



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 07:30 AM UTC

PDB ID : 7Y18 / pdb_00007y18
Title : Crystal structure of ribosomal ITS2 pre-rRNA processing complex from *Saccharomyces cerevisiae*
Authors : Chen, J.; Liu, L.
Deposited on : 2022-06-07
Resolution : 3.69 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:

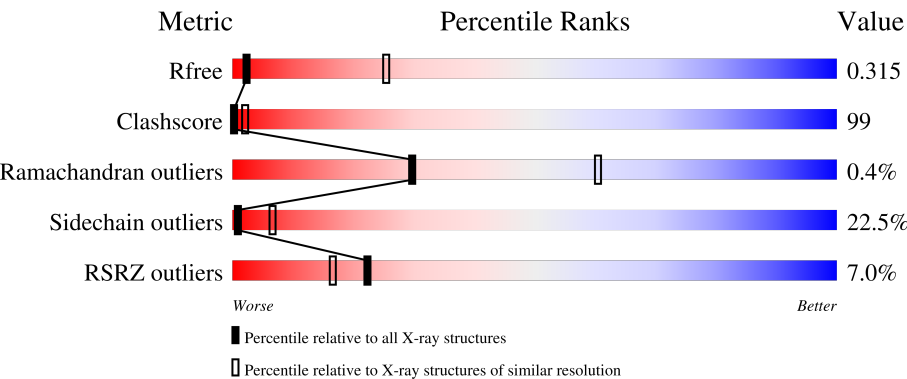
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.69 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	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	632	4% 17% 45% 21% • 16%
1	B	632	12% 23% 41% 18% • 16%
1	E	632	3% 22% 44% 17% • 17%
2	C	502	4% 32% 38% 14% • 14%
2	D	502	5% 34% 39% 11% • 15%

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Mol	Chain	Length	Quality of chain
2	F	502	6% 33% 34% 11% • 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23039 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 Polynucleotide 5'-hydroxyl-kinase GRC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4122	2649	693	771	9			
1	B	528	Total	C	N	O	S	0	0	0
			4069	2607	693	759	10			
1	E	527	Total	C	N	O	S	0	0	0
			4076	2614	691	761	10			

- Molecule 2 is a protein called Protein LAS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	430	Total	C	N	O	S	0	0	0
			3614	2324	629	652	9			
2	D	429	Total	C	N	O	S	0	0	0
			3614	2325	628	652	9			
2	F	397	Total	C	N	O	S	0	0	0
			3364	2176	584	595	9			

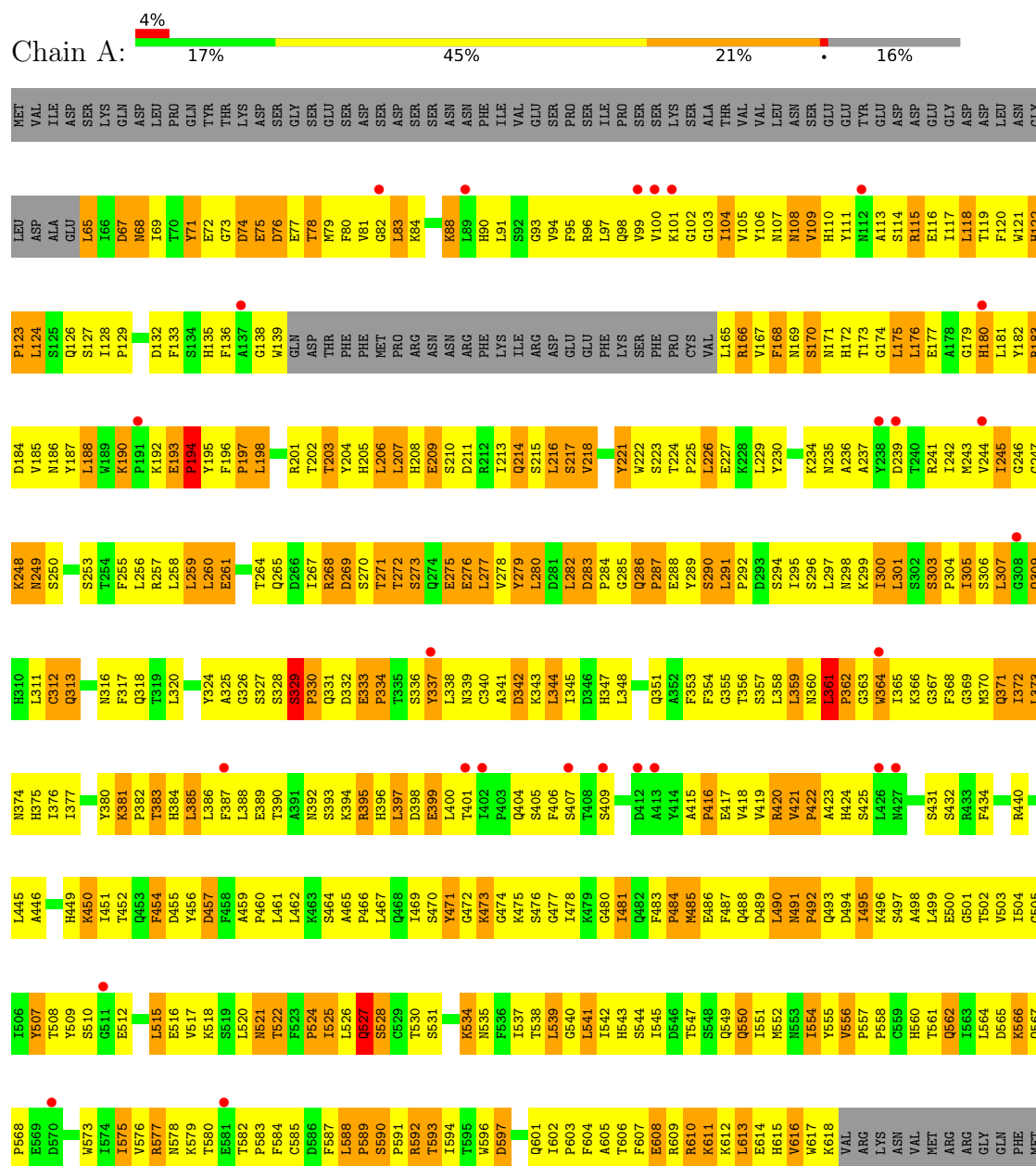
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total	O	0	0
			36	36		
3	C	31	Total	O	0	0
			31	31		
3	D	21	Total	O	0	0
			21	21		
3	B	30	Total	O	0	0
			30	30		
3	E	43	Total	O	0	0
			43	43		
3	F	19	Total	O	0	0
			19	19		

3 Residue-property plots

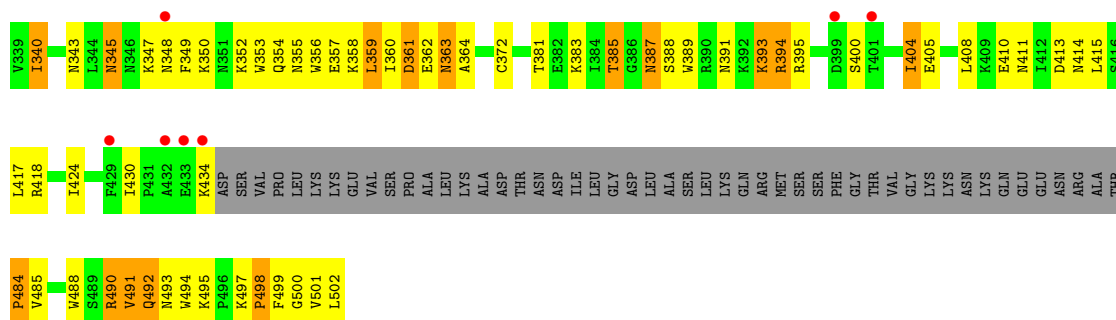
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Polynucleotide 5'-hydroxyl-kinase GRC3

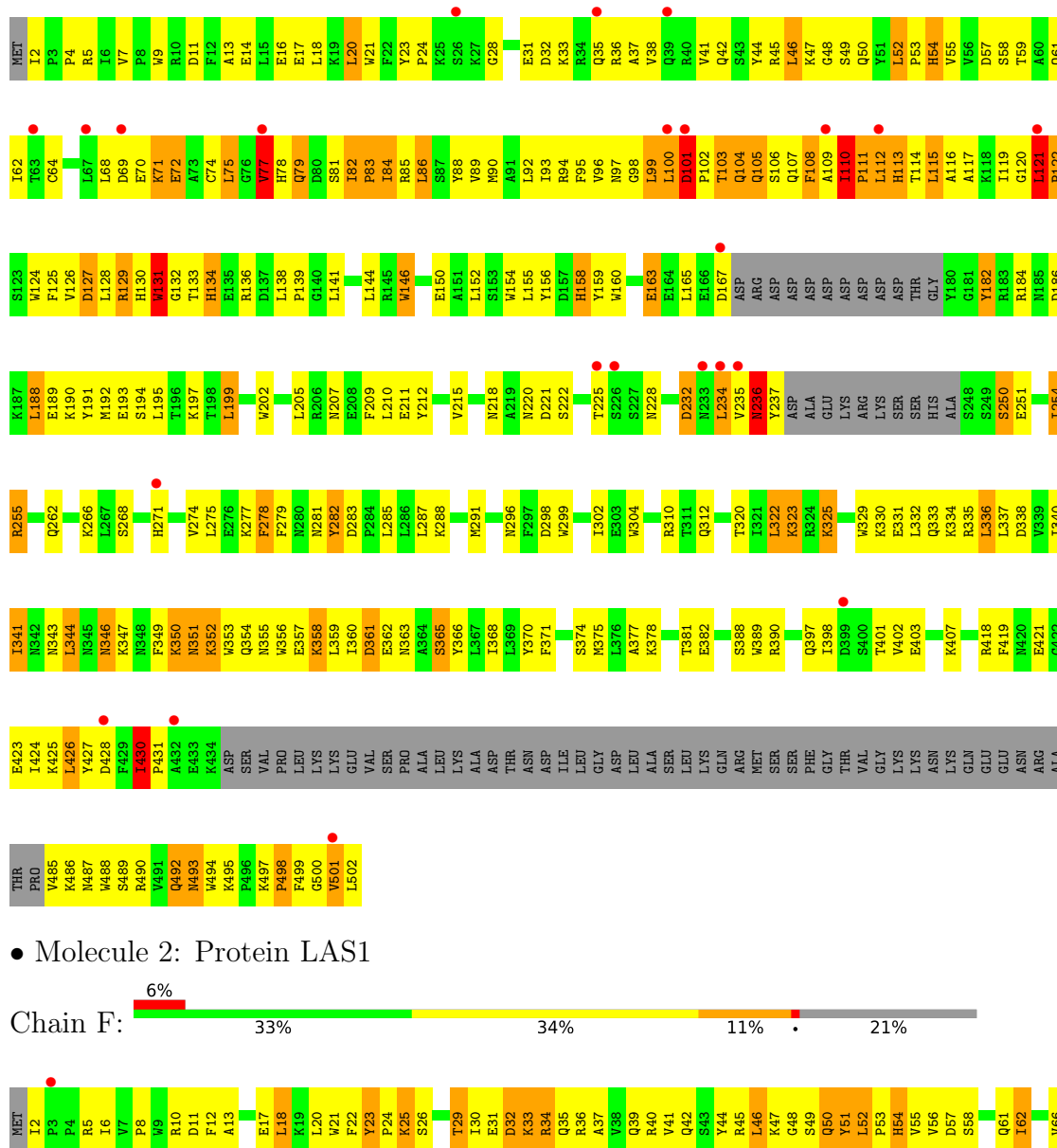


LEU	ASP	VAL	ASP	VAL	MET
ALA	ALA	ILE	ILE	VAL	
GLU	GLU	ASP	ASP	GLN	
LEU	LEU	SER	SER	LYS	
I66	I66	LYS	GLN	GLN	
I69	I69	ASP	ASP	ASP	
T70	T70	LEU	LEU	PRO	
Y71	Y71	PRO	PRO	GLN	
E72	E72	GLN	GLN	TVR	
G73	G73	TVR	TVR	THR	
D74	D74	THR	THR	LYS	
E75	E75	ASP	ASP	ASP	
D76	D76	SER	SER	SER	
E77	E77	SER	SER	GLY	
T78	T78	GLY	GLY	SER	
M79	M79	SER	SER	GLU	
F80	F80	GLU	GLU	SER	
V81	V81	SER	SER	ASP	
G82	G82	ASP	ASP	SER	
L83	L83	SER	SER	ASP	
K84	K84	ASP	ASP	SER	
E85	E85	SER	SER	SER	
				ASN	
K88	K88	ASN	ASN	ASN	
L89	L89	ASN	ASN	PHE	
H90	H90	PHE	PHE	ILE	
L91	L91	ILE	ILE	VAL	
				GLU	
F95	F95	GLU	GLU	SER	
R96	R96	SER	SER	PRO	
L97	L97	PRO	PRO	SER	
Q98	Q98	SER	SER	ILE	
V99	V99	ILE	ILE	PRO	
V100	V100	PRO	PRO	SER	
I101	I101	SER	SER	SER	
G102	G102	SER	SER	LYS	
G103	G103	LYS	LYS	SER	
I104	I104	SER	SER	ALA	
V105	V105	ALA	ALA	THR	
V106	V106	THR	THR	VAL	
I107	I107	VAL	VAL	VAL	
M108	M108	VAL	VAL	LEU	
V109	V109	LEU	LEU	ASN	
H110	H110	ASN	ASN	SER	
Y111	Y111	SER	SER	GLU	
M112	M112	GLU	GLU	GLY	
S114	S114	GLY	GLY	GLU	
T115	T115	GLU	GLU	ASP	
E116	E116	ASP	ASP	ASP	
I117	I117	ASP	ASP	GLU	
L118	L118	GLU	GLU	GLY	
T119	T119	GLY	GLY	ASP	
F120	F120	ASP	ASP	LEU	
W121	W121	LEU	LEU	ASN	
H122	H122	ASN	ASN	GLY	
P123	P123	GLY	GLY		



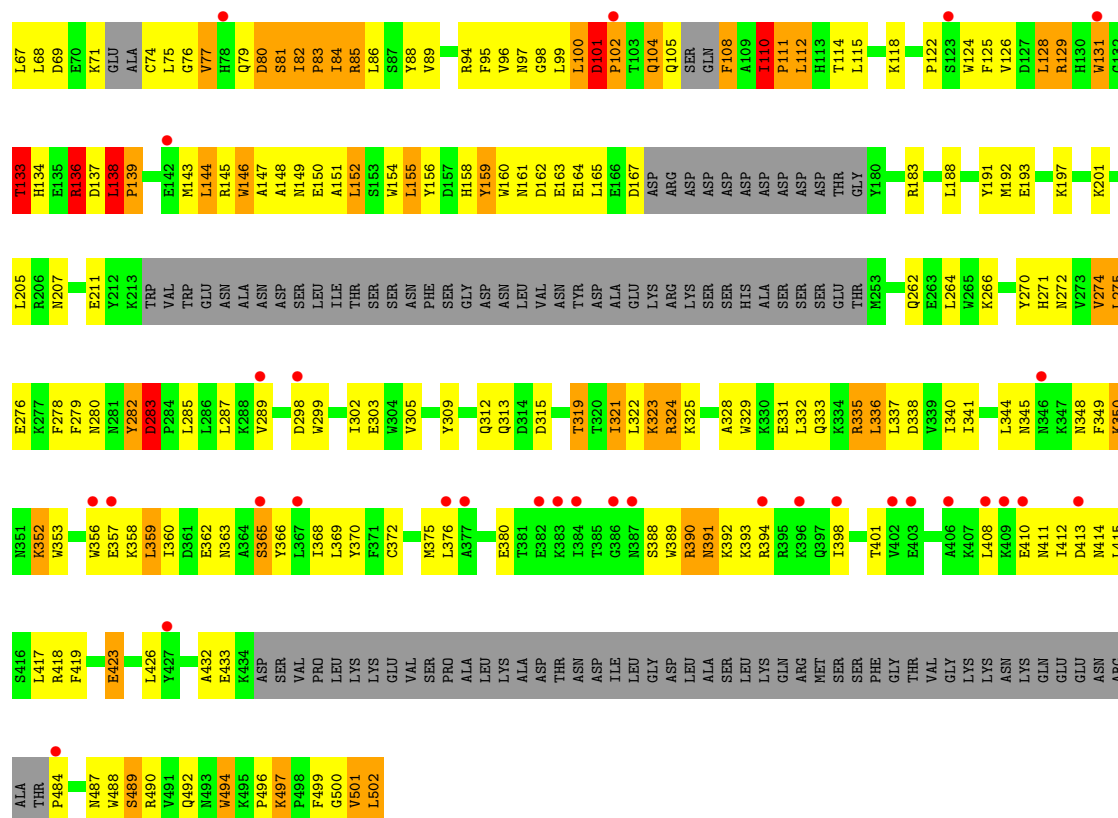


• Molecule 2: Protein LAS1



• Molecule 2: Protein LAS1





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	233.56Å 116.14Å 159.31Å 90.00° 96.41° 90.00°	Depositor
Resolution (Å)	48.63 – 3.69 48.63 – 3.69	Depositor EDS
% Data completeness (in resolution range)	80.1 (48.63-3.69) 80.2 (48.63-3.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.03 (at 3.67Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.278 , 0.318 0.278 , 0.315	Depositor DCC
R_{free} test set	1824 reflections (3.97%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 74.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	23039	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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	0.71	31/4230 (0.7%)	1.11	46/5764 (0.8%)
1	B	0.58	24/4169 (0.6%)	1.10	48/5676 (0.8%)
1	E	0.62	30/4179 (0.7%)	1.03	38/5690 (0.7%)
2	C	0.52	11/3703 (0.3%)	0.88	19/5016 (0.4%)
2	D	0.51	12/3704 (0.3%)	0.85	18/5017 (0.4%)
2	F	0.51	12/3445 (0.3%)	0.86	20/4658 (0.4%)
All	All	0.58	120/23430 (0.5%)	0.98	189/31821 (0.6%)

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	283	ASP	C-N	7.90	1.40	1.33
1	A	556	VAL	C-N	6.42	1.41	1.33
1	B	190	LYS	C-N	6.31	1.40	1.33
1	E	381	LYS	C-N	6.24	1.41	1.33
2	C	23	TYR	C-N	6.24	1.41	1.33
2	D	52	LEU	C-N	6.21	1.41	1.33
2	C	101	ASP	C-N	6.15	1.40	1.33
1	A	381	LYS	C-N	6.11	1.40	1.33
1	B	196	PHE	C-N	6.04	1.41	1.33
1	A	588	LEU	C-N	6.04	1.40	1.33
1	B	483	PHE	C-N	6.03	1.40	1.33
1	E	483	PHE	C-N	6.03	1.40	1.33
1	A	483	PHE	C-N	5.92	1.40	1.33
1	A	421	VAL	C-N	5.89	1.41	1.33
2	C	138	LEU	C-N	5.85	1.40	1.33
2	D	121	LEU	C-N	5.85	1.41	1.33
1	A	329	SER	C-N	5.83	1.40	1.33
1	B	193	GLU	C-N	5.83	1.40	1.33
2	D	110	ILE	C-N	5.79	1.41	1.33
1	E	567	GLN	C-N	5.79	1.41	1.33
2	F	110	ILE	C-N	5.78	1.41	1.33
2	D	430	ILE	C-N	5.76	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	122	HIS	C-N	5.75	1.41	1.33
2	F	138	LEU	C-N	5.75	1.40	1.33
1	A	459	ALA	C-N	5.74	1.41	1.33
1	A	602	ILE	C-N	5.74	1.41	1.34
1	E	304	PRO	N-CD	5.72	1.55	1.47
1	E	459	ALA	C-N	5.71	1.41	1.33
1	A	361	LEU	C-N	5.68	1.41	1.33
1	A	218	VAL	C-N	5.67	1.41	1.33
1	E	218	VAL	C-N	5.67	1.41	1.33
1	E	582	THR	C-N	5.67	1.41	1.33
1	B	567	GLN	C-N	5.65	1.41	1.33
1	E	602	ILE	C-N	5.64	1.40	1.33
1	E	588	LEU	C-N	5.63	1.40	1.33
1	B	459	ALA	C-N	5.61	1.41	1.33
1	E	190	LYS	C-N	5.60	1.40	1.33
1	A	304	PRO	N-CD	5.55	1.55	1.47
1	A	122	HIS	C-N	5.54	1.40	1.33
1	B	286	GLN	C-N	5.53	1.40	1.33
1	A	286	GLN	C-N	5.52	1.40	1.33
1	B	283	ASP	C-N	5.49	1.40	1.34
1	B	191	PRO	N-CD	5.46	1.55	1.47
1	B	194	PRO	N-CD	5.45	1.55	1.47
1	B	123	PRO	N-CD	5.45	1.55	1.47
2	F	23	TYR	C-N	5.43	1.41	1.33
1	B	329	SER	C-N	5.43	1.40	1.34
2	C	102	PRO	N-CD	5.42	1.55	1.47
1	E	523	PHE	C-N	5.41	1.40	1.33
2	D	24	PRO	N-CD	5.39	1.55	1.47
2	F	139	PRO	N-CD	5.39	1.55	1.47
1	A	589	PRO	N-CD	5.36	1.55	1.47
2	D	498	PRO	N-CD	5.35	1.55	1.47
1	A	197	PRO	N-CD	5.33	1.55	1.47
2	F	283	ASP	C-N	5.33	1.41	1.34
1	A	382	PRO	N-CD	5.33	1.55	1.47
1	A	123	PRO	N-CD	5.32	1.55	1.47
1	B	484	PRO	N-CD	5.32	1.55	1.47
1	E	191	PRO	N-CD	5.32	1.55	1.47
2	C	139	PRO	N-CD	5.32	1.55	1.47
1	E	568	PRO	N-CD	5.31	1.55	1.47
1	A	334	PRO	N-CD	5.31	1.55	1.47
2	D	101	ASP	C-N	5.29	1.41	1.34
2	C	498	PRO	N-CD	5.29	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	329	SER	C-N	5.28	1.40	1.33
1	E	603	PRO	N-CD	5.28	1.55	1.47
1	E	291	LEU	C-N	5.28	1.40	1.33
1	E	492	PRO	N-CD	5.27	1.55	1.47
1	A	330	PRO	N-CD	5.25	1.55	1.47
1	E	330	PRO	N-CD	5.25	1.55	1.47
1	A	287	PRO	N-CD	5.24	1.55	1.47
2	C	111	PRO	N-CD	5.24	1.55	1.47
1	A	591	PRO	N-CD	5.23	1.55	1.47
1	B	524	PRO	N-CD	5.23	1.55	1.47
1	B	287	PRO	N-CD	5.23	1.55	1.47
1	B	197	PRO	N-CD	5.22	1.55	1.47
1	E	292	PRO	N-CD	5.21	1.55	1.47
2	C	82	ILE	C-N	5.20	1.41	1.34
1	E	484	PRO	N-CD	5.20	1.55	1.47
1	A	484	PRO	N-CD	5.20	1.55	1.47
1	E	589	PRO	N-CD	5.20	1.55	1.47
2	D	111	PRO	N-CD	5.19	1.55	1.47
2	F	82	ILE	C-N	5.19	1.41	1.34
1	B	284	PRO	N-CD	5.19	1.55	1.47
1	B	492	PRO	N-CD	5.19	1.55	1.47
1	A	492	PRO	N-CD	5.18	1.54	1.47
2	D	82	ILE	C-N	5.17	1.41	1.34
1	E	460	PRO	N-CD	5.16	1.54	1.47
1	E	591	PRO	N-CD	5.16	1.54	1.47
1	E	491	ASN	C-N	5.15	1.40	1.33
1	A	568	PRO	N-CD	5.14	1.54	1.47
2	F	111	PRO	N-CD	5.14	1.54	1.47
2	C	283	ASP	C-N	5.14	1.41	1.34
2	F	24	PRO	N-CD	5.14	1.54	1.47
2	F	496	PRO	N-CD	5.13	1.54	1.47
2	F	101	ASP	C-N	5.12	1.41	1.34
1	E	333	GLU	C-N	5.11	1.41	1.34
1	E	219	PRO	N-CD	5.11	1.54	1.47
1	A	524	PRO	N-CD	5.10	1.54	1.47
1	B	333	GLU	C-N	5.10	1.41	1.34
2	D	83	PRO	N-CD	5.10	1.54	1.47
1	E	334	PRO	N-CD	5.10	1.54	1.47
1	A	422	PRO	N-CD	5.09	1.54	1.47
1	E	524	PRO	N-CD	5.09	1.54	1.47
2	C	284	PRO	N-CD	5.09	1.54	1.47
1	B	330	PRO	N-CD	5.09	1.54	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	558	PRO	N-CD	5.08	1.54	1.47
2	D	431	PRO	N-CD	5.07	1.54	1.47
2	F	102	PRO	N-CD	5.07	1.54	1.47
2	C	24	PRO	N-CD	5.06	1.54	1.47
1	B	460	PRO	N-CD	5.06	1.54	1.47
1	E	382	PRO	N-CD	5.06	1.54	1.47
1	A	362	PRO	N-CD	5.05	1.54	1.47
1	E	583	PRO	N-CD	5.04	1.54	1.47
1	A	491	ASN	C-N	5.04	1.40	1.34
2	D	122	PRO	N-CD	5.03	1.54	1.47
2	F	83	PRO	N-CD	5.03	1.54	1.47
1	B	491	ASN	C-N	5.02	1.40	1.34
1	A	590	SER	C-N	5.01	1.40	1.34
1	B	568	PRO	N-CD	5.00	1.54	1.47

All (189) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	197	PRO	N-CA-C	-17.90	76.42	111.69
1	B	198	LEU	N-CA-CB	-12.20	90.87	110.51
1	B	617	TRP	N-CA-C	-11.63	90.42	109.96
1	B	618	LYS	N-CA-C	-10.53	81.53	111.00
1	B	197	PRO	CB-CA-C	-10.49	93.57	110.25
1	B	617	TRP	CB-CA-C	-9.47	93.90	109.53
1	A	415	ALA	N-CA-C	8.00	115.42	108.22
1	E	303	SER	C-N-CD	7.87	137.91	120.60
1	A	247	GLY	N-CA-C	-7.81	102.07	112.14
2	F	159	TYR	N-CA-C	7.78	119.54	111.14
1	E	392	ASN	N-CA-C	7.77	119.75	111.28
1	A	556	VAL	CA-C-N	-7.53	112.62	120.38
1	A	556	VAL	C-N-CA	-7.53	112.62	120.38
1	E	523	PHE	CA-C-N	-7.32	112.44	119.76
1	E	523	PHE	C-N-CA	-7.32	112.44	119.76
1	E	474	GLY	N-CA-C	7.30	121.49	112.73
1	B	193	GLU	CA-C-N	-7.29	113.21	120.21
1	B	193	GLU	C-N-CA	-7.29	113.21	120.21
1	A	483	PHE	CA-C-N	-7.24	113.26	120.21
1	A	483	PHE	C-N-CA	-7.24	113.26	120.21
2	C	101	ASP	CA-C-N	-7.16	113.30	120.31
2	C	101	ASP	C-N-CA	-7.16	113.30	120.31
1	A	588	LEU	CA-C-N	-7.13	112.97	120.03
1	A	588	LEU	C-N-CA	-7.13	112.97	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	567	GLN	CA-C-N	-7.12	112.42	119.76
1	B	567	GLN	C-N-CA	-7.12	112.42	119.76
2	C	317	ASN	N-CA-C	7.11	119.03	111.28
1	E	483	PHE	CA-C-N	-7.11	112.99	120.03
1	E	483	PHE	C-N-CA	-7.11	112.99	120.03
2	F	110	ILE	CA-C-N	-7.03	112.52	119.76
2	F	110	ILE	C-N-CA	-7.03	112.52	119.76
1	A	416	PRO	N-CA-CB	7.03	110.63	103.25
1	A	361	LEU	CA-C-N	-6.98	112.78	119.76
1	A	361	LEU	C-N-CA	-6.98	112.78	119.76
1	A	510	SER	N-CA-C	-6.96	101.35	110.53
1	B	483	PHE	CA-C-N	-6.95	113.15	120.03
1	B	483	PHE	C-N-CA	-6.95	113.15	120.03
1	B	124	LEU	N-CA-C	6.94	118.92	111.36
1	B	286	GLN	CA-C-N	-6.93	112.62	119.76
1	B	286	GLN	C-N-CA	-6.93	112.62	119.76
2	D	110	ILE	CA-C-N	-6.90	112.88	119.85
2	D	110	ILE	C-N-CA	-6.90	112.88	119.85
1	E	416	PRO	N-CA-CB	6.89	110.49	103.25
2	F	138	LEU	CA-C-N	-6.88	113.21	120.03
2	F	138	LEU	C-N-CA	-6.88	113.21	120.03
2	C	484	PRO	N-CA-CB	6.88	110.57	103.00
2	F	133	THR	N-CA-C	6.86	118.54	111.14
1	E	588	LEU	CA-C-N	-6.83	112.95	119.85
1	E	588	LEU	C-N-CA	-6.83	112.95	119.85
1	E	381	LYS	CA-C-N	-6.82	112.74	119.90
1	E	381	LYS	C-N-CA	-6.82	112.74	119.90
2	D	121	LEU	CA-C-N	-6.82	112.74	119.76
2	D	121	LEU	C-N-CA	-6.82	112.74	119.76
1	E	582	THR	CA-C-N	-6.79	112.97	119.76
1	E	582	THR	C-N-CA	-6.79	112.97	119.76
2	C	138	LEU	CA-C-N	-6.78	113.32	120.03
2	C	138	LEU	C-N-CA	-6.78	113.32	120.03
1	B	190	LYS	CA-C-N	-6.77	113.68	120.31
1	B	190	LYS	C-N-CA	-6.77	113.68	120.31
1	A	421	VAL	CA-C-N	-6.76	112.79	119.76
1	A	421	VAL	C-N-CA	-6.76	112.79	119.76
1	B	474	GLY	N-CA-C	6.75	120.83	112.73
1	E	609	ARG	CB-CA-C	-6.74	108.81	116.63
2	F	484	PRO	N-CA-CB	6.74	110.42	103.00
1	E	602	ILE	CA-C-N	-6.74	113.04	119.85
1	E	602	ILE	C-N-CA	-6.74	113.04	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	218	VAL	CA-C-N	-6.74	113.02	119.76
1	A	218	VAL	C-N-CA	-6.74	113.02	119.76
1	A	122	HIS	CA-C-N	-6.72	113.06	119.85
1	A	122	HIS	C-N-CA	-6.72	113.06	119.85
1	B	459	ALA	CA-C-N	-6.71	112.85	119.76
1	B	459	ALA	C-N-CA	-6.71	112.85	119.76
1	E	190	LYS	CA-C-N	-6.70	113.08	119.85
1	E	190	LYS	C-N-CA	-6.70	113.08	119.85
1	A	459	ALA	CA-C-N	-6.68	112.87	119.76
1	A	459	ALA	C-N-CA	-6.68	112.87	119.76
2	D	430	ILE	CA-C-N	-6.68	113.10	119.85
2	D	430	ILE	C-N-CA	-6.68	113.10	119.85
1	B	416	PRO	N-CA-CB	6.67	110.26	103.25
1	E	459	ALA	CA-C-N	-6.64	112.92	119.76
1	E	459	ALA	C-N-CA	-6.64	112.92	119.76
1	E	291	LEU	CA-C-N	-6.63	112.93	119.76
1	E	291	LEU	C-N-CA	-6.63	112.93	119.76
2	F	23	TYR	CA-C-N	-6.63	112.95	119.78
2	F	23	TYR	C-N-CA	-6.63	112.95	119.78
1	E	218	VAL	CA-C-N	-6.63	112.93	119.76
1	E	218	VAL	C-N-CA	-6.63	112.93	119.76
2	C	23	TYR	CA-C-N	-6.62	112.68	119.83
2	C	23	TYR	C-N-CA	-6.62	112.68	119.83
2	D	52	LEU	CA-C-N	-6.61	113.48	120.03
2	D	52	LEU	C-N-CA	-6.61	113.48	120.03
1	A	286	GLN	CA-C-N	-6.54	113.22	119.76
1	A	286	GLN	C-N-CA	-6.54	113.22	119.76
1	E	567	GLN	CA-C-N	-6.51	113.28	119.85
1	E	567	GLN	C-N-CA	-6.51	113.28	119.85
1	B	85	GLU	CB-CA-C	-6.46	109.14	116.63
1	B	122	HIS	CA-C-N	-6.40	113.39	119.85
1	B	122	HIS	C-N-CA	-6.40	113.39	119.85
1	E	415	ALA	N-CA-C	6.32	113.91	108.22
1	A	381	LYS	CA-C-N	-6.32	113.27	119.90
1	A	381	LYS	C-N-CA	-6.32	113.27	119.90
2	D	78	HIS	N-CA-C	6.29	118.22	111.36
2	C	223	LEU	N-CA-C	6.29	118.21	111.36
2	D	158	HIS	N-CA-C	6.27	118.19	111.36
1	A	283	ASP	CA-C-N	-6.26	113.32	120.89
1	A	283	ASP	C-N-CA	-6.26	113.32	120.89
1	B	263	PHE	N-CA-C	-6.25	104.46	111.28
1	B	329	SER	CA-C-N	-6.21	113.28	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	SER	C-N-CA	-6.21	113.28	119.56
1	B	422	PRO	N-CA-CB	6.18	109.74	103.25
1	B	466	PRO	N-CA-CB	6.14	109.69	103.25
2	F	136	ARG	N-CA-C	6.13	117.97	111.28
1	A	235	ASN	N-CA-C	6.10	117.93	111.28
1	A	329	SER	CA-C-N	-5.95	113.49	119.56
1	A	329	SER	C-N-CA	-5.95	113.49	119.56
1	B	392	ASN	N-CA-C	5.92	117.73	111.28
1	E	611	LYS	N-CA-C	-5.87	102.23	110.50
2	C	100	LEU	N-CA-C	5.78	117.39	111.14
1	E	491	ASN	CA-C-N	-5.78	112.92	119.28
1	E	491	ASN	C-N-CA	-5.78	112.92	119.28
1	B	400	LEU	N-CA-C	5.77	117.57	111.28
2	D	101	ASP	CA-C-N	-5.72	112.70	119.05
2	D	101	ASP	C-N-CA	-5.72	112.70	119.05
2	C	216	TRP	N-CA-C	5.70	117.57	111.36
2	C	85	ARG	N-CA-C	-5.69	105.08	111.28
2	F	82	ILE	O-C-N	5.59	124.04	120.07
1	E	333	GLU	CA-C-N	-5.57	112.87	119.05
1	E	333	GLU	C-N-CA	-5.57	112.87	119.05
2	C	82	ILE	CA-C-N	-5.56	112.88	119.05
2	C	82	ILE	C-N-CA	-5.56	112.88	119.05
1	A	74	ASP	CB-CA-C	-5.55	110.16	116.54
1	A	590	SER	CA-C-N	-5.53	112.91	119.05
1	A	590	SER	C-N-CA	-5.53	112.91	119.05
1	A	491	ASN	CA-C-N	-5.50	112.95	119.05
1	A	491	ASN	C-N-CA	-5.50	112.95	119.05
1	A	527	GLN	N-CA-C	5.49	117.27	111.28
2	D	28	GLY	N-CA-C	5.49	119.13	110.96
1	A	193	GLU	CA-C-N	-5.48	112.99	119.84
1	A	193	GLU	C-N-CA	-5.48	112.99	119.84
1	B	523	PHE	CA-C-N	-5.46	113.01	119.84
1	B	523	PHE	C-N-CA	-5.46	113.01	119.84
2	F	413	ASP	N-CA-C	-5.46	105.33	111.28
1	B	196	PHE	CA-C-N	-5.45	112.89	120.25
1	B	196	PHE	C-N-CA	-5.45	112.89	120.25
2	F	101	ASP	CA-C-N	-5.45	113.00	119.05
2	F	101	ASP	C-N-CA	-5.45	113.00	119.05
1	A	471	TYR	N-CA-C	-5.42	102.86	110.50
2	F	82	ILE	CA-C-N	-5.42	113.04	119.05
2	F	82	ILE	C-N-CA	-5.42	113.04	119.05
2	F	283	ASP	CA-C-N	-5.41	113.04	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	283	ASP	C-N-CA	-5.41	113.04	119.05
2	F	29	THR	N-CA-C	-5.41	106.73	113.55
1	E	369	GLY	N-CA-C	-5.35	106.31	112.73
2	C	44	TYR	N-CA-C	-5.35	105.45	111.28
1	B	491	ASN	CA-C-N	-5.34	113.12	119.05
1	B	491	ASN	C-N-CA	-5.34	113.12	119.05
1	E	329	SER	CA-C-N	-5.29	113.46	119.28
1	E	329	SER	C-N-CA	-5.29	113.46	119.28
1	A	279	TYR	N-CA-C	-5.29	103.05	110.50
2	C	29	THR	N-CA-C	5.27	116.71	111.07
2	D	82	ILE	CA-C-N	-5.27	113.20	119.05
2	D	82	ILE	C-N-CA	-5.27	113.20	119.05
1	E	510	SER	N-CA-C	-5.27	103.58	110.53
1	B	428	HIS	N-CA-C	-5.24	103.97	110.41
1	A	602	ILE	CA-C-N	-5.24	113.14	118.85
1	A	602	ILE	C-N-CA	-5.24	113.14	118.85
1	B	344	LEU	N-CA-C	5.24	117.07	111.36
2	C	283	ASP	CA-C-N	-5.22	113.25	119.05
2	C	283	ASP	C-N-CA	-5.22	113.25	119.05
1	B	475	LYS	CA-C-N	-5.21	114.47	122.87
1	B	475	LYS	C-N-CA	-5.21	114.47	122.87
1	A	557	PRO	CA-C-N	-5.20	113.28	119.05
1	A	557	PRO	C-N-CA	-5.20	113.28	119.05
1	A	333	GLU	CA-C-N	-5.20	113.28	119.05
1	A	333	GLU	C-N-CA	-5.20	113.28	119.05
1	B	333	GLU	CA-C-N	-5.19	113.29	119.05
1	B	333	GLU	C-N-CA	-5.19	113.29	119.05
2	C	215	VAL	N-CA-C	5.17	115.39	110.42
1	B	338	LEU	N-CA-C	-5.17	105.64	111.28
1	B	173	THR	N-CA-C	5.16	116.98	111.36
1	B	233	HIS	N-CA-C	5.12	116.87	111.28
2	D	236	ASN	N-CA-C	5.11	116.85	111.28
2	D	50	GLN	N-CA-C	-5.09	105.91	112.68
1	B	370	MET	N-CA-C	-5.09	105.73	111.28
1	E	530	THR	CB-CA-C	-5.08	110.74	116.63
2	F	32	ASP	N-CA-C	-5.05	101.36	109.39
1	A	194	PRO	CA-N-CD	-5.04	104.95	112.00
2	D	77	VAL	N-CA-C	5.02	115.74	110.62
1	B	530	THR	CB-CA-C	-5.02	110.41	117.23

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	4122	0	3931	1042	0
1	B	4069	0	3873	974	0
1	E	4076	0	3880	900	3
2	C	3614	0	3553	708	0
2	D	3614	0	3551	682	0
2	F	3364	0	3350	547	6
3	A	36	0	0	4	0
3	B	30	0	0	2	0
3	C	31	0	0	4	0
3	D	21	0	0	1	0
3	E	43	0	0	8	0
3	F	19	0	0	1	0
All	All	23039	0	22138	4466	6

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 99.

All (4466) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:LYS:CB	1:A:139:TRP:CD1	1.77	1.65
2:C:202:TRP:CZ3	2:C:209:PHE:CE1	1.77	1.62
2:D:4:PRO:HB3	1:B:607:PHE:CE1	1.10	1.62
1:E:331:GLN:HG3	1:E:364:TRP:CZ2	1.21	1.62
1:A:607:PHE:CE1	2:C:4:PRO:CB	1.82	1.62
1:B:366:LYS:HB3	1:B:396:HIS:CD2	1.38	1.58
2:D:69:ASP:CA	2:D:77:VAL:HG21	1.26	1.58
1:B:79:MET:CA	1:B:167:VAL:HG21	1.32	1.57
2:D:202:TRP:CZ3	2:D:209:PHE:CE2	1.92	1.56
1:A:331:GLN:CG	1:A:364:TRP:HZ2	1.09	1.56
1:A:504:ILE:HD12	1:A:575:ILE:CG2	1.13	1.56
2:D:4:PRO:CB	1:B:607:PHE:CE1	1.86	1.56
1:E:331:GLN:CG	1:E:364:TRP:HZ2	1.12	1.55
1:B:90:HIS:CE1	1:B:128:ILE:HD11	1.42	1.55
1:E:96:ARG:HG3	1:E:168:PHE:CE2	1.06	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:ILE:HA	1:A:397:LEU:CD2	1.36	1.54
2:D:202:TRP:HZ3	2:D:209:PHE:CE2	1.24	1.53
2:D:69:ASP:HA	2:D:77:VAL:CG2	1.33	1.53
2:C:278:PHE:CE2	2:C:286:LEU:HD23	1.37	1.52
1:E:469:ILE:HG21	1:E:478:ILE:CD1	1.09	1.52
1:B:177:GLU:HG2	1:B:458:PHE:CD2	1.45	1.52
1:E:96:ARG:CG	1:E:168:PHE:CE2	1.90	1.50
1:A:607:PHE:CE1	2:C:4:PRO:CD	1.88	1.50
1:B:79:MET:N	1:B:167:VAL:CG2	1.70	1.50
2:C:202:TRP:HZ3	2:C:209:PHE:CE1	1.09	1.50
2:C:23:TYR:CD2	2:C:156:TYR:HD2	1.26	1.49
2:D:5:ARG:CD	1:B:610:ARG:HE	1.23	1.47
1:A:504:ILE:CD1	1:A:575:ILE:CG2	1.91	1.47
2:C:202:TRP:CZ3	2:C:209:PHE:HE1	1.17	1.46
2:F:128:LEU:HB2	2:F:131:TRP:CZ3	1.48	1.46
2:D:312:GLN:NE2	2:D:323:LYS:HG3	1.20	1.46
1:A:538:THR:HB	1:A:560:HIS:CD2	1.47	1.46
1:A:607:PHE:CZ	2:C:4:PRO:CG	1.99	1.45
1:B:172:HIS:CD2	1:B:454:PHE:HA	1.52	1.45
1:B:504:ILE:HD12	1:B:575:ILE:CG2	1.47	1.45
2:F:68:LEU:HD22	2:F:84:ILE:CD1	1.46	1.44
1:E:614:GLU:OE2	2:F:159:TYR:CE1	1.68	1.43
1:A:331:GLN:CG	1:A:364:TRP:CZ2	1.98	1.43
1:B:96:ARG:NH2	1:B:171:ASN:HD21	1.01	1.43
1:B:366:LYS:HG2	1:B:396:HIS:CB	1.48	1.43
1:E:301:LEU:CD1	1:E:316:ASN:O	1.67	1.42
1:B:366:LYS:HA	1:B:396:HIS:CE1	1.52	1.42
2:D:202:TRP:CZ3	2:D:209:PHE:CD2	2.04	1.42
2:D:329:TRP:CE2	2:D:424:ILE:CD1	2.02	1.42
1:A:326:GLY:HA3	1:A:578:ASN:ND2	1.10	1.42
1:A:538:THR:CB	1:A:560:HIS:HD2	1.29	1.41
1:B:471:TYR:HE1	1:B:550:GLN:CA	1.32	1.41
2:C:206:ARG:O	2:C:210:LEU:CD1	1.66	1.41
2:D:202:TRP:HZ3	2:D:209:PHE:CZ	1.38	1.41
2:D:329:TRP:CD2	2:D:424:ILE:CD1	2.00	1.41
1:A:98:GLN:NE2	1:A:115:ARG:CG	1.83	1.41
1:A:488:GLN:NE2	1:A:527:GLN:HE22	0.98	1.41
1:A:589:PRO:HD2	1:A:596:TRP:CH2	1.56	1.41
1:A:105:VAL:CB	1:A:132:ASP:HB2	1.49	1.40
1:B:174:GLY:O	1:B:458:PHE:CE2	1.71	1.40
1:A:502:THR:HB	1:A:577:ARG:NH2	1.34	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:LYS:CE	1:A:395:ARG:HH22	1.35	1.39
1:A:368:PHE:HE1	2:D:146:TRP:NE1	1.15	1.39
1:A:488:GLN:NE2	1:A:527:GLN:NE2	1.68	1.39
1:A:366:LYS:CE	1:A:395:ARG:NH2	1.86	1.39
1:A:105:VAL:HB	1:A:132:ASP:CB	1.51	1.39
2:D:146:TRP:CH2	2:D:150:GLU:OE1	1.75	1.39
2:D:146:TRP:CZ3	2:D:150:GLU:HB2	1.57	1.38
2:F:18:LEU:CD2	2:F:22:PHE:CE2	2.05	1.38
1:A:607:PHE:CE1	2:C:4:PRO:CA	2.06	1.38
1:E:182:TYR:HE1	1:E:184:ASP:CG	0.93	1.38
2:C:80:ASP:OD1	2:C:82:ILE:CG2	1.69	1.38
2:D:312:GLN:HE22	2:D:323:LYS:CG	1.35	1.37
1:E:169:ASN:OD1	1:E:203:THR:CG2	1.71	1.37
2:C:202:TRP:CZ3	2:C:209:PHE:CD1	2.10	1.37
1:B:366:LYS:CB	1:B:396:HIS:CD2	2.05	1.37
2:D:23:TYR:CD2	2:D:156:TYR:HD2	1.42	1.36
1:A:607:PHE:HE1	2:C:4:PRO:N	1.20	1.36
2:D:4:PRO:HB3	1:B:607:PHE:CZ	1.60	1.36
2:D:23:TYR:CD2	2:D:156:TYR:CD2	2.12	1.36
1:A:589:PRO:CD	1:A:596:TRP:HH2	1.38	1.36
1:E:469:ILE:CG2	1:E:478:ILE:CD1	2.04	1.35
1:B:366:LYS:HA	1:B:396:HIS:ND1	1.41	1.35
1:A:607:PHE:CZ	2:C:4:PRO:HB3	1.61	1.35
2:F:272:ASN:HA	2:F:275:LEU:CD1	1.52	1.34
1:A:84:LYS:CB	1:A:139:TRP:CG	2.09	1.34
2:F:272:ASN:CA	2:F:275:LEU:CD1	2.05	1.34
1:A:216:LEU:CD1	1:A:425:SER:OG	1.72	1.34
2:D:84:ILE:HD11	2:D:88:TYR:CE2	1.61	1.34
2:C:23:TYR:CD2	2:C:156:TYR:CD2	2.16	1.34
1:A:84:LYS:CB	1:A:139:TRP:HB3	1.57	1.33
1:A:592:ARG:NH2	2:C:184:ARG:NH2	1.74	1.33
1:E:364:TRP:HD1	1:E:369:GLY:N	1.20	1.33
1:B:239:ASP:CB	1:B:355:GLY:H	1.39	1.33
1:A:388:LEU:O	1:A:423:ALA:CB	1.75	1.32
1:A:607:PHE:HE1	2:C:4:PRO:CD	1.27	1.32
1:E:469:ILE:CG2	1:E:478:ILE:HD11	1.55	1.32
1:B:230:TYR:CE1	1:B:263:PHE:HE1	1.44	1.32
2:F:272:ASN:CA	2:F:275:LEU:HD13	1.60	1.32
1:A:607:PHE:CE1	2:C:4:PRO:HD3	1.57	1.32
2:F:350:LYS:NZ	2:F:401:THR:HG22	1.41	1.32
2:D:23:TYR:CE2	2:D:156:TYR:HD2	1.48	1.31

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:HIS:CE1	1:B:128:ILE:HB	1.62	1.31
1:B:230:TYR:CE1	1:B:263:PHE:CE1	2.17	1.31
1:B:177:GLU:CG	1:B:458:PHE:HD2	1.42	1.31
1:E:187:TYR:CE1	1:E:192:LYS:CB	2.13	1.31
1:E:109:VAL:HG23	1:E:111:TYR:CE1	1.65	1.30
2:F:312:GLN:OE1	2:F:323:LYS:CE	1.78	1.30
1:A:488:GLN:HE21	1:A:527:GLN:NE2	1.23	1.30
2:C:54:HIS:NE2	2:C:98:GLY:HA3	1.45	1.30
2:D:5:ARG:HD2	1:B:610:ARG:NE	1.42	1.30
2:D:77:VAL:CG1	2:D:84:ILE:HG12	1.61	1.30
1:E:519:SER:O	1:E:520:LEU:HD23	1.18	1.30
2:C:497:LYS:HD2	2:C:502:LEU:O	1.15	1.30
1:A:181:LEU:CD1	1:A:585:CYS:SG	2.18	1.29
2:C:180:TYR:O	2:C:184:ARG:HG2	1.17	1.29
2:D:146:TRP:CH2	2:D:150:GLU:HB2	1.66	1.29
1:A:607:PHE:CE1	2:C:4:PRO:CG	2.14	1.29
1:A:507:TYR:HD1	1:A:535:ASN:O	1.08	1.29
1:B:79:MET:O	1:B:167:VAL:CG2	1.81	1.29
1:B:90:HIS:CE1	1:B:128:ILE:CD1	2.13	1.29
1:A:84:LYS:CB	1:A:139:TRP:CB	2.11	1.29
1:A:366:LYS:HE3	1:A:395:ARG:NH2	1.43	1.29
1:B:366:LYS:HA	1:B:396:HIS:CG	1.66	1.29
2:F:312:GLN:NE2	2:F:323:LYS:HD2	1.44	1.29
1:B:361:LEU:CD2	1:B:376:ILE:HD12	1.59	1.28
1:A:607:PHE:CZ	2:C:4:PRO:CB	2.10	1.28
2:C:278:PHE:HE2	2:C:286:LEU:CD2	1.44	1.28
1:B:471:TYR:CE1	1:B:550:GLN:HA	1.66	1.28
2:F:98:GLY:O	2:F:102:PRO:HD3	1.33	1.28
1:B:219:PRO:HB3	1:B:221:TYR:CE2	1.69	1.28
1:E:83:LEU:HD13	1:E:101:LYS:O	1.34	1.28
2:F:58:SER:O	2:F:62:ILE:CG1	1.81	1.28
1:A:387:PHE:O	1:A:421:VAL:HG22	1.21	1.28
1:A:607:PHE:CE1	2:C:4:PRO:HB3	1.53	1.28
1:A:589:PRO:CD	1:A:596:TRP:CH2	2.15	1.28
1:A:96:ARG:O	1:A:168:PHE:CE1	1.86	1.27
1:A:226:LEU:HD11	1:A:230:TYR:OH	1.16	1.27
2:C:85:ARG:HD3	1:B:486:GLU:OE2	1.22	1.27
1:B:96:ARG:NH2	1:B:171:ASN:ND2	1.82	1.27
1:E:487:PHE:O	1:E:490:LEU:HD11	1.13	1.27
1:E:182:TYR:CE1	1:E:184:ASP:CG	1.77	1.27
2:C:64:CYS:SG	2:D:82:ILE:HG21	1.73	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:58:SER:O	2:F:62:ILE:HG13	1.10	1.27
2:D:69:ASP:C	2:D:77:VAL:HG21	1.58	1.27
2:F:131:TRP:HE1	2:F:139:PRO:CG	1.46	1.26
1:B:79:MET:C	1:B:167:VAL:HG21	1.60	1.26
1:E:96:ARG:CG	1:E:168:PHE:HE2	1.31	1.26
2:C:206:ARG:O	2:C:210:LEU:HD11	1.08	1.26
1:E:609:ARG:O	2:F:5:ARG:NH1	1.66	1.25
1:A:98:GLN:CD	1:A:115:ARG:HA	1.59	1.25
2:D:23:TYR:CE2	2:D:156:TYR:CD2	2.25	1.25
1:E:538:THR:OG1	1:E:560:HIS:HD2	1.20	1.25
1:E:222:TRP:NE1	1:E:422:PRO:O	1.67	1.24
1:B:90:HIS:CE1	1:B:213:ILE:HD11	1.72	1.24
2:F:68:LEU:CD2	2:F:84:ILE:HD13	1.65	1.24
1:A:246:GLY:O	1:A:363:GLY:HA3	1.33	1.24
2:C:497:LYS:HD2	2:C:502:LEU:C	1.59	1.24
2:F:97:ASN:OD1	2:F:129:ARG:NH2	1.71	1.24
1:A:365:ILE:HG22	1:A:397:LEU:CD2	1.68	1.24
2:D:146:TRP:HH2	2:D:150:GLU:OE1	1.06	1.24
1:E:487:PHE:O	1:E:490:LEU:CD1	1.84	1.24
1:A:326:GLY:CA	1:A:578:ASN:ND2	1.99	1.23
1:B:96:ARG:CZ	1:B:171:ASN:HD21	1.51	1.23
2:F:18:LEU:HD23	2:F:22:PHE:CE2	1.66	1.23
1:A:366:LYS:HG3	1:A:396:HIS:CB	1.65	1.23
1:A:216:LEU:HD12	1:A:425:SER:OG	1.19	1.23
1:A:365:ILE:CA	1:A:397:LEU:CD2	2.15	1.23
2:C:288:LYS:HE2	2:C:343:ASN:OD1	1.31	1.23
1:B:174:GLY:O	1:B:458:PHE:HE2	0.89	1.23
2:D:98:GLY:O	2:D:102:PRO:HD3	1.37	1.23
1:E:614:GLU:OE2	2:F:159:TYR:CZ	1.90	1.23
1:A:98:GLN:NE2	1:A:115:ARG:CA	2.02	1.23
2:D:23:TYR:CE2	2:D:156:TYR:HB2	1.73	1.23
1:B:166:ARG:O	1:B:167:VAL:HG22	1.37	1.22
1:B:297:LEU:CB	1:B:344:LEU:HD11	1.67	1.22
1:A:592:ARG:HH21	2:C:184:ARG:NH2	1.34	1.22
2:C:86:LEU:CD2	2:C:138:LEU:HD11	1.70	1.22
2:C:119:ILE:HD11	2:C:121:LEU:CB	1.70	1.22
1:A:96:ARG:HG3	1:A:168:PHE:CE1	1.75	1.21
1:A:607:PHE:CZ	2:C:4:PRO:HG3	1.69	1.21
1:E:289:TYR:HD1	1:E:317:PHE:CD2	1.57	1.21
1:A:359:LEU:HD12	1:A:360:ASN:N	1.56	1.21
1:E:289:TYR:HB3	1:E:317:PHE:CE2	1.73	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:LYS:HG2	1:A:395:ARG:NH1	1.55	1.21
2:C:86:LEU:CD2	2:C:138:LEU:CD1	2.19	1.21
1:A:226:LEU:HD11	1:A:230:TYR:CZ	1.75	1.21
2:C:119:ILE:CD1	2:C:121:LEU:HB2	1.69	1.21
1:B:270:SER:OG	1:B:273:SER:OG	1.56	1.21
1:E:169:ASN:OD1	1:E:203:THR:HG23	1.25	1.21
1:A:98:GLN:NE2	1:A:115:ARG:HA	1.53	1.21
1:A:464:SER:O	2:C:494:TRP:CZ3	1.92	1.20
1:E:97:LEU:HD21	1:E:120:PHE:CE1	1.74	1.20
2:D:279:PHE:CE1	2:D:304:TRP:CZ3	2.28	1.20
2:C:80:ASP:OD1	2:C:82:ILE:HG22	1.29	1.20
2:F:17:GLU:OE2	2:F:21:TRP:CH2	1.93	1.20
2:F:18:LEU:CD2	2:F:22:PHE:CZ	2.24	1.20
2:F:365:SER:CA	2:F:419:PHE:HE1	1.55	1.20
1:B:172:HIS:HD2	1:B:454:PHE:CA	1.54	1.19
1:E:331:GLN:CG	1:E:364:TRP:CZ2	1.98	1.19
2:D:329:TRP:CE2	2:D:424:ILE:HD11	1.70	1.19
1:B:172:HIS:HA	1:B:454:PHE:O	1.40	1.19
1:B:367:GLY:H	1:B:396:HIS:CE1	1.59	1.19
1:A:84:LYS:CB	1:A:139:TRP:HD1	1.25	1.19
1:A:492:PRO:O	1:A:495:ILE:HG13	1.38	1.19
2:D:159:TYR:CE1	1:B:614:GLU:HG2	1.78	1.19
1:E:246:GLY:O	1:E:363:GLY:HA2	1.40	1.19
2:F:313:GLN:NE2	2:F:423:GLU:OE1	1.74	1.19
2:D:362:GLU:OE1	2:D:490:ARG:CD	1.91	1.18
2:F:128:LEU:HB2	2:F:131:TRP:CE3	1.76	1.18
1:E:369:GLY:HA2	1:E:372:ILE:HG22	1.18	1.18
1:A:331:GLN:HG3	1:A:364:TRP:CZ2	1.65	1.18
2:C:32:ASP:OD1	2:C:34:ARG:NE	1.74	1.18
2:C:86:LEU:HD23	2:C:138:LEU:CD1	1.72	1.18
2:D:36:ARG:HD3	1:B:491:ASN:OD1	1.44	1.18
1:B:79:MET:N	1:B:167:VAL:HG23	1.41	1.18
2:F:151:ALA:O	2:F:155:LEU:CD1	1.91	1.18
2:C:23:TYR:CE2	2:C:156:TYR:HD2	1.61	1.18
1:E:232:SER:O	1:E:236:ALA:HB2	1.38	1.18
2:F:365:SER:HA	2:F:419:PHE:CE1	1.78	1.18
1:A:98:GLN:NE2	1:A:115:ARG:CB	2.06	1.18
1:A:98:GLN:HE22	1:A:115:ARG:HG3	1.04	1.18
1:A:367:GLY:N	1:A:396:HIS:CE1	2.12	1.18
2:C:110:ILE:CG2	2:C:114:THR:HB	1.74	1.18
2:D:96:VAL:O	2:D:100:LEU:HB2	1.38	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:75:LEU:O	2:F:77:VAL:HG22	1.39	1.17
1:A:365:ILE:CA	1:A:397:LEU:HD22	1.71	1.17
2:C:291:MET:CE	2:C:340:ILE:HG22	1.74	1.17
2:F:126:VAL:O	2:F:129:ARG:CG	1.91	1.17
1:A:538:THR:CB	1:A:560:HIS:CD2	2.13	1.17
1:A:469:ILE:CD1	2:C:488:TRP:CH2	2.27	1.17
1:B:321:LEU:HD21	1:B:344:LEU:CD1	1.74	1.17
1:E:97:LEU:CD2	1:E:120:PHE:CE1	2.27	1.17
1:E:246:GLY:O	1:E:363:GLY:CA	1.92	1.17
1:E:469:ILE:HG21	1:E:478:ILE:HD12	1.26	1.17
2:F:350:LYS:NZ	2:F:401:THR:CG2	2.07	1.17
2:C:52:LEU:HD12	2:C:53:PRO:CD	1.73	1.16
1:E:190:LYS:NZ	1:E:202:THR:OG1	1.77	1.16
2:F:74:CYS:HB3	2:F:75:LEU:HB2	1.23	1.16
1:B:504:ILE:CD1	1:B:575:ILE:HG21	1.75	1.16
1:A:331:GLN:CD	1:A:364:TRP:HZ2	1.50	1.16
1:B:366:LYS:CA	1:B:396:HIS:CD2	2.28	1.16
1:A:469:ILE:HD13	2:C:488:TRP:CH2	1.79	1.16
2:D:329:TRP:CE3	2:D:424:ILE:HD13	1.81	1.16
2:D:329:TRP:CZ2	2:D:424:ILE:HD11	1.79	1.16
1:E:121:TRP:CB	1:E:309:GLN:O	1.93	1.16
1:A:181:LEU:HD13	1:A:585:CYS:SG	1.83	1.16
2:C:52:LEU:HD12	2:C:53:PRO:N	1.61	1.16
2:D:489:SER:O	1:B:467:LEU:HB2	1.43	1.16
1:B:510:SER:HB3	1:B:535:ASN:OD1	1.43	1.16
1:E:364:TRP:CD1	1:E:369:GLY:N	2.13	1.16
1:A:181:LEU:HD11	1:A:585:CYS:SG	1.78	1.15
1:B:80:PHE:HE1	1:B:166:ARG:N	1.44	1.15
1:A:491:ASN:OD1	1:A:494:ASP:OD1	1.61	1.15
2:D:159:TYR:HE1	1:B:614:GLU:CG	1.59	1.15
1:B:311:LEU:O	1:B:313:GLN:OE1	1.63	1.15
1:B:471:TYR:CD1	1:B:550:GLN:O	1.99	1.15
1:E:118:LEU:CD1	1:E:305:ILE:HG21	1.77	1.15
1:A:368:PHE:CE1	2:D:146:TRP:NE1	2.06	1.15
2:D:423:GLU:HA	2:D:426:LEU:HG	1.18	1.15
1:E:96:ARG:HG3	1:E:168:PHE:CD2	1.81	1.15
1:A:469:ILE:CG2	2:C:488:TRP:H	1.60	1.14
1:A:615:HIS:HD2	2:C:102:PRO:CG	1.60	1.14
1:E:187:TYR:CZ	1:E:192:LYS:CB	2.30	1.14
2:F:126:VAL:O	2:F:129:ARG:HG2	1.45	1.14
1:A:331:GLN:CD	1:A:364:TRP:CZ2	2.23	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:PHE:HE1	2:C:4:PRO:CA	1.51	1.14
1:B:471:TYR:CE1	1:B:550:GLN:CA	2.24	1.14
1:A:507:TYR:CD1	1:A:535:ASN:O	2.01	1.14
2:C:278:PHE:CE2	2:C:286:LEU:CD2	2.21	1.14
1:B:79:MET:CA	1:B:167:VAL:CG2	2.17	1.14
1:E:118:LEU:HB3	1:E:305:ILE:HB	1.27	1.14
2:F:280:ASN:O	2:F:325:LYS:NZ	1.80	1.14
1:E:301:LEU:HD12	1:E:316:ASN:O	1.27	1.14
1:E:369:GLY:HA2	1:E:372:ILE:CG2	1.77	1.14
1:E:491:ASN:ND2	2:F:36:ARG:NE	1.94	1.14
1:A:388:LEU:C	1:A:423:ALA:HB2	1.73	1.14
2:F:55:VAL:HG11	2:F:159:TYR:CD1	1.83	1.14
2:D:362:GLU:OE1	2:D:490:ARG:HD3	0.96	1.13
2:D:329:TRP:CD2	2:D:424:ILE:HD13	1.75	1.13
1:E:98:GLN:HG3	1:E:117:ILE:HG23	1.19	1.13
1:A:98:GLN:HE21	1:A:115:ARG:CG	1.53	1.13
1:A:366:LYS:CG	1:A:395:ARG:HH12	1.61	1.13
2:C:52:LEU:HD11	2:C:56:VAL:HB	1.27	1.13
1:A:74:ASP:OD1	1:A:75:GLU:N	1.82	1.12
1:A:528:SER:OG	3:A:701:HOH:O	1.58	1.12
2:C:136:ARG:O	2:D:94:ARG:NH2	1.80	1.12
2:D:296:ASN:OD1	2:D:352:LYS:NZ	1.81	1.12
1:B:364:TRP:HB3	1:B:369:GLY:HA3	1.16	1.13
1:B:366:LYS:CA	1:B:396:HIS:CG	2.32	1.12
1:E:188:LEU:CD1	1:E:434:PHE:CZ	2.32	1.13
1:E:188:LEU:HD12	1:E:434:PHE:CZ	1.83	1.13
2:F:333:GLN:HG3	2:F:337:LEU:HD21	1.19	1.13
2:D:159:TYR:CE1	1:B:614:GLU:CG	2.32	1.12
1:B:366:LYS:CG	1:B:396:HIS:HB2	1.80	1.12
1:B:230:TYR:HE1	1:B:263:PHE:CE1	1.57	1.12
1:E:121:TRP:HB3	1:E:309:GLN:O	1.44	1.12
1:E:524:PRO:C	1:E:525:ILE:HD13	1.74	1.12
2:C:52:LEU:CD1	2:C:53:PRO:HD2	1.79	1.12
1:B:175:LEU:HB2	1:B:456:TYR:CD2	1.83	1.12
1:A:555:TYR:OH	2:C:494:TRP:HH2	1.31	1.11
2:D:329:TRP:CD2	2:D:424:ILE:HD12	1.76	1.11
2:D:356:TRP:O	2:D:360:ILE:HG13	1.49	1.11
1:B:79:MET:C	1:B:167:VAL:CG2	2.19	1.11
1:E:590:SER:OG	1:E:593:THR:OG1	1.67	1.11
2:D:36:ARG:CD	1:B:491:ASN:OD1	1.98	1.11
2:D:146:TRP:CE3	2:D:146:TRP:O	2.02	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:324:TYR:HB2	1:E:536:PHE:CE2	1.84	1.11
2:D:5:ARG:CD	1:B:610:ARG:NE	2.03	1.11
2:D:46:LEU:HD11	1:B:483:PHE:CE1	1.83	1.11
1:B:80:PHE:CE1	1:B:166:ARG:N	2.17	1.11
1:B:366:LYS:CB	1:B:396:HIS:CG	2.34	1.11
2:F:52:LEU:HD21	2:F:57:ASP:HB2	1.31	1.11
1:A:96:ARG:O	1:A:168:PHE:CD1	2.03	1.11
2:D:96:VAL:O	2:D:100:LEU:CB	1.98	1.11
1:E:96:ARG:CG	1:E:168:PHE:CD2	2.32	1.11
1:E:364:TRP:HB3	1:E:369:GLY:HA3	1.14	1.11
1:E:431:SER:OG	1:E:434:PHE:N	1.84	1.11
2:D:4:PRO:CB	1:B:607:PHE:HE1	1.34	1.11
1:B:611:LYS:HB2	1:B:614:GLU:OE2	1.49	1.11
1:E:491:ASN:ND2	2:F:36:ARG:CD	2.14	1.11
2:F:139:PRO:HG2	2:F:144:LEU:HD11	1.28	1.11
2:F:350:LYS:HZ2	2:F:401:THR:CG2	1.62	1.11
1:A:365:ILE:CG2	1:A:397:LEU:HD23	1.81	1.10
2:C:23:TYR:CE2	2:C:156:TYR:HB2	1.86	1.10
2:C:102:PRO:HA	2:C:104:GLN:OE1	1.48	1.10
1:B:449:HIS:HB3	1:B:457:ASP:O	1.49	1.10
2:F:312:GLN:CD	2:F:323:LYS:CD	2.24	1.10
1:B:321:LEU:HD21	1:B:344:LEU:HD12	1.24	1.10
1:B:367:GLY:N	1:B:396:HIS:NE2	1.97	1.10
1:E:468:GLN:O	2:F:487:ASN:O	1.69	1.10
1:A:466:PRO:O	2:C:491:VAL:HG23	1.48	1.10
2:D:77:VAL:HG12	2:D:84:ILE:HG21	1.22	1.10
2:D:312:GLN:OE1	2:D:430:ILE:HG13	1.48	1.10
1:B:589:PRO:HD2	1:B:596:TRP:CH2	1.85	1.10
1:E:109:VAL:CG2	1:E:111:TYR:CE1	2.34	1.10
1:A:226:LEU:CD1	1:A:230:TYR:CZ	2.34	1.10
1:A:367:GLY:H	1:A:396:HIS:CE1	1.70	1.10
1:A:372:ILE:HG23	1:A:373:LEU:HD23	1.24	1.10
2:C:202:TRP:CH2	2:C:209:PHE:HD1	1.69	1.10
1:E:589:PRO:HD2	1:E:596:TRP:CH2	1.86	1.10
2:F:152:LEU:HA	2:F:155:LEU:CD1	1.82	1.10
1:A:388:LEU:O	1:A:423:ALA:HB2	0.93	1.09
2:C:210:LEU:HD12	2:C:210:LEU:H	1.16	1.09
2:C:291:MET:HE1	2:C:340:ILE:HG22	1.15	1.09
2:D:358:LYS:HA	2:D:361:ASP:OD2	1.52	1.09
1:E:109:VAL:CG2	1:E:111:TYR:HE1	1.64	1.09
1:A:98:GLN:HE21	1:A:115:ARG:CA	1.63	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:78:HIS:HB2	2:D:35:GLN:NE2	1.64	1.09
2:D:485:VAL:CG2	1:B:470:SER:HB3	1.82	1.09
1:B:252:LYS:NZ	1:B:361:LEU:O	1.84	1.09
1:B:361:LEU:HD21	1:B:376:ILE:HD12	1.31	1.09
1:B:79:MET:O	1:B:167:VAL:CG1	2.01	1.09
1:B:485:MET:SD	1:B:486:GLU:N	2.24	1.09
1:A:336:SER:OG	1:A:340:CYS:SG	2.09	1.09
2:D:77:VAL:CG1	2:D:84:ILE:CG1	2.28	1.09
1:B:366:LYS:CG	1:B:396:HIS:CB	2.29	1.09
1:B:450:LYS:CD	1:B:456:TYR:OH	2.00	1.09
2:D:77:VAL:HG11	2:D:84:ILE:CG1	1.81	1.09
2:D:329:TRP:CE2	2:D:424:ILE:HD12	1.79	1.09
2:F:312:GLN:CD	2:F:323:LYS:HD2	1.78	1.09
1:B:99:VAL:CG2	1:B:166:ARG:NH2	2.17	1.08
1:A:98:GLN:CG	1:A:115:ARG:HA	1.83	1.08
1:A:226:LEU:CD1	1:A:230:TYR:OH	2.00	1.08
2:D:95:PHE:CE1	2:D:155:LEU:HD21	1.89	1.08
2:C:136:ARG:HD3	1:B:617:TRP:O	1.50	1.08
2:C:224:ILE:HB	2:C:229:PHE:HE2	1.19	1.08
1:B:239:ASP:CB	1:B:355:GLY:N	2.16	1.08
1:B:366:LYS:HG2	1:B:396:HIS:HB2	1.30	1.08
1:B:366:LYS:HA	1:B:396:HIS:CD2	1.86	1.08
1:A:502:THR:CB	1:A:577:ARG:NH2	2.17	1.08
2:D:95:PHE:HE1	2:D:155:LEU:HD21	1.15	1.08
1:A:338:LEU:HD21	1:A:372:ILE:HG13	1.35	1.08
1:A:469:ILE:HG22	2:C:488:TRP:N	1.67	1.08
2:C:80:ASP:OD1	2:C:82:ILE:HG21	1.48	1.08
1:B:277:LEU:HD23	1:B:277:LEU:H	1.16	1.08
1:B:366:LYS:CA	1:B:396:HIS:CE1	2.36	1.08
1:A:589:PRO:HG3	1:A:594:ILE:HD12	1.27	1.07
2:C:96:VAL:HG21	2:C:128:LEU:HD21	1.30	1.07
2:C:497:LYS:CD	2:C:502:LEU:O	2.02	1.07
1:B:99:VAL:CG2	1:B:166:ARG:HH21	1.66	1.07
1:B:395:ARG:NH1	1:B:396:HIS:HD2	1.50	1.07
1:E:589:PRO:HD2	1:E:596:TRP:HH2	1.06	1.07
1:A:480:GLY:HA2	1:A:524:PRO:O	1.54	1.07
1:E:289:TYR:CD1	1:E:317:PHE:CD2	2.42	1.07
1:E:567:GLN:HE21	1:E:567:GLN:HA	1.17	1.07
1:A:75:GLU:HA	2:C:259:ARG:HH21	1.18	1.07
1:A:265:GLN:OE1	1:A:268:ARG:NH1	1.88	1.07
1:A:365:ILE:HA	1:A:397:LEU:HD22	1.23	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:PHE:CZ	1:B:165:LEU:HA	1.89	1.07
1:E:548:SER:OG	1:E:549:GLN:NE2	1.88	1.07
2:F:18:LEU:HD22	2:F:22:PHE:CE2	1.87	1.07
1:A:246:GLY:O	1:A:363:GLY:CA	2.03	1.07
1:A:504:ILE:HD12	1:A:575:ILE:HG23	1.14	1.07
1:A:566:LYS:HZ3	1:A:566:LYS:HA	1.19	1.07
2:C:52:LEU:CD1	2:C:53:PRO:CD	2.32	1.07
2:C:312:GLN:OE1	2:C:323:LYS:HD2	1.53	1.07
2:D:251:GLU:OE1	2:D:255:ARG:NH2	1.88	1.07
1:B:348:LEU:HD11	1:B:353:PHE:CD1	1.89	1.07
1:B:496:LYS:NZ	1:B:500:GLU:OE2	1.88	1.07
2:F:338:ASP:HA	2:F:341:ILE:HD12	1.10	1.07
1:A:169:ASN:OD1	1:A:204:TYR:HE1	1.36	1.06
1:A:388:LEU:HA	1:A:421:VAL:HG23	1.22	1.06
1:A:116:GLU:OE1	1:A:116:GLU:N	1.89	1.06
1:A:496:LYS:NZ	1:A:500:GLU:OE2	1.88	1.06
2:C:86:LEU:HD21	2:C:138:LEU:HD11	1.35	1.06
2:D:358:LYS:HD3	2:D:490:ARG:HH21	1.17	1.06
1:B:469:ILE:HD13	1:B:554:ILE:HG21	1.09	1.06
1:E:510:SER:HB2	1:E:533:SER:O	1.52	1.06
2:F:98:GLY:O	2:F:102:PRO:CD	2.03	1.06
1:A:592:ARG:HH21	2:C:184:ARG:CZ	1.67	1.06
2:D:202:TRP:CZ3	2:D:209:PHE:CZ	2.30	1.06
1:B:210:SER:O	1:B:212:ARG:NH2	1.88	1.06
1:B:230:TYR:CD1	1:B:263:PHE:CE1	2.41	1.06
1:E:210:SER:O	1:E:212:ARG:NH2	1.87	1.06
2:D:46:LEU:HD11	1:B:483:PHE:HE1	1.00	1.06
1:E:301:LEU:HD11	1:E:316:ASN:O	1.54	1.06
1:A:107:ASN:O	1:A:108:ASN:ND2	1.88	1.06
2:D:77:VAL:CG1	2:D:84:ILE:CB	2.33	1.06
2:D:120:GLY:O	2:D:158:HIS:HE1	1.38	1.06
1:B:179:GLY:O	1:B:182:TYR:O	1.72	1.06
1:E:471:TYR:O	1:E:550:GLN:O	1.74	1.06
2:F:128:LEU:CB	2:F:131:TRP:CZ3	2.37	1.06
1:A:98:GLN:HE21	1:A:115:ARG:HG2	1.20	1.05
1:B:310:HIS:CD2	1:B:314:GLY:HA3	1.90	1.05
1:E:188:LEU:CD1	1:E:434:PHE:CE1	2.38	1.05
2:F:152:LEU:CA	2:F:155:LEU:CD1	2.32	1.05
1:A:366:LYS:HG3	1:A:396:HIS:HB2	1.37	1.05
1:A:469:ILE:CD1	2:C:488:TRP:CZ2	2.39	1.05
2:C:136:ARG:HG3	1:B:617:TRP:HB3	1.36	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:509:TYR:CE2	1:B:513:ASP:HB2	1.91	1.05
2:F:88:TYR:HB3	2:F:144:LEU:HD23	1.37	1.05
2:F:145:ARG:O	2:F:149:ASN:ND2	1.88	1.05
1:B:107:ASN:O	1:B:108:ASN:ND2	1.89	1.05
1:E:397:LEU:HD12	1:E:397:LEU:H	1.22	1.05
1:A:469:ILE:HD13	2:C:488:TRP:CZ3	1.92	1.05
1:E:118:LEU:HD13	1:E:305:ILE:HG21	1.34	1.05
2:C:202:TRP:CE3	2:C:209:PHE:HE1	1.75	1.05
2:D:23:TYR:HD2	2:D:156:TYR:CD2	1.59	1.05
1:B:197:PRO:O	1:B:197:PRO:CG	2.02	1.05
2:F:350:LYS:NZ	2:F:401:THR:CB	2.19	1.05
2:D:96:VAL:HG13	2:D:100:LEU:HG	1.35	1.04
2:D:202:TRP:CE3	2:D:209:PHE:CE2	2.45	1.04
1:B:175:LEU:HB2	1:B:456:TYR:HD2	0.91	1.04
2:C:307:ARG:HB2	2:C:307:ARG:HH11	1.19	1.04
2:D:485:VAL:HG23	1:B:470:SER:HB3	1.07	1.04
1:E:469:ILE:HD13	1:E:478:ILE:HD11	1.36	1.04
1:E:612:LYS:CD	2:F:164:GLU:CD	2.30	1.04
1:B:366:LYS:HG2	1:B:396:HIS:HB3	1.34	1.04
1:E:289:TYR:CB	1:E:317:PHE:CE2	2.41	1.04
1:A:245:ILE:CD1	1:A:363:GLY:HA2	1.86	1.04
1:A:615:HIS:CD2	2:C:102:PRO:HG3	1.91	1.04
1:A:616:VAL:HG23	1:A:618:LYS:HE2	1.35	1.04
2:C:202:TRP:CH2	2:C:209:PHE:CD1	2.44	1.04
2:D:279:PHE:CE1	2:D:304:TRP:HZ3	1.71	1.04
2:D:487:ASN:CG	2:D:488:TRP:H	1.62	1.04
1:B:367:GLY:N	1:B:396:HIS:CE1	2.24	1.04
2:C:23:TYR:CE2	2:C:156:TYR:CD2	2.41	1.04
2:D:209:PHE:CZ	2:D:254:ILE:HG23	1.93	1.04
1:B:309:GLN:OE1	1:B:311:LEU:N	1.88	1.04
1:A:226:LEU:CD1	1:A:230:TYR:CE1	2.40	1.03
1:A:336:SER:O	1:A:340:CYS:N	1.90	1.03
1:E:241:ARG:N	1:E:383:THR:OG1	1.91	1.03
2:F:275:LEU:H	2:F:275:LEU:HD12	1.19	1.03
1:A:615:HIS:CD2	2:C:102:PRO:CG	2.40	1.03
2:C:95:PHE:CE1	2:C:155:LEU:HD11	1.92	1.03
2:D:279:PHE:CD1	2:D:304:TRP:CZ3	2.46	1.03
2:D:69:ASP:CA	2:D:77:VAL:CG2	2.07	1.03
2:D:278:PHE:CD1	2:D:279:PHE:HD2	1.77	1.03
2:F:365:SER:HA	2:F:419:PHE:HE1	0.89	1.03
1:A:127:SER:OG	1:A:216:LEU:HD22	1.56	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:364:TRP:HB3	1:E:369:GLY:CA	1.88	1.03
1:E:431:SER:OG	1:E:434:PHE:C	2.02	1.03
1:E:538:THR:OG1	1:E:560:HIS:CD2	2.12	1.03
1:A:607:PHE:CZ	2:C:4:PRO:HD3	1.92	1.03
1:E:169:ASN:CG	1:E:203:THR:HG23	1.84	1.03
1:E:524:PRO:O	1:E:525:ILE:HD13	1.59	1.03
1:A:290:SER:OG	1:A:296:SER:OG	1.73	1.02
1:B:397:LEU:HG	1:B:400:LEU:HD21	1.06	1.02
2:F:131:TRP:HE1	2:F:139:PRO:CD	1.70	1.02
2:D:69:ASP:O	2:D:77:VAL:CG2	2.07	1.02
1:B:247:GLY:N	1:B:365:ILE:HG23	1.72	1.02
1:E:301:LEU:HD11	1:E:316:ASN:C	1.83	1.02
2:C:310:ARG:NH2	2:C:314:ASP:OD1	1.93	1.02
2:D:329:TRP:CG	2:D:424:ILE:HD12	1.93	1.02
1:E:293:ASP:OD2	1:E:327:SER:C	2.02	1.02
1:E:389:GLU:CG	1:E:394:LYS:HA	1.90	1.02
2:F:139:PRO:HG2	2:F:144:LEU:CD1	1.89	1.02
2:F:270:TYR:O	2:F:274:VAL:HG23	1.59	1.02
1:A:607:PHE:HZ	2:C:4:PRO:HG3	0.85	1.02
2:D:77:VAL:HG13	2:D:84:ILE:HB	1.35	1.02
1:B:197:PRO:O	1:B:197:PRO:HG2	1.54	1.02
1:B:515:LEU:HD23	1:B:515:LEU:H	1.23	1.02
1:E:245:ILE:HD13	1:E:373:LEU:HD13	1.40	1.02
2:C:99:LEU:HD22	2:C:99:LEU:H	1.22	1.02
2:D:77:VAL:HG12	2:D:84:ILE:CG2	1.88	1.02
1:B:79:MET:O	1:B:167:VAL:HG22	1.56	1.02
1:B:297:LEU:HB2	1:B:344:LEU:CD1	1.88	1.02
2:F:18:LEU:HD23	2:F:22:PHE:CZ	1.91	1.02
2:F:22:PHE:CE1	2:F:37:ALA:HB1	1.95	1.02
1:A:364:TRP:HD1	1:A:369:GLY:CA	1.73	1.01
1:B:509:TYR:HE2	1:B:513:ASP:HB2	1.20	1.01
1:B:589:PRO:CD	1:B:596:TRP:CH2	2.42	1.01
1:E:83:LEU:CD1	1:E:101:LYS:O	2.07	1.01
1:E:359:LEU:HD11	1:E:361:LEU:HG	1.35	1.01
1:E:369:GLY:CA	1:E:372:ILE:HG22	1.89	1.01
1:E:614:GLU:OE2	2:F:159:TYR:OH	1.78	1.01
2:C:97:ASN:ND2	2:C:129:ARG:CD	2.23	1.01
2:D:357:GLU:O	2:D:361:ASP:OD2	1.75	1.01
1:B:166:ARG:O	1:B:167:VAL:CG2	2.08	1.01
2:F:128:LEU:HA	2:F:131:TRP:HE3	1.26	1.01
1:A:365:ILE:HA	1:A:397:LEU:HD21	1.03	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:PHE:O	1:A:421:VAL:CG2	2.08	1.01
1:A:504:ILE:CD1	1:A:575:ILE:HG21	1.88	1.01
1:A:607:PHE:HZ	2:C:4:PRO:CG	1.50	1.01
2:C:125:PHE:HA	2:C:128:LEU:HD23	1.39	1.01
1:A:99:VAL:HG21	1:A:104:ILE:HD11	1.40	1.01
1:A:592:ARG:NH2	2:C:184:ARG:HH21	1.42	1.01
2:C:434:LYS:HE2	3:C:612:HOH:O	1.60	1.01
2:D:46:LEU:HD21	1:B:577:ARG:HD3	1.43	1.01
1:B:214:GLN:OE1	1:B:426:LEU:CB	2.09	1.01
1:E:213:ILE:HD11	1:E:215:SER:HB3	1.42	1.01
1:A:365:ILE:CG2	1:A:397:LEU:CD2	2.34	1.01
2:D:84:ILE:CD1	2:D:88:TYR:HE2	1.72	1.01
2:D:358:LYS:HB3	2:D:490:ARG:HE	1.22	1.01
1:E:482:GLN:HB3	1:E:576:VAL:HG22	1.41	1.01
2:F:270:TYR:O	2:F:274:VAL:CG2	2.07	1.01
1:A:290:SER:OG	1:A:296:SER:CB	2.09	1.00
1:A:366:LYS:CG	1:A:395:ARG:NH1	2.21	1.00
1:B:79:MET:N	1:B:167:VAL:HG21	1.47	1.00
1:E:199:ASN:HB3	1:E:202:THR:HG23	1.43	1.00
2:F:151:ALA:O	2:F:155:LEU:HD11	1.59	1.00
1:A:368:PHE:CE1	2:D:146:TRP:CD1	2.49	1.00
2:D:125:PHE:O	2:D:128:LEU:HB3	1.61	1.00
2:D:495:LYS:O	2:D:497:LYS:HG3	1.61	1.00
1:E:241:ARG:NE	1:E:381:LYS:HD3	1.75	1.00
1:B:219:PRO:CB	1:B:221:TYR:CE2	2.43	1.00
1:E:450:LYS:HE3	1:E:453:GLN:HA	1.39	1.00
2:D:84:ILE:CD1	2:D:88:TYR:CE2	2.43	1.00
1:E:364:TRP:CD1	1:E:369:GLY:CA	2.44	1.00
1:A:348:LEU:HD11	1:A:353:PHE:HB3	1.37	1.00
2:C:180:TYR:O	2:C:184:ARG:CG	2.08	1.00
1:B:330:PRO:HB3	1:B:337:TYR:CD1	1.96	1.00
1:B:361:LEU:HD22	1:B:376:ILE:HD12	1.40	1.00
1:A:481:ILE:CG2	1:A:575:ILE:HB	1.92	1.00
2:C:138:LEU:HD21	2:D:94:ARG:HD2	1.43	1.00
1:B:175:LEU:CB	1:B:456:TYR:HD2	1.75	1.00
1:B:369:GLY:HA2	1:B:372:ILE:HG22	1.44	1.00
1:A:98:GLN:NE2	1:A:115:ARG:HG3	1.64	0.99
1:E:97:LEU:CD2	1:E:120:PHE:HE1	1.69	0.99
2:F:131:TRP:NE1	2:F:139:PRO:CG	2.25	0.99
1:A:331:GLN:HG2	1:A:364:TRP:CZ2	1.97	0.99
2:D:358:LYS:CA	2:D:361:ASP:OD2	2.10	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:469:ILE:HD13	1:B:554:ILE:CG2	1.91	0.99
1:E:610:ARG:HD2	2:F:167:ASP:CB	1.92	0.99
2:D:430:ILE:H	2:D:430:ILE:HD13	1.23	0.99
2:F:151:ALA:O	2:F:155:LEU:HD12	1.60	0.99
2:D:485:VAL:HG23	1:B:470:SER:CB	1.93	0.99
1:B:387:PHE:CE2	1:B:397:LEU:HD21	1.97	0.99
1:B:327:SER:CB	1:B:332:ASP:OD2	2.09	0.99
1:B:471:TYR:CE1	1:B:550:GLN:C	2.40	0.99
1:A:469:ILE:HD13	2:C:488:TRP:CZ2	1.97	0.99
2:C:202:TRP:CE3	2:C:209:PHE:CE1	2.49	0.99
2:D:184:ARG:HB3	1:B:592:ARG:CD	1.92	0.99
1:B:366:LYS:CD	1:B:396:HIS:HB2	1.92	0.99
1:B:578:ASN:OD1	1:B:579:LYS:N	1.96	0.99
2:F:312:GLN:OE1	2:F:323:LYS:HE2	1.58	0.99
2:C:304:TRP:CD2	2:C:308:ASN:ND2	2.30	0.99
1:E:97:LEU:HD21	1:E:120:PHE:HE1	1.23	0.99
1:E:106:TYR:OH	1:E:122:HIS:NE2	1.95	0.99
1:E:496:LYS:NZ	3:E:701:HOH:O	1.93	0.99
2:C:209:PHE:CE2	2:C:254:ILE:HG23	1.98	0.98
2:C:17:GLU:OE2	2:C:40:ARG:NH1	1.94	0.98
1:B:365:ILE:CD1	1:B:366:LYS:HG3	1.92	0.98
1:B:589:PRO:CD	1:B:596:TRP:HH2	1.76	0.98
1:E:491:ASN:ND2	2:F:36:ARG:HD2	1.79	0.98
2:F:338:ASP:HA	2:F:341:ILE:CD1	1.93	0.98
2:C:224:ILE:HB	2:C:229:PHE:CE2	1.97	0.98
1:A:469:ILE:HG22	2:C:488:TRP:H	0.82	0.98
2:C:345:ASN:OD1	2:C:348:ASN:N	1.96	0.98
2:F:312:GLN:OE1	2:F:323:LYS:NZ	1.96	0.98
2:D:336:LEU:HD11	2:D:340:ILE:HD11	1.43	0.98
1:A:169:ASN:OD1	1:A:204:TYR:CE1	2.17	0.98
1:E:450:LYS:CE	1:E:453:GLN:HA	1.92	0.98
1:B:366:LYS:HA	1:B:396:HIS:NE2	1.77	0.98
1:E:182:TYR:HE1	1:E:184:ASP:OD1	1.46	0.98
2:F:18:LEU:HD22	2:F:22:PHE:HE2	1.23	0.98
1:A:507:TYR:HD1	1:A:535:ASN:C	1.71	0.98
2:D:146:TRP:CZ3	2:D:150:GLU:CB	2.46	0.98
2:D:202:TRP:CZ3	2:D:209:PHE:CG	2.51	0.98
1:B:589:PRO:HG2	1:B:596:TRP:CH2	1.99	0.98
1:E:491:ASN:CG	2:F:36:ARG:CD	2.36	0.98
1:B:348:LEU:CD1	1:B:353:PHE:HB3	1.93	0.98
1:B:390:THR:HG23	1:B:391:ALA:H	1.26	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:616:VAL:HG11	2:C:50:GLN:O	1.64	0.97
1:B:86:LYS:HA	1:B:133:PHE:HB3	1.45	0.97
1:B:471:TYR:HE1	1:B:550:GLN:HA	0.82	0.97
1:A:216:LEU:HD12	1:A:425:SER:HG	1.16	0.97
1:A:245:ILE:HD12	1:A:246:GLY:N	1.79	0.97
1:E:289:TYR:HB3	1:E:317:PHE:HE2	1.19	0.97
1:A:616:VAL:HG23	1:A:618:LYS:CE	1.93	0.97
2:D:4:PRO:CG	1:B:607:PHE:HE1	1.76	0.97
2:D:202:TRP:CH2	2:D:209:PHE:CG	2.53	0.97
1:A:169:ASN:CG	1:A:203:THR:HG23	1.90	0.97
1:A:592:ARG:HD2	2:C:184:ARG:HE	1.29	0.97
2:F:280:ASN:HA	2:F:325:LYS:HE3	1.46	0.97
1:A:364:TRP:HD1	1:A:369:GLY:HA2	1.26	0.97
2:D:278:PHE:HD1	2:D:279:PHE:HD2	1.09	0.97
1:E:364:TRP:HD1	1:E:369:GLY:CA	1.76	0.97
2:F:333:GLN:CG	2:F:337:LEU:HD21	1.94	0.97
2:D:69:ASP:C	2:D:77:VAL:CG2	2.30	0.97
1:E:241:ARG:CZ	1:E:381:LYS:HD3	1.95	0.97
1:E:491:ASN:HD21	2:F:36:ARG:HD2	1.28	0.96
2:F:104:GLN:OE1	2:F:105:GLN:N	1.98	0.96
2:F:312:GLN:OE1	2:F:323:LYS:CD	2.11	0.96
1:A:399:GLU:OE2	1:A:400:LEU:N	1.98	0.96
2:D:4:PRO:CA	1:B:607:PHE:CE1	2.46	0.96
1:B:99:VAL:HG22	1:B:166:ARG:NH2	1.80	0.96
1:B:105:VAL:HG21	1:B:134:SER:OG	1.64	0.96
1:E:175:LEU:HD22	1:E:189:TRP:NE1	1.79	0.96
1:A:370:MET:CB	1:A:400:LEU:CB	2.44	0.96
1:E:175:LEU:CD2	1:E:189:TRP:HE1	1.77	0.96
2:F:350:LYS:HZ3	2:F:401:THR:HG22	1.25	0.96
1:A:603:PRO:O	2:C:10:ARG:O	1.82	0.96
2:C:206:ARG:O	2:C:210:LEU:HD12	1.66	0.96
2:D:97:ASN:O	2:D:101:ASP:N	1.98	0.96
2:F:52:LEU:CD2	2:F:57:ASP:HB2	1.94	0.96
1:A:326:GLY:HA3	1:A:578:ASN:CG	1.89	0.96
1:B:366:LYS:HD3	1:B:395:ARG:HE	1.29	0.96
1:A:365:ILE:CB	1:A:397:LEU:CD2	2.42	0.96
1:A:590:SER:OG	2:C:184:ARG:NE	1.98	0.96
2:D:69:ASP:HA	2:D:77:VAL:HG22	1.45	0.96
1:B:79:MET:CB	1:B:167:VAL:HG21	1.94	0.96
1:B:366:LYS:HB3	1:B:396:HIS:HD2	1.15	0.96
2:C:288:LYS:CE	2:C:343:ASN:OD1	2.13	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:133:THR:HG22	2:D:97:ASN:ND2	1.81	0.96
2:C:234:LEU:O	2:C:235:VAL:HG23	1.64	0.96
1:B:96:ARG:CZ	1:B:171:ASN:ND2	2.22	0.96
1:A:367:GLY:N	1:A:396:HIS:HE1	1.54	0.96
2:D:5:ARG:CZ	1:B:610:ARG:HG2	1.96	0.96
1:E:99:VAL:O	1:E:113:ALA:O	1.78	0.96
2:F:55:VAL:HG21	2:F:159:TYR:CB	1.95	0.96
2:F:152:LEU:C	2:F:155:LEU:CD1	2.39	0.96
1:B:247:GLY:N	1:B:365:ILE:CG2	2.30	0.95
1:E:612:LYS:HD2	2:F:164:GLU:CD	1.90	0.95
2:D:485:VAL:CG2	1:B:470:SER:CB	2.44	0.95
1:B:219:PRO:HB3	1:B:221:TYR:HE2	1.01	0.95
1:B:361:LEU:CD2	1:B:376:ILE:CD1	2.44	0.95
1:B:365:ILE:HD12	1:B:366:LYS:HG3	1.47	0.95
1:A:206:LEU:C	1:A:207:LEU:HD23	1.91	0.95
1:B:348:LEU:HD12	1:B:353:PHE:HB3	1.48	0.95
1:B:361:LEU:HD22	1:B:376:ILE:CD1	1.96	0.95
1:B:366:LYS:CA	1:B:396:HIS:NE2	2.30	0.95
2:D:497:LYS:O	1:B:543:HIS:NE2	2.00	0.95
1:B:89:LEU:HD13	1:B:90:HIS:N	1.82	0.95
1:E:612:LYS:HD3	2:F:164:GLU:CD	1.89	0.95
1:A:98:GLN:NE2	1:A:115:ARG:HG2	1.76	0.95
1:A:616:VAL:CG1	2:C:50:GLN:O	2.15	0.95
1:B:397:LEU:CG	1:B:400:LEU:HD21	1.95	0.95
2:F:282:TYR:HE2	2:F:287:LEU:HD22	1.30	0.95
1:A:96:ARG:O	1:A:168:PHE:HE1	1.49	0.95
1:A:331:GLN:HG3	1:A:364:TRP:CH2	2.02	0.95
1:B:208:HIS:ND1	1:B:209:GLU:HG2	1.80	0.95
1:B:249:ASN:OD1	1:B:424:HIS:NE2	1.99	0.95
1:B:397:LEU:HD12	1:B:400:LEU:HD11	1.45	0.95
2:F:88:TYR:HB3	2:F:144:LEU:CD2	1.96	0.95
1:A:326:GLY:CA	1:A:578:ASN:HD22	1.69	0.94
1:A:504:ILE:HD12	1:A:575:ILE:HG22	0.97	0.94
1:A:607:PHE:CZ	2:C:4:PRO:CD	2.30	0.94
1:B:100:VAL:HB	3:B:708:HOH:O	1.65	0.94
1:B:243:MET:SD	1:B:361:LEU:HD11	2.07	0.94
1:A:311:LEU:O	1:A:313:GLN:NE2	1.99	0.94
1:E:519:SER:O	1:E:520:LEU:CD2	2.13	0.94
1:A:331:GLN:HE21	1:A:364:TRP:HE1	1.14	0.94
2:D:154:TRP:CE3	2:D:155:LEU:HD23	2.02	0.94
2:F:18:LEU:HD21	2:F:22:PHE:CZ	2.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:103:GLY:HA3	1:E:134:SER:O	1.68	0.94
1:E:469:ILE:CD1	1:E:478:ILE:HD11	1.95	0.94
1:B:541:LEU:HD12	1:B:542:ILE:N	1.83	0.94
2:F:128:LEU:CB	2:F:131:TRP:CE3	2.49	0.94
2:C:138:LEU:CD2	2:D:94:ARG:NH1	2.29	0.94
1:B:366:LYS:HD3	1:B:396:HIS:HB2	1.46	0.94
2:F:272:ASN:C	2:F:275:LEU:HD13	1.93	0.94
1:A:589:PRO:CG	1:A:594:ILE:HD12	1.98	0.94
1:E:452:THR:OG1	1:E:455:ASP:OD2	1.85	0.94
2:F:350:LYS:HZ1	2:F:401:THR:CB	1.81	0.94
1:A:366:LYS:HE2	1:A:395:ARG:NH2	1.58	0.94
1:A:502:THR:HB	1:A:577:ARG:HH21	1.15	0.94
1:A:604:PHE:HE2	2:C:10:ARG:NH1	1.66	0.94
2:C:97:ASN:HD21	2:C:129:ARG:CD	1.81	0.94
1:B:330:PRO:HD2	1:B:364:TRP:CZ2	2.03	0.94
1:E:206:LEU:C	1:E:207:LEU:HD23	1.91	0.94
2:F:32:ASP:OD2	2:F:34:ARG:NE	2.01	0.94
2:F:272:ASN:HA	2:F:275:LEU:HD13	0.95	0.94
1:A:366:LYS:HG2	1:A:395:ARG:HH12	0.78	0.94
1:A:406:PHE:HD1	1:A:407:SER:H	1.15	0.94
2:C:79:GLN:O	2:C:79:GLN:NE2	2.00	0.94
2:D:489:SER:O	1:B:467:LEU:CB	2.15	0.94
1:E:499:LEU:O	1:E:502:THR:OG1	1.85	0.94
2:F:338:ASP:CA	2:F:341:ILE:HD12	1.97	0.94
1:A:226:LEU:HD12	1:A:230:TYR:CE1	2.02	0.94
1:A:368:PHE:CE2	1:A:372:ILE:HB	2.03	0.94
2:C:105:GLN:HA	2:C:105:GLN:NE2	1.83	0.94
2:D:96:VAL:CG1	2:D:100:LEU:HG	1.98	0.94
1:B:288:GLU:HG2	1:B:289:TYR:CE2	2.03	0.94
1:B:449:HIS:NE2	1:B:461:LEU:HG	1.82	0.94
2:F:272:ASN:C	2:F:275:LEU:CD1	2.39	0.94
2:D:154:TRP:CZ2	2:D:158:HIS:ND1	2.36	0.93
2:D:209:PHE:CE1	2:D:254:ILE:CG2	2.51	0.93
1:B:395:ARG:NH1	1:B:396:HIS:CD2	2.35	0.93
1:A:592:ARG:NH2	2:C:184:ARG:CZ	2.27	0.93
2:D:329:TRP:CD1	2:D:424:ILE:HD12	2.04	0.93
1:B:389:GLU:O	1:B:390:THR:HG22	1.68	0.93
2:C:138:LEU:HD23	2:D:94:ARG:NH1	1.83	0.93
1:B:388:LEU:HA	1:B:421:VAL:O	1.67	0.93
1:A:365:ILE:HG22	1:A:397:LEU:HD23	0.95	0.93
1:A:395:ARG:NH1	1:A:396:HIS:HB2	1.83	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:23:TYR:CZ	2:C:156:TYR:HB2	2.02	0.93
2:D:358:LYS:HB3	2:D:490:ARG:NE	1.82	0.93
1:A:100:VAL:HG12	3:A:704:HOH:O	1.68	0.93
2:C:133:THR:HG23	2:D:93:ILE:CG2	1.98	0.93
2:C:307:ARG:O	2:C:311:THR:OG1	1.85	0.93
1:B:115:ARG:HB2	1:B:115:ARG:NH2	1.84	0.93
2:D:312:GLN:OE1	2:D:427:TYR:CD2	2.21	0.93
1:A:467:LEU:CD2	1:A:556:VAL:HG22	1.99	0.93
1:A:589:PRO:HD2	1:A:596:TRP:CZ3	2.03	0.93
1:B:588:LEU:H	1:B:588:LEU:HD12	1.31	0.93
1:E:100:VAL:HG12	1:E:101:LYS:HG2	1.49	0.93
1:A:366:LYS:HE2	1:A:395:ARG:HH22	0.77	0.93
2:D:122:PRO:HB2	2:D:125:PHE:HD2	1.30	0.93
1:E:289:TYR:HB3	1:E:317:PHE:CD2	2.04	0.93
1:E:610:ARG:HD2	2:F:167:ASP:HB2	1.49	0.93
1:A:471:TYR:HD1	1:A:552:MET:HG3	1.30	0.93
2:C:359:LEU:O	2:C:363:ASN:ND2	2.02	0.93
1:A:99:VAL:HB	1:A:113:ALA:HA	1.48	0.93
1:E:610:ARG:HG2	1:E:610:ARG:HH11	1.34	0.93
2:C:312:GLN:OE1	2:C:323:LYS:CD	2.17	0.92
2:D:23:TYR:HE2	2:D:156:TYR:HB2	1.35	0.92
1:B:247:GLY:O	1:B:250:SER:OG	1.85	0.92
1:E:289:TYR:CB	1:E:317:PHE:HE2	1.80	0.92
1:A:365:ILE:HD12	1:A:366:LYS:H	1.31	0.92
2:D:84:ILE:HD11	2:D:88:TYR:HE2	0.79	0.92
2:D:209:PHE:CZ	2:D:254:ILE:CG2	2.52	0.92
1:B:541:LEU:HD12	1:B:542:ILE:H	1.33	0.92
1:E:467:LEU:CD1	2:F:488:TRP:HB3	1.98	0.92
1:A:126:GLN:HE22	1:A:257:ARG:NH1	1.67	0.92
1:B:310:HIS:HD2	1:B:314:GLY:HA3	1.24	0.92
1:B:449:HIS:HE2	1:B:461:LEU:HG	1.32	0.92
2:F:131:TRP:NE1	2:F:139:PRO:HG3	1.83	0.92
1:A:96:ARG:NH2	1:A:171:ASN:OD1	2.02	0.92
2:D:358:LYS:O	2:D:362:GLU:N	2.01	0.92
1:B:471:TYR:CE1	1:B:550:GLN:O	2.21	0.92
1:E:612:LYS:HD2	2:F:164:GLU:OE2	1.69	0.92
1:A:365:ILE:CA	1:A:397:LEU:HD21	1.89	0.92
1:A:368:PHE:HE1	2:D:146:TRP:CD1	1.86	0.92
1:A:538:THR:OG1	1:A:560:HIS:CD2	2.22	0.92
1:E:175:LEU:HD22	1:E:189:TRP:HE1	1.30	0.92
2:F:126:VAL:O	2:F:129:ARG:HG3	1.69	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:LEU:O	1:A:294:SER:HB3	1.67	0.92
2:D:278:PHE:CD1	2:D:279:PHE:CD2	2.58	0.92
1:B:268:ARG:NH1	1:B:305:ILE:HD12	1.84	0.92
1:B:327:SER:HB2	1:B:332:ASP:OD2	1.69	0.92
1:E:169:ASN:OD1	1:E:203:THR:HG21	1.67	0.92
1:E:615:HIS:ND1	1:E:615:HIS:O	2.03	0.92
1:E:615:HIS:CE1	2:F:102:PRO:HG3	2.05	0.92
2:F:126:VAL:HG13	2:F:129:ARG:HD3	1.52	0.92
2:F:131:TRP:HE1	2:F:139:PRO:HG3	1.31	0.92
2:D:418:ARG:HB2	2:D:419:PHE:CD2	2.04	0.91
2:D:423:GLU:CA	2:D:426:LEU:HG	1.99	0.91
1:E:383:THR:HB	1:E:384:HIS:HD2	1.34	0.91
1:A:98:GLN:HE21	1:A:115:ARG:CB	1.73	0.91
2:D:23:TYR:CE2	2:D:156:TYR:CB	2.52	0.91
1:A:250:SER:O	1:A:423:ALA:O	1.87	0.91
1:A:369:GLY:HA2	1:A:372:ILE:CG2	2.00	0.91
1:A:469:ILE:HD11	2:C:488:TRP:CH2	2.02	0.91
1:B:546:ASP:HB3	1:B:549:GLN:HG3	1.52	0.91
1:E:301:LEU:HD12	1:E:301:LEU:H	1.31	0.91
1:B:297:LEU:HB2	1:B:344:LEU:HD11	0.94	0.91
1:E:182:TYR:CE1	1:E:184:ASP:CB	2.52	0.91
1:E:83:LEU:HD23	1:E:83:LEU:H	1.31	0.91
1:A:207:LEU:HD12	1:A:213:ILE:HG12	1.50	0.91
2:D:122:PRO:HB2	2:D:125:PHE:CD2	2.06	0.91
1:B:611:LYS:HB2	1:B:614:GLU:CD	1.95	0.91
1:A:196:PHE:HB3	1:A:205:HIS:HE1	1.33	0.91
1:B:591:PRO:O	1:B:592:ARG:HB3	1.69	0.91
1:A:451:ILE:HG22	1:A:452:THR:HG23	1.51	0.91
1:A:464:SER:O	2:C:494:TRP:HZ3	1.36	0.91
2:C:95:PHE:O	2:C:99:LEU:CD2	2.19	0.91
1:B:357:SER:C	1:B:358:LEU:HD13	1.96	0.91
2:C:97:ASN:ND2	2:C:129:ARG:HD3	1.85	0.91
2:D:54:HIS:CD2	2:D:98:GLY:HA3	2.05	0.91
1:E:109:VAL:HG23	1:E:111:TYR:HE1	1.06	0.91
1:E:310:HIS:CD2	1:E:314:GLY:HA3	2.04	0.91
2:C:383:LYS:NZ	2:C:405:GLU:OE1	2.04	0.91
2:D:487:ASN:ND2	2:D:488:TRP:N	2.18	0.91
1:B:239:ASP:CB	1:B:355:GLY:O	2.20	0.91
1:B:324:TYR:HB2	1:B:536:PHE:CE2	2.04	0.91
2:F:365:SER:CA	2:F:419:PHE:CE1	2.46	0.91
1:A:282:LEU:HD12	1:A:359:LEU:CD1	2.01	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:23:TYR:HD2	2:C:156:TYR:CD2	1.86	0.90
2:D:82:ILE:HG22	2:D:83:PRO:HD3	1.50	0.90
2:D:159:TYR:CZ	1:B:614:GLU:HG2	2.06	0.90
2:D:487:ASN:ND2	2:D:488:TRP:H	1.69	0.90
1:B:450:LYS:HD3	1:B:456:TYR:HH	1.19	0.90
1:E:121:TRP:HB2	1:E:309:GLN:O	1.69	0.90
1:E:222:TRP:HE1	1:E:422:PRO:C	1.79	0.90
1:A:365:ILE:O	1:A:396:HIS:CE1	2.25	0.90
1:A:368:PHE:HE2	1:A:372:ILE:HB	1.34	0.90
1:A:245:ILE:HD11	1:A:363:GLY:HA2	1.53	0.90
1:B:321:LEU:HD13	1:B:347:HIS:HD1	1.36	0.90
1:E:71:TYR:CD1	1:E:80:PHE:CE2	2.59	0.90
1:E:118:LEU:CB	1:E:305:ILE:HB	2.01	0.90
2:F:152:LEU:HA	2:F:155:LEU:HD13	1.49	0.90
1:A:366:LYS:HG3	1:A:396:HIS:CG	1.95	0.90
1:E:389:GLU:HG2	1:E:394:LYS:HA	1.50	0.90
1:A:566:LYS:HA	1:A:566:LYS:NZ	1.86	0.90
1:A:589:PRO:HD2	1:A:596:TRP:HH2	0.93	0.90
2:C:10:ARG:HG2	2:C:10:ARG:HH11	1.36	0.90
2:D:96:VAL:O	2:D:100:LEU:N	2.05	0.90
2:D:418:ARG:HB2	2:D:419:PHE:CE2	2.06	0.90
1:A:96:ARG:C	1:A:168:PHE:HE1	1.80	0.90
1:A:604:PHE:HE2	2:C:10:ARG:HH12	1.18	0.90
1:B:397:LEU:HD12	1:B:400:LEU:CD1	2.01	0.90
2:D:358:LYS:O	2:D:362:GLU:HB2	1.71	0.90
1:E:245:ILE:CD1	1:E:373:LEU:HD13	2.01	0.90
1:A:398:ASP:OD2	1:A:399:GLU:N	2.05	0.90
2:C:85:ARG:CD	1:B:486:GLU:OE2	2.18	0.90
2:D:423:GLU:HA	2:D:426:LEU:CG	2.01	0.90
1:B:366:LYS:HG2	1:B:396:HIS:CG	2.06	0.90
1:A:126:GLN:HE22	1:A:257:ARG:NH2	1.70	0.90
2:D:44:TYR:O	2:D:48:GLY:N	2.04	0.90
2:D:312:GLN:OE1	2:D:427:TYR:HD2	1.55	0.90
1:B:219:PRO:HB2	1:B:221:TYR:CD2	2.06	0.90
1:E:96:ARG:HG2	1:E:168:PHE:CD2	2.04	0.90
1:A:325:ALA:O	1:A:578:ASN:ND2	2.05	0.89
2:C:304:TRP:CE2	2:C:308:ASN:ND2	2.39	0.89
2:C:362:GLU:HG3	2:C:490:ARG:HG2	1.53	0.89
2:D:120:GLY:O	2:D:158:HIS:CE1	2.25	0.89
1:B:197:PRO:O	1:B:197:PRO:CD	2.09	0.89
1:B:219:PRO:CB	1:B:221:TYR:CD2	2.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:359:LEU:HD23	2:F:360:ILE:N	1.85	0.89
1:B:246:GLY:O	1:B:363:GLY:CA	2.19	0.89
1:E:98:GLN:HG3	1:E:117:ILE:CG2	2.01	0.89
2:F:152:LEU:HA	2:F:155:LEU:HD11	1.51	0.89
1:A:282:LEU:O	1:A:337:TYR:OH	1.90	0.89
1:A:365:ILE:CB	1:A:397:LEU:HD22	2.02	0.89
1:A:615:HIS:CD2	2:C:102:PRO:HG2	2.07	0.89
2:D:156:TYR:HA	2:D:160:TRP:HD1	1.36	0.89
2:D:349:PHE:HE2	2:D:356:TRP:CD2	1.89	0.89
1:B:246:GLY:O	1:B:363:GLY:HA3	1.73	0.89
1:E:364:TRP:CB	1:E:369:GLY:HA3	2.01	0.89
1:A:170:SER:OG	1:A:172:HIS:ND1	2.05	0.89
2:C:133:THR:CG2	2:D:93:ILE:CG2	2.51	0.89
2:D:77:VAL:CG1	2:D:84:ILE:HB	1.99	0.89
1:B:174:GLY:C	1:B:458:PHE:HE2	1.81	0.89
1:B:175:LEU:HD13	1:B:456:TYR:CD2	2.07	0.89
1:A:381:LYS:CB	1:A:409:SER:CB	2.50	0.89
2:D:154:TRP:CZ3	2:D:155:LEU:HD23	2.08	0.89
2:F:20:LEU:O	2:F:23:TYR:O	1.89	0.89
1:A:475:LYS:CB	1:A:478:ILE:O	2.20	0.89
1:A:592:ARG:CD	2:C:184:ARG:HE	1.85	0.89
1:A:615:HIS:HD2	2:C:102:PRO:HG3	1.30	0.89
2:C:209:PHE:HE2	2:C:254:ILE:HG23	1.36	0.89
1:B:259:LEU:O	1:B:263:PHE:CD1	2.26	0.89
1:E:491:ASN:ND2	2:F:39:GLN:HB3	1.88	0.89
2:C:138:LEU:HD21	2:D:94:ARG:CD	2.02	0.89
1:B:177:GLU:CG	1:B:458:PHE:CD2	2.30	0.89
1:B:365:ILE:HD12	1:B:366:LYS:N	1.88	0.89
1:A:465:ALA:HA	2:C:494:TRP:CE3	2.07	0.89
2:D:69:ASP:O	2:D:77:VAL:HG23	1.72	0.89
1:E:449:HIS:HB3	1:E:457:ASP:O	1.72	0.89
1:A:477:GLY:O	1:A:573:TRP:HB2	1.73	0.89
2:D:69:ASP:CG	2:D:88:TYR:OH	2.16	0.89
1:E:241:ARG:HD3	1:E:381:LYS:O	1.72	0.89
2:F:131:TRP:HE1	2:F:139:PRO:CB	1.86	0.89
2:F:155:LEU:HD12	2:F:155:LEU:H	1.37	0.89
2:F:272:ASN:CA	2:F:275:LEU:HD11	1.89	0.89
1:A:222:TRP:O	1:A:225:PRO:HD2	1.73	0.88
1:B:80:PHE:HE1	1:B:165:LEU:C	1.80	0.88
1:A:181:LEU:HD13	1:A:585:CYS:HG	1.33	0.88
2:C:291:MET:CE	2:C:340:ILE:CG2	2.50	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4:PRO:CD	1:B:607:PHE:HE1	1.87	0.88
2:D:23:TYR:HE2	2:D:156:TYR:CD2	1.89	0.88
1:B:233:HIS:CE1	1:B:275:GLU:OE1	2.27	0.88
1:B:247:GLY:CA	1:B:365:ILE:HG23	2.03	0.88
1:E:77:GLU:OE2	1:E:169:ASN:ND2	2.05	0.88
1:B:366:LYS:HB3	1:B:395:ARG:HH11	1.38	0.88
1:E:383:THR:HB	1:E:384:HIS:CD2	2.08	0.88
2:C:95:PHE:O	2:C:99:LEU:HD21	1.73	0.88
2:C:100:LEU:HG	2:C:101:ASP:OD1	1.74	0.88
1:B:92:SER:HB2	1:B:207:LEU:HD11	1.52	0.88
1:B:366:LYS:CG	1:B:396:HIS:CG	2.57	0.88
2:F:389:TRP:NE1	2:F:390:ARG:HD2	1.89	0.88
1:A:614:GLU:OE2	2:C:159:TYR:OH	1.91	0.88
2:D:69:ASP:O	2:D:77:VAL:HG21	1.69	0.88
1:B:90:HIS:HE1	1:B:128:ILE:CD1	1.81	0.88
1:E:529:CYS:O	1:E:530:THR:OG1	1.92	0.88
2:C:310:ARG:NE	2:C:314:ASP:OD2	2.06	0.88
1:E:172:HIS:HA	1:E:454:PHE:O	1.74	0.88
1:E:194:PRO:HB2	1:E:205:HIS:CE1	2.09	0.88
1:E:245:ILE:CD1	1:E:373:LEU:CD1	2.52	0.88
1:E:592:ARG:HH21	1:E:592:ARG:HG3	1.39	0.88
1:A:77:GLU:O	1:A:204:TYR:OH	1.91	0.88
1:A:84:LYS:CA	1:A:139:TRP:HB3	2.04	0.88
1:A:357:SER:HG	1:A:380:TYR:HH	1.08	0.88
1:B:180:HIS:HB3	1:B:592:ARG:HH12	1.39	0.88
1:B:589:PRO:CG	1:B:596:TRP:CH2	2.57	0.88
1:A:504:ILE:CD1	1:A:575:ILE:HG23	1.79	0.88
2:D:77:VAL:HG11	2:D:84:ILE:HG12	0.90	0.88
1:A:98:GLN:HE22	1:A:115:ARG:CG	1.64	0.87
1:A:589:PRO:CG	1:A:596:TRP:CH2	2.57	0.87
1:A:369:GLY:HA2	1:A:372:ILE:HG22	1.53	0.87
1:B:90:HIS:ND1	1:B:128:ILE:CD1	2.37	0.87
2:F:128:LEU:HA	2:F:131:TRP:CE3	2.09	0.87
1:B:99:VAL:HG21	1:B:166:ARG:NH2	1.87	0.87
1:B:306:SER:C	1:B:307:LEU:HD23	1.98	0.87
1:B:504:ILE:CD1	1:B:575:ILE:CG2	2.43	0.87
1:E:246:GLY:O	1:E:363:GLY:HA3	1.71	0.87
1:A:273:SER:HB3	1:A:275:GLU:OE1	1.74	0.87
1:B:178:ALA:N	1:B:458:PHE:CD2	2.43	0.87
1:E:213:ILE:CD1	1:E:215:SER:HB3	2.05	0.87
1:A:126:GLN:HE22	1:A:257:ARG:CZ	1.86	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:GLY:O	1:A:478:ILE:HD13	1.74	0.87
1:A:592:ARG:HH22	2:C:184:ARG:NH2	1.68	0.87
2:C:86:LEU:HD23	2:C:138:LEU:HD13	1.55	0.87
1:B:504:ILE:HD12	1:B:575:ILE:HG21	0.87	0.87
1:B:545:ILE:CD1	1:B:552:MET:HE3	2.05	0.87
1:E:123:PRO:HG3	1:E:309:GLN:HG2	1.55	0.87
1:A:282:LEU:HD11	1:A:359:LEU:HD22	1.55	0.87
1:A:491:ASN:HD21	2:C:36:ARG:CZ	1.87	0.87
1:A:541:LEU:HD12	1:A:542:ILE:N	1.90	0.87
2:C:362:GLU:CG	2:C:490:ARG:HG2	2.04	0.87
1:E:96:ARG:CD	1:E:168:PHE:CE2	2.57	0.87
1:A:401:THR:O	1:A:405:SER:N	2.06	0.87
1:B:80:PHE:HZ	1:B:165:LEU:HA	1.31	0.87
1:E:128:ILE:O	1:E:215:SER:HB2	1.74	0.87
1:E:232:SER:O	1:E:236:ALA:CB	2.23	0.87
2:F:17:GLU:OE2	2:F:21:TRP:CZ2	2.27	0.87
1:A:388:LEU:HA	1:A:421:VAL:CG2	2.05	0.87
2:D:279:PHE:HE1	2:D:304:TRP:HZ3	1.23	0.87
1:B:571:ALA:O	1:B:573:TRP:NE1	2.07	0.87
1:E:504:ILE:O	1:E:540:GLY:N	2.08	0.87
1:E:590:SER:OG	1:E:592:ARG:NH2	2.08	0.87
1:A:99:VAL:O	1:A:113:ALA:O	1.92	0.86
1:A:615:HIS:HD2	2:C:102:PRO:HG2	1.37	0.86
1:B:469:ILE:CD1	1:B:554:ILE:HG21	2.00	0.86
1:B:589:PRO:HD2	1:B:596:TRP:CZ2	2.09	0.86
2:C:136:ARG:CG	1:B:617:TRP:HB3	2.05	0.86
1:A:96:ARG:CG	1:A:168:PHE:CE1	2.57	0.86
1:A:282:LEU:HD12	1:A:359:LEU:HD13	1.56	0.86
1:B:366:LYS:HD3	1:B:395:ARG:NE	1.90	0.86
1:B:369:GLY:CA	1:B:372:ILE:HG22	2.05	0.86
1:E:103:GLY:CA	1:E:134:SER:O	2.23	0.86
1:A:105:VAL:CG1	1:A:132:ASP:HB2	2.06	0.86
1:B:172:HIS:CA	1:B:454:PHE:O	2.24	0.86
1:B:369:GLY:HA2	1:B:372:ILE:CG2	2.05	0.86
1:A:348:LEU:CD1	1:A:353:PHE:HB3	2.06	0.86
2:C:96:VAL:HG11	2:C:128:LEU:HD11	1.57	0.86
2:C:110:ILE:HG22	2:C:114:THR:HB	1.57	0.86
1:B:91:LEU:HD11	1:B:204:TYR:HB2	1.56	0.86
1:B:364:TRP:HB3	1:B:369:GLY:CA	2.04	0.86
1:E:365:ILE:O	1:E:396:HIS:CB	2.23	0.86
2:F:151:ALA:C	2:F:155:LEU:HD11	2.00	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:SER:OG	1:A:296:SER:HB3	1.74	0.86
1:A:390:THR:OG1	1:A:421:VAL:O	1.93	0.86
2:D:184:ARG:HB3	1:B:592:ARG:HD3	1.56	0.86
1:E:118:LEU:HD23	1:E:118:LEU:H	1.40	0.86
2:F:128:LEU:HB2	2:F:131:TRP:HZ3	1.32	0.86
1:A:216:LEU:HD23	1:A:217:SER:N	1.91	0.86
1:A:471:TYR:HA	1:A:478:ILE:HB	1.57	0.86
1:A:492:PRO:HA	1:A:495:ILE:HD11	1.56	0.86
1:B:105:VAL:CG2	1:B:134:SER:OG	2.23	0.86
1:E:85:GLU:O	1:E:133:PHE:HD1	1.57	0.86
1:E:469:ILE:CG2	1:E:478:ILE:HD12	1.89	0.86
1:E:614:GLU:OE2	2:F:159:TYR:HE1	1.27	0.86
1:A:73:GLY:HA3	1:A:78:THR:HG23	1.58	0.86
1:A:187:TYR:CE2	1:A:192:LYS:CB	2.59	0.86
1:A:226:LEU:HD11	1:A:230:TYR:HH	0.96	0.86
1:A:383:THR:HB	1:A:384:HIS:ND1	1.91	0.86
1:A:75:GLU:CA	2:C:259:ARG:HH21	1.88	0.85
1:B:90:HIS:ND1	1:B:128:ILE:HD11	1.90	0.85
1:B:105:VAL:HA	1:B:109:VAL:O	1.75	0.85
2:F:58:SER:OG	2:F:62:ILE:HD11	1.75	0.85
2:F:163:GLU:O	2:F:165:LEU:HD22	1.76	0.85
2:C:307:ARG:HH11	2:C:307:ARG:CB	1.88	0.85
1:B:364:TRP:CB	1:B:369:GLY:HA3	2.04	0.85
2:C:54:HIS:CD2	2:C:98:GLY:HA3	2.10	0.85
2:F:152:LEU:CA	2:F:155:LEU:HD11	2.03	0.85
1:A:105:VAL:HB	1:A:132:ASP:HB2	0.85	0.85
1:A:124:LEU:HB2	1:A:188:LEU:O	1.76	0.85
2:C:93:ILE:O	2:C:97:ASN:HB2	1.76	0.85
2:C:358:LYS:CB	2:C:490:ARG:NH1	2.40	0.85
2:D:96:VAL:C	2:D:100:LEU:HB2	2.01	0.85
1:B:338:LEU:HD21	1:B:372:ILE:HD12	1.57	0.85
1:A:331:GLN:HG2	1:A:364:TRP:HZ2	1.28	0.85
2:D:99:LEU:HD12	2:D:99:LEU:H	1.41	0.85
2:D:487:ASN:HD21	2:D:488:TRP:CD1	1.95	0.85
1:B:321:LEU:O	1:B:321:LEU:HD23	1.77	0.85
1:B:387:PHE:CZ	1:B:401:THR:HG23	2.11	0.85
1:B:589:PRO:HD2	1:B:596:TRP:HH2	1.30	0.85
1:E:487:PHE:CE2	2:F:46:LEU:HA	2.12	0.85
2:F:337:LEU:HD22	2:F:370:TYR:CD1	2.09	0.85
1:A:488:GLN:HE22	1:A:527:GLN:NE2	1.75	0.85
1:B:450:LYS:HD3	1:B:456:TYR:OH	1.03	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:545:ILE:HD11	1:B:552:MET:HE3	1.59	0.85
1:E:245:ILE:HD11	1:E:373:LEU:CD1	2.04	0.85
1:E:349:GLU:OE2	1:E:381:LYS:NZ	2.08	0.85
2:C:82:ILE:CG2	2:D:64:CYS:SG	2.64	0.85
2:D:202:TRP:HZ3	2:D:209:PHE:CE1	1.95	0.85
2:D:288:LYS:HG3	2:D:343:ASN:ND2	1.92	0.85
2:F:389:TRP:HE1	2:F:390:ARG:HD2	1.40	0.85
1:E:469:ILE:HG21	1:E:478:ILE:CG1	2.07	0.85
2:D:68:LEU:O	2:D:71:LYS:HG3	1.76	0.85
1:B:327:SER:OG	1:B:332:ASP:OD2	1.93	0.85
1:E:267:ILE:HD11	1:E:302:SER:HB3	1.58	0.85
2:F:25:LYS:HE2	2:F:25:LYS:O	1.76	0.85
1:A:226:LEU:HD11	1:A:230:TYR:CE1	2.08	0.85
1:B:261:GLU:HA	1:B:264:THR:OG1	1.77	0.85
1:E:493:GLN:NE2	2:F:36:ARG:NH2	2.23	0.85
1:A:365:ILE:O	1:A:396:HIS:ND1	1.98	0.84
2:C:125:PHE:O	2:C:128:LEU:HG	1.77	0.84
2:D:159:TYR:HE1	1:B:614:GLU:HG3	1.40	0.84
1:B:207:LEU:HD13	1:B:213:ILE:HD13	1.59	0.84
2:F:312:GLN:NE2	2:F:323:LYS:CD	2.33	0.84
1:A:126:GLN:NE2	1:A:257:ARG:HH12	1.74	0.84
2:C:125:PHE:O	2:C:128:LEU:N	2.09	0.84
2:D:207:ASN:O	2:D:211:GLU:HG3	1.78	0.84
2:D:323:LYS:CG	2:D:427:TYR:HE2	1.90	0.84
1:B:90:HIS:HE1	1:B:128:ILE:CG1	1.90	0.84
1:B:400:LEU:HD23	1:B:401:THR:N	1.92	0.84
1:B:425:SER:HA	1:B:426:LEU:C	2.03	0.84
2:F:17:GLU:OE2	2:F:21:TRP:HH2	1.60	0.84
1:A:366:LYS:CG	1:A:396:HIS:CB	2.53	0.84
1:A:481:ILE:HG22	1:A:575:ILE:HB	1.59	0.84
1:A:282:LEU:HA	1:A:295:ILE:HG23	1.59	0.84
1:A:331:GLN:HE21	1:A:364:TRP:NE1	1.76	0.84
1:A:545:ILE:HG12	1:A:552:MET:HG2	1.60	0.84
2:C:68:LEU:O	2:C:68:LEU:HD12	1.78	0.84
2:D:46:LEU:CD2	1:B:577:ARG:HD3	2.07	0.84
2:D:79:GLN:NE2	2:D:79:GLN:HA	1.92	0.84
2:F:152:LEU:O	2:F:155:LEU:HD13	1.77	0.84
2:C:32:ASP:OD1	2:C:34:ARG:CZ	2.25	0.84
2:D:146:TRP:CH2	2:D:150:GLU:CB	2.59	0.84
2:F:52:LEU:HD21	2:F:57:ASP:CB	2.07	0.84
2:F:283:ASP:OD1	2:F:285:LEU:N	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:302:ILE:HD11	2:F:340:ILE:HG21	1.58	0.84
2:D:5:ARG:HD3	1:B:610:ARG:NE	1.91	0.84
2:D:71:LYS:NZ	2:D:71:LYS:HB3	1.91	0.84
1:B:365:ILE:O	1:B:396:HIS:ND1	2.11	0.84
1:E:615:HIS:NE2	2:F:102:PRO:HG3	1.92	0.84
2:C:95:PHE:CE1	2:C:155:LEU:CD1	2.60	0.83
1:B:99:VAL:HG22	1:B:166:ARG:CZ	2.08	0.83
1:B:105:VAL:HG23	1:B:134:SER:HB2	1.60	0.83
1:B:357:SER:O	1:B:358:LEU:HD13	1.78	0.83
2:C:278:PHE:HZ	2:C:287:LEU:HD13	1.44	0.83
2:D:121:LEU:HD12	2:D:122:PRO:CD	2.08	0.83
2:D:156:TYR:HA	2:D:160:TRP:CD1	2.13	0.83
2:D:312:GLN:NE2	2:D:323:LYS:CG	2.09	0.83
1:B:448:PHE:HB3	1:B:461:LEU:CD2	2.07	0.83
2:F:350:LYS:HZ1	2:F:401:THR:CA	1.90	0.83
2:F:372:CYS:C	2:F:412:ILE:HD11	2.01	0.83
1:A:364:TRP:CD1	1:A:369:GLY:CA	2.61	0.83
1:A:471:TYR:CD1	1:A:552:MET:HG3	2.13	0.83
1:B:99:VAL:CG1	1:B:166:ARG:HH21	1.91	0.83
2:F:350:LYS:HZ1	2:F:401:THR:HA	1.44	0.83
1:A:216:LEU:HD13	1:A:425:SER:OG	1.79	0.83
2:D:146:TRP:O	2:D:146:TRP:HE3	1.61	0.83
2:D:188:LEU:HD12	2:D:188:LEU:O	1.77	0.83
2:D:487:ASN:CG	2:D:488:TRP:N	2.34	0.83
1:B:615:HIS:ND1	1:B:615:HIS:O	2.11	0.83
1:E:369:GLY:O	1:E:373:LEU:HG	1.77	0.83
2:F:98:GLY:O	2:F:102:PRO:CG	2.27	0.83
1:A:388:LEU:O	1:A:423:ALA:CA	2.26	0.83
2:D:358:LYS:HD3	2:D:490:ARG:NH2	1.92	0.83
2:C:278:PHE:CZ	2:C:287:LEU:CD1	2.62	0.83
1:E:71:TYR:CE1	1:E:80:PHE:CE2	2.66	0.83
1:A:381:LYS:HB3	1:A:409:SER:CB	2.09	0.83
1:A:460:PRO:HB2	1:A:594:ILE:HD11	1.61	0.83
2:D:4:PRO:CG	1:B:607:PHE:CE1	2.57	0.83
1:E:491:ASN:ND2	2:F:36:ARG:HE	1.74	0.83
2:C:125:PHE:HD1	2:C:128:LEU:CD2	1.92	0.83
2:D:53:PRO:HB3	1:B:614:GLU:O	1.77	0.83
2:D:278:PHE:HD1	2:D:279:PHE:CD2	1.94	0.83
2:F:350:LYS:HZ2	2:F:401:THR:HG22	1.07	0.83
1:A:181:LEU:HD13	1:A:181:LEU:O	1.78	0.83
2:C:54:HIS:NE2	2:C:98:GLY:CA	2.36	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:86:LEU:HD12	2:D:138:LEU:CD2	2.09	0.83
2:D:336:LEU:HD12	2:D:340:ILE:HG13	1.61	0.83
2:C:217:GLU:HB3	2:C:218:ASN:OD1	1.79	0.82
1:B:284:PRO:O	1:B:287:PRO:HD3	1.79	0.82
1:E:118:LEU:HD12	1:E:305:ILE:HG21	1.58	0.82
1:A:451:ILE:HG22	1:A:452:THR:CG2	2.08	0.82
1:A:504:ILE:CD1	1:A:575:ILE:HG22	1.81	0.82
2:F:85:ARG:HB3	2:F:138:LEU:HD22	1.59	0.82
2:F:131:TRP:NE1	2:F:139:PRO:HB3	1.93	0.82
2:C:62:ILE:HG21	2:C:152:LEU:HD21	1.60	0.82
1:B:247:GLY:H	1:B:365:ILE:CG2	1.91	0.82
1:E:471:TYR:OH	1:E:523:PHE:CE1	2.32	0.82
2:F:312:GLN:HE22	2:F:323:LYS:HD2	1.39	0.82
2:F:492:GLN:NE2	2:F:492:GLN:H	1.78	0.82
1:A:249:ASN:O	1:A:249:ASN:ND2	2.13	0.82
2:C:59:THR:OG1	2:C:155:LEU:HD22	1.78	0.82
2:C:75:LEU:HD23	2:C:76:GLY:O	1.78	0.82
2:D:356:TRP:O	2:D:360:ILE:CG1	2.26	0.82
2:C:96:VAL:HG21	2:C:128:LEU:CD2	2.07	0.82
1:E:360:ASN:ND2	1:E:360:ASN:O	2.12	0.82
1:E:487:PHE:HE2	2:F:46:LEU:HA	1.44	0.82
1:E:537:ILE:HD12	1:E:573:TRP:HZ3	1.42	0.82
1:A:270:SER:HB2	1:A:273:SER:OG	1.79	0.82
2:C:78:HIS:HB2	2:D:35:GLN:HE22	1.41	0.82
2:C:276:GLU:O	2:C:280:ASN:ND2	2.12	0.82
2:D:52:LEU:O	1:B:616:VAL:HG13	1.77	0.82
1:B:331:GLN:O	1:B:334:PRO:HD3	1.80	0.82
1:B:467:LEU:O	1:B:467:LEU:HD23	1.79	0.82
1:B:473:LYS:HE2	1:B:474:GLY:H	1.42	0.82
1:E:89:LEU:HB3	1:E:131:ILE:HB	1.62	0.82
2:F:55:VAL:HG21	2:F:159:TYR:CG	2.15	0.82
2:C:156:TYR:HA	2:C:160:TRP:HB2	1.61	0.82
2:D:279:PHE:CD1	2:D:304:TRP:CH2	2.67	0.82
1:B:210:SER:O	1:B:212:ARG:HD3	1.80	0.82
1:B:517:VAL:HG12	1:B:526:LEU:HD12	1.61	0.82
2:F:152:LEU:O	2:F:155:LEU:CD1	2.27	0.82
1:A:388:LEU:CA	1:A:421:VAL:HG23	2.08	0.82
1:A:608:GLU:N	1:A:608:GLU:OE2	2.13	0.82
2:C:291:MET:HE1	2:C:340:ILE:CG2	2.06	0.82
1:E:519:SER:C	1:E:520:LEU:HD23	2.04	0.82
2:D:352:LYS:O	2:D:355:ASN:HB2	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:PRO:HB2	1:B:221:TYR:HD2	1.42	0.82
1:B:288:GLU:HG2	1:B:289:TYR:HE2	1.42	0.82
1:B:390:THR:HG23	1:B:391:ALA:N	1.91	0.82
1:E:310:HIS:HB2	1:E:314:GLY:N	1.94	0.82
2:F:80:ASP:O	2:F:83:PRO:HD2	1.80	0.82
2:C:357:GLU:O	2:C:361:ASP:N	2.13	0.81
2:D:358:LYS:O	2:D:362:GLU:CB	2.27	0.81
1:B:400:LEU:HD23	1:B:401:THR:H	1.43	0.81
1:A:69:ILE:HG21	1:A:80:PHE:HB3	1.62	0.81
2:C:61:GLN:OE1	2:D:138:LEU:HD11	1.80	0.81
2:C:125:PHE:CA	2:C:128:LEU:HD23	2.10	0.81
2:D:54:HIS:CD2	2:D:99:LEU:HD12	2.15	0.81
1:E:188:LEU:HD11	1:E:434:PHE:CE1	2.14	0.81
2:F:111:PRO:HG2	2:F:114:THR:CB	2.10	0.81
1:A:491:ASN:ND2	2:C:36:ARG:NE	2.28	0.81
2:C:96:VAL:CB	2:C:128:LEU:HD11	2.09	0.81
2:D:199:LEU:CD1	2:D:281:ASN:OD1	2.29	0.81
1:E:467:LEU:HD11	2:F:488:TRP:HB3	1.61	0.81
2:F:54:HIS:CE1	2:F:58:SER:HB2	2.14	0.81
2:F:74:CYS:HB3	2:F:75:LEU:CB	2.10	0.81
1:A:79:MET:SD	1:A:80:PHE:N	2.54	0.81
1:A:507:TYR:CD1	1:A:535:ASN:C	2.51	0.81
1:A:607:PHE:CE1	2:C:4:PRO:HA	2.15	0.81
2:C:393:LYS:HE2	2:C:393:LYS:HA	1.62	0.81
1:B:241:ARG:C	1:B:242:ILE:HD12	2.05	0.81
2:C:59:THR:OG1	2:C:155:LEU:CD2	2.28	0.81
1:A:226:LEU:HD12	1:A:226:LEU:O	1.80	0.81
2:C:23:TYR:CE2	2:C:156:TYR:CB	2.63	0.81
2:D:98:GLY:O	2:D:102:PRO:CD	2.26	0.81
2:D:131:TRP:HA	2:D:131:TRP:CE3	2.16	0.81
2:F:362:GLU:C	2:F:363:ASN:HD22	1.88	0.81
1:A:381:LYS:HA	1:A:409:SER:CB	2.11	0.81
2:C:97:ASN:ND2	2:C:129:ARG:NE	2.28	0.81
2:C:133:THR:HG23	2:D:93:ILE:HG21	1.61	0.81
2:F:88:TYR:CB	2:F:144:LEU:CD2	2.58	0.81
2:C:101:ASP:HA	2:C:105:GLN:HG2	1.63	0.81
2:C:136:ARG:HA	1:B:617:TRP:CD2	2.15	0.81
1:B:90:HIS:HE1	1:B:213:ILE:HD11	1.44	0.81
1:B:172:HIS:HD2	1:B:454:PHE:HA	0.78	0.81
1:B:309:GLN:OE1	1:B:310:HIS:N	2.13	0.81
1:B:364:TRP:CD1	1:B:372:ILE:HG21	2.16	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:136:ARG:HG3	1:B:617:TRP:CB	2.10	0.81
2:C:352:LYS:HB3	2:C:355:ASN:HD22	1.44	0.81
2:D:336:LEU:HD12	2:D:336:LEU:O	1.81	0.81
1:B:397:LEU:HG	1:B:400:LEU:CD2	2.01	0.81
1:E:537:ILE:HD12	1:E:573:TRP:CZ3	2.14	0.81
1:A:488:GLN:NE2	1:A:527:GLN:CD	2.38	0.81
1:B:337:TYR:OH	1:B:362:PRO:HG2	1.81	0.81
1:E:385:LEU:H	1:E:417:GLU:HB3	1.44	0.81
2:C:234:LEU:O	2:C:235:VAL:CG2	2.29	0.80
1:B:96:ARG:HH22	1:B:171:ASN:HD21	1.26	0.80
2:F:372:CYS:O	2:F:412:ILE:HD11	1.80	0.80
1:A:256:LEU:HD12	1:A:279:TYR:OH	1.82	0.80
1:A:306:SER:OG	1:A:316:ASN:ND2	2.14	0.80
2:C:182:TYR:CE1	2:F:183:ARG:HG3	2.17	0.80
1:B:488:GLN:NE2	1:B:488:GLN:HA	1.95	0.80
2:F:350:LYS:NZ	2:F:401:THR:CA	2.44	0.80
2:F:353:TRP:NE1	2:F:357:GLU:OE2	2.13	0.80
1:A:99:VAL:HG21	1:A:104:ILE:CD1	2.11	0.80
2:C:64:CYS:SG	2:D:82:ILE:CG2	2.64	0.80
2:C:353:TRP:HH2	2:C:408:LEU:CD2	1.94	0.80
2:D:323:LYS:HG3	2:D:427:TYR:HE2	1.45	0.80
1:A:280:LEU:CD1	1:A:297:LEU:HD12	2.10	0.80
2:C:96:VAL:CG1	2:C:128:LEU:HD11	2.12	0.80
1:B:123:PRO:HG3	1:B:309:GLN:HG3	1.61	0.80
2:F:125:PHE:HA	2:F:128:LEU:HD23	1.64	0.80
2:D:4:PRO:CA	1:B:607:PHE:HE1	1.90	0.80
1:B:79:MET:O	1:B:167:VAL:CB	2.30	0.80
1:E:359:LEU:HD12	1:E:360:ASN:N	1.97	0.80
2:F:328:ALA:HB3	2:F:331:GLU:HG3	1.61	0.80
1:A:616:VAL:O	1:A:618:LYS:HG3	1.82	0.80
2:D:126:VAL:O	2:D:129:ARG:HG3	1.80	0.80
2:F:319:THR:HG21	2:F:433:GLU:H	1.47	0.80
1:A:290:SER:HG	1:A:296:SER:CB	1.92	0.80
2:D:349:PHE:HE2	2:D:356:TRP:CE2	1.99	0.80
2:D:96:VAL:HG13	2:D:100:LEU:CG	2.12	0.80
2:D:146:TRP:CZ2	2:D:150:GLU:OE1	2.35	0.80
1:B:79:MET:O	1:B:167:VAL:HG13	1.79	0.80
1:B:590:SER:O	1:B:593:THR:OG1	2.00	0.80
1:A:467:LEU:HD22	1:A:556:VAL:HG22	1.62	0.80
2:C:288:LYS:O	2:C:292:LEU:HG	1.82	0.80
2:D:86:LEU:CD1	2:D:138:LEU:CD2	2.60	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:359:LEU:HD12	1:B:360:ASN:N	1.97	0.80
2:F:55:VAL:HG21	2:F:159:TYR:HB3	1.62	0.80
2:F:128:LEU:HD12	2:F:128:LEU:O	1.82	0.80
1:A:372:ILE:HG23	1:A:373:LEU:CD2	2.11	0.80
2:D:122:PRO:HG2	2:D:125:PHE:CE2	2.16	0.80
1:B:90:HIS:CE1	1:B:213:ILE:CD1	2.62	0.80
1:B:544:SER:OG	1:B:553:ASN:OD1	1.99	0.80
1:E:118:LEU:CD1	1:E:305:ILE:CG2	2.58	0.80
1:E:549:GLN:HB2	1:E:551:ILE:HG23	1.62	0.80
1:E:589:PRO:CD	1:E:596:TRP:CH2	2.65	0.80
1:A:222:TRP:NE1	1:A:422:PRO:O	2.13	0.79
1:A:324:TYR:HH	1:A:580:THR:HG1	1.26	0.79
1:A:607:PHE:CD1	2:C:4:PRO:CA	2.66	0.79
2:D:350:LYS:NZ	2:D:401:THR:HG22	1.96	0.79
2:C:53:PRO:HD2	2:C:56:VAL:CG2	2.12	0.79
2:C:388:SER:O	2:C:391:ASN:ND2	2.16	0.79
2:F:54:HIS:HE1	2:F:58:SER:HB2	1.47	0.79
2:F:131:TRP:HE1	2:F:139:PRO:HD3	1.44	0.79
1:E:212:ARG:HH21	1:E:212:ARG:HG3	1.48	0.79
1:E:395:ARG:HH21	1:E:395:ARG:HG3	1.46	0.79
1:A:102:GLY:O	1:A:113:ALA:HB2	1.83	0.79
1:A:196:PHE:HB3	1:A:205:HIS:CE1	2.17	0.79
2:C:206:ARG:C	2:C:210:LEU:HD11	2.05	0.79
1:E:245:ILE:CD1	1:E:373:LEU:HD22	2.12	0.79
1:A:282:LEU:CD1	1:A:359:LEU:CD2	2.61	0.79
1:A:589:PRO:HD3	1:A:596:TRP:HH2	1.43	0.79
1:E:79:MET:O	1:E:166:ARG:O	2.00	0.79
1:A:105:VAL:HG12	1:A:132:ASP:OD2	1.82	0.79
1:A:327:SER:OG	1:A:329:SER:O	1.99	0.79
2:C:52:LEU:HD12	2:C:53:PRO:HD2	1.47	0.79
2:C:133:THR:CG2	2:D:93:ILE:HG21	2.13	0.79
1:B:331:GLN:HA	1:B:334:PRO:HG3	1.63	0.79
1:B:571:ALA:O	1:B:573:TRP:CD1	2.35	0.79
1:E:491:ASN:CG	2:F:36:ARG:HD3	2.08	0.79
2:F:152:LEU:C	2:F:155:LEU:HD12	2.07	0.79
2:C:103:THR:N	2:C:104:GLN:HA	1.95	0.79
1:B:330:PRO:HB3	1:B:337:TYR:CE1	2.18	0.79
1:B:590:SER:N	1:B:593:THR:OG1	2.15	0.79
2:D:5:ARG:HD2	1:B:610:ARG:HE	0.62	0.79
2:D:349:PHE:CE2	2:D:356:TRP:CE2	2.71	0.79
1:B:366:LYS:C	1:B:396:HIS:NE2	2.40	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:408:THR:CB	1:B:414:TYR:HA	2.13	0.79
1:E:601:GLN:NE2	1:E:601:GLN:HA	1.98	0.79
2:F:17:GLU:CD	2:F:21:TRP:CZ2	2.60	0.79
1:A:174:GLY:HA2	1:A:177:GLU:OE1	1.83	0.79
1:A:394:LYS:O	1:A:394:LYS:HD2	1.82	0.79
1:B:387:PHE:CE2	1:B:397:LEU:CD2	2.66	0.79
1:B:387:PHE:CE1	1:B:401:THR:CG2	2.66	0.79
1:B:559:CYS:SG	1:B:560:HIS:ND1	2.56	0.79
1:E:289:TYR:CA	1:E:317:PHE:CE2	2.66	0.79
1:E:471:TYR:CE1	1:E:550:GLN:HA	2.18	0.79
1:A:555:TYR:OH	2:C:494:TRP:CH2	2.14	0.79
2:C:156:TYR:CZ	2:C:161:ASN:ND2	2.51	0.79
2:C:207:ASN:HA	2:C:210:LEU:HD13	1.65	0.79
2:D:84:ILE:HD12	2:D:84:ILE:O	1.81	0.79
1:E:106:TYR:HE2	1:E:120:PHE:CD2	2.01	0.79
1:A:207:LEU:CD1	1:A:213:ILE:HG12	2.12	0.78
2:C:46:LEU:O	2:C:46:LEU:HD22	1.84	0.78
2:D:74:CYS:O	2:D:75:LEU:HD13	1.82	0.78
2:D:312:GLN:OE1	2:D:430:ILE:CG1	2.28	0.78
2:D:362:GLU:CD	2:D:490:ARG:HD3	2.04	0.78
1:B:348:LEU:HD11	1:B:353:PHE:CG	2.17	0.78
2:F:131:TRP:NE1	2:F:139:PRO:HD3	1.98	0.78
1:A:331:GLN:NE2	1:A:364:TRP:NE1	2.32	0.78
1:B:574:ILE:C	1:B:575:ILE:HD13	2.08	0.78
1:A:207:LEU:O	1:A:208:HIS:ND1	2.15	0.78
2:C:231:GLY:HA3	2:C:234:LEU:HD21	1.66	0.78
1:B:181:LEU:HD21	1:B:460:PRO:HG3	1.65	0.78
1:B:249:ASN:OD1	1:B:424:HIS:CD2	2.36	0.78
1:E:245:ILE:CD1	1:E:373:LEU:CD2	2.61	0.78
2:F:68:LEU:CD2	2:F:84:ILE:CD1	2.42	0.78
2:F:128:LEU:CA	2:F:131:TRP:HE3	1.96	0.78
1:A:301:LEU:CD2	1:A:318:GLN:HE21	1.95	0.78
2:C:156:TYR:CE1	2:C:161:ASN:ND2	2.48	0.78
1:E:176:LEU:HD22	1:E:176:LEU:H	1.47	0.78
2:F:111:PRO:HG2	2:F:114:THR:OG1	1.84	0.78
2:F:337:LEU:HD12	2:F:338:ASP:N	1.99	0.78
1:A:221:TYR:HB2	1:A:422:PRO:HG2	1.65	0.78
2:C:97:ASN:HD21	2:C:129:ARG:NE	1.82	0.78
1:B:105:VAL:HG23	1:B:134:SER:CB	2.14	0.78
1:B:387:PHE:CZ	1:B:401:THR:CG2	2.66	0.78
1:A:105:VAL:HB	1:A:132:ASP:HB3	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:PHE:HE1	1:A:355:GLY:C	1.92	0.78
1:B:388:LEU:H	1:B:388:LEU:HD12	1.48	0.78
1:A:607:PHE:CE1	2:C:4:PRO:N	2.11	0.78
2:D:329:TRP:NE1	2:D:424:ILE:HD12	1.96	0.78
1:B:177:GLU:HG2	1:B:458:PHE:CE2	2.16	0.78
1:B:219:PRO:CB	1:B:221:TYR:HE2	1.87	0.78
2:F:17:GLU:CG	2:F:21:TRP:CZ2	2.67	0.78
2:F:88:TYR:CB	2:F:144:LEU:HD22	2.13	0.78
2:F:98:GLY:C	2:F:102:PRO:HD3	2.09	0.78
1:A:527:GLN:NE2	1:A:527:GLN:O	2.17	0.78
2:F:152:LEU:CA	2:F:155:LEU:HD13	2.08	0.78
1:A:480:GLY:H	1:A:524:PRO:HG2	1.46	0.78
1:A:607:PHE:CD1	2:C:4:PRO:HA	2.18	0.78
1:B:172:HIS:CD2	1:B:454:PHE:CA	2.42	0.78
1:E:309:GLN:OE1	1:E:311:LEU:HD13	1.84	0.78
2:C:138:LEU:HD21	2:D:94:ARG:CZ	2.14	0.78
2:C:138:LEU:CD2	2:D:94:ARG:CZ	2.62	0.78
2:C:278:PHE:CZ	2:C:287:LEU:HD13	2.19	0.78
1:E:470:SER:O	1:E:477:GLY:HA3	1.84	0.78
2:F:88:TYR:HB2	2:F:144:LEU:HD22	1.63	0.78
1:A:395:ARG:CZ	1:A:396:HIS:HB2	2.13	0.77
1:A:489:ASP:HB2	2:D:79:GLN:O	1.84	0.77
2:C:133:THR:HG23	2:D:93:ILE:HG22	1.65	0.77
2:D:58:SER:HA	2:D:61:GLN:HB2	1.65	0.77
1:E:188:LEU:HD13	1:E:434:PHE:CE1	2.17	0.77
1:E:384:HIS:HA	1:E:417:GLU:CB	2.15	0.77
2:F:350:LYS:HZ1	2:F:401:THR:HB	1.49	0.77
1:A:606:THR:CG2	2:C:5:ARG:NH1	2.47	0.77
2:C:34:ARG:HG3	2:C:67:LEU:HD11	1.66	0.77
2:D:128:LEU:O	2:D:128:LEU:HD23	1.84	0.77
2:D:212:TYR:CE2	2:D:250:SER:CB	2.68	0.77
1:B:529:CYS:O	1:B:530:THR:OG1	2.02	0.77
2:F:359:LEU:HD21	2:F:368:ILE:HD13	1.64	0.77
1:A:282:LEU:CD1	1:A:359:LEU:HD22	2.14	0.77
1:A:371:GLN:NE2	1:A:371:GLN:O	2.17	0.77
1:B:216:LEU:HD23	1:B:217:SER:N	2.00	0.77
2:F:270:TYR:O	2:F:274:VAL:HG22	1.83	0.77
2:C:130:HIS:HB2	2:C:134:HIS:ND1	1.99	0.77
2:D:489:SER:O	1:B:467:LEU:CA	2.33	0.77
2:F:497:LYS:HE2	2:F:502:LEU:O	1.84	0.77
1:A:305:ILE:HG22	1:A:307:LEU:HD11	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:53:PRO:HB2	2:C:56:VAL:HG23	1.65	0.77
2:D:98:GLY:C	2:D:102:PRO:HD3	2.08	0.77
1:B:321:LEU:CD2	1:B:344:LEU:CD1	2.60	0.77
1:E:241:ARG:CZ	1:E:381:LYS:CD	2.62	0.77
2:F:131:TRP:NE1	2:F:139:PRO:CB	2.45	0.77
1:A:256:LEU:HD11	1:A:360:ASN:HB3	1.65	0.77
1:A:366:LYS:CG	1:A:396:HIS:HB2	2.14	0.77
2:C:336:LEU:HD12	2:C:336:LEU:O	1.84	0.77
1:B:175:LEU:HD13	1:B:456:TYR:CE2	2.20	0.77
1:B:369:GLY:O	1:B:372:ILE:HG22	1.85	0.77
2:D:190:LYS:NZ	3:D:601:HOH:O	2.16	0.77
2:D:357:GLU:O	2:D:361:ASP:CG	2.27	0.77
1:E:289:TYR:CA	1:E:317:PHE:HE2	1.98	0.77
2:F:129:ARG:HB3	2:F:129:ARG:HH21	1.50	0.77
2:F:280:ASN:CA	2:F:325:LYS:HE3	2.15	0.77
1:A:83:LEU:HD23	1:A:166:ARG:NH1	2.00	0.77
1:A:467:LEU:HD21	1:A:556:VAL:HG22	1.65	0.77
2:D:23:TYR:CZ	2:D:156:TYR:HB2	2.19	0.77
2:D:202:TRP:CH2	2:D:209:PHE:CD1	2.73	0.77
1:B:395:ARG:HH11	1:B:396:HIS:CD2	1.97	0.77
1:E:169:ASN:CG	1:E:203:THR:CG2	2.52	0.77
2:C:410:GLU:O	2:C:414:ASN:ND2	2.18	0.77
1:B:261:GLU:C	1:B:264:THR:OG1	2.28	0.77
2:F:22:PHE:CD1	2:F:37:ALA:HB1	2.20	0.77
2:F:271:HIS:CA	2:F:274:VAL:HG23	2.15	0.77
1:A:196:PHE:CG	1:A:197:PRO:HD2	2.20	0.77
1:A:592:ARG:HH21	2:C:184:ARG:NE	1.82	0.77
2:D:105:GLN:HG2	1:B:615:HIS:CD2	2.19	0.77
1:B:261:GLU:C	1:B:264:THR:HG1	1.93	0.77
2:C:111:PRO:HG2	2:C:114:THR:OG1	1.85	0.76
2:D:23:TYR:HD2	2:D:156:TYR:CE2	2.02	0.76
2:F:131:TRP:CE2	2:F:139:PRO:HG3	2.20	0.76
2:C:82:ILE:O	2:C:86:LEU:HG	1.85	0.76
1:E:214:GLN:OE1	1:E:427:ASN:N	2.17	0.76
1:E:301:LEU:HD13	1:E:301:LEU:O	1.85	0.76
1:E:399:GLU:OE2	1:E:400:LEU:N	2.18	0.76
1:E:469:ILE:HG22	1:E:470:SER:H	1.48	0.76
2:F:271:HIS:HA	2:F:274:VAL:HG23	1.66	0.76
1:A:313:GLN:HG3	1:A:456:TYR:OH	1.85	0.76
1:A:592:ARG:HD2	2:C:184:ARG:NE	1.98	0.76
1:A:270:SER:CB	1:A:273:SER:OG	2.32	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:LEU:O	1:A:359:LEU:HD13	1.84	0.76
1:A:502:THR:CB	1:A:577:ARG:HH21	1.85	0.76
2:C:82:ILE:HG23	2:D:64:CYS:SG	2.23	0.76
2:D:154:TRP:CE2	2:D:158:HIS:ND1	2.51	0.76
1:B:261:GLU:CA	1:B:264:THR:OG1	2.32	0.76
1:A:555:TYR:HH	2:C:494:TRP:HH2	0.81	0.76
1:B:175:LEU:HA	1:B:458:PHE:CZ	2.20	0.76
1:B:311:LEU:N	1:B:311:LEU:HD22	2.01	0.76
1:B:389:GLU:O	1:B:390:THR:CG2	2.33	0.76
1:A:381:LYS:HD3	1:A:409:SER:CB	2.13	0.76
2:C:99:LEU:HD22	2:C:99:LEU:N	2.00	0.76
2:D:125:PHE:O	2:D:128:LEU:CB	2.34	0.76
2:D:184:ARG:HB3	1:B:592:ARG:HD2	1.65	0.76
1:B:245:ILE:HD13	1:B:361:LEU:HB2	1.66	0.76
2:F:350:LYS:NZ	2:F:401:THR:HA	1.99	0.76
1:A:98:GLN:HG3	1:A:115:ARG:C	2.11	0.76
2:C:40:ARG:HD3	2:C:44:TYR:OH	1.85	0.76
1:B:243:MET:HE3	1:B:380:TYR:HD2	1.49	0.76
1:E:106:TYR:HE2	1:E:120:PHE:HD2	1.34	0.76
2:F:55:VAL:HG11	2:F:159:TYR:CE1	2.21	0.76
2:F:332:LEU:HD23	2:F:332:LEU:O	1.86	0.76
1:A:226:LEU:HD12	1:A:230:TYR:CZ	2.16	0.76
1:A:469:ILE:HD13	2:C:488:TRP:CE3	2.21	0.76
2:C:79:GLN:N	2:C:79:GLN:HE21	1.82	0.76
2:C:209:PHE:CE2	2:C:254:ILE:HG12	2.20	0.76
2:D:113:HIS:ND1	2:D:126:VAL:HG11	2.00	0.76
2:D:354:GLN:O	2:D:358:LYS:HG2	1.86	0.76
1:E:364:TRP:HD1	1:E:369:GLY:H	1.32	0.76
1:E:364:TRP:CD2	3:E:705:HOH:O	2.38	0.76
1:A:331:GLN:NE2	1:A:364:TRP:CZ2	2.53	0.76
2:C:62:ILE:CG2	2:C:152:LEU:HD21	2.16	0.76
2:C:363:ASN:HA	2:C:492:GLN:O	1.85	0.76
2:D:23:TYR:CE2	2:D:156:TYR:CG	2.73	0.76
1:A:280:LEU:HD11	1:A:297:LEU:HD12	1.66	0.75
1:A:469:ILE:HD13	2:C:488:TRP:CE2	2.20	0.75
1:A:614:GLU:HB3	2:C:159:TYR:CE1	2.21	0.75
2:D:349:PHE:HE2	2:D:356:TRP:CG	2.04	0.75
1:E:245:ILE:HD11	1:E:373:LEU:HD11	1.66	0.75
1:B:364:TRP:CD1	1:B:369:GLY:HA2	2.21	0.75
1:B:469:ILE:CG1	1:B:552:MET:HB3	2.17	0.75
1:B:588:LEU:HD12	1:B:588:LEU:N	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:100:LEU:N	2:F:100:LEU:HD23	2.02	0.75
1:A:307:LEU:HD12	1:A:307:LEU:N	2.01	0.75
2:D:278:PHE:CE1	2:D:279:PHE:CD2	2.74	0.75
2:F:128:LEU:CA	2:F:131:TRP:CE3	2.67	0.75
1:A:179:GLY:HA2	1:A:182:TYR:O	1.86	0.75
1:A:361:LEU:HD11	1:A:376:ILE:HD11	1.68	0.75
1:A:539:LEU:N	1:A:539:LEU:HD23	2.02	0.75
2:C:80:ASP:CG	2:C:82:ILE:HG22	2.10	0.75
2:D:113:HIS:CE1	2:D:126:VAL:HG11	2.21	0.75
2:D:212:TYR:CE2	2:D:250:SER:HB2	2.20	0.75
1:E:103:GLY:O	1:E:134:SER:N	2.17	0.75
1:A:118:LEU:N	1:A:118:LEU:HD23	2.02	0.75
2:C:133:THR:CG2	2:D:93:ILE:HG22	2.16	0.75
1:B:106:TYR:O	1:B:109:VAL:HG22	1.86	0.75
2:F:101:ASP:HB2	2:F:105:GLN:HB2	1.66	0.75
1:B:577:ARG:NH2	1:B:578:ASN:O	2.19	0.75
2:F:58:SER:C	2:F:62:ILE:HG13	2.07	0.75
1:E:307:LEU:N	1:E:307:LEU:HD12	2.02	0.75
1:B:165:LEU:HD12	1:B:165:LEU:N	2.02	0.75
2:F:58:SER:O	2:F:62:ILE:HG12	1.85	0.75
2:F:131:TRP:NE1	2:F:139:PRO:CD	2.49	0.75
1:A:126:GLN:HE22	1:A:257:ARG:HH22	1.32	0.75
2:C:64:CYS:HG	2:D:82:ILE:HG21	1.51	0.75
1:E:199:ASN:CB	1:E:202:THR:HG23	2.16	0.75
1:A:471:TYR:OH	1:A:547:THR:HA	1.87	0.74
2:C:10:ARG:HB2	2:C:11:ASP:OD2	1.87	0.74
1:B:68:ASN:CB	1:B:82:GLY:H	2.00	0.74
2:F:411:ASN:O	2:F:415:LEU:N	2.20	0.74
2:D:88:TYR:HB2	2:D:144:LEU:HD13	1.69	0.74
1:B:590:SER:CA	1:B:593:THR:OG1	2.35	0.74
1:E:472:GLY:O	1:E:475:LYS:CB	2.35	0.74
2:D:68:LEU:O	2:D:77:VAL:HG22	1.86	0.74
1:E:212:ARG:NH2	1:E:212:ARG:HG3	2.01	0.74
2:C:119:ILE:HD11	2:C:121:LEU:HB2	0.81	0.74
2:D:333:GLN:NE2	2:D:370:TYR:CE2	2.56	0.74
1:B:230:TYR:HE1	1:B:263:PHE:HE1	0.81	0.74
1:E:175:LEU:O	1:E:175:LEU:HD23	1.87	0.74
2:C:100:LEU:HB2	2:C:115:LEU:HD13	1.70	0.74
2:D:184:ARG:CB	1:B:592:ARG:HD2	2.17	0.74
2:D:312:GLN:HE22	2:D:427:TYR:HE2	1.33	0.74
1:B:103:GLY:O	1:B:134:SER:HB2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:SER:O	1:B:307:LEU:HD23	1.87	0.74
1:B:395:ARG:HE	1:B:396:HIS:HB2	1.52	0.74
1:E:98:GLN:CG	1:E:117:ILE:HG23	2.08	0.74
1:A:604:PHE:CE2	2:C:10:ARG:NH1	2.54	0.74
2:C:75:LEU:CD2	2:C:76:GLY:O	2.36	0.74
2:D:36:ARG:NE	1:B:491:ASN:OD1	2.19	0.74
1:E:241:ARG:H	1:E:383:THR:HG1	1.34	0.74
2:F:125:PHE:O	2:F:128:LEU:HG	1.87	0.74
1:A:288:GLU:HG2	1:A:289:TYR:HD2	1.51	0.74
2:D:5:ARG:HD2	1:B:610:ARG:CZ	2.18	0.74
1:B:358:LEU:HD22	1:B:358:LEU:N	2.02	0.74
1:E:76:ASP:O	1:E:77:GLU:HG2	1.88	0.74
1:A:517:VAL:HG23	1:A:524:PRO:HB2	1.69	0.74
2:C:231:GLY:CA	2:C:234:LEU:HD21	2.18	0.74
2:D:77:VAL:HG13	2:D:84:ILE:CB	2.03	0.74
2:D:112:LEU:O	2:D:116:ALA:N	2.21	0.74
1:B:80:PHE:CZ	1:B:165:LEU:CA	2.68	0.74
1:B:268:ARG:NH1	1:B:305:ILE:CD1	2.51	0.74
2:F:68:LEU:HD23	2:F:68:LEU:C	2.13	0.74
1:A:213:ILE:O	1:A:213:ILE:HD12	1.88	0.74
2:C:52:LEU:CD1	2:C:56:VAL:HB	2.13	0.74
2:C:92:LEU:N	2:C:92:LEU:HD23	2.02	0.74
1:B:178:ALA:N	1:B:458:PHE:CE2	2.56	0.74
1:E:177:GLU:O	1:E:180:HIS:HB2	1.88	0.74
1:E:331:GLN:CG	1:E:364:TRP:CE2	2.70	0.74
2:F:111:PRO:HG2	2:F:114:THR:HB	1.69	0.74
1:A:83:LEU:HD23	1:A:83:LEU:N	2.03	0.74
1:A:126:GLN:HE22	1:A:257:ARG:HH12	1.28	0.74
1:A:616:VAL:O	1:A:618:LYS:HE2	1.87	0.74
2:C:90:MET:HB3	2:D:86:LEU:HG	1.70	0.74
2:D:159:TYR:CE1	1:B:614:GLU:HG3	2.17	0.74
1:B:297:LEU:HB3	1:B:321:LEU:CD2	2.18	0.74
2:F:280:ASN:O	2:F:325:LYS:CE	2.34	0.74
1:A:207:LEU:HD23	1:A:207:LEU:N	2.02	0.73
1:A:301:LEU:HD21	1:A:318:GLN:HE21	1.51	0.73
2:C:54:HIS:CD2	2:C:98:GLY:C	2.66	0.73
2:C:278:PHE:CD2	2:C:286:LEU:CD2	2.70	0.73
1:E:609:ARG:O	2:F:5:ARG:CZ	2.36	0.73
2:F:23:TYR:OH	2:F:152:LEU:O	2.06	0.73
2:D:329:TRP:CE3	2:D:424:ILE:CD1	2.54	0.73
2:D:336:LEU:HD11	2:D:340:ILE:CD1	2.16	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:LEU:HD12	1:A:65:LEU:N	2.03	0.73
2:D:112:LEU:HD23	2:D:112:LEU:N	2.02	0.73
2:D:310:ARG:NH2	2:D:495:LYS:HE3	2.04	0.73
1:B:525:ILE:HD13	1:B:525:ILE:N	2.04	0.73
1:B:611:LYS:HD3	1:B:614:GLU:OE2	1.87	0.73
1:E:194:PRO:HB2	1:E:205:HIS:HE1	1.53	0.73
1:A:79:MET:HE1	1:A:81:VAL:CG2	2.18	0.73
1:A:94:VAL:O	1:A:203:THR:OG1	2.05	0.73
1:B:175:LEU:O	1:B:458:PHE:CZ	2.41	0.73
1:B:181:LEU:CD2	1:B:460:PRO:HG3	2.18	0.73
1:A:245:ILE:HD12	1:A:363:GLY:HA2	1.71	0.73
2:D:333:GLN:NE2	2:D:370:TYR:CZ	2.55	0.73
1:B:365:ILE:HD13	1:B:366:LYS:HG3	1.70	0.73
1:E:118:LEU:HB3	1:E:305:ILE:CB	2.15	0.73
1:E:324:TYR:HB3	1:E:507:TYR:OH	1.88	0.73
1:E:384:HIS:HA	1:E:417:GLU:HB2	1.70	0.73
1:A:337:TYR:HA	1:A:340:CYS:HB2	1.70	0.73
1:A:471:TYR:HE1	1:A:545:ILE:HG23	1.53	0.73
2:D:4:PRO:HA	1:B:607:PHE:CD1	2.23	0.73
2:D:346:ASN:ND2	2:D:382:GLU:OE1	2.21	0.73
1:E:400:LEU:N	1:E:400:LEU:HD12	2.03	0.73
1:A:390:THR:OG1	1:A:422:PRO:HA	1.89	0.73
2:C:133:THR:HG22	2:D:97:ASN:HD21	1.54	0.73
1:B:366:LYS:CA	1:B:396:HIS:ND1	2.35	0.73
1:E:97:LEU:HD21	1:E:120:PHE:CZ	2.24	0.73
1:E:469:ILE:HD13	1:E:478:ILE:CD1	2.14	0.73
1:E:577:ARG:HD2	1:E:578:ASN:N	2.02	0.73
1:A:331:GLN:NE2	1:A:364:TRP:HE1	1.86	0.73
1:A:488:GLN:HE21	1:A:527:GLN:CD	1.96	0.73
2:C:77:VAL:HB	2:C:79:GLN:HG3	1.69	0.73
2:D:184:ARG:CB	1:B:592:ARG:CD	2.66	0.73
1:B:90:HIS:HE1	1:B:128:ILE:HG12	1.53	0.73
1:B:263:PHE:O	1:B:267:ILE:HG23	1.89	0.73
1:E:118:LEU:HD12	1:E:305:ILE:CG2	2.18	0.73
1:A:126:GLN:NE2	1:A:257:ARG:HH22	1.87	0.73
2:D:356:TRP:O	2:D:360:ILE:N	2.18	0.73
2:D:359:LEU:HD23	2:D:359:LEU:C	2.14	0.73
1:B:124:LEU:HB3	1:B:434:PHE:HE2	1.54	0.73
1:B:241:ARG:HB3	1:B:380:TYR:CZ	2.24	0.73
1:E:83:LEU:HD23	1:E:83:LEU:N	2.03	0.73
1:E:259:LEU:O	1:E:263:PHE:HD1	1.72	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:365:ILE:CD1	1:E:366:LYS:H	2.02	0.73
1:A:98:GLN:CG	1:A:115:ARG:CA	2.65	0.73
2:C:312:GLN:HE22	2:C:323:LYS:HB2	1.53	0.73
2:D:113:HIS:HA	2:D:116:ALA:HB3	1.71	0.73
1:B:174:GLY:HA3	1:B:177:GLU:OE2	1.89	0.73
1:E:469:ILE:CD1	1:E:478:ILE:CD1	2.65	0.73
1:A:303:SER:O	3:A:702:HOH:O	2.06	0.72
1:A:480:GLY:H	1:A:524:PRO:CG	2.01	0.72
2:C:10:ARG:NH1	2:C:10:ARG:HG2	2.02	0.72
2:C:105:GLN:HA	2:C:105:GLN:HE21	1.50	0.72
2:D:350:LYS:HZ3	2:D:401:THR:HG22	1.52	0.72
1:B:478:ILE:HD13	1:B:478:ILE:N	2.03	0.72
1:B:559:CYS:HG	1:B:560:HIS:HD1	1.36	0.72
1:E:473:LYS:HD2	1:E:473:LYS:N	2.03	0.72
1:E:491:ASN:OD1	2:F:36:ARG:HD3	1.88	0.72
1:E:610:ARG:HG2	1:E:610:ARG:NH1	1.98	0.72
2:F:76:GLY:O	2:F:77:VAL:HG13	1.89	0.72
2:F:282:TYR:CE2	2:F:287:LEU:HD22	2.21	0.72
1:A:90:HIS:NE2	1:A:213:ILE:HD11	2.04	0.72
1:A:99:VAL:HB	1:A:113:ALA:CA	2.19	0.72
1:A:276:GLU:N	1:A:276:GLU:OE2	2.22	0.72
1:A:326:GLY:HA3	1:A:578:ASN:HD22	0.91	0.72
1:B:330:PRO:HB3	1:B:337:TYR:HD1	1.50	0.72
1:B:387:PHE:CD2	1:B:397:LEU:CD2	2.73	0.72
1:E:289:TYR:O	1:E:317:PHE:CE2	2.42	0.72
2:C:86:LEU:HD21	2:C:138:LEU:CD1	2.03	0.72
2:C:332:LEU:HD23	2:C:332:LEU:C	2.14	0.72
1:B:174:GLY:O	1:B:458:PHE:CD2	2.39	0.72
1:E:358:LEU:HD23	1:E:358:LEU:H	1.53	0.72
1:E:592:ARG:HD2	1:E:592:ARG:C	2.14	0.72
1:A:288:GLU:HG2	1:A:289:TYR:CD2	2.23	0.72
2:C:54:HIS:CD2	2:C:98:GLY:CA	2.72	0.72
2:C:85:ARG:NE	2:C:138:LEU:HB2	2.05	0.72
2:D:2:ILE:HG12	1:B:609:ARG:HE	1.55	0.72
2:D:121:LEU:HD12	2:D:122:PRO:HD2	1.69	0.72
2:D:202:TRP:CZ3	2:D:209:PHE:CE1	2.71	0.72
1:B:124:LEU:HB3	1:B:434:PHE:CE2	2.24	0.72
1:B:260:LEU:O	1:B:264:THR:OG1	2.05	0.72
1:A:105:VAL:N	1:A:132:ASP:O	2.20	0.72
1:A:226:LEU:HD12	1:A:226:LEU:C	2.15	0.72
1:A:466:PRO:O	2:C:491:VAL:CG2	2.34	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:VAL:HG22	1:B:166:ARG:NE	2.04	0.72
1:E:100:VAL:C	1:E:101:LYS:HG2	2.13	0.72
1:E:362:PRO:HB2	3:E:705:HOH:O	1.88	0.72
2:F:337:LEU:HD12	2:F:337:LEU:C	2.15	0.72
1:A:541:LEU:HD12	1:A:541:LEU:C	2.14	0.72
2:C:102:PRO:C	2:C:104:GLN:HA	2.13	0.72
2:C:138:LEU:HD21	2:D:94:ARG:NH1	2.05	0.72
2:C:400:SER:O	2:C:404:ILE:HG13	1.89	0.72
2:D:88:TYR:O	2:D:92:LEU:HG	1.90	0.72
2:D:278:PHE:CE1	2:D:279:PHE:CE2	2.78	0.72
1:B:321:LEU:HD23	1:B:321:LEU:C	2.15	0.72
1:E:331:GLN:HG2	1:E:364:TRP:CZ2	2.18	0.72
1:A:538:THR:HB	1:A:560:HIS:HD2	0.57	0.72
2:C:112:LEU:N	2:C:112:LEU:HD23	2.03	0.72
2:C:350:LYS:HG2	2:C:404:ILE:HD12	1.70	0.72
2:D:322:LEU:HD23	2:D:322:LEU:C	2.15	0.72
2:D:357:GLU:C	2:D:361:ASP:OD2	2.31	0.72
1:B:392:ASN:N	1:B:393:SER:HA	2.04	0.72
1:A:267:ILE:HD11	1:A:277:LEU:CD2	2.20	0.72
1:B:277:LEU:HD23	1:B:277:LEU:N	2.00	0.72
1:B:388:LEU:HD12	1:B:388:LEU:N	2.03	0.72
1:E:365:ILE:N	1:E:365:ILE:HD12	2.04	0.72
1:A:206:LEU:HD22	1:A:207:LEU:N	2.05	0.72
1:A:471:TYR:HE1	1:A:545:ILE:CG2	2.03	0.72
2:C:158:HIS:O	2:C:162:ASP:HB3	1.89	0.72
1:E:310:HIS:CB	1:E:314:GLY:CA	2.68	0.72
1:E:480:GLY:H	1:E:524:PRO:CG	2.02	0.72
2:F:54:HIS:CD2	2:F:98:GLY:HA3	2.25	0.72
1:A:84:LYS:N	1:A:139:TRP:HB3	2.05	0.71
1:A:347:HIS:NE2	1:A:351:GLN:OE1	2.23	0.71
1:A:373:LEU:HD23	1:A:373:LEU:N	2.05	0.71
2:C:52:LEU:HD13	2:C:53:PRO:CD	2.18	0.71
2:C:159:TYR:HE2	2:C:160:TRP:CZ3	2.08	0.71
1:B:80:PHE:CD1	1:B:166:ARG:HB2	2.24	0.71
1:B:347:HIS:CD2	1:B:351:GLN:HG2	2.25	0.71
1:E:397:LEU:HD12	1:E:397:LEU:N	2.01	0.71
1:E:599:ASN:OD1	1:E:600:ILE:N	2.23	0.71
1:A:105:VAL:O	1:A:132:ASP:HB2	1.89	0.71
1:A:502:THR:CG2	1:A:577:ARG:NH2	2.52	0.71
2:C:45:ARG:NH2	2:C:57:ASP:OD1	2.23	0.71
2:C:68:LEU:O	2:C:71:LYS:HD2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:LEU:HD13	1:B:347:HIS:ND1	2.05	0.71
1:B:408:THR:CB	1:B:415:ALA:N	2.53	0.71
1:E:469:ILE:HG22	1:E:470:SER:N	2.03	0.71
2:F:89:VAL:HG23	2:F:144:LEU:HD21	1.71	0.71
1:A:369:GLY:CA	1:A:372:ILE:HG22	2.20	0.71
1:A:395:ARG:O	1:A:398:ASP:OD1	2.09	0.71
2:C:100:LEU:C	2:C:100:LEU:HD12	2.15	0.71
2:D:99:LEU:HD12	2:D:99:LEU:N	2.05	0.71
1:B:172:HIS:HD2	1:B:454:PHE:C	1.97	0.71
1:B:451:ILE:HD13	1:B:451:ILE:N	2.04	0.71
1:E:97:LEU:HD22	1:E:120:PHE:CE1	2.23	0.71
1:E:116:GLU:OE1	1:E:116:GLU:N	2.23	0.71
1:A:466:PRO:HB2	1:A:554:ILE:O	1.91	0.71
1:B:96:ARG:CZ	1:B:171:ASN:CG	2.63	0.71
1:B:324:TYR:HB2	1:B:536:PHE:CD2	2.24	0.71
1:E:199:ASN:O	1:E:202:THR:OG1	2.08	0.71
2:F:68:LEU:HD22	2:F:84:ILE:HD13	0.76	0.71
1:A:359:LEU:HD12	1:A:359:LEU:C	2.15	0.71
1:A:364:TRP:CD1	1:A:369:GLY:HA2	2.17	0.71
1:B:79:MET:O	1:B:167:VAL:HG11	1.89	0.71
1:E:110:HIS:C	1:E:111:TYR:HD1	1.98	0.71
1:E:118:LEU:HD23	1:E:118:LEU:N	2.04	0.71
1:E:357:SER:OG	1:E:380:TYR:OH	2.05	0.71
2:F:305:VAL:HG21	2:F:336:LEU:HD21	1.72	0.71
2:F:389:TRP:CD1	2:F:390:ARG:HD2	2.25	0.71
1:A:126:GLN:NE2	1:A:257:ARG:NH1	2.34	0.71
2:D:46:LEU:CD1	1:B:483:PHE:CE1	2.71	0.71
1:B:337:TYR:OH	1:B:362:PRO:CG	2.38	0.71
1:B:364:TRP:HD1	1:B:369:GLY:HA2	1.55	0.71
1:B:521:ASN:O	1:B:522:THR:HG22	1.90	0.71
1:B:575:ILE:HD13	1:B:575:ILE:N	2.04	0.71
1:E:103:GLY:C	1:E:104:ILE:HD12	2.15	0.71
1:E:166:ARG:HG2	1:E:166:ARG:NH1	2.04	0.71
1:E:331:GLN:CD	1:E:364:TRP:CZ2	2.66	0.71
2:F:359:LEU:HD23	2:F:359:LEU:C	2.15	0.71
1:A:245:ILE:HD11	1:A:363:GLY:O	1.89	0.71
1:A:299:LYS:C	1:A:300:ILE:HD12	2.16	0.71
1:A:359:LEU:HD12	1:A:360:ASN:H	1.55	0.71
1:A:521:ASN:O	1:A:522:THR:HG22	1.91	0.71
2:C:102:PRO:CA	2:C:104:GLN:OE1	2.35	0.71
2:C:209:PHE:HE2	2:C:254:ILE:CG2	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:224:ILE:HG21	2:C:229:PHE:HZ	1.54	0.71
2:D:88:TYR:CB	2:D:144:LEU:HD13	2.20	0.71
2:D:363:ASN:O	2:D:368:ILE:HD12	1.90	0.71
1:B:366:LYS:HB3	1:B:395:ARG:NH1	2.05	0.71
1:B:480:GLY:HA2	1:B:524:PRO:O	1.91	0.71
1:E:364:TRP:CD1	1:E:369:GLY:H	2.05	0.71
1:E:387:PHE:CE1	1:E:401:THR:CG2	2.74	0.71
1:B:612:LYS:O	1:B:613:LEU:HD12	1.90	0.71
2:C:23:TYR:CE2	2:C:160:TRP:HD1	2.09	0.71
1:B:474:GLY:N	1:B:475:LYS:HA	2.06	0.71
1:E:166:ARG:HG2	1:E:166:ARG:HH11	1.56	0.71
2:F:131:TRP:CZ2	2:F:139:PRO:HG3	2.26	0.71
1:A:75:GLU:HA	2:C:259:ARG:NH2	2.01	0.71
2:D:130:HIS:O	2:D:132:GLY:N	2.23	0.71
1:B:259:LEU:O	1:B:263:PHE:HD1	1.71	0.71
1:B:503:VAL:CG1	1:B:539:LEU:HD22	2.21	0.71
1:A:420:ARG:HG2	1:A:420:ARG:HH21	1.56	0.70
2:C:75:LEU:HD23	2:C:75:LEU:C	2.14	0.70
2:C:106:SER:OG	2:C:108:PHE:O	2.07	0.70
1:B:348:LEU:HD11	1:B:353:PHE:HB3	1.69	0.70
1:B:359:LEU:HD12	1:B:359:LEU:C	2.15	0.70
1:E:390:THR:OG1	1:E:423:ALA:N	2.24	0.70
2:F:54:HIS:NE2	2:F:98:GLY:HA3	2.06	0.70
2:F:278:PHE:O	2:F:282:TYR:N	2.24	0.70
1:A:196:PHE:CD2	1:A:197:PRO:HD2	2.26	0.70
1:A:223:SER:O	1:A:227:GLU:N	2.20	0.70
2:D:69:ASP:HA	2:D:77:VAL:CB	2.20	0.70
1:B:65:LEU:C	1:B:65:LEU:HD12	2.15	0.70
1:B:366:LYS:C	1:B:396:HIS:CE1	2.68	0.70
2:F:500:GLY:C	2:F:501:VAL:HG23	2.16	0.70
1:A:440:ARG:NH1	3:A:703:HOH:O	2.22	0.70
2:D:23:TYR:HE2	2:D:156:TYR:CB	1.97	0.70
1:E:123:PRO:HG3	1:E:309:GLN:CG	2.22	0.70
1:E:359:LEU:HD12	1:E:359:LEU:C	2.15	0.70
2:F:68:LEU:HB3	2:F:84:ILE:HD11	1.72	0.70
1:A:469:ILE:CG2	2:C:488:TRP:N	2.38	0.70
2:C:210:LEU:HD12	2:C:210:LEU:N	2.01	0.70
2:C:309:TYR:HE1	2:C:313:GLN:NE2	1.89	0.70
1:B:515:LEU:HD23	1:B:515:LEU:N	2.03	0.70
1:B:544:SER:OG	1:B:553:ASN:HB2	1.92	0.70
1:A:245:ILE:HD12	1:A:246:GLY:H	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:PHE:CE1	1:A:355:GLY:C	2.70	0.70
1:A:381:LYS:CA	1:A:409:SER:CB	2.69	0.70
2:C:52:LEU:HD12	2:C:52:LEU:C	2.15	0.70
1:B:90:HIS:ND1	1:B:128:ILE:HD13	2.05	0.70
1:B:123:PRO:HG3	1:B:309:GLN:CG	2.21	0.70
1:B:517:VAL:HB	1:B:525:ILE:O	1.91	0.70
1:E:395:ARG:HG3	1:E:395:ARG:NH2	2.00	0.70
1:E:397:LEU:H	1:E:397:LEU:CD1	2.03	0.70
1:E:450:LYS:HE3	1:E:453:GLN:CA	2.19	0.70
2:F:333:GLN:HA	2:F:337:LEU:HD23	1.72	0.70
1:A:91:LEU:HD21	1:A:167:VAL:HG11	1.72	0.70
1:A:214:GLN:HG2	1:A:214:GLN:O	1.92	0.70
1:A:305:ILE:CG2	1:A:307:LEU:HD11	2.21	0.70
2:D:128:LEU:HD23	2:D:128:LEU:C	2.16	0.70
1:B:473:LYS:CE	1:B:474:GLY:H	2.04	0.70
1:E:83:LEU:CD1	1:E:101:LYS:C	2.63	0.70
1:E:241:ARG:NH1	1:E:381:LYS:CD	2.54	0.70
1:E:293:ASP:OD2	1:E:328:SER:N	2.25	0.70
1:E:450:LYS:HE2	1:E:453:GLN:HA	1.72	0.70
1:E:469:ILE:HG21	1:E:478:ILE:HD11	0.71	0.70
2:F:99:LEU:O	2:F:102:PRO:HD2	1.91	0.70
1:A:331:GLN:NE2	1:A:364:TRP:CE2	2.59	0.70
1:A:616:VAL:HG12	2:C:50:GLN:O	1.92	0.70
2:C:53:PRO:HD2	2:C:56:VAL:HG21	1.74	0.70
2:C:110:ILE:CG2	2:C:114:THR:CB	2.64	0.70
2:C:110:ILE:HG21	2:C:114:THR:HB	1.72	0.70
1:B:99:VAL:HG22	1:B:166:ARG:HH21	1.41	0.70
1:B:471:TYR:HD1	1:B:550:GLN:O	1.71	0.70
2:F:271:HIS:HA	2:F:274:VAL:CG2	2.21	0.70
1:A:105:VAL:CB	1:A:132:ASP:CB	2.34	0.70
2:C:182:TYR:OH	2:F:183:ARG:HG3	1.92	0.70
2:D:288:LYS:HG3	2:D:343:ASN:HD22	1.56	0.70
1:B:243:MET:SD	1:B:361:LEU:CD1	2.80	0.70
1:E:213:ILE:C	1:E:213:ILE:HD12	2.16	0.70
1:A:365:ILE:O	1:A:396:HIS:CG	2.45	0.70
1:A:491:ASN:HD21	2:C:36:ARG:NE	1.88	0.70
2:D:72:GLU:OE1	2:D:72:GLU:HA	1.91	0.70
2:D:96:VAL:CG1	2:D:100:LEU:CG	2.70	0.70
1:B:348:LEU:HD11	1:B:353:PHE:HD1	1.56	0.70
1:B:387:PHE:CD2	1:B:397:LEU:HD21	2.27	0.70
1:E:105:VAL:HA	1:E:109:VAL:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:577:ARG:HD2	1:E:578:ASN:H	1.57	0.70
2:F:25:LYS:HE2	2:F:25:LYS:C	2.16	0.70
1:A:590:SER:OG	2:C:184:ARG:CD	2.39	0.70
2:D:86:LEU:CD1	2:D:138:LEU:HD21	2.22	0.70
1:B:243:MET:HE3	1:B:380:TYR:CD2	2.27	0.70
1:B:246:GLY:O	1:B:363:GLY:HA2	1.91	0.70
1:A:105:VAL:O	1:A:132:ASP:CB	2.39	0.69
1:A:618:LYS:C	2:C:104:GLN:HE22	2.00	0.69
1:B:80:PHE:CE1	1:B:165:LEU:C	2.64	0.69
1:B:166:ARG:C	1:B:167:VAL:HG22	2.15	0.69
1:E:85:GLU:O	1:E:133:PHE:CD1	2.43	0.69
1:E:109:VAL:HG21	1:E:111:TYR:CE1	2.26	0.69
1:E:179:GLY:HA2	1:E:185:VAL:HG13	1.74	0.69
1:E:491:ASN:CG	2:F:36:ARG:NE	2.45	0.69
2:F:30:ILE:C	2:F:30:ILE:HD12	2.17	0.69
1:A:104:ILE:HD12	1:A:104:ILE:N	2.07	0.69
2:C:38:VAL:HG11	2:C:64:CYS:SG	2.31	0.69
1:B:91:LEU:HD11	1:B:204:TYR:CB	2.22	0.69
1:E:306:SER:C	1:E:307:LEU:HD12	2.17	0.69
1:E:431:SER:OG	1:E:434:PHE:CA	2.40	0.69
2:F:372:CYS:C	2:F:412:ILE:CD1	2.63	0.69
1:B:590:SER:C	1:B:593:THR:OG1	2.36	0.69
1:E:213:ILE:HD12	1:E:213:ILE:O	1.92	0.69
1:E:451:ILE:O	1:E:452:THR:OG1	2.10	0.69
1:A:504:ILE:HD13	1:A:575:ILE:HG21	1.71	0.69
1:B:398:ASP:OD2	1:B:398:ASP:N	2.24	0.69
1:B:599:ASN:ND2	1:B:600:ILE:HD13	2.08	0.69
1:E:230:TYR:HB3	1:E:262:LYS:NZ	2.07	0.69
1:E:241:ARG:HB2	1:E:383:THR:H	1.56	0.69
2:F:79:GLN:HA	2:F:83:PRO:HG2	1.73	0.69
1:A:480:GLY:N	1:A:524:PRO:HG2	2.07	0.69
2:D:202:TRP:CH2	2:D:209:PHE:CD2	2.73	0.69
2:F:332:LEU:HD23	2:F:332:LEU:C	2.17	0.69
2:C:125:PHE:CD1	2:C:128:LEU:CD2	2.75	0.69
2:D:202:TRP:CZ3	2:D:209:PHE:CD1	2.81	0.69
1:B:400:LEU:HD22	1:B:400:LEU:H	1.56	0.69
1:E:89:LEU:O	1:E:130:THR:HG22	1.93	0.69
1:E:493:GLN:HE21	2:F:36:ARG:HH22	1.39	0.69
1:A:106:TYR:O	1:A:109:VAL:HG13	1.93	0.69
1:A:353:PHE:CE1	1:A:355:GLY:N	2.60	0.69
2:D:139:PRO:HG2	2:D:144:LEU:HD21	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:ILE:O	1:B:69:ILE:HD13	1.93	0.69
1:B:96:ARG:CZ	1:B:171:ASN:OD1	2.40	0.69
1:B:230:TYR:CE1	1:B:263:PHE:CD1	2.80	0.69
1:B:366:LYS:CD	1:B:395:ARG:HH11	2.06	0.69
1:B:389:GLU:HG3	1:B:393:SER:O	1.91	0.69
1:B:578:ASN:OD1	1:B:579:LYS:HG2	1.91	0.69
1:E:613:LEU:O	2:F:159:TYR:HD1	1.75	0.69
2:F:322:LEU:HD21	2:F:332:LEU:HD11	1.75	0.69
1:A:106:TYR:O	1:A:109:VAL:HG22	1.92	0.69
2:C:82:ILE:CG2	2:D:64:CYS:HG	2.05	0.69
2:C:349:PHE:CZ	2:C:353:TRP:CZ3	2.81	0.69
2:D:336:LEU:HD12	2:D:336:LEU:C	2.15	0.69
1:B:92:SER:CB	1:B:207:LEU:HD11	2.22	0.69
1:B:471:TYR:HA	1:B:478:ILE:HG12	1.74	0.69
1:B:506:ILE:HD11	1:B:540:GLY:HA3	1.72	0.69
1:B:546:ASP:HB3	1:B:549:GLN:CG	2.22	0.69
1:E:96:ARG:HG2	1:E:168:PHE:HD2	1.57	0.69
1:E:245:ILE:HD11	1:E:373:LEU:CD2	2.22	0.69
1:E:477:GLY:O	1:E:478:ILE:HG13	1.93	0.69
1:E:548:SER:CB	1:E:549:GLN:HE21	2.05	0.69
2:F:278:PHE:CE2	2:F:282:TYR:HA	2.28	0.69
2:F:366:TYR:N	2:F:419:PHE:CD1	2.60	0.69
1:A:165:LEU:N	1:A:165:LEU:HD12	2.07	0.69
1:A:245:ILE:HD11	1:A:363:GLY:CA	2.23	0.69
2:C:314:ASP:CB	2:C:495:LYS:HZ1	2.06	0.69
1:B:114:SER:C	1:B:115:ARG:HG3	2.15	0.69
1:B:243:MET:CE	1:B:380:TYR:CD2	2.76	0.69
1:E:205:HIS:O	1:E:207:LEU:CD2	2.40	0.69
1:E:240:THR:OG1	1:E:356:THR:HG22	1.93	0.69
1:E:561:THR:HG23	1:E:562:GLN:HA	1.75	0.69
1:A:180:HIS:HB2	2:C:269:ILE:HD12	1.74	0.69
2:C:353:TRP:HH2	2:C:408:LEU:HD21	1.57	0.69
1:B:122:HIS:HE1	1:B:128:ILE:HB	1.48	0.69
1:E:181:LEU:O	1:E:181:LEU:HD13	1.93	0.69
1:E:390:THR:HG22	1:E:391:ALA:H	1.56	0.69
1:E:489:ASP:OD1	1:E:489:ASP:N	2.25	0.69
1:A:105:VAL:CA	1:A:132:ASP:HB2	2.24	0.68
1:A:108:ASN:HD22	1:A:108:ASN:C	2.01	0.68
1:A:174:GLY:CA	1:A:177:GLU:OE1	2.41	0.68
2:C:101:ASP:O	2:C:105:GLN:N	2.26	0.68
2:D:86:LEU:HD11	2:D:138:LEU:HD21	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:349:PHE:CE2	2:D:356:TRP:CD1	2.82	0.68
1:B:480:GLY:HA2	1:B:524:PRO:HG2	1.75	0.68
1:E:169:ASN:ND2	1:E:203:THR:HG23	2.07	0.68
1:E:389:GLU:OE1	1:E:389:GLU:HA	1.93	0.68
2:F:365:SER:C	2:F:419:PHE:CE1	2.71	0.68
2:F:418:ARG:C	2:F:419:PHE:HD2	2.01	0.68
1:A:507:TYR:CD2	1:A:576:VAL:HG21	2.28	0.68
2:C:353:TRP:CH2	2:C:408:LEU:HD21	2.27	0.68
1:B:359:LEU:HD12	1:B:360:ASN:C	2.18	0.68
1:B:509:TYR:O	1:B:510:SER:OG	2.10	0.68
1:B:510:SER:CB	1:B:535:ASN:OD1	2.34	0.68
1:A:265:GLN:HA	1:A:268:ARG:HH11	1.57	0.68
1:A:617:TRP:HD1	1:A:618:LYS:N	1.91	0.68
2:C:357:GLU:O	2:C:361:ASP:HB2	1.93	0.68
2:D:323:LYS:CG	2:D:427:TYR:CE2	2.74	0.68
1:E:103:GLY:N	1:E:134:SER:O	2.26	0.68
1:E:222:TRP:CD1	1:E:422:PRO:HB2	2.28	0.68
1:A:392:ASN:N	1:A:393:SER:HA	2.09	0.68
1:A:469:ILE:HG21	2:C:488:TRP:CD2	2.29	0.68
1:B:211:ASP:O	1:B:212:ARG:HB2	1.94	0.68
1:E:79:MET:HG2	1:E:80:PHE:N	2.07	0.68
1:E:521:ASN:O	1:E:522:THR:HG22	1.92	0.68
1:A:77:GLU:HG3	1:A:201:ARG:O	1.94	0.68
1:A:93:GLY:H	1:A:122:HIS:HB2	1.59	0.68
1:A:353:PHE:CE1	1:A:355:GLY:CA	2.77	0.68
2:C:125:PHE:C	2:C:128:LEU:HG	2.18	0.68
2:D:138:LEU:HD12	2:D:138:LEU:H	1.58	0.68
2:D:188:LEU:HD12	2:D:188:LEU:C	2.18	0.68
1:B:108:ASN:C	1:B:108:ASN:HD22	2.01	0.68
1:B:265:GLN:HA	1:B:268:ARG:HH21	1.57	0.68
2:C:95:PHE:O	2:C:99:LEU:HD22	1.93	0.68
2:D:99:LEU:O	2:D:102:PRO:HD2	1.93	0.68
1:B:455:ASP:OD1	1:B:455:ASP:N	2.27	0.68
1:E:289:TYR:O	1:E:317:PHE:HE2	1.76	0.68
1:E:310:HIS:HB2	1:E:314:GLY:CA	2.22	0.68
1:E:472:GLY:C	1:E:475:LYS:CB	2.67	0.68
1:A:96:ARG:C	1:A:168:PHE:CE1	2.59	0.68
1:A:377:ILE:HD13	1:A:385:LEU:HD11	1.76	0.68
1:A:507:TYR:HA	1:A:535:ASN:O	1.93	0.68
2:C:78:HIS:HB2	2:D:35:GLN:CD	2.18	0.68
1:B:364:TRP:HD1	1:B:372:ILE:CG2	2.06	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:366:TYR:N	2:F:419:PHE:HD1	1.91	0.68
1:A:83:LEU:HD23	1:A:83:LEU:H	1.59	0.68
1:A:103:GLY:C	1:A:104:ILE:HD12	2.18	0.68
1:A:381:LYS:CD	1:A:409:SER:CB	2.72	0.68
1:A:420:ARG:HG2	1:A:420:ARG:NH2	2.08	0.68
1:B:507:TYR:HB2	1:B:574:ILE:O	1.94	0.68
1:E:88:LYS:HG2	1:E:132:ASP:OD1	1.94	0.68
1:A:105:VAL:O	1:A:132:ASP:CG	2.37	0.68
1:A:374:ASN:OD1	1:A:404:GLN:CB	2.42	0.68
1:A:507:TYR:HD2	1:A:576:VAL:HG21	1.58	0.68
2:D:4:PRO:CD	1:B:607:PHE:CE1	2.75	0.68
2:D:84:ILE:CD1	2:D:88:TYR:CD2	2.76	0.68
1:A:74:ASP:CG	1:A:75:GLU:N	2.49	0.68
1:A:313:GLN:N	1:A:313:GLN:HE21	1.92	0.68
1:A:502:THR:HB	1:A:577:ARG:HH22	1.54	0.68
2:D:212:TYR:CZ	2:D:250:SER:CB	2.77	0.68
2:D:500:GLY:O	2:D:501:VAL:HG22	1.93	0.68
1:E:592:ARG:HG3	1:E:592:ARG:NH2	2.01	0.68
2:F:272:ASN:HA	2:F:275:LEU:HD11	1.55	0.68
1:A:541:LEU:O	1:A:554:ILE:HG13	1.93	0.67
2:F:338:ASP:OD1	2:F:370:TYR:OH	2.12	0.67
2:F:350:LYS:NZ	2:F:401:THR:HB	2.03	0.67
1:A:597:ASP:N	1:A:597:ASP:OD1	2.27	0.67
2:D:99:LEU:H	2:D:99:LEU:CD1	2.05	0.67
2:D:119:ILE:HD11	2:D:121:LEU:HD22	1.76	0.67
1:B:400:LEU:HD22	1:B:400:LEU:N	2.08	0.67
1:E:106:TYR:CE2	1:E:120:PHE:CD2	2.82	0.67
2:F:80:ASP:OD1	2:F:83:PRO:HD3	1.93	0.67
1:A:181:LEU:HD13	1:A:181:LEU:C	2.19	0.67
1:A:267:ILE:HD11	1:A:277:LEU:HD23	1.75	0.67
1:A:365:ILE:HD12	1:A:366:LYS:N	2.08	0.67
2:C:97:ASN:ND2	2:C:129:ARG:HE	1.92	0.67
2:C:182:TYR:CZ	2:F:183:ARG:HG3	2.29	0.67
2:D:495:LYS:O	2:D:497:LYS:CG	2.41	0.67
1:B:67:ASP:OD2	1:B:67:ASP:N	2.27	0.67
2:F:333:GLN:O	2:F:337:LEU:HG	1.94	0.67
1:A:481:ILE:HG23	1:A:575:ILE:HB	1.73	0.67
2:D:430:ILE:HD13	2:D:430:ILE:N	2.04	0.67
1:B:239:ASP:CB	1:B:355:GLY:CA	2.71	0.67
1:E:75:GLU:OE1	1:E:76:ASP:N	2.27	0.67
1:E:207:LEU:HD23	1:E:207:LEU:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:431:SER:HG	1:E:434:PHE:N	1.91	0.67
2:F:126:VAL:C	2:F:129:ARG:HG2	2.19	0.67
2:F:418:ARG:O	2:F:419:PHE:HD2	1.78	0.67
1:A:264:THR:O	1:A:268:ARG:HD3	1.93	0.67
1:A:589:PRO:CB	1:A:594:ILE:HD12	2.24	0.67
2:C:11:ASP:OD2	2:C:11:ASP:N	2.26	0.67
2:D:45:ARG:NH2	2:D:57:ASP:OD2	2.27	0.67
2:F:312:GLN:CD	2:F:323:LYS:CE	2.59	0.67
2:D:5:ARG:NE	1:B:610:ARG:CG	2.58	0.67
1:B:97:LEU:HB2	1:B:120:PHE:HE1	1.59	0.67
1:E:385:LEU:O	1:E:419:VAL:CG2	2.43	0.67
1:E:493:GLN:HE21	2:F:36:ARG:NH2	1.91	0.67
1:B:549:GLN:O	1:B:550:GLN:HB2	1.95	0.67
1:E:88:LYS:HB3	1:E:130:THR:HG21	1.75	0.67
1:E:324:TYR:HB2	1:E:536:PHE:CD2	2.28	0.67
1:E:368:PHE:O	1:E:372:ILE:N	2.27	0.67
1:E:390:THR:HG22	1:E:391:ALA:N	2.10	0.67
1:E:536:PHE:HD1	1:E:537:ILE:N	1.92	0.67
1:E:592:ARG:HH21	1:E:593:THR:N	1.93	0.67
2:F:331:GLU:O	2:F:335:ARG:HB2	1.94	0.67
1:B:115:ARG:HB2	1:B:115:ARG:CZ	2.24	0.67
2:F:128:LEU:HD12	2:F:128:LEU:C	2.20	0.67
2:C:349:PHE:CZ	2:C:353:TRP:HZ3	2.12	0.67
2:D:486:LYS:O	2:D:486:LYS:HD3	1.93	0.67
1:B:490:LEU:HD12	1:B:491:ASN:N	2.10	0.67
2:C:86:LEU:HD23	2:C:138:LEU:HD12	1.75	0.67
2:C:234:LEU:C	2:C:235:VAL:HG23	2.20	0.67
1:B:471:TYR:OH	1:B:547:THR:HA	1.94	0.67
1:E:538:THR:HG22	1:E:539:LEU:O	1.95	0.67
3:E:701:HOH:O	2:F:502:LEU:CD2	2.43	0.67
2:F:22:PHE:CE1	2:F:37:ALA:CB	2.75	0.67
2:F:501:VAL:O	2:F:502:LEU:HD12	1.94	0.67
1:A:471:TYR:HD1	1:A:552:MET:CG	2.04	0.66
1:A:590:SER:HB3	1:A:593:THR:OG1	1.95	0.66
2:C:210:LEU:CD1	2:C:210:LEU:H	1.96	0.66
2:D:54:HIS:NE2	2:D:99:LEU:HD12	2.10	0.66
2:D:62:ILE:HG21	2:D:152:LEU:HD21	1.77	0.66
2:D:77:VAL:HG12	2:D:84:ILE:CB	2.11	0.66
1:B:230:TYR:HD1	1:B:263:PHE:CE1	2.07	0.66
1:B:450:LYS:HB3	1:B:450:LYS:NZ	2.10	0.66
1:E:369:GLY:HA2	1:E:372:ILE:HG21	1.71	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:128:LEU:CB	2:F:131:TRP:HZ3	1.94	0.66
1:A:106:TYR:HD2	1:A:120:PHE:HE2	1.40	0.66
1:A:216:LEU:HD23	1:A:217:SER:H	1.59	0.66
1:A:381:LYS:CG	1:A:409:SER:CB	2.72	0.66
2:D:209:PHE:CE1	2:D:254:ILE:HG23	2.24	0.66
1:B:365:ILE:HD12	1:B:366:LYS:CG	2.23	0.66
1:B:470:SER:HA	1:B:551:ILE:HA	1.76	0.66
1:E:257:ARG:HD2	1:E:308:GLY:O	1.96	0.66
1:E:310:HIS:HD2	1:E:314:GLY:HA3	1.57	0.66
2:F:151:ALA:C	2:F:155:LEU:CD1	2.65	0.66
2:F:333:GLN:HA	2:F:337:LEU:CD2	2.25	0.66
1:A:261:GLU:HG2	1:A:307:LEU:HD23	1.76	0.66
2:F:48:GLY:HA2	2:F:50:GLN:O	1.95	0.66
1:A:331:GLN:O	1:A:334:PRO:HD3	1.94	0.66
1:A:543:HIS:HE1	2:C:502:LEU:C	2.03	0.66
2:D:146:TRP:CE3	2:D:146:TRP:C	2.73	0.66
1:E:205:HIS:O	1:E:207:LEU:HD21	1.95	0.66
1:E:473:LYS:HD2	1:E:474:GLY:H	1.60	0.66
1:A:229:LEU:HD12	1:A:259:LEU:HD21	1.77	0.66
1:A:589:PRO:HG3	1:A:594:ILE:CD1	2.16	0.66
2:C:95:PHE:CZ	2:C:155:LEU:HD12	2.29	0.66
2:C:138:LEU:HD21	2:D:94:ARG:NE	2.09	0.66
2:C:337:LEU:O	2:C:337:LEU:HD23	1.96	0.66
1:B:79:MET:C	1:B:167:VAL:HG22	2.04	0.66
1:B:364:TRP:HD1	1:B:372:ILE:HG21	1.59	0.66
1:B:599:ASN:HD21	1:B:600:ILE:CD1	2.07	0.66
1:E:364:TRP:CD1	1:E:369:GLY:HA2	2.29	0.66
2:D:291:MET:HE1	2:D:340:ILE:HG23	1.77	0.66
1:B:369:GLY:C	1:B:372:ILE:HG22	2.20	0.66
1:B:599:ASN:HD21	1:B:600:ILE:HD13	1.61	0.66
1:B:288:GLU:HG2	1:B:289:TYR:CD2	2.30	0.66
1:B:348:LEU:HD11	1:B:353:PHE:CB	2.25	0.66
1:E:289:TYR:HD1	1:E:317:PHE:CG	2.12	0.66
1:A:107:ASN:ND2	1:A:258:LEU:HD21	2.10	0.66
1:A:504:ILE:HD13	1:A:575:ILE:CG2	2.15	0.66
2:D:96:VAL:O	2:D:100:LEU:CA	2.43	0.66
2:D:202:TRP:HH2	2:D:209:PHE:CD1	2.14	0.66
1:E:562:GLN:O	1:E:565:ASP:N	2.29	0.66
2:D:108:PHE:H	2:D:108:PHE:HD2	1.44	0.66
2:D:133:THR:HB	2:D:134:HIS:CD2	2.31	0.66
1:E:260:LEU:O	1:E:264:THR:OG1	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:306:SER:O	1:E:307:LEU:HG	1.95	0.66
1:E:364:TRP:CB	1:E:369:GLY:CA	2.67	0.66
1:E:561:THR:HA	1:E:564:LEU:HD12	1.76	0.66
1:E:567:GLN:HA	1:E:567:GLN:NE2	1.99	0.66
1:E:610:ARG:CD	2:F:167:ASP:CG	2.69	0.66
1:A:614:GLU:HB3	2:C:159:TYR:HE1	1.57	0.66
2:C:182:TYR:OH	2:F:183:ARG:CG	2.44	0.66
1:B:471:TYR:CE1	1:B:550:GLN:CB	2.79	0.66
1:E:324:TYR:HB2	1:E:536:PHE:HE2	1.52	0.66
1:E:390:THR:O	1:E:394:LYS:HG3	1.95	0.66
1:E:546:ASP:OD1	1:E:549:GLN:NE2	2.29	0.66
1:E:612:LYS:HD3	2:F:164:GLU:OE1	1.96	0.66
2:C:207:ASN:CA	2:C:210:LEU:HD13	2.26	0.65
2:D:46:LEU:CD1	1:B:483:PHE:HE1	1.92	0.65
2:D:323:LYS:HG3	2:D:427:TYR:CE2	2.29	0.65
1:B:408:THR:CB	1:B:414:TYR:C	2.69	0.65
1:B:515:LEU:H	1:B:515:LEU:CD2	1.97	0.65
1:A:374:ASN:CG	1:A:404:GLN:CB	2.69	0.65
2:C:100:LEU:HD13	2:C:115:LEU:HD12	1.77	0.65
1:B:80:PHE:CE1	1:B:165:LEU:HA	2.29	0.65
1:A:81:VAL:H	1:A:166:ARG:HG2	1.62	0.65
1:A:366:LYS:HG3	1:A:395:ARG:NH1	2.09	0.65
1:B:110:HIS:O	1:B:111:TYR:HD1	1.79	0.65
1:B:277:LEU:H	1:B:277:LEU:CD2	1.97	0.65
1:E:188:LEU:HD12	1:E:434:PHE:CE2	2.32	0.65
1:E:333:GLU:OE1	1:E:336:SER:HB2	1.95	0.65
2:F:53:PRO:HB2	2:F:56:VAL:HG23	1.78	0.65
2:F:66:VAL:HA	2:F:88:TYR:OH	1.97	0.65
1:A:90:HIS:O	1:A:206:LEU:HD23	1.96	0.65
2:C:381:THR:O	2:C:385:THR:OG1	2.13	0.65
1:B:107:ASN:O	1:B:109:VAL:HG13	1.96	0.65
1:E:233:HIS:HB2	1:E:263:PHE:HE2	1.60	0.65
1:E:584:PHE:CE1	1:E:588:LEU:HD12	2.31	0.65
1:A:366:LYS:HE3	1:A:395:ARG:CZ	2.20	0.65
1:A:386:LEU:HD23	1:A:419:VAL:HG23	1.76	0.65
1:A:607:PHE:CD1	2:C:4:PRO:HB3	2.27	0.65
2:C:387:ASN:N	2:C:387:ASN:OD1	2.30	0.65
2:D:2:ILE:CG1	1:B:609:ARG:HE	2.10	0.65
2:D:349:PHE:CE2	2:D:356:TRP:CD2	2.80	0.65
1:B:297:LEU:CB	1:B:344:LEU:CD1	2.61	0.65
2:F:152:LEU:C	2:F:155:LEU:HD13	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:501:VAL:C	2:F:502:LEU:HG	2.22	0.65
1:E:310:HIS:CG	1:E:314:GLY:HA3	2.30	0.65
2:C:40:ARG:O	2:C:43:SER:N	2.28	0.65
2:D:70:GLU:HG3	2:D:70:GLU:O	1.96	0.65
2:D:99:LEU:C	2:D:102:PRO:HD2	2.21	0.65
2:D:184:ARG:HD3	1:B:592:ARG:HD3	1.79	0.65
1:B:347:HIS:NE2	1:B:351:GLN:CD	2.55	0.65
1:A:368:PHE:HE1	2:D:146:TRP:HE1	0.66	0.65
1:A:406:PHE:HD1	1:A:407:SER:N	1.90	0.65
2:D:493:ASN:HD22	2:D:493:ASN:N	1.94	0.65
1:B:98:GLN:OE1	1:B:165:LEU:HD11	1.96	0.65
1:B:471:TYR:HE1	1:B:550:GLN:CB	2.08	0.65
1:E:293:ASP:OD2	1:E:327:SER:O	2.14	0.65
2:F:82:ILE:HG22	2:F:83:PRO:HD3	1.78	0.65
1:A:105:VAL:CG1	1:A:132:ASP:CB	2.70	0.65
1:A:246:GLY:C	1:A:363:GLY:HA3	2.18	0.65
2:D:31:GLU:HA	2:D:31:GLU:OE1	1.97	0.65
2:D:218:ASN:ND2	2:D:221:ASP:OD2	2.30	0.65
2:D:337:LEU:O	2:D:341:ILE:HG13	1.95	0.65
2:D:349:PHE:HE2	2:D:356:TRP:CD1	2.15	0.65
1:E:257:ARG:CD	1:E:308:GLY:O	2.45	0.65
1:E:359:LEU:HD12	1:E:360:ASN:C	2.22	0.65
2:F:17:GLU:OE2	2:F:40:ARG:NH1	2.30	0.65
2:F:99:LEU:C	2:F:102:PRO:HD2	2.22	0.65
2:F:337:LEU:CD2	2:F:370:TYR:CZ	2.72	0.65
2:F:345:ASN:HB3	2:F:348:ASN:HB2	1.78	0.65
2:F:312:GLN:CD	2:F:323:LYS:NZ	2.54	0.65
1:B:261:GLU:O	1:B:264:THR:OG1	2.14	0.64
1:B:397:LEU:CD1	1:B:400:LEU:HD11	2.22	0.64
1:E:230:TYR:HB3	1:E:262:LYS:HZ3	1.60	0.64
1:E:615:HIS:NE2	2:F:102:PRO:CG	2.60	0.64
2:D:46:LEU:CD2	1:B:577:ARG:CD	2.75	0.64
2:F:312:GLN:CD	2:F:323:LYS:HD3	2.21	0.64
1:A:106:TYR:CD2	1:A:120:PHE:HE2	2.15	0.64
1:A:348:LEU:HD11	1:A:353:PHE:CB	2.22	0.64
2:D:312:GLN:NE2	2:D:427:TYR:HE2	1.96	0.64
1:B:389:GLU:C	1:B:390:THR:HG22	2.22	0.64
1:E:613:LEU:O	2:F:159:TYR:CD1	2.51	0.64
1:A:196:PHE:CD1	1:A:197:PRO:HD2	2.32	0.64
1:A:592:ARG:HH21	2:C:184:ARG:HH21	1.02	0.64
1:B:185:VAL:HG23	1:B:188:LEU:HD12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:346:ASP:OD1	1:E:379:LYS:NZ	2.27	0.64
1:A:301:LEU:CD2	1:A:318:GLN:NE2	2.60	0.64
1:A:371:GLN:HE21	1:A:371:GLN:HA	1.63	0.64
2:C:75:LEU:HD23	2:C:76:GLY:N	2.12	0.64
2:C:231:GLY:O	2:C:234:LEU:HG	1.98	0.64
2:D:62:ILE:CG2	2:D:152:LEU:HD21	2.28	0.64
2:D:68:LEU:O	2:D:71:LYS:CG	2.45	0.64
1:B:469:ILE:HG12	1:B:552:MET:O	1.98	0.64
1:B:469:ILE:HG13	1:B:552:MET:HB3	1.79	0.64
1:B:538:THR:HG22	1:B:539:LEU:O	1.98	0.64
1:E:256:LEU:HD22	1:E:358:LEU:HD12	1.80	0.64
1:E:369:GLY:C	1:E:372:ILE:HG22	2.22	0.64
1:E:491:ASN:ND2	2:F:39:GLN:CB	2.59	0.64
2:F:11:ASP:OD2	2:F:13:ALA:HB3	1.97	0.64
1:A:98:GLN:HE21	1:A:115:ARG:C	2.05	0.64
1:A:491:ASN:ND2	2:C:36:ARG:CZ	2.59	0.64
1:A:492:PRO:HA	1:A:495:ILE:CD1	2.26	0.64
2:C:307:ARG:HB2	2:C:307:ARG:NH1	2.02	0.64
1:E:106:TYR:CD2	1:E:120:PHE:HE2	2.15	0.64
1:A:265:GLN:OE1	1:A:265:GLN:HA	1.96	0.64
1:A:395:ARG:HG3	1:A:396:HIS:N	2.12	0.64
1:A:590:SER:CB	2:C:184:ARG:CZ	2.75	0.64
2:C:80:ASP:O	2:C:81:SER:OG	2.08	0.64
1:E:471:TYR:OH	1:E:523:PHE:CD1	2.47	0.64
2:C:6:ILE:HG21	2:C:51:TYR:CE1	2.33	0.64
2:C:55:VAL:HG23	2:C:155:LEU:CD2	2.27	0.64
2:D:312:GLN:NE2	2:D:427:TYR:CE2	2.66	0.64
1:E:123:PRO:CG	1:E:309:GLN:HG2	2.27	0.64
1:E:269:ASP:N	1:E:269:ASP:OD2	2.28	0.64
2:C:104:GLN:OE1	2:C:104:GLN:HA	1.98	0.64
2:C:130:HIS:HB2	2:C:134:HIS:CE1	2.33	0.64
1:B:207:LEU:HD13	1:B:213:ILE:CD1	2.28	0.64
1:B:242:ILE:HD12	1:B:242:ILE:N	2.12	0.64
1:B:288:GLU:C	1:B:289:TYR:HD2	2.06	0.64
1:B:408:THR:CB	1:B:414:TYR:CA	2.75	0.64
1:E:71:TYR:HD1	1:E:80:PHE:CD2	2.16	0.64
1:E:241:ARG:O	1:E:383:THR:N	2.31	0.64
2:F:34:ARG:O	2:F:37:ALA:N	2.30	0.64
1:A:299:LYS:O	1:A:300:ILE:HD12	1.97	0.64
1:A:469:ILE:CD1	2:C:488:TRP:CZ3	2.70	0.64
2:D:131:TRP:HA	2:D:131:TRP:HE3	1.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:350:LYS:NZ	2:D:401:THR:CG2	2.61	0.64
1:E:385:LEU:N	1:E:417:GLU:HB3	2.13	0.64
1:E:567:GLN:HE21	1:E:567:GLN:CA	2.01	0.64
1:E:615:HIS:CE1	2:F:102:PRO:CG	2.80	0.64
2:F:352:LYS:O	2:F:356:TRP:HD1	1.81	0.64
1:A:590:SER:OG	2:C:184:ARG:CZ	2.46	0.63
2:C:12:PHE:O	2:C:12:PHE:HD1	1.80	0.63
2:C:291:MET:HE3	2:C:340:ILE:HG22	1.77	0.63
2:D:82:ILE:CG2	2:D:83:PRO:HD3	2.25	0.63
1:B:338:LEU:HD21	1:B:372:ILE:CD1	2.27	0.63
1:B:395:ARG:HD2	1:B:395:ARG:C	2.23	0.63
1:E:358:LEU:HD23	1:E:358:LEU:N	2.13	0.63
1:A:489:ASP:CB	2:D:79:GLN:O	2.46	0.63
1:E:400:LEU:HD12	1:E:400:LEU:H	1.63	0.63
2:C:156:TYR:OH	2:C:161:ASN:ND2	2.31	0.63
2:C:352:LYS:HB3	2:C:355:ASN:ND2	2.13	0.63
2:C:362:GLU:HG2	2:C:490:ARG:HG2	1.80	0.63
1:B:450:LYS:O	1:B:559:CYS:HB3	1.97	0.63
1:E:295:ILE:HD11	1:E:337:TYR:CD2	2.33	0.63
2:D:202:TRP:CE3	2:D:209:PHE:CD2	2.75	0.63
2:D:329:TRP:CH2	2:D:424:ILE:HD11	2.31	0.63
1:B:128:ILE:HG12	1:B:213:ILE:HD12	1.81	0.63
1:B:469:ILE:CD1	1:B:554:ILE:CG2	2.71	0.63
1:A:71:TYR:HD2	1:A:72:GLU:N	1.96	0.63
1:A:286:GLN:HG3	1:A:286:GLN:O	1.97	0.63
1:A:301:LEU:HD23	1:A:318:GLN:NE2	2.13	0.63
2:C:95:PHE:HE1	2:C:155:LEU:HD11	1.61	0.63
2:C:181:GLY:O	2:C:185:ASN:HB2	1.99	0.63
1:B:174:GLY:O	1:B:177:GLU:HG2	1.99	0.63
1:B:365:ILE:HD12	1:B:366:LYS:H	1.60	0.63
2:F:75:LEU:O	2:F:77:VAL:CG2	2.32	0.63
1:A:96:ARG:HG3	1:A:168:PHE:CD1	2.33	0.63
1:A:489:ASP:CG	2:D:79:GLN:O	2.41	0.63
2:C:79:GLN:NE2	3:C:601:HOH:O	2.30	0.63
2:C:336:LEU:HD12	2:C:336:LEU:C	2.22	0.63
2:D:5:ARG:NE	1:B:610:ARG:HG2	2.14	0.63
1:B:105:VAL:CG2	1:B:134:SER:CB	2.76	0.63
1:B:545:ILE:HD13	1:B:552:MET:HE3	1.79	0.63
1:A:126:GLN:NE2	1:A:257:ARG:NH2	2.43	0.63
2:C:52:LEU:HD13	2:C:53:PRO:HD2	1.73	0.63
2:C:99:LEU:H	2:C:99:LEU:CD2	2.02	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:290:LEU:HD12	2:C:297:PHE:CZ	2.34	0.63
1:B:194:PRO:HG3	1:B:205:HIS:NE2	2.13	0.63
1:B:233:HIS:HE1	1:B:275:GLU:OE1	1.79	0.63
1:B:239:ASP:CB	1:B:355:GLY:C	2.71	0.63
1:E:83:LEU:HD12	1:E:138:GLY:HA3	1.81	0.63
2:F:411:ASN:HA	2:F:414:ASN:HB3	1.80	0.63
2:C:90:MET:HE2	2:D:89:VAL:CG1	2.28	0.63
2:C:304:TRP:O	2:C:308:ASN:ND2	2.30	0.63
1:E:71:TYR:CD1	1:E:80:PHE:CD2	2.86	0.63
2:F:328:ALA:HB3	2:F:331:GLU:CG	2.29	0.63
2:F:369:LEU:HA	2:F:415:LEU:HD12	1.81	0.63
1:A:123:PRO:HG3	1:A:309:GLN:HG2	1.80	0.63
1:A:182:TYR:HB3	1:A:185:VAL:HG12	1.81	0.63
1:A:366:LYS:HG3	1:A:396:HIS:HB3	1.71	0.63
1:A:386:LEU:HD23	1:A:419:VAL:CG2	2.28	0.63
1:E:186:ASN:C	1:E:186:ASN:HD22	2.05	0.63
1:A:507:TYR:HD2	1:A:576:VAL:CG2	2.12	0.62
1:B:297:LEU:HB3	1:B:344:LEU:HD11	1.76	0.62
1:B:364:TRP:HA	1:B:364:TRP:CE3	2.33	0.62
1:B:387:PHE:CD2	1:B:397:LEU:HD22	2.34	0.62
1:B:546:ASP:CB	1:B:549:GLN:HG3	2.28	0.62
1:E:614:GLU:CD	2:F:159:TYR:OH	2.41	0.62
1:A:469:ILE:HD13	2:C:488:TRP:CD2	2.34	0.62
1:A:516:GLU:O	1:A:516:GLU:HG2	1.97	0.62
1:B:252:LYS:HD2	1:B:360:ASN:HB2	1.80	0.62
1:B:594:ILE:HG22	1:B:596:TRP:H	1.64	0.62
1:E:301:LEU:CD1	1:E:301:LEU:H	2.08	0.62
1:E:562:GLN:CA	1:E:565:ASP:HB2	2.29	0.62
2:C:119:ILE:CG1	2:C:121:LEU:H	2.12	0.62
2:D:341:ILE:HD13	2:D:374:SER:CB	2.29	0.62
1:B:387:PHE:HE2	1:B:397:LEU:HD11	1.64	0.62
1:B:590:SER:C	1:B:593:THR:HG1	2.05	0.62
1:E:471:TYR:CZ	1:E:523:PHE:CE1	2.88	0.62
2:C:80:ASP:CG	2:D:64:CYS:HG	2.07	0.62
2:D:69:ASP:HB3	2:D:84:ILE:HD11	1.82	0.62
2:D:184:ARG:CB	1:B:592:ARG:HD3	2.29	0.62
2:D:310:ARG:CZ	2:D:495:LYS:HE3	2.30	0.62
1:B:120:PHE:HA	1:B:307:LEU:O	1.99	0.62
1:E:100:VAL:HG12	1:E:101:LYS:HE2	1.81	0.62
1:E:169:ASN:OD1	1:E:203:THR:CB	2.46	0.62
1:E:522:THR:OG1	1:E:550:GLN:NE2	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:577:ARG:NE	1:E:578:ASN:O	2.29	0.62
1:A:206:LEU:HD21	1:A:208:HIS:CE1	2.34	0.62
1:A:342:ASP:OD1	1:A:375:HIS:NE2	2.31	0.62
2:C:96:VAL:HB	2:C:128:LEU:HD11	1.80	0.62
2:D:146:TRP:CH2	2:D:150:GLU:CD	2.73	0.62
1:B:96:ARG:NE	1:B:171:ASN:OD1	2.32	0.62
1:B:128:ILE:HG12	1:B:213:ILE:CD1	2.29	0.62
1:B:333:GLU:OE2	1:B:336:SER:N	2.22	0.62
1:E:106:TYR:HH	1:E:122:HIS:CD2	2.14	0.62
1:A:617:TRP:O	2:D:136:ARG:HD3	1.99	0.62
1:E:71:TYR:CE2	1:E:73:GLY:HA3	2.35	0.62
1:E:507:TYR:CD1	1:E:536:PHE:HA	2.33	0.62
2:C:129:ARG:NH1	2:C:129:ARG:HG2	2.15	0.62
2:D:278:PHE:HE1	2:D:279:PHE:CE2	2.16	0.62
1:B:359:LEU:HD11	1:B:361:LEU:HG	1.82	0.62
1:E:106:TYR:O	1:E:109:VAL:HG22	1.99	0.62
1:E:451:ILE:C	1:E:452:THR:HG23	2.25	0.62
2:F:298:ASP:CG	2:F:356:TRP:HZ2	2.07	0.62
1:A:69:ILE:HB	1:A:80:PHE:O	2.00	0.62
1:A:365:ILE:C	1:A:397:LEU:HD22	2.25	0.62
1:A:365:ILE:HB	1:A:397:LEU:HD22	1.82	0.62
2:C:209:PHE:CE2	2:C:254:ILE:CG2	2.77	0.62
2:D:492:GLN:HB2	2:D:493:ASN:ND2	2.15	0.62
1:B:91:LEU:CD1	1:B:204:TYR:HB2	2.28	0.62
1:B:121:TRP:N	1:B:307:LEU:O	2.30	0.62
1:E:118:LEU:HB2	1:E:305:ILE:HG22	1.81	0.62
1:E:245:ILE:HD12	1:E:373:LEU:HD22	1.81	0.62
1:E:471:TYR:OH	1:E:523:PHE:HE1	1.81	0.62
2:F:129:ARG:NH2	2:F:129:ARG:HB3	2.15	0.62
2:F:148:ALA:O	2:F:152:LEU:HB2	2.00	0.62
1:A:366:LYS:HD2	1:A:396:HIS:HB3	1.82	0.62
1:B:86:LYS:CA	1:B:133:PHE:HB3	2.24	0.62
1:A:472:GLY:HA2	1:A:550:GLN:HE21	1.65	0.62
1:A:492:PRO:C	1:A:495:ILE:HG13	2.22	0.62
2:C:98:GLY:O	2:C:102:PRO:HD3	2.00	0.62
2:D:86:LEU:CD1	2:D:138:LEU:HD22	2.29	0.62
2:D:333:GLN:HG2	2:D:338:ASP:OD2	2.00	0.62
1:E:280:LEU:HG	1:E:297:LEU:HD12	1.81	0.62
1:E:471:TYR:HH	1:E:523:PHE:HD1	1.45	0.62
2:F:158:HIS:O	2:F:162:ASP:OD2	2.18	0.62
1:A:395:ARG:HH21	1:A:395:ARG:CG	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:59:THR:HG21	2:C:160:TRP:HE1	1.63	0.61
2:C:191:TYR:OH	2:C:264:LEU:O	2.18	0.61
1:B:80:PHE:CE1	1:B:165:LEU:CA	2.82	0.61
1:B:240:THR:OG1	1:B:242:ILE:HD11	1.99	0.61
1:E:106:TYR:OH	1:E:122:HIS:CD2	2.53	0.61
1:E:287:PRO:O	1:E:443:LYS:NZ	2.33	0.61
1:E:603:PRO:O	1:E:604:PHE:HB2	2.00	0.61
1:A:471:TYR:CE1	1:A:545:ILE:HG23	2.35	0.61
2:C:316:SER:OG	2:C:317:ASN:OD1	2.18	0.61
1:E:387:PHE:CE1	1:E:401:THR:HG21	2.35	0.61
1:E:387:PHE:HE1	1:E:401:THR:CG2	2.13	0.61
2:C:497:LYS:CD	2:C:502:LEU:C	2.54	0.61
2:D:105:GLN:HG2	1:B:615:HIS:HD2	1.65	0.61
2:D:494:TRP:HH2	2:D:497:LYS:HB2	1.66	0.61
2:D:501:VAL:O	2:D:501:VAL:HG23	2.00	0.61
1:B:449:HIS:CB	1:B:457:ASP:O	2.39	0.61
1:B:461:LEU:HD12	1:B:461:LEU:H	1.65	0.61
1:E:376:ILE:O	1:E:380:TYR:N	2.28	0.61
1:E:469:ILE:HD11	2:F:488:TRP:CH2	2.34	0.61
2:D:430:ILE:H	2:D:430:ILE:CD1	1.97	0.61
1:E:272:THR:HG22	3:E:707:HOH:O	1.99	0.61
1:E:364:TRP:CG	1:E:369:GLY:CA	2.83	0.61
1:E:507:TYR:HD1	1:E:536:PHE:HA	1.65	0.61
1:A:282:LEU:HD12	1:A:359:LEU:HD11	1.83	0.61
1:A:481:ILE:HG22	1:A:575:ILE:O	2.01	0.61
2:C:202:TRP:CE2	2:C:286:LEU:HD12	2.35	0.61
2:D:336:LEU:CD1	2:D:340:ILE:HG13	2.31	0.61
1:B:247:GLY:H	1:B:365:ILE:HG21	1.65	0.61
1:A:185:VAL:HG22	1:A:185:VAL:O	2.00	0.61
1:A:333:GLU:OE2	1:A:333:GLU:HA	2.00	0.61
1:A:589:PRO:CD	1:A:596:TRP:CZ3	2.75	0.61
2:D:323:LYS:HG2	2:D:427:TYR:CE2	2.36	0.61
1:B:243:MET:CE	1:B:380:TYR:HD2	2.13	0.61
1:B:326:GLY:O	1:B:578:ASN:OD1	2.12	0.61
1:B:347:HIS:HD2	1:B:351:GLN:HG2	1.66	0.61
1:B:366:LYS:CB	1:B:395:ARG:HH11	2.10	0.61
1:B:529:CYS:C	1:B:530:THR:OG1	2.38	0.61
1:E:230:TYR:CG	1:E:262:LYS:NZ	2.68	0.61
1:E:549:GLN:HB2	1:E:551:ILE:CG2	2.30	0.61
1:A:603:PRO:HB2	1:A:604:PHE:HD2	1.66	0.61
2:C:278:PHE:HZ	2:C:287:LEU:CD1	2.07	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:485:VAL:HG21	1:B:470:SER:CB	2.29	0.61
1:B:321:LEU:CD2	1:B:344:LEU:HD12	2.17	0.61
1:E:110:HIS:HD2	1:E:111:TYR:N	1.98	0.61
1:E:185:VAL:O	1:E:185:VAL:HG22	2.00	0.61
1:E:507:TYR:HE1	1:E:536:PHE:HB2	1.65	0.61
2:F:8:PRO:HD3	2:F:51:TYR:O	2.00	0.61
2:F:275:LEU:CD1	2:F:275:LEU:H	1.94	0.61
1:A:76:ASP:OD2	1:A:78:THR:HG22	2.01	0.61
2:C:216:TRP:CD1	2:C:216:TRP:H	2.18	0.61
1:B:527:GLN:O	1:B:528:SER:OG	2.15	0.61
1:E:71:TYR:CE1	1:E:80:PHE:HE2	2.13	0.61
1:E:365:ILE:HD12	1:E:365:ILE:H	1.66	0.61
1:E:480:GLY:H	1:E:524:PRO:CB	2.14	0.61
1:E:531:SER:O	1:E:534:LYS:HE2	2.00	0.61
1:E:546:ASP:CG	1:E:549:GLN:HE22	2.09	0.61
1:A:110:HIS:O	1:A:111:TYR:HD1	1.83	0.61
1:A:174:GLY:C	1:A:177:GLU:OE1	2.44	0.61
2:C:280:ASN:O	2:C:281:ASN:OD1	2.19	0.61
2:D:188:LEU:HD11	2:D:192:MET:HG3	1.83	0.61
2:D:494:TRP:CH2	2:D:497:LYS:HB2	2.35	0.61
2:D:499:PHE:HD1	1:B:543:HIS:HA	1.66	0.61
1:E:482:GLN:CB	1:E:576:VAL:HG22	2.25	0.61
2:F:66:VAL:HA	2:F:88:TYR:HH	1.65	0.61
1:A:522:THR:OG1	1:A:550:GLN:OE1	2.19	0.61
2:C:80:ASP:OD1	2:D:64:CYS:SG	2.56	0.61
2:D:485:VAL:HG13	2:D:485:VAL:O	2.01	0.61
1:B:90:HIS:CE1	1:B:128:ILE:CG1	2.71	0.61
1:A:97:LEU:O	1:A:118:LEU:HD23	2.01	0.60
1:A:213:ILE:HD12	1:A:213:ILE:C	2.26	0.60
2:C:314:ASP:HB3	2:C:495:LYS:HZ1	1.64	0.60
2:D:71:LYS:HB3	2:D:71:LYS:HZ3	1.66	0.60
1:B:566:LYS:O	1:B:567:GLN:HG2	2.00	0.60
2:F:335:ARG:HH11	2:F:335:ARG:CG	2.13	0.60
1:A:79:MET:SD	1:A:81:VAL:HG23	2.41	0.60
1:A:177:GLU:HG2	2:C:267:LEU:CD2	2.30	0.60
1:A:589:PRO:CG	1:A:596:TRP:CZ3	2.83	0.60
2:C:64:CYS:CB	2:D:82:ILE:HG21	2.31	0.60
2:C:159:TYR:CE2	2:C:160:TRP:CZ3	2.89	0.60
2:C:310:ARG:HH11	2:C:310:ARG:CG	2.14	0.60
1:B:123:PRO:HB3	1:B:311:LEU:HD21	1.82	0.60
1:B:562:GLN:O	1:B:566:LYS:N	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ASN:HD22	1:A:258:LEU:CD2	2.14	0.60
1:A:284:PRO:C	1:A:287:PRO:HD3	2.27	0.60
2:C:54:HIS:HD2	2:C:98:GLY:C	2.07	0.60
2:C:141:LEU:HD23	2:C:145:ARG:NH2	2.16	0.60
2:C:345:ASN:HB3	2:C:348:ASN:HB2	1.83	0.60
2:D:188:LEU:HD11	2:D:192:MET:CG	2.31	0.60
1:B:90:HIS:CD2	1:B:207:LEU:O	2.54	0.60
1:E:185:VAL:HG23	1:E:188:LEU:HD22	1.82	0.60
1:E:187:TYR:CD1	1:E:192:LYS:CB	2.81	0.60
1:E:610:ARG:HD2	2:F:167:ASP:CG	2.26	0.60
2:F:408:LEU:O	2:F:412:ILE:HG13	2.02	0.60
1:A:284:PRO:O	1:A:287:PRO:HD3	2.00	0.60
2:C:110:ILE:HG23	2:C:114:THR:HB	1.77	0.60
2:D:133:THR:C	2:D:134:HIS:HD2	2.09	0.60
2:D:212:TYR:CZ	2:D:250:SER:OG	2.53	0.60
1:B:115:ARG:HB2	1:B:115:ARG:HH21	1.61	0.60
1:B:473:LYS:HG2	1:B:474:GLY:N	2.15	0.60
2:F:154:TRP:CE3	2:F:155:LEU:HA	2.36	0.60
1:A:241:ARG:HB3	1:A:380:TYR:CZ	2.37	0.60
1:A:467:LEU:HD21	1:A:556:VAL:CG2	2.31	0.60
1:A:588:LEU:HD11	2:C:6:ILE:HD13	1.82	0.60
2:C:125:PHE:HB3	2:C:128:LEU:HD21	1.82	0.60
2:C:394:ARG:HH11	2:C:394:ARG:CG	2.15	0.60
1:B:80:PHE:HD1	1:B:166:ARG:CB	2.15	0.60
1:B:103:GLY:N	1:B:134:SER:O	2.23	0.60
1:E:262:LYS:HD2	1:E:262:LYS:O	2.01	0.60
2:F:275:LEU:HD12	2:F:275:LEU:N	2.04	0.60
1:A:172:HIS:HA	1:A:454:PHE:O	1.99	0.60
2:C:100:LEU:HD12	2:C:100:LEU:O	2.02	0.60
2:D:101:ASP:O	2:D:103:THR:OG1	2.17	0.60
2:D:105:GLN:OE1	2:D:105:GLN:N	2.34	0.60
2:D:124:TRP:HA	2:D:127:ASP:OD1	2.02	0.60
1:B:99:VAL:CB	1:B:166:ARG:HH21	2.13	0.60
1:E:525:ILE:HD13	1:E:525:ILE:N	2.15	0.60
2:F:50:GLN:HB2	2:F:51:TYR:CD2	2.37	0.60
2:D:199:LEU:HD11	2:D:281:ASN:CB	2.30	0.60
2:D:209:PHE:CE2	2:D:254:ILE:HG23	2.35	0.60
1:E:91:LEU:O	1:E:122:HIS:ND1	2.28	0.60
1:E:522:THR:HG23	1:E:522:THR:O	2.01	0.60
2:F:278:PHE:CE2	2:F:282:TYR:HB2	2.37	0.60
1:A:121:TRP:N	1:A:307:LEU:O	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ASN:O	1:A:343:LYS:HG3	2.01	0.60
1:A:366:LYS:CD	1:A:396:HIS:HB3	2.31	0.60
2:D:38:VAL:HG11	2:D:64:CYS:HB2	1.84	0.60
2:D:489:SER:O	1:B:467:LEU:HA	2.00	0.60
1:B:167:VAL:O	1:B:204:TYR:CE1	2.54	0.60
1:E:289:TYR:C	1:E:317:PHE:HE2	2.10	0.60
2:F:126:VAL:CG1	2:F:129:ARG:HD3	2.30	0.60
1:A:75:GLU:O	1:A:76:ASP:OD2	2.18	0.60
1:A:96:ARG:CB	1:A:168:PHE:HE1	2.15	0.60
2:C:345:ASN:OD1	2:C:347:LYS:N	2.34	0.60
2:C:349:PHE:HZ	2:C:353:TRP:HZ3	1.50	0.60
1:B:590:SER:HB2	1:B:593:THR:OG1	2.02	0.60
2:F:272:ASN:C	2:F:275:LEU:HD12	2.23	0.60
1:A:121:TRP:HB3	1:A:309:GLN:O	2.02	0.60
1:A:174:GLY:O	1:A:177:GLU:OE1	2.20	0.60
1:A:370:MET:O	1:A:374:ASN:CG	2.45	0.60
1:A:509:TYR:CZ	1:A:512:GLU:CB	2.85	0.60
2:D:36:ARG:NH1	1:B:494:ASP:OD1	2.34	0.60
2:D:492:GLN:C	2:D:493:ASN:HD22	2.10	0.60
1:B:80:PHE:HZ	1:B:165:LEU:CA	2.06	0.60
1:B:174:GLY:HA3	1:B:456:TYR:O	2.02	0.60
1:B:175:LEU:CD1	1:B:456:TYR:CD2	2.83	0.60
1:E:166:ARG:HH11	1:E:166:ARG:CG	2.15	0.60
2:C:501:VAL:O	2:C:501:VAL:HG12	2.02	0.59
2:D:322:LEU:HD23	2:D:323:LYS:N	2.17	0.59
1:B:121:TRP:HB3	1:B:309:GLN:O	2.02	0.59
1:B:397:LEU:HD12	1:B:400:LEU:CG	2.32	0.59
1:E:70:THR:HG22	1:E:70:THR:O	2.02	0.59
1:E:118:LEU:HB2	1:E:305:ILE:CG2	2.32	0.59
1:E:212:ARG:HH21	1:E:212:ARG:CG	2.14	0.59
1:A:190:LYS:HD3	1:A:205:HIS:HB2	1.84	0.59
1:A:206:LEU:HD22	1:A:207:LEU:H	1.67	0.59
1:A:374:ASN:HD21	1:A:400:LEU:C	2.10	0.59
1:B:445:LEU:HD11	1:B:586:ASP:HB2	1.84	0.59
1:B:559:CYS:SG	1:B:560:HIS:N	2.74	0.59
1:A:465:ALA:HA	2:C:494:TRP:CZ3	2.37	0.59
1:B:175:LEU:HA	1:B:458:PHE:HZ	1.67	0.59
1:B:207:LEU:HA	1:B:211:ASP:OD1	2.01	0.59
1:B:283:ASP:OD1	1:B:285:GLY:N	2.34	0.59
1:E:216:LEU:HG	1:E:217:SER:O	2.02	0.59
1:E:268:ARG:HH11	1:E:268:ARG:CG	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:493:GLN:NE2	2:F:36:ARG:HH22	1.96	0.59
2:F:102:PRO:O	2:F:104:GLN:HG2	2.02	0.59
2:F:275:LEU:O	2:F:279:PHE:HD2	1.85	0.59
1:A:509:TYR:CE2	1:A:512:GLU:CB	2.86	0.59
2:D:54:HIS:NE2	2:D:98:GLY:HA3	2.17	0.59
2:D:84:ILE:HD12	2:D:88:TYR:CD2	2.38	0.59
2:D:312:GLN:OE1	2:D:427:TYR:CE2	2.55	0.59
2:D:492:GLN:HB2	2:D:493:ASN:HD22	1.67	0.59
1:B:104:ILE:HD11	1:B:166:ARG:HH22	1.67	0.59
1:B:169:ASN:OD1	1:B:203:THR:N	2.33	0.59
1:B:390:THR:O	1:B:394:LYS:HB3	2.02	0.59
1:E:233:HIS:HB2	1:E:263:PHE:CE2	2.37	0.59
1:A:234:LYS:CE	1:A:270:SER:OG	2.50	0.59
1:A:256:LEU:O	1:A:260:LEU:N	2.34	0.59
1:A:395:ARG:HG3	1:A:396:HIS:H	1.66	0.59
1:A:471:TYR:HH	1:A:547:THR:HA	1.67	0.59
2:C:82:ILE:HG21	2:D:64:CYS:SG	2.43	0.59
1:B:231:LEU:O	1:B:235:ASN:ND2	2.35	0.59
1:B:364:TRP:CD1	1:B:369:GLY:CA	2.86	0.59
1:E:71:TYR:CE2	1:E:73:GLY:CA	2.85	0.59
1:E:584:PHE:CZ	1:E:588:LEU:CD1	2.86	0.59
2:F:337:LEU:HD21	2:F:370:TYR:CZ	2.37	0.59
1:A:67:ASP:N	1:A:67:ASP:OD2	2.35	0.59
1:A:185:VAL:CG2	1:A:188:LEU:HD12	2.32	0.59
2:C:129:ARG:CG	2:C:129:ARG:HH11	2.15	0.59
2:C:224:ILE:CG2	2:C:229:PHE:HZ	2.16	0.59
2:D:96:VAL:C	2:D:100:LEU:CB	2.69	0.59
2:D:133:THR:CB	2:D:134:HIS:CD2	2.85	0.59
1:B:391:ALA:C	1:B:393:SER:HA	2.26	0.59
1:B:448:PHE:HB3	1:B:461:LEU:HD21	1.85	0.59
1:E:100:VAL:HG12	1:E:101:LYS:CG	2.26	0.59
2:F:66:VAL:HA	2:F:88:TYR:CE1	2.37	0.59
1:A:69:ILE:HG22	1:A:69:ILE:O	2.02	0.59
2:D:359:LEU:HA	2:D:362:GLU:HB3	1.84	0.59
2:D:426:LEU:N	2:D:426:LEU:HD23	2.17	0.59
1:B:177:GLU:HG2	1:B:458:PHE:HD2	0.68	0.59
1:B:461:LEU:O	1:B:555:TYR:CE2	2.55	0.59
1:E:98:GLN:CG	1:E:117:ILE:CG2	2.74	0.59
1:E:408:THR:CB	1:E:414:TYR:CB	2.81	0.59
2:F:262:GLN:O	2:F:266:LYS:HG3	2.03	0.59
1:A:183:ARG:HH21	1:A:183:ARG:CG	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:336:LEU:O	2:D:340:ILE:HG13	2.01	0.59
1:B:478:ILE:HG23	1:B:575:ILE:HD11	1.85	0.59
1:E:333:GLU:CD	1:E:336:SER:HB2	2.28	0.59
1:E:365:ILE:HD12	1:E:366:LYS:H	1.67	0.59
1:E:491:ASN:OD1	2:F:36:ARG:CD	2.47	0.59
2:F:329:TRP:O	2:F:333:GLN:N	2.31	0.59
1:A:183:ARG:NH2	1:A:183:ARG:HG2	2.16	0.59
1:A:359:LEU:HD12	1:A:360:ASN:C	2.27	0.59
1:A:406:PHE:CD1	1:A:407:SER:N	2.68	0.59
2:D:353:TRP:HA	2:D:356:TRP:HD1	1.65	0.59
1:B:105:VAL:O	1:B:132:ASP:HB2	2.03	0.59
1:B:542:ILE:CD1	1:B:552:MET:HE2	2.33	0.59
1:E:248:LYS:O	1:E:249:ASN:HB3	2.01	0.59
1:E:496:LYS:O	1:E:500:GLU:HG3	2.03	0.59
1:A:353:PHE:HE1	1:A:355:GLY:O	1.85	0.59
2:C:97:ASN:CG	2:C:129:ARG:HE	2.09	0.59
2:C:304:TRP:CE3	2:C:308:ASN:ND2	2.71	0.59
2:C:314:ASP:CB	2:C:495:LYS:NZ	2.66	0.59
2:D:23:TYR:HE2	2:D:156:TYR:CG	2.16	0.59
1:B:280:LEU:O	1:B:359:LEU:HB2	2.03	0.59
1:B:389:GLU:HB3	1:B:394:LYS:HA	1.85	0.59
1:A:90:HIS:HE2	1:A:213:ILE:CD1	2.17	0.58
2:D:122:PRO:CG	2:D:125:PHE:CE2	2.86	0.58
1:B:80:PHE:CD1	1:B:166:ARG:CB	2.85	0.58
1:E:85:GLU:C	1:E:133:PHE:HD1	2.11	0.58
1:E:310:HIS:CB	1:E:314:GLY:HA3	2.32	0.58
1:A:288:GLU:O	1:A:289:TYR:HB2	2.01	0.58
2:C:314:ASP:HB3	2:C:495:LYS:NZ	2.17	0.58
1:B:247:GLY:CA	1:B:365:ILE:CG2	2.75	0.58
1:B:359:LEU:HD12	1:B:360:ASN:CA	2.32	0.58
1:B:448:PHE:HB3	1:B:461:LEU:HD23	1.83	0.58
1:E:233:HIS:CG	1:E:263:PHE:CE2	2.91	0.58
1:A:489:ASP:OD1	2:D:79:GLN:O	2.21	0.58
1:A:617:TRP:C	1:A:618:LYS:HG3	2.28	0.58
2:C:23:TYR:CE2	2:C:156:TYR:CG	2.89	0.58
2:C:307:ARG:HH11	2:C:307:ARG:CG	2.15	0.58
2:D:113:HIS:CE1	2:D:126:VAL:CG1	2.86	0.58
1:E:241:ARG:CA	1:E:383:THR:OG1	2.50	0.58
1:E:489:ASP:C	1:E:490:LEU:HD12	2.28	0.58
1:A:502:THR:CB	1:A:577:ARG:HH22	2.12	0.58
2:C:207:ASN:HA	2:C:210:LEU:CD1	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:184:ARG:HE	1:B:183:ARG:HH12	1.49	0.58
1:B:98:GLN:HB3	1:B:165:LEU:CD1	2.32	0.58
1:B:389:GLU:HB3	1:B:394:LYS:CB	2.33	0.58
1:B:499:LEU:O	1:B:502:THR:OG1	2.21	0.58
1:E:77:GLU:CD	1:E:169:ASN:HD22	2.09	0.58
1:E:96:ARG:HD3	1:E:169:ASN:O	2.03	0.58
1:E:193:GLU:N	1:E:194:PRO:HD3	2.18	0.58
1:E:259:LEU:O	1:E:263:PHE:CD1	2.54	0.58
1:E:276:GLU:O	1:E:353:PHE:HZ	1.87	0.58
1:A:83:LEU:CD2	1:A:166:ARG:NH1	2.66	0.58
1:A:562:GLN:CB	1:A:565:ASP:HB2	2.33	0.58
2:C:312:GLN:CD	2:C:323:LYS:HD2	2.27	0.58
2:D:354:GLN:O	2:D:358:LYS:CG	2.50	0.58
1:B:103:GLY:O	1:B:134:SER:N	2.36	0.58
1:B:275:GLU:HG3	1:B:275:GLU:O	2.04	0.58
1:B:310:HIS:C	1:B:311:LEU:HD22	2.27	0.58
1:E:549:GLN:CB	1:E:551:ILE:HG23	2.33	0.58
2:F:89:VAL:CG2	2:F:144:LEU:HD21	2.32	0.58
1:A:327:SER:OG	1:A:332:ASP:OD2	2.17	0.58
2:C:191:TYR:CE2	2:C:264:LEU:HD22	2.38	0.58
2:D:159:TYR:OH	1:B:614:GLU:HG2	2.04	0.58
2:D:499:PHE:HE2	1:B:587:PHE:HA	1.68	0.58
1:B:128:ILE:O	1:B:128:ILE:HD12	2.03	0.58
1:E:259:LEU:HG	1:E:263:PHE:HE1	1.68	0.58
1:E:365:ILE:HD13	1:E:366:LYS:H	1.67	0.58
1:E:461:LEU:HB2	1:E:586:ASP:OD2	2.03	0.58
1:E:610:ARG:NE	2:F:167:ASP:CG	2.62	0.58
1:A:79:MET:HE1	1:A:81:VAL:HG21	1.84	0.58
1:A:83:LEU:CD2	1:A:166:ARG:CZ	2.82	0.58
1:A:325:ALA:C	1:A:578:ASN:ND2	2.61	0.58
1:A:527:GLN:HE21	1:A:527:GLN:C	2.10	0.58
1:A:543:HIS:HE1	2:C:502:LEU:CA	2.17	0.58
2:C:95:PHE:CZ	2:C:155:LEU:CD1	2.86	0.58
2:C:119:ILE:HG13	2:C:121:LEU:N	2.18	0.58
2:D:54:HIS:CD2	2:D:98:GLY:CA	2.84	0.58
1:B:578:ASN:CG	1:B:579:LYS:N	2.62	0.58
1:E:188:LEU:HD13	1:E:434:PHE:CZ	2.35	0.58
1:E:230:TYR:CB	1:E:262:LYS:NZ	2.66	0.58
2:F:55:VAL:HG11	2:F:159:TYR:CG	2.35	0.58
2:F:272:ASN:O	2:F:275:LEU:HD13	2.03	0.58
1:A:198:LEU:CD2	1:A:205:HIS:CD2	2.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:GLY:CA	1:A:524:PRO:HG2	2.33	0.58
1:A:517:VAL:CG2	1:A:524:PRO:HB2	2.32	0.58
2:C:68:LEU:HD12	2:C:68:LEU:C	2.29	0.58
2:C:97:ASN:HD22	2:C:129:ARG:HD3	1.67	0.58
2:C:103:THR:N	2:C:104:GLN:CA	2.64	0.58
2:C:136:ARG:CD	1:B:617:TRP:O	2.39	0.58
1:B:515:LEU:O	1:B:517:VAL:HG13	2.04	0.58
1:E:268:ARG:HG3	1:E:268:ARG:NH1	2.17	0.58
1:E:301:LEU:HD11	1:E:316:ASN:CA	2.34	0.58
1:E:471:TYR:CD1	1:E:550:GLN:C	2.82	0.58
2:F:66:VAL:O	2:F:69:ASP:OD1	2.21	0.58
2:F:115:LEU:O	2:F:115:LEU:HD23	2.03	0.58
2:F:372:CYS:O	2:F:412:ILE:CD1	2.50	0.58
2:C:72:GLU:OE1	2:C:72:GLU:HA	2.04	0.58
2:D:111:PRO:HG2	2:D:114:THR:OG1	2.03	0.58
1:E:118:LEU:CB	1:E:305:ILE:CB	2.77	0.58
1:E:609:ARG:HD2	2:F:2:ILE:HG12	1.85	0.58
1:A:221:TYR:CB	1:A:422:PRO:HG2	2.34	0.58
2:C:90:MET:HE2	2:D:89:VAL:HG12	1.85	0.58
1:E:289:TYR:HA	1:E:317:PHE:CE2	2.38	0.58
1:E:364:TRP:HD1	1:E:368:PHE:C	2.05	0.58
1:E:538:THR:HG22	1:E:539:LEU:N	2.18	0.58
1:A:245:ILE:HD12	1:A:245:ILE:C	2.27	0.57
1:B:79:MET:HB3	1:B:167:VAL:HG21	1.81	0.57
1:B:209:GLU:N	1:B:209:GLU:OE2	2.37	0.57
1:E:193:GLU:N	1:E:194:PRO:CD	2.67	0.57
1:E:467:LEU:HD12	2:F:488:TRP:HB3	1.85	0.57
2:F:133:THR:HB	2:F:134:HIS:ND1	2.20	0.57
2:F:278:PHE:HE2	2:F:282:TYR:HA	1.68	0.57
2:F:337:LEU:HD12	2:F:341:ILE:HD11	1.86	0.57
2:F:492:GLN:H	2:F:492:GLN:CD	2.11	0.57
1:A:98:GLN:HG3	1:A:116:GLU:N	2.19	0.57
2:C:23:TYR:CE2	2:C:160:TRP:CD1	2.90	0.57
2:D:4:PRO:CA	1:B:607:PHE:CD1	2.81	0.57
2:D:69:ASP:HA	2:D:77:VAL:CG1	2.34	0.57
2:D:349:PHE:CE2	2:D:356:TRP:CG	2.90	0.57
1:B:231:LEU:O	1:B:235:ASN:OD1	2.22	0.57
1:E:71:TYR:HD1	1:E:80:PHE:CE2	2.19	0.57
2:F:18:LEU:HD21	2:F:22:PHE:HZ	1.58	0.57
2:F:152:LEU:O	2:F:155:LEU:HD12	2.01	0.57
1:A:96:ARG:CB	1:A:168:PHE:CE1	2.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:127:ASP:OD2	2:D:127:ASP:N	2.36	0.57
2:D:363:ASN:O	2:D:368:ILE:CD1	2.52	0.57
1:E:451:ILE:HG22	1:E:452:THR:HG23	1.86	0.57
2:F:365:SER:C	2:F:419:PHE:CD1	2.82	0.57
2:F:410:GLU:O	2:F:414:ASN:HB2	2.04	0.57
1:A:90:HIS:NE2	1:A:213:ILE:CD1	2.67	0.57
2:C:43:SER:O	2:C:46:LEU:N	2.38	0.57
2:C:74:CYS:HA	2:C:75:LEU:C	2.30	0.57
2:C:314:ASP:OD2	2:C:495:LYS:HE3	2.04	0.57
2:C:387:ASN:HA	2:C:391:ASN:HD21	1.68	0.57
1:B:89:LEU:HD13	1:B:89:LEU:C	2.30	0.57
1:B:122:HIS:CE1	1:B:128:ILE:CB	2.59	0.57
1:B:454:PHE:C	1:B:455:ASP:OD1	2.48	0.57
1:E:97:LEU:H	1:E:97:LEU:HD23	1.70	0.57
1:A:96:ARG:HG3	1:A:168:PHE:CZ	2.36	0.57
1:A:196:PHE:CB	1:A:205:HIS:HE1	2.14	0.57
1:A:486:GLU:O	1:A:487:PHE:CB	2.52	0.57
1:A:488:GLN:OE1	1:A:488:GLN:HA	2.05	0.57
1:B:538:THR:HG22	1:B:539:LEU:N	2.19	0.57
1:E:301:LEU:HD12	1:E:301:LEU:N	2.11	0.57
1:E:510:SER:CB	1:E:533:SER:O	2.41	0.57
1:E:617:TRP:HD1	1:E:617:TRP:O	1.88	0.57
2:F:75:LEU:HG	2:F:76:GLY:N	2.19	0.57
2:C:36:ARG:HA	2:C:39:GLN:NE2	2.20	0.57
1:B:80:PHE:HD1	1:B:166:ARG:HB2	1.69	0.57
1:B:105:VAL:CG1	1:B:108:ASN:HA	2.35	0.57
1:B:232:SER:O	1:B:236:ALA:HB2	2.03	0.57
1:B:369:GLY:O	1:B:373:LEU:HG	2.05	0.57
1:E:305:ILE:CG2	1:E:307:LEU:HD11	2.34	0.57
1:E:561:THR:CA	1:E:564:LEU:HD12	2.34	0.57
1:E:597:ASP:OD1	1:E:597:ASP:N	2.34	0.57
1:A:267:ILE:CD1	1:A:277:LEU:CD2	2.82	0.57
2:C:309:TYR:CE1	2:C:313:GLN:NE2	2.73	0.57
2:D:69:ASP:HA	2:D:77:VAL:HG21	0.85	0.57
2:D:498:PRO:CG	1:B:602:ILE:HG23	2.34	0.57
1:B:387:PHE:CE1	1:B:401:THR:HG21	2.38	0.57
1:B:504:ILE:HD12	1:B:575:ILE:HG22	1.72	0.57
1:B:590:SER:O	1:B:594:ILE:O	2.22	0.57
1:E:91:LEU:HB3	1:E:95:PHE:CE1	2.39	0.57
1:E:98:GLN:CB	1:E:117:ILE:HG22	2.35	0.57
2:F:51:TYR:CD2	2:F:51:TYR:N	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:58:SER:OG	2:F:95:PHE:HB2	2.04	0.57
2:F:201:LYS:O	2:F:205:LEU:HG	2.05	0.57
2:F:349:PHE:CD1	2:F:375:MET:CE	2.87	0.57
2:F:349:PHE:CE1	2:F:375:MET:CE	2.87	0.57
2:F:389:TRP:CD1	2:F:390:ARG:CD	2.88	0.57
1:A:399:GLU:OE2	1:A:399:GLU:N	2.38	0.57
2:D:96:VAL:CG1	2:D:100:LEU:CB	2.83	0.57
2:D:494:TRP:CH2	2:D:497:LYS:CG	2.88	0.57
1:B:289:TYR:CD2	1:B:289:TYR:N	2.73	0.57
1:A:278:VAL:O	1:A:278:VAL:HG23	2.04	0.57
2:C:108:PHE:CD1	2:C:108:PHE:N	2.73	0.57
2:C:312:GLN:OE1	2:C:323:LYS:CE	2.52	0.57
2:D:199:LEU:HD11	2:D:281:ASN:HB2	1.87	0.57
1:B:469:ILE:O	1:B:552:MET:N	2.38	0.57
1:E:392:ASN:N	1:E:393:SER:HA	2.20	0.57
1:E:509:TYR:CD1	1:E:510:SER:N	2.73	0.57
1:A:239:ASP:CB	1:A:355:GLY:H	2.17	0.57
1:A:374:ASN:ND2	1:A:400:LEU:O	2.38	0.57
2:D:351:ASN:OD1	2:D:351:ASN:N	2.37	0.57
1:B:76:ASP:O	1:B:169:ASN:HB2	2.05	0.57
1:E:106:TYR:HD2	1:E:120:PHE:HE2	1.52	0.57
1:E:417:GLU:OE1	1:E:417:GLU:HA	2.04	0.57
2:F:272:ASN:O	2:F:276:GLU:HG3	2.05	0.57
1:A:194:PRO:O	1:A:211:ASP:OD1	2.22	0.56
1:A:359:LEU:HD12	1:A:360:ASN:CA	2.31	0.56
1:A:467:LEU:CD2	1:A:556:VAL:CG2	2.81	0.56
2:C:53:PRO:CD	2:C:56:VAL:HG21	2.35	0.56
2:C:125:PHE:O	2:C:128:LEU:CG	2.49	0.56
1:B:347:HIS:CD2	1:B:351:GLN:CG	2.88	0.56
1:B:348:LEU:CD1	1:B:353:PHE:CB	2.75	0.56
1:B:366:LYS:CD	1:B:395:ARG:NH1	2.68	0.56
1:E:610:ARG:HE	2:F:167:ASP:CG	2.13	0.56
1:A:486:GLU:O	1:A:487:PHE:HB2	2.04	0.56
2:C:125:PHE:CA	2:C:128:LEU:CD2	2.81	0.56
2:D:108:PHE:CD2	2:D:108:PHE:N	2.73	0.56
2:D:122:PRO:HD3	2:D:154:TRP:NE1	2.20	0.56
2:D:125:PHE:HA	2:D:128:LEU:HB2	1.87	0.56
2:D:349:PHE:CE2	2:D:356:TRP:NE1	2.72	0.56
1:B:80:PHE:CE1	1:B:166:ARG:HB2	2.40	0.56
1:B:92:SER:OG	1:B:189:TRP:O	2.23	0.56
1:B:405:SER:O	1:B:407:SER:O	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:485:MET:SD	1:B:485:MET:N	2.78	0.56
1:E:133:PHE:CD2	1:E:134:SER:N	2.73	0.56
1:E:245:ILE:HD13	1:E:373:LEU:CD1	2.19	0.56
1:E:333:GLU:OE1	1:E:336:SER:N	2.28	0.56
1:E:531:SER:O	1:E:534:LYS:HG3	2.06	0.56
2:F:369:LEU:HD12	2:F:415:LEU:HB3	1.86	0.56
1:A:128:ILE:O	1:A:215:SER:CB	2.53	0.56
1:A:236:ALA:O	1:A:237:ALA:HB3	2.05	0.56
2:C:97:ASN:HD21	2:C:129:ARG:HD2	1.70	0.56
2:C:145:ARG:NH2	3:C:602:HOH:O	2.39	0.56
2:C:207:ASN:C	2:C:210:LEU:HD13	2.30	0.56
2:D:154:TRP:HE3	2:D:155:LEU:HD23	1.60	0.56
1:B:313:GLN:HB3	1:B:456:TYR:OH	2.04	0.56
1:B:588:LEU:O	1:B:588:LEU:HD13	2.05	0.56
1:E:106:TYR:CE2	1:E:120:PHE:HD2	2.18	0.56
1:E:118:LEU:CB	1:E:305:ILE:CG2	2.84	0.56
1:E:359:LEU:HD12	1:E:360:ASN:CA	2.35	0.56
2:F:139:PRO:CG	2:F:144:LEU:HD11	2.18	0.56
2:F:280:ASN:O	2:F:325:LYS:HE3	2.06	0.56
2:C:314:ASP:CG	2:C:495:LYS:HZ1	2.14	0.56
2:D:69:ASP:HB3	2:D:84:ILE:CD1	2.36	0.56
2:D:84:ILE:O	2:D:88:TYR:HD2	1.89	0.56
1:B:127:SER:HB3	1:B:214:GLN:HG3	1.87	0.56
1:E:100:VAL:CG1	1:E:101:LYS:HE2	2.35	0.56
1:E:353:PHE:CE1	1:E:355:GLY:HA3	2.41	0.56
1:E:493:GLN:HE22	2:F:36:ARG:NH2	2.02	0.56
2:F:280:ASN:C	2:F:325:LYS:HE3	2.30	0.56
1:A:71:TYR:CD2	1:A:72:GLU:N	2.73	0.56
1:A:96:ARG:O	1:A:168:PHE:HD1	1.80	0.56
1:A:187:TYR:CZ	1:A:192:LYS:CB	2.88	0.56
1:A:223:SER:O	1:A:227:GLU:HB3	2.06	0.56
1:B:105:VAL:O	1:B:105:VAL:HG12	2.05	0.56
1:B:243:MET:HE3	1:B:382:PRO:HB3	1.87	0.56
1:E:182:TYR:C	1:E:182:TYR:HD1	2.14	0.56
1:A:365:ILE:C	1:A:396:HIS:CE1	2.77	0.56
2:D:122:PRO:HG2	2:D:125:PHE:HE2	1.69	0.56
2:D:188:LEU:CD1	2:D:192:MET:HG2	2.36	0.56
1:B:388:LEU:CA	1:B:421:VAL:O	2.48	0.56
1:B:573:TRP:CD1	1:B:573:TRP:N	2.73	0.56
1:E:106:TYR:CE2	1:E:120:PHE:CE2	2.93	0.56
1:E:394:LYS:HD2	1:E:394:LYS:C	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:LYS:C	1:A:300:ILE:CD1	2.79	0.56
1:A:353:PHE:HE1	1:A:355:GLY:CA	2.15	0.56
1:A:365:ILE:HD13	1:A:366:LYS:HD3	1.88	0.56
2:D:122:PRO:HD2	2:D:125:PHE:CD2	2.41	0.56
2:D:194:SER:HA	2:D:197:LYS:HB2	1.85	0.56
1:B:124:LEU:HB2	1:B:188:LEU:O	2.05	0.56
2:F:110:ILE:HG21	2:F:114:THR:HG22	1.87	0.56
1:A:218:VAL:O	1:A:218:VAL:HG13	2.05	0.56
1:A:365:ILE:CD1	1:A:366:LYS:H	2.14	0.56
1:A:518:LYS:O	1:A:525:ILE:N	2.33	0.56
2:C:133:THR:HG22	2:D:97:ASN:HD22	1.68	0.56
2:D:336:LEU:CD1	2:D:340:ILE:HD11	2.29	0.56
1:B:221:TYR:CD2	1:B:221:TYR:N	2.73	0.56
1:B:569:GLU:HG3	1:B:570:ASP:N	2.20	0.56
1:E:360:ASN:HD22	1:E:360:ASN:H	1.53	0.56
1:E:561:THR:CG2	1:E:562:GLN:HA	2.36	0.56
2:F:21:TRP:HE3	2:F:37:ALA:HA	1.71	0.56
2:F:98:GLY:O	2:F:102:PRO:HG3	2.04	0.56
2:F:152:LEU:N	2:F:155:LEU:HD11	2.20	0.56
1:A:96:ARG:HD3	1:A:170:SER:HA	1.87	0.56
1:A:248:LYS:O	1:A:249:ASN:HB3	2.05	0.56
2:C:388:SER:N	2:C:391:ASN:HD21	2.03	0.56
2:D:82:ILE:HG22	2:D:83:PRO:CD	2.32	0.56
1:B:331:GLN:HG3	1:B:364:TRP:CZ2	2.41	0.56
1:B:389:GLU:HA	1:B:389:GLU:OE2	2.04	0.56
1:E:83:LEU:HD22	1:E:166:ARG:HE	1.71	0.56
1:E:111:TYR:N	1:E:111:TYR:CD1	2.73	0.56
1:A:81:VAL:HG12	1:A:82:GLY:N	2.21	0.56
1:A:282:LEU:CD1	1:A:359:LEU:HD21	2.35	0.56
1:A:477:GLY:C	1:A:478:ILE:HD13	2.30	0.56
1:A:617:TRP:CD1	1:A:618:LYS:N	2.73	0.56
2:C:53:PRO:CB	2:C:56:VAL:HG23	2.35	0.56
2:D:46:LEU:HD22	1:B:577:ARG:CD	2.35	0.56
2:D:134:HIS:CD2	2:D:134:HIS:N	2.73	0.56
1:E:74:ASP:OD2	1:E:75:GLU:N	2.34	0.56
1:E:123:PRO:HB3	1:E:311:LEU:CD2	2.35	0.56
2:F:122:PRO:HB2	2:F:124:TRP:HD1	1.69	0.56
1:A:471:TYR:CE1	1:A:545:ILE:CG2	2.88	0.55
1:A:562:GLN:HB2	1:A:565:ASP:HB2	1.89	0.55
2:C:224:ILE:CG2	2:C:229:PHE:CZ	2.89	0.55
2:C:359:LEU:C	2:C:359:LEU:HD23	2.31	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4:PRO:CB	1:B:607:PHE:CZ	2.51	0.55
2:D:5:ARG:CZ	1:B:610:ARG:CG	2.80	0.55
2:D:96:VAL:HG13	2:D:100:LEU:CB	2.36	0.55
2:D:102:PRO:O	2:D:104:GLN:N	2.34	0.55
1:B:77:GLU:O	1:B:204:TYR:OH	2.23	0.55
1:B:211:ASP:HA	1:B:212:ARG:NH2	2.21	0.55
1:E:245:ILE:HD11	1:E:373:LEU:HD21	1.87	0.55
1:E:384:HIS:CD2	1:E:384:HIS:N	2.73	0.55
1:E:389:GLU:HB3	1:E:394:LYS:HB3	1.87	0.55
1:A:311:LEU:HD22	1:A:311:LEU:N	2.21	0.55
1:A:460:PRO:CB	1:A:594:ILE:HD11	2.33	0.55
1:A:518:LYS:CB	1:A:527:GLN:HG2	2.36	0.55
2:C:32:ASP:OD1	2:C:34:ARG:HG2	2.06	0.55
2:C:112:LEU:HD23	2:C:112:LEU:H	1.71	0.55
2:C:209:PHE:HD2	2:C:254:ILE:HD13	1.71	0.55
2:C:353:TRP:CE3	2:C:404:ILE:CG2	2.89	0.55
2:D:329:TRP:CB	2:D:424:ILE:HG23	2.36	0.55
1:B:230:TYR:CD1	1:B:263:PHE:CD1	2.93	0.55
1:B:236:ALA:O	1:B:237:ALA:HB3	2.06	0.55
1:B:570:ASP:N	1:B:570:ASP:OD2	2.38	0.55
1:E:95:PHE:CE2	1:E:120:PHE:CG	2.95	0.55
1:E:205:HIS:O	1:E:207:LEU:HD23	2.06	0.55
1:E:241:ARG:NH1	1:E:381:LYS:HD2	2.21	0.55
1:E:301:LEU:CD1	1:E:316:ASN:C	2.47	0.55
1:E:536:PHE:HD1	1:E:536:PHE:C	2.15	0.55
1:A:69:ILE:HG21	1:A:80:PHE:CB	2.34	0.55
1:A:84:LYS:H	1:A:139:TRP:CB	2.19	0.55
1:A:106:TYR:HE2	1:A:120:PHE:CD2	2.25	0.55
1:A:127:SER:HG	1:A:216:LEU:HD22	1.65	0.55
2:C:78:HIS:ND1	2:C:78:HIS:O	2.39	0.55
2:C:119:ILE:HG12	2:C:121:LEU:H	1.71	0.55
2:D:356:TRP:C	2:D:360:ILE:HG13	2.29	0.55
1:B:99:VAL:HG22	1:B:166:ARG:HE	1.68	0.55
1:B:387:PHE:HE2	1:B:397:LEU:CD1	2.19	0.55
1:B:523:PHE:HB2	1:B:525:ILE:HD11	1.88	0.55
1:E:105:VAL:O	1:E:105:VAL:HG12	2.06	0.55
1:E:389:GLU:HG3	1:E:394:LYS:HA	1.80	0.55
1:A:168:PHE:HD1	1:A:168:PHE:H	1.55	0.55
1:A:361:LEU:HD11	1:A:376:ILE:CD1	2.35	0.55
1:A:373:LEU:HD23	1:A:373:LEU:H	1.69	0.55
1:B:589:PRO:HG2	1:B:596:TRP:CZ2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:ASP:CG	1:E:75:GLU:H	2.07	0.55
1:E:111:TYR:HD1	1:E:111:TYR:N	2.03	0.55
2:F:51:TYR:N	2:F:51:TYR:HD2	2.05	0.55
1:A:502:THR:CG2	1:A:577:ARG:HH22	2.19	0.55
1:A:562:GLN:O	1:A:565:ASP:HB2	2.07	0.55
2:D:341:ILE:HD13	2:D:374:SER:HB3	1.88	0.55
1:E:395:ARG:HH21	1:E:395:ARG:CG	2.15	0.55
1:E:504:ILE:HG13	1:E:540:GLY:O	2.05	0.55
1:E:518:LYS:O	1:E:525:ILE:N	2.26	0.55
2:F:17:GLU:HG2	2:F:21:TRP:CZ2	2.41	0.55
2:F:298:ASP:CG	2:F:356:TRP:CZ2	2.85	0.55
1:A:255:PHE:CE2	1:A:259:LEU:CD2	2.89	0.55
1:E:179:GLY:HA2	1:E:185:VAL:CG1	2.36	0.55
1:A:74:ASP:OD1	1:A:75:GLU:CA	2.55	0.55
1:A:480:GLY:HA2	1:A:524:PRO:HG2	1.88	0.55
2:D:209:PHE:CZ	2:D:254:ILE:HG22	2.39	0.55
1:B:482:GLN:OE1	1:B:526:LEU:CD2	2.55	0.55
1:E:546:ASP:HB3	1:E:551:ILE:HG12	1.89	0.55
2:F:191:TYR:OH	2:F:264:LEU:O	2.21	0.55
2:F:276:GLU:O	2:F:280:ASN:ND2	2.40	0.55
2:F:335:ARG:HG3	2:F:335:ARG:NH1	2.21	0.55
1:A:353:PHE:HE1	1:A:355:GLY:N	2.05	0.55
1:A:518:LYS:O	1:A:525:ILE:CG1	2.55	0.55
2:C:55:VAL:HG23	2:C:155:LEU:HD21	1.89	0.55
2:C:283:ASP:HB3	2:C:286:LEU:HB2	1.89	0.55
2:D:108:PHE:O	2:D:109:ALA:HB3	2.07	0.55
2:D:312:GLN:NE2	2:D:323:LYS:CD	2.68	0.55
2:D:329:TRP:CG	2:D:424:ILE:HG23	2.41	0.55
1:B:90:HIS:HE1	1:B:213:ILE:CD1	2.13	0.55
1:B:485:MET:HE3	1:B:485:MET:H	1.72	0.55
2:F:147:ALA:O	2:F:151:ALA:N	2.34	0.55
1:A:561:THR:HG23	1:A:562:GLN:HA	1.89	0.55
2:C:52:LEU:CD1	2:C:53:PRO:N	2.53	0.55
2:D:193:GLU:O	2:D:197:LYS:HG3	2.07	0.55
2:D:218:ASN:ND2	2:D:221:ASP:HB2	2.21	0.55
2:D:358:LYS:CB	2:D:490:ARG:NE	2.66	0.55
1:B:65:LEU:HD12	1:B:65:LEU:O	2.07	0.55
1:E:214:GLN:OE1	1:E:427:ASN:CA	2.54	0.55
2:F:111:PRO:O	2:F:114:THR:HB	2.06	0.55
2:F:154:TRP:CE3	2:F:154:TRP:C	2.85	0.55
1:A:347:HIS:C	1:A:347:HIS:CD2	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:562:GLN:O	1:A:565:ASP:N	2.40	0.55
2:C:309:TYR:CD1	2:C:309:TYR:C	2.85	0.55
2:C:329:TRP:CG	2:C:424:ILE:HG23	2.41	0.55
2:D:90:MET:O	2:D:94:ARG:HG3	2.06	0.55
2:D:156:TYR:C	2:D:156:TYR:CD1	2.85	0.55
1:B:93:GLY:H	1:B:122:HIS:HB3	1.71	0.55
1:E:454:PHE:CD2	1:E:454:PHE:N	2.73	0.55
2:F:410:GLU:O	2:F:414:ASN:CB	2.55	0.55
1:A:353:PHE:CD1	1:A:353:PHE:C	2.85	0.54
2:C:332:LEU:HD23	2:C:337:LEU:HB2	1.89	0.54
2:D:21:TRP:HB3	2:D:37:ALA:HB2	1.89	0.54
2:D:154:TRP:CE3	2:D:154:TRP:C	2.85	0.54
2:D:154:TRP:CE3	2:D:155:LEU:HA	2.42	0.54
2:D:188:LEU:CD1	2:D:192:MET:CG	2.86	0.54
1:B:397:LEU:CD1	1:B:400:LEU:CG	2.86	0.54
2:F:131:TRP:CD1	2:F:139:PRO:HD3	2.42	0.54
1:A:606:THR:HG23	2:C:5:ARG:NH1	2.22	0.54
2:C:83:PRO:HB3	2:D:68:LEU:HD22	1.88	0.54
2:C:359:LEU:O	2:C:359:LEU:HD23	2.07	0.54
1:B:180:HIS:HB3	1:B:592:ARG:NH1	2.15	0.54
1:B:587:PHE:C	1:B:587:PHE:CD2	2.85	0.54
1:B:589:PRO:N	1:B:596:TRP:HH2	2.03	0.54
1:E:385:LEU:O	1:E:419:VAL:HG23	2.07	0.54
1:E:471:TYR:CZ	1:E:523:PHE:HE1	2.25	0.54
1:E:587:PHE:C	1:E:587:PHE:CD2	2.85	0.54
2:F:22:PHE:CD1	2:F:37:ALA:CB	2.91	0.54
2:F:110:ILE:CG2	2:F:114:THR:CG2	2.86	0.54
2:F:391:ASN:N	2:F:391:ASN:OD1	2.38	0.54
1:A:353:PHE:CE1	1:A:354:PHE:C	2.86	0.54
2:C:125:PHE:O	2:C:127:ASP:N	2.41	0.54
2:D:499:PHE:CD1	1:B:543:HIS:HA	2.41	0.54
1:A:101:LYS:HA	1:A:113:ALA:HB3	1.90	0.54
1:A:503:VAL:HG22	1:A:582:THR:HB	1.89	0.54
1:A:589:PRO:CB	1:A:594:ILE:CD1	2.85	0.54
2:C:83:PRO:O	2:C:86:LEU:HB2	2.06	0.54
2:C:350:LYS:HG2	2:C:404:ILE:CD1	2.37	0.54
2:D:282:TYR:CD1	2:D:282:TYR:C	2.86	0.54
1:B:79:MET:O	1:B:79:MET:HE3	2.06	0.54
1:B:395:ARG:HE	1:B:396:HIS:CB	2.20	0.54
1:B:544:SER:OG	1:B:553:ASN:CB	2.56	0.54
1:E:83:LEU:H	1:E:83:LEU:CD2	2.01	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:474:GLY:N	1:E:475:LYS:HA	2.21	0.54
1:E:480:GLY:H	1:E:524:PRO:HB2	1.72	0.54
1:E:562:GLN:HA	1:E:565:ASP:HB2	1.88	0.54
1:A:90:HIS:HE2	1:A:213:ILE:HD11	1.73	0.54
1:A:255:PHE:HE2	1:A:259:LEU:CD2	2.21	0.54
2:C:61:GLN:HE22	2:C:94:ARG:HE	1.55	0.54
2:C:101:ASP:OD1	2:C:101:ASP:N	2.38	0.54
2:C:325:LYS:C	2:C:326:PHE:CD1	2.85	0.54
2:D:122:PRO:CB	2:D:125:PHE:CD2	2.86	0.54
2:D:344:LEU:O	2:D:378:LYS:NZ	2.38	0.54
1:B:364:TRP:CE3	1:B:364:TRP:CA	2.90	0.54
1:B:467:LEU:HD23	1:B:554:ILE:O	2.07	0.54
1:E:257:ARG:HE	1:E:308:GLY:C	2.14	0.54
2:F:131:TRP:CD1	2:F:131:TRP:C	2.85	0.54
2:F:146:TRP:C	2:F:146:TRP:CD1	2.85	0.54
1:A:91:LEU:HD23	1:A:95:PHE:CE2	2.42	0.54
1:A:95:PHE:CE2	1:A:120:PHE:HB2	2.43	0.54
1:A:245:ILE:HD11	1:A:363:GLY:C	2.33	0.54
1:A:282:LEU:HD13	1:A:359:LEU:HD21	1.89	0.54
1:A:317:PHE:C	1:A:317:PHE:CD2	2.86	0.54
1:A:369:GLY:O	1:A:373:LEU:HG	2.07	0.54
2:C:53:PRO:CD	2:C:56:VAL:CG2	2.86	0.54
2:C:310:ARG:HH21	2:C:314:ASP:CG	2.12	0.54
2:C:323:LYS:HA	2:C:326:PHE:O	2.07	0.54
1:B:484:PRO:HG2	1:B:487:PHE:HD1	1.71	0.54
1:E:110:HIS:C	1:E:110:HIS:CD2	2.85	0.54
1:E:487:PHE:CE2	2:F:46:LEU:CA	2.82	0.54
2:F:68:LEU:HD22	2:F:84:ILE:CG1	2.31	0.54
2:F:270:TYR:C	2:F:274:VAL:HG23	2.31	0.54
2:F:282:TYR:CD1	2:F:282:TYR:C	2.86	0.54
2:F:305:VAL:HG21	2:F:336:LEU:CD2	2.36	0.54
1:A:449:HIS:HB3	1:A:457:ASP:O	2.07	0.54
1:B:361:LEU:HD22	1:B:376:ILE:HD11	1.84	0.54
1:B:435:HIS:HB2	1:B:438:GLN:HB3	1.88	0.54
1:B:595:THR:O	1:B:595:THR:HG22	2.06	0.54
2:C:31:GLU:HG2	2:C:31:GLU:O	2.07	0.54
2:C:82:ILE:CG2	2:C:83:PRO:HD3	2.37	0.54
2:C:138:LEU:CD2	2:D:94:ARG:HH11	2.18	0.54
2:C:138:LEU:HD23	2:D:94:ARG:CZ	2.30	0.54
2:D:79:GLN:HA	2:D:79:GLN:HE21	1.73	0.54
1:B:172:HIS:CD2	1:B:454:PHE:C	2.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:544:SER:OG	1:B:553:ASN:CG	2.50	0.54
1:E:199:ASN:CB	1:E:202:THR:CG2	2.85	0.54
1:E:471:TYR:CE2	1:E:523:PHE:HD1	2.26	0.54
1:E:549:GLN:HE21	1:E:549:GLN:N	2.06	0.54
2:F:62:ILE:HD12	2:F:155:LEU:HD21	1.89	0.54
2:F:312:GLN:NE2	2:F:323:LYS:NZ	2.55	0.54
2:F:349:PHE:CE1	2:F:375:MET:HE2	2.42	0.54
1:A:97:LEU:O	1:A:118:LEU:N	2.31	0.54
1:A:105:VAL:C	1:A:132:ASP:HB2	2.33	0.54
1:A:226:LEU:CD1	1:A:230:TYR:HE1	2.14	0.54
2:D:191:TYR:CD1	2:D:191:TYR:C	2.86	0.54
2:D:350:LYS:HZ1	2:D:401:THR:HG22	1.72	0.54
2:D:494:TRP:CH2	2:D:497:LYS:HG3	2.42	0.54
1:B:590:SER:CB	1:B:593:THR:OG1	2.55	0.54
1:A:120:PHE:HA	1:A:307:LEU:O	2.08	0.54
1:A:234:LYS:HE2	1:A:270:SER:OG	2.08	0.54
1:A:503:VAL:CG2	1:A:582:THR:HB	2.38	0.54
2:C:54:HIS:O	2:C:54:HIS:ND1	2.42	0.54
2:D:96:VAL:HG13	2:D:100:LEU:HB2	1.89	0.54
2:D:279:PHE:HD1	2:D:304:TRP:CH2	2.24	0.54
1:B:254:THR:O	1:B:258:LEU:HG	2.08	0.54
1:B:337:TYR:C	1:B:337:TYR:CD2	2.85	0.54
1:E:133:PHE:CD2	1:E:133:PHE:C	2.86	0.54
1:E:181:LEU:HD13	1:E:181:LEU:C	2.32	0.54
1:E:210:SER:O	1:E:212:ARG:HG3	2.08	0.54
1:E:384:HIS:HA	1:E:417:GLU:HB3	1.87	0.54
1:E:424:HIS:C	1:E:424:HIS:CD2	2.85	0.54
1:E:451:ILE:HB	1:E:455:ASP:OD1	2.07	0.54
2:F:125:PHE:HD1	2:F:128:LEU:HD23	1.73	0.54
1:A:183:ARG:HH21	1:A:183:ARG:HG2	1.73	0.53
1:A:388:LEU:O	1:A:423:ALA:N	2.42	0.53
1:A:471:TYR:C	1:A:471:TYR:CD2	2.85	0.53
2:C:110:ILE:N	2:C:110:ILE:HD12	2.23	0.53
2:D:154:TRP:CZ3	2:D:155:LEU:CD2	2.86	0.53
2:D:389:TRP:CD1	2:D:389:TRP:C	2.86	0.53
1:B:288:GLU:C	1:B:289:TYR:CD2	2.85	0.53
1:B:545:ILE:HG12	1:B:552:MET:HG3	1.90	0.53
1:E:175:LEU:HD21	1:E:189:TRP:HE1	1.70	0.53
2:F:271:HIS:C	2:F:274:VAL:HG23	2.33	0.53
1:A:91:LEU:HD12	1:A:205:HIS:O	2.09	0.53
1:A:337:TYR:CD1	1:A:337:TYR:C	2.86	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:82:ILE:CG2	2:D:83:PRO:CD	2.86	0.53
2:D:331:GLU:O	2:D:335:ARG:HB2	2.06	0.53
1:B:99:VAL:HG13	1:B:166:ARG:HH21	1.70	0.53
1:B:366:LYS:HD3	1:B:395:ARG:CZ	2.38	0.53
1:B:490:LEU:CD1	1:B:491:ASN:H	2.21	0.53
1:E:188:LEU:HD11	1:E:434:PHE:CD1	2.43	0.53
1:A:128:ILE:O	1:A:215:SER:HB2	2.09	0.53
1:A:269:ASP:OD2	1:A:269:ASP:N	2.41	0.53
2:C:75:LEU:HD23	2:C:76:GLY:C	2.34	0.53
1:B:110:HIS:HD2	1:B:111:TYR:N	2.06	0.53
1:B:324:TYR:CB	1:B:536:PHE:CE2	2.85	0.53
1:E:289:TYR:CB	1:E:317:PHE:CD2	2.81	0.53
1:E:385:LEU:O	1:E:419:VAL:HG22	2.07	0.53
1:E:471:TYR:O	1:E:550:GLN:CB	2.56	0.53
2:D:21:TRP:N	2:D:21:TRP:CD1	2.73	0.53
1:B:387:PHE:CE2	1:B:397:LEU:HD11	2.42	0.53
1:B:397:LEU:CD1	1:B:400:LEU:HG	2.39	0.53
1:E:473:LYS:HD2	1:E:473:LYS:H	1.71	0.53
1:E:501:GLY:HA3	2:F:499:PHE:HD1	1.74	0.53
1:E:554:ILE:HG21	2:F:488:TRP:CZ3	2.44	0.53
1:A:124:LEU:H	1:A:188:LEU:CD2	2.22	0.53
1:A:267:ILE:CD1	1:A:277:LEU:HD21	2.39	0.53
1:A:518:LYS:O	1:A:525:ILE:HG13	2.09	0.53
2:D:278:PHE:CD1	2:D:278:PHE:C	2.86	0.53
2:D:336:LEU:CD1	2:D:340:ILE:CD1	2.86	0.53
2:D:350:LYS:HZ1	2:D:401:THR:CG2	2.21	0.53
1:B:122:HIS:ND1	1:B:128:ILE:HB	2.14	0.53
1:B:175:LEU:O	1:B:458:PHE:HZ	1.88	0.53
1:B:208:HIS:CE1	1:B:209:GLU:HG2	2.42	0.53
1:E:168:PHE:CD2	1:E:168:PHE:C	2.85	0.53
1:E:241:ARG:HB2	1:E:383:THR:N	2.23	0.53
1:E:486:GLU:O	2:F:42:GLN:OE1	2.27	0.53
1:E:562:GLN:CB	1:E:565:ASP:HB2	2.39	0.53
1:E:562:GLN:HB2	1:E:565:ASP:HB3	1.90	0.53
1:E:584:PHE:C	1:E:584:PHE:CD1	2.86	0.53
1:A:504:ILE:HD11	1:A:575:ILE:HG23	1.81	0.53
2:C:160:TRP:HA	2:C:160:TRP:CE3	2.43	0.53
2:D:312:GLN:CD	2:D:427:TYR:CE2	2.87	0.53
1:E:295:ILE:HD11	1:E:337:TYR:CE2	2.43	0.53
2:F:312:GLN:HE22	2:F:323:LYS:NZ	2.07	0.53
2:F:418:ARG:C	2:F:419:PHE:CD2	2.85	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:HD23	1:A:277:LEU:CD1	2.39	0.53
1:A:617:TRP:CH2	2:D:133:THR:O	2.61	0.53
2:C:207:ASN:CA	2:C:210:LEU:CD1	2.87	0.53
1:B:73:GLY:HA2	1:B:74:ASP:C	2.33	0.53
1:B:536:PHE:CD1	1:B:536:PHE:C	2.85	0.53
1:B:589:PRO:CD	1:B:596:TRP:CZ2	2.84	0.53
1:E:324:TYR:CB	1:E:536:PHE:CE2	2.76	0.53
1:E:444:ILE:HD12	1:E:581:GLU:OE1	2.09	0.53
1:E:612:LYS:CD	2:F:164:GLU:CG	2.87	0.53
2:F:108:PHE:N	2:F:108:PHE:CD2	2.77	0.53
2:F:298:ASP:OD2	2:F:356:TRP:HZ2	1.91	0.53
2:C:497:LYS:CE	2:C:502:LEU:O	2.57	0.53
2:D:69:ASP:CB	2:D:77:VAL:HG11	2.38	0.53
1:B:92:SER:HB2	1:B:207:LEU:CD1	2.33	0.53
1:B:264:THR:O	1:B:267:ILE:HG12	2.09	0.53
1:B:381:LYS:HD3	1:B:410:LEU:HA	1.90	0.53
1:E:559:CYS:SG	1:E:560:HIS:N	2.81	0.53
1:A:97:LEU:O	1:A:117:ILE:HA	2.09	0.53
1:A:541:LEU:C	1:A:554:ILE:HG13	2.34	0.53
2:D:199:LEU:HD13	2:D:281:ASN:OD1	2.08	0.53
2:D:283:ASP:OD1	2:D:285:LEU:N	2.40	0.53
2:D:333:GLN:O	2:D:338:ASP:N	2.37	0.53
1:E:182:TYR:HD1	1:E:184:ASP:H	1.55	0.53
1:E:222:TRP:HD1	1:E:422:PRO:HB2	1.69	0.53
1:A:84:LYS:H	1:A:139:TRP:HB3	1.74	0.53
1:A:305:ILE:HG22	1:A:307:LEU:CD1	2.35	0.53
1:A:478:ILE:HD13	1:A:573:TRP:HB2	1.91	0.53
2:C:86:LEU:CD2	2:C:138:LEU:HD12	2.29	0.53
2:C:110:ILE:HG23	2:C:111:PRO:HD2	1.90	0.53
2:C:332:LEU:CD2	2:C:337:LEU:HB2	2.39	0.53
2:C:349:PHE:HZ	2:C:353:TRP:CZ3	2.24	0.53
1:B:286:GLN:HG3	1:B:286:GLN:O	2.09	0.53
1:E:114:SER:O	1:E:115:ARG:HB3	2.07	0.53
1:E:175:LEU:CD2	1:E:189:TRP:NE1	2.50	0.53
1:E:211:ASP:C	1:E:212:ARG:HG3	2.33	0.53
1:E:471:TYR:CZ	1:E:523:PHE:CD1	2.97	0.53
1:E:488:GLN:HB3	1:E:489:ASP:OD1	2.09	0.53
1:A:198:LEU:CD2	1:A:205:HIS:NE2	2.73	0.52
2:C:78:HIS:CB	2:D:35:GLN:NE2	2.55	0.52
2:C:235:VAL:HG12	2:C:236:ASN:N	2.22	0.52
2:D:4:PRO:HD3	1:B:607:PHE:CE1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:262:GLN:O	2:D:266:LYS:HG3	2.09	0.52
1:B:175:LEU:CA	1:B:458:PHE:CZ	2.91	0.52
1:A:257:ARG:HA	1:A:260:LEU:HB2	1.91	0.52
2:C:207:ASN:O	2:C:210:LEU:HD13	2.08	0.52
2:D:84:ILE:HD12	2:D:84:ILE:C	2.34	0.52
2:D:349:PHE:CD2	2:D:356:TRP:NE1	2.77	0.52
1:B:321:LEU:HD21	1:B:344:LEU:HD13	1.81	0.52
1:B:562:GLN:HB2	1:B:565:ASP:HB2	1.91	0.52
1:E:96:ARG:HG2	1:E:168:PHE:O	2.09	0.52
2:F:155:LEU:CD1	2:F:155:LEU:H	2.10	0.52
2:F:394:ARG:O	2:F:398:ILE:HG13	2.10	0.52
1:A:446:ALA:O	1:A:450:LYS:HB2	2.09	0.52
1:A:472:GLY:N	1:A:475:LYS:CB	2.72	0.52
1:A:603:PRO:HG2	2:C:500:GLY:HA3	1.91	0.52
2:C:337:LEU:HD23	2:C:337:LEU:C	2.35	0.52
2:D:133:THR:C	2:D:134:HIS:CD2	2.87	0.52
2:D:358:LYS:O	2:D:362:GLU:CA	2.56	0.52
1:B:503:VAL:HG12	1:B:539:LEU:HD22	1.91	0.52
1:E:120:PHE:HA	1:E:307:LEU:O	2.08	0.52
1:E:182:TYR:C	1:E:182:TYR:CD1	2.85	0.52
1:E:388:LEU:HD12	1:E:388:LEU:N	2.24	0.52
1:A:83:LEU:HD12	1:A:138:GLY:HA3	1.90	0.52
1:A:106:TYR:HE2	1:A:120:PHE:HD2	1.55	0.52
1:A:488:GLN:HE21	1:A:527:GLN:HE22	0.52	0.52
1:A:584:PHE:CD1	1:A:584:PHE:C	2.86	0.52
2:C:119:ILE:CG1	2:C:121:LEU:HB2	2.38	0.52
2:C:394:ARG:HH11	2:C:394:ARG:HG2	1.74	0.52
1:E:587:PHE:O	1:E:587:PHE:HD2	1.92	0.52
2:F:145:ARG:C	2:F:149:ASN:HD22	2.08	0.52
1:A:311:LEU:N	1:A:311:LEU:CD2	2.73	0.52
1:A:359:LEU:CD1	1:A:360:ASN:C	2.82	0.52
1:A:366:LYS:CE	1:A:395:ARG:CZ	2.79	0.52
1:A:464:SER:C	2:C:494:TRP:CZ3	2.81	0.52
1:A:480:GLY:N	1:A:524:PRO:CG	2.70	0.52
2:D:5:ARG:NE	1:B:610:ARG:HG3	2.24	0.52
2:D:77:VAL:HG13	2:D:84:ILE:CG1	2.30	0.52
2:D:113:HIS:HA	2:D:116:ALA:CB	2.39	0.52
2:D:302:ILE:HD12	2:D:356:TRP:HZ3	1.74	0.52
1:B:242:ILE:N	1:B:242:ILE:CD1	2.73	0.52
1:E:81:VAL:HG12	1:E:82:GLY:N	2.25	0.52
1:E:112:ASN:OD1	1:E:112:ASN:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:196:PHE:CD2	1:E:197:PRO:HD2	2.44	0.52
1:E:264:THR:O	1:E:268:ARG:NH1	2.43	0.52
1:E:383:THR:C	1:E:384:HIS:CD2	2.88	0.52
1:E:493:GLN:HE22	2:F:36:ARG:HH21	1.58	0.52
1:E:518:LYS:HB3	1:E:525:ILE:O	2.09	0.52
2:C:223:LEU:N	2:C:223:LEU:CD2	2.73	0.52
1:B:395:ARG:NE	1:B:396:HIS:CA	2.73	0.52
1:E:184:ASP:OD1	1:E:184:ASP:N	2.42	0.52
1:E:233:HIS:CB	1:E:263:PHE:HE2	2.23	0.52
1:A:115:ARG:HG2	1:A:115:ARG:O	2.09	0.52
1:A:270:SER:HB3	1:A:273:SER:OG	2.09	0.52
1:A:338:LEU:HD21	1:A:372:ILE:CG1	2.22	0.52
2:C:101:ASP:O	2:C:104:GLN:OE1	2.28	0.52
2:C:129:ARG:HG2	2:C:129:ARG:HH11	1.72	0.52
2:C:191:TYR:HE2	2:C:264:LEU:HD22	1.74	0.52
2:C:312:GLN:NE2	2:C:323:LYS:HB2	2.23	0.52
2:D:341:ILE:HG23	2:D:375:MET:SD	2.50	0.52
1:B:318:GLN:HG3	1:B:318:GLN:O	2.09	0.52
1:E:106:TYR:CD2	1:E:120:PHE:CE2	2.97	0.52
1:E:588:LEU:HD11	2:F:6:ILE:HD11	1.92	0.52
1:A:330:PRO:HG2	1:A:362:PRO:HG3	1.91	0.52
1:A:431:SER:O	1:A:434:PHE:N	2.36	0.52
2:D:84:ILE:HD12	2:D:88:TYR:HD2	1.74	0.52
2:D:291:MET:CE	2:D:340:ILE:HG23	2.39	0.52
2:D:329:TRP:CZ3	2:D:424:ILE:HD13	2.38	0.52
2:D:358:LYS:C	2:D:361:ASP:OD2	2.51	0.52
1:B:268:ARG:CZ	1:B:305:ILE:HD12	2.39	0.52
1:B:549:GLN:HB2	1:B:551:ILE:HG23	1.91	0.52
1:E:182:TYR:CE1	1:E:184:ASP:OD1	2.33	0.52
1:E:280:LEU:HD11	1:E:345:ILE:HG12	1.92	0.52
1:E:365:ILE:CD1	1:E:366:LYS:N	2.73	0.52
1:E:536:PHE:C	1:E:536:PHE:CD1	2.86	0.52
2:F:108:PHE:N	2:F:108:PHE:HD2	2.06	0.52
2:F:278:PHE:C	2:F:278:PHE:CD2	2.86	0.52
1:A:77:GLU:HG3	1:A:201:ARG:C	2.35	0.52
1:A:491:ASN:HD22	2:C:36:ARG:CD	2.23	0.52
1:A:617:TRP:HA	2:C:102:PRO:HB3	1.92	0.52
2:C:404:ILE:O	2:C:408:LEU:HD12	2.10	0.52
2:D:96:VAL:CG1	2:D:100:LEU:HB2	2.40	0.52
2:D:250:SER:O	2:D:254:ILE:HG13	2.10	0.52
1:B:97:LEU:HB2	1:B:120:PHE:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:PRO:HG3	1:B:292:PRO:HA	1.92	0.52
1:B:471:TYR:CD1	1:B:471:TYR:N	2.76	0.52
1:B:478:ILE:HD13	1:B:478:ILE:H	1.72	0.52
1:B:482:GLN:HB2	1:B:526:LEU:HD22	1.92	0.52
2:F:129:ARG:NH2	2:F:129:ARG:CB	2.73	0.52
2:F:299:TRP:O	2:F:303:GLU:N	2.37	0.52
1:A:74:ASP:OD1	1:A:75:GLU:O	2.28	0.52
1:A:469:ILE:CD1	2:C:488:TRP:CE2	2.87	0.52
1:B:68:ASN:CB	1:B:81:VAL:HA	2.40	0.52
1:B:490:LEU:CD1	1:B:491:ASN:N	2.73	0.52
1:B:538:THR:CG2	1:B:539:LEU:N	2.73	0.52
1:E:268:ARG:CG	1:E:268:ARG:NH1	2.73	0.52
1:E:305:ILE:HG22	1:E:307:LEU:HD11	1.91	0.52
1:E:358:LEU:N	1:E:358:LEU:CD2	2.73	0.52
1:E:449:HIS:HD2	1:E:458:PHE:HA	1.75	0.52
2:F:34:ARG:O	2:F:35:GLN:C	2.50	0.52
1:A:385:LEU:HD23	1:A:386:LEU:N	2.25	0.51
2:C:356:TRP:CE3	2:C:359:LEU:HD13	2.45	0.51
2:D:113:HIS:O	2:D:117:ALA:N	2.42	0.51
2:D:232:ASP:OD1	2:D:232:ASP:N	2.37	0.51
1:B:175:LEU:HA	1:B:458:PHE:CE2	2.45	0.51
1:B:289:TYR:HD2	1:B:289:TYR:N	2.08	0.51
1:B:311:LEU:N	1:B:311:LEU:CD2	2.73	0.51
1:B:450:LYS:NZ	1:B:450:LYS:CB	2.73	0.51
1:B:589:PRO:CG	1:B:596:TRP:CZ2	2.93	0.51
1:E:289:TYR:HD1	1:E:317:PHE:HD2	1.45	0.51
1:E:469:ILE:CB	1:E:478:ILE:HD11	2.33	0.51
1:E:524:PRO:O	1:E:525:ILE:CD1	2.46	0.51
1:E:560:HIS:O	1:E:563:ILE:HB	2.09	0.51
2:F:68:LEU:HD22	2:F:84:ILE:HD11	1.72	0.51
2:F:154:TRP:CE2	2:F:158:HIS:ND1	2.76	0.51
1:A:176:LEU:CD2	1:A:176:LEU:N	2.73	0.51
1:A:418:VAL:O	1:A:419:VAL:HG13	2.10	0.51
2:C:40:ARG:HD3	2:C:44:TYR:CZ	2.44	0.51
2:D:312:GLN:OE1	2:D:430:ILE:CD1	2.58	0.51
2:D:346:ASN:HD22	2:D:382:GLU:CD	2.17	0.51
1:B:213:ILE:O	1:B:213:ILE:HG13	2.09	0.51
1:B:289:TYR:HA	1:B:317:PHE:CE1	2.45	0.51
1:E:75:GLU:OE1	1:E:76:ASP:HB2	2.09	0.51
1:E:88:LYS:HB3	1:E:130:THR:CG2	2.40	0.51
1:E:562:GLN:O	1:E:566:LYS:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:315:ASP:OD2	3:F:601:HOH:O	2.19	0.51
1:A:77:GLU:CG	1:A:201:ARG:O	2.58	0.51
1:A:104:ILE:CD1	1:A:104:ILE:N	2.73	0.51
1:A:124:LEU:CB	1:A:188:LEU:O	2.54	0.51
1:A:196:PHE:CE2	1:A:197:PRO:HD2	2.46	0.51
2:C:358:LYS:O	2:C:362:GLU:HB2	2.10	0.51
2:D:95:PHE:CZ	2:D:155:LEU:HD21	2.42	0.51
2:D:212:TYR:CE2	2:D:250:SER:HB3	2.46	0.51
2:D:218:ASN:ND2	2:D:221:ASP:CB	2.73	0.51
2:D:329:TRP:N	2:D:428:ASP:OD1	2.43	0.51
1:B:400:LEU:CD2	1:B:400:LEU:N	2.73	0.51
1:E:104:ILE:N	1:E:104:ILE:CD1	2.73	0.51
1:E:175:LEU:HD23	1:E:175:LEU:C	2.35	0.51
1:E:468:GLN:O	2:F:488:TRP:HA	2.10	0.51
1:E:490:LEU:HD12	1:E:490:LEU:N	2.25	0.51
2:F:36:ARG:HH12	2:F:40:ARG:HH21	1.56	0.51
1:A:183:ARG:CG	1:A:183:ARG:NH2	2.73	0.51
1:A:498:ALA:O	1:A:502:THR:CG2	2.59	0.51
2:C:110:ILE:N	2:C:110:ILE:CD1	2.73	0.51
2:C:128:LEU:HD12	2:C:129:ARG:N	2.25	0.51
1:B:79:MET:C	1:B:79:MET:SD	2.94	0.51
1:B:114:SER:O	1:B:115:ARG:NE	2.43	0.51
1:B:473:LYS:CE	1:B:474:GLY:N	2.73	0.51
1:E:97:LEU:CB	1:E:167:VAL:H	2.23	0.51
1:E:612:LYS:HD3	2:F:164:GLU:CG	2.40	0.51
2:F:158:HIS:O	2:F:162:ASP:CG	2.54	0.51
1:A:508:THR:OG1	1:A:537:ILE:HD11	2.10	0.51
2:C:209:PHE:CE2	2:C:254:ILE:CG1	2.92	0.51
2:C:209:PHE:HE2	2:C:254:ILE:HG12	1.67	0.51
1:B:99:VAL:CG1	1:B:166:ARG:NH2	2.68	0.51
1:E:233:HIS:CB	1:E:263:PHE:CE2	2.94	0.51
1:E:289:TYR:CD1	1:E:317:PHE:HD2	2.21	0.51
1:E:587:PHE:C	1:E:587:PHE:HD2	2.18	0.51
2:F:52:LEU:HD23	2:F:57:ASP:HB2	1.89	0.51
1:A:107:ASN:HD22	1:A:258:LEU:HD21	1.72	0.51
1:B:69:ILE:N	1:B:69:ILE:CD1	2.73	0.51
1:B:85:GLU:O	1:B:133:PHE:CD1	2.64	0.51
1:B:310:HIS:CD2	1:B:314:GLY:CA	2.79	0.51
1:B:503:VAL:HG12	1:B:539:LEU:CD2	2.40	0.51
1:E:469:ILE:CG2	1:E:470:SER:N	2.73	0.51
1:E:491:ASN:HD22	2:F:36:ARG:HE	1.53	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:TYR:CD2	1:A:71:TYR:C	2.89	0.51
1:A:79:MET:SD	1:A:79:MET:C	2.94	0.51
1:A:169:ASN:CB	1:A:203:THR:HG23	2.41	0.51
1:A:176:LEU:N	1:A:176:LEU:HD22	2.26	0.51
1:A:291:LEU:CD1	1:A:291:LEU:N	2.73	0.51
1:A:603:PRO:O	2:C:10:ARG:C	2.53	0.51
2:C:119:ILE:CG1	2:C:121:LEU:N	2.74	0.51
2:C:160:TRP:HA	2:C:160:TRP:HE3	1.76	0.51
2:D:209:PHE:CE1	2:D:254:ILE:HG21	2.43	0.51
1:B:467:LEU:CD2	1:B:554:ILE:O	2.59	0.51
1:E:71:TYR:C	1:E:71:TYR:CD2	2.89	0.51
1:E:95:PHE:CE2	1:E:120:PHE:HB2	2.45	0.51
1:E:389:GLU:HB3	1:E:394:LYS:CB	2.40	0.51
1:E:592:ARG:NH2	1:E:593:THR:N	2.57	0.51
1:E:599:ASN:OD1	1:E:600:ILE:HG12	2.10	0.51
1:A:371:GLN:NE2	1:A:371:GLN:CA	2.73	0.51
2:C:405:GLU:HA	2:C:408:LEU:HD12	1.93	0.51
1:B:175:LEU:C	1:B:458:PHE:CZ	2.89	0.51
1:E:387:PHE:CZ	1:E:401:THR:CG2	2.94	0.51
1:E:528:SER:C	1:E:529:CYS:SG	2.94	0.51
1:A:177:GLU:HG2	2:C:267:LEU:HD23	1.91	0.51
1:A:226:LEU:CG	1:A:230:TYR:OH	2.58	0.51
1:A:300:ILE:CD1	1:A:300:ILE:N	2.73	0.51
1:A:365:ILE:CG2	1:A:397:LEU:HD21	2.34	0.51
1:A:603:PRO:O	2:C:10:ARG:HA	2.10	0.51
2:C:96:VAL:HG11	2:C:128:LEU:CD1	2.35	0.51
2:C:122:PRO:HB2	2:C:124:TRP:CD1	2.46	0.51
2:C:127:ASP:O	2:C:131:TRP:HB2	2.10	0.51
2:C:206:ARG:C	2:C:210:LEU:CD1	2.69	0.51
2:D:88:TYR:HB3	2:D:144:LEU:HD13	1.92	0.51
1:E:265:GLN:O	1:E:269:ASP:OD2	2.29	0.51
1:E:280:LEU:O	1:E:359:LEU:HB2	2.10	0.51
2:F:45:ARG:O	2:F:48:GLY:O	2.28	0.51
1:A:395:ARG:NH2	1:A:395:ARG:CG	2.73	0.51
2:D:182:TYR:O	2:D:186:ASP:N	2.42	0.51
1:B:175:LEU:CA	1:B:458:PHE:CE2	2.94	0.51
1:B:347:HIS:CD2	1:B:347:HIS:C	2.87	0.51
1:E:245:ILE:CG2	1:E:387:PHE:CE2	2.94	0.51
1:E:588:LEU:HD21	2:F:6:ILE:CD1	2.40	0.51
1:E:601:GLN:NE2	1:E:601:GLN:CA	2.73	0.51
2:F:12:PHE:O	2:F:12:PHE:HD1	1.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:53:PRO:HD2	2:F:56:VAL:HG21	1.93	0.51
2:F:359:LEU:HD23	2:F:360:ILE:CA	2.40	0.51
1:A:84:LYS:CB	1:A:139:TRP:C	2.84	0.50
2:C:129:ARG:NH1	2:C:129:ARG:CG	2.73	0.50
2:C:212:TYR:N	2:C:212:TYR:CD2	2.79	0.50
2:C:224:ILE:CB	2:C:229:PHE:CE2	2.86	0.50
2:D:102:PRO:HG3	1:B:615:HIS:NE2	2.26	0.50
2:D:329:TRP:HB2	2:D:424:ILE:HG23	1.93	0.50
1:B:245:ILE:O	1:B:388:LEU:CD1	2.59	0.50
1:B:536:PHE:HD1	1:B:537:ILE:N	2.09	0.50
1:A:198:LEU:HD23	1:A:205:HIS:HE2	1.76	0.50
1:A:527:GLN:NE2	1:A:527:GLN:CA	2.73	0.50
1:B:98:GLN:HB3	1:B:165:LEU:HD13	1.92	0.50
1:B:311:LEU:O	1:B:312:CYS:HB2	2.12	0.50
1:B:467:LEU:HD23	1:B:467:LEU:C	2.36	0.50
1:E:364:TRP:CE3	3:E:705:HOH:O	2.64	0.50
1:E:538:THR:CG2	1:E:539:LEU:N	2.73	0.50
1:E:546:ASP:HB3	1:E:551:ILE:CG1	2.40	0.50
1:A:71:TYR:CE2	1:A:73:GLY:N	2.73	0.50
1:A:481:ILE:HG23	1:A:575:ILE:CG1	2.41	0.50
1:A:524:PRO:O	1:A:524:PRO:HG2	2.10	0.50
2:C:310:ARG:HE	2:C:314:ASP:CG	2.11	0.50
2:D:154:TRP:HZ3	2:D:155:LEU:HD23	1.71	0.50
2:D:159:TYR:HE1	1:B:614:GLU:CD	2.17	0.50
2:D:193:GLU:O	2:D:197:LYS:CG	2.60	0.50
1:B:358:LEU:N	1:B:358:LEU:CD2	2.73	0.50
1:E:491:ASN:HD21	2:F:39:GLN:CB	2.23	0.50
1:A:106:TYR:CD2	1:A:120:PHE:CE2	2.98	0.50
1:A:165:LEU:N	1:A:165:LEU:CD1	2.73	0.50
1:A:469:ILE:CG2	2:C:488:TRP:CD2	2.94	0.50
2:C:387:ASN:C	2:C:391:ASN:HD21	2.19	0.50
2:D:133:THR:HB	2:D:134:HIS:HD2	1.76	0.50
2:D:336:LEU:CD1	2:D:340:ILE:CG1	2.90	0.50
1:B:92:SER:HA	1:B:122:HIS:HB3	1.93	0.50
1:B:121:TRP:CB	1:B:309:GLN:O	2.59	0.50
1:B:175:LEU:HD22	1:B:456:TYR:HE2	1.76	0.50
1:B:448:PHE:CB	1:B:461:LEU:HD21	2.41	0.50
1:B:450:LYS:CD	1:B:456:TYR:HH	2.04	0.50
1:E:98:GLN:CB	1:E:117:ILE:CG2	2.89	0.50
1:E:118:LEU:N	1:E:118:LEU:CD2	2.73	0.50
1:E:399:GLU:OE2	1:E:400:LEU:CA	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:66:VAL:HA	2:F:88:TYR:CZ	2.45	0.50
1:A:97:LEU:HA	1:A:166:ARG:O	2.11	0.50
1:A:204:TYR:CD1	1:A:204:TYR:N	2.79	0.50
1:A:224:THR:HB	1:A:225:PRO:HD3	1.94	0.50
1:A:589:PRO:HG2	1:A:596:TRP:CZ3	2.46	0.50
2:C:96:VAL:CG2	2:C:128:LEU:HD11	2.42	0.50
2:D:69:ASP:CB	2:D:77:VAL:HG21	2.27	0.50
2:D:330:LYS:O	2:D:334:LYS:HG2	2.11	0.50
1:B:103:GLY:O	1:B:134:SER:CB	2.56	0.50
1:B:211:ASP:CA	1:B:212:ARG:NH2	2.75	0.50
1:B:488:GLN:HA	1:B:488:GLN:HE21	1.77	0.50
1:E:97:LEU:HB2	1:E:167:VAL:H	1.76	0.50
1:E:98:GLN:HB2	1:E:117:ILE:CG2	2.42	0.50
1:E:213:ILE:HD12	1:E:215:SER:N	2.26	0.50
1:E:267:ILE:CD1	1:E:302:SER:HB3	2.38	0.50
1:E:584:PHE:CE1	1:E:588:LEU:CD1	2.95	0.50
2:F:398:ILE:HA	2:F:401:THR:HG23	1.92	0.50
1:A:83:LEU:O	1:A:133:PHE:CD2	2.64	0.50
1:A:174:GLY:HA3	1:A:456:TYR:O	2.11	0.50
1:A:471:TYR:O	1:A:550:GLN:O	2.30	0.50
2:D:199:LEU:HD12	2:D:281:ASN:OD1	2.11	0.50
1:B:174:GLY:C	1:B:458:PHE:CE2	2.67	0.50
1:B:184:ASP:HB3	1:B:438:GLN:OE1	2.12	0.50
1:B:536:PHE:C	1:B:536:PHE:HD1	2.19	0.50
1:E:84:LYS:HA	1:E:133:PHE:CZ	2.45	0.50
1:E:110:HIS:CD2	1:E:111:TYR:N	2.80	0.50
1:E:331:GLN:HG3	1:E:364:TRP:CH2	2.19	0.50
1:A:241:ARG:NE	1:A:380:TYR:O	2.43	0.50
1:A:265:GLN:HA	1:A:268:ARG:NH1	2.26	0.50
1:A:484:PRO:HG2	1:A:487:PHE:CD1	2.47	0.50
2:D:112:LEU:N	2:D:112:LEU:CD2	2.73	0.50
2:D:184:ARG:CG	1:B:592:ARG:CD	2.90	0.50
2:D:210:LEU:HG	2:D:285:LEU:HD11	1.93	0.50
1:B:167:VAL:O	1:B:204:TYR:CZ	2.65	0.50
1:B:334:PRO:O	1:B:338:LEU:HD12	2.11	0.50
1:B:482:GLN:HB3	1:B:576:VAL:HG22	1.92	0.50
1:B:541:LEU:O	1:B:555:TYR:N	2.45	0.50
1:E:353:PHE:HE1	1:E:355:GLY:HA3	1.77	0.50
2:F:359:LEU:HD21	2:F:368:ILE:CD1	2.37	0.50
1:A:105:VAL:HG12	1:A:105:VAL:O	2.10	0.50
1:A:267:ILE:CD1	1:A:277:LEU:HD23	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:ASN:ND2	2:C:36:ARG:CD	2.74	0.50
1:E:182:TYR:CE1	1:E:184:ASP:HB2	2.42	0.50
1:E:549:GLN:NE2	1:E:549:GLN:N	2.60	0.50
2:F:110:ILE:CG2	2:F:114:THR:HG22	2.42	0.50
2:F:350:LYS:HZ3	2:F:401:THR:CG2	1.98	0.50
1:A:307:LEU:N	1:A:307:LEU:CD1	2.73	0.50
1:A:371:GLN:NE2	1:A:371:GLN:HA	2.25	0.50
1:A:457:ASP:OD2	2:C:268:SER:HB2	2.12	0.50
2:C:357:GLU:HG2	2:C:361:ASP:OD1	2.12	0.50
1:B:450:LYS:HB3	1:B:450:LYS:HZ3	1.75	0.50
1:E:76:ASP:C	1:E:77:GLU:HG2	2.37	0.50
1:E:268:ARG:HH11	1:E:268:ARG:HG3	1.74	0.50
1:E:474:GLY:N	1:E:475:LYS:CA	2.74	0.50
1:E:589:PRO:CG	1:E:596:TRP:CH2	2.95	0.50
2:F:53:PRO:HD2	2:F:56:VAL:CG2	2.41	0.50
1:A:589:PRO:HG3	1:A:596:TRP:CH2	2.46	0.49
1:A:617:TRP:HD1	1:A:618:LYS:H	1.60	0.49
2:C:307:ARG:NH1	2:C:307:ARG:CG	2.73	0.49
2:D:69:ASP:OD1	2:D:88:TYR:OH	2.20	0.49
1:B:389:GLU:HB3	1:B:394:LYS:CA	2.42	0.49
1:B:390:THR:CG2	1:B:391:ALA:H	2.02	0.49
1:E:214:GLN:HG3	1:E:214:GLN:O	2.12	0.49
1:E:445:LEU:HD13	1:E:583:PRO:HG3	1.93	0.49
1:E:473:LYS:HD2	1:E:474:GLY:N	2.27	0.49
1:E:473:LYS:CD	1:E:474:GLY:H	2.25	0.49
1:E:549:GLN:NE2	1:E:549:GLN:H	2.10	0.49
2:C:23:TYR:HD2	2:C:156:TYR:CE2	2.29	0.49
2:C:292:LEU:N	2:C:292:LEU:HD23	2.26	0.49
2:C:359:LEU:C	2:C:359:LEU:CD2	2.85	0.49
1:B:167:VAL:HG23	1:B:167:VAL:O	2.11	0.49
1:E:71:TYR:CZ	1:E:73:GLY:HA3	2.47	0.49
1:E:279:TYR:HB2	1:E:300:ILE:HD11	1.93	0.49
1:E:523:PHE:CB	1:E:525:ILE:HD11	2.42	0.49
2:F:319:THR:HG21	2:F:433:GLU:N	2.23	0.49
2:F:332:LEU:C	2:F:332:LEU:CD2	2.85	0.49
2:C:260:GLN:O	2:C:264:LEU:HG	2.11	0.49
1:E:195:TYR:CD1	1:E:208:HIS:HB3	2.47	0.49
1:E:208:HIS:ND1	1:E:209:GLU:N	2.60	0.49
1:A:107:ASN:O	1:A:109:VAL:HG13	2.12	0.49
1:A:169:ASN:HB3	1:A:203:THR:CG2	2.42	0.49
1:A:392:ASN:CB	1:A:393:SER:C	2.85	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:SER:HB2	1:A:550:GLN:O	2.12	0.49
1:A:592:ARG:HH21	2:C:184:ARG:HE	1.58	0.49
1:A:617:TRP:C	1:A:618:LYS:CG	2.85	0.49
2:D:69:ASP:HB2	2:D:77:VAL:HG11	1.93	0.49
2:D:82:ILE:HG23	2:D:83:PRO:N	2.28	0.49
1:B:195:TYR:O	1:B:196:PHE:HD1	1.96	0.49
1:B:490:LEU:HD12	1:B:491:ASN:H	1.74	0.49
1:E:389:GLU:HB2	1:E:397:LEU:HD11	1.94	0.49
1:E:394:LYS:C	1:E:394:LYS:CD	2.86	0.49
2:F:188:LEU:O	2:F:192:MET:HG2	2.12	0.49
2:F:349:PHE:CD1	2:F:375:MET:HE2	2.47	0.49
1:A:169:ASN:ND2	1:A:203:THR:HG23	2.26	0.49
1:A:541:LEU:HD11	2:C:499:PHE:HE1	1.77	0.49
1:A:614:GLU:HB2	2:C:53:PRO:HB3	1.94	0.49
2:C:209:PHE:HD2	2:C:254:ILE:CD1	2.25	0.49
2:C:332:LEU:C	2:C:332:LEU:CD2	2.85	0.49
2:D:99:LEU:C	2:D:102:PRO:CD	2.86	0.49
2:D:278:PHE:CE1	2:D:279:PHE:HE2	2.30	0.49
1:B:94:VAL:HG12	1:B:95:PHE:N	2.28	0.49
1:E:182:TYR:CD1	1:E:184:ASP:N	2.79	0.49
1:E:236:ALA:O	1:E:237:ALA:HB3	2.13	0.49
1:E:245:ILE:HG21	1:E:387:PHE:HE2	1.77	0.49
1:E:365:ILE:HG21	1:E:389:GLU:OE2	2.13	0.49
1:E:390:THR:O	1:E:394:LYS:CG	2.61	0.49
1:A:552:MET:O	1:A:554:ILE:HG22	2.11	0.49
1:A:592:ARG:NH2	2:C:184:ARG:NE	2.53	0.49
1:A:603:PRO:HD3	2:C:498:PRO:HG2	1.94	0.49
2:C:131:TRP:CH2	2:C:143:MET:HE3	2.48	0.49
2:C:291:MET:HE3	2:C:340:ILE:CG2	2.36	0.49
2:D:154:TRP:HZ3	2:D:155:LEU:CD2	2.25	0.49
2:D:359:LEU:C	2:D:359:LEU:CD2	2.86	0.49
2:D:487:ASN:ND2	2:D:488:TRP:CD1	2.75	0.49
1:E:181:LEU:C	1:E:181:LEU:CD1	2.86	0.49
2:F:54:HIS:ND1	2:F:54:HIS:O	2.43	0.49
2:F:80:ASP:OD1	2:F:80:ASP:N	2.35	0.49
1:A:169:ASN:HB3	1:A:203:THR:HG21	1.94	0.49
1:A:472:GLY:CA	1:A:475:LYS:CB	2.91	0.49
2:C:46:LEU:HD22	2:C:46:LEU:C	2.38	0.49
2:C:128:LEU:O	2:C:131:TRP:HB3	2.12	0.49
2:C:218:ASN:OD1	2:C:218:ASN:N	2.45	0.49
2:C:337:LEU:C	2:C:337:LEU:CD2	2.86	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:489:SER:C	1:B:467:LEU:HB2	2.29	0.49
1:B:93:GLY:O	1:B:95:PHE:CE1	2.65	0.49
1:B:245:ILE:HD12	1:B:246:GLY:H	1.77	0.49
1:B:277:LEU:HA	1:B:356:THR:O	2.12	0.49
1:B:364:TRP:HE3	1:B:364:TRP:H	1.60	0.49
1:E:316:ASN:O	1:E:316:ASN:ND2	2.44	0.49
2:F:98:GLY:O	2:F:102:PRO:CB	2.61	0.49
2:F:372:CYS:HB3	2:F:412:ILE:HD11	1.93	0.49
1:A:129:PRO:HB3	1:A:217:SER:HA	1.93	0.49
1:A:205:HIS:ND1	1:A:206:LEU:N	2.60	0.49
1:A:243:MET:SD	1:A:361:LEU:CD2	3.01	0.49
1:A:280:LEU:HD11	1:A:297:LEU:CD1	2.39	0.49
1:A:383:THR:HB	1:A:384:HIS:CE1	2.47	0.49
2:C:353:TRP:CH2	2:C:408:LEU:CD2	2.82	0.49
1:B:65:LEU:HD12	1:B:66:ILE:O	2.13	0.49
1:B:122:HIS:HE1	1:B:128:ILE:HD13	1.78	0.49
1:E:76:ASP:C	1:E:77:GLU:CG	2.85	0.49
1:E:103:GLY:O	1:E:104:ILE:HD12	2.13	0.49
1:E:233:HIS:CD2	1:E:356:THR:HG21	2.48	0.49
1:E:431:SER:OG	1:E:435:HIS:N	2.45	0.49
1:E:477:GLY:C	1:E:478:ILE:HG13	2.37	0.49
1:E:538:THR:HG21	1:E:557:PRO:HD2	1.94	0.49
2:F:154:TRP:HE3	2:F:155:LEU:N	2.11	0.49
1:A:168:PHE:CD1	1:A:168:PHE:N	2.81	0.49
1:A:364:TRP:CD1	1:A:369:GLY:HA3	2.43	0.49
2:C:125:PHE:CD1	2:C:128:LEU:HD23	2.48	0.49
2:C:202:TRP:HH2	2:C:289:VAL:HG21	1.77	0.49
2:D:146:TRP:C	2:D:146:TRP:CD2	2.90	0.49
2:D:423:GLU:O	2:D:426:LEU:HB2	2.13	0.49
1:B:247:GLY:HA3	1:B:365:ILE:CG2	2.43	0.49
1:B:305:ILE:HG22	1:B:307:LEU:HD21	1.95	0.49
1:B:471:TYR:CZ	1:B:550:GLN:HA	2.39	0.49
1:E:100:VAL:C	1:E:101:LYS:CG	2.86	0.49
1:E:389:GLU:CD	1:E:392:ASN:CB	2.86	0.49
1:A:280:LEU:CG	1:A:297:LEU:HD12	2.42	0.49
1:A:357:SER:OG	1:A:380:TYR:OH	1.95	0.49
1:A:517:VAL:HG13	1:A:517:VAL:O	2.13	0.49
1:A:615:HIS:ND1	1:A:615:HIS:N	2.60	0.49
2:C:312:GLN:OE1	2:C:323:LYS:NZ	2.45	0.49
2:D:128:LEU:C	2:D:128:LEU:CD2	2.86	0.49
2:D:419:PHE:CD2	2:D:419:PHE:N	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:LEU:CD2	1:B:401:THR:H	2.21	0.49
1:B:509:TYR:CZ	1:B:513:ASP:HB2	2.44	0.49
1:E:243:MET:SD	1:E:377:ILE:HG12	2.52	0.49
1:E:317:PHE:HD1	1:E:317:PHE:H	1.59	0.49
1:E:501:GLY:CA	2:F:499:PHE:HD1	2.26	0.49
1:E:562:GLN:H	1:E:562:GLN:CD	2.20	0.49
1:A:388:LEU:HG	1:A:421:VAL:HG21	1.95	0.48
2:C:62:ILE:HG12	2:C:91:ALA:HB1	1.94	0.48
2:C:202:TRP:CH2	2:C:289:VAL:HG21	2.48	0.48
1:B:469:ILE:HB	1:B:478:ILE:HD11	1.94	0.48
2:F:125:PHE:HD1	2:F:128:LEU:CD2	2.25	0.48
2:F:159:TYR:C	2:F:159:TYR:CD2	2.91	0.48
1:A:171:ASN:O	1:A:454:PHE:HB2	2.12	0.48
1:A:261:GLU:CG	1:A:307:LEU:HD23	2.43	0.48
1:A:306:SER:C	1:A:307:LEU:HD12	2.37	0.48
1:A:373:LEU:CD2	1:A:373:LEU:N	2.73	0.48
1:A:487:PHE:HD2	2:C:42:GLN:OE1	1.96	0.48
2:D:5:ARG:CD	1:B:610:ARG:CG	2.91	0.48
2:D:54:HIS:HE1	2:D:58:SER:OG	1.96	0.48
1:B:534:LYS:N	1:B:534:LYS:HD2	2.28	0.48
1:E:214:GLN:OE1	1:E:427:ASN:CB	2.60	0.48
1:E:306:SER:C	1:E:307:LEU:CD1	2.85	0.48
1:E:390:THR:OG1	1:E:422:PRO:HA	2.13	0.48
1:E:473:LYS:H	1:E:473:LYS:CD	2.25	0.48
2:F:337:LEU:CD1	2:F:338:ASP:N	2.73	0.48
1:A:75:GLU:CA	2:C:259:ARG:NH2	2.63	0.48
1:A:256:LEU:CD1	1:A:360:ASN:HB3	2.40	0.48
1:A:282:LEU:CD1	1:A:359:LEU:CD1	2.85	0.48
1:A:330:PRO:HB3	1:A:337:TYR:CD2	2.48	0.48
1:A:472:GLY:HA2	1:A:550:GLN:NE2	2.28	0.48
1:A:611:LYS:HA	2:C:164:GLU:O	2.14	0.48
2:C:23:TYR:HE2	2:C:160:TRP:HD1	1.57	0.48
2:C:197:LYS:O	2:C:201:LYS:HG3	2.12	0.48
2:D:71:LYS:HB3	2:D:71:LYS:HZ2	1.77	0.48
2:D:329:TRP:CG	2:D:424:ILE:CD1	2.65	0.48
1:B:127:SER:CB	1:B:214:GLN:HG3	2.43	0.48
1:B:507:TYR:HD1	1:B:535:ASN:O	1.96	0.48
1:E:309:GLN:CD	1:E:311:LEU:HD13	2.37	0.48
2:F:30:ILE:C	2:F:30:ILE:CD1	2.85	0.48
2:F:67:LEU:O	2:F:67:LEU:HD23	2.14	0.48
1:A:71:TYR:CD2	1:A:73:GLY:N	2.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLN:HG2	1:A:115:ARG:HA	1.85	0.48
1:A:253:SER:O	1:A:257:ARG:HG3	2.14	0.48
1:A:492:PRO:HB3	1:A:521:ASN:HB2	1.95	0.48
2:C:182:TYR:HE1	2:F:183:ARG:HG3	1.69	0.48
2:C:202:TRP:CE2	2:C:286:LEU:CD1	2.97	0.48
2:C:325:LYS:O	2:C:326:PHE:HD1	1.95	0.48
2:C:353:TRP:CE3	2:C:404:ILE:HG23	2.48	0.48
1:B:359:LEU:CD1	1:B:360:ASN:C	2.86	0.48
1:B:599:ASN:ND2	1:B:600:ILE:N	2.60	0.48
1:A:313:GLN:NE2	1:A:313:GLN:N	2.60	0.48
2:C:125:PHE:CB	2:C:128:LEU:CD2	2.91	0.48
2:C:148:ALA:O	2:C:152:LEU:HG	2.14	0.48
2:C:278:PHE:HE2	2:C:286:LEU:HD23	0.51	0.48
2:D:110:ILE:HG22	2:D:111:PRO:O	2.14	0.48
1:B:395:ARG:NE	1:B:396:HIS:HA	2.28	0.48
1:B:405:SER:O	1:B:406:PHE:C	2.55	0.48
1:E:195:TYR:HD1	1:E:210:SER:OG	1.97	0.48
1:E:254:THR:HA	1:E:257:ARG:NH1	2.28	0.48
1:A:196:PHE:CG	1:A:197:PRO:CD	2.94	0.48
1:A:481:ILE:HG23	1:A:575:ILE:CB	2.41	0.48
1:A:543:HIS:CE1	2:C:502:LEU:C	2.89	0.48
2:C:130:HIS:CB	2:C:134:HIS:ND1	2.73	0.48
2:C:310:ARG:HH11	2:C:310:ARG:HG3	1.77	0.48
2:D:215:VAL:HG13	2:D:255:ARG:NH2	2.28	0.48
2:F:99:LEU:C	2:F:102:PRO:CD	2.86	0.48
1:A:81:VAL:HG12	1:A:82:GLY:H	1.79	0.48
2:C:96:VAL:HG21	2:C:128:LEU:HD11	1.96	0.48
2:C:278:PHE:CE1	2:C:287:LEU:CD1	2.97	0.48
1:B:76:ASP:HB3	1:B:169:ASN:HB2	1.95	0.48
1:E:480:GLY:N	1:E:524:PRO:HB2	2.28	0.48
1:A:244:VAL:HB	1:A:256:LEU:HD21	1.96	0.48
1:A:401:THR:HA	1:A:404:GLN:CB	2.43	0.48
1:A:541:LEU:C	1:A:541:LEU:CD1	2.85	0.48
1:A:543:HIS:HE1	2:C:502:LEU:HA	1.77	0.48
1:A:617:TRP:HH2	2:D:133:THR:O	1.96	0.48
2:C:15:LEU:O	2:C:15:LEU:HD23	2.14	0.48
2:D:21:TRP:HB3	2:D:33:LYS:O	2.14	0.48
2:D:278:PHE:HE1	2:D:279:PHE:CD2	2.27	0.48
2:D:320:THR:OG1	2:D:323:LYS:HB2	2.13	0.48
2:D:423:GLU:O	2:D:426:LEU:N	2.46	0.48
1:B:263:PHE:HD1	1:B:263:PHE:H	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:347:HIS:HA	1:B:350:GLU:HB2	1.96	0.48
1:B:488:GLN:NE2	1:B:488:GLN:CA	2.73	0.48
1:E:240:THR:OG1	1:E:240:THR:O	2.30	0.48
1:E:295:ILE:HG22	1:E:344:LEU:HD21	1.94	0.48
1:E:297:LEU:HB3	1:E:321:LEU:HD23	1.96	0.48
1:A:100:VAL:O	1:A:101:LYS:HD2	2.14	0.48
1:A:124:LEU:H	1:A:188:LEU:HD23	1.79	0.48
1:A:451:ILE:C	1:A:452:THR:CG2	2.86	0.48
2:D:69:ASP:CB	2:D:84:ILE:HG12	2.44	0.48
2:D:334:LYS:HA	2:D:338:ASP:HB2	1.96	0.48
2:D:492:GLN:H	2:D:492:GLN:HG2	1.46	0.48
1:B:263:PHE:CD1	1:B:263:PHE:N	2.82	0.48
1:B:395:ARG:C	1:B:395:ARG:CD	2.86	0.48
1:E:223:SER:O	1:E:227:GLU:N	2.47	0.48
1:E:282:LEU:HD23	1:E:295:ILE:HG23	1.94	0.48
1:E:394:LYS:HD2	1:E:395:ARG:N	2.28	0.48
1:E:452:THR:HB	1:E:454:PHE:HE2	1.79	0.48
1:A:472:GLY:H	1:A:475:LYS:CB	2.27	0.48
2:C:88:TYR:O	2:C:92:LEU:HG	2.13	0.48
2:C:141:LEU:HD23	2:C:145:ARG:HH22	1.79	0.48
2:D:54:HIS:NE2	2:D:99:LEU:CD1	2.75	0.48
1:E:83:LEU:O	1:E:133:PHE:CD1	2.66	0.48
1:E:96:ARG:O	1:E:168:PHE:N	2.47	0.48
1:E:233:HIS:CG	1:E:263:PHE:HE2	2.30	0.48
2:F:337:LEU:CD1	2:F:341:ILE:HD11	2.44	0.48
1:A:181:LEU:CD1	1:A:181:LEU:C	2.85	0.47
1:A:396:HIS:C	1:A:396:HIS:CD2	2.92	0.47
2:D:59:THR:OG1	2:D:155:LEU:CD1	2.62	0.47
2:D:493:ASN:N	2:D:493:ASN:ND2	2.60	0.47
1:B:73:GLY:CA	1:B:74:ASP:C	2.86	0.47
1:B:611:LYS:O	1:B:614:GLU:HG3	2.14	0.47
1:E:74:ASP:CG	1:E:75:GLU:N	2.70	0.47
1:E:263:PHE:O	1:E:267:ILE:HG23	2.14	0.47
1:E:389:GLU:CB	1:E:394:LYS:HA	2.42	0.47
1:E:480:GLY:H	1:E:524:PRO:HG3	1.79	0.47
2:F:193:GLU:HG2	2:F:197:LYS:HD2	1.96	0.47
2:F:285:LEU:O	2:F:289:VAL:HG23	2.14	0.47
1:A:288:GLU:OE2	1:A:289:TYR:HE2	1.96	0.47
1:A:465:ALA:CA	2:C:494:TRP:CE3	2.88	0.47
1:A:616:VAL:HG23	1:A:618:LYS:NZ	2.28	0.47
2:C:182:TYR:OH	2:F:183:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:55:VAL:HG21	2:D:159:TYR:CG	2.49	0.47
2:D:279:PHE:CE1	2:D:304:TRP:CE3	2.98	0.47
1:B:241:ARG:HB3	1:B:380:TYR:CE2	2.49	0.47
1:E:100:VAL:HG12	1:E:101:LYS:CE	2.43	0.47
1:E:182:TYR:HD1	1:E:183:ARG:N	2.12	0.47
1:E:444:ILE:CD1	1:E:581:GLU:OE1	2.63	0.47
1:E:471:TYR:CE2	1:E:523:PHE:CD1	3.01	0.47
1:E:495:ILE:HG21	1:E:523:PHE:HD2	1.78	0.47
2:F:333:GLN:HG3	2:F:370:TYR:CZ	2.49	0.47
1:A:114:SER:O	1:A:114:SER:OG	2.29	0.47
1:A:348:LEU:HD12	1:A:348:LEU:O	2.14	0.47
2:C:394:ARG:CG	2:C:394:ARG:NH1	2.73	0.47
2:D:86:LEU:HD12	2:D:138:LEU:HD22	1.89	0.47
2:D:312:GLN:CD	2:D:430:ILE:HG13	2.33	0.47
1:B:94:VAL:C	1:B:95:PHE:CD1	2.92	0.47
1:B:583:PRO:HG2	1:B:586:ASP:HB3	1.97	0.47
1:E:289:TYR:CG	1:E:317:PHE:CD2	2.99	0.47
1:E:481:ILE:HG13	1:E:524:PRO:O	2.14	0.47
1:E:529:CYS:C	1:E:530:THR:OG1	2.54	0.47
2:F:324:ARG:HB3	2:F:324:ARG:HH11	1.78	0.47
2:F:349:PHE:CE1	2:F:375:MET:HE3	2.49	0.47
1:A:367:GLY:O	2:D:124:TRP:HB3	2.14	0.47
2:C:209:PHE:HE2	2:C:254:ILE:CG1	2.25	0.47
2:C:387:ASN:CA	2:C:391:ASN:HD21	2.28	0.47
2:D:112:LEU:HD23	2:D:112:LEU:H	1.73	0.47
2:D:209:PHE:CE1	2:D:254:ILE:HG22	2.45	0.47
2:D:329:TRP:CZ3	2:D:424:ILE:CD1	2.97	0.47
1:E:103:GLY:C	1:E:104:ILE:CD1	2.85	0.47
1:E:361:LEU:CD2	1:E:376:ILE:HD11	2.44	0.47
1:E:537:ILE:C	1:E:538:THR:HG1	2.22	0.47
2:F:501:VAL:C	2:F:502:LEU:CG	2.86	0.47
1:A:97:LEU:O	1:A:118:LEU:CD2	2.63	0.47
1:A:184:ASP:N	1:A:184:ASP:OD1	2.48	0.47
1:A:330:PRO:HG3	1:A:337:TYR:CE2	2.49	0.47
2:C:54:HIS:HD2	2:C:98:GLY:O	1.98	0.47
2:C:232:ASP:OD1	2:C:232:ASP:N	2.47	0.47
2:C:333:GLN:HG2	2:C:338:ASP:OD2	2.14	0.47
1:B:230:TYR:HE1	1:B:263:PHE:CD1	2.20	0.47
1:E:71:TYR:CD1	1:E:80:PHE:HE2	2.26	0.47
1:E:109:VAL:HG21	1:E:111:TYR:OH	2.12	0.47
1:E:199:ASN:HB3	1:E:202:THR:CG2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:491:ASN:HB2	1:E:494:ASP:OD1	2.15	0.47
1:A:371:GLN:NE2	1:A:371:GLN:C	2.73	0.47
1:A:462:LEU:HD11	2:C:499:PHE:CD2	2.49	0.47
2:C:85:ARG:HE	2:C:138:LEU:HD12	1.79	0.47
2:C:133:THR:HG21	2:D:93:ILE:HG21	1.93	0.47
2:C:163:GLU:O	2:C:165:LEU:HD13	2.15	0.47
2:C:484:PRO:N	2:C:485:VAL:C	2.73	0.47
2:D:79:GLN:NE2	2:D:79:GLN:CA	2.73	0.47
2:D:163:GLU:O	2:D:165:LEU:HD22	2.14	0.47
1:B:110:HIS:C	1:B:110:HIS:CD2	2.92	0.47
1:B:313:GLN:CD	1:B:313:GLN:N	2.73	0.47
1:B:408:THR:CB	1:B:415:ALA:H	2.26	0.47
1:E:364:TRP:CD1	1:E:368:PHE:C	2.89	0.47
1:E:387:PHE:CE1	1:E:401:THR:HG23	2.48	0.47
1:A:83:LEU:O	1:A:133:PHE:CG	2.68	0.47
1:A:271:THR:HA	1:A:272:THR:HA	1.45	0.47
1:A:390:THR:OG1	1:A:422:PRO:CA	2.62	0.47
1:A:399:GLU:N	1:A:399:GLU:CD	2.73	0.47
1:A:531:SER:O	1:A:534:LYS:HG3	2.14	0.47
1:A:543:HIS:CE1	2:C:502:LEU:HA	2.50	0.47
1:A:562:GLN:O	1:A:566:LYS:N	2.48	0.47
2:C:14:GLU:O	2:C:17:GLU:HB3	2.14	0.47
2:C:85:ARG:NH1	1:B:486:GLU:OE1	2.48	0.47
2:C:135:GLU:O	2:C:136:ARG:C	2.56	0.47
2:C:136:ARG:HA	1:B:617:TRP:CG	2.48	0.47
2:C:271:HIS:ND1	2:C:300:LYS:HE3	2.30	0.47
1:B:207:LEU:CD1	1:B:213:ILE:HD13	2.38	0.47
1:B:211:ASP:C	1:B:212:ARG:NH2	2.73	0.47
1:B:288:GLU:O	1:B:289:TYR:HB2	2.14	0.47
1:B:331:GLN:HG3	1:B:364:TRP:HZ2	1.80	0.47
1:B:358:LEU:HD22	1:B:358:LEU:H	1.77	0.47
1:B:543:HIS:ND1	1:B:543:HIS:C	2.73	0.47
1:B:593:THR:HG1	1:B:594:ILE:H	1.61	0.47
1:E:301:LEU:CD1	1:E:301:LEU:N	2.73	0.47
1:E:467:LEU:HB2	2:F:489:SER:C	2.40	0.47
1:E:502:THR:O	1:E:541:LEU:HD12	2.14	0.47
1:E:562:GLN:CD	1:E:562:GLN:N	2.73	0.47
2:F:8:PRO:CD	2:F:51:TYR:O	2.63	0.47
2:F:96:VAL:HG11	2:F:129:ARG:HD2	1.95	0.47
1:A:73:GLY:CA	1:A:78:THR:HG23	2.40	0.47
1:A:462:LEU:HD11	2:C:499:PHE:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:SER:HB3	2:C:485:VAL:CG2	2.44	0.47
1:A:589:PRO:HD3	1:A:596:TRP:CH2	2.29	0.47
2:C:34:ARG:HA	2:C:37:ALA:HB3	1.97	0.47
2:D:113:HIS:ND1	2:D:113:HIS:N	2.62	0.47
2:D:278:PHE:HZ	2:D:287:LEU:HD13	1.78	0.47
1:B:469:ILE:HG12	1:B:552:MET:HB3	1.95	0.47
1:E:195:TYR:HD1	1:E:210:SER:HG	1.61	0.47
1:E:235:ASN:N	1:E:235:ASN:ND2	2.60	0.47
1:E:324:TYR:CB	1:E:536:PHE:HE2	2.25	0.47
1:E:471:TYR:O	1:E:550:GLN:HB2	2.14	0.47
1:E:504:ILE:HD11	1:E:554:ILE:HD11	1.97	0.47
1:E:546:ASP:CG	1:E:549:GLN:NE2	2.73	0.47
2:F:110:ILE:HG23	2:F:111:PRO:HD2	1.97	0.47
2:F:207:ASN:O	2:F:211:GLU:HG3	2.14	0.47
1:A:99:VAL:HB	1:A:113:ALA:CB	2.45	0.47
1:A:242:ILE:HB	1:A:358:LEU:HD23	1.96	0.47
1:A:369:GLY:C	1:A:372:ILE:HG22	2.40	0.47
2:C:310:ARG:CG	2:C:310:ARG:NH1	2.73	0.47
2:D:36:ARG:CD	1:B:491:ASN:CG	2.84	0.47
2:D:47:LYS:HG2	1:B:502:THR:HG21	1.97	0.47
2:D:111:PRO:HG2	2:D:114:THR:CB	2.45	0.47
2:D:184:ARG:CG	1:B:592:ARG:HD3	2.44	0.47
1:B:65:LEU:HD12	1:B:66:ILE:C	2.40	0.47
1:B:94:VAL:C	1:B:95:PHE:HD1	2.23	0.47
1:B:371:GLN:HA	1:B:371:GLN:NE2	2.27	0.47
1:B:395:ARG:CD	1:B:396:HIS:N	2.78	0.47
1:B:531:SER:O	1:B:531:SER:OG	2.30	0.47
1:A:79:MET:CE	1:A:81:VAL:CG2	2.90	0.47
1:A:383:THR:C	1:A:384:HIS:ND1	2.73	0.47
1:A:466:PRO:HD3	2:C:494:TRP:CZ2	2.50	0.47
1:A:490:LEU:HD11	2:C:43:SER:CB	2.44	0.47
2:C:12:PHE:C	2:C:12:PHE:CD1	2.93	0.47
2:C:78:HIS:ND1	2:C:78:HIS:C	2.73	0.47
1:B:175:LEU:C	1:B:458:PHE:CE2	2.93	0.47
1:B:231:LEU:O	1:B:235:ASN:CG	2.58	0.47
1:E:178:ALA:O	1:E:458:PHE:CD1	2.68	0.47
1:E:224:THR:HB	1:E:225:PRO:HD3	1.96	0.47
1:E:295:ILE:HD11	1:E:337:TYR:HD2	1.78	0.47
1:E:361:LEU:HD21	1:E:376:ILE:CD1	2.45	0.47
1:E:592:ARG:NH2	1:E:592:ARG:CG	2.73	0.47
1:A:69:ILE:CG2	1:A:80:PHE:CB	2.92	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:MET:HE1	1:A:81:VAL:HG23	1.97	0.46
1:A:198:LEU:CD2	1:A:205:HIS:HE2	2.28	0.46
1:A:226:LEU:CD1	1:A:230:TYR:HH	1.92	0.46
1:A:366:LYS:CG	1:A:396:HIS:HB3	2.34	0.46
1:A:469:ILE:HG23	2:C:488:TRP:CE3	2.49	0.46
2:C:128:LEU:HA	2:C:131:TRP:CB	2.45	0.46
2:C:332:LEU:HD23	2:C:332:LEU:O	2.14	0.46
2:D:102:PRO:O	2:D:104:GLN:CD	2.58	0.46
2:D:494:TRP:CH2	2:D:497:LYS:CB	2.98	0.46
1:B:599:ASN:ND2	1:B:599:ASN:C	2.73	0.46
1:E:95:PHE:C	1:E:95:PHE:CD2	2.92	0.46
1:E:171:ASN:ND2	1:E:454:PHE:CD1	2.83	0.46
1:E:460:PRO:HG2	1:E:593:THR:HG22	1.98	0.46
1:A:94:VAL:HG12	1:A:170:SER:CB	2.45	0.46
1:A:188:LEU:CD2	1:A:188:LEU:C	2.88	0.46
1:A:501:GLY:O	1:A:582:THR:HG21	2.14	0.46
2:C:92:LEU:N	2:C:92:LEU:CD2	2.73	0.46
2:D:11:ASP:OD1	2:D:13:ALA:HB3	2.15	0.46
2:D:139:PRO:CG	2:D:144:LEU:HD21	2.42	0.46
1:B:89:LEU:HD13	1:B:90:HIS:C	2.40	0.46
1:B:216:LEU:HD23	1:B:216:LEU:C	2.41	0.46
1:B:450:LYS:HA	1:B:456:TYR:HD1	1.80	0.46
1:B:615:HIS:ND1	1:B:615:HIS:C	2.73	0.46
1:E:398:ASP:OD2	1:E:398:ASP:N	2.40	0.46
2:F:48:GLY:HA2	2:F:49:SER:C	2.39	0.46
2:F:50:GLN:C	2:F:51:TYR:CD2	2.93	0.46
1:A:214:GLN:HE21	1:A:214:GLN:HB3	1.56	0.46
1:A:267:ILE:HD12	1:A:277:LEU:HD21	1.97	0.46
2:D:397:GLN:O	2:D:401:THR:HG23	2.15	0.46
1:B:342:ASP:HA	1:B:345:ILE:HD12	1.98	0.46
1:B:364:TRP:CD1	1:B:372:ILE:CG2	2.86	0.46
1:B:524:PRO:O	1:B:524:PRO:HG2	2.15	0.46
1:E:247:GLY:C	1:E:250:SER:HG	2.22	0.46
2:F:84:ILE:HD12	2:F:84:ILE:HA	1.77	0.46
2:F:154:TRP:HE3	2:F:155:LEU:CA	2.28	0.46
1:A:392:ASN:N	1:A:393:SER:CA	2.78	0.46
1:A:588:LEU:HD11	2:C:6:ILE:CD1	2.46	0.46
2:C:61:GLN:O	2:C:64:CYS:HB2	2.15	0.46
1:B:233:HIS:HD1	1:B:233:HIS:C	2.21	0.46
1:E:360:ASN:ND2	1:E:360:ASN:H	2.13	0.46
1:E:360:ASN:N	1:E:360:ASN:HD22	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:32:ASP:OD2	2:F:34:ARG:HG3	2.15	0.46
2:F:48:GLY:CA	2:F:49:SER:C	2.88	0.46
2:F:337:LEU:HD12	2:F:338:ASP:CA	2.45	0.46
2:F:337:LEU:C	2:F:337:LEU:CD1	2.86	0.46
1:A:364:TRP:HB3	1:A:369:GLY:HA3	1.97	0.46
1:A:554:ILE:HG12	1:A:555:TYR:N	2.31	0.46
1:A:587:PHE:HD2	1:A:587:PHE:O	1.97	0.46
2:C:130:HIS:CG	2:C:134:HIS:ND1	2.83	0.46
2:D:96:VAL:HG12	2:D:100:LEU:CB	2.46	0.46
2:D:222:SER:O	2:D:222:SER:OG	2.28	0.46
1:B:90:HIS:CE1	1:B:128:ILE:HG12	2.43	0.46
1:B:347:HIS:NE2	1:B:351:GLN:OE1	2.48	0.46
1:E:228:LYS:HB2	1:E:228:LYS:HE2	1.58	0.46
1:E:316:ASN:C	1:E:316:ASN:ND2	2.73	0.46
1:E:387:PHE:HE1	1:E:401:THR:HG21	1.75	0.46
2:F:335:ARG:HH11	2:F:335:ARG:HG3	1.78	0.46
1:A:229:LEU:HD11	1:A:386:LEU:HD11	1.96	0.46
1:A:311:LEU:C	1:A:312:CYS:SG	2.99	0.46
2:C:360:ILE:HD13	2:C:372:CYS:SG	2.56	0.46
2:D:167:ASP:HA	1:B:612:LYS:HG2	1.96	0.46
2:D:220:ASN:ND2	2:D:220:ASN:C	2.73	0.46
1:B:389:GLU:CG	1:B:394:LYS:HA	2.45	0.46
1:E:186:ASN:C	1:E:186:ASN:ND2	2.73	0.46
1:E:280:LEU:HB3	1:E:359:LEU:HB2	1.97	0.46
1:E:487:PHE:CZ	2:F:46:LEU:HA	2.51	0.46
2:F:54:HIS:ND1	2:F:54:HIS:C	2.73	0.46
2:F:100:LEU:N	2:F:100:LEU:CD2	2.73	0.46
1:A:79:MET:SD	1:A:80:PHE:C	2.98	0.46
1:A:607:PHE:HE1	2:C:4:PRO:CG	1.83	0.46
2:C:12:PHE:HD1	2:C:12:PHE:C	2.23	0.46
2:C:125:PHE:HD1	2:C:128:LEU:HD23	1.75	0.46
2:D:46:LEU:O	2:D:46:LEU:HD23	2.16	0.46
2:D:55:VAL:HG13	2:D:159:TYR:CE2	2.50	0.46
1:B:65:LEU:C	1:B:65:LEU:CD1	2.86	0.46
1:B:216:LEU:HD23	1:B:217:SER:H	1.75	0.46
1:B:317:PHE:C	1:B:317:PHE:CD2	2.93	0.46
1:B:349:GLU:C	1:B:352:ALA:H	2.23	0.46
1:E:501:GLY:CA	2:F:499:PHE:CD1	2.99	0.46
2:F:278:PHE:CE2	2:F:282:TYR:CB	2.99	0.46
1:A:83:LEU:N	1:A:83:LEU:CD2	2.73	0.46
1:A:98:GLN:CG	1:A:115:ARG:C	2.82	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:LEU:HD12	1:A:120:PHE:CZ	2.50	0.46
2:C:125:PHE:CB	2:C:128:LEU:HD21	2.44	0.46
2:D:14:GLU:O	2:D:17:GLU:HG2	2.16	0.46
2:D:278:PHE:CZ	2:D:287:LEU:HD13	2.51	0.46
2:D:358:LYS:N	2:D:361:ASP:OD2	2.48	0.46
1:B:330:PRO:HD2	1:B:364:TRP:HZ2	1.70	0.46
1:B:353:PHE:CG	1:B:354:PHE:N	2.84	0.46
1:B:388:LEU:N	1:B:388:LEU:CD1	2.73	0.46
1:B:431:SER:HB2	1:B:434:PHE:O	2.16	0.46
1:E:206:LEU:O	1:E:207:LEU:HD23	2.14	0.46
1:E:369:GLY:O	1:E:372:ILE:HG22	2.16	0.46
1:E:376:ILE:HA	1:E:379:LYS:HB3	1.97	0.46
1:E:491:ASN:HD22	2:F:36:ARG:NE	2.00	0.46
1:E:562:GLN:HB2	1:E:565:ASP:CB	2.45	0.46
2:F:280:ASN:OD1	2:F:321:ILE:CG2	2.63	0.46
2:C:146:TRP:CD1	2:C:146:TRP:C	2.94	0.46
2:C:291:MET:SD	2:C:340:ILE:HG23	2.56	0.46
2:D:184:ARG:CD	1:B:592:ARG:HD3	2.44	0.46
2:D:283:ASP:OD1	2:D:285:LEU:HB2	2.16	0.46
1:B:177:GLU:OE2	1:B:456:TYR:O	2.34	0.46
1:B:297:LEU:HB3	1:B:321:LEU:HD22	1.95	0.46
1:E:169:ASN:HD21	1:E:203:THR:HG23	1.79	0.46
1:E:245:ILE:CG2	1:E:387:PHE:HE2	2.28	0.46
1:E:291:LEU:O	1:E:294:SER:HB3	2.14	0.46
1:E:536:PHE:HZ	1:E:539:LEU:HD23	1.81	0.46
1:E:543:HIS:CE1	2:F:494:TRP:HZ2	2.34	0.46
2:F:79:GLN:O	2:F:79:GLN:HG2	2.16	0.46
2:F:322:LEU:HD21	2:F:332:LEU:CD1	2.45	0.46
1:A:81:VAL:H	1:A:166:ARG:CG	2.28	0.46
1:A:169:ASN:CB	1:A:203:THR:CG2	2.93	0.46
1:A:196:PHE:CE1	1:A:197:PRO:HD2	2.51	0.46
1:A:366:LYS:HG2	1:A:395:ARG:CZ	2.37	0.46
1:A:370:MET:O	1:A:374:ASN:CB	2.64	0.46
1:A:398:ASP:CG	1:A:399:GLU:N	2.73	0.46
2:C:9:TRP:HA	2:C:14:GLU:OE2	2.15	0.46
2:C:116:ALA:HB2	2:C:126:VAL:HG21	1.98	0.46
2:C:327:ASN:OD1	2:C:331:GLU:OE2	2.34	0.46
2:D:36:ARG:HH11	1:B:494:ASP:CG	2.24	0.46
2:D:371:PHE:CZ	2:D:375:MET:HG3	2.51	0.46
2:D:492:GLN:C	2:D:493:ASN:ND2	2.73	0.46
1:B:271:THR:HA	1:B:272:THR:HA	1.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:541:LEU:O	1:B:554:ILE:HG13	2.15	0.46
1:E:96:ARG:HB3	1:E:119:THR:HG22	1.97	0.46
1:E:241:ARG:HH11	1:E:381:LYS:HD2	1.80	0.46
1:E:306:SER:C	1:E:307:LEU:CG	2.89	0.46
2:F:68:LEU:CD2	2:F:68:LEU:C	2.86	0.46
2:F:362:GLU:O	2:F:363:ASN:ND2	2.39	0.46
1:A:264:THR:HG22	1:A:268:ARG:HD3	1.97	0.45
1:A:498:ALA:O	1:A:502:THR:HG23	2.16	0.45
1:A:534:LYS:HG3	1:A:534:LYS:H	1.50	0.45
1:A:567:GLN:HA	1:A:567:GLN:NE2	2.31	0.45
2:C:21:TRP:CZ3	2:C:36:ARG:HG3	2.51	0.45
2:C:54:HIS:ND1	2:C:54:HIS:C	2.73	0.45
2:D:346:ASN:N	2:D:346:ASN:OD1	2.49	0.45
2:D:377:ALA:O	2:D:381:THR:HG23	2.15	0.45
2:D:488:TRP:HE3	1:B:467:LEU:HG	1.81	0.45
1:B:507:TYR:CD1	1:B:535:ASN:O	2.69	0.45
1:E:98:GLN:HB2	1:E:117:ILE:HG22	1.95	0.45
1:E:105:VAL:CG1	1:E:108:ASN:HA	2.45	0.45
1:E:289:TYR:CD1	1:E:317:PHE:CE2	3.03	0.45
2:F:83:PRO:O	2:F:86:LEU:HB2	2.15	0.45
2:F:492:GLN:CD	2:F:492:GLN:N	2.73	0.45
1:A:246:GLY:O	1:A:363:GLY:HA2	2.09	0.45
1:A:299:LYS:HB2	1:A:320:LEU:HD11	1.98	0.45
1:B:93:GLY:N	1:B:122:HIS:HB3	2.31	0.45
1:B:110:HIS:CD2	1:B:111:TYR:N	2.84	0.45
1:B:321:LEU:CD1	1:B:347:HIS:HD1	2.20	0.45
1:E:208:HIS:ND1	1:E:210:SER:N	2.60	0.45
1:E:432:SER:O	1:E:432:SER:OG	2.31	0.45
1:E:504:ILE:HD13	1:E:575:ILE:HD13	1.98	0.45
2:F:122:PRO:HB2	2:F:124:TRP:CD1	2.49	0.45
2:F:372:CYS:CB	2:F:412:ILE:HD11	2.46	0.45
2:F:376:LEU:O	2:F:380:GLU:N	2.50	0.45
1:A:123:PRO:HG3	1:A:311:LEU:HD21	1.98	0.45
1:A:173:THR:O	1:A:177:GLU:OE2	2.35	0.45
1:A:249:ASN:ND2	1:A:249:ASN:C	2.73	0.45
1:A:289:TYR:HD1	1:A:298:ASN:HD21	1.63	0.45
1:A:326:GLY:N	1:A:578:ASN:ND2	2.59	0.45
1:A:588:LEU:HD21	1:A:605:ALA:CB	2.47	0.45
2:D:113:HIS:O	2:D:116:ALA:HB3	2.14	0.45
2:D:154:TRP:HE3	2:D:155:LEU:N	2.13	0.45
2:D:288:LYS:CG	2:D:343:ASN:ND2	2.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:312:GLN:HE22	2:D:323:LYS:HG3	0.43	0.45
1:E:109:VAL:HG21	1:E:111:TYR:CZ	2.50	0.45
1:E:375:HIS:O	1:E:378:ARG:HB3	2.17	0.45
2:F:349:PHE:C	2:F:349:PHE:CD2	2.93	0.45
1:A:194:PRO:HG3	1:A:198:LEU:CD2	2.46	0.45
1:A:540:GLY:HA3	1:A:554:ILE:HD11	1.99	0.45
2:C:110:ILE:HG22	2:C:111:PRO:O	2.15	0.45
1:B:451:ILE:N	1:B:451:ILE:CD1	2.73	0.45
1:B:506:ILE:CD1	1:B:540:GLY:HA3	2.45	0.45
1:E:389:GLU:CG	1:E:393:SER:O	2.64	0.45
1:E:399:GLU:OE2	1:E:400:LEU:HA	2.15	0.45
1:E:454:PHE:HD2	1:E:454:PHE:H	1.62	0.45
1:E:592:ARG:HD2	1:E:592:ARG:O	2.16	0.45
2:F:146:TRP:NE1	2:F:150:GLU:OE1	2.46	0.45
1:A:110:HIS:C	1:A:111:TYR:CD1	2.95	0.45
1:A:116:GLU:O	1:A:118:LEU:HD23	2.17	0.45
1:A:187:TYR:CD2	1:A:192:LYS:CB	2.98	0.45
1:A:190:LYS:NZ	1:A:202:THR:O	2.43	0.45
1:A:249:ASN:C	1:A:249:ASN:HD22	2.25	0.45
1:A:313:GLN:CG	1:A:456:TYR:OH	2.61	0.45
2:C:36:ARG:HA	2:C:39:GLN:HE21	1.82	0.45
1:B:392:ASN:N	1:B:393:SER:CA	2.77	0.45
1:E:481:ILE:HA	1:E:575:ILE:O	2.17	0.45
2:F:45:ARG:NH2	2:F:61:GLN:HE21	2.14	0.45
2:F:500:GLY:C	2:F:501:VAL:CG2	2.85	0.45
1:A:88:LYS:H	1:A:88:LYS:HG3	1.59	0.45
2:D:220:ASN:ND2	2:D:220:ASN:O	2.50	0.45
2:D:502:LEU:CB	1:B:546:ASP:OD1	2.65	0.45
1:B:90:HIS:CG	1:B:207:LEU:HB2	2.51	0.45
1:E:537:ILE:O	1:E:538:THR:OG1	2.32	0.45
2:F:89:VAL:HG21	2:F:138:LEU:HD23	1.98	0.45
1:A:100:VAL:C	1:A:101:LYS:HG2	2.42	0.45
1:A:348:LEU:CD1	1:A:353:PHE:CB	2.86	0.45
2:C:53:PRO:CG	2:C:56:VAL:CG2	2.94	0.45
1:B:114:SER:C	1:B:115:ARG:CG	2.85	0.45
1:B:467:LEU:CD2	1:B:467:LEU:N	2.80	0.45
1:E:491:ASN:CG	2:F:36:ARG:HD2	2.25	0.45
1:A:223:SER:O	1:A:227:GLU:CB	2.65	0.45
1:A:255:PHE:CE2	1:A:259:LEU:HD22	2.51	0.45
1:A:607:PHE:CE2	2:C:4:PRO:HB3	2.37	0.45
2:D:426:LEU:O	2:D:430:ILE:CD1	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:599:ASN:C	1:B:599:ASN:HD22	2.25	0.45
1:E:241:ARG:HB2	1:E:383:THR:OG1	2.16	0.45
1:E:359:LEU:CD1	1:E:360:ASN:C	2.90	0.45
1:E:365:ILE:HD13	1:E:366:LYS:N	2.29	0.45
1:E:562:GLN:CB	1:E:565:ASP:CB	2.95	0.45
2:F:97:ASN:CG	2:F:129:ARG:HH22	2.13	0.45
2:F:156:TYR:CZ	2:F:161:ASN:ND2	2.82	0.45
2:F:389:TRP:NE1	2:F:390:ARG:CD	2.73	0.45
1:A:83:LEU:HD23	1:A:166:ARG:CZ	2.47	0.45
1:A:123:PRO:HD3	1:A:309:GLN:O	2.17	0.45
1:A:326:GLY:N	1:A:578:ASN:HD22	2.13	0.45
1:A:617:TRP:C	1:A:617:TRP:CD1	2.95	0.45
2:C:34:ARG:HH21	2:C:67:LEU:HG	1.81	0.45
2:C:82:ILE:HG23	2:C:83:PRO:HD3	1.98	0.45
2:C:128:LEU:HA	2:C:131:TRP:HB2	1.99	0.45
2:C:235:VAL:CG1	2:C:236:ASN:N	2.79	0.45
2:D:320:THR:HG1	2:D:323:LYS:H	1.64	0.45
1:B:317:PHE:CD2	1:B:317:PHE:O	2.70	0.45
1:E:95:PHE:CD2	1:E:95:PHE:O	2.70	0.45
1:E:194:PRO:CB	1:E:205:HIS:CE1	2.91	0.45
1:E:425:SER:OG	1:E:426:LEU:HA	2.16	0.45
1:E:452:THR:OG1	1:E:454:PHE:CD2	2.70	0.45
1:E:473:LYS:CD	1:E:474:GLY:N	2.80	0.45
1:E:523:PHE:HB3	1:E:525:ILE:HD11	1.98	0.45
1:E:549:GLN:C	1:E:550:GLN:HG2	2.42	0.45
1:E:590:SER:O	1:E:591:PRO:C	2.60	0.45
2:F:108:PHE:CG	2:F:108:PHE:O	2.70	0.45
1:A:294:SER:OG	1:A:295:ILE:N	2.50	0.45
1:A:396:HIS:CD2	1:A:396:HIS:O	2.70	0.45
1:A:613:LEU:O	1:A:615:HIS:CE1	2.70	0.45
2:C:50:GLN:OE1	2:C:51:TYR:CE2	2.70	0.45
2:C:107:GLN:OE1	2:C:108:PHE:CD2	2.70	0.45
2:D:17:GLU:O	2:D:21:TRP:CD1	2.70	0.45
2:D:124:TRP:HA	2:D:127:ASP:CG	2.41	0.45
1:B:473:LYS:CG	1:B:474:GLY:N	2.80	0.45
1:B:599:ASN:ND2	1:B:600:ILE:CD1	2.73	0.45
1:E:317:PHE:C	1:E:317:PHE:CD1	2.95	0.45
1:E:331:GLN:HG3	1:E:364:TRP:HZ2	0.30	0.45
1:E:460:PRO:HG2	1:E:593:THR:CG2	2.47	0.45
2:F:12:PHE:O	2:F:12:PHE:CD1	2.70	0.45
2:F:52:LEU:HD21	2:F:57:ASP:CA	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:606:THR:HG23	2:C:5:ARG:HH11	1.80	0.44
2:C:84:ILE:O	2:C:88:TYR:CD2	2.70	0.44
2:C:130:HIS:CB	2:C:134:HIS:CE1	3.01	0.44
2:C:364:ALA:H	2:C:493:ASN:ND2	2.14	0.44
2:D:133:THR:OG1	2:D:134:HIS:CD2	2.70	0.44
2:D:237:TYR:CD1	2:D:237:TYR:O	2.71	0.44
2:D:323:LYS:HD2	2:D:430:ILE:HG13	1.99	0.44
1:B:175:LEU:CB	1:B:456:TYR:CD2	2.67	0.44
1:E:241:ARG:CB	1:E:383:THR:OG1	2.65	0.44
2:F:275:LEU:HB3	2:F:279:PHE:HE2	1.82	0.44
2:F:349:PHE:CD2	2:F:349:PHE:O	2.70	0.44
1:A:168:PHE:HD1	1:A:168:PHE:N	2.15	0.44
1:A:288:GLU:OE2	1:A:289:TYR:CE2	2.70	0.44
1:A:339:ASN:O	1:A:343:LYS:CG	2.64	0.44
1:A:587:PHE:C	1:A:587:PHE:CD2	2.95	0.44
1:B:294:SER:OG	1:B:323:PHE:O	2.29	0.44
1:E:208:HIS:CG	1:E:209:GLU:N	2.85	0.44
1:E:257:ARG:NE	1:E:308:GLY:O	2.50	0.44
1:A:168:PHE:CD1	1:A:168:PHE:O	2.70	0.44
1:A:195:TYR:O	1:A:195:TYR:CD1	2.70	0.44
1:A:394:LYS:HD2	1:A:394:LYS:C	2.42	0.44
2:C:51:TYR:N	2:C:51:TYR:CD2	2.84	0.44
2:C:62:ILE:O	2:C:65:ALA:N	2.50	0.44
2:C:122:PRO:HD2	2:C:125:PHE:CD2	2.52	0.44
2:C:224:ILE:HG21	2:C:229:PHE:CZ	2.40	0.44
2:D:298:ASP:OD1	2:D:299:TRP:N	2.50	0.44
2:D:488:TRP:CH2	1:B:469:ILE:HG21	2.52	0.44
1:B:260:LEU:HD23	1:B:277:LEU:HD12	1.99	0.44
2:F:156:TYR:HA	2:F:160:TRP:HB2	2.00	0.44
1:A:128:ILE:O	1:A:215:SER:HA	2.18	0.44
1:A:188:LEU:O	1:A:188:LEU:HD23	2.17	0.44
1:A:388:LEU:HG	1:A:421:VAL:CG2	2.47	0.44
1:A:445:LEU:HD13	1:A:583:PRO:HG3	2.00	0.44
1:A:469:ILE:HD12	2:C:488:TRP:CZ2	2.41	0.44
1:A:471:TYR:CE2	1:A:522:THR:O	2.71	0.44
1:A:589:PRO:HB2	1:A:594:ILE:HG13	1.98	0.44
2:D:4:PRO:N	1:B:607:PHE:HE1	2.15	0.44
1:B:75:GLU:C	1:B:76:ASP:CG	2.85	0.44
1:B:347:HIS:CD2	1:B:347:HIS:O	2.70	0.44
1:E:261:GLU:HG2	1:E:307:LEU:HD23	1.98	0.44
2:F:278:PHE:O	2:F:278:PHE:CD2	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:CA	1:A:168:PHE:HE1	2.31	0.44
1:A:222:TRP:C	1:A:225:PRO:HD2	2.41	0.44
2:C:207:ASN:C	2:C:210:LEU:CD1	2.89	0.44
2:C:364:ALA:H	2:C:493:ASN:HD21	1.65	0.44
2:C:497:LYS:NZ	2:C:501:VAL:O	2.44	0.44
2:D:82:ILE:CG2	2:D:83:PRO:N	2.80	0.44
1:B:471:TYR:CD1	1:B:471:TYR:O	2.71	0.44
1:E:271:THR:HA	1:E:272:THR:HA	1.64	0.44
1:E:342:ASP:OD2	1:E:375:HIS:NE2	2.38	0.44
1:E:495:ILE:HG21	1:E:523:PHE:CD2	2.52	0.44
1:E:501:GLY:HA2	2:F:499:PHE:CE1	2.53	0.44
1:E:531:SER:O	1:E:531:SER:OG	2.30	0.44
1:E:588:LEU:HD21	2:F:6:ILE:HD13	1.98	0.44
1:E:617:TRP:CD1	1:E:617:TRP:C	2.94	0.44
2:F:411:ASN:O	2:F:414:ASN:HB3	2.18	0.44
1:A:260:LEU:CD2	1:A:277:LEU:HD12	2.48	0.44
1:A:317:PHE:CD2	1:A:317:PHE:O	2.70	0.44
1:A:347:HIS:CE1	1:A:351:GLN:OE1	2.70	0.44
2:D:403:GLU:O	2:D:407:LYS:HG3	2.18	0.44
1:B:167:VAL:O	1:B:204:TYR:OH	2.33	0.44
1:B:172:HIS:CB	1:B:454:PHE:O	2.66	0.44
1:E:313:GLN:OE1	1:E:450:LYS:NZ	2.50	0.44
2:F:499:PHE:N	2:F:499:PHE:CD2	2.84	0.44
1:A:226:LEU:CD1	1:A:226:LEU:C	2.85	0.44
1:A:491:ASN:HD22	2:C:36:ARG:HD3	1.81	0.44
1:A:603:PRO:HB2	1:A:604:PHE:CD2	2.51	0.44
2:C:107:GLN:OE1	2:C:108:PHE:CZ	2.71	0.44
1:B:463:LYS:HE2	1:B:594:ILE:HG12	1.98	0.44
2:F:278:PHE:CD2	2:F:282:TYR:HA	2.53	0.44
1:A:108:ASN:ND2	1:A:108:ASN:C	2.73	0.44
1:A:195:TYR:O	1:A:195:TYR:CG	2.70	0.44
1:A:280:LEU:HG	1:A:297:LEU:HD12	1.98	0.44
1:A:353:PHE:CD1	1:A:354:PHE:N	2.86	0.44
1:A:365:ILE:CD1	1:A:366:LYS:N	2.77	0.44
1:A:613:LEU:O	1:A:615:HIS:ND1	2.51	0.44
1:A:614:GLU:O	1:A:614:GLU:HG3	2.17	0.44
2:C:84:ILE:O	2:C:88:TYR:HD2	2.00	0.44
2:C:202:TRP:CZ2	2:C:286:LEU:HD12	2.53	0.44
1:B:103:GLY:O	1:B:134:SER:CA	2.65	0.44
1:E:311:LEU:O	1:E:312:CYS:HB2	2.17	0.44
1:E:385:LEU:HD22	1:E:387:PHE:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:389:GLU:HG2	1:E:397:LEU:HD11	2.00	0.44
1:E:462:LEU:O	2:F:494:TRP:HZ3	2.01	0.44
1:E:496:LYS:HG2	1:E:500:GLU:OE2	2.17	0.44
2:F:108:PHE:CD2	2:F:108:PHE:O	2.70	0.44
2:F:278:PHE:CE2	2:F:282:TYR:CA	3.00	0.44
1:A:485:MET:H	1:A:485:MET:HG2	1.58	0.44
1:A:515:LEU:H	1:A:515:LEU:HG	1.57	0.44
2:D:102:PRO:O	2:D:104:GLN:NE2	2.51	0.44
1:B:89:LEU:HD13	1:B:90:HIS:CA	2.47	0.44
1:B:265:GLN:HA	1:B:265:GLN:OE1	2.17	0.44
1:B:273:SER:HB3	1:B:275:GLU:HG2	1.99	0.44
1:B:482:GLN:CD	1:B:526:LEU:HD23	2.43	0.44
1:E:317:PHE:CD1	1:E:317:PHE:O	2.70	0.44
1:E:482:GLN:HE21	1:E:576:VAL:CG1	2.31	0.44
2:F:309:TYR:OH	2:F:423:GLU:OE2	2.36	0.44
1:A:105:VAL:CG1	1:A:132:ASP:OD2	2.62	0.43
1:A:166:ARG:HB3	1:A:167:VAL:H	1.60	0.43
1:A:248:LYS:H	1:A:248:LYS:HG2	1.56	0.43
1:A:398:ASP:CG	1:A:399:GLU:H	2.25	0.43
1:A:473:LYS:H	1:A:473:LYS:HG2	1.45	0.43
2:C:54:HIS:HE1	2:C:58:SER:OG	2.00	0.43
2:C:107:GLN:OE1	2:C:108:PHE:CD1	2.71	0.43
2:C:107:GLN:OE1	2:C:108:PHE:CG	2.71	0.43
2:C:278:PHE:CZ	2:C:287:LEU:HD12	2.52	0.43
2:C:285:LEU:O	2:C:285:LEU:HD22	2.18	0.43
2:D:188:LEU:CD1	2:D:192:MET:HG3	2.48	0.43
2:D:356:TRP:O	2:D:360:ILE:CB	2.66	0.43
1:B:108:ASN:ND2	1:B:108:ASN:O	2.51	0.43
1:B:122:HIS:HE1	1:B:128:ILE:CD1	2.31	0.43
1:B:421:VAL:O	1:B:421:VAL:HG23	2.18	0.43
1:E:431:SER:CB	1:E:434:PHE:C	2.89	0.43
1:E:494:ASP:OD1	1:E:494:ASP:N	2.47	0.43
1:E:587:PHE:CD2	1:E:587:PHE:O	2.71	0.43
2:F:17:GLU:CG	2:F:21:TRP:CE2	3.01	0.43
1:A:255:PHE:HE2	1:A:259:LEU:HD21	1.83	0.43
2:C:136:ARG:C	2:D:94:ARG:HH22	2.10	0.43
2:D:389:TRP:CD1	2:D:389:TRP:O	2.70	0.43
1:E:213:ILE:CD1	1:E:213:ILE:C	2.86	0.43
1:E:348:LEU:HB3	1:E:349:GLU:OE1	2.19	0.43
1:E:469:ILE:CG2	1:E:470:SER:H	2.22	0.43
1:E:562:GLN:C	1:E:565:ASP:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:101:ASP:N	2:F:102:PRO:CD	2.82	0.43
2:F:352:LYS:HE3	2:F:352:LYS:HB2	1.94	0.43
1:A:368:PHE:CD2	1:A:368:PHE:O	2.70	0.43
2:C:125:PHE:CD1	2:C:128:LEU:HD21	2.51	0.43
2:C:329:TRP:CD1	2:C:424:ILE:CG2	3.02	0.43
1:B:90:HIS:CE1	1:B:128:ILE:HD13	2.30	0.43
1:B:97:LEU:HD13	1:B:120:PHE:CE1	2.53	0.43
1:B:368:PHE:O	1:B:372:ILE:N	2.48	0.43
1:B:591:PRO:O	1:B:592:ARG:CB	2.49	0.43
1:E:133:PHE:HD2	1:E:134:SER:N	2.15	0.43
1:E:424:HIS:CD2	1:E:424:HIS:O	2.70	0.43
1:E:424:HIS:O	1:E:424:HIS:CG	2.70	0.43
1:E:509:TYR:HE1	1:E:533:SER:HB3	1.83	0.43
1:E:541:LEU:HD12	1:E:542:ILE:H	1.83	0.43
2:F:81:SER:O	2:F:84:ILE:HG22	2.17	0.43
2:F:98:GLY:O	2:F:102:PRO:HB3	2.18	0.43
2:F:426:LEU:HD23	2:F:426:LEU:HA	1.89	0.43
1:A:105:VAL:HG12	1:A:132:ASP:HB2	1.96	0.43
1:A:241:ARG:O	1:A:383:THR:OG1	2.21	0.43
1:A:389:GLU:HB3	1:A:394:LYS:HB3	1.98	0.43
1:A:420:ARG:HH21	1:A:420:ARG:CG	2.23	0.43
1:A:502:THR:HG22	1:A:577:ARG:HH22	1.84	0.43
1:A:505:GLY:HA2	1:A:539:LEU:HA	1.99	0.43
1:A:561:THR:CG2	1:A:562:GLN:HA	2.48	0.43
2:C:90:MET:CB	2:D:86:LEU:HG	2.45	0.43
2:C:107:GLN:OE1	2:C:108:PHE:CE1	2.70	0.43
2:C:209:PHE:CD2	2:C:254:ILE:HG12	2.53	0.43
2:D:358:LYS:HG2	2:D:358:LYS:H	1.58	0.43
2:D:365:SER:O	2:D:368:ILE:N	2.51	0.43
2:D:427:TYR:CD2	2:D:427:TYR:O	2.70	0.43
1:B:175:LEU:HD12	1:B:458:PHE:HZ	1.84	0.43
1:B:194:PRO:CG	1:B:205:HIS:NE2	2.81	0.43
1:B:317:PHE:O	1:B:317:PHE:HD2	2.01	0.43
1:B:366:LYS:HD3	1:B:395:ARG:NH1	2.33	0.43
1:E:277:LEU:HD23	1:E:277:LEU:H	1.83	0.43
1:E:518:LYS:O	1:E:525:ILE:O	2.36	0.43
1:A:170:SER:OG	1:A:172:HIS:CE1	2.70	0.43
1:A:341:ALA:O	1:A:344:LEU:N	2.50	0.43
2:C:209:PHE:CD2	2:C:254:ILE:HD13	2.51	0.43
2:C:333:GLN:HA	2:C:337:LEU:HB3	2.00	0.43
2:C:389:TRP:CE3	2:C:389:TRP:HA	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:488:TRP:CZ3	1:B:469:ILE:CG2	3.01	0.43
1:B:208:HIS:O	1:B:210:SER:N	2.41	0.43
1:B:453:GLN:H	1:B:453:GLN:HG2	1.49	0.43
1:E:189:TRP:HA	1:E:189:TRP:CE3	2.54	0.43
1:E:234:LYS:HA	1:E:234:LYS:HD2	1.74	0.43
1:E:252:LYS:HE3	1:E:361:LEU:O	2.19	0.43
1:E:617:TRP:O	1:E:617:TRP:CD1	2.70	0.43
2:F:17:GLU:HG2	2:F:21:TRP:CE2	2.53	0.43
2:F:163:GLU:O	2:F:164:GLU:C	2.61	0.43
2:F:333:GLN:CB	2:F:337:LEU:HD21	2.46	0.43
1:A:177:GLU:HG2	2:C:267:LEU:HD22	1.99	0.43
1:A:549:GLN:HB3	1:A:551:ILE:HG23	2.01	0.43
2:C:79:GLN:CD	3:C:601:HOH:O	2.61	0.43
2:C:107:GLN:OE1	2:C:108:PHE:CE2	2.70	0.43
2:C:340:ILE:H	2:C:340:ILE:HG13	1.56	0.43
2:D:188:LEU:HD12	2:D:192:MET:HG2	2.00	0.43
2:D:330:LYS:O	2:D:334:LYS:CG	2.66	0.43
1:B:111:TYR:CE1	1:B:265:GLN:HB2	2.54	0.43
1:B:178:ALA:HA	1:B:458:PHE:CB	2.25	0.43
1:B:337:TYR:OH	1:B:362:PRO:CD	2.66	0.43
1:E:389:GLU:HG3	1:E:393:SER:O	2.17	0.43
2:F:99:LEU:HD23	2:F:99:LEU:HA	1.82	0.43
1:A:282:LEU:O	1:A:337:TYR:CZ	2.72	0.43
1:A:417:GLU:HG3	1:A:418:VAL:N	2.34	0.43
1:A:450:LYS:HB2	1:A:456:TYR:CE1	2.54	0.43
1:A:484:PRO:HG2	1:A:487:PHE:HD1	1.84	0.43
2:D:71:LYS:NZ	2:D:71:LYS:CB	2.73	0.43
1:B:241:ARG:NE	1:B:380:TYR:O	2.51	0.43
1:B:310:HIS:N	1:B:310:HIS:ND1	2.60	0.43
1:B:365:ILE:O	1:B:396:HIS:CG	2.70	0.43
1:B:467:LEU:HD22	1:B:467:LEU:H	1.84	0.43
1:E:615:HIS:ND1	1:E:615:HIS:C	2.73	0.43
1:A:399:GLU:CD	1:A:399:GLU:H	2.27	0.43
2:C:82:ILE:HG22	2:C:83:PRO:HD3	2.01	0.43
2:C:116:ALA:O	2:C:119:ILE:HG12	2.19	0.43
2:C:310:ARG:NE	2:C:314:ASP:CG	2.73	0.43
2:D:88:TYR:CD1	2:D:144:LEU:HB3	2.54	0.43
2:D:152:LEU:N	2:D:152:LEU:HD23	2.33	0.43
2:D:352:LYS:O	2:D:355:ASN:CB	2.62	0.43
2:D:497:LYS:HD2	2:D:501:VAL:HG23	1.99	0.43
1:B:344:LEU:O	1:B:347:HIS:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:372:ILE:HG23	1:B:373:LEU:N	2.33	0.43
1:B:471:TYR:HD1	1:B:471:TYR:O	2.01	0.43
1:B:471:TYR:O	1:B:550:GLN:NE2	2.46	0.43
1:E:361:LEU:HD21	1:E:376:ILE:HD11	2.01	0.43
2:F:319:THR:CG2	2:F:432:ALA:HA	2.48	0.43
1:A:208:HIS:O	1:A:209:GLU:HB2	2.18	0.43
1:A:291:LEU:N	1:A:291:LEU:HD13	2.32	0.43
1:A:615:HIS:N	1:A:615:HIS:HD1	2.17	0.43
2:C:112:LEU:N	2:C:112:LEU:CD2	2.73	0.43
2:C:257:ASN:O	2:C:261:TRP:HD1	2.00	0.43
2:C:280:ASN:C	2:C:281:ASN:OD1	2.61	0.43
1:B:338:LEU:HD11	1:B:372:ILE:HD13	2.00	0.43
1:B:364:TRP:HA	1:B:364:TRP:HE3	1.81	0.43
1:B:397:LEU:HD12	1:B:400:LEU:HG	1.98	0.43
1:B:522:THR:HG23	1:B:522:THR:O	2.18	0.43
1:E:81:VAL:CG1	1:E:82:GLY:N	2.81	0.43
2:F:312:GLN:OE1	2:F:323:LYS:HD3	2.09	0.43
2:F:353:TRP:CE2	2:F:357:GLU:OE2	2.70	0.43
2:F:359:LEU:C	2:F:359:LEU:CD2	2.86	0.43
1:A:431:SER:C	1:A:434:PHE:H	2.25	0.43
1:A:612:LYS:HA	1:A:613:LEU:HA	1.45	0.43
2:C:116:ALA:HB2	2:C:126:VAL:CG2	2.48	0.43
2:C:209:PHE:HE2	2:C:254:ILE:CB	2.32	0.43
2:D:212:TYR:HH	2:D:250:SER:HG	1.66	0.43
2:D:489:SER:O	1:B:468:GLN:N	2.52	0.43
1:B:611:LYS:N	1:B:614:GLU:OE1	2.51	0.43
1:E:491:ASN:HD21	2:F:39:GLN:HB2	1.83	0.43
1:E:508:THR:N	1:E:535:ASN:O	2.36	0.43
2:F:48:GLY:HA2	2:F:50:GLN:N	2.34	0.43
2:F:126:VAL:HA	2:F:129:ARG:HD3	1.99	0.43
1:A:75:GLU:O	1:A:76:ASP:CG	2.62	0.42
1:A:283:ASP:OD1	1:A:285:GLY:N	2.35	0.42
1:A:502:THR:O	1:A:504:ILE:HG23	2.19	0.42
2:C:122:PRO:HD2	2:C:125:PHE:CE2	2.54	0.42
2:C:128:LEU:HD12	2:C:129:ARG:HA	2.00	0.42
2:C:411:ASN:O	2:C:415:LEU:HG	2.18	0.42
2:C:490:ARG:HE	2:C:490:ARG:HB2	1.54	0.42
2:D:195:LEU:HD22	2:D:274:VAL:HG22	2.00	0.42
1:B:245:ILE:O	1:B:388:LEU:HD11	2.19	0.42
1:B:471:TYR:CD1	1:B:550:GLN:HB3	2.54	0.42
1:B:542:ILE:HD11	1:B:552:MET:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:83:LEU:HD12	1:E:101:LYS:C	2.44	0.42
1:E:331:GLN:NE2	1:E:368:PHE:CB	2.82	0.42
1:E:385:LEU:HB2	1:E:417:GLU:O	2.19	0.42
1:E:389:GLU:HG3	1:E:392:ASN:CB	2.49	0.42
2:F:68:LEU:HD23	2:F:68:LEU:O	2.19	0.42
2:F:340:ILE:HG22	2:F:344:LEU:HD11	1.99	0.42
2:C:357:GLU:O	2:C:361:ASP:CB	2.65	0.42
1:B:69:ILE:HD13	1:B:69:ILE:N	2.34	0.42
1:B:115:ARG:HH21	1:B:115:ARG:CB	2.30	0.42
1:B:347:HIS:NE2	1:B:351:GLN:CG	2.82	0.42
1:E:431:SER:HB2	1:E:435:HIS:HA	2.01	0.42
1:E:504:ILE:N	1:E:540:GLY:O	2.34	0.42
1:A:291:LEU:O	1:A:292:PRO:C	2.63	0.42
1:A:587:PHE:HD2	1:A:587:PHE:C	2.27	0.42
2:D:104:GLN:HG2	2:D:105:GLN:OE1	2.19	0.42
1:B:395:ARG:HE	1:B:396:HIS:CA	2.32	0.42
1:B:461:LEU:O	1:B:555:TYR:CZ	2.73	0.42
1:B:530:THR:HB	1:B:531:SER:H	1.63	0.42
2:F:497:LYS:HG2	2:F:501:VAL:HB	2.01	0.42
1:A:68:ASN:HB3	1:A:69:ILE:HG13	2.01	0.42
1:A:265:GLN:O	1:A:268:ARG:HG2	2.20	0.42
1:A:466:PRO:HD3	2:C:494:TRP:CH2	2.54	0.42
1:A:604:PHE:HE1	2:C:47:LYS:HD2	1.85	0.42
2:C:96:VAL:CG2	2:C:128:LEU:HD21	2.22	0.42
2:C:353:TRP:CZ3	2:C:404:ILE:CG2	3.02	0.42
2:D:115:LEU:O	2:D:115:LEU:HD23	2.20	0.42
2:D:296:ASN:HB3	2:D:299:TRP:CZ2	2.54	0.42
1:B:100:VAL:HG23	1:B:101:LYS:N	2.34	0.42
1:B:105:VAL:O	1:B:132:ASP:OD2	2.38	0.42
1:B:485:MET:SD	1:B:485:MET:C	2.94	0.42
1:E:123:PRO:CB	1:E:311:LEU:HD21	2.49	0.42
1:E:169:ASN:OD1	1:E:203:THR:OG1	2.31	0.42
1:E:239:ASP:HA	1:E:355:GLY:O	2.20	0.42
2:F:97:ASN:OD1	2:F:129:ARG:CZ	2.56	0.42
1:A:507:TYR:CE1	1:A:535:ASN:C	2.97	0.42
2:C:54:HIS:CE1	2:C:58:SER:OG	2.72	0.42
2:D:7:VAL:HB	2:D:9:TRP:CE2	2.55	0.42
2:D:81:SER:OG	2:D:141:LEU:HD22	2.19	0.42
1:B:130:THR:HG23	1:B:215:SER:HB2	2.02	0.42
1:B:169:ASN:HD21	1:B:202:THR:HA	1.85	0.42
1:B:233:HIS:C	1:B:233:HIS:ND1	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:534:LYS:HD2	1:B:534:LYS:H	1.84	0.42
1:E:214:GLN:CD	1:E:427:ASN:O	2.62	0.42
1:E:280:LEU:HB3	1:E:359:LEU:CB	2.50	0.42
1:E:610:ARG:CD	2:F:167:ASP:CB	2.78	0.42
2:F:54:HIS:CD2	2:F:98:GLY:CA	3.00	0.42
1:A:181:LEU:HD22	1:A:181:LEU:HA	1.84	0.42
1:A:606:THR:HG21	2:C:5:ARG:NH1	2.31	0.42
2:C:89:VAL:HG11	2:D:90:MET:HE2	2.01	0.42
2:C:192:MET:HE3	2:C:192:MET:HB3	1.86	0.42
2:C:272:ASN:O	2:C:276:GLU:HG3	2.19	0.42
2:C:323:LYS:HE2	2:C:430:ILE:HB	2.01	0.42
2:D:61:GLN:OE1	2:D:94:ARG:NE	2.53	0.42
2:D:279:PHE:HE1	2:D:304:TRP:CZ3	2.01	0.42
1:B:263:PHE:HD1	1:B:263:PHE:N	2.17	0.42
1:B:372:ILE:HD12	1:B:372:ILE:O	2.19	0.42
1:B:509:TYR:OH	1:B:513:ASP:HB3	2.18	0.42
1:E:295:ILE:HG22	1:E:344:LEU:CD2	2.50	0.42
1:E:469:ILE:HD12	1:E:478:ILE:CD1	2.45	0.42
2:F:21:TRP:HB3	2:F:37:ALA:HB2	2.00	0.42
1:A:289:TYR:HD1	1:A:298:ASN:ND2	2.18	0.42
1:A:301:LEU:HD12	1:A:301:LEU:H	1.85	0.42
2:C:85:ARG:HH11	1:B:486:GLU:CD	2.28	0.42
2:C:359:LEU:HD23	2:C:363:ASN:HD21	1.85	0.42
1:B:69:ILE:HD13	1:B:69:ILE:C	2.45	0.42
1:E:100:VAL:O	1:E:101:LYS:HD3	2.20	0.42
1:E:462:LEU:O	2:F:494:TRP:CZ3	2.72	0.42
2:F:139:PRO:HG2	2:F:144:LEU:HD12	1.91	0.42
2:F:154:TRP:CE3	2:F:155:LEU:CA	3.01	0.42
2:F:500:GLY:O	2:F:501:VAL:HG23	2.19	0.42
1:A:105:VAL:HG12	1:A:132:ASP:CG	2.45	0.42
1:A:471:TYR:HB3	1:A:552:MET:SD	2.59	0.42
1:A:474:GLY:N	1:A:475:LYS:HA	2.35	0.42
1:A:527:GLN:NE2	1:A:527:GLN:C	2.73	0.42
2:C:128:LEU:HD12	2:C:129:ARG:CA	2.49	0.42
2:D:69:ASP:HB3	2:D:88:TYR:HE2	1.84	0.42
2:D:498:PRO:HG2	1:B:602:ILE:HG23	2.01	0.42
1:B:210:SER:C	1:B:212:ARG:HH21	2.03	0.42
1:B:491:ASN:HD22	1:B:491:ASN:HA	1.62	0.42
1:E:254:THR:HA	1:E:257:ARG:HH11	1.85	0.42
1:E:301:LEU:HD11	1:E:316:ASN:HA	2.00	0.42
1:A:175:LEU:HD23	1:A:175:LEU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:20:LEU:HD23	2:D:20:LEU:HA	1.87	0.42
2:D:502:LEU:C	1:B:544:SER:CB	2.93	0.42
1:B:474:GLY:N	1:B:475:LYS:CA	2.79	0.42
1:B:482:GLN:CG	1:B:526:LEU:HD23	2.50	0.42
1:B:503:VAL:HG11	1:B:539:LEU:HD22	2.00	0.42
1:B:575:ILE:N	1:B:575:ILE:CD1	2.73	0.42
1:E:464:SER:O	2:F:494:TRP:CZ3	2.72	0.42
1:E:501:GLY:HA2	2:F:499:PHE:CD1	2.55	0.42
3:E:701:HOH:O	2:F:502:LEU:HD21	2.13	0.42
2:F:275:LEU:O	2:F:279:PHE:CD2	2.70	0.42
1:A:588:LEU:HD21	1:A:605:ALA:HB2	2.00	0.42
2:C:6:ILE:HG21	2:C:51:TYR:CD1	2.54	0.42
2:C:55:VAL:HG23	2:C:155:LEU:HD23	2.00	0.42
2:C:79:GLN:NE2	2:C:79:GLN:C	2.73	0.42
2:C:82:ILE:HG23	2:C:83:PRO:CD	2.50	0.42
2:C:125:PHE:HB3	2:C:128:LEU:CD2	2.49	0.42
2:D:195:LEU:HD21	2:D:277:LYS:HB3	2.02	0.42
1:B:175:LEU:HD22	1:B:456:TYR:CE2	2.55	0.42
1:B:364:TRP:CA	1:B:364:TRP:HE3	2.33	0.42
1:B:366:LYS:HD2	1:B:395:ARG:NH1	2.34	0.42
1:B:397:LEU:CG	1:B:400:LEU:HD11	2.49	0.42
1:E:96:ARG:NE	1:E:168:PHE:CE2	2.87	0.42
1:E:306:SER:C	1:E:307:LEU:HG	2.44	0.42
1:E:493:GLN:HE21	1:E:493:GLN:HB2	1.68	0.42
1:E:548:SER:H	1:E:548:SER:HG	1.52	0.42
1:E:573:TRP:NE1	2:F:487:ASN:OD1	2.53	0.42
2:F:10:ARG:HE	2:F:10:ARG:HB3	1.65	0.42
2:F:50:GLN:O	2:F:51:TYR:HB2	2.19	0.42
2:F:154:TRP:HE3	2:F:155:LEU:HA	1.81	0.42
2:F:499:PHE:N	2:F:499:PHE:HD2	2.18	0.42
1:A:367:GLY:C	2:D:124:TRP:HB3	2.45	0.41
1:A:368:PHE:O	1:A:368:PHE:CG	2.72	0.41
1:A:386:LEU:CD2	1:A:419:VAL:HG21	2.50	0.41
1:A:498:ALA:O	1:A:502:THR:HG21	2.20	0.41
1:A:610:ARG:HD2	2:C:167:ASP:OD2	2.20	0.41
2:C:53:PRO:HD2	2:C:56:VAL:HG23	1.98	0.41
1:B:96:ARG:HG2	1:B:119:THR:OG1	2.20	0.41
1:B:431:SER:O	1:B:434:PHE:HB2	2.20	0.41
1:E:123:PRO:CB	1:E:311:LEU:CD2	2.98	0.41
1:E:171:ASN:ND2	1:E:454:PHE:HD1	2.18	0.41
1:E:244:VAL:HG13	1:E:388:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:31:GLU:O	2:F:33:LYS:N	2.52	0.41
1:A:480:GLY:H	1:A:524:PRO:HG3	1.82	0.41
2:C:228:ASN:OD1	2:C:228:ASN:N	2.31	0.41
2:D:36:ARG:NH1	1:B:494:ASP:CG	2.78	0.41
2:D:42:GLN:NE2	1:B:487:PHE:CE2	2.88	0.41
2:D:349:PHE:CD2	2:D:356:TRP:CE2	3.07	0.41
1:B:472:GLY:HA3	1:B:476:SER:H	1.84	0.41
1:E:96:ARG:O	1:E:168:PHE:CD2	2.73	0.41
1:E:175:LEU:CD2	1:E:175:LEU:C	2.93	0.41
1:E:391:ALA:C	1:E:393:SER:HA	2.44	0.41
1:E:469:ILE:CG1	1:E:478:ILE:HD11	2.50	0.41
2:F:112:LEU:H	2:F:112:LEU:HG	1.58	0.41
1:A:291:LEU:HD13	1:A:291:LEU:H	1.85	0.41
1:A:584:PHE:C	1:A:584:PHE:HD1	2.27	0.41
2:C:89:VAL:CG1	2:D:90:MET:HE2	2.50	0.41
2:C:314:ASP:OD2	2:C:495:LYS:CE	2.68	0.41
2:C:356:TRP:O	2:C:360:ILE:N	2.31	0.41
2:C:413:ASP:O	2:C:417:LEU:HG	2.20	0.41
2:D:85:ARG:NH2	2:D:138:LEU:O	2.53	0.41
2:D:92:LEU:O	2:D:95:PHE:HB3	2.20	0.41
2:D:234:LEU:HD13	2:D:236:ASN:HB2	2.02	0.41
2:D:322:LEU:C	2:D:322:LEU:CD2	2.86	0.41
2:D:336:LEU:C	2:D:336:LEU:CD1	2.86	0.41
1:B:390:THR:CG2	1:B:391:ALA:N	2.63	0.41
1:B:588:LEU:N	1:B:588:LEU:CD1	2.73	0.41
2:F:137:ASP:O	2:F:138:LEU:C	2.59	0.41
2:F:272:ASN:O	2:F:275:LEU:CD1	2.65	0.41
1:A:79:MET:SD	1:A:80:PHE:O	2.79	0.41
1:A:135:HIS:HA	1:A:136:PHE:HA	1.83	0.41
1:A:226:LEU:HD13	1:A:259:LEU:HD13	2.03	0.41
1:A:395:ARG:HH21	1:A:395:ARG:HG2	1.84	0.41
1:A:527:GLN:NE2	1:A:527:GLN:HA	2.35	0.41
1:A:617:TRP:HZ2	2:D:134:HIS:HA	1.84	0.41
2:C:336:LEU:O	2:C:340:ILE:HG13	2.20	0.41
2:D:49:SER:O	2:D:49:SER:OG	2.34	0.41
2:D:115:LEU:C	2:D:115:LEU:CD2	2.92	0.41
2:D:154:TRP:C	2:D:154:TRP:CD2	2.97	0.41
1:B:293:ASP:OD2	1:B:580:THR:HG23	2.21	0.41
1:B:338:LEU:HD11	1:B:372:ILE:CD1	2.50	0.41
1:B:385:LEU:O	1:B:386:LEU:HG	2.19	0.41
1:E:96:ARG:O	1:E:168:PHE:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:239:ASP:CB	1:E:355:GLY:O	2.68	0.41
1:E:289:TYR:CG	1:E:317:PHE:CE2	3.07	0.41
1:E:581:GLU:H	1:E:581:GLU:HG3	1.63	0.41
2:F:36:ARG:HD2	2:F:36:ARG:HA	1.63	0.41
1:A:221:TYR:CD1	1:A:221:TYR:N	2.88	0.41
1:A:592:ARG:HD3	2:C:184:ARG:HE	1.77	0.41
2:C:125:PHE:O	2:C:126:VAL:C	2.63	0.41
2:C:312:GLN:HE21	2:C:320:THR:HG23	1.85	0.41
2:D:268:SER:HA	2:D:271:HIS:CD2	2.55	0.41
2:D:329:TRP:CH2	2:D:424:ILE:CD1	2.99	0.41
1:B:96:ARG:HH22	1:B:171:ASN:ND2	1.97	0.41
1:B:321:LEU:CD2	1:B:321:LEU:C	2.86	0.41
1:B:506:ILE:HD11	1:B:540:GLY:CA	2.47	0.41
1:B:519:SER:O	1:B:520:LEU:HD23	2.21	0.41
1:E:554:ILE:HG21	2:F:488:TRP:HZ3	1.83	0.41
1:E:568:PRO:HG2	1:E:571:ALA:HB2	2.01	0.41
2:F:154:TRP:C	2:F:154:TRP:CD2	2.98	0.41
1:A:173:THR:O	1:A:177:GLU:OE1	2.39	0.41
1:A:387:PHE:C	1:A:388:LEU:HD12	2.46	0.41
1:A:492:PRO:HA	1:A:495:ILE:CG1	2.49	0.41
1:A:492:PRO:HB3	1:A:520:LEU:HB3	2.02	0.41
2:C:96:VAL:HA	2:C:99:LEU:HD23	2.03	0.41
2:C:136:ARG:HA	1:B:617:TRP:CE3	2.54	0.41
2:D:81:SER:HA	2:D:84:ILE:HG22	2.03	0.41
2:D:359:LEU:HD23	2:D:360:ILE:N	2.36	0.41
1:B:566:LYS:C	1:B:567:GLN:HG2	2.46	0.41
1:E:178:ALA:C	1:E:458:PHE:CD1	2.81	0.41
1:E:487:PHE:O	1:E:490:LEU:HD12	2.04	0.41
1:E:600:ILE:HG12	1:E:600:ILE:H	1.63	0.41
2:F:41:VAL:O	2:F:44:TYR:N	2.48	0.41
1:A:97:LEU:HG	1:A:166:ARG:O	2.21	0.41
1:A:225:PRO:HG2	1:A:421:VAL:HG12	2.02	0.41
1:A:446:ALA:O	1:A:450:LYS:CB	2.69	0.41
1:A:488:GLN:NE2	1:A:527:GLN:OE1	2.52	0.41
2:C:143:MET:O	2:C:143:MET:SD	2.79	0.41
2:D:271:HIS:O	2:D:275:LEU:HG	2.21	0.41
2:D:325:LYS:HD3	2:D:325:LYS:HA	1.62	0.41
1:B:521:ASN:O	1:B:523:PHE:CD2	2.74	0.41
1:E:387:PHE:HE1	1:E:401:THR:HG23	1.82	0.41
1:E:389:GLU:CB	1:E:397:LEU:HD11	2.50	0.41
1:E:449:HIS:CD2	1:E:458:PHE:HA	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:519:SER:C	1:E:520:LEU:CD2	2.83	0.41
2:F:68:LEU:O	2:F:71:LYS:HB2	2.20	0.41
2:F:191:TYR:CE2	2:F:264:LEU:HD22	2.56	0.41
1:A:180:HIS:HB2	2:C:269:ILE:CD1	2.47	0.41
1:A:306:SER:HG	1:A:316:ASN:ND2	2.17	0.41
1:A:347:HIS:CD2	1:A:347:HIS:O	2.74	0.41
2:C:415:LEU:O	2:C:418:ARG:N	2.48	0.41
2:D:302:ILE:HD12	2:D:356:TRP:CZ3	2.55	0.41
2:D:365:SER:O	2:D:366:TYR:C	2.63	0.41
1:B:107:ASN:HA	1:B:218:VAL:HG12	2.03	0.41
1:B:337:TYR:CZ	1:B:362:PRO:HG2	2.55	0.41
1:B:480:GLY:CA	1:B:524:PRO:O	2.66	0.41
1:A:98:GLN:HB3	1:A:165:LEU:N	2.35	0.41
1:A:395:ARG:NH2	1:A:395:ARG:HG3	2.35	0.41
1:A:492:PRO:HG3	1:A:520:LEU:HB3	2.03	0.41
2:C:310:ARG:NH2	2:C:314:ASP:CG	2.73	0.41
2:D:312:GLN:CD	2:D:427:TYR:CD2	2.96	0.41
2:D:489:SER:OG	1:B:468:GLN:HG2	2.21	0.41
1:B:93:GLY:O	1:B:95:PHE:CD1	2.74	0.41
1:B:175:LEU:N	1:B:456:TYR:HB2	2.35	0.41
1:B:177:GLU:HG3	1:B:458:PHE:CD2	2.43	0.41
1:B:295:ILE:O	1:B:323:PHE:N	2.34	0.41
1:B:364:TRP:CG	1:B:369:GLY:HA3	2.55	0.41
1:E:76:ASP:OD1	1:E:169:ASN:HB3	2.20	0.41
1:E:166:ARG:C	1:E:167:VAL:HG23	2.46	0.41
1:E:310:HIS:CG	1:E:314:GLY:CA	3.02	0.41
1:E:421:VAL:HB	1:E:422:PRO:HD2	2.03	0.41
1:E:471:TYR:HA	1:E:478:ILE:HB	2.02	0.41
1:E:509:TYR:HD1	1:E:510:SER:H	1.69	0.41
1:A:106:TYR:CE2	1:A:120:PHE:CD2	3.06	0.41
1:A:173:THR:O	1:A:177:GLU:CD	2.64	0.41
1:A:337:TYR:C	1:A:337:TYR:HD1	2.27	0.41
1:A:461:LEU:HD22	1:A:555:TYR:CD2	2.56	0.41
1:A:469:ILE:CG2	2:C:488:TRP:CA	2.98	0.41
2:C:388:SER:N	2:C:391:ASN:ND2	2.69	0.41
2:D:374:SER:O	2:D:377:ALA:N	2.53	0.41
2:D:398:ILE:O	2:D:402:VAL:HG23	2.21	0.41
1:B:366:LYS:CG	1:B:395:ARG:HH11	2.34	0.41
1:B:387:PHE:CE2	1:B:397:LEU:CD1	3.01	0.41
1:B:526:LEU:HD12	1:B:526:LEU:HA	1.77	0.41
1:E:440:ARG:O	1:E:444:ILE:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:546:ASP:OD1	1:E:548:SER:OG	2.38	0.41
2:F:18:LEU:CD1	2:F:44:TYR:HE2	2.34	0.41
2:F:100:LEU:HD23	2:F:100:LEU:H	1.83	0.41
2:F:154:TRP:CE3	2:F:155:LEU:N	2.89	0.41
1:A:105:VAL:HB	1:A:132:ASP:C	2.45	0.40
1:A:480:GLY:CA	1:A:524:PRO:O	2.45	0.40
1:A:502:THR:CG2	1:A:577:ARG:HH21	2.25	0.40
2:C:96:VAL:HA	2:C:99:LEU:CD2	2.51	0.40
2:C:136:ARG:NE	2:D:49:SER:O	2.54	0.40
2:D:418:ARG:CB	2:D:419:PHE:CE2	2.92	0.40
2:D:427:TYR:HD2	2:D:430:ILE:HD11	1.87	0.40
2:D:487:ASN:O	1:B:468:GLN:O	2.39	0.40
1:B:96:ARG:HA	1:B:119:THR:HA	2.02	0.40
1:B:96:ARG:O	1:B:168:PHE:CB	2.69	0.40
1:E:89:LEU:N	1:E:131:ILE:O	2.46	0.40
1:E:127:SER:O	1:E:129:PRO:HD3	2.20	0.40
1:E:176:LEU:N	1:E:176:LEU:HD13	2.36	0.40
1:E:268:ARG:HD3	1:E:302:SER:HB2	2.01	0.40
1:E:471:TYR:OH	1:E:522:THR:O	2.38	0.40
2:F:333:GLN:CA	2:F:337:LEU:CD2	2.98	0.40
1:A:168:PHE:CD1	1:A:168:PHE:C	2.98	0.40
1:A:268:ARG:HG2	1:A:268:ARG:H	1.59	0.40
2:C:38:VAL:O	2:C:42:GLN:HB2	2.20	0.40
2:C:74:CYS:HB2	2:C:75:LEU:HA	2.03	0.40
2:C:325:LYS:O	2:C:326:PHE:CD1	2.73	0.40
2:D:5:ARG:CD	1:B:610:ARG:HG3	2.52	0.40
2:D:41:VAL:O	2:D:45:ARG:HG3	2.21	0.40
2:D:237:TYR:O	2:D:237:TYR:HD1	2.04	0.40
2:D:341:ILE:CD1	2:D:374:SER:HB3	2.52	0.40
2:D:492:GLN:HE21	2:D:492:GLN:HB3	1.61	0.40
1:B:436:ALA:O	1:B:440:ARG:HB2	2.21	0.40
1:E:97:LEU:HA	1:E:167:VAL:H	1.87	0.40
1:E:168:PHE:HD2	1:E:168:PHE:C	2.28	0.40
1:E:168:PHE:HD2	1:E:168:PHE:O	2.05	0.40
1:E:362:PRO:CB	3:E:705:HOH:O	2.60	0.40
1:E:507:TYR:HD1	1:E:535:ASN:O	2.03	0.40
2:F:18:LEU:HD11	2:F:44:TYR:HE2	1.86	0.40
2:F:126:VAL:HA	2:F:129:ARG:CD	2.50	0.40
2:F:270:TYR:C	2:F:274:VAL:CG2	2.88	0.40
2:F:372:CYS:HB2	2:F:412:ILE:HG12	2.03	0.40
2:F:411:ASN:CA	2:F:414:ASN:HB3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:358:LYS:CB	2:C:490:ARG:HH12	2.29	0.40
1:B:521:ASN:O	1:B:523:PHE:HD2	2.03	0.40
1:B:600:ILE:CG2	3:B:703:HOH:O	2.70	0.40
1:E:474:GLY:N	1:E:475:LYS:CB	2.85	0.40
2:F:34:ARG:HA	2:F:37:ALA:HB3	2.04	0.40
2:F:298:ASP:HB2	2:F:356:TRP:HH2	1.86	0.40
1:A:324:TYR:OH	1:A:580:THR:OG1	2.04	0.40
2:C:195:LEU:O	2:C:198:THR:N	2.52	0.40
2:C:237:TYR:HD1	2:C:237:TYR:HA	1.82	0.40
2:C:256:GLU:O	2:C:260:GLN:HG3	2.22	0.40
2:C:287:LEU:HD12	2:C:287:LEU:HA	1.85	0.40
1:B:243:MET:HE3	1:B:243:MET:HB2	1.79	0.40
1:B:472:GLY:O	1:B:475:LYS:CB	2.69	0.40
1:E:121:TRP:O	1:E:123:PRO:HD3	2.21	0.40
1:E:373:LEU:O	1:E:377:ILE:HG13	2.22	0.40
2:F:143:MET:HE2	2:F:143:MET:HB2	1.99	0.40
2:F:156:TYR:OH	2:F:161:ASN:ND2	2.54	0.40
1:A:197:PRO:HG2	1:A:197:PRO:O	2.22	0.40
1:A:544:SER:OG	1:A:545:ILE:N	2.54	0.40
1:A:562:GLN:H	1:A:562:GLN:HG2	1.57	0.40
2:C:291:MET:SD	2:C:340:ILE:CG2	3.10	0.40
1:B:289:TYR:CD1	1:B:317:PHE:HD1	2.39	0.40
1:E:175:LEU:HD22	1:E:189:TRP:CD1	2.53	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:331:GLN:O	2:F:143:MET:CE[2_555]	1.76	0.44
2:F:49:SER:C	2:F:136:ARG:NH2[2_555]	1.94	0.26
2:F:49:SER:O	2:F:136:ARG:NH2[2_555]	1.99	0.21
1:E:486:GLU:O	2:F:81:SER:OG[2_555]	2.08	0.12
2:F:94:ARG:NH2	2:F:136:ARG:O[2_555]	2.08	0.12
1:E:371:GLN:NE2	2:F:150:GLU:OE1[2_555]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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	525/632 (83%)	494 (94%)	29 (6%)	2 (0%)	30	60
1	B	522/632 (83%)	488 (94%)	31 (6%)	3 (1%)	21	52
1	E	521/632 (82%)	492 (94%)	28 (5%)	1 (0%)	43	72
2	C	422/502 (84%)	404 (96%)	18 (4%)	0	100	100
2	D	421/502 (84%)	399 (95%)	20 (5%)	2 (0%)	24	56
2	F	385/502 (77%)	372 (97%)	11 (3%)	2 (0%)	24	56
All	All	2796/3402 (82%)	2649 (95%)	137 (5%)	10 (0%)	30	60

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	PRO
2	D	131	TRP
1	B	416	PRO
1	E	416	PRO
2	F	501	VAL
1	B	422	PRO
1	A	194	PRO
1	B	466	PRO
2	D	101	ASP
2	F	101	ASP

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	441/579 (76%)	313 (71%)	128 (29%)	0	2
1	B	430/579 (74%)	327 (76%)	103 (24%)	1	5
1	E	433/579 (75%)	320 (74%)	113 (26%)	0	4
2	C	392/461 (85%)	318 (81%)	74 (19%)	1	10
2	D	391/461 (85%)	319 (82%)	72 (18%)	1	11
2	F	364/461 (79%)	302 (83%)	62 (17%)	2	13
All	All	2451/3120 (79%)	1899 (78%)	552 (22%)	1	6

All (552) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	67	ASP
1	A	68	ASN
1	A	71	TYR
1	A	75	GLU
1	A	76	ASP
1	A	78	THR
1	A	83	LEU
1	A	88	LYS
1	A	104	ILE
1	A	108	ASN
1	A	109	VAL
1	A	115	ARG
1	A	118	LEU
1	A	119	THR
1	A	124	LEU
1	A	166	ARG
1	A	168	PHE
1	A	170	SER
1	A	175	LEU
1	A	176	LEU
1	A	180	HIS
1	A	183	ARG
1	A	186	ASN
1	A	188	LEU
1	A	190	LYS
1	A	193	GLU
1	A	198	LEU
1	A	203	THR
1	A	206	LEU

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Mol	Chain	Res	Type
1	A	207	LEU
1	A	209	GLU
1	A	210	SER
1	A	214	GLN
1	A	216	LEU
1	A	217	SER
1	A	221	TYR
1	A	226	LEU
1	A	245	ILE
1	A	248	LYS
1	A	249	ASN
1	A	259	LEU
1	A	260	LEU
1	A	261	GLU
1	A	268	ARG
1	A	269	ASP
1	A	271	THR
1	A	272	THR
1	A	273	SER
1	A	275	GLU
1	A	276	GLU
1	A	277	LEU
1	A	280	LEU
1	A	282	LEU
1	A	290	SER
1	A	291	LEU
1	A	300	ILE
1	A	301	LEU
1	A	303	SER
1	A	305	ILE
1	A	307	LEU
1	A	309	GLN
1	A	312	CYS
1	A	313	GLN
1	A	328	SER
1	A	329	SER
1	A	337	TYR
1	A	342	ASP
1	A	344	LEU
1	A	345	ILE
1	A	356	THR
1	A	359	LEU

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Mol	Chain	Res	Type
1	A	361	LEU
1	A	364	TRP
1	A	371	GLN
1	A	372	ILE
1	A	373	LEU
1	A	383	THR
1	A	385	LEU
1	A	395	ARG
1	A	397	LEU
1	A	399	GLU
1	A	420	ARG
1	A	424	HIS
1	A	432	SER
1	A	450	LYS
1	A	454	PHE
1	A	455	ASP
1	A	457	ASP
1	A	473	LYS
1	A	476	SER
1	A	481	ILE
1	A	485	MET
1	A	490	LEU
1	A	493	GLN
1	A	495	ILE
1	A	497	SER
1	A	499	LEU
1	A	507	TYR
1	A	515	LEU
1	A	521	ASN
1	A	522	THR
1	A	525	ILE
1	A	526	LEU
1	A	527	GLN
1	A	528	SER
1	A	530	THR
1	A	534	LYS
1	A	539	LEU
1	A	541	LEU
1	A	550	GLN
1	A	554	ILE
1	A	562	GLN
1	A	564	LEU

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Mol	Chain	Res	Type
1	A	566	LYS
1	A	575	ILE
1	A	577	ARG
1	A	579	LYS
1	A	592	ARG
1	A	593	THR
1	A	597	ASP
1	A	601	GLN
1	A	608	GLU
1	A	609	ARG
1	A	610	ARG
1	A	611	LYS
1	A	613	LEU
1	A	616	VAL
2	C	11	ASP
2	C	15	LEU
2	C	29	THR
2	C	30	ILE
2	C	46	LEU
2	C	49	SER
2	C	50	GLN
2	C	52	LEU
2	C	54	HIS
2	C	55	VAL
2	C	56	VAL
2	C	68	LEU
2	C	71	LYS
2	C	77	VAL
2	C	78	HIS
2	C	79	GLN
2	C	80	ASP
2	C	87	SER
2	C	92	LEU
2	C	97	ASN
2	C	99	LEU
2	C	100	LEU
2	C	101	ASP
2	C	105	GLN
2	C	107	GLN
2	C	108	PHE
2	C	110	ILE
2	C	112	LEU

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Mol	Chain	Res	Type
2	C	115	LEU
2	C	129	ARG
2	C	141	LEU
2	C	142	GLU
2	C	143	MET
2	C	155	LEU
2	C	160	TRP
2	C	163	GLU
2	C	182	TYR
2	C	210	LEU
2	C	213	LYS
2	C	217	GLU
2	C	218	ASN
2	C	221	ASP
2	C	223	LEU
2	C	224	ILE
2	C	228	ASN
2	C	232	ASP
2	C	234	LEU
2	C	236	ASN
2	C	285	LEU
2	C	287	LEU
2	C	288	LYS
2	C	307	ARG
2	C	310	ARG
2	C	311	THR
2	C	312	GLN
2	C	317	ASN
2	C	325	LYS
2	C	327	ASN
2	C	330	LYS
2	C	340	ILE
2	C	345	ASN
2	C	354	GLN
2	C	359	LEU
2	C	361	ASP
2	C	363	ASN
2	C	385	THR
2	C	387	ASN
2	C	393	LYS
2	C	394	ARG
2	C	395	ARG

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Mol	Chain	Res	Type
2	C	404	ILE
2	C	490	ARG
2	C	491	VAL
2	C	492	GLN
2	D	16	GLU
2	D	18	LEU
2	D	20	LEU
2	D	32	ASP
2	D	46	LEU
2	D	54	HIS
2	D	71	LYS
2	D	72	GLU
2	D	75	LEU
2	D	77	VAL
2	D	79	GLN
2	D	84	ILE
2	D	86	LEU
2	D	99	LEU
2	D	100	LEU
2	D	103	THR
2	D	104	GLN
2	D	105	GLN
2	D	106	SER
2	D	107	GLN
2	D	108	PHE
2	D	110	ILE
2	D	112	LEU
2	D	113	HIS
2	D	115	LEU
2	D	121	LEU
2	D	127	ASP
2	D	129	ARG
2	D	131	TRP
2	D	134	HIS
2	D	146	TRP
2	D	163	GLU
2	D	182	TYR
2	D	188	LEU
2	D	189	GLU
2	D	199	LEU
2	D	205	LEU
2	D	225	THR

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Mol	Chain	Res	Type
2	D	228	ASN
2	D	232	ASP
2	D	234	LEU
2	D	235	VAL
2	D	236	ASN
2	D	250	SER
2	D	254	ILE
2	D	255	ARG
2	D	278	PHE
2	D	282	TYR
2	D	322	LEU
2	D	323	LYS
2	D	325	LYS
2	D	332	LEU
2	D	336	LEU
2	D	341	ILE
2	D	344	LEU
2	D	346	ASN
2	D	347	LYS
2	D	350	LYS
2	D	351	ASN
2	D	352	LYS
2	D	358	LYS
2	D	361	ASP
2	D	365	SER
2	D	388	SER
2	D	390	ARG
2	D	421	GLU
2	D	425	LYS
2	D	426	LEU
2	D	430	ILE
2	D	492	GLN
2	D	493	ASN
2	D	501	VAL
1	B	65	LEU
1	B	67	ASP
1	B	69	ILE
1	B	74	ASP
1	B	78	THR
1	B	79	MET
1	B	90	HIS
1	B	108	ASN

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Mol	Chain	Res	Type
1	B	115	ARG
1	B	117	ILE
1	B	122	HIS
1	B	124	LEU
1	B	165	LEU
1	B	166	ARG
1	B	173	THR
1	B	176	LEU
1	B	181	LEU
1	B	190	LYS
1	B	196	PHE
1	B	209	GLU
1	B	210	SER
1	B	212	ARG
1	B	217	SER
1	B	221	TYR
1	B	242	ILE
1	B	243	MET
1	B	250	SER
1	B	252	LYS
1	B	253	SER
1	B	264	THR
1	B	268	ARG
1	B	273	SER
1	B	277	LEU
1	B	289	TYR
1	B	307	LEU
1	B	310	HIS
1	B	313	GLN
1	B	318	GLN
1	B	321	LEU
1	B	332	ASP
1	B	333	GLU
1	B	337	TYR
1	B	345	ILE
1	B	350	GLU
1	B	356	THR
1	B	358	LEU
1	B	359	LEU
1	B	364	TRP
1	B	370	MET
1	B	371	GLN

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Mol	Chain	Res	Type
1	B	372	ILE
1	B	388	LEU
1	B	389	GLU
1	B	394	LYS
1	B	395	ARG
1	B	397	LEU
1	B	398	ASP
1	B	399	GLU
1	B	400	LEU
1	B	401	THR
1	B	425	SER
1	B	429	THR
1	B	450	LYS
1	B	451	ILE
1	B	453	GLN
1	B	455	ASP
1	B	461	LEU
1	B	462	LEU
1	B	467	LEU
1	B	469	ILE
1	B	471	TYR
1	B	473	LYS
1	B	476	SER
1	B	478	ILE
1	B	481	ILE
1	B	485	MET
1	B	486	GLU
1	B	488	GLN
1	B	490	LEU
1	B	491	ASN
1	B	499	LEU
1	B	515	LEU
1	B	520	LEU
1	B	522	THR
1	B	524	PRO
1	B	525	ILE
1	B	530	THR
1	B	534	LYS
1	B	539	LEU
1	B	549	GLN
1	B	551	ILE
1	B	569	GLU

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Mol	Chain	Res	Type
1	B	570	ASP
1	B	575	ILE
1	B	577	ARG
1	B	585	CYS
1	B	588	LEU
1	B	592	ARG
1	B	599	ASN
1	B	612	LYS
1	B	613	LEU
1	B	615	HIS
1	B	616	VAL
1	E	69	ILE
1	E	71	TYR
1	E	72	GLU
1	E	75	GLU
1	E	79	MET
1	E	83	LEU
1	E	98	GLN
1	E	104	ILE
1	E	111	TYR
1	E	112	ASN
1	E	114	SER
1	E	117	ILE
1	E	118	LEU
1	E	130	THR
1	E	166	ARG
1	E	167	VAL
1	E	168	PHE
1	E	170	SER
1	E	176	LEU
1	E	177	GLU
1	E	180	HIS
1	E	181	LEU
1	E	182	TYR
1	E	184	ASP
1	E	188	LEU
1	E	196	PHE
1	E	199	ASN
1	E	203	THR
1	E	206	LEU
1	E	207	LEU
1	E	209	GLU

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Mol	Chain	Res	Type
1	E	212	ARG
1	E	216	LEU
1	E	234	LYS
1	E	235	ASN
1	E	245	ILE
1	E	248	LYS
1	E	267	ILE
1	E	268	ARG
1	E	269	ASP
1	E	273	SER
1	E	290	SER
1	E	291	LEU
1	E	293	ASP
1	E	301	LEU
1	E	307	LEU
1	E	310	HIS
1	E	311	LEU
1	E	316	ASN
1	E	317	PHE
1	E	327	SER
1	E	332	ASP
1	E	333	GLU
1	E	336	SER
1	E	356	THR
1	E	358	LEU
1	E	359	LEU
1	E	360	ASN
1	E	365	ILE
1	E	381	LYS
1	E	383	THR
1	E	384	HIS
1	E	385	LEU
1	E	386	LEU
1	E	388	LEU
1	E	393	SER
1	E	394	LYS
1	E	395	ARG
1	E	397	LEU
1	E	399	GLU
1	E	400	LEU
1	E	417	GLU
1	E	450	LYS

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Mol	Chain	Res	Type
1	E	451	ILE
1	E	454	PHE
1	E	471	TYR
1	E	473	LYS
1	E	481	ILE
1	E	489	ASP
1	E	493	GLN
1	E	499	LEU
1	E	502	THR
1	E	517	VAL
1	E	525	ILE
1	E	526	LEU
1	E	529	CYS
1	E	534	LYS
1	E	539	LEU
1	E	547	THR
1	E	548	SER
1	E	549	GLN
1	E	560	HIS
1	E	562	GLN
1	E	564	LEU
1	E	565	ASP
1	E	566	LYS
1	E	567	GLN
1	E	575	ILE
1	E	581	GLU
1	E	582	THR
1	E	588	LEU
1	E	592	ARG
1	E	594	ILE
1	E	595	THR
1	E	597	ASP
1	E	598	ASP
1	E	601	GLN
1	E	608	GLU
1	E	609	ARG
1	E	610	ARG
1	E	612	LYS
1	E	614	GLU
1	E	618	LYS
2	F	18	LEU
2	F	25	LYS

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Mol	Chain	Res	Type
2	F	26	SER
2	F	29	THR
2	F	33	LYS
2	F	34	ARG
2	F	46	LEU
2	F	47	LYS
2	F	50	GLN
2	F	51	TYR
2	F	52	LEU
2	F	54	HIS
2	F	62	ILE
2	F	77	VAL
2	F	80	ASP
2	F	81	SER
2	F	84	ILE
2	F	85	ARG
2	F	100	LEU
2	F	101	ASP
2	F	104	GLN
2	F	108	PHE
2	F	110	ILE
2	F	112	LEU
2	F	118	LYS
2	F	128	LEU
2	F	129	ARG
2	F	131	TRP
2	F	133	THR
2	F	136	ARG
2	F	138	LEU
2	F	144	LEU
2	F	146	TRP
2	F	152	LEU
2	F	155	LEU
2	F	274	VAL
2	F	275	LEU
2	F	282	TYR
2	F	283	ASP
2	F	319	THR
2	F	321	ILE
2	F	323	LYS
2	F	324	ARG
2	F	335	ARG

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Mol	Chain	Res	Type
2	F	336	LEU
2	F	350	LYS
2	F	352	LYS
2	F	358	LYS
2	F	359	LEU
2	F	365	SER
2	F	388	SER
2	F	390	ARG
2	F	391	ASN
2	F	392	LYS
2	F	393	LYS
2	F	417	LEU
2	F	423	GLU
2	F	489	SER
2	F	490	ARG
2	F	494	TRP
2	F	497	LYS
2	F	502	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	98	GLN
1	A	107	ASN
1	A	108	ASN
1	A	126	GLN
1	A	186	ASN
1	A	214	GLN
1	A	298	ASN
1	A	313	GLN
1	A	316	ASN
1	A	318	GLN
1	A	331	GLN
1	A	371	GLN
1	A	438	GLN
1	A	453	GLN
1	A	482	GLN
1	A	488	GLN
1	A	491	ASN
1	A	493	GLN
1	A	543	HIS

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Mol	Chain	Res	Type
1	A	560	HIS
1	A	567	GLN
1	A	615	HIS
2	C	39	GLN
2	C	54	HIS
2	C	61	GLN
2	C	79	GLN
2	C	97	ASN
2	C	105	GLN
2	C	158	HIS
2	C	161	ASN
2	C	185	ASN
2	C	272	ASN
2	C	313	GLN
2	C	355	ASN
2	C	363	ASN
2	C	391	ASN
2	D	79	GLN
2	D	104	GLN
2	D	134	HIS
2	D	161	ASN
2	D	218	ASN
2	D	220	ASN
2	D	257	ASN
2	D	312	GLN
2	D	327	ASN
2	D	342	ASN
2	D	343	ASN
2	D	397	GLN
2	D	492	GLN
2	D	493	ASN
1	B	90	HIS
1	B	108	ASN
1	B	171	ASN
1	B	172	HIS
1	B	233	HIS
1	B	286	GLN
1	B	318	GLN
1	B	339	ASN
1	B	396	HIS
1	B	424	HIS
1	B	435	HIS

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Mol	Chain	Res	Type
1	B	438	GLN
1	B	488	GLN
1	B	549	GLN
1	B	599	ASN
1	E	110	HIS
1	E	205	HIS
1	E	316	ASN
1	E	351	GLN
1	E	360	ASN
1	E	371	GLN
1	E	384	HIS
1	E	424	HIS
1	E	482	GLN
1	E	491	ASN
1	E	493	GLN
1	E	549	GLN
1	E	560	HIS
1	E	567	GLN
1	E	601	GLN
2	F	42	GLN
2	F	105	GLN
2	F	130	HIS
2	F	161	ASN
2	F	257	ASN
2	F	333	GLN
2	F	345	ASN
2	F	492	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	529/632 (83%)	0.63	27 (5%)	33	22	30, 74, 134, 150	0
1	B	528/632 (83%)	1.09	78 (14%)	5	7	28, 109, 157, 177	0
1	E	527/632 (83%)	0.64	16 (3%)	52	32	49, 89, 133, 163	0
2	C	430/502 (85%)	0.55	22 (5%)	33	22	29, 72, 158, 200	0
2	D	429/502 (85%)	0.68	23 (5%)	31	21	45, 93, 152, 198	0
2	F	397/502 (79%)	0.84	32 (8%)	18	14	45, 133, 176, 198	0
All	All	2840/3402 (83%)	0.74	198 (6%)	22	16	28, 91, 158, 200	0

All (198) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	397	LEU	5.9
1	B	301	LEU	4.9
1	B	280	LEU	4.6
1	A	401	THR	4.4
2	C	85	ARG	4.3
1	B	278	VAL	4.3
1	A	100	VAL	4.2
1	E	138	GLY	4.2
1	B	178	ALA	4.1
2	C	218	ASN	4.0
1	B	483	PHE	4.0
1	B	206	LEU	4.0
1	E	412	ASP	3.9
2	C	432	ALA	3.9
1	B	401	THR	3.9
1	A	409	SER	3.8
2	C	78	HIS	3.8
1	E	137	ALA	3.8
1	A	180	HIS	3.8

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Mol	Chain	Res	Type	RSRZ
2	F	387	ASN	3.6
2	D	101	ASP	3.6
2	D	77	VAL	3.6
2	F	382	GLU	3.6
2	F	413	ASP	3.6
2	C	233	ASN	3.5
1	B	297	LEU	3.5
2	F	403	GLU	3.4
1	B	255	PHE	3.3
1	B	411	ARG	3.3
1	B	316	ASN	3.3
1	B	300	ILE	3.3
1	B	276	GLU	3.2
2	C	76	GLY	3.2
2	F	386	GLY	3.2
1	B	230	TYR	3.2
2	F	377	ALA	3.2
2	C	433	GLU	3.2
2	D	233	ASN	3.1
1	A	412	ASP	3.1
1	B	201	ARG	3.1
1	B	91	LEU	3.1
1	E	401	THR	3.1
1	A	581	GLU	3.0
2	C	106	SER	3.0
2	C	399	ASP	3.0
1	B	427	ASN	3.0
2	D	35	GLN	3.0
2	C	348	ASN	3.0
2	D	235	VAL	3.0
2	C	429	PHE	3.0
2	C	235	VAL	3.0
2	C	180	TYR	2.9
1	B	111	TYR	2.9
1	B	303	SER	2.9
2	D	67	LEU	2.9
1	E	238	TYR	2.9
1	A	82	GLY	2.8
1	B	196	PHE	2.8
2	D	100	LEU	2.8
1	B	87	GLN	2.8
1	B	438	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
2	D	399	ASP	2.8
1	E	187	TYR	2.8
1	A	99	VAL	2.8
1	B	82	GLY	2.8
1	B	240	THR	2.8
2	C	158	HIS	2.7
1	A	239	ASP	2.7
2	C	167	ASP	2.7
1	A	407	SER	2.7
2	F	357	GLU	2.7
1	B	451	ILE	2.6
2	C	237	TYR	2.6
2	D	26	SER	2.6
2	D	271	HIS	2.6
1	B	78	THR	2.6
1	B	193	GLU	2.6
2	D	234	LEU	2.6
1	B	518	LYS	2.6
1	E	474	GLY	2.6
1	B	119	THR	2.6
1	B	173	THR	2.6
2	D	112	LEU	2.6
2	C	434	LYS	2.6
1	E	312	CYS	2.6
2	F	346	ASN	2.6
1	B	581	GLU	2.5
1	B	100	VAL	2.5
1	B	488	GLN	2.5
2	D	39	GLN	2.5
1	B	138	GLY	2.5
1	B	216	LEU	2.5
2	F	131	TRP	2.5
1	A	238	TYR	2.5
1	B	81	VAL	2.5
2	F	427	TYR	2.5
1	B	121	TRP	2.5
1	A	112	ASN	2.5
2	F	396	LYS	2.5
1	E	239	ASP	2.5
2	F	376	LEU	2.5
1	B	321	LEU	2.4
2	F	123	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	427	ASN	2.4
2	F	3	PRO	2.4
2	F	142	GLU	2.4
1	B	292	PRO	2.4
2	F	484	PRO	2.4
1	A	511	GLY	2.4
2	F	383	LYS	2.4
2	F	408	LEU	2.4
1	A	137	ALA	2.4
1	E	216	LEU	2.4
1	A	413	ALA	2.4
1	B	375	HIS	2.4
1	B	315	SER	2.4
2	C	26	SER	2.4
2	C	77	VAL	2.3
1	B	197	PRO	2.3
1	B	617	TRP	2.3
1	B	378	ARG	2.3
1	B	101	LYS	2.3
1	E	237	ALA	2.3
1	B	425	SER	2.3
2	F	78	HIS	2.3
1	B	139	TRP	2.3
2	D	225	THR	2.3
1	A	101	LYS	2.3
1	A	244	VAL	2.3
2	F	402	VAL	2.3
1	B	609	ARG	2.3
1	E	455	ASP	2.3
1	B	344	LEU	2.2
1	B	423	ALA	2.2
2	F	365	SER	2.2
1	A	387	PHE	2.2
1	B	365	ILE	2.2
1	A	364	TRP	2.2
1	A	308	GLY	2.2
1	B	218	VAL	2.2
2	F	394	ARG	2.2
2	F	410	GLU	2.2
1	B	112	ASN	2.2
2	F	406	ALA	2.2
2	F	409	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	412	ASP	2.2
1	B	110	HIS	2.2
1	B	175	LEU	2.2
2	F	398	ILE	2.2
1	A	426	LEU	2.2
1	E	409	SER	2.2
2	F	102	PRO	2.2
2	C	401	THR	2.2
1	B	306	SER	2.1
2	D	167	ASP	2.1
1	E	289	TYR	2.1
1	B	434	PHE	2.1
1	B	479	LYS	2.1
2	D	432	ALA	2.1
1	A	402	ILE	2.1
2	C	75	LEU	2.1
2	F	367	LEU	2.1
1	B	616	VAL	2.1
1	A	337	TYR	2.1
1	E	139	TRP	2.1
1	B	102	GLY	2.1
1	B	247	GLY	2.1
1	B	571	ALA	2.1
1	B	442	PHE	2.1
1	A	89	LEU	2.1
1	B	238	TYR	2.1
1	E	320	LEU	2.1
1	B	123	PRO	2.1
2	F	384	ILE	2.1
2	C	125	PHE	2.1
1	B	596	TRP	2.1
2	F	298	ASP	2.1
2	F	356	TRP	2.1
1	B	478	ILE	2.1
2	D	109	ALA	2.1
2	D	226	SER	2.1
1	B	458	PHE	2.1
2	F	289	VAL	2.1
1	B	414	TYR	2.0
1	A	191	PRO	2.0
1	B	568	PRO	2.0
1	A	570	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	569	GLU	2.0
2	D	63	THR	2.0
1	B	286	GLN	2.0
2	D	501	VAL	2.0
1	B	117	ILE	2.0
1	B	177	GLU	2.0
2	D	69	ASP	2.0
2	D	428	ASP	2.0
2	D	121	LEU	2.0
1	B	229	LEU	2.0
1	B	185	VAL	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.