



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:24 PM GMT

PDB ID : 4XF2
Title : Tetragonal structure of Arp2/3 complex
Authors : Jurgenson, C.T.; Pollard, T.P.
Deposited on : 2014-12-25
Resolution : 5.00 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

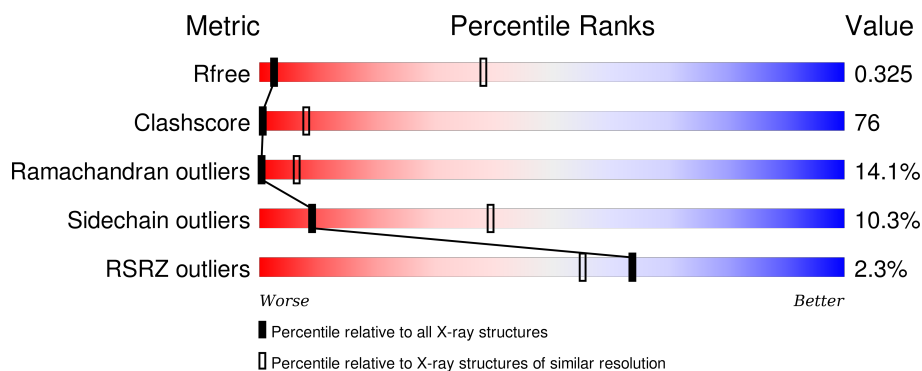
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1119 (6.22-3.60)
Clashscore	102246	1019 (6.22-3.66)
Ramachandran outliers	100387	1158 (6.22-3.60)
Sidechain outliers	100360	1136 (6.22-3.60)
RSRZ outliers	91569	1122 (6.22-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	418	<div> <div>24%</div> <div>58%</div> <div>11%</div> <div>6%</div> </div>
1	T	418	<div> <div>25%</div> <div>56%</div> <div>11%</div> <div>6%</div> </div>
2	B	394	<div> <div>22%</div> <div>26%</div> <div>9%</div> <div>42%</div> </div>
2	U	394	<div> <div>20%</div> <div>28%</div> <div>9%</div> <div>42%</div> </div>
3	C	372	<div> <div>19%</div> <div>54%</div> <div>20%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
3	V	372	
4	D	300	
4	W	300	
5	E	178	
5	X	178	
6	F	168	
6	Y	168	
7	G	151	
7	Z	151	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 27556 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Actin-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			3146	2022	522	587	15			
1	T	392	Total	C	N	O	S	0	0	0
			3146	2022	522	587	15			

- Molecule 2 is a protein called Actin-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	228	Total	C	N	O	S	0	0	0
			1734	1105	303	322	4			
2	U	228	Total	C	N	O	S	0	0	0
			1738	1108	304	322	4			

- Molecule 3 is a protein called Actin-related protein 2/3 complex subunit 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	354	Total	C	N	O	S	0	0	0
			2758	1747	487	505	19			
3	V	354	Total	C	N	O	S	0	0	0
			2758	1747	487	505	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	VAL	ILE	conflict	UNP Q58CQ2
V	58	VAL	ILE	conflict	UNP Q58CQ2

- Molecule 4 is a protein called Actin-related protein 2/3 complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	284	Total	C	N	O	S	0	0	0
			2292	1456	397	431	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	W	284	Total	C	N	O	S	0	0	0
			2292	1456	397	431	8			

- Molecule 5 is a protein called Actin-related protein 2/3 complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	174	Total	C	N	O	S	0	0	0
			1415	908	236	262	9			
5	X	174	Total	C	N	O	S	0	0	0
			1415	908	236	262	9			

- Molecule 6 is a protein called Actin-related protein 2/3 complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	167	Total	C	N	O	S	0	0	0
			1371	875	239	248	9			
6	Y	167	Total	C	N	O	S	0	0	0
			1371	875	239	248	9			

- Molecule 7 is a protein called Actin-related protein 2/3 complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	139	Total	C	N	O	S	0	0	0
			1060	661	185	211	3			
7	Z	139	Total	C	N	O	S	0	0	0
			1060	661	185	211	3			

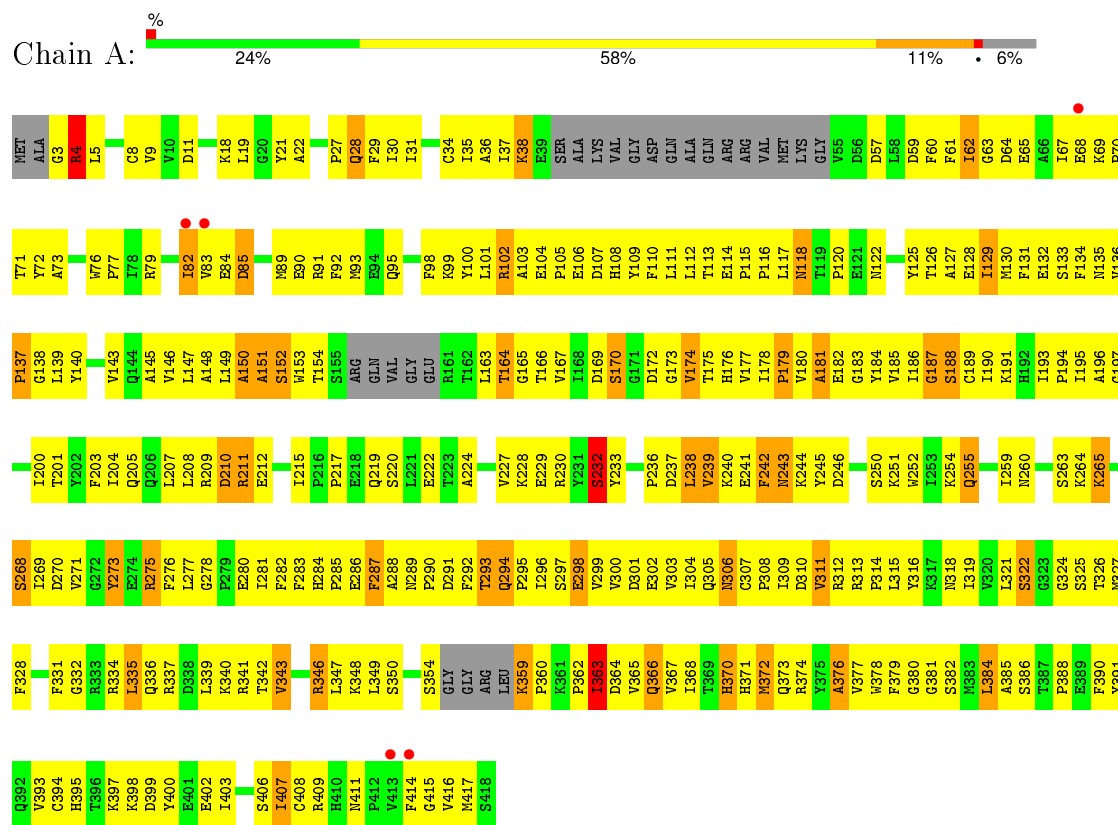
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	17	ASP	GLY	conflict	UNP Q3SYX9
G	28	ASP	GLU	conflict	UNP Q3SYX9
Z	17	ASP	GLY	conflict	UNP Q3SYX9
Z	28	ASP	GLU	conflict	UNP Q3SYX9

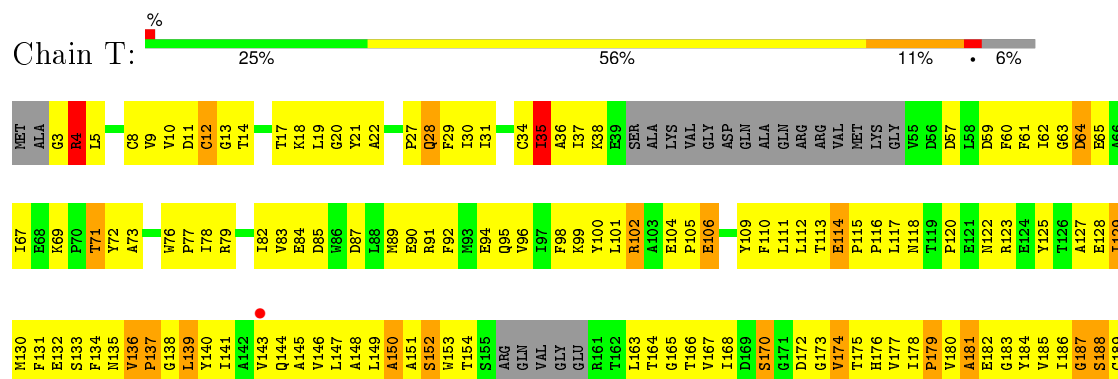
3 Residue-property plots

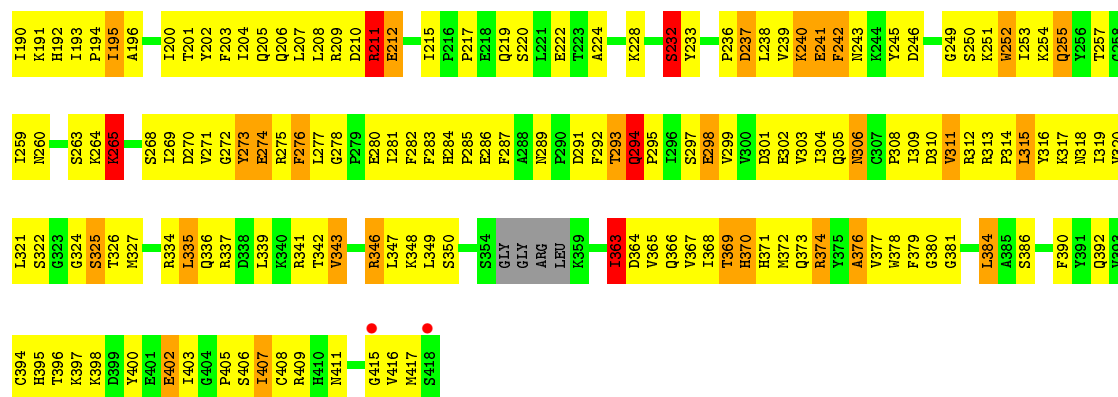
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

• Molecule 1: Actin-related protein 3

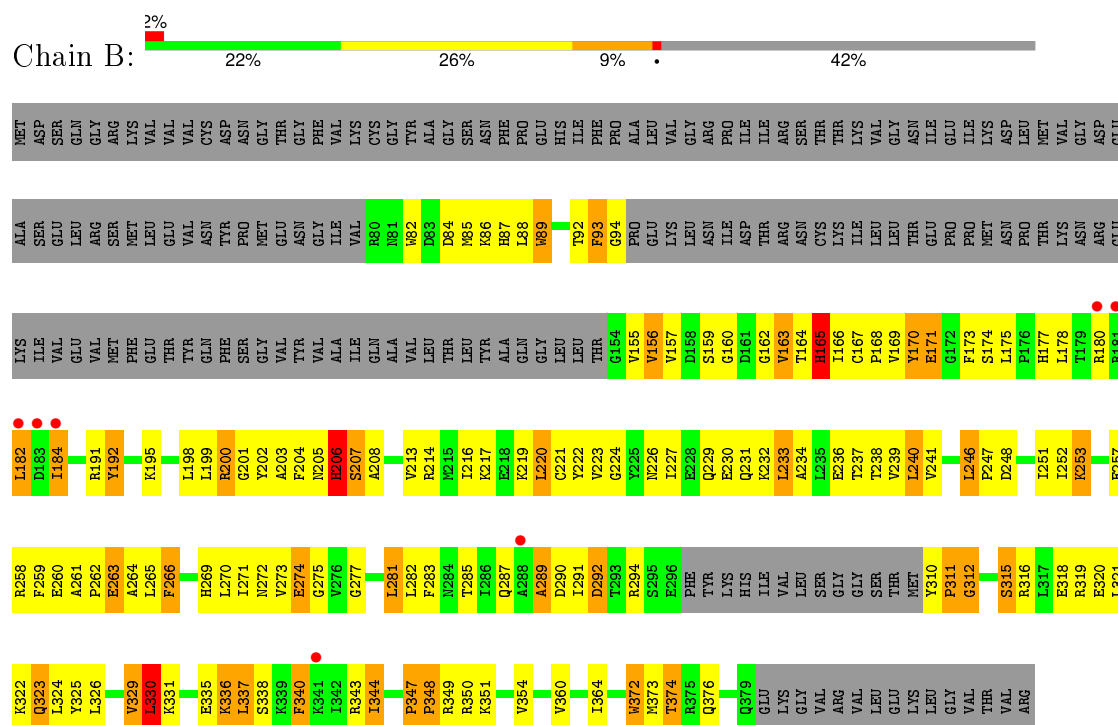


• Molecule 1: Actin-related protein 3

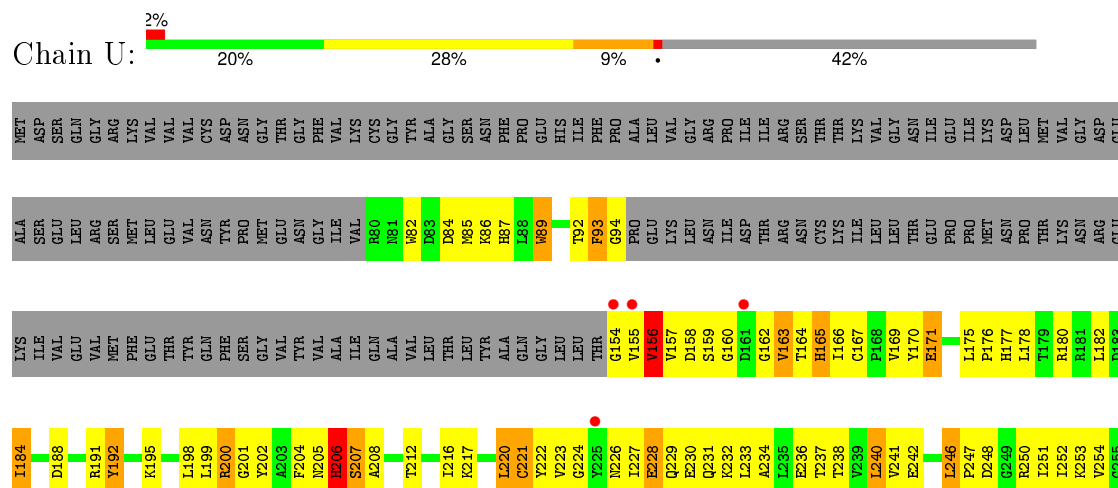


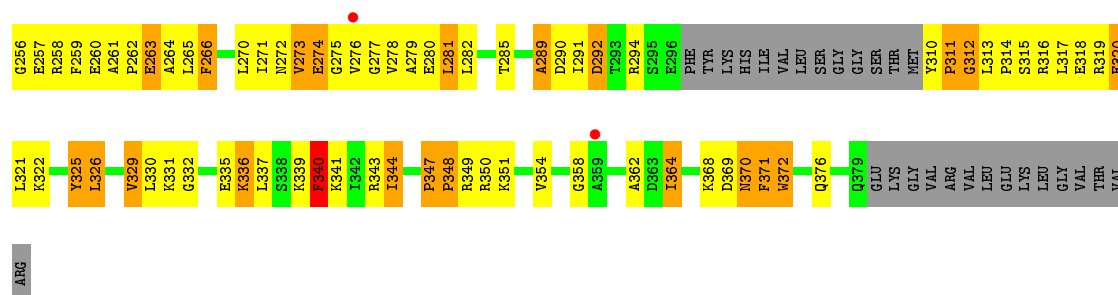


• Molecule 2: Actin-related protein 2

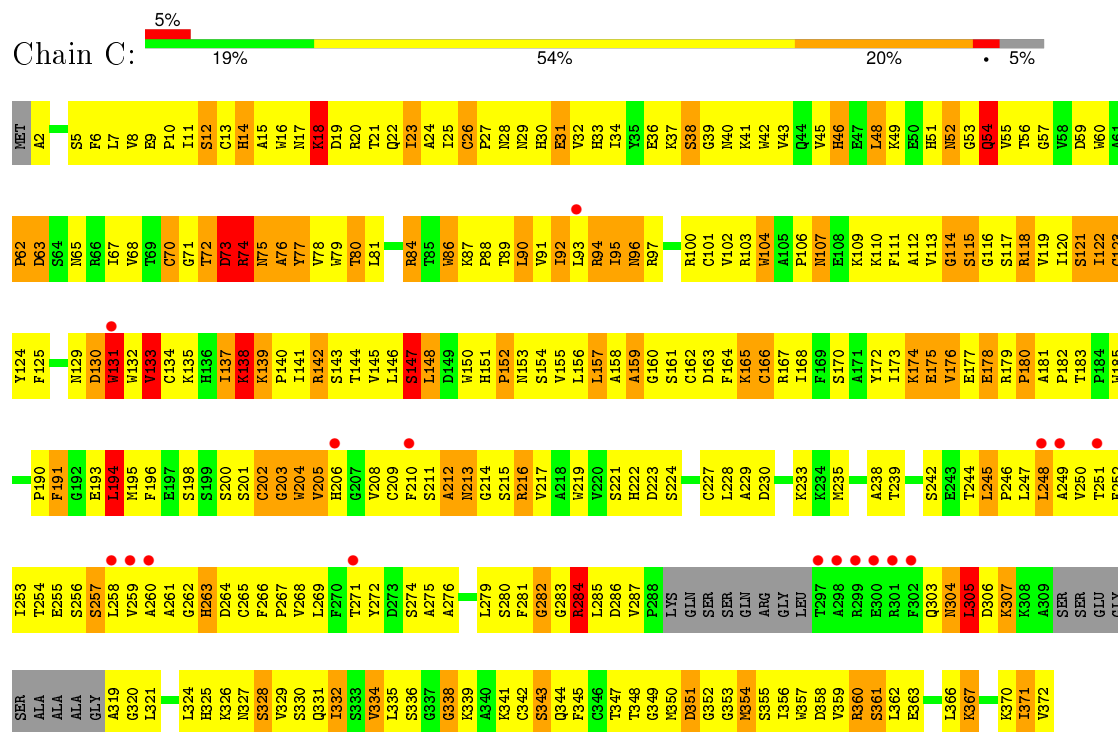


• Molecule 2: Actin-related protein 2

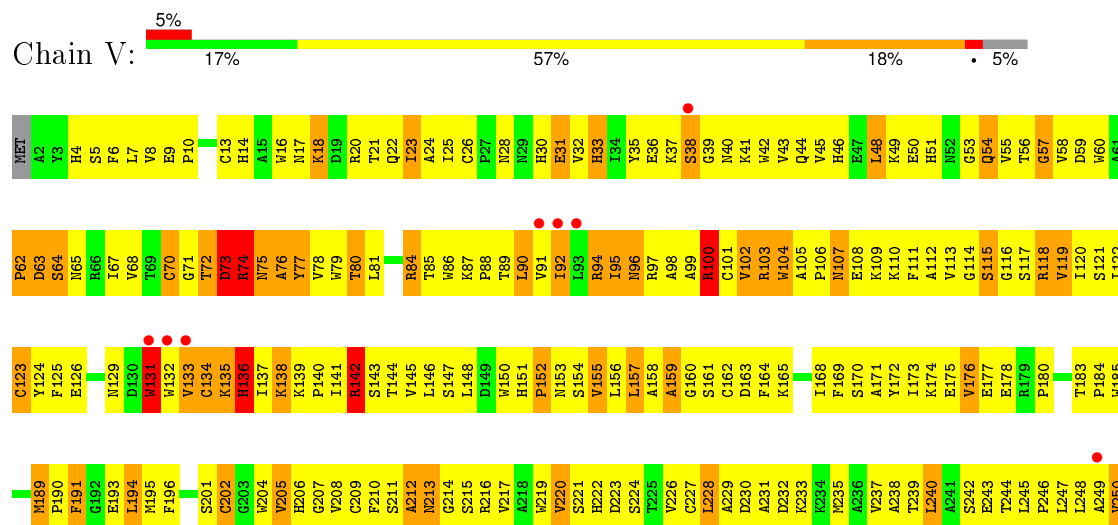


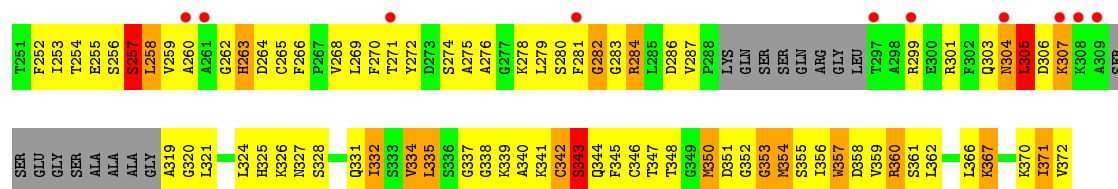


• Molecule 3: Actin-related protein 2/3 complex subunit 1B

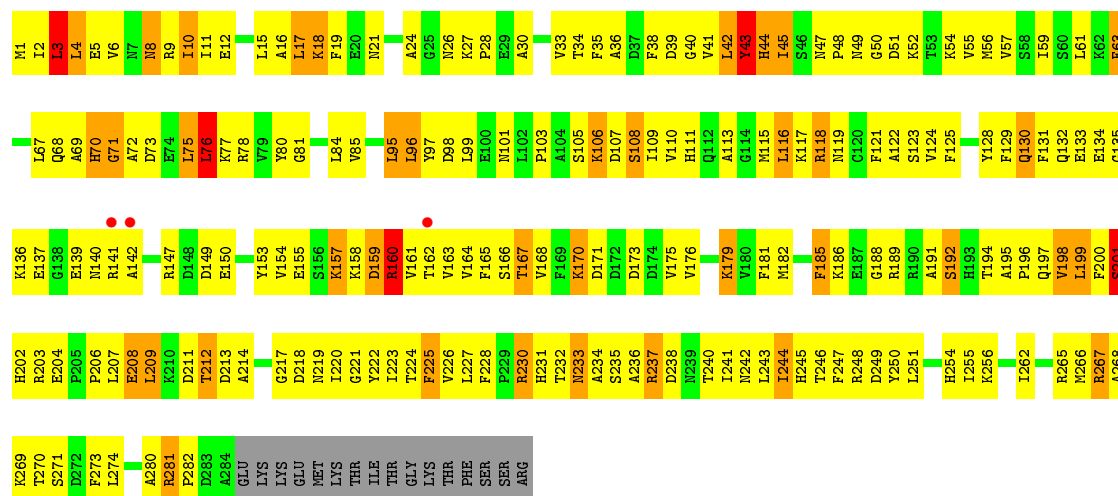


• Molecule 3: Actin-related protein 2/3 complex subunit 1B

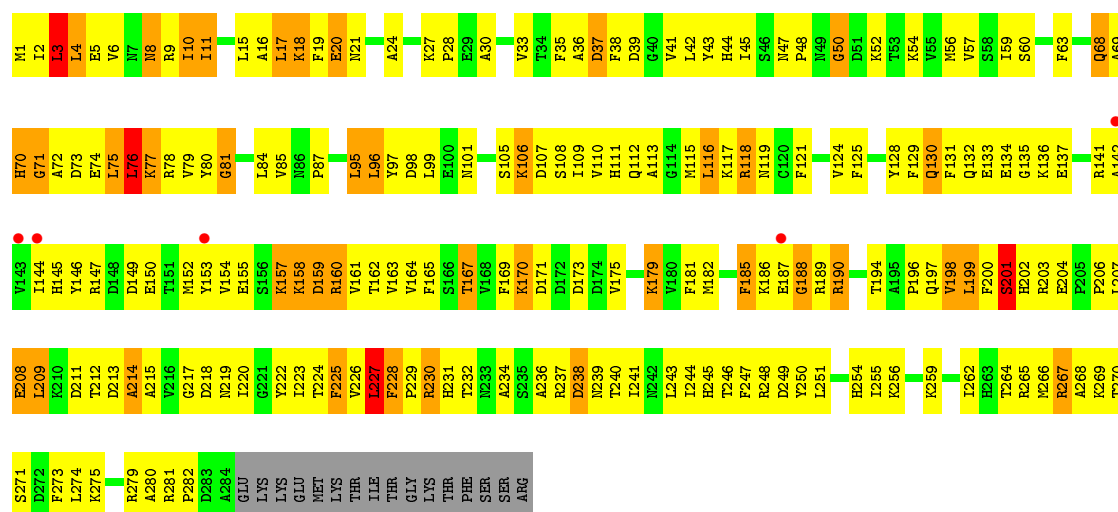




• Molecule 4: Actin-related protein 2/3 complex subunit 2



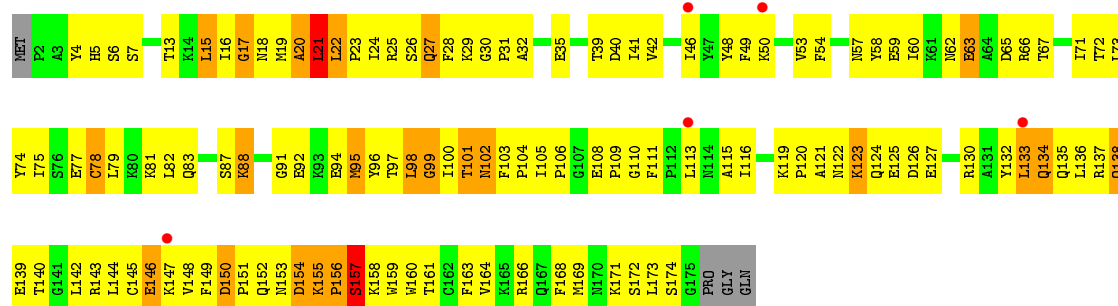
• Molecule 4: Actin-related protein 2/3 complex subunit 2



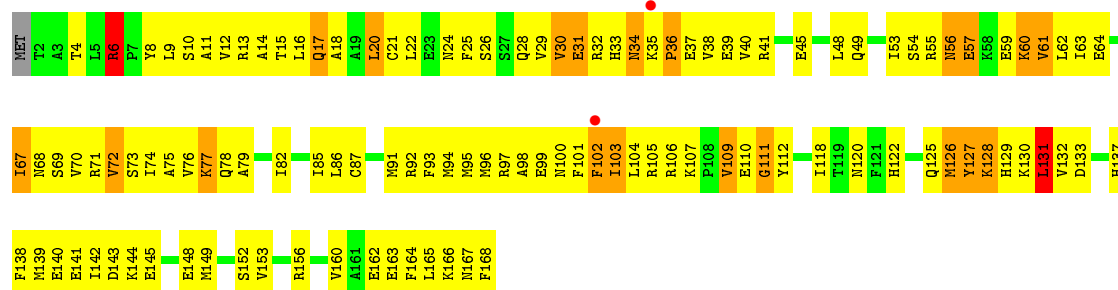
• Molecule 5: Actin-related protein 2/3 complex subunit 3



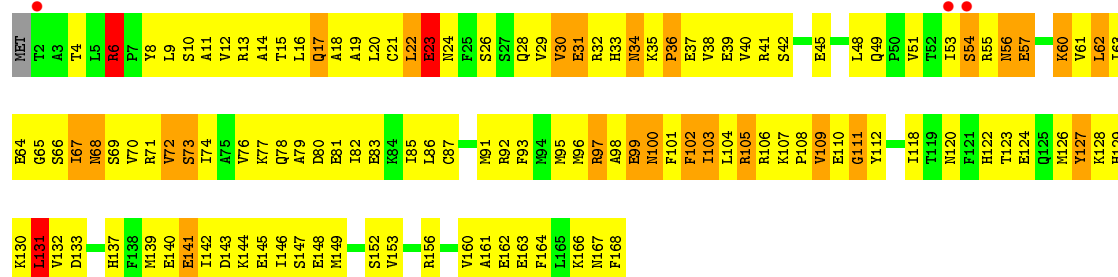
- Molecule 5: Actin-related protein 2/3 complex subunit 3



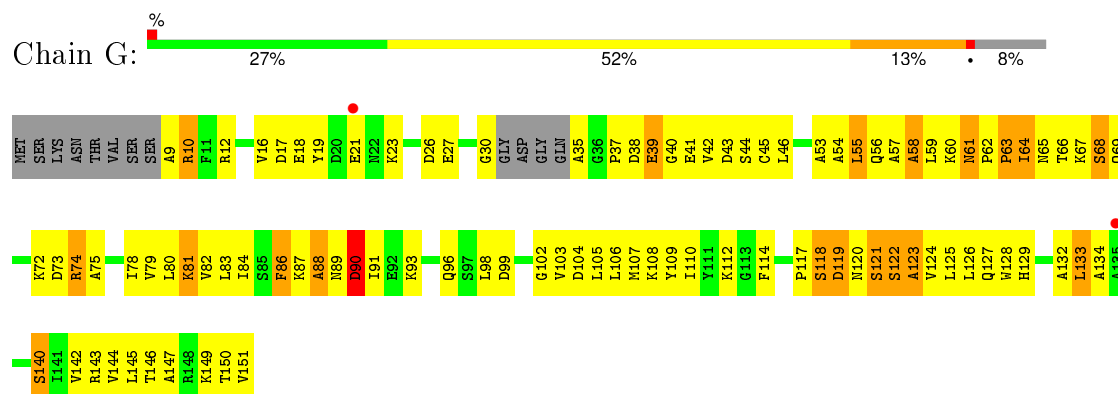
- Molecule 6: Actin-related protein 2/3 complex subunit 4



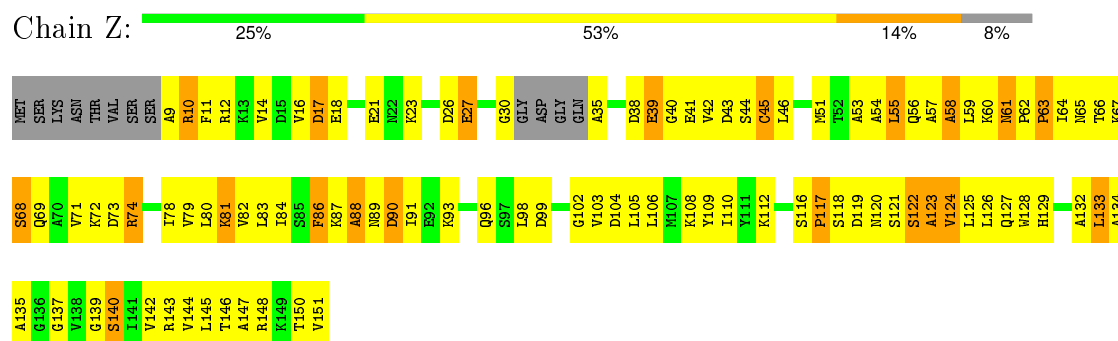
- Molecule 6: Actin-related protein 2/3 complex subunit 4



- Molecule 7: Actin-related protein 2/3 complex subunit 5



• Molecule 7: Actin-related protein 2/3 complex subunit 5



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	149.93Å 149.93Å 265.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.54 – 5.00 47.54 – 4.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (47.54-5.00) 81.1 (47.54-4.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 4.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.275 , 0.303 0.298 , 0.325	Depositor DCC
R_{free} test set	1215 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	185.4	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 282.2	EDS
Estimated twinning fraction	0.368 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 32376 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	27556	wwPDB-VP
Average B, all atoms (Å ²)	256.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.42	0/3226	0.83	4/4376 (0.1%)
1	T	0.33	0/3226	0.64	2/4376 (0.0%)
2	B	0.40	0/1764	0.84	5/2389 (0.2%)
2	U	0.33	0/1768	0.67	4/2393 (0.2%)
3	C	0.35	0/2827	0.74	2/3832 (0.1%)
3	V	0.32	0/2827	0.62	0/3832
4	D	0.37	0/2341	0.72	2/3161 (0.1%)
4	W	0.33	0/2341	0.63	2/3161 (0.1%)
5	E	0.37	0/1449	0.71	0/1954
5	X	0.36	0/1449	0.65	0/1954
6	F	0.40	0/1393	0.80	1/1868 (0.1%)
6	Y	0.36	0/1393	0.73	1/1868 (0.1%)
7	G	0.33	0/1072	0.63	0/1442
7	Z	0.38	0/1072	0.67	0/1442
All	All	0.36	0/28148	0.71	23/38048 (0.1%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	LYS	C-N-CD	-9.01	100.78	120.60
4	D	267	ARG	NE-CZ-NH1	-6.56	117.02	120.30
4	D	96	LEU	CA-CB-CG	6.55	130.37	115.30
4	W	96	LEU	CA-CB-CG	6.54	130.35	115.30
6	Y	131	LEU	CA-CB-CG	6.50	130.24	115.30
6	F	131	LEU	CA-CB-CG	6.45	130.13	115.30
2	B	347	PRO	N-CA-CB	6.15	110.68	103.30
2	U	347	PRO	N-CA-CB	6.11	110.63	103.30
2	B	348	PRO	N-CA-CB	6.09	110.61	103.30
2	U	348	PRO	N-CA-CB	6.03	110.53	103.30
3	C	203	GLY	N-CA-C	5.90	127.84	113.10
1	T	139	LEU	CA-CB-CG	5.75	128.53	115.30
2	U	281	LEU	CA-CB-CG	5.63	128.24	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	W	267	ARG	NE-CZ-NH1	-5.56	117.52	120.30
2	B	319	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	A	139	LEU	CA-CB-CG	5.44	127.81	115.30
3	C	194	LEU	CA-CB-CG	5.39	127.70	115.30
1	A	275	ARG	NE-CZ-NH1	-5.34	117.63	120.30
2	B	281	LEU	CA-CB-CG	5.25	127.37	115.30
2	U	281	LEU	CB-CG-CD1	-5.13	102.28	111.00
1	A	346	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	T	346	ARG	NE-CZ-NH2	-5.10	117.75	120.30
2	B	330	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3146	0	3089	442	0
1	T	3146	0	3087	561	0
2	B	1734	0	1641	156	0
2	U	1738	0	1653	224	0
3	C	2758	0	2713	539	0
3	V	2758	0	2711	609	0
4	D	2292	0	2257	444	2
4	W	2292	0	2257	391	1
5	E	1415	0	1416	181	1
5	X	1415	0	1416	230	2
6	F	1371	0	1410	202	0
6	Y	1371	0	1410	257	0
7	G	1060	0	1065	114	0
7	Z	1060	0	1065	119	0
All	All	27556	0	27190	4138	3

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 76.

All (4138) 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:T:193:ILE:HG23	1:T:292:PHE:CE1	1.28	1.67
4:D:165:PHE:CZ	4:D:247:PHE:CE2	1.77	1.67
1:T:194:PRO:HD2	1:T:292:PHE:CE1	1.29	1.64
3:V:99:ALA:HA	3:V:115:SER:CB	1.19	1.59
2:B:202:TYR:CE2	2:B:252:ILE:HB	1.11	1.57
6:Y:61:VAL:HG22	6:Y:74:ILE:CG2	1.14	1.57
5:X:24:ILE:CG2	5:X:41:ILE:HG22	1.34	1.55
5:X:19:MET:HE1	5:X:67:THR:CA	1.37	1.54
6:Y:61:VAL:CG2	6:Y:74:ILE:HG21	1.41	1.50
3:C:245:LEU:HD13	3:C:263:HIS:CE1	1.42	1.50
1:A:62:ILE:HD13	1:A:92:PHE:CE1	1.48	1.48
6:Y:61:VAL:CG2	6:Y:74:ILE:CG2	1.89	1.47
1:A:336:GLN:CG	1:A:367:VAL:HG23	1.41	1.47
1:A:336:GLN:HG3	1:A:367:VAL:CG2	1.41	1.46
4:D:165:PHE:CG	4:D:223:ILE:HB	1.51	1.46
1:T:194:PRO:HD2	1:T:292:PHE:CD1	1.51	1.44
1:T:151:ALA:HB3	1:T:370:HIS:CD2	1.52	1.44
3:V:99:ALA:HA	3:V:115:SER:CA	1.43	1.44
3:V:245:LEU:HD13	3:V:263:HIS:CE1	1.53	1.43
3:V:77:TYR:CB	3:V:89:THR:O	1.65	1.41
4:D:165:PHE:CB	4:D:223:ILE:HB	1.50	1.41
3:V:99:ALA:C	3:V:115:SER:HA	1.38	1.41
4:D:162:THR:CB	4:D:225:PHE:O	1.65	1.40
3:C:77:TYR:CB	3:C:89:THR:O	1.67	1.40
4:D:165:PHE:CZ	4:D:247:PHE:CD2	2.11	1.38
5:X:149:PHE:CE2	5:X:156:PRO:HG3	1.57	1.37
4:D:41:VAL:CG1	4:D:59:ILE:HD11	1.53	1.37
2:U:321:LEU:HB3	2:U:340:PHE:CE1	1.61	1.36
3:C:249:ALA:O	3:C:260:ALA:CB	1.74	1.36
2:U:204:PHE:CZ	2:U:250:ARG:NH1	1.92	1.35
3:C:120:ILE:CB	3:C:137:ILE:HD11	1.56	1.35
2:B:202:TYR:CE2	2:B:252:ILE:CB	2.08	1.35
3:V:77:TYR:CD2	3:V:89:THR:O	1.77	1.35
3:V:99:ALA:CA	3:V:115:SER:HA	1.58	1.34
1:A:102:ARG:HG3	4:D:38:PHE:CE2	1.63	1.34
1:T:194:PRO:CG	1:T:292:PHE:HD1	1.41	1.33
7:Z:63:PRO:HD2	7:Z:109:TYR:OH	1.18	1.32
3:C:146:LEU:HD12	3:C:205:VAL:O	1.28	1.32
6:Y:60:LYS:O	6:Y:74:ILE:CG2	1.77	1.31
4:D:165:PHE:HZ	4:D:247:PHE:CD2	1.49	1.30
3:V:5:SER:HA	3:V:352:GLY:O	1.21	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:193:ILE:HG23	1:T:292:PHE:CZ	1.64	1.29
3:V:77:TYR:CG	3:V:89:THR:O	1.85	1.29
3:V:99:ALA:HB1	3:V:114:GLY:O	1.24	1.28
3:C:146:LEU:CD1	3:C:206:HIS:HA	1.61	1.27
5:X:24:ILE:HG21	5:X:41:ILE:CG2	1.64	1.26
3:V:10:PRO:HA	3:V:350:MET:O	1.14	1.26
3:V:98:ALA:O	3:V:115:SER:HB2	1.23	1.26
2:U:321:LEU:HD22	2:U:340:PHE:CG	1.70	1.26
1:T:194:PRO:CD	1:T:292:PHE:CD1	2.18	1.26
3:V:123:CYS:N	3:V:134:CYS:SG	2.09	1.25
5:X:24:ILE:CG2	5:X:41:ILE:CG2	2.14	1.25
3:C:77:TYR:CD2	3:C:90:LEU:HA	1.70	1.25
1:T:195:ILE:CG1	1:T:285:PRO:HB3	1.66	1.25
3:V:99:ALA:CA	3:V:115:SER:CB	2.13	1.24
6:Y:60:LYS:O	6:Y:74:ILE:HG23	1.26	1.24
3:C:77:TYR:HB3	3:C:89:THR:O	1.06	1.23
4:D:45:ILE:CG1	4:D:57:VAL:HG22	1.67	1.23
3:C:77:TYR:CD2	3:C:89:THR:O	1.92	1.23
4:D:45:ILE:HG13	4:D:57:VAL:CG2	1.69	1.22
1:A:165:GLY:O	1:A:180:VAL:HG23	1.39	1.22
2:B:202:TYR:HE2	2:B:252:ILE:CB	1.44	1.22
3:V:99:ALA:CA	3:V:115:SER:CA	2.15	1.22
4:W:69:ALA:O	4:W:71:GLY:N	1.70	1.22
3:C:245:LEU:CD1	3:C:263:HIS:CE1	2.23	1.22
2:U:321:LEU:HB3	2:U:340:PHE:CD1	1.75	1.21
4:D:165:PHE:CD2	4:D:223:ILE:HB	1.76	1.21
3:V:77:TYR:CD2	3:V:90:LEU:HA	1.76	1.21
1:T:193:ILE:CG2	1:T:292:PHE:CE1	2.25	1.20
7:G:63:PRO:HD2	7:G:109:TYR:OH	1.39	1.20
6:F:18:ALA:CB	7:G:142:VAL:HG22	1.70	1.19
2:U:204:PHE:CE2	2:U:250:ARG:NH1	2.08	1.19
3:V:73:ASP:OD2	6:Y:32:ARG:NE	1.74	1.19
1:A:62:ILE:CD1	1:A:92:PHE:HE1	1.55	1.19
4:W:186:LYS:HD3	4:W:198:VAL:C	1.63	1.19
6:Y:95:MET:SD	6:Y:106:ARG:O	2.02	1.18
3:C:120:ILE:HB	3:C:137:ILE:CD1	1.74	1.17
1:T:194:PRO:CD	1:T:292:PHE:CE1	2.25	1.17
1:T:35:ILE:HG13	1:T:61:PHE:O	1.42	1.17
3:C:10:PRO:HA	3:C:350:MET:O	1.45	1.17
4:D:161:VAL:O	4:D:227:LEU:HB2	1.45	1.17
4:D:165:PHE:HB2	4:D:223:ILE:CA	1.73	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:263:HIS:HA	3:C:328:SER:HB3	1.22	1.16
3:V:77:TYR:HB3	3:V:89:THR:O	1.05	1.16
4:D:165:PHE:CD2	4:D:223:ILE:CG2	2.29	1.16
3:C:21:THR:O	3:C:42:TRP:CH2	1.98	1.16
1:T:178:ILE:HG22	1:T:190:ILE:HD13	1.17	1.16
7:Z:63:PRO:CD	7:Z:109:TYR:OH	1.93	1.16
6:Y:61:VAL:CG1	6:Y:74:ILE:HG12	1.76	1.16
6:Y:9:LEU:CD1	6:Y:140:GLU:HG3	1.76	1.15
2:U:318:GLU:OE1	3:V:97:ARG:NH2	1.79	1.15
6:Y:61:VAL:HG13	6:Y:74:ILE:CG1	1.76	1.15
3:C:77:TYR:CG	3:C:89:THR:O	1.99	1.15
5:X:19:MET:CE	5:X:67:THR:HA	1.77	1.15
3:C:76:ALA:HB3	3:C:91:VAL:O	1.47	1.15
1:T:195:ILE:HG13	1:T:285:PRO:CB	1.77	1.14
3:C:165:LYS:HB3	3:C:198:SER:CB	1.76	1.14
5:X:19:MET:CE	5:X:67:THR:CA	2.24	1.14
6:Y:61:VAL:CG2	6:Y:74:ILE:HG23	1.71	1.14
1:T:194:PRO:CG	1:T:292:PHE:CD1	2.31	1.13
3:C:250:VAL:HA	3:C:260:ALA:HB2	1.24	1.13
5:E:19:MET:HE1	5:E:67:THR:HA	1.15	1.13
6:Y:22:LEU:HD22	6:Y:67:ILE:O	1.47	1.12
3:C:143:SER:HB2	3:C:162:CYS:HB2	1.25	1.12
3:V:79:TRP:HA	3:V:87:LYS:O	1.47	1.13
3:C:120:ILE:HD12	3:C:137:ILE:HD12	1.27	1.12
5:X:26:SER:HB2	5:X:139:GLU:HG2	1.27	1.12
1:T:115:PRO:HG3	1:T:144:GLN:OE1	1.49	1.12
1:T:194:PRO:HG2	1:T:292:PHE:HD1	1.07	1.12
1:A:35:ILE:HB	1:A:62:ILE:HG22	1.25	1.12
4:D:36:ALA:HA	4:D:42:LEU:HB3	1.30	1.12
3:C:148:LEU:HD23	3:C:159:ALA:HB3	1.29	1.12
6:Y:127:TYR:O	6:Y:131:LEU:HD13	1.50	1.12
1:T:163:LEU:O	1:T:180:VAL:HG11	1.48	1.12
3:V:18:LYS:HG3	3:V:62:PRO:HB3	1.29	1.12
4:W:77:LYS:HG3	4:W:84:LEU:HB3	1.30	1.12
4:D:165:PHE:CB	4:D:223:ILE:CB	2.28	1.11
1:T:114:GLU:HG2	1:T:141:ILE:HG22	1.30	1.11
1:T:136:VAL:HB	1:T:137:PRO:HD2	1.27	1.11
3:C:93:LEU:HD22	3:C:123:CYS:SG	1.90	1.11
3:V:102:VAL:HG22	3:V:103:ARG:N	1.61	1.11
1:T:194:PRO:HG2	1:T:292:PHE:CD1	1.87	1.10
4:D:41:VAL:HG11	4:D:59:ILE:HD11	1.27	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:77:TYR:HE2	3:C:90:LEU:HD23	1.10	1.10
3:V:99:ALA:HA	3:V:115:SER:HB3	1.31	1.10
4:D:165:PHE:CE1	4:D:247:PHE:CE2	2.38	1.09
5:X:24:ILE:HG21	5:X:41:ILE:HG22	1.09	1.09
3:C:253:ILE:HG13	3:C:257:SER:HB3	1.34	1.09
3:V:245:LEU:CD1	3:V:263:HIS:CE1	2.35	1.09
3:C:165:LYS:CB	3:C:198:SER:HB3	1.83	1.09
3:C:123:CYS:HA	3:C:134:CYS:HA	1.18	1.09
3:C:153:ASN:HD21	3:C:156:LEU:N	1.49	1.09
3:V:10:PRO:CA	3:V:350:MET:O	1.99	1.09
3:C:153:ASN:ND2	3:C:156:LEU:H	1.49	1.09
3:C:97:ARG:CB	3:C:117:SER:HB2	1.82	1.09
3:C:327:ASN:ND2	3:C:351:ASP:HB3	1.67	1.09
3:C:97:ARG:HB2	3:C:117:SER:HB2	1.35	1.09
3:C:263:HIS:CD2	6:F:21:CYS:HB3	1.87	1.08
7:G:38:ASP:HB2	7:G:41:GLU:HB3	1.32	1.08
3:V:254:THR:HG23	3:V:341:LYS:HD3	1.35	1.08
3:V:123:CYS:HB2	3:V:133:VAL:O	1.52	1.08
3:V:77:TYR:HE2	3:V:90:LEU:HD23	1.17	1.08
2:U:241:VAL:CG1	2:U:253:LYS:HD2	1.82	1.08
1:A:237:ASP:HB3	1:A:240:LYS:HB2	1.25	1.08
4:D:34:THR:HG23	4:D:44:HIS:CG	1.89	1.07
4:D:165:PHE:CE1	4:D:247:PHE:CD2	2.41	1.07
1:T:241:GLU:O	1:T:243:ASN:N	1.87	1.07
3:V:21:THR:O	3:V:42:TRP:CH2	2.08	1.07
4:D:165:PHE:HB2	4:D:223:ILE:CB	1.84	1.07
1:A:62:ILE:CD1	1:A:92:PHE:CE1	2.33	1.07
4:D:45:ILE:HG13	4:D:57:VAL:HG22	1.11	1.07
6:Y:9:LEU:CD1	6:Y:140:GLU:CG	2.32	1.07
4:D:199:LEU:HB2	4:D:224:THR:OG1	1.54	1.06
3:V:148:LEU:HD23	3:V:159:ALA:CB	1.83	1.06
5:X:24:ILE:HG22	5:X:41:ILE:HG22	1.15	1.06
1:T:145:ALA:HB2	1:T:178:ILE:HD12	1.35	1.06
4:W:132:GLN:CG	4:W:160:ARG:N	2.18	1.06
7:G:106:LEU:O	7:G:110:ILE:HG12	1.53	1.06
4:D:165:PHE:CD2	4:D:223:ILE:CB	2.38	1.06
3:V:102:VAL:CG2	3:V:103:ARG:H	1.66	1.06
5:X:42:VAL:HG22	5:X:140:THR:HG22	1.37	1.06
6:F:38:VAL:HG12	6:F:69:SER:HB2	1.06	1.06
3:C:10:PRO:HB3	3:C:350:MET:HB3	1.36	1.06
2:U:241:VAL:HG11	2:U:253:LYS:CD	1.85	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:73:ASP:OD2	6:Y:32:ARG:CD	2.04	1.06
1:T:193:ILE:CG2	1:T:292:PHE:CZ	2.39	1.05
4:D:43:TYR:HE2	4:D:116:LEU:HD22	1.15	1.05
3:C:148:LEU:HD23	3:C:159:ALA:CB	1.85	1.05
3:V:215:SER:OG	3:V:216:ARG:NH1	1.87	1.05
3:V:24:ALA:HB1	3:V:32:VAL:HG11	1.36	1.05
6:Y:67:ILE:HG23	6:Y:68:ASN:H	1.15	1.05
5:X:149:PHE:CE2	5:X:156:PRO:CG	2.39	1.05
3:V:5:SER:CA	3:V:352:GLY:O	2.04	1.05
6:F:8:TYR:CG	6:F:55:ARG:HB2	1.91	1.05
6:F:18:ALA:CA	7:G:142:VAL:HG22	1.84	1.05
3:C:327:ASN:HD22	3:C:351:ASP:HB3	1.11	1.05
3:C:8:VAL:HG23	4:D:282:PRO:HG2	1.33	1.05
4:D:41:VAL:HG13	4:D:59:ILE:HD11	1.37	1.05
2:B:241:VAL:HG11	2:B:253:LYS:HD2	1.09	1.05
3:C:77:TYR:CE2	3:C:90:LEU:HD23	1.93	1.04
3:C:21:THR:O	3:C:42:TRP:CZ3	2.10	1.04
6:Y:9:LEU:HD13	6:Y:140:GLU:OE2	1.57	1.04
1:T:120:PRO:HG2	2:U:202:TYR:CE2	1.90	1.04
3:C:18:LYS:HG3	3:C:62:PRO:HB3	1.34	1.04
6:Y:9:LEU:HD11	6:Y:140:GLU:HG3	1.36	1.04
7:G:42:VAL:HG21	7:G:57:ALA:CB	1.87	1.04
1:T:390:PHE:O	1:T:394:CYS:HB2	1.57	1.04
5:E:26:SER:HB2	5:E:139:GLU:CG	1.88	1.04
1:T:174:VAL:CG2	1:T:193:ILE:O	2.06	1.04
4:W:37:ASP:HB2	4:W:43:TYR:HE2	1.17	1.04
3:V:343:SER:HA	3:V:359:VAL:HB	1.37	1.04
5:E:19:MET:HE1	5:E:67:THR:CA	1.88	1.04
3:V:99:ALA:CB	3:V:114:GLY:O	2.04	1.04
6:Y:61:VAL:HG13	6:Y:74:ILE:HG12	1.05	1.04
3:V:8:VAL:HG23	4:W:282:PRO:HG2	1.39	1.04
3:C:67:ILE:O	3:C:78:VAL:HG13	1.58	1.04
3:V:252:PHE:CE2	3:V:258:LEU:HD11	1.93	1.04
3:C:14:HIS:CE1	3:C:348:THR:OG1	2.11	1.03
3:V:97:ARG:HB2	3:V:117:SER:HB2	1.39	1.03
2:U:336:LYS:HG2	7:Z:21:GLU:CD	1.78	1.03
7:Z:133:LEU:HG	7:Z:134:ALA:H	1.21	1.03
3:V:102:VAL:HG23	3:V:112:ALA:O	1.56	1.03
3:V:64:SER:OG	3:V:108:GLU:OE1	1.73	1.03
6:Y:9:LEU:HD11	6:Y:140:GLU:CG	1.87	1.03
1:T:363:ILE:H	1:T:363:ILE:HD13	1.19	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:247:LEU:HB3	3:C:261:ALA:O	1.57	1.03
7:G:42:VAL:HG21	7:G:57:ALA:HB1	1.37	1.03
1:A:177:VAL:O	1:A:179:PRO:HD3	1.57	1.03
2:U:329:VAL:HG12	2:U:330:LEU:HD12	1.40	1.03
3:V:212:ALA:HB2	3:V:339:LYS:CB	1.88	1.03
1:T:285:PRO:HB2	1:T:292:PHE:HB3	1.39	1.03
1:T:203:PHE:HZ	5:X:54:PHE:CE2	1.77	1.03
4:D:166:SER:O	4:D:167:THR:O	1.75	1.02
3:V:77:TYR:HB3	3:V:89:THR:C	1.78	1.02
3:V:72:THR:CG2	6:Y:26:SER:OG	2.07	1.02
3:V:257:SER:OG	3:V:371:ILE:HA	1.57	1.02
3:V:253:ILE:HB	3:V:342:CYS:SG	1.98	1.02
6:F:20:LEU:HG	6:F:21:CYS:H	1.19	1.02
2:U:321:LEU:HD13	2:U:340:PHE:CD1	1.93	1.02
1:T:35:ILE:CG1	1:T:61:PHE:O	2.08	1.02
6:Y:9:LEU:CD1	6:Y:140:GLU:OE2	2.06	1.02
4:W:150:GLU:HG2	4:W:167:THR:HA	1.37	1.02
6:Y:38:VAL:HG12	6:Y:69:SER:HB2	1.41	1.02
3:C:249:ALA:O	3:C:260:ALA:HB1	0.84	1.02
2:U:236:GLU:O	6:Y:105:ARG:HG2	1.57	1.02
5:E:26:SER:HB2	5:E:139:GLU:HG2	1.06	1.01
1:T:99:LYS:HG3	4:W:5:GLU:HG3	1.41	1.01
4:W:244:ILE:HG23	4:W:245:HIS:H	1.23	1.01
1:T:239:VAL:HG22	5:X:4:TYR:CZ	1.94	1.01
6:F:61:VAL:HG13	6:F:74:ILE:HG12	1.40	1.01
3:V:106:PRO:HD2	3:V:154:SER:HA	1.39	1.01
1:A:270:ASP:O	5:E:159:TRP:HH2	1.44	1.01
5:X:79:LEU:HD22	5:X:164:VAL:HB	1.43	1.01
4:W:226:VAL:HG12	4:W:227:LEU:H	1.26	1.01
1:T:36:ALA:HB3	1:T:73:ALA:O	1.58	1.01
2:B:202:TYR:CD2	2:B:252:ILE:HB	1.96	1.00
1:T:313:ARG:HB3	1:T:314:PRO:HD3	1.38	1.00
2:B:241:VAL:HG11	2:B:253:LYS:CD	1.91	1.00
2:B:241:VAL:CG1	2:B:253:LYS:HD2	1.90	1.00
6:F:18:ALA:HB2	7:G:142:VAL:HG22	1.43	1.00
4:D:41:VAL:CG1	4:D:59:ILE:CD1	2.39	1.00
1:A:208:LEU:HD21	1:A:215:ILE:HD12	1.43	1.00
6:Y:144:LYS:O	6:Y:148:GLU:HB2	1.61	1.00
1:A:336:GLN:CD	1:A:367:VAL:H	1.64	1.00
3:C:215:SER:OG	3:C:216:ARG:NH1	1.95	1.00
7:G:124:VAL:HG13	7:G:125:LEU:H	1.24	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:195:ILE:HG13	1:T:285:PRO:HB3	1.00	1.00
3:V:4:HIS:O	3:V:354:MET:CB	2.09	1.00
3:V:122:ILE:C	3:V:134:CYS:SG	2.39	1.00
2:U:237:THR:HG22	6:Y:105:ARG:NE	1.76	1.00
3:V:158:ALA:CB	3:V:168:ILE:HG13	1.90	0.99
4:W:165:PHE:HE2	4:W:225:PHE:CD2	1.79	0.99
6:Y:8:TYR:CG	6:Y:55:ARG:HB2	1.96	0.99
1:T:174:VAL:HA	1:T:196:ALA:HB2	1.41	0.99
4:D:36:ALA:CA	4:D:42:LEU:HB3	1.92	0.99
3:C:146:LEU:HD11	3:C:206:HIS:HA	1.44	0.99
1:A:270:ASP:O	5:E:159:TRP:CH2	2.15	0.99
1:A:82:ILE:HA	1:A:115:PRO:HG2	1.43	0.99
5:E:26:SER:CB	5:E:139:GLU:HG2	1.93	0.99
3:V:67:ILE:O	3:V:78:VAL:HG13	1.62	0.99
4:D:63:PHE:HD2	4:D:67:LEU:HD12	1.23	0.99
1:T:9:VAL:O	1:T:378:TRP:NE1	1.95	0.99
4:W:75:LEU:CD2	4:W:78:ARG:HB3	1.93	0.99
1:T:138:GLY:HA3	1:T:395:HIS:O	1.62	0.98
1:T:151:ALA:CB	1:T:370:HIS:CD2	2.45	0.98
3:C:77:TYR:CE2	3:C:90:LEU:HA	1.99	0.98
1:T:238:LEU:O	1:T:242:PHE:HD2	1.45	0.98
4:D:244:ILE:HG23	4:D:245:HIS:H	1.24	0.98
3:V:21:THR:O	3:V:42:TRP:HH2	1.43	0.98
3:V:334:VAL:HG12	3:V:335:LEU:H	1.27	0.98
6:F:38:VAL:HG12	6:F:69:SER:CB	1.92	0.98
2:U:322:LYS:HB3	7:Z:16:VAL:HG21	1.45	0.98
7:Z:124:VAL:HG13	7:Z:125:LEU:H	1.24	0.98
2:U:241:VAL:HG11	2:U:253:LYS:HD2	0.98	0.98
1:T:336:GLN:HG3	1:T:367:VAL:CG2	1.93	0.98
1:A:238:LEU:HD21	1:A:280:GLU:HG2	1.42	0.98
6:Y:60:LYS:O	6:Y:74:ILE:HG22	1.64	0.98
4:W:106:LYS:O	4:W:108:SER:N	1.97	0.98
5:X:149:PHE:CZ	5:X:156:PRO:HG3	1.99	0.97
3:V:68:VAL:HB	3:V:104:TRP:CZ2	1.99	0.97
6:F:38:VAL:CG1	6:F:69:SER:HB2	1.92	0.97
6:F:18:ALA:HA	7:G:142:VAL:HG22	1.45	0.97
4:W:186:LYS:HB2	4:W:198:VAL:O	1.62	0.97
5:E:152:GLN:OE1	5:E:155:LYS:NZ	1.97	0.97
3:V:269:LEU:H	3:V:283:GLY:HA3	1.22	0.97
4:D:162:THR:HB	4:D:225:PHE:O	0.80	0.97
1:T:211:ARG:NH1	1:T:274:GLU:OE1	1.96	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:104:PRO:HB2	5:X:111:PHE:HB2	1.43	0.97
3:C:14:HIS:CE1	3:C:348:THR:HG1	1.82	0.97
6:Y:67:ILE:HG23	6:Y:68:ASN:N	1.74	0.97
4:D:75:LEU:CD2	4:D:78:ARG:HB3	1.94	0.97
2:B:246:LEU:HB3	2:B:247:PRO:HD2	1.46	0.97
7:G:108:LYS:HG2	7:G:144:VAL:HG13	1.46	0.97
3:V:76:ALA:HB3	3:V:91:VAL:O	1.63	0.97
3:V:102:VAL:HG22	3:V:103:ARG:H	0.80	0.97
4:W:36:ALA:CB	4:W:42:LEU:HA	1.95	0.97
1:A:18:LYS:HG3	1:A:30:ILE:HG12	1.44	0.96
2:U:234:ALA:HB2	2:U:259:PHE:HZ	1.30	0.96
1:T:336:GLN:HG3	1:T:367:VAL:HG23	1.45	0.96
4:D:165:PHE:HD2	4:D:223:ILE:HG22	1.28	0.96
4:W:132:GLN:CG	4:W:160:ARG:H	1.78	0.96
3:C:30:HIS:HB3	3:C:51:HIS:O	1.63	0.96
1:A:180:VAL:HG12	1:A:181:ALA:H	1.29	0.96
1:T:304:ILE:HD12	1:T:316:TYR:CE1	2.01	0.96
4:W:132:GLN:HG2	4:W:159:ASP:HA	1.44	0.96
3:V:259:VAL:HG12	3:V:260:ALA:H	1.31	0.96
6:F:138:PHE:O	6:F:142:ILE:HG23	1.64	0.96
4:D:128:TYR:CE2	4:D:154:VAL:HG21	2.00	0.96
3:C:93:LEU:CD2	3:C:123:CYS:SG	2.54	0.96
3:C:79:TRP:HA	3:C:87:LYS:O	1.64	0.96
3:V:157:LEU:O	3:V:168:ILE:HG23	1.64	0.95
3:V:99:ALA:HA	3:V:115:SER:HB2	1.32	0.95
4:W:45:ILE:HG13	4:W:57:VAL:HG13	1.46	0.95
3:V:53:GLY:HA3	3:V:73:ASP:OD1	1.65	0.95
3:V:123:CYS:CB	3:V:133:VAL:O	2.13	0.95
4:D:41:VAL:HG22	4:D:61:LEU:HD12	1.45	0.95
2:U:253:LYS:HE3	6:Y:99:GLU:HB3	1.47	0.95
5:E:148:VAL:HG13	5:E:160:TRP:HE3	1.30	0.95
3:V:99:ALA:C	3:V:115:SER:CA	2.32	0.95
3:V:212:ALA:HB2	3:V:339:LYS:HB3	1.47	0.95
3:V:77:TYR:CE2	3:V:90:LEU:HD23	2.01	0.95
2:B:336:LYS:HB3	7:G:21:GLU:OE2	1.65	0.95
1:A:313:ARG:HB3	1:A:314:PRO:HD3	1.45	0.95
1:T:114:GLU:HG2	1:T:141:ILE:CG2	1.96	0.95
2:B:168:PRO:HG2	2:B:178:LEU:O	1.67	0.94
1:T:204:ILE:HG23	1:T:274:GLU:HB2	1.49	0.94
4:W:186:LYS:CD	4:W:198:VAL:H	1.79	0.94
2:U:246:LEU:HB3	2:U:247:PRO:HD2	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:248:ARG:NH1	4:W:249:ASP:OD1	2.00	0.94
4:W:27:LYS:HD3	4:W:28:PRO:HD2	1.47	0.94
1:T:136:VAL:HB	1:T:137:PRO:CD	1.98	0.94
7:Z:57:ALA:O	7:Z:59:LEU:N	2.00	0.94
3:V:135:LYS:HG3	3:V:191:PHE:CE2	2.02	0.94
1:A:102:ARG:CG	4:D:38:PHE:CE2	2.49	0.94
1:A:132:GLU:HG3	1:A:400:TYR:OH	1.66	0.94
6:F:152:SER:O	6:F:156:ARG:HB2	1.66	0.94
1:T:255:GLN:NE2	1:T:270:ASP:OD1	2.00	0.94
3:V:72:THR:HG21	6:Y:26:SER:OG	1.68	0.94
3:V:254:THR:HG22	3:V:255:GLU:H	1.29	0.94
3:C:115:SER:OG	3:C:119:VAL:O	1.85	0.94
3:C:24:ALA:HB1	3:C:32:VAL:HG11	1.48	0.94
2:U:318:GLU:CD	3:V:97:ARG:HH22	1.71	0.94
1:T:203:PHE:CZ	5:X:54:PHE:CE2	2.56	0.94
1:A:363:ILE:H	1:A:363:ILE:HD13	1.33	0.94
7:Z:63:PRO:HD2	7:Z:109:TYR:HH	0.86	0.93
3:C:77:TYR:HD2	3:C:90:LEU:CA	1.80	0.93
1:T:180:VAL:HG12	1:T:181:ALA:H	1.32	0.93
1:T:5:LEU:CD2	4:W:42:LEU:HD11	1.98	0.93
1:T:36:ALA:CB	1:T:73:ALA:O	2.16	0.93
3:V:148:LEU:HD23	3:V:159:ALA:HB3	1.48	0.93
3:V:173:ILE:CG2	3:V:176:VAL:HG22	1.98	0.93
5:X:19:MET:HE2	5:X:67:THR:OG1	1.68	0.93
1:A:177:VAL:HG11	1:A:303:VAL:HG21	1.50	0.93
6:F:61:VAL:HG22	6:F:74:ILE:HG23	1.47	0.93
4:D:77:LYS:HG3	4:D:84:LEU:HB3	1.50	0.93
5:X:19:MET:CE	5:X:67:THR:N	2.32	0.93
3:C:245:LEU:CD1	3:C:263:HIS:HE1	1.71	0.93
3:C:146:LEU:CD1	3:C:205:VAL:O	2.17	0.93
3:C:77:TYR:HB3	3:C:89:THR:C	1.88	0.93
3:C:146:LEU:CD1	3:C:206:HIS:CA	2.47	0.93
6:Y:101:PHE:O	6:Y:103:ILE:N	2.00	0.93
6:Y:61:VAL:HG22	6:Y:74:ILE:CB	1.98	0.93
3:C:120:ILE:HD12	3:C:137:ILE:CD1	1.97	0.93
5:E:104:PRO:HB2	5:E:111:PHE:HB2	1.48	0.93
5:X:63:GLU:HA	5:X:66:ARG:HD3	1.51	0.92
4:W:227:LEU:HD23	4:W:231:HIS:HB2	1.48	0.92
3:V:77:TYR:HD2	3:V:90:LEU:HA	1.14	0.92
6:F:101:PHE:O	6:F:103:ILE:N	2.02	0.92
3:V:153:ASN:HD21	3:V:156:LEU:H	1.00	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:172:TYR:CD2	3:V:180:PRO:HD3	2.04	0.92
4:W:132:GLN:HE21	4:W:159:ASP:C	1.72	0.92
3:C:76:ALA:O	3:C:91:VAL:HB	1.69	0.92
3:V:253:ILE:HG13	3:V:257:SER:HB3	1.52	0.92
2:U:313:LEU:HG	2:U:317:LEU:HG	1.52	0.92
1:A:236:PRO:O	1:A:334:ARG:NH1	2.03	0.92
4:D:186:LYS:HZ3	4:D:199:LEU:HD12	1.34	0.92
2:U:182:LEU:HD11	2:U:281:LEU:HD11	1.48	0.92
1:A:120:PRO:HG3	2:B:201:GLY:CA	1.99	0.92
3:V:30:HIS:HB3	3:V:51:HIS:O	1.70	0.92
4:D:36:ALA:HB1	4:D:42:LEU:HD23	1.49	0.92
4:D:132:GLN:HG2	4:D:159:ASP:HA	1.49	0.92
3:V:14:HIS:CE1	3:V:348:THR:OG1	2.23	0.92
1:A:62:ILE:HD13	1:A:92:PHE:CD1	2.04	0.92
4:W:165:PHE:HE2	4:W:225:PHE:HD2	1.00	0.92
4:D:27:LYS:HD3	4:D:28:PRO:HD2	1.52	0.92
3:V:24:ALA:HB1	3:V:32:VAL:CG1	1.99	0.92
2:U:326:LEU:HB2	2:U:335:GLU:OE1	1.70	0.92
3:V:151:HIS:O	3:V:153:ASN:N	2.03	0.91
3:C:151:HIS:O	3:C:153:ASN:N	2.03	0.91
4:W:132:GLN:HE21	4:W:159:ASP:CA	1.83	0.91
5:X:15:LEU:HA	5:X:20:ALA:HB2	1.52	0.91
4:D:43:TYR:CE2	4:D:116:LEU:HD22	2.03	0.91
5:X:113:LEU:HD21	5:X:171:LYS:HG3	1.51	0.91
3:C:30:HIS:HD1	3:C:53:GLY:C	1.74	0.91
4:W:132:GLN:HG2	4:W:160:ARG:N	1.81	0.91
3:V:13:CYS:SG	3:V:56:THR:O	2.28	0.91
1:T:37:ILE:HG22	1:T:59:ASP:O	1.71	0.91
5:X:26:SER:CB	5:X:139:GLU:HG2	2.00	0.91
1:A:35:ILE:HD12	1:A:62:ILE:CG2	2.01	0.91
4:W:165:PHE:CE2	4:W:225:PHE:CD2	2.59	0.91
2:U:175:LEU:O	2:U:177:HIS:N	2.03	0.91
1:T:406:SER:HB2	1:T:409:ARG:HE	1.32	0.91
5:E:155:LYS:O	5:E:157:SER:N	2.03	0.91
4:D:121:PHE:O	4:D:124:VAL:HG12	1.69	0.91
4:D:165:PHE:CG	4:D:223:ILE:CB	2.47	0.91
5:X:79:LEU:CD2	5:X:164:VAL:HB	2.01	0.91
6:F:8:TYR:CD1	6:F:55:ARG:HB2	2.06	0.91
7:Z:116:SER:O	7:Z:118:SER:N	2.03	0.91
4:D:162:THR:HG22	4:D:226:VAL:HA	1.50	0.90
3:C:30:HIS:ND1	3:C:53:GLY:C	2.24	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:336:GLN:CG	1:T:367:VAL:HG23	1.99	0.90
7:Z:104:ASP:OD2	7:Z:143:ARG:NH1	2.04	0.90
1:T:285:PRO:HG2	1:T:292:PHE:CD2	2.05	0.90
4:D:165:PHE:HZ	4:D:247:PHE:CE2	1.44	0.90
3:V:77:TYR:HD2	3:V:90:LEU:CA	1.83	0.90
2:U:241:VAL:HG13	2:U:253:LYS:HG2	1.51	0.90
3:V:243:GLU:HB3	7:Z:137:GLY:HA3	1.54	0.90
3:V:183:THR:HG23	3:V:184:PRO:HD2	1.53	0.90
5:E:19:MET:CE	5:E:67:THR:HA	2.00	0.90
3:V:4:HIS:O	3:V:354:MET:HB2	1.70	0.90
1:T:18:LYS:HG3	1:T:30:ILE:HG12	1.53	0.90
7:G:57:ALA:O	7:G:59:LEU:N	2.05	0.90
3:C:72:THR:O	3:C:74:ARG:N	2.03	0.90
7:G:63:PRO:CD	7:G:109:TYR:OH	2.19	0.90
4:W:37:ASP:HB2	4:W:43:TYR:CE2	2.05	0.90
1:A:166:THR:OG1	1:A:315:LEU:HG	1.71	0.90
3:V:110:LYS:HD3	3:V:173:ILE:HD11	1.51	0.90
1:T:308:PRO:O	1:T:311:VAL:HG12	1.70	0.90
4:D:63:PHE:CD2	4:D:67:LEU:HD12	2.06	0.90
3:V:224:SER:HA	3:V:246:PRO:HA	1.50	0.90
6:Y:61:VAL:HG23	6:Y:74:ILE:CG2	1.99	0.90
3:V:106:PRO:HB2	3:V:154:SER:HB3	1.52	0.90
6:Y:9:LEU:CD1	6:Y:140:GLU:CD	2.41	0.89
1:T:128:GLU:HG2	1:T:129:ILE:H	1.35	0.89
1:T:284:HIS:CB	1:T:287:PHE:HB2	2.03	0.89
1:A:102:ARG:HG3	4:D:38:PHE:CD2	2.07	0.89
3:C:143:SER:HB2	3:C:162:CYS:CB	2.02	0.89
4:D:69:ALA:O	4:D:71:GLY:N	2.06	0.89
7:Z:80:LEU:O	7:Z:84:ILE:HG13	1.71	0.89
2:B:241:VAL:HG13	2:B:253:LYS:HG2	1.54	0.89
2:U:321:LEU:HD13	2:U:340:PHE:HD1	1.33	0.89
3:C:249:ALA:HB1	3:C:332:ILE:HG22	1.52	0.89
6:Y:9:LEU:HD13	6:Y:140:GLU:HG3	1.52	0.89
3:C:165:LYS:HB3	3:C:198:SER:HB3	0.94	0.89
3:C:165:LYS:HG2	3:C:200:SER:O	1.72	0.89
1:T:304:ILE:HG21	1:T:316:TYR:CE2	2.08	0.89
1:A:308:PRO:O	1:A:311:VAL:HG12	1.73	0.89
4:D:214:ALA:HB1	4:D:222:TYR:OH	1.72	0.89
3:C:269:LEU:H	3:C:283:GLY:HA3	1.35	0.89
3:C:10:PRO:HB3	3:C:350:MET:CB	2.02	0.89
5:E:63:GLU:HA	5:E:66:ARG:HD3	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:194:PRO:HD2	1:T:292:PHE:HE1	1.09	0.89
4:D:165:PHE:HB2	4:D:223:ILE:N	1.87	0.89
3:C:21:THR:O	3:C:42:TRP:HH2	1.47	0.89
6:F:63:ILE:CD1	6:F:72:VAL:HG13	2.03	0.89
1:A:128:GLU:HG2	1:A:129:ILE:H	1.37	0.89
4:W:182:MET:HG3	4:W:200:PHE:CE1	2.08	0.89
4:D:165:PHE:CZ	4:D:247:PHE:HE2	1.60	0.88
3:V:158:ALA:HB1	3:V:168:ILE:HG13	1.51	0.88
2:U:321:LEU:HD22	2:U:340:PHE:CD2	2.08	0.88
4:W:80:TYR:OH	4:W:112:GLN:O	1.89	0.88
4:W:165:PHE:CE2	4:W:225:PHE:HD2	1.90	0.88
1:A:120:PRO:HG3	2:B:201:GLY:HA3	1.52	0.88
4:D:30:ALA:HB2	4:D:52:LYS:HG2	1.55	0.88
3:V:72:THR:O	3:V:74:ARG:N	2.05	0.88
3:C:326:LYS:HB2	3:C:351:ASP:OD2	1.74	0.88
4:W:132:GLN:HG3	4:W:160:ARG:N	1.87	0.88
4:D:75:LEU:HD21	4:D:78:ARG:HB3	1.54	0.88
1:T:116:PRO:HB3	1:T:185:VAL:HG11	1.53	0.88
2:U:261:ALA:HB3	2:U:262:PRO:HD3	1.56	0.88
3:C:14:HIS:O	3:C:331:GLN:NE2	2.06	0.88
4:D:8:ASN:OD1	4:D:43:TYR:CE1	2.26	0.88
1:A:370:HIS:CD2	1:A:371:HIS:H	1.92	0.88
5:X:26:SER:OG	5:X:139:GLU:CD	2.11	0.88
1:T:151:ALA:HB3	1:T:370:HIS:HD2	0.96	0.88
4:D:165:PHE:HD2	4:D:223:ILE:CG2	1.76	0.88
4:D:36:ALA:CB	4:D:42:LEU:HB3	2.04	0.88
1:T:239:VAL:HG13	5:X:4:TYR:CE1	2.08	0.88
1:T:99:LYS:HG3	4:W:5:GLU:CG	2.04	0.88
4:W:106:LYS:C	4:W:108:SER:H	1.78	0.88
7:G:118:SER:HB3	7:G:121:SER:HB3	1.56	0.88
1:A:205:GLN:HE22	1:A:220:SER:C	1.78	0.88
3:V:173:ILE:HG21	3:V:176:VAL:HG22	1.56	0.87
3:V:245:LEU:HD13	3:V:263:HIS:HE1	0.88	0.87
2:U:223:VAL:H	2:U:312:GLY:HA3	1.38	0.87
2:B:182:LEU:HD11	2:B:281:LEU:HD11	1.53	0.87
3:V:48:LEU:HD11	3:V:86:TRP:HB2	1.56	0.87
1:A:21:TYR:CE1	4:D:35:PHE:HB2	2.08	0.87
4:D:36:ALA:CB	4:D:42:LEU:HD23	2.05	0.87
4:D:142:ALA:H	4:D:154:VAL:CG2	1.85	0.87
5:X:19:MET:HE1	5:X:67:THR:N	1.87	0.87
3:C:263:HIS:HA	3:C:328:SER:CB	2.05	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:321:LEU:CB	2:U:340:PHE:CD1	2.56	0.87
4:D:45:ILE:CG1	4:D:57:VAL:CG2	2.38	0.87
4:W:237:ARG:C	4:W:241:ILE:HD13	1.95	0.87
1:T:304:ILE:HD13	1:T:315:LEU:O	1.73	0.87
1:A:208:LEU:CD2	1:A:215:ILE:HD12	2.03	0.87
1:A:193:ILE:HD11	1:A:299:VAL:HG11	1.57	0.87
3:V:347:THR:H	3:V:355:SER:HB3	1.38	0.87
7:G:104:ASP:OD2	7:G:143:ARG:NH1	2.07	0.87
3:V:253:ILE:CG1	3:V:257:SER:HB3	2.05	0.86
1:A:9:VAL:O	1:A:378:TRP:NE1	2.06	0.86
3:C:245:LEU:HB3	3:C:246:PRO:HD2	1.56	0.86
1:T:178:ILE:HG22	1:T:190:ILE:CD1	2.03	0.86
1:A:211:ARG:HD3	5:E:159:TRP:CZ3	2.10	0.86
6:Y:8:TYR:CD1	6:Y:55:ARG:HB2	2.10	0.86
5:X:5:HIS:CD2	5:X:58:TYR:CZ	2.62	0.86
1:T:241:GLU:C	1:T:243:ASN:H	1.77	0.86
3:V:98:ALA:C	3:V:115:SER:HB2	1.94	0.86
4:W:165:PHE:CZ	4:W:247:PHE:CD2	2.64	0.86
3:V:102:VAL:O	3:V:103:ARG:HG2	1.75	0.86
3:C:123:CYS:HB3	3:C:133:VAL:O	1.74	0.86
3:V:98:ALA:O	3:V:115:SER:CB	2.19	0.86
3:C:327:ASN:HD22	3:C:351:ASP:CB	1.89	0.86
3:V:247:LEU:O	3:V:248:LEU:HD22	1.74	0.86
4:D:45:ILE:HD12	4:D:45:ILE:H	1.39	0.86
4:D:10:ILE:C	4:D:11:ILE:HD12	1.97	0.86
3:C:334:VAL:HG12	3:C:335:LEU:H	1.41	0.85
1:T:37:ILE:HA	1:T:72:TYR:HD2	1.41	0.85
1:A:165:GLY:HA3	1:A:318:ASN:HB3	1.56	0.85
1:T:240:LYS:O	1:T:242:PHE:N	2.09	0.85
1:T:203:PHE:HZ	5:X:54:PHE:CD2	1.93	0.85
1:A:82:ILE:HG12	1:A:83:VAL:N	1.89	0.85
6:Y:102:PHE:O	6:Y:122:HIS:NE2	2.10	0.85
1:A:21:TYR:OH	1:A:101:LEU:O	1.92	0.85
4:W:280:ALA:HB3	6:Y:126:MET:SD	2.17	0.85
3:C:155:VAL:HG21	3:C:180:PRO:HB3	1.59	0.85
3:V:121:SER:HB3	3:V:136:HIS:CE1	2.11	0.85
3:V:258:LEU:O	3:V:270:PHE:HB2	1.76	0.85
4:D:165:PHE:HB2	4:D:223:ILE:HB	1.38	0.85
5:X:15:LEU:HA	5:X:20:ALA:CB	2.06	0.85
3:C:104:TRP:O	3:C:150:TRP:NE1	2.09	0.85
1:A:278:GLY:O	1:A:281:ILE:HG13	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:129:ASN:ND2	3:V:131:TRP:CE3	2.44	0.85
4:W:194:THR:HB	4:W:230:ARG:CZ	2.07	0.85
1:T:211:ARG:HD2	1:T:212:GLU:H	1.40	0.85
5:E:149:PHE:CD2	5:E:156:PRO:HA	2.11	0.85
4:D:59:ILE:HD12	4:D:116:LEU:HD11	1.58	0.85
3:V:269:LEU:N	3:V:283:GLY:HA3	1.91	0.85
1:A:336:GLN:OE1	1:A:367:VAL:N	2.10	0.85
5:X:155:LYS:C	5:X:157:SER:H	1.80	0.85
2:U:321:LEU:CD2	2:U:340:PHE:CG	2.59	0.85
3:C:253:ILE:CG1	3:C:257:SER:HB3	2.06	0.85
3:C:116:GLY:HA2	3:C:145:VAL:N	1.92	0.84
1:T:120:PRO:HG2	2:U:202:TYR:CZ	2.11	0.84
4:D:68:GLN:HG3	4:D:73:ASP:CG	1.96	0.84
1:T:278:GLY:O	1:T:281:ILE:HG13	1.77	0.84
3:C:73:ASP:OD2	6:F:32:ARG:CD	2.24	0.84
1:T:321:LEU:HB3	1:T:326:THR:HB	1.59	0.84
3:C:146:LEU:HD13	3:C:206:HIS:HA	1.60	0.84
2:U:237:THR:HG22	6:Y:105:ARG:HE	1.38	0.84
4:D:8:ASN:ND2	4:D:43:TYR:OH	2.09	0.84
3:C:116:GLY:HA2	3:C:145:VAL:H	1.43	0.84
4:W:35:PHE:O	4:W:43:TYR:N	2.10	0.84
1:A:181:ALA:CB	1:A:186:ILE:HD11	2.07	0.84
1:T:69:LYS:HD2	1:T:72:TYR:CD1	2.12	0.84
3:V:120:ILE:O	3:V:121:SER:OG	1.95	0.84
4:D:106:LYS:O	4:D:106:LYS:HD2	1.78	0.84
1:T:177:VAL:HG11	1:T:303:VAL:HG21	1.59	0.84
3:C:97:ARG:HG3	3:C:117:SER:CB	2.08	0.84
4:W:132:GLN:HG2	4:W:159:ASP:CA	2.08	0.84
1:A:103:ALA:C	4:D:38:PHE:HE1	1.81	0.84
1:A:138:GLY:HA3	1:A:395:HIS:O	1.78	0.84
5:X:26:SER:OG	5:X:139:GLU:OE2	1.95	0.84
3:C:158:ALA:HB2	3:C:168:ILE:HG13	1.59	0.84
1:A:211:ARG:HD3	5:E:159:TRP:CH2	2.13	0.84
6:F:102:PHE:O	6:F:122:HIS:NE2	2.10	0.84
2:U:154:GLY:O	2:U:169:VAL:HB	1.78	0.84
3:V:160:GLY:HA3	3:V:205:VAL:HG11	1.58	0.84
4:D:280:ALA:O	6:F:127:TYR:HD1	1.61	0.84
1:A:135:ASN:OD1	1:A:397:LYS:HD2	1.78	0.84
2:B:223:VAL:H	2:B:312:GLY:HA3	1.41	0.83
1:T:186:ILE:CG2	1:T:189:CYS:HB2	2.08	0.83
7:Z:118:SER:HB3	7:Z:121:SER:HB3	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:76:VAL:HB	6:F:78:GLN:HE22	1.42	0.83
5:E:23:PRO:HB3	5:E:32:ALA:HB1	1.60	0.83
1:T:151:ALA:CB	1:T:370:HIS:HD2	1.87	0.83
4:D:41:VAL:HG22	4:D:61:LEU:CD1	2.08	0.83
3:C:77:TYR:CD2	3:C:90:LEU:CA	2.55	0.83
1:T:208:LEU:HG	1:T:211:ARG:HH21	1.43	0.83
5:E:136:LEU:O	5:E:140:THR:OG1	1.95	0.83
4:W:153:TYR:O	4:W:164:VAL:N	2.12	0.83
1:T:5:LEU:HD22	4:W:42:LEU:HD11	1.60	0.83
3:V:104:TRP:O	3:V:150:TRP:NE1	2.11	0.83
4:D:116:LEU:HD23	4:D:117:LYS:N	1.93	0.83
3:V:102:VAL:HA	3:V:112:ALA:O	1.78	0.83
1:A:336:GLN:OE1	1:A:366:GLN:HA	1.78	0.83
3:V:77:TYR:CE2	3:V:90:LEU:HA	2.12	0.83
3:C:332:ILE:HB	3:C:347:THR:HG22	1.57	0.83
7:G:80:LEU:O	7:G:84:ILE:HG13	1.78	0.83
6:Y:145:GLU:O	6:Y:149:MET:HG2	1.79	0.83
6:Y:60:LYS:C	6:Y:74:ILE:HG23	1.97	0.83
2:U:321:LEU:CD1	2:U:340:PHE:HB2	2.09	0.83
2:U:169:VAL:HG12	2:U:170:TYR:H	1.44	0.83
3:V:158:ALA:HB2	3:V:168:ILE:CG1	2.09	0.83
3:V:72:THR:HG22	6:Y:26:SER:OG	1.76	0.83
3:C:116:GLY:HA3	3:C:144:THR:HA	1.61	0.83
3:C:205:VAL:HA	3:C:221:SER:HA	1.60	0.83
4:D:45:ILE:CB	4:D:57:VAL:HG22	2.08	0.83
3:C:70:CYS:SG	3:C:113:VAL:HG11	2.18	0.82
1:T:151:ALA:O	1:T:154:THR:HG22	1.79	0.82
3:C:263:HIS:CA	3:C:328:SER:HB3	2.08	0.82
3:C:172:TYR:HE1	3:C:174:LYS:HG2	1.43	0.82
1:A:237:ASP:HB3	1:A:240:LYS:CB	2.06	0.82
4:D:130:GLN:HG3	4:D:134:GLU:CD	1.99	0.82
3:V:102:VAL:HG23	3:V:112:ALA:C	1.98	0.82
6:F:18:ALA:HA	7:G:142:VAL:CG2	2.09	0.82
3:C:164:PHE:O	3:C:205:VAL:HG23	1.79	0.82
3:C:286:ASP:OD1	3:C:287:VAL:N	2.12	0.82
1:T:178:ILE:CG2	1:T:190:ILE:HD13	2.07	0.82
3:C:10:PRO:CA	3:C:350:MET:O	2.27	0.82
1:A:134:PHE:CD1	4:D:256:LYS:HD3	2.14	0.82
4:W:116:LEU:HD23	4:W:117:LYS:N	1.94	0.82
1:A:205:GLN:NE2	1:A:220:SER:O	2.11	0.82
3:V:140:PRO:HD2	3:V:169:PHE:CZ	2.14	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ILE:CB	1:A:62:ILE:HG22	2.09	0.82
1:T:201:THR:HB	1:T:224:ALA:HB1	1.60	0.82
2:U:204:PHE:HZ	2:U:250:ARG:NH1	1.74	0.82
4:W:186:LYS:HD3	4:W:198:VAL:O	1.79	0.82
1:T:31:ILE:HD12	1:T:63:GLY:HA3	1.62	0.82
1:T:114:GLU:HB2	1:T:118:ASN:HD22	1.43	0.82
2:U:204:PHE:CZ	2:U:250:ARG:CZ	2.62	0.82
3:V:158:ALA:HB2	3:V:168:ILE:HG13	1.61	0.82
4:D:36:ALA:HA	4:D:42:LEU:CB	2.10	0.82
2:U:313:LEU:N	2:U:314:PRO:CD	2.42	0.82
3:V:102:VAL:CG2	3:V:112:ALA:O	2.27	0.82
3:C:152:PRO:HG2	3:C:212:ALA:HA	1.62	0.82
2:U:202:TYR:CE1	2:U:252:ILE:HB	2.13	0.82
1:A:134:PHE:HD1	4:D:256:LYS:HD3	1.45	0.82
7:Z:38:ASP:HB2	7:Z:41:GLU:HB3	1.59	0.82
4:W:215:ALA:O	4:W:222:TYR:OH	1.96	0.81
6:F:63:ILE:HD13	6:F:72:VAL:HG13	1.62	0.81
1:A:211:ARG:NH1	5:E:159:TRP:HZ3	1.78	0.81
2:B:168:PRO:CG	2:B:178:LEU:O	2.28	0.81
1:T:285:PRO:HB2	1:T:292:PHE:CB	2.10	0.81
5:X:136:LEU:O	5:X:140:THR:OG1	1.98	0.81
3:C:120:ILE:CG1	3:C:137:ILE:HD11	2.08	0.81
3:V:8:VAL:HG13	3:V:9:GLU:H	1.43	0.81
1:A:165:GLY:N	1:A:180:VAL:HG21	1.95	0.81
4:W:77:LYS:HG3	4:W:84:LEU:CB	2.08	0.81
6:Y:61:VAL:CB	6:Y:74:ILE:HG12	2.10	0.81
1:A:99:LYS:HG3	4:D:5:GLU:HG3	1.62	0.81
2:U:241:VAL:CG1	2:U:253:LYS:CG	2.59	0.81
3:V:143:SER:HB2	3:V:162:CYS:HB2	1.62	0.81
4:D:202:HIS:CD2	4:D:203:ARG:HG3	2.16	0.81
3:C:24:ALA:HB1	3:C:32:VAL:CG1	2.10	0.81
6:F:76:VAL:HB	6:F:78:GLN:NE2	1.96	0.81
1:A:260:ASN:HB2	1:A:265:LYS:O	1.81	0.81
7:Z:87:LYS:N	7:Z:87:LYS:HD3	1.96	0.81
3:V:115:SER:H	3:V:145:VAL:HB	1.45	0.81
2:U:241:VAL:CG1	2:U:253:LYS:CD	2.51	0.81
1:T:304:ILE:CD1	1:T:316:TYR:CE1	2.64	0.81
3:C:123:CYS:HA	3:C:134:CYS:CA	2.07	0.81
3:C:8:VAL:HG13	3:C:9:GLU:H	1.46	0.81
1:T:102:ARG:HG2	4:W:37:ASP:OD1	1.79	0.81
5:E:83:GLN:HG3	5:E:161:THR:HG1	1.46	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:173:ILE:HB	3:C:176:VAL:CG2	2.11	0.81
1:A:71:THR:HG23	1:A:72:TYR:CD1	2.16	0.81
5:E:19:MET:CE	5:E:67:THR:CA	2.59	0.81
1:T:116:PRO:HB3	1:T:185:VAL:CG1	2.10	0.80
3:C:97:ARG:HB2	3:C:117:SER:CB	2.11	0.80
3:V:73:ASP:OD2	6:Y:32:ARG:HD3	1.79	0.80
3:V:107:ASN:HD22	3:V:109:LYS:H	1.27	0.80
5:X:19:MET:CE	5:X:67:THR:OG1	2.29	0.80
3:C:143:SER:CB	3:C:162:CYS:HB2	2.09	0.80
4:W:75:LEU:HD21	4:W:78:ARG:HB3	1.59	0.80
6:Y:54:SER:OG	7:Z:117:PRO:HG2	1.81	0.80
4:D:165:PHE:HB3	4:D:223:ILE:HD12	1.63	0.80
3:V:100:ARG:HG2	3:V:146:LEU:HD23	1.63	0.80
2:B:253:LYS:HE3	6:F:99:GLU:HB3	1.63	0.80
6:F:61:VAL:HG13	6:F:74:ILE:CG1	2.12	0.80
2:U:220:LEU:H	2:U:220:LEU:HD12	1.45	0.80
3:C:116:GLY:CA	3:C:144:THR:HA	2.12	0.80
1:T:193:ILE:HG23	1:T:292:PHE:CD1	2.13	0.80
3:C:30:HIS:CB	3:C:51:HIS:O	2.28	0.80
7:Z:74:ARG:O	7:Z:78:ILE:HG13	1.82	0.80
1:A:35:ILE:HD11	1:A:60:PHE:HD2	1.45	0.80
3:C:253:ILE:HG13	3:C:257:SER:CB	2.12	0.80
4:D:63:PHE:HD2	4:D:67:LEU:CD1	1.95	0.80
1:T:207:LEU:O	1:T:207:LEU:HD23	1.82	0.80
4:D:153:TYR:HB2	4:D:164:VAL:HB	1.63	0.80
1:A:120:PRO:HG3	2:B:201:GLY:C	2.03	0.80
3:C:73:ASP:OD2	6:F:32:ARG:NE	2.15	0.80
1:A:114:GLU:HB2	1:A:118:ASN:HD22	1.47	0.80
1:A:100:TYR:O	4:D:10:ILE:HG12	1.82	0.79
3:C:116:GLY:CA	3:C:145:VAL:H	1.96	0.79
5:E:148:VAL:HG13	5:E:160:TRP:CE3	2.15	0.79
5:X:19:MET:HE1	5:X:67:THR:HA	0.81	0.79
6:Y:36:PRO:HA	6:Y:69:SER:HB3	1.64	0.79
4:W:165:PHE:CE1	4:W:247:PHE:CD2	2.70	0.79
1:T:71:THR:HG23	1:T:72:TYR:CD1	2.17	0.79
4:D:165:PHE:HB2	4:D:223:ILE:C	2.01	0.79
6:Y:73:SER:C	6:Y:74:ILE:HG13	2.02	0.79
1:T:317:LYS:HE2	1:T:364:ASP:OD2	1.82	0.79
4:D:165:PHE:HB3	4:D:223:ILE:CD1	2.12	0.79
3:V:156:LEU:HD23	3:V:170:SER:HB2	1.65	0.79
3:C:261:ALA:HB1	3:C:266:PHE:O	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:77:LYS:CG	4:W:84:LEU:HB3	2.10	0.79
3:C:152:PRO:CG	3:C:212:ALA:HA	2.11	0.79
2:U:329:VAL:CG1	2:U:330:LEU:HD12	2.12	0.79
3:V:212:ALA:HB2	3:V:339:LYS:HB2	1.64	0.79
7:G:87:LYS:HD3	7:G:87:LYS:N	1.97	0.79
7:G:74:ARG:O	7:G:78:ILE:HG13	1.83	0.79
2:U:371:PHE:O	2:U:372:TRP:CB	2.31	0.79
5:X:60:ILE:HD12	5:X:60:ILE:H	1.46	0.79
6:Y:139:MET:O	6:Y:142:ILE:HG12	1.83	0.79
3:V:173:ILE:CB	3:V:176:VAL:HG22	2.12	0.79
6:Y:67:ILE:CG2	6:Y:68:ASN:H	1.90	0.79
3:C:34:ILE:O	3:C:45:VAL:N	2.15	0.79
4:W:188:GLY:O	4:W:190:ARG:HG2	1.83	0.79
1:T:326:THR:O	1:T:373:GLN:OE1	2.01	0.79
6:F:18:ALA:HB1	7:G:142:VAL:HA	1.63	0.79
4:W:186:LYS:HD2	4:W:198:VAL:H	1.46	0.79
3:C:123:CYS:SG	3:C:134:CYS:HB2	2.23	0.79
5:E:26:SER:CB	5:E:139:GLU:CG	2.58	0.79
3:V:101:CYS:SG	3:V:147:SER:HA	2.23	0.79
3:C:122:ILE:HG23	3:C:135:LYS:HB2	1.63	0.79
4:D:165:PHE:CE2	4:D:225:PHE:CE1	2.71	0.79
4:D:165:PHE:CB	4:D:223:ILE:N	2.45	0.79
6:Y:36:PRO:HG2	6:Y:39:GLU:HB2	1.63	0.78
3:C:172:TYR:HE1	3:C:174:LYS:CG	1.95	0.78
3:C:97:ARG:CG	3:C:117:SER:HB2	2.12	0.78
1:T:120:PRO:HG3	2:U:201:GLY:O	1.82	0.78
1:A:31:ILE:HD12	1:A:63:GLY:HA3	1.63	0.78
1:T:114:GLU:HB2	1:T:118:ASN:ND2	1.98	0.78
4:W:132:GLN:HG2	4:W:160:ARG:H	1.39	0.78
4:W:37:ASP:N	4:W:41:VAL:O	2.16	0.78
1:T:208:LEU:HG	1:T:211:ARG:NH2	1.98	0.78
4:W:146:TYR:OH	4:W:150:GLU:HB3	1.83	0.78
1:T:194:PRO:CD	1:T:292:PHE:HD1	1.70	0.78
1:A:208:LEU:HD21	1:A:215:ILE:CD1	2.12	0.78
1:T:284:HIS:HB2	1:T:287:PHE:HB2	1.64	0.78
4:W:59:ILE:HD12	4:W:116:LEU:HD11	1.65	0.78
5:X:149:PHE:HE2	5:X:156:PRO:HG3	1.43	0.78
1:T:165:GLY:O	1:T:180:VAL:HG23	1.82	0.78
3:V:332:ILE:HG13	3:V:347:THR:HG22	1.65	0.78
3:V:122:ILE:O	3:V:135:LYS:N	2.13	0.78
4:D:165:PHE:CE2	4:D:225:PHE:CD1	2.71	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:165:PHE:CE1	4:W:247:PHE:HD2	2.02	0.78
4:D:124:VAL:HG13	4:D:125:PHE:CD1	2.17	0.78
3:V:14:HIS:CE1	3:V:348:THR:HG23	2.19	0.78
4:D:186:LYS:NZ	4:D:199:LEU:HD12	1.97	0.78
6:Y:61:VAL:CA	6:Y:74:ILE:HG23	2.14	0.78
6:F:22:LEU:HD22	6:F:67:ILE:HA	1.64	0.78
2:B:241:VAL:CG1	2:B:253:LYS:HG2	2.14	0.78
6:Y:62:LEU:HD21	6:Y:71:ARG:HH21	1.49	0.78
4:D:165:PHE:CE1	4:D:247:PHE:HE2	1.91	0.78
5:X:16:ILE:O	5:X:18:ASN:N	2.17	0.78
5:X:83:GLN:OE1	5:X:164:VAL:HG11	1.83	0.78
3:V:79:TRP:CH2	3:V:88:PRO:HB3	2.19	0.78
1:T:11:ASP:O	1:T:18:LYS:HE2	1.83	0.78
1:A:260:ASN:ND2	1:A:263:SER:OG	2.17	0.78
4:D:41:VAL:HG11	4:D:59:ILE:CD1	2.10	0.77
1:A:165:GLY:H	1:A:180:VAL:CG2	1.97	0.77
3:V:153:ASN:HD21	3:V:156:LEU:N	1.79	0.77
1:T:21:TYR:CE2	4:W:35:PHE:HB2	2.20	0.77
3:V:102:VAL:O	3:V:103:ARG:CG	2.33	0.77
3:V:70:CYS:SG	3:V:113:VAL:HG11	2.24	0.77
3:V:343:SER:CA	3:V:359:VAL:HB	2.13	0.77
3:V:344:GLN:N	3:V:359:VAL:HG23	2.00	0.77
5:X:24:ILE:HG12	5:X:135:GLN:NE2	1.98	0.77
4:D:199:LEU:CB	4:D:224:THR:OG1	2.32	0.77
2:U:321:LEU:CD1	2:U:340:PHE:CD1	2.68	0.77
2:U:321:LEU:HD13	2:U:340:PHE:HB2	1.66	0.77
5:E:26:SER:OG	5:E:139:GLU:CD	2.23	0.77
1:T:363:ILE:H	1:T:363:ILE:CD1	1.97	0.77
1:A:211:ARG:NH1	5:E:159:TRP:CZ3	2.53	0.77
3:V:135:LYS:HB3	3:V:191:PHE:CZ	2.18	0.77
3:C:120:ILE:HB	3:C:137:ILE:HD11	0.80	0.77
4:D:165:PHE:CE1	4:D:247:PHE:HD2	1.97	0.77
3:V:107:ASN:OD1	3:V:154:SER:HB2	1.84	0.77
2:B:336:LYS:HD3	7:G:21:GLU:HG2	1.65	0.77
4:D:194:THR:O	4:D:231:HIS:NE2	2.17	0.77
7:Z:99:ASP:O	7:Z:103:VAL:HG23	1.83	0.77
3:C:261:ALA:HB2	3:C:267:PRO:HA	1.67	0.77
4:D:34:THR:HG23	4:D:44:HIS:CD2	2.18	0.77
4:D:106:LYS:HZ3	4:D:106:LYS:H	1.32	0.77
4:W:116:LEU:HD23	4:W:117:LYS:H	1.49	0.77
1:A:114:GLU:HB2	1:A:118:ASN:ND2	1.99	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:68:GLN:HG3	4:W:73:ASP:OD2	1.85	0.77
4:D:165:PHE:CD2	4:D:223:ILE:HG22	2.06	0.77
4:D:198:VAL:HG13	4:D:224:THR:O	1.85	0.77
3:C:120:ILE:CD1	3:C:137:ILE:HD12	2.13	0.77
1:T:238:LEU:O	1:T:242:PHE:CD2	2.36	0.77
4:W:30:ALA:HB2	4:W:52:LYS:HG2	1.65	0.77
2:B:241:VAL:CG1	2:B:253:LYS:CD	2.58	0.77
4:W:36:ALA:HB2	4:W:42:LEU:HA	1.65	0.77
2:U:322:LYS:HG2	7:Z:16:VAL:HG11	1.67	0.77
5:E:162:CYS:O	5:E:164:VAL:N	2.18	0.77
3:V:14:HIS:ND1	3:V:348:THR:OG1	2.17	0.77
5:X:23:PRO:HB2	5:X:35:GLU:HG2	1.66	0.77
5:E:91:GLY:HA2	5:E:94:GLU:OE1	1.85	0.77
3:V:99:ALA:CA	3:V:115:SER:HB3	1.98	0.77
3:C:72:THR:HG21	6:F:26:SER:OG	1.84	0.77
3:C:77:TYR:HD2	3:C:89:THR:O	1.46	0.76
4:W:155:GLU:HB2	4:W:162:THR:OG1	1.86	0.76
1:A:82:ILE:CA	1:A:115:PRO:HG2	2.13	0.76
5:X:108:GLU:O	5:X:110:GLY:N	2.18	0.76
4:W:153:TYR:HB2	4:W:164:VAL:HB	1.66	0.76
1:T:118:ASN:OD1	1:T:123:ARG:HG3	1.85	0.76
1:T:104:GLU:OE2	4:W:248:ARG:NH1	2.17	0.76
6:Y:61:VAL:HG22	6:Y:74:ILE:HG21	0.77	0.76
7:G:105:LEU:H	7:G:105:LEU:HD12	1.50	0.76
3:C:327:ASN:HB2	3:C:351:ASP:OD1	1.85	0.76
2:U:313:LEU:H	2:U:314:PRO:CD	1.97	0.76
4:D:158:LYS:HG3	4:D:159:ASP:OD2	1.85	0.76
4:D:182:MET:HG3	4:D:200:PHE:CE1	2.21	0.76
3:V:99:ALA:CB	3:V:115:SER:HB3	2.15	0.76
6:F:24:ASN:OD1	6:F:120:ASN:ND2	2.19	0.76
5:E:26:SER:HA	5:E:139:GLU:OE1	1.85	0.76
4:W:130:GLN:HG3	4:W:134:GLU:CD	2.05	0.76
3:C:223:ASP:HB3	7:G:146:THR:HB	1.65	0.76
4:W:48:PRO:HG3	4:W:54:LYS:HD2	1.68	0.76
4:D:186:LYS:HD3	4:D:198:VAL:C	2.06	0.76
5:X:19:MET:HE3	5:X:67:THR:N	2.00	0.76
5:E:16:ILE:HG22	5:E:20:ALA:O	1.85	0.76
3:V:79:TRP:CA	3:V:87:LYS:O	2.30	0.76
3:V:79:TRP:CZ3	3:V:88:PRO:HD3	2.21	0.76
6:F:61:VAL:CG1	6:F:74:ILE:HG12	2.14	0.76
2:U:315:SER:HB2	6:Y:31:GLU:HB3	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:234:ALA:HB2	2:B:259:PHE:HZ	1.49	0.76
1:T:211:ARG:CD	1:T:212:GLU:H	1.98	0.76
4:D:116:LEU:HD23	4:D:117:LYS:H	1.51	0.76
1:T:304:ILE:HG21	1:T:316:TYR:CZ	2.21	0.76
4:W:75:LEU:CD1	4:W:78:ARG:HD3	2.16	0.76
1:T:281:ILE:HD12	1:T:282:PHE:N	2.01	0.76
5:X:19:MET:HE1	5:X:67:THR:CB	2.15	0.75
1:T:163:LEU:O	1:T:180:VAL:CG1	2.31	0.75
1:T:186:ILE:HG21	1:T:189:CYS:HB2	1.68	0.75
1:T:102:ARG:NH1	4:W:5:GLU:HB2	2.01	0.75
4:D:203:ARG:O	4:D:204:GLU:HG2	1.86	0.75
1:A:69:LYS:HD2	1:A:72:TYR:CD1	2.22	0.75
3:C:77:TYR:HD2	3:C:90:LEU:HA	1.16	0.75
3:V:10:PRO:HB3	3:V:350:MET:CA	2.17	0.75
4:W:207:LEU:O	4:W:209:LEU:N	2.19	0.75
7:G:124:VAL:HG22	7:G:126:LEU:H	1.50	0.75
5:X:16:ILE:CG1	5:X:125:GLU:HG2	2.15	0.75
3:C:144:THR:HB	3:C:162:CYS:SG	2.26	0.75
4:W:207:LEU:C	4:W:209:LEU:H	1.89	0.75
4:W:80:TYR:CZ	4:W:112:GLN:O	2.40	0.75
4:W:132:GLN:NE2	4:W:159:ASP:C	2.40	0.75
2:B:273:VAL:HG12	2:B:275:GLY:H	1.51	0.75
5:X:26:SER:HA	5:X:139:GLU:OE1	1.85	0.75
4:D:8:ASN:OD1	4:D:43:TYR:CZ	2.39	0.75
2:U:237:THR:HG22	6:Y:105:ARG:CD	2.16	0.75
4:D:75:LEU:HD11	4:D:78:ARG:CZ	2.16	0.75
3:V:153:ASN:ND2	3:V:156:LEU:H	1.81	0.75
3:V:173:ILE:HD12	3:V:173:ILE:N	2.02	0.75
3:V:173:ILE:HB	3:V:176:VAL:HG22	1.68	0.75
1:A:319:ILE:HB	1:A:367:VAL:HA	1.68	0.75
2:U:277:GLY:O	2:U:281:LEU:HB2	1.85	0.75
3:V:183:THR:CG2	3:V:184:PRO:HD2	2.16	0.75
6:F:18:ALA:O	7:G:145:LEU:HD12	1.86	0.75
3:C:123:CYS:CA	3:C:134:CYS:HA	2.08	0.75
3:C:173:ILE:HB	3:C:176:VAL:HG22	1.67	0.75
1:A:112:LEU:HD13	1:A:113:THR:O	1.85	0.75
7:G:63:PRO:HD2	7:G:109:TYR:HH	1.50	0.75
4:D:109:ILE:HG13	4:D:110:VAL:N	2.02	0.75
2:B:220:LEU:HD12	2:B:220:LEU:N	2.01	0.75
2:B:372:TRP:O	2:B:374:THR:N	2.19	0.75
1:T:193:ILE:HG23	1:T:194:PRO:HD2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:172:TYR:CE2	3:V:180:PRO:HD3	2.22	0.75
3:V:343:SER:HA	3:V:359:VAL:CB	2.16	0.75
6:Y:9:LEU:HD12	6:Y:140:GLU:OE2	1.85	0.75
3:V:252:PHE:CZ	3:V:258:LEU:HD21	2.21	0.75
3:V:140:PRO:HD2	3:V:169:PHE:HZ	1.51	0.75
5:X:26:SER:HB2	5:X:139:GLU:CG	2.15	0.75
3:V:254:THR:HG22	3:V:255:GLU:N	2.02	0.75
3:V:215:SER:HG	3:V:216:ARG:NH1	1.80	0.75
2:U:237:THR:CG2	6:Y:105:ARG:HE	1.98	0.75
6:F:102:PHE:HD1	6:F:122:HIS:CD2	2.05	0.75
2:B:220:LEU:HD12	2:B:220:LEU:H	1.52	0.75
4:W:203:ARG:O	4:W:204:GLU:HG2	1.86	0.75
3:V:135:LYS:CG	3:V:191:PHE:CE2	2.69	0.74
3:C:10:PRO:HB3	3:C:350:MET:CA	2.16	0.74
7:G:38:ASP:O	7:G:40:GLY:N	2.20	0.74
5:X:22:LEU:HD12	5:X:23:PRO:HD2	1.68	0.74
3:C:271:THR:HG21	3:C:370:LYS:HB2	1.69	0.74
1:T:164:THR:HA	1:T:180:VAL:CB	2.17	0.74
6:Y:56:ASN:OD1	6:Y:57:GLU:N	2.20	0.74
1:T:9:VAL:HG13	1:T:111:LEU:HD22	1.67	0.74
4:D:244:ILE:HG23	4:D:245:HIS:N	2.02	0.74
1:A:134:PHE:CE1	4:D:256:LYS:HB3	2.21	0.74
7:Z:41:GLU:HG3	7:Z:42:VAL:HG23	1.69	0.74
4:D:226:VAL:HG12	4:D:227:LEU:H	1.52	0.74
6:Y:9:LEU:HD13	6:Y:140:GLU:CD	2.07	0.74
3:C:233:LYS:O	3:C:233:LYS:HD3	1.87	0.74
1:T:38:LYS:NZ	1:T:59:ASP:OD2	2.20	0.74
3:C:72:THR:CG2	6:F:26:SER:OG	2.35	0.74
5:X:26:SER:CB	5:X:139:GLU:CG	2.65	0.74
5:E:162:CYS:C	5:E:164:VAL:H	1.90	0.74
3:V:14:HIS:CE1	3:V:348:THR:CG2	2.71	0.74
4:W:202:HIS:NE2	4:W:203:ARG:HG3	2.02	0.74
1:T:319:ILE:HB	1:T:366:GLN:O	1.88	0.74
7:G:99:ASP:O	7:G:103:VAL:HG23	1.87	0.74
2:B:241:VAL:CG1	2:B:253:LYS:CG	2.65	0.74
3:C:97:ARG:HG3	3:C:117:SER:OG	1.88	0.74
2:B:233:LEU:HG	2:B:233:LEU:O	1.85	0.74
6:Y:76:VAL:HB	6:Y:78:GLN:NE2	2.03	0.74
3:V:343:SER:C	3:V:359:VAL:HG23	2.07	0.74
1:T:200:ILE:HG12	1:T:281:ILE:CD1	2.18	0.74
3:V:332:ILE:CG1	3:V:347:THR:HG22	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:284:HIS:HB3	1:T:287:PHE:HB2	1.67	0.74
1:T:304:ILE:HA	1:T:315:LEU:HD23	1.69	0.74
3:C:73:ASP:OD2	6:F:32:ARG:HD3	1.87	0.74
5:E:20:ALA:O	5:E:21:LEU:HB2	1.86	0.74
7:Z:38:ASP:O	7:Z:40:GLY:N	2.20	0.74
1:T:167:VAL:HG13	1:T:320:VAL:HB	1.70	0.74
1:A:102:ARG:HG3	4:D:38:PHE:CZ	2.22	0.74
6:Y:101:PHE:HD2	6:Y:103:ILE:HD11	1.53	0.74
4:W:75:LEU:HD11	4:W:78:ARG:CZ	2.18	0.74
3:C:173:ILE:CG2	3:C:176:VAL:HG22	2.17	0.74
3:V:137:ILE:HD12	3:V:169:PHE:CD2	2.21	0.74
1:T:202:TYR:O	1:T:206:GLN:HB2	1.88	0.74
6:F:149:MET:O	6:F:153:VAL:HG22	1.87	0.74
6:Y:61:VAL:HG13	6:Y:74:ILE:CD1	2.18	0.74
3:C:30:HIS:ND1	3:C:53:GLY:O	2.20	0.74
3:C:269:LEU:N	3:C:283:GLY:HA3	2.03	0.74
3:V:41:LYS:HD3	3:V:41:LYS:N	2.02	0.74
3:V:148:LEU:HD23	3:V:159:ALA:HB2	1.70	0.73
4:W:150:GLU:CG	4:W:167:THR:HA	2.16	0.73
2:B:331:LYS:O	2:B:331:LYS:HD3	1.88	0.73
1:A:35:ILE:HD11	1:A:60:PHE:CD2	2.22	0.73
2:U:241:VAL:CG1	2:U:253:LYS:HG2	2.18	0.73
3:V:6:PHE:CE2	3:V:354:MET:HG3	2.23	0.73
2:B:246:LEU:HB3	2:B:247:PRO:CD	2.17	0.73
4:D:280:ALA:HB3	6:F:126:MET:SD	2.28	0.73
1:A:241:GLU:O	1:A:243:ASN:N	2.21	0.73
1:T:175:THR:OG1	1:T:193:ILE:HB	1.88	0.73
6:Y:102:PHE:HD1	6:Y:122:HIS:CD2	2.06	0.73
4:D:202:HIS:NE2	4:D:203:ARG:HG3	2.04	0.73
6:Y:68:ASN:HB2	6:Y:120:ASN:OD1	1.89	0.73
3:C:250:VAL:CA	3:C:260:ALA:HB2	2.11	0.73
1:A:187:GLY:O	1:A:188:SER:OG	2.07	0.73
4:W:244:ILE:HG23	4:W:245:HIS:N	2.02	0.73
2:U:233:LEU:O	2:U:233:LEU:HG	1.88	0.73
5:E:26:SER:CB	5:E:139:GLU:CD	2.55	0.73
5:E:26:SER:OG	5:E:139:GLU:OE2	2.06	0.73
7:Z:83:LEU:O	7:Z:86:PHE:HB2	1.88	0.73
3:V:173:ILE:HB	3:V:177:GLU:HG2	1.71	0.73
6:F:22:LEU:HD13	6:F:67:ILE:O	1.89	0.73
4:D:124:VAL:HG13	4:D:125:PHE:HD1	1.51	0.73
6:F:67:ILE:HG23	6:F:68:ASN:H	1.51	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ALA:C	4:D:38:PHE:CE1	2.61	0.73
3:C:14:HIS:ND1	3:C:348:THR:OG1	2.19	0.73
6:Y:128:LYS:O	6:Y:132:VAL:HG23	1.89	0.73
3:V:202:CYS:SG	7:Z:147:ALA:HA	2.28	0.73
3:V:224:SER:N	3:V:246:PRO:HG3	2.04	0.73
3:V:115:SER:O	3:V:145:VAL:HB	1.88	0.73
6:Y:67:ILE:CG2	6:Y:68:ASN:N	2.48	0.73
3:V:259:VAL:HG12	3:V:260:ALA:N	2.02	0.73
3:V:146:LEU:CD1	3:V:206:HIS:HA	2.19	0.73
5:X:19:MET:CE	5:X:67:THR:CB	2.66	0.73
4:W:154:VAL:O	4:W:155:GLU:HG3	1.89	0.73
1:T:316:TYR:O	1:T:365:VAL:HA	1.89	0.73
6:F:62:LEU:HD21	6:F:71:ARG:HH21	1.53	0.73
4:D:68:GLN:HG3	4:D:73:ASP:OD2	1.87	0.73
7:G:91:ILE:HG23	7:G:128:TRP:CE3	2.24	0.73
4:W:132:GLN:HE21	4:W:159:ASP:CB	2.02	0.73
6:F:48:LEU:HD13	7:G:145:LEU:HB3	1.70	0.72
6:Y:23:GLU:HA	6:Y:120:ASN:HB2	1.71	0.72
1:A:180:VAL:HG12	1:A:181:ALA:N	2.04	0.72
3:C:334:VAL:HB	3:C:338:GLY:HA2	1.71	0.72
1:T:273:TYR:H	1:T:273:TYR:HD1	1.36	0.72
3:V:21:THR:O	3:V:42:TRP:CZ3	2.41	0.72
6:F:56:ASN:OD1	6:F:57:GLU:N	2.22	0.72
1:A:363:ILE:N	1:A:363:ILE:HD13	2.03	0.72
3:C:158:ALA:O	3:C:159:ALA:HB2	1.89	0.72
1:T:271:VAL:HG13	1:T:274:GLU:OE2	1.89	0.72
2:U:169:VAL:HG12	2:U:170:TYR:N	2.03	0.72
7:Z:91:ILE:HG23	7:Z:128:TRP:CE3	2.23	0.72
3:V:102:VAL:CA	3:V:112:ALA:O	2.37	0.72
4:D:45:ILE:HD12	4:D:45:ILE:N	2.03	0.72
3:C:153:ASN:O	3:C:154:SER:OG	2.08	0.72
5:E:145:CYS:O	5:E:149:PHE:HD1	1.73	0.72
4:D:265:ARG:HB3	6:F:145:GLU:OE2	1.89	0.72
1:T:233:TYR:HH	1:T:245:TYR:HH	1.06	0.72
7:Z:30:GLY:HA2	7:Z:65:ASN:O	1.90	0.72
4:D:45:ILE:CG2	4:D:57:VAL:HG22	2.18	0.72
3:V:48:LEU:HD11	3:V:86:TRP:CB	2.19	0.72
1:T:313:ARG:HB3	1:T:314:PRO:CD	2.17	0.72
3:V:211:SER:HB3	3:V:252:PHE:CE2	2.23	0.72
1:T:206:GLN:HA	1:T:209:ARG:HD2	1.70	0.72
6:Y:35:LYS:HB3	6:Y:36:PRO:HD2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:249:ALA:HB1	3:C:332:ILE:CG2	2.19	0.72
3:V:119:VAL:HG23	3:V:138:LYS:HA	1.71	0.72
1:T:112:LEU:HD13	1:T:113:THR:O	1.89	0.72
1:T:5:LEU:HD21	4:W:42:LEU:HD11	1.71	0.72
4:D:75:LEU:O	4:D:77:LYS:N	2.22	0.72
1:A:152:SER:HA	1:A:370:HIS:HB3	1.71	0.72
4:W:179:LYS:HB3	4:W:179:LYS:NZ	2.04	0.72
3:C:146:LEU:HD12	3:C:206:HIS:HA	1.70	0.72
3:V:10:PRO:CB	3:V:350:MET:HA	2.19	0.72
3:C:107:ASN:HD22	3:C:109:LYS:H	1.37	0.72
5:E:157:SER:O	5:E:159:TRP:N	2.21	0.72
6:F:101:PHE:HD2	6:F:103:ILE:HD11	1.54	0.72
1:A:134:PHE:HE1	4:D:256:LYS:HB3	1.54	0.72
3:V:4:HIS:O	3:V:354:MET:HB3	1.90	0.72
4:D:63:PHE:CD2	4:D:67:LEU:CD1	2.72	0.72
3:V:20:ARG:CD	3:V:335:LEU:HD22	2.20	0.72
4:D:8:ASN:CG	4:D:43:TYR:OH	2.28	0.72
3:C:250:VAL:HA	3:C:260:ALA:CB	2.13	0.72
4:W:106:LYS:H	4:W:106:LYS:HZ3	1.35	0.72
4:D:132:GLN:CG	4:D:160:ARG:H	2.02	0.72
1:A:370:HIS:CG	1:A:371:HIS:H	2.06	0.72
3:V:217:VAL:CG1	3:V:229:ALA:HB3	2.20	0.72
1:A:287:PHE:HZ	5:E:51:ALA:HB1	1.53	0.72
4:W:227:LEU:HD23	4:W:231:HIS:CB	2.19	0.72
1:T:114:GLU:CG	1:T:141:ILE:HG22	2.15	0.72
3:C:16:TRP:CE2	3:C:23:ILE:HD12	2.25	0.72
3:V:286:ASP:OD1	3:V:287:VAL:N	2.22	0.72
4:D:132:GLN:HE21	4:D:159:ASP:CA	2.03	0.72
1:T:174:VAL:HG22	1:T:175:THR:N	2.05	0.71
1:A:367:VAL:HG12	1:A:368:ILE:N	2.05	0.71
5:X:79:LEU:HD22	5:X:164:VAL:CB	2.18	0.71
1:T:111:LEU:HD23	1:T:111:LEU:O	1.89	0.71
3:C:73:ASP:O	3:C:74:ARG:HD3	1.90	0.71
6:F:20:LEU:HG	6:F:21:CYS:N	2.00	0.71
1:T:164:THR:HA	1:T:180:VAL:HB	1.70	0.71
4:D:162:THR:CA	4:D:225:PHE:O	2.38	0.71
5:X:71:ILE:HG12	5:X:136:LEU:HD22	1.71	0.71
4:W:45:ILE:HG13	4:W:57:VAL:CG1	2.20	0.71
1:A:102:ARG:CG	4:D:38:PHE:CD2	2.72	0.71
3:C:123:CYS:CB	3:C:134:CYS:HB2	2.20	0.71
3:V:152:PRO:HG2	3:V:212:ALA:HA	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:228:LEU:HD13	3:V:279:LEU:CD2	2.20	0.71
5:E:95:MET:HB3	5:E:138:GLN:HE22	1.53	0.71
3:V:8:VAL:HG13	3:V:9:GLU:N	2.05	0.71
4:W:2:ILE:HG21	6:Y:163:GLU:HG2	1.73	0.71
3:C:360:ARG:C	3:C:362:LEU:H	1.93	0.71
6:F:35:LYS:HB3	6:F:36:PRO:HD2	1.71	0.71
3:C:77:TYR:HD2	3:C:89:THR:C	1.92	0.71
1:T:304:ILE:HG23	1:T:315:LEU:HB3	1.73	0.71
4:D:75:LEU:CD1	4:D:78:ARG:HD3	2.21	0.71
3:V:335:LEU:HB2	3:V:344:GLN:O	1.89	0.71
1:A:363:ILE:CD1	1:A:363:ILE:H	2.04	0.71
5:E:83:GLN:HG3	5:E:161:THR:OG1	1.91	0.71
5:E:60:ILE:HD12	5:E:60:ILE:H	1.54	0.71
3:V:172:TYR:HA	3:V:177:GLU:OE1	1.90	0.71
3:C:159:ALA:HA	3:C:208:VAL:HG21	1.72	0.71
2:U:314:PRO:HB2	6:Y:31:GLU:OE2	1.90	0.71
3:C:114:GLY:CA	3:C:148:LEU:HD11	2.20	0.71
1:T:272:GLY:O	1:T:275:ARG:HB2	1.90	0.71
5:X:77:GLU:HG3	5:X:103:PHE:HZ	1.55	0.71
2:U:206:HIS:O	2:U:208:ALA:N	2.24	0.71
3:V:106:PRO:HG2	3:V:154:SER:H	1.56	0.71
6:Y:61:VAL:HG22	6:Y:74:ILE:CG1	2.21	0.71
5:X:106:PRO:O	5:X:119:LYS:HB3	1.91	0.71
3:V:77:TYR:HD2	3:V:89:THR:C	1.93	0.71
4:D:132:GLN:CG	4:D:160:ARG:N	2.54	0.71
4:W:202:HIS:CD2	4:W:203:ARG:HG3	2.25	0.71
1:T:285:PRO:HB2	1:T:292:PHE:CD2	2.24	0.70
4:D:165:PHE:CD2	4:D:223:ILE:HG21	2.22	0.70
4:D:163:VAL:H	4:D:225:PHE:HB3	1.56	0.70
3:V:115:SER:O	3:V:145:VAL:N	2.23	0.70
6:Y:37:GLU:O	6:Y:41:ARG:N	2.24	0.70
1:A:102:ARG:NH1	4:D:5:GLU:HB2	2.05	0.70
4:W:186:LYS:CB	4:W:198:VAL:O	2.37	0.70
4:W:212:THR:HG22	4:W:213:ASP:H	1.54	0.70
1:T:35:ILE:HD11	1:T:60:PHE:HD2	1.55	0.70
3:C:32:VAL:HG12	3:C:33:HIS:N	2.06	0.70
5:E:53:VAL:HG23	5:E:167:GLN:C	2.12	0.70
3:V:165:LYS:HE3	3:V:201:SER:HB2	1.71	0.70
3:C:261:ALA:CB	3:C:266:PHE:O	2.39	0.70
3:V:76:ALA:O	3:V:91:VAL:HB	1.91	0.70
4:W:75:LEU:HD11	4:W:78:ARG:NH1	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:36:ALA:CA	4:W:42:LEU:HA	2.21	0.70
4:W:35:PHE:HE1	4:W:45:ILE:CD1	2.04	0.70
2:U:177:HIS:O	2:U:178:LEU:HG	1.90	0.70
3:V:343:SER:O	3:V:344:GLN:HG3	1.91	0.70
6:Y:61:VAL:HG22	6:Y:74:ILE:HG23	1.35	0.70
3:C:160:GLY:HA3	3:C:205:VAL:HG11	1.71	0.70
4:W:118:ARG:NH1	4:W:119:ASN:OD1	2.25	0.70
3:V:254:THR:HG23	3:V:341:LYS:CD	2.19	0.70
3:V:32:VAL:HG12	3:V:33:HIS:N	2.05	0.70
2:U:313:LEU:H	2:U:314:PRO:HD3	1.55	0.70
4:D:158:LYS:HD2	4:D:159:ASP:OD1	1.90	0.70
2:U:246:LEU:HB3	2:U:247:PRO:CD	2.20	0.70
2:B:206:HIS:O	2:B:208:ALA:N	2.24	0.70
1:T:174:VAL:HG23	1:T:193:ILE:O	1.88	0.70
4:D:45:ILE:HG23	4:D:57:VAL:HG22	1.74	0.70
1:A:290:PRO:O	1:A:292:PHE:N	2.25	0.70
7:Z:63:PRO:CD	7:Z:109:TYR:HH	1.81	0.70
4:D:241:ILE:HD12	4:D:241:ILE:N	2.06	0.70
3:V:172:TYR:HE2	3:V:178:GLU:C	1.94	0.70
6:F:17:GLN:HA	6:F:20:LEU:HD22	1.72	0.70
4:W:237:ARG:O	4:W:241:ILE:HD13	1.91	0.70
7:G:104:ASP:OD2	7:G:143:ARG:HD2	1.92	0.70
1:A:304:ILE:HG21	1:A:316:TYR:CZ	2.26	0.70
4:D:165:PHE:CE2	4:D:247:PHE:CE2	2.70	0.70
3:V:102:VAL:O	3:V:103:ARG:CB	2.39	0.70
7:G:104:ASP:OD1	7:G:140:SER:OG	2.07	0.70
4:D:165:PHE:CB	4:D:223:ILE:H	2.04	0.70
3:V:101:CYS:O	3:V:114:GLY:N	2.19	0.70
6:Y:18:ALA:HA	7:Z:142:VAL:HG22	1.74	0.70
3:C:120:ILE:CD1	3:C:137:ILE:CD1	2.69	0.70
3:C:77:TYR:HE2	3:C:90:LEU:CD2	1.98	0.70
4:W:75:LEU:HD11	4:W:78:ARG:HD3	1.74	0.70
2:U:220:LEU:HD12	2:U:220:LEU:N	2.06	0.70
3:C:329:VAL:HG12	3:C:330:SER:N	2.06	0.70
6:Y:80:ASP:OD1	6:Y:82:ILE:HG22	1.91	0.70
3:V:68:VAL:HG12	3:V:104:TRP:NE1	2.06	0.69
3:C:14:HIS:HE1	3:C:348:THR:OG1	1.72	0.69
4:W:227:LEU:CD2	4:W:231:HIS:HB2	2.19	0.69
3:C:173:ILE:O	3:C:177:GLU:HG2	1.91	0.69
3:C:97:ARG:HG3	3:C:117:SER:HB2	1.72	0.69
4:D:75:LEU:HD11	4:D:78:ARG:NH1	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:27:LYS:HD3	4:W:28:PRO:CD	2.20	0.69
1:T:37:ILE:CG2	1:T:59:ASP:O	2.39	0.69
1:T:246:ASP:OD1	1:T:273:TYR:OH	2.09	0.69
3:C:223:ASP:HB3	7:G:146:THR:CB	2.22	0.69
4:D:2:ILE:HG21	6:F:163:GLU:HG2	1.72	0.69
4:D:165:PHE:HE2	4:D:225:PHE:CE1	2.09	0.69
1:T:215:ILE:HD11	1:T:269:ILE:HD13	1.73	0.69
4:W:186:LYS:HD3	4:W:198:VAL:H	1.56	0.69
4:W:163:VAL:HB	4:W:225:PHE:CB	2.22	0.69
3:C:17:ASN:HD21	3:C:22:GLN:H	1.40	0.69
3:V:253:ILE:CB	3:V:342:CYS:SG	2.78	0.69
7:G:124:VAL:HG13	7:G:125:LEU:N	2.04	0.69
4:D:75:LEU:HD11	4:D:78:ARG:HD3	1.75	0.69
4:D:109:ILE:HG13	4:D:110:VAL:H	1.54	0.69
1:A:367:VAL:HG12	1:A:368:ILE:H	1.58	0.69
1:A:165:GLY:O	1:A:180:VAL:CG2	2.30	0.69
6:Y:9:LEU:HD13	6:Y:140:GLU:CG	2.10	0.69
1:A:241:GLU:HB3	1:A:245:TYR:CD1	2.27	0.69
2:B:321:LEU:HD13	2:B:340:PHE:CD1	2.28	0.69
4:W:226:VAL:HG12	4:W:227:LEU:N	2.04	0.69
4:W:132:GLN:HG3	4:W:160:ARG:H	1.47	0.69
4:W:10:ILE:O	4:W:11:ILE:HG13	1.93	0.69
7:Z:26:ASP:OD2	7:Z:148:ARG:NE	2.21	0.69
1:T:233:TYR:OH	1:T:245:TYR:OH	1.88	0.69
1:T:260:ASN:ND2	1:T:263:SER:OG	2.25	0.69
6:F:36:PRO:HG2	6:F:39:GLU:HB2	1.73	0.69
6:F:61:VAL:HG22	6:F:74:ILE:HG12	1.75	0.69
1:T:122:ASN:HA	1:T:125:TYR:HD2	1.58	0.69
3:V:173:ILE:HD12	3:V:173:ILE:H	1.57	0.69
3:C:173:ILE:CB	3:C:176:VAL:HG22	2.23	0.69
7:G:41:GLU:HG3	7:G:42:VAL:N	2.07	0.69
2:U:237:THR:HA	6:Y:105:ARG:HG2	1.74	0.69
1:A:207:LEU:CD1	5:E:54:PHE:HZ	2.06	0.69
3:V:153:ASN:O	3:V:154:SER:OG	2.09	0.69
1:A:164:THR:HA	1:A:180:VAL:HG11	1.73	0.69
4:W:75:LEU:O	4:W:77:LYS:N	2.25	0.69
7:Z:133:LEU:HG	7:Z:134:ALA:N	2.01	0.69
1:T:37:ILE:HA	1:T:72:TYR:CD2	2.27	0.69
1:A:151:ALA:HB2	1:A:379:PHE:CE2	2.28	0.69
5:E:94:GLU:HB3	5:E:98:LEU:CD1	2.22	0.69
6:Y:76:VAL:HG12	6:Y:77:LYS:N	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:87:SER:HB2	5:E:153:ASN:OD1	1.92	0.69
3:C:164:PHE:HA	3:C:204:TRP:HA	1.75	0.69
3:C:10:PRO:CB	3:C:350:MET:HB3	2.18	0.69
3:V:116:GLY:HA2	3:V:144:THR:HA	1.75	0.69
3:C:263:HIS:CD2	6:F:21:CYS:CB	2.70	0.69
3:C:120:ILE:CB	3:C:137:ILE:CD1	2.51	0.69
4:W:241:ILE:N	4:W:241:ILE:HD12	2.07	0.69
4:W:36:ALA:HA	4:W:42:LEU:HA	1.75	0.69
1:A:208:LEU:HD23	1:A:208:LEU:C	2.14	0.69
7:Z:124:VAL:HG13	7:Z:125:LEU:N	2.04	0.69
7:Z:42:VAL:HG13	7:Z:45:CYS:HB2	1.75	0.69
6:F:18:ALA:HB2	7:G:142:VAL:CG2	2.21	0.68
1:A:165:GLY:H	1:A:180:VAL:HG21	1.57	0.68
1:A:181:ALA:HB2	1:A:186:ILE:HD11	1.73	0.68
6:F:61:VAL:HG22	6:F:74:ILE:CG2	2.19	0.68
3:V:269:LEU:HB3	3:V:283:GLY:HA2	1.75	0.68
3:C:101:CYS:HB2	3:C:147:SER:HA	1.74	0.68
4:D:130:GLN:HG3	4:D:134:GLU:OE1	1.93	0.68
3:V:228:LEU:C	3:V:228:LEU:HD23	2.14	0.68
1:A:103:ALA:N	4:D:38:PHE:CE1	2.61	0.68
3:C:147:SER:C	3:C:148:LEU:HG	2.14	0.68
5:E:20:ALA:O	5:E:21:LEU:CB	2.40	0.68
7:Z:133:LEU:CG	7:Z:134:ALA:H	2.04	0.68
1:T:285:PRO:CB	1:T:292:PHE:CD2	2.77	0.68
3:V:173:ILE:HG21	3:V:176:VAL:CG2	2.23	0.68
3:C:347:THR:H	3:C:355:SER:HB3	1.56	0.68
1:T:181:ALA:CB	1:T:186:ILE:HD11	2.24	0.68
1:T:239:VAL:HG13	5:X:4:TYR:CD1	2.27	0.68
3:C:8:VAL:HG13	3:C:9:GLU:N	2.08	0.68
6:F:37:GLU:O	6:F:41:ARG:N	2.20	0.68
7:Z:56:GLN:O	7:Z:59:LEU:HG	1.94	0.68
1:A:305:GLN:HG3	1:A:346:ARG:NH2	2.09	0.68
3:C:329:VAL:HG12	3:C:330:SER:H	1.58	0.68
3:V:107:ASN:ND2	3:V:109:LYS:HG2	2.08	0.68
6:Y:51:VAL:O	6:Y:62:LEU:HD12	1.94	0.68
4:W:186:LYS:NZ	4:W:197:GLN:HB3	2.08	0.68
4:W:186:LYS:HZ3	4:W:199:LEU:HD12	1.58	0.68
5:E:19:MET:HE3	5:E:67:THR:N	2.08	0.68
3:C:107:ASN:OD1	3:C:154:SER:HB2	1.93	0.68
6:F:145:GLU:O	6:F:149:MET:HG2	1.94	0.68
5:E:13:THR:HG21	5:E:20:ALA:HB1	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:118:ASN:OD1	1:T:123:ARG:CG	2.42	0.68
1:T:207:LEU:CD1	5:X:54:PHE:HZ	2.06	0.68
6:F:122:HIS:O	6:F:126:MET:HB2	1.93	0.68
1:T:285:PRO:CG	1:T:292:PHE:CD2	2.75	0.68
3:V:172:TYR:HD2	3:V:180:PRO:HD3	1.56	0.68
5:X:16:ILE:H	5:X:20:ALA:HA	1.57	0.68
5:X:16:ILE:N	5:X:20:ALA:HA	2.08	0.68
3:C:332:ILE:CB	3:C:347:THR:HG22	2.23	0.68
3:V:30:HIS:CB	3:V:51:HIS:O	2.41	0.68
4:D:132:GLN:HG3	4:D:160:ARG:H	1.57	0.68
6:Y:80:ASP:OD1	6:Y:83:GLU:HG3	1.93	0.68
3:C:5:SER:HB3	3:C:352:GLY:HA3	1.76	0.68
3:V:183:THR:HG22	3:V:185:TRP:H	1.58	0.68
3:C:68:VAL:HB	3:C:104:TRP:CZ2	2.28	0.68
3:V:347:THR:H	3:V:355:SER:CB	2.05	0.68
3:V:115:SER:O	3:V:145:VAL:CB	2.42	0.68
1:T:135:ASN:OD1	1:T:397:LYS:HD2	1.93	0.68
3:V:32:VAL:HG12	3:V:33:HIS:H	1.58	0.68
3:V:271:THR:HG21	3:V:370:LYS:HB2	1.76	0.68
2:U:266:PHE:O	7:Z:12:ARG:NH2	2.26	0.68
2:B:236:GLU:O	6:F:105:ARG:HG2	1.93	0.67
6:Y:73:SER:HB2	6:Y:112:TYR:HD2	1.59	0.67
2:U:234:ALA:HB2	2:U:259:PHE:CZ	2.21	0.67
4:D:181:PHE:O	4:D:185:PHE:HD2	1.77	0.67
2:U:321:LEU:CB	2:U:340:PHE:CE1	2.57	0.67
3:V:72:THR:HG21	6:Y:26:SER:HG	1.59	0.67
4:D:80:TYR:HE1	4:D:113:ALA:HA	1.60	0.67
3:C:117:SER:C	3:C:118:ARG:HD2	2.14	0.67
5:E:5:HIS:CD2	5:E:61:LYS:HG3	2.30	0.67
5:E:73:LEU:HB3	5:E:173:LEU:HD22	1.76	0.67
1:T:321:LEU:HB3	1:T:326:THR:CB	2.25	0.67
3:C:115:SER:H	3:C:145:VAL:HB	1.58	0.67
3:C:160:GLY:HA3	3:C:205:VAL:CG1	2.25	0.67
5:X:155:LYS:O	5:X:157:SER:N	2.27	0.67
4:W:80:TYR:CE1	4:W:112:GLN:O	2.47	0.67
1:T:305:GLN:HG3	1:T:346:ARG:NH2	2.10	0.67
3:V:331:GLN:HG2	3:V:332:ILE:H	1.59	0.67
3:V:106:PRO:HG2	3:V:154:SER:N	2.10	0.67
1:A:165:GLY:CA	1:A:318:ASN:HB3	2.25	0.67
1:T:187:GLY:O	1:T:188:SER:OG	2.08	0.67
1:T:316:TYR:HB3	1:T:364:ASP:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:41:GLU:HG3	7:G:42:VAL:HG23	1.76	0.67
1:T:102:ARG:HH12	4:W:5:GLU:HB2	1.60	0.67
2:U:336:LYS:HG2	7:Z:21:GLU:CG	2.25	0.67
5:E:152:GLN:CB	5:E:155:LYS:HD2	2.24	0.67
4:D:106:LYS:NZ	4:D:106:LYS:H	1.93	0.67
1:T:289:ASN:HB3	1:T:291:ASP:OD2	1.95	0.67
5:X:31:PRO:HD2	5:X:135:GLN:OE1	1.95	0.67
1:T:186:ILE:HD13	2:U:205:ASN:HB3	1.77	0.67
1:T:140:TYR:HB3	1:T:390:PHE:HE1	1.60	0.67
5:E:71:ILE:HG12	5:E:136:LEU:HD22	1.75	0.67
7:G:81:LYS:O	7:G:84:ILE:N	2.20	0.67
3:V:228:LEU:O	3:V:228:LEU:HD23	1.94	0.67
3:C:202:CYS:SG	7:G:147:ALA:HA	2.34	0.67
5:X:91:GLY:HA2	5:X:94:GLU:OE1	1.93	0.67
1:T:174:VAL:HG22	1:T:175:THR:H	1.60	0.67
1:T:321:LEU:HD12	1:T:373:GLN:OE1	1.94	0.67
3:V:168:ILE:HD13	3:V:196:PHE:HB3	1.76	0.67
3:C:224:SER:N	3:C:246:PRO:HB3	2.10	0.67
4:D:8:ASN:HB3	4:D:11:ILE:HD13	1.77	0.67
1:T:163:LEU:C	1:T:180:VAL:HG11	2.15	0.67
4:W:75:LEU:HG	4:W:78:ARG:HD3	1.77	0.67
3:C:216:ARG:HB3	3:C:252:PHE:CE2	2.30	0.67
3:V:152:PRO:CG	3:V:212:ALA:HA	2.25	0.67
4:D:132:GLN:HG3	4:D:160:ARG:N	2.10	0.67
4:D:27:LYS:HD3	4:D:28:PRO:CD	2.25	0.67
4:D:179:LYS:NZ	4:D:179:LYS:HB3	2.10	0.67
4:D:165:PHE:HE2	4:D:225:PHE:CD1	2.12	0.66
3:V:205:VAL:HA	3:V:220:VAL:O	1.94	0.66
3:C:224:SER:H	3:C:246:PRO:HB3	1.60	0.66
4:D:41:VAL:HG13	4:D:59:ILE:CD1	2.19	0.66
5:X:22:LEU:CD1	5:X:23:PRO:HD2	2.24	0.66
4:W:98:ASP:HB3	4:W:101:ASN:HB3	1.76	0.66
3:V:146:LEU:HD13	3:V:206:HIS:HA	1.76	0.66
4:W:11:ILE:HD11	4:W:35:PHE:CZ	2.30	0.66
4:D:153:TYR:HB2	4:D:164:VAL:CB	2.24	0.66
1:A:128:GLU:HG2	1:A:129:ILE:N	2.10	0.66
5:E:23:PRO:HB3	5:E:32:ALA:CB	2.25	0.66
1:A:252:TRP:O	1:A:275:ARG:NH1	2.27	0.66
5:X:24:ILE:HG21	5:X:41:ILE:HG21	1.68	0.66
6:Y:38:VAL:HG12	6:Y:69:SER:CB	2.21	0.66
5:E:134:GLN:HA	5:E:137:ARG:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:304:ILE:CG2	1:T:316:TYR:CE2	2.79	0.66
4:W:280:ALA:O	6:Y:127:TYR:HD1	1.77	0.66
4:D:45:ILE:HG23	4:D:57:VAL:CG2	2.25	0.66
6:Y:95:MET:CG	6:Y:106:ARG:O	2.43	0.66
2:U:326:LEU:HD23	2:U:326:LEU:C	2.15	0.66
1:A:112:LEU:HD12	1:A:126:THR:HG21	1.78	0.66
1:A:305:GLN:HG3	1:A:346:ARG:HH22	1.60	0.66
1:A:120:PRO:CG	2:B:201:GLY:HA3	2.24	0.66
1:A:205:GLN:O	1:A:209:ARG:HG3	1.95	0.66
4:D:186:LYS:HD3	4:D:198:VAL:O	1.95	0.66
5:X:24:ILE:HG22	5:X:41:ILE:CG2	2.02	0.66
3:C:120:ILE:O	3:C:121:SER:OG	2.05	0.66
1:A:211:ARG:HD2	1:A:212:GLU:H	1.59	0.66
3:V:155:VAL:HG11	3:V:180:PRO:CG	2.26	0.66
7:G:105:LEU:HD12	7:G:105:LEU:N	2.10	0.66
6:Y:148:GLU:O	6:Y:152:SER:HB3	1.96	0.66
1:A:207:LEU:HD23	1:A:207:LEU:O	1.96	0.66
2:U:217:LYS:O	2:U:221:CYS:HB2	1.95	0.66
4:D:226:VAL:HG12	4:D:227:LEU:N	2.10	0.66
4:D:165:PHE:HE1	4:D:247:PHE:CD2	2.12	0.66
1:A:35:ILE:HG13	1:A:61:PHE:O	1.96	0.66
1:A:181:ALA:HB1	1:A:186:ILE:HD11	1.76	0.66
4:W:77:LYS:O	4:W:81:GLY:N	2.25	0.66
4:W:45:ILE:CG1	4:W:57:VAL:HG22	2.26	0.66
6:F:60:LYS:NZ	6:F:112:TYR:CE1	2.64	0.66
4:D:132:GLN:HG2	4:D:159:ASP:CA	2.24	0.66
3:V:14:HIS:ND1	3:V:348:THR:CG2	2.58	0.66
4:D:6:VAL:O	4:D:115:MET:HB3	1.95	0.66
3:C:271:THR:HG21	3:C:370:LYS:CB	2.25	0.66
3:C:239:THR:HA	3:C:279:LEU:HD12	1.78	0.66
5:E:113:LEU:HD21	5:E:171:LYS:HG3	1.77	0.66
7:Z:106:LEU:O	7:Z:110:ILE:HG12	1.94	0.66
6:F:36:PRO:HA	6:F:69:SER:HB3	1.78	0.66
3:V:18:LYS:HG3	3:V:62:PRO:CB	2.17	0.66
3:C:74:ARG:HG3	3:C:95:ILE:HD11	1.76	0.66
4:D:133:GLU:HG2	4:D:133:GLU:O	1.96	0.66
3:V:156:LEU:CD2	3:V:170:SER:HB2	2.26	0.66
5:X:26:SER:OG	5:X:139:GLU:CG	2.44	0.66
6:Y:21:CYS:C	6:Y:22:LEU:HG	2.14	0.66
2:U:321:LEU:CG	2:U:340:PHE:CD1	2.79	0.66
3:C:321:LEU:H	3:C:326:LYS:HZ2	1.41	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Z:59:LEU:HD22	7:Z:105:LEU:HD23	1.77	0.66
3:V:228:LEU:HD13	3:V:279:LEU:HD23	1.78	0.66
3:C:141:ILE:O	3:C:142:ARG:HG3	1.96	0.66
4:W:158:LYS:HG3	4:W:159:ASP:OD2	1.96	0.66
1:A:313:ARG:HB3	1:A:314:PRO:CD	2.23	0.66
6:Y:41:ARG:HH21	6:Y:71:ARG:HH12	1.45	0.65
3:V:233:LYS:HD3	3:V:233:LYS:O	1.95	0.65
2:U:326:LEU:O	2:U:331:LYS:HA	1.96	0.65
1:A:321:LEU:HB3	1:A:326:THR:HB	1.78	0.65
3:V:239:THR:O	3:V:240:LEU:HB2	1.95	0.65
2:U:321:LEU:HD22	2:U:340:PHE:CD1	2.31	0.65
4:W:186:LYS:HD3	4:W:198:VAL:CA	2.25	0.65
5:E:22:LEU:O	5:E:132:TYR:OH	2.08	0.65
3:C:97:ARG:CG	3:C:117:SER:CB	2.73	0.65
1:A:238:LEU:O	1:A:242:PHE:HD2	1.80	0.65
1:T:207:LEU:HD12	5:X:54:PHE:CZ	2.31	0.65
3:V:207:GLY:O	3:V:220:VAL:HG22	1.96	0.65
1:A:336:GLN:CG	1:A:367:VAL:N	2.58	0.65
1:T:208:LEU:HD23	1:T:208:LEU:C	2.17	0.65
1:T:203:PHE:CZ	5:X:54:PHE:CD2	2.80	0.65
1:A:82:ILE:HB	1:A:115:PRO:HB2	1.77	0.65
2:B:311:PRO:HB3	6:F:32:ARG:HD2	1.79	0.65
6:Y:76:VAL:HB	6:Y:78:GLN:HE22	1.62	0.65
1:A:284:HIS:O	1:A:287:PHE:HB2	1.96	0.65
4:D:186:LYS:HD3	4:D:198:VAL:H	1.61	0.65
3:C:245:LEU:HB3	3:C:246:PRO:CD	2.26	0.65
3:C:71:GLY:H	3:C:75:ASN:HB2	1.61	0.65
7:G:105:LEU:H	7:G:105:LEU:CD1	2.10	0.65
3:V:252:PHE:CE1	3:V:258:LEU:HD21	2.31	0.65
1:T:336:GLN:HG2	1:T:367:VAL:HG23	1.79	0.65
7:G:108:LYS:HE3	7:G:144:VAL:HA	1.78	0.65
3:C:166:CYS:SG	3:C:167:ARG:N	2.68	0.65
1:A:336:GLN:CD	1:A:367:VAL:N	2.45	0.65
1:T:271:VAL:HG12	1:T:275:ARG:HG3	1.77	0.65
2:U:321:LEU:HD22	2:U:340:PHE:CB	2.25	0.65
2:U:241:VAL:HG13	2:U:253:LYS:CG	2.22	0.65
6:Y:137:HIS:O	6:Y:141:GLU:HB2	1.97	0.65
5:X:134:GLN:HA	5:X:137:ARG:HG3	1.77	0.65
6:F:21:CYS:O	6:F:22:LEU:HG	1.96	0.65
1:A:100:TYR:O	4:D:10:ILE:CG1	2.44	0.65
3:C:215:SER:HG	3:C:216:ARG:NH1	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:GLU:O	1:A:114:GLU:HG3	1.94	0.65
3:C:267:PRO:HG3	3:C:357:TRP:CZ2	2.32	0.65
6:F:18:ALA:CB	7:G:142:VAL:CG2	2.62	0.65
6:F:33:HIS:HB3	6:F:35:LYS:HE2	1.78	0.65
6:F:22:LEU:HD22	6:F:67:ILE:CA	2.26	0.65
4:D:77:LYS:HG3	4:D:84:LEU:CB	2.26	0.65
7:G:83:LEU:HD22	7:G:128:TRP:CZ2	2.32	0.65
2:U:278:VAL:HG13	2:U:320:GLU:OE1	1.95	0.65
4:D:199:LEU:N	4:D:224:THR:OG1	2.29	0.65
5:X:20:ALA:O	5:X:21:LEU:HB2	1.96	0.65
3:C:13:CYS:O	3:C:14:HIS:HB3	1.96	0.65
1:T:34:CYS:SG	1:T:67:ILE:HG23	2.37	0.65
1:T:35:ILE:HD11	1:T:60:PHE:CD2	2.31	0.65
4:W:132:GLN:HG2	4:W:159:ASP:C	2.16	0.65
6:F:41:ARG:NH2	6:F:71:ARG:HH12	1.94	0.65
7:Z:122:SER:OG	7:Z:123:ALA:N	2.30	0.65
1:A:63:GLY:O	1:A:65:GLU:N	2.27	0.65
2:B:226:ASN:O	2:B:230:GLU:HG2	1.96	0.65
2:B:289:ALA:O	2:B:291:ILE:N	2.30	0.65
3:C:144:THR:O	3:C:161:SER:OG	2.11	0.65
5:E:19:MET:HG2	5:E:66:ARG:HB3	1.79	0.65
7:Z:11:PHE:O	7:Z:14:VAL:HG12	1.97	0.65
4:W:135:GLY:O	4:W:136:LYS:HB2	1.96	0.65
5:X:59:GLU:HG3	5:X:59:GLU:O	1.97	0.65
3:V:343:SER:C	3:V:359:VAL:CG2	2.65	0.65
5:X:24:ILE:CD1	5:X:26:SER:HB2	2.27	0.65
1:T:117:LEU:HD23	1:T:117:LEU:O	1.96	0.65
2:U:262:PRO:C	2:U:264:ALA:H	2.00	0.65
1:T:368:ILE:HG22	1:T:369:THR:N	2.11	0.65
4:D:162:THR:CG2	4:D:225:PHE:O	2.43	0.64
4:W:237:ARG:O	4:W:241:ILE:CD1	2.45	0.64
2:U:253:LYS:NZ	2:U:253:LYS:HB3	2.12	0.64
1:T:102:ARG:HH12	4:W:5:GLU:CB	2.09	0.64
1:A:371:HIS:O	1:A:373:GLN:N	2.26	0.64
4:D:110:VAL:HG13	4:D:111:HIS:N	2.12	0.64
4:W:185:PHE:HZ	6:Y:160:VAL:HG12	1.60	0.64
3:V:100:ARG:HG2	3:V:146:LEU:HA	1.79	0.64
3:V:172:TYR:CD2	3:V:180:PRO:CD	2.80	0.64
5:X:13:THR:HG22	5:X:20:ALA:CB	2.27	0.64
1:T:89:MET:CE	1:T:92:PHE:HD2	2.10	0.64
1:A:208:LEU:HG	1:A:211:ARG:NH2	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:LYS:O	1:A:232:SER:OG	2.15	0.64
3:V:343:SER:N	3:V:359:VAL:HG21	2.13	0.64
4:W:197:GLN:HB2	4:W:226:VAL:HG21	1.79	0.64
1:A:201:THR:HB	1:A:224:ALA:HB1	1.78	0.64
1:A:9:VAL:HG13	1:A:111:LEU:HD22	1.80	0.64
3:V:155:VAL:HG11	3:V:180:PRO:HG2	1.79	0.64
5:X:155:LYS:C	5:X:157:SER:N	2.46	0.64
4:W:186:LYS:HD3	4:W:198:VAL:N	2.11	0.64
1:T:89:MET:HE1	1:T:92:PHE:HD2	1.63	0.64
1:T:203:PHE:CE1	5:X:54:PHE:CZ	2.85	0.64
4:W:159:ASP:O	4:W:160:ARG:HB3	1.97	0.64
4:D:223:ILE:HG22	4:D:224:THR:N	2.12	0.64
6:F:21:CYS:C	6:F:22:LEU:HG	2.18	0.64
3:V:77:TYR:HD2	3:V:89:THR:O	1.37	0.64
1:T:35:ILE:CB	1:T:61:PHE:O	2.45	0.64
2:U:237:THR:CG2	6:Y:105:ARG:NE	2.55	0.64
3:C:129:ASN:O	3:C:130:ASP:HB2	1.97	0.64
3:V:242:SER:OG	3:V:244:THR:HG22	1.97	0.64
5:X:149:PHE:CD2	5:X:156:PRO:HA	2.33	0.64
4:W:243:LEU:H	4:W:243:LEU:HD23	1.62	0.64
4:W:75:LEU:CG	4:W:78:ARG:HD3	2.27	0.64
3:C:107:ASN:ND2	3:C:109:LYS:H	1.96	0.64
1:A:172:ASP:O	1:A:196:ALA:HB1	1.96	0.64
1:T:239:VAL:CG1	5:X:4:TYR:CD1	2.81	0.64
2:U:232:LYS:HG2	2:U:232:LYS:O	1.97	0.64
1:A:409:ARG:HD3	2:B:200:ARG:O	1.97	0.64
4:D:163:VAL:H	4:D:225:PHE:CB	2.10	0.64
6:Y:61:VAL:HG23	6:Y:74:ILE:HG23	1.66	0.64
4:W:141:ARG:HH11	4:W:209:LEU:HD13	1.62	0.64
3:C:21:THR:O	3:C:42:TRP:HZ3	1.73	0.64
6:F:102:PHE:CD1	6:F:122:HIS:CD2	2.86	0.64
6:Y:54:SER:OG	7:Z:117:PRO:CG	2.45	0.64
1:A:304:ILE:HG21	1:A:316:TYR:CE2	2.31	0.64
3:V:271:THR:HG21	3:V:370:LYS:CB	2.27	0.64
1:A:271:VAL:HG12	1:A:275:ARG:HD2	1.79	0.64
6:Y:61:VAL:HA	6:Y:74:ILE:HG23	1.80	0.64
1:A:36:ALA:HB3	1:A:72:TYR:HB3	1.80	0.64
1:A:365:VAL:O	1:A:366:GLN:HB2	1.96	0.64
4:W:231:HIS:HB3	4:W:240:THR:HG21	1.79	0.64
1:T:35:ILE:HD12	1:T:62:ILE:CG2	2.27	0.64
1:A:270:ASP:O	5:E:159:TRP:CZ2	2.50	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:313:LEU:HD12	2:U:316:ARG:HB3	1.80	0.64
4:W:194:THR:HB	4:W:230:ARG:NE	2.12	0.64
5:E:42:VAL:HG22	5:E:140:THR:HG22	1.80	0.64
5:E:59:GLU:O	5:E:59:GLU:HG3	1.98	0.64
3:V:360:ARG:C	3:V:362:LEU:H	2.01	0.64
1:T:363:ILE:N	1:T:363:ILE:HD13	2.02	0.64
4:D:80:TYR:CE1	4:D:113:ALA:HA	2.33	0.64
7:Z:83:LEU:HD22	7:Z:128:TRP:CZ2	2.33	0.64
3:C:114:GLY:O	3:C:115:SER:HB3	1.97	0.64
4:W:163:VAL:HB	4:W:225:PHE:HB2	1.80	0.64
4:W:227:LEU:CD2	4:W:231:HIS:CB	2.76	0.64
4:W:35:PHE:CE1	4:W:45:ILE:CD1	2.81	0.64
7:Z:133:LEU:O	7:Z:135:ALA:N	2.27	0.64
3:C:166:CYS:O	3:C:167:ARG:HD2	1.98	0.64
4:D:165:PHE:HE1	4:D:247:PHE:HD2	1.41	0.63
4:W:130:GLN:HG3	4:W:134:GLU:OE1	1.98	0.63
4:W:47:ASN:HB3	4:W:48:PRO:HD2	1.80	0.63
3:V:39:GLY:O	3:V:40:ASN:HB2	1.97	0.63
3:V:107:ASN:ND2	3:V:109:LYS:H	1.97	0.63
3:V:135:LYS:HB3	3:V:191:PHE:CE2	2.33	0.63
3:C:158:ALA:CB	3:C:168:ILE:HG13	2.26	0.63
4:W:6:VAL:O	4:W:115:MET:HB3	1.98	0.63
1:T:186:ILE:O	1:T:188:SER:N	2.32	0.63
4:W:201:SER:OG	4:W:206:PRO:HD3	1.97	0.63
1:T:151:ALA:O	1:T:370:HIS:HB3	1.98	0.63
3:C:120:ILE:CG1	3:C:137:ILE:CD1	2.75	0.63
1:T:115:PRO:CG	1:T:144:GLN:OE1	2.39	0.63
1:T:181:ALA:O	1:T:182:GLU:HB2	1.99	0.63
3:C:123:CYS:HB3	3:C:134:CYS:HB2	1.80	0.63
1:T:409:ARG:HB3	2:U:201:GLY:HA3	1.79	0.63
4:W:150:GLU:HG2	4:W:167:THR:CA	2.20	0.63
1:A:208:LEU:HG	1:A:211:ARG:HH21	1.64	0.63
4:D:159:ASP:O	4:D:160:ARG:HB3	1.97	0.63
3:C:238:ALA:O	3:C:239:THR:OG1	2.14	0.63
4:D:268:ALA:C	4:D:270:THR:H	2.02	0.63
3:V:31:GLU:HB3	3:V:49:LYS:HA	1.79	0.63
4:D:135:GLY:O	4:D:136:LYS:HB2	1.97	0.63
2:B:192:TYR:CE2	2:B:270:LEU:HB3	2.33	0.63
3:V:141:ILE:HG22	3:V:142:ARG:N	2.13	0.63
7:G:40:GLY:HA2	7:G:43:ASP:HB2	1.80	0.63
1:A:151:ALA:O	1:A:154:THR:HG22	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:41:ILE:HG23	5:E:42:VAL:N	2.12	0.63
3:V:144:THR:OG1	6:Y:28:GLN:CG	2.46	0.63
5:E:5:HIS:HB3	5:E:65:ASP:OD1	1.99	0.63
2:B:195:LYS:O	2:B:199:LEU:HG	1.97	0.63
3:V:77:TYR:CD2	3:V:90:LEU:CA	2.62	0.63
1:A:186:ILE:O	1:A:188:SER:N	2.32	0.63
1:A:255:GLN:HA	1:A:269:ILE:O	1.98	0.63
1:A:82:ILE:HG12	1:A:83:VAL:H	1.64	0.63
2:U:312:GLY:HA2	6:Y:33:HIS:NE2	2.14	0.63
2:U:184:ILE:HB	2:U:271:ILE:HD11	1.80	0.63
4:D:165:PHE:HB3	4:D:223:ILE:HB	1.73	0.63
3:V:334:VAL:HG13	3:V:345:PHE:HB3	1.80	0.63
1:A:60:PHE:CE2	1:A:95:GLN:HG2	2.33	0.63
1:A:95:GLN:O	1:A:100:TYR:HD2	1.81	0.63
3:C:173:ILE:HG22	3:C:176:VAL:HG22	1.79	0.63
4:D:158:LYS:HG3	4:D:159:ASP:CG	2.18	0.63
4:D:41:VAL:C	4:D:42:LEU:HG	2.18	0.63
1:T:203:PHE:HE1	5:X:54:PHE:CE1	2.16	0.63
4:D:141:ARG:HB2	4:D:154:VAL:O	1.99	0.63
3:V:106:PRO:CD	3:V:154:SER:HA	2.21	0.63
3:V:79:TRP:CZ2	3:V:88:PRO:HB3	2.34	0.63
3:V:253:ILE:CD1	3:V:257:SER:HB3	2.29	0.63
1:T:305:GLN:HG3	1:T:346:ARG:HH22	1.63	0.63
5:E:25:ARG:HB3	5:E:40:ASP:OD2	1.98	0.63
4:D:118:ARG:NH1	4:D:119:ASN:OD1	2.28	0.63
1:T:13:GLY:O	1:T:78:ILE:HG21	1.99	0.63
3:C:31:GLU:HB3	3:C:49:LYS:HA	1.79	0.63
5:X:149:PHE:CE2	5:X:156:PRO:CD	2.81	0.63
3:V:74:ARG:HG3	3:V:95:ILE:HD11	1.80	0.63
4:D:98:ASP:HB3	4:D:101:ASN:HB3	1.79	0.63
2:B:261:ALA:HB3	2:B:262:PRO:HD3	1.81	0.63
2:U:289:ALA:O	2:U:291:ILE:N	2.31	0.63
3:V:99:ALA:CA	3:V:115:SER:HB2	2.05	0.62
3:V:334:VAL:HG12	3:V:335:LEU:N	2.06	0.62
5:X:26:SER:CB	5:X:139:GLU:CD	2.67	0.62
5:X:145:CYS:O	5:X:149:PHE:HD1	1.81	0.62
1:T:105:PRO:HB2	1:T:134:PHE:HB3	1.80	0.62
3:V:259:VAL:HG13	3:V:268:VAL:O	1.99	0.62
1:A:304:ILE:HD12	1:A:316:TYR:CE1	2.34	0.62
3:C:185:TRP:HH2	3:C:217:VAL:HG11	1.64	0.62
3:C:39:GLY:O	3:C:40:ASN:HB2	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:165:PHE:HB2	4:D:223:ILE:H	1.61	0.62
3:V:160:GLY:HA3	3:V:205:VAL:CG1	2.28	0.62
1:T:200:ILE:HG23	1:T:281:ILE:CG1	2.30	0.62
3:C:18:LYS:HG3	3:C:62:PRO:CB	2.21	0.62
2:U:326:LEU:HD12	2:U:335:GLU:OE1	1.99	0.62
4:D:208:GLU:O	4:D:209:LEU:HB2	1.98	0.62
2:B:257:GLU:HA	2:B:260:GLU:HB2	1.80	0.62
5:X:24:ILE:CG2	5:X:41:ILE:HG21	2.24	0.62
3:V:5:SER:CB	3:V:352:GLY:O	2.47	0.62
5:E:132:TYR:O	5:E:134:GLN:N	2.31	0.62
1:T:105:PRO:HG2	4:W:256:LYS:CE	2.29	0.62
6:F:128:LYS:O	6:F:132:VAL:HG23	1.98	0.62
5:X:113:LEU:HD21	5:X:171:LYS:CG	2.28	0.62
2:B:343:ARG:HH22	3:C:92:ILE:HG22	1.64	0.62
2:B:315:SER:HB2	6:F:31:GLU:HB3	1.81	0.62
1:A:354:SER:HG	1:A:359:LYS:N	1.96	0.62
3:V:157:LEU:O	3:V:168:ILE:CG2	2.41	0.62
1:T:128:GLU:HG2	1:T:129:ILE:N	2.10	0.62
4:D:128:TYR:OH	4:D:142:ALA:N	2.33	0.62
2:B:262:PRO:C	2:B:264:ALA:H	2.03	0.62
3:V:107:ASN:HD22	3:V:109:LYS:HG2	1.63	0.62
2:B:202:TYR:CD2	2:B:252:ILE:CB	2.69	0.62
4:D:41:VAL:O	4:D:42:LEU:HG	1.99	0.62
3:C:101:CYS:CB	3:C:147:SER:HA	2.30	0.62
3:C:147:SER:O	3:C:148:LEU:HG	1.99	0.62
6:Y:101:PHE:CD2	6:Y:103:ILE:HD11	2.34	0.62
5:E:21:LEU:HG	5:E:21:LEU:O	1.98	0.62
2:U:322:LYS:CG	7:Z:16:VAL:HG11	2.29	0.62
5:X:22:LEU:HD13	5:X:23:PRO:HD3	1.81	0.62
1:T:285:PRO:HG2	1:T:292:PHE:CE2	2.34	0.62
1:A:38:LYS:NZ	1:A:59:ASP:OD2	2.30	0.62
4:D:40:GLY:O	4:D:42:LEU:HG	2.00	0.62
1:A:195:ILE:HD11	1:A:285:PRO:HB3	1.82	0.62
1:T:240:LYS:O	1:T:241:GLU:C	2.37	0.62
1:T:200:ILE:HG23	1:T:281:ILE:HG12	1.81	0.62
4:W:137:GLU:OE1	4:W:158:LYS:HE2	1.99	0.62
1:T:211:ARG:CG	1:T:212:GLU:H	2.10	0.62
3:V:5:SER:HB3	3:V:352:GLY:HA3	1.80	0.62
4:W:186:LYS:CD	4:W:198:VAL:O	2.47	0.62
4:W:10:ILE:O	4:W:10:ILE:HG22	2.00	0.62
3:V:249:ALA:O	3:V:250:VAL:HB	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:194:THR:HB	4:D:230:ARG:NE	2.13	0.62
5:X:22:LEU:CD1	5:X:23:PRO:CD	2.78	0.62
5:E:5:HIS:HA	5:E:58:TYR:OH	1.99	0.62
5:X:13:THR:HG22	5:X:20:ALA:HB1	1.81	0.62
1:T:211:ARG:HD2	1:T:212:GLU:HB3	1.82	0.62
1:T:239:VAL:HG22	5:X:4:TYR:CE1	2.34	0.62
4:D:103:PRO:O	4:D:106:LYS:HE3	2.00	0.62
2:U:321:LEU:HD13	2:U:340:PHE:CB	2.29	0.62
4:W:128:TYR:HE2	4:W:142:ALA:HB2	1.65	0.62
3:C:172:TYR:HE2	3:C:178:GLU:C	2.02	0.62
5:X:53:VAL:HG21	5:X:166:ARG:CB	2.29	0.62
4:D:155:GLU:OE2	4:D:208:GLU:HG2	2.00	0.62
4:D:165:PHE:CE2	4:D:225:PHE:HE1	2.15	0.62
3:V:135:LYS:CB	3:V:191:PHE:CZ	2.82	0.62
1:A:82:ILE:HG13	1:A:115:PRO:HD2	1.82	0.62
5:X:132:TYR:O	5:X:134:GLN:N	2.33	0.62
7:G:16:VAL:HA	7:G:19:TYR:HD2	1.65	0.62
4:W:95:LEU:HD11	4:W:97:TYR:CZ	2.35	0.62
4:W:268:ALA:C	4:W:270:THR:H	2.03	0.62
1:T:286:GLU:HB3	1:T:292:PHE:O	1.99	0.61
3:C:334:VAL:HG13	3:C:345:PHE:HB3	1.81	0.61
1:T:106:GLU:HG3	4:W:256:LYS:HE3	1.82	0.61
4:W:42:LEU:HB2	4:W:60:SER:OG	1.99	0.61
3:C:32:VAL:HG12	3:C:33:HIS:H	1.64	0.61
7:G:98:LEU:HB2	7:G:103:VAL:HG22	1.81	0.61
1:A:241:GLU:O	1:A:244:LYS:N	2.33	0.61
3:V:219:TRP:CG	3:V:227:CYS:HB2	2.02	0.61
7:Z:108:LYS:HG2	7:Z:144:VAL:HG13	1.80	0.61
4:D:165:PHE:CE2	4:D:225:PHE:HD1	2.15	0.61
3:V:122:ILE:HG23	3:V:122:ILE:O	2.00	0.61
3:C:107:ASN:ND2	3:C:109:LYS:HG2	2.15	0.61
3:C:151:HIS:NE2	3:C:214:GLY:CA	2.63	0.61
5:E:49:PHE:HA	5:E:52:ASN:HB2	1.83	0.61
2:U:166:ILE:HG12	2:U:285:THR:HG21	1.82	0.61
2:U:242:GLU:O	2:U:254:VAL:HG12	2.00	0.61
3:V:114:GLY:O	3:V:115:SER:HB3	2.00	0.61
6:Y:41:ARG:NH2	6:Y:71:ARG:HH12	1.99	0.61
1:A:103:ALA:O	4:D:38:PHE:HE1	1.83	0.61
6:Y:20:LEU:HD23	6:Y:20:LEU:H	1.66	0.61
3:C:114:GLY:HA2	3:C:148:LEU:HD11	1.82	0.61
1:A:11:ASP:O	1:A:18:LYS:HB2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:ILE:C	1:A:311:VAL:H	2.03	0.61
1:T:263:SER:O	1:T:264:LYS:HB2	2.00	0.61
1:T:193:ILE:HD11	1:T:299:VAL:HG11	1.82	0.61
1:A:336:GLN:CG	1:A:367:VAL:H	2.13	0.61
1:A:175:THR:CG2	1:A:195:ILE:HB	2.30	0.61
3:V:259:VAL:CG1	3:V:260:ALA:H	2.11	0.61
6:Y:76:VAL:HG21	6:Y:87:CYS:SG	2.41	0.61
4:D:43:TYR:CE2	4:D:116:LEU:CD2	2.81	0.61
1:A:336:GLN:OE1	1:A:366:GLN:CA	2.47	0.61
1:A:332:GLY:O	1:A:367:VAL:HG21	2.01	0.61
6:Y:102:PHE:CD1	6:Y:122:HIS:CD2	2.87	0.61
1:T:120:PRO:HG3	2:U:201:GLY:C	2.21	0.61
1:A:128:GLU:CG	1:A:129:ILE:H	2.08	0.61
2:B:224:GLY:O	2:B:316:ARG:NH1	2.33	0.61
4:D:95:LEU:HD11	4:D:97:TYR:CZ	2.36	0.61
1:T:174:VAL:HG21	1:T:193:ILE:O	1.97	0.61
6:F:20:LEU:O	6:F:22:LEU:HG	2.00	0.61
3:V:10:PRO:HB2	3:V:350:MET:HA	1.81	0.61
7:G:151:VAL:O	7:G:151:VAL:HG23	2.00	0.61
1:T:31:ILE:HD12	1:T:63:GLY:CA	2.29	0.61
4:W:36:ALA:HB1	4:W:41:VAL:O	2.01	0.61
7:Z:83:LEU:HD22	7:Z:128:TRP:CE2	2.36	0.61
5:X:81:LYS:HB2	5:X:98:LEU:CD1	2.31	0.61
4:D:214:ALA:CB	4:D:222:TYR:OH	2.47	0.61
6:Y:36:PRO:CG	6:Y:39:GLU:HB2	2.31	0.61
1:T:204:ILE:CG2	1:T:274:GLU:HB2	2.27	0.61
6:Y:102:PHE:O	6:Y:103:ILE:HG23	2.01	0.61
4:W:244:ILE:CG2	4:W:245:HIS:H	2.06	0.61
3:V:332:ILE:HD12	3:V:347:THR:HG21	1.82	0.61
4:D:111:HIS:CE1	4:D:115:MET:SD	2.94	0.61
6:F:8:TYR:CD2	6:F:55:ARG:HB2	2.34	0.61
4:D:75:LEU:HD23	4:D:76:LEU:N	2.15	0.61
4:D:153:TYR:HB2	4:D:164:VAL:CG2	2.30	0.61
2:B:336:LYS:HB3	7:G:21:GLU:CD	2.20	0.61
7:Z:81:LYS:O	7:Z:84:ILE:N	2.33	0.61
7:G:69:GLN:O	7:G:73:ASP:N	2.34	0.61
1:T:176:HIS:HD2	1:T:192:HIS:CD2	2.18	0.61
7:Z:151:VAL:HG23	7:Z:151:VAL:O	2.00	0.61
3:V:10:PRO:CB	3:V:350:MET:CA	2.77	0.61
1:T:145:ALA:CB	1:T:178:ILE:HD12	2.23	0.61
3:V:141:ILE:O	3:V:142:ARG:HG3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:176:VAL:HG23	3:C:177:GLU:N	2.16	0.61
4:W:35:PHE:HE1	4:W:45:ILE:HD13	1.65	0.61
2:U:325:TYR:CE1	2:U:330:LEU:HD13	2.36	0.61
2:U:313:LEU:N	2:U:314:PRO:HD2	2.14	0.61
5:E:78:CYS:C	5:E:82:LEU:HB3	2.21	0.61
1:T:205:GLN:O	1:T:209:ARG:HG3	1.99	0.61
2:U:192:TYR:HE2	2:U:270:LEU:HD22	1.66	0.61
1:A:62:ILE:HD12	1:A:92:PHE:HE1	1.59	0.61
6:F:102:PHE:O	6:F:103:ILE:HG23	2.01	0.61
2:U:212:THR:O	2:U:216:ILE:HG12	2.01	0.61
4:W:133:GLU:HG2	4:W:133:GLU:O	2.01	0.61
3:V:148:LEU:CD2	3:V:159:ALA:HB3	2.29	0.60
5:X:164:VAL:O	5:X:164:VAL:HG22	2.00	0.60
4:D:45:ILE:HG13	4:D:57:VAL:HG21	1.79	0.60
1:T:309:ILE:C	1:T:311:VAL:H	2.04	0.60
7:G:42:VAL:HG21	7:G:57:ALA:HB3	1.81	0.60
6:Y:56:ASN:O	6:Y:57:GLU:HB3	2.01	0.60
4:D:191:ALA:CB	6:F:165:LEU:HB3	2.30	0.60
1:A:348:LYS:O	1:A:350:SER:N	2.31	0.60
5:X:42:VAL:CG2	5:X:140:THR:HG22	2.21	0.60
1:A:186:ILE:HG21	1:A:189:CYS:HB2	1.82	0.60
4:W:146:TYR:CZ	4:W:150:GLU:HB3	2.36	0.60
7:Z:116:SER:N	7:Z:117:PRO:HD3	2.16	0.60
2:B:343:ARG:HH12	3:C:92:ILE:HG21	1.64	0.60
1:A:207:LEU:CD1	5:E:54:PHE:CZ	2.84	0.60
4:D:199:LEU:HB2	4:D:224:THR:HG1	1.62	0.60
4:D:202:HIS:CE1	4:D:220:ILE:O	2.54	0.60
2:B:252:ILE:HD12	2:B:252:ILE:O	2.02	0.60
3:V:77:TYR:HB3	3:V:89:THR:CA	2.30	0.60
3:C:144:THR:HG1	6:F:25:PHE:HZ	1.49	0.60
3:C:107:ASN:HD22	3:C:109:LYS:HG2	1.66	0.60
4:D:141:ARG:HH11	4:D:209:LEU:HD13	1.65	0.60
5:X:102:ASN:HA	5:X:137:ARG:HH12	1.66	0.60
1:T:194:PRO:CD	1:T:292:PHE:HE1	1.87	0.60
2:B:253:LYS:NZ	2:B:253:LYS:HB3	2.17	0.60
3:C:164:PHE:O	3:C:205:VAL:CG2	2.50	0.60
1:A:181:ALA:O	1:A:182:GLU:HB2	2.01	0.60
1:T:35:ILE:HD11	1:T:60:PHE:HB2	1.82	0.60
1:T:36:ALA:HB2	1:T:73:ALA:O	2.01	0.60
3:V:30:HIS:HA	3:V:55:VAL:HG23	1.82	0.60
3:V:223:ASP:HB3	7:Z:146:THR:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:118:SER:HB3	7:G:121:SER:CB	2.30	0.60
1:T:167:VAL:CG1	1:T:320:VAL:HB	2.31	0.60
2:U:192:TYR:CE2	2:U:270:LEU:HB3	2.36	0.60
2:U:343:ARG:HH22	3:V:92:ILE:HG22	1.67	0.60
5:E:105:ILE:HG22	5:E:133:LEU:HD22	1.84	0.60
6:F:144:LYS:O	6:F:148:GLU:HB2	2.01	0.60
1:A:8:CYS:HB2	1:A:110:PHE:CE1	2.37	0.60
3:V:68:VAL:HG12	3:V:104:TRP:HE1	1.64	0.60
3:V:158:ALA:HB2	3:V:168:ILE:HG23	1.84	0.60
6:Y:73:SER:HB2	6:Y:112:TYR:CD2	2.36	0.60
6:F:36:PRO:CA	6:F:69:SER:HB3	2.32	0.60
1:A:102:ARG:HH12	4:D:5:GLU:CB	2.15	0.60
5:X:83:GLN:OE1	5:X:164:VAL:CG1	2.49	0.60
6:Y:95:MET:HA	6:Y:104:LEU:HD21	1.82	0.60
1:T:180:VAL:HG12	1:T:181:ALA:N	2.11	0.60
3:V:269:LEU:H	3:V:283:GLY:CA	2.05	0.60
4:D:142:ALA:H	4:D:154:VAL:HG22	1.64	0.60
7:Z:99:ASP:O	7:Z:103:VAL:N	2.34	0.60
1:T:297:SER:O	1:T:339:LEU:HD13	2.02	0.60
5:X:105:ILE:HB	5:X:106:PRO:HD2	1.83	0.60
1:A:69:LYS:HD2	1:A:72:TYR:CE1	2.36	0.60
3:C:51:HIS:CE1	3:C:75:ASN:HB3	2.37	0.60
3:C:287:VAL:HG23	3:C:287:VAL:O	2.02	0.60
3:V:10:PRO:HB3	3:V:350:MET:C	2.22	0.60
3:C:10:PRO:CB	3:C:350:MET:CA	2.80	0.60
3:V:211:SER:O	3:V:213:ASN:N	2.35	0.60
7:Z:118:SER:HB3	7:Z:121:SER:CB	2.28	0.60
5:E:23:PRO:HG2	5:E:35:GLU:HG2	1.84	0.60
4:W:251:LEU:O	4:W:255:ILE:HG12	2.02	0.60
4:W:111:HIS:CE1	4:W:115:MET:SD	2.95	0.60
4:W:141:ARG:NH2	4:W:155:GLU:HG2	2.17	0.60
1:T:186:ILE:HD13	2:U:205:ASN:CB	2.32	0.60
3:C:124:TYR:O	3:C:133:VAL:HG23	2.01	0.60
4:D:189:ARG:HB2	4:D:189:ARG:CZ	2.32	0.60
4:D:165:PHE:CZ	4:D:225:PHE:HE1	2.20	0.60
3:V:101:CYS:CB	3:V:147:SER:HA	2.31	0.60
5:X:119:LYS:HB2	5:X:120:PRO:HD2	1.82	0.60
6:F:22:LEU:HD22	6:F:67:ILE:C	2.21	0.60
1:A:242:PHE:CZ	1:A:277:LEU:HD22	2.37	0.60
1:A:200:ILE:HG12	1:A:281:ILE:HD11	1.83	0.60
5:X:53:VAL:HG13	5:X:54:PHE:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:35:TYR:HB3	3:V:42:TRP:HE3	1.67	0.60
2:U:315:SER:OG	6:Y:30:VAL:C	2.40	0.60
1:T:286:GLU:OE1	1:T:293:THR:HG23	2.01	0.60
2:U:321:LEU:HD13	2:U:340:PHE:CG	2.35	0.60
1:A:82:ILE:HG13	1:A:115:PRO:CG	2.32	0.60
4:D:128:TYR:HE2	4:D:142:ALA:HB2	1.67	0.60
5:X:22:LEU:HD13	5:X:23:PRO:CD	2.31	0.60
4:W:217:GLY:HA3	4:W:220:ILE:HD13	1.83	0.60
2:B:170:TYR:C	2:B:171:GLU:HG2	2.22	0.60
6:F:137:HIS:O	6:F:141:GLU:HG3	2.02	0.60
1:A:117:LEU:O	1:A:117:LEU:HD23	2.02	0.60
4:W:71:GLY:HA2	4:W:74:GLU:HB2	1.82	0.60
3:V:6:PHE:CE2	3:V:354:MET:CG	2.84	0.60
4:D:248:ARG:NH1	4:D:249:ASP:OD1	2.35	0.60
3:C:56:THR:OG1	3:C:57:GLY:N	2.34	0.59
7:Z:124:VAL:HG22	7:Z:126:LEU:H	1.67	0.59
2:B:343:ARG:HH21	3:C:94:ARG:HA	1.67	0.59
6:F:11:ALA:O	6:F:15:THR:HG23	2.02	0.59
1:T:193:ILE:HG12	1:T:292:PHE:HZ	1.67	0.59
1:A:319:ILE:HG13	1:A:366:GLN:O	2.02	0.59
3:V:247:LEU:C	3:V:248:LEU:HD22	2.21	0.59
3:C:172:TYR:CE1	3:C:174:LYS:HG2	2.33	0.59
3:V:346:CYS:SG	3:V:347:THR:N	2.75	0.59
3:V:250:VAL:HG23	3:V:259:VAL:O	2.01	0.59
3:V:137:ILE:HD12	3:V:169:PHE:CG	2.37	0.59
6:Y:87:CYS:O	6:Y:91:MET:HG2	2.03	0.59
4:D:241:ILE:HD12	4:D:241:ILE:H	1.67	0.59
2:B:318:GLU:O	2:B:321:LEU:HG	2.02	0.59
5:E:5:HIS:CG	5:E:61:LYS:HE2	2.36	0.59
1:T:292:PHE:O	1:T:293:THR:OG1	2.18	0.59
4:D:186:LYS:CD	4:D:198:VAL:H	2.15	0.59
1:T:211:ARG:NH1	5:X:159:TRP:CZ3	2.71	0.59
6:F:56:ASN:O	6:F:57:GLU:HB3	2.02	0.59
1:A:90:GLU:CD	1:A:129:ILE:HG23	2.23	0.59
7:Z:18:GLU:HA	7:Z:23:LYS:NZ	2.17	0.59
1:A:399:ASP:HA	1:A:402:GLU:OE1	2.01	0.59
3:V:335:LEU:HD12	3:V:344:GLN:O	2.01	0.59
5:E:13:THR:HG21	5:E:22:LEU:HD22	1.84	0.59
3:C:252:PHE:CZ	3:C:258:LEU:HD21	2.37	0.59
3:C:122:ILE:HG23	3:C:122:ILE:O	2.03	0.59
3:C:151:HIS:NE2	3:C:214:GLY:HA2	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:104:GLU:CD	1:T:105:PRO:HD2	2.22	0.59
4:W:203:ARG:HG2	4:W:218:ASP:HA	1.83	0.59
2:B:184:ILE:HB	2:B:271:ILE:HD11	1.84	0.59
5:X:24:ILE:HD12	5:X:26:SER:HB2	1.85	0.59
3:C:245:LEU:HB2	3:C:264:ASP:OD1	2.02	0.59
1:A:186:ILE:O	1:A:186:ILE:HG22	2.02	0.59
4:W:75:LEU:HD23	4:W:76:LEU:N	2.17	0.59
3:C:48:LEU:HD11	3:C:86:TRP:HB2	1.84	0.59
1:A:177:VAL:HG12	1:A:177:VAL:O	2.01	0.59
4:D:132:GLN:HE21	4:D:159:ASP:HA	1.67	0.59
5:X:157:SER:O	5:X:161:THR:HG22	2.02	0.59
3:V:118:ARG:O	3:V:119:VAL:HB	2.03	0.59
1:T:390:PHE:O	1:T:394:CYS:CB	2.43	0.59
7:G:114:PHE:CZ	7:G:125:LEU:O	2.56	0.59
2:U:313:LEU:CG	2:U:317:LEU:HG	2.29	0.59
1:T:173:GLY:O	1:T:174:VAL:HB	2.02	0.59
3:C:269:LEU:HB3	3:C:283:GLY:HA2	1.84	0.59
4:W:241:ILE:O	4:W:244:ILE:HG22	2.03	0.59
3:V:18:LYS:CG	3:V:62:PRO:HB3	2.19	0.59
1:A:211:ARG:CD	1:A:212:GLU:H	2.14	0.59
3:V:144:THR:OG1	6:Y:28:GLN:HG2	2.03	0.59
4:D:12:GLU:HG3	4:D:110:VAL:HG21	1.84	0.59
3:V:156:LEU:HD23	3:V:170:SER:CB	2.32	0.59
3:C:152:PRO:HG3	3:C:212:ALA:HA	1.84	0.59
5:E:149:PHE:HE2	5:E:156:PRO:HG3	1.68	0.59
6:F:87:CYS:O	6:F:91:MET:HG2	2.02	0.59
3:V:193:GLU:O	3:V:195:MET:HG2	2.03	0.59
3:V:207:GLY:H	3:V:220:VAL:HG23	1.68	0.59
4:W:248:ARG:HD3	4:W:248:ARG:C	2.23	0.59
3:V:217:VAL:O	3:V:228:LEU:HA	2.03	0.59
5:E:72:THR:HA	5:E:75:ILE:HD12	1.85	0.59
1:T:193:ILE:HG12	1:T:292:PHE:CZ	2.38	0.59
4:W:110:VAL:HG13	4:W:111:HIS:N	2.18	0.59
5:E:97:THR:O	5:E:101:THR:HG23	2.03	0.59
1:T:135:ASN:ND2	4:W:171:ASP:OD1	2.36	0.59
3:C:327:ASN:ND2	3:C:351:ASP:CB	2.55	0.59
3:V:254:THR:CG2	3:V:255:GLU:H	2.11	0.59
6:F:63:ILE:HD11	6:F:72:VAL:HG13	1.81	0.59
2:U:315:SER:OG	6:Y:30:VAL:HA	2.03	0.59
1:A:207:LEU:HD11	5:E:54:PHE:HZ	1.68	0.59
6:Y:20:LEU:O	6:Y:22:LEU:HG	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:271:VAL:HG13	1:T:274:GLU:CG	2.33	0.58
3:C:331:GLN:HG2	3:C:332:ILE:H	1.67	0.58
5:E:19:MET:CE	5:E:67:THR:N	2.66	0.58
5:X:53:VAL:HG21	5:X:166:ARG:HB3	1.85	0.58
4:D:191:ALA:O	4:D:192:SER:HB3	2.02	0.58
6:Y:11:ALA:O	6:Y:15:THR:HG23	2.03	0.58
1:T:285:PRO:CB	1:T:292:PHE:HB3	2.25	0.58
3:V:99:ALA:O	3:V:115:SER:HA	1.96	0.58
4:W:207:LEU:C	4:W:209:LEU:N	2.57	0.58
4:W:240:THR:HG22	6:Y:168:PHE:HD1	1.66	0.58
3:C:252:PHE:CE2	3:C:258:LEU:HD11	2.38	0.58
1:A:343:VAL:HG13	1:A:363:ILE:HD11	1.86	0.58
4:W:194:THR:HB	4:W:230:ARG:NH2	2.18	0.58
4:W:2:ILE:HG21	6:Y:163:GLU:HB3	1.86	0.58
2:B:192:TYR:HE2	2:B:270:LEU:HD22	1.68	0.58
1:A:403:ILE:HB	1:A:407:ILE:HD13	1.85	0.58
2:B:238:THR:HG22	6:F:106:ARG:NH2	2.18	0.58
3:V:344:GLN:HG3	3:V:358:ASP:OD2	2.03	0.58
3:V:245:LEU:HB2	3:V:264:ASP:OD1	2.04	0.58
3:C:268:VAL:HA	3:C:284:ARG:H	1.68	0.58
4:W:186:LYS:CE	4:W:197:GLN:HB3	2.33	0.58
4:W:162:THR:HA	4:W:225:PHE:O	2.03	0.58
2:U:233:LEU:O	2:U:240:LEU:HD21	2.03	0.58
3:V:253:ILE:HD11	3:V:257:SER:OG	2.03	0.58
3:V:268:VAL:HA	3:V:284:ARG:H	1.67	0.58
4:D:142:ALA:HB3	4:D:154:VAL:HG22	1.85	0.58
4:D:142:ALA:H	4:D:154:VAL:HG23	1.67	0.58
7:G:133:LEU:HG	7:G:134:ALA:H	1.67	0.58
3:V:150:TRP:HZ3	3:V:155:VAL:O	1.85	0.58
1:A:4:ARG:CZ	1:A:5:LEU:HD21	2.34	0.58
7:Z:63:PRO:HD3	7:Z:109:TYR:OH	1.98	0.58
2:U:236:GLU:OE1	6:Y:105:ARG:NH2	2.37	0.58
3:C:329:VAL:HA	3:C:349:GLY:HA2	1.85	0.58
1:T:285:PRO:HB2	1:T:292:PHE:CG	2.37	0.58
3:V:224:SER:HB2	3:V:246:PRO:CD	2.34	0.58
1:A:103:ALA:HB1	1:A:108:HIS:CD2	2.39	0.58
4:D:34:THR:HG1	4:D:44:HIS:CD2	2.22	0.58
6:F:55:ARG:HH21	6:F:56:ASN:ND2	2.02	0.58
3:V:14:HIS:ND1	3:V:348:THR:HG21	2.18	0.58
1:T:194:PRO:O	1:T:195:ILE:HG12	2.03	0.58
1:T:195:ILE:HG22	1:T:195:ILE:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:285:LEU:O	3:C:286:ASP:HB2	2.04	0.58
3:V:340:ALA:O	3:V:341:LYS:HG2	2.04	0.58
1:T:207:LEU:HD12	5:X:54:PHE:HZ	1.67	0.58
4:D:70:HIS:C	4:D:72:ALA:H	2.07	0.58
4:W:21:ASN:OD1	4:W:28:PRO:HA	2.03	0.58
1:T:318:ASN:OD1	1:T:368:ILE:CD1	2.52	0.58
1:A:116:PRO:O	1:A:117:LEU:HB3	2.04	0.58
1:T:195:ILE:CD1	1:T:285:PRO:HB3	2.30	0.58
3:V:135:LYS:HB3	3:V:191:PHE:HZ	1.63	0.58
5:X:16:ILE:HG13	5:X:125:GLU:HG2	1.85	0.58
3:C:269:LEU:HB3	3:C:283:GLY:CA	2.33	0.58
1:A:292:PHE:HE2	1:A:294:GLN:HB3	1.69	0.58
1:T:99:LYS:HE2	4:W:9:ARG:NH1	2.17	0.58
5:X:97:THR:O	5:X:101:THR:HG23	2.02	0.58
7:G:16:VAL:HA	7:G:19:TYR:CD2	2.39	0.58
3:V:180:PRO:HB2	3:V:189:MET:SD	2.43	0.58
4:D:35:PHE:CE2	4:D:43:TYR:HD1	2.22	0.58
3:C:113:VAL:O	3:C:120:ILE:O	2.22	0.58
3:C:51:HIS:ND1	3:C:75:ASN:CG	2.57	0.58
1:T:62:ILE:HG21	1:T:92:PHE:HD1	1.68	0.58
7:Z:62:PRO:O	7:Z:64:ILE:N	2.37	0.58
4:D:165:PHE:HB3	4:D:223:ILE:CB	2.32	0.58
3:V:110:LYS:CD	3:V:173:ILE:HD11	2.29	0.58
6:F:20:LEU:HD23	6:F:20:LEU:N	2.19	0.58
4:W:75:LEU:HG	4:W:78:ARG:CB	2.33	0.58
3:C:215:SER:O	3:C:230:ASP:HA	2.02	0.58
4:D:217:GLY:HA3	4:D:220:ILE:HD13	1.86	0.58
1:T:181:ALA:HB2	1:T:186:ILE:HD11	1.86	0.58
1:T:128:GLU:CG	1:T:129:ILE:H	2.09	0.58
1:T:99:LYS:HE2	4:W:9:ARG:HH11	1.69	0.58
4:W:11:ILE:HG22	4:W:11:ILE:O	2.03	0.58
1:A:82:ILE:HG13	1:A:115:PRO:HG2	1.86	0.58
1:T:348:LYS:O	1:T:350:SER:N	2.30	0.58
5:X:72:THR:HA	5:X:75:ILE:HD12	1.85	0.58
1:T:127:ALA:O	1:T:131:PHE:HD2	1.87	0.58
1:A:395:HIS:CE1	1:A:408:CYS:HA	2.39	0.57
3:C:158:ALA:O	3:C:159:ALA:CB	2.52	0.57
5:X:149:PHE:CD2	5:X:156:PRO:CA	2.87	0.57
7:Z:63:PRO:HB2	7:Z:151:VAL:OXT	2.04	0.57
1:T:35:ILE:HB	1:T:61:PHE:O	2.03	0.57
3:V:269:LEU:HB3	3:V:283:GLY:CA	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:254:HIS:CE1	6:Y:160:VAL:HG22	2.39	0.57
1:T:13:GLY:O	1:T:78:ILE:HB	2.04	0.57
3:V:65:ASN:O	3:V:65:ASN:ND2	2.37	0.57
1:T:192:HIS:O	1:T:193:ILE:HG13	2.04	0.57
3:C:259:VAL:HG13	3:C:268:VAL:O	2.03	0.57
2:B:234:ALA:HB2	2:B:259:PHE:CZ	2.36	0.57
3:C:65:ASN:O	3:C:65:ASN:ND2	2.37	0.57
1:T:371:HIS:O	1:T:373:GLN:N	2.26	0.57
4:D:165:PHE:CZ	4:D:225:PHE:CE1	2.92	0.57
3:V:159:ALA:HA	3:V:208:VAL:HG21	1.85	0.57
5:X:42:VAL:HG22	5:X:140:THR:CG2	2.24	0.57
3:C:245:LEU:HD13	3:C:263:HIS:HE1	0.74	0.57
3:V:73:ASP:O	3:V:74:ARG:HD3	2.04	0.57
4:W:6:VAL:O	4:W:6:VAL:HG12	2.04	0.57
1:T:57:ASP:OD2	6:Y:156:ARG:NH2	2.37	0.57
3:C:174:LYS:C	3:C:176:VAL:H	2.08	0.57
1:T:237:ASP:OD2	5:X:4:TYR:OH	2.21	0.57
1:T:99:LYS:HA	1:T:102:ARG:NH1	2.19	0.57
3:C:262:GLY:HA2	3:C:329:VAL:HB	1.85	0.57
6:Y:48:LEU:HB3	7:Z:145:LEU:HB3	1.85	0.57
1:A:200:ILE:HG12	1:A:281:ILE:CD1	2.34	0.57
2:U:236:GLU:O	6:Y:105:ARG:CG	2.42	0.57
1:A:270:ASP:OD2	5:E:158:LYS:NZ	2.33	0.57
5:E:160:TRP:C	5:E:162:CYS:H	2.07	0.57
2:B:262:PRO:O	2:B:264:ALA:N	2.37	0.57
5:X:48:TYR:O	5:X:49:PHE:HB3	2.03	0.57
2:U:349:ARG:O	2:U:351:LYS:N	2.37	0.57
4:D:48:PRO:O	4:D:49:ASN:HB2	2.04	0.57
4:D:206:PRO:HG2	4:D:224:THR:CG2	2.34	0.57
3:V:343:SER:CA	3:V:359:VAL:CG2	2.82	0.57
1:A:35:ILE:HD12	1:A:62:ILE:HG21	1.84	0.57
4:W:80:TYR:CE1	4:W:113:ALA:HA	2.40	0.57
3:C:18:LYS:CG	3:C:62:PRO:HB3	2.23	0.57
4:W:45:ILE:HG23	4:W:57:VAL:HG22	1.85	0.57
6:F:60:LYS:NZ	6:F:112:TYR:CD1	2.73	0.57
3:C:360:ARG:O	3:C:362:LEU:N	2.36	0.57
6:Y:80:ASP:CG	6:Y:82:ILE:HG22	2.24	0.57
3:C:183:THR:HG22	3:C:185:TRP:HD1	1.70	0.57
3:C:57:GLY:N	3:C:70:CYS:O	2.38	0.57
6:Y:102:PHE:CD1	6:Y:122:HIS:HD2	2.22	0.57
3:C:34:ILE:HB	3:C:45:VAL:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:406:SER:HB2	1:T:409:ARG:NE	2.14	0.57
2:U:237:THR:HA	6:Y:105:ARG:CG	2.34	0.57
5:X:25:ARG:O	5:X:25:ARG:HG3	2.04	0.57
1:A:127:ALA:O	1:A:131:PHE:HD2	1.86	0.57
4:D:9:ARG:C	4:D:11:ILE:H	2.08	0.57
3:C:30:HIS:HA	3:C:55:VAL:HG23	1.86	0.57
1:T:271:VAL:HA	1:T:274:GLU:OE2	2.03	0.57
2:B:202:TYR:HB3	2:B:204:PHE:CE2	2.40	0.57
2:U:253:LYS:HE3	6:Y:99:GLU:CB	2.30	0.57
1:T:21:TYR:OH	1:T:101:LEU:O	2.15	0.57
4:D:75:LEU:HD11	4:D:78:ARG:CD	2.34	0.57
4:D:77:LYS:CG	4:D:84:LEU:HB3	2.31	0.57
2:U:315:SER:OG	6:Y:30:VAL:CA	2.53	0.57
3:V:219:TRP:CD2	3:V:227:CYS:CB	2.62	0.57
3:V:272:TYR:HE1	3:V:278:LYS:O	1.88	0.57
5:E:95:MET:HB3	5:E:138:GLN:NE2	2.19	0.57
3:V:173:ILE:HD13	3:V:177:GLU:CD	2.25	0.57
1:A:99:LYS:HG3	4:D:5:GLU:CG	2.32	0.57
1:A:180:VAL:O	1:A:181:ALA:HB2	2.05	0.57
3:C:211:SER:O	3:C:213:ASN:N	2.37	0.57
4:W:9:ARG:C	4:W:11:ILE:H	2.08	0.57
4:W:36:ALA:HB2	4:W:42:LEU:HG	1.87	0.57
3:V:253:ILE:HD11	3:V:257:SER:CB	2.34	0.57
6:F:138:PHE:O	6:F:142:ILE:CG2	2.48	0.57
7:G:83:LEU:HD22	7:G:128:TRP:CE2	2.40	0.57
1:T:205:GLN:HG2	1:T:209:ARG:NH2	2.20	0.57
3:V:202:CYS:SG	7:Z:148:ARG:N	2.75	0.57
4:W:185:PHE:CZ	6:Y:160:VAL:HG12	2.39	0.57
4:W:121:PHE:O	4:W:124:VAL:HG12	2.05	0.57
2:B:349:ARG:O	2:B:351:LYS:N	2.38	0.57
4:W:149:ASP:OD1	4:W:149:ASP:N	2.37	0.57
3:V:281:PHE:CD1	3:V:282:GLY:N	2.73	0.57
3:V:173:ILE:HG22	3:V:175:GLU:H	1.69	0.57
3:C:146:LEU:HD12	3:C:206:HIS:CA	2.31	0.57
3:V:32:VAL:O	3:V:33:HIS:ND1	2.27	0.57
1:A:120:PRO:HB3	1:A:409:ARG:HD3	1.87	0.57
1:T:18:LYS:N	1:T:18:LYS:HD3	2.20	0.57
2:U:370:ASN:C	2:U:372:TRP:H	2.07	0.57
1:T:205:GLN:HG2	1:T:209:ARG:HH21	1.70	0.57
7:Z:53:ALA:O	7:Z:55:LEU:N	2.38	0.57
3:V:158:ALA:CB	3:V:168:ILE:CG1	2.67	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:TYR:CE2	2:B:252:ILE:CG2	2.87	0.56
1:A:102:ARG:HH12	4:D:5:GLU:HB2	1.66	0.56
3:C:75:ASN:O	3:C:76:ALA:HB2	2.05	0.56
1:T:271:VAL:HG13	1:T:274:GLU:HG2	1.86	0.56
6:Y:122:HIS:O	6:Y:126:MET:HB2	2.05	0.56
4:W:165:PHE:CD2	4:W:223:ILE:HB	2.40	0.56
1:A:237:ASP:CB	1:A:240:LYS:HB2	2.17	0.56
4:D:164:VAL:HG11	4:D:209:LEU:HD23	1.87	0.56
3:V:121:SER:CB	3:V:136:HIS:CE1	2.87	0.56
1:T:219:GLN:NE2	1:T:222:GLU:OE1	2.37	0.56
1:T:228:LYS:O	1:T:232:SER:OG	2.21	0.56
5:X:73:LEU:HB3	5:X:173:LEU:HD22	1.86	0.56
7:G:53:ALA:O	7:G:55:LEU:N	2.38	0.56
7:Z:35:ALA:HA	7:Z:61:ASN:HD22	1.69	0.56
1:T:295:PRO:O	1:T:299:VAL:HG23	2.05	0.56
6:Y:61:VAL:CB	6:Y:74:ILE:HG23	2.32	0.56
6:Y:23:GLU:CA	6:Y:120:ASN:HB2	2.33	0.56
3:C:146:LEU:HD13	3:C:206:HIS:O	2.05	0.56
4:W:75:LEU:CG	4:W:78:ARG:HB3	2.35	0.56
3:C:254:THR:HB	3:C:257:SER:HB2	1.87	0.56
7:G:44:SER:C	7:G:46:LEU:H	2.08	0.56
1:A:238:LEU:HD21	1:A:280:GLU:CG	2.24	0.56
1:T:200:ILE:HG12	1:T:281:ILE:HD11	1.87	0.56
7:Z:122:SER:O	7:Z:123:ALA:HB3	2.05	0.56
4:D:173:ASP:HB2	6:F:85:ILE:HG21	1.87	0.56
4:W:3:LEU:O	4:W:4:LEU:HG	2.06	0.56
3:V:20:ARG:HD3	3:V:335:LEU:HD22	1.87	0.56
2:B:202:TYR:HE2	2:B:252:ILE:CA	2.16	0.56
6:Y:23:GLU:C	6:Y:120:ASN:CB	2.74	0.56
5:E:102:ASN:HA	5:E:137:ARG:HH12	1.70	0.56
5:E:16:ILE:O	5:E:16:ILE:HG23	2.05	0.56
5:E:152:GLN:HB2	5:E:155:LYS:HD2	1.86	0.56
1:A:82:ILE:CG1	1:A:83:VAL:N	2.66	0.56
3:C:74:ARG:CG	3:C:95:ILE:HD11	2.35	0.56
7:G:128:TRP:O	7:G:132:ALA:HB2	2.05	0.56
3:C:129:ASN:ND2	3:C:131:TRP:CE2	2.73	0.56
1:T:13:GLY:O	1:T:78:ILE:CB	2.53	0.56
4:W:228:PHE:HB3	4:W:229:PRO:HD2	1.87	0.56
2:U:226:ASN:HD22	2:U:229:GLN:HB2	1.69	0.56
1:T:286:GLU:OE1	1:T:293:THR:HA	2.04	0.56
3:V:222:HIS:O	3:V:246:PRO:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ILE:HG22	1:A:189:CYS:H	1.70	0.56
1:A:238:LEU:C	1:A:240:LYS:H	2.07	0.56
5:E:162:CYS:C	5:E:164:VAL:N	2.58	0.56
2:U:343:ARG:HH12	3:V:92:ILE:HG21	1.71	0.56
6:F:104:LEU:HD23	6:F:104:LEU:C	2.26	0.56
4:D:3:LEU:O	4:D:4:LEU:HG	2.06	0.56
4:W:187:GLU:HG2	4:W:187:GLU:O	2.05	0.56
3:V:263:HIS:CD2	6:Y:21:CYS:HB3	2.39	0.56
4:W:241:ILE:HD12	4:W:241:ILE:H	1.69	0.56
3:C:10:PRO:HB3	3:C:350:MET:C	2.26	0.56
1:T:304:ILE:CG2	1:T:316:TYR:CZ	2.89	0.56
2:U:177:HIS:C	2:U:178:LEU:HG	2.26	0.56
3:V:146:LEU:HD12	3:V:205:VAL:O	2.05	0.56
5:X:17:GLY:N	5:X:125:GLU:OE1	2.33	0.56
6:Y:17:GLN:HA	6:Y:20:LEU:HD22	1.87	0.56
1:T:273:TYR:CD1	1:T:273:TYR:N	2.73	0.56
5:X:103:PHE:HB3	5:X:104:PRO:HD2	1.86	0.56
4:W:132:GLN:CG	4:W:159:ASP:HA	2.28	0.56
1:A:11:ASP:HA	1:A:113:THR:CG2	2.35	0.56
2:U:262:PRO:O	2:U:264:ALA:N	2.37	0.56
3:V:217:VAL:HG12	3:V:229:ALA:HB3	1.87	0.56
1:A:398:LYS:O	1:A:402:GLU:HG3	2.05	0.56
3:V:156:LEU:CD2	3:V:170:SER:CB	2.84	0.56
2:B:198:LEU:HD21	2:B:204:PHE:O	2.06	0.56
6:Y:22:LEU:HD22	6:Y:67:ILE:C	2.25	0.56
3:V:75:ASN:O	3:V:76:ALA:HB2	2.05	0.56
2:B:336:LYS:HD3	7:G:21:GLU:CG	2.33	0.56
2:U:224:GLY:O	2:U:316:ARG:HD2	2.05	0.56
1:T:69:LYS:HD2	1:T:72:TYR:HD1	1.68	0.56
1:A:304:ILE:HD13	1:A:315:LEU:O	2.06	0.56
4:D:238:ASP:O	4:D:242:ASN:N	2.37	0.56
5:X:19:MET:O	5:X:20:ALA:HB2	2.05	0.56
3:C:259:VAL:HG22	3:C:269:LEU:HD12	1.88	0.56
4:W:237:ARG:O	4:W:241:ILE:HG12	2.06	0.56
1:T:120:PRO:CG	2:U:202:TYR:CE2	2.80	0.56
4:D:244:ILE:CG2	4:D:245:HIS:H	2.07	0.56
2:U:282:LEU:O	2:U:285:THR:OG1	2.24	0.56
7:Z:83:LEU:HB3	7:Z:128:TRP:NE1	2.21	0.56
4:D:179:LYS:HZ1	4:D:179:LYS:HB3	1.69	0.56
4:W:129:PHE:O	4:W:133:GLU:HB3	2.05	0.56
3:C:15:ALA:HB2	3:C:59:ASP:HA	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:122:ILE:O	3:V:135:LYS:HB2	2.06	0.56
2:U:311:PRO:HB3	6:Y:32:ARG:HH11	1.71	0.56
1:T:179:PRO:HB2	1:T:315:LEU:HD11	1.88	0.56
4:W:11:ILE:HD11	4:W:35:PHE:HZ	1.68	0.56
7:G:9:ALA:O	7:G:10:ARG:HB2	2.05	0.56
2:B:169:VAL:HG22	2:B:174:SER:HA	1.88	0.56
3:V:104:TRP:O	3:V:105:ALA:HB2	2.05	0.56
6:Y:36:PRO:CA	6:Y:69:SER:HB3	2.35	0.56
3:C:204:TRP:O	3:C:221:SER:CB	2.54	0.56
4:W:213:ASP:O	4:W:214:ALA:HB2	2.06	0.56
4:W:240:THR:O	4:W:244:ILE:HB	2.05	0.56
6:F:55:ARG:NH2	6:F:56:ASN:HD21	2.03	0.56
1:A:283:PHE:O	1:A:295:PRO:HB3	2.06	0.56
1:A:205:GLN:HG2	1:A:209:ARG:CZ	2.35	0.56
1:T:205:GLN:NE2	1:T:220:SER:O	2.24	0.56
3:V:228:LEU:HD13	3:V:279:LEU:HD21	1.87	0.56
1:T:60:PHE:HE2	1:T:95:GLN:HG2	1.71	0.55
1:A:238:LEU:CD2	1:A:280:GLU:HG2	2.27	0.55
1:T:239:VAL:CG1	5:X:4:TYR:CE1	2.86	0.55
4:D:207:LEU:C	4:D:209:LEU:H	2.08	0.55
4:D:132:GLN:HG2	4:D:160:ARG:H	1.71	0.55
1:A:370:HIS:CG	1:A:371:HIS:N	2.75	0.55
3:V:143:SER:CB	3:V:162:CYS:HB2	2.34	0.55
3:C:259:VAL:O	3:C:260:ALA:HB2	2.05	0.55
3:C:348:THR:HG22	3:C:354:MET:HG2	1.88	0.55
7:G:114:PHE:CE1	7:G:125:LEU:O	2.59	0.55
2:U:171:GLU:O	2:U:171:GLU:HG3	2.07	0.55
1:T:131:PHE:HB3	1:T:400:TYR:CZ	2.40	0.55
4:W:124:VAL:HG13	4:W:125:PHE:HD1	1.71	0.55
3:V:102:VAL:O	3:V:103:ARG:HB2	2.06	0.55
6:Y:73:SER:O	6:Y:74:ILE:HG13	2.06	0.55
3:C:245:LEU:HD12	3:C:263:HIS:CE1	2.34	0.55
2:U:319:ARG:C	2:U:321:LEU:H	2.08	0.55
4:W:186:LYS:CG	4:W:198:VAL:O	2.55	0.55
1:T:316:TYR:CD1	1:T:365:VAL:HG12	2.41	0.55
1:T:237:ASP:HB3	1:T:240:LYS:CB	2.37	0.55
1:T:105:PRO:HG2	4:W:256:LYS:CD	2.37	0.55
6:Y:8:TYR:CD2	6:Y:55:ARG:HB2	2.40	0.55
1:A:82:ILE:CB	1:A:115:PRO:HG2	2.35	0.55
1:A:326:THR:O	1:A:373:GLN:OE1	2.24	0.55
5:X:5:HIS:CD2	5:X:58:TYR:OH	2.60	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:131:PHE:HE1	4:W:136:LYS:HE3	1.70	0.55
3:V:204:TRP:O	3:V:221:SER:OG	2.21	0.55
3:V:151:HIS:NE2	3:V:214:GLY:CA	2.70	0.55
3:V:56:THR:OG1	3:V:57:GLY:N	2.39	0.55
2:B:202:TYR:OH	2:B:253:LYS:N	2.39	0.55
3:C:162:CYS:HB3	6:F:45:GLU:OE2	2.07	0.55
5:X:77:GLU:HG3	5:X:103:PHE:CZ	2.40	0.55
3:V:328:SER:H	3:V:350:MET:HE2	1.71	0.55
4:W:186:LYS:NZ	4:W:199:LEU:HD12	2.21	0.55
4:W:240:THR:HA	6:Y:168:PHE:CE1	2.42	0.55
4:W:132:GLN:NE2	4:W:159:ASP:CA	2.63	0.55
1:A:304:ILE:CD1	1:A:316:TYR:CE1	2.89	0.55
1:T:318:ASN:OD1	1:T:368:ILE:HD11	2.07	0.55
1:A:297:SER:O	1:A:339:LEU:HD13	2.05	0.55
6:Y:62:LEU:N	6:Y:73:SER:O	2.30	0.55
6:F:68:ASN:HB2	6:F:120:ASN:OD1	2.07	0.55
1:A:71:THR:CG2	1:A:72:TYR:CD1	2.88	0.55
3:C:332:ILE:HG12	3:C:332:ILE:O	2.06	0.55
3:C:152:PRO:HG2	3:C:212:ALA:CA	2.36	0.55
5:X:113:LEU:CD2	5:X:171:LYS:HG3	2.31	0.55
1:T:170:SER:O	1:T:325:SER:OG	2.23	0.55
3:V:306:ASP:O	3:V:307:LYS:HB2	2.05	0.55
4:D:165:PHE:N	4:D:223:ILE:O	2.34	0.55
1:T:255:GLN:CD	1:T:270:ASP:OD1	2.45	0.55
3:V:118:ARG:HB3	3:V:142:ARG:HA	1.88	0.55
4:W:132:GLN:NE2	4:W:159:ASP:HB3	2.22	0.55
1:T:4:ARG:CZ	1:T:5:LEU:HD21	2.36	0.55
1:A:82:ILE:HA	1:A:115:PRO:CG	2.26	0.55
4:D:75:LEU:HG	4:D:78:ARG:HD3	1.88	0.55
6:F:101:PHE:CD2	6:F:103:ILE:HD11	2.40	0.55
4:D:197:GLN:HB2	4:D:226:VAL:HG21	1.89	0.55
4:D:203:ARG:HG2	4:D:218:ASP:HA	1.88	0.55
1:A:105:PRO:HB2	1:A:136:VAL:HG12	1.86	0.55
4:W:208:GLU:O	4:W:209:LEU:HB2	2.07	0.55
3:V:79:TRP:CZ3	3:V:88:PRO:CD	2.90	0.55
1:T:203:PHE:CZ	5:X:54:PHE:CZ	2.95	0.55
6:Y:146:ILE:O	6:Y:149:MET:HB2	2.07	0.55
5:X:16:ILE:HD11	5:X:125:GLU:HG2	1.87	0.55
3:C:224:SER:CA	3:C:246:PRO:HB3	2.36	0.55
4:W:75:LEU:HD11	4:W:78:ARG:CD	2.35	0.55
7:Z:44:SER:C	7:Z:46:LEU:H	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:223:ASP:CB	7:G:146:THR:HB	2.36	0.55
4:D:107:ASP:C	4:D:109:ILE:H	2.09	0.55
4:W:202:HIS:CE1	4:W:220:ILE:O	2.60	0.55
1:A:233:TYR:OH	1:A:245:TYR:OH	2.11	0.55
4:W:70:HIS:C	4:W:72:ALA:H	2.09	0.55
7:G:62:PRO:O	7:G:64:ILE:N	2.39	0.55
1:T:286:GLU:CD	1:T:293:THR:HG23	2.27	0.55
3:V:334:VAL:HB	3:V:338:GLY:HA2	1.87	0.55
1:T:273:TYR:C	1:T:275:ARG:H	2.11	0.55
3:C:212:ALA:HB2	3:C:339:LYS:HB3	1.87	0.55
1:T:237:ASP:HB3	1:T:240:LYS:HB3	1.89	0.55
4:D:75:LEU:CG	4:D:78:ARG:HD3	2.37	0.55
6:F:139:MET:O	6:F:142:ILE:HG12	2.07	0.55
2:B:166:ILE:HG12	2:B:285:THR:HG21	1.87	0.55
1:A:260:ASN:HB3	1:A:265:LYS:N	2.21	0.55
4:D:240:THR:OG1	4:D:241:ILE:HD12	2.06	0.55
2:U:278:VAL:HG13	2:U:320:GLU:OE2	2.07	0.55
4:D:234:ALA:HA	4:D:237:ARG:HB2	1.88	0.55
7:Z:14:VAL:HG13	7:Z:14:VAL:O	2.06	0.55
1:T:292:PHE:HE2	1:T:294:GLN:O	1.89	0.55
3:C:77:TYR:HB3	3:C:89:THR:H	1.70	0.55
1:T:273:TYR:N	1:T:273:TYR:HD1	2.04	0.55
1:T:120:PRO:HB3	1:T:409:ARG:HD3	1.89	0.55
4:D:150:GLU:HG2	4:D:168:VAL:H	1.71	0.55
2:U:170:TYR:O	2:U:171:GLU:HG2	2.06	0.55
1:T:122:ASN:HA	1:T:125:TYR:CD2	2.39	0.55
1:T:369:THR:O	1:T:369:THR:HG22	2.05	0.55
7:Z:17:ASP:O	7:Z:23:LYS:HD2	2.06	0.55
3:C:208:VAL:HG12	3:C:219:TRP:HB2	1.89	0.54
1:T:211:ARG:NH1	5:X:159:TRP:HZ3	2.04	0.54
3:V:10:PRO:HB3	3:V:350:MET:CB	2.37	0.54
4:W:128:TYR:CE2	4:W:142:ALA:HB2	2.41	0.54
1:A:285:PRO:HB2	1:A:292:PHE:HB3	1.90	0.54
6:F:61:VAL:CG2	6:F:74:ILE:HG23	2.29	0.54
4:D:132:GLN:HG2	4:D:160:ARG:N	2.22	0.54
1:T:13:GLY:O	1:T:78:ILE:CG2	2.55	0.54
2:B:184:ILE:HD11	2:B:264:ALA:HB1	1.87	0.54
3:V:22:GLN:O	3:V:23:ILE:HB	2.08	0.54
2:B:232:LYS:O	2:B:232:LYS:HG2	2.05	0.54
6:Y:4:THR:HG23	6:Y:4:THR:O	2.07	0.54
1:T:28:GLN:NE2	4:W:33:VAL:HG13	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y:61:VAL:CA	6:Y:74:ILE:HG12	2.36	0.54
1:T:208:LEU:CG	1:T:211:ARG:NH2	2.70	0.54
1:A:242:PHE:HZ	1:A:277:LEU:HD13	1.71	0.54
1:T:105:PRO:O	1:T:106:GLU:CG	2.55	0.54
4:D:75:LEU:HG	4:D:78:ARG:CB	2.38	0.54
2:U:315:SER:HB3	6:Y:30:VAL:HG12	1.89	0.54
2:U:169:VAL:CG1	2:U:170:TYR:H	2.17	0.54
1:A:219:GLN:NE2	1:A:222:GLU:OE1	2.40	0.54
1:A:114:GLU:OE1	1:A:118:ASN:HB3	2.08	0.54
4:D:250:TYR:OH	6:F:160:VAL:HG13	2.06	0.54
2:U:278:VAL:HG13	2:U:320:GLU:CD	2.27	0.54
4:W:181:PHE:O	4:W:185:PHE:HD2	1.90	0.54
1:T:249:GLY:O	1:T:253:ILE:HB	2.07	0.54
5:E:13:THR:OG1	5:E:22:LEU:HD22	2.06	0.54
2:U:252:ILE:HD12	2:U:252:ILE:O	2.08	0.54
3:V:256:SER:O	3:V:258:LEU:HD12	2.07	0.54
3:V:331:GLN:HG2	3:V:332:ILE:N	2.21	0.54
1:A:135:ASN:OD1	1:A:397:LYS:CD	2.54	0.54
4:D:110:VAL:HG13	4:D:111:HIS:H	1.71	0.54
4:W:2:ILE:HG21	6:Y:163:GLU:CG	2.37	0.54
3:C:217:VAL:O	3:C:217:VAL:HG13	2.07	0.54
1:A:28:GLN:HE21	4:D:33:VAL:HG13	1.70	0.54
3:V:77:TYR:HB3	3:V:89:THR:H	1.71	0.54
3:C:77:TYR:HD2	3:C:90:LEU:N	2.05	0.54
5:E:13:THR:CG2	5:E:22:LEU:HD22	2.38	0.54
3:C:254:THR:HG22	3:C:255:GLU:H	1.71	0.54
3:C:20:ARG:HD3	3:C:335:LEU:HD22	1.90	0.54
3:V:253:ILE:HD11	3:V:257:SER:HB3	1.89	0.54
2:B:169:VAL:HA	2:B:174:SER:HA	1.89	0.54
7:G:67:LYS:O	7:G:68:SER:HB2	2.06	0.54
1:T:370:HIS:CG	1:T:371:HIS:H	2.26	0.54
5:X:24:ILE:HG12	5:X:135:GLN:HE22	1.73	0.54
4:W:214:ALA:HB1	4:W:222:TYR:OH	2.08	0.54
4:W:237:ARG:O	4:W:241:ILE:CG1	2.56	0.54
6:F:55:ARG:HH21	6:F:56:ASN:HD21	1.56	0.54
3:V:284:ARG:NH1	3:V:286:ASP:HB3	2.22	0.54
3:V:287:VAL:O	3:V:287:VAL:HG23	2.07	0.54
2:B:329:VAL:HG12	2:B:330:LEU:HD12	1.89	0.54
6:Y:9:LEU:HD11	6:Y:140:GLU:HG2	1.86	0.54
6:F:138:PHE:O	6:F:142:ILE:HG12	2.08	0.54
4:D:280:ALA:O	6:F:127:TYR:CD1	2.52	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:6:VAL:O	4:D:6:VAL:HG12	2.06	0.54
1:A:390:PHE:O	1:A:394:CYS:HB2	2.08	0.54
3:V:122:ILE:HD13	3:V:171:ALA:HB2	1.90	0.54
2:U:230:GLU:O	2:U:233:LEU:HB3	2.07	0.54
1:T:185:VAL:HG12	1:T:186:ILE:N	2.23	0.54
7:G:58:ALA:HB1	7:G:79:VAL:HG12	1.89	0.54
4:W:11:ILE:HG22	4:W:15:LEU:HG	1.88	0.54
6:F:126:MET:HB3	6:F:131:LEU:HD12	1.89	0.54
3:V:14:HIS:HE1	3:V:348:THR:OG1	1.87	0.54
1:T:236:PRO:O	1:T:334:ARG:NH1	2.39	0.54
6:Y:82:ILE:O	6:Y:86:LEU:HG	2.07	0.54
3:V:224:SER:HA	3:V:246:PRO:CA	2.31	0.54
6:Y:16:LEU:O	6:Y:18:ALA:N	2.38	0.54
1:T:395:HIS:CE1	1:T:408:CYS:HA	2.43	0.54
1:A:151:ALA:HB2	1:A:379:PHE:HE2	1.68	0.54
5:E:24:ILE:HG22	5:E:41:ILE:H	1.72	0.54
1:A:37:ILE:HG22	1:A:59:ASP:O	2.08	0.54
3:V:74:ARG:CG	3:V:95:ILE:HD11	2.38	0.54
4:W:243:LEU:O	6:Y:168:PHE:HZ	1.90	0.54
4:W:158:LYS:HD2	4:W:159:ASP:OD1	2.08	0.54
3:C:281:PHE:CD1	3:C:282:GLY:N	2.76	0.54
3:V:158:ALA:HB3	3:V:210:PHE:HE2	1.73	0.54
6:Y:34:ASN:O	6:Y:35:LYS:HG2	2.08	0.54
1:T:208:LEU:CG	1:T:211:ARG:HH21	2.17	0.54
1:A:175:THR:HG23	1:A:195:ILE:HB	1.90	0.54
2:U:236:GLU:C	6:Y:105:ARG:HG2	2.28	0.54
6:F:41:ARG:HH21	6:F:71:ARG:HH12	1.55	0.54
1:T:294:GLN:HG2	1:T:299:VAL:HG22	1.89	0.53
1:A:3:GLY:C	1:A:5:LEU:H	2.11	0.53
6:Y:20:LEU:HG	6:Y:21:CYS:N	2.24	0.53
1:T:116:PRO:O	1:T:117:LEU:HB3	2.07	0.53
1:T:181:ALA:HB1	1:T:186:ILE:HD11	1.89	0.53
1:T:137:PRO:O	1:T:397:LYS:N	2.41	0.53
4:W:132:GLN:CG	4:W:159:ASP:C	2.76	0.53
1:T:3:GLY:C	1:T:5:LEU:H	2.11	0.53
3:V:257:SER:HB2	3:V:372:VAL:H	1.74	0.53
1:A:169:ASP:CB	1:A:178:ILE:HD11	2.38	0.53
7:Z:124:VAL:HG22	7:Z:125:LEU:N	2.23	0.53
4:D:77:LYS:O	4:D:81:GLY:N	2.38	0.53
4:D:191:ALA:HB3	6:F:165:LEU:HB3	1.91	0.53
6:F:77:LYS:HE3	6:F:79:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:173:ASP:HB2	6:Y:85:ILE:HG21	1.89	0.53
3:V:172:TYR:HE2	3:V:178:GLU:O	1.90	0.53
5:X:79:LEU:HD23	5:X:164:VAL:HB	1.88	0.53
6:F:128:LYS:HA	6:F:131:LEU:HD22	1.89	0.53
3:V:14:HIS:CE1	3:V:348:THR:HG1	2.05	0.53
3:C:73:ASP:OD2	6:F:32:ARG:CZ	2.56	0.53
3:C:5:SER:CB	3:C:352:GLY:HA3	2.38	0.53
1:A:143:VAL:HG23	1:A:146:VAL:HB	1.90	0.53
3:V:102:VAL:HB	3:V:113:VAL:HA	1.90	0.53
6:Y:60:LYS:NZ	6:Y:112:TYR:CE1	2.76	0.53
3:C:146:LEU:HD12	3:C:205:VAL:C	2.17	0.53
1:A:186:ILE:HD13	2:B:205:ASN:HB3	1.90	0.53
3:C:79:TRP:O	3:C:86:TRP:HE3	1.91	0.53
1:A:169:ASP:HB2	1:A:178:ILE:HD11	1.90	0.53
7:G:124:VAL:HG22	7:G:125:LEU:N	2.23	0.53
6:F:142:ILE:HG13	6:F:143:ASP:N	2.23	0.53
1:A:135:ASN:OD1	1:A:397:LYS:HG3	2.08	0.53
5:E:94:GLU:O	5:E:98:LEU:HG	2.08	0.53
3:C:306:ASP:O	3:C:307:LYS:HB2	2.07	0.53
1:T:195:ILE:HG13	1:T:285:PRO:CG	2.37	0.53
3:V:102:VAL:CG2	3:V:103:ARG:N	2.37	0.53
3:V:172:TYR:HD2	3:V:180:PRO:CD	2.19	0.53
4:W:240:THR:OG1	4:W:241:ILE:HD12	2.08	0.53
1:T:304:ILE:HD13	1:T:316:TYR:CD1	2.43	0.53
3:C:17:ASN:O	3:C:19:ASP:N	2.36	0.53
3:C:97:ARG:CG	3:C:117:SER:OG	2.56	0.53
7:G:43:ASP:O	7:G:46:LEU:HB2	2.08	0.53
4:W:35:PHE:CE1	4:W:45:ILE:HD11	2.42	0.53
1:A:140:TYR:CE1	1:A:411:ASN:HB3	2.44	0.53
2:U:273:VAL:HG12	2:U:275:GLY:H	1.74	0.53
3:V:122:ILE:HD13	3:V:171:ALA:CB	2.39	0.53
3:V:204:TRP:O	3:V:221:SER:CB	2.56	0.53
3:C:206:HIS:NE2	3:C:222:HIS:HB2	2.24	0.53
1:T:164:THR:HA	1:T:180:VAL:CG1	2.38	0.53
1:T:180:VAL:O	1:T:181:ALA:HB2	2.07	0.53
4:W:132:GLN:HE21	4:W:159:ASP:HB3	1.73	0.53
1:T:102:ARG:HG3	4:W:38:PHE:CE2	2.44	0.53
4:W:38:PHE:HB3	4:W:249:ASP:CG	2.29	0.53
1:T:209:ARG:HG2	1:T:209:ARG:HH11	1.73	0.53
1:A:207:LEU:HD11	5:E:54:PHE:CZ	2.44	0.53
4:D:173:ASP:O	4:D:176:VAL:HB	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:137:HIS:O	6:F:141:GLU:CG	2.56	0.53
5:X:19:MET:HA	5:X:63:GLU:HB3	1.90	0.53
4:D:11:ILE:HD12	4:D:11:ILE:N	2.22	0.53
3:C:30:HIS:CG	3:C:52:ASN:O	2.62	0.53
2:U:321:LEU:CD2	2:U:340:PHE:CB	2.86	0.53
4:W:186:LYS:CD	4:W:198:VAL:N	2.58	0.53
4:W:75:LEU:HD23	4:W:78:ARG:HB3	1.88	0.53
4:W:44:HIS:O	4:W:57:VAL:HG13	2.09	0.53
1:A:409:ARG:CD	2:B:200:ARG:O	2.56	0.53
6:Y:76:VAL:HG12	6:Y:77:LYS:H	1.70	0.53
2:B:202:TYR:CD2	2:B:252:ILE:CG2	2.92	0.53
3:C:115:SER:C	3:C:145:VAL:H	2.09	0.53
3:V:319:ALA:N	6:Y:127:TYR:HH	2.06	0.53
1:T:239:VAL:CG2	5:X:4:TYR:CZ	2.83	0.53
3:V:211:SER:HB3	3:V:252:PHE:CD2	2.44	0.53
1:A:179:PRO:HD2	1:A:190:ILE:HG12	1.90	0.53
3:V:6:PHE:HE2	3:V:354:MET:CG	2.22	0.53
3:V:268:VAL:HG12	3:V:284:ARG:HA	1.91	0.53
1:T:69:LYS:HD2	1:T:72:TYR:CE1	2.42	0.53
2:U:195:LYS:O	2:U:199:LEU:HG	2.09	0.53
2:B:266:PHE:O	7:G:12:ARG:NH2	2.42	0.53
4:W:241:ILE:H	4:W:241:ILE:CD1	2.22	0.53
5:X:53:VAL:HG13	5:X:54:PHE:H	1.72	0.53
6:F:95:MET:SD	6:F:106:ARG:O	2.67	0.53
6:F:67:ILE:HG23	6:F:68:ASN:N	2.21	0.53
5:X:149:PHE:HE2	5:X:156:PRO:CD	2.22	0.53
4:W:128:TYR:OH	4:W:142:ALA:N	2.42	0.53
4:W:234:ALA:HA	4:W:237:ARG:HB2	1.91	0.53
1:T:238:LEU:HD21	1:T:280:GLU:HG2	1.90	0.53
3:V:325:HIS:CE1	3:V:353:GLY:O	2.62	0.53
1:T:177:VAL:HG12	1:T:177:VAL:O	2.09	0.53
4:D:186:LYS:HZ2	4:D:198:VAL:N	2.07	0.53
6:Y:61:VAL:CG2	6:Y:74:ILE:HG12	2.38	0.53
5:X:120:PRO:HB2	5:X:122:ASN:OD1	2.09	0.53
5:X:120:PRO:HG3	5:X:125:GLU:HB3	1.91	0.53
6:Y:67:ILE:C	6:Y:69:SER:H	2.12	0.53
3:C:168:ILE:HD13	3:C:196:PHE:HD2	1.74	0.53
1:T:211:ARG:HD2	1:T:212:GLU:N	2.16	0.53
1:T:115:PRO:HA	1:T:144:GLN:HG3	1.91	0.53
3:C:230:ASP:HB2	3:C:233:LYS:HB3	1.90	0.53
7:G:42:VAL:CG2	7:G:57:ALA:CB	2.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:45:ILE:HG13	4:W:57:VAL:HG22	1.91	0.53
4:D:150:GLU:HG2	4:D:167:THR:HA	1.90	0.53
7:Z:99:ASP:C	7:Z:103:VAL:HG23	2.29	0.53
5:E:53:VAL:HG21	5:E:166:ARG:C	2.29	0.53
4:W:131:PHE:HA	4:W:135:GLY:O	2.09	0.53
5:X:96:TYR:O	5:X:100:ILE:HG13	2.09	0.53
3:V:59:ASP:HB3	3:V:104:TRP:CD1	2.45	0.52
6:Y:51:VAL:CG2	6:Y:63:ILE:O	2.57	0.52
3:C:101:CYS:O	3:C:114:GLY:N	2.40	0.52
2:U:321:LEU:O	2:U:340:PHE:CZ	2.62	0.52
1:T:110:PHE:HB2	1:T:139:LEU:HD12	1.91	0.52
3:C:107:ASN:HB3	3:C:154:SER:HB2	1.91	0.52
3:C:153:ASN:ND2	3:C:155:VAL:HB	2.24	0.52
3:C:68:VAL:O	3:C:68:VAL:HG13	2.09	0.52
1:T:140:TYR:CB	1:T:390:PHE:HE1	2.22	0.52
2:U:322:LYS:CB	7:Z:16:VAL:HG21	2.30	0.52
5:E:149:PHE:CE2	5:E:156:PRO:HA	2.43	0.52
1:T:28:GLN:HE21	4:W:33:VAL:HG13	1.72	0.52
1:A:239:VAL:HG22	5:E:4:TYR:CZ	2.43	0.52
3:V:183:THR:CG2	3:V:184:PRO:CD	2.85	0.52
3:V:189:MET:N	3:V:190:PRO:HD3	2.24	0.52
3:V:246:PRO:HD3	7:Z:142:VAL:HG11	1.90	0.52
3:V:334:VAL:CB	3:V:338:GLY:HA2	2.40	0.52
1:A:35:ILE:HD12	1:A:62:ILE:HG23	1.88	0.52
1:A:36:ALA:HB2	1:A:73:ALA:O	2.09	0.52
1:A:28:GLN:NE2	4:D:33:VAL:HG13	2.24	0.52
4:D:33:VAL:O	4:D:44:HIS:HD2	1.92	0.52
3:C:172:TYR:CE1	3:C:174:LYS:CG	2.86	0.52
6:F:61:VAL:CG2	6:F:74:ILE:HG12	2.38	0.52
4:D:70:HIS:O	4:D:72:ALA:N	2.40	0.52
3:C:31:GLU:HB3	3:C:49:LYS:CA	2.39	0.52
1:T:285:PRO:CB	1:T:292:PHE:CB	2.85	0.52
4:D:165:PHE:O	4:D:222:TYR:HA	2.09	0.52
3:V:173:ILE:HD12	3:V:177:GLU:OE1	2.09	0.52
3:C:206:HIS:CD2	3:C:221:SER:O	2.62	0.52
3:V:10:PRO:HG3	6:Y:124:GLU:HG2	1.91	0.52
3:C:172:TYR:HD2	3:C:180:PRO:HD3	1.74	0.52
1:T:207:LEU:HD11	5:X:54:PHE:HZ	1.74	0.52
4:W:38:PHE:HB3	4:W:249:ASP:OD1	2.08	0.52
5:E:24:ILE:HA	5:E:40:ASP:HB2	1.90	0.52
3:C:131:TRP:CD1	3:C:131:TRP:N	2.76	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Z:66:THR:OG1	7:Z:71:VAL:HG11	2.08	0.52
3:V:135:LYS:CB	3:V:191:PHE:CE2	2.93	0.52
1:A:131:PHE:HZ	1:A:138:GLY:HA2	1.74	0.52
2:U:198:LEU:HD21	2:U:204:PHE:H	1.75	0.52
1:T:137:PRO:O	1:T:396:THR:C	2.48	0.52
3:C:22:GLN:O	3:C:23:ILE:HB	2.10	0.52
7:Z:133:LEU:C	7:Z:135:ALA:H	2.11	0.52
1:A:305:GLN:CG	1:A:346:ARG:HH22	2.22	0.52
3:V:223:ASP:HB3	7:Z:146:THR:CB	2.39	0.52
3:C:129:ASN:ND2	3:C:131:TRP:CZ2	2.73	0.52
2:B:337:LEU:HG	2:B:338:SER:H	1.75	0.52
4:W:282:PRO:HA	6:Y:127:TYR:HE1	1.75	0.52
2:U:238:THR:HG22	6:Y:106:ARG:NH2	2.24	0.52
7:G:42:VAL:CG2	7:G:57:ALA:HB1	2.26	0.52
4:D:228:PHE:HB2	4:D:231:HIS:HD2	1.73	0.52
3:C:31:GLU:HB3	3:C:49:LYS:CB	2.39	0.52
4:D:186:LYS:NZ	4:D:197:GLN:HB3	2.25	0.52
3:V:122:ILE:HG23	3:V:135:LYS:HB2	1.91	0.52
3:V:207:GLY:N	3:V:220:VAL:HG23	2.25	0.52
4:W:165:PHE:O	4:W:222:TYR:CD2	2.63	0.52
3:C:173:ILE:CB	3:C:176:VAL:CG2	2.86	0.52
5:E:48:TYR:O	5:E:49:PHE:HB3	2.10	0.52
3:V:332:ILE:CB	3:V:347:THR:HG22	2.38	0.52
5:E:148:VAL:HG22	5:E:160:TRP:HZ3	1.74	0.52
2:B:157:VAL:HA	2:B:167:CYS:SG	2.49	0.52
1:A:122:ASN:HA	1:A:125:TYR:HD2	1.73	0.52
3:V:107:ASN:ND2	3:V:109:LYS:CG	2.73	0.52
3:V:205:VAL:HA	3:V:221:SER:HA	1.92	0.52
5:X:16:ILE:CD1	5:X:125:GLU:HG2	2.38	0.52
3:C:56:THR:HB	3:C:100:ARG:NH1	2.25	0.52
3:C:146:LEU:HD13	3:C:206:HIS:CA	2.29	0.52
3:C:216:ARG:HD3	3:C:256:SER:HA	1.91	0.52
5:X:54:PHE:HE1	5:X:166:ARG:HD2	1.73	0.52
1:A:347:LEU:HD12	1:A:363:ILE:CD1	2.40	0.52
4:D:129:PHE:O	4:D:133:GLU:HB3	2.10	0.52
3:C:102:VAL:HA	3:C:112:ALA:O	2.10	0.52
3:C:147:SER:O	3:C:159:ALA:HB1	2.10	0.52
2:B:166:ILE:HG13	2:B:167:CYS:H	1.75	0.52
5:X:81:LYS:HB2	5:X:98:LEU:HD11	1.91	0.52
4:W:254:HIS:CD2	6:Y:160:VAL:HG13	2.45	0.52
3:V:107:ASN:HD22	3:V:109:LYS:N	2.03	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:24:ILE:CG1	5:X:135:GLN:NE2	2.70	0.52
1:A:71:THR:HG23	1:A:72:TYR:CE1	2.45	0.52
4:D:38:PHE:C	4:D:40:GLY:H	2.12	0.52
3:C:208:VAL:HG12	3:C:219:TRP:CB	2.40	0.52
3:V:8:VAL:CG1	3:V:9:GLU:H	2.18	0.52
1:T:120:PRO:CG	2:U:201:GLY:O	2.57	0.52
1:T:105:PRO:HG2	4:W:256:LYS:HE3	1.92	0.52
4:D:137:GLU:OE1	4:D:158:LYS:HE2	2.09	0.52
3:C:27:PRO:O	3:C:29:ASN:N	2.43	0.52
3:V:124:TYR:HD2	3:V:125:PHE:O	1.93	0.52
1:A:367:VAL:CG1	1:A:368:ILE:H	2.23	0.52
3:C:115:SER:N	3:C:145:VAL:HB	2.10	0.52
1:A:165:GLY:N	1:A:180:VAL:CG2	2.60	0.52
7:G:72:LYS:HD3	7:G:151:VAL:O	2.09	0.52
4:W:109:ILE:HG13	4:W:110:VAL:N	2.24	0.52
3:C:135:LYS:HD2	3:C:191:PHE:HE2	1.75	0.52
1:A:281:ILE:HD12	1:A:282:PHE:N	2.24	0.52
3:V:32:VAL:CG1	3:V:33:HIS:N	2.73	0.52
1:T:105:PRO:CG	4:W:256:LYS:CD	2.88	0.52
3:V:331:GLN:O	3:V:347:THR:HB	2.10	0.52
2:B:282:LEU:O	2:B:285:THR:OG1	2.25	0.52
3:C:24:ALA:HA	3:C:33:HIS:O	2.09	0.52
1:A:309:ILE:O	1:A:311:VAL:N	2.43	0.52
5:X:92:GLU:O	5:X:95:MET:HB2	2.10	0.52
1:T:174:VAL:CG2	1:T:175:THR:N	2.73	0.51
4:D:206:PRO:HG2	4:D:224:THR:HG22	1.92	0.51
3:V:123:CYS:HB3	3:V:133:VAL:O	1.97	0.51
3:V:222:HIS:O	3:V:246:PRO:CG	2.58	0.51
5:X:15:LEU:HB3	5:X:63:GLU:OE1	2.10	0.51
6:Y:21:CYS:O	6:Y:22:LEU:HD23	2.11	0.51
4:W:75:LEU:CD1	4:W:78:ARG:NH1	2.73	0.51
3:C:155:VAL:HG11	3:C:180:PRO:CG	2.39	0.51
3:C:173:ILE:HD12	3:C:173:ILE:N	2.25	0.51
3:C:172:TYR:CD2	3:C:180:PRO:HD3	2.44	0.51
7:G:42:VAL:HG11	7:G:57:ALA:HB3	1.91	0.51
4:D:75:LEU:HD11	4:D:78:ARG:NE	2.24	0.51
4:D:75:LEU:CD1	4:D:78:ARG:NH1	2.73	0.51
3:V:284:ARG:NH1	3:V:286:ASP:CB	2.73	0.51
6:F:102:PHE:CD1	6:F:122:HIS:HD2	2.27	0.51
2:U:155:VAL:HG13	2:U:167:CYS:O	2.11	0.51
5:X:97:THR:C	5:X:99:GLY:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2:ALA:HB3	3:C:356:ILE:O	2.10	0.51
3:C:161:SER:HB3	3:C:163:ASP:OD1	2.10	0.51
2:U:253:LYS:NZ	2:U:253:LYS:CB	2.73	0.51
3:V:32:VAL:CG1	3:V:33:HIS:H	2.23	0.51
1:T:140:TYR:CE1	1:T:411:ASN:HB3	2.45	0.51
7:Z:58:ALA:HB1	7:Z:79:VAL:HG12	1.92	0.51
5:E:145:CYS:O	5:E:149:PHE:CD1	2.59	0.51
5:E:41:ILE:CG2	5:E:42:VAL:N	2.73	0.51
2:B:237:THR:HG22	6:F:105:ARG:HE	1.75	0.51
5:E:5:HIS:HB2	5:E:61:LYS:HE2	1.92	0.51
5:E:88:LYS:C	5:E:90:GLN:H	2.14	0.51
5:X:16:ILE:HG22	5:X:20:ALA:O	2.11	0.51
3:C:34:ILE:O	3:C:45:VAL:HB	2.10	0.51
3:V:141:ILE:CG2	3:V:142:ARG:N	2.73	0.51
1:T:164:THR:HA	1:T:180:VAL:HG11	1.93	0.51
1:T:240:LYS:C	1:T:242:PHE:N	2.63	0.51
4:D:75:LEU:CG	4:D:78:ARG:HB3	2.41	0.51
3:C:32:VAL:CG1	3:C:33:HIS:N	2.73	0.51
1:A:130:MET:HA	1:A:133:SER:OG	2.09	0.51
1:A:209:ARG:HG2	1:A:209:ARG:HH11	1.75	0.51
1:T:233:TYR:CZ	1:T:276:PHE:HB3	2.45	0.51
1:A:207:LEU:HD12	5:E:54:PHE:CZ	2.46	0.51
3:C:5:SER:HB3	3:C:352:GLY:CA	2.40	0.51
4:D:181:PHE:O	4:D:185:PHE:CD2	2.60	0.51
2:B:162:GLY:O	2:B:163:VAL:HG12	2.11	0.51
3:V:100:ARG:CG	3:V:146:LEU:HA	2.41	0.51
1:A:102:ARG:CD	4:D:38:PHE:CE2	2.94	0.51
3:C:259:VAL:CG2	3:C:269:LEU:HD12	2.40	0.51
7:Z:72:LYS:HD3	7:Z:151:VAL:O	2.10	0.51
4:W:161:VAL:HG12	4:W:162:THR:N	2.26	0.51
4:W:165:PHE:CZ	4:W:247:PHE:CE2	2.99	0.51
3:C:176:VAL:CG2	3:C:177:GLU:N	2.73	0.51
3:V:257:SER:O	3:V:258:LEU:HD12	2.11	0.51
1:A:211:ARG:CD	5:E:159:TRP:CZ3	2.89	0.51
4:D:75:LEU:CD2	4:D:76:LEU:N	2.73	0.51
7:G:87:LYS:O	7:G:88:ALA:HB2	2.11	0.51
1:T:219:GLN:NE2	1:T:259:ILE:O	2.43	0.51
4:D:270:THR:HA	4:D:273:PHE:HB2	1.91	0.51
1:T:143:VAL:HG23	1:T:146:VAL:HB	1.92	0.51
3:C:139:LYS:HB3	3:C:140:PRO:HA	1.92	0.51
3:V:189:MET:N	3:V:190:PRO:CD	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:253:ILE:HD12	1:T:272:GLY:HA3	1.91	0.51
4:D:45:ILE:CG1	4:D:57:VAL:HG21	2.34	0.51
1:A:193:ILE:HG23	1:A:292:PHE:CE1	2.46	0.51
1:T:133:SER:OG	1:T:134:PHE:N	2.43	0.51
5:E:158:LYS:HG3	5:E:158:LYS:O	2.09	0.51
3:V:6:PHE:HB3	3:V:7:LEU:HD23	1.91	0.51
1:A:82:ILE:CG1	1:A:115:PRO:HG2	2.40	0.51
3:V:269:LEU:CA	3:V:283:GLY:HA3	2.39	0.51
3:V:30:HIS:ND1	3:V:54:GLN:HA	2.25	0.51
3:V:162:CYS:HB3	6:Y:45:GLU:OE2	2.10	0.51
1:T:368:ILE:CG2	1:T:369:THR:N	2.73	0.51
2:U:364:ILE:O	2:U:368:LYS:CB	2.58	0.51
3:C:11:ILE:HG23	3:C:26:CYS:O	2.10	0.51
1:T:174:VAL:HG22	1:T:193:ILE:O	2.03	0.51
3:V:134:CYS:SG	3:V:135:LYS:N	2.83	0.51
2:U:321:LEU:HD11	2:U:340:PHE:HB2	1.89	0.51
3:C:14:HIS:O	3:C:331:GLN:CD	2.49	0.51
1:T:304:ILE:HD12	1:T:316:TYR:HE1	1.68	0.51
1:A:193:ILE:HG23	1:A:292:PHE:CD1	2.46	0.51
1:T:207:LEU:CD1	5:X:54:PHE:CZ	2.88	0.51
4:W:132:GLN:HG3	4:W:160:ARG:CA	2.40	0.51
3:V:230:ASP:O	3:V:235:MET:HA	2.11	0.51
2:U:180:ARG:NH1	2:U:285:THR:HA	2.26	0.51
3:V:14:HIS:CE1	3:V:348:THR:CB	2.94	0.51
6:F:70:VAL:HB	6:F:118:ILE:HB	1.92	0.51
1:T:174:VAL:CG2	1:T:175:THR:H	2.24	0.51
6:Y:61:VAL:HG22	6:Y:74:ILE:HG12	1.93	0.51
1:A:406:SER:O	1:A:408:CYS:N	2.39	0.51
3:V:248:LEU:HB2	3:V:262:GLY:CA	2.41	0.51
4:W:196:PRO:HD3	4:W:231:HIS:CE1	2.46	0.51
4:W:186:LYS:HZ3	4:W:199:LEU:CD1	2.23	0.51
1:T:114:GLU:CB	1:T:118:ASN:ND2	2.73	0.51
3:V:253:ILE:HB	3:V:342:CYS:HG	1.73	0.51
3:C:37:LYS:O	3:C:38:SER:HB2	2.10	0.51
6:F:4:THR:O	6:F:4:THR:HG23	2.10	0.51
3:C:6:PHE:HB3	3:C:7:LEU:HD23	1.92	0.51
3:V:358:ASP:OD1	3:V:360:ARG:N	2.43	0.51
5:X:120:PRO:C	5:X:122:ASN:H	2.14	0.51
3:C:247:LEU:CB	3:C:261:ALA:O	2.45	0.51
1:T:134:PHE:HD1	4:W:256:LYS:HD3	1.76	0.51
3:V:355:SER:O	3:V:356:ILE:HD13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:128:TYR:CE2	4:D:142:ALA:HB2	2.46	0.51
1:T:371:HIS:C	1:T:373:GLN:H	2.14	0.51
4:D:186:LYS:HB2	4:D:198:VAL:O	2.11	0.51
4:D:198:VAL:CG1	4:D:224:THR:O	2.58	0.51
4:W:241:ILE:N	4:W:241:ILE:CD1	2.73	0.51
1:T:63:GLY:O	1:T:65:GLU:N	2.35	0.51
3:V:118:ARG:HG3	3:V:142:ARG:O	2.11	0.51
6:F:62:LEU:HG	6:F:63:ILE:N	2.24	0.51
2:B:168:PRO:HG3	2:B:178:LEU:O	2.10	0.51
5:E:53:VAL:HG23	5:E:167:GLN:O	2.11	0.51
1:A:77:PRO:O	1:A:84:GLU:HB2	2.11	0.51
2:U:263:GLU:OE2	2:U:263:GLU:N	2.43	0.51
1:T:321:LEU:CD1	1:T:373:GLN:OE1	2.59	0.51
4:D:165:PHE:CZ	4:D:247:PHE:CZ	2.79	0.51
4:D:223:ILE:CG2	4:D:224:THR:N	2.73	0.51
2:B:253:LYS:NZ	2:B:253:LYS:CB	2.73	0.51
5:X:24:ILE:HG12	5:X:135:GLN:HE21	1.74	0.51
6:F:16:LEU:O	6:F:18:ALA:N	2.40	0.51
3:C:148:LEU:CD2	3:C:159:ALA:CB	2.76	0.51
3:C:125:PHE:HB2	3:C:132:TRP:CZ2	2.46	0.51
4:W:158:LYS:HG3	4:W:159:ASP:CG	2.32	0.51
3:V:252:PHE:CD2	3:V:258:LEU:HD11	2.41	0.51
4:D:274:LEU:HD13	6:F:101:PHE:CE1	2.46	0.51
7:Z:87:LYS:O	7:Z:88:ALA:HB2	2.10	0.51
6:F:95:MET:HA	6:F:104:LEU:HD21	1.93	0.51
4:W:85:VAL:HG21	4:W:96:LEU:HD22	1.93	0.51
3:V:206:HIS:NE2	3:V:222:HIS:HB2	2.25	0.50
5:X:16:ILE:HG13	5:X:125:GLU:CG	2.41	0.50
6:F:22:LEU:HD22	6:F:67:ILE:HD12	1.94	0.50
6:Y:127:TYR:O	6:Y:131:LEU:CD1	2.40	0.50
1:A:186:ILE:CG2	1:A:189:CYS:HB2	2.42	0.50
3:C:10:PRO:CB	3:C:350:MET:HA	2.40	0.50
2:U:318:GLU:OE2	3:V:97:ARG:NH1	2.37	0.50
7:G:56:GLN:O	7:G:59:LEU:HG	2.11	0.50
1:A:242:PHE:CE1	1:A:277:LEU:HD22	2.46	0.50
5:X:168:PHE:CE1	5:X:169:MET:HG2	2.46	0.50
3:V:347:THR:N	3:V:355:SER:HB3	2.17	0.50
2:U:169:VAL:CG1	2:U:170:TYR:N	2.73	0.50
1:T:368:ILE:O	1:T:369:THR:OG1	2.26	0.50
4:W:270:THR:HA	4:W:273:PHE:HB2	1.91	0.50
1:A:246:ASP:OD1	1:A:273:TYR:OH	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:202:HIS:C	4:D:204:GLU:H	2.15	0.50
1:A:99:LYS:HD2	4:D:1:MET:SD	2.51	0.50
6:Y:23:GLU:CA	6:Y:120:ASN:CB	2.90	0.50
3:V:77:TYR:HB3	3:V:89:THR:N	2.25	0.50
4:W:165:PHE:CE2	4:W:225:PHE:CE2	2.98	0.50
3:C:334:VAL:HG12	3:C:335:LEU:N	2.19	0.50
1:A:281:ILE:HD12	1:A:281:ILE:C	2.30	0.50
3:C:8:VAL:CG1	3:C:9:GLU:H	2.21	0.50
1:T:305:GLN:CG	1:T:346:ARG:HH22	2.24	0.50
3:V:354:MET:SD	3:V:355:SER:N	2.83	0.50
1:A:205:GLN:HG2	1:A:209:ARG:NH2	2.26	0.50
4:D:115:MET:HE3	4:D:118:ARG:NH1	2.26	0.50
4:W:201:SER:HB2	4:W:204:GLU:O	2.11	0.50
4:W:2:ILE:CG2	6:Y:163:GLU:HG2	2.41	0.50
4:D:181:PHE:CD1	4:D:255:ILE:HD13	2.46	0.50
5:E:6:SER:N	5:E:65:ASP:OD1	2.36	0.50
1:T:13:GLY:C	1:T:78:ILE:HG21	2.31	0.50
1:T:324:GLY:O	1:T:325:SER:HB3	2.11	0.50
5:E:106:PRO:O	5:E:119:LYS:HB2	2.11	0.50
3:V:180:PRO:HD2	3:V:189:MET:SD	2.51	0.50
6:Y:55:ARG:HH21	6:Y:56:ASN:ND2	2.09	0.50
1:A:82:ILE:HG13	1:A:115:PRO:CD	2.40	0.50
7:Z:116:SER:N	7:Z:117:PRO:CD	2.74	0.50
2:B:343:ARG:HH21	3:C:94:ARG:CA	2.25	0.50
4:D:107:ASP:O	4:D:110:VAL:HG12	2.11	0.50
4:D:17:LEU:O	4:D:17:LEU:HG	2.11	0.50
1:T:294:GLN:HG2	1:T:299:VAL:CG2	2.41	0.50
3:V:70:CYS:SG	3:V:71:GLY:N	2.84	0.50
2:B:202:TYR:CE2	2:B:252:ILE:CD1	2.94	0.50
4:D:41:VAL:CG1	4:D:59:ILE:CG1	2.90	0.50
4:W:75:LEU:CD2	4:W:76:LEU:N	2.73	0.50
3:C:104:TRP:CE3	3:C:111:PHE:HB3	2.47	0.50
3:V:337:GLY:O	3:V:342:CYS:N	2.44	0.50
1:A:347:LEU:HD12	1:A:363:ILE:HD13	1.93	0.50
5:E:78:CYS:O	5:E:82:LEU:HD22	2.12	0.50
4:W:267:ARG:O	4:W:271:SER:N	2.35	0.50
3:V:137:ILE:CD1	3:V:169:PHE:CD2	2.92	0.50
1:T:27:PRO:O	1:T:29:PHE:N	2.44	0.50
2:U:162:GLY:O	2:U:163:VAL:HG12	2.11	0.50
2:B:274:GLU:OE1	2:B:274:GLU:HA	2.11	0.50
3:V:190:PRO:O	3:V:191:PHE:C	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:151:HIS:NE2	3:V:214:GLY:HA2	2.26	0.50
4:D:45:ILE:CG2	4:D:55:VAL:CG1	2.88	0.50
1:A:186:ILE:HD13	2:B:205:ASN:CB	2.41	0.50
1:T:92:PHE:O	1:T:96:VAL:HG23	2.12	0.50
6:F:73:SER:HB2	6:F:112:TYR:HD2	1.75	0.50
1:T:87:ASP:OD1	4:W:264:THR:HG22	2.10	0.50
3:V:144:THR:OG1	6:Y:28:GLN:CD	2.50	0.50
4:D:241:ILE:H	4:D:241:ILE:CD1	2.23	0.50
5:E:5:HIS:CD2	5:E:58:TYR:CZ	2.99	0.50
6:F:162:GLU:C	6:F:164:PHE:H	2.15	0.50
4:D:212:THR:HG22	4:D:213:ASP:H	1.76	0.50
7:G:35:ALA:HA	7:G:61:ASN:HD22	1.74	0.50
1:A:204:ILE:HG21	1:A:227:VAL:HG11	1.92	0.50
3:C:257:SER:C	3:C:258:LEU:HD12	2.32	0.50
4:W:11:ILE:CG2	4:W:15:LEU:HG	2.42	0.50
1:T:20:GLY:HA3	1:T:378:TRP:CZ2	2.46	0.50
1:A:313:ARG:CB	1:A:314:PRO:HD3	2.31	0.50
4:D:106:LYS:HD2	4:D:106:LYS:C	2.32	0.50
2:B:220:LEU:HD22	2:B:258:ARG:NE	2.26	0.50
4:D:2:ILE:O	4:D:254:HIS:NE2	2.42	0.50
4:D:2:ILE:HG21	6:F:163:GLU:CG	2.41	0.50
5:E:62:ASN:O	5:E:65:ASP:HB2	2.11	0.50
3:C:217:VAL:HG12	3:C:229:ALA:O	2.12	0.50
3:V:327:ASN:HB2	3:V:351:ASP:CG	2.30	0.50
7:G:122:SER:OG	7:G:123:ALA:N	2.45	0.50
1:T:193:ILE:HG21	1:T:292:PHE:CZ	2.43	0.50
3:V:185:TRP:CZ2	3:V:210:PHE:HE1	2.29	0.50
1:A:95:GLN:O	1:A:100:TYR:CD2	2.62	0.50
4:W:109:ILE:HG13	4:W:110:VAL:H	1.77	0.50
3:V:258:LEU:N	3:V:270:PHE:O	2.44	0.50
4:D:142:ALA:HB3	4:D:154:VAL:CG2	2.41	0.50
3:C:329:VAL:CG1	3:C:330:SER:H	2.24	0.50
5:X:81:LYS:HB2	5:X:98:LEU:HD13	1.93	0.50
4:W:95:LEU:HD11	4:W:97:TYR:CE1	2.46	0.50
7:G:120:ASN:C	7:G:122:SER:H	2.15	0.50
4:W:236:ALA:C	4:W:238:ASP:H	2.15	0.50
1:T:194:PRO:C	1:T:195:ILE:HG12	2.32	0.50
1:T:194:PRO:O	1:T:195:ILE:HD13	2.12	0.50
1:A:131:PHE:HB3	1:A:400:TYR:CZ	2.47	0.50
4:D:36:ALA:CB	4:D:42:LEU:CD2	2.86	0.50
3:C:332:ILE:CG1	3:C:347:THR:HG22	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:199:LEU:HB2	4:W:224:THR:OG1	2.11	0.50
3:C:335:LEU:HB2	3:C:344:GLN:O	2.11	0.50
5:E:5:HIS:CB	5:E:61:LYS:HE2	2.42	0.50
4:D:95:LEU:HD11	4:D:97:TYR:CE1	2.46	0.50
2:B:169:VAL:HG22	2:B:174:SER:HB3	1.94	0.50
2:U:273:VAL:HG12	2:U:274:GLU:N	2.27	0.50
1:T:147:LEU:C	1:T:149:LEU:H	2.16	0.50
3:V:99:ALA:N	3:V:115:SER:HB2	2.26	0.50
6:Y:35:LYS:HB3	6:Y:36:PRO:CD	2.41	0.50
3:C:76:ALA:C	3:C:77:TYR:CD1	2.86	0.50
5:X:104:PRO:O	5:X:111:PHE:HB2	2.12	0.50
1:T:304:ILE:HD13	1:T:316:TYR:CE1	2.46	0.50
3:C:170:SER:O	3:C:191:PHE:HA	2.12	0.50
3:C:172:TYR:H	3:C:191:PHE:HD1	1.60	0.50
2:U:253:LYS:HZ3	2:U:253:LYS:HB3	1.77	0.50
1:A:170:SER:HA	1:A:176:HIS:ND1	2.27	0.50
1:T:203:PHE:CE1	5:X:54:PHE:CE1	3.00	0.50
5:E:152:GLN:HB3	5:E:155:LYS:HD2	1.92	0.50
3:V:194:LEU:H	3:V:194:LEU:HD12	1.76	0.50
3:V:104:TRP:CE3	3:V:111:PHE:HB3	2.47	0.49
3:V:173:ILE:HB	3:V:176:VAL:CG2	2.40	0.49
6:Y:73:SER:OG	6:Y:109:VAL:HG21	2.11	0.49
2:U:311:PRO:HB3	6:Y:32:ARG:HD2	1.94	0.49
1:T:112:LEU:H	1:T:139:LEU:HD21	1.76	0.49
3:C:173:ILE:CG2	3:C:176:VAL:CG2	2.88	0.49
1:A:211:ARG:CG	1:A:212:GLU:H	2.25	0.49
7:Z:80:LEU:HG	7:Z:84:ILE:HD11	1.92	0.49
5:E:53:VAL:HG13	5:E:54:PHE:N	2.27	0.49
7:G:122:SER:O	7:G:123:ALA:HB3	2.12	0.49
5:X:24:ILE:HD11	5:X:26:SER:HB2	1.93	0.49
6:F:67:ILE:C	6:F:69:SER:H	2.14	0.49
4:D:35:PHE:CE2	4:D:43:TYR:CD1	3.00	0.49
3:V:248:LEU:HD23	3:V:263:HIS:H	1.76	0.49
3:V:76:ALA:C	3:V:77:TYR:CD1	2.86	0.49
5:X:157:SER:O	5:X:159:TRP:N	2.35	0.49
4:W:280:ALA:CB	6:Y:126:MET:SD	2.97	0.49
4:W:237:ARG:C	4:W:241:ILE:CD1	2.76	0.49
3:V:243:GLU:CB	7:Z:137:GLY:HA3	2.34	0.49
3:V:219:TRP:HH2	3:V:237:VAL:HG13	1.76	0.49
2:U:289:ALA:O	2:U:291:ILE:HG12	2.12	0.49
7:G:64:ILE:HG23	7:G:149:LYS:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y:162:GLU:C	6:Y:164:PHE:H	2.16	0.49
4:D:202:HIS:ND1	4:D:220:ILE:O	2.46	0.49
1:A:165:GLY:H	1:A:180:VAL:CB	2.26	0.49
1:T:35:ILE:HB	1:T:62:ILE:HG22	1.93	0.49
3:C:254:THR:CB	3:C:257:SER:HB2	2.43	0.49
1:T:120:PRO:CD	2:U:202:TYR:CE1	2.96	0.49
4:D:241:ILE:CD1	4:D:241:ILE:N	2.73	0.49
1:A:252:TRP:O	1:A:254:LYS:HG3	2.13	0.49
4:W:16:ALA:HB1	4:W:20:GLU:OE1	2.13	0.49
4:D:170:LYS:HE2	4:D:170:LYS:HA	1.94	0.49
3:V:104:TRP:HA	3:V:111:PHE:HA	1.93	0.49
1:A:35:ILE:CD1	1:A:62:ILE:CG2	2.84	0.49
3:V:77:TYR:CD1	3:V:77:TYR:N	2.81	0.49
1:T:271:VAL:HG12	1:T:272:GLY:N	2.28	0.49
3:C:14:HIS:N	3:C:331:GLN:OE1	2.45	0.49
4:W:246:THR:O	4:W:250:TYR:N	2.44	0.49
4:W:243:LEU:O	6:Y:168:PHE:CZ	2.65	0.49
1:A:304:ILE:HG12	1:A:315:LEU:HD23	1.94	0.49
3:C:239:THR:CA	3:C:279:LEU:HD12	2.42	0.49
3:V:147:SER:O	3:V:159:ALA:HB1	2.13	0.49
3:V:176:VAL:HG23	3:V:177:GLU:N	2.26	0.49
6:Y:61:VAL:HA	6:Y:74:ILE:HG12	1.93	0.49
4:D:45:ILE:CD1	4:D:45:ILE:H	2.16	0.49
1:T:89:MET:HE1	1:T:92:PHE:CD2	2.46	0.49
3:C:172:TYR:CE2	3:C:178:GLU:C	2.86	0.49
6:F:41:ARG:NH2	6:F:71:ARG:NH1	2.60	0.49
4:D:80:TYR:HB2	4:D:84:LEU:HB2	1.94	0.49
2:B:344:ILE:O	3:C:74:ARG:NH2	2.46	0.49
1:T:283:PHE:O	1:T:284:HIS:ND1	2.45	0.49
4:D:130:GLN:O	4:D:134:GLU:HB2	2.13	0.49
3:C:360:ARG:C	3:C:362:LEU:N	2.65	0.49
4:W:185:PHE:CE1	6:Y:161:ALA:HA	2.48	0.49
2:U:343:ARG:HH21	3:V:94:ARG:HA	1.76	0.49
1:T:348:LYS:C	1:T:350:SER:H	2.14	0.49
5:X:78:CYS:C	5:X:82:LEU:HB3	2.31	0.49
3:V:163:ASP:C	3:V:164:PHE:CD2	2.86	0.49
3:C:194:LEU:HD12	3:C:194:LEU:H	1.76	0.49
1:T:193:ILE:CG2	1:T:194:PRO:HD2	2.39	0.49
1:T:194:PRO:O	1:T:195:ILE:CG1	2.60	0.49
3:V:76:ALA:C	3:V:77:TYR:CG	2.86	0.49
3:C:113:VAL:O	3:C:114:GLY:O	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:247:PHE:HA	4:W:250:TYR:HB3	1.95	0.49
4:W:75:LEU:HD11	4:W:78:ARG:NE	2.28	0.49
1:T:130:MET:HA	1:T:133:SER:OG	2.12	0.49
1:A:167:VAL:O	1:A:178:ILE:O	2.30	0.49
6:Y:8:TYR:HE1	6:Y:53:ILE:O	1.96	0.49
2:B:180:ARG:NH1	2:B:285:THR:HA	2.27	0.49
3:V:140:PRO:CD	3:V:169:PHE:HZ	2.24	0.49
3:V:144:THR:HG1	6:Y:28:GLN:CD	2.16	0.49
6:F:94:MET:HB3	6:F:104:LEU:CD1	2.42	0.49
6:Y:63:ILE:HD13	6:Y:72:VAL:HG13	1.94	0.49
3:V:77:TYR:CB	3:V:89:THR:H	2.26	0.49
3:C:77:TYR:HB3	3:C:89:THR:N	2.27	0.49
5:X:104:PRO:HB2	5:X:111:PHE:CB	2.31	0.49
3:C:284:ARG:NH1	3:C:286:ASP:HB3	2.27	0.49
3:V:10:PRO:CB	3:V:350:MET:O	2.60	0.49
3:V:78:VAL:HG12	3:V:79:TRP:N	2.28	0.49
3:C:265:CYS:O	3:C:325:HIS:HB2	2.13	0.49
1:A:129:ILE:O	1:A:133:SER:N	2.45	0.49
4:W:265:ARG:HB3	6:Y:145:GLU:OE2	2.12	0.49
3:V:31:GLU:HB3	3:V:49:LYS:CA	2.43	0.49
4:D:236:ALA:C	4:D:238:ASP:H	2.15	0.49
3:V:321:LEU:HB2	3:V:326:LYS:HD3	1.95	0.49
1:A:147:LEU:C	1:A:149:LEU:H	2.16	0.49
1:A:388:PRO:O	1:A:391:TYR:HB2	2.13	0.49
4:W:170:LYS:HE2	4:W:170:LYS:HA	1.93	0.49
3:V:135:LYS:HG3	3:V:191:PHE:CZ	2.44	0.49
3:V:151:HIS:HB3	3:V:156:LEU:O	2.13	0.49
3:V:158:ALA:HB3	3:V:210:PHE:CE2	2.48	0.49
3:V:206:HIS:CD2	3:V:222:HIS:HB2	2.48	0.49
3:V:360:ARG:O	3:V:362:LEU:N	2.45	0.49
3:C:77:TYR:HB3	3:C:89:THR:CA	2.41	0.49
1:T:211:ARG:HD2	1:T:212:GLU:CB	2.43	0.49
4:W:165:PHE:CZ	4:W:225:PHE:CE2	3.01	0.49
3:C:20:ARG:CD	3:C:335:LEU:HD22	2.42	0.49
1:T:241:GLU:C	1:T:243:ASN:N	2.46	0.49
4:D:166:SER:O	4:D:167:THR:C	2.44	0.49
7:G:124:VAL:HG23	7:G:126:LEU:HD12	1.94	0.49
5:E:148:VAL:HG22	5:E:160:TRP:CZ3	2.48	0.49
1:T:283:PHE:CZ	1:T:334:ARG:HG3	2.47	0.49
4:D:182:MET:HG3	4:D:200:PHE:HE1	1.77	0.49
1:A:125:TYR:HD1	6:F:97:ARG:HH21	1.58	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:LEU:HB2	1:A:377:VAL:HG13	1.94	0.49
2:B:217:LYS:O	2:B:221:CYS:HB2	2.13	0.49
4:D:36:ALA:HB1	4:D:42:LEU:CD2	2.32	0.49
5:E:63:GLU:HA	5:E:66:ARG:CD	2.35	0.49
1:T:110:PHE:O	1:T:139:LEU:HG	2.11	0.49
3:C:212:ALA:HB2	3:C:339:LYS:CB	2.43	0.49
1:T:105:PRO:O	1:T:106:GLU:HG2	2.13	0.49
1:A:208:LEU:CG	1:A:211:ARG:NH2	2.76	0.49
4:W:106:LYS:C	4:W:108:SER:N	2.47	0.49
1:A:120:PRO:CB	2:B:201:GLY:HA3	2.43	0.49
3:V:139:LYS:HB3	3:V:140:PRO:HA	1.93	0.49
4:W:202:HIS:C	4:W:204:GLU:H	2.15	0.49
5:E:5:HIS:CD2	5:E:59:GLU:O	2.65	0.49
7:Z:9:ALA:O	7:Z:10:ARG:HB2	2.11	0.49
2:U:200:ARG:HD2	2:U:257:GLU:OE2	2.13	0.49
6:Y:18:ALA:HB1	7:Z:142:VAL:HA	1.95	0.49
5:X:105:ILE:HB	5:X:106:PRO:CD	2.43	0.49
6:Y:20:LEU:HD23	6:Y:20:LEU:N	2.27	0.49
3:C:115:SER:H	3:C:145:VAL:CB	2.25	0.49
1:T:62:ILE:HD12	1:T:92:PHE:HE1	1.78	0.49
1:T:186:ILE:HG22	1:T:189:CYS:HB2	1.89	0.49
3:V:165:LYS:HE3	3:V:201:SER:CB	2.43	0.49
3:C:166:CYS:HG	3:C:167:ARG:H	1.59	0.49
5:X:99:GLY:O	5:X:137:ARG:HB3	2.13	0.49
5:X:78:CYS:O	5:X:82:LEU:HD22	2.12	0.49
1:T:337:ARG:HD2	1:T:341:ARG:NH2	2.28	0.49
2:B:213:VAL:O	2:B:216:ILE:HB	2.13	0.49
3:V:124:TYR:O	3:V:132:TRP:CE3	2.66	0.48
5:X:106:PRO:HB2	5:X:119:LYS:HB3	1.95	0.48
6:F:22:LEU:HD22	6:F:67:ILE:O	2.13	0.48
1:A:132:GLU:CG	1:A:400:TYR:OH	2.53	0.48
5:X:154:ASP:O	5:X:155:LYS:HG3	2.13	0.48
1:A:180:VAL:CG1	1:A:181:ALA:H	2.11	0.48
4:W:115:MET:CE	4:W:118:ARG:HD3	2.43	0.48
6:Y:95:MET:HA	6:Y:104:LEU:CD2	2.43	0.48
5:E:66:ARG:HE	5:E:116:ILE:HG21	1.77	0.48
1:T:207:LEU:C	1:T:207:LEU:HD23	2.33	0.48
1:T:120:PRO:HD2	2:U:202:TYR:CE1	2.48	0.48
1:T:129:ILE:O	1:T:133:SER:N	2.46	0.48
2:B:289:ALA:O	2:B:291:ILE:HG12	2.13	0.48
1:A:399:ASP:O	1:A:407:ILE:HD11	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:64:ILE:O	7:G:64:ILE:HG22	2.13	0.48
6:F:82:ILE:O	6:F:86:LEU:HG	2.13	0.48
1:T:392:GLN:HA	1:T:392:GLN:OE1	2.13	0.48
4:D:36:ALA:HB2	4:D:42:LEU:HD23	1.90	0.48
4:W:75:LEU:HG	4:W:78:ARG:HB3	1.95	0.48
3:V:24:ALA:HA	3:V:33:HIS:O	2.13	0.48
1:T:106:GLU:HG3	4:W:256:LYS:CE	2.43	0.48
1:T:71:THR:HG23	1:T:72:TYR:CE1	2.49	0.48
1:A:403:ILE:HD12	1:A:407:ILE:HG21	1.95	0.48
7:G:17:ASP:O	7:G:23:LYS:HD2	2.13	0.48
3:V:226:VAL:HG13	3:V:226:VAL:O	2.13	0.48
3:V:178:GLU:O	3:V:180:PRO:HD3	2.12	0.48
3:V:77:TYR:HD2	3:V:90:LEU:N	2.11	0.48
1:T:253:ILE:CD1	1:T:272:GLY:HA3	2.43	0.48
5:X:77:GLU:OE2	5:X:174:SER:HB2	2.13	0.48
4:D:45:ILE:HG13	4:D:57:VAL:CG1	2.42	0.48
1:T:239:VAL:HG22	5:X:4:TYR:CE2	2.45	0.48
1:T:301:ASP:OD1	1:T:346:ARG:NH2	2.46	0.48
2:B:155:VAL:HG13	2:B:167:CYS:O	2.13	0.48
3:C:329:VAL:CG1	3:C:330:SER:N	2.74	0.48
5:E:87:SER:CB	5:E:153:ASN:OD1	2.60	0.48
5:X:150:ASP:C	5:X:152:GLN:H	2.17	0.48
2:B:263:GLU:N	2:B:263:GLU:OE2	2.45	0.48
5:X:135:GLN:O	5:X:139:GLU:N	2.35	0.48
3:C:219:TRP:CE2	3:C:227:CYS:CB	2.97	0.48
3:C:76:ALA:C	3:C:77:TYR:CG	2.86	0.48
4:D:45:ILE:CG2	4:D:57:VAL:CG2	2.87	0.48
3:C:10:PRO:CB	3:C:350:MET:CB	2.83	0.48
2:U:336:LYS:HG2	7:Z:21:GLU:OE2	2.13	0.48
6:Y:145:GLU:HA	6:Y:145:GLU:OE1	2.13	0.48
3:V:59:ASP:OD2	3:V:103:ARG:HA	2.14	0.48
3:V:248:LEU:HB2	3:V:262:GLY:HA3	1.95	0.48
3:V:264:ASP:HB3	3:V:266:PHE:CE2	2.48	0.48
3:C:163:ASP:N	3:C:163:ASP:OD1	2.43	0.48
3:C:77:TYR:N	3:C:77:TYR:CD1	2.81	0.48
4:W:226:VAL:CG1	4:W:227:LEU:H	2.09	0.48
1:T:77:PRO:O	1:T:84:GLU:HB2	2.13	0.48
3:C:342:CYS:SG	3:C:359:VAL:HG11	2.53	0.48
3:V:216:ARG:HG3	3:V:230:ASP:OD2	2.14	0.48
1:T:343:VAL:HG23	1:T:346:ARG:HH21	1.79	0.48
1:A:305:GLN:HG3	1:A:346:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:115:MET:CE	4:D:118:ARG:HD3	2.42	0.48
6:Y:76:VAL:CG1	6:Y:77:LYS:N	2.73	0.48
7:Z:83:LEU:HD13	7:Z:128:TRP:CG	2.49	0.48
5:E:5:HIS:NE2	5:E:59:GLU:O	2.46	0.48
1:T:286:GLU:HA	1:T:289:ASN:O	2.13	0.48
6:F:22:LEU:CD2	6:F:67:ILE:HA	2.39	0.48
1:T:253:ILE:HG23	1:T:271:VAL:O	2.14	0.48
6:F:73:SER:OG	6:F:109:VAL:HG21	2.13	0.48
5:E:158:LYS:HG3	5:E:159:TRP:CD1	2.48	0.48
4:D:129:PHE:CD2	4:D:237:ARG:HG3	2.48	0.48
5:X:74:TYR:OH	5:X:99:GLY:HA2	2.13	0.48
1:T:14:THR:HA	1:T:78:ILE:O	2.14	0.48
3:C:81:LEU:HD11	3:C:84:ARG:HA	1.94	0.48
4:D:267:ARG:O	4:D:271:SER:N	2.38	0.48
3:V:101:CYS:HB2	3:V:147:SER:HA	1.94	0.48
3:V:343:SER:CA	3:V:359:VAL:CB	2.84	0.48
5:X:105:ILE:O	5:X:108:GLU:HG2	2.13	0.48
6:F:35:LYS:CB	6:F:36:PRO:HD2	2.40	0.48
3:C:206:HIS:CD2	3:C:222:HIS:HB2	2.48	0.48
3:C:14:HIS:O	3:C:331:GLN:OE1	2.31	0.48
3:C:32:VAL:CG1	3:C:33:HIS:H	2.26	0.48
6:Y:149:MET:O	6:Y:153:VAL:HG22	2.13	0.48
7:Z:90:ASP:HA	7:Z:93:LYS:HE3	1.95	0.48
1:T:194:PRO:O	1:T:195:ILE:CD1	2.62	0.48
3:C:14:HIS:CE1	3:C:348:THR:CG2	2.97	0.48
3:V:10:PRO:CB	3:V:350:MET:C	2.82	0.48
1:A:197:GLY:O	1:A:201:THR:HG23	2.13	0.48
6:Y:55:ARG:HH21	6:Y:56:ASN:HD21	1.62	0.48
3:V:223:ASP:O	7:Z:143:ARG:HG3	2.13	0.48
1:A:260:ASN:HB3	1:A:265:LYS:H	1.77	0.48
7:Z:88:ALA:O	7:Z:90:ASP:N	2.43	0.48
4:W:179:LYS:HB3	4:W:179:LYS:HZ3	1.77	0.48
2:U:343:ARG:HH21	3:V:94:ARG:CA	2.27	0.48
1:A:337:ARG:HD2	1:A:341:ARG:NH2	2.29	0.48
2:U:86:LYS:HA	2:U:89:TRP:CZ2	2.48	0.48
6:Y:6:ARG:O	6:Y:10:SER:N	2.44	0.48
4:D:165:PHE:O	4:D:222:TYR:CD2	2.67	0.48
3:V:17:ASN:O	3:V:20:ARG:NH1	2.46	0.48
2:B:202:TYR:CE2	2:B:252:ILE:CG1	2.94	0.48
2:B:223:VAL:O	6:F:33:HIS:NE2	2.46	0.48
4:D:36:ALA:HB1	4:D:42:LEU:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:10:PRO:HB3	3:V:350:MET:HB3	1.95	0.48
4:W:152:MET:HA	4:W:164:VAL:O	2.14	0.48
4:W:163:VAL:HB	4:W:225:PHE:HB3	1.96	0.48
3:C:23:ILE:O	3:C:23:ILE:HG23	2.14	0.48
1:A:63:GLY:C	1:A:65:GLU:H	2.14	0.48
1:T:233:TYR:OH	1:T:245:TYR:CZ	2.65	0.48
1:A:140:TYR:HB3	1:A:390:PHE:HE1	1.78	0.48
2:B:322:LYS:O	2:B:324:LEU:N	2.47	0.48
1:T:172:ASP:O	1:T:196:ALA:HB1	2.14	0.48
1:T:286:GLU:OE2	1:T:293:THR:HG23	2.14	0.48
3:V:158:ALA:O	3:V:159:ALA:HB2	2.14	0.48
1:A:367:VAL:CG1	1:A:368:ILE:N	2.73	0.48
3:C:101:CYS:O	3:C:113:VAL:HA	2.14	0.48
3:C:30:HIS:HB2	3:C:51:HIS:O	2.14	0.48
1:A:189:CYS:HG	1:A:307:CYS:HG	1.61	0.48
3:C:123:CYS:SG	3:C:134:CYS:CB	3.00	0.48
3:C:334:VAL:HG21	3:C:338:GLY:O	2.14	0.48
2:U:336:LYS:CG	7:Z:21:GLU:CD	2.66	0.48
1:A:212:GLU:CD	1:A:269:ILE:HB	2.35	0.48
2:U:222:TYR:OH	2:U:259:PHE:CD2	2.61	0.48
2:U:310:TYR:O	2:U:312:GLY:N	2.47	0.48
2:U:177:HIS:ND1	2:U:178:LEU:HG	2.28	0.48
1:A:219:GLN:HE21	1:A:222:GLU:CD	2.17	0.48
1:T:219:GLN:OE1	1:T:260:ASN:C	2.52	0.48
2:B:236:GLU:OE1	6:F:105:ARG:NH2	2.46	0.48
3:C:238:ALA:HB1	3:C:279:LEU:H	1.79	0.48
1:A:348:LYS:C	1:A:350:SER:H	2.17	0.48
4:W:169:PHE:HB2	4:W:175:VAL:HG22	1.95	0.48
1:A:84:GLU:HB3	1:A:85:ASP:H	1.51	0.48
3:C:190:PRO:HG2	3:C:193:GLU:HB2	1.96	0.48
1:T:403:ILE:O	1:T:403:ILE:HG22	2.14	0.48
1:T:151:ALA:HB2	1:T:379:PHE:CE2	2.49	0.47
1:T:254:LYS:O	1:T:271:VAL:N	2.36	0.47
4:W:282:PRO:HA	6:Y:127:TYR:CE1	2.48	0.47
1:A:293:THR:O	1:A:294:GLN:HB2	2.14	0.47
1:A:298:GLU:OE1	1:A:342:THR:HG21	2.14	0.47
7:Z:91:ILE:CD1	7:Z:127:GLN:HB3	2.44	0.47
3:V:217:VAL:HG13	3:V:217:VAL:O	2.13	0.47
3:C:60:TRP:HE1	3:C:65:ASN:HA	1.79	0.47
2:B:86:LYS:HA	2:B:89:TRP:CZ2	2.48	0.47
6:F:6:ARG:O	6:F:10:SER:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:358:ASP:HB3	3:C:361:SER:OG	2.14	0.47
6:Y:123:THR:O	6:Y:123:THR:HG22	2.13	0.47
4:D:201:SER:OG	4:D:206:PRO:HD3	2.15	0.47
5:X:41:ILE:HG23	5:X:42:VAL:N	2.29	0.47
1:A:98:PHE:O	1:A:99:LYS:HB3	2.14	0.47
3:C:56:THR:H	3:C:71:GLY:HA2	1.79	0.47
5:X:149:PHE:HE2	5:X:156:PRO:HD3	1.79	0.47
4:W:115:MET:HE3	4:W:118:ARG:NH1	2.29	0.47
1:T:180:VAL:CG1	1:T:181:ALA:H	2.15	0.47
1:T:309:ILE:O	1:T:311:VAL:N	2.48	0.47
4:W:77:LYS:HG2	4:W:81:GLY:O	2.15	0.47
1:A:242:PHE:CZ	1:A:277:LEU:HD13	2.49	0.47
1:T:277:LEU:O	1:T:280:GLU:HB3	2.14	0.47
1:T:203:PHE:HE1	5:X:54:PHE:CZ	2.30	0.47
3:V:257:SER:CB	3:V:372:VAL:H	2.27	0.47
1:A:178:ILE:HG22	1:A:190:ILE:HD13	1.96	0.47
3:V:238:ALA:HB1	3:V:279:LEU:N	2.29	0.47
4:D:39:ASP:OD1	4:D:248:ARG:HD2	2.13	0.47
3:V:265:CYS:O	3:V:325:HIS:HB2	2.14	0.47
3:V:321:LEU:HD22	3:V:326:LYS:HA	1.95	0.47
3:V:115:SER:O	3:V:145:VAL:CA	2.62	0.47
6:F:39:GLU:HA	6:F:39:GLU:OE1	2.14	0.47
1:A:102:ARG:NH1	4:D:5:GLU:CB	2.76	0.47
6:Y:19:ALA:O	6:Y:22:LEU:HD21	2.13	0.47
1:T:255:GLN:HA	1:T:269:ILE:O	2.14	0.47
3:C:269:LEU:CA	3:C:283:GLY:HA3	2.44	0.47
1:T:35:ILE:CD1	1:T:60:PHE:HD2	2.27	0.47
3:C:165:LYS:HE3	3:C:201:SER:HB2	1.97	0.47
3:V:79:TRP:CZ3	3:V:88:PRO:HB3	2.49	0.47
6:F:110:GLU:OE2	6:F:111:GLY:N	2.47	0.47
1:A:82:ILE:HB	1:A:115:PRO:CB	2.42	0.47
2:U:155:VAL:HG13	2:U:167:CYS:HB2	1.96	0.47
1:A:9:VAL:CG1	1:A:111:LEU:HD22	2.45	0.47
4:D:250:TYR:OH	6:F:160:VAL:CG1	2.62	0.47
4:W:169:PHE:O	4:W:219:ASN:ND2	2.47	0.47
3:C:59:ASP:OD2	3:C:103:ARG:HA	2.14	0.47
3:V:161:SER:HB3	3:V:163:ASP:OD1	2.14	0.47
1:A:393:VAL:HG21	1:A:414:PHE:CD1	2.49	0.47
1:T:193:ILE:HG22	1:T:194:PRO:N	2.28	0.47
6:Y:110:GLU:OE2	6:Y:111:GLY:N	2.48	0.47
1:A:319:ILE:CG1	1:A:366:GLN:O	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:163:ASP:O	3:C:164:PHE:HB2	2.15	0.47
3:C:30:HIS:CE1	3:C:53:GLY:C	2.87	0.47
2:U:231:GLN:C	2:U:233:LEU:H	2.17	0.47
6:Y:9:LEU:HD12	6:Y:140:GLU:CD	2.29	0.47
3:C:8:VAL:CG1	3:C:9:GLU:N	2.78	0.47
1:T:104:GLU:HG3	1:T:105:PRO:N	2.28	0.47
1:A:219:GLN:OE1	1:A:260:ASN:C	2.53	0.47
1:T:205:GLN:CG	1:T:209:ARG:NH2	2.76	0.47
2:B:321:LEU:HD13	2:B:340:PHE:HD1	1.75	0.47
3:V:102:VAL:CG2	3:V:113:VAL:HG22	2.45	0.47
3:V:158:ALA:HB2	3:V:168:ILE:CG2	2.44	0.47
6:F:20:LEU:CG	6:F:21:CYS:H	2.03	0.47
6:F:35:LYS:CB	6:F:36:PRO:CD	2.93	0.47
1:A:131:PHE:CE1	1:A:136:VAL:O	2.68	0.47
4:W:243:LEU:N	4:W:243:LEU:HD23	2.29	0.47
3:C:257:SER:O	3:C:258:LEU:HG	2.14	0.47
1:A:194:PRO:HD2	1:A:292:PHE:CD1	2.49	0.47
3:V:37:LYS:O	3:V:38:SER:HB2	2.15	0.47
4:W:2:ILE:HG21	6:Y:163:GLU:CB	2.44	0.47
5:E:168:PHE:CE1	5:E:169:MET:HG2	2.49	0.47
4:D:131:PHE:HA	4:D:135:GLY:O	2.14	0.47
3:V:109:LYS:HZ3	3:V:176:VAL:HG23	1.80	0.47
3:C:264:ASP:HB3	3:C:266:PHE:CE2	2.49	0.47
4:D:10:ILE:O	4:D:10:ILE:HG22	2.14	0.47
1:T:165:GLY:HA2	1:T:315:LEU:HA	1.96	0.47
3:C:150:TRP:HZ3	3:C:155:VAL:O	1.98	0.47
1:T:305:GLN:HG3	1:T:346:ARG:CZ	2.44	0.47
3:C:72:THR:HG22	6:F:26:SER:OG	2.14	0.47
1:T:202:TYR:O	1:T:206:GLN:N	2.39	0.47
1:A:287:PHE:CZ	5:E:51:ALA:HB1	2.42	0.47
3:V:23:ILE:O	3:V:23:ILE:HG23	2.14	0.47
6:F:9:LEU:HD13	6:F:140:GLU:OE2	2.14	0.47
4:D:165:PHE:HB3	4:D:223:ILE:N	2.28	0.47
2:B:202:TYR:HD2	2:B:252:ILE:HG21	1.79	0.47
6:Y:62:LEU:HG	6:Y:63:ILE:N	2.30	0.47
5:X:18:ASN:ND2	5:X:19:MET:HG2	2.30	0.47
2:B:223:VAL:HB	2:B:312:GLY:O	2.14	0.47
4:D:34:THR:CG2	4:D:44:HIS:CD2	2.95	0.47
4:D:59:ILE:HD12	4:D:116:LEU:CD1	2.39	0.47
1:A:59:ASP:OD2	1:A:72:TYR:OH	2.32	0.47
5:X:157:SER:C	5:X:159:TRP:H	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:63:PRO:HB2	7:G:151:VAL:OXT	2.15	0.47
3:C:34:ILE:C	3:C:45:VAL:HB	2.34	0.47
3:C:43:VAL:O	3:C:45:VAL:HG23	2.14	0.47
5:E:50:LYS:HA	5:E:50:LYS:HD2	1.64	0.47
4:W:15:LEU:HB3	4:W:19:PHE:HE2	1.79	0.47
1:T:104:GLU:OE2	4:W:248:ARG:CZ	2.63	0.47
1:T:134:PHE:CD1	4:W:256:LYS:HB3	2.49	0.47
6:F:73:SER:HB2	6:F:112:TYR:CD2	2.49	0.47
6:F:61:VAL:HG22	6:F:74:ILE:CG1	2.43	0.47
1:A:270:ASP:HB2	5:E:159:TRP:HZ2	1.79	0.47
2:B:166:ILE:HG23	2:B:168:PRO:HD3	1.97	0.47
4:D:132:GLN:HE21	4:D:159:ASP:HB3	1.80	0.47
1:T:59:ASP:CG	1:T:72:TYR:HH	2.18	0.47
5:E:82:LEU:HA	5:E:85:CYS:SG	2.55	0.47
5:E:77:GLU:O	5:E:79:LEU:N	2.46	0.47
2:B:234:ALA:HA	2:B:240:LEU:CD1	2.45	0.47
4:D:250:TYR:OH	6:F:160:VAL:O	2.32	0.47
5:X:102:ASN:HA	5:X:137:ARG:NH1	2.28	0.47
2:U:226:ASN:HD21	2:U:228:GLU:HB3	1.78	0.47
1:A:34:CYS:HB3	1:A:76:TRP:CE2	2.49	0.47
7:G:30:GLY:HA2	7:G:66:THR:HA	1.97	0.47
3:C:228:LEU:HD23	3:C:228:LEU:C	2.34	0.47
3:V:358:ASP:OD1	3:V:360:ARG:HB2	2.15	0.47
3:V:117:SER:C	3:V:118:ARG:HD2	2.35	0.47
1:T:165:GLY:N	1:T:180:VAL:CG2	2.78	0.47
2:U:253:LYS:CE	6:Y:99:GLU:OE1	2.62	0.47
7:G:104:ASP:OD2	7:G:143:ARG:CZ	2.63	0.47
6:F:102:PHE:HB2	6:F:122:HIS:HE2	1.80	0.47
4:D:132:GLN:HE21	4:D:159:ASP:CB	2.27	0.47
4:W:48:PRO:O	4:W:50:GLY:N	2.43	0.47
5:E:96:TYR:HA	5:E:138:GLN:OE1	2.15	0.47
4:W:17:LEU:HG	4:W:17:LEU:O	2.14	0.47
3:V:344:GLN:CG	3:V:358:ASP:OD2	2.63	0.47
6:F:152:SER:O	6:F:156:ARG:CB	2.51	0.47
1:A:319:ILE:O	1:A:368:ILE:HB	2.15	0.47
3:V:89:THR:HG22	3:V:90:LEU:N	2.29	0.47
3:C:268:VAL:HG12	3:C:284:ARG:HA	1.97	0.47
1:T:309:ILE:C	1:T:311:VAL:N	2.68	0.47
1:T:304:ILE:CD1	1:T:315:LEU:O	2.56	0.47
3:C:172:TYR:HE1	3:C:174:LYS:HG3	1.78	0.47
1:T:99:LYS:HG3	4:W:5:GLU:HG2	1.92	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:GLN:HB2	1:A:268:SER:OG	2.15	0.47
5:E:24:ILE:HG22	5:E:41:ILE:N	2.30	0.47
2:B:326:LEU:HB2	2:B:335:GLU:OE1	2.15	0.47
2:U:343:ARG:HH21	3:V:94:ARG:N	2.12	0.47
1:A:8:CYS:HB2	1:A:110:PHE:CD1	2.50	0.47
1:A:37:ILE:HD13	1:A:91:ARG:HH22	1.79	0.47
5:X:156:PRO:O	5:X:157:SER:CB	2.62	0.47
6:F:64:GLU:OE1	6:F:71:ARG:NH2	2.47	0.47
1:A:11:ASP:O	1:A:18:LYS:HE2	2.15	0.47
1:A:371:HIS:C	1:A:373:GLN:H	2.14	0.47
4:D:246:THR:O	4:D:250:TYR:N	2.46	0.47
1:A:252:TRP:C	1:A:275:ARG:HH12	2.18	0.47
2:B:184:ILE:HD11	2:B:264:ALA:CB	2.45	0.47
5:E:123:LYS:HD2	5:E:123:LYS:N	2.30	0.47
1:T:150:ALA:C	1:T:152:SER:H	2.16	0.46
3:V:171:ALA:HA	3:V:191:PHE:CE1	2.50	0.46
6:Y:64:GLU:OE1	6:Y:71:ARG:NH2	2.48	0.46
6:Y:102:PHE:HB2	6:Y:122:HIS:HE2	1.80	0.46
6:Y:128:LYS:HA	6:Y:131:LEU:HD22	1.96	0.46
1:A:181:ALA:HB2	1:A:186:ILE:CD1	2.43	0.46
3:C:254:THR:HG23	3:C:341:LYS:HD3	1.96	0.46
3:C:327:ASN:HB2	3:C:351:ASP:CG	2.34	0.46
1:T:102:ARG:NH1	4:W:5:GLU:CB	2.72	0.46
3:C:78:VAL:HG12	3:C:79:TRP:N	2.30	0.46
3:V:14:HIS:HB2	3:V:25:ILE:HG22	1.97	0.46
2:B:234:ALA:HA	2:B:240:LEU:HD11	1.97	0.46
4:W:124:VAL:HG13	4:W:125:PHE:CD1	2.49	0.46
1:T:298:GLU:OE1	1:T:342:THR:HG21	2.15	0.46
1:A:68:GLU:O	1:A:70:PRO:HD3	2.14	0.46
6:Y:51:VAL:HG23	6:Y:63:ILE:HB	1.96	0.46
4:D:43:TYR:O	4:D:44:HIS:HB2	2.15	0.46
4:D:9:ARG:O	4:D:11:ILE:N	2.47	0.46
1:T:212:GLU:CD	1:T:269:ILE:HB	2.36	0.46
1:T:186:ILE:HG21	1:T:189:CYS:CB	2.43	0.46
1:T:105:PRO:CG	4:W:256:LYS:HD2	2.45	0.46
4:W:11:ILE:CG1	4:W:35:PHE:HZ	2.28	0.46
4:D:142:ALA:N	4:D:154:VAL:HG22	2.30	0.46
1:A:295:PRO:O	1:A:298:GLU:HB2	2.15	0.46
2:B:206:HIS:HB2	2:B:207:SER:H	1.17	0.46
7:Z:55:LEU:HD23	7:Z:55:LEU:H	1.80	0.46
4:D:15:LEU:HB3	4:D:19:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:165:PHE:HB2	4:D:223:ILE:O	2.15	0.46
6:F:22:LEU:CD1	6:F:67:ILE:O	2.61	0.46
3:C:161:SER:OG	3:C:162:CYS:N	2.47	0.46
3:C:259:VAL:HG12	3:C:260:ALA:N	2.31	0.46
1:T:314:PRO:C	1:T:316:TYR:H	2.19	0.46
3:C:79:TRP:CH2	3:C:88:PRO:HB3	2.50	0.46
1:A:177:VAL:O	1:A:179:PRO:CD	2.47	0.46
6:F:62:LEU:HB2	6:F:112:TYR:HE2	1.80	0.46
3:C:32:VAL:O	3:C:33:HIS:ND1	2.40	0.46
1:T:37:ILE:CA	1:T:72:TYR:HD2	2.18	0.46
1:A:205:GLN:NE2	1:A:220:SER:HB3	2.29	0.46
6:Y:76:VAL:CG1	6:Y:77:LYS:H	2.28	0.46
3:V:219:TRP:CD2	3:V:227:CYS:HB2	2.33	0.46
4:D:181:PHE:O	4:D:185:PHE:HB2	2.15	0.46
5:X:72:THR:O	5:X:75:ILE:HB	2.15	0.46
3:V:163:ASP:N	3:V:163:ASP:OD1	2.49	0.46
1:A:27:PRO:O	1:A:29:PHE:N	2.48	0.46
3:V:334:VAL:CG1	3:V:335:LEU:H	2.07	0.46
1:A:163:LEU:O	1:A:180:VAL:HG11	2.16	0.46
3:V:97:ARG:HB2	3:V:117:SER:CB	2.27	0.46
1:T:120:PRO:CG	2:U:202:TYR:CZ	2.92	0.46
5:E:26:SER:OG	5:E:139:GLU:CG	2.63	0.46
6:F:62:LEU:CB	6:F:112:TYR:HE2	2.27	0.46
7:G:124:VAL:CG1	7:G:125:LEU:H	2.05	0.46
3:V:346:CYS:SG	3:V:355:SER:HB3	2.56	0.46
1:T:9:VAL:CG1	1:T:111:LEU:HD22	2.40	0.46
4:D:80:TYR:HD2	4:D:84:LEU:HD12	1.79	0.46
1:T:11:ASP:O	1:T:18:LYS:HB2	2.15	0.46
4:W:56:MET:C	4:W:56:MET:SD	2.94	0.46
5:X:42:VAL:O	5:X:46:ILE:HG13	2.16	0.46
6:F:34:ASN:C	6:F:35:LYS:HG3	2.36	0.46
1:A:131:PHE:CZ	1:A:138:GLY:HA2	2.50	0.46
1:A:57:ASP:OD2	6:F:156:ARG:NH2	2.48	0.46
1:A:60:PHE:HE2	1:A:95:GLN:HG2	1.78	0.46
3:C:116:GLY:HA2	3:C:144:THR:HA	1.92	0.46
3:C:30:HIS:CE1	3:C:53:GLY:HA2	2.51	0.46
4:W:243:LEU:O	4:W:243:LEU:HG	2.14	0.46
1:T:62:ILE:HD12	1:T:92:PHE:CE1	2.51	0.46
3:C:36:GLU:C	3:C:42:TRP:CE3	2.88	0.46
3:C:233:LYS:HG3	3:C:274:SER:OG	2.16	0.46
4:D:166:SER:O	4:D:221:GLY:O	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:PHE:O	1:A:295:PRO:CB	2.64	0.46
2:B:343:ARG:HG2	2:B:344:ILE:H	1.81	0.46
7:G:117:PRO:O	7:G:119:ASP:N	2.49	0.46
5:X:94:GLU:HB3	5:X:98:LEU:CD1	2.45	0.46
1:T:132:GLU:CG	1:T:400:TYR:OH	2.63	0.46
2:B:169:VAL:HG22	2:B:174:SER:CB	2.46	0.46
1:A:109:TYR:HB3	1:A:390:PHE:HE2	1.79	0.46
1:T:168:ILE:CD1	1:T:177:VAL:HA	2.45	0.46
4:D:203:ARG:C	4:D:204:GLU:HG2	2.35	0.46
3:V:146:LEU:HD23	3:V:146:LEU:HA	1.82	0.46
4:D:8:ASN:OD1	4:D:11:ILE:HD11	2.15	0.46
6:Y:23:GLU:C	6:Y:120:ASN:HB3	2.36	0.46
6:Y:39:GLU:HA	6:Y:39:GLU:OE1	2.16	0.46
3:C:119:VAL:HG22	3:C:120:ILE:N	2.31	0.46
3:C:204:TRP:O	3:C:221:SER:HB3	2.15	0.46
1:T:255:GLN:HB2	1:T:268:SER:OG	2.15	0.46
5:X:53:VAL:CG2	5:X:166:ARG:HB3	2.45	0.46
3:V:110:LYS:NZ	3:V:173:ILE:CD1	2.79	0.46
1:A:5:LEU:HD22	4:D:42:LEU:HD21	1.98	0.46
4:W:110:VAL:HG13	4:W:111:HIS:H	1.79	0.46
3:V:356:ILE:O	3:V:357:TRP:HB3	2.16	0.46
4:D:125:PHE:HE2	4:D:244:ILE:HG21	1.79	0.46
3:V:259:VAL:CG1	3:V:268:VAL:O	2.63	0.46
2:B:166:ILE:HG13	2:B:167:CYS:N	2.30	0.46
1:A:219:GLN:NE2	1:A:259:ILE:O	2.48	0.46
4:D:85:VAL:HG21	4:D:96:LEU:HD22	1.97	0.46
1:T:376:ALA:O	1:T:377:VAL:HB	2.15	0.46
6:Y:51:VAL:HG22	6:Y:63:ILE:O	2.16	0.46
1:T:304:ILE:CD1	1:T:316:TYR:CD1	2.98	0.46
1:A:174:VAL:HG23	1:A:194:PRO:HA	1.97	0.46
4:D:153:TYR:CB	4:D:164:VAL:HB	2.40	0.46
2:B:343:ARG:HH21	3:C:94:ARG:N	2.14	0.46
5:E:77:GLU:C	5:E:79:LEU:H	2.18	0.46
1:A:147:LEU:CB	1:A:377:VAL:HG13	2.46	0.46
4:D:56:MET:SD	4:D:56:MET:C	2.94	0.46
2:B:292:ASP:OD1	2:B:292:ASP:N	2.49	0.46
3:V:102:VAL:O	3:V:148:LEU:O	2.33	0.46
3:V:20:ARG:CZ	3:V:335:LEU:HD22	2.46	0.46
5:X:120:PRO:O	5:X:122:ASN:N	2.37	0.46
6:F:17:GLN:O	7:G:142:VAL:CG2	2.64	0.46
1:A:89:MET:HE3	1:A:92:PHE:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y:67:ILE:HG13	6:Y:68:ASN:H	1.81	0.46
1:T:118:ASN:OD1	1:T:123:ARG:HG2	2.15	0.46
6:F:60:LYS:HG2	6:F:60:LYS:H	1.51	0.46
1:A:11:ASP:HA	1:A:113:THR:HG21	1.98	0.46
4:W:95:LEU:HD21	4:W:97:TYR:CE2	2.51	0.46
6:Y:70:VAL:HB	6:Y:118:ILE:HB	1.96	0.46
7:Z:69:GLN:O	7:Z:73:ASP:N	2.49	0.46
4:D:266:MET:SD	6:F:93:PHE:HB2	2.56	0.46
3:V:107:ASN:O	3:V:108:GLU:HB2	2.16	0.46
3:V:207:GLY:O	3:V:220:VAL:CG2	2.63	0.46
3:V:224:SER:HB2	3:V:246:PRO:HD3	1.97	0.46
1:A:103:ALA:O	1:A:105:PRO:HD3	2.16	0.46
3:C:116:GLY:HA2	3:C:144:THR:CA	2.46	0.46
4:W:80:TYR:HB2	4:W:84:LEU:HB2	1.98	0.46
3:V:37:LYS:HG3	3:V:42:TRP:CZ2	2.51	0.46
4:D:153:TYR:HB2	4:D:164:VAL:HG21	1.97	0.46
2:U:315:SER:CB	6:Y:30:VAL:HG12	2.46	0.46
1:T:17:THR:O	1:T:30:ILE:HA	2.15	0.46
1:A:233:TYR:CZ	1:A:276:PHE:HB3	2.50	0.46
7:Z:91:ILE:HD13	7:Z:127:GLN:HB3	1.98	0.46
5:X:123:LYS:HD2	5:X:123:LYS:N	2.31	0.45
4:D:34:THR:HG23	4:D:44:HIS:CB	2.45	0.45
5:X:155:LYS:HE3	5:X:155:LYS:HB2	1.59	0.45
5:X:77:GLU:C	5:X:79:LEU:H	2.18	0.45
1:T:60:PHE:CE2	1:T:95:GLN:HG2	2.51	0.45
3:V:78:VAL:HG12	3:V:80:THR:H	1.81	0.45
3:C:106:PRO:HD2	3:C:154:SER:HA	1.96	0.45
4:D:128:TYR:HE1	4:D:140:ASN:O	1.99	0.45
2:U:223:VAL:HB	2:U:312:GLY:C	2.36	0.45
1:T:167:VAL:HG13	1:T:320:VAL:CB	2.43	0.45
4:D:2:ILE:HG21	6:F:163:GLU:HB3	1.98	0.45
2:B:262:PRO:C	2:B:264:ALA:N	2.69	0.45
1:T:302:GLU:O	1:T:306:ASN:HB2	2.15	0.45
6:Y:55:ARG:NH2	6:Y:56:ASN:HD21	2.14	0.45
2:U:157:VAL:HA	2:U:167:CYS:SG	2.57	0.45
1:A:302:GLU:O	1:A:306:ASN:HB2	2.16	0.45
1:T:373:GLN:O	1:T:373:GLN:HG2	2.15	0.45
6:Y:60:LYS:NZ	6:Y:112:TYR:CD1	2.85	0.45
1:A:104:GLU:O	1:A:108:HIS:HD2	1.99	0.45
1:A:35:ILE:CG1	1:A:62:ILE:HG22	2.46	0.45
1:T:204:ILE:O	1:T:208:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:16:TRP:CE2	3:C:23:ILE:CD1	2.98	0.45
3:C:16:TRP:CE3	3:C:335:LEU:HD21	2.51	0.45
3:C:17:ASN:C	3:C:19:ASP:H	2.17	0.45
3:C:106:PRO:HB2	3:C:154:SER:HB3	1.98	0.45
7:G:107:MET:O	7:G:110:ILE:HB	2.16	0.45
5:E:139:GLU:OE1	5:E:143:ARG:HG3	2.17	0.45
1:A:145:ALA:HB2	1:A:178:ILE:HD12	1.98	0.45
6:F:73:SER:C	6:F:74:ILE:HG13	2.36	0.45
1:T:20:GLY:C	1:T:378:TRP:HZ2	2.19	0.45
1:A:11:ASP:HA	1:A:113:THR:HG23	1.98	0.45
1:A:309:ILE:C	1:A:311:VAL:N	2.69	0.45
5:X:60:ILE:CD1	5:X:60:ILE:H	2.23	0.45
2:B:291:ILE:HA	2:B:294:ARG:HD2	1.99	0.45
7:Z:108:LYS:HE3	7:Z:144:VAL:HA	1.99	0.45
3:V:351:ASP:C	3:V:353:GLY:H	2.20	0.45
3:C:27:PRO:C	3:C:29:ASN:N	2.69	0.45
2:U:276:VAL:HB	2:U:280:GLU:HB3	1.98	0.45
1:A:191:LYS:HB2	1:A:191:LYS:HE3	1.68	0.45
3:V:123:CYS:HB3	3:V:133:VAL:C	2.12	0.45
4:D:42:LEU:N	4:D:42:LEU:HD12	2.32	0.45
6:F:92:ARG:O	6:F:96:MET:HG2	2.16	0.45
5:E:99:GLY:HA3	5:E:137:ARG:O	2.16	0.45
3:V:79:TRP:O	3:V:86:TRP:HE3	1.99	0.45
1:A:175:THR:OG1	1:A:193:ILE:HB	2.17	0.45
1:A:301:ASP:OD1	1:A:346:ARG:NH2	2.49	0.45
7:Z:40:GLY:HA2	7:Z:43:ASP:HB2	1.98	0.45
4:D:196:PRO:HD3	4:D:231:HIS:CE1	2.52	0.45
4:W:48:PRO:C	4:W:50:GLY:H	2.20	0.45
3:V:238:ALA:HB1	3:V:278:LYS:HA	1.98	0.45
5:E:5:HIS:HE2	5:E:59:GLU:CG	2.30	0.45
3:C:181:ALA:HA	3:C:182:PRO:HD3	1.69	0.45
6:Y:18:ALA:O	7:Z:145:LEU:HD12	2.17	0.45
6:Y:51:VAL:HG23	6:Y:63:ILE:O	2.16	0.45
2:U:198:LEU:CD2	2:U:204:PHE:H	2.30	0.45
1:T:62:ILE:CD1	1:T:92:PHE:CE1	2.99	0.45
1:A:281:ILE:HG21	1:A:288:ALA:HB2	1.98	0.45
5:X:22:LEU:HD12	5:X:23:PRO:CD	2.40	0.45
1:T:219:GLN:HE21	1:T:222:GLU:CD	2.19	0.45
4:W:268:ALA:O	4:W:270:THR:N	2.50	0.45
2:B:169:VAL:HG22	2:B:174:SER:CA	2.45	0.45
2:B:198:LEU:CD2	2:B:204:PHE:H	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:22:LEU:CD2	6:F:67:ILE:HD12	2.47	0.45
1:A:35:ILE:CD1	1:A:60:PHE:HD2	2.20	0.45
1:T:271:VAL:CG1	1:T:274:GLU:HG2	2.46	0.45
4:W:165:PHE:CZ	4:W:225:PHE:CD2	3.05	0.45
3:C:345:PHE:CD2	3:C:359:VAL:HG22	2.52	0.45
6:F:8:TYR:HE1	6:F:53:ILE:O	1.99	0.45
3:V:250:VAL:HG23	3:V:260:ALA:HB2	1.98	0.45
3:C:319:ALA:N	6:F:127:TYR:HH	2.15	0.45
1:A:76:TRP:HA	1:A:77:PRO:HD3	1.73	0.45
6:F:129:HIS:CG	6:F:130:LYS:N	2.85	0.45
2:B:202:TYR:CE2	2:B:252:ILE:HD13	2.51	0.45
3:C:119:VAL:O	3:C:145:VAL:HG21	2.17	0.45
3:C:157:LEU:O	3:C:168:ILE:HG23	2.17	0.45
5:E:19:MET:HE1	5:E:67:THR:CB	2.44	0.45
1:T:10:VAL:O	1:T:113:THR:HG23	2.17	0.45
1:T:239:VAL:HG11	5:X:4:TYR:CD1	2.52	0.45
1:A:208:LEU:HD23	1:A:208:LEU:O	2.16	0.45
2:U:184:ILE:HD11	2:U:264:ALA:HB1	1.99	0.45
7:G:80:LEU:HG	7:G:84:ILE:HD11	1.99	0.45
4:D:268:ALA:O	4:D:270:THR:N	2.49	0.45
5:E:120:PRO:HG3	5:E:125:GLU:HB3	1.99	0.45
4:D:16:ALA:C	4:D:18:LYS:H	2.20	0.45
4:W:259:LYS:HA	4:W:262:ILE:HD12	1.99	0.45
3:V:124:TYR:N	3:V:134:CYS:HA	2.31	0.45
3:V:17:ASN:HB3	3:V:60:TRP:CD2	2.51	0.45
1:A:89:MET:HE2	1:A:93:MET:HG2	1.99	0.45
4:D:41:VAL:C	4:D:42:LEU:CG	2.86	0.45
3:C:144:THR:OG1	6:F:25:PHE:HZ	1.97	0.45
1:T:271:VAL:HG13	1:T:274:GLU:CD	2.38	0.45
5:X:104:PRO:O	5:X:111:PHE:CD1	2.70	0.45
4:D:45:ILE:HG21	4:D:55:VAL:CG1	2.47	0.45
1:T:35:ILE:HD12	1:T:62:ILE:HG23	1.98	0.45
5:E:102:ASN:HA	5:E:137:ARG:NH1	2.31	0.45
3:C:124:TYR:C	3:C:124:TYR:CD1	2.90	0.45
3:C:117:SER:O	3:C:118:ARG:HD2	2.17	0.45
1:A:208:LEU:HD22	1:A:215:ILE:HD12	1.93	0.45
4:D:132:GLN:CG	4:D:159:ASP:HA	2.35	0.45
4:D:110:VAL:CG1	4:D:111:HIS:N	2.78	0.45
2:U:206:HIS:HB2	2:U:207:SER:H	1.18	0.45
2:B:214:ARG:O	2:B:217:LYS:HB3	2.17	0.45
4:D:243:LEU:N	4:D:243:LEU:HD23	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:46:ILE:CD1	5:E:147:LYS:HD2	2.47	0.45
1:T:191:LYS:HB2	1:T:191:LYS:HE3	1.65	0.45
4:D:199:LEU:CA	4:D:224:THR:OG1	2.65	0.45
3:V:107:ASN:HB2	3:V:109:LYS:HG2	1.99	0.45
5:X:103:PHE:HD1	5:X:104:PRO:HD2	1.81	0.45
3:C:269:LEU:H	3:C:283:GLY:CA	2.20	0.45
4:W:186:LYS:HZ1	4:W:197:GLN:HB3	1.79	0.45
3:C:117:SER:O	3:C:117:SER:OG	2.31	0.45
1:A:242:PHE:CD1	5:E:50:LYS:HE2	2.52	0.45
1:A:281:ILE:C	1:A:281:ILE:CD1	2.86	0.45
1:A:134:PHE:CD1	4:D:256:LYS:HB3	2.52	0.45
6:Y:82:ILE:HG23	6:Y:83:GLU:N	2.31	0.45
3:C:217:VAL:CG1	3:C:229:ALA:HB3	2.46	0.45
1:T:174:VAL:CA	1:T:196:ALA:HB2	2.30	0.45
1:T:370:HIS:O	1:T:371:HIS:CG	2.70	0.45
3:V:123:CYS:HA	3:V:135:LYS:N	2.28	0.45
3:V:100:ARG:HG2	3:V:145:VAL:O	2.17	0.45
3:V:110:LYS:HZ2	3:V:173:ILE:CD1	2.30	0.45
5:X:24:ILE:HG22	5:X:41:ILE:H	1.82	0.45
5:X:119:LYS:HE3	5:X:126:ASP:OD2	2.17	0.45
6:F:18:ALA:CB	7:G:142:VAL:HA	2.39	0.45
5:E:99:GLY:O	5:E:137:ARG:HB3	2.16	0.45
1:T:304:ILE:HG21	1:T:316:TYR:CD2	2.49	0.45
3:C:211:SER:HB3	3:C:216:ARG:HB2	1.99	0.45
3:C:257:SER:O	3:C:258:LEU:HD12	2.17	0.45
1:A:286:GLU:HB3	1:A:292:PHE:O	2.17	0.45
1:A:208:LEU:CG	1:A:211:ARG:HH21	2.30	0.45
5:E:158:LYS:O	5:E:159:TRP:CD1	2.70	0.45
3:V:219:TRP:CD1	3:V:219:TRP:O	2.70	0.45
1:T:264:LYS:HA	1:T:264:LYS:HD3	1.55	0.45
4:D:251:LEU:O	4:D:255:ILE:HG12	2.17	0.45
1:T:398:LYS:O	1:T:402:GLU:HG3	2.16	0.45
4:D:186:LYS:HD3	4:D:198:VAL:N	2.29	0.44
6:Y:60:LYS:H	6:Y:60:LYS:HG2	1.58	0.44
1:A:104:GLU:OE1	1:A:106:GLU:HG3	2.17	0.44
1:A:21:TYR:CE1	4:D:35:PHE:CB	2.92	0.44
3:C:164:PHE:CA	3:C:203:GLY:O	2.65	0.44
4:D:45:ILE:HG23	4:D:57:VAL:HG23	2.00	0.44
5:E:101:THR:O	5:E:102:ASN:C	2.55	0.44
1:T:365:VAL:O	1:T:365:VAL:HG23	2.17	0.44
4:W:79:VAL:HG13	4:W:112:GLN:HE22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:136:VAL:CB	1:T:137:PRO:CD	2.75	0.44
3:C:16:TRP:CD2	3:C:23:ILE:HD12	2.52	0.44
3:C:252:PHE:CD2	3:C:257:SER:O	2.70	0.44
3:C:156:LEU:CD2	3:C:170:SER:CB	2.95	0.44
1:T:281:ILE:HD12	1:T:281:ILE:C	2.36	0.44
1:T:130:MET:HE3	1:T:134:PHE:HD2	1.81	0.44
6:F:73:SER:CB	6:F:112:TYR:HD2	2.30	0.44
1:A:283:PHE:CZ	1:A:334:ARG:HG3	2.52	0.44
5:E:78:CYS:O	5:E:82:LEU:HB3	2.18	0.44
6:Y:147:SER:C	6:Y:149:MET:H	2.21	0.44
4:D:194:THR:HB	4:D:230:ARG:CZ	2.47	0.44
7:Z:91:ILE:HG23	7:Z:128:TRP:CZ3	2.52	0.44
2:U:343:ARG:HG2	2:U:344:ILE:H	1.82	0.44
2:B:170:TYR:HB2	2:B:175:LEU:HD11	1.98	0.44
3:C:102:VAL:HG23	3:C:112:ALA:O	2.17	0.44
3:V:17:ASN:HB3	3:V:60:TRP:CE3	2.52	0.44
3:C:224:SER:HA	3:C:246:PRO:HA	1.99	0.44
1:A:57:ASP:O	1:A:60:PHE:CD1	2.71	0.44
4:W:144:ILE:HD12	4:W:152:MET:CB	2.47	0.44
4:W:186:LYS:HE3	4:W:197:GLN:HB3	1.99	0.44
4:W:227:LEU:CD2	4:W:231:HIS:HB3	2.48	0.44
1:T:90:GLU:CD	1:T:129:ILE:HG23	2.37	0.44
4:D:75:LEU:HG	4:D:78:ARG:HB2	1.98	0.44
6:Y:142:ILE:HG13	6:Y:143:ASP:N	2.32	0.44
4:D:181:PHE:C	4:D:185:PHE:HD2	2.20	0.44
4:D:98:ASP:CG	4:D:101:ASN:H	2.21	0.44
5:X:150:ASP:O	5:X:152:GLN:N	2.51	0.44
1:T:251:LYS:O	1:T:252:TRP:CG	2.71	0.44
3:C:367:LYS:HE3	3:C:367:LYS:HB2	1.81	0.44
1:T:175:THR:O	1:T:176:HIS:CD2	2.71	0.44
4:D:226:VAL:CG1	4:D:227:LEU:N	2.79	0.44
3:V:360:ARG:HB3	3:V:360:ARG:HE	1.53	0.44
6:Y:41:ARG:NH2	6:Y:71:ARG:NH1	2.66	0.44
4:W:224:THR:O	4:W:225:PHE:CD2	2.70	0.44
3:C:34:ILE:HG22	3:C:45:VAL:HB	1.98	0.44
1:T:313:ARG:HH11	1:T:313:ARG:HG3	1.82	0.44
3:C:155:VAL:HG11	3:C:180:PRO:HG2	1.98	0.44
1:A:280:GLU:O	1:A:280:GLU:HG3	2.18	0.44
1:T:200:ILE:HG12	1:T:281:ILE:HD13	1.98	0.44
1:T:240:LYS:HG2	1:T:241:GLU:N	2.33	0.44
3:V:357:TRP:O	3:V:357:TRP:CD1	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:134:GLN:CA	5:X:137:ARG:HG3	2.45	0.44
4:W:254:HIS:CD2	6:Y:160:VAL:CG1	3.01	0.44
6:Y:110:GLU:O	6:Y:112:TYR:N	2.38	0.44
6:Y:34:ASN:C	6:Y:35:LYS:CG	2.86	0.44
1:T:201:THR:CB	1:T:224:ALA:HB1	2.40	0.44
3:V:85:THR:O	3:V:87:LYS:HG2	2.17	0.44
1:T:186:ILE:CD1	2:U:205:ASN:HB3	2.45	0.44
1:T:203:PHE:HD2	1:T:278:GLY:HA2	1.82	0.44
4:D:122:ALA:O	4:D:125:PHE:HB2	2.17	0.44
1:A:150:ALA:HB1	1:A:379:PHE:HD2	1.82	0.44
3:C:304:ASN:N	3:C:304:ASN:OD1	2.51	0.44
1:A:107:ASP:OD2	4:D:147:ARG:NH1	2.51	0.44
1:T:293:THR:O	1:T:294:GLN:HB2	2.18	0.44
6:Y:23:GLU:C	6:Y:120:ASN:HB2	2.37	0.44
6:Y:23:GLU:HA	6:Y:120:ASN:CB	2.45	0.44
1:T:201:THR:HA	1:T:204:ILE:HD12	2.00	0.44
5:X:149:PHE:HE2	5:X:156:PRO:CG	2.09	0.44
1:T:309:ILE:O	1:T:312:ARG:HG2	2.17	0.44
3:C:211:SER:CB	3:C:216:ARG:HB2	2.48	0.44
3:V:340:ALA:C	3:V:341:LYS:HG2	2.38	0.44
5:E:47:TYR:O	5:E:48:TYR:CD1	2.70	0.44
5:E:48:TYR:C	5:E:50:LYS:H	2.21	0.44
1:T:343:VAL:HG13	1:T:363:ILE:HD11	2.00	0.44
3:V:332:ILE:O	3:V:332:ILE:HG23	2.18	0.44
3:V:332:ILE:HD12	3:V:347:THR:CG2	2.46	0.44
1:A:90:GLU:CD	1:A:129:ILE:CG2	2.86	0.44
4:W:59:ILE:HD12	4:W:116:LEU:CD1	2.43	0.44
7:Z:98:LEU:HB2	7:Z:103:VAL:HG22	1.98	0.44
5:X:22:LEU:HA	5:X:22:LEU:HD13	1.87	0.44
4:W:98:ASP:CG	4:W:101:ASN:H	2.21	0.44
5:X:74:TYR:CZ	5:X:137:ARG:HA	2.53	0.44
4:W:268:ALA:C	4:W:270:THR:N	2.71	0.44
5:X:48:TYR:C	5:X:50:LYS:H	2.21	0.44
3:V:16:TRP:CE2	3:V:23:ILE:HD12	2.53	0.44
1:A:273:TYR:N	1:A:273:TYR:CD1	2.84	0.44
4:D:243:LEU:O	6:F:168:PHE:HZ	2.01	0.44
3:C:304:ASN:O	3:C:305:LEU:HB2	2.18	0.44
3:V:304:ASN:OD1	3:V:304:ASN:N	2.50	0.44
3:C:219:TRP:O	3:C:219:TRP:CD1	2.70	0.44
4:W:199:LEU:HB2	4:W:224:THR:CG2	2.47	0.44
5:E:13:THR:OG1	5:E:22:LEU:CD2	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:110:LYS:HD3	3:C:173:ILE:HD13	2.00	0.44
6:F:55:ARG:NH2	6:F:56:ASN:ND2	2.64	0.44
1:A:343:VAL:HG23	1:A:346:ARG:HH21	1.83	0.44
4:W:203:ARG:C	4:W:204:GLU:HG2	2.37	0.44
2:B:330:LEU:HB2	2:B:335:GLU:OE2	2.18	0.44
2:B:326:LEU:HA	2:B:330:LEU:O	2.17	0.44
4:D:48:PRO:HG3	4:D:54:LYS:HD2	1.98	0.44
1:A:183:GLY:O	1:A:184:TYR:CD1	2.71	0.44
5:E:18:ASN:O	5:E:18:ASN:ND2	2.50	0.44
4:D:149:ASP:OD1	4:D:149:ASP:N	2.51	0.44
1:T:174:VAL:O	1:T:176:HIS:CE1	2.70	0.44
4:D:199:LEU:HB2	4:D:224:THR:CB	2.46	0.44
5:X:139:GLU:OE1	5:X:143:ARG:HG3	2.18	0.44
6:F:48:LEU:HD13	7:G:145:LEU:HD13	2.00	0.44
1:A:100:TYR:O	4:D:10:ILE:CD1	2.65	0.44
1:A:35:ILE:HG12	1:A:36:ALA:N	2.33	0.44
1:A:103:ALA:CA	4:D:38:PHE:CE1	3.01	0.44
3:C:250:VAL:CA	3:C:260:ALA:CB	2.87	0.44
4:W:274:LEU:HD13	6:Y:101:PHE:CE1	2.53	0.44
1:T:109:TYR:O	1:T:110:PHE:CD1	2.70	0.44
3:C:212:ALA:O	3:C:213:ASN:HB3	2.18	0.44
1:T:280:GLU:O	1:T:280:GLU:HG3	2.18	0.44
7:G:106:LEU:O	7:G:106:LEU:HG	2.18	0.44
2:U:326:LEU:HA	2:U:330:LEU:O	2.17	0.44
1:T:336:GLN:HG3	1:T:367:VAL:CB	2.48	0.44
3:V:137:ILE:O	3:V:139:LYS:N	2.50	0.44
5:E:77:GLU:OE2	5:E:174:SER:HB2	2.18	0.44
4:D:230:ARG:O	4:D:230:ARG:HG2	2.18	0.44
4:D:131:PHE:HE1	4:D:136:LYS:HE3	1.82	0.44
6:F:12:VAL:C	6:F:14:ALA:H	2.20	0.44
7:Z:69:GLN:O	7:Z:73:ASP:HB2	2.18	0.44
3:V:299:ARG:C	3:V:301:ARG:H	2.21	0.44
2:U:292:ASP:N	2:U:292:ASP:OD1	2.51	0.44
3:V:151:HIS:NE2	3:V:214:GLY:HA3	2.33	0.44
3:V:343:SER:C	3:V:359:VAL:HB	2.38	0.44
6:Y:48:LEU:HD13	7:Z:145:LEU:HB3	2.00	0.44
2:B:202:TYR:CD2	2:B:252:ILE:HG21	2.53	0.44
3:C:265:CYS:SG	3:C:327:ASN:C	2.96	0.44
2:U:336:LYS:CG	7:Z:21:GLU:CG	2.94	0.44
2:U:325:TYR:CE1	2:U:330:LEU:CD1	3.00	0.44
6:F:60:LYS:HG2	6:F:75:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:67:LEU:O	4:D:72:ALA:HB3	2.17	0.44
1:A:305:GLN:HG3	1:A:346:ARG:NH1	2.33	0.44
1:T:209:ARG:HG2	1:T:209:ARG:NH1	2.32	0.44
2:B:326:LEU:O	2:B:331:LYS:HA	2.18	0.44
1:T:125:TYR:HD1	6:Y:97:ARG:HH21	1.63	0.44
2:U:279:ALA:HB2	2:U:320:GLU:OE1	2.18	0.44
4:D:85:VAL:HG11	4:D:96:LEU:HD23	2.00	0.44
1:T:327:MET:SD	1:T:374:ARG:HG2	2.58	0.44
1:A:22:ALA:HB1	1:A:386:SER:OG	2.17	0.44
1:A:210:ASP:N	1:A:210:ASP:OD1	2.49	0.44
6:Y:20:LEU:CD2	6:Y:20:LEU:H	2.30	0.44
1:T:211:ARG:CG	1:T:212:GLU:N	2.79	0.44
3:C:274:SER:C	3:C:276:ALA:H	2.20	0.44
3:V:274:SER:C	3:V:276:ALA:H	2.21	0.44
1:T:347:LEU:HD12	1:T:363:ILE:CD1	2.47	0.44
4:D:128:TYR:CE2	4:D:154:VAL:CG2	2.89	0.44
5:X:5:HIS:CD2	5:X:58:TYR:CE2	3.05	0.44
7:G:81:LYS:O	7:G:83:LEU:N	2.50	0.44
4:W:265:ARG:C	4:W:267:ARG:H	2.20	0.44
4:W:59:ILE:HB	4:W:116:LEU:HD11	1.99	0.44
1:T:276:PHE:H	1:T:276:PHE:HD1	1.64	0.44
4:W:18:LYS:HB3	4:W:99:LEU:HD21	2.00	0.44
1:T:285:PRO:CB	1:T:292:PHE:CG	2.98	0.43
3:V:173:ILE:CD1	3:V:173:ILE:N	2.73	0.43
3:V:343:SER:O	3:V:359:VAL:N	2.51	0.43
6:F:35:LYS:HB3	6:F:36:PRO:CD	2.43	0.43
3:C:146:LEU:HD13	3:C:206:HIS:C	2.38	0.43
1:A:165:GLY:H	1:A:180:VAL:HB	1.83	0.43
5:E:19:MET:CE	5:E:67:THR:OG1	2.66	0.43
1:T:179:PRO:CB	1:T:315:LEU:HD11	2.48	0.43
1:A:197:GLY:HA2	1:A:200:ILE:HD12	2.00	0.43
6:F:110:GLU:O	6:F:112:TYR:N	2.41	0.43
1:A:82:ILE:CG1	1:A:83:VAL:H	2.29	0.43
1:A:347:LEU:CD1	1:A:362:PRO:HA	2.48	0.43
2:B:277:GLY:O	2:B:281:LEU:HB2	2.18	0.43
5:E:149:PHE:CE2	5:E:156:PRO:CB	3.01	0.43
3:V:217:VAL:HG13	3:V:219:TRP:HZ3	1.83	0.43
3:C:129:ASN:O	3:C:131:TRP:CD1	2.70	0.43
7:Z:18:GLU:HA	7:Z:23:LYS:HZ3	1.82	0.43
6:Y:12:VAL:C	6:Y:14:ALA:H	2.20	0.43
3:V:36:GLU:HB2	3:V:45:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:50:GLU:HG3	3:V:50:GLU:O	2.17	0.43
3:V:224:SER:H	3:V:246:PRO:HB3	1.83	0.43
2:B:253:LYS:HZ3	2:B:253:LYS:HB3	1.81	0.43
3:C:263:HIS:HA	3:C:328:SER:CA	2.49	0.43
6:Y:67:ILE:HG13	6:Y:68:ASN:N	2.33	0.43
1:T:116:PRO:HB3	1:T:185:VAL:HG13	1.97	0.43
1:T:238:LEU:C	1:T:240:LYS:H	2.20	0.43
6:F:112:TYR:CD1	6:F:112:TYR:N	2.86	0.43
3:V:14:HIS:CB	3:V:25:ILE:HG22	2.48	0.43
1:A:321:LEU:O	1:A:322:SER:HB2	2.18	0.43
2:U:170:TYR:CD2	2:U:170:TYR:O	2.70	0.43
1:T:87:ASP:HB2	4:W:267:ARG:HD2	1.99	0.43
2:B:222:TYR:OH	2:B:259:PHE:CD2	2.66	0.43
4:D:118:ARG:HH11	4:D:118:ARG:HB3	1.83	0.43
4:D:2:ILE:CG2	6:F:163:GLU:HG2	2.46	0.43
1:T:259:ILE:HD12	1:T:259:ILE:N	2.32	0.43
3:V:239:THR:HG22	3:V:240:LEU:N	2.33	0.43
4:D:268:ALA:C	4:D:270:THR:N	2.70	0.43
1:A:273:TYR:N	1:A:273:TYR:HD1	2.16	0.43
5:E:107:GLY:HA3	5:E:119:LYS:HD3	2.00	0.43
5:X:150:ASP:C	5:X:152:GLN:N	2.71	0.43
1:A:22:ALA:HA	1:A:382:SER:OG	2.18	0.43
2:U:256:GLY:O	2:U:260:GLU:HG3	2.18	0.43
6:Y:129:HIS:CG	6:Y:130:LYS:N	2.86	0.43
1:T:64:ASP:N	1:T:64:ASP:OD1	2.52	0.43
4:W:275:LYS:O	4:W:279:ARG:HG3	2.18	0.43
1:T:168:ILE:O	1:T:321:LEU:O	2.36	0.43
4:D:165:PHE:CE2	4:D:223:ILE:HG21	2.52	0.43
3:V:56:THR:O	3:V:58:VAL:HG23	2.18	0.43
6:Y:35:LYS:CB	6:Y:36:PRO:CD	2.96	0.43
7:G:105:LEU:O	7:G:109:TYR:HD2	2.01	0.43
4:W:239:ASN:ND2	6:Y:168:PHE:O	2.50	0.43
1:T:312:ARG:HG3	1:T:313:ARG:N	2.33	0.43
3:C:133:VAL:HB	3:C:134:CYS:H	1.68	0.43
3:C:253:ILE:HB	3:C:342:CYS:SG	2.58	0.43
3:C:172:TYR:C	3:C:172:TYR:CD1	2.91	0.43
3:C:321:LEU:HD22	3:C:326:LYS:HA	1.99	0.43
4:W:158:LYS:C	4:W:158:LYS:HD3	2.38	0.43
6:F:73:SER:O	6:F:74:ILE:HG13	2.18	0.43
3:V:4:HIS:O	3:V:354:MET:N	2.52	0.43
1:T:20:GLY:CA	1:T:378:TRP:CZ2	3.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:12:CYS:HA	1:T:17:THR:HG23	2.00	0.43
1:A:321:LEU:HB3	1:A:326:THR:CB	2.47	0.43
1:A:205:GLN:OE1	1:A:209:ARG:NH2	2.51	0.43
7:G:133:LEU:HG	7:G:134:ALA:N	2.32	0.43
3:V:304:ASN:O	3:V:305:LEU:HB2	2.18	0.43
1:A:328:PHE:HB2	1:A:331:PHE:HB2	1.99	0.43
5:X:27:GLN:O	5:X:28:PHE:CD1	2.71	0.43
2:B:93:PHE:HB3	2:B:94:GLY:H	1.52	0.43
2:U:337:LEU:HD12	2:U:337:LEU:HA	1.80	0.43
4:D:165:PHE:HD2	4:D:223:ILE:CB	2.07	0.43
1:A:71:THR:CG2	1:A:72:TYR:CE1	3.01	0.43
1:A:102:ARG:NH2	4:D:8:ASN:HA	2.33	0.43
4:W:197:GLN:HB2	4:W:226:VAL:CG2	2.47	0.43
1:T:95:GLN:O	1:T:100:TYR:CD1	2.71	0.43
3:C:125:PHE:HB2	3:C:132:TRP:CH2	2.53	0.43
4:W:11:ILE:CD1	4:W:35:PHE:HZ	2.30	0.43
3:C:78:VAL:HG12	3:C:80:THR:H	1.84	0.43
4:W:230:ARG:HG2	4:W:230:ARG:O	2.18	0.43
2:U:170:TYR:C	2:U:171:GLU:HG2	2.38	0.43
2:B:220:LEU:HD22	2:B:258:ARG:CZ	2.48	0.43
4:D:262:ILE:HG23	6:F:149:MET:CE	2.47	0.43
5:X:91:GLY:O	5:X:94:GLU:HB2	2.18	0.43
4:D:95:LEU:HD21	4:D:97:TYR:CE2	2.53	0.43
1:T:403:ILE:HB	1:T:407:ILE:HD13	2.00	0.43
1:A:153:TRP:HZ3	1:A:384:LEU:CD1	2.32	0.43
1:T:22:ALA:HB1	1:T:386:SER:OG	2.18	0.43
7:Z:27:GLU:H	7:Z:27:GLU:HG3	1.52	0.43
6:Y:61:VAL:CG2	6:Y:74:ILE:CG1	2.94	0.43
4:D:34:THR:OG1	4:D:44:HIS:CD2	2.70	0.43
4:D:8:ASN:OD1	4:D:43:TYR:OH	2.36	0.43
1:T:271:VAL:CG1	1:T:275:ARG:HG3	2.46	0.43
4:W:144:ILE:HD12	4:W:152:MET:HB3	2.00	0.43
4:W:197:GLN:O	4:W:198:VAL:HG22	2.17	0.43
1:T:76:TRP:HA	1:T:77:PRO:HD3	1.73	0.43
5:E:134:GLN:CA	5:E:137:ARG:HG3	2.46	0.43
5:E:74:TYR:CZ	5:E:137:ARG:HA	2.53	0.43
4:W:75:LEU:HD23	4:W:75:LEU:C	2.39	0.43
4:W:137:GLU:HG3	4:W:158:LYS:HA	2.00	0.43
5:E:135:GLN:O	5:E:139:GLU:N	2.35	0.43
4:W:45:ILE:CG1	4:W:57:VAL:CG2	2.95	0.43
3:V:253:ILE:CD1	3:V:257:SER:CB	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:160:TRP:C	5:E:162:CYS:N	2.72	0.43
2:U:166:ILE:HG13	2:U:167:CYS:N	2.32	0.43
1:A:128:GLU:CG	1:A:129:ILE:N	2.77	0.43
5:E:79:LEU:HA	5:E:83:GLN:H	1.83	0.43
7:G:90:ASP:HA	7:G:93:LYS:HE3	2.00	0.43
5:X:22:LEU:HA	5:X:23:PRO:HD3	1.86	0.43
5:X:94:GLU:HB3	5:X:98:LEU:HG	2.00	0.43
6:F:12:VAL:HA	6:F:15:THR:OG1	2.19	0.43
4:W:16:ALA:C	4:W:18:LYS:H	2.22	0.43
4:D:47:ASN:ND2	4:D:51:ASP:O	2.42	0.43
3:V:81:LEU:HD11	3:V:84:ARG:HA	1.99	0.43
6:Y:107:LYS:HA	6:Y:108:PRO:HD3	1.90	0.43
1:T:373:GLN:HE21	1:T:373:GLN:HB3	1.65	0.43
4:D:186:LYS:HZ2	4:D:197:GLN:HB3	1.83	0.43
4:D:199:LEU:H	4:D:224:THR:HG1	1.63	0.43
3:V:245:LEU:HD12	3:V:263:HIS:CE1	2.44	0.43
3:C:158:ALA:HB3	3:C:210:PHE:HE2	1.84	0.43
3:V:215:SER:O	3:V:231:ALA:N	2.50	0.43
3:V:233:LYS:HG3	3:V:274:SER:OG	2.19	0.43
7:Z:58:ALA:O	7:Z:59:LEU:HD23	2.18	0.43
4:W:175:VAL:HG21	4:W:219:ASN:OD1	2.19	0.43
3:V:124:TYR:C	3:V:132:TRP:CZ3	2.92	0.43
5:X:29:LYS:C	5:X:31:PRO:HD3	2.39	0.43
5:X:122:ASN:C	5:X:123:LYS:HD2	2.39	0.43
2:U:238:THR:HG21	6:Y:98:ALA:HB3	2.01	0.43
1:T:35:ILE:HD12	1:T:62:ILE:HG22	1.99	0.43
4:W:75:LEU:HG	4:W:78:ARG:HB2	2.00	0.43
3:V:4:HIS:O	3:V:354:MET:CA	2.66	0.43
2:U:291:ILE:HA	2:U:294:ARG:HD2	2.00	0.43
1:A:8:CYS:HB2	1:A:110:PHE:HE1	1.80	0.43
7:G:55:LEU:H	7:G:55:LEU:HD23	1.84	0.43
3:V:173:ILE:CD1	3:V:173:ILE:H	2.27	0.43
3:V:59:ASP:OD1	3:V:60:TRP:N	2.51	0.43
3:V:264:ASP:HB3	3:V:266:PHE:CZ	2.54	0.43
1:A:165:GLY:HA3	1:A:318:ASN:CB	2.39	0.43
1:A:173:GLY:O	1:A:174:VAL:HB	2.18	0.43
1:A:281:ILE:O	1:A:285:PRO:HA	2.18	0.43
1:T:128:GLU:CG	1:T:129:ILE:N	2.78	0.43
4:W:15:LEU:HB3	4:W:19:PHE:CE2	2.54	0.43
3:V:253:ILE:CG2	3:V:342:CYS:SG	3.06	0.43
1:A:208:LEU:C	1:A:208:LEU:CD2	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:106:LYS:O	4:W:106:LYS:HD2	2.19	0.43
2:U:220:LEU:HB2	2:U:258:ARG:HH21	1.84	0.43
5:X:50:LYS:HD2	5:X:50:LYS:HA	1.71	0.43
3:V:327:ASN:HD22	3:V:351:ASP:HB3	1.83	0.43
1:A:372:MET:O	1:A:376:ALA:HB2	2.19	0.43
4:W:147:ARG:HD3	4:W:147:ARG:HA	1.78	0.43
2:B:269:HIS:H	2:B:269:HIS:CD2	2.37	0.43
3:V:57:GLY:N	3:V:70:CYS:O	2.52	0.43
3:C:77:TYR:CD2	3:C:89:THR:C	2.71	0.43
4:D:45:ILE:HG12	4:D:57:VAL:CG2	2.39	0.43
4:W:186:LYS:NZ	4:W:197:GLN:CB	2.77	0.43
1:T:57:ASP:O	1:T:60:PHE:CD1	2.71	0.43
3:V:118:ARG:CG	3:V:142:ARG:O	2.66	0.43
1:T:309:ILE:HG13	1:T:312:ARG:HD2	2.01	0.43
3:V:230:ASP:HB2	3:V:233:LYS:HB3	2.00	0.43
6:F:61:VAL:HA	6:F:74:ILE:HA	2.01	0.43
7:G:88:ALA:O	7:G:90:ASP:N	2.47	0.43
1:A:34:CYS:SG	1:A:67:ILE:HG23	2.59	0.43
5:X:30:GLY:C	5:X:32:ALA:N	2.73	0.43
2:B:229:GLN:HG2	6:F:40:VAL:HG13	2.01	0.43
4:D:201:SER:HB2	4:D:204:GLU:O	2.19	0.43
3:V:102:VAL:CB	3:V:113:VAL:HA	2.48	0.43
3:V:176:VAL:CG2	3:V:177:GLU:N	2.81	0.43
5:X:15:LEU:HA	5:X:20:ALA:CA	2.48	0.43
1:A:127:ALA:O	1:A:131:PHE:CD2	2.70	0.43
1:A:132:GLU:HG3	1:A:400:TYR:HH	1.75	0.43
1:A:36:ALA:CB	1:A:72:TYR:HB3	2.49	0.43
3:V:77:TYR:HE2	3:V:90:LEU:CD2	2.06	0.43
3:C:51:HIS:CB	3:C:55:VAL:CG2	2.96	0.43
1:T:255:GLN:HA	1:T:270:ASP:HA	2.01	0.43
5:X:103:PHE:CD1	5:X:104:PRO:HD2	2.54	0.43
5:X:83:GLN:HG3	5:X:161:THR:OG1	2.19	0.43
2:U:321:LEU:CD2	2:U:340:PHE:CD1	2.95	0.43
3:V:8:VAL:CG1	3:V:9:GLU:N	2.75	0.43
1:T:60:PHE:HE2	1:T:95:GLN:CG	2.31	0.43
6:F:139:MET:O	6:F:142:ILE:CG1	2.67	0.43
4:D:106:LYS:NZ	4:D:106:LYS:N	2.64	0.43
7:G:91:ILE:HD13	7:G:127:GLN:HB3	2.01	0.43
2:B:170:TYR:HB2	2:B:175:LEU:CD1	2.49	0.43
1:T:183:GLY:C	1:T:184:TYR:CD1	2.92	0.43
1:T:257:THR:O	1:T:257:THR:OG1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:197:GLN:O	4:D:198:VAL:HG22	2.19	0.42
3:V:56:THR:HB	3:V:100:ARG:HH12	1.84	0.42
3:V:150:TRP:CE3	3:V:157:LEU:HB3	2.54	0.42
6:Y:24:ASN:OD1	6:Y:120:ASN:ND2	2.52	0.42
3:C:164:PHE:HB3	3:C:203:GLY:O	2.19	0.42
1:T:253:ILE:CD1	1:T:272:GLY:CA	2.97	0.42
3:C:79:TRP:C	3:C:86:TRP:HE3	2.23	0.42
1:T:305:GLN:HA	1:T:305:GLN:OE1	2.18	0.42
1:T:305:GLN:HG3	1:T:346:ARG:NH1	2.34	0.42
3:V:268:VAL:HA	3:V:284:ARG:N	2.32	0.42
2:U:312:GLY:H	2:U:314:PRO:HD2	1.84	0.42
2:U:312:GLY:N	2:U:314:PRO:HD2	2.34	0.42
5:E:94:GLU:HB3	5:E:98:LEU:HD11	2.00	0.42
4:W:47:ASN:HB3	4:W:48:PRO:CD	2.49	0.42
3:V:219:TRP:CH2	3:V:237:VAL:HG13	2.54	0.42
5:E:53:VAL:HA	5:E:168:PHE:HA	2.01	0.42
2:U:226:ASN:ND2	2:U:228:GLU:HB3	2.34	0.42
3:C:11:ILE:HG21	3:C:25:ILE:HB	2.01	0.42
5:E:119:LYS:HE3	5:E:126:ASP:OD2	2.19	0.42
3:V:20:ARG:NH1	3:V:335:LEU:HD22	2.34	0.42
3:C:244:THR:OG1	3:C:245:LEU:N	2.51	0.42
3:C:101:CYS:SG	3:C:147:SER:HB3	2.59	0.42
4:W:141:ARG:NH1	4:W:209:LEU:HD13	2.32	0.42
4:W:246:THR:O	4:W:250:TYR:HB2	2.19	0.42
3:C:174:LYS:H	3:C:174:LYS:HG3	1.64	0.42
2:U:325:TYR:O	2:U:330:LEU:HB2	2.19	0.42
7:G:118:SER:O	7:G:119:ASP:HB3	2.18	0.42
4:W:130:GLN:O	4:W:134:GLU:HB2	2.19	0.42
7:Z:26:ASP:OD2	7:Z:148:ARG:HG3	2.19	0.42
2:U:272:ASN:O	2:U:273:VAL:O	2.37	0.42
5:X:148:VAL:HG22	5:X:160:TRP:CE3	2.54	0.42
1:T:172:ASP:O	1:T:196:ALA:CB	2.67	0.42
3:V:190:PRO:HG2	3:V:193:GLU:HB2	2.00	0.42
3:C:263:HIS:CG	6:F:21:CYS:CB	3.03	0.42
3:C:332:ILE:O	3:C:332:ILE:HG23	2.19	0.42
4:W:6:VAL:HG21	4:W:246:THR:CG2	2.50	0.42
5:E:100:ILE:O	5:E:102:ASN:N	2.52	0.42
1:A:238:LEU:O	1:A:240:LYS:N	2.52	0.42
5:E:26:SER:CA	5:E:139:GLU:OE1	2.63	0.42
3:V:268:VAL:CA	3:V:284:ARG:H	2.30	0.42
1:A:130:MET:O	1:A:134:PHE:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:62:ASN:O	5:X:65:ASP:HB2	2.19	0.42
5:E:94:GLU:HB3	5:E:98:LEU:HG	2.01	0.42
5:E:51:ALA:O	5:E:55:PHE:HB2	2.19	0.42
7:G:120:ASN:O	7:G:122:SER:N	2.43	0.42
3:C:264:ASP:HB3	3:C:266:PHE:CZ	2.54	0.42
3:C:56:THR:HB	3:C:100:ARG:HH11	1.84	0.42
3:C:332:ILE:HG13	3:C:347:THR:CG2	2.50	0.42
1:A:164:THR:HA	1:A:180:VAL:CG1	2.47	0.42
4:W:197:GLN:C	4:W:198:VAL:CG2	2.87	0.42
4:W:246:THR:O	4:W:250:TYR:CB	2.67	0.42
4:D:153:TYR:O	4:D:164:VAL:N	2.40	0.42
2:U:313:LEU:C	2:U:315:SER:N	2.73	0.42
2:U:156:VAL:HB	2:U:157:VAL:H	1.72	0.42
1:A:309:ILE:O	1:A:312:ARG:HG2	2.19	0.42
5:X:5:HIS:HB3	5:X:65:ASP:OD1	2.20	0.42
2:B:315:SER:OG	6:F:30:VAL:HA	2.20	0.42
5:X:95:MET:HB3	5:X:138:GLN:HE22	1.83	0.42
5:E:122:ASN:C	5:E:123:LYS:HD2	2.40	0.42
5:E:124:GLN:HG3	5:E:125:GLU:H	1.85	0.42
1:A:183:GLY:C	1:A:184:TYR:CD1	2.93	0.42
3:V:367:LYS:HE3	3:V:367:LYS:HB2	1.83	0.42
2:B:202:TYR:HE2	2:B:252:ILE:HB	0.64	0.42
3:C:247:LEU:O	3:C:248:LEU:HD22	2.18	0.42
3:C:269:LEU:HB3	3:C:283:GLY:HA3	2.00	0.42
1:T:112:LEU:O	1:T:141:ILE:HG23	2.19	0.42
4:W:38:PHE:O	4:W:39:ASP:HB2	2.19	0.42
4:W:36:ALA:HB1	4:W:41:VAL:C	2.40	0.42
7:Z:104:ASP:OD2	7:Z:143:ARG:CZ	2.64	0.42
5:E:149:PHE:CE2	5:E:156:PRO:HB3	2.53	0.42
2:B:237:THR:HG22	6:F:105:ARG:NE	2.34	0.42
2:B:287:GLN:HA	2:B:294:ARG:NH1	2.35	0.42
4:D:16:ALA:O	4:D:18:LYS:N	2.52	0.42
2:B:84:ASP:CG	2:B:85:MET:H	2.22	0.42
1:A:296:ILE:O	1:A:300:VAL:HG23	2.20	0.42
1:T:168:ILE:HG23	1:T:176:HIS:O	2.19	0.42
3:V:102:VAL:CB	3:V:112:ALA:O	2.67	0.42
1:A:132:GLU:OE1	6:F:92:ARG:HD2	2.20	0.42
3:V:244:THR:OG1	3:V:245:LEU:N	2.52	0.42
6:Y:35:LYS:CB	6:Y:36:PRO:HD2	2.45	0.42
3:C:76:ALA:O	3:C:91:VAL:CB	2.55	0.42
4:W:128:TYR:CE2	4:W:154:VAL:HG21	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:80:TYR:HE1	4:W:113:ALA:HA	1.85	0.42
1:T:8:CYS:HB2	1:T:110:PHE:CD1	2.55	0.42
1:T:240:LYS:CG	1:T:241:GLU:H	2.32	0.42
1:T:240:LYS:CG	1:T:241:GLU:N	2.82	0.42
2:U:237:THR:HG22	6:Y:105:ARG:CG	2.49	0.42
5:E:150:ASP:C	5:E:152:GLN:N	2.73	0.42
4:D:280:ALA:CB	6:F:126:MET:SD	3.05	0.42
3:V:140:PRO:CD	3:V:169:PHE:CZ	2.94	0.42
1:A:241:GLU:HB3	1:A:245:TYR:CE1	2.54	0.42
7:Z:26:ASP:OD2	7:Z:148:ARG:CG	2.68	0.42
1:T:289:ASN:C	1:T:291:ASP:N	2.73	0.42
2:B:310:TYR:O	2:B:312:GLY:N	2.53	0.42
3:C:51:HIS:CB	3:C:55:VAL:HG22	2.49	0.42
3:C:45:VAL:O	3:C:46:HIS:C	2.58	0.42
4:W:80:TYR:HB2	4:W:84:LEU:HD12	2.02	0.42
1:A:208:LEU:HD11	1:A:215:ILE:HD11	2.01	0.42
4:D:158:LYS:HD3	4:D:158:LYS:C	2.40	0.42
2:U:184:ILE:HD11	2:U:264:ALA:CB	2.49	0.42
1:A:209:ARG:HG2	1:A:209:ARG:NH1	2.34	0.42
4:D:195:ALA:HB1	6:F:165:LEU:HG	2.01	0.42
2:B:175:LEU:C	2:B:177:HIS:N	2.73	0.42
1:A:385:ALA:HA	1:A:390:PHE:HB2	2.01	0.42
4:D:163:VAL:O	4:D:225:PHE:HB2	2.20	0.42
5:X:24:ILE:HA	5:X:40:ASP:HB2	2.01	0.42
5:X:120:PRO:CB	5:X:125:GLU:HB3	2.50	0.42
3:C:261:ALA:HB2	3:C:267:PRO:CA	2.45	0.42
1:A:102:ARG:HA	4:D:38:PHE:CZ	2.55	0.42
4:W:223:ILE:HG22	4:W:224:THR:N	2.35	0.42
3:C:20:ARG:NE	3:C:335:LEU:HB3	2.35	0.42
3:C:230:ASP:OD2	3:C:272:TYR:HE2	2.02	0.42
4:W:10:ILE:C	4:W:11:ILE:HD12	2.40	0.42
4:D:75:LEU:C	4:D:75:LEU:HD23	2.40	0.42
7:Z:43:ASP:O	7:Z:46:LEU:HB2	2.19	0.42
4:W:54:LYS:HE3	4:W:54:LYS:HB2	1.87	0.42
4:D:107:ASP:C	4:D:109:ILE:N	2.73	0.42
2:B:283:PHE:CZ	2:B:329:VAL:HG21	2.55	0.42
7:Z:51:MET:HB3	7:Z:86:PHE:CZ	2.55	0.42
4:D:197:GLN:C	4:D:198:VAL:CG2	2.88	0.42
3:V:155:VAL:HG11	3:V:180:PRO:CB	2.49	0.42
3:C:224:SER:HA	3:C:246:PRO:HB3	2.02	0.42
1:A:89:MET:HE1	1:A:92:PHE:HD2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:ILE:HB	1:A:366:GLN:O	2.20	0.42
2:U:319:ARG:C	2:U:321:LEU:N	2.73	0.42
3:V:209:CYS:O	3:V:252:PHE:HE1	2.02	0.42
3:V:355:SER:OG	3:V:357:TRP:CZ2	2.73	0.42
2:B:246:LEU:CB	2:B:247:PRO:CD	2.88	0.42
5:E:160:TRP:O	5:E:162:CYS:N	2.52	0.42
1:A:334:ARG:O	1:A:335:LEU:HB2	2.19	0.42
5:E:140:THR:O	5:E:144:LEU:HB3	2.20	0.42
1:A:63:GLY:C	1:A:65:GLU:N	2.73	0.42
1:T:265:LYS:HA	1:T:265:LYS:HD2	1.66	0.42
1:T:318:ASN:OD1	1:T:368:ILE:HD12	2.19	0.42
6:F:98:ALA:HB2	6:F:104:LEU:HD22	2.02	0.42
3:V:126:GLU:OE2	3:V:133:VAL:HG21	2.20	0.42
3:V:360:ARG:C	3:V:362:LEU:N	2.72	0.42
6:Y:73:SER:CB	6:Y:112:TYR:HD2	2.30	0.42
5:X:16:ILE:CG1	5:X:125:GLU:CG	2.90	0.42
3:C:148:LEU:HA	3:C:159:ALA:HB2	2.01	0.42
4:D:45:ILE:HG13	4:D:57:VAL:CB	2.44	0.42
5:E:20:ALA:HB2	5:E:63:GLU:HB2	2.01	0.42
3:C:107:ASN:CB	3:C:154:SER:HB2	2.50	0.42
3:C:97:ARG:HD2	6:F:28:GLN:O	2.20	0.42
1:T:238:LEU:C	1:T:240:LYS:N	2.73	0.42
7:Z:128:TRP:O	7:Z:132:ALA:HB2	2.20	0.42
5:X:50:LYS:NZ	5:X:163:PHE:CE2	2.88	0.42
1:A:125:TYR:HE1	6:F:97:ARG:HE	1.67	0.42
4:W:145:HIS:C	4:W:147:ARG:N	2.73	0.42
1:T:286:GLU:CD	1:T:293:THR:HA	2.39	0.41
1:T:292:PHE:CE2	1:T:294:GLN:O	2.72	0.41
2:B:253:LYS:CE	6:F:99:GLU:OE1	2.68	0.41
1:A:131:PHE:HE1	1:A:136:VAL:O	2.02	0.41
5:E:66:ARG:HE	5:E:116:ILE:CG2	2.34	0.41
1:T:137:PRO:HG2	1:T:138:GLY:H	1.84	0.41
3:C:174:LYS:O	3:C:176:VAL:N	2.53	0.41
3:C:96:ASN:O	3:C:97:ARG:NH1	2.43	0.41
1:T:278:GLY:C	1:T:280:GLU:N	2.73	0.41
5:E:30:GLY:HA2	5:E:135:GLN:OE1	2.19	0.41
4:W:11:ILE:HD11	4:W:35:PHE:CE2	2.54	0.41
5:E:25:ARG:N	5:E:40:ASP:OD2	2.40	0.41
5:E:91:GLY:HA2	5:E:94:GLU:CD	2.40	0.41
2:U:266:PHE:CZ	2:U:278:VAL:HG11	2.55	0.41
3:V:31:GLU:HB3	3:V:49:LYS:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:16:VAL:C	7:G:18:GLU:N	2.73	0.41
1:T:384:LEU:HD23	1:T:384:LEU:HA	1.80	0.41
1:T:168:ILE:HD12	1:T:177:VAL:HA	2.01	0.41
3:V:115:SER:N	3:V:145:VAL:HB	2.24	0.41
3:V:173:ILE:CD1	3:V:177:GLU:CD	2.87	0.41
3:V:172:TYR:CE2	3:V:178:GLU:O	2.73	0.41
5:X:46:ILE:HD13	5:X:147:LYS:HD3	2.02	0.41
5:X:77:GLU:O	5:X:79:LEU:N	2.47	0.41
6:Y:98:ALA:C	6:Y:100:ASN:N	2.73	0.41
4:W:80:TYR:O	4:W:81:GLY:C	2.58	0.41
3:C:170:SER:HB3	3:C:195:MET:CE	2.50	0.41
1:A:278:GLY:C	1:A:280:GLU:N	2.73	0.41
1:T:120:PRO:HG2	2:U:202:TYR:CD2	2.51	0.41
4:W:38:PHE:HB3	4:W:249:ASP:OD2	2.20	0.41
3:V:223:ASP:CB	7:Z:146:THR:HB	2.49	0.41
1:T:334:ARG:O	1:T:335:LEU:HB2	2.20	0.41
2:U:262:PRO:C	2:U:264:ALA:N	2.67	0.41
7:G:117:PRO:C	7:G:119:ASP:N	2.73	0.41
4:W:202:HIS:C	4:W:204:GLU:N	2.73	0.41
1:T:217:PRO:O	1:T:220:SER:HB2	2.20	0.41
2:U:192:TYR:CE2	2:U:270:LEU:HD22	2.50	0.41
5:E:72:THR:O	5:E:75:ILE:HB	2.19	0.41
7:Z:64:ILE:HG22	7:Z:64:ILE:O	2.19	0.41
3:C:138:LYS:HG3	3:C:139:LYS:HG3	2.01	0.41
4:D:202:HIS:C	4:D:204:GLU:N	2.73	0.41
1:A:100:TYR:O	4:D:10:ILE:HD11	2.19	0.41
2:U:321:LEU:O	2:U:340:PHE:CE1	2.72	0.41
3:C:175:GLU:C	3:C:176:VAL:HG13	2.40	0.41
6:F:61:VAL:CB	6:F:74:ILE:HG12	2.50	0.41
3:V:259:VAL:O	3:V:260:ALA:HB2	2.20	0.41
2:U:184:ILE:HA	2:U:188:ASP:OD2	2.21	0.41
4:D:106:LYS:C	4:D:108:SER:N	2.73	0.41
4:D:254:HIS:CD2	6:F:160:VAL:HG13	2.55	0.41
4:D:131:PHE:CG	4:D:139:GLU:HG3	2.55	0.41
4:W:251:LEU:HD11	4:W:255:ILE:HD11	2.01	0.41
5:E:46:ILE:HD13	5:E:147:LYS:CD	2.51	0.41
2:U:84:ASP:CG	2:U:85:MET:H	2.23	0.41
2:B:159:SER:OG	2:B:164:THR:HA	2.20	0.41
3:C:336:SER:HB2	3:C:343:SER:OG	2.20	0.41
1:A:264:LYS:HD3	1:A:264:LYS:HA	1.83	0.41
6:Y:92:ARG:O	6:Y:96:MET:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V:99:ALA:CA	3:V:114:GLY:O	2.66	0.41
3:V:99:ALA:HB2	3:V:115:SER:HB3	1.99	0.41
3:V:153:ASN:ND2	3:V:155:VAL:HB	2.35	0.41
6:Y:112:TYR:N	6:Y:112:TYR:CD1	2.88	0.41
5:X:124:GLN:HG3	5:X:125:GLU:H	1.86	0.41
3:C:30:HIS:CD2	3:C:52:ASN:O	2.74	0.41
1:A:238:LEU:C	1:A:240:LYS:N	2.73	0.41
4:D:123:SER:C	4:D:125:PHE:N	2.73	0.41
2:U:220:LEU:O	2:U:222:TYR:N	2.53	0.41
1:A:311:VAL:O	1:A:311:VAL:HG22	2.20	0.41
4:W:179:LYS:HB3	4:W:179:LYS:HZ2	1.82	0.41
4:D:281:ARG:HB3	6:F:125:GLN:O	2.20	0.41
7:G:37:PRO:HD2	7:G:75:ALA:O	2.20	0.41
2:B:219:LYS:HA	2:B:219:LYS:HD2	1.74	0.41
4:W:266:MET:SD	6:Y:93:PHE:HB2	2.60	0.41
3:V:103:ARG:HG3	3:V:148:LEU:O	2.21	0.41
3:V:109:LYS:HZ1	3:V:176:VAL:HB	1.86	0.41
2:B:202:TYR:HB3	2:B:204:PHE:HE2	1.86	0.41
5:X:26:SER:HA	5:X:139:GLU:CD	2.40	0.41
5:X:18:ASN:ND2	5:X:19:MET:CG	2.84	0.41
3:C:263:HIS:NE2	6:F:21:CYS:HB3	2.28	0.41
4:D:9:ARG:C	4:D:11:ILE:N	2.74	0.41
2:U:321:LEU:CD1	2:U:340:PHE:CB	2.90	0.41
7:Z:63:PRO:HD2	7:Z:109:TYR:CZ	2.35	0.41
4:W:153:TYR:O	4:W:163:VAL:HA	2.20	0.41
3:V:96:ASN:O	3:V:97:ARG:NH1	2.48	0.41
3:C:345:PHE:CE2	3:C:359:VAL:HG22	2.55	0.41
3:C:156:LEU:HD23	3:C:170:SER:HA	2.03	0.41
3:V:243:GLU:O	7:Z:139:GLY:N	2.51	0.41
1:A:217:PRO:O	1:A:220:SER:HB2	2.21	0.41
2:U:370:ASN:O	2:U:372:TRP:N	2.51	0.41
4:D:192:SER:C	4:D:194:THR:N	2.73	0.41
4:W:202:HIS:ND1	4:W:220:ILE:O	2.53	0.41
4:W:4:LEU:HA	4:W:4:LEU:HD23	1.79	0.41
4:W:70:HIS:C	4:W:72:ALA:N	2.73	0.41
4:W:236:ALA:C	4:W:238:ASP:N	2.73	0.41
1:T:150:ALA:C	1:T:152:SER:N	2.74	0.41
3:V:158:ALA:HB2	3:V:168:ILE:CB	2.50	0.41
3:V:344:GLN:N	3:V:359:VAL:CG2	2.78	0.41
5:X:41:ILE:CG2	5:X:42:VAL:N	2.83	0.41
1:T:34:CYS:HB3	1:T:76:TRP:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:168:PHE:CZ	5:X:169:MET:HG2	2.55	0.41
1:T:134:PHE:CD1	4:W:256:LYS:HD3	2.53	0.41
3:V:371:ILE:O	3:V:372:VAL:HB	2.20	0.41
1:A:179:PRO:CD	1:A:190:ILE:HG12	2.51	0.41
7:G:140:SER:O	7:G:144:VAL:HG23	2.20	0.41
3:V:26:CYS:SG	3:V:55:VAL:HB	2.60	0.41
7:Z:137:GLY:C	7:Z:139:GLY:H	2.24	0.41
1:T:132:GLU:HG3	1:T:400:TYR:OH	2.20	0.41
3:C:138:LYS:HG3	3:C:139:LYS:H	1.84	0.41
3:C:371:ILE:O	3:C:372:VAL:HB	2.20	0.41
1:T:193:ILE:CG2	1:T:194:PRO:N	2.83	0.41
1:T:150:ALA:HB1	1:T:379:PHE:HD2	1.85	0.41
2:U:238:THR:C	2:U:240:LEU:H	2.24	0.41
1:T:34:CYS:O	1:T:35:ILE:HB	2.20	0.41
1:T:61:PHE:C	1:T:62:ILE:HG23	2.41	0.41
3:C:254:THR:HG22	3:C:255:GLU:N	2.35	0.41
4:W:158:LYS:HG3	4:W:159:ASP:N	2.36	0.41
4:W:45:ILE:CG1	4:W:57:VAL:HG13	2.34	0.41
4:D:166:SER:C	4:D:167:THR:O	2.55	0.41
6:F:71:ARG:C	6:F:72:VAL:HG23	2.41	0.41
5:E:155:LYS:C	5:E:157:SER:N	2.73	0.41
3:C:242:SER:O	7:G:143:ARG:NH2	2.54	0.41
5:E:82:LEU:HD21	5:E:149:PHE:CZ	2.56	0.41
4:D:106:LYS:C	4:D:108:SER:H	2.23	0.41
7:G:129:HIS:O	7:G:132:ALA:HB3	2.21	0.41
4:D:192:SER:C	4:D:194:THR:H	2.22	0.41
3:C:262:GLY:C	3:C:329:VAL:H	2.23	0.41
6:F:105:ARG:HB3	6:F:107:LYS:O	2.21	0.41
4:W:173:ASP:HB2	6:Y:85:ILE:CG2	2.50	0.41
5:E:18:ASN:ND2	5:E:117:TYR:HA	2.36	0.41
1:T:371:HIS:C	1:T:373:GLN:N	2.73	0.41
5:X:120:PRO:CG	5:X:125:GLU:HB3	2.51	0.41
4:W:161:VAL:HG23	4:W:232:THR:HG21	2.02	0.41
6:F:55:ARG:NH1	6:F:59:GLU:OE2	2.53	0.41
1:T:101:LEU:HA	1:T:101:LEU:HD23	1.88	0.41
1:T:21:TYR:CZ	4:W:35:PHE:HB2	2.55	0.41
6:F:62:LEU:HB3	6:F:73:SER:HB2	2.03	0.41
7:Z:118:SER:O	7:Z:120:ASN:N	2.54	0.41
1:A:371:HIS:C	1:A:373:GLN:N	2.73	0.41
5:E:24:ILE:HD13	5:E:42:VAL:CG2	2.51	0.41
5:X:74:TYR:OH	5:X:99:GLY:CA	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:368:ILE:CG2	1:T:369:THR:H	2.34	0.41
2:B:170:TYR:C	2:B:171:GLU:CG	2.88	0.41
6:Y:12:VAL:HA	6:Y:15:THR:OG1	2.21	0.41
4:W:70:HIS:O	4:W:72:ALA:N	2.54	0.41
2:B:227:ILE:O	2:B:231:GLN:HB3	2.20	0.41
4:D:175:VAL:HG21	4:D:219:ASN:ND2	2.35	0.41
4:D:227:LEU:HB3	4:D:232:THR:CG2	2.51	0.41
3:V:100:ARG:N	3:V:115:SER:HA	2.17	0.41
3:V:20:ARG:NE	3:V:335:LEU:HD22	2.36	0.41
5:X:63:GLU:HA	5:X:66:ARG:CD	2.38	0.41
6:Y:21:CYS:O	6:Y:22:LEU:HG	2.20	0.41
3:C:164:PHE:O	3:C:203:GLY:O	2.39	0.41
3:C:219:TRP:CE2	3:C:227:CYS:HB2	2.56	0.41
3:C:77:TYR:CB	3:C:89:THR:H	2.34	0.41
3:C:77:TYR:CA	3:C:89:THR:O	2.57	0.41
3:C:269:LEU:H	3:C:284:ARG:H	1.69	0.41
3:C:331:GLN:HG2	3:C:332:ILE:N	2.35	0.41
6:Y:124:GLU:C	6:Y:126:MET:H	2.24	0.41
5:E:63:GLU:H	5:E:63:GLU:HG3	1.41	0.41
3:C:68:VAL:HG12	3:C:104:TRP:NE1	2.36	0.41
3:C:111:PHE:HE2	3:C:132:TRP:CZ3	2.38	0.41
1:A:196:ALA:O	1:A:197:GLY:C	2.58	0.41
3:V:232:ASP:OD1	3:V:233:LYS:N	2.54	0.41
4:W:42:LEU:HD12	4:W:42:LEU:N	2.36	0.41
1:T:99:LYS:HD2	4:W:1:MET:SD	2.60	0.41
4:W:45:ILE:HG13	4:W:57:VAL:CG2	2.51	0.41
2:U:330:LEU:C	2:U:332:GLY:H	2.23	0.41
1:A:215:ILE:HD11	1:A:269:ILE:HD13	2.03	0.41
3:V:346:CYS:C	3:V:347:THR:CG2	2.89	0.41
3:V:346:CYS:O	3:V:347:THR:HG22	2.21	0.41
6:Y:55:ARG:O	6:Y:55:ARG:HG2	2.20	0.41
4:D:70:HIS:C	4:D:72:ALA:N	2.73	0.41
2:U:166:ILE:HD13	2:U:281:LEU:HD22	2.02	0.41
1:T:284:HIS:O	1:T:287:PHE:HB2	2.20	0.41
1:A:151:ALA:HB3	1:A:370:HIS:CD2	2.55	0.41
2:U:370:ASN:C	2:U:372:TRP:N	2.73	0.41
4:D:110:VAL:CG1	4:D:111:HIS:H	2.33	0.41
7:G:98:LEU:CB	7:G:103:VAL:HG22	2.50	0.41
4:D:254:HIS:CE1	6:F:160:VAL:HG22	2.56	0.41
1:T:260:ASN:HB3	1:T:265:LYS:N	2.36	0.41
3:C:279:LEU:HD23	3:C:279:LEU:HA	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:129:PHE:CE2	4:D:237:ARG:HG3	2.56	0.41
2:U:192:TYR:CE1	2:U:195:LYS:HD3	2.55	0.41
4:W:169:PHE:HZ	4:W:251:LEU:HD23	1.86	0.41
3:C:139:LYS:CB	3:C:140:PRO:HA	2.50	0.41
4:W:145:HIS:C	4:W:147:ARG:H	2.25	0.41
6:Y:40:VAL:HG12	6:Y:42:SER:OG	2.20	0.41
4:W:189:ARG:NH1	4:W:189:ARG:HB2	2.35	0.41
3:V:151:HIS:C	3:V:153:ASN:N	2.73	0.41
6:Y:61:VAL:N	6:Y:74:ILE:HG23	2.32	0.41
5:X:120:PRO:C	5:X:122:ASN:N	2.75	0.41
5:X:120:PRO:HB2	5:X:122:ASN:CG	2.41	0.41
3:C:90:LEU:O	3:C:91:VAL:HG23	2.21	0.41
3:V:72:THR:CG2	6:Y:26:SER:HG	2.20	0.41
1:T:31:ILE:HD11	1:T:62:ILE:HD12	2.02	0.41
3:C:230:ASP:O	3:C:235:MET:HA	2.21	0.41
7:G:58:ALA:O	7:G:59:LEU:HD23	2.21	0.41
3:V:215:SER:O	3:V:230:ASP:HA	2.22	0.41
5:E:41:ILE:HG12	5:E:71:ILE:CD1	2.51	0.41
4:D:265:ARG:HD3	6:F:145:GLU:OE2	2.21	0.41
5:X:99:GLY:HA3	5:X:137:ARG:O	2.21	0.41
4:D:21:ASN:HB3	4:D:26:ASN:O	2.21	0.41
2:U:358:GLY:O	2:U:362:ALA:HB3	2.21	0.41
1:A:185:VAL:HB	2:B:203:ALA:HB1	2.02	0.41
3:V:204:TRP:C	3:V:205:VAL:HG23	2.42	0.40
5:X:66:ARG:HE	5:X:116:ILE:HG21	1.86	0.40
4:D:38:PHE:C	4:D:40:GLY:N	2.73	0.40
3:C:30:HIS:HD1	3:C:54:GLN:N	2.18	0.40
1:T:208:LEU:HD21	1:T:215:ILE:HD12	2.02	0.40
3:C:14:HIS:CE1	3:C:348:THR:CB	3.04	0.40
6:Y:127:TYR:HB3	6:Y:128:LYS:H	1.74	0.40
1:A:181:ALA:HB2	1:A:186:ILE:CG1	2.50	0.40
6:Y:98:ALA:O	6:Y:100:ASN:N	2.54	0.40
1:T:164:THR:HA	1:T:180:VAL:CG2	2.52	0.40
1:T:242:PHE:HZ	1:T:277:LEU:HD13	1.86	0.40
5:X:53:VAL:HA	5:X:168:PHE:HA	2.03	0.40
2:U:232:LYS:HE2	2:U:236:GLU:CD	2.42	0.40
4:D:123:SER:O	4:D:125:PHE:N	2.54	0.40
3:C:59:ASP:OD1	3:C:60:TRP:N	2.52	0.40
4:W:125:PHE:N	4:W:125:PHE:CD1	2.88	0.40
2:B:86:LYS:O	2:B:88:LEU:N	2.49	0.40
4:D:18:LYS:HB3	4:D:99:LEU:HD21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:LEU:HA	1:A:384:LEU:HD23	1.84	0.40
2:B:320:GLU:HA	2:B:323:GLN:HG3	2.03	0.40
2:U:159:SER:OG	2:U:164:THR:HA	2.21	0.40
3:C:63:ASP:OD1	3:C:63:ASP:N	2.54	0.40
1:A:251:LYS:HB3	1:A:251:LYS:HE2	1.91	0.40
4:D:197:GLN:C	4:D:198:VAL:HG23	2.42	0.40
3:V:100:ARG:HA	3:V:100:ARG:HD2	1.59	0.40
6:Y:60:LYS:O	6:Y:61:VAL:HG23	2.21	0.40
1:T:84:GLU:HB3	1:T:85:ASP:H	1.62	0.40
1:A:174:VAL:O	1:A:176:HIS:CE1	2.74	0.40
2:U:220:LEU:HB2	2:U:258:ARG:HE	1.86	0.40
2:U:180:ARG:HH12	2:U:285:THR:HA	1.86	0.40
5:X:6:SER:N	5:X:65:ASP:OD1	2.45	0.40
7:G:86:PHE:C	7:G:87:LYS:HD3	2.40	0.40
7:G:93:LYS:HG3	7:G:93:LYS:H	1.68	0.40
4:W:228:PHE:HB3	4:W:229:PRO:CD	2.49	0.40
3:C:138:LYS:HA	3:C:138:LYS:HD2	1.68	0.40
3:V:163:ASP:O	3:V:164:PHE:HD2	2.05	0.40
2:U:93:PHE:HB3	2:U:94:GLY:H	1.49	0.40
5:X:108:GLU:OE1	5:X:108:GLU:HA	2.22	0.40
2:B:223:VAL:HB	2:B:312:GLY:C	2.42	0.40
1:A:340:LYS:HB2	1:A:365:VAL:CG2	2.51	0.40
1:T:254:LYS:O	1:T:270:ASP:HA	2.20	0.40
4:W:77:LYS:C	4:W:79:VAL:N	2.73	0.40
3:C:152:PRO:HG2	3:C:213:ASN:N	2.36	0.40
3:C:135:LYS:HD2	3:C:191:PHE:CE2	2.55	0.40
5:E:158:LYS:O	5:E:159:TRP:CG	2.74	0.40
3:V:346:CYS:C	3:V:347:THR:HG23	2.41	0.40
4:D:244:ILE:CG2	4:D:245:HIS:N	2.73	0.40
7:Z:57:ALA:C	7:Z:59:LEU:N	2.73	0.40
7:Z:120:ASN:C	7:Z:122:SER:H	2.24	0.40
2:U:261:ALA:HB3	2:U:262:PRO:CD	2.39	0.40
7:Z:41:GLU:HG3	7:Z:42:VAL:N	2.37	0.40
1:A:203:PHE:CZ	1:A:207:LEU:HD12	2.57	0.40
3:C:40:ASN:C	3:C:41:LYS:HD3	2.40	0.40
1:T:132:GLU:HG2	1:T:400:TYR:OH	2.22	0.40
5:E:46:ILE:HD13	5:E:147:LYS:HD2	2.03	0.40
2:B:164:THR:O	2:B:165:HIS:CB	2.69	0.40
1:T:94:GLU:O	1:T:98:PHE:HD2	2.04	0.40
3:C:209:CYS:SG	3:C:251:THR:HA	2.61	0.40
3:V:43:VAL:HG12	3:V:44:GLN:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:226:VAL:CG1	4:D:227:LEU:H	2.26	0.40
3:V:148:LEU:HA	3:V:159:ALA:HB2	2.04	0.40
3:V:343:SER:CA	3:V:359:VAL:HG21	2.51	0.40
1:A:99:LYS:HA	1:A:102:ARG:NH1	2.35	0.40
1:A:136:VAL:HB	1:A:137:PRO:HD2	2.03	0.40
3:C:116:GLY:N	3:C:145:VAL:H	2.19	0.40
3:C:146:LEU:HB2	3:C:160:GLY:O	2.21	0.40
3:C:158:ALA:HB3	3:C:210:PHE:CE2	2.57	0.40
3:C:51:HIS:HB3	3:C:55:VAL:HG22	2.04	0.40
4:W:245:HIS:C	4:W:247:PHE:N	2.75	0.40
3:C:36:GLU:HB2	3:C:45:VAL:HG21	2.03	0.40
3:C:151:HIS:C	3:C:153:ASN:N	2.73	0.40
4:W:9:ARG:C	4:W:11:ILE:N	2.74	0.40
7:Z:137:GLY:C	7:Z:139:GLY:N	2.73	0.40
3:V:143:SER:HB2	3:V:144:THR:H	1.70	0.40
4:W:30:ALA:CB	4:W:52:LYS:HG2	2.44	0.40
3:C:360:ARG:HG2	3:C:363:GLU:OE2	2.21	0.40
2:U:226:ASN:O	2:U:227:ILE:C	2.60	0.40
4:D:233:ASN:HD22	4:D:235:SER:N	2.20	0.40
1:T:151:ALA:C	1:T:153:TRP:H	2.24	0.40
3:V:103:ARG:HA	3:V:103:ARG:HD3	1.97	0.40
3:V:68:VAL:CG1	3:V:104:TRP:NE1	2.81	0.40
3:V:173:ILE:CB	3:V:176:VAL:CG2	2.92	0.40
6:Y:48:LEU:HG	6:Y:65:GLY:O	2.20	0.40
4:D:36:ALA:HA	4:D:42:LEU:CA	2.52	0.40
4:W:197:GLN:C	4:W:198:VAL:HG23	2.42	0.40
1:T:185:VAL:CG1	1:T:186:ILE:N	2.84	0.40
1:T:109:TYR:CE1	1:T:137:PRO:CG	3.05	0.40
1:T:281:ILE:C	1:T:281:ILE:CD1	2.90	0.40
6:F:60:LYS:O	6:F:61:VAL:HG23	2.22	0.40
3:V:347:THR:N	3:V:355:SER:CB	2.78	0.40
2:U:369:ASP:HA	2:U:372:TRP:O	2.22	0.40
7:Z:129:HIS:O	7:Z:132:ALA:HB3	2.21	0.40
1:T:233:TYR:OH	1:T:245:TYR:CE2	2.75	0.40
4:D:176:VAL:O	4:D:179:LYS:HB2	2.21	0.40
6:Y:12:VAL:O	6:Y:14:ALA:N	2.55	0.40
4:D:15:LEU:HB3	4:D:19:PHE:HE2	1.87	0.40
7:Z:67:LYS:HE2	7:Z:67:LYS:HB3	1.95	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:200:PHE:O	5:X:88:LYS:NZ[3_555]	1.85	0.35
5:E:88:LYS:NZ	4:W:200:PHE:O[3_545]	1.90	0.30
4:D:199:LEU:CD2	5:X:146:GLU:OE1[3_555]	2.10	0.10

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	384/418 (92%)	270 (70%)	66 (17%)	48 (12%)	0	8
1	T	384/418 (92%)	264 (69%)	69 (18%)	51 (13%)	0	7
2	B	222/394 (56%)	139 (63%)	48 (22%)	35 (16%)	0	5
2	U	222/394 (56%)	132 (60%)	55 (25%)	35 (16%)	0	5
3	C	348/372 (94%)	207 (60%)	82 (24%)	59 (17%)	0	5
3	V	348/372 (94%)	208 (60%)	80 (23%)	60 (17%)	0	4
4	D	282/300 (94%)	189 (67%)	65 (23%)	28 (10%)	1	13
4	W	282/300 (94%)	186 (66%)	63 (22%)	33 (12%)	0	9
5	E	172/178 (97%)	124 (72%)	30 (17%)	18 (10%)	1	12
5	X	172/178 (97%)	116 (67%)	34 (20%)	22 (13%)	0	8
6	F	165/168 (98%)	120 (73%)	23 (14%)	22 (13%)	0	7
6	Y	165/168 (98%)	113 (68%)	29 (18%)	23 (14%)	0	6
7	G	135/151 (89%)	91 (67%)	21 (16%)	23 (17%)	0	5
7	Z	135/151 (89%)	84 (62%)	27 (20%)	24 (18%)	0	4
All	All	3416/3962 (86%)	2243 (66%)	692 (20%)	481 (14%)	0	6

All (481) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	28	GLN

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Mol	Chain	Res	Type
1	A	150	ALA
1	A	181	ALA
1	A	232	SER
1	A	242	PHE
1	A	291	ASP
1	A	325	SER
1	A	349	LEU
1	A	360	PRO
1	A	363	ILE
1	A	370	HIS
2	B	163	VAL
2	B	165	HIS
2	B	206	HIS
2	B	207	SER
2	B	325	TYR
2	B	344	ILE
2	B	347	PRO
2	B	348	PRO
2	B	350	ARG
2	B	373	MET
2	B	376	GLN
3	C	12	SER
3	C	23	ILE
3	C	38	SER
3	C	62	PRO
3	C	73	ASP
3	C	76	ALA
3	C	80	THR
3	C	96	ASN
3	C	104	TRP
3	C	212	ALA
3	C	213	ASN
3	C	307	LYS
3	C	332	ILE
3	C	353	GLY
3	C	366	LEU
3	C	367	LYS
3	C	371	ILE
4	D	70	HIS
4	D	76	LEU
4	D	167	THR
4	D	170	LYS

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Mol	Chain	Res	Type
4	D	209	LEU
5	E	21	LEU
5	E	29	LYS
5	E	57	ASN
5	E	115	ALA
5	E	133	LEU
5	E	158	LYS
5	E	163	PHE
6	F	20	LEU
6	F	57	GLU
6	F	67	ILE
6	F	102	PHE
6	F	109	VAL
6	F	127	TYR
7	G	10	ARG
7	G	39	GLU
7	G	54	ALA
7	G	58	ALA
7	G	81	LYS
7	G	82	VAL
7	G	90	ASP
1	T	4	ARG
1	T	28	GLN
1	T	35	ILE
1	T	136	VAL
1	T	150	ALA
1	T	170	SER
1	T	174	VAL
1	T	181	ALA
1	T	188	SER
1	T	232	SER
1	T	240	LYS
1	T	241	GLU
1	T	242	PHE
1	T	325	SER
1	T	349	LEU
1	T	370	HIS
2	U	163	VAL
2	U	206	HIS
2	U	207	SER
2	U	273	VAL
2	U	329	VAL

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Mol	Chain	Res	Type
2	U	344	ILE
2	U	347	PRO
2	U	348	PRO
2	U	350	ARG
2	U	370	ASN
2	U	372	TRP
2	U	376	GLN
3	V	23	ILE
3	V	38	SER
3	V	62	PRO
3	V	72	THR
3	V	73	ASP
3	V	76	ALA
3	V	80	THR
3	V	96	ASN
3	V	102	VAL
3	V	103	ARG
3	V	119	VAL
3	V	159	ALA
3	V	250	VAL
3	V	307	LYS
3	V	366	LEU
3	V	367	LYS
3	V	371	ILE
4	W	70	HIS
4	W	76	LEU
4	W	107	ASP
4	W	158	LYS
4	W	170	LYS
4	W	208	GLU
4	W	209	LEU
4	W	227	LEU
5	X	17	GLY
5	X	20	ALA
5	X	57	ASN
5	X	87	SER
5	X	115	ALA
5	X	133	LEU
6	Y	57	GLU
6	Y	67	ILE
6	Y	102	PHE
6	Y	109	VAL

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Mol	Chain	Res	Type
7	Z	17	ASP
7	Z	39	GLU
7	Z	54	ALA
7	Z	58	ALA
7	Z	68	SER
7	Z	81	LYS
7	Z	82	VAL
7	Z	90	ASP
7	Z	124	VAL
1	A	38	LYS
1	A	64	ASP
1	A	82	ILE
1	A	102	ARG
1	A	118	ASN
1	A	129	ILE
1	A	148	ALA
1	A	170	SER
1	A	174	VAL
1	A	187	GLY
1	A	188	SER
1	A	239	VAL
1	A	243	ASN
1	A	310	ASP
1	A	311	VAL
1	A	324	GLY
1	A	335	LEU
1	A	372	MET
1	A	376	ALA
1	A	380	GLY
1	A	381	GLY
1	A	407	ILE
2	B	246	LEU
2	B	251	ILE
2	B	263	GLU
2	B	266	PHE
2	B	290	ASP
2	B	323	GLN
2	B	336	LYS
2	B	337	LEU
2	B	374	THR
3	C	18	LYS
3	C	28	ASN

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Mol	Chain	Res	Type
3	C	72	THR
3	C	84	ARG
3	C	86	TRP
3	C	95	ILE
3	C	114	GLY
3	C	159	ALA
3	C	166	CYS
3	C	175	GLU
3	C	204	TRP
3	C	275	ALA
3	C	320	GLY
3	C	361	SER
4	D	3	LEU
4	D	10	ILE
4	D	24	ALA
4	D	43	TYR
4	D	44	HIS
4	D	63	PHE
4	D	157	LYS
4	D	199	LEU
5	E	15	LEU
5	E	101	THR
5	E	161	THR
6	F	13	ARG
6	F	111	GLY
6	F	128	LYS
7	G	26	ASP
7	G	45	CYS
7	G	88	ALA
7	G	118	SER
7	G	150	THR
1	T	12	CYS
1	T	102	ARG
1	T	137	PRO
1	T	148	ALA
1	T	187	GLY
1	T	195	ILE
1	T	310	ASP
1	T	335	LEU
1	T	363	ILE
1	T	372	MET
1	T	374	ARG

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Mol	Chain	Res	Type
1	T	376	ALA
1	T	381	GLY
1	T	407	ILE
2	U	165	HIS
2	U	221	CYS
2	U	251	ILE
2	U	263	GLU
2	U	266	PHE
2	U	290	ASP
2	U	340	PHE
2	U	354	VAL
2	U	364	ILE
2	U	371	PHE
3	V	46	HIS
3	V	84	ARG
3	V	95	ILE
3	V	131	TRP
3	V	191	PHE
3	V	194	LEU
3	V	202	CYS
3	V	212	ALA
3	V	213	ASN
3	V	240	LEU
3	V	275	ALA
3	V	282	GLY
3	V	320	GLY
3	V	332	ILE
3	V	343	SER
4	W	3	LEU
4	W	10	ILE
4	W	11	ILE
4	W	24	ALA
4	W	63	PHE
4	W	68	GLN
4	W	105	SER
4	W	157	LYS
4	W	160	ARG
4	W	199	LEU
4	W	214	ALA
5	X	21	LEU
5	X	154	ASP
5	X	158	LYS

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Mol	Chain	Res	Type
6	Y	13	ARG
6	Y	111	GLY
7	Z	10	ARG
7	Z	45	CYS
7	Z	88	ALA
7	Z	122	SER
7	Z	133	LEU
7	Z	150	THR
1	A	85	ASP
1	A	151	ALA
1	A	364	ASP
1	A	366	GLN
1	A	374	ARG
2	B	171	GLU
2	B	265	LEU
2	B	289	ALA
2	B	311	PRO
2	B	312	GLY
3	C	46	HIS
3	C	70	CYS
3	C	75	ASN
3	C	130	ASP
3	C	152	PRO
3	C	176	VAL
3	C	191	PHE
3	C	282	GLY
3	C	343	SER
4	D	17	LEU
4	D	75	LEU
4	D	105	SER
4	D	108	SER
4	D	160	ARG
4	D	192	SER
4	D	201	SER
4	D	208	GLU
5	E	78	CYS
5	E	134	GLN
5	E	156	PRO
5	E	157	SER
6	F	17	GLN
6	F	34	ASN
6	F	103	ILE

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Mol	Chain	Res	Type
6	F	133	ASP
7	G	102	GLY
7	G	121	SER
7	G	122	SER
7	G	123	ALA
7	G	133	LEU
1	T	64	ASP
1	T	129	ILE
1	T	212	GLU
1	T	274	GLU
1	T	293	THR
1	T	322	SER
1	T	369	THR
1	T	380	GLY
1	T	402	GLU
2	U	160	GLY
2	U	171	GLU
2	U	176	PRO
2	U	246	LEU
2	U	265	LEU
2	U	289	ALA
2	U	311	PRO
2	U	312	GLY
2	U	320	GLU
3	V	75	ASN
3	V	104	TRP
3	V	115	SER
3	V	133	VAL
3	V	138	LYS
3	V	152	PRO
3	V	228	LEU
3	V	303	GLN
3	V	357	TRP
3	V	361	SER
4	W	17	LEU
4	W	75	LEU
4	W	188	GLY
4	W	201	SER
5	X	78	CYS
5	X	101	THR
5	X	102	ASN
5	X	109	PRO

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Mol	Chain	Res	Type
5	X	121	ALA
5	X	134	GLN
5	X	151	PRO
6	Y	17	GLN
6	Y	34	ASN
6	Y	68	ASN
6	Y	103	ILE
6	Y	127	TYR
6	Y	133	ASP
7	Z	89	ASN
7	Z	117	PRO
7	Z	119	ASP
7	Z	123	ALA
1	A	230	ARG
1	A	384	LEU
2	B	87	HIS
2	B	160	GLY
2	B	329	VAL
2	B	354	VAL
2	B	364	ILE
3	C	54	GLN
3	C	131	TRP
3	C	138	LYS
3	C	303	GLN
3	C	305	LEU
3	C	334	VAL
3	C	351	ASP
4	D	237	ARG
4	D	269	LYS
5	E	102	ASN
6	F	30	VAL
6	F	49	GLN
7	G	61	ASN
7	G	63	PRO
7	G	89	ASN
7	G	119	ASP
1	T	211	ARG
1	T	252	TRP
1	T	265	LYS
1	T	384	LEU
2	U	87	HIS
2	U	341	LYS

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Mol	Chain	Res	Type
3	V	28	ASN
3	V	100	ARG
3	V	155	VAL
3	V	257	SER
3	V	305	LEU
3	V	342	CYS
4	W	8	ASN
4	W	50	GLY
4	W	167	THR
4	W	269	LYS
5	X	98	LEU
5	X	155	LYS
5	X	157	SER
5	X	172	SER
6	Y	29	VAL
6	Y	49	GLN
6	Y	56	ASN
7	Z	60	LYS
7	Z	61	ASN
7	Z	63	PRO
7	Z	140	SER
1	A	179	PRO
1	A	415	GLY
2	B	156	VAL
2	B	372	TRP
3	C	14	HIS
3	C	52	ASN
3	C	74	ARG
3	C	115	SER
3	C	147	SER
3	C	245	LEU
3	C	284	ARG
3	C	304	ASN
4	D	4	LEU
6	F	6	ARG
6	F	29	VAL
6	F	56	ASN
6	F	72	VAL
7	G	60	LYS
7	G	64	ILE
1	T	83	VAL
1	T	106	GLU

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Mol	Chain	Res	Type
1	T	294	GLN
1	T	315	LEU
1	T	405	PRO
1	T	415	GLY
2	U	156	VAL
3	V	63	ASP
3	V	74	ARG
3	V	136	HIS
3	V	142	ARG
3	V	205	VAL
3	V	304	ASN
3	V	334	VAL
3	V	335	LEU
3	V	350	MET
3	V	353	GLY
4	W	4	LEU
5	X	156	PRO
6	Y	6	ARG
6	Y	23	GLU
6	Y	30	VAL
6	Y	66	SER
6	Y	99	GLU
1	A	137	PRO
1	A	229	GLU
1	A	238	LEU
1	A	322	SER
2	B	170	TYR
3	C	121	SER
4	D	50	GLY
4	D	198	VAL
5	E	3	ALA
5	E	172	SER
6	F	77	LYS
2	U	325	TYR
4	W	71	GLY
4	W	198	VAL
5	X	99	GLY
6	Y	79	ALA
2	B	360	VAL
3	C	338	GLY
1	T	179	PRO
7	Z	102	GLY

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Mol	Chain	Res	Type
3	C	205	VAL
4	D	71	GLY
3	V	57	GLY
2	B	239	VAL
4	W	87	PRO
1	A	294	GLN
4	D	188	GLY
6	F	61	VAL
3	V	176	VAL
6	Y	72	VAL
3	C	133	VAL
5	E	110	GLY
6	F	36	PRO
1	T	311	VAL
4	W	81	GLY
4	W	228	PHE
6	Y	36	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/363 (95%)	321 (93%)	24 (7%)	19	58
1	T	345/363 (95%)	319 (92%)	26 (8%)	17	55
2	B	168/345 (49%)	144 (86%)	24 (14%)	4	27
2	U	169/345 (49%)	147 (87%)	22 (13%)	5	30
3	C	301/313 (96%)	257 (85%)	44 (15%)	4	25
3	V	301/313 (96%)	264 (88%)	37 (12%)	6	32
4	D	249/264 (94%)	223 (90%)	26 (10%)	9	39
4	W	249/264 (94%)	225 (90%)	24 (10%)	10	43
5	E	156/159 (98%)	142 (91%)	14 (9%)	12	46
5	X	156/159 (98%)	136 (87%)	20 (13%)	5	30
6	F	154/155 (99%)	145 (94%)	9 (6%)	25	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Y	154/155 (99%)	138 (90%)	16 (10%)	9	39
7	G	114/124 (92%)	103 (90%)	11 (10%)	10	43
7	Z	114/124 (92%)	105 (92%)	9 (8%)	15	53
All	All	2975/3446 (86%)	2669 (90%)	306 (10%)	9	39

All (306) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	19	LEU
1	A	62	ILE
1	A	79	ARG
1	A	152	SER
1	A	164	THR
1	A	210	ASP
1	A	211	ARG
1	A	232	SER
1	A	250	SER
1	A	255	GLN
1	A	265	LYS
1	A	268	SER
1	A	273	TYR
1	A	287	PHE
1	A	289	ASN
1	A	293	THR
1	A	298	GLU
1	A	306	ASN
1	A	327	MET
1	A	343	VAL
1	A	363	ILE
1	A	416	VAL
1	A	417	MET
2	B	82	TRP
2	B	89	TRP
2	B	92	THR
2	B	93	PHE
2	B	156	VAL
2	B	165	HIS
2	B	173	PHE
2	B	182	LEU
2	B	184	ILE

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Mol	Chain	Res	Type
2	B	191	ARG
2	B	192	TYR
2	B	200	ARG
2	B	206	HIS
2	B	220	LEU
2	B	233	LEU
2	B	240	LEU
2	B	248	ASP
2	B	253	LYS
2	B	272	ASN
2	B	274	GLU
2	B	292	ASP
2	B	315	SER
2	B	330	LEU
2	B	340	PHE
3	C	12	SER
3	C	18	LYS
3	C	26	CYS
3	C	31	GLU
3	C	48	LEU
3	C	54	GLN
3	C	63	ASP
3	C	73	ASP
3	C	74	ARG
3	C	77	TYR
3	C	90	LEU
3	C	92	ILE
3	C	94	ARG
3	C	107	ASN
3	C	118	ARG
3	C	122	ILE
3	C	123	CYS
3	C	131	TRP
3	C	133	VAL
3	C	137	ILE
3	C	138	LYS
3	C	139	LYS
3	C	142	ARG
3	C	147	SER
3	C	148	LEU
3	C	157	LEU
3	C	165	LYS

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Mol	Chain	Res	Type
3	C	174	LYS
3	C	178	GLU
3	C	179	ARG
3	C	180	PRO
3	C	194	LEU
3	C	202	CYS
3	C	216	ARG
3	C	248	LEU
3	C	257	SER
3	C	263	HIS
3	C	280	SER
3	C	284	ARG
3	C	305	LEU
3	C	324	LEU
3	C	328	SER
3	C	354	MET
3	C	360	ARG
4	D	3	LEU
4	D	8	ASN
4	D	18	LYS
4	D	42	LEU
4	D	43	TYR
4	D	45	ILE
4	D	76	LEU
4	D	95	LEU
4	D	106	LYS
4	D	116	LEU
4	D	118	ARG
4	D	130	GLN
4	D	157	LYS
4	D	159	ASP
4	D	160	ARG
4	D	171	ASP
4	D	179	LYS
4	D	185	PHE
4	D	201	SER
4	D	211	ASP
4	D	212	THR
4	D	225	PHE
4	D	230	ARG
4	D	233	ASN
4	D	244	ILE

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Mol	Chain	Res	Type
4	D	281	ARG
5	E	7	SER
5	E	10	ASP
5	E	39	THR
5	E	63	GLU
5	E	88	LYS
5	E	95	MET
5	E	123	LYS
5	E	127	GLU
5	E	130	ARG
5	E	138	GLN
5	E	142	LEU
5	E	144	LEU
5	E	146	GLU
5	E	150	ASP
6	F	6	ARG
6	F	31	GLU
6	F	54	SER
6	F	60	LYS
6	F	100	ASN
6	F	126	MET
6	F	131	LEU
6	F	166	LYS
6	F	167	ASN
7	G	27	GLU
7	G	39	GLU
7	G	55	LEU
7	G	65	ASN
7	G	68	SER
7	G	74	ARG
7	G	86	PHE
7	G	90	ASP
7	G	96	GLN
7	G	112	LYS
7	G	140	SER
1	T	4	ARG
1	T	19	LEU
1	T	35	ILE
1	T	71	THR
1	T	79	ARG
1	T	82	ILE
1	T	91	ARG

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Mol	Chain	Res	Type
1	T	114	GLU
1	T	152	SER
1	T	166	THR
1	T	210	ASP
1	T	211	ARG
1	T	232	SER
1	T	237	ASP
1	T	250	SER
1	T	255	GLN
1	T	265	LYS
1	T	273	TYR
1	T	276	PHE
1	T	294	GLN
1	T	298	GLU
1	T	306	ASN
1	T	343	VAL
1	T	363	ILE
1	T	416	VAL
1	T	417	MET
2	U	82	TRP
2	U	89	TRP
2	U	92	THR
2	U	93	PHE
2	U	156	VAL
2	U	158	ASP
2	U	165	HIS
2	U	184	ILE
2	U	191	ARG
2	U	192	TYR
2	U	200	ARG
2	U	206	HIS
2	U	220	LEU
2	U	228	GLU
2	U	240	LEU
2	U	248	ASP
2	U	274	GLU
2	U	292	ASP
2	U	326	LEU
2	U	336	LYS
2	U	339	LYS
2	U	340	PHE
3	V	18	LYS

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Mol	Chain	Res	Type
3	V	31	GLU
3	V	33	HIS
3	V	48	LEU
3	V	54	GLN
3	V	63	ASP
3	V	64	SER
3	V	70	CYS
3	V	73	ASP
3	V	74	ARG
3	V	77	TYR
3	V	90	LEU
3	V	92	ILE
3	V	94	ARG
3	V	100	ARG
3	V	107	ASN
3	V	118	ARG
3	V	123	CYS
3	V	131	TRP
3	V	134	CYS
3	V	135	LYS
3	V	136	HIS
3	V	142	ARG
3	V	157	LEU
3	V	174	LYS
3	V	189	MET
3	V	220	VAL
3	V	257	SER
3	V	258	LEU
3	V	263	HIS
3	V	280	SER
3	V	284	ARG
3	V	305	LEU
3	V	324	LEU
3	V	343	SER
3	V	354	MET
3	V	360	ARG
4	W	3	LEU
4	W	8	ASN
4	W	18	LYS
4	W	20	GLU
4	W	37	ASP
4	W	76	LEU

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Mol	Chain	Res	Type
4	W	77	LYS
4	W	95	LEU
4	W	106	LYS
4	W	116	LEU
4	W	118	ARG
4	W	130	GLN
4	W	157	LYS
4	W	159	ASP
4	W	179	LYS
4	W	185	PHE
4	W	190	ARG
4	W	201	SER
4	W	211	ASP
4	W	225	PHE
4	W	227	LEU
4	W	230	ARG
4	W	238	ASP
4	W	281	ARG
5	X	7	SER
5	X	15	LEU
5	X	21	LEU
5	X	22	LEU
5	X	27	GLN
5	X	39	THR
5	X	63	GLU
5	X	88	LYS
5	X	95	MET
5	X	123	LYS
5	X	127	GLU
5	X	130	ARG
5	X	133	LEU
5	X	138	GLN
5	X	142	LEU
5	X	144	LEU
5	X	146	GLU
5	X	150	ASP
5	X	153	ASN
5	X	157	SER
6	Y	6	ARG
6	Y	22	LEU
6	Y	23	GLU
6	Y	31	GLU

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Mol	Chain	Res	Type
6	Y	54	SER
6	Y	60	LYS
6	Y	62	LEU
6	Y	73	SER
6	Y	81	GLU
6	Y	97	ARG
6	Y	100	ASN
6	Y	105	ARG
6	Y	131	LEU
6	Y	141	GLU
6	Y	166	LYS
6	Y	167	ASN
7	Z	27	GLU
7	Z	39	GLU
7	Z	55	LEU
7	Z	68	SER
7	Z	74	ARG
7	Z	86	PHE
7	Z	96	GLN
7	Z	112	LYS
7	Z	140	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	HIS
1	A	144	GLN
1	A	192	HIS
1	A	205	GLN
1	A	260	ASN
1	A	370	HIS
3	C	14	HIS
3	C	54	GLN
3	C	107	ASN
3	C	153	ASN
3	C	213	ASN
3	C	263	HIS
3	C	327	ASN
4	D	111	HIS
4	D	219	ASN
4	D	233	ASN
5	E	18	ASN

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Mol	Chain	Res	Type
5	E	102	ASN
5	E	138	GLN
6	F	78	GLN
6	F	129	HIS
7	G	61	ASN
7	G	129	HIS
1	T	108	HIS
1	T	176	HIS
1	T	192	HIS
1	T	260	ASN
1	T	294	GLN
2	U	226	ASN
3	V	107	ASN
3	V	136	HIS
3	V	153	ASN
3	V	213	ASN
3	V	263	HIS
4	W	111	HIS
4	W	132	GLN
5	X	5	HIS
5	X	18	ASN
5	X	138	GLN
6	Y	78	GLN
7	Z	61	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	392/418 (93%)	-0.36	5 (1%) 79 72	234, 254, 267, 283	0
1	T	392/418 (93%)	-0.42	3 (0%) 87 82	234, 254, 266, 280	0
2	B	228/394 (57%)	-0.18	7 (3%) 52 43	210, 253, 272, 281	0
2	U	228/394 (57%)	-0.18	6 (2%) 59 50	207, 253, 270, 282	0
3	C	354/372 (95%)	-0.21	17 (4%) 34 28	241, 259, 276, 296	0
3	V	354/372 (95%)	-0.16	18 (5%) 32 26	242, 259, 278, 291	0
4	D	284/300 (94%)	-0.46	3 (1%) 82 76	237, 256, 269, 278	0
4	W	284/300 (94%)	-0.44	5 (1%) 71 63	233, 256, 269, 278	0
5	E	174/178 (97%)	-0.33	5 (2%) 55 45	244, 259, 271, 281	0
5	X	174/178 (97%)	-0.40	5 (2%) 55 45	245, 258, 270, 282	0
6	F	167/168 (99%)	-0.26	2 (1%) 81 74	232, 251, 264, 274	0
6	Y	167/168 (99%)	-0.23	3 (1%) 71 63	231, 251, 265, 274	0
7	G	139/151 (92%)	-0.41	2 (1%) 78 70	243, 258, 275, 285	0
7	Z	139/151 (92%)	-0.44	0 100 100	241, 258, 275, 288	0
All	All	3476/3962 (87%)	-0.32	81 (2%) 64 55	207, 256, 271, 296	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	299	ARG	6.8
4	W	143	VAL	6.1
3	C	298	ALA	5.7
3	V	249	ALA	5.3
3	V	132	TRP	5.3
4	W	153	TYR	4.2
3	V	307	LYS	4.1
3	C	301	ARG	4.1

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Mol	Chain	Res	Type	RSRZ
3	V	261	ALA	3.9
1	T	415	GLY	3.6
3	C	302	PHE	3.6
7	G	21	GLU	3.6
3	V	281	PHE	3.6
3	V	133	VAL	3.6
4	W	142	ALA	3.4
3	V	260	ALA	3.4
2	U	225	TYR	3.3
3	C	258	LEU	3.3
1	A	414	PHE	3.3
3	C	300	GLU	3.3
2	U	155	VAL	3.3
5	E	52	ASN	3.3
3	C	297	THR	3.3
5	E	24	ILE	3.1
2	B	184	ILE	3.1
3	V	309	ALA	3.1
4	D	141	ARG	3.0
2	B	180	ARG	3.0
2	U	154	GLY	2.9
6	Y	53	ILE	2.9
2	B	181	ARG	2.9
3	V	92	ILE	2.9
3	C	206	HIS	2.9
2	B	341	LYS	2.8
5	X	50	LYS	2.8
6	Y	2	THR	2.8
3	V	304	ASN	2.7
3	C	249	ALA	2.7
3	V	271	THR	2.7
3	V	131	TRP	2.7
1	T	418	SER	2.7
1	A	68	GLU	2.7
5	E	50	LYS	2.6
3	V	297	THR	2.6
5	E	71	ILE	2.6
3	C	248	LEU	2.5
5	E	51	ALA	2.5
3	V	308	LYS	2.5
2	B	288	ALA	2.5
2	B	183	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
6	F	35	LYS	2.5
3	V	91	VAL	2.4
1	A	83	VAL	2.4
5	X	113	LEU	2.4
3	V	38	SER	2.4
7	G	135	ALA	2.4
1	T	143	VAL	2.3
5	X	133	LEU	2.3
3	V	93	LEU	2.3
4	W	144	ILE	2.3
4	D	142	ALA	2.3
2	U	359	ALA	2.3
3	C	259	VAL	2.3
3	C	131	TRP	2.3
4	D	162	THR	2.2
6	F	102	PHE	2.2
3	C	93	LEU	2.2
3	C	251	THR	2.2
3	V	299	ARG	2.2
3	C	260	ALA	2.2
1	A	82	ILE	2.2
5	X	46	ILE	2.1
5	X	147	LYS	2.1
3	C	210	PHE	2.1
2	B	182	LEU	2.1
2	U	276	VAL	2.1
4	W	187	GLU	2.1
6	Y	54	SER	2.1
3	C	271	THR	2.1
1	A	413	VAL	2.0
2	U	161	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.