



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2017 – 04:31 PM EDT

PDB ID : 2R92
Title : Elongation complex of RNA polymerase II with artificial RdRP scaffold
Authors : Lehmann, E.; Brueckner, F.; Cramer, P.
Deposited on : unknown
Resolution : 3.80 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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

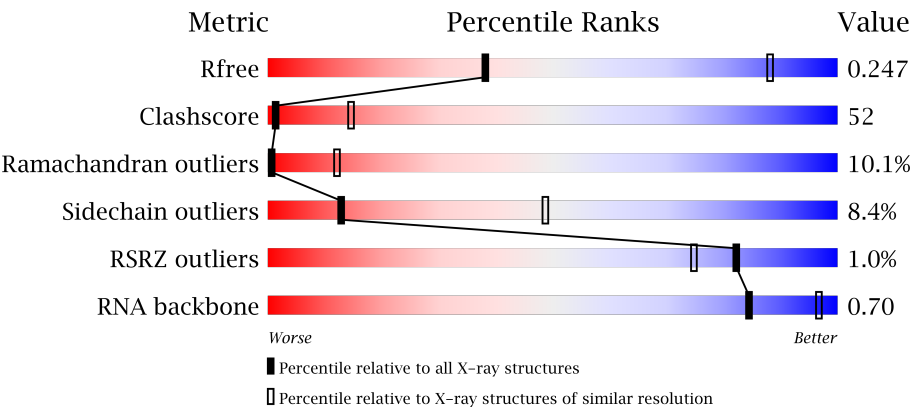
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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.



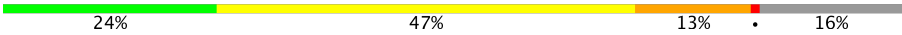
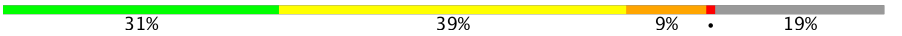


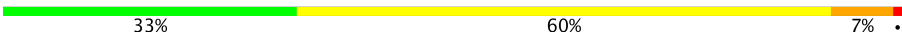
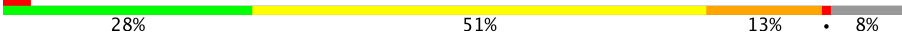
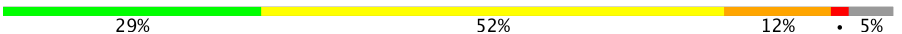
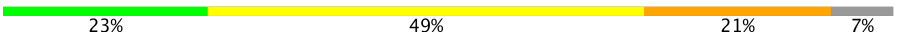
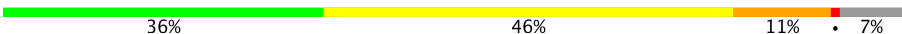

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1019 (4.08-3.52)
Clashscore	112137	1030 (4.04-3.56)
Ramachandran outliers	110173	1011 (4.06-3.54)
Sidechain outliers	110143	1005 (4.06-3.54)
RSRZ outliers	101464	1032 (4.08-3.52)
RNA backbone	2435	1016 (4.70-2.90)

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	P	16	<div><div>13%</div><div>13%38%6%44%</div></div>
2	T	17	<div><div>41%</div><div>6%29%6%18%41%</div></div>
3	A	1733	<div><div>27%44%9%18%</div></div>
4	B	1224	<div><div>%</div><div>27%53%10%9%</div></div>

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Mol	Chain	Length	Quality of chain
5	C	318	
6	D	221	
7	E	215	
8	F	155	
9	G	171	
10	H	146	
11	I	122	
12	J	70	
13	K	120	
14	L	70	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 31611 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 RNA (5'-R(*UP*GP*CP*AP*UP*AP*AP*AP*GP*AP*CP*CP*AP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	9	Total	C	N	O	P	0	0	0
			192	87	39	58	8			

- Molecule 2 is a RNA chain called RNA (5'-R(*CP*UP*UP*GP*AP*CP*GP*CP*CP*UP*GP*GP*UP*CP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	10	Total	C	N	O	P	0	0	0
			208	94	36	69	9			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	1422	Total	C	N	O	S	0	0	0
			11194	7054	1959	2119	62			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	1112	Total	C	N	O	S	0	0	0
			8841	5596	1550	1640	55			

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	267	Total	C	N	O	S	0	0	0
			2101	1320	349	419	13			

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	178	Total	C	N	O	S	0	0	0
			1434	887	257	288	2			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	88	Total	C	N	O	S	0	0	0
			712	455	120	134	3			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	171	Total	C	N	O	S	0	0	0
			1340	861	222	249	8			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	135	Total	C	N	O	S	0	0	0
			1084	683	183	214	4			

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	116	Total	C	N	O	S	0	0	0
			944	581	172	181	10			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	112	Total	C	N	O	S	0	0	0
			904	580	154	168	2			

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	46	Total	C	N	O	S	0	0	0
			364	224	72	64	4			

- Molecule 15 is ZINC ION (three-letter code: ZN) (formula: Zn).

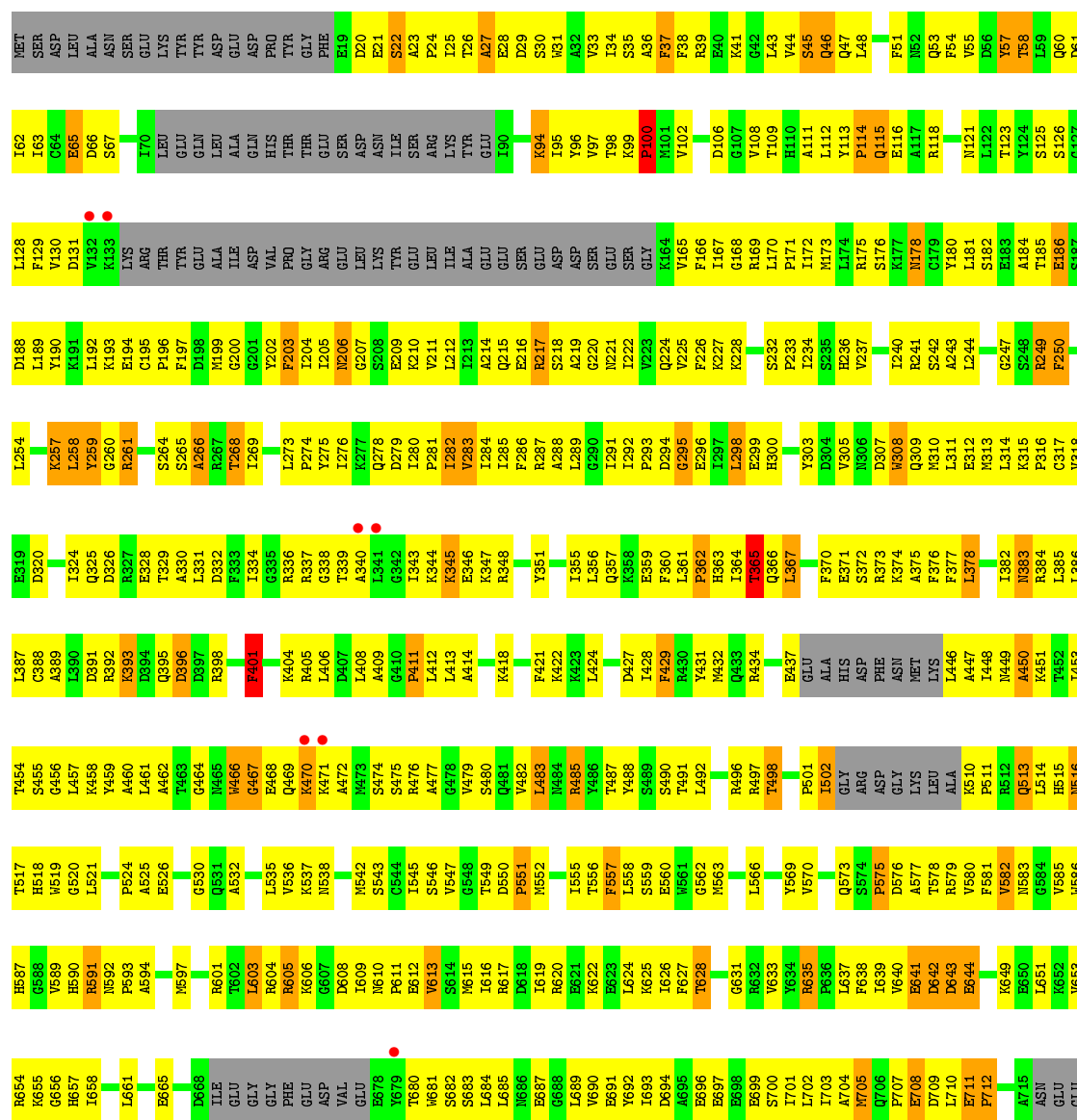
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	J	1	Total	Zn	0	0
			1	1		
15	B	1	Total	Zn	0	0
			1	1		
15	I	2	Total	Zn	0	0
			2	2		
15	C	1	Total	Zn	0	0
			1	1		
15	A	2	Total	Zn	0	0
			2	2		
15	L	1	Total	Zn	0	0
			1	1		

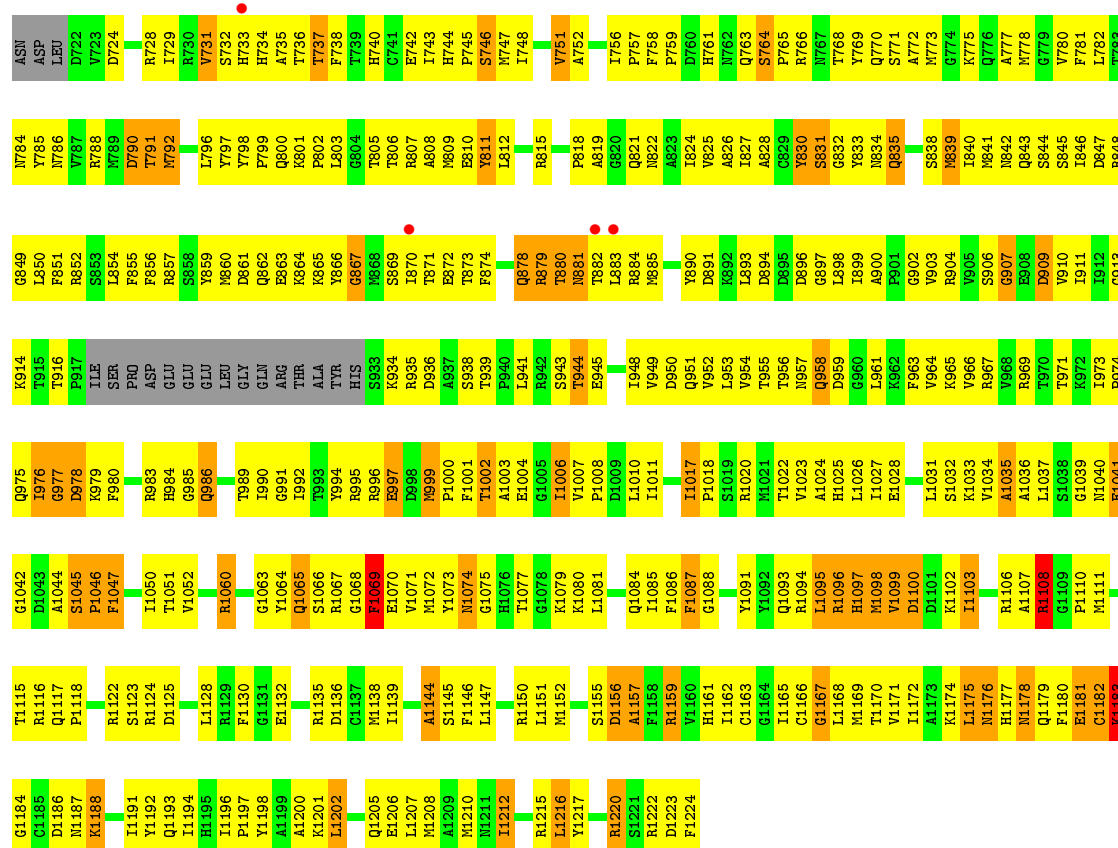
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	1	Total	Mg	0	0
			1	1		

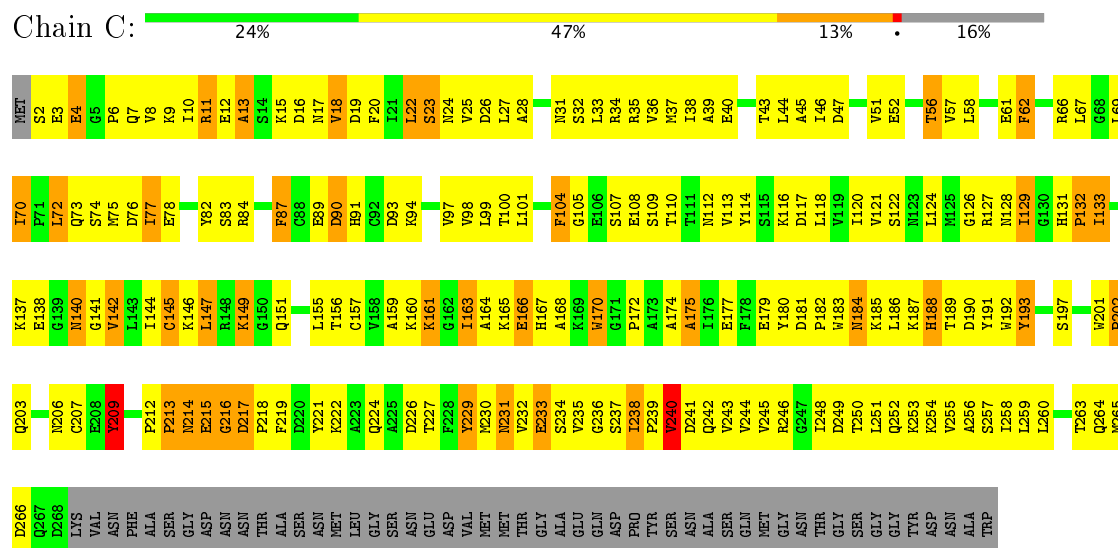


- Molecule 4: DNA-directed RNA polymerase II subunit RPB2

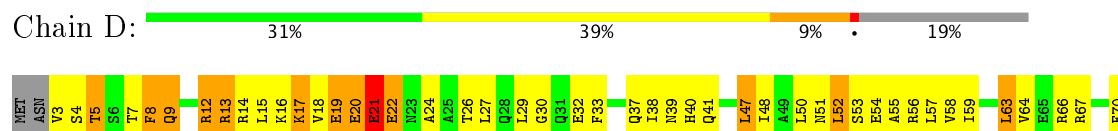


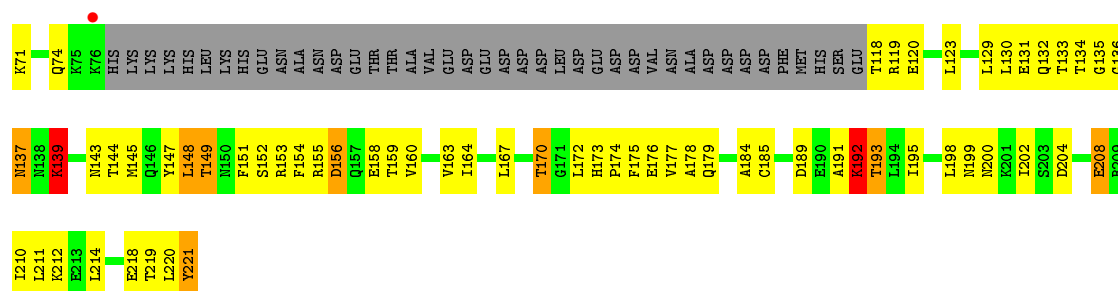


• Molecule 5: DNA-directed RNA polymerase II subunit RPB3

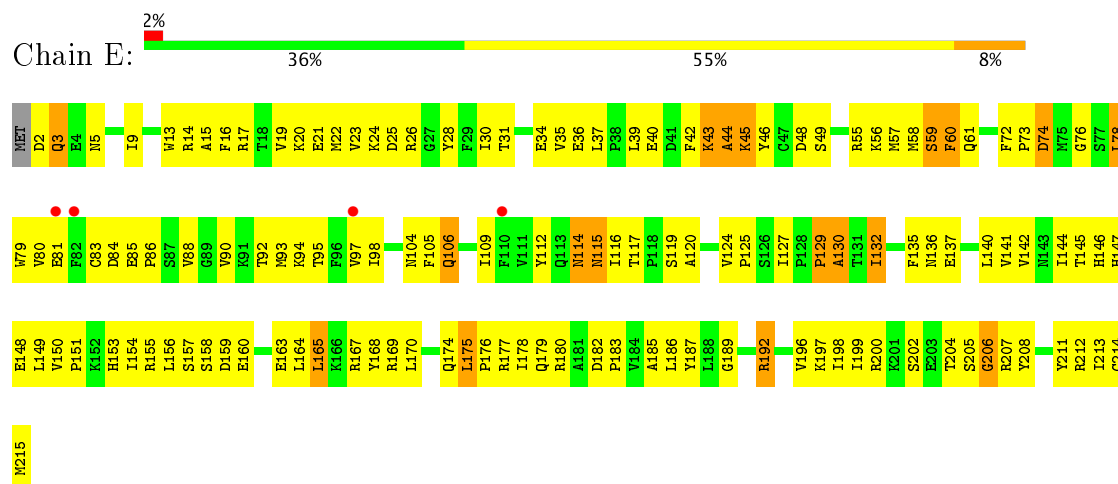


• Molecule 6: DNA-directed RNA polymerase II subunit RPB4

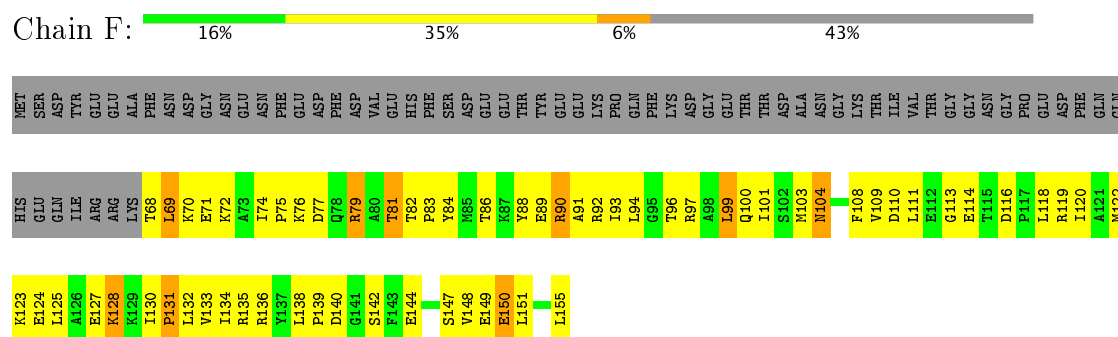




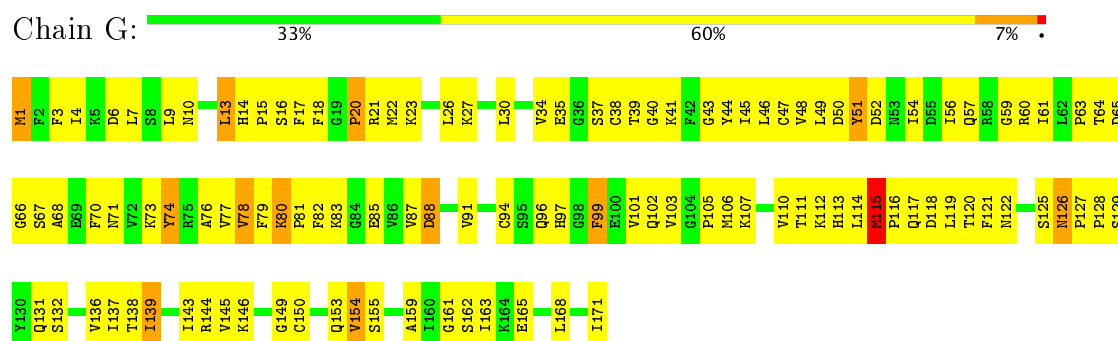
- Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1



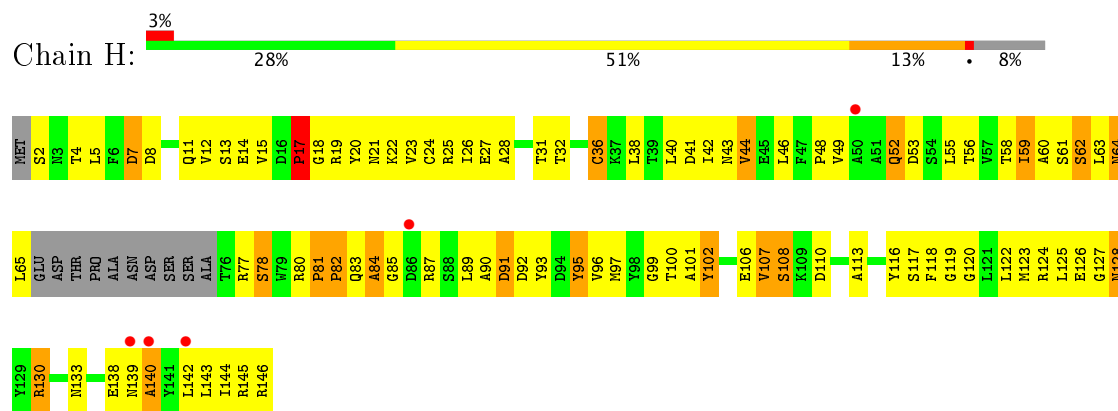
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC2



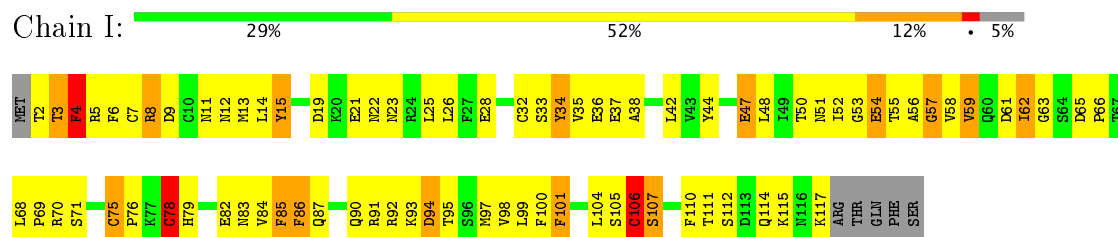
- Molecule 9: DNA-directed RNA polymerase II subunit RPB7



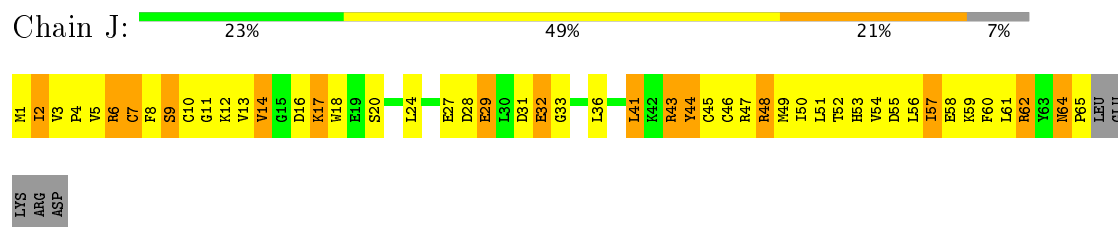
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3



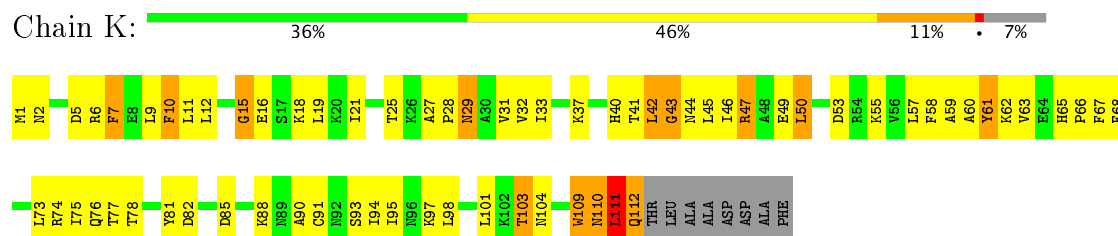
- Molecule 11: DNA-directed RNA polymerase II subunit RPB9



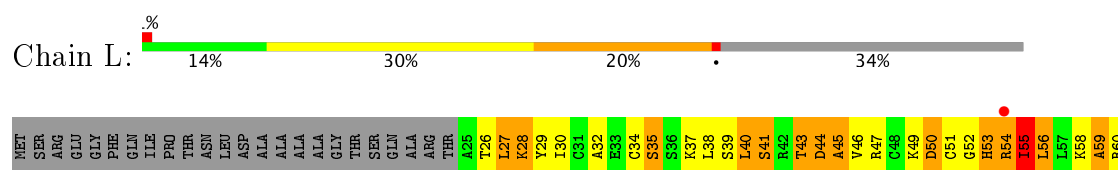
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC5

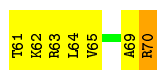


- Molecule 13: DNA-directed RNA polymerase II subunit RPB11



- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC4





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	222.68Å 393.85Å 283.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.80 48.51 – 3.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.80) 99.9 (48.51-3.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.44 (at 3.77Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.212 , 0.246 0.217 , 0.247	Depositor DCC
R_{free} test set	2431 reflections (1.99%)	DCC
Wilson B-factor (Å ²)	114.7	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 67.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.038 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.037 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	31611	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	P	0.63	0/215	0.81	0/334
2	T	0.71	0/231	1.32	5/358 (1.4%)
3	A	0.42	0/11394	0.73	7/15407 (0.0%)
4	B	0.41	0/9012	0.68	1/12149 (0.0%)
5	C	0.43	0/2138	0.71	0/2896
6	D	0.39	0/1444	0.66	0/1935
7	E	0.39	0/1788	0.63	0/2406
8	F	0.45	0/724	0.76	0/977
9	G	0.45	0/1368	0.72	0/1844
10	H	0.37	0/1102	0.62	0/1492
11	I	0.38	0/962	0.65	0/1295
12	J	0.47	0/541	0.75	0/727
13	K	0.45	0/922	0.68	0/1244
14	L	0.46	0/366	0.69	0/485
All	All	0.42	0/32207	0.71	13/43549 (0.0%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1176	LEU	CA-CB-CG	13.45	146.23	115.30
2	T	12	G	N9-C1'-C2'	9.04	125.76	114.00
2	T	12	G	O4'-C1'-N9	8.14	114.72	108.20
2	T	13	U	O4'-C1'-N1	7.87	114.50	108.20
3	A	1176	LEU	CB-CA-C	-7.05	96.81	110.20
3	A	1177	LEU	N-CA-C	-6.94	92.26	111.00
2	T	14	C	O4'-C1'-N1	6.57	113.45	108.20
3	A	452	LYS	N-CA-C	-6.12	94.48	111.00
3	A	1176	LEU	CA-C-O	5.52	131.68	120.10
2	T	13	U	N1-C1'-C2'	5.32	120.91	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1176	LEU	CA-C-N	-5.30	105.53	117.20
4	B	111	ALA	N-CA-C	-5.22	96.91	111.00
3	A	567	LYS	C-N-CD	5.02	138.94	128.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	192	0	101	6	0
2	T	208	0	110	16	0
3	A	11194	0	11278	1259	0
4	B	8841	0	8874	1006	0
5	C	2101	0	2055	275	0
6	D	1434	0	1460	146	0
7	E	1752	0	1776	163	0
8	F	712	0	738	89	0
9	G	1340	0	1357	182	0
10	H	1084	0	1057	140	0
11	I	944	0	903	120	0
12	J	532	0	542	90	0
13	K	904	0	911	93	0
14	L	364	0	388	54	0
15	A	2	0	0	0	0
15	B	1	0	0	0	0
15	C	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	L	1	0	0	0	0
16	A	1	0	0	0	0
All	All	31611	0	31550	3310	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 52.

All (3310) 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)
3:A:58:LEU:HD12	3:A:59:GLY:H	0.99	1.11
4:B:343:ILE:HG23	4:B:347:LYS:HB2	1.25	1.09
4:B:510:LYS:HG2	4:B:511:PRO:HD3	1.22	1.08
3:A:53:LEU:HD23	3:A:54:ASN:N	1.68	1.08
5:C:43:THR:HG22	5:C:44:LEU:H	0.98	1.07
6:D:40:HIS:HB3	9:G:73:LYS:HZ3	1.12	1.06
3:A:63:ARG:HA	3:A:74:MET:HE1	1.32	1.05
3:A:868:TYR:CE1	3:A:1064:VAL:HG11	1.90	1.05
12:J:5:VAL:HG12	12:J:6:ARG:HG3	1.39	1.05
4:B:589:VAL:HG12	4:B:590:HIS:H	1.20	1.04
4:B:882:THR:HG22	4:B:884:ARG:H	1.18	1.04
4:B:521:LEU:HD22	4:B:633:VAL:HG12	1.38	1.03
7:E:94:LYS:HE2	7:E:98:ILE:HD11	1.35	1.03
4:B:273:LEU:HB2	4:B:276:ILE:HD12	1.37	1.02
4:B:37:PHE:HE1	4:B:41:LYS:HG3	1.25	1.02
3:A:901:LEU:H	3:A:926:GLN:NE2	1.55	1.02
3:A:254:GLU:HB2	4:B:935:ARG:HH12	1.25	1.02
10:H:100:THR:HG23	10:H:138:GLU:HA	1.40	1.02
3:A:53:LEU:HD23	3:A:54:ASN:H	0.89	1.00
11:I:115:LYS:HD3	11:I:117:LYS:HE3	1.40	0.99
3:A:1161:THR:HG22	3:A:1163:ILE:H	1.25	0.98
3:A:1329:THR:HG22	3:A:1331:SER:H	1.27	0.98
4:B:583:ASN:HD21	4:B:628:THR:HG22	1.26	0.98
9:G:15:PRO:HA	9:G:18:PHE:CD1	1.99	0.97
3:A:34:LYS:HE2	3:A:57:ARG:HH22	1.28	0.97
4:B:37:PHE:CE1	4:B:41:LYS:HG3	1.98	0.97
3:A:567:LYS:CG	3:A:568:PRO:HD2	1.96	0.96
3:A:225:ASN:HD22	3:A:228:PHE:H	1.08	0.96
5:C:43:THR:HG22	5:C:44:LEU:N	1.80	0.96
10:H:4:THR:HA	10:H:60:ALA:HB2	1.42	0.96
3:A:754:SER:H	3:A:757:ASN:HD22	1.00	0.95
4:B:287:ARG:HG2	4:B:292:ILE:HA	1.46	0.95
3:A:446:ARG:HD3	3:A:480:ALA:HB2	1.48	0.95
9:G:138:THR:HG22	9:G:139:ILE:H	1.32	0.95
4:B:364:ILE:HG12	4:B:585:VAL:HG13	1.44	0.95
12:J:64:ASN:HB3	12:J:65:PRO:CD	1.97	0.95
3:A:1063:MET:SD	3:A:1436:ILE:HG12	2.07	0.95
4:B:1072:MET:CE	4:B:1085:ILE:HB	1.97	0.94
11:I:34:TYR:HD2	11:I:35:VAL:N	1.63	0.94
3:A:58:LEU:HD12	3:A:59:GLY:N	1.82	0.94
3:A:779:PHE:HE1	3:A:785:PRO:HD3	1.29	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:49:GLU:HG3	13:K:94:ILE:HG12	1.49	0.94
3:A:855:THR:HG21	3:A:857:ARG:HE	1.32	0.93
2:T:13:U:O2'	2:T:14:C:O5'	1.84	0.93
5:C:43:THR:CG2	5:C:44:LEU:H	1.82	0.93
6:D:40:HIS:HB3	9:G:73:LYS:NZ	1.84	0.93
4:B:1002:THR:HG23	4:B:1006:ILE:HG13	1.50	0.93
3:A:767:GLN:NE2	3:A:774:ARG:HB3	1.84	0.93
6:D:56:ARG:HB2	6:D:148:LEU:HD22	1.50	0.93
14:L:32:ALA:HB3	14:L:55:ILE:HD12	1.51	0.93
3:A:535:THR:HG21	3:A:616:VAL:HA	1.49	0.92
5:C:47:ASP:HA	14:L:69:ALA:HB3	1.52	0.92
4:B:999:MET:HG3	4:B:1000:PRO:HD2	1.52	0.92
5:C:57:VAL:HG11	12:J:60:PHE:HB3	1.49	0.92
3:A:58:LEU:CD1	3:A:59:GLY:H	1.83	0.92
5:C:39:ALA:HA	5:C:164:ALA:HB3	1.48	0.92
10:H:130:ARG:H	10:H:130:ARG:HD2	1.35	0.92
4:B:746:SER:HB2	4:B:1046:PRO:HG2	1.51	0.91
4:B:806:THR:HG22	4:B:808:ALA:H	1.33	0.91
6:D:17:LYS:HE3	6:D:17:LYS:HA	1.52	0.91
3:A:1127:ASP:HB3	3:A:1130:GLN:HB3	1.52	0.91
4:B:336:ARG:HG2	4:B:348:ARG:HD3	1.50	0.91
7:E:19:VAL:O	7:E:23:VAL:HG23	1.71	0.91
4:B:637:LEU:HD12	4:B:693:ILE:HD12	1.53	0.90
3:A:903:ASN:HD22	3:A:904:THR:N	1.69	0.90
3:A:1438:THR:HB	4:B:1144:ALA:HB3	1.50	0.90
4:B:172:ILE:HD13	4:B:178:ASN:HB3	1.51	0.90
12:J:1:MET:H1	12:J:57:ILE:H	0.93	0.90
3:A:1445:ILE:H	3:A:1445:ILE:HD12	1.37	0.90
3:A:563:PRO:HG3	3:A:572:TRP:CZ2	2.07	0.90
4:B:247:GLY:H	4:B:418:LYS:NZ	1.70	0.90
3:A:53:LEU:CD2	3:A:54:ASN:H	1.82	0.89
4:B:1177:HIS:HB2	4:B:1179:GLN:HE21	1.35	0.89
4:B:510:LYS:HG2	4:B:511:PRO:CD	2.02	0.89
5:C:32:SER:O	5:C:36:VAL:HG23	1.72	0.89
4:B:1159:ARG:HD3	4:B:1193:GLN:HG3	1.54	0.89
3:A:1004:ASN:ND2	7:E:167:ARG:HD2	1.86	0.89
12:J:16:ASP:OD1	12:J:17:LYS:HD2	1.72	0.89
3:A:399:HIS:HB3	3:A:400:PRO:HD3	1.53	0.89
4:B:879:ARG:NH1	4:B:883:LEU:HD22	1.85	0.89
4:B:800:GLN:HB3	12:J:52:THR:HG21	1.54	0.89
12:J:3:VAL:HG21	12:J:18:TRP:HB2	1.51	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:39:THR:HG22	9:G:40:GLY:H	1.37	0.88
3:A:658:LEU:HD13	4:B:831:SER:H	1.37	0.88
3:A:19:PHE:O	3:A:1416:ALA:HA	1.73	0.88
4:B:549:THR:HG22	4:B:550:ASP:H	1.37	0.88
4:B:577:ALA:HB1	4:B:589:VAL:HG11	1.56	0.88
3:A:567:LYS:HB3	10:H:96:VAL:H	1.38	0.88
3:A:901:LEU:H	3:A:926:GLN:HE21	0.90	0.88
12:J:64:ASN:HB3	12:J:65:PRO:HD3	1.56	0.88
3:A:567:LYS:CD	3:A:568:PRO:HD2	2.04	0.87
4:B:515:HIS:H	4:B:518:HIS:HD2	1.22	0.87
9:G:111:THR:HG22	9:G:113:HIS:H	1.37	0.87
3:A:763:ALA:O	3:A:803:SER:HB3	1.74	0.87
11:I:26:LEU:HD23	11:I:37:GLU:HA	1.53	0.87
7:E:180:ARG:HH21	7:E:192:ARG:HB2	1.38	0.87
3:A:93:VAL:HG13	3:A:301:ALA:HB1	1.57	0.86
5:C:101:LEU:HD13	5:C:118:LEU:HD23	1.58	0.86
6:D:144:THR:O	6:D:148:LEU:HB2	1.73	0.86
3:A:356:ASP:HB2	3:A:469:ARG:NH1	1.89	0.86
4:B:467:GLY:H	4:B:475:SER:HB3	1.37	0.86
3:A:590:ARG:NH2	3:A:620:LYS:HB3	1.91	0.86
13:K:47:ARG:HB3	13:K:47:ARG:HH11	1.41	0.86
9:G:26:LEU:HD12	9:G:56:ILE:HD13	1.58	0.85
3:A:963:ILE:HD11	3:A:1048:ASN:HB3	1.58	0.85
5:C:164:ALA:HA	5:C:167:HIS:O	1.75	0.85
3:A:868:TYR:HE1	3:A:1064:VAL:HG11	1.38	0.85
5:C:166:GLU:HG3	13:K:10:PHE:HZ	1.42	0.85
3:A:1345:ARG:HG3	3:A:1376:THR:HG21	1.58	0.85
1:P:9:G:H2'	1:P:10:A:C8	2.12	0.85
13:K:65:HIS:HD2	13:K:67:PHE:H	1.24	0.85
11:I:34:TYR:CD2	11:I:35:VAL:N	2.45	0.85
11:I:85:PHE:HD2	11:I:85:PHE:H	1.25	0.85
4:B:1072:MET:HE1	4:B:1085:ILE:HB	1.59	0.84
4:B:112:LEU:HD12	4:B:113:TYR:H	1.40	0.84
5:C:6:PRO:HB3	5:C:25:VAL:HG12	1.57	0.84
3:A:560:ILE:HG13	10:H:78:SER:HB2	1.59	0.84
9:G:7:LEU:HB2	9:G:74:TYR:CE2	2.11	0.84
3:A:164:ARG:HG3	3:A:165:GLY:H	1.42	0.84
3:A:33:ALA:HB1	3:A:56:PRO:HB2	1.58	0.84
3:A:40:THR:HG22	3:A:41:MET:HG3	1.56	0.84
4:B:879:ARG:HH11	4:B:883:LEU:HD22	1.39	0.84
5:C:99:LEU:HD12	5:C:118:LEU:HB3	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:44:LEU:HB2	5:C:77:ILE:HD11	1.57	0.84
7:E:198:ILE:HD11	7:E:212:ARG:HG3	1.60	0.84
3:A:308:ILE:HG22	3:A:309:ALA:H	1.42	0.84
4:B:343:ILE:CG2	4:B:347:LYS:HB2	2.07	0.84
3:A:1017:LEU:HB2	7:E:206:GLY:H	1.41	0.84
3:A:265:LYS:HD2	3:A:265:LYS:H	1.42	0.83
3:A:901:LEU:N	3:A:926:GLN:HE21	1.75	0.83
4:B:1201:LYS:HE2	4:B:1205:GLN:OE1	1.78	0.83
12:J:1:MET:H1	12:J:57:ILE:N	1.74	0.83
9:G:143:ILE:HG22	9:G:144:ARG:N	1.93	0.83
5:C:98:VAL:O	5:C:99:LEU:HD22	1.78	0.83
4:B:212:LEU:HD23	4:B:480:SER:HB2	1.59	0.83
3:A:34:LYS:HE2	3:A:57:ARG:NH2	1.93	0.83
3:A:899:VAL:HB	3:A:929:LEU:HD11	1.61	0.83
3:A:1420:ASP:HB3	3:A:1422:ARG:HG3	1.59	0.83
3:A:699:ALA:HB1	11:I:114:GLN:HB2	1.58	0.83
5:C:77:ILE:HG23	5:C:161:LYS:HE3	1.61	0.82
9:G:1:MET:SD	9:G:79:PHE:HD1	2.03	0.82
9:G:138:THR:HG22	9:G:139:ILE:N	1.92	0.82
8:F:99:LEU:O	8:F:103:MET:HG2	1.80	0.82
6:D:40:HIS:CB	9:G:73:LYS:NZ	2.41	0.82
4:B:613:VAL:HG13	4:B:627:PHE:O	1.79	0.82
4:B:770:GLN:OE1	4:B:983:ARG:HA	1.78	0.82
13:K:21:ILE:HG12	13:K:33:ILE:HG12	1.59	0.82
3:A:265:LYS:HD2	3:A:265:LYS:N	1.94	0.82
6:D:47:LEU:HD13	6:D:48:ILE:N	1.95	0.81
8:F:93:ILE:HD11	8:F:134:ILE:HD11	1.59	0.81
3:A:1424:VAL:HG11	4:B:1139:ILE:HD13	1.61	0.81
11:I:8:ARG:HG3	11:I:34:TYR:HE1	1.44	0.81
11:I:75:CYS:HG	11:I:78:CYS:HG	1.23	0.81
3:A:913:LEU:HD12	3:A:914:GLU:H	1.46	0.81
5:C:239:PRO:HB2	5:C:241:ASP:OD1	1.81	0.81
3:A:1325:THR:O	7:E:148:GLU:HB2	1.79	0.81
3:A:779:PHE:CE1	3:A:785:PRO:HD3	2.15	0.81
4:B:121:ASN:HA	4:B:207:GLY:HA2	1.61	0.81
3:A:58:LEU:HD11	3:A:243:PRO:HB3	1.61	0.81
3:A:34:LYS:CE	3:A:57:ARG:HH12	1.92	0.81
3:A:666:ILE:HD12	3:A:667:GLY:H	1.46	0.81
4:B:115:GLN:HG2	4:B:193:LYS:HB2	1.63	0.81
6:D:134:THR:HG22	6:D:135:GLY:N	1.95	0.81
3:A:679:ILE:HG12	3:A:732:LEU:HD12	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1028:THR:O	3:A:1032:LEU:HD12	1.79	0.81
4:B:654:ARG:H	4:B:657:HIS:HD2	1.28	0.81
3:A:442:VAL:HB	3:A:489:LEU:HD11	1.61	0.81
3:A:451:HIS:CD2	3:A:1074:GLU:HG3	2.16	0.81
3:A:225:ASN:ND2	3:A:228:PHE:H	1.79	0.81
3:A:1312:ASN:O	3:A:1316:VAL:HG23	1.81	0.81
3:A:518:LYS:HE2	3:A:624:SER:O	1.80	0.80
4:B:35:SER:O	4:B:39:ARG:HG3	1.82	0.80
4:B:778:MET:CE	4:B:1094:ARG:HD3	2.10	0.80
4:B:1007:VAL:HG22	4:B:1008:PRO:HD2	1.63	0.80
7:E:16:PHE:CZ	7:E:20:LYS:HE2	2.15	0.80
9:G:1:MET:SD	9:G:79:PHE:CD1	2.75	0.80
3:A:598:LEU:HA	10:H:122:LEU:HD13	1.64	0.80
3:A:629:LEU:O	3:A:633:VAL:HG23	1.82	0.80
3:A:1189:SER:O	3:A:1241:ARG:HD3	1.82	0.80
5:C:238:ILE:HG23	5:C:242:GLN:HB2	1.63	0.80
10:H:93:TYR:HB3	10:H:144:ILE:O	1.82	0.80
11:I:8:ARG:HG3	11:I:34:TYR:CE1	2.17	0.80
3:A:1120:LEU:HD12	3:A:1120:LEU:N	1.98	0.79
4:B:902:GLY:O	14:L:65:VAL:HG11	1.82	0.79
3:A:567:LYS:HD2	3:A:568:PRO:HD2	1.63	0.79
4:B:22:SER:HA	4:B:654:ARG:CB	2.11	0.79
5:C:66:ARG:NH1	12:J:2:ILE:HG21	1.97	0.79
3:A:70:CYS:O	3:A:72:GLU:HG2	1.82	0.79
4:B:370:PHE:HE2	4:B:373:ARG:HH11	1.31	0.79
8:F:86:THR:OG1	8:F:89:GLU:HG3	1.83	0.79
9:G:49:LEU:HD21	9:G:77:VAL:HG23	1.65	0.79
4:B:882:THR:HG22	4:B:884:ARG:N	1.98	0.79
9:G:127:PRO:HG2	9:G:138:THR:HG21	1.63	0.79
3:A:868:TYR:HD2	3:A:1058:VAL:HG21	1.45	0.79
3:A:577:ILE:O	3:A:580:VAL:HG23	1.82	0.79
6:D:159:THR:O	6:D:163:VAL:HG23	1.82	0.79
8:F:69:LEU:C	8:F:71:GLU:H	1.83	0.79
3:A:58:LEU:HD11	3:A:243:PRO:CB	2.12	0.78
3:A:855:THR:HG21	3:A:857:ARG:NE	1.98	0.78
3:A:567:LYS:HD3	10:H:95:TYR:CD2	2.18	0.78
3:A:244:PRO:HG2	3:A:245:PRO:HD3	1.64	0.78
4:B:467:GLY:N	4:B:475:SER:HB3	1.97	0.78
7:E:22:MET:HE3	7:E:26:ARG:HE	1.46	0.78
4:B:23:ALA:HB1	4:B:24:PRO:HD2	1.66	0.78
4:B:899:ILE:HD11	4:B:911:ILE:HA	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:13:LEU:HD21	9:G:17:PHE:HB2	1.64	0.78
13:K:49:GLU:HG3	13:K:94:ILE:CG1	2.13	0.78
4:B:65:GLU:HG3	4:B:66:ASP:H	1.48	0.78
4:B:1183:LYS:HE3	4:B:1183:LYS:N	1.99	0.78
4:B:622:LYS:HE2	11:I:59:VAL:HG22	1.65	0.78
4:B:955:THR:HG22	4:B:956:THR:N	1.97	0.77
9:G:122:ASN:ND2	9:G:125:SER:HB3	1.99	0.77
13:K:40:HIS:HD1	13:K:61:TYR:HH	1.24	0.77
9:G:34:VAL:HG12	9:G:45:ILE:HG21	1.64	0.77
3:A:665:GLY:O	3:A:667:GLY:N	2.18	0.77
3:A:709:THR:HG22	3:A:711:ARG:H	1.49	0.77
4:B:906:SER:O	4:B:941:LEU:HD23	1.85	0.77
3:A:858:ASN:HD22	3:A:858:ASN:C	1.84	0.77
4:B:1095:LEU:HD12	4:B:1095:LEU:H	1.49	0.77
6:D:153:ARG:NH2	6:D:184:ALA:HA	2.00	0.77
12:J:36:LEU:HD22	12:J:41:LEU:HD12	1.66	0.77
4:B:579:ARG:HB2	4:B:586:TRP:NE1	1.99	0.77
4:B:860:MET:HB2	4:B:965:LYS:HG2	1.67	0.77
3:A:23:SER:HA	3:A:233:TRP:NE1	2.00	0.77
3:A:381:THR:HG23	3:A:383:TYR:H	1.50	0.77
5:C:18:VAL:O	5:C:18:VAL:HG12	1.84	0.77
3:A:866:PHE:C	3:A:867:ILE:HD12	2.06	0.77
4:B:232:SER:HB3	4:B:261:ARG:HH21	1.50	0.77
4:B:580:VAL:HG22	4:B:624:LEU:HB3	1.66	0.77
4:B:1072:MET:HE3	4:B:1085:ILE:HB	1.65	0.77
4:B:801:LYS:O	12:J:52:THR:HG23	1.84	0.77
4:B:516:ASN:N	4:B:516:ASN:HD22	1.80	0.76
7:E:124:VAL:HG13	7:E:132:ILE:HD12	1.67	0.76
3:A:1032:LEU:O	3:A:1036:ARG:HD3	1.85	0.76
3:A:1341:ILE:HD12	3:A:1379:GLY:O	1.85	0.76
3:A:332:LYS:HG3	3:A:333:GLU:HG2	1.67	0.76
3:A:61:ILE:HG22	3:A:62:ASP:H	1.49	0.76
4:B:502:ILE:H	4:B:502:ILE:HD12	1.48	0.76
6:D:39:ASN:HD21	6:D:41:GLN:NE2	1.82	0.76
3:A:384:ASN:OD1	3:A:388:LEU:HD12	1.85	0.76
7:E:192:ARG:HH11	7:E:192:ARG:HG3	1.50	0.76
12:J:43:ARG:HG3	12:J:45:CYS:SG	2.26	0.76
3:A:902:LEU:HG	3:A:926:GLN:HG3	1.67	0.76
4:B:515:HIS:HD2	4:B:517:THR:H	1.31	0.76
4:B:22:SER:HA	4:B:654:ARG:HB3	1.66	0.76
13:K:65:HIS:CD2	13:K:67:PHE:H	2.04	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:216:GLU:OE1	4:B:537:LYS:HE2	1.85	0.76
4:B:589:VAL:HG12	4:B:590:HIS:N	2.00	0.76
5:C:241:ASP:O	5:C:245:VAL:HG23	1.86	0.76
9:G:88:ASP:HB3	9:G:144:ARG:HA	1.68	0.76
3:A:1002:GLY:HA3	3:A:1007:ILE:HG21	1.67	0.76
3:A:738:LYS:HB2	3:A:740:LEU:HG	1.67	0.76
3:A:768:GLN:HG2	3:A:816:HIS:HA	1.66	0.76
4:B:882:THR:CG2	4:B:884:ARG:HB2	2.16	0.76
4:B:1202:LEU:O	4:B:1206:GLU:HG3	1.85	0.75
6:D:173:HIS:O	6:D:177:VAL:HG23	1.86	0.75
4:B:1065:GLN:HE21	4:B:1067:ARG:N	1.84	0.75
4:B:1065:GLN:HE21	4:B:1067:ARG:H	1.34	0.75
4:B:806:THR:HG22	4:B:808:ALA:N	2.00	0.75
3:A:93:VAL:HG22	3:A:301:ALA:HA	1.68	0.75
3:A:821:ARG:HH11	3:A:821:ARG:HB2	1.51	0.75
3:A:87:ALA:CB	3:A:276:LEU:HD23	2.17	0.75
4:B:642:ASP:HB3	4:B:649:LYS:HD2	1.69	0.75
3:A:164:ARG:HG3	3:A:165:GLY:N	2.01	0.75
4:B:114:PRO:HG2	4:B:115:GLN:H	1.51	0.75
4:B:798:TYR:HE2	5:C:62:PHE:CE2	2.04	0.75
7:E:202:SER:HB3	7:E:205:SER:O	1.86	0.75
3:A:1329:THR:HG22	3:A:1331:SER:N	2.01	0.75
3:A:1332:PHE:H	3:A:1332:PHE:HD2	1.34	0.75
3:A:321:PRO:O	3:A:322:VAL:HB	1.87	0.75
3:A:382:PRO:HB3	3:A:428:TYR:HE2	1.50	0.75
3:A:567:LYS:HG3	3:A:568:PRO:HD2	1.67	0.75
4:B:1163:CYS:SG	4:B:1165:ILE:HB	2.25	0.75
4:B:611:PRO:HB3	4:B:685:LEU:HD11	1.68	0.75
6:D:12:ARG:HG2	6:D:14:ARG:HG3	1.69	0.75
2:T:12:G:O2'	2:T:13:U:O5'	2.02	0.75
3:A:699:ALA:HB3	3:A:701:LEU:HG	1.68	0.74
4:B:800:GLN:HB3	12:J:52:THR:CG2	2.17	0.74
3:A:249:SER:O	3:A:250:ILE:HG13	1.87	0.74
4:B:1162:ILE:HD11	4:B:1194:ILE:HD13	1.67	0.74
3:A:34:LYS:CE	3:A:57:ARG:HH22	2.00	0.74
3:A:69:THR:O	3:A:71:GLN:N	2.20	0.74
4:B:758:PHE:CE1	4:B:1027:ILE:HG22	2.22	0.74
11:I:34:TYR:HE2	11:I:36:GLU:HB3	1.52	0.74
3:A:351:THR:HB	4:B:1103:ILE:HD12	1.70	0.74
4:B:642:ASP:HA	4:B:649:LYS:HA	1.67	0.74
10:H:102:TYR:OH	10:H:122:LEU:HD22	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:59:ILE:HG22	10:H:60:ALA:N	2.01	0.74
3:A:853:ASP:O	3:A:854:ASN:HB2	1.86	0.74
3:A:337:ARG:HD3	4:B:1132:GLU:OE1	1.88	0.74
4:B:53:GLN:HG2	4:B:547:VAL:HG22	1.69	0.74
5:C:8:VAL:HG12	5:C:9:LYS:H	1.53	0.74
9:G:14:HIS:ND1	9:G:15:PRO:HD2	2.03	0.74
3:A:239:LEU:HD12	3:A:240:PRO:HD2	1.69	0.74
3:A:67:CYS:O	3:A:70:CYS:HB3	1.87	0.74
4:B:60:GLN:O	4:B:63:ILE:HG22	1.88	0.74
5:C:189:THR:HG22	5:C:190:ASP:N	2.03	0.74
3:A:541:ILE:HG21	3:A:549:MET:HE1	1.68	0.74
3:A:62:ASP:HB3	3:A:64:ASN:ND2	2.02	0.74
10:H:40:LEU:HD13	10:H:123:MET:HB2	1.70	0.74
3:A:534:LEU:O	3:A:574:GLY:HA3	1.85	0.74
3:A:783:THR:HG21	3:A:815:PHE:CZ	2.22	0.74
3:A:774:ARG:NH2	3:A:797:LYS:HG3	2.03	0.74
3:A:836:TYR:CE2	3:A:840:ARG:HD2	2.23	0.73
4:B:483:LEU:HD11	4:B:491:THR:HG23	1.70	0.73
5:C:212:PRO:HB3	5:C:213:PRO:HD2	1.69	0.73
10:H:38:LEU:HD12	10:H:124:ARG:O	1.87	0.73
13:K:45:LEU:HG	13:K:94:ILE:HD13	1.68	0.73
4:B:336:ARG:HH22	4:B:345:LYS:HE2	1.54	0.73
3:A:1100:ARG:HH21	3:A:1351:GLU:HG2	1.53	0.73
4:B:745:PRO:O	4:B:748:ILE:HG12	1.87	0.73
6:D:153:ARG:HB3	6:D:154:PHE:CE1	2.22	0.73
9:G:119:LEU:HD12	9:G:131:GLN:O	1.88	0.73
10:H:4:THR:HA	10:H:60:ALA:CB	2.18	0.73
3:A:1244:ARG:HB3	3:A:1245:PRO:HD2	1.69	0.73
3:A:114:LEU:HD13	3:A:171:GLN:HE22	1.53	0.73
13:K:21:ILE:HG23	13:K:31:VAL:HG11	1.71	0.73
13:K:90:ALA:O	13:K:94:ILE:HG13	1.88	0.73
10:H:89:LEU:O	10:H:91:ASP:N	2.22	0.73
3:A:1118:VAL:HG12	3:A:1327:ILE:HG13	1.69	0.73
3:A:152:VAL:CG1	3:A:153:PRO:HD2	2.17	0.73
3:A:55:ASP:N	3:A:56:PRO:HD3	2.04	0.73
3:A:868:TYR:CD2	3:A:1058:VAL:HG21	2.23	0.73
3:A:1198:ASP:HB3	3:A:1201:ALA:HB3	1.68	0.73
3:A:1116:LEU:N	3:A:1308:THR:HG22	2.04	0.73
3:A:754:SER:N	3:A:757:ASN:HD22	1.83	0.73
3:A:896:ARG:HD3	3:A:897:TYR:HE1	1.54	0.73
4:B:244:LEU:HD11	4:B:366:GLN:HE22	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:579:ARG:HB2	4:B:586:TRP:HE1	1.54	0.73
6:D:47:LEU:HD13	6:D:48:ILE:H	1.53	0.73
1:P:11:C:H2'	1:P:12:C:H6	1.54	0.73
6:D:189:ASP:O	6:D:193:THR:HB	1.88	0.73
3:A:1174:PHE:HA	3:A:1176:LEU:HD23	1.70	0.72
3:A:34:LYS:HE2	3:A:57:ARG:HH12	1.52	0.72
4:B:1187:ASN:O	4:B:1188:LYS:HB2	1.89	0.72
6:D:134:THR:HG22	6:D:135:GLY:H	1.52	0.72
12:J:48:ARG:HE	12:J:49:MET:HE2	1.54	0.72
3:A:345:VAL:HG21	4:B:1150:ARG:NH1	2.04	0.72
4:B:1172:ILE:O	4:B:1172:ILE:HG22	1.89	0.72
4:B:359:GLU:O	4:B:362:PRO:HD3	1.89	0.72
4:B:167:ILE:HG22	4:B:453:ILE:HD12	1.70	0.72
4:B:642:ASP:HB3	4:B:649:LYS:CD	2.19	0.72
14:L:30:ILE:O	14:L:56:LEU:HA	1.88	0.72
4:B:863:GLU:OE2	4:B:873:THR:HA	1.89	0.72
7:E:157:SER:OG	7:E:160:GLU:HG3	1.88	0.72
3:A:244:PRO:HG2	3:A:245:PRO:CD	2.19	0.72
3:A:285:PRO:HG2	3:A:288:ALA:HB3	1.71	0.72
4:B:880:THR:O	4:B:881:ASN:HB2	1.88	0.72
3:A:230:ARG:H	3:A:233:TRP:HE3	1.32	0.72
3:A:63:ARG:HA	3:A:74:MET:CE	2.18	0.72
4:B:336:ARG:NH2	4:B:345:LYS:HE2	2.05	0.72
4:B:340:ALA:CB	4:B:343:ILE:HD12	2.18	0.72
3:A:1242:VAL:HG12	3:A:1243:VAL:H	1.55	0.72
4:B:365:THR:HG23	4:B:367:LEU:H	1.54	0.72
10:H:100:THR:OG1	10:H:138:GLU:HG3	1.88	0.72
12:J:57:ILE:HA	12:J:60:PHE:HD2	1.54	0.72
4:B:1115:THR:HG22	4:B:1117:GLN:HG3	1.70	0.72
5:C:238:ILE:HD11	5:C:246:ARG:NH1	2.04	0.72
10:H:41:ASP:O	10:H:42:ILE:HG13	1.89	0.72
10:H:89:LEU:C	10:H:91:ASP:H	1.92	0.72
3:A:1017:LEU:HB2	7:E:206:GLY:N	2.02	0.72
3:A:896:ARG:NH2	3:A:1030:ARG:HH21	1.88	0.72
4:B:1159:ARG:HE	4:B:1193:GLN:HE21	1.35	0.72
9:G:143:ILE:HG22	9:G:144:ARG:H	1.52	0.72
8:F:103:MET:CE	9:G:66:GLY:H	2.03	0.72
3:A:885:THR:O	3:A:940:ARG:HD2	1.90	0.72
4:B:582:VAL:HG23	4:B:626:ILE:HB	1.70	0.72
12:J:3:VAL:HG21	12:J:18:TRP:CB	2.19	0.72
3:A:69:THR:C	3:A:71:GLN:H	1.93	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:247:GLY:H	4:B:418:LYS:HZ1	1.35	0.71
4:B:847:ASP:HB3	5:C:167:HIS:NE2	2.05	0.71
2:T:10:U:H2'	2:T:11:G:O4'	1.89	0.71
3:A:1120:LEU:CD1	3:A:1120:LEU:H	2.03	0.71
3:A:1124:HIS:HB3	3:A:1130:GLN:HG2	1.71	0.71
3:A:1116:LEU:HB2	3:A:1329:THR:OG1	1.90	0.71
3:A:32:VAL:HG21	3:A:68:GLN:NE2	2.05	0.71
3:A:855:THR:HG23	3:A:857:ARG:HG3	1.71	0.71
8:F:69:LEU:O	8:F:71:GLU:N	2.23	0.71
3:A:986:ILE:HG22	3:A:987:VAL:N	2.05	0.71
4:B:193:LYS:NZ	14:L:32:ALA:HB1	2.05	0.71
4:B:975:GLN:HG2	4:B:976:ILE:H	1.56	0.71
4:B:859:TYR:OH	4:B:941:LEU:HD12	1.91	0.71
6:D:170:THR:HB	6:D:172:LEU:HG	1.70	0.71
14:L:32:ALA:HB3	14:L:55:ILE:CD1	2.20	0.71
3:A:913:LEU:HD12	3:A:914:GLU:N	2.05	0.71
4:B:842:ASN:ND2	4:B:845:SER:H	1.88	0.71
5:C:36:VAL:HG21	5:C:251:LEU:HD22	1.72	0.71
3:A:821:ARG:NH1	3:A:821:ARG:HB2	2.05	0.71
4:B:112:LEU:HD12	4:B:113:TYR:N	2.06	0.71
4:B:815:ARG:HD3	4:B:1041:GLU:OE2	1.91	0.71
5:C:35:ARG:NH1	13:K:41:THR:N	2.38	0.71
3:A:1030:ARG:HG3	3:A:1034:GLU:OE2	1.91	0.71
3:A:477:PRO:HG2	3:A:521:MET:HG2	1.72	0.71
3:A:960:ILE:O	3:A:963:ILE:HG22	1.91	0.71
3:A:2:VAL:HG21	4:B:1157:ALA:HB1	1.73	0.71
3:A:1115:SER:O	3:A:1116:LEU:HB3	1.89	0.70
3:A:438:ASP:O	3:A:439:ASN:HB2	1.88	0.70
3:A:646:PHE:O	3:A:650:GLN:HG3	1.91	0.70
4:B:708:GLU:O	4:B:710:LEU:N	2.24	0.70
4:B:862:GLN:HG2	4:B:963:PHE:HD1	1.54	0.70
3:A:139:TRP:O	3:A:143:LYS:HB3	1.90	0.70
5:C:213:PRO:O	5:C:214:ASN:HB2	1.91	0.70
5:C:46:ILE:HD12	5:C:67:LEU:HB3	1.72	0.70
9:G:81:PRO:HG3	9:G:106:MET:SD	2.31	0.70
14:L:58:LYS:O	14:L:58:LYS:HG2	1.90	0.70
3:A:1121:GLU:HG2	3:A:1122:PRO:HD2	1.72	0.70
3:A:1343:ALA:HB2	7:E:150:VAL:HG22	1.73	0.70
3:A:445:ASN:HB2	3:A:455:MET:HG2	1.73	0.70
3:A:58:LEU:HD13	3:A:80:HIS:O	1.91	0.70
4:B:39:ARG:NH2	4:B:665:GLU:HG2	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:35:ILE:O	3:A:35:ILE:HG22	1.90	0.70
5:C:209:TYR:H	5:C:209:TYR:HD1	1.40	0.70
11:I:82:GLU:OE2	11:I:104:LEU:HD12	1.90	0.70
4:B:343:ILE:CG2	4:B:348:ARG:HG3	2.22	0.70
6:D:40:HIS:CE1	6:D:41:GLN:HG3	2.27	0.70
8:F:103:MET:O	8:F:104:ASN:HB2	1.90	0.70
8:F:119:ARG:HG3	8:F:119:ARG:HH11	1.56	0.70
12:J:12:LYS:O	12:J:14:VAL:HG23	1.92	0.70
3:A:1208:THR:O	3:A:1212:VAL:HG23	1.92	0.70
3:A:761:MET:HA	3:A:804:TYR:HB2	1.72	0.70
3:A:899:VAL:HB	3:A:929:LEU:CD1	2.21	0.70
7:E:22:MET:HE3	7:E:26:ARG:NE	2.06	0.70
4:B:205:ILE:N	4:B:205:ILE:HD12	2.07	0.70
3:A:993:LEU:HD22	3:A:1046:LEU:HD22	1.73	0.70
3:A:34:LYS:NZ	3:A:57:ARG:HH12	1.90	0.70
3:A:794:PRO:HG2	3:A:795:GLU:OE2	1.91	0.70
3:A:1161:THR:HG22	3:A:1163:ILE:N	2.05	0.70
3:A:412:ARG:NH2	4:B:1108:ARG:NH1	2.39	0.70
4:B:498:THR:HG22	4:B:537:LYS:H	1.55	0.70
4:B:971:THR:OG1	5:C:61:GLU:HG3	1.92	0.70
3:A:451:HIS:NE2	3:A:1074:GLU:HG3	2.07	0.69
3:A:1261:LYS:O	3:A:1264:GLU:HB3	1.92	0.69
9:G:143:ILE:CG2	9:G:144:ARG:H	2.05	0.69
4:B:778:MET:HE1	4:B:1094:ARG:HD3	1.73	0.69
4:B:98:THR:O	4:B:126:SER:HB2	1.91	0.69
13:K:46:ILE:O	13:K:50:LEU:HB2	1.92	0.69
6:D:175:PHE:HZ	9:G:85:GLU:HG3	1.57	0.69
12:J:36:LEU:HD12	12:J:47:ARG:NH1	2.07	0.69
5:C:232:VAL:HG21	5:C:244:VAL:HG22	1.73	0.69
3:A:541:ILE:HG21	3:A:549:MET:CE	2.21	0.69
3:A:79:GLY:HA3	3:A:243:PRO:HG3	1.74	0.69
3:A:901:LEU:N	3:A:926:GLN:NE2	2.37	0.69
4:B:168:GLY:H	4:B:450:ALA:HB1	1.57	0.69
5:C:66:ARG:NH2	12:J:3:VAL:O	2.24	0.69
11:I:50:THR:HG22	11:I:52:ILE:H	1.58	0.69
3:A:50:ILE:C	3:A:52:GLY:H	1.96	0.69
10:H:127:GLY:O	10:H:128:ASN:HB2	1.93	0.69
10:H:61:SER:O	10:H:62:SER:HB3	1.91	0.69
3:A:254:GLU:HB2	4:B:935:ARG:NH1	2.03	0.69
3:A:472:LEU:HD11	4:B:835:GLN:NE2	2.08	0.69
4:B:975:GLN:O	4:B:990:ILE:HD12	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:709:THR:HG23	11:I:94:ASP:HA	1.73	0.69
4:B:830:TYR:CE2	4:B:1000:PRO:HD3	2.28	0.69
5:C:184:ASN:ND2	5:C:187:LYS:HA	2.08	0.69
3:A:1015:VAL:HG12	3:A:1019:CYS:SG	2.33	0.69
3:A:84:ILE:HD11	3:A:270:LEU:HD13	1.74	0.69
4:B:811:TYR:N	4:B:811:TYR:CD1	2.60	0.69
7:E:117:THR:HG22	7:E:119:SER:H	1.58	0.69
3:A:1030:ARG:HG3	3:A:1034:GLU:CD	2.13	0.69
3:A:443:LEU:HD21	3:A:455:MET:HB3	1.75	0.69
3:A:446:ARG:CD	3:A:480:ALA:HB2	2.22	0.69
4:B:515:HIS:CD2	4:B:516:ASN:H	2.10	0.69
3:A:567:LYS:HB3	10:H:96:VAL:N	2.07	0.69
4:B:25:ILE:HD11	4:B:653:VAL:O	1.92	0.69
4:B:710:LEU:HA	4:B:733:HIS:HB3	1.75	0.69
3:A:353:ILE:HG21	3:A:487:MET:HE3	1.73	0.68
3:A:344:ARG:HD2	4:B:1118:PRO:O	1.92	0.68
4:B:615:MET:C	4:B:616:ILE:HD12	2.14	0.68
9:G:79:PHE:CZ	9:G:106:MET:HE2	2.28	0.68
3:A:1171:GLN:HA	3:A:1174:PHE:CD1	2.29	0.68
3:A:477:PRO:CG	3:A:521:MET:HG2	2.23	0.68
9:G:143:ILE:CG2	9:G:144:ARG:N	2.57	0.68
4:B:1006:ILE:HD13	12:J:44:TYR:HE2	1.58	0.68
3:A:903:ASN:ND2	3:A:904:THR:N	2.42	0.68
4:B:1087:PHE:HD2	4:B:1088:GLY:N	1.91	0.68
4:B:295:GLY:H	4:B:298:LEU:HD23	1.57	0.68
4:B:378:LEU:O	4:B:378:LEU:HD12	1.93	0.68
4:B:526:GLU:HG2	4:B:538:ASN:HD22	1.58	0.68
4:B:65:GLU:HG3	4:B:66:ASP:N	2.08	0.68
3:A:567:LYS:HD3	10:H:95:TYR:CG	2.28	0.68
11:I:111:THR:HG22	11:I:112:SER:N	2.08	0.68
3:A:903:ASN:HD22	3:A:904:THR:H	1.41	0.68
10:H:36:CYS:HA	10:H:126:GLU:O	1.92	0.68
3:A:528:LEU:O	3:A:531:ILE:HG22	1.93	0.68
3:A:590:ARG:HD3	3:A:604:GLY:HA2	1.74	0.68
3:A:886:ILE:HD11	3:A:943:LEU:HB3	1.74	0.68
4:B:1006:ILE:HD13	12:J:44:TYR:CE2	2.29	0.68
5:C:191:TYR:HD2	5:C:201:TRP:CD1	2.11	0.68
9:G:128:PRO:O	9:G:138:THR:HG23	1.93	0.68
3:A:694:THR:O	3:A:698:GLN:HG3	1.93	0.68
4:B:351:TYR:O	4:B:355:ILE:HG13	1.94	0.68
6:D:17:LYS:HE3	6:D:17:LYS:CA	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:109:VAL:HG11	8:F:123:LYS:HD3	1.74	0.68
8:F:90:ARG:HD3	8:F:155:LEU:CD1	2.23	0.68
3:A:443:LEU:HD12	4:B:1146:PHE:CE2	2.28	0.68
3:A:836:TYR:CD2	3:A:840:ARG:HD2	2.27	0.68
4:B:661:LEU:HD11	4:B:684:LEU:HD21	1.74	0.68
10:H:84:ALA:HA	10:H:87:ARG:HB2	1.76	0.68
3:A:535:THR:CG2	3:A:616:VAL:HA	2.24	0.68
6:D:50:LEU:HD13	6:D:55:ALA:HA	1.76	0.68
10:H:58:THR:HG22	10:H:59:ILE:H	1.59	0.68
4:B:288:ALA:HA	4:B:331:LEU:HD12	1.73	0.68
4:B:653:VAL:HG22	4:B:689:LEU:HB3	1.76	0.68
5:C:73:GLN:HB3	5:C:131:HIS:H	1.58	0.68
5:C:40:GLU:HA	5:C:163:ILE:HG21	1.74	0.68
10:H:59:ILE:HG22	10:H:60:ALA:H	1.58	0.68
13:K:58:PHE:HB3	13:K:76:GLN:HB3	1.76	0.68
3:A:1402:PHE:CE1	3:A:1403:GLU:HG3	2.28	0.67
3:A:18:GLN:HB2	4:B:1215:ARG:HB2	1.77	0.67
4:B:113:TYR:HB3	4:B:114:PRO:HD2	1.75	0.67
4:B:123:THR:OG1	4:B:458:LYS:HE2	1.94	0.67
5:C:189:THR:HG22	5:C:190:ASP:H	1.59	0.67
10:H:25:ARG:HA	10:H:41:ASP:HA	1.76	0.67
4:B:1085:ILE:HD12	4:B:1085:ILE:N	2.09	0.67
5:C:40:GLU:HA	5:C:163:ILE:CG2	2.24	0.67
5:C:244:VAL:O	5:C:248:ILE:HG13	1.94	0.67
3:A:567:LYS:HB3	10:H:95:TYR:HA	1.76	0.67
3:A:1094:VAL:HG12	3:A:1095:THR:H	1.60	0.67
3:A:182:VAL:HG22	3:A:201:VAL:HA	1.75	0.67
3:A:849:MET:HE1	3:A:1061:GLY:HA2	1.75	0.67
4:B:859:TYR:CZ	4:B:941:LEU:HD12	2.30	0.67
6:D:56:ARG:HA	6:D:148:LEU:HD13	1.76	0.67
12:J:1:MET:N	12:J:57:ILE:H	1.81	0.67
3:A:963:ILE:HD11	3:A:1048:ASN:CB	2.25	0.67
4:B:1096:ARG:O	4:B:1097:HIS:HB2	1.93	0.67
4:B:467:GLY:H	4:B:475:SER:CB	2.07	0.67
4:B:654:ARG:H	4:B:657:HIS:CD2	2.12	0.67
5:C:35:ARG:HH12	13:K:41:THR:H	1.41	0.67
8:F:118:LEU:O	8:F:122:MET:HG3	1.95	0.67
3:A:666:ILE:H	4:B:1026:LEU:HD13	1.59	0.67
6:D:47:LEU:HD11	9:G:3:PHE:CD2	2.30	0.67
3:A:388:LEU:O	3:A:392:VAL:HG23	1.95	0.67
4:B:606:LYS:HD2	4:B:608:ASP:OD2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:183:TRP:CZ2	5:C:207:CYS:HB3	2.30	0.67
7:E:207:ARG:HB2	7:E:207:ARG:HH11	1.60	0.67
10:H:64:ASN:O	10:H:65:LEU:HB2	1.94	0.67
3:A:1120:LEU:HD12	3:A:1120:LEU:H	1.59	0.67
3:A:253:ASN:HB3	4:B:935:ARG:CZ	2.24	0.67
4:B:429:PHE:HA	4:B:432:MET:HE2	1.75	0.67
4:B:408:LEU:HD22	4:B:545:ILE:HD12	1.77	0.67
4:B:603:LEU:HD13	4:B:608:ASP:HB2	1.77	0.67
5:C:34:ARG:O	5:C:38:ILE:HG13	1.95	0.67
6:D:134:THR:HG22	6:D:136:GLY:H	1.59	0.67
11:I:111:THR:HG22	11:I:112:SER:H	1.59	0.67
12:J:57:ILE:HA	12:J:60:PHE:CD2	2.30	0.67
3:A:335:ARG:HA	3:A:339:ASN:HB2	1.77	0.67
2:T:8:C:H4'	3:A:447:GLN:NE2	2.09	0.67
3:A:92:HIS:O	3:A:94:GLY:N	2.28	0.67
4:B:532:ALA:HA	4:B:535:LEU:HD12	1.77	0.67
5:C:133:ILE:CD1	5:C:237:SER:HA	2.25	0.67
3:A:1420:ASP:O	3:A:1421:CYS:HB2	1.95	0.67
3:A:152:VAL:HG12	3:A:153:PRO:HD2	1.77	0.67
4:B:604:ARG:NH1	4:B:691:GLU:OE2	2.28	0.67
7:E:22:MET:HE1	7:E:26:ARG:HH21	1.59	0.67
3:A:34:LYS:HE2	3:A:57:ARG:NH1	2.10	0.66
5:C:251:LEU:O	5:C:255:VAL:HG23	1.96	0.66
8:F:130:ILE:HB	8:F:148:VAL:HG21	1.76	0.66
10:H:81:PRO:CB	10:H:82:PRO:HD2	2.25	0.66
11:I:52:ILE:HG13	11:I:52:ILE:O	1.95	0.66
11:I:55:THR:HG22	11:I:58:VAL:CG2	2.26	0.66
11:I:85:PHE:CD1	11:I:99:LEU:HD13	2.30	0.66
3:A:1100:ARG:O	3:A:1103:GLU:HB3	1.96	0.66
3:A:458:HIS:CE1	3:A:507:VAL:HG21	2.31	0.66
3:A:356:ASP:HB2	3:A:469:ARG:HH12	1.58	0.66
5:C:8:VAL:HG12	5:C:9:LYS:N	2.10	0.66
6:D:8:PHE:CE2	9:G:6:ASP:HB2	2.30	0.66
3:A:396:PRO:HG3	3:A:416:ARG:HB3	1.78	0.66
4:B:847:ASP:C	4:B:849:GLY:H	1.98	0.66
7:E:135:PHE:HB3	7:E:140:LEU:HD11	1.76	0.66
4:B:737:THR:HG21	11:I:66:PRO:HA	1.76	0.66
12:J:14:VAL:HG12	12:J:50:ILE:HD11	1.77	0.66
3:A:1027:ALA:O	3:A:1031:VAL:HG23	1.95	0.66
3:A:335:ARG:NH1	4:B:1202:LEU:HD13	2.10	0.66
3:A:466:SER:O	4:B:1103:ILE:HD11	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1127:ASP:HB3	3:A:1130:GLN:CB	2.25	0.66
3:A:798:GLY:HA2	3:A:815:PHE:CD1	2.30	0.66
4:B:60:GLN:HE22	4:B:94:LYS:HA	1.61	0.66
5:C:35:ARG:NH1	13:K:41:THR:H	1.92	0.66
3:A:1100:ARG:HH21	3:A:1351:GLU:CG	2.07	0.66
4:B:955:THR:CG2	4:B:956:THR:N	2.59	0.66
4:B:999:MET:HB3	4:B:1007:VAL:HG21	1.76	0.66
2:T:12:G:O2'	2:T:13:U:H3'	1.94	0.66
4:B:361:LEU:HD21	4:B:377:PHE:CD2	2.31	0.66
4:B:792:MET:HA	4:B:856:PHE:O	1.96	0.66
7:E:157:SER:C	7:E:159:ASP:H	1.99	0.66
8:F:116:ASP:HB3	8:F:119:ARG:HB2	1.78	0.66
6:D:40:HIS:CB	9:G:73:LYS:HZ3	1.93	0.66
3:A:698:GLN:HA	11:I:97:MET:O	1.96	0.66
3:A:254:GLU:O	3:A:256:GLN:N	2.28	0.66
3:A:856:THR:HB	3:A:865:GLN:HB2	1.77	0.66
4:B:642:ASP:O	4:B:644:GLU:N	2.28	0.66
4:B:857:ARG:HD2	4:B:945:GLU:OE1	1.94	0.66
4:B:999:MET:HA	4:B:999:MET:CE	2.26	0.66
3:A:541:ILE:HG22	3:A:546:VAL:HG23	1.76	0.66
4:B:121:ASN:HA	4:B:207:GLY:CA	2.26	0.66
9:G:96:GLN:HG3	9:G:97:HIS:HD2	1.60	0.66
3:A:1372:VAL:O	3:A:1376:THR:HG22	1.95	0.66
3:A:63:ARG:HD3	3:A:74:MET:CE	2.26	0.66
4:B:1023:VAL:O	4:B:1026:LEU:HB2	1.95	0.66
4:B:114:PRO:HG3	4:B:181:LEU:HD11	1.77	0.66
4:B:525:ALA:O	4:B:768:THR:HA	1.96	0.66
4:B:35:SER:HA	4:B:811:TYR:HE2	1.61	0.66
8:F:103:MET:HE2	9:G:66:GLY:H	1.61	0.66
6:D:58:VAL:HG11	9:G:4:ILE:HD11	1.78	0.66
13:K:65:HIS:CD2	13:K:67:PHE:HB2	2.31	0.66
3:A:1094:VAL:HG13	3:A:1113:THR:HG21	1.77	0.65
3:A:1373:ASP:HA	3:A:1376:THR:CG2	2.26	0.65
3:A:475:THR:HG23	3:A:476:SER:N	2.10	0.65
4:B:830:TYR:O	4:B:832:GLY:N	2.29	0.65
5:C:11:ARG:HD3	5:C:209:TYR:CE2	2.31	0.65
5:C:161:LYS:O	5:C:170:TRP:NE1	2.28	0.65
10:H:126:GLU:C	10:H:130:ARG:HH22	2.00	0.65
3:A:590:ARG:NH2	3:A:620:LYS:CB	2.59	0.65
3:A:87:ALA:HB3	3:A:276:LEU:HD23	1.77	0.65
3:A:842:VAL:HG11	4:B:1136:ASP:OD2	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:47:LEU:HD11	9:G:3:PHE:CE2	2.31	0.65
11:I:76:PRO:CG	11:I:110:PHE:HB3	2.27	0.65
4:B:364:ILE:HG12	4:B:585:VAL:CG1	2.25	0.65
4:B:39:ARG:HG2	4:B:39:ARG:HH11	1.61	0.65
6:D:130:LEU:O	6:D:132:GLN:N	2.29	0.65
7:E:114:ASN:O	7:E:115:ASN:HB3	1.97	0.65
10:H:81:PRO:HB2	10:H:82:PRO:HD2	1.78	0.65
10:H:42:ILE:HG23	10:H:95:TYR:HE1	1.61	0.65
5:C:146:LYS:HB2	12:J:61:LEU:HD11	1.78	0.65
3:A:1130:GLN:HE21	3:A:1134:ILE:HD11	1.61	0.65
3:A:1164:PRO:HG2	3:A:1165:GLU:H	1.59	0.65
3:A:254:GLU:HG3	4:B:935:ARG:HH22	1.60	0.65
3:A:35:ILE:HA	3:A:52:GLY:O	1.97	0.65
4:B:1162:ILE:HD11	4:B:1194:ILE:CD1	2.27	0.65
4:B:799:PRO:HB3	4:B:818:PRO:HG2	1.77	0.65
6:D:130:LEU:C	6:D:132:GLN:H	2.00	0.65
11:I:58:VAL:HG13	11:I:62:ILE:HD13	1.78	0.65
4:B:351:TYR:CE1	4:B:355:ILE:HD11	2.32	0.65
4:B:763:GLN:HG2	4:B:765:PRO:HD2	1.79	0.65
7:E:176:PRO:O	7:E:212:ARG:HA	1.96	0.65
9:G:1:MET:HG3	9:G:85:GLU:OE2	1.96	0.65
3:A:356:ASP:OD2	13:K:65:HIS:HE1	1.78	0.65
3:A:450:LEU:HB3	3:A:838:GLN:HE21	1.61	0.65
4:B:601:ARG:O	4:B:605:ARG:HG3	1.97	0.65
8:F:111:LEU:H	8:F:111:LEU:HD12	1.60	0.65
13:K:31:VAL:HG12	13:K:32:VAL:N	2.12	0.65
14:L:70:ARG:HG2	14:L:70:ARG:HH11	1.62	0.65
3:A:1038:THR:H	3:A:1041:ALA:HB3	1.62	0.65
3:A:211:PHE:HA	3:A:214:ILE:HG13	1.78	0.65
3:A:896:ARG:HD3	3:A:897:TYR:CE1	2.31	0.65
4:B:807:ARG:HG2	4:B:1045:SER:OG	1.97	0.65
10:H:62:SER:HB2	10:H:64:ASN:HD22	1.61	0.65
3:A:809:THR:H	3:A:812:GLU:HB2	1.62	0.65
4:B:294:ASP:O	4:B:296:GLU:N	2.29	0.65
4:B:549:THR:HB	4:B:628:THR:OG1	1.97	0.65
9:G:122:ASN:HD22	9:G:125:SER:HB3	1.61	0.65
3:A:743:VAL:O	3:A:747:VAL:HG23	1.97	0.65
4:B:515:HIS:CD2	4:B:517:THR:H	2.15	0.65
4:B:953:LEU:HD21	4:B:965:LYS:HB2	1.78	0.65
3:A:698:GLN:NE2	11:I:99:LEU:HD21	2.12	0.65
4:B:1180:PHE:HB3	4:B:1191:ILE:HD12	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:38:PHE:HD1	4:B:811:TYR:CD2	2.15	0.65
4:B:782:LEU:HD12	4:B:788:ARG:HH11	1.62	0.65
4:B:842:ASN:O	4:B:846:ILE:HG13	1.97	0.65
9:G:18:PHE:HA	9:G:22:MET:CE	2.27	0.65
6:D:29:LEU:HB3	9:G:82:PHE:HE2	1.60	0.65
2:T:13:U:O2'	2:T:14:C:H6	1.80	0.65
7:E:48:ASP:CG	7:E:49:SER:H	2.00	0.64
3:A:1118:VAL:O	3:A:1305:VAL:HG13	1.97	0.64
3:A:366:VAL:HG21	3:A:460:VAL:HG22	1.78	0.64
4:B:1069:PHE:HD1	4:B:1069:PHE:H	1.44	0.64
5:C:39:ALA:CA	5:C:164:ALA:HB3	2.26	0.64
4:B:185:THR:H	4:B:188:ASP:HB2	1.62	0.64
6:D:67:ARG:HB2	6:D:133:THR:HG21	1.78	0.64
3:A:628:GLY:O	3:A:632:VAL:HG23	1.97	0.64
4:B:1159:ARG:NE	4:B:1193:GLN:HE21	1.96	0.64
5:C:174:ALA:HB2	5:C:235:VAL:HG22	1.80	0.64
3:A:547:LEU:HD22	13:K:58:PHE:CE1	2.32	0.64
3:A:738:LYS:HD2	3:A:740:LEU:HD21	1.80	0.64
3:A:853:ASP:OD1	3:A:855:THR:HB	1.98	0.64
4:B:705:MET:H	4:B:710:LEU:CD1	2.11	0.64
8:F:68:THR:HB	8:F:71:GLU:HB2	1.80	0.64
6:D:29:LEU:HD22	9:G:82:PHE:CE2	2.32	0.64
3:A:215:SER:HB3	3:A:218:ASP:HB2	1.79	0.64
3:A:88:LYS:HE3	3:A:280:GLU:OE2	1.98	0.64
5:C:18:VAL:HG23	5:C:240:VAL:HB	1.80	0.64
9:G:45:ILE:HD13	9:G:78:VAL:HG13	1.78	0.64
11:I:55:THR:HG23	11:I:86:PHE:HZ	1.62	0.64
3:A:1317:MET:O	3:A:1322:ILE:HD11	1.96	0.64
4:B:46:GLN:HG3	4:B:47:GLN:H	1.62	0.64
4:B:865:LYS:NZ	4:B:869:SER:HA	2.12	0.64
4:B:955:THR:HG22	4:B:956:THR:H	1.61	0.64
5:C:67:LEU:HD11	5:C:155:LEU:CD1	2.27	0.64
7:E:198:ILE:HD11	7:E:212:ARG:CG	2.28	0.64
8:F:90:ARG:HD3	8:F:155:LEU:HD11	1.79	0.64
3:A:886:ILE:HG13	3:A:943:LEU:HD12	1.78	0.64
4:B:798:TYR:HE2	5:C:62:PHE:CZ	2.16	0.64
9:G:1:MET:HE3	9:G:80:LYS:C	2.17	0.64
3:A:537:ARG:HD2	10:H:20:TYR:CE1	2.33	0.64
3:A:42:ASP:HB3	3:A:45:GLN:H	1.63	0.64
3:A:844:ALA:O	3:A:845:LEU:HD23	1.97	0.64
4:B:1002:THR:CG2	4:B:1006:ILE:HG13	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:603:LEU:HD12	4:B:609:ILE:HG13	1.80	0.64
4:B:955:THR:CG2	4:B:956:THR:H	2.11	0.64
8:F:99:LEU:HD12	8:F:99:LEU:O	1.96	0.64
9:G:119:LEU:HD13	9:G:132:SER:HB2	1.80	0.64
3:A:372:LYS:HA	3:A:435:HIS:ND1	2.13	0.64
5:C:6:PRO:CB	5:C:25:VAL:HG12	2.28	0.64
3:A:154:SER:HB3	3:A:162:VAL:HG21	1.79	0.63
3:A:79:GLY:HA3	3:A:243:PRO:CG	2.29	0.63
3:A:441:PRO:HD2	3:A:498:ARG:NH2	2.13	0.63
3:A:616:VAL:HG12	3:A:617:VAL:H	1.64	0.63
3:A:590:ARG:HH21	3:A:620:LYS:HB3	1.62	0.63
3:A:68:GLN:C	3:A:70:CYS:H	2.00	0.63
4:B:434:ARG:O	4:B:437:GLU:HB2	1.98	0.63
3:A:1329:THR:CG2	3:A:1331:SER:H	2.06	0.63
3:A:1313:LEU:HD23	3:A:1338:VAL:HG21	1.80	0.63
3:A:1438:THR:HB	4:B:1144:ALA:CB	2.28	0.63
3:A:215:SER:HB3	3:A:218:ASP:OD2	1.99	0.63
3:A:311:GLN:O	3:A:312:PRO:C	2.36	0.63
3:A:728:LYS:O	3:A:732:LEU:HG	1.97	0.63
4:B:847:ASP:HB3	5:C:167:HIS:CD2	2.34	0.63
3:A:105:CYS:O	3:A:114:LEU:HG	1.98	0.63
3:A:914:GLU:HB2	3:A:979:SER:O	1.98	0.63
4:B:824:ILE:CG2	4:B:1087:PHE:HE2	2.12	0.63
5:C:253:LYS:O	5:C:256:ALA:HB3	1.98	0.63
9:G:79:PHE:HZ	9:G:106:MET:HE2	1.62	0.63
3:A:1385:THR:HG22	3:A:1386:ARG:N	2.13	0.63
3:A:310:GLY:O	3:A:312:PRO:HD2	1.99	0.63
4:B:273:LEU:HD12	4:B:280:ILE:HD12	1.80	0.63
4:B:411:PRO:O	4:B:414:ALA:HB3	1.97	0.63
5:C:67:LEU:HA	5:C:70:ILE:HD12	1.79	0.63
6:D:71:LYS:HA	6:D:74:GLN:HB2	1.79	0.63
7:E:192:ARG:NH1	7:E:192:ARG:HG3	2.13	0.63
7:E:55:ARG:C	7:E:57:MET:H	2.00	0.63
8:F:130:ILE:O	8:F:148:VAL:HG21	1.98	0.63
3:A:567:LYS:HB2	3:A:568:PRO:CD	2.29	0.63
4:B:305:VAL:O	4:B:305:VAL:HG12	1.99	0.63
4:B:952:VAL:HG12	4:B:953:LEU:N	2.13	0.63
11:I:34:TYR:CE2	11:I:36:GLU:HB3	2.33	0.63
12:J:3:VAL:HG21	12:J:18:TRP:CG	2.34	0.63
3:A:34:LYS:O	3:A:35:ILE:HB	1.99	0.63
4:B:227:LYS:HB2	4:B:395:GLN:OE1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:179:GLU:HG2	5:C:180:TYR:N	2.13	0.63
3:A:144:THR:O	3:A:146:MET:HG3	1.98	0.63
3:A:984:LYS:O	3:A:988:LEU:HB2	1.98	0.63
4:B:1001:PHE:CZ	4:B:1073:TYR:HB2	2.33	0.63
5:C:101:LEU:HD13	5:C:118:LEU:CD2	2.27	0.63
6:D:134:THR:CG2	6:D:135:GLY:H	2.10	0.63
6:D:134:THR:CG2	6:D:135:GLY:N	2.61	0.63
7:E:5:ASN:O	7:E:9:ILE:HG13	1.98	0.63
3:A:871:ASP:OD2	3:A:873:MET:HB2	1.98	0.63
5:C:45:ALA:HA	5:C:72:LEU:CD1	2.28	0.63
12:J:2:ILE:H	12:J:57:ILE:CG2	2.12	0.63
3:A:1006:ILE:HD12	7:E:163:GLU:HG3	1.80	0.62
4:B:792:MET:HG3	4:B:855:PHE:CE1	2.34	0.62
5:C:73:GLN:CB	5:C:131:HIS:H	2.11	0.62
7:E:144:ILE:HG13	7:E:145:THR:N	2.14	0.62
2:T:13:U:HO2'	2:T:14:C:C5'	2.08	0.62
3:A:858:ASN:ND2	3:A:860:LEU:H	1.97	0.62
4:B:363:HIS:O	4:B:364:ILE:HB	1.99	0.62
4:B:219:ALA:HB2	4:B:405:ARG:NH1	2.14	0.62
3:A:427:GLN:HB2	3:A:430:TRP:CE2	2.34	0.62
3:A:442:VAL:HG21	3:A:460:VAL:HG23	1.80	0.62
3:A:685:GLU:HG3	3:A:686:ALA:N	2.15	0.62
5:C:17:ASN:O	5:C:18:VAL:HG23	1.99	0.62
12:J:7:CYS:SG	12:J:49:MET:HE3	2.39	0.62
3:A:7:SER:HB3	4:B:1175:LEU:HD22	1.81	0.62
4:B:792:MET:HG3	4:B:855:PHE:HE1	1.64	0.62
8:F:69:LEU:C	8:F:71:GLU:N	2.52	0.62
4:B:1099:VAL:CG1	4:B:1100:ASP:N	2.62	0.62
4:B:842:ASN:HD22	4:B:845:SER:CB	2.13	0.62
9:G:165:GLU:HB2	9:G:168:LEU:HD12	1.80	0.62
10:H:139:ASN:O	10:H:140:ALA:HB2	1.99	0.62
12:J:44:TYR:HD2	12:J:44:TYR:N	1.98	0.62
4:B:516:ASN:ND2	4:B:516:ASN:N	2.46	0.62
9:G:51:TYR:O	9:G:54:ILE:HG13	1.99	0.62
3:A:202:LEU:HB3	3:A:207:ILE:HD11	1.81	0.62
3:A:252:PHE:O	3:A:253:ASN:HB2	1.99	0.62
3:A:714:PHE:O	3:A:718:VAL:HG23	2.00	0.62
4:B:1180:PHE:O	4:B:1181:GLU:O	2.18	0.62
4:B:218:SER:HB3	4:B:241:ARG:NH1	2.15	0.62
6:D:12:ARG:NE	6:D:14:ARG:HD2	2.15	0.62
7:E:124:VAL:HG13	7:E:132:ILE:HB	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:22:MET:CE	7:E:26:ARG:HH21	2.12	0.62
12:J:44:TYR:HA	12:J:47:ARG:CB	2.30	0.62
13:K:42:LEU:CD2	13:K:46:ILE:HD11	2.30	0.62
3:A:1036:ARG:HH11	3:A:1036:ARG:HG2	1.65	0.62
3:A:1174:PHE:C	3:A:1176:LEU:N	2.53	0.62
7:E:213:ILE:HG12	7:E:214:CYS:N	2.13	0.62
13:K:60:ALA:O	13:K:73:LEU:HD12	1.99	0.62
4:B:224:GLN:HA	4:B:396:ASP:OD2	2.00	0.62
4:B:616:ILE:N	4:B:616:ILE:HD12	2.14	0.62
5:C:69:LEU:N	5:C:69:LEU:HD12	2.15	0.62
7:E:124:VAL:HA	7:E:132:ILE:HD12	1.82	0.62
8:F:89:GLU:OE2	8:F:134:ILE:HG21	1.99	0.62
14:L:27:LEU:O	14:L:28:LYS:HG2	2.00	0.62
3:A:993:LEU:HD22	3:A:1046:LEU:CD2	2.30	0.61
3:A:767:GLN:HE22	3:A:774:ARG:HB3	1.62	0.61
4:B:751:VAL:HG13	4:B:812:LEU:HD22	1.81	0.61
4:B:373:ARG:HG3	4:B:566:LEU:HD23	1.80	0.61
4:B:744:HIS:HD2	4:B:746:SER:OG	1.82	0.61
6:D:4:SER:O	6:D:5:THR:HB	1.99	0.61
3:A:1095:THR:O	3:A:1095:THR:HG22	2.00	0.61
3:A:1227:ILE:HG22	3:A:1228:TRP:N	2.14	0.61
3:A:1348:LEU:O	3:A:1352:VAL:HG23	2.00	0.61
3:A:399:HIS:HB3	3:A:400:PRO:CD	2.29	0.61
3:A:785:PRO:HG2	3:A:786:HIS:HD2	1.65	0.61
3:A:786:HIS:CD2	3:A:786:HIS:N	2.67	0.61
4:B:1183:LYS:N	4:B:1183:LYS:CE	2.62	0.61
3:A:870:GLU:HG2	7:E:208:TYR:CG	2.36	0.61
4:B:1181:GLU:HG3	4:B:1188:LYS:HE3	1.80	0.61
5:C:20:PHE:HE1	5:C:22:LEU:HD12	1.65	0.61
9:G:131:GLN:HG2	9:G:136:VAL:HG22	1.83	0.61
3:A:1114:PRO:O	3:A:1115:SER:O	2.18	0.61
3:A:107:CYS:N	3:A:114:LEU:HD21	2.15	0.61
3:A:1436:ILE:O	3:A:1437:GLY:C	2.39	0.61
4:B:1002:THR:O	4:B:1004:GLU:N	2.32	0.61
3:A:746:MET:HE3	4:B:1018:PRO:HG2	1.82	0.61
4:B:58:THR:O	4:B:62:ILE:HG13	2.00	0.61
3:A:818:MET:HA	4:B:514:LEU:HB3	1.82	0.61
3:A:984:LYS:HG2	3:A:988:LEU:HD12	1.81	0.61
4:B:217:ARG:HE	4:B:405:ARG:HB2	1.66	0.61
4:B:515:HIS:CD2	4:B:516:ASN:N	2.69	0.61
9:G:48:VAL:HG13	9:G:74:TYR:HD1	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:84:ALA:CB	10:H:87:ARG:HB2	2.29	0.61
3:A:1121:GLU:CG	3:A:1122:PRO:HD2	2.30	0.61
3:A:1224:LEU:HD11	3:A:1240:CYS:HB2	1.83	0.61
4:B:1177:HIS:HB2	4:B:1179:GLN:NE2	2.12	0.61
4:B:999:MET:HE3	4:B:999:MET:HA	1.83	0.61
5:C:45:ALA:HA	5:C:72:LEU:HD13	1.83	0.61
3:A:567:LYS:CB	10:H:95:TYR:HA	2.30	0.61
3:A:1279:ILE:HD11	3:A:1316:VAL:HG21	1.83	0.61
6:D:13:ARG:HA	6:D:17:LYS:HZ3	1.66	0.61
3:A:1226:VAL:HG22	3:A:1240:CYS:HB3	1.83	0.61
3:A:1313:LEU:O	3:A:1315:GLU:N	2.34	0.61
3:A:87:ALA:HB1	3:A:276:LEU:HD23	1.82	0.61
4:B:278:GLN:HG2	4:B:279:ASP:H	1.65	0.61
4:B:393:LYS:HA	4:B:393:LYS:HE3	1.82	0.61
4:B:842:ASN:HB3	4:B:845:SER:OG	2.00	0.61
7:E:84:ASP:O	7:E:86:PRO:HD3	2.00	0.61
9:G:39:THR:HG22	9:G:40:GLY:N	2.12	0.61
3:A:1206:ASP:HB3	3:A:1274:ARG:HH12	1.65	0.61
3:A:268:ASP:HB3	3:A:299:HIS:ND1	2.16	0.61
4:B:39:ARG:HH21	4:B:665:GLU:HG2	1.64	0.61
4:B:900:ALA:O	4:B:903:VAL:HG23	2.01	0.61
5:C:112:ASN:HB2	5:C:114:TYR:CE1	2.36	0.61
3:A:1451:VAL:O	3:A:1454:MET:HG2	2.00	0.60
3:A:596:THR:C	3:A:598:LEU:H	2.05	0.60
4:B:291:ILE:HD13	4:B:300:HIS:NE2	2.16	0.60
4:B:583:ASN:ND2	4:B:628:THR:HG22	2.09	0.60
5:C:98:VAL:HG23	5:C:122:SER:HB3	1.82	0.60
5:C:105:GLY:HA3	5:C:149:LYS:O	2.00	0.60
7:E:207:ARG:CB	7:E:207:ARG:HH11	2.14	0.60
5:C:66:ARG:CZ	12:J:2:ILE:HG21	2.30	0.60
2:T:12:G:HO2'	2:T:13:U:C5'	2.11	0.60
3:A:1305:VAL:HG12	3:A:1306:LEU:N	2.16	0.60
3:A:1348:LEU:HG	3:A:1372:VAL:HG23	1.82	0.60
3:A:549:MET:SD	3:A:577:ILE:HD11	2.41	0.60
3:A:552:TRP:HE3	3:A:651:LYS:HB3	1.66	0.60
4:B:1180:PHE:HB3	4:B:1191:ILE:CD1	2.31	0.60
4:B:234:ILE:HG12	4:B:257:LYS:HD3	1.83	0.60
4:B:803:LEU:HD13	4:B:1032:SER:HB3	1.82	0.60
4:B:97:VAL:HG12	4:B:178:ASN:HD21	1.65	0.60
6:D:173:HIS:ND1	6:D:174:PRO:HD2	2.16	0.60
9:G:39:THR:HG22	9:G:41:LYS:H	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1293:SER:OG	3:A:1294:PRO:HD2	2.01	0.60
3:A:381:THR:CG2	3:A:383:TYR:H	2.14	0.60
3:A:578:LEU:HD23	3:A:612:ILE:CD1	2.31	0.60
3:A:672:ASP:HB2	3:A:736:ASN:OD1	2.01	0.60
4:B:796:LEU:HD12	4:B:852:ARG:O	2.01	0.60
5:C:175:ALA:HB2	12:J:10:CYS:HB2	1.82	0.60
5:C:238:ILE:CG2	5:C:242:GLN:HB2	2.31	0.60
10:H:11:GLN:HA	10:H:53:ASP:O	2.01	0.60
11:I:55:THR:HG23	11:I:86:PHE:CZ	2.37	0.60
1:P:11:C:H2'	1:P:12:C:C6	2.35	0.60
3:A:11:LEU:O	3:A:11:LEU:HD23	2.01	0.60
3:A:471:ASN:OD1	3:A:472:LEU:N	2.34	0.60
4:B:378:LEU:O	4:B:382:ILE:HG13	2.01	0.60
4:B:364:ILE:CG1	4:B:585:VAL:HG13	2.25	0.60
4:B:866:TYR:HB2	4:B:870:ILE:HB	1.83	0.60
6:D:192:LYS:HE3	6:D:204:ASP:OD1	2.02	0.60
2:T:13:U:C2'	2:T:14:C:O5'	2.49	0.60
3:A:1073:GLY:O	3:A:1076:ALA:HB3	2.02	0.60
3:A:41:MET:HB3	3:A:49:LYS:HA	1.83	0.60
3:A:423:ASP:O	3:A:424:ILE:HB	2.02	0.60
4:B:1034:VAL:HG12	4:B:1035:ALA:N	2.16	0.60
4:B:547:VAL:HG12	4:B:612:GLU:OE2	2.01	0.60
4:B:1001:PHE:CD2	5:C:34:ARG:NH2	2.69	0.60
12:J:44:TYR:N	12:J:44:TYR:CD2	2.68	0.60
3:A:852:TYR:CD2	3:A:1060:PRO:HB2	2.37	0.60
3:A:416:ARG:C	3:A:417:TYR:HD2	2.05	0.60
3:A:600:PRO:HG2	3:A:601:LYS:H	1.65	0.60
4:B:1031:LEU:HD11	4:B:1042:GLY:HA3	1.84	0.60
4:B:1115:THR:O	4:B:1116:ARG:HB2	2.02	0.60
4:B:976:ILE:O	4:B:990:ILE:HB	2.01	0.60
11:I:106:CYS:O	11:I:107:SER:HB2	2.02	0.60
13:K:53:ASP:OD1	13:K:55:LYS:HB2	2.02	0.60
3:A:565:ILE:O	3:A:570:PRO:HA	2.02	0.60
4:B:269:ILE:HD11	4:B:386:LEU:HD21	1.83	0.60
4:B:873:THR:O	4:B:914:LYS:HA	2.02	0.60
11:I:25:LEU:HB3	11:I:38:ALA:HB2	1.82	0.60
3:A:1004:ASN:O	3:A:1008:GLN:HB2	2.01	0.60
3:A:34:LYS:HG2	3:A:57:ARG:HH22	1.66	0.60
3:A:709:THR:HB	3:A:712:GLU:HG3	1.83	0.60
4:B:232:SER:HB3	4:B:261:ARG:NH2	2.17	0.60
4:B:821:GLN:HE22	4:B:851:PHE:HA	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:39:LEU:O	7:E:42:PHE:HB3	2.01	0.60
3:A:709:THR:HG22	3:A:710:LEU:N	2.17	0.60
5:C:144:ILE:O	5:C:145:CYS:HB3	2.01	0.60
9:G:27:LYS:HE2	9:G:54:ILE:HB	1.84	0.60
10:H:48:PRO:O	10:H:49:VAL:HG23	2.02	0.60
11:I:101:PHE:N	11:I:101:PHE:CD1	2.70	0.60
13:K:101:LEU:HD23	13:K:101:LEU:O	2.01	0.60
3:A:14:VAL:N	3:A:1432:GLN:HE22	2.00	0.60
3:A:284:ALA:O	3:A:286:HIS:N	2.34	0.60
3:A:567:LYS:CB	3:A:568:PRO:CD	2.80	0.60
3:A:56:PRO:O	3:A:57:ARG:NE	2.35	0.60
3:A:683:ILE:HD13	3:A:801:GLU:HG3	1.84	0.60
4:B:100:PRO:HD3	4:B:172:ILE:HD12	1.84	0.60
10:H:84:ALA:CA	10:H:87:ARG:HB2	2.32	0.60
3:A:12:ARG:HE	4:B:1192:TYR:HE2	1.50	0.59
3:A:427:GLN:HG3	3:A:430:TRP:CZ2	2.36	0.59
3:A:53:LEU:HD22	3:A:54:ASN:HD22	1.66	0.59
4:B:483:LEU:HD11	4:B:491:THR:CG2	2.31	0.59
7:E:13:TRP:O	7:E:16:PHE:HB3	2.02	0.59
9:G:35:GLU:OE2	9:G:48:VAL:HG23	2.01	0.59
9:G:51:TYR:C	9:G:51:TYR:CD2	2.75	0.59
3:A:1076:ALA:HA	3:A:1079:MET:CE	2.31	0.59
3:A:1289:ARG:HD2	3:A:1303:GLU:OE2	2.02	0.59
3:A:1341:ILE:HG23	3:A:1342:GLU:N	2.18	0.59
3:A:683:ILE:HG21	3:A:801:GLU:HG3	1.84	0.59
3:A:768:GLN:CG	3:A:816:HIS:HA	2.31	0.59
4:B:431:TYR:CE2	4:B:447:ALA:HB2	2.37	0.59
4:B:696:GLU:O	4:B:699:GLU:HB2	2.02	0.59
6:D:119:ARG:HD3	6:D:221:TYR:CE2	2.37	0.59
7:E:78:LEU:HD21	7:E:80:VAL:HG23	1.83	0.59
3:A:369:SER:HB2	13:K:2:ASN:OD1	2.02	0.59
3:A:407:ARG:HG2	3:A:430:TRP:CZ2	2.37	0.59
4:B:487:THR:O	4:B:490:SER:HB3	2.02	0.59
8:F:90:ARG:HG3	8:F:91:ALA:N	2.17	0.59
9:G:144:ARG:HG2	9:G:168:LEU:HD23	1.84	0.59
10:H:81:PRO:CB	10:H:82:PRO:CD	2.81	0.59
10:H:95:TYR:HB3	10:H:144:ILE:HB	1.84	0.59
3:A:115:LEU:O	3:A:122:MET:HE2	2.02	0.59
3:A:14:VAL:H	3:A:1432:GLN:HE22	1.50	0.59
3:A:90:VAL:CG1	3:A:297:GLN:HA	2.32	0.59
3:A:414:ASP:OD1	3:A:416:ARG:HG2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:265:SER:O	4:B:266:ALA:HB3	2.03	0.59
4:B:446:LEU:O	4:B:447:ALA:HB3	2.02	0.59
4:B:871:THR:HG22	4:B:872:GLU:O	2.01	0.59
5:C:238:ILE:HG22	5:C:243:VAL:HG23	1.84	0.59
6:D:7:THR:HG21	6:D:32:GLU:OE2	2.01	0.59
9:G:1:MET:O	9:G:3:PHE:CD1	2.56	0.59
3:A:224:PHE:CE2	3:A:231:PRO:HG3	2.37	0.59
3:A:34:LYS:HB3	3:A:36:ARG:HE	1.67	0.59
3:A:53:LEU:CD2	3:A:54:ASN:HD22	2.15	0.59
3:A:49:LYS:NZ	3:A:61:ILE:HG13	2.18	0.59
3:A:630:ILE:HD13	3:A:646:PHE:CZ	2.38	0.59
3:A:682:THR:HA	3:A:685:GLU:HG2	1.85	0.59
4:B:705:MET:N	4:B:710:LEU:HD12	2.18	0.59
4:B:803:LEU:CD1	4:B:1032:SER:HB3	2.32	0.59
5:C:165:LYS:O	13:K:6:ARG:NH1	2.35	0.59
4:B:1077:THR:HG22	13:K:44:ASN:ND2	2.17	0.59
3:A:496:GLU:O	3:A:499:ALA:HB3	2.02	0.59
4:B:745:PRO:O	4:B:747:MET:N	2.35	0.59
7:E:212:ARG:HH11	7:E:212:ARG:HG3	1.68	0.59
7:E:60:PHE:CE2	7:E:80:VAL:HB	2.37	0.59
10:H:58:THR:HB	10:H:143:LEU:HD13	1.84	0.59
3:A:710:LEU:HD13	11:I:94:ASP:O	2.02	0.59
12:J:48:ARG:HE	12:J:49:MET:CE	2.14	0.59
3:A:547:LEU:HD22	13:K:58:PHE:CD1	2.38	0.59
3:A:981:LEU:CD2	3:A:1039:LYS:HA	2.33	0.59
3:A:1198:ASP:O	3:A:1202:MET:HG2	2.02	0.59
3:A:1242:VAL:HG12	3:A:1243:VAL:N	2.18	0.59
3:A:34:LYS:HE2	3:A:57:ARG:CZ	2.33	0.59
3:A:53:LEU:CD2	3:A:54:ASN:N	2.55	0.59
3:A:90:VAL:HG13	3:A:297:GLN:HA	1.84	0.59
4:B:824:ILE:HG23	4:B:1087:PHE:HE2	1.68	0.59
3:A:1447:GLU:OE2	9:G:23:LYS:HB2	2.02	0.59
3:A:1171:GLN:HA	3:A:1174:PHE:HD1	1.68	0.59
3:A:55:ASP:C	3:A:57:ARG:H	2.05	0.59
4:B:1187:ASN:O	4:B:1188:LYS:CB	2.51	0.59
4:B:653:VAL:CG2	4:B:689:LEU:HB3	2.32	0.59
4:B:309:GLN:HG3	11:I:52:ILE:CD1	2.33	0.59
3:A:427:GLN:HB2	3:A:430:TRP:NE1	2.18	0.59
3:A:858:ASN:ND2	3:A:858:ASN:C	2.56	0.59
4:B:641:GLU:HB3	4:B:643:ASP:OD2	2.03	0.59
9:G:49:LEU:HG	9:G:76:ALA:HA	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:80:LYS:HG2	9:G:80:LYS:O	2.02	0.59
6:D:29:LEU:HD13	9:G:82:PHE:CZ	2.37	0.59
11:I:50:THR:HG22	11:I:51:ASN:N	2.16	0.59
14:L:38:LEU:O	14:L:39:SER:HB3	2.01	0.59
3:A:1370:LEU:O	3:A:1374:VAL:HG23	2.03	0.59
3:A:34:LYS:NZ	3:A:57:ARG:NH1	2.50	0.59
3:A:783:THR:HG21	3:A:815:PHE:CE2	2.38	0.59
3:A:855:THR:CG2	3:A:857:ARG:HE	2.13	0.59
4:B:247:GLY:H	4:B:418:LYS:HZ3	1.49	0.59
5:C:203:GLN:HG2	5:C:207:CYS:SG	2.41	0.59
9:G:88:ASP:OD2	9:G:88:ASP:N	2.35	0.59
12:J:14:VAL:HG12	12:J:14:VAL:O	2.03	0.59
3:A:1030:ARG:NH1	3:A:1035:TYR:OH	2.35	0.58
3:A:23:SER:HB3	3:A:233:TRP:CZ2	2.38	0.58
3:A:332:LYS:H	3:A:337:ARG:HB3	1.68	0.58
3:A:722:LEU:HD22	3:A:799:PHE:CD1	2.37	0.58
4:B:221:ASN:N	4:B:241:ARG:O	2.30	0.58
4:B:546:SER:OG	4:B:631:GLY:N	2.32	0.58
3:A:1450:LEU:HG	3:A:1450:LEU:O	2.03	0.58
3:A:897:TYR:HD2	3:A:936:LEU:HD13	1.67	0.58
4:B:911:ILE:HD11	4:B:941:LEU:HD13	1.86	0.58
5:C:145:CYS:HA	12:J:2:ILE:HD11	1.85	0.58
6:D:53:SER:H	6:D:148:LEU:CD2	2.15	0.58
3:A:1373:ASP:HA	3:A:1376:THR:HG22	1.85	0.58
3:A:168:GLY:O	3:A:169:ASN:C	2.42	0.58
3:A:782:ARG:NH2	4:B:699:GLU:O	2.36	0.58
3:A:901:LEU:HD22	3:A:919:ILE:CG2	2.33	0.58
4:B:702:LEU:HD12	4:B:703:ILE:H	1.67	0.58
10:H:23:VAL:HG22	10:H:43:ASN:HA	1.85	0.58
13:K:21:ILE:HG23	13:K:31:VAL:CG1	2.33	0.58
3:A:444:PHE:HB2	3:A:458:HIS:HD2	1.67	0.58
3:A:541:ILE:HD13	3:A:549:MET:CE	2.34	0.58
3:A:596:THR:O	3:A:598:LEU:N	2.35	0.58
8:F:109:VAL:HG12	8:F:110:ASP:N	2.18	0.58
10:H:102:TYR:N	10:H:102:TYR:CD2	2.72	0.58
11:I:115:LYS:HB3	11:I:117:LYS:HG3	1.85	0.58
12:J:44:TYR:HA	12:J:47:ARG:HB2	1.85	0.58
3:A:1100:ARG:NH2	3:A:1351:GLU:HG2	2.19	0.58
4:B:995:ARG:HH12	5:C:165:LYS:HG2	1.69	0.58
5:C:254:LYS:O	5:C:258:ILE:HD13	2.02	0.58
8:F:130:ILE:O	8:F:148:VAL:CG2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1065:GLN:HG3	4:B:1067:ARG:H	1.68	0.58
4:B:418:LYS:HG2	4:B:422:LYS:HE3	1.86	0.58
4:B:856:PHE:HD2	4:B:967:ARG:HD2	1.68	0.58
5:C:17:ASN:N	5:C:240:VAL:HG11	2.18	0.58
11:I:76:PRO:HG2	11:I:110:PHE:HB3	1.84	0.58
12:J:2:ILE:H	12:J:57:ILE:HG22	1.67	0.58
3:A:1445:ILE:N	3:A:1445:ILE:HD12	2.13	0.58
3:A:399:HIS:CB	3:A:400:PRO:HD3	2.30	0.58
3:A:524:VAL:HG12	3:A:525:GLN:H	1.69	0.58
3:A:845:LEU:HD22	3:A:1374:VAL:HG21	1.84	0.58
4:B:1152:MET:CE	4:B:1157:ALA:HA	2.34	0.58
3:A:828:ALA:CB	4:B:530:GLY:HA2	2.34	0.58
5:C:131:HIS:O	5:C:133:ILE:N	2.36	0.58
11:I:85:PHE:CE1	11:I:99:LEU:HD13	2.39	0.58
12:J:1:MET:N	12:J:57:ILE:HG22	2.19	0.58
3:A:1147:THR:HB	11:I:48:LEU:HD12	1.84	0.58
3:A:871:ASP:OD1	3:A:1366:ARG:NH2	2.37	0.58
3:A:901:LEU:HD22	3:A:919:ILE:HG22	1.85	0.58
4:B:557:PHE:CD2	4:B:557:PHE:C	2.76	0.58
4:B:580:VAL:HG22	4:B:624:LEU:CB	2.33	0.58
5:C:209:TYR:N	5:C:209:TYR:CD1	2.72	0.58
7:E:22:MET:HE1	7:E:26:ARG:NH2	2.19	0.58
7:E:60:PHE:HE2	7:E:80:VAL:HB	1.68	0.58
10:H:17:PRO:HB3	10:H:24:CYS:SG	2.43	0.58
10:H:12:VAL:HG13	10:H:26:ILE:HG23	1.86	0.58
10:H:40:LEU:HD22	10:H:123:MET:CE	2.33	0.58
11:I:50:THR:CG2	11:I:52:ILE:HG12	2.34	0.58
3:A:1141:THR:OG1	3:A:1205:LYS:HD3	2.04	0.58
3:A:23:SER:HA	3:A:233:TRP:CD1	2.38	0.58
3:A:940:ARG:HG2	3:A:940:ARG:HH11	1.69	0.58
6:D:22:GLU:H	6:D:22:GLU:CD	2.07	0.58
9:G:138:THR:CG2	9:G:139:ILE:H	2.02	0.58
3:A:935:GLN:HE21	3:A:1023:ARG:NH1	2.01	0.58
3:A:1445:ILE:H	3:A:1445:ILE:CD1	2.04	0.58
3:A:264:PHE:O	3:A:267:ALA:HB3	2.04	0.58
4:B:193:LYS:HZ1	14:L:32:ALA:HB1	1.68	0.58
4:B:583:ASN:HD21	4:B:628:THR:CG2	2.08	0.58
9:G:59:GLY:HA3	9:G:70:PHE:CD2	2.38	0.58
10:H:62:SER:C	10:H:64:ASN:H	2.06	0.58
4:B:309:GLN:HG3	11:I:52:ILE:HD11	1.85	0.58
3:A:547:LEU:HD13	13:K:58:PHE:CD1	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1343:ALA:O	3:A:1346:ALA:HB3	2.03	0.57
3:A:172:PRO:HD3	3:A:185:TRP:NE1	2.18	0.57
4:B:357:GLN:O	4:B:366:GLN:HA	2.03	0.57
4:B:365:THR:HG23	4:B:367:LEU:N	2.18	0.57
4:B:969:ARG:NH1	5:C:61:GLU:OE1	2.37	0.57
5:C:124:LEU:O	5:C:127:ARG:HG2	2.04	0.57
7:E:24:LYS:HB3	7:E:30:ILE:HD12	1.85	0.57
9:G:14:HIS:CD2	9:G:16:SER:HB2	2.40	0.57
3:A:1227:ILE:HG22	3:A:1228:TRP:H	1.67	0.57
3:A:1445:ILE:HD11	9:G:68:ALA:HB1	1.87	0.57
3:A:55:ASP:CG	3:A:55:ASP:O	2.41	0.57
4:B:185:THR:O	4:B:188:ASP:HB2	2.04	0.57
4:B:218:SER:HB3	4:B:241:ARG:HH11	1.70	0.57
4:B:846:ILE:HG23	4:B:974:PRO:HG2	1.85	0.57
4:B:997:GLU:H	4:B:997:GLU:CD	2.06	0.57
5:C:212:PRO:CB	5:C:213:PRO:HD2	2.34	0.57
14:L:28:LYS:HB2	14:L:39:SER:HB2	1.86	0.57
2:T:13:U:HO2'	2:T:14:C:P	2.24	0.57
3:A:1002:GLY:HA3	3:A:1007:ILE:CG2	2.33	0.57
3:A:382:PRO:CB	3:A:428:TYR:HE2	2.18	0.57
3:A:598:LEU:HD22	10:H:25:ARG:NH1	2.19	0.57
3:A:979:SER:OG	3:A:980:ASP:N	2.35	0.57
4:B:1103:ILE:O	4:B:1122:ARG:NH1	2.37	0.57
4:B:214:ALA:HB3	4:B:498:THR:HA	1.86	0.57
5:C:172:PRO:O	5:C:235:VAL:HG23	2.05	0.57
5:C:31:ASN:OD1	5:C:34:ARG:HD3	2.04	0.57
12:J:1:MET:N	12:J:56:LEU:N	2.53	0.57
3:A:1097:GLY:O	3:A:1100:ARG:HB3	2.05	0.57
3:A:1342:GLU:OE2	7:E:212:ARG:NH1	2.38	0.57
3:A:24:PRO:HD2	3:A:233:TRP:CD1	2.38	0.57
7:E:153:HIS:HB3	7:E:196:VAL:HG11	1.86	0.57
9:G:18:PHE:HA	9:G:22:MET:HE3	1.85	0.57
10:H:100:THR:HG22	10:H:101:ALA:N	2.19	0.57
12:J:64:ASN:CB	12:J:65:PRO:CD	2.79	0.57
14:L:40:LEU:HD22	14:L:44:ASP:CB	2.34	0.57
3:A:1222:ASN:O	3:A:1223:ASP:HB3	2.05	0.57
3:A:1454:MET:O	3:A:1454:MET:HG3	2.04	0.57
3:A:427:GLN:HB2	3:A:430:TRP:CD1	2.40	0.57
3:A:535:THR:HG21	3:A:616:VAL:CA	2.30	0.57
3:A:675:THR:OG1	3:A:736:ASN:ND2	2.37	0.57
3:A:875:ALA:HA	3:A:878:ILE:CD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1222:ARG:O	4:B:1222:ARG:HG2	2.05	0.57
4:B:340:ALA:HB2	4:B:343:ILE:HD12	1.86	0.57
6:D:4:SER:O	6:D:5:THR:CB	2.51	0.57
7:E:154:ILE:H	7:E:196:VAL:HG13	1.70	0.57
7:E:207:ARG:HB2	7:E:207:ARG:NH1	2.18	0.57
3:A:1193:LEU:HD12	3:A:1194:ARG:N	2.20	0.57
3:A:1299:VAL:HG12	3:A:1300:LYS:N	2.20	0.57
3:A:215:SER:HB3	3:A:218:ASP:CG	2.24	0.57
3:A:567:LYS:HD2	3:A:568:PRO:CD	2.33	0.57
3:A:754:SER:H	3:A:757:ASN:ND2	1.86	0.57
3:A:886:ILE:HG22	3:A:887:GLY:N	2.18	0.57
3:A:886:ILE:HG13	3:A:943:LEU:CD1	2.34	0.57
4:B:166:PHE:C	4:B:167:ILE:HG13	2.25	0.57
4:B:189:LEU:O	4:B:192:LEU:N	2.34	0.57
4:B:27:ALA:O	4:B:29:ASP:N	2.37	0.57
4:B:466:TRP:O	4:B:468:GLU:N	2.37	0.57
4:B:549:THR:HG22	4:B:550:ASP:N	2.15	0.57
4:B:872:GLU:HG2	4:B:916:THR:OG1	2.04	0.57
5:C:36:VAL:HG21	5:C:251:LEU:HB2	1.85	0.57
6:D:119:ARG:HG2	6:D:120:GLU:N	2.19	0.57
10:H:41:ASP:OD2	10:H:122:LEU:N	2.37	0.57
3:A:1377:THR:O	3:A:1379:GLY:N	2.38	0.57
3:A:222:LEU:O	3:A:224:PHE:N	2.37	0.57
2:T:8:C:H4'	3:A:447:GLN:HE22	1.70	0.57
3:A:69:THR:C	3:A:71:GLN:N	2.56	0.57
3:A:841:LEU:O	3:A:845:LEU:HG	2.05	0.57
4:B:128:LEU:HD11	4:B:170:LEU:HB2	1.87	0.57
4:B:237:VAL:HG22	4:B:257:LYS:HA	1.87	0.57
8:F:119:ARG:NH1	8:F:119:ARG:HG3	2.20	0.57
8:F:68:THR:HG21	8:F:71:GLU:OE2	2.03	0.57
9:G:145:VAL:HG12	9:G:146:LYS:N	2.19	0.57
9:G:1:MET:O	9:G:3:PHE:CE1	2.58	0.57
3:A:119:ASN:O	3:A:122:MET:HB3	2.05	0.57
4:B:1096:ARG:O	4:B:1097:HIS:CB	2.53	0.57
4:B:751:VAL:HG13	4:B:812:LEU:CD2	2.35	0.57
4:B:957:ASN:O	4:B:959:ASP:N	2.38	0.57
13:K:59:ALA:HA	13:K:74:ARG:O	2.05	0.57
3:A:1244:ARG:HB3	3:A:1245:PRO:CD	2.35	0.57
3:A:341:MET:CE	3:A:843:LYS:NZ	2.68	0.57
3:A:351:THR:HB	4:B:1103:ILE:CD1	2.35	0.57
3:A:821:ARG:HD2	3:A:825:ILE:HD11	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1099:VAL:HG13	4:B:1100:ASP:N	2.19	0.57
4:B:118:ARG:HH11	4:B:204:ILE:HD11	1.69	0.57
4:B:203:PHE:N	4:B:203:PHE:CD1	2.73	0.57
5:C:99:LEU:HB2	5:C:157:CYS:HB2	1.87	0.57
9:G:17:PHE:CD2	9:G:17:PHE:N	2.71	0.57
3:A:42:ASP:C	3:A:44:THR:H	2.06	0.57
3:A:61:ILE:O	3:A:63:ARG:N	2.38	0.57
3:A:901:LEU:HB2	3:A:926:GLN:HG2	1.86	0.57
4:B:758:PHE:CE2	4:B:1044:ALA:HA	2.40	0.57
6:D:55:ALA:HB3	6:D:148:LEU:HD21	1.86	0.57
8:F:97:ARG:O	8:F:101:ILE:HG13	2.05	0.57
10:H:143:LEU:N	10:H:143:LEU:HD12	2.20	0.57
11:I:55:THR:HG22	11:I:58:VAL:HG21	1.87	0.57
3:A:268:ASP:HB3	3:A:299:HIS:CE1	2.39	0.56
3:A:666:ILE:HG23	4:B:1026:LEU:HB3	1.87	0.56
4:B:1073:TYR:CE2	4:B:1080:LYS:HG2	2.39	0.56
4:B:217:ARG:NE	4:B:405:ARG:HB2	2.20	0.56
4:B:242:SER:HB2	4:B:362:PRO:HG2	1.86	0.56
4:B:899:ILE:CD1	4:B:911:ILE:HA	2.34	0.56
5:C:2:SER:N	5:C:3:GLU:N	2.53	0.56
7:E:135:PHE:HD2	7:E:140:LEU:HD21	1.70	0.56
9:G:20:PRO:HG2	9:G:21:ARG:H	1.69	0.56
13:K:12:LEU:H	13:K:12:LEU:HD12	1.69	0.56
3:A:84:ILE:HG22	3:A:239:LEU:HB3	1.87	0.56
3:A:401:GLY:C	3:A:435:HIS:HD2	2.09	0.56
4:B:745:PRO:C	4:B:747:MET:H	2.08	0.56
6:D:160:VAL:O	6:D:164:ILE:HG13	2.05	0.56
6:D:18:VAL:O	6:D:18:VAL:HG13	2.05	0.56
9:G:1:MET:O	9:G:1:MET:SD	2.63	0.56
3:A:1035:TYR:O	3:A:1037:LEU:N	2.38	0.56
3:A:1174:PHE:C	3:A:1176:LEU:H	2.07	0.56
3:A:244:PRO:CG	3:A:245:PRO:HD3	2.35	0.56
3:A:590:ARG:O	3:A:591:PHE:HB2	2.04	0.56
3:A:63:ARG:HD3	3:A:74:MET:HE3	1.86	0.56
4:B:126:SER:OG	4:B:172:ILE:HD11	2.04	0.56
4:B:865:LYS:HE2	4:B:871:THR:OG1	2.05	0.56
5:C:147:LEU:HB2	5:C:151:GLN:HB2	1.86	0.56
5:C:133:ILE:HD12	5:C:237:SER:HA	1.87	0.56
7:E:153:HIS:HB3	7:E:196:VAL:CG1	2.35	0.56
10:H:99:GLY:HA3	10:H:118:PHE:HA	1.86	0.56
3:A:711:ARG:HA	11:I:97:MET:HE1	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:9:G:H2'	1:P:10:A:H8	1.67	0.56
3:A:1213:GLY:O	3:A:1216:ILE:N	2.39	0.56
3:A:1289:ARG:NH1	3:A:1326:ARG:NH1	2.54	0.56
3:A:114:LEU:HD13	3:A:171:GLN:NE2	2.19	0.56
3:A:298:PHE:CZ	3:A:314:ALA:HB2	2.41	0.56
3:A:418:SER:C	3:A:420:ARG:H	2.08	0.56
3:A:450:LEU:HB3	3:A:838:GLN:NE2	2.21	0.56
3:A:798:GLY:HA2	3:A:815:PHE:HD1	1.70	0.56
3:A:349:ALA:C	4:B:1128:LEU:HD11	2.25	0.56
5:C:107:SER:C	5:C:109:SER:H	2.09	0.56
6:D:33:PHE:CE2	9:G:80:LYS:NZ	2.68	0.56
7:E:46:TYR:CD2	7:E:58:MET:HG2	2.41	0.56
8:F:79:ARG:HG3	8:F:144:GLU:OE1	2.05	0.56
3:A:1369:ALA:O	3:A:1372:VAL:HG12	2.05	0.56
3:A:563:PRO:HG3	3:A:572:TRP:CE2	2.40	0.56
3:A:601:LYS:HB2	3:A:603:ASN:HD21	1.70	0.56
3:A:785:PRO:HG2	3:A:786:HIS:CD2	2.41	0.56
4:B:1001:PHE:CE1	4:B:1073:TYR:HB2	2.39	0.56
4:B:819:ALA:O	4:B:1093:GLN:HG2	2.05	0.56
4:B:118:ARG:HH22	4:B:194:GLU:CD	2.08	0.56
4:B:811:TYR:HD1	4:B:811:TYR:H	1.53	0.56
3:A:288:ALA:HA	3:A:291:GLU:OE2	2.05	0.56
3:A:345:VAL:HG21	4:B:1150:ARG:HH11	1.70	0.56
4:B:557:PHE:C	4:B:557:PHE:HD2	2.08	0.56
4:B:847:ASP:C	4:B:849:GLY:N	2.59	0.56
4:B:865:LYS:HZ3	4:B:869:SER:HA	1.70	0.56
4:B:900:ALA:HB3	14:L:61:THR:OG1	2.06	0.56
5:C:66:ARG:NH2	12:J:5:VAL:HG23	2.20	0.56
6:D:52:LEU:HD21	6:D:147:TYR:HE2	1.69	0.56
6:D:8:PHE:CD1	6:D:8:PHE:O	2.58	0.56
9:G:1:MET:HE3	9:G:80:LYS:O	2.04	0.56
9:G:47:CYS:O	9:G:76:ALA:HB1	2.05	0.56
3:A:215:SER:HB3	3:A:218:ASP:CB	2.36	0.56
3:A:41:MET:HB3	3:A:48:ALA:O	2.06	0.56
3:A:18:GLN:O	4:B:1215:ARG:HG2	2.06	0.56
4:B:39:ARG:HG2	4:B:39:ARG:NH1	2.19	0.56
4:B:844:SER:O	4:B:847:ASP:HB2	2.05	0.56
5:C:22:LEU:HB2	5:C:230:MET:HE3	1.88	0.56
5:C:31:ASN:O	5:C:34:ARG:HB3	2.05	0.56
3:A:1445:ILE:HD12	9:G:59:GLY:O	2.05	0.56
11:I:61:ASP:C	11:I:63:GLY:H	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:154:SER:CB	3:A:162:VAL:HG21	2.36	0.56
3:A:34:LYS:CE	3:A:57:ARG:NH1	2.66	0.56
3:A:504:LEU:HD12	3:A:504:LEU:N	2.21	0.56
4:B:1106:ARG:NH1	4:B:1110:PRO:HG2	2.21	0.56
3:A:106:VAL:HG13	3:A:112:LYS:O	2.06	0.56
3:A:1412:ALA:HA	3:A:1417:GLU:OE2	2.06	0.56
4:B:424:LEU:O	4:B:428:ILE:HG13	2.05	0.56
4:B:770:GLN:CD	4:B:983:ARG:HA	2.26	0.56
6:D:24:ALA:C	6:D:26:THR:H	2.09	0.56
7:E:198:ILE:CD1	7:E:212:ARG:HG3	2.35	0.56
9:G:138:THR:HG22	9:G:139:ILE:HG13	1.88	0.56
13:K:109:TRP:O	13:K:111:LEU:N	2.39	0.56
4:B:295:GLY:N	4:B:298:LEU:HD23	2.20	0.56
4:B:810:GLU:HG3	4:B:815:ARG:HH22	1.69	0.56
5:C:168:ALA:C	5:C:170:TRP:H	2.10	0.56
5:C:187:LYS:C	5:C:189:THR:H	2.10	0.56
5:C:22:LEU:HD13	5:C:230:MET:CE	2.36	0.56
3:A:869:GLY:O	7:E:204:THR:HG21	2.05	0.56
10:H:113:ALA:HB1	10:H:125:LEU:O	2.06	0.56
3:A:744:LYS:HG2	3:A:748:MET:CE	2.36	0.56
3:A:963:ILE:HD13	3:A:1049:ILE:CG1	2.36	0.56
4:B:125:SER:HA	4:B:171:PRO:HA	1.88	0.56
4:B:280:ILE:HG21	4:B:285:ILE:HG13	1.87	0.56
4:B:431:TYR:CZ	4:B:447:ALA:HB2	2.41	0.56
4:B:582:VAL:HG12	4:B:587:HIS:CD2	2.41	0.56
5:C:98:VAL:C	5:C:99:LEU:HD22	2.25	0.56
8:F:75:PRO:O	8:F:77:ASP:O	2.23	0.56
13:K:15:GLY:O	13:K:16:GLU:HG3	2.06	0.56
2:T:12:G:O2'	2:T:13:U:C3'	2.54	0.56
3:A:1166:ASP:OD2	3:A:1239:ARG:HD2	2.05	0.55
3:A:265:LYS:O	3:A:269:ILE:HG13	2.06	0.55
3:A:470:LEU:HD22	3:A:487:MET:CE	2.36	0.55
3:A:696:GLU:HG2	3:A:696:GLU:O	2.06	0.55
3:A:744:LYS:HG2	3:A:748:MET:HE2	1.88	0.55
4:B:282:ILE:HD12	4:B:382:ILE:HD13	1.89	0.55
4:B:589:VAL:CG1	4:B:590:HIS:H	2.03	0.55
5:C:18:VAL:O	5:C:20:PHE:HD2	1.89	0.55
6:D:29:LEU:HB3	9:G:82:PHE:CE2	2.41	0.55
7:E:124:VAL:HG13	7:E:132:ILE:CD1	2.36	0.55
7:E:79:TRP:HE1	7:E:81:GLU:HB2	1.71	0.55
10:H:89:LEU:C	10:H:91:ASP:N	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:308:TRP:HA	4:B:311:LEU:HD12	1.88	0.55
4:B:638:PHE:HD2	4:B:690:VAL:HG22	1.71	0.55
9:G:27:LYS:O	9:G:30:LEU:HB3	2.06	0.55
12:J:27:GLU:C	12:J:29:GLU:H	2.10	0.55
3:A:543:LEU:H	3:A:572:TRP:HZ3	1.54	0.55
3:A:49:LYS:HZ1	3:A:61:ILE:HG13	1.71	0.55
3:A:683:ILE:HD13	3:A:801:GLU:CG	2.36	0.55
3:A:829:VAL:C	3:A:831:THR:H	2.10	0.55
3:A:84:ILE:HG23	3:A:84:ILE:O	2.06	0.55
3:A:863:VAL:HG11	3:A:866:PHE:CD2	2.41	0.55
3:A:907:THR:CG2	3:A:908:LEU:N	2.68	0.55
4:B:1097:HIS:H	4:B:1098:MET:HE2	1.71	0.55
4:B:978:ASP:OD2	4:B:1098:MET:HG2	2.06	0.55
4:B:336:ARG:NE	4:B:348:ARG:HH11	2.03	0.55
4:B:247:GLY:N	4:B:418:LYS:HZ1	2.04	0.55
4:B:757:PRO:HG3	4:B:1028:GLU:OE2	2.06	0.55
4:B:955:THR:HG23	14:L:54:ARG:O	2.07	0.55
9:G:9:LEU:HD12	9:G:10:ASN:H	1.71	0.55
13:K:47:ARG:C	13:K:47:ARG:HD2	2.27	0.55
13:K:65:HIS:HD2	13:K:67:PHE:HB2	1.71	0.55
3:A:250:ILE:O	3:A:258:GLY:HA3	2.05	0.55
3:A:450:LEU:N	3:A:450:LEU:HD12	2.22	0.55
3:A:49:LYS:HZ1	3:A:61:ILE:N	2.04	0.55
3:A:58:LEU:HD21	3:A:243:PRO:HA	1.88	0.55
4:B:850:LEU:HD12	4:B:851:PHE:H	1.72	0.55
4:B:997:GLU:N	4:B:997:GLU:OE2	2.29	0.55
7:E:169:ARG:HH12	8:F:74:ILE:HD11	1.72	0.55
11:I:105:SER:O	11:I:106:CYS:HB3	2.06	0.55
11:I:26:LEU:CD2	11:I:37:GLU:HA	2.30	0.55
3:A:1332:PHE:CD2	3:A:1332:PHE:N	2.73	0.55
3:A:500:GLU:OE2	4:B:1145:SER:HB2	2.06	0.55
3:A:590:ARG:HH22	3:A:620:LYS:HB3	1.72	0.55
3:A:663:SER:OG	3:A:664:THR:N	2.40	0.55
4:B:243:ALA:HA	4:B:250:PHE:O	2.07	0.55
4:B:95:ILE:CG1	4:B:130:VAL:HG22	2.37	0.55
4:B:95:ILE:HG13	4:B:130:VAL:HG22	1.86	0.55
3:A:857:ARG:NH1	8:F:139:PRO:HB2	2.21	0.55
4:B:190:TYR:CE2	12:J:62:ARG:HB3	2.41	0.55
3:A:973:ILE:HD11	3:A:1041:ALA:HB2	1.87	0.55
3:A:478:TYR:O	3:A:479:ASN:HB3	2.06	0.55
3:A:825:ILE:HG22	3:A:826:ASP:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:909:ASP:OD1	4:B:909:ASP:N	2.40	0.55
4:B:999:MET:HB3	4:B:1007:VAL:CG2	2.36	0.55
5:C:257:SER:HA	5:C:260:LEU:HB3	1.88	0.55
7:E:55:ARG:C	7:E:57:MET:N	2.60	0.55
7:E:85:GLU:HB2	7:E:88:VAL:HG22	1.87	0.55
11:I:115:LYS:HD3	11:I:117:LYS:CE	2.26	0.55
3:A:1008:GLN:O	3:A:1011:GLN:HB3	2.07	0.55
3:A:44:THR:O	3:A:45:GLN:HB2	2.06	0.55
3:A:469:ARG:HH11	3:A:469:ARG:HB3	1.71	0.55
3:A:53:LEU:HD22	3:A:54:ASN:ND2	2.21	0.55
4:B:1223:ASP:O	4:B:1224:PHE:HB2	2.07	0.55
4:B:129:PHE:HA	4:B:165:VAL:O	2.06	0.55
7:E:197:LYS:HE2	7:E:199:ILE:HD11	1.89	0.55
7:E:44:ALA:O	7:E:45:LYS:HB2	2.06	0.55
14:L:34:CYS:SG	14:L:34:CYS:O	2.64	0.55
3:A:1198:ASP:HB3	3:A:1201:ALA:CB	2.36	0.55
3:A:407:ARG:HG2	3:A:430:TRP:CH2	2.41	0.55
3:A:567:LYS:NZ	10:H:46:LEU:HB2	2.21	0.55
3:A:567:LYS:CB	3:A:568:PRO:HD2	2.36	0.55
4:B:1174:LYS:O	4:B:1176:ASN:N	2.39	0.55
4:B:336:ARG:CZ	4:B:348:ARG:HH11	2.20	0.55
4:B:899:ILE:CG2	4:B:949:VAL:HG21	2.37	0.55
6:D:145:MET:O	6:D:149:THR:HB	2.07	0.55
7:E:157:SER:C	7:E:159:ASP:N	2.60	0.55
7:E:23:VAL:O	7:E:28:TYR:HB2	2.06	0.55
9:G:117:GLN:C	9:G:119:LEU:H	2.09	0.55
10:H:40:LEU:HD22	10:H:123:MET:HE2	1.87	0.55
5:C:145:CYS:HA	12:J:2:ILE:CD1	2.37	0.55
13:K:19:LEU:HD22	13:K:33:ILE:CG2	2.37	0.55
3:A:1064:VAL:HG12	3:A:1064:VAL:O	2.05	0.55
3:A:266:LEU:HD21	3:A:303:TYR:CE1	2.41	0.55
3:A:590:ARG:NH1	3:A:590:ARG:HG3	2.21	0.55
4:B:1177:HIS:CB	4:B:1179:GLN:HE21	2.14	0.55
4:B:287:ARG:NH1	4:B:324:ILE:O	2.40	0.55
4:B:687:GLU:O	4:B:689:LEU:HG	2.06	0.55
12:J:1:MET:H3	12:J:56:LEU:N	2.05	0.55
3:A:1076:ALA:HA	3:A:1079:MET:HE2	1.88	0.55
3:A:1116:LEU:HD11	3:A:1118:VAL:HG13	1.88	0.55
3:A:1409:LEU:O	3:A:1412:ALA:HB3	2.06	0.55
3:A:49:LYS:HZ2	3:A:60:SER:HA	1.70	0.55
3:A:537:ARG:HH12	10:H:122:LEU:HG	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:167:LEU:O	6:D:170:THR:OG1	2.25	0.55
3:A:537:ARG:HD2	10:H:20:TYR:HE1	1.72	0.55
10:H:38:LEU:HD13	10:H:125:LEU:HD13	1.87	0.55
14:L:29:TYR:N	14:L:29:TYR:CD2	2.73	0.55
3:A:60:SER:C	3:A:61:ILE:HG13	2.26	0.54
3:A:767:GLN:HA	3:A:799:PHE:HA	1.88	0.54
4:B:63:ILE:HD12	4:B:421:PHE:CE2	2.41	0.54
4:B:557:PHE:HE1	4:B:603:LEU:HD11	1.72	0.54
8:F:111:LEU:N	8:F:111:LEU:HD12	2.22	0.54
9:G:13:LEU:CD2	9:G:17:PHE:HB2	2.36	0.54
3:A:222:LEU:O	3:A:224:PHE:HD1	1.90	0.54
3:A:472:LEU:O	3:A:475:THR:HB	2.06	0.54
3:A:559:VAL:O	3:A:559:VAL:HG12	2.06	0.54
4:B:847:ASP:O	4:B:849:GLY:N	2.40	0.54
5:C:186:LEU:HD21	5:C:224:GLN:O	2.08	0.54
5:C:234:SER:CB	5:C:240:VAL:HG13	2.38	0.54
8:F:76:LYS:O	8:F:79:ARG:HD3	2.07	0.54
10:H:15:VAL:HG22	10:H:26:ILE:HG12	1.90	0.54
3:A:1349:TYR:HB2	3:A:1372:VAL:HG21	1.90	0.54
3:A:356:ASP:HB2	3:A:469:ARG:HH11	1.72	0.54
4:B:575:PRO:HG2	4:B:576:ASP:H	1.72	0.54
5:C:166:GLU:HG3	13:K:10:PHE:CZ	2.33	0.54
3:A:1340:GLY:HA2	7:E:183:PRO:HD2	1.89	0.54
3:A:720:ARG:HB3	3:A:720:ARG:NH1	2.21	0.54
3:A:346:ASP:HB3	4:B:1108:ARG:H	1.71	0.54
4:B:1182:CYS:SG	4:B:1182:CYS:O	2.65	0.54
4:B:39:ARG:HH21	4:B:665:GLU:CD	2.11	0.54
4:B:209:GLU:OE2	4:B:483:LEU:HD23	2.07	0.54
6:D:208:GLU:O	6:D:212:LYS:HG3	2.06	0.54
8:F:82:THR:HG22	8:F:84:TYR:H	1.70	0.54
11:I:50:THR:HG22	11:I:51:ASN:H	1.72	0.54
14:L:70:ARG:HG2	14:L:70:ARG:NH1	2.21	0.54
3:A:1025:ARG:O	3:A:1026:LEU:HD23	2.07	0.54
3:A:1176:LEU:HD12	3:A:1177:LEU:O	2.07	0.54
3:A:605:MET:HE2	3:A:607:ILE:HG13	1.88	0.54
4:B:1007:VAL:CG2	4:B:1008:PRO:HD2	2.37	0.54
4:B:102:VAL:HG23	4:B:112:LEU:HB2	1.88	0.54
4:B:615:MET:HB3	4:B:626:ILE:HG12	1.89	0.54
3:A:58:LEU:CD1	3:A:243:PRO:HB3	2.32	0.54
3:A:673:GLY:O	3:A:676:MET:HB2	2.07	0.54
3:A:746:MET:CE	4:B:1018:PRO:HG2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:192:LEU:O	4:B:193:LYS:HB2	2.07	0.54
4:B:44:VAL:HG11	4:B:199:MET:HG2	1.89	0.54
7:E:93:MET:SD	7:E:97:VAL:HG23	2.47	0.54
6:D:40:HIS:CB	9:G:73:LYS:HZ2	2.18	0.54
11:I:58:VAL:HG13	11:I:62:ILE:CD1	2.37	0.54
11:I:90:GLN:NE2	11:I:92:ARG:HD3	2.23	0.54
3:A:1062:GLU:OE2	8:F:88:TYR:OH	2.24	0.54
3:A:37:PHE:N	3:A:37:PHE:CD1	2.76	0.54
3:A:666:ILE:HD11	4:B:1067:ARG:O	2.06	0.54
4:B:228:LYS:CB	4:B:261:ARG:HH22	2.21	0.54
4:B:731:VAL:HG12	4:B:732:SER:N	2.23	0.54
3:A:89:PRO:HB2	3:A:204:THR:HG22	1.88	0.54
3:A:345:VAL:HG23	3:A:346:ASP:O	2.07	0.54
3:A:404:TYR:HB2	3:A:433:GLU:HB2	1.89	0.54
4:B:1065:GLN:NE2	4:B:1066:SER:N	2.56	0.54
4:B:57:TYR:HD1	4:B:57:TYR:N	2.05	0.54
4:B:806:THR:O	4:B:809:MET:HG3	2.08	0.54
4:B:952:VAL:HG12	4:B:953:LEU:H	1.71	0.54
4:B:798:TYR:CE2	5:C:62:PHE:CE2	2.92	0.54
6:D:220:LEU:O	6:D:221:TYR:HD1	1.90	0.54
8:F:125:LEU:HB2	8:F:130:ILE:HD11	1.88	0.54
4:B:39:ARG:HH21	4:B:665:GLU:CG	2.20	0.54
4:B:247:GLY:N	4:B:418:LYS:NZ	2.50	0.54
4:B:616:ILE:HG13	4:B:697:GLU:HG3	1.90	0.54
4:B:96:TYR:HB2	4:B:129:PHE:HB2	1.89	0.54
5:C:263:THR:C	5:C:265:MET:H	2.09	0.54
6:D:71:LYS:HA	6:D:74:GLN:CB	2.37	0.54
7:E:127:ILE:O	7:E:127:ILE:HG13	2.08	0.54
11:I:7:CYS:N	11:I:14:LEU:HD21	2.22	0.54
11:I:8:ARG:CG	11:I:34:TYR:HE1	2.17	0.54
13:K:42:LEU:HD21	13:K:46:ILE:HD11	1.90	0.54
14:L:53:HIS:HB3	14:L:55:ILE:CD1	2.38	0.54
3:A:1102:LYS:O	3:A:1106:ASN:ND2	2.40	0.54
3:A:1130:GLN:O	3:A:1134:ILE:HG13	2.08	0.54
3:A:19:PHE:HB3	3:A:1413:GLY:HA2	1.88	0.54
3:A:207:ILE:O	3:A:211:PHE:HD1	1.91	0.54
4:B:126:SER:O	4:B:169:ARG:HA	2.07	0.54
4:B:459:TYR:CE1	4:B:469:GLN:HG2	2.43	0.54
5:C:7:GLN:HG2	13:K:104:ASN:HD22	1.72	0.54
6:D:191:ALA:O	6:D:193:THR:N	2.41	0.54
8:F:89:GLU:HB3	8:F:134:ILE:CD1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:40:LEU:CD1	10:H:123:MET:HB2	2.36	0.54
13:K:6:ARG:O	13:K:9:LEU:HG	2.08	0.54
14:L:49:LYS:O	14:L:50:ASP:CB	2.55	0.54
3:A:1435:PRO:HA	3:A:1439:GLY:O	2.08	0.53
3:A:350:ARG:HH11	3:A:350:ARG:HG3	1.74	0.53
4:B:217:ARG:C	4:B:217:ARG:HD2	2.28	0.53
4:B:570:VAL:CG2	4:B:573:GLN:HB3	2.38	0.53
4:B:590:HIS:HD2	4:B:593:PRO:HB3	1.73	0.53
6:D:64:VAL:C	6:D:66:ARG:H	2.10	0.53
10:H:15:VAL:HG22	10:H:26:ILE:CD1	2.38	0.53
13:K:63:VAL:HG23	13:K:63:VAL:O	2.08	0.53
3:A:1239:ARG:HH22	3:A:1241:ARG:HH22	1.55	0.53
3:A:849:MET:CE	3:A:1061:GLY:HA2	2.37	0.53
4:B:1196:ILE:HB	4:B:1197:PRO:HD2	1.89	0.53
4:B:315:LYS:N	4:B:316:PRO:HD2	2.23	0.53
4:B:459:TYR:CZ	4:B:469:GLN:HG2	2.42	0.53
4:B:591:ARG:O	4:B:593:PRO:HD3	2.08	0.53
4:B:654:ARG:O	4:B:656:GLY:N	2.42	0.53
4:B:704:ALA:HB2	4:B:738:PHE:CD2	2.44	0.53
5:C:23:SER:O	5:C:24:ASN:HB3	2.07	0.53
6:D:153:ARG:HB3	6:D:154:PHE:CD1	2.43	0.53
3:A:1004:ASN:CG	7:E:167:ARG:HD2	2.28	0.53
13:K:10:PHE:CD2	13:K:10:PHE:N	2.76	0.53
3:A:341:MET:HE1	4:B:1135:ARG:NH1	2.24	0.53
3:A:399:HIS:O	3:A:401:GLY:N	2.41	0.53
3:A:442:VAL:CG2	3:A:460:VAL:HG23	2.38	0.53
3:A:699:ALA:CB	3:A:701:LEU:HG	2.36	0.53
3:A:341:MET:CE	3:A:843:LYS:HZ3	2.21	0.53
4:B:758:PHE:CE1	4:B:1027:ILE:CG2	2.92	0.53
4:B:337:ARG:C	4:B:338:GLY:N	2.61	0.53
4:B:476:ARG:NH2	4:B:501:PRO:HG3	2.23	0.53
4:B:705:MET:H	4:B:710:LEU:HD12	1.73	0.53
5:C:46:ILE:HG23	5:C:157:CYS:HB3	1.89	0.53
8:F:109:VAL:HG13	8:F:127:GLU:OE1	2.08	0.53
9:G:114:LEU:HG	9:G:162:SER:HB3	1.91	0.53
3:A:117:GLU:H	3:A:117:GLU:CD	2.12	0.53
3:A:1430:LEU:O	4:B:1196:ILE:HG22	2.09	0.53
3:A:166:GLY:O	3:A:167:CYS:SG	2.67	0.53
3:A:4:GLN:O	3:A:5:GLN:HB2	2.08	0.53
3:A:774:ARG:O	3:A:775:ILE:C	2.45	0.53
3:A:816:HIS:HE2	4:B:764:SER:H	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1034:VAL:O	4:B:1037:LEU:N	2.41	0.53
4:B:758:PHE:CZ	4:B:1044:ALA:HA	2.43	0.53
4:B:1147:LEU:HD23	4:B:1147:LEU:C	2.28	0.53
4:B:326:ASP:OD2	4:B:328:GLU:HB2	2.07	0.53
4:B:57:TYR:CD1	4:B:57:TYR:N	2.74	0.53
4:B:825:VAL:CG1	4:B:826:ALA:N	2.71	0.53
5:C:17:ASN:O	5:C:18:VAL:CG2	2.57	0.53
3:A:1291:VAL:HG22	3:A:1292:PRO:HD2	1.90	0.53
3:A:339:ASN:O	3:A:343:LYS:HG2	2.09	0.53
4:B:189:LEU:O	4:B:192:LEU:HB2	2.08	0.53
4:B:240:ILE:CG2	4:B:254:LEU:HB3	2.38	0.53
4:B:313:MET:CE	4:B:386:LEU:HD22	2.38	0.53
4:B:594:ALA:HA	4:B:617:ARG:NH1	2.24	0.53
4:B:785:TYR:CD1	4:B:786:ASN:N	2.76	0.53
7:E:154:ILE:O	7:E:196:VAL:HA	2.09	0.53
11:I:69:PRO:HG2	11:I:85:PHE:CE2	2.44	0.53
3:A:666:ILE:HD12	3:A:667:GLY:N	2.20	0.53
4:B:746:SER:CB	4:B:1046:PRO:HG2	2.32	0.53
4:B:983:ARG:HD2	4:B:1091:TYR:HB3	1.89	0.53
4:B:129:PHE:HD2	4:B:166:PHE:HA	1.72	0.53
10:H:58:THR:HG22	10:H:59:ILE:N	2.24	0.53
3:A:698:GLN:HE21	11:I:99:LEU:HD21	1.73	0.53
3:A:1134:ILE:O	3:A:1138:ILE:HG13	2.08	0.53
3:A:115:LEU:HB2	3:A:122:MET:CE	2.38	0.53
3:A:1394:THR:HG21	3:A:1398:MET:SD	2.48	0.53
3:A:1397:LEU:O	3:A:1400:CYS:HB3	2.09	0.53
3:A:30:ILE:HG23	4:B:1170:THR:HG23	1.91	0.53
3:A:64:ASN:O	3:A:65:LEU:C	2.46	0.53
3:A:711:ARG:NH2	11:I:87:GLN:OE1	2.41	0.53
3:A:73:GLY:O	3:A:75:ASN:N	2.42	0.53
4:B:233:PRO:HG2	4:B:234:ILE:CD1	2.39	0.53
4:B:343:ILE:HG21	4:B:348:ARG:HG3	1.90	0.53
4:B:479:VAL:O	4:B:480:SER:HB3	2.08	0.53
5:C:3:GLU:O	5:C:4:GLU:HB2	2.06	0.53
3:A:862:ASN:HA	7:E:174:GLN:HB3	1.91	0.53
9:G:106:MET:HG2	9:G:107:LYS:N	2.22	0.53
3:A:347:PHE:CE2	3:A:375:THR:HG23	2.43	0.53
3:A:475:THR:CG2	3:A:476:SER:N	2.72	0.53
3:A:618:GLU:O	3:A:620:LYS:N	2.42	0.53
3:A:710:LEU:H	3:A:710:LEU:HD12	1.74	0.53
4:B:642:ASP:HB3	4:B:649:LYS:CG	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:1:MET:C	9:G:1:MET:SD	2.86	0.53
10:H:64:ASN:O	10:H:65:LEU:CB	2.57	0.53
3:A:1308:THR:HG23	3:A:1309:ASP:N	2.23	0.53
3:A:997:LEU:HD13	3:A:1018:PHE:CE2	2.44	0.53
4:B:102:VAL:CG2	4:B:112:LEU:HD22	2.38	0.53
4:B:1071:VAL:O	4:B:1072:MET:HG3	2.08	0.53
3:A:340:LEU:HD21	4:B:1200:ALA:N	2.24	0.53
4:B:233:PRO:HG2	4:B:234:ILE:HD12	1.90	0.53
4:B:502:ILE:N	4:B:502:ILE:HD12	2.20	0.53
3:A:828:ALA:HB2	4:B:530:GLY:HA2	1.91	0.53
3:A:472:LEU:CD1	4:B:835:GLN:NE2	2.71	0.53
4:B:986:GLN:OE1	4:B:986:GLN:HA	2.09	0.53
5:C:214:ASN:HB3	5:C:217:ASP:OD2	2.09	0.53
7:E:28:TYR:CE1	7:E:78:LEU:HD13	2.44	0.53
3:A:1444:MET:HG3	9:G:60:ARG:HA	1.90	0.53
12:J:9:SER:HB2	12:J:45:CYS:HB2	1.90	0.53
13:K:47:ARG:CB	13:K:47:ARG:HH11	2.17	0.53
3:A:50:ILE:O	3:A:52:GLY:N	2.42	0.53
3:A:61:ILE:HG22	3:A:62:ASP:N	2.23	0.53
3:A:901:LEU:HA	3:A:907:THR:OG1	2.09	0.53
4:B:1065:GLN:NE2	4:B:1066:SER:H	2.07	0.53
4:B:582:VAL:HA	4:B:626:ILE:O	2.09	0.53
8:F:109:VAL:HG21	8:F:124:GLU:HA	1.90	0.53
3:A:1348:LEU:HG	3:A:1372:VAL:CG2	2.39	0.52
3:A:219:PHE:CE2	3:A:231:PRO:HD2	2.43	0.52
3:A:382:PRO:HB3	3:A:428:TYR:CE2	2.38	0.52
3:A:446:ARG:HB2	3:A:487:MET:SD	2.49	0.52
4:B:766:ARG:NH2	4:B:1020:ARG:HH11	2.06	0.52
4:B:169:ARG:HB2	4:B:454:THR:HG23	1.91	0.52
4:B:487:THR:CG2	4:B:488:TYR:N	2.73	0.52
4:B:693:ILE:HD11	4:B:740:HIS:CD2	2.44	0.52
4:B:693:ILE:HD13	4:B:701:ILE:HD13	1.90	0.52
4:B:1001:PHE:CE2	5:C:34:ARG:NE	2.77	0.52
11:I:32:CYS:SG	11:I:33:SER:N	2.81	0.52
4:B:822:ASN:O	12:J:48:ARG:NH1	2.41	0.52
3:A:113:LEU:HG	3:A:218:ASP:OD1	2.09	0.52
3:A:326:ARG:NH2	3:A:1407:GLU:HG3	2.24	0.52
3:A:300:VAL:O	3:A:300:VAL:HG12	2.08	0.52
3:A:767:GLN:HE21	3:A:774:ARG:HB3	1.71	0.52
4:B:216:GLU:HA	4:B:406:LEU:CD2	2.40	0.52
4:B:542:MET:HG2	4:B:747:MET:HE3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:797:TYR:HE1	4:B:854:LEU:CD2	2.23	0.52
4:B:797:TYR:HE1	4:B:854:LEU:HD23	1.72	0.52
5:C:177:GLU:HB2	5:C:231:ASN:HB3	1.89	0.52
8:F:100:GLN:O	8:F:103:MET:HB2	2.09	0.52
9:G:15:PRO:HA	9:G:18:PHE:CE1	2.43	0.52
13:K:31:VAL:CG1	13:K:32:VAL:N	2.71	0.52
3:A:1215:ARG:HA	3:A:1218:GLN:HG2	1.90	0.52
3:A:34:LYS:HB3	3:A:36:ARG:NE	2.24	0.52
4:B:464:GLY:HA2	4:B:479:VAL:O	2.09	0.52
4:B:515:HIS:H	4:B:518:HIS:CD2	2.14	0.52
4:B:641:GLU:C	4:B:643:ASP:H	2.12	0.52
6:D:8:PHE:HE1	6:D:38:ILE:H	1.57	0.52
6:D:56:ARG:NH2	6:D:57:LEU:HD21	2.23	0.52
7:E:202:SER:OG	7:E:204:THR:HG22	2.09	0.52
9:G:94:CYS:HA	9:G:99:PHE:HA	1.90	0.52
12:J:20:SER:O	12:J:24:LEU:HG	2.09	0.52
13:K:93:SER:O	13:K:97:LYS:HG3	2.09	0.52
3:A:208:LEU:HD21	3:A:212:LYS:HE3	1.90	0.52
3:A:471:ASN:O	3:A:474:VAL:HG12	2.10	0.52
3:A:504:LEU:HD11	8:F:91:ALA:HB1	1.92	0.52
3:A:738:LYS:C	3:A:740:LEU:H	2.13	0.52
3:A:996:ASN:C	3:A:998:LEU:HD12	2.29	0.52
4:B:843:GLN:O	4:B:844:SER:C	2.48	0.52
5:C:15:LYS:O	5:C:240:VAL:HG22	2.09	0.52
10:H:130:ARG:HB3	10:H:133:ASN:HB2	1.91	0.52
11:I:7:CYS:HB3	11:I:14:LEU:HD21	1.90	0.52
4:B:1039:GLY:HA2	12:J:51:LEU:HD21	1.91	0.52
13:K:42:LEU:O	13:K:46:ILE:HG13	2.08	0.52
3:A:971:PHE:CE2	3:A:1040:GLN:HG2	2.45	0.52
3:A:12:ARG:O	4:B:1194:ILE:HG22	2.09	0.52
3:A:1324:PRO:HB2	7:E:142:VAL:HG11	1.91	0.52
3:A:1333:ILE:O	3:A:1337:GLU:HG3	2.09	0.52
3:A:1445:ILE:HG12	9:G:18:PHE:CE2	2.44	0.52
3:A:335:ARG:O	3:A:339:ASN:HB2	2.08	0.52
3:A:960:ILE:HA	3:A:963:ILE:HG22	1.90	0.52
4:B:1081:LEU:HD12	4:B:1085:ILE:HD11	1.91	0.52
3:A:1017:LEU:CB	7:E:206:GLY:H	2.20	0.52
8:F:109:VAL:CG1	8:F:123:LYS:HD3	2.39	0.52
10:H:24:CYS:HB2	10:H:44:VAL:HG21	1.92	0.52
11:I:101:PHE:HB2	11:I:110:PHE:CE2	2.45	0.52
12:J:27:GLU:O	12:J:29:GLU:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:546:VAL:HG21	3:A:572:TRP:CE3	2.44	0.52
3:A:898:ARG:HB2	3:A:933:TYR:HE1	1.75	0.52
4:B:225:VAL:HA	4:B:237:VAL:O	2.10	0.52
4:B:563:MET:CE	4:B:580:VAL:HB	2.40	0.52
10:H:4:THR:CA	10:H:60:ALA:HB2	2.28	0.52
3:A:1397:LEU:HB2	3:A:1426:GLU:OE1	2.10	0.52
3:A:298:PHE:HZ	3:A:314:ALA:HB2	1.74	0.52
3:A:353:ILE:HD13	3:A:487:MET:HE2	1.92	0.52
3:A:626:ASN:O	3:A:631:HIS:CD2	2.63	0.52
3:A:68:GLN:O	3:A:70:CYS:N	2.37	0.52
4:B:171:PRO:HD2	4:B:457:LEU:HD13	1.90	0.52
4:B:281:PRO:HG2	4:B:284:ILE:HG13	1.92	0.52
5:C:189:THR:CG2	5:C:190:ASP:H	2.21	0.52
5:C:182:PRO:HG3	5:C:206:ASN:O	2.09	0.52
6:D:198:LEU:O	6:D:200:ASN:N	2.43	0.52
9:G:119:LEU:CD1	9:G:132:SER:HB2	2.39	0.52
9:G:96:GLN:HB3	9:G:121:PHE:CE2	2.45	0.52
3:A:567:LYS:HE3	10:H:46:LEU:HB2	1.90	0.52
3:A:1147:THR:HB	11:I:48:LEU:CD1	2.39	0.52
3:A:265:LYS:HE2	3:A:322:VAL:HG11	1.91	0.52
3:A:779:PHE:O	3:A:780:VAL:C	2.48	0.52
4:B:1124:ARG:O	4:B:1125:ASP:HB3	2.08	0.52
4:B:834:ASN:HA	4:B:838:SER:O	2.09	0.52
5:C:251:LEU:O	5:C:251:LEU:HD12	2.09	0.52
5:C:69:LEU:O	12:J:6:ARG:HD2	2.09	0.52
11:I:62:ILE:O	11:I:62:ILE:HG12	2.10	0.52
4:B:824:ILE:HG12	12:J:48:ARG:HH12	1.75	0.52
13:K:18:LYS:NZ	13:K:37:LYS:O	2.43	0.52
3:A:253:ASN:HB3	4:B:935:ARG:NH2	2.24	0.52
3:A:512:VAL:HA	3:A:519:PRO:HA	1.92	0.52
4:B:228:LYS:HB2	4:B:261:ARG:HH22	1.75	0.52
4:B:562:GLY:C	4:B:590:HIS:HD1	2.13	0.52
4:B:995:ARG:NH1	5:C:165:LYS:HG2	2.24	0.52
5:C:34:ARG:NH1	5:C:35:ARG:HG2	2.25	0.52
6:D:5:THR:O	6:D:5:THR:HG23	2.10	0.52
8:F:111:LEU:C	8:F:113:GLY:H	2.13	0.52
9:G:73:LYS:HE2	9:G:74:TYR:O	2.10	0.52
11:I:71:SER:OG	11:I:83:ASN:HB2	2.08	0.52
13:K:55:LYS:HB3	13:K:81:TYR:CD1	2.45	0.52
4:B:1166:CYS:HB2	4:B:1215:ARG:NH1	2.24	0.52
4:B:244:LEU:HD11	4:B:366:GLN:NE2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:363:HIS:CD2	4:B:585:VAL:HG22	2.45	0.52
4:B:370:PHE:HE2	4:B:373:ARG:NH1	2.05	0.52
4:B:466:TRP:CE3	4:B:466:TRP:HA	2.43	0.52
4:B:616:ILE:CG1	4:B:697:GLU:HA	2.40	0.52
4:B:871:THR:HG22	4:B:872:GLU:N	2.24	0.52
4:B:948:ILE:HG22	4:B:949:VAL:O	2.09	0.52
10:H:18:GLY:O	10:H:19:ARG:HB2	2.10	0.52
12:J:2:ILE:HG12	12:J:57:ILE:HD12	1.92	0.52
3:A:42:ASP:HA	3:A:46:THR:O	2.10	0.51
3:A:50:ILE:C	3:A:52:GLY:N	2.62	0.51
3:A:54:ASN:N	3:A:54:ASN:HD22	2.08	0.51
3:A:722:LEU:O	3:A:725:ALA:HB3	2.11	0.51
3:A:666:ILE:N	4:B:1026:LEU:HD13	2.25	0.51
4:B:681:TRP:HA	4:B:684:LEU:CD1	2.40	0.51
4:B:1065:GLN:HB2	5:C:201:TRP:CZ3	2.44	0.51
6:D:29:LEU:HD22	9:G:82:PHE:CD2	2.45	0.51
10:H:123:MET:HE1	10:H:142:LEU:HD11	1.92	0.51
13:K:110:ASN:O	13:K:111:LEU:CB	2.57	0.51
3:A:1400:CYS:O	3:A:1405:THR:HG23	2.10	0.51
4:B:824:ILE:HG12	12:J:48:ARG:NH1	2.25	0.51
4:B:1063:GLY:O	5:C:202:PRO:HG2	2.11	0.51
9:G:56:ILE:O	9:G:57:GLN:HB2	2.09	0.51
3:A:1018:PHE:O	3:A:1021:LEU:HB3	2.11	0.51
3:A:1305:VAL:CG1	3:A:1306:LEU:N	2.73	0.51
3:A:1120:LEU:O	3:A:1323:ASP:HB2	2.10	0.51
3:A:846:GLU:OE1	3:A:1425:SER:OG	2.29	0.51
4:B:1087:PHE:HD2	4:B:1088:GLY:H	1.58	0.51
4:B:1197:PRO:HG2	4:B:1200:ALA:CB	2.41	0.51
4:B:542:MET:HG2	4:B:747:MET:HB3	1.91	0.51
4:B:882:THR:HG22	4:B:884:ARG:HB2	1.93	0.51
5:C:3:GLU:O	5:C:4:GLU:CB	2.59	0.51
10:H:113:ALA:HB2	10:H:126:GLU:HG3	1.92	0.51
13:K:57:LEU:HD12	13:K:77:THR:O	2.10	0.51
3:A:172:PRO:HD3	3:A:185:TRP:HE1	1.76	0.51
3:A:475:THR:HG23	3:A:476:SER:H	1.76	0.51
4:B:1074:ASN:HB2	4:B:1081:LEU:HD21	1.92	0.51
3:A:666:ILE:HD11	4:B:1086:PHE:HE1	1.75	0.51
4:B:1106:ARG:HH21	4:B:1111:MET:CE	2.24	0.51
3:A:806:ARG:HH12	4:B:729:ILE:CD1	2.23	0.51
5:C:235:VAL:HG13	12:J:13:VAL:HG23	1.92	0.51
7:E:16:PHE:HZ	7:E:20:LYS:HE2	1.70	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:99:PHE:HZ	9:G:163:ILE:HD13	1.76	0.51
10:H:130:ARG:N	10:H:130:ARG:HD2	2.16	0.51
5:C:52:GLU:HA	14:L:64:LEU:HD22	1.91	0.51
3:A:152:VAL:HG12	3:A:153:PRO:CD	2.40	0.51
3:A:525:GLN:HG3	4:B:835:GLN:HG2	1.93	0.51
3:A:897:TYR:CD2	3:A:936:LEU:HD13	2.45	0.51
3:A:907:THR:HG23	3:A:908:LEU:N	2.26	0.51
4:B:1050:ILE:HG22	4:B:1051:THR:N	2.26	0.51
3:A:29:ALA:HB1	4:B:1184:GLY:HA2	1.93	0.51
4:B:340:ALA:HB1	4:B:343:ILE:HD12	1.92	0.51
4:B:833:TYR:N	4:B:833:TYR:CD1	2.77	0.51
4:B:872:GLU:CD	4:B:914:LYS:HE2	2.31	0.51
4:B:862:GLN:CG	4:B:963:PHE:HD1	2.21	0.51
5:C:183:TRP:O	5:C:185:LYS:N	2.43	0.51
6:D:173:HIS:CD2	6:D:175:PHE:H	2.29	0.51
6:D:63:LEU:HD23	9:G:47:CYS:SG	2.51	0.51
9:G:149:GLY:O	9:G:159:ALA:HB1	2.11	0.51
10:H:127:GLY:N	10:H:130:ARG:HH22	2.07	0.51
14:L:43:THR:O	14:L:43:THR:HG22	2.10	0.51
3:A:1283:VAL:HG12	3:A:1284:MET:N	2.25	0.51
3:A:1436:ILE:CD1	4:B:1139:ILE:HG23	2.41	0.51
3:A:332:LYS:HB2	3:A:337:ARG:CZ	2.41	0.51
3:A:382:PRO:HD3	3:A:428:TYR:CD2	2.45	0.51
3:A:62:ASP:HB3	3:A:64:ASN:HD21	1.74	0.51
3:A:794:PRO:C	3:A:796:SER:H	2.13	0.51
3:A:898:ARG:HB2	3:A:933:TYR:CE1	2.46	0.51
3:A:903:ASN:C	3:A:903:ASN:ND2	2.64	0.51
4:B:29:ASP:OD1	4:B:658:ILE:HD13	2.10	0.51
4:B:343:ILE:HG22	4:B:348:ARG:HG3	1.91	0.51
4:B:336:ARG:CZ	4:B:348:ARG:NH1	2.73	0.51
4:B:212:LEU:CD2	4:B:480:SER:HB2	2.36	0.51
5:C:20:PHE:CE1	5:C:22:LEU:HD12	2.45	0.51
6:D:8:PHE:CD2	9:G:6:ASP:O	2.63	0.51
3:A:116:ASP:O	3:A:118:HIS:N	2.43	0.51
3:A:148:CYS:O	3:A:168:GLY:HA2	2.09	0.51
3:A:412:ARG:NH2	4:B:1108:ARG:HH12	2.08	0.51
4:B:168:GLY:HA2	4:B:454:THR:OG1	2.11	0.51
4:B:785:TYR:CD1	4:B:785:TYR:C	2.83	0.51
4:B:839:MET:HE1	4:B:980:PHE:HB2	1.92	0.51
7:E:165:LEU:N	7:E:165:LEU:HD23	2.25	0.51
11:I:69:PRO:HG2	11:I:85:PHE:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:85:PHE:N	11:I:85:PHE:HD2	2.02	0.51
3:A:1066:VAL:O	3:A:1070:GLN:HG3	2.10	0.51
3:A:351:THR:HG22	4:B:1103:ILE:HA	1.91	0.51
4:B:984:HIS:NE2	4:B:1025:HIS:HA	2.26	0.51
4:B:361:LEU:N	4:B:362:PRO:CD	2.73	0.51
4:B:460:ALA:HB1	4:B:466:TRP:CZ3	2.46	0.51
5:C:259:LEU:HD13	13:K:91:CYS:CB	2.40	0.51
4:B:1001:PHE:CE2	5:C:34:ARG:CZ	2.94	0.51
6:D:123:LEU:HD23	6:D:149:THR:HG21	1.93	0.51
3:A:1371:LEU:O	3:A:1375:MET:HG3	2.10	0.51
3:A:896:ARG:NH2	3:A:1030:ARG:NH2	2.59	0.51
4:B:944:THR:HG21	4:B:1122:ARG:NH2	2.26	0.51
4:B:216:GLU:HA	4:B:406:LEU:HD23	1.93	0.51
4:B:840:ILE:HG21	4:B:994:TYR:HD1	1.75	0.51
5:C:213:PRO:O	5:C:214:ASN:CB	2.58	0.51
7:E:24:LYS:HG3	7:E:25:ASP:N	2.26	0.51
7:E:55:ARG:O	7:E:57:MET:N	2.44	0.51
8:F:96:THR:O	8:F:100:GLN:HG3	2.11	0.51
3:A:1220:PHE:O	3:A:1221:LYS:HB2	2.11	0.51
3:A:89:PRO:HB3	3:A:208:LEU:HD12	1.93	0.51
3:A:58:LEU:HD11	3:A:244:PRO:HD2	1.91	0.51
4:B:176:SER:O	4:B:182:SER:HB3	2.11	0.51
4:B:329:THR:O	4:B:332:ASP:HB3	2.10	0.51
4:B:288:ALA:O	4:B:331:LEU:HD11	2.11	0.51
4:B:640:VAL:O	4:B:641:GLU:C	2.49	0.51
4:B:885:MET:HA	4:B:936:ASP:HB2	1.92	0.51
5:C:97:VAL:HB	5:C:159:ALA:HB3	1.93	0.51
10:H:128:ASN:O	10:H:128:ASN:OD1	2.29	0.51
11:I:7:CYS:SG	11:I:8:ARG:O	2.69	0.51
3:A:1149:ALA:HB2	11:I:47:GLU:HA	1.92	0.50
3:A:152:VAL:HG13	3:A:153:PRO:HD2	1.90	0.50
3:A:527:THR:CG2	3:A:650:GLN:HA	2.41	0.50
3:A:591:PHE:HA	3:A:595:THR:HG21	1.92	0.50
3:A:75:ASN:O	3:A:76:GLU:CB	2.59	0.50
3:A:982:THR:O	3:A:985:ASP:HB2	2.11	0.50
4:B:1040:ASN:O	4:B:1042:GLY:N	2.43	0.50
3:A:347:PHE:H	4:B:1107:ALA:HA	1.76	0.50
4:B:23:ALA:H	4:B:654:ARG:HB3	1.77	0.50
4:B:637:LEU:O	4:B:690:VAL:HG13	2.11	0.50
5:C:112:ASN:HB2	5:C:114:TYR:HE1	1.74	0.50
5:C:184:ASN:HD21	5:C:187:LYS:HA	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:62:PHE:O	5:C:66:ARG:HG3	2.10	0.50
9:G:127:PRO:HG2	9:G:138:THR:CG2	2.37	0.50
3:A:1197:LEU:HD11	3:A:1238:ILE:HD11	1.93	0.50
4:B:1176:ASN:C	4:B:1178:ASN:H	2.15	0.50
3:A:1410:PHE:HD2	4:B:1212:ILE:HD12	1.76	0.50
4:B:215:GLN:OE1	4:B:479:VAL:HG22	2.11	0.50
4:B:309:GLN:OE1	11:I:52:ILE:HD11	2.11	0.50
4:B:731:VAL:HG12	4:B:732:SER:H	1.76	0.50
4:B:882:THR:HB	4:B:934:LYS:O	2.11	0.50
3:A:1446:ASP:HB2	8:F:133:VAL:HG23	1.93	0.50
11:I:6:PHE:HA	11:I:14:LEU:HG	1.92	0.50
3:A:1425:SER:O	3:A:1429:ILE:HG13	2.11	0.50
3:A:317:LYS:O	3:A:318:SER:CB	2.58	0.50
3:A:648:ASN:O	3:A:649:ILE:C	2.48	0.50
3:A:718:VAL:O	3:A:721:PHE:HB2	2.10	0.50
3:A:805:LEU:CD1	4:B:1052:VAL:HG21	2.42	0.50
3:A:357:PRO:HD2	4:B:833:TYR:CE1	2.46	0.50
5:C:138:GLU:N	5:C:138:GLU:OE1	2.42	0.50
5:C:241:ASP:OD1	5:C:242:GLN:N	2.42	0.50
6:D:4:SER:OG	6:D:5:THR:N	2.45	0.50
6:D:8:PHE:O	6:D:9:GLN:HB2	2.11	0.50
7:E:112:TYR:CE1	7:E:136:ASN:HB2	2.46	0.50
10:H:91:ASP:O	10:H:93:TYR:N	2.41	0.50
3:A:1149:ALA:CB	11:I:47:GLU:HA	2.41	0.50
12:J:14:VAL:CG1	12:J:50:ILE:HD11	2.39	0.50
4:B:822:ASN:ND2	12:J:52:THR:HG21	2.26	0.50
3:A:207:ILE:HG22	3:A:211:PHE:CE1	2.47	0.50
3:A:325:ILE:HG21	4:B:1210:MET:HG3	1.94	0.50
3:A:719:VAL:C	3:A:721:PHE:H	2.14	0.50
3:A:720:ARG:HB3	3:A:720:ARG:CZ	2.42	0.50
3:A:31:SER:HA	3:A:81:PHE:O	2.12	0.50
4:B:313:MET:HE2	4:B:386:LEU:HD22	1.93	0.50
5:C:263:THR:C	5:C:265:MET:N	2.64	0.50
5:C:31:ASN:O	5:C:32:SER:C	2.50	0.50
6:D:63:LEU:HD13	6:D:133:THR:OG1	2.10	0.50
6:D:153:ARG:C	6:D:154:PHE:CD1	2.85	0.50
9:G:35:GLU:CG	9:G:48:VAL:HG23	2.41	0.50
3:A:295:LEU:O	3:A:298:PHE:HB3	2.11	0.50
3:A:837:ILE:HA	3:A:840:ARG:HD3	1.92	0.50
4:B:295:GLY:O	4:B:299:GLU:HG2	2.12	0.50
4:B:683:SER:O	4:B:687:GLU:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:798:TYR:HE2	5:C:62:PHE:HE2	1.56	0.50
5:C:70:ILE:HD11	5:C:144:ILE:HG12	1.93	0.50
6:D:56:ARG:HD3	6:D:149:THR:HA	1.91	0.50
3:A:852:TYR:CD1	8:F:136:ARG:HB3	2.46	0.50
9:G:44:TYR:CD2	9:G:105:PRO:HB2	2.47	0.50
10:H:26:ILE:CG2	10:H:27:GLU:N	2.75	0.50
3:A:571:LEU:HD22	10:H:46:LEU:HD11	1.94	0.50
3:A:1120:LEU:O	3:A:1323:ASP:N	2.44	0.50
3:A:16:GLU:HB3	3:A:1418:LEU:HD11	1.94	0.50
3:A:675:THR:O	3:A:679:ILE:HG13	2.12	0.50
4:B:824:ILE:CG2	4:B:1087:PHE:CE2	2.93	0.50
4:B:526:GLU:OE2	4:B:752:ALA:HB2	2.12	0.50
4:B:638:PHE:HB3	4:B:651:LEU:HD22	1.94	0.50
5:C:89:GLU:O	5:C:90:ASP:HB3	2.11	0.50
9:G:34:VAL:CG1	9:G:45:ILE:HG21	2.37	0.50
3:A:1101:LEU:HB2	3:A:1355:VAL:HG11	1.93	0.50
3:A:224:PHE:HD2	3:A:229:SER:O	1.95	0.50
4:B:100:PRO:HB2	4:B:180:TYR:HE1	1.75	0.50
4:B:169:ARG:HD2	4:B:454:THR:HG21	1.93	0.50
6:D:195:ILE:HG22	6:D:198:LEU:HG	1.93	0.50
6:D:39:ASN:HD21	6:D:41:GLN:HE21	1.54	0.50
7:E:145:THR:HG21	7:E:187:TYR:CD2	2.46	0.50
8:F:68:THR:O	8:F:69:LEU:HB3	2.12	0.50
9:G:137:ILE:HG21	9:G:143:ILE:HD11	1.94	0.50
9:G:80:LYS:HD3	9:G:80:LYS:N	2.26	0.50
12:J:7:CYS:O	12:J:11:GLY:HA2	2.12	0.50
12:J:55:ASP:OD2	12:J:58:GLU:HG2	2.12	0.50
3:A:1144:LYS:HB2	3:A:1268:LEU:O	2.11	0.50
3:A:1120:LEU:CD1	3:A:1304:TRP:O	2.60	0.50
3:A:1364:ASN:O	3:A:1365:TYR:C	2.50	0.50
3:A:180:LYS:NZ	3:A:294:SER:HB3	2.26	0.50
3:A:606:LEU:HG	3:A:613:ILE:HD12	1.93	0.50
3:A:853:ASP:OD1	3:A:855:THR:CB	2.60	0.50
3:A:920:LEU:HD23	3:A:921:GLY:N	2.27	0.50
4:B:1162:ILE:HG22	4:B:1163:CYS:H	1.77	0.50
4:B:291:ILE:HD13	4:B:300:HIS:CD2	2.47	0.50
4:B:289:LEU:HD13	4:B:375:ALA:HB2	1.93	0.50
4:B:639:ILE:HG22	4:B:641:GLU:HG2	1.94	0.50
9:G:115:MET:CB	9:G:116:PRO:HD2	2.42	0.50
9:G:145:VAL:CG1	9:G:146:LYS:N	2.74	0.50
14:L:40:LEU:HD13	14:L:44:ASP:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:43:GLU:O	3:A:44:THR:HB	2.12	0.50
3:A:852:TYR:CE2	3:A:1060:PRO:HB2	2.47	0.50
4:B:1045:SER:O	4:B:1046:PRO:O	2.30	0.50
3:A:346:ASP:HB3	4:B:1108:ARG:N	2.25	0.50
4:B:171:PRO:HD2	4:B:457:LEU:CD1	2.42	0.50
4:B:281:PRO:O	4:B:283:VAL:N	2.45	0.50
4:B:840:ILE:HD13	4:B:994:TYR:HE1	1.77	0.50
4:B:976:ILE:O	4:B:978:ASP:N	2.45	0.50
5:C:168:ALA:C	5:C:170:TRP:N	2.65	0.50
5:C:11:ARG:HD3	5:C:209:TYR:CZ	2.46	0.50
8:F:114:GLU:OE2	8:F:119:ARG:HG2	2.12	0.50
3:A:1446:ASP:HB2	8:F:133:VAL:CG2	2.41	0.50
9:G:115:MET:HB3	9:G:116:PRO:HD2	1.93	0.50
10:H:55:LEU:HD22	10:H:144:ILE:CG2	2.42	0.50
12:J:31:ASP:O	12:J:32:GLU:C	2.50	0.50
3:A:1401:SER:O	3:A:1402:PHE:HB2	2.11	0.49
3:A:7:SER:CB	4:B:1175:LEU:HD22	2.42	0.49
3:A:827:THR:O	3:A:831:THR:HB	2.11	0.49
3:A:845:LEU:O	3:A:846:GLU:C	2.50	0.49
3:A:963:ILE:HD13	3:A:1049:ILE:HG13	1.93	0.49
4:B:33:VAL:O	4:B:36:ALA:HB3	2.11	0.49
4:B:654:ARG:C	4:B:656:GLY:H	2.15	0.49
5:C:18:VAL:CG2	5:C:240:VAL:HB	2.42	0.49
7:E:124:VAL:HG13	7:E:132:ILE:CG1	2.42	0.49
3:A:1017:LEU:HB3	7:E:205:SER:HA	1.93	0.49
8:F:109:VAL:HG23	8:F:124:GLU:HG2	1.94	0.49
9:G:80:LYS:O	9:G:82:PHE:CE1	2.65	0.49
9:G:96:GLN:HG3	9:G:97:HIS:CD2	2.45	0.49
11:I:14:LEU:HD22	11:I:28:GLU:O	2.12	0.49
3:A:1313:LEU:HD23	3:A:1338:VAL:CG2	2.41	0.49
3:A:1450:LEU:O	3:A:1450:LEU:CG	2.59	0.49
3:A:187:LYS:NZ	3:A:198:GLU:OE2	2.39	0.49
3:A:224:PHE:CD2	3:A:231:PRO:HG3	2.47	0.49
3:A:93:VAL:CG2	3:A:301:ALA:HA	2.41	0.49
3:A:616:VAL:HG12	3:A:617:VAL:N	2.27	0.49
3:A:621:THR:O	3:A:629:LEU:HB2	2.12	0.49
3:A:720:ARG:O	3:A:724:GLU:HB2	2.11	0.49
3:A:981:LEU:HD21	3:A:1039:LYS:HA	1.94	0.49
4:B:1182:CYS:C	4:B:1183:LYS:HE3	2.32	0.49
4:B:521:LEU:HB3	4:B:633:VAL:HG11	1.94	0.49
4:B:640:VAL:O	4:B:640:VAL:HG12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:76:ASP:OD2	5:C:128:ASN:N	2.44	0.49
5:C:74:SER:HB2	5:C:77:ILE:HG12	1.95	0.49
4:B:1077:THR:HG22	13:K:44:ASN:HD21	1.77	0.49
3:A:1007:ILE:HD13	7:E:168:TYR:HE2	1.77	0.49
3:A:997:LEU:HD13	3:A:1018:PHE:HE2	1.76	0.49
3:A:322:VAL:HG12	3:A:322:VAL:O	2.11	0.49
3:A:341:MET:HE2	3:A:843:LYS:HZ1	1.77	0.49
4:B:281:PRO:HB3	4:B:320:ASP:OD2	2.12	0.49
9:G:14:HIS:CD2	9:G:16:SER:CB	2.95	0.49
11:I:15:TYR:N	11:I:15:TYR:CD1	2.80	0.49
3:A:783:THR:HG22	3:A:784:LEU:HG	1.93	0.49
3:A:808:LEU:HD23	3:A:813:PHE:HA	1.93	0.49
4:B:896:ASP:CG	14:L:58:LYS:HZ2	2.16	0.49
7:E:157:SER:O	7:E:159:ASP:N	2.45	0.49
7:E:156:LEU:HA	7:E:160:GLU:OE1	2.12	0.49
3:A:1006:ILE:HB	7:E:167:ARG:HG3	1.95	0.49
3:A:857:ARG:CZ	8:F:139:PRO:HG3	2.43	0.49
10:H:101:ALA:HB2	10:H:116:TYR:CE1	2.48	0.49
10:H:13:SER:O	10:H:14:GLU:HB2	2.13	0.49
3:A:939:ASP:OD1	3:A:1023:ARG:NH1	2.46	0.49
3:A:106:VAL:HG12	3:A:107:CYS:N	2.28	0.49
3:A:1283:VAL:HG12	3:A:1284:MET:H	1.78	0.49
3:A:438:ASP:OD1	3:A:461:LYS:HA	2.12	0.49
3:A:440:ASP:O	3:A:442:VAL:HG22	2.12	0.49
4:B:1072:MET:HE3	4:B:1085:ILE:HD13	1.94	0.49
4:B:777:ALA:HA	4:B:1095:LEU:HA	1.94	0.49
4:B:1174:LYS:O	4:B:1176:ASN:HB2	2.11	0.49
4:B:409:ALA:O	4:B:413:LEU:HG	2.12	0.49
4:B:37:PHE:CD1	4:B:41:LYS:HG3	2.45	0.49
4:B:680:THR:O	4:B:684:LEU:HD12	2.12	0.49
7:E:22:MET:CE	7:E:26:ARG:NH2	2.74	0.49
10:H:87:ARG:O	10:H:89:LEU:HG	2.12	0.49
14:L:39:SER:O	14:L:40:LEU:HG	2.11	0.49
3:A:1211:GLN:O	3:A:1212:VAL:C	2.51	0.49
3:A:51:GLY:HA2	3:A:56:PRO:HA	1.94	0.49
4:B:204:ILE:HG22	4:B:204:ILE:O	2.12	0.49
4:B:745:PRO:C	4:B:747:MET:N	2.66	0.49
4:B:843:GLN:O	4:B:846:ILE:N	2.45	0.49
7:E:23:VAL:HB	7:E:30:ILE:HD11	1.95	0.49
11:I:51:ASN:O	11:I:54:GLU:HG3	2.12	0.49
11:I:85:PHE:HD1	11:I:99:LEU:HD13	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:35:ILE:HD13	3:A:241:VAL:HG11	1.94	0.49
3:A:364:VAL:O	3:A:364:VAL:HG13	2.11	0.49
3:A:578:LEU:O	3:A:578:LEU:HG	2.13	0.49
3:A:806:ARG:NH1	4:B:729:ILE:HG13	2.28	0.49
4:B:1216:LEU:C	4:B:1217:TYR:HD1	2.16	0.49
4:B:189:LEU:CD1	4:B:196:PRO:HA	2.42	0.49
4:B:769:TYR:C	4:B:771:SER:N	2.65	0.49
4:B:784:ASN:O	4:B:788:ARG:HG3	2.13	0.49
4:B:882:THR:HG21	4:B:884:ARG:HB2	1.93	0.49
3:A:1004:ASN:HD21	7:E:167:ARG:HD2	1.73	0.49
9:G:51:TYR:HD2	9:G:51:TYR:C	2.16	0.49
9:G:88:ASP:HB3	9:G:144:ARG:CA	2.42	0.49
10:H:83:GLN:C	10:H:85:GLY:H	2.15	0.49
12:J:56:LEU:O	12:J:59:LYS:N	2.44	0.49
3:A:1237:ILE:HG22	3:A:1238:ILE:N	2.28	0.49
3:A:1256:GLU:O	3:A:1260:LEU:HB3	2.12	0.49
3:A:1272:THR:C	3:A:1273:LEU:HD12	2.33	0.49
3:A:1323:ASP:C	3:A:1325:THR:H	2.15	0.49
3:A:269:ILE:HG23	3:A:300:VAL:CG2	2.43	0.49
3:A:590:ARG:HH21	3:A:620:LYS:CB	2.22	0.49
3:A:605:MET:CE	3:A:612:ILE:HG23	2.42	0.49
4:B:1220:ARG:HB3	4:B:1220:ARG:CZ	2.43	0.49
4:B:280:ILE:CG2	4:B:285:ILE:HG13	2.42	0.49
4:B:642:ASP:CA	4:B:649:LYS:HA	2.40	0.49
4:B:729:ILE:O	4:B:729:ILE:HG22	2.11	0.49
5:C:146:LYS:HB2	12:J:57:ILE:HD11	1.93	0.49
6:D:210:ILE:O	6:D:214:LEU:HG	2.13	0.49
6:D:39:ASN:HD22	6:D:41:GLN:HB2	1.78	0.49
7:E:135:PHE:CD2	7:E:140:LEU:HD21	2.48	0.49
7:E:13:TRP:CE3	7:E:39:LEU:HD13	2.47	0.49
9:G:106:MET:CG	9:G:107:LYS:N	2.75	0.49
9:G:129:SER:HB3	9:G:138:THR:OG1	2.12	0.49
9:G:7:LEU:CD1	9:G:45:ILE:HD11	2.43	0.49
13:K:110:ASN:O	13:K:111:LEU:HB3	2.12	0.49
3:A:120:GLU:C	3:A:122:MET:N	2.66	0.49
3:A:70:CYS:SG	3:A:70:CYS:O	2.71	0.49
3:A:735:VAL:O	3:A:735:VAL:HG12	2.12	0.49
3:A:7:SER:C	3:A:9:ALA:H	2.15	0.49
3:A:984:LYS:HG2	3:A:988:LEU:CD1	2.43	0.49
4:B:311:LEU:O	4:B:312:GLU:C	2.49	0.49
4:B:866:TYR:O	4:B:867:GLY:C	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:112:ASN:CB	5:C:114:TYR:CE1	2.95	0.49
5:C:234:SER:HB3	5:C:240:VAL:HG13	1.95	0.49
8:F:128:LYS:HD3	8:F:149:GLU:O	2.12	0.49
9:G:74:TYR:HD2	9:G:74:TYR:H	1.61	0.49
9:G:7:LEU:O	9:G:73:LYS:HD2	2.13	0.49
10:H:12:VAL:HB	10:H:52:GLN:H	1.77	0.49
11:I:2:THR:O	11:I:3:THR:C	2.51	0.49
11:I:3:THR:O	11:I:3:THR:HG22	2.13	0.49
13:K:47:ARG:O	13:K:47:ARG:HD2	2.13	0.49
4:B:770:GLN:HG2	4:B:983:ARG:O	2.13	0.49
4:B:850:LEU:HD12	4:B:851:PHE:N	2.28	0.49
5:C:147:LEU:HD23	5:C:147:LEU:N	2.28	0.49
5:C:46:ILE:CD1	5:C:67:LEU:HB3	2.40	0.49
6:D:19:GLU:O	6:D:21:GLU:N	2.46	0.49
7:E:28:TYR:HE1	7:E:78:LEU:HD13	1.78	0.49
14:L:32:ALA:CB	14:L:55:ILE:HD12	2.33	0.49
3:A:335:ARG:HA	3:A:339:ASN:HD22	1.78	0.48
3:A:546:VAL:O	3:A:550:LEU:HG	2.13	0.48
3:A:527:THR:O	3:A:653:VAL:HG11	2.13	0.48
3:A:981:LEU:HD21	3:A:1038:THR:O	2.13	0.48
3:A:29:ALA:HB1	4:B:1184:GLY:CA	2.43	0.48
4:B:234:ILE:N	4:B:234:ILE:HD12	2.28	0.48
4:B:550:ASP:OD1	4:B:551:PRO:HD2	2.13	0.48
4:B:1084:GLN:OE1	5:C:189:THR:CG2	2.61	0.48
5:C:226:ASP:O	5:C:227:THR:HB	2.12	0.48
5:C:243:VAL:HG12	5:C:243:VAL:O	2.13	0.48
6:D:53:SER:H	6:D:148:LEU:HD23	1.78	0.48
7:E:124:VAL:HB	7:E:125:PRO:HD3	1.95	0.48
11:I:34:TYR:C	11:I:34:TYR:CD2	2.86	0.48
13:K:61:TYR:C	13:K:61:TYR:CD2	2.85	0.48
4:B:992:ILE:HD11	13:K:66:PRO:HB2	1.95	0.48
3:A:166:GLY:O	3:A:167:CYS:CB	2.61	0.48
3:A:227:VAL:HG12	6:D:15:LEU:HD23	1.94	0.48
3:A:573:SER:OG	3:A:576:GLN:HB2	2.12	0.48
3:A:605:MET:HE1	3:A:612:ILE:HG23	1.95	0.48
3:A:18:GLN:HB3	4:B:1215:ARG:HG3	1.94	0.48
4:B:129:PHE:CD2	4:B:166:PHE:HA	2.48	0.48
4:B:615:MET:HA	4:B:625:LYS:O	2.13	0.48
7:E:15:ALA:O	7:E:19:VAL:HG23	2.13	0.48
11:I:21:GLU:O	11:I:21:GLU:HG2	2.14	0.48
13:K:65:HIS:HD2	13:K:67:PHE:N	2.03	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1219:THR:HG21	3:A:1271:ILE:HD11	1.94	0.48
3:A:1385:THR:CG2	3:A:1386:ARG:N	2.76	0.48
3:A:618:GLU:O	3:A:621:THR:N	2.41	0.48
3:A:719:VAL:C	3:A:721:PHE:N	2.67	0.48
4:B:1022:THR:HG23	4:B:1022:THR:O	2.12	0.48
4:B:1068:GLY:O	4:B:1069:PHE:O	2.32	0.48
4:B:1106:ARG:NH2	4:B:1111:MET:CE	2.76	0.48
4:B:1166:CYS:O	4:B:1166:CYS:SG	2.70	0.48
4:B:806:THR:HA	4:B:1045:SER:OG	2.13	0.48
4:B:810:GLU:HB3	4:B:811:TYR:CE1	2.48	0.48
4:B:879:ARG:O	4:B:880:THR:HB	2.13	0.48
5:C:70:ILE:HG12	5:C:142:VAL:HG11	1.95	0.48
11:I:56:ALA:O	11:I:57:GLY:O	2.31	0.48
4:B:737:THR:CG2	11:I:66:PRO:HA	2.43	0.48
3:A:1280:GLU:O	3:A:1281:ARG:C	2.52	0.48
3:A:18:GLN:H	4:B:1215:ARG:HB2	1.79	0.48
3:A:507:VAL:N	3:A:508:PRO:CD	2.77	0.48
4:B:1102:LYS:O	4:B:1103:ILE:C	2.52	0.48
4:B:581:PHE:HA	4:B:585:VAL:O	2.13	0.48
4:B:54:PHE:HA	4:B:58:THR:HB	1.93	0.48
4:B:893:LEU:HD22	4:B:897:GLY:C	2.34	0.48
8:F:90:ARG:HD3	8:F:155:LEU:HD12	1.93	0.48
10:H:145:ARG:O	10:H:146:ARG:HB2	2.13	0.48
3:A:1094:VAL:HG12	3:A:1095:THR:N	2.26	0.48
3:A:1319:VAL:HG13	3:A:1320:PRO:HD2	1.96	0.48
3:A:474:VAL:C	3:A:477:PRO:HD2	2.34	0.48
4:B:365:THR:HG23	4:B:367:LEU:HG	1.96	0.48
4:B:498:THR:O	4:B:536:VAL:HA	2.13	0.48
4:B:363:HIS:HD2	4:B:585:VAL:HG22	1.78	0.48
5:C:181:ASP:CG	5:C:186:LEU:HD13	2.32	0.48
5:C:221:TYR:CE1	5:C:222:LYS:HG3	2.49	0.48
7:E:13:TRP:CZ3	7:E:39:LEU:HB2	2.48	0.48
7:E:78:LEU:C	7:E:78:LEU:HD23	2.33	0.48
11:I:111:THR:CG2	11:I:112:SER:N	2.77	0.48
12:J:44:TYR:HA	12:J:47:ARG:HB3	1.95	0.48
3:A:1029:ARG:HG3	3:A:1029:ARG:HH11	1.79	0.48
3:A:981:LEU:HD23	3:A:1039:LYS:HA	1.96	0.48
3:A:423:ASP:O	3:A:424:ILE:CB	2.62	0.48
3:A:475:THR:CG2	3:A:476:SER:H	2.26	0.48
3:A:98:LYS:O	3:A:102:VAL:HG23	2.14	0.48
4:B:1167:GLY:N	4:B:1217:TYR:HE1	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:324:ILE:HD13	4:B:330:ALA:HA	1.96	0.48
4:B:711:GLU:H	4:B:712:PRO:HD2	1.78	0.48
4:B:913:GLY:HA2	4:B:938:SER:OG	2.13	0.48
5:C:249:ASP:O	5:C:252:GLN:HB3	2.13	0.48
7:E:2:ASP:HB3	7:E:3:GLN:H	1.46	0.48
3:A:1444:MET:CG	9:G:60:ARG:HA	2.43	0.48
3:A:1005:GLU:O	3:A:1009:ASN:HB2	2.13	0.48
3:A:167:CYS:O	3:A:167:CYS:SG	2.72	0.48
3:A:185:TRP:CZ3	3:A:200:ARG:HG2	2.48	0.48
3:A:341:MET:HE1	4:B:1135:ARG:HH12	1.79	0.48
4:B:1072:MET:CE	4:B:1087:PHE:HD1	2.26	0.48
3:A:1409:LEU:HD13	4:B:1207:LEU:HD21	1.95	0.48
4:B:954:VAL:O	14:L:55:ILE:O	2.31	0.48
5:C:11:ARG:HH21	5:C:229:TYR:HB3	1.79	0.48
7:E:55:ARG:HD2	7:E:83:CYS:O	2.14	0.48
10:H:91:ASP:C	10:H:93:TYR:H	2.15	0.48
3:A:207:ILE:CG2	3:A:211:PHE:CE1	2.97	0.48
3:A:407:ARG:HD2	3:A:413:ILE:HD11	1.96	0.48
3:A:442:VAL:CB	3:A:489:LEU:HD11	2.40	0.48
3:A:613:ILE:O	3:A:614:PHE:HB3	2.13	0.48
3:A:666:ILE:CD1	3:A:667:GLY:H	2.20	0.48
4:B:1072:MET:SD	4:B:1087:PHE:HD1	2.37	0.48
4:B:314:LEU:O	4:B:317:CYS:HB3	2.14	0.48
4:B:744:HIS:CG	4:B:745:PRO:HD2	2.49	0.48
4:B:121:ASN:OD1	4:B:963:PHE:HZ	1.96	0.48
5:C:146:LYS:C	5:C:147:LEU:HD23	2.33	0.48
5:C:147:LEU:HD12	5:C:151:GLN:O	2.13	0.48
5:C:174:ALA:O	5:C:175:ALA:HB2	2.14	0.48
6:D:135:GLY:C	6:D:137:ASN:H	2.16	0.48
6:D:191:ALA:C	6:D:193:THR:H	2.17	0.48
7:E:213:ILE:HG12	7:E:214:CYS:H	1.78	0.48
10:H:116:TYR:HE2	10:H:140:ALA:CB	2.27	0.48
12:J:1:MET:H2	12:J:57:ILE:HG22	1.78	0.48
14:L:47:ARG:HH21	14:L:54:ARG:NH2	2.12	0.48
3:A:1398:MET:HB2	3:A:1426:GLU:OE2	2.13	0.48
3:A:399:HIS:CB	3:A:400:PRO:CD	2.90	0.48
4:B:1097:HIS:N	4:B:1098:MET:HE2	2.29	0.48
4:B:345:LYS:O	4:B:348:ARG:N	2.47	0.48
4:B:519:TRP:C	4:B:519:TRP:CD1	2.87	0.48
4:B:790:ASP:N	4:B:790:ASP:OD2	2.45	0.48
6:D:51:ASN:O	6:D:52:LEU:O	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:99:GLY:CA	10:H:118:PHE:HA	2.44	0.48
3:A:1120:LEU:HD13	3:A:1304:TRP:O	2.14	0.48
3:A:568:PRO:HB2	5:C:221:TYR:CZ	2.49	0.48
3:A:608:ILE:HD12	3:A:613:ILE:CD1	2.44	0.48
3:A:79:GLY:H	4:B:1205:GLN:HE22	1.61	0.48
4:B:557:PHE:O	4:B:557:PHE:HD2	1.96	0.48
4:B:954:VAL:HA	4:B:964:VAL:HG22	1.95	0.48
9:G:153:GLN:CG	9:G:154:VAL:HG23	2.44	0.48
10:H:20:TYR:O	10:H:22:LYS:N	2.46	0.48
14:L:61:THR:HG22	14:L:62:LYS:N	2.28	0.48
3:A:1438:THR:CG2	8:F:92:ARG:HD2	2.44	0.47
3:A:1438:THR:HG22	8:F:92:ARG:HD2	1.96	0.47
3:A:444:PHE:CB	3:A:458:HIS:HD2	2.26	0.47
3:A:98:LYS:O	3:A:99:ILE:C	2.52	0.47
4:B:955:THR:HG22	4:B:956:THR:O	2.14	0.47
5:C:186:LEU:HD12	5:C:186:LEU:N	2.29	0.47
8:F:138:LEU:HB3	8:F:139:PRO:HD2	1.95	0.47
9:G:43:GLY:HA3	9:G:80:LYS:HB3	1.96	0.47
3:A:1349:TYR:CA	3:A:1372:VAL:HG21	2.44	0.47
3:A:146:MET:HA	3:A:171:GLN:HB2	1.97	0.47
3:A:514:PRO:C	3:A:516:SER:H	2.16	0.47
3:A:903:ASN:ND2	3:A:905:ASP:H	2.12	0.47
4:B:1023:VAL:O	4:B:1026:LEU:N	2.47	0.47
4:B:200:GLY:HA2	4:B:202:TYR:CE2	2.49	0.47
4:B:294:ASP:C	4:B:296:GLU:H	2.16	0.47
4:B:801:LYS:O	12:J:52:THR:CG2	2.58	0.47
4:B:43:LEU:HD11	4:B:811:TYR:O	2.15	0.47
6:D:52:LEU:CD2	6:D:147:TYR:HE2	2.27	0.47
8:F:68:THR:O	8:F:69:LEU:CB	2.62	0.47
5:C:35:ARG:HH11	13:K:41:THR:CA	2.27	0.47
4:B:193:LYS:HZ3	14:L:32:ALA:HB1	1.74	0.47
3:A:282:ASN:O	3:A:284:ALA:N	2.47	0.47
3:A:352:VAL:O	3:A:467:THR:HG22	2.15	0.47
4:B:314:LEU:O	4:B:318:VAL:HG23	2.15	0.47
4:B:38:PHE:CD1	4:B:811:TYR:CD2	3.00	0.47
4:B:557:PHE:O	4:B:557:PHE:CD2	2.67	0.47
4:B:628:THR:O	4:B:628:THR:HG23	2.14	0.47
4:B:842:ASN:ND2	4:B:845:SER:OG	2.38	0.47
4:B:878:GLN:O	4:B:879:ARG:C	2.52	0.47
5:C:263:THR:O	5:C:265:MET:N	2.47	0.47
14:L:46:VAL:HG12	14:L:46:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1048:ASN:O	3:A:1049:ILE:C	2.52	0.47
3:A:1376:THR:O	3:A:1377:THR:C	2.53	0.47
3:A:42:ASP:C	3:A:44:THR:N	2.67	0.47
3:A:90:VAL:HG13	3:A:297:GLN:CD	2.35	0.47
3:A:961:ARG:HH11	3:A:961:ARG:HG3	1.80	0.47
4:B:1198:TYR:CD2	4:B:1198:TYR:O	2.67	0.47
4:B:300:HIS:O	4:B:303:TYR:HE2	1.98	0.47
4:B:310:MET:O	4:B:313:MET:HB2	2.13	0.47
4:B:44:VAL:O	4:B:45:SER:C	2.52	0.47
4:B:897:GLY:O	4:B:898:LEU:HD23	2.13	0.47
4:B:838:SER:HB2	4:B:989:THR:O	2.15	0.47
5:C:18:VAL:O	5:C:18:VAL:CG1	2.56	0.47
5:C:215:GLU:O	5:C:216:GLY:C	2.51	0.47
5:C:43:THR:CG2	5:C:44:LEU:N	2.52	0.47
6:D:185:CYS:O	6:D:211:LEU:HD22	2.14	0.47
7:E:164:LEU:HD11	7:E:211:TYR:CE1	2.50	0.47
8:F:74:ILE:HG23	8:F:75:PRO:HD2	1.96	0.47
10:H:123:MET:HG2	10:H:124:ARG:N	2.28	0.47
3:A:262:LEU:O	3:A:264:PHE:N	2.47	0.47
4:B:1069:PHE:HA	4:B:1085:ILE:O	2.14	0.47
4:B:118:ARG:CG	4:B:204:ILE:HD13	2.45	0.47
4:B:298:LEU:CD2	4:B:298:LEU:N	2.78	0.47
4:B:604:ARG:C	4:B:606:LYS:H	2.17	0.47
5:C:22:LEU:O	5:C:227:THR:HA	2.15	0.47
5:C:67:LEU:HD11	5:C:155:LEU:HD12	1.97	0.47
6:D:151:PHE:N	6:D:151:PHE:CD1	2.81	0.47
8:F:77:ASP:C	8:F:79:ARG:H	2.16	0.47
4:B:258:LEU:O	4:B:258:LEU:HG	2.13	0.47
4:B:293:PRO:HG2	4:B:296:GLU:CB	2.44	0.47
4:B:51:PHE:CD2	4:B:173:MET:HB3	2.49	0.47
4:B:376:PHE:O	4:B:586:TRP:HZ3	1.97	0.47
4:B:769:TYR:C	4:B:771:SER:H	2.17	0.47
7:E:145:THR:HG21	7:E:187:TYR:CE2	2.50	0.47
5:C:84:ARG:NE	13:K:11:LEU:HD11	2.29	0.47
3:A:106:VAL:HG13	3:A:112:LYS:C	2.35	0.47
3:A:1313:LEU:C	3:A:1315:GLU:H	2.18	0.47
3:A:567:LYS:CG	3:A:568:PRO:CD	2.80	0.47
4:B:1152:MET:HE1	4:B:1157:ALA:HA	1.96	0.47
4:B:114:PRO:O	4:B:116:GLU:N	2.48	0.47
4:B:247:GLY:C	4:B:249:ARG:H	2.17	0.47
4:B:273:LEU:CB	4:B:276:ILE:HD12	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:460:ALA:HB1	4:B:466:TRP:CE3	2.50	0.47
4:B:604:ARG:O	4:B:606:LYS:N	2.47	0.47
5:C:100:THR:OG1	5:C:121:VAL:HG21	2.14	0.47
5:C:116:LYS:HD3	5:C:140:ASN:HA	1.96	0.47
5:C:189:THR:CG2	5:C:190:ASP:N	2.69	0.47
5:C:69:LEU:HB3	12:J:6:ARG:HD3	1.97	0.47
6:D:48:ILE:HG21	9:G:4:ILE:HB	1.96	0.47
8:F:103:MET:HE3	9:G:66:GLY:H	1.80	0.47
3:A:816:HIS:CD2	4:B:764:SER:HB2	2.50	0.47
4:B:220:GLY:O	4:B:222:ILE:HG13	2.14	0.47
6:D:54:GLU:O	6:D:58:VAL:HG23	2.14	0.47
11:I:22:ASN:O	11:I:23:ASN:HB2	2.15	0.47
3:A:1036:ARG:HH11	3:A:1036:ARG:CG	2.28	0.47
3:A:1236:LEU:C	3:A:1237:ILE:HG13	2.35	0.47
3:A:47:ARG:O	3:A:48:ALA:HB2	2.15	0.47
3:A:55:ASP:N	3:A:56:PRO:CD	2.77	0.47
3:A:902:LEU:CG	3:A:926:GLN:HG3	2.43	0.47
4:B:485:ARG:HG3	4:B:781:PHE:CD1	2.49	0.47
4:B:54:PHE:O	4:B:58:THR:HB	2.15	0.47
4:B:735:ALA:O	4:B:738:PHE:HE1	1.98	0.47
4:B:882:THR:HG21	4:B:934:LYS:O	2.15	0.47
5:C:98:VAL:HG12	5:C:99:LEU:N	2.29	0.47
7:E:144:ILE:HG13	7:E:145:THR:H	1.79	0.47
7:E:205:SER:O	7:E:206:GLY:C	2.54	0.47
7:E:93:MET:SD	7:E:97:VAL:CG2	3.03	0.47
5:C:259:LEU:HD13	13:K:91:CYS:HB2	1.96	0.47
14:L:52:GLY:O	14:L:53:HIS:C	2.53	0.47
3:A:1114:PRO:HB2	3:A:1311:VAL:HG23	1.95	0.47
3:A:1453:TYR:O	3:A:1454:MET:HB3	2.14	0.47
3:A:211:PHE:HA	3:A:214:ILE:CD1	2.45	0.47
3:A:590:ARG:HH11	3:A:590:ARG:HG3	1.79	0.47
4:B:569:TYR:CE1	4:B:589:VAL:HG21	2.49	0.47
4:B:826:ALA:HB2	4:B:1008:PRO:HB3	1.96	0.47
4:B:839:MET:CE	4:B:980:PHE:HB2	2.44	0.47
4:B:903:VAL:HG12	4:B:904:ARG:N	2.30	0.47
4:B:882:THR:CB	4:B:934:LYS:O	2.62	0.47
5:C:100:THR:HG22	5:C:101:LEU:N	2.30	0.47
5:C:121:VAL:O	5:C:121:VAL:HG12	2.15	0.47
6:D:185:CYS:HB2	6:D:211:LEU:HD21	1.97	0.47
10:H:99:GLY:HA3	10:H:117:SER:O	2.14	0.47
10:H:7:ASP:O	10:H:8:ASP:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:5:ARG:HD3	11:I:36:GLU:OE2	2.15	0.47
14:L:38:LEU:CD1	14:L:49:LYS:HE2	2.44	0.47
3:A:246:VAL:O	3:A:328:ARG:NH1	2.41	0.47
3:A:506:ALA:HB1	3:A:508:PRO:HD2	1.96	0.47
3:A:601:LYS:HB2	3:A:603:ASN:ND2	2.29	0.47
3:A:793:SER:HB2	3:A:794:PRO:HD2	1.96	0.47
4:B:1167:GLY:H	4:B:1215:ARG:HD2	1.80	0.47
4:B:1161:HIS:NE2	4:B:1175:LEU:HD21	2.30	0.47
4:B:373:ARG:CG	4:B:566:LEU:HD23	2.45	0.47
4:B:44:VAL:HG21	4:B:199:MET:O	2.15	0.47
4:B:642:ASP:H	4:B:649:LYS:HE3	1.79	0.47
4:B:616:ILE:HG12	4:B:697:GLU:HA	1.97	0.47
5:C:179:GLU:HG2	5:C:180:TYR:H	1.78	0.47
7:E:78:LEU:HD11	7:E:109:ILE:HD12	1.97	0.47
9:G:126:ASN:HD22	9:G:127:PRO:HA	1.80	0.47
4:B:1070:GLU:O	4:B:1084:GLN:HB3	2.16	0.46
4:B:195:CYS:SG	4:B:197:PHE:HB2	2.55	0.46
4:B:525:ALA:O	4:B:768:THR:HG23	2.15	0.46
3:A:254:GLU:CG	4:B:935:ARG:HH22	2.27	0.46
4:B:860:MET:CB	4:B:965:LYS:HG2	2.43	0.46
5:C:112:ASN:HD22	5:C:112:ASN:N	2.13	0.46
5:C:234:SER:OG	5:C:235:VAL:N	2.46	0.46
8:F:131:PRO:C	8:F:132:LEU:HD23	2.36	0.46
9:G:87:VAL:HB	9:G:103:VAL:HG11	1.97	0.46
9:G:91:VAL:HA	9:G:101:VAL:HA	1.97	0.46
10:H:26:ILE:HG22	10:H:27:GLU:N	2.31	0.46
11:I:53:GLY:C	11:I:55:THR:H	2.19	0.46
3:A:1015:VAL:CG1	3:A:1019:CYS:SG	3.03	0.46
3:A:347:PHE:HE2	3:A:375:THR:HG23	1.79	0.46
3:A:961:ARG:O	3:A:965:GLN:HG3	2.15	0.46
4:B:115:GLN:HG2	4:B:193:LYS:CB	2.40	0.46
4:B:1183:LYS:HE3	4:B:1183:LYS:O	2.15	0.46
4:B:773:MET:CE	4:B:985:GLY:HA2	2.45	0.46
4:B:824:ILE:O	4:B:824:ILE:HG22	2.15	0.46
7:E:151:PRO:HB3	7:E:200:ARG:HB3	1.96	0.46
9:G:115:MET:CB	9:G:116:PRO:CD	2.93	0.46
3:A:1121:GLU:O	3:A:1122:PRO:C	2.53	0.46
3:A:247:ARG:HH11	3:A:247:ARG:HG3	1.81	0.46
3:A:350:ARG:NH1	3:A:350:ARG:HG3	2.31	0.46
3:A:567:LYS:CE	10:H:46:LEU:HB2	2.44	0.46
3:A:90:VAL:HG13	3:A:297:GLN:OE1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:967:ALA:HA	3:A:1044:TRP:CZ3	2.51	0.46
5:C:47:ASP:HA	14:L:69:ALA:CB	2.33	0.46
6:D:33:PHE:CE1	9:G:80:LYS:HE3	2.50	0.46
7:E:124:VAL:CA	7:E:132:ILE:HD12	2.46	0.46
7:E:35:VAL:C	7:E:37:LEU:H	2.19	0.46
7:E:61:GLN:NE2	7:E:105:PHE:CZ	2.82	0.46
9:G:99:PHE:C	9:G:99:PHE:CD1	2.87	0.46
10:H:38:LEU:HD13	10:H:125:LEU:CD1	2.46	0.46
10:H:139:ASN:O	10:H:140:ALA:CB	2.63	0.46
10:H:11:GLN:O	10:H:28:ALA:HB1	2.15	0.46
3:A:963:ILE:HD13	3:A:1049:ILE:HG12	1.96	0.46
3:A:1377:THR:O	3:A:1378:GLN:C	2.53	0.46
3:A:371:ALA:HB2	3:A:462:VAL:HG12	1.97	0.46
3:A:49:LYS:HZ1	3:A:61:ILE:CG1	2.27	0.46
3:A:957:PRO:O	3:A:958:VAL:HB	2.16	0.46
4:B:372:SER:O	4:B:376:PHE:HD1	1.98	0.46
4:B:840:ILE:HD13	4:B:994:TYR:CE1	2.51	0.46
5:C:124:LEU:CD2	5:C:129:ILE:HG22	2.46	0.46
9:G:3:PHE:CD1	9:G:80:LYS:NZ	2.72	0.46
9:G:61:ILE:HG23	9:G:66:GLY:O	2.16	0.46
3:A:537:ARG:NH1	10:H:120:GLY:O	2.47	0.46
11:I:106:CYS:SG	11:I:107:SER:N	2.89	0.46
3:A:709:THR:HG21	11:I:93:LYS:O	2.15	0.46
13:K:7:PHE:HA	13:K:10:PHE:CE2	2.50	0.46
14:L:46:VAL:CG1	14:L:56:LEU:HD12	2.46	0.46
3:A:211:PHE:HA	3:A:214:ILE:CG1	2.46	0.46
3:A:701:LEU:HD23	11:I:115:LYS:HG3	1.96	0.46
3:A:787:PHE:CE1	3:A:796:SER:HA	2.51	0.46
3:A:986:ILE:CG2	3:A:987:VAL:N	2.76	0.46
4:B:563:MET:HE3	4:B:580:VAL:HB	1.96	0.46
5:C:175:ALA:HB3	12:J:43:ARG:HH22	1.79	0.46
5:C:74:SER:CB	5:C:77:ILE:HG12	2.46	0.46
6:D:154:PHE:CE2	6:D:163:VAL:HG21	2.50	0.46
6:D:219:THR:HG22	6:D:220:LEU:N	2.30	0.46
10:H:27:GLU:HA	10:H:38:LEU:O	2.15	0.46
2:T:6:C:H2'	2:T:7:G:O4'	2.16	0.46
3:A:377:PRO:HD3	3:A:493:GLN:OE1	2.15	0.46
3:A:562:THR:HA	3:A:563:PRO:HD3	1.82	0.46
3:A:676:MET:O	3:A:679:ILE:HB	2.16	0.46
3:A:683:ILE:HG21	3:A:801:GLU:CG	2.45	0.46
4:B:240:ILE:HG23	4:B:240:ILE:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:344:LYS:O	4:B:346:GLU:N	2.48	0.46
4:B:616:ILE:HG23	4:B:700:SER:OG	2.15	0.46
4:B:957:ASN:O	4:B:958:GLN:C	2.54	0.46
4:B:973:ILE:HG23	4:B:974:PRO:HD2	1.98	0.46
5:C:234:SER:HB2	5:C:240:VAL:HG13	1.98	0.46
9:G:48:VAL:HG13	9:G:74:TYR:CD1	2.49	0.46
3:A:1279:ILE:CD1	3:A:1316:VAL:HG21	2.46	0.46
3:A:1345:ARG:HG3	3:A:1376:THR:CG2	2.39	0.46
3:A:230:ARG:HB2	3:A:233:TRP:CE3	2.51	0.46
3:A:768:GLN:HG2	3:A:816:HIS:CA	2.42	0.46
3:A:899:VAL:CB	3:A:929:LEU:HD11	2.39	0.46
4:B:189:LEU:HD12	4:B:196:PRO:HA	1.97	0.46
4:B:280:ILE:HD13	4:B:334:ILE:HG12	1.98	0.46
4:B:378:LEU:HD12	4:B:378:LEU:C	2.34	0.46
4:B:212:LEU:HD21	4:B:461:LEU:HG	1.98	0.46
6:D:144:THR:HG21	9:G:46:LEU:HD13	1.98	0.46
6:D:40:HIS:CG	6:D:41:GLN:N	2.83	0.46
7:E:92:THR:O	7:E:95:THR:HB	2.15	0.46
9:G:18:PHE:HZ	9:G:68:ALA:HB2	1.81	0.46
3:A:701:LEU:CD2	11:I:115:LYS:HG3	2.45	0.46
12:J:45:CYS:O	12:J:48:ARG:HG3	2.15	0.46
14:L:30:ILE:HD11	14:L:59:ALA:HB2	1.98	0.46
4:B:343:ILE:HG21	4:B:348:ARG:N	2.30	0.46
5:C:242:GLN:C	5:C:244:VAL:N	2.69	0.46
7:E:90:VAL:O	7:E:93:MET:HB3	2.16	0.46
10:H:59:ILE:O	10:H:60:ALA:HB3	2.16	0.46
10:H:95:TYR:CE2	10:H:97:MET:HG3	2.51	0.46
14:L:61:THR:HG21	14:L:63:ARG:CG	2.46	0.46
3:A:1116:LEU:CD1	3:A:1118:VAL:HG13	2.45	0.46
3:A:241:VAL:HG13	3:A:266:LEU:HD13	1.97	0.46
3:A:269:ILE:CG2	3:A:300:VAL:HG22	2.46	0.46
3:A:302:THR:HA	3:A:305:ASP:O	2.16	0.46
3:A:65:LEU:O	3:A:66:LYS:O	2.34	0.46
4:B:96:TYR:N	4:B:129:PHE:O	2.39	0.46
4:B:185:THR:O	4:B:186:GLU:C	2.54	0.46
4:B:376:PHE:CE2	4:B:569:TYR:HD2	2.34	0.46
4:B:834:ASN:O	4:B:838:SER:O	2.34	0.46
6:D:185:CYS:HB2	6:D:211:LEU:CD2	2.46	0.46
7:E:90:VAL:HG23	7:E:120:ALA:HA	1.97	0.46
3:A:1325:THR:OG1	7:E:146:HIS:O	2.27	0.46
7:E:179:GLN:HB2	7:E:182:ASP:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:17:ARG:O	7:E:20:LYS:HB2	2.16	0.46
9:G:22:MET:O	9:G:23:LYS:C	2.54	0.46
9:G:44:TYR:O	9:G:78:VAL:HG12	2.16	0.46
12:J:56:LEU:O	12:J:57:ILE:C	2.55	0.46
3:A:115:LEU:HB2	3:A:122:MET:HE2	1.97	0.46
3:A:219:PHE:O	3:A:222:LEU:O	2.34	0.46
3:A:308:ILE:HG22	3:A:309:ALA:N	2.20	0.46
3:A:418:SER:C	3:A:420:ARG:N	2.69	0.46
3:A:710:LEU:N	3:A:710:LEU:HD12	2.29	0.46
3:A:84:ILE:O	3:A:84:ILE:CG2	2.64	0.46
3:A:900:ASP:HA	3:A:926:GLN:NE2	2.31	0.46
4:B:758:PHE:HZ	4:B:1031:LEU:HD22	1.81	0.46
4:B:1151:LEU:N	4:B:1151:LEU:CD1	2.78	0.46
5:C:160:LYS:O	5:C:161:LYS:O	2.34	0.46
5:C:133:ILE:HD13	5:C:236:GLY:C	2.37	0.46
5:C:256:ALA:O	5:C:259:LEU:N	2.47	0.46
5:C:2:SER:N	5:C:3:GLU:O	2.49	0.46
6:D:56:ARG:CA	6:D:148:LEU:HD13	2.45	0.46
10:H:44:VAL:HG12	10:H:44:VAL:O	2.16	0.46
11:I:19:ASP:OD1	11:I:22:ASN:HB2	2.16	0.46
12:J:6:ARG:HG2	12:J:13:VAL:HA	1.98	0.46
12:J:2:ILE:HG22	12:J:3:VAL:O	2.16	0.46
14:L:27:LEU:HD23	14:L:27:LEU:N	2.30	0.46
3:A:883:LEU:CD2	3:A:1021:LEU:HB2	2.46	0.45
3:A:852:TYR:HA	3:A:1060:PRO:HB3	1.97	0.45
3:A:425:GLN:N	3:A:425:GLN:OE1	2.49	0.45
3:A:728:LYS:HA	3:A:731:ARG:HB2	1.98	0.45
3:A:335:ARG:NH1	4:B:1202:LEU:HD22	2.31	0.45
4:B:570:VAL:HG23	4:B:573:GLN:HB3	1.98	0.45
4:B:860:MET:HG2	4:B:861:ASP:N	2.31	0.45
5:C:104:PHE:HD2	5:C:105:GLY:N	2.14	0.45
5:C:22:LEU:HD13	5:C:230:MET:HE1	1.96	0.45
5:C:254:LYS:O	5:C:256:ALA:N	2.49	0.45
4:B:798:TYR:CE2	5:C:62:PHE:HE2	2.30	0.45
5:C:67:LEU:HD11	5:C:155:LEU:HD13	1.98	0.45
6:D:195:ILE:HB	6:D:198:LEU:CD1	2.46	0.45
11:I:70:ARG:HA	11:I:83:ASN:O	2.15	0.45
3:A:116:ASP:C	3:A:118:HIS:N	2.66	0.45
3:A:954:TRP:HB3	3:A:955:PRO:HD2	1.98	0.45
3:A:964:ILE:O	3:A:967:ALA:HB3	2.16	0.45
3:A:7:SER:OG	4:B:1193:GLN:NE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:283:VAL:O	4:B:286:PHE:N	2.45	0.45
4:B:558:LEU:C	4:B:560:GLU:H	2.19	0.45
4:B:827:ILE:HD12	4:B:1086:PHE:CD2	2.51	0.45
4:B:827:ILE:HD12	4:B:1086:PHE:HD2	1.81	0.45
4:B:880:THR:O	4:B:880:THR:HG22	2.17	0.45
5:C:11:ARG:NH2	5:C:229:TYR:HB3	2.31	0.45
5:C:40:GLU:HA	5:C:163:ILE:HG22	1.98	0.45
6:D:175:PHE:O	6:D:179:GLN:HG2	2.16	0.45
7:E:178:ILE:CD1	7:E:185:ALA:HB2	2.47	0.45
7:E:48:ASP:CG	7:E:49:SER:N	2.68	0.45
11:I:53:GLY:C	11:I:55:THR:N	2.70	0.45
3:A:1362:TYR:CD1	3:A:1363:VAL:N	2.84	0.45
3:A:416:ARG:O	3:A:417:TYR:HD2	2.00	0.45
3:A:683:ILE:HG21	3:A:801:GLU:CD	2.36	0.45
3:A:901:LEU:O	3:A:921:GLY:N	2.35	0.45
4:B:1159:ARG:CD	4:B:1193:GLN:HE21	2.30	0.45
4:B:232:SER:CB	4:B:261:ARG:HH21	2.24	0.45
4:B:579:ARG:HG2	4:B:579:ARG:HH11	1.81	0.45
6:D:156:ASP:C	6:D:158:GLU:N	2.70	0.45
9:G:37:SER:OG	9:G:45:ILE:HB	2.16	0.45
11:I:111:THR:CG2	11:I:112:SER:H	2.27	0.45
11:I:68:LEU:HB3	11:I:84:VAL:HG23	1.98	0.45
13:K:110:ASN:O	13:K:111:LEU:HD23	2.17	0.45
3:A:248:PRO:O	3:A:260:ASP:HB2	2.15	0.45
3:A:33:ALA:CB	3:A:56:PRO:HB2	2.38	0.45
3:A:59:GLY:HA2	3:A:67:CYS:SG	2.56	0.45
3:A:878:ILE:HG22	3:A:956:LEU:N	2.30	0.45
3:A:919:ILE:HD13	3:A:983:ILE:HD12	1.97	0.45
4:B:980:PHE:HE2	4:B:1094:ARG:HB2	1.81	0.45
4:B:25:ILE:HD11	4:B:653:VAL:C	2.36	0.45
4:B:469:GLN:HB2	4:B:470:LYS:H	1.50	0.45
4:B:401:PHE:HB2	4:B:517:THR:OG1	2.16	0.45
4:B:603:LEU:HB3	4:B:609:ILE:CD1	2.47	0.45
6:D:8:PHE:HD1	6:D:8:PHE:O	1.99	0.45
9:G:13:LEU:O	9:G:67:SER:HA	2.17	0.45
11:I:101:PHE:HE1	11:I:112:SER:HB2	1.80	0.45
12:J:64:ASN:HB3	12:J:65:PRO:HD2	1.90	0.45
14:L:58:LYS:O	14:L:59:ALA:O	2.34	0.45
3:A:150:THR:HG22	3:A:150:THR:O	2.16	0.45
3:A:21:LEU:HD11	3:A:1414:ALA:HA	1.98	0.45
3:A:445:ASN:HB2	3:A:454:SER:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:469:ARG:NH1	3:A:469:ARG:HB3	2.31	0.45
3:A:634:THR:HG1	3:A:642:CYS:HG	1.63	0.45
3:A:961:ARG:HG2	3:A:965:GLN:HE21	1.81	0.45
3:A:967:ALA:O	3:A:968:GLN:O	2.35	0.45
4:B:1197:PRO:HG2	4:B:1200:ALA:HB2	1.99	0.45
4:B:118:ARG:HG2	4:B:204:ILE:HD13	1.98	0.45
4:B:265:SER:O	4:B:266:ALA:CB	2.65	0.45
4:B:520:GLY:H	4:B:748:ILE:HG22	1.81	0.45
4:B:63:ILE:O	4:B:67:SER:HB3	2.16	0.45
4:B:744:HIS:ND1	4:B:745:PRO:HD2	2.31	0.45
4:B:780:VAL:HG12	4:B:782:LEU:O	2.17	0.45
4:B:95:ILE:CB	4:B:130:VAL:HG22	2.47	0.45
4:B:979:LYS:HG2	4:B:1095:LEU:HD13	1.97	0.45
8:F:147:SER:OG	8:F:150:GLU:HG3	2.16	0.45
14:L:61:THR:CG2	14:L:63:ARG:HG2	2.47	0.45
3:A:1410:PHE:C	3:A:1412:ALA:H	2.20	0.45
3:A:185:TRP:HZ3	3:A:200:ARG:HG2	1.81	0.45
3:A:317:LYS:O	3:A:318:SER:HB3	2.17	0.45
3:A:374:LEU:HD13	3:A:491:VAL:CG2	2.47	0.45
3:A:590:ARG:HH11	3:A:590:ARG:CG	2.29	0.45
3:A:695:LYS:C	3:A:697:ALA:H	2.20	0.45
3:A:774:ARG:NH2	3:A:797:LYS:CG	2.78	0.45
4:B:1034:VAL:O	4:B:1036:ALA:N	2.50	0.45
4:B:542:MET:CE	4:B:743:ILE:HG13	2.47	0.45
5:C:16:ASP:O	5:C:17:ASN:CG	2.55	0.45
5:C:45:ALA:HA	5:C:72:LEU:HD12	1.97	0.45
7:E:19:VAL:HG11	7:E:80:VAL:HG11	1.98	0.45
9:G:101:VAL:HG12	9:G:102:GLN:N	2.31	0.45
10:H:106:GLU:O	10:H:108:SER:N	2.50	0.45
10:H:43:ASN:OD1	10:H:46:LEU:HG	2.17	0.45
13:K:50:LEU:HD11	13:K:75:ILE:CD1	2.47	0.45
3:A:107:CYS:SG	3:A:171:GLN:HG2	2.57	0.45
3:A:1265:ASN:O	3:A:1268:LEU:N	2.48	0.45
3:A:24:PRO:HB3	3:A:237:THR:HB	1.99	0.45
3:A:399:HIS:O	3:A:400:PRO:C	2.53	0.45
3:A:427:GLN:O	3:A:428:TYR:C	2.52	0.45
3:A:547:LEU:HD22	13:K:58:PHE:HE1	1.80	0.45
3:A:586:ILE:HD11	3:A:633:VAL:HA	1.99	0.45
4:B:980:PHE:CE2	4:B:1094:ARG:HG3	2.51	0.45
4:B:1130:PHE:HZ	4:B:1138:MET:HG2	1.82	0.45
4:B:226:PHE:CD1	4:B:398:ARG:NH2	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:758:PHE:HB2	4:B:1024:ALA:HB1	1.98	0.45
4:B:806:THR:CG2	4:B:808:ALA:HB3	2.47	0.45
4:B:55:VAL:CG1	4:B:97:VAL:HG21	2.47	0.45
5:C:56:THR:HG22	5:C:57:VAL:H	1.81	0.45
6:D:155:ARG:O	6:D:155:ARG:HG2	2.15	0.45
7:E:14:ARG:HH21	7:E:141:VAL:HG12	1.82	0.45
7:E:31:THR:O	7:E:35:VAL:HG23	2.16	0.45
3:A:1438:THR:HG23	8:F:92:ARG:HB2	1.99	0.45
9:G:138:THR:CG2	9:G:139:ILE:N	2.62	0.45
9:G:1:MET:CE	9:G:1:MET:O	2.64	0.45
3:A:1265:ASN:C	3:A:1267:MET:N	2.68	0.45
3:A:1389:PHE:CD1	3:A:1389:PHE:C	2.90	0.45
3:A:353:ILE:HG21	3:A:487:MET:HG3	1.98	0.45
3:A:578:LEU:HD23	3:A:612:ILE:HD11	1.99	0.45
4:B:1045:SER:HB3	4:B:1046:PRO:HD2	1.99	0.45
4:B:30:SER:HB3	4:B:743:ILE:O	2.17	0.45
4:B:799:PRO:CB	4:B:818:PRO:HG2	2.43	0.45
4:B:860:MET:HG2	4:B:861:ASP:H	1.81	0.45
6:D:64:VAL:C	6:D:66:ARG:N	2.70	0.45
7:E:124:VAL:HG13	7:E:132:ILE:CB	2.45	0.45
8:F:97:ARG:HA	8:F:97:ARG:HD2	1.82	0.45
9:G:38:CYS:HB3	9:G:155:SER:HA	1.97	0.45
8:F:103:MET:HE1	9:G:65:ASP:HB2	1.99	0.45
10:H:128:ASN:CG	10:H:128:ASN:O	2.55	0.45
3:A:1341:ILE:CG2	3:A:1342:GLU:N	2.79	0.45
3:A:347:PHE:N	3:A:347:PHE:CD1	2.85	0.45
3:A:560:ILE:HG13	10:H:78:SER:CB	2.40	0.45
3:A:57:ARG:O	3:A:68:GLN:HG3	2.16	0.45
3:A:657:LEU:HD12	3:A:657:LEU:O	2.16	0.45
3:A:844:ALA:C	3:A:845:LEU:HD23	2.36	0.45
3:A:853:ASP:C	3:A:853:ASP:OD1	2.56	0.45
3:A:78:PRO:HA	4:B:1201:LYS:NZ	2.32	0.45
4:B:879:ARG:HH11	4:B:883:LEU:CD2	2.20	0.45
6:D:67:ARG:CB	6:D:133:THR:HG21	2.45	0.45
7:E:112:TYR:CZ	7:E:136:ASN:HB2	2.52	0.45
8:F:125:LEU:HB2	8:F:130:ILE:CD1	2.47	0.45
9:G:50:ASP:O	9:G:51:TYR:C	2.54	0.45
13:K:61:TYR:O	13:K:61:TYR:CD2	2.69	0.45
3:A:1021:LEU:O	3:A:1024:SER:HB3	2.17	0.45
3:A:1115:SER:OG	3:A:1116:LEU:N	2.50	0.45
3:A:1299:VAL:CG1	3:A:1300:LYS:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:417:TYR:N	3:A:417:TYR:CD2	2.85	0.45
3:A:709:THR:CG2	3:A:710:LEU:N	2.80	0.45
3:A:875:ALA:HA	3:A:878:ILE:HD11	1.98	0.45
4:B:99:LYS:HB3	4:B:100:PRO:HD2	1.99	0.45
4:B:1017:ILE:HB	4:B:1018:PRO:HD3	1.98	0.45
7:E:31:THR:OG1	7:E:34:GLU:N	2.47	0.45
10:H:127:GLY:O	10:H:128:ASN:CB	2.59	0.45
11:I:55:THR:O	11:I:55:THR:HG22	2.16	0.45
14:L:53:HIS:O	14:L:55:ILE:HG12	2.16	0.45
2:T:12:G:H4'	2:T:13:U:OP1	2.17	0.45
3:A:58:LEU:CD1	3:A:59:GLY:N	2.62	0.44
4:B:1162:ILE:HG22	4:B:1163:CYS:N	2.31	0.44
4:B:953:LEU:O	4:B:953:LEU:HD23	2.17	0.44
7:E:151:PRO:CB	7:E:200:ARG:HB3	2.47	0.44
9:G:125:SER:OG	9:G:128:PRO:HA	2.16	0.44
3:A:1291:VAL:HG22	3:A:1292:PRO:CD	2.47	0.44
3:A:1385:THR:C	3:A:1387:HIS:N	2.69	0.44
3:A:416:ARG:C	3:A:417:TYR:CD2	2.89	0.44
3:A:590:ARG:HD3	3:A:604:GLY:CA	2.45	0.44
3:A:93:VAL:HG21	3:A:301:ALA:O	2.17	0.44
4:B:1182:CYS:O	4:B:1183:LYS:C	2.55	0.44
4:B:471:LYS:O	4:B:472:ALA:HB2	2.17	0.44
4:B:874:PHE:HA	4:B:913:GLY:O	2.16	0.44
4:B:1079:LYS:CA	5:C:27:LEU:HD21	2.47	0.44
8:F:86:THR:HG23	8:F:89:GLU:OE1	2.18	0.44
9:G:117:GLN:C	9:G:119:LEU:N	2.70	0.44
9:G:20:PRO:HG2	9:G:21:ARG:N	2.32	0.44
11:I:34:TYR:C	11:I:34:TYR:HD2	2.16	0.44
3:A:1219:THR:HG21	3:A:1271:ILE:CD1	2.47	0.44
3:A:1293:SER:OG	3:A:1295:THR:HG23	2.17	0.44
3:A:207:ILE:HG23	3:A:211:PHE:HE1	1.82	0.44
3:A:262:LEU:C	3:A:264:PHE:N	2.71	0.44
3:A:418:SER:O	3:A:420:ARG:N	2.50	0.44
3:A:717:ASN:HA	3:A:720:ARG:HH12	1.81	0.44
3:A:786:HIS:CD2	3:A:786:HIS:H	2.35	0.44
3:A:341:MET:CE	4:B:1135:ARG:NH1	2.80	0.44
4:B:128:LEU:HD11	4:B:170:LEU:CB	2.48	0.44
4:B:339:THR:O	4:B:339:THR:HG22	2.16	0.44
4:B:611:PRO:O	4:B:692:TYR:HB2	2.17	0.44
5:C:66:ARG:NH1	5:C:144:ILE:O	2.50	0.44
5:C:87:PHE:CD1	5:C:87:PHE:N	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:87:PHE:HD1	5:C:87:PHE:H	1.65	0.44
6:D:119:ARG:HD3	6:D:221:TYR:CD2	2.53	0.44
7:E:180:ARG:HH21	7:E:192:ARG:CB	2.20	0.44
9:G:10:ASN:OD1	9:G:71:ASN:HA	2.18	0.44
9:G:153:GLN:HG2	9:G:154:VAL:HG23	1.97	0.44
9:G:48:VAL:HA	9:G:76:ALA:HB2	1.98	0.44
13:K:12:LEU:N	13:K:12:LEU:HD12	2.32	0.44
3:A:1072:ILE:O	3:A:1075:PRO:HG2	2.17	0.44
3:A:34:LYS:HG2	3:A:57:ARG:NH2	2.32	0.44
3:A:406:ILE:HG13	3:A:431:LYS:HB2	2.00	0.44
3:A:543:LEU:N	3:A:572:TRP:HZ3	2.15	0.44
3:A:693:VAL:HA	3:A:696:GLU:HB3	2.00	0.44
3:A:829:VAL:C	3:A:831:THR:N	2.70	0.44
4:B:1095:LEU:HD12	4:B:1095:LEU:N	2.25	0.44
3:A:343:LYS:NZ	4:B:1151:LEU:O	2.41	0.44
4:B:1165:ILE:HG22	4:B:1166:CYS:N	2.32	0.44
3:A:806:ARG:HD3	4:B:728:ARG:HA	1.99	0.44
4:B:833:TYR:N	4:B:833:TYR:HD1	2.15	0.44
9:G:126:ASN:HA	9:G:126:ASN:HD22	1.60	0.44
9:G:110:VAL:HG22	9:G:161:GLY:O	2.16	0.44
3:A:1445:ILE:HG12	9:G:18:PHE:HE2	1.83	0.44
10:H:40:LEU:HB2	10:H:123:MET:HG3	1.98	0.44
3:A:310:GLY:C	3:A:312:PRO:HD2	2.38	0.44
3:A:415:LEU:HA	3:A:415:LEU:HD23	1.80	0.44
3:A:608:ILE:HG13	3:A:613:ILE:HD12	1.99	0.44
4:B:205:ILE:N	4:B:205:ILE:CD1	2.74	0.44
4:B:834:ASN:HB3	4:B:840:ILE:HG13	1.98	0.44
4:B:94:LYS:HG2	4:B:95:ILE:N	2.32	0.44
5:C:69:LEU:N	5:C:69:LEU:CD1	2.81	0.44
5:C:90:ASP:O	5:C:91:HIS:HB3	2.17	0.44
7:E:186:LEU:O	7:E:189:GLY:N	2.50	0.44
11:I:98:VAL:HG12	11:I:99:LEU:N	2.33	0.44
5:C:35:ARG:HH11	13:K:41:THR:N	2.13	0.44
1:P:13:A:O2'	1:P:14:G:H5'	2.18	0.44
3:A:108:MET:O	3:A:109:HIS:HB2	2.18	0.44
3:A:1213:GLY:O	3:A:1214:GLU:C	2.56	0.44
3:A:31:SER:OG	3:A:82:GLY:HA2	2.18	0.44
4:B:1116:ARG:HD2	4:B:1198:TYR:CD1	2.53	0.44
3:A:1409:LEU:HD13	4:B:1207:LEU:CD2	2.48	0.44
4:B:234:ILE:HG21	4:B:237:VAL:CG2	2.48	0.44
4:B:562:GLY:HA3	4:B:590:HIS:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:957:ASN:HD22	4:B:961:LEU:HD12	1.83	0.44
5:C:193:TYR:HD2	5:C:197:SER:HB3	1.83	0.44
5:C:44:LEU:HD21	5:C:159:ALA:HB1	1.99	0.44
5:C:8:VAL:O	5:C:9:LYS:HG3	2.17	0.44
6:D:47:LEU:HD11	9:G:3:PHE:HD2	1.81	0.44
7:E:124:VAL:CG1	7:E:132:ILE:HD12	2.43	0.44
7:E:182:ASP:OD1	7:E:183:PRO:HD2	2.17	0.44
7:E:42:PHE:CE1	7:E:58:MET:HE3	2.53	0.44
9:G:106:MET:HB3	9:G:106:MET:HE2	1.90	0.44
9:G:154:VAL:HG12	9:G:155:SER:N	2.32	0.44
11:I:12:ASN:HB3	11:I:13:MET:H	1.55	0.44
14:L:28:LYS:HB2	14:L:39:SER:CB	2.48	0.44
3:A:1116:LEU:C	3:A:1116:LEU:HD12	2.38	0.44
3:A:1226:VAL:HG13	3:A:1239:ARG:O	2.17	0.44
3:A:1445:ILE:HG21	9:G:18:PHE:CD2	2.53	0.44
3:A:889:SER:HB3	3:A:1297:GLU:HG2	1.99	0.44
4:B:1001:PHE:CD1	4:B:1001:PHE:C	2.91	0.44
3:A:1436:ILE:HD11	4:B:1139:ILE:HG23	2.00	0.44
4:B:387:LEU:O	4:B:392:ARG:HB2	2.17	0.44
4:B:401:PHE:HA	4:B:404:LYS:HG3	1.99	0.44
4:B:882:THR:O	4:B:883:LEU:HB2	2.17	0.44
9:G:20:PRO:CG	9:G:21:ARG:H	2.31	0.44
10:H:99:GLY:N	10:H:118:PHE:CD2	2.86	0.44
10:H:89:LEU:HB3	10:H:91:ASP:OD1	2.18	0.44
11:I:78:CYS:SG	11:I:106:CYS:HB3	2.58	0.44
3:A:1209:MET:SD	3:A:1236:LEU:HD22	2.57	0.44
3:A:1345:ARG:HD2	3:A:1373:ASP:OD1	2.17	0.44
3:A:719:VAL:O	3:A:721:PHE:N	2.50	0.44
3:A:738:LYS:CD	3:A:740:LEU:HD21	2.46	0.44
3:A:818:MET:N	4:B:514:LEU:HD23	2.33	0.44
3:A:821:ARG:HD2	3:A:825:ILE:CD1	2.47	0.44
3:A:867:ILE:N	3:A:867:ILE:HD12	2.32	0.44
4:B:1106:ARG:HH21	4:B:1111:MET:HE1	1.82	0.44
4:B:1207:LEU:HB3	4:B:1212:ILE:HG22	2.00	0.44
4:B:766:ARG:HD3	4:B:766:ARG:HA	1.69	0.44
5:C:254:LYS:C	5:C:256:ALA:N	2.70	0.44
6:D:51:ASN:O	6:D:52:LEU:C	2.56	0.44
6:D:8:PHE:CE2	9:G:6:ASP:O	2.71	0.44
3:A:600:PRO:HA	10:H:25:ARG:NH2	2.32	0.44
10:H:4:THR:HG22	10:H:5:LEU:H	1.83	0.44
13:K:55:LYS:HB3	13:K:81:TYR:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:82:ASP:O	13:K:85:ASP:HB2	2.18	0.44
3:A:1011:GLN:HE21	3:A:1015:VAL:HG21	1.83	0.44
3:A:1191:TRP:HB3	3:A:1260:LEU:HD23	2.00	0.44
3:A:1410:PHE:HA	4:B:1212:ILE:HD11	2.00	0.44
3:A:14:VAL:HG21	4:B:1216:LEU:CD1	2.48	0.44
3:A:224:PHE:CZ	3:A:234:MET:HE2	2.52	0.44
3:A:332:LYS:C	3:A:334:GLY:H	2.20	0.44
3:A:382:PRO:HD3	3:A:428:TYR:HD2	1.83	0.44
3:A:442:VAL:O	3:A:457:ALA:HA	2.18	0.44
3:A:608:ILE:C	3:A:610:GLY:H	2.21	0.44
3:A:896:ARG:HB3	3:A:897:TYR:CD1	2.53	0.44
3:A:986:ILE:HD12	3:A:1032:LEU:HD11	1.99	0.44
4:B:199:MET:N	4:B:199:MET:SD	2.88	0.44
4:B:274:PRO:O	4:B:275:TYR:HB2	2.18	0.44
4:B:298:LEU:N	4:B:298:LEU:HD22	2.33	0.44
4:B:408:LEU:HA	4:B:408:LEU:HD12	1.75	0.44
5:C:26:ASP:O	5:C:27:LEU:C	2.56	0.44
7:E:169:ARG:HB3	8:F:140:ASP:OD2	2.17	0.44
10:H:142:LEU:C	10:H:143:LEU:HD12	2.37	0.44
10:H:12:VAL:HB	10:H:52:GLN:N	2.33	0.44
12:J:41:LEU:N	12:J:41:LEU:HD23	2.33	0.44
13:K:68:PHE:CD2	13:K:68:PHE:N	2.83	0.44
3:A:1225:PHE:CE2	3:A:1227:ILE:HD11	2.52	0.43
3:A:164:ARG:CG	3:A:165:GLY:H	2.12	0.43
3:A:285:PRO:CG	3:A:288:ALA:HB3	2.44	0.43
3:A:42:ASP:HB3	3:A:45:GLN:N	2.33	0.43
3:A:621:THR:HG22	3:A:621:THR:O	2.18	0.43
3:A:814:PHE:O	3:A:817:ALA:HB3	2.17	0.43
3:A:897:TYR:N	3:A:897:TYR:CD1	2.86	0.43
3:A:805:LEU:HD11	4:B:1052:VAL:HG21	1.98	0.43
4:B:1166:CYS:SG	4:B:1168:LEU:HD12	2.57	0.43
4:B:210:LYS:HE2	4:B:462:ALA:HA	2.00	0.43
4:B:515:HIS:HD2	4:B:516:ASN:N	2.14	0.43
5:C:113:VAL:O	5:C:144:ILE:N	2.50	0.43
5:C:98:VAL:CG2	5:C:122:SER:HB3	2.48	0.43
7:E:129:PRO:O	7:E:130:ALA:C	2.57	0.43
7:E:168:TYR:HB2	7:E:170:LEU:HG	2.00	0.43
7:E:178:ILE:HG22	7:E:213:ILE:O	2.18	0.43
8:F:72:LYS:O	8:F:142:SER:HA	2.18	0.43
12:J:1:MET:O	12:J:1:MET:HG3	2.17	0.43
13:K:10:PHE:HA	13:K:37:LYS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:43:GLY:HA3	13:K:61:TYR:CE1	2.53	0.43
13:K:7:PHE:CD1	13:K:7:PHE:C	2.91	0.43
14:L:40:LEU:HD22	14:L:44:ASP:HB3	1.99	0.43
3:A:1076:ALA:HA	3:A:1079:MET:HE3	2.00	0.43
3:A:1151:GLU:HA	11:I:44:TYR:O	2.17	0.43
3:A:279:LEU:O	3:A:284:ALA:HB2	2.17	0.43
3:A:514:PRO:CB	3:A:875:ALA:HB3	2.47	0.43
3:A:523:ILE:CD1	3:A:649:ILE:HG21	2.48	0.43
3:A:966:ASN:O	3:A:967:ALA:C	2.56	0.43
4:B:1115:THR:CG2	4:B:1117:GLN:HG3	2.43	0.43
4:B:1197:PRO:O	4:B:1200:ALA:N	2.48	0.43
4:B:593:PRO:HG2	4:B:617:ARG:NH2	2.33	0.43
4:B:769:TYR:O	4:B:771:SER:N	2.51	0.43
4:B:497:ARG:NH2	4:B:775:LYS:NZ	2.66	0.43
5:C:101:LEU:HA	5:C:101:LEU:HD12	1.79	0.43
5:C:113:VAL:HG23	5:C:147:LEU:HD21	1.99	0.43
5:C:131:HIS:HA	5:C:132:PRO:HD3	1.89	0.43
5:C:242:GLN:C	5:C:244:VAL:H	2.20	0.43
6:D:8:PHE:CE1	6:D:37:GLN:HB2	2.53	0.43
9:G:34:VAL:HG11	9:G:74:TYR:CE1	2.54	0.43
3:A:1147:THR:O	11:I:48:LEU:HD12	2.18	0.43
3:A:18:GLN:HB2	4:B:1215:ARG:CB	2.47	0.43
3:A:218:ASP:O	3:A:219:PHE:C	2.57	0.43
3:A:278:THR:O	3:A:282:ASN:HB2	2.18	0.43
3:A:546:VAL:HA	3:A:549:MET:HE2	1.99	0.43
3:A:858:ASN:ND2	3:A:861:GLY:H	2.15	0.43
3:A:965:GLN:HA	3:A:968:GLN:HG3	2.00	0.43
4:B:773:MET:HB3	4:B:1095:LEU:HD23	2.01	0.43
4:B:1156:ASP:HB3	4:B:1198:TYR:H	1.84	0.43
4:B:278:GLN:HG2	4:B:279:ASP:N	2.33	0.43
4:B:756:ILE:O	4:B:759:PRO:HD3	2.19	0.43
4:B:95:ILE:HB	4:B:130:VAL:HG22	2.00	0.43
4:B:996:ARG:HG2	4:B:1007:VAL:HG11	1.99	0.43
7:E:147:HIS:CD2	7:E:149:LEU:H	2.36	0.43
8:F:81:THR:HB	8:F:136:ARG:HH11	1.83	0.43
6:D:40:HIS:HB2	9:G:73:LYS:HZ2	1.83	0.43
10:H:82:PRO:C	10:H:84:ALA:H	2.21	0.43
11:I:7:CYS:HB2	11:I:34:TYR:CD1	2.53	0.43
3:A:1153:TYR:CE1	11:I:42:LEU:HD13	2.54	0.43
4:B:309:GLN:CG	11:I:52:ILE:HD11	2.48	0.43
12:J:41:LEU:HD11	12:J:50:ILE:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:34:CYS:O	14:L:35:SER:C	2.57	0.43
3:A:1095:THR:OG1	3:A:1113:THR:HB	2.19	0.43
3:A:1409:LEU:HA	3:A:1409:LEU:HD23	1.87	0.43
3:A:1410:PHE:HA	4:B:1212:ILE:CD1	2.48	0.43
3:A:86:LEU:HD12	3:A:236:LEU:O	2.18	0.43
3:A:244:PRO:CG	3:A:245:PRO:CD	2.92	0.43
3:A:58:LEU:O	3:A:59:GLY:O	2.37	0.43
3:A:753:GLY:HA2	3:A:757:ASN:ND2	2.33	0.43
3:A:351:THR:CB	4:B:1103:ILE:HD12	2.46	0.43
4:B:542:MET:SD	4:B:747:MET:HE2	2.59	0.43
4:B:885:MET:HA	4:B:936:ASP:CB	2.47	0.43
4:B:1001:PHE:HD2	5:C:34:ARG:NH2	2.14	0.43
5:C:82:TYR:O	5:C:83:SER:C	2.56	0.43
6:D:20:GLU:HA	6:D:20:GLU:OE2	2.19	0.43
7:E:149:LEU:HD23	7:E:149:LEU:N	2.33	0.43
3:A:560:ILE:CG1	10:H:78:SER:HB2	2.39	0.43
12:J:3:VAL:CG2	12:J:18:TRP:CG	3.02	0.43
12:J:53:HIS:CD2	12:J:54:VAL:N	2.86	0.43
3:A:1011:GLN:O	3:A:1015:VAL:HG23	2.19	0.43
3:A:1162:VAL:HG12	3:A:1162:VAL:O	2.17	0.43
3:A:1349:TYR:O	3:A:1350:LYS:C	2.56	0.43
3:A:401:GLY:C	3:A:435:HIS:CD2	2.89	0.43
4:B:102:VAL:O	4:B:109:THR:HA	2.18	0.43
4:B:114:PRO:HG2	4:B:115:GLN:N	2.28	0.43
4:B:221:ASN:OD1	4:B:242:SER:HA	2.18	0.43
4:B:303:TYR:N	4:B:303:TYR:CD2	2.86	0.43
4:B:351:TYR:CD1	4:B:355:ILE:HD11	2.54	0.43
4:B:383:ASN:O	4:B:384:ARG:C	2.57	0.43
4:B:46:GLN:OE1	4:B:47:GLN:HG2	2.19	0.43
4:B:53:GLN:HG2	4:B:547:VAL:CG2	2.45	0.43
3:A:806:ARG:HH12	4:B:729:ILE:HD12	1.83	0.43
4:B:977:GLY:HA3	4:B:1099:VAL:HB	2.01	0.43
5:C:12:GLU:O	5:C:13:ALA:HB2	2.18	0.43
7:E:204:THR:HG23	7:E:205:SER:N	2.34	0.43
7:E:94:LYS:CE	7:E:98:ILE:HD11	2.26	0.43
10:H:48:PRO:O	10:H:49:VAL:CG2	2.66	0.43
13:K:10:PHE:CD1	13:K:11:LEU:CD2	3.01	0.43
3:A:1171:GLN:HA	3:A:1174:PHE:CE1	2.54	0.43
3:A:1285:MET:O	3:A:1304:TRP:HA	2.18	0.43
3:A:1315:GLU:C	3:A:1317:MET:N	2.70	0.43
3:A:1311:VAL:HG11	3:A:1329:THR:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:17:VAL:HA	4:B:1215:ARG:O	2.18	0.43
3:A:247:ARG:HG3	3:A:247:ARG:O	2.18	0.43
3:A:325:ILE:HG22	4:B:1210:MET:HE1	2.00	0.43
3:A:402:ALA:CB	3:A:434:ARG:HA	2.49	0.43
3:A:667:GLY:HA3	5:C:192:TRP:CH2	2.54	0.43
4:B:29:ASP:HB3	4:B:658:ILE:CD1	2.49	0.43
4:B:225:VAL:HG11	4:B:385:LEU:HA	2.01	0.43
4:B:383:ASN:O	4:B:387:LEU:HD13	2.18	0.43
4:B:519:TRP:HE1	4:B:635:ARG:NH2	2.16	0.43
4:B:97:VAL:HG12	4:B:178:ASN:ND2	2.32	0.43
5:C:8:VAL:CG1	5:C:9:LYS:N	2.80	0.43
7:E:178:ILE:HD11	7:E:185:ALA:HB2	2.01	0.43
3:A:1118:VAL:HG12	3:A:1327:ILE:CG1	2.43	0.43
3:A:477:PRO:HG3	3:A:521:MET:HG2	1.98	0.43
3:A:577:ILE:C	3:A:579:SER:N	2.71	0.43
3:A:604:GLY:O	3:A:605:MET:HB2	2.19	0.43
3:A:647:GLY:O	3:A:651:LYS:HG3	2.19	0.43
3:A:818:MET:HG2	4:B:514:LEU:HG	2.01	0.43
4:B:1034:VAL:C	4:B:1036:ALA:N	2.71	0.43
4:B:1074:ASN:HB2	4:B:1081:LEU:CD2	2.49	0.43
4:B:1159:ARG:HB3	4:B:1159:ARG:NH1	2.34	0.43
4:B:282:ILE:CD1	4:B:382:ILE:HD13	2.48	0.43
4:B:700:SER:O	4:B:701:ILE:HG22	2.19	0.43
5:C:22:LEU:HD13	5:C:230:MET:HE3	2.00	0.43
6:D:119:ARG:HG2	6:D:120:GLU:H	1.81	0.43
6:D:4:SER:C	6:D:5:THR:HG22	2.39	0.43
7:E:175:LEU:HD23	7:E:176:PRO:HD2	2.00	0.43
7:E:72:PHE:CE2	7:E:155:ARG:NH2	2.87	0.43
10:H:2:SER:HA	10:H:62:SER:OG	2.19	0.43
11:I:101:PHE:HD1	11:I:101:PHE:H	1.66	0.43
3:A:369:SER:CB	13:K:2:ASN:OD1	2.67	0.43
13:K:49:GLU:OE2	13:K:97:LYS:HE3	2.19	0.43
14:L:61:THR:CG2	14:L:63:ARG:CG	2.97	0.43
3:A:1156:PRO:HA	3:A:1190:PRO:CB	2.49	0.43
3:A:1193:LEU:HB2	3:A:1260:LEU:HD11	2.01	0.43
3:A:50:ILE:HG22	3:A:52:GLY:N	2.33	0.43
3:A:541:ILE:HD13	3:A:549:MET:HE3	2.00	0.43
3:A:567:LYS:HB3	10:H:95:TYR:CA	2.46	0.43
3:A:658:LEU:HD12	4:B:830:TYR:CD1	2.53	0.43
3:A:717:ASN:HA	3:A:720:ARG:NH1	2.34	0.43
3:A:89:PRO:HB2	3:A:204:THR:CG2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:971:PHE:HE2	3:A:1040:GLN:HG2	1.83	0.43
4:B:839:MET:HG3	4:B:1010:LEU:HD11	2.01	0.43
4:B:1031:LEU:HD11	4:B:1042:GLY:CA	2.48	0.43
4:B:168:GLY:N	4:B:450:ALA:HB1	2.29	0.43
4:B:701:ILE:HD11	4:B:703:ILE:HD11	2.01	0.43
7:E:42:PHE:O	7:E:43:LYS:C	2.57	0.43
3:A:1066:VAL:HG11	4:B:1136:ASP:O	2.19	0.43
3:A:1215:ARG:HH11	3:A:1215:ARG:HG2	1.83	0.43
3:A:184:SER:HB3	3:A:199:LEU:CD2	2.48	0.43
3:A:208:LEU:C	3:A:208:LEU:HD23	2.39	0.43
3:A:302:THR:HG22	3:A:303:TYR:N	2.34	0.43
3:A:37:PHE:H	3:A:37:PHE:HD1	1.66	0.43
3:A:515:GLN:O	3:A:516:SER:HB3	2.18	0.43
3:A:535:THR:CG2	3:A:575:LYS:HE2	2.48	0.43
3:A:551:TYR:CE2	13:K:62:LYS:HG2	2.53	0.43
3:A:765:VAL:HG23	3:A:802:ASN:O	2.18	0.43
3:A:722:LEU:HD22	3:A:799:PHE:CG	2.54	0.43
4:B:1060:ARG:HD2	4:B:1060:ARG:HA	1.57	0.43
4:B:1079:LYS:HA	5:C:27:LEU:HD21	2.01	0.43
4:B:980:PHE:CE2	4:B:1094:ARG:HB2	2.54	0.43
3:A:335:ARG:HH11	4:B:1202:LEU:HD13	1.82	0.43
4:B:38:PHE:HD1	4:B:811:TYR:HD2	1.64	0.43
4:B:597:MET:CE	4:B:597:MET:HA	2.49	0.43
4:B:758:PHE:N	4:B:759:PRO:CD	2.82	0.43
5:C:120:ILE:CD1	5:C:124:LEU:HD11	2.48	0.43
6:D:66:ARG:HD2	6:D:133:THR:HB	2.00	0.43
7:E:177:ARG:HD3	7:E:215:MET:HG3	2.01	0.43
11:I:99:LEU:C	11:I:100:PHE:HD1	2.21	0.43
5:C:47:ASP:CA	14:L:69:ALA:HB3	2.36	0.43
3:A:527:THR:HG23	3:A:650:GLN:HA	2.00	0.43
3:A:789:LYS:NZ	4:B:620:ARG:HH11	2.17	0.43
3:A:866:PHE:O	3:A:867:ILE:HD12	2.19	0.43
4:B:412:LEU:HB3	4:B:466:TRP:CZ2	2.54	0.43
4:B:764:SER:HB3	4:B:765:PRO:CD	2.49	0.43
5:C:252:GLN:HB2	13:K:98:LEU:HD13	2.01	0.43
5:C:8:VAL:CG1	5:C:9:LYS:H	2.27	0.43
8:F:111:LEU:H	8:F:111:LEU:CD1	2.29	0.43
8:F:93:ILE:HD13	8:F:148:VAL:HG12	2.01	0.43
11:I:53:GLY:O	11:I:55:THR:N	2.52	0.43
3:A:1004:ASN:HD21	3:A:1007:ILE:HG12	1.84	0.42
3:A:1424:VAL:HG11	4:B:1139:ILE:CD1	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1434:ALA:HA	3:A:1435:PRO:HD3	1.90	0.42
3:A:470:LEU:HD22	3:A:487:MET:HE1	2.01	0.42
3:A:478:TYR:O	3:A:479:ASN:CB	2.65	0.42
3:A:939:ASP:O	3:A:940:ARG:C	2.58	0.42
4:B:1065:GLN:NE2	4:B:1067:ARG:H	2.11	0.42
4:B:205:ILE:O	4:B:207:GLY:N	2.52	0.42
4:B:642:ASP:CA	4:B:649:LYS:HG3	2.48	0.42
4:B:769:TYR:O	4:B:772:ALA:N	2.52	0.42
5:C:238:ILE:HD11	5:C:246:ARG:CZ	2.47	0.42
7:E:105:PHE:O	7:E:106:GLN:HB2	2.19	0.42
9:G:14:HIS:ND1	9:G:15:PRO:CD	2.77	0.42
11:I:100:PHE:N	11:I:100:PHE:CD1	2.87	0.42
14:L:40:LEU:HD13	14:L:44:ASP:CB	2.49	0.42
3:A:1163:ILE:HG22	3:A:1164:PRO:HD2	2.01	0.42
3:A:1191:TRP:CD1	3:A:1256:GLU:HB2	2.54	0.42
3:A:1280:GLU:O	3:A:1281:ARG:O	2.37	0.42
3:A:336:ILE:HG22	3:A:337:ARG:N	2.33	0.42
3:A:367:PRO:HB3	3:A:465:TYR:O	2.19	0.42
3:A:37:PHE:HB2	3:A:52:GLY:HA3	2.01	0.42
3:A:629:LEU:HD22	3:A:633:VAL:CG2	2.50	0.42
3:A:65:LEU:O	3:A:66:LYS:C	2.57	0.42
3:A:767:GLN:OE1	3:A:799:PHE:HB2	2.19	0.42
4:B:100:PRO:HB2	4:B:180:TYR:CE1	2.53	0.42
4:B:360:PHE:C	4:B:360:PHE:CD2	2.92	0.42
4:B:51:PHE:HE2	4:B:172:ILE:HG23	1.84	0.42
4:B:952:VAL:CG1	4:B:953:LEU:N	2.81	0.42
10:H:31:THR:O	10:H:31:THR:HG22	2.19	0.42
3:A:1215:ARG:HA	3:A:1218:GLN:HE21	1.84	0.42
3:A:1239:ARG:HH22	3:A:1241:ARG:NH2	2.15	0.42
3:A:1280:GLU:O	3:A:1282:VAL:HG23	2.19	0.42
3:A:172:PRO:HB3	3:A:185:TRP:CE2	2.54	0.42
3:A:353:ILE:HD13	3:A:487:MET:CE	2.49	0.42
3:A:560:ILE:HG12	3:A:560:ILE:H	1.55	0.42
3:A:608:ILE:C	3:A:610:GLY:N	2.72	0.42
3:A:614:PHE:C	3:A:614:PHE:CD1	2.92	0.42
3:A:645:LEU:CD1	3:A:649:ILE:HG13	2.50	0.42
3:A:742:ASN:O	3:A:745:GLN:HB2	2.19	0.42
4:B:360:PHE:O	4:B:361:LEU:C	2.58	0.42
4:B:502:ILE:N	4:B:502:ILE:CD1	2.82	0.42
4:B:515:HIS:CD2	4:B:517:THR:HG23	2.54	0.42
4:B:515:HIS:N	4:B:518:HIS:HD2	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:867:GLY:C	4:B:869:SER:H	2.22	0.42
5:C:133:ILE:HD13	5:C:236:GLY:O	2.18	0.42
6:D:56:ARG:CB	6:D:148:LEU:HD22	2.36	0.42
7:E:157:SER:HG	7:E:160:GLU:HG3	1.82	0.42
1:P:14:G:O2'	1:P:15:G:H5'	2.19	0.42
3:A:1394:THR:CG2	3:A:1398:MET:SD	3.06	0.42
3:A:1424:VAL:HG13	3:A:1436:ILE:HD12	2.02	0.42
3:A:224:PHE:CD2	3:A:231:PRO:HD3	2.54	0.42
3:A:40:THR:C	3:A:41:MET:HG3	2.37	0.42
3:A:41:MET:HB2	3:A:42:ASP:H	1.39	0.42
3:A:481:ASP:OD1	3:A:483:ASP:OD2	2.37	0.42
3:A:55:ASP:C	3:A:57:ARG:N	2.71	0.42
3:A:577:ILE:HG13	3:A:578:LEU:N	2.33	0.42
3:A:598:LEU:O	3:A:599:SER:C	2.57	0.42
3:A:626:ASN:C	3:A:628:GLY:H	2.22	0.42
3:A:553:VAL:HG22	3:A:652:VAL:CG2	2.49	0.42
3:A:894:GLU:HG3	3:A:933:TYR:OH	2.18	0.42
3:A:896:ARG:HB3	3:A:897:TYR:HD1	1.84	0.42
4:B:1096:ARG:CG	4:B:1097:HIS:N	2.82	0.42
4:B:259:TYR:HB2	4:B:268:THR:HG23	2.01	0.42
4:B:467:GLY:CA	4:B:475:SER:HB3	2.48	0.42
4:B:707:PRO:HG2	4:B:708:GLU:H	1.82	0.42
5:C:69:LEU:HB3	12:J:6:ARG:CD	2.49	0.42
6:D:29:LEU:HD23	6:D:29:LEU:N	2.33	0.42
7:E:149:LEU:O	7:E:151:PRO:HD3	2.19	0.42
10:H:84:ALA:HB1	10:H:87:ARG:HB2	1.98	0.42
5:C:147:LEU:HA	12:J:61:LEU:HD21	2.01	0.42
3:A:1015:VAL:O	3:A:1016:THR:C	2.57	0.42
3:A:1164:PRO:HG2	3:A:1165:GLU:HG3	2.02	0.42
3:A:120:GLU:C	3:A:122:MET:H	2.23	0.42
3:A:1332:PHE:HA	3:A:1335:ILE:HB	2.00	0.42
3:A:332:LYS:HG3	3:A:333:GLU:CG	2.43	0.42
3:A:362:ASP:OD2	3:A:459:ARG:HD3	2.19	0.42
3:A:514:PRO:HB2	3:A:875:ALA:HB3	2.01	0.42
3:A:977:LYS:HB3	3:A:978:PRO:HD2	2.00	0.42
4:B:1010:LEU:HA	4:B:1010:LEU:HD12	1.74	0.42
4:B:1167:GLY:O	4:B:1215:ARG:HA	2.20	0.42
4:B:455:SER:O	4:B:456:GLY:C	2.58	0.42
5:C:73:GLN:HB2	5:C:131:HIS:HB2	2.00	0.42
7:E:117:THR:C	7:E:119:SER:H	2.22	0.42
9:G:117:GLN:O	9:G:119:LEU:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:83:LYS:HE2	9:G:150:CYS:H	1.84	0.42
10:H:110:ASP:O	10:H:128:ASN:ND2	2.53	0.42
10:H:4:THR:O	10:H:5:LEU:HD23	2.19	0.42
10:H:95:TYR:HE2	10:H:97:MET:CG	2.31	0.42
13:K:103:THR:HG22	13:K:104:ASN:N	2.34	0.42
3:A:1161:THR:C	3:A:1163:ILE:H	2.22	0.42
3:A:1444:MET:N	3:A:1444:MET:HE2	2.35	0.42
3:A:244:PRO:CB	3:A:245:PRO:HD3	2.49	0.42
3:A:346:ASP:OD1	4:B:1108:ARG:HA	2.19	0.42
3:A:622:VAL:O	3:A:622:VAL:HG13	2.19	0.42
3:A:780:VAL:O	3:A:780:VAL:HG12	2.19	0.42
3:A:794:PRO:C	3:A:796:SER:N	2.73	0.42
4:B:1159:ARG:HD3	4:B:1193:GLN:CG	2.39	0.42
4:B:377:PHE:HE1	4:B:581:PHE:HE2	1.66	0.42
4:B:578:THR:C	4:B:589:VAL:HG13	2.40	0.42
4:B:96:TYR:HE1	4:B:131:ASP:OD2	2.02	0.42
5:C:114:TYR:CD2	5:C:140:ASN:HB2	2.55	0.42
5:C:27:LEU:O	5:C:28:ALA:C	2.58	0.42
6:D:67:ARG:CA	6:D:133:THR:HG21	2.49	0.42
7:E:179:GLN:O	7:E:182:ASP:HB2	2.20	0.42
7:E:85:GLU:O	7:E:88:VAL:HG23	2.19	0.42
10:H:62:SER:C	10:H:64:ASN:N	2.73	0.42
11:I:101:PHE:CE1	11:I:112:SER:HB2	2.55	0.42
11:I:90:GLN:HE21	11:I:92:ARG:HB2	1.85	0.42
13:K:111:LEU:O	13:K:112:GLN:CB	2.67	0.42
14:L:53:HIS:HB3	14:L:55:ILE:HD11	2.01	0.42
3:A:1107:VAL:O	3:A:1107:VAL:HG12	2.19	0.42
3:A:1265:ASN:O	3:A:1267:MET:N	2.53	0.42
3:A:1385:THR:O	3:A:1387:HIS:N	2.52	0.42
3:A:154:SER:OG	3:A:162:VAL:HG21	2.20	0.42
3:A:20:GLY:O	3:A:21:LEU:HD23	2.20	0.42
3:A:388:LEU:HD22	3:A:432:VAL:HB	2.01	0.42
3:A:68:GLN:C	3:A:70:CYS:N	2.70	0.42
3:A:890:ASP:H	3:A:1296:GLY:HA3	1.84	0.42
3:A:919:ILE:HD13	3:A:983:ILE:CD1	2.50	0.42
3:A:960:ILE:HA	3:A:963:ILE:CG2	2.50	0.42
4:B:1039:GLY:HA2	12:J:51:LEU:CD2	2.48	0.42
4:B:205:ILE:O	4:B:206:ASN:C	2.58	0.42
4:B:332:ASP:OD1	4:B:336:ARG:NE	2.53	0.42
5:C:18:VAL:O	5:C:19:ASP:C	2.58	0.42
6:D:118:THR:O	6:D:118:THR:HG22	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:179:GLN:NE2	6:D:179:GLN:HA	2.33	0.42
6:D:39:ASN:ND2	6:D:41:GLN:NE2	2.60	0.42
7:E:136:ASN:OD1	7:E:137:GLU:N	2.52	0.42
8:F:118:LEU:O	8:F:118:LEU:HD12	2.20	0.42
8:F:94:LEU:HD21	8:F:122:MET:HA	2.02	0.42
10:H:42:ILE:HG12	10:H:95:TYR:CE1	2.55	0.42
11:I:2:THR:O	11:I:4:PHE:N	2.52	0.42
12:J:7:CYS:SG	12:J:49:MET:CE	3.05	0.42
13:K:88:LYS:O	13:K:91:CYS:HB2	2.19	0.42
3:A:1059:HIS:ND1	8:F:86:THR:HA	2.33	0.42
3:A:1339:LEU:HD13	7:E:147:HIS:CD2	2.54	0.42
3:A:453:MET:C	3:A:455:MET:H	2.23	0.42
3:A:652:VAL:O	3:A:653:VAL:C	2.58	0.42
3:A:870:GLU:HB2	7:E:204:THR:HG21	2.02	0.42
3:A:90:VAL:HG12	3:A:91:PHE:N	2.35	0.42
4:B:293:PRO:C	4:B:294:ASP:O	2.58	0.42
4:B:31:TRP:CE3	4:B:34:ILE:HD12	2.54	0.42
4:B:356:LEU:O	4:B:374:LYS:NZ	2.48	0.42
4:B:492:LEU:HD13	4:B:812:LEU:HD23	2.02	0.42
4:B:854:LEU:HB3	4:B:856:PHE:HE1	1.85	0.42
4:B:911:ILE:HG22	4:B:966:VAL:HG21	2.02	0.42
5:C:250:THR:O	5:C:253:LYS:N	2.53	0.42
6:D:7:THR:O	6:D:9:GLN:N	2.52	0.42
10:H:102:TYR:N	10:H:102:TYR:HD2	2.16	0.42
11:I:13:MET:HG3	11:I:14:LEU:N	2.34	0.42
3:A:883:LEU:HD11	3:A:1017:LEU:HD11	2.02	0.42
3:A:1150:SER:O	3:A:1151:GLU:HG3	2.20	0.42
3:A:1154:TYR:HD1	3:A:1191:TRP:CH2	2.38	0.42
3:A:114:LEU:O	3:A:115:LEU:HG	2.19	0.42
3:A:1219:THR:CB	3:A:1271:ILE:HD11	2.50	0.42
3:A:1279:ILE:HD11	3:A:1316:VAL:CG2	2.49	0.42
3:A:1297:GLU:HG3	3:A:1297:GLU:H	1.56	0.42
3:A:367:PRO:HA	3:A:463:ILE:O	2.20	0.42
3:A:354:SER:O	3:A:469:ARG:HA	2.19	0.42
3:A:605:MET:HG2	3:A:621:THR:HG21	2.01	0.42
3:A:664:THR:CG2	3:A:665:GLY:N	2.82	0.42
3:A:940:ARG:HG2	3:A:940:ARG:NH1	2.34	0.42
4:B:1070:GLU:OE1	12:J:44:TYR:OH	2.37	0.42
4:B:828:ALA:HB2	4:B:1085:ILE:HG23	2.01	0.42
4:B:234:ILE:O	4:B:261:ARG:NH2	2.53	0.42
4:B:293:PRO:HG2	4:B:296:GLU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:449:ASN:C	4:B:451:LYS:H	2.23	0.42
4:B:461:LEU:HD12	4:B:461:LEU:N	2.35	0.42
4:B:611:PRO:CB	4:B:685:LEU:HD21	2.50	0.42
5:C:46:ILE:HD13	5:C:157:CYS:SG	2.60	0.42
5:C:66:ARG:CZ	12:J:2:ILE:CG2	2.98	0.42
5:C:93:ASP:OD1	5:C:122:SER:HB2	2.20	0.42
6:D:27:LEU:HD22	6:D:173:HIS:CD2	2.54	0.42
9:G:21:ARG:HD3	9:G:21:ARG:HA	1.79	0.42
10:H:107:VAL:HG21	10:H:126:GLU:OE2	2.20	0.42
11:I:105:SER:O	11:I:106:CYS:CB	2.68	0.42
13:K:55:LYS:HB2	13:K:81:TYR:HE1	1.83	0.42
3:A:1074:GLU:HB3	3:A:1075:PRO:CD	2.50	0.42
3:A:1226:VAL:HG22	3:A:1240:CYS:CB	2.49	0.42
3:A:1260:LEU:CG	3:A:1260:LEU:O	2.68	0.42
3:A:1120:LEU:HD11	3:A:1305:VAL:HA	2.01	0.42
3:A:1348:LEU:HD21	3:A:1375:MET:SD	2.60	0.42
3:A:1437:GLY:HA3	8:F:88:TYR:CD2	2.55	0.42
3:A:1441:PHE:CZ	8:F:89:GLU:HA	2.55	0.42
3:A:370:ILE:O	3:A:373:THR:N	2.45	0.42
3:A:532:ARG:HD3	3:A:749:ALA:HB2	2.02	0.42
3:A:979:SER:HG	3:A:980:ASP:H	1.66	0.42
4:B:1002:THR:HG21	4:B:1006:ILE:HD12	2.01	0.42
4:B:222:ILE:O	4:B:240:ILE:HA	2.19	0.42
4:B:307:ASP:O	4:B:308:TRP:C	2.57	0.42
4:B:383:ASN:C	4:B:387:LEU:HD13	2.40	0.42
4:B:582:VAL:HG23	4:B:626:ILE:CB	2.46	0.42
4:B:603:LEU:HB3	4:B:609:ILE:HG13	2.01	0.42
5:C:174:ALA:O	12:J:10:CYS:HB2	2.19	0.42
5:C:191:TYR:CD2	5:C:201:TRP:CD1	3.00	0.42
5:C:6:PRO:HB3	5:C:25:VAL:CG1	2.40	0.42
6:D:24:ALA:C	6:D:26:THR:N	2.73	0.42
9:G:39:THR:CG2	9:G:40:GLY:H	2.18	0.42
10:H:11:GLN:C	10:H:28:ALA:HB1	2.41	0.42
10:H:80:ARG:HA	10:H:81:PRO:HD3	1.87	0.42
10:H:83:GLN:O	10:H:85:GLY:N	2.51	0.42
14:L:40:LEU:HD22	14:L:44:ASP:CG	2.40	0.42
3:A:875:ALA:HB2	3:A:1366:ARG:HD2	2.02	0.41
3:A:383:TYR:N	3:A:383:TYR:CD2	2.88	0.41
3:A:404:TYR:CD2	3:A:414:ASP:HA	2.54	0.41
3:A:470:LEU:HD22	3:A:487:MET:HE3	2.01	0.41
3:A:494:SER:O	3:A:497:THR:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:500:GLU:O	3:A:504:LEU:HD13	2.20	0.41
3:A:699:ALA:O	3:A:700:ASN:HB3	2.20	0.41
4:B:839:MET:HG3	4:B:1010:LEU:CD1	2.50	0.41
4:B:1106:ARG:HD2	4:B:1125:ASP:O	2.20	0.41
4:B:22:SER:HA	4:B:654:ARG:CG	2.50	0.41
4:B:376:PHE:HB3	4:B:586:TRP:CZ3	2.55	0.41
4:B:654:ARG:C	4:B:656:GLY:N	2.72	0.41
4:B:736:THR:O	4:B:736:THR:HG22	2.20	0.41
4:B:806:THR:HG22	4:B:808:ALA:CB	2.50	0.41
4:B:841:MET:SD	4:B:846:ILE:HD11	2.59	0.41
4:B:60:GLN:NE2	4:B:94:LYS:HA	2.31	0.41
5:C:107:SER:C	5:C:109:SER:N	2.72	0.41
5:C:246:ARG:HA	5:C:249:ASP:HB3	2.02	0.41
5:C:77:ILE:HD13	5:C:77:ILE:HA	1.84	0.41
7:E:177:ARG:HD3	7:E:215:MET:CG	2.49	0.41
8:F:89:GLU:HB3	8:F:134:ILE:HD13	2.02	0.41
10:H:95:TYR:CE2	10:H:97:MET:CG	3.02	0.41
13:K:46:ILE:O	13:K:46:ILE:HG22	2.20	0.41
13:K:67:PHE:C	13:K:68:PHE:HD2	2.24	0.41
3:A:1010:ALA:O	3:A:1013:ASP:HB2	2.19	0.41
3:A:1053:PHE:O	3:A:1055:ARG:N	2.53	0.41
3:A:18:GLN:CB	4:B:1215:ARG:HG3	2.50	0.41
3:A:269:ILE:HG23	3:A:300:VAL:HG22	2.02	0.41
3:A:289:ILE:C	3:A:291:GLU:H	2.23	0.41
3:A:510:GLN:HA	3:A:510:GLN:OE1	2.19	0.41
3:A:567:LYS:HD3	10:H:95:TYR:HA	2.02	0.41
3:A:719:VAL:CG2	3:A:774:ARG:HD3	2.50	0.41
3:A:714:PHE:HE2	3:A:792:TYR:HD2	1.67	0.41
3:A:857:ARG:HD3	3:A:861:GLY:O	2.20	0.41
4:B:761:HIS:HB2	4:B:1024:ALA:HB2	2.02	0.41
4:B:1208:MET:HA	4:B:1212:ILE:O	2.19	0.41
3:A:822:GLU:HG3	4:B:513:GLN:NE2	2.35	0.41
5:C:187:LYS:HG3	5:C:219:PHE:CE1	2.54	0.41
5:C:254:LYS:C	5:C:256:ALA:H	2.23	0.41
5:C:45:ALA:O	5:C:159:ALA:HA	2.19	0.41
5:C:89:GLU:O	5:C:90:ASP:CB	2.68	0.41
6:D:156:ASP:HB3	6:D:159:THR:H	1.85	0.41
6:D:8:PHE:HE1	6:D:37:GLN:HB2	1.86	0.41
3:A:870:GLU:HG2	7:E:208:TYR:CD1	2.55	0.41
7:E:93:MET:HE2	7:E:120:ALA:HB1	2.01	0.41
11:I:50:THR:CG2	11:I:51:ASN:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1025:ARG:NH1	3:A:1025:ARG:HG3	2.34	0.41
3:A:1072:ILE:HG23	3:A:1356:ILE:HD11	2.02	0.41
3:A:1192:LEU:HG	3:A:1193:LEU:N	2.35	0.41
3:A:182:VAL:CG2	3:A:201:VAL:HA	2.49	0.41
3:A:48:ALA:O	3:A:49:LYS:HG2	2.20	0.41
3:A:492:PRO:O	3:A:493:GLN:NE2	2.53	0.41
3:A:809:THR:OG1	3:A:812:GLU:HG3	2.21	0.41
3:A:746:MET:CE	4:B:1018:PRO:CG	2.98	0.41
4:B:1064:TYR:O	4:B:1065:GLN:C	2.59	0.41
4:B:1085:ILE:CD1	4:B:1085:ILE:N	2.79	0.41
4:B:165:VAL:HG11	4:B:448:ILE:HD13	2.02	0.41
4:B:616:ILE:HG13	4:B:697:GLU:HA	2.03	0.41
4:B:906:SER:O	4:B:907:GLY:O	2.38	0.41
5:C:239:PRO:O	5:C:241:ASP:N	2.53	0.41
6:D:139:LYS:O	6:D:143:ASN:ND2	2.50	0.41
6:D:156:ASP:C	6:D:158:GLU:H	2.23	0.41
6:D:13:ARG:CA	6:D:17:LYS:NZ	2.83	0.41
8:F:101:ILE:HD13	8:F:120:ILE:CG2	2.51	0.41
8:F:103:MET:CE	9:G:65:ASP:HB2	2.50	0.41
12:J:16:ASP:O	12:J:18:TRP:N	2.54	0.41
13:K:55:LYS:CB	13:K:81:TYR:CE1	3.03	0.41
14:L:61:THR:HG22	14:L:63:ARG:HG2	2.01	0.41
3:A:1205:LYS:O	3:A:1206:ASP:C	2.58	0.41
3:A:1209:MET:CE	3:A:1236:LEU:HB3	2.50	0.41
3:A:1263:ILE:O	3:A:1267:MET:HG3	2.20	0.41
3:A:532:ARG:O	3:A:535:THR:HB	2.20	0.41
3:A:577:ILE:O	3:A:578:LEU:C	2.59	0.41
3:A:34:LYS:CG	3:A:57:ARG:HH22	2.33	0.41
3:A:965:GLN:O	3:A:968:GLN:HB2	2.20	0.41
4:B:1207:LEU:HD23	4:B:1207:LEU:HA	1.93	0.41
4:B:806:THR:HG22	4:B:808:ALA:HB3	2.02	0.41
5:C:94:LYS:HE3	5:C:94:LYS:HB2	1.76	0.41
6:D:154:PHE:HB2	6:D:160:VAL:HG22	2.02	0.41
6:D:38:ILE:HG22	6:D:39:ASN:O	2.20	0.41
7:E:164:LEU:HD21	7:E:211:TYR:CG	2.54	0.41
3:A:1450:LEU:CD1	8:F:108:PHE:CZ	3.04	0.41
8:F:82:THR:HG23	8:F:83:PRO:HD2	2.03	0.41
9:G:79:PHE:HZ	9:G:106:MET:CE	2.31	0.41
3:A:1289:ARG:HH12	3:A:1326:ARG:NH1	2.18	0.41
3:A:693:VAL:O	3:A:693:VAL:HG12	2.20	0.41
3:A:929:LEU:HD23	3:A:983:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1034:VAL:C	4:B:1036:ALA:H	2.22	0.41
4:B:1085:ILE:HG22	4:B:1086:PHE:N	2.35	0.41
4:B:1167:GLY:CA	4:B:1217:TYR:HE1	2.34	0.41
4:B:259:TYR:H	4:B:259:TYR:HD1	1.68	0.41
4:B:654:ARG:N	4:B:657:HIS:HD2	2.05	0.41
4:B:990:ILE:HG22	4:B:991:GLY:N	2.36	0.41
5:C:168:ALA:O	5:C:170:TRP:N	2.54	0.41
5:C:73:GLN:CD	5:C:74:SER:H	2.24	0.41
8:F:119:ARG:CG	8:F:119:ARG:NH1	2.83	0.41
9:G:65:ASP:OD2	9:G:67:SER:HB2	2.20	0.41
11:I:100:PHE:N	11:I:100:PHE:HD1	2.18	0.41
13:K:27:ALA:HB1	13:K:28:PRO:HD2	2.03	0.41
14:L:55:ILE:H	14:L:55:ILE:HG12	1.45	0.41
3:A:172:PRO:HB3	3:A:185:TRP:CD2	2.55	0.41
3:A:412:ARG:HH21	4:B:1108:ARG:NH1	2.17	0.41
4:B:21:GLU:O	4:B:22:SER:O	2.38	0.41
5:C:217:ASP:HA	5:C:218:PRO:HD3	1.85	0.41
5:C:252:GLN:HE21	13:K:95:ILE:HG23	1.85	0.41
6:D:137:ASN:C	6:D:137:ASN:HD22	2.23	0.41
9:G:39:THR:CG2	9:G:41:LYS:H	2.29	0.41
10:H:91:ASP:CG	10:H:91:ASP:O	2.57	0.41
3:A:1152:ILE:HG13	11:I:44:TYR:HB3	2.03	0.41
11:I:54:GLU:HB3	11:I:100:PHE:CE2	2.55	0.41
14:L:43:THR:C	14:L:45:ALA:H	2.24	0.41
3:A:404:TYR:CE2	3:A:414:ASP:HA	2.56	0.41
3:A:474:VAL:HG22	3:A:474:VAL:O	2.21	0.41
3:A:684:ALA:O	3:A:687:LYS:HB2	2.21	0.41
3:A:958:VAL:O	3:A:958:VAL:HG12	2.20	0.41
4:B:1033:LYS:NZ	4:B:1070:GLU:OE1	2.48	0.41
4:B:23:ALA:H	4:B:654:ARG:HD2	1.86	0.41
4:B:464:GLY:O	4:B:477:ALA:HA	2.21	0.41
4:B:864:LYS:HB2	4:B:872:GLU:OE1	2.21	0.41
7:E:114:ASN:O	7:E:115:ASN:CB	2.63	0.41
7:E:17:ARG:O	7:E:21:GLU:HG3	2.21	0.41
7:E:30:ILE:HG22	7:E:31:THR:N	2.35	0.41
6:D:48:ILE:CG2	9:G:4:ILE:HB	2.51	0.41
9:G:23:LYS:HG3	9:G:56:ILE:CD1	2.50	0.41
10:H:61:SER:O	10:H:62:SER:CB	2.64	0.41
3:A:1019:CYS:O	3:A:1022:LEU:HB3	2.21	0.41
3:A:1115:SER:HB3	3:A:1330:ASN:HD21	1.86	0.41
3:A:335:ARG:HB2	3:A:335:ARG:HE	1.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:341:MET:HE2	3:A:843:LYS:NZ	2.34	0.41
3:A:42:ASP:O	3:A:44:THR:N	2.41	0.41
3:A:666:ILE:HD11	4:B:1086:PHE:CE1	2.55	0.41
3:A:77:CYS:C	3:A:78:PRO:O	2.58	0.41
4:B:307:ASP:O	4:B:309:GLN:N	2.54	0.41
4:B:800:GLN:O	4:B:801:LYS:C	2.58	0.41
3:A:667:GLY:HA3	5:C:192:TRP:HH2	1.85	0.41
6:D:63:LEU:O	6:D:129:LEU:HD11	2.21	0.41
7:E:168:TYR:CB	7:E:170:LEU:HG	2.50	0.41
9:G:59:GLY:CA	9:G:70:PHE:CD2	3.02	0.41
3:A:1101:LEU:HD11	3:A:1105:LEU:HD11	2.02	0.41
3:A:1153:TYR:CD2	3:A:1163:ILE:HD11	2.55	0.41
3:A:399:HIS:CG	3:A:400:PRO:N	2.88	0.41
3:A:43:GLU:HB2	3:A:46:THR:HB	2.03	0.41
3:A:784:LEU:HB3	3:A:785:PRO:HD2	2.03	0.41
3:A:866:PHE:HE1	7:E:211:TYR:H	1.68	0.41
3:A:899:VAL:CG2	3:A:1029:ARG:HG2	2.51	0.41
4:B:211:VAL:HG23	4:B:483:LEU:HB2	2.03	0.41
4:B:487:THR:H	4:B:490:SER:HB3	1.85	0.41
4:B:711:GLU:HB2	4:B:712:PRO:CD	2.51	0.41
4:B:890:TYR:CZ	4:B:910:VAL:HG21	2.55	0.41
7:E:116:ILE:CG2	7:E:120:ALA:HB3	2.50	0.41
9:G:102:GLN:HG3	9:G:106:MET:O	2.21	0.41
9:G:114:LEU:HD12	9:G:114:LEU:HA	1.96	0.41
11:I:86:PHE:CE1	11:I:100:PHE:HB2	2.55	0.41
11:I:6:PHE:C	11:I:14:LEU:HD11	2.41	0.41
3:A:102:VAL:O	3:A:105:CYS:HB2	2.21	0.41
3:A:1126:ALA:O	3:A:1128:GLN:N	2.54	0.41
3:A:1214:GLU:O	3:A:1218:GLN:HG2	2.21	0.41
3:A:384:ASN:O	3:A:385:ILE:C	2.59	0.41
3:A:385:ILE:HG22	3:A:386:ASP:N	2.35	0.41
3:A:608:ILE:HD12	3:A:613:ILE:HD11	2.03	0.41
3:A:818:MET:HB3	3:A:818:MET:HE2	1.88	0.41
4:B:284:ILE:HG23	4:B:324:ILE:HD12	2.03	0.41
4:B:324:ILE:CG2	4:B:325:GLN:N	2.82	0.41
4:B:619:ILE:HD12	11:I:65:ASP:HB2	2.02	0.41
5:C:221:TYR:CD1	5:C:222:LYS:HG3	2.56	0.41
5:C:33:LEU:O	5:C:37:MET:HG3	2.21	0.41
7:E:114:ASN:HD22	7:E:114:ASN:HA	1.62	0.41
8:F:82:THR:HA	8:F:83:PRO:HD3	1.80	0.41
9:G:15:PRO:O	9:G:18:PHE:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:207:ILE:CG2	3:A:211:PHE:HE1	2.33	0.41
3:A:244:PRO:O	3:A:246:VAL:N	2.53	0.41
3:A:298:PHE:HD2	3:A:299:HIS:CD2	2.39	0.41
3:A:306:ASN:HB2	3:A:324:SER:HB3	2.02	0.41
3:A:53:LEU:O	3:A:54:ASN:C	2.60	0.41
3:A:709:THR:HB	3:A:712:GLU:H	1.86	0.41
3:A:781:ASP:O	3:A:789:LYS:HA	2.21	0.41
3:A:852:TYR:CD2	3:A:1060:PRO:CB	3.03	0.41
3:A:898:ARG:O	3:A:1029:ARG:NH1	2.54	0.41
3:A:899:VAL:CG2	3:A:908:LEU:HD21	2.51	0.41
4:B:1000:PRO:O	4:B:1000:PRO:HG2	2.21	0.41
4:B:1106:ARG:NH2	4:B:1111:MET:HE2	2.36	0.41
4:B:1132:GLU:O	4:B:1135:ARG:HB3	2.20	0.41
4:B:555:ILE:HG22	4:B:556:THR:N	2.35	0.41
4:B:622:LYS:HE2	11:I:59:VAL:CG2	2.42	0.41
4:B:693:ILE:HG22	4:B:694:ASP:O	2.20	0.41
4:B:818:PRO:HB2	4:B:1091:TYR:OH	2.21	0.41
5:C:167:HIS:CD2	5:C:168:ALA:H	2.39	0.41
6:D:14:ARG:O	6:D:15:LEU:HB3	2.21	0.41
6:D:176:GLU:C	6:D:178:ALA:N	2.73	0.41
6:D:176:GLU:O	6:D:178:ALA:N	2.54	0.41
10:H:56:THR:HB	10:H:145:ARG:HG2	2.02	0.41
11:I:15:TYR:O	11:I:28:GLU:HG2	2.20	0.41
11:I:58:VAL:O	11:I:58:VAL:HG12	2.21	0.41
13:K:78:THR:O	13:K:81:TYR:HB3	2.21	0.41
3:A:1025:ARG:HH11	3:A:1025:ARG:HG3	1.85	0.40
3:A:497:THR:HG23	4:B:1146:PHE:HD1	1.85	0.40
4:B:175:ARG:HH11	4:B:175:ARG:HG2	1.87	0.40
4:B:46:GLN:CG	4:B:47:GLN:H	2.32	0.40
4:B:681:TRP:O	4:B:683:SER:N	2.54	0.40
4:B:542:MET:CG	4:B:747:MET:HB3	2.51	0.40
4:B:826:ALA:O	4:B:1011:ILE:HA	2.21	0.40
4:B:899:ILE:HG22	4:B:903:VAL:CG2	2.50	0.40
5:C:174:ALA:O	12:J:10:CYS:O	2.39	0.40
5:C:82:TYR:CD2	5:C:161:LYS:HB3	2.55	0.40
9:G:7:LEU:CB	9:G:74:TYR:CE2	2.97	0.40
11:I:61:ASP:C	11:I:63:GLY:N	2.73	0.40
5:C:259:LEU:CD1	13:K:91:CYS:HB2	2.51	0.40
2:T:12:G:C2'	2:T:13:U:O5'	2.69	0.40
3:A:874:ASP:CA	3:A:1058:VAL:HG22	2.51	0.40
3:A:108:MET:SD	3:A:108:MET:N	2.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:241:VAL:HG13	3:A:266:LEU:CD1	2.51	0.40
3:A:84:ILE:HD11	3:A:270:LEU:HD22	2.02	0.40
3:A:503:GLN:OE1	8:F:90:ARG:NH2	2.48	0.40
3:A:738:LYS:HB2	3:A:740:LEU:CG	2.45	0.40
3:A:821:ARG:CB	3:A:821:ARG:HH11	2.27	0.40
3:A:89:PRO:C	3:A:204:THR:HG21	2.42	0.40
3:A:961:ARG:HG3	3:A:961:ARG:NH1	2.35	0.40
4:B:728:ARG:HH12	4:B:1047:PHE:HB3	1.86	0.40
4:B:250:PHE:HA	4:B:250:PHE:HD2	1.69	0.40
4:B:388:CYS:O	4:B:391:ASP:N	2.51	0.40
4:B:552:MET:HA	4:B:555:ILE:HB	2.03	0.40
4:B:558:LEU:O	4:B:560:GLU:N	2.54	0.40
4:B:591:ARG:O	4:B:592:ASN:C	2.59	0.40
4:B:732:SER:HB2	4:B:734:HIS:CD2	2.56	0.40
4:B:950:ASP:O	4:B:951:GLN:HB2	2.21	0.40
9:G:111:THR:HG22	9:G:113:HIS:N	2.20	0.40
8:F:99:LEU:HD21	9:G:64:THR:O	2.21	0.40
9:G:82:PHE:N	9:G:82:PHE:CD1	2.89	0.40
13:K:95:ILE:O	13:K:98:LEU:HB2	2.21	0.40
14:L:40:LEU:HB3	14:L:41:SER:H	1.47	0.40
3:A:1364:ASN:HD22	3:A:1365:TYR:N	2.19	0.40
3:A:699:ALA:O	3:A:700:ASN:CB	2.69	0.40
4:B:984:HIS:CD2	4:B:1025:HIS:HB2	2.56	0.40
4:B:1080:LYS:HD2	5:C:188:HIS:HB2	2.04	0.40
4:B:258:LEU:CG	4:B:258:LEU:O	2.69	0.40
4:B:311:LEU:O	4:B:314:LEU:N	2.51	0.40
4:B:446:LEU:N	4:B:446:LEU:HD23	2.36	0.40
4:B:376:PHE:CZ	4:B:569:TYR:HB3	2.56	0.40
4:B:610:ASN:HA	4:B:611:PRO:HD3	1.89	0.40
4:B:791:THR:O	4:B:792:MET:O	2.38	0.40
4:B:835:GLN:HE21	4:B:835:GLN:HB2	1.65	0.40
4:B:953:LEU:CD2	4:B:965:LYS:HB2	2.50	0.40
6:D:154:PHE:CE2	6:D:163:VAL:CG2	3.04	0.40
6:D:195:ILE:O	6:D:198:LEU:HG	2.21	0.40
8:F:111:LEU:C	8:F:113:GLY:N	2.73	0.40
9:G:88:ASP:CB	9:G:144:ARG:HA	2.44	0.40
10:H:113:ALA:CB	10:H:125:LEU:O	2.70	0.40
12:J:47:ARG:HH11	12:J:47:ARG:HG2	1.85	0.40
13:K:67:PHE:C	13:K:68:PHE:CD2	2.94	0.40
14:L:58:LYS:O	14:L:58:LYS:CG	2.65	0.40
3:A:1441:PHE:HB2	8:F:135:ARG:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:491:VAL:HG12	3:A:492:PRO:O	2.21	0.40
3:A:576:GLN:HG3	10:H:119:GLY:HA3	2.04	0.40
3:A:95:PHE:O	3:A:96:ILE:C	2.58	0.40
4:B:984:HIS:CG	4:B:1025:HIS:HB2	2.56	0.40
4:B:1159:ARG:HB3	4:B:1159:ARG:HH11	1.87	0.40
4:B:236:HIS:CE1	4:B:389:ALA:HA	2.57	0.40
4:B:26:THR:O	4:B:29:ASP:HB2	2.21	0.40
4:B:382:ILE:O	4:B:385:LEU:HB3	2.21	0.40
4:B:680:THR:O	4:B:684:LEU:CD1	2.69	0.40
5:C:179:GLU:CG	5:C:180:TYR:N	2.84	0.40
6:D:24:ALA:HB3	6:D:26:THR:OG1	2.21	0.40
7:E:212:ARG:CG	7:E:212:ARG:HH11	2.34	0.40
8:F:77:ASP:C	8:F:79:ARG:N	2.75	0.40
9:G:112:LYS:NZ	9:G:120:THR:HA	2.37	0.40
10:H:100:THR:CG2	10:H:101:ALA:N	2.83	0.40
12:J:3:VAL:HA	12:J:4:PRO:HD3	1.92	0.40
13:K:29:ASN:O	13:K:76:GLN:HG3	2.21	0.40
3:A:1097:GLY:HA2	3:A:1355:VAL:HG13	2.04	0.40
3:A:1291:VAL:HG13	3:A:1292:PRO:N	2.36	0.40
3:A:1369:ALA:O	3:A:1370:LEU:C	2.58	0.40
3:A:24:PRO:HD2	3:A:233:TRP:NE1	2.36	0.40
3:A:43:GLU:O	3:A:44:THR:CB	2.68	0.40
3:A:49:LYS:NZ	3:A:60:SER:HA	2.36	0.40
4:B:1017:ILE:HD13	4:B:1017:ILE:HA	1.92	0.40
4:B:114:PRO:O	4:B:115:GLN:C	2.60	0.40
4:B:802:PRO:HG2	4:B:805:THR:HG22	2.03	0.40
6:D:191:ALA:C	6:D:193:THR:N	2.75	0.40
7:E:58:MET:O	7:E:59:SER:O	2.39	0.40
9:G:3:PHE:CE1	9:G:80:LYS:HE2	2.56	0.40
2:T:12:G:HO2'	2:T:13:U:C4'	2.35	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	
3	A	1412/1733 (82%)	1030 (73%)	249 (18%)	133 (9%)	1	14
4	B	1094/1224 (89%)	780 (71%)	214 (20%)	100 (9%)	1	15
5	C	264/318 (83%)	164 (62%)	64 (24%)	36 (14%)	0	5
6	D	174/221 (79%)	126 (72%)	30 (17%)	18 (10%)	0	11
7	E	212/215 (99%)	158 (74%)	36 (17%)	18 (8%)	1	16
8	F	86/155 (56%)	69 (80%)	9 (10%)	8 (9%)	1	14
9	G	169/171 (99%)	130 (77%)	33 (20%)	6 (4%)	4	37
10	H	131/146 (90%)	74 (56%)	36 (28%)	21 (16%)	0	4
11	I	114/122 (93%)	69 (60%)	30 (26%)	15 (13%)	0	6
12	J	63/70 (90%)	39 (62%)	10 (16%)	14 (22%)	0	1
13	K	110/120 (92%)	87 (79%)	15 (14%)	8 (7%)	1	21
14	L	44/70 (63%)	18 (41%)	10 (23%)	16 (36%)	0	0
All	All	3873/4565 (85%)	2744 (71%)	736 (19%)	393 (10%)	1	12

All (393) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	4	GLN
3	A	44	THR
3	A	48	ALA
3	A	54	ASN
3	A	57	ARG
3	A	58	LEU
3	A	62	ASP
3	A	65	LEU
3	A	66	LYS
3	A	70	CYS
3	A	74	MET
3	A	93	VAL
3	A	154	SER
3	A	167	CYS
3	A	223	GLY
3	A	250	ILE
3	A	255	SER
3	A	286	HIS
3	A	311	GLN

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Mol	Chain	Res	Type
3	A	318	SER
3	A	335	ARG
3	A	399	HIS
3	A	516	SER
3	A	517	ASN
3	A	536	LEU
3	A	567	LYS
3	A	597	LEU
3	A	619	LYS
3	A	626	ASN
3	A	666	ILE
3	A	780	VAL
3	A	968	GLN
3	A	986	ILE
3	A	1016	THR
3	A	1036	ARG
3	A	1115	SER
3	A	1116	LEU
3	A	1120	LEU
3	A	1122	PRO
3	A	1124	HIS
3	A	1127	ASP
3	A	1176	LEU
3	A	1212	VAL
3	A	1223	ASP
3	A	1233	ASP
3	A	1314	SER
3	A	1365	TYR
3	A	1378	GLN
3	A	1405	THR
4	B	22	SER
4	B	28	GLU
4	B	45	SER
4	B	108	VAL
4	B	186	GLU
4	B	206	ASN
4	B	258	LEU
4	B	266	ALA
4	B	367	LEU
4	B	467	GLY
4	B	643	ASP
4	B	709	ASP

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Mol	Chain	Res	Type
4	B	731	VAL
4	B	792	MET
4	B	879	ARG
4	B	881	ASN
4	B	907	GLY
4	B	958	GLN
4	B	1003	ALA
4	B	1041	GLU
4	B	1046	PRO
4	B	1069	PHE
4	B	1097	HIS
4	B	1156	ASP
4	B	1171	VAL
4	B	1175	LEU
4	B	1181	GLU
4	B	1182	CYS
4	B	1188	LYS
5	C	4	GLU
5	C	18	VAL
5	C	110	THR
5	C	132	PRO
5	C	149	LYS
5	C	156	THR
5	C	161	LYS
5	C	184	ASN
5	C	214	ASN
5	C	215	GLU
5	C	216	GLY
6	D	5	THR
6	D	8	PHE
6	D	20	GLU
6	D	131	GLU
6	D	199	ASN
7	E	3	GLN
7	E	45	LYS
7	E	59	SER
7	E	73	PRO
7	E	106	GLN
7	E	130	ALA
8	F	81	THR
9	G	63	PRO
10	H	21	ASN

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Mol	Chain	Res	Type
10	H	62	SER
10	H	78	SER
10	H	128	ASN
10	H	140	ALA
11	I	3	THR
11	I	57	GLY
11	I	106	CYS
12	J	2	ILE
12	J	28	ASP
12	J	32	GLU
12	J	41	LEU
12	J	64	ASN
13	K	109	TRP
13	K	110	ASN
13	K	111	LEU
14	L	50	ASP
14	L	59	ALA
3	A	42	ASP
3	A	59	GLY
3	A	61	ILE
3	A	71	GLN
3	A	76	GLU
3	A	117	GLU
3	A	128	ILE
3	A	253	ASN
3	A	257	ARG
3	A	283	GLY
3	A	312	PRO
3	A	322	VAL
3	A	331	GLY
3	A	332	LYS
3	A	419	LYS
3	A	543	LEU
3	A	592	ASP
3	A	649	ILE
3	A	753	GLY
3	A	765	VAL
3	A	888	GLY
3	A	969	GLN
3	A	1002	GLY
3	A	1281	ARG
3	A	1377	THR

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Mol	Chain	Res	Type
3	A	1438	THR
4	B	46	GLN
4	B	58	THR
4	B	65	GLU
4	B	100	PRO
4	B	115	GLN
4	B	261	ARG
4	B	282	ILE
4	B	345	LYS
4	B	543	SER
4	B	605	ARG
4	B	641	GLU
4	B	655	LYS
4	B	746	SER
4	B	751	VAL
4	B	831	SER
4	B	848	ARG
4	B	867	GLY
4	B	891	ASP
4	B	1065	GLN
4	B	1075	GLY
4	B	1155	SER
4	B	1186	ASP
5	C	78	GLU
5	C	141	GLY
5	C	142	VAL
5	C	213	PRO
5	C	231	ASN
6	D	9	GLN
6	D	12	ARG
6	D	16	LYS
6	D	19	GLU
6	D	21	GLU
6	D	30	GLY
6	D	52	LEU
6	D	192	LYS
7	E	36	GLU
7	E	44	ALA
7	E	74	ASP
7	E	76	GLY
7	E	192	ARG
7	E	206	GLY

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Mol	Chain	Res	Type
8	F	69	LEU
8	F	70	LYS
8	F	150	GLU
8	F	151	LEU
9	G	139	ILE
10	H	17	PRO
10	H	59	ILE
10	H	77	ARG
10	H	81	PRO
10	H	82	PRO
10	H	84	ALA
10	H	90	ALA
10	H	107	VAL
10	H	108	SER
11	I	11	ASN
11	I	59	VAL
11	I	95	THR
12	J	6	ARG
12	J	9	SER
12	J	14	VAL
12	J	17	LYS
12	J	29	GLU
12	J	33	GLY
13	K	15	GLY
14	L	53	HIS
14	L	60	ARG
3	A	67	CYS
3	A	169	ASN
3	A	219	PHE
3	A	263	THR
3	A	336	ILE
3	A	424	ILE
3	A	465	TYR
3	A	591	PHE
3	A	652	VAL
3	A	846	GLU
3	A	847	ASP
3	A	871	ASP
3	A	875	ALA
3	A	926	GLN
3	A	972	HIS
3	A	1054	LEU

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Mol	Chain	Res	Type
3	A	1221	LYS
4	B	184	ALA
4	B	257	LYS
4	B	259	TYR
4	B	264	SER
4	B	401	PHE
4	B	470	LYS
4	B	642	ASP
4	B	708	GLU
4	B	711	GLU
4	B	943	SER
4	B	1100	ASP
4	B	1178	ASN
4	B	1183	LYS
5	C	90	ASP
5	C	117	ASP
5	C	217	ASP
5	C	233	GLU
6	D	47	LEU
7	E	43	LYS
7	E	115	ASN
7	E	158	SER
8	F	128	LYS
9	G	20	PRO
9	G	118	ASP
9	G	154	VAL
10	H	52	GLN
10	H	63	LEU
10	H	64	ASN
10	H	92	ASP
11	I	9	ASP
11	I	78	CYS
11	I	91	ARG
11	I	107	SER
12	J	8	PHE
13	K	29	ASN
14	L	35	SER
14	L	37	LYS
3	A	69	THR
3	A	84	ILE
3	A	410	GLY
3	A	439	ASN

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Mol	Chain	Res	Type
3	A	483	ASP
3	A	648	ASN
3	A	706	HIS
3	A	775	ILE
3	A	789	LYS
3	A	1114	PRO
3	A	1136	SER
4	B	48	LEU
4	B	114	PRO
4	B	249	ARG
4	B	260	GLY
4	B	308	TRP
4	B	362	PRO
4	B	450	ALA
4	B	474	SER
4	B	483	LEU
4	B	559	SER
4	B	575	PRO
4	B	764	SER
4	B	880	THR
4	B	977	GLY
4	B	1017	ILE
4	B	1035	ALA
4	B	1074	ASN
4	B	1108	ARG
4	B	1144	ALA
4	B	1157	ALA
5	C	11	ARG
5	C	87	PHE
5	C	175	ALA
5	C	188	HIS
5	C	240	VAL
6	D	218	GLU
7	E	40	GLU
7	E	56	LYS
9	G	115	MET
10	H	32	THR
10	H	44	VAL
11	I	47	GLU
11	I	79	HIS
12	J	62	ARG
13	K	7	PHE

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Mol	Chain	Res	Type
14	L	26	THR
14	L	28	LYS
14	L	40	LEU
14	L	43	THR
14	L	45	ALA
3	A	35	ILE
3	A	43	GLU
3	A	55	ASP
3	A	113	LEU
3	A	130	ASP
3	A	164	ARG
3	A	317	LYS
3	A	605	MET
3	A	739	ASP
3	A	783	THR
3	A	891	ALA
3	A	1366	ARG
3	A	1392	SER
4	B	27	ALA
4	B	365	THR
4	B	383	ASN
4	B	513	GLN
4	B	551	PRO
4	B	705	MET
4	B	712	PRO
4	B	1045	SER
5	C	10	ILE
5	C	13	ALA
5	C	108	GLU
5	C	264	GLN
8	F	104	ASN
11	I	4	PHE
11	I	54	GLU
11	I	62	ILE
13	K	103	THR
14	L	41	SER
14	L	44	ASP
14	L	54	ARG
3	A	5	GLN
3	A	245	PRO
3	A	249	SER
3	A	830	LYS

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Mol	Chain	Res	Type
3	A	958	VAL
3	A	1094	VAL
3	A	1123	GLY
3	A	1454	MET
4	B	20	ASP
4	B	94	LYS
4	B	295	GLY
5	C	70	ILE
5	C	133	ILE
5	C	137	LYS
5	C	209	TYR
6	D	139	LYS
10	H	36	CYS
12	J	57	ILE
14	L	56	LEU
3	A	400	PRO
3	A	604	GLY
3	A	1164	PRO
4	B	1167	GLY
5	C	51	VAL
3	A	599	SER
3	A	1324	PRO
5	C	126	GLY
5	C	202	PRO
3	A	51	GLY
3	A	825	ILE
6	D	59	ILE
8	F	131	PRO
13	K	43	GLY
3	A	600	PRO
3	A	622	VAL
4	B	411	PRO
4	B	613	VAL
4	B	976	ILE
6	D	202	ILE
14	L	55	ILE
4	B	524	PRO
7	E	129	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	1245/1520 (82%)	1129 (91%)	116 (9%)	10	43
4	B	964/1061 (91%)	890 (92%)	74 (8%)	15	52
5	C	235/274 (86%)	212 (90%)	23 (10%)	9	40
6	D	160/200 (80%)	142 (89%)	18 (11%)	7	34
7	E	196/197 (100%)	188 (96%)	8 (4%)	35	69
8	F	78/137 (57%)	75 (96%)	3 (4%)	38	70
9	G	152/152 (100%)	140 (92%)	12 (8%)	14	51
10	H	119/128 (93%)	113 (95%)	6 (5%)	28	65
11	I	110/116 (95%)	99 (90%)	11 (10%)	9	39
12	J	60/65 (92%)	55 (92%)	5 (8%)	13	49
13	K	97/102 (95%)	87 (90%)	10 (10%)	8	38
14	L	40/57 (70%)	36 (90%)	4 (10%)	9	39
All	All	3456/4009 (86%)	3166 (92%)	290 (8%)	13	49

All (290) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	2	VAL
3	A	11	LEU
3	A	37	PHE
3	A	38	PRO
3	A	41	MET
3	A	54	ASN
3	A	62	ASP
3	A	67	CYS
3	A	83	HIS
3	A	93	VAL
3	A	108	MET
3	A	122	MET
3	A	131	SER
3	A	188	ASP

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Mol	Chain	Res	Type
3	A	200	ARG
3	A	221	SER
3	A	236	LEU
3	A	245	PRO
3	A	261	ASP
3	A	265	LYS
3	A	270	LEU
3	A	302	THR
3	A	312	PRO
3	A	326	ARG
3	A	335	ARG
3	A	337	ARG
3	A	345	VAL
3	A	381	THR
3	A	385	ILE
3	A	406	ILE
3	A	408	ASP
3	A	425	GLN
3	A	434	ARG
3	A	442	VAL
3	A	443	LEU
3	A	445	ASN
3	A	450	LEU
3	A	462	VAL
3	A	469	ARG
3	A	470	LEU
3	A	481	ASP
3	A	504	LEU
3	A	515	GLN
3	A	518	LYS
3	A	524	VAL
3	A	560	ILE
3	A	562	THR
3	A	584	ASN
3	A	618	GLU
3	A	622	VAL
3	A	626	ASN
3	A	629	LEU
3	A	635	ARG
3	A	659	HIS
3	A	666	ILE
3	A	685	GLU

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Mol	Chain	Res	Type
3	A	741	ASN
3	A	768	GLN
3	A	779	PHE
3	A	786	HIS
3	A	821	ARG
3	A	827	THR
3	A	831	THR
3	A	834	THR
3	A	852	TYR
3	A	858	ASN
3	A	871	ASP
3	A	886	ILE
3	A	890	ASP
3	A	903	ASN
3	A	907	THR
3	A	929	LEU
3	A	940	ARG
3	A	941	LYS
3	A	969	GLN
3	A	992	ASP
3	A	1001	ARG
3	A	1029	ARG
3	A	1035	TYR
3	A	1052	GLN
3	A	1067	LEU
3	A	1116	LEU
3	A	1122	PRO
3	A	1138	ILE
3	A	1170	ILE
3	A	1176	LEU
3	A	1177	LEU
3	A	1193	LEU
3	A	1206	ASP
3	A	1240	CYS
3	A	1245	PRO
3	A	1264	GLU
3	A	1271	ILE
3	A	1291	VAL
3	A	1295	THR
3	A	1309	ASP
3	A	1325	THR
3	A	1332	PHE

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Mol	Chain	Res	Type
3	A	1333	ILE
3	A	1336	MET
3	A	1359	ASP
3	A	1364	ASN
3	A	1366	ARG
3	A	1372	VAL
3	A	1386	ARG
3	A	1389	PHE
3	A	1393	ASN
3	A	1394	THR
3	A	1405	THR
3	A	1433	MET
3	A	1436	ILE
3	A	1442	ASP
3	A	1443	VAL
3	A	1444	MET
3	A	1445	ILE
3	A	1447	GLU
4	B	37	PHE
4	B	57	TYR
4	B	61	ASP
4	B	100	PRO
4	B	106	ASP
4	B	178	ASN
4	B	203	PHE
4	B	217	ARG
4	B	250	PHE
4	B	268	THR
4	B	283	VAL
4	B	298	LEU
4	B	365	THR
4	B	371	GLU
4	B	378	LEU
4	B	393	LYS
4	B	396	ASP
4	B	401	PHE
4	B	427	ASP
4	B	429	PHE
4	B	466	TRP
4	B	482	VAL
4	B	485	ARG
4	B	496	ARG

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Mol	Chain	Res	Type
4	B	498	THR
4	B	502	ILE
4	B	516	ASN
4	B	557	PHE
4	B	582	VAL
4	B	591	ARG
4	B	603	LEU
4	B	628	THR
4	B	635	ARG
4	B	644	GLU
4	B	682	SER
4	B	724	ASP
4	B	737	THR
4	B	742	GLU
4	B	790	ASP
4	B	791	THR
4	B	811	TYR
4	B	830	TYR
4	B	835	GLN
4	B	839	MET
4	B	878	GLN
4	B	894	ASP
4	B	909	ASP
4	B	939	THR
4	B	944	THR
4	B	978	ASP
4	B	986	GLN
4	B	997	GLU
4	B	999	MET
4	B	1002	THR
4	B	1006	ILE
4	B	1047	PHE
4	B	1060	ARG
4	B	1069	PHE
4	B	1087	PHE
4	B	1095	LEU
4	B	1096	ARG
4	B	1098	MET
4	B	1099	VAL
4	B	1103	ILE
4	B	1108	ARG
4	B	1123	SER

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Mol	Chain	Res	Type
4	B	1159	ARG
4	B	1169	MET
4	B	1176	ASN
4	B	1183	LYS
4	B	1202	LEU
4	B	1212	ILE
4	B	1216	LEU
4	B	1220	ARG
5	C	22	LEU
5	C	23	SER
5	C	56	THR
5	C	58	LEU
5	C	62	PHE
5	C	72	LEU
5	C	75	MET
5	C	77	ILE
5	C	104	PHE
5	C	129	ILE
5	C	140	ASN
5	C	145	CYS
5	C	147	LEU
5	C	163	ILE
5	C	166	GLU
5	C	170	TRP
5	C	193	TYR
5	C	209	TYR
5	C	229	TYR
5	C	233	GLU
5	C	238	ILE
5	C	240	VAL
5	C	266	ASP
6	D	3	VAL
6	D	13	ARG
6	D	17	LYS
6	D	21	GLU
6	D	22	GLU
6	D	63	LEU
6	D	70	PHE
6	D	137	ASN
6	D	139	LYS
6	D	148	LEU
6	D	149	THR

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Mol	Chain	Res	Type
6	D	152	SER
6	D	156	ASP
6	D	170	THR
6	D	192	LYS
6	D	193	THR
6	D	208	GLU
6	D	221	TYR
7	E	60	PHE
7	E	74	ASP
7	E	78	LEU
7	E	104	ASN
7	E	114	ASN
7	E	132	ILE
7	E	165	LEU
7	E	175	LEU
8	F	79	ARG
8	F	90	ARG
8	F	99	LEU
9	G	1	MET
9	G	13	LEU
9	G	51	TYR
9	G	52	ASP
9	G	74	TYR
9	G	78	VAL
9	G	80	LYS
9	G	88	ASP
9	G	99	PHE
9	G	115	MET
9	G	126	ASN
9	G	171	ILE
10	H	7	ASP
10	H	17	PRO
10	H	91	ASP
10	H	95	TYR
10	H	102	TYR
10	H	130	ARG
11	I	4	PHE
11	I	8	ARG
11	I	15	TYR
11	I	34	TYR
11	I	75	CYS
11	I	78	CYS

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Mol	Chain	Res	Type
11	I	85	PHE
11	I	86	PHE
11	I	94	ASP
11	I	101	PHE
11	I	106	CYS
12	J	7	CYS
12	J	43	ARG
12	J	44	TYR
12	J	46	CYS
12	J	48	ARG
13	K	1	MET
13	K	5	ASP
13	K	10	PHE
13	K	25	THR
13	K	42	LEU
13	K	47	ARG
13	K	50	LEU
13	K	61	TYR
13	K	111	LEU
13	K	112	GLN
14	L	27	LEU
14	L	51	CYS
14	L	55	ILE
14	L	70	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	54	ASN
3	A	64	ASN
3	A	71	GLN
3	A	225	ASN
3	A	256	GLN
3	A	299	HIS
3	A	339	ASN
3	A	358	ASN
3	A	394	ASN
3	A	435	HIS
3	A	479	ASN
3	A	525	GLN
3	A	603	ASN
3	A	631	HIS

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Mol	Chain	Res	Type
3	A	654	ASN
3	A	723	ASN
3	A	736	ASN
3	A	741	ASN
3	A	745	GLN
3	A	757	ASN
3	A	768	GLN
3	A	786	HIS
3	A	838	GLN
3	A	858	ASN
3	A	877	HIS
3	A	903	ASN
3	A	926	GLN
3	A	935	GLN
3	A	994	GLN
3	A	1130	GLN
3	A	1140	HIS
3	A	1188	GLN
3	A	1218	GLN
3	A	1364	ASN
3	A	1432	GLN
4	B	60	GLN
4	B	121	ASN
4	B	178	ASN
4	B	215	GLN
4	B	236	HIS
4	B	350	GLN
4	B	363	HIS
4	B	366	GLN
4	B	465	ASN
4	B	513	GLN
4	B	515	HIS
4	B	516	ASN
4	B	518	HIS
4	B	538	ASN
4	B	706	GLN
4	B	744	HIS
4	B	821	GLN
4	B	842	ASN
4	B	957	ASN
4	B	975	GLN
4	B	1015	HIS

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Mol	Chain	Res	Type
4	B	1025	HIS
4	B	1065	GLN
4	B	1117	GLN
4	B	1176	ASN
4	B	1179	GLN
4	B	1193	GLN
5	C	24	ASN
5	C	73	GLN
5	C	112	ASN
5	C	167	HIS
5	C	252	GLN
6	D	39	ASN
6	D	40	HIS
6	D	41	GLN
6	D	137	ASN
6	D	179	GLN
7	E	8	ASN
7	E	101	GLN
7	E	104	ASN
7	E	114	ASN
7	E	147	HIS
9	G	53	ASN
9	G	57	GLN
9	G	97	HIS
9	G	122	ASN
9	G	126	ASN
10	H	64	ASN
10	H	133	ASN
10	H	137	GLN
11	I	12	ASN
11	I	46	HIS
11	I	90	GLN
11	I	108	HIS
12	J	53	HIS
12	J	64	ASN
13	K	44	ASN
13	K	65	HIS
13	K	76	GLN
13	K	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	P	8/16 (50%)	1 (12%)	0
2	T	9/17 (52%)	5 (55%)	2 (22%)
All	All	17/33 (51%)	6 (35%)	2 (11%)

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	P	9	G
2	T	11	G
2	T	12	G
2	T	13	U
2	T	14	C
2	T	15	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	T	12	G
2	T	13	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](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	B	1
5	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2:SER	C	3:GLU	N	3.04
1	B	337:ARG	C	338:GLY	N	2.61

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	P	9/16 (56%)	1.99	2 (22%) 1 1	194, 200, 200, 200	0
2	T	10/17 (58%)	2.20	7 (70%) 0 0	180, 190, 200, 200	0
3	A	1422/1733 (82%)	-0.26	7 (0%) 90 86	56, 116, 175, 200	0
4	B	1112/1224 (90%)	-0.19	11 (0%) 82 75	57, 126, 188, 200	0
5	C	267/318 (83%)	-0.29	0 100 100	74, 110, 158, 180	0
6	D	178/221 (80%)	-0.26	1 (0%) 89 85	87, 133, 184, 198	0
7	E	214/215 (99%)	-0.25	4 (1%) 67 58	90, 159, 197, 200	0
8	F	88/155 (56%)	-0.52	0 100 100	65, 91, 129, 140	0
9	G	171/171 (100%)	-0.30	0 100 100	88, 112, 155, 163	0
10	H	135/146 (92%)	0.34	5 (3%) 42 34	139, 166, 190, 200	0
11	I	116/122 (95%)	0.06	0 100 100	114, 163, 191, 200	0
12	J	65/70 (92%)	-0.49	0 100 100	79, 108, 146, 153	0
13	K	112/120 (93%)	-0.31	0 100 100	81, 114, 139, 167	0
14	L	46/70 (65%)	0.01	1 (2%) 62 53	111, 166, 194, 196	0
All	All	3945/4598 (85%)	-0.21	38 (0%) 82 75	56, 123, 187, 200	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	471	LYS	5.2
1	P	9	G	4.6
3	A	1092	LYS	3.7
1	P	8	A	3.5
2	T	15	A	3.5
2	T	6	C	3.4
10	H	140	ALA	3.1
4	B	882	THR	3.0

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Mol	Chain	Res	Type	RSRZ
3	A	1455	PRO	2.9
4	B	132	VAL	2.9
4	B	733	HIS	2.9
4	B	883	LEU	2.9
2	T	14	C	2.8
7	E	82	PHE	2.8
14	L	54	ARG	2.8
3	A	188	ASP	2.8
3	A	253	ASN	2.5
10	H	86	ASP	2.4
3	A	1256	GLU	2.4
10	H	50	ALA	2.4
7	E	97	VAL	2.4
2	T	12	G	2.4
7	E	110	PHE	2.4
7	E	81	GLU	2.3
2	T	7	G	2.3
3	A	115	LEU	2.3
10	H	139	ASN	2.3
10	H	142	LEU	2.3
2	T	11	G	2.2
6	D	76	LYS	2.2
4	B	133	LYS	2.2
2	T	8	C	2.1
4	B	679	TYR	2.1
4	B	340	ALA	2.1
3	A	1244	ARG	2.1
4	B	341	LEU	2.1
4	B	870	ILE	2.0
4	B	470	LYS	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
15	ZN	B	1307	1/1	1.00	0.22	0.80	83,83,83,83	0
15	ZN	I	203	1/1	0.99	0.16	0.27	120,120,120,120	0
15	ZN	C	302	1/1	1.00	0.13	-0.56	82,82,82,82	0
15	ZN	A	1508	1/1	1.00	0.14	-0.96	83,83,83,83	0
15	ZN	J	101	1/1	1.00	0.25	-0.97	100,100,100,100	0
15	ZN	L	105	1/1	0.97	0.10	-1.12	155,155,155,155	0
15	ZN	I	204	1/1	0.99	0.04	-1.70	181,181,181,181	0
15	ZN	A	1506	1/1	0.95	0.08	-2.66	121,121,121,121	0
16	MG	A	1	1/1	0.97	0.18	-	79,79,79,79	0

6.5 Other polymers

There are no such residues in this entry.