



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 06:17 AM UTC

PDB ID : 3LRC / pdb_00003lrc
Title : Structure of E. coli AdiC (P1)
Authors : Gao, X.; Lu, F.; Zhou, L.; Shi, Y.
Deposited on : 2010-02-11
Resolution : 4.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

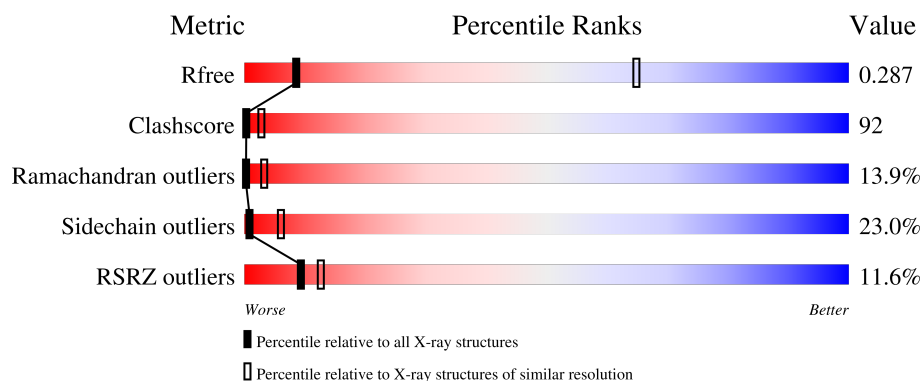
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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}	180053	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
Sidechain outliers	187428	1055 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	445	6% 15% 56% 19% 8%
1	B	445	15% 17% 52% 21% 8%
1	C	445	17% 16% 52% 21% 8%
1	D	445	6% 16% 54% 20% 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12144 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.

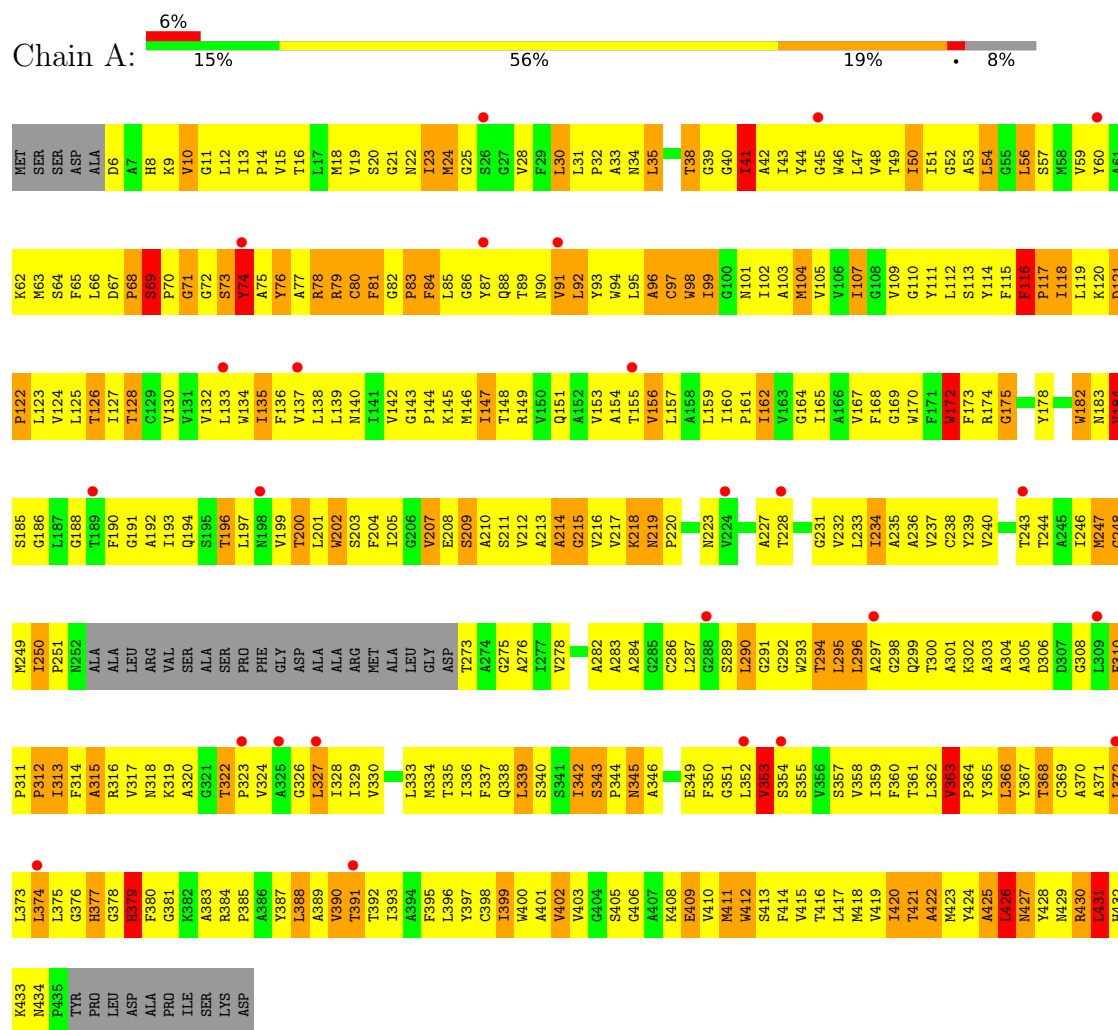
- Molecule 1 is a protein called Arginine/agmatine antiporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	0	0	0
			3036	2020	481	514	21			
1	B	410	Total	C	N	O	S	0	0	0
			3036	2020	481	514	21			
1	C	410	Total	C	N	O	S	0	0	0
			3036	2020	481	514	21			
1	D	410	Total	C	N	O	S	0	0	0
			3036	2020	481	514	21			

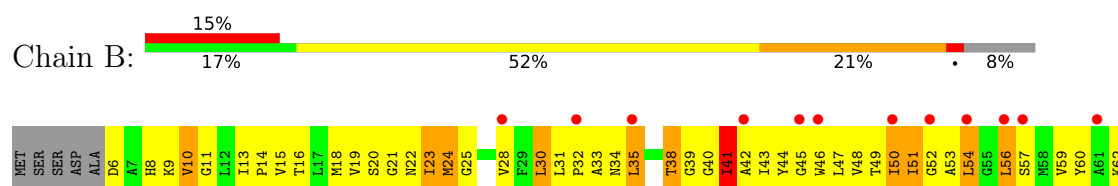
3 Residue-property plots

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

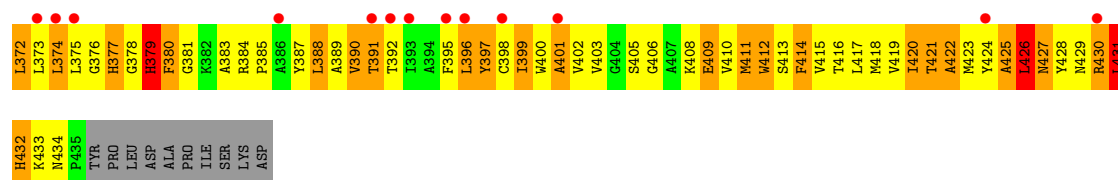
• Molecule 1: Arginine/agmatine antiporter



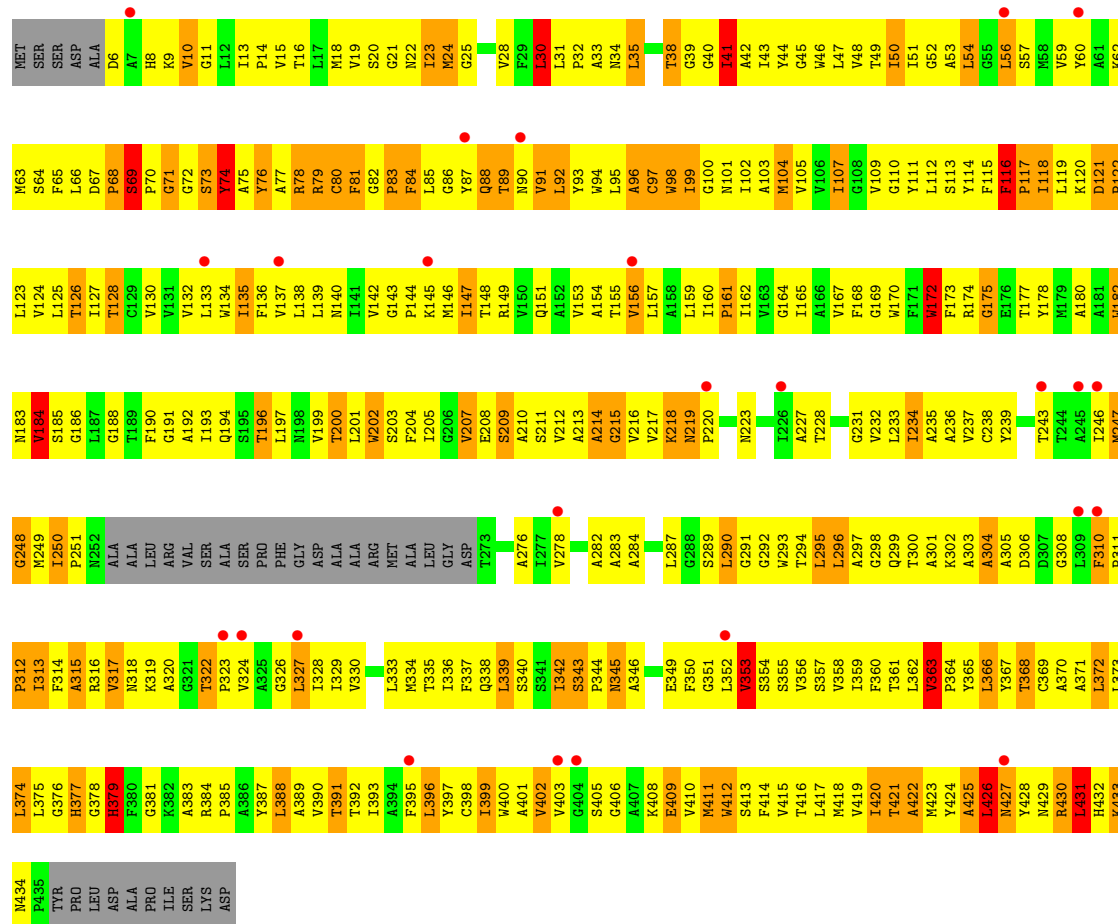
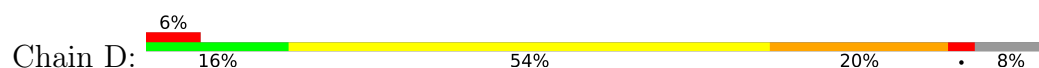
• Molecule 1: Arginine/agmatine antiporter







● Molecule 1: Arginine/agmatine antiporter



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	81.88Å 111.67Å 113.76Å 80.03° 74.34° 68.83°	Depositor
Resolution (Å)	30.00 – 4.00 30.00 – 4.00	Depositor EDS
% Data completeness (in resolution range)	95.7 (30.00-4.00) 96.7 (30.00-4.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 3.99Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.319 , 0.331 0.283 , 0.287	Depositor DCC
R_{free} test set	1472 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	184.3	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 322.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12144	wwPDB-VP
Average B, all atoms (Å ²)	301.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.60	1/3115 (0.0%)	1.02	9/4264 (0.2%)
1	B	0.62	1/3115 (0.0%)	1.03	11/4264 (0.3%)
1	C	0.61	1/3115 (0.0%)	1.02	11/4264 (0.3%)
1	D	0.60	1/3115 (0.0%)	1.03	9/4264 (0.2%)
All	All	0.61	4/12460 (0.0%)	1.02	40/17056 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	363	VAL	CA-CB	7.89	1.58	1.54
1	D	363	VAL	CA-CB	7.61	1.57	1.54
1	A	363	VAL	CA-CB	6.93	1.57	1.54
1	C	363	VAL	CA-CB	6.58	1.57	1.54

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	425	ALA	N-CA-C	-8.08	103.56	113.41
1	A	425	ALA	N-CA-C	-8.00	103.65	113.41
1	B	402	VAL	N-CA-C	-7.80	106.30	113.71
1	B	80	CYS	N-CA-C	-7.73	103.31	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	425	ALA	N-CA-C	-7.56	104.19	113.41
1	B	425	ALA	N-CA-C	-7.54	104.21	113.41
1	B	342	ILE	N-CA-C	7.17	117.26	110.30
1	C	80	CYS	N-CA-C	-7.08	104.11	112.89
1	D	342	ILE	N-CA-C	7.04	117.13	110.30
1	C	342	ILE	N-CA-C	6.99	117.08	110.30
1	A	342	ILE	N-CA-C	6.86	116.96	110.30
1	D	80	CYS	N-CA-C	-6.86	104.39	112.89
1	C	370	ALA	N-CA-C	-6.30	104.51	111.82
1	A	402	VAL	N-CA-C	-6.22	107.80	113.71
1	A	80	CYS	N-CA-C	-6.17	105.24	112.89
1	B	311	PRO	CA-C-N	6.16	127.54	119.84
1	B	311	PRO	C-N-CA	6.16	127.54	119.84
1	B	186	GLY	N-CA-C	-6.07	105.65	112.33
1	A	186	GLY	N-CA-C	-5.79	105.28	111.93
1	C	311	PRO	CA-C-N	5.78	127.06	119.84
1	C	311	PRO	C-N-CA	5.78	127.06	119.84
1	C	186	GLY	N-CA-C	-5.76	105.30	111.93
1	B	110	GLY	N-CA-C	-5.63	108.15	114.40
1	C	110	GLY	N-CA-C	-5.60	108.18	114.40
1	D	186	GLY	N-CA-C	-5.49	105.61	111.93
1	D	110	GLY	N-CA-C	-5.46	108.34	114.40
1	D	402	VAL	N-CA-C	-5.45	108.53	113.71
1	A	110	GLY	N-CA-C	-5.45	108.35	114.40
1	D	342	ILE	CA-C-N	5.34	131.32	121.70
1	D	342	ILE	C-N-CA	5.34	131.32	121.70
1	C	432	HIS	N-CA-C	5.31	122.11	110.80
1	C	342	ILE	CA-C-N	5.29	131.21	121.70
1	C	342	ILE	C-N-CA	5.29	131.21	121.70
1	A	342	ILE	CA-C-N	5.28	131.21	121.70
1	A	342	ILE	C-N-CA	5.28	131.21	121.70
1	B	342	ILE	CA-C-N	5.27	131.18	121.70
1	B	342	ILE	C-N-CA	5.27	131.18	121.70
1	D	363	VAL	O-C-N	5.23	123.77	120.42
1	A	294	THR	N-CA-C	-5.20	105.61	111.28
1	B	370	ALA	N-CA-C	-5.04	105.91	111.71

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	431	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	A	79	ARG	Peptide
1	B	431	LEU	Peptide
1	B	79	ARG	Peptide
1	C	431	LEU	Peptide
1	C	79	ARG	Peptide
1	D	431	LEU	Peptide
1	D	79	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3036	0	3141	601	0
1	B	3036	0	3141	608	0
1	C	3036	0	3141	599	0
1	D	3036	0	3141	594	0
All	All	12144	0	12564	2268	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 92.

All (2268) 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:D:188:GLY:O	1:D:192:ALA:HB2	1.29	1.30
1:B:188:GLY:O	1:B:192:ALA:HB2	1.29	1.29
1:A:188:GLY:O	1:A:192:ALA:HB2	1.29	1.27
1:C:188:GLY:O	1:C:192:ALA:HB2	1.30	1.26
1:B:38:THR:HB	1:B:39:GLY:HA3	1.29	1.14
1:D:38:THR:HB	1:D:39:GLY:HA3	1.29	1.14
1:B:66:LEU:O	1:B:68:PRO:HD3	1.50	1.11
1:C:85:LEU:HD21	1:D:85:LEU:HD21	1.14	1.11
1:C:92:LEU:HD11	1:C:363:VAL:HG21	1.11	1.11
1:C:315:ALA:HB1	1:C:316:ARG:HA	1.10	1.10
1:D:315:ALA:HB1	1:D:316:ARG:HA	1.09	1.09
1:A:85:LEU:HD21	1:B:85:LEU:HD21	1.13	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:THR:HB	1:A:39:GLY:HA3	1.28	1.09
1:A:66:LEU:O	1:A:68:PRO:HD3	1.53	1.09
1:C:66:LEU:O	1:C:68:PRO:HD3	1.49	1.08
1:D:66:LEU:O	1:D:68:PRO:HD3	1.53	1.08
1:A:92:LEU:HD11	1:A:363:VAL:HG21	1.11	1.08
1:D:24:MET:HE1	1:D:238:CYS:SG	1.94	1.08
1:D:92:LEU:HD11	1:D:363:VAL:HG21	1.10	1.07
1:B:92:LEU:HD11	1:B:363:VAL:HG21	1.09	1.07
1:A:24:MET:HE3	1:A:162:ILE:HD12	1.36	1.06
1:A:315:ALA:HB1	1:A:316:ARG:HA	1.11	1.05
1:C:16:THR:HG22	1:C:227:ALA:HA	1.37	1.05
1:D:60:TYR:CE2	1:D:368:THR:HG21	1.91	1.05
1:B:311:PRO:HD3	1:B:426:LEU:HD21	1.05	1.05
1:B:315:ALA:HB1	1:B:316:ARG:HA	1.10	1.04
1:C:38:THR:HB	1:C:39:GLY:HA3	1.29	1.04
1:C:60:TYR:CE2	1:C:368:THR:HG21	1.92	1.04
1:D:60:TYR:HE2	1:D:368:THR:HG21	1.23	1.04
1:A:60:TYR:CE2	1:A:368:THR:HG21	1.92	1.04
1:B:16:THR:HG22	1:B:227:ALA:HA	1.40	1.04
1:B:60:TYR:CE2	1:B:368:THR:HG21	1.93	1.03
1:A:24:MET:HE1	1:A:238:CYS:SG	1.98	1.03
1:A:16:THR:HG22	1:A:227:ALA:HA	1.40	1.02
1:D:24:MET:HE3	1:D:162:ILE:HD12	1.37	1.02
1:C:311:PRO:HD3	1:C:426:LEU:HD21	1.04	1.02
1:D:64:SER:O	1:D:68:PRO:HG3	1.59	1.02
1:A:164:GLY:O	1:A:168:PHE:HB2	1.61	1.01
1:B:24:MET:HE3	1:B:162:ILE:HD12	1.42	1.01
1:B:360:PHE:HE1	1:B:413:SER:HA	1.23	1.01
1:C:360:PHE:HE1	1:C:413:SER:HA	1.24	1.01
1:C:60:TYR:HE2	1:C:368:THR:HG21	1.25	1.01
1:C:24:MET:HE3	1:C:162:ILE:HD12	1.43	1.01
1:B:24:MET:HE1	1:B:238:CYS:SG	1.99	1.00
1:B:313:ILE:O	1:B:315:ALA:HB3	1.59	1.00
1:C:24:MET:HE1	1:C:238:CYS:SG	2.01	1.00
1:D:16:THR:HG22	1:D:227:ALA:HA	1.41	1.00
1:D:313:ILE:O	1:D:315:ALA:HB3	1.62	1.00
1:A:421:THR:HG22	1:A:422:ALA:N	1.76	0.99
1:C:313:ILE:O	1:C:315:ALA:HB3	1.61	0.99
1:D:311:PRO:HD3	1:D:426:LEU:CD2	1.91	0.99
1:B:302:LYS:HG2	1:B:323:PRO:HB3	1.45	0.99
1:B:365:TYR:HB3	1:B:398:CYS:SG	2.02	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:TYR:HE2	1:A:368:THR:HG21	1.22	0.99
1:A:414:PHE:HB2	1:B:414:PHE:HD1	1.26	0.99
1:D:311:PRO:CD	1:D:426:LEU:HD21	1.92	0.99
1:B:64:SER:O	1:B:68:PRO:HG3	1.63	0.99
1:D:164:GLY:O	1:D:168:PHE:HB2	1.60	0.98
1:A:64:SER:O	1:A:68:PRO:HG3	1.64	0.98
1:A:313:ILE:O	1:A:315:ALA:HB3	1.62	0.98
1:A:311:PRO:HD3	1:A:426:LEU:CD2	1.93	0.98
1:C:164:GLY:O	1:C:168:PHE:HB2	1.62	0.98
1:D:92:LEU:CD1	1:D:363:VAL:HG21	1.94	0.97
1:A:311:PRO:HD3	1:A:426:LEU:HD21	0.98	0.97
1:B:92:LEU:CD1	1:B:363:VAL:HG21	1.95	0.97
1:C:81:PHE:HB3	1:C:82:GLY:HA2	1.47	0.96
1:A:302:LYS:HG2	1:A:323:PRO:HB3	1.47	0.96
1:B:164:GLY:O	1:B:168:PHE:HB2	1.63	0.96
1:C:64:SER:O	1:C:68:PRO:HG3	1.64	0.96
1:D:302:LYS:HG2	1:D:323:PRO:HB3	1.47	0.96
1:A:365:TYR:HB3	1:A:398:CYS:SG	2.06	0.96
1:A:84:PHE:CE1	1:B:85:LEU:HD11	2.01	0.96
1:C:41:ILE:HG22	1:C:246:ILE:HD13	1.46	0.96
1:A:311:PRO:CD	1:A:426:LEU:HD21	1.94	0.95
1:D:421:THR:HG22	1:D:422:ALA:N	1.78	0.95
1:C:302:LYS:HG2	1:C:323:PRO:HB3	1.45	0.95
1:B:60:TYR:HE2	1:B:368:THR:HG21	1.27	0.95
1:D:92:LEU:HD21	1:D:363:VAL:HG23	1.48	0.95
1:B:41:ILE:HG22	1:B:246:ILE:HD13	1.48	0.95
1:B:92:LEU:HD21	1:B:363:VAL:HG23	1.49	0.95
1:B:81:PHE:HB3	1:B:82:GLY:HA2	1.47	0.95
1:B:209:SER:HA	1:B:296:LEU:HD11	1.49	0.95
1:C:365:TYR:HB3	1:C:398:CYS:SG	2.05	0.95
1:D:360:PHE:HE1	1:D:413:SER:HA	1.31	0.95
1:A:85:LEU:HD11	1:B:84:PHE:CE1	2.02	0.94
1:A:118:ILE:HD12	1:A:119:LEU:O	1.68	0.94
1:B:421:THR:HG22	1:B:422:ALA:N	1.81	0.94
1:A:360:PHE:HE1	1:A:413:SER:HA	1.33	0.93
1:B:116:PHE:HB3	1:B:117:PRO:HD2	1.49	0.93
1:B:315:ALA:CB	1:B:316:ARG:HA	1.98	0.93
1:A:209:SER:HA	1:A:296:LEU:HD11	1.51	0.92
1:B:118:ILE:HD12	1:B:119:LEU:O	1.69	0.92
1:A:92:LEU:CD1	1:A:363:VAL:HG21	1.97	0.92
1:D:116:PHE:HB3	1:D:117:PRO:HD2	1.50	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:209:SER:HA	1:D:296:LEU:HD11	1.48	0.92
1:C:92:LEU:CD1	1:C:363:VAL:HG21	1.97	0.92
1:C:421:THR:HG22	1:C:422:ALA:N	1.84	0.92
1:C:250:ILE:H	1:C:251:PRO:HD2	1.33	0.92
1:D:119:LEU:HD13	1:D:124:VAL:HG11	1.52	0.92
1:C:116:PHE:HB3	1:C:117:PRO:HD2	1.49	0.92
1:C:315:ALA:HB1	1:C:316:ARG:CA	2.00	0.92
1:B:111:TYR:HB3	1:B:283:ALA:HB2	1.52	0.91
1:D:342:ILE:HB	1:D:343:SER:HB2	1.53	0.91
1:A:116:PHE:HB3	1:A:117:PRO:HD2	1.49	0.91
1:D:365:TYR:HB3	1:D:398:CYS:SG	2.10	0.91
1:A:342:ILE:HB	1:A:343:SER:HB2	1.51	0.91
1:C:119:LEU:HD13	1:C:124:VAL:HG11	1.51	0.91
1:D:84:PHE:CE1	1:D:85:LEU:HD23	2.06	0.91
1:C:92:LEU:HD21	1:C:363:VAL:HG23	1.49	0.91
1:C:414:PHE:HD1	1:D:414:PHE:HB2	1.35	0.91
1:C:111:TYR:HB3	1:C:283:ALA:HB2	1.50	0.91
1:B:315:ALA:HB1	1:B:316:ARG:CA	2.00	0.91
1:D:315:ALA:HB1	1:D:316:ARG:CA	2.00	0.91
1:B:250:ILE:H	1:B:251:PRO:HD2	1.34	0.90
1:B:342:ILE:HB	1:B:343:SER:HB2	1.53	0.90
1:B:119:LEU:HD13	1:B:124:VAL:HG11	1.51	0.90
1:D:118:ILE:HD12	1:D:119:LEU:O	1.71	0.90
1:A:250:ILE:H	1:A:251:PRO:HD2	1.35	0.90
1:A:85:LEU:HD21	1:B:85:LEU:CD2	2.00	0.90
1:A:315:ALA:HB1	1:A:316:ARG:CA	2.00	0.90
1:A:188:GLY:O	1:A:192:ALA:CB	2.19	0.90
1:D:32:PRO:HG3	1:D:243:THR:HG22	1.54	0.90
1:D:311:PRO:HD3	1:D:426:LEU:HD21	0.96	0.90
1:D:250:ILE:H	1:D:251:PRO:HD2	1.35	0.89
1:D:119:LEU:HD22	1:D:124:VAL:HG21	1.54	0.89
1:A:111:TYR:HB3	1:A:283:ALA:HB2	1.54	0.89
1:A:85:LEU:CD2	1:B:85:LEU:HD21	2.01	0.89
1:C:118:ILE:HD12	1:C:119:LEU:O	1.71	0.89
1:C:63:MET:HG3	1:C:76:TYR:CE2	2.07	0.89
1:A:81:PHE:HB3	1:A:82:GLY:HA2	1.53	0.89
1:A:119:LEU:HD13	1:A:124:VAL:HG11	1.53	0.89
1:D:111:TYR:HB3	1:D:283:ALA:HB2	1.55	0.89
1:C:84:PHE:CE1	1:D:85:LEU:HD11	2.07	0.89
1:A:85:LEU:HD11	1:B:84:PHE:CD1	2.08	0.89
1:D:425:ALA:C	1:D:427:ASN:H	1.78	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:LEU:HD11	1:D:84:PHE:CE1	2.07	0.88
1:A:41:ILE:HG22	1:A:246:ILE:HD13	1.56	0.88
1:A:119:LEU:HD22	1:A:124:VAL:HG21	1.55	0.88
1:C:311:PRO:HD3	1:C:426:LEU:CD2	1.98	0.88
1:B:425:ALA:C	1:B:427:ASN:H	1.80	0.88
1:C:425:ALA:C	1:C:427:ASN:H	1.81	0.88
1:A:84:PHE:CE1	1:A:85:LEU:HD23	2.08	0.88
1:B:119:LEU:HD22	1:B:124:VAL:HG21	1.56	0.88
1:C:24:MET:HB3	1:C:25:GLY:HA2	1.56	0.88
1:D:92:LEU:HD21	1:D:363:VAL:CG2	2.04	0.88
1:A:414:PHE:HB2	1:B:414:PHE:CD1	2.08	0.87
1:C:250:ILE:H	1:C:251:PRO:CD	1.87	0.87
1:D:90:ASN:OD1	1:D:300:THR:O	1.91	0.87
1:D:188:GLY:O	1:D:192:ALA:CB	2.20	0.87
1:C:119:LEU:HD22	1:C:124:VAL:HG21	1.56	0.87
1:C:209:SER:HA	1:C:296:LEU:HD11	1.52	0.87
1:C:342:ILE:HB	1:C:343:SER:HB2	1.53	0.87
1:D:24:MET:HB3	1:D:25:GLY:HA2	1.56	0.87
1:B:188:GLY:O	1:B:192:ALA:CB	2.20	0.87
1:B:32:PRO:HG3	1:B:243:THR:HG22	1.57	0.87
1:C:85:LEU:CD2	1:D:85:LEU:HD21	2.04	0.87
1:A:24:MET:HB3	1:A:25:GLY:HA2	1.57	0.86
1:A:425:ALA:C	1:A:427:ASN:H	1.81	0.86
1:D:81:PHE:HB3	1:D:82:GLY:HA2	1.56	0.86
1:B:250:ILE:H	1:B:251:PRO:CD	1.87	0.86
1:C:92:LEU:HD21	1:C:363:VAL:CG2	2.05	0.86
1:B:84:PHE:CE1	1:B:85:LEU:HD23	2.10	0.86
1:A:250:ILE:H	1:A:251:PRO:CD	1.88	0.86
1:B:311:PRO:HD3	1:B:426:LEU:CD2	1.99	0.86
1:A:373:LEU:HD13	1:B:428:TYR:OH	1.76	0.85
1:A:41:ILE:HG13	1:A:43:ILE:CG1	2.06	0.85
1:C:188:GLY:O	1:C:192:ALA:CB	2.20	0.85
1:D:202:TRP:CE3	1:D:358:VAL:HG11	2.12	0.85
1:D:250:ILE:H	1:D:251:PRO:CD	1.89	0.85
1:B:41:ILE:CG2	1:B:246:ILE:HD13	2.06	0.85
1:B:92:LEU:HD21	1:B:363:VAL:CG2	2.06	0.85
1:C:32:PRO:HG3	1:C:243:THR:HG22	1.58	0.85
1:D:315:ALA:CB	1:D:316:ARG:HA	1.98	0.85
1:A:92:LEU:HD21	1:A:363:VAL:HG23	1.57	0.85
1:A:90:ASN:OD1	1:A:300:THR:O	1.94	0.85
1:A:342:ILE:N	1:A:343:SER:HB2	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:41:ILE:HG22	1:D:246:ILE:HD13	1.57	0.85
1:C:41:ILE:CG2	1:C:246:ILE:HD13	2.06	0.84
1:A:315:ALA:CB	1:A:316:ARG:HA	1.99	0.84
1:A:78:ARG:HA	1:A:82:GLY:HA3	1.58	0.84
1:B:24:MET:HB3	1:B:25:GLY:HA2	1.57	0.84
1:B:202:TRP:CE3	1:B:358:VAL:HG11	2.11	0.84
1:A:202:TRP:CE3	1:A:358:VAL:HG11	2.13	0.84
1:B:365:TYR:HB3	1:B:398:CYS:HG	1.37	0.84
1:C:84:PHE:CE1	1:C:85:LEU:HD23	2.11	0.84
1:C:133:LEU:HD23	1:C:290:LEU:HD11	1.60	0.84
1:D:78:ARG:HA	1:D:82:GLY:HA3	1.57	0.83
1:B:412:TRP:HA	1:B:412:TRP:CE3	2.12	0.83
1:C:376:GLY:C	1:C:379:HIS:H	1.87	0.83
1:D:412:TRP:CE3	1:D:412:TRP:HA	2.12	0.83
1:A:414:PHE:HD1	1:B:414:PHE:HB2	1.43	0.83
1:D:342:ILE:N	1:D:343:SER:HB2	1.94	0.83
1:B:360:PHE:CE1	1:B:413:SER:HA	2.13	0.83
1:C:412:TRP:HA	1:C:412:TRP:CE3	2.12	0.83
1:C:202:TRP:CE3	1:C:358:VAL:HG11	2.13	0.82
1:B:310:PHE:HB3	1:B:311:PRO:C	2.04	0.82
1:C:93:TYR:CE2	1:C:97:CYS:SG	2.72	0.82
1:D:412:TRP:HA	1:D:412:TRP:HE3	1.45	0.82
1:A:38:THR:HB	1:A:39:GLY:CA	2.09	0.82
1:A:210:ALA:HB3	1:A:228:THR:HG22	1.61	0.82
1:C:38:THR:HB	1:C:39:GLY:CA	2.09	0.82
1:A:32:PRO:HG3	1:A:243:THR:HG22	1.61	0.82
1:B:78:ARG:HA	1:B:82:GLY:HA3	1.61	0.82
1:B:342:ILE:N	1:B:343:SER:HB2	1.94	0.82
1:B:38:THR:HB	1:B:39:GLY:CA	2.08	0.81
1:C:311:PRO:CD	1:C:426:LEU:HD21	2.00	0.81
1:D:133:LEU:HD23	1:D:290:LEU:HD11	1.61	0.81
1:B:406:GLY:HA3	1:B:409:GLU:OE2	1.81	0.81
1:C:73:SER:H	1:C:76:TYR:HE1	1.23	0.81
1:C:310:PHE:HB3	1:C:311:PRO:C	2.06	0.81
1:D:421:THR:HG22	1:D:422:ALA:H	1.42	0.81
1:C:342:ILE:N	1:C:343:SER:HB2	1.95	0.81
1:A:412:TRP:CE3	1:A:412:TRP:HA	2.11	0.81
1:A:412:TRP:HA	1:A:412:TRP:HE3	1.44	0.81
1:C:85:LEU:HD21	1:D:85:LEU:CD2	2.05	0.81
1:A:38:THR:CB	1:A:39:GLY:HA3	2.10	0.81
1:A:60:TYR:HE2	1:A:368:THR:CG2	1.94	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:ILE:CA	1:A:343:SER:HB2	2.11	0.81
1:D:78:ARG:CA	1:D:82:GLY:HA3	2.10	0.81
1:A:133:LEU:HD23	1:A:290:LEU:HD11	1.61	0.81
1:D:210:ALA:HB3	1:D:228:THR:HG22	1.61	0.81
1:A:41:ILE:HG13	1:A:43:ILE:HG13	1.63	0.81
1:B:73:SER:H	1:B:76:TYR:HE1	1.26	0.81
1:D:38:THR:HB	1:D:39:GLY:CA	2.10	0.81
1:D:41:ILE:HG13	1:D:43:ILE:CG1	2.11	0.81
1:C:38:THR:CB	1:C:39:GLY:HA3	2.11	0.81
1:D:60:TYR:HE2	1:D:368:THR:CG2	1.94	0.81
1:A:411:MET:HG3	1:A:412:TRP:N	1.96	0.80
1:B:342:ILE:CA	1:B:343:SER:HB2	2.11	0.80
1:A:421:THR:HG22	1:A:422:ALA:H	1.42	0.80
1:C:412:TRP:HA	1:C:412:TRP:HE3	1.45	0.80
1:C:201:LEU:HG	1:C:401:ALA:HB2	1.63	0.80
1:D:84:PHE:HE1	1:D:85:LEU:HD23	1.44	0.80
1:A:92:LEU:HD21	1:A:363:VAL:CG2	2.11	0.80
1:C:173:PHE:HA	1:C:174:ARG:HB2	1.64	0.80
1:D:342:ILE:CA	1:D:343:SER:HB2	2.11	0.80
1:A:84:PHE:HE1	1:A:85:LEU:HD23	1.46	0.80
1:A:24:MET:O	1:A:28:VAL:HG23	1.82	0.80
1:A:342:ILE:HB	1:A:343:SER:CB	2.12	0.80
1:B:376:GLY:C	1:B:379:HIS:H	1.88	0.80
1:A:84:PHE:CD1	1:B:85:LEU:HD11	2.16	0.80
1:B:173:PHE:HA	1:B:174:ARG:HB2	1.64	0.80
1:C:78:ARG:HA	1:C:82:GLY:HA3	1.61	0.80
1:A:78:ARG:CA	1:A:82:GLY:HA3	2.11	0.80
1:A:173:PHE:HA	1:A:174:ARG:HB2	1.64	0.80
1:C:35:LEU:HD23	1:C:196:THR:HG22	1.64	0.79
1:C:84:PHE:CD1	1:D:85:LEU:HD11	2.16	0.79
1:C:374:LEU:O	1:C:375:LEU:HD23	1.81	0.79
1:A:95:LEU:HA	1:A:98:TRP:CZ3	2.18	0.79
1:A:140:ASN:HB3	1:A:327:LEU:HD22	1.62	0.79
1:B:133:LEU:HD23	1:B:290:LEU:HD11	1.61	0.79
1:C:56:LEU:HD11	1:C:365:TYR:HD1	1.47	0.79
1:B:210:ALA:HB3	1:B:228:THR:HG22	1.64	0.79
1:C:210:ALA:HB3	1:C:228:THR:HG22	1.64	0.79
1:B:412:TRP:HA	1:B:412:TRP:HE3	1.45	0.79
1:A:19:VAL:HG21	1:A:210:ALA:HB2	1.63	0.79
1:B:19:VAL:HG21	1:B:210:ALA:HB2	1.65	0.79
1:D:355:SER:O	1:D:358:VAL:HB	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:ILE:CB	1:A:343:SER:HB2	2.12	0.79
1:C:78:ARG:CA	1:C:82:GLY:HA3	2.13	0.79
1:C:315:ALA:CB	1:C:316:ARG:HA	1.98	0.79
1:C:342:ILE:CA	1:C:343:SER:HB2	2.12	0.79
1:B:35:LEU:HD23	1:B:196:THR:HG22	1.64	0.79
1:C:406:GLY:HA3	1:C:409:GLU:OE2	1.82	0.79
1:D:73:SER:H	1:D:76:TYR:HE1	1.30	0.79
1:B:342:ILE:CB	1:B:343:SER:HB2	2.13	0.79
1:B:38:THR:CB	1:B:39:GLY:HA3	2.11	0.78
1:B:79:ARG:HB3	1:B:375:LEU:HD21	1.64	0.78
1:D:41:ILE:HG13	1:D:43:ILE:HG13	1.65	0.78
1:D:95:LEU:HA	1:D:98:TRP:CZ3	2.18	0.78
1:A:81:PHE:HD2	1:A:81:PHE:C	1.90	0.78
1:B:421:THR:HG22	1:B:422:ALA:H	1.47	0.78
1:C:360:PHE:CE1	1:C:413:SER:HA	2.15	0.78
1:C:414:PHE:HB2	1:D:414:PHE:HD1	1.48	0.78
1:C:19:VAL:HG21	1:C:210:ALA:HB2	1.65	0.78
1:A:24:MET:HB3	1:A:25:GLY:CA	2.14	0.78
1:B:409:GLU:O	1:B:412:TRP:HB2	1.83	0.78
1:C:116:PHE:HB3	1:C:117:PRO:CD	2.13	0.78
1:D:24:MET:HB3	1:D:25:GLY:CA	2.14	0.78
1:A:310:PHE:HB3	1:A:311:PRO:C	2.08	0.78
1:D:342:ILE:CB	1:D:343:SER:HB2	2.13	0.78
1:A:116:PHE:HB3	1:A:117:PRO:CD	2.14	0.78
1:B:56:LEU:HD11	1:B:365:TYR:HD1	1.49	0.78
1:A:411:MET:O	1:A:415:VAL:HG23	1.84	0.78
1:C:74:TYR:CZ	1:C:304:ALA:HB2	2.18	0.78
1:B:74:TYR:CZ	1:B:304:ALA:HB2	2.18	0.78
1:B:78:ARG:CA	1:B:82:GLY:HA3	2.13	0.78
1:C:90:ASN:OD1	1:C:300:THR:O	2.02	0.78
1:C:342:ILE:CB	1:C:343:SER:HB2	2.13	0.78
1:D:60:TYR:CE2	1:D:368:THR:CG2	2.67	0.78
1:A:35:LEU:HD23	1:A:196:THR:HG22	1.66	0.78
1:D:81:PHE:HD2	1:D:81:PHE:C	1.91	0.78
1:A:93:TYR:CE2	1:A:97:CYS:SG	2.77	0.77
1:C:79:ARG:HB3	1:C:375:LEU:HD21	1.67	0.77
1:D:173:PHE:HA	1:D:174:ARG:HB2	1.64	0.77
1:D:201:LEU:HG	1:D:401:ALA:HB2	1.66	0.77
1:A:414:PHE:CD1	1:B:414:PHE:HB2	2.19	0.77
1:B:24:MET:HB3	1:B:25:GLY:CA	2.15	0.77
1:D:140:ASN:HB3	1:D:327:LEU:HD22	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:310:PHE:HB3	1:D:311:PRO:C	2.09	0.77
1:B:411:MET:O	1:B:415:VAL:HG23	1.84	0.77
1:C:24:MET:HB3	1:C:25:GLY:CA	2.13	0.77
1:D:24:MET:O	1:D:28:VAL:HG23	1.84	0.77
1:B:355:SER:O	1:B:358:VAL:HB	1.85	0.77
1:D:19:VAL:HG21	1:D:210:ALA:HB2	1.63	0.77
1:C:342:ILE:HB	1:C:343:SER:CB	2.15	0.77
1:D:342:ILE:HB	1:D:343:SER:CB	2.15	0.77
1:A:63:MET:HG3	1:A:76:TYR:CE2	2.20	0.77
1:A:355:SER:O	1:A:358:VAL:HB	1.84	0.77
1:B:116:PHE:HB3	1:B:117:PRO:CD	2.14	0.77
1:B:201:LEU:HG	1:B:401:ALA:HB2	1.65	0.77
1:D:406:GLY:HA3	1:D:409:GLU:OE2	1.85	0.77
1:A:15:VAL:HG21	1:A:217:VAL:HG13	1.65	0.76
1:B:140:ASN:HB3	1:B:327:LEU:HD22	1.66	0.76
1:C:355:SER:O	1:C:358:VAL:HB	1.85	0.76
1:A:79:ARG:HB3	1:A:375:LEU:HD21	1.68	0.76
1:D:66:LEU:C	1:D:68:PRO:HD3	2.09	0.76
1:A:362:LEU:HG	1:A:402:VAL:CG2	2.16	0.76
1:A:374:LEU:O	1:A:375:LEU:HD23	1.85	0.76
1:A:406:GLY:HA3	1:A:409:GLU:OE2	1.85	0.76
1:B:24:MET:O	1:B:28:VAL:HG23	1.85	0.76
1:B:90:ASN:OD1	1:B:300:THR:O	2.02	0.76
1:D:93:TYR:CE2	1:D:97:CYS:SG	2.78	0.76
1:B:115:PHE:HE1	1:B:276:ALA:HA	1.51	0.76
1:C:41:ILE:HG13	1:C:43:ILE:HG13	1.67	0.76
1:D:411:MET:HG3	1:D:412:TRP:N	1.98	0.76
1:D:116:PHE:HB3	1:D:117:PRO:CD	2.15	0.76
1:D:374:LEU:O	1:D:375:LEU:HD23	1.86	0.76
1:B:63:MET:HG3	1:B:76:TYR:CE2	2.20	0.76
1:D:35:LEU:HD23	1:D:196:THR:HG22	1.67	0.76
1:B:311:PRO:CD	1:B:426:LEU:HD21	2.01	0.76
1:B:342:ILE:HB	1:B:343:SER:CB	2.15	0.76
1:C:80:CYS:HA	1:C:374:LEU:HD23	1.68	0.76
1:A:115:PHE:HE1	1:A:276:ALA:HA	1.51	0.75
1:A:346:ALA:HB3	1:A:351:GLY:HA2	1.68	0.75
1:C:84:PHE:HE1	1:C:85:LEU:HD23	1.51	0.75
1:D:15:VAL:HG21	1:D:217:VAL:HG13	1.68	0.75
1:B:411:MET:HG3	1:B:412:TRP:N	2.02	0.75
1:A:366:LEU:CD1	1:B:421:THR:HG21	2.15	0.75
1:A:411:MET:HA	1:B:410:VAL:HG12	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:SER:H	1:A:76:TYR:HE1	1.35	0.75
1:C:411:MET:O	1:C:415:VAL:HG23	1.86	0.75
1:C:414:PHE:CD1	1:D:414:PHE:HB2	2.22	0.75
1:C:24:MET:O	1:C:28:VAL:HG23	1.86	0.75
1:B:102:ILE:HG23	1:B:338:GLN:HG2	1.69	0.75
1:C:115:PHE:HE1	1:C:276:ALA:HA	1.51	0.75
1:D:314:PHE:HA	1:D:315:ALA:C	2.12	0.75
1:B:80:CYS:HA	1:B:374:LEU:HD23	1.68	0.75
1:B:374:LEU:O	1:B:375:LEU:HD23	1.86	0.75
1:A:72:GLY:O	1:A:74:TYR:N	2.20	0.75
1:A:421:THR:O	1:A:423:MET:N	2.20	0.75
1:B:346:ALA:HB3	1:B:351:GLY:HA2	1.68	0.75
1:A:201:LEU:HG	1:A:401:ALA:HB2	1.66	0.74
1:A:376:GLY:C	1:A:379:HIS:H	1.95	0.74
1:B:41:ILE:HG13	1:B:43:ILE:HG13	1.68	0.74
1:C:406:GLY:HA3	1:C:409:GLU:CD	2.12	0.74
1:C:411:MET:HG3	1:C:412:TRP:N	2.00	0.74
1:C:433:LYS:CB	1:D:78:ARG:HH11	1.99	0.74
1:B:368:THR:HG22	1:B:369:CYS:N	2.00	0.74
1:D:74:TYR:CZ	1:D:304:ALA:HB2	2.23	0.74
1:D:115:PHE:HE1	1:D:276:ALA:HA	1.49	0.74
1:A:62:LYS:HA	1:A:65:PHE:HB2	1.69	0.74
1:A:109:VAL:HG11	1:A:128:THR:HG21	1.70	0.74
1:C:409:GLU:O	1:C:412:TRP:HB2	1.85	0.74
1:A:10:VAL:HG12	1:A:11:GLY:H	1.53	0.74
1:B:63:MET:SD	1:B:372:LEU:HD12	2.27	0.74
1:B:84:PHE:HE1	1:B:85:LEU:HD23	1.50	0.74
1:C:10:VAL:HG12	1:C:11:GLY:H	1.51	0.74
1:C:314:PHE:HA	1:C:315:ALA:C	2.12	0.74
1:C:346:ALA:HB3	1:C:351:GLY:HA2	1.68	0.74
1:C:15:VAL:HG21	1:C:217:VAL:HG13	1.70	0.74
1:B:56:LEU:HD11	1:B:365:TYR:CD1	2.23	0.74
1:D:79:ARG:HB3	1:D:375:LEU:HD21	1.69	0.74
1:C:41:ILE:HG13	1:C:43:ILE:CG1	2.18	0.74
1:A:314:PHE:HA	1:A:315:ALA:C	2.13	0.74
1:D:139:LEU:O	1:D:147:ILE:HD13	1.88	0.73
1:D:346:ALA:HB3	1:D:351:GLY:HA2	1.68	0.73
1:A:366:LEU:HD11	1:B:421:THR:HG21	1.70	0.73
1:C:102:ILE:HG23	1:C:338:GLN:HG2	1.68	0.73
1:A:41:ILE:CG2	1:A:246:ILE:HD13	2.18	0.73
1:B:10:VAL:HG12	1:B:11:GLY:H	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:ASN:HB3	1:C:327:LEU:HD22	1.68	0.73
1:D:41:ILE:CG2	1:D:246:ILE:HD13	2.18	0.73
1:C:56:LEU:HD11	1:C:365:TYR:CD1	2.22	0.73
1:C:95:LEU:HA	1:C:98:TRP:CZ3	2.23	0.73
1:D:376:GLY:C	1:D:379:HIS:H	1.95	0.73
1:A:60:TYR:CE2	1:A:368:THR:CG2	2.67	0.73
1:A:80:CYS:HA	1:A:374:LEU:HD23	1.71	0.73
1:B:72:GLY:O	1:B:74:TYR:N	2.21	0.73
1:B:95:LEU:HA	1:B:98:TRP:CZ3	2.23	0.73
1:C:60:TYR:CE2	1:C:368:THR:CG2	2.71	0.73
1:A:74:TYR:CZ	1:A:304:ALA:HB2	2.23	0.73
1:C:85:LEU:HD11	1:D:84:PHE:CD1	2.23	0.73
1:D:81:PHE:C	1:D:81:PHE:CD2	2.65	0.73
1:D:202:TRP:HE3	1:D:358:VAL:HG11	1.54	0.73
1:A:292:GLY:O	1:A:296:LEU:HD23	1.89	0.73
1:B:400:TRP:O	1:B:403:VAL:HG12	1.89	0.73
1:B:15:VAL:HG21	1:B:217:VAL:HG13	1.71	0.72
1:D:38:THR:CB	1:D:39:GLY:HA3	2.11	0.72
1:D:292:GLY:O	1:D:296:LEU:HD23	1.88	0.72
1:A:395:PHE:CD1	1:B:422:ALA:HB2	2.24	0.72
1:C:81:PHE:HD2	1:C:81:PHE:C	1.97	0.72
1:A:78:ARG:HH11	1:B:433:LYS:CB	2.01	0.72
1:A:400:TRP:O	1:A:403:VAL:HG12	1.89	0.72
1:B:314:PHE:HA	1:B:315:ALA:C	2.12	0.72
1:B:362:LEU:HG	1:B:402:VAL:CG2	2.19	0.72
1:C:66:LEU:C	1:C:68:PRO:HD3	2.13	0.72
1:C:368:THR:HG22	1:C:369:CYS:N	2.02	0.72
1:D:10:VAL:HG12	1:D:11:GLY:H	1.53	0.72
1:D:63:MET:SD	1:D:372:LEU:HD12	2.29	0.72
1:A:63:MET:SD	1:A:372:LEU:HD12	2.30	0.72
1:D:78:ARG:C	1:D:82:GLY:HA3	2.14	0.72
1:D:184:VAL:HG12	1:D:185:SER:H	1.54	0.72
1:A:410:VAL:HG12	1:B:411:MET:HA	1.72	0.72
1:D:362:LEU:HG	1:D:402:VAL:CG2	2.18	0.72
1:B:60:TYR:CE2	1:B:368:THR:CG2	2.72	0.72
1:B:81:PHE:HD2	1:B:81:PHE:C	1.98	0.72
1:A:116:PHE:O	1:A:118:ILE:HG22	1.90	0.71
1:B:62:LYS:HA	1:B:65:PHE:HB2	1.70	0.71
1:B:201:LEU:CG	1:B:401:ALA:HB2	2.20	0.71
1:B:416:THR:HA	1:B:419:VAL:HG12	1.71	0.71
1:D:102:ILE:HG23	1:D:338:GLN:HG2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:SER:O	1:A:118:ILE:HD13	1.91	0.71
1:A:409:GLU:O	1:A:412:TRP:HB2	1.90	0.71
1:C:62:LYS:HA	1:C:65:PHE:HB2	1.72	0.71
1:C:201:LEU:CG	1:C:401:ALA:HB2	2.19	0.71
1:C:362:LEU:HG	1:C:402:VAL:CG2	2.20	0.71
1:D:62:LYS:HA	1:D:65:PHE:HB2	1.71	0.71
1:A:66:LEU:C	1:A:68:PRO:HD3	2.16	0.71
1:B:41:ILE:HG13	1:B:43:ILE:CG1	2.20	0.71
1:C:139:LEU:O	1:C:147:ILE:HD13	1.91	0.71
1:D:63:MET:HG3	1:D:76:TYR:CE2	2.26	0.71
1:D:80:CYS:HA	1:D:374:LEU:HD23	1.71	0.71
1:B:109:VAL:HG11	1:B:128:THR:HG21	1.73	0.71
1:C:156:VAL:HA	1:C:159:LEU:HD12	1.73	0.71
1:A:184:VAL:HG12	1:A:185:SER:H	1.55	0.71
1:D:116:PHE:O	1:D:118:ILE:HG22	1.90	0.71
1:D:411:MET:O	1:D:415:VAL:HG23	1.90	0.71
1:A:368:THR:HG22	1:A:369:CYS:N	2.06	0.71
1:C:140:ASN:ND2	1:C:147:ILE:HG12	2.06	0.71
1:C:292:GLY:O	1:C:296:LEU:HD23	1.91	0.71
1:D:140:ASN:ND2	1:D:147:ILE:HG12	2.05	0.71
1:B:93:TYR:CE2	1:B:97:CYS:SG	2.84	0.70
1:A:361:THR:O	1:A:365:TYR:CD2	2.45	0.70
1:B:184:VAL:HG12	1:B:185:SER:H	1.54	0.70
1:B:66:LEU:C	1:B:68:PRO:HD3	2.15	0.70
1:B:202:TRP:HE3	1:B:358:VAL:HG11	1.55	0.70
1:C:78:ARG:C	1:C:82:GLY:HA3	2.17	0.70
1:D:120:LYS:H	1:D:120:LYS:HE2	1.57	0.70
1:A:78:ARG:C	1:A:82:GLY:HA3	2.16	0.70
1:A:361:THR:O	1:A:365:TYR:HD2	1.75	0.70
1:A:362:LEU:O	1:A:365:TYR:HB2	1.91	0.70
1:C:109:VAL:HG11	1:C:128:THR:HG21	1.71	0.70
1:B:60:TYR:HE2	1:B:368:THR:CG2	2.02	0.70
1:A:81:PHE:C	1:A:81:PHE:CD2	2.65	0.70
1:A:93:TYR:HB2	1:A:364:PRO:HG2	1.74	0.70
1:B:406:GLY:HA3	1:B:409:GLU:CD	2.16	0.70
1:C:23:ILE:HG21	1:C:204:PHE:CD1	2.27	0.70
1:C:184:VAL:HG12	1:C:185:SER:H	1.56	0.70
1:D:368:THR:HG22	1:D:369:CYS:N	2.06	0.70
1:D:421:THR:CG2	1:D:422:ALA:N	2.53	0.70
1:C:421:THR:HG22	1:C:422:ALA:H	1.55	0.70
1:D:379:HIS:C	1:D:381:GLY:H	1.99	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:LYS:HE2	1:C:120:LYS:H	1.56	0.70
1:D:56:LEU:HD11	1:D:365:TYR:HD1	1.57	0.70
1:A:56:LEU:HD11	1:A:365:TYR:HD1	1.56	0.69
1:A:428:TYR:O	1:A:429:ASN:OD1	2.10	0.69
1:D:46:TRP:CZ3	1:D:239:TYR:HB3	2.28	0.69
1:D:77:ALA:C	1:D:79:ARG:H	1.99	0.69
1:D:302:LYS:H	1:D:302:LYS:HD3	1.57	0.69
1:A:139:LEU:O	1:A:147:ILE:HD13	1.90	0.69
1:B:139:LEU:O	1:B:147:ILE:HD13	1.92	0.69
1:C:410:VAL:HG12	1:D:411:MET:HA	1.74	0.69
1:D:156:VAL:HA	1:D:159:LEU:HD12	1.74	0.69
1:C:72:GLY:O	1:C:74:TYR:N	2.24	0.69
1:A:56:LEU:HD11	1:A:365:TYR:CD1	2.27	0.69
1:D:109:VAL:HG11	1:D:128:THR:HG21	1.73	0.69
1:D:409:GLU:O	1:D:412:TRP:HB2	1.92	0.69
1:B:72:GLY:N	1:B:211:SER:O	2.26	0.69
1:B:78:ARG:C	1:B:82:GLY:HA3	2.17	0.69
1:D:360:PHE:CE1	1:D:413:SER:HA	2.22	0.69
1:D:400:TRP:O	1:D:403:VAL:HG12	1.92	0.69
1:A:57:SER:CB	1:A:232:VAL:HG21	2.22	0.69
1:A:301:ALA:HB1	1:A:310:PHE:HE1	1.58	0.69
1:A:377:HIS:HE1	1:B:430:ARG:C	2.01	0.69
1:A:416:THR:HA	1:A:419:VAL:HG12	1.73	0.69
1:C:201:LEU:C	1:C:203:SER:H	2.01	0.69
1:C:379:HIS:C	1:C:381:GLY:H	2.01	0.69
1:D:56:LEU:HD11	1:D:365:TYR:CD1	2.28	0.69
1:D:94:TRP:HA	1:D:97:CYS:HB2	1.75	0.69
1:D:421:THR:O	1:D:423:MET:N	2.26	0.69
1:D:428:TYR:O	1:D:429:ASN:OD1	2.11	0.69
1:A:302:LYS:H	1:A:302:LYS:HD3	1.57	0.69
1:A:395:PHE:CE1	1:B:422:ALA:HB2	2.28	0.69
1:C:53:ALA:HB2	1:C:397:TYR:CE2	2.28	0.69
1:A:359:ILE:HD11	1:A:409:GLU:HB3	1.73	0.69
1:B:41:ILE:HG22	1:B:246:ILE:CD1	2.23	0.69
1:B:379:HIS:C	1:B:381:GLY:H	1.99	0.69
1:C:63:MET:HG3	1:C:76:TYR:CD2	2.28	0.69
1:A:46:TRP:CZ3	1:A:239:TYR:HB3	2.28	0.68
1:C:93:TYR:HB2	1:C:364:PRO:HG2	1.73	0.68
1:A:202:TRP:HE3	1:A:358:VAL:HG11	1.56	0.68
1:B:156:VAL:HA	1:B:159:LEU:HD12	1.73	0.68
1:B:361:THR:O	1:B:365:TYR:HD2	1.77	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:ILE:HD13	1:C:337:PHE:HD2	1.59	0.68
1:C:178:TYR:HD2	1:C:247:MET:HA	1.59	0.68
1:D:300:THR:O	1:D:300:THR:HG22	1.93	0.68
1:A:156:VAL:HA	1:A:159:LEU:HD12	1.75	0.68
1:C:202:TRP:HE3	1:C:358:VAL:HG11	1.56	0.68
1:C:302:LYS:HD3	1:C:302:LYS:H	1.58	0.68
1:D:93:TYR:HB2	1:D:364:PRO:HG2	1.74	0.68
1:A:120:LYS:HE2	1:A:120:LYS:H	1.58	0.68
1:B:359:ILE:HD11	1:B:409:GLU:HB3	1.76	0.68
1:C:399:ILE:HG13	1:D:418:MET:HE2	1.75	0.68
1:D:72:GLY:O	1:D:74:TYR:N	2.26	0.68
1:D:102:ILE:HD13	1:D:337:PHE:HD2	1.59	0.68
1:B:298:GLY:O	1:B:302:LYS:HD3	1.93	0.68
1:D:359:ILE:HD11	1:D:409:GLU:HB3	1.75	0.68
1:C:433:LYS:CB	1:D:78:ARG:NH1	2.55	0.68
1:A:90:ASN:O	1:A:91:VAL:C	2.37	0.68
1:B:160:ILE:HB	1:B:161:PRO:HD3	1.74	0.68
1:D:93:TYR:HE1	1:D:208:GLU:CD	2.01	0.68
1:D:425:ALA:C	1:D:427:ASN:N	2.47	0.68
1:A:23:ILE:HG21	1:A:204:PHE:CD1	2.29	0.68
1:A:102:ILE:HG23	1:A:338:GLN:HG2	1.76	0.68
1:B:46:TRP:CZ3	1:B:239:TYR:HB3	2.29	0.68
1:B:81:PHE:C	1:B:81:PHE:CD2	2.72	0.68
1:C:395:PHE:CE1	1:D:422:ALA:HB2	2.28	0.68
1:C:428:TYR:O	1:C:429:ASN:OD1	2.12	0.68
1:B:301:ALA:HB1	1:B:310:PHE:HE1	1.59	0.68
1:C:201:LEU:CD2	1:C:401:ALA:HB2	2.23	0.68
1:B:120:LYS:H	1:B:120:LYS:HE2	1.58	0.67
1:B:178:TYR:HD2	1:B:247:MET:HA	1.59	0.67
1:B:184:VAL:HG11	1:C:184:VAL:HG11	1.77	0.67
1:D:57:SER:CB	1:D:232:VAL:HG21	2.24	0.67
1:A:72:GLY:N	1:A:211:SER:O	2.27	0.67
1:B:23:ILE:HG21	1:B:204:PHE:CD1	2.29	0.67
1:A:379:HIS:C	1:A:381:GLY:H	2.01	0.67
1:C:116:PHE:O	1:C:118:ILE:HG22	1.95	0.67
1:A:54:LEU:HD11	1:A:233:LEU:HD23	1.76	0.67
1:A:92:LEU:HD21	1:A:364:PRO:HD3	1.77	0.67
1:B:201:LEU:CD2	1:B:401:ALA:HB2	2.24	0.67
1:D:301:ALA:HB1	1:D:310:PHE:HE1	1.57	0.67
1:A:425:ALA:C	1:A:427:ASN:N	2.50	0.67
1:B:201:LEU:C	1:B:203:SER:H	2.00	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:THR:O	1:B:365:TYR:CD2	2.48	0.67
1:C:60:TYR:HE2	1:C:368:THR:CG2	2.02	0.67
1:A:109:VAL:HG11	1:A:128:THR:CG2	2.25	0.67
1:A:379:HIS:HB3	1:A:381:GLY:O	1.95	0.67
1:C:111:TYR:HE2	1:C:282:ALA:HB1	1.60	0.67
1:C:411:MET:HA	1:D:410:VAL:HG12	1.77	0.67
1:D:90:ASN:O	1:D:91:VAL:C	2.38	0.67
1:A:140:ASN:ND2	1:A:147:ILE:HG12	2.09	0.67
1:B:425:ALA:C	1:B:427:ASN:N	2.49	0.67
1:B:53:ALA:HB2	1:B:397:TYR:CE2	2.29	0.67
1:C:160:ILE:HB	1:C:161:PRO:HD3	1.75	0.67
1:C:416:THR:HA	1:C:419:VAL:HG12	1.77	0.67
1:D:178:TYR:HD2	1:D:247:MET:HA	1.60	0.67
1:A:77:ALA:C	1:A:79:ARG:H	2.03	0.67
1:A:111:TYR:HE2	1:A:282:ALA:HB1	1.59	0.67
1:D:111:TYR:HE2	1:D:282:ALA:HB1	1.59	0.67
1:D:201:LEU:C	1:D:203:SER:H	2.02	0.67
1:A:94:TRP:HA	1:A:97:CYS:HB2	1.77	0.66
1:B:93:TYR:HB2	1:B:364:PRO:HG2	1.76	0.66
1:A:178:TYR:HD2	1:A:247:MET:HA	1.61	0.66
1:A:292:GLY:O	1:A:295:LEU:HB3	1.95	0.66
1:A:300:THR:O	1:A:300:THR:HG22	1.94	0.66
1:B:77:ALA:C	1:B:79:ARG:H	2.03	0.66
1:B:87:TYR:OH	1:B:308:GLY:HA3	1.94	0.66
1:C:72:GLY:N	1:C:212:VAL:HA	2.11	0.66
1:A:201:LEU:C	1:A:203:SER:H	2.03	0.66
1:B:292:GLY:O	1:B:296:LEU:HD23	1.95	0.66
1:C:72:GLY:N	1:C:211:SER:O	2.28	0.66
1:C:72:GLY:H	1:C:212:VAL:HA	1.60	0.66
1:C:359:ILE:HD11	1:C:409:GLU:HB3	1.76	0.66
1:C:414:PHE:HB2	1:D:414:PHE:CD1	2.28	0.66
1:C:46:TRP:CZ3	1:C:239:TYR:HB3	2.29	0.66
1:B:109:VAL:HG11	1:B:128:THR:CG2	2.26	0.66
1:C:298:GLY:O	1:C:302:LYS:HD3	1.95	0.66
1:D:23:ILE:HG21	1:D:204:PHE:CD1	2.30	0.66
1:A:41:ILE:HG13	1:A:43:ILE:HG12	1.74	0.66
1:B:111:TYR:HE2	1:B:282:ALA:HB1	1.59	0.66
1:B:302:LYS:HD3	1:B:302:LYS:H	1.60	0.66
1:C:87:TYR:HB3	1:C:424:TYR:OH	1.95	0.66
1:C:113:SER:O	1:C:118:ILE:HD13	1.95	0.66
1:D:84:PHE:HE1	1:D:85:LEU:CD2	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:PHE:C	1:C:81:PHE:CD2	2.72	0.66
1:C:87:TYR:OH	1:C:308:GLY:HA3	1.96	0.66
1:C:301:ALA:HB1	1:C:310:PHE:HE1	1.59	0.66
1:C:302:LYS:HG2	1:C:323:PRO:CB	2.23	0.66
1:C:400:TRP:O	1:C:403:VAL:HG12	1.95	0.66
1:D:379:HIS:HB3	1:D:381:GLY:O	1.95	0.66
1:C:41:ILE:HG22	1:C:246:ILE:CD1	2.25	0.66
1:C:77:ALA:C	1:C:79:ARG:H	2.03	0.66
1:C:94:TRP:HA	1:C:97:CYS:HB2	1.77	0.66
1:C:361:THR:O	1:C:365:TYR:CD2	2.49	0.65
1:A:11:GLY:O	1:A:15:VAL:HG23	1.95	0.65
1:C:143:GLY:HA2	1:C:146:MET:H	1.61	0.65
1:C:425:ALA:C	1:C:427:ASN:N	2.50	0.65
1:D:136:PHE:CD2	1:D:290:LEU:HB3	2.31	0.65
1:C:102:ILE:HD13	1:C:337:PHE:CD2	2.31	0.65
1:C:428:TYR:OH	1:D:373:LEU:HD13	1.95	0.65
1:D:292:GLY:O	1:D:295:LEU:HB3	1.97	0.65
1:A:78:ARG:NH1	1:B:433:LYS:CB	2.59	0.65
1:B:428:TYR:O	1:B:429:ASN:OD1	2.13	0.65
1:D:72:GLY:N	1:D:211:SER:O	2.29	0.65
1:B:94:TRP:HA	1:B:97:CYS:HB2	1.77	0.65
1:D:102:ILE:HD13	1:D:337:PHE:CD2	2.31	0.65
1:D:126:THR:HB	1:D:342:ILE:HG23	1.79	0.65
1:A:126:THR:HB	1:A:342:ILE:HG23	1.79	0.65
1:B:140:ASN:ND2	1:B:147:ILE:HG12	2.11	0.65
1:D:420:ILE:O	1:D:421:THR:O	2.14	0.65
1:A:371:ALA:C	1:A:373:LEU:H	2.04	0.65
1:B:362:LEU:O	1:B:365:TYR:HB2	1.96	0.65
1:C:109:VAL:HG11	1:C:128:THR:CG2	2.26	0.65
1:D:109:VAL:HG11	1:D:128:THR:CG2	2.26	0.65
1:C:41:ILE:HA	1:C:42:ALA:C	2.21	0.65
1:D:350:PHE:HA	1:D:355:SER:HB3	1.79	0.65
1:D:298:GLY:O	1:D:302:LYS:HD3	1.96	0.65
1:A:49:THR:HG21	1:A:200:THR:HB	1.79	0.65
1:B:87:TYR:HB3	1:B:424:TYR:OH	1.97	0.65
1:B:173:PHE:HB3	1:B:178:TYR:OH	1.97	0.65
1:C:422:ALA:HB2	1:D:395:PHE:CD1	2.32	0.64
1:D:41:ILE:HA	1:D:42:ALA:C	2.21	0.64
1:D:201:LEU:CG	1:D:401:ALA:HB2	2.27	0.64
1:A:298:GLY:O	1:A:302:LYS:HD3	1.98	0.64
1:A:414:PHE:CB	1:B:414:PHE:HD1	2.04	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:ALA:HB2	1:B:395:PHE:CE1	2.32	0.64
1:C:91:VAL:HB	1:C:420:ILE:HD11	1.79	0.64
1:B:84:PHE:HE1	1:B:85:LEU:CD2	2.09	0.64
1:B:113:SER:O	1:B:118:ILE:HD13	1.97	0.64
1:C:376:GLY:O	1:C:378:GLY:N	2.30	0.64
1:D:87:TYR:OH	1:D:308:GLY:HA3	1.98	0.64
1:A:57:SER:HB3	1:A:232:VAL:HG21	1.80	0.64
1:A:84:PHE:HE1	1:A:85:LEU:CD2	2.09	0.64
1:B:102:ILE:HD13	1:B:337:PHE:HD2	1.62	0.64
1:B:300:THR:O	1:B:300:THR:HG22	1.96	0.64
1:C:371:ALA:C	1:C:373:LEU:H	2.06	0.64
1:A:41:ILE:HA	1:A:42:ALA:C	2.21	0.64
1:A:111:TYR:CE2	1:A:282:ALA:HB1	2.33	0.64
1:A:406:GLY:HA3	1:A:409:GLU:CD	2.23	0.64
1:A:420:ILE:HG22	1:A:421:THR:N	2.13	0.64
1:B:344:PRO:O	1:B:345:ASN:HB2	1.97	0.64
1:D:113:SER:O	1:D:118:ILE:HD13	1.97	0.64
1:A:53:ALA:HB2	1:A:397:TYR:CE2	2.32	0.64
1:A:201:LEU:CG	1:A:401:ALA:HB2	2.28	0.64
1:C:57:SER:CB	1:C:232:VAL:HG21	2.28	0.64
1:C:84:PHE:HE1	1:C:85:LEU:CD2	2.11	0.64
1:D:54:LEU:HD11	1:D:233:LEU:HD23	1.77	0.64
1:A:247:MET:HG2	1:A:248:GLY:N	2.13	0.64
1:C:173:PHE:HB3	1:C:178:TYR:OH	1.97	0.64
1:D:111:TYR:CE2	1:D:282:ALA:HB1	2.33	0.64
1:D:173:PHE:HB3	1:D:178:TYR:OH	1.98	0.64
1:A:360:PHE:CE1	1:A:413:SER:HA	2.24	0.64
1:B:102:ILE:HD13	1:B:337:PHE:CD2	2.33	0.64
1:B:371:ALA:C	1:B:373:LEU:H	2.06	0.64
1:A:344:PRO:O	1:A:345:ASN:HB2	1.98	0.64
1:B:116:PHE:O	1:B:118:ILE:HG22	1.98	0.64
1:C:362:LEU:O	1:C:365:TYR:HB2	1.98	0.64
1:A:366:LEU:CD2	1:B:421:THR:HG21	2.29	0.63
1:C:344:PRO:O	1:C:345:ASN:HB2	1.98	0.63
1:D:416:THR:HA	1:D:419:VAL:HG12	1.79	0.63
1:A:207:VAL:HG12	1:A:232:VAL:CG2	2.28	0.63
1:A:362:LEU:HG	1:A:402:VAL:HG21	1.80	0.63
1:C:247:MET:HG2	1:C:248:GLY:N	2.13	0.63
1:A:133:LEU:HD22	1:A:334:MET:HE3	1.79	0.63
1:A:337:PHE:CZ	1:A:353:VAL:HG11	2.34	0.63
1:B:136:PHE:CD2	1:B:290:LEU:HB3	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:VAL:HG12	1:C:232:VAL:CG2	2.29	0.63
1:C:361:THR:O	1:C:365:TYR:HD2	1.80	0.63
1:D:384:ARG:HB3	1:D:385:PRO:HD3	1.81	0.63
1:A:87:TYR:OH	1:A:308:GLY:HA3	1.99	0.63
1:A:403:VAL:HG23	1:B:415:VAL:HG11	1.80	0.63
1:B:91:VAL:O	1:B:95:LEU:HB3	1.99	0.63
1:B:302:LYS:HG2	1:B:323:PRO:CB	2.24	0.63
1:B:425:ALA:HA	1:B:428:TYR:CZ	2.34	0.63
1:C:78:ARG:HH11	1:D:433:LYS:CB	2.12	0.63
1:D:72:GLY:H	1:D:212:VAL:HA	1.64	0.63
1:A:93:TYR:HE1	1:A:208:GLU:CD	2.06	0.63
1:C:399:ILE:CG1	1:D:418:MET:HE2	2.28	0.63
1:D:160:ILE:HB	1:D:161:PRO:HD3	1.81	0.63
1:B:420:ILE:HG22	1:B:421:THR:N	2.13	0.63
1:C:136:PHE:CD2	1:C:290:LEU:HB3	2.33	0.63
1:C:323:PRO:HD2	1:C:327:LEU:HD11	1.81	0.63
1:D:371:ALA:C	1:D:373:LEU:H	2.05	0.63
1:A:420:ILE:O	1:A:421:THR:O	2.16	0.63
1:B:376:GLY:O	1:B:378:GLY:N	2.32	0.63
1:C:73:SER:N	1:C:76:TYR:HE1	1.96	0.63
1:C:78:ARG:NH1	1:D:433:LYS:CB	2.62	0.63
1:C:93:TYR:HE2	1:C:97:CYS:SG	2.20	0.63
1:A:136:PHE:CD2	1:A:290:LEU:HB3	2.34	0.63
1:B:111:TYR:CE2	1:B:282:ALA:HB1	2.33	0.63
1:B:247:MET:HG2	1:B:248:GLY:N	2.14	0.63
1:C:300:THR:O	1:C:300:THR:HG22	1.99	0.63
1:C:420:ILE:O	1:C:421:THR:O	2.17	0.62
1:D:247:MET:HG2	1:D:248:GLY:N	2.12	0.62
1:B:72:GLY:H	1:B:212:VAL:HA	1.64	0.62
1:B:143:GLY:HA2	1:B:146:MET:H	1.62	0.62
1:C:292:GLY:O	1:C:295:LEU:HB3	1.98	0.62
1:D:41:ILE:HG13	1:D:43:ILE:HG12	1.80	0.62
1:A:363:VAL:HG23	1:A:364:PRO:HD3	1.81	0.62
1:B:57:SER:CB	1:B:232:VAL:HG21	2.29	0.62
1:C:111:TYR:CE2	1:C:282:ALA:HB1	2.34	0.62
1:D:57:SER:HB3	1:D:232:VAL:HG21	1.80	0.62
1:B:346:ALA:CB	1:B:351:GLY:HA2	2.29	0.62
1:C:421:THR:HG21	1:D:366:LEU:CD1	2.30	0.62
1:D:53:ALA:HB2	1:D:397:TYR:CE2	2.35	0.62
1:D:344:PRO:O	1:D:345:ASN:HB2	1.97	0.62
1:A:160:ILE:HB	1:A:161:PRO:HD3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:ALA:CB	1:A:351:GLY:HA2	2.29	0.62
1:D:346:ALA:CB	1:D:351:GLY:HA2	2.29	0.62
1:D:425:ALA:HA	1:D:428:TYR:CZ	2.35	0.62
1:A:173:PHE:HB3	1:A:178:TYR:OH	2.00	0.62
1:C:104:MET:HE1	1:C:286:CYS:SG	2.39	0.62
1:C:376:GLY:O	1:C:379:HIS:N	2.30	0.62
1:D:13:ILE:HB	1:D:14:PRO:HD3	1.81	0.62
1:D:92:LEU:HD23	1:D:92:LEU:C	2.24	0.62
1:A:350:PHE:HA	1:A:355:SER:HB3	1.82	0.62
1:B:379:HIS:HB3	1:B:381:GLY:O	1.99	0.62
1:B:337:PHE:CZ	1:B:353:VAL:HG11	2.34	0.62
1:C:10:VAL:HG12	1:C:11:GLY:N	2.14	0.62
1:C:54:LEU:HD11	1:C:233:LEU:HD23	1.82	0.62
1:A:102:ILE:HD13	1:A:337:PHE:HD2	1.65	0.62
1:B:41:ILE:HA	1:B:42:ALA:C	2.24	0.62
1:C:346:ALA:CB	1:C:351:GLY:HA2	2.29	0.62
1:A:302:LYS:HG2	1:A:323:PRO:CB	2.26	0.62
1:A:342:ILE:H	1:A:343:SER:HB2	1.63	0.62
1:C:342:ILE:H	1:C:343:SER:HB2	1.65	0.62
1:D:173:PHE:HA	1:D:174:ARG:CB	2.30	0.62
1:A:81:PHE:CD2	1:A:83:PRO:HD2	2.35	0.61
1:C:178:TYR:CD2	1:C:247:MET:HA	2.35	0.61
1:D:82:GLY:N	1:D:83:PRO:HD2	2.15	0.61
1:D:246:ILE:O	1:D:246:ILE:HG23	2.00	0.61
1:A:197:LEU:O	1:A:201:LEU:HB2	1.99	0.61
1:A:246:ILE:O	1:A:246:ILE:HG23	2.00	0.61
1:B:10:VAL:HG12	1:B:11:GLY:N	2.15	0.61
1:B:246:ILE:HG23	1:B:246:ILE:O	2.00	0.61
1:D:60:TYR:CD2	1:D:368:THR:HG21	2.35	0.61
1:A:81:PHE:HB3	1:A:82:GLY:CA	2.30	0.61
1:A:425:ALA:HA	1:A:428:TYR:CZ	2.35	0.61
1:B:63:MET:SD	1:B:372:LEU:CD1	2.88	0.61
1:C:421:THR:O	1:C:423:MET:N	2.33	0.61
1:C:422:ALA:HB2	1:D:395:PHE:CE1	2.35	0.61
1:D:16:THR:CG2	1:D:227:ALA:HA	2.24	0.61
1:D:337:PHE:CZ	1:D:353:VAL:HG11	2.35	0.61
1:D:49:THR:HG21	1:D:200:THR:HB	1.82	0.61
1:A:395:PHE:CD1	1:B:422:ALA:CB	2.82	0.61
1:B:72:GLY:N	1:B:212:VAL:HA	2.14	0.61
1:B:292:GLY:O	1:B:295:LEU:HB3	2.00	0.61
1:B:384:ARG:HB3	1:B:385:PRO:HD3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:337:PHE:CZ	1:C:353:VAL:HG11	2.36	0.61
1:C:359:ILE:O	1:C:362:LEU:HB2	2.01	0.61
1:B:60:TYR:CD2	1:B:368:THR:HG21	2.36	0.61
1:B:360:PHE:O	1:B:363:VAL:HG23	2.00	0.61
1:B:421:THR:O	1:B:423:MET:N	2.34	0.61
1:C:368:THR:O	1:C:371:ALA:N	2.31	0.61
1:B:81:PHE:HB3	1:B:82:GLY:CA	2.27	0.61
1:B:178:TYR:CD2	1:B:247:MET:HA	2.35	0.61
1:B:207:VAL:CG1	1:B:232:VAL:CG2	2.78	0.61
1:C:49:THR:HG21	1:C:200:THR:HB	1.83	0.61
1:C:379:HIS:HB3	1:C:381:GLY:O	2.01	0.61
1:C:421:THR:HG21	1:D:366:LEU:HD11	1.83	0.61
1:D:143:GLY:HA2	1:D:146:MET:H	1.66	0.61
1:A:87:TYR:HB3	1:A:424:TYR:OH	2.01	0.61
1:A:102:ILE:HD13	1:A:337:PHE:CD2	2.35	0.61
1:B:207:VAL:HG12	1:B:232:VAL:CG2	2.30	0.61
1:D:362:LEU:O	1:D:365:TYR:HB2	1.99	0.61
1:A:119:LEU:CD2	1:A:124:VAL:HG21	2.30	0.61
1:A:421:THR:CG2	1:A:422:ALA:N	2.52	0.61
1:C:60:TYR:CD2	1:C:368:THR:HG21	2.35	0.61
1:C:173:PHE:HA	1:C:174:ARG:CB	2.30	0.61
1:A:143:GLY:HA2	1:A:146:MET:H	1.65	0.61
1:B:91:VAL:HB	1:B:420:ILE:HD11	1.82	0.61
1:B:350:PHE:HA	1:B:355:SER:HB3	1.82	0.61
1:A:418:MET:HE2	1:B:399:ILE:CG1	2.31	0.60
1:B:92:LEU:HD21	1:B:364:PRO:HD3	1.83	0.60
1:C:38:THR:CB	1:C:39:GLY:CA	2.75	0.60
1:D:120:LYS:HE2	1:D:120:LYS:N	2.16	0.60
1:D:302:LYS:CD	1:D:302:LYS:N	2.64	0.60
1:A:178:TYR:CD2	1:A:247:MET:HA	2.37	0.60
1:B:213:ALA:O	1:B:214:ALA:C	2.44	0.60
1:B:342:ILE:H	1:B:343:SER:HB2	1.65	0.60
1:C:246:ILE:HG23	1:C:246:ILE:O	2.01	0.60
1:A:63:MET:HG3	1:A:76:TYR:CD2	2.35	0.60
1:B:13:ILE:HB	1:B:14:PRO:HD3	1.83	0.60
1:C:81:PHE:HB3	1:C:82:GLY:CA	2.27	0.60
1:C:144:PRO:HD3	1:C:322:THR:CG2	2.31	0.60
1:C:207:VAL:CG1	1:C:232:VAL:CG2	2.79	0.60
1:C:213:ALA:O	1:C:214:ALA:C	2.45	0.60
1:D:342:ILE:H	1:D:343:SER:HB2	1.64	0.60
1:A:72:GLY:H	1:A:212:VAL:HA	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:GLY:N	1:A:83:PRO:HD2	2.16	0.60
1:B:88:GLN:HA	1:B:91:VAL:HG23	1.83	0.60
1:C:201:LEU:HD23	1:C:401:ALA:HB2	1.82	0.60
1:C:350:PHE:HA	1:C:355:SER:HB3	1.82	0.60
1:D:10:VAL:HG12	1:D:11:GLY:N	2.16	0.60
1:D:178:TYR:CD2	1:D:247:MET:HA	2.36	0.60
1:D:361:THR:O	1:D:365:TYR:CD2	2.53	0.60
1:A:38:THR:CB	1:A:39:GLY:CA	2.75	0.60
1:B:57:SER:HB3	1:B:232:VAL:HG21	1.83	0.60
1:B:201:LEU:HD23	1:B:401:ALA:HB2	1.82	0.60
1:A:302:LYS:N	1:A:302:LYS:CD	2.64	0.60
1:A:421:THR:HG21	1:B:366:LEU:HD11	1.83	0.60
1:C:94:TRP:O	1:C:97:CYS:HB2	2.01	0.60
1:C:197:LEU:O	1:C:201:LEU:HB2	2.02	0.60
1:C:302:LYS:CD	1:C:302:LYS:N	2.65	0.60
1:C:425:ALA:HA	1:C:428:TYR:CZ	2.36	0.60
1:D:54:LEU:HD11	1:D:233:LEU:CD2	2.31	0.60
1:C:420:ILE:HG22	1:C:421:THR:N	2.17	0.60
1:A:207:VAL:CG1	1:A:232:VAL:CG2	2.80	0.60
1:B:155:THR:O	1:B:159:LEU:HG	2.02	0.60
1:C:76:TYR:OH	1:C:211:SER:OG	2.15	0.60
1:D:119:LEU:CD2	1:D:124:VAL:HG21	2.30	0.60
1:D:213:ALA:O	1:D:214:ALA:C	2.44	0.60
1:A:60:TYR:CD2	1:A:368:THR:HG21	2.36	0.60
1:A:366:LEU:HD21	1:B:421:THR:CG2	2.32	0.60
1:D:197:LEU:O	1:D:201:LEU:HB2	2.00	0.60
1:D:406:GLY:HA3	1:D:409:GLU:CD	2.26	0.60
1:A:13:ILE:HB	1:A:14:PRO:HD3	1.82	0.60
1:B:90:ASN:ND2	1:B:310:PHE:CZ	2.70	0.60
1:D:89:THR:HG23	1:D:364:PRO:HG3	1.84	0.60
1:D:420:ILE:HG22	1:D:421:THR:N	2.15	0.60
1:A:10:VAL:HG12	1:A:11:GLY:N	2.16	0.59
1:C:11:GLY:O	1:C:15:VAL:HG23	2.01	0.59
1:D:138:LEU:O	1:D:142:VAL:HG23	2.02	0.59
1:A:422:ALA:HB2	1:B:395:PHE:CD1	2.37	0.59
1:B:144:PRO:HD3	1:B:322:THR:CG2	2.32	0.59
1:C:418:MET:HE2	1:D:399:ILE:CG1	2.32	0.59
1:D:11:GLY:O	1:D:15:VAL:HG23	2.02	0.59
1:D:72:GLY:N	1:D:212:VAL:HA	2.17	0.59
1:B:49:THR:HG21	1:B:200:THR:HB	1.83	0.59
1:B:54:LEU:HD11	1:B:233:LEU:HD23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:VAL:HB	1:D:420:ILE:HD11	1.83	0.59
1:D:302:LYS:HG2	1:D:323:PRO:CB	2.27	0.59
1:A:92:LEU:HD23	1:A:92:LEU:C	2.28	0.59
1:C:79:ARG:HB2	1:C:375:LEU:HD11	1.84	0.59
1:C:88:GLN:HA	1:C:91:VAL:HG23	1.85	0.59
1:C:421:THR:HG21	1:D:366:LEU:CD2	2.33	0.59
1:D:363:VAL:HG23	1:D:364:PRO:HD3	1.83	0.59
1:B:323:PRO:HD2	1:B:327:LEU:HD11	1.83	0.59
1:D:362:LEU:HG	1:D:402:VAL:HG21	1.84	0.59
1:A:72:GLY:N	1:A:212:VAL:HA	2.18	0.59
1:A:144:PRO:HD3	1:A:322:THR:CG2	2.32	0.59
1:C:20:SER:HA	1:C:23:ILE:HD12	1.84	0.59
1:D:361:THR:O	1:D:365:TYR:HD2	1.85	0.59
1:B:120:LYS:NZ	1:B:124:VAL:HG12	2.18	0.59
1:C:395:PHE:CD1	1:D:422:ALA:HB2	2.38	0.59
1:D:20:SER:HB2	1:D:231:GLY:HA2	1.85	0.59
1:D:247:MET:HE2	1:D:249:MET:HB2	1.85	0.59
1:A:16:THR:CG2	1:A:227:ALA:HA	2.25	0.59
1:B:94:TRP:O	1:B:97:CYS:HB2	2.03	0.59
1:C:107:ILE:O	1:C:111:TYR:HD1	1.85	0.59
1:C:126:THR:HB	1:C:342:ILE:HG23	1.84	0.59
1:C:421:THR:CG2	1:C:422:ALA:N	2.57	0.59
1:A:213:ALA:O	1:A:214:ALA:C	2.45	0.59
1:B:20:SER:HB2	1:B:231:GLY:HA2	1.85	0.59
1:B:82:GLY:N	1:B:83:PRO:HD2	2.18	0.59
1:B:126:THR:HB	1:B:342:ILE:HG23	1.83	0.59
1:B:368:THR:O	1:B:371:ALA:N	2.35	0.59
1:C:13:ILE:HB	1:C:14:PRO:HD3	1.84	0.59
1:C:376:GLY:C	1:C:378:GLY:N	2.59	0.59
1:C:421:THR:HG21	1:D:366:LEU:HD21	1.84	0.59
1:D:426:LEU:O	1:D:427:ASN:ND2	2.34	0.59
1:A:120:LYS:HE2	1:A:120:LYS:N	2.17	0.58
1:A:421:THR:HG21	1:B:366:LEU:CD1	2.33	0.58
1:B:119:LEU:CD2	1:B:124:VAL:HG21	2.31	0.58
1:B:376:GLY:O	1:B:379:HIS:N	2.32	0.58
1:C:57:SER:HB3	1:C:232:VAL:HG21	1.83	0.58
1:B:362:LEU:HG	1:B:402:VAL:HG21	1.84	0.58
1:B:376:GLY:C	1:B:378:GLY:N	2.60	0.58
1:A:210:ALA:HB3	1:A:228:THR:CG2	2.33	0.58
1:B:79:ARG:HB2	1:B:375:LEU:HD11	1.84	0.58
1:B:120:LYS:HE2	1:B:120:LYS:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:LEU:O	1:B:201:LEU:HB2	2.03	0.58
1:B:302:LYS:CD	1:B:302:LYS:N	2.66	0.58
1:B:315:ALA:HB1	1:B:316:ARG:HD3	1.85	0.58
1:C:384:ARG:HB3	1:C:385:PRO:HD3	1.85	0.58
1:D:155:THR:O	1:D:159:LEU:HG	2.03	0.58
1:B:11:GLY:O	1:B:15:VAL:HG23	2.04	0.58
1:C:120:LYS:HE2	1:C:120:LYS:N	2.17	0.58
1:A:54:LEU:HD11	1:A:233:LEU:CD2	2.32	0.58
1:A:365:TYR:HB3	1:A:398:CYS:HG	1.66	0.58
1:A:426:LEU:O	1:A:427:ASN:ND2	2.34	0.58
1:B:81:PHE:CD2	1:B:83:PRO:HD2	2.38	0.58
1:B:209:SER:CA	1:B:296:LEU:HD11	2.30	0.58
1:B:250:ILE:N	1:B:251:PRO:CD	2.60	0.58
1:A:366:LEU:HD21	1:B:421:THR:HG21	1.85	0.58
1:A:384:ARG:HB3	1:A:385:PRO:HD3	1.85	0.58
1:B:115:PHE:CE1	1:B:276:ALA:HA	2.37	0.58
1:D:63:MET:SD	1:D:372:LEU:CD1	2.91	0.58
1:A:8:HIS:HB3	1:A:9:LYS:HE2	1.85	0.58
1:A:79:ARG:HB2	1:A:375:LEU:HD11	1.85	0.58
1:A:366:LEU:HD13	1:A:367:TYR:CD2	2.39	0.58
1:A:403:VAL:HG23	1:B:415:VAL:CG1	2.34	0.58
1:B:426:LEU:O	1:B:427:ASN:ND2	2.37	0.58
1:C:81:PHE:CD2	1:C:83:PRO:HD2	2.38	0.58
1:C:120:LYS:NZ	1:C:124:VAL:HG12	2.18	0.58
1:D:81:PHE:CD2	1:D:83:PRO:HD2	2.38	0.58
1:A:213:ALA:O	1:A:215:GLY:N	2.37	0.58
1:C:284:ALA:HA	1:C:287:LEU:HB2	1.86	0.58
1:D:302:LYS:HD3	1:D:302:LYS:N	2.19	0.58
1:D:368:THR:O	1:D:371:ALA:N	2.36	0.58
1:B:184:VAL:HG11	1:C:184:VAL:CG1	2.34	0.57
1:C:8:HIS:HB3	1:C:9:LYS:HE2	1.85	0.57
1:C:16:THR:CG2	1:C:227:ALA:HA	2.22	0.57
1:C:310:PHE:HB3	1:C:311:PRO:CA	2.34	0.57
1:D:77:ALA:C	1:D:79:ARG:N	2.61	0.57
1:D:144:PRO:HD3	1:D:322:THR:CG2	2.33	0.57
1:D:207:VAL:HG12	1:D:232:VAL:CG2	2.33	0.57
1:A:138:LEU:O	1:A:142:VAL:HG23	2.04	0.57
1:A:155:THR:O	1:A:159:LEU:HG	2.03	0.57
1:A:428:TYR:OH	1:B:373:LEU:HD13	2.04	0.57
1:B:213:ALA:O	1:B:215:GLY:N	2.36	0.57
1:C:54:LEU:HD11	1:C:233:LEU:CD2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:PHE:CE1	1:D:276:ALA:HA	2.36	0.57
1:A:63:MET:SD	1:A:372:LEU:CD1	2.92	0.57
1:A:120:LYS:NZ	1:A:124:VAL:HG12	2.20	0.57
1:A:191:GLY:O	1:A:194:GLN:HB2	2.04	0.57
1:C:155:THR:O	1:C:159:LEU:HG	2.03	0.57
1:C:357:SER:O	1:C:361:THR:HG23	2.04	0.57
1:D:8:HIS:HB3	1:D:9:LYS:HE2	1.85	0.57
1:D:91:VAL:HG21	1:D:420:ILE:HG12	1.86	0.57
1:B:138:LEU:O	1:B:142:VAL:HG23	2.04	0.57
1:D:49:THR:HB	1:D:197:LEU:HD23	1.86	0.57
1:A:77:ALA:HB1	1:A:86:GLY:HA2	1.87	0.57
1:A:377:HIS:CE1	1:B:431:LEU:N	2.72	0.57
1:C:63:MET:CG	1:C:76:TYR:CE2	2.85	0.57
1:C:91:VAL:O	1:C:95:LEU:HB3	2.04	0.57
1:C:213:ALA:O	1:C:215:GLY:N	2.36	0.57
1:D:430:ARG:O	1:D:431:LEU:CB	2.53	0.57
1:A:107:ILE:O	1:A:111:TYR:HD1	1.87	0.57
1:B:20:SER:HA	1:B:23:ILE:HD12	1.87	0.57
1:B:99:ILE:HA	1:B:102:ILE:HD12	1.87	0.57
1:C:373:LEU:HD13	1:D:428:TYR:OH	2.05	0.57
1:D:79:ARG:HD3	1:D:375:LEU:HD11	1.87	0.57
1:A:133:LEU:HD22	1:A:334:MET:CE	2.33	0.57
1:A:359:ILE:O	1:A:362:LEU:HB2	2.04	0.57
1:B:107:ILE:O	1:B:111:TYR:HD1	1.87	0.57
1:B:201:LEU:O	1:B:203:SER:N	2.38	0.57
1:C:53:ALA:HB2	1:C:397:TYR:HE2	1.70	0.57
1:C:119:LEU:CD2	1:C:124:VAL:HG21	2.31	0.57
1:D:301:ALA:C	1:D:303:ALA:H	2.12	0.57
1:A:68:PRO:HA	1:A:69:SER:CB	2.34	0.57
1:A:302:LYS:HD3	1:A:302:LYS:N	2.19	0.57
1:B:188:GLY:C	1:B:192:ALA:HB2	2.24	0.57
1:B:310:PHE:HB3	1:B:311:PRO:CA	2.34	0.57
1:B:421:THR:CG2	1:B:422:ALA:N	2.55	0.57
1:C:63:MET:CG	1:C:76:TYR:CD2	2.87	0.57
1:C:67:ASP:C	1:C:67:ASP:OD1	2.48	0.57
1:C:360:PHE:O	1:C:363:VAL:HG23	2.04	0.57
1:C:414:PHE:C	1:C:414:PHE:CD2	2.83	0.57
1:D:6:ASP:HB3	1:D:9:LYS:HG2	1.87	0.57
1:D:87:TYR:HB3	1:D:424:TYR:OH	2.04	0.57
1:D:120:LYS:NZ	1:D:124:VAL:HG12	2.19	0.57
1:A:79:ARG:HG2	1:B:433:LYS:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:ILE:HG21	1:C:246:ILE:HG21	1.85	0.57
1:C:73:SER:N	1:C:76:TYR:CE1	2.72	0.57
1:C:204:PHE:HB3	1:C:397:TYR:OH	2.05	0.57
1:D:81:PHE:HB3	1:D:82:GLY:CA	2.34	0.57
1:B:84:PHE:CD1	1:B:85:LEU:N	2.73	0.57
1:B:218:LYS:HB2	1:B:223:ASN:HD22	1.70	0.57
1:B:284:ALA:HA	1:B:287:LEU:HB2	1.87	0.57
1:C:92:LEU:HD23	1:C:92:LEU:C	2.30	0.57
1:A:99:ILE:HA	1:A:102:ILE:HD12	1.87	0.56
1:C:49:THR:HB	1:C:197:LEU:HD23	1.87	0.56
1:C:90:ASN:ND2	1:C:310:PHE:CZ	2.72	0.56
1:B:357:SER:O	1:B:361:THR:HG23	2.05	0.56
1:B:420:ILE:O	1:B:421:THR:O	2.23	0.56
1:C:214:ALA:O	1:C:216:VAL:N	2.38	0.56
1:C:250:ILE:N	1:C:251:PRO:CD	2.60	0.56
1:C:362:LEU:HG	1:C:402:VAL:HG21	1.86	0.56
1:A:81:PHE:CB	1:A:82:GLY:HA2	2.24	0.56
1:A:140:ASN:CB	1:A:327:LEU:HD22	2.34	0.56
1:A:376:GLY:O	1:A:378:GLY:N	2.38	0.56
1:B:8:HIS:HB3	1:B:9:LYS:HE2	1.87	0.56
1:B:81:PHE:CB	1:B:82:GLY:HA2	2.19	0.56
1:B:210:ALA:HB3	1:B:228:THR:CG2	2.35	0.56
1:C:20:SER:HB2	1:C:231:GLY:HA2	1.86	0.56
1:C:133:LEU:HD22	1:C:334:MET:HE3	1.87	0.56
1:D:68:PRO:HA	1:D:69:SER:CB	2.35	0.56
1:D:93:TYR:CE1	1:D:208:GLU:CD	2.83	0.56
1:D:140:ASN:CB	1:D:327:LEU:HD22	2.35	0.56
1:D:204:PHE:HB3	1:D:397:TYR:OH	2.04	0.56
1:A:247:MET:HG2	1:A:248:GLY:H	1.71	0.56
1:A:315:ALA:HB1	1:A:316:ARG:HD3	1.86	0.56
1:A:373:LEU:HB3	1:B:428:TYR:CE1	2.41	0.56
1:B:173:PHE:HA	1:B:174:ARG:CB	2.30	0.56
1:B:204:PHE:HB3	1:B:397:TYR:OH	2.06	0.56
1:C:315:ALA:HB1	1:C:316:ARG:HD3	1.87	0.56
1:D:247:MET:HG2	1:D:248:GLY:H	1.70	0.56
1:D:315:ALA:HB1	1:D:316:ARG:HD3	1.87	0.56
1:B:167:VAL:O	1:B:170:TRP:HB3	2.06	0.56
1:C:138:LEU:O	1:C:142:VAL:HG23	2.05	0.56
1:A:234:ILE:HG22	1:A:235:ALA:N	2.20	0.56
1:A:247:MET:HE2	1:A:249:MET:HB2	1.88	0.56
1:B:53:ALA:HB2	1:B:397:TYR:HE2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ILE:HA	1:C:102:ILE:HD12	1.88	0.56
1:D:212:VAL:CG1	1:D:296:LEU:HD13	2.35	0.56
1:D:310:PHE:HB3	1:D:311:PRO:CA	2.36	0.56
1:A:34:ASN:HB3	1:A:199:VAL:HG11	1.88	0.56
1:A:79:ARG:HD3	1:A:375:LEU:HD11	1.88	0.56
1:A:431:LEU:N	1:B:377:HIS:CE1	2.74	0.56
1:B:67:ASP:C	1:B:67:ASP:OD1	2.49	0.56
1:B:92:LEU:C	1:B:92:LEU:HD23	2.31	0.56
1:C:92:LEU:HD21	1:C:364:PRO:HD3	1.87	0.56
1:C:201:LEU:C	1:C:203:SER:N	2.62	0.56
1:C:426:LEU:O	1:C:427:ASN:ND2	2.37	0.56
1:D:250:ILE:N	1:D:251:PRO:CD	2.61	0.56
1:A:310:PHE:HB3	1:A:311:PRO:CA	2.36	0.56
1:A:430:ARG:O	1:A:431:LEU:CB	2.53	0.56
1:B:73:SER:N	1:B:76:TYR:HE1	2.00	0.56
1:B:214:ALA:O	1:B:216:VAL:N	2.39	0.56
1:B:379:HIS:CE1	1:B:387:TYR:HD2	2.24	0.56
1:C:82:GLY:N	1:C:83:PRO:HD2	2.21	0.56
1:C:210:ALA:HB3	1:C:228:THR:CG2	2.35	0.56
1:C:302:LYS:HD3	1:C:302:LYS:N	2.20	0.56
1:C:433:LYS:O	1:D:79:ARG:HG2	2.06	0.56
1:D:88:GLN:HG2	1:D:89:THR:N	2.20	0.56
1:A:88:GLN:HG2	1:A:89:THR:N	2.19	0.56
1:A:284:ALA:HA	1:A:287:LEU:HB2	1.88	0.56
1:B:71:GLY:O	1:B:212:VAL:HA	2.06	0.56
1:A:379:HIS:CE1	1:A:387:TYR:HD2	2.24	0.56
1:B:172:TRP:CE3	1:B:173:PHE:HD2	2.24	0.56
1:D:20:SER:HA	1:D:23:ILE:HD12	1.86	0.56
1:D:284:ALA:HA	1:D:287:LEU:HB2	1.88	0.56
1:D:379:HIS:CE1	1:D:387:TYR:HD2	2.24	0.56
1:A:41:ILE:HG21	1:A:246:ILE:HG21	1.88	0.55
1:A:68:PRO:HA	1:A:69:SER:HB3	1.87	0.55
1:A:91:VAL:HB	1:A:420:ILE:HD11	1.89	0.55
1:A:377:HIS:CE1	1:B:430:ARG:C	2.84	0.55
1:C:379:HIS:CE1	1:C:387:TYR:HD2	2.23	0.55
1:D:38:THR:CB	1:D:39:GLY:CA	2.76	0.55
1:D:63:MET:HG3	1:D:76:TYR:CD2	2.40	0.55
1:D:213:ALA:O	1:D:215:GLY:N	2.38	0.55
1:D:363:VAL:O	1:D:366:LEU:HB3	2.06	0.55
1:A:123:LEU:O	1:A:126:THR:HG23	2.07	0.55
1:A:20:SER:HB2	1:A:231:GLY:HA2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:THR:HB	1:A:197:LEU:HD23	1.89	0.55
1:C:172:TRP:CE3	1:C:173:PHE:HD2	2.25	0.55
1:B:119:LEU:HD13	1:B:124:VAL:CG1	2.32	0.55
1:B:133:LEU:HD23	1:B:290:LEU:CD1	2.36	0.55
1:B:359:ILE:O	1:B:362:LEU:HB2	2.06	0.55
1:C:167:VAL:O	1:C:170:TRP:HB3	2.06	0.55
1:C:400:TRP:HA	1:C:403:VAL:HG12	1.88	0.55
1:D:118:ILE:HA	1:D:119:LEU:C	2.32	0.55
1:D:121:ASP:H	1:D:122:PRO:CD	2.19	0.55
1:D:207:VAL:CG1	1:D:232:VAL:CG2	2.84	0.55
1:D:359:ILE:O	1:D:362:LEU:HB2	2.05	0.55
1:A:20:SER:HA	1:A:23:ILE:HD12	1.87	0.55
1:A:201:LEU:C	1:A:203:SER:N	2.65	0.55
1:C:312:PRO:HA	1:C:313:ILE:HB	1.89	0.55
1:D:81:PHE:CB	1:D:82:GLY:HA2	2.25	0.55
1:C:63:MET:SD	1:C:372:LEU:HD12	2.46	0.55
1:A:204:PHE:O	1:A:204:PHE:HD1	1.90	0.55
1:A:430:ARG:C	1:B:377:HIS:HE1	2.15	0.55
1:B:121:ASP:H	1:B:122:PRO:CD	2.19	0.55
1:C:173:PHE:CA	1:C:174:ARG:HB2	2.37	0.55
1:C:201:LEU:O	1:C:203:SER:N	2.40	0.55
1:C:399:ILE:HA	1:D:418:MET:HE1	1.88	0.55
1:D:24:MET:HE3	1:D:162:ILE:CD1	2.25	0.55
1:D:167:VAL:O	1:D:170:TRP:HB3	2.07	0.55
1:A:201:LEU:CD2	1:A:401:ALA:HB2	2.37	0.55
1:B:73:SER:N	1:B:76:TYR:CE1	2.74	0.55
1:B:302:LYS:HD3	1:B:302:LYS:N	2.21	0.55
1:A:84:PHE:CD1	1:A:85:LEU:N	2.75	0.55
1:B:41:ILE:HG21	1:B:246:ILE:HG21	1.88	0.55
1:B:63:MET:HG3	1:B:76:TYR:CD2	2.41	0.55
1:B:77:ALA:C	1:B:79:ARG:N	2.63	0.55
1:B:104:MET:HE1	1:B:286:CYS:SG	2.47	0.55
1:C:68:PRO:HB2	1:C:220:PRO:HB3	1.88	0.55
1:C:115:PHE:CE1	1:C:276:ALA:HA	2.37	0.55
1:D:234:ILE:HG22	1:D:235:ALA:N	2.21	0.55
1:D:376:GLY:O	1:D:378:GLY:N	2.40	0.55
1:A:115:PHE:CE1	1:A:276:ALA:HA	2.37	0.55
1:A:120:LYS:HZ3	1:A:124:VAL:HG12	1.72	0.55
1:A:294:THR:O	1:A:297:ALA:HB3	2.07	0.55
1:B:72:GLY:C	1:B:74:TYR:H	2.15	0.55
1:C:123:LEU:O	1:C:126:THR:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:214:ALA:O	1:D:216:VAL:N	2.40	0.55
1:A:204:PHE:HB3	1:A:397:TYR:OH	2.06	0.54
1:A:301:ALA:C	1:A:303:ALA:H	2.13	0.54
1:A:312:PRO:HA	1:A:313:ILE:HB	1.89	0.54
1:B:118:ILE:HA	1:B:119:LEU:C	2.32	0.54
1:D:34:ASN:HB3	1:D:199:VAL:HG11	1.89	0.54
1:D:88:GLN:HA	1:D:91:VAL:HG23	1.89	0.54
1:D:107:ILE:O	1:D:111:TYR:HD1	1.89	0.54
1:A:167:VAL:O	1:A:170:TRP:HB3	2.07	0.54
1:B:68:PRO:HA	1:B:69:SER:CB	2.37	0.54
1:B:90:ASN:O	1:B:91:VAL:C	2.49	0.54
1:C:247:MET:HG2	1:C:248:GLY:H	1.71	0.54
1:A:118:ILE:HA	1:A:119:LEU:C	2.31	0.54
1:B:38:THR:CB	1:B:39:GLY:CA	2.74	0.54
1:B:88:GLN:HG2	1:B:89:THR:N	2.23	0.54
1:C:68:PRO:HA	1:C:69:SER:CB	2.38	0.54
1:C:119:LEU:HD13	1:C:124:VAL:CG1	2.32	0.54
1:A:71:GLY:O	1:A:212:VAL:HA	2.08	0.54
1:A:172:TRP:CE3	1:A:173:PHE:HD2	2.25	0.54
1:D:92:LEU:HD21	1:D:364:PRO:HD3	1.88	0.54
1:D:201:LEU:CD2	1:D:401:ALA:HB2	2.37	0.54
1:D:210:ALA:HB3	1:D:228:THR:CG2	2.34	0.54
1:A:10:VAL:HG22	1:A:145:LYS:HA	1.89	0.54
1:A:400:TRP:HA	1:A:403:VAL:HG12	1.89	0.54
1:B:430:ARG:O	1:B:431:LEU:CB	2.55	0.54
1:C:71:GLY:O	1:C:212:VAL:HA	2.08	0.54
1:C:118:ILE:HA	1:C:119:LEU:C	2.32	0.54
1:C:396:LEU:O	1:C:397:TYR:C	2.50	0.54
1:D:172:TRP:CE3	1:D:173:PHE:HD2	2.25	0.54
1:A:212:VAL:CG1	1:A:296:LEU:HD13	2.38	0.54
1:D:188:GLY:C	1:D:192:ALA:HB2	2.24	0.54
1:A:6:ASP:HB3	1:A:9:LYS:HG2	1.90	0.54
1:A:41:ILE:HG22	1:A:246:ILE:CD1	2.35	0.54
1:A:57:SER:HB2	1:A:232:VAL:HG21	1.89	0.54
1:A:373:LEU:CB	1:B:428:TYR:CE1	2.91	0.54
1:B:54:LEU:HD11	1:B:233:LEU:CD2	2.37	0.54
1:B:77:ALA:HB1	1:B:86:GLY:HA2	1.90	0.54
1:B:132:VAL:O	1:B:135:ILE:HB	2.08	0.54
1:B:201:LEU:C	1:B:203:SER:N	2.62	0.54
1:C:218:LYS:HB2	1:C:223:ASN:HD22	1.71	0.54
1:C:323:PRO:HB2	1:C:326:GLY:HA3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:415:VAL:HG11	1:D:403:VAL:HG23	1.88	0.54
1:D:77:ALA:HB1	1:D:86:GLY:HA2	1.90	0.54
1:D:314:PHE:O	1:D:314:PHE:HD2	1.91	0.54
1:A:77:ALA:C	1:A:79:ARG:N	2.64	0.54
1:C:68:PRO:HA	1:C:69:SER:HB3	1.90	0.54
1:C:144:PRO:HB2	1:C:216:VAL:HG11	1.90	0.54
1:D:8:HIS:HB3	1:D:9:LYS:NZ	2.23	0.54
1:B:247:MET:HG2	1:B:248:GLY:H	1.72	0.54
1:C:23:ILE:HG21	1:C:204:PHE:HD1	1.72	0.54
1:C:81:PHE:CB	1:C:82:GLY:HA2	2.19	0.54
1:B:68:PRO:HB2	1:B:220:PRO:HB3	1.89	0.54
1:C:15:VAL:O	1:C:19:VAL:HG23	2.07	0.54
1:C:67:ASP:OD1	1:C:69:SER:HA	2.08	0.54
1:A:314:PHE:HD2	1:A:314:PHE:O	1.91	0.53
1:C:69:SER:OG	1:C:70:PRO:HA	2.08	0.53
1:C:376:GLY:O	1:C:377:HIS:C	2.51	0.53
1:D:15:VAL:O	1:D:19:VAL:HG23	2.06	0.53
1:D:68:PRO:HA	1:D:69:SER:HB3	1.88	0.53
1:B:68:PRO:HA	1:B:69:SER:HB3	1.90	0.53
1:B:323:PRO:HB2	1:B:326:GLY:HA3	1.90	0.53
1:C:84:PHE:CE1	1:C:85:LEU:CD2	2.88	0.53
1:C:379:HIS:C	1:C:381:GLY:N	2.66	0.53
1:D:81:PHE:CE2	1:D:83:PRO:HG2	2.43	0.53
1:D:133:LEU:HD22	1:D:334:MET:HE3	1.90	0.53
1:A:81:PHE:CE2	1:A:83:PRO:HG2	2.43	0.53
1:A:114:TYR:C	1:A:115:PHE:HD2	2.16	0.53
1:A:132:VAL:O	1:A:135:ILE:HB	2.08	0.53
1:A:218:LYS:HB2	1:A:223:ASN:HD22	1.73	0.53
1:C:71:GLY:C	1:C:212:VAL:HA	2.33	0.53
1:C:132:VAL:O	1:C:135:ILE:HB	2.09	0.53
1:D:133:LEU:HD22	1:D:334:MET:SD	2.48	0.53
1:D:218:LYS:HB2	1:D:223:ASN:HD22	1.72	0.53
1:D:312:PRO:HA	1:D:313:ILE:HB	1.89	0.53
1:D:366:LEU:HD13	1:D:367:TYR:CD2	2.43	0.53
1:A:67:ASP:C	1:A:67:ASP:OD1	2.52	0.53
1:A:367:TYR:O	1:A:370:ALA:HB3	2.08	0.53
1:B:312:PRO:HA	1:B:313:ILE:HB	1.89	0.53
1:B:400:TRP:HA	1:B:403:VAL:HG12	1.89	0.53
1:C:54:LEU:HD12	1:C:232:VAL:HG12	1.91	0.53
1:C:133:LEU:HD23	1:C:290:LEU:CD1	2.35	0.53
1:C:188:GLY:C	1:C:192:ALA:HB2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:TYR:C	1:D:115:PHE:HD2	2.16	0.53
1:D:376:GLY:C	1:D:378:GLY:N	2.66	0.53
1:A:15:VAL:O	1:A:19:VAL:HG23	2.08	0.53
1:A:73:SER:N	1:A:76:TYR:HE1	2.06	0.53
1:B:8:HIS:O	1:B:9:LYS:HD3	2.08	0.53
1:C:74:TYR:CE1	1:C:304:ALA:HB2	2.43	0.53
1:C:78:ARG:C	1:C:79:ARG:HG3	2.33	0.53
1:C:90:ASN:O	1:C:91:VAL:C	2.50	0.53
1:D:73:SER:N	1:D:76:TYR:CE1	2.76	0.53
1:D:191:GLY:O	1:D:194:GLN:HB2	2.09	0.53
1:C:247:MET:HE2	1:C:249:MET:HB2	1.91	0.53
1:D:79:ARG:HB2	1:D:375:LEU:HD11	1.90	0.53
1:D:133:LEU:HD22	1:D:334:MET:CE	2.38	0.53
1:B:396:LEU:O	1:B:397:TYR:C	2.51	0.53
1:C:6:ASP:HB3	1:C:9:LYS:HG2	1.89	0.53
1:A:121:ASP:H	1:A:122:PRO:CD	2.20	0.53
1:A:418:MET:HE2	1:B:399:ILE:HG13	1.90	0.53
1:C:121:ASP:H	1:C:122:PRO:CD	2.22	0.53
1:A:323:PRO:HD2	1:A:327:LEU:HD11	1.91	0.53
1:A:376:GLY:C	1:A:378:GLY:N	2.65	0.53
1:B:144:PRO:HB2	1:B:216:VAL:HG11	1.90	0.53
1:C:430:ARG:C	1:D:377:HIS:HE1	2.16	0.53
1:D:201:LEU:O	1:D:203:SER:N	2.41	0.53
1:D:400:TRP:HA	1:D:403:VAL:HG12	1.91	0.53
1:D:425:ALA:O	1:D:427:ASN:N	2.42	0.53
1:A:363:VAL:O	1:A:366:LEU:HB3	2.09	0.53
1:B:205:ILE:HD13	1:B:361:THR:OG1	2.09	0.53
1:B:234:ILE:HG22	1:B:235:ALA:N	2.24	0.53
1:C:93:TYR:C	1:C:93:TYR:CD2	2.87	0.53
1:D:204:PHE:O	1:D:204:PHE:HD1	1.92	0.53
1:A:173:PHE:CA	1:A:174:ARG:HB2	2.38	0.52
1:B:71:GLY:C	1:B:212:VAL:HA	2.34	0.52
1:B:96:ALA:HA	1:B:357:SER:HB2	1.91	0.52
1:B:426:LEU:O	1:B:426:LEU:HG	2.10	0.52
1:C:41:ILE:HG13	1:C:43:ILE:HG12	1.91	0.52
1:C:77:ALA:HB1	1:C:86:GLY:HA2	1.90	0.52
1:C:367:TYR:O	1:C:370:ALA:HB3	2.09	0.52
1:A:88:GLN:HA	1:A:91:VAL:HG23	1.90	0.52
1:A:91:VAL:HG21	1:A:420:ILE:HG12	1.91	0.52
1:B:6:ASP:HB3	1:B:9:LYS:HG2	1.90	0.52
1:B:412:TRP:CZ3	1:B:415:VAL:HG21	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:414:PHE:C	1:B:414:PHE:CD2	2.87	0.52
1:D:123:LEU:O	1:D:126:THR:HG23	2.09	0.52
1:A:214:ALA:O	1:A:216:VAL:N	2.42	0.52
1:A:414:PHE:HD1	1:B:414:PHE:CB	2.16	0.52
1:B:376:GLY:O	1:B:377:HIS:C	2.52	0.52
1:C:96:ALA:HA	1:C:357:SER:HB2	1.90	0.52
1:C:114:TYR:C	1:C:115:PHE:HD2	2.18	0.52
1:D:149:ARG:O	1:D:153:VAL:HG23	2.10	0.52
1:D:323:PRO:HB2	1:D:326:GLY:HA3	1.92	0.52
1:A:90:ASN:ND2	1:A:310:PHE:CZ	2.77	0.52
1:B:10:VAL:HG22	1:B:145:LYS:HA	1.92	0.52
1:B:49:THR:HB	1:B:197:LEU:HD23	1.91	0.52
1:C:8:HIS:O	1:C:9:LYS:HD3	2.09	0.52
1:C:84:PHE:CD1	1:C:85:LEU:N	2.77	0.52
1:D:84:PHE:CD1	1:D:85:LEU:N	2.78	0.52
1:A:433:LYS:CB	1:B:78:ARG:HH11	2.21	0.52
1:B:114:TYR:C	1:B:115:PHE:HD2	2.18	0.52
1:B:247:MET:HE2	1:B:249:MET:HB2	1.90	0.52
1:C:216:VAL:O	1:C:216:VAL:HG12	2.10	0.52
1:C:420:ILE:O	1:C:421:THR:C	2.53	0.52
1:D:41:ILE:HG21	1:D:246:ILE:HG21	1.90	0.52
1:B:15:VAL:O	1:B:19:VAL:HG23	2.09	0.52
1:B:16:THR:CG2	1:B:227:ALA:HA	2.25	0.52
1:B:389:ALA:O	1:B:392:THR:N	2.43	0.52
1:C:91:VAL:HG21	1:C:420:ILE:HG12	1.91	0.52
1:C:209:SER:CA	1:C:296:LEU:HD11	2.33	0.52
1:C:377:HIS:HE1	1:D:430:ARG:N	2.08	0.52
1:D:31:LEU:HB2	1:D:32:PRO:HD3	1.91	0.52
1:B:149:ARG:O	1:B:153:VAL:HG23	2.10	0.52
1:B:212:VAL:CG1	1:B:296:LEU:HD13	2.40	0.52
1:B:379:HIS:C	1:B:381:GLY:N	2.65	0.52
1:C:426:LEU:O	1:C:426:LEU:HG	2.10	0.52
1:A:433:LYS:CB	1:B:78:ARG:NH1	2.73	0.52
1:C:204:PHE:HD1	1:C:204:PHE:O	1.92	0.52
1:D:83:PRO:O	1:D:84:PHE:C	2.52	0.52
1:D:301:ALA:C	1:D:303:ALA:N	2.68	0.52
1:D:314:PHE:HA	1:D:315:ALA:O	2.10	0.52
1:A:82:GLY:N	1:A:83:PRO:CD	2.73	0.52
1:A:201:LEU:O	1:A:203:SER:N	2.43	0.52
1:A:216:VAL:HG12	1:A:216:VAL:O	2.09	0.52
1:C:10:VAL:HG22	1:C:145:LYS:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:PRO:HA	1:C:35:LEU:HD12	1.91	0.52
1:C:299:GLN:OE1	1:C:299:GLN:HA	2.09	0.52
1:C:389:ALA:O	1:C:392:THR:N	2.43	0.52
1:D:99:ILE:HA	1:D:102:ILE:HD12	1.91	0.52
1:A:319:LYS:O	1:A:320:ALA:HB3	2.10	0.52
1:C:31:LEU:HB2	1:C:32:PRO:HD3	1.92	0.52
1:D:139:LEU:HB3	1:D:146:MET:HE1	1.92	0.52
1:D:201:LEU:C	1:D:203:SER:N	2.64	0.52
1:A:323:PRO:HB2	1:A:326:GLY:HA3	1.92	0.51
1:A:418:MET:CE	1:B:399:ILE:HA	2.40	0.51
1:B:204:PHE:O	1:B:204:PHE:HD1	1.92	0.51
1:C:415:VAL:CG1	1:D:403:VAL:HG23	2.40	0.51
1:A:85:LEU:CD1	1:B:84:PHE:CE1	2.88	0.51
1:A:379:HIS:C	1:A:381:GLY:N	2.67	0.51
1:A:412:TRP:CZ3	1:A:415:VAL:HG21	2.45	0.51
1:B:173:PHE:CA	1:B:174:ARG:HB2	2.37	0.51
1:B:184:VAL:O	1:B:185:SER:HB2	2.10	0.51
1:C:77:ALA:C	1:C:79:ARG:N	2.64	0.51
1:C:184:VAL:O	1:C:185:SER:HB2	2.10	0.51
1:C:399:ILE:HA	1:D:418:MET:CE	2.39	0.51
1:C:430:ARG:O	1:C:431:LEU:CB	2.57	0.51
1:A:377:HIS:HE1	1:B:430:ARG:N	2.08	0.51
1:B:123:LEU:O	1:B:126:THR:HG23	2.10	0.51
1:C:88:GLN:HG2	1:C:89:THR:N	2.25	0.51
1:C:149:ARG:O	1:C:153:VAL:HG23	2.10	0.51
1:C:151:GLN:HE22	1:C:289:SER:HA	1.75	0.51
1:D:41:ILE:HG22	1:D:246:ILE:CD1	2.36	0.51
1:D:82:GLY:N	1:D:83:PRO:CD	2.74	0.51
1:D:216:VAL:O	1:D:216:VAL:HG12	2.11	0.51
1:C:72:GLY:C	1:C:74:TYR:H	2.19	0.51
1:D:144:PRO:HG2	1:D:216:VAL:HG11	1.93	0.51
1:A:119:LEU:HD22	1:A:124:VAL:CG2	2.36	0.51
1:B:216:VAL:O	1:B:216:VAL:HG12	2.10	0.51
1:C:18:MET:HA	1:C:151:GLN:HG2	1.93	0.51
1:C:56:LEU:CD1	1:C:365:TYR:CD1	2.93	0.51
1:D:10:VAL:HG22	1:D:145:LYS:HA	1.92	0.51
1:D:372:LEU:HG	1:D:372:LEU:O	2.10	0.51
1:A:31:LEU:HB2	1:A:32:PRO:HD3	1.93	0.51
1:A:93:TYR:CE1	1:A:208:GLU:CD	2.87	0.51
1:B:32:PRO:HA	1:B:35:LEU:HD12	1.93	0.51
1:C:41:ILE:O	1:C:41:ILE:HG12	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:306:ASP:C	1:D:308:GLY:N	2.69	0.51
1:D:367:TYR:O	1:D:370:ALA:HB3	2.11	0.51
1:A:78:ARG:C	1:A:79:ARG:HG3	2.35	0.51
1:B:41:ILE:HG13	1:B:43:ILE:HG12	1.93	0.51
1:C:32:PRO:HA	1:C:35:LEU:CD1	2.41	0.51
1:C:111:TYR:CB	1:C:283:ALA:HB2	2.33	0.51
1:D:90:ASN:ND2	1:D:310:PHE:CZ	2.78	0.51
1:D:93:TYR:HE1	1:D:208:GLU:OE2	1.92	0.51
1:A:306:ASP:C	1:A:308:GLY:N	2.68	0.51
1:A:372:LEU:HG	1:A:372:LEU:O	2.11	0.51
1:B:23:ILE:HG21	1:B:204:PHE:HD1	1.76	0.51
1:B:69:SER:OG	1:B:70:PRO:HA	2.11	0.51
1:B:74:TYR:CE1	1:B:304:ALA:HB2	2.45	0.51
1:B:299:GLN:OE1	1:B:299:GLN:HA	2.11	0.51
1:B:319:LYS:O	1:B:320:ALA:HB3	2.11	0.51
1:D:8:HIS:HB3	1:D:9:LYS:CE	2.41	0.51
1:D:310:PHE:CE1	1:D:314:PHE:HE2	2.29	0.51
1:D:420:ILE:O	1:D:421:THR:C	2.54	0.51
1:A:377:HIS:CE1	1:B:430:ARG:N	2.79	0.51
1:B:69:SER:OG	1:B:71:GLY:N	2.43	0.51
1:B:301:ALA:C	1:B:303:ALA:H	2.18	0.51
1:C:301:ALA:C	1:C:303:ALA:H	2.16	0.51
1:D:57:SER:HB2	1:D:232:VAL:HG21	1.92	0.51
1:D:67:ASP:C	1:D:67:ASP:OD1	2.52	0.51
1:D:132:VAL:O	1:D:135:ILE:HB	2.11	0.51
1:A:80:CYS:O	1:B:81:PHE:CE1	2.64	0.51
1:A:396:LEU:O	1:A:397:TYR:C	2.54	0.51
1:B:44:TYR:O	1:B:47:LEU:N	2.44	0.51
1:C:205:ILE:HD13	1:C:361:THR:OG1	2.11	0.51
1:C:421:THR:CG2	1:D:366:LEU:HD21	2.41	0.51
1:A:72:GLY:C	1:A:74:TYR:H	2.19	0.50
1:A:376:GLY:O	1:A:377:HIS:C	2.53	0.50
1:C:44:TYR:O	1:C:47:LEU:N	2.44	0.50
1:D:67:ASP:OD1	1:D:69:SER:HA	2.11	0.50
1:D:376:GLY:O	1:D:377:HIS:C	2.53	0.50
1:A:44:TYR:O	1:A:47:LEU:N	2.44	0.50
1:A:54:LEU:HD12	1:A:232:VAL:HG12	1.92	0.50
1:B:93:TYR:HE1	1:B:208:GLU:CD	2.19	0.50
1:B:119:LEU:CD1	1:B:124:VAL:HG11	2.35	0.50
1:C:218:LYS:O	1:C:220:PRO:HD3	2.12	0.50
1:C:319:LYS:O	1:C:320:ALA:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:PRO:HB2	1:D:220:PRO:HB3	1.93	0.50
1:A:8:HIS:O	1:A:9:LYS:HD3	2.11	0.50
1:A:73:SER:N	1:A:76:TYR:CE1	2.79	0.50
1:A:80:CYS:O	1:B:81:PHE:HE1	1.94	0.50
1:A:133:LEU:HD23	1:A:290:LEU:CD1	2.38	0.50
1:A:154:ALA:O	1:A:157:LEU:HB2	2.11	0.50
1:A:424:TYR:CD1	1:A:430:ARG:NH2	2.79	0.50
1:B:18:MET:HA	1:B:151:GLN:HG2	1.92	0.50
1:B:32:PRO:HA	1:B:35:LEU:CD1	2.42	0.50
1:B:139:LEU:HB3	1:B:146:MET:HE1	1.92	0.50
1:B:218:LYS:O	1:B:220:PRO:HD3	2.11	0.50
1:B:420:ILE:O	1:B:421:THR:C	2.54	0.50
1:C:139:LEU:HB3	1:C:146:MET:HE1	1.93	0.50
1:B:89:THR:HG23	1:B:364:PRO:HG3	1.93	0.50
1:B:91:VAL:HG21	1:B:420:ILE:HG12	1.92	0.50
1:D:302:LYS:HG3	1:D:314:PHE:HB2	1.94	0.50
1:D:323:PRO:HD2	1:D:327:LEU:HD11	1.93	0.50
1:D:326:GLY:O	1:D:330:VAL:HG23	2.11	0.50
1:A:8:HIS:HB3	1:A:9:LYS:NZ	2.26	0.50
1:A:68:PRO:HB2	1:A:220:PRO:HB3	1.93	0.50
1:A:301:ALA:C	1:A:303:ALA:N	2.70	0.50
1:A:416:THR:CA	1:A:419:VAL:HG12	2.42	0.50
1:B:67:ASP:OD1	1:B:69:SER:HA	2.11	0.50
1:C:412:TRP:CZ3	1:C:415:VAL:HG21	2.46	0.50
1:D:18:MET:HA	1:D:151:GLN:HG2	1.94	0.50
1:D:56:LEU:HD12	1:D:397:TYR:CE1	2.46	0.50
1:D:92:LEU:O	1:D:360:PHE:HB3	2.12	0.50
1:D:133:LEU:HD23	1:D:290:LEU:CD1	2.34	0.50
1:A:119:LEU:HD13	1:A:124:VAL:CG1	2.33	0.50
1:A:144:PRO:HG2	1:A:216:VAL:HG11	1.93	0.50
1:A:149:ARG:O	1:A:153:VAL:HG23	2.12	0.50
1:A:330:VAL:O	1:A:334:MET:HB2	2.11	0.50
1:B:330:VAL:O	1:B:334:MET:HB2	2.12	0.50
1:C:104:MET:CE	1:C:286:CYS:SG	3.00	0.50
1:C:414:PHE:O	1:C:418:MET:HG3	2.12	0.50
1:D:205:ILE:HD13	1:D:361:THR:OG1	2.12	0.50
1:D:319:LYS:O	1:D:320:ALA:HB3	2.12	0.50
1:A:313:ILE:HG22	1:A:314:PHE:N	2.27	0.50
1:B:31:LEU:HB2	1:B:32:PRO:HD3	1.92	0.50
1:B:326:GLY:O	1:B:330:VAL:HG23	2.12	0.50
1:C:314:PHE:HD2	1:C:314:PHE:O	1.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:PRO:HA	1:D:35:LEU:HD12	1.93	0.50
1:A:421:THR:HG21	1:B:366:LEU:HD21	1.93	0.50
1:C:79:ARG:HD3	1:C:375:LEU:HD11	1.93	0.50
1:C:366:LEU:HD11	1:D:421:THR:HG21	1.94	0.50
1:C:418:MET:HE2	1:D:399:ILE:HG12	1.94	0.50
1:D:32:PRO:HA	1:D:35:LEU:CD1	2.41	0.50
1:D:74:TYR:OH	1:D:304:ALA:HA	2.12	0.50
1:A:50:ILE:HD13	1:A:236:ALA:HB1	1.94	0.50
1:A:84:PHE:CE1	1:A:85:LEU:CD2	2.88	0.50
1:A:89:THR:HG23	1:A:364:PRO:HG3	1.94	0.50
1:A:133:LEU:HD22	1:A:334:MET:SD	2.52	0.50
1:A:420:ILE:HG22	1:A:421:THR:H	1.75	0.50
1:C:410:VAL:CG1	1:D:411:MET:HA	2.42	0.50
1:D:184:VAL:O	1:D:185:SER:HB2	2.12	0.50
1:D:294:THR:O	1:D:297:ALA:HB3	2.11	0.50
1:D:396:LEU:O	1:D:397:TYR:C	2.54	0.50
1:A:83:PRO:O	1:A:84:PHE:C	2.55	0.49
1:B:351:GLY:C	1:B:353:VAL:H	2.19	0.49
1:B:372:LEU:C	1:B:373:LEU:HG	2.36	0.49
1:B:416:THR:CA	1:B:419:VAL:HG12	2.40	0.49
1:D:71:GLY:O	1:D:212:VAL:HA	2.11	0.49
1:D:313:ILE:HG22	1:D:314:PHE:N	2.26	0.49
1:A:32:PRO:HA	1:A:35:LEU:CD1	2.42	0.49
1:A:53:ALA:HB2	1:A:397:TYR:HE2	1.76	0.49
1:B:72:GLY:C	1:B:74:TYR:N	2.69	0.49
1:C:119:LEU:CD1	1:C:124:VAL:HG11	2.35	0.49
1:C:310:PHE:CE1	1:C:314:PHE:HE2	2.30	0.49
1:A:371:ALA:C	1:A:373:LEU:N	2.70	0.49
1:A:426:LEU:C	1:A:427:ASN:HD22	2.19	0.49
1:B:104:MET:HB3	1:B:290:LEU:HD23	1.94	0.49
1:B:133:LEU:HD22	1:B:334:MET:HE3	1.93	0.49
1:C:330:VAL:O	1:C:334:MET:HB2	2.12	0.49
1:C:411:MET:HE1	1:D:403:VAL:O	2.12	0.49
1:D:218:LYS:O	1:D:220:PRO:HD3	2.11	0.49
1:D:303:ALA:C	1:D:305:ALA:H	2.20	0.49
1:D:330:VAL:O	1:D:334:MET:HB2	2.11	0.49
1:D:412:TRP:CZ3	1:D:415:VAL:HG21	2.47	0.49
1:A:23:ILE:HG21	1:A:204:PHE:HD1	1.74	0.49
1:A:74:TYR:OH	1:A:304:ALA:HA	2.11	0.49
1:A:111:TYR:CB	1:A:283:ALA:HB2	2.36	0.49
1:A:303:ALA:C	1:A:305:ALA:H	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:LEU:O	1:A:377:HIS:CD2	2.65	0.49
1:B:78:ARG:C	1:B:79:ARG:HG3	2.37	0.49
1:B:371:ALA:C	1:B:373:LEU:N	2.70	0.49
1:C:23:ILE:HG23	1:C:204:PHE:O	2.13	0.49
1:C:69:SER:OG	1:C:71:GLY:N	2.42	0.49
1:C:426:LEU:C	1:C:427:ASN:HD22	2.21	0.49
1:D:140:ASN:HD21	1:D:147:ILE:HG12	1.77	0.49
1:D:357:SER:O	1:D:361:THR:HG23	2.12	0.49
1:D:379:HIS:C	1:D:381:GLY:N	2.65	0.49
1:A:8:HIS:HB3	1:A:9:LYS:CE	2.43	0.49
1:A:165:ILE:O	1:A:169:GLY:HA3	2.11	0.49
1:A:218:LYS:O	1:A:220:PRO:HD3	2.12	0.49
1:A:421:THR:HG21	1:B:366:LEU:CD2	2.43	0.49
1:B:151:GLN:HE22	1:B:289:SER:HA	1.77	0.49
1:B:363:VAL:O	1:B:366:LEU:HB3	2.12	0.49
1:B:366:LEU:HD13	1:B:367:TYR:CD2	2.47	0.49
1:B:385:PRO:HA	1:B:388:LEU:HB2	1.95	0.49
1:C:326:GLY:O	1:C:330:VAL:HG23	2.13	0.49
1:C:351:GLY:C	1:C:353:VAL:H	2.20	0.49
1:C:430:ARG:N	1:D:377:HIS:HE1	2.10	0.49
1:D:8:HIS:O	1:D:9:LYS:HD3	2.11	0.49
1:D:93:TYR:HE2	1:D:97:CYS:SG	2.35	0.49
1:D:120:LYS:HZ3	1:D:124:VAL:HG12	1.76	0.49
1:D:173:PHE:CA	1:D:174:ARG:HB2	2.36	0.49
1:D:209:SER:CA	1:D:296:LEU:HD11	2.30	0.49
1:A:35:LEU:CD2	1:A:196:THR:HG22	2.41	0.49
1:A:379:HIS:CE1	1:A:387:TYR:CD2	3.01	0.49
1:B:23:ILE:HG23	1:B:204:PHE:O	2.13	0.49
1:B:191:GLY:O	1:B:194:GLN:HB2	2.13	0.49
1:B:298:GLY:HA2	1:B:302:LYS:NZ	2.27	0.49
1:B:302:LYS:HG3	1:B:314:PHE:HB2	1.94	0.49
1:B:314:PHE:O	1:B:314:PHE:HD2	1.95	0.49
1:C:133:LEU:HD22	1:C:334:MET:CE	2.43	0.49
1:C:154:ALA:O	1:C:157:LEU:HB2	2.13	0.49
1:D:54:LEU:HD12	1:D:232:VAL:HG12	1.94	0.49
1:D:165:ILE:O	1:D:169:GLY:HA3	2.13	0.49
1:A:71:GLY:C	1:A:212:VAL:HA	2.37	0.49
1:A:360:PHE:O	1:A:363:VAL:HG23	2.13	0.49
1:A:425:ALA:O	1:A:427:ASN:N	2.43	0.49
1:B:49:THR:OG1	1:B:201:LEU:CD1	2.61	0.49
1:B:119:LEU:HD22	1:B:124:VAL:CG2	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:LEU:HA	1:B:342:ILE:HG13	1.95	0.49
1:B:374:LEU:O	1:B:377:HIS:CD2	2.66	0.49
1:D:119:LEU:HD22	1:D:124:VAL:CG2	2.35	0.49
1:D:379:HIS:CE1	1:D:387:TYR:CD2	3.01	0.49
1:A:32:PRO:HA	1:A:35:LEU:HD12	1.94	0.49
1:A:79:ARG:HD3	1:A:375:LEU:CD1	2.42	0.49
1:A:93:TYR:HE2	1:A:97:CYS:SG	2.31	0.49
1:A:363:VAL:CB	1:A:364:PRO:HD3	2.43	0.49
1:B:41:ILE:O	1:B:41:ILE:HG12	2.11	0.49
1:B:56:LEU:CD1	1:B:365:TYR:CD1	2.94	0.49
1:B:63:MET:HB2	1:B:372:LEU:HD13	1.94	0.49
1:C:50:ILE:HD13	1:C:236:ALA:HB1	1.95	0.49
1:C:234:ILE:HG22	1:C:235:ALA:N	2.25	0.49
1:C:422:ALA:CB	1:D:395:PHE:CD1	2.95	0.49
1:C:428:TYR:CE1	1:D:373:LEU:HB3	2.47	0.49
1:D:210:ALA:C	1:D:212:VAL:H	2.20	0.49
1:D:298:GLY:HA2	1:D:302:LYS:NZ	2.28	0.49
1:A:92:LEU:O	1:A:360:PHE:HB3	2.12	0.49
1:A:376:GLY:HA3	1:A:379:HIS:CD2	2.48	0.49
1:A:420:ILE:O	1:A:421:THR:C	2.56	0.49
1:C:104:MET:HB3	1:C:290:LEU:HD23	1.95	0.49
1:D:351:GLY:C	1:D:353:VAL:H	2.21	0.49
1:A:49:THR:OG1	1:A:201:LEU:CD1	2.61	0.49
1:A:302:LYS:HG3	1:A:314:PHE:HB2	1.94	0.49
1:B:50:ILE:HD13	1:B:236:ALA:HB1	1.93	0.49
1:A:67:ASP:OD1	1:A:69:SER:HA	2.13	0.48
1:A:351:GLY:C	1:A:353:VAL:H	2.21	0.48
1:C:79:ARG:HD3	1:C:375:LEU:CD1	2.43	0.48
1:C:379:HIS:CE1	1:C:387:TYR:CD2	3.01	0.48
1:D:78:ARG:C	1:D:79:ARG:HG3	2.38	0.48
1:D:79:ARG:HD3	1:D:375:LEU:CD1	2.43	0.48
1:A:14:PRO:HB2	1:A:148:THR:OG1	2.13	0.48
1:A:151:GLN:HE22	1:A:289:SER:HA	1.77	0.48
1:A:314:PHE:HA	1:A:315:ALA:O	2.13	0.48
1:B:363:VAL:CB	1:B:364:PRO:HD3	2.43	0.48
1:C:8:HIS:HB3	1:C:9:LYS:NZ	2.28	0.48
1:D:21:GLY:HA2	1:D:24:MET:HB2	1.94	0.48
1:D:24:MET:CB	1:D:25:GLY:CA	2.88	0.48
1:A:209:SER:CA	1:A:296:LEU:HD11	2.34	0.48
1:C:8:HIS:HB3	1:C:9:LYS:CE	2.43	0.48
1:C:367:TYR:O	1:C:368:THR:C	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:TYR:HE1	1:A:208:GLU:OE2	1.95	0.48
1:B:363:VAL:HG23	1:B:364:PRO:HD3	1.94	0.48
1:C:294:THR:O	1:C:297:ALA:HB3	2.13	0.48
1:D:74:TYR:CE1	1:D:304:ALA:HB2	2.47	0.48
1:D:154:ALA:O	1:D:157:LEU:HB2	2.13	0.48
1:A:139:LEU:HB3	1:A:146:MET:HE1	1.95	0.48
1:A:310:PHE:CE1	1:A:314:PHE:HE2	2.30	0.48
1:B:74:TYR:OH	1:B:304:ALA:HA	2.13	0.48
1:B:206:GLY:O	1:B:208:GLU:N	2.47	0.48
1:B:372:LEU:O	1:B:373:LEU:HG	2.13	0.48
1:B:379:HIS:CE1	1:B:387:TYR:CD2	3.01	0.48
1:C:49:THR:OG1	1:C:201:LEU:CD1	2.61	0.48
1:C:311:PRO:HG2	1:C:426:LEU:HD11	1.95	0.48
1:A:56:LEU:HD12	1:A:397:TYR:CE1	2.48	0.48
1:A:250:ILE:N	1:A:251:PRO:CD	2.61	0.48
1:B:8:HIS:HB3	1:B:9:LYS:NZ	2.28	0.48
1:B:165:ILE:O	1:B:169:GLY:HA3	2.13	0.48
1:C:74:TYR:OH	1:C:304:ALA:HA	2.14	0.48
1:D:114:TYR:CE1	1:D:118:ILE:HG12	2.49	0.48
1:A:72:GLY:C	1:A:74:TYR:N	2.69	0.48
1:A:81:PHE:HA	1:B:81:PHE:CZ	2.49	0.48
1:A:205:ILE:HD13	1:A:361:THR:OG1	2.13	0.48
1:B:30:LEU:O	1:B:33:ALA:HB3	2.14	0.48
1:B:56:LEU:CD1	1:B:365:TYR:HD1	2.24	0.48
1:B:136:PHE:HB3	1:B:291:GLY:HA2	1.96	0.48
1:B:144:PRO:HD3	1:B:322:THR:HG23	1.96	0.48
1:B:314:PHE:HA	1:B:315:ALA:O	2.13	0.48
1:C:366:LEU:CD1	1:D:421:THR:HG21	2.43	0.48
1:D:374:LEU:O	1:D:377:HIS:CD2	2.66	0.48
1:D:426:LEU:C	1:D:427:ASN:HD22	2.19	0.48
1:A:18:MET:HA	1:A:151:GLN:HG2	1.95	0.48
1:B:84:PHE:CE1	1:B:85:LEU:CD2	2.87	0.48
1:B:114:TYR:CE1	1:B:118:ILE:HG12	2.49	0.48
1:B:294:THR:O	1:B:297:ALA:HB3	2.13	0.48
1:C:191:GLY:O	1:C:194:GLN:HB2	2.13	0.48
1:C:342:ILE:CB	1:C:343:SER:CB	2.86	0.48
1:D:74:TYR:CZ	1:D:304:ALA:CB	2.96	0.48
1:D:93:TYR:CE1	1:D:208:GLU:OE1	2.66	0.48
1:A:74:TYR:CE1	1:A:304:ALA:HB2	2.48	0.48
1:A:218:LYS:HB3	1:A:219:ASN:H	1.52	0.48
1:A:342:ILE:HB	1:A:343:SER:OG	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:SER:O	1:A:361:THR:HG23	2.14	0.48
1:B:46:TRP:CH2	1:B:200:THR:HG22	2.49	0.48
1:B:54:LEU:HD12	1:B:232:VAL:HG12	1.95	0.48
1:B:82:GLY:N	1:B:83:PRO:CD	2.77	0.48
1:B:140:ASN:CB	1:B:327:LEU:HD22	2.38	0.48
1:B:154:ALA:O	1:B:157:LEU:HB2	2.14	0.48
1:C:46:TRP:CH2	1:C:200:THR:HG22	2.49	0.48
1:C:302:LYS:HG3	1:C:314:PHE:HB2	1.95	0.48
1:D:69:SER:OG	1:D:70:PRO:HA	2.14	0.48
1:B:218:LYS:HB3	1:B:219:ASN:H	1.52	0.48
1:C:363:VAL:O	1:C:366:LEU:HB3	2.13	0.48
1:D:44:TYR:O	1:D:47:LEU:N	2.47	0.48
1:D:77:ALA:O	1:D:79:ARG:N	2.46	0.48
1:D:424:TYR:CD1	1:D:430:ARG:NH2	2.82	0.48
1:B:19:VAL:CG2	1:B:210:ALA:HB2	2.40	0.47
1:B:313:ILE:HG22	1:B:314:PHE:N	2.29	0.47
1:C:114:TYR:CE1	1:C:118:ILE:HG12	2.49	0.47
1:C:322:THR:HA	1:C:323:PRO:HD3	1.76	0.47
1:C:389:ALA:O	1:C:390:VAL:C	2.56	0.47
1:D:56:LEU:HD12	1:D:397:TYR:CD1	2.49	0.47
1:A:74:TYR:CZ	1:A:304:ALA:CB	2.97	0.47
1:B:81:PHE:CE2	1:B:83:PRO:HG2	2.48	0.47
1:C:93:TYR:HE1	1:C:208:GLU:CD	2.22	0.47
1:C:339:LEU:HA	1:C:342:ILE:HG13	1.96	0.47
1:C:374:LEU:O	1:C:377:HIS:CD2	2.68	0.47
1:A:30:LEU:O	1:A:33:ALA:HB3	2.14	0.47
1:A:95:LEU:HD23	1:A:95:LEU:O	2.14	0.47
1:A:133:LEU:CD1	1:A:338:GLN:HG3	2.44	0.47
1:C:56:LEU:CD1	1:C:365:TYR:HD1	2.23	0.47
1:C:314:PHE:HA	1:C:315:ALA:O	2.12	0.47
1:C:366:LEU:HD13	1:C:367:TYR:CD2	2.50	0.47
1:A:23:ILE:HG23	1:A:204:PHE:O	2.13	0.47
1:B:311:PRO:HG2	1:B:426:LEU:HD11	1.96	0.47
1:C:92:LEU:O	1:C:360:PHE:HB3	2.14	0.47
1:D:376:GLY:HA3	1:D:379:HIS:CD2	2.50	0.47
1:A:69:SER:OG	1:A:70:PRO:HA	2.15	0.47
1:A:188:GLY:C	1:A:192:ALA:HB2	2.24	0.47
1:A:299:GLN:OE1	1:A:299:GLN:HA	2.14	0.47
1:B:88:GLN:O	1:B:91:VAL:N	2.47	0.47
1:B:376:GLY:HA3	1:B:379:HIS:CD2	2.49	0.47
1:C:313:ILE:HG22	1:C:314:PHE:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:PRO:HB2	1:D:148:THR:OG1	2.14	0.47
1:B:302:LYS:HE3	1:B:326:GLY:CA	2.45	0.47
1:B:420:ILE:HG22	1:B:421:THR:H	1.79	0.47
1:C:83:PRO:O	1:C:84:PHE:C	2.57	0.47
1:C:144:PRO:HD3	1:C:322:THR:HG23	1.96	0.47
1:C:298:GLY:HA2	1:C:302:LYS:NZ	2.30	0.47
1:D:414:PHE:C	1:D:414:PHE:CD2	2.92	0.47
1:A:41:ILE:O	1:A:41:ILE:HG12	2.14	0.47
1:A:326:GLY:O	1:A:330:VAL:HG23	2.15	0.47
1:A:372:LEU:C	1:A:373:LEU:HG	2.40	0.47
1:A:426:LEU:O	1:A:426:LEU:HG	2.15	0.47
1:B:22:ASN:HB3	1:B:293:TRP:HE1	1.79	0.47
1:B:121:ASP:HB2	1:B:122:PRO:HD3	1.97	0.47
1:B:235:ALA:O	1:B:238:CYS:HB2	2.15	0.47
1:B:388:LEU:HD23	1:B:388:LEU:HA	1.63	0.47
1:B:421:THR:O	1:B:424:TYR:N	2.37	0.47
1:C:14:PRO:HB2	1:C:148:THR:OG1	2.14	0.47
1:C:31:LEU:HD11	1:C:239:TYR:CE2	2.50	0.47
1:C:34:ASN:HB3	1:C:199:VAL:HG11	1.97	0.47
1:C:165:ILE:O	1:C:169:GLY:HA3	2.14	0.47
1:C:212:VAL:CG1	1:C:296:LEU:HD13	2.45	0.47
1:C:363:VAL:HG23	1:C:364:PRO:HD3	1.97	0.47
1:D:133:LEU:CD1	1:D:338:GLN:HG3	2.44	0.47
1:D:339:LEU:HA	1:D:342:ILE:HG13	1.96	0.47
1:D:360:PHE:O	1:D:363:VAL:HG23	2.15	0.47
1:A:376:GLY:O	1:A:379:HIS:N	2.42	0.47
1:B:8:HIS:HB3	1:B:9:LYS:CE	2.44	0.47
1:B:128:THR:O	1:B:132:VAL:HG23	2.15	0.47
1:B:367:TYR:O	1:B:370:ALA:HB3	2.14	0.47
1:C:136:PHE:HB3	1:C:291:GLY:HA2	1.95	0.47
1:C:301:ALA:C	1:C:303:ALA:N	2.73	0.47
1:C:363:VAL:CB	1:C:364:PRO:HD3	2.45	0.47
1:C:418:MET:HE2	1:D:399:ILE:HG13	1.95	0.47
1:C:418:MET:CE	1:D:399:ILE:HA	2.44	0.47
1:D:119:LEU:HD13	1:D:124:VAL:CG1	2.33	0.47
1:A:414:PHE:C	1:A:414:PHE:CD2	2.93	0.47
1:B:14:PRO:HB2	1:B:148:THR:OG1	2.15	0.47
1:B:79:ARG:HD3	1:B:375:LEU:HD11	1.96	0.47
1:C:201:LEU:HD23	1:C:401:ALA:CB	2.44	0.47
1:C:210:ALA:C	1:C:212:VAL:H	2.21	0.47
1:C:306:ASP:C	1:C:308:GLY:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:LEU:HD13	1:D:47:LEU:C	2.40	0.47
1:D:104:MET:HB3	1:D:290:LEU:HD23	1.97	0.47
1:A:107:ILE:HG23	1:A:111:TYR:CE1	2.50	0.47
1:A:136:PHE:HB3	1:A:291:GLY:HA2	1.97	0.47
1:A:173:PHE:HA	1:A:174:ARG:CB	2.31	0.47
1:A:400:TRP:HA	1:A:403:VAL:CG1	2.45	0.47
1:C:371:ALA:C	1:C:373:LEU:N	2.70	0.47
1:C:377:HIS:HE1	1:D:430:ARG:C	2.23	0.47
1:C:377:HIS:CE1	1:D:431:LEU:N	2.83	0.47
1:D:19:VAL:CG2	1:D:210:ALA:HB2	2.40	0.47
1:D:306:ASP:C	1:D:308:GLY:H	2.22	0.47
1:D:339:LEU:HA	1:D:342:ILE:CG1	2.45	0.47
1:A:22:ASN:HB3	1:A:293:TRP:HE1	1.80	0.46
1:A:161:PRO:O	1:A:165:ILE:HG13	2.15	0.46
1:B:79:ARG:HD3	1:B:375:LEU:CD1	2.45	0.46
1:B:389:ALA:O	1:B:390:VAL:C	2.58	0.46
1:B:416:THR:O	1:B:419:VAL:HG12	2.15	0.46
1:B:420:ILE:CG2	1:B:421:THR:N	2.78	0.46
1:C:41:ILE:HG21	1:C:246:ILE:CG2	2.44	0.46
1:A:21:GLY:HA2	1:A:24:MET:HB2	1.96	0.46
1:A:56:LEU:HD12	1:A:397:TYR:CD1	2.50	0.46
1:A:306:ASP:C	1:A:308:GLY:H	2.22	0.46
1:A:368:THR:O	1:A:371:ALA:N	2.39	0.46
1:B:305:ALA:HA	1:B:312:PRO:HG2	1.98	0.46
1:C:57:SER:HB2	1:C:232:VAL:HG21	1.96	0.46
1:C:431:LEU:N	1:D:377:HIS:CE1	2.83	0.46
1:D:115:PHE:CD2	1:D:115:PHE:N	2.83	0.46
1:D:217:VAL:O	1:D:218:LYS:O	2.33	0.46
1:D:376:GLY:O	1:D:379:HIS:N	2.43	0.46
1:A:104:MET:HB3	1:A:290:LEU:HD23	1.96	0.46
1:A:184:VAL:O	1:A:185:SER:HB2	2.15	0.46
1:A:363:VAL:CG2	1:A:364:PRO:HD3	2.44	0.46
1:B:88:GLN:O	1:B:91:VAL:HG23	2.14	0.46
1:B:133:LEU:HD22	1:B:334:MET:SD	2.55	0.46
1:B:400:TRP:HA	1:B:403:VAL:CG1	2.46	0.46
1:C:128:THR:O	1:C:132:VAL:HG23	2.15	0.46
1:D:426:LEU:O	1:D:426:LEU:HG	2.16	0.46
1:C:67:ASP:OD1	1:C:67:ASP:O	2.33	0.46
1:C:82:GLY:N	1:C:83:PRO:CD	2.78	0.46
1:C:144:PRO:HG2	1:C:216:VAL:HG11	1.97	0.46
1:C:206:GLY:O	1:C:208:GLU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:ILE:HD13	1:D:236:ALA:HB1	1.97	0.46
1:D:352:LEU:HD21	1:D:408:LYS:HB2	1.98	0.46
1:A:342:ILE:CB	1:A:343:SER:CB	2.84	0.46
1:B:133:LEU:CD1	1:B:338:GLN:HG3	2.46	0.46
1:B:144:PRO:HG2	1:B:216:VAL:HG11	1.97	0.46
1:B:147:ILE:HD12	1:B:147:ILE:HA	1.70	0.46
1:B:306:ASP:C	1:B:308:GLY:N	2.73	0.46
1:B:425:ALA:O	1:B:427:ASN:N	2.48	0.46
1:C:99:ILE:HG21	1:C:357:SER:HB3	1.98	0.46
1:D:84:PHE:N	1:D:430:ARG:NH1	2.64	0.46
1:D:151:GLN:HE22	1:D:289:SER:HA	1.80	0.46
1:D:219:ASN:N	1:D:219:ASN:HD22	2.14	0.46
1:A:62:LYS:HA	1:A:65:PHE:CB	2.42	0.46
1:A:144:PRO:HB2	1:A:216:VAL:HG11	1.98	0.46
1:B:310:PHE:CE1	1:B:314:PHE:HE2	2.33	0.46
1:C:121:ASP:HB2	1:C:122:PRO:HD3	1.97	0.46
1:C:133:LEU:HD22	1:C:334:MET:SD	2.54	0.46
1:C:219:ASN:HD22	1:C:219:ASN:N	2.12	0.46
1:D:56:LEU:CD1	1:D:365:TYR:CD1	2.99	0.46
1:D:98:TRP:O	1:D:101:ASN:HB2	2.16	0.46
1:A:10:VAL:CG1	1:A:148:THR:HG21	2.46	0.46
1:A:201:LEU:HD12	1:A:201:LEU:HA	1.83	0.46
1:B:99:ILE:HG21	1:B:357:SER:HB3	1.97	0.46
1:B:111:TYR:CB	1:B:283:ALA:HB2	2.34	0.46
1:B:217:VAL:O	1:B:218:LYS:O	2.34	0.46
1:C:379:HIS:HE1	1:C:387:TYR:CD2	2.34	0.46
1:C:400:TRP:HA	1:C:403:VAL:CG1	2.45	0.46
1:B:44:TYR:O	1:B:45:GLY:C	2.58	0.46
1:B:93:TYR:CD2	1:B:93:TYR:C	2.93	0.46
1:C:119:LEU:HD22	1:C:124:VAL:CG2	2.37	0.46
1:C:217:VAL:O	1:C:218:LYS:O	2.34	0.46
1:D:71:GLY:C	1:D:212:VAL:HA	2.39	0.46
1:D:103:ALA:HB2	1:D:354:SER:OG	2.16	0.46
1:A:217:VAL:O	1:A:218:LYS:O	2.33	0.46
1:B:74:TYR:CZ	1:B:304:ALA:CB	2.94	0.46
1:B:92:LEU:CD2	1:B:363:VAL:CG2	2.89	0.46
1:C:47:LEU:C	1:C:47:LEU:HD13	2.41	0.46
1:C:376:GLY:HA3	1:C:379:HIS:CD2	2.51	0.46
1:D:72:GLY:C	1:D:74:TYR:H	2.23	0.46
1:D:92:LEU:CD2	1:D:363:VAL:CG2	2.88	0.46
1:A:113:SER:HA	1:A:120:LYS:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ILE:HG22	1:A:136:PHE:N	2.30	0.46
1:A:299:GLN:C	1:A:301:ALA:H	2.24	0.46
1:A:314:PHE:O	1:A:314:PHE:CD2	2.69	0.46
1:A:379:HIS:HE1	1:A:387:TYR:CD2	2.34	0.46
1:B:10:VAL:O	1:B:218:LYS:HG3	2.15	0.46
1:B:31:LEU:HD11	1:B:239:TYR:CE2	2.51	0.46
1:B:205:ILE:O	1:B:205:ILE:HG22	2.16	0.46
1:C:44:TYR:O	1:C:45:GLY:C	2.58	0.46
1:C:140:ASN:CB	1:C:327:LEU:HD22	2.40	0.46
1:C:403:VAL:O	1:D:411:MET:HE1	2.17	0.46
1:D:31:LEU:HD13	1:D:46:TRP:HH2	1.81	0.46
1:D:416:THR:O	1:D:419:VAL:HG12	2.16	0.46
1:A:94:TRP:O	1:A:97:CYS:HB2	2.16	0.45
1:A:411:MET:HB2	1:B:410:VAL:CG1	2.46	0.45
1:B:83:PRO:O	1:B:84:PHE:C	2.59	0.45
1:B:93:TYR:HE2	1:B:97:CYS:SG	2.35	0.45
1:B:426:LEU:C	1:B:427:ASN:HD22	2.21	0.45
1:C:84:PHE:N	1:C:430:ARG:NH1	2.65	0.45
1:C:104:MET:HB3	1:C:104:MET:HE2	1.71	0.45
1:C:107:ILE:O	1:C:111:TYR:CD1	2.68	0.45
1:C:301:ALA:HB1	1:C:310:PHE:CE1	2.47	0.45
1:C:425:ALA:O	1:C:427:ASN:N	2.48	0.45
1:D:22:ASN:HB3	1:D:293:TRP:HE1	1.81	0.45
1:D:299:GLN:C	1:D:301:ALA:H	2.24	0.45
1:D:359:ILE:HD11	1:D:409:GLU:CB	2.45	0.45
1:A:385:PRO:HA	1:A:388:LEU:HB2	1.98	0.45
1:A:413:SER:O	1:A:416:THR:HB	2.16	0.45
1:B:115:PHE:CD2	1:B:115:PHE:N	2.84	0.45
1:B:210:ALA:C	1:B:212:VAL:H	2.24	0.45
1:C:63:MET:SD	1:C:372:LEU:CD1	3.04	0.45
1:C:89:THR:HG23	1:C:364:PRO:HG3	1.97	0.45
1:C:120:LYS:HZ3	1:C:124:VAL:HG12	1.81	0.45
1:C:413:SER:O	1:C:416:THR:HB	2.16	0.45
1:D:69:SER:OG	1:D:71:GLY:N	2.45	0.45
1:D:136:PHE:HD2	1:D:290:LEU:HD12	1.82	0.45
1:D:379:HIS:HE1	1:D:387:TYR:CD2	2.34	0.45
1:A:41:ILE:HG21	1:A:246:ILE:CG2	2.47	0.45
1:C:115:PHE:N	1:C:115:PHE:CD2	2.84	0.45
1:C:140:ASN:HD21	1:C:147:ILE:HG12	1.79	0.45
1:C:385:PRO:HA	1:C:388:LEU:HB2	1.98	0.45
1:D:72:GLY:C	1:D:74:TYR:N	2.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:LEU:HD12	1:D:201:LEU:HA	1.83	0.45
1:D:372:LEU:C	1:D:373:LEU:HG	2.41	0.45
1:A:19:VAL:CG2	1:A:210:ALA:HB2	2.40	0.45
1:A:69:SER:OG	1:A:71:GLY:N	2.45	0.45
1:A:201:LEU:HD23	1:A:401:ALA:HB2	1.99	0.45
1:A:418:MET:HE2	1:B:399:ILE:HG12	1.96	0.45
1:A:422:ALA:CB	1:B:395:PHE:CD1	2.99	0.45
1:B:120:LYS:HZ3	1:B:124:VAL:HG12	1.81	0.45
1:C:22:ASN:HB3	1:C:293:TRP:HE1	1.82	0.45
1:C:30:LEU:O	1:C:33:ALA:HB3	2.16	0.45
1:C:81:PHE:HE1	1:D:80:CYS:O	2.00	0.45
1:C:414:PHE:C	1:C:414:PHE:HD2	2.24	0.45
1:D:10:VAL:CG1	1:D:148:THR:HG21	2.47	0.45
1:D:41:ILE:O	1:D:41:ILE:HG12	2.16	0.45
1:D:63:MET:HB2	1:D:372:LEU:HD13	1.99	0.45
1:B:301:ALA:C	1:B:303:ALA:N	2.74	0.45
1:B:339:LEU:HA	1:B:342:ILE:CG1	2.46	0.45
1:C:28:VAL:HA	1:C:31:LEU:HG	1.99	0.45
1:C:98:TRP:O	1:C:101:ASN:HB2	2.17	0.45
1:C:302:LYS:HE3	1:C:326:GLY:CA	2.46	0.45
1:D:104:MET:HB3	1:D:104:MET:HE2	1.66	0.45
1:D:363:VAL:CB	1:D:364:PRO:HD3	2.46	0.45
1:A:47:LEU:HD13	1:A:47:LEU:C	2.40	0.45
1:B:98:TRP:O	1:B:101:ASN:HB2	2.16	0.45
1:B:219:ASN:HD22	1:B:219:ASN:N	2.13	0.45
1:C:19:VAL:CG2	1:C:210:ALA:HB2	2.41	0.45
1:C:88:GLN:HG3	1:C:420:ILE:HG21	1.98	0.45
1:A:60:TYR:HH	1:A:368:THR:HG1	1.64	0.45
1:A:119:LEU:CD1	1:A:124:VAL:HG11	2.36	0.45
1:A:339:LEU:HA	1:A:342:ILE:HG13	1.98	0.45
1:A:345:ASN:O	1:A:346:ALA:HB3	2.16	0.45
1:A:373:LEU:HD11	1:A:391:THR:HB	1.97	0.45
1:B:35:LEU:CD2	1:B:196:THR:HG22	2.40	0.45
1:C:235:ALA:O	1:C:238:CYS:HB2	2.17	0.45
1:C:306:ASP:C	1:C:308:GLY:H	2.25	0.45
1:C:342:ILE:HB	1:C:343:SER:OG	2.16	0.45
1:C:411:MET:HA	1:D:410:VAL:CG1	2.46	0.45
1:D:44:TYR:O	1:D:45:GLY:C	2.59	0.45
1:D:135:ILE:O	1:D:139:LEU:HG	2.16	0.45
1:A:46:TRP:CH2	1:A:200:THR:HG22	2.52	0.45
1:B:113:SER:HA	1:B:120:LYS:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:342:ILE:HB	1:B:343:SER:OG	2.16	0.45
1:C:21:GLY:HA2	1:C:24:MET:HB2	1.98	0.45
1:C:49:THR:OG1	1:C:201:LEU:HD12	2.17	0.45
1:D:107:ILE:HG23	1:D:111:TYR:CE1	2.52	0.45
1:D:172:TRP:HE3	1:D:173:PHE:N	2.15	0.45
1:D:345:ASN:O	1:D:346:ALA:HB3	2.16	0.45
1:A:388:LEU:HD23	1:A:388:LEU:HA	1.70	0.45
1:B:41:ILE:HG21	1:B:246:ILE:CG2	2.46	0.45
1:B:47:LEU:C	1:B:47:LEU:HD13	2.42	0.45
1:B:92:LEU:O	1:B:360:PHE:HB3	2.17	0.45
1:B:303:ALA:C	1:B:305:ALA:H	2.24	0.45
1:B:352:LEU:HD21	1:B:408:LYS:HB2	1.99	0.45
1:C:10:VAL:O	1:C:218:LYS:HG3	2.17	0.45
1:C:113:SER:HA	1:C:120:LYS:HG3	1.98	0.45
1:C:303:ALA:C	1:C:305:ALA:H	2.24	0.45
1:C:345:ASN:O	1:C:346:ALA:HB3	2.17	0.45
1:D:23:ILE:HG21	1:D:204:PHE:HD1	1.79	0.45
1:D:32:PRO:CG	1:D:243:THR:HG22	2.37	0.45
1:D:121:ASP:N	1:D:122:PRO:CD	2.80	0.45
1:D:121:ASP:HB2	1:D:122:PRO:HD3	1.99	0.45
1:D:136:PHE:HB3	1:D:291:GLY:HA2	1.97	0.45
1:D:385:PRO:HA	1:D:388:LEU:HB2	1.98	0.45
1:A:104:MET:HB3	1:A:104:MET:HE2	1.66	0.45
1:A:302:LYS:HE3	1:A:326:GLY:CA	2.47	0.45
1:A:352:LEU:HD21	1:A:408:LYS:HB2	1.99	0.45
1:A:373:LEU:HB2	1:B:428:TYR:CE1	2.52	0.45
1:A:376:GLY:HA3	1:A:379:HIS:HD2	1.82	0.45
1:C:31:LEU:HD13	1:C:46:TRP:HH2	1.82	0.45
1:D:49:THR:OG1	1:D:201:LEU:CD1	2.64	0.45
1:D:135:ILE:HG22	1:D:136:PHE:N	2.32	0.45
1:D:201:LEU:HD23	1:D:401:ALA:HB2	1.99	0.45
1:D:314:PHE:O	1:D:314:PHE:CD2	2.68	0.45
1:D:413:SER:O	1:D:416:THR:HB	2.17	0.45
1:A:298:GLY:HA2	1:A:302:LYS:NZ	2.31	0.44
1:A:412:TRP:CE3	1:A:415:VAL:HG21	2.52	0.44
1:A:420:ILE:CG2	1:A:421:THR:N	2.77	0.44
1:B:317:VAL:HA	1:B:322:THR:O	2.17	0.44
1:C:83:PRO:HB2	1:C:84:PHE:H	1.58	0.44
1:C:119:LEU:HB3	1:C:120:LYS:H	1.59	0.44
1:C:136:PHE:HD2	1:C:290:LEU:HD12	1.82	0.44
1:D:116:PHE:O	1:D:117:PRO:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:311:PRO:HG2	1:D:426:LEU:HD11	2.00	0.44
1:D:342:ILE:CB	1:D:343:SER:CB	2.86	0.44
1:D:418:MET:HE2	1:D:418:MET:HB3	1.71	0.44
1:A:98:TRP:O	1:A:101:ASN:HB2	2.17	0.44
1:B:59:VAL:HG22	1:B:391:THR:HG22	1.98	0.44
1:B:379:HIS:HE1	1:B:387:TYR:CD2	2.35	0.44
1:C:19:VAL:HG11	1:C:228:THR:HA	2.00	0.44
1:C:81:PHE:CE2	1:C:83:PRO:HG2	2.52	0.44
1:C:372:LEU:C	1:C:373:LEU:HG	2.42	0.44
1:C:377:HIS:CE1	1:D:430:ARG:N	2.86	0.44
1:D:28:VAL:O	1:D:30:LEU:N	2.45	0.44
1:D:46:TRP:CH2	1:D:200:THR:HG22	2.52	0.44
1:D:113:SER:HA	1:D:120:LYS:HG3	1.99	0.44
1:D:342:ILE:HB	1:D:343:SER:OG	2.17	0.44
1:D:420:ILE:CG2	1:D:421:THR:N	2.80	0.44
1:A:31:LEU:HD13	1:A:46:TRP:HH2	1.81	0.44
1:A:82:GLY:O	1:A:83:PRO:O	2.35	0.44
1:A:135:ILE:O	1:A:139:LEU:HG	2.17	0.44
1:A:136:PHE:HD2	1:A:290:LEU:HD12	1.81	0.44
1:A:219:ASN:N	1:A:219:ASN:HD22	2.14	0.44
1:A:418:MET:HE1	1:B:399:ILE:HA	1.97	0.44
1:B:82:GLY:O	1:B:83:PRO:O	2.36	0.44
1:B:290:LEU:HD22	1:B:290:LEU:HA	1.63	0.44
1:B:337:PHE:HZ	1:B:353:VAL:HG11	1.80	0.44
1:B:367:TYR:O	1:B:368:THR:C	2.59	0.44
1:C:205:ILE:HG22	1:C:205:ILE:O	2.17	0.44
1:C:299:GLN:C	1:C:301:ALA:H	2.26	0.44
1:D:136:PHE:CE1	1:D:287:LEU:O	2.71	0.44
1:D:314:PHE:CA	1:D:315:ALA:O	2.65	0.44
1:A:49:THR:HB	1:A:197:LEU:CD2	2.46	0.44
1:A:114:TYR:CE1	1:A:118:ILE:HG12	2.52	0.44
1:A:115:PHE:CD2	1:A:115:PHE:N	2.84	0.44
1:A:305:ALA:HA	1:A:312:PRO:HG2	2.00	0.44
1:A:389:ALA:O	1:A:392:THR:N	2.50	0.44
1:B:21:GLY:HA2	1:B:24:MET:HB2	1.99	0.44
1:B:49:THR:OG1	1:B:201:LEU:HD12	2.17	0.44
1:B:351:GLY:C	1:B:353:VAL:N	2.76	0.44
1:B:356:VAL:HA	1:B:359:ILE:HD12	1.99	0.44
1:B:412:TRP:CE3	1:B:415:VAL:HG21	2.52	0.44
1:C:74:TYR:CZ	1:C:304:ALA:CB	2.93	0.44
1:C:201:LEU:HD23	1:C:401:ALA:CA	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:GLY:O	1:D:41:ILE:C	2.60	0.44
1:D:49:THR:HB	1:D:197:LEU:CD2	2.46	0.44
1:D:95:LEU:HD23	1:D:95:LEU:O	2.18	0.44
1:D:363:VAL:CG2	1:D:364:PRO:HD3	2.47	0.44
1:D:389:ALA:O	1:D:392:THR:N	2.50	0.44
1:D:400:TRP:HA	1:D:403:VAL:CG1	2.47	0.44
1:A:28:VAL:O	1:A:30:LEU:N	2.45	0.44
1:A:81:PHE:CB	1:A:82:GLY:CA	2.92	0.44
1:A:93:TYR:CE1	1:A:208:GLU:OE1	2.71	0.44
1:B:133:LEU:HD22	1:B:334:MET:CE	2.48	0.44
1:B:315:ALA:CB	1:B:316:ARG:CA	2.77	0.44
1:C:59:VAL:HG22	1:C:391:THR:CG2	2.48	0.44
1:C:59:VAL:HG22	1:C:391:THR:HG22	1.98	0.44
1:C:317:VAL:O	1:C:318:ASN:C	2.61	0.44
1:D:128:THR:O	1:D:132:VAL:HG23	2.18	0.44
1:D:161:PRO:O	1:D:165:ILE:HG13	2.17	0.44
1:A:121:ASP:HB2	1:A:122:PRO:HD3	1.99	0.44
1:B:34:ASN:HB3	1:B:199:VAL:HG11	1.98	0.44
1:B:93:TYR:CE1	1:B:208:GLU:CD	2.96	0.44
1:B:116:PHE:O	1:B:117:PRO:C	2.61	0.44
1:B:346:ALA:HB3	1:B:351:GLY:CA	2.43	0.44
1:C:352:LEU:HD21	1:C:408:LYS:HB2	1.99	0.44
1:D:373:LEU:HD11	1:D:391:THR:HB	1.98	0.44
1:A:60:TYR:OH	1:A:368:THR:OG1	2.34	0.44
1:A:337:PHE:HZ	1:A:353:VAL:HG11	1.81	0.44
1:B:136:PHE:HD2	1:B:290:LEU:HD12	1.82	0.44
1:B:344:PRO:O	1:B:345:ASN:CB	2.65	0.44
1:C:49:THR:HB	1:C:197:LEU:CD2	2.48	0.44
1:D:91:VAL:O	1:D:95:LEU:HB3	2.17	0.44
1:D:92:LEU:HD11	1:D:363:VAL:CG2	2.07	0.44
1:D:133:LEU:CD2	1:D:290:LEU:HD11	2.42	0.44
1:A:144:PRO:HD3	1:A:322:THR:HG23	1.99	0.44
1:A:359:ILE:HD11	1:A:409:GLU:CB	2.44	0.44
1:A:414:PHE:HB2	1:B:414:PHE:HB2	2.00	0.44
1:A:421:THR:C	1:A:423:MET:N	2.75	0.44
1:B:201:LEU:HD12	1:B:201:LEU:HA	1.81	0.44
1:D:24:MET:HE2	1:D:159:LEU:HD23	1.99	0.44
1:D:81:PHE:CB	1:D:82:GLY:CA	2.95	0.44
1:A:88:GLN:O	1:A:91:VAL:HG23	2.17	0.44
1:A:116:PHE:O	1:A:117:PRO:C	2.60	0.44
1:A:116:PHE:CB	1:A:117:PRO:CD	2.93	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:LEU:HD11	1:A:391:THR:CB	2.48	0.44
1:B:31:LEU:HD13	1:B:46:TRP:HH2	1.82	0.44
1:B:345:ASN:O	1:B:346:ALA:HB3	2.17	0.44
1:C:81:PHE:CE1	1:D:80:CYS:O	2.71	0.44
1:C:339:LEU:HA	1:C:342:ILE:CG1	2.48	0.44
1:C:396:LEU:HD23	1:C:396:LEU:HA	1.72	0.44
1:D:19:VAL:HG11	1:D:228:THR:HA	2.00	0.44
1:D:53:ALA:HB2	1:D:397:TYR:HE2	1.80	0.44
1:D:299:GLN:OE1	1:D:299:GLN:HA	2.17	0.44
1:A:23:ILE:HG23	1:A:204:PHE:C	2.43	0.43
1:A:114:TYR:C	1:A:115:PHE:CD2	2.96	0.43
1:A:172:TRP:HE3	1:A:173:PHE:N	2.16	0.43
1:B:107:ILE:O	1:B:111:TYR:CD1	2.71	0.43
1:B:121:ASP:N	1:B:122:PRO:CD	2.80	0.43
1:B:318:ASN:HB2	1:B:324:VAL:CG2	2.48	0.43
1:C:351:GLY:C	1:C:353:VAL:N	2.76	0.43
1:C:403:VAL:HG23	1:D:415:VAL:HG11	2.00	0.43
1:A:311:PRO:HG2	1:A:426:LEU:HD11	1.99	0.43
1:A:311:PRO:HA	1:A:312:PRO:HD3	1.85	0.43
1:A:339:LEU:HA	1:A:342:ILE:CG1	2.48	0.43
1:A:344:PRO:O	1:A:345:ASN:CB	2.65	0.43
1:B:24:MET:HE3	1:B:162:ILE:CD1	2.31	0.43
1:B:57:SER:HB2	1:B:232:VAL:HG21	1.98	0.43
1:C:91:VAL:HB	1:C:420:ILE:CD1	2.46	0.43
1:C:133:LEU:CD1	1:C:338:GLN:HG3	2.48	0.43
1:C:418:MET:HE2	1:C:418:MET:HB3	1.74	0.43
1:D:8:HIS:ND1	1:D:9:LYS:NZ	2.65	0.43
1:D:78:ARG:O	1:D:79:ARG:HG3	2.18	0.43
1:D:88:GLN:O	1:D:91:VAL:HG23	2.19	0.43
1:D:94:TRP:O	1:D:97:CYS:HB2	2.17	0.43
1:D:111:TYR:CB	1:D:283:ALA:HB2	2.37	0.43
1:D:174:ARG:HA	1:D:175:GLY:HA3	1.92	0.43
1:D:212:VAL:HG11	1:D:296:LEU:HD13	1.98	0.43
1:A:84:PHE:N	1:A:430:ARG:NH1	2.66	0.43
1:B:212:VAL:HG11	1:B:296:LEU:HD13	1.99	0.43
1:C:359:ILE:H	1:C:359:ILE:HG13	1.69	0.43
1:A:78:ARG:O	1:A:79:ARG:HG3	2.18	0.43
1:A:306:ASP:O	1:A:308:GLY:N	2.52	0.43
1:B:10:VAL:CG1	1:B:148:THR:HG21	2.48	0.43
1:B:83:PRO:HB2	1:B:84:PHE:H	1.56	0.43
1:B:104:MET:CE	1:B:286:CYS:SG	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:PHE:CB	1:B:117:PRO:CD	2.92	0.43
1:B:172:TRP:HE3	1:B:173:PHE:N	2.16	0.43
1:B:201:LEU:HD23	1:B:401:ALA:CB	2.46	0.43
1:B:376:GLY:HA3	1:B:379:HIS:HD2	1.84	0.43
1:B:413:SER:O	1:B:416:THR:HB	2.18	0.43
1:C:395:PHE:CD1	1:D:422:ALA:CB	3.02	0.43
1:C:430:ARG:N	1:D:377:HIS:CE1	2.85	0.43
1:D:133:LEU:HD11	1:D:338:GLN:HG3	2.00	0.43
1:A:63:MET:HB2	1:A:372:LEU:HD13	2.00	0.43
1:A:210:ALA:C	1:A:212:VAL:H	2.26	0.43
1:A:415:VAL:HG11	1:B:403:VAL:HG23	2.00	0.43
1:C:116:PHE:CB	1:C:117:PRO:CD	2.92	0.43
1:C:416:THR:CA	1:C:419:VAL:HG12	2.47	0.43
1:D:99:ILE:HG22	1:D:100:GLY:N	2.33	0.43
1:B:19:VAL:HG11	1:B:228:THR:HA	2.00	0.43
1:C:107:ILE:HG23	1:C:111:TYR:CE1	2.53	0.43
1:C:372:LEU:HG	1:C:372:LEU:O	2.19	0.43
1:D:317:VAL:O	1:D:318:ASN:C	2.60	0.43
1:A:44:TYR:O	1:A:45:GLY:C	2.60	0.43
1:A:88:GLN:O	1:A:91:VAL:N	2.52	0.43
1:B:28:VAL:O	1:B:30:LEU:N	2.47	0.43
1:B:428:TYR:C	1:B:429:ASN:CG	2.87	0.43
1:C:96:ALA:O	1:C:293:TRP:HZ3	2.00	0.43
1:C:359:ILE:HB	1:C:413:SER:OG	2.19	0.43
1:C:416:THR:O	1:C:419:VAL:HG12	2.19	0.43
1:C:420:ILE:HG22	1:C:421:THR:H	1.82	0.43
1:C:423:MET:HG2	1:C:423:MET:O	2.19	0.43
1:D:116:PHE:CB	1:D:117:PRO:CD	2.93	0.43
1:D:337:PHE:HZ	1:D:353:VAL:HG11	1.82	0.43
1:A:52:GLY:HA2	1:A:393:ILE:CG2	2.49	0.43
1:A:128:THR:O	1:A:132:VAL:HG23	2.19	0.43
1:A:410:VAL:C	1:A:412:TRP:N	2.74	0.43
1:B:56:LEU:HD12	1:B:397:TYR:CE1	2.54	0.43
1:C:10:VAL:CG1	1:C:148:THR:HG21	2.49	0.43
1:C:56:LEU:HD12	1:C:397:TYR:CE1	2.53	0.43
1:C:72:GLY:C	1:C:74:TYR:N	2.71	0.43
1:C:172:TRP:HE3	1:C:173:PHE:N	2.17	0.43
1:C:187:LEU:N	1:C:187:LEU:HD23	2.33	0.43
1:C:218:LYS:HB3	1:C:219:ASN:H	1.52	0.43
1:C:414:PHE:HE2	1:C:418:MET:SD	2.42	0.43
1:D:30:LEU:O	1:D:33:ALA:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:VAL:HG23	1:B:159:LEU:HD12	2.01	0.43
1:B:317:VAL:O	1:B:318:ASN:C	2.62	0.43
1:C:82:GLY:O	1:C:83:PRO:O	2.36	0.43
1:C:116:PHE:O	1:C:117:PRO:C	2.61	0.43
1:D:10:VAL:HG11	1:D:148:THR:HG21	2.01	0.43
1:D:41:ILE:HG21	1:D:246:ILE:CG2	2.48	0.43
1:D:410:VAL:C	1:D:412:TRP:N	2.75	0.43
1:A:56:LEU:CD1	1:A:365:TYR:CD1	2.99	0.43
1:A:215:GLY:O	1:A:216:VAL:HG22	2.19	0.43
1:B:76:TYR:OH	1:B:211:SER:OG	2.23	0.43
1:B:81:PHE:CB	1:B:82:GLY:CA	2.90	0.43
1:B:84:PHE:N	1:B:430:ARG:NH1	2.66	0.43
1:C:290:LEU:O	1:C:294:THR:HG23	2.18	0.43
1:C:344:PRO:O	1:C:345:ASN:CB	2.65	0.43
1:D:52:GLY:HA2	1:D:393:ILE:CG2	2.49	0.43
1:D:88:GLN:O	1:D:91:VAL:N	2.52	0.43
1:D:95:LEU:O	1:D:96:ALA:HB2	2.19	0.43
1:D:388:LEU:HD23	1:D:388:LEU:HA	1.70	0.43
1:A:40:GLY:O	1:A:41:ILE:C	2.61	0.42
1:A:359:ILE:HB	1:A:413:SER:OG	2.19	0.42
1:B:107:ILE:HG23	1:B:111:TYR:CE1	2.54	0.42
1:B:302:LYS:HE3	1:B:326:GLY:HA3	2.01	0.42
1:B:359:ILE:HD11	1:B:409:GLU:CB	2.46	0.42
1:C:23:ILE:O	1:C:24:MET:C	2.61	0.42
1:C:311:PRO:HA	1:C:312:PRO:HD3	1.85	0.42
1:C:356:VAL:HA	1:C:359:ILE:HD12	2.01	0.42
1:D:60:TYR:HE2	1:D:368:THR:CB	2.32	0.42
1:D:139:LEU:C	1:D:147:ILE:HD13	2.43	0.42
1:A:104:MET:HE1	1:A:286:CYS:SG	2.59	0.42
1:A:317:VAL:O	1:A:318:ASN:C	2.62	0.42
1:B:206:GLY:C	1:B:208:GLU:N	2.77	0.42
1:B:414:PHE:O	1:B:418:MET:HG3	2.19	0.42
1:C:67:ASP:O	1:C:69:SER:HA	2.19	0.42
1:D:114:TYR:C	1:D:115:PHE:CD2	2.96	0.42
1:D:144:PRO:HD3	1:D:322:THR:HG23	1.98	0.42
1:A:10:VAL:HG11	1:A:148:THR:HG21	2.01	0.42
1:A:103:ALA:HB2	1:A:354:SER:OG	2.19	0.42
1:B:290:LEU:O	1:B:294:THR:HG23	2.20	0.42
1:B:410:VAL:C	1:B:412:TRP:N	2.75	0.42
1:C:24:MET:HE2	1:C:159:LEU:HD23	2.00	0.42
1:C:421:THR:O	1:C:424:TYR:N	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:144:PRO:HB2	1:D:216:VAL:HG11	2.01	0.42
1:D:412:TRP:CE3	1:D:415:VAL:HG21	2.55	0.42
1:A:389:ALA:O	1:A:390:VAL:C	2.63	0.42
1:A:421:THR:O	1:A:424:TYR:N	2.44	0.42
1:A:431:LEU:N	1:B:377:HIS:HE1	2.17	0.42
1:B:88:GLN:HG3	1:B:420:ILE:HG21	2.01	0.42
1:B:299:GLN:C	1:B:301:ALA:H	2.27	0.42
1:C:139:LEU:HB3	1:C:147:ILE:HD13	2.00	0.42
1:C:318:ASN:HB2	1:C:324:VAL:CG2	2.49	0.42
1:C:363:VAL:HB	1:C:364:PRO:HD3	2.01	0.42
1:C:420:ILE:CG2	1:C:421:THR:N	2.81	0.42
1:D:59:VAL:HG11	1:D:369:CYS:SG	2.59	0.42
1:D:62:LYS:HA	1:D:65:PHE:CB	2.43	0.42
1:D:318:ASN:HB2	1:D:324:VAL:CG2	2.49	0.42
1:A:114:TYR:O	1:A:115:PHE:HB2	2.19	0.42
1:A:366:LEU:HD11	1:B:421:THR:CG2	2.46	0.42
1:A:421:THR:CG2	1:B:366:LEU:HD21	2.49	0.42
1:A:430:ARG:N	1:B:377:HIS:HE1	2.17	0.42
1:B:67:ASP:OD1	1:B:67:ASP:O	2.38	0.42
1:B:139:LEU:HB3	1:B:147:ILE:HD13	2.01	0.42
1:D:147:ILE:HD12	1:D:147:ILE:HA	1.71	0.42
1:D:215:GLY:O	1:D:216:VAL:HG22	2.19	0.42
1:A:8:HIS:ND1	1:A:9:LYS:NZ	2.65	0.42
1:A:50:ILE:CD1	1:A:236:ALA:HB1	2.50	0.42
1:A:318:ASN:HB2	1:A:324:VAL:CG2	2.50	0.42
1:B:24:MET:HE2	1:B:159:LEU:HD23	2.00	0.42
1:B:50:ILE:CD1	1:B:236:ALA:HB1	2.49	0.42
1:B:59:VAL:HG22	1:B:391:THR:CG2	2.50	0.42
1:B:135:ILE:O	1:B:139:LEU:HG	2.19	0.42
1:B:314:PHE:O	1:B:314:PHE:CD2	2.73	0.42
1:B:359:ILE:H	1:B:359:ILE:HG13	1.69	0.42
1:D:218:LYS:HB3	1:D:219:ASN:H	1.51	0.42
1:D:356:VAL:HA	1:D:359:ILE:HD12	2.02	0.42
1:D:376:GLY:HA3	1:D:379:HIS:HD2	1.83	0.42
1:A:88:GLN:HG3	1:A:420:ILE:HG21	2.01	0.42
1:A:136:PHE:CE1	1:A:287:LEU:O	2.72	0.42
1:A:290:LEU:O	1:A:294:THR:HG23	2.19	0.42
1:B:161:PRO:O	1:B:165:ILE:HG13	2.19	0.42
1:C:135:ILE:O	1:C:139:LEU:HG	2.19	0.42
1:C:135:ILE:HG22	1:C:136:PHE:N	2.34	0.42
1:C:156:VAL:HG23	1:C:159:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:LEU:CD1	1:D:124:VAL:HG11	2.36	0.42
1:A:19:VAL:HG11	1:A:228:THR:HA	2.01	0.42
1:A:59:VAL:HG11	1:A:369:CYS:SG	2.59	0.42
1:A:77:ALA:O	1:A:79:ARG:N	2.53	0.42
1:A:236:ALA:O	1:A:239:TYR:HB2	2.20	0.42
1:B:28:VAL:HA	1:B:31:LEU:HG	2.01	0.42
1:B:46:TRP:CH2	1:B:239:TYR:HB3	2.55	0.42
1:B:114:TYR:C	1:B:115:PHE:CD2	2.97	0.42
1:B:397:TYR:C	1:B:397:TYR:CD1	2.97	0.42
1:C:50:ILE:CD1	1:C:236:ALA:HB1	2.49	0.42
1:C:114:TYR:C	1:C:115:PHE:CD2	2.97	0.42
1:D:172:TRP:HB3	1:D:173:PHE:H	1.65	0.42
1:D:199:VAL:O	1:D:199:VAL:HG12	2.18	0.42
1:D:305:ALA:HA	1:D:312:PRO:HG2	2.01	0.42
1:D:344:PRO:O	1:D:345:ASN:CB	2.64	0.42
1:A:10:VAL:O	1:A:218:LYS:HG3	2.19	0.42
1:A:93:TYR:CD2	1:A:93:TYR:C	2.98	0.42
1:A:117:PRO:C	1:A:118:ILE:HG22	2.45	0.42
1:A:133:LEU:HD11	1:A:338:GLN:HG3	2.01	0.42
1:A:290:LEU:HA	1:A:290:LEU:HD22	1.64	0.42
1:A:314:PHE:CA	1:A:315:ALA:O	2.68	0.42
1:B:69:SER:N	1:B:70:PRO:HA	2.34	0.42
1:B:134:TRP:HA	1:B:137:VAL:HB	2.01	0.42
1:B:365:TYR:CB	1:B:398:CYS:SG	2.92	0.42
1:C:69:SER:N	1:C:70:PRO:HA	2.35	0.42
1:C:92:LEU:CD2	1:C:363:VAL:CG2	2.88	0.42
1:C:101:ASN:O	1:C:104:MET:HB2	2.20	0.42
1:C:410:VAL:C	1:C:412:TRP:N	2.76	0.42
1:D:92:LEU:HD21	1:D:363:VAL:HG21	1.94	0.42
1:D:235:ALA:O	1:D:238:CYS:HB2	2.20	0.42
1:A:147:ILE:HA	1:A:147:ILE:HD12	1.70	0.42
1:A:421:THR:C	1:A:423:MET:H	2.27	0.42
1:B:67:ASP:O	1:B:69:SER:HA	2.20	0.42
1:B:136:PHE:CE1	1:B:287:LEU:O	2.73	0.42
1:C:95:LEU:HD12	1:C:98:TRP:HH2	1.85	0.42
1:C:305:ALA:HA	1:C:312:PRO:HG2	2.01	0.42
1:C:359:ILE:HD11	1:C:409:GLU:CB	2.47	0.42
1:C:412:TRP:CE3	1:C:412:TRP:CA	2.96	0.42
1:C:428:TYR:CE1	1:D:373:LEU:CB	3.03	0.42
1:D:60:TYR:OH	1:D:368:THR:OG1	2.35	0.42
1:D:69:SER:N	1:D:70:PRO:HA	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:VAL:HG23	1:D:159:LEU:HD12	2.01	0.42
1:A:273:THR:C	1:A:275:GLY:H	2.28	0.41
1:A:368:THR:O	1:A:371:ALA:HB3	2.20	0.41
1:B:306:ASP:C	1:B:308:GLY:H	2.27	0.41
1:C:136:PHE:CE1	1:C:287:LEU:O	2.73	0.41
1:D:420:ILE:HG22	1:D:421:THR:H	1.80	0.41
1:A:63:MET:CG	1:A:76:TYR:CD2	3.03	0.41
1:A:96:ALA:HA	1:A:357:SER:HB2	2.02	0.41
1:B:13:ILE:CB	1:B:14:PRO:HD3	2.50	0.41
1:C:88:GLN:O	1:C:91:VAL:HG23	2.21	0.41
1:D:99:ILE:HG21	1:D:357:SER:HB3	2.02	0.41
1:D:107:ILE:O	1:D:111:TYR:CD1	2.72	0.41
1:D:371:ALA:C	1:D:373:LEU:N	2.72	0.41
1:A:99:ILE:HG21	1:A:357:SER:HB3	2.02	0.41
1:A:107:ILE:O	1:A:111:TYR:CD1	2.71	0.41
1:A:134:TRP:HA	1:A:137:VAL:HB	2.02	0.41
1:B:23:ILE:O	1:B:24:MET:C	2.63	0.41
1:B:101:ASN:O	1:B:104:MET:HB2	2.20	0.41
1:B:249:MET:C	1:B:250:ILE:HG12	2.45	0.41
1:C:273:THR:C	1:C:275:GLY:H	2.28	0.41
1:D:114:TYR:O	1:D:115:PHE:HB2	2.20	0.41
1:D:317:VAL:HA	1:D:322:THR:O	2.20	0.41
1:D:351:GLY:C	1:D:353:VAL:N	2.78	0.41
1:A:92:LEU:CG	1:A:363:VAL:HG21	2.50	0.41
1:A:121:ASP:N	1:A:122:PRO:CD	2.81	0.41
1:A:212:VAL:HG11	1:A:296:LEU:HD13	2.03	0.41
1:A:352:LEU:HD23	1:A:352:LEU:HA	1.93	0.41
1:B:49:THR:HB	1:B:197:LEU:CD2	2.50	0.41
1:B:51:ILE:HG22	1:B:52:GLY:N	2.35	0.41
1:C:35:LEU:CD2	1:C:196:THR:HG22	2.42	0.41
1:C:317:VAL:HA	1:C:322:THR:O	2.20	0.41
1:D:290:LEU:O	1:D:294:THR:HG23	2.20	0.41
1:D:389:ALA:O	1:D:390:VAL:C	2.62	0.41
1:A:49:THR:OG1	1:A:201:LEU:HD12	2.21	0.41
1:A:69:SER:N	1:A:70:PRO:HA	2.35	0.41
1:A:359:ILE:HD13	1:A:410:VAL:HA	2.02	0.41
1:B:135:ILE:HG22	1:B:136:PHE:N	2.34	0.41
1:C:54:LEU:HD12	1:C:232:VAL:CG1	2.50	0.41
1:C:95:LEU:HD23	1:C:95:LEU:O	2.20	0.41
1:D:210:ALA:C	1:D:212:VAL:N	2.78	0.41
1:D:311:PRO:HA	1:D:312:PRO:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:LEU:HD11	1:D:391:THR:CB	2.50	0.41
1:A:24:MET:HE2	1:A:159:LEU:HD23	2.03	0.41
1:A:139:LEU:C	1:A:147:ILE:HD13	2.45	0.41
1:A:174:ARG:HA	1:A:175:GLY:HA3	1.93	0.41
1:A:395:PHE:O	1:A:399:ILE:HB	2.21	0.41
1:B:8:HIS:ND1	1:B:9:LYS:NZ	2.66	0.41
1:B:374:LEU:HD12	1:B:374:LEU:HA	1.86	0.41
1:C:28:VAL:O	1:C:30:LEU:N	2.46	0.41
1:C:314:PHE:CA	1:C:315:ALA:O	2.68	0.41
1:C:376:GLY:CA	1:C:379:HIS:H	2.33	0.41
1:D:82:GLY:O	1:D:83:PRO:O	2.39	0.41
1:D:88:GLN:O	1:D:89:THR:C	2.63	0.41
1:D:301:ALA:HB1	1:D:310:PHE:CE1	2.46	0.41
1:D:302:LYS:HE3	1:D:326:GLY:CA	2.50	0.41
1:A:366:LEU:HD13	1:A:367:TYR:HD2	1.81	0.41
1:C:310:PHE:HB3	1:C:311:PRO:O	2.20	0.41
1:C:346:ALA:HB3	1:C:351:GLY:CA	2.44	0.41
1:D:35:LEU:CD2	1:D:196:THR:HG22	2.43	0.41
1:D:60:TYR:HH	1:D:368:THR:HG1	1.68	0.41
1:A:81:PHE:HE1	1:B:80:CYS:O	2.03	0.41
1:A:173:PHE:CE1	1:A:247:MET:SD	3.14	0.41
1:A:300:THR:O	1:A:300:THR:CG2	2.64	0.41
1:B:94:TRP:CA	1:B:97:CYS:HB2	2.47	0.41
1:B:359:ILE:HB	1:B:413:SER:OG	2.21	0.41
1:B:363:VAL:HB	1:B:364:PRO:HD3	2.02	0.41
1:C:211:SER:O	1:C:211:SER:OG	2.33	0.41
1:C:212:VAL:HG11	1:C:296:LEU:HD13	2.02	0.41
1:D:69:SER:HB2	1:D:75:ALA:HB2	2.02	0.41
1:D:117:PRO:C	1:D:118:ILE:HG22	2.45	0.41
1:D:306:ASP:O	1:D:308:GLY:N	2.54	0.41
1:A:10:VAL:CG2	1:A:145:LYS:HA	2.51	0.41
1:A:215:GLY:C	1:A:216:VAL:CG2	2.94	0.41
1:A:351:GLY:C	1:A:353:VAL:N	2.78	0.41
1:B:133:LEU:HD11	1:B:338:GLN:HG3	2.02	0.41
1:B:187:LEU:N	1:B:187:LEU:HD23	2.35	0.41
1:B:215:GLY:C	1:B:216:VAL:CG2	2.94	0.41
1:B:289:SER:O	1:B:292:GLY:N	2.54	0.41
1:B:301:ALA:HB1	1:B:310:PHE:CE1	2.47	0.41
1:B:314:PHE:CA	1:B:315:ALA:O	2.69	0.41
1:C:40:GLY:O	1:C:41:ILE:C	2.64	0.41
1:C:69:SER:HB2	1:C:75:ALA:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:TRP:HA	1:C:137:VAL:HB	2.03	0.41
1:C:209:SER:HA	1:C:296:LEU:CD1	2.38	0.41
1:C:397:TYR:C	1:C:397:TYR:CD1	2.98	0.41
1:C:418:MET:HE2	1:D:399:ILE:HA	2.03	0.41
1:D:88:GLN:HG3	1:D:420:ILE:HG21	2.02	0.41
1:D:349:GLU:O	1:D:350:PHE:HB2	2.21	0.41
1:D:368:THR:O	1:D:371:ALA:HB3	2.20	0.41
1:A:399:ILE:O	1:A:403:VAL:HB	2.21	0.41
1:B:77:ALA:O	1:B:79:ARG:N	2.54	0.41
1:B:92:LEU:CG	1:B:363:VAL:HG21	2.48	0.41
1:B:174:ARG:HA	1:B:175:GLY:HA3	1.93	0.41
1:B:214:ALA:C	1:B:216:VAL:N	2.79	0.41
1:B:217:VAL:HG12	1:B:218:LYS:N	2.36	0.41
1:C:147:ILE:HD12	1:C:147:ILE:HA	1.71	0.41
1:C:215:GLY:O	1:C:216:VAL:HG22	2.21	0.41
1:D:6:ASP:HB3	1:D:9:LYS:CG	2.49	0.41
1:D:28:VAL:HA	1:D:31:LEU:HG	2.03	0.41
1:D:31:LEU:HD11	1:D:239:TYR:CE2	2.56	0.41
1:D:95:LEU:HA	1:D:98:TRP:HZ3	1.80	0.41
1:D:214:ALA:C	1:D:216:VAL:N	2.79	0.41
1:D:303:ALA:C	1:D:305:ALA:N	2.79	0.41
1:D:416:THR:CA	1:D:419:VAL:HG12	2.47	0.41
1:A:74:TYR:O	1:A:75:ALA:C	2.64	0.40
1:A:433:LYS:O	1:B:79:ARG:HG2	2.21	0.40
1:B:93:TYR:HE1	1:B:208:GLU:OE2	2.04	0.40
1:B:342:ILE:CB	1:B:343:SER:CB	2.86	0.40
1:C:77:ALA:O	1:C:79:ARG:N	2.54	0.40
1:C:92:LEU:HD21	1:C:363:VAL:HG21	1.95	0.40
1:C:366:LEU:HD21	1:D:421:THR:HG21	2.02	0.40
1:D:134:TRP:HA	1:D:137:VAL:HB	2.03	0.40
1:A:28:VAL:HA	1:A:31:LEU:HG	2.03	0.40
1:A:101:ASN:O	1:A:104:MET:HB2	2.21	0.40
1:B:295:LEU:C	1:B:295:LEU:CD2	2.95	0.40
1:B:311:PRO:HA	1:B:312:PRO:HD3	1.85	0.40
1:B:322:THR:HA	1:B:323:PRO:HD3	1.76	0.40
1:C:72:GLY:CA	1:C:211:SER:O	2.70	0.40
1:C:114:TYR:O	1:C:115:PHE:HB2	2.20	0.40
1:C:202:TRP:CH2	1:C:350:PHE:CE1	3.09	0.40
1:C:214:ALA:C	1:C:216:VAL:N	2.78	0.40
1:C:376:GLY:HA3	1:C:379:HIS:HD2	1.85	0.40
1:D:84:PHE:CE1	1:D:85:LEU:CD2	2.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:PRO:O	1:D:118:ILE:CG2	2.68	0.40
1:D:177:THR:O	1:D:180:ALA:HB3	2.21	0.40
1:D:215:GLY:C	1:D:216:VAL:CG2	2.94	0.40
1:D:397:TYR:C	1:D:397:TYR:CD1	2.99	0.40
1:D:421:THR:C	1:D:423:MET:N	2.79	0.40
1:A:54:LEU:HD12	1:A:232:VAL:CG1	2.51	0.40
1:A:79:ARG:NE	1:B:433:LYS:O	2.55	0.40
1:A:240:VAL:O	1:A:244:THR:HG23	2.22	0.40
1:A:249:MET:C	1:A:250:ILE:HG12	2.46	0.40
1:A:317:VAL:HA	1:A:322:THR:O	2.22	0.40
1:A:349:GLU:O	1:A:350:PHE:HB2	2.22	0.40
1:A:416:THR:O	1:A:419:VAL:HG12	2.21	0.40
1:B:114:TYR:O	1:B:115:PHE:HB2	2.20	0.40
1:C:95:LEU:HD12	1:C:98:TRP:CH2	2.57	0.40
1:C:218:LYS:HB2	1:C:223:ASN:ND2	2.35	0.40
1:C:366:LEU:CD2	1:D:421:THR:HG21	2.51	0.40
1:D:54:LEU:HD12	1:D:232:VAL:CG1	2.52	0.40
1:A:67:ASP:OD1	1:A:67:ASP:O	2.39	0.40
1:A:69:SER:HB2	1:A:75:ALA:HB2	2.02	0.40
1:A:214:ALA:C	1:A:216:VAL:N	2.79	0.40
1:B:207:VAL:HG12	1:B:232:VAL:HG23	2.02	0.40
1:B:378:GLY:O	1:B:379:HIS:O	2.40	0.40
1:C:10:VAL:CG1	1:C:11:GLY:H	2.28	0.40
1:C:24:MET:HE3	1:C:162:ILE:CD1	2.32	0.40
1:C:29:PHE:O	1:C:30:LEU:HG	2.21	0.40
1:C:302:LYS:HE3	1:C:326:GLY:HA3	2.03	0.40
1:C:412:TRP:CE3	1:C:415:VAL:HG21	2.56	0.40
1:D:67:ASP:OD1	1:D:67:ASP:O	2.39	0.40
1:D:367:TYR:O	1:D:368:THR:C	2.65	0.40
1:A:202:TRP:CH2	1:A:350:PHE:CE1	3.10	0.40
1:A:355:SER:OG	1:A:409:GLU:HG2	2.21	0.40
1:A:395:PHE:CE1	1:B:422:ALA:CB	3.01	0.40
1:B:40:GLY:O	1:B:41:ILE:C	2.64	0.40
1:B:91:VAL:O	1:B:95:LEU:CB	2.66	0.40
1:B:177:THR:O	1:B:180:ALA:HB3	2.21	0.40
1:B:207:VAL:CG1	1:B:232:VAL:HG21	2.52	0.40
1:B:215:GLY:O	1:B:216:VAL:HG22	2.21	0.40
1:C:60:TYR:CE1	1:C:208:GLU:HA	2.57	0.40
1:C:117:PRO:C	1:C:118:ILE:HG22	2.47	0.40
1:C:249:MET:C	1:C:250:ILE:HG12	2.46	0.40
1:D:46:TRP:CH2	1:D:239:TYR:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:374:LEU:HD12	1:D:374:LEU:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	406/445 (91%)	275 (68%)	79 (20%)	52 (13%)	0	4
1	B	406/445 (91%)	274 (68%)	76 (19%)	56 (14%)	0	3
1	C	406/445 (91%)	278 (68%)	67 (16%)	61 (15%)	0	3
1	D	406/445 (91%)	274 (68%)	76 (19%)	56 (14%)	0	3
All	All	1624/1780 (91%)	1101 (68%)	298 (18%)	225 (14%)	0	3

All (225) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	30	LEU
1	A	41	ILE
1	A	69	SER
1	A	73	SER
1	A	83	PRO
1	A	96	ALA
1	A	117	PRO
1	A	121	ASP
1	A	172	TRP
1	A	182	TRP
1	A	183	ASN
1	A	184	VAL
1	A	214	ALA

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Mol	Chain	Res	Type
1	A	218	LYS
1	A	345	ASN
1	A	377	HIS
1	A	421	THR
1	A	422	ALA
1	A	426	LEU
1	A	431	LEU
1	B	10	VAL
1	B	30	LEU
1	B	41	ILE
1	B	69	SER
1	B	73	SER
1	B	83	PRO
1	B	96	ALA
1	B	117	PRO
1	B	121	ASP
1	B	172	TRP
1	B	182	TRP
1	B	183	ASN
1	B	184	VAL
1	B	214	ALA
1	B	218	LYS
1	B	345	ASN
1	B	377	HIS
1	B	421	THR
1	B	431	LEU
1	C	10	VAL
1	C	30	LEU
1	C	41	ILE
1	C	69	SER
1	C	73	SER
1	C	83	PRO
1	C	96	ALA
1	C	117	PRO
1	C	121	ASP
1	C	172	TRP
1	C	182	TRP
1	C	183	ASN
1	C	184	VAL
1	C	214	ALA
1	C	218	LYS
1	C	345	ASN

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Mol	Chain	Res	Type
1	C	377	HIS
1	C	421	THR
1	C	431	LEU
1	D	10	VAL
1	D	30	LEU
1	D	41	ILE
1	D	69	SER
1	D	73	SER
1	D	83	PRO
1	D	96	ALA
1	D	117	PRO
1	D	121	ASP
1	D	172	TRP
1	D	182	TRP
1	D	183	ASN
1	D	184	VAL
1	D	214	ALA
1	D	218	LYS
1	D	345	ASN
1	D	377	HIS
1	D	421	THR
1	D	422	ALA
1	D	426	LEU
1	D	431	LEU
1	D	432	HIS
1	A	24	MET
1	A	68	PRO
1	A	116	PHE
1	A	118	ILE
1	A	122	PRO
1	A	190	PHE
1	A	202	TRP
1	A	215	GLY
1	A	250	ILE
1	A	310	PHE
1	A	372	LEU
1	A	379	HIS
1	A	432	HIS
1	B	24	MET
1	B	116	PHE
1	B	118	ILE
1	B	122	PRO

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Mol	Chain	Res	Type
1	B	190	PHE
1	B	202	TRP
1	B	215	GLY
1	B	250	ILE
1	B	310	PHE
1	B	379	HIS
1	B	422	ALA
1	B	426	LEU
1	C	24	MET
1	C	116	PHE
1	C	118	ILE
1	C	122	PRO
1	C	190	PHE
1	C	202	TRP
1	C	215	GLY
1	C	250	ILE
1	C	310	PHE
1	C	379	HIS
1	C	401	ALA
1	C	422	ALA
1	C	426	LEU
1	D	24	MET
1	D	116	PHE
1	D	118	ILE
1	D	122	PRO
1	D	190	PHE
1	D	202	TRP
1	D	215	GLY
1	D	250	ILE
1	D	310	PHE
1	D	372	LEU
1	D	379	HIS
1	A	248	GLY
1	A	312	PRO
1	A	313	ILE
1	A	315	ALA
1	A	343	SER
1	B	68	PRO
1	B	143	GLY
1	B	248	GLY
1	B	312	PRO
1	B	313	ILE

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Mol	Chain	Res	Type
1	B	315	ALA
1	B	340	SER
1	B	368	THR
1	B	372	LEU
1	B	390	VAL
1	B	432	HIS
1	C	68	PRO
1	C	78	ARG
1	C	248	GLY
1	C	312	PRO
1	C	313	ILE
1	C	315	ALA
1	C	340	SER
1	C	368	THR
1	C	372	LEU
1	C	432	HIS
1	D	68	PRO
1	D	78	ARG
1	D	248	GLY
1	D	312	PRO
1	D	313	ILE
1	D	315	ALA
1	D	340	SER
1	D	343	SER
1	A	38	THR
1	A	74	TYR
1	A	78	ARG
1	A	322	THR
1	A	340	SER
1	A	368	THR
1	A	380	PHE
1	B	38	THR
1	B	78	ARG
1	B	322	THR
1	B	343	SER
1	B	401	ALA
1	C	38	THR
1	C	143	GLY
1	C	322	THR
1	C	343	SER
1	C	390	VAL
1	C	396	LEU

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Mol	Chain	Res	Type
1	D	38	THR
1	D	74	TYR
1	D	322	THR
1	D	368	THR
1	D	434	ASN
1	A	383	ALA
1	B	304	ALA
1	B	380	PHE
1	B	383	ALA
1	B	396	LEU
1	C	74	TYR
1	C	304	ALA
1	C	380	PHE
1	C	383	ALA
1	D	383	ALA
1	D	433	LYS
1	B	74	TYR
1	B	220	PRO
1	C	397	TYR
1	D	89	THR
1	D	304	ALA
1	D	396	LEU
1	A	175	GLY
1	B	71	GLY
1	B	175	GLY
1	C	71	GLY
1	C	175	GLY
1	D	175	GLY
1	A	71	GLY
1	A	434	ASN
1	C	220	PRO
1	D	71	GLY
1	B	205	ILE
1	C	207	VAL
1	C	161	PRO
1	C	205	ILE
1	C	434	ASN
1	A	353	VAL
1	A	390	VAL
1	C	353	VAL
1	D	161	PRO
1	D	317	VAL

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Mol	Chain	Res	Type
1	D	353	VAL

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	314/343 (92%)	241 (77%)	73 (23%)	1	5
1	B	314/343 (92%)	243 (77%)	71 (23%)	1	6
1	C	314/343 (92%)	242 (77%)	72 (23%)	1	6
1	D	314/343 (92%)	241 (77%)	73 (23%)	1	5
All	All	1256/1372 (92%)	967 (77%)	289 (23%)	1	6

All (289) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	23	ILE
1	A	35	LEU
1	A	41	ILE
1	A	48	VAL
1	A	50	ILE
1	A	51	ILE
1	A	54	LEU
1	A	56	LEU
1	A	69	SER
1	A	74	TYR
1	A	76	TYR
1	A	81	PHE
1	A	84	PHE
1	A	91	VAL
1	A	92	LEU
1	A	97	CYS
1	A	98	TRP
1	A	99	ILE
1	A	104	MET

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Mol	Chain	Res	Type
1	A	105	VAL
1	A	107	ILE
1	A	112	LEU
1	A	116	PHE
1	A	125	LEU
1	A	126	THR
1	A	127	ILE
1	A	128	THR
1	A	130	VAL
1	A	135	ILE
1	A	147	ILE
1	A	156	VAL
1	A	162	ILE
1	A	172	TRP
1	A	182	TRP
1	A	184	VAL
1	A	193	ILE
1	A	196	THR
1	A	200	THR
1	A	207	VAL
1	A	209	SER
1	A	219	ASN
1	A	234	ILE
1	A	237	VAL
1	A	247	MET
1	A	278	VAL
1	A	290	LEU
1	A	295	LEU
1	A	296	LEU
1	A	327	LEU
1	A	328	ILE
1	A	329	ILE
1	A	333	LEU
1	A	335	THR
1	A	336	ILE
1	A	339	LEU
1	A	353	VAL
1	A	363	VAL
1	A	366	LEU
1	A	374	LEU
1	A	379	HIS
1	A	388	LEU

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Mol	Chain	Res	Type
1	A	391	THR
1	A	399	ILE
1	A	405	SER
1	A	409	GLU
1	A	411	MET
1	A	412	TRP
1	A	417	LEU
1	A	420	ILE
1	A	426	LEU
1	A	427	ASN
1	A	430	ARG
1	B	23	ILE
1	B	35	LEU
1	B	41	ILE
1	B	48	VAL
1	B	50	ILE
1	B	51	ILE
1	B	54	LEU
1	B	56	LEU
1	B	69	SER
1	B	74	TYR
1	B	76	TYR
1	B	81	PHE
1	B	84	PHE
1	B	88	GLN
1	B	91	VAL
1	B	92	LEU
1	B	97	CYS
1	B	98	TRP
1	B	99	ILE
1	B	104	MET
1	B	105	VAL
1	B	107	ILE
1	B	112	LEU
1	B	116	PHE
1	B	125	LEU
1	B	126	THR
1	B	127	ILE
1	B	128	THR
1	B	130	VAL
1	B	135	ILE
1	B	147	ILE

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Mol	Chain	Res	Type
1	B	156	VAL
1	B	172	TRP
1	B	182	TRP
1	B	184	VAL
1	B	196	THR
1	B	200	THR
1	B	207	VAL
1	B	209	SER
1	B	219	ASN
1	B	234	ILE
1	B	237	VAL
1	B	247	MET
1	B	278	VAL
1	B	290	LEU
1	B	295	LEU
1	B	296	LEU
1	B	327	LEU
1	B	328	ILE
1	B	329	ILE
1	B	333	LEU
1	B	335	THR
1	B	339	LEU
1	B	353	VAL
1	B	363	VAL
1	B	366	LEU
1	B	374	LEU
1	B	379	HIS
1	B	388	LEU
1	B	391	THR
1	B	399	ILE
1	B	405	SER
1	B	409	GLU
1	B	411	MET
1	B	412	TRP
1	B	414	PHE
1	B	417	LEU
1	B	420	ILE
1	B	426	LEU
1	B	427	ASN
1	B	430	ARG
1	C	23	ILE
1	C	35	LEU

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Mol	Chain	Res	Type
1	C	41	ILE
1	C	48	VAL
1	C	50	ILE
1	C	51	ILE
1	C	54	LEU
1	C	56	LEU
1	C	69	SER
1	C	74	TYR
1	C	76	TYR
1	C	81	PHE
1	C	84	PHE
1	C	88	GLN
1	C	91	VAL
1	C	92	LEU
1	C	97	CYS
1	C	98	TRP
1	C	99	ILE
1	C	104	MET
1	C	105	VAL
1	C	107	ILE
1	C	112	LEU
1	C	116	PHE
1	C	125	LEU
1	C	126	THR
1	C	127	ILE
1	C	128	THR
1	C	130	VAL
1	C	135	ILE
1	C	147	ILE
1	C	156	VAL
1	C	172	TRP
1	C	182	TRP
1	C	184	VAL
1	C	196	THR
1	C	200	THR
1	C	207	VAL
1	C	209	SER
1	C	219	ASN
1	C	234	ILE
1	C	237	VAL
1	C	247	MET
1	C	278	VAL

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Mol	Chain	Res	Type
1	C	290	LEU
1	C	295	LEU
1	C	296	LEU
1	C	327	LEU
1	C	328	ILE
1	C	329	ILE
1	C	333	LEU
1	C	335	THR
1	C	339	LEU
1	C	353	VAL
1	C	363	VAL
1	C	366	LEU
1	C	374	LEU
1	C	379	HIS
1	C	380	PHE
1	C	388	LEU
1	C	391	THR
1	C	399	ILE
1	C	405	SER
1	C	409	GLU
1	C	411	MET
1	C	412	TRP
1	C	414	PHE
1	C	417	LEU
1	C	420	ILE
1	C	426	LEU
1	C	427	ASN
1	C	430	ARG
1	D	23	ILE
1	D	30	LEU
1	D	35	LEU
1	D	41	ILE
1	D	48	VAL
1	D	50	ILE
1	D	51	ILE
1	D	54	LEU
1	D	56	LEU
1	D	69	SER
1	D	74	TYR
1	D	76	TYR
1	D	81	PHE
1	D	84	PHE

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Mol	Chain	Res	Type
1	D	88	GLN
1	D	91	VAL
1	D	92	LEU
1	D	97	CYS
1	D	98	TRP
1	D	99	ILE
1	D	104	MET
1	D	105	VAL
1	D	107	ILE
1	D	112	LEU
1	D	116	PHE
1	D	125	LEU
1	D	126	THR
1	D	127	ILE
1	D	128	THR
1	D	130	VAL
1	D	135	ILE
1	D	147	ILE
1	D	156	VAL
1	D	172	TRP
1	D	182	TRP
1	D	184	VAL
1	D	193	ILE
1	D	196	THR
1	D	200	THR
1	D	207	VAL
1	D	209	SER
1	D	219	ASN
1	D	234	ILE
1	D	237	VAL
1	D	247	MET
1	D	278	VAL
1	D	290	LEU
1	D	295	LEU
1	D	296	LEU
1	D	327	LEU
1	D	328	ILE
1	D	329	ILE
1	D	333	LEU
1	D	335	THR
1	D	336	ILE
1	D	339	LEU

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Mol	Chain	Res	Type
1	D	353	VAL
1	D	363	VAL
1	D	366	LEU
1	D	374	LEU
1	D	379	HIS
1	D	388	LEU
1	D	391	THR
1	D	399	ILE
1	D	405	SER
1	D	409	GLU
1	D	411	MET
1	D	412	TRP
1	D	417	LEU
1	D	420	ILE
1	D	426	LEU
1	D	427	ASN
1	D	430	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	140	ASN
1	A	219	ASN
1	A	223	ASN
1	A	377	HIS
1	A	379	HIS
1	B	22	ASN
1	B	140	ASN
1	B	219	ASN
1	B	223	ASN
1	B	377	HIS
1	B	379	HIS
1	C	22	ASN
1	C	140	ASN
1	C	219	ASN
1	C	223	ASN
1	C	377	HIS
1	C	379	HIS
1	D	22	ASN
1	D	140	ASN
1	D	219	ASN

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Mol	Chain	Res	Type
1	D	223	ASN
1	D	377	HIS
1	D	379	HIS

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 oligosaccharides 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	410/445 (92%)	0.35	25 (6%) 27 24	144, 300, 447, 565	0
1	B	410/445 (92%)	1.00	65 (15%) 5 8	133, 299, 453, 567	0
1	C	410/445 (92%)	1.00	75 (18%) 3 6	136, 297, 453, 569	0
1	D	410/445 (92%)	0.48	25 (6%) 27 24	141, 299, 442, 563	0
All	All	1640/1780 (92%)	0.71	190 (11%) 9 12	133, 299, 452, 569	0

All (190) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	196	THR	6.0
1	B	300	THR	6.0
1	B	155	THR	5.6
1	D	243	THR	5.3
1	C	125	LEU	5.1
1	B	287	LEU	5.0
1	B	45	GLY	4.9
1	C	293	TRP	4.9
1	B	354	SER	4.7
1	C	196	THR	4.6
1	C	87	TYR	4.5
1	B	32	PRO	4.5
1	C	32	PRO	4.3
1	D	145	LYS	4.2
1	A	87	TYR	4.2
1	D	87	TYR	4.2
1	B	133	LEU	4.1
1	B	347	THR	4.1
1	D	60	TYR	3.9
1	D	245	ALA	3.9
1	C	142	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	199	VAL	3.9
1	C	300	THR	3.9
1	C	375	LEU	3.8
1	C	373	LEU	3.8
1	C	207	VAL	3.8
1	B	56	LEU	3.8
1	B	42	ALA	3.8
1	B	244	THR	3.7
1	C	278	VAL	3.7
1	B	151	GLN	3.7
1	C	287	LEU	3.6
1	B	369	CYS	3.6
1	B	54	LEU	3.6
1	C	197	LEU	3.6
1	D	133	LEU	3.6
1	B	87	TYR	3.6
1	B	197	LEU	3.5
1	C	228	THR	3.5
1	C	163	VAL	3.5
1	C	424	TYR	3.5
1	A	189	THR	3.5
1	C	133	LEU	3.4
1	A	243	THR	3.4
1	C	302	LYS	3.4
1	C	45	GLY	3.4
1	A	391	THR	3.4
1	B	200	THR	3.3
1	C	220	PRO	3.3
1	A	133	LEU	3.3
1	C	369	CYS	3.3
1	C	392	THR	3.3
1	C	35	LEU	3.2
1	A	198	ASN	3.2
1	C	109	VAL	3.2
1	B	386	ALA	3.2
1	B	228	THR	3.1
1	B	207	VAL	3.1
1	C	8	HIS	3.1
1	C	374	LEU	3.1
1	B	220	PRO	3.1
1	B	64	SER	3.1
1	D	278	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	155	THR	3.0
1	B	181	ALA	3.0
1	C	401	ALA	3.0
1	D	137	VAL	3.0
1	B	35	LEU	2.9
1	B	278	VAL	2.9
1	C	15	VAL	2.9
1	C	34	ASN	2.9
1	A	323	PRO	2.8
1	C	33	ALA	2.8
1	C	370	ALA	2.8
1	C	209	SER	2.8
1	A	137	VAL	2.8
1	B	375	LEU	2.8
1	A	45	GLY	2.8
1	A	60	TYR	2.8
1	C	200	THR	2.8
1	B	353	VAL	2.7
1	C	50	ILE	2.7
1	B	89	THR	2.7
1	C	226	ILE	2.7
1	B	232	VAL	2.7
1	B	46	TRP	2.7
1	C	56	LEU	2.7
1	B	184	VAL	2.7
1	C	22	ASN	2.7
1	B	61	ALA	2.6
1	B	293	TRP	2.6
1	B	157	LEU	2.6
1	C	29	PHE	2.6
1	C	391	THR	2.6
1	B	74	TYR	2.6
1	C	240	VAL	2.6
1	B	66	LEU	2.6
1	A	352	LEU	2.6
1	C	64	SER	2.6
1	D	309	LEU	2.6
1	C	395	PHE	2.6
1	B	245	ALA	2.5
1	B	178	TYR	2.5
1	B	394	ALA	2.5
1	C	181	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	391	THR	2.5
1	C	89	THR	2.5
1	C	398	CYS	2.5
1	C	201	LEU	2.5
1	C	224	VAL	2.5
1	D	156	VAL	2.5
1	C	206	GLY	2.5
1	B	373	LEU	2.5
1	C	180	ALA	2.5
1	C	314	PHE	2.4
1	A	74	TYR	2.4
1	C	61	ALA	2.4
1	A	327	LEU	2.4
1	D	404	GLY	2.4
1	C	195	SER	2.4
1	D	427	ASN	2.4
1	B	114	TYR	2.4
1	C	120	LYS	2.4
1	D	220	PRO	2.4
1	A	354	SER	2.4
1	B	209	SER	2.4
1	B	398	CYS	2.4
1	C	364	PRO	2.3
1	A	325	ALA	2.3
1	C	42	ALA	2.3
1	C	57	SER	2.3
1	D	90	ASN	2.3
1	D	395	PHE	2.3
1	A	155	THR	2.3
1	B	136	PHE	2.3
1	B	132	VAL	2.3
1	B	302	LYS	2.3
1	C	46	TRP	2.3
1	B	50	ILE	2.3
1	A	91	VAL	2.3
1	C	204	PHE	2.3
1	D	310	PHE	2.3
1	C	393	ILE	2.3
1	B	125	LEU	2.3
1	C	396	LEU	2.3
1	B	195	SER	2.3
1	C	36	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	28	VAL	2.3
1	C	31	LEU	2.3
1	C	217	VAL	2.3
1	C	162	ILE	2.2
1	B	430	ARG	2.2
1	C	193	ILE	2.2
1	B	233	LEU	2.2
1	D	403	VAL	2.2
1	B	370	ALA	2.2
1	B	52	GLY	2.2
1	B	243	THR	2.2
1	D	324	VAL	2.2
1	C	386	ALA	2.2
1	A	309	LEU	2.2
1	A	297	ALA	2.2
1	B	204	PHE	2.2
1	B	202	TRP	2.2
1	C	252	ASN	2.1
1	D	56	LEU	2.1
1	D	352	LEU	2.1
1	B	199	VAL	2.1
1	B	246	ILE	2.1
1	B	392	THR	2.1
1	C	296	LEU	2.1
1	A	228	THR	2.1
1	C	74	TYR	2.1
1	B	57	SER	2.1
1	A	372	LEU	2.1
1	D	226	ILE	2.1
1	B	109	VAL	2.1
1	C	430	ARG	2.1
1	A	288	GLY	2.1
1	A	26	SER	2.1
1	D	7	ALA	2.1
1	D	246	ILE	2.1
1	C	94	TRP	2.1
1	A	224	VAL	2.1
1	C	184	VAL	2.1
1	A	374	LEU	2.0
1	B	225	PRO	2.0
1	C	232	VAL	2.0
1	D	323	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	327	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.