M	197[A]	LEU	5.2
1	2-M	197[B]	LEU	5.2
1	3-M	197[C]	LEU	5.2
1	4-M	197[D]	LEU	5.2
1	1-O	76[A]	VAL	5.2
1	1-O	261[A]	ASP	5.2
1	2-O	76[B]	VAL	5.2
1	2-O	261[B]	ASP	5.2
1	3-O	76[C]	VAL	5.2
1	3-O	261[C]	ASP	5.2
1	4-O	76[D]	VAL	5.2
1	4-O	261[D]	ASP	5.2
1	1-J	173[A]	ALA	5.2
1	2-J	173[B]	ALA	5.2
1	3-J	173[C]	ALA	5.2
1	4-J	173[D]	ALA	5.2
1	1-P	119[A]	ARG	5.2
1	2-P	119[B]	ARG	5.2
1	3-P	119[C]	ARG	5.2
1	4-P	119[D]	ARG	5.2
1	1-M	121[A]	GLY	5.2
1	2-M	121[B]	GLY	5.2
1	3-M	121[C]	GLY	5.2
1	4-M	121[D]	GLY	5.2
1	1-O	302[A]	VAL	5.1
1	1-P	242[A]	THR	5.1
1	2-O	302[B]	VAL	5.1
1	2-P	242[B]	THR	5.1
1	3-O	302[C]	VAL	5.1
1	3-P	242[C]	THR	5.1
1	4-O	302[D]	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
1	4-P	242[D]	THR	5.1
1	1-K	174[A]	TRP	5.1
1	1-L	131[A]	TRP	5.1
1	1-N	23[A]	TYR	5.1
1	2-K	174[B]	TRP	5.1
1	2-L	131[B]	TRP	5.1
1	1-O	175[A]	ASN	5.1
1	2-N	23[B]	TYR	5.1
1	3-K	174[C]	TRP	5.1
1	3-L	131[C]	TRP	5.1
1	3-N	23[C]	TYR	5.1
1	4-K	174[D]	TRP	5.1
1	4-L	131[D]	TRP	5.1
1	2-O	175[B]	ASN	5.1
1	3-O	175[C]	ASN	5.1
1	4-N	23[D]	TYR	5.1
1	4-O	175[D]	ASN	5.1
1	1-N	247[A]	HIS	5.1
1	1-P	228[A]	ILE	5.1
1	2-N	247[B]	HIS	5.1
1	2-P	228[B]	ILE	5.1
1	3-N	247[C]	HIS	5.1
1	3-P	228[C]	ILE	5.1
1	4-N	247[D]	HIS	5.1
1	4-P	228[D]	ILE	5.1
1	1-I	56[A]	PHE	5.1
1	2-I	56[B]	PHE	5.1
1	3-I	56[C]	PHE	5.1
1	4-I	56[D]	PHE	5.1
1	1-J	275[A]	ARG	5.1
1	2-J	275[B]	ARG	5.1
1	3-J	275[C]	ARG	5.1
1	4-J	275[D]	ARG	5.1
1	1-L	108[A]	GLU	5.1
1	2-L	108[B]	GLU	5.1
1	3-L	108[C]	GLU	5.1
1	4-L	108[D]	GLU	5.1
1	1-M	220[A]	LEU	5.1
1	2-M	220[B]	LEU	5.1
1	3-M	220[C]	LEU	5.1
1	4-M	220[D]	LEU	5.1
1	1-M	182[A]	MET	5.1

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Mol	Chain	Res	Type	RSRZ
1	1-N	317[A]	ALA	5.1
1	2-M	182[B]	MET	5.1
1	2-N	317[B]	ALA	5.1
1	3-M	182[C]	MET	5.1
1	3-N	317[C]	ALA	5.1
1	4-M	182[D]	MET	5.1
1	4-N	317[D]	ALA	5.1
1	1-M	21[A]	TYR	5.1
1	2-M	21[B]	TYR	5.1
1	3-M	21[C]	TYR	5.1
1	4-M	21[D]	TYR	5.1
1	1-O	248[A]	GLU	5.1
1	2-O	248[B]	GLU	5.1
1	3-O	248[C]	GLU	5.1
1	4-O	248[D]	GLU	5.1
1	1-P	249[A]	PHE	5.1
1	2-P	249[B]	PHE	5.1
1	3-P	249[C]	PHE	5.1
1	4-P	249[D]	PHE	5.1
1	1-M	141[A]	ALA	5.1
1	2-M	141[B]	ALA	5.1
1	3-M	141[C]	ALA	5.1
1	4-M	141[D]	ALA	5.1
1	1-K	147[A]	GLY	5.1
1	2-K	147[B]	GLY	5.1
1	3-K	147[C]	GLY	5.1
1	4-K	147[D]	GLY	5.1
1	1-N	21[A]	TYR	5.1
1	1-N	231[A]	TYR	5.1
1	2-N	21[B]	TYR	5.1
1	2-N	231[B]	TYR	5.1
1	3-N	21[C]	TYR	5.1
1	3-N	231[C]	TYR	5.1
1	4-N	21[D]	TYR	5.1
1	4-N	231[D]	TYR	5.1
1	1-I	274[A]	PRO	5.1
1	1-P	203[A]	PRO	5.1
1	2-I	274[B]	PRO	5.1
1	2-P	203[B]	PRO	5.1
1	3-I	274[C]	PRO	5.1
1	3-P	203[C]	PRO	5.1
1	4-I	274[D]	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
1	4-P	203[D]	PRO	5.1
1	1-I	261[A]	ASP	5.1
1	1-J	90[A]	ALA	5.1
1	2-I	261[B]	ASP	5.1
1	2-J	90[B]	ALA	5.1
1	3-I	261[C]	ASP	5.1
1	3-J	90[C]	ALA	5.1
1	4-I	261[D]	ASP	5.1
1	4-J	90[D]	ALA	5.1
1	1-L	30[A]	ILE	5.1
1	2-L	30[B]	ILE	5.1
1	3-L	30[C]	ILE	5.1
1	4-L	30[D]	ILE	5.1
1	1-K	83[A]	PHE	5.1
1	1-L	39[A]	ASP	5.1
1	1-P	277[A]	PHE	5.1
1	2-K	83[B]	PHE	5.1
1	2-L	39[B]	ASP	5.1
1	2-P	277[B]	PHE	5.1
1	3-K	83[C]	PHE	5.1
1	3-L	39[C]	ASP	5.1
1	3-P	277[C]	PHE	5.1
1	4-K	83[D]	PHE	5.1
1	4-L	39[D]	ASP	5.1
1	4-P	277[D]	PHE	5.1
1	1-K	67[A]	THR	5.1
1	2-K	67[B]	THR	5.1
1	3-K	67[C]	THR	5.1
1	4-K	67[D]	THR	5.1
1	1-A	141[A]	ALA	5.1
1	2-A	141[B]	ALA	5.1
1	3-A	141[C]	ALA	5.1
1	4-A	141[D]	ALA	5.1
1	1-B	212[A]	LEU	5.1
1	1-H	204[A]	GLY	5.1
1	1-L	99[A]	GLY	5.1
1	2-B	212[B]	LEU	5.1
1	2-H	204[B]	GLY	5.1
1	2-L	99[B]	GLY	5.1
1	3-B	212[C]	LEU	5.1
1	3-H	204[C]	GLY	5.1
1	3-L	99[C]	GLY	5.1

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Mol	Chain	Res	Type	RSRZ
1	4-B	212[D]	LEU	5.1
1	4-H	204[D]	GLY	5.1
1	4-L	99[D]	GLY	5.1
1	1-M	227[A]	ASN	5.1
1	2-M	227[B]	ASN	5.1
1	3-M	227[C]	ASN	5.1
1	4-M	227[D]	ASN	5.1
1	1-P	151[A]	ASP	5.1
1	2-P	151[B]	ASP	5.1
1	3-P	151[C]	ASP	5.1
1	4-P	151[D]	ASP	5.1
1	1-I	277[A]	PHE	5.1
1	1-K	193[A]	PHE	5.1
1	2-I	277[B]	PHE	5.1
1	2-K	193[B]	PHE	5.1
1	3-I	277[C]	PHE	5.1
1	3-K	193[C]	PHE	5.1
1	4-I	277[D]	PHE	5.1
1	4-K	193[D]	PHE	5.1
1	1-I	137[A]	GLU	5.1
1	1-I	288[A]	GLU	5.1
1	2-I	137[B]	GLU	5.1
1	2-I	288[B]	GLU	5.1
1	3-I	137[C]	GLU	5.1
1	3-I	288[C]	GLU	5.1
1	4-I	137[D]	GLU	5.1
1	4-I	288[D]	GLU	5.1
1	1-H	197[A]	LEU	5.1
1	2-H	197[B]	LEU	5.1
1	3-H	197[C]	LEU	5.1
1	4-H	197[D]	LEU	5.1
1	1-J	215[A]	GLN	5.0
1	1-K	286[A]	LYS	5.0
1	2-J	215[B]	GLN	5.0
1	2-K	286[B]	LYS	5.0
1	3-J	215[C]	GLN	5.0
1	3-K	286[C]	LYS	5.0
1	4-J	215[D]	GLN	5.0
1	4-K	286[D]	LYS	5.0
1	1-C	316[A]	SER	5.0
1	1-J	262[A]	HIS	5.0
1	1-L	278[A]	PRO	5.0

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Mol	Chain	Res	Type	RSRZ
1	2-C	316[B]	SER	5.0
1	2-J	262[B]	HIS	5.0
1	2-L	278[B]	PRO	5.0
1	3-C	316[C]	SER	5.0
1	3-J	262[C]	HIS	5.0
1	3-L	278[C]	PRO	5.0
1	4-C	316[D]	SER	5.0
1	4-J	262[D]	HIS	5.0
1	4-L	278[D]	PRO	5.0
1	1-K	311[A]	ILE	5.0
1	1-P	170[A]	ILE	5.0
1	2-K	311[B]	ILE	5.0
1	2-P	170[B]	ILE	5.0
1	3-K	311[C]	ILE	5.0
1	3-P	170[C]	ILE	5.0
1	4-K	311[D]	ILE	5.0
1	4-P	170[D]	ILE	5.0
1	1-I	99[A]	GLY	5.0
1	2-I	99[B]	GLY	5.0
1	3-I	99[C]	GLY	5.0
1	4-I	99[D]	GLY	5.0
1	1-N	104[A]	ASN	5.0
1	1-N	162[A]	ASN	5.0
1	2-N	104[B]	ASN	5.0
1	2-N	162[B]	ASN	5.0
1	3-N	104[C]	ASN	5.0
1	3-N	162[C]	ASN	5.0
1	4-N	104[D]	ASN	5.0
1	4-N	162[D]	ASN	5.0
1	1-K	102[A]	ASP	5.0
1	1-M	144[A]	ASP	5.0
1	2-K	102[B]	ASP	5.0
1	2-M	144[B]	ASP	5.0
1	3-K	102[C]	ASP	5.0
1	3-M	144[C]	ASP	5.0
1	4-K	102[D]	ASP	5.0
1	4-M	144[D]	ASP	5.0
1	1-P	146[A]	LYS	5.0
1	2-P	146[B]	LYS	5.0
1	3-P	146[C]	LYS	5.0
1	4-P	146[D]	LYS	5.0
1	1-P	44[A]	GLY	5.0

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Mol	Chain	Res	Type	RSRZ
1	2-P	44[B]	GLY	5.0
1	3-P	44[C]	GLY	5.0
1	4-P	44[D]	GLY	5.0
1	1-J	315[A]	MET	5.0
1	1-K	88[A]	THR	5.0
1	1-K	315[A]	MET	5.0
1	2-J	315[B]	MET	5.0
1	2-K	88[B]	THR	5.0
1	2-K	315[B]	MET	5.0
1	3-J	315[C]	MET	5.0
1	3-K	88[C]	THR	5.0
1	3-K	315[C]	MET	5.0
1	4-J	315[D]	MET	5.0
1	4-K	88[D]	THR	5.0
1	4-K	315[D]	MET	5.0
1	1-P	138[A]	TYR	5.0
1	2-P	138[B]	TYR	5.0
1	3-P	138[C]	TYR	5.0
1	4-P	138[D]	TYR	5.0
1	1-I	142[A]	ASP	5.0
1	1-L	91[A]	LYS	5.0
1	2-I	142[B]	ASP	5.0
1	2-L	91[B]	LYS	5.0
1	3-I	142[C]	ASP	5.0
1	3-L	91[C]	LYS	5.0
1	4-I	142[D]	ASP	5.0
1	4-L	91[D]	LYS	5.0
1	1-L	52[A]	PRO	5.0
1	1-M	125[A]	PRO	5.0
1	2-L	52[B]	PRO	5.0
1	2-M	125[B]	PRO	5.0
1	3-L	52[C]	PRO	5.0
1	3-M	125[C]	PRO	5.0
1	4-L	52[D]	PRO	5.0
1	4-M	125[D]	PRO	5.0
1	1-L	116[A]	GLY	5.0
1	1-N	124[A]	GLY	5.0
1	2-L	116[B]	GLY	5.0
1	2-N	124[B]	GLY	5.0
1	3-L	116[C]	GLY	5.0
1	3-N	124[C]	GLY	5.0
1	4-L	116[D]	GLY	5.0

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Mol	Chain	Res	Type	RSRZ
1	4-N	124[D]	GLY	5.0
1	1-K	187[A]	CYS	5.0
1	2-K	187[B]	CYS	5.0
1	3-K	187[C]	CYS	5.0
1	4-K	187[D]	CYS	5.0
1	1-K	237[A]	MET	5.0
1	2-K	237[B]	MET	5.0
1	3-K	237[C]	MET	5.0
1	4-K	237[D]	MET	5.0
1	1-J	152[A]	GLN	5.0
1	1-P	22[A]	GLN	5.0
1	2-J	152[B]	GLN	5.0
1	2-P	22[B]	GLN	5.0
1	3-J	152[C]	GLN	5.0
1	3-P	22[C]	GLN	5.0
1	4-J	152[D]	GLN	5.0
1	4-P	22[D]	GLN	5.0
1	1-A	14[A]	SER	5.0
1	1-K	257[A]	HIS	5.0
1	1-L	222[A]	LEU	5.0
1	2-A	14[B]	SER	5.0
1	2-K	257[B]	HIS	5.0
1	2-L	222[B]	LEU	5.0
1	3-A	14[C]	SER	5.0
1	3-K	257[C]	HIS	5.0
1	3-L	222[C]	LEU	5.0
1	4-A	14[D]	SER	5.0
1	4-K	257[D]	HIS	5.0
1	4-L	222[D]	LEU	5.0
1	1-C	203[A]	PRO	5.0
1	2-C	203[B]	PRO	5.0
1	3-C	203[C]	PRO	5.0
1	4-C	203[D]	PRO	5.0
1	1-E	36[A]	VAL	5.0
1	1-K	309[A]	GLY	5.0
1	1-P	36[A]	VAL	5.0
1	2-E	36[B]	VAL	5.0
1	2-K	309[B]	GLY	5.0
1	2-P	36[B]	VAL	5.0
1	3-E	36[C]	VAL	5.0
1	3-K	309[C]	GLY	5.0
1	3-P	36[C]	VAL	5.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	4-E	36[D]	VAL	5.0
1	4-K	309[D]	GLY	5.0
1	4-P	36[D]	VAL	5.0
1	1-I	227[A]	ASN	5.0
1	1-L	252[A]	GLN	5.0
1	2-I	227[B]	ASN	5.0
1	2-L	252[B]	GLN	5.0
1	3-I	227[C]	ASN	5.0
1	3-L	252[C]	GLN	5.0
1	4-I	227[D]	ASN	5.0
1	4-L	252[D]	GLN	5.0
1	1-M	59[A]	ALA	5.0
1	2-M	59[B]	ALA	5.0
1	3-M	59[C]	ALA	5.0
1	4-M	59[D]	ALA	5.0
1	1-K	157[A]	ILE	5.0
1	2-K	157[B]	ILE	5.0
1	3-K	157[C]	ILE	5.0
1	4-K	157[D]	ILE	5.0
1	1-I	145[A]	TYR	5.0
1	1-J	23[A]	TYR	5.0
1	1-N	127[A]	TYR	5.0
1	2-I	145[B]	TYR	5.0
1	2-J	23[B]	TYR	5.0
1	2-N	127[B]	TYR	5.0
1	3-I	145[C]	TYR	5.0
1	3-J	23[C]	TYR	5.0
1	3-N	127[C]	TYR	5.0
1	4-I	145[D]	TYR	5.0
1	4-J	23[D]	TYR	5.0
1	4-N	127[D]	TYR	5.0
1	1-K	117[A]	HIS	5.0
1	2-K	117[B]	HIS	5.0
1	3-K	117[C]	HIS	5.0
1	4-K	117[D]	HIS	5.0
1	1-L	70[A]	ARG	5.0
1	2-L	70[B]	ARG	5.0
1	3-L	70[C]	ARG	5.0
1	4-L	70[D]	ARG	5.0
1	1-I	39[A]	ASP	5.0
1	1-I	254[A]	GLY	5.0
1	1-K	17[A]	ASP	5.0

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Mol	Chain	Res	Type	RSRZ
1	1-L	143[A]	GLY	5.0
1	2-I	39[B]	ASP	5.0
1	2-I	254[B]	GLY	5.0
1	2-K	17[B]	ASP	5.0
1	2-L	143[B]	GLY	5.0
1	3-I	39[C]	ASP	5.0
1	3-I	254[C]	GLY	5.0
1	3-K	17[C]	ASP	5.0
1	3-L	143[C]	GLY	5.0
1	4-I	39[D]	ASP	5.0
1	4-I	254[D]	GLY	5.0
1	4-K	17[D]	ASP	5.0
1	4-L	143[D]	GLY	5.0
1	1-P	213[A]	MET	5.0
1	2-P	213[B]	MET	5.0
1	3-P	213[C]	MET	5.0
1	4-P	213[D]	MET	5.0
1	1-I	173[A]	ALA	5.0
1	1-M	50[A]	ALA	5.0
1	2-I	173[B]	ALA	5.0
1	2-M	50[B]	ALA	5.0
1	3-I	173[C]	ALA	5.0
1	3-M	50[C]	ALA	5.0
1	4-I	173[D]	ALA	5.0
1	4-M	50[D]	ALA	5.0
1	1-C	260[A]	ARG	5.0
1	1-K	284[A]	ARG	5.0
1	1-K	217[A]	SER	5.0
1	1-L	137[A]	GLU	5.0
1	2-C	260[B]	ARG	5.0
1	2-K	284[B]	ARG	5.0
1	2-K	217[B]	SER	5.0
1	2-L	137[B]	GLU	5.0
1	3-C	260[C]	ARG	5.0
1	3-K	284[C]	ARG	5.0
1	3-K	217[C]	SER	5.0
1	3-L	137[C]	GLU	5.0
1	4-C	260[D]	ARG	5.0
1	4-K	284[D]	ARG	5.0
1	4-K	217[D]	SER	5.0
1	4-L	137[D]	GLU	5.0
1	1-L	23[A]	TYR	5.0

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Mol	Chain	Res	Type	RSRZ
1	1-L	274[A]	PRO	5.0
1	2-L	23[B]	TYR	5.0
1	1-L	295[A]	PHE	5.0
1	2-L	274[B]	PRO	5.0
1	3-L	23[C]	TYR	5.0
1	3-L	274[C]	PRO	5.0
1	4-L	23[D]	TYR	5.0
1	2-L	295[B]	PHE	5.0
1	3-L	295[C]	PHE	5.0
1	4-L	274[D]	PRO	5.0
1	4-L	295[D]	PHE	5.0
1	1-I	71[A]	VAL	4.9
1	1-L	313[A]	MET	4.9
1	1-N	263[A]	VAL	4.9
1	2-I	71[B]	VAL	4.9
1	2-L	313[B]	MET	4.9
1	2-N	263[B]	VAL	4.9
1	3-I	71[C]	VAL	4.9
1	3-L	313[C]	MET	4.9
1	3-N	263[C]	VAL	4.9
1	4-I	71[D]	VAL	4.9
1	4-L	313[D]	MET	4.9
1	4-N	263[D]	VAL	4.9
1	1-P	136[A]	ALA	4.9
1	2-P	136[B]	ALA	4.9
1	3-P	136[C]	ALA	4.9
1	4-P	136[D]	ALA	4.9
1	1-K	299[A]	ASP	4.9
1	2-K	299[B]	ASP	4.9
1	3-K	299[C]	ASP	4.9
1	4-K	299[D]	ASP	4.9
1	1-A	111[A]	GLU	4.9
1	1-K	222[A]	LEU	4.9
1	2-A	111[B]	GLU	4.9
1	2-K	222[B]	LEU	4.9
1	3-A	111[C]	GLU	4.9
1	3-K	222[C]	LEU	4.9
1	4-A	111[D]	GLU	4.9
1	4-K	222[D]	LEU	4.9
1	1-K	118[A]	ARG	4.9
1	2-K	118[B]	ARG	4.9
1	3-K	118[C]	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
1	4-K	118[D]	ARG	4.9
1	1-I	297[A]	VAL	4.9
1	2-I	297[B]	VAL	4.9
1	3-I	297[C]	VAL	4.9
1	4-I	297[D]	VAL	4.9
1	1-M	183[A]	ALA	4.9
1	2-M	183[B]	ALA	4.9
1	3-M	183[C]	ALA	4.9
1	4-M	183[D]	ALA	4.9
1	1-J	294[A]	GLY	4.9
1	2-J	294[B]	GLY	4.9
1	3-J	294[C]	GLY	4.9
1	4-J	294[D]	GLY	4.9
1	1-N	174[A]	TRP	4.9
1	2-N	174[B]	TRP	4.9
1	3-N	174[C]	TRP	4.9
1	4-N	174[D]	TRP	4.9
1	1-O	40[A]	ARG	4.9
1	2-O	40[B]	ARG	4.9
1	3-O	40[C]	ARG	4.9
1	4-O	40[D]	ARG	4.9
1	1-M	129[A]	PHE	4.9
1	2-M	129[B]	PHE	4.9
1	3-M	129[C]	PHE	4.9
1	4-M	129[D]	PHE	4.9
1	1-N	98[A]	VAL	4.9
1	1-O	32[A]	ASN	4.9
1	1-O	306[A]	LYS	4.9
1	2-N	98[B]	VAL	4.9
1	2-O	32[B]	ASN	4.9
1	2-O	306[B]	LYS	4.9
1	3-N	98[C]	VAL	4.9
1	3-O	32[C]	ASN	4.9
1	3-O	306[C]	LYS	4.9
1	4-N	98[D]	VAL	4.9
1	4-O	32[D]	ASN	4.9
1	4-O	306[D]	LYS	4.9
1	1-E	44[A]	GLY	4.9
1	2-E	44[B]	GLY	4.9
1	3-E	44[C]	GLY	4.9
1	4-E	44[D]	GLY	4.9
1	1-K	180[A]	PRO	4.9

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Mol	Chain	Res	Type	RSRZ
1	2-K	180[B]	PRO	4.9
1	3-K	180[C]	PRO	4.9
1	4-K	180[D]	PRO	4.9
1	1-M	228[A]	ILE	4.9
1	2-M	228[B]	ILE	4.9
1	3-M	228[C]	ILE	4.9
1	4-M	228[D]	ILE	4.9
1	1-K	140[A]	ASP	4.9
1	1-O	142[A]	ASP	4.9
1	2-K	140[B]	ASP	4.9
1	2-O	142[B]	ASP	4.9
1	3-K	140[C]	ASP	4.9
1	3-O	142[C]	ASP	4.9
1	4-K	140[D]	ASP	4.9
1	4-O	142[D]	ASP	4.9
1	1-P	295[A]	PHE	4.9
1	2-P	295[B]	PHE	4.9
1	3-P	295[C]	PHE	4.9
1	4-P	295[D]	PHE	4.9
1	1-N	212[A]	LEU	4.9
1	2-N	212[B]	LEU	4.9
1	3-N	212[C]	LEU	4.9
1	4-N	212[D]	LEU	4.9
1	1-I	57[A]	SER	4.9
1	1-K	205[A]	SER	4.9
1	1-O	90[A]	ALA	4.9
1	2-I	57[B]	SER	4.9
1	2-K	205[B]	SER	4.9
1	2-O	90[B]	ALA	4.9
1	3-I	57[C]	SER	4.9
1	3-K	205[C]	SER	4.9
1	3-O	90[C]	ALA	4.9
1	4-I	57[D]	SER	4.9
1	4-K	205[D]	SER	4.9
1	4-O	90[D]	ALA	4.9
1	1-A	290[A]	GLY	4.9
1	2-A	290[B]	GLY	4.9
1	3-A	290[C]	GLY	4.9
1	4-A	290[D]	GLY	4.9
1	1-L	140[A]	ASP	4.9
1	2-L	140[B]	ASP	4.9
1	3-L	140[C]	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
1	4-L	140[D]	ASP	4.9
1	1-G	137[A]	GLU	4.9
1	1-L	35[A]	GLU	4.9
1	2-G	137[B]	GLU	4.9
1	2-L	35[B]	GLU	4.9
1	3-G	137[C]	GLU	4.9
1	3-L	35[C]	GLU	4.9
1	4-G	137[D]	GLU	4.9
1	4-L	35[D]	GLU	4.9
1	1-B	14[A]	SER	4.9
1	1-I	80[A]	LEU	4.9
1	1-L	72[A]	PHE	4.9
1	2-B	14[B]	SER	4.9
1	3-B	14[C]	SER	4.9
1	1-J	317[A]	ALA	4.9
1	1-K	304[A]	GLY	4.9
1	1-O	23[A]	TYR	4.9
1	2-I	80[B]	LEU	4.9
1	2-L	72[B]	PHE	4.9
1	4-B	14[D]	SER	4.9
1	2-J	317[B]	ALA	4.9
1	2-K	304[B]	GLY	4.9
1	2-O	23[B]	TYR	4.9
1	3-I	80[C]	LEU	4.9
1	3-L	72[C]	PHE	4.9
1	3-J	317[C]	ALA	4.9
1	3-K	304[C]	GLY	4.9
1	3-O	23[C]	TYR	4.9
1	4-I	80[D]	LEU	4.9
1	4-L	72[D]	PHE	4.9
1	4-J	317[D]	ALA	4.9
1	4-K	304[D]	GLY	4.9
1	4-O	23[D]	TYR	4.9
1	1-L	112[A]	LYS	4.9
1	1-O	64[A]	PRO	4.9
1	2-L	112[B]	LYS	4.9
1	2-O	64[B]	PRO	4.9
1	3-L	112[C]	LYS	4.9
1	3-O	64[C]	PRO	4.9
1	4-L	112[D]	LYS	4.9
1	4-O	64[D]	PRO	4.9
1	1-D	243[A]	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
1	2-D	243[B]	ASP	4.9
1	3-D	243[C]	ASP	4.9
1	4-D	243[D]	ASP	4.9
1	1-I	248[A]	GLU	4.9
1	2-I	248[B]	GLU	4.9
1	3-I	248[C]	GLU	4.9
1	4-I	248[D]	GLU	4.9
1	1-A	15[A]	ASN	4.9
1	1-J	227[A]	ASN	4.9
1	2-A	15[B]	ASN	4.9
1	2-J	227[B]	ASN	4.9
1	3-A	15[C]	ASN	4.9
1	3-J	227[C]	ASN	4.9
1	4-A	15[D]	ASN	4.9
1	4-J	227[D]	ASN	4.9
1	1-O	262[A]	HIS	4.9
1	2-O	262[B]	HIS	4.9
1	3-O	262[C]	HIS	4.9
1	4-O	262[D]	HIS	4.9
1	1-H	160[A]	ILE	4.9
1	2-H	160[B]	ILE	4.9
1	3-H	160[C]	ILE	4.9
1	4-H	160[D]	ILE	4.9
1	1-J	189[A]	MET	4.9
1	2-J	189[B]	MET	4.9
1	3-J	189[C]	MET	4.9
1	4-J	189[D]	MET	4.9
1	1-J	83[A]	PHE	4.8
1	1-L	56[A]	PHE	4.8
1	2-J	83[B]	PHE	4.8
1	2-L	56[B]	PHE	4.8
1	3-J	83[C]	PHE	4.8
1	3-L	56[C]	PHE	4.8
1	4-J	83[D]	PHE	4.8
1	4-L	56[D]	PHE	4.8
1	1-J	255[A]	ASP	4.8
1	2-J	255[B]	ASP	4.8
1	3-J	255[C]	ASP	4.8
1	4-J	255[D]	ASP	4.8
1	1-O	213[A]	MET	4.8
1	2-O	213[B]	MET	4.8
1	3-O	213[C]	MET	4.8

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Mol	Chain	Res	Type	RSRZ
1	4-O	213[D]	MET	4.8
1	1-B	201[A]	ASP	4.8
1	1-J	166[A]	ASP	4.8
1	2-B	201[B]	ASP	4.8
1	2-J	166[B]	ASP	4.8
1	3-B	201[C]	ASP	4.8
1	3-J	166[C]	ASP	4.8
1	4-B	201[D]	ASP	4.8
1	4-J	166[D]	ASP	4.8
1	1-M	164[A]	PRO	4.8
1	2-M	164[B]	PRO	4.8
1	3-M	164[C]	PRO	4.8
1	4-M	164[D]	PRO	4.8
1	1-B	197[A]	LEU	4.8
1	1-L	209[A]	LEU	4.8
1	1-P	209[A]	LEU	4.8
1	2-B	197[B]	LEU	4.8
1	2-L	209[B]	LEU	4.8
1	2-P	209[B]	LEU	4.8
1	3-B	197[C]	LEU	4.8
1	3-L	209[C]	LEU	4.8
1	3-P	209[C]	LEU	4.8
1	4-B	197[D]	LEU	4.8
1	4-L	209[D]	LEU	4.8
1	4-P	209[D]	LEU	4.8
1	1-M	156[A]	VAL	4.8
1	1-M	224[A]	VAL	4.8
1	2-M	156[B]	VAL	4.8
1	2-M	224[B]	VAL	4.8
1	3-M	156[C]	VAL	4.8
1	3-M	224[C]	VAL	4.8
1	4-M	156[D]	VAL	4.8
1	4-M	224[D]	VAL	4.8
1	1-I	273[A]	GLU	4.8
1	1-P	215[A]	GLN	4.8
1	2-I	273[B]	GLU	4.8
1	2-P	215[B]	GLN	4.8
1	3-I	273[C]	GLU	4.8
1	3-P	215[C]	GLN	4.8
1	4-I	273[D]	GLU	4.8
1	4-P	215[D]	GLN	4.8
1	1-J	57[A]	SER	4.8

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Mol	Chain	Res	Type	RSRZ
1	1-J	149[A]	GLY	4.8
1	2-J	57[B]	SER	4.8
1	2-J	149[B]	GLY	4.8
1	3-J	57[C]	SER	4.8
1	3-J	149[C]	GLY	4.8
1	4-J	57[D]	SER	4.8
1	4-J	149[D]	GLY	4.8
1	1-K	51[A]	PRO	4.8
1	2-K	51[B]	PRO	4.8
1	3-K	51[C]	PRO	4.8
1	4-K	51[D]	PRO	4.8
1	1-K	81[A]	LEU	4.8
1	2-K	81[B]	LEU	4.8
1	3-K	81[C]	LEU	4.8
1	4-K	81[D]	LEU	4.8
1	1-J	33[A]	VAL	4.8
1	2-J	33[B]	VAL	4.8
1	3-J	33[C]	VAL	4.8
1	4-J	33[D]	VAL	4.8
1	1-P	178[A]	ASP	4.8
1	2-P	178[B]	ASP	4.8
1	3-P	178[C]	ASP	4.8
1	4-P	178[D]	ASP	4.8
1	1-K	62[A]	THR	4.8
1	2-K	62[B]	THR	4.8
1	3-K	62[C]	THR	4.8
1	4-K	62[D]	THR	4.8
1	1-K	78[A]	ALA	4.8
1	1-O	317[A]	ALA	4.8
1	2-K	78[B]	ALA	4.8
1	2-O	317[B]	ALA	4.8
1	3-K	78[C]	ALA	4.8
1	3-O	317[C]	ALA	4.8
1	4-K	78[D]	ALA	4.8
1	4-O	317[D]	ALA	4.8
1	1-L	312[A]	ASP	4.8
1	1-M	193[A]	PHE	4.8
1	1-O	72[A]	PHE	4.8
1	2-L	312[B]	ASP	4.8
1	2-M	193[B]	PHE	4.8
1	2-O	72[B]	PHE	4.8
1	3-L	312[C]	ASP	4.8

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Mol	Chain	Res	Type	RSRZ
1	3-M	193[C]	PHE	4.8
1	3-O	72[C]	PHE	4.8
1	4-L	312[D]	ASP	4.8
1	4-M	193[D]	PHE	4.8
1	4-O	72[D]	PHE	4.8
1	1-H	271[A]	GLU	4.8
1	2-H	271[B]	GLU	4.8
1	3-H	271[C]	GLU	4.8
1	4-H	271[D]	GLU	4.8
1	1-I	199[A]	PRO	4.8
1	1-K	32[A]	ASN	4.8
1	1-M	186[A]	PRO	4.8
1	2-I	199[B]	PRO	4.8
1	2-K	32[B]	ASN	4.8
1	2-M	186[B]	PRO	4.8
1	3-I	199[C]	PRO	4.8
1	3-K	32[C]	ASN	4.8
1	3-M	186[C]	PRO	4.8
1	4-I	199[D]	PRO	4.8
1	4-K	32[D]	ASN	4.8
1	4-M	186[D]	PRO	4.8
1	1-I	312[A]	ASP	4.8
1	1-L	236[A]	HIS	4.8
1	2-I	312[B]	ASP	4.8
1	2-L	236[B]	HIS	4.8
1	3-I	312[C]	ASP	4.8
1	3-L	236[C]	HIS	4.8
1	4-I	312[D]	ASP	4.8
1	4-L	236[D]	HIS	4.8
1	1-A	294[A]	GLY	4.8
1	1-E	116[A]	GLY	4.8
1	1-M	109[A]	PHE	4.8
1	1-N	264[A]	GLU	4.8
1	2-A	294[B]	GLY	4.8
1	2-E	116[B]	GLY	4.8
1	2-M	109[B]	PHE	4.8
1	2-N	264[B]	GLU	4.8
1	3-A	294[C]	GLY	4.8
1	3-E	116[C]	GLY	4.8
1	3-M	109[C]	PHE	4.8
1	3-N	264[C]	GLU	4.8
1	4-A	294[D]	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
1	4-E	116[D]	GLY	4.8
1	4-M	109[D]	PHE	4.8
1	4-N	264[D]	GLU	4.8
1	1-K	216[A]	ARG	4.8
1	1-P	132[A]	ARG	4.8
1	2-K	216[B]	ARG	4.8
1	2-P	132[B]	ARG	4.8
1	3-K	216[C]	ARG	4.8
1	3-P	132[C]	ARG	4.8
1	4-K	216[D]	ARG	4.8
1	4-P	132[D]	ARG	4.8
1	1-I	189[A]	MET	4.8
1	2-I	189[B]	MET	4.8
1	3-I	189[C]	MET	4.8
1	4-I	189[D]	MET	4.8
1	1-K	207[A]	PRO	4.8
1	2-K	207[B]	PRO	4.8
1	3-K	207[C]	PRO	4.8
1	4-K	207[D]	PRO	4.8
1	1-A	200[A]	ALA	4.8
1	1-J	140[A]	ASP	4.8
1	1-P	256[A]	ALA	4.8
1	2-A	200[B]	ALA	4.8
1	2-J	140[B]	ASP	4.8
1	2-P	256[B]	ALA	4.8
1	3-A	200[C]	ALA	4.8
1	3-J	140[C]	ASP	4.8
1	3-P	256[C]	ALA	4.8
1	4-A	200[D]	ALA	4.8
1	4-J	140[D]	ASP	4.8
1	4-P	256[D]	ALA	4.8
1	1-N	160[A]	ILE	4.8
1	2-N	160[B]	ILE	4.8
1	3-N	160[C]	ILE	4.8
1	4-N	160[D]	ILE	4.8
1	1-P	172[A]	SER	4.8
1	2-P	172[B]	SER	4.8
1	3-P	172[C]	SER	4.8
1	4-P	172[D]	SER	4.8
1	1-K	123[A]	LEU	4.7
1	2-K	123[B]	LEU	4.7
1	3-K	123[C]	LEU	4.7

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Mol	Chain	Res	Type	RSRZ
1	4-K	123[D]	LEU	4.7
1	1-F	203[A]	PRO	4.7
1	1-K	189[A]	MET	4.7
1	2-F	203[B]	PRO	4.7
1	2-K	189[B]	MET	4.7
1	3-F	203[C]	PRO	4.7
1	3-K	189[C]	MET	4.7
1	4-F	203[D]	PRO	4.7
1	4-K	189[D]	MET	4.7
1	1-I	286[A]	LYS	4.7
1	2-I	286[B]	LYS	4.7
1	3-I	286[C]	LYS	4.7
1	4-I	286[D]	LYS	4.7
1	1-L	216[A]	ARG	4.7
1	2-L	216[B]	ARG	4.7
1	3-L	216[C]	ARG	4.7
1	4-L	216[D]	ARG	4.7
1	1-P	135[A]	GLY	4.7
1	2-P	135[B]	GLY	4.7
1	3-P	135[C]	GLY	4.7
1	4-P	135[D]	GLY	4.7
1	1-L	28[A]	ARG	4.7
1	1-L	40[A]	ARG	4.7
1	2-L	28[B]	ARG	4.7
1	2-L	40[B]	ARG	4.7
1	3-L	28[C]	ARG	4.7
1	3-L	40[C]	ARG	4.7
1	4-L	28[D]	ARG	4.7
1	4-L	40[D]	ARG	4.7
1	1-K	161[A]	LYS	4.7
1	2-K	161[B]	LYS	4.7
1	3-K	161[C]	LYS	4.7
1	4-K	161[D]	LYS	4.7
1	1-I	276[A]	ASP	4.7
1	1-J	151[A]	ASP	4.7
1	2-I	276[B]	ASP	4.7
1	2-J	151[B]	ASP	4.7
1	3-I	276[C]	ASP	4.7
1	3-J	151[C]	ASP	4.7
1	4-I	276[D]	ASP	4.7
1	4-J	151[D]	ASP	4.7
1	1-L	225[A]	PRO	4.7

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Mol	Chain	Res	Type	RSRZ
1	2-L	225[B]	PRO	4.7
1	3-L	225[C]	PRO	4.7
1	4-L	225[D]	PRO	4.7
1	1-L	92[A]	MET	4.7
1	2-L	92[B]	MET	4.7
1	3-L	92[C]	MET	4.7
1	4-L	92[D]	MET	4.7
1	1-N	150[A]	VAL	4.7
1	2-N	150[B]	VAL	4.7
1	3-N	150[C]	VAL	4.7
1	4-N	150[D]	VAL	4.7
1	1-L	44[A]	GLY	4.7
1	1-L	231[A]	TYR	4.7
1	2-L	44[B]	GLY	4.7
1	2-L	231[B]	TYR	4.7
1	3-L	44[C]	GLY	4.7
1	3-L	231[C]	TYR	4.7
1	4-L	44[D]	GLY	4.7
1	4-L	231[D]	TYR	4.7
1	1-N	271[A]	GLU	4.7
1	2-N	271[B]	GLU	4.7
1	3-N	271[C]	GLU	4.7
1	4-N	271[D]	GLU	4.7
1	1-J	276[A]	ASP	4.7
1	2-J	276[B]	ASP	4.7
1	3-J	276[C]	ASP	4.7
1	4-J	276[D]	ASP	4.7
1	1-I	241[A]	ILE	4.7
1	1-P	278[A]	PRO	4.7
1	2-I	241[B]	ILE	4.7
1	2-P	278[B]	PRO	4.7
1	3-I	241[C]	ILE	4.7
1	3-P	278[C]	PRO	4.7
1	4-I	241[D]	ILE	4.7
1	4-P	278[D]	PRO	4.7
1	1-O	189[A]	MET	4.7
1	2-O	189[B]	MET	4.7
1	3-O	189[C]	MET	4.7
1	4-O	189[D]	MET	4.7
1	1-N	19[A]	GLU	4.7
1	1-N	277[A]	PHE	4.7
1	2-N	19[B]	GLU	4.7

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Mol	Chain	Res	Type	RSRZ
1	2-N	277[B]	PHE	4.7
1	3-N	19[C]	GLU	4.7
1	3-N	277[C]	PHE	4.7
1	4-N	19[D]	GLU	4.7
1	4-N	277[D]	PHE	4.7
1	1-M	18[A]	HIS	4.7
1	1-M	208[A]	LYS	4.7
1	1-M	247[A]	HIS	4.7
1	2-M	18[B]	HIS	4.7
1	2-M	208[B]	LYS	4.7
1	2-M	247[B]	HIS	4.7
1	3-M	18[C]	HIS	4.7
1	3-M	208[C]	LYS	4.7
1	3-M	247[C]	HIS	4.7
1	4-M	18[D]	HIS	4.7
1	4-M	208[D]	LYS	4.7
1	4-M	247[D]	HIS	4.7
1	1-L	184[A]	LEU	4.7
1	1-P	163[A]	ASN	4.7
1	2-L	184[B]	LEU	4.7
1	2-P	163[B]	ASN	4.7
1	3-L	184[C]	LEU	4.7
1	3-P	163[C]	ASN	4.7
1	4-L	184[D]	LEU	4.7
1	4-P	163[D]	ASN	4.7
1	1-G	202[A]	SER	4.7
1	1-N	39[A]	ASP	4.7
1	1-N	106[A]	SER	4.7
1	2-G	202[B]	SER	4.7
1	2-N	39[B]	ASP	4.7
1	2-N	106[B]	SER	4.7
1	3-G	202[C]	SER	4.7
1	3-N	39[C]	ASP	4.7
1	3-N	106[C]	SER	4.7
1	4-G	202[D]	SER	4.7
1	4-N	39[D]	ASP	4.7
1	4-N	106[D]	SER	4.7
1	1-L	29[A]	ARG	4.7
1	2-L	29[B]	ARG	4.7
1	3-L	29[C]	ARG	4.7
1	4-L	29[D]	ARG	4.7
1	1-M	314[A]	LYS	4.7

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Mol	Chain	Res	Type	RSRZ
1	2-M	314[B]	LYS	4.7
1	3-M	314[C]	LYS	4.7
1	4-M	314[D]	LYS	4.7
1	1-G	204[A]	GLY	4.6
1	1-J	77[A]	ILE	4.6
1	2-G	204[B]	GLY	4.6
1	2-J	77[B]	ILE	4.6
1	3-G	204[C]	GLY	4.6
1	3-J	77[C]	ILE	4.6
1	4-G	204[D]	GLY	4.6
1	4-J	77[D]	ILE	4.6
1	1-N	58[A]	LEU	4.6
1	2-N	58[B]	LEU	4.6
1	3-N	58[C]	LEU	4.6
1	4-N	58[D]	LEU	4.6
1	1-I	69[A]	LYS	4.6
1	1-K	177[A]	LYS	4.6
1	2-I	69[B]	LYS	4.6
1	2-K	177[B]	LYS	4.6
1	3-I	69[C]	LYS	4.6
1	3-K	177[C]	LYS	4.6
1	4-I	69[D]	LYS	4.6
1	4-K	177[D]	LYS	4.6
1	1-P	126[A]	VAL	4.6
1	2-P	126[B]	VAL	4.6
1	3-P	126[C]	VAL	4.6
1	4-P	126[D]	VAL	4.6
1	1-C	42[A]	GLY	4.6
1	1-J	310[A]	LYS	4.6
1	1-L	135[A]	GLY	4.6
1	2-C	42[B]	GLY	4.6
1	2-J	310[B]	LYS	4.6
1	2-L	135[B]	GLY	4.6
1	3-C	42[C]	GLY	4.6
1	3-J	310[C]	LYS	4.6
1	3-L	135[C]	GLY	4.6
1	4-C	42[D]	GLY	4.6
1	4-J	310[D]	LYS	4.6
1	4-L	135[D]	GLY	4.6
1	1-K	181[A]	LEU	4.6
1	1-O	209[A]	LEU	4.6
1	2-K	181[B]	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	2-O	209[B]	LEU	4.6
1	3-K	181[C]	LEU	4.6
1	3-O	209[C]	LEU	4.6
1	4-K	181[D]	LEU	4.6
1	4-O	209[D]	LEU	4.6
1	1-L	301[A]	VAL	4.6
1	1-O	71[A]	VAL	4.6
1	2-L	301[B]	VAL	4.6
1	2-O	71[B]	VAL	4.6
1	3-L	301[C]	VAL	4.6
1	3-O	71[C]	VAL	4.6
1	4-L	301[D]	VAL	4.6
1	4-O	71[D]	VAL	4.6
1	1-A	312[A]	ASP	4.6
1	1-N	125[A]	PRO	4.6
1	1-N	307[A]	PRO	4.6
1	1-O	51[A]	PRO	4.6
1	2-A	312[B]	ASP	4.6
1	2-N	125[B]	PRO	4.6
1	2-N	307[B]	PRO	4.6
1	2-O	51[B]	PRO	4.6
1	3-A	312[C]	ASP	4.6
1	3-N	125[C]	PRO	4.6
1	3-N	307[C]	PRO	4.6
1	3-O	51[C]	PRO	4.6
1	4-A	312[D]	ASP	4.6
1	4-N	125[D]	PRO	4.6
1	4-N	307[D]	PRO	4.6
1	4-O	51[D]	PRO	4.6
1	1-J	29[A]	ARG	4.6
1	1-J	208[A]	LYS	4.6
1	1-L	260[A]	ARG	4.6
1	2-J	29[B]	ARG	4.6
1	2-J	208[B]	LYS	4.6
1	2-L	260[B]	ARG	4.6
1	3-J	29[C]	ARG	4.6
1	3-J	208[C]	LYS	4.6
1	3-L	260[C]	ARG	4.6
1	4-J	29[D]	ARG	4.6
1	4-J	208[D]	LYS	4.6
1	4-L	260[D]	ARG	4.6
1	1-J	182[A]	MET	4.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	2-J	182[B]	MET	4.6
1	3-J	182[C]	MET	4.6
1	4-J	182[D]	MET	4.6
1	1-P	252[A]	GLN	4.6
1	2-P	252[B]	GLN	4.6
1	3-P	252[C]	GLN	4.6
1	4-P	252[D]	GLN	4.6
1	1-O	170[A]	ILE	4.6
1	1-O	292[A]	ILE	4.6
1	2-O	170[B]	ILE	4.6
1	2-O	292[B]	ILE	4.6
1	3-O	170[C]	ILE	4.6
1	3-O	292[C]	ILE	4.6
1	4-O	170[D]	ILE	4.6
1	4-O	292[D]	ILE	4.6
1	1-J	117[A]	HIS	4.6
1	1-J	158[A]	ASP	4.6
1	1-M	133[A]	HIS	4.6
1	2-J	117[B]	HIS	4.6
1	2-J	158[B]	ASP	4.6
1	2-M	133[B]	HIS	4.6
1	3-J	117[C]	HIS	4.6
1	3-J	158[C]	ASP	4.6
1	3-M	133[C]	HIS	4.6
1	4-J	117[D]	HIS	4.6
1	4-J	158[D]	ASP	4.6
1	4-M	133[D]	HIS	4.6
1	1-E	111[A]	GLU	4.6
1	1-P	76[A]	VAL	4.6
1	2-E	111[B]	GLU	4.6
1	2-P	76[B]	VAL	4.6
1	3-E	111[C]	GLU	4.6
1	3-P	76[C]	VAL	4.6
1	4-E	111[D]	GLU	4.6
1	4-P	76[D]	VAL	4.6
1	1-O	177[A]	LYS	4.6
1	2-O	177[B]	LYS	4.6
1	3-O	177[C]	LYS	4.6
1	4-O	177[D]	LYS	4.6
1	1-O	58[A]	LEU	4.6
1	2-O	58[B]	LEU	4.6
1	3-O	58[C]	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	4-O	58[D]	LEU	4.6
1	1-P	124[A]	GLY	4.6
1	2-P	124[B]	GLY	4.6
1	3-P	124[C]	GLY	4.6
1	4-P	124[D]	GLY	4.6
1	1-N	69[A]	LYS	4.6
1	2-N	69[B]	LYS	4.6
1	3-N	69[C]	LYS	4.6
1	4-N	69[D]	LYS	4.6
1	1-L	100[A]	ILE	4.6
1	1-O	164[A]	PRO	4.6
1	1-P	30[A]	ILE	4.6
1	2-L	100[B]	ILE	4.6
1	2-O	164[B]	PRO	4.6
1	2-P	30[B]	ILE	4.6
1	3-L	100[C]	ILE	4.6
1	3-O	164[C]	PRO	4.6
1	3-P	30[C]	ILE	4.6
1	4-L	100[D]	ILE	4.6
1	4-O	164[D]	PRO	4.6
1	4-P	30[D]	ILE	4.6
1	1-P	221[A]	GLY	4.6
1	2-P	221[B]	GLY	4.6
1	3-P	221[C]	GLY	4.6
1	4-P	221[D]	GLY	4.6
1	1-H	205[A]	SER	4.6
1	1-P	150[A]	VAL	4.6
1	2-H	205[B]	SER	4.6
1	2-P	150[B]	VAL	4.6
1	3-H	205[C]	SER	4.6
1	3-P	150[C]	VAL	4.6
1	4-H	205[D]	SER	4.6
1	4-P	150[D]	VAL	4.6
1	1-A	315[A]	MET	4.6
1	2-A	315[B]	MET	4.6
1	3-A	315[C]	MET	4.6
1	4-A	315[D]	MET	4.6
1	1-P	257[A]	HIS	4.6
1	2-P	257[B]	HIS	4.6
1	3-P	257[C]	HIS	4.6
1	4-P	257[D]	HIS	4.6
1	1-G	23[A]	TYR	4.6

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Mol	Chain	Res	Type	RSRZ
1	2-G	23[B]	TYR	4.6
1	3-G	23[C]	TYR	4.6
1	4-G	23[D]	TYR	4.6
1	1-H	199[A]	PRO	4.5
1	1-I	207[A]	PRO	4.5
1	1-J	148[A]	LYS	4.5
1	1-K	64[A]	PRO	4.5
1	1-P	264[A]	GLU	4.5
1	2-H	199[B]	PRO	4.5
1	2-I	207[B]	PRO	4.5
1	2-J	148[B]	LYS	4.5
1	2-K	64[B]	PRO	4.5
1	2-P	264[B]	GLU	4.5
1	3-H	199[C]	PRO	4.5
1	3-I	207[C]	PRO	4.5
1	3-J	148[C]	LYS	4.5
1	3-K	64[C]	PRO	4.5
1	3-P	264[C]	GLU	4.5
1	4-H	199[D]	PRO	4.5
1	4-I	207[D]	PRO	4.5
1	4-J	148[D]	LYS	4.5
1	4-K	64[D]	PRO	4.5
1	4-P	264[D]	GLU	4.5
1	1-L	213[A]	MET	4.5
1	2-L	213[B]	MET	4.5
1	3-L	213[C]	MET	4.5
1	4-L	213[D]	MET	4.5
1	1-P	109[A]	PHE	4.5
1	2-P	109[B]	PHE	4.5
1	3-P	109[C]	PHE	4.5
1	4-P	109[D]	PHE	4.5
1	1-I	296[A]	LYS	4.5
1	1-O	245[A]	GLU	4.5
1	2-I	296[B]	LYS	4.5
1	2-O	245[B]	GLU	4.5
1	3-I	296[C]	LYS	4.5
1	3-O	245[C]	GLU	4.5
1	4-I	296[D]	LYS	4.5
1	4-O	245[D]	GLU	4.5
1	1-K	106[A]	SER	4.5
1	1-M	118[A]	ARG	4.5
1	2-K	106[B]	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	2-M	118[B]	ARG	4.5
1	3-K	106[C]	SER	4.5
1	3-M	118[C]	ARG	4.5
1	4-K	106[D]	SER	4.5
1	4-M	118[D]	ARG	4.5
1	1-L	241[A]	ILE	4.5
1	1-M	280[A]	LEU	4.5
1	1-P	282[A]	TRP	4.5
1	2-L	241[B]	ILE	4.5
1	2-M	280[B]	LEU	4.5
1	2-P	282[B]	TRP	4.5
1	3-L	241[C]	ILE	4.5
1	3-M	280[C]	LEU	4.5
1	3-P	282[C]	TRP	4.5
1	4-L	241[D]	ILE	4.5
1	4-M	280[D]	LEU	4.5
1	4-P	282[D]	TRP	4.5
1	1-I	91[A]	LYS	4.5
1	1-I	218[A]	CYS	4.5
1	1-K	120[A]	GLU	4.5
1	1-L	288[A]	GLU	4.5
1	1-O	267[A]	LYS	4.5
1	2-I	91[B]	LYS	4.5
1	2-I	218[B]	CYS	4.5
1	2-K	120[B]	GLU	4.5
1	2-L	288[B]	GLU	4.5
1	2-O	267[B]	LYS	4.5
1	3-I	91[C]	LYS	4.5
1	3-I	218[C]	CYS	4.5
1	3-K	120[C]	GLU	4.5
1	3-L	288[C]	GLU	4.5
1	3-O	267[C]	LYS	4.5
1	4-I	91[D]	LYS	4.5
1	4-I	218[D]	CYS	4.5
1	4-K	120[D]	GLU	4.5
1	4-L	288[D]	GLU	4.5
1	4-O	267[D]	LYS	4.5
1	1-O	307[A]	PRO	4.5
1	1-P	16[A]	PRO	4.5
1	2-O	307[B]	PRO	4.5
1	2-P	16[B]	PRO	4.5
1	3-O	307[C]	PRO	4.5

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Mol	Chain	Res	Type	RSRZ
1	3-P	16[C]	PRO	4.5
1	4-O	307[D]	PRO	4.5
1	4-P	16[D]	PRO	4.5
1	1-E	14[A]	SER	4.5
1	1-E	202[A]	SER	4.5
1	2-E	14[B]	SER	4.5
1	2-E	202[B]	SER	4.5
1	3-E	14[C]	SER	4.5
1	3-E	202[C]	SER	4.5
1	4-E	14[D]	SER	4.5
1	4-E	202[D]	SER	4.5
1	1-G	111[A]	GLU	4.5
1	1-I	154[A]	GLN	4.5
1	1-L	130[A]	GLN	4.5
1	1-L	245[A]	GLU	4.5
1	2-G	111[B]	GLU	4.5
1	2-I	154[B]	GLN	4.5
1	2-L	130[B]	GLN	4.5
1	2-L	245[B]	GLU	4.5
1	3-G	111[C]	GLU	4.5
1	3-I	154[C]	GLN	4.5
1	3-L	130[C]	GLN	4.5
1	3-L	245[C]	GLU	4.5
1	4-G	111[D]	GLU	4.5
1	4-I	154[D]	GLN	4.5
1	4-L	130[D]	GLN	4.5
1	4-L	245[D]	GLU	4.5
1	1-J	160[A]	ILE	4.5
1	1-K	66[A]	LEU	4.5
1	2-J	160[B]	ILE	4.5
1	2-K	66[B]	LEU	4.5
1	3-J	160[C]	ILE	4.5
1	3-K	66[C]	LEU	4.5
1	4-J	160[D]	ILE	4.5
1	4-K	66[D]	LEU	4.5
1	1-O	244[A]	THR	4.5
1	2-O	244[B]	THR	4.5
1	3-O	244[C]	THR	4.5
1	4-O	244[D]	THR	4.5
1	1-J	86[A]	GLY	4.5
1	2-J	86[B]	GLY	4.5
1	3-J	86[C]	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
1	4-J	86[D]	GLY	4.5
1	1-J	286[A]	LYS	4.5
1	1-L	148[A]	LYS	4.5
1	1-P	96[A]	GLN	4.5
1	1-P	285[A]	SER	4.5
1	2-J	286[B]	LYS	4.5
1	2-L	148[B]	LYS	4.5
1	2-P	96[B]	GLN	4.5
1	2-P	285[B]	SER	4.5
1	3-J	286[C]	LYS	4.5
1	3-L	148[C]	LYS	4.5
1	3-P	96[C]	GLN	4.5
1	3-P	285[C]	SER	4.5
1	4-J	286[D]	LYS	4.5
1	4-L	148[D]	LYS	4.5
1	4-P	96[D]	GLN	4.5
1	4-P	285[D]	SER	4.5
1	1-I	182[A]	MET	4.5
1	1-K	58[A]	LEU	4.5
1	2-I	182[B]	MET	4.5
1	2-K	58[B]	LEU	4.5
1	3-I	182[C]	MET	4.5
1	3-K	58[C]	LEU	4.5
1	4-I	182[D]	MET	4.5
1	4-K	58[D]	LEU	4.5
1	1-F	17[A]	ASP	4.5
1	1-I	303[A]	GLU	4.5
1	1-L	248[A]	GLU	4.5
1	1-M	263[A]	VAL	4.5
1	2-F	17[B]	ASP	4.5
1	2-I	303[B]	GLU	4.5
1	2-L	248[B]	GLU	4.5
1	2-M	263[B]	VAL	4.5
1	3-F	17[C]	ASP	4.5
1	3-I	303[C]	GLU	4.5
1	3-L	248[C]	GLU	4.5
1	3-M	263[C]	VAL	4.5
1	4-F	17[D]	ASP	4.5
1	4-I	303[D]	GLU	4.5
1	4-L	248[D]	GLU	4.5
1	4-M	263[D]	VAL	4.5
1	1-M	154[A]	GLN	4.5

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Mol	Chain	Res	Type	RSRZ
1	2-M	154[B]	GLN	4.5
1	3-M	154[C]	GLN	4.5
1	4-M	154[D]	GLN	4.5
1	1-G	190[A]	PHE	4.5
1	1-I	90[A]	ALA	4.5
1	1-J	295[A]	PHE	4.5
1	1-L	226[A]	PHE	4.5
1	2-G	190[B]	PHE	4.5
1	2-I	90[B]	ALA	4.5
1	2-J	295[B]	PHE	4.5
1	2-L	226[B]	PHE	4.5
1	3-G	190[C]	PHE	4.5
1	3-I	90[C]	ALA	4.5
1	3-J	295[C]	PHE	4.5
1	3-L	226[C]	PHE	4.5
1	4-G	190[D]	PHE	4.5
1	4-I	90[D]	ALA	4.5
1	4-J	295[D]	PHE	4.5
1	4-L	226[D]	PHE	4.5
1	1-O	162[A]	ASN	4.5
1	2-O	162[B]	ASN	4.5
1	3-O	162[C]	ASN	4.5
1	4-O	162[D]	ASN	4.5
1	1-I	18[A]	HIS	4.5
1	2-I	18[B]	HIS	4.5
1	3-I	18[C]	HIS	4.5
1	4-I	18[D]	HIS	4.5
1	1-J	298[A]	GLU	4.5
1	1-M	271[A]	GLU	4.5
1	2-J	298[B]	GLU	4.5
1	2-M	271[B]	GLU	4.5
1	3-J	298[C]	GLU	4.5
1	3-M	271[C]	GLU	4.5
1	4-J	298[D]	GLU	4.5
1	4-M	271[D]	GLU	4.5
1	1-K	152[A]	GLN	4.5
1	1-L	238[A]	ILE	4.5
1	1-N	270[A]	LEU	4.5
1	2-K	152[B]	GLN	4.5
1	2-L	238[B]	ILE	4.5
1	2-N	270[B]	LEU	4.5
1	3-K	152[C]	GLN	4.5

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Mol	Chain	Res	Type	RSRZ
1	3-L	238[C]	ILE	4.5
1	3-N	270[C]	LEU	4.5
1	4-L	238[D]	ILE	4.5
1	4-N	270[D]	LEU	4.5
1	4-K	152[D]	GLN	4.5
1	1-D	61[A]	ASN	4.5
1	2-D	61[B]	ASN	4.5
1	3-D	61[C]	ASN	4.5
1	4-D	61[D]	ASN	4.5
1	1-G	47[A]	ALA	4.5
1	1-K	256[A]	ALA	4.5
1	2-G	47[B]	ALA	4.5
1	2-K	256[B]	ALA	4.5
1	3-G	47[C]	ALA	4.5
1	3-K	256[C]	ALA	4.5
1	4-G	47[D]	ALA	4.5
1	4-K	256[D]	ALA	4.5
1	1-O	167[A]	ARG	4.5
1	2-O	167[B]	ARG	4.5
1	3-O	167[C]	ARG	4.5
1	4-O	167[D]	ARG	4.5
1	1-I	298[A]	GLU	4.5
1	1-M	262[A]	HIS	4.5
1	2-I	298[B]	GLU	4.5
1	2-M	262[B]	HIS	4.5
1	3-I	298[C]	GLU	4.5
1	3-M	262[C]	HIS	4.5
1	4-I	298[D]	GLU	4.5
1	4-M	262[D]	HIS	4.5
1	1-F	197[A]	LEU	4.4
1	1-J	67[A]	THR	4.4
1	1-J	153[A]	LEU	4.4
1	2-F	197[B]	LEU	4.4
1	2-J	67[B]	THR	4.4
1	2-J	153[B]	LEU	4.4
1	3-F	197[C]	LEU	4.4
1	3-J	67[C]	THR	4.4
1	3-J	153[C]	LEU	4.4
1	4-F	197[D]	LEU	4.4
1	4-J	67[D]	THR	4.4
1	4-J	153[D]	LEU	4.4
1	1-O	163[A]	ASN	4.4

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Mol	Chain	Res	Type	RSRZ
1	2-O	163[B]	ASN	4.4
1	3-O	163[C]	ASN	4.4
1	4-O	163[D]	ASN	4.4
1	1-F	14[A]	SER	4.4
1	1-P	57[A]	SER	4.4
1	2-F	14[B]	SER	4.4
1	2-P	57[B]	SER	4.4
1	3-F	14[C]	SER	4.4
1	3-P	57[C]	SER	4.4
1	4-F	14[D]	SER	4.4
1	4-P	57[D]	SER	4.4
1	1-J	248[A]	GLU	4.4
1	1-M	173[A]	ALA	4.4
1	1-P	317[A]	ALA	4.4
1	2-J	248[B]	GLU	4.4
1	2-M	173[B]	ALA	4.4
1	2-P	317[B]	ALA	4.4
1	3-J	248[C]	GLU	4.4
1	3-M	173[C]	ALA	4.4
1	3-P	317[C]	ALA	4.4
1	4-J	248[D]	GLU	4.4
1	4-M	173[D]	ALA	4.4
1	4-P	317[D]	ALA	4.4
1	1-F	201[A]	ASP	4.4
1	1-M	236[A]	HIS	4.4
1	2-F	201[B]	ASP	4.4
1	2-M	236[B]	HIS	4.4
1	3-F	201[C]	ASP	4.4
1	3-M	236[C]	HIS	4.4
1	4-F	201[D]	ASP	4.4
1	4-M	236[D]	HIS	4.4
1	1-K	34[A]	GLY	4.4
1	2-K	34[B]	GLY	4.4
1	3-K	34[C]	GLY	4.4
1	4-K	34[D]	GLY	4.4
1	1-G	199[A]	PRO	4.4
1	1-J	288[A]	GLU	4.4
1	1-M	207[A]	PRO	4.4
1	2-G	199[B]	PRO	4.4
1	2-J	288[B]	GLU	4.4
1	2-M	207[B]	PRO	4.4
1	3-G	199[C]	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	3-J	288[C]	GLU	4.4
1	3-M	207[C]	PRO	4.4
1	4-G	199[D]	PRO	4.4
1	4-J	288[D]	GLU	4.4
1	4-M	207[D]	PRO	4.4
1	1-J	123[A]	LEU	4.4
1	1-J	138[A]	TYR	4.4
1	1-K	184[A]	LEU	4.4
1	1-P	216[A]	ARG	4.4
1	2-J	123[B]	LEU	4.4
1	2-J	138[B]	TYR	4.4
1	2-K	184[B]	LEU	4.4
1	2-P	216[B]	ARG	4.4
1	3-J	123[C]	LEU	4.4
1	3-J	138[C]	TYR	4.4
1	3-K	184[C]	LEU	4.4
1	3-P	216[C]	ARG	4.4
1	4-J	123[D]	LEU	4.4
1	4-J	138[D]	TYR	4.4
1	4-K	184[D]	LEU	4.4
1	4-P	216[D]	ARG	4.4
1	1-K	27[A]	ILE	4.4
1	1-P	160[A]	ILE	4.4
1	2-K	27[B]	ILE	4.4
1	2-P	160[B]	ILE	4.4
1	3-K	27[C]	ILE	4.4
1	3-P	160[C]	ILE	4.4
1	4-K	27[D]	ILE	4.4
1	4-P	160[D]	ILE	4.4
1	1-I	25[A]	ASP	4.4
1	2-I	25[B]	ASP	4.4
1	3-I	25[C]	ASP	4.4
1	4-I	25[D]	ASP	4.4
1	1-O	130[A]	GLN	4.4
1	2-O	130[B]	GLN	4.4
1	3-O	130[C]	GLN	4.4
1	4-O	130[D]	GLN	4.4
1	1-F	271[A]	GLU	4.4
1	1-G	44[A]	GLY	4.4
1	2-F	271[B]	GLU	4.4
1	2-G	44[B]	GLY	4.4
1	3-F	271[C]	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	3-G	44[C]	GLY	4.4
1	4-F	271[D]	GLU	4.4
1	4-G	44[D]	GLY	4.4
1	1-N	176[A]	PRO	4.4
1	2-N	176[B]	PRO	4.4
1	3-N	176[C]	PRO	4.4
1	4-N	176[D]	PRO	4.4
1	1-N	158[A]	ASP	4.4
1	2-N	158[B]	ASP	4.4
1	3-N	158[C]	ASP	4.4
1	4-N	158[D]	ASP	4.4
1	1-I	61[A]	ASN	4.4
1	2-I	61[B]	ASN	4.4
1	3-I	61[C]	ASN	4.4
1	4-I	61[D]	ASN	4.4
1	1-O	295[A]	PHE	4.4
1	2-O	295[B]	PHE	4.4
1	3-O	295[C]	PHE	4.4
1	4-O	295[D]	PHE	4.4
1	1-N	185[A]	PRO	4.4
1	2-N	185[B]	PRO	4.4
1	3-N	185[C]	PRO	4.4
1	4-N	185[D]	PRO	4.4
1	1-K	252[A]	GLN	4.4
1	2-K	252[B]	GLN	4.4
1	3-K	252[C]	GLN	4.4
1	4-K	252[D]	GLN	4.4
1	1-M	81[A]	LEU	4.4
1	2-M	81[B]	LEU	4.4
1	3-M	81[C]	LEU	4.4
1	4-M	81[D]	LEU	4.4
1	1-L	132[A]	ARG	4.4
1	1-O	29[A]	ARG	4.4
1	2-L	132[B]	ARG	4.4
1	2-O	29[B]	ARG	4.4
1	3-L	132[C]	ARG	4.4
1	3-O	29[C]	ARG	4.4
1	4-L	132[D]	ARG	4.4
1	4-O	29[D]	ARG	4.4
1	1-L	154[A]	GLN	4.4
1	1-M	269[A]	GLN	4.4
1	2-L	154[B]	GLN	4.4

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Mol	Chain	Res	Type	RSRZ
1	2-M	269[B]	GLN	4.4
1	3-L	154[C]	GLN	4.4
1	3-M	269[C]	GLN	4.4
1	4-L	154[D]	GLN	4.4
1	4-M	269[D]	GLN	4.4
1	1-N	41[A]	THR	4.4
1	1-O	19[A]	GLU	4.4
1	2-N	41[B]	THR	4.4
1	2-O	19[B]	GLU	4.4
1	3-N	41[C]	THR	4.4
1	3-O	19[C]	GLU	4.4
1	4-N	41[D]	THR	4.4
1	4-O	19[D]	GLU	4.4
1	1-N	188[A]	HIS	4.4
1	2-N	188[B]	HIS	4.4
1	3-N	188[C]	HIS	4.4
1	4-N	188[D]	HIS	4.4
1	1-P	37[A]	ARG	4.4
1	2-P	37[B]	ARG	4.4
1	3-P	37[C]	ARG	4.4
1	4-P	37[D]	ARG	4.4
1	1-K	291[A]	ASP	4.4
1	2-K	291[B]	ASP	4.4
1	3-K	291[C]	ASP	4.4
1	4-K	291[D]	ASP	4.4
1	1-K	91[A]	LYS	4.4
1	1-P	107[A]	LYS	4.4
1	2-K	91[B]	LYS	4.4
1	2-P	107[B]	LYS	4.4
1	3-K	91[C]	LYS	4.4
1	3-P	107[C]	LYS	4.4
1	4-K	91[D]	LYS	4.4
1	4-P	107[D]	LYS	4.4
1	1-M	37[A]	ARG	4.4
1	2-M	37[B]	ARG	4.4
1	3-M	37[C]	ARG	4.4
1	4-M	37[D]	ARG	4.4
1	1-C	110[A]	LEU	4.3
1	1-J	111[A]	GLU	4.3
1	1-P	60[A]	ASP	4.3
1	1-M	267[A]	LYS	4.3
1	1-N	171[A]	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
1	1-P	123[A]	LEU	4.3
1	1-P	166[A]	ASP	4.3
1	1-P	179[A]	LEU	4.3
1	1-P	220[A]	LEU	4.3
1	2-C	110[B]	LEU	4.3
1	2-J	111[B]	GLU	4.3
1	2-P	60[B]	ASP	4.3
1	2-M	267[B]	LYS	4.3
1	2-N	171[B]	LEU	4.3
1	2-P	123[B]	LEU	4.3
1	2-P	166[B]	ASP	4.3
1	2-P	179[B]	LEU	4.3
1	2-P	220[B]	LEU	4.3
1	3-C	110[C]	LEU	4.3
1	3-J	111[C]	GLU	4.3
1	3-P	60[C]	ASP	4.3
1	3-M	267[C]	LYS	4.3
1	3-N	171[C]	LEU	4.3
1	3-P	123[C]	LEU	4.3
1	3-P	166[C]	ASP	4.3
1	3-P	179[C]	LEU	4.3
1	3-P	220[C]	LEU	4.3
1	4-C	110[D]	LEU	4.3
1	4-J	111[D]	GLU	4.3
1	4-M	267[D]	LYS	4.3
1	4-N	171[D]	LEU	4.3
1	4-P	60[D]	ASP	4.3
1	4-P	123[D]	LEU	4.3
1	4-P	166[D]	ASP	4.3
1	4-P	179[D]	LEU	4.3
1	4-P	220[D]	LEU	4.3
1	1-J	150[A]	VAL	4.3
1	1-J	164[A]	PRO	4.3
1	2-J	150[B]	VAL	4.3
1	2-J	164[B]	PRO	4.3
1	3-J	150[C]	VAL	4.3
1	3-J	164[C]	PRO	4.3
1	4-J	150[D]	VAL	4.3
1	4-J	164[D]	PRO	4.3
1	1-I	74[A]	ARG	4.3
1	2-I	74[B]	ARG	4.3
1	3-I	74[C]	ARG	4.3

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Mol	Chain	Res	Type	RSRZ
1	4-I	74[D]	ARG	4.3
1	1-O	273[A]	GLU	4.3
1	2-O	273[B]	GLU	4.3
1	3-O	273[C]	GLU	4.3
1	4-O	273[D]	GLU	4.3
1	1-J	219[A]	ASP	4.3
1	2-J	219[B]	ASP	4.3
1	3-J	219[C]	ASP	4.3
1	4-J	219[D]	ASP	4.3
1	1-B	283[A]	ALA	4.3
1	1-I	136[A]	ALA	4.3
1	1-I	223[A]	GLY	4.3
1	1-P	42[A]	GLY	4.3
1	2-B	283[B]	ALA	4.3
1	2-I	136[B]	ALA	4.3
1	2-I	223[B]	GLY	4.3
1	2-P	42[B]	GLY	4.3
1	3-B	283[C]	ALA	4.3
1	3-I	136[C]	ALA	4.3
1	3-I	223[C]	GLY	4.3
1	3-P	42[C]	GLY	4.3
1	4-B	283[D]	ALA	4.3
1	4-I	136[D]	ALA	4.3
1	4-I	223[D]	GLY	4.3
1	4-P	42[D]	GLY	4.3
1	1-B	199[A]	PRO	4.3
1	1-N	92[A]	MET	4.3
1	1-P	169[A]	ILE	4.3
1	2-B	199[B]	PRO	4.3
1	2-N	92[B]	MET	4.3
1	2-P	169[B]	ILE	4.3
1	3-B	199[C]	PRO	4.3
1	3-N	92[C]	MET	4.3
1	3-P	169[C]	ILE	4.3
1	4-B	199[D]	PRO	4.3
1	4-N	92[D]	MET	4.3
1	4-P	169[D]	ILE	4.3
1	1-I	163[A]	ASN	4.3
1	2-I	163[B]	ASN	4.3
1	3-I	163[C]	ASN	4.3
1	4-I	163[D]	ASN	4.3
1	1-B	165[A]	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	1-L	87[A]	CYS	4.3
1	2-B	165[B]	THR	4.3
1	2-L	87[B]	CYS	4.3
1	3-B	165[C]	THR	4.3
1	3-L	87[C]	CYS	4.3
1	4-B	165[D]	THR	4.3
1	4-L	87[D]	CYS	4.3
1	1-J	147[A]	GLY	4.3
1	1-N	143[A]	GLY	4.3
1	2-J	147[B]	GLY	4.3
1	2-N	143[B]	GLY	4.3
1	3-J	147[C]	GLY	4.3
1	3-N	143[C]	GLY	4.3
1	4-J	147[D]	GLY	4.3
1	4-N	143[D]	GLY	4.3
1	1-M	185[A]	PRO	4.3
1	2-M	185[B]	PRO	4.3
1	3-M	185[C]	PRO	4.3
1	4-M	185[D]	PRO	4.3
1	1-N	236[A]	HIS	4.3
1	2-N	236[B]	HIS	4.3
1	3-N	236[C]	HIS	4.3
1	4-N	236[D]	HIS	4.3
1	1-L	163[A]	ASN	4.3
1	2-L	163[B]	ASN	4.3
1	3-L	163[C]	ASN	4.3
1	4-L	163[D]	ASN	4.3
1	1-C	294[A]	GLY	4.3
1	2-C	294[B]	GLY	4.3
1	3-C	294[C]	GLY	4.3
1	4-C	294[D]	GLY	4.3
1	1-K	211[A]	CYS	4.3
1	2-K	211[B]	CYS	4.3
1	3-K	211[C]	CYS	4.3
1	4-K	211[D]	CYS	4.3
1	1-C	200[A]	ALA	4.3
1	2-C	200[B]	ALA	4.3
1	3-C	200[C]	ALA	4.3
1	4-C	200[D]	ALA	4.3
1	1-O	111[A]	GLU	4.3
1	2-O	111[B]	GLU	4.3
1	3-O	111[C]	GLU	4.3

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Mol	Chain	Res	Type	RSRZ
1	4-O	111[D]	GLU	4.3
1	1-N	95[A]	SER	4.3
1	2-N	95[B]	SER	4.3
1	3-N	95[C]	SER	4.3
1	4-N	95[D]	SER	4.3
1	1-K	255[A]	ASP	4.3
1	1-L	26[A]	LEU	4.3
1	1-N	179[A]	LEU	4.3
1	1-P	153[A]	LEU	4.3
1	2-K	255[B]	ASP	4.3
1	2-L	26[B]	LEU	4.3
1	2-N	179[B]	LEU	4.3
1	2-P	153[B]	LEU	4.3
1	3-K	255[C]	ASP	4.3
1	3-L	26[C]	LEU	4.3
1	3-N	179[C]	LEU	4.3
1	3-P	153[C]	LEU	4.3
1	4-K	255[D]	ASP	4.3
1	4-L	26[D]	LEU	4.3
1	4-N	179[D]	LEU	4.3
1	4-P	153[D]	LEU	4.3
1	1-N	71[A]	VAL	4.3
1	2-N	71[B]	VAL	4.3
1	3-N	71[C]	VAL	4.3
1	4-N	71[D]	VAL	4.3
1	1-I	284[A]	ARG	4.3
1	1-N	121[A]	GLY	4.3
1	2-I	284[B]	ARG	4.3
1	2-N	121[B]	GLY	4.3
1	3-I	284[C]	ARG	4.3
1	3-N	121[C]	GLY	4.3
1	4-I	284[D]	ARG	4.3
1	4-N	121[D]	GLY	4.3
1	1-P	23[A]	TYR	4.3
1	2-P	23[B]	TYR	4.3
1	3-P	23[C]	TYR	4.3
1	4-P	23[D]	TYR	4.3
1	1-O	296[A]	LYS	4.3
1	2-O	296[B]	LYS	4.3
1	3-O	296[C]	LYS	4.3
1	4-O	296[D]	LYS	4.3
1	1-D	198[A]	PRO	4.3

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Mol	Chain	Res	Type	RSRZ
1	1-J	162[A]	ASN	4.3
1	1-K	274[A]	PRO	4.3
1	1-L	142[A]	ASP	4.3
1	1-L	176[A]	PRO	4.3
1	1-N	164[A]	PRO	4.3
1	2-D	198[B]	PRO	4.3
1	2-J	162[B]	ASN	4.3
1	2-K	274[B]	PRO	4.3
1	2-L	142[B]	ASP	4.3
1	2-L	176[B]	PRO	4.3
1	2-N	164[B]	PRO	4.3
1	3-D	198[C]	PRO	4.3
1	3-J	162[C]	ASN	4.3
1	3-K	274[C]	PRO	4.3
1	3-L	142[C]	ASP	4.3
1	3-L	176[C]	PRO	4.3
1	3-N	164[C]	PRO	4.3
1	4-D	198[D]	PRO	4.3
1	4-J	162[D]	ASN	4.3
1	4-K	274[D]	PRO	4.3
1	4-L	142[D]	ASP	4.3
1	4-L	176[D]	PRO	4.3
1	4-N	164[D]	PRO	4.3
1	1-P	313[A]	MET	4.3
1	2-P	313[B]	MET	4.3
1	3-P	313[C]	MET	4.3
1	4-P	313[D]	MET	4.3
1	1-P	24[A]	LEU	4.3
1	2-P	24[B]	LEU	4.3
1	3-P	24[C]	LEU	4.3
1	4-P	24[D]	LEU	4.3
1	1-J	40[A]	ARG	4.3
1	1-K	29[A]	ARG	4.3
1	2-J	40[B]	ARG	4.3
1	2-K	29[B]	ARG	4.3
1	3-J	40[C]	ARG	4.3
1	3-K	29[C]	ARG	4.3
1	4-J	40[D]	ARG	4.3
1	4-K	29[D]	ARG	4.3
1	1-O	91[A]	LYS	4.3
1	1-O	314[A]	LYS	4.3
1	2-O	91[B]	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
1	2-O	314[B]	LYS	4.3
1	3-O	91[C]	LYS	4.3
1	3-O	314[C]	LYS	4.3
1	4-O	91[D]	LYS	4.3
1	4-O	314[D]	LYS	4.3
1	1-N	76[A]	VAL	4.3
1	2-N	76[B]	VAL	4.3
1	3-N	76[C]	VAL	4.3
1	4-N	76[D]	VAL	4.3
1	1-J	154[A]	GLN	4.3
1	1-M	130[A]	GLN	4.3
1	2-J	154[B]	GLN	4.3
1	2-M	130[B]	GLN	4.3
1	3-J	154[C]	GLN	4.3
1	3-M	130[C]	GLN	4.3
1	4-J	154[D]	GLN	4.3
1	4-M	130[D]	GLN	4.3
1	1-D	201[A]	ASP	4.3
1	2-D	201[B]	ASP	4.3
1	3-D	201[C]	ASP	4.3
1	4-D	201[D]	ASP	4.3
1	1-I	133[A]	HIS	4.3
1	1-K	176[A]	PRO	4.3
1	2-I	133[B]	HIS	4.3
1	2-K	176[B]	PRO	4.3
1	3-I	133[C]	HIS	4.3
1	3-K	176[C]	PRO	4.3
1	4-I	133[D]	HIS	4.3
1	4-K	176[D]	PRO	4.3
1	1-B	277[A]	PHE	4.2
1	2-B	277[B]	PHE	4.2
1	3-B	277[C]	PHE	4.2
1	4-B	277[D]	PHE	4.2
1	1-I	40[A]	ARG	4.2
1	2-I	40[B]	ARG	4.2
1	3-I	40[C]	ARG	4.2
1	4-I	40[D]	ARG	4.2
1	1-P	154[A]	GLN	4.2
1	2-P	154[B]	GLN	4.2
1	3-P	154[C]	GLN	4.2
1	4-P	154[D]	GLN	4.2
1	1-H	203[A]	PRO	4.2

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Mol	Chain	Res	Type	RSRZ
1	1-I	185[A]	PRO	4.2
1	1-J	38[A]	PRO	4.2
1	2-H	203[B]	PRO	4.2
1	2-I	185[B]	PRO	4.2
1	2-J	38[B]	PRO	4.2
1	3-H	203[C]	PRO	4.2
1	3-I	185[C]	PRO	4.2
1	3-J	38[C]	PRO	4.2
1	4-H	203[D]	PRO	4.2
1	4-I	185[D]	PRO	4.2
1	4-J	38[D]	PRO	4.2
1	1-M	155[A]	ARG	4.2
1	2-M	155[B]	ARG	4.2
1	3-M	155[C]	ARG	4.2
1	4-M	155[D]	ARG	4.2
1	1-L	237[A]	MET	4.2
1	2-L	237[B]	MET	4.2
1	3-L	237[C]	MET	4.2
1	4-L	237[D]	MET	4.2
1	1-P	121[A]	GLY	4.2
1	2-P	121[B]	GLY	4.2
1	3-P	121[C]	GLY	4.2
1	4-P	121[D]	GLY	4.2
1	1-I	291[A]	ASP	4.2
1	2-I	291[B]	ASP	4.2
1	3-I	291[C]	ASP	4.2
1	4-I	291[D]	ASP	4.2
1	1-N	175[A]	ASN	4.2
1	2-N	175[B]	ASN	4.2
1	3-N	175[C]	ASN	4.2
1	4-N	175[D]	ASN	4.2
1	1-L	172[A]	SER	4.2
1	2-L	172[B]	SER	4.2
1	3-L	172[C]	SER	4.2
1	4-L	172[D]	SER	4.2
1	1-I	31[A]	ILE	4.2
1	1-J	236[A]	HIS	4.2
1	1-O	133[A]	HIS	4.2
1	2-I	31[B]	ILE	4.2
1	2-J	236[B]	HIS	4.2
1	2-O	133[B]	HIS	4.2
1	3-I	31[C]	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	3-J	236[C]	HIS	4.2
1	3-O	133[C]	HIS	4.2
1	4-I	31[D]	ILE	4.2
1	4-J	236[D]	HIS	4.2
1	4-O	133[D]	HIS	4.2
1	1-J	143[A]	GLY	4.2
1	2-J	143[B]	GLY	4.2
1	3-J	143[C]	GLY	4.2
1	4-J	143[D]	GLY	4.2
1	1-N	62[A]	THR	4.2
1	1-N	242[A]	THR	4.2
1	2-N	62[B]	THR	4.2
1	2-N	242[B]	THR	4.2
1	3-N	62[C]	THR	4.2
1	3-N	242[C]	THR	4.2
1	4-N	62[D]	THR	4.2
1	4-N	242[D]	THR	4.2
1	1-B	202[A]	SER	4.2
1	1-D	95[A]	SER	4.2
1	1-I	66[A]	LEU	4.2
1	1-L	210[A]	SER	4.2
1	1-P	260[A]	ARG	4.2
1	2-B	202[B]	SER	4.2
1	2-D	95[B]	SER	4.2
1	2-I	66[B]	LEU	4.2
1	2-L	210[B]	SER	4.2
1	2-P	260[B]	ARG	4.2
1	3-B	202[C]	SER	4.2
1	3-D	95[C]	SER	4.2
1	3-I	66[C]	LEU	4.2
1	3-L	210[C]	SER	4.2
1	3-P	260[C]	ARG	4.2
1	4-B	202[D]	SER	4.2
1	4-D	95[D]	SER	4.2
1	4-I	66[D]	LEU	4.2
1	4-L	210[D]	SER	4.2
1	4-P	260[D]	ARG	4.2
1	1-P	297[A]	VAL	4.2
1	2-P	297[B]	VAL	4.2
1	3-P	297[C]	VAL	4.2
1	4-P	297[D]	VAL	4.2
1	1-M	35[A]	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
1	2-M	35[B]	GLU	4.2
1	3-M	35[C]	GLU	4.2
1	4-M	35[D]	GLU	4.2
1	1-M	147[A]	GLY	4.2
1	1-O	286[A]	LYS	4.2
1	2-M	147[B]	GLY	4.2
1	2-O	286[B]	LYS	4.2
1	3-M	147[C]	GLY	4.2
1	3-O	286[C]	LYS	4.2
1	4-M	147[D]	GLY	4.2
1	4-O	286[D]	LYS	4.2
1	1-O	193[A]	PHE	4.2
1	2-O	193[B]	PHE	4.2
1	3-O	193[C]	PHE	4.2
1	4-O	193[D]	PHE	4.2
1	1-J	20[A]	GLU	4.2
1	1-J	264[A]	GLU	4.2
1	1-L	111[A]	GLU	4.2
1	2-J	20[B]	GLU	4.2
1	2-J	264[B]	GLU	4.2
1	2-L	111[B]	GLU	4.2
1	3-J	20[C]	GLU	4.2
1	3-J	264[C]	GLU	4.2
1	3-L	111[C]	GLU	4.2
1	4-J	20[D]	GLU	4.2
1	4-J	264[D]	GLU	4.2
1	4-L	111[D]	GLU	4.2
1	1-N	267[A]	LYS	4.2
1	1-M	39[A]	ASP	4.2
1	1-P	191[A]	CYS	4.2
1	2-N	267[B]	LYS	4.2
1	2-M	39[B]	ASP	4.2
1	2-P	191[B]	CYS	4.2
1	3-N	267[C]	LYS	4.2
1	3-M	39[C]	ASP	4.2
1	3-P	191[C]	CYS	4.2
1	4-N	267[D]	LYS	4.2
1	4-M	39[D]	ASP	4.2
1	4-P	191[D]	CYS	4.2
1	1-A	42[A]	GLY	4.2
1	2-A	42[B]	GLY	4.2
1	3-A	42[C]	GLY	4.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	4-A	42[D]	GLY	4.2
1	1-I	79[A]	GLU	4.2
1	1-O	269[A]	GLN	4.2
1	2-I	79[B]	GLU	4.2
1	2-O	269[B]	GLN	4.2
1	3-I	79[C]	GLU	4.2
1	3-O	269[C]	GLN	4.2
1	4-I	79[D]	GLU	4.2
1	4-O	269[D]	GLN	4.2
1	1-L	107[A]	LYS	4.2
1	2-L	107[B]	LYS	4.2
1	3-L	107[C]	LYS	4.2
1	4-L	107[D]	LYS	4.2
1	1-I	246[A]	PRO	4.2
1	2-I	246[B]	PRO	4.2
1	3-I	246[C]	PRO	4.2
1	4-I	246[D]	PRO	4.2
1	1-G	60[A]	ASP	4.2
1	1-M	179[A]	LEU	4.2
1	2-G	60[B]	ASP	4.2
1	2-M	179[B]	LEU	4.2
1	3-G	60[C]	ASP	4.2
1	3-M	179[C]	LEU	4.2
1	4-G	60[D]	ASP	4.2
1	4-M	179[D]	LEU	4.2
1	1-C	317[A]	ALA	4.2
1	1-I	183[A]	ALA	4.2
1	1-L	232[A]	ALA	4.2
1	1-L	317[A]	ALA	4.2
1	1-N	283[A]	ALA	4.2
1	2-C	317[B]	ALA	4.2
1	2-I	183[B]	ALA	4.2
1	2-L	232[B]	ALA	4.2
1	2-L	317[B]	ALA	4.2
1	2-N	283[B]	ALA	4.2
1	3-C	317[C]	ALA	4.2
1	3-I	183[C]	ALA	4.2
1	3-L	232[C]	ALA	4.2
1	3-L	317[C]	ALA	4.2
1	3-N	283[C]	ALA	4.2
1	4-C	317[D]	ALA	4.2
1	4-I	183[D]	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
1	4-L	232[D]	ALA	4.2
1	4-L	317[D]	ALA	4.2
1	4-N	283[D]	ALA	4.2
1	1-J	224[A]	VAL	4.2
1	1-K	168[A]	ARG	4.2
1	2-J	224[B]	VAL	4.2
1	2-K	168[B]	ARG	4.2
1	3-J	224[C]	VAL	4.2
1	3-K	168[C]	ARG	4.2
1	4-J	224[D]	VAL	4.2
1	4-K	168[D]	ARG	4.2
1	1-K	264[A]	GLU	4.2
1	2-K	264[B]	GLU	4.2
1	3-K	264[C]	GLU	4.2
1	4-K	264[D]	GLU	4.2
1	1-J	172[A]	SER	4.2
1	2-J	172[B]	SER	4.2
1	3-J	172[C]	SER	4.2
1	4-J	172[D]	SER	4.2
1	1-M	225[A]	PRO	4.1
1	2-M	225[B]	PRO	4.1
1	3-M	225[C]	PRO	4.1
1	4-M	225[D]	PRO	4.1
1	1-J	42[A]	GLY	4.1
1	2-J	42[B]	GLY	4.1
1	3-J	42[C]	GLY	4.1
1	4-J	42[D]	GLY	4.1
1	1-N	288[A]	GLU	4.1
1	2-N	288[B]	GLU	4.1
1	3-N	288[C]	GLU	4.1
1	4-N	288[D]	GLU	4.1
1	1-L	113[A]	VAL	4.1
1	1-L	152[A]	GLN	4.1
1	1-P	112[A]	LYS	4.1
1	2-L	113[B]	VAL	4.1
1	2-L	152[B]	GLN	4.1
1	2-P	112[B]	LYS	4.1
1	3-L	113[C]	VAL	4.1
1	3-L	152[C]	GLN	4.1
1	3-P	112[C]	LYS	4.1
1	4-L	113[D]	VAL	4.1
1	4-L	152[D]	GLN	4.1

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Mol	Chain	Res	Type	RSRZ
1	4-P	112[D]	LYS	4.1
1	1-J	247[A]	HIS	4.1
1	1-M	316[A]	SER	4.1
1	1-P	18[A]	HIS	4.1
1	2-J	247[B]	HIS	4.1
1	2-M	316[B]	SER	4.1
1	2-P	18[B]	HIS	4.1
1	3-J	247[C]	HIS	4.1
1	3-M	316[C]	SER	4.1
1	3-P	18[C]	HIS	4.1
1	4-J	247[D]	HIS	4.1
1	4-M	316[D]	SER	4.1
1	4-P	18[D]	HIS	4.1
1	1-H	42[A]	GLY	4.1
1	1-J	114[A]	GLY	4.1
1	1-M	163[A]	ASN	4.1
1	2-H	42[B]	GLY	4.1
1	2-J	114[B]	GLY	4.1
1	2-M	163[B]	ASN	4.1
1	3-H	42[C]	GLY	4.1
1	3-J	114[C]	GLY	4.1
1	3-M	163[C]	ASN	4.1
1	4-H	42[D]	GLY	4.1
1	4-J	114[D]	GLY	4.1
1	4-M	163[D]	ASN	4.1
1	1-A	90[A]	ALA	4.1
1	2-A	90[B]	ALA	4.1
1	3-A	90[C]	ALA	4.1
1	4-A	90[D]	ALA	4.1
1	1-J	113[A]	VAL	4.1
1	2-J	113[B]	VAL	4.1
1	3-J	113[C]	VAL	4.1
1	4-J	113[D]	VAL	4.1
1	1-K	144[A]	ASP	4.1
1	1-N	85[A]	SER	4.1
1	2-K	144[B]	ASP	4.1
1	2-N	85[B]	SER	4.1
1	3-K	144[C]	ASP	4.1
1	3-N	85[C]	SER	4.1
1	4-K	144[D]	ASP	4.1
1	4-N	85[D]	SER	4.1
1	1-B	203[A]	PRO	4.1

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Mol	Chain	Res	Type	RSRZ
1	1-M	45[A]	THR	4.1
1	1-O	67[A]	THR	4.1
1	2-B	203[B]	PRO	4.1
1	2-M	45[B]	THR	4.1
1	2-O	67[B]	THR	4.1
1	3-B	203[C]	PRO	4.1
1	3-M	45[C]	THR	4.1
1	3-O	67[C]	THR	4.1
1	4-B	203[D]	PRO	4.1
1	4-M	45[D]	THR	4.1
1	4-O	67[D]	THR	4.1
1	1-M	107[A]	LYS	4.1
1	1-M	306[A]	LYS	4.1
1	2-M	107[B]	LYS	4.1
1	2-M	306[B]	LYS	4.1
1	3-M	107[C]	LYS	4.1
1	3-M	306[C]	LYS	4.1
1	4-M	107[D]	LYS	4.1
1	4-M	306[D]	LYS	4.1
1	1-D	190[A]	PHE	4.1
1	1-N	229[A]	ALA	4.1
1	2-D	190[B]	PHE	4.1
1	2-N	229[B]	ALA	4.1
1	3-D	190[C]	PHE	4.1
1	3-N	229[C]	ALA	4.1
1	4-D	190[D]	PHE	4.1
1	4-N	229[D]	ALA	4.1
1	1-I	155[A]	ARG	4.1
1	1-M	245[A]	GLU	4.1
1	1-P	155[A]	ARG	4.1
1	2-I	155[B]	ARG	4.1
1	2-M	245[B]	GLU	4.1
1	2-P	155[B]	ARG	4.1
1	3-I	155[C]	ARG	4.1
1	3-M	245[C]	GLU	4.1
1	3-P	155[C]	ARG	4.1
1	4-I	155[D]	ARG	4.1
1	4-M	245[D]	GLU	4.1
1	4-P	155[D]	ARG	4.1
1	1-L	36[A]	VAL	4.1
1	2-L	36[B]	VAL	4.1
1	3-L	36[C]	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	4-L	36[D]	VAL	4.1
1	1-N	170[A]	ILE	4.1
1	2-N	170[B]	ILE	4.1
1	3-N	170[C]	ILE	4.1
1	4-N	170[D]	ILE	4.1
1	1-L	41[A]	THR	4.1
1	1-L	62[A]	THR	4.1
1	2-L	41[B]	THR	4.1
1	2-L	62[B]	THR	4.1
1	3-L	41[C]	THR	4.1
1	3-L	62[C]	THR	4.1
1	4-L	41[D]	THR	4.1
1	4-L	62[D]	THR	4.1
1	1-E	136[A]	ALA	4.1
1	1-L	191[A]	CYS	4.1
1	2-E	136[B]	ALA	4.1
1	2-L	191[B]	CYS	4.1
1	3-E	136[C]	ALA	4.1
1	3-L	191[C]	CYS	4.1
1	4-E	136[D]	ALA	4.1
1	4-L	191[D]	CYS	4.1
1	1-J	106[A]	SER	4.1
1	1-L	57[A]	SER	4.1
1	2-J	106[B]	SER	4.1
1	2-L	57[B]	SER	4.1
1	3-J	106[C]	SER	4.1
1	3-L	57[C]	SER	4.1
1	4-J	106[D]	SER	4.1
1	4-L	57[D]	SER	4.1
1	1-J	92[A]	MET	4.1
1	1-J	213[A]	MET	4.1
1	2-J	92[B]	MET	4.1
1	2-J	213[B]	MET	4.1
1	3-J	92[C]	MET	4.1
1	3-J	213[C]	MET	4.1
1	4-J	92[D]	MET	4.1
1	4-J	213[D]	MET	4.1
1	1-M	36[A]	VAL	4.1
1	2-M	36[B]	VAL	4.1
1	3-M	36[C]	VAL	4.1
1	4-M	36[D]	VAL	4.1
1	1-I	68[A]	THR	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-M	42[A]	GLY	4.1
1	2-I	68[B]	THR	4.1
1	2-M	42[B]	GLY	4.1
1	3-I	68[C]	THR	4.1
1	3-M	42[C]	GLY	4.1
1	4-I	68[D]	THR	4.1
1	4-M	42[D]	GLY	4.1
1	1-N	79[A]	GLU	4.1
1	2-N	79[B]	GLU	4.1
1	3-N	79[C]	GLU	4.1
1	4-N	79[D]	GLU	4.1
1	1-K	119[A]	ARG	4.1
1	1-O	37[A]	ARG	4.1
1	2-K	119[B]	ARG	4.1
1	2-O	37[B]	ARG	4.1
1	3-K	119[C]	ARG	4.1
1	3-O	37[C]	ARG	4.1
1	4-K	119[D]	ARG	4.1
1	4-O	37[D]	ARG	4.1
1	1-E	308[A]	TRP	4.1
1	2-E	308[B]	TRP	4.1
1	3-E	308[C]	TRP	4.1
1	4-E	308[D]	TRP	4.1
1	1-P	217[A]	SER	4.1
1	2-P	217[B]	SER	4.1
1	3-P	217[C]	SER	4.1
1	4-P	217[D]	SER	4.1
1	1-O	252[A]	GLN	4.1
1	2-O	252[B]	GLN	4.1
1	3-O	252[C]	GLN	4.1
1	4-O	252[D]	GLN	4.1
1	1-A	203[A]	PRO	4.1
1	1-C	16[A]	PRO	4.1
1	1-I	294[A]	GLY	4.1
1	1-P	307[A]	PRO	4.1
1	2-A	203[B]	PRO	4.1
1	2-C	16[B]	PRO	4.1
1	2-I	294[B]	GLY	4.1
1	2-P	307[B]	PRO	4.1
1	3-A	203[C]	PRO	4.1
1	3-C	16[C]	PRO	4.1
1	3-I	294[C]	GLY	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-P	307[C]	PRO	4.1
1	4-A	203[D]	PRO	4.1
1	4-C	16[D]	PRO	4.1
1	4-I	294[D]	GLY	4.1
1	4-P	307[D]	PRO	4.1
1	1-M	151[A]	ASP	4.1
1	2-M	151[B]	ASP	4.1
1	3-M	151[C]	ASP	4.1
1	4-M	151[D]	ASP	4.1
1	1-C	271[A]	GLU	4.0
1	1-J	237[A]	MET	4.0
1	2-C	271[B]	GLU	4.0
1	2-J	237[B]	MET	4.0
1	3-C	271[C]	GLU	4.0
1	3-J	237[C]	MET	4.0
1	4-C	271[D]	GLU	4.0
1	4-J	237[D]	MET	4.0
1	1-I	122[A]	ASP	4.0
1	1-I	132[A]	ARG	4.0
1	1-K	28[A]	ARG	4.0
1	1-O	274[A]	PRO	4.0
1	2-I	122[B]	ASP	4.0
1	2-I	132[B]	ARG	4.0
1	2-K	28[B]	ARG	4.0
1	2-O	274[B]	PRO	4.0
1	3-I	122[C]	ASP	4.0
1	3-I	132[C]	ARG	4.0
1	3-K	28[C]	ARG	4.0
1	3-O	274[C]	PRO	4.0
1	4-I	122[D]	ASP	4.0
1	4-I	132[D]	ARG	4.0
1	4-K	28[D]	ARG	4.0
1	4-O	274[D]	PRO	4.0
1	1-M	192[A]	GLN	4.0
1	2-M	192[B]	GLN	4.0
1	3-M	192[C]	GLN	4.0
1	4-M	192[D]	GLN	4.0
1	1-N	78[A]	ALA	4.0
1	2-N	78[B]	ALA	4.0
1	3-N	78[C]	ALA	4.0
1	4-N	78[D]	ALA	4.0
1	1-P	55[A]	ARG	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-E	204[A]	GLY	4.0
1	1-J	39[A]	ASP	4.0
1	1-P	144[A]	ASP	4.0
1	2-P	55[B]	ARG	4.0
1	1-K	38[A]	PRO	4.0
1	1-K	254[A]	GLY	4.0
1	2-E	204[B]	GLY	4.0
1	2-J	39[B]	ASP	4.0
1	2-P	144[B]	ASP	4.0
1	3-P	55[C]	ARG	4.0
1	3-E	204[C]	GLY	4.0
1	3-J	39[C]	ASP	4.0
1	3-P	144[C]	ASP	4.0
1	4-E	204[D]	GLY	4.0
1	4-J	39[D]	ASP	4.0
1	4-P	55[D]	ARG	4.0
1	2-K	38[B]	PRO	4.0
1	2-K	254[B]	GLY	4.0
1	3-K	38[C]	PRO	4.0
1	3-K	254[C]	GLY	4.0
1	4-K	38[D]	PRO	4.0
1	4-K	254[D]	GLY	4.0
1	4-P	144[D]	ASP	4.0
1	1-K	137[A]	GLU	4.0
1	1-O	271[A]	GLU	4.0
1	2-K	137[B]	GLU	4.0
1	2-O	271[B]	GLU	4.0
1	3-K	137[C]	GLU	4.0
1	3-O	271[C]	GLU	4.0
1	4-K	137[D]	GLU	4.0
1	4-O	271[D]	GLU	4.0
1	1-M	175[A]	ASN	4.0
1	2-M	175[B]	ASN	4.0
1	3-M	175[C]	ASN	4.0
1	4-M	175[D]	ASN	4.0
1	1-O	47[A]	ALA	4.0
1	1-P	78[A]	ALA	4.0
1	2-O	47[B]	ALA	4.0
1	2-P	78[B]	ALA	4.0
1	3-O	47[C]	ALA	4.0
1	3-P	78[C]	ALA	4.0
1	4-O	47[D]	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	4-P	78[D]	ALA	4.0
1	1-K	219[A]	ASP	4.0
1	1-L	17[A]	ASP	4.0
1	2-K	219[B]	ASP	4.0
1	2-L	17[B]	ASP	4.0
1	3-K	219[C]	ASP	4.0
1	3-L	17[C]	ASP	4.0
1	4-K	219[D]	ASP	4.0
1	4-L	17[D]	ASP	4.0
1	1-K	221[A]	GLY	4.0
1	2-K	221[B]	GLY	4.0
1	3-K	221[C]	GLY	4.0
1	4-K	221[D]	GLY	4.0
1	1-O	185[A]	PRO	4.0
1	2-O	185[B]	PRO	4.0
1	3-O	185[C]	PRO	4.0
1	4-O	185[D]	PRO	4.0
1	1-M	298[A]	GLU	4.0
1	2-M	298[B]	GLU	4.0
1	3-M	298[C]	GLU	4.0
1	4-M	298[D]	GLU	4.0
1	1-I	268[A]	THR	4.0
1	1-J	214[A]	TYR	4.0
1	1-O	159[A]	THR	4.0
1	2-I	268[B]	THR	4.0
1	2-J	214[B]	TYR	4.0
1	2-O	159[B]	THR	4.0
1	3-I	268[C]	THR	4.0
1	3-J	214[C]	TYR	4.0
1	3-O	159[C]	THR	4.0
1	4-I	268[D]	THR	4.0
1	4-J	214[D]	TYR	4.0
1	4-O	159[D]	THR	4.0
1	1-L	118[A]	ARG	4.0
1	1-L	297[A]	VAL	4.0
1	2-L	118[B]	ARG	4.0
1	2-L	297[B]	VAL	4.0
1	3-L	118[C]	ARG	4.0
1	3-L	297[C]	VAL	4.0
1	4-L	118[D]	ARG	4.0
1	4-L	297[D]	VAL	4.0
1	1-N	255[A]	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	2-N	255[B]	ASP	4.0
1	3-N	255[C]	ASP	4.0
1	4-N	255[D]	ASP	4.0
1	1-H	245[A]	GLU	4.0
1	2-H	245[B]	GLU	4.0
1	3-H	245[C]	GLU	4.0
1	4-H	245[D]	GLU	4.0
1	1-N	213[A]	MET	4.0
1	2-N	213[B]	MET	4.0
1	3-N	213[C]	MET	4.0
1	4-N	213[D]	MET	4.0
1	1-N	133[A]	HIS	4.0
1	1-O	18[A]	HIS	4.0
1	2-N	133[B]	HIS	4.0
1	2-O	18[B]	HIS	4.0
1	3-N	133[C]	HIS	4.0
1	3-O	18[C]	HIS	4.0
1	4-N	133[D]	HIS	4.0
1	4-O	18[D]	HIS	4.0
1	1-C	231[A]	TYR	4.0
1	2-C	231[B]	TYR	4.0
1	3-C	231[C]	TYR	4.0
1	4-C	231[D]	TYR	4.0
1	1-G	113[A]	VAL	4.0
1	1-L	287[A]	GLU	4.0
1	2-G	113[B]	VAL	4.0
1	2-L	287[B]	GLU	4.0
1	3-G	113[C]	VAL	4.0
1	3-L	287[C]	GLU	4.0
1	4-G	113[D]	VAL	4.0
1	4-L	287[D]	GLU	4.0
1	1-N	154[A]	GLN	4.0
1	2-N	154[B]	GLN	4.0
1	3-N	154[C]	GLN	4.0
1	4-N	154[D]	GLN	4.0
1	1-C	111[A]	GLU	4.0
1	1-G	17[A]	ASP	4.0
1	1-K	178[A]	ASP	4.0
1	1-N	57[A]	SER	4.0
1	2-C	111[B]	GLU	4.0
1	2-G	17[B]	ASP	4.0
1	2-K	178[B]	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	2-N	57[B]	SER	4.0
1	3-C	111[C]	GLU	4.0
1	3-G	17[C]	ASP	4.0
1	3-K	178[C]	ASP	4.0
1	3-N	57[C]	SER	4.0
1	4-C	111[D]	GLU	4.0
1	4-G	17[D]	ASP	4.0
1	4-K	178[D]	ASP	4.0
1	4-N	57[D]	SER	4.0
1	1-D	270[A]	LEU	4.0
1	2-D	270[B]	LEU	4.0
1	3-D	270[C]	LEU	4.0
1	4-D	270[D]	LEU	4.0
1	1-O	112[A]	LYS	4.0
1	2-O	112[B]	LYS	4.0
1	3-O	112[C]	LYS	4.0
1	4-O	112[D]	LYS	4.0
1	1-K	258[A]	VAL	4.0
1	1-M	136[A]	ALA	4.0
1	2-K	258[B]	VAL	4.0
1	2-M	136[B]	ALA	4.0
1	3-K	258[C]	VAL	4.0
1	3-M	136[C]	ALA	4.0
1	4-K	258[D]	VAL	4.0
1	4-M	136[D]	ALA	4.0
1	1-J	125[A]	PRO	4.0
1	2-J	125[B]	PRO	4.0
1	3-J	125[C]	PRO	4.0
1	4-J	125[D]	PRO	4.0
1	1-O	158[A]	ASP	3.9
1	1-P	39[A]	ASP	3.9
1	2-O	158[B]	ASP	3.9
1	2-P	39[B]	ASP	3.9
1	3-O	158[C]	ASP	3.9
1	3-P	39[C]	ASP	3.9
1	4-O	158[D]	ASP	3.9
1	4-P	39[D]	ASP	3.9
1	1-F	143[A]	GLY	3.9
1	1-I	143[A]	GLY	3.9
1	1-N	83[A]	PHE	3.9
1	2-F	143[B]	GLY	3.9
1	2-I	143[B]	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	2-N	83[B]	PHE	3.9
1	3-F	143[C]	GLY	3.9
1	3-I	143[C]	GLY	3.9
1	3-N	83[C]	PHE	3.9
1	4-F	143[D]	GLY	3.9
1	4-I	143[D]	GLY	3.9
1	4-N	83[D]	PHE	3.9
1	1-N	169[A]	ILE	3.9
1	2-N	169[B]	ILE	3.9
1	3-N	169[C]	ILE	3.9
1	4-N	169[D]	ILE	3.9
1	1-K	132[A]	ARG	3.9
1	2-K	132[B]	ARG	3.9
1	3-K	132[C]	ARG	3.9
1	4-K	132[D]	ARG	3.9
1	1-J	69[A]	LYS	3.9
1	1-J	312[A]	ASP	3.9
1	1-K	166[A]	ASP	3.9
1	1-M	261[A]	ASP	3.9
1	2-J	69[B]	LYS	3.9
1	2-J	312[B]	ASP	3.9
1	2-K	166[B]	ASP	3.9
1	2-M	261[B]	ASP	3.9
1	3-J	69[C]	LYS	3.9
1	3-J	312[C]	ASP	3.9
1	3-K	166[C]	ASP	3.9
1	3-M	261[C]	ASP	3.9
1	4-J	69[D]	LYS	3.9
1	4-J	312[D]	ASP	3.9
1	4-K	166[D]	ASP	3.9
1	4-M	261[D]	ASP	3.9
1	1-E	113[A]	VAL	3.9
1	1-J	18[A]	HIS	3.9
1	1-J	156[A]	VAL	3.9
1	2-E	113[B]	VAL	3.9
1	2-J	18[B]	HIS	3.9
1	2-J	156[B]	VAL	3.9
1	3-E	113[C]	VAL	3.9
1	3-J	18[C]	HIS	3.9
1	3-J	156[C]	VAL	3.9
1	4-E	113[D]	VAL	3.9
1	4-J	18[D]	HIS	3.9

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Mol	Chain	Res	Type	RSRZ
1	4-J	156[D]	VAL	3.9
1	1-N	285[A]	SER	3.9
1	1-P	250[A]	ILE	3.9
1	2-N	285[B]	SER	3.9
1	2-P	250[B]	ILE	3.9
1	3-N	285[C]	SER	3.9
1	3-P	250[C]	ILE	3.9
1	4-N	285[D]	SER	3.9
1	4-P	250[D]	ILE	3.9
1	1-I	271[A]	GLU	3.9
1	1-K	111[A]	GLU	3.9
1	2-I	271[B]	GLU	3.9
1	2-K	111[B]	GLU	3.9
1	3-I	271[C]	GLU	3.9
1	3-K	111[C]	GLU	3.9
1	4-I	271[D]	GLU	3.9
1	4-K	111[D]	GLU	3.9
1	1-O	284[A]	ARG	3.9
1	2-O	284[B]	ARG	3.9
1	3-O	284[C]	ARG	3.9
1	4-O	284[D]	ARG	3.9
1	1-L	281[A]	LYS	3.9
1	1-K	25[A]	ASP	3.9
1	1-K	162[A]	ASN	3.9
1	2-L	281[B]	LYS	3.9
1	2-K	25[B]	ASP	3.9
1	2-K	162[B]	ASN	3.9
1	3-L	281[C]	LYS	3.9
1	3-K	25[C]	ASP	3.9
1	3-K	162[C]	ASN	3.9
1	4-K	25[D]	ASP	3.9
1	4-K	162[D]	ASN	3.9
1	4-L	281[D]	LYS	3.9
1	1-J	48[A]	LEU	3.9
1	2-J	48[B]	LEU	3.9
1	3-J	48[C]	LEU	3.9
1	4-J	48[D]	LEU	3.9
1	1-L	300[A]	PHE	3.9
1	2-L	300[B]	PHE	3.9
1	3-L	300[C]	PHE	3.9
1	4-L	300[D]	PHE	3.9
1	1-A	113[A]	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	1-I	156[A]	VAL	3.9
1	2-A	113[B]	VAL	3.9
1	2-I	156[B]	VAL	3.9
1	3-A	113[C]	VAL	3.9
1	3-I	156[C]	VAL	3.9
1	4-A	113[D]	VAL	3.9
1	4-I	156[D]	VAL	3.9
1	1-N	75[A]	GLY	3.9
1	1-O	221[A]	GLY	3.9
1	2-N	75[B]	GLY	3.9
1	2-O	221[B]	GLY	3.9
1	3-N	75[C]	GLY	3.9
1	3-O	221[C]	GLY	3.9
1	4-N	75[D]	GLY	3.9
1	4-O	221[D]	GLY	3.9
1	1-P	261[A]	ASP	3.9
1	2-P	261[B]	ASP	3.9
1	3-P	261[C]	ASP	3.9
1	4-P	261[D]	ASP	3.9
1	1-G	287[A]	GLU	3.9
1	1-P	35[A]	GLU	3.9
1	2-G	287[B]	GLU	3.9
1	2-P	35[B]	GLU	3.9
1	3-G	287[C]	GLU	3.9
1	3-P	35[C]	GLU	3.9
1	4-G	287[D]	GLU	3.9
1	4-P	35[D]	GLU	3.9
1	1-M	270[A]	LEU	3.9
1	1-P	80[A]	LEU	3.9
1	2-M	270[B]	LEU	3.9
1	2-P	80[B]	LEU	3.9
1	3-M	270[C]	LEU	3.9
1	3-P	80[C]	LEU	3.9
1	4-M	270[D]	LEU	3.9
1	4-P	80[D]	LEU	3.9
1	1-L	284[A]	ARG	3.9
1	1-N	53[A]	SER	3.9
1	1-N	132[A]	ARG	3.9
1	2-L	284[B]	ARG	3.9
1	2-N	53[B]	SER	3.9
1	2-N	132[B]	ARG	3.9
1	3-L	284[C]	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
1	3-N	53[C]	SER	3.9
1	3-N	132[C]	ARG	3.9
1	4-L	284[D]	ARG	3.9
1	4-N	53[D]	SER	3.9
1	4-N	132[D]	ARG	3.9
1	1-I	135[A]	GLY	3.9
1	1-O	276[A]	ASP	3.9
1	2-I	135[B]	GLY	3.9
1	2-O	276[B]	ASP	3.9
1	3-I	135[C]	GLY	3.9
1	3-O	276[C]	ASP	3.9
1	4-I	135[D]	GLY	3.9
1	4-O	276[D]	ASP	3.9
1	1-I	96[A]	GLN	3.9
1	2-I	96[B]	GLN	3.9
1	3-I	96[C]	GLN	3.9
1	4-I	96[D]	GLN	3.9
1	1-M	74[A]	ARG	3.9
1	1-N	173[A]	ALA	3.9
1	2-M	74[B]	ARG	3.9
1	2-N	173[B]	ALA	3.9
1	3-M	74[C]	ARG	3.9
1	3-N	173[C]	ALA	3.9
1	4-M	74[D]	ARG	3.9
1	4-N	173[D]	ALA	3.9
1	1-P	53[A]	SER	3.9
1	2-P	53[B]	SER	3.9
1	3-P	53[C]	SER	3.9
1	4-P	53[D]	SER	3.9
1	1-L	158[A]	ASP	3.9
1	1-L	219[A]	ASP	3.9
1	1-M	219[A]	ASP	3.9
1	1-N	276[A]	ASP	3.9
1	2-L	158[B]	ASP	3.9
1	2-L	219[B]	ASP	3.9
1	2-M	219[B]	ASP	3.9
1	2-N	276[B]	ASP	3.9
1	3-L	158[C]	ASP	3.9
1	3-L	219[C]	ASP	3.9
1	3-M	219[C]	ASP	3.9
1	3-N	276[C]	ASP	3.9
1	4-L	158[D]	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
1	4-L	219[D]	ASP	3.9
1	4-M	219[D]	ASP	3.9
1	4-N	276[D]	ASP	3.9
1	1-I	116[A]	GLY	3.9
1	2-I	116[B]	GLY	3.9
1	3-I	116[C]	GLY	3.9
1	4-I	116[D]	GLY	3.9
1	1-K	23[A]	TYR	3.9
1	2-K	23[B]	TYR	3.9
1	3-K	23[C]	TYR	3.9
1	4-K	23[D]	TYR	3.9
1	1-P	238[A]	ILE	3.9
1	2-P	238[B]	ILE	3.9
1	3-P	238[C]	ILE	3.9
1	4-P	238[D]	ILE	3.9
1	1-K	19[A]	GLU	3.8
1	2-K	19[B]	GLU	3.8
1	3-K	19[C]	GLU	3.8
1	4-K	19[D]	GLU	3.8
1	1-J	99[A]	GLY	3.8
1	1-O	114[A]	GLY	3.8
1	2-J	99[B]	GLY	3.8
1	2-O	114[B]	GLY	3.8
1	3-J	99[C]	GLY	3.8
1	3-O	114[C]	GLY	3.8
1	4-J	99[D]	GLY	3.8
1	4-O	114[D]	GLY	3.8
1	1-G	109[A]	PHE	3.8
1	1-J	314[A]	LYS	3.8
1	2-G	109[B]	PHE	3.8
1	2-J	314[B]	LYS	3.8
1	3-G	109[C]	PHE	3.8
1	3-J	314[C]	LYS	3.8
1	4-G	109[D]	PHE	3.8
1	4-J	314[D]	LYS	3.8
1	1-C	13[A]	ARG	3.8
1	1-L	244[A]	THR	3.8
1	2-C	13[B]	ARG	3.8
1	2-L	244[B]	THR	3.8
1	3-C	13[C]	ARG	3.8
1	3-L	244[C]	THR	3.8
1	4-C	13[D]	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
1	4-L	244[D]	THR	3.8
1	1-K	94[A]	SER	3.8
1	2-K	94[B]	SER	3.8
1	3-K	94[C]	SER	3.8
1	4-K	94[D]	SER	3.8
1	1-B	159[A]	THR	3.8
1	2-B	159[B]	THR	3.8
1	3-B	159[C]	THR	3.8
1	4-B	159[D]	THR	3.8
1	1-M	198[A]	PRO	3.8
1	2-M	198[B]	PRO	3.8
1	3-M	198[C]	PRO	3.8
1	4-M	198[D]	PRO	3.8
1	1-I	178[A]	ASP	3.8
1	2-I	178[B]	ASP	3.8
1	3-I	178[C]	ASP	3.8
1	4-I	178[D]	ASP	3.8
1	1-L	94[A]	SER	3.8
1	2-L	94[B]	SER	3.8
1	3-L	94[C]	SER	3.8
1	4-L	94[D]	SER	3.8
1	1-L	264[A]	GLU	3.8
1	2-L	264[B]	GLU	3.8
1	3-L	264[C]	GLU	3.8
1	4-L	264[D]	GLU	3.8
1	1-L	153[A]	LEU	3.8
1	1-M	181[A]	LEU	3.8
1	2-L	153[B]	LEU	3.8
1	2-M	181[B]	LEU	3.8
1	3-L	153[C]	LEU	3.8
1	3-M	181[C]	LEU	3.8
1	4-L	153[D]	LEU	3.8
1	4-M	181[D]	LEU	3.8
1	1-L	144[A]	ASP	3.8
1	1-P	140[A]	ASP	3.8
1	2-L	144[B]	ASP	3.8
1	2-P	140[B]	ASP	3.8
1	3-L	144[C]	ASP	3.8
1	3-P	140[C]	ASP	3.8
1	4-L	144[D]	ASP	3.8
1	4-P	140[D]	ASP	3.8
1	1-C	190[A]	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
1	1-I	281[A]	LYS	3.8
1	1-O	98[A]	VAL	3.8
1	2-C	190[B]	PHE	3.8
1	2-I	281[B]	LYS	3.8
1	2-O	98[B]	VAL	3.8
1	3-C	190[C]	PHE	3.8
1	3-I	281[C]	LYS	3.8
1	3-O	98[C]	VAL	3.8
1	4-C	190[D]	PHE	3.8
1	4-I	281[D]	LYS	3.8
1	4-O	98[D]	VAL	3.8
1	1-P	162[A]	ASN	3.8
1	2-P	162[B]	ASN	3.8
1	3-P	162[C]	ASN	3.8
1	4-P	162[D]	ASN	3.8
1	1-J	272[A]	ARG	3.8
1	1-L	275[A]	ARG	3.8
1	2-J	272[B]	ARG	3.8
1	2-L	275[B]	ARG	3.8
1	3-J	272[C]	ARG	3.8
1	3-L	275[C]	ARG	3.8
1	4-J	272[D]	ARG	3.8
1	4-L	275[D]	ARG	3.8
1	1-K	42[A]	GLY	3.8
1	1-L	315[A]	MET	3.8
1	2-K	42[B]	GLY	3.8
1	2-L	315[B]	MET	3.8
1	3-K	42[C]	GLY	3.8
1	3-L	315[C]	MET	3.8
1	4-K	42[D]	GLY	3.8
1	4-L	315[D]	MET	3.8
1	1-N	306[A]	LYS	3.8
1	2-N	306[B]	LYS	3.8
1	3-N	306[C]	LYS	3.8
1	4-N	306[D]	LYS	3.8
1	1-I	26[A]	LEU	3.8
1	1-K	159[A]	THR	3.8
1	1-L	179[A]	LEU	3.8
1	1-O	123[A]	LEU	3.8
1	1-P	222[A]	LEU	3.8
1	2-I	26[B]	LEU	3.8
1	2-K	159[B]	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	2-L	179[B]	LEU	3.8
1	2-O	123[B]	LEU	3.8
1	2-P	222[B]	LEU	3.8
1	3-I	26[C]	LEU	3.8
1	3-K	159[C]	THR	3.8
1	3-L	179[C]	LEU	3.8
1	3-O	123[C]	LEU	3.8
1	3-P	222[C]	LEU	3.8
1	4-I	26[D]	LEU	3.8
1	4-K	159[D]	THR	3.8
1	4-L	179[D]	LEU	3.8
1	4-O	123[D]	LEU	3.8
1	4-P	222[D]	LEU	3.8
1	1-B	190[A]	PHE	3.8
1	1-M	72[A]	PHE	3.8
1	2-B	190[B]	PHE	3.8
1	2-M	72[B]	PHE	3.8
1	3-B	190[C]	PHE	3.8
1	3-M	72[C]	PHE	3.8
1	4-B	190[D]	PHE	3.8
1	4-M	72[D]	PHE	3.8
1	1-O	75[A]	GLY	3.8
1	2-O	75[B]	GLY	3.8
1	3-O	75[C]	GLY	3.8
1	4-O	75[D]	GLY	3.8
1	1-H	308[A]	TRP	3.8
1	1-J	253[A]	MET	3.8
1	2-H	308[B]	TRP	3.8
1	2-J	253[B]	MET	3.8
1	3-H	308[C]	TRP	3.8
1	3-J	253[C]	MET	3.8
1	4-H	308[D]	TRP	3.8
1	4-J	253[D]	MET	3.8
1	1-N	252[A]	GLN	3.8
1	2-N	252[B]	GLN	3.8
1	3-N	252[C]	GLN	3.8
1	4-N	252[D]	GLN	3.8
1	1-K	233[A]	LEU	3.8
1	2-K	233[B]	LEU	3.8
1	3-K	233[C]	LEU	3.8
1	4-K	233[D]	LEU	3.8
1	1-I	146[A]	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
1	1-J	116[A]	GLY	3.8
1	2-I	146[B]	LYS	3.8
1	2-J	116[B]	GLY	3.8
1	3-I	146[C]	LYS	3.8
1	3-J	116[C]	GLY	3.8
1	4-I	146[D]	LYS	3.8
1	4-J	116[D]	GLY	3.8
1	1-N	22[A]	GLN	3.8
1	1-P	141[A]	ALA	3.8
1	2-N	22[B]	GLN	3.8
1	2-P	141[B]	ALA	3.8
1	3-N	22[C]	GLN	3.8
1	3-P	141[C]	ALA	3.8
1	4-N	22[D]	GLN	3.8
1	4-P	141[D]	ALA	3.8
1	1-N	131[A]	TRP	3.7
1	2-N	131[B]	TRP	3.7
1	3-N	131[C]	TRP	3.7
1	4-N	131[D]	TRP	3.7
1	1-M	235[A]	THR	3.7
1	2-M	235[B]	THR	3.7
1	3-M	235[C]	THR	3.7
1	4-M	235[D]	THR	3.7
1	1-F	205[A]	SER	3.7
1	2-F	205[B]	SER	3.7
1	3-F	205[C]	SER	3.7
1	4-F	205[D]	SER	3.7
1	1-I	121[A]	GLY	3.7
1	2-I	121[B]	GLY	3.7
1	3-I	121[C]	GLY	3.7
1	4-I	121[D]	GLY	3.7
1	1-F	200[A]	ALA	3.7
1	1-K	236[A]	HIS	3.7
1	1-P	271[A]	GLU	3.7
1	2-F	200[B]	ALA	3.7
1	2-K	236[B]	HIS	3.7
1	2-P	271[B]	GLU	3.7
1	3-F	200[C]	ALA	3.7
1	3-K	236[C]	HIS	3.7
1	3-P	271[C]	GLU	3.7
1	4-F	200[D]	ALA	3.7
1	4-K	236[D]	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	4-P	271[D]	GLU	3.7
1	1-M	180[A]	PRO	3.7
1	2-M	180[B]	PRO	3.7
1	3-M	180[C]	PRO	3.7
1	4-M	180[D]	PRO	3.7
1	1-L	150[A]	VAL	3.7
1	1-M	29[A]	ARG	3.7
1	2-L	150[B]	VAL	3.7
1	2-M	29[B]	ARG	3.7
1	3-L	150[C]	VAL	3.7
1	3-M	29[C]	ARG	3.7
1	4-L	150[D]	VAL	3.7
1	4-M	29[D]	ARG	3.7
1	1-J	267[A]	LYS	3.7
1	2-J	267[B]	LYS	3.7
1	3-J	267[C]	LYS	3.7
1	4-J	267[D]	LYS	3.7
1	1-A	202[A]	SER	3.7
1	2-A	202[B]	SER	3.7
1	3-A	202[C]	SER	3.7
1	4-A	202[D]	SER	3.7
1	1-E	17[A]	ASP	3.7
1	2-E	17[B]	ASP	3.7
1	3-E	17[C]	ASP	3.7
1	4-E	17[D]	ASP	3.7
1	1-A	204[A]	GLY	3.7
1	2-A	204[B]	GLY	3.7
1	3-A	204[C]	GLY	3.7
1	4-A	204[D]	GLY	3.7
1	1-J	22[A]	GLN	3.7
1	1-F	307[A]	PRO	3.7
1	1-L	49[A]	PHE	3.7
1	2-J	22[B]	GLN	3.7
1	1-M	278[A]	PRO	3.7
1	2-F	307[B]	PRO	3.7
1	2-L	49[B]	PHE	3.7
1	3-J	22[C]	GLN	3.7
1	3-F	307[C]	PRO	3.7
1	3-L	49[C]	PHE	3.7
1	4-J	22[D]	GLN	3.7
1	1-P	219[A]	ASP	3.7
1	2-M	278[B]	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	3-M	278[C]	PRO	3.7
1	4-F	307[D]	PRO	3.7
1	4-L	49[D]	PHE	3.7
1	2-P	219[B]	ASP	3.7
1	3-P	219[C]	ASP	3.7
1	4-M	278[D]	PRO	3.7
1	4-P	219[D]	ASP	3.7
1	1-D	86[A]	GLY	3.7
1	1-H	155[A]	ARG	3.7
1	1-P	67[A]	THR	3.7
1	2-D	86[B]	GLY	3.7
1	2-H	155[B]	ARG	3.7
1	2-P	67[B]	THR	3.7
1	3-D	86[C]	GLY	3.7
1	3-H	155[C]	ARG	3.7
1	3-P	67[C]	THR	3.7
1	4-D	86[D]	GLY	3.7
1	4-H	155[D]	ARG	3.7
1	4-P	67[D]	THR	3.7
1	1-I	188[A]	HIS	3.7
1	2-I	188[B]	HIS	3.7
1	3-I	188[C]	HIS	3.7
1	4-I	188[D]	HIS	3.7
1	1-A	317[A]	ALA	3.7
1	1-M	248[A]	GLU	3.7
1	1-O	298[A]	GLU	3.7
1	2-A	317[B]	ALA	3.7
1	2-M	248[B]	GLU	3.7
1	2-O	298[B]	GLU	3.7
1	1-N	152[A]	GLN	3.7
1	2-N	152[B]	GLN	3.7
1	3-A	317[C]	ALA	3.7
1	3-M	248[C]	GLU	3.7
1	3-O	298[C]	GLU	3.7
1	3-N	152[C]	GLN	3.7
1	4-A	317[D]	ALA	3.7
1	4-M	248[D]	GLU	3.7
1	4-O	298[D]	GLU	3.7
1	4-N	152[D]	GLN	3.7
1	1-B	263[A]	VAL	3.7
1	1-K	84[A]	VAL	3.7
1	2-B	263[B]	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	2-K	84[B]	VAL	3.7
1	3-B	263[C]	VAL	3.7
1	3-K	84[C]	VAL	3.7
1	4-B	263[D]	VAL	3.7
1	4-K	84[D]	VAL	3.7
1	1-L	207[A]	PRO	3.7
1	2-L	207[B]	PRO	3.7
1	3-L	207[C]	PRO	3.7
1	4-L	207[D]	PRO	3.7
1	1-K	155[A]	ARG	3.7
1	2-K	155[B]	ARG	3.7
1	3-K	155[C]	ARG	3.7
1	4-K	155[D]	ARG	3.7
1	1-C	32[A]	ASN	3.7
1	1-K	175[A]	ASN	3.7
1	1-L	77[A]	ILE	3.7
1	2-C	32[B]	ASN	3.7
1	2-K	175[B]	ASN	3.7
1	2-L	77[B]	ILE	3.7
1	3-C	32[C]	ASN	3.7
1	3-K	175[C]	ASN	3.7
1	3-L	77[C]	ILE	3.7
1	4-C	32[D]	ASN	3.7
1	4-K	175[D]	ASN	3.7
1	4-L	77[D]	ILE	3.7
1	1-L	299[A]	ASP	3.7
1	2-L	299[B]	ASP	3.7
1	3-L	299[C]	ASP	3.7
1	4-L	299[D]	ASP	3.7
1	1-H	26[A]	LEU	3.7
1	1-M	286[A]	LYS	3.7
1	2-H	26[B]	LEU	3.7
1	2-M	286[B]	LYS	3.7
1	3-H	26[C]	LEU	3.7
1	3-M	286[C]	LYS	3.7
1	4-H	26[D]	LEU	3.7
1	4-M	286[D]	LYS	3.7
1	1-B	95[A]	SER	3.7
1	1-K	40[A]	ARG	3.7
1	1-L	307[A]	PRO	3.7
1	1-N	168[A]	ARG	3.7
1	2-B	95[B]	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	2-K	40[B]	ARG	3.7
1	2-L	307[B]	PRO	3.7
1	2-N	168[B]	ARG	3.7
1	3-B	95[C]	SER	3.7
1	3-K	40[C]	ARG	3.7
1	3-L	307[C]	PRO	3.7
1	3-N	168[C]	ARG	3.7
1	4-B	95[D]	SER	3.7
1	4-K	40[D]	ARG	3.7
1	4-L	307[D]	PRO	3.7
1	4-N	168[D]	ARG	3.7
1	1-N	298[A]	GLU	3.7
1	1-P	287[A]	GLU	3.7
1	2-N	298[B]	GLU	3.7
1	2-P	287[B]	GLU	3.7
1	3-N	298[C]	GLU	3.7
1	3-P	287[C]	GLU	3.7
1	4-N	298[D]	GLU	3.7
1	4-P	287[D]	GLU	3.7
1	1-L	22[A]	GLN	3.6
1	2-L	22[B]	GLN	3.6
1	3-L	22[C]	GLN	3.6
1	4-L	22[D]	GLN	3.6
1	1-A	151[A]	ASP	3.6
1	1-I	166[A]	ASP	3.6
1	1-J	296[A]	LYS	3.6
1	1-P	89[A]	ASP	3.6
1	2-A	151[B]	ASP	3.6
1	2-I	166[B]	ASP	3.6
1	2-J	296[B]	LYS	3.6
1	2-P	89[B]	ASP	3.6
1	3-A	151[C]	ASP	3.6
1	3-I	166[C]	ASP	3.6
1	3-J	296[C]	LYS	3.6
1	3-P	89[C]	ASP	3.6
1	4-A	151[D]	ASP	3.6
1	4-I	166[D]	ASP	3.6
1	4-J	296[D]	LYS	3.6
1	4-P	89[D]	ASP	3.6
1	1-C	141[A]	ALA	3.6
1	1-M	239[A]	ALA	3.6
1	2-C	141[B]	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	2-M	239[B]	ALA	3.6
1	3-C	141[C]	ALA	3.6
1	3-M	239[C]	ALA	3.6
1	4-C	141[D]	ALA	3.6
1	4-M	239[D]	ALA	3.6
1	1-J	240[A]	LEU	3.6
1	1-M	176[A]	PRO	3.6
1	1-O	230[A]	SER	3.6
1	2-J	240[B]	LEU	3.6
1	2-M	176[B]	PRO	3.6
1	2-O	230[B]	SER	3.6
1	3-J	240[C]	LEU	3.6
1	3-M	176[C]	PRO	3.6
1	3-O	230[C]	SER	3.6
1	4-J	240[D]	LEU	3.6
1	4-M	176[D]	PRO	3.6
1	4-O	230[D]	SER	3.6
1	1-M	22[A]	GLN	3.6
1	2-M	22[B]	GLN	3.6
1	3-M	22[C]	GLN	3.6
1	4-M	22[D]	GLN	3.6
1	1-J	137[A]	GLU	3.6
1	1-O	157[A]	ILE	3.6
1	2-J	137[B]	GLU	3.6
1	2-O	157[B]	ILE	3.6
1	3-J	137[C]	GLU	3.6
1	3-O	157[C]	ILE	3.6
1	4-J	137[D]	GLU	3.6
1	4-O	157[D]	ILE	3.6
1	1-K	210[A]	SER	3.6
1	2-K	210[B]	SER	3.6
1	3-K	210[C]	SER	3.6
1	4-K	210[D]	SER	3.6
1	1-D	204[A]	GLY	3.6
1	2-D	204[B]	GLY	3.6
1	3-D	204[C]	GLY	3.6
1	4-D	204[D]	GLY	3.6
1	1-L	192[A]	GLN	3.6
1	1-M	104[A]	ASN	3.6
1	2-L	192[B]	GLN	3.6
1	2-M	104[B]	ASN	3.6
1	3-L	192[C]	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
1	3-M	104[C]	ASN	3.6
1	4-L	192[D]	GLN	3.6
1	4-M	104[D]	ASN	3.6
1	1-O	275[A]	ARG	3.6
1	2-O	275[B]	ARG	3.6
1	3-O	275[C]	ARG	3.6
1	4-O	275[D]	ARG	3.6
1	1-L	83[A]	PHE	3.6
1	2-L	83[B]	PHE	3.6
1	3-L	83[C]	PHE	3.6
1	4-L	83[D]	PHE	3.6
1	1-K	213[A]	MET	3.6
1	1-O	187[A]	CYS	3.6
1	2-K	213[B]	MET	3.6
1	2-O	187[B]	CYS	3.6
1	3-K	213[C]	MET	3.6
1	3-O	187[C]	CYS	3.6
1	4-K	213[D]	MET	3.6
1	4-O	187[D]	CYS	3.6
1	1-J	185[A]	PRO	3.6
1	2-J	185[B]	PRO	3.6
1	3-J	185[C]	PRO	3.6
1	4-J	185[D]	PRO	3.6
1	1-M	73[A]	LEU	3.6
1	1-O	272[A]	ARG	3.6
1	1-P	270[A]	LEU	3.6
1	2-M	73[B]	LEU	3.6
1	2-O	272[B]	ARG	3.6
1	2-P	270[B]	LEU	3.6
1	3-M	73[C]	LEU	3.6
1	3-O	272[C]	ARG	3.6
1	3-P	270[C]	LEU	3.6
1	4-M	73[D]	LEU	3.6
1	4-O	272[D]	ARG	3.6
1	4-P	270[D]	LEU	3.6
1	1-B	43[A]	THR	3.6
1	2-B	43[B]	THR	3.6
1	3-B	43[C]	THR	3.6
1	4-B	43[D]	THR	3.6
1	1-K	223[A]	GLY	3.6
1	2-K	223[B]	GLY	3.6
1	3-K	223[C]	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	4-K	223[D]	GLY	3.6
1	1-O	219[A]	ASP	3.6
1	1-B	155[A]	ARG	3.6
1	1-K	170[A]	ILE	3.6
1	2-O	219[B]	ASP	3.6
1	2-B	155[B]	ARG	3.6
1	2-K	170[B]	ILE	3.6
1	3-K	170[C]	ILE	3.6
1	3-O	219[C]	ASP	3.6
1	4-K	170[D]	ILE	3.6
1	4-O	219[D]	ASP	3.6
1	3-B	155[C]	ARG	3.6
1	4-B	155[D]	ARG	3.6
1	1-O	222[A]	LEU	3.6
1	2-O	222[B]	LEU	3.6
1	3-O	222[C]	LEU	3.6
1	4-O	222[D]	LEU	3.6
1	1-J	120[A]	GLU	3.6
1	2-J	120[B]	GLU	3.6
1	3-J	120[C]	GLU	3.6
1	4-J	120[D]	GLU	3.6
1	1-G	193[A]	PHE	3.6
1	1-J	226[A]	PHE	3.6
1	1-K	52[A]	PRO	3.6
1	1-O	216[A]	ARG	3.6
1	2-G	193[B]	PHE	3.6
1	2-J	226[B]	PHE	3.6
1	2-K	52[B]	PRO	3.6
1	2-O	216[B]	ARG	3.6
1	3-G	193[C]	PHE	3.6
1	3-J	226[C]	PHE	3.6
1	3-K	52[C]	PRO	3.6
1	3-O	216[C]	ARG	3.6
1	4-G	193[D]	PHE	3.6
1	4-J	226[D]	PHE	3.6
1	4-K	52[D]	PRO	3.6
1	4-O	216[D]	ARG	3.6
1	1-O	257[A]	HIS	3.6
1	2-O	257[B]	HIS	3.6
1	3-O	257[C]	HIS	3.6
1	4-O	257[D]	HIS	3.6
1	1-N	191[A]	CYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	2-N	191[B]	CYS	3.6
1	3-N	191[C]	CYS	3.6
1	4-N	191[D]	CYS	3.6
1	1-A	118[A]	ARG	3.6
1	1-E	309[A]	GLY	3.6
1	1-I	28[A]	ARG	3.6
1	1-I	290[A]	GLY	3.6
1	1-J	89[A]	ASP	3.6
1	2-A	118[B]	ARG	3.6
1	2-E	309[B]	GLY	3.6
1	2-I	28[B]	ARG	3.6
1	2-I	290[B]	GLY	3.6
1	2-J	89[B]	ASP	3.6
1	3-A	118[C]	ARG	3.6
1	3-E	309[C]	GLY	3.6
1	3-I	28[C]	ARG	3.6
1	3-I	290[C]	GLY	3.6
1	3-J	89[C]	ASP	3.6
1	4-A	118[D]	ARG	3.6
1	4-E	309[D]	GLY	3.6
1	4-I	28[D]	ARG	3.6
1	4-I	290[D]	GLY	3.6
1	4-J	89[D]	ASP	3.6
1	1-L	125[A]	PRO	3.6
1	2-L	125[B]	PRO	3.6
1	3-L	125[C]	PRO	3.6
1	4-L	125[D]	PRO	3.6
1	1-I	130[A]	GLN	3.5
1	2-I	130[B]	GLN	3.5
1	3-I	130[C]	GLN	3.5
1	4-I	130[D]	GLN	3.5
1	1-J	70[A]	ARG	3.5
1	1-N	32[A]	ASN	3.5
1	1-O	178[A]	ASP	3.5
1	2-J	70[B]	ARG	3.5
1	2-N	32[B]	ASN	3.5
1	2-O	178[B]	ASP	3.5
1	3-J	70[C]	ARG	3.5
1	3-N	32[C]	ASN	3.5
1	3-O	178[C]	ASP	3.5
1	4-J	70[D]	ARG	3.5
1	4-N	32[D]	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	4-O	178[D]	ASP	3.5
1	1-C	263[A]	VAL	3.5
1	2-C	263[B]	VAL	3.5
1	3-C	263[C]	VAL	3.5
1	4-C	263[D]	VAL	3.5
1	1-P	247[A]	HIS	3.5
1	2-P	247[B]	HIS	3.5
1	3-P	247[C]	HIS	3.5
1	4-P	247[D]	HIS	3.5
1	1-G	108[A]	GLU	3.5
1	1-K	269[A]	GLN	3.5
1	1-M	120[A]	GLU	3.5
1	2-G	108[B]	GLU	3.5
1	2-K	269[B]	GLN	3.5
1	2-M	120[B]	GLU	3.5
1	3-G	108[C]	GLU	3.5
1	3-K	269[C]	GLN	3.5
1	3-M	120[C]	GLU	3.5
1	4-G	108[D]	GLU	3.5
1	4-K	269[D]	GLN	3.5
1	4-M	120[D]	GLU	3.5
1	1-B	60[A]	ASP	3.5
1	1-D	162[A]	ASN	3.5
1	1-F	155[A]	ARG	3.5
1	1-H	15[A]	ASN	3.5
1	1-I	89[A]	ASP	3.5
1	1-J	216[A]	ARG	3.5
1	1-N	299[A]	ASP	3.5
1	2-B	60[B]	ASP	3.5
1	2-D	162[B]	ASN	3.5
1	2-F	155[B]	ARG	3.5
1	2-H	15[B]	ASN	3.5
1	2-I	89[B]	ASP	3.5
1	2-J	216[B]	ARG	3.5
1	2-N	299[B]	ASP	3.5
1	3-B	60[C]	ASP	3.5
1	3-D	162[C]	ASN	3.5
1	3-F	155[C]	ARG	3.5
1	3-H	15[C]	ASN	3.5
1	3-I	89[C]	ASP	3.5
1	3-J	216[C]	ARG	3.5
1	3-N	299[C]	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	4-B	60[D]	ASP	3.5
1	4-D	162[D]	ASN	3.5
1	4-F	155[D]	ARG	3.5
1	4-H	15[D]	ASN	3.5
1	4-I	89[D]	ASP	3.5
1	4-J	216[D]	ARG	3.5
1	4-N	299[D]	ASP	3.5
1	1-C	95[A]	SER	3.5
1	1-I	230[A]	SER	3.5
1	2-C	95[B]	SER	3.5
1	2-I	230[B]	SER	3.5
1	3-C	95[C]	SER	3.5
1	3-I	230[C]	SER	3.5
1	4-C	95[D]	SER	3.5
1	4-I	230[D]	SER	3.5
1	1-A	220[A]	LEU	3.5
1	1-L	123[A]	LEU	3.5
1	1-M	65[A]	LEU	3.5
1	2-A	220[B]	LEU	3.5
1	2-L	123[B]	LEU	3.5
1	2-M	65[B]	LEU	3.5
1	3-A	220[C]	LEU	3.5
1	3-L	123[C]	LEU	3.5
1	3-M	65[C]	LEU	3.5
1	4-A	220[D]	LEU	3.5
1	4-L	123[D]	LEU	3.5
1	4-M	65[D]	LEU	3.5
1	1-O	247[A]	HIS	3.5
1	2-O	247[B]	HIS	3.5
1	3-O	247[C]	HIS	3.5
1	4-O	247[D]	HIS	3.5
1	1-D	59[A]	ALA	3.5
1	2-D	59[B]	ALA	3.5
1	3-D	59[C]	ALA	3.5
1	4-D	59[D]	ALA	3.5
1	1-M	275[A]	ARG	3.5
1	2-M	275[B]	ARG	3.5
1	3-M	275[C]	ARG	3.5
1	4-M	275[D]	ARG	3.5
1	1-O	107[A]	LYS	3.5
1	2-O	107[B]	LYS	3.5
1	3-O	107[C]	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	4-O	107[D]	LYS	3.5
1	1-N	38[A]	PRO	3.5
1	2-N	38[B]	PRO	3.5
1	3-N	38[C]	PRO	3.5
1	4-N	38[D]	PRO	3.5
1	1-I	73[A]	LEU	3.5
1	2-I	73[B]	LEU	3.5
1	3-I	73[C]	LEU	3.5
1	4-I	73[D]	LEU	3.5
1	1-J	74[A]	ARG	3.5
1	1-J	112[A]	LYS	3.5
1	1-K	272[A]	ARG	3.5
1	2-J	74[B]	ARG	3.5
1	2-J	112[B]	LYS	3.5
1	2-K	272[B]	ARG	3.5
1	3-J	74[C]	ARG	3.5
1	3-J	112[C]	LYS	3.5
1	3-K	272[C]	ARG	3.5
1	4-J	74[D]	ARG	3.5
1	4-J	112[D]	LYS	3.5
1	4-K	272[D]	ARG	3.5
1	1-M	243[A]	ASP	3.5
1	2-M	243[B]	ASP	3.5
1	3-M	243[C]	ASP	3.5
1	4-M	243[D]	ASP	3.5
1	1-K	121[A]	GLY	3.5
1	1-L	106[A]	SER	3.5
1	2-K	121[B]	GLY	3.5
1	2-L	106[B]	SER	3.5
1	3-K	121[C]	GLY	3.5
1	3-L	106[C]	SER	3.5
1	4-K	121[D]	GLY	3.5
1	4-L	106[D]	SER	3.5
1	1-N	261[A]	ASP	3.5
1	2-N	261[B]	ASP	3.5
1	3-N	261[C]	ASP	3.5
1	4-N	261[D]	ASP	3.5
1	1-F	273[A]	GLU	3.5
1	1-N	20[A]	GLU	3.5
1	2-F	273[B]	GLU	3.5
1	2-N	20[B]	GLU	3.5
1	3-F	273[C]	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	3-N	20[C]	GLU	3.5
1	4-F	273[D]	GLU	3.5
1	4-N	20[D]	GLU	3.5
1	1-D	214[A]	TYR	3.5
1	1-F	308[A]	TRP	3.5
1	1-I	50[A]	ALA	3.5
1	2-D	214[B]	TYR	3.5
1	2-F	308[B]	TRP	3.5
1	2-I	50[B]	ALA	3.5
1	3-D	214[C]	TYR	3.5
1	3-F	308[C]	TRP	3.5
1	3-I	50[C]	ALA	3.5
1	4-D	214[D]	TYR	3.5
1	4-F	308[D]	TRP	3.5
1	4-I	50[D]	ALA	3.5
1	1-N	205[A]	SER	3.5
1	1-O	34[A]	GLY	3.5
1	2-N	205[B]	SER	3.5
1	2-O	34[B]	GLY	3.5
1	3-N	205[C]	SER	3.5
1	3-O	34[C]	GLY	3.5
1	4-N	205[D]	SER	3.5
1	4-O	34[D]	GLY	3.5
1	1-C	139[A]	THR	3.5
1	2-C	139[B]	THR	3.5
1	3-C	139[C]	THR	3.5
1	4-C	139[D]	THR	3.5
1	1-N	52[A]	PRO	3.5
1	1-N	246[A]	PRO	3.5
1	2-N	52[B]	PRO	3.5
1	2-N	246[B]	PRO	3.5
1	3-N	52[C]	PRO	3.5
1	3-N	246[C]	PRO	3.5
1	4-N	52[D]	PRO	3.5
1	4-N	246[D]	PRO	3.5
1	1-O	151[A]	ASP	3.5
1	2-O	151[B]	ASP	3.5
1	3-O	151[C]	ASP	3.5
1	4-O	151[D]	ASP	3.5
1	1-K	160[A]	ILE	3.5
1	2-K	160[B]	ILE	3.5
1	3-K	160[C]	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	4-K	160[D]	ILE	3.5
1	1-B	112[A]	LYS	3.5
1	1-J	107[A]	LYS	3.5
1	2-B	112[B]	LYS	3.5
1	2-J	107[B]	LYS	3.5
1	3-B	112[C]	LYS	3.5
1	3-J	107[C]	LYS	3.5
1	4-B	112[D]	LYS	3.5
1	4-J	107[D]	LYS	3.5
1	1-J	124[A]	GLY	3.5
1	2-J	124[B]	GLY	3.5
1	3-J	124[C]	GLY	3.5
1	4-J	124[D]	GLY	3.5
1	1-F	284[A]	ARG	3.5
1	2-F	284[B]	ARG	3.5
1	3-F	284[C]	ARG	3.5
1	4-F	284[D]	ARG	3.5
1	1-F	218[A]	CYS	3.4
1	2-F	218[B]	CYS	3.4
1	3-F	218[C]	CYS	3.4
1	4-F	218[D]	CYS	3.4
1	1-I	104[A]	ASN	3.4
1	2-I	104[B]	ASN	3.4
1	3-I	104[C]	ASN	3.4
1	4-I	104[D]	ASN	3.4
1	1-I	251[A]	LEU	3.4
1	2-I	251[B]	LEU	3.4
1	3-I	251[C]	LEU	3.4
1	4-I	251[D]	LEU	3.4
1	1-K	271[A]	GLU	3.4
1	1-P	20[A]	GLU	3.4
1	2-K	271[B]	GLU	3.4
1	2-P	20[B]	GLU	3.4
1	3-K	271[C]	GLU	3.4
1	3-P	20[C]	GLU	3.4
1	4-K	271[D]	GLU	3.4
1	4-P	20[D]	GLU	3.4
1	1-N	293[A]	ASP	3.4
1	2-N	293[B]	ASP	3.4
1	3-N	293[C]	ASP	3.4
1	4-N	293[D]	ASP	3.4
1	1-I	307[A]	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	2-I	307[B]	PRO	3.4
1	3-I	307[C]	PRO	3.4
1	4-I	307[D]	PRO	3.4
1	1-H	189[A]	MET	3.4
1	1-O	55[A]	ARG	3.4
1	1-P	288[A]	GLU	3.4
1	2-H	189[B]	MET	3.4
1	2-O	55[B]	ARG	3.4
1	2-P	288[B]	GLU	3.4
1	3-H	189[C]	MET	3.4
1	3-O	55[C]	ARG	3.4
1	3-P	288[C]	GLU	3.4
1	4-H	189[D]	MET	3.4
1	4-O	55[D]	ARG	3.4
1	4-P	288[D]	GLU	3.4
1	1-D	309[A]	GLY	3.4
1	1-L	290[A]	GLY	3.4
1	2-D	309[B]	GLY	3.4
1	2-L	290[B]	GLY	3.4
1	3-D	309[C]	GLY	3.4
1	3-L	290[C]	GLY	3.4
1	4-D	309[D]	GLY	3.4
1	4-L	290[D]	GLY	3.4
1	1-O	53[A]	SER	3.4
1	1-P	293[A]	ASP	3.4
1	2-O	53[B]	SER	3.4
1	2-P	293[B]	ASP	3.4
1	3-O	53[C]	SER	3.4
1	3-P	293[C]	ASP	3.4
1	4-O	53[D]	SER	3.4
1	4-P	293[D]	ASP	3.4
1	1-P	148[A]	LYS	3.4
1	2-P	148[B]	LYS	3.4
1	3-P	148[C]	LYS	3.4
1	4-P	148[D]	LYS	3.4
1	1-P	79[A]	GLU	3.4
1	2-P	79[B]	GLU	3.4
1	3-P	79[C]	GLU	3.4
1	4-P	79[D]	GLU	3.4
1	1-E	60[A]	ASP	3.4
1	1-J	97[A]	GLY	3.4
1	1-O	243[A]	ASP	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	2-E	60[B]	ASP	3.4
1	2-J	97[B]	GLY	3.4
1	2-O	243[B]	ASP	3.4
1	3-E	60[C]	ASP	3.4
1	3-J	97[C]	GLY	3.4
1	3-O	243[C]	ASP	3.4
1	4-E	60[D]	ASP	3.4
1	4-J	97[D]	GLY	3.4
1	4-O	243[D]	ASP	3.4
1	1-I	47[A]	ALA	3.4
1	2-I	47[B]	ALA	3.4
1	3-I	47[C]	ALA	3.4
1	4-I	47[D]	ALA	3.4
1	1-K	35[A]	GLU	3.4
1	2-K	35[B]	GLU	3.4
1	3-K	35[C]	GLU	3.4
1	4-K	35[D]	GLU	3.4
1	1-B	214[A]	TYR	3.4
1	2-B	214[B]	TYR	3.4
1	3-B	214[C]	TYR	3.4
1	4-B	214[D]	TYR	3.4
1	1-N	219[A]	ASP	3.4
1	2-N	219[B]	ASP	3.4
1	3-N	219[C]	ASP	3.4
1	4-N	219[D]	ASP	3.4
1	1-C	92[A]	MET	3.4
1	1-H	290[A]	GLY	3.4
1	1-M	128[A]	GLY	3.4
1	1-M	206[A]	LYS	3.4
1	1-N	103[A]	GLY	3.4
1	2-C	92[B]	MET	3.4
1	2-H	290[B]	GLY	3.4
1	2-M	128[B]	GLY	3.4
1	2-M	206[B]	LYS	3.4
1	2-N	103[B]	GLY	3.4
1	3-C	92[C]	MET	3.4
1	3-H	290[C]	GLY	3.4
1	3-M	128[C]	GLY	3.4
1	3-M	206[C]	LYS	3.4
1	3-N	103[C]	GLY	3.4
1	4-C	92[D]	MET	3.4
1	4-H	290[D]	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	4-M	128[D]	GLY	3.4
1	4-M	206[D]	LYS	3.4
1	4-N	103[D]	GLY	3.4
1	1-K	129[A]	PHE	3.4
1	2-K	129[B]	PHE	3.4
1	3-K	129[C]	PHE	3.4
1	4-K	129[D]	PHE	3.4
1	1-A	13[A]	ARG	3.4
1	1-L	115[A]	LEU	3.4
1	1-L	266[A]	LEU	3.4
1	2-A	13[B]	ARG	3.4
1	2-L	115[B]	LEU	3.4
1	2-L	266[B]	LEU	3.4
1	3-A	13[C]	ARG	3.4
1	3-L	115[C]	LEU	3.4
1	3-L	266[C]	LEU	3.4
1	4-A	13[D]	ARG	3.4
1	4-L	115[D]	LEU	3.4
1	4-L	266[D]	LEU	3.4
1	1-E	302[A]	VAL	3.4
1	2-E	302[B]	VAL	3.4
1	3-E	302[C]	VAL	3.4
1	4-E	302[D]	VAL	3.4
1	1-D	202[A]	SER	3.4
1	1-J	104[A]	ASN	3.4
1	2-D	202[B]	SER	3.4
1	2-J	104[B]	ASN	3.4
1	3-D	202[C]	SER	3.4
1	3-J	104[C]	ASN	3.4
1	4-D	202[D]	SER	3.4
1	4-J	104[D]	ASN	3.4
1	1-K	136[A]	ALA	3.4
1	1-N	74[A]	ARG	3.4
1	2-K	136[B]	ALA	3.4
1	2-N	74[B]	ARG	3.4
1	3-K	136[C]	ALA	3.4
1	3-N	74[C]	ARG	3.4
1	4-K	136[D]	ALA	3.4
1	4-N	74[D]	ARG	3.4
1	1-D	267[A]	LYS	3.4
1	1-N	177[A]	LYS	3.4
1	2-D	267[B]	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	2-N	177[B]	LYS	3.4
1	3-D	267[C]	LYS	3.4
1	3-N	177[C]	LYS	3.4
1	4-D	267[D]	LYS	3.4
1	4-N	177[D]	LYS	3.4
1	1-D	15[A]	ASN	3.3
1	1-I	217[A]	SER	3.3
1	2-D	15[B]	ASN	3.3
1	2-I	217[B]	SER	3.3
1	3-D	15[C]	ASN	3.3
1	3-I	217[C]	SER	3.3
1	4-D	15[D]	ASN	3.3
1	4-I	217[D]	SER	3.3
1	1-L	185[A]	PRO	3.3
1	2-L	185[B]	PRO	3.3
1	3-L	185[C]	PRO	3.3
1	4-L	185[D]	PRO	3.3
1	1-E	287[A]	GLU	3.3
1	1-N	273[A]	GLU	3.3
1	2-E	287[B]	GLU	3.3
1	2-N	273[B]	GLU	3.3
1	3-E	287[C]	GLU	3.3
1	3-N	273[C]	GLU	3.3
1	4-E	287[D]	GLU	3.3
1	4-N	273[D]	GLU	3.3
1	1-E	63[A]	LEU	3.3
1	1-G	115[A]	LEU	3.3
1	2-E	63[B]	LEU	3.3
1	2-G	115[B]	LEU	3.3
1	3-E	63[C]	LEU	3.3
1	3-G	115[C]	LEU	3.3
1	4-E	63[D]	LEU	3.3
1	4-G	115[D]	LEU	3.3
1	1-A	135[A]	GLY	3.3
1	1-M	221[A]	GLY	3.3
1	2-A	135[B]	GLY	3.3
1	2-M	221[B]	GLY	3.3
1	3-A	135[C]	GLY	3.3
1	3-M	221[C]	GLY	3.3
1	4-A	135[D]	GLY	3.3
1	4-M	221[D]	GLY	3.3
1	1-A	21[A]	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	1-A	271[A]	GLU	3.3
1	1-J	25[A]	ASP	3.3
1	2-A	21[B]	TYR	3.3
1	2-A	271[B]	GLU	3.3
1	2-J	25[B]	ASP	3.3
1	3-A	21[C]	TYR	3.3
1	3-A	271[C]	GLU	3.3
1	3-J	25[C]	ASP	3.3
1	4-A	21[D]	TYR	3.3
1	4-A	271[D]	GLU	3.3
1	4-J	25[D]	ASP	3.3
1	1-K	185[A]	PRO	3.3
1	2-K	185[B]	PRO	3.3
1	3-K	185[C]	PRO	3.3
1	4-K	185[D]	PRO	3.3
1	1-I	72[A]	PHE	3.3
1	2-I	72[B]	PHE	3.3
1	3-I	72[C]	PHE	3.3
1	4-I	72[D]	PHE	3.3
1	1-F	97[A]	GLY	3.3
1	1-J	37[A]	ARG	3.3
1	1-L	157[A]	ILE	3.3
1	1-M	244[A]	THR	3.3
1	2-F	97[B]	GLY	3.3
1	2-J	37[B]	ARG	3.3
1	2-L	157[B]	ILE	3.3
1	2-M	244[B]	THR	3.3
1	3-F	97[C]	GLY	3.3
1	3-J	37[C]	ARG	3.3
1	3-L	157[C]	ILE	3.3
1	3-M	244[C]	THR	3.3
1	4-F	97[D]	GLY	3.3
1	4-J	37[D]	ARG	3.3
1	4-L	157[D]	ILE	3.3
1	4-M	244[D]	THR	3.3
1	1-O	208[A]	LYS	3.3
1	2-O	208[B]	LYS	3.3
1	3-O	208[C]	LYS	3.3
1	4-O	208[D]	LYS	3.3
1	1-N	189[A]	MET	3.3
1	2-N	189[B]	MET	3.3
1	3-N	189[C]	MET	3.3

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Mol	Chain	Res	Type	RSRZ
1	4-N	189[D]	MET	3.3
1	1-H	142[A]	ASP	3.3
1	1-I	158[A]	ASP	3.3
1	1-N	312[A]	ASP	3.3
1	2-H	142[B]	ASP	3.3
1	2-I	158[B]	ASP	3.3
1	2-N	312[B]	ASP	3.3
1	3-H	142[C]	ASP	3.3
1	3-I	158[C]	ASP	3.3
1	3-N	312[C]	ASP	3.3
1	4-H	142[D]	ASP	3.3
1	4-I	158[D]	ASP	3.3
1	4-N	312[D]	ASP	3.3
1	1-N	105[A]	GLY	3.3
1	1-N	149[A]	GLY	3.3
1	2-N	105[B]	GLY	3.3
1	2-N	149[B]	GLY	3.3
1	3-N	105[C]	GLY	3.3
1	3-N	149[C]	GLY	3.3
1	4-N	105[D]	GLY	3.3
1	4-N	149[D]	GLY	3.3
1	1-I	20[A]	GLU	3.3
1	1-L	298[A]	GLU	3.3
1	1-P	120[A]	GLU	3.3
1	2-I	20[B]	GLU	3.3
1	2-L	298[B]	GLU	3.3
1	2-P	120[B]	GLU	3.3
1	3-I	20[C]	GLU	3.3
1	3-L	298[C]	GLU	3.3
1	3-P	120[C]	GLU	3.3
1	4-I	20[D]	GLU	3.3
1	4-L	298[D]	GLU	3.3
1	4-P	120[D]	GLU	3.3
1	1-N	40[A]	ARG	3.3
1	2-N	40[B]	ARG	3.3
1	3-N	40[C]	ARG	3.3
1	4-N	40[D]	ARG	3.3
1	1-J	163[A]	ASN	3.3
1	2-J	163[B]	ASN	3.3
1	3-J	163[C]	ASN	3.3
1	4-J	163[D]	ASN	3.3
1	1-B	276[A]	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	1-F	268[A]	THR	3.3
1	1-N	45[A]	THR	3.3
1	1-N	102[A]	ASP	3.3
1	2-B	276[B]	ASP	3.3
1	2-F	268[B]	THR	3.3
1	2-N	45[B]	THR	3.3
1	2-N	102[B]	ASP	3.3
1	3-B	276[C]	ASP	3.3
1	3-F	268[C]	THR	3.3
1	3-N	45[C]	THR	3.3
1	3-N	102[C]	ASP	3.3
1	4-B	276[D]	ASP	3.3
1	4-F	268[D]	THR	3.3
1	4-N	45[D]	THR	3.3
1	4-N	102[D]	ASP	3.3
1	1-E	47[A]	ALA	3.3
1	2-E	47[B]	ALA	3.3
1	3-E	47[C]	ALA	3.3
1	4-E	47[D]	ALA	3.3
1	1-I	192[A]	GLN	3.3
1	1-N	192[A]	GLN	3.3
1	2-I	192[B]	GLN	3.3
1	2-N	192[B]	GLN	3.3
1	3-I	192[C]	GLN	3.3
1	3-N	192[C]	GLN	3.3
1	4-I	192[D]	GLN	3.3
1	4-N	192[D]	GLN	3.3
1	1-F	49[A]	PHE	3.3
1	2-F	49[B]	PHE	3.3
1	3-F	49[C]	PHE	3.3
1	4-F	49[D]	PHE	3.3
1	1-G	184[A]	LEU	3.3
1	2-G	184[B]	LEU	3.3
1	3-G	184[C]	LEU	3.3
1	4-G	184[D]	LEU	3.3
1	1-B	64[A]	PRO	3.3
1	2-B	64[B]	PRO	3.3
1	3-B	64[C]	PRO	3.3
1	4-B	64[D]	PRO	3.3
1	1-N	304[A]	GLY	3.2
1	2-N	304[B]	GLY	3.2
1	3-N	304[C]	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	4-N	304[D]	GLY	3.2
1	1-N	146[A]	LYS	3.2
1	2-N	146[B]	LYS	3.2
1	3-N	146[C]	LYS	3.2
1	4-N	146[D]	LYS	3.2
1	1-L	285[A]	SER	3.2
1	2-L	285[B]	SER	3.2
1	3-L	285[C]	SER	3.2
1	4-L	285[D]	SER	3.2
1	1-O	20[A]	GLU	3.2
1	2-O	20[B]	GLU	3.2
1	3-O	20[C]	GLU	3.2
1	4-O	20[D]	GLU	3.2
1	1-K	208[A]	LYS	3.2
1	2-K	208[B]	LYS	3.2
1	3-K	208[C]	LYS	3.2
1	4-K	208[D]	LYS	3.2
1	1-I	215[A]	GLN	3.2
1	1-N	294[A]	GLY	3.2
1	2-I	215[B]	GLN	3.2
1	2-N	294[B]	GLY	3.2
1	3-I	215[C]	GLN	3.2
1	3-N	294[C]	GLY	3.2
1	4-I	215[D]	GLN	3.2
1	4-N	294[D]	GLY	3.2
1	1-E	137[A]	GLU	3.2
1	1-I	245[A]	GLU	3.2
1	1-J	35[A]	GLU	3.2
1	2-E	137[B]	GLU	3.2
1	2-I	245[B]	GLU	3.2
1	2-J	35[B]	GLU	3.2
1	3-E	137[C]	GLU	3.2
1	3-I	245[C]	GLU	3.2
1	3-J	35[C]	GLU	3.2
1	4-E	137[D]	GLU	3.2
1	4-I	245[D]	GLU	3.2
1	4-J	35[D]	GLU	3.2
1	1-P	210[A]	SER	3.2
1	2-P	210[B]	SER	3.2
1	3-P	210[C]	SER	3.2
1	4-P	210[D]	SER	3.2
1	1-J	41[A]	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	2-J	41[B]	THR	3.2
1	3-J	41[C]	THR	3.2
1	4-J	41[D]	THR	3.2
1	1-C	197[A]	LEU	3.2
1	1-I	147[A]	GLY	3.2
1	1-M	123[A]	LEU	3.2
1	1-N	135[A]	GLY	3.2
1	2-C	197[B]	LEU	3.2
1	2-I	147[B]	GLY	3.2
1	2-M	123[B]	LEU	3.2
1	2-N	135[B]	GLY	3.2
1	3-C	197[C]	LEU	3.2
1	3-I	147[C]	GLY	3.2
1	3-M	123[C]	LEU	3.2
1	3-N	135[C]	GLY	3.2
1	4-C	197[D]	LEU	3.2
1	4-I	147[D]	GLY	3.2
1	4-M	123[D]	LEU	3.2
1	4-N	135[D]	GLY	3.2
1	1-O	132[A]	ARG	3.2
1	2-O	132[B]	ARG	3.2
1	3-O	132[C]	ARG	3.2
1	4-O	132[D]	ARG	3.2
1	1-H	14[A]	SER	3.2
1	2-H	14[B]	SER	3.2
1	3-H	14[C]	SER	3.2
1	4-H	14[D]	SER	3.2
1	1-A	107[A]	LYS	3.2
1	1-F	146[A]	LYS	3.2
1	1-K	41[A]	THR	3.2
1	2-A	107[B]	LYS	3.2
1	2-F	146[B]	LYS	3.2
1	2-K	41[B]	THR	3.2
1	3-A	107[C]	LYS	3.2
1	3-F	146[C]	LYS	3.2
1	3-K	41[C]	THR	3.2
1	4-A	107[D]	LYS	3.2
1	4-F	146[D]	LYS	3.2
1	4-K	41[D]	THR	3.2
1	1-L	86[A]	GLY	3.2
1	2-L	86[B]	GLY	3.2
1	3-L	86[C]	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	4-L	86[D]	GLY	3.2
1	1-D	277[A]	PHE	3.2
1	1-H	54[A]	PHE	3.2
1	1-J	72[A]	PHE	3.2
1	1-K	280[A]	LEU	3.2
1	2-D	277[B]	PHE	3.2
1	2-H	54[B]	PHE	3.2
1	2-J	72[B]	PHE	3.2
1	1-J	87[A]	CYS	3.2
1	1-J	218[A]	CYS	3.2
1	1-L	27[A]	ILE	3.2
1	2-K	280[B]	LEU	3.2
1	3-D	277[C]	PHE	3.2
1	3-H	54[C]	PHE	3.2
1	3-J	72[C]	PHE	3.2
1	3-K	280[C]	LEU	3.2
1	4-D	277[D]	PHE	3.2
1	4-H	54[D]	PHE	3.2
1	4-J	72[D]	PHE	3.2
1	2-J	87[B]	CYS	3.2
1	2-J	218[B]	CYS	3.2
1	2-L	27[B]	ILE	3.2
1	3-J	87[C]	CYS	3.2
1	3-J	218[C]	CYS	3.2
1	3-L	27[C]	ILE	3.2
1	4-K	280[D]	LEU	3.2
1	4-J	87[D]	CYS	3.2
1	4-J	218[D]	CYS	3.2
1	4-L	27[D]	ILE	3.2
1	1-D	203[A]	PRO	3.2
1	1-F	260[A]	ARG	3.2
1	1-M	216[A]	ARG	3.2
1	2-D	203[B]	PRO	3.2
1	2-F	260[B]	ARG	3.2
1	2-M	216[B]	ARG	3.2
1	3-D	203[C]	PRO	3.2
1	3-F	260[C]	ARG	3.2
1	3-M	216[C]	ARG	3.2
1	4-D	203[D]	PRO	3.2
1	4-F	260[D]	ARG	3.2
1	4-M	216[D]	ARG	3.2
1	1-P	69[A]	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	1-P	296[A]	LYS	3.2
1	2-P	69[B]	LYS	3.2
1	2-P	296[B]	LYS	3.2
1	3-P	69[C]	LYS	3.2
1	3-P	296[C]	LYS	3.2
1	4-P	69[D]	LYS	3.2
1	4-P	296[D]	LYS	3.2
1	1-A	95[A]	SER	3.2
1	2-A	95[B]	SER	3.2
1	3-A	95[C]	SER	3.2
1	4-A	95[D]	SER	3.2
1	1-N	151[A]	ASP	3.2
1	2-N	151[B]	ASP	3.2
1	3-N	151[C]	ASP	3.2
1	4-N	151[D]	ASP	3.2
1	1-O	87[A]	CYS	3.2
1	2-O	87[B]	CYS	3.2
1	3-O	87[C]	CYS	3.2
1	4-O	87[D]	CYS	3.2
1	1-D	70[A]	ARG	3.2
1	2-D	70[B]	ARG	3.2
1	3-D	70[C]	ARG	3.2
1	4-D	70[D]	ARG	3.2
1	1-I	44[A]	GLY	3.2
1	1-P	149[A]	GLY	3.2
1	1-P	254[A]	GLY	3.2
1	2-I	44[B]	GLY	3.2
1	2-P	149[B]	GLY	3.2
1	2-P	254[B]	GLY	3.2
1	3-I	44[C]	GLY	3.2
1	3-P	149[C]	GLY	3.2
1	3-P	254[C]	GLY	3.2
1	4-I	44[D]	GLY	3.2
1	4-P	149[D]	GLY	3.2
1	4-P	254[D]	GLY	3.2
1	1-C	59[A]	ALA	3.2
1	1-M	166[A]	ASP	3.2
1	2-C	59[B]	ALA	3.2
1	2-M	166[B]	ASP	3.2
1	3-C	59[C]	ALA	3.2
1	3-M	166[C]	ASP	3.2
1	4-C	59[D]	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	4-M	166[D]	ASP	3.2
1	1-O	233[A]	LEU	3.2
1	2-O	233[B]	LEU	3.2
1	3-O	233[C]	LEU	3.2
1	4-O	233[D]	LEU	3.2
1	1-A	131[A]	TRP	3.2
1	1-D	282[A]	TRP	3.2
1	2-A	131[B]	TRP	3.2
1	2-D	282[B]	TRP	3.2
1	3-A	131[C]	TRP	3.2
1	3-D	282[C]	TRP	3.2
1	4-A	131[D]	TRP	3.2
1	4-D	282[D]	TRP	3.2
1	1-B	38[A]	PRO	3.1
1	1-C	290[A]	GLY	3.1
1	1-D	176[A]	PRO	3.1
1	2-B	38[B]	PRO	3.1
1	2-C	290[B]	GLY	3.1
1	2-D	176[B]	PRO	3.1
1	3-B	38[C]	PRO	3.1
1	3-C	290[C]	GLY	3.1
1	3-D	176[C]	PRO	3.1
1	4-B	38[D]	PRO	3.1
1	4-C	290[D]	GLY	3.1
1	4-D	176[D]	PRO	3.1
1	1-L	133[A]	HIS	3.1
1	2-L	133[B]	HIS	3.1
1	3-L	133[C]	HIS	3.1
1	4-L	133[D]	HIS	3.1
1	1-M	152[A]	GLN	3.1
1	1-P	85[A]	SER	3.1
1	2-M	152[B]	GLN	3.1
1	2-P	85[B]	SER	3.1
1	3-M	152[C]	GLN	3.1
1	3-P	85[C]	SER	3.1
1	4-M	152[D]	GLN	3.1
1	4-P	85[D]	SER	3.1
1	1-H	200[A]	ALA	3.1
1	1-H	260[A]	ARG	3.1
1	1-J	132[A]	ARG	3.1
1	2-H	200[B]	ALA	3.1
1	2-H	260[B]	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	2-J	132[B]	ARG	3.1
1	3-H	200[C]	ALA	3.1
1	3-H	260[C]	ARG	3.1
1	3-J	132[C]	ARG	3.1
1	4-H	200[D]	ALA	3.1
1	4-H	260[D]	ARG	3.1
1	4-J	132[D]	ARG	3.1
1	1-A	112[A]	LYS	3.1
1	1-K	279[A]	LYS	3.1
1	1-M	281[A]	LYS	3.1
1	2-A	112[B]	LYS	3.1
1	2-K	279[B]	LYS	3.1
1	2-M	281[B]	LYS	3.1
1	3-A	112[C]	LYS	3.1
1	3-K	279[C]	LYS	3.1
1	3-M	281[C]	LYS	3.1
1	4-A	112[D]	LYS	3.1
1	4-K	279[D]	LYS	3.1
1	4-M	281[D]	LYS	3.1
1	1-O	305[A]	TYR	3.1
1	2-O	305[B]	TYR	3.1
1	3-O	305[C]	TYR	3.1
1	4-O	305[D]	TYR	3.1
1	1-H	249[A]	PHE	3.1
1	2-H	249[B]	PHE	3.1
1	3-H	249[C]	PHE	3.1
1	4-H	249[D]	PHE	3.1
1	1-A	38[A]	PRO	3.1
1	1-M	46[A]	VAL	3.1
1	2-A	38[B]	PRO	3.1
1	2-M	46[B]	VAL	3.1
1	3-A	38[C]	PRO	3.1
1	3-M	46[C]	VAL	3.1
1	4-A	38[D]	PRO	3.1
1	4-M	46[D]	VAL	3.1
1	1-C	315[A]	MET	3.1
1	1-O	215[A]	GLN	3.1
1	2-C	315[B]	MET	3.1
1	2-O	215[B]	GLN	3.1
1	3-C	315[C]	MET	3.1
1	3-O	215[C]	GLN	3.1
1	4-C	315[D]	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	4-O	215[D]	GLN	3.1
1	1-F	144[A]	ASP	3.1
1	2-F	144[B]	ASP	3.1
1	3-F	144[C]	ASP	3.1
1	4-F	144[D]	ASP	3.1
1	1-B	260[A]	ARG	3.1
1	1-M	148[A]	LYS	3.1
1	2-B	260[B]	ARG	3.1
1	2-M	148[B]	LYS	3.1
1	3-B	260[C]	ARG	3.1
1	3-M	148[C]	LYS	3.1
1	4-B	260[D]	ARG	3.1
1	4-M	148[D]	LYS	3.1
1	1-H	283[A]	ALA	3.1
1	1-H	317[A]	ALA	3.1
1	1-M	229[A]	ALA	3.1
1	2-H	283[B]	ALA	3.1
1	2-H	317[B]	ALA	3.1
1	2-M	229[B]	ALA	3.1
1	3-H	283[C]	ALA	3.1
1	3-H	317[C]	ALA	3.1
1	3-M	229[C]	ALA	3.1
1	4-H	283[D]	ALA	3.1
1	4-H	317[D]	ALA	3.1
1	4-M	229[D]	ALA	3.1
1	1-A	43[A]	THR	3.1
1	1-B	147[A]	GLY	3.1
1	2-A	43[B]	THR	3.1
1	2-B	147[B]	GLY	3.1
1	3-A	43[C]	THR	3.1
1	3-B	147[C]	GLY	3.1
1	4-A	43[D]	THR	3.1
1	4-B	147[D]	GLY	3.1
1	1-K	281[A]	LYS	3.1
1	2-K	281[B]	LYS	3.1
1	3-K	281[C]	LYS	3.1
1	4-K	281[D]	LYS	3.1
1	1-E	283[A]	ALA	3.1
1	1-M	211[A]	CYS	3.1
1	2-E	283[B]	ALA	3.1
1	2-M	211[B]	CYS	3.1
1	3-E	283[C]	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	3-M	211[C]	CYS	3.1
1	4-E	283[D]	ALA	3.1
1	4-M	211[D]	CYS	3.1
1	1-O	128[A]	GLY	3.1
1	2-O	128[B]	GLY	3.1
1	3-O	128[C]	GLY	3.1
1	4-O	128[D]	GLY	3.1
1	1-K	303[A]	GLU	3.1
1	1-M	111[A]	GLU	3.1
1	2-K	303[B]	GLU	3.1
1	2-M	111[B]	GLU	3.1
1	3-K	303[C]	GLU	3.1
1	3-M	111[C]	GLU	3.1
1	4-K	303[D]	GLU	3.1
1	4-M	111[D]	GLU	3.1
1	1-E	23[A]	TYR	3.1
1	2-E	23[B]	TYR	3.1
1	3-E	23[C]	TYR	3.1
1	4-E	23[D]	TYR	3.1
1	1-J	76[A]	VAL	3.1
1	1-L	84[A]	VAL	3.1
1	2-J	76[B]	VAL	3.1
1	2-L	84[B]	VAL	3.1
1	3-J	76[C]	VAL	3.1
1	3-L	84[C]	VAL	3.1
1	4-J	76[D]	VAL	3.1
1	4-L	84[D]	VAL	3.1
1	1-C	174[A]	TRP	3.1
1	2-C	174[B]	TRP	3.1
1	3-C	174[C]	TRP	3.1
1	4-C	174[D]	TRP	3.1
1	1-P	286[A]	LYS	3.1
1	2-P	286[B]	LYS	3.1
1	3-P	286[C]	LYS	3.1
1	4-P	286[D]	LYS	3.1
1	1-B	70[A]	ARG	3.1
1	1-O	35[A]	GLU	3.1
1	1-P	25[A]	ASP	3.1
1	1-D	18[A]	HIS	3.1
1	1-F	70[A]	ARG	3.1
1	2-B	70[B]	ARG	3.1
1	2-O	35[B]	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	2-P	25[B]	ASP	3.1
1	2-D	18[B]	HIS	3.1
1	2-F	70[B]	ARG	3.1
1	3-B	70[C]	ARG	3.1
1	3-O	35[C]	GLU	3.1
1	3-P	25[C]	ASP	3.1
1	3-D	18[C]	HIS	3.1
1	3-F	70[C]	ARG	3.1
1	4-B	70[D]	ARG	3.1
1	4-D	18[D]	HIS	3.1
1	4-F	70[D]	ARG	3.1
1	4-O	35[D]	GLU	3.1
1	4-P	25[D]	ASP	3.1
1	1-P	171[A]	LEU	3.1
1	2-P	171[B]	LEU	3.1
1	3-P	171[C]	LEU	3.1
1	4-P	171[D]	LEU	3.1
1	1-E	193[A]	PHE	3.1
1	1-H	295[A]	PHE	3.1
1	1-N	134[A]	PHE	3.1
1	2-E	193[B]	PHE	3.1
1	2-H	295[B]	PHE	3.1
1	2-N	134[B]	PHE	3.1
1	3-E	193[C]	PHE	3.1
1	3-H	295[C]	PHE	3.1
1	3-N	134[C]	PHE	3.1
1	4-E	193[D]	PHE	3.1
1	4-H	295[D]	PHE	3.1
1	4-N	134[D]	PHE	3.1
1	1-L	286[A]	LYS	3.1
1	2-L	286[B]	LYS	3.1
1	3-L	286[C]	LYS	3.1
1	4-L	286[D]	LYS	3.1
1	1-L	141[A]	ALA	3.1
1	2-L	141[B]	ALA	3.1
1	3-L	141[C]	ALA	3.1
1	4-L	141[D]	ALA	3.1
1	1-B	246[A]	PRO	3.1
1	2-B	246[B]	PRO	3.1
1	3-B	246[C]	PRO	3.1
1	4-B	246[D]	PRO	3.1
1	1-K	192[A]	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	2-K	192[B]	GLN	3.1
1	3-K	192[C]	GLN	3.1
1	4-K	192[D]	GLN	3.1
1	1-C	312[A]	ASP	3.1
1	1-N	72[A]	PHE	3.1
1	2-C	312[B]	ASP	3.1
1	2-N	72[B]	PHE	3.1
1	3-C	312[C]	ASP	3.1
1	3-N	72[C]	PHE	3.1
1	4-C	312[D]	ASP	3.1
1	4-N	72[D]	PHE	3.1
1	1-J	223[A]	GLY	3.0
1	2-J	223[B]	GLY	3.0
1	3-J	223[C]	GLY	3.0
1	4-J	223[D]	GLY	3.0
1	1-O	310[A]	LYS	3.0
1	2-O	310[B]	LYS	3.0
1	3-O	310[C]	LYS	3.0
1	4-O	310[D]	LYS	3.0
1	1-K	130[A]	GLN	3.0
1	1-O	165[A]	THR	3.0
1	2-K	130[B]	GLN	3.0
1	2-O	165[B]	THR	3.0
1	3-K	130[C]	GLN	3.0
1	3-O	165[C]	THR	3.0
1	4-K	130[D]	GLN	3.0
1	4-O	165[D]	THR	3.0
1	1-B	13[A]	ARG	3.0
1	2-B	13[B]	ARG	3.0
1	3-B	13[C]	ARG	3.0
1	4-B	13[D]	ARG	3.0
1	1-H	266[A]	LEU	3.0
1	2-H	266[B]	LEU	3.0
1	3-H	266[C]	LEU	3.0
1	4-H	266[D]	LEU	3.0
1	1-F	15[A]	ASN	3.0
1	1-L	61[A]	ASN	3.0
1	1-D	116[A]	GLY	3.0
1	1-E	98[A]	VAL	3.0
1	1-M	277[A]	PHE	3.0
1	2-F	15[B]	ASN	3.0
1	2-L	61[B]	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	1-N	297[A]	VAL	3.0
1	2-D	116[B]	GLY	3.0
1	2-E	98[B]	VAL	3.0
1	2-M	277[B]	PHE	3.0
1	3-F	15[C]	ASN	3.0
1	3-L	61[C]	ASN	3.0
1	3-D	116[C]	GLY	3.0
1	3-E	98[C]	VAL	3.0
1	3-M	277[C]	PHE	3.0
1	4-F	15[D]	ASN	3.0
1	4-L	61[D]	ASN	3.0
1	2-N	297[B]	VAL	3.0
1	3-N	297[C]	VAL	3.0
1	4-D	116[D]	GLY	3.0
1	4-E	98[D]	VAL	3.0
1	4-M	277[D]	PHE	3.0
1	4-N	297[D]	VAL	3.0
1	1-B	176[A]	PRO	3.0
1	1-I	264[A]	GLU	3.0
1	1-O	180[A]	PRO	3.0
1	2-B	176[B]	PRO	3.0
1	2-I	264[B]	GLU	3.0
1	2-O	180[B]	PRO	3.0
1	3-B	176[C]	PRO	3.0
1	3-I	264[C]	GLU	3.0
1	3-O	180[C]	PRO	3.0
1	4-B	176[D]	PRO	3.0
1	4-I	264[D]	GLU	3.0
1	4-O	180[D]	PRO	3.0
1	1-L	85[A]	SER	3.0
1	2-L	85[B]	SER	3.0
1	3-L	85[C]	SER	3.0
1	4-L	85[D]	SER	3.0
1	1-A	140[A]	ASP	3.0
1	2-A	140[B]	ASP	3.0
1	3-A	140[C]	ASP	3.0
1	4-A	140[D]	ASP	3.0
1	1-G	308[A]	TRP	3.0
1	1-L	93[A]	LEU	3.0
1	1-L	267[A]	LYS	3.0
1	2-G	308[B]	TRP	3.0
1	2-L	93[B]	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	2-L	267[B]	LYS	3.0
1	3-G	308[C]	TRP	3.0
1	3-L	93[C]	LEU	3.0
1	3-L	267[C]	LYS	3.0
1	4-G	308[D]	TRP	3.0
1	4-L	93[D]	LEU	3.0
1	4-L	267[D]	LYS	3.0
1	1-A	106[A]	SER	3.0
1	2-A	106[B]	SER	3.0
1	3-A	106[C]	SER	3.0
1	4-A	106[D]	SER	3.0
1	1-M	159[A]	THR	3.0
1	2-M	159[B]	THR	3.0
1	3-M	159[C]	THR	3.0
1	4-M	159[D]	THR	3.0
1	1-L	69[A]	LYS	3.0
1	1-O	206[A]	LYS	3.0
1	2-L	69[B]	LYS	3.0
1	2-O	206[B]	LYS	3.0
1	3-L	69[C]	LYS	3.0
1	3-O	206[C]	LYS	3.0
1	4-L	69[D]	LYS	3.0
1	4-O	206[D]	LYS	3.0
1	1-G	15[A]	ASN	3.0
1	1-P	245[A]	GLU	3.0
1	2-G	15[B]	ASN	3.0
1	2-P	245[B]	GLU	3.0
1	3-G	15[C]	ASN	3.0
1	3-P	245[C]	GLU	3.0
1	4-G	15[D]	ASN	3.0
1	4-P	245[D]	GLU	3.0
1	1-A	114[A]	GLY	3.0
1	2-A	114[B]	GLY	3.0
1	3-A	114[C]	GLY	3.0
1	4-A	114[D]	GLY	3.0
1	1-P	284[A]	ARG	3.0
1	2-P	284[B]	ARG	3.0
1	3-P	284[C]	ARG	3.0
1	4-P	284[D]	ARG	3.0
1	1-O	144[A]	ASP	3.0
1	2-O	144[B]	ASP	3.0
1	3-O	144[C]	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	4-O	144[D]	ASP	3.0
1	1-B	134[A]	PHE	3.0
1	2-B	134[B]	PHE	3.0
1	3-B	134[C]	PHE	3.0
1	4-B	134[D]	PHE	3.0
1	1-F	187[A]	CYS	3.0
1	2-F	187[B]	CYS	3.0
1	3-F	187[C]	CYS	3.0
1	4-F	187[D]	CYS	3.0
1	1-K	215[A]	GLN	3.0
1	1-P	309[A]	GLY	3.0
1	2-K	215[B]	GLN	3.0
1	2-P	309[B]	GLY	3.0
1	3-K	215[C]	GLN	3.0
1	3-P	309[C]	GLY	3.0
1	4-K	215[D]	GLN	3.0
1	4-P	309[D]	GLY	3.0
1	1-C	55[A]	ARG	3.0
1	1-N	284[A]	ARG	3.0
1	2-C	55[B]	ARG	3.0
1	2-N	284[B]	ARG	3.0
1	3-C	55[C]	ARG	3.0
1	3-N	284[C]	ARG	3.0
1	4-C	55[D]	ARG	3.0
1	4-N	284[D]	ARG	3.0
1	1-D	212[A]	LEU	3.0
1	1-D	310[A]	LYS	3.0
1	1-H	279[A]	LYS	3.0
1	1-M	161[A]	LYS	3.0
1	2-D	212[B]	LEU	3.0
1	2-D	310[B]	LYS	3.0
1	2-H	279[B]	LYS	3.0
1	2-M	161[B]	LYS	3.0
1	3-D	212[C]	LEU	3.0
1	3-D	310[C]	LYS	3.0
1	3-H	279[C]	LYS	3.0
1	3-M	161[C]	LYS	3.0
1	4-D	212[D]	LEU	3.0
1	4-D	310[D]	LYS	3.0
1	4-H	279[D]	LYS	3.0
1	4-M	161[D]	LYS	3.0
1	1-P	108[A]	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	2-P	108[B]	GLU	3.0
1	3-P	108[C]	GLU	3.0
1	4-P	108[D]	GLU	3.0
1	1-D	82[A]	TRP	3.0
1	1-E	101[A]	TRP	3.0
1	2-D	82[B]	TRP	3.0
1	2-E	101[B]	TRP	3.0
1	3-D	82[C]	TRP	3.0
1	3-E	101[C]	TRP	3.0
1	4-D	82[D]	TRP	3.0
1	4-E	101[D]	TRP	3.0
1	1-A	300[A]	PHE	3.0
1	2-A	300[B]	PHE	3.0
1	3-A	300[C]	PHE	3.0
1	4-A	300[D]	PHE	3.0
1	1-D	260[A]	ARG	3.0
1	1-L	121[A]	GLY	3.0
1	1-O	147[A]	GLY	3.0
1	2-D	260[B]	ARG	3.0
1	2-L	121[B]	GLY	3.0
1	2-O	147[B]	GLY	3.0
1	3-D	260[C]	ARG	3.0
1	3-L	121[C]	GLY	3.0
1	3-O	147[C]	GLY	3.0
1	4-D	260[D]	ARG	3.0
1	4-L	121[D]	GLY	3.0
1	4-O	147[D]	GLY	3.0
1	1-K	273[A]	GLU	3.0
1	2-K	273[B]	GLU	3.0
1	3-K	273[C]	GLU	3.0
1	4-K	273[D]	GLU	3.0
1	1-A	274[A]	PRO	3.0
1	1-C	51[A]	PRO	3.0
1	1-E	205[A]	SER	3.0
1	2-A	274[B]	PRO	3.0
1	2-C	51[B]	PRO	3.0
1	2-E	205[B]	SER	3.0
1	3-A	274[C]	PRO	3.0
1	3-C	51[C]	PRO	3.0
1	3-E	205[C]	SER	3.0
1	4-A	274[D]	PRO	3.0
1	4-C	51[D]	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	4-E	205[D]	SER	3.0
1	1-E	194[A]	PHE	2.9
1	1-H	49[A]	PHE	2.9
1	2-E	194[B]	PHE	2.9
1	2-H	49[B]	PHE	2.9
1	3-E	194[C]	PHE	2.9
1	3-H	49[C]	PHE	2.9
1	4-E	194[D]	PHE	2.9
1	4-H	49[D]	PHE	2.9
1	1-E	117[A]	HIS	2.9
1	2-E	117[B]	HIS	2.9
1	3-E	117[C]	HIS	2.9
1	4-E	117[D]	HIS	2.9
1	1-G	312[A]	ASP	2.9
1	1-L	166[A]	ASP	2.9
1	1-M	25[A]	ASP	2.9
1	2-G	312[B]	ASP	2.9
1	2-L	166[B]	ASP	2.9
1	2-M	25[B]	ASP	2.9
1	3-G	312[C]	ASP	2.9
1	3-L	166[C]	ASP	2.9
1	3-M	25[C]	ASP	2.9
1	4-G	312[D]	ASP	2.9
1	4-L	166[D]	ASP	2.9
1	4-M	25[D]	ASP	2.9
1	1-K	96[A]	GLN	2.9
1	2-K	96[B]	GLN	2.9
1	3-K	96[C]	GLN	2.9
1	4-K	96[D]	GLN	2.9
1	1-F	24[A]	LEU	2.9
1	1-K	55[A]	ARG	2.9
1	2-F	24[B]	LEU	2.9
1	2-K	55[B]	ARG	2.9
1	3-F	24[C]	LEU	2.9
1	3-K	55[C]	ARG	2.9
1	4-F	24[D]	LEU	2.9
1	4-K	55[D]	ARG	2.9
1	1-A	34[A]	GLY	2.9
1	1-N	97[A]	GLY	2.9
1	1-P	62[A]	THR	2.9
1	1-P	27[A]	ILE	2.9
1	2-A	34[B]	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	2-N	97[B]	GLY	2.9
1	2-P	62[B]	THR	2.9
1	2-P	27[B]	ILE	2.9
1	3-A	34[C]	GLY	2.9
1	3-N	97[C]	GLY	2.9
1	3-P	62[C]	THR	2.9
1	3-P	27[C]	ILE	2.9
1	4-A	34[D]	GLY	2.9
1	4-N	97[D]	GLY	2.9
1	4-P	62[D]	THR	2.9
1	4-P	27[D]	ILE	2.9
1	1-J	313[A]	MET	2.9
1	2-J	313[B]	MET	2.9
1	3-J	313[C]	MET	2.9
1	4-J	313[D]	MET	2.9
1	1-C	131[A]	TRP	2.9
1	2-C	131[B]	TRP	2.9
1	3-C	131[C]	TRP	2.9
1	4-C	131[D]	TRP	2.9
1	1-P	175[A]	ASN	2.9
1	2-P	175[B]	ASN	2.9
1	3-P	175[C]	ASN	2.9
1	4-P	175[D]	ASN	2.9
1	1-K	69[A]	LYS	2.9
1	2-K	69[B]	LYS	2.9
1	3-K	69[C]	LYS	2.9
1	4-K	69[D]	LYS	2.9
1	1-F	290[A]	GLY	2.9
1	2-F	290[B]	GLY	2.9
1	3-F	290[C]	GLY	2.9
1	4-F	290[D]	GLY	2.9
1	1-D	235[A]	THR	2.9
1	1-G	139[A]	THR	2.9
1	2-D	235[B]	THR	2.9
1	2-G	139[B]	THR	2.9
1	3-D	235[C]	THR	2.9
1	3-G	139[C]	THR	2.9
1	4-D	235[D]	THR	2.9
1	4-G	139[D]	THR	2.9
1	1-C	33[A]	VAL	2.9
1	2-C	33[B]	VAL	2.9
1	3-C	33[C]	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	4-C	33[D]	VAL	2.9
1	1-E	109[A]	PHE	2.9
1	2-E	109[B]	PHE	2.9
1	3-E	109[C]	PHE	2.9
1	4-E	109[D]	PHE	2.9
1	1-M	69[A]	LYS	2.9
1	1-N	310[A]	LYS	2.9
1	2-M	69[B]	LYS	2.9
1	2-N	310[B]	LYS	2.9
1	3-M	69[C]	LYS	2.9
1	3-N	310[C]	LYS	2.9
1	4-M	69[D]	LYS	2.9
1	4-N	310[D]	LYS	2.9
1	1-K	164[A]	PRO	2.9
1	2-K	164[B]	PRO	2.9
1	3-K	164[C]	PRO	2.9
1	4-K	164[D]	PRO	2.9
1	1-E	184[A]	LEU	2.9
1	1-H	43[A]	THR	2.9
1	1-M	66[A]	LEU	2.9
1	2-E	184[B]	LEU	2.9
1	2-H	43[B]	THR	2.9
1	2-M	66[B]	LEU	2.9
1	3-E	184[C]	LEU	2.9
1	3-H	43[C]	THR	2.9
1	3-M	66[C]	LEU	2.9
1	4-E	184[D]	LEU	2.9
1	4-H	43[D]	THR	2.9
1	4-M	66[D]	LEU	2.9
1	1-G	33[A]	VAL	2.9
1	1-P	40[A]	ARG	2.9
1	2-G	33[B]	VAL	2.9
1	2-P	40[B]	ARG	2.9
1	3-G	33[C]	VAL	2.9
1	3-P	40[C]	ARG	2.9
1	4-G	33[D]	VAL	2.9
1	4-P	40[D]	ARG	2.9
1	1-F	190[A]	PHE	2.9
1	1-G	180[A]	PRO	2.9
1	2-F	190[B]	PHE	2.9
1	2-G	180[B]	PRO	2.9
1	3-F	190[C]	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	3-G	180[C]	PRO	2.9
1	4-F	190[D]	PHE	2.9
1	4-G	180[D]	PRO	2.9
1	1-F	229[A]	ALA	2.9
1	1-I	105[A]	GLY	2.9
1	2-F	229[B]	ALA	2.9
1	2-I	105[B]	GLY	2.9
1	3-F	229[C]	ALA	2.9
1	3-I	105[C]	GLY	2.9
1	4-F	229[D]	ALA	2.9
1	4-I	105[D]	GLY	2.9
1	1-I	119[A]	ARG	2.9
1	2-I	119[B]	ARG	2.9
1	3-I	119[C]	ARG	2.9
1	4-I	119[D]	ARG	2.9
1	1-A	33[A]	VAL	2.9
1	1-B	33[A]	VAL	2.9
1	1-B	301[A]	VAL	2.9
1	1-C	38[A]	PRO	2.9
1	1-F	164[A]	PRO	2.9
1	2-A	33[B]	VAL	2.9
1	2-B	33[B]	VAL	2.9
1	2-B	301[B]	VAL	2.9
1	2-C	38[B]	PRO	2.9
1	2-F	164[B]	PRO	2.9
1	3-A	33[C]	VAL	2.9
1	3-B	33[C]	VAL	2.9
1	3-B	301[C]	VAL	2.9
1	3-C	38[C]	PRO	2.9
1	3-F	164[C]	PRO	2.9
1	4-A	33[D]	VAL	2.9
1	4-B	33[D]	VAL	2.9
1	4-B	301[D]	VAL	2.9
1	4-C	38[D]	PRO	2.9
1	4-F	164[D]	PRO	2.9
1	1-M	264[A]	GLU	2.9
1	2-M	264[B]	GLU	2.9
1	3-M	264[C]	GLU	2.9
1	4-M	264[D]	GLU	2.9
1	1-H	309[A]	GLY	2.9
1	1-I	149[A]	GLY	2.9
1	2-H	309[B]	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	2-I	149[B]	GLY	2.9
1	3-H	309[C]	GLY	2.9
1	3-I	149[C]	GLY	2.9
1	4-H	309[D]	GLY	2.9
1	4-I	149[D]	GLY	2.9
1	1-B	21[A]	TYR	2.9
1	2-B	21[B]	TYR	2.9
1	3-B	21[C]	TYR	2.9
1	4-B	21[D]	TYR	2.9
1	1-L	261[A]	ASP	2.9
1	1-M	53[A]	SER	2.9
1	1-M	230[A]	SER	2.9
1	1-O	293[A]	ASP	2.9
1	2-L	261[B]	ASP	2.9
1	2-M	53[B]	SER	2.9
1	2-M	230[B]	SER	2.9
1	2-O	293[B]	ASP	2.9
1	3-L	261[C]	ASP	2.9
1	3-M	53[C]	SER	2.9
1	3-M	230[C]	SER	2.9
1	3-O	293[C]	ASP	2.9
1	4-L	261[D]	ASP	2.9
1	4-M	53[D]	SER	2.9
1	4-M	230[D]	SER	2.9
1	4-O	293[D]	ASP	2.9
1	1-C	274[A]	PRO	2.9
1	1-K	79[A]	GLU	2.9
1	1-L	279[A]	LYS	2.9
1	1-M	279[A]	LYS	2.9
1	1-N	107[A]	LYS	2.9
1	2-C	274[B]	PRO	2.9
1	2-K	79[B]	GLU	2.9
1	2-L	279[B]	LYS	2.9
1	2-M	279[B]	LYS	2.9
1	2-N	107[B]	LYS	2.9
1	3-C	274[C]	PRO	2.9
1	3-K	79[C]	GLU	2.9
1	3-L	279[C]	LYS	2.9
1	3-M	279[C]	LYS	2.9
1	3-N	107[C]	LYS	2.9
1	4-C	274[D]	PRO	2.9
1	4-K	79[D]	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	4-L	279[D]	LYS	2.9
1	4-M	279[D]	LYS	2.9
1	4-N	107[D]	LYS	2.9
1	1-H	33[A]	VAL	2.8
1	2-H	33[B]	VAL	2.8
1	3-H	33[C]	VAL	2.8
1	4-H	33[D]	VAL	2.8
1	1-H	259[A]	TYR	2.8
1	2-H	259[B]	TYR	2.8
1	3-H	259[C]	TYR	2.8
1	4-H	259[D]	TYR	2.8
1	1-D	43[A]	THR	2.8
1	1-O	108[A]	GLU	2.8
1	2-D	43[B]	THR	2.8
1	2-O	108[B]	GLU	2.8
1	3-D	43[C]	THR	2.8
1	3-O	108[C]	GLU	2.8
1	4-D	43[D]	THR	2.8
1	4-O	108[D]	GLU	2.8
1	1-H	13[A]	ARG	2.8
1	2-H	13[B]	ARG	2.8
1	3-H	13[C]	ARG	2.8
1	4-H	13[D]	ARG	2.8
1	1-G	116[A]	GLY	2.8
1	1-H	187[A]	CYS	2.8
1	1-I	301[A]	VAL	2.8
1	1-J	44[A]	GLY	2.8
1	1-N	128[A]	GLY	2.8
1	2-G	116[B]	GLY	2.8
1	2-H	187[B]	CYS	2.8
1	2-I	301[B]	VAL	2.8
1	2-J	44[B]	GLY	2.8
1	2-N	128[B]	GLY	2.8
1	3-G	116[C]	GLY	2.8
1	3-H	187[C]	CYS	2.8
1	3-I	301[C]	VAL	2.8
1	3-J	44[C]	GLY	2.8
1	3-N	128[C]	GLY	2.8
1	4-G	116[D]	GLY	2.8
1	4-H	187[D]	CYS	2.8
1	4-I	301[D]	VAL	2.8
1	4-J	44[D]	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	4-N	128[D]	GLY	2.8
1	1-I	120[A]	GLU	2.8
1	1-L	60[A]	ASP	2.8
1	2-I	120[B]	GLU	2.8
1	2-L	60[B]	ASP	2.8
1	3-I	120[C]	GLU	2.8
1	3-L	60[C]	ASP	2.8
1	4-I	120[D]	GLU	2.8
1	4-L	60[D]	ASP	2.8
1	1-B	164[A]	PRO	2.8
1	2-B	164[B]	PRO	2.8
1	3-B	164[C]	PRO	2.8
1	4-B	164[D]	PRO	2.8
1	1-O	188[A]	HIS	2.8
1	2-O	188[B]	HIS	2.8
1	3-O	188[C]	HIS	2.8
1	4-O	188[D]	HIS	2.8
1	1-A	97[A]	GLY	2.8
1	1-H	143[A]	GLY	2.8
1	1-P	147[A]	GLY	2.8
1	2-A	97[B]	GLY	2.8
1	2-H	143[B]	GLY	2.8
1	2-P	147[B]	GLY	2.8
1	3-A	97[C]	GLY	2.8
1	3-H	143[C]	GLY	2.8
1	3-P	147[C]	GLY	2.8
1	4-A	97[D]	GLY	2.8
1	4-H	143[D]	GLY	2.8
1	4-P	147[D]	GLY	2.8
1	1-C	30[A]	ILE	2.8
1	1-D	31[A]	ILE	2.8
1	2-C	30[B]	ILE	2.8
1	2-D	31[B]	ILE	2.8
1	3-C	30[C]	ILE	2.8
1	3-D	31[C]	ILE	2.8
1	4-C	30[D]	ILE	2.8
1	4-D	31[D]	ILE	2.8
1	1-B	298[A]	GLU	2.8
1	2-B	298[B]	GLU	2.8
1	3-B	298[C]	GLU	2.8
1	4-B	298[D]	GLU	2.8
1	1-D	263[A]	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	2-D	263[B]	VAL	2.8
1	3-D	263[C]	VAL	2.8
1	4-D	263[D]	VAL	2.8
1	1-M	282[A]	TRP	2.8
1	1-O	229[A]	ALA	2.8
1	2-M	282[B]	TRP	2.8
1	2-O	229[B]	ALA	2.8
1	3-M	282[C]	TRP	2.8
1	3-O	229[C]	ALA	2.8
1	4-M	282[D]	TRP	2.8
1	4-O	229[D]	ALA	2.8
1	1-A	289[A]	ILE	2.8
1	1-N	94[A]	SER	2.8
1	2-A	289[B]	ILE	2.8
1	2-N	94[B]	SER	2.8
1	3-A	289[C]	ILE	2.8
1	3-N	94[C]	SER	2.8
1	4-A	289[D]	ILE	2.8
1	4-N	94[D]	SER	2.8
1	1-E	45[A]	THR	2.8
1	1-G	43[A]	THR	2.8
1	1-J	177[A]	LYS	2.8
1	2-E	45[B]	THR	2.8
1	2-G	43[B]	THR	2.8
1	2-J	177[B]	LYS	2.8
1	3-E	45[C]	THR	2.8
1	3-G	43[C]	THR	2.8
1	3-J	177[C]	LYS	2.8
1	4-E	45[D]	THR	2.8
1	4-G	43[D]	THR	2.8
1	4-J	177[D]	LYS	2.8
1	1-K	246[A]	PRO	2.8
1	2-K	246[B]	PRO	2.8
1	3-K	246[C]	PRO	2.8
1	4-K	246[D]	PRO	2.8
1	1-C	98[A]	VAL	2.8
1	1-F	279[A]	LYS	2.8
1	1-M	57[A]	SER	2.8
1	1-N	296[A]	LYS	2.8
1	2-C	98[B]	VAL	2.8
1	2-F	279[B]	LYS	2.8
1	2-M	57[B]	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	2-N	296[B]	LYS	2.8
1	3-C	98[C]	VAL	2.8
1	3-F	279[C]	LYS	2.8
1	3-M	57[C]	SER	2.8
1	3-N	296[C]	LYS	2.8
1	4-C	98[D]	VAL	2.8
1	4-F	279[D]	LYS	2.8
1	4-M	57[D]	SER	2.8
1	4-N	296[D]	LYS	2.8
1	1-E	43[A]	THR	2.8
1	1-I	242[A]	THR	2.8
1	2-E	43[B]	THR	2.8
1	2-I	242[B]	THR	2.8
1	3-E	43[C]	THR	2.8
1	3-I	242[C]	THR	2.8
1	4-E	43[D]	THR	2.8
1	4-I	242[D]	THR	2.8
1	1-F	189[A]	MET	2.8
1	1-L	304[A]	GLY	2.8
1	2-F	189[B]	MET	2.8
1	2-L	304[B]	GLY	2.8
1	3-F	189[C]	MET	2.8
1	3-L	304[C]	GLY	2.8
1	4-F	189[D]	MET	2.8
1	4-L	304[D]	GLY	2.8
1	1-G	138[A]	TYR	2.8
1	1-K	298[A]	GLU	2.8
1	2-G	138[B]	TYR	2.8
1	2-K	298[B]	GLU	2.8
1	3-G	138[C]	TYR	2.8
1	3-K	298[C]	GLU	2.8
1	4-G	138[D]	TYR	2.8
1	4-K	298[D]	GLU	2.8
1	1-E	33[A]	VAL	2.7
1	2-E	33[B]	VAL	2.7
1	3-E	33[C]	VAL	2.7
1	4-E	33[D]	VAL	2.7
1	1-D	199[A]	PRO	2.7
1	1-G	38[A]	PRO	2.7
1	2-D	199[B]	PRO	2.7
1	2-G	38[B]	PRO	2.7
1	3-D	199[C]	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	3-G	38[C]	PRO	2.7
1	4-D	199[D]	PRO	2.7
1	4-G	38[D]	PRO	2.7
1	1-F	309[A]	GLY	2.7
1	1-M	254[A]	GLY	2.7
1	2-F	309[B]	GLY	2.7
1	2-M	254[B]	GLY	2.7
1	3-F	309[C]	GLY	2.7
1	3-M	254[C]	GLY	2.7
1	4-F	309[D]	GLY	2.7
1	4-M	254[D]	GLY	2.7
1	1-J	110[A]	LEU	2.7
1	2-J	110[B]	LEU	2.7
1	3-J	110[C]	LEU	2.7
1	4-J	110[D]	LEU	2.7
1	1-K	186[A]	PRO	2.7
1	2-K	186[B]	PRO	2.7
1	3-K	186[C]	PRO	2.7
1	4-K	186[D]	PRO	2.7
1	1-A	316[A]	SER	2.7
1	1-M	60[A]	ASP	2.7
1	2-A	316[B]	SER	2.7
1	2-M	60[B]	ASP	2.7
1	3-A	316[C]	SER	2.7
1	3-M	60[C]	ASP	2.7
1	4-A	316[D]	SER	2.7
1	4-M	60[D]	ASP	2.7
1	1-B	32[A]	ASN	2.7
1	1-B	281[A]	LYS	2.7
1	2-B	32[B]	ASN	2.7
1	2-B	281[B]	LYS	2.7
1	3-B	32[C]	ASN	2.7
1	3-B	281[C]	LYS	2.7
1	4-B	32[D]	ASN	2.7
1	4-B	281[D]	LYS	2.7
1	1-B	305[A]	TYR	2.7
1	1-C	270[A]	LEU	2.7
1	2-B	305[B]	TYR	2.7
1	1-M	52[A]	PRO	2.7
1	2-C	270[B]	LEU	2.7
1	3-B	305[C]	TYR	2.7
1	3-C	270[C]	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	4-B	305[D]	TYR	2.7
1	2-M	52[B]	PRO	2.7
1	3-M	52[C]	PRO	2.7
1	4-C	270[D]	LEU	2.7
1	4-M	52[D]	PRO	2.7
1	1-A	103[A]	GLY	2.7
1	1-E	124[A]	GLY	2.7
1	1-L	105[A]	GLY	2.7
1	2-A	103[B]	GLY	2.7
1	2-E	124[B]	GLY	2.7
1	2-L	105[B]	GLY	2.7
1	3-A	103[C]	GLY	2.7
1	3-E	124[C]	GLY	2.7
1	3-L	105[C]	GLY	2.7
1	4-A	103[D]	GLY	2.7
1	4-E	124[D]	GLY	2.7
1	4-L	105[D]	GLY	2.7
1	1-A	92[A]	MET	2.7
1	2-A	92[B]	MET	2.7
1	3-A	92[C]	MET	2.7
1	4-A	92[D]	MET	2.7
1	1-I	219[A]	ASP	2.7
1	2-I	219[B]	ASP	2.7
1	3-I	219[C]	ASP	2.7
1	4-I	219[D]	ASP	2.7
1	1-D	101[A]	TRP	2.7
1	2-D	101[B]	TRP	2.7
1	3-D	101[C]	TRP	2.7
1	4-D	101[D]	TRP	2.7
1	1-C	97[A]	GLY	2.7
1	1-C	103[A]	GLY	2.7
1	2-C	97[B]	GLY	2.7
1	2-C	103[B]	GLY	2.7
1	3-C	97[C]	GLY	2.7
1	3-C	103[C]	GLY	2.7
1	4-C	97[D]	GLY	2.7
1	4-C	103[D]	GLY	2.7
1	1-E	179[A]	LEU	2.7
1	1-E	259[A]	TYR	2.7
1	2-E	179[B]	LEU	2.7
1	2-E	259[B]	TYR	2.7
1	3-E	179[C]	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	3-E	259[C]	TYR	2.7
1	4-E	179[D]	LEU	2.7
1	4-E	259[D]	TYR	2.7
1	1-D	45[A]	THR	2.7
1	2-D	45[B]	THR	2.7
1	3-D	45[C]	THR	2.7
1	4-D	45[D]	THR	2.7
1	1-G	301[A]	VAL	2.7
1	2-G	301[B]	VAL	2.7
1	3-G	301[C]	VAL	2.7
1	4-G	301[D]	VAL	2.7
1	1-O	39[A]	ASP	2.7
1	2-O	39[B]	ASP	2.7
1	3-O	39[C]	ASP	2.7
1	4-O	39[D]	ASP	2.7
1	1-D	27[A]	ILE	2.7
1	2-D	27[B]	ILE	2.7
1	3-D	27[C]	ILE	2.7
1	4-D	27[D]	ILE	2.7
1	1-G	103[A]	GLY	2.7
1	2-G	103[B]	GLY	2.7
1	3-G	103[C]	GLY	2.7
1	4-G	103[D]	GLY	2.7
1	1-N	303[A]	GLU	2.7
1	2-N	303[B]	GLU	2.7
1	3-N	303[C]	GLU	2.7
1	4-N	303[D]	GLU	2.7
1	1-D	312[A]	ASP	2.7
1	1-E	68[A]	THR	2.7
1	1-L	25[A]	ASP	2.7
1	1-P	255[A]	ASP	2.7
1	2-D	312[B]	ASP	2.7
1	2-E	68[B]	THR	2.7
1	2-L	25[B]	ASP	2.7
1	2-P	255[B]	ASP	2.7
1	3-D	312[C]	ASP	2.7
1	3-E	68[C]	THR	2.7
1	3-L	25[C]	ASP	2.7
1	3-P	255[C]	ASP	2.7
1	4-D	312[D]	ASP	2.7
1	4-E	68[D]	THR	2.7
1	4-L	25[D]	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	4-P	255[D]	ASP	2.7
1	1-H	28[A]	ARG	2.7
1	1-M	119[A]	ARG	2.7
1	2-H	28[B]	ARG	2.7
1	2-M	119[B]	ARG	2.7
1	3-H	28[C]	ARG	2.7
1	3-M	119[C]	ARG	2.7
1	4-H	28[D]	ARG	2.7
1	4-M	119[D]	ARG	2.7
1	1-A	277[A]	PHE	2.7
1	1-F	103[A]	GLY	2.7
1	1-G	295[A]	PHE	2.7
1	1-O	103[A]	GLY	2.7
1	1-P	111[A]	GLU	2.7
1	2-A	277[B]	PHE	2.7
1	2-F	103[B]	GLY	2.7
1	2-G	295[B]	PHE	2.7
1	2-O	103[B]	GLY	2.7
1	2-P	111[B]	GLU	2.7
1	3-F	103[C]	GLY	2.7
1	3-G	295[C]	PHE	2.7
1	3-O	103[C]	GLY	2.7
1	3-P	111[C]	GLU	2.7
1	4-F	103[D]	GLY	2.7
1	4-O	103[D]	GLY	2.7
1	4-P	111[D]	GLU	2.7
1	3-A	277[C]	PHE	2.7
1	4-A	277[D]	PHE	2.7
1	4-G	295[D]	PHE	2.7
1	1-C	118[A]	ARG	2.7
1	2-C	118[B]	ARG	2.7
1	3-C	118[C]	ARG	2.7
1	4-C	118[D]	ARG	2.7
1	1-M	212[A]	LEU	2.7
1	1-O	93[A]	LEU	2.7
1	2-M	212[B]	LEU	2.7
1	2-O	93[B]	LEU	2.7
1	3-M	212[C]	LEU	2.7
1	3-O	93[C]	LEU	2.7
1	4-M	212[D]	LEU	2.7
1	4-O	93[D]	LEU	2.7
1	1-H	113[A]	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	2-H	113[B]	VAL	2.6
1	3-H	113[C]	VAL	2.6
1	4-H	113[D]	VAL	2.6
1	1-B	206[A]	LYS	2.6
1	1-L	161[A]	LYS	2.6
1	2-B	206[B]	LYS	2.6
1	2-L	161[B]	LYS	2.6
1	3-B	206[C]	LYS	2.6
1	3-L	161[C]	LYS	2.6
1	4-B	206[D]	LYS	2.6
1	4-L	161[D]	LYS	2.6
1	1-E	27[A]	ILE	2.6
1	2-E	27[B]	ILE	2.6
1	3-E	27[C]	ILE	2.6
1	4-E	27[D]	ILE	2.6
1	1-C	277[A]	PHE	2.6
1	1-N	90[A]	ALA	2.6
1	2-C	277[B]	PHE	2.6
1	2-N	90[B]	ALA	2.6
1	3-C	277[C]	PHE	2.6
1	3-N	90[C]	ALA	2.6
1	4-C	277[D]	PHE	2.6
1	4-N	90[D]	ALA	2.6
1	1-D	161[A]	LYS	2.6
1	2-D	161[B]	LYS	2.6
1	3-D	161[C]	LYS	2.6
1	4-D	161[D]	LYS	2.6
1	1-C	46[A]	VAL	2.6
1	1-D	224[A]	VAL	2.6
1	2-C	46[B]	VAL	2.6
1	2-D	224[B]	VAL	2.6
1	3-C	46[C]	VAL	2.6
1	3-D	224[C]	VAL	2.6
1	4-C	46[D]	VAL	2.6
1	4-D	224[D]	VAL	2.6
1	1-H	124[A]	GLY	2.6
1	1-K	276[A]	ASP	2.6
1	2-H	124[B]	GLY	2.6
1	2-K	276[B]	ASP	2.6
1	3-H	124[C]	GLY	2.6
1	3-K	276[C]	ASP	2.6
1	4-H	124[D]	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	4-K	276[D]	ASP	2.6
1	1-A	16[A]	PRO	2.6
1	1-F	16[A]	PRO	2.6
1	2-A	16[B]	PRO	2.6
1	2-F	16[B]	PRO	2.6
1	3-A	16[C]	PRO	2.6
1	3-F	16[C]	PRO	2.6
1	4-A	16[D]	PRO	2.6
1	4-F	16[D]	PRO	2.6
1	1-F	108[A]	GLU	2.6
1	1-G	317[A]	ALA	2.6
1	1-H	287[A]	GLU	2.6
1	2-F	108[B]	GLU	2.6
1	2-G	317[B]	ALA	2.6
1	2-H	287[B]	GLU	2.6
1	3-F	108[C]	GLU	2.6
1	3-G	317[C]	ALA	2.6
1	3-H	287[C]	GLU	2.6
1	4-F	108[D]	GLU	2.6
1	4-G	317[D]	ALA	2.6
1	4-H	287[D]	GLU	2.6
1	1-C	146[A]	LYS	2.6
1	1-C	300[A]	PHE	2.6
1	1-P	281[A]	LYS	2.6
1	2-C	146[B]	LYS	2.6
1	2-C	300[B]	PHE	2.6
1	2-P	281[B]	LYS	2.6
1	3-C	146[C]	LYS	2.6
1	3-C	300[C]	PHE	2.6
1	3-P	281[C]	LYS	2.6
1	4-C	146[D]	LYS	2.6
1	4-C	300[D]	PHE	2.6
1	4-P	281[D]	LYS	2.6
1	1-H	144[A]	ASP	2.6
1	2-H	144[B]	ASP	2.6
1	3-H	144[C]	ASP	2.6
1	4-H	144[D]	ASP	2.6
1	1-G	272[A]	ARG	2.6
1	2-G	272[B]	ARG	2.6
1	3-G	272[C]	ARG	2.6
1	4-G	272[D]	ARG	2.6
1	1-A	174[A]	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	2-A	174[B]	TRP	2.6
1	3-A	174[C]	TRP	2.6
1	4-A	174[D]	TRP	2.6
1	1-F	169[A]	ILE	2.6
1	2-F	169[B]	ILE	2.6
1	3-F	169[C]	ILE	2.6
1	4-F	169[D]	ILE	2.6
1	1-O	152[A]	GLN	2.6
1	2-O	152[B]	GLN	2.6
1	3-O	152[C]	GLN	2.6
1	4-O	152[D]	GLN	2.6
1	1-E	260[A]	ARG	2.6
1	2-E	260[B]	ARG	2.6
1	3-E	260[C]	ARG	2.6
1	4-E	260[D]	ARG	2.6
1	1-E	93[A]	LEU	2.6
1	2-E	93[B]	LEU	2.6
1	3-E	93[C]	LEU	2.6
1	4-E	93[D]	LEU	2.6
1	1-C	21[A]	TYR	2.6
1	2-C	21[B]	TYR	2.6
1	3-C	21[C]	TYR	2.6
1	4-C	21[D]	TYR	2.6
1	1-L	59[A]	ALA	2.6
1	2-L	59[B]	ALA	2.6
1	3-L	59[C]	ALA	2.6
1	4-L	59[D]	ALA	2.6
1	1-B	27[A]	ILE	2.6
1	1-D	292[A]	ILE	2.6
1	1-E	272[A]	ARG	2.6
1	1-H	169[A]	ILE	2.6
1	2-B	27[B]	ILE	2.6
1	2-D	292[B]	ILE	2.6
1	2-E	272[B]	ARG	2.6
1	2-H	169[B]	ILE	2.6
1	3-B	27[C]	ILE	2.6
1	3-D	292[C]	ILE	2.6
1	3-E	272[C]	ARG	2.6
1	3-H	169[C]	ILE	2.6
1	4-B	27[D]	ILE	2.6
1	4-D	292[D]	ILE	2.6
1	4-E	272[D]	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	4-H	169[D]	ILE	2.6
1	1-J	179[A]	LEU	2.6
1	2-J	179[B]	LEU	2.6
1	3-J	179[C]	LEU	2.6
1	4-J	179[D]	LEU	2.6
1	1-E	142[A]	ASP	2.6
1	1-L	291[A]	ASP	2.6
1	1-P	152[A]	GLN	2.6
1	2-E	142[B]	ASP	2.6
1	2-L	291[B]	ASP	2.6
1	2-P	152[B]	GLN	2.6
1	3-E	142[C]	ASP	2.6
1	3-L	291[C]	ASP	2.6
1	3-P	152[C]	GLN	2.6
1	4-E	142[D]	ASP	2.6
1	4-L	291[D]	ASP	2.6
1	4-P	152[D]	GLN	2.6
1	1-O	146[A]	LYS	2.6
1	2-O	146[B]	LYS	2.6
1	3-O	146[C]	LYS	2.6
1	4-O	146[D]	LYS	2.6
1	1-C	117[A]	HIS	2.6
1	2-C	117[B]	HIS	2.6
1	3-C	117[C]	HIS	2.6
1	4-C	117[D]	HIS	2.6
1	1-D	308[A]	TRP	2.6
1	2-D	308[B]	TRP	2.6
1	3-D	308[C]	TRP	2.6
1	4-D	308[D]	TRP	2.6
1	1-A	32[A]	ASN	2.6
1	1-G	61[A]	ASN	2.6
1	1-G	226[A]	PHE	2.6
1	2-A	32[B]	ASN	2.6
1	2-G	61[B]	ASN	2.6
1	2-G	226[B]	PHE	2.6
1	3-A	32[C]	ASN	2.6
1	3-G	61[C]	ASN	2.6
1	3-G	226[C]	PHE	2.6
1	4-A	32[D]	ASN	2.6
1	4-G	61[D]	ASN	2.6
1	4-G	226[D]	PHE	2.6
1	1-H	218[A]	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	2-H	218[B]	CYS	2.6
1	3-H	218[C]	CYS	2.6
1	4-H	218[D]	CYS	2.6
1	1-O	212[A]	LEU	2.6
1	2-O	212[B]	LEU	2.6
1	3-O	212[C]	LEU	2.6
1	4-O	212[D]	LEU	2.6
1	1-K	314[A]	LYS	2.5
1	2-K	314[B]	LYS	2.5
1	3-K	314[C]	LYS	2.5
1	4-K	314[D]	LYS	2.5
1	1-A	285[A]	SER	2.5
1	2-A	285[B]	SER	2.5
1	3-A	285[C]	SER	2.5
1	4-A	285[D]	SER	2.5
1	1-H	315[A]	MET	2.5
1	2-H	315[B]	MET	2.5
1	3-H	315[C]	MET	2.5
1	4-H	315[D]	MET	2.5
1	1-B	129[A]	PHE	2.5
1	1-B	282[A]	TRP	2.5
1	1-E	185[A]	PRO	2.5
1	2-B	129[B]	PHE	2.5
1	2-B	282[B]	TRP	2.5
1	2-E	185[B]	PRO	2.5
1	3-B	129[C]	PHE	2.5
1	3-B	282[C]	TRP	2.5
1	3-E	185[C]	PRO	2.5
1	4-B	129[D]	PHE	2.5
1	4-B	282[D]	TRP	2.5
1	4-E	185[D]	PRO	2.5
1	1-C	181[A]	LEU	2.5
1	1-C	266[A]	LEU	2.5
1	2-C	181[B]	LEU	2.5
1	2-C	266[B]	LEU	2.5
1	3-C	181[C]	LEU	2.5
1	3-C	266[C]	LEU	2.5
1	4-C	181[D]	LEU	2.5
1	4-C	266[D]	LEU	2.5
1	1-C	245[A]	GLU	2.5
1	1-G	143[A]	GLY	2.5
1	1-H	223[A]	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	1-A	41[A]	THR	2.5
1	1-O	227[A]	ASN	2.5
1	2-C	245[B]	GLU	2.5
1	2-G	143[B]	GLY	2.5
1	2-H	223[B]	GLY	2.5
1	2-A	41[B]	THR	2.5
1	2-O	227[B]	ASN	2.5
1	3-C	245[C]	GLU	2.5
1	3-G	143[C]	GLY	2.5
1	3-H	223[C]	GLY	2.5
1	3-O	227[C]	ASN	2.5
1	4-C	245[D]	GLU	2.5
1	4-G	143[D]	GLY	2.5
1	4-H	223[D]	GLY	2.5
1	3-A	41[C]	THR	2.5
1	4-A	41[D]	THR	2.5
1	4-O	227[D]	ASN	2.5
1	1-H	17[A]	ASP	2.5
1	1-J	265[A]	PRO	2.5
1	2-H	17[B]	ASP	2.5
1	2-J	265[B]	PRO	2.5
1	3-H	17[C]	ASP	2.5
1	3-J	265[C]	PRO	2.5
1	4-H	17[D]	ASP	2.5
1	4-J	265[D]	PRO	2.5
1	1-B	57[A]	SER	2.5
1	1-A	110[A]	LEU	2.5
1	1-D	247[A]	HIS	2.5
1	2-B	57[B]	SER	2.5
1	2-D	247[B]	HIS	2.5
1	3-B	57[C]	SER	2.5
1	3-D	247[C]	HIS	2.5
1	4-B	57[D]	SER	2.5
1	2-A	110[B]	LEU	2.5
1	3-A	110[C]	LEU	2.5
1	4-A	110[D]	LEU	2.5
1	4-D	247[D]	HIS	2.5
1	1-A	314[A]	LYS	2.5
1	1-C	34[A]	GLY	2.5
1	1-E	173[A]	ALA	2.5
1	1-G	187[A]	CYS	2.5
1	1-O	104[A]	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	2-A	314[B]	LYS	2.5
1	2-C	34[B]	GLY	2.5
1	2-E	173[B]	ALA	2.5
1	2-G	187[B]	CYS	2.5
1	2-O	104[B]	ASN	2.5
1	3-A	314[C]	LYS	2.5
1	3-C	34[C]	GLY	2.5
1	3-E	173[C]	ALA	2.5
1	3-G	187[C]	CYS	2.5
1	3-O	104[C]	ASN	2.5
1	4-A	314[D]	LYS	2.5
1	4-C	34[D]	GLY	2.5
1	4-E	173[D]	ALA	2.5
1	4-G	187[D]	CYS	2.5
1	4-O	104[D]	ASN	2.5
1	1-D	155[A]	ARG	2.5
1	1-P	98[A]	VAL	2.5
1	2-D	155[B]	ARG	2.5
1	2-P	98[B]	VAL	2.5
1	3-D	155[C]	ARG	2.5
1	3-P	98[C]	VAL	2.5
1	4-D	155[D]	ARG	2.5
1	4-P	98[D]	VAL	2.5
1	1-F	259[A]	TYR	2.5
1	2-F	259[B]	TYR	2.5
1	3-F	259[C]	TYR	2.5
1	4-F	259[D]	TYR	2.5
1	1-L	215[A]	GLN	2.5
1	1-L	269[A]	GLN	2.5
1	1-B	270[A]	LEU	2.5
1	1-E	121[A]	GLY	2.5
1	1-J	26[A]	LEU	2.5
1	1-J	171[A]	LEU	2.5
1	1-K	275[A]	ARG	2.5
1	2-L	215[B]	GLN	2.5
1	2-L	269[B]	GLN	2.5
1	2-B	270[B]	LEU	2.5
1	2-E	121[B]	GLY	2.5
1	2-J	26[B]	LEU	2.5
1	2-J	171[B]	LEU	2.5
1	2-K	275[B]	ARG	2.5
1	3-L	215[C]	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	3-L	269[C]	GLN	2.5
1	3-B	270[C]	LEU	2.5
1	3-E	121[C]	GLY	2.5
1	3-J	26[C]	LEU	2.5
1	3-J	171[C]	LEU	2.5
1	3-K	275[C]	ARG	2.5
1	4-E	121[D]	GLY	2.5
1	4-J	26[D]	LEU	2.5
1	4-J	171[D]	LEU	2.5
1	4-K	275[D]	ARG	2.5
1	4-L	215[D]	GLN	2.5
1	4-L	269[D]	GLN	2.5
1	4-B	270[D]	LEU	2.5
1	1-G	218[A]	CYS	2.5
1	2-G	218[B]	CYS	2.5
1	3-G	218[C]	CYS	2.5
1	4-G	218[D]	CYS	2.5
1	1-O	287[A]	GLU	2.5
1	2-O	287[B]	GLU	2.5
1	3-O	287[C]	GLU	2.5
1	4-O	287[D]	GLU	2.5
1	1-D	21[A]	TYR	2.5
1	2-D	21[B]	TYR	2.5
1	3-D	21[C]	TYR	2.5
1	4-D	21[D]	TYR	2.5
1	1-G	85[A]	SER	2.5
1	2-G	85[B]	SER	2.5
1	3-G	85[C]	SER	2.5
1	4-G	85[D]	SER	2.5
1	1-A	119[A]	ARG	2.5
1	2-A	119[B]	ARG	2.5
1	3-A	119[C]	ARG	2.5
1	4-A	119[D]	ARG	2.5
1	1-G	304[A]	GLY	2.5
1	2-G	304[B]	GLY	2.5
1	3-G	304[C]	GLY	2.5
1	4-G	304[D]	GLY	2.5
1	1-B	47[A]	ALA	2.5
1	1-E	251[A]	LEU	2.5
1	1-E	266[A]	LEU	2.5
1	2-B	47[B]	ALA	2.5
1	2-E	251[B]	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	2-E	266[B]	LEU	2.5
1	3-B	47[C]	ALA	2.5
1	3-E	251[C]	LEU	2.5
1	3-E	266[C]	LEU	2.5
1	4-B	47[D]	ALA	2.5
1	4-E	251[D]	LEU	2.5
1	4-E	266[D]	LEU	2.5
1	1-D	206[A]	LYS	2.5
1	1-M	242[A]	THR	2.5
1	2-D	206[B]	LYS	2.5
1	2-M	242[B]	THR	2.5
1	3-D	206[C]	LYS	2.5
1	3-M	242[C]	THR	2.5
1	4-D	206[D]	LYS	2.5
1	4-M	242[D]	THR	2.5
1	1-D	305[A]	TYR	2.5
1	1-O	25[A]	ASP	2.5
1	2-D	305[B]	TYR	2.5
1	2-O	25[B]	ASP	2.5
1	3-D	305[C]	TYR	2.5
1	3-O	25[C]	ASP	2.5
1	4-D	305[D]	TYR	2.5
1	4-O	25[D]	ASP	2.5
1	1-D	288[A]	GLU	2.5
1	1-F	147[A]	GLY	2.5
1	2-D	288[B]	GLU	2.5
1	2-F	147[B]	GLY	2.5
1	3-D	288[C]	GLU	2.5
1	3-F	147[C]	GLY	2.5
1	4-D	288[D]	GLU	2.5
1	4-F	147[D]	GLY	2.5
1	1-F	317[A]	ALA	2.5
1	2-F	317[B]	ALA	2.5
1	3-F	317[C]	ALA	2.5
1	4-F	317[D]	ALA	2.5
1	1-A	28[A]	ARG	2.4
1	1-H	284[A]	ARG	2.4
1	2-A	28[B]	ARG	2.4
1	2-H	284[B]	ARG	2.4
1	3-A	28[C]	ARG	2.4
1	3-H	284[C]	ARG	2.4
1	4-A	28[D]	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	4-H	284[D]	ARG	2.4
1	1-B	104[A]	ASN	2.4
1	2-B	104[B]	ASN	2.4
1	3-B	104[C]	ASN	2.4
1	4-B	104[D]	ASN	2.4
1	1-B	196[A]	SER	2.4
1	1-O	303[A]	GLU	2.4
1	2-B	196[B]	SER	2.4
1	2-O	303[B]	GLU	2.4
1	3-B	196[C]	SER	2.4
1	3-O	303[C]	GLU	2.4
1	4-B	196[D]	SER	2.4
1	4-O	303[D]	GLU	2.4
1	1-G	124[A]	GLY	2.4
1	2-G	124[B]	GLY	2.4
1	3-G	124[C]	GLY	2.4
1	4-G	124[D]	GLY	2.4
1	1-C	31[A]	ILE	2.4
1	2-C	31[B]	ILE	2.4
1	3-C	31[C]	ILE	2.4
1	4-C	31[D]	ILE	2.4
1	1-F	54[A]	PHE	2.4
1	1-F	92[A]	MET	2.4
1	1-H	92[A]	MET	2.4
1	2-F	54[B]	PHE	2.4
1	1-I	235[A]	THR	2.4
1	2-F	92[B]	MET	2.4
1	2-H	92[B]	MET	2.4
1	3-F	54[C]	PHE	2.4
1	3-F	92[C]	MET	2.4
1	3-H	92[C]	MET	2.4
1	4-F	54[D]	PHE	2.4
1	2-I	235[B]	THR	2.4
1	3-I	235[C]	THR	2.4
1	4-F	92[D]	MET	2.4
1	4-H	92[D]	MET	2.4
1	4-I	235[D]	THR	2.4
1	1-A	98[A]	VAL	2.4
1	2-A	98[B]	VAL	2.4
1	3-A	98[C]	VAL	2.4
1	4-A	98[D]	VAL	2.4
1	1-E	143[A]	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	1-G	121[A]	GLY	2.4
1	2-E	143[B]	GLY	2.4
1	2-G	121[B]	GLY	2.4
1	3-E	143[C]	GLY	2.4
1	3-G	121[C]	GLY	2.4
1	4-E	143[D]	GLY	2.4
1	4-G	121[D]	GLY	2.4
1	1-D	167[A]	ARG	2.4
1	1-E	250[A]	ILE	2.4
1	1-G	31[A]	ILE	2.4
1	2-D	167[B]	ARG	2.4
1	2-E	250[B]	ILE	2.4
1	2-G	31[B]	ILE	2.4
1	3-D	167[C]	ARG	2.4
1	3-E	250[C]	ILE	2.4
1	3-G	31[C]	ILE	2.4
1	4-D	167[D]	ARG	2.4
1	4-E	250[D]	ILE	2.4
1	4-G	31[D]	ILE	2.4
1	1-K	90[A]	ALA	2.4
1	2-K	90[B]	ALA	2.4
1	3-K	90[C]	ALA	2.4
1	4-K	90[D]	ALA	2.4
1	1-H	306[A]	LYS	2.4
1	1-J	261[A]	ASP	2.4
1	2-H	306[B]	LYS	2.4
1	2-J	261[B]	ASP	2.4
1	3-H	306[C]	LYS	2.4
1	3-J	261[C]	ASP	2.4
1	4-H	306[D]	LYS	2.4
1	4-J	261[D]	ASP	2.4
1	1-A	190[A]	PHE	2.4
1	1-E	226[A]	PHE	2.4
1	2-A	190[B]	PHE	2.4
1	2-E	226[B]	PHE	2.4
1	3-A	190[C]	PHE	2.4
1	3-E	226[C]	PHE	2.4
1	4-A	190[D]	PHE	2.4
1	4-E	226[D]	PHE	2.4
1	1-D	131[A]	TRP	2.4
1	1-D	148[A]	LYS	2.4
1	2-D	131[B]	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	2-D	148[B]	LYS	2.4
1	3-D	131[C]	TRP	2.4
1	3-D	148[C]	LYS	2.4
1	4-D	131[D]	TRP	2.4
1	4-D	148[D]	LYS	2.4
1	1-F	142[A]	ASP	2.4
1	2-F	142[B]	ASP	2.4
1	3-F	142[C]	ASP	2.4
1	4-F	142[D]	ASP	2.4
1	1-B	207[A]	PRO	2.4
1	1-N	136[A]	ALA	2.4
1	2-B	207[B]	PRO	2.4
1	2-N	136[B]	ALA	2.4
1	3-B	207[C]	PRO	2.4
1	3-N	136[C]	ALA	2.4
1	4-B	207[D]	PRO	2.4
1	4-N	136[D]	ALA	2.4
1	1-B	87[A]	CYS	2.4
1	2-B	87[B]	CYS	2.4
1	3-B	87[C]	CYS	2.4
1	4-B	87[D]	CYS	2.4
1	1-K	85[A]	SER	2.4
1	2-K	85[B]	SER	2.4
1	3-K	85[C]	SER	2.4
1	4-K	85[D]	SER	2.4
1	1-G	120[A]	GLU	2.4
1	1-K	20[A]	GLU	2.4
1	1-N	42[A]	GLY	2.4
1	2-G	120[B]	GLU	2.4
1	2-K	20[B]	GLU	2.4
1	2-N	42[B]	GLY	2.4
1	3-G	120[C]	GLU	2.4
1	3-K	20[C]	GLU	2.4
1	3-N	42[C]	GLY	2.4
1	4-G	120[D]	GLU	2.4
1	4-K	20[D]	GLU	2.4
1	4-N	42[D]	GLY	2.4
1	1-H	32[A]	ASN	2.4
1	2-H	32[B]	ASN	2.4
1	3-H	32[C]	ASN	2.4
1	4-H	32[D]	ASN	2.4
1	1-A	265[A]	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	1-C	90[A]	ALA	2.4
1	2-A	265[B]	PRO	2.4
1	2-C	90[B]	ALA	2.4
1	3-A	265[C]	PRO	2.4
1	3-C	90[C]	ALA	2.4
1	4-A	265[D]	PRO	2.4
1	4-C	90[D]	ALA	2.4
1	1-A	313[A]	MET	2.4
1	2-A	313[B]	MET	2.4
1	3-A	313[C]	MET	2.4
1	4-A	313[D]	MET	2.4
1	1-E	145[A]	TYR	2.4
1	1-I	106[A]	SER	2.4
1	1-N	230[A]	SER	2.4
1	2-E	145[B]	TYR	2.4
1	2-I	106[B]	SER	2.4
1	2-N	230[B]	SER	2.4
1	3-E	145[C]	TYR	2.4
1	3-I	106[C]	SER	2.4
1	3-N	230[C]	SER	2.4
1	4-E	145[D]	TYR	2.4
1	4-I	106[D]	SER	2.4
1	4-N	230[D]	SER	2.4
1	1-G	112[A]	LYS	2.4
1	1-H	55[A]	ARG	2.4
1	1-N	216[A]	ARG	2.4
1	2-G	112[B]	LYS	2.4
1	2-H	55[B]	ARG	2.4
1	2-N	216[B]	ARG	2.4
1	3-G	112[C]	LYS	2.4
1	3-H	55[C]	ARG	2.4
1	3-N	216[C]	ARG	2.4
1	4-G	112[D]	LYS	2.4
1	4-H	55[D]	ARG	2.4
1	4-N	216[D]	ARG	2.4
1	1-G	194[A]	PHE	2.4
1	2-G	194[B]	PHE	2.4
1	3-G	194[C]	PHE	2.4
1	4-G	194[D]	PHE	2.4
1	1-D	46[A]	VAL	2.4
1	2-D	46[B]	VAL	2.4
1	3-D	46[C]	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	4-D	46[D]	VAL	2.4
1	1-B	137[A]	GLU	2.4
1	2-B	137[B]	GLU	2.4
1	3-B	137[C]	GLU	2.4
1	4-B	137[D]	GLU	2.4
1	1-C	112[A]	LYS	2.4
1	1-F	55[A]	ARG	2.4
1	2-C	112[B]	LYS	2.4
1	2-F	55[B]	ARG	2.4
1	3-C	112[C]	LYS	2.4
1	3-F	55[C]	ARG	2.4
1	4-C	112[D]	LYS	2.4
1	4-F	55[D]	ARG	2.4
1	1-P	294[A]	GLY	2.4
1	2-P	294[B]	GLY	2.4
1	3-P	294[C]	GLY	2.4
1	4-P	294[D]	GLY	2.4
1	1-F	56[A]	PHE	2.3
1	2-F	56[B]	PHE	2.3
1	3-F	56[C]	PHE	2.3
1	4-F	56[D]	PHE	2.3
1	1-G	273[A]	GLU	2.3
1	2-G	273[B]	GLU	2.3
1	3-G	273[C]	GLU	2.3
1	4-G	273[D]	GLU	2.3
1	1-A	146[A]	LYS	2.3
1	1-B	71[A]	VAL	2.3
1	1-B	267[A]	LYS	2.3
1	1-C	64[A]	PRO	2.3
1	1-C	107[A]	LYS	2.3
1	1-H	84[A]	VAL	2.3
1	1-G	247[A]	HIS	2.3
1	2-A	146[B]	LYS	2.3
1	2-B	71[B]	VAL	2.3
1	2-B	267[B]	LYS	2.3
1	2-C	64[B]	PRO	2.3
1	2-C	107[B]	LYS	2.3
1	2-H	84[B]	VAL	2.3
1	2-G	247[B]	HIS	2.3
1	3-A	146[C]	LYS	2.3
1	3-B	71[C]	VAL	2.3
1	3-B	267[C]	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	3-C	64[C]	PRO	2.3
1	3-C	107[C]	LYS	2.3
1	3-H	84[C]	VAL	2.3
1	3-G	247[C]	HIS	2.3
1	4-A	146[D]	LYS	2.3
1	4-B	71[D]	VAL	2.3
1	4-B	267[D]	LYS	2.3
1	4-C	107[D]	LYS	2.3
1	4-H	84[D]	VAL	2.3
1	1-I	275[A]	ARG	2.3
1	2-I	275[B]	ARG	2.3
1	3-I	275[C]	ARG	2.3
1	4-C	64[D]	PRO	2.3
1	4-G	247[D]	HIS	2.3
1	4-I	275[D]	ARG	2.3
1	1-E	235[A]	THR	2.3
1	1-P	304[A]	GLY	2.3
1	2-E	235[B]	THR	2.3
1	2-P	304[B]	GLY	2.3
1	3-E	235[C]	THR	2.3
1	3-P	304[C]	GLY	2.3
1	4-E	235[D]	THR	2.3
1	4-P	304[D]	GLY	2.3
1	1-D	60[A]	ASP	2.3
1	2-D	60[B]	ASP	2.3
1	3-D	60[C]	ASP	2.3
1	4-D	60[D]	ASP	2.3
1	1-B	148[A]	LYS	2.3
1	2-B	148[B]	LYS	2.3
1	3-B	148[C]	LYS	2.3
1	4-B	148[D]	LYS	2.3
1	1-G	63[A]	LEU	2.3
1	2-G	63[B]	LEU	2.3
1	3-G	63[C]	LEU	2.3
1	4-G	63[D]	LEU	2.3
1	1-A	133[A]	HIS	2.3
1	1-K	125[A]	PRO	2.3
1	1-M	51[A]	PRO	2.3
1	2-A	133[B]	HIS	2.3
1	2-K	125[B]	PRO	2.3
1	2-M	51[B]	PRO	2.3
1	3-A	133[C]	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	3-K	125[C]	PRO	2.3
1	3-M	51[C]	PRO	2.3
1	4-A	133[D]	HIS	2.3
1	4-K	125[D]	PRO	2.3
1	4-M	51[D]	PRO	2.3
1	1-E	147[A]	GLY	2.3
1	1-G	92[A]	MET	2.3
1	1-G	142[A]	ASP	2.3
1	1-O	140[A]	ASP	2.3
1	2-E	147[B]	GLY	2.3
1	2-G	92[B]	MET	2.3
1	2-G	142[B]	ASP	2.3
1	2-O	140[B]	ASP	2.3
1	3-E	147[C]	GLY	2.3
1	3-G	92[C]	MET	2.3
1	3-G	142[C]	ASP	2.3
1	3-O	140[C]	ASP	2.3
1	4-E	147[D]	GLY	2.3
1	4-G	92[D]	MET	2.3
1	4-G	142[D]	ASP	2.3
1	4-O	140[D]	ASP	2.3
1	1-C	81[A]	LEU	2.3
1	2-C	81[B]	LEU	2.3
1	3-C	81[C]	LEU	2.3
1	4-C	81[D]	LEU	2.3
1	1-B	59[A]	ALA	2.3
1	2-B	59[B]	ALA	2.3
1	3-B	59[C]	ALA	2.3
1	4-B	59[D]	ALA	2.3
1	1-B	61[A]	ASN	2.3
1	2-B	61[B]	ASN	2.3
1	3-B	61[C]	ASN	2.3
1	4-B	61[D]	ASN	2.3
1	1-A	236[A]	HIS	2.3
1	2-A	236[B]	HIS	2.3
1	3-A	236[C]	HIS	2.3
1	4-A	236[D]	HIS	2.3
1	1-G	201[A]	ASP	2.3
1	2-G	201[B]	ASP	2.3
1	3-G	201[C]	ASP	2.3
1	4-G	201[D]	ASP	2.3
1	1-E	114[A]	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	1-G	14[A]	SER	2.3
1	1-L	296[A]	LYS	2.3
1	2-E	114[B]	GLY	2.3
1	2-G	14[B]	SER	2.3
1	2-L	296[B]	LYS	2.3
1	3-E	114[C]	GLY	2.3
1	3-G	14[C]	SER	2.3
1	3-L	296[C]	LYS	2.3
1	4-E	114[D]	GLY	2.3
1	4-G	14[D]	SER	2.3
1	4-L	296[D]	LYS	2.3
1	1-A	50[A]	ALA	2.3
1	1-C	28[A]	ARG	2.3
1	1-D	317[A]	ALA	2.3
1	1-F	258[A]	VAL	2.3
1	1-G	82[A]	TRP	2.3
1	1-H	71[A]	VAL	2.3
1	1-H	258[A]	VAL	2.3
1	2-A	50[B]	ALA	2.3
1	2-C	28[B]	ARG	2.3
1	2-D	317[B]	ALA	2.3
1	2-F	258[B]	VAL	2.3
1	2-G	82[B]	TRP	2.3
1	2-H	71[B]	VAL	2.3
1	2-H	258[B]	VAL	2.3
1	3-A	50[C]	ALA	2.3
1	3-C	28[C]	ARG	2.3
1	3-D	317[C]	ALA	2.3
1	3-F	258[C]	VAL	2.3
1	3-G	82[C]	TRP	2.3
1	3-H	71[C]	VAL	2.3
1	3-H	258[C]	VAL	2.3
1	4-A	50[D]	ALA	2.3
1	4-C	28[D]	ARG	2.3
1	4-D	317[D]	ALA	2.3
1	4-F	258[D]	VAL	2.3
1	4-G	82[D]	TRP	2.3
1	4-H	71[D]	VAL	2.3
1	4-H	258[D]	VAL	2.3
1	1-F	264[A]	GLU	2.3
1	2-F	264[B]	GLU	2.3
1	3-F	264[C]	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	4-F	264[D]	GLU	2.3
1	1-A	144[A]	ASP	2.3
1	1-F	312[A]	ASP	2.3
1	2-A	144[B]	ASP	2.3
1	2-F	312[B]	ASP	2.3
1	3-A	144[C]	ASP	2.3
1	3-F	312[C]	ASP	2.3
1	4-A	144[D]	ASP	2.3
1	4-F	312[D]	ASP	2.3
1	1-E	100[A]	ILE	2.3
1	2-E	100[B]	ILE	2.3
1	3-E	100[C]	ILE	2.3
1	4-E	100[D]	ILE	2.3
1	1-G	237[A]	MET	2.3
1	2-G	237[B]	MET	2.3
1	3-G	237[C]	MET	2.3
1	4-G	237[D]	MET	2.3
1	1-B	113[A]	VAL	2.3
1	2-B	113[B]	VAL	2.3
1	3-B	113[C]	VAL	2.3
1	4-B	113[D]	VAL	2.3
1	1-C	114[A]	GLY	2.3
1	1-C	204[A]	GLY	2.3
1	2-C	114[B]	GLY	2.3
1	2-C	204[B]	GLY	2.3
1	3-C	114[C]	GLY	2.3
1	3-C	204[C]	GLY	2.3
1	4-C	114[D]	GLY	2.3
1	4-C	204[D]	GLY	2.3
1	1-B	31[A]	ILE	2.3
1	1-E	108[A]	GLU	2.3
1	2-B	31[B]	ILE	2.3
1	2-E	108[B]	GLU	2.3
1	3-B	31[C]	ILE	2.3
1	3-E	108[C]	GLU	2.3
1	4-B	31[D]	ILE	2.3
1	4-E	108[D]	GLU	2.3
1	1-F	234[A]	LEU	2.2
1	1-L	234[A]	LEU	2.2
1	1-O	270[A]	LEU	2.2
1	2-F	234[B]	LEU	2.2
1	2-L	234[B]	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	2-O	270[B]	LEU	2.2
1	3-F	234[C]	LEU	2.2
1	3-L	234[C]	LEU	2.2
1	3-O	270[C]	LEU	2.2
1	4-F	234[D]	LEU	2.2
1	4-L	234[D]	LEU	2.2
1	4-O	270[D]	LEU	2.2
1	1-D	302[A]	VAL	2.2
1	1-G	302[A]	VAL	2.2
1	2-D	302[B]	VAL	2.2
1	2-G	302[B]	VAL	2.2
1	3-D	302[C]	VAL	2.2
1	3-G	302[C]	VAL	2.2
1	4-D	302[D]	VAL	2.2
1	4-G	302[D]	VAL	2.2
1	1-A	128[A]	GLY	2.2
1	1-B	309[A]	GLY	2.2
1	1-E	103[A]	GLY	2.2
1	1-F	32[A]	ASN	2.2
1	1-G	186[A]	PRO	2.2
1	1-I	278[A]	PRO	2.2
1	2-A	128[B]	GLY	2.2
1	2-B	309[B]	GLY	2.2
1	2-E	103[B]	GLY	2.2
1	2-F	32[B]	ASN	2.2
1	2-G	186[B]	PRO	2.2
1	2-I	278[B]	PRO	2.2
1	3-A	128[C]	GLY	2.2
1	3-B	309[C]	GLY	2.2
1	3-E	103[C]	GLY	2.2
1	3-F	32[C]	ASN	2.2
1	3-G	186[C]	PRO	2.2
1	3-I	278[C]	PRO	2.2
1	4-A	128[D]	GLY	2.2
1	4-B	309[D]	GLY	2.2
1	4-E	103[D]	GLY	2.2
1	4-F	32[D]	ASN	2.2
1	4-G	186[D]	PRO	2.2
1	4-I	278[D]	PRO	2.2
1	1-G	122[A]	ASP	2.2
1	1-L	122[A]	ASP	2.2
1	1-P	142[A]	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	2-G	122[B]	ASP	2.2
1	2-L	122[B]	ASP	2.2
1	2-P	142[B]	ASP	2.2
1	3-G	122[C]	ASP	2.2
1	3-L	122[C]	ASP	2.2
1	3-P	142[C]	ASP	2.2
1	4-G	122[D]	ASP	2.2
1	4-L	122[D]	ASP	2.2
1	4-P	142[D]	ASP	2.2
1	1-G	136[A]	ALA	2.2
1	2-G	136[B]	ALA	2.2
1	3-G	136[C]	ALA	2.2
1	4-G	136[D]	ALA	2.2
1	1-B	41[A]	THR	2.2
1	2-B	41[B]	THR	2.2
1	3-B	41[C]	THR	2.2
1	4-B	41[D]	THR	2.2
1	1-A	120[A]	GLU	2.2
1	1-J	133[A]	HIS	2.2
1	2-A	120[B]	GLU	2.2
1	2-J	133[B]	HIS	2.2
1	3-A	120[C]	GLU	2.2
1	3-J	133[C]	HIS	2.2
1	4-A	120[D]	GLU	2.2
1	4-J	133[D]	HIS	2.2
1	1-C	70[A]	ARG	2.2
1	1-E	70[A]	ARG	2.2
1	1-F	297[A]	VAL	2.2
1	2-C	70[B]	ARG	2.2
1	2-E	70[B]	ARG	2.2
1	2-F	297[B]	VAL	2.2
1	3-C	70[C]	ARG	2.2
1	3-E	70[C]	ARG	2.2
1	3-F	297[C]	VAL	2.2
1	4-C	70[D]	ARG	2.2
1	4-E	70[D]	ARG	2.2
1	4-F	297[D]	VAL	2.2
1	1-A	116[A]	GLY	2.2
1	1-B	97[A]	GLY	2.2
1	2-A	116[B]	GLY	2.2
1	2-B	97[B]	GLY	2.2
1	3-A	116[C]	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	3-B	97[C]	GLY	2.2
1	4-A	116[D]	GLY	2.2
1	4-B	97[D]	GLY	2.2
1	1-G	101[A]	TRP	2.2
1	2-G	101[B]	TRP	2.2
1	3-G	101[C]	TRP	2.2
1	4-G	101[D]	TRP	2.2
1	1-A	288[A]	GLU	2.2
1	1-C	289[A]	ILE	2.2
1	1-G	250[A]	ILE	2.2
1	2-A	288[B]	GLU	2.2
1	2-C	289[B]	ILE	2.2
1	2-G	250[B]	ILE	2.2
1	3-A	288[C]	GLU	2.2
1	3-C	289[C]	ILE	2.2
1	3-G	250[C]	ILE	2.2
1	4-A	288[D]	GLU	2.2
1	4-C	289[D]	ILE	2.2
1	4-G	250[D]	ILE	2.2
1	1-E	232[A]	ALA	2.2
1	2-E	232[B]	ALA	2.2
1	3-E	232[C]	ALA	2.2
1	4-E	232[D]	ALA	2.2
1	1-E	65[A]	LEU	2.2
1	2-E	65[B]	LEU	2.2
1	3-E	65[C]	LEU	2.2
1	4-E	65[D]	LEU	2.2
1	1-C	246[A]	PRO	2.2
1	1-G	98[A]	VAL	2.2
1	1-H	36[A]	VAL	2.2
1	2-C	246[B]	PRO	2.2
1	2-G	98[B]	VAL	2.2
1	2-H	36[B]	VAL	2.2
1	3-C	246[C]	PRO	2.2
1	3-G	98[C]	VAL	2.2
1	3-H	36[C]	VAL	2.2
1	4-C	246[D]	PRO	2.2
1	4-G	98[D]	VAL	2.2
1	4-H	36[D]	VAL	2.2
1	1-C	306[A]	LYS	2.2
1	1-D	146[A]	LYS	2.2
1	1-E	247[A]	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	2-C	306[B]	LYS	2.2
1	2-D	146[B]	LYS	2.2
1	2-E	247[B]	HIS	2.2
1	3-C	306[C]	LYS	2.2
1	3-D	146[C]	LYS	2.2
1	3-E	247[C]	HIS	2.2
1	4-C	306[D]	LYS	2.2
1	4-D	146[D]	LYS	2.2
1	4-E	247[D]	HIS	2.2
1	1-B	228[A]	ILE	2.2
1	1-E	15[A]	ASN	2.2
1	2-B	228[B]	ILE	2.2
1	2-E	15[B]	ASN	2.2
1	3-B	228[C]	ILE	2.2
1	3-E	15[C]	ASN	2.2
1	4-B	228[D]	ILE	2.2
1	4-E	15[D]	ASN	2.2
1	1-J	34[A]	GLY	2.2
1	1-N	218[A]	CYS	2.2
1	2-J	34[B]	GLY	2.2
1	2-N	218[B]	CYS	2.2
1	3-J	34[C]	GLY	2.2
1	3-N	218[C]	CYS	2.2
1	4-J	34[D]	GLY	2.2
1	4-N	218[D]	CYS	2.2
1	1-A	264[A]	GLU	2.2
1	1-D	265[A]	PRO	2.2
1	1-K	230[A]	SER	2.2
1	2-D	265[B]	PRO	2.2
1	2-K	230[B]	SER	2.2
1	3-D	265[C]	PRO	2.2
1	3-K	230[C]	SER	2.2
1	4-D	265[D]	PRO	2.2
1	4-K	230[D]	SER	2.2
1	2-A	264[B]	GLU	2.2
1	3-A	264[C]	GLU	2.2
1	4-A	264[D]	GLU	2.2
1	1-F	126[A]	VAL	2.2
1	2-F	126[B]	VAL	2.2
1	3-F	126[C]	VAL	2.2
1	4-F	126[D]	VAL	2.2
1	1-H	296[A]	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	1-P	29[A]	ARG	2.2
1	2-H	296[B]	LYS	2.2
1	2-P	29[B]	ARG	2.2
1	3-H	296[C]	LYS	2.2
1	3-P	29[C]	ARG	2.2
1	4-H	296[D]	LYS	2.2
1	4-P	29[D]	ARG	2.2
1	1-B	92[A]	MET	2.2
1	2-B	92[B]	MET	2.2
1	3-B	92[C]	MET	2.2
1	4-B	92[D]	MET	2.2
1	1-D	47[A]	ALA	2.2
1	2-D	47[B]	ALA	2.2
1	3-D	47[C]	ALA	2.2
1	4-D	47[D]	ALA	2.2
1	1-H	137[A]	GLU	2.2
1	2-H	137[B]	GLU	2.2
1	3-H	137[C]	GLU	2.2
1	4-H	137[D]	GLU	2.2
1	1-D	228[A]	ILE	2.2
1	1-E	82[A]	TRP	2.2
1	2-D	228[B]	ILE	2.2
1	2-E	82[B]	TRP	2.2
1	3-D	228[C]	ILE	2.2
1	3-E	82[C]	TRP	2.2
1	4-D	228[D]	ILE	2.2
1	4-E	82[D]	TRP	2.2
1	1-F	240[A]	LEU	2.2
1	1-G	52[A]	PRO	2.2
1	2-F	240[B]	LEU	2.2
1	2-G	52[B]	PRO	2.2
1	3-F	240[C]	LEU	2.2
1	3-G	52[C]	PRO	2.2
1	4-F	240[D]	LEU	2.2
1	4-G	52[D]	PRO	2.2
1	1-F	87[A]	CYS	2.2
1	1-J	168[A]	ARG	2.2
1	2-F	87[B]	CYS	2.2
1	2-J	168[B]	ARG	2.2
1	3-F	87[C]	CYS	2.2
1	3-J	168[C]	ARG	2.2
1	4-F	87[D]	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	4-J	168[D]	ARG	2.2
1	1-A	127[A]	TYR	2.2
1	1-F	21[A]	TYR	2.2
1	2-A	127[B]	TYR	2.2
1	2-F	21[B]	TYR	2.2
1	3-A	127[C]	TYR	2.2
1	3-F	21[C]	TYR	2.2
1	4-A	127[D]	TYR	2.2
1	4-F	21[D]	TYR	2.2
1	1-A	117[A]	HIS	2.2
1	2-A	117[B]	HIS	2.2
1	3-A	117[C]	HIS	2.2
1	4-A	117[D]	HIS	2.2
1	1-C	137[A]	GLU	2.2
1	1-O	288[A]	GLU	2.2
1	2-C	137[B]	GLU	2.2
1	2-O	288[B]	GLU	2.2
1	3-C	137[C]	GLU	2.2
1	3-O	288[C]	GLU	2.2
1	4-C	137[D]	GLU	2.2
1	4-O	288[D]	GLU	2.2
1	1-F	43[A]	THR	2.2
1	2-F	43[B]	THR	2.2
1	3-F	43[C]	THR	2.2
1	4-F	43[D]	THR	2.2
1	1-H	314[A]	LYS	2.2
1	1-L	306[A]	LYS	2.2
1	2-H	314[B]	LYS	2.2
1	2-L	306[B]	LYS	2.2
1	3-H	314[C]	LYS	2.2
1	3-L	306[C]	LYS	2.2
1	4-H	314[D]	LYS	2.2
1	4-L	306[D]	LYS	2.2
1	1-N	77[A]	ILE	2.1
1	2-N	77[B]	ILE	2.1
1	3-N	77[C]	ILE	2.1
1	4-N	77[D]	ILE	2.1
1	1-B	58[A]	LEU	2.1
1	1-B	131[A]	TRP	2.1
1	1-D	66[A]	LEU	2.1
1	1-E	282[A]	TRP	2.1
1	2-B	58[B]	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	2-B	131[B]	TRP	2.1
1	2-D	66[B]	LEU	2.1
1	2-E	282[B]	TRP	2.1
1	3-B	58[C]	LEU	2.1
1	3-B	131[C]	TRP	2.1
1	3-D	66[C]	LEU	2.1
1	3-E	282[C]	TRP	2.1
1	4-B	58[D]	LEU	2.1
1	4-B	131[D]	TRP	2.1
1	4-D	66[D]	LEU	2.1
1	4-E	282[D]	TRP	2.1
1	1-E	295[A]	PHE	2.1
1	1-G	145[A]	TYR	2.1
1	2-E	295[B]	PHE	2.1
1	2-G	145[B]	TYR	2.1
1	3-E	295[C]	PHE	2.1
1	3-G	145[C]	TYR	2.1
1	4-E	295[D]	PHE	2.1
1	4-G	145[D]	TYR	2.1
1	1-B	146[A]	LYS	2.1
1	1-G	243[A]	ASP	2.1
1	1-K	293[A]	ASP	2.1
1	2-B	146[B]	LYS	2.1
1	2-G	243[B]	ASP	2.1
1	2-K	293[B]	ASP	2.1
1	3-B	146[C]	LYS	2.1
1	3-G	243[C]	ASP	2.1
1	3-K	293[C]	ASP	2.1
1	4-B	146[D]	LYS	2.1
1	4-G	243[D]	ASP	2.1
1	4-K	293[D]	ASP	2.1
1	1-B	239[A]	ALA	2.1
1	1-G	309[A]	GLY	2.1
1	1-O	97[A]	GLY	2.1
1	1-O	223[A]	GLY	2.1
1	2-B	239[B]	ALA	2.1
1	2-G	309[B]	GLY	2.1
1	2-O	97[B]	GLY	2.1
1	2-O	223[B]	GLY	2.1
1	3-B	239[C]	ALA	2.1
1	3-G	309[C]	GLY	2.1
1	3-O	97[C]	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	3-O	223[C]	GLY	2.1
1	3-C	202[C]	SER	2.1
1	3-G	45[C]	THR	2.1
1	3-L	96[C]	GLN	2.1
1	4-B	239[D]	ALA	2.1
1	4-G	309[D]	GLY	2.1
1	4-O	97[D]	GLY	2.1
1	4-O	223[D]	GLY	2.1
1	1-C	202[A]	SER	2.1
1	1-G	45[A]	THR	2.1
1	1-L	96[A]	GLN	2.1
1	2-C	202[B]	SER	2.1
1	2-G	45[B]	THR	2.1
1	2-L	96[B]	GLN	2.1
1	4-C	202[D]	SER	2.1
1	4-G	45[D]	THR	2.1
1	4-L	96[D]	GLN	2.1
1	1-B	170[A]	ILE	2.1
1	2-B	170[B]	ILE	2.1
1	3-B	170[C]	ILE	2.1
1	4-B	170[D]	ILE	2.1
1	1-A	81[A]	LEU	2.1
1	1-C	26[A]	LEU	2.1
1	1-M	162[A]	ASN	2.1
1	2-A	81[B]	LEU	2.1
1	2-C	26[B]	LEU	2.1
1	2-M	162[B]	ASN	2.1
1	3-A	81[C]	LEU	2.1
1	3-C	26[C]	LEU	2.1
1	3-M	162[C]	ASN	2.1
1	4-A	81[D]	LEU	2.1
1	4-C	26[D]	LEU	2.1
1	4-M	162[D]	ASN	2.1
1	1-F	296[A]	LYS	2.1
1	1-G	117[A]	HIS	2.1
1	2-F	296[B]	LYS	2.1
1	2-G	117[B]	HIS	2.1
1	3-F	296[C]	LYS	2.1
1	3-G	117[C]	HIS	2.1
1	4-F	296[D]	LYS	2.1
1	4-G	117[D]	HIS	2.1
1	1-E	297[A]	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	1-P	122[A]	ASP	2.1
1	2-E	297[B]	VAL	2.1
1	2-P	122[B]	ASP	2.1
1	3-E	297[C]	VAL	2.1
1	3-P	122[C]	ASP	2.1
1	4-E	297[D]	VAL	2.1
1	4-P	122[D]	ASP	2.1
1	1-A	74[A]	ARG	2.1
1	2-A	74[B]	ARG	2.1
1	3-A	74[C]	ARG	2.1
1	4-A	74[D]	ARG	2.1
1	1-D	136[A]	ALA	2.1
1	1-G	268[A]	THR	2.1
1	1-H	229[A]	ALA	2.1
1	1-H	285[A]	SER	2.1
1	2-D	136[B]	ALA	2.1
1	2-H	229[B]	ALA	2.1
1	2-H	285[B]	SER	2.1
1	3-D	136[C]	ALA	2.1
1	3-G	268[C]	THR	2.1
1	3-H	229[C]	ALA	2.1
1	3-H	285[C]	SER	2.1
1	4-D	136[D]	ALA	2.1
1	4-H	229[D]	ALA	2.1
1	4-H	285[D]	SER	2.1
1	2-G	268[B]	THR	2.1
1	4-G	268[D]	THR	2.1
1	1-C	314[A]	LYS	2.1
1	1-E	107[A]	LYS	2.1
1	2-C	314[B]	LYS	2.1
1	2-E	107[B]	LYS	2.1
1	3-C	314[C]	LYS	2.1
1	3-E	107[C]	LYS	2.1
1	4-C	314[D]	LYS	2.1
1	4-E	107[D]	LYS	2.1
1	1-B	18[A]	HIS	2.1
1	1-C	238[A]	ILE	2.1
1	2-B	18[B]	HIS	2.1
1	2-C	238[B]	ILE	2.1
1	3-B	18[C]	HIS	2.1
1	3-C	238[C]	ILE	2.1
1	4-B	18[D]	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	4-C	238[D]	ILE	2.1
1	1-A	115[A]	LEU	2.1
1	2-A	115[B]	LEU	2.1
1	3-A	115[C]	LEU	2.1
1	4-A	115[D]	LEU	2.1
1	1-B	36[A]	VAL	2.1
1	1-D	97[A]	GLY	2.1
1	2-B	36[B]	VAL	2.1
1	2-D	97[B]	GLY	2.1
1	3-B	36[C]	VAL	2.1
1	3-D	97[C]	GLY	2.1
1	4-B	36[D]	VAL	2.1
1	4-D	97[D]	GLY	2.1
1	1-A	246[A]	PRO	2.1
1	2-A	246[B]	PRO	2.1
1	3-A	246[C]	PRO	2.1
1	4-A	246[D]	PRO	2.1
1	1-F	13[A]	ARG	2.1
1	1-I	168[A]	ARG	2.1
1	2-F	13[B]	ARG	2.1
1	2-I	168[B]	ARG	2.1
1	3-F	13[C]	ARG	2.1
1	3-I	168[C]	ARG	2.1
1	4-F	13[D]	ARG	2.1
1	4-I	168[D]	ARG	2.1
1	1-E	120[A]	GLU	2.1
1	2-E	120[B]	GLU	2.1
1	3-E	120[C]	GLU	2.1
1	4-E	120[D]	GLU	2.1
1	1-G	241[A]	ILE	2.1
1	1-J	170[A]	ILE	2.1
1	2-G	241[B]	ILE	2.1
1	2-J	170[B]	ILE	2.1
1	3-G	241[C]	ILE	2.1
1	3-J	170[C]	ILE	2.1
1	4-G	241[D]	ILE	2.1
1	4-J	170[D]	ILE	2.1
1	1-H	126[A]	VAL	2.1
1	2-H	126[B]	VAL	2.1
1	3-H	126[C]	VAL	2.1
1	4-H	126[D]	VAL	2.1
1	1-B	300[A]	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	1-D	134[A]	PHE	2.1
1	1-F	64[A]	PRO	2.1
1	1-G	265[A]	PRO	2.1
1	1-H	307[A]	PRO	2.1
1	2-B	300[B]	PHE	2.1
1	2-D	134[B]	PHE	2.1
1	2-F	64[B]	PRO	2.1
1	2-G	265[B]	PRO	2.1
1	2-H	307[B]	PRO	2.1
1	3-B	300[C]	PHE	2.1
1	3-D	134[C]	PHE	2.1
1	3-F	64[C]	PRO	2.1
1	3-G	265[C]	PRO	2.1
1	3-H	307[C]	PRO	2.1
1	4-B	300[D]	PHE	2.1
1	4-D	134[D]	PHE	2.1
1	4-F	64[D]	PRO	2.1
1	4-G	265[D]	PRO	2.1
1	4-H	307[D]	PRO	2.1
1	1-B	74[A]	ARG	2.1
1	1-G	25[A]	ASP	2.1
1	2-B	74[B]	ARG	2.1
1	2-G	25[B]	ASP	2.1
1	1-B	188[A]	HIS	2.1
1	1-L	20[A]	GLU	2.1
1	3-B	74[C]	ARG	2.1
1	3-G	25[C]	ASP	2.1
1	4-B	74[D]	ARG	2.1
1	4-G	25[D]	ASP	2.1
1	2-B	188[B]	HIS	2.1
1	2-L	20[B]	GLU	2.1
1	3-B	188[C]	HIS	2.1
1	3-L	20[C]	GLU	2.1
1	4-B	188[D]	HIS	2.1
1	4-L	20[D]	GLU	2.1
1	1-G	87[A]	CYS	2.1
1	2-G	87[B]	CYS	2.1
1	3-G	87[C]	CYS	2.1
1	4-G	87[D]	CYS	2.1
1	1-C	309[A]	GLY	2.1
1	1-K	114[A]	GLY	2.1
1	1-L	177[A]	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	2-C	309[B]	GLY	2.1
1	2-K	114[B]	GLY	2.1
1	2-L	177[B]	LYS	2.1
1	3-C	309[C]	GLY	2.1
1	3-K	114[C]	GLY	2.1
1	3-L	177[C]	LYS	2.1
1	4-C	309[D]	GLY	2.1
1	4-K	114[D]	GLY	2.1
1	4-L	177[D]	LYS	2.1
1	1-D	250[A]	ILE	2.1
1	1-F	53[A]	SER	2.1
1	2-D	250[B]	ILE	2.1
1	2-F	53[B]	SER	2.1
1	3-D	250[C]	ILE	2.1
1	3-F	53[C]	SER	2.1
1	4-D	250[D]	ILE	2.1
1	4-F	53[D]	SER	2.1
1	1-D	163[A]	ASN	2.1
1	1-E	237[A]	MET	2.1
1	2-B	16[B]	PRO	2.1
1	2-B	278[B]	PRO	2.1
1	2-D	163[B]	ASN	2.1
1	2-E	237[B]	MET	2.1
1	3-E	237[C]	MET	2.1
1	3-B	278[C]	PRO	2.1
1	3-D	163[C]	ASN	2.1
1	4-D	163[D]	ASN	2.1
1	4-E	237[D]	MET	2.1
1	1-B	16[A]	PRO	2.1
1	1-B	278[A]	PRO	2.1
1	1-F	248[A]	GLU	2.1
1	1-J	293[A]	ASP	2.1
1	2-F	248[B]	GLU	2.1
1	2-J	293[B]	ASP	2.1
1	3-B	16[C]	PRO	2.1
1	3-F	248[C]	GLU	2.1
1	3-J	293[C]	ASP	2.1
1	4-B	16[D]	PRO	2.1
1	4-B	278[D]	PRO	2.1
1	4-F	248[D]	GLU	2.1
1	4-J	293[D]	ASP	2.1
1	1-D	165[A]	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	1-F	41[A]	THR	2.1
1	2-D	165[B]	THR	2.1
1	2-F	41[B]	THR	2.1
1	3-D	165[C]	THR	2.1
1	3-F	41[C]	THR	2.1
1	4-D	165[D]	THR	2.1
1	4-F	41[D]	THR	2.1
1	1-A	83[A]	PHE	2.1
1	1-E	54[A]	PHE	2.1
1	2-A	83[B]	PHE	2.1
1	2-E	54[B]	PHE	2.1
1	3-A	83[C]	PHE	2.1
1	3-E	54[C]	PHE	2.1
1	4-A	83[D]	PHE	2.1
1	4-E	54[D]	PHE	2.1
1	1-G	279[A]	LYS	2.1
1	2-G	279[B]	LYS	2.1
1	3-G	279[C]	LYS	2.1
1	4-G	279[D]	LYS	2.1
1	1-A	309[A]	GLY	2.1
1	1-M	149[A]	GLY	2.1
1	2-A	309[B]	GLY	2.1
1	2-M	149[B]	GLY	2.1
1	3-A	309[C]	GLY	2.1
1	3-M	149[C]	GLY	2.1
1	4-A	309[D]	GLY	2.1
1	4-M	149[D]	GLY	2.1
1	1-H	53[A]	SER	2.0
1	2-H	53[B]	SER	2.0
1	3-H	53[C]	SER	2.0
1	4-H	53[D]	SER	2.0
1	1-A	270[A]	LEU	2.0
1	1-A	311[A]	ILE	2.0
1	1-C	140[A]	ASP	2.0
1	1-E	228[A]	ILE	2.0
1	1-H	293[A]	ASP	2.0
1	2-A	270[B]	LEU	2.0
1	2-A	311[B]	ILE	2.0
1	2-C	140[B]	ASP	2.0
1	2-E	228[B]	ILE	2.0
1	2-H	293[B]	ASP	2.0
1	2-D	52[B]	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	2-D	154[B]	GLN	2.0
1	3-A	270[C]	LEU	2.0
1	3-A	311[C]	ILE	2.0
1	3-C	140[C]	ASP	2.0
1	3-E	228[C]	ILE	2.0
1	3-H	293[C]	ASP	2.0
1	3-D	52[C]	PRO	2.0
1	3-D	154[C]	GLN	2.0
1	4-A	270[D]	LEU	2.0
1	4-A	311[D]	ILE	2.0
1	4-C	140[D]	ASP	2.0
1	4-E	228[D]	ILE	2.0
1	4-H	293[D]	ASP	2.0
1	1-D	52[A]	PRO	2.0
1	1-D	154[A]	GLN	2.0
1	4-D	52[D]	PRO	2.0
1	4-D	154[D]	GLN	2.0
1	1-D	41[A]	THR	2.0
1	1-F	59[A]	ALA	2.0
1	1-F	283[A]	ALA	2.0
1	2-D	41[B]	THR	2.0
1	2-F	59[B]	ALA	2.0
1	2-F	283[B]	ALA	2.0
1	3-D	41[C]	THR	2.0
1	3-F	59[C]	ALA	2.0
1	3-F	283[C]	ALA	2.0
1	4-D	41[D]	THR	2.0
1	4-F	59[D]	ALA	2.0
1	4-F	283[D]	ALA	2.0
1	1-B	194[A]	PHE	2.0
1	2-B	194[B]	PHE	2.0
1	3-B	194[C]	PHE	2.0
1	4-B	194[D]	PHE	2.0
1	1-A	259[A]	TYR	2.0
1	1-F	23[A]	TYR	2.0
1	2-A	259[B]	TYR	2.0
1	2-F	23[B]	TYR	2.0
1	3-A	259[C]	TYR	2.0
1	3-F	23[C]	TYR	2.0
1	4-A	259[D]	TYR	2.0
1	4-F	23[D]	TYR	2.0
1	1-E	61[A]	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	1-E	74[A]	ARG	2.0
1	1-G	205[A]	SER	2.0
1	2-E	61[B]	ASN	2.0
1	2-E	74[B]	ARG	2.0
1	2-G	205[B]	SER	2.0
1	3-E	61[C]	ASN	2.0
1	3-E	74[C]	ARG	2.0
1	3-G	205[C]	SER	2.0
1	4-E	61[D]	ASN	2.0
1	4-E	74[D]	ARG	2.0
1	4-G	205[D]	SER	2.0
1	1-C	313[A]	MET	2.0
1	1-D	87[A]	CYS	2.0
1	1-D	180[A]	PRO	2.0
1	1-H	208[A]	LYS	2.0
1	2-C	313[B]	MET	2.0
1	2-D	87[B]	CYS	2.0
1	2-D	180[B]	PRO	2.0
1	2-H	208[B]	LYS	2.0
1	3-C	313[C]	MET	2.0
1	3-D	87[C]	CYS	2.0
1	3-D	180[C]	PRO	2.0
1	3-H	208[C]	LYS	2.0
1	4-C	313[D]	MET	2.0
1	4-D	87[D]	CYS	2.0
1	4-D	180[D]	PRO	2.0
1	4-H	208[D]	LYS	2.0
1	1-E	211[A]	CYS	2.0
1	2-E	211[B]	CYS	2.0
1	3-E	211[C]	CYS	2.0
1	4-E	211[D]	CYS	2.0
1	1-F	179[A]	LEU	2.0
1	2-F	179[B]	LEU	2.0
1	3-F	179[C]	LEU	2.0
1	4-F	179[D]	LEU	2.0
1	1-F	287[A]	GLU	2.0
1	1-G	46[A]	VAL	2.0
1	2-F	287[B]	GLU	2.0
1	2-G	46[B]	VAL	2.0
1	3-F	287[C]	GLU	2.0
1	3-G	46[C]	VAL	2.0
1	4-F	287[D]	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	4-G	46[D]	VAL	2.0
1	1-K	122[A]	ASP	2.0
1	2-K	122[B]	ASP	2.0
1	3-K	122[C]	ASP	2.0
1	4-K	122[D]	ASP	2.0
1	1-A	225[A]	PRO	2.0
1	2-A	225[B]	PRO	2.0
1	3-A	225[C]	PRO	2.0
1	4-A	225[D]	PRO	2.0
1	1-H	313[A]	MET	2.0
1	1-M	253[A]	MET	2.0
1	2-H	313[B]	MET	2.0
1	2-M	253[B]	MET	2.0
1	3-H	313[C]	MET	2.0
1	3-M	253[C]	MET	2.0
1	4-H	313[D]	MET	2.0
1	4-M	253[D]	MET	2.0
1	1-E	273[A]	GLU	2.0
1	2-E	273[B]	GLU	2.0
1	3-E	273[C]	GLU	2.0
1	4-E	273[D]	GLU	2.0
1	1-P	165[A]	THR	2.0
1	2-P	165[B]	THR	2.0
1	3-P	165[C]	THR	2.0
1	4-P	165[D]	THR	2.0
1	1-D	25[A]	ASP	2.0
1	1-E	25[A]	ASP	2.0
1	1-G	258[A]	VAL	2.0
1	1-H	34[A]	GLY	2.0
1	1-I	279[A]	LYS	2.0
1	2-D	25[B]	ASP	2.0
1	2-E	25[B]	ASP	2.0
1	2-G	258[B]	VAL	2.0
1	2-H	34[B]	GLY	2.0
1	2-I	279[B]	LYS	2.0
1	3-D	25[C]	ASP	2.0
1	3-E	25[C]	ASP	2.0
1	3-G	258[C]	VAL	2.0
1	3-H	34[C]	GLY	2.0
1	3-I	279[C]	LYS	2.0
1	4-D	25[D]	ASP	2.0
1	4-E	25[D]	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	4-G	258[D]	VAL	2.0
1	4-H	34[D]	GLY	2.0
1	4-I	279[D]	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	UMP	4-J	400[D]	20/20	0.51	0.59	49,61,70,70	20
2	UMP	1-J	400[A]	20/20	0.51	0.59	48,61,70,71	20
2	UMP	3-J	400[C]	20/20	0.51	0.59	49,60,70,70	20
2	UMP	2-J	400[B]	20/20	0.51	0.59	49,61,71,71	20
2	UMP	1-I	350[A]	20/20	0.58	0.52	50,62,74,74	20
2	UMP	3-I	350[C]	20/20	0.58	0.52	50,62,74,74	20
2	UMP	2-I	350[B]	20/20	0.58	0.52	50,62,74,74	20
2	UMP	4-I	350[D]	20/20	0.58	0.52	50,62,74,74	20
2	UMP	3-N	600[C]	20/20	0.60	0.54	48,60,72,72	20
2	UMP	2-N	600[B]	20/20	0.60	0.54	49,61,72,72	20
2	UMP	1-N	600[A]	20/20	0.60	0.54	48,61,72,72	20
2	UMP	4-N	600[D]	20/20	0.60	0.54	48,60,72,72	20
2	UMP	1-K	450[A]	20/20	0.62	0.50	49,62,73,73	20
2	UMP	2-K	450[B]	20/20	0.62	0.50	49,62,73,73	20
2	UMP	4-K	450[D]	20/20	0.62	0.50	50,62,73,73	20
2	UMP	3-K	450[C]	20/20	0.62	0.50	49,62,73,73	20
2	UMP	1-M	550[A]	20/20	0.66	0.41	49,62,73,73	20
2	UMP	2-M	550[B]	20/20	0.66	0.41	50,62,73,73	20
2	UMP	3-M	550[C]	20/20	0.66	0.41	49,62,72,72	20

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	UMP	4-M	550[D]	20/20	0.66	0.41	50,61,73,73	20
2	UMP	1-L	500[A]	20/20	0.70	0.45	49,61,71,71	20
2	UMP	3-L	500[C]	20/20	0.70	0.45	49,61,71,71	20
2	UMP	2-L	500[B]	20/20	0.70	0.45	49,61,71,71	20
2	UMP	4-L	500[D]	20/20	0.70	0.45	49,61,71,71	20
2	UMP	2-P	700[B]	20/20	0.75	0.46	48,60,70,70	20
2	UMP	1-P	700[A]	20/20	0.75	0.46	48,60,70,70	20
2	UMP	4-P	700[D]	20/20	0.75	0.46	49,60,70,70	20
2	UMP	3-P	700[C]	20/20	0.75	0.46	49,60,70,70	20
3	CB3	4-H	2701[D]	35/35	0.82	0.21	14,22,31,36	35
3	CB3	3-H	2701[C]	35/35	0.82	0.21	14,22,31,36	35
3	CB3	1-H	2701[A]	35/35	0.82	0.21	14,22,31,36	35
3	CB3	2-H	2701[B]	35/35	0.82	0.21	14,22,31,36	35
2	UMP	2-O	650[B]	20/20	0.83	0.31	17,19,19,19	20
2	UMP	3-O	650[C]	20/20	0.83	0.31	17,19,20,22	20
2	UMP	4-O	650[D]	20/20	0.83	0.31	17,18,19,20	20
2	UMP	1-O	650[A]	20/20	0.83	0.31	17,18,19,19	20
3	CB3	1-F	2601[A]	35/35	0.85	0.23	16,23,32,39	35
3	CB3	4-F	2601[D]	35/35	0.85	0.23	16,23,32,39	35
3	CB3	3-F	2601[C]	35/35	0.85	0.23	16,23,32,39	35
3	CB3	2-F	2601[B]	35/35	0.85	0.23	16,23,32,39	35
3	CB3	1-B	2401[A]	35/35	0.86	0.19	18,22,38,40	35
3	CB3	2-B	2401[B]	35/35	0.86	0.19	18,22,38,40	35
3	CB3	3-B	2401[C]	35/35	0.86	0.19	18,22,38,40	35
3	CB3	4-B	2401[D]	35/35	0.86	0.19	18,22,38,40	35
3	CB3	3-D	2501[C]	35/35	0.87	0.20	14,23,41,44	35
3	CB3	1-D	2501[A]	35/35	0.87	0.20	14,23,41,44	35
3	CB3	4-D	2501[D]	35/35	0.87	0.20	14,23,41,44	35
3	CB3	2-D	2501[B]	35/35	0.87	0.20	14,23,41,44	35
3	CB3	1-E	2551[A]	35/35	0.88	0.20	15,23,37,37	35
3	CB3	4-E	2551[D]	35/35	0.88	0.20	15,23,37,37	35
3	CB3	2-E	2551[B]	35/35	0.88	0.20	15,23,37,37	35
3	CB3	3-E	2551[C]	35/35	0.88	0.20	15,23,37,37	35
2	UMP	1-C	450[A]	20/20	0.89	0.22	17,21,27,27	20
2	UMP	3-C	450[C]	20/20	0.89	0.22	17,21,27,27	20
2	UMP	4-C	450[D]	20/20	0.89	0.22	17,21,27,27	20
2	UMP	2-C	450[B]	20/20	0.89	0.22	17,21,27,27	20
2	UMP	4-A	350[D]	20/20	0.90	0.22	18,23,27,29	20
2	UMP	3-A	350[C]	20/20	0.90	0.22	18,23,27,29	20
3	CB3	1-G	2651[A]	35/35	0.90	0.23	18,24,32,37	35
3	CB3	4-G	2651[D]	35/35	0.90	0.23	18,24,32,37	35
3	CB3	4-C	2451[D]	35/35	0.90	0.21	20,26,32,37	35

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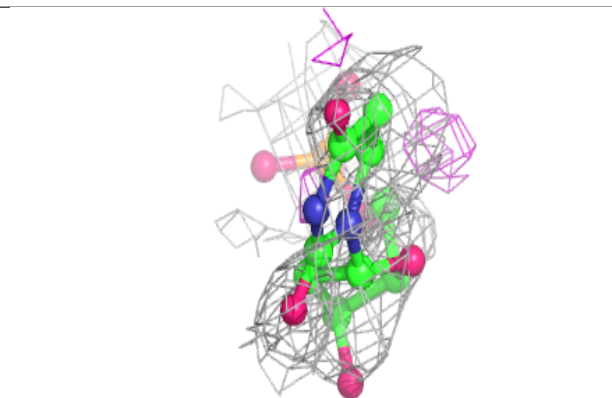
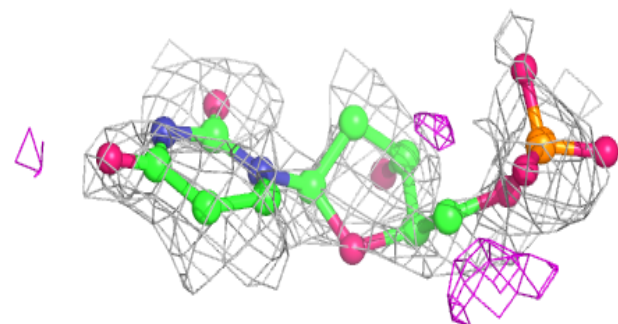
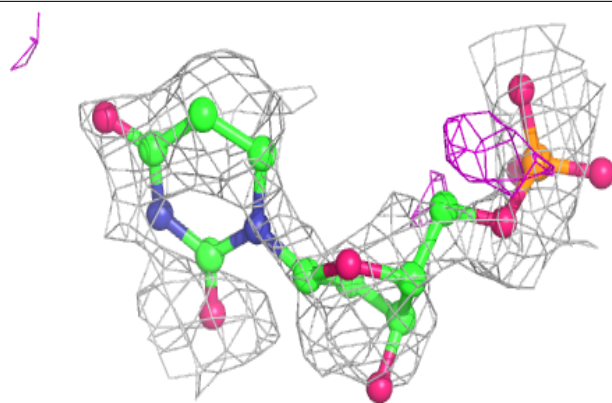
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	UMP	1-A	350[A]	20/20	0.90	0.22	18,23,27,29	20
3	CB3	1-C	2451[A]	35/35	0.90	0.21	20,26,32,37	35
2	UMP	2-A	350[B]	20/20	0.90	0.22	18,23,27,29	20
3	CB3	2-C	2451[B]	35/35	0.90	0.21	20,26,32,37	35
3	CB3	3-G	2651[C]	35/35	0.90	0.23	18,24,32,37	35
3	CB3	2-G	2651[B]	35/35	0.90	0.23	18,24,32,37	35
3	CB3	3-C	2451[C]	35/35	0.90	0.21	20,26,32,37	35
3	CB3	4-A	2351[D]	35/35	0.91	0.18	16,24,31,35	35
3	CB3	1-A	2351[A]	35/35	0.91	0.18	16,24,31,35	35
3	CB3	3-A	2351[C]	35/35	0.91	0.18	16,24,31,35	35
3	CB3	2-A	2351[B]	35/35	0.91	0.18	16,24,31,35	35
2	UMP	1-E	550[A]	20/20	0.92	0.16	20,22,24,24	20
2	UMP	4-G	650[D]	20/20	0.92	0.18	18,21,23,26	20
2	UMP	4-E	550[D]	20/20	0.92	0.16	20,22,24,24	20
2	UMP	1-G	650[A]	20/20	0.92	0.18	18,21,23,26	20
2	UMP	3-G	650[C]	20/20	0.92	0.18	18,21,23,26	20
2	UMP	2-E	550[B]	20/20	0.92	0.16	20,22,24,24	20
2	UMP	3-E	550[C]	20/20	0.92	0.16	20,22,24,24	20
2	UMP	2-G	650[B]	20/20	0.92	0.18	18,21,23,26	20
2	UMP	3-B	400[C]	20/20	0.94	0.17	13,17,22,22	20
2	UMP	1-D	500[A]	20/20	0.94	0.16	14,19,22,25	20
2	UMP	2-B	400[B]	20/20	0.94	0.17	13,17,22,22	20
2	UMP	4-B	400[D]	20/20	0.94	0.17	13,17,22,22	20
2	UMP	1-B	400[A]	20/20	0.94	0.17	13,17,22,22	20
2	UMP	3-D	500[C]	20/20	0.94	0.16	14,19,22,25	20
2	UMP	2-D	500[B]	20/20	0.94	0.16	14,19,22,25	20
2	UMP	4-D	500[D]	20/20	0.94	0.16	14,19,22,25	20
2	UMP	2-F	600[B]	20/20	0.95	0.15	15,18,22,22	20
2	UMP	4-F	600[D]	20/20	0.95	0.15	15,18,22,22	20
2	UMP	3-F	600[C]	20/20	0.95	0.15	15,18,22,22	20
2	UMP	1-F	600[A]	20/20	0.95	0.15	15,18,22,22	20
2	UMP	1-H	700[A]	20/20	0.96	0.12	13,19,30,56	20
2	UMP	4-H	700[D]	20/20	0.96	0.12	13,19,30,56	20
2	UMP	3-H	700[C]	20/20	0.96	0.12	13,19,30,56	20
2	UMP	2-H	700[B]	20/20	0.96	0.12	13,19,30,56	20

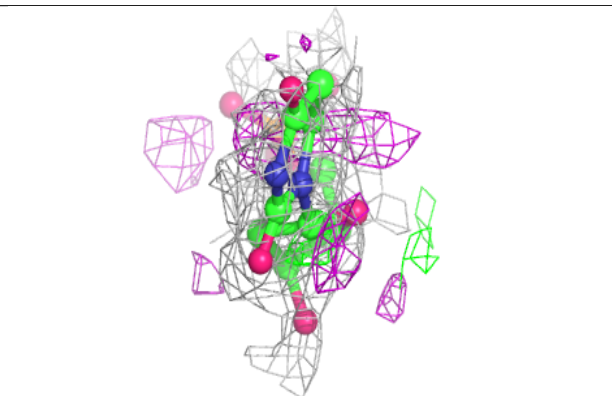
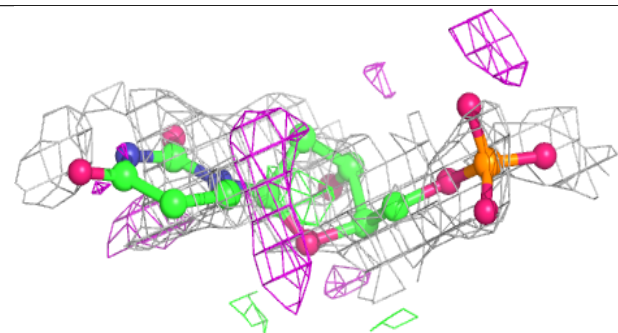
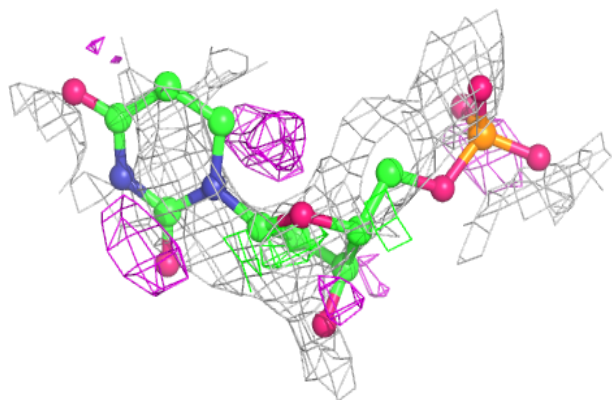
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around UMP J 400 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around UMP I 350 (A):**

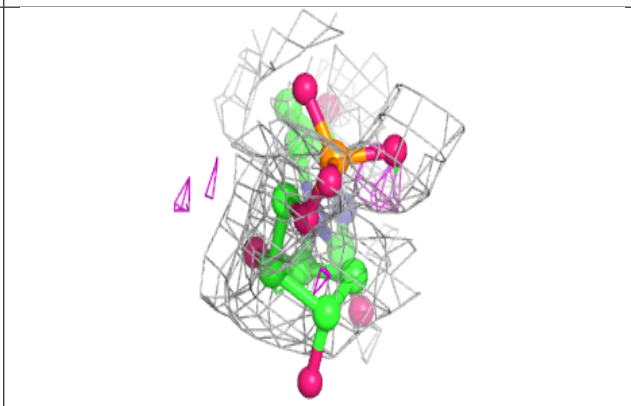
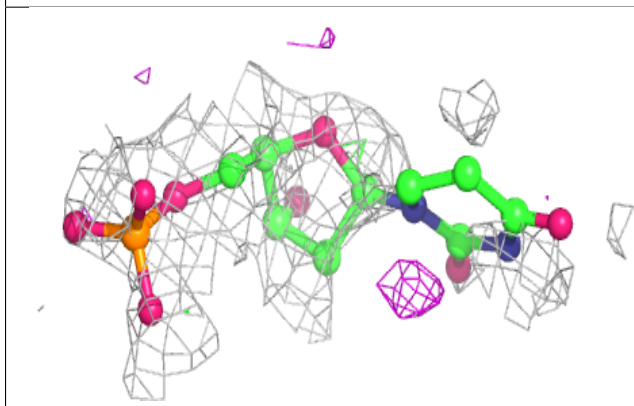
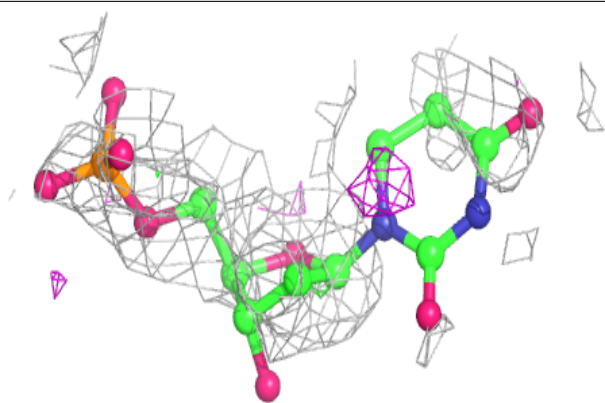
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



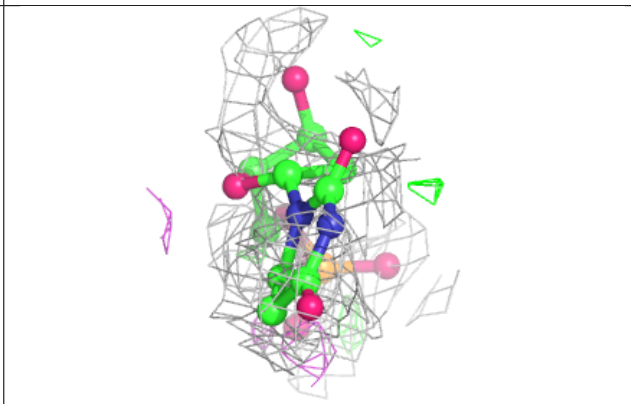
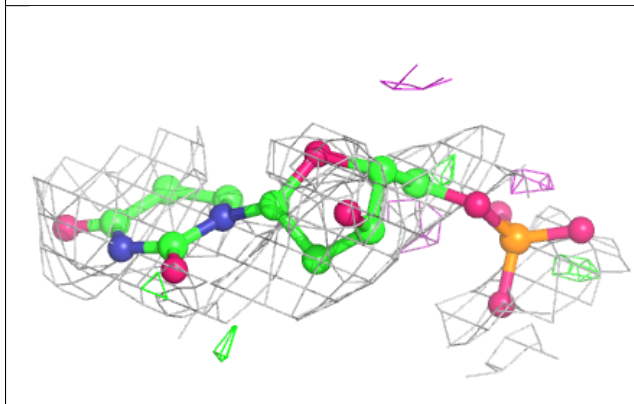
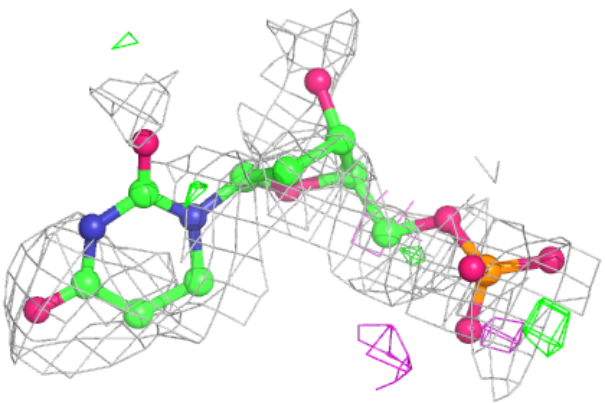


**Electron density around UMP N 600 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

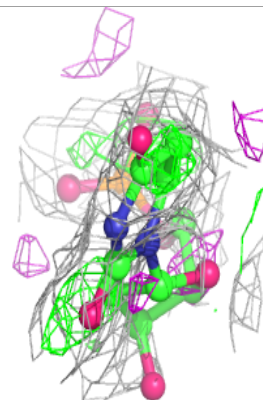
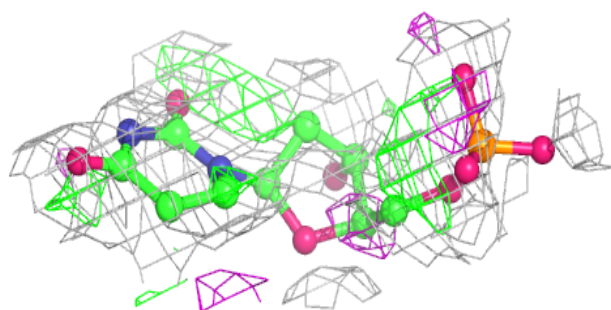
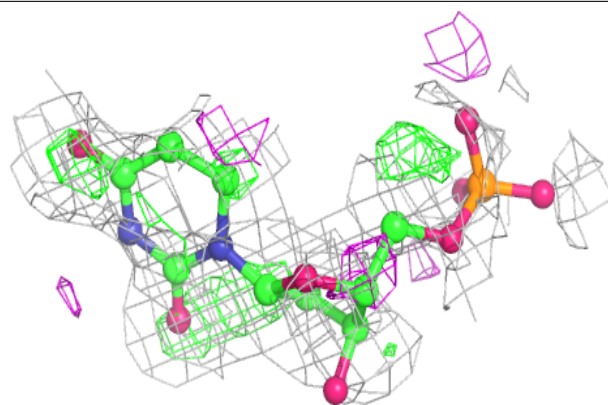
**Electron density around UMP K 450 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

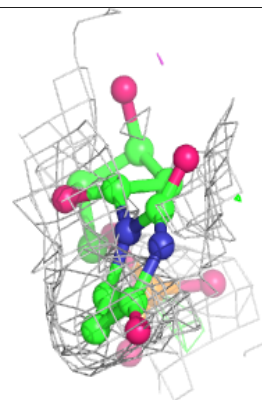
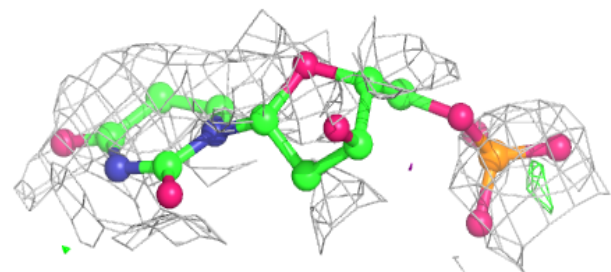
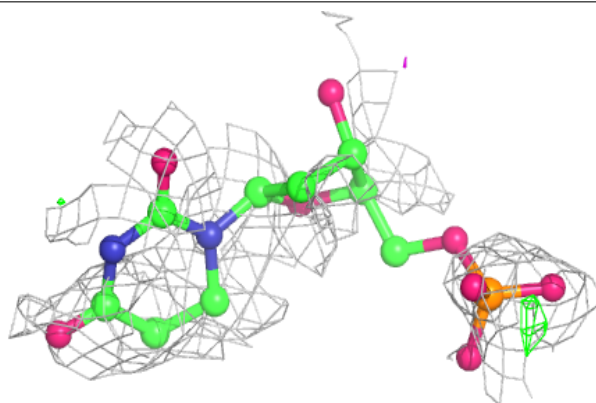


**Electron density around UMP M 550 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

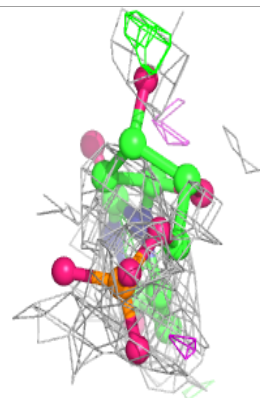
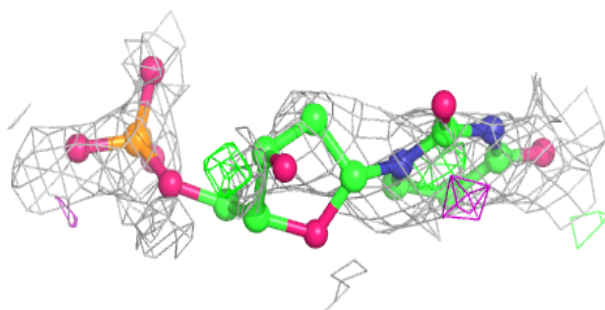
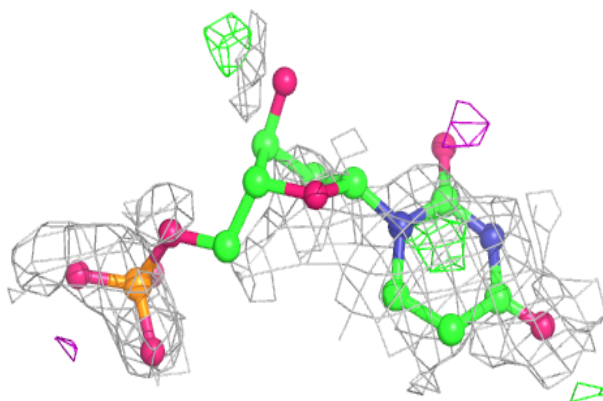
**Electron density around UMP L 500 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

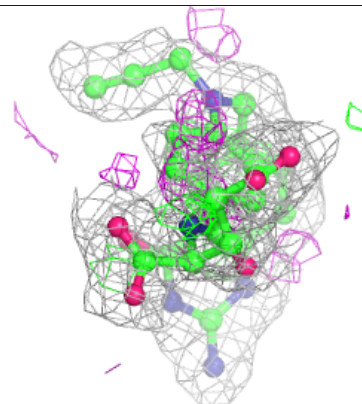
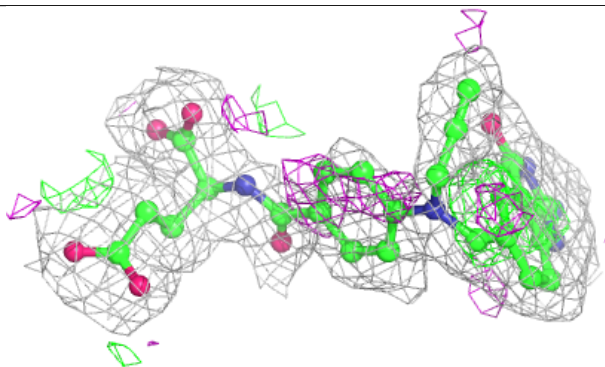
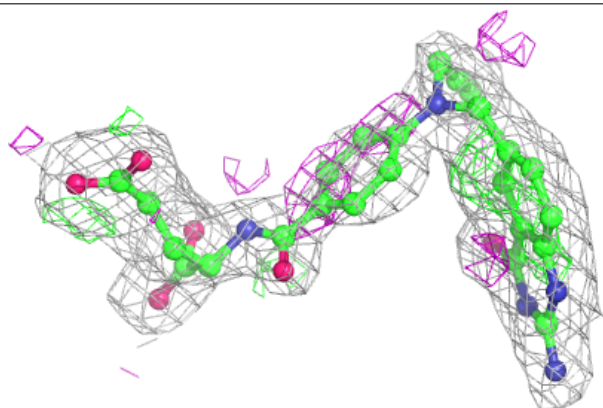


**Electron density around UMP P 700 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

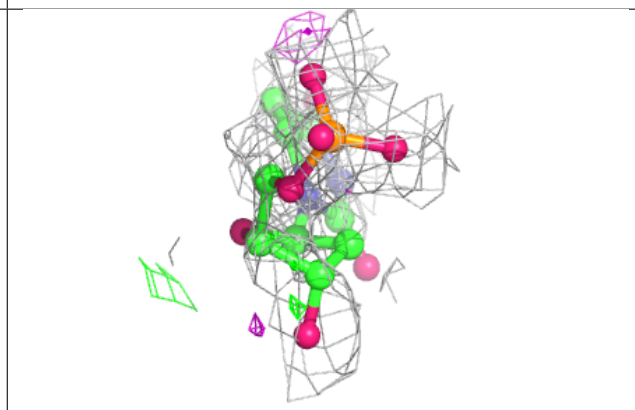
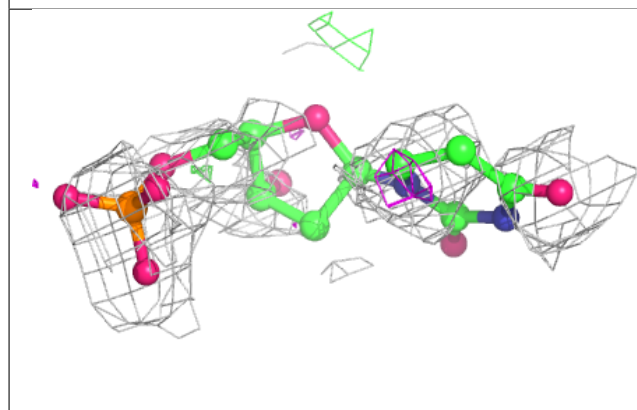
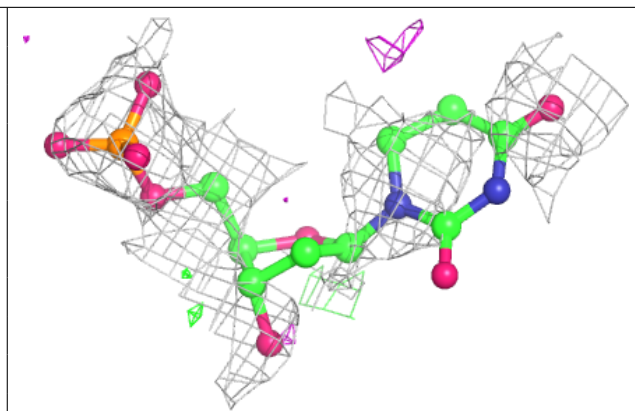
**Electron density around CB3 H 2701 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

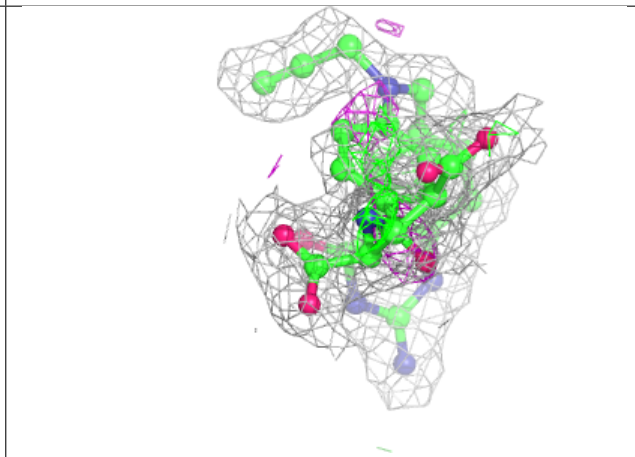
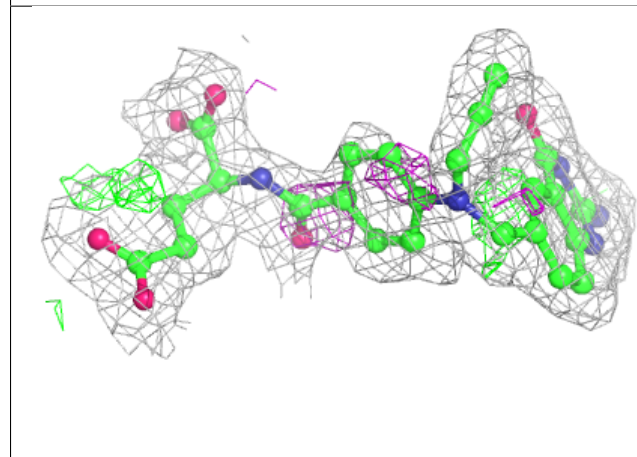
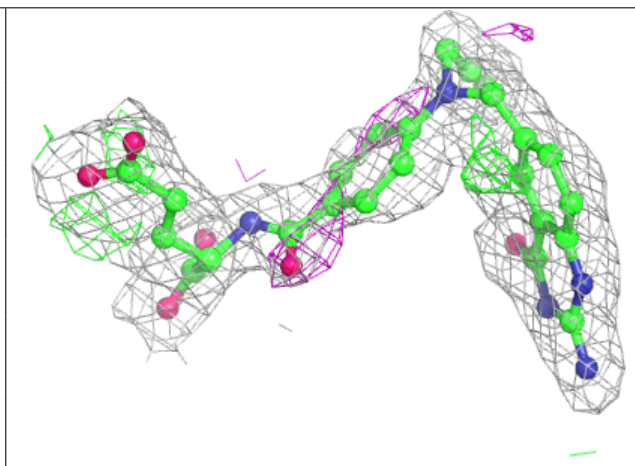


**Electron density around UMP O 650 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around CB3 F 2601 (A):**

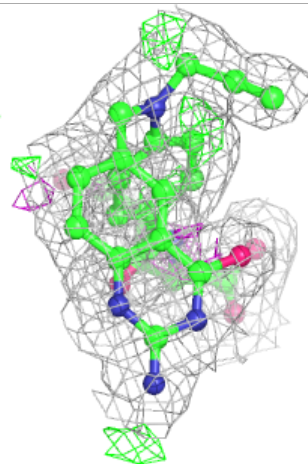
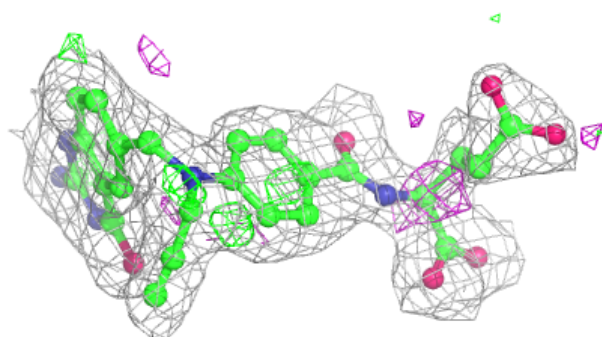
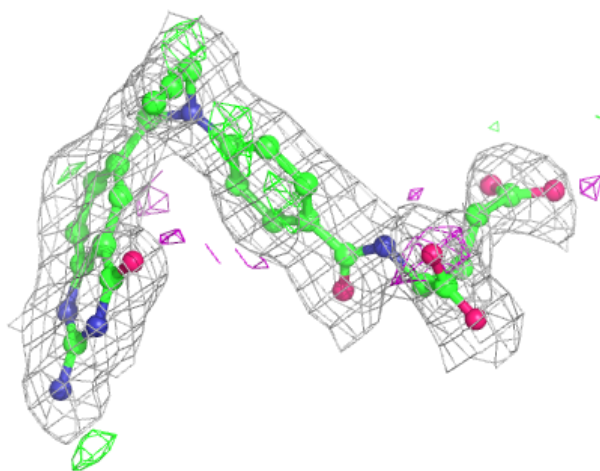
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





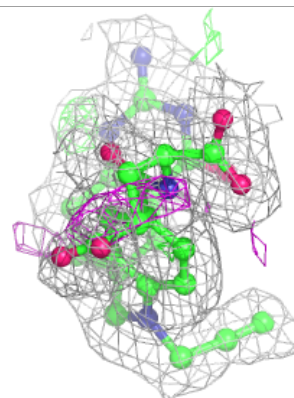
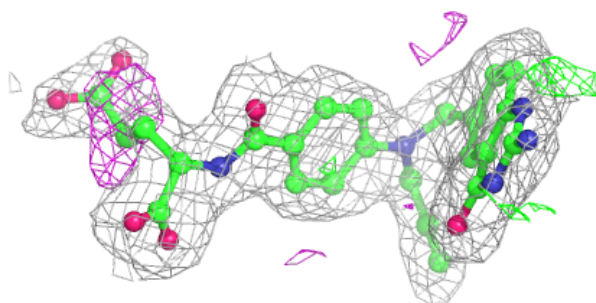
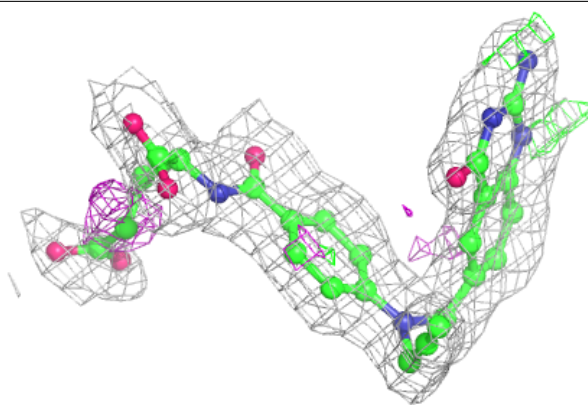
**Electron density around CB3 B 2401 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

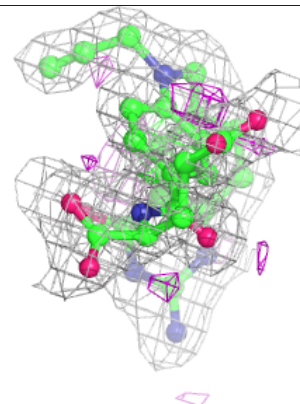
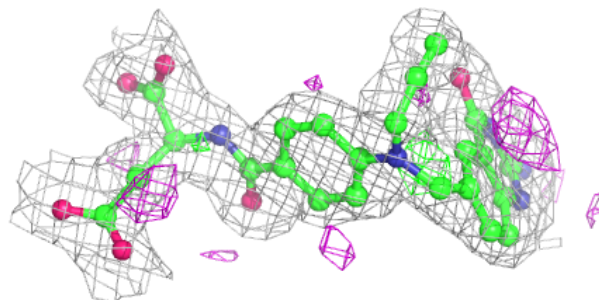
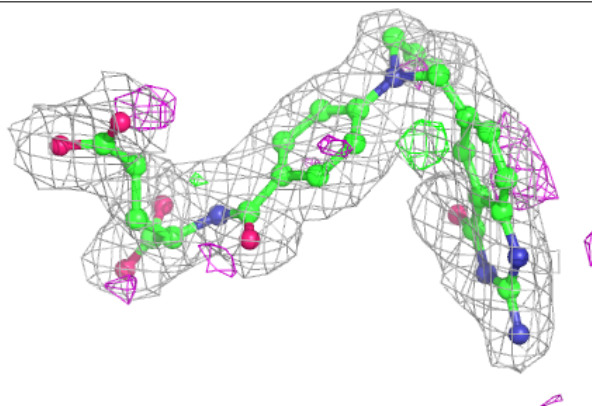


**Electron density around CB3 D 2501 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

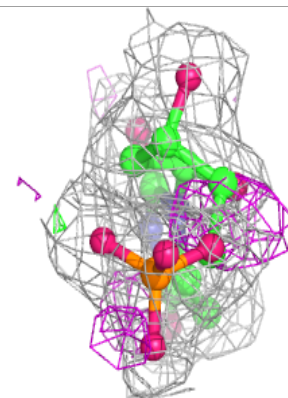
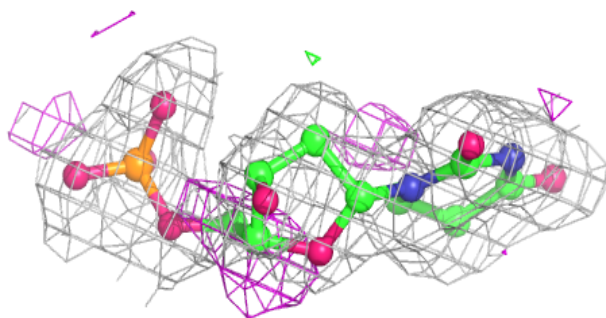
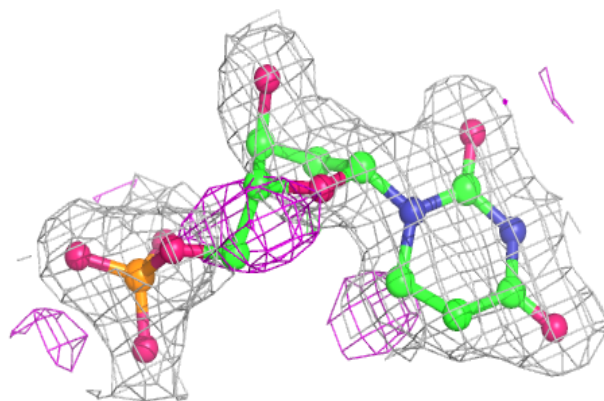
**Electron density around CB3 E 2551 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

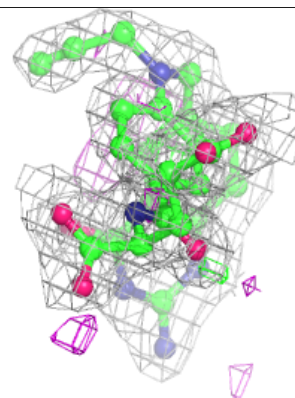
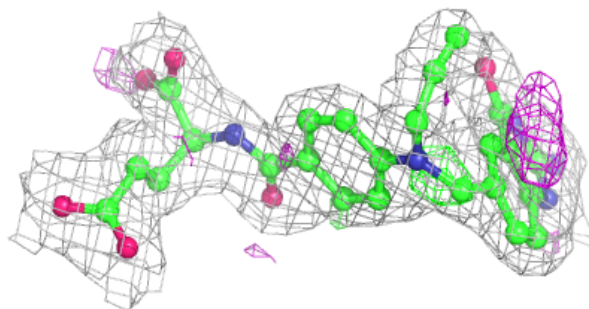
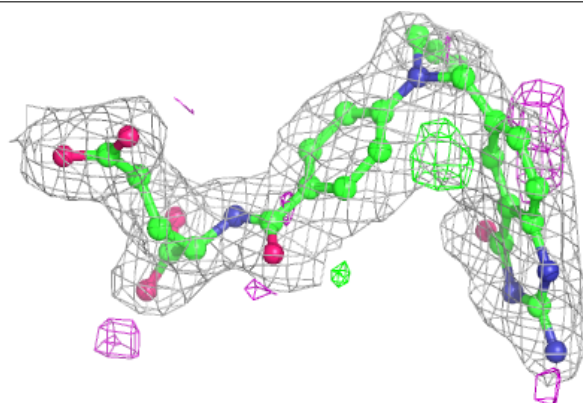


**Electron density around UMP C 450 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

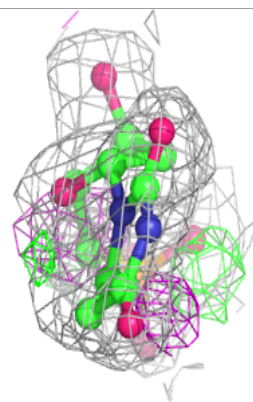
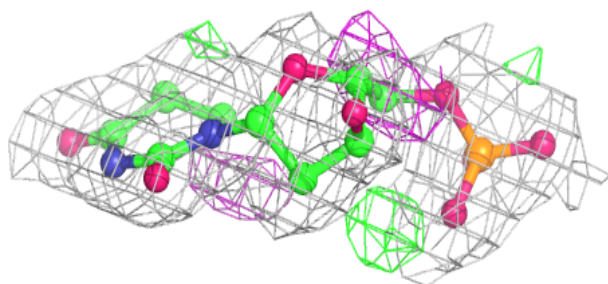
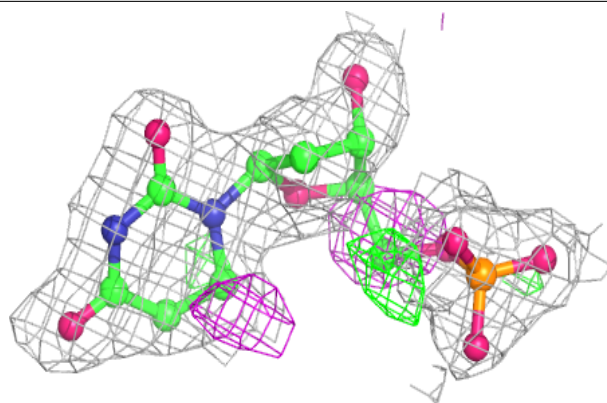
**Electron density around CB3 G 2651 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

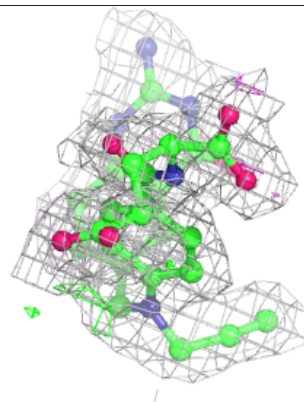
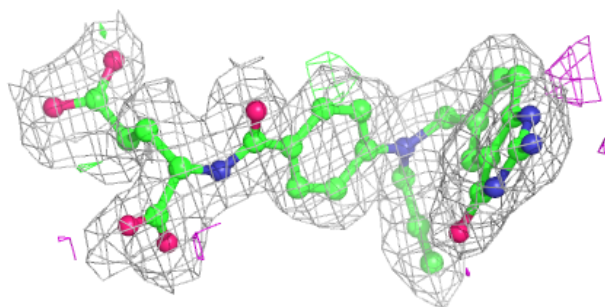
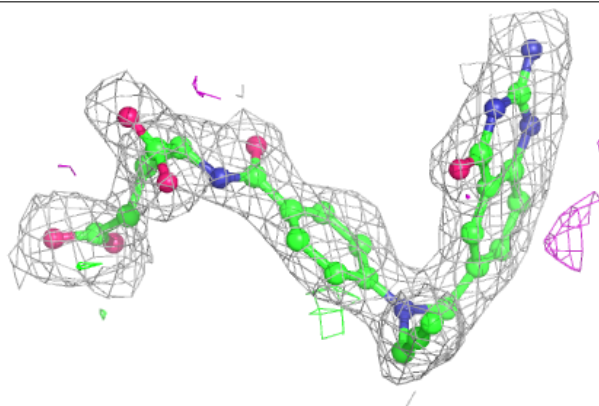


**Electron density around UMP A 350 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around CB3 C 2451 (A):**

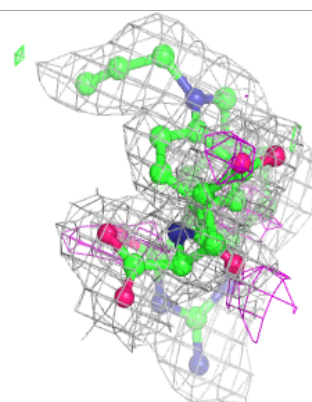
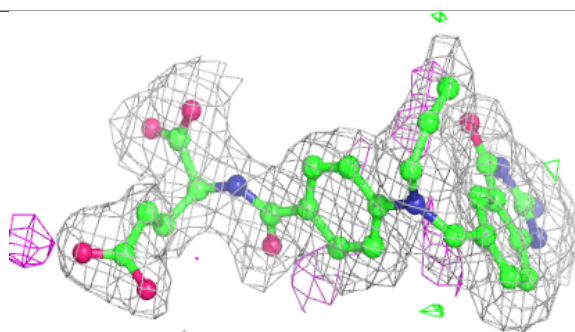
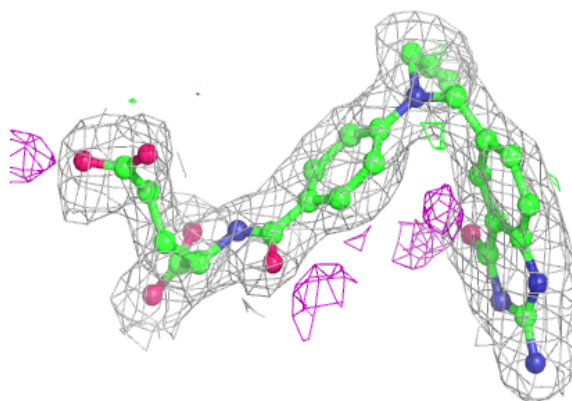
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



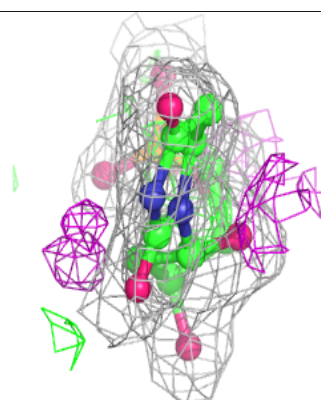
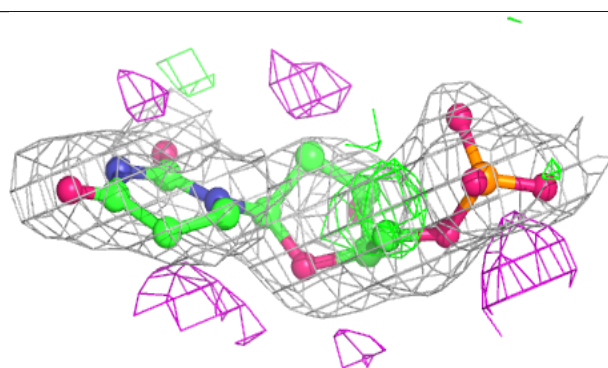
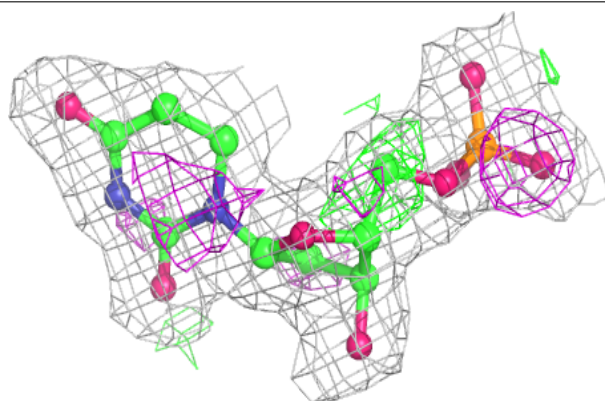


**Electron density around CB3 A 2351 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

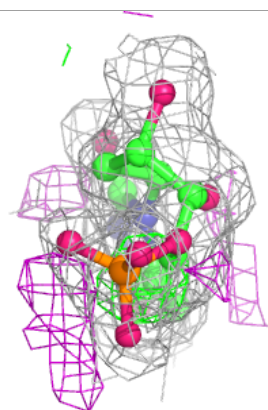
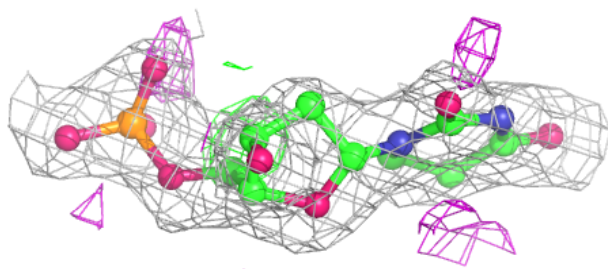
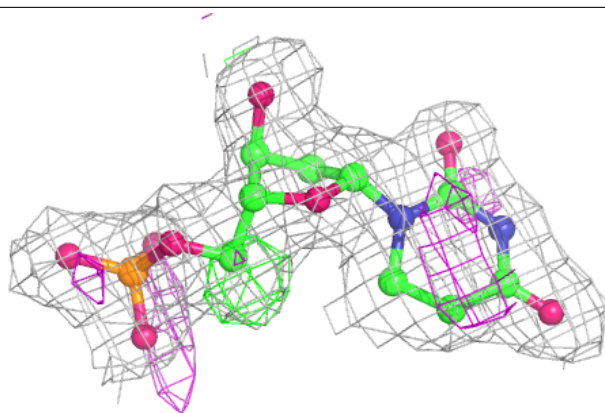
**Electron density around UMP E 550 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

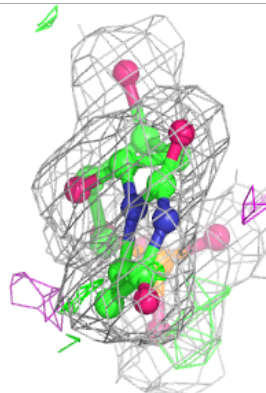
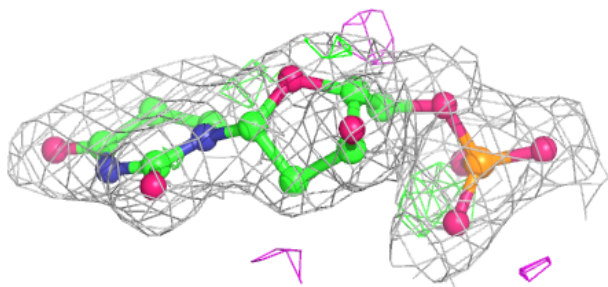
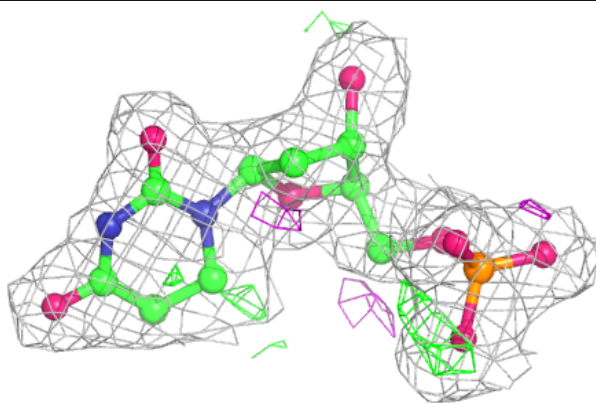


**Electron density around UMP G 650 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

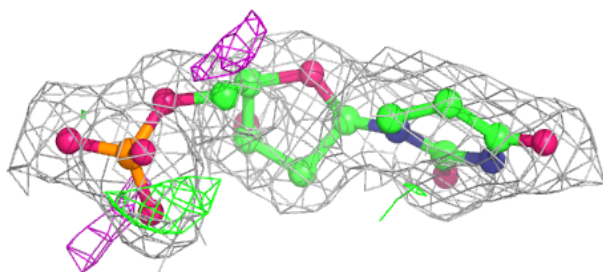
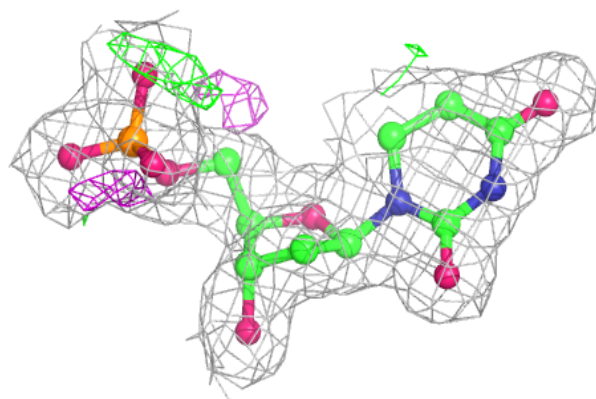
**Electron density around UMP D 500 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

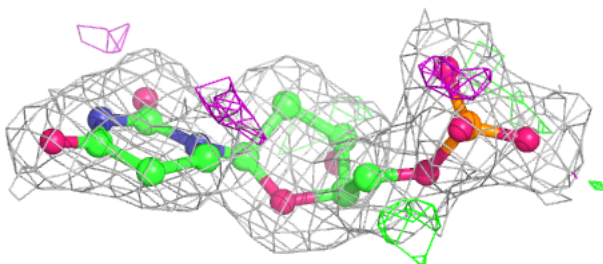
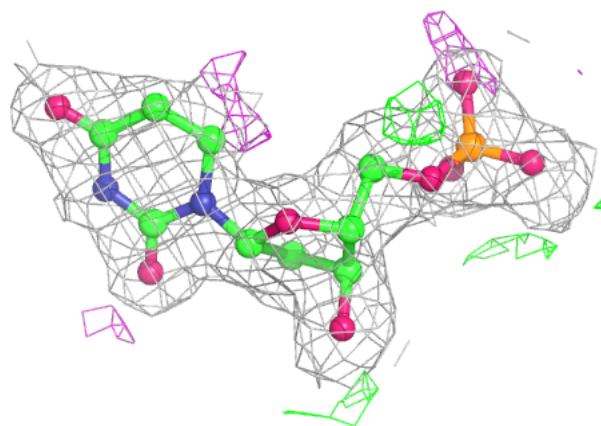


**Electron density around UMP B 400 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

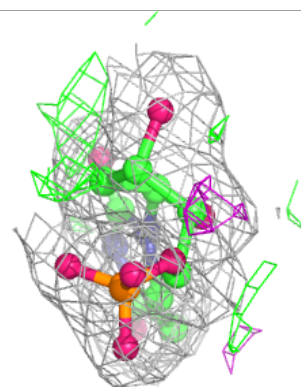
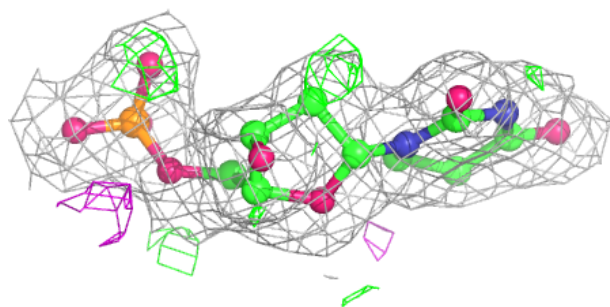
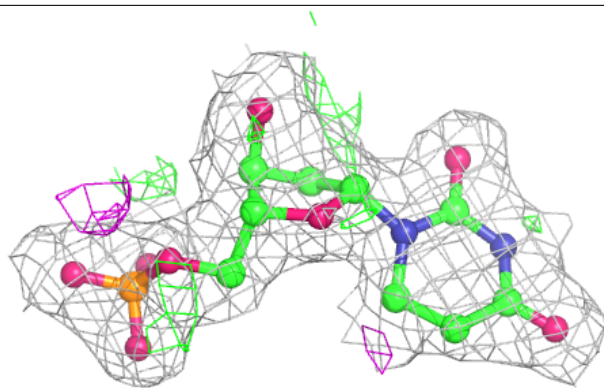
**Electron density around UMP F 600 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around UMP H 700 (A):**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.