



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:03 AM UTC

PDB ID : 2V8N / pdb_00002v8n
Title : Wild-type Structure of Lactose Permease
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Deposited on : 2007-08-09
Resolution : 3.60 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

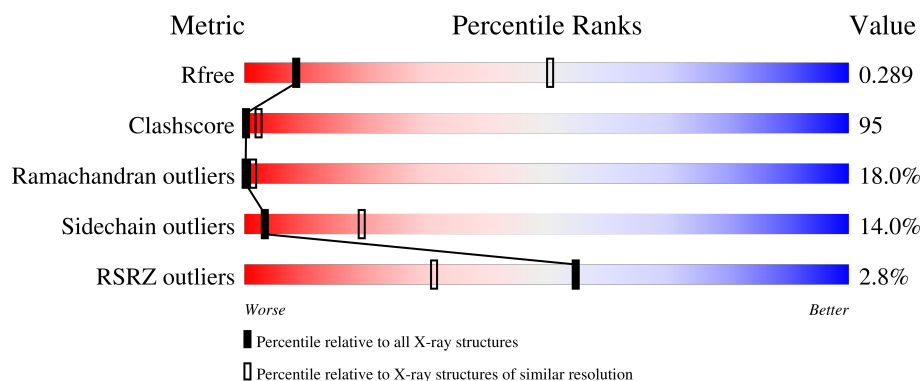
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	417	2% 17% 50% 31% .
1	B	417	4% 15% 53% 29% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6584 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.

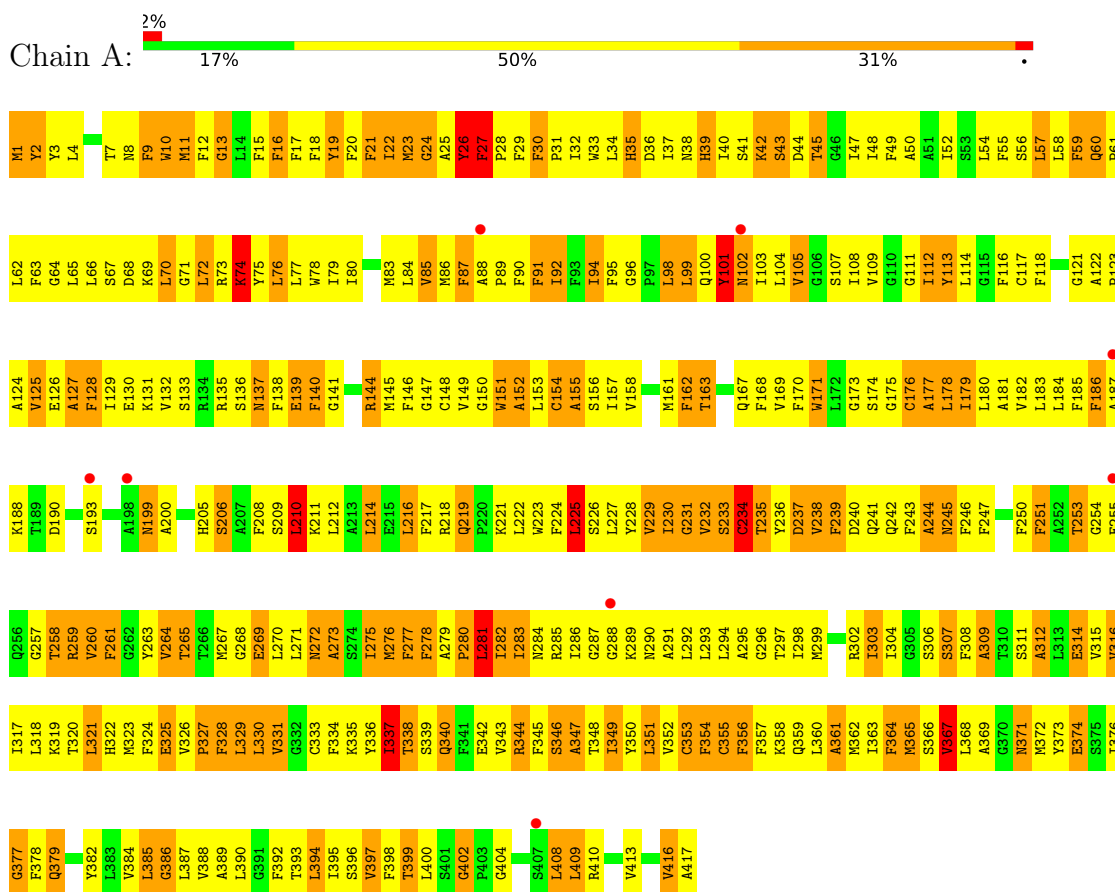
- Molecule 1 is a protein called LACTOSE PERMEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3292	2223	506	541	22			
1	B	417	Total	C	N	O	S	0	0	0
			3292	2223	506	541	22			

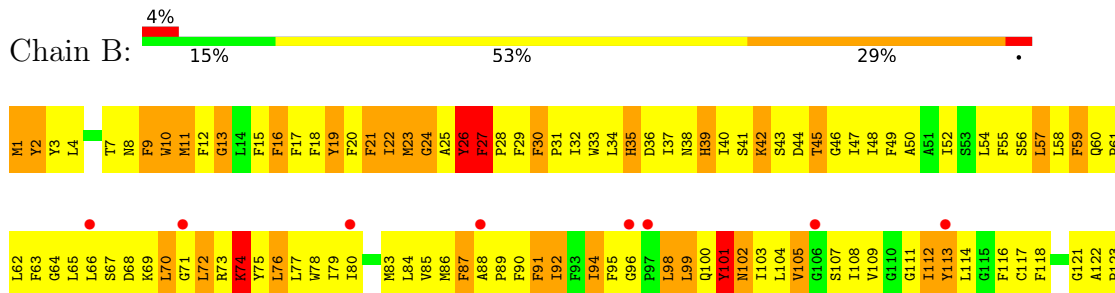
3 Residue-property plots

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: LACTOSE PERMEASE



• Molecule 1: LACTOSE PERMEASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	101.37Å 127.40Å 188.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 3.60 10.00 – 3.60	Depositor EDS
% Data completeness (in resolution range)	82.7 (10.00-3.60) 81.0 (10.00-3.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 3.47Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.294 , 0.333 0.308 , 0.289	Depositor DCC
R_{free} test set	1308 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	87.1	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 101.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6584	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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	0.64	0/3389	1.26	51/4591 (1.1%)
1	B	0.64	0/3389	1.26	50/4591 (1.1%)
All	All	0.64	0/6778	1.26	101/9182 (1.1%)

There are no bond length outliers.

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	113	TYR	N-CA-C	-12.24	98.62	113.19
1	A	113	TYR	N-CA-C	-11.91	99.02	113.19
1	A	314	GLU	N-CA-C	-10.98	98.66	112.72
1	B	314	GLU	N-CA-C	-10.87	98.81	112.72
1	A	151	TRP	N-CA-C	-10.25	99.80	110.97
1	B	151	TRP	N-CA-C	-10.24	99.81	110.97
1	A	13	GLY	N-CA-C	-10.00	102.26	114.66
1	B	13	GLY	N-CA-C	-9.90	102.39	114.66
1	B	303	ILE	N-CA-C	-9.29	103.82	111.81
1	A	397	VAL	N-CA-C	-8.58	102.06	110.72
1	B	397	VAL	N-CA-C	-8.57	102.06	110.72
1	B	272	ASN	N-CA-C	-8.46	102.05	112.38
1	A	272	ASN	N-CA-C	-8.30	102.25	112.38
1	B	45	THR	N-CA-C	-8.16	103.53	113.97
1	A	45	THR	N-CA-C	-8.10	103.53	113.50
1	B	225	LEU	N-CA-C	-8.06	101.56	111.40
1	B	101	TYR	N-CA-C	-7.94	101.45	112.25
1	A	225	LEU	N-CA-C	-7.87	101.80	111.40
1	A	101	TYR	N-CA-C	-7.76	101.69	112.25
1	B	402	GLY	CA-C-N	7.72	129.49	119.84
1	B	402	GLY	C-N-CA	7.72	129.49	119.84
1	A	219	GLN	CA-C-N	7.70	127.24	118.85
1	A	219	GLN	C-N-CA	7.70	127.24	118.85
1	A	377	GLY	N-CA-C	7.67	122.34	112.68
1	B	377	GLY	N-CA-C	7.58	122.23	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	402	GLY	CA-C-N	7.58	129.31	119.84
1	A	402	GLY	C-N-CA	7.58	129.31	119.84
1	A	125	VAL	N-CA-C	-7.56	103.31	110.42
1	B	219	GLN	CA-C-N	7.50	127.03	118.85
1	B	219	GLN	C-N-CA	7.50	127.03	118.85
1	A	386	GLY	N-CA-C	-7.48	104.41	113.99
1	B	219	GLN	N-CA-C	7.48	120.49	109.50
1	A	219	GLN	N-CA-C	7.30	120.23	109.50
1	B	23	MET	N-CA-C	-7.29	103.36	111.82
1	B	125	VAL	N-CA-C	-7.28	103.58	110.42
1	B	386	GLY	N-CA-C	-7.25	104.70	113.99
1	A	19	TYR	N-CA-C	-7.04	103.57	112.93
1	A	237	ASP	N-CA-C	-6.97	103.38	110.97
1	A	23	MET	N-CA-C	-6.90	103.81	111.82
1	B	273	ALA	N-CA-C	-6.74	103.55	111.03
1	B	19	TYR	N-CA-C	-6.67	104.05	112.93
1	A	273	ALA	N-CA-C	-6.63	103.67	111.03
1	B	63	PHE	N-CA-C	-6.58	105.26	113.55
1	B	361	ALA	N-CA-C	-6.58	104.19	111.36
1	A	321	LEU	N-CA-C	-6.57	104.30	113.37
1	A	9	PHE	N-CA-C	-6.56	103.39	111.40
1	A	63	PHE	N-CA-C	-6.52	105.33	113.55
1	B	9	PHE	N-CA-C	-6.49	103.49	111.40
1	B	321	LEU	N-CA-C	-6.41	104.53	113.37
1	A	361	ALA	N-CA-C	-6.38	104.40	111.36
1	B	186	PHE	N-CA-C	-6.36	104.67	112.88
1	A	186	PHE	N-CA-C	-6.23	104.85	112.88
1	B	237	ASP	N-CA-C	-6.21	104.20	110.97
1	A	307	SER	N-CA-C	-6.19	104.61	111.36
1	A	312	ALA	N-CA-C	-6.18	105.87	113.41
1	B	312	ALA	N-CA-C	-6.10	105.97	113.41
1	A	72	LEU	N-CA-C	-6.08	103.17	111.56
1	A	297	THR	N-CA-C	-6.04	104.78	111.36
1	A	206	SER	N-CA-C	-6.00	102.58	110.43
1	A	216	LEU	N-CA-C	-5.97	106.54	113.88
1	B	307	SER	N-CA-C	-5.97	104.86	111.36
1	B	297	THR	N-CA-C	-5.92	104.90	111.36
1	B	261	PHE	N-CA-C	-5.91	103.62	111.24
1	B	216	LEU	N-CA-C	-5.85	106.68	113.88
1	A	177	ALA	N-CA-C	-5.84	104.33	112.45
1	B	206	SER	N-CA-C	-5.83	102.79	110.43
1	A	210	LEU	N-CA-C	-5.82	104.85	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	72	LEU	N-CA-C	-5.79	103.57	111.56
1	A	261	PHE	N-CA-C	-5.71	103.87	111.24
1	B	177	ALA	N-CA-C	-5.70	104.53	112.45
1	A	94	ILE	N-CA-C	5.57	116.72	111.48
1	B	145	MET	N-CA-C	-5.54	106.22	112.87
1	B	250	PHE	N-CA-C	5.54	119.14	112.38
1	A	250	PHE	N-CA-C	5.54	119.14	112.38
1	A	145	MET	N-CA-C	-5.47	106.30	112.87
1	A	21	PHE	N-CA-C	-5.47	105.31	111.28
1	B	74	LYS	N-CA-C	5.46	119.77	113.38
1	B	371	ASN	N-CA-C	-5.42	105.81	112.90
1	B	176	CYS	N-CA-C	-5.39	106.40	112.87
1	A	176	CYS	N-CA-C	-5.37	106.43	112.87
1	B	234	CYS	CA-CB-SG	5.37	126.75	114.40
1	A	316	VAL	N-CA-C	-5.36	105.50	110.53
1	B	210	LEU	N-CA-C	-5.31	105.39	111.07
1	B	94	ILE	N-CA-C	5.30	116.46	111.48
1	A	234	CYS	CA-CB-SG	5.29	126.57	114.40
1	B	374	GLU	N-CA-C	5.27	117.03	111.28
1	A	74	LYS	N-CA-C	5.25	119.52	113.38
1	A	402	GLY	N-CA-C	5.18	122.92	112.34
1	B	27	PHE	N-CA-C	5.18	121.25	109.81
1	A	371	ASN	N-CA-C	-5.17	106.13	112.90
1	B	21	PHE	N-CA-C	-5.17	105.65	111.28
1	B	46	GLY	N-CA-C	-5.14	107.41	113.99
1	B	402	GLY	N-CA-C	5.13	122.80	112.34
1	B	316	VAL	N-CA-C	-5.12	105.72	110.53
1	A	27	PHE	N-CA-C	5.12	121.12	109.81
1	A	251	PHE	N-CA-C	5.10	117.77	109.86
1	A	270	LEU	N-CA-C	-5.10	107.12	113.19
1	B	144	ARG	N-CA-C	-5.09	105.42	111.69
1	A	374	GLU	N-CA-C	5.09	116.83	111.28
1	A	144	ARG	N-CA-C	-5.07	105.45	111.69
1	A	85	VAL	N-CA-C	-5.05	106.35	112.76

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3292	0	3335	622	0
1	B	3292	0	3335	638	0
All	All	6584	0	6670	1259	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 95.

All (1259) 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:B:264:VAL:HG13	1:B:265:THR:H	1.09	1.10
1:B:302:ARG:HH22	1:B:319:LYS:HD2	1.10	1.09
1:A:396:SER:HA	1:A:399:THR:HB	1.34	1.09
1:B:396:SER:HA	1:B:399:THR:HB	1.33	1.09
1:A:302:ARG:HH22	1:A:319:LYS:HD2	1.09	1.08
1:A:264:VAL:HG13	1:A:265:THR:H	1.11	1.07
1:A:246:PHE:HB2	1:A:378:PHE:CD2	1.91	1.06
1:B:246:PHE:HB2	1:B:378:PHE:CD2	1.90	1.05
1:A:246:PHE:HB2	1:A:378:PHE:HD2	1.18	1.05
1:A:22:ILE:HD11	1:A:177:ALA:HB2	1.42	1.02
1:B:22:ILE:HD11	1:B:177:ALA:HB2	1.42	1.02
1:B:385:LEU:HA	1:B:388:VAL:HG12	1.40	0.99
1:A:385:LEU:HA	1:A:388:VAL:HG12	1.42	0.99
1:B:246:PHE:HB2	1:B:378:PHE:HD2	1.17	0.99
1:A:139:GLU:HG2	1:A:141:GLY:H	1.26	0.99
1:B:30:PHE:HB3	1:B:31:PRO:HD3	1.44	0.98
1:A:281:LEU:HD22	1:A:281:LEU:H	1.23	0.98
1:B:323:MET:HE3	1:B:326:VAL:HG21	1.42	0.97
1:A:296:GLY:HA2	1:A:299:MET:HE3	1.47	0.97
1:B:139:GLU:HG2	1:B:141:GLY:H	1.27	0.97
1:B:281:LEU:HD22	1:B:281:LEU:H	1.24	0.97
1:A:323:MET:HE3	1:A:326:VAL:HG21	1.44	0.96
1:B:296:GLY:HA2	1:B:299:MET:HE3	1.48	0.96
1:A:30:PHE:HB3	1:A:31:PRO:HD3	1.46	0.94
1:A:272:ASN:HB2	1:A:323:MET:HG3	1.50	0.94
1:B:272:ASN:HB2	1:B:323:MET:HG3	1.50	0.94
1:B:413:VAL:HG13	1:B:417:ALA:HB3	1.49	0.94
1:B:210:LEU:HD23	1:B:210:LEU:H	1.30	0.93
1:A:210:LEU:HD23	1:A:210:LEU:H	1.32	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:VAL:HG13	1:A:417:ALA:HB3	1.50	0.93
1:B:209:SER:HB3	1:B:212:LEU:HB2	1.51	0.93
1:A:302:ARG:NH2	1:A:319:LYS:HD2	1.84	0.93
1:B:238:VAL:O	1:B:241:GLN:HG2	1.69	0.92
1:B:302:ARG:NH2	1:B:319:LYS:HD2	1.84	0.92
1:B:289:LYS:HE3	1:B:400:LEU:HB3	1.52	0.91
1:A:230:ILE:O	1:A:234:CYS:HB3	1.70	0.91
1:A:33:TRP:HA	1:A:37:ILE:HD12	1.53	0.91
1:B:311:SER:HB2	1:B:314:GLU:HB2	1.53	0.91
1:B:73:ARG:C	1:B:74:LYS:HD2	1.96	0.90
1:A:73:ARG:C	1:A:74:LYS:HD2	1.96	0.90
1:A:209:SER:HB3	1:A:212:LEU:HB2	1.52	0.90
1:A:311:SER:HB2	1:A:314:GLU:HB2	1.54	0.89
1:B:33:TRP:HA	1:B:37:ILE:HD12	1.54	0.89
1:A:29:PHE:HA	1:A:261:PHE:CZ	2.08	0.89
1:B:26:TYR:O	1:B:30:PHE:HB2	1.73	0.88
1:B:45:THR:HG22	1:B:48:ILE:HD12	1.56	0.88
1:B:302:ARG:HH21	1:B:322:HIS:HB2	1.39	0.88
1:A:26:TYR:O	1:A:30:PHE:HB2	1.72	0.88
1:B:230:ILE:O	1:B:234:CYS:HB3	1.73	0.87
1:A:289:LYS:HE3	1:A:400:LEU:HB3	1.54	0.87
1:A:355:CYS:C	1:A:357:PHE:H	1.82	0.87
1:A:238:VAL:O	1:A:241:GLN:HG2	1.75	0.87
1:B:355:CYS:C	1:B:357:PHE:H	1.83	0.87
1:B:29:PHE:HA	1:B:261:PHE:CZ	2.10	0.86
1:B:19:TYR:O	1:B:22:ILE:HG22	1.76	0.86
1:A:302:ARG:HH21	1:A:322:HIS:HB2	1.41	0.85
1:A:19:TYR:O	1:A:22:ILE:HG22	1.76	0.85
1:A:45:THR:HG22	1:A:48:ILE:HD12	1.56	0.85
1:A:211:LYS:HA	1:A:214:LEU:HD22	1.58	0.84
1:A:392:PHE:HA	1:A:395:ILE:HG22	1.59	0.83
1:A:29:PHE:HA	1:A:261:PHE:HZ	1.40	0.83
1:B:261:PHE:O	1:B:264:VAL:HG12	1.79	0.82
1:A:264:VAL:HG13	1:A:265:THR:N	1.89	0.82
1:B:272:ASN:OD1	1:B:275:ILE:HD11	1.79	0.82
1:B:302:ARG:NH2	1:B:319:LYS:HA	1.94	0.82
1:A:251:PHE:HB2	1:A:257:GLY:HA2	1.61	0.82
1:B:264:VAL:HG13	1:B:265:THR:N	1.87	0.82
1:B:392:PHE:HA	1:B:395:ILE:HG22	1.59	0.82
1:A:302:ARG:NH2	1:A:319:LYS:HA	1.94	0.81
1:B:211:LYS:HA	1:B:214:LEU:HD22	1.59	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:385:LEU:HA	1:B:388:VAL:CG1	2.09	0.81
1:B:29:PHE:HA	1:B:261:PHE:HZ	1.43	0.81
1:A:258:THR:O	1:A:260:VAL:N	2.13	0.81
1:A:7:THR:HG23	1:A:8:ASN:H	1.45	0.81
1:B:104:LEU:O	1:B:108:ILE:HG12	1.81	0.80
1:A:177:ALA:O	1:A:181:ALA:HB3	1.81	0.80
1:B:177:ALA:O	1:B:181:ALA:HB3	1.80	0.80
1:A:24:GLY:HA2	1:A:151:TRP:CZ3	2.17	0.80
1:A:385:LEU:HA	1:A:388:VAL:CG1	2.11	0.80
1:A:104:LEU:O	1:A:108:ILE:HG12	1.82	0.80
1:B:251:PHE:HB2	1:B:257:GLY:HA2	1.62	0.80
1:B:174:SER:O	1:B:177:ALA:HB3	1.82	0.80
1:A:264:VAL:HG21	1:A:319:LYS:HG2	1.64	0.79
1:A:272:ASN:OD1	1:A:275:ILE:HD11	1.81	0.79
1:B:258:THR:O	1:B:260:VAL:N	2.15	0.79
1:B:7:THR:HG23	1:B:8:ASN:H	1.46	0.79
1:B:264:VAL:HG21	1:B:319:LYS:HG2	1.65	0.79
1:A:233:SER:O	1:A:236:TYR:HB3	1.82	0.78
1:A:55:PHE:O	1:A:59:PHE:HB2	1.83	0.78
1:B:112:ILE:C	1:B:114:LEU:H	1.88	0.78
1:B:233:SER:O	1:B:236:TYR:HB3	1.83	0.78
1:B:55:PHE:O	1:B:59:PHE:HB2	1.83	0.78
1:A:261:PHE:O	1:A:264:VAL:HG12	1.84	0.78
1:B:24:GLY:HA2	1:B:151:TRP:CZ3	2.19	0.78
1:A:112:ILE:C	1:A:114:LEU:H	1.89	0.77
1:B:234:CYS:H	1:B:358:LYS:HZ3	1.30	0.77
1:B:308:PHE:O	1:B:309:ALA:C	2.27	0.77
1:B:42:LYS:H	1:B:42:LYS:HD3	1.48	0.77
1:B:337:ILE:O	1:B:338:THR:C	2.27	0.77
1:A:337:ILE:O	1:A:338:THR:C	2.28	0.77
1:B:243:PHE:O	1:B:246:PHE:HB3	1.85	0.77
1:B:279:ALA:O	1:B:283:ILE:HG12	1.85	0.77
1:A:330:LEU:HD12	1:A:331:VAL:HG12	1.67	0.76
1:A:281:LEU:HD22	1:A:281:LEU:N	1.98	0.76
1:B:282:ILE:O	1:B:286:ILE:HG12	1.85	0.76
1:A:243:PHE:O	1:A:246:PHE:HB3	1.85	0.76
1:B:210:LEU:O	1:B:214:LEU:HD13	1.85	0.76
1:B:259:ARG:C	1:B:261:PHE:H	1.92	0.76
1:A:174:SER:O	1:A:177:ALA:HB3	1.86	0.76
1:A:259:ARG:C	1:A:261:PHE:H	1.92	0.76
1:A:234:CYS:HB2	1:A:358:LYS:HE2	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:LEU:HD22	1:B:281:LEU:N	1.99	0.76
1:A:279:ALA:O	1:A:283:ILE:HG12	1.85	0.76
1:A:237:ASP:HB2	1:A:362:MET:HE1	1.68	0.76
1:A:88:ALA:HB2	1:A:170:PHE:C	2.11	0.75
1:A:282:ILE:O	1:A:286:ILE:HG12	1.86	0.75
1:A:76:LEU:HD12	1:A:79:ILE:HD12	1.69	0.75
1:B:88:ALA:HB2	1:B:170:PHE:C	2.11	0.75
1:B:16:PHE:HD2	1:B:144:ARG:HA	1.52	0.75
1:A:355:CYS:O	1:A:357:PHE:N	2.19	0.75
1:A:16:PHE:HD2	1:A:144:ARG:HA	1.50	0.75
1:A:308:PHE:O	1:A:309:ALA:C	2.27	0.75
1:B:76:LEU:HD12	1:B:79:ILE:HD12	1.68	0.74
1:B:234:CYS:HB2	1:B:358:LYS:HE2	1.68	0.74
1:A:234:CYS:HB2	1:A:358:LYS:CE	2.16	0.74
1:A:279:ALA:HB3	1:A:280:PRO:HD3	1.69	0.74
1:B:35:HIS:O	1:B:39:HIS:HA	1.87	0.74
1:B:88:ALA:HB3	1:B:89:PRO:HD3	1.69	0.74
1:B:234:CYS:HB2	1:B:358:LYS:CE	2.17	0.74
1:A:62:LEU:HD12	1:A:62:LEU:H	1.52	0.74
1:B:62:LEU:HD12	1:B:62:LEU:H	1.53	0.74
1:A:221:LYS:HD3	1:A:340:GLN:HG3	1.69	0.74
1:A:22:ILE:CD1	1:A:177:ALA:HB2	2.18	0.73
1:B:278:PHE:C	1:B:281:LEU:HD23	2.13	0.73
1:A:35:HIS:O	1:A:39:HIS:HA	1.89	0.73
1:B:330:LEU:HD12	1:B:331:VAL:HG12	1.70	0.73
1:A:128:PHE:CD1	1:A:128:PHE:C	2.66	0.73
1:A:48:ILE:O	1:A:52:ILE:HG13	1.89	0.73
1:B:355:CYS:O	1:B:357:PHE:N	2.20	0.73
1:B:279:ALA:HB3	1:B:280:PRO:HD3	1.68	0.73
1:B:15:PHE:HD1	1:B:184:LEU:HD12	1.52	0.73
1:B:48:ILE:O	1:B:52:ILE:HG13	1.87	0.73
1:A:234:CYS:H	1:A:358:LYS:HZ1	1.34	0.73
1:B:302:ARG:HH22	1:B:319:LYS:HA	1.52	0.73
1:A:296:GLY:CA	1:A:299:MET:HE3	2.19	0.73
1:B:52:ILE:HG12	1:B:112:ILE:HG21	1.70	0.72
1:B:128:PHE:C	1:B:128:PHE:CD1	2.66	0.72
1:A:52:ILE:HG12	1:A:112:ILE:HG21	1.69	0.72
1:A:80:ILE:O	1:A:84:LEU:HD23	1.90	0.72
1:A:278:PHE:C	1:A:281:LEU:HD23	2.15	0.72
1:B:237:ASP:HB2	1:B:362:MET:HE1	1.71	0.72
1:A:210:LEU:O	1:A:214:LEU:HD13	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:ILE:HD12	1:A:349:ILE:H	1.54	0.72
1:B:22:ILE:CD1	1:B:177:ALA:HB2	2.18	0.72
1:B:111:GLY:C	1:B:113:TYR:H	1.95	0.72
1:A:15:PHE:HD1	1:A:184:LEU:HD12	1.54	0.72
1:A:302:ARG:HH22	1:A:319:LYS:HA	1.52	0.72
1:B:349:ILE:HD12	1:B:349:ILE:H	1.55	0.72
1:A:227:LEU:HA	1:A:230:ILE:HD12	1.72	0.72
1:B:22:ILE:CG2	1:B:23:MET:N	2.53	0.72
1:B:157:ILE:HD11	1:B:168:PHE:HE2	1.55	0.72
1:A:157:ILE:HD11	1:A:168:PHE:HE2	1.53	0.71
1:B:258:THR:O	1:B:261:PHE:N	2.23	0.71
1:A:320:THR:C	1:A:322:HIS:H	1.99	0.71
1:B:279:ALA:C	1:B:283:ILE:HG12	2.16	0.71
1:B:368:LEU:O	1:B:372:MET:HB2	1.90	0.71
1:A:42:LYS:H	1:A:42:LYS:HD3	1.53	0.71
1:A:258:THR:O	1:A:261:PHE:N	2.22	0.70
1:A:279:ALA:C	1:A:283:ILE:HG12	2.16	0.70
1:A:22:ILE:CG2	1:A:23:MET:N	2.54	0.70
1:A:111:GLY:C	1:A:113:TYR:H	1.96	0.70
1:A:312:ALA:O	1:A:316:VAL:HG23	1.91	0.70
1:B:244:ALA:O	1:B:246:PHE:N	2.25	0.70
1:A:88:ALA:HB3	1:A:89:PRO:HD3	1.72	0.70
1:B:231:GLY:HA3	1:B:392:PHE:CD2	2.27	0.70
1:B:312:ALA:O	1:B:316:VAL:HG23	1.91	0.70
1:A:128:PHE:CD1	1:A:129:ILE:HD13	2.27	0.69
1:A:244:ALA:O	1:A:246:PHE:N	2.25	0.69
1:A:90:PHE:CE2	1:A:95:PHE:HB2	2.26	0.69
1:B:227:LEU:HA	1:B:230:ILE:HD12	1.73	0.69
1:A:355:CYS:C	1:A:357:PHE:N	2.51	0.69
1:B:90:PHE:CE2	1:B:95:PHE:HB2	2.27	0.69
1:B:76:LEU:CD1	1:B:79:ILE:HD12	2.23	0.69
1:B:268:GLY:O	1:B:272:ASN:N	2.25	0.69
1:B:41:SER:HB3	1:B:44:ASP:OD2	1.92	0.69
1:B:80:ILE:O	1:B:84:LEU:HD23	1.93	0.69
1:B:221:LYS:HD3	1:B:340:GLN:HG3	1.73	0.69
1:B:379:GLN:H	1:B:379:GLN:HE21	1.41	0.69
1:A:40:ILE:HG13	1:A:44:ASP:HB2	1.75	0.69
1:A:273:ALA:O	1:A:276:MET:HB3	1.92	0.69
1:B:40:ILE:HG13	1:B:44:ASP:HB2	1.75	0.69
1:A:21:PHE:CD1	1:A:154:CYS:HB2	2.28	0.68
1:A:157:ILE:HD11	1:A:168:PHE:CE2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:GLY:CA	1:B:299:MET:HE3	2.23	0.68
1:A:76:LEU:CD1	1:A:79:ILE:HD12	2.22	0.68
1:B:320:THR:C	1:B:322:HIS:H	2.00	0.68
1:A:41:SER:HB3	1:A:44:ASP:OD2	1.94	0.68
1:B:128:PHE:CD1	1:B:129:ILE:HD13	2.28	0.68
1:A:176:CYS:O	1:A:180:LEU:HB2	1.93	0.68
1:A:368:LEU:O	1:A:372:MET:HB2	1.92	0.68
1:B:273:ALA:O	1:B:276:MET:HB3	1.94	0.68
1:A:44:ASP:O	1:A:47:ILE:HG22	1.94	0.68
1:A:231:GLY:HA3	1:A:392:PHE:CD2	2.28	0.68
1:B:281:LEU:O	1:B:285:ARG:HB2	1.94	0.68
1:A:128:PHE:HD1	1:A:129:ILE:N	1.92	0.68
1:A:302:ARG:NH2	1:A:319:LYS:O	2.27	0.68
1:A:112:ILE:C	1:A:114:LEU:N	2.51	0.68
1:A:285:ARG:O	1:A:286:ILE:HD13	1.95	0.67
1:B:176:CYS:O	1:B:180:LEU:HB2	1.93	0.67
1:B:302:ARG:NH2	1:B:319:LYS:O	2.27	0.67
1:B:44:ASP:O	1:B:47:ILE:HG22	1.94	0.67
1:B:211:LYS:CA	1:B:214:LEU:HD22	2.24	0.67
1:A:225:LEU:HD23	1:A:226:SER:N	2.09	0.67
1:B:157:ILE:HD11	1:B:168:PHE:CE2	2.29	0.67
1:A:255:GLU:O	1:A:259:ARG:HB2	1.94	0.67
1:A:268:GLY:O	1:A:272:ASN:N	2.25	0.67
1:A:382:TYR:O	1:A:386:GLY:N	2.25	0.67
1:A:408:LEU:H	1:A:408:LEU:HD23	1.60	0.67
1:B:255:GLU:O	1:B:259:ARG:HB2	1.95	0.67
1:A:169:VAL:HG23	1:A:170:PHE:N	2.10	0.67
1:B:128:PHE:HD1	1:B:129:ILE:N	1.93	0.67
1:B:230:ILE:O	1:B:231:GLY:C	2.37	0.67
1:A:283:ILE:O	1:A:287:GLY:N	2.28	0.67
1:B:21:PHE:CD1	1:B:154:CYS:HB2	2.28	0.67
1:B:76:LEU:O	1:B:79:ILE:N	2.27	0.67
1:A:258:THR:OG1	1:A:259:ARG:N	2.29	0.67
1:B:22:ILE:HG22	1:B:23:MET:N	2.09	0.67
1:A:319:LYS:O	1:A:322:HIS:HB2	1.95	0.66
1:B:112:ILE:C	1:B:114:LEU:N	2.49	0.66
1:B:225:LEU:HD23	1:B:226:SER:N	2.10	0.66
1:A:379:GLN:H	1:A:379:GLN:HE21	1.42	0.66
1:B:351:LEU:C	1:B:351:LEU:CD2	2.69	0.66
1:B:319:LYS:O	1:B:322:HIS:HB2	1.94	0.66
1:A:22:ILE:HG22	1:A:23:MET:N	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LEU:O	1:A:79:ILE:N	2.28	0.66
1:B:1:MET:HE2	1:B:4:LEU:HD13	1.77	0.66
1:B:112:ILE:H	1:B:112:ILE:CD1	2.08	0.66
1:B:283:ILE:O	1:B:287:GLY:N	2.29	0.66
1:B:285:ARG:O	1:B:286:ILE:HD13	1.96	0.66
1:B:385:LEU:CA	1:B:388:VAL:HG12	2.19	0.66
1:B:271:LEU:HD23	1:B:271:LEU:C	2.21	0.66
1:B:162:PHE:CG	1:B:163:THR:N	2.63	0.65
1:A:112:ILE:H	1:A:112:ILE:CD1	2.09	0.65
1:A:162:PHE:CG	1:A:163:THR:N	2.64	0.65
1:A:271:LEU:C	1:A:271:LEU:HD23	2.20	0.65
1:B:254:GLY:O	1:B:258:THR:HG23	1.96	0.65
1:A:20:PHE:O	1:A:24:GLY:N	2.29	0.65
1:A:169:VAL:HG23	1:A:170:PHE:H	1.62	0.65
1:A:72:LEU:HD11	1:A:131:LYS:HD3	1.79	0.65
1:A:351:LEU:C	1:A:351:LEU:CD2	2.70	0.65
1:B:351:LEU:C	1:B:351:LEU:HD23	2.21	0.65
1:A:54:LEU:C	1:A:54:LEU:HD23	2.22	0.65
1:A:281:LEU:O	1:A:285:ARG:HB2	1.96	0.65
1:B:48:ILE:HG22	1:B:52:ILE:HD11	1.77	0.65
1:A:251:PHE:HB2	1:A:257:GLY:CA	2.26	0.65
1:B:408:LEU:HD23	1:B:408:LEU:H	1.62	0.65
1:A:169:VAL:HG23	1:A:170:PHE:HD1	1.62	0.65
1:A:211:LYS:CA	1:A:214:LEU:HD22	2.24	0.65
1:A:48:ILE:HG22	1:A:52:ILE:HD11	1.79	0.64
1:A:312:ALA:O	1:A:315:VAL:HG22	1.98	0.64
1:B:199:ASN:HD22	1:B:200:ALA:N	1.96	0.64
1:A:29:PHE:CA	1:A:261:PHE:HZ	2.10	0.64
1:A:330:LEU:HD13	1:A:331:VAL:N	2.12	0.64
1:B:72:LEU:HD11	1:B:131:LYS:HD3	1.79	0.64
1:B:169:VAL:HG23	1:B:170:PHE:N	2.12	0.64
1:B:251:PHE:HB2	1:B:257:GLY:CA	2.27	0.64
1:B:337:ILE:O	1:B:340:GLN:N	2.31	0.64
1:A:337:ILE:O	1:A:340:GLN:N	2.31	0.64
1:A:359:GLN:O	1:A:363:ILE:HG13	1.98	0.64
1:A:1:MET:HE2	1:A:4:LEU:HD13	1.77	0.64
1:B:54:LEU:C	1:B:54:LEU:HD23	2.23	0.64
1:A:345:PHE:HB3	1:A:349:ILE:HD11	1.80	0.64
1:B:29:PHE:CA	1:B:261:PHE:HZ	2.11	0.64
1:B:345:PHE:HB3	1:B:349:ILE:HD11	1.80	0.64
1:A:351:LEU:C	1:A:351:LEU:HD23	2.23	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:ARG:O	1:A:306:SER:OG	2.16	0.63
1:B:20:PHE:O	1:B:24:GLY:N	2.30	0.63
1:B:154:CYS:O	1:B:157:ILE:HG22	1.98	0.63
1:A:337:ILE:CD1	1:A:350:TYR:HE1	2.11	0.63
1:A:385:LEU:CA	1:A:388:VAL:HG12	2.21	0.63
1:B:312:ALA:O	1:B:315:VAL:HG22	1.99	0.63
1:B:330:LEU:HD13	1:B:331:VAL:N	2.13	0.63
1:A:154:CYS:O	1:A:157:ILE:HG22	1.99	0.63
1:A:229:VAL:HG12	1:A:358:LYS:HE3	1.81	0.63
1:B:122:ALA:N	1:B:123:PRO:HD2	2.12	0.63
1:A:45:THR:HA	1:A:48:ILE:HD12	1.79	0.63
1:B:52:ILE:HG23	1:B:112:ILE:HG21	1.81	0.63
1:B:169:VAL:HG23	1:B:170:PHE:HD1	1.63	0.63
1:B:337:ILE:CD1	1:B:350:TYR:HE1	2.11	0.63
1:B:42:LYS:H	1:B:42:LYS:CD	2.08	0.63
1:B:104:LEU:HD12	1:B:104:LEU:H	1.63	0.63
1:B:216:LEU:HD12	1:B:219:GLN:NE2	2.14	0.63
1:A:122:ALA:N	1:A:123:PRO:HD2	2.12	0.63
1:A:254:GLY:O	1:A:258:THR:HG23	1.98	0.63
1:A:155:ALA:O	1:A:158:VAL:HG22	1.99	0.63
1:B:112:ILE:N	1:B:112:ILE:HD13	2.13	0.63
1:A:112:ILE:HD13	1:A:112:ILE:N	2.14	0.62
1:A:7:THR:HG23	1:A:8:ASN:N	2.14	0.62
1:B:139:GLU:HG2	1:B:141:GLY:N	2.09	0.62
1:B:282:ILE:C	1:B:286:ILE:HG12	2.24	0.62
1:A:104:LEU:HD12	1:A:104:LEU:H	1.64	0.62
1:B:11:MET:HE3	1:B:187:ALA:HB1	1.80	0.62
1:B:45:THR:HA	1:B:48:ILE:HD12	1.81	0.62
1:B:289:LYS:HG2	1:B:400:LEU:HD23	1.82	0.62
1:A:199:ASN:HD22	1:A:200:ALA:N	1.96	0.62
1:B:7:THR:HG23	1:B:8:ASN:N	2.14	0.62
1:A:33:TRP:CE3	1:A:34:LEU:HD23	2.35	0.62
1:A:216:LEU:HD12	1:A:219:GLN:NE2	2.14	0.62
1:B:26:TYR:CD1	1:B:27:PHE:N	2.67	0.62
1:A:11:MET:HE3	1:A:187:ALA:HB1	1.80	0.62
1:A:136:SER:O	1:A:137:ASN:HB2	1.99	0.62
1:A:35:HIS:O	1:A:39:HIS:N	2.32	0.62
1:A:337:ILE:HD13	1:A:350:TYR:HE1	1.65	0.62
1:A:121:GLY:O	1:A:124:ALA:HB3	2.00	0.62
1:A:211:LYS:O	1:A:212:LEU:C	2.43	0.62
1:B:258:THR:OG1	1:B:259:ARG:N	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:CYS:SG	1:B:365:MET:HG3	2.40	0.61
1:B:355:CYS:C	1:B:357:PHE:N	2.52	0.61
1:A:33:TRP:CA	1:A:37:ILE:HD12	2.28	0.61
1:A:52:ILE:HG23	1:A:112:ILE:HG21	1.82	0.61
1:A:275:ILE:CD1	1:A:327:PRO:HB3	2.30	0.61
1:A:275:ILE:HD13	1:A:327:PRO:HB3	1.83	0.61
1:B:23:MET:C	1:B:25:ALA:H	2.08	0.61
1:B:179:ILE:O	1:B:183:LEU:HB2	2.01	0.61
1:B:337:ILE:HD13	1:B:350:TYR:HE1	1.65	0.61
1:B:392:PHE:CA	1:B:395:ILE:HG22	2.29	0.61
1:A:139:GLU:HG2	1:A:141:GLY:N	2.08	0.61
1:B:16:PHE:CD2	1:B:144:ARG:HA	2.35	0.61
1:B:128:PHE:CE1	1:B:129:ILE:HD13	2.36	0.61
1:B:35:HIS:O	1:B:39:HIS:N	2.32	0.61
1:B:121:GLY:O	1:B:124:ALA:HB3	2.01	0.61
1:B:229:VAL:HG12	1:B:358:LYS:HE3	1.81	0.61
1:B:359:GLN:O	1:B:363:ILE:HG13	2.00	0.61
1:A:117:CYS:O	1:A:121:GLY:HA3	1.99	0.61
1:B:117:CYS:O	1:B:121:GLY:HA3	2.01	0.61
1:B:136:SER:O	1:B:137:ASN:HB2	2.00	0.61
1:A:16:PHE:CD2	1:A:144:ARG:HA	2.33	0.61
1:A:282:ILE:O	1:A:283:ILE:C	2.42	0.61
1:A:23:MET:C	1:A:25:ALA:H	2.08	0.61
1:B:155:ALA:O	1:B:158:VAL:HG22	2.01	0.61
1:B:167:GLN:O	1:B:171:TRP:HB2	2.00	0.61
1:A:128:PHE:CD1	1:A:129:ILE:N	2.69	0.61
1:A:230:ILE:O	1:A:231:GLY:C	2.42	0.61
1:A:282:ILE:C	1:A:286:ILE:HG12	2.26	0.61
1:B:30:PHE:HB3	1:B:31:PRO:CD	2.26	0.61
1:B:337:ILE:HG21	1:B:349:ILE:HG21	1.82	0.61
1:A:44:ASP:O	1:A:48:ILE:HG13	2.00	0.61
1:A:272:ASN:O	1:A:275:ILE:HG13	2.01	0.61
1:B:128:PHE:CD1	1:B:129:ILE:N	2.69	0.61
1:B:140:PHE:HD1	1:B:140:PHE:H	1.49	0.61
1:B:275:ILE:CD1	1:B:327:PRO:HB3	2.30	0.61
1:A:179:ILE:O	1:A:183:LEU:HB2	1.99	0.60
1:B:169:VAL:HG23	1:B:170:PHE:H	1.63	0.60
1:A:26:TYR:CD1	1:A:27:PHE:N	2.69	0.60
1:B:272:ASN:O	1:B:275:ILE:HG13	2.01	0.60
1:B:416:VAL:HG12	1:B:416:VAL:O	2.02	0.60
1:A:128:PHE:CE1	1:A:129:ILE:HD13	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:PHE:CA	1:A:395:ILE:HG22	2.29	0.60
1:B:154:CYS:O	1:B:156:SER:N	2.34	0.60
1:B:282:ILE:HG23	1:B:286:ILE:HG13	1.83	0.60
1:B:302:ARG:O	1:B:306:SER:OG	2.17	0.60
1:B:311:SER:O	1:B:315:VAL:HG13	2.01	0.60
1:B:244:ALA:O	1:B:247:PHE:N	2.34	0.60
1:A:49:PHE:CD2	1:A:241:GLN:HB2	2.36	0.60
1:A:52:ILE:HA	1:A:112:ILE:HG13	1.82	0.60
1:B:33:TRP:CE3	1:B:34:LEU:HD23	2.37	0.60
1:A:244:ALA:O	1:A:247:PHE:N	2.34	0.60
1:A:289:LYS:HG2	1:A:400:LEU:HD23	1.83	0.60
1:B:33:TRP:CA	1:B:37:ILE:HD12	2.29	0.60
1:B:99:LEU:HD23	1:B:107:SER:HB3	1.83	0.60
1:A:57:LEU:HD12	1:A:359:GLN:HB2	1.83	0.60
1:A:167:GLN:O	1:A:171:TRP:HB2	2.00	0.60
1:B:246:PHE:HZ	1:B:309:ALA:CB	2.15	0.60
1:A:9:PHE:HD2	1:A:10:TRP:HE3	1.48	0.60
1:A:154:CYS:O	1:A:156:SER:N	2.35	0.60
1:B:231:GLY:O	1:B:235:THR:HG23	2.01	0.60
1:A:272:ASN:HB2	1:A:323:MET:CG	2.30	0.60
1:B:9:PHE:HD2	1:B:10:TRP:HE3	1.48	0.60
1:B:303:ILE:HB	1:B:386:GLY:HA2	1.82	0.60
1:A:254:GLY:O	1:A:258:THR:N	2.34	0.59
1:A:280:PRO:O	1:A:281:LEU:C	2.45	0.59
1:B:272:ASN:HB2	1:B:323:MET:CG	2.30	0.59
1:A:337:ILE:HG21	1:A:349:ILE:HG21	1.83	0.59
1:B:78:TRP:CZ2	1:B:185:PHE:HB3	2.38	0.59
1:B:241:GLN:HE22	1:B:366:SER:HB2	1.66	0.59
1:A:140:PHE:HD1	1:A:140:PHE:H	1.49	0.59
1:A:116:PHE:CG	1:A:117:CYS:N	2.71	0.59
1:A:246:PHE:HZ	1:A:309:ALA:CB	2.15	0.59
1:A:416:VAL:HG12	1:A:416:VAL:O	2.02	0.59
1:B:2:TYR:HD1	1:B:2:TYR:H	1.49	0.59
1:A:246:PHE:HB2	1:A:378:PHE:CE2	2.38	0.59
1:B:413:VAL:HG13	1:B:417:ALA:CB	2.29	0.59
1:A:188:LYS:C	1:A:188:LYS:HD2	2.28	0.59
1:B:44:ASP:O	1:B:48:ILE:HG13	2.02	0.59
1:A:282:ILE:HG23	1:A:286:ILE:HG13	1.83	0.59
1:B:275:ILE:HD13	1:B:327:PRO:HB3	1.83	0.59
1:B:188:LYS:HD2	1:B:188:LYS:C	2.28	0.59
1:B:232:VAL:O	1:B:236:TYR:CB	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:PHE:HB2	1:B:378:PHE:CE2	2.37	0.59
1:A:23:MET:O	1:A:25:ALA:N	2.36	0.59
1:B:49:PHE:CD2	1:B:241:GLN:HB2	2.38	0.59
1:A:135:ARG:C	1:A:135:ARG:HD2	2.28	0.58
1:A:251:PHE:CE2	1:A:260:VAL:HG21	2.38	0.58
1:A:232:VAL:O	1:A:236:TYR:CB	2.52	0.58
1:B:23:MET:O	1:B:25:ALA:N	2.36	0.58
1:B:90:PHE:O	1:B:94:ILE:N	2.26	0.58
1:A:112:ILE:H	1:A:112:ILE:HD13	1.67	0.58
1:A:331:VAL:HG23	1:A:335:LYS:HD3	1.84	0.58
1:B:52:ILE:HA	1:B:112:ILE:HG13	1.85	0.58
1:B:211:LYS:HA	1:B:214:LEU:CD2	2.31	0.58
1:B:227:LEU:CA	1:B:230:ILE:HD12	2.34	0.58
1:B:104:LEU:H	1:B:104:LEU:CD1	2.16	0.58
1:A:330:LEU:CD1	1:A:331:VAL:N	2.66	0.58
1:B:282:ILE:O	1:B:283:ILE:C	2.45	0.58
1:A:241:GLN:HE22	1:A:366:SER:HB2	1.67	0.58
1:B:382:TYR:O	1:B:386:GLY:N	2.24	0.58
1:A:2:TYR:H	1:A:2:TYR:HD1	1.50	0.58
1:A:15:PHE:CD1	1:A:184:LEU:HD12	2.36	0.58
1:A:211:LYS:HA	1:A:214:LEU:CD2	2.31	0.58
1:B:112:ILE:H	1:B:112:ILE:HD13	1.67	0.58
1:B:302:ARG:NH2	1:B:319:LYS:CA	2.66	0.58
1:A:99:LEU:HD23	1:A:107:SER:HB3	1.85	0.58
1:A:234:CYS:SG	1:A:365:MET:HG3	2.44	0.58
1:B:127:ALA:O	1:B:130:GLU:N	2.33	0.58
1:B:337:ILE:HD13	1:B:350:TYR:CE1	2.39	0.58
1:A:78:TRP:CZ2	1:A:185:PHE:HB3	2.39	0.58
1:A:258:THR:O	1:A:259:ARG:C	2.46	0.58
1:A:259:ARG:C	1:A:261:PHE:N	2.59	0.58
1:A:303:ILE:HB	1:A:386:GLY:HA2	1.85	0.58
1:B:111:GLY:C	1:B:113:TYR:N	2.62	0.58
1:B:331:VAL:HG23	1:B:335:LYS:HD3	1.85	0.58
1:B:398:PHE:O	1:B:399:THR:C	2.47	0.58
1:A:231:GLY:HA3	1:A:392:PHE:CE2	2.38	0.57
1:B:54:LEU:HD23	1:B:54:LEU:O	2.04	0.57
1:A:129:ILE:O	1:A:133:SER:HB3	2.04	0.57
1:A:337:ILE:HD13	1:A:350:TYR:CE1	2.39	0.57
1:B:231:GLY:HA3	1:B:392:PHE:CE2	2.39	0.57
1:B:392:PHE:HA	1:B:395:ILE:CG2	2.30	0.57
1:A:295:ALA:HB2	1:A:328:PHE:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:CYS:O	1:B:334:PHE:C	2.47	0.57
1:A:231:GLY:O	1:A:235:THR:HG23	2.05	0.57
1:A:413:VAL:HG13	1:A:417:ALA:CB	2.30	0.57
1:B:224:PHE:HA	1:B:227:LEU:HD12	1.86	0.57
1:B:234:CYS:H	1:B:358:LYS:NZ	2.02	0.57
1:B:259:ARG:C	1:B:261:PHE:N	2.59	0.57
1:A:94:ILE:O	1:A:98:LEU:HD13	2.05	0.57
1:A:251:PHE:CZ	1:A:260:VAL:HG21	2.38	0.57
1:A:398:PHE:O	1:A:399:THR:C	2.47	0.57
1:B:211:LYS:O	1:B:212:LEU:C	2.46	0.57
1:B:330:LEU:CD1	1:B:331:VAL:N	2.67	0.57
1:A:169:VAL:HG23	1:A:170:PHE:CD1	2.39	0.57
1:A:311:SER:O	1:A:315:VAL:HG13	2.04	0.57
1:B:35:HIS:O	1:B:39:HIS:CA	2.52	0.57
1:B:135:ARG:HD2	1:B:135:ARG:C	2.29	0.57
1:B:280:PRO:O	1:B:281:LEU:C	2.47	0.57
1:B:348:THR:O	1:B:352:VAL:N	2.37	0.57
1:A:50:ALA:HB2	1:A:366:SER:OG	2.04	0.57
1:A:224:PHE:HA	1:A:227:LEU:HD12	1.87	0.57
1:B:57:LEU:HD11	1:B:360:LEU:HB2	1.87	0.57
1:A:104:LEU:H	1:A:104:LEU:CD1	2.17	0.57
1:B:251:PHE:CE2	1:B:260:VAL:HG21	2.40	0.57
1:B:258:THR:O	1:B:259:ARG:C	2.47	0.57
1:B:351:LEU:HD22	1:B:352:VAL:N	2.20	0.57
1:B:105:VAL:O	1:B:109:VAL:HG23	2.05	0.57
1:A:333:CYS:O	1:A:334:PHE:C	2.47	0.57
1:B:15:PHE:CD1	1:B:184:LEU:HD12	2.36	0.57
1:B:234:CYS:SG	1:B:361:ALA:HB1	2.44	0.57
1:A:90:PHE:O	1:A:94:ILE:N	2.28	0.56
1:A:111:GLY:C	1:A:113:TYR:N	2.62	0.56
1:A:365:MET:O	1:A:368:LEU:HB2	2.05	0.56
1:B:116:PHE:CG	1:B:117:CYS:N	2.73	0.56
1:A:348:THR:O	1:A:352:VAL:N	2.38	0.56
1:B:238:VAL:HG13	1:B:366:SER:HA	1.87	0.56
1:B:251:PHE:CZ	1:B:260:VAL:HG21	2.40	0.56
1:B:261:PHE:O	1:B:264:VAL:CG1	2.51	0.56
1:B:275:ILE:HD13	1:B:327:PRO:HD3	1.88	0.56
1:A:234:CYS:H	1:A:358:LYS:NZ	2.01	0.56
1:A:234:CYS:SG	1:A:361:ALA:HB1	2.45	0.56
1:B:57:LEU:HD12	1:B:359:GLN:HB2	1.87	0.56
1:B:295:ALA:O	1:B:298:ILE:HB	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ALA:O	1:A:130:GLU:N	2.34	0.56
1:A:351:LEU:HD22	1:A:352:VAL:N	2.21	0.56
1:A:30:PHE:HB3	1:A:31:PRO:CD	2.27	0.56
1:B:17:PHE:HA	1:B:147:GLY:HA2	1.88	0.56
1:B:129:ILE:O	1:B:133:SER:HB3	2.05	0.56
1:B:177:ALA:O	1:B:181:ALA:CB	2.53	0.56
1:B:229:VAL:O	1:B:233:SER:HB3	2.06	0.56
1:B:254:GLY:O	1:B:258:THR:N	2.35	0.56
1:A:17:PHE:HA	1:A:147:GLY:HA2	1.87	0.56
1:A:35:HIS:O	1:A:39:HIS:CA	2.53	0.56
1:A:168:PHE:HE1	1:B:186:PHE:HB2	1.71	0.56
1:B:210:LEU:C	1:B:214:LEU:HD22	2.31	0.56
1:B:365:MET:O	1:B:368:LEU:HB2	2.06	0.56
1:A:105:VAL:O	1:A:109:VAL:HG23	2.06	0.56
1:A:229:VAL:O	1:A:233:SER:HB3	2.05	0.56
1:B:94:ILE:O	1:B:98:LEU:HD13	2.06	0.56
1:A:392:PHE:HA	1:A:395:ILE:CG2	2.31	0.55
1:B:100:GLN:C	1:B:102:ASN:H	2.14	0.55
1:B:190:ASP:O	1:B:192:PRO:HD3	2.06	0.55
1:B:269:GLU:C	1:B:271:LEU:H	2.15	0.55
1:A:100:GLN:C	1:A:102:ASN:H	2.15	0.55
1:A:210:LEU:H	1:A:210:LEU:CD2	2.08	0.55
1:B:33:TRP:CH2	1:B:96:GLY:HA2	2.41	0.55
1:B:112:ILE:CD1	1:B:112:ILE:N	2.70	0.55
1:B:376:ILE:HG22	1:B:376:ILE:O	2.07	0.55
1:A:277:PHE:O	1:A:280:PRO:HD2	2.05	0.55
1:B:235:THR:HG22	1:B:365:MET:SD	2.46	0.55
1:A:227:LEU:CA	1:A:230:ILE:HD12	2.34	0.55
1:A:325:GLU:O	1:A:326:VAL:C	2.49	0.55
1:A:33:TRP:CH2	1:A:96:GLY:HA2	2.41	0.55
1:A:54:LEU:HD23	1:A:54:LEU:O	2.06	0.55
1:B:57:LEU:HD12	1:B:360:LEU:N	2.22	0.55
1:B:277:PHE:O	1:B:280:PRO:HD2	2.06	0.55
1:B:348:THR:O	1:B:352:VAL:HB	2.06	0.55
1:A:376:ILE:HG22	1:A:376:ILE:O	2.07	0.55
1:B:92:ILE:HG22	1:B:92:ILE:O	2.06	0.55
1:B:150:GLY:O	1:B:154:CYS:HB2	2.07	0.55
1:B:278:PHE:HA	1:B:281:LEU:CD2	2.36	0.55
1:A:240:ASP:C	1:A:242:GLN:H	2.14	0.55
1:A:349:ILE:HD12	1:A:349:ILE:N	2.21	0.55
1:B:55:PHE:CE2	1:B:113:TYR:HA	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:357:PHE:O	1:B:360:LEU:HB3	2.07	0.55
1:B:125:VAL:O	1:B:126:GLU:C	2.50	0.55
1:B:337:ILE:CG2	1:B:349:ILE:HG21	2.37	0.55
1:A:1:MET:O	1:A:4:LEU:HB2	2.07	0.54
1:A:59:PHE:O	1:A:62:LEU:N	2.39	0.54
1:A:299:MET:O	1:A:302:ARG:HB3	2.06	0.54
1:B:67:SER:O	1:B:68:ASP:C	2.50	0.54
1:B:342:GLU:O	1:B:344:ARG:N	2.39	0.54
1:A:67:SER:O	1:A:68:ASP:C	2.50	0.54
1:A:275:ILE:HD13	1:A:327:PRO:HD3	1.88	0.54
1:B:169:VAL:HG23	1:B:170:PHE:CD1	2.41	0.54
1:A:52:ILE:CG1	1:A:112:ILE:HG21	2.37	0.54
1:A:295:ALA:O	1:A:298:ILE:HB	2.06	0.54
1:A:302:ARG:NH2	1:A:319:LYS:CA	2.67	0.54
1:A:42:LYS:H	1:A:42:LYS:CD	2.12	0.54
1:A:275:ILE:O	1:A:276:MET:C	2.51	0.54
1:A:278:PHE:HA	1:A:281:LEU:CD2	2.38	0.54
1:A:342:GLU:O	1:A:344:ARG:N	2.40	0.54
1:B:219:GLN:O	1:B:222:LEU:HB3	2.07	0.54
1:B:368:LEU:O	1:B:372:MET:N	2.35	0.54
1:A:357:PHE:O	1:A:360:LEU:HB3	2.06	0.54
1:B:28:PRO:HG2	1:B:29:PHE:H	1.72	0.54
1:B:295:ALA:HB2	1:B:328:PHE:HB3	1.88	0.54
1:B:67:SER:HA	1:B:71:GLY:O	2.06	0.54
1:A:17:PHE:CE1	1:A:150:GLY:HA2	2.43	0.54
1:A:219:GLN:O	1:A:222:LEU:HB3	2.08	0.54
1:A:251:PHE:CB	1:A:257:GLY:HA2	2.34	0.54
1:A:389:ALA:O	1:A:392:PHE:HB2	2.07	0.54
1:B:76:LEU:HD12	1:B:79:ILE:HB	1.90	0.54
1:B:175:GLY:C	1:B:177:ALA:N	2.66	0.54
1:B:389:ALA:O	1:B:392:PHE:HB2	2.08	0.54
1:A:76:LEU:HD12	1:A:79:ILE:HB	1.90	0.54
1:B:241:GLN:NE2	1:B:366:SER:HB2	2.23	0.54
1:B:306:SER:O	1:B:379:GLN:HG3	2.08	0.54
1:A:364:PHE:O	1:A:365:MET:C	2.50	0.54
1:A:369:ALA:HA	1:A:372:MET:CB	2.38	0.54
1:B:394:LEU:O	1:B:397:VAL:HG23	2.08	0.54
1:A:238:VAL:HG13	1:A:366:SER:HA	1.90	0.53
1:A:269:GLU:C	1:A:271:LEU:H	2.14	0.53
1:A:330:LEU:HD13	1:A:330:LEU:C	2.33	0.53
1:A:348:THR:O	1:A:352:VAL:HB	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:LYS:O	1:B:214:LEU:N	2.42	0.53
1:B:298:ILE:O	1:B:299:MET:C	2.51	0.53
1:B:232:VAL:O	1:B:236:TYR:HB2	2.08	0.53
1:B:344:ARG:HG2	1:B:345:PHE:HD1	1.73	0.53
1:A:92:ILE:HG22	1:A:92:ILE:O	2.06	0.53
1:A:101:TYR:O	1:A:103:ILE:HG12	2.08	0.53
1:A:337:ILE:CG2	1:A:349:ILE:HG21	2.38	0.53
1:B:99:LEU:HD23	1:B:99:LEU:H	1.73	0.53
1:A:55:PHE:CE2	1:A:113:TYR:HA	2.44	0.53
1:A:175:GLY:C	1:A:177:ALA:H	2.16	0.53
1:B:59:PHE:O	1:B:62:LEU:N	2.41	0.53
1:A:67:SER:HA	1:A:71:GLY:O	2.09	0.53
1:A:109:VAL:C	1:A:111:GLY:H	2.16	0.53
1:A:150:GLY:O	1:A:154:CYS:HB2	2.08	0.53
1:A:175:GLY:C	1:A:177:ALA:N	2.66	0.53
1:B:12:PHE:HE2	1:B:128:PHE:HE1	1.57	0.53
1:B:88:ALA:HB2	1:B:170:PHE:O	2.09	0.53
1:B:210:LEU:H	1:B:210:LEU:CD2	2.07	0.53
1:B:237:ASP:O	1:B:240:ASP:N	2.41	0.53
1:A:12:PHE:HE2	1:A:128:PHE:HE1	1.57	0.53
1:A:33:TRP:HA	1:A:37:ILE:CD1	2.34	0.53
1:A:241:GLN:NE2	1:A:366:SER:HB2	2.24	0.53
1:A:368:LEU:O	1:A:372:MET:N	2.36	0.53
1:B:101:TYR:O	1:B:103:ILE:N	2.42	0.53
1:B:182:VAL:HA	1:B:185:PHE:HD2	1.74	0.53
1:A:232:VAL:O	1:A:236:TYR:HB2	2.08	0.53
1:A:298:ILE:O	1:A:299:MET:C	2.50	0.53
1:B:1:MET:O	1:B:4:LEU:HB2	2.08	0.53
1:B:85:VAL:O	1:B:174:SER:HB3	2.08	0.53
1:B:109:VAL:C	1:B:111:GLY:H	2.16	0.53
1:B:390:LEU:O	1:B:394:LEU:HB3	2.09	0.53
1:A:88:ALA:HB2	1:A:170:PHE:O	2.09	0.53
1:B:208:PHE:CE2	1:B:348:THR:HG22	2.43	0.53
1:B:275:ILE:O	1:B:276:MET:C	2.52	0.53
1:B:384:VAL:O	1:B:388:VAL:HB	2.09	0.53
1:A:211:LYS:O	1:A:214:LEU:N	2.41	0.53
1:B:379:GLN:H	1:B:379:GLN:NE2	2.06	0.53
1:B:307:SER:O	1:B:379:GLN:HG2	2.09	0.53
1:B:330:LEU:HD13	1:B:330:LEU:C	2.34	0.53
1:B:336:TYR:OH	1:B:400:LEU:HD11	2.08	0.53
1:A:99:LEU:HD23	1:A:99:LEU:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ASN:C	1:A:286:ILE:H	2.16	0.52
1:A:326:VAL:N	1:A:327:PRO:HD2	2.24	0.52
1:B:240:ASP:C	1:B:242:GLN:H	2.16	0.52
1:B:364:PHE:O	1:B:365:MET:C	2.51	0.52
1:B:369:ALA:HA	1:B:372:MET:CB	2.39	0.52
1:A:90:PHE:CZ	1:A:95:PHE:HB2	2.44	0.52
1:A:135:ARG:HD2	1:A:135:ARG:O	2.09	0.52
1:A:394:LEU:O	1:A:397:VAL:HG23	2.09	0.52
1:B:90:PHE:CZ	1:B:95:PHE:HB2	2.44	0.52
1:B:116:PHE:CD2	1:B:117:CYS:N	2.77	0.52
1:B:349:ILE:HD12	1:B:349:ILE:N	2.23	0.52
1:A:28:PRO:HG2	1:A:29:PHE:H	1.74	0.52
1:A:244:ALA:O	1:A:245:ASN:C	2.51	0.52
1:B:101:TYR:O	1:B:103:ILE:HG12	2.09	0.52
1:A:52:ILE:HG23	1:A:112:ILE:CG2	2.39	0.52
1:A:272:ASN:HA	1:A:275:ILE:HG12	1.91	0.52
1:A:306:SER:O	1:A:379:GLN:HG3	2.09	0.52
1:B:17:PHE:CE1	1:B:150:GLY:HA2	2.44	0.52
1:B:52:ILE:HG23	1:B:112:ILE:CG2	2.39	0.52
1:B:320:THR:C	1:B:322:HIS:N	2.68	0.52
1:A:125:VAL:O	1:A:126:GLU:C	2.50	0.52
1:A:390:LEU:O	1:A:394:LEU:HB3	2.09	0.52
1:B:22:ILE:HG22	1:B:23:MET:H	1.72	0.52
1:B:128:PHE:CZ	1:B:132:VAL:HG21	2.45	0.52
1:B:228:TYR:O	1:B:229:VAL:C	2.52	0.52
1:B:325:GLU:O	1:B:326:VAL:C	2.51	0.52
1:A:29:PHE:HE2	1:A:170:PHE:CE1	2.28	0.52
1:A:101:TYR:O	1:A:103:ILE:N	2.42	0.52
1:B:52:ILE:CG1	1:B:112:ILE:HG21	2.39	0.52
1:B:104:LEU:HD12	1:B:104:LEU:N	2.24	0.52
1:B:351:LEU:CD2	1:B:352:VAL:N	2.73	0.52
1:B:33:TRP:HA	1:B:37:ILE:CD1	2.35	0.52
1:B:44:ASP:C	1:B:47:ILE:HG22	2.34	0.52
1:B:369:ALA:O	1:B:373:TYR:CD2	2.62	0.52
1:A:16:PHE:CZ	1:A:126:GLU:HA	2.44	0.52
1:A:369:ALA:HA	1:A:372:MET:HB3	1.92	0.52
1:B:385:LEU:C	1:B:387:LEU:N	2.63	0.52
1:B:303:ILE:HG21	1:B:385:LEU:HD12	1.91	0.52
1:A:59:PHE:HA	1:A:62:LEU:HD13	1.91	0.51
1:A:177:ALA:O	1:A:181:ALA:CB	2.54	0.51
1:A:344:ARG:HG2	1:A:345:PHE:HD1	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:PHE:HA	1:B:62:LEU:HD13	1.91	0.51
1:A:22:ILE:HG22	1:A:23:MET:H	1.75	0.51
1:A:307:SER:O	1:A:379:GLN:HG2	2.10	0.51
1:A:366:SER:O	1:A:367:VAL:C	2.53	0.51
1:B:29:PHE:HE2	1:B:170:PHE:CE1	2.28	0.51
1:B:272:ASN:HA	1:B:275:ILE:HG12	1.91	0.51
1:A:85:VAL:O	1:A:174:SER:HB3	2.10	0.51
1:A:237:ASP:O	1:A:238:VAL:C	2.53	0.51
1:B:135:ARG:HD2	1:B:135:ARG:O	2.11	0.51
1:B:268:GLY:O	1:B:271:LEU:HB3	2.10	0.51
1:B:284:ASN:C	1:B:286:ILE:H	2.18	0.51
1:A:182:VAL:HA	1:A:185:PHE:HD2	1.74	0.51
1:A:226:SER:O	1:A:230:ILE:HG13	2.11	0.51
1:A:345:PHE:O	1:A:347:ALA:N	2.44	0.51
1:A:388:VAL:CG1	1:A:389:ALA:N	2.73	0.51
1:B:388:VAL:CG1	1:B:389:ALA:N	2.74	0.51
1:A:116:PHE:CD2	1:A:117:CYS:N	2.76	0.51
1:A:268:GLY:O	1:A:271:LEU:HB3	2.10	0.51
1:A:279:ALA:O	1:A:280:PRO:C	2.52	0.51
1:B:55:PHE:HE2	1:B:113:TYR:HA	1.76	0.51
1:B:251:PHE:CB	1:B:257:GLY:HA2	2.35	0.51
1:B:409:LEU:HD12	1:B:409:LEU:C	2.36	0.51
1:A:22:ILE:HG13	1:A:176:CYS:SG	2.51	0.51
1:A:104:LEU:HD12	1:A:104:LEU:N	2.26	0.51
1:A:369:ALA:O	1:A:373:TYR:CD2	2.64	0.51
1:B:264:VAL:O	1:B:265:THR:C	2.53	0.51
1:B:17:PHE:CA	1:B:147:GLY:HA2	2.41	0.51
1:B:326:VAL:N	1:B:327:PRO:HD2	2.25	0.51
1:A:409:LEU:C	1:A:409:LEU:HD12	2.36	0.51
1:B:16:PHE:CZ	1:B:126:GLU:HA	2.45	0.51
1:B:99:LEU:HD23	1:B:99:LEU:N	2.26	0.51
1:B:244:ALA:O	1:B:245:ASN:C	2.53	0.51
1:B:279:ALA:O	1:B:280:PRO:C	2.53	0.51
1:A:128:PHE:CZ	1:A:132:VAL:HG21	2.45	0.51
1:A:154:CYS:O	1:A:155:ALA:C	2.54	0.51
1:A:385:LEU:C	1:A:387:LEU:N	2.64	0.51
1:B:281:LEU:N	1:B:281:LEU:CD2	2.70	0.51
1:B:294:LEU:O	1:B:298:ILE:HG12	2.11	0.51
1:B:376:ILE:O	1:B:376:ILE:CG2	2.59	0.51
1:A:44:ASP:C	1:A:47:ILE:HG22	2.35	0.51
1:A:242:GLN:HB3	1:A:373:TYR:HE2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:PHE:O	1:A:264:VAL:CG1	2.56	0.51
1:B:226:SER:C	1:B:230:ILE:HD12	2.36	0.51
1:A:1:MET:HE2	1:A:4:LEU:CD1	2.42	0.50
1:A:158:VAL:O	1:A:162:PHE:HB3	2.12	0.50
1:A:349:ILE:H	1:A:349:ILE:CD1	2.24	0.50
1:A:373:TYR:O	1:A:377:GLY:N	2.39	0.50
1:B:175:GLY:C	1:B:177:ALA:H	2.16	0.50
1:B:237:ASP:O	1:B:238:VAL:C	2.54	0.50
1:B:299:MET:O	1:B:302:ARG:HB3	2.10	0.50
1:B:304:ILE:HG12	1:B:386:GLY:O	2.10	0.50
1:A:17:PHE:CA	1:A:147:GLY:HA2	2.40	0.50
1:A:294:LEU:O	1:A:298:ILE:HG12	2.11	0.50
1:A:303:ILE:HG21	1:A:385:LEU:HD12	1.92	0.50
1:A:317:ILE:N	1:A:317:ILE:HD12	2.26	0.50
1:A:384:VAL:O	1:A:388:VAL:HB	2.11	0.50
1:B:1:MET:HE2	1:B:4:LEU:CD1	2.41	0.50
1:A:275:ILE:HG13	1:A:276:MET:H	1.76	0.50
1:A:320:THR:C	1:A:322:HIS:N	2.66	0.50
1:A:336:TYR:OH	1:A:400:LEU:HD11	2.10	0.50
1:B:23:MET:HG3	1:B:118:PHE:CD1	2.46	0.50
1:A:22:ILE:HD11	1:A:173:GLY:O	2.11	0.50
1:A:125:VAL:O	1:A:129:ILE:HG12	2.11	0.50
1:A:228:TYR:O	1:A:229:VAL:C	2.54	0.50
1:B:45:THR:HA	1:B:48:ILE:CG1	2.42	0.50
1:B:158:VAL:O	1:B:162:PHE:HB3	2.12	0.50
1:B:317:ILE:HD12	1:B:317:ILE:N	2.26	0.50
1:A:136:SER:O	1:A:137:ASN:CB	2.59	0.50
1:A:33:TRP:CZ3	1:A:34:LEU:HD23	2.47	0.50
1:B:125:VAL:O	1:B:129:ILE:HG12	2.12	0.50
1:B:369:ALA:HA	1:B:372:MET:HB3	1.92	0.50
1:A:117:CYS:C	1:A:121:GLY:HA3	2.36	0.50
1:A:351:LEU:CD2	1:A:352:VAL:N	2.74	0.50
1:B:24:GLY:HA2	1:B:151:TRP:CE3	2.47	0.50
1:B:199:ASN:HD22	1:B:199:ASN:C	2.19	0.50
1:A:329:LEU:O	1:A:330:LEU:C	2.55	0.50
1:A:45:THR:HA	1:A:48:ILE:CG1	2.41	0.50
1:A:395:ILE:C	1:A:397:VAL:H	2.18	0.50
1:B:329:LEU:O	1:B:330:LEU:C	2.54	0.50
1:A:23:MET:HG3	1:A:118:PHE:CD1	2.47	0.49
1:B:116:PHE:O	1:B:121:GLY:N	2.45	0.49
1:B:154:CYS:O	1:B:155:ALA:C	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:PHE:CB	1:A:31:PRO:HD3	2.30	0.49
1:A:334:PHE:HD2	1:A:335:LYS:HD2	1.77	0.49
1:B:226:SER:HB3	1:B:230:ILE:HD11	1.93	0.49
1:B:333:CYS:O	1:B:337:ILE:HG13	2.12	0.49
1:B:334:PHE:HD2	1:B:335:LYS:HD2	1.77	0.49
1:A:24:GLY:HA2	1:A:151:TRP:CE3	2.47	0.49
1:A:99:LEU:HD23	1:A:99:LEU:N	2.27	0.49
1:A:376:ILE:O	1:A:376:ILE:CG2	2.58	0.49
1:B:395:ILE:C	1:B:397:VAL:H	2.19	0.49
1:A:55:PHE:HE2	1:A:113:TYR:HA	1.78	0.49
1:A:240:ASP:C	1:A:242:GLN:N	2.70	0.49
1:B:42:LYS:HD3	1:B:42:LYS:N	2.21	0.49
1:B:178:LEU:O	1:B:180:LEU:N	2.45	0.49
1:B:326:VAL:HB	1:B:327:PRO:CD	2.42	0.49
1:A:33:TRP:HH2	1:A:96:GLY:HA2	1.76	0.49
1:A:109:VAL:C	1:A:111:GLY:N	2.71	0.49
1:A:116:PHE:O	1:A:121:GLY:N	2.45	0.49
1:A:199:ASN:HD22	1:A:199:ASN:C	2.20	0.49
1:A:237:ASP:O	1:A:240:ASP:N	2.45	0.49
1:A:269:GLU:C	1:A:271:LEU:N	2.69	0.49
1:A:326:VAL:HB	1:A:327:PRO:CD	2.41	0.49
1:B:242:GLN:HB3	1:B:373:TYR:HE2	1.77	0.49
1:B:275:ILE:HG13	1:B:276:MET:H	1.77	0.49
1:B:373:TYR:O	1:B:377:GLY:N	2.39	0.49
1:A:178:LEU:O	1:A:180:LEU:N	2.45	0.49
1:B:75:TYR:O	1:B:76:LEU:C	2.55	0.49
1:B:234:CYS:HB2	1:B:358:LYS:CD	2.42	0.49
1:B:244:ALA:C	1:B:246:PHE:N	2.70	0.49
1:B:269:GLU:C	1:B:271:LEU:N	2.69	0.49
1:B:278:PHE:HA	1:B:281:LEU:HD21	1.95	0.49
1:A:264:VAL:O	1:A:265:THR:C	2.54	0.49
1:B:12:PHE:HE2	1:B:128:PHE:CE1	2.30	0.49
1:B:349:ILE:H	1:B:349:ILE:CD1	2.25	0.49
1:B:226:SER:O	1:B:230:ILE:HG13	2.13	0.49
1:A:19:TYR:HD2	1:A:20:PHE:HD1	1.60	0.49
1:A:223:TRP:O	1:A:226:SER:HB2	2.13	0.49
1:A:282:ILE:O	1:A:286:ILE:N	2.46	0.49
1:B:253:THR:HB	1:B:254:GLY:H	1.45	0.49
1:A:379:GLN:H	1:A:379:GLN:NE2	2.08	0.48
1:B:33:TRP:HH2	1:B:96:GLY:HA2	1.77	0.48
1:B:84:LEU:C	1:B:86:MET:N	2.70	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:GLY:C	1:B:123:PRO:HD2	2.38	0.48
1:B:345:PHE:O	1:B:347:ALA:N	2.46	0.48
1:A:45:THR:HA	1:A:48:ILE:CD1	2.42	0.48
1:B:22:ILE:HD11	1:B:173:GLY:O	2.13	0.48
1:B:33:TRP:CZ3	1:B:34:LEU:HD23	2.48	0.48
1:B:136:SER:O	1:B:137:ASN:CB	2.60	0.48
1:A:235:THR:HG22	1:A:365:MET:SD	2.53	0.48
1:A:242:GLN:HB3	1:A:373:TYR:CE2	2.48	0.48
1:B:214:LEU:N	1:B:214:LEU:CD1	2.75	0.48
1:B:223:TRP:O	1:B:226:SER:HB2	2.13	0.48
1:B:117:CYS:C	1:B:121:GLY:HA3	2.37	0.48
1:B:289:LYS:HG2	1:B:400:LEU:CD2	2.43	0.48
1:B:45:THR:HA	1:B:48:ILE:CD1	2.43	0.48
1:B:91:PHE:CG	1:B:170:PHE:CE2	3.01	0.48
1:A:75:TYR:O	1:A:76:LEU:C	2.56	0.48
1:A:214:LEU:N	1:A:214:LEU:CD1	2.77	0.48
1:B:223:TRP:HA	1:B:223:TRP:CE3	2.49	0.48
1:A:12:PHE:HD2	1:A:129:ILE:HD12	1.79	0.48
1:A:234:CYS:HB2	1:A:358:LYS:CD	2.43	0.48
1:A:345:PHE:O	1:A:346:SER:C	2.55	0.48
1:B:152:ALA:HA	1:B:266:THR:HG23	1.96	0.48
1:B:395:ILE:C	1:B:397:VAL:N	2.72	0.48
1:A:226:SER:C	1:A:230:ILE:HD12	2.39	0.48
1:B:78:TRP:HH2	1:B:186:PHE:HE2	1.61	0.48
1:B:99:LEU:O	1:B:102:ASN:N	2.47	0.48
1:A:244:ALA:C	1:A:246:PHE:N	2.69	0.48
1:A:298:ILE:HG22	1:A:299:MET:N	2.28	0.48
1:A:388:VAL:HG13	1:A:389:ALA:N	2.29	0.48
1:B:19:TYR:CD2	1:B:19:TYR:C	2.91	0.48
1:B:62:LEU:HD12	1:B:62:LEU:N	2.26	0.48
1:B:366:SER:O	1:B:367:VAL:C	2.56	0.48
1:A:12:PHE:HE2	1:A:128:PHE:CE1	2.30	0.48
1:A:64:GLY:C	1:A:66:LEU:H	2.22	0.48
1:B:150:GLY:O	1:B:154:CYS:CB	2.62	0.48
1:B:234:CYS:SG	1:B:361:ALA:CB	3.02	0.48
1:B:288:GLY:O	1:B:292:LEU:HB2	2.14	0.48
1:A:288:GLY:O	1:A:292:LEU:HB2	2.14	0.47
1:B:42:LYS:HG2	1:B:374:GLU:HB2	1.95	0.47
1:B:282:ILE:O	1:B:286:ILE:N	2.47	0.47
1:A:234:CYS:SG	1:A:361:ALA:CB	3.03	0.47
1:B:109:VAL:C	1:B:111:GLY:N	2.71	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:VAL:O	1:B:230:ILE:O	2.32	0.47
1:B:242:GLN:HB3	1:B:373:TYR:CE2	2.48	0.47
1:A:282:ILE:HG22	1:A:283:ILE:N	2.30	0.47
1:A:327:PRO:HG2	1:A:328:PHE:H	1.79	0.47
1:B:23:MET:HA	1:B:118:PHE:CE1	2.50	0.47
1:A:19:TYR:CD2	1:A:19:TYR:C	2.92	0.47
1:A:62:LEU:HD12	1:A:62:LEU:N	2.26	0.47
1:A:162:PHE:CD2	1:A:163:THR:N	2.83	0.47
1:A:226:SER:HB3	1:A:230:ILE:HD11	1.95	0.47
1:B:44:ASP:HB3	1:B:104:LEU:HD21	1.95	0.47
1:B:289:LYS:O	1:B:293:LEU:HD13	2.15	0.47
1:B:319:LYS:C	1:B:321:LEU:N	2.73	0.47
1:B:345:PHE:O	1:B:346:SER:C	2.57	0.47
1:A:42:LYS:HD3	1:A:42:LYS:N	2.26	0.47
1:A:99:LEU:H	1:A:99:LEU:CD2	2.26	0.47
1:A:234:CYS:N	1:A:358:LYS:NZ	2.62	0.47
1:A:333:CYS:O	1:A:337:ILE:HG13	2.15	0.47
1:B:42:LYS:O	1:B:45:THR:OG1	2.29	0.47
1:B:214:LEU:HD13	1:B:214:LEU:N	2.28	0.47
1:A:44:ASP:HB3	1:A:104:LEU:HD21	1.96	0.47
1:A:78:TRP:HH2	1:A:186:PHE:HE2	1.61	0.47
1:A:91:PHE:HA	1:A:95:PHE:HB3	1.95	0.47
1:A:109:VAL:O	1:A:113:TYR:HB2	2.14	0.47
1:A:154:CYS:SG	1:A:158:VAL:CG1	3.03	0.47
1:A:214:LEU:HD13	1:A:214:LEU:N	2.30	0.47
1:A:229:VAL:O	1:A:230:ILE:O	2.33	0.47
1:A:230:ILE:C	1:A:234:CYS:HB3	2.37	0.47
1:A:233:SER:O	1:A:234:CYS:C	2.57	0.47
1:A:260:VAL:HG12	1:A:260:VAL:O	2.14	0.47
1:A:278:PHE:HA	1:A:281:LEU:HD21	1.97	0.47
1:A:304:ILE:HG12	1:A:386:GLY:O	2.14	0.47
1:A:306:SER:HB3	1:A:382:TYR:CE2	2.50	0.47
1:A:395:ILE:C	1:A:397:VAL:N	2.72	0.47
1:B:12:PHE:HD2	1:B:129:ILE:HD12	1.79	0.47
1:B:19:TYR:HD2	1:B:20:PHE:HD1	1.62	0.47
1:B:34:LEU:HD13	1:B:45:THR:HG22	1.97	0.47
1:B:152:ALA:O	1:B:153:LEU:C	2.58	0.47
1:B:162:PHE:CD2	1:B:163:THR:N	2.83	0.47
1:B:234:CYS:N	1:B:358:LYS:NZ	2.63	0.47
1:B:243:PHE:O	1:B:244:ALA:C	2.58	0.47
1:B:281:LEU:O	1:B:285:ARG:CB	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:VAL:HG13	1:B:389:ALA:N	2.30	0.47
1:A:17:PHE:HB2	1:A:146:PHE:O	2.14	0.47
1:A:121:GLY:C	1:A:123:PRO:HD2	2.40	0.47
1:A:208:PHE:CE2	1:A:348:THR:HG22	2.49	0.47
1:B:11:MET:C	1:B:12:PHE:CD1	2.93	0.47
1:B:222:LEU:HG	1:B:223:TRP:N	2.30	0.47
1:B:84:LEU:HD11	1:B:118:PHE:CE2	2.50	0.47
1:B:233:SER:O	1:B:234:CYS:C	2.58	0.47
1:B:240:ASP:C	1:B:242:GLN:N	2.72	0.47
1:B:298:ILE:HG22	1:B:299:MET:N	2.30	0.47
1:A:99:LEU:O	1:A:102:ASN:N	2.48	0.47
1:A:289:LYS:HD3	1:A:289:LYS:C	2.40	0.47
1:B:144:ARG:C	1:B:146:PHE:N	2.73	0.47
1:B:306:SER:HB3	1:B:382:TYR:CE2	2.51	0.47
1:B:327:PRO:HG2	1:B:328:PHE:H	1.80	0.47
1:A:33:TRP:HE3	1:A:34:LEU:HD23	1.78	0.46
1:A:52:ILE:HA	1:A:112:ILE:HG21	1.97	0.46
1:A:84:LEU:HD11	1:A:118:PHE:CE2	2.49	0.46
1:B:233:SER:O	1:B:236:TYR:N	2.48	0.46
1:B:245:ASN:H	1:B:245:ASN:ND2	2.13	0.46
1:A:150:GLY:O	1:A:154:CYS:CB	2.63	0.46
1:B:50:ALA:HB2	1:B:366:SER:OG	2.15	0.46
1:B:224:PHE:CD1	1:B:224:PHE:N	2.84	0.46
1:B:232:VAL:O	1:B:236:TYR:HB3	2.15	0.46
1:B:366:SER:O	1:B:369:ALA:N	2.48	0.46
1:A:42:LYS:HG2	1:A:374:GLU:HB2	1.96	0.46
1:B:57:LEU:HD22	1:B:58:LEU:HG	1.97	0.46
1:B:23:MET:C	1:B:25:ALA:N	2.73	0.46
1:B:91:PHE:HA	1:B:95:PHE:HB3	1.96	0.46
1:B:216:LEU:O	1:B:219:GLN:HB2	2.16	0.46
1:B:282:ILE:HG22	1:B:283:ILE:N	2.29	0.46
1:A:27:PHE:O	1:A:28:PRO:C	2.58	0.46
1:B:279:ALA:HB3	1:B:280:PRO:CD	2.42	0.46
1:B:64:GLY:C	1:B:66:LEU:H	2.24	0.46
1:B:109:VAL:O	1:B:113:TYR:HB2	2.16	0.46
1:B:289:LYS:HD3	1:B:289:LYS:C	2.40	0.46
1:B:319:LYS:C	1:B:321:LEU:H	2.23	0.46
1:A:52:ILE:HG12	1:A:112:ILE:CG2	2.40	0.46
1:A:91:PHE:CG	1:A:170:PHE:CE2	3.04	0.46
1:A:124:ALA:O	1:A:127:ALA:HB3	2.16	0.46
1:A:223:TRP:HA	1:A:223:TRP:CE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ASN:H	1:A:245:ASN:ND2	2.14	0.46
1:B:33:TRP:HE3	1:B:34:LEU:HD23	1.80	0.46
1:B:66:LEU:HG	1:B:67:SER:N	2.31	0.46
1:B:124:ALA:O	1:B:127:ALA:HB3	2.16	0.46
1:B:149:VAL:O	1:B:149:VAL:HG22	2.16	0.46
1:A:18:PHE:CG	1:A:180:LEU:HD13	2.50	0.46
1:A:295:ALA:O	1:A:299:MET:HG3	2.15	0.46
1:B:12:PHE:CD1	1:B:12:PHE:N	2.82	0.46
1:B:52:ILE:HA	1:B:112:ILE:HG21	1.98	0.46
1:A:224:PHE:CD1	1:A:224:PHE:N	2.83	0.46
1:A:358:LYS:HA	1:A:358:LYS:HD3	1.73	0.46
1:A:366:SER:O	1:A:369:ALA:N	2.49	0.46
1:B:57:LEU:HB2	1:B:359:GLN:HB2	1.98	0.46
1:B:99:LEU:C	1:B:101:TYR:N	2.74	0.46
1:A:12:PHE:N	1:A:12:PHE:CD1	2.84	0.45
1:A:38:ASN:O	1:A:39:HIS:C	2.59	0.45
1:A:349:ILE:O	1:A:353:CYS:CB	2.63	0.45
1:B:29:PHE:CA	1:B:261:PHE:CZ	2.89	0.45
1:B:30:PHE:CB	1:B:31:PRO:HD3	2.28	0.45
1:B:91:PHE:CD1	1:B:170:PHE:HE2	2.34	0.45
1:A:23:MET:HA	1:A:118:PHE:CE1	2.51	0.45
1:A:64:GLY:C	1:A:66:LEU:N	2.75	0.45
1:A:264:VAL:HG22	1:A:265:THR:N	2.31	0.45
1:B:16:PHE:CE2	1:B:144:ARG:HD3	2.51	0.45
1:B:122:ALA:O	1:B:126:GLU:N	2.41	0.45
1:B:260:VAL:HG12	1:B:260:VAL:O	2.15	0.45
1:A:34:LEU:HD13	1:A:45:THR:HG22	1.97	0.45
1:A:319:LYS:O	1:A:322:HIS:CB	2.65	0.45
1:A:367:VAL:CG1	1:A:368:LEU:N	2.79	0.45
1:B:72:LEU:O	1:B:74:LYS:NZ	2.49	0.45
1:B:223:TRP:HA	1:B:223:TRP:HE3	1.81	0.45
1:B:251:PHE:CG	1:B:257:GLY:HA2	2.51	0.45
1:B:264:VAL:HG22	1:B:265:THR:N	2.31	0.45
1:B:322:HIS:C	1:B:324:PHE:H	2.24	0.45
1:A:281:LEU:O	1:A:285:ARG:CB	2.64	0.45
1:B:26:TYR:CD1	1:B:27:PHE:HB2	2.51	0.45
1:B:27:PHE:O	1:B:28:PRO:C	2.58	0.45
1:B:227:LEU:N	1:B:230:ILE:HD12	2.32	0.45
1:A:13:GLY:HA3	1:A:146:PHE:HD2	1.82	0.45
1:A:30:PHE:O	1:A:33:TRP:HB3	2.16	0.45
1:A:122:ALA:O	1:A:126:GLU:N	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:VAL:HG22	1:A:149:VAL:O	2.17	0.45
1:A:152:ALA:O	1:A:153:LEU:C	2.59	0.45
1:A:344:ARG:HG3	1:A:344:ARG:HH11	1.80	0.45
1:B:353:CYS:O	1:B:357:PHE:HB2	2.16	0.45
1:B:367:VAL:CG1	1:B:368:LEU:N	2.79	0.45
1:A:27:PHE:HB3	1:A:28:PRO:CD	2.47	0.45
1:A:57:LEU:HD11	1:A:360:LEU:HB2	1.99	0.45
1:A:154:CYS:O	1:A:157:ILE:N	2.48	0.45
1:A:237:ASP:CB	1:A:362:MET:HE1	2.44	0.45
1:B:127:ALA:O	1:B:128:PHE:C	2.59	0.45
1:A:127:ALA:O	1:A:128:PHE:C	2.60	0.45
1:A:149:VAL:O	1:A:152:ALA:HB3	2.17	0.45
1:A:289:LYS:HG2	1:A:400:LEU:CD2	2.45	0.45
1:B:52:ILE:HG12	1:B:112:ILE:CG2	2.42	0.45
1:B:344:ARG:HG3	1:B:344:ARG:HH11	1.81	0.45
1:A:11:MET:C	1:A:12:PHE:CD1	2.95	0.45
1:A:353:CYS:O	1:A:357:PHE:HB2	2.16	0.45
1:B:26:TYR:HB2	1:B:87:PHE:CZ	2.52	0.45
1:B:49:PHE:HA	1:B:52:ILE:HG13	1.99	0.45
1:B:99:LEU:H	1:B:99:LEU:CD2	2.25	0.45
1:B:349:ILE:O	1:B:353:CYS:CB	2.65	0.45
1:A:26:TYR:HB2	1:A:87:PHE:CZ	2.52	0.45
1:A:253:THR:HB	1:A:254:GLY:H	1.45	0.45
1:B:9:PHE:CD2	1:B:10:TRP:HE3	2.32	0.45
1:B:91:PHE:CG	1:B:170:PHE:HE2	2.34	0.45
1:B:243:PHE:CE2	1:B:247:PHE:HB2	2.51	0.45
1:A:116:PHE:C	1:A:118:PHE:N	2.75	0.45
1:A:223:TRP:HA	1:A:223:TRP:HE3	1.82	0.45
1:A:347:ALA:O	1:A:351:LEU:N	2.45	0.45
1:B:234:CYS:O	1:B:236:TYR:N	2.50	0.45
1:B:246:PHE:CB	1:B:378:PHE:HD2	2.07	0.45
1:B:334:PHE:HD1	1:B:350:TYR:OH	2.00	0.45
1:B:345:PHE:C	1:B:349:ILE:HD13	2.42	0.45
1:B:354:PHE:CD1	1:B:354:PHE:N	2.85	0.45
1:A:85:VAL:O	1:A:85:VAL:HG12	2.17	0.44
1:A:127:ALA:O	1:A:130:GLU:HB3	2.17	0.44
1:A:319:LYS:C	1:A:321:LEU:N	2.75	0.44
1:A:334:PHE:HD1	1:A:350:TYR:OH	2.00	0.44
1:A:345:PHE:C	1:A:349:ILE:HD13	2.41	0.44
1:B:64:GLY:C	1:B:66:LEU:N	2.75	0.44
1:B:279:ALA:O	1:B:282:ILE:HB	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:GLU:O	1:B:374:GLU:HG2	2.17	0.44
1:B:398:PHE:O	1:B:400:LEU:N	2.49	0.44
1:A:1:MET:C	1:A:3:TYR:H	2.25	0.44
1:A:210:LEU:C	1:A:214:LEU:HD22	2.42	0.44
1:A:251:PHE:CG	1:A:257:GLY:HA2	2.53	0.44
1:B:230:ILE:C	1:B:234:CYS:HB3	2.40	0.44
1:B:246:PHE:HZ	1:B:309:ALA:HB2	1.83	0.44
1:A:84:LEU:C	1:A:86:MET:H	2.24	0.44
1:A:222:LEU:HG	1:A:223:TRP:N	2.30	0.44
1:A:279:ALA:HB3	1:A:280:PRO:CD	2.43	0.44
1:A:299:MET:O	1:A:302:ARG:N	2.45	0.44
1:B:17:PHE:HB2	1:B:146:PHE:O	2.16	0.44
1:B:319:LYS:O	1:B:322:HIS:CB	2.63	0.44
1:A:9:PHE:CD2	1:A:10:TRP:HE3	2.33	0.44
1:A:16:PHE:CE2	1:A:144:ARG:HD3	2.53	0.44
1:A:57:LEU:HD12	1:A:360:LEU:N	2.33	0.44
1:A:66:LEU:HG	1:A:67:SER:N	2.32	0.44
1:A:84:LEU:C	1:A:86:MET:N	2.71	0.44
1:A:86:MET:HE2	1:A:89:PRO:HB2	1.99	0.44
1:A:226:SER:O	1:A:227:LEU:C	2.61	0.44
1:A:246:PHE:HZ	1:A:309:ALA:HB2	1.82	0.44
1:A:289:LYS:O	1:A:293:LEU:HD13	2.17	0.44
1:B:3:TYR:HB3	1:B:138:PHE:CD2	2.52	0.44
1:B:289:LYS:HZ3	1:B:402:GLY:HA2	1.81	0.44
1:B:302:ARG:CZ	1:B:318:LEU:O	2.66	0.44
1:A:12:PHE:CE2	1:A:128:PHE:HE1	2.36	0.44
1:A:57:LEU:HD22	1:A:58:LEU:HG	2.00	0.44
1:A:233:SER:O	1:A:236:TYR:N	2.49	0.44
1:A:259:ARG:O	1:A:261:PHE:N	2.50	0.44
1:A:398:PHE:O	1:A:400:LEU:N	2.50	0.44
1:B:299:MET:HG2	1:B:325:GLU:HG3	2.00	0.44
1:B:1:MET:C	1:B:3:TYR:H	2.25	0.44
1:B:7:THR:CG2	1:B:8:ASN:H	2.25	0.44
1:B:259:ARG:O	1:B:261:PHE:N	2.50	0.44
1:B:304:ILE:HD11	1:B:386:GLY:C	2.42	0.44
1:B:387:LEU:O	1:B:390:LEU:N	2.50	0.44
1:A:209:SER:O	1:A:212:LEU:HB3	2.17	0.44
1:B:33:TRP:HA	1:B:37:ILE:HB	2.00	0.44
1:B:57:LEU:HB2	1:B:359:GLN:CB	2.48	0.44
1:A:7:THR:O	1:A:10:TRP:N	2.50	0.44
1:A:45:THR:CG2	1:A:48:ILE:HD12	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:GLY:O	1:A:66:LEU:N	2.50	0.44
1:A:275:ILE:HD12	1:A:327:PRO:HB3	2.00	0.44
1:B:84:LEU:C	1:B:86:MET:H	2.23	0.44
1:B:209:SER:O	1:B:212:LEU:HB3	2.17	0.44
1:B:263:TYR:HD1	1:B:263:TYR:H	1.65	0.44
1:A:216:LEU:O	1:A:219:GLN:HB2	2.17	0.44
1:A:246:PHE:CD1	1:A:247:PHE:N	2.86	0.44
1:B:78:TRP:HZ2	1:B:185:PHE:HB3	1.82	0.44
1:B:149:VAL:O	1:B:152:ALA:HB3	2.17	0.44
1:B:234:CYS:C	1:B:236:TYR:N	2.75	0.44
1:A:50:ALA:HB1	1:A:363:ILE:O	2.18	0.43
1:A:60:GLN:HE21	1:A:60:GLN:HB2	1.60	0.43
1:A:175:GLY:O	1:A:178:LEU:N	2.51	0.43
1:B:275:ILE:HD12	1:B:327:PRO:HB3	2.00	0.43
1:B:392:PHE:O	1:B:395:ILE:HG22	2.18	0.43
1:B:416:VAL:O	1:B:417:ALA:HB2	2.17	0.43
1:A:26:TYR:CD1	1:A:27:PHE:HB2	2.53	0.43
1:A:279:ALA:O	1:A:282:ILE:HB	2.18	0.43
1:A:299:MET:HG2	1:A:325:GLU:HG3	2.00	0.43
1:A:319:LYS:C	1:A:321:LEU:H	2.25	0.43
1:A:374:GLU:O	1:A:374:GLU:HG2	2.18	0.43
1:A:387:LEU:O	1:A:390:LEU:N	2.51	0.43
1:B:337:ILE:HB	1:B:338:THR:H	1.60	0.43
1:A:243:PHE:CE2	1:A:247:PHE:HB2	2.53	0.43
1:A:275:ILE:HD13	1:A:327:PRO:CB	2.48	0.43
1:A:281:LEU:N	1:A:281:LEU:CD2	2.69	0.43
1:A:284:ASN:C	1:A:286:ILE:N	2.76	0.43
1:A:344:ARG:HG3	1:A:344:ARG:NH1	2.33	0.43
1:B:85:VAL:O	1:B:85:VAL:HG12	2.17	0.43
1:B:101:TYR:HD2	1:B:101:TYR:HA	1.65	0.43
1:B:154:CYS:O	1:B:157:ILE:N	2.49	0.43
1:B:275:ILE:HD13	1:B:327:PRO:CB	2.48	0.43
1:B:395:ILE:HG12	1:B:399:THR:OG1	2.18	0.43
1:A:59:PHE:C	1:A:61:PRO:HD2	2.43	0.43
1:A:72:LEU:O	1:A:74:LYS:NZ	2.51	0.43
1:A:169:VAL:CG2	1:A:170:PHE:H	2.30	0.43
1:A:230:ILE:HA	1:A:358:LYS:HE2	2.00	0.43
1:B:27:PHE:HB3	1:B:28:PRO:CD	2.48	0.43
1:B:154:CYS:SG	1:B:158:VAL:CG1	3.06	0.43
1:B:246:PHE:CD1	1:B:247:PHE:N	2.86	0.43
1:A:91:PHE:CD1	1:A:170:PHE:HE2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:LEU:C	1:A:101:TYR:N	2.75	0.43
1:A:354:PHE:N	1:A:354:PHE:CD1	2.86	0.43
1:A:395:ILE:HG12	1:A:399:THR:OG1	2.19	0.43
1:A:416:VAL:O	1:A:417:ALA:HB2	2.18	0.43
1:B:16:PHE:HZ	1:B:126:GLU:HA	1.82	0.43
1:B:22:ILE:HG13	1:B:176:CYS:SG	2.58	0.43
1:B:57:LEU:HD12	1:B:359:GLN:C	2.43	0.43
1:B:59:PHE:C	1:B:61:PRO:HD2	2.43	0.43
1:B:210:LEU:O	1:B:214:LEU:HD22	2.18	0.43
1:B:299:MET:O	1:B:302:ARG:N	2.44	0.43
1:B:358:LYS:O	1:B:361:ALA:N	2.51	0.43
1:A:3:TYR:HB3	1:A:138:PHE:CD2	2.53	0.43
1:A:33:TRP:HA	1:A:37:ILE:HB	2.01	0.43
1:A:234:CYS:C	1:A:236:TYR:N	2.76	0.43
1:A:283:ILE:HD13	1:A:283:ILE:H	1.84	0.43
1:A:295:ALA:HB2	1:A:328:PHE:CB	2.48	0.43
1:A:322:HIS:C	1:A:324:PHE:H	2.26	0.43
1:B:7:THR:O	1:B:10:TRP:N	2.51	0.43
1:B:13:GLY:HA3	1:B:146:PHE:HD2	1.83	0.43
1:B:18:PHE:CG	1:B:180:LEU:HD13	2.53	0.43
1:B:211:LYS:O	1:B:214:LEU:HB2	2.18	0.43
1:B:354:PHE:HD1	1:B:354:PHE:H	1.66	0.43
1:A:16:PHE:HZ	1:A:126:GLU:HA	1.83	0.43
1:B:69:LYS:O	1:B:70:LEU:C	2.61	0.43
1:A:19:TYR:HD2	1:A:20:PHE:CD1	2.37	0.43
1:A:29:PHE:CA	1:A:261:PHE:CZ	2.89	0.43
1:B:336:TYR:CZ	1:B:400:LEU:HD11	2.53	0.43
1:B:38:ASN:O	1:B:39:HIS:C	2.60	0.43
1:B:62:LEU:H	1:B:62:LEU:CD1	2.26	0.43
1:B:229:VAL:HG12	1:B:358:LYS:CE	2.48	0.43
1:B:295:ALA:O	1:B:299:MET:HG3	2.18	0.43
1:B:345:PHE:HB3	1:B:349:ILE:CD1	2.47	0.43
1:A:91:PHE:CE1	1:A:95:PHE:HD2	2.37	0.43
1:A:154:CYS:SG	1:A:158:VAL:HG13	2.58	0.43
1:A:155:ALA:C	1:A:158:VAL:HG22	2.44	0.43
1:A:358:LYS:O	1:A:361:ALA:N	2.51	0.43
1:B:271:LEU:C	1:B:273:ALA:N	2.73	0.43
1:A:32:ILE:HG22	1:A:33:TRP:N	2.33	0.42
1:A:49:PHE:HA	1:A:52:ILE:HG13	2.01	0.42
1:A:246:PHE:HD2	1:A:378:PHE:HB3	1.83	0.42
1:B:88:ALA:C	1:B:90:PHE:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:LEU:O	1:A:179:ILE:C	2.62	0.42
1:A:232:VAL:O	1:A:236:TYR:HB3	2.18	0.42
1:A:263:TYR:HD1	1:A:263:TYR:H	1.66	0.42
1:A:293:LEU:HD21	1:A:396:SER:C	2.45	0.42
1:A:408:LEU:O	1:A:409:LEU:HB3	2.20	0.42
1:B:74:LYS:CE	1:B:190:ASP:HB2	2.49	0.42
1:B:169:VAL:CG2	1:B:170:PHE:H	2.32	0.42
1:B:169:VAL:CG2	1:B:170:PHE:N	2.81	0.42
1:B:211:LYS:N	1:B:214:LEU:HD22	2.33	0.42
1:B:246:PHE:HD2	1:B:378:PHE:HB3	1.83	0.42
1:A:7:THR:C	1:A:9:PHE:H	2.26	0.42
1:A:302:ARG:CZ	1:A:318:LEU:O	2.68	0.42
1:B:48:ILE:C	1:B:52:ILE:HG13	2.45	0.42
1:B:344:ARG:HG3	1:B:344:ARG:NH1	2.33	0.42
1:A:243:PHE:O	1:A:244:ALA:C	2.62	0.42
1:A:302:ARG:O	1:A:302:ARG:HG2	2.19	0.42
1:B:127:ALA:O	1:B:130:GLU:HB3	2.18	0.42
1:B:261:PHE:C	1:B:264:VAL:HG12	2.41	0.42
1:B:278:PHE:O	1:B:281:LEU:HD23	2.20	0.42
1:B:344:ARG:NE	1:B:345:PHE:HE1	2.18	0.42
1:A:69:LYS:O	1:A:70:LEU:C	2.62	0.42
1:A:88:ALA:C	1:A:90:PHE:N	2.77	0.42
1:B:19:TYR:HD2	1:B:20:PHE:CD1	2.38	0.42
1:B:30:PHE:CB	1:B:31:PRO:CD	2.93	0.42
1:B:255:GLU:O	1:B:259:ARG:CB	2.66	0.42
1:B:278:PHE:HA	1:B:281:LEU:HD23	2.00	0.42
1:B:358:LYS:C	1:B:360:LEU:N	2.75	0.42
1:A:17:PHE:O	1:A:21:PHE:HB2	2.19	0.42
1:A:62:LEU:H	1:A:62:LEU:CD1	2.26	0.42
1:A:144:ARG:C	1:A:146:PHE:N	2.73	0.42
1:A:364:PHE:O	1:A:366:SER:N	2.52	0.42
1:B:23:MET:HA	1:B:118:PHE:CZ	2.55	0.42
1:B:116:PHE:C	1:B:118:PHE:N	2.76	0.42
1:A:29:PHE:O	1:A:30:PHE:C	2.62	0.42
1:B:64:GLY:O	1:B:66:LEU:N	2.51	0.42
1:B:275:ILE:HD13	1:B:327:PRO:CD	2.49	0.42
1:A:16:PHE:HB3	1:A:147:GLY:HA3	2.01	0.42
1:A:74:LYS:CE	1:A:190:ASP:HB2	2.49	0.42
1:A:75:TYR:O	1:A:77:LEU:N	2.53	0.42
1:A:255:GLU:O	1:A:259:ARG:CB	2.66	0.42
1:B:9:PHE:HD2	1:B:10:TRP:CE3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:PHE:CE1	1:B:95:PHE:HD2	2.38	0.42
1:B:408:LEU:O	1:B:409:LEU:HB3	2.20	0.42
1:A:227:LEU:N	1:A:230:ILE:HD12	2.35	0.42
1:B:26:TYR:HB2	1:B:87:PHE:CE1	2.55	0.42
1:B:75:TYR:O	1:B:77:LEU:N	2.53	0.42
1:B:95:PHE:O	1:B:96:GLY:C	2.62	0.42
1:B:385:LEU:H	1:B:385:LEU:HG	1.44	0.42
1:A:42:LYS:O	1:A:45:THR:OG1	2.34	0.42
1:A:91:PHE:CG	1:A:170:PHE:HE2	2.37	0.42
1:A:186:PHE:N	1:A:186:PHE:CD2	2.87	0.42
1:B:88:ALA:N	1:B:89:PRO:CD	2.83	0.42
1:B:293:LEU:HD21	1:B:396:SER:C	2.45	0.42
1:A:7:THR:C	1:A:9:PHE:N	2.77	0.41
1:A:234:CYS:O	1:A:236:TYR:N	2.52	0.41
1:A:278:PHE:HA	1:A:281:LEU:HD23	2.01	0.41
1:A:349:ILE:O	1:A:353:CYS:HB3	2.20	0.41
1:A:369:ALA:HA	1:A:372:MET:HB2	2.01	0.41
1:B:17:PHE:O	1:B:21:PHE:HB2	2.19	0.41
1:B:122:ALA:O	1:B:126:GLU:HG3	2.20	0.41
1:B:260:VAL:O	1:B:264:VAL:HB	2.20	0.41
1:B:302:ARG:O	1:B:302:ARG:HG2	2.20	0.41
1:B:378:PHE:O	1:B:382:TYR:CG	2.73	0.41
1:A:41:SER:O	1:A:44:ASP:HB2	2.21	0.41
1:A:169:VAL:CG2	1:A:170:PHE:N	2.78	0.41
1:A:271:LEU:C	1:A:273:ALA:N	2.74	0.41
1:A:275:ILE:HD13	1:A:327:PRO:CD	2.50	0.41
1:B:286:ILE:CG2	1:B:291:ALA:HB2	2.50	0.41
1:A:11:MET:HG2	1:A:187:ALA:O	2.20	0.41
1:A:151:TRP:O	1:A:155:ALA:N	2.53	0.41
1:A:337:ILE:HG13	1:A:337:ILE:H	1.48	0.41
1:B:1:MET:CG	1:B:4:LEU:HD22	2.50	0.41
1:B:2:TYR:HE2	1:B:137:ASN:OD1	2.03	0.41
1:B:41:SER:O	1:B:42:LYS:C	2.62	0.41
1:B:76:LEU:C	1:B:78:TRP:N	2.77	0.41
1:B:264:VAL:CG1	1:B:265:THR:N	2.59	0.41
1:B:303:ILE:HB	1:B:386:GLY:CA	2.48	0.41
1:B:394:LEU:O	1:B:397:VAL:CG2	2.67	0.41
1:A:1:MET:C	1:A:3:TYR:N	2.78	0.41
1:A:41:SER:O	1:A:42:LYS:C	2.62	0.41
1:A:229:VAL:HG12	1:A:358:LYS:CE	2.49	0.41
1:A:336:TYR:CZ	1:A:400:LEU:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:TYR:CD1	1:B:26:TYR:C	2.95	0.41
1:B:284:ASN:C	1:B:286:ILE:N	2.77	0.41
1:A:17:PHE:CE1	1:A:150:GLY:CA	3.04	0.41
1:A:94:ILE:O	1:A:98:LEU:HB2	2.20	0.41
1:A:246:PHE:CZ	1:A:309:ALA:CB	3.01	0.41
1:A:358:LYS:C	1:A:360:LEU:N	2.76	0.41
1:B:1:MET:C	1:B:3:TYR:N	2.78	0.41
1:B:175:GLY:O	1:B:178:LEU:N	2.54	0.41
1:B:336:TYR:OH	1:B:400:LEU:CD1	2.69	0.41
1:A:247:PHE:CD1	1:A:315:VAL:HG23	2.55	0.41
1:A:286:ILE:CG2	1:A:291:ALA:HB2	2.50	0.41
1:A:304:ILE:HD11	1:A:386:GLY:C	2.46	0.41
1:A:392:PHE:O	1:A:395:ILE:HG22	2.21	0.41
1:B:7:THR:C	1:B:9:PHE:H	2.28	0.41
1:B:11:MET:C	1:B:12:PHE:HD1	2.29	0.41
1:B:178:LEU:O	1:B:179:ILE:C	2.63	0.41
1:A:15:PHE:HB2	1:A:184:LEU:HD13	2.03	0.41
1:A:19:TYR:CD2	1:A:20:PHE:N	2.88	0.41
1:A:26:TYR:CD1	1:A:26:TYR:C	2.96	0.41
1:A:43:SER:HB2	1:A:371:ASN:OD1	2.21	0.41
1:A:52:ILE:CB	1:A:112:ILE:HG21	2.51	0.41
1:B:32:ILE:HG22	1:B:33:TRP:N	2.35	0.41
1:B:246:PHE:CD1	1:B:246:PHE:C	2.98	0.41
1:B:358:LYS:O	1:B:359:GLN:C	2.63	0.41
1:A:263:TYR:O	1:A:264:VAL:O	2.39	0.41
1:A:394:LEU:O	1:A:397:VAL:CG2	2.67	0.41
1:B:186:PHE:N	1:B:186:PHE:CD2	2.89	0.41
1:B:247:PHE:CD1	1:B:315:VAL:HG23	2.56	0.41
1:A:88:ALA:N	1:A:89:PRO:CD	2.84	0.41
1:A:104:LEU:O	1:A:105:VAL:C	2.64	0.41
1:A:211:LYS:O	1:A:214:LEU:HB2	2.21	0.41
1:A:246:PHE:CD1	1:A:246:PHE:C	2.99	0.41
1:A:246:PHE:CB	1:A:378:PHE:HD2	2.08	0.41
1:A:298:ILE:HD13	1:A:298:ILE:HA	1.83	0.41
1:A:346:SER:O	1:A:347:ALA:C	2.63	0.41
1:B:11:MET:HG2	1:B:187:ALA:O	2.21	0.41
1:B:16:PHE:HB3	1:B:147:GLY:HA3	2.02	0.41
1:B:29:PHE:O	1:B:30:PHE:C	2.63	0.41
1:B:86:MET:HE2	1:B:89:PRO:HB2	2.02	0.41
1:B:154:CYS:SG	1:B:158:VAL:HG13	2.61	0.41
1:B:226:SER:C	1:B:230:ILE:CD1	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:GLN:O	1:B:257:GLY:C	2.63	0.41
1:B:273:ALA:O	1:B:274:SER:C	2.64	0.41
1:B:283:ILE:H	1:B:283:ILE:HD13	1.85	0.41
1:B:317:ILE:N	1:B:317:ILE:CD1	2.84	0.41
1:A:1:MET:CG	1:A:4:LEU:HD22	2.50	0.41
1:A:7:THR:CG2	1:A:8:ASN:H	2.24	0.41
1:A:239:PHE:CE2	1:A:243:PHE:HD1	2.39	0.41
1:B:12:PHE:CE2	1:B:128:PHE:HE1	2.36	0.41
1:B:155:ALA:C	1:B:158:VAL:HG22	2.45	0.41
1:B:226:SER:O	1:B:227:LEU:C	2.62	0.41
1:B:19:TYR:CD2	1:B:20:PHE:N	2.89	0.40
1:B:230:ILE:HG13	1:B:230:ILE:H	1.70	0.40
1:B:246:PHE:CZ	1:B:309:ALA:CB	3.01	0.40
1:B:369:ALA:HA	1:B:372:MET:HB2	2.03	0.40
1:A:2:TYR:HE2	1:A:137:ASN:OD1	2.04	0.40
1:A:205:HIS:O	1:A:206:SER:C	2.64	0.40
1:A:345:PHE:HB3	1:A:349:ILE:CD1	2.48	0.40
1:B:94:ILE:O	1:B:98:LEU:HB2	2.22	0.40
1:B:205:HIS:O	1:B:206:SER:C	2.64	0.40
1:B:349:ILE:O	1:B:353:CYS:HB3	2.20	0.40
1:A:23:MET:HA	1:A:118:PHE:CZ	2.57	0.40
1:A:25:ALA:O	1:A:26:TYR:C	2.64	0.40
1:A:42:LYS:O	1:A:44:ASP:N	2.53	0.40
1:A:59:PHE:O	1:A:60:GLN:C	2.64	0.40
1:A:265:THR:C	1:A:267:MET:N	2.78	0.40
1:A:278:PHE:O	1:A:281:LEU:HD23	2.21	0.40
1:A:289:LYS:C	1:A:289:LYS:CD	2.95	0.40
1:B:30:PHE:O	1:B:33:TRP:HB3	2.21	0.40
1:B:44:ASP:O	1:B:47:ILE:CG2	2.68	0.40
1:B:289:LYS:C	1:B:289:LYS:CD	2.94	0.40
1:B:297:THR:O	1:B:301:VAL:HG23	2.21	0.40
1:B:337:ILE:HG13	1:B:337:ILE:H	1.47	0.40
1:B:385:LEU:C	1:B:387:LEU:H	2.29	0.40
1:A:144:ARG:C	1:A:146:PHE:H	2.29	0.40
1:A:99:LEU:CD2	1:A:107:SER:HB3	2.52	0.40
1:A:354:PHE:HD1	1:A:354:PHE:H	1.68	0.40
1:B:19:TYR:O	1:B:22:ILE:CG2	2.60	0.40
1:B:45:THR:CG2	1:B:48:ILE:HD12	2.38	0.40
1:B:52:ILE:CG2	1:B:112:ILE:HG21	2.50	0.40
1:B:299:MET:O	1:B:300:SER:C	2.64	0.40
1:B:317:ILE:C	1:B:319:LYS:H	2.29	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	415/417 (100%)	228 (55%)	113 (27%)	74 (18%)	0	1
1	B	415/417 (100%)	229 (55%)	111 (27%)	75 (18%)	0	1
All	All	830/834 (100%)	457 (55%)	224 (27%)	149 (18%)	0	1

All (149) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	ASP
1	A	39	HIS
1	A	70	LEU
1	A	102	ASN
1	A	105	VAL
1	A	127	ALA
1	A	137	ASN
1	A	139	GLU
1	A	152	ALA
1	A	155	ALA
1	A	178	LEU
1	A	230	ILE
1	A	234	CYS
1	A	244	ALA
1	A	245	ASN
1	A	259	ARG
1	A	264	VAL
1	A	282	ILE
1	A	283	ILE
1	A	327	PRO
1	A	328	PHE
1	A	343	VAL

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Mol	Chain	Res	Type
1	A	346	SER
1	A	356	PHE
1	A	365	MET
1	A	399	THR
1	A	402	GLY
1	A	409	LEU
1	B	36	ASP
1	B	39	HIS
1	B	70	LEU
1	B	102	ASN
1	B	105	VAL
1	B	127	ALA
1	B	137	ASN
1	B	139	GLU
1	B	152	ALA
1	B	155	ALA
1	B	178	LEU
1	B	230	ILE
1	B	234	CYS
1	B	244	ALA
1	B	245	ASN
1	B	259	ARG
1	B	264	VAL
1	B	282	ILE
1	B	283	ILE
1	B	327	PRO
1	B	328	PHE
1	B	337	ILE
1	B	343	VAL
1	B	346	SER
1	B	356	PHE
1	B	365	MET
1	B	399	THR
1	B	402	GLY
1	B	409	LEU
1	A	24	GLY
1	A	30	PHE
1	A	35	HIS
1	A	56	SER
1	A	76	LEU
1	A	91	PHE
1	A	179	ILE

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Mol	Chain	Res	Type
1	A	231	GLY
1	A	258	THR
1	A	277	PHE
1	A	309	ALA
1	A	330	LEU
1	A	337	ILE
1	A	338	THR
1	A	353	CYS
1	A	355	CYS
1	A	404	GLY
1	B	24	GLY
1	B	30	PHE
1	B	35	HIS
1	B	56	SER
1	B	76	LEU
1	B	91	PHE
1	B	179	ILE
1	B	231	GLY
1	B	258	THR
1	B	277	PHE
1	B	309	ALA
1	B	330	LEU
1	B	338	THR
1	B	353	CYS
1	B	355	CYS
1	B	404	GLY
1	A	26	TYR
1	A	193	SER
1	A	278	PHE
1	A	339	SER
1	A	340	GLN
1	A	364	PHE
1	B	26	TYR
1	B	193	SER
1	B	265	THR
1	B	278	PHE
1	B	339	SER
1	B	340	GLN
1	B	349	ILE
1	B	364	PHE
1	A	65	LEU
1	A	87	PHE

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Mol	Chain	Res	Type
1	A	232	VAL
1	A	235	THR
1	A	265	THR
1	A	276	MET
1	A	290	ASN
1	A	349	ILE
1	A	354	PHE
1	B	65	LEU
1	B	87	PHE
1	B	154	CYS
1	B	233	SER
1	B	276	MET
1	B	290	ASN
1	B	354	PHE
1	A	43	SER
1	A	154	CYS
1	A	233	SER
1	A	260	VAL
1	A	280	PRO
1	A	281	LEU
1	A	367	VAL
1	B	43	SER
1	B	232	VAL
1	B	280	PRO
1	B	281	LEU
1	B	323	MET
1	A	57	LEU
1	A	347	ALA
1	B	57	LEU
1	B	235	THR
1	B	260	VAL
1	B	347	ALA
1	B	367	VAL
1	B	229	VAL
1	A	27	PHE
1	A	229	VAL
1	A	238	VAL
1	B	238	VAL
1	A	92	ILE
1	A	416	VAL
1	B	27	PHE
1	B	416	VAL

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Mol	Chain	Res	Type
1	B	92	ILE

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	346/346 (100%)	297 (86%)	49 (14%)	3	19
1	B	346/346 (100%)	298 (86%)	48 (14%)	3	19
All	All	692/692 (100%)	595 (86%)	97 (14%)	3	19

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	TYR
1	A	10	TRP
1	A	11	MET
1	A	16	PHE
1	A	22	ILE
1	A	26	TYR
1	A	42	LYS
1	A	59	PHE
1	A	60	GLN
1	A	74	LYS
1	A	83	MET
1	A	98	LEU
1	A	99	LEU
1	A	101	TYR
1	A	112	ILE
1	A	128	PHE
1	A	140	PHE
1	A	148	CYS
1	A	161	MET
1	A	162	PHE
1	A	163	THR

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Mol	Chain	Res	Type
1	A	171	TRP
1	A	199	ASN
1	A	210	LEU
1	A	214	LEU
1	A	217	PHE
1	A	218	ARG
1	A	225	LEU
1	A	239	PHE
1	A	253	THR
1	A	269	GLU
1	A	275	ILE
1	A	281	LEU
1	A	303	ILE
1	A	325	GLU
1	A	329	LEU
1	A	331	VAL
1	A	337	ILE
1	A	344	ARG
1	A	351	LEU
1	A	356	PHE
1	A	367	VAL
1	A	379	GLN
1	A	385	LEU
1	A	393	THR
1	A	394	LEU
1	A	408	LEU
1	A	410	ARG
1	B	1	MET
1	B	2	TYR
1	B	10	TRP
1	B	11	MET
1	B	16	PHE
1	B	22	ILE
1	B	26	TYR
1	B	42	LYS
1	B	59	PHE
1	B	60	GLN
1	B	74	LYS
1	B	83	MET
1	B	98	LEU
1	B	99	LEU
1	B	101	TYR

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Mol	Chain	Res	Type
1	B	112	ILE
1	B	128	PHE
1	B	140	PHE
1	B	148	CYS
1	B	161	MET
1	B	162	PHE
1	B	163	THR
1	B	171	TRP
1	B	199	ASN
1	B	210	LEU
1	B	214	LEU
1	B	217	PHE
1	B	218	ARG
1	B	225	LEU
1	B	239	PHE
1	B	253	THR
1	B	269	GLU
1	B	275	ILE
1	B	281	LEU
1	B	325	GLU
1	B	329	LEU
1	B	331	VAL
1	B	337	ILE
1	B	344	ARG
1	B	351	LEU
1	B	356	PHE
1	B	367	VAL
1	B	379	GLN
1	B	385	LEU
1	B	393	THR
1	B	394	LEU
1	B	408	LEU
1	B	410	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	60	GLN
1	A	199	ASN
1	A	219	GLN
1	A	241	GLN

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Mol	Chain	Res	Type
1	A	245	ASN
1	A	379	GLN
1	B	8	ASN
1	B	60	GLN
1	B	166	ASN
1	B	199	ASN
1	B	219	GLN
1	B	241	GLN
1	B	242	GLN
1	B	245	ASN
1	B	359	GLN
1	B	379	GLN

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	417/417 (100%)	0.13	8 (1%) 66 39	15, 81, 164, 196	0
1	B	417/417 (100%)	0.18	15 (3%) 46 26	21, 80, 164, 196	0
All	All	834/834 (100%)	0.15	23 (2%) 55 31	15, 81, 164, 196	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	404	GLY	4.7
1	B	97	PRO	3.7
1	A	198	ALA	3.4
1	B	96	GLY	3.4
1	A	407	SER	3.3
1	B	113	TYR	3.3
1	A	102	ASN	3.2
1	A	88	ALA	3.2
1	B	195	ALA	3.2
1	A	193	SER	2.8
1	B	106	GLY	2.7
1	A	255	GLU	2.5
1	B	80	ILE	2.5
1	B	88	ALA	2.5
1	A	187	ALA	2.4
1	A	288	GLY	2.4
1	B	66	LEU	2.4
1	B	196	THR	2.2
1	B	71	GLY	2.2
1	B	198	ALA	2.1
1	B	197	VAL	2.1
1	B	173	GLY	2.0
1	B	407	SER	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.