



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 02:55 PM GMT

PDB ID : 1WZ2  
Title : The crystal structure of Leucyl-tRNA synthetase and tRNA(leucine) complex  
Authors : Fukunaga, R.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2005-02-21  
Resolution : 3.21 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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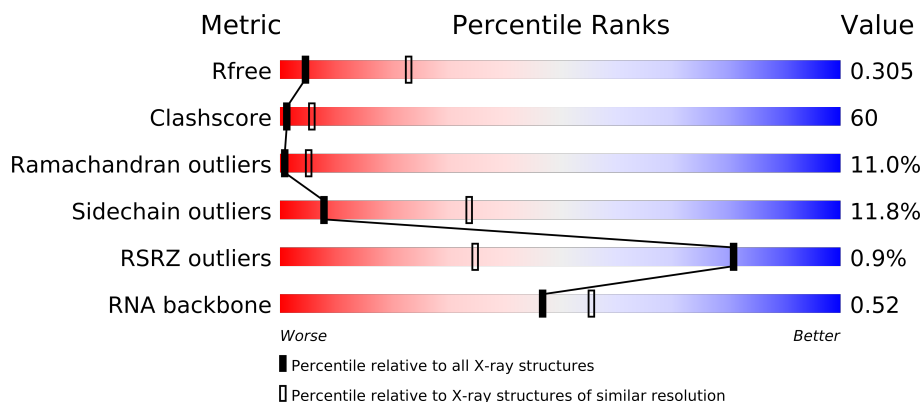
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.21 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))
$R_{free}$	66092	1205 (3.30-3.14)
Clashscore	79885	1072 (3.28-3.16)
Ramachandran outliers	78287	1052 (3.28-3.16)
Sidechain outliers	78261	1051 (3.28-3.16)
RSRZ outliers	66119	1206 (3.30-3.14)
RNA backbone	1838	1004 (3.74-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	C	88	
1	D	88	
2	A	967	
2	B	967	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19578 atoms, of which 0 are hydrogen and 0 are deuterium.

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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	88	Total	C	N	O	P	0	0	0
			1880	836	339	617	88			
1	D	88	Total	C	N	O	P	0	0	0
			1880	836	339	617	88			

- Molecule 2 is a protein called Leucyl-tRNA synthetase.

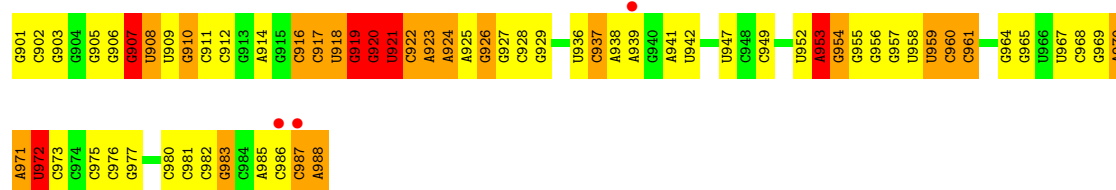
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	948	Total	C	N	O	S	0	0	0
			7909	5132	1323	1430	24			
2	B	948	Total	C	N	O	S	0	0	0
			7909	5132	1323	1430	24			

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

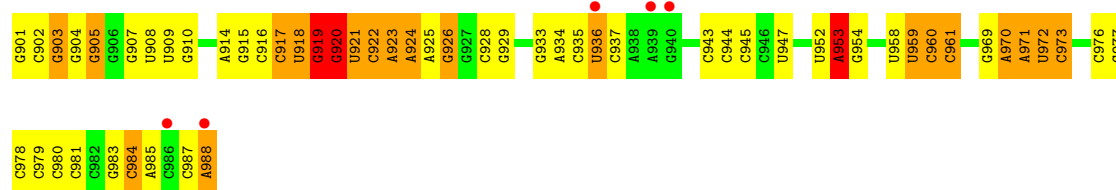
#### • Molecule 1: tRNA

Chain C: 



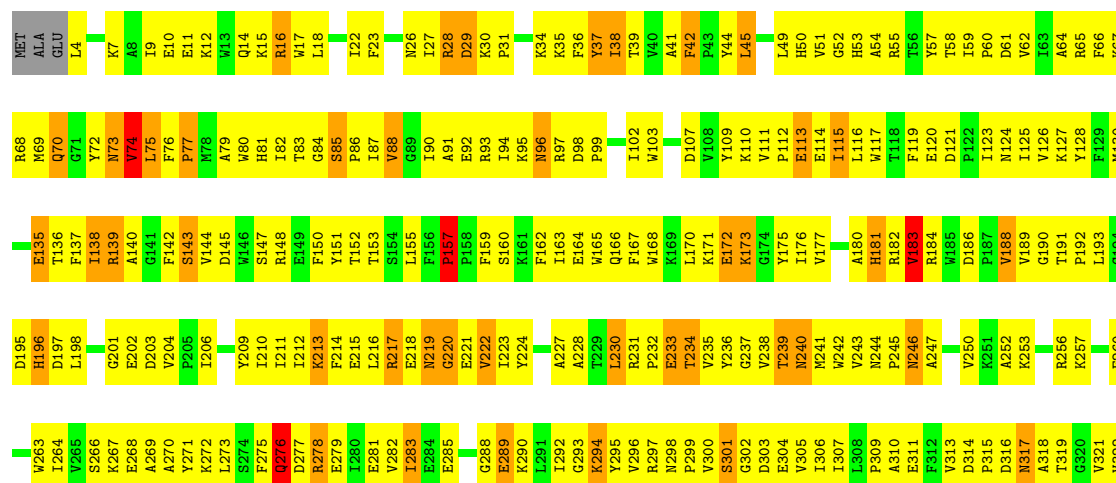
#### • Molecule 1: tRNA

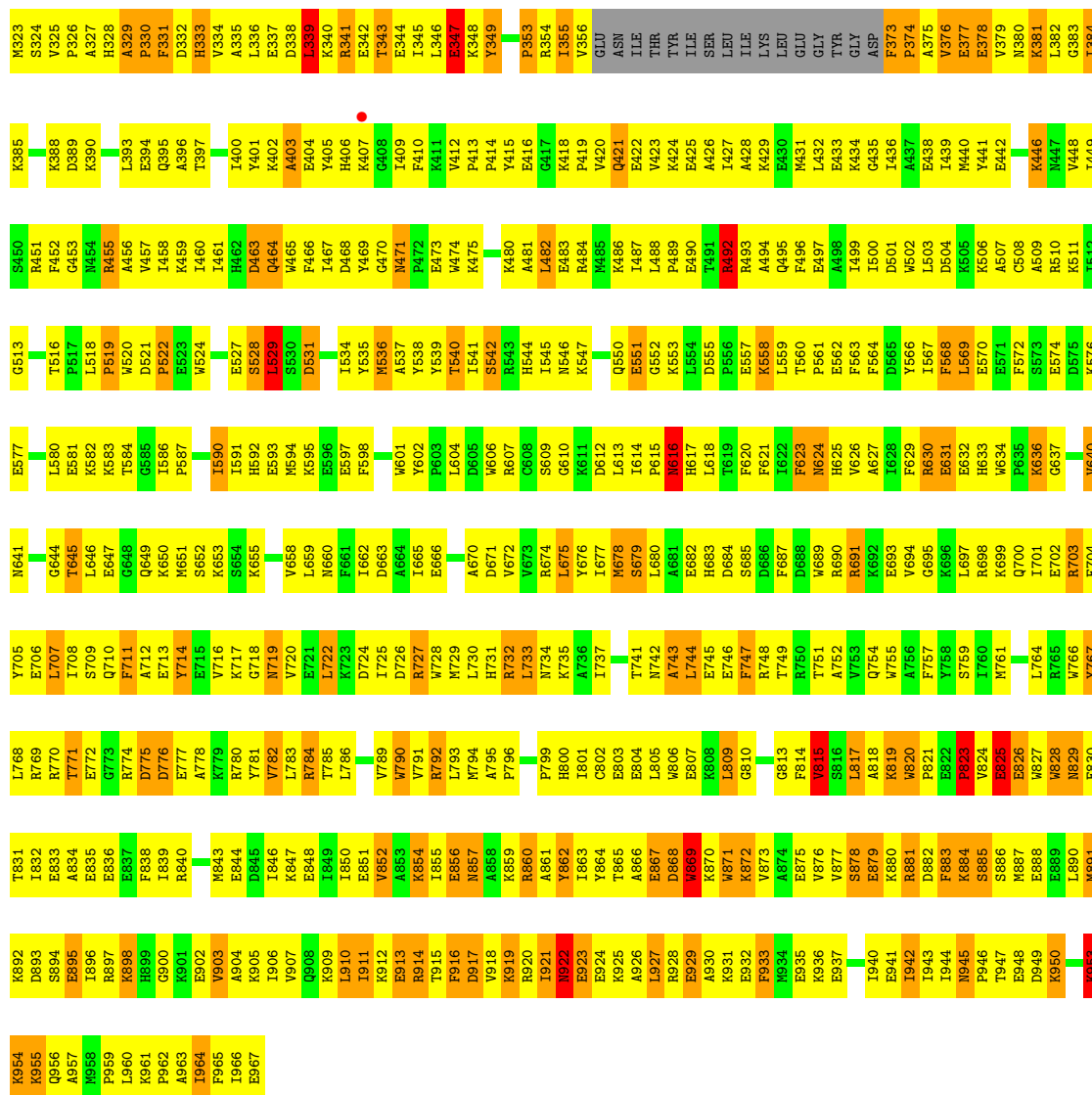
Chain D: 



#### • Molecule 2: Leucyl-tRNA synthetase

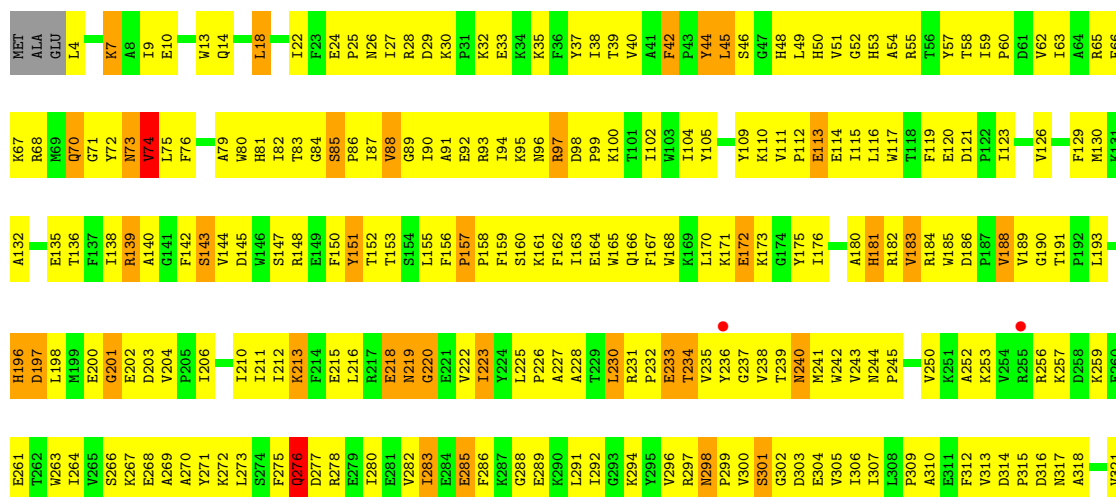
Chain A: 





## • Molecule 2: Leucyl-tRNA synthetase

### Chain B:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	120.55Å 231.13Å 118.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.21 48.69 – 3.21	Depositor EDS
% Data completeness (in resolution range)	90.7 (14.99-3.21) 90.8 (48.69-3.21)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.22 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.241 , 0.305 0.245 , 0.305	Depositor DCC
$R_{free}$ test set	5012 reflections (11.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	75.5	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 36.2	EDS
Estimated twinning fraction	0.046 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 49816 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	19578	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality i

### 5.1 Standard geometry i

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	C	0.55	1/2099 (0.0%)	0.82	7/3270 (0.2%)
1	D	0.52	1/2099 (0.0%)	0.81	3/3270 (0.1%)
2	A	0.59	0/8115	0.76	6/10953 (0.1%)
2	B	0.42	0/8115	0.67	2/10953 (0.0%)
All	All	0.52	2/20428 (0.0%)	0.74	18/28446 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	6
1	D	0	5
2	A	0	2
All	All	0	13

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	901	G	OP3-P	-7.18	1.52	1.61
1	D	901	G	OP3-P	-7.06	1.52	1.61

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	675	LEU	CA-CB-CG	10.29	138.97	115.30
2	A	815	VAL	CB-CA-C	-8.02	96.17	111.40
1	C	919	G	N9-C1'-C2'	7.77	124.10	114.00
1	D	953	A	N9-C1'-C2'	7.42	123.64	114.00
1	C	907	G	N9-C1'-C2'	7.18	123.33	114.00
1	D	920	G	N9-C1'-C2'	7.04	123.15	114.00
1	C	953	A	N9-C1'-C2'	6.38	122.30	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	972	U	N1-C1'-C2'	5.87	121.63	114.00
1	D	920	G	O4'-C1'-N9	5.84	112.87	108.20
1	C	953	A	C1'-O4'-C4'	-5.72	105.32	109.90
1	C	920	G	N9-C1'-C2'	5.71	121.43	114.00
2	A	927	LEU	CA-CB-CG	5.69	128.38	115.30
1	C	953	A	O4'-C1'-N9	5.62	112.70	108.20
2	B	680	LEU	N-CA-C	5.50	125.84	111.00
2	A	680	LEU	N-CA-C	5.44	125.68	111.00
2	A	74	VAL	N-CA-C	5.33	125.39	111.00
2	A	492	ARG	CG-CD-NE	5.05	122.41	111.80
2	B	74	VAL	N-CA-C	5.04	124.61	111.00

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	535	TYR	Sidechain
2	A	767	TYR	Sidechain
1	C	907	G	Sidechain
1	C	919	G	Sidechain
1	C	920	G	Sidechain
1	C	921	U	Sidechain
1	C	926	G	Sidechain
1	C	959	U	Sidechain
1	D	919	G	Sidechain
1	D	920	G	Sidechain
1	D	926	G	Sidechain
1	D	953	A	Sidechain
1	D	959	U	Sidechain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1880	0	956	88	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1880	0	956	65	0
2	A	7909	0	7908	1115	0
2	B	7909	0	7908	1018	0
All	All	19578	0	17728	2256	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 60.

All (2256) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:866:ALA:N	2:A:955:LYS:HZ3	1.39	1.18
2:A:30:LYS:HB2	2:A:73:ASN:HD22	1.11	1.13
2:A:170:LEU:HB3	2:A:176:ILE:HD11	1.23	1.09
2:A:616:ASN:HD22	2:A:617:HIS:N	1.51	1.08
2:A:68:ARG:HH22	2:A:143:SER:HB3	1.15	1.07
2:A:924:GLU:HB3	2:A:928:ARG:HH21	1.12	1.07
2:B:920:ARG:HA	2:B:920:ARG:HE	1.12	1.06
2:B:26:ASN:HB3	2:B:28:ARG:NH2	1.70	1.06
2:A:921:ILE:HD12	2:A:928:ARG:HH12	1.20	1.05
2:A:480:LYS:HE2	2:A:484:ARG:HH22	1.17	1.05
2:A:922:ASN:HD22	2:A:923:GLU:N	1.53	1.05
2:B:703:ARG:HB2	2:B:703:ARG:HH11	1.18	1.05
2:A:724:ASP:HA	2:A:727:ARG:HG3	1.33	1.04
2:A:771:THR:HG21	2:A:774:ARG:HH11	1.18	1.04
2:B:198:LEU:HB2	2:B:202:GLU:HG2	1.40	1.02
2:A:924:GLU:HB3	2:A:928:ARG:NH2	1.75	1.02
2:B:733:LEU:HD11	2:B:789:VAL:HG11	1.41	1.02
2:B:866:ALA:H	2:B:955:LYS:NZ	1.58	1.01
2:A:616:ASN:ND2	2:A:617:HIS:H	1.57	1.01
2:B:860:ARG:NH1	2:B:943:ILE:H	1.59	1.01
2:B:558:LYS:HB3	2:B:584:THR:HA	1.43	1.01
2:B:650:LYS:HE2	2:B:651:MET:H	1.22	1.00
2:A:529:LEU:H	2:A:529:LEU:HD12	1.27	1.00
2:A:163:ILE:HD12	2:A:531:ASP:HB2	1.40	1.00
2:A:722:LEU:HD22	2:A:722:LEU:H	1.22	1.00
2:A:87:ILE:HG13	2:A:88:VAL:H	1.24	0.99
2:B:703:ARG:HB2	2:B:703:ARG:NH1	1.77	0.99
2:A:188:VAL:HG23	2:A:189:VAL:H	1.28	0.99
1:D:904:G:H2'	1:D:905:G:H5''	1.45	0.98
2:A:848:GLU:O	2:A:852:VAL:HG23	1.63	0.98
2:B:227:ALA:HA	2:B:321:VAL:HG23	1.45	0.98
2:A:567:ILE:HA	2:A:595:LYS:HD2	1.44	0.97

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:916:C:H5'	1:C:917:C:C5	1.99	0.97
2:A:227:ALA:HA	2:A:321:VAL:HG23	1.46	0.97
2:A:426:ALA:HA	2:A:429:LYS:HE2	1.45	0.97
2:A:922:ASN:C	2:A:922:ASN:HD22	1.68	0.96
2:A:690:ARG:NH1	2:A:693:GLU:HG3	1.79	0.96
2:A:68:ARG:NH2	2:A:143:SER:HB3	1.79	0.96
2:A:890:LEU:HD12	2:A:906:ILE:HD11	1.48	0.96
2:A:345:ILE:HG12	2:A:346:LEU:H	1.29	0.95
1:C:986:C:H4'	1:C:987:C:H5"	1.47	0.95
2:B:88:VAL:HG21	2:B:513:GLY:HA2	1.48	0.95
2:A:68:ARG:HH22	2:A:143:SER:CB	1.80	0.95
2:A:558:LYS:HB3	2:A:584:THR:HA	1.48	0.94
2:B:860:ARG:HH11	2:B:943:ILE:N	1.66	0.94
2:A:792:ARG:HG3	2:A:792:ARG:HH21	1.30	0.94
2:A:660:ASN:HB2	2:A:663:ASP:HB3	1.50	0.93
2:A:741:THR:HG1	2:A:820:TRP:HZ3	1.04	0.93
2:B:866:ALA:H	2:B:955:LYS:HZ3	1.01	0.93
2:A:860:ARG:NH1	2:A:861:ALA:HA	1.84	0.93
2:A:771:THR:HG21	2:A:774:ARG:NH1	1.82	0.93
2:B:429:LYS:O	2:B:433:GLU:HG2	1.67	0.92
2:A:182:ARG:HD2	2:A:206:ILE:HG21	1.49	0.92
2:A:28:ARG:HE	2:A:28:ARG:H	1.01	0.92
2:A:860:ARG:NH1	2:A:943:ILE:H	1.66	0.92
2:A:139:ARG:HG3	2:A:139:ARG:HH11	1.34	0.92
2:A:866:ALA:H	2:A:955:LYS:HZ3	0.98	0.92
2:B:784:ARG:HH22	2:B:810:GLY:H	1.15	0.92
2:B:927:LEU:HD12	2:B:944:ILE:HD12	1.50	0.91
2:A:770:ARG:HD2	2:A:933:PHE:CE2	2.06	0.91
2:B:82:ILE:HG21	2:B:126:VAL:HG13	1.50	0.91
2:A:866:ALA:H	2:A:955:LYS:NZ	1.69	0.91
2:A:480:LYS:HE2	2:A:484:ARG:NH2	1.84	0.91
2:B:49:LEU:HD12	2:B:49:LEU:H	1.34	0.91
2:B:734:ASN:HD21	2:B:824:VAL:H	1.12	0.91
2:B:233:GLU:HA	2:B:427:ILE:HD12	1.51	0.91
2:B:355:ILE:HG22	2:B:356:VAL:H	1.36	0.91
2:B:860:ARG:HH11	2:B:943:ILE:H	0.99	0.90
2:A:210:ILE:HD11	2:A:232:PRO:HG3	1.54	0.90
2:B:26:ASN:HB3	2:B:28:ARG:HH22	1.34	0.90
2:B:167:PHE:HA	2:B:170:LEU:HD12	1.55	0.89
2:B:826:GLU:C	2:B:828:TRP:H	1.70	0.89
2:A:567:ILE:HG22	2:A:595:LYS:HB2	1.51	0.89
2:B:920:ARG:HA	2:B:920:ARG:NE	1.85	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:198:LEU:HB2	2:A:202:GLU:HG2	1.52	0.89
2:A:49:LEU:HD12	2:A:49:LEU:H	1.35	0.89
2:A:771:THR:CG2	2:A:774:ARG:HH11	1.86	0.89
2:A:496:PHE:CE1	2:A:614:ILE:HG12	2.08	0.89
2:A:730:LEU:HB3	2:A:827:TRP:NE1	1.88	0.88
2:A:230:LEU:HD23	2:A:230:LEU:H	1.37	0.88
2:B:870:LYS:HE3	2:B:905:LYS:HE3	1.55	0.88
2:A:826:GLU:C	2:A:828:TRP:H	1.70	0.88
2:A:343:THR:HG23	2:A:344:GLU:H	1.37	0.88
2:A:111:VAL:HG22	2:A:128:TYR:HE2	1.39	0.88
1:D:983:G:H2'	1:D:984:C:H5''	1.53	0.88
2:B:83:THR:HG22	2:B:515:GLY:HA2	1.56	0.88
2:B:675:LEU:HD23	2:B:697:LEU:HD21	1.54	0.87
2:B:567:ILE:HG22	2:B:595:LYS:HB2	1.55	0.87
1:D:922:C:H4'	1:D:923:A:O5'	1.72	0.87
2:B:555:ASP:HB3	2:B:558:LYS:HG2	1.55	0.87
2:A:489:PRO:HG3	2:A:684:ASP:OD2	1.75	0.87
2:B:714:TYR:HD2	2:B:714:TYR:H	1.21	0.87
2:A:471:ASN:OD1	2:A:473:GLU:HG2	1.73	0.87
2:A:219:ASN:ND2	2:A:220:GLY:H	1.72	0.87
2:B:188:VAL:HG23	2:B:189:VAL:H	1.40	0.87
2:A:921:ILE:HB	2:A:928:ARG:HH22	1.40	0.87
2:A:211:ILE:HG22	2:A:228:ALA:HB2	1.57	0.86
1:C:902:C:H2'	1:C:903:G:O4'	1.74	0.86
2:A:482:LEU:HD23	2:A:482:LEU:O	1.75	0.86
2:B:44:TYR:HE1	2:B:87:ILE:HD11	1.39	0.86
2:A:496:PHE:HE1	2:A:614:ILE:HG12	1.40	0.86
2:B:351:ILE:HD12	2:B:351:ILE:H	1.39	0.86
2:A:836:GLU:O	2:A:840:ARG:HG3	1.74	0.86
2:A:204:VAL:HG21	2:A:448:VAL:CG2	2.05	0.86
2:B:342:GLU:HG2	2:B:343:THR:H	1.40	0.86
2:B:882:ASP:CG	2:B:883:PHE:H	1.79	0.85
2:A:829:ASN:OD1	2:A:832:ILE:HG13	1.77	0.85
2:B:587:PRO:HB2	2:B:590:ILE:HG12	1.56	0.85
2:B:182:ARG:HD2	2:B:206:ILE:HG21	1.59	0.84
2:B:413:PRO:HB2	2:B:414:PRO:HD3	1.57	0.84
2:A:819:LYS:H	2:A:819:LYS:HE3	1.43	0.84
2:A:803:GLU:HA	2:A:815:VAL:CG2	2.07	0.84
2:B:446:LYS:HD2	2:B:446:LYS:N	1.92	0.84
1:C:928:C:H2'	1:C:929:G:C8	2.13	0.84
2:B:703:ARG:HD2	2:B:707:LEU:HD11	1.60	0.84
1:C:928:C:H2'	1:C:929:G:H8	1.42	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:145:ASP:OD1	2:A:147:SER:HB3	1.78	0.83
2:B:866:ALA:N	2:B:955:LYS:HZ3	1.76	0.83
2:A:731:HIS:HE1	2:A:833:GLU:OE1	1.60	0.83
2:B:705:TYR:CE2	2:B:805:LEU:HD21	2.13	0.83
2:A:671:ASP:OD2	2:A:800:HIS:HB2	1.78	0.83
2:B:4:LEU:HD23	2:B:4:LEU:O	1.79	0.83
2:A:966:ILE:O	2:A:967:GLU:HB2	1.79	0.83
2:B:186:ASP:HB2	2:B:193:LEU:HD11	1.59	0.83
2:A:770:ARG:HD2	2:A:933:PHE:HE2	1.41	0.83
2:B:86:PRO:O	2:B:90:ILE:HG12	1.78	0.83
2:A:732:ARG:HH11	2:A:735:LYS:HD3	1.45	0.82
2:A:28:ARG:H	2:A:28:ARG:NE	1.76	0.82
2:B:935:GLU:OE1	2:B:941:GLU:HA	1.80	0.82
1:D:923:A:H4'	1:D:924:A:O5'	1.79	0.82
2:A:59:ILE:HG12	2:A:678:MET:HE1	1.60	0.82
2:B:13:TRP:CE2	2:B:803:GLU:HB3	2.15	0.82
2:A:51:VAL:O	2:A:54:ALA:HB3	1.80	0.82
2:A:238:VAL:HG11	2:A:298:ASN:HD22	1.45	0.81
2:A:345:ILE:HG12	2:A:346:LEU:N	1.94	0.81
2:A:384:ILE:HG22	2:A:385:LYS:H	1.45	0.81
2:A:859:LYS:HB3	2:A:941:GLU:HB3	1.63	0.81
2:A:355:ILE:HG22	2:A:356:VAL:H	1.45	0.81
1:C:922:C:H4'	1:C:923:A:O5'	1.78	0.81
2:B:230:LEU:H	2:B:230:LEU:HD23	1.45	0.81
2:A:722:LEU:N	2:A:722:LEU:HD22	1.95	0.81
2:B:860:ARG:HB3	2:B:966:ILE:HG22	1.61	0.81
2:B:340:LYS:NZ	2:B:341:ARG:HH12	1.79	0.81
2:A:895:GLU:OE1	2:A:898:LYS:HD2	1.81	0.81
2:A:690:ARG:HH11	2:A:693:GLU:HG3	1.45	0.80
2:B:641:ASN:HA	2:B:683:HIS:O	1.80	0.80
2:B:268:GLU:HG3	2:B:316:ASP:HA	1.63	0.80
2:B:170:LEU:HB2	2:B:176:ILE:HD11	1.62	0.80
2:A:660:ASN:HB2	2:A:663:ASP:CB	2.10	0.80
2:B:186:ASP:HB3	2:B:191:THR:HG23	1.61	0.80
2:A:412:VAL:HG23	2:A:414:PRO:HD2	1.64	0.80
1:C:986:C:N3	2:A:506:LYS:HG2	1.97	0.80
2:B:384:ILE:HG22	2:B:385:LYS:H	1.47	0.80
2:A:73:ASN:O	2:A:601:TRP:HH2	1.64	0.80
2:A:39:THR:HG23	2:A:604:LEU:HD11	1.63	0.79
2:B:860:ARG:HE	2:B:942:ILE:HA	1.48	0.79
1:D:904:G:C2'	1:D:905:G:H5''	2.11	0.79
2:A:931:LYS:O	2:A:935:GLU:HG3	1.80	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:863:ILE:HB	2:B:953:LYS:HD3	1.64	0.79
1:C:911:C:H2'	1:C:912:C:H6	1.47	0.79
2:B:157:PRO:HB2	2:B:158:PRO:HD3	1.65	0.79
2:A:170:LEU:CB	2:A:176:ILE:HD11	2.11	0.79
2:A:922:ASN:ND2	2:A:923:GLU:N	2.30	0.79
2:A:82:ILE:HG13	2:A:153:THR:HG23	1.63	0.79
2:A:732:ARG:NH1	2:A:735:LYS:HD3	1.98	0.79
2:B:547:LYS:HE2	2:B:547:LYS:HA	1.63	0.79
2:B:116:LEU:HD12	2:B:119:PHE:CD2	2.17	0.79
2:B:919:LYS:O	2:B:922:ASN:HB2	1.82	0.79
2:A:297:ARG:HG2	2:A:304:GLU:HG2	1.63	0.79
2:B:826:GLU:C	2:B:828:TRP:N	2.34	0.79
2:A:487:ILE:HG22	2:A:489:PRO:O	1.82	0.79
2:B:297:ARG:HG2	2:B:304:GLU:HG2	1.63	0.79
1:D:902:C:H3'	1:D:903:G:H5''	1.64	0.79
2:A:867:GLU:H	2:A:867:GLU:CD	1.86	0.78
2:A:924:GLU:CB	2:A:928:ARG:HH21	1.94	0.78
2:B:343:THR:HG23	2:B:344:GLU:H	1.47	0.78
2:B:345:ILE:HG12	2:B:346:LEU:H	1.47	0.78
2:B:464:GLN:HA	2:B:524:TRP:CH2	2.18	0.78
2:A:186:ASP:HB3	2:A:191:THR:HG23	1.65	0.78
2:B:722:LEU:CD2	2:B:722:LEU:H	1.97	0.78
2:B:949:ASP:HB2	2:B:954:LYS:HE2	1.64	0.78
2:A:204:VAL:HG21	2:A:448:VAL:HG22	1.66	0.78
1:C:986:C:H4'	1:C:987:C:C5'	2.14	0.78
2:B:51:VAL:O	2:B:54:ALA:HB3	1.84	0.78
2:A:348:LYS:NZ	2:A:348:LYS:HB3	1.99	0.78
2:A:871:TRP:CZ3	2:A:918:VAL:HG13	2.18	0.78
2:A:826:GLU:C	2:A:828:TRP:N	2.34	0.78
2:B:471:ASN:ND2	2:B:473:GLU:HG2	1.99	0.78
2:B:55:ARG:O	2:B:59:ILE:HG13	1.83	0.78
2:A:482:LEU:HD12	2:A:500:ILE:HD11	1.66	0.78
2:A:87:ILE:HG13	2:A:88:VAL:N	1.98	0.78
2:B:333:HIS:HA	2:B:336:LEU:HB2	1.66	0.78
2:B:45:LEU:HD11	2:B:80:TRP:HB3	1.64	0.78
2:A:393:LEU:HD12	2:A:396:ALA:HB3	1.66	0.78
2:A:482:LEU:HD11	2:A:496:PHE:HB3	1.66	0.77
2:A:650:LYS:HD2	2:A:651:MET:H	1.48	0.77
2:B:731:HIS:CD2	2:B:829:ASN:H	2.02	0.77
2:B:801:ILE:O	2:B:805:LEU:HG	1.84	0.77
2:B:540:THR:HG23	2:B:541:ILE:HG23	1.64	0.77
2:A:529:LEU:CD1	2:A:529:LEU:H	1.96	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:209:TYR:HE1	2:A:317:ASN:HD21	1.30	0.77
1:C:985:A:H61	2:A:504:ASP:HB2	1.47	0.77
2:A:860:ARG:HB3	2:A:966:ILE:HG22	1.64	0.77
2:A:871:TRP:CD1	2:A:959:PRO:HG3	2.18	0.77
2:A:242:TRP:HH2	2:A:332:ASP:HA	1.50	0.77
1:C:986:C:N3	2:A:507:ALA:N	2.32	0.77
2:B:446:LYS:HD2	2:B:446:LYS:H	1.47	0.77
2:B:834:ALA:HA	2:B:837:GLU:OE2	1.83	0.77
2:A:819:LYS:H	2:A:819:LYS:CE	1.97	0.77
2:B:866:ALA:N	2:B:955:LYS:NZ	2.31	0.77
2:A:722:LEU:H	2:A:722:LEU:CD2	1.98	0.77
2:B:150:PHE:HD1	2:B:151:TYR:O	1.68	0.77
2:A:919:LYS:HD2	2:A:960:LEU:CD1	2.16	0.76
2:A:770:ARG:NH1	2:A:933:PHE:HD2	1.81	0.76
2:B:845:ASP:O	2:B:849:ILE:HG13	1.84	0.76
2:B:880:LYS:HG3	2:B:885:SER:HB2	1.67	0.76
2:A:198:LEU:HB2	2:A:202:GLU:CG	2.14	0.76
2:B:631:GLU:HA	2:B:634:TRP:CE2	2.20	0.76
2:A:27:ILE:N	2:A:28:ARG:HH21	1.83	0.76
2:B:914:ARG:HH21	2:B:915:THR:HG23	1.51	0.76
2:A:28:ARG:HE	2:A:28:ARG:N	1.81	0.76
2:A:488:LEU:HD12	2:A:606:TRP:CH2	2.21	0.76
2:A:88:VAL:HG21	2:A:513:GLY:HA2	1.66	0.76
2:A:731:HIS:CE1	2:A:833:GLU:OE1	2.39	0.76
2:A:928:ARG:O	2:A:930:ALA:N	2.18	0.76
2:B:931:LYS:O	2:B:935:GLU:HG3	1.86	0.76
2:B:82:ILE:HG21	2:B:126:VAL:CG1	2.16	0.76
2:B:887:MET:SD	2:B:906:ILE:HD12	2.26	0.76
2:B:165:TRP:CD1	2:B:561:PRO:HA	2.21	0.75
1:D:929:G:H1	1:D:947:U:H3	1.35	0.75
2:A:238:VAL:CG1	2:A:298:ASN:HD22	1.98	0.75
2:A:949:ASP:HB2	2:A:954:LYS:HE2	1.69	0.75
2:A:641:ASN:HA	2:A:683:HIS:O	1.85	0.75
2:B:767:TYR:HE2	2:B:783:LEU:HD11	1.49	0.75
2:B:678:MET:HB3	2:B:749:THR:HB	1.68	0.75
2:A:492:ARG:CG	2:A:492:ARG:HH11	1.99	0.75
2:A:17:TRP:CH2	2:A:800:HIS:HD2	2.04	0.75
2:A:957:ALA:HB2	2:A:963:ALA:HB2	1.67	0.75
2:B:846:ILE:HG12	2:B:964:ILE:CD1	2.16	0.75
2:B:211:ILE:HG22	2:B:228:ALA:HB2	1.68	0.74
2:A:139:ARG:NH1	2:A:139:ARG:HG3	1.95	0.74
2:A:624:ASN:HD22	2:A:624:ASN:H	1.35	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:631:GLU:HA	2:B:634:TRP:NE1	2.01	0.74
2:A:213:LYS:HD2	2:A:435:GLY:O	1.87	0.74
2:B:681:ALA:HA	2:B:750:ARG:HG3	1.68	0.74
2:B:89:GLY:O	2:B:93:ARG:HG3	1.87	0.74
2:A:551:GLU:O	2:A:553:LYS:HG2	1.86	0.74
2:A:755:TRP:O	2:A:759:SER:HB3	1.87	0.74
2:A:645:THR:HG22	2:A:650:LYS:HA	1.68	0.74
1:C:908:U:H5'	1:C:961:C:OP2	1.88	0.74
1:D:902:C:C3'	1:D:903:G:H5''	2.17	0.74
2:B:836:GLU:O	2:B:840:ARG:HG3	1.87	0.74
2:A:432:LEU:HD11	2:A:439:ILE:HG13	1.70	0.74
2:A:354:ARG:HD2	2:A:376:VAL:CG1	2.17	0.74
2:A:30:LYS:HB2	2:A:73:ASN:ND2	1.96	0.73
2:B:26:ASN:CB	2:B:28:ARG:HH22	2.01	0.73
2:A:230:LEU:CD2	2:A:230:LEU:H	2.01	0.73
2:A:882:ASP:CG	2:A:883:PHE:H	1.92	0.73
2:B:928:ARG:O	2:B:930:ALA:N	2.21	0.73
2:B:859:LYS:HB3	2:B:941:GLU:HB3	1.69	0.73
2:B:703:ARG:HH11	2:B:703:ARG:CB	2.00	0.73
2:A:566:TYR:HA	2:A:570:GLU:HB2	1.70	0.73
2:A:766:TRP:CH2	2:A:770:ARG:HD3	2.23	0.73
2:B:957:ALA:HB2	2:B:963:ALA:HB2	1.67	0.73
2:B:857:ASN:ND2	2:B:967:GLU:HG2	2.03	0.73
2:B:198:LEU:CB	2:B:202:GLU:HG2	2.19	0.73
2:A:345:ILE:HG23	2:A:346:LEU:HD13	1.71	0.73
2:B:544:HIS:O	2:B:548:LEU:HG	1.87	0.73
2:B:867:GLU:CD	2:B:867:GLU:H	1.92	0.73
2:A:537:ALA:O	2:A:540:THR:HG22	1.88	0.73
2:A:413:PRO:HB2	2:A:414:PRO:HD3	1.70	0.73
1:C:982:C:H2'	1:C:983:G:C8	2.24	0.73
2:A:691:ARG:O	2:A:694:VAL:HG12	1.88	0.73
2:A:42:PHE:CD1	2:A:81:HIS:HB2	2.24	0.73
2:A:233:GLU:HB3	2:A:423:VAL:HG23	1.68	0.73
2:A:832:ILE:HA	2:A:835:GLU:HG3	1.71	0.73
2:A:792:ARG:HG3	2:A:792:ARG:NH2	2.04	0.73
2:A:17:TRP:CH2	2:A:800:HIS:CD2	2.76	0.73
2:A:373:PHE:CD1	2:A:374:PRO:HD3	2.24	0.73
2:A:342:GLU:HG2	2:A:343:THR:H	1.54	0.72
2:A:250:VAL:HG12	2:A:285:GLU:HA	1.70	0.72
2:B:925:LYS:HA	2:B:928:ARG:HG2	1.68	0.72
2:B:734:ASN:HD21	2:B:824:VAL:N	1.86	0.72
2:A:558:LYS:HD2	2:A:583:LYS:O	1.89	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:860:ARG:NH2	2:A:862:TYR:HB3	2.04	0.72
2:B:803:GLU:OE2	2:B:815:VAL:N	2.23	0.72
2:A:771:THR:HG22	2:A:774:ARG:HD3	1.70	0.72
2:B:695:GLY:O	2:B:698:ARG:HB3	1.90	0.72
2:B:848:GLU:O	2:B:852:VAL:HG23	1.89	0.72
2:A:488:LEU:HD12	2:A:606:TRP:CZ3	2.24	0.72
2:A:239:THR:CG2	2:A:326:PRO:HD2	2.20	0.72
2:B:757:PHE:HD1	2:B:794:MET:SD	2.12	0.72
2:B:480:LYS:HA	2:B:483:GLU:OE1	1.89	0.72
2:B:167:PHE:HA	2:B:170:LEU:CD1	2.19	0.72
2:B:467:ILE:HG13	2:B:508:CYS:SG	2.30	0.72
2:A:863:ILE:HB	2:A:953:LYS:HD3	1.70	0.71
2:A:342:GLU:HG2	2:A:343:THR:N	2.04	0.71
2:A:119:PHE:CD1	2:A:125:ILE:HG12	2.24	0.71
2:A:690:ARG:HD3	2:A:693:GLU:OE2	1.89	0.71
2:B:32:LYS:HG2	2:B:600:TYR:CD1	2.25	0.71
2:B:957:ALA:HB2	2:B:963:ALA:CB	2.21	0.71
2:A:922:ASN:C	2:A:922:ASN:ND2	2.34	0.71
2:A:860:ARG:HH22	2:A:862:TYR:N	1.87	0.71
2:B:784:ARG:NH2	2:B:810:GLY:H	1.88	0.71
2:B:22:ILE:HG13	2:B:817:LEU:HD21	1.73	0.71
2:A:731:HIS:CD2	2:A:829:ASN:H	2.08	0.71
2:A:219:ASN:HD22	2:A:220:GLY:H	1.37	0.71
2:A:770:ARG:NH1	2:A:933:PHE:CD2	2.59	0.71
2:A:957:ALA:HB2	2:A:963:ALA:CB	2.20	0.71
2:A:67:LYS:HD3	2:A:70:GLN:HE21	1.54	0.71
2:B:890:LEU:HD12	2:B:906:ILE:HD11	1.73	0.71
2:A:734:ASN:OD1	2:A:823:PRO:HA	1.91	0.71
2:B:30:LYS:HE3	2:B:71:GLY:O	1.90	0.71
2:A:730:LEU:HB3	2:A:827:TRP:HE1	1.54	0.70
2:A:198:LEU:HD22	2:A:202:GLU:HA	1.73	0.70
2:A:631:GLU:HA	2:A:634:TRP:CE2	2.26	0.70
2:B:282:VAL:HG12	2:B:283:ILE:N	2.07	0.70
2:A:419:PRO:HG2	2:A:422:GLU:HG3	1.71	0.70
2:A:857:ASN:O	2:A:940:ILE:HD11	1.90	0.70
2:B:826:GLU:O	2:B:827:TRP:HB3	1.91	0.70
2:B:471:ASN:HD21	2:B:473:GLU:HG2	1.55	0.70
2:A:276:GLN:HA	2:A:460:ILE:HD13	1.71	0.70
2:A:824:VAL:HG11	2:A:827:TRP:HE3	1.56	0.70
1:C:970:A:H4'	1:C:971:A:OP1	1.91	0.70
2:B:487:ILE:HG22	2:B:489:PRO:O	1.91	0.70
2:A:613:LEU:O	2:A:618:LEU:HB2	1.91	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:140:ALA:HB2	2:A:665:ILE:HD11	1.72	0.70
2:A:826:GLU:O	2:A:827:TRP:HB3	1.90	0.70
2:A:333:HIS:HA	2:A:336:LEU:HB2	1.73	0.70
2:A:204:VAL:HG21	2:A:448:VAL:HG21	1.74	0.70
2:A:795:ALA:HB3	2:A:796:PRO:HD3	1.72	0.70
2:B:803:GLU:OE2	2:B:815:VAL:HG12	1.91	0.70
2:A:12:LYS:NZ	2:A:16:ARG:HH12	1.90	0.70
2:A:866:ALA:N	2:A:955:LYS:NZ	2.27	0.69
2:A:919:LYS:O	2:A:922:ASN:HB2	1.92	0.69
2:B:927:LEU:CD1	2:B:944:ILE:HD12	2.23	0.69
2:B:297:ARG:NH2	2:B:297:ARG:HB3	2.07	0.69
1:C:920:G:H5''	1:C:921:U:H5	1.57	0.69
2:B:660:ASN:HB2	2:B:663:ASP:CB	2.22	0.69
2:A:374:PRO:HG2	2:A:379:VAL:HG21	1.74	0.69
2:B:95:LYS:C	2:B:97:ARG:H	1.96	0.69
2:A:339:LEU:HD22	2:A:340:LYS:N	2.08	0.69
2:B:690:ARG:HB3	2:B:690:ARG:NH1	2.06	0.69
2:A:22:ILE:HG23	2:A:23:PHE:CD1	2.27	0.69
2:A:165:TRP:HD1	2:A:561:PRO:HA	1.58	0.69
2:B:741:THR:HG1	2:B:820:TRP:HZ3	1.41	0.69
2:B:770:ARG:HD2	2:B:933:PHE:CE2	2.27	0.69
1:C:923:A:H4'	1:C:924:A:O5'	1.91	0.69
2:B:400:ILE:HD12	2:B:401:TYR:N	2.06	0.69
2:A:91:ALA:O	2:A:94:ILE:HG13	1.91	0.69
2:B:675:LEU:CD2	2:B:697:LEU:HD21	2.22	0.69
2:B:675:LEU:HD22	2:B:701:ILE:HD11	1.74	0.69
2:A:577:GLU:OE2	2:A:592:HIS:HB2	1.92	0.69
2:B:7:LYS:HB2	2:B:7:LYS:NZ	2.07	0.69
2:A:163:ILE:CD1	2:A:531:ASP:HB2	2.22	0.69
2:B:35:LYS:HB2	2:B:601:TRP:CZ3	2.28	0.69
2:A:863:ILE:HG22	2:A:953:LYS:HG2	1.74	0.69
2:A:449:ILE:N	2:A:449:ILE:HD12	2.08	0.69
2:A:221:GLU:HA	2:A:221:GLU:OE2	1.93	0.69
2:A:45:LEU:HD11	2:A:80:TRP:HB3	1.75	0.69
2:A:10:GLU:O	2:A:14:GLN:HG3	1.93	0.69
2:B:920:ARG:C	2:B:922:ASN:H	1.97	0.68
2:A:480:LYS:CE	2:A:484:ARG:HH22	1.99	0.68
2:A:730:LEU:HB3	2:A:827:TRP:CD1	2.28	0.68
2:B:341:ARG:HD3	2:B:341:ARG:N	2.07	0.68
2:A:920:ARG:C	2:A:922:ASN:H	1.96	0.68
2:B:882:ASP:CG	2:B:883:PHE:N	2.47	0.68
2:A:95:LYS:C	2:A:97:ARG:H	1.96	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:566:TYR:HA	2:B:570:GLU:HB3	1.75	0.68
2:B:14:GLN:O	2:B:18:LEU:HB2	1.93	0.68
2:A:30:LYS:CB	2:A:73:ASN:HD22	1.98	0.68
2:B:871:TRP:NE1	2:B:959:PRO:HB3	2.09	0.68
2:B:650:LYS:HE2	2:B:651:MET:N	2.03	0.68
2:A:239:THR:HG23	2:A:326:PRO:HD2	1.74	0.68
2:A:198:LEU:CB	2:A:202:GLU:HG2	2.23	0.68
2:A:62:VAL:HG21	2:A:678:MET:HE3	1.75	0.68
2:B:65:ARG:HA	2:B:68:ARG:NH1	2.08	0.68
2:B:116:LEU:HD12	2:B:119:PHE:HD2	1.59	0.68
2:B:767:TYR:CE2	2:B:783:LEU:HD11	2.27	0.68
2:A:629:PHE:O	2:A:631:GLU:N	2.25	0.68
2:B:276:GLN:O	2:B:460:ILE:HD12	1.92	0.68
2:B:28:ARG:HG3	2:B:28:ARG:HH11	1.59	0.68
2:B:678:MET:HE3	2:B:749:THR:HG21	1.74	0.68
2:A:717:LYS:HD3	2:A:717:LYS:O	1.94	0.68
2:A:82:ILE:HG21	2:A:126:VAL:HG13	1.74	0.68
2:A:722:LEU:N	2:A:722:LEU:CD2	2.55	0.68
2:A:652:SER:OG	2:A:655:LYS:HB2	1.94	0.68
2:B:770:ARG:HA	2:B:933:PHE:HE2	1.58	0.68
2:B:26:ASN:HB2	2:B:29:ASP:OD2	1.93	0.68
2:B:198:LEU:HD12	2:B:198:LEU:H	1.59	0.68
2:B:734:ASN:ND2	2:B:823:PRO:HA	2.07	0.68
1:C:988:A:H5''	2:A:528:SER:OG	1.94	0.68
2:B:237:GLY:O	2:B:325:VAL:HG13	1.94	0.68
2:B:300:VAL:HG13	2:B:301:SER:H	1.59	0.68
2:A:803:GLU:CD	2:A:815:VAL:HG23	2.14	0.68
1:C:929:G:H1	1:C:947:U:H3	1.42	0.68
2:A:75:LEU:HD12	2:A:75:LEU:C	2.14	0.67
2:B:185:TRP:CZ2	2:B:190:GLY:HA2	2.29	0.67
2:B:345:ILE:HG12	2:B:346:LEU:N	2.09	0.67
1:D:920:G:H5''	1:D:921:U:H5	1.59	0.67
2:B:555:ASP:HB3	2:B:558:LYS:CG	2.24	0.67
2:B:92:GLU:O	2:B:95:LYS:HB3	1.94	0.67
2:A:423:VAL:C	2:A:425:GLU:H	1.95	0.67
2:B:795:ALA:HB3	2:B:796:PRO:HD3	1.77	0.67
2:A:919:LYS:H	2:A:919:LYS:CE	2.07	0.67
2:B:26:ASN:CB	2:B:28:ARG:NH2	2.55	0.67
2:A:872:LYS:O	2:A:876:VAL:HG23	1.94	0.67
2:A:404:GLU:O	2:A:420:VAL:HG21	1.95	0.67
2:B:423:VAL:C	2:B:425:GLU:H	1.97	0.67
1:D:977:G:H2'	1:D:978:C:C6	2.30	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:242:TRP:CH2	2:A:332:ASP:HA	2.29	0.67
2:B:614:ILE:N	2:B:615:PRO:HD2	2.09	0.67
2:A:870:LYS:HE2	2:A:905:LYS:HE3	1.77	0.67
2:A:139:ARG:NH2	2:A:666:GLU:OE1	2.27	0.67
1:C:916:C:H4'	1:C:916:C:OP1	1.93	0.66
2:A:428:ALA:O	2:A:432:LEU:HD23	1.95	0.66
2:B:57:TYR:O	2:B:60:PRO:HG2	1.95	0.66
2:B:741:THR:OG1	2:B:820:TRP:HZ3	1.78	0.66
2:A:891:MET:SD	2:A:897:ARG:HG3	2.35	0.66
2:A:529:LEU:N	2:A:529:LEU:HD12	2.06	0.66
2:A:536:MET:SD	2:A:607:ARG:NH1	2.69	0.66
2:B:326:PRO:HA	2:B:332:ASP:HB2	1.77	0.66
2:B:136:THR:HG22	2:B:661:PHE:HD2	1.60	0.66
2:A:717:LYS:HD3	2:A:717:LYS:C	2.15	0.66
2:A:682:GLU:OE1	2:A:748:ARG:HB3	1.95	0.66
2:B:935:GLU:HG2	2:B:942:ILE:HD13	1.78	0.66
2:A:488:LEU:HD22	2:A:683:HIS:CE1	2.31	0.66
2:A:266:SER:HB2	2:A:269:ALA:HB2	1.78	0.66
2:B:871:TRP:CZ3	2:B:918:VAL:HG13	2.30	0.66
2:A:703:ARG:HG3	2:A:707:LEU:HD12	1.78	0.66
2:B:921:ILE:HB	2:B:928:ARG:NH2	2.09	0.66
2:B:793:LEU:CD2	2:B:821:PRO:HG2	2.25	0.66
2:A:921:ILE:HD12	2:A:928:ARG:NH1	2.03	0.66
2:A:188:VAL:HG23	2:A:189:VAL:N	2.06	0.66
2:B:171:LYS:HG2	2:B:176:ILE:HD12	1.78	0.66
2:B:459:LYS:NZ	2:B:461:ILE:HD13	2.11	0.66
2:B:690:ARG:HB3	2:B:690:ARG:CZ	2.25	0.66
2:A:434:LYS:HB3	2:A:436:ILE:HG12	1.77	0.66
2:A:198:LEU:HB2	2:A:202:GLU:CD	2.15	0.66
2:B:256:ARG:HG3	2:B:257:LYS:H	1.61	0.66
2:A:947:THR:HG23	2:A:948:GLU:N	2.11	0.66
2:A:784:ARG:HH22	2:A:810:GLY:H	1.45	0.65
2:B:139:ARG:HH11	2:B:139:ARG:HG3	1.60	0.65
2:B:650:LYS:CE	2:B:651:MET:H	2.05	0.65
2:A:860:ARG:NH1	2:A:943:ILE:N	2.41	0.65
1:D:983:G:C2'	1:D:984:C:H5''	2.25	0.65
2:B:197:ASP:HB3	2:B:451:ARG:HB2	1.78	0.65
2:B:198:LEU:HB2	2:B:202:GLU:CG	2.20	0.65
2:A:83:THR:HG23	2:A:152:THR:HB	1.78	0.65
2:B:537:ALA:HB2	2:B:602:TYR:CZ	2.31	0.65
2:A:354:ARG:HD2	2:A:376:VAL:HG12	1.78	0.65
2:A:914:ARG:NH2	2:A:915:THR:HG23	2.11	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:730:LEU:HD22	2:A:827:TRP:CZ2	2.31	0.65
2:A:82:ILE:HG21	2:A:126:VAL:CG1	2.26	0.65
2:A:210:ILE:CD1	2:A:232:PRO:HG3	2.24	0.65
2:A:297:ARG:HG2	2:A:304:GLU:CG	2.25	0.65
2:A:86:PRO:O	2:A:90:ILE:HG13	1.95	0.65
2:A:647:GLU:OE2	2:A:690:ARG:HA	1.97	0.65
2:B:50:HIS:CE1	2:B:52:GLY:HA3	2.31	0.65
1:C:967:U:H2'	1:C:969:G:N7	2.11	0.65
2:A:914:ARG:HH21	2:A:915:THR:HG23	1.62	0.65
2:B:616:ASN:ND2	2:B:617:HIS:H	1.93	0.65
2:A:109:TYR:OH	2:A:653:LYS:HE2	1.96	0.65
2:A:590:ILE:O	2:A:594:MET:HG3	1.97	0.65
2:A:767:TYR:HE2	2:A:783:LEU:CD1	2.09	0.65
2:A:233:GLU:HA	2:A:427:ILE:HD12	1.77	0.65
2:B:87:ILE:HD13	2:B:126:VAL:CG2	2.27	0.65
2:B:540:THR:CG2	2:B:541:ILE:HG23	2.25	0.65
2:B:909:LYS:NZ	2:B:914:ARG:O	2.29	0.65
2:A:4:LEU:O	2:A:4:LEU:HD23	1.97	0.65
2:B:924:GLU:O	2:B:928:ARG:N	2.28	0.64
2:B:924:GLU:HB3	2:B:928:ARG:HH21	1.62	0.64
2:B:300:VAL:HG13	2:B:301:SER:N	2.12	0.64
2:A:197:ASP:HB3	2:A:451:ARG:HB2	1.78	0.64
2:A:650:LYS:HD2	2:A:651:MET:N	2.11	0.64
2:B:39:THR:HG22	2:B:40:VAL:H	1.60	0.64
2:B:922:ASN:HD22	2:B:923:GLU:N	1.96	0.64
2:B:724:ASP:HA	2:B:727:ARG:HG3	1.79	0.64
2:B:27:ILE:HG13	2:B:28:ARG:N	2.13	0.64
2:B:198:LEU:HD22	2:B:202:GLU:HA	1.78	0.64
2:A:345:ILE:CG1	2:A:346:LEU:H	2.06	0.64
2:B:880:LYS:CG	2:B:885:SER:HB2	2.28	0.64
2:A:467:ILE:HG13	2:A:508:CYS:HB3	1.80	0.64
2:B:958:MET:CE	2:B:959:PRO:HD2	2.27	0.64
2:B:563:PHE:CD1	2:B:584:THR:HG21	2.33	0.64
2:A:139:ARG:CG	2:A:139:ARG:HH11	2.09	0.64
2:B:632:GLU:HG3	2:B:633:HIS:ND1	2.13	0.64
2:B:33:GLU:CD	2:B:33:GLU:H	2.00	0.64
2:A:890:LEU:CD1	2:A:906:ILE:HD11	2.27	0.64
2:B:729:MET:HE3	2:B:763:ASP:O	1.97	0.64
2:B:570:GLU:OE1	2:B:576:LYS:HE2	1.98	0.64
2:A:313:VAL:HG12	2:A:322:VAL:HG21	1.78	0.64
2:B:289:GLU:O	2:B:292:ILE:HB	1.98	0.64
2:A:492:ARG:HG2	2:A:492:ARG:HH11	1.63	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:920:G:H5''	1:C:921:U:C5	2.33	0.64
1:D:977:G:H2'	1:D:978:C:H6	1.62	0.64
2:A:871:TRP:HH2	2:A:919:LYS:HE3	1.61	0.64
2:B:660:ASN:HB2	2:B:663:ASP:HB3	1.80	0.64
2:A:475:LYS:NZ	2:A:503:LEU:O	2.31	0.64
2:B:860:ARG:HB3	2:B:966:ILE:HA	1.78	0.64
2:A:212:ILE:HD13	2:A:235:VAL:CG1	2.27	0.64
1:D:943:C:H2'	1:D:944:C:C6	2.33	0.64
2:B:864:TYR:HH	2:B:871:TRP:HZ2	1.45	0.64
2:A:136:THR:HG23	2:A:662:ILE:HB	1.80	0.64
2:A:49:LEU:HD12	2:A:49:LEU:N	2.10	0.63
2:B:73:ASN:O	2:B:601:TRP:HH2	1.81	0.63
2:A:92:GLU:O	2:A:95:LYS:HB3	1.99	0.63
2:A:924:GLU:O	2:A:928:ARG:N	2.28	0.63
2:A:342:GLU:CG	2:A:343:THR:H	2.11	0.63
2:B:373:PHE:N	2:B:374:PRO:HD2	2.14	0.63
2:B:256:ARG:HH11	2:B:278:ARG:HG3	1.63	0.63
2:B:213:LYS:HD2	2:B:435:GLY:O	1.99	0.63
2:A:924:GLU:CD	2:A:927:LEU:HD13	2.19	0.63
2:A:343:THR:HG23	2:A:344:GLU:N	2.12	0.63
2:B:755:TRP:O	2:B:759:SER:HB3	1.99	0.63
2:A:272:LYS:HE3	2:A:442:GLU:OE1	1.98	0.63
2:A:616:ASN:ND2	2:A:617:HIS:N	2.24	0.63
2:B:10:GLU:O	2:B:14:GLN:HG3	1.97	0.63
2:A:724:ASP:HA	2:A:727:ARG:CG	2.19	0.63
2:B:681:ALA:CA	2:B:750:ARG:HG3	2.28	0.63
2:A:85:SER:H	2:A:86:PRO:CD	2.12	0.63
2:B:139:ARG:HG3	2:B:139:ARG:NH1	2.13	0.63
2:B:428:ALA:O	2:B:432:LEU:HD23	1.98	0.63
2:B:87:ILE:HD13	2:B:126:VAL:HG22	1.79	0.63
2:B:495:GLN:HE21	2:B:614:ILE:HG21	1.63	0.63
2:A:924:GLU:O	2:A:927:LEU:HB3	1.99	0.63
2:A:728:TRP:HE3	2:A:729:MET:N	1.97	0.63
2:B:826:GLU:N	2:B:826:GLU:CD	2.52	0.63
2:B:45:LEU:HD11	2:B:80:TRP:CB	2.29	0.63
2:A:631:GLU:HA	2:A:634:TRP:NE1	2.14	0.63
2:A:282:VAL:HG12	2:A:283:ILE:H	1.64	0.63
2:B:332:ASP:O	2:B:333:HIS:HB2	1.99	0.62
2:B:894:SER:C	2:B:896:ILE:H	2.03	0.62
2:A:268:GLU:N	2:A:268:GLU:OE1	2.26	0.62
2:A:544:HIS:H	2:A:544:HIS:CD2	2.15	0.62
2:B:764:LEU:HD13	2:B:786:LEU:HD13	1.80	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:26:ASN:HB2	2:B:29:ASP:CG	2.19	0.62
2:A:180:ALA:O	2:A:181:HIS:HB2	1.99	0.62
1:C:918:U:H5''	1:C:919:G:OP1	1.98	0.62
2:B:216:LEU:HD11	2:B:294:LYS:HB3	1.80	0.62
2:A:235:VAL:HB	2:A:300:VAL:HG11	1.79	0.62
2:B:51:VAL:HG11	2:B:689:TRP:CE3	2.33	0.62
2:A:730:LEU:CB	2:A:827:TRP:HE1	2.12	0.62
2:A:724:ASP:CA	2:A:727:ARG:HG3	2.20	0.62
2:A:126:VAL:HG12	2:A:126:VAL:O	1.99	0.62
2:A:41:ALA:HA	2:A:607:ARG:NH2	2.15	0.62
1:C:911:C:H2'	1:C:912:C:C6	2.33	0.62
2:A:733:LEU:O	2:A:737:ILE:HG13	1.99	0.62
2:A:540:THR:OG1	2:A:598:PHE:HA	2.00	0.62
2:A:94:ILE:HD12	2:A:95:LYS:N	2.14	0.62
2:A:306:ILE:HG12	2:A:307:ILE:N	2.14	0.62
2:A:894:SER:C	2:A:896:ILE:H	2.02	0.62
2:A:168:TRP:CH2	2:A:520:TRP:HB3	2.34	0.62
2:B:181:HIS:ND1	2:B:464:GLN:HG2	2.14	0.62
2:B:531:ASP:OD2	2:B:532:SER:N	2.32	0.62
2:A:7:LYS:NZ	2:A:7:LYS:HB2	2.15	0.62
2:B:218:GLU:CD	2:B:219:ASN:HD22	2.03	0.62
2:A:933:PHE:C	2:A:933:PHE:CD1	2.72	0.62
2:B:126:VAL:O	2:B:126:VAL:HG12	1.99	0.62
2:B:85:SER:H	2:B:86:PRO:HD3	1.64	0.62
2:B:212:ILE:HD13	2:B:235:VAL:HG12	1.82	0.62
2:A:213:LYS:HB2	2:A:224:TYR:CD2	2.35	0.62
2:B:68:ARG:NH2	2:B:143:SER:HB3	2.14	0.62
2:B:277:ASP:O	2:B:278:ARG:HG3	1.99	0.62
2:B:234:THR:HG22	2:B:325:VAL:HG11	1.80	0.62
2:A:186:ASP:HB2	2:A:193:LEU:HD11	1.82	0.62
2:A:702:GLU:O	2:A:706:GLU:HG3	2.00	0.62
1:C:914:A:H1'	1:C:925:A:C6	2.35	0.62
2:A:860:ARG:HH11	2:A:943:ILE:H	1.48	0.62
2:B:709:SER:O	2:B:712:ALA:HB3	2.00	0.62
2:A:709:SER:O	2:A:712:ALA:HB3	1.99	0.62
2:B:140:ALA:O	2:B:674:ARG:NH1	2.31	0.62
2:A:776:ASP:OD2	2:A:778:ALA:HB3	1.99	0.62
2:A:906:ILE:O	2:A:910:LEU:HB2	2.00	0.61
2:B:49:LEU:HD12	2:B:49:LEU:N	2.13	0.61
2:B:793:LEU:HD21	2:B:821:PRO:HG2	1.81	0.61
1:D:970:A:H2'	1:D:972:U:OP2	2.00	0.61
2:A:297:ARG:CB	2:A:297:ARG:NH2	2.63	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:745:GLU:OE2	2:B:745:GLU:HA	1.99	0.61
1:C:986:C:C2	2:A:507:ALA:HB3	2.36	0.61
2:B:44:TYR:CE1	2:B:87:ILE:HD11	2.30	0.61
2:A:102:ILE:HD12	2:A:103:TRP:N	2.15	0.61
2:A:11:GLU:O	2:A:15:LYS:HG3	2.00	0.61
2:B:264:ILE:HG21	2:B:291:LEU:HD21	1.81	0.61
2:B:920:ARG:CA	2:B:920:ARG:HE	2.01	0.61
2:A:326:PRO:HA	2:A:332:ASP:HB2	1.81	0.61
2:B:44:TYR:OH	2:B:87:ILE:HG13	2.00	0.61
2:A:803:GLU:HA	2:A:815:VAL:HG23	1.82	0.61
2:B:401:TYR:O	2:B:405:TYR:HB2	2.00	0.61
2:B:723:LYS:HG3	2:B:724:ASP:H	1.66	0.61
2:A:864:TYR:CZ	2:A:922:ASN:OD1	2.53	0.61
2:A:82:ILE:H	2:A:152:THR:HG1	1.45	0.61
2:B:345:ILE:CG1	2:B:346:LEU:H	2.13	0.61
2:B:91:ALA:O	2:B:94:ILE:HG13	1.99	0.61
2:A:924:GLU:OE2	2:A:927:LEU:HD13	2.01	0.61
2:A:297:ARG:NH2	2:A:297:ARG:HB3	2.15	0.61
2:A:857:ASN:ND2	2:A:967:GLU:HG2	2.16	0.61
2:A:26:ASN:O	2:A:29:ASP:HB2	2.01	0.61
2:B:879:GLU:O	2:B:880:LYS:HD2	2.00	0.61
2:A:618:LEU:O	2:A:621:PHE:HB3	2.00	0.61
2:B:890:LEU:CD1	2:B:906:ILE:HD11	2.31	0.61
2:B:277:ASP:OD1	2:B:462:HIS:NE2	2.33	0.61
2:A:919:LYS:HD2	2:A:960:LEU:HD11	1.82	0.61
2:B:914:ARG:NE	2:B:915:THR:O	2.34	0.61
2:A:893:ASP:OD1	2:A:894:SER:O	2.19	0.61
2:B:145:ASP:OD1	2:B:147:SER:HB3	1.99	0.61
2:B:28:ARG:H	2:B:28:ARG:NH1	1.98	0.61
2:A:866:ALA:CA	2:A:955:LYS:HZ3	2.11	0.61
2:B:770:ARG:HA	2:B:933:PHE:CE2	2.35	0.61
1:D:970:A:H4'	1:D:971:A:OP1	2.01	0.61
2:A:492:ARG:HD2	2:A:614:ILE:CD1	2.30	0.60
2:A:94:ILE:HD11	2:A:120:GLU:N	2.15	0.60
2:B:448:VAL:HG12	2:B:456:ALA:HB3	1.82	0.60
2:A:567:ILE:O	2:A:568:PHE:CG	2.54	0.60
2:B:730:LEU:HB3	2:B:827:TRP:NE1	2.16	0.60
2:A:803:GLU:OE2	2:A:814:PHE:HB3	2.01	0.60
2:A:241:MET:HB2	2:A:307:ILE:HA	1.81	0.60
2:A:123:ILE:O	2:A:127:LYS:HB2	2.00	0.60
2:A:427:ILE:O	2:A:431:MET:HG3	2.00	0.60
2:A:860:ARG:NE	2:A:860:ARG:O	2.35	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:45:LEU:HD11	2:A:80:TRP:CB	2.31	0.60
2:A:381:LYS:HB3	2:A:382:LEU:HD12	1.83	0.60
2:A:594:MET:O	2:A:597:GLU:HB2	2.01	0.60
2:B:748:ARG:HH11	2:B:748:ARG:HB3	1.67	0.60
2:A:210:ILE:HG22	2:A:439:ILE:HG12	1.83	0.60
2:A:234:THR:HG22	2:A:325:VAL:HG11	1.83	0.60
2:B:166:GLN:O	2:B:170:LEU:HG	2.01	0.60
2:B:186:ASP:HB3	2:B:191:THR:CG2	2.32	0.60
2:A:461:ILE:CG2	2:A:464:GLN:HB2	2.32	0.60
1:C:976:C:O2'	1:C:977:G:H5'	2.01	0.60
2:A:266:SER:HB2	2:A:269:ALA:CB	2.32	0.60
2:A:12:LYS:HZ3	2:A:16:ARG:HH12	1.50	0.60
1:C:953:A:H5'	1:C:954:G:OP1	2.02	0.60
2:A:919:LYS:H	2:A:919:LYS:HE3	1.66	0.60
2:A:919:LYS:NZ	2:A:960:LEU:HD11	2.16	0.60
2:B:85:SER:H	2:B:86:PRO:CD	2.14	0.60
2:B:32:LYS:HG2	2:B:600:TYR:HD1	1.65	0.60
2:B:266:SER:HB3	2:B:269:ALA:HB2	1.83	0.60
2:A:412:VAL:CG2	2:A:414:PRO:HD2	2.32	0.60
2:B:781:TYR:CE2	2:B:785:THR:HG21	2.37	0.60
2:B:781:TYR:O	2:B:785:THR:HG23	2.02	0.60
1:D:979:C:H2'	1:D:980:C:C6	2.37	0.60
2:B:79:ALA:HB1	2:B:150:PHE:O	2.01	0.60
2:B:282:VAL:HG12	2:B:283:ILE:H	1.66	0.60
2:A:560:THR:HB	2:A:561:PRO:HD2	1.84	0.60
2:A:767:TYR:CZ	2:A:782:VAL:HG11	2.37	0.60
2:B:725:ILE:HG21	2:B:771:THR:CG2	2.31	0.59
2:A:857:ASN:OD1	2:A:967:GLU:HA	2.02	0.59
2:A:297:ARG:HH21	2:A:297:ARG:HB2	1.67	0.59
2:B:569:LEU:HA	2:B:630:ARG:HD3	1.85	0.59
2:A:17:TRP:HH2	2:A:800:HIS:CD2	2.20	0.59
2:B:540:THR:OG1	2:B:598:PHE:HA	2.01	0.59
2:A:354:ARG:HD2	2:A:376:VAL:HG13	1.82	0.59
2:A:915:THR:OG1	2:A:916:PHE:N	2.31	0.59
2:B:746:GLU:HB2	2:B:748:ARG:HD2	1.84	0.59
2:A:960:LEU:HD22	2:A:960:LEU:N	2.17	0.59
2:A:678:MET:HB3	2:A:749:THR:HB	1.84	0.59
2:A:895:GLU:OE1	2:A:898:LYS:CD	2.50	0.59
2:B:935:GLU:OE1	2:B:942:ILE:N	2.34	0.59
2:B:339:LEU:HD22	2:B:340:LYS:N	2.17	0.59
2:A:711:PHE:HA	2:A:714:TYR:CD2	2.38	0.59
2:A:914:ARG:NE	2:A:915:THR:O	2.35	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:475:LYS:HG2	2:B:479:ARG:NH2	2.18	0.59
2:A:75:LEU:HD23	2:A:601:TRP:CD2	2.37	0.59
2:A:79:ALA:HB1	2:A:150:PHE:O	2.01	0.59
2:A:824:VAL:HG11	2:A:827:TRP:CE3	2.37	0.59
2:A:182:ARG:O	2:A:183:VAL:HB	2.02	0.59
2:A:860:ARG:CB	2:A:966:ILE:HG22	2.33	0.59
2:B:711:PHE:CD1	2:B:783:LEU:HB3	2.38	0.59
2:B:241:MET:HB2	2:B:307:ILE:HA	1.84	0.59
2:B:100:LYS:HE2	2:B:104:ILE:HD11	1.83	0.59
2:A:921:ILE:HB	2:A:928:ARG:NH2	2.16	0.59
2:A:152:THR:HG22	2:A:159:PHE:HE1	1.67	0.59
1:C:986:C:C2	2:A:506:LYS:HG2	2.37	0.59
2:B:594:MET:O	2:B:597:GLU:HB2	2.02	0.59
2:A:819:LYS:HD2	2:A:819:LYS:N	2.17	0.59
2:A:560:THR:O	2:A:563:PHE:HB3	2.03	0.59
2:B:618:LEU:O	2:B:621:PHE:HB3	2.03	0.59
2:B:112:PRO:O	2:B:114:GLU:N	2.36	0.59
2:A:242:TRP:CE3	2:A:324:SER:HB2	2.38	0.59
2:A:401:TYR:O	2:A:405:TYR:HB2	2.03	0.59
2:B:94:ILE:HD12	2:B:95:LYS:N	2.18	0.59
1:D:916:C:O2'	1:D:972:U:H4'	2.03	0.59
2:B:227:ALA:CA	2:B:321:VAL:HG23	2.26	0.59
2:A:231:ARG:HB3	2:A:233:GLU:OE2	2.02	0.59
2:B:233:GLU:HB3	2:B:423:VAL:HG23	1.84	0.59
2:B:250:VAL:O	2:B:264:ILE:HA	2.02	0.59
2:B:921:ILE:HD12	2:B:928:ARG:HH22	1.68	0.59
2:B:943:ILE:HG22	2:B:946:PRO:HG3	1.84	0.59
2:B:966:ILE:O	2:B:967:GLU:HB2	2.03	0.59
2:A:211:ILE:CG2	2:A:228:ALA:HB2	2.30	0.59
2:A:297:ARG:CB	2:A:297:ARG:HH21	2.16	0.59
2:B:50:HIS:H	2:B:53:HIS:CD2	2.21	0.59
2:B:404:GLU:HA	2:B:407:LYS:O	2.03	0.59
2:B:722:LEU:HD23	2:B:722:LEU:H	1.68	0.58
2:A:66:PHE:CD1	2:A:744:LEU:HD12	2.37	0.58
2:B:355:ILE:HG22	2:B:356:VAL:N	2.12	0.58
2:B:641:ASN:HD22	2:B:641:ASN:C	2.06	0.58
2:A:393:LEU:HG	2:A:397:THR:OG1	2.03	0.58
2:A:378:GLU:HA	2:A:378:GLU:OE2	2.02	0.58
2:A:882:ASP:CG	2:A:883:PHE:N	2.56	0.58
2:A:250:VAL:O	2:A:264:ILE:HA	2.04	0.58
2:A:547:LYS:O	2:A:550:GLN:HB3	2.03	0.58
2:A:847:LYS:O	2:A:851:GLU:HG3	2.03	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:75:LEU:HD12	2:A:77:PRO:HD3	1.85	0.58
1:D:904:G:C3'	1:D:905:G:H5''	2.33	0.58
2:A:966:ILE:O	2:A:967:GLU:CB	2.50	0.58
2:B:49:LEU:CD1	2:B:49:LEU:H	2.12	0.58
2:B:105:TYR:O	2:B:111:VAL:HG23	2.03	0.58
2:A:263:TRP:HH2	2:A:438:GLU:OE1	1.86	0.58
2:A:216:LEU:HG	2:A:216:LEU:O	2.03	0.58
2:B:857:ASN:O	2:B:940:ILE:HD11	2.03	0.58
2:A:920:ARG:O	2:A:922:ASN:N	2.36	0.58
2:B:733:LEU:HD13	2:B:737:ILE:HG13	1.85	0.58
2:A:860:ARG:HH22	2:A:862:TYR:HB3	1.68	0.58
2:A:860:ARG:HH11	2:A:943:ILE:N	2.01	0.58
2:A:819:LYS:CD	2:A:819:LYS:N	2.66	0.58
2:A:729:MET:SD	2:A:764:LEU:HA	2.44	0.58
2:A:235:VAL:HA	2:A:323:MET:HE3	1.85	0.58
2:A:27:ILE:H	2:A:28:ARG:NH2	2.01	0.58
2:A:541:ILE:HB	2:A:594:MET:HE2	1.86	0.58
2:B:901:LYS:O	2:B:901:LYS:HD3	2.03	0.58
2:A:410:PHE:O	2:A:416:GLU:HB3	2.03	0.58
2:B:429:LYS:NZ	2:B:429:LYS:HB3	2.19	0.58
2:B:180:ALA:O	2:B:181:HIS:HB2	2.04	0.58
2:B:660:ASN:HB2	2:B:663:ASP:HB2	1.86	0.58
2:A:944:ILE:HG22	2:A:945:ASN:N	2.18	0.58
2:B:60:PRO:HB2	2:B:76:PHE:CE1	2.39	0.58
2:B:342:GLU:HG2	2:B:343:THR:N	2.15	0.58
2:B:804:GLU:O	2:B:807:GLU:HB3	2.03	0.58
2:B:50:HIS:HE1	2:B:52:GLY:HA3	1.68	0.58
2:B:238:VAL:HA	2:B:325:VAL:HG22	1.85	0.58
2:A:566:TYR:O	2:A:595:LYS:HD2	2.04	0.58
2:A:239:THR:O	2:A:240:ASN:HB3	2.03	0.58
2:B:713:GLU:HA	2:B:713:GLU:OE2	2.04	0.58
2:B:495:GLN:O	2:B:499:ILE:HG12	2.04	0.58
2:A:710:GLN:O	2:A:712:ALA:N	2.37	0.58
2:B:682:GLU:OE1	2:B:748:ARG:HB3	2.03	0.58
2:B:652:SER:OG	2:B:655:LYS:HB2	2.04	0.58
2:A:167:PHE:O	2:A:170:LEU:HB2	2.04	0.58
2:A:482:LEU:HD23	2:A:482:LEU:C	2.24	0.58
2:B:835:GLU:OE1	2:B:921:ILE:HG13	2.03	0.58
2:B:211:ILE:HG12	2:B:438:GLU:O	2.03	0.58
2:A:862:TYR:C	2:A:862:TYR:CD2	2.77	0.58
2:B:410:PHE:O	2:B:416:GLU:HB3	2.04	0.58
2:B:377:GLU:OE2	2:B:380:ASN:HB2	2.04	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:860:ARG:O	2:B:860:ARG:CZ	2.52	0.57
2:A:871:TRP:HZ3	2:A:918:VAL:HG22	1.69	0.57
2:A:860:ARG:NE	2:A:860:ARG:C	2.57	0.57
2:B:467:ILE:HG13	2:B:508:CYS:HB3	1.85	0.57
1:C:937:C:O5'	1:C:937:C:H6	1.87	0.57
2:A:355:ILE:HG23	2:A:412:VAL:CG1	2.34	0.57
2:B:629:PHE:O	2:B:631:GLU:N	2.29	0.57
2:B:459:LYS:HZ3	2:B:461:ILE:HD13	1.70	0.57
2:A:112:PRO:O	2:A:114:GLU:N	2.37	0.57
2:A:614:ILE:N	2:A:615:PRO:HD2	2.19	0.57
2:B:727:ARG:HH11	2:B:727:ARG:HG2	1.69	0.57
2:B:831:THR:O	2:B:835:GLU:HG3	2.05	0.57
2:B:563:PHE:CE1	2:B:584:THR:HG21	2.39	0.57
2:A:404:GLU:HA	2:A:407:LYS:O	2.05	0.57
2:A:646:LEU:O	2:A:647:GLU:HB2	2.04	0.57
2:A:145:ASP:OD1	2:A:145:ASP:C	2.43	0.57
1:D:943:C:H2'	1:D:944:C:H6	1.66	0.57
2:A:42:PHE:HD1	2:A:42:PHE:O	1.87	0.57
2:B:784:ARG:O	2:B:784:ARG:HD3	2.05	0.57
2:B:631:GLU:HA	2:B:634:TRP:CD1	2.40	0.57
2:A:348:LYS:HB3	2:A:348:LYS:HZ3	1.70	0.57
2:A:541:ILE:HB	2:A:594:MET:CE	2.34	0.57
2:A:860:ARG:CB	2:A:966:ILE:HA	2.34	0.57
2:B:116:LEU:HD12	2:B:119:PHE:CE2	2.40	0.57
2:B:541:ILE:O	2:B:545:ILE:HG12	2.05	0.57
2:B:793:LEU:CD2	2:B:821:PRO:CG	2.82	0.57
2:A:757:PHE:HD1	2:A:794:MET:SD	2.27	0.57
2:B:846:ILE:HG12	2:B:964:ILE:HD13	1.86	0.57
2:A:770:ARG:HD2	2:A:933:PHE:CD2	2.39	0.57
2:B:410:PHE:CE2	2:B:423:VAL:HG11	2.40	0.57
2:B:32:LYS:O	2:B:35:LYS:HG3	2.04	0.57
2:A:559:LEU:HD22	2:A:563:PHE:CE2	2.40	0.57
2:A:331:PHE:O	2:A:334:VAL:HG23	2.04	0.57
2:B:928:ARG:C	2:B:930:ALA:H	2.09	0.57
2:B:697:LEU:O	2:B:701:ILE:HG12	2.05	0.57
2:A:233:GLU:HA	2:A:427:ILE:CD1	2.34	0.57
2:B:242:TRP:CH2	2:B:332:ASP:HA	2.40	0.57
2:A:551:GLU:O	2:A:553:LYS:N	2.37	0.57
2:A:804:GLU:O	2:A:807:GLU:HB3	2.05	0.57
2:B:624:ASN:HD22	2:B:624:ASN:H	1.51	0.57
2:A:253:LYS:HD3	2:A:260:GLU:OE1	2.04	0.57
1:D:928:C:OP1	2:B:696:LYS:HE3	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:745:GLU:HA	2:A:745:GLU:OE2	2.05	0.57
2:B:151:TYR:CD1	2:B:156:PHE:HB2	2.40	0.57
2:A:171:LYS:HE2	2:A:520:TRP:CE2	2.40	0.57
2:A:920:ARG:C	2:A:922:ASN:N	2.58	0.56
2:A:83:THR:HG22	2:A:153:THR:HG22	1.87	0.56
2:B:662:ILE:HG23	2:B:663:ASP:H	1.70	0.56
2:A:256:ARG:HH11	2:A:278:ARG:HD3	1.70	0.56
2:B:239:THR:O	2:B:240:ASN:HB3	2.04	0.56
2:B:870:LYS:HE2	2:B:957:ALA:O	2.05	0.56
2:B:161:LYS:HD2	2:B:559:LEU:O	2.05	0.56
2:A:840:ARG:O	2:A:844:GLU:HG3	2.04	0.56
2:B:57:TYR:C	2:B:60:PRO:HD2	2.26	0.56
2:B:212:ILE:HD13	2:B:235:VAL:CG1	2.35	0.56
2:B:705:TYR:CD2	2:B:805:LEU:HD21	2.40	0.56
2:B:918:VAL:HG11	2:B:920:ARG:HD2	1.87	0.56
2:A:864:TYR:HD2	2:A:962:PRO:HB3	1.70	0.56
2:A:877:VAL:HG22	2:A:906:ILE:HG23	1.85	0.56
2:A:196:HIS:CD2	2:A:197:ASP:H	2.22	0.56
2:A:93:ARG:HG2	2:A:451:ARG:NH2	2.21	0.56
2:B:867:GLU:CD	2:B:867:GLU:N	2.57	0.56
2:B:95:LYS:C	2:B:97:ARG:N	2.58	0.56
2:B:432:LEU:HD11	2:B:439:ILE:HG13	1.87	0.56
2:B:609:SER:O	2:B:640:VAL:HA	2.05	0.56
2:B:135:GLU:O	2:B:138:ILE:HG22	2.06	0.56
2:B:389:ASP:O	2:B:390:LYS:HD3	2.05	0.56
2:B:725:ILE:HD13	2:B:770:ARG:NH2	2.21	0.56
2:A:481:ALA:O	2:A:484:ARG:N	2.34	0.56
2:B:165:TRP:HD1	2:B:561:PRO:HA	1.70	0.56
2:B:44:TYR:HE1	2:B:87:ILE:CD1	2.16	0.56
2:A:93:ARG:HD3	2:A:451:ARG:NH2	2.20	0.56
2:B:884:LYS:O	2:B:887:MET:N	2.38	0.56
2:B:743:ALA:HB2	2:B:751:THR:HG22	1.87	0.56
2:A:928:ARG:C	2:A:930:ALA:H	2.08	0.56
2:B:920:ARG:O	2:B:922:ASN:N	2.37	0.56
2:A:325:VAL:N	2:A:332:ASP:OD2	2.39	0.56
2:A:662:ILE:HG23	2:A:663:ASP:N	2.19	0.56
2:B:53:HIS:O	2:B:57:TYR:HD2	1.89	0.56
2:B:852:VAL:HG12	2:B:852:VAL:O	2.06	0.56
2:A:825:GLU:HG2	2:A:826:GLU:HG2	1.87	0.56
2:B:236:TYR:CE2	2:B:414:PRO:HG2	2.41	0.56
2:B:708:ILE:HB	2:B:805:LEU:HD13	1.87	0.56
2:A:384:ILE:HG22	2:A:385:LYS:N	2.18	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:16:ARG:CG	2:A:16:ARG:HH11	2.19	0.56
2:B:742:ASN:HD22	2:B:742:ASN:N	2.03	0.56
2:A:45:LEU:HD21	2:A:80:TRP:HB3	1.87	0.56
1:D:979:C:H2'	1:D:980:C:H6	1.71	0.56
2:B:272:LYS:HE2	2:B:442:GLU:OE1	2.05	0.56
2:B:98:ASP:O	2:B:102:ILE:HG23	2.06	0.56
2:A:831:THR:O	2:A:835:GLU:HG3	2.06	0.56
2:A:771:THR:CG2	2:A:774:ARG:HD3	2.35	0.56
2:B:797:PHE:CD2	2:B:797:PHE:N	2.73	0.56
2:A:27:ILE:N	2:A:28:ARG:NH2	2.53	0.56
2:B:779:LYS:O	2:B:783:LEU:HD13	2.04	0.56
2:A:95:LYS:C	2:A:97:ARG:N	2.58	0.56
2:A:884:LYS:O	2:A:887:MET:N	2.38	0.56
2:B:374:PRO:HG3	2:B:379:VAL:HG21	1.88	0.56
2:B:475:LYS:HG2	2:B:475:LYS:O	2.06	0.56
2:A:355:ILE:HD12	2:A:412:VAL:HG11	1.88	0.56
2:A:953:LYS:NZ	2:A:953:LYS:HB3	2.19	0.56
2:A:706:GLU:O	2:A:709:SER:HB2	2.06	0.56
2:A:212:ILE:HD13	2:A:235:VAL:HG12	1.88	0.56
2:A:690:ARG:HH12	2:A:693:GLU:HG3	1.70	0.56
2:A:67:LYS:CE	2:A:70:GLN:NE2	2.69	0.56
2:A:860:ARG:HH22	2:A:862:TYR:CB	2.18	0.56
2:B:767:TYR:HE2	2:B:783:LEU:CD1	2.19	0.56
2:A:866:ALA:HB3	2:A:955:LYS:NZ	2.21	0.56
2:B:935:GLU:CD	2:B:942:ILE:H	2.09	0.56
2:A:82:ILE:HG13	2:A:153:THR:CG2	2.33	0.56
2:B:744:LEU:HD23	2:B:752:ALA:HB2	1.87	0.56
2:A:708:ILE:HD12	2:A:791:VAL:HG23	1.87	0.56
2:B:551:GLU:O	2:B:553:LYS:N	2.39	0.56
1:C:905:G:H2'	1:C:906:G:O4'	2.06	0.56
2:A:468:ASP:C	2:A:470:GLY:H	2.08	0.55
2:B:868:ASP:O	2:B:870:LYS:N	2.39	0.55
2:A:728:TRP:O	2:A:731:HIS:N	2.38	0.55
2:A:863:ILE:HG13	2:A:945:ASN:OD1	2.05	0.55
2:B:613:LEU:O	2:B:618:LEU:HB2	2.06	0.55
2:B:746:GLU:O	2:B:748:ARG:HG3	2.06	0.55
2:A:675:LEU:HD12	2:A:697:LEU:HD21	1.88	0.55
2:B:727:ARG:HG2	2:B:727:ARG:NH1	2.21	0.55
2:B:167:PHE:O	2:B:170:LEU:HB2	2.06	0.55
2:A:112:PRO:HG2	2:A:115:ILE:HD12	1.87	0.55
2:A:331:PHE:HD1	2:A:334:VAL:HG21	1.72	0.55
2:B:920:ARG:C	2:B:922:ASN:N	2.60	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:555:ASP:OD2	2:B:558:LYS:HE2	2.07	0.55
2:A:198:LEU:H	2:A:198:LEU:HD12	1.70	0.55
2:A:933:PHE:C	2:A:933:PHE:HD1	2.08	0.55
2:B:468:ASP:C	2:B:470:GLY:H	2.09	0.55
2:A:631:GLU:HA	2:A:634:TRP:CD1	2.42	0.55
1:C:920:G:H4'	1:C:920:G:OP1	2.06	0.55
2:B:636:LYS:HB3	2:B:636:LYS:HZ2	1.71	0.55
2:A:84:GLY:O	2:A:513:GLY:HA3	2.07	0.55
2:A:859:LYS:CB	2:A:941:GLU:HB3	2.33	0.55
2:A:644:GLY:O	2:A:650:LYS:NZ	2.38	0.55
2:A:767:TYR:HE2	2:A:783:LEU:HD13	1.70	0.55
1:D:980:C:O2'	1:D:981:C:H5'	2.06	0.55
2:A:349:TYR:HD1	2:A:349:TYR:H	1.55	0.55
2:A:868:ASP:O	2:A:870:LYS:N	2.40	0.55
2:B:878:SER:CB	2:B:915:THR:HG22	2.36	0.55
2:B:835:GLU:O	2:B:838:PHE:HB3	2.07	0.55
2:A:297:ARG:HG2	2:A:304:GLU:CD	2.27	0.55
2:A:488:LEU:HA	2:A:489:PRO:C	2.27	0.55
2:B:847:LYS:O	2:B:851:GLU:HG3	2.06	0.55
2:B:314:ASP:HB3	2:B:317:ASN:HB3	1.88	0.55
2:B:860:ARG:C	2:B:860:ARG:CZ	2.75	0.55
2:B:142:PHE:C	2:B:144:VAL:H	2.10	0.55
2:B:235:VAL:HB	2:B:300:VAL:HG11	1.88	0.55
2:B:884:LYS:HG2	2:B:888:GLU:OE1	2.07	0.55
2:A:884:LYS:O	2:A:886:SER:N	2.40	0.55
2:A:142:PHE:C	2:A:144:VAL:H	2.11	0.55
2:A:469:TYR:HB3	2:A:503:LEU:HD23	1.89	0.55
2:A:567:ILE:HA	2:A:595:LYS:CD	2.28	0.55
2:A:66:PHE:CE2	2:A:70:GLN:NE2	2.69	0.55
2:B:508:CYS:O	2:B:509:ALA:HB2	2.06	0.55
2:A:555:ASP:OD2	2:A:558:LYS:HG2	2.07	0.55
2:B:537:ALA:O	2:B:540:THR:HG22	2.07	0.55
2:B:489:PRO:HG3	2:B:684:ASP:OD2	2.06	0.55
2:A:733:LEU:HD11	2:A:789:VAL:HG21	1.89	0.55
2:B:864:TYR:HD2	2:B:962:PRO:HB3	1.72	0.54
2:B:84:GLY:O	2:B:513:GLY:HA3	2.07	0.54
2:A:766:TRP:CH2	2:A:836:GLU:OE1	2.60	0.54
2:A:342:GLU:CG	2:A:343:THR:N	2.68	0.54
2:A:58:THR:O	2:A:62:VAL:HG23	2.07	0.54
2:B:471:ASN:CG	2:B:473:GLU:HG2	2.28	0.54
2:A:714:TYR:CD1	2:A:780:ARG:HG2	2.42	0.54
2:B:139:ARG:HH11	2:B:139:ARG:CG	2.19	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:152:THR:HG22	2:A:159:PHE:CE1	2.43	0.54
2:B:136:THR:HG22	2:B:661:PHE:CD2	2.41	0.54
2:B:219:ASN:OD1	2:B:220:GLY:N	2.41	0.54
1:D:933:G:O2'	1:D:934:A:H5'	2.07	0.54
2:A:480:LYS:CE	2:A:484:ARG:NH2	2.64	0.54
2:B:432:LEU:HD13	2:B:437:ALA:O	2.06	0.54
2:A:784:ARG:CZ	2:A:809:LEU:HD23	2.37	0.54
2:A:388:LYS:HD3	2:A:389:ASP:N	2.21	0.54
2:A:75:LEU:HD12	2:A:76:PHE:N	2.22	0.54
2:A:922:ASN:HD22	2:A:923:GLU:CA	2.18	0.54
2:B:753:VAL:HG23	2:B:797:PHE:CE1	2.42	0.54
1:C:986:C:C5	2:A:181:HIS:NE2	2.72	0.54
2:A:27:ILE:H	2:A:28:ARG:HH21	1.54	0.54
2:B:728:TRP:O	2:B:731:HIS:N	2.38	0.54
2:A:49:LEU:CD1	2:A:49:LEU:H	2.13	0.54
2:B:536:MET:SD	2:B:536:MET:N	2.81	0.54
2:A:67:LYS:HE2	2:A:70:GLN:NE2	2.23	0.54
2:A:964:ILE:HD12	2:A:965:PHE:N	2.23	0.54
2:B:730:LEU:HD22	2:B:827:TRP:CZ2	2.42	0.54
2:A:623:PHE:O	2:A:626:VAL:HG22	2.08	0.54
2:A:282:VAL:HG12	2:A:283:ILE:N	2.22	0.54
2:B:173:LYS:HB3	2:B:175:TYR:CE2	2.43	0.54
2:B:298:ASN:HD22	2:B:299:PRO:HD2	1.71	0.54
2:B:729:MET:HG3	2:B:729:MET:O	2.07	0.54
2:A:343:THR:HG23	2:A:344:GLU:HG2	1.89	0.54
2:B:567:ILE:O	2:B:568:PHE:CG	2.60	0.54
2:B:206:ILE:HG22	2:B:206:ILE:O	2.08	0.54
2:A:98:ASP:O	2:A:102:ILE:HG23	2.07	0.54
2:A:377:GLU:O	2:A:378:GLU:HB2	2.07	0.54
2:B:757:PHE:CD1	2:B:794:MET:SD	2.99	0.54
2:A:734:ASN:OD1	2:A:823:PRO:CA	2.56	0.54
2:B:275:PHE:O	2:B:277:ASP:N	2.39	0.54
2:A:75:LEU:HD23	2:A:601:TRP:CG	2.42	0.54
2:A:724:ASP:HB2	2:A:929:GLU:OE2	2.07	0.54
1:D:914:A:H4'	2:B:750:ARG:HH22	1.72	0.54
2:B:50:HIS:ND1	2:B:52:GLY:N	2.56	0.54
2:B:413:PRO:CB	2:B:414:PRO:HD3	2.33	0.54
2:B:343:THR:HG23	2:B:344:GLU:N	2.21	0.54
2:A:51:VAL:HG23	2:A:52:GLY:N	2.23	0.54
2:A:560:THR:HB	2:A:561:PRO:CD	2.38	0.54
2:B:213:LYS:HB3	2:B:213:LYS:NZ	2.21	0.54
1:D:960:C:O2'	1:D:961:C:OP2	2.16	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:226:PRO:HG3	2:B:263:TRP:CE3	2.43	0.54
2:B:48:HIS:HB2	2:B:109:TYR:HD1	1.73	0.54
2:A:67:LYS:CD	2:A:70:GLN:HE21	2.18	0.54
2:B:45:LEU:HD13	2:B:130:MET:CB	2.38	0.54
2:B:467:ILE:HG13	2:B:508:CYS:CB	2.37	0.54
2:B:475:LYS:HA	2:B:623:PHE:HE1	1.72	0.54
2:B:347:GLU:OE1	2:B:348:LYS:N	2.39	0.54
2:B:838:PHE:O	2:B:842:VAL:HG23	2.07	0.54
2:A:923:GLU:CD	2:A:923:GLU:N	2.61	0.54
2:A:860:ARG:NH2	2:A:862:TYR:N	2.56	0.54
2:B:188:VAL:HG23	2:B:189:VAL:N	2.16	0.54
2:B:51:VAL:HG23	2:B:659:LEU:HB3	1.89	0.54
2:A:388:LYS:HD3	2:A:389:ASP:HB2	1.89	0.54
2:B:393:LEU:HD12	2:B:396:ALA:HB3	1.88	0.54
2:B:776:ASP:OD2	2:B:778:ALA:HB3	2.08	0.54
2:A:150:PHE:HD1	2:A:151:TYR:O	1.91	0.54
2:A:495:GLN:HG2	2:A:614:ILE:HG21	1.90	0.54
2:A:824:VAL:CG1	2:A:827:TRP:HE3	2.20	0.54
2:B:243:VAL:HG12	2:B:321:VAL:HG12	1.90	0.54
2:A:420:VAL:C	2:A:422:GLU:H	2.12	0.54
2:A:420:VAL:HG12	2:A:424:LYS:NZ	2.23	0.54
2:A:62:VAL:HG21	2:A:678:MET:CE	2.38	0.54
2:A:867:GLU:N	2:A:867:GLU:CD	2.58	0.54
1:C:955:G:OP1	2:A:961:LYS:NZ	2.39	0.54
2:A:609:SER:O	2:A:640:VAL:HA	2.08	0.54
2:A:508:CYS:O	2:A:509:ALA:HB2	2.07	0.53
2:B:871:TRP:CD1	2:B:959:PRO:HB3	2.42	0.53
1:C:985:A:H2'	1:C:986:C:C4	2.43	0.53
2:B:710:GLN:O	2:B:712:ALA:N	2.41	0.53
2:B:55:ARG:HD2	2:B:687:PHE:CE1	2.44	0.53
2:A:953:LYS:HB3	2:A:953:LYS:HZ3	1.72	0.53
2:A:216:LEU:HB2	2:A:296:VAL:HG12	1.91	0.53
2:A:15:LYS:NZ	2:A:15:LYS:HB3	2.23	0.53
2:B:725:ILE:HD13	2:B:770:ARG:HH21	1.72	0.53
2:B:733:LEU:CD1	2:B:789:VAL:HG11	2.28	0.53
2:A:193:LEU:HG	2:A:197:ASP:HB2	1.90	0.53
2:A:12:LYS:NZ	2:A:16:ARG:NH1	2.55	0.53
2:B:616:ASN:HA	2:B:620:PHE:CE1	2.44	0.53
2:B:855:ILE:O	2:B:856:GLU:HB2	2.07	0.53
2:A:730:LEU:O	2:A:827:TRP:NE1	2.42	0.53
2:A:263:TRP:CH2	2:A:438:GLU:OE1	2.62	0.53
2:A:233:GLU:HB3	2:A:423:VAL:CG2	2.36	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:555:ASP:OD2	2:A:558:LYS:HE2	2.09	0.53
2:B:235:VAL:HG23	2:B:236:TYR:N	2.23	0.53
2:B:729:MET:HA	2:B:729:MET:HE2	1.90	0.53
2:B:182:ARG:O	2:B:183:VAL:HB	2.07	0.53
2:B:66:PHE:CG	2:B:744:LEU:HD12	2.43	0.53
2:B:240:ASN:HA	2:B:305:VAL:HB	1.90	0.53
2:B:966:ILE:O	2:B:967:GLU:CB	2.57	0.53
2:A:826:GLU:O	2:A:828:TRP:N	2.40	0.53
2:A:860:ARG:HB3	2:A:966:ILE:HA	1.90	0.53
2:B:166:GLN:NE2	2:B:534:ILE:HG12	2.23	0.53
2:A:39:THR:HG23	2:A:604:LEU:CD1	2.36	0.53
2:B:475:LYS:O	2:B:479:ARG:NH1	2.41	0.53
2:B:42:PHE:O	2:B:42:PHE:HD1	1.91	0.53
2:A:923:GLU:H	2:A:923:GLU:CD	2.11	0.53
2:A:242:TRP:CD1	2:A:310:ALA:HB2	2.44	0.53
2:A:336:LEU:O	2:A:338:ASP:N	2.42	0.53
2:B:461:ILE:CG2	2:B:464:GLN:HB2	2.39	0.53
2:A:459:LYS:HG2	2:A:460:ILE:N	2.22	0.53
2:B:681:ALA:N	2:B:750:ARG:HG3	2.23	0.53
2:B:797:PHE:HD2	2:B:797:PHE:H	1.56	0.53
2:B:340:LYS:HZ2	2:B:341:ARG:HH12	1.55	0.53
2:B:253:LYS:NZ	2:B:283:ILE:HD11	2.23	0.53
2:B:488:LEU:HA	2:B:489:PRO:C	2.29	0.53
2:A:884:LYS:NZ	2:A:884:LYS:HB2	2.23	0.53
2:A:733:LEU:HD11	2:A:789:VAL:CB	2.38	0.53
2:A:256:ARG:NH1	2:A:278:ARG:HD3	2.24	0.53
2:B:336:LEU:O	2:B:338:ASP:N	2.42	0.53
2:B:79:ALA:HB2	2:B:539:TYR:HE2	1.73	0.53
2:B:620:PHE:CD1	2:B:620:PHE:N	2.76	0.53
2:B:39:THR:HG22	2:B:40:VAL:N	2.23	0.53
2:B:860:ARG:NE	2:B:942:ILE:HA	2.20	0.53
2:A:198:LEU:HD13	2:A:202:GLU:OE1	2.09	0.53
1:C:985:A:H2'	1:C:986:C:C5	2.44	0.53
2:B:171:LYS:HD2	2:B:520:TRP:CZ3	2.44	0.53
2:B:384:ILE:HG22	2:B:385:LYS:N	2.20	0.53
2:B:884:LYS:O	2:B:886:SER:N	2.41	0.53
2:B:66:PHE:CE2	2:B:744:LEU:HB3	2.44	0.53
2:A:887:MET:HE2	2:A:891:MET:HG2	1.90	0.53
2:B:395:GLN:HG3	2:B:396:ALA:N	2.24	0.53
2:A:173:LYS:HD3	2:A:175:TYR:CE2	2.44	0.53
2:B:860:ARG:HA	2:B:966:ILE:HA	1.90	0.53
2:A:235:VAL:HA	2:A:323:MET:CE	2.38	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:44:TYR:CD1	2:B:44:TYR:C	2.82	0.53
2:A:51:VAL:HG13	2:A:659:LEU:HB3	1.90	0.53
2:A:751:THR:O	2:A:752:ALA:C	2.48	0.53
2:B:751:THR:O	2:B:752:ALA:C	2.47	0.53
2:A:676:TYR:HB2	2:A:697:LEU:HD23	1.91	0.53
2:A:150:PHE:CE2	2:A:538:TYR:HD2	2.27	0.53
1:C:988:A:C5'	2:A:528:SER:OG	2.57	0.53
1:D:902:C:C2'	1:D:903:G:H5''	2.38	0.53
2:B:54:ALA:HB1	2:B:661:PHE:CE1	2.44	0.53
2:A:136:THR:CG2	2:A:662:ILE:HB	2.39	0.52
2:A:17:TRP:CZ3	2:A:800:HIS:CD2	2.97	0.52
2:B:687:PHE:C	2:B:687:PHE:CD2	2.82	0.52
2:B:733:LEU:O	2:B:737:ILE:HG13	2.09	0.52
2:B:761:MET:SD	2:B:790:TRP:HH2	2.32	0.52
2:A:528:SER:OG	2:A:529:LEU:HD12	2.09	0.52
2:A:766:TRP:CZ3	2:A:836:GLU:OE1	2.63	0.52
2:B:781:TYR:CZ	2:B:785:THR:HG21	2.44	0.52
2:A:241:MET:HG3	2:A:296:VAL:HG21	1.90	0.52
2:A:801:ILE:O	2:A:805:LEU:HG	2.10	0.52
2:A:716:VAL:O	2:A:716:VAL:HG12	2.09	0.52
2:A:826:GLU:OE2	2:A:826:GLU:N	2.42	0.52
2:B:703:ARG:HD2	2:B:707:LEU:CD1	2.37	0.52
2:A:662:ILE:HG23	2:A:663:ASP:H	1.74	0.52
2:B:782:VAL:HG12	2:B:783:LEU:HD12	1.91	0.52
2:A:188:VAL:CG2	2:A:189:VAL:H	2.07	0.52
2:B:83:THR:HG23	2:B:152:THR:HB	1.91	0.52
2:B:82:ILE:HG13	2:B:153:THR:HG23	1.91	0.52
2:B:297:ARG:NH2	2:B:297:ARG:CB	2.72	0.52
2:B:420:VAL:C	2:B:422:GLU:H	2.12	0.52
2:B:624:ASN:HD22	2:B:624:ASN:N	2.08	0.52
2:B:720:VAL:HG12	2:B:777:GLU:HG2	1.91	0.52
2:B:625:HIS:CD2	2:B:635:PRO:HD3	2.44	0.52
2:B:486:LYS:H	2:B:637:GLY:HA2	1.74	0.52
1:D:988:A:C8	2:B:529:LEU:HD21	2.44	0.52
2:A:482:LEU:CD1	2:A:500:ILE:HD11	2.38	0.52
2:B:722:LEU:HD22	2:B:722:LEU:H	1.71	0.52
2:B:723:LYS:HG3	2:B:724:ASP:N	2.24	0.52
2:B:661:PHE:CE2	2:B:665:ILE:HD11	2.44	0.52
2:A:292:ILE:HD13	2:A:307:ILE:HG22	1.91	0.52
2:B:223:ILE:HD11	2:B:264:ILE:HG13	1.92	0.52
2:B:764:LEU:O	2:B:768:LEU:HG	2.08	0.52
2:A:234:THR:O	2:A:325:VAL:HG21	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:860:ARG:O	2:A:860:ARG:CZ	2.58	0.52
2:B:356:VAL:HG21	2:B:411:LYS:HB2	1.91	0.52
2:A:752:ALA:O	2:A:755:TRP:N	2.43	0.52
2:A:14:GLN:O	2:A:18:LEU:HB2	2.08	0.52
2:B:100:LYS:O	2:B:104:ILE:HG13	2.10	0.52
2:A:355:ILE:HG22	2:A:356:VAL:N	2.21	0.52
2:A:342:GLU:N	2:A:342:GLU:OE2	2.41	0.52
2:B:803:GLU:HG2	2:B:815:VAL:HG12	1.92	0.52
2:A:323:MET:HG3	2:A:323:MET:O	2.08	0.52
2:B:826:GLU:O	2:B:828:TRP:N	2.42	0.52
2:B:671:ASP:OD1	2:B:799:PRO:HD2	2.10	0.52
2:B:676:TYR:O	2:B:679:SER:HB3	2.10	0.52
2:A:37:TYR:HD2	2:A:38:ILE:H	1.58	0.52
2:B:345:ILE:CG1	2:B:346:LEU:N	2.73	0.52
2:B:241:MET:HG3	2:B:296:VAL:HG21	1.91	0.52
2:A:480:LYS:HG2	2:A:484:ARG:NH2	2.24	0.52
2:B:558:LYS:O	2:B:584:THR:HG22	2.10	0.52
2:B:433:GLU:HA	2:B:433:GLU:OE2	2.10	0.52
2:B:233:GLU:OE2	2:B:234:THR:N	2.42	0.52
2:B:232:PRO:HD2	2:B:424:LYS:HG3	1.92	0.52
2:B:24:GLU:CD	2:B:147:SER:HB2	2.30	0.52
2:A:864:TYR:CG	2:A:865:THR:N	2.77	0.51
2:A:177:VAL:HG23	2:A:466:PHE:HB2	1.92	0.51
2:B:44:TYR:C	2:B:44:TYR:HD1	2.14	0.51
2:B:266:SER:HB3	2:B:269:ALA:CB	2.41	0.51
2:B:956:GLN:HG2	2:B:956:GLN:O	2.09	0.51
2:A:496:PHE:HE1	2:A:614:ILE:CG1	2.18	0.51
2:A:44:TYR:OH	2:A:87:ILE:HG12	2.09	0.51
2:A:326:PRO:HA	2:A:332:ASP:CB	2.40	0.51
2:A:860:ARG:CZ	2:A:861:ALA:HA	2.39	0.51
2:B:35:LYS:HB2	2:B:601:TRP:HZ3	1.75	0.51
2:B:834:ALA:O	2:B:837:GLU:OE2	2.29	0.51
2:B:915:THR:O	2:B:916:PHE:HD2	1.93	0.51
2:A:373:PHE:HD1	2:A:374:PRO:HD3	1.68	0.51
2:B:273:LEU:HA	2:B:276:GLN:HG3	1.92	0.51
2:A:486:LYS:H	2:A:637:GLY:HA2	1.75	0.51
2:A:65:ARG:O	2:A:68:ARG:N	2.44	0.51
2:B:863:ILE:HG22	2:B:953:LYS:HG2	1.92	0.51
2:B:679:SER:O	2:B:750:ARG:HG2	2.10	0.51
2:A:555:ASP:HB3	2:A:558:LYS:HG2	1.93	0.51
2:B:427:ILE:HG22	2:B:431:MET:SD	2.50	0.51
2:A:36:PHE:O	2:A:36:PHE:CD2	2.64	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:789:VAL:O	2:A:790:TRP:C	2.49	0.51
2:A:672:VAL:HG21	2:A:698:ARG:HG3	1.93	0.51
2:B:62:VAL:HG21	2:B:678:MET:CE	2.39	0.51
2:B:235:VAL:HG23	2:B:236:TYR:H	1.76	0.51
2:A:102:ILE:HD12	2:A:102:ILE:C	2.30	0.51
2:A:148:ARG:NH1	2:A:597:GLU:OE1	2.43	0.51
2:B:946:PRO:HG2	2:B:953:LYS:HE2	1.92	0.51
2:B:789:VAL:O	2:B:790:TRP:C	2.49	0.51
2:A:722:LEU:O	2:A:722:LEU:HD23	2.10	0.51
2:A:488:LEU:HD22	2:A:683:HIS:HE1	1.75	0.51
2:B:913:GLU:O	2:B:914:ARG:O	2.29	0.51
2:B:678:MET:CE	2:B:749:THR:HG21	2.40	0.51
2:A:423:VAL:C	2:A:425:GLU:N	2.64	0.51
2:B:44:TYR:OH	2:B:86:PRO:HD2	2.11	0.51
2:B:297:ARG:CB	2:B:297:ARG:HH21	2.24	0.51
2:A:306:ILE:CG1	2:A:307:ILE:N	2.74	0.51
2:A:268:GLU:O	2:A:271:TYR:HB3	2.11	0.51
2:A:630:ARG:O	2:A:632:GLU:N	2.38	0.51
2:B:391:GLU:HG3	2:B:394:GLU:HB2	1.93	0.51
2:A:53:HIS:O	2:A:57:TYR:HD2	1.93	0.51
2:B:717:LYS:O	2:B:717:LYS:HD3	2.11	0.51
2:B:67:LYS:HE3	2:B:72:TYR:CE1	2.45	0.51
2:B:870:LYS:O	2:B:872:LYS:N	2.43	0.51
2:A:480:LYS:HA	2:A:483:GLU:OE1	2.11	0.51
2:A:803:GLU:OE1	2:A:815:VAL:HG23	2.11	0.51
2:B:547:LYS:O	2:B:550:GLN:HB3	2.10	0.51
2:B:636:LYS:HB3	2:B:636:LYS:NZ	2.25	0.51
1:C:916:C:O2'	1:C:972:U:H1'	2.10	0.51
2:A:860:ARG:CZ	2:A:861:ALA:CA	2.89	0.51
2:A:51:VAL:O	2:A:54:ALA:CB	2.56	0.51
2:B:45:LEU:HD13	2:B:130:MET:HA	1.92	0.51
2:B:793:LEU:HD23	2:B:821:PRO:HG3	1.93	0.51
2:A:913:GLU:O	2:A:914:ARG:O	2.29	0.51
2:A:268:GLU:H	2:A:268:GLU:CD	2.12	0.51
1:D:961:C:H2'	1:D:961:C:O2	2.10	0.51
2:A:838:PHE:HE2	2:A:922:ASN:ND2	2.09	0.51
2:A:239:THR:HG21	2:A:326:PRO:HD2	1.92	0.51
2:A:690:ARG:HH11	2:A:693:GLU:CG	2.20	0.51
2:B:630:ARG:O	2:B:632:GLU:N	2.41	0.51
2:A:93:ARG:HG3	2:A:93:ARG:HH11	1.74	0.51
2:B:742:ASN:O	2:B:743:ALA:C	2.49	0.51
2:A:95:LYS:O	2:A:97:ARG:N	2.44	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:168:TRP:NE1	2:A:519:PRO:HB2	2.25	0.51
2:A:112:PRO:CG	2:A:115:ILE:HD12	2.41	0.51
1:C:949:C:C2	1:C:957:G:N2	2.79	0.51
2:B:860:ARG:CB	2:B:966:ILE:HA	2.41	0.51
2:A:871:TRP:NE1	2:A:959:PRO:HB3	2.26	0.51
2:A:873:VAL:CG1	2:A:906:ILE:HG12	2.40	0.51
2:A:819:LYS:H	2:A:819:LYS:CD	2.24	0.51
2:B:200:GLU:HG2	2:B:201:GLY:N	2.26	0.51
2:A:490:GLU:OE1	2:A:493:ARG:HB2	2.11	0.50
2:A:919:LYS:HD2	2:A:960:LEU:HD13	1.93	0.50
1:D:902:C:H2'	1:D:903:G:H5''	1.92	0.50
2:A:332:ASP:O	2:A:333:HIS:HB2	2.11	0.50
2:B:915:THR:OG1	2:B:916:PHE:N	2.44	0.50
2:A:751:THR:O	2:A:754:GLN:N	2.43	0.50
2:B:160:SER:O	2:B:164:GLU:HG3	2.11	0.50
2:B:51:VAL:CG2	2:B:659:LEU:HB3	2.41	0.50
2:A:269:ALA:O	2:A:273:LEU:HD12	2.10	0.50
2:A:950:LYS:H	2:A:953:LYS:NZ	2.10	0.50
2:B:743:ALA:HB2	2:B:751:THR:CG2	2.41	0.50
2:A:880:LYS:HG3	2:A:886:SER:HA	1.92	0.50
2:A:217:ARG:HH21	2:A:222:VAL:CG1	2.24	0.50
2:A:135:GLU:O	2:A:138:ILE:HG22	2.11	0.50
2:B:730:LEU:HB3	2:B:827:TRP:CD1	2.46	0.50
2:B:51:VAL:CG2	2:B:659:LEU:HD23	2.40	0.50
2:B:51:VAL:HG21	2:B:659:LEU:HD23	1.92	0.50
2:B:148:ARG:HB3	2:B:542:SER:HB3	1.93	0.50
2:B:540:THR:HG21	2:B:598:PHE:HD1	1.76	0.50
2:B:210:ILE:C	2:B:210:ILE:HD12	2.31	0.50
2:A:676:TYR:HA	2:A:697:LEU:CD2	2.41	0.50
2:A:793:LEU:HD23	2:A:821:PRO:CG	2.41	0.50
2:A:871:TRP:CD2	2:A:920:ARG:NH2	2.78	0.50
2:A:240:ASN:O	2:A:324:SER:HB3	2.11	0.50
2:B:242:TRP:HH2	2:B:332:ASP:HA	1.75	0.50
2:A:41:ALA:HA	2:A:607:ARG:HH22	1.75	0.50
2:A:275:PHE:O	2:A:277:ASP:N	2.39	0.50
2:B:94:ILE:HD11	2:B:120:GLU:N	2.27	0.50
2:A:884:LYS:HG3	2:A:888:GLU:HG3	1.93	0.50
2:B:395:GLN:O	2:B:399:THR:HG23	2.10	0.50
2:B:910:LEU:C	2:B:910:LEU:HD13	2.32	0.50
2:A:172:GLU:N	2:A:172:GLU:OE1	2.45	0.50
1:C:941:A:O3'	2:A:699:LYS:NZ	2.32	0.50
2:A:235:VAL:HG23	2:A:236:TYR:N	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:381:LYS:C	2:A:381:LYS:NZ	2.64	0.50
2:B:782:VAL:HG12	2:B:783:LEU:N	2.26	0.50
2:A:354:ARG:HE	2:A:375:ALA:C	2.13	0.50
2:B:495:GLN:HG2	2:B:614:ILE:HG21	1.92	0.50
2:A:61:ASP:OD1	2:A:143:SER:N	2.25	0.50
2:A:413:PRO:CB	2:A:414:PRO:HD3	2.42	0.50
2:B:327:ALA:HB2	2:B:353:PRO:O	2.12	0.50
2:A:72:TYR:O	2:A:74:VAL:HG23	2.11	0.50
2:B:244:ASN:HB2	2:B:313:VAL:HG23	1.94	0.50
2:A:231:ARG:HB3	2:A:233:GLU:CD	2.32	0.50
2:A:235:VAL:HG11	2:A:431:MET:CE	2.42	0.50
2:A:862:TYR:OH	2:A:926:ALA:HB1	2.11	0.50
2:B:587:PRO:HB2	2:B:590:ILE:CG1	2.35	0.50
2:A:98:ASP:OD2	2:A:99:PRO:HD2	2.11	0.50
2:A:863:ILE:CB	2:A:953:LYS:HD3	2.41	0.50
2:B:482:LEU:HD11	2:B:496:PHE:HB3	1.94	0.50
2:B:196:HIS:CD2	2:B:197:ASP:H	2.30	0.50
2:A:389:ASP:O	2:A:390:LYS:HD3	2.12	0.50
2:A:817:LEU:N	2:A:817:LEU:HD23	2.27	0.50
2:A:781:TYR:O	2:A:785:THR:HG23	2.12	0.50
2:A:569:LEU:HD12	2:A:569:LEU:N	2.26	0.50
2:A:235:VAL:HG23	2:A:236:TYR:H	1.76	0.50
2:A:300:VAL:HG13	2:A:301:SER:N	2.27	0.50
2:A:425:GLU:O	2:A:429:LYS:HD3	2.11	0.50
2:A:860:ARG:HA	2:A:966:ILE:HA	1.93	0.50
2:A:931:LYS:HE2	2:A:942:ILE:HG22	1.92	0.50
2:A:947:THR:HG23	2:A:948:GLU:H	1.77	0.50
2:B:866:ALA:HB3	2:B:869:TRP:CD1	2.47	0.50
2:A:232:PRO:HD2	2:A:424:LYS:HG3	1.93	0.50
2:A:855:ILE:HG23	2:A:855:ILE:O	2.10	0.50
2:A:382:LEU:C	2:A:384:ILE:H	2.15	0.50
1:C:909:U:H5''	1:C:910:G:OP2	2.12	0.50
2:A:292:ILE:HG13	2:A:309:PRO:HB3	1.94	0.50
2:A:252:ALA:HB2	2:A:282:VAL:HA	1.94	0.50
2:A:474:TRP:NE1	2:A:627:ALA:HB2	2.27	0.50
2:A:79:ALA:HB2	2:A:539:TYR:HE2	1.76	0.49
2:B:871:TRP:CE3	2:B:920:ARG:NH1	2.80	0.49
2:B:921:ILE:HD12	2:B:928:ARG:NH2	2.27	0.49
2:A:85:SER:H	2:A:86:PRO:HD3	1.78	0.49
2:A:568:PHE:HD1	2:A:598:PHE:CE2	2.30	0.49
1:C:916:C:C5'	1:C:917:C:C5	2.86	0.49
2:B:49:LEU:HA	2:B:53:HIS:HD2	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:268:GLU:OE2	2:B:315:PRO:HB2	2.11	0.49
2:A:393:LEU:C	2:A:395:GLN:H	2.15	0.49
2:B:330:PRO:CD	2:B:400:ILE:HG12	2.42	0.49
2:A:924:GLU:OE1	2:A:927:LEU:HD22	2.13	0.49
2:B:966:ILE:O	2:B:966:ILE:HG13	2.12	0.49
2:A:870:LYS:O	2:A:872:LYS:N	2.44	0.49
2:B:185:TRP:CD1	2:B:186:ASP:N	2.81	0.49
2:B:587:PRO:O	2:B:591:ILE:HG12	2.12	0.49
2:A:45:LEU:HD13	2:A:130:MET:HB2	1.94	0.49
2:B:175:TYR:CE1	2:B:474:TRP:HB2	2.47	0.49
2:A:142:PHE:O	2:A:144:VAL:N	2.45	0.49
2:A:111:VAL:HG22	2:A:128:TYR:CE2	2.31	0.49
2:A:41:ALA:HB2	2:A:607:ARG:HH21	1.76	0.49
2:B:662:ILE:HG23	2:B:663:ASP:N	2.25	0.49
2:B:282:VAL:CG1	2:B:283:ILE:N	2.72	0.49
2:B:196:HIS:HD2	2:B:197:ASP:H	1.58	0.49
2:A:878:SER:CB	2:A:915:THR:HG22	2.42	0.49
2:A:697:LEU:O	2:A:701:ILE:HG12	2.12	0.49
2:A:616:ASN:HB2	2:A:620:PHE:CE2	2.47	0.49
2:B:846:ILE:HD12	2:B:938:LEU:HD21	1.94	0.49
2:B:297:ARG:CZ	2:B:297:ARG:HB3	2.41	0.49
2:B:95:LYS:O	2:B:97:ARG:N	2.45	0.49
2:A:717:LYS:HD2	2:A:777:GLU:OE2	2.12	0.49
2:A:894:SER:C	2:A:896:ILE:N	2.65	0.49
2:B:746:GLU:OE1	2:B:748:ARG:HD2	2.13	0.49
2:B:42:PHE:O	2:B:42:PHE:CD1	2.65	0.49
2:B:907:VAL:O	2:B:910:LEU:HB3	2.12	0.49
2:B:354:ARG:HD2	2:B:376:VAL:HG12	1.95	0.49
2:B:455:ARG:HG2	2:B:455:ARG:HH11	1.78	0.49
2:A:467:ILE:HG21	2:A:469:TYR:CZ	2.47	0.49
2:B:423:VAL:C	2:B:425:GLU:N	2.66	0.49
2:B:185:TRP:HZ2	2:B:190:GLY:HA2	1.75	0.49
2:A:691:ARG:CG	2:A:691:ARG:HH11	2.26	0.49
2:B:273:LEU:HB3	2:B:280:ILE:HD11	1.94	0.49
1:C:958:U:H6	1:C:958:U:H3'	1.78	0.49
2:B:724:ASP:HB2	2:B:929:GLU:OE2	2.11	0.49
2:A:218:GLU:HG3	2:A:219:ASN:N	2.28	0.49
2:B:79:ALA:O	2:B:80:TRP:CE3	2.65	0.49
2:B:488:LEU:HD12	2:B:606:TRP:CZ3	2.46	0.49
2:B:741:THR:HA	2:B:820:TRP:CH2	2.47	0.49
2:A:730:LEU:HD22	2:A:827:TRP:HZ2	1.78	0.49
2:A:214:PHE:CE2	2:A:298:ASN:HA	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:240:ASN:HA	2:A:305:VAL:HB	1.93	0.49
2:A:66:PHE:CZ	2:A:70:GLN:OE1	2.66	0.49
2:A:947:THR:CG2	2:A:948:GLU:N	2.75	0.49
2:B:298:ASN:HD22	2:B:299:PRO:CD	2.25	0.49
2:B:889:GLU:O	2:B:889:GLU:HG3	2.11	0.49
2:A:871:TRP:CZ3	2:A:918:VAL:HA	2.47	0.49
2:A:184:ARG:NH1	2:A:195:ASP:OD2	2.46	0.49
2:A:184:ARG:NH2	2:A:202:GLU:O	2.45	0.49
2:B:163:ILE:O	2:B:166:GLN:HB3	2.13	0.49
1:C:910:G:C6	1:C:911:C:N4	2.81	0.49
2:B:151:TYR:CE1	2:B:156:PHE:HD1	2.30	0.49
2:A:691:ARG:HG2	2:A:691:ARG:NH1	2.26	0.49
2:B:22:ILE:CG1	2:B:817:LEU:HD21	2.42	0.49
2:B:474:TRP:CZ2	2:B:623:PHE:HB3	2.47	0.49
2:B:393:LEU:C	2:B:395:GLN:H	2.16	0.49
1:C:941:A:H2'	1:C:942:U:C6	2.48	0.49
2:B:860:ARG:HH22	2:B:861:ALA:C	2.16	0.49
2:B:922:ASN:O	2:B:925:LYS:N	2.44	0.49
2:A:826:GLU:CD	2:A:826:GLU:N	2.63	0.49
2:A:227:ALA:CA	2:A:321:VAL:HG23	2.31	0.49
2:B:212:ILE:HD13	2:B:431:MET:HE1	1.94	0.49
2:B:540:THR:HG21	2:B:598:PHE:HB2	1.93	0.49
2:B:751:THR:O	2:B:754:GLN:N	2.45	0.49
2:B:213:LYS:HZ2	2:B:213:LYS:HB3	1.77	0.49
1:D:935:C:H5'	1:D:936:U:H5''	1.95	0.49
2:B:172:GLU:N	2:B:172:GLU:OE1	2.46	0.49
2:B:868:ASP:O	2:B:869:TRP:C	2.52	0.49
2:B:760:ILE:HD12	2:B:790:TRP:CD1	2.48	0.49
2:A:237:GLY:C	2:A:325:VAL:HG22	2.33	0.49
2:A:840:ARG:O	2:A:843:MET:HB2	2.12	0.49
2:A:196:HIS:CD2	2:A:197:ASP:N	2.81	0.49
2:B:45:LEU:HD13	2:B:130:MET:HB2	1.95	0.49
2:A:311:GLU:HG2	2:A:389:ASP:OD2	2.12	0.49
2:B:37:TYR:HD2	2:B:38:ILE:H	1.60	0.49
2:B:676:TYR:CZ	2:B:680:LEU:HD11	2.48	0.48
2:A:570:GLU:O	2:A:595:LYS:HE2	2.13	0.48
2:A:355:ILE:HD12	2:A:412:VAL:CG1	2.43	0.48
2:A:836:GLU:HA	2:A:839:ILE:HD11	1.94	0.48
2:B:166:GLN:CG	2:B:534:ILE:HD11	2.43	0.48
2:B:728:TRP:C	2:B:730:LEU:N	2.67	0.48
2:B:834:ALA:O	2:B:837:GLU:CD	2.52	0.48
2:B:65:ARG:O	2:B:68:ARG:N	2.46	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:256:ARG:CZ	2:B:277:ASP:OD2	2.61	0.48
2:A:782:VAL:HG12	2:A:783:LEU:N	2.28	0.48
2:A:65:ARG:HG2	2:A:143:SER:OG	2.13	0.48
1:D:953:A:O2'	2:B:849:ILE:HG23	2.12	0.48
2:A:933:PHE:HD1	2:A:933:PHE:O	1.95	0.48
2:B:282:VAL:CG1	2:B:283:ILE:H	2.25	0.48
2:A:165:TRP:CD1	2:A:561:PRO:HA	2.44	0.48
2:A:880:LYS:HG3	2:A:886:SER:HB3	1.95	0.48
2:B:375:ALA:O	2:B:377:GLU:N	2.40	0.48
2:B:389:ASP:C	2:B:390:LYS:HD3	2.33	0.48
2:B:67:LYS:HD2	2:B:70:GLN:NE2	2.28	0.48
2:A:467:ILE:HG13	2:A:508:CYS:CB	2.43	0.48
2:A:126:VAL:CG1	2:A:126:VAL:O	2.60	0.48
2:A:242:TRP:HZ3	2:A:332:ASP:CG	2.17	0.48
2:A:931:LYS:HE2	2:A:942:ILE:O	2.13	0.48
2:B:35:LYS:HD2	2:B:35:LYS:C	2.34	0.48
2:A:488:LEU:CD1	2:A:606:TRP:CH2	2.92	0.48
2:B:382:LEU:C	2:B:384:ILE:H	2.16	0.48
2:B:741:THR:O	2:B:745:GLU:HG2	2.13	0.48
2:B:275:PHE:C	2:B:277:ASP:H	2.17	0.48
2:B:496:PHE:CE1	2:B:614:ILE:HG23	2.49	0.48
2:B:614:ILE:N	2:B:615:PRO:CD	2.75	0.48
2:A:289:GLU:O	2:A:292:ILE:HB	2.13	0.48
2:A:388:LYS:CD	2:A:389:ASP:HB2	2.42	0.48
2:A:170:LEU:O	2:A:176:ILE:HG12	2.13	0.48
2:A:501:ASP:O	2:A:503:LEU:N	2.39	0.48
2:B:775:ASP:C	2:B:775:ASP:OD1	2.51	0.48
2:A:871:TRP:C	2:A:875:GLU:OE2	2.52	0.48
2:B:677:ILE:HG22	2:B:678:MET:N	2.28	0.48
2:A:42:PHE:CD1	2:A:42:PHE:O	2.66	0.48
2:A:227:ALA:HA	2:A:321:VAL:O	2.12	0.48
2:B:429:LYS:O	2:B:433:GLU:CG	2.52	0.48
2:A:725:ILE:CD1	2:A:770:ARG:HE	2.26	0.48
2:B:601:TRP:HA	2:B:601:TRP:CE3	2.48	0.48
2:B:351:ILE:CD1	2:B:351:ILE:H	2.16	0.48
2:B:340:LYS:HB3	2:B:341:ARG:HH11	1.77	0.48
2:B:79:ALA:N	2:B:539:TYR:OH	2.46	0.48
2:B:256:ARG:HG3	2:B:257:LYS:N	2.28	0.48
2:A:784:ARG:HH22	2:A:810:GLY:N	2.11	0.48
1:C:954:G:N2	2:A:961:LYS:HG3	2.29	0.48
2:A:256:ARG:HG3	2:A:257:LYS:H	1.78	0.48
2:B:42:PHE:CD1	2:B:81:HIS:HB2	2.49	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:505:LYS:H	2:B:505:LYS:HD2	1.78	0.48
1:C:916:C:H2'	1:C:972:U:O3'	2.12	0.48
2:A:742:ASN:O	2:A:743:ALA:C	2.51	0.48
2:A:855:ILE:HG13	2:A:856:GLU:HG2	1.95	0.48
2:A:964:ILE:HD11	2:A:966:ILE:HG23	1.96	0.48
2:A:725:ILE:HD13	2:A:770:ARG:HE	1.78	0.48
2:A:631:GLU:C	2:A:633:HIS:H	2.16	0.48
2:B:752:ALA:O	2:B:755:TRP:N	2.46	0.48
2:B:894:SER:C	2:B:896:ILE:N	2.66	0.48
2:B:500:ILE:HG23	2:B:623:PHE:CZ	2.49	0.48
2:B:327:ALA:HB1	2:B:354:ARG:CB	2.44	0.48
2:B:37:TYR:CD2	2:B:38:ILE:N	2.82	0.48
2:B:501:ASP:O	2:B:503:LEU:N	2.41	0.48
2:A:162:PHE:HA	2:A:564:PHE:CE2	2.49	0.48
2:A:198:LEU:HD22	2:A:202:GLU:CA	2.43	0.48
2:B:126:VAL:O	2:B:126:VAL:CG1	2.61	0.48
2:A:41:ALA:CA	2:A:607:ARG:NH2	2.77	0.48
2:B:464:GLN:NE2	2:B:507:ALA:HB1	2.28	0.48
2:B:377:GLU:O	2:B:378:GLU:HB2	2.13	0.48
2:A:705:TYR:CD2	2:A:805:LEU:HD11	2.48	0.48
2:B:354:ARG:HD2	2:B:376:VAL:CG1	2.42	0.48
2:B:732:ARG:HH11	2:B:732:ARG:HB3	1.77	0.48
1:D:917:C:O5'	1:D:917:C:H6	1.96	0.48
2:A:892:LYS:O	2:A:892:LYS:HG2	2.13	0.48
2:B:471:ASN:C	2:B:471:ASN:ND2	2.66	0.48
2:A:449:ILE:CD1	2:A:449:ILE:N	2.75	0.48
2:A:868:ASP:O	2:A:869:TRP:C	2.52	0.48
2:A:860:ARG:CZ	2:A:860:ARG:C	2.82	0.48
2:B:356:VAL:HB	2:B:409:ILE:O	2.14	0.48
2:B:423:VAL:HA	2:B:426:ALA:HB3	1.95	0.48
2:B:171:LYS:CG	2:B:176:ILE:HD12	2.42	0.48
2:B:345:ILE:O	2:B:346:LEU:HB2	2.13	0.48
1:C:920:G:H1'	1:C:969:G:H21	1.78	0.48
2:B:623:PHE:O	2:B:624:ASN:C	2.52	0.48
2:B:48:HIS:HB2	2:B:109:TYR:CD1	2.48	0.48
1:D:958:U:O5'	1:D:958:U:H6	1.97	0.48
2:B:198:LEU:HD23	2:B:448:VAL:HG13	1.95	0.48
2:B:560:THR:HB	2:B:561:PRO:HD2	1.95	0.48
2:A:792:ARG:HH21	2:A:792:ARG:CG	2.15	0.48
2:A:860:ARG:NH2	2:A:861:ALA:C	2.67	0.48
2:B:53:HIS:O	2:B:57:TYR:CD2	2.67	0.48
2:B:420:VAL:HG12	2:B:424:LYS:NZ	2.28	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:894:SER:O	2:B:896:ILE:N	2.47	0.48
1:D:970:A:O2'	1:D:971:A:O5'	2.32	0.48
2:B:112:PRO:O	2:B:113:GLU:C	2.52	0.48
1:C:941:A:H4'	2:A:699:LYS:NZ	2.29	0.48
2:B:732:ARG:HB3	2:B:732:ARG:NH1	2.29	0.48
2:B:710:GLN:O	2:B:713:GLU:HG2	2.13	0.48
2:A:953:LYS:NZ	2:A:953:LYS:CB	2.76	0.48
2:A:956:GLN:HG2	2:A:956:GLN:O	2.14	0.48
2:A:188:VAL:HG23	2:A:190:GLY:H	1.79	0.47
2:A:419:PRO:O	2:A:422:GLU:HB2	2.14	0.47
2:A:877:VAL:C	2:A:879:GLU:H	2.16	0.47
2:B:568:PHE:C	2:B:569:LEU:HD12	2.34	0.47
2:A:55:ARG:O	2:A:59:ILE:HG13	2.14	0.47
2:B:276:GLN:O	2:B:277:ASP:HB3	2.14	0.47
2:B:793:LEU:HD23	2:B:821:PRO:CG	2.44	0.47
2:A:846:ILE:O	2:A:850:ILE:HG13	2.14	0.47
2:A:827:TRP:HD1	2:A:827:TRP:O	1.95	0.47
2:B:704:PHE:HE1	2:B:790:TRP:CD2	2.31	0.47
2:A:770:ARG:CD	2:A:933:PHE:HE2	2.19	0.47
2:B:233:GLU:HA	2:B:427:ILE:CD1	2.33	0.47
1:D:984:C:H6	1:D:984:C:H5'	1.79	0.47
2:A:671:ASP:OD1	2:A:799:PRO:HD2	2.13	0.47
2:B:646:LEU:HD12	2:B:689:TRP:HB3	1.96	0.47
2:A:717:LYS:HD2	2:A:718:GLY:O	2.14	0.47
2:A:279:GLU:OE1	2:A:281:GLU:OE1	2.32	0.47
1:C:958:U:H3'	1:C:958:U:C6	2.49	0.47
2:B:701:ILE:O	2:B:704:PHE:HB3	2.13	0.47
2:A:42:PHE:CE1	2:A:81:HIS:HB2	2.48	0.47
1:C:986:C:H5	2:A:181:HIS:HE2	1.56	0.47
2:A:854:LYS:HE2	2:A:967:GLU:CD	2.34	0.47
2:B:340:LYS:CB	2:B:341:ARG:HH11	2.28	0.47
2:A:375:ALA:O	2:A:377:GLU:N	2.40	0.47
2:B:68:ARG:HB2	2:B:74:VAL:HG11	1.96	0.47
2:A:746:GLU:O	2:A:748:ARG:HG3	2.14	0.47
2:A:714:TYR:HD1	2:A:780:ARG:CG	2.27	0.47
2:A:767:TYR:CE2	2:A:782:VAL:HG11	2.49	0.47
2:A:112:PRO:O	2:A:113:GLU:C	2.53	0.47
2:B:725:ILE:CD1	2:B:770:ARG:HE	2.27	0.47
2:B:734:ASN:HD21	2:B:823:PRO:HA	1.75	0.47
2:A:568:PHE:HB2	2:A:569:LEU:HD12	1.96	0.47
2:A:238:VAL:HA	2:A:325:VAL:HG22	1.96	0.47
2:B:326:PRO:HA	2:B:332:ASP:CB	2.44	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:145:ASP:OD1	2:A:145:ASP:O	2.32	0.47
1:C:922:C:H4'	1:C:923:A:C5'	2.44	0.47
2:A:37:TYR:HD2	2:A:38:ILE:N	2.12	0.47
2:A:695:GLY:O	2:A:698:ARG:HB3	2.15	0.47
2:A:53:HIS:O	2:A:57:TYR:CD2	2.67	0.47
2:A:198:LEU:CD2	2:A:202:GLU:HA	2.44	0.47
2:A:964:ILE:CD1	2:A:966:ILE:HG23	2.45	0.47
2:B:729:MET:HE3	2:B:763:ASP:C	2.35	0.47
2:B:400:ILE:C	2:B:400:ILE:HD12	2.34	0.47
2:A:710:GLN:C	2:A:712:ALA:N	2.68	0.47
2:A:609:SER:OG	2:A:610:GLY:N	2.46	0.47
2:B:830:GLU:HG3	2:B:831:THR:N	2.29	0.47
2:A:871:TRP:CH2	2:A:919:LYS:HE3	2.47	0.47
2:A:922:ASN:O	2:A:925:LYS:N	2.47	0.47
2:B:58:THR:HG22	2:B:678:MET:HE1	1.96	0.47
2:A:942:ILE:C	2:A:943:ILE:HG13	2.35	0.47
2:B:85:SER:N	2:B:86:PRO:CD	2.77	0.47
2:B:45:LEU:HD13	2:B:130:MET:CA	2.45	0.47
2:A:944:ILE:HG22	2:A:945:ASN:H	1.78	0.47
2:A:12:LYS:HZ2	2:A:16:ARG:NH1	2.12	0.47
2:B:277:ASP:O	2:B:277:ASP:CG	2.50	0.47
2:A:546:ASN:O	2:A:550:GLN:HB2	2.14	0.47
2:A:267:LYS:O	2:A:270:ALA:HB3	2.14	0.47
2:A:866:ALA:HB3	2:A:955:LYS:HZ1	1.78	0.47
2:A:75:LEU:CD1	2:A:77:PRO:HD3	2.44	0.47
2:B:860:ARG:NH1	2:B:861:ALA:HA	2.30	0.47
2:B:862:TYR:HB3	2:B:964:ILE:HB	1.95	0.47
2:B:864:TYR:CG	2:B:865:THR:N	2.82	0.47
2:B:951:GLY:HA3	2:B:965:PHE:CE1	2.49	0.47
2:A:835:GLU:O	2:A:838:PHE:HB3	2.15	0.47
2:A:877:VAL:CG2	2:A:906:ILE:HG23	2.45	0.47
2:B:83:THR:CG2	2:B:153:THR:HG22	2.44	0.47
2:B:212:ILE:CD1	2:B:235:VAL:CG1	2.93	0.47
2:A:99:PRO:O	2:A:102:ILE:HG13	2.14	0.47
2:B:150:PHE:CD1	2:B:151:TYR:O	2.58	0.47
2:B:540:THR:HG21	2:B:598:PHE:CD1	2.50	0.47
2:A:318:ALA:HA	2:A:440:MET:SD	2.55	0.47
2:B:256:ARG:CG	2:B:257:LYS:H	2.23	0.47
2:B:216:LEU:CD1	2:B:294:LYS:HB3	2.43	0.47
2:A:894:SER:O	2:A:896:ILE:N	2.47	0.47
2:A:518:LEU:HD12	2:A:524:TRP:CB	2.44	0.47
2:B:395:GLN:HG3	2:B:396:ALA:H	1.80	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:393:LEU:HG	2:B:397:THR:OG1	2.14	0.47
2:B:554:LEU:HD12	2:B:586:ILE:HD11	1.97	0.47
2:A:728:TRP:C	2:A:730:LEU:N	2.68	0.47
2:A:830:GLU:HG3	2:A:831:THR:N	2.30	0.47
2:A:423:VAL:HA	2:A:426:ALA:HB3	1.96	0.47
2:A:558:LYS:HB3	2:A:584:THR:CA	2.34	0.47
2:B:238:VAL:O	2:B:238:VAL:HG13	2.15	0.47
2:B:519:PRO:HG2	2:B:520:TRP:CE3	2.49	0.47
2:A:348:LYS:HZ2	2:A:348:LYS:HB3	1.77	0.47
1:C:919:G:C6	1:C:969:G:C6	3.03	0.47
2:B:690:ARG:HB2	2:B:693:GLU:HG3	1.97	0.47
2:A:767:TYR:HE2	2:A:783:LEU:HD11	1.79	0.47
2:A:241:MET:HG3	2:A:296:VAL:CG2	2.45	0.47
2:B:135:GLU:HA	2:B:138:ILE:HG22	1.97	0.47
1:C:957:G:O2'	1:C:958:U:H5'	2.15	0.47
2:B:958:MET:HE1	2:B:959:PRO:HD2	1.95	0.47
2:A:825:GLU:OE2	2:A:825:GLU:O	2.33	0.47
1:D:914:A:H2'	1:D:915:G:O4'	2.15	0.47
2:A:210:ILE:HG22	2:A:439:ILE:HG23	1.97	0.47
2:A:860:ARG:O	2:A:860:ARG:NH1	2.47	0.47
2:A:59:ILE:HB	2:A:60:PRO:CD	2.45	0.47
2:A:314:ASP:HB3	2:A:317:ASN:HB3	1.95	0.47
2:A:327:ALA:HB2	2:A:353:PRO:O	2.15	0.47
2:A:16:ARG:CG	2:A:16:ARG:NH1	2.77	0.47
2:B:402:LYS:O	2:B:405:TYR:HB3	2.15	0.47
2:A:880:LYS:HG3	2:A:886:SER:CA	2.45	0.47
2:B:793:LEU:HD21	2:B:821:PRO:CG	2.43	0.47
2:A:461:ILE:HG21	2:A:464:GLN:HB2	1.97	0.47
2:A:747:PHE:CD1	2:A:747:PHE:N	2.83	0.47
2:B:167:PHE:HA	2:B:170:LEU:CG	2.44	0.47
2:A:800:HIS:O	2:A:802:CYS:N	2.48	0.47
2:A:93:ARG:O	2:A:98:ASP:HB2	2.15	0.47
2:A:354:ARG:HH11	2:A:354:ARG:HG3	1.80	0.47
2:A:215:GLU:O	2:A:296:VAL:HA	2.15	0.47
2:A:544:HIS:H	2:A:544:HIS:HD2	1.59	0.47
2:A:168:TRP:CE2	2:A:519:PRO:HB2	2.49	0.47
2:B:63:ILE:O	2:B:67:LYS:HG2	2.15	0.47
2:B:521:ASP:N	2:B:522:PRO:HD3	2.30	0.47
2:A:576:LYS:O	2:A:580:LEU:HD13	2.15	0.47
2:A:75:LEU:HD23	2:A:601:TRP:CE2	2.50	0.46
2:B:164:GLU:O	2:B:165:TRP:C	2.54	0.46
2:A:275:PHE:C	2:A:277:ASP:H	2.18	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:482:LEU:CD1	2:B:496:PHE:HB3	2.45	0.46
2:A:243:VAL:HG22	2:A:292:ILE:HD11	1.95	0.46
1:D:980:C:H2'	1:D:981:C:H6	1.79	0.46
2:A:331:PHE:CD1	2:A:334:VAL:HG21	2.51	0.46
2:B:259:LYS:HE2	2:B:261:GLU:OE1	2.15	0.46
2:A:587:PRO:O	2:A:591:ILE:HG12	2.15	0.46
2:B:766:TRP:HH2	2:B:836:GLU:OE1	1.97	0.46
1:D:953:A:C2	2:B:966:ILE:HG12	2.50	0.46
2:B:860:ARG:CB	2:B:966:ILE:HG22	2.40	0.46
2:B:698:ARG:HG3	2:B:698:ARG:HH11	1.80	0.46
2:B:733:LEU:CD1	2:B:737:ILE:HD11	2.45	0.46
2:B:558:LYS:HG3	2:B:584:THR:O	2.14	0.46
2:A:238:VAL:HG11	2:A:298:ASN:HB2	1.97	0.46
2:A:381:LYS:HZ2	2:A:382:LEU:HD12	1.80	0.46
2:A:196:HIS:HD2	2:A:197:ASP:H	1.64	0.46
2:B:45:LEU:CD1	2:B:80:TRP:HB3	2.40	0.46
2:A:626:VAL:HG12	2:A:634:TRP:CE2	2.50	0.46
2:A:213:LYS:HB3	2:A:213:LYS:NZ	2.30	0.46
2:B:495:GLN:HE21	2:B:614:ILE:CG2	2.27	0.46
2:A:268:GLU:HG3	2:A:316:ASP:HA	1.97	0.46
2:A:544:HIS:O	2:A:547:LYS:HB3	2.14	0.46
2:A:457:VAL:HG23	2:A:458:ILE:N	2.31	0.46
2:A:772:GLU:OE1	2:A:936:LYS:HE3	2.15	0.46
2:A:150:PHE:CD1	2:A:150:PHE:C	2.88	0.46
2:B:933:PHE:CD1	2:B:933:PHE:C	2.89	0.46
2:A:42:PHE:CE1	2:A:81:HIS:CG	3.04	0.46
2:A:768:LEU:O	2:A:769:ARG:C	2.53	0.46
2:B:829:ASN:OD1	2:B:832:ILE:HG13	2.16	0.46
2:B:546:ASN:O	2:B:550:GLN:HB2	2.15	0.46
2:B:834:ALA:CA	2:B:837:GLU:OE2	2.60	0.46
2:A:164:GLU:O	2:A:165:TRP:C	2.53	0.46
2:B:418:LYS:HB3	2:B:419:PRO:HD2	1.97	0.46
2:B:616:ASN:HD22	2:B:617:HIS:H	1.60	0.46
2:B:67:LYS:O	2:B:72:TYR:HD1	1.99	0.46
2:B:436:ILE:O	2:B:436:ILE:HG22	2.16	0.46
2:A:297:ARG:CZ	2:A:297:ARG:HB3	2.45	0.46
2:A:355:ILE:HG23	2:A:412:VAL:HG11	1.97	0.46
2:A:412:VAL:HG23	2:A:414:PRO:CD	2.39	0.46
2:A:204:VAL:O	2:A:204:VAL:HG23	2.16	0.46
2:A:933:PHE:HE1	2:A:937:GLU:HB2	1.81	0.46
2:B:418:LYS:HG3	2:B:422:GLU:OE2	2.16	0.46
2:A:717:LYS:NZ	2:A:719:ASN:HB2	2.29	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:728:TRP:CE3	2:A:729:MET:N	2.80	0.46
2:A:918:VAL:HG11	2:A:920:ARG:HD2	1.97	0.46
2:A:210:ILE:HD11	2:A:232:PRO:CG	2.37	0.46
2:A:393:LEU:C	2:A:395:GLN:N	2.69	0.46
2:A:809:LEU:O	2:A:810:GLY:C	2.54	0.46
2:A:455:ARG:HD3	2:A:456:ALA:N	2.30	0.46
2:B:722:LEU:HG	2:B:727:ARG:NH1	2.31	0.46
2:A:860:ARG:NH1	2:A:861:ALA:CA	2.69	0.46
2:B:238:VAL:HB	2:B:323:MET:HE1	1.96	0.46
2:A:327:ALA:HB1	2:A:354:ARG:CB	2.46	0.46
2:A:50:HIS:H	2:A:53:HIS:CD2	2.34	0.46
1:C:956:G:O2'	1:C:957:G:H5'	2.16	0.46
2:A:911:ILE:O	2:A:911:ILE:HG13	2.15	0.46
2:B:204:VAL:HG11	2:B:443:PHE:HB3	1.97	0.46
1:D:954:G:O6	2:B:963:ALA:HA	2.16	0.46
2:A:872:LYS:HA	2:A:875:GLU:OE2	2.15	0.46
2:B:789:VAL:O	2:B:792:ARG:N	2.49	0.46
2:B:789:VAL:O	2:B:791:VAL:N	2.49	0.46
2:B:734:ASN:ND2	2:B:824:VAL:H	1.94	0.46
2:A:356:VAL:HB	2:A:409:ILE:O	2.16	0.46
2:A:678:MET:N	2:A:678:MET:SD	2.88	0.46
2:B:722:LEU:N	2:B:722:LEU:HD23	2.30	0.46
2:B:918:VAL:CG1	2:B:920:ARG:HD2	2.46	0.46
2:B:824:VAL:O	2:B:825:GLU:C	2.53	0.46
2:B:557:GLU:O	2:B:559:LEU:N	2.49	0.46
2:A:424:LYS:NZ	2:A:424:LYS:HB2	2.31	0.46
2:A:183:VAL:HG13	2:A:184:ARG:O	2.16	0.46
2:B:631:GLU:C	2:B:633:HIS:H	2.17	0.46
2:A:806:TRP:CB	2:A:815:VAL:HG22	2.45	0.46
2:B:459:LYS:HZ2	2:B:461:ILE:CD1	2.29	0.46
2:A:93:ARG:HG2	2:A:451:ARG:HH21	1.80	0.46
2:B:877:VAL:C	2:B:879:GLU:H	2.18	0.46
2:A:863:ILE:HG22	2:A:953:LYS:CG	2.44	0.46
2:B:65:ARG:O	2:B:68:ARG:HB3	2.16	0.46
2:B:717:LYS:C	2:B:717:LYS:HD3	2.36	0.46
2:B:839:ILE:C	2:B:839:ILE:HD12	2.36	0.46
2:A:64:ALA:O	2:A:68:ARG:HB2	2.16	0.46
2:A:731:HIS:HD2	2:A:828:TRP:HA	1.80	0.46
2:A:232:PRO:HG2	2:A:428:ALA:HB2	1.98	0.46
2:B:710:GLN:C	2:B:712:ALA:N	2.69	0.46
2:B:476:GLU:HA	2:B:476:GLU:OE1	2.16	0.46
2:B:328:HIS:O	2:B:329:ALA:C	2.53	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:159:PHE:O	2:A:162:PHE:HB3	2.16	0.46
2:A:660:ASN:HB2	2:A:663:ASP:HB2	1.94	0.46
2:B:234:THR:O	2:B:325:VAL:HG21	2.16	0.46
2:A:230:LEU:N	2:A:230:LEU:CD2	2.76	0.46
2:A:489:PRO:HD3	2:A:683:HIS:HB3	1.98	0.46
2:A:382:LEU:HD12	2:A:382:LEU:N	2.31	0.46
2:B:641:ASN:ND2	2:B:641:ASN:C	2.69	0.46
2:A:395:GLN:HG3	2:A:396:ALA:H	1.81	0.46
2:A:624:ASN:HD22	2:A:624:ASN:N	2.07	0.46
2:A:173:LYS:HB3	2:A:175:TYR:CE2	2.51	0.46
2:B:70:GLN:HB3	2:B:72:TYR:CD1	2.51	0.46
2:B:516:THR:O	2:B:526:ILE:HG13	2.15	0.46
2:A:297:ARG:O	2:A:299:PRO:HD3	2.16	0.45
2:A:903:VAL:HG12	2:A:906:ILE:HG13	1.97	0.45
2:A:183:VAL:O	2:A:184:ARG:C	2.54	0.45
2:B:231:ARG:HB3	2:B:233:GLU:OE2	2.17	0.45
2:B:882:ASP:O	2:B:883:PHE:HB3	2.15	0.45
2:A:393:LEU:O	2:A:395:GLN:N	2.49	0.45
2:A:545:ILE:HG12	2:A:594:MET:HE3	1.98	0.45
1:C:949:C:C2	1:C:957:G:C2	3.04	0.45
2:A:741:THR:O	2:A:745:GLU:HG2	2.17	0.45
2:A:855:ILE:O	2:A:856:GLU:HB2	2.15	0.45
2:A:51:VAL:CG2	2:A:52:GLY:N	2.79	0.45
2:B:914:ARG:HE	2:B:915:THR:N	2.13	0.45
2:B:292:ILE:HG13	2:B:309:PRO:HB3	1.98	0.45
2:B:505:LYS:HD2	2:B:505:LYS:N	2.30	0.45
2:A:23:PHE:CD2	2:A:143:SER:HA	2.51	0.45
2:B:928:ARG:C	2:B:930:ALA:N	2.69	0.45
2:A:186:ASP:HB3	2:A:191:THR:CG2	2.41	0.45
2:A:950:LYS:HG2	2:A:953:LYS:HZ1	1.82	0.45
1:D:919:G:H1'	1:D:970:A:C2	2.52	0.45
2:B:9:ILE:HD13	2:B:804:GLU:HG2	1.97	0.45
2:B:535:TYR:CE1	2:B:536:MET:SD	3.10	0.45
2:A:166:GLN:HB2	2:A:534:ILE:HD11	1.97	0.45
2:A:328:HIS:O	2:A:329:ALA:C	2.54	0.45
2:A:61:ASP:OD2	2:A:674:ARG:NH2	2.45	0.45
1:D:905:G:H5'	1:D:905:G:H8	1.82	0.45
2:A:211:ILE:HG21	2:A:319:THR:CG2	2.46	0.45
2:A:742:ASN:O	2:A:744:LEU:N	2.50	0.45
2:B:412:VAL:H	2:B:416:GLU:HG2	1.82	0.45
2:B:136:THR:CG2	2:B:661:PHE:HD2	2.26	0.45
1:C:918:U:O2	1:C:918:U:H2'	2.15	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:155:LEU:C	2:A:157:PRO:HD3	2.37	0.45
2:A:464:GLN:NE2	2:A:465:TRP:O	2.49	0.45
2:B:485:MET:SD	2:B:635:PRO:HB2	2.57	0.45
2:B:953:LYS:HB3	2:B:953:LYS:NZ	2.30	0.45
2:B:676:TYR:HA	2:B:697:LEU:CD2	2.46	0.45
2:B:411:LYS:HA	2:B:416:GLU:CD	2.37	0.45
2:B:729:MET:CE	2:B:729:MET:HA	2.47	0.45
2:A:17:TRP:CZ2	2:A:803:GLU:HG3	2.52	0.45
2:B:306:ILE:HG12	2:B:307:ILE:N	2.31	0.45
2:B:266:SER:O	2:B:269:ALA:HB3	2.16	0.45
2:A:838:PHE:HE2	2:A:922:ASN:HD21	1.63	0.45
2:B:142:PHE:O	2:B:144:VAL:N	2.49	0.45
2:B:231:ARG:HB3	2:B:233:GLU:CD	2.37	0.45
2:B:713:GLU:CA	2:B:713:GLU:OE2	2.65	0.45
2:A:294:LYS:N	2:A:294:LYS:HD2	2.32	0.45
2:B:342:GLU:OE2	2:B:342:GLU:N	2.50	0.45
2:B:711:PHE:HE1	2:B:783:LEU:HD23	1.82	0.45
2:A:377:GLU:CD	2:A:377:GLU:C	2.75	0.45
2:A:713:GLU:O	2:A:714:TYR:C	2.53	0.45
1:D:944:C:H2'	1:D:945:C:H6	1.81	0.45
2:A:544:HIS:CD2	2:A:544:HIS:N	2.85	0.45
2:B:393:LEU:C	2:B:395:GLN:N	2.70	0.45
2:B:393:LEU:CD1	2:B:396:ALA:HB3	2.46	0.45
2:A:582:LYS:H	2:A:582:LYS:HD2	1.81	0.45
2:B:921:ILE:HB	2:B:928:ARG:HH22	1.77	0.45
2:B:83:THR:HG22	2:B:153:THR:HG22	1.97	0.45
2:B:730:LEU:HA	2:B:730:LEU:HD23	1.84	0.45
2:B:123:ILE:HD11	2:B:155:LEU:CD1	2.47	0.45
2:B:55:ARG:HD2	2:B:687:PHE:CD1	2.51	0.45
1:C:960:C:H4'	1:C:961:C:OP2	2.17	0.45
2:B:252:ALA:HB2	2:B:282:VAL:HA	1.99	0.45
2:A:557:GLU:O	2:A:559:LEU:N	2.49	0.45
2:B:742:ASN:O	2:B:745:GLU:N	2.50	0.45
2:B:232:PRO:HG2	2:B:428:ALA:HB2	1.99	0.45
2:A:80:TRP:CD1	2:A:130:MET:HG3	2.51	0.45
2:A:211:ILE:HA	2:A:227:ALA:O	2.17	0.45
2:A:211:ILE:HG21	2:A:319:THR:HG21	1.99	0.45
2:A:210:ILE:O	2:A:210:ILE:HG13	2.16	0.45
2:A:426:ALA:HA	2:A:429:LYS:CE	2.31	0.45
2:A:218:GLU:OE2	2:A:294:LYS:HE2	2.16	0.45
2:A:93:ARG:HG3	2:A:93:ARG:NH1	2.32	0.45
2:B:51:VAL:O	2:B:54:ALA:CB	2.62	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:54:ALA:CB	2:B:661:PHE:CD1	3.00	0.45
2:A:277:ASP:HB2	2:A:460:ILE:HB	1.99	0.45
2:A:717:LYS:C	2:A:717:LYS:CD	2.83	0.45
2:A:112:PRO:HB2	2:A:115:ILE:HG13	1.99	0.45
2:A:341:ARG:HG2	2:A:341:ARG:HH11	1.81	0.45
2:A:482:LEU:C	2:A:482:LEU:CD2	2.85	0.45
2:A:61:ASP:OD2	2:A:674:ARG:NH1	2.48	0.45
2:B:766:TRP:HZ3	2:B:836:GLU:CG	2.30	0.45
2:B:950:LYS:H	2:B:953:LYS:NZ	2.15	0.45
2:A:831:THR:O	2:A:835:GLU:CG	2.65	0.45
2:B:227:ALA:HA	2:B:321:VAL:O	2.15	0.45
1:C:916:C:H5'	1:C:917:C:H5	1.66	0.45
2:A:840:ARG:HE	2:A:840:ARG:HB3	1.60	0.45
2:B:731:HIS:HE1	2:B:833:GLU:OE1	2.00	0.45
1:D:921:U:OP2	1:D:922:C:H3'	2.17	0.45
2:A:266:SER:O	2:A:269:ALA:HB3	2.17	0.45
2:B:7:LYS:HB2	2:B:7:LYS:HZ3	1.81	0.45
2:B:387:GLN:HE21	2:B:387:GLN:HA	1.82	0.45
2:B:387:GLN:HG3	2:B:388:LYS:N	2.32	0.45
2:B:245:PRO:O	2:B:288:GLY:HA3	2.17	0.45
1:C:939:A:OP1	1:C:939:A:H4'	2.16	0.45
2:B:28:ARG:HG3	2:B:28:ARG:NH1	2.30	0.45
2:A:728:TRP:HE3	2:A:729:MET:CA	2.29	0.45
2:A:568:PHE:CB	2:A:569:LEU:HD12	2.46	0.45
2:B:713:GLU:O	2:B:714:TYR:C	2.55	0.45
2:B:890:LEU:O	2:B:892:LYS:N	2.50	0.45
2:A:250:VAL:HG12	2:A:285:GLU:HG3	1.99	0.45
2:B:682:GLU:OE1	2:B:748:ARG:NH1	2.49	0.45
2:A:463:ASP:O	2:A:464:GLN:C	2.55	0.45
2:B:911:ILE:O	2:B:911:ILE:HG13	2.16	0.45
2:B:860:ARG:HB3	2:B:966:ILE:CG2	2.40	0.44
2:A:800:HIS:C	2:A:802:CYS:H	2.21	0.44
2:A:800:HIS:C	2:A:802:CYS:N	2.70	0.44
2:A:553:LYS:NZ	2:A:553:LYS:HB3	2.32	0.44
2:A:94:ILE:HD11	2:A:120:GLU:CA	2.46	0.44
2:A:916:PHE:HB3	2:A:917:ASP:H	1.67	0.44
2:B:373:PHE:N	2:B:374:PRO:CD	2.80	0.44
2:A:518:LEU:HD12	2:A:524:TRP:HB3	1.98	0.44
1:D:960:C:H4'	1:D:961:C:H5''	1.98	0.44
2:A:902:GLU:C	2:A:904:ALA:H	2.21	0.44
2:A:67:LYS:HE2	2:A:70:GLN:HE22	1.82	0.44
2:B:429:LYS:HZ2	2:B:429:LYS:HB3	1.82	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:26:ASN:C	2:A:28:ARG:HH21	2.20	0.44
2:B:714:TYR:CD2	2:B:714:TYR:N	2.73	0.44
2:B:511:LYS:HE3	2:B:524:TRP:CE2	2.51	0.44
2:B:215:GLU:O	2:B:296:VAL:HA	2.17	0.44
2:B:42:PHE:N	2:B:42:PHE:CD1	2.85	0.44
2:A:482:LEU:O	2:A:493:ARG:NH1	2.50	0.44
2:B:860:ARG:O	2:B:860:ARG:NH1	2.50	0.44
2:A:85:SER:N	2:A:86:PRO:CD	2.77	0.44
2:B:211:ILE:O	2:B:211:ILE:HG13	2.16	0.44
2:B:809:LEU:O	2:B:810:GLY:C	2.56	0.44
2:A:768:LEU:O	2:A:770:ARG:N	2.49	0.44
2:B:57:TYR:O	2:B:60:PRO:CG	2.62	0.44
2:B:234:THR:HA	2:B:355:ILE:CD1	2.47	0.44
2:B:170:LEU:CB	2:B:176:ILE:HD11	2.41	0.44
2:A:119:PHE:C	2:A:121:ASP:N	2.69	0.44
2:B:476:GLU:HA	2:B:479:ARG:NH1	2.32	0.44
2:A:69:MET:HB3	2:A:818:ALA:O	2.17	0.44
2:A:31:PRO:HD2	2:A:34:LYS:HG3	1.98	0.44
2:B:902:GLU:C	2:B:904:ALA:H	2.21	0.44
2:A:730:LEU:CA	2:A:827:TRP:HE1	2.30	0.44
2:A:234:THR:HB	2:A:325:VAL:HG21	1.99	0.44
2:A:432:LEU:HD11	2:A:439:ILE:CG1	2.45	0.44
2:A:766:TRP:O	2:A:770:ARG:N	2.47	0.44
2:B:518:LEU:HD22	2:B:520:TRP:CZ2	2.52	0.44
2:B:186:ASP:OD2	2:B:188:VAL:HG13	2.18	0.44
2:B:150:PHE:C	2:B:150:PHE:CD1	2.90	0.44
2:B:742:ASN:ND2	2:B:742:ASN:N	2.65	0.44
2:A:400:ILE:HD12	2:A:400:ILE:C	2.37	0.44
2:B:846:ILE:HG12	2:B:964:ILE:HD12	1.94	0.44
2:B:866:ALA:H	2:B:955:LYS:HZ1	1.57	0.44
2:A:872:LYS:HA	2:A:872:LYS:HZ2	1.83	0.44
2:B:679:SER:HA	2:B:753:VAL:HG11	2.00	0.44
2:B:750:ARG:HB3	2:B:750:ARG:HE	1.50	0.44
2:A:933:PHE:CE1	2:A:937:GLU:HB2	2.51	0.44
2:B:340:LYS:HG2	2:B:341:ARG:NH1	2.32	0.44
2:B:783:LEU:N	2:B:783:LEU:HD12	2.33	0.44
2:A:703:ARG:HG2	2:A:761:MET:CE	2.48	0.44
2:A:878:SER:HB2	2:A:914:ARG:HB2	1.99	0.44
2:B:718:GLY:O	2:B:720:VAL:HG13	2.18	0.44
2:B:490:GLU:C	2:B:492:ARG:H	2.21	0.44
2:B:768:LEU:O	2:B:769:ARG:C	2.55	0.44
2:B:725:ILE:HG21	2:B:771:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:902:C:H2'	1:D:903:G:C4'	2.47	0.44
2:B:330:PRO:HD3	2:B:400:ILE:HG12	2.00	0.44
2:B:216:LEU:O	2:B:216:LEU:HG	2.17	0.44
2:A:789:VAL:O	2:A:791:VAL:N	2.50	0.44
2:A:518:LEU:HD22	2:A:520:TRP:CZ2	2.53	0.44
1:D:972:U:H5''	1:D:973:C:OP2	2.18	0.44
2:B:393:LEU:O	2:B:395:GLN:N	2.51	0.44
2:B:908:GLN:HE22	2:B:958:MET:HG3	1.83	0.44
2:A:862:TYR:HB2	2:A:964:ILE:HA	1.99	0.44
2:B:339:LEU:HD13	2:B:339:LEU:N	2.33	0.44
2:A:244:ASN:HB2	2:A:313:VAL:HG23	1.99	0.44
2:B:218:GLU:CD	2:B:219:ASN:ND2	2.70	0.44
2:B:261:GLU:HB2	2:B:263:TRP:HE1	1.81	0.44
2:A:50:HIS:CE1	2:A:53:HIS:CE1	3.06	0.44
1:C:957:G:C2	1:C:958:U:C2	3.06	0.44
2:B:449:ILE:HG23	2:B:454:ASN:O	2.18	0.44
2:B:168:TRP:NE1	2:B:519:PRO:HB2	2.33	0.44
2:B:729:MET:HB2	2:B:729:MET:HE2	1.78	0.44
2:B:75:LEU:HD22	2:B:601:TRP:CD1	2.53	0.44
2:B:463:ASP:O	2:B:464:GLN:C	2.56	0.44
2:A:863:ILE:CG2	2:A:953:LYS:HD3	2.48	0.44
2:B:250:VAL:HG12	2:B:285:GLU:HG3	2.00	0.44
2:B:104:ILE:HG21	2:B:653:LYS:HD3	1.99	0.44
1:D:937:C:H2'	1:D:937:C:O2	2.18	0.44
1:D:953:A:H1'	2:B:849:ILE:CG2	2.48	0.44
2:B:58:THR:HA	2:B:142:PHE:HE1	1.83	0.44
2:A:803:GLU:HA	2:A:815:VAL:HG21	1.98	0.44
2:B:79:ALA:HB2	2:B:539:TYR:CE2	2.51	0.44
2:B:739:GLU:HB3	2:B:755:TRP:CD1	2.53	0.44
2:A:243:VAL:HG23	2:A:244:ASN:N	2.33	0.44
2:B:331:PHE:O	2:B:334:VAL:HG23	2.17	0.44
2:B:724:ASP:OD2	2:B:928:ARG:HD3	2.18	0.43
2:A:824:VAL:CG1	2:A:827:TRP:CE3	3.00	0.43
1:C:972:U:H5'	1:C:973:C:OP2	2.18	0.43
2:A:238:VAL:HG13	2:A:238:VAL:O	2.16	0.43
2:A:966:ILE:HG13	2:A:966:ILE:O	2.17	0.43
2:B:57:TYR:O	2:B:60:PRO:HD2	2.17	0.43
2:A:49:LEU:HD22	2:A:137:PHE:HE1	1.83	0.43
1:D:923:A:HO2'	1:D:924:A:P	2.40	0.43
2:B:459:LYS:HZ2	2:B:461:ILE:HD13	1.82	0.43
2:B:711:PHE:CE1	2:B:783:LEU:HD23	2.53	0.43
2:A:703:ARG:HG3	2:A:707:LEU:CD1	2.47	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:767:TYR:CE2	2:A:783:LEU:HD11	2.52	0.43
1:C:937:C:H2'	1:C:938:A:O4'	2.18	0.43
1:C:958:U:C3'	1:C:958:U:C6	3.01	0.43
1:C:941:A:H4'	2:A:699:LYS:HZ1	1.82	0.43
2:B:267:LYS:O	2:B:270:ALA:HB3	2.18	0.43
2:A:636:LYS:HB3	2:A:636:LYS:NZ	2.32	0.43
2:B:738:LYS:HB3	2:B:738:LYS:NZ	2.33	0.43
2:A:245:PRO:O	2:A:288:GLY:HA3	2.18	0.43
2:A:921:ILE:O	2:A:924:GLU:HB3	2.17	0.43
2:A:81:HIS:HD2	2:A:152:THR:HG21	1.83	0.43
2:A:83:THR:O	2:A:528:SER:HB3	2.17	0.43
2:A:420:VAL:HG12	2:A:424:LYS:HZ1	1.82	0.43
2:A:890:LEU:O	2:A:892:LYS:N	2.51	0.43
2:B:355:ILE:HG23	2:B:412:VAL:CG1	2.49	0.43
2:A:381:LYS:HZ2	2:A:381:LYS:HB3	1.83	0.43
2:B:742:ASN:O	2:B:744:LEU:N	2.51	0.43
2:B:331:PHE:HD1	2:B:334:VAL:HG21	1.83	0.43
2:A:675:LEU:CD1	2:A:697:LEU:HD21	2.48	0.43
2:A:701:ILE:O	2:A:704:PHE:HB3	2.16	0.43
2:A:677:ILE:HD11	2:A:689:TRP:HZ3	1.83	0.43
2:A:75:LEU:CD1	2:A:75:LEU:C	2.84	0.43
2:A:490:GLU:C	2:A:492:ARG:H	2.22	0.43
2:A:824:VAL:HB	2:A:827:TRP:CE3	2.53	0.43
2:B:188:VAL:HG23	2:B:190:GLY:H	1.84	0.43
2:A:58:THR:HG22	2:A:62:VAL:CG2	2.49	0.43
2:B:339:LEU:HD22	2:B:340:LYS:HG3	2.00	0.43
2:B:618:LEU:HA	2:B:618:LEU:HD23	1.88	0.43
2:A:244:ASN:HD22	2:A:313:VAL:HG23	1.82	0.43
2:A:166:GLN:NE2	2:A:534:ILE:HG12	2.33	0.43
2:B:911:ILE:O	2:B:912:LYS:HG3	2.18	0.43
2:B:449:ILE:HG22	2:B:450:SER:N	2.33	0.43
2:B:860:ARG:HH12	2:B:861:ALA:HA	1.83	0.43
2:A:919:LYS:H	2:A:919:LYS:HE2	1.82	0.43
1:C:985:A:H61	2:A:504:ASP:CB	2.24	0.43
2:B:412:VAL:HG23	2:B:414:PRO:HD2	2.00	0.43
2:B:163:ILE:HA	2:B:163:ILE:HD13	1.92	0.43
2:B:644:GLY:HA2	2:B:687:PHE:O	2.18	0.43
2:B:877:VAL:HG22	2:B:906:ILE:HG23	2.01	0.43
2:B:210:ILE:HG22	2:B:439:ILE:HG12	1.99	0.43
2:B:373:PHE:N	2:B:373:PHE:CD1	2.86	0.43
1:D:917:C:C2	1:D:918:U:C5	3.06	0.43
2:B:577:GLU:OE1	2:B:592:HIS:HB2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:988:A:N7	2:A:529:LEU:HD21	2.33	0.43
2:B:119:PHE:C	2:B:121:ASP:N	2.70	0.43
2:A:623:PHE:O	2:A:624:ASN:C	2.56	0.43
2:A:460:ILE:HD12	2:A:460:ILE:N	2.33	0.43
2:A:884:LYS:C	2:A:886:SER:N	2.72	0.43
2:A:446:LYS:HD2	2:A:446:LYS:H	1.84	0.43
2:B:310:ALA:HB1	2:B:312:PHE:CE1	2.53	0.43
2:A:508:CYS:O	2:A:508:CYS:SG	2.77	0.43
2:B:198:LEU:CD1	2:B:198:LEU:H	2.29	0.43
2:B:62:VAL:HG21	2:B:678:MET:HE2	1.98	0.43
2:A:183:VAL:CG1	2:A:183:VAL:O	2.65	0.43
2:A:27:ILE:HG12	2:A:28:ARG:CZ	2.49	0.43
2:B:171:LYS:HD2	2:B:520:TRP:CE3	2.54	0.43
2:B:340:LYS:CE	2:B:341:ARG:HH12	2.32	0.43
2:B:401:TYR:OH	2:B:424:LYS:HE3	2.19	0.43
2:A:45:LEU:CD1	2:A:80:TRP:HB3	2.47	0.43
2:B:114:GLU:OE1	2:B:114:GLU:HA	2.18	0.43
2:A:330:PRO:CD	2:A:400:ILE:HG12	2.48	0.43
1:C:964:G:O2'	1:C:965:G:H5'	2.18	0.43
2:B:922:ASN:ND2	2:B:923:GLU:N	2.63	0.43
2:B:923:GLU:HB2	2:B:945:ASN:HD21	1.84	0.43
2:A:728:TRP:O	2:A:730:LEU:N	2.51	0.43
2:A:960:LEU:CD2	2:A:960:LEU:N	2.81	0.43
2:B:211:ILE:HA	2:B:227:ALA:O	2.19	0.43
2:A:138:ILE:HD12	2:A:138:ILE:HA	1.87	0.43
2:B:183:VAL:O	2:B:184:ARG:C	2.57	0.43
2:B:546:ASN:HA	2:B:546:ASN:HD22	1.59	0.43
2:B:45:LEU:HD11	2:B:130:MET:HG3	2.00	0.43
2:A:273:LEU:HD21	2:A:440:MET:HG3	2.00	0.43
2:B:573:SER:HB2	2:B:576:LYS:HG2	2.00	0.43
2:A:703:ARG:O	2:A:707:LEU:HD12	2.18	0.43
1:C:955:G:P	2:A:961:LYS:HZ3	2.40	0.43
2:A:198:LEU:HD22	2:A:202:GLU:CB	2.49	0.43
1:C:986:C:O3'	2:A:510:ARG:HD2	2.19	0.43
2:A:742:ASN:O	2:A:745:GLU:N	2.52	0.43
2:A:128:TYR:O	2:A:128:TYR:CD1	2.71	0.43
2:B:337:GLU:HG2	2:B:337:GLU:O	2.18	0.43
2:A:36:PHE:O	2:A:38:ILE:HG22	2.18	0.43
2:A:94:ILE:HD12	2:A:94:ILE:C	2.39	0.43
1:D:976:C:O2'	1:D:977:G:H5'	2.18	0.43
2:B:379:VAL:O	2:B:383:GLY:HA3	2.19	0.43
2:B:218:GLU:O	2:B:219:ASN:C	2.56	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:173:LYS:HD2	2:B:175:TYR:CE2	2.54	0.43
2:B:481:ALA:O	2:B:484:ARG:N	2.34	0.43
2:B:864:TYR:OH	2:B:871:TRP:HZ2	2.02	0.43
2:B:953:LYS:O	2:B:954:LYS:C	2.57	0.43
2:A:566:TYR:OH	2:A:572:PHE:HD1	2.01	0.43
2:A:182:ARG:O	2:A:183:VAL:CB	2.66	0.43
2:B:728:TRP:HZ3	2:B:729:MET:CE	2.32	0.43
2:B:343:THR:HG23	2:B:344:GLU:HG2	2.00	0.43
2:B:803:GLU:CG	2:B:815:VAL:HG12	2.49	0.43
2:A:380:ASN:O	2:A:384:ILE:HG13	2.19	0.43
2:A:37:TYR:CE2	2:A:39:THR:CG2	3.01	0.43
2:B:646:LEU:O	2:B:647:GLU:HB2	2.19	0.43
2:B:539:TYR:HA	2:B:542:SER:HB2	2.01	0.43
2:B:273:LEU:CB	2:B:280:ILE:HD11	2.49	0.43
2:B:33:GLU:N	2:B:33:GLU:OE2	2.39	0.43
1:D:969:G:O2'	1:D:970:A:H5'	2.18	0.43
2:B:25:PRO:HD2	2:B:145:ASP:OD2	2.19	0.43
2:A:246:ASN:OD1	2:A:247:ALA:N	2.52	0.43
2:B:560:THR:O	2:B:563:PHE:HB3	2.19	0.43
2:A:214:PHE:HA	2:A:299:PRO:CG	2.49	0.43
2:A:231:ARG:O	2:A:234:THR:OG1	2.36	0.43
2:B:231:ARG:O	2:B:234:THR:OG1	2.37	0.43
2:B:471:ASN:OD1	2:B:473:GLU:HG2	2.18	0.43
2:A:544:HIS:HE1	2:A:593:GLU:OE2	2.01	0.43
2:A:511:LYS:HE2	2:A:524:TRP:CE2	2.53	0.43
2:B:98:ASP:OD2	2:B:99:PRO:HD2	2.19	0.43
2:A:475:LYS:HE3	2:A:500:ILE:O	2.19	0.42
2:B:840:ARG:O	2:B:844:GLU:HG3	2.18	0.42
2:B:698:ARG:O	2:B:701:ILE:HB	2.18	0.42
2:B:737:ILE:HG22	2:B:823:PRO:HD3	2.00	0.42
2:B:680:LEU:C	2:B:750:ARG:HG3	2.39	0.42
2:A:232:PRO:O	2:A:427:ILE:HG21	2.19	0.42
2:A:184:ARG:HD3	2:A:198:LEU:HD21	2.01	0.42
2:A:198:LEU:HD23	2:A:448:VAL:HG13	2.01	0.42
1:D:920:G:H5''	1:D:921:U:C5	2.48	0.42
2:A:470:GLY:O	2:A:471:ASN:C	2.57	0.42
2:A:384:ILE:CG2	2:A:385:LYS:H	2.19	0.42
2:B:22:ILE:HA	2:B:22:ILE:HD12	1.82	0.42
2:B:614:ILE:HA	2:B:618:LEU:HB2	2.01	0.42
2:A:884:LYS:HZ3	2:A:884:LYS:HB2	1.82	0.42
2:B:373:PHE:HB2	2:B:374:PRO:HD3	2.02	0.42
2:B:374:PRO:HG3	2:B:379:VAL:CG2	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:223:ILE:HG23	2:B:223:ILE:O	2.19	0.42
2:A:311:GLU:OE2	2:A:335:ALA:HB2	2.19	0.42
1:C:941:A:H2'	1:C:942:U:H6	1.84	0.42
1:C:964:G:N2	1:C:975:C:C2	2.86	0.42
2:A:521:ASP:N	2:A:522:PRO:HD3	2.34	0.42
2:B:872:LYS:HA	2:B:872:LYS:HD3	1.88	0.42
2:A:959:PRO:C	2:A:960:LEU:CD2	2.87	0.42
2:A:890:LEU:C	2:A:892:LYS:N	2.72	0.42
2:A:854:LYS:HG3	2:A:855:ILE:H	1.83	0.42
2:B:355:ILE:CG2	2:B:410:PHE:CE1	3.02	0.42
2:B:706:GLU:O	2:B:709:SER:HB2	2.19	0.42
2:B:54:ALA:HB2	2:B:661:PHE:CD1	2.54	0.42
2:A:314:ASP:HA	2:A:315:PRO:HD3	1.89	0.42
2:A:714:TYR:N	2:A:714:TYR:CD2	2.88	0.42
1:D:916:C:O2'	1:D:972:U:O3'	2.36	0.42
2:A:675:LEU:CD1	2:A:697:LEU:HD11	2.48	0.42
1:C:958:U:H2'	1:C:959:U:O5'	2.19	0.42
1:D:958:U:H2'	1:D:959:U:O5'	2.19	0.42
2:A:786:LEU:C	2:A:786:LEU:HD23	2.40	0.42
2:A:469:TYR:CE2	2:A:620:PHE:CD1	3.07	0.42
2:A:774:ARG:HG2	2:A:775:ASP:N	2.34	0.42
2:B:165:TRP:HZ2	2:B:565:ASP:OD2	2.02	0.42
2:B:159:PHE:O	2:B:162:PHE:HB3	2.19	0.42
2:B:827:TRP:HD1	2:B:827:TRP:O	2.02	0.42
2:B:884:LYS:O	2:B:885:SER:C	2.57	0.42
1:C:960:C:C2	1:C:971:A:H1'	2.54	0.42
2:A:244:ASN:ND2	2:A:313:VAL:HG23	2.34	0.42
2:A:614:ILE:HA	2:A:618:LEU:HB2	2.02	0.42
1:D:953:A:HO2'	1:D:954:G:H8	1.62	0.42
2:A:572:PHE:HE1	2:A:595:LYS:HB3	1.85	0.42
2:A:860:ARG:NH2	2:A:862:TYR:CB	2.77	0.42
2:A:218:GLU:O	2:A:219:ASN:C	2.57	0.42
2:A:691:ARG:CG	2:A:691:ARG:NH1	2.80	0.42
2:A:373:PHE:N	2:A:374:PRO:CD	2.83	0.42
2:B:388:LYS:H	2:B:390:LYS:HE2	1.84	0.42
2:B:720:VAL:CG1	2:B:777:GLU:HG2	2.48	0.42
2:A:724:ASP:C	2:A:726:ASP:N	2.73	0.42
2:A:195:ASP:C	2:A:202:GLU:OE1	2.57	0.42
1:C:985:A:O3'	1:C:986:C:C6	2.72	0.42
2:A:191:THR:HA	2:A:192:PRO:HD3	1.88	0.42
2:A:733:LEU:HD11	2:A:789:VAL:CG2	2.48	0.42
2:B:225:LEU:HD12	2:B:264:ILE:O	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:160:SER:HB3	2:A:516:THR:HG23	2.01	0.42
2:B:800:HIS:O	2:B:802:CYS:N	2.53	0.42
2:B:819:LYS:HD2	2:B:819:LYS:N	2.34	0.42
2:A:211:ILE:HG12	2:A:438:GLU:O	2.20	0.42
1:D:922:C:H4'	1:D:923:A:C5'	2.46	0.42
2:A:37:TYR:OH	2:A:536:MET:O	2.30	0.42
1:C:982:C:O5'	1:C:982:C:H6	2.02	0.42
2:B:616:ASN:O	2:B:619:THR:N	2.52	0.42
2:A:256:ARG:NH1	2:A:278:ARG:NH1	2.68	0.42
2:B:581:GLU:HG3	2:B:586:ILE:O	2.20	0.42
2:A:911:ILE:HG13	2:A:912:LYS:HG3	2.02	0.42
2:B:764:LEU:HD13	2:B:786:LEU:CD1	2.48	0.42
2:B:766:TRP:O	2:B:770:ARG:N	2.45	0.42
2:A:730:LEU:HD23	2:A:730:LEU:HA	1.90	0.42
2:A:83:THR:HA	2:A:153:THR:HG22	2.02	0.42
2:B:176:ILE:HD13	2:B:520:TRP:CH2	2.55	0.42
2:B:728:TRP:O	2:B:730:LEU:N	2.53	0.42
1:D:922:C:H5''	1:D:923:A:OP1	2.20	0.42
2:A:145:ASP:OD1	2:A:147:SER:N	2.52	0.42
2:B:470:GLY:O	2:B:471:ASN:C	2.58	0.42
2:B:890:LEU:C	2:B:892:LYS:N	2.71	0.42
2:A:379:VAL:O	2:A:383:GLY:HA3	2.19	0.42
2:A:276:GLN:HE21	2:A:276:GLN:HB3	1.62	0.42
2:A:947:THR:CG2	2:A:948:GLU:H	2.33	0.42
2:A:767:TYR:OH	2:A:782:VAL:HG21	2.19	0.42
2:B:469:TYR:HB2	2:B:504:ASP:O	2.20	0.42
2:B:721:GLU:HA	2:B:721:GLU:OE2	2.19	0.42
2:B:645:THR:OG1	2:B:688:ASP:OD1	2.28	0.42
2:B:775:ASP:O	2:B:775:ASP:OD1	2.38	0.42
2:B:921:ILE:HD12	2:B:928:ARG:HH12	1.85	0.42
2:A:931:LYS:NZ	2:A:935:GLU:OE2	2.42	0.42
2:B:661:PHE:O	2:B:665:ILE:HG13	2.20	0.42
2:A:560:THR:O	2:A:563:PHE:N	2.52	0.42
2:A:711:PHE:CD1	2:A:711:PHE:N	2.88	0.42
2:A:544:HIS:HE1	2:A:593:GLU:CD	2.23	0.42
2:B:478:ALA:HB2	2:B:623:PHE:CD1	2.55	0.42
2:B:129:PHE:HA	2:B:132:ALA:HB3	2.01	0.42
2:B:725:ILE:CD1	2:B:770:ARG:NE	2.82	0.42
2:B:871:TRP:CD2	2:B:920:ARG:NH2	2.80	0.42
2:A:181:HIS:ND1	2:A:182:ARG:O	2.52	0.42
2:A:67:LYS:HA	2:A:70:GLN:HB2	2.01	0.42
2:B:152:THR:HG22	2:B:159:PHE:CE1	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:714:TYR:CD1	2:B:780:ARG:HD3	2.55	0.42
1:C:927:G:C6	1:C:928:C:C4	3.08	0.42
2:A:12:LYS:HZ1	2:A:16:ARG:HH22	1.67	0.42
2:B:576:LYS:O	2:B:580:LEU:HD13	2.20	0.42
2:B:277:ASP:OD2	2:B:462:HIS:CE1	2.73	0.42
2:A:519:PRO:HG2	2:A:520:TRP:CE3	2.55	0.42
2:B:147:SER:OG	2:B:543:ARG:HG3	2.20	0.42
1:C:953:A:C5'	1:C:954:G:OP1	2.68	0.42
2:B:317:ASN:O	2:B:318:ALA:HB3	2.20	0.42
2:A:924:GLU:HA	2:A:927:LEU:HB3	2.02	0.42
2:B:734:ASN:HD22	2:B:734:ASN:HA	1.51	0.42
2:A:418:LYS:HB3	2:A:422:GLU:OE2	2.20	0.42
2:B:567:ILE:HG21	2:B:594:MET:HE3	2.01	0.42
2:B:32:LYS:HA	2:B:600:TYR:CE1	2.55	0.42
1:D:923:A:O2'	1:D:924:A:OP2	2.30	0.42
2:A:887:MET:CE	2:A:891:MET:HG2	2.49	0.42
2:A:434:LYS:HB3	2:A:436:ILE:CG1	2.46	0.42
2:A:708:ILE:HD12	2:A:791:VAL:CG2	2.49	0.42
2:B:800:HIS:C	2:B:802:CYS:N	2.72	0.42
2:A:347:GLU:C	2:A:347:GLU:CD	2.78	0.42
2:A:290:LYS:HE3	2:A:290:LYS:HB3	1.95	0.42
2:A:402:LYS:O	2:A:403:ALA:C	2.58	0.42
1:D:953:A:N1	2:B:966:ILE:HG12	2.35	0.41
2:A:87:ILE:O	2:A:90:ILE:HB	2.20	0.41
1:D:903:G:H2'	1:D:904:G:O4'	2.20	0.41
2:A:235:VAL:HG11	2:A:431:MET:HE3	2.02	0.41
2:B:325:VAL:N	2:B:332:ASP:OD2	2.51	0.41
1:C:926:G:O2'	1:C:927:G:H5'	2.20	0.41
1:C:923:A:O2'	1:C:924:A:OP2	2.34	0.41
2:A:123:ILE:HD11	2:A:155:LEU:HD11	2.02	0.41
2:B:553:LYS:HE3	2:B:553:LYS:HB3	1.80	0.41
2:B:671:ASP:HB3	2:B:798:THR:HG22	2.02	0.41
2:B:768:LEU:O	2:B:770:ARG:N	2.52	0.41
2:A:824:VAL:O	2:A:825:GLU:C	2.57	0.41
2:B:677:ILE:HD13	2:B:677:ILE:HA	1.85	0.41
2:B:824:VAL:HG12	2:B:825:GLU:N	2.35	0.41
2:B:825:GLU:O	2:B:825:GLU:CG	2.68	0.41
2:B:412:VAL:O	2:B:416:GLU:OE1	2.37	0.41
2:B:728:TRP:HE3	2:B:729:MET:N	2.18	0.41
2:B:803:GLU:CD	2:B:815:VAL:HG12	2.41	0.41
2:A:711:PHE:O	2:A:784:ARG:HG2	2.20	0.41
1:C:976:C:C2'	1:C:977:G:H5'	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:934:MET:O	2:B:938:LEU:HD13	2.21	0.41
2:A:871:TRP:CE3	2:A:920:ARG:NH2	2.88	0.41
2:A:236:TYR:CE2	2:A:414:PRO:HG2	2.55	0.41
1:C:970:A:O2'	1:C:971:A:O5'	2.38	0.41
2:A:691:ARG:O	2:A:694:VAL:CG1	2.64	0.41
2:A:250:VAL:CG1	2:A:285:GLU:HG3	2.50	0.41
2:A:264:ILE:O	2:A:264:ILE:HG22	2.18	0.41
2:A:9:ILE:HD13	2:A:804:GLU:HG2	2.02	0.41
2:B:289:GLU:N	2:B:289:GLU:OE2	2.53	0.41
2:B:264:ILE:HG23	2:B:286:PHE:CE2	2.55	0.41
2:B:263:TRP:CD1	2:B:263:TRP:N	2.88	0.41
1:D:988:A:N7	2:B:529:LEU:HD21	2.36	0.41
2:A:341:ARG:N	2:A:341:ARG:HD3	2.36	0.41
2:A:499:ILE:HG12	2:A:615:PRO:HA	2.02	0.41
2:B:212:ILE:CD1	2:B:235:VAL:HG12	2.47	0.41
2:B:730:LEU:O	2:B:827:TRP:NE1	2.53	0.41
2:A:459:LYS:CG	2:A:460:ILE:N	2.83	0.41
2:A:12:LYS:NZ	2:A:16:ARG:HH22	2.18	0.41
2:A:710:GLN:O	2:A:711:PHE:C	2.57	0.41
2:A:909:LYS:NZ	2:A:913:GLU:O	2.52	0.41
2:A:148:ARG:HB3	2:A:542:SER:HB3	2.02	0.41
2:B:173:LYS:HD2	2:B:175:TYR:HE2	1.85	0.41
2:B:847:LYS:HE3	2:B:847:LYS:HB2	1.89	0.41
2:B:510:ARG:HA	2:B:510:ARG:HE	1.84	0.41
2:A:61:ASP:O	2:A:64:ALA:N	2.53	0.41
2:B:774:ARG:CG	2:B:775:ASP:N	2.84	0.41
2:A:410:PHE:CZ	2:A:412:VAL:HG21	2.54	0.41
1:C:987:C:H5	2:A:506:LYS:NZ	2.18	0.41
2:B:182:ARG:O	2:B:183:VAL:CB	2.69	0.41
2:A:395:GLN:HG3	2:A:396:ALA:N	2.34	0.41
2:A:317:ASN:O	2:A:318:ALA:HB3	2.21	0.41
2:A:16:ARG:HG3	2:A:16:ARG:NH1	2.36	0.41
2:A:574:GLU:HA	2:A:577:GLU:OE1	2.20	0.41
2:A:45:LEU:HD13	2:A:130:MET:CB	2.51	0.41
2:B:570:GLU:OE1	2:B:576:LYS:HG3	2.20	0.41
2:A:767:TYR:OH	2:A:782:VAL:HG11	2.21	0.41
2:B:506:LYS:HE3	2:B:527:GLU:OE1	2.21	0.41
2:B:725:ILE:HD13	2:B:770:ARG:NE	2.36	0.41
1:D:902:C:H2'	1:D:903:G:C5'	2.51	0.41
2:A:540:THR:HG21	2:A:598:PHE:CD1	2.55	0.41
2:B:884:LYS:C	2:B:886:SER:N	2.73	0.41
1:C:960:C:H2'	1:C:971:A:H1'	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:711:PHE:HA	2:A:714:TYR:CE2	2.56	0.41
2:B:196:HIS:CD2	2:B:197:ASP:N	2.89	0.41
2:A:544:HIS:CE1	2:A:593:GLU:OE2	2.73	0.41
2:B:241:MET:HG3	2:B:296:VAL:CG2	2.51	0.41
2:A:612:ASP:OD1	2:A:613:LEU:HD23	2.21	0.41
2:A:614:ILE:N	2:A:615:PRO:CD	2.83	0.41
2:B:856:GLU:O	2:B:857:ASN:O	2.38	0.41
2:B:863:ILE:HG13	2:B:945:ASN:HA	2.03	0.41
2:A:412:VAL:H	2:A:416:GLU:HG2	1.86	0.41
2:B:136:THR:HG23	2:B:662:ILE:HB	2.02	0.41
2:B:880:LYS:O	2:B:881:ARG:C	2.59	0.41
2:A:950:LYS:H	2:A:953:LYS:HZ3	1.68	0.41
1:C:920:G:C4'	1:C:920:G:OP1	2.68	0.41
2:A:7:LYS:HZ3	2:A:7:LYS:HB2	1.85	0.41
2:B:860:ARG:HH21	2:B:860:ARG:HB2	1.86	0.41
2:A:405:TYR:HE2	2:A:424:LYS:HZ3	1.68	0.41
2:A:181:HIS:HD2	2:A:466:PHE:CE1	2.38	0.41
2:A:382:LEU:C	2:A:384:ILE:N	2.74	0.41
2:B:471:ASN:HD22	2:B:471:ASN:C	2.23	0.41
2:A:626:VAL:HG12	2:A:634:TRP:CD2	2.56	0.41
2:B:65:ARG:HA	2:B:68:ARG:HH11	1.81	0.41
2:B:276:GLN:HE21	2:B:460:ILE:HD11	1.86	0.41
2:A:884:LYS:O	2:A:885:SER:C	2.58	0.41
1:D:944:C:OP1	2:B:765:ARG:HD3	2.20	0.41
2:B:623:PHE:O	2:B:626:VAL:HG22	2.21	0.41
2:A:676:TYR:O	2:A:679:SER:HB3	2.21	0.41
2:A:793:LEU:HD23	2:A:821:PRO:HG3	2.03	0.41
2:A:116:LEU:C	2:A:116:LEU:HD23	2.41	0.41
2:A:467:ILE:CG1	2:A:508:CYS:HB3	2.50	0.41
2:B:849:ILE:HD12	2:B:964:ILE:CD1	2.51	0.41
2:B:725:ILE:HB	2:B:929:GLU:OE1	2.20	0.41
2:B:846:ILE:HD12	2:B:938:LEU:CD2	2.51	0.41
2:B:944:ILE:HG22	2:B:945:ASN:N	2.36	0.41
2:B:964:ILE:HG13	2:B:965:PHE:N	2.34	0.41
2:A:872:LYS:O	2:A:876:VAL:CG2	2.65	0.41
2:A:831:THR:O	2:A:834:ALA:HB3	2.21	0.41
2:A:872:LYS:HA	2:A:875:GLU:CD	2.41	0.41
2:B:749:THR:O	2:B:750:ARG:C	2.57	0.41
2:B:560:THR:HB	2:B:561:PRO:CD	2.51	0.41
2:A:644:GLY:HA2	2:A:687:PHE:O	2.20	0.41
2:A:882:ASP:C	2:A:883:PHE:HD1	2.24	0.41
2:A:714:TYR:CE1	2:A:780:ARG:HG2	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:914:A:H1'	1:C:925:A:N1	2.36	0.41
2:B:652:SER:HG	2:B:655:LYS:HB2	1.85	0.41
2:A:112:PRO:HD2	2:A:115:ILE:HD12	2.02	0.41
2:A:175:TYR:CE1	2:A:474:TRP:HB2	2.56	0.41
1:C:958:U:C2'	1:C:959:U:O5'	2.68	0.41
1:D:925:A:H2'	1:D:926:G:O4'	2.21	0.41
2:A:293:GLY:O	2:A:295:TYR:CD1	2.74	0.41
2:A:406:HIS:ND1	2:A:421:GLN:OE1	2.54	0.41
2:B:771:THR:HB	2:B:774:ARG:HD3	2.03	0.41
2:B:786:LEU:HD23	2:B:786:LEU:C	2.41	0.41
2:B:846:ILE:HA	2:B:849:ILE:HD12	2.03	0.41
2:B:870:LYS:HE3	2:B:905:LYS:CE	2.40	0.41
2:A:232:PRO:O	2:A:235:VAL:HG22	2.21	0.41
2:A:135:GLU:O	2:A:139:ARG:HB2	2.21	0.41
2:B:412:VAL:O	2:B:413:PRO:C	2.60	0.41
2:B:488:LEU:HA	2:B:488:LEU:HD23	1.81	0.41
2:A:252:ALA:HB1	2:A:281:GLU:O	2.21	0.41
2:A:168:TRP:CZ3	2:A:520:TRP:CE3	3.09	0.41
2:A:173:LYS:CB	2:A:175:TYR:CE2	3.04	0.41
2:B:949:ASP:HB2	2:B:954:LYS:CE	2.45	0.40
2:B:704:PHE:HD1	2:B:790:TRP:CH2	2.39	0.40
2:A:345:ILE:O	2:A:346:LEU:HB2	2.20	0.40
1:C:986:C:C2	2:A:507:ALA:N	2.89	0.40
2:B:152:THR:HG22	2:B:159:PHE:CZ	2.56	0.40
2:B:155:LEU:C	2:B:157:PRO:HD3	2.42	0.40
2:B:914:ARG:CZ	2:B:915:THR:O	2.69	0.40
2:B:914:ARG:HH21	2:B:915:THR:CG2	2.27	0.40
2:B:914:ARG:NH2	2:B:915:THR:HG23	2.29	0.40
2:A:9:ILE:O	2:A:12:LYS:HB3	2.22	0.40
2:B:482:LEU:C	2:B:482:LEU:HD23	2.41	0.40
2:B:240:ASN:O	2:B:324:SER:HB3	2.21	0.40
2:B:334:VAL:HG13	2:B:388:LYS:O	2.20	0.40
1:C:980:C:H2'	1:C:981:C:H6	1.86	0.40
2:A:581:GLU:HG3	2:A:586:ILE:O	2.21	0.40
2:B:381:LYS:C	2:B:381:LYS:HD2	2.40	0.40
2:A:824:VAL:CG1	2:A:825:GLU:N	2.84	0.40
2:A:232:PRO:CG	2:A:428:ALA:HB2	2.51	0.40
2:A:646:LEU:O	2:A:647:GLU:CB	2.69	0.40
2:A:803:GLU:HA	2:A:803:GLU:OE1	2.20	0.40
2:A:9:ILE:O	2:A:10:GLU:C	2.60	0.40
2:A:339:LEU:N	2:A:339:LEU:HD13	2.36	0.40
2:A:713:GLU:O	2:A:714:TYR:O	2.40	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:914:ARG:HH21	2:A:915:THR:C	2.25	0.40
2:A:733:LEU:HD11	2:A:789:VAL:HB	2.02	0.40
2:B:497:GLU:O	2:B:500:ILE:N	2.54	0.40
2:B:871:TRP:HZ3	2:B:918:VAL:HA	1.87	0.40
2:A:959:PRO:O	2:A:960:LEU:HB2	2.20	0.40
2:B:597:GLU:O	2:B:600:TYR:N	2.53	0.40
2:B:186:ASP:CB	2:B:193:LEU:HD11	2.42	0.40
2:B:13:TRP:CZ2	2:B:803:GLU:HB3	2.53	0.40
2:B:337:GLU:O	2:B:339:LEU:HD12	2.21	0.40
2:B:461:ILE:HB	2:B:464:GLN:HB2	2.03	0.40
2:B:915:THR:O	2:B:916:PHE:CD2	2.74	0.40
2:B:783:LEU:N	2:B:783:LEU:CD1	2.84	0.40
2:A:441:TYR:O	2:A:442:GLU:OE2	2.40	0.40
2:B:216:LEU:HB2	2:B:296:VAL:HG12	2.04	0.40
2:A:173:LYS:HD3	2:A:175:TYR:HE2	1.86	0.40
2:A:50:HIS:H	2:A:53:HIS:HD2	1.68	0.40
2:A:77:PRO:HG3	2:A:539:TYR:CD1	2.56	0.40
2:A:497:GLU:O	2:A:500:ILE:N	2.54	0.40
2:B:849:ILE:HD12	2:B:964:ILE:HD11	2.04	0.40
2:A:918:VAL:HG11	2:A:920:ARG:NH1	2.37	0.40
2:B:555:ASP:OD2	2:B:557:GLU:HB2	2.22	0.40
2:A:953:LYS:O	2:A:954:LYS:C	2.59	0.40
2:A:14:GLN:H	2:A:14:GLN:HG3	1.61	0.40
2:A:518:LEU:C	2:A:520:TRP:H	2.24	0.40
2:B:48:HIS:NE2	2:B:132:ALA:HB1	2.36	0.40
2:B:718:GLY:O	2:B:719:ASN:C	2.60	0.40
2:B:70:GLN:HB3	2:B:72:TYR:CE1	2.56	0.40
2:A:217:ARG:HE	2:A:217:ARG:HB3	1.62	0.40
2:B:349:TYR:O	2:B:349:TYR:CG	2.74	0.40
2:B:724:ASP:C	2:B:726:ASP:N	2.75	0.40
2:B:919:LYS:NZ	2:B:960:LEU:HD11	2.36	0.40
2:B:921:ILE:O	2:B:924:GLU:CB	2.69	0.40
2:B:44:TYR:O	2:B:46:SER:N	2.54	0.40
2:B:780:ARG:O	2:B:781:TYR:C	2.59	0.40
2:A:867:GLU:N	2:A:867:GLU:OE1	2.38	0.40
2:B:646:LEU:O	2:B:647:GLU:CB	2.69	0.40
2:A:559:LEU:HA	2:A:563:PHE:CD2	2.57	0.40
2:A:330:PRO:HD3	2:A:400:ILE:HG12	2.04	0.40
2:A:96:ASN:ND2	2:A:96:ASN:N	2.70	0.40
2:B:525:VAL:HG13	2:B:525:VAL:O	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	
2	A	944/967 (98%)	630 (67%)	211 (22%)	103 (11%)	1	5
2	B	944/967 (98%)	632 (67%)	208 (22%)	104 (11%)	1	5
All	All	1888/1934 (98%)	1262 (67%)	419 (22%)	207 (11%)	1	5

All (207) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	74	VAL
2	A	110	LYS
2	A	143	SER
2	A	183	VAL
2	A	188	VAL
2	A	276	GLN
2	A	333	HIS
2	A	347	GLU
2	A	377	GLU
2	A	378	GLU
2	A	552	GLY
2	A	630	ARG
2	A	714	TYR
2	A	854	LYS
2	A	867	GLU
2	A	871	TRP
2	A	883	PHE
2	A	913	GLU
2	A	914	ARG
2	A	929	GLU
2	A	953	LYS
2	B	45	LEU
2	B	74	VAL
2	B	110	LYS
2	B	183	VAL
2	B	188	VAL
2	B	276	GLN

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Mol	Chain	Res	Type
2	B	333	HIS
2	B	347	GLU
2	B	377	GLU
2	B	378	GLU
2	B	552	GLY
2	B	630	ARG
2	B	714	TYR
2	B	854	LYS
2	B	867	GLU
2	B	871	TRP
2	B	883	PHE
2	B	913	GLU
2	B	914	ARG
2	B	929	GLU
2	B	953	LYS
2	A	45	LEU
2	A	113	GLU
2	A	181	HIS
2	A	201	GLY
2	A	219	ASN
2	A	301	SER
2	A	343	THR
2	A	374	PRO
2	A	376	VAL
2	A	415	TYR
2	A	464	GLN
2	A	494	ALA
2	A	502	TRP
2	A	528	SER
2	A	529	LEU
2	A	568	PHE
2	A	616	ASN
2	A	711	PHE
2	A	782	VAL
2	A	857	ASN
2	A	868	ASP
2	A	869	TRP
2	A	885	SER
2	A	900	GLY
2	A	921	ILE
2	A	922	ASN
2	A	950	LYS

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Mol	Chain	Res	Type
2	A	954	LYS
2	A	955	LYS
2	B	113	GLU
2	B	143	SER
2	B	181	HIS
2	B	201	GLY
2	B	219	ASN
2	B	301	SER
2	B	343	THR
2	B	374	PRO
2	B	376	VAL
2	B	415	TYR
2	B	464	GLN
2	B	502	TRP
2	B	528	SER
2	B	529	LEU
2	B	568	PHE
2	B	616	ASN
2	B	782	VAL
2	B	857	ASN
2	B	868	ASP
2	B	869	TRP
2	B	885	SER
2	B	900	GLY
2	B	921	ILE
2	B	922	ASN
2	B	950	LYS
2	B	954	LYS
2	B	955	LYS
2	A	73	ASN
2	A	223	ILE
2	A	240	ASN
2	A	453	GLY
2	A	482	LEU
2	A	558	LYS
2	A	631	GLU
2	A	775	ASP
2	A	825	GLU
2	A	895	GLU
2	A	911	ILE
2	B	73	ASN
2	B	96	ASN

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Mol	Chain	Res	Type
2	B	220	GLY
2	B	223	ILE
2	B	240	ASN
2	B	453	GLY
2	B	494	ALA
2	B	558	LYS
2	B	631	GLU
2	B	711	PHE
2	B	775	ASP
2	B	825	GLU
2	B	891	MET
2	B	895	GLU
2	B	911	ILE
2	A	85	SER
2	A	96	ASN
2	A	117	TRP
2	A	220	GLY
2	A	283	ILE
2	A	421	GLN
2	A	542	SER
2	A	623	PHE
2	A	670	ALA
2	A	719	ASN
2	A	856	GLU
2	A	881	ARG
2	A	891	MET
2	A	903	VAL
2	A	907	VAL
2	B	85	SER
2	B	117	TRP
2	B	421	GLN
2	B	482	LEU
2	B	623	PHE
2	B	670	ALA
2	B	719	ASN
2	B	790	TRP
2	B	856	GLU
2	B	881	ARG
2	B	903	VAL
2	B	907	VAL
2	A	157	PRO
2	A	337	GLU

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Mol	Chain	Res	Type
2	A	339	LEU
2	A	394	GLU
2	A	452	PHE
2	A	519	PRO
2	A	790	TRP
2	A	878	SER
2	A	898	LYS
2	B	157	PRO
2	B	283	ILE
2	B	339	LEU
2	B	403	ALA
2	B	452	PHE
2	B	519	PRO
2	B	540	THR
2	B	542	SER
2	B	743	ALA
2	B	878	SER
2	A	303	ASP
2	A	403	ALA
2	A	743	ALA
2	A	813	GLY
2	B	337	GLU
2	B	394	GLU
2	B	495	GLN
2	A	945	ASN
2	A	946	PRO
2	B	945	ASN
2	B	946	PRO
2	A	88	VAL
2	A	471	ASN
2	A	522	PRO
2	A	823	PRO
2	B	471	ASN
2	B	522	PRO
2	B	789	VAL
2	A	302	GLY
2	A	353	PRO
2	A	355	ILE
2	A	384	ILE
2	B	222	VAL
2	B	302	GLY
2	B	353	PRO

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Mol	Chain	Res	Type
2	B	355	ILE
2	B	384	ILE
2	A	115	ILE
2	A	222	VAL
2	A	329	ALA
2	A	330	PRO
2	B	88	VAL
2	B	115	ILE
2	B	329	ALA
2	B	330	PRO
2	B	813	GLY
2	B	823	PRO

### 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	
2	A	841/857 (98%)	731 (87%)	110 (13%)	6	28
2	B	841/857 (98%)	752 (89%)	89 (11%)	10	38
All	All	1682/1714 (98%)	1483 (88%)	199 (12%)	8	34

All (199) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	16	ARG
2	A	28	ARG
2	A	29	ASP
2	A	35	LYS
2	A	37	TYR
2	A	38	ILE
2	A	42	PHE
2	A	70	GLN
2	A	75	LEU
2	A	77	PRO
2	A	107	ASP
2	A	124	ASN
2	A	135	GLU

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Mol	Chain	Res	Type
2	A	138	ILE
2	A	139	ARG
2	A	157	PRO
2	A	172	GLU
2	A	173	LYS
2	A	183	VAL
2	A	196	HIS
2	A	203	ASP
2	A	213	LYS
2	A	217	ARG
2	A	230	LEU
2	A	233	GLU
2	A	234	THR
2	A	239	THR
2	A	246	ASN
2	A	276	GLN
2	A	278	ARG
2	A	289	GLU
2	A	294	LYS
2	A	317	ASN
2	A	331	PHE
2	A	339	LEU
2	A	341	ARG
2	A	347	GLU
2	A	349	TYR
2	A	373	PHE
2	A	381	LYS
2	A	433	GLU
2	A	446	LYS
2	A	455	ARG
2	A	463	ASP
2	A	492	ARG
2	A	527	GLU
2	A	529	LEU
2	A	531	ASP
2	A	536	MET
2	A	540	THR
2	A	551	GLU
2	A	562	GLU
2	A	569	LEU
2	A	590	ILE
2	A	602	TYR

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Mol	Chain	Res	Type
2	A	616	ASN
2	A	624	ASN
2	A	625	HIS
2	A	636	LYS
2	A	640	VAL
2	A	645	THR
2	A	649	GLN
2	A	658	VAL
2	A	678	MET
2	A	679	SER
2	A	685	SER
2	A	691	ARG
2	A	700	GLN
2	A	703	ARG
2	A	707	LEU
2	A	720	VAL
2	A	722	LEU
2	A	727	ARG
2	A	732	ARG
2	A	733	LEU
2	A	744	LEU
2	A	747	PHE
2	A	771	THR
2	A	776	ASP
2	A	784	ARG
2	A	792	ARG
2	A	809	LEU
2	A	815	VAL
2	A	817	LEU
2	A	819	LYS
2	A	820	TRP
2	A	823	PRO
2	A	825	GLU
2	A	826	GLU
2	A	828	TRP
2	A	829	ASN
2	A	852	VAL
2	A	860	ARG
2	A	862	TYR
2	A	869	TRP
2	A	872	LYS
2	A	879	GLU

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Mol	Chain	Res	Type
2	A	881	ARG
2	A	884	LYS
2	A	910	LEU
2	A	916	PHE
2	A	917	ASP
2	A	919	LYS
2	A	922	ASN
2	A	923	GLU
2	A	932	GLU
2	A	933	PHE
2	A	942	ILE
2	A	953	LYS
2	A	964	ILE
2	B	7	LYS
2	B	18	LEU
2	B	42	PHE
2	B	44	TYR
2	B	70	GLN
2	B	97	ARG
2	B	139	ARG
2	B	151	TYR
2	B	172	GLU
2	B	196	HIS
2	B	197	ASP
2	B	203	ASP
2	B	213	LYS
2	B	218	GLU
2	B	230	LEU
2	B	233	GLU
2	B	234	THR
2	B	271	TYR
2	B	276	GLN
2	B	285	GLU
2	B	298	ASN
2	B	303	ASP
2	B	331	PHE
2	B	332	ASP
2	B	338	ASP
2	B	339	LEU
2	B	341	ARG
2	B	347	GLU
2	B	381	LYS

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Mol	Chain	Res	Type
2	B	405	TYR
2	B	415	TYR
2	B	429	LYS
2	B	451	ARG
2	B	471	ASN
2	B	479	ARG
2	B	504	ASP
2	B	505	LYS
2	B	510	ARG
2	B	511	LYS
2	B	528	SER
2	B	533	THR
2	B	536	MET
2	B	540	THR
2	B	546	ASN
2	B	547	LYS
2	B	551	GLU
2	B	557	GLU
2	B	565	ASP
2	B	599	GLU
2	B	602	TYR
2	B	607	ARG
2	B	624	ASN
2	B	625	HIS
2	B	630	ARG
2	B	641	ASN
2	B	649	GLN
2	B	650	LYS
2	B	658	VAL
2	B	674	ARG
2	B	675	LEU
2	B	690	ARG
2	B	703	ARG
2	B	714	TYR
2	B	722	LEU
2	B	726	ASP
2	B	729	MET
2	B	734	ASN
2	B	744	LEU
2	B	748	ARG
2	B	750	ARG
2	B	812	GLU

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Mol	Chain	Res	Type
2	B	819	LYS
2	B	820	TRP
2	B	825	GLU
2	B	826	GLU
2	B	828	TRP
2	B	829	ASN
2	B	855	ILE
2	B	860	ARG
2	B	869	TRP
2	B	885	SER
2	B	886	SER
2	B	889	GLU
2	B	917	ASP
2	B	919	LYS
2	B	920	ARG
2	B	940	ILE
2	B	953	LYS
2	B	964	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	5	ASN
2	A	53	HIS
2	A	70	GLN
2	A	73	ASN
2	A	81	HIS
2	A	96	ASN
2	A	124	ASN
2	A	166	GLN
2	A	196	HIS
2	A	219	ASN
2	A	276	GLN
2	A	317	ASN
2	A	421	GLN
2	A	447	ASN
2	A	464	GLN
2	A	544	HIS
2	A	546	ASN
2	A	616	ASN
2	A	624	ASN
2	A	625	HIS

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Mol	Chain	Res	Type
2	A	683	HIS
2	A	731	HIS
2	A	742	ASN
2	A	800	HIS
2	A	922	ASN
2	B	53	HIS
2	B	70	GLN
2	B	73	ASN
2	B	124	ASN
2	B	166	GLN
2	B	196	HIS
2	B	276	GLN
2	B	298	ASN
2	B	317	ASN
2	B	387	GLN
2	B	421	GLN
2	B	447	ASN
2	B	471	ASN
2	B	495	GLN
2	B	546	ASN
2	B	616	ASN
2	B	731	HIS
2	B	734	ASN
2	B	742	ASN
2	B	908	GLN
2	B	922	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	87/88 (98%)	24 (27%)	7 (8%)
1	D	87/88 (98%)	22 (25%)	8 (9%)
All	All	174/176 (98%)	46 (26%)	15 (8%)

All (46) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	907	G
1	C	908	U
1	C	910	G
1	C	916	C

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Mol	Chain	Res	Type
1	C	917	C
1	C	918	U
1	C	919	G
1	C	920	G
1	C	921	U
1	C	922	C
1	C	923	A
1	C	924	A
1	C	936	U
1	C	937	C
1	C	952	U
1	C	953	A
1	C	954	G
1	C	961	C
1	C	968	C
1	C	971	A
1	C	972	U
1	C	983	G
1	C	987	C
1	C	988	A
1	D	903	G
1	D	905	G
1	D	908	U
1	D	909	U
1	D	910	G
1	D	917	C
1	D	918	U
1	D	919	G
1	D	920	G
1	D	921	U
1	D	923	A
1	D	924	A
1	D	936	U
1	D	952	U
1	D	961	C
1	D	971	A
1	D	972	U
1	D	973	C
1	D	984	C
1	D	985	A
1	D	987	C
1	D	988	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C	907	G
1	C	922	C
1	C	923	A
1	C	953	A
1	C	960	C
1	C	970	A
1	C	972	U
1	D	907	G
1	D	920	G
1	D	922	C
1	D	923	A
1	D	953	A
1	D	960	C
1	D	970	A
1	D	972	U

#### 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 ⓘ

There are no ligands in this entry.

#### 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	C	88/88 (100%)	0.16	3 (3%) 43 9	53, 78, 126, 149	0
1	D	88/88 (100%)	0.26	5 (5%) 23 5	53, 91, 146, 150	0
2	A	948/967 (98%)	-0.10	1 (0%) 93 75	8, 59, 131, 150	0
2	B	948/967 (98%)	0.08	9 (0%) 81 35	48, 102, 149, 150	0
All	All	2072/2110 (98%)	0.01	18 (0%) 81 35	8, 82, 143, 150	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	939	A	5.3
1	D	936	U	4.2
2	B	920	ARG	3.9
1	D	986	C	3.5
2	B	236	TYR	3.2
1	C	987	C	3.1
1	C	939	A	3.0
2	B	862	TYR	3.0
1	C	986	C	2.9
1	D	988	A	2.9
2	B	895	GLU	2.9
1	D	940	G	2.7
2	B	784	ARG	2.2
2	A	407	LYS	2.2
2	B	255	ARG	2.1
2	B	524	TRP	2.1
2	B	865	THR	2.1
2	B	464	GLN	2.1

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.