



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:17 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 X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

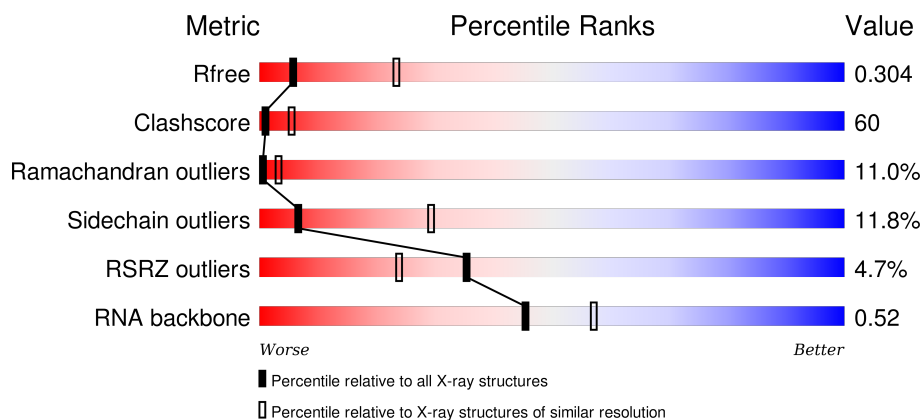
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	1095 (3.26-3.18)
Clashscore	102246	1046 (3.24-3.20)
Ramachandran outliers	100387	1026 (3.24-3.20)
Sidechain outliers	100360	1025 (3.24-3.20)
RSRZ outliers	91569	1100 (3.26-3.18)
RNA backbone	2183	1004 (3.72-2.72)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	88	<div> <div>6%</div> <div>27% 44% 22% 7%</div> </div>
1	D	88	<div> <div>8%</div> <div>36% 39% 22% .</div> </div>
2	A	967	<div> <div>3%</div> <div>21% 60% 16% ..</div> </div>
2	B	967	<div> <div>6%</div> <div>22% 61% 14% ..</div> </div>

2 Entry composition

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

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

- Molecule 1 is a 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			

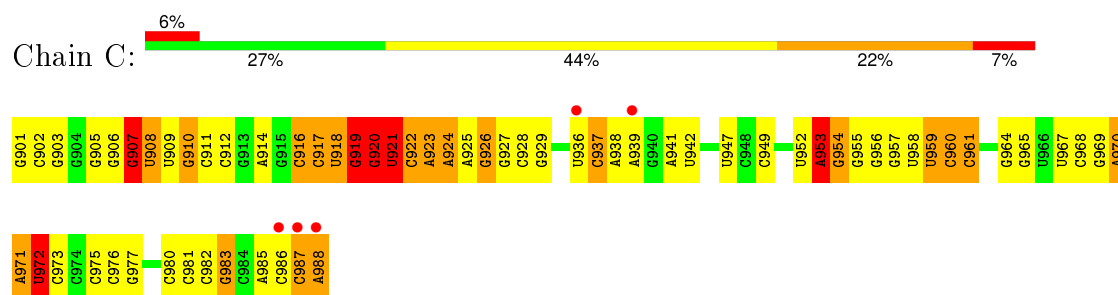
- Molecule 2 is a protein called Leucyl-tRNA synthetase.

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			

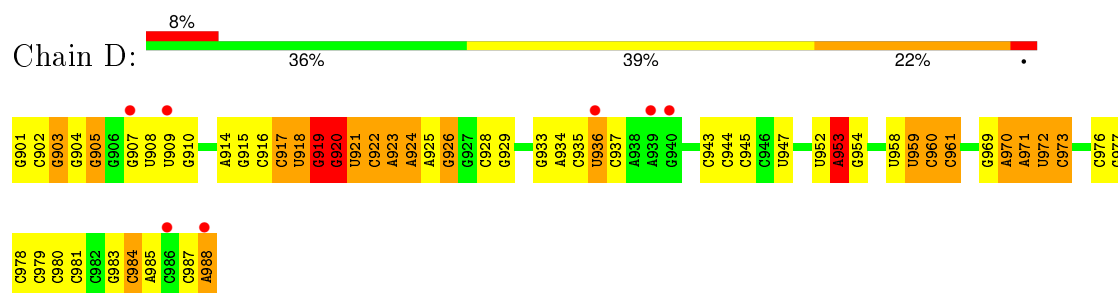
3 Residue-property plots

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.

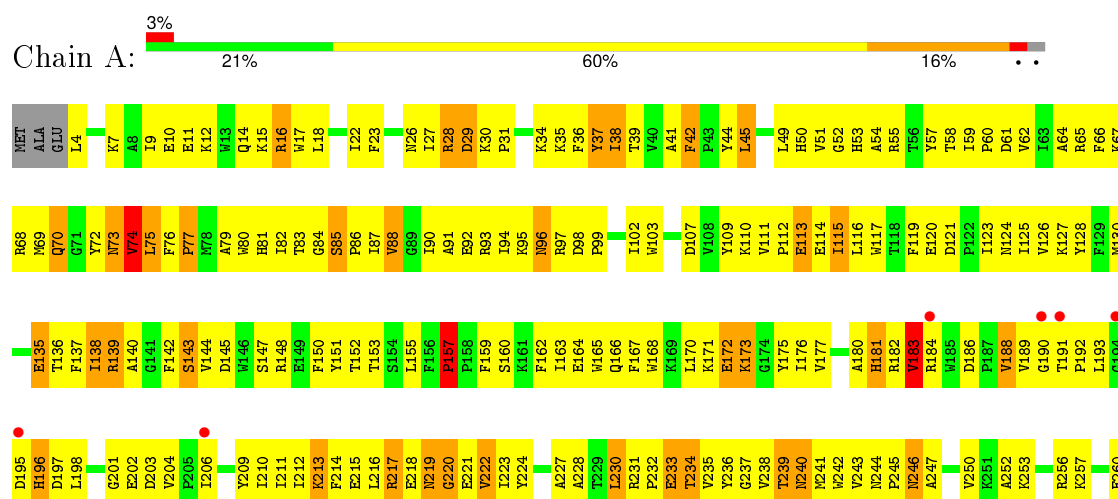
• Molecule 1: tRNA



• Molecule 1: tRNA



• Molecule 2: Leucyl-tRNA synthetase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.305 0.243 , 0.304	Depositor DCC
R_{free} test set	4957 reflections (10.07%)	DCC
Wilson B-factor (Å ²)	75.5	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 76.5	EDS
Estimated twinning fraction	0.046 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 49816 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	19578	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1880	0	956	88	0
1	D	1880	0	956	65	0
2	A	7909	0	7908	1115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	7909	0	7908	1018	0
All	All	19578	0	17728	2256	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 60.

All (2256) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	Interatomic distance (Å)	Clash overlap (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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:920:ARG:HA	2:B:920:ARG:NE	1.85	0.89
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:54:ALA:CB	2:B:661:PHE:CD1	3.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	Interatomic distance (Å)	Clash overlap (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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:725:ILE:HG21	2:B:771:THR:HG21	1.99	0.44
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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 [i](#)

5.3.1 Protein backbone [i](#)

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%)	0	3
2	B	944/967 (98%)	632 (67%)	208 (22%)	104 (11%)	0	3
All	All	1888/1934 (98%)	1262 (67%)	419 (22%)	207 (11%)	0	3

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	A	841/857 (98%)	731 (87%)	110 (13%)	5 24
2	B	841/857 (98%)	752 (89%)	89 (11%)	8 34
All	All	1682/1714 (98%)	1483 (88%)	199 (12%)	6 29

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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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 ²)	Q<0.9
1	C	88/88 (100%)	0.24	5 (5%) 27 17	53, 78, 126, 149	0
1	D	88/88 (100%)	0.45	7 (7%) 15 9	53, 91, 146, 150	0
2	A	948/967 (98%)	-0.06	30 (3%) 51 38	8, 59, 131, 150	0
2	B	948/967 (98%)	0.29	55 (5%) 26 16	48, 102, 149, 150	0
All	All	2072/2110 (98%)	0.13	97 (4%) 35 24	8, 82, 143, 150	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	407	LYS	5.5
1	D	936	U	5.5
2	B	524	TRP	5.3
1	D	939	A	5.1
2	B	236	TYR	5.1
2	B	386	SER	4.9
2	B	862	TYR	4.8
2	A	456	ALA	4.2
2	B	403	ALA	4.0
2	B	920	ARG	4.0
2	A	457	VAL	3.9
2	B	895	GLU	3.8
2	B	891	MET	3.7
2	A	869	TRP	3.7
2	B	869	TRP	3.7
2	B	265	VAL	3.7
2	A	406	HIS	3.6
2	A	455	ARG	3.6
2	B	583	LYS	3.5
1	D	909	U	3.5
2	B	457	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	167	PHE	3.3
2	B	291	LEU	3.3
2	B	887	MET	3.3
2	B	405	TYR	3.3
2	B	310	ALA	3.3
1	D	988	A	3.2
2	A	915	THR	3.2
2	A	586	ILE	3.2
1	D	986	C	3.1
2	B	255	ARG	3.1
2	B	784	ARG	3.1
2	B	280	ILE	3.0
2	A	404	GLU	3.0
2	A	291	LEU	3.0
2	A	450	SER	2.9
2	B	300	VAL	2.9
2	B	387	GLN	2.8
2	B	929	GLU	2.8
2	B	263	TRP	2.8
2	B	938	LEU	2.8
1	D	907	G	2.8
2	B	966	ILE	2.7
2	B	264	ILE	2.7
2	B	883	PHE	2.7
2	B	238	VAL	2.7
2	B	399	THR	2.7
2	A	447	ASN	2.6
2	A	448	VAL	2.6
2	A	191	THR	2.6
2	A	917	ASP	2.6
2	B	455	ARG	2.6
2	B	381	LYS	2.6
2	B	865	THR	2.6
1	C	987	C	2.5
2	A	862	TYR	2.5
2	B	242	TRP	2.4
2	B	355	ILE	2.4
1	C	986	C	2.4
2	B	453	GLY	2.4
2	B	870	LYS	2.4
2	A	449	ILE	2.4
2	A	868	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
2	A	502	TRP	2.4
2	B	919	LYS	2.4
2	B	353	PRO	2.3
2	B	400	ILE	2.3
2	A	584	THR	2.3
2	B	964	ILE	2.3
2	B	279	GLU	2.3
2	B	286	PHE	2.3
1	D	940	G	2.3
2	B	323	MET	2.3
2	B	354	ARG	2.2
2	B	404	GLU	2.2
2	B	352	ASP	2.2
2	B	458	ILE	2.2
2	B	251	LYS	2.2
2	B	967	GLU	2.2
2	B	409	ILE	2.2
1	C	939	A	2.2
1	C	988	A	2.2
2	B	346	LEU	2.1
2	A	452	PHE	2.1
2	B	319	THR	2.1
2	A	190	GLY	2.1
2	A	206	ILE	2.1
2	A	890	LEU	2.1
2	A	195	ASP	2.1
2	A	194	GLY	2.1
2	A	384	ILE	2.1
2	A	881	ARG	2.0
1	C	936	U	2.0
2	B	464	GLN	2.0
2	A	184	ARG	2.0
2	B	382	LEU	2.0
2	A	349	TYR	2.0

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 [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.