wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 01:47 PM BST

PDB ID	:	3J6H
EMDB ID:	:	EMD-5916
Title	:	Nucleotide-free Kinesin motor domain complexed with GMPCPP-microtubule
Authors	:	Morikawa, M.; Yajima, H.; Nitta, R.; Inoue, S.; Ogura, T.; Sato, C.; Hirokawa, N.
Deposited on	:	2014-02-21
Resolution	:	8.10 Å(reported)
Based on PDB ID	:	1JFF,1JFF,3WRD

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

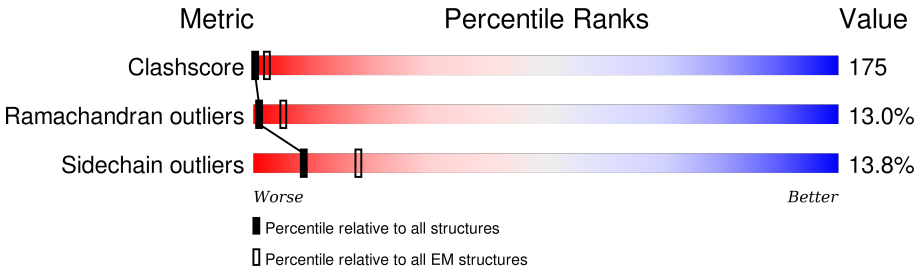
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.10 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	436	15% 58% 18% • 6%
2	B	426	19% 58% 21% •
3	K	352	25% 39% 13% • 21%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GTP	A	502	-	-	X	-
6	G2P	B	602	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8810 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	410	3213	2036	549	608	20	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	265	GLY	ALA	SEE REMARK 999	UNP P02550

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	426	3351	2105	575	646	25	0	0

- Molecule 3 is a protein called Kinesin heavy chain isoform 5C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	K	277	2175	1369	375	417	14	0	0

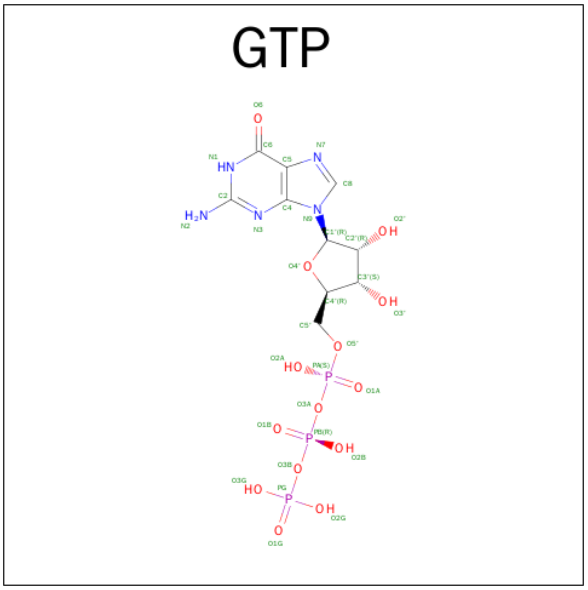
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	346	HIS	-	EXPRESSION TAG	UNP P28738
K	347	HIS	-	EXPRESSION TAG	UNP P28738
K	348	HIS	-	EXPRESSION TAG	UNP P28738
K	349	HIS	-	EXPRESSION TAG	UNP P28738
K	350	HIS	-	EXPRESSION TAG	UNP P28738
K	351	HIS	-	EXPRESSION TAG	UNP P28738
K	352	HIS	-	EXPRESSION TAG	UNP P28738

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

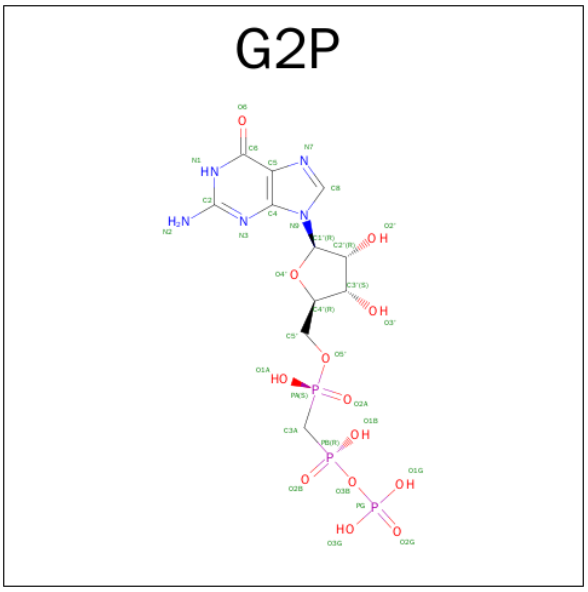
Mol	Chain	Residues	Atoms	AltConf
4	B	1	Total Mg 1 1	0
4	A	1	Total Mg 1 1	0

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



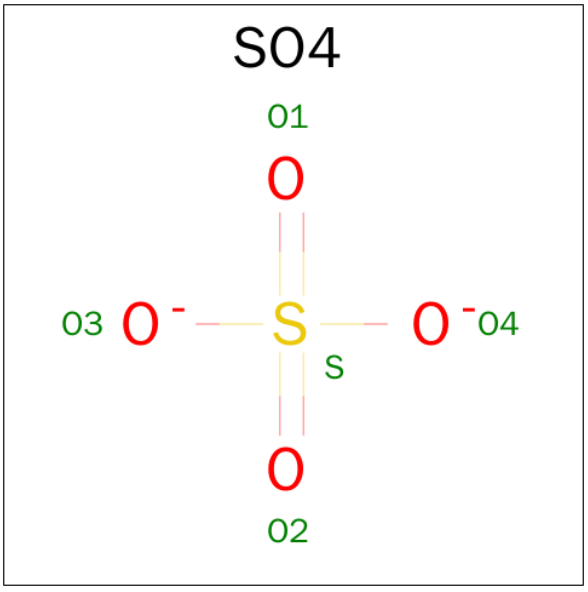
Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total C N O P 32 10 5 14 3	0

- Molecule 6 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: G2P) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
6	B	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



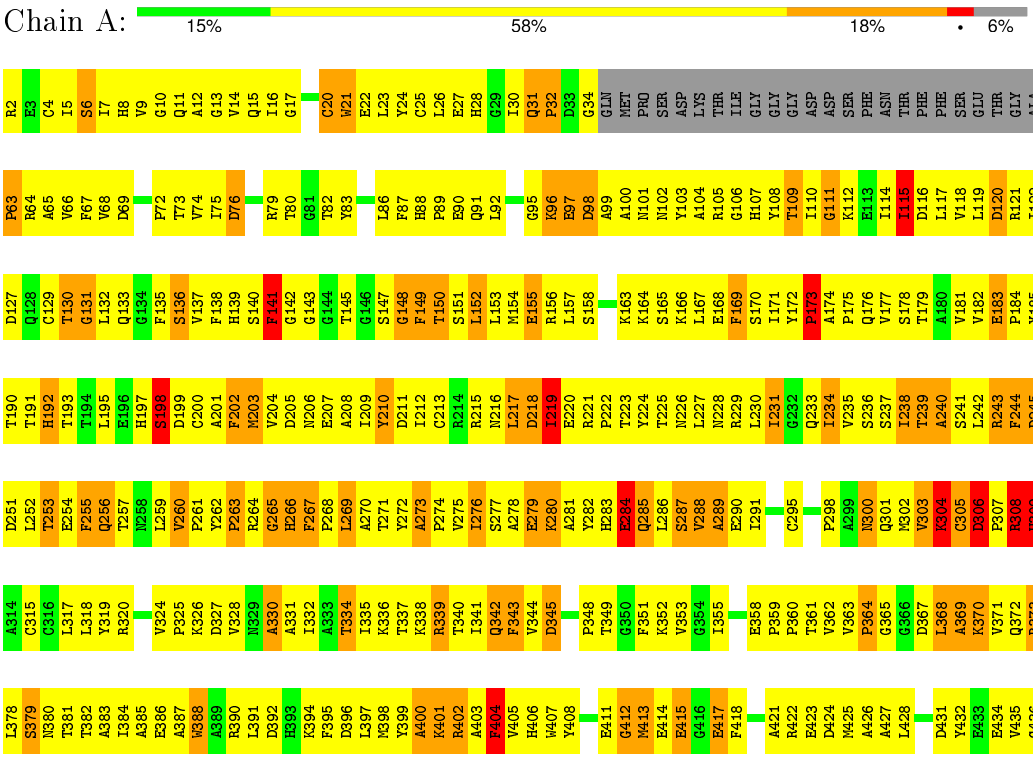
Mol	Chain	Residues	Atoms			AltConf
7	K	1	Total	O	S	0
			5	4	1	

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

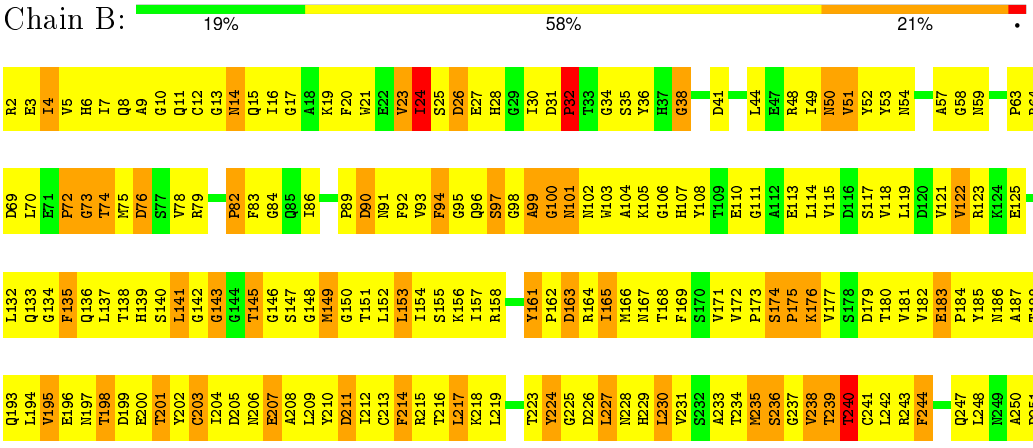
- Molecule 1: Tubulin alpha-1A chain

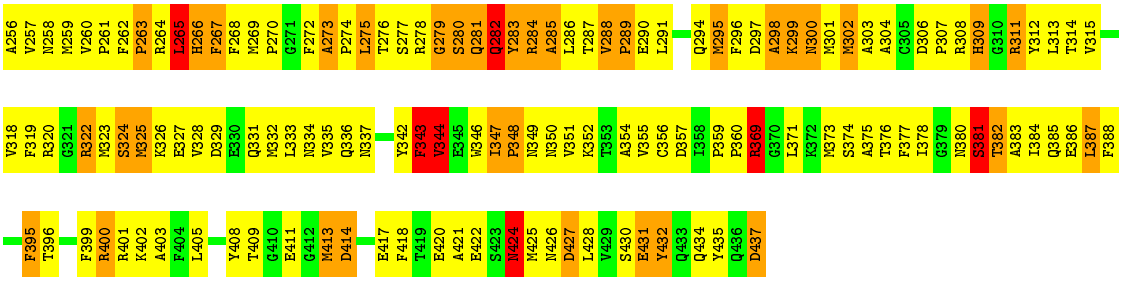
Chain A:



- Molecule 2: Tubulin beta chain

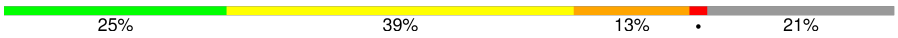
Chain B:

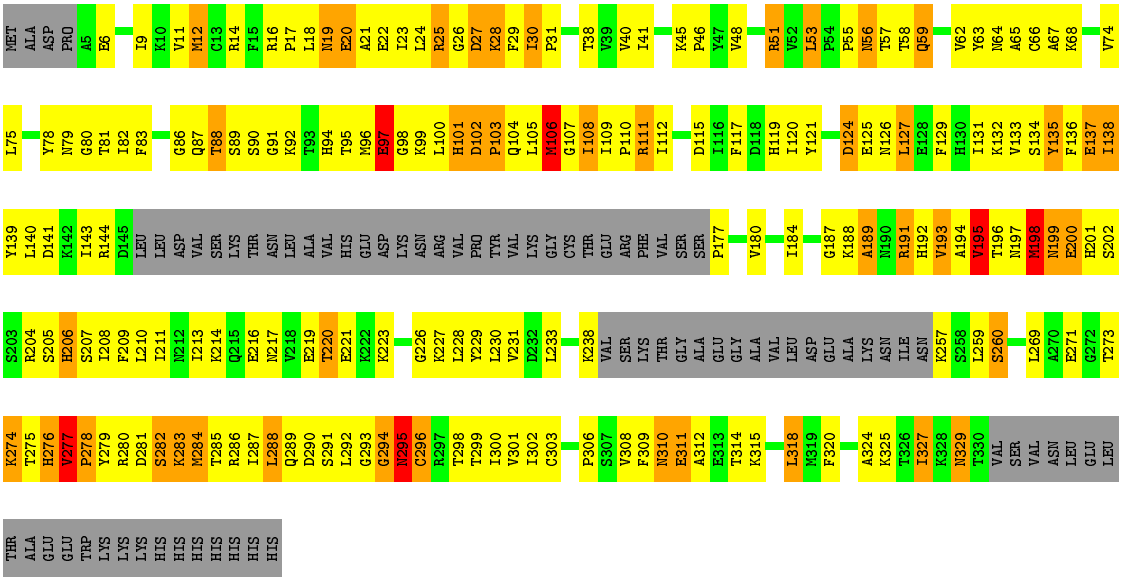




- Molecule 3: Kinesin heavy chain isoform 5C

Chain K:





4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	302000	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Each filament	Depositor
Microscope	JEM-2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	10	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	40000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, SO4, G2P

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	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	0.55	0/3286	0.90	12/4463 (0.3%)
2	B	0.56	1/3426 (0.0%)	0.81	8/4642 (0.2%)
3	K	0.56	1/2210 (0.0%)	0.88	11/2973 (0.4%)
All	All	0.56	2/8922 (0.0%)	0.86	31/12078 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
3	K	0	6
All	All	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	381	SER	C-N	11.04	1.59	1.34
3	K	189	ALA	C-N	-5.46	1.21	1.34

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	381	SER	O-C-N	-11.14	104.88	122.70
1	A	136	SER	CB-CA-C	-10.93	89.34	110.10
1	A	312	TYR	CB-CG-CD1	10.62	127.38	121.00
2	B	145	THR	CA-CB-CG2	-8.71	100.20	112.40
3	K	97	GLU	C-N-CA	8.31	139.75	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	K	200	GLU	O-C-N	-8.20	109.59	122.70
2	B	4	ILE	C-N-CA	-7.73	102.38	121.70
1	A	136	SER	C-N-CA	-7.35	103.33	121.70
1	A	312	TYR	CB-CG-CD2	-7.25	116.65	121.00
1	A	304	LYS	N-CA-CB	7.22	123.60	110.60
3	K	200	GLU	C-N-CA	6.46	137.86	121.70
3	K	277	VAL	C-N-CD	6.32	141.68	128.40
2	B	235	MET	CG-SD-CE	6.12	109.99	100.20
1	A	202	PHE	C-N-CA	-6.08	106.49	121.70
1	A	306	ASP	C-N-CD	6.04	141.08	128.40
3	K	137	GLU	C-N-CA	6.02	136.74	121.70
1	A	309	HIS	N-CA-CB	5.91	121.24	110.60
3	K	295	ASN	CA-CB-CG	5.75	126.05	113.40
3	K	296	CYS	C-N-CA	-5.71	107.44	121.70
3	K	260	SER	N-CA-CB	5.49	118.73	110.50
2	B	143	GLY	C-N-CA	5.43	133.70	122.30
3	K	189	ALA	O-C-N	-5.42	114.03	122.70
2	B	344	VAL	C-N-CA	5.41	135.23	121.70
1	A	198	SER	C-N-CA	-5.35	108.33	121.70
2	B	217	LEU	N-CA-C	-5.34	96.57	111.00
3	K	295	ASN	N-CA-C	5.28	125.27	111.00
1	A	309	HIS	N-CA-C	-5.21	96.95	111.00
1	A	343	PHE	C-N-CA	5.21	134.71	121.70
3	K	296	CYS	CA-C-N	5.16	128.56	117.20
1	A	203	MET	CB-CA-C	5.14	120.67	110.40
2	B	145	THR	N-CA-C	-5.09	97.25	111.00

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	MET	Peptide
2	B	143	GLY	Mainchain
2	B	381	SER	Mainchain
3	K	189	ALA	Mainchain
3	K	193	VAL	Peptide
3	K	199	ASN	Mainchain
3	K	200	GLU	Mainchain
3	K	206	HIS	Mainchain
3	K	97	GLU	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in 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	A	3213	0	3121	1412	0
2	B	3351	0	3224	1072	0
3	K	2175	0	2169	707	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	32	0	10	74	0
6	B	32	0	13	17	0
7	K	5	0	0	0	0
All	All	8810	0	8537	3039	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 175.

All (3039) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:PHE:CZ	1:A:234:ILE:HD13	1.26	1.65
3:K:83:PHE:CE1	3:K:231:VAL:HG23	1.32	1.64
1:A:312:TYR:CD1	1:A:381:THR:CG2	1.76	1.64
1:A:169:PHE:CG	1:A:235:VAL:HA	1.13	1.64
1:A:169:PHE:CD2	1:A:235:VAL:HA	1.21	1.64
1:A:176:GLN:HA	1:A:394:LYS:CE	1.23	1.63
1:A:172:TYR:CD2	1:A:388:TRP:HZ3	1.17	1.61
2:B:103:TRP:CE2	2:B:189:LEU:HB3	1.18	1.61
2:B:103:TRP:CD2	2:B:189:LEU:HD13	1.31	1.60
1:A:185:TYR:HD2	1:A:408:TYR:CE2	1.02	1.60
3:K:139:TYR:H	3:K:206:HIS:CE1	1.07	1.60
3:K:83:PHE:CE2	3:K:288:LEU:HA	1.35	1.60
1:A:189:LEU:HD12	1:A:413:MET:CE	1.14	1.59
1:A:175:PRO:CD	1:A:207:GLU:HB2	1.17	1.59
1:A:227:LEU:HB2	5:A:502:GTP:C5	1.21	1.59
1:A:227:LEU:CB	5:A:502:GTP:C5	1.75	1.59
3:K:9:ILE:CB	3:K:327:ILE:CD1	1.75	1.58
2:B:68:VAL:HG21	2:B:153:LEU:CD2	1.33	1.58
3:K:62:VAL:CG2	3:K:106:MET:HG3	1.22	1.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:VAL:CG1	1:A:384:ILE:HG21	1.22	1.57
3:K:83:PHE:CZ	3:K:231:VAL:CG2	1.75	1.57
3:K:83:PHE:CZ	3:K:231:VAL:HG23	1.09	1.56
2:B:93:VAL:CG1	2:B:114:LEU:HG	1.30	1.56
3:K:105:LEU:HD11	3:K:301:VAL:CG1	1.20	1.56
1:A:303:VAL:CG1	1:A:384:ILE:HD13	1.16	1.55
3:K:139:TYR:HB3	3:K:283:LYS:CB	1.12	1.55
1:A:202:PHE:CD1	1:A:378:LEU:HD22	1.07	1.54
3:K:139:TYR:CB	3:K:283:LYS:CA	1.83	1.54
1:A:204:VAL:HG23	1:A:302:MET:CB	1.34	1.54
1:A:169:PHE:CD2	1:A:235:VAL:CA	1.90	1.53
2:B:70:LEU:HD11	2:B:106:GLY:CA	1.33	1.53
2:B:103:TRP:CE3	2:B:189:LEU:HD13	1.06	1.53
1:A:185:TYR:CD2	1:A:408:TYR:CE2	1.95	1.52
1:A:202:PHE:CD1	1:A:378:LEU:CD2	1.82	1.52
1:A:312:TYR:HD1	1:A:381:THR:CG2	0.94	1.52
1:A:397:LEU:CD1	2:B:348:PRO:HG2	1.40	1.52
2:B:93:VAL:CG2	2:B:118:VAL:HG22	1.38	1.52
3:K:59:GLN:CG	3:K:106:MET:CB	1.86	1.52
3:K:59:GLN:HG2	3:K:106:MET:CB	1.38	1.51
1:A:303:VAL:CB	1:A:384:ILE:CD1	1.85	1.51
3:K:292:LEU:HD13	3:K:320:PHE:CZ	1.42	1.51
3:K:139:TYR:HB3	3:K:283:LYS:CA	1.07	1.50
2:B:11:GLN:H	6:B:602:G2P:PB	1.34	1.50
1:A:169:PHE:CD1	1:A:235:VAL:HG22	1.47	1.50
1:A:303:VAL:HG11	1:A:384:ILE:CG2	1.40	1.50
1:A:301:GLN:HE22	1:A:383:ALA:CB	1.24	1.50
3:K:139:TYR:CG	3:K:283:LYS:HA	1.46	1.50
1:A:303:VAL:HG12	1:A:387:ALA:CB	1.04	1.50
1:A:189:LEU:CD1	1:A:413:MET:CE	1.90	1.49
2:B:64:ARG:CG	2:B:125:GLU:HB3	1.37	1.49
2:B:104:ALA:HB2	2:B:413:MET:SD	1.51	1.49
2:B:9:ALA:CB	2:B:150:GLY:HA3	1.42	1.49
1:A:182:VAL:HG21	1:A:407:TRP:CZ3	1.48	1.48
2:B:103:TRP:CB	2:B:189:LEU:HD12	1.38	1.48
1:A:169:PHE:CG	1:A:235:VAL:CA	1.96	1.48
2:B:93:VAL:CB	2:B:118:VAL:HG22	1.38	1.48
3:K:9:ILE:HB	3:K:327:ILE:CD1	1.03	1.48
1:A:303:VAL:C	1:A:384:ILE:HD11	1.28	1.47
1:A:224:TYR:CE2	2:B:325:MET:CG	1.94	1.47
3:K:83:PHE:CD2	3:K:291:SER:OG	1.65	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:SER:CB	1:A:243:ARG:NH2	1.71	1.47
2:B:93:VAL:HG21	2:B:118:VAL:CG2	1.44	1.47
1:A:165:SER:HB2	1:A:243:ARG:NH2	1.15	1.47
2:B:103:TRP:CD2	2:B:189:LEU:CD1	1.95	1.46
1:A:169:PHE:CD2	1:A:238:ILE:HG12	1.49	1.46
1:A:224:TYR:CE2	2:B:325:MET:HG2	1.43	1.46
1:A:169:PHE:CE2	1:A:238:ILE:HG12	1.46	1.46
1:A:224:TYR:CD2	2:B:325:MET:HG2	1.50	1.46
1:A:301:GLN:NE2	1:A:383:ALA:HB3	1.22	1.46
2:B:103:TRP:N	2:B:408:TYR:CE2	1.79	1.46
1:A:169:PHE:CB	1:A:235:VAL:HG13	1.39	1.45
3:K:62:VAL:HA	3:K:104:GLN:CG	1.17	1.45
3:K:105:LEU:CD1	3:K:301:VAL:CG1	1.94	1.45
1:A:165:SER:HB3	1:A:252:LEU:CB	1.46	1.45
3:K:83:PHE:CD2	3:K:288:LEU:HA	1.50	1.45
1:A:172:TYR:CE2	1:A:388:TRP:HZ3	1.34	1.45
1:A:303:VAL:C	1:A:384:ILE:CD1	1.86	1.45
1:A:172:TYR:CD2	1:A:388:TRP:CZ3	2.04	1.44
2:B:93:VAL:C	2:B:114:LEU:CD2	1.85	1.44
2:B:93:VAL:C	2:B:114:LEU:HD21	1.09	1.44
1:A:209:ILE:CG2	1:A:212:ILE:HD12	1.47	1.44
2:B:93:VAL:CB	2:B:118:VAL:CG2	1.95	1.43
1:A:303:VAL:CB	1:A:384:ILE:HD13	1.46	1.43
3:K:292:LEU:CD1	3:K:320:PHE:CZ	1.98	1.43
1:A:224:TYR:CZ	2:B:325:MET:CG	2.01	1.43
1:A:298:PRO:HB3	1:A:307:PRO:CD	1.45	1.43
3:K:53:LEU:CD1	3:K:104:GLN:OE1	1.68	1.42
2:B:94:PHE:N	2:B:114:LEU:HD21	1.19	1.42
3:K:139:TYR:CB	3:K:283:LYS:CB	1.97	1.42
3:K:9:ILE:CG1	3:K:327:ILE:HD13	1.49	1.42
3:K:208:ILE:HD13	3:K:287:ILE:CD1	1.49	1.42
2:B:431:GLU:HB2	3:K:274:LYS:CD	1.49	1.42
1:A:303:VAL:HG12	1:A:384:ILE:CD1	1.50	1.42
3:K:62:VAL:CA	3:K:104:GLN:HG2	1.09	1.41
1:A:227:LEU:HB2	5:A:502:GTP:C4	1.25	1.41
1:A:204:VAL:CG1	1:A:231:ILE:HG23	1.49	1.41
3:K:14:ARG:NH1	3:K:95:THR:HG22	1.28	1.41
3:K:14:ARG:HH21	3:K:103:PRO:CD	1.29	1.41
2:B:93:VAL:CG2	2:B:118:VAL:CG2	1.98	1.40
1:A:407:TRP:HA	2:B:257:VAL:CG2	1.51	1.40
2:B:431:GLU:HB3	3:K:274:LYS:NZ	1.24	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:94:PHE:CA	2:B:114:LEU:CD2	2.00	1.39
3:K:62:VAL:HG23	3:K:106:MET:CG	1.49	1.39
2:B:97:SER:HB3	2:B:110:GLU:CD	1.40	1.39
3:K:95:THR:CB	3:K:105:LEU:HB2	1.48	1.39
3:K:14:ARG:CZ	3:K:103:PRO:HD2	1.50	1.39
2:B:94:PHE:C	2:B:114:LEU:HD22	1.04	1.39
1:A:101:ASN:O	1:A:407:TRP:CZ3	1.74	1.39
2:B:93:VAL:CG1	2:B:118:VAL:HG23	1.52	1.39
1:A:167:LEU:H	1:A:252:LEU:CD1	1.32	1.39
1:A:172:TYR:CE2	1:A:391:LEU:HD22	1.56	1.39
3:K:139:TYR:HB2	3:K:284:MET:N	1.32	1.39
1:A:169:PHE:CZ	1:A:234:ILE:CD1	2.06	1.39
1:A:169:PHE:CD1	1:A:235:VAL:HA	1.55	1.39
2:B:93:VAL:O	2:B:114:LEU:CD2	1.68	1.39
1:A:101:ASN:CB	1:A:407:TRP:CH2	2.03	1.38
2:B:68:VAL:CG2	2:B:153:LEU:HD21	1.53	1.38
3:K:14:ARG:NE	3:K:103:PRO:CG	1.85	1.38
2:B:103:TRP:CG	2:B:189:LEU:HD12	1.59	1.38
3:K:139:TYR:N	3:K:206:HIS:CE1	1.73	1.38
3:K:139:TYR:CB	3:K:283:LYS:HB2	1.50	1.38
3:K:139:TYR:CA	3:K:206:HIS:HE1	1.36	1.38
3:K:62:VAL:CG2	3:K:106:MET:CG	1.96	1.38
1:A:303:VAL:CG1	1:A:387:ALA:HB1	1.30	1.37
2:B:264:ARG:HH22	3:K:276:HIS:CE1	1.42	1.37
3:K:206:HIS:CD2	3:K:287:ILE:HD12	1.45	1.37
1:A:210:TYR:CE1	5:A:502:GTP:C6	2.11	1.37
3:K:274:LYS:CB	3:K:281:ASP:OD2	1.69	1.37
2:B:103:TRP:CE3	2:B:189:LEU:CD1	2.02	1.37
3:K:14:ARG:NE	3:K:103:PRO:HG2	1.10	1.37
1:A:101:ASN:CB	1:A:407:TRP:HH2	1.33	1.37
1:A:175:PRO:CD	1:A:207:GLU:CB	2.01	1.37
1:A:204:VAL:CG2	1:A:302:MET:HB3	1.53	1.37
1:A:384:ILE:HG23	1:A:388:TRP:N	1.37	1.36
1:A:266:HIS:CE1	1:A:431:ASP:OD2	1.76	1.36
1:A:165:SER:CB	1:A:252:LEU:HB2	1.52	1.36
1:A:380:ASN:HB3	1:A:432:TYR:CE1	1.58	1.36
1:A:209:ILE:HG23	1:A:212:ILE:CD1	1.55	1.36
1:A:172:TYR:CE2	1:A:391:LEU:CD2	2.07	1.36
1:A:169:PHE:CE1	1:A:234:ILE:HG23	1.60	1.35
1:A:206:ASN:OD1	5:A:502:GTP:N3	1.57	1.35
1:A:174:ALA:CB	1:A:207:GLU:H	1.38	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:HIS:CE1	1:A:431:ASP:CG	2.00	1.35
3:K:83:PHE:CG	3:K:231:VAL:HB	1.60	1.35
3:K:14:ARG:NH2	3:K:103:PRO:CD	1.84	1.35
1:A:269:LEU:C	1:A:378:LEU:HD12	1.44	1.35
2:B:66:ILE:HG21	2:B:118:VAL:CG1	1.54	1.35
1:A:169:PHE:CD1	1:A:235:VAL:CG2	2.09	1.34
3:K:139:TYR:N	3:K:206:HIS:HE1	1.04	1.34
2:B:13:GLY:CA	2:B:139:HIS:HA	1.53	1.34
2:B:94:PHE:C	2:B:114:LEU:CD2	1.95	1.34
3:K:208:ILE:CD1	3:K:287:ILE:CD1	2.05	1.34
3:K:20:GLU:HG3	3:K:198:MET:SD	1.67	1.34
3:K:139:TYR:CD1	3:K:283:LYS:HA	1.63	1.34
2:B:97:SER:CB	2:B:110:GLU:OE1	1.73	1.34
1:A:189:LEU:HD11	1:A:417:GLU:CB	1.57	1.33
3:K:9:ILE:CB	3:K:327:ILE:HD13	1.37	1.33
2:B:103:TRP:CD2	2:B:189:LEU:HB3	1.62	1.33
1:A:172:TYR:CE2	1:A:388:TRP:CZ3	2.12	1.33
1:A:243:ARG:NH2	1:A:251:ASP:OD1	1.59	1.32
3:K:208:ILE:CD1	3:K:287:ILE:HD13	1.59	1.32
1:A:101:ASN:HB2	1:A:407:TRP:CZ2	1.64	1.32
2:B:93:VAL:CG1	2:B:114:LEU:O	1.76	1.32
1:A:102:ASN:HD21	1:A:411:GLU:C	1.32	1.32
1:A:398:MET:O	1:A:403:ALA:CB	1.76	1.32
2:B:12:CYS:SG	2:B:140:SER:HB3	1.70	1.32
1:A:101:ASN:O	1:A:407:TRP:CH2	1.82	1.32
3:K:14:ARG:HE	3:K:103:PRO:CG	1.40	1.32
2:B:103:TRP:CG	2:B:189:LEU:CD1	2.11	1.31
1:A:312:TYR:O	1:A:381:THR:CB	1.76	1.31
1:A:174:ALA:CB	5:A:502:GTP:O2'	1.78	1.31
3:K:59:GLN:O	3:K:106:MET:CG	1.79	1.31
2:B:103:TRP:N	2:B:408:TYR:HE2	1.16	1.31
3:K:140:LEU:HD11	3:K:284:MET:SD	1.69	1.31
1:A:312:TYR:O	1:A:381:THR:HB	1.19	1.31
1:A:167:LEU:N	1:A:252:LEU:HD13	1.42	1.31
1:A:206:ASN:CG	5:A:502:GTP:N3	1.83	1.31
1:A:195:LEU:HD22	1:A:265:GLY:C	1.48	1.30
1:A:169:PHE:CD2	1:A:238:ILE:CG1	2.11	1.30
1:A:224:TYR:CZ	2:B:325:MET:HG3	1.60	1.30
3:K:83:PHE:CD2	3:K:288:LEU:CA	2.14	1.30
3:K:105:LEU:CD1	3:K:301:VAL:HG11	1.56	1.30
3:K:135:TYR:CE2	3:K:187:GLY:HA3	1.65	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:ARG:CD	2:B:125:GLU:HB3	1.60	1.30
2:B:431:GLU:CB	3:K:274:LYS:HZ2	1.43	1.30
2:B:64:ARG:HG3	2:B:125:GLU:CB	1.62	1.30
3:K:139:TYR:CA	3:K:283:LYS:HB2	1.61	1.30
2:B:7:ILE:O	2:B:137:LEU:HD12	1.32	1.29
3:K:9:ILE:CD1	3:K:327:ILE:HD13	1.60	1.29
1:A:169:PHE:HB3	1:A:235:VAL:CG1	1.62	1.29
1:A:175:PRO:CG	1:A:208:ALA:N	1.96	1.29
2:B:93:VAL:HG12	2:B:114:LEU:CG	1.62	1.29
1:A:303:VAL:O	1:A:384:ILE:CD1	1.75	1.29
2:B:258:ASN:ND2	2:B:352:LYS:HZ3	1.28	1.29
1:A:189:LEU:CD1	1:A:413:MET:HE2	1.56	1.29
1:A:398:MET:HB3	1:A:404:PHE:CE1	1.68	1.29
2:B:175:PRO:HD2	2:B:207:GLU:OE2	1.14	1.29
2:B:103:TRP:CE2	2:B:189:LEU:CB	2.14	1.29
2:B:6:HIS:HA	2:B:136:GLN:O	1.32	1.29
1:A:266:HIS:HE1	1:A:431:ASP:CG	1.35	1.28
1:A:169:PHE:CE1	1:A:234:ILE:CD1	2.16	1.28
1:A:195:LEU:HD22	1:A:265:GLY:O	1.33	1.28
1:A:208:ALA:HB2	1:A:304:LYS:CA	1.63	1.28
3:K:102:ASP:HB3	3:K:103:PRO:CD	1.57	1.28
1:A:191:THR:O	1:A:195:LEU:HG	1.12	1.27
2:B:431:GLU:CB	3:K:274:LYS:CD	2.12	1.27
1:A:207:GLU:OE1	1:A:394:LYS:HE2	1.26	1.27
1:A:185:TYR:HB3	1:A:418:PHE:CE1	1.70	1.27
3:K:14:ARG:NH1	3:K:104:GLN:O	1.64	1.27
1:A:166:LYS:CA	1:A:252:LEU:HD13	1.64	1.27
2:B:66:ILE:CG2	2:B:118:VAL:HG13	1.64	1.26
3:K:83:PHE:CE1	3:K:231:VAL:N	2.02	1.26
2:B:94:PHE:CA	2:B:114:LEU:HD21	1.62	1.26
1:A:176:GLN:CA	1:A:394:LYS:CE	2.12	1.26
2:B:431:GLU:CB	3:K:274:LYS:HD2	1.62	1.26
1:A:179:THR:CG2	2:B:248:LEU:HD13	1.64	1.26
3:K:136:PHE:CD2	3:K:139:TYR:OH	1.73	1.26
1:A:380:ASN:O	1:A:432:TYR:CD1	1.88	1.26
3:K:291:SER:O	3:K:300:ILE:HG12	1.31	1.26
3:K:83:PHE:CE2	3:K:231:VAL:HG21	1.69	1.26
3:K:292:LEU:HD13	3:K:320:PHE:CE2	1.69	1.26
1:A:173:PRO:O	1:A:205:ASP:CG	1.74	1.25
2:B:97:SER:CB	2:B:110:GLU:CD	2.02	1.25
3:K:89:SER:HB3	3:K:199:ASN:OD1	1.28	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ASN:HB2	5:A:502:GTP:C1'	1.66	1.25
1:A:204:VAL:HG21	1:A:302:MET:SD	1.74	1.25
2:B:93:VAL:HG11	2:B:118:VAL:CG2	1.67	1.25
2:B:93:VAL:HG21	2:B:118:VAL:CA	1.64	1.25
1:A:174:ALA:HB1	1:A:207:GLU:N	1.49	1.25
1:A:206:ASN:HB3	5:A:502:GTP:N3	1.51	1.25
1:A:301:GLN:CD	1:A:383:ALA:HB3	1.57	1.25
1:A:189:LEU:CD1	1:A:417:GLU:HB3	1.66	1.25
1:A:269:LEU:O	1:A:378:LEU:HD12	1.13	1.25
3:K:105:LEU:CG	3:K:301:VAL:HG11	1.40	1.25
1:A:210:TYR:CE1	5:A:502:GTP:C5	2.23	1.25
3:K:14:ARG:NH2	3:K:103:PRO:HD2	0.93	1.25
1:A:172:TYR:CD1	1:A:173:PRO:HD2	1.71	1.24
1:A:206:ASN:CB	5:A:502:GTP:N3	1.98	1.24
1:A:189:LEU:CD1	1:A:413:MET:SD	2.26	1.24
1:A:169:PHE:CD1	1:A:235:VAL:CA	2.17	1.24
1:A:176:GLN:CA	1:A:394:LYS:HE2	1.65	1.24
3:K:283:LYS:NZ	3:K:286:ARG:HD2	1.49	1.24
1:A:171:ILE:HA	1:A:204:VAL:CG1	1.68	1.23
1:A:195:LEU:CB	1:A:265:GLY:HA3	1.67	1.23
1:A:202:PHE:CG	1:A:378:LEU:HD22	1.74	1.23
2:B:93:VAL:CG1	2:B:118:VAL:CG2	2.15	1.23
1:A:175:PRO:CD	1:A:208:ALA:H	1.49	1.23
3:K:83:PHE:CD2	3:K:288:LEU:CB	2.20	1.23
1:A:101:ASN:HB3	1:A:407:TRP:CH2	1.65	1.22
1:A:174:ALA:HB2	5:A:502:GTP:O2'	1.34	1.22
2:B:70:LEU:CD1	2:B:106:GLY:HA2	1.67	1.22
1:A:102:ASN:ND2	1:A:412:GLY:N	1.87	1.22
3:K:83:PHE:CE2	3:K:231:VAL:CG2	2.22	1.22
1:A:397:LEU:HD13	2:B:348:PRO:CG	1.69	1.22
1:A:175:PRO:HD2	1:A:207:GLU:CA	1.68	1.22
1:A:195:LEU:CD2	1:A:265:GLY:O	1.86	1.21
1:A:175:PRO:CD	1:A:208:ALA:N	2.03	1.21
1:A:105:ARG:HB2	1:A:411:GLU:O	1.07	1.21
2:B:266:HIS:HB3	2:B:432:TYR:OH	1.39	1.21
1:A:176:GLN:HG2	1:A:394:LYS:NZ	1.56	1.20
2:B:93:VAL:O	2:B:114:LEU:HD21	1.30	1.20
2:B:103:TRP:CD1	2:B:189:LEU:HB2	1.77	1.20
3:K:274:LYS:HB2	3:K:281:ASP:OD2	1.05	1.20
1:A:269:LEU:HD13	1:A:384:ILE:CB	1.71	1.20
3:K:137:GLU:OE1	3:K:191:ARG:HA	1.39	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:5:VAL:O	2:B:135:PHE:HB3	1.40	1.20
1:A:182:VAL:CG2	1:A:407:TRP:CZ3	2.24	1.20
1:A:175:PRO:O	1:A:394:LYS:CE	1.89	1.20
3:K:53:LEU:HD13	3:K:104:GLN:CB	1.69	1.20
1:A:208:ALA:HB2	1:A:304:LYS:N	1.54	1.19
3:K:139:TYR:C	3:K:283:LYS:HB2	1.62	1.19
2:B:66:ILE:HD11	2:B:122:VAL:CG1	1.73	1.19
3:K:53:LEU:CD1	3:K:104:GLN:HB2	1.72	1.19
2:B:205:ASP:OD2	2:B:304:ALA:N	1.75	1.19
1:A:262:TYR:O	1:A:266:HIS:CD2	1.94	1.19
1:A:269:LEU:HD11	1:A:384:ILE:C	1.39	1.19
3:K:139:TYR:CB	3:K:284:MET:N	2.05	1.19
1:A:169:PHE:CE1	1:A:234:ILE:HD12	1.76	1.19
2:B:93:VAL:HG21	2:B:118:VAL:CB	1.72	1.19
1:A:312:TYR:O	1:A:381:THR:CG2	1.90	1.19
3:K:324:ALA:O	3:K:327:ILE:HG13	1.05	1.18
1:A:269:LEU:C	1:A:378:LEU:CD1	2.09	1.18
2:B:336:GLN:OE1	2:B:347:ILE:O	1.59	1.18
2:B:66:ILE:CD1	2:B:122:VAL:HG12	1.71	1.18
1:A:177:VAL:N	1:A:207:GLU:CD	1.97	1.18
1:A:172:TYR:O	1:A:205:ASP:HA	1.40	1.18
1:A:202:PHE:HE2	1:A:238:ILE:HG23	1.07	1.18
1:A:191:THR:OG1	1:A:267:PHE:CE2	1.94	1.18
3:K:135:TYR:CD2	3:K:187:GLY:HA3	1.77	1.18
1:A:185:TYR:CD1	1:A:418:PHE:CG	2.30	1.18
1:A:301:GLN:NE2	1:A:383:ALA:CB	1.91	1.18
2:B:93:VAL:HB	2:B:118:VAL:HG22	1.20	1.18
3:K:83:PHE:CD1	3:K:231:VAL:HB	1.79	1.18
1:A:303:VAL:CA	1:A:384:ILE:CD1	2.21	1.17
1:A:303:VAL:CG1	1:A:384:ILE:CG2	2.07	1.17
3:K:53:LEU:CD2	3:K:104:GLN:OE1	1.93	1.17
2:B:9:ALA:CB	2:B:150:GLY:CA	2.21	1.17
3:K:139:TYR:CB	3:K:283:LYS:HA	1.59	1.17
1:A:227:LEU:HB3	5:A:502:GTP:N7	1.60	1.17
1:A:312:TYR:CD1	1:A:381:THR:HG21	1.71	1.17
1:A:398:MET:CB	1:A:404:PHE:HE1	1.58	1.17
3:K:139:TYR:CB	3:K:206:HIS:CE1	2.12	1.16
3:K:102:ASP:HB3	3:K:103:PRO:HD3	1.26	1.16
1:A:269:LEU:CD1	1:A:384:ILE:C	2.11	1.16
2:B:97:SER:OG	2:B:110:GLU:OE1	1.62	1.16
2:B:68:VAL:CB	2:B:153:LEU:HD21	1.74	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:175:PRO:CD	2:B:207:GLU:OE2	1.92	1.16
3:K:89:SER:CB	3:K:199:ASN:OD1	1.93	1.16
1:A:27:GLU:HG3	1:A:358:GLU:CD	1.65	1.16
1:A:405:VAL:HG22	1:A:418:PHE:CD2	1.80	1.16
1:A:182:VAL:HG21	1:A:407:TRP:CE3	1.80	1.16
1:A:380:ASN:HB3	1:A:432:TYR:CD1	1.81	1.15
3:K:14:ARG:CD	3:K:103:PRO:HG2	1.75	1.15
3:K:59:GLN:HG2	3:K:106:MET:CA	1.76	1.15
2:B:103:TRP:NE1	2:B:189:LEU:HB3	1.59	1.15
1:A:185:TYR:CD2	1:A:408:TYR:CD2	2.33	1.15
2:B:104:ALA:CB	2:B:413:MET:CE	2.25	1.15
2:B:66:ILE:CD1	2:B:122:VAL:CG1	2.25	1.15
1:A:204:VAL:CG2	1:A:209:ILE:HD13	1.76	1.15
1:A:303:VAL:CG1	1:A:384:ILE:CD1	1.97	1.15
2:B:196:GLU:OE1	3:K:280:ARG:NH1	1.79	1.15
2:B:234:THR:HG21	2:B:270:PRO:HB2	1.22	1.15
1:A:176:GLN:N	1:A:207:GLU:HB3	1.58	1.15
1:A:102:ASN:ND2	1:A:411:GLU:C	1.98	1.15
1:A:169:PHE:CD2	1:A:235:VAL:C	2.18	1.15
2:B:258:ASN:ND2	2:B:352:LYS:NZ	1.93	1.15
3:K:139:TYR:CB	3:K:283:LYS:C	2.14	1.15
1:A:206:ASN:CG	5:A:502:GTP:C4	2.14	1.14
3:K:324:ALA:O	3:K:327:ILE:CG1	1.95	1.14
3:K:139:TYR:HB2	3:K:206:HIS:CE1	1.81	1.14
1:A:210:TYR:CZ	5:A:502:GTP:C5	2.35	1.14
2:B:7:ILE:HB	2:B:137:LEU:HD13	1.26	1.14
1:A:165:SER:O	1:A:252:LEU:HD12	1.47	1.14
2:B:381:SER:C	2:B:383:ALA:H	1.51	1.14
1:A:179:THR:HG22	2:B:248:LEU:CD1	1.76	1.14
1:A:166:LYS:C	1:A:252:LEU:HD13	1.68	1.14
1:A:380:ASN:O	1:A:432:TYR:CG	2.00	1.14
1:A:176:GLN:HA	1:A:394:LYS:NZ	1.61	1.13
1:A:303:VAL:CB	1:A:384:ILE:HD12	1.58	1.13
1:A:398:MET:O	1:A:403:ALA:HB2	0.99	1.13
2:B:94:PHE:O	2:B:114:LEU:HD22	1.47	1.13
1:A:204:VAL:HG11	1:A:231:ILE:CG2	1.77	1.13
2:B:266:HIS:CB	2:B:432:TYR:OH	1.94	1.13
1:A:243:ARG:NH2	1:A:252:LEU:H	1.46	1.13
2:B:94:PHE:O	2:B:114:LEU:HD13	1.47	1.13
2:B:70:LEU:CD1	2:B:106:GLY:CA	2.24	1.13
3:K:107:GLY:O	3:K:110:PRO:HD2	1.48	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:14:ARG:HH21	3:K:102:ASP:HB3	1.09	1.12
3:K:59:GLN:CG	3:K:106:MET:HB3	1.65	1.12
3:K:83:PHE:CG	3:K:291:SER:OG	2.02	1.12
1:A:195:LEU:HB3	1:A:265:GLY:CA	1.79	1.12
1:A:227:LEU:CD1	1:A:231:ILE:HD11	1.80	1.12
2:B:103:TRP:CD2	2:B:189:LEU:CB	2.28	1.12
3:K:9:ILE:CD1	3:K:327:ILE:HG21	1.79	1.12
3:K:59:GLN:CA	3:K:106:MET:HB3	1.78	1.12
1:A:298:PRO:CB	1:A:307:PRO:HD2	1.78	1.12
2:B:9:ALA:HB2	2:B:150:GLY:HA3	1.29	1.12
3:K:83:PHE:CE1	3:K:231:VAL:CG2	2.12	1.12
3:K:59:GLN:CG	3:K:106:MET:CA	2.28	1.12
1:A:189:LEU:HD11	1:A:413:MET:SD	1.89	1.11
2:B:9:ALA:HB1	2:B:150:GLY:HA3	1.25	1.11
1:A:175:PRO:C	1:A:394:LYS:HE2	1.70	1.11
1:A:27:GLU:CG	1:A:358:GLU:OE2	1.99	1.11
1:A:227:LEU:HB2	5:A:502:GTP:C6	1.84	1.11
1:A:171:ILE:CG2	1:A:231:ILE:HG13	1.64	1.11
2:B:336:GLN:OE1	2:B:349:ASN:O	1.68	1.11
3:K:283:LYS:O	3:K:286:ARG:HB3	1.50	1.11
1:A:176:GLN:H	1:A:207:GLU:CB	1.60	1.11
1:A:298:PRO:CB	1:A:307:PRO:CD	2.29	1.11
3:K:83:PHE:CD1	3:K:231:VAL:N	2.13	1.11
3:K:53:LEU:HD13	3:K:104:GLN:CG	1.79	1.11
3:K:20:GLU:CG	3:K:198:MET:SD	2.37	1.11
1:A:102:ASN:HD21	1:A:412:GLY:N	1.47	1.10
1:A:382:THR:O	1:A:385:ALA:CB	1.99	1.10
2:B:262:PHE:HZ	3:K:271:GLU:OE2	1.30	1.10
1:A:208:ALA:HB2	1:A:304:LYS:HA	1.29	1.10
1:A:428:LEU:HG	1:A:432:TYR:CE2	1.84	1.10
1:A:398:MET:C	1:A:403:ALA:HB2	1.72	1.10
2:B:167:ASN:HD21	2:B:252:LEU:HD22	1.05	1.10
3:K:62:VAL:HG22	3:K:106:MET:HG3	1.28	1.10
3:K:53:LEU:HD11	3:K:104:GLN:OE1	1.37	1.10
2:B:205:ASP:O	2:B:209:LEU:HD13	1.51	1.10
1:A:169:PHE:CD2	1:A:235:VAL:O	2.04	1.10
1:A:6:SER:HA	1:A:136:SER:HB3	1.31	1.10
3:K:95:THR:HB	3:K:105:LEU:CB	1.82	1.10
1:A:165:SER:HB3	1:A:252:LEU:CA	1.80	1.10
2:B:103:TRP:HB3	2:B:189:LEU:CD1	1.80	1.10
2:B:94:PHE:CA	2:B:114:LEU:HD22	1.67	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:THR:OG1	5:A:502:GTP:H5'	1.52	1.09
2:B:103:TRP:CD1	2:B:189:LEU:CB	2.35	1.09
2:B:431:GLU:CB	3:K:274:LYS:NZ	2.07	1.09
2:B:100:GLY:N	2:B:105:LYS:HD3	1.63	1.09
1:A:105:ARG:O	1:A:110:ILE:HG22	1.49	1.09
2:B:228:ASN:OD1	6:B:602:G2P:N1	1.84	1.09
3:K:14:ARG:NH1	3:K:95:THR:CG2	2.14	1.09
1:A:266:HIS:ND1	1:A:431:ASP:OD2	1.85	1.09
2:B:68:VAL:CG2	2:B:153:LEU:CD2	2.16	1.09
1:A:166:LYS:HA	1:A:252:LEU:HD13	1.35	1.09
2:B:13:GLY:HA3	2:B:139:HIS:HA	1.24	1.09
1:A:185:TYR:HD2	1:A:408:TYR:CD2	1.66	1.09
1:A:165:SER:HB3	1:A:243:ARG:NH2	1.65	1.09
2:B:69:ASP:H	2:B:149:MET:HE1	1.14	1.09
3:K:274:LYS:HB2	3:K:281:ASP:CG	1.71	1.09
2:B:264:ARG:HD3	3:K:274:LYS:HD3	1.10	1.08
3:K:83:PHE:CD1	3:K:231:VAL:CB	2.37	1.08
3:K:105:LEU:HG	3:K:301:VAL:HG11	1.28	1.08
2:B:103:TRP:HB3	2:B:189:LEU:HD12	1.08	1.08
3:K:208:ILE:CD1	3:K:287:ILE:HD12	1.83	1.08
3:K:290:ASP:O	3:K:298:THR:CG2	2.00	1.08
1:A:176:GLN:HA	1:A:394:LYS:HE3	1.34	1.08
1:A:210:TYR:CD1	5:A:502:GTP:C2	2.41	1.08
1:A:267:PHE:H	1:A:428:LEU:HD11	0.96	1.08
1:A:302:MET:O	1:A:303:VAL:HG23	1.52	1.08
2:B:9:ALA:HB2	2:B:150:GLY:CA	1.83	1.08
2:B:264:ARG:HD3	3:K:274:LYS:CD	1.83	1.08
2:B:204:ILE:HG23	2:B:302:MET:HB3	1.29	1.08
1:A:175:PRO:HG3	1:A:208:ALA:N	1.68	1.07
1:A:204:VAL:HG23	1:A:209:ILE:CD1	1.84	1.07
3:K:291:SER:O	3:K:300:ILE:CG1	2.01	1.07
3:K:53:LEU:HD13	3:K:104:GLN:HB2	1.18	1.07
3:K:59:GLN:O	3:K:106:MET:HG2	1.48	1.07
1:A:181:VAL:CG1	1:A:404:PHE:CD2	2.37	1.07
1:A:173:PRO:O	1:A:205:ASP:CB	2.02	1.07
2:B:267:PHE:HB2	2:B:384:ILE:HD13	1.37	1.07
3:K:108:ILE:O	3:K:112:ILE:HG13	1.54	1.07
1:A:174:ALA:HB1	1:A:207:GLU:CA	1.84	1.07
1:A:267:PHE:H	1:A:428:LEU:CD1	1.66	1.07
1:A:380:ASN:CB	1:A:432:TYR:CE1	2.36	1.07
1:A:261:PRO:HG2	1:A:435:VAL:HG21	1.36	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:59:GLN:CG	3:K:106:MET:HB2	1.67	1.07
1:A:312:TYR:CG	1:A:381:THR:HG21	1.88	1.07
2:B:103:TRP:CB	2:B:189:LEU:CD1	2.29	1.07
1:A:176:GLN:N	1:A:394:LYS:HE2	1.68	1.07
2:B:262:PHE:CE2	2:B:435:TYR:CE1	2.42	1.07
2:B:104:ALA:CB	2:B:413:MET:SD	2.43	1.07
2:B:93:VAL:HG11	2:B:114:LEU:O	1.48	1.07
1:A:5:ILE:HD11	1:A:135:PHE:CE1	1.88	1.07
1:A:165:SER:CA	1:A:252:LEU:HB2	1.84	1.06
1:A:227:LEU:HB3	5:A:502:GTP:C5	1.62	1.06
2:B:11:GLN:OE1	6:B:602:G2P:O1A	1.71	1.06
1:A:136:SER:HB2	1:A:239:THR:HG21	1.08	1.06
2:B:68:VAL:C	2:B:149:MET:SD	2.33	1.06
2:B:93:VAL:HG13	2:B:114:LEU:O	1.44	1.06
3:K:59:GLN:HG3	3:K:106:MET:HB3	1.37	1.06
3:K:59:GLN:O	3:K:106:MET:HG3	1.51	1.06
3:K:62:VAL:CG2	3:K:106:MET:CB	2.32	1.06
1:A:204:VAL:CG2	1:A:302:MET:SD	2.43	1.06
1:A:413:MET:SD	1:A:417:GLU:HB3	1.96	1.06
1:A:167:LEU:N	1:A:252:LEU:CD1	2.04	1.06
3:K:53:LEU:HD22	3:K:104:GLN:CD	1.75	1.06
1:A:27:GLU:CD	1:A:358:GLU:CG	2.24	1.06
1:A:209:ILE:O	1:A:212:ILE:N	1.87	1.06
1:A:224:TYR:CG	2:B:325:MET:HG2	1.90	1.06
2:B:264:ARG:CD	3:K:274:LYS:HD3	1.83	1.06
3:K:14:ARG:CZ	3:K:103:PRO:CD	2.28	1.06
1:A:204:VAL:CG1	1:A:231:ILE:CG2	2.32	1.06
3:K:206:HIS:CD2	3:K:287:ILE:CD1	2.38	1.06
1:A:172:TYR:CD2	1:A:205:ASP:OD2	2.09	1.06
1:A:312:TYR:HD1	1:A:381:THR:HG22	0.89	1.06
1:A:105:ARG:CB	1:A:411:GLU:O	2.04	1.06
2:B:66:ILE:CG2	2:B:118:VAL:CG1	2.27	1.06
1:A:206:ASN:O	1:A:210:TYR:N	1.88	1.06
1:A:269:LEU:O	1:A:378:LEU:CD1	2.00	1.06
1:A:398:MET:HB3	1:A:404:PHE:HE1	0.89	1.06
3:K:83:PHE:CE2	3:K:288:LEU:CA	2.31	1.06
1:A:185:TYR:OH	1:A:402:ARG:O	1.73	1.05
2:B:64:ARG:HG3	2:B:125:GLU:CG	1.86	1.05
2:B:93:VAL:CG1	2:B:114:LEU:CG	2.24	1.05
1:A:195:LEU:HD22	1:A:265:GLY:CA	1.85	1.05
2:B:93:VAL:O	2:B:114:LEU:HD23	1.57	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:LEU:CB	5:A:502:GTP:C6	2.39	1.05
1:A:312:TYR:CD1	1:A:381:THR:HG23	1.64	1.05
1:A:202:PHE:HE2	1:A:238:ILE:CG2	1.55	1.05
2:B:11:GLN:N	6:B:602:G2P:PB	2.18	1.05
2:B:104:ALA:HB1	2:B:413:MET:HE3	1.39	1.05
1:A:174:ALA:CB	1:A:207:GLU:N	2.10	1.05
1:A:175:PRO:HA	1:A:391:LEU:HD12	1.38	1.05
1:A:208:ALA:CB	1:A:304:LYS:N	2.19	1.04
2:B:172:VAL:HG11	2:B:387:LEU:HD21	1.37	1.04
1:A:165:SER:C	1:A:252:LEU:HB2	1.78	1.04
3:K:57:THR:O	3:K:103:PRO:HA	1.57	1.04
1:A:224:TYR:CE2	2:B:325:MET:HG3	1.76	1.04
1:A:303:VAL:HG12	1:A:387:ALA:HB3	1.37	1.04
2:B:264:ARG:NH2	3:K:276:HIS:HE1	1.54	1.04
3:K:59:GLN:HG3	3:K:106:MET:CB	1.85	1.04
1:A:109:THR:HG22	1:A:110:ILE:N	1.71	1.04
1:A:397:LEU:CD1	2:B:348:PRO:CG	2.29	1.04
3:K:94:HIS:NE2	3:K:102:ASP:HB2	1.70	1.04
2:B:68:VAL:HG21	2:B:153:LEU:HD23	1.38	1.04
1:A:27:GLU:OE1	1:A:358:GLU:HG2	1.58	1.04
1:A:169:PHE:CE1	1:A:234:ILE:HD13	1.87	1.04
2:B:11:GLN:N	6:B:602:G2P:O2B	1.88	1.04
2:B:70:LEU:HD12	2:B:145:THR:HG22	1.39	1.04
1:A:185:TYR:CD1	1:A:418:PHE:CD1	2.46	1.03
1:A:303:VAL:HB	1:A:384:ILE:CD1	1.60	1.03
3:K:59:GLN:HA	3:K:106:MET:HB3	1.35	1.03
1:A:169:PHE:CE2	1:A:235:VAL:CA	2.08	1.03
2:B:104:ALA:HB1	2:B:413:MET:CE	1.88	1.03
1:A:174:ALA:HB3	5:A:502:GTP:O3'	1.58	1.03
1:A:27:GLU:CD	1:A:358:GLU:HG2	1.77	1.03
1:A:175:PRO:CG	1:A:207:GLU:HB2	1.87	1.03
1:A:101:ASN:HB2	1:A:407:TRP:CH2	1.81	1.03
1:A:407:TRP:CA	2:B:257:VAL:CG2	2.37	1.03
1:A:102:ASN:CG	1:A:411:GLU:HB2	1.78	1.03
3:K:14:ARG:NE	3:K:103:PRO:CD	2.22	1.03
1:A:28:HIS:NE2	1:A:358:GLU:OE1	1.90	1.03
1:A:101:ASN:O	1:A:407:TRP:HZ3	1.38	1.03
2:B:70:LEU:HD21	2:B:111:GLY:CA	1.87	1.03
3:K:59:GLN:O	3:K:62:VAL:HG22	1.58	1.03
1:A:102:ASN:ND2	1:A:411:GLU:HB2	1.73	1.02
2:B:103:TRP:CG	2:B:189:LEU:CB	2.42	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LEU:HD13	1:A:384:ILE:HB	1.07	1.02
1:A:303:VAL:HG12	1:A:384:ILE:CG1	1.89	1.02
2:B:9:ALA:HB1	2:B:150:GLY:CA	1.88	1.02
2:B:347:ILE:O	2:B:349:ASN:N	1.91	1.02
1:A:175:PRO:HG3	1:A:208:ALA:CA	1.88	1.02
1:A:204:VAL:CG2	1:A:209:ILE:CD1	2.36	1.02
3:K:105:LEU:CG	3:K:301:VAL:CG1	2.23	1.02
1:A:243:ARG:HH21	1:A:252:LEU:N	1.57	1.02
1:A:169:PHE:CD2	1:A:238:ILE:CB	2.43	1.02
2:B:64:ARG:CG	2:B:125:GLU:CB	2.24	1.02
2:B:70:LEU:HD21	2:B:111:GLY:N	1.75	1.02
1:A:224:TYR:HD2	2:B:247:GLN:HB3	1.17	1.02
1:A:224:TYR:CZ	2:B:325:MET:HG2	1.76	1.02
1:A:27:GLU:CG	1:A:358:GLU:CD	2.28	1.02
2:B:264:ARG:NH2	3:K:276:HIS:CE1	2.27	1.02
3:K:292:LEU:HD11	3:K:320:PHE:CZ	1.91	1.02
1:A:103:TYR:CD1	1:A:148:GLY:HA2	1.94	1.02
1:A:405:VAL:HG22	1:A:418:PHE:CE2	1.94	1.02
3:K:63:TYR:HA	3:K:106:MET:CE	1.90	1.02
1:A:169:PHE:HE1	1:A:234:ILE:CG2	1.71	1.01
1:A:171:ILE:HA	1:A:204:VAL:HG13	1.38	1.01
1:A:4:CYS:HB3	1:A:243:ARG:HB3	1.38	1.01
1:A:169:PHE:HD2	1:A:238:ILE:HB	1.23	1.01
1:A:188:ILE:C	1:A:421:ALA:HB1	1.59	1.01
2:B:64:ARG:HG3	2:B:125:GLU:HB3	1.05	1.01
3:K:9:ILE:CG2	3:K:327:ILE:CD1	2.38	1.01
1:A:166:LYS:CA	1:A:252:LEU:CD1	2.38	1.01
1:A:171:ILE:HG21	1:A:231:ILE:HG13	1.37	1.01
3:K:9:ILE:HD12	3:K:327:ILE:HG21	1.37	1.01
3:K:82:ILE:O	3:K:83:PHE:CD1	2.14	1.01
1:A:202:PHE:CE2	1:A:238:ILE:HG23	1.96	1.01
1:A:206:ASN:OD1	5:A:502:GTP:C2	2.12	1.01
1:A:176:GLN:HG2	1:A:394:LYS:HZ1	1.23	1.01
2:B:346:TRP:HB3	2:B:349:ASN:HD21	1.25	1.01
3:K:63:TYR:HA	3:K:106:MET:HE2	1.05	1.01
3:K:65:ALA:CB	3:K:104:GLN:NE2	2.23	1.01
2:B:69:ASP:N	2:B:149:MET:HE1	1.75	1.01
1:A:181:VAL:HG12	1:A:404:PHE:CD2	1.95	1.01
3:K:95:THR:OG1	3:K:105:LEU:HB2	1.60	1.01
1:A:11:GLN:HG3	1:A:74:VAL:HG11	1.43	1.01
1:A:27:GLU:OE1	1:A:358:GLU:CG	2.09	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:VAL:CG2	1:A:407:TRP:CE3	2.43	1.00
1:A:312:TYR:CB	1:A:381:THR:HG21	1.90	1.00
2:B:4:ILE:HA	2:B:134:GLY:O	1.61	1.00
1:A:167:LEU:H	1:A:252:LEU:CG	1.58	1.00
1:A:202:PHE:CE2	1:A:238:ILE:CG2	2.44	1.00
3:K:63:TYR:CA	3:K:106:MET:HE2	1.91	1.00
1:A:189:LEU:HD12	1:A:413:MET:HE1	1.39	1.00
1:A:169:PHE:CG	1:A:235:VAL:CB	2.45	1.00
3:K:233:LEU:HD11	3:K:288:LEU:HD11	1.44	1.00
3:K:95:THR:HB	3:K:105:LEU:HB2	1.03	1.00
2:B:100:GLY:CA	2:B:105:LYS:HD3	1.91	1.00
2:B:347:ILE:HB	2:B:348:PRO:HD3	1.40	1.00
2:B:70:LEU:HD11	2:B:106:GLY:HA3	1.43	1.00
1:A:101:ASN:HB3	1:A:407:TRP:HH2	0.91	1.00
2:B:7:ILE:CB	2:B:137:LEU:HD13	1.90	1.00
3:K:62:VAL:HG21	3:K:106:MET:CB	1.91	1.00
1:A:166:LYS:HA	1:A:252:LEU:CD1	1.91	1.00
1:A:171:ILE:HA	1:A:204:VAL:HG12	1.39	1.00
1:A:413:MET:SD	1:A:417:GLU:CB	2.50	1.00
1:A:185:TYR:CB	1:A:418:PHE:CE1	2.45	1.00
1:A:101:ASN:HB2	1:A:407:TRP:HZ2	1.24	0.99
1:A:169:PHE:HE1	1:A:234:ILE:HG23	0.84	0.99
2:B:236:SER:O	2:B:240:THR:HG23	1.60	0.99
1:A:165:SER:CB	1:A:252:LEU:H	1.76	0.99
1:A:208:ALA:CB	1:A:304:LYS:CA	2.40	0.99
1:A:402:ARG:HH22	1:A:415:GLU:CD	1.51	0.99
3:K:292:LEU:HA	3:K:300:ILE:HD11	1.44	0.99
1:A:191:THR:O	1:A:195:LEU:CG	2.09	0.99
1:A:195:LEU:HB3	1:A:265:GLY:HA3	1.01	0.99
2:B:195:VAL:HA	2:B:265:LEU:HD23	1.42	0.99
1:A:174:ALA:CA	1:A:207:GLU:H	1.75	0.99
1:A:181:VAL:HG21	2:B:352:LYS:CG	1.93	0.99
3:K:83:PHE:CD2	3:K:291:SER:CB	2.44	0.99
2:B:66:ILE:HG21	2:B:118:VAL:HG11	1.40	0.99
3:K:83:PHE:CZ	3:K:231:VAL:HG21	1.79	0.99
1:A:206:ASN:CB	5:A:502:GTP:C1'	2.34	0.98
2:B:94:PHE:O	2:B:114:LEU:CD1	2.11	0.98
2:B:299:LYS:H	2:B:299:LYS:HD3	1.24	0.98
3:K:208:ILE:HD13	3:K:287:ILE:HD13	1.01	0.98
2:B:431:GLU:HB2	3:K:274:LYS:CE	1.93	0.98
1:A:407:TRP:CA	2:B:257:VAL:HG21	1.93	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:139:TYR:HD1	3:K:282:SER:O	1.46	0.98
2:B:13:GLY:HA2	2:B:139:HIS:HA	1.41	0.98
2:B:103:TRP:NE1	2:B:189:LEU:CB	2.19	0.98
2:B:5:VAL:H	2:B:135:PHE:HA	1.25	0.98
1:A:188:ILE:HD12	1:A:421:ALA:O	1.63	0.98
3:K:14:ARG:HH11	3:K:95:THR:HG22	1.18	0.98
2:B:204:ILE:CD1	2:B:231:VAL:HG13	1.93	0.98
3:K:139:TYR:HB3	3:K:283:LYS:C	1.80	0.98
1:A:175:PRO:HD2	1:A:207:GLU:CB	1.79	0.97
1:A:182:VAL:HG21	1:A:407:TRP:HZ3	1.26	0.97
2:B:93:VAL:C	2:B:114:LEU:CG	2.31	0.97
1:A:176:GLN:H	1:A:207:GLU:HB3	0.82	0.97
1:A:208:ALA:HB1	1:A:304:LYS:O	1.63	0.97
2:B:176:LYS:HD2	2:B:207:GLU:HB2	1.46	0.97
1:A:176:GLN:CG	1:A:394:LYS:NZ	2.28	0.97
1:A:101:ASN:C	1:A:407:TRP:CH2	2.37	0.97
1:A:133:GLN:OE1	1:A:251:ASP:OD2	1.80	0.97
2:B:6:HIS:NE2	2:B:138:THR:HG23	1.78	0.97
2:B:93:VAL:HG21	2:B:118:VAL:HA	1.44	0.97
3:K:135:TYR:CE2	3:K:187:GLY:CA	2.48	0.97
3:K:14:ARG:HE	3:K:103:PRO:CD	1.77	0.97
1:A:178:SER:HA	5:A:502:GTP:O3'	1.65	0.97
1:A:269:LEU:CD1	1:A:384:ILE:CA	2.42	0.97
1:A:380:ASN:C	1:A:432:TYR:CD1	2.36	0.97
1:A:303:VAL:O	1:A:384:ILE:HD11	0.80	0.97
2:B:167:ASN:ND2	2:B:252:LEU:HD22	1.78	0.97
3:K:53:LEU:CD2	3:K:104:GLN:CD	2.30	0.97
1:A:380:ASN:CB	1:A:432:TYR:CD1	2.47	0.97
3:K:208:ILE:CG1	3:K:287:ILE:HD13	1.94	0.96
3:K:53:LEU:CG	3:K:104:GLN:OE1	2.12	0.96
3:K:14:ARG:CZ	3:K:95:THR:HG22	1.94	0.96
1:A:172:TYR:CZ	1:A:391:LEU:CD2	2.48	0.96
3:K:59:GLN:CB	3:K:106:MET:HB3	1.94	0.96
3:K:184:ILE:HG12	3:K:209:PHE:CE2	2.01	0.96
1:A:227:LEU:N	5:A:502:GTP:C6	2.33	0.96
1:A:165:SER:CB	1:A:251:ASP:OD1	2.13	0.96
1:A:189:LEU:CD1	1:A:417:GLU:CG	2.42	0.96
1:A:165:SER:HB3	1:A:252:LEU:N	1.79	0.96
3:K:83:PHE:HB2	3:K:291:SER:CB	1.95	0.96
3:K:59:GLN:CB	3:K:106:MET:CB	2.42	0.96
3:K:14:ARG:HH11	3:K:95:THR:CG2	1.72	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:VAL:CA	1:A:384:ILE:HD13	1.91	0.96
1:A:208:ALA:CB	1:A:303:VAL:C	2.33	0.96
1:A:181:VAL:HG21	2:B:352:LYS:HG3	1.46	0.96
1:A:267:PHE:N	1:A:428:LEU:HD11	1.80	0.96
2:B:104:ALA:HB2	2:B:413:MET:CE	1.91	0.96
1:A:173:PRO:O	1:A:205:ASP:HB3	1.62	0.95
1:A:384:ILE:CG2	1:A:388:TRP:N	2.28	0.95
1:A:165:SER:HB2	1:A:251:ASP:OD1	1.65	0.95
1:A:210:TYR:HE1	5:A:502:GTP:C6	1.60	0.95
1:A:209:ILE:CB	1:A:212:ILE:HD12	1.96	0.95
3:K:59:GLN:HG2	3:K:106:MET:HB2	0.98	0.95
2:B:431:GLU:CB	3:K:274:LYS:CE	2.43	0.95
2:B:70:LEU:CD2	2:B:111:GLY:N	2.29	0.95
3:K:139:TYR:HB2	3:K:284:MET:H	1.18	0.95
1:A:169:PHE:CB	1:A:235:VAL:CG1	2.33	0.95
1:A:227:LEU:HD12	1:A:231:ILE:HD11	1.44	0.95
1:A:269:LEU:HD13	1:A:384:ILE:CA	1.96	0.95
3:K:139:TYR:HB2	3:K:283:LYS:C	1.84	0.95
1:A:227:LEU:HB2	5:A:502:GTP:N3	1.81	0.95
2:B:93:VAL:HG13	2:B:114:LEU:HG	1.47	0.95
3:K:233:LEU:HD11	3:K:288:LEU:CD1	1.95	0.95
1:A:175:PRO:HD2	1:A:208:ALA:N	1.75	0.95
1:A:175:PRO:O	1:A:394:LYS:HE2	1.62	0.95
1:A:407:TRP:HA	2:B:257:VAL:HG21	0.96	0.95
3:K:83:PHE:HE2	3:K:288:LEU:HA	1.23	0.94
1:A:169:PHE:CE2	1:A:235:VAL:C	2.38	0.94
1:A:202:PHE:CD1	1:A:378:LEU:HD23	2.00	0.94
3:K:136:PHE:CE2	3:K:139:TYR:OH	2.19	0.94
3:K:53:LEU:HD13	3:K:104:GLN:CD	1.87	0.94
1:A:169:PHE:CG	1:A:235:VAL:HG13	2.02	0.94
1:A:224:TYR:CE1	2:B:325:MET:CG	2.51	0.94
3:K:9:ILE:HD12	3:K:327:ILE:HD13	1.46	0.94
1:A:172:TYR:O	1:A:205:ASP:CA	2.14	0.94
3:K:14:ARG:CG	3:K:103:PRO:HG2	1.97	0.94
2:B:273:ALA:HB3	2:B:274:PRO:HD3	1.48	0.94
1:A:169:PHE:CD1	1:A:235:VAL:CB	2.50	0.94
2:B:262:PHE:CZ	3:K:271:GLU:OE2	2.20	0.94
3:K:139:TYR:CG	3:K:283:LYS:CA	2.32	0.94
3:K:208:ILE:HD13	3:K:287:ILE:HD12	1.45	0.94
1:A:175:PRO:CG	1:A:207:GLU:C	2.36	0.94
2:B:68:VAL:HG21	2:B:153:LEU:HD21	1.03	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:102:ASP:CB	3:K:103:PRO:HD3	1.97	0.94
2:B:132:LEU:HD23	2:B:164:ARG:HG3	1.50	0.94
3:K:206:HIS:HD2	3:K:208:ILE:HD11	1.32	0.94
3:K:9:ILE:HB	3:K:327:ILE:HD11	1.45	0.94
1:A:402:ARG:NH2	1:A:415:GLU:OE2	2.01	0.94
2:B:281:GLN:O	2:B:283:TYR:N	2.00	0.94
1:A:106:GLY:O	1:A:111:GLY:HA3	1.64	0.94
1:A:165:SER:CB	1:A:252:LEU:N	2.30	0.94
1:A:169:PHE:CD2	1:A:238:ILE:HB	2.01	0.94
1:A:202:PHE:CE1	1:A:378:LEU:CD2	2.51	0.94
3:K:19:ASN:HB2	3:K:198:MET:HE2	1.50	0.94
3:K:38:THR:HG22	3:K:48:VAL:HG22	1.50	0.94
1:A:251:ASP:N	1:A:254:GLU:HG3	1.83	0.94
1:A:384:ILE:N	1:A:385:ALA:HB3	1.82	0.94
2:B:103:TRP:CD2	2:B:189:LEU:CG	2.51	0.94
2:B:167:ASN:OD1	2:B:252:LEU:HD13	1.68	0.94
3:K:283:LYS:NZ	3:K:286:ARG:CD	2.31	0.94
3:K:9:ILE:HD12	3:K:327:ILE:CG2	1.98	0.94
3:K:53:LEU:HD22	3:K:104:GLN:NE2	1.83	0.94
1:A:363:VAL:O	1:A:365:GLY:N	2.01	0.93
3:K:53:LEU:HD21	3:K:104:GLN:OE1	1.67	0.93
1:A:189:LEU:CD1	1:A:417:GLU:CB	2.35	0.93
3:K:9:ILE:HD12	3:K:327:ILE:CG1	1.98	0.93
1:A:177:VAL:N	1:A:207:GLU:OE2	1.99	0.93
1:A:384:ILE:CG2	1:A:388:TRP:H	1.80	0.93
3:K:102:ASP:CB	3:K:103:PRO:CD	2.46	0.93
1:A:28:HIS:CD2	1:A:358:GLU:OE1	2.20	0.93
2:B:66:ILE:HG23	2:B:118:VAL:HG13	1.46	0.93
1:A:175:PRO:HD2	1:A:208:ALA:H	1.32	0.93
2:B:424:ASN:HA	3:K:276:HIS:CD2	2.03	0.93
1:A:169:PHE:CE1	1:A:235:VAL:CA	2.33	0.93
1:A:237:SER:HB2	1:A:376:CYS:SG	2.08	0.93
1:A:166:LYS:N	1:A:252:LEU:HB3	1.84	0.93
2:B:264:ARG:O	2:B:265:LEU:HB3	1.69	0.93
1:A:165:SER:OG	1:A:251:ASP:CG	2.06	0.93
2:B:11:GLN:HB3	6:B:602:G2P:PA	2.09	0.93
3:K:83:PHE:CE1	3:K:231:VAL:CB	2.49	0.93
3:K:88:THR:C	3:K:196:THR:OG1	2.07	0.93
1:A:103:TYR:CE1	1:A:148:GLY:HA2	2.03	0.92
1:A:382:THR:O	1:A:385:ALA:HB2	1.67	0.92
2:B:381:SER:C	2:B:383:ALA:N	2.20	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:HB3	1:A:193:THR:HG21	1.51	0.92
3:K:109:ILE:HG22	3:K:184:ILE:HD13	1.51	0.92
1:A:227:LEU:HD11	1:A:231:ILE:HD11	1.51	0.92
1:A:175:PRO:HG3	1:A:208:ALA:CB	1.99	0.92
1:A:227:LEU:CA	5:A:502:GTP:C6	2.53	0.92
3:K:9:ILE:CD1	3:K:327:ILE:CD1	2.47	0.92
3:K:20:GLU:CB	3:K:198:MET:SD	2.58	0.92
2:B:93:VAL:CG2	2:B:118:VAL:CA	2.47	0.92
3:K:62:VAL:HG23	3:K:106:MET:HE3	1.51	0.92
1:A:27:GLU:CD	1:A:358:GLU:OE2	2.08	0.92
1:A:224:TYR:CE1	2:B:325:MET:HB3	2.03	0.92
3:K:83:PHE:CD2	3:K:231:VAL:HB	2.05	0.92
1:A:169:PHE:CE1	1:A:234:ILE:CG2	2.49	0.92
1:A:298:PRO:HB3	1:A:307:PRO:HD3	1.50	0.92
2:B:90:ASP:O	2:B:121:VAL:HG21	1.68	0.92
2:B:13:GLY:CA	2:B:139:HIS:CA	2.47	0.92
3:K:274:LYS:CA	3:K:281:ASP:OD2	2.16	0.92
2:B:102:ASN:HA	2:B:408:TYR:CZ	2.05	0.91
1:A:208:ALA:HB1	1:A:304:LYS:C	1.90	0.91
1:A:227:LEU:CB	5:A:502:GTP:C4	2.00	0.91
2:B:94:PHE:N	2:B:114:LEU:CD2	1.97	0.91
3:K:231:VAL:CG1	3:K:288:LEU:HB3	1.99	0.91
3:K:83:PHE:HD2	3:K:288:LEU:CA	1.74	0.91
1:A:204:VAL:HG23	1:A:209:ILE:HD11	1.50	0.91
1:A:428:LEU:HD11	1:A:432:TYR:CZ	2.06	0.91
3:K:105:LEU:CD1	3:K:301:VAL:CB	2.48	0.91
1:A:98:ASP:HB2	1:A:105:ARG:HH21	1.35	0.91
2:B:431:GLU:HG3	3:K:274:LYS:HD3	1.52	0.91
3:K:290:ASP:O	3:K:298:THR:HG23	1.69	0.91
2:B:258:ASN:HD22	2:B:352:LYS:HZ3	0.98	0.91
1:A:175:PRO:HD2	1:A:207:GLU:N	1.83	0.91
1:A:167:LEU:N	1:A:252:LEU:CG	2.24	0.91
1:A:209:ILE:HA	1:A:212:ILE:CD1	2.00	0.91
1:A:380:ASN:HB3	1:A:432:TYR:HE1	1.14	0.91
1:A:428:LEU:HG	1:A:432:TYR:HE2	1.29	0.91
2:B:93:VAL:CG2	2:B:118:VAL:HA	1.99	0.91
1:A:31:GLN:HB3	1:A:32:PRO:HD2	1.51	0.91
1:A:224:TYR:CD2	2:B:325:MET:CG	2.39	0.91
3:K:83:PHE:CE2	3:K:291:SER:OG	2.24	0.91
3:K:105:LEU:HD11	3:K:301:VAL:CB	2.00	0.91
3:K:62:VAL:C	3:K:106:MET:HE3	1.91	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:TYR:HE2	1:A:391:LEU:HD22	1.10	0.90
2:B:6:HIS:CA	2:B:136:GLN:O	2.20	0.90
2:B:204:ILE:HG21	2:B:231:VAL:HG22	1.53	0.90
1:A:208:ALA:CB	1:A:304:LYS:O	2.18	0.90
3:K:292:LEU:HD13	3:K:320:PHE:HZ	1.20	0.90
3:K:53:LEU:CD1	3:K:104:GLN:CD	2.39	0.90
3:K:137:GLU:CD	3:K:191:ARG:HG2	1.92	0.90
1:A:137:VAL:HG11	1:A:150:THR:HG21	1.53	0.90
1:A:301:GLN:OE1	1:A:383:ALA:HB3	1.71	0.90
1:A:383:ALA:C	1:A:385:ALA:HB3	1.92	0.90
3:K:140:LEU:CD1	3:K:284:MET:SD	2.59	0.90
3:K:105:LEU:HD11	3:K:301:VAL:HG12	0.90	0.90
2:B:54:ASN:OD1	2:B:128:SER:HB2	1.70	0.90
3:K:283:LYS:HZ1	3:K:286:ARG:HB2	1.35	0.90
1:A:175:PRO:O	1:A:394:LYS:CD	2.20	0.90
1:A:176:GLN:CG	1:A:394:LYS:HZ1	1.84	0.90
2:B:93:VAL:HG11	2:B:118:VAL:HG23	0.91	0.90
2:B:94:PHE:O	2:B:114:LEU:CD2	2.11	0.90
3:K:139:TYR:CD1	3:K:283:LYS:CA	2.55	0.90
3:K:83:PHE:CD2	3:K:288:LEU:HB2	2.03	0.90
1:A:169:PHE:CE2	1:A:238:ILE:CG1	2.43	0.90
1:A:206:ASN:HB2	5:A:502:GTP:C2'	2.01	0.90
1:A:302:MET:O	1:A:303:VAL:CG2	2.20	0.90
2:B:262:PHE:CD2	2:B:435:TYR:CZ	2.60	0.90
3:K:283:LYS:HZ3	3:K:286:ARG:HD2	1.27	0.90
3:K:83:PHE:CD2	3:K:288:LEU:HB3	2.05	0.90
3:K:9:ILE:CG2	3:K:327:ILE:HD11	2.01	0.90
1:A:207:GLU:OE1	1:A:394:LYS:CE	2.15	0.90
2:B:8:GLN:OE1	2:B:67:LEU:HD22	1.72	0.90
3:K:290:ASP:O	3:K:298:THR:HG21	1.72	0.90
3:K:139:TYR:CB	3:K:284:MET:H	1.76	0.89
3:K:9:ILE:HD12	3:K:327:ILE:CD1	2.01	0.89
1:A:251:ASP:H	1:A:254:GLU:HG3	1.35	0.89
2:B:66:ILE:HD13	2:B:122:VAL:CG1	2.02	0.89
2:B:91:ASN:HD22	2:B:121:VAL:HG11	1.34	0.89
2:B:93:VAL:HB	2:B:118:VAL:CG2	1.82	0.89
1:A:136:SER:HB2	1:A:239:THR:CG2	2.00	0.89
2:B:54:ASN:OD1	2:B:128:SER:CB	2.21	0.89
1:A:119:LEU:HD23	1:A:122:ILE:HD11	1.54	0.89
1:A:185:TYR:CD2	1:A:408:TYR:HE2	1.56	0.89
3:K:53:LEU:HD13	3:K:104:GLN:OE1	1.70	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LEU:HD13	1:A:417:GLU:HG3	1.54	0.89
1:A:229:ARG:NH1	1:A:363:VAL:HG21	1.86	0.89
1:A:301:GLN:HE22	1:A:383:ALA:HB1	1.38	0.89
2:B:431:GLU:CG	3:K:274:LYS:CD	2.51	0.89
3:K:109:ILE:CG2	3:K:184:ILE:HD13	2.03	0.89
1:A:169:PHE:HZ	1:A:234:ILE:HD13	1.36	0.89
3:K:74:VAL:HG21	3:K:228:LEU:HD13	1.55	0.88
1:A:171:ILE:CG2	1:A:231:ILE:CG1	2.51	0.88
1:A:185:TYR:CG	1:A:418:PHE:CE1	2.61	0.88
2:B:103:TRP:N	2:B:408:TYR:CD2	2.42	0.88
2:B:7:ILE:HB	2:B:137:LEU:CD1	2.02	0.88
2:B:64:ARG:CD	2:B:125:GLU:CB	2.50	0.88
3:K:59:GLN:HG3	3:K:106:MET:HA	1.56	0.88
1:A:303:VAL:HB	1:A:384:ILE:HD12	0.88	0.88
1:A:202:PHE:HA	1:A:378:LEU:CD2	2.04	0.88
1:A:384:ILE:HG23	1:A:388:TRP:H	0.96	0.88
1:A:179:THR:OG1	5:A:502:GTP:C5'	2.22	0.88
2:B:66:ILE:HD11	2:B:122:VAL:HG12	1.42	0.88
2:B:264:ARG:HB2	2:B:266:HIS:CD2	2.08	0.88
3:K:283:LYS:HZ1	3:K:286:ARG:HD2	1.33	0.88
2:B:103:TRP:HE3	2:B:189:LEU:HD13	1.17	0.88
3:K:83:PHE:HB2	3:K:291:SER:HB3	1.54	0.88
3:K:283:LYS:O	3:K:286:ARG:CB	2.20	0.88
1:A:147:SER:HB2	1:A:190:THR:OG1	1.73	0.88
1:A:204:VAL:HG22	1:A:209:ILE:HD13	1.53	0.88
1:A:110:ILE:HG23	1:A:111:GLY:H	1.38	0.88
3:K:81:THR:CG2	3:K:291:SER:OG	2.21	0.88
1:A:166:LYS:N	1:A:252:LEU:CB	2.37	0.88
1:A:175:PRO:HG3	1:A:208:ALA:HB2	1.54	0.88
3:K:83:PHE:HD1	3:K:231:VAL:H	1.19	0.88
1:A:399:TYR:HA	1:A:403:ALA:HB3	1.56	0.87
1:A:267:PHE:HZ	1:A:424:ASP:OD1	1.57	0.87
2:B:97:SER:HB3	2:B:110:GLU:OE1	1.46	0.87
1:A:224:TYR:CE1	2:B:325:MET:CB	2.58	0.87
1:A:402:ARG:O	1:A:405:VAL:HG23	1.73	0.87
1:A:175:PRO:CG	1:A:207:GLU:CB	2.50	0.87
1:A:26:LEU:HD23	1:A:361:THR:HG23	1.57	0.87
2:B:311:ARG:HD3	2:B:342:TYR:HA	1.56	0.87
3:K:206:HIS:HD2	3:K:287:ILE:HD12	1.09	0.87
2:B:70:LEU:HD22	2:B:110:GLU:CB	2.04	0.87
3:K:233:LEU:HD21	3:K:288:LEU:HD11	1.53	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:TYR:CG	1:A:418:PHE:CD1	2.63	0.87
1:A:189:LEU:HD13	1:A:417:GLU:CG	2.04	0.87
2:B:52:TYR:HE1	2:B:136:GLN:HG3	1.37	0.87
1:A:122:ILE:HD12	1:A:157:LEU:HD21	1.54	0.87
1:A:224:TYR:CE1	2:B:325:MET:HG2	2.09	0.87
3:K:274:LYS:C	3:K:281:ASP:OD2	2.12	0.87
3:K:95:THR:CB	3:K:105:LEU:CB	2.44	0.87
1:A:185:TYR:HB3	1:A:418:PHE:HE1	1.39	0.87
1:A:206:ASN:CB	5:A:502:GTP:C4	2.53	0.87
2:B:52:TYR:CE1	2:B:136:GLN:HG3	2.09	0.87
1:A:175:PRO:HG2	1:A:207:GLU:C	1.94	0.87
2:B:6:HIS:CE1	2:B:8:GLN:HG2	2.10	0.87
1:A:202:PHE:CZ	1:A:255:PHE:HE2	1.93	0.86
1:A:227:LEU:N	5:A:502:GTP:O6	2.08	0.86
3:K:19:ASN:HB2	3:K:198:MET:CE	2.05	0.86
2:B:276:THR:HB	2:B:281:GLN:HG3	1.56	0.86
1:A:133:GLN:HG3	1:A:251:ASP:OD1	1.76	0.86
1:A:208:ALA:CB	1:A:304:LYS:C	2.43	0.86
1:A:298:PRO:CB	1:A:307:PRO:HD3	2.00	0.86
3:K:292:LEU:HA	3:K:300:ILE:CD1	2.05	0.86
3:K:82:ILE:O	3:K:83:PHE:HD1	1.54	0.86
2:B:204:ILE:HD13	2:B:231:VAL:HG13	1.57	0.86
3:K:139:TYR:O	3:K:283:LYS:CB	2.23	0.86
3:K:62:VAL:CG2	3:K:106:MET:H	1.87	0.86
2:B:94:PHE:HA	2:B:114:LEU:CD2	2.04	0.86
2:B:5:VAL:N	2:B:135:PHE:HA	1.90	0.86
1:A:408:TYR:HB2	1:A:418:PHE:HZ	1.39	0.86
2:B:153:LEU:O	2:B:157:ILE:HG12	1.75	0.86
3:K:291:SER:O	3:K:300:ILE:CD1	2.22	0.86
1:A:136:SER:CB	1:A:239:THR:HG21	2.00	0.86
3:K:208:ILE:HD11	3:K:287:ILE:HD12	1.55	0.86
3:K:83:PHE:CG	3:K:231:VAL:CB	2.53	0.86
1:A:109:THR:HG22	1:A:110:ILE:H	1.33	0.86
1:A:398:MET:C	1:A:403:ALA:CB	2.36	0.86
1:A:267:PHE:CE1	1:A:428:LEU:HB2	2.07	0.86
2:B:255:LEU:O	2:B:259:MET:HG3	1.75	0.86
1:A:384:ILE:HG23	1:A:387:ALA:C	1.96	0.86
2:B:94:PHE:O	2:B:114:LEU:CG	2.23	0.86
1:A:397:LEU:HD13	2:B:348:PRO:HG2	0.87	0.86
1:A:176:GLN:HG2	1:A:394:LYS:HZ3	1.41	0.86
2:B:7:ILE:CG2	2:B:137:LEU:HD13	2.06	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:PHE:CG	1:A:235:VAL:CG1	2.59	0.85
1:A:175:PRO:HD2	1:A:207:GLU:C	1.96	0.85
1:A:182:VAL:HG11	1:A:407:TRP:HE3	1.39	0.85
3:K:139:TYR:CD1	3:K:282:SER:O	2.29	0.85
2:B:360:PRO:HG2	2:B:371:LEU:HB3	1.56	0.85
1:A:224:TYR:CD2	2:B:247:GLN:HB3	2.08	0.85
2:B:195:VAL:HG13	2:B:196:GLU:HG2	1.57	0.85
2:B:250:ALA:HA	2:B:254:LYS:HE2	1.58	0.85
2:B:66:ILE:CD1	2:B:122:VAL:HG11	2.05	0.85
2:B:13:GLY:HA3	2:B:139:HIS:CA	2.05	0.85
2:B:19:LYS:HG3	2:B:228:ASN:HB3	1.57	0.85
3:K:83:PHE:HZ	3:K:229:TYR:HB3	1.41	0.85
1:A:27:GLU:CD	1:A:358:GLU:CD	2.35	0.85
2:B:234:THR:HG21	2:B:270:PRO:CB	2.06	0.85
3:K:105:LEU:HB3	3:K:108:ILE:HD11	1.58	0.85
3:K:197:ASN:O	3:K:199:ASN:OD1	1.93	0.85
1:A:185:TYR:HB3	1:A:418:PHE:CD1	2.11	0.85
2:B:242:LEU:HD22	2:B:250:ALA:H	1.42	0.85
1:A:102:ASN:ND2	1:A:411:GLU:CB	2.40	0.85
3:K:62:VAL:HG21	3:K:106:MET:N	1.90	0.85
1:A:192:HIS:HB2	1:A:424:ASP:OD2	1.76	0.85
1:A:181:VAL:HG12	1:A:404:PHE:CG	2.12	0.85
2:B:427:ASP:OD2	3:K:276:HIS:ND1	2.00	0.85
3:K:65:ALA:HB3	3:K:104:GLN:NE2	1.90	0.85
1:A:165:SER:HB3	1:A:252:LEU:HB2	0.92	0.85
1:A:202:PHE:CE1	1:A:378:LEU:HD23	2.10	0.85
2:B:150:GLY:HA2	2:B:153:LEU:HD22	1.59	0.85
3:K:102:ASP:HB3	3:K:103:PRO:HD2	1.55	0.85
1:A:204:VAL:HG23	1:A:302:MET:CG	2.05	0.85
1:A:206:ASN:HA	1:A:209:ILE:HB	1.56	0.85
1:A:195:LEU:CD2	1:A:265:GLY:HA3	2.06	0.85
3:K:283:LYS:C	3:K:283:LYS:HE2	1.96	0.85
3:K:14:ARG:NH2	3:K:102:ASP:HB3	1.91	0.85
3:K:59:GLN:HG3	3:K:106:MET:CA	2.02	0.85
3:K:62:VAL:HG21	3:K:106:MET:CA	2.07	0.85
1:A:102:ASN:CG	1:A:411:GLU:CB	2.44	0.84
1:A:405:VAL:HG22	1:A:418:PHE:HD2	1.38	0.84
2:B:431:GLU:HG3	3:K:274:LYS:CD	2.06	0.84
3:K:65:ALA:CB	3:K:104:GLN:HE22	1.88	0.84
3:K:59:GLN:CG	3:K:106:MET:HA	2.06	0.84
3:K:238:LYS:O	3:K:259:LEU:CD1	2.25	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:68:VAL:HG21	2:B:153:LEU:CG	2.08	0.84
1:A:234:ILE:HG13	1:A:270:ALA:HB1	1.59	0.84
2:B:347:ILE:C	2:B:349:ASN:H	1.80	0.84
2:B:54:ASN:ND2	2:B:125:GLU:OE1	2.09	0.84
1:A:141:PHE:CD2	1:A:172:TYR:HD1	1.94	0.84
1:A:176:GLN:C	1:A:207:GLU:CD	2.35	0.84
2:B:336:GLN:CD	2:B:349:ASN:O	2.15	0.84
3:K:206:HIS:CD2	3:K:208:ILE:HD11	2.12	0.84
2:B:431:GLU:HB2	3:K:274:LYS:HD2	0.86	0.84
3:K:107:GLY:O	3:K:110:PRO:CD	2.25	0.84
1:A:380:ASN:CB	1:A:432:TYR:HE1	1.82	0.84
3:K:83:PHE:HD2	3:K:288:LEU:CB	1.75	0.84
3:K:20:GLU:HB2	3:K:198:MET:SD	2.18	0.84
1:A:133:GLN:CD	1:A:251:ASP:OD2	2.16	0.84
2:B:10:GLY:HA2	2:B:145:THR:OG1	1.76	0.84
2:B:20:PHE:CD1	2:B:235:MET:SD	2.71	0.84
3:K:231:VAL:HG11	3:K:288:LEU:HB3	1.58	0.84
3:K:9:ILE:CB	3:K:327:ILE:HD11	2.02	0.84
3:K:9:ILE:HD11	3:K:327:ILE:HG21	1.57	0.84
1:A:264:ARG:O	1:A:266:HIS:N	2.09	0.84
1:A:261:PRO:HG2	1:A:435:VAL:CG2	2.06	0.84
1:A:165:SER:C	1:A:252:LEU:CB	2.46	0.84
1:A:101:ASN:CA	1:A:407:TRP:HH2	1.90	0.84
1:A:380:ASN:CA	1:A:432:TYR:CE1	2.60	0.83
1:A:174:ALA:HB1	5:A:502:GTP:O2'	1.78	0.83
1:A:133:GLN:HG3	1:A:251:ASP:CG	1.98	0.83
1:A:406:HIS:CB	2:B:257:VAL:HA	2.08	0.83
2:B:253:ARG:O	2:B:257:VAL:HG22	1.78	0.83
2:B:7:ILE:O	2:B:137:LEU:CD1	2.21	0.83
3:K:83:PHE:HD2	3:K:288:LEU:HB2	1.38	0.83
1:A:175:PRO:O	1:A:394:LYS:HD2	1.78	0.83
1:A:308:ARG:O	1:A:309:HIS:C	2.17	0.83
1:A:185:TYR:HD2	1:A:408:TYR:HE2	0.85	0.83
2:B:428:LEU:HA	3:K:274:LYS:HZ3	1.43	0.83
2:B:431:GLU:CG	3:K:274:LYS:HD3	2.08	0.83
1:A:172:TYR:O	1:A:204:VAL:O	1.97	0.83
1:A:209:ILE:HG23	1:A:212:ILE:HD12	0.83	0.83
1:A:195:LEU:CG	1:A:265:GLY:HA3	2.06	0.83
1:A:189:LEU:HD21	1:A:417:GLU:HA	1.60	0.83
1:A:6:SER:HA	1:A:136:SER:CB	2.07	0.83
2:B:148:GLY:O	2:B:151:THR:HG22	1.79	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:CB	1:A:193:THR:HG21	2.09	0.83
1:A:303:VAL:CG1	1:A:387:ALA:HB3	1.93	0.83
1:A:312:TYR:O	1:A:381:THR:HG21	1.79	0.83
1:A:195:LEU:HD22	1:A:265:GLY:HA3	1.59	0.83
3:K:83:PHE:CD1	3:K:231:VAL:CA	2.61	0.83
2:B:70:LEU:HD22	2:B:110:GLU:HB2	1.59	0.83
1:A:189:LEU:HD21	1:A:417:GLU:CA	2.06	0.83
1:A:171:ILE:HG23	1:A:231:ILE:HG13	1.61	0.83
1:A:304:LYS:O	1:A:305:CYS:SG	2.37	0.83
1:A:298:PRO:HB3	1:A:307:PRO:HD2	0.83	0.83
1:A:428:LEU:O	1:A:432:TYR:CD2	2.32	0.83
1:A:189:LEU:CD1	1:A:413:MET:HE1	2.02	0.82
3:K:143:ILE:HD11	3:K:282:SER:O	1.78	0.82
3:K:139:TYR:O	3:K:283:LYS:HB2	1.77	0.82
3:K:208:ILE:HD11	3:K:287:ILE:CD1	2.08	0.82
1:A:224:TYR:HD2	2:B:247:GLN:CB	1.92	0.82
1:A:269:LEU:CD1	1:A:384:ILE:HB	2.02	0.82
2:B:110:GLU:O	2:B:113:GLU:HG2	1.79	0.82
2:B:191:VAL:HG11	2:B:425:MET:HG3	1.60	0.82
1:A:165:SER:C	1:A:252:LEU:HD12	1.98	0.82
1:A:169:PHE:HD2	1:A:238:ILE:CB	1.84	0.82
1:A:206:ASN:HB2	5:A:502:GTP:O2'	1.78	0.82
1:A:428:LEU:CG	1:A:432:TYR:CE2	2.62	0.82
3:K:292:LEU:CD2	3:K:320:PHE:HZ	1.93	0.82
3:K:59:GLN:CA	3:K:106:MET:CB	2.58	0.82
1:A:210:TYR:CE1	5:A:502:GTP:N1	2.47	0.82
2:B:431:GLU:HB3	3:K:274:LYS:CE	2.09	0.82
2:B:209:LEU:HB3	2:B:227:LEU:HD22	1.59	0.82
3:K:59:GLN:HE22	3:K:100:LEU:HA	1.43	0.82
1:A:262:TYR:O	1:A:266:HIS:HD2	1.54	0.82
3:K:59:GLN:CB	3:K:106:MET:HB2	2.06	0.82
1:A:348:PRO:O	1:A:349:THR:OG1	1.96	0.82
1:A:362:VAL:HG13	1:A:368:LEU:HD12	1.61	0.82
2:B:264:ARG:HB2	2:B:266:HIS:HD2	1.45	0.82
1:A:224:TYR:CD1	2:B:325:MET:HG2	2.14	0.82
2:B:156:LYS:HE2	2:B:156:LYS:HA	1.61	0.82
1:A:175:PRO:O	1:A:394:LYS:NZ	2.12	0.81
3:K:95:THR:O	3:K:108:ILE:HG13	1.80	0.81
2:B:10:GLY:CA	6:B:602:G2P:O2B	2.28	0.81
1:A:188:ILE:O	1:A:421:ALA:HB1	1.78	0.81
3:K:59:GLN:O	3:K:62:VAL:CG2	2.29	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:137:GLU:OE2	3:K:192:HIS:N	2.12	0.81
1:A:301:GLN:NE2	1:A:383:ALA:HB1	1.94	0.81
1:A:101:ASN:CA	1:A:407:TRP:CH2	2.64	0.81
1:A:248:LEU:HD23	1:A:353:VAL:O	1.80	0.81
1:A:191:THR:OG1	1:A:267:PHE:CD2	2.29	0.81
1:A:202:PHE:HD1	1:A:378:LEU:CG	1.92	0.81
3:K:83:PHE:HE1	3:K:231:VAL:N	1.75	0.81
2:B:427:ASP:OD2	3:K:274:LYS:HB3	1.80	0.81
1:A:109:THR:CG2	1:A:110:ILE:N	2.44	0.81
1:A:267:PHE:CD1	1:A:267:PHE:N	2.49	0.81
2:B:69:ASP:N	2:B:149:MET:CE	2.44	0.81
2:B:20:PHE:CZ	2:B:24:ILE:HD12	2.15	0.81
2:B:10:GLY:HA3	6:B:602:G2P:O2B	1.80	0.81
1:A:169:PHE:CE2	1:A:234:ILE:HD13	2.13	0.81
3:K:283:LYS:HZ3	3:K:286:ARG:CD	1.90	0.81
2:B:100:GLY:HA3	2:B:105:LYS:HD3	1.62	0.81
1:A:169:PHE:HD2	1:A:235:VAL:O	1.63	0.81
1:A:7:ILE:HG22	1:A:66:VAL:HG22	1.63	0.81
2:B:324:SER:HB3	2:B:327:GLU:HG2	1.60	0.81
2:B:431:GLU:CG	3:K:274:LYS:HD2	2.11	0.80
2:B:54:ASN:HD21	2:B:64:ARG:HD3	1.46	0.80
2:B:262:PHE:CZ	3:K:271:GLU:CD	2.53	0.80
3:K:14:ARG:HD2	3:K:95:THR:HG21	1.62	0.80
2:B:287:THR:O	2:B:288:VAL:HG23	1.78	0.80
1:A:169:PHE:HD1	1:A:235:VAL:HG22	0.98	0.80
1:A:192:HIS:CB	1:A:424:ASP:OD2	2.30	0.80
2:B:147:SER:HB2	2:B:190:SER:HB3	1.63	0.80
2:B:136:GLN:NE2	2:B:239:THR:HG21	1.95	0.80
3:K:62:VAL:HG23	3:K:106:MET:CE	2.11	0.80
3:K:137:GLU:CD	3:K:191:ARG:HA	2.01	0.80
1:A:143:GLY:HA3	5:A:502:GTP:O2G	1.81	0.80
1:A:205:ASP:C	1:A:209:ILE:HD12	2.01	0.80
1:A:171:ILE:HG23	1:A:231:ILE:CD1	2.12	0.80
2:B:70:LEU:CD1	2:B:145:THR:HG22	2.12	0.80
1:A:220:GLU:C	1:A:222:PRO:HD3	2.01	0.80
2:B:103:TRP:CD1	2:B:189:LEU:HB3	2.12	0.80
3:K:277:VAL:H	3:K:278:PRO:HD3	1.46	0.80
3:K:281:ASP:O	3:K:282:SER:CB	2.29	0.80
1:A:173:PRO:O	1:A:391:LEU:HD11	1.81	0.80
2:B:236:SER:O	2:B:240:THR:CG2	2.29	0.80
1:A:406:HIS:HB3	2:B:257:VAL:HA	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:9:ILE:HD11	3:K:295:ASN:OD1	1.80	0.80
1:A:100:ALA:CB	1:A:105:ARG:HD3	2.11	0.80
1:A:141:PHE:CD2	1:A:172:TYR:CD1	2.69	0.80
1:A:182:VAL:HG11	1:A:408:TYR:CD2	2.11	0.80
2:B:97:SER:HB2	2:B:110:GLU:CG	2.12	0.80
3:K:139:TYR:C	3:K:283:LYS:CB	2.48	0.80
1:A:241:SER:O	1:A:244:PHE:HB3	1.82	0.80
3:K:14:ARG:CZ	3:K:103:PRO:CG	2.59	0.80
1:A:176:GLN:CA	1:A:394:LYS:NZ	2.34	0.79
2:B:97:SER:HB2	2:B:110:GLU:CD	2.03	0.79
2:B:413:MET:HG3	2:B:414:ASP:H	1.47	0.79
1:A:132:LEU:HD23	1:A:132:LEU:H	1.46	0.79
2:B:97:SER:HB3	2:B:110:GLU:OE2	1.82	0.79
1:A:173:PRO:O	1:A:205:ASP:OD2	1.99	0.79
1:A:398:MET:HG2	2:B:349:ASN:CB	2.12	0.79
3:K:62:VAL:HG23	3:K:106:MET:HG3	0.79	0.79
3:K:184:ILE:CG1	3:K:209:PHE:CE2	2.66	0.79
1:A:20:CYS:HB2	1:A:236:SER:HB2	1.64	0.79
2:B:136:GLN:NE2	2:B:239:THR:CG2	2.46	0.79
2:B:346:TRP:HB3	2:B:349:ASN:ND2	1.97	0.79
1:A:259:LEU:O	1:A:380:ASN:ND2	2.15	0.79
2:B:196:GLU:OE1	3:K:280:ARG:CD	2.31	0.79
3:K:83:PHE:CZ	3:K:229:TYR:HB3	2.17	0.79
3:K:194:ALA:O	3:K:195:VAL:HG13	1.83	0.79
1:A:173:PRO:C	1:A:205:ASP:CG	2.41	0.79
3:K:62:VAL:CG2	3:K:106:MET:HB3	2.13	0.79
3:K:106:MET:SD	3:K:106:MET:N	2.56	0.79
2:B:396:THR:HG23	2:B:422:GLU:OE2	1.83	0.79
1:A:175:PRO:CD	1:A:207:GLU:C	2.51	0.79
2:B:265:LEU:HD12	2:B:265:LEU:O	1.83	0.79
3:K:231:VAL:HG11	3:K:288:LEU:CB	2.13	0.79
1:A:177:VAL:H	1:A:207:GLU:CD	1.80	0.78
1:A:22:GLU:CD	1:A:364:PRO:HD3	2.03	0.78
2:B:262:PHE:CD2	2:B:435:TYR:CE1	2.71	0.78
3:K:216:GLU:HG3	3:K:223:LYS:HG2	1.63	0.78
1:A:234:ILE:HG21	1:A:302:MET:HE1	1.65	0.78
3:K:197:ASN:O	3:K:199:ASN:CG	2.21	0.78
2:B:35:SER:HB3	2:B:59:ASN:HA	1.65	0.78
1:A:399:TYR:HA	1:A:403:ALA:CB	2.14	0.78
3:K:14:ARG:NH2	3:K:94:HIS:CD2	2.51	0.78
2:B:347:ILE:HB	2:B:348:PRO:CD	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:ARG:HH21	1:A:252:LEU:H	0.80	0.78
2:B:100:GLY:H	2:B:105:LYS:HD3	1.46	0.78
1:A:69:ASP:HA	1:A:145:THR:HG21	1.66	0.78
1:A:173:PRO:HB2	1:A:391:LEU:HD21	1.66	0.78
1:A:200:CYS:CB	1:A:255:PHE:HB3	2.14	0.78
1:A:182:VAL:HG11	1:A:407:TRP:CE3	2.18	0.78
2:B:259:MET:HA	2:B:314:THR:HG21	1.65	0.78
3:K:281:ASP:O	3:K:282:SER:HB3	1.82	0.78
3:K:19:ASN:C	3:K:19:ASN:HD22	1.87	0.78
1:A:165:SER:OG	1:A:253:THR:N	2.17	0.78
3:K:62:VAL:HG21	3:K:106:MET:H	1.46	0.78
2:B:256:ALA:O	2:B:260:VAL:HG22	1.83	0.78
1:A:200:CYS:HB2	1:A:255:PHE:HB3	1.64	0.78
1:A:301:GLN:CD	1:A:383:ALA:CB	2.40	0.78
1:A:185:TYR:CE1	1:A:418:PHE:CD2	2.72	0.78
1:A:204:VAL:HG22	1:A:209:ILE:CD1	2.11	0.78
1:A:231:ILE:HA	1:A:234:ILE:HG22	1.66	0.78
1:A:262:TYR:O	1:A:266:HIS:NE2	2.17	0.78
2:B:6:HIS:CD2	2:B:138:THR:HG23	2.18	0.78
1:A:209:ILE:CA	1:A:212:ILE:HD12	2.13	0.77
1:A:204:VAL:HG11	1:A:231:ILE:HG23	0.80	0.77
1:A:269:LEU:HD12	1:A:382:THR:OG1	1.84	0.77
2:B:167:ASN:HD21	2:B:252:LEU:CD2	1.91	0.77
3:K:105:LEU:CD1	3:K:301:VAL:HB	2.14	0.77
3:K:62:VAL:HG23	3:K:106:MET:SD	2.24	0.77
2:B:104:ALA:CB	2:B:413:MET:HE1	2.14	0.77
3:K:14:ARG:NE	3:K:103:PRO:HD2	1.89	0.77
1:A:304:LYS:O	1:A:305:CYS:CB	2.32	0.77
1:A:398:MET:CG	1:A:404:PHE:HE1	1.96	0.77
2:B:428:LEU:HA	3:K:274:LYS:NZ	1.99	0.77
1:A:269:LEU:HD11	1:A:384:ILE:CA	2.10	0.77
1:A:301:GLN:OE1	1:A:383:ALA:CB	2.33	0.77
2:B:165:ILE:HG13	2:B:252:LEU:HD12	1.66	0.77
2:B:266:HIS:CG	2:B:432:TYR:CZ	2.72	0.77
2:B:205:ASP:OD2	2:B:304:ALA:CA	2.33	0.77
1:A:202:PHE:HA	1:A:378:LEU:HD21	1.66	0.77
1:A:303:VAL:CG1	1:A:384:ILE:CB	2.62	0.77
1:A:210:TYR:OH	5:A:502:GTP:N7	2.17	0.77
2:B:262:PHE:CG	2:B:435:TYR:CZ	2.73	0.77
3:K:19:ASN:HD21	3:K:22:GLU:HG3	1.49	0.77
2:B:100:GLY:N	2:B:105:LYS:CD	2.44	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:TYR:CB	1:A:418:PHE:CD1	2.66	0.77
1:A:165:SER:CB	1:A:252:LEU:CA	2.62	0.77
1:A:186:ASN:ND2	1:A:408:TYR:HE1	1.82	0.77
1:A:210:TYR:CZ	5:A:502:GTP:N7	2.52	0.77
2:B:259:MET:HG2	2:B:314:THR:HG21	1.67	0.77
1:A:11:GLN:HG3	1:A:74:VAL:CG1	2.13	0.77
1:A:362:VAL:HG13	1:A:368:LEU:CG	2.13	0.77
2:B:68:VAL:CG1	2:B:153:LEU:HD21	2.15	0.77
2:B:7:ILE:HG22	2:B:137:LEU:CD1	2.14	0.77
1:A:110:ILE:HG23	1:A:111:GLY:N	1.99	0.77
1:A:399:TYR:O	1:A:401:LYS:N	2.18	0.77
2:B:267:PHE:CD1	2:B:388:PHE:HE2	2.02	0.77
1:A:179:THR:HG22	2:B:248:LEU:HD13	0.84	0.76
1:A:407:TRP:HA	2:B:257:VAL:HG23	1.67	0.76
2:B:168:THR:HB	2:B:201:THR:HG23	1.67	0.76
1:A:398:MET:HG2	2:B:349:ASN:HB3	1.66	0.76
2:B:70:LEU:HD11	2:B:106:GLY:HA2	0.79	0.76
2:B:205:ASP:OD2	2:B:304:ALA:CB	2.34	0.76
2:B:66:ILE:HD13	2:B:122:VAL:HG12	1.59	0.76
2:B:205:ASP:OD2	2:B:304:ALA:HB2	1.86	0.76
2:B:192:HIS:ND1	2:B:424:ASN:OD1	2.18	0.76
2:B:174:SER:HB2	2:B:207:GLU:OE1	1.84	0.76
1:A:202:PHE:CE1	1:A:378:LEU:HB3	2.20	0.76
1:A:204:VAL:CG2	1:A:302:MET:CB	2.30	0.76
1:A:203:MET:HB3	1:A:388:TRP:HH2	1.51	0.76
3:K:9:ILE:HB	3:K:327:ILE:HD12	0.77	0.76
3:K:132:LYS:HE2	3:K:214:LYS:HE3	1.68	0.76
1:A:185:TYR:CE1	1:A:418:PHE:CG	2.73	0.76
1:A:208:ALA:HB3	1:A:303:VAL:C	2.05	0.76
2:B:7:ILE:CG2	2:B:137:LEU:CD1	2.63	0.76
3:K:9:ILE:CG2	3:K:327:ILE:HD13	2.06	0.76
1:A:401:LYS:NZ	2:B:346:TRP:HE1	1.83	0.76
2:B:95:GLY:N	2:B:114:LEU:HD22	1.96	0.76
1:A:163:LYS:O	1:A:164:LYS:HG2	1.86	0.76
1:A:221:ARG:HD3	1:A:221:ARG:O	1.85	0.76
1:A:223:THR:HB	1:A:225:THR:HG22	1.67	0.76
1:A:407:TRP:CZ3	1:A:408:TYR:CE1	2.74	0.76
1:A:176:GLN:CB	1:A:394:LYS:HZ1	1.98	0.76
1:A:210:TYR:CE1	5:A:502:GTP:C4	2.73	0.76
2:B:234:THR:CG2	2:B:270:PRO:HB2	2.11	0.76
1:A:331:ALA:O	1:A:335:ILE:HG12	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ALA:HA	1:A:207:GLU:H	1.51	0.75
1:A:276:ILE:HG23	1:A:369:ALA:CB	2.16	0.75
1:A:388:TRP:CD1	1:A:432:TYR:CE2	2.75	0.75
2:B:262:PHE:HZ	3:K:271:GLU:CD	1.88	0.75
2:B:264:ARG:HD3	3:K:274:LYS:CG	2.16	0.75
2:B:2:ARG:O	2:B:51:VAL:HG22	1.86	0.75
3:K:38:THR:CG2	3:K:48:VAL:HG22	2.16	0.75
1:A:6:SER:CA	1:A:136:SER:HB3	2.15	0.75
1:A:172:TYR:CZ	1:A:391:LEU:HD23	2.20	0.75
1:A:226:ASN:HB2	5:A:502:GTP:O6	1.87	0.75
1:A:172:TYR:N	1:A:204:VAL:O	2.19	0.75
2:B:5:VAL:H	2:B:135:PHE:CA	1.99	0.75
1:A:227:LEU:HB2	5:A:502:GTP:C2	2.21	0.75
1:A:401:LYS:HZ2	2:B:346:TRP:HE1	1.32	0.75
2:B:102:ASN:HA	2:B:408:TYR:CE2	2.20	0.75
2:B:12:CYS:CB	2:B:140:SER:HB3	2.16	0.75
2:B:6:HIS:NE2	2:B:138:THR:CG2	2.50	0.75
3:K:83:PHE:CG	3:K:291:SER:CB	2.68	0.75
3:K:137:GLU:OE2	3:K:205:SER:OG	2.04	0.75
1:A:172:TYR:CD2	1:A:388:TRP:CH2	2.75	0.75
1:A:4:CYS:HB3	1:A:243:ARG:CB	2.16	0.75
1:A:266:HIS:HE1	1:A:431:ASP:OD1	1.67	0.75
1:A:381:THR:O	1:A:385:ALA:HB2	1.85	0.75
2:B:64:ARG:NH1	2:B:128:SER:OG	2.20	0.75
2:B:250:ALA:HB1	2:B:254:LYS:HB2	1.69	0.75
2:B:8:GLN:CD	2:B:67:LEU:HD22	2.07	0.75
3:K:276:HIS:HB3	3:K:278:PRO:CD	2.17	0.75
1:A:225:THR:O	1:A:229:ARG:HG3	1.85	0.75
1:A:227:LEU:HB3	5:A:502:GTP:C8	2.21	0.75
2:B:64:ARG:HD2	2:B:125:GLU:HB3	1.65	0.75
2:B:9:ALA:HB2	2:B:150:GLY:HA2	1.67	0.75
3:K:295:ASN:OD1	3:K:329:ASN:OD1	2.03	0.75
1:A:203:MET:SD	1:A:267:PHE:HB3	2.27	0.75
1:A:268:PRO:HA	1:A:380:ASN:HA	1.67	0.75
2:B:103:TRP:CG	2:B:189:LEU:HB2	2.12	0.75
1:A:102:ASN:HD22	1:A:412:GLY:N	1.79	0.74
1:A:172:TYR:CE2	1:A:391:LEU:HD21	2.20	0.74
1:A:181:VAL:HG11	1:A:404:PHE:CD2	2.21	0.74
1:A:428:LEU:HD11	1:A:432:TYR:OH	1.87	0.74
2:B:13:GLY:HA2	2:B:139:HIS:CA	2.15	0.74
2:B:243:ARG:HH22	2:B:252:LEU:HG	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:59:GLN:NE2	3:K:100:LEU:HA	2.00	0.74
3:K:89:SER:OG	3:K:197:ASN:N	2.19	0.74
3:K:95:THR:OG1	3:K:105:LEU:CB	2.35	0.74
1:A:186:ASN:HD21	1:A:408:TYR:HE1	1.32	0.74
1:A:227:LEU:O	1:A:227:LEU:HD12	1.87	0.74
1:A:407:TRP:CD1	2:B:258:ASN:ND2	2.55	0.74
2:B:11:GLN:HB3	6:B:602:G2P:O1A	1.86	0.74
2:B:196:GLU:OE1	3:K:280:ARG:HD2	1.87	0.74
1:A:27:GLU:OE2	1:A:358:GLU:OE2	2.05	0.74
1:A:122:ILE:HB	1:A:135:PHE:HE1	1.52	0.74
2:B:266:HIS:CG	2:B:432:TYR:OH	2.41	0.74
2:B:100:GLY:H	2:B:105:LYS:CD	2.00	0.74
2:B:64:ARG:HD2	2:B:125:GLU:C	2.08	0.74
2:B:266:HIS:CA	2:B:432:TYR:OH	2.36	0.74
2:B:102:ASN:C	2:B:408:TYR:CE2	2.61	0.74
1:A:7:ILE:HD12	1:A:153:LEU:HD21	1.67	0.74
1:A:165:SER:OG	1:A:252:LEU:N	2.20	0.74
1:A:188:ILE:C	1:A:421:ALA:CB	2.44	0.74
2:B:100:GLY:H	2:B:105:LYS:CE	2.00	0.74
1:A:16:ILE:HD11	1:A:231:ILE:O	1.87	0.74
1:A:308:ARG:O	1:A:309:HIS:O	2.05	0.74
1:A:404:PHE:HB3	2:B:258:ASN:OD1	1.87	0.74
2:B:91:ASN:ND2	2:B:121:VAL:HG11	2.03	0.74
2:B:196:GLU:CD	3:K:280:ARG:HH11	1.90	0.74
3:K:206:HIS:HB3	3:K:284:MET:HG3	1.68	0.74
3:K:9:ILE:CB	3:K:327:ILE:HD12	1.71	0.74
1:A:362:VAL:CG1	1:A:368:LEU:HB2	2.18	0.74
1:A:189:LEU:HD13	1:A:413:MET:SD	2.28	0.74
1:A:210:TYR:CD1	5:A:502:GTP:N1	2.55	0.74
1:A:312:TYR:CD1	1:A:381:THR:HG22	1.76	0.74
1:A:143:GLY:CA	5:A:502:GTP:O2G	2.36	0.74
2:B:267:PHE:CZ	2:B:428:LEU:HD21	2.22	0.74
2:B:102:ASN:CA	2:B:408:TYR:CE2	2.71	0.74
2:B:209:LEU:HG	2:B:230:LEU:HD22	1.69	0.74
1:A:103:TYR:CD1	1:A:148:GLY:CA	2.71	0.74
1:A:172:TYR:CE2	1:A:388:TRP:CE3	2.76	0.74
1:A:242:LEU:HG	1:A:250:VAL:O	1.88	0.74
1:A:105:ARG:N	1:A:412:GLY:HA3	2.01	0.74
2:B:19:LYS:HG3	2:B:228:ASN:CB	2.17	0.74
3:K:290:ASP:HA	3:K:295:ASN:HB3	1.70	0.74
3:K:83:PHE:CB	3:K:291:SER:CB	2.65	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:ILE:HD13	2:B:136:GLN:HE21	1.53	0.73
1:A:176:GLN:HA	1:A:394:LYS:HZ1	1.51	0.73
2:B:7:ILE:CB	2:B:137:LEU:CD1	2.62	0.73
2:B:217:LEU:C	2:B:219:LEU:H	1.90	0.73
2:B:94:PHE:HA	2:B:114:LEU:HD21	1.66	0.73
3:K:139:TYR:CA	3:K:206:HIS:CE1	2.26	0.73
3:K:139:TYR:CA	3:K:283:LYS:CB	2.51	0.73
3:K:95:THR:HB	3:K:105:LEU:C	2.08	0.73
2:B:217:LEU:O	2:B:219:LEU:N	2.22	0.73
1:A:101:ASN:CB	1:A:407:TRP:CZ2	2.40	0.73
1:A:264:ARG:C	1:A:266:HIS:H	1.91	0.73
1:A:303:VAL:CG1	1:A:384:ILE:CG1	2.59	0.73
3:K:14:ARG:HG3	3:K:103:PRO:HB2	1.70	0.73
1:A:362:VAL:HG13	1:A:368:LEU:CD1	2.19	0.73
2:B:66:ILE:HD11	2:B:122:VAL:HG11	1.66	0.73
3:K:276:HIS:HB2	3:K:281:ASP:HB3	1.70	0.73
3:K:292:LEU:CD2	3:K:320:PHE:CZ	2.71	0.73
3:K:292:LEU:CD1	3:K:320:PHE:HZ	1.65	0.73
3:K:65:ALA:HB2	3:K:104:GLN:NE2	2.01	0.73
2:B:100:GLY:H	2:B:105:LYS:NZ	1.86	0.73
1:A:181:VAL:HG21	2:B:352:LYS:HZ2	1.54	0.73
1:A:313:MET:HG3	1:A:315:CYS:SG	2.29	0.73
1:A:105:ARG:H	1:A:412:GLY:HA3	1.52	0.73
1:A:172:TYR:OH	1:A:391:LEU:HD23	1.89	0.73
1:A:63:PRO:O	1:A:64:ARG:HG2	1.88	0.73
1:A:169:PHE:CG	1:A:235:VAL:HG22	2.21	0.73
2:B:111:GLY:O	2:B:115:VAL:HG23	1.89	0.73
2:B:267:PHE:CD2	2:B:388:PHE:HZ	2.07	0.73
3:K:105:LEU:CD1	3:K:301:VAL:HG12	1.86	0.73
2:B:274:PRO:HG2	2:B:371:LEU:HD21	1.69	0.73
1:A:202:PHE:CD1	1:A:378:LEU:CG	2.69	0.73
1:A:169:PHE:HB3	1:A:235:VAL:HG13	0.73	0.73
1:A:380:ASN:CA	1:A:432:TYR:CD1	2.71	0.73
2:B:93:VAL:HG12	2:B:114:LEU:HG	0.73	0.73
1:A:202:PHE:HD1	1:A:378:LEU:HD22	0.90	0.73
1:A:269:LEU:CD1	1:A:384:ILE:CB	2.60	0.73
2:B:138:THR:HG22	2:B:235:MET:CE	2.19	0.73
2:B:69:ASP:N	2:B:149:MET:SD	2.61	0.73
2:B:94:PHE:N	2:B:114:LEU:HD11	2.04	0.73
3:K:59:GLN:HG2	3:K:106:MET:C	2.08	0.73
2:B:76:ASP:HA	2:B:79:ARG:HG2	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:PHE:HZ	1:A:255:PHE:HE2	1.37	0.72
2:B:262:PHE:CE1	3:K:271:GLU:OE1	2.42	0.72
3:K:231:VAL:CB	3:K:288:LEU:HB3	2.19	0.72
3:K:19:ASN:ND2	3:K:22:GLU:HG3	2.03	0.72
1:A:317:LEU:HB3	1:A:319:TYR:HE1	1.52	0.72
2:B:242:LEU:HD13	2:B:250:ALA:C	2.08	0.72
1:A:362:VAL:HG11	1:A:368:LEU:O	1.89	0.72
1:A:234:ILE:HD13	1:A:234:ILE:O	1.81	0.72
1:A:313:MET:SD	1:A:382:THR:N	2.62	0.72
2:B:12:CYS:HB3	2:B:140:SER:OG	1.89	0.72
2:B:191:VAL:CG1	2:B:425:MET:HG3	2.19	0.72
1:A:165:SER:CB	1:A:243:ARG:HH21	1.98	0.72
1:A:242:LEU:HD21	1:A:250:VAL:HB	1.71	0.72
3:K:27:ASP:HA	3:K:28:LYS:NZ	2.05	0.72
1:A:31:GLN:HB3	1:A:32:PRO:CD	2.18	0.72
1:A:105:ARG:O	1:A:110:ILE:CG2	2.33	0.72
1:A:303:VAL:HG11	1:A:384:ILE:CB	2.18	0.72
2:B:93:VAL:CG1	2:B:114:LEU:C	2.58	0.72
1:A:209:ILE:CA	1:A:212:ILE:CD1	2.68	0.72
2:B:6:HIS:HE1	2:B:8:GLN:HG2	1.52	0.72
1:A:112:LYS:O	1:A:115:ILE:HG22	1.89	0.72
1:A:174:ALA:CB	5:A:502:GTP:O3'	2.38	0.72
1:A:202:PHE:HE1	1:A:378:LEU:HB3	1.55	0.72
1:A:407:TRP:HZ3	1:A:408:TYR:CE1	2.06	0.72
3:K:63:TYR:CA	3:K:106:MET:CE	2.59	0.72
3:K:137:GLU:HG2	3:K:205:SER:CB	2.19	0.72
1:A:172:TYR:CE2	1:A:391:LEU:HD23	2.17	0.71
1:A:165:SER:HB3	1:A:252:LEU:H	1.41	0.71
2:B:243:ARG:NH2	2:B:252:LEU:HG	2.05	0.71
3:K:324:ALA:C	3:K:327:ILE:HG13	2.06	0.71
1:A:12:ALA:HB3	1:A:140:SER:OG	1.91	0.71
1:A:176:GLN:CG	1:A:394:LYS:HZ3	1.98	0.71
2:B:138:THR:HG22	2:B:235:MET:HE1	1.71	0.71
2:B:237:GLY:O	2:B:241:CYS:HB3	1.91	0.71
2:B:48:ARG:HG2	2:B:243:ARG:O	1.90	0.71
1:A:165:SER:HB2	1:A:243:ARG:CZ	2.13	0.71
1:A:208:ALA:HB3	1:A:303:VAL:CA	2.21	0.71
2:B:2:ARG:HD3	2:B:130:ASP:OD2	1.91	0.71
1:A:171:ILE:HG23	1:A:231:ILE:CG1	2.18	0.71
1:A:269:LEU:CD2	1:A:388:TRP:NE1	2.53	0.71
1:A:25:CYS:HB2	1:A:30:ILE:O	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:CYS:HB3	1:A:377:MET:HE2	1.70	0.71
3:K:9:ILE:HD12	3:K:327:ILE:CB	2.20	0.71
1:A:402:ARG:NH2	1:A:415:GLU:CD	2.30	0.71
1:A:176:GLN:CA	1:A:394:LYS:HZ1	2.04	0.71
1:A:400:ALA:O	1:A:401:LYS:HB2	1.91	0.71
1:A:5:ILE:HD11	1:A:135:PHE:HE1	1.49	0.71
3:K:231:VAL:HB	3:K:288:LEU:HB3	1.73	0.71
1:A:178:SER:CA	5:A:502:GTP:O3'	2.33	0.71
2:B:431:GLU:OE1	2:B:432:TYR:HA	1.91	0.71
3:K:231:VAL:HG22	3:K:287:ILE:HG22	1.73	0.71
2:B:204:ILE:CG2	2:B:209:LEU:HD11	2.21	0.71
1:A:27:GLU:OE1	1:A:358:GLU:HG3	1.90	0.71
3:K:120:ILE:HG23	3:K:129:PHE:CD2	2.25	0.71
1:A:165:SER:CB	1:A:253:THR:H	2.04	0.71
1:A:148:GLY:O	1:A:151:SER:HB2	1.91	0.70
1:A:182:VAL:CG1	1:A:407:TRP:CE3	2.73	0.70
1:A:269:LEU:CD1	1:A:384:ILE:N	2.54	0.70
1:A:22:GLU:OE1	1:A:364:PRO:HD3	1.91	0.70
2:B:70:LEU:CD2	2:B:111:GLY:CA	2.66	0.70
1:A:88:HIS:C	1:A:90:GLU:H	1.94	0.70
1:A:192:HIS:HA	1:A:195:LEU:HD12	1.72	0.70
2:B:8:GLN:NE2	2:B:17:GLY:HA3	2.06	0.70
2:B:356:CYS:SG	2:B:357:ASP:N	2.63	0.70
1:A:317:LEU:HD12	1:A:351:PHE:HD1	1.56	0.70
1:A:202:PHE:HD1	1:A:378:LEU:CD2	1.51	0.70
2:B:64:ARG:HD2	2:B:125:GLU:O	1.90	0.70
1:A:175:PRO:HD3	1:A:208:ALA:H	1.49	0.70
1:A:173:PRO:O	1:A:391:LEU:CD1	2.38	0.70
1:A:400:ALA:O	1:A:401:LYS:HD2	1.91	0.70
1:A:315:CYS:HA	1:A:379:SER:OG	1.92	0.70
1:A:384:ILE:HA	1:A:385:ALA:C	2.09	0.70
2:B:4:ILE:HG21	2:B:136:GLN:HG2	1.72	0.70
1:A:165:SER:OG	1:A:251:ASP:OD1	2.05	0.70
2:B:10:GLY:O	2:B:14:ASN:HB2	1.91	0.70
1:A:237:SER:CB	1:A:376:CYS:SG	2.80	0.70
1:A:202:PHE:CD1	1:A:378:LEU:CB	2.73	0.70
1:A:204:VAL:HG23	1:A:209:ILE:HD13	1.52	0.70
1:A:63:PRO:C	1:A:64:ARG:HG2	2.12	0.70
2:B:66:ILE:HD13	2:B:118:VAL:HG12	1.71	0.70
3:K:276:HIS:HB3	3:K:278:PRO:HD2	1.73	0.70
1:A:269:LEU:CD1	1:A:384:ILE:H	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:291:LEU:O	2:B:295:MET:HG3	1.91	0.70
1:A:399:TYR:O	1:A:400:ALA:C	2.30	0.70
2:B:267:PHE:CE1	2:B:428:LEU:HD21	2.27	0.70
3:K:231:VAL:CG2	3:K:287:ILE:HG22	2.21	0.70
1:A:137:VAL:HG11	1:A:150:THR:CG2	2.21	0.70
1:A:175:PRO:HG2	1:A:207:GLU:CB	2.21	0.70
1:A:195:LEU:HD23	1:A:265:GLY:O	1.86	0.70
1:A:269:LEU:HD22	1:A:384:ILE:HG22	1.73	0.70
3:K:14:ARG:CG	3:K:103:PRO:CG	2.70	0.70
1:A:362:VAL:HG13	1:A:368:LEU:HB2	1.73	0.70
1:A:135:PHE:O	1:A:252:LEU:HD11	1.91	0.69
3:K:290:ASP:OD1	3:K:295:ASN:CB	2.40	0.69
1:A:224:TYR:CZ	2:B:325:MET:CB	2.75	0.69
2:B:336:GLN:HG3	2:B:351:VAL:HG21	1.74	0.69
3:K:63:TYR:N	3:K:106:MET:HE3	2.06	0.69
1:A:209:ILE:HG23	1:A:212:ILE:HD13	1.70	0.69
1:A:23:LEU:CD1	1:A:361:THR:C	2.60	0.69
3:K:233:LEU:HD21	3:K:288:LEU:CD1	2.14	0.69
3:K:79:ASN:HD21	3:K:226:GLY:HA2	1.56	0.69
1:A:133:GLN:CG	1:A:251:ASP:CG	2.60	0.69
1:A:195:LEU:CD2	1:A:265:GLY:CA	2.63	0.69
1:A:408:TYR:CD2	1:A:418:PHE:CZ	2.81	0.69
1:A:222:PRO:HD2	2:B:326:LYS:HB3	1.74	0.69
2:B:427:ASP:CG	3:K:276:HIS:CG	2.60	0.69
3:K:292:LEU:CG	3:K:320:PHE:HZ	2.04	0.69
1:A:229:ARG:NH1	1:A:363:VAL:CG2	2.55	0.69
2:B:424:ASN:HA	3:K:276:HIS:HD2	1.57	0.69
2:B:359:PRO:HB2	2:B:360:PRO:HD2	1.74	0.69
3:K:79:ASN:ND2	3:K:226:GLY:HA2	2.07	0.69
1:A:158:SER:HB2	1:A:197:HIS:HD2	1.57	0.69
1:A:312:TYR:C	1:A:313:MET:HG2	2.12	0.69
1:A:189:LEU:HD11	1:A:413:MET:CE	2.05	0.69
2:B:234:THR:O	2:B:238:VAL:HG23	1.91	0.69
2:B:262:PHE:CZ	2:B:435:TYR:CE1	2.79	0.69
1:A:185:TYR:CD1	1:A:418:PHE:CD2	2.81	0.69
3:K:206:HIS:CD2	3:K:208:ILE:CD1	2.75	0.69
1:A:406:HIS:HB2	2:B:257:VAL:CA	2.23	0.69
2:B:325:MET:HE3	2:B:325:MET:HA	1.75	0.69
3:K:59:GLN:C	3:K:62:VAL:HG22	2.13	0.69
3:K:59:GLN:HA	3:K:62:VAL:HG22	1.74	0.69
2:B:209:LEU:HD23	2:B:227:LEU:HB3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:VAL:HG12	1:A:372:GLN:H	1.57	0.69
1:A:195:LEU:HD23	1:A:199:ASP:OD1	1.92	0.69
3:K:96:MET:O	3:K:109:ILE:HG13	1.92	0.69
1:A:210:TYR:HA	5:A:502:GTP:N2	2.08	0.69
3:K:292:LEU:HD22	3:K:320:PHE:HZ	1.56	0.69
3:K:9:ILE:CG1	3:K:327:ILE:CD1	2.35	0.69
1:A:217:LEU:HD12	1:A:277:SER:HB3	1.76	0.68
1:A:210:TYR:CZ	5:A:502:GTP:C4	2.81	0.68
2:B:68:VAL:HG11	2:B:153:LEU:HD11	1.74	0.68
2:B:70:LEU:HD21	2:B:111:GLY:HA2	1.75	0.68
1:A:102:ASN:OD1	1:A:105:ARG:HB3	1.93	0.68
2:B:24:ILE:HD11	2:B:52:TYR:CE2	2.28	0.68
1:A:244:PHE:HD1	1:A:245:ASP:N	1.89	0.68
1:A:413:MET:SD	1:A:417:GLU:HB2	2.32	0.68
1:A:428:LEU:CD1	1:A:432:TYR:CZ	2.76	0.68
1:A:202:PHE:CZ	1:A:255:PHE:CE2	2.81	0.68
2:B:167:ASN:ND2	2:B:252:LEU:CD2	2.54	0.68
3:K:83:PHE:CE1	3:K:231:VAL:CA	2.77	0.68
2:B:180:THR:HG22	2:B:181:VAL:N	2.07	0.68
1:A:221:ARG:N	1:A:222:PRO:HD3	2.09	0.68
1:A:191:THR:OG1	1:A:267:PHE:HE2	1.50	0.68
1:A:427:ALA:O	1:A:431:ASP:CG	2.32	0.68
1:A:177:VAL:H	1:A:207:GLU:CG	2.06	0.68
2:B:103:TRP:CZ2	2:B:189:LEU:HB3	2.14	0.68
1:A:181:VAL:HG21	2:B:352:LYS:NZ	2.09	0.68
2:B:70:LEU:H	2:B:145:THR:HG21	1.58	0.68
3:K:133:VAL:HG11	3:K:180:VAL:HG13	1.74	0.68
1:A:189:LEU:HD12	1:A:413:MET:HE2	0.68	0.68
3:K:9:ILE:HG21	3:K:327:ILE:CD1	2.23	0.68
1:A:206:ASN:OD1	5:A:502:GTP:C4	2.17	0.68
2:B:196:GLU:OE2	3:K:279:TYR:CD1	2.47	0.68
2:B:136:GLN:NE2	2:B:239:THR:OG1	2.25	0.68
2:B:44:LEU:HD12	2:B:49:ILE:HD13	1.76	0.68
3:K:95:THR:HB	3:K:105:LEU:CA	2.24	0.68
1:A:191:THR:HG1	1:A:267:PHE:HE2	0.72	0.67
2:B:242:LEU:CD2	2:B:250:ALA:H	2.07	0.67
2:B:332:MET:HE2	2:B:351:VAL:HG12	1.74	0.67
3:K:276:HIS:CE1	3:K:279:TYR:OH	2.46	0.67
1:A:206:ASN:C	1:A:210:TYR:H	1.98	0.67
1:A:205:ASP:N	1:A:302:MET:O	2.18	0.67
1:A:210:TYR:CD2	5:A:502:GTP:H2'	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:325:MET:CE	2:B:355:VAL:HG21	2.24	0.67
1:A:175:PRO:HG3	1:A:304:LYS:HA	1.77	0.67
1:A:202:PHE:HD1	1:A:378:LEU:CB	2.07	0.67
1:A:407:TRP:CZ2	2:B:254:LYS:NZ	2.59	0.67
1:A:406:HIS:HB2	2:B:257:VAL:HA	1.75	0.67
1:A:312:TYR:HB2	1:A:381:THR:HG21	1.73	0.67
1:A:398:MET:CG	1:A:404:PHE:CE1	2.75	0.67
1:A:7:ILE:HD12	1:A:153:LEU:CD2	2.24	0.67
2:B:70:LEU:HD22	2:B:110:GLU:C	2.15	0.67
2:B:97:SER:CB	2:B:110:GLU:CG	2.72	0.67
1:A:167:LEU:HA	1:A:200:CYS:SG	2.35	0.67
1:A:399:TYR:CA	1:A:403:ALA:CB	2.72	0.67
1:A:95:GLY:O	1:A:97:GLU:N	2.27	0.67
3:K:136:PHE:HD2	3:K:139:TYR:OH	1.36	0.67
3:K:81:THR:HG22	3:K:291:SER:OG	1.94	0.67
1:A:204:VAL:HG23	1:A:302:MET:HB2	1.66	0.67
1:A:115:ILE:CD1	1:A:119:LEU:HG	2.23	0.67
1:A:141:PHE:O	1:A:147:SER:HB3	1.94	0.67
1:A:181:VAL:HG21	2:B:352:LYS:HG2	1.75	0.67
1:A:101:ASN:C	1:A:407:TRP:HH2	1.87	0.67
1:A:181:VAL:CG2	2:B:352:LYS:CG	2.72	0.67
2:B:381:SER:O	2:B:383:ALA:N	2.27	0.67
1:A:269:LEU:CA	1:A:378:LEU:HD12	2.25	0.67
1:A:172:TYR:H	1:A:204:VAL:H	1.42	0.67
3:K:83:PHE:CD2	3:K:231:VAL:CB	2.77	0.67
3:K:83:PHE:CD2	3:K:291:SER:HB2	2.30	0.67
2:B:299:LYS:N	2:B:299:LYS:HD3	2.04	0.67
3:K:92:LYS:HB2	3:K:92:LYS:NZ	2.09	0.67
2:B:94:PHE:N	2:B:114:LEU:CD1	2.57	0.67
2:B:182:VAL:HG23	2:B:186:ASN:HD21	1.60	0.67
2:B:66:ILE:C	2:B:67:LEU:HD23	2.15	0.67
1:A:174:ALA:CA	1:A:207:GLU:N	2.53	0.66
2:B:107:HIS:CD2	2:B:151:THR:CG2	2.77	0.66
2:B:313:LEU:HD21	2:B:382:THR:HG23	1.76	0.66
1:A:408:TYR:CB	1:A:418:PHE:HZ	2.07	0.66
1:A:406:HIS:CB	2:B:257:VAL:CA	2.72	0.66
2:B:262:PHE:HE1	3:K:271:GLU:OE1	1.77	0.66
1:A:174:ALA:HB2	5:A:502:GTP:C2'	2.25	0.66
2:B:103:TRP:CG	2:B:189:LEU:HB3	2.16	0.66
1:A:407:TRP:HB2	2:B:258:ASN:ND2	2.10	0.66
2:B:328:VAL:O	2:B:332:MET:HG2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:346:TRP:CB	2:B:349:ASN:HD21	2.04	0.66
1:A:171:ILE:CA	1:A:204:VAL:HG13	2.21	0.66
2:B:54:ASN:OD1	2:B:128:SER:HB3	1.95	0.66
2:B:267:PHE:CD1	2:B:267:PHE:N	2.62	0.66
1:A:427:ALA:O	1:A:431:ASP:OD2	2.13	0.66
3:K:100:LEU:O	3:K:101:HIS:HB2	1.93	0.66
3:K:194:ALA:O	3:K:195:VAL:CG1	2.43	0.66
1:A:105:ARG:HG3	1:A:105:ARG:HH11	1.60	0.66
1:A:251:ASP:O	1:A:254:GLU:HB2	1.95	0.66
3:K:283:LYS:HZ1	3:K:286:ARG:CB	2.09	0.66
3:K:292:LEU:CD1	3:K:320:PHE:CE2	2.50	0.66
3:K:17:PRO:HG3	3:K:55:PRO:HB3	1.78	0.66
1:A:102:ASN:CB	1:A:411:GLU:HB2	2.26	0.66
1:A:138:PHE:HE1	1:A:235:VAL:C	1.95	0.66
1:A:172:TYR:HE2	1:A:391:LEU:CD2	1.77	0.66
1:A:408:TYR:HB3	1:A:413:MET:HB2	1.78	0.66
1:A:7:ILE:HD11	1:A:137:VAL:HG22	1.77	0.66
2:B:265:LEU:HD12	2:B:265:LEU:C	2.16	0.66
1:A:203:MET:CE	1:A:267:PHE:HB3	2.25	0.66
1:A:276:ILE:O	1:A:369:ALA:HB2	1.95	0.66
1:A:399:TYR:CA	1:A:403:ALA:HB2	2.25	0.66
1:A:341:ILE:HG12	1:A:341:ILE:O	1.95	0.66
1:A:175:PRO:HA	1:A:391:LEU:CD1	2.23	0.66
1:A:407:TRP:CA	2:B:257:VAL:HG23	2.23	0.66
2:B:251:ASP:O	2:B:253:ARG:N	2.29	0.66
2:B:3:GLU:C	2:B:132:LEU:HD12	2.16	0.66
3:K:24:LEU:C	3:K:26:GLY:H	1.99	0.66
1:A:397:LEU:HD12	2:B:348:PRO:HG2	1.64	0.66
2:B:267:PHE:CD1	2:B:388:PHE:CE2	2.84	0.66
2:B:108:TYR:CD1	2:B:413:MET:HE1	2.31	0.66
1:A:152:LEU:HA	1:A:155:GLU:HB2	1.77	0.65
1:A:388:TRP:HA	1:A:388:TRP:CE3	2.31	0.65
2:B:204:ILE:HG22	2:B:209:LEU:HD11	1.78	0.65
1:A:184:PRO:C	1:A:395:PHE:HE2	1.98	0.65
2:B:167:ASN:OD1	2:B:252:LEU:CD1	2.43	0.65
2:B:251:ASP:O	2:B:254:LYS:N	2.29	0.65
2:B:413:MET:HG2	2:B:418:PHE:HE1	1.61	0.65
2:B:230:LEU:HD23	2:B:231:VAL:N	2.10	0.65
3:K:127:LEU:HA	3:K:216:GLU:O	1.96	0.65
1:A:68:VAL:HG11	1:A:149:PHE:CZ	2.30	0.65
1:A:210:TYR:CD1	5:A:502:GTP:N3	2.63	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:70:LEU:HD22	2:B:111:GLY:N	2.11	0.65
1:A:266:HIS:HA	1:A:428:LEU:HD13	1.78	0.65
2:B:251:ASP:O	2:B:252:LEU:C	2.34	0.65
3:K:25:ARG:HG2	3:K:25:ARG:O	1.97	0.65
2:B:4:ILE:CA	2:B:134:GLY:O	2.41	0.65
2:B:250:ALA:HB1	2:B:254:LYS:CB	2.27	0.65
2:B:281:GLN:O	2:B:283:TYR:HB2	1.96	0.65
1:A:407:TRP:HA	2:B:257:VAL:CB	2.26	0.65
2:B:66:ILE:HD11	2:B:122:VAL:CB	2.26	0.65
3:K:9:ILE:HG21	3:K:327:ILE:HD11	1.79	0.65
3:K:62:VAL:HG22	3:K:106:MET:CG	1.99	0.65
2:B:103:TRP:CG	2:B:189:LEU:CG	2.75	0.65
3:K:53:LEU:CD1	3:K:104:GLN:CB	2.47	0.65
2:B:282:GLN:O	2:B:282:GLN:HG2	1.97	0.65
2:B:158:ARG:NE	2:B:197:ASN:O	2.30	0.65
2:B:431:GLU:O	2:B:434:GLN:HG2	1.97	0.65
2:B:4:ILE:HB	2:B:51:VAL:O	1.97	0.65
3:K:14:ARG:HD2	3:K:95:THR:CG2	2.26	0.65
1:A:372:GLN:O	1:A:373:ARG:HB3	1.96	0.65
2:B:276:THR:HB	2:B:281:GLN:CG	2.25	0.65
2:B:35:SER:HB3	2:B:59:ASN:CA	2.26	0.65
1:A:304:LYS:O	1:A:305:CYS:HB3	1.98	0.64
3:K:294:GLY:HA2	3:K:329:ASN:HB3	1.79	0.64
3:K:137:GLU:HG2	3:K:205:SER:HB2	1.77	0.64
1:A:175:PRO:CB	1:A:304:LYS:HA	2.27	0.64
1:A:217:LEU:HD11	1:A:367:ASP:O	1.96	0.64
1:A:380:ASN:CB	1:A:432:TYR:HD1	2.04	0.64
2:B:114:LEU:O	2:B:118:VAL:HG23	1.97	0.64
3:K:283:LYS:HZ1	3:K:286:ARG:CD	2.01	0.64
1:A:115:ILE:HG23	1:A:116:ASP:N	2.12	0.64
1:A:406:HIS:HB2	2:B:257:VAL:O	1.97	0.64
2:B:12:CYS:SG	2:B:140:SER:CB	2.66	0.64
1:A:276:ILE:HG23	1:A:369:ALA:HB2	1.80	0.64
2:B:241:CYS:O	2:B:244:PHE:HB2	1.98	0.64
2:B:427:ASP:O	2:B:430:SER:HB3	1.97	0.64
1:A:227:LEU:O	1:A:231:ILE:HG12	1.96	0.64
1:A:304:LYS:HE3	1:A:305:CYS:SG	2.38	0.64
1:A:308:ARG:C	1:A:309:HIS:O	2.28	0.64
2:B:12:CYS:CB	2:B:140:SER:CB	2.76	0.64
2:B:172:VAL:HG11	2:B:387:LEU:CD2	2.22	0.64
2:B:262:PHE:CG	2:B:435:TYR:OH	2.49	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:TYR:HD2	1:A:205:ASP:OD2	1.79	0.64
1:A:382:THR:O	1:A:385:ALA:HB3	1.95	0.64
1:A:398:MET:O	1:A:403:ALA:HB1	1.91	0.64
1:A:267:PHE:N	1:A:428:LEU:CD1	2.51	0.64
1:A:224:TYR:OH	2:B:325:MET:HG3	1.98	0.64
2:B:262:PHE:CE2	2:B:435:TYR:CD1	2.86	0.64
1:A:185:TYR:HE1	1:A:399:TYR:CD1	2.16	0.64
2:B:299:LYS:O	2:B:300:ASN:HB2	1.98	0.64
1:A:179:THR:OG1	1:A:224:TYR:CE1	2.51	0.64
1:A:185:TYR:OH	1:A:405:VAL:HG23	1.96	0.64
1:A:271:THR:HG23	1:A:300:ASN:O	1.97	0.64
2:B:267:PHE:HB2	2:B:384:ILE:CD1	2.22	0.64
2:B:424:ASN:O	3:K:276:HIS:NE2	2.31	0.64
3:K:83:PHE:HB2	3:K:291:SER:HB2	1.78	0.64
1:A:151:SER:O	1:A:155:GLU:HB2	1.98	0.64
1:A:264:ARG:O	1:A:266:HIS:CD2	2.51	0.63
1:A:302:MET:C	1:A:303:VAL:HG23	2.18	0.63
1:A:303:VAL:C	1:A:384:ILE:HD13	1.83	0.63
2:B:258:ASN:ND2	2:B:352:LYS:HZ2	1.94	0.63
2:B:264:ARG:HH22	3:K:276:HIS:HE1	0.74	0.63
2:B:336:GLN:NE2	2:B:351:VAL:HG23	2.12	0.63
2:B:284:ARG:O	2:B:286:LEU:N	2.30	0.63
1:A:362:VAL:HG13	1:A:368:LEU:CB	2.27	0.63
1:A:317:LEU:HD12	1:A:351:PHE:CD1	2.33	0.63
3:K:92:LYS:HB2	3:K:92:LYS:HZ3	1.62	0.63
1:A:169:PHE:CD1	1:A:235:VAL:HG23	2.29	0.63
1:A:206:ASN:HB3	5:A:502:GTP:C4	2.25	0.63
1:A:210:TYR:CE2	5:A:502:GTP:H2'	2.33	0.63
2:B:264:ARG:NH2	3:K:279:TYR:OH	2.31	0.63
3:K:87:GLN:HG3	3:K:87:GLN:O	1.97	0.63
1:A:203:MET:HE1	1:A:267:PHE:HB3	1.80	0.63
2:B:104:ALA:CB	2:B:413:MET:HE3	2.05	0.63
2:B:9:ALA:HB1	2:B:150:GLY:N	2.13	0.63
3:K:294:GLY:HA2	3:K:329:ASN:CB	2.25	0.63
2:B:180:THR:CG2	2:B:181:VAL:N	2.61	0.63
3:K:117:PHE:HB2	3:K:177:PRO:HG3	1.79	0.63
1:A:165:SER:C	1:A:252:LEU:CD1	2.65	0.63
1:A:173:PRO:C	1:A:205:ASP:CB	2.66	0.63
1:A:227:LEU:HD12	1:A:231:ILE:CD1	2.26	0.63
1:A:268:PRO:CA	1:A:379:SER:O	2.47	0.63
1:A:102:ASN:ND2	1:A:412:GLY:CA	2.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:325:MET:HE2	2:B:355:VAL:HG21	1.80	0.63
1:A:152:LEU:HD12	1:A:153:LEU:N	2.14	0.63
1:A:188:ILE:CD1	1:A:421:ALA:O	2.41	0.63
2:B:137:LEU:HD22	2:B:154:ILE:CG2	2.28	0.63
2:B:68:VAL:HB	2:B:153:LEU:HD21	1.76	0.63
2:B:254:LYS:O	2:B:258:ASN:HB2	1.99	0.63
3:K:20:GLU:N	3:K:198:MET:SD	2.71	0.63
1:A:16:ILE:HD11	1:A:235:VAL:HB	1.81	0.63
2:B:204:ILE:HD12	2:B:231:VAL:HG13	1.81	0.63
1:A:398:MET:CG	2:B:349:ASN:HB3	2.27	0.63
2:B:242:LEU:CD1	2:B:255:LEU:HD11	2.28	0.63
2:B:422:GLU:O	2:B:426:ASN:HB2	1.97	0.63
1:A:208:ALA:HB3	1:A:303:VAL:N	2.13	0.63
1:A:380:ASN:HA	1:A:432:TYR:CE1	2.32	0.63
2:B:107:HIS:HD2	2:B:151:THR:CG2	2.12	0.63
3:K:94:HIS:NE2	3:K:102:ASP:CB	2.56	0.63
3:K:127:LEU:O	3:K:127:LEU:HD12	1.98	0.63
1:A:315:CYS:HB3	1:A:377:MET:CE	2.29	0.63
1:A:213:CYS:SG	5:A:502:GTP:N2	2.72	0.63
3:K:95:THR:HB	3:K:104:GLN:O	1.97	0.63
3:K:105:LEU:CB	3:K:108:ILE:HD11	2.29	0.63
3:K:21:ALA:O	3:K:25:ARG:N	2.27	0.63
1:A:269:LEU:C	1:A:378:LEU:HD13	2.14	0.62
1:A:278:ALA:HA	1:A:282:TYR:OH	1.99	0.62
1:A:7:ILE:HG22	1:A:66:VAL:CG2	2.28	0.62
2:B:115:VAL:HG21	2:B:152:LEU:CD2	2.29	0.62
2:B:192:HIS:O	2:B:195:VAL:HG12	1.98	0.62
2:B:133:GLN:HG3	2:B:165:ILE:HD11	1.80	0.62
1:A:206:ASN:O	1:A:209:ILE:N	2.32	0.62
2:B:93:VAL:HG21	2:B:118:VAL:N	2.13	0.62
3:K:59:GLN:CA	3:K:62:VAL:HG22	2.29	0.62
2:B:205:ASP:HB2	2:B:208:ALA:HB3	1.80	0.62
3:K:126:ASN:O	3:K:127:LEU:HD12	1.98	0.62
2:B:68:VAL:CG2	2:B:153:LEU:HD23	2.10	0.62
1:A:215:ARG:C	1:A:216:ASN:HD22	2.03	0.62
3:K:273:THR:O	3:K:274:LYS:O	2.17	0.62
1:A:273:ALA:HB3	1:A:274:PRO:HD3	1.81	0.62
1:A:119:LEU:CD2	1:A:122:ILE:HD11	2.28	0.62
1:A:175:PRO:CD	1:A:207:GLU:CA	2.46	0.62
2:B:12:CYS:HG	2:B:140:SER:HB3	1.64	0.62
2:B:93:VAL:HG21	2:B:118:VAL:HG23	1.61	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ILE:HA	1:A:212:ILE:CG1	2.30	0.62
1:A:381:THR:O	1:A:385:ALA:CB	2.47	0.62
2:B:267:PHE:CD2	2:B:388:PHE:CZ	2.88	0.62
2:B:313:LEU:HD21	2:B:382:THR:CG2	2.30	0.62
1:A:313:MET:HB3	1:A:381:THR:HB	1.82	0.62
1:A:203:MET:HB3	1:A:388:TRP:CH2	2.35	0.62
2:B:93:VAL:HG13	2:B:114:LEU:CG	2.14	0.62
3:K:283:LYS:N	3:K:283:LYS:HD3	2.14	0.62
3:K:195:VAL:C	3:K:202:SER:OG	2.31	0.62
1:A:267:PHE:HD1	1:A:267:PHE:H	1.47	0.62
1:A:185:TYR:OH	1:A:399:TYR:HD1	1.82	0.62
2:B:3:GLU:HB2	2:B:132:LEU:HA	1.82	0.62
2:B:205:ASP:HB2	2:B:208:ALA:CB	2.30	0.62
2:B:211:ASP:OD1	2:B:212:ILE:N	2.33	0.62
2:B:230:LEU:O	2:B:233:ALA:HB3	2.00	0.62
1:A:209:ILE:CG2	1:A:212:ILE:CD1	2.39	0.62
1:A:188:ILE:O	1:A:421:ALA:CB	2.47	0.62
1:A:267:PHE:CZ	1:A:424:ASP:OD1	2.48	0.62
2:B:315:VAL:HG13	2:B:377:PHE:CE1	2.34	0.62
2:B:179:ASP:HB2	6:B:602:G2P:O2'	1.99	0.62
3:K:81:THR:HG21	3:K:291:SER:OG	2.00	0.62
3:K:59:GLN:C	3:K:106:MET:CG	2.65	0.62
3:K:25:ARG:HH12	3:K:309:PHE:HB2	1.65	0.62
1:A:317:LEU:HD11	1:A:351:PHE:HE1	1.65	0.62
1:A:192:HIS:CA	1:A:424:ASP:OD2	2.47	0.61
1:A:172:TYR:CD2	1:A:205:ASP:CG	2.73	0.61
2:B:114:LEU:HD23	2:B:149:MET:CE	2.30	0.61
1:A:88:HIS:O	1:A:90:GLU:N	2.33	0.61
3:K:45:LYS:HD3	3:K:45:LYS:N	2.13	0.61
2:B:324:SER:C	2:B:326:LYS:H	2.03	0.61
3:K:83:PHE:CB	3:K:291:SER:HB3	2.27	0.61
3:K:109:ILE:HG22	3:K:184:ILE:CD1	2.29	0.61
2:B:285:ALA:HB1	2:B:290:GLU:HG2	1.83	0.61
1:A:317:LEU:HB3	1:A:319:TYR:CE1	2.33	0.61
2:B:63:PRO:HD2	2:B:86:ILE:HG12	1.80	0.61
1:A:102:ASN:ND2	1:A:411:GLU:CA	2.63	0.61
2:B:428:LEU:CA	3:K:274:LYS:HZ3	2.13	0.61
3:K:63:TYR:N	3:K:106:MET:CE	2.63	0.61
1:A:412:GLY:O	1:A:413:MET:HG2	2.00	0.61
1:A:181:VAL:HG11	1:A:404:PHE:HD2	1.63	0.61
2:B:97:SER:HB2	2:B:110:GLU:HB3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:250:ALA:CA	2:B:254:LYS:HE2	2.30	0.61
1:A:27:GLU:HG2	1:A:358:GLU:OE2	1.95	0.61
2:B:318:VAL:HA	2:B:354:ALA:HB3	1.81	0.61
2:B:103:TRP:CA	2:B:408:TYR:HE2	2.09	0.61
3:K:81:THR:OG1	3:K:290:ASP:HB3	2.01	0.61
3:K:83:PHE:CG	3:K:288:LEU:HB3	2.35	0.61
2:B:204:ILE:HG23	2:B:302:MET:CB	2.17	0.61
1:A:118:VAL:HG11	1:A:149:PHE:HZ	1.65	0.61
1:A:176:GLN:C	1:A:207:GLU:OE2	2.38	0.61
1:A:169:PHE:CG	1:A:238:ILE:CG1	2.82	0.61
1:A:167:LEU:HG	1:A:255:PHE:CG	2.34	0.61
1:A:301:GLN:HE22	1:A:383:ALA:CA	2.06	0.61
3:K:22:GLU:HA	3:K:27:ASP:OD2	2.01	0.61
1:A:248:LEU:CD2	1:A:353:VAL:O	2.49	0.61
1:A:179:THR:OG1	1:A:224:TYR:CZ	2.48	0.61
1:A:236:SER:O	1:A:240:ALA:HB3	1.99	0.61
1:A:397:LEU:HD12	2:B:348:PRO:CB	2.31	0.61
1:A:185:TYR:CD1	1:A:418:PHE:CB	2.83	0.61
1:A:428:LEU:CD1	1:A:432:TYR:CE2	2.83	0.61
2:B:427:ASP:HB3	3:K:276:HIS:CD2	2.36	0.61
3:K:233:LEU:HD11	3:K:288:LEU:HD13	1.82	0.61
3:K:111:ARG:CG	3:K:111:ARG:HH11	2.14	0.61
1:A:115:ILE:HG13	1:A:152:LEU:HD13	1.81	0.61
1:A:174:ALA:HA	1:A:207:GLU:N	2.15	0.61
3:K:291:SER:HA	3:K:298:THR:CG2	2.31	0.61
3:K:97:GLU:HB3	3:K:109:ILE:HD12	1.83	0.61
1:A:398:MET:SD	1:A:404:PHE:CE1	2.93	0.61
3:K:207:SER:C	3:K:208:ILE:HD12	2.21	0.61
3:K:277:VAL:H	3:K:278:PRO:CD	2.14	0.61
3:K:53:LEU:HD12	3:K:104:GLN:HB2	1.77	0.61
1:A:202:PHE:CB	1:A:378:LEU:HD22	2.29	0.60
1:A:315:CYS:CA	1:A:379:SER:OG	2.48	0.60
2:B:68:VAL:HG11	2:B:153:LEU:HD21	1.82	0.60
3:K:278:PRO:HG2	3:K:279:TYR:HD2	1.66	0.60
3:K:12:MET:HG3	3:K:51:ARG:HB3	1.82	0.60
1:A:266:HIS:ND1	1:A:431:ASP:CG	2.41	0.60
2:B:115:VAL:HG21	2:B:152:LEU:HD23	1.83	0.60
2:B:324:SER:O	2:B:328:VAL:HG23	2.01	0.60
2:B:172:VAL:CG1	2:B:387:LEU:HD21	2.24	0.60
3:K:283:LYS:NZ	3:K:286:ARG:HB2	2.13	0.60
2:B:66:ILE:HD13	2:B:122:VAL:HG11	1.76	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:62:VAL:HG21	3:K:106:MET:HB3	1.74	0.60
2:B:176:LYS:HD2	2:B:207:GLU:CB	2.27	0.60
1:A:288:VAL:O	1:A:290:GLU:N	2.33	0.60
1:A:268:PRO:HA	1:A:379:SER:O	2.02	0.60
1:A:400:ALA:O	1:A:401:LYS:CB	2.48	0.60
2:B:66:ILE:CG1	2:B:122:VAL:HG12	2.31	0.60
2:B:4:ILE:CG2	2:B:136:GLN:HG2	2.31	0.60
3:K:81:THR:OG1	3:K:290:ASP:OD2	2.18	0.60
3:K:292:LEU:HD22	3:K:320:PHE:CZ	2.35	0.60
1:A:284:GLU:O	1:A:286:LEU:N	2.35	0.60
1:A:209:ILE:HA	1:A:212:ILE:HG13	1.83	0.60
1:A:388:TRP:HA	1:A:388:TRP:HE3	1.65	0.60
2:B:93:VAL:CB	2:B:118:VAL:HG23	1.92	0.60
2:B:10:GLY:C	6:B:602:G2P:O2B	2.39	0.60
2:B:174:SER:OG	2:B:206:ASN:HB2	2.02	0.60
1:A:205:ASP:O	1:A:209:ILE:HD12	2.01	0.60
1:A:27:GLU:OE1	1:A:359:PRO:O	2.18	0.60
1:A:170:SER:O	1:A:204:VAL:HG12	2.01	0.60
1:A:155:GLU:HA	1:A:197:HIS:CD2	2.36	0.60
1:A:22:GLU:CD	1:A:364:PRO:CD	2.70	0.60
1:A:270:ALA:N	1:A:378:LEU:CD1	2.65	0.60
1:A:270:ALA:N	1:A:378:LEU:HD13	2.17	0.60
1:A:408:TYR:O	1:A:412:GLY:N	2.30	0.60
2:B:408:TYR:CG	2:B:418:PHE:HZ	2.20	0.60
3:K:278:PRO:HG2	3:K:279:TYR:CD2	2.37	0.60
1:A:100:ALA:HB2	1:A:105:ARG:HD3	1.83	0.60
1:A:172:TYR:CZ	1:A:391:LEU:HD21	2.34	0.60
1:A:23:LEU:HD13	1:A:361:THR:CA	2.30	0.60
2:B:19:LYS:CG	2:B:228:ASN:HB3	2.31	0.60
2:B:161:TYR:C	2:B:163:ASP:H	2.05	0.60
1:A:172:TYR:HD2	1:A:388:TRP:CZ3	2.07	0.59
2:B:128:SER:OG	2:B:129:CYS:N	2.34	0.59
1:A:210:TYR:CE1	5:A:502:GTP:C2	2.87	0.59
1:A:16:ILE:CD1	1:A:231:ILE:C	2.70	0.59
1:A:202:PHE:CA	1:A:378:LEU:CD2	2.80	0.59
2:B:262:PHE:CE1	3:K:271:GLU:CD	2.75	0.59
3:K:111:ARG:HH11	3:K:111:ARG:HG2	1.67	0.59
3:K:14:ARG:NH2	3:K:94:HIS:HD2	1.98	0.59
2:B:279:GLY:O	2:B:282:GLN:HB3	2.01	0.59
2:B:141:LEU:N	2:B:141:LEU:CD1	2.65	0.59
1:A:119:LEU:O	1:A:122:ILE:HG12	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:ALA:O	1:A:370:LYS:HB3	2.03	0.59
3:K:276:HIS:HB3	3:K:278:PRO:HD3	1.82	0.59
1:A:166:LYS:N	1:A:252:LEU:CD1	2.65	0.59
1:A:311:LYS:HE2	1:A:312:TYR:CE2	2.37	0.59
2:B:349:ASN:O	2:B:350:ASN:HB2	2.01	0.59
1:A:181:VAL:CG2	2:B:352:LYS:HG3	2.25	0.59
2:B:49:ILE:O	2:B:51:VAL:N	2.35	0.59
3:K:233:LEU:CD1	3:K:288:LEU:HD11	2.14	0.59
1:A:115:ILE:HD13	1:A:115:ILE:O	2.02	0.59
1:A:166:LYS:HA	1:A:252:LEU:HD12	1.83	0.59
1:A:209:ILE:CB	1:A:212:ILE:CD1	2.78	0.59
1:A:266:HIS:CE1	1:A:431:ASP:CB	2.83	0.59
1:A:7:ILE:CD1	1:A:137:VAL:HG22	2.31	0.59
3:K:109:ILE:CG2	3:K:184:ILE:CD1	2.79	0.59
1:A:172:TYR:H	1:A:204:VAL:N	2.01	0.59
1:A:264:ARG:HB2	1:A:266:HIS:CE1	2.37	0.59
3:K:62:VAL:HG22	3:K:106:MET:HB3	1.85	0.59
1:A:172:TYR:CG	1:A:173:PRO:HD2	2.32	0.59
1:A:202:PHE:O	1:A:203:MET:HG3	2.03	0.59
1:A:23:LEU:HD13	1:A:361:THR:H	1.68	0.59
2:B:64:ARG:CD	2:B:125:GLU:O	2.51	0.59
3:K:62:VAL:CG2	3:K:106:MET:HE3	2.30	0.59
2:B:30:ILE:HD13	2:B:53:TYR:CE2	2.38	0.59
3:K:131:ILE:N	3:K:131:ILE:HD12	2.17	0.59
1:A:305:CYS:O	1:A:306:ASP:HB2	2.01	0.59
2:B:183:GLU:HB3	2:B:184:PRO:CD	2.33	0.59
2:B:94:PHE:O	2:B:114:LEU:HB2	2.03	0.59
1:A:11:GLN:HE21	1:A:74:VAL:HG22	1.66	0.59
1:A:371:VAL:HG12	1:A:372:GLN:N	2.17	0.59
3:K:74:VAL:HA	3:K:78:TYR:O	2.02	0.59
1:A:204:VAL:CG1	1:A:231:ILE:HD12	2.33	0.59
1:A:298:PRO:HB2	1:A:307:PRO:HD3	1.83	0.59
1:A:312:TYR:HA	1:A:342:GLN:O	2.03	0.59
2:B:97:SER:HB2	2:B:110:GLU:CB	2.32	0.59
1:A:174:ALA:HA	1:A:205:ASP:HB3	1.85	0.58
1:A:435:VAL:HG12	1:A:435:VAL:O	2.02	0.58
3:K:14:ARG:CZ	3:K:103:PRO:HG2	2.14	0.58
1:A:269:LEU:N	1:A:379:SER:O	2.36	0.58
1:A:278:ALA:HB2	1:A:369:ALA:HA	1.85	0.58
2:B:165:ILE:HG13	2:B:252:LEU:CD1	2.33	0.58
1:A:173:PRO:C	1:A:205:ASP:HB3	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:THR:HA	1:A:432:TYR:HB3	1.86	0.58
2:B:267:PHE:CE1	2:B:388:PHE:HE2	2.22	0.58
2:B:70:LEU:CD2	2:B:111:GLY:HA2	2.33	0.58
3:K:279:TYR:CD1	3:K:280:ARG:N	2.72	0.58
2:B:299:LYS:O	2:B:300:ASN:CB	2.51	0.58
1:A:312:TYR:C	1:A:381:THR:HG21	2.22	0.58
1:A:405:VAL:CG2	1:A:418:PHE:HD2	2.12	0.58
2:B:151:THR:OG1	2:B:193:GLN:HB3	2.03	0.58
3:K:83:PHE:CG	3:K:288:LEU:CB	2.84	0.58
1:A:384:ILE:HG23	1:A:387:ALA:CA	2.24	0.58
1:A:179:THR:CG2	2:B:248:LEU:HB2	2.33	0.58
2:B:332:MET:CE	2:B:351:VAL:CG1	2.81	0.58
1:A:397:LEU:CD1	2:B:348:PRO:CB	2.81	0.58
1:A:243:ARG:NH2	1:A:252:LEU:N	2.28	0.58
1:A:63:PRO:HD3	1:A:86:LEU:O	2.04	0.58
2:B:5:VAL:C	2:B:135:PHE:HB3	2.21	0.58
1:A:181:VAL:CG2	2:B:352:LYS:HG2	2.33	0.58
3:K:83:PHE:CD2	3:K:231:VAL:CG2	2.86	0.58
3:K:29:PHE:CE2	3:K:55:PRO:HG2	2.39	0.58
1:A:103:TYR:HH	1:A:107:HIS:CE1	2.21	0.58
2:B:243:ARG:HH21	2:B:252:LEU:H	1.52	0.58
2:B:307:PRO:HB3	2:B:312:TYR:OH	2.04	0.58
2:B:70:LEU:C	2:B:99:ALA:HB2	2.24	0.58
2:B:98:GLY:HA3	2:B:105:LYS:HZ1	1.68	0.58
1:A:2:ARG:N	1:A:131:GLY:O	2.37	0.58
1:A:169:PHE:CZ	1:A:234:ILE:CG1	2.74	0.58
1:A:169:PHE:CE1	1:A:235:VAL:CG2	2.80	0.58
2:B:427:ASP:OD2	3:K:276:HIS:CG	2.57	0.58
2:B:2:ARG:HG2	2:B:48:ARG:HH12	1.68	0.58
2:B:54:ASN:ND2	2:B:64:ARG:HD3	2.15	0.58
2:B:30:ILE:HA	2:B:35:SER:O	2.04	0.58
1:A:98:ASP:CB	1:A:105:ARG:HH21	2.13	0.58
1:A:182:VAL:HG22	1:A:407:TRP:CZ3	2.31	0.58
1:A:179:THR:CB	5:A:502:GTP:H5'	2.34	0.58
2:B:174:SER:CB	2:B:207:GLU:CD	2.73	0.58
1:A:171:ILE:HG23	1:A:231:ILE:HD12	1.86	0.57
2:B:324:SER:CB	2:B:327:GLU:HG2	2.30	0.57
3:K:19:ASN:O	3:K:23:ILE:HG22	2.04	0.57
2:B:100:GLY:H	2:B:105:LYS:HZ3	1.51	0.57
1:A:243:ARG:CZ	1:A:251:ASP:OD1	2.46	0.57
1:A:176:GLN:CB	1:A:394:LYS:NZ	2.63	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:TYR:HD1	1:A:418:PHE:CG	2.16	0.57
2:B:203:CYS:SG	2:B:267:PHE:HB3	2.44	0.57
1:A:185:TYR:CE1	1:A:399:TYR:CD1	2.92	0.57
1:A:191:THR:CG2	1:A:267:PHE:HE2	2.16	0.57
1:A:210:TYR:HD1	5:A:502:GTP:C2	2.16	0.57
2:B:149:MET:O	2:B:153:LEU:HD13	2.05	0.57
3:K:293:GLY:HA2	3:K:327:ILE:CG2	2.35	0.57
2:B:319:PHE:HA	2:B:375:ALA:HA	1.86	0.57
1:A:175:PRO:CG	1:A:304:LYS:HA	2.33	0.57
2:B:428:LEU:HA	3:K:274:LYS:CE	2.35	0.57
1:A:286:LEU:HD12	1:A:290:GLU:HG2	1.87	0.57
3:K:194:ALA:C	3:K:195:VAL:CG1	2.73	0.57
1:A:363:VAL:O	1:A:364:PRO:C	2.43	0.57
2:B:106:GLY:O	2:B:149:MET:CA	2.52	0.57
2:B:251:ASP:H	2:B:254:LYS:HB2	1.70	0.57
3:K:53:LEU:CD2	3:K:104:GLN:NE2	2.58	0.57
1:A:218:ASP:O	1:A:219:ILE:HG23	2.04	0.57
2:B:103:TRP:CZ3	2:B:189:LEU:HD22	2.39	0.57
2:B:264:ARG:HD3	2:B:431:GLU:HG3	1.87	0.57
2:B:320:ARG:O	2:B:359:PRO:HA	2.04	0.57
2:B:12:CYS:HB3	2:B:140:SER:CB	2.34	0.57
2:B:89:PRO:HA	2:B:92:PHE:CD2	2.38	0.57
2:B:217:LEU:C	2:B:219:LEU:N	2.55	0.57
1:A:268:PRO:HB2	1:A:378:LEU:HG	1.86	0.57
2:B:283:TYR:C	2:B:284:ARG:HG2	2.25	0.57
1:A:117:LEU:HD11	1:A:121:ARG:HH22	1.69	0.57
1:A:309:HIS:CD2	1:A:310:GLY:H	2.22	0.57
2:B:70:LEU:CD2	2:B:110:GLU:C	2.71	0.57
3:K:136:PHE:HD2	3:K:139:TYR:CZ	2.23	0.57
3:K:137:GLU:HG2	3:K:205:SER:OG	2.05	0.57
1:A:139:HIS:CE1	1:A:170:SER:HB3	2.39	0.57
1:A:204:VAL:CG2	1:A:302:MET:CG	2.76	0.57
1:A:307:PRO:HA	1:A:386:GLU:HG3	1.87	0.57
1:A:269:LEU:CA	1:A:378:LEU:CD1	2.83	0.57
2:B:182:VAL:HG23	2:B:186:ASN:ND2	2.20	0.57
2:B:103:TRP:HZ3	2:B:417:GLU:HG3	1.69	0.57
1:A:317:LEU:HD11	1:A:351:PHE:CE1	2.40	0.57
1:A:216:ASN:O	1:A:217:LEU:HB2	2.05	0.56
1:A:224:TYR:CD2	2:B:247:GLN:CB	2.78	0.56
2:B:169:PHE:CZ	2:B:235:MET:HB2	2.39	0.56
2:B:270:PRO:HA	2:B:377:PHE:O	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:ARG:NH1	2:B:128:SER:CB	2.68	0.56
2:B:274:PRO:CG	2:B:371:LEU:HD21	2.34	0.56
1:A:88:HIS:C	1:A:90:GLU:N	2.57	0.56
1:A:189:LEU:HD11	1:A:417:GLU:HB3	0.71	0.56
1:A:399:TYR:O	1:A:402:ARG:N	2.38	0.56
1:A:312:TYR:CD2	1:A:437:VAL:CG2	2.88	0.56
2:B:4:ILE:HD12	2:B:51:VAL:CG1	2.35	0.56
2:B:50:ASN:O	2:B:64:ARG:NH2	2.38	0.56
3:K:279:TYR:HD1	3:K:280:ARG:H	1.51	0.56
1:A:152:LEU:HA	1:A:155:GLU:CB	2.35	0.56
1:A:398:MET:HB3	1:A:404:PHE:CD1	2.36	0.56
2:B:428:LEU:CA	3:K:274:LYS:NZ	2.68	0.56
1:A:231:ILE:HA	1:A:234:ILE:CG2	2.36	0.56
2:B:14:ASN:OD1	2:B:75:MET:HG2	2.05	0.56
2:B:312:TYR:O	2:B:344:VAL:HB	2.05	0.56
3:K:282:SER:HA	3:K:286:ARG:NH1	2.20	0.56
3:K:105:LEU:HD13	3:K:301:VAL:HB	1.87	0.56
2:B:216:THR:O	2:B:217:LEU:HD12	2.05	0.56
2:B:319:PHE:CD2	2:B:375:ALA:HB2	2.40	0.56
1:A:331:ALA:O	1:A:334:THR:HG22	2.05	0.56
1:A:338:LYS:O	1:A:340:THR:N	2.34	0.56
2:B:273:ALA:CB	2:B:274:PRO:HD3	2.30	0.56
1:A:209:ILE:O	1:A:212:ILE:CB	2.53	0.56
1:A:191:THR:CB	1:A:267:PHE:HE2	2.18	0.56
1:A:5:ILE:HD11	1:A:135:PHE:CD1	2.38	0.56
2:B:324:SER:C	2:B:326:LYS:N	2.59	0.56
2:B:332:MET:HE2	2:B:351:VAL:CG1	2.34	0.56
2:B:94:PHE:HD1	2:B:114:LEU:HD13	1.69	0.56
1:A:185:TYR:HB2	1:A:408:TYR:CZ	2.41	0.56
1:A:172:TYR:CE2	1:A:205:ASP:OD2	2.58	0.56
1:A:308:ARG:O	1:A:310:GLY:O	2.24	0.56
1:A:407:TRP:CD1	2:B:254:LYS:HA	2.40	0.56
2:B:165:ILE:H	2:B:165:ILE:HD13	1.70	0.56
2:B:19:LYS:O	2:B:23:VAL:HG23	2.06	0.56
1:A:7:ILE:HG12	1:A:136:SER:O	2.06	0.56
2:B:264:ARG:CG	3:K:274:LYS:HD3	2.36	0.56
1:A:312:TYR:CA	1:A:381:THR:HG21	2.35	0.56
1:A:388:TRP:CE3	1:A:425:MET:HE1	2.41	0.56
2:B:267:PHE:CE1	2:B:388:PHE:CE2	2.93	0.56
3:K:290:ASP:OD1	3:K:295:ASN:HB2	2.05	0.56
3:K:109:ILE:HB	3:K:110:PRO:HD3	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:91:GLY:O	3:K:95:THR:HG23	2.05	0.56
1:A:408:TYR:HB2	1:A:418:PHE:CZ	2.31	0.56
2:B:119:LEU:O	2:B:123:ARG:HG3	2.06	0.56
2:B:169:PHE:CD1	2:B:235:MET:HE2	2.40	0.56
3:K:62:VAL:CG2	3:K:106:MET:N	2.56	0.56
2:B:273:ALA:HB3	2:B:274:PRO:CD	2.29	0.56
3:K:238:LYS:O	3:K:259:LEU:HD11	2.03	0.56
2:B:180:THR:CG2	2:B:181:VAL:H	2.17	0.56
2:B:145:THR:HG23	6:B:602:G2P:O2G	2.06	0.56
3:K:211:ILE:HD12	3:K:228:LEU:HD23	1.88	0.56
1:A:177:VAL:N	1:A:207:GLU:CG	2.68	0.55
1:A:22:GLU:OE1	1:A:364:PRO:CD	2.53	0.55
1:A:253:THR:O	1:A:256:GLN:HG2	2.06	0.55
2:B:94:PHE:O	2:B:114:LEU:CB	2.54	0.55
3:K:269:LEU:HD21	3:K:283:LYS:HE3	1.88	0.55
1:A:390:ARG:HG3	1:A:390:ARG:HH11	1.71	0.55
1:A:269:LEU:HD21	1:A:388:TRP:CD1	2.41	0.55
2:B:299:LYS:CD	2:B:299:LYS:H	2.07	0.55
1:A:16:ILE:HD12	1:A:171:ILE:HD11	1.87	0.55
1:A:208:ALA:CA	1:A:304:LYS:O	2.54	0.55
1:A:202:PHE:CA	1:A:378:LEU:HD22	2.35	0.55
1:A:175:PRO:CA	1:A:391:LEU:HD12	2.23	0.55
2:B:311:ARG:HG2	2:B:311:ARG:HH11	1.71	0.55
2:B:424:ASN:HD22	2:B:424:ASN:C	2.10	0.55
2:B:93:VAL:O	2:B:114:LEU:CG	2.46	0.55
2:B:272:PHE:HB3	2:B:275:LEU:HD22	1.88	0.55
2:B:169:PHE:CZ	2:B:235:MET:HA	2.41	0.55
2:B:301:MET:CE	2:B:377:PHE:HE2	2.18	0.55
2:B:66:ILE:HD13	2:B:118:VAL:CG1	2.37	0.55
3:K:62:VAL:HA	3:K:104:GLN:CD	2.16	0.55
2:B:223:THR:HG22	2:B:224:TYR:N	2.21	0.55
1:A:174:ALA:CA	1:A:205:ASP:HB3	2.36	0.55
1:A:407:TRP:HD1	2:B:254:LYS:HA	1.71	0.55
2:B:151:THR:OG1	2:B:193:GLN:CB	2.54	0.55
2:B:191:VAL:HA	2:B:194:LEU:HD12	1.87	0.55
2:B:11:GLN:CD	6:B:602:G2P:O1A	2.42	0.55
3:K:292:LEU:HD11	3:K:320:PHE:CE1	2.40	0.55
3:K:292:LEU:CA	3:K:300:ILE:HD11	2.27	0.55
3:K:184:ILE:CG1	3:K:209:PHE:HE2	2.15	0.55
2:B:311:ARG:HD2	2:B:344:VAL:H	1.71	0.55
2:B:6:HIS:HB3	2:B:65:ALA:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:9:ILE:HD13	3:K:295:ASN:HD21	1.72	0.55
3:K:216:GLU:CG	3:K:223:LYS:HG2	2.36	0.55
2:B:31:ASP:O	2:B:32:PRO:C	2.44	0.55
1:A:176:GLN:N	1:A:207:GLU:CB	2.34	0.55
1:A:269:LEU:O	1:A:378:LEU:HA	2.06	0.55
1:A:205:ASP:OD2	1:A:391:LEU:HD22	2.07	0.55
2:B:139:HIS:HE1	2:B:168:THR:HG23	1.71	0.55
3:K:14:ARG:HH21	3:K:102:ASP:CB	2.00	0.55
2:B:210:TYR:HD1	2:B:227:LEU:HD21	1.71	0.55
1:A:110:ILE:CG2	1:A:111:GLY:H	2.15	0.55
1:A:150:THR:O	1:A:153:LEU:N	2.40	0.55
1:A:26:LEU:HD23	1:A:361:THR:CG2	2.33	0.55
2:B:258:ASN:CG	2:B:352:LYS:NZ	2.58	0.55
2:B:424:ASN:HA	3:K:276:HIS:NE2	2.22	0.55
2:B:176:LYS:HE3	2:B:207:GLU:HG3	1.88	0.55
3:K:137:GLU:CG	3:K:205:SER:OG	2.55	0.55
1:A:209:ILE:O	1:A:210:TYR:C	2.45	0.55
2:B:94:PHE:HD1	2:B:114:LEU:CD1	2.20	0.55
2:B:239:THR:HG22	2:B:240:THR:N	2.22	0.55
2:B:259:MET:CG	2:B:314:THR:HG21	2.36	0.55
2:B:297:ASP:OD1	2:B:298:ALA:N	2.39	0.55
2:B:166:MET:HB3	2:B:198:THR:OG1	2.06	0.54
2:B:20:PHE:CE1	2:B:24:ILE:HD12	2.42	0.54
3:K:139:TYR:O	3:K:283:LYS:CG	2.55	0.54
1:A:269:LEU:HD21	1:A:388:TRP:NE1	2.22	0.54
1:A:202:PHE:CE1	1:A:378:LEU:CB	2.91	0.54
2:B:93:VAL:HG13	2:B:114:LEU:CD1	2.37	0.54
2:B:239:THR:O	2:B:241:CYS:N	2.41	0.54
2:B:255:LEU:O	2:B:259:MET:CG	2.53	0.54
1:A:406:HIS:HB2	2:B:257:VAL:C	2.27	0.54
2:B:67:LEU:HD23	2:B:67:LEU:N	2.22	0.54
3:K:211:ILE:HB	3:K:228:LEU:HB3	1.89	0.54
1:A:248:LEU:HB3	1:A:355:ILE:H	1.72	0.54
3:K:41:ILE:HG22	3:K:41:ILE:O	2.06	0.54
3:K:284:MET:C	3:K:286:ARG:N	2.59	0.54
1:A:175:PRO:HB3	1:A:304:LYS:H	1.71	0.54
1:A:17:GLY:O	1:A:21:TRP:HB2	2.08	0.54
1:A:169:PHE:HE1	1:A:234:ILE:HD12	1.56	0.54
1:A:381:THR:C	1:A:385:ALA:HB2	2.28	0.54
2:B:12:CYS:CB	2:B:140:SER:OG	2.56	0.54
2:B:147:SER:CB	2:B:190:SER:HB3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:190:SER:O	2:B:194:LEU:HG	2.06	0.54
3:K:26:GLY:O	3:K:27:ASP:O	2.25	0.54
2:B:7:ILE:HG22	2:B:137:LEU:HD11	1.89	0.54
3:K:302:ILE:HG13	3:K:302:ILE:O	2.07	0.54
1:A:115:ILE:C	1:A:115:ILE:HD13	2.28	0.54
1:A:301:GLN:HE21	1:A:384:ILE:HG13	1.73	0.54
2:B:64:ARG:HH11	2:B:128:SER:HB3	1.72	0.54
1:A:163:LYS:O	1:A:163:LYS:HG2	2.08	0.54
1:A:143:GLY:HA2	5:A:502:GTP:PG	2.48	0.54
2:B:259:MET:CA	2:B:314:THR:HG21	2.35	0.54
2:B:325:MET:CE	2:B:355:VAL:HG11	2.38	0.54
3:K:283:LYS:O	3:K:283:LYS:HE2	2.06	0.54
3:K:324:ALA:O	3:K:327:ILE:CD1	2.53	0.54
2:B:98:GLY:CA	2:B:105:LYS:NZ	2.67	0.54
1:A:198:SER:HA	1:A:256:GLN:NE2	2.23	0.54
1:A:311:LYS:HE2	1:A:312:TYR:HE2	1.73	0.54
1:A:381:THR:HG22	1:A:382:THR:N	2.23	0.54
2:B:427:ASP:OD1	2:B:428:LEU:N	2.41	0.54
3:K:59:GLN:NE2	3:K:100:LEU:HD13	2.23	0.54
2:B:206:ASN:O	2:B:209:LEU:HB2	2.08	0.54
3:K:220:THR:O	3:K:221:GLU:HB2	2.08	0.54
1:A:23:LEU:HD13	1:A:361:THR:C	2.27	0.54
2:B:107:HIS:HD2	2:B:151:THR:HG22	1.72	0.54
2:B:242:LEU:HD22	2:B:250:ALA:N	2.19	0.54
2:B:201:THR:OG1	2:B:265:LEU:HD11	2.07	0.54
3:K:291:SER:HA	3:K:298:THR:HG23	1.90	0.54
3:K:62:VAL:C	3:K:106:MET:CE	2.73	0.54
2:B:213:CYS:SG	2:B:219:LEU:HD23	2.48	0.54
2:B:27:GLU:HG2	2:B:27:GLU:O	2.08	0.54
1:A:103:TYR:HE1	1:A:151:SER:OG	1.90	0.54
2:B:138:THR:CG2	2:B:235:MET:HE1	2.38	0.54
2:B:194:LEU:C	2:B:196:GLU:H	2.11	0.54
2:B:44:LEU:O	2:B:49:ILE:HG12	2.07	0.54
2:B:331:GLN:O	2:B:335:VAL:HG23	2.08	0.54
1:A:118:VAL:HG21	1:A:149:PHE:CZ	2.42	0.53
2:B:325:MET:O	2:B:329:ASP:HB2	2.07	0.53
3:K:65:ALA:HB2	3:K:104:GLN:HE22	1.65	0.53
2:B:31:ASP:HB3	2:B:32:PRO:HD2	1.89	0.53
1:A:324:VAL:O	1:A:327:ASP:HB2	2.08	0.53
1:A:102:ASN:HD21	1:A:412:GLY:CA	2.17	0.53
1:A:98:ASP:O	1:A:110:ILE:HD13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LEU:CD2	1:A:388:TRP:CE2	2.91	0.53
2:B:431:GLU:O	2:B:434:GLN:CG	2.56	0.53
3:K:277:VAL:HG12	3:K:277:VAL:O	2.08	0.53
1:A:242:LEU:C	1:A:244:PHE:H	2.09	0.53
1:A:6:SER:O	1:A:65:ALA:HB1	2.07	0.53
2:B:11:GLN:CB	6:B:602:G2P:O1A	2.56	0.53
1:A:210:TYR:CD1	5:A:502:GTP:C4	2.95	0.53
2:B:323:MET:HG3	2:B:328:VAL:HG21	1.90	0.53
3:K:137:GLU:CG	3:K:191:ARG:HG2	2.39	0.53
1:A:110:ILE:O	1:A:112:LYS:N	2.41	0.53
1:A:179:THR:CG2	2:B:248:LEU:CD1	2.56	0.53
1:A:182:VAL:O	1:A:184:PRO:N	2.41	0.53
1:A:133:GLN:CD	1:A:251:ASP:CG	2.66	0.53
1:A:407:TRP:CB	2:B:257:VAL:HG23	2.38	0.53
2:B:343:PHE:O	2:B:344:VAL:O	2.26	0.53
2:B:347:ILE:CB	2:B:348:PRO:HD3	2.27	0.53
2:B:5:VAL:O	2:B:5:VAL:HG23	2.09	0.53
1:A:339:ARG:C	1:A:341:ILE:H	2.11	0.53
1:A:121:ARG:O	1:A:125:LEU:HB2	2.08	0.53
2:B:322:ARG:HG3	2:B:322:ARG:HH11	1.73	0.53
1:A:211:ASP:O	1:A:215:ARG:N	2.41	0.53
1:A:9:VAL:CG1	1:A:139:HIS:HB3	2.38	0.53
2:B:93:VAL:C	2:B:114:LEU:CD1	2.76	0.53
2:B:226:ASP:O	2:B:227:LEU:C	2.46	0.53
1:A:11:GLN:CG	1:A:74:VAL:HG11	2.28	0.53
1:A:224:TYR:CE2	2:B:325:MET:SD	2.99	0.53
2:B:259:MET:HG2	2:B:314:THR:CG2	2.38	0.53
3:K:9:ILE:HD11	3:K:295:ASN:CG	2.29	0.53
2:B:229:HIS:ND1	2:B:229:HIS:C	2.62	0.53
1:A:213:CYS:O	1:A:219:ILE:HG13	2.08	0.53
1:A:380:ASN:O	1:A:432:TYR:CE1	2.57	0.53
2:B:114:LEU:HD23	2:B:149:MET:HE1	1.91	0.53
2:B:64:ARG:HD3	2:B:125:GLU:HB3	1.80	0.53
2:B:343:PHE:O	2:B:350:ASN:ND2	2.42	0.53
2:B:347:ILE:C	2:B:349:ASN:N	2.49	0.53
2:B:98:GLY:HA3	2:B:105:LYS:NZ	2.23	0.53
3:K:29:PHE:CD1	3:K:31:PRO:HD2	2.43	0.53
3:K:56:ASN:O	3:K:56:ASN:ND2	2.42	0.53
1:A:243:ARG:CZ	1:A:252:LEU:HG	2.39	0.53
1:A:303:VAL:HG11	1:A:384:ILE:HG21	0.54	0.53
2:B:36:TYR:CZ	2:B:38:GLY:HA3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:PRO:CA	1:A:207:GLU:CB	2.62	0.53
2:B:7:ILE:N	2:B:136:GLN:O	2.42	0.53
2:B:336:GLN:CG	2:B:351:VAL:HG21	2.39	0.53
2:B:21:TRP:CZ2	2:B:65:ALA:HB2	2.44	0.53
3:K:284:MET:HE3	3:K:285:THR:HG23	1.90	0.53
3:K:28:LYS:HE2	3:K:308:VAL:HG11	1.90	0.53
1:A:283:HIS:O	1:A:284:GLU:C	2.47	0.53
2:B:64:ARG:HH11	2:B:128:SER:CB	2.22	0.52
2:B:64:ARG:HD2	2:B:125:GLU:CB	2.31	0.52
2:B:70:LEU:HD12	2:B:145:THR:CG2	2.27	0.52
3:K:24:LEU:C	3:K:26:GLY:N	2.62	0.52
1:A:204:VAL:HG13	1:A:231:ILE:HD12	1.90	0.52
1:A:231:ILE:HD13	1:A:231:ILE:N	2.25	0.52
1:A:244:PHE:CD1	1:A:245:ASP:N	2.76	0.52
1:A:399:TYR:CE1	1:A:402:ARG:HA	2.43	0.52
1:A:226:ASN:CB	5:A:502:GTP:O6	2.57	0.52
2:B:2:ARG:HH12	2:B:50:ASN:HD22	1.56	0.52
3:K:59:GLN:C	3:K:106:MET:HG2	2.27	0.52
2:B:174:SER:HB2	2:B:207:GLU:CD	2.30	0.52
1:A:224:TYR:CD1	2:B:325:MET:CG	2.87	0.52
1:A:301:GLN:NE2	1:A:384:ILE:HG13	2.23	0.52
2:B:93:VAL:HA	2:B:114:LEU:HD11	1.91	0.52
2:B:94:PHE:N	2:B:114:LEU:CG	2.64	0.52
3:K:14:ARG:HE	3:K:103:PRO:HG2	1.01	0.52
2:B:226:ASP:O	2:B:229:HIS:N	2.42	0.52
1:A:23:LEU:HD13	1:A:361:THR:N	2.23	0.52
1:A:407:TRP:CG	2:B:258:ASN:ND2	2.77	0.52
1:A:182:VAL:CG1	1:A:408:TYR:CD2	2.56	0.52
2:B:8:GLN:OE1	2:B:14:ASN:ND2	2.42	0.52
2:B:64:ARG:HG3	2:B:125:GLU:CD	2.29	0.52
3:K:277:VAL:N	3:K:278:PRO:CD	2.73	0.52
3:K:135:TYR:CE2	3:K:187:GLY:C	2.83	0.52
2:B:93:VAL:HG22	2:B:117:SER:C	2.30	0.52
2:B:7:ILE:C	2:B:137:LEU:HD12	2.20	0.52
2:B:147:SER:O	2:B:151:THR:HB	2.09	0.52
3:K:284:MET:C	3:K:286:ARG:H	2.12	0.52
3:K:293:GLY:C	3:K:295:ASN:OD1	2.47	0.52
2:B:212:ILE:O	2:B:216:THR:HB	2.09	0.52
3:K:89:SER:CA	3:K:199:ASN:OD1	2.57	0.52
1:A:119:LEU:HD11	1:A:156:ARG:CD	2.40	0.52
2:B:264:ARG:HA	2:B:264:ARG:HE	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:105:LEU:HA	3:K:108:ILE:HD11	1.92	0.52
2:B:210:TYR:CD1	2:B:227:LEU:HD21	2.44	0.52
2:B:295:MET:SD	2:B:375:ALA:O	2.68	0.52
2:B:133:GLN:NE2	2:B:251:ASP:OD2	2.40	0.52
2:B:424:ASN:C	2:B:424:ASN:ND2	2.62	0.52
1:A:137:VAL:HG21	1:A:154:MET:HG2	1.92	0.52
1:A:150:THR:O	1:A:151:SER:C	2.47	0.52
1:A:209:ILE:HA	1:A:212:ILE:HD11	1.87	0.52
1:A:417:GLU:OE1	1:A:417:GLU:HA	2.10	0.52
2:B:169:PHE:CZ	2:B:235:MET:CB	2.93	0.52
1:A:181:VAL:HG11	2:B:258:ASN:OD1	2.09	0.52
2:B:425:MET:O	2:B:428:LEU:HB3	2.09	0.52
2:B:262:PHE:CZ	2:B:435:TYR:HE1	2.28	0.52
1:A:167:LEU:N	1:A:252:LEU:CB	2.73	0.52
1:A:23:LEU:CD1	1:A:361:THR:O	2.58	0.52
1:A:383:ALA:O	1:A:386:GLU:HB2	2.10	0.52
2:B:188:THR:HA	2:B:425:MET:CE	2.40	0.52
2:B:4:ILE:HG12	2:B:134:GLY:O	2.09	0.52
2:B:70:LEU:CD1	2:B:106:GLY:HA3	2.18	0.52
1:A:275:VAL:HG21	1:A:300:ASN:OD1	2.09	0.52
1:A:147:SER:CB	1:A:190:THR:OG1	2.52	0.52
2:B:107:HIS:CD2	2:B:151:THR:HG22	2.45	0.52
3:K:143:ILE:CD1	3:K:282:SER:O	2.53	0.52
3:K:324:ALA:O	3:K:325:LYS:C	2.48	0.52
3:K:59:GLN:O	3:K:106:MET:CB	2.55	0.52
2:B:320:ARG:HA	2:B:356:CYS:HB3	1.92	0.52
1:A:172:TYR:CE1	1:A:173:PRO:HD2	2.39	0.51
1:A:182:VAL:HG12	1:A:404:PHE:O	2.10	0.51
1:A:210:TYR:CZ	5:A:502:GTP:C8	2.99	0.51
1:A:311:LYS:HG2	1:A:311:LYS:O	2.10	0.51
2:B:147:SER:HB2	2:B:190:SER:CB	2.37	0.51
3:K:283:LYS:N	3:K:283:LYS:CD	2.73	0.51
3:K:233:LEU:CD1	3:K:288:LEU:CD1	2.67	0.51
3:K:59:GLN:HA	3:K:62:VAL:CG2	2.40	0.51
3:K:19:ASN:C	3:K:19:ASN:ND2	2.61	0.51
2:B:209:LEU:O	2:B:210:TYR:C	2.48	0.51
2:B:431:GLU:OE1	2:B:432:TYR:CA	2.57	0.51
2:B:9:ALA:C	2:B:146:GLY:HA2	2.30	0.51
3:K:104:GLN:C	3:K:106:MET:N	2.60	0.51
3:K:14:ARG:NH2	3:K:103:PRO:N	2.56	0.51
1:A:166:LYS:C	1:A:252:LEU:HB3	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:LYS:HB2	1:A:198:SER:HB2	1.92	0.51
2:B:132:LEU:CD2	2:B:164:ARG:HG3	2.32	0.51
2:B:314:THR:CG2	2:B:315:VAL:N	2.73	0.51
2:B:64:ARG:HG3	2:B:125:GLU:HG3	1.85	0.51
3:K:194:ALA:C	3:K:195:VAL:HG12	2.30	0.51
1:A:191:THR:HG23	1:A:424:ASP:OD2	2.09	0.51
1:A:191:THR:HG23	1:A:192:HIS:N	2.25	0.51
1:A:202:PHE:HZ	1:A:255:PHE:CE2	2.23	0.51
1:A:407:TRP:N	2:B:257:VAL:CB	2.56	0.51
2:B:149:MET:O	2:B:153:LEU:HD22	2.10	0.51
2:B:168:THR:CB	2:B:201:THR:HG23	2.38	0.51
2:B:49:ILE:O	2:B:50:ASN:C	2.48	0.51
3:K:29:PHE:HE2	3:K:55:PRO:HG2	1.74	0.51
1:A:8:HIS:HB3	1:A:13:GLY:O	2.10	0.51
2:B:106:GLY:O	2:B:149:MET:HB2	2.10	0.51
2:B:103:TRP:CZ2	2:B:189:LEU:O	2.64	0.51
2:B:21:TRP:HZ2	2:B:65:ALA:HB2	1.76	0.51
2:B:422:GLU:O	2:B:426:ASN:N	2.37	0.51
1:A:231:ILE:CA	1:A:234:ILE:HG22	2.38	0.51
1:A:268:PRO:HB3	1:A:380:ASN:OD1	2.10	0.51
2:B:149:MET:HG2	2:B:149:MET:O	2.10	0.51
2:B:3:GLU:O	2:B:4:ILE:HG13	2.09	0.51
3:K:9:ILE:HD12	3:K:327:ILE:HG12	1.88	0.51
3:K:107:GLY:C	3:K:110:PRO:HD2	2.27	0.51
2:B:260:VAL:HG23	2:B:260:VAL:O	2.11	0.51
1:A:239:THR:O	1:A:240:ALA:C	2.48	0.51
1:A:238:ILE:O	1:A:242:LEU:HB2	2.11	0.51
1:A:307:PRO:O	1:A:311:LYS:HB2	2.11	0.51
1:A:268:PRO:CB	1:A:379:SER:O	2.59	0.51
1:A:398:MET:CB	1:A:404:PHE:CE1	2.50	0.51
2:B:253:ARG:HH11	2:B:253:ARG:CG	2.24	0.51
2:B:265:LEU:O	2:B:266:HIS:O	2.29	0.51
3:K:59:GLN:HB3	3:K:106:MET:HB2	1.90	0.51
1:A:341:ILE:HD13	1:A:343:PHE:CZ	2.45	0.51
1:A:171:ILE:O	1:A:171:ILE:HG22	2.10	0.51
1:A:397:LEU:HD13	2:B:348:PRO:CD	2.38	0.51
1:A:67:PHE:HE2	1:A:87:PHE:CE2	2.29	0.51
1:A:140:SER:O	1:A:142:GLY:N	2.44	0.51
2:B:103:TRP:NE1	2:B:189:LEU:C	2.65	0.51
2:B:242:LEU:HD12	2:B:255:LEU:HD11	1.93	0.51
2:B:99:ALA:HB1	6:B:602:G2P:O2G	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:277:SER:OG	2:B:281:GLN:HB2	2.10	0.51
1:A:172:TYR:HB2	1:A:203:MET:HB3	1.92	0.51
1:A:224:TYR:CD1	2:B:325:MET:CB	2.93	0.51
1:A:269:LEU:HD12	1:A:382:THR:HG1	1.76	0.51
1:A:405:VAL:HG22	1:A:418:PHE:HE2	1.67	0.51
1:A:119:LEU:HA	1:A:122:ILE:HG12	1.93	0.50
1:A:227:LEU:HB2	5:A:502:GTP:N1	2.23	0.50
1:A:229:ARG:CZ	1:A:363:VAL:HG21	2.40	0.50
1:A:407:TRP:CA	2:B:257:VAL:CB	2.86	0.50
1:A:388:TRP:HD1	1:A:432:TYR:CE2	2.28	0.50
2:B:333:LEU:O	2:B:336:GLN:N	2.45	0.50
2:B:346:TRP:O	2:B:350:ASN:ND2	2.44	0.50
2:B:267:PHE:CG	2:B:388:PHE:CZ	2.99	0.50
2:B:298:ALA:O	2:B:299:LYS:C	2.50	0.50
1:A:270:ALA:CA	1:A:378:LEU:HD13	2.42	0.50
1:A:360:PRO:O	1:A:370:LYS:NZ	2.43	0.50
1:A:185:TYR:CG	1:A:408:TYR:CE2	2.88	0.50
2:B:93:VAL:CB	2:B:114:LEU:HG	2.27	0.50
3:K:83:PHE:HD2	3:K:291:SER:HB2	1.73	0.50
3:K:137:GLU:OE2	3:K:191:ARG:HG2	2.09	0.50
2:B:369:ARG:C	2:B:369:ARG:HD2	2.32	0.50
1:A:115:ILE:HD11	1:A:119:LEU:HG	1.92	0.50
1:A:202:PHE:HB3	1:A:270:ALA:HB2	1.93	0.50
1:A:261:PRO:HB2	1:A:262:TYR:CD2	2.46	0.50
1:A:301:GLN:HE22	1:A:383:ALA:HB3	0.85	0.50
1:A:143:GLY:HA2	5:A:502:GTP:O2G	2.11	0.50
2:B:280:SER:O	2:B:282:GLN:N	2.45	0.50
3:K:40:VAL:CG2	3:K:46:PRO:HB3	2.41	0.50
1:A:22:GLU:OE2	1:A:364:PRO:CG	2.59	0.50
1:A:320:ARG:HD3	1:A:360:PRO:HB3	1.94	0.50
2:B:103:TRP:CE3	2:B:189:LEU:CG	2.86	0.50
2:B:106:GLY:O	2:B:149:MET:N	2.45	0.50
2:B:24:ILE:HG22	2:B:25:SER:N	2.27	0.50
2:B:383:ALA:C	2:B:385:GLN:H	2.15	0.50
2:B:3:GLU:OE1	2:B:50:ASN:HB3	2.11	0.50
3:K:14:ARG:NH1	3:K:95:THR:CB	2.73	0.50
1:A:16:ILE:CD1	1:A:231:ILE:O	2.59	0.50
2:B:265:LEU:HD12	2:B:266:HIS:O	2.12	0.50
3:K:89:SER:OG	3:K:199:ASN:OD1	2.30	0.50
3:K:87:GLN:O	3:K:90:SER:HB3	2.11	0.50
1:A:141:PHE:HD2	1:A:172:TYR:CD1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:173:PRO:HB3	2:B:183:GLU:HG2	1.93	0.50
2:B:196:GLU:OE2	3:K:280:ARG:HD3	2.10	0.50
2:B:49:ILE:HG13	2:B:50:ASN:H	1.75	0.50
1:A:132:LEU:CD2	1:A:164:LYS:HE3	2.41	0.50
1:A:172:TYR:CG	1:A:205:ASP:OD1	2.65	0.50
1:A:185:TYR:CG	1:A:418:PHE:CZ	2.98	0.50
2:B:173:PRO:HB3	2:B:183:GLU:CG	2.42	0.50
3:K:59:GLN:C	3:K:106:MET:CB	2.80	0.50
1:A:344:VAL:HG22	1:A:345:ASP:N	2.27	0.50
1:A:12:ALA:CB	1:A:140:SER:OG	2.59	0.50
1:A:405:VAL:CG2	1:A:418:PHE:CD2	2.73	0.50
1:A:397:LEU:HD12	2:B:348:PRO:CG	2.26	0.50
2:B:175:PRO:CD	2:B:207:GLU:CD	2.76	0.50
2:B:230:LEU:HD21	2:B:302:MET:HE2	1.94	0.50
1:A:138:PHE:CE1	1:A:235:VAL:C	2.76	0.50
1:A:264:ARG:C	1:A:266:HIS:N	2.60	0.50
2:B:188:THR:HA	2:B:425:MET:HE3	1.93	0.50
3:K:81:THR:CB	3:K:290:ASP:OD2	2.60	0.50
3:K:83:PHE:HE1	3:K:230:LEU:C	2.15	0.50
3:K:79:ASN:ND2	3:K:227:LYS:H	2.10	0.50
2:B:313:LEU:CD2	2:B:382:THR:HG23	2.39	0.50
1:A:16:ILE:HG23	1:A:17:GLY:N	2.26	0.49
1:A:230:LEU:O	1:A:233:GLN:N	2.35	0.49
1:A:208:ALA:HA	1:A:304:LYS:O	2.12	0.49
2:B:196:GLU:OE1	3:K:280:ARG:CZ	2.57	0.49
2:B:258:ASN:CG	2:B:352:LYS:HZ2	2.15	0.49
2:B:323:MET:HG3	2:B:328:VAL:CG2	2.41	0.49
3:K:74:VAL:CG1	3:K:213:ILE:HD12	2.42	0.49
1:A:9:VAL:HG21	1:A:149:PHE:CD1	2.46	0.49
1:A:185:TYR:CE1	1:A:418:PHE:HB3	2.47	0.49
1:A:209:ILE:O	1:A:212:ILE:HG13	2.12	0.49
2:B:296:PHE:CZ	2:B:315:VAL:HG11	2.46	0.49
3:K:206:HIS:HD2	3:K:287:ILE:CD1	1.96	0.49
3:K:135:TYR:HE2	3:K:184:ILE:O	1.94	0.49
2:B:240:THR:HG23	2:B:241:CYS:H	1.76	0.49
1:A:115:ILE:CG2	1:A:116:ASP:N	2.75	0.49
1:A:266:HIS:ND1	1:A:431:ASP:CB	2.74	0.49
2:B:113:GLU:HG3	2:B:114:LEU:N	2.26	0.49
2:B:64:ARG:HH12	2:B:128:SER:HG	1.58	0.49
2:B:128:SER:HG	2:B:129:CYS:H	1.60	0.49
3:K:89:SER:CB	3:K:197:ASN:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:HB3	1:A:193:THR:CG2	2.34	0.49
1:A:169:PHE:CE1	1:A:234:ILE:CB	2.94	0.49
1:A:242:LEU:C	1:A:244:PHE:N	2.66	0.49
1:A:407:TRP:CE3	1:A:408:TYR:CE1	2.97	0.49
2:B:168:THR:O	2:B:201:THR:HA	2.12	0.49
2:B:387:LEU:HD23	2:B:388:PHE:CD1	2.47	0.49
2:B:428:LEU:O	3:K:274:LYS:NZ	2.45	0.49
2:B:93:VAL:C	2:B:114:LEU:HD11	2.32	0.49
1:A:251:ASP:OD1	1:A:252:LEU:N	2.44	0.49
3:K:89:SER:OG	3:K:196:THR:OG1	2.29	0.49
3:K:74:VAL:HG11	3:K:213:ILE:HD12	1.94	0.49
1:A:191:THR:C	1:A:195:LEU:HG	2.15	0.49
1:A:182:VAL:HG22	1:A:407:TRP:CE3	2.41	0.49
2:B:93:VAL:C	2:B:114:LEU:HG	2.18	0.49
2:B:266:HIS:ND1	2:B:432:TYR:CE1	2.81	0.49
2:B:11:GLN:CG	6:B:602:G2P:O1A	2.61	0.49
3:K:27:ASP:HA	3:K:28:LYS:HZ2	1.77	0.49
1:A:414:GLU:OE1	1:A:414:GLU:N	2.45	0.49
2:B:431:GLU:CB	3:K:274:LYS:HD3	2.21	0.49
3:K:81:THR:HG23	3:K:83:PHE:CZ	2.48	0.49
3:K:99:LYS:HG3	3:K:100:LEU:H	1.77	0.49
1:A:11:GLN:O	1:A:14:VAL:HB	2.12	0.49
1:A:269:LEU:N	1:A:378:LEU:HD12	2.27	0.49
1:A:399:TYR:N	1:A:403:ALA:HB2	2.22	0.49
1:A:185:TYR:CD1	1:A:418:PHE:HB3	2.46	0.49
2:B:262:PHE:O	2:B:264:ARG:N	2.45	0.49
3:K:233:LEU:CD2	3:K:288:LEU:HD11	2.21	0.49
3:K:87:GLN:O	3:K:88:THR:C	2.51	0.49
1:A:191:THR:CG2	1:A:192:HIS:N	2.76	0.49
1:A:398:MET:HG2	2:B:349:ASN:HB2	1.93	0.49
2:B:93:VAL:CG2	2:B:118:VAL:HG23	2.02	0.49
3:K:107:GLY:O	3:K:108:ILE:C	2.50	0.49
1:A:283:HIS:O	1:A:285:GLN:N	2.46	0.49
1:A:274:PRO:CB	1:A:371:VAL:HG21	2.43	0.49
1:A:186:ASN:ND2	1:A:408:TYR:CE1	2.70	0.48
1:A:244:PHE:C	1:A:244:PHE:CD1	2.84	0.48
1:A:407:TRP:O	1:A:411:GLU:HG3	2.12	0.48
1:A:96:LYS:O	1:A:97:GLU:O	2.31	0.48
2:B:191:VAL:HG13	2:B:192:HIS:N	2.28	0.48
2:B:266:HIS:HA	2:B:432:TYR:OH	2.12	0.48
3:K:111:ARG:CG	3:K:111:ARG:NH1	2.73	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:88:THR:O	3:K:196:THR:OG1	2.30	0.48
1:A:122:ILE:HB	1:A:135:PHE:CE1	2.40	0.48
1:A:182:VAL:CG1	1:A:407:TRP:HB3	2.43	0.48
1:A:177:VAL:H	1:A:207:GLU:CB	2.24	0.48
2:B:169:PHE:CE1	2:B:235:MET:HB2	2.48	0.48
2:B:296:PHE:HZ	2:B:315:VAL:HG11	1.78	0.48
3:K:109:ILE:N	3:K:110:PRO:HD2	2.28	0.48
1:A:104:ALA:HB2	1:A:413:MET:HA	1.96	0.48
1:A:231:ILE:O	1:A:235:VAL:HG23	2.12	0.48
2:B:93:VAL:CA	2:B:114:LEU:HD11	2.43	0.48
2:B:137:LEU:HD22	2:B:154:ILE:HG21	1.95	0.48
2:B:336:GLN:CD	2:B:351:VAL:HG23	2.33	0.48
2:B:431:GLU:HA	2:B:434:GLN:CG	2.42	0.48
1:A:27:GLU:CG	1:A:358:GLU:CG	2.85	0.48
1:A:115:ILE:O	1:A:116:ASP:C	2.51	0.48
1:A:149:PHE:HE1	1:A:153:LEU:HD22	1.77	0.48
1:A:269:LEU:N	1:A:378:LEU:CD1	2.76	0.48
1:A:401:LYS:HD2	2:B:346:TRP:CZ2	2.49	0.48
3:K:277:VAL:N	3:K:278:PRO:HD3	2.21	0.48
3:K:283:LYS:HE2	3:K:284:MET:O	2.13	0.48
1:A:328:VAL:C	1:A:330:ALA:H	2.15	0.48
1:A:167:LEU:N	1:A:252:LEU:HB3	2.29	0.48
1:A:188:ILE:O	1:A:191:THR:HG22	2.13	0.48
1:A:174:ALA:HB2	1:A:207:GLU:H	1.59	0.48
1:A:165:SER:CB	1:A:253:THR:N	2.72	0.48
1:A:6:SER:OG	1:A:65:ALA:HB2	2.14	0.48
2:B:104:ALA:HA	2:B:413:MET:HE1	1.95	0.48
2:B:93:VAL:CG2	2:B:118:VAL:N	2.74	0.48
2:B:237:GLY:O	2:B:241:CYS:CB	2.61	0.48
2:B:431:GLU:OE1	2:B:432:TYR:N	2.46	0.48
3:K:208:ILE:N	3:K:208:ILE:HD12	2.28	0.48
3:K:82:ILE:HA	3:K:299:THR:O	2.13	0.48
3:K:83:PHE:HE2	3:K:287:ILE:O	1.96	0.48
3:K:102:ASP:CG	3:K:103:PRO:HD3	2.34	0.48
2:B:209:LEU:CD2	2:B:227:LEU:HD13	2.43	0.48
3:K:86:GLY:O	3:K:92:LYS:HE3	2.13	0.48
1:A:172:TYR:O	1:A:204:VAL:C	2.52	0.48
1:A:171:ILE:CA	1:A:204:VAL:HG12	2.29	0.48
1:A:262:TYR:HB2	1:A:266:HIS:NE2	2.29	0.48
1:A:99:ALA:O	1:A:100:ALA:HB3	2.14	0.48
2:B:308:ARG:HG3	2:B:342:TYR:OH	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:ILE:HG13	2:B:50:ASN:N	2.28	0.48
2:B:8:GLN:HB3	2:B:14:ASN:HA	1.95	0.48
2:B:281:GLN:C	2:B:283:TYR:N	2.67	0.48
3:K:124:ASP:OD1	3:K:124:ASP:C	2.51	0.48
1:A:118:VAL:HG21	1:A:149:PHE:CE2	2.48	0.48
1:A:165:SER:CA	1:A:252:LEU:CB	2.76	0.48
1:A:169:PHE:CD2	1:A:238:ILE:HG13	2.33	0.48
1:A:224:TYR:O	1:A:228:ASN:ND2	2.46	0.48
1:A:425:MET:HE3	1:A:428:LEU:HD23	1.95	0.48
2:B:269:MET:HB3	2:B:303:ALA:HB2	1.94	0.48
2:B:413:MET:HG3	2:B:414:ASP:N	2.22	0.48
3:K:109:ILE:HB	3:K:110:PRO:CD	2.43	0.48
2:B:209:LEU:O	2:B:213:CYS:N	2.47	0.48
3:K:90:SER:OG	3:K:303:CYS:HB2	2.13	0.48
1:A:105:ARG:NH1	1:A:105:ARG:HG3	2.27	0.48
1:A:163:LYS:C	1:A:164:LYS:HG2	2.33	0.48
1:A:185:TYR:HH	1:A:405:VAL:HG23	1.77	0.48
2:B:154:ILE:HG22	2:B:166:MET:CE	2.44	0.48
3:K:140:LEU:HD21	3:K:284:MET:CE	2.43	0.48
3:K:291:SER:O	3:K:300:ILE:HD11	2.10	0.48
1:A:392:ASP:O	1:A:395:PHE:HB3	2.13	0.48
2:B:142:GLY:HA3	2:B:183:GLU:OE2	2.13	0.48
2:B:199:ASP:O	2:B:200:GLU:HG3	2.13	0.48
2:B:104:ALA:CA	2:B:413:MET:HE1	2.44	0.48
2:B:399:PHE:O	2:B:400:ARG:C	2.51	0.48
1:A:172:TYR:CD1	1:A:173:PRO:CD	2.67	0.48
2:B:115:VAL:CG2	2:B:152:LEU:HD23	2.43	0.48
2:B:101:ASN:HD21	2:B:186:ASN:ND2	2.12	0.48
2:B:263:PRO:O	2:B:264:ARG:C	2.52	0.48
3:K:25:ARG:HH12	3:K:309:PHE:CB	2.27	0.48
2:B:204:ILE:HD13	2:B:231:VAL:HG22	1.96	0.48
1:A:369:ALA:O	1:A:370:LYS:CB	2.62	0.47
2:B:20:PHE:O	2:B:24:ILE:HB	2.14	0.47
1:A:335:ILE:O	1:A:337:THR:N	2.47	0.47
1:A:154:MET:HA	1:A:157:LEU:HD12	1.96	0.47
1:A:166:LYS:H	1:A:252:LEU:HB3	1.74	0.47
1:A:269:LEU:HD23	1:A:388:TRP:NE1	2.27	0.47
2:B:196:GLU:CD	3:K:280:ARG:HD3	2.35	0.47
2:B:3:GLU:CD	2:B:64:ARG:HH22	2.17	0.47
1:A:97:GLU:HB2	1:A:110:ILE:HD11	1.96	0.47
1:A:132:LEU:H	1:A:132:LEU:CD2	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:VAL:O	1:A:260:VAL:CG2	2.63	0.47
1:A:399:TYR:N	1:A:403:ALA:CB	2.77	0.47
1:A:407:TRP:O	1:A:411:GLU:CG	2.63	0.47
2:B:242:LEU:CD1	2:B:250:ALA:HB3	2.45	0.47
1:A:407:TRP:HZ2	2:B:254:LYS:NZ	2.10	0.47
2:B:266:HIS:CG	2:B:432:TYR:CE1	3.02	0.47
2:B:24:ILE:CD1	2:B:52:TYR:CE2	2.97	0.47
3:K:28:LYS:H	3:K:28:LYS:HD2	1.78	0.47
3:K:138:ILE:H	3:K:205:SER:HB2	1.80	0.47
2:B:297:ASP:OD2	2:B:299:LYS:HE2	2.14	0.47
1:A:132:LEU:HD21	1:A:164:LYS:HE3	1.96	0.47
2:B:101:ASN:O	2:B:101:ASN:ND2	2.47	0.47
2:B:176:LYS:HG3	2:B:177:VAL:H	1.78	0.47
3:K:121:TYR:OH	3:K:177:PRO:HD3	2.14	0.47
1:A:312:TYR:CD2	1:A:437:VAL:HG22	2.49	0.47
1:A:9:VAL:HG11	1:A:150:THR:OG1	2.13	0.47
2:B:20:PHE:CG	2:B:235:MET:SD	3.07	0.47
2:B:264:ARG:HA	2:B:264:ARG:NE	2.29	0.47
2:B:336:GLN:NE2	2:B:351:VAL:CG2	2.77	0.47
2:B:427:ASP:CB	3:K:276:HIS:CD2	2.98	0.47
2:B:93:VAL:HG12	2:B:114:LEU:CB	2.39	0.47
1:A:362:VAL:HG13	1:A:368:LEU:HG	1.94	0.47
1:A:107:HIS:CE1	1:A:152:LEU:HB3	2.49	0.47
1:A:388:TRP:HD1	1:A:432:TYR:CD2	2.32	0.47
2:B:101:ASN:HD21	2:B:186:ASN:HD21	1.63	0.47
2:B:198:THR:HG23	2:B:200:GLU:H	1.79	0.47
2:B:91:ASN:ND2	2:B:121:VAL:CG1	2.76	0.47
3:K:139:TYR:CD1	3:K:143:ILE:HG12	2.50	0.47
3:K:290:ASP:OD1	3:K:295:ASN:HB3	2.14	0.47
2:B:211:ASP:OD1	2:B:212:ILE:HG13	2.14	0.47
3:K:89:SER:N	3:K:196:THR:OG1	2.47	0.47
1:A:11:GLN:O	1:A:15:GLN:HG3	2.15	0.47
3:K:132:LYS:HE2	3:K:214:LYS:CE	2.42	0.47
1:A:434:GLU:C	1:A:436:GLY:H	2.18	0.47
1:A:147:SER:O	1:A:190:THR:HG23	2.14	0.47
1:A:217:LEU:CD1	1:A:277:SER:HA	2.44	0.47
1:A:255:PHE:O	1:A:256:GLN:C	2.53	0.47
2:B:134:GLY:HA3	2:B:165:ILE:HG12	1.97	0.47
2:B:147:SER:HB2	2:B:186:ASN:O	2.15	0.47
1:A:122:ILE:CD1	1:A:157:LEU:HD21	2.35	0.47
1:A:155:GLU:HG2	1:A:197:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:GLN:HA	1:A:260:VAL:HG13	1.97	0.47
1:A:265:GLY:O	1:A:266:HIS:O	2.33	0.47
1:A:267:PHE:CE1	1:A:428:LEU:CB	2.82	0.47
2:B:264:ARG:CD	3:K:274:LYS:CG	2.88	0.47
2:B:307:PRO:HB3	2:B:312:TYR:CZ	2.49	0.47
3:K:184:ILE:HG13	3:K:209:PHE:CE2	2.46	0.47
3:K:21:ALA:HA	3:K:24:LEU:HB3	1.97	0.47
3:K:137:GLU:HG2	3:K:138:ILE:HG23	1.86	0.47
1:A:34:GLY:C	1:A:61:HIS:N	2.68	0.47
1:A:145:THR:O	1:A:149:PHE:HB3	2.15	0.47
1:A:209:ILE:HG12	1:A:302:MET:HG2	1.40	0.47
1:A:169:PHE:HE2	1:A:238:ILE:H	1.60	0.47
2:B:332:MET:HE3	2:B:351:VAL:CG1	2.43	0.47
2:B:3:GLU:HA	2:B:51:VAL:HA	1.97	0.47
2:B:68:VAL:HG21	2:B:153:LEU:HG	1.95	0.47
3:K:284:MET:O	3:K:285:THR:OG1	2.32	0.47
3:K:88:THR:O	3:K:89:SER:HB2	2.15	0.47
2:B:287:THR:N	2:B:290:GLU:OE1	2.48	0.47
1:A:392:ASP:OD1	1:A:422:ARG:NE	2.48	0.47
2:B:169:PHE:CD1	2:B:235:MET:CE	2.98	0.47
3:K:83:PHE:HE1	3:K:230:LEU:CA	2.28	0.47
2:B:226:ASP:O	2:B:229:HIS:HB3	2.14	0.47
1:A:286:LEU:CD1	1:A:290:GLU:HG2	2.44	0.47
2:B:35:SER:CB	2:B:59:ASN:HA	2.42	0.47
1:A:203:MET:CB	1:A:388:TRP:CH2	2.98	0.47
1:A:278:ALA:O	1:A:279:GLU:HG2	2.15	0.47
1:A:399:TYR:CA	1:A:403:ALA:HB3	2.35	0.47
2:B:196:GLU:O	2:B:197:ASN:OD1	2.33	0.47
3:K:283:LYS:H	3:K:286:ARG:HD3	1.80	0.47
3:K:293:GLY:HA2	3:K:327:ILE:HG23	1.96	0.47
1:A:226:ASN:O	1:A:229:ARG:N	2.48	0.46
1:A:241:SER:HB3	1:A:320:ARG:NH2	2.29	0.46
1:A:253:THR:O	1:A:254:GLU:C	2.52	0.46
3:K:231:VAL:HG21	3:K:287:ILE:HG22	1.97	0.46
3:K:14:ARG:HG3	3:K:103:PRO:CB	2.40	0.46
3:K:138:ILE:N	3:K:205:SER:HB2	2.29	0.46
1:A:10:GLY:O	1:A:11:GLN:C	2.53	0.46
3:K:75:LEU:HD23	3:K:213:ILE:HG21	1.96	0.46
1:A:120:ASP:O	1:A:124:LYS:HB2	2.15	0.46
1:A:151:SER:OG	1:A:193:THR:HG21	2.13	0.46
1:A:22:GLU:O	1:A:23:LEU:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:103:TRP:HZ3	2:B:417:GLU:CG	2.27	0.46
2:B:387:LEU:O	2:B:387:LEU:HG	2.15	0.46
2:B:267:PHE:CG	2:B:388:PHE:HZ	2.32	0.46
3:K:11:VAL:HG22	3:K:300:ILE:HB	1.97	0.46
2:B:175:PRO:O	2:B:176:LYS:C	2.52	0.46
1:A:339:ARG:C	1:A:341:ILE:N	2.67	0.46
1:A:164:LYS:O	1:A:253:THR:HG23	2.15	0.46
1:A:206:ASN:O	1:A:210:TYR:HB2	2.15	0.46
1:A:209:ILE:O	1:A:212:ILE:CA	2.60	0.46
1:A:209:ILE:O	1:A:212:ILE:CG1	2.63	0.46
1:A:396:ASP:O	1:A:397:LEU:C	2.53	0.46
2:B:243:ARG:N	2:B:243:ARG:HD3	2.25	0.46
2:B:336:GLN:CG	2:B:351:VAL:CG2	2.94	0.46
2:B:165:ILE:CG1	2:B:252:LEU:HD12	2.40	0.46
2:B:307:PRO:C	2:B:309:HIS:H	2.18	0.46
2:B:70:LEU:O	2:B:99:ALA:HB2	2.15	0.46
3:K:14:ARG:HH21	3:K:103:PRO:HD2	0.63	0.46
1:A:115:ILE:HG23	1:A:116:ASP:H	1.79	0.46
1:A:7:ILE:HG13	1:A:137:VAL:HG22	1.97	0.46
1:A:200:CYS:CB	1:A:255:PHE:CB	2.91	0.46
1:A:4:CYS:CB	1:A:243:ARG:HB3	2.26	0.46
1:A:256:GLN:O	1:A:260:VAL:HG13	2.15	0.46
1:A:185:TYR:HE2	1:A:404:PHE:C	2.18	0.46
1:A:25:CYS:SG	1:A:83:TYR:HE2	2.38	0.46
2:B:52:TYR:CZ	2:B:136:GLN:HG3	2.51	0.46
2:B:185:TYR:HD1	2:B:395:PHE:CE1	2.33	0.46
2:B:237:GLY:HA3	2:B:376:THR:OG1	2.15	0.46
3:K:206:HIS:HD2	3:K:208:ILE:CD1	2.09	0.46
3:K:231:VAL:HG21	3:K:288:LEU:HA	1.95	0.46
2:B:209:LEU:HD23	2:B:227:LEU:HD13	1.98	0.46
1:A:286:LEU:O	1:A:287:SER:O	2.34	0.46
1:A:234:ILE:CG1	1:A:270:ALA:HB1	2.38	0.46
1:A:278:ALA:HB2	1:A:369:ALA:CA	2.45	0.46
1:A:22:GLU:OE2	1:A:364:PRO:HG2	2.16	0.46
1:A:423:GLU:O	1:A:426:ALA:HB3	2.16	0.46
2:B:262:PHE:CZ	3:K:271:GLU:OE1	2.67	0.46
2:B:66:ILE:HD11	2:B:122:VAL:HB	1.96	0.46
1:A:317:LEU:CD1	1:A:351:PHE:CD1	2.97	0.46
1:A:148:GLY:O	1:A:149:PHE:C	2.54	0.46
1:A:185:TYR:OH	1:A:399:TYR:CD1	2.66	0.46
2:B:133:GLN:O	2:B:165:ILE:CD1	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:196:GLU:CD	3:K:280:ARG:CD	2.83	0.46
3:K:293:GLY:HA2	3:K:327:ILE:HG21	1.97	0.46
3:K:30:ILE:HD13	3:K:308:VAL:HB	1.98	0.46
2:B:208:ALA:O	2:B:212:ILE:HG13	2.16	0.46
1:A:9:VAL:HG21	1:A:149:PHE:HD1	1.80	0.46
1:A:148:GLY:O	1:A:151:SER:CB	2.62	0.46
1:A:241:SER:C	1:A:244:PHE:HB3	2.36	0.46
1:A:200:CYS:HB3	1:A:255:PHE:HB3	1.95	0.46
2:B:135:PHE:CD1	2:B:135:PHE:N	2.84	0.46
2:B:428:LEU:C	3:K:274:LYS:NZ	2.69	0.46
2:B:6:HIS:HB3	2:B:21:TRP:HZ2	1.81	0.46
3:K:136:PHE:HD2	3:K:139:TYR:HH	0.52	0.46
2:B:424:ASN:ND2	3:K:276:HIS:NE2	2.58	0.46
2:B:175:PRO:N	2:B:207:GLU:OE1	2.49	0.46
1:A:202:PHE:CE2	1:A:238:ILE:HG21	2.46	0.46
1:A:207:GLU:N	5:A:502:GTP:O2'	2.49	0.46
1:A:266:HIS:HA	1:A:428:LEU:CD1	2.45	0.46
1:A:303:VAL:C	1:A:387:ALA:CB	2.80	0.46
2:B:113:GLU:CG	2:B:114:LEU:N	2.79	0.46
2:B:154:ILE:HD12	2:B:155:SER:N	2.31	0.46
2:B:70:LEU:CD1	2:B:106:GLY:N	2.79	0.46
3:K:139:TYR:HE2	3:K:208:ILE:HD13	1.76	0.46
3:K:16:ARG:HG3	3:K:16:ARG:HH11	1.81	0.46
1:A:324:VAL:HG12	1:A:326:LYS:H	1.81	0.46
1:A:384:ILE:HA	1:A:387:ALA:N	2.31	0.46
2:B:408:TYR:O	2:B:411:GLU:HB2	2.16	0.46
3:K:82:ILE:C	3:K:83:PHE:CD1	2.85	0.46
3:K:16:ARG:NE	3:K:89:SER:O	2.49	0.46
2:B:273:ALA:CB	2:B:274:PRO:CD	2.93	0.46
1:A:288:VAL:HA	1:A:291:ILE:HG12	1.97	0.46
1:A:267:PHE:CE1	1:A:428:LEU:HD13	2.18	0.45
1:A:143:GLY:HA2	5:A:502:GTP:O3G	2.16	0.45
2:B:64:ARG:HA	2:B:125:GLU:OE2	2.16	0.45
2:B:103:TRP:CA	2:B:408:TYR:CE2	2.89	0.45
1:A:362:VAL:CG1	1:A:368:LEU:CB	2.89	0.45
3:K:29:PHE:CE1	3:K:31:PRO:HD2	2.51	0.45
1:A:117:LEU:HD12	1:A:121:ARG:HH12	1.80	0.45
3:K:18:LEU:HD23	3:K:306:PRO:HG2	1.97	0.45
1:A:7:ILE:CG1	1:A:137:VAL:HG22	2.46	0.45
1:A:169:PHE:CE1	1:A:235:VAL:HG23	2.50	0.45
1:A:212:ILE:HD11	1:A:302:MET:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:384:ILE:HG23	2:B:384:ILE:O	2.14	0.45
3:K:282:SER:HA	3:K:286:ARG:HD3	1.98	0.45
1:A:286:LEU:HG	1:A:290:GLU:HB2	1.98	0.45
2:B:224:TYR:O	2:B:225:GLY:C	2.53	0.45
1:A:114:ILE:O	1:A:118:VAL:HG23	2.16	0.45
1:A:115:ILE:CG1	1:A:152:LEU:HD13	2.46	0.45
2:B:115:VAL:HG21	2:B:152:LEU:HD21	1.98	0.45
2:B:253:ARG:HH11	2:B:253:ARG:HG2	1.79	0.45
2:B:72:PRO:O	2:B:74:THR:N	2.50	0.45
2:B:210:TYR:CE1	2:B:227:LEU:HD11	2.52	0.45
2:B:100:GLY:HA3	2:B:105:LYS:CD	2.40	0.45
2:B:360:PRO:O	2:B:369:ARG:C	2.54	0.45
1:A:291:ILE:HD12	1:A:375:VAL:HG23	1.99	0.45
2:B:288:VAL:N	2:B:289:PRO:CD	2.79	0.45
1:A:169:PHE:CG	1:A:238:ILE:HG13	2.51	0.45
1:A:23:LEU:O	1:A:26:LEU:HB3	2.17	0.45
2:B:137:LEU:HD22	2:B:154:ILE:HG23	1.98	0.45
2:B:242:LEU:HD11	2:B:250:ALA:HB3	1.97	0.45
2:B:332:MET:CE	2:B:351:VAL:HG12	2.40	0.45
2:B:4:ILE:HG23	2:B:135:PHE:HA	1.99	0.45
2:B:176:LYS:HG2	2:B:207:GLU:OE1	2.16	0.45
1:A:274:PRO:HB2	1:A:371:VAL:HG21	1.98	0.45
1:A:286:LEU:O	1:A:287:SER:C	2.55	0.45
1:A:334:THR:CG2	1:A:335:ILE:N	2.79	0.45
1:A:309:HIS:NE2	1:A:338:LYS:HD3	2.32	0.45
1:A:202:PHE:CA	1:A:378:LEU:HD21	2.42	0.45
2:B:103:TRP:CZ3	2:B:417:GLU:HG3	2.51	0.45
3:K:14:ARG:CD	3:K:95:THR:CG2	2.94	0.45
1:A:11:GLN:HE21	1:A:74:VAL:CG2	2.29	0.45
1:A:182:VAL:O	1:A:184:PRO:CD	2.65	0.45
1:A:276:ILE:HG12	1:A:277:SER:N	2.32	0.45
1:A:381:THR:O	1:A:385:ALA:N	2.50	0.45
1:A:185:TYR:CE1	1:A:399:TYR:HD1	2.33	0.45
1:A:407:TRP:CB	2:B:258:ASN:ND2	2.79	0.45
2:B:4:ILE:HG21	2:B:136:GLN:CG	2.45	0.45
2:B:94:PHE:N	2:B:94:PHE:CD1	2.84	0.45
3:K:19:ASN:N	3:K:22:GLU:OE1	2.37	0.45
1:A:117:LEU:HD11	1:A:121:ARG:NH2	2.30	0.45
1:A:280:LYS:HB3	1:A:281:ALA:H	1.49	0.45
3:K:310:ASN:O	3:K:312:ALA:N	2.49	0.45
2:B:202:TYR:HE2	2:B:378:ILE:HG21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ARG:HH11	1:A:363:VAL:HG21	1.73	0.45
1:A:392:ASP:OD1	1:A:422:ARG:CZ	2.64	0.45
2:B:242:LEU:HA	2:B:242:LEU:HD23	1.76	0.45
2:B:254:LYS:HB3	2:B:254:LYS:HE3	1.88	0.45
2:B:323:MET:CE	2:B:328:VAL:HG22	2.46	0.45
3:K:194:ALA:HB1	3:K:204:ARG:HE	1.80	0.45
3:K:217:ASN:CG	3:K:220:THR:HG23	2.36	0.45
1:A:152:LEU:HD12	1:A:152:LEU:C	2.38	0.45
1:A:407:TRP:HB2	2:B:257:VAL:HG23	1.98	0.45
2:B:324:SER:OG	2:B:326:LYS:HB3	2.16	0.45
3:K:279:TYR:HD1	3:K:280:ARG:N	2.13	0.45
3:K:20:GLU:O	3:K:23:ILE:HG22	2.16	0.45
1:A:27:GLU:HG3	1:A:358:GLU:OE1	2.14	0.45
2:B:288:VAL:N	2:B:289:PRO:HD2	2.32	0.45
3:K:194:ALA:CB	3:K:204:ARG:HE	2.30	0.45
1:A:363:VAL:C	1:A:365:GLY:N	2.69	0.45
2:B:11:GLN:O	2:B:14:ASN:HB3	2.16	0.45
2:B:269:MET:HE1	2:B:381:SER:OG	2.16	0.45
2:B:258:ASN:CB	2:B:352:LYS:HD2	2.47	0.45
3:K:139:TYR:O	3:K:283:LYS:HG3	2.17	0.45
2:B:212:ILE:O	2:B:212:ILE:HG22	2.17	0.45
1:A:271:THR:O	1:A:376:CYS:HA	2.17	0.45
3:K:194:ALA:HB2	3:K:204:ARG:HG2	1.98	0.45
1:A:119:LEU:HD11	1:A:156:ARG:HD2	1.97	0.45
1:A:229:ARG:NH1	1:A:229:ARG:HG2	2.31	0.45
1:A:407:TRP:CE3	1:A:408:TYR:CD1	3.05	0.45
1:A:407:TRP:CZ3	1:A:408:TYR:CD1	3.05	0.45
1:A:63:PRO:C	1:A:64:ARG:CG	2.83	0.45
1:A:95:GLY:C	1:A:97:GLU:N	2.69	0.45
2:B:167:ASN:HA	2:B:200:GLU:O	2.17	0.45
2:B:266:HIS:CE1	2:B:432:TYR:CE1	3.05	0.45
2:B:70:LEU:HD22	2:B:110:GLU:HB3	1.95	0.45
2:B:67:LEU:HD12	2:B:92:PHE:CD1	2.51	0.45
3:K:310:ASN:O	3:K:311:GLU:C	2.55	0.45
1:A:243:ARG:NH2	1:A:252:LEU:CB	2.78	0.44
1:A:165:SER:HG	1:A:253:THR:H	1.53	0.44
1:A:295:CYS:HB3	1:A:377:MET:HG2	1.99	0.44
2:B:324:SER:O	2:B:326:LYS:N	2.50	0.44
2:B:431:GLU:HA	2:B:434:GLN:HG3	1.97	0.44
3:K:324:ALA:O	3:K:327:ILE:N	2.51	0.44
3:K:9:ILE:CD1	3:K:327:ILE:CG2	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:LEU:O	1:A:157:LEU:HG	2.18	0.44
1:A:218:ASP:C	1:A:219:ILE:HG12	2.37	0.44
1:A:234:ILE:CG2	1:A:302:MET:HE1	2.42	0.44
2:B:133:GLN:HE21	2:B:243:ARG:NH2	2.16	0.44
2:B:253:ARG:CG	2:B:253:ARG:NH1	2.80	0.44
3:K:105:LEU:CA	3:K:108:ILE:HD11	2.48	0.44
2:B:287:THR:O	2:B:288:VAL:CG2	2.58	0.44
1:A:317:LEU:CD1	1:A:351:PHE:CE1	3.01	0.44
2:B:399:PHE:O	2:B:402:LYS:N	2.29	0.44
3:K:315:LYS:HG2	3:K:315:LYS:O	2.17	0.44
1:A:224:TYR:HD1	5:A:502:GTP:C8	2.36	0.44
1:A:16:ILE:HD12	1:A:231:ILE:C	2.38	0.44
1:A:202:PHE:HA	1:A:378:LEU:HD22	1.81	0.44
1:A:408:TYR:CG	1:A:418:PHE:CZ	3.05	0.44
2:B:23:VAL:O	2:B:25:SER:N	2.50	0.44
2:B:52:TYR:HE2	2:B:240:THR:HB	1.83	0.44
2:B:259:MET:HE3	2:B:268:PHE:CE2	2.53	0.44
2:B:156:LYS:CE	2:B:156:LYS:HA	2.38	0.44
2:B:242:LEU:C	2:B:244:PHE:H	2.19	0.44
2:B:189:LEU:HD23	2:B:421:ALA:CB	2.48	0.44
2:B:8:GLN:CG	2:B:67:LEU:HD22	2.47	0.44
1:A:287:SER:N	1:A:290:GLU:OE1	2.51	0.44
1:A:328:VAL:O	1:A:330:ALA:N	2.38	0.44
1:A:210:TYR:HE1	5:A:502:GTP:O6	1.92	0.44
2:B:11:GLN:O	2:B:15:GLN:N	2.41	0.44
2:B:93:VAL:HG22	2:B:117:SER:O	2.18	0.44
2:B:313:LEU:CG	2:B:382:THR:HG23	2.48	0.44
3:K:45:LYS:CD	3:K:45:LYS:N	2.78	0.44
1:A:255:PHE:O	1:A:259:LEU:N	2.50	0.44
1:A:400:ALA:O	1:A:401:LYS:CD	2.64	0.44
2:B:103:TRP:O	2:B:103:TRP:CD2	2.71	0.44
2:B:250:ALA:CB	2:B:254:LYS:HE2	2.48	0.44
1:A:397:LEU:HD11	2:B:348:PRO:HG2	1.71	0.44
2:B:346:TRP:HB2	2:B:349:ASN:OD1	2.18	0.44
2:B:7:ILE:HD11	2:B:157:ILE:HG13	1.99	0.44
3:K:139:TYR:CG	3:K:283:LYS:C	2.83	0.44
1:A:121:ARG:NH1	1:A:121:ARG:HG2	2.33	0.44
1:A:388:TRP:CD1	1:A:432:TYR:HE2	2.31	0.44
2:B:239:THR:O	2:B:240:THR:C	2.56	0.44
2:B:431:GLU:O	2:B:434:GLN:N	2.48	0.44
2:B:68:VAL:CB	2:B:153:LEU:CD2	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:274:PRO:HG2	2:B:371:LEU:CD2	2.43	0.44
1:A:173:PRO:O	1:A:391:LEU:HD13	2.17	0.44
1:A:175:PRO:HG2	1:A:207:GLU:HB3	1.97	0.44
2:B:301:MET:O	2:B:303:ALA:N	2.51	0.44
2:B:67:LEU:HD12	2:B:92:PHE:CE1	2.53	0.44
1:A:121:ARG:HG2	1:A:121:ARG:HH11	1.83	0.44
1:A:72:PRO:HG2	1:A:73:THR:H	1.83	0.44
1:A:383:ALA:O	1:A:386:GLU:N	2.50	0.44
1:A:408:TYR:CG	1:A:418:PHE:HZ	2.35	0.44
1:A:63:PRO:HG2	1:A:91:GLN:OE1	2.18	0.44
2:B:14:ASN:O	2:B:17:GLY:N	2.50	0.44
2:B:243:ARG:HH21	2:B:252:LEU:N	2.15	0.44
3:K:206:HIS:O	3:K:208:ILE:HD12	2.17	0.44
3:K:53:LEU:CG	3:K:104:GLN:CD	2.77	0.44
3:K:66:CYS:HB2	3:K:67:ALA:H	1.66	0.44
3:K:137:GLU:CD	3:K:192:HIS:H	2.17	0.44
2:B:295:MET:SD	2:B:375:ALA:HB3	2.57	0.44
1:A:272:TYR:CE2	1:A:274:PRO:HD2	2.53	0.44
1:A:13:GLY:C	1:A:16:ILE:HG22	2.38	0.43
1:A:179:THR:HG23	1:A:224:TYR:OH	2.18	0.43
1:A:278:ALA:CA	1:A:282:TYR:OH	2.65	0.43
2:B:242:LEU:HD22	2:B:250:ALA:O	2.17	0.43
2:B:307:PRO:C	2:B:309:HIS:N	2.71	0.43
1:A:110:ILE:CG2	1:A:111:GLY:N	2.71	0.43
1:A:175:PRO:CG	1:A:207:GLU:CA	2.92	0.43
1:A:175:PRO:CG	1:A:208:ALA:HB2	2.37	0.43
1:A:142:GLY:O	5:A:502:GTP:O3G	2.35	0.43
2:B:13:GLY:N	2:B:139:HIS:HA	2.21	0.43
1:A:406:HIS:CB	2:B:257:VAL:CB	2.96	0.43
2:B:312:TYR:HA	2:B:381:SER:HA	1.99	0.43
2:B:409:THR:HA	2:B:413:MET:HB3	1.99	0.43
2:B:359:PRO:CB	2:B:360:PRO:HD2	2.45	0.43
1:A:106:GLY:O	1:A:111:GLY:CA	2.51	0.43
2:B:428:LEU:HA	3:K:274:LYS:HE2	2.00	0.43
3:K:184:ILE:HG12	3:K:209:PHE:HE2	1.64	0.43
2:B:82:PRO:C	2:B:84:GLY:H	2.20	0.43
3:K:64:ASN:HA	3:K:68:LYS:HB2	2.00	0.43
2:B:138:THR:HG22	2:B:235:MET:HE3	1.97	0.43
2:B:182:VAL:O	2:B:183:GLU:C	2.56	0.43
2:B:26:ASP:C	2:B:28:HIS:H	2.21	0.43
2:B:409:THR:C	2:B:411:GLU:H	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:GLN:O	2:B:282:GLN:CG	2.65	0.43
2:B:161:TYR:N	2:B:161:TYR:CD1	2.86	0.43
1:A:104:ALA:H	1:A:413:MET:HG2	1.83	0.43
1:A:102:ASN:CG	1:A:411:GLU:HB3	2.32	0.43
2:B:204:ILE:HG22	2:B:209:LEU:CD1	2.47	0.43
1:A:11:GLN:NE2	1:A:74:VAL:HG22	2.30	0.43
2:B:280:SER:OG	2:B:281:GLN:N	2.49	0.43
2:B:141:LEU:N	2:B:141:LEU:HD12	2.33	0.43
1:A:202:PHE:C	1:A:203:MET:HG3	2.39	0.43
1:A:191:THR:HG21	1:A:267:PHE:HE2	1.83	0.43
1:A:4:CYS:HB3	1:A:243:ARG:CD	2.48	0.43
2:B:168:THR:CG2	2:B:201:THR:HG23	2.48	0.43
2:B:24:ILE:CG2	2:B:25:SER:N	2.80	0.43
2:B:265:LEU:C	2:B:265:LEU:CD1	2.83	0.43
2:B:6:HIS:HB3	2:B:65:ALA:CB	2.49	0.43
1:A:283:HIS:ND1	1:A:283:HIS:O	2.50	0.43
3:K:80:GLY:O	3:K:228:LEU:HD12	2.19	0.43
3:K:314:THR:HG23	3:K:318:LEU:CD2	2.48	0.43
1:A:8:HIS:CD2	1:A:138:PHE:CD2	3.07	0.43
1:A:231:ILE:H	1:A:231:ILE:HD13	1.82	0.43
2:B:255:LEU:HD12	2:B:255:LEU:N	2.34	0.43
2:B:103:TRP:CB	2:B:408:TYR:HE2	2.32	0.43
3:K:14:ARG:HG2	3:K:103:PRO:CG	2.47	0.43
2:B:210:TYR:O	2:B:211:ASP:C	2.57	0.43
3:K:126:ASN:O	3:K:127:LEU:CD1	2.64	0.43
1:A:16:ILE:CG2	1:A:17:GLY:N	2.82	0.43
1:A:185:TYR:HB2	1:A:408:TYR:CE2	2.54	0.43
2:B:240:THR:HG23	2:B:241:CYS:N	2.33	0.43
2:B:262:PHE:HA	2:B:263:PRO:HD2	1.65	0.43
2:B:435:TYR:C	2:B:437:ASP:N	2.72	0.43
2:B:48:ARG:HG2	2:B:243:ARG:HB3	2.01	0.43
2:B:72:PRO:HG2	2:B:73:GLY:H	1.83	0.43
3:K:117:PHE:CD2	3:K:177:PRO:CA	3.02	0.43
2:B:194:LEU:C	2:B:196:GLU:N	2.70	0.43
3:K:62:VAL:HG12	3:K:104:GLN:HG3	1.50	0.43
1:A:174:ALA:HB3	1:A:207:GLU:HG2	1.03	0.43
1:A:209:ILE:O	1:A:211:ASP:N	2.52	0.43
2:B:70:LEU:HB2	2:B:99:ALA:CB	2.48	0.43
1:A:115:ILE:C	1:A:115:ILE:CD1	2.87	0.42
2:B:154:ILE:HG22	2:B:166:MET:HE1	2.01	0.42
2:B:179:ASP:CB	6:B:602:G2P:O2'	2.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:68:VAL:HG11	2:B:153:LEU:CD1	2.46	0.42
2:B:175:PRO:CG	2:B:207:GLU:OE2	2.59	0.42
1:A:76:ASP:O	1:A:79:ARG:N	2.52	0.42
1:A:154:MET:CE	1:A:166:LYS:HB3	2.48	0.42
1:A:154:MET:HE3	1:A:166:LYS:HB3	2.01	0.42
1:A:230:LEU:O	1:A:231:ILE:C	2.57	0.42
1:A:263:PRO:O	1:A:264:ARG:C	2.56	0.42
1:A:185:TYR:CZ	1:A:405:VAL:HG23	2.55	0.42
2:B:428:LEU:C	3:K:274:LYS:HZ3	2.23	0.42
3:K:284:MET:O	3:K:286:ARG:N	2.52	0.42
2:B:175:PRO:N	2:B:207:GLU:OE2	2.49	0.42
3:K:238:LYS:C	3:K:259:LEU:HD12	2.40	0.42
2:B:161:TYR:O	2:B:163:ASP:N	2.51	0.42
3:K:134:SER:HB2	3:K:210:LEU:HB3	2.01	0.42
1:A:231:ILE:C	1:A:233:GLN:N	2.73	0.42
1:A:384:ILE:CA	1:A:385:ALA:C	2.85	0.42
1:A:185:TYR:HE2	1:A:404:PHE:O	2.01	0.42
2:B:333:LEU:HD11	2:B:337:ASN:HD21	1.85	0.42
3:K:292:LEU:HA	3:K:300:ILE:HD13	1.94	0.42
3:K:109:ILE:HG21	3:K:184:ILE:HD13	1.96	0.42
2:B:204:ILE:HD13	2:B:231:VAL:CG1	2.41	0.42
1:A:16:ILE:HD11	1:A:231:ILE:C	2.38	0.42
1:A:269:LEU:HD22	1:A:384:ILE:CG2	2.47	0.42
1:A:312:TYR:O	1:A:381:THR:HG22	2.03	0.42
2:B:118:VAL:O	2:B:122:VAL:HG13	2.19	0.42
2:B:336:GLN:NE2	2:B:349:ASN:O	2.52	0.42
2:B:72:PRO:O	2:B:73:GLY:C	2.57	0.42
3:K:22:GLU:O	3:K:27:ASP:HB2	2.19	0.42
2:B:210:TYR:O	2:B:214:PHE:N	2.52	0.42
3:K:197:ASN:O	3:K:199:ASN:N	2.52	0.42
1:A:67:PHE:HB2	1:A:92:LEU:HD23	2.02	0.42
3:K:40:VAL:HG22	3:K:46:PRO:HB3	2.01	0.42
1:A:110:ILE:O	1:A:111:GLY:C	2.58	0.42
1:A:149:PHE:O	1:A:150:THR:C	2.56	0.42
1:A:119:LEU:HD11	1:A:156:ARG:HD3	2.02	0.42
1:A:158:SER:HB2	1:A:197:HIS:CD2	2.46	0.42
1:A:205:ASP:OD2	1:A:391:LEU:CD2	2.68	0.42
1:A:252:LEU:O	1:A:253:THR:C	2.56	0.42
1:A:21:TRP:HE1	1:A:63:PRO:HB3	1.83	0.42
2:B:103:TRP:CE3	2:B:189:LEU:HD22	2.55	0.42
2:B:187:ALA:O	2:B:188:THR:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:65:ALA:HB3	3:K:104:GLN:CD	2.39	0.42
2:B:210:TYR:O	2:B:213:CYS:N	2.49	0.42
3:K:117:PHE:CD2	3:K:177:PRO:HA	2.54	0.42
3:K:117:PHE:CD2	3:K:177:PRO:N	2.88	0.42
1:A:13:GLY:HA2	1:A:16:ILE:CG2	2.50	0.42
1:A:4:CYS:CB	1:A:243:ARG:CB	2.94	0.42
2:B:136:GLN:OE1	2:B:239:THR:OG1	2.34	0.42
2:B:138:THR:O	2:B:139:HIS:HB3	2.19	0.42
2:B:261:PRO:HB2	2:B:262:PHE:CD2	2.54	0.42
2:B:64:ARG:CD	2:B:125:GLU:CA	2.98	0.42
3:K:220:THR:O	3:K:221:GLU:CB	2.67	0.42
1:A:104:ALA:HB2	1:A:413:MET:HG2	2.02	0.42
1:A:143:GLY:CA	5:A:502:GTP:PG	3.08	0.42
1:A:147:SER:HB2	1:A:186:ASN:O	2.19	0.42
1:A:25:CYS:SG	1:A:26:LEU:N	2.92	0.42
1:A:311:LYS:O	1:A:312:TYR:CD2	2.73	0.42
1:A:210:TYR:CA	5:A:502:GTP:N2	2.80	0.42
2:B:333:LEU:O	2:B:334:ASN:C	2.58	0.42
3:K:208:ILE:HG12	3:K:287:ILE:HD13	1.83	0.42
3:K:89:SER:CB	3:K:196:THR:OG1	2.68	0.42
1:A:335:ILE:C	1:A:337:THR:N	2.73	0.42
1:A:198:SER:HA	1:A:256:GLN:HE22	1.83	0.42
1:A:206:ASN:O	1:A:207:GLU:C	2.58	0.42
1:A:104:ALA:HB2	1:A:413:MET:CA	2.49	0.42
2:B:106:GLY:O	2:B:149:MET:HA	2.20	0.42
2:B:196:GLU:OE1	3:K:280:ARG:HD3	2.17	0.42
2:B:242:LEU:HB3	2:B:250:ALA:O	2.20	0.42
2:B:2:ARG:HG2	2:B:48:ARG:NH1	2.33	0.42
1:A:8:HIS:HA	1:A:138:PHE:HB2	2.00	0.42
1:A:95:GLY:C	1:A:97:GLU:H	2.23	0.42
2:B:427:ASP:OD1	2:B:427:ASP:C	2.57	0.42
2:B:273:ALA:HB1	2:B:291:LEU:HG	2.01	0.42
1:A:192:HIS:HA	1:A:195:LEU:CD1	2.46	0.42
1:A:210:TYR:HA	1:A:210:TYR:HD1	1.71	0.42
1:A:206:ASN:CB	5:A:502:GTP:O2'	2.60	0.42
2:B:383:ALA:C	2:B:385:GLN:N	2.72	0.42
3:K:282:SER:O	3:K:282:SER:OG	2.37	0.42
2:B:175:PRO:O	2:B:177:VAL:N	2.53	0.42
1:A:27:GLU:OE2	1:A:358:GLU:HG2	2.17	0.42
2:B:98:GLY:O	2:B:100:GLY:N	2.49	0.42
3:K:126:ASN:OD1	3:K:127:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ILE:O	1:A:212:ILE:HB	2.20	0.41
1:A:224:TYR:CD2	2:B:325:MET:SD	3.12	0.41
1:A:238:ILE:O	1:A:242:LEU:CB	2.67	0.41
2:B:153:LEU:HD13	2:B:153:LEU:N	2.34	0.41
2:B:133:GLN:CG	2:B:165:ILE:HD11	2.49	0.41
2:B:192:HIS:NE2	2:B:420:GLU:HG2	2.34	0.41
3:K:81:THR:HB	3:K:290:ASP:OD2	2.19	0.41
3:K:81:THR:HG21	3:K:291:SER:N	2.34	0.41
3:K:95:THR:O	3:K:106:MET:O	2.38	0.41
3:K:135:TYR:CE2	3:K:188:LYS:N	2.88	0.41
3:K:62:VAL:HG22	3:K:106:MET:CB	2.28	0.41
3:K:137:GLU:CD	3:K:144:ARG:HH22	2.23	0.41
2:B:16:ILE:HD11	2:B:171:VAL:HG21	2.02	0.41
1:A:243:ARG:NH2	1:A:252:LEU:HG	2.35	0.41
1:A:255:PHE:O	1:A:257:THR:N	2.53	0.41
3:K:278:PRO:CD	3:K:279:TYR:H	2.33	0.41
3:K:290:ASP:OD1	3:K:296:CYS:N	2.54	0.41
3:K:24:LEU:O	3:K:26:GLY:N	2.52	0.41
1:A:168:GLU:CG	1:A:201:ALA:HA	2.49	0.41
1:A:169:PHE:HD1	1:A:235:VAL:CG2	1.84	0.41
1:A:262:TYR:HB3	1:A:263:PRO:HD2	2.00	0.41
1:A:303:VAL:HG12	1:A:387:ALA:HB1	0.41	0.41
1:A:306:ASP:H	1:A:307:PRO:HD3	1.86	0.41
1:A:192:HIS:HA	1:A:424:ASP:OD2	2.19	0.41
2:B:118:VAL:O	2:B:121:VAL:N	2.54	0.41
2:B:192:HIS:HD1	2:B:424:ASN:CG	2.20	0.41
2:B:421:ALA:O	2:B:422:GLU:C	2.58	0.41
3:K:79:ASN:ND2	3:K:226:GLY:CA	2.79	0.41
2:B:399:PHE:O	2:B:401:ARG:N	2.53	0.41
1:A:242:LEU:HD11	1:A:250:VAL:HG23	2.02	0.41
1:A:405:VAL:HG13	1:A:418:PHE:HE2	1.85	0.41
2:B:103:TRP:H	2:B:408:TYR:HE2	0.44	0.41
2:B:25:SER:O	2:B:28:HIS:N	2.53	0.41
2:B:307:PRO:O	2:B:309:HIS:N	2.53	0.41
1:A:181:VAL:CG2	2:B:352:LYS:NZ	2.82	0.41
3:K:83:PHE:CE2	3:K:287:ILE:O	2.73	0.41
3:K:287:ILE:C	3:K:289:GLN:H	2.23	0.41
1:A:23:LEU:HD13	1:A:361:THR:O	2.21	0.41
1:A:313:MET:CB	1:A:381:THR:HB	2.50	0.41
2:B:169:PHE:CE2	2:B:235:MET:CB	3.03	0.41
2:B:182:VAL:O	2:B:184:PRO:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:294:GLY:N	3:K:295:ASN:OD1	2.53	0.41
3:K:59:GLN:HE21	3:K:59:GLN:HB2	1.62	0.41
3:K:14:ARG:CD	3:K:95:THR:HG21	2.41	0.41
3:K:20:GLU:O	3:K:24:LEU:N	2.54	0.41
1:A:288:VAL:C	1:A:290:GLU:N	2.71	0.41
2:B:288:VAL:C	2:B:290:GLU:N	2.70	0.41
3:K:194:ALA:CA	3:K:204:ARG:HG2	2.51	0.41
3:K:127:LEU:HA	3:K:217:ASN:HA	2.03	0.41
2:B:12:CYS:C	2:B:14:ASN:N	2.71	0.41
2:B:103:TRP:HE3	2:B:189:LEU:CD1	1.93	0.41
2:B:136:GLN:HE22	2:B:239:THR:CG2	2.31	0.41
2:B:395:PHE:HB3	2:B:396:THR:H	1.73	0.41
2:B:409:THR:C	2:B:411:GLU:N	2.73	0.41
1:A:344:VAL:HG22	1:A:345:ASP:H	1.85	0.41
3:K:6:GLU:HG3	3:K:6:GLU:O	2.21	0.41
1:A:152:LEU:CD1	1:A:152:LEU:C	2.89	0.41
1:A:188:ILE:HD13	1:A:425:MET:HG3	2.03	0.41
1:A:174:ALA:HB2	1:A:206:ASN:HB2	2.02	0.41
1:A:207:GLU:O	1:A:211:ASP:OD2	2.38	0.41
2:B:119:LEU:O	2:B:122:VAL:HG22	2.21	0.41
2:B:311:ARG:NH1	2:B:311:ARG:HG2	2.34	0.41
3:K:58:THR:O	3:K:62:VAL:HG13	2.20	0.41
2:B:174:SER:HB3	2:B:207:GLU:H	1.84	0.41
1:A:289:ALA:HB3	1:A:290:GLU:OE2	2.20	0.41
2:B:161:TYR:C	2:B:163:ASP:N	2.71	0.41
1:A:328:VAL:C	1:A:330:ALA:N	2.73	0.41
1:A:204:VAL:HG23	1:A:302:MET:SD	2.36	0.41
1:A:224:TYR:HA	5:A:502:GTP:N7	2.36	0.41
1:A:204:VAL:HG12	1:A:231:ILE:CG2	2.37	0.41
1:A:269:LEU:CD1	1:A:382:THR:HG1	2.34	0.41
1:A:384:ILE:CA	1:A:385:ALA:HB3	2.50	0.41
1:A:266:HIS:HD1	1:A:431:ASP:CB	2.33	0.41
2:B:12:CYS:O	2:B:13:GLY:C	2.59	0.41
2:B:3:GLU:HB2	2:B:132:LEU:HD12	2.03	0.41
2:B:135:PHE:CD1	2:B:166:MET:SD	3.13	0.41
2:B:239:THR:HG22	2:B:240:THR:H	1.86	0.41
2:B:258:ASN:HB3	2:B:352:LYS:HD2	2.02	0.41
3:K:206:HIS:O	3:K:206:HIS:CG	2.74	0.41
3:K:206:HIS:O	3:K:208:ILE:CD1	2.69	0.41
3:K:233:LEU:HD23	3:K:233:LEU:HA	1.90	0.41
1:A:332:ILE:CD1	1:A:353:VAL:HG22	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:THR:O	1:A:131:GLY:C	2.59	0.41
1:A:67:PHE:CE2	1:A:87:PHE:CE2	3.08	0.41
1:A:203:MET:HB2	1:A:388:TRP:CZ2	2.56	0.41
1:A:305:CYS:O	1:A:305:CYS:SG	2.79	0.41
1:A:377:MET:O	1:A:377:MET:HG3	2.18	0.41
2:B:48:ARG:CG	2:B:243:ARG:O	2.66	0.41
1:A:115:ILE:CG2	1:A:116:ASP:H	2.32	0.41
1:A:206:ASN:C	1:A:209:ILE:H	2.24	0.41
1:A:404:PHE:CD1	1:A:404:PHE:N	2.83	0.41
2:B:23:VAL:O	2:B:24:ILE:C	2.59	0.41
3:K:9:ILE:CD1	3:K:295:ASN:HD21	2.33	0.41
3:K:106:MET:SD	3:K:107:GLY:N	2.94	0.41
3:K:63:TYR:CE1	3:K:67:ALA:HB3	2.56	0.41
3:K:198:MET:HE2	3:K:198:MET:O	2.21	0.41
3:K:28:LYS:H	3:K:28:LYS:CD	2.34	0.41
2:B:275:LEU:HD12	2:B:275:LEU:HA	1.78	0.41
2:B:417:GLU:O	2:B:420:GLU:HB3	2.21	0.41
2:B:424:ASN:ND2	3:K:279:TYR:OH	2.54	0.41
3:K:63:TYR:HB2	3:K:111:ARG:HD3	2.02	0.41
2:B:274:PRO:HD3	2:B:374:SER:HA	2.02	0.41
2:B:171:VAL:HG12	2:B:171:VAL:O	2.20	0.41
1:A:177:VAL:HG11	1:A:210:TYR:CD2	2.56	0.40
1:A:312:TYR:CD2	1:A:437:VAL:HG23	2.55	0.40
2:B:20:PHE:CD1	2:B:235:MET:CG	3.04	0.40
3:K:231:VAL:HG11	3:K:288:LEU:CG	2.51	0.40
3:K:206:HIS:CB	3:K:284:MET:HG3	2.44	0.40
2:B:291:LEU:HD21	2:B:373:MET:HG2	2.03	0.40
1:A:272:TYR:O	1:A:300:ASN:ND2	2.54	0.40
2:B:78:VAL:O	2:B:84:GLY:HA3	2.21	0.40
1:A:76:ASP:O	1:A:80:THR:N	2.53	0.40
1:A:307:PRO:C	1:A:308:ARG:HG2	2.40	0.40
2:B:102:ASN:C	2:B:104:ALA:H	2.25	0.40
2:B:114:LEU:HD12	2:B:117:SER:OG	2.21	0.40
2:B:12:CYS:O	2:B:14:ASN:N	2.55	0.40
1:A:407:TRP:CB	2:B:258:ASN:HD21	2.35	0.40
2:B:325:MET:HE1	2:B:355:VAL:HG11	2.03	0.40
2:B:11:GLN:HA	2:B:74:THR:HG21	2.03	0.40
3:K:138:ILE:HD12	3:K:141:ASP:HB2	2.04	0.40
1:A:318:LEU:HB2	1:A:376:CYS:SG	2.61	0.40
2:B:35:SER:HB3	2:B:59:ASN:OD1	2.21	0.40
3:K:115:ASP:OD1	3:K:119:HIS:CE1	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:MET:O	1:A:426:ALA:C	2.60	0.40
2:B:132:LEU:O	2:B:164:ARG:HD2	2.21	0.40
2:B:188:THR:O	2:B:191:VAL:HG12	2.22	0.40
2:B:70:LEU:HD13	2:B:110:GLU:HB2	2.03	0.40
3:K:278:PRO:HD2	3:K:279:TYR:H	1.85	0.40
1:A:273:ALA:HB2	1:A:375:VAL:HB	2.02	0.40
2:B:405:LEU:O	2:B:405:LEU:HD23	2.21	0.40
1:A:175:PRO:C	1:A:207:GLU:CB	2.88	0.40
1:A:209:ILE:HD11	1:A:302:MET:O	2.02	0.40
1:A:172:TYR:CG	1:A:388:TRP:CH2	3.09	0.40
2:B:93:VAL:CA	2:B:114:LEU:HG	2.50	0.40
2:B:183:GLU:HB3	2:B:184:PRO:HD3	2.03	0.40
2:B:108:TYR:CE1	2:B:413:MET:HE1	2.56	0.40
3:K:283:LYS:HZ1	3:K:286:ARG:CG	2.34	0.40
3:K:27:ASP:HA	3:K:28:LYS:HZ3	1.79	0.40
1:A:14:VAL:HG11	1:A:75:ILE:HD13	2.04	0.40
1:A:133:GLN:O	1:A:243:ARG:NH1	2.52	0.40
1:A:149:PHE:CD1	1:A:150:THR:N	2.89	0.40
1:A:30:ILE:HG22	1:A:30:ILE:O	2.21	0.40
2:B:150:GLY:HA2	2:B:153:LEU:CD2	2.41	0.40
2:B:95:GLY:C	2:B:97:SER:H	2.25	0.40
3:K:273:THR:C	3:K:274:LYS:O	2.60	0.40
3:K:20:GLU:O	3:K:24:LEU:HB2	2.21	0.40
2:B:98:GLY:C	2:B:100:GLY:H	2.24	0.40
1:A:371:VAL:CG1	1:A:372:GLN:H	2.32	0.40
3:K:194:ALA:HA	3:K:204:ARG:HG2	2.03	0.40
2:B:322:ARG:CG	2:B:322:ARG:HH11	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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	406/436 (93%)	262 (64%)	83 (20%)	61 (15%)	0 5
2	B	424/426 (100%)	268 (63%)	100 (24%)	56 (13%)	0 7
3	K	271/352 (77%)	209 (77%)	36 (13%)	26 (10%)	1 15
All	All	1101/1214 (91%)	739 (67%)	219 (20%)	143 (13%)	1 7

All (143) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	LYS
1	A	97	GLU
1	A	108	TYR
1	A	109	THR
1	A	141	PHE
1	A	183	GLU
1	A	217	LEU
1	A	240	ALA
1	A	249	ASN
1	A	255	PHE
1	A	266	HIS
1	A	280	LYS
1	A	284	GLU
1	A	285	GLN
1	A	287	SER
1	A	289	ALA
1	A	304	LYS
1	A	305	CYS
1	A	306	ASP
1	A	309	HIS
1	A	364	PRO
1	A	370	LYS
1	A	400	ALA
1	A	401	LYS
2	B	23	VAL
2	B	24	ILE
2	B	32	PRO
2	B	50	ASN
2	B	82	PRO
2	B	97	SER
2	B	128	SER
2	B	176	LYS
2	B	183	GLU
2	B	218	LYS

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Mol	Chain	Res	Type
2	B	238	VAL
2	B	239	THR
2	B	240	THR
2	B	252	LEU
2	B	263	PRO
2	B	266	HIS
2	B	273	ALA
2	B	278	ARG
2	B	280	SER
2	B	281	GLN
2	B	282	GLN
2	B	288	VAL
2	B	294	GLN
2	B	295	MET
2	B	311	ARG
2	B	343	PHE
2	B	344	VAL
2	B	348	PRO
2	B	369	ARG
2	B	382	THR
2	B	403	ALA
3	K	27	ASP
3	K	98	GLY
3	K	101	HIS
3	K	102	ASP
3	K	106	MET
3	K	138	ILE
3	K	198	MET
3	K	274	LYS
3	K	278	PRO
3	K	282	SER
1	A	24	TYR
1	A	63	PRO
1	A	111	GLY
1	A	131	GLY
1	A	198	SER
1	A	218	ASP
1	A	219	ILE
1	A	238	ILE
1	A	265	GLY
1	A	312	TYR
1	A	339	ARG

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Mol	Chain	Res	Type
1	A	342	GLN
1	A	373	ARG
2	B	38	GLY
2	B	73	GLY
2	B	175	PRO
2	B	265	LEU
2	B	279	GLY
2	B	298	ALA
2	B	300	ASN
3	K	20	GLU
3	K	88	THR
3	K	108	ILE
3	K	219	GLU
3	K	294	GLY
3	K	311	GLU
3	K	327	ILE
1	A	148	GLY
1	A	149	PHE
1	A	239	THR
1	A	245	ASP
1	A	263	PRO
1	A	279	GLU
1	A	288	VAL
1	A	303	VAL
1	A	308	ARG
1	A	330	ALA
1	A	336	LYS
1	A	345	ASP
1	A	369	ALA
1	A	404	PHE
2	B	83	PHE
2	B	99	ALA
2	B	100	GLY
2	B	302	MET
2	B	386	GLU
3	K	25	ARG
3	K	195	VAL
3	K	201	HIS
3	K	276	HIS
3	K	284	MET
1	A	89	PRO
1	A	300	ASN

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Mol	Chain	Res	Type
2	B	34	GLY
2	B	96	GLN
2	B	395	PHE
3	K	103	PRO
3	K	277	VAL
1	A	129	CYS
1	A	256	GLN
1	A	313	MET
1	A	412	GLY
2	B	57	ALA
2	B	74	THR
2	B	285	ALA
3	K	127	LEU
3	K	329	ASN
1	A	31	GLN
1	A	273	ALA
2	B	51	VAL
2	B	58	GLY
2	B	162	PRO
2	B	400	ARG
2	B	424	ASN
1	A	173	PRO
2	B	195	VAL
1	A	115	ILE
2	B	72	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	345/365 (94%)	299 (87%)	46 (13%)	5 28
2	B	367/367 (100%)	307 (84%)	60 (16%)	3 20
3	K	243/311 (78%)	217 (89%)	26 (11%)	8 36
All	All	955/1043 (92%)	823 (86%)	132 (14%)	8 27

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	20	CYS
1	A	21	TRP
1	A	32	PRO
1	A	76	ASP
1	A	82	THR
1	A	98	ASP
1	A	115	ILE
1	A	120	ASP
1	A	125	LEU
1	A	127	ASP
1	A	130	THR
1	A	141	PHE
1	A	150	THR
1	A	152	LEU
1	A	155	GLU
1	A	169	PHE
1	A	173	PRO
1	A	183	GLU
1	A	192	HIS
1	A	210	TYR
1	A	219	ILE
1	A	231	ILE
1	A	234	ILE
1	A	243	ARG
1	A	244	PHE
1	A	253	THR
1	A	260	VAL
1	A	267	PHE
1	A	269	LEU
1	A	276	ILE
1	A	284	GLU
1	A	308	ARG
1	A	312	TYR
1	A	325	PRO
1	A	334	THR
1	A	352	LYS
1	A	368	LEU
1	A	376	CYS
1	A	379	SER
1	A	388	TRP
1	A	402	ARG

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Mol	Chain	Res	Type
1	A	404	PHE
1	A	413	MET
1	A	415	GLU
1	A	417	GLU
2	B	14	ASN
2	B	24	ILE
2	B	26	ASP
2	B	32	PRO
2	B	41	ASP
2	B	68	VAL
2	B	76	ASP
2	B	90	ASP
2	B	94	PHE
2	B	101	ASN
2	B	122	VAL
2	B	129	CYS
2	B	135	PHE
2	B	141	LEU
2	B	149	MET
2	B	153	LEU
2	B	161	TYR
2	B	163	ASP
2	B	165	ILE
2	B	174	SER
2	B	198	THR
2	B	201	THR
2	B	203	CYS
2	B	207	GLU
2	B	211	ASP
2	B	214	PHE
2	B	215	ARG
2	B	224	TYR
2	B	227	LEU
2	B	230	LEU
2	B	236	SER
2	B	240	THR
2	B	244	PHE
2	B	253	ARG
2	B	265	LEU
2	B	267	PHE
2	B	275	LEU
2	B	282	GLN

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Mol	Chain	Res	Type
2	B	283	TYR
2	B	284	ARG
2	B	289	PRO
2	B	299	LYS
2	B	306	ASP
2	B	309	HIS
2	B	322	ARG
2	B	324	SER
2	B	325	MET
2	B	343	PHE
2	B	344	VAL
2	B	347	ILE
2	B	369	ARG
2	B	380	ASN
2	B	387	LEU
2	B	413	MET
2	B	414	ASP
2	B	424	ASN
2	B	427	ASP
2	B	431	GLU
2	B	432	TYR
2	B	437	ASP
3	K	12	MET
3	K	19	ASN
3	K	28	LYS
3	K	30	ILE
3	K	51	ARG
3	K	53	LEU
3	K	56	ASN
3	K	59	GLN
3	K	106	MET
3	K	111	ARG
3	K	124	ASP
3	K	125	GLU
3	K	135	TYR
3	K	191	ARG
3	K	193	VAL
3	K	195	VAL
3	K	198	MET
3	K	220	THR
3	K	257	LYS
3	K	260	SER

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Mol	Chain	Res	Type
3	K	275	THR
3	K	283	LYS
3	K	288	LEU
3	K	295	ASN
3	K	310	ASN
3	K	318	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	15	GLN
1	A	101	ASN
1	A	102	ASN
1	A	128	GLN
1	A	139	HIS
1	A	176	GLN
1	A	197	HIS
1	A	216	ASN
1	A	226	ASN
1	A	228	ASN
1	A	256	GLN
1	A	266	HIS
1	A	301	GLN
1	A	309	HIS
1	A	406	HIS
2	B	11	GLN
2	B	14	ASN
2	B	50	ASN
2	B	91	ASN
2	B	107	HIS
2	B	136	GLN
2	B	186	ASN
2	B	197	ASN
2	B	258	ASN
2	B	282	GLN
2	B	331	GLN
2	B	334	ASN
2	B	337	ASN
2	B	380	ASN
2	B	406	HIS
2	B	424	ASN

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Mol	Chain	Res	Type
3	K	19	ASN
3	K	56	ASN
3	K	59	GLN
3	K	69	GLN
3	K	79	ASN
3	K	94	HIS
3	K	130	HIS
3	K	310	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	GTP	A	502	4	26,34,34	1.12	2 (7%)	29,54,54	1.82	5 (17%)
6	G2P	B	602	4	29,34,34	5.63	22 (75%)	32,54,54	4.64	19 (59%)
7	SO4	K	500	-	4,4,4	0.39	0	6,6,6	0.17	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GTP	A	502	4	-	0/18/38/38	0/3/3/3
6	G2P	B	602	4	-	0/15/38/38	0/3/3/3
7	SO4	K	500	-	-	0/0/0/0	0/0/0/0

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	602	G2P	PB-C3A	-18.82	1.60	1.80
6	B	602	G2P	PA-C3A	-9.81	1.70	1.80
6	B	602	G2P	O2'-C2'	-6.08	1.28	1.43
6	B	602	G2P	PA-O1A	-5.79	1.42	1.56
6	B	602	G2P	C8-N7	-4.99	1.25	1.34
6	B	602	G2P	O5'-C5'	-3.98	1.28	1.44
6	B	602	G2P	PG-O1G	-3.31	1.43	1.54
6	B	602	G2P	O6-C6	-2.29	1.18	1.24
6	B	602	G2P	C2'-C3'	-2.25	1.47	1.53
6	B	602	G2P	PB-O1B	2.01	1.61	1.56
6	B	602	G2P	C3'-C4'	2.30	1.59	1.53
6	B	602	G2P	O4'-C4'	2.57	1.50	1.45
6	B	602	G2P	O4'-C1'	2.66	1.45	1.41
6	B	602	G2P	PG-O2G	2.96	1.60	1.50
5	A	502	GTP	C5-C4	3.11	1.47	1.40
5	A	502	GTP	C6-C5	3.62	1.48	1.41
6	B	602	G2P	PA-O2A	4.01	1.62	1.51
6	B	602	G2P	C6-C5	4.28	1.50	1.41
6	B	602	G2P	C4-N3	4.77	1.43	1.35
6	B	602	G2P	C2'-C1'	4.97	1.61	1.53
6	B	602	G2P	O3'-C3'	6.31	1.57	1.43
6	B	602	G2P	C2-N1	6.38	1.47	1.35
6	B	602	G2P	C2-N2	6.94	1.48	1.34
6	B	602	G2P	PA-O5'	8.95	1.67	1.57

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	602	G2P	N3-C2-N1	-10.56	113.20	127.56
6	B	602	G2P	O4'-C4'-C3'	-7.36	90.23	105.16
6	B	602	G2P	C1'-N9-C4	-6.48	119.58	126.81
6	B	602	G2P	C5-C6-N1	-4.79	117.26	123.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	602	G2P	O5'-PA-O2A	-4.76	100.88	114.05
6	B	602	G2P	O2'-C2'-C3'	-4.72	96.60	111.86
5	A	502	GTP	C5-C6-N1	-4.22	118.01	123.52
6	B	602	G2P	O2A-PA-C3A	-3.62	98.22	108.82
5	A	502	GTP	N3-C2-N1	-3.42	122.90	127.56
5	A	502	GTP	C6-C5-C4	-3.14	117.27	120.86
6	B	602	G2P	C6-C5-C4	-2.68	117.80	120.86
6	B	602	G2P	O5'-PA-C3A	-2.63	96.76	104.23
5	A	502	GTP	C4'-O4'-C1'	2.03	111.79	109.64
6	B	602	G2P	O3'-C3'-C2'	2.11	118.68	111.86
6	B	602	G2P	O2'-C2'-C1'	2.35	118.96	111.61
6	B	602	G2P	O3G-PG-O1G	2.39	116.22	107.44
6	B	602	G2P	O1A-PA-C3A	3.83	125.71	107.14
6	B	602	G2P	O1B-PB-O2B	4.99	126.18	110.24
5	A	502	GTP	C6-N1-C2	5.47	122.29	115.88
6	B	602	G2P	N2-C2-N3	6.17	129.31	117.72
6	B	602	G2P	C4'-O4'-C1'	6.74	116.79	109.64
6	B	602	G2P	O1A-PA-O5'	7.44	125.53	106.69
6	B	602	G2P	PA-O5'-C5'	8.23	145.75	122.23
6	B	602	G2P	C6-N1-C2	10.07	127.68	115.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 91 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	502	GTP	74	0
6	B	602	G2P	17	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.