



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:48 AM UTC

PDB ID : 3FH6 / pdb_00003fh6
Title : Crystal structure of the resting state maltose transporter from E. coli
Authors : Khare, D.; Oldham, M.L.; Orelle, C.; Davidson, A.L.; Chen, J.
Deposited on : 2008-12-08
Resolution : 4.50 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:

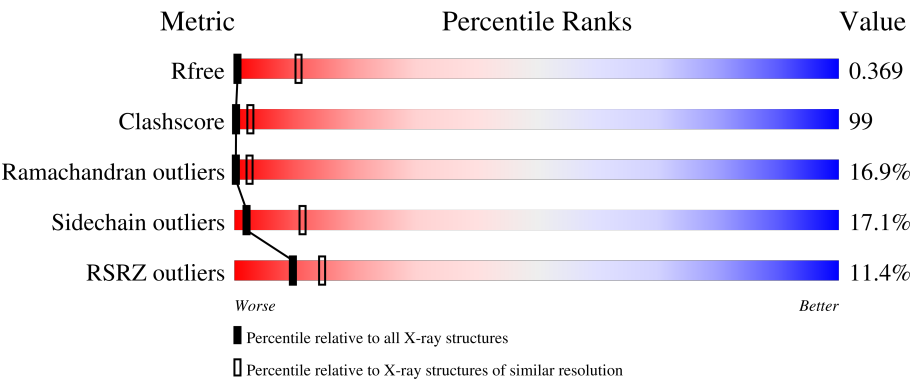
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 4.50 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	1127 (5.10-3.90)
Clashscore	190562	1002 (5.06-3.94)
Ramachandran outliers	187476	1060 (5.10-3.90)
Sidechain outliers	187428	1043 (5.10-3.90)
RSRZ outliers	180081	1122 (5.10-3.90)

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	F	480	8% 8%38%19% • 34%
1	H	480	6% 7%38%19% • 34%
2	G	296	7% 14%45%23% • 14%
2	I	296	9% 14%45%23% • 14%
3	A	381	15% 9%55%28%6% •

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Mol	Chain	Length	Quality of chain
3	B	381	13% 12% 54% 27% 5%
3	C	381	11% 9% 53% 28% 6%
3	D	381	10% 13% 53% 27% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20236 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 Maltose transport system permease protein malF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	316	Total	C	N	O	S	0	0	0
			2418	1607	378	418	15			
1	H	316	Total	C	N	O	S	0	0	0
			2418	1607	378	418	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	35	MET	-	expression tag	UNP P02916
H	35	MET	-	expression tag	UNP P02916

- Molecule 2 is a protein called Maltose transport system permease protein malG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	254	Total	C	N	O	S	0	0	0
			1942	1308	306	319	9			
2	I	254	Total	C	N	O	S	0	0	0
			1942	1308	306	319	9			

- Molecule 3 is a protein called Maltose/maltodextrin import ATP-binding protein malK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	371	Total	C	N	O	S	0	0	0
			2876	1819	515	529	13			
3	B	372	Total	C	N	O	S	0	0	0
			2882	1822	516	531	13			
3	C	371	Total	C	N	O	S	0	0	0
			2876	1819	515	529	13			
3	D	372	Total	C	N	O	S	0	0	0
			2882	1822	516	531	13			

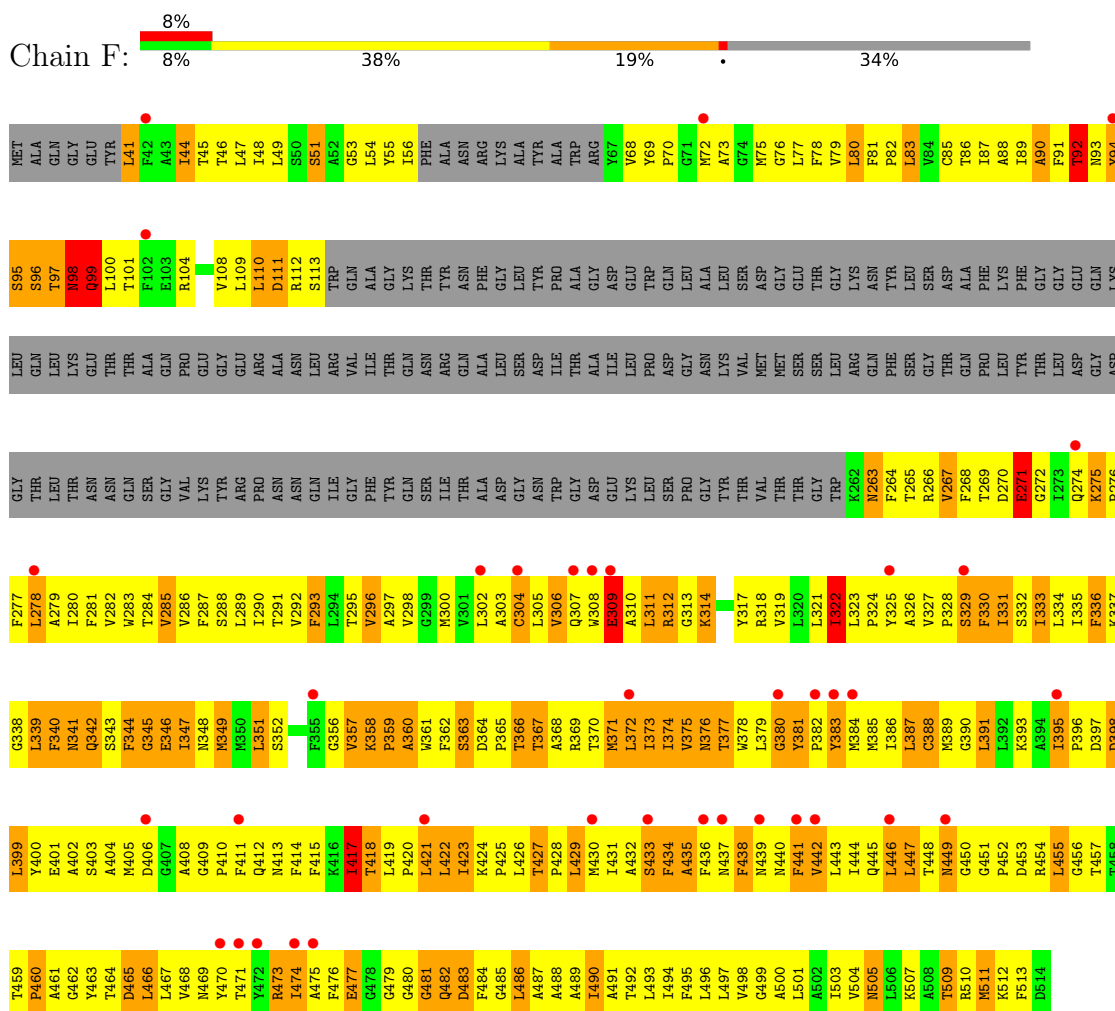
There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	372	ALA	-	expression tag	UNP P68187
A	373	SER	-	expression tag	UNP P68187
A	374	ALA	-	expression tag	UNP P68187
A	375	SER	-	expression tag	UNP P68187
A	376	HIS	-	expression tag	UNP P68187
A	377	HIS	-	expression tag	UNP P68187
A	378	HIS	-	expression tag	UNP P68187
A	379	HIS	-	expression tag	UNP P68187
A	380	HIS	-	expression tag	UNP P68187
A	381	HIS	-	expression tag	UNP P68187
B	372	ALA	-	expression tag	UNP P68187
B	373	SER	-	expression tag	UNP P68187
B	374	ALA	-	expression tag	UNP P68187
B	375	SER	-	expression tag	UNP P68187
B	376	HIS	-	expression tag	UNP P68187
B	377	HIS	-	expression tag	UNP P68187
B	378	HIS	-	expression tag	UNP P68187
B	379	HIS	-	expression tag	UNP P68187
B	380	HIS	-	expression tag	UNP P68187
B	381	HIS	-	expression tag	UNP P68187
C	372	ALA	-	expression tag	UNP P68187
C	373	SER	-	expression tag	UNP P68187
C	374	ALA	-	expression tag	UNP P68187
C	375	SER	-	expression tag	UNP P68187
C	376	HIS	-	expression tag	UNP P68187
C	377	HIS	-	expression tag	UNP P68187
C	378	HIS	-	expression tag	UNP P68187
C	379	HIS	-	expression tag	UNP P68187
C	380	HIS	-	expression tag	UNP P68187
C	381	HIS	-	expression tag	UNP P68187
D	372	ALA	-	expression tag	UNP P68187
D	373	SER	-	expression tag	UNP P68187
D	374	ALA	-	expression tag	UNP P68187
D	375	SER	-	expression tag	UNP P68187
D	376	HIS	-	expression tag	UNP P68187
D	377	HIS	-	expression tag	UNP P68187
D	378	HIS	-	expression tag	UNP P68187
D	379	HIS	-	expression tag	UNP P68187
D	380	HIS	-	expression tag	UNP P68187
D	381	HIS	-	expression tag	UNP P68187

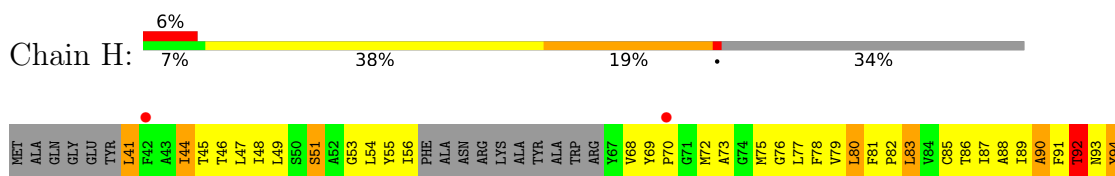
3 Residue-property plots

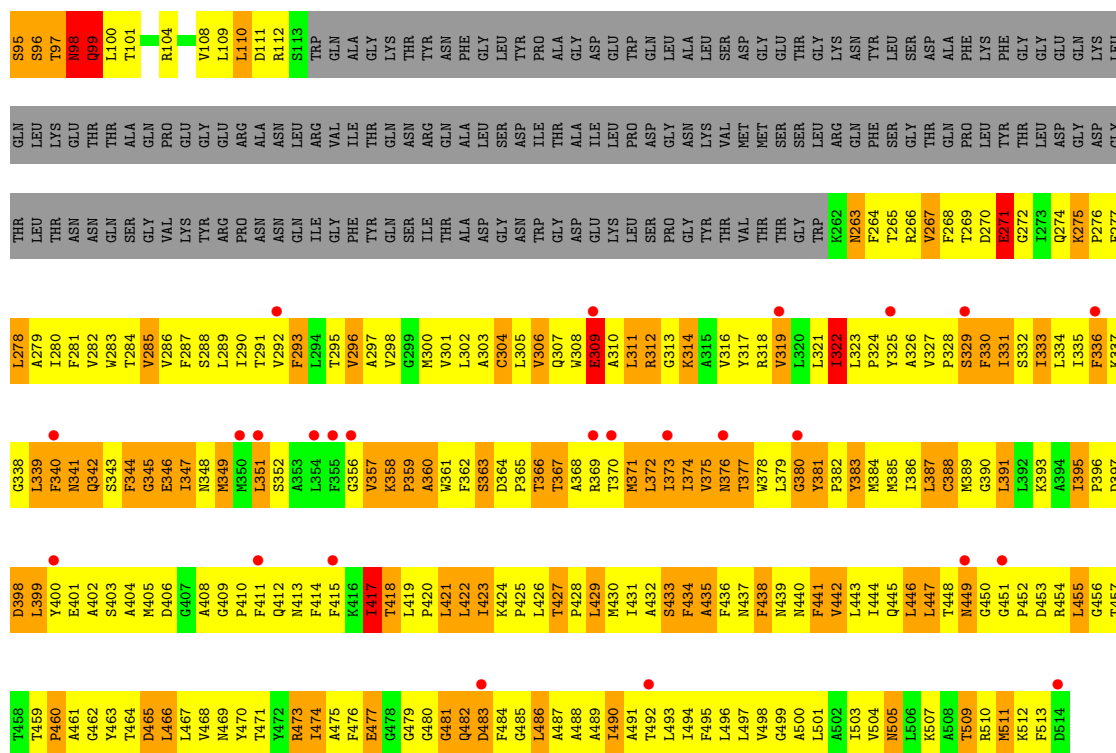
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Maltose transport system permease protein malF

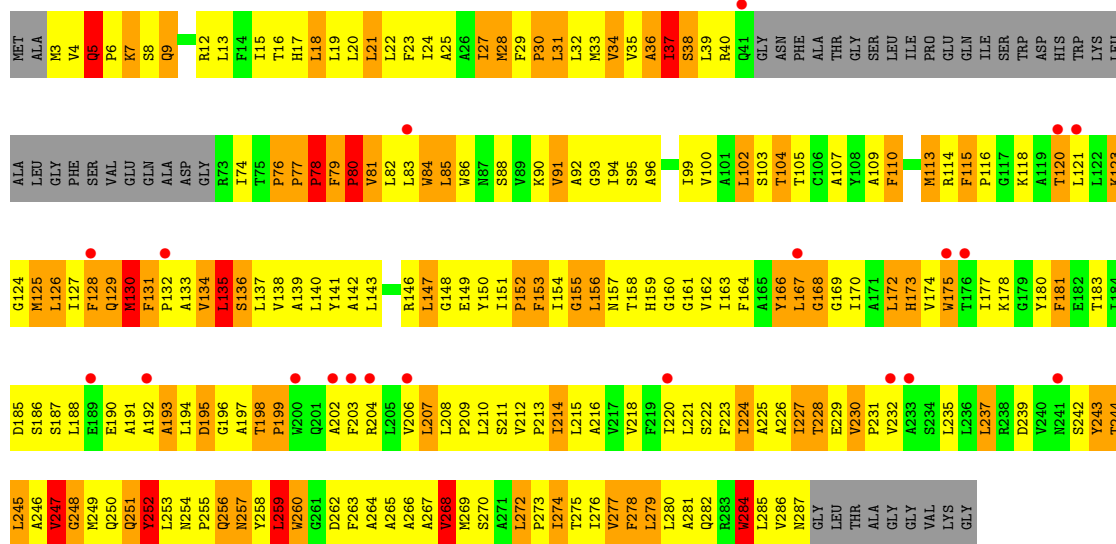
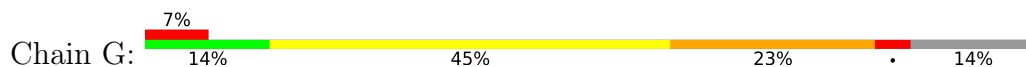


- Molecule 1: Maltose transport system permease protein malF

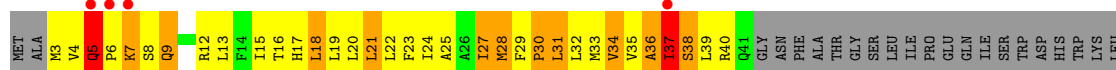
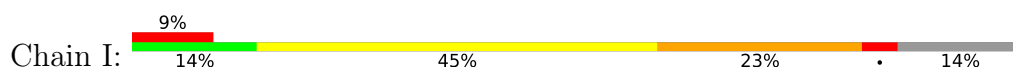


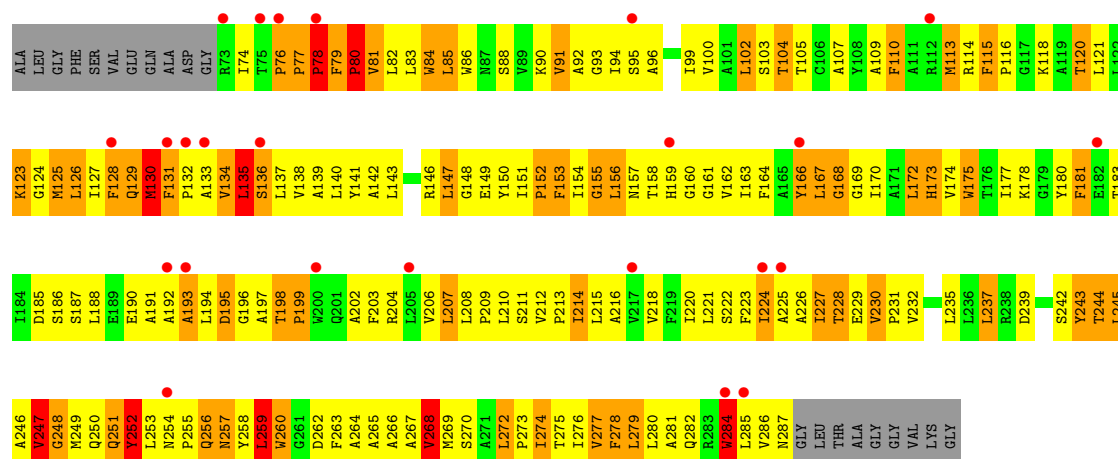


• Molecule 2: Maltose transport system permease protein malG

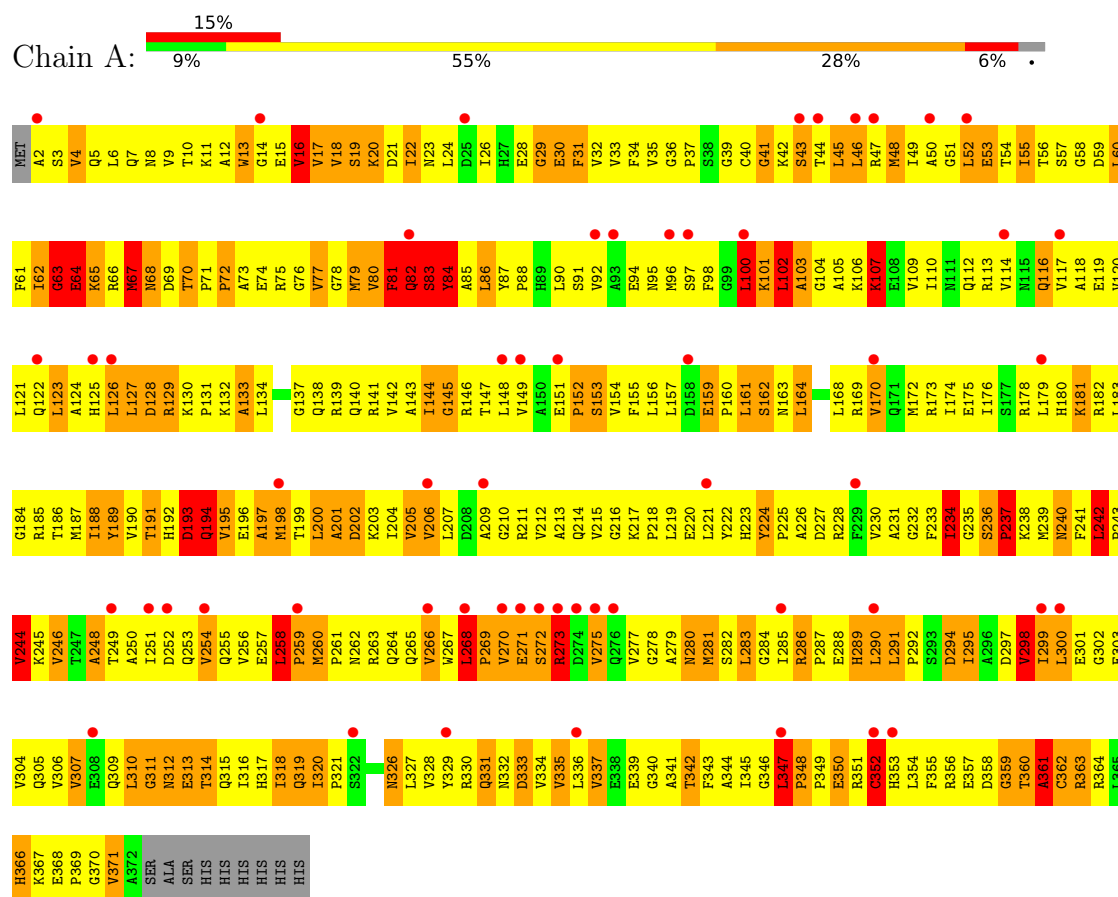


• Molecule 2: Maltose transport system permease protein malG

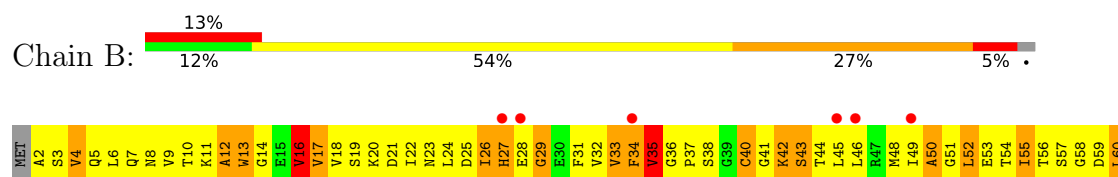


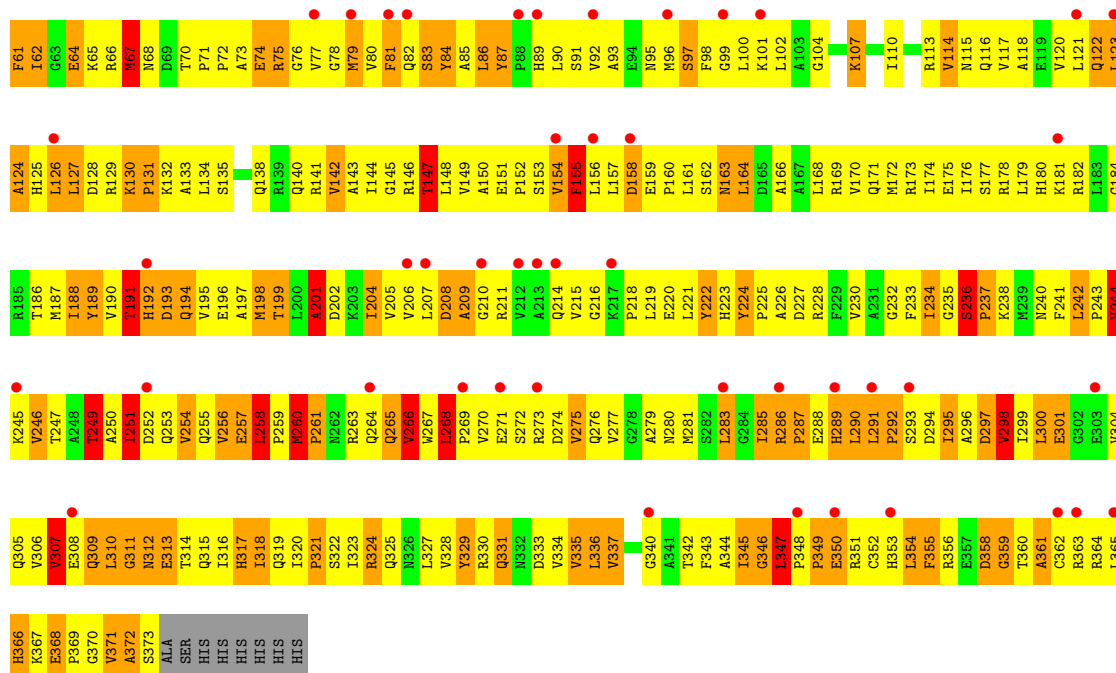


• Molecule 3: Maltose/maltodextrin import ATP-binding protein malK

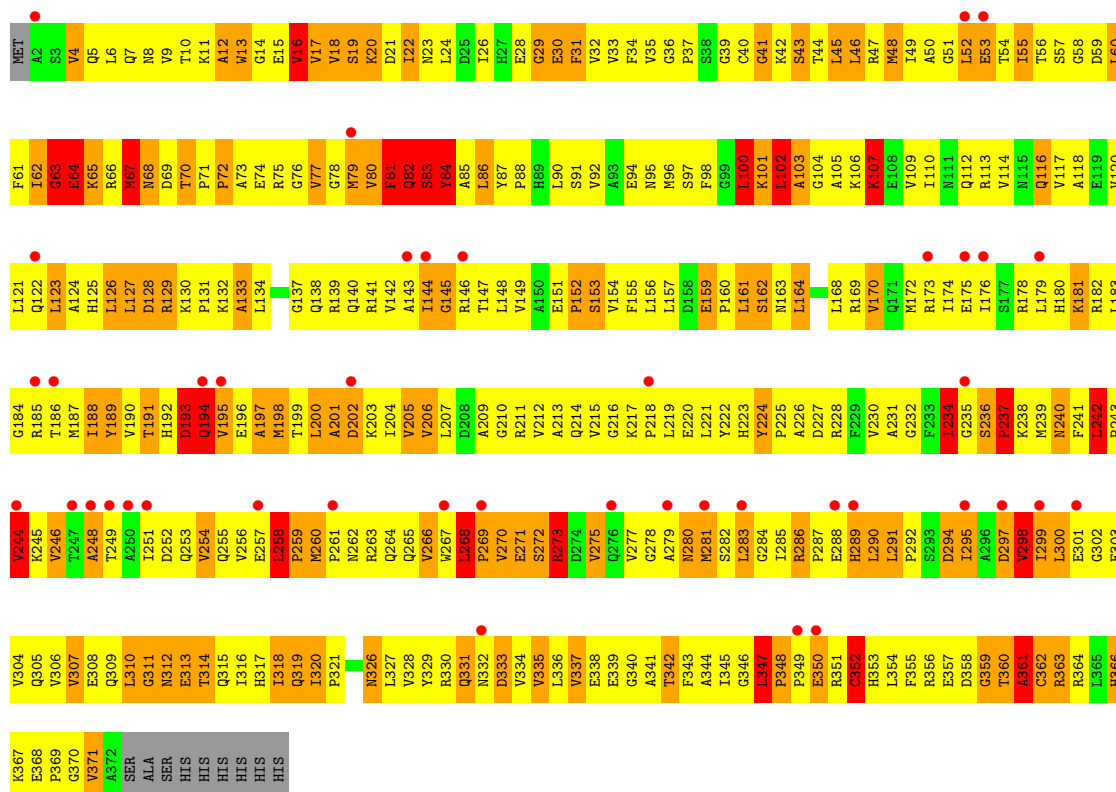
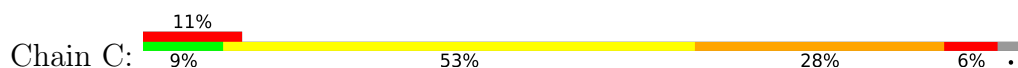


• Molecule 3: Maltose/maltodextrin import ATP-binding protein malK

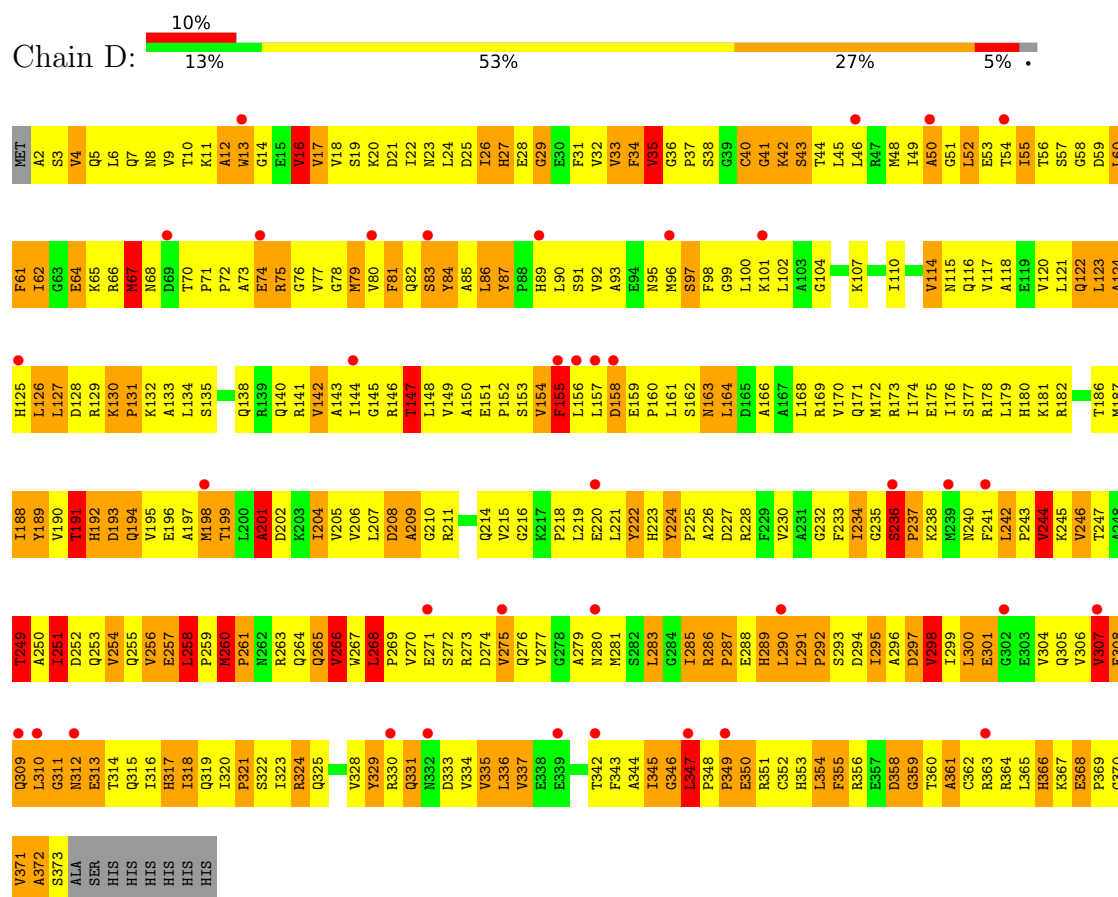




• Molecule 3: Maltose/maltodextrin import ATP-binding protein malK



• Molecule 3: Maltose/maltodextrin import ATP-binding protein malK



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	171.10Å 209.48Å 438.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.50 50.00 – 4.50	Depositor EDS
% Data completeness (in resolution range)	85.2 (50.00-4.50) 85.1 (50.00-4.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 4.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.340 , 0.363 0.354 , 0.369	Depositor DCC
R_{free} test set	2038 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	216.6	Xtriage
Anisotropy	0.633	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 228.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	20236	wwPDB-VP
Average B, all atoms (Å ²)	300.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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	F	0.66	0/2473	1.36	40/3365 (1.2%)
1	H	0.66	0/2473	1.36	40/3365 (1.2%)
2	G	0.68	0/1992	1.47	41/2724 (1.5%)
2	I	0.68	0/1992	1.47	41/2724 (1.5%)
3	A	0.62	0/2926	1.41	56/3968 (1.4%)
3	B	0.63	0/2932	1.46	52/3976 (1.3%)
3	C	0.62	0/2926	1.42	56/3968 (1.4%)
3	D	0.63	0/2932	1.46	53/3976 (1.3%)
All	All	0.64	0/20646	1.43	379/28066 (1.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	0	1
3	C	0	1
All	All	0	2

There are no bond length outliers.

All (379) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	236	SER	CA-C-N	-16.10	104.75	120.21
3	D	236	SER	C-N-CA	-16.10	104.75	120.21
3	B	236	SER	CA-C-N	-16.10	104.76	120.21
3	B	236	SER	C-N-CA	-16.10	104.76	120.21
3	D	347	LEU	CA-C-N	-12.73	107.27	120.38
3	D	347	LEU	C-N-CA	-12.73	107.27	120.38
3	B	347	LEU	CA-C-N	-12.72	107.28	120.38
3	B	347	LEU	C-N-CA	-12.72	107.28	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	99	GLN	N-CA-C	-12.64	97.49	111.14
1	H	99	GLN	N-CA-C	-12.63	97.50	111.14
3	C	200	LEU	N-CA-C	12.57	124.67	110.97
3	A	294	ASP	N-CA-C	12.28	124.66	111.03
3	A	200	LEU	N-CA-C	12.27	124.65	111.03
3	C	294	ASP	N-CA-C	12.27	124.64	111.03
1	F	95	SER	N-CA-C	-12.22	98.00	111.07
1	H	95	SER	N-CA-C	-12.21	98.00	111.07
2	G	136	SER	N-CA-C	-11.74	98.48	111.28
2	I	136	SER	N-CA-C	-11.71	98.52	111.28
2	G	186	SER	N-CA-C	11.41	123.69	111.03
2	I	186	SER	N-CA-C	11.38	123.67	111.03
3	C	201	ALA	N-CA-C	11.02	125.33	110.35
3	A	201	ALA	N-CA-C	11.00	125.31	110.35
2	G	207	LEU	N-CA-C	10.38	122.34	111.14
2	I	207	LEU	N-CA-C	10.37	122.33	111.14
1	H	380	GLY	N-CA-C	10.25	129.24	113.86
1	F	380	GLY	N-CA-C	10.25	129.23	113.86
3	B	154	VAL	N-CA-C	10.19	122.37	106.88
3	D	154	VAL	N-CA-C	10.16	122.32	106.88
3	D	216	GLY	N-CA-C	10.03	122.90	110.96
3	B	216	GLY	N-CA-C	10.03	122.89	110.96
3	A	41	GLY	N-CA-C	-9.71	101.80	115.30
2	I	79	PHE	CA-C-N	9.71	131.98	119.84
2	I	79	PHE	C-N-CA	9.71	131.98	119.84
3	C	41	GLY	N-CA-C	-9.71	101.80	115.30
2	G	79	PHE	CA-C-N	9.70	131.97	119.84
2	G	79	PHE	C-N-CA	9.70	131.97	119.84
3	C	81	PHE	N-CA-C	9.61	122.23	110.41
2	G	196	GLY	N-CA-C	9.58	129.66	114.90
2	I	196	GLY	N-CA-C	9.58	129.66	114.90
3	A	81	PHE	N-CA-C	9.58	122.19	110.41
2	G	77	PRO	N-CA-C	9.44	122.21	110.70
2	I	77	PRO	N-CA-C	9.44	122.21	110.70
3	C	164	LEU	N-CA-C	9.11	120.72	107.88
3	A	164	LEU	N-CA-C	9.10	120.72	107.88
2	G	259	LEU	N-CA-C	-9.06	91.50	110.80
2	I	259	LEU	N-CA-C	-9.06	91.51	110.80
2	I	39	LEU	N-CA-C	8.88	123.71	111.55
2	G	39	LEU	N-CA-C	8.85	123.68	111.55
2	I	248	GLY	N-CA-C	8.85	123.35	112.73
2	G	248	GLY	N-CA-C	8.83	123.32	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	283	LEU	N-CA-C	8.79	122.70	108.63
3	A	283	LEU	N-CA-C	8.77	122.67	108.63
2	I	260	TRP	N-CA-C	-8.77	101.72	111.28
2	G	260	TRP	N-CA-C	-8.73	101.76	111.28
3	A	100	LEU	N-CA-C	8.69	120.44	110.97
3	C	100	LEU	N-CA-C	8.65	120.40	110.97
3	B	81	PHE	N-CA-C	8.63	121.02	110.41
3	D	81	PHE	N-CA-C	8.62	121.01	110.41
1	F	442	VAL	N-CA-C	8.61	119.40	110.36
1	H	442	VAL	N-CA-C	8.61	119.40	110.36
1	H	329	SER	N-CA-C	-8.59	100.92	111.40
1	F	329	SER	N-CA-C	-8.59	100.92	111.40
2	G	245	LEU	N-CA-C	-8.50	101.94	111.71
2	I	245	LEU	N-CA-C	-8.48	101.96	111.71
3	B	283	LEU	N-CA-C	8.45	122.77	108.23
3	D	283	LEU	N-CA-C	8.44	122.75	108.23
1	H	322	ILE	N-CA-C	8.43	118.52	110.42
1	F	322	ILE	N-CA-C	8.43	118.51	110.42
3	C	151	GLU	CA-C-N	8.40	130.34	119.84
3	C	151	GLU	C-N-CA	8.40	130.34	119.84
3	A	151	GLU	CA-C-N	8.38	130.31	119.84
3	A	151	GLU	C-N-CA	8.38	130.31	119.84
2	G	257	ASN	N-CA-C	8.36	120.69	110.91
2	I	257	ASN	N-CA-C	8.34	120.67	110.91
3	D	286	ARG	CA-C-N	8.31	128.00	119.19
3	D	286	ARG	C-N-CA	8.31	128.00	119.19
3	B	336	LEU	N-CA-C	-8.30	99.44	110.24
3	B	286	ARG	CA-C-N	8.29	127.98	119.19
3	B	286	ARG	C-N-CA	8.29	127.98	119.19
3	D	336	LEU	N-CA-C	-8.29	99.47	110.24
1	H	495	PHE	N-CA-C	8.22	119.93	110.97
1	F	495	PHE	N-CA-C	8.21	119.92	110.97
2	G	76	PRO	CA-C-N	8.05	128.68	120.38
2	G	76	PRO	C-N-CA	8.05	128.68	120.38
2	I	76	PRO	CA-C-N	8.05	128.67	120.38
2	I	76	PRO	C-N-CA	8.05	128.67	120.38
3	C	258	LEU	CA-C-N	8.01	128.09	119.28
3	C	258	LEU	C-N-CA	8.01	128.09	119.28
3	A	258	LEU	CA-C-N	8.00	128.08	119.28
3	A	258	LEU	C-N-CA	8.00	128.08	119.28
3	D	164	LEU	N-CA-C	7.99	119.17	108.38
3	B	164	LEU	N-CA-C	7.99	119.17	108.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	76	PRO	N-CA-C	7.98	120.43	110.70
2	I	76	PRO	N-CA-C	7.97	120.42	110.70
3	C	194	GLN	N-CA-C	-7.80	98.57	111.37
3	A	194	GLN	N-CA-C	-7.80	98.58	111.37
3	C	144	ILE	N-CA-C	-7.78	101.76	110.62
3	D	128	ASP	N-CA-C	7.77	119.53	111.14
3	B	128	ASP	N-CA-C	7.76	119.52	111.14
3	A	144	ILE	N-CA-C	-7.75	101.79	110.62
3	B	201	ALA	N-CA-C	7.70	127.21	110.80
3	D	201	ALA	N-CA-C	7.70	127.21	110.80
3	B	74	GLU	N-CA-C	7.63	119.23	111.07
3	D	74	GLU	N-CA-C	7.63	119.23	111.07
2	I	247	VAL	N-CA-C	7.62	117.58	110.42
2	G	247	VAL	N-CA-C	7.60	117.56	110.42
2	G	173	HIS	N-CA-C	7.59	119.19	111.07
1	H	511	MET	N-CA-C	7.58	117.89	107.73
1	F	511	MET	N-CA-C	7.57	117.88	107.73
2	I	173	HIS	N-CA-C	7.57	119.17	111.07
3	C	361	ALA	N-CA-C	7.54	126.85	110.80
3	A	361	ALA	N-CA-C	7.53	126.84	110.80
3	A	289	HIS	N-CA-C	7.39	119.41	111.36
3	C	68	ASN	N-CA-C	-7.39	103.23	111.28
3	C	289	HIS	N-CA-C	7.38	119.41	111.36
1	F	482	GLN	N-CA-C	-7.35	103.26	111.28
3	D	237	PRO	N-CA-C	-7.33	100.96	111.22
1	H	482	GLN	N-CA-C	-7.32	103.30	111.28
3	B	237	PRO	N-CA-C	-7.31	100.98	111.22
3	B	163	ASN	N-CA-C	7.25	120.92	109.39
3	D	163	ASN	N-CA-C	7.25	120.92	109.39
2	I	274	ILE	N-CA-C	7.25	117.33	110.30
2	G	274	ILE	N-CA-C	7.22	117.31	110.30
3	D	155	PHE	N-CA-C	7.11	121.52	108.58
3	B	155	PHE	N-CA-C	7.10	121.51	108.58
3	A	291	LEU	CA-C-N	7.10	128.71	119.84
3	A	291	LEU	C-N-CA	7.10	128.71	119.84
3	A	79	MET	N-CA-C	7.07	117.85	107.88
3	C	291	LEU	CA-C-N	7.06	128.67	119.84
3	C	291	LEU	C-N-CA	7.06	128.67	119.84
3	C	79	MET	N-CA-C	7.06	117.83	107.88
2	I	78	PRO	N-CA-CB	7.04	110.64	103.25
2	G	78	PRO	N-CA-CB	7.04	110.64	103.25
3	D	346	GLY	N-CA-C	7.02	125.00	111.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	346	GLY	N-CA-C	7.02	125.00	111.31
3	A	202	ASP	N-CA-C	-6.99	103.74	111.36
3	C	202	ASP	N-CA-C	-6.98	103.75	111.36
3	A	360	THR	N-CA-C	6.97	119.32	110.33
3	A	20	LYS	N-CA-C	6.97	121.26	108.58
3	C	360	THR	N-CA-C	6.97	119.32	110.33
3	C	20	LYS	N-CA-C	6.96	121.25	108.58
3	C	273	ARG	N-CA-C	-6.87	101.31	110.24
3	A	273	ARG	N-CA-C	-6.85	101.34	110.24
1	H	80	LEU	N-CA-C	6.76	118.30	111.07
1	F	80	LEU	N-CA-C	6.72	118.26	111.07
3	A	68	ASN	N-CA-C	-6.68	103.25	111.33
2	I	244	THR	N-CA-C	-6.67	100.59	110.46
2	G	244	THR	N-CA-C	-6.66	100.61	110.46
1	H	477	GLU	N-CA-C	-6.65	103.13	110.91
3	C	326	ASN	N-CA-C	-6.65	101.17	110.35
1	F	477	GLU	N-CA-C	-6.65	103.13	110.91
3	B	50	ALA	N-CA-C	-6.64	103.73	110.97
3	A	326	ASN	N-CA-C	-6.63	101.20	110.35
3	D	50	ALA	N-CA-C	-6.62	103.75	110.97
3	B	42	LYS	N-CA-C	-6.62	103.32	111.33
3	D	42	LYS	N-CA-C	-6.60	103.34	111.33
3	C	98	PHE	N-CA-C	6.51	118.07	110.97
3	A	98	PHE	N-CA-C	6.50	118.06	110.97
2	G	193	ALA	N-CA-C	-6.47	103.50	111.33
1	F	372	LEU	N-CA-C	6.47	117.99	111.07
2	I	193	ALA	N-CA-C	-6.46	103.51	111.33
2	G	77	PRO	N-CA-CB	6.45	109.34	103.08
1	H	372	LEU	N-CA-C	6.45	117.97	111.07
2	I	77	PRO	N-CA-CB	6.45	109.34	103.08
1	H	70	PRO	N-CA-CB	6.44	110.17	103.15
3	B	361	ALA	N-CA-C	6.44	120.55	110.32
1	F	70	PRO	N-CA-CB	6.42	110.15	103.15
1	F	429	LEU	N-CA-C	6.42	118.16	111.03
3	D	361	ALA	N-CA-C	6.40	120.50	110.32
1	H	429	LEU	N-CA-C	6.40	118.13	111.03
1	F	387	LEU	N-CA-C	-6.39	104.00	110.97
1	F	417	ILE	N-CA-C	6.39	122.63	109.34
1	H	417	ILE	N-CA-C	6.39	122.62	109.34
3	D	54	THR	N-CA-C	6.38	119.93	110.48
1	H	387	LEU	N-CA-C	-6.38	104.02	110.97
3	B	54	THR	N-CA-C	6.38	119.92	110.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	129	GLN	N-CA-C	6.37	118.02	111.14
2	I	129	GLN	N-CA-C	6.33	117.98	111.14
1	F	44	ILE	N-CA-C	6.30	116.41	110.30
1	H	427	THR	N-CA-C	6.30	122.09	113.77
1	H	446	LEU	N-CA-C	6.30	118.14	111.28
1	F	446	LEU	N-CA-C	6.29	118.14	111.28
3	A	234	ILE	N-CA-C	6.29	122.42	109.34
3	C	234	ILE	N-CA-C	6.29	122.42	109.34
1	F	427	THR	N-CA-C	6.27	122.05	113.77
1	H	418	THR	N-CA-C	6.27	118.64	111.11
1	H	44	ILE	N-CA-C	6.26	116.37	110.30
3	D	317	HIS	N-CA-C	-6.25	102.11	110.55
1	F	418	THR	N-CA-C	6.25	118.61	111.11
3	B	305	GLN	N-CA-C	6.25	121.03	112.04
3	D	305	GLN	N-CA-C	6.25	121.03	112.04
3	B	317	HIS	N-CA-C	-6.24	102.12	110.55
2	I	5	GLN	CA-C-N	6.23	125.64	118.85
2	I	5	GLN	C-N-CA	6.23	125.64	118.85
2	G	5	GLN	CA-C-N	6.23	125.64	118.85
2	G	5	GLN	C-N-CA	6.23	125.64	118.85
3	C	159	GLU	N-CA-C	6.19	123.49	109.81
3	A	159	GLU	N-CA-C	6.19	123.48	109.81
1	H	109	LEU	N-CA-C	6.17	117.80	111.14
3	A	286	ARG	CA-C-N	6.14	125.55	118.85
3	A	286	ARG	C-N-CA	6.14	125.55	118.85
1	F	109	LEU	N-CA-C	6.13	117.76	111.14
3	B	251	ILE	N-CA-C	6.09	122.00	109.34
3	C	286	ARG	CA-C-N	6.08	125.48	118.85
3	C	286	ARG	C-N-CA	6.08	125.48	118.85
3	D	251	ILE	N-CA-C	6.07	121.97	109.34
2	G	120	THR	N-CA-C	6.06	117.56	111.07
2	I	120	THR	N-CA-C	6.05	117.54	111.07
1	F	360	ALA	N-CA-C	6.01	119.52	108.58
1	H	341	ASN	N-CA-C	-6.00	102.61	110.53
1	H	360	ALA	N-CA-C	5.99	119.48	108.58
1	F	341	ASN	N-CA-C	-5.98	102.63	110.53
3	B	124	ALA	N-CA-C	-5.98	104.33	111.69
3	D	258	LEU	CA-C-N	5.98	127.32	119.84
3	D	258	LEU	C-N-CA	5.98	127.32	119.84
2	G	76	PRO	N-CA-CB	5.97	108.87	103.08
1	H	435	ALA	N-CA-C	-5.97	103.95	111.11
1	F	435	ALA	N-CA-C	-5.97	103.95	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	258	LEU	CA-C-N	5.96	127.29	119.84
3	B	258	LEU	C-N-CA	5.96	127.29	119.84
3	D	124	ALA	N-CA-C	-5.96	104.36	111.69
1	F	359	PRO	N-CA-C	5.95	124.72	112.47
1	H	359	PRO	N-CA-C	5.94	124.71	112.47
3	A	248	ALA	N-CA-C	5.93	116.11	108.34
3	C	248	ALA	N-CA-C	5.93	116.11	108.34
2	I	76	PRO	N-CA-CB	5.93	108.83	103.08
2	I	123	LYS	N-CA-C	-5.92	104.00	111.11
3	C	242	LEU	CA-C-N	5.92	127.23	119.84
3	C	242	LEU	C-N-CA	5.92	127.23	119.84
3	A	242	LEU	CA-C-N	5.90	127.22	119.84
3	A	242	LEU	C-N-CA	5.90	127.22	119.84
3	C	209	ALA	N-CA-C	-5.89	103.28	111.52
2	G	123	LYS	N-CA-C	-5.89	104.04	111.11
3	B	209	ALA	N-CA-C	-5.89	103.33	111.28
3	A	209	ALA	N-CA-C	-5.88	103.29	111.52
3	D	209	ALA	N-CA-C	-5.87	103.36	111.28
2	I	243	TYR	N-CA-C	-5.85	103.22	110.41
2	G	243	TYR	N-CA-C	-5.84	103.22	110.41
3	D	249	THR	N-CA-C	5.84	117.02	108.14
3	B	249	THR	N-CA-C	5.83	117.00	108.14
3	D	268	LEU	CA-C-N	5.82	127.11	119.84
3	D	268	LEU	C-N-CA	5.82	127.11	119.84
3	B	268	LEU	CA-C-N	5.81	127.10	119.84
3	B	268	LEU	C-N-CA	5.81	127.10	119.84
2	I	110	PHE	N-CA-C	5.78	118.06	111.02
1	F	44	ILE	CB-CA-C	-5.76	104.61	111.81
1	H	44	ILE	CB-CA-C	-5.76	104.61	111.81
2	G	110	PHE	N-CA-C	5.76	118.04	111.02
2	G	279	LEU	N-CA-C	5.75	117.22	111.07
2	I	279	LEU	N-CA-C	5.74	117.21	111.07
2	I	34	VAL	N-CA-C	-5.69	104.13	110.62
2	G	34	VAL	N-CA-C	-5.69	104.13	110.62
1	F	278	LEU	N-CA-C	5.68	117.47	111.28
2	I	80	PRO	N-CA-C	5.67	124.16	112.47
2	G	80	PRO	N-CA-C	5.67	124.14	112.47
1	H	278	LEU	N-CA-C	5.63	117.42	111.28
3	A	259	PRO	N-CA-C	5.62	121.24	113.65
3	B	222	TYR	N-CA-C	5.62	117.10	110.97
3	C	259	PRO	N-CA-C	5.62	121.24	113.65
3	D	222	TYR	N-CA-C	5.62	117.09	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	122	GLN	N-CA-C	-5.61	103.71	111.28
3	D	265	GLN	N-CA-C	-5.60	103.10	110.33
3	B	265	GLN	N-CA-C	-5.60	103.11	110.33
3	D	122	GLN	N-CA-C	-5.60	103.72	111.28
3	A	268	LEU	CA-C-N	5.58	126.81	119.84
3	A	268	LEU	C-N-CA	5.58	126.81	119.84
3	C	268	LEU	CA-C-N	5.56	126.80	119.84
3	C	268	LEU	C-N-CA	5.56	126.80	119.84
2	G	232	VAL	N-CA-C	5.55	115.75	110.42
2	I	232	VAL	N-CA-C	5.54	115.74	110.42
3	D	258	LEU	N-CA-C	5.54	116.80	109.93
2	G	251	GLN	N-CA-C	5.53	120.50	111.37
3	B	258	LEU	N-CA-C	5.52	116.78	109.93
1	H	438	PHE	N-CA-C	-5.52	104.28	111.02
3	C	83	SER	N-CA-C	-5.52	99.05	110.80
3	C	271	GLU	N-CA-C	5.51	117.09	111.14
3	A	83	SER	N-CA-C	-5.51	99.06	110.80
2	I	251	GLN	N-CA-C	5.51	120.46	111.37
1	F	438	PHE	N-CA-C	-5.51	104.30	111.02
1	F	339	LEU	N-CA-C	-5.50	104.14	111.24
3	A	271	GLU	N-CA-C	5.50	117.08	111.14
1	H	339	LEU	N-CA-C	-5.50	104.14	111.24
3	D	287	PRO	N-CA-C	-5.50	106.37	113.57
3	C	39	GLY	N-CA-C	-5.49	105.81	114.10
3	A	282	SER	N-CA-C	5.49	116.40	107.23
3	A	39	GLY	N-CA-C	-5.49	105.81	114.10
3	B	287	PRO	N-CA-C	-5.49	106.38	113.57
3	C	282	SER	N-CA-C	5.49	116.39	107.23
3	A	63	GLY	N-CA-C	-5.49	100.18	113.18
3	C	63	GLY	N-CA-C	-5.48	100.18	113.18
3	C	170	VAL	N-CA-C	5.46	115.59	110.30
3	A	170	VAL	N-CA-C	5.45	115.58	110.30
3	C	137	GLY	N-CA-C	5.43	119.06	112.49
3	A	137	GLY	N-CA-C	5.43	119.06	112.49
3	A	320	ILE	CA-C-N	-5.42	114.12	119.92
3	A	320	ILE	C-N-CA	-5.42	114.12	119.92
1	H	358	LYS	CA-C-N	5.41	126.61	119.84
1	H	358	LYS	C-N-CA	5.41	126.61	119.84
3	C	320	ILE	CA-C-N	-5.41	114.14	119.92
3	C	320	ILE	C-N-CA	-5.41	114.14	119.92
1	F	358	LYS	CA-C-N	5.40	126.59	119.84
1	F	358	LYS	C-N-CA	5.40	126.59	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	268	VAL	N-CA-C	-5.39	104.62	110.23
2	I	268	VAL	N-CA-C	-5.39	104.62	110.23
3	B	261	PRO	N-CA-C	5.38	121.77	113.75
3	C	128	ASP	N-CA-C	5.38	117.22	111.36
3	B	147	THR	N-CA-C	-5.38	104.66	111.11
3	A	128	ASP	N-CA-C	5.37	117.22	111.36
3	D	147	THR	N-CA-C	-5.37	104.67	111.11
1	H	433	SER	N-CA-C	-5.37	105.43	111.28
3	D	261	PRO	N-CA-C	5.37	121.74	113.75
1	F	386	ILE	N-CA-C	5.34	115.55	110.42
1	F	433	SER	N-CA-C	-5.34	105.45	111.28
3	D	199	THR	N-CA-C	5.34	117.54	111.02
3	B	289	HIS	N-CA-C	5.33	120.44	113.88
1	H	386	ILE	N-CA-C	5.33	115.54	110.42
2	I	166	TYR	N-CA-C	5.33	117.09	111.28
3	D	289	HIS	N-CA-C	5.31	120.42	113.88
3	B	199	THR	N-CA-C	5.30	117.49	111.02
3	D	291	LEU	CA-C-N	5.30	126.47	119.84
3	D	291	LEU	C-N-CA	5.30	126.47	119.84
3	C	181	LYS	N-CA-C	-5.30	104.91	111.33
2	G	166	TYR	N-CA-C	5.30	117.05	111.28
3	A	181	LYS	N-CA-C	-5.27	104.95	111.33
3	C	272	SER	N-CA-C	5.25	121.99	110.80
3	C	352	CYS	N-CA-C	5.25	121.98	110.80
3	B	291	LEU	CA-C-N	5.25	126.40	119.84
3	B	291	LEU	C-N-CA	5.25	126.40	119.84
2	G	195	ASP	N-CA-C	5.24	120.33	113.20
3	A	272	SER	N-CA-C	5.24	121.96	110.80
3	A	352	CYS	N-CA-C	5.24	121.96	110.80
2	I	195	ASP	N-CA-C	5.24	120.32	113.20
3	B	67	MET	N-CA-C	5.22	121.92	110.80
1	H	68	VAL	N-CA-C	5.21	115.43	110.53
1	H	395	ILE	CA-C-N	5.21	126.35	119.84
1	H	395	ILE	C-N-CA	5.21	126.35	119.84
3	A	62	ILE	N-CA-C	-5.21	100.35	107.75
3	D	67	MET	N-CA-C	5.21	121.89	110.80
3	A	82	GLN	N-CA-C	-5.20	105.61	111.28
3	C	62	ILE	N-CA-C	-5.20	100.37	107.75
1	F	68	VAL	N-CA-C	5.20	115.41	110.53
1	H	441	PHE	N-CA-C	5.19	117.35	111.02
1	F	395	ILE	CA-C-N	5.19	126.32	119.84
1	F	395	ILE	C-N-CA	5.19	126.32	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	490	ILE	N-CA-C	5.18	115.40	110.42
3	C	107	LYS	N-CA-C	5.17	117.32	111.11
1	H	306	VAL	CB-CA-C	-5.17	105.08	111.70
1	F	306	VAL	CB-CA-C	-5.17	105.08	111.70
1	F	441	PHE	N-CA-C	5.16	117.32	111.02
3	C	82	GLN	N-CA-C	-5.16	105.65	111.28
1	F	490	ILE	N-CA-C	5.16	115.37	110.42
3	A	107	LYS	N-CA-C	5.16	117.30	111.11
3	C	145	GLY	N-CA-C	5.12	120.54	113.99
3	A	145	GLY	N-CA-C	5.12	120.54	113.99
1	H	473	ARG	N-CA-C	5.12	116.55	110.97
1	F	473	ARG	N-CA-C	5.11	116.53	110.97
2	I	102	LEU	N-CA-C	5.11	116.65	111.14
3	D	114	VAL	N-CA-C	5.09	115.24	110.30
3	B	114	VAL	N-CA-C	5.09	115.24	110.30
2	G	102	LEU	N-CA-C	5.09	116.64	111.14
3	B	130	LYS	CA-C-N	5.09	126.20	119.84
3	B	130	LYS	C-N-CA	5.09	126.20	119.84
3	A	314	THR	N-CA-C	-5.08	101.40	108.96
3	C	314	THR	N-CA-C	-5.07	101.40	108.96
3	B	40	CYS	N-CA-C	-5.07	105.75	111.28
3	A	298	VAL	N-CA-C	5.06	119.87	109.34
3	C	298	VAL	N-CA-C	5.05	119.85	109.34
3	D	130	LYS	CA-C-N	5.05	126.16	119.84
3	D	130	LYS	C-N-CA	5.05	126.16	119.84
3	B	191	THR	N-CA-C	5.05	121.55	110.80
3	D	191	THR	N-CA-C	5.04	121.53	110.80
3	D	40	CYS	N-CA-C	-5.04	105.79	111.28
3	D	296	ALA	N-CA-C	5.03	116.60	110.41
2	G	134	VAL	N-CA-C	-5.02	102.62	109.55
3	D	319	GLN	N-CA-C	5.01	116.65	108.63
3	B	319	GLN	N-CA-C	5.01	116.65	108.63
3	B	296	ALA	N-CA-C	5.01	116.57	110.41
2	I	134	VAL	N-CA-C	-5.00	102.65	109.55
3	D	41	GLY	N-CA-C	-5.00	106.18	114.48

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	84	TYR	Sidechain
3	C	84	TYR	Sidechain

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	F	2418	0	2476	572	0
1	H	2418	0	2476	573	0
2	G	1942	0	2008	379	0
2	I	1942	0	2008	382	0
3	A	2876	0	2942	609	15
3	B	2882	0	2947	582	12
3	C	2876	0	2942	598	9
3	D	2882	0	2947	574	5
All	All	20236	0	20746	4050	31

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 (4050) 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:F:347:ILE:HG23	1:F:348:ASN:H	1.03	1.15
3:D:157:LEU:HD23	3:D:160:PRO:HG3	1.30	1.13
1:F:275:LYS:H	1:F:276:PRO:HD2	1.07	1.13
1:F:387:LEU:HD21	1:F:429:LEU:HD13	1.29	1.12
3:C:79:MET:HG2	3:C:80:VAL:H	1.14	1.12
1:H:284:THR:HG22	1:H:466:LEU:HA	1.16	1.12
3:A:40:CYS:HB2	3:A:42:LYS:HG3	1.27	1.12
1:H:486:LEU:HD22	2:I:135:LEU:HD21	1.14	1.12
3:D:301:GLU:HA	3:D:344:ALA:HB2	1.28	1.11
3:B:157:LEU:HD23	3:B:160:PRO:HG3	1.30	1.11
1:F:100:LEU:HB3	1:F:104:ARG:HG3	1.31	1.11
1:F:328:PRO:HD3	2:G:274:ILE:HG12	1.29	1.11
3:A:144:ILE:HG22	3:A:148:LEU:HD11	1.32	1.11
1:H:328:PRO:HD3	2:I:274:ILE:HG12	1.29	1.10
1:H:490:ILE:HG12	2:I:135:LEU:HD23	1.33	1.10
1:F:486:LEU:HD22	2:G:135:LEU:HD21	1.14	1.10
1:H:100:LEU:HB3	1:H:104:ARG:HG3	1.31	1.10
1:H:347:ILE:HG23	1:H:348:ASN:H	1.03	1.10
2:I:188:LEU:H	2:I:188:LEU:HD12	1.17	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:275:LYS:H	1:H:276:PRO:HD2	1.07	1.09
3:C:144:ILE:HG22	3:C:148:LEU:HD11	1.32	1.08
3:B:301:GLU:HA	3:B:344:ALA:HB2	1.28	1.08
1:F:490:ILE:HG12	2:G:135:LEU:HD23	1.33	1.08
1:F:284:THR:HG22	1:F:466:LEU:HA	1.16	1.08
3:C:40:CYS:HB2	3:C:42:LYS:HG3	1.27	1.08
1:H:387:LEU:HD21	1:H:429:LEU:HD13	1.29	1.07
1:F:357:VAL:HG12	1:F:358:LYS:H	1.13	1.06
3:A:79:MET:HG2	3:A:80:VAL:H	1.14	1.06
1:H:357:VAL:HG12	1:H:358:LYS:H	1.13	1.05
3:A:117:VAL:O	3:A:120:VAL:HG22	1.56	1.05
2:G:188:LEU:H	2:G:188:LEU:HD12	1.16	1.04
3:C:317:HIS:O	3:C:318:ILE:HG13	1.55	1.04
3:A:317:HIS:O	3:A:318:ILE:HG13	1.55	1.04
3:C:117:VAL:O	3:C:120:VAL:HG22	1.56	1.04
1:F:373:ILE:HG13	1:F:374:ILE:H	1.23	1.03
3:D:44:THR:HG22	3:D:48:MET:HE2	1.39	1.03
3:B:44:THR:HG22	3:B:48:MET:HE2	1.39	1.03
1:H:373:ILE:HG13	1:H:374:ILE:H	1.23	1.03
3:A:315:GLN:HE21	3:A:330:ARG:HG2	1.25	1.02
3:C:84:TYR:HB3	3:C:86:LEU:HD21	1.39	1.02
3:D:204:ILE:HG22	3:D:205:VAL:H	1.23	1.02
3:C:315:GLN:HE21	3:C:330:ARG:HG2	1.25	1.01
3:B:298:VAL:HG11	3:B:347:LEU:HB3	1.42	1.01
1:H:100:LEU:HD22	1:H:104:ARG:HE	1.24	1.01
1:H:327:VAL:HA	2:I:274:ILE:HG21	1.43	1.01
3:D:298:VAL:HG11	3:D:347:LEU:HB3	1.42	1.01
1:F:373:ILE:HG13	1:F:374:ILE:N	1.76	1.01
3:B:226:ALA:HB3	3:B:230:VAL:HG21	1.39	1.01
3:A:42:LYS:HG2	3:A:207:LEU:HD12	1.42	1.00
3:C:42:LYS:HG2	3:C:207:LEU:HD12	1.42	1.00
3:A:225:PRO:HD2	3:A:353:HIS:NE2	1.77	1.00
1:H:348:ASN:HB3	1:H:358:LYS:HG3	1.41	1.00
2:I:31:LEU:HD23	2:I:31:LEU:H	1.25	1.00
1:F:391:LEU:HD21	1:F:425:PRO:HB2	1.43	1.00
1:F:327:VAL:HA	2:G:274:ILE:HG21	1.43	0.99
1:F:100:LEU:HD22	1:F:104:ARG:HE	1.24	0.99
3:A:84:TYR:HB3	3:A:86:LEU:HD21	1.39	0.99
1:H:391:LEU:HD21	1:H:425:PRO:HB2	1.43	0.99
3:D:226:ALA:HB3	3:D:230:VAL:HG21	1.39	0.99
2:G:195:ASP:HB2	3:A:102:LEU:HD23	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:204:ILE:HG22	3:B:205:VAL:H	1.23	0.99
3:D:368:GLU:HB3	3:D:369:PRO:HD2	1.43	0.99
3:A:183:LEU:HD22	3:A:185:ARG:HH12	1.26	0.99
3:B:368:GLU:HB3	3:B:369:PRO:HD2	1.43	0.99
3:C:225:PRO:HD2	3:C:353:HIS:NE2	1.77	0.99
1:F:348:ASN:HB3	1:F:358:LYS:HG3	1.41	0.99
1:F:497:LEU:HD13	2:G:132:PRO:HD3	1.45	0.99
2:I:115:PHE:HB2	2:I:116:PRO:HD2	1.42	0.99
1:H:341:ASN:ND2	1:H:344:PHE:HB2	1.78	0.98
2:G:115:PHE:HB2	2:G:116:PRO:HD2	1.42	0.98
1:H:497:LEU:HD13	2:I:132:PRO:HD3	1.45	0.98
3:D:34:PHE:O	3:D:35:VAL:HG13	1.64	0.98
2:G:31:LEU:HD23	2:G:31:LEU:H	1.25	0.98
2:I:255:PRO:HB2	2:I:259:LEU:HG	1.46	0.98
3:C:183:LEU:HD22	3:C:185:ARG:HH12	1.26	0.98
1:F:341:ASN:ND2	1:F:344:PHE:HB2	1.78	0.98
3:C:66:ARG:O	3:C:67:MET:HG2	1.63	0.98
3:B:34:PHE:O	3:B:35:VAL:HG13	1.64	0.98
3:B:243:PRO:HB2	3:B:259:PRO:HG3	1.43	0.98
3:D:260:MET:HB2	3:D:261:PRO:HD2	1.44	0.97
1:F:486:LEU:HD13	1:F:490:ILE:HD11	1.46	0.97
3:D:301:GLU:HA	3:D:344:ALA:CB	1.94	0.97
1:F:303:ALA:HA	1:F:385:MET:HE1	1.46	0.97
3:A:66:ARG:O	3:A:67:MET:HG2	1.63	0.97
3:A:368:GLU:HG2	3:A:369:PRO:HD2	1.47	0.97
1:H:346:GLU:HA	1:H:349:MET:HG3	1.46	0.96
3:A:223:HIS:O	3:A:225:PRO:HD3	1.64	0.96
3:B:260:MET:HB2	3:B:261:PRO:HD2	1.44	0.96
1:H:303:ALA:HA	1:H:385:MET:HE1	1.46	0.96
3:D:243:PRO:HB2	3:D:259:PRO:HG3	1.43	0.96
2:G:255:PRO:HB2	2:G:259:LEU:HG	1.46	0.96
3:C:368:GLU:HG2	3:C:369:PRO:HD2	1.47	0.96
3:B:301:GLU:HA	3:B:344:ALA:CB	1.94	0.96
3:B:356:ARG:HB2	3:B:358:ASP:OD1	1.66	0.96
1:F:347:ILE:CG2	1:F:348:ASN:H	1.80	0.95
2:I:195:ASP:HB2	3:C:102:LEU:HD23	1.44	0.95
3:C:223:HIS:O	3:C:225:PRO:HD3	1.64	0.95
3:D:91:SER:HA	3:D:131:PRO:HD3	1.46	0.95
3:B:46:LEU:HD11	3:B:156:LEU:HB3	1.47	0.95
1:H:486:LEU:HD13	1:H:490:ILE:HD11	1.46	0.94
3:C:96:MET:HB3	3:C:149:VAL:HG21	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:347:ILE:HG23	1:F:348:ASN:N	1.75	0.94
3:B:358:ASP:CG	3:B:359:GLY:H	1.75	0.94
3:D:356:ARG:HB2	3:D:358:ASP:OD1	1.66	0.94
2:G:158:THR:HG23	2:G:161:GLY:H	1.31	0.94
1:H:424:LYS:HZ1	1:H:511:MET:HE2	1.32	0.94
3:D:358:ASP:CG	3:D:359:GLY:H	1.75	0.94
3:B:189:TYR:HD2	3:B:190:VAL:N	1.65	0.94
3:A:96:MET:HB3	3:A:149:VAL:HG21	1.49	0.94
3:B:91:SER:HA	3:B:131:PRO:HD3	1.46	0.94
3:A:281:MET:HB3	3:A:354:LEU:HD11	1.49	0.94
1:H:347:ILE:CG2	1:H:348:ASN:H	1.80	0.94
1:H:410:PRO:HA	1:H:413:ASN:ND2	1.82	0.94
2:G:245:LEU:HG	2:G:249:MET:HE2	1.50	0.94
3:C:226:ALA:O	3:C:361:ALA:HB2	1.68	0.94
1:F:410:PRO:HA	1:F:413:ASN:ND2	1.82	0.94
3:D:189:TYR:HD2	3:D:190:VAL:N	1.65	0.93
2:I:245:LEU:HG	2:I:249:MET:HE2	1.50	0.93
3:D:46:LEU:HD11	3:D:156:LEU:HB3	1.47	0.93
1:F:284:THR:CG2	1:F:466:LEU:HA	1.97	0.93
3:A:70:THR:HG22	3:A:71:PRO:HD2	1.48	0.93
3:D:268:LEU:HD12	3:D:270:VAL:CG2	1.98	0.93
1:F:372:LEU:HD12	1:F:443:LEU:HD21	1.48	0.93
3:A:79:MET:HG2	3:A:80:VAL:N	1.83	0.93
3:B:268:LEU:HD12	3:B:270:VAL:CG2	1.97	0.93
3:A:109:VAL:HG12	3:A:113:ARG:HD2	1.50	0.93
3:B:204:ILE:HG22	3:B:205:VAL:N	1.84	0.93
3:D:320:ILE:HG23	3:D:321:PRO:HD2	1.50	0.93
1:F:346:GLU:HA	1:F:349:MET:HG3	1.46	0.92
3:C:109:VAL:HG12	3:C:113:ARG:HD2	1.50	0.92
3:D:40:CYS:SG	3:D:42:LYS:HG3	2.09	0.92
1:H:284:THR:CG2	1:H:466:LEU:HA	1.97	0.92
3:D:100:LEU:HD12	3:D:101:LYS:N	1.85	0.92
3:B:40:CYS:SG	3:B:42:LYS:HG3	2.09	0.92
3:D:117:VAL:O	3:D:120:VAL:HG22	1.68	0.92
1:H:373:ILE:HG13	1:H:374:ILE:N	1.76	0.92
3:C:70:THR:HG22	3:C:71:PRO:HD2	1.48	0.92
1:H:372:LEU:HD12	1:H:443:LEU:HD21	1.48	0.92
3:C:204:ILE:HG22	3:C:205:VAL:H	1.33	0.92
3:C:214:GLN:CD	3:C:226:ALA:HB2	1.95	0.92
2:G:18:LEU:HD23	2:G:19:LEU:H	1.33	0.92
2:G:150:TYR:O	2:G:152:PRO:HD3	1.70	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:150:TYR:O	2:I:152:PRO:HD3	1.70	0.92
3:A:226:ALA:O	3:A:361:ALA:HB2	1.68	0.92
3:A:287:PRO:HA	3:A:290:LEU:HD12	1.52	0.92
3:A:214:GLN:CD	3:A:226:ALA:HB2	1.95	0.92
2:I:35:VAL:O	2:I:37:ILE:N	2.02	0.92
2:I:158:THR:HG23	2:I:161:GLY:H	1.32	0.92
2:I:185:ASP:O	2:I:188:LEU:HD13	1.69	0.92
1:H:284:THR:HG22	1:H:466:LEU:CA	2.00	0.92
3:C:287:PRO:HA	3:C:290:LEU:HD12	1.52	0.92
3:D:42:LYS:HG2	3:D:207:LEU:HD12	1.51	0.92
2:G:185:ASP:O	2:G:188:LEU:HD13	1.69	0.91
2:G:195:ASP:CB	3:A:102:LEU:HD23	2.01	0.91
3:A:55:ILE:HD12	3:A:55:ILE:H	1.33	0.91
2:I:18:LEU:HD23	2:I:19:LEU:H	1.33	0.91
2:G:254:ASN:HB2	2:G:255:PRO:CD	2.01	0.91
3:C:301:GLU:HA	3:C:344:ALA:HB2	1.53	0.91
2:G:35:VAL:O	2:G:37:ILE:N	2.02	0.91
1:H:347:ILE:HG23	1:H:348:ASN:N	1.75	0.91
3:C:281:MET:HB3	3:C:354:LEU:HD11	1.50	0.91
3:A:11:LYS:HA	3:A:56:THR:HB	1.52	0.91
3:B:117:VAL:O	3:B:120:VAL:HG22	1.68	0.91
3:C:55:ILE:H	3:C:55:ILE:HD12	1.33	0.91
3:B:320:ILE:HG23	3:B:321:PRO:HD2	1.50	0.91
3:B:42:LYS:HG2	3:B:207:LEU:HD12	1.51	0.90
3:B:100:LEU:HD12	3:B:101:LYS:N	1.85	0.90
1:F:284:THR:HG22	1:F:466:LEU:CA	2.00	0.90
2:I:177:ILE:HD12	2:I:214:ILE:HG21	1.53	0.90
2:I:254:ASN:HB2	2:I:255:PRO:CD	2.01	0.90
3:A:301:GLU:HA	3:A:344:ALA:HB2	1.53	0.90
3:C:11:LYS:HA	3:C:56:THR:HB	1.52	0.90
2:I:195:ASP:CB	3:C:102:LEU:HD23	2.01	0.90
1:H:87:ILE:HA	1:H:490:ILE:CG2	2.02	0.90
2:G:135:LEU:HG	2:G:138:VAL:HG21	1.55	0.89
2:G:204:ARG:O	2:G:209:PRO:HD2	1.72	0.89
2:I:135:LEU:HG	2:I:138:VAL:HG21	1.55	0.89
2:G:220:ILE:HG13	2:G:221:LEU:N	1.86	0.89
1:F:317:TYR:CE2	2:G:20:LEU:HG	2.07	0.89
3:A:11:LYS:HA	3:A:56:THR:CB	2.03	0.89
3:D:204:ILE:HG22	3:D:205:VAL:N	1.84	0.89
3:A:204:ILE:HG22	3:A:205:VAL:H	1.33	0.89
2:G:207:LEU:O	2:G:210:LEU:HB2	1.73	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:275:LYS:N	1:F:276:PRO:HD2	1.87	0.89
3:B:11:LYS:HA	3:B:56:THR:HB	1.55	0.89
1:F:89:ILE:O	1:F:91:PHE:N	2.06	0.89
3:B:5:GLN:C	3:B:6:LEU:HD12	1.98	0.89
1:H:317:TYR:CE2	2:I:20:LEU:HG	2.07	0.89
1:F:501:LEU:HB3	2:G:127:ILE:HG23	1.54	0.88
2:G:28:MET:O	2:G:31:LEU:HG	1.73	0.88
2:G:177:ILE:HD12	2:G:214:ILE:HG21	1.53	0.88
1:H:89:ILE:O	1:H:91:PHE:N	2.06	0.88
2:I:220:ILE:HG13	2:I:221:LEU:N	1.86	0.88
1:F:87:ILE:HA	1:F:490:ILE:CG2	2.02	0.88
3:C:334:VAL:HG12	3:C:335:VAL:H	1.38	0.88
3:D:11:LYS:HA	3:D:56:THR:HB	1.55	0.88
2:I:28:MET:HA	2:I:31:LEU:HD21	1.55	0.88
1:F:381:TYR:HD1	1:F:382:PRO:N	1.70	0.88
2:G:188:LEU:H	2:G:188:LEU:CD1	1.87	0.88
1:H:381:TYR:HD1	1:H:382:PRO:N	1.70	0.88
2:I:204:ARG:O	2:I:209:PRO:HD2	1.72	0.88
2:G:28:MET:HA	2:G:31:LEU:HD21	1.55	0.88
2:I:28:MET:O	2:I:31:LEU:HG	1.73	0.88
1:F:450:GLY:HA2	1:F:464:THR:HB	1.56	0.88
2:I:188:LEU:H	2:I:188:LEU:CD1	1.87	0.88
1:F:486:LEU:O	1:F:490:ILE:HG13	1.74	0.88
3:C:11:LYS:HA	3:C:56:THR:CB	2.03	0.88
1:F:267:VAL:HA	1:F:488:ALA:HB2	1.55	0.87
1:H:92:THR:HG23	1:H:93:ASN:H	1.39	0.87
1:H:99:GLN:HE22	2:I:146:ARG:HH12	1.15	0.87
2:I:29:PHE:HB3	2:I:30:PRO:HD3	1.57	0.87
3:C:145:GLY:HA2	3:C:148:LEU:HD12	1.56	0.87
3:D:5:GLN:C	3:D:6:LEU:HD12	1.98	0.87
3:D:349:PRO:O	3:D:352:CYS:HB2	1.74	0.87
1:F:92:THR:HG23	1:F:93:ASN:H	1.39	0.87
1:H:275:LYS:N	1:H:276:PRO:HD2	1.87	0.87
2:I:207:LEU:O	2:I:210:LEU:HB2	1.73	0.87
1:F:99:GLN:HE22	2:G:146:ARG:HH12	1.15	0.87
3:B:180:HIS:HA	3:B:187:MET:HE1	1.56	0.87
1:H:267:VAL:HA	1:H:488:ALA:HB2	1.56	0.87
1:F:442:VAL:HG13	2:G:230:VAL:HG11	1.56	0.86
1:H:501:LEU:HB3	2:I:127:ILE:HG23	1.54	0.86
2:I:212:VAL:HA	2:I:215:LEU:HG	1.56	0.86
3:B:283:LEU:HD11	3:B:352:CYS:SG	2.14	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:110:ILE:O	3:C:114:VAL:HG23	1.76	0.86
3:A:317:HIS:C	3:A:318:ILE:HG13	2.00	0.86
3:D:283:LEU:HD11	3:D:352:CYS:SG	2.14	0.86
3:A:334:VAL:HG12	3:A:335:VAL:H	1.38	0.86
3:C:170:VAL:O	3:C:173:ARG:HB3	1.76	0.86
3:D:180:HIS:HA	3:D:187:MET:HE1	1.55	0.86
2:G:29:PHE:HB3	2:G:30:PRO:HD3	1.57	0.86
3:B:349:PRO:O	3:B:352:CYS:HB2	1.74	0.86
1:H:275:LYS:H	1:H:276:PRO:CD	1.88	0.86
1:H:308:TRP:CH2	1:H:410:PRO:HB3	2.10	0.86
1:H:486:LEU:O	1:H:490:ILE:HG13	1.74	0.86
1:H:409:GLY:H	1:H:412:GLN:HB2	1.40	0.85
1:H:442:VAL:HG13	2:I:230:VAL:HG11	1.56	0.85
3:A:164:LEU:HD22	3:A:168:LEU:HD23	1.58	0.85
1:H:450:GLY:HA2	1:H:464:THR:HB	1.56	0.85
3:D:26:ILE:H	3:D:26:ILE:HD12	1.39	0.85
3:D:242:LEU:HB3	3:D:323:ILE:HD11	1.57	0.85
3:A:110:ILE:O	3:A:114:VAL:HG23	1.76	0.85
3:C:204:ILE:HG22	3:C:205:VAL:N	1.91	0.85
1:F:494:ILE:O	1:F:498:VAL:HG23	1.76	0.85
2:G:172:LEU:HD23	2:G:173:HIS:H	1.42	0.85
3:A:113:ARG:O	3:A:117:VAL:HG23	1.76	0.85
3:C:79:MET:HG2	3:C:80:VAL:N	1.83	0.85
3:B:242:LEU:HB3	3:B:323:ILE:HD11	1.57	0.85
3:C:317:HIS:C	3:C:318:ILE:HG13	2.00	0.85
2:G:24:ILE:HD12	2:G:25:ALA:N	1.92	0.85
2:G:212:VAL:HA	2:G:215:LEU:HG	1.56	0.85
2:G:132:PRO:O	2:G:134:VAL:N	2.10	0.85
3:C:285:ILE:HD12	3:C:286:ARG:H	1.40	0.85
3:C:84:TYR:CB	3:C:86:LEU:HD21	2.07	0.84
1:F:308:TRP:CH2	1:F:410:PRO:HB3	2.10	0.84
3:A:170:VAL:O	3:A:173:ARG:HB3	1.76	0.84
3:D:307:VAL:HG12	3:D:309:GLN:HE22	1.41	0.84
2:G:92:ALA:HB2	2:G:227:ILE:HD13	1.59	0.84
3:A:300:LEU:HD11	3:A:347:LEU:HD23	1.59	0.84
1:H:88:ALA:HA	1:H:264:PHE:HZ	1.42	0.84
3:C:113:ARG:O	3:C:117:VAL:HG23	1.76	0.84
3:D:269:PRO:HB2	3:D:365:LEU:HB2	1.59	0.84
1:F:396:PRO:CG	1:F:399:LEU:HD12	2.06	0.84
3:B:241:PHE:C	3:B:242:LEU:HG	2.03	0.84
3:D:188:ILE:HD12	3:D:188:ILE:N	1.92	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:84:TYR:CB	3:A:86:LEU:HD21	2.07	0.84
3:B:26:ILE:HD12	3:B:26:ILE:H	1.39	0.84
3:B:188:ILE:HD12	3:B:188:ILE:N	1.92	0.84
3:B:307:VAL:HG12	3:B:309:GLN:HE22	1.41	0.84
1:F:88:ALA:HA	1:F:264:PHE:HZ	1.42	0.84
3:C:214:GLN:HG2	3:C:215:VAL:N	1.93	0.84
1:F:335:ILE:HD12	1:F:339:LEU:HD11	1.60	0.84
3:A:145:GLY:HA2	3:A:148:LEU:HD12	1.56	0.84
1:H:280:ILE:O	1:H:284:THR:HG23	1.77	0.84
1:H:396:PRO:CG	1:H:399:LEU:HD12	2.06	0.84
2:I:35:VAL:C	2:I:37:ILE:H	1.85	0.84
1:F:275:LYS:H	1:F:276:PRO:CD	1.88	0.84
1:F:280:ILE:O	1:F:284:THR:HG23	1.77	0.84
2:I:93:GLY:HA2	2:I:223:PHE:HE1	1.42	0.84
3:D:135:SER:OG	3:D:138:GLN:HG3	1.77	0.84
3:A:62:ILE:O	3:A:64:GLU:N	2.11	0.84
3:A:144:ILE:O	3:A:148:LEU:HG	1.78	0.84
3:A:285:ILE:HD12	3:A:286:ARG:H	1.40	0.84
1:F:357:VAL:HG12	1:F:358:LYS:N	1.93	0.83
2:G:35:VAL:C	2:G:37:ILE:H	1.85	0.83
1:H:405:MET:HE3	3:D:78:GLY:HA2	1.60	0.83
1:F:282:VAL:O	1:F:286:VAL:HG23	1.78	0.83
2:G:93:GLY:HA2	2:G:223:PHE:HE1	1.42	0.83
1:H:494:ILE:O	1:H:498:VAL:HG23	1.76	0.83
3:B:84:TYR:HB3	3:B:86:LEU:HD21	1.59	0.83
1:H:327:VAL:CA	2:I:274:ILE:HG21	2.08	0.83
3:A:124:ALA:O	3:A:127:LEU:HD13	1.78	0.83
1:H:335:ILE:HD12	1:H:339:LEU:HD11	1.60	0.83
3:D:236:SER:HB3	3:D:237:PRO:HD3	1.60	0.83
3:D:254:VAL:HB	3:D:270:VAL:HG21	1.59	0.83
3:B:269:PRO:HB2	3:B:365:LEU:HB2	1.59	0.83
2:I:24:ILE:HD12	2:I:25:ALA:N	1.92	0.83
2:I:92:ALA:HB2	2:I:227:ILE:HD13	1.59	0.83
3:C:300:LEU:HD11	3:C:347:LEU:HD23	1.59	0.83
3:B:11:LYS:HA	3:B:56:THR:CB	2.08	0.83
1:H:282:VAL:O	1:H:286:VAL:HG23	1.78	0.83
3:C:164:LEU:HD22	3:C:168:LEU:HD23	1.58	0.83
1:H:308:TRP:O	1:H:310:ALA:N	2.12	0.83
2:I:172:LEU:HD23	2:I:173:HIS:H	1.42	0.83
2:I:173:HIS:CE1	2:I:218:VAL:HG13	2.13	0.83
2:I:188:LEU:HD12	2:I:188:LEU:N	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:12:ALA:O	3:D:14:GLY:N	2.11	0.83
3:B:12:ALA:O	3:B:14:GLY:N	2.11	0.83
2:I:132:PRO:O	2:I:134:VAL:N	2.10	0.83
3:C:62:ILE:O	3:C:64:GLU:N	2.11	0.83
3:C:124:ALA:O	3:C:127:LEU:HD13	1.78	0.83
2:G:173:HIS:CE1	2:G:218:VAL:HG13	2.13	0.82
3:C:144:ILE:O	3:C:148:LEU:HG	1.78	0.82
3:D:84:TYR:HB3	3:D:86:LEU:HD21	1.59	0.82
1:F:409:GLY:H	1:F:412:GLN:HB2	1.41	0.82
2:G:229:GLU:O	2:G:230:VAL:HG23	1.79	0.82
3:B:135:SER:OG	3:B:138:GLN:HG3	1.77	0.82
3:B:254:VAL:HB	3:B:270:VAL:HG21	1.59	0.82
1:H:460:PRO:HD2	1:H:474:ILE:HG22	1.62	0.82
1:F:448:THR:O	1:F:450:GLY:N	2.12	0.82
2:I:229:GLU:O	2:I:230:VAL:HG23	1.79	0.82
3:D:11:LYS:HA	3:D:56:THR:CB	2.08	0.82
1:F:280:ILE:HD13	1:F:470:TYR:HD1	1.44	0.82
1:F:284:THR:HG21	1:F:467:LEU:N	1.95	0.82
3:A:288:GLU:HG2	3:B:312:ASN:HB2	1.61	0.82
3:D:241:PHE:C	3:D:242:LEU:HG	2.03	0.82
1:F:312:ARG:HD2	1:F:313:GLY:H	1.43	0.82
1:H:280:ILE:HD13	1:H:470:TYR:HD1	1.44	0.82
1:F:308:TRP:O	1:F:310:ALA:N	2.12	0.82
1:H:312:ARG:HD2	1:H:313:GLY:H	1.43	0.82
1:F:327:VAL:CA	2:G:274:ILE:HG21	2.08	0.82
3:A:214:GLN:HG2	3:A:215:VAL:N	1.93	0.81
1:H:424:LYS:NZ	1:H:511:MET:HE2	1.95	0.81
2:I:229:GLU:CD	2:I:230:VAL:H	1.88	0.81
1:F:267:VAL:HG22	1:F:488:ALA:N	1.96	0.81
1:F:289:LEU:HD23	1:F:434:PHE:CE2	2.15	0.81
1:F:424:LYS:HZ1	1:F:511:MET:HE2	1.44	0.81
2:G:148:GLY:HA2	2:G:155:GLY:HA3	1.61	0.81
2:G:158:THR:O	2:G:162:VAL:HG23	1.80	0.81
3:B:189:TYR:HD2	3:B:190:VAL:H	1.29	0.81
3:B:236:SER:HB3	3:B:237:PRO:HD3	1.60	0.81
1:H:284:THR:HG21	1:H:467:LEU:N	1.95	0.81
1:H:357:VAL:HG12	1:H:358:LYS:N	1.93	0.81
1:H:448:THR:O	1:H:450:GLY:N	2.12	0.81
2:I:148:GLY:HA2	2:I:155:GLY:HA3	1.60	0.81
2:I:158:THR:O	2:I:162:VAL:HG23	1.80	0.81
3:C:288:GLU:HG2	3:D:312:ASN:HB2	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:144:ILE:O	3:D:148:LEU:HG	1.80	0.81
1:F:405:MET:HE3	3:B:78:GLY:HA2	1.60	0.81
1:H:357:VAL:CG1	1:H:358:LYS:H	1.92	0.81
3:D:268:LEU:O	3:D:270:VAL:HG23	1.79	0.81
1:F:87:ILE:HA	1:F:490:ILE:HG22	1.62	0.81
1:F:317:TYR:HE2	2:G:20:LEU:HG	1.43	0.81
3:D:204:ILE:CG2	3:D:205:VAL:H	1.94	0.81
3:D:189:TYR:HD2	3:D:190:VAL:H	1.29	0.81
3:A:204:ILE:HG22	3:A:205:VAL:N	1.91	0.81
3:A:256:VAL:HG13	3:A:268:LEU:HD21	1.61	0.81
3:C:183:LEU:HD22	3:C:185:ARG:NH1	1.95	0.81
3:D:170:VAL:O	3:D:173:ARG:HB3	1.81	0.81
3:B:204:ILE:CG2	3:B:205:VAL:H	1.94	0.81
1:H:289:LEU:HD23	1:H:434:PHE:CE2	2.15	0.81
1:F:41:LEU:HD12	1:F:89:ILE:HD11	1.62	0.81
1:F:337:LYS:HZ3	2:G:253:LEU:HG	1.45	0.81
1:H:87:ILE:HA	1:H:490:ILE:HG22	1.62	0.81
1:F:424:LYS:NZ	1:F:511:MET:HE2	1.95	0.81
1:H:329:SER:O	1:H:333:ILE:HG13	1.81	0.81
3:C:40:CYS:HB2	3:C:42:LYS:CG	2.10	0.81
3:C:236:SER:HB3	3:C:237:PRO:CD	2.11	0.81
3:A:183:LEU:HD22	3:A:185:ARG:NH1	1.95	0.80
3:A:241:PHE:HD1	3:A:284:GLY:HA2	1.45	0.80
3:B:144:ILE:O	3:B:148:LEU:HG	1.81	0.80
3:B:170:VAL:O	3:B:173:ARG:HB3	1.81	0.80
1:H:41:LEU:HD12	1:H:89:ILE:HD11	1.62	0.80
1:H:317:TYR:HE2	2:I:20:LEU:HG	1.43	0.80
3:C:241:PHE:HD1	3:C:284:GLY:HA2	1.45	0.80
2:G:153:PHE:O	2:G:158:THR:HG21	1.81	0.80
3:A:236:SER:HB3	3:A:237:PRO:CD	2.11	0.80
1:H:267:VAL:HG22	1:H:488:ALA:N	1.96	0.80
1:H:486:LEU:HD13	1:H:490:ILE:CD1	2.11	0.80
3:C:44:THR:HG22	3:C:48:MET:HE2	1.62	0.80
3:C:96:MET:HE3	3:C:142:VAL:O	1.80	0.80
2:G:220:ILE:HG13	2:G:221:LEU:H	1.43	0.80
3:B:268:LEU:O	3:B:270:VAL:HG23	1.79	0.80
2:G:36:ALA:C	2:G:37:ILE:HG12	2.05	0.80
3:A:315:GLN:HA	3:A:329:TYR:O	1.81	0.80
1:F:486:LEU:HD13	1:F:490:ILE:CD1	2.11	0.80
3:A:96:MET:HE3	3:A:142:VAL:O	1.80	0.80
3:A:306:VAL:HG12	3:A:307:VAL:H	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:346:GLU:CA	1:H:349:MET:HG3	2.12	0.80
2:I:153:PHE:O	2:I:158:THR:HG21	1.81	0.80
2:I:172:LEU:HD23	2:I:173:HIS:N	1.96	0.80
2:G:177:ILE:HD12	2:G:214:ILE:CG2	2.11	0.80
2:I:120:THR:O	2:I:123:LYS:HB3	1.82	0.80
3:D:268:LEU:HD12	3:D:270:VAL:HG21	1.63	0.80
1:F:357:VAL:CG1	1:F:358:LYS:H	1.92	0.80
3:A:87:TYR:H	3:A:95:ASN:HD21	1.29	0.80
1:H:486:LEU:CD2	2:I:135:LEU:HD21	2.07	0.80
3:A:44:THR:HG22	3:A:48:MET:HE2	1.62	0.80
1:F:333:ILE:O	1:F:336:PHE:HB2	1.82	0.80
2:G:172:LEU:HD23	2:G:173:HIS:N	1.96	0.80
3:B:285:ILE:HD11	3:B:289:HIS:HB2	1.64	0.80
2:I:220:ILE:HG13	2:I:221:LEU:H	1.43	0.80
1:F:281:PHE:HA	1:F:467:LEU:HD21	1.64	0.79
1:F:460:PRO:HD2	1:F:474:ILE:HG22	1.61	0.79
2:I:36:ALA:C	2:I:37:ILE:HG12	2.05	0.79
2:I:177:ILE:HD12	2:I:214:ILE:CG2	2.11	0.79
3:C:315:GLN:HA	3:C:329:TYR:O	1.81	0.79
1:F:312:ARG:CD	1:F:313:GLY:H	1.95	0.79
3:C:256:VAL:HG13	3:C:268:LEU:HD21	1.61	0.79
2:G:229:GLU:CD	2:G:230:VAL:H	1.88	0.79
1:F:330:PHE:CE2	2:G:246:ALA:HA	2.18	0.79
1:F:490:ILE:HG12	2:G:135:LEU:CD2	2.12	0.79
3:B:189:TYR:CD2	3:B:190:VAL:N	2.50	0.79
2:G:188:LEU:HD12	2:G:188:LEU:N	1.94	0.79
3:B:336:LEU:O	3:B:337:VAL:HG23	1.82	0.79
1:H:281:PHE:HA	1:H:467:LEU:HD21	1.64	0.79
1:H:330:PHE:CE2	2:I:246:ALA:HA	2.18	0.79
1:H:462:GLY:HA3	1:H:465:ASP:OD2	1.83	0.79
3:C:87:TYR:H	3:C:95:ASN:HD21	1.29	0.79
3:D:189:TYR:CD2	3:D:190:VAL:N	2.50	0.79
2:G:202:ALA:O	2:G:206:VAL:HB	1.83	0.79
3:A:12:ALA:O	3:A:14:GLY:N	2.16	0.79
1:H:312:ARG:CD	1:H:313:GLY:H	1.95	0.79
3:D:164:LEU:HD13	3:D:168:LEU:HD23	1.65	0.79
3:C:300:LEU:CD1	3:C:347:LEU:HD23	2.13	0.79
3:D:240:ASN:HD21	3:D:328:VAL:HB	1.48	0.79
3:D:336:LEU:O	3:D:337:VAL:HG23	1.82	0.79
1:F:100:LEU:HD22	1:F:104:ARG:NE	1.98	0.78
1:F:346:GLU:CA	1:F:349:MET:HG3	2.12	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:120:THR:O	2:G:123:LYS:HB3	1.82	0.78
3:C:12:ALA:O	3:C:14:GLY:N	2.16	0.78
3:D:126:LEU:HD11	3:D:138:GLN:NE2	1.99	0.78
1:F:329:SER:O	1:F:333:ILE:HG13	1.81	0.78
3:A:306:VAL:HG12	3:A:307:VAL:N	1.98	0.78
3:B:268:LEU:HD12	3:B:270:VAL:HG21	1.63	0.78
1:H:333:ILE:O	1:H:336:PHE:HB2	1.82	0.78
3:B:95:ASN:O	3:B:98:PHE:HB2	1.83	0.78
1:H:406:ASP:OD2	3:D:99:GLY:HA2	1.84	0.78
3:C:306:VAL:HG12	3:C:307:VAL:H	1.47	0.78
3:B:126:LEU:HD11	3:B:138:GLN:NE2	1.99	0.78
3:B:334:VAL:HG12	3:B:335:VAL:N	1.98	0.78
1:H:341:ASN:HD22	1:H:344:PHE:HB2	1.47	0.78
1:F:94:TYR:CZ	1:F:99:GLN:HA	2.18	0.78
1:H:94:TYR:CZ	1:H:99:GLN:HA	2.18	0.78
1:H:409:GLY:N	1:H:412:GLN:HB2	1.98	0.78
3:B:240:ASN:HD21	3:B:328:VAL:HB	1.48	0.78
2:I:84:TRP:NE1	2:I:248:GLY:HA3	1.99	0.78
1:F:409:GLY:N	1:F:412:GLN:HB2	1.98	0.78
1:F:341:ASN:HD22	1:F:344:PHE:HB2	1.47	0.78
3:A:300:LEU:CD1	3:A:347:LEU:HD23	2.13	0.78
2:I:202:ALA:O	2:I:206:VAL:HB	1.83	0.78
1:F:322:ILE:C	1:F:324:PRO:HD2	2.09	0.77
2:G:13:LEU:O	2:G:17:HIS:HB2	1.84	0.77
1:F:406:ASP:OD2	3:B:99:GLY:HA2	1.84	0.77
3:A:334:VAL:O	3:A:335:VAL:HG23	1.84	0.77
3:D:285:ILE:HD11	3:D:289:HIS:HB2	1.64	0.77
1:F:335:ILE:O	1:F:339:LEU:HG	1.85	0.77
1:F:462:GLY:HA3	1:F:465:ASP:OD2	1.83	0.77
3:C:270:VAL:HG13	3:C:271:GLU:N	1.97	0.77
3:A:270:VAL:HG13	3:A:271:GLU:N	1.97	0.77
3:A:299:ILE:HG22	3:A:300:LEU:H	1.49	0.77
1:H:100:LEU:HD22	1:H:104:ARG:NE	1.98	0.77
1:H:322:ILE:C	1:H:324:PRO:HD2	2.09	0.77
1:H:490:ILE:HG12	2:I:135:LEU:CD2	2.12	0.77
3:C:214:GLN:HG2	3:C:215:VAL:H	1.48	0.77
3:D:60:LEU:HD12	3:D:61:PHE:N	2.00	0.77
3:A:234:ILE:HG22	3:A:235:GLY:H	1.49	0.77
3:C:306:VAL:HG12	3:C:307:VAL:N	1.98	0.77
3:A:10:THR:HA	3:A:19:SER:O	1.85	0.77
3:B:11:LYS:HZ3	3:B:53:GLU:HG3	1.50	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:95:ASN:O	3:D:98:PHE:HB2	1.83	0.77
2:G:84:TRP:NE1	2:G:248:GLY:HA3	1.99	0.77
2:G:32:LEU:O	2:G:35:VAL:HB	1.85	0.77
3:A:270:VAL:HG22	3:A:362:CYS:HB3	1.66	0.77
3:D:186:THR:O	3:D:187:MET:HG3	1.85	0.77
1:F:468:VAL:HG23	2:G:134:VAL:CG2	2.14	0.77
3:B:244:VAL:HG23	3:B:281:MET:O	1.85	0.77
1:H:346:GLU:H	1:H:346:GLU:CD	1.92	0.77
2:I:3:MET:HE3	3:D:72:PRO:HG2	1.67	0.76
3:C:33:VAL:C	3:C:34:PHE:HD2	1.94	0.76
3:B:164:LEU:HD13	3:B:168:LEU:HD23	1.65	0.76
3:C:55:ILE:HD12	3:C:55:ILE:N	1.99	0.76
3:A:55:ILE:HD12	3:A:55:ILE:N	1.99	0.76
3:B:60:LEU:HD12	3:B:61:PHE:N	2.00	0.76
3:B:100:LEU:HD12	3:B:101:LYS:H	1.50	0.76
3:C:270:VAL:HG22	3:C:362:CYS:HB3	1.66	0.76
3:C:334:VAL:O	3:C:335:VAL:HG23	1.84	0.76
3:C:346:GLY:O	3:C:348:PRO:HD3	1.85	0.76
3:D:334:VAL:HG12	3:D:335:VAL:N	1.98	0.76
3:A:369:PRO:O	3:A:371:VAL:HG23	1.86	0.76
1:H:468:VAL:HG23	2:I:134:VAL:CG2	2.14	0.76
3:C:92:VAL:HG13	3:C:142:VAL:HG11	1.68	0.76
3:C:203:LYS:HD3	3:C:215:VAL:CG1	2.16	0.76
3:A:40:CYS:HB2	3:A:42:LYS:CG	2.10	0.76
2:I:32:LEU:O	2:I:35:VAL:HB	1.85	0.76
3:C:10:THR:HA	3:C:19:SER:O	1.85	0.76
3:D:175:GLU:O	3:D:179:LEU:HD23	1.85	0.76
3:D:244:VAL:HG23	3:D:281:MET:O	1.85	0.76
3:A:33:VAL:C	3:A:34:PHE:HD2	1.94	0.76
3:B:358:ASP:CG	3:B:359:GLY:N	2.43	0.76
2:I:13:LEU:O	2:I:17:HIS:HB2	1.84	0.76
3:A:92:VAL:HG13	3:A:142:VAL:HG11	1.68	0.76
3:C:369:PRO:O	3:C:371:VAL:HG23	1.86	0.76
1:F:77:LEU:O	1:F:81:PHE:HB3	1.86	0.76
2:G:3:MET:HE3	3:B:72:PRO:HG2	1.67	0.76
3:A:286:ARG:HB3	3:A:288:GLU:OE1	1.86	0.76
3:A:346:GLY:O	3:A:348:PRO:HD3	1.85	0.76
1:H:77:LEU:O	1:H:81:PHE:HB3	1.86	0.76
3:C:178:ARG:O	3:C:182:ARG:HB2	1.86	0.76
3:C:194:GLN:O	3:C:197:ALA:HB3	1.86	0.76
3:D:11:LYS:HZ3	3:D:53:GLU:HG3	1.51	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:145:GLY:HA2	3:D:148:LEU:HD12	1.67	0.76
3:A:203:LYS:HD3	3:A:215:VAL:CG1	2.16	0.76
3:C:286:ARG:HB3	3:C:288:GLU:OE1	1.86	0.76
1:H:358:LYS:O	1:H:358:LYS:HG2	1.86	0.76
3:C:299:ILE:HG22	3:C:300:LEU:H	1.49	0.76
3:D:89:HIS:CD2	3:D:90:LEU:HG	2.21	0.76
2:G:244:THR:OG1	2:G:246:ALA:HB3	1.86	0.75
3:B:89:HIS:CD2	3:B:90:LEU:HG	2.22	0.75
3:C:77:VAL:HG12	3:C:78:GLY:H	1.49	0.75
3:A:145:GLY:O	3:A:149:VAL:HG23	1.86	0.75
1:F:346:GLU:CD	1:F:346:GLU:H	1.92	0.75
3:A:178:ARG:O	3:A:182:ARG:HB2	1.86	0.75
3:B:240:ASN:HB2	3:B:285:ILE:O	1.86	0.75
1:H:342:GLN:NE2	1:H:362:PHE:HB2	2.02	0.75
1:H:465:ASP:CG	1:H:473:ARG:HH22	1.95	0.75
1:H:501:LEU:HD13	2:I:127:ILE:HG23	1.68	0.75
1:F:465:ASP:CG	1:F:473:ARG:HH22	1.95	0.75
1:F:501:LEU:HD13	2:G:127:ILE:HG23	1.68	0.75
3:A:18:VAL:HG13	3:A:18:VAL:O	1.85	0.75
3:C:55:ILE:H	3:C:55:ILE:CD1	2.00	0.75
3:A:353:HIS:NE2	3:A:364:ARG:HD3	2.02	0.75
1:H:270:ASP:HB3	1:H:274:GLN:HB3	1.68	0.75
3:C:18:VAL:HG13	3:C:18:VAL:O	1.85	0.75
3:D:70:THR:HG23	3:D:71:PRO:HD2	1.69	0.75
1:F:396:PRO:HG2	1:F:399:LEU:HD12	1.69	0.75
3:A:188:ILE:H	3:A:188:ILE:HD12	1.51	0.75
3:B:70:THR:HG23	3:B:71:PRO:HD2	1.69	0.75
2:G:282:GLN:OE1	2:G:282:GLN:HA	1.87	0.75
3:A:194:GLN:O	3:A:197:ALA:HB3	1.86	0.75
3:B:307:VAL:HG12	3:B:309:GLN:NE2	2.01	0.75
2:I:9:GLN:OE1	2:I:9:GLN:HA	1.87	0.75
3:C:145:GLY:O	3:C:149:VAL:HG23	1.86	0.75
1:F:270:ASP:HB3	1:F:274:GLN:HB3	1.68	0.75
3:A:77:VAL:HG12	3:A:78:GLY:H	1.49	0.75
3:A:267:TRP:C	3:A:268:LEU:HD23	2.12	0.75
2:G:84:TRP:HB3	2:G:245:LEU:HA	1.69	0.74
3:B:186:THR:O	3:B:187:MET:HG3	1.85	0.74
1:F:100:LEU:HB3	1:F:104:ARG:CG	2.15	0.74
1:F:431:ILE:O	1:F:434:PHE:HB3	1.87	0.74
2:G:84:TRP:CD1	2:G:248:GLY:HA3	2.22	0.74
2:G:207:LEU:HA	2:G:210:LEU:HD12	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:145:GLY:HA2	3:B:148:LEU:HD12	1.67	0.74
3:B:157:LEU:CD2	3:B:160:PRO:HG3	2.15	0.74
1:H:90:ALA:CB	1:H:490:ILE:HD12	2.17	0.74
1:H:335:ILE:O	1:H:339:LEU:HG	1.85	0.74
2:I:207:LEU:HA	2:I:210:LEU:HD12	1.69	0.74
3:D:157:LEU:CD2	3:D:160:PRO:HG3	2.15	0.74
3:D:307:VAL:HG12	3:D:309:GLN:NE2	2.01	0.74
2:I:84:TRP:HB3	2:I:245:LEU:HA	1.69	0.74
3:C:234:ILE:HG22	3:C:235:GLY:H	1.49	0.74
2:I:244:THR:OG1	2:I:246:ALA:HB3	1.86	0.74
3:D:306:VAL:HG12	3:D:307:VAL:H	1.52	0.74
3:A:214:GLN:HG2	3:A:215:VAL:H	1.48	0.74
3:B:175:GLU:O	3:B:179:LEU:HD23	1.85	0.74
3:A:206:VAL:O	3:A:213:ALA:HB3	1.88	0.74
1:H:431:ILE:HG13	1:H:432:ALA:N	2.02	0.74
1:F:328:PRO:HD3	2:G:274:ILE:CG1	2.16	0.74
3:A:40:CYS:SG	3:A:41:GLY:N	2.61	0.74
3:A:116:GLN:O	3:A:120:VAL:HG13	1.87	0.74
3:A:130:LYS:HB2	3:A:131:PRO:CD	2.18	0.74
2:I:84:TRP:CD1	2:I:248:GLY:HA3	2.22	0.74
3:C:130:LYS:HB2	3:C:131:PRO:CD	2.18	0.74
3:D:240:ASN:OD1	3:D:328:VAL:HG23	1.88	0.74
2:G:212:VAL:HG22	2:G:215:LEU:HD12	1.69	0.74
1:F:431:ILE:HG13	1:F:432:ALA:N	2.02	0.74
3:A:241:PHE:CD1	3:A:284:GLY:HA2	2.23	0.74
3:C:188:ILE:H	3:C:188:ILE:HD12	1.52	0.74
3:C:353:HIS:NE2	3:C:364:ARG:HD3	2.02	0.74
3:D:100:LEU:HD12	3:D:101:LYS:H	1.50	0.74
3:D:240:ASN:HB2	3:D:285:ILE:O	1.87	0.74
1:F:90:ALA:CB	1:F:490:ILE:HD12	2.17	0.74
3:B:300:LEU:HB2	3:B:345:ILE:O	1.88	0.74
1:H:419:LEU:O	1:H:421:LEU:N	2.19	0.74
3:C:40:CYS:SG	3:C:41:GLY:N	2.61	0.74
1:F:302:LEU:HD22	1:F:321:LEU:HD13	1.70	0.73
1:F:358:LYS:HG2	1:F:358:LYS:O	1.86	0.73
3:A:204:ILE:CG2	3:A:205:VAL:H	2.02	0.73
3:A:254:VAL:O	3:A:268:LEU:HG	1.88	0.73
2:I:162:VAL:HG12	2:I:166:TYR:CE2	2.23	0.73
1:F:498:VAL:HA	1:F:501:LEU:HD12	1.71	0.73
1:H:374:ILE:C	1:H:374:ILE:HD12	2.13	0.73
2:I:194:LEU:HA	3:C:73:ALA:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:267:TRP:C	3:C:268:LEU:HD23	2.12	0.73
3:A:55:ILE:H	3:A:55:ILE:CD1	2.00	0.73
3:B:123:LEU:HD21	3:B:142:VAL:HG22	1.71	0.73
3:C:116:GLN:O	3:C:120:VAL:HG13	1.87	0.73
3:C:241:PHE:CD1	3:C:284:GLY:HA2	2.23	0.73
3:D:298:VAL:HG21	3:D:347:LEU:O	1.89	0.73
1:F:342:GLN:NE2	1:F:362:PHE:HB2	2.02	0.73
3:B:276:GLN:HE21	3:B:277:VAL:HG22	1.54	0.73
3:B:337:VAL:O	3:B:337:VAL:HG12	1.89	0.73
1:H:423:ILE:HD13	1:H:424:LYS:H	1.54	0.73
3:C:254:VAL:O	3:C:268:LEU:HG	1.88	0.73
3:A:123:LEU:CD1	3:A:141:ARG:HH21	2.02	0.73
3:B:298:VAL:HG21	3:B:347:LEU:O	1.89	0.73
2:G:9:GLN:OE1	2:G:9:GLN:HA	1.87	0.73
3:B:84:TYR:CB	3:B:86:LEU:HD21	2.19	0.73
3:B:87:TYR:H	3:B:95:ASN:HD21	1.36	0.73
1:F:296:VAL:HG23	1:F:384:MET:SD	2.29	0.73
1:H:431:ILE:O	1:H:434:PHE:HB3	1.87	0.73
3:C:344:ALA:O	3:C:345:ILE:HG23	1.89	0.73
3:B:123:LEU:CD2	3:B:142:VAL:HG22	2.19	0.73
3:B:317:HIS:O	3:B:318:ILE:HG13	1.89	0.73
2:I:212:VAL:HG22	2:I:215:LEU:HD12	1.70	0.73
3:D:311:GLY:C	3:D:313:GLU:H	1.96	0.73
2:G:194:LEU:HA	3:A:73:ALA:HB2	1.70	0.72
3:A:126:LEU:HD13	3:A:134:LEU:HD22	1.71	0.72
1:H:372:LEU:HD12	1:H:443:LEU:CD2	2.19	0.72
1:H:396:PRO:HG2	1:H:399:LEU:HD12	1.68	0.72
3:C:126:LEU:HD13	3:C:134:LEU:HD22	1.71	0.72
3:C:206:VAL:O	3:C:213:ALA:HB3	1.88	0.72
3:A:33:VAL:HG13	3:A:201:ALA:HB2	1.70	0.72
1:H:314:LYS:H	1:H:314:LYS:HD2	1.53	0.72
3:C:33:VAL:HG13	3:C:201:ALA:HB2	1.70	0.72
2:G:162:VAL:HG12	2:G:166:TYR:CE2	2.23	0.72
1:H:498:VAL:HA	1:H:501:LEU:HD12	1.71	0.72
3:C:123:LEU:CD1	3:C:141:ARG:HH21	2.02	0.72
3:C:306:VAL:H	3:C:317:HIS:HB2	1.54	0.72
3:D:84:TYR:CB	3:D:86:LEU:HD21	2.19	0.72
3:D:300:LEU:HB2	3:D:345:ILE:O	1.88	0.72
2:G:135:LEU:HG	2:G:138:VAL:CG2	2.19	0.72
3:A:344:ALA:O	3:A:345:ILE:HG23	1.89	0.72
1:H:270:ASP:HB3	1:H:274:GLN:CB	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:135:LEU:HG	2:I:138:VAL:CG2	2.19	0.72
3:C:204:ILE:CG2	3:C:205:VAL:H	2.02	0.72
3:A:183:LEU:CD2	3:A:185:ARG:HH12	2.01	0.72
3:B:244:VAL:HG23	3:B:281:MET:C	2.15	0.72
3:C:55:ILE:HG12	3:C:68:ASN:ND2	2.05	0.72
1:F:374:ILE:C	1:F:374:ILE:HD12	2.13	0.72
3:B:85:ALA:O	3:B:146:ARG:NH2	2.20	0.72
3:B:240:ASN:OD1	3:B:328:VAL:HG23	1.88	0.72
1:H:302:LEU:HD22	1:H:321:LEU:HD13	1.70	0.72
2:I:148:GLY:CA	2:I:155:GLY:HA3	2.19	0.72
3:A:10:THR:HB	3:A:57:SER:HB3	1.69	0.72
3:A:79:MET:CG	3:A:80:VAL:H	2.00	0.72
3:B:306:VAL:HG12	3:B:307:VAL:H	1.52	0.72
2:I:282:GLN:OE1	2:I:282:GLN:HA	1.87	0.72
3:C:156:LEU:O	3:C:157:LEU:HD12	1.90	0.72
3:D:87:TYR:HB3	3:D:89:HIS:CE1	2.24	0.72
3:D:272:SER:O	3:D:275:VAL:HG22	1.88	0.72
2:G:85:LEU:HD22	2:G:245:LEU:HD22	1.72	0.72
3:A:156:LEU:O	3:A:157:LEU:HD12	1.90	0.72
3:B:97:SER:O	3:B:101:LYS:HB2	1.89	0.72
1:F:270:ASP:HB3	1:F:274:GLN:CB	2.19	0.72
2:G:148:GLY:CA	2:G:155:GLY:HA3	2.19	0.72
3:A:55:ILE:HG12	3:A:68:ASN:ND2	2.04	0.72
3:B:298:VAL:HB	3:B:347:LEU:H	1.55	0.72
3:B:87:TYR:HB3	3:B:89:HIS:CE1	2.24	0.72
1:H:486:LEU:H	1:H:486:LEU:HD12	1.55	0.72
2:I:275:THR:O	2:I:279:LEU:HB2	1.90	0.72
3:C:10:THR:HB	3:C:57:SER:HB3	1.69	0.72
1:F:419:LEU:O	1:F:421:LEU:N	2.19	0.71
1:F:486:LEU:H	1:F:486:LEU:HD12	1.55	0.71
2:G:275:THR:O	2:G:279:LEU:HB2	1.90	0.71
3:A:301:GLU:HA	3:A:344:ALA:CB	2.20	0.71
1:H:296:VAL:HG23	1:H:384:MET:SD	2.29	0.71
3:D:85:ALA:O	3:D:146:ARG:NH2	2.20	0.71
3:D:169:ARG:NH1	3:D:169:ARG:HB2	2.05	0.71
3:D:244:VAL:HG23	3:D:281:MET:C	2.15	0.71
3:D:337:VAL:O	3:D:337:VAL:HG12	1.89	0.71
1:F:314:LYS:H	1:F:314:LYS:HD2	1.53	0.71
1:F:423:ILE:HD13	1:F:424:LYS:H	1.54	0.71
2:G:244:THR:OG1	2:G:247:VAL:HG23	1.91	0.71
3:B:169:ARG:HB2	3:B:169:ARG:NH1	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:281:PHE:CA	1:H:467:LEU:HD21	2.20	0.71
3:C:206:VAL:HG11	3:C:230:VAL:HG22	1.72	0.71
3:D:123:LEU:CD2	3:D:142:VAL:HG22	2.19	0.71
3:D:276:GLN:HE21	3:D:277:VAL:HG22	1.54	0.71
3:D:298:VAL:HB	3:D:347:LEU:H	1.55	0.71
1:H:284:THR:HA	1:H:466:LEU:HD22	1.73	0.71
3:D:123:LEU:HD21	3:D:142:VAL:HG22	1.71	0.71
1:F:100:LEU:CD2	1:F:104:ARG:HE	2.03	0.71
1:F:284:THR:HA	1:F:466:LEU:HD22	1.73	0.71
1:F:285:VAL:HG23	1:F:438:PHE:HE2	1.56	0.71
1:F:419:LEU:C	1:F:421:LEU:H	1.97	0.71
3:B:55:ILE:HG21	3:B:68:ASN:CG	2.16	0.71
3:B:272:SER:O	3:B:275:VAL:HG22	1.88	0.71
1:H:337:LYS:HZ3	2:I:253:LEU:CD1	2.04	0.71
1:H:423:ILE:HG12	1:H:424:LYS:N	2.06	0.71
3:C:5:GLN:C	3:C:6:LEU:HD12	2.16	0.71
2:G:36:ALA:O	2:G:37:ILE:HG23	1.91	0.71
2:I:85:LEU:HD22	2:I:245:LEU:HD22	1.72	0.71
3:C:183:LEU:CD2	3:C:185:ARG:HH12	2.01	0.71
3:C:236:SER:HB3	3:C:237:PRO:HD2	1.71	0.71
3:A:236:SER:HB3	3:A:237:PRO:HD2	1.71	0.71
3:B:311:GLY:C	3:B:313:GLU:H	1.96	0.71
1:H:457:THR:CG2	1:H:461:ALA:HB3	2.20	0.71
3:C:10:THR:HG22	3:C:11:LYS:N	2.06	0.71
3:C:60:LEU:HD12	3:C:61:PHE:H	1.55	0.71
3:D:317:HIS:O	3:D:318:ILE:HG13	1.89	0.71
3:A:223:HIS:C	3:A:225:PRO:HD3	2.16	0.71
3:D:97:SER:O	3:D:101:LYS:HB2	1.89	0.71
3:A:13:TRP:HH2	3:A:53:GLU:OE2	1.74	0.71
3:A:306:VAL:H	3:A:317:HIS:HB2	1.54	0.71
1:H:419:LEU:C	1:H:421:LEU:H	1.98	0.71
1:F:87:ILE:HA	1:F:490:ILE:HG21	1.71	0.71
3:A:7:GLN:HA	3:A:23:ASN:OD1	1.91	0.71
3:A:270:VAL:HG13	3:A:271:GLU:H	1.55	0.71
3:C:13:TRP:HH2	3:C:53:GLU:OE2	1.74	0.71
3:D:198:MET:HE2	3:D:234:ILE:CG2	2.21	0.71
1:F:281:PHE:CA	1:F:467:LEU:HD21	2.20	0.71
1:F:284:THR:OG1	1:F:467:LEU:HD23	1.91	0.71
1:F:376:ASN:HD22	1:F:379:LEU:HB3	1.56	0.71
1:F:387:LEU:CD2	1:F:429:LEU:HD13	2.15	0.71
1:F:457:THR:CG2	1:F:461:ALA:HB3	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:301:GLU:HA	3:C:344:ALA:CB	2.20	0.71
1:F:289:LEU:HD23	1:F:434:PHE:HE2	1.56	0.70
1:F:372:LEU:HD12	1:F:443:LEU:CD2	2.19	0.70
3:B:77:VAL:HG12	3:B:78:GLY:N	2.06	0.70
3:C:307:VAL:O	3:C:307:VAL:HG12	1.90	0.70
3:D:55:ILE:HG21	3:D:68:ASN:CG	2.15	0.70
3:D:350:GLU:HB2	3:D:366:HIS:CE1	2.26	0.70
1:F:362:PHE:O	1:F:452:PRO:HD3	1.91	0.70
2:G:93:GLY:HA2	2:G:223:PHE:CE1	2.26	0.70
1:H:322:ILE:HG21	2:I:278:PHE:CE1	2.26	0.70
1:H:387:LEU:CD2	1:H:429:LEU:HD13	2.15	0.70
3:C:7:GLN:HA	3:C:23:ASN:OD1	1.91	0.70
3:A:351:ARG:HE	3:A:368:GLU:CD	1.99	0.70
1:H:328:PRO:HD3	2:I:274:ILE:CG1	2.16	0.70
2:I:5:GLN:OE1	2:I:7:LYS:HB2	1.91	0.70
3:D:77:VAL:HG12	3:D:78:GLY:N	2.06	0.70
1:F:86:THR:O	1:F:490:ILE:HG21	1.91	0.70
1:F:374:ILE:HD12	1:F:375:VAL:N	2.07	0.70
1:H:376:ASN:HD22	1:H:379:LEU:HB3	1.56	0.70
2:I:36:ALA:O	2:I:37:ILE:HG23	1.91	0.70
2:I:212:VAL:N	2:I:213:PRO:HD2	2.06	0.70
3:D:180:HIS:HA	3:D:187:MET:CE	2.21	0.70
1:F:72:MET:HE1	1:F:75:MET:SD	2.32	0.70
2:G:5:GLN:OE1	2:G:7:LYS:HB2	1.91	0.70
3:A:203:LYS:HD3	3:A:215:VAL:HG11	1.73	0.70
3:A:206:VAL:HG11	3:A:230:VAL:HG22	1.72	0.70
1:H:87:ILE:HA	1:H:490:ILE:HG21	1.71	0.70
2:I:244:THR:OG1	2:I:247:VAL:HG23	1.91	0.70
2:I:254:ASN:HB2	2:I:255:PRO:HD2	1.73	0.70
1:F:322:ILE:HG21	2:G:278:PHE:CE1	2.26	0.70
2:G:198:THR:OG1	2:G:199:PRO:HD2	1.91	0.70
2:G:212:VAL:N	2:G:213:PRO:HD2	2.06	0.70
3:A:60:LEU:HD12	3:A:61:PHE:H	1.56	0.70
3:A:178:ARG:O	3:A:181:LYS:HG2	1.92	0.70
1:H:374:ILE:HD12	1:H:375:VAL:N	2.07	0.70
2:I:18:LEU:HD23	2:I:19:LEU:N	2.07	0.70
3:B:10:THR:HB	3:B:57:SER:HB2	1.73	0.70
1:H:100:LEU:HB3	1:H:104:ARG:CG	2.15	0.70
1:H:285:VAL:HG23	1:H:438:PHE:HE2	1.56	0.70
1:H:362:PHE:O	1:H:452:PRO:HD3	1.91	0.70
3:C:351:ARG:HE	3:C:368:GLU:CD	1.99	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:298:VAL:HG12	1:F:302:LEU:HD12	1.73	0.70
3:A:85:ALA:C	3:A:86:LEU:HD23	2.16	0.70
3:A:91:SER:HB2	3:A:129:ARG:O	1.92	0.70
3:A:334:VAL:HG12	3:A:335:VAL:N	2.06	0.70
3:B:174:ILE:O	3:B:177:SER:HB3	1.92	0.70
3:B:198:MET:HE2	3:B:234:ILE:CG2	2.21	0.70
3:C:91:SER:HB2	3:C:129:ARG:O	1.91	0.70
3:D:87:TYR:H	3:D:95:ASN:HD21	1.36	0.70
1:F:423:ILE:HG12	1:F:424:LYS:N	2.06	0.70
3:B:350:GLU:HB2	3:B:366:HIS:CE1	2.26	0.70
1:H:86:THR:O	1:H:490:ILE:HG21	1.91	0.70
1:H:298:VAL:HG12	1:H:302:LEU:HD12	1.72	0.70
3:C:203:LYS:HD3	3:C:215:VAL:HG11	1.73	0.70
3:D:174:ILE:O	3:D:177:SER:HB3	1.92	0.70
3:A:153:SER:O	3:A:185:ARG:HB3	1.92	0.70
3:B:18:VAL:HG13	3:B:19:SER:N	2.07	0.70
3:B:34:PHE:N	3:B:34:PHE:HD2	1.90	0.70
3:B:180:HIS:HA	3:B:187:MET:CE	2.21	0.70
3:B:368:GLU:HB3	3:B:369:PRO:CD	2.20	0.70
3:C:130:LYS:HB2	3:C:131:PRO:HD2	1.74	0.70
3:A:5:GLN:C	3:A:6:LEU:HD12	2.16	0.69
3:A:353:HIS:CD2	3:A:364:ARG:HD3	2.27	0.69
2:I:93:GLY:HA2	2:I:223:PHE:CE1	2.26	0.69
3:C:178:ARG:O	3:C:181:LYS:HG2	1.92	0.69
3:D:10:THR:HB	3:D:57:SER:HB2	1.73	0.69
1:F:371:MET:SD	1:F:447:LEU:HD11	2.33	0.69
2:G:114:ARG:HG2	2:G:118:LYS:HZ1	1.55	0.69
3:A:10:THR:HG22	3:A:11:LYS:N	2.06	0.69
1:H:72:MET:HE1	1:H:75:MET:SD	2.31	0.69
2:I:249:MET:SD	2:I:266:ALA:HB1	2.32	0.69
1:H:337:LYS:HZ3	2:I:253:LEU:HG	1.55	0.69
2:I:198:THR:OG1	2:I:199:PRO:HD2	1.91	0.69
3:C:65:LYS:CD	3:C:65:LYS:H	2.03	0.69
3:C:353:HIS:CD2	3:C:364:ARG:HD3	2.27	0.69
3:D:34:PHE:HB2	3:D:190:VAL:HG22	1.74	0.69
3:B:34:PHE:HB2	3:B:190:VAL:HG22	1.74	0.69
1:H:289:LEU:HD23	1:H:434:PHE:HE2	1.55	0.69
2:I:265:ALA:O	2:I:268:VAL:HB	1.93	0.69
3:C:334:VAL:HG12	3:C:335:VAL:N	2.06	0.69
3:D:316:ILE:HG22	3:D:317:HIS:O	1.92	0.69
3:A:307:VAL:O	3:A:307:VAL:HG12	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:284:THR:OG1	1:H:467:LEU:HD23	1.91	0.69
3:A:130:LYS:HB2	3:A:131:PRO:HD2	1.74	0.69
3:A:156:LEU:C	3:A:157:LEU:HD12	2.18	0.69
3:B:316:ILE:HG22	3:B:317:HIS:O	1.92	0.69
1:H:286:VAL:O	1:H:290:ILE:HG12	1.93	0.69
3:C:223:HIS:C	3:C:225:PRO:HD3	2.16	0.69
1:F:486:LEU:CD2	2:G:135:LEU:HD21	2.07	0.69
2:G:18:LEU:HD23	2:G:19:LEU:N	2.07	0.69
1:F:468:VAL:HG23	2:G:134:VAL:HG23	1.74	0.69
2:G:284:TRP:O	2:G:286:VAL:N	2.26	0.69
3:A:46:LEU:HD23	3:A:79:MET:HE2	1.75	0.69
3:A:76:GLY:O	3:A:152:PRO:HB2	1.93	0.69
3:A:88:PRO:HA	3:A:131:PRO:HG2	1.75	0.69
3:B:4:VAL:HG13	3:B:26:ILE:HB	1.75	0.69
1:H:510:ARG:HG3	2:I:175:TRP:CH2	2.28	0.69
3:C:85:ALA:C	3:C:86:LEU:HD23	2.16	0.69
3:C:214:GLN:CG	3:C:215:VAL:H	2.05	0.69
3:C:270:VAL:CG2	3:C:362:CYS:HB3	2.23	0.69
3:D:4:VAL:HG13	3:D:26:ILE:HB	1.75	0.69
3:D:276:GLN:NE2	3:D:277:VAL:HG22	2.07	0.69
2:G:249:MET:SD	2:G:266:ALA:HB1	2.33	0.69
2:G:254:ASN:HB2	2:G:255:PRO:HD2	1.73	0.69
3:A:96:MET:HE2	3:A:145:GLY:HA3	1.75	0.69
3:D:11:LYS:HG3	3:D:12:ALA:H	1.58	0.69
3:A:65:LYS:CD	3:A:65:LYS:H	2.03	0.69
3:A:188:ILE:HD12	3:A:188:ILE:N	2.08	0.69
3:D:34:PHE:HD2	3:D:34:PHE:N	1.90	0.69
3:A:11:LYS:CA	3:A:56:THR:HB	2.23	0.68
3:A:180:HIS:O	3:A:184:GLY:N	2.26	0.68
3:B:34:PHE:C	3:B:35:VAL:HG22	2.17	0.68
3:B:194:GLN:O	3:B:197:ALA:HB3	1.94	0.68
3:B:246:VAL:HG21	3:B:281:MET:HE3	1.75	0.68
3:B:292:PRO:C	3:B:345:ILE:HG22	2.19	0.68
1:H:100:LEU:CD2	1:H:104:ARG:HE	2.03	0.68
3:C:112:GLN:O	3:C:116:GLN:HB2	1.93	0.68
1:F:510:ARG:HG3	2:G:175:TRP:CH2	2.28	0.68
2:G:265:ALA:O	2:G:268:VAL:HB	1.93	0.68
1:H:284:THR:HG21	1:H:467:LEU:HD23	1.75	0.68
3:C:96:MET:HE2	3:C:145:GLY:HA3	1.75	0.68
3:C:270:VAL:HG13	3:C:271:GLU:H	1.55	0.68
3:B:354:LEU:HD12	3:B:355:PHE:H	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:284:TRP:O	2:I:286:VAL:N	2.26	0.68
3:C:11:LYS:CA	3:C:56:THR:HB	2.23	0.68
3:D:287:PRO:HA	3:D:290:LEU:HD12	1.75	0.68
3:D:306:VAL:HG12	3:D:307:VAL:N	2.08	0.68
1:F:279:ALA:HB1	1:F:454:ARG:NH2	2.08	0.68
3:A:65:LYS:H	3:A:65:LYS:HD3	1.58	0.68
3:A:270:VAL:CG2	3:A:362:CYS:HB3	2.23	0.68
3:B:11:LYS:NZ	3:B:53:GLU:HG3	2.09	0.68
1:H:339:LEU:O	1:H:345:GLY:HA3	1.94	0.68
3:D:32:VAL:HG12	3:D:33:VAL:H	1.57	0.68
3:D:223:HIS:O	3:D:225:PRO:HD3	1.93	0.68
1:F:75:MET:HE1	2:G:125:MET:SD	2.34	0.68
1:F:284:THR:HG21	1:F:467:LEU:HD23	1.75	0.68
3:A:214:GLN:CG	3:A:215:VAL:H	2.05	0.68
3:A:316:ILE:O	3:A:329:TYR:HB3	1.93	0.68
3:B:32:VAL:HG12	3:B:33:VAL:H	1.58	0.68
3:B:100:LEU:HD13	3:B:110:ILE:HG12	1.76	0.68
3:C:33:VAL:CG1	3:C:201:ALA:HB2	2.23	0.68
3:C:65:LYS:H	3:C:65:LYS:HD3	1.58	0.68
3:C:316:ILE:O	3:C:329:TYR:HB3	1.93	0.68
3:D:19:SER:OG	3:D:48:MET:HE1	1.93	0.68
3:D:34:PHE:C	3:D:35:VAL:HG22	2.17	0.68
1:F:286:VAL:O	1:F:290:ILE:HG12	1.93	0.68
3:A:33:VAL:CG1	3:A:201:ALA:HB2	2.23	0.68
3:A:262:ASN:OD1	3:A:264:GLN:HG3	1.93	0.68
2:I:103:SER:OG	2:I:170:ILE:HG22	1.94	0.68
3:C:180:HIS:O	3:C:184:GLY:N	2.26	0.68
3:A:81:PHE:H	3:A:81:PHE:HD1	1.42	0.68
3:B:350:GLU:CD	3:B:350:GLU:N	2.51	0.68
1:H:371:MET:SD	1:H:447:LEU:HD11	2.33	0.68
3:C:156:LEU:C	3:C:157:LEU:HD12	2.18	0.68
3:C:262:ASN:OD1	3:C:264:GLN:HG3	1.93	0.68
3:D:10:THR:HG22	3:D:11:LYS:H	1.58	0.68
3:B:276:GLN:NE2	3:B:277:VAL:HG22	2.08	0.68
3:B:287:PRO:HA	3:B:290:LEU:HD12	1.75	0.68
3:C:336:LEU:O	3:C:337:VAL:HG23	1.94	0.68
3:C:368:GLU:CG	3:C:369:PRO:HD2	2.23	0.68
3:D:18:VAL:HG13	3:D:19:SER:N	2.07	0.68
3:D:194:GLN:O	3:D:197:ALA:HB3	1.94	0.68
3:D:292:PRO:C	3:D:345:ILE:HG22	2.19	0.68
2:G:129:GLN:C	2:G:131:PHE:H	2.02	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:34:PHE:N	3:B:34:PHE:CD2	2.62	0.68
3:B:83:SER:O	3:B:84:TYR:CG	2.47	0.68
1:H:87:ILE:HG12	1:H:494:ILE:CB	2.24	0.68
2:I:23:PHE:O	2:I:27:ILE:HG12	1.94	0.68
2:I:129:GLN:O	2:I:131:PHE:N	2.25	0.68
3:C:81:PHE:CD1	3:C:81:PHE:N	2.59	0.68
1:F:366:THR:CG2	1:F:367:THR:N	2.57	0.68
3:A:231:ALA:HB1	3:A:239:MET:SD	2.34	0.68
3:B:306:VAL:O	3:B:316:ILE:HG23	1.94	0.68
3:C:76:GLY:O	3:C:152:PRO:HB2	1.93	0.68
3:C:153:SER:O	3:C:185:ARG:HB3	1.92	0.68
3:C:231:ALA:HB1	3:C:239:MET:SD	2.34	0.68
3:D:350:GLU:CD	3:D:350:GLU:N	2.51	0.68
3:A:112:GLN:O	3:A:116:GLN:HB2	1.93	0.67
3:A:330:ARG:NH1	3:B:312:ASN:OD1	2.26	0.67
1:H:280:ILE:HD12	1:H:467:LEU:HA	1.77	0.67
1:H:335:ILE:CD1	1:H:339:LEU:HD11	2.25	0.67
1:H:468:VAL:HG23	2:I:134:VAL:HG23	1.74	0.67
3:C:188:ILE:HD12	3:C:188:ILE:N	2.08	0.67
1:F:317:TYR:O	1:F:321:LEU:HG	1.95	0.67
1:F:330:PHE:HE2	2:G:246:ALA:O	1.76	0.67
3:A:315:GLN:HE21	3:A:330:ARG:CG	2.05	0.67
3:B:10:THR:HG22	3:B:11:LYS:H	1.58	0.67
3:B:223:HIS:O	3:B:225:PRO:HD3	1.93	0.67
3:C:79:MET:CG	3:C:80:VAL:H	2.00	0.67
3:D:100:LEU:HD13	3:D:110:ILE:HG12	1.76	0.67
3:B:258:LEU:HD22	3:B:258:LEU:N	2.10	0.67
3:B:306:VAL:HG12	3:B:307:VAL:N	2.08	0.67
1:H:279:ALA:HB1	1:H:454:ARG:NH2	2.08	0.67
3:C:138:GLN:O	3:C:142:VAL:HG23	1.95	0.67
1:H:87:ILE:O	1:H:90:ALA:HB3	1.95	0.67
3:C:86:LEU:O	3:C:88:PRO:HD3	1.94	0.67
3:D:306:VAL:O	3:D:316:ILE:HG23	1.94	0.67
3:D:344:ALA:O	3:D:345:ILE:HG23	1.95	0.67
1:F:280:ILE:HD12	1:F:467:LEU:HA	1.76	0.67
1:F:337:LYS:HZ3	2:G:253:LEU:CG	2.07	0.67
3:C:315:GLN:HE21	3:C:330:ARG:CG	2.05	0.67
1:F:365:PRO:HG3	1:F:452:PRO:HG3	1.76	0.67
2:G:274:ILE:O	2:G:278:PHE:HB3	1.95	0.67
3:A:336:LEU:O	3:A:337:VAL:HG23	1.94	0.67
3:A:357:GLU:C	3:A:359:GLY:H	2.02	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:75:MET:HE1	2:I:125:MET:SD	2.34	0.67
3:D:246:VAL:HG21	3:D:281:MET:HE3	1.75	0.67
1:F:87:ILE:O	1:F:90:ALA:HB3	1.95	0.67
2:G:103:SER:OG	2:G:170:ILE:HG22	1.94	0.67
3:A:368:GLU:CG	3:A:369:PRO:HD2	2.23	0.67
3:B:289:HIS:CE1	3:B:351:ARG:HD2	2.30	0.67
1:H:365:PRO:HG3	1:H:452:PRO:HG3	1.76	0.67
3:C:46:LEU:HD23	3:C:79:MET:HE2	1.75	0.67
3:D:287:PRO:HB3	3:D:330:ARG:H	1.59	0.67
3:A:81:PHE:CD1	3:A:81:PHE:N	2.59	0.67
2:I:21:LEU:O	2:I:24:ILE:HG13	1.95	0.67
2:I:129:GLN:C	2:I:131:PHE:H	2.02	0.67
3:C:357:GLU:C	3:C:359:GLY:H	2.02	0.67
3:D:354:LEU:HD12	3:D:355:PHE:H	1.59	0.67
1:F:468:VAL:O	1:F:471:THR:HB	1.95	0.67
3:A:86:LEU:O	3:A:88:PRO:HD3	1.94	0.67
3:B:6:LEU:O	3:B:7:GLN:HG3	1.95	0.67
1:H:366:THR:CG2	1:H:367:THR:N	2.57	0.67
3:C:310:LEU:O	3:C:310:LEU:HD23	1.95	0.67
3:D:4:VAL:CG2	3:D:5:GLN:N	2.58	0.67
1:F:460:PRO:HD2	1:F:474:ILE:CG2	2.25	0.67
3:B:19:SER:OG	3:B:48:MET:HE1	1.93	0.67
1:H:283:TRP:NE1	1:H:464:THR:O	2.29	0.67
1:H:460:PRO:HD2	1:H:474:ILE:CG2	2.25	0.67
1:H:468:VAL:O	1:H:471:THR:HB	1.95	0.67
2:I:274:ILE:O	2:I:278:PHE:HB3	1.95	0.67
3:C:44:THR:CG2	3:C:48:MET:HE2	2.25	0.67
3:D:11:LYS:NZ	3:D:53:GLU:HG3	2.09	0.67
3:B:11:LYS:HG3	3:B:12:ALA:H	1.58	0.66
3:B:344:ALA:O	3:B:345:ILE:HG23	1.95	0.66
3:D:258:LEU:HD22	3:D:258:LEU:N	2.10	0.66
1:F:339:LEU:O	1:F:345:GLY:HA3	1.94	0.66
2:G:129:GLN:O	2:G:131:PHE:N	2.25	0.66
3:A:10:THR:HG22	3:A:11:LYS:H	1.60	0.66
3:B:240:ASN:ND2	3:B:328:VAL:HB	2.10	0.66
3:B:258:LEU:HD22	3:B:258:LEU:H	1.60	0.66
1:H:82:PRO:HG3	2:I:143:LEU:HD22	1.77	0.66
3:D:40:CYS:SG	3:D:41:GLY:N	2.69	0.66
3:D:281:MET:HB3	3:D:354:LEU:HD11	1.76	0.66
1:F:79:VAL:HG22	2:G:168:GLY:HA3	1.78	0.66
1:F:86:THR:O	1:F:90:ALA:HB2	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:335:ILE:CD1	1:F:339:LEU:HD11	2.25	0.66
3:B:281:MET:HB3	3:B:354:LEU:HD11	1.76	0.66
1:H:100:LEU:CB	1:H:104:ARG:HG3	2.19	0.66
1:H:330:PHE:HE2	2:I:246:ALA:O	1.77	0.66
3:D:240:ASN:ND2	3:D:328:VAL:HB	2.10	0.66
3:D:347:LEU:O	3:D:348:PRO:C	2.36	0.66
1:F:87:ILE:HG12	1:F:494:ILE:CB	2.24	0.66
2:G:24:ILE:O	2:G:28:MET:HG2	1.94	0.66
3:A:84:TYR:OH	3:A:163:ASN:HB2	1.95	0.66
3:B:249:THR:OG1	3:B:250:ALA:N	2.28	0.66
3:B:287:PRO:HB3	3:B:330:ARG:H	1.59	0.66
1:H:91:PHE:O	1:H:263:ASN:ND2	2.29	0.66
3:D:6:LEU:O	3:D:7:GLN:HG3	1.95	0.66
3:D:353:HIS:CD2	3:D:364:ARG:HD3	2.30	0.66
1:F:91:PHE:O	1:F:263:ASN:ND2	2.29	0.66
1:F:284:THR:HG21	1:F:467:LEU:H	1.61	0.66
3:A:138:GLN:O	3:A:142:VAL:HG23	1.95	0.66
3:A:193:ASP:O	3:A:194:GLN:C	2.37	0.66
3:B:40:CYS:SG	3:B:41:GLY:N	2.69	0.66
3:B:243:PRO:C	3:B:244:VAL:HG22	2.21	0.66
3:B:353:HIS:CD2	3:B:364:ARG:HD3	2.30	0.66
1:H:86:THR:O	1:H:90:ALA:HB2	1.95	0.66
3:C:291:LEU:O	3:C:346:GLY:N	2.27	0.66
3:D:18:VAL:CG1	3:D:19:SER:N	2.59	0.66
3:D:83:SER:O	3:D:84:TYR:CG	2.47	0.66
1:F:332:SER:O	1:F:335:ILE:HG13	1.96	0.66
1:F:381:TYR:CD1	1:F:382:PRO:HD3	2.31	0.66
2:G:23:PHE:O	2:G:27:ILE:HG12	1.94	0.66
1:H:317:TYR:O	1:H:321:LEU:HG	1.94	0.66
1:H:332:SER:O	1:H:335:ILE:HG13	1.96	0.66
3:C:88:PRO:HA	3:C:131:PRO:HG2	1.75	0.66
3:C:363:ARG:HG3	3:C:363:ARG:O	1.95	0.66
3:D:289:HIS:CE1	3:D:351:ARG:HD2	2.30	0.66
1:F:396:PRO:HG2	1:F:399:LEU:HB2	1.78	0.66
2:G:21:LEU:O	2:G:24:ILE:HG13	1.95	0.66
3:B:274:ASP:HB3	3:B:356:ARG:HH21	1.61	0.66
2:I:24:ILE:O	2:I:28:MET:HG2	1.94	0.66
3:D:198:MET:HE2	3:D:234:ILE:HG21	1.78	0.66
1:F:457:THR:HG21	1:F:461:ALA:HB3	1.78	0.66
1:F:499:GLY:O	1:F:503:ILE:HG12	1.96	0.66
2:G:25:ALA:O	2:G:28:MET:HB2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:156:LEU:C	3:B:157:LEU:HD12	2.21	0.66
1:H:267:VAL:HG13	1:H:488:ALA:HA	1.77	0.66
1:H:499:GLY:O	1:H:503:ILE:HG12	1.96	0.66
3:C:33:VAL:C	3:C:34:PHE:CD2	2.74	0.66
3:C:193:ASP:O	3:C:194:GLN:C	2.37	0.66
3:D:23:ASN:O	3:D:24:LEU:HD23	1.96	0.66
3:D:156:LEU:C	3:D:157:LEU:HD12	2.21	0.66
3:D:298:VAL:CG1	3:D:347:LEU:HB3	2.23	0.66
3:D:358:ASP:CG	3:D:359:GLY:N	2.43	0.66
3:A:44:THR:CG2	3:A:48:MET:HE2	2.25	0.66
3:A:126:LEU:HD11	3:A:138:GLN:NE2	2.11	0.66
3:A:291:LEU:O	3:A:346:GLY:N	2.27	0.66
3:A:310:LEU:HD23	3:A:310:LEU:O	1.95	0.66
3:B:4:VAL:CG2	3:B:5:GLN:N	2.58	0.66
1:H:384:MET:O	1:H:388:CYS:HB2	1.96	0.66
3:C:299:ILE:HG22	3:C:300:LEU:N	2.11	0.66
3:C:351:ARG:O	3:C:352:CYS:O	2.14	0.66
3:D:243:PRO:C	3:D:244:VAL:HG22	2.21	0.66
1:F:267:VAL:HG13	1:F:488:ALA:HA	1.77	0.66
1:F:488:ALA:O	1:F:492:THR:HG22	1.96	0.66
3:A:315:GLN:NE2	3:A:330:ARG:HG2	2.06	0.66
3:B:242:LEU:CD1	3:B:283:LEU:HB3	2.26	0.66
2:I:25:ALA:O	2:I:28:MET:HB2	1.95	0.66
1:F:330:PHE:CD1	1:F:331:ILE:N	2.64	0.65
1:F:423:ILE:CD1	1:F:424:LYS:H	2.08	0.65
3:A:236:SER:O	3:A:237:PRO:O	2.14	0.65
3:A:363:ARG:HG3	3:A:363:ARG:O	1.95	0.65
3:B:23:ASN:O	3:B:24:LEU:HD23	1.96	0.65
1:H:410:PRO:O	1:H:413:ASN:HB2	1.96	0.65
1:H:423:ILE:CD1	1:H:424:LYS:H	2.08	0.65
2:I:146:ARG:HA	2:I:149:GLU:OE2	1.96	0.65
3:C:10:THR:HG22	3:C:11:LYS:H	1.60	0.65
3:C:11:LYS:HA	3:C:56:THR:OG1	1.96	0.65
1:F:82:PRO:HG3	2:G:143:LEU:HD22	1.77	0.65
3:A:299:ILE:HG22	3:A:300:LEU:N	2.11	0.65
1:H:88:ALA:O	1:H:263:ASN:ND2	2.28	0.65
1:H:486:LEU:HD12	1:H:486:LEU:N	2.11	0.65
2:I:174:VAL:HA	2:I:177:ILE:HG22	1.78	0.65
3:C:81:PHE:H	3:C:81:PHE:HD1	1.42	0.65
3:D:242:LEU:CD1	3:D:283:LEU:HB3	2.26	0.65
1:F:486:LEU:HD12	1:F:486:LEU:N	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:126:LEU:HD22	2:G:127:ILE:HG13	1.77	0.65
2:G:141:TYR:CE1	2:G:156:LEU:HD11	2.32	0.65
3:C:126:LEU:HD11	3:C:138:GLN:NE2	2.11	0.65
1:F:384:MET:O	1:F:388:CYS:HB2	1.96	0.65
2:G:187:SER:HA	2:G:190:GLU:HG3	1.78	0.65
3:A:306:VAL:O	3:A:316:ILE:HG23	1.97	0.65
1:H:457:THR:HG21	1:H:461:ALA:HB3	1.78	0.65
1:H:510:ARG:O	1:H:511:MET:HG3	1.97	0.65
2:I:141:TYR:CE1	2:I:156:LEU:HD11	2.32	0.65
3:D:368:GLU:HB3	3:D:369:PRO:CD	2.21	0.65
3:B:18:VAL:CG1	3:B:19:SER:N	2.59	0.65
3:B:188:ILE:N	3:B:188:ILE:CD1	2.60	0.65
1:H:79:VAL:HG22	2:I:168:GLY:HA3	1.77	0.65
1:H:81:PHE:HB3	1:H:82:PRO:HD3	1.78	0.65
1:H:396:PRO:HG2	1:H:399:LEU:HB2	1.78	0.65
3:C:12:ALA:HA	3:C:17:VAL:HA	1.79	0.65
3:C:174:ILE:HG22	3:C:178:ARG:HG3	1.77	0.65
1:F:100:LEU:CB	1:F:104:ARG:HG3	2.19	0.65
1:F:468:VAL:HG13	1:F:469:ASN:N	2.11	0.65
2:G:92:ALA:HA	2:G:226:ALA:CB	2.27	0.65
3:A:121:LEU:O	3:A:123:LEU:HD13	1.97	0.65
3:A:219:LEU:O	3:A:222:TYR:N	2.30	0.65
3:B:214:GLN:CD	3:B:226:ALA:HB2	2.21	0.65
3:B:298:VAL:CG1	3:B:347:LEU:HB3	2.23	0.65
3:D:274:ASP:HB3	3:D:356:ARG:HH21	1.61	0.65
1:F:410:PRO:O	1:F:413:ASN:HB2	1.96	0.65
2:G:146:ARG:HA	2:G:149:GLU:OE2	1.96	0.65
2:G:174:VAL:HA	2:G:177:ILE:HG22	1.78	0.65
3:A:29:GLY:HA2	3:A:184:GLY:O	1.96	0.65
3:A:174:ILE:HG22	3:A:178:ARG:HG3	1.77	0.65
1:H:488:ALA:O	1:H:492:THR:HG22	1.96	0.65
3:D:96:MET:C	3:D:98:PHE:H	2.05	0.65
3:B:6:LEU:C	3:B:7:GLN:HG3	2.22	0.65
3:B:96:MET:O	3:B:98:PHE:N	2.27	0.65
1:H:330:PHE:CD1	1:H:331:ILE:N	2.64	0.65
3:C:29:GLY:HA2	3:C:184:GLY:O	1.96	0.65
3:C:186:THR:O	3:C:187:MET:HG3	1.95	0.65
3:C:219:LEU:O	3:C:222:TYR:N	2.30	0.65
1:F:360:ALA:HB1	1:F:363:SER:HB2	1.79	0.65
3:B:96:MET:C	3:B:98:PHE:H	2.05	0.65
1:H:468:VAL:HG13	1:H:469:ASN:N	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:121:LEU:O	3:C:123:LEU:HD13	1.97	0.65
3:C:236:SER:O	3:C:237:PRO:O	2.14	0.65
3:C:354:LEU:O	3:C:362:CYS:HB2	1.96	0.65
1:F:81:PHE:HB3	1:F:82:PRO:HD3	1.78	0.65
1:F:283:TRP:NE1	1:F:464:THR:O	2.28	0.65
1:F:497:LEU:HD22	2:G:131:PHE:HD2	1.63	0.65
3:A:214:GLN:CG	3:A:215:VAL:N	2.59	0.65
1:H:422:LEU:C	1:H:425:PRO:HD2	2.22	0.65
3:C:84:TYR:OH	3:C:163:ASN:HB2	1.95	0.65
3:A:351:ARG:O	3:A:352:CYS:O	2.14	0.64
3:B:4:VAL:HG22	3:B:5:GLN:N	2.13	0.64
3:D:34:PHE:N	3:D:34:PHE:CD2	2.62	0.64
3:D:214:GLN:CD	3:D:226:ALA:HB2	2.21	0.64
3:D:285:ILE:HD12	3:D:286:ARG:H	1.62	0.64
1:F:337:LYS:HZ3	2:G:253:LEU:CD1	2.11	0.64
3:A:354:LEU:O	3:A:362:CYS:HB2	1.96	0.64
1:H:337:LYS:HG3	1:H:362:PHE:HZ	1.62	0.64
1:H:381:TYR:CD1	1:H:382:PRO:HD3	2.31	0.64
2:I:187:SER:HA	2:I:190:GLU:HG3	1.78	0.64
1:F:510:ARG:O	1:F:511:MET:HG3	1.97	0.64
2:G:204:ARG:O	2:G:209:PRO:CD	2.45	0.64
3:A:28:GLU:HG3	3:A:29:GLY:N	2.11	0.64
3:A:133:ALA:O	3:A:134:LEU:HG	1.97	0.64
3:A:279:ALA:HB1	3:A:281:MET:HE3	1.78	0.64
3:B:285:ILE:HD12	3:B:286:ARG:H	1.62	0.64
3:B:314:THR:HG22	3:B:315:GLN:N	2.12	0.64
3:C:307:VAL:HG23	3:C:339:GLU:HG2	1.79	0.64
1:F:497:LEU:HD22	2:G:131:PHE:CD2	2.33	0.64
3:B:198:MET:HE2	3:B:234:ILE:HG21	1.78	0.64
1:H:414:PHE:CE1	1:H:419:LEU:HD12	2.32	0.64
3:C:65:LYS:HD3	3:C:65:LYS:N	2.13	0.64
3:D:4:VAL:HG22	3:D:5:GLN:N	2.13	0.64
1:F:307:GLN:C	1:F:309:GLU:H	2.05	0.64
3:A:11:LYS:HA	3:A:56:THR:OG1	1.96	0.64
3:A:12:ALA:HA	3:A:17:VAL:HA	1.79	0.64
3:A:33:VAL:C	3:A:34:PHE:CD2	2.74	0.64
3:A:190:VAL:HG12	3:A:191:THR:N	2.12	0.64
3:A:270:VAL:CG1	3:A:271:GLU:N	2.61	0.64
3:A:307:VAL:HG23	3:A:339:GLU:HG2	1.79	0.64
1:H:360:ALA:HB1	1:H:363:SER:HB2	1.78	0.64
2:I:126:LEU:HD22	2:I:127:ILE:HG13	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:GLU:HG3	3:C:29:GLY:N	2.11	0.64
3:C:164:LEU:HD13	3:C:168:LEU:HG	1.79	0.64
3:D:314:THR:HG22	3:D:315:GLN:N	2.12	0.64
3:D:371:VAL:O	3:D:371:VAL:HG12	1.96	0.64
1:F:422:LEU:C	1:F:425:PRO:HD2	2.22	0.64
2:G:281:ALA:O	2:G:284:TRP:HB2	1.97	0.64
3:A:298:VAL:HB	3:A:347:LEU:HB3	1.78	0.64
3:B:5:GLN:O	3:B:6:LEU:HD12	1.98	0.64
3:C:270:VAL:CG1	3:C:271:GLU:N	2.61	0.64
3:C:306:VAL:O	3:C:316:ILE:HG23	1.97	0.64
3:D:6:LEU:C	3:D:7:GLN:HG3	2.22	0.64
3:D:227:ASP:HB2	3:D:359:GLY:O	1.98	0.64
1:H:422:LEU:HD23	1:H:425:PRO:HG3	1.80	0.64
2:I:92:ALA:HA	2:I:226:ALA:CB	2.27	0.64
3:C:83:SER:O	3:C:84:TYR:CG	2.51	0.64
3:C:133:ALA:O	3:C:134:LEU:HG	1.97	0.64
3:C:190:VAL:HG12	3:C:191:THR:N	2.12	0.64
3:C:279:ALA:HB1	3:C:281:MET:HE3	1.78	0.64
3:C:298:VAL:HB	3:C:347:LEU:HB3	1.78	0.64
3:C:330:ARG:NH1	3:D:312:ASN:OD1	2.26	0.64
3:D:249:THR:OG1	3:D:250:ALA:N	2.28	0.64
3:A:186:THR:O	3:A:187:MET:HG3	1.96	0.64
3:A:186:THR:HG22	3:A:187:MET:N	2.13	0.64
2:I:204:ARG:O	2:I:209:PRO:CD	2.45	0.64
3:C:169:ARG:HD3	3:C:193:ASP:OD2	1.98	0.64
3:D:67:MET:HE3	3:D:75:ARG:HA	1.78	0.64
1:F:486:LEU:CD1	1:F:490:ILE:HD11	2.26	0.64
2:G:194:LEU:HD23	3:A:72:PRO:HB2	1.80	0.64
3:A:224:TYR:CE2	3:A:371:VAL:HG11	2.33	0.64
3:B:336:LEU:O	3:B:337:VAL:CG2	2.45	0.64
1:H:373:ILE:CG1	1:H:374:ILE:N	2.59	0.64
1:H:497:LEU:HD22	2:I:131:PHE:HD2	1.63	0.64
2:I:187:SER:HA	2:I:190:GLU:CG	2.28	0.64
3:D:354:LEU:HG	3:D:355:PHE:N	2.12	0.64
1:F:278:LEU:H	1:F:278:LEU:HD22	1.62	0.64
2:G:187:SER:HA	2:G:190:GLU:CG	2.28	0.64
3:A:83:SER:O	3:A:84:TYR:CG	2.51	0.64
3:A:240:ASN:CG	3:A:327:LEU:HD12	2.23	0.64
3:A:334:VAL:O	3:A:335:VAL:CG2	2.46	0.64
1:H:278:LEU:HD22	1:H:278:LEU:H	1.62	0.64
1:H:298:VAL:O	1:H:302:LEU:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:115:PHE:HB2	2:I:116:PRO:CD	2.23	0.64
1:F:337:LYS:HG3	1:F:362:PHE:HZ	1.62	0.63
3:B:334:VAL:CG1	3:B:335:VAL:N	2.61	0.63
1:H:41:LEU:CD1	1:H:89:ILE:HD11	2.28	0.63
1:H:501:LEU:HD13	2:I:127:ILE:CG2	2.28	0.63
2:I:28:MET:SD	2:I:31:LEU:HD11	2.38	0.63
2:I:254:ASN:HB2	2:I:255:PRO:HD3	1.80	0.63
3:C:186:THR:HG22	3:C:187:MET:N	2.13	0.63
3:C:240:ASN:ND2	3:C:327:LEU:HD12	2.13	0.63
3:D:188:ILE:N	3:D:188:ILE:CD1	2.60	0.63
1:F:298:VAL:O	1:F:302:LEU:HB2	1.97	0.63
1:F:414:PHE:CE1	1:F:419:LEU:HD12	2.32	0.63
2:G:82:LEU:CD2	2:G:269:MET:HE1	2.28	0.63
3:B:67:MET:HE3	3:B:75:ARG:HA	1.79	0.63
1:H:410:PRO:HA	1:H:413:ASN:HD22	1.62	0.63
3:D:258:LEU:HD22	3:D:258:LEU:H	1.60	0.63
3:D:334:VAL:CG1	3:D:335:VAL:N	2.61	0.63
3:D:350:GLU:HB3	3:D:366:HIS:CD2	2.33	0.63
3:A:65:LYS:HD3	3:A:65:LYS:N	2.13	0.63
3:A:130:LYS:HE2	3:A:132:LYS:HE2	1.80	0.63
3:B:227:ASP:HB2	3:B:359:GLY:O	1.98	0.63
3:B:350:GLU:CD	3:B:350:GLU:H	2.04	0.63
3:B:350:GLU:HB3	3:B:366:HIS:CD2	2.34	0.63
3:B:371:VAL:O	3:B:371:VAL:HG12	1.96	0.63
3:C:83:SER:O	3:C:84:TYR:CD2	2.51	0.63
1:F:391:LEU:HD23	1:F:422:LEU:CD2	2.28	0.63
1:F:398:ASP:O	1:F:401:GLU:N	2.31	0.63
3:A:83:SER:O	3:A:84:TYR:CD2	2.51	0.63
1:H:381:TYR:HD1	1:H:382:PRO:CD	2.11	0.63
1:H:396:PRO:HG3	1:H:399:LEU:HD12	1.79	0.63
1:H:497:LEU:HD22	2:I:131:PHE:CD2	2.33	0.63
2:I:148:GLY:HA2	2:I:155:GLY:CA	2.28	0.63
3:D:198:MET:CE	3:D:234:ILE:HG21	2.29	0.63
2:G:31:LEU:O	2:G:34:VAL:HB	1.99	0.63
1:H:438:PHE:HD1	1:H:439:ASN:OD1	1.82	0.63
2:I:281:ALA:O	2:I:284:TRP:HB2	1.97	0.63
3:C:87:TYR:N	3:C:95:ASN:HD21	1.96	0.63
3:D:8:ASN:O	3:D:58:GLY:HA3	1.98	0.63
3:D:46:LEU:HD12	3:D:156:LEU:HD13	1.81	0.63
3:D:350:GLU:CD	3:D:350:GLU:H	2.04	0.63
1:F:422:LEU:HD23	1:F:425:PRO:HG3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:501:LEU:HD13	2:G:127:ILE:CG2	2.28	0.63
3:B:8:ASN:O	3:B:58:GLY:HA3	1.98	0.63
3:B:223:HIS:HE1	3:B:369:PRO:HG2	1.63	0.63
3:B:226:ALA:HB3	3:B:230:VAL:CG2	2.22	0.63
3:B:292:PRO:HA	3:B:345:ILE:HG22	1.80	0.63
1:H:284:THR:HG21	1:H:467:LEU:H	1.61	0.63
3:C:12:ALA:HB2	3:C:17:VAL:HG13	1.79	0.63
3:C:130:LYS:HE2	3:C:132:LYS:HE2	1.80	0.63
3:C:179:LEU:O	3:C:183:LEU:N	2.30	0.63
3:C:253:GLN:HB2	3:C:267:TRP:CE3	2.34	0.63
3:D:292:PRO:HA	3:D:345:ILE:HG22	1.81	0.63
3:D:300:LEU:HD11	3:D:347:LEU:HB2	1.81	0.63
3:D:334:VAL:HG12	3:D:335:VAL:H	1.64	0.63
3:D:336:LEU:O	3:D:337:VAL:CG2	2.45	0.63
2:G:107:ALA:HB2	2:G:174:VAL:HG22	1.81	0.63
3:B:354:LEU:HG	3:B:355:PHE:N	2.12	0.63
1:H:328:PRO:CD	2:I:274:ILE:HG12	2.19	0.63
1:F:41:LEU:CD1	1:F:89:ILE:HD11	2.28	0.63
2:G:31:LEU:HD23	2:G:31:LEU:N	2.07	0.63
3:A:87:TYR:N	3:A:95:ASN:HD21	1.96	0.63
3:A:164:LEU:HD13	3:A:168:LEU:HG	1.80	0.63
3:A:253:GLN:HB2	3:A:267:TRP:CE3	2.34	0.63
3:A:283:LEU:HD12	3:A:353:HIS:O	1.98	0.63
3:B:46:LEU:HD12	3:B:156:LEU:HD13	1.81	0.63
1:H:268:PHE:O	1:H:270:ASP:N	2.32	0.63
1:H:330:PHE:O	1:H:333:ILE:HD12	1.99	0.63
1:H:348:ASN:HA	1:H:351:LEU:HB2	1.81	0.63
1:H:383:TYR:CD2	1:H:384:MET:HE2	2.33	0.63
1:H:391:LEU:HD23	1:H:422:LEU:CD2	2.28	0.63
2:I:107:ALA:HB2	2:I:174:VAL:HG22	1.81	0.63
2:I:173:HIS:ND1	2:I:218:VAL:HG13	2.14	0.63
3:C:145:GLY:CA	3:C:148:LEU:HD12	2.28	0.63
3:C:283:LEU:HD12	3:C:353:HIS:O	1.98	0.63
1:F:51:SER:O	1:F:55:TYR:HB2	1.99	0.63
1:F:341:ASN:HD22	1:F:344:PHE:CB	2.12	0.63
1:F:381:TYR:HD1	1:F:382:PRO:CD	2.11	0.63
1:F:422:LEU:HA	1:F:425:PRO:HG3	1.81	0.63
3:A:40:CYS:HB3	3:A:42:LYS:NZ	2.14	0.63
3:A:240:ASN:ND2	3:A:327:LEU:HD12	2.13	0.63
2:I:82:LEU:CD2	2:I:269:MET:HE1	2.28	0.63
3:C:306:VAL:CG1	3:C:307:VAL:H	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:96:MET:O	3:D:98:PHE:N	2.27	0.63
3:B:198:MET:CE	3:B:234:ILE:HG21	2.29	0.62
3:B:315:GLN:HA	3:B:329:TYR:O	1.98	0.62
1:H:337:LYS:NZ	2:I:253:LEU:HG	2.14	0.62
1:H:423:ILE:CG1	1:H:424:LYS:N	2.62	0.62
3:C:224:TYR:CE2	3:C:371:VAL:HG11	2.33	0.62
3:C:306:VAL:HB	3:C:317:HIS:CG	2.35	0.62
3:C:334:VAL:O	3:C:335:VAL:CG2	2.46	0.62
3:D:356:ARG:HD2	3:D:360:THR:OG1	1.99	0.62
1:F:383:TYR:CD2	1:F:384:MET:HE2	2.33	0.62
2:G:28:MET:SD	2:G:31:LEU:HD11	2.38	0.62
3:A:32:VAL:HG12	3:A:33:VAL:N	2.14	0.62
3:A:306:VAL:HB	3:A:317:HIS:CG	2.34	0.62
3:B:347:LEU:O	3:B:348:PRO:C	2.36	0.62
1:H:51:SER:O	1:H:55:TYR:HB2	1.99	0.62
1:H:307:GLN:C	1:H:309:GLU:H	2.05	0.62
1:H:337:LYS:HZ3	2:I:253:LEU:CG	2.11	0.62
1:H:341:ASN:HD22	1:H:344:PHE:CB	2.12	0.62
2:I:31:LEU:HD23	2:I:31:LEU:N	2.07	0.62
3:C:32:VAL:HG12	3:C:33:VAL:H	1.64	0.62
3:D:292:PRO:HD2	3:D:295:ILE:HD12	1.81	0.62
3:A:243:PRO:O	3:A:244:VAL:HG22	2.00	0.62
1:H:398:ASP:O	1:H:401:GLU:N	2.31	0.62
2:G:91:VAL:HG12	2:G:92:ALA:N	2.15	0.62
1:H:287:PHE:HE2	1:H:437:ASN:O	1.82	0.62
1:H:333:ILE:HA	1:H:336:PHE:HB2	1.81	0.62
3:C:32:VAL:HG12	3:C:33:VAL:N	2.14	0.62
3:C:96:MET:CE	3:C:145:GLY:HA3	2.29	0.62
1:F:330:PHE:O	1:F:333:ILE:HD12	1.99	0.62
1:F:410:PRO:HA	1:F:413:ASN:HD22	1.62	0.62
2:G:85:LEU:CD2	2:G:245:LEU:HD22	2.29	0.62
3:A:12:ALA:HB2	3:A:17:VAL:HG13	1.79	0.62
1:H:422:LEU:HA	1:H:425:PRO:HG3	1.81	0.62
3:D:6:LEU:HD23	3:D:9:VAL:HG21	1.81	0.62
1:F:396:PRO:HG3	1:F:399:LEU:HD12	1.79	0.62
1:F:438:PHE:HD1	1:F:439:ASN:OD1	1.82	0.62
2:G:86:TRP:NE1	2:G:90:LYS:HD2	2.15	0.62
3:A:164:LEU:CD2	3:A:168:LEU:HD23	2.29	0.62
3:A:169:ARG:HD3	3:A:193:ASP:OD2	1.98	0.62
3:B:255:GLN:NE2	3:B:267:TRP:NE1	2.48	0.62
3:B:292:PRO:HD2	3:B:295:ILE:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:356:ARG:HD2	3:B:360:THR:OG1	1.99	0.62
2:I:91:VAL:HG12	2:I:92:ALA:N	2.15	0.62
2:G:173:HIS:ND1	2:G:218:VAL:HG13	2.14	0.62
3:B:355:PHE:HB3	3:B:360:THR:O	2.00	0.62
2:I:31:LEU:O	2:I:34:VAL:HB	1.99	0.62
2:I:194:LEU:HD23	3:C:72:PRO:HB2	1.80	0.62
2:I:255:PRO:CB	2:I:259:LEU:HG	2.27	0.62
3:D:223:HIS:HE1	3:D:369:PRO:HG2	1.63	0.62
3:D:261:PRO:O	3:D:263:ARG:HG2	2.00	0.62
3:D:315:GLN:HA	3:D:329:TYR:O	1.98	0.62
3:A:306:VAL:CG1	3:A:307:VAL:H	2.12	0.62
3:A:351:ARG:HH11	3:A:351:ARG:HG3	1.65	0.62
3:B:315:GLN:C	3:B:316:ILE:HG13	2.25	0.62
1:H:503:ILE:HG22	1:H:507:LYS:HZ2	1.64	0.62
3:C:55:ILE:HD13	3:C:68:ASN:HB3	1.82	0.62
2:G:78:PRO:O	2:G:80:PRO:HD3	2.00	0.62
2:G:126:LEU:HD23	2:G:127:ILE:N	2.15	0.62
3:B:32:VAL:HG12	3:B:33:VAL:N	2.15	0.62
2:I:180:TYR:HE2	2:I:211:SER:HA	1.65	0.62
3:C:40:CYS:HB3	3:C:42:LYS:NZ	2.14	0.62
3:C:240:ASN:CG	3:C:327:LEU:HD12	2.23	0.62
3:C:251:ILE:O	3:C:272:SER:HB3	2.00	0.62
3:C:315:GLN:NE2	3:C:330:ARG:HG2	2.06	0.62
1:F:283:TRP:CZ3	1:F:369:ARG:HB3	2.35	0.62
1:F:348:ASN:HA	1:F:351:LEU:HB2	1.81	0.62
3:A:96:MET:CE	3:A:145:GLY:HA3	2.29	0.62
3:A:223:HIS:O	3:A:225:PRO:CD	2.46	0.62
3:B:152:PRO:O	3:B:154:VAL:N	2.33	0.62
3:B:223:HIS:C	3:B:225:PRO:HD3	2.24	0.62
2:I:85:LEU:CD2	2:I:245:LEU:HD22	2.29	0.62
3:D:266:VAL:HG22	3:D:267:TRP:O	2.00	0.62
1:F:99:GLN:HE22	2:G:146:ARG:NH1	1.93	0.61
3:D:255:GLN:NE2	3:D:267:TRP:NE1	2.48	0.61
1:F:414:PHE:HA	1:F:418:THR:CG2	2.31	0.61
1:F:439:ASN:ND2	2:G:132:PRO:HB2	2.15	0.61
1:F:454:ARG:HB2	1:F:457:THR:CG2	2.30	0.61
3:B:9:VAL:HG22	3:B:59:ASP:O	2.00	0.61
3:B:334:VAL:HG12	3:B:335:VAL:H	1.64	0.61
3:C:168:LEU:HD12	3:C:172:MET:HG2	1.82	0.61
3:C:243:PRO:O	3:C:244:VAL:HG22	1.99	0.61
3:C:351:ARG:HH11	3:C:351:ARG:HG3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:44:THR:CG2	3:D:48:MET:HE2	2.25	0.61
3:D:355:PHE:HB3	3:D:360:THR:O	1.99	0.61
1:F:423:ILE:CG1	1:F:424:LYS:N	2.62	0.61
1:F:439:ASN:HD22	2:G:132:PRO:HB2	1.65	0.61
1:F:501:LEU:CB	2:G:127:ILE:HG23	2.28	0.61
1:H:439:ASN:ND2	2:I:132:PRO:HB2	2.15	0.61
2:I:230:VAL:HB	2:I:231:PRO:HD3	1.82	0.61
3:D:9:VAL:HG22	3:D:59:ASP:O	2.00	0.61
1:F:333:ILE:HA	1:F:336:PHE:HB2	1.81	0.61
2:G:148:GLY:HA2	2:G:155:GLY:CA	2.28	0.61
3:B:188:ILE:HD12	3:B:188:ILE:H	1.65	0.61
3:B:242:LEU:HB3	3:B:323:ILE:CD1	2.30	0.61
3:C:331:GLN:HE22	3:C:335:VAL:HG21	1.65	0.61
3:D:55:ILE:HD12	3:D:55:ILE:N	2.15	0.61
1:F:268:PHE:O	1:F:270:ASP:N	2.32	0.61
3:D:5:GLN:O	3:D:6:LEU:HD12	1.98	0.61
3:A:145:GLY:CA	3:A:148:LEU:HD12	2.28	0.61
3:B:10:THR:HG22	3:B:11:LYS:N	2.15	0.61
3:B:138:GLN:O	3:B:142:VAL:HG23	2.00	0.61
3:B:142:VAL:O	3:B:145:GLY:N	2.33	0.61
3:B:261:PRO:O	3:B:263:ARG:HG2	2.00	0.61
3:B:300:LEU:HD11	3:B:347:LEU:HB2	1.81	0.61
1:H:302:LEU:HB3	1:H:385:MET:SD	2.41	0.61
1:H:454:ARG:HB2	1:H:457:THR:CG2	2.30	0.61
2:I:78:PRO:O	2:I:80:PRO:HD3	2.00	0.61
3:C:312:ASN:O	3:C:313:GLU:HB3	1.99	0.61
3:D:32:VAL:HG12	3:D:33:VAL:N	2.15	0.61
3:D:328:VAL:HG12	3:D:329:TYR:H	1.65	0.61
1:F:337:LYS:NZ	2:G:253:LEU:HG	2.14	0.61
1:F:373:ILE:CG1	1:F:374:ILE:N	2.59	0.61
2:G:180:TYR:HE2	2:G:211:SER:HA	1.65	0.61
3:A:251:ILE:O	3:A:272:SER:HB3	2.00	0.61
3:B:328:VAL:HG12	3:B:329:TYR:H	1.65	0.61
1:H:283:TRP:CZ3	1:H:369:ARG:HB3	2.35	0.61
2:I:86:TRP:NE1	2:I:90:LYS:HD2	2.15	0.61
3:C:188:ILE:HG22	3:C:189:TYR:N	2.16	0.61
3:D:138:GLN:HA	3:D:141:ARG:HD3	1.83	0.61
3:D:223:HIS:C	3:D:225:PRO:HD3	2.24	0.61
1:F:53:GLY:HA2	1:F:69:TYR:CB	2.31	0.61
1:F:88:ALA:O	1:F:263:ASN:ND2	2.28	0.61
1:F:287:PHE:HE2	1:F:437:ASN:O	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:381:TYR:CD1	1:F:382:PRO:CD	2.84	0.61
3:A:46:LEU:HD13	3:A:190:VAL:HG23	1.83	0.61
3:A:102:LEU:O	3:A:103:ALA:HB3	2.00	0.61
3:A:188:ILE:HG22	3:A:189:TYR:N	2.16	0.61
3:A:312:ASN:O	3:A:313:GLU:HB3	2.00	0.61
3:B:6:LEU:HD23	3:B:9:VAL:HG21	1.81	0.61
3:B:266:VAL:HG22	3:B:267:TRP:O	2.00	0.61
3:B:335:VAL:O	3:B:337:VAL:HG23	2.01	0.61
1:H:96:SER:HB2	1:H:481:GLY:HA3	1.83	0.61
1:H:414:PHE:HA	1:H:418:THR:CG2	2.31	0.61
2:I:274:ILE:HG22	2:I:275:THR:N	2.15	0.61
3:D:10:THR:HG22	3:D:11:LYS:N	2.15	0.61
3:D:152:PRO:O	3:D:154:VAL:N	2.33	0.61
1:H:358:LYS:N	1:H:359:PRO:HD3	2.15	0.61
1:H:381:TYR:CD1	1:H:382:PRO:CD	2.84	0.61
1:H:439:ASN:HD22	2:I:132:PRO:HB2	1.65	0.61
1:F:302:LEU:HB3	1:F:385:MET:SD	2.41	0.61
1:F:358:LYS:N	1:F:359:PRO:HD3	2.15	0.61
1:F:468:VAL:HG13	1:F:469:ASN:H	1.65	0.61
3:A:8:ASN:H	3:A:23:ASN:CG	2.08	0.61
3:A:179:LEU:O	3:A:183:LEU:N	2.30	0.61
3:B:55:ILE:N	3:B:55:ILE:HD12	2.15	0.61
1:H:366:THR:HG22	1:H:367:THR:H	1.66	0.61
3:C:194:GLN:O	3:C:198:MET:HG2	2.01	0.61
3:D:70:THR:CG2	3:D:71:PRO:HD2	2.30	0.61
3:D:138:GLN:O	3:D:142:VAL:HG23	2.00	0.61
3:D:315:GLN:C	3:D:316:ILE:HG13	2.25	0.61
2:G:4:VAL:CG1	3:B:72:PRO:HD3	2.31	0.60
2:G:230:VAL:HB	2:G:231:PRO:HD3	1.82	0.60
3:A:11:LYS:HD2	3:A:56:THR:OG1	2.01	0.60
3:A:234:ILE:HG22	3:A:235:GLY:N	2.16	0.60
3:D:145:GLY:O	3:D:149:VAL:HG23	2.01	0.60
1:F:303:ALA:CA	1:F:385:MET:HE1	2.28	0.60
3:A:55:ILE:HD13	3:A:68:ASN:HB3	1.82	0.60
3:A:168:LEU:HD12	3:A:172:MET:HG2	1.82	0.60
3:B:124:ALA:O	3:B:127:LEU:HD13	2.01	0.60
3:B:145:GLY:O	3:B:149:VAL:HG23	2.01	0.60
3:B:335:VAL:HG12	3:B:337:VAL:CG2	2.32	0.60
3:C:234:ILE:HG22	3:C:235:GLY:N	2.16	0.60
3:D:66:ARG:HG2	3:D:66:ARG:HH11	1.66	0.60
3:D:188:ILE:HD12	3:D:188:ILE:H	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:194:GLN:O	3:A:198:MET:HG2	2.01	0.60
3:B:50:ALA:O	3:B:75:ARG:HD2	2.00	0.60
1:H:53:GLY:HA2	1:H:69:TYR:CB	2.31	0.60
2:I:126:LEU:HD23	2:I:127:ILE:N	2.15	0.60
3:C:8:ASN:H	3:C:23:ASN:CG	2.08	0.60
3:C:84:TYR:HE1	3:C:140:GLN:HE21	1.49	0.60
3:D:124:ALA:O	3:D:127:LEU:HD13	2.01	0.60
3:D:335:VAL:HG12	3:D:337:VAL:CG2	2.31	0.60
2:G:208:LEU:O	2:G:209:PRO:C	2.44	0.60
2:G:274:ILE:HG22	2:G:275:THR:N	2.15	0.60
3:A:154:VAL:HG12	3:A:155:PHE:H	1.66	0.60
3:A:169:ARG:NH1	3:A:169:ARG:HB2	2.16	0.60
3:A:193:ASP:HB3	3:A:196:GLU:HB2	1.84	0.60
3:B:138:GLN:HA	3:B:141:ARG:HD3	1.83	0.60
1:H:96:SER:O	1:H:97:THR:HG23	2.01	0.60
1:H:108:VAL:O	1:H:112:ARG:HG3	2.02	0.60
1:H:341:ASN:ND2	2:I:256:GLN:OE1	2.34	0.60
3:C:169:ARG:NH1	3:C:169:ARG:HB2	2.16	0.60
2:G:254:ASN:HB2	2:G:255:PRO:HD3	1.80	0.60
2:G:279:LEU:O	2:G:282:GLN:HB2	2.02	0.60
3:B:334:VAL:O	3:B:335:VAL:HG22	2.02	0.60
2:I:114:ARG:HG2	2:I:118:LYS:NZ	2.17	0.60
2:I:255:PRO:O	2:I:259:LEU:HG	2.01	0.60
3:D:334:VAL:O	3:D:335:VAL:HG22	2.02	0.60
3:D:335:VAL:O	3:D:337:VAL:HG23	2.01	0.60
3:A:232:GLY:HA3	3:A:238:LYS:HZ1	1.67	0.60
3:B:20:LYS:HB3	3:B:211:ARG:HG2	1.83	0.60
3:D:140:GLN:O	3:D:144:ILE:HG13	2.02	0.60
2:G:15:ILE:HA	2:G:18:LEU:HD22	1.84	0.60
3:A:331:GLN:HE22	3:A:335:VAL:HG21	1.65	0.60
3:B:285:ILE:HD12	3:B:286:ARG:N	2.17	0.60
1:H:468:VAL:HG13	1:H:469:ASN:H	1.65	0.60
3:D:142:VAL:O	3:D:145:GLY:N	2.33	0.60
3:B:140:GLN:O	3:B:144:ILE:HG13	2.02	0.60
1:H:88:ALA:HA	1:H:264:PHE:CZ	2.31	0.60
1:H:283:TRP:CZ3	1:H:369:ARG:HD3	2.37	0.60
1:H:284:THR:CG2	1:H:467:LEU:HD23	2.32	0.60
1:H:339:LEU:O	1:H:347:ILE:CG2	2.50	0.60
2:I:255:PRO:O	2:I:259:LEU:HB3	2.02	0.60
2:I:279:LEU:O	2:I:282:GLN:HB2	2.02	0.60
3:C:102:LEU:O	3:C:103:ALA:HB3	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:334:VAL:CG1	3:D:335:VAL:H	2.15	0.60
1:F:96:SER:O	1:F:97:THR:HG23	2.01	0.60
1:F:341:ASN:ND2	2:G:256:GLN:OE1	2.34	0.60
1:F:366:THR:HG22	1:F:367:THR:H	1.66	0.60
3:A:32:VAL:HG12	3:A:33:VAL:H	1.64	0.60
3:B:70:THR:CG2	3:B:71:PRO:HD2	2.30	0.60
3:C:232:GLY:HA3	3:C:238:LYS:HZ1	1.65	0.60
3:D:50:ALA:O	3:D:75:ARG:HD2	2.00	0.60
1:F:96:SER:HB2	1:F:481:GLY:HA3	1.83	0.60
2:G:158:THR:CG2	2:G:161:GLY:H	2.09	0.60
2:G:255:PRO:O	2:G:259:LEU:HG	2.01	0.60
2:G:255:PRO:O	2:G:259:LEU:HB3	2.02	0.60
3:C:46:LEU:HD13	3:C:190:VAL:HG23	1.83	0.60
3:C:92:VAL:HG13	3:C:142:VAL:CG1	2.32	0.60
3:C:193:ASP:HB3	3:C:196:GLU:HB2	1.84	0.60
3:C:300:LEU:HB2	3:C:345:ILE:O	2.02	0.60
1:F:330:PHE:CZ	2:G:249:MET:HE3	2.37	0.59
1:F:339:LEU:O	1:F:347:ILE:CG2	2.49	0.59
1:F:342:GLN:HE22	1:F:363:SER:N	1.99	0.59
1:F:381:TYR:CD1	1:F:381:TYR:C	2.80	0.59
3:A:20:LYS:O	3:A:21:ASP:OD2	2.20	0.59
1:H:331:ILE:C	1:H:331:ILE:HD13	2.27	0.59
1:F:278:LEU:O	1:F:282:VAL:HG23	2.01	0.59
1:F:283:TRP:CZ3	1:F:369:ARG:HD3	2.37	0.59
3:B:66:ARG:HH11	3:B:66:ARG:HG2	1.66	0.59
1:H:342:GLN:HE22	1:H:363:SER:N	1.99	0.59
1:F:381:TYR:N	1:F:382:PRO:HD2	2.17	0.59
1:H:381:TYR:CD1	1:H:381:TYR:C	2.80	0.59
2:I:4:VAL:CG1	3:D:72:PRO:HD3	2.31	0.59
3:C:11:LYS:HD2	3:C:56:THR:OG1	2.01	0.59
3:D:226:ALA:HB3	3:D:230:VAL:CG2	2.22	0.59
1:F:108:VAL:O	1:F:112:ARG:HG3	2.02	0.59
2:G:86:TRP:HE1	2:G:90:LYS:HD2	1.67	0.59
3:A:92:VAL:HG13	3:A:142:VAL:CG1	2.32	0.59
3:A:242:LEU:CD1	3:A:283:LEU:HB3	2.32	0.59
3:A:75:ARG:CB	3:A:77:VAL:HG23	2.32	0.59
3:B:334:VAL:CG1	3:B:335:VAL:H	2.15	0.59
1:H:381:TYR:CD1	1:H:382:PRO:N	2.62	0.59
1:H:400:TYR:OH	1:H:418:THR:HB	2.02	0.59
2:I:15:ILE:HA	2:I:18:LEU:HD22	1.83	0.59
2:I:208:LEU:O	2:I:209:PRO:C	2.44	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:20:LYS:O	3:C:21:ASP:OD2	2.20	0.59
3:C:164:LEU:CD2	3:C:168:LEU:HD23	2.29	0.59
3:B:251:ILE:HG22	3:B:252:ASP:OD1	2.03	0.59
1:H:87:ILE:HG23	1:H:491:ALA:HA	1.85	0.59
1:H:278:LEU:O	1:H:282:VAL:HG23	2.01	0.59
2:I:86:TRP:HE1	2:I:90:LYS:HD2	1.67	0.59
3:C:154:VAL:HG12	3:C:155:PHE:H	1.66	0.59
1:F:400:TYR:OH	1:F:418:THR:HB	2.02	0.59
2:G:134:VAL:O	2:G:136:SER:N	2.36	0.59
2:G:224:ILE:O	2:G:228:THR:HG22	2.02	0.59
2:G:245:LEU:CG	2:G:249:MET:HE2	2.30	0.59
3:A:144:ILE:HG22	3:A:148:LEU:CD1	2.21	0.59
3:A:195:VAL:O	3:A:199:THR:HG23	2.03	0.59
1:H:381:TYR:N	1:H:382:PRO:HD2	2.17	0.59
2:I:29:PHE:O	2:I:32:LEU:HB2	2.03	0.59
3:D:193:ASP:O	3:D:194:GLN:C	2.46	0.59
1:F:87:ILE:HG23	1:F:491:ALA:HA	1.85	0.59
1:F:284:THR:CG2	1:F:467:LEU:HD23	2.32	0.59
1:F:442:VAL:CG1	2:G:230:VAL:HG11	2.29	0.59
3:A:335:VAL:HG12	3:A:337:VAL:HG23	1.85	0.59
3:A:336:LEU:O	3:A:337:VAL:CG2	2.51	0.59
3:B:28:GLU:HG3	3:B:29:GLY:N	2.18	0.59
3:B:193:ASP:O	3:B:194:GLN:C	2.46	0.59
3:B:243:PRO:O	3:B:244:VAL:HG13	2.03	0.59
1:H:381:TYR:HD1	1:H:381:TYR:C	2.10	0.59
1:H:441:PHE:HD2	1:H:468:VAL:HG22	1.68	0.59
3:D:46:LEU:HA	3:D:49:ILE:HD12	1.85	0.59
1:F:323:LEU:O	1:F:326:ALA:N	2.36	0.59
1:F:510:ARG:HG3	2:G:175:TRP:HH2	1.68	0.59
1:H:330:PHE:CZ	2:I:249:MET:HE3	2.37	0.59
1:H:368:ALA:O	1:H:371:MET:HB2	2.03	0.59
2:I:224:ILE:O	2:I:228:THR:HG22	2.02	0.59
3:C:12:ALA:HB1	3:C:17:VAL:HG22	1.84	0.59
3:C:75:ARG:CB	3:C:77:VAL:HG23	2.32	0.59
3:C:242:LEU:CD1	3:C:283:LEU:HB3	2.32	0.59
3:D:335:VAL:O	3:D:336:LEU:C	2.45	0.59
1:F:285:VAL:HG12	1:F:286:VAL:N	2.17	0.59
3:A:33:VAL:O	3:A:34:PHE:HD2	1.86	0.59
3:A:240:ASN:O	3:A:241:PHE:CD1	2.55	0.59
1:H:298:VAL:HG11	1:H:381:TYR:HD2	1.68	0.59
1:H:442:VAL:CG1	2:I:230:VAL:HG11	2.29	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:486:LEU:CD1	1:H:490:ILE:HD11	2.26	0.59
3:D:20:LYS:HB3	3:D:211:ARG:HG2	1.83	0.59
3:D:285:ILE:HD12	3:D:286:ARG:N	2.17	0.59
1:F:317:TYR:CD2	2:G:20:LEU:HG	2.38	0.58
3:A:6:LEU:HD23	3:A:9:VAL:HG21	1.85	0.58
3:A:86:LEU:HA	3:A:146:ARG:NH2	2.18	0.58
3:A:123:LEU:CD2	3:A:142:VAL:HG22	2.33	0.58
3:A:300:LEU:HB2	3:A:345:ILE:O	2.02	0.58
3:A:306:VAL:CG1	3:A:307:VAL:N	2.66	0.58
3:C:239:MET:O	3:C:240:ASN:O	2.21	0.58
3:C:240:ASN:O	3:C:241:PHE:CD1	2.55	0.58
3:D:251:ILE:HG22	3:D:252:ASP:OD1	2.03	0.58
2:G:115:PHE:HB2	2:G:116:PRO:CD	2.23	0.58
2:G:146:ARG:O	2:G:149:GLU:HG2	2.04	0.58
2:G:276:ILE:HG22	2:G:277:VAL:N	2.18	0.58
3:A:60:LEU:HD12	3:A:61:PHE:N	2.17	0.58
1:H:323:LEU:O	1:H:324:PRO:C	2.46	0.58
2:I:158:THR:CG2	2:I:161:GLY:H	2.09	0.58
3:C:84:TYR:HE1	3:C:140:GLN:NE2	2.01	0.58
3:C:123:LEU:CD2	3:C:142:VAL:HG22	2.33	0.58
3:C:144:ILE:HG22	3:C:148:LEU:CD1	2.21	0.58
3:D:45:LEU:CD1	3:D:207:LEU:HD11	2.33	0.58
1:F:88:ALA:HA	1:F:264:PHE:CZ	2.31	0.58
1:F:368:ALA:O	1:F:371:MET:HB2	2.03	0.58
2:G:82:LEU:HD21	2:G:269:MET:HE1	1.86	0.58
3:A:12:ALA:HB1	3:A:17:VAL:HG22	1.85	0.58
3:A:53:GLU:HG3	3:A:54:THR:H	1.68	0.58
3:A:94:GLU:HA	3:A:97:SER:OG	2.03	0.58
1:H:323:LEU:O	1:H:326:ALA:N	2.36	0.58
1:H:446:LEU:HD21	2:I:250:GLN:HG3	1.85	0.58
2:I:134:VAL:O	2:I:136:SER:N	2.36	0.58
3:C:354:LEU:HG	3:C:362:CYS:SG	2.43	0.58
3:D:158:ASP:O	3:D:159:GLU:HB2	2.03	0.58
1:F:381:TYR:HD1	1:F:381:TYR:C	2.10	0.58
1:F:399:LEU:O	1:F:402:ALA:HB3	2.03	0.58
2:G:29:PHE:O	2:G:32:LEU:HB2	2.03	0.58
2:G:255:PRO:CB	2:G:259:LEU:HG	2.27	0.58
3:A:62:ILE:C	3:A:64:GLU:N	2.60	0.58
3:A:154:VAL:HG12	3:A:155:PHE:N	2.18	0.58
3:B:45:LEU:CD1	3:B:207:LEU:HD11	2.33	0.58
3:B:46:LEU:CD1	3:B:156:LEU:HD13	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:46:LEU:HA	3:B:49:ILE:HD12	1.85	0.58
3:B:92:VAL:HG23	3:B:129:ARG:O	2.03	0.58
1:H:501:LEU:CB	2:I:127:ILE:HG23	2.28	0.58
1:H:510:ARG:HG3	2:I:175:TRP:HH2	1.68	0.58
2:I:276:ILE:HG22	2:I:277:VAL:N	2.18	0.58
3:C:62:ILE:C	3:C:64:GLU:N	2.60	0.58
3:C:306:VAL:CG1	3:C:307:VAL:N	2.66	0.58
3:C:310:LEU:CD2	3:C:312:ASN:ND2	2.66	0.58
3:C:310:LEU:HD22	3:C:312:ASN:ND2	2.19	0.58
3:D:97:SER:HB2	3:D:100:LEU:HD11	1.85	0.58
3:D:151:GLU:N	3:D:152:PRO:HD3	2.18	0.58
3:A:271:GLU:HG2	3:A:273:ARG:HH21	1.68	0.58
3:A:286:ARG:HD3	3:A:288:GLU:OE2	2.04	0.58
1:H:284:THR:HG21	1:H:467:LEU:CD2	2.33	0.58
1:H:398:ASP:O	1:H:401:GLU:HB2	2.04	0.58
2:I:99:ILE:HD12	2:I:222:SER:HB3	1.85	0.58
1:F:283:TRP:CE3	1:F:369:ARG:HD3	2.38	0.58
1:F:330:PHE:CZ	2:G:246:ALA:HA	2.39	0.58
1:F:331:ILE:HD13	1:F:331:ILE:C	2.27	0.58
1:F:333:ILE:HA	1:F:336:PHE:HD1	1.69	0.58
1:F:450:GLY:HA3	1:F:465:ASP:OD2	2.04	0.58
2:G:114:ARG:HG2	2:G:118:LYS:NZ	2.17	0.58
3:A:239:MET:O	3:A:240:ASN:C	2.47	0.58
3:B:26:ILE:HD12	3:B:26:ILE:N	2.14	0.58
3:B:151:GLU:N	3:B:152:PRO:HD3	2.18	0.58
3:B:260:MET:CB	3:B:261:PRO:HD2	2.26	0.58
1:H:340:PHE:HA	1:H:347:ILE:HG21	1.86	0.58
1:H:399:LEU:O	1:H:402:ALA:HB3	2.03	0.58
3:C:236:SER:O	3:C:237:PRO:C	2.47	0.58
3:C:306:VAL:HG21	3:C:317:HIS:ND1	2.18	0.58
3:D:28:GLU:HG3	3:D:29:GLY:N	2.18	0.58
3:D:92:VAL:HG23	3:D:129:ARG:O	2.03	0.58
3:D:186:THR:HG22	3:D:187:MET:N	2.19	0.58
3:D:270:VAL:HG12	3:D:271:GLU:N	2.19	0.58
1:F:264:PHE:O	1:F:265:THR:C	2.47	0.58
1:F:398:ASP:O	1:F:401:GLU:HB2	2.04	0.58
2:G:3:MET:HG2	2:G:4:VAL:N	2.19	0.58
3:A:75:ARG:HB2	3:A:77:VAL:HG23	1.86	0.58
3:A:84:TYR:HE1	3:A:140:GLN:NE2	2.01	0.58
3:A:84:TYR:HE1	3:A:140:GLN:HE21	1.49	0.58
3:A:310:LEU:HD22	3:A:312:ASN:ND2	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:354:LEU:HG	3:A:362:CYS:SG	2.43	0.58
3:B:158:ASP:O	3:B:159:GLU:HB2	2.03	0.58
3:B:186:THR:HG22	3:B:187:MET:N	2.19	0.58
3:B:255:GLN:O	3:B:256:VAL:HG13	2.04	0.58
3:B:270:VAL:HG12	3:B:271:GLU:N	2.19	0.58
3:B:270:VAL:HG12	3:B:272:SER:H	1.68	0.58
3:B:291:LEU:O	3:B:345:ILE:HB	2.03	0.58
3:C:94:GLU:HA	3:C:97:SER:OG	2.03	0.58
3:D:291:LEU:O	3:D:345:ILE:HB	2.03	0.58
1:F:329:SER:OG	1:F:379:LEU:HD11	2.04	0.58
1:F:466:LEU:N	1:F:469:ASN:OD1	2.37	0.58
1:F:468:VAL:HG13	1:F:469:ASN:ND2	2.19	0.58
3:A:85:ALA:O	3:A:146:ARG:NH2	2.36	0.58
3:A:306:VAL:HG21	3:A:317:HIS:ND1	2.18	0.58
3:B:60:LEU:HD12	3:B:61:PHE:O	2.04	0.58
1:H:330:PHE:CZ	2:I:246:ALA:HA	2.39	0.58
1:H:424:LYS:N	1:H:425:PRO:HD2	2.19	0.58
3:C:53:GLU:HG3	3:C:54:THR:H	1.68	0.58
3:D:60:LEU:HD12	3:D:61:PHE:O	2.04	0.58
3:D:242:LEU:HB3	3:D:323:ILE:CD1	2.30	0.58
1:F:284:THR:HG21	1:F:467:LEU:CD2	2.33	0.58
1:F:340:PHE:HA	1:F:347:ILE:HG21	1.86	0.58
1:F:473:ARG:C	1:F:475:ALA:H	2.11	0.58
2:G:24:ILE:CD1	2:G:25:ALA:N	2.67	0.58
3:A:20:LYS:HB3	3:A:211:ARG:NH1	2.19	0.58
3:B:156:LEU:N	3:B:156:LEU:HD23	2.18	0.58
3:B:194:GLN:H	3:B:194:GLN:CD	2.12	0.58
1:H:450:GLY:HA3	1:H:465:ASP:OD2	2.04	0.58
3:C:33:VAL:O	3:C:34:PHE:HD2	1.86	0.58
3:C:154:VAL:HG12	3:C:155:PHE:N	2.18	0.58
3:C:336:LEU:O	3:C:337:VAL:CG2	2.51	0.58
3:D:93:ALA:N	3:D:127:LEU:O	2.37	0.58
3:D:272:SER:O	3:D:275:VAL:CG2	2.52	0.58
1:F:497:LEU:O	1:F:500:ALA:HB3	2.04	0.58
2:G:99:ILE:HD12	2:G:222:SER:HB3	1.85	0.58
3:B:299:ILE:O	3:B:300:LEU:HG	2.04	0.58
1:H:329:SER:OG	1:H:379:LEU:HD11	2.04	0.58
2:I:3:MET:HG2	2:I:4:VAL:N	2.19	0.58
3:C:6:LEU:HD23	3:C:9:VAL:HG21	1.85	0.58
3:C:83:SER:OG	3:C:84:TYR:N	2.37	0.58
3:C:195:VAL:O	3:C:199:THR:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:300:LEU:HD22	3:C:320:ILE:HD13	1.85	0.58
3:C:335:VAL:HG12	3:C:337:VAL:HG23	1.85	0.58
3:D:227:ASP:OD1	3:D:230:VAL:HG23	2.04	0.58
3:D:243:PRO:O	3:D:244:VAL:HG13	2.03	0.58
3:D:251:ILE:HD13	3:D:251:ILE:H	1.69	0.58
1:F:275:LYS:N	1:F:276:PRO:CD	2.58	0.57
1:F:378:TRP:HD1	2:G:27:ILE:HG22	1.69	0.57
1:F:441:PHE:HD2	1:F:468:VAL:HG22	1.68	0.57
2:G:195:ASP:HB3	3:A:102:LEU:HD23	1.85	0.57
3:B:33:VAL:O	3:B:204:ILE:HG23	2.04	0.57
3:B:34:PHE:O	3:B:35:VAL:CG1	2.48	0.57
3:B:196:GLU:O	3:B:199:THR:OG1	2.20	0.57
1:H:285:VAL:HG12	1:H:286:VAL:N	2.17	0.57
1:H:473:ARG:C	1:H:475:ALA:H	2.11	0.57
3:C:60:LEU:HD12	3:C:61:PHE:N	2.17	0.57
3:C:86:LEU:HA	3:C:146:ARG:NH2	2.18	0.57
3:D:46:LEU:CD1	3:D:156:LEU:HD13	2.33	0.57
1:F:79:VAL:CG2	2:G:168:GLY:HA3	2.34	0.57
1:F:317:TYR:CE2	2:G:20:LEU:CG	2.86	0.57
1:F:323:LEU:O	1:F:324:PRO:C	2.46	0.57
1:F:441:PHE:HB2	1:F:468:VAL:HG21	1.86	0.57
1:F:446:LEU:HD21	2:G:250:GLN:HG3	1.85	0.57
3:A:239:MET:O	3:A:240:ASN:O	2.21	0.57
3:A:310:LEU:CD2	3:A:312:ASN:ND2	2.66	0.57
1:H:79:VAL:CG2	2:I:168:GLY:HA3	2.34	0.57
2:I:146:ARG:O	2:I:149:GLU:HG2	2.04	0.57
1:F:352:SER:HA	1:F:357:VAL:O	2.03	0.57
2:G:191:ALA:O	2:G:194:LEU:HB2	2.04	0.57
3:A:77:VAL:HG12	3:A:78:GLY:N	2.19	0.57
3:A:257:GLU:HB2	3:A:265:GLN:HG2	1.86	0.57
3:B:97:SER:HB2	3:B:100:LEU:HD11	1.85	0.57
1:H:283:TRP:CE3	1:H:369:ARG:HD3	2.38	0.57
1:H:352:SER:HA	1:H:357:VAL:O	2.03	0.57
1:H:441:PHE:HB2	1:H:468:VAL:HG21	1.86	0.57
1:H:466:LEU:N	1:H:469:ASN:OD1	2.37	0.57
1:H:468:VAL:HG13	1:H:469:ASN:ND2	2.19	0.57
2:I:194:LEU:CD2	3:C:72:PRO:HB2	2.34	0.57
3:C:286:ARG:HD3	3:C:288:GLU:OE2	2.04	0.57
3:D:33:VAL:O	3:D:204:ILE:HG23	2.04	0.57
3:D:196:GLU:O	3:D:199:THR:OG1	2.19	0.57
1:F:298:VAL:HG11	1:F:381:TYR:HD2	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:323:LEU:N	1:F:324:PRO:HD2	2.19	0.57
3:A:346:GLY:O	3:A:348:PRO:CD	2.51	0.57
3:B:188:ILE:HG22	3:B:189:TYR:N	2.19	0.57
3:B:251:ILE:HD13	3:B:251:ILE:H	1.69	0.57
1:H:264:PHE:O	1:H:265:THR:C	2.47	0.57
1:H:317:TYR:CD2	2:I:20:LEU:HG	2.38	0.57
2:I:134:VAL:C	2:I:136:SER:H	2.12	0.57
3:B:335:VAL:O	3:B:336:LEU:C	2.45	0.57
1:H:333:ILE:HA	1:H:336:PHE:HD1	1.69	0.57
2:I:94:ILE:CD1	2:I:163:ILE:HD13	2.35	0.57
2:I:191:ALA:O	2:I:194:LEU:HB2	2.04	0.57
3:C:311:GLY:C	3:C:313:GLU:H	2.12	0.57
3:C:336:LEU:C	3:C:337:VAL:HG23	2.30	0.57
3:D:223:HIS:CE1	3:D:369:PRO:HG2	2.40	0.57
1:F:278:LEU:HD22	1:F:278:LEU:N	2.19	0.57
3:A:126:LEU:HD13	3:A:134:LEU:CD2	2.34	0.57
3:A:300:LEU:HD22	3:A:320:ILE:HD13	1.85	0.57
3:A:336:LEU:C	3:A:337:VAL:HG23	2.30	0.57
3:B:93:ALA:N	3:B:127:LEU:O	2.37	0.57
3:B:122:GLN:O	3:B:123:LEU:HD12	2.05	0.57
3:C:13:TRP:HB2	3:C:16:VAL:HB	1.87	0.57
3:C:305:GLN:HG3	3:C:326:ASN:ND2	2.20	0.57
1:F:110:LEU:HD23	1:F:110:LEU:C	2.30	0.57
3:A:285:ILE:HD12	3:A:286:ARG:N	2.16	0.57
3:B:226:ALA:O	3:B:361:ALA:HB3	2.04	0.57
3:B:271:GLU:OE1	3:B:271:GLU:O	2.23	0.57
1:H:278:LEU:HD22	1:H:278:LEU:N	2.19	0.57
2:I:82:LEU:HD21	2:I:269:MET:HE1	1.86	0.57
3:C:172:MET:O	3:C:175:GLU:HB2	2.04	0.57
3:C:257:GLU:HB2	3:C:265:GLN:HG2	1.86	0.57
3:D:260:MET:CB	3:D:261:PRO:HD2	2.26	0.57
3:D:350:GLU:O	3:D:364:ARG:NH1	2.37	0.57
1:F:280:ILE:HD13	1:F:470:TYR:CD1	2.34	0.57
2:G:24:ILE:O	2:G:28:MET:CG	2.53	0.57
2:G:134:VAL:C	2:G:136:SER:H	2.12	0.57
2:G:252:TYR:N	2:G:252:TYR:CD1	2.73	0.57
3:A:13:TRP:HB2	3:A:16:VAL:HB	1.87	0.57
3:B:272:SER:O	3:B:275:VAL:CG2	2.52	0.57
1:H:75:MET:SD	2:I:125:MET:HE3	2.45	0.57
2:I:272:LEU:HD23	2:I:273:PRO:HD3	1.86	0.57
3:C:20:LYS:HB3	3:C:211:ARG:NH1	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:279:ALA:CB	3:C:281:MET:HE3	2.35	0.57
3:D:122:GLN:O	3:D:123:LEU:HD12	2.05	0.57
3:D:156:LEU:HD23	3:D:156:LEU:N	2.18	0.57
3:D:270:VAL:HG12	3:D:272:SER:H	1.68	0.57
3:D:299:ILE:O	3:D:300:LEU:HG	2.04	0.57
1:F:298:VAL:HG11	1:F:381:TYR:CD2	2.40	0.57
1:F:424:LYS:N	1:F:425:PRO:HD2	2.19	0.57
1:F:501:LEU:HD23	2:G:130:MET:SD	2.45	0.57
3:A:279:ALA:CB	3:A:281:MET:HE3	2.35	0.57
1:H:501:LEU:HD23	2:I:130:MET:SD	2.45	0.57
3:C:271:GLU:HG2	3:C:273:ARG:HH21	1.68	0.57
3:D:60:LEU:C	3:D:61:PHE:CD1	2.83	0.57
3:D:279:ALA:O	3:D:281:MET:N	2.37	0.57
3:D:281:MET:CB	3:D:354:LEU:HD11	2.35	0.57
3:D:368:GLU:CB	3:D:369:PRO:HD2	2.28	0.57
1:F:312:ARG:CD	1:F:313:GLY:N	2.68	0.57
1:F:343:SER:OG	1:F:344:PHE:N	2.37	0.57
2:G:194:LEU:CD2	3:A:72:PRO:HB2	2.34	0.57
3:B:60:LEU:C	3:B:61:PHE:CD1	2.83	0.57
1:H:56:ILE:HD11	1:H:69:TYR:CB	2.35	0.57
3:C:80:VAL:HG22	3:C:160:PRO:HB3	1.87	0.57
3:C:346:GLY:O	3:C:348:PRO:CD	2.51	0.57
2:G:29:PHE:CE1	2:G:33:MET:SD	2.98	0.56
3:A:172:MET:O	3:A:175:GLU:HB2	2.04	0.56
3:B:350:GLU:O	3:B:364:ARG:NH1	2.37	0.56
1:H:343:SER:OG	1:H:344:PHE:N	2.37	0.56
2:I:24:ILE:O	2:I:28:MET:CG	2.53	0.56
2:G:94:ILE:CD1	2:G:163:ILE:HD13	2.35	0.56
2:G:227:ILE:C	2:G:229:GLU:H	2.13	0.56
3:B:330:ARG:O	3:B:331:GLN:HB2	2.04	0.56
1:H:110:LEU:C	1:H:110:LEU:HD23	2.30	0.56
1:H:323:LEU:N	1:H:324:PRO:HD2	2.19	0.56
1:H:365:PRO:HG3	1:H:452:PRO:CG	2.35	0.56
3:D:226:ALA:O	3:D:361:ALA:HB3	2.05	0.56
3:D:320:ILE:HG23	3:D:321:PRO:CD	2.31	0.56
1:F:48:ILE:HG13	1:F:49:LEU:N	2.20	0.56
1:F:277:PHE:O	1:F:280:ILE:HG12	2.06	0.56
1:F:280:ILE:HG13	1:F:281:PHE:N	2.20	0.56
1:F:328:PRO:CD	2:G:274:ILE:HG12	2.19	0.56
1:F:334:LEU:HD11	2:G:250:GLN:HA	1.87	0.56
3:A:224:TYR:HE2	3:A:371:VAL:HG11	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:243:PRO:C	3:A:244:VAL:HG22	2.31	0.56
3:A:275:VAL:O	3:A:275:VAL:HG12	2.05	0.56
3:A:311:GLY:C	3:A:313:GLU:H	2.12	0.56
3:A:312:ASN:O	3:A:312:ASN:OD1	2.23	0.56
3:A:314:THR:OG1	3:A:334:VAL:HA	2.05	0.56
3:B:223:HIS:CE1	3:B:369:PRO:HG2	2.40	0.56
1:H:284:THR:HA	1:H:466:LEU:CD2	2.35	0.56
2:I:94:ILE:HG13	2:I:163:ILE:HG21	1.87	0.56
2:I:166:TYR:OH	2:I:229:GLU:HG2	2.06	0.56
2:I:230:VAL:CB	2:I:231:PRO:HD3	2.35	0.56
2:I:252:TYR:N	2:I:252:TYR:CD1	2.73	0.56
3:C:224:TYR:HE2	3:C:371:VAL:HG11	1.70	0.56
3:C:312:ASN:O	3:C:312:ASN:OD1	2.23	0.56
3:C:314:THR:OG1	3:C:334:VAL:HA	2.05	0.56
3:D:188:ILE:HG22	3:D:189:TYR:N	2.19	0.56
3:D:255:GLN:O	3:D:256:VAL:HG13	2.04	0.56
1:F:284:THR:HA	1:F:466:LEU:CD2	2.35	0.56
2:G:4:VAL:HG22	2:G:6:PRO:HD3	1.86	0.56
2:G:92:ALA:CB	2:G:227:ILE:HD13	2.34	0.56
3:B:279:ALA:O	3:B:281:MET:N	2.37	0.56
1:H:48:ILE:HG13	1:H:49:LEU:N	2.20	0.56
1:H:277:PHE:O	1:H:280:ILE:HG12	2.06	0.56
1:H:334:LEU:HD11	2:I:250:GLN:HA	1.88	0.56
1:H:378:TRP:HD1	2:I:27:ILE:HG22	1.69	0.56
3:C:304:VAL:HG13	3:C:316:ILE:CG2	2.36	0.56
1:F:366:THR:CG2	1:F:367:THR:H	2.19	0.56
1:F:421:LEU:HD13	3:B:89:HIS:HB3	1.87	0.56
3:A:258:LEU:N	3:A:258:LEU:HD22	2.20	0.56
1:H:342:GLN:CD	1:H:362:PHE:HB2	2.31	0.56
1:H:497:LEU:O	1:H:500:ALA:HB3	2.04	0.56
2:I:29:PHE:CE1	2:I:33:MET:SD	2.98	0.56
3:D:253:GLN:HB2	3:D:267:TRP:CE3	2.40	0.56
3:D:330:ARG:O	3:D:331:GLN:HB2	2.04	0.56
1:F:284:THR:CG2	1:F:466:LEU:CA	2.74	0.56
2:G:230:VAL:CB	2:G:231:PRO:HD3	2.35	0.56
3:B:253:GLN:HB2	3:B:267:TRP:CE3	2.40	0.56
1:H:281:PHE:N	1:H:467:LEU:HD21	2.21	0.56
2:G:99:ILE:HD12	2:G:222:SER:CB	2.36	0.56
3:A:347:LEU:O	3:A:349:PRO:HD3	2.06	0.56
3:B:130:LYS:HG3	3:B:133:ALA:HB3	1.88	0.56
1:H:345:GLY:C	1:H:347:ILE:N	2.62	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:366:THR:CG2	1:H:367:THR:H	2.19	0.56
2:I:4:VAL:HG22	2:I:6:PRO:HD3	1.86	0.56
2:I:115:PHE:CB	2:I:116:PRO:HD2	2.27	0.56
3:C:107:LYS:HA	3:C:110:ILE:HD12	1.88	0.56
3:C:169:ARG:HD3	3:C:196:GLU:OE2	2.05	0.56
3:C:239:MET:O	3:C:240:ASN:C	2.47	0.56
3:D:130:LYS:HG3	3:D:133:ALA:HB3	1.88	0.56
3:D:286:ARG:HD3	3:D:288:GLU:OE2	2.06	0.56
3:D:336:LEU:C	3:D:337:VAL:HG23	2.31	0.56
1:F:56:ILE:HD11	1:F:69:TYR:CB	2.35	0.56
1:F:333:ILE:O	1:F:336:PHE:CB	2.53	0.56
1:F:486:LEU:HD13	1:F:490:ILE:CG1	2.36	0.56
2:G:166:TYR:OH	2:G:229:GLU:HG2	2.06	0.56
3:B:222:TYR:CE1	3:B:286:ARG:NE	2.74	0.56
1:H:486:LEU:HD13	1:H:490:ILE:CG1	2.36	0.56
2:I:24:ILE:CD1	2:I:25:ALA:N	2.67	0.56
2:I:99:ILE:HD12	2:I:222:SER:CB	2.36	0.56
3:C:75:ARG:HB2	3:C:77:VAL:HG23	1.86	0.56
3:C:243:PRO:C	3:C:244:VAL:HG22	2.31	0.56
3:C:258:LEU:HD22	3:C:258:LEU:N	2.20	0.56
3:C:307:VAL:CG2	3:C:339:GLU:HG2	2.36	0.56
1:F:345:GLY:C	1:F:347:ILE:N	2.62	0.56
1:F:365:PRO:HG3	1:F:452:PRO:CG	2.35	0.56
2:G:272:LEU:HD23	2:G:273:PRO:HD3	1.86	0.56
3:A:107:LYS:HA	3:A:110:ILE:HD12	1.88	0.56
3:A:305:GLN:HG3	3:A:326:ASN:ND2	2.20	0.56
3:B:42:LYS:HE2	3:B:190:VAL:CG1	2.36	0.56
3:B:227:ASP:OD1	3:B:230:VAL:HG23	2.04	0.56
3:B:286:ARG:HD3	3:B:288:GLU:OE2	2.06	0.56
1:H:41:LEU:HD23	1:H:44:ILE:HD12	1.88	0.56
1:H:280:ILE:HG13	1:H:281:PHE:N	2.20	0.56
1:H:298:VAL:HG11	1:H:381:TYR:CD2	2.40	0.56
3:D:42:LYS:HE2	3:D:190:VAL:CG1	2.36	0.56
1:F:80:LEU:O	1:F:83:LEU:HB2	2.06	0.56
2:G:286:VAL:O	2:G:287:ASN:CG	2.49	0.56
3:A:309:GLN:O	3:A:310:LEU:HB2	2.06	0.56
3:B:281:MET:CB	3:B:354:LEU:HD11	2.35	0.56
1:H:281:PHE:HA	1:H:467:LEU:CD2	2.36	0.56
1:H:421:LEU:HD13	3:D:89:HIS:HB3	1.87	0.56
1:H:431:ILE:HG13	1:H:432:ALA:H	1.71	0.56
2:I:164:PHE:HA	2:I:167:LEU:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:286:VAL:O	2:I:287:ASN:CG	2.49	0.56
3:C:275:VAL:O	3:C:275:VAL:HG12	2.05	0.56
3:D:90:LEU:O	3:D:131:PRO:HG2	2.06	0.56
1:F:88:ALA:O	1:F:89:ILE:C	2.49	0.55
1:F:281:PHE:N	1:F:467:LEU:HD21	2.21	0.55
1:F:339:LEU:O	1:F:347:ILE:HG22	2.06	0.55
2:G:94:ILE:HG13	2:G:163:ILE:HG21	1.87	0.55
3:A:230:VAL:O	3:A:234:ILE:HG13	2.06	0.55
1:H:267:VAL:HG22	1:H:488:ALA:CA	2.37	0.55
1:H:459:THR:HB	1:H:460:PRO:CD	2.36	0.55
1:H:509:THR:O	1:H:510:ARG:HB2	2.05	0.55
2:I:195:ASP:HB3	3:C:102:LEU:HD23	1.85	0.55
3:C:126:LEU:HD13	3:C:134:LEU:CD2	2.34	0.55
3:D:194:GLN:CD	3:D:194:GLN:H	2.12	0.55
3:D:271:GLU:O	3:D:271:GLU:OE1	2.23	0.55
1:F:75:MET:SD	2:G:125:MET:HE3	2.45	0.55
1:F:342:GLN:CD	1:F:362:PHE:HB2	2.31	0.55
2:G:29:PHE:HB3	2:G:30:PRO:CD	2.33	0.55
3:A:80:VAL:HG22	3:A:160:PRO:HB3	1.87	0.55
3:A:258:LEU:H	3:A:258:LEU:CD2	2.19	0.55
1:H:312:ARG:CD	1:H:313:GLY:N	2.68	0.55
1:H:330:PHE:CE2	2:I:246:ALA:O	2.59	0.55
2:I:227:ILE:C	2:I:229:GLU:H	2.13	0.55
3:C:34:PHE:O	3:C:35:VAL:CG1	2.55	0.55
3:C:195:VAL:HG13	3:D:310:LEU:HD21	1.88	0.55
3:C:223:HIS:O	3:C:225:PRO:CD	2.46	0.55
3:C:347:LEU:O	3:C:349:PRO:HD3	2.06	0.55
3:D:62:ILE:HD12	3:D:67:MET:HG3	1.89	0.55
3:D:314:THR:HG22	3:D:315:GLN:H	1.70	0.55
1:F:330:PHE:CE2	2:G:246:ALA:O	2.59	0.55
1:F:398:ASP:O	1:F:399:LEU:C	2.49	0.55
3:A:169:ARG:HD3	3:A:196:GLU:OE2	2.04	0.55
3:B:155:PHE:N	3:B:155:PHE:CD1	2.74	0.55
2:I:181:PHE:HZ	2:I:203:PHE:HE2	1.54	0.55
3:C:152:PRO:HG2	3:C:155:PHE:CE1	2.41	0.55
3:D:222:TYR:CE1	3:D:286:ARG:NE	2.74	0.55
3:D:287:PRO:HG3	3:D:328:VAL:HB	1.88	0.55
2:G:115:PHE:CB	2:G:116:PRO:HD2	2.27	0.55
3:A:83:SER:OG	3:A:84:TYR:N	2.37	0.55
3:A:86:LEU:HA	3:A:146:ARG:HH22	1.72	0.55
3:A:304:VAL:HG13	3:A:316:ILE:CG2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:62:ILE:HD12	3:B:67:MET:HG3	1.89	0.55
1:H:341:ASN:CG	1:H:344:PHE:HB2	2.31	0.55
1:F:459:THR:HB	1:F:460:PRO:CD	2.36	0.55
2:G:181:PHE:HZ	2:G:203:PHE:HE2	1.54	0.55
3:A:272:SER:O	3:A:273:ARG:C	2.50	0.55
3:A:285:ILE:CD1	3:A:286:ARG:H	2.16	0.55
3:A:307:VAL:CG2	3:A:339:GLU:HG2	2.36	0.55
3:B:90:LEU:O	3:B:131:PRO:HG2	2.06	0.55
3:B:140:GLN:O	3:B:143:ALA:HB3	2.07	0.55
3:B:236:SER:CB	3:B:237:PRO:HD3	2.35	0.55
3:B:247:THR:HG21	3:B:265:GLN:CD	2.31	0.55
2:I:187:SER:O	2:I:190:GLU:N	2.40	0.55
3:C:77:VAL:HG12	3:C:78:GLY:N	2.19	0.55
3:C:188:ILE:H	3:C:188:ILE:CD1	2.20	0.55
3:D:247:THR:HG21	3:D:265:GLN:CD	2.31	0.55
1:F:41:LEU:HD23	1:F:44:ILE:HD12	1.88	0.55
1:F:333:ILE:C	1:F:336:PHE:HB2	2.31	0.55
3:B:44:THR:CG2	3:B:48:MET:HE2	2.25	0.55
3:B:226:ALA:CB	3:B:230:VAL:HG21	2.27	0.55
3:B:266:VAL:CG2	3:B:267:TRP:N	2.70	0.55
3:B:292:PRO:CA	3:B:345:ILE:HG22	2.37	0.55
1:H:409:GLY:HA2	1:H:412:GLN:H	1.72	0.55
3:D:59:ASP:OD1	3:D:66:ARG:NH2	2.40	0.55
1:F:341:ASN:CG	1:F:344:PHE:HB2	2.31	0.55
1:F:419:LEU:C	1:F:421:LEU:N	2.59	0.55
3:A:34:PHE:O	3:A:35:VAL:CG1	2.55	0.55
3:A:195:VAL:HG13	3:B:310:LEU:HD21	1.88	0.55
3:A:236:SER:O	3:A:237:PRO:C	2.47	0.55
3:B:38:SER:C	3:B:40:CYS:H	2.15	0.55
3:B:59:ASP:OD1	3:B:66:ARG:NH2	2.40	0.55
3:B:336:LEU:C	3:B:337:VAL:HG23	2.31	0.55
1:H:434:PHE:CD1	1:H:434:PHE:C	2.84	0.55
3:D:26:ILE:H	3:D:26:ILE:CD1	2.14	0.55
3:D:155:PHE:N	3:D:155:PHE:CD1	2.74	0.55
3:D:242:LEU:HD12	3:D:283:LEU:HB3	1.88	0.55
2:G:12:ARG:HG2	2:G:12:ARG:HH11	1.72	0.55
2:G:33:MET:O	2:G:36:ALA:HB3	2.07	0.55
3:A:13:TRP:HH2	3:A:53:GLU:CD	2.15	0.55
3:A:334:VAL:C	3:A:335:VAL:HG23	2.32	0.55
1:H:274:GLN:HG2	1:H:274:GLN:O	2.06	0.55
1:H:333:ILE:O	1:H:336:PHE:CB	2.53	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:486:LEU:H	1:H:486:LEU:CD1	2.10	0.55
3:C:10:THR:CB	3:C:57:SER:HB3	2.37	0.55
3:D:77:VAL:CG1	3:D:78:GLY:N	2.70	0.55
3:D:140:GLN:O	3:D:143:ALA:HB3	2.06	0.55
2:G:137:LEU:HA	2:G:140:LEU:HD12	1.89	0.55
2:G:164:PHE:HA	2:G:167:LEU:HD13	1.88	0.55
3:A:51:GLY:HA3	3:A:72:PRO:HG3	1.87	0.55
1:H:93:ASN:O	1:H:95:SER:N	2.40	0.55
2:I:15:ILE:O	2:I:18:LEU:HD23	2.06	0.55
3:C:258:LEU:H	3:C:258:LEU:CD2	2.19	0.55
3:D:292:PRO:CA	3:D:345:ILE:HG22	2.37	0.55
1:F:503:ILE:HG22	1:F:507:LYS:HZ2	1.72	0.55
3:A:102:LEU:O	3:A:103:ALA:CB	2.55	0.55
1:H:333:ILE:C	1:H:336:PHE:HB2	2.31	0.55
3:C:4:VAL:HG22	3:C:5:GLN:N	2.21	0.55
3:C:34:PHE:C	3:C:35:VAL:HG13	2.32	0.55
3:C:190:VAL:O	3:C:191:THR:HB	2.07	0.55
3:D:77:VAL:HG12	3:D:78:GLY:H	1.71	0.55
3:D:226:ALA:CB	3:D:230:VAL:HG21	2.27	0.55
3:D:236:SER:HB3	3:D:237:PRO:CD	2.34	0.55
3:D:260:MET:HB2	3:D:261:PRO:CD	2.29	0.55
1:F:347:ILE:CG2	1:F:348:ASN:N	2.47	0.54
3:A:123:LEU:HD12	3:A:141:ARG:HH21	1.71	0.54
3:B:77:VAL:CG1	3:B:78:GLY:N	2.70	0.54
3:B:189:TYR:O	3:B:190:VAL:HG23	2.07	0.54
3:B:236:SER:HB3	3:B:237:PRO:CD	2.34	0.54
1:H:264:PHE:O	1:H:267:VAL:HG23	2.07	0.54
1:H:317:TYR:CE2	2:I:20:LEU:CG	2.86	0.54
1:H:339:LEU:O	1:H:347:ILE:HG22	2.06	0.54
3:C:51:GLY:HA3	3:C:72:PRO:HG3	1.87	0.54
3:C:86:LEU:HA	3:C:146:ARG:HH22	1.72	0.54
3:C:272:SER:O	3:C:273:ARG:C	2.50	0.54
3:D:281:MET:HB3	3:D:355:PHE:O	2.07	0.54
1:F:509:THR:O	1:F:510:ARG:HB2	2.05	0.54
2:G:28:MET:CA	2:G:31:LEU:HD21	2.33	0.54
1:H:457:THR:HB	1:H:461:ALA:HB3	1.89	0.54
2:I:33:MET:O	2:I:36:ALA:HB3	2.07	0.54
3:C:13:TRP:HH2	3:C:53:GLU:CD	2.15	0.54
3:C:123:LEU:HD12	3:C:141:ARG:HH21	1.71	0.54
3:C:258:LEU:HB3	3:C:260:MET:SD	2.48	0.54
3:C:355:PHE:HB3	3:C:360:THR:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:267:VAL:HG22	1:F:488:ALA:CA	2.36	0.54
1:F:500:ALA:O	1:F:504:VAL:HG23	2.07	0.54
2:G:15:ILE:O	2:G:18:LEU:HD23	2.06	0.54
3:A:4:VAL:HG22	3:A:5:GLN:N	2.21	0.54
3:A:335:VAL:HG12	3:A:335:VAL:O	2.06	0.54
3:B:242:LEU:HD12	3:B:283:LEU:HB3	1.88	0.54
1:H:80:LEU:O	1:H:83:LEU:HB2	2.06	0.54
1:H:439:ASN:HB3	2:I:132:PRO:HB2	1.89	0.54
3:C:85:ALA:O	3:C:146:ARG:NH2	2.36	0.54
3:C:285:ILE:CD1	3:C:286:ARG:H	2.16	0.54
3:D:191:THR:OG1	3:D:192:HIS:N	2.39	0.54
3:D:266:VAL:CG2	3:D:267:TRP:N	2.70	0.54
2:G:187:SER:O	2:G:190:GLU:N	2.40	0.54
3:A:152:PRO:HG2	3:A:155:PHE:CE1	2.42	0.54
3:A:258:LEU:HB3	3:A:260:MET:SD	2.48	0.54
3:B:255:GLN:C	3:B:256:VAL:HG13	2.33	0.54
3:B:314:THR:HG22	3:B:315:GLN:H	1.70	0.54
3:C:309:GLN:O	3:C:310:LEU:HB2	2.06	0.54
3:C:335:VAL:HG12	3:C:335:VAL:O	2.06	0.54
1:F:431:ILE:HG13	1:F:432:ALA:H	1.71	0.54
1:F:434:PHE:CD1	1:F:434:PHE:C	2.84	0.54
2:G:239:ASP:O	2:G:243:TYR:CE2	2.61	0.54
3:A:339:GLU:C	3:A:341:ALA:H	2.15	0.54
3:A:355:PHE:HB3	3:A:360:THR:O	2.08	0.54
3:B:354:LEU:CG	3:B:355:PHE:N	2.70	0.54
2:I:137:LEU:HA	2:I:140:LEU:HD12	1.89	0.54
3:C:102:LEU:O	3:C:103:ALA:CB	2.55	0.54
3:D:18:VAL:CG1	3:D:19:SER:H	2.20	0.54
3:D:189:TYR:O	3:D:190:VAL:HG23	2.07	0.54
3:D:255:GLN:C	3:D:256:VAL:HG13	2.33	0.54
3:D:354:LEU:CG	3:D:355:PHE:N	2.70	0.54
1:F:383:TYR:CE2	1:F:384:MET:HE2	2.43	0.54
1:F:457:THR:CB	1:F:461:ALA:HB3	2.38	0.54
3:A:294:ASP:OD1	3:A:295:ILE:HG13	2.08	0.54
3:B:163:ASN:O	3:B:164:LEU:HG	2.07	0.54
3:B:287:PRO:HG3	3:B:328:VAL:HB	1.88	0.54
3:B:334:VAL:O	3:B:335:VAL:CG2	2.56	0.54
1:H:457:THR:CB	1:H:461:ALA:HB3	2.38	0.54
2:I:34:VAL:O	2:I:37:ILE:O	2.26	0.54
2:I:230:VAL:HG12	2:I:231:PRO:N	2.23	0.54
3:C:9:VAL:HG22	3:C:59:ASP:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:230:VAL:O	3:C:234:ILE:HG13	2.07	0.54
3:C:294:ASP:OD1	3:C:295:ILE:HG13	2.08	0.54
3:C:334:VAL:C	3:C:335:VAL:HG23	2.32	0.54
3:D:45:LEU:HD12	3:D:207:LEU:HD11	1.90	0.54
1:F:91:PHE:O	1:F:263:ASN:CG	2.51	0.54
1:F:336:PHE:HA	1:F:339:LEU:HD12	1.89	0.54
1:F:439:ASN:HB3	2:G:132:PRO:HB2	1.89	0.54
2:G:34:VAL:O	2:G:37:ILE:O	2.26	0.54
2:G:147:LEU:HD21	2:G:154:ILE:HD11	1.90	0.54
3:B:20:LYS:HG2	3:B:211:ARG:HD3	1.90	0.54
3:B:22:ILE:O	3:B:23:ASN:CG	2.51	0.54
3:D:26:ILE:HD12	3:D:26:ILE:N	2.14	0.54
1:F:264:PHE:O	1:F:267:VAL:HG23	2.07	0.54
2:G:187:SER:O	2:G:188:LEU:C	2.50	0.54
2:G:254:ASN:CB	2:G:255:PRO:CD	2.82	0.54
3:A:96:MET:HE3	3:A:142:VAL:HG12	1.90	0.54
3:A:188:ILE:HG22	3:A:189:TYR:H	1.73	0.54
3:B:32:VAL:O	3:B:33:VAL:HG12	2.08	0.54
3:B:126:LEU:HD11	3:B:138:GLN:CD	2.32	0.54
1:H:446:LEU:HD11	2:I:250:GLN:OE1	2.08	0.54
2:I:12:ARG:HG2	2:I:12:ARG:HH11	1.72	0.54
3:C:339:GLU:C	3:C:341:ALA:H	2.15	0.54
2:G:24:ILE:HD12	2:G:25:ALA:CA	2.38	0.54
2:G:109:ALA:HA	2:G:113:MET:HE3	1.90	0.54
2:G:134:VAL:C	2:G:136:SER:N	2.66	0.54
3:A:15:GLU:O	3:A:17:VAL:HG23	2.08	0.54
3:B:186:THR:O	3:B:187:MET:CG	2.55	0.54
3:B:320:ILE:HG23	3:B:321:PRO:CD	2.31	0.54
1:H:280:ILE:HD13	1:H:470:TYR:CD1	2.34	0.54
2:I:3:MET:HG2	2:I:4:VAL:H	1.73	0.54
3:C:43:SER:O	3:C:46:LEU:HB2	2.08	0.54
3:C:186:THR:HG22	3:C:187:MET:H	1.73	0.54
3:D:126:LEU:HD11	3:D:138:GLN:CD	2.32	0.54
3:D:272:SER:O	3:D:273:ARG:C	2.51	0.54
1:H:91:PHE:O	1:H:263:ASN:CG	2.51	0.54
1:H:275:LYS:N	1:H:276:PRO:CD	2.58	0.54
1:H:500:ALA:O	1:H:504:VAL:HG23	2.07	0.54
2:I:94:ILE:HD12	2:I:163:ILE:HD13	1.90	0.54
2:I:178:LYS:O	2:I:181:PHE:HB2	2.08	0.54
1:F:274:GLN:O	1:F:274:GLN:HG2	2.06	0.53
1:F:408:ALA:HB1	1:F:412:GLN:CB	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:409:GLY:HA2	1:F:412:GLN:H	1.72	0.53
1:F:496:LEU:HD12	1:F:496:LEU:O	2.08	0.53
2:G:94:ILE:HD12	2:G:163:ILE:HD13	1.90	0.53
2:G:173:HIS:CD2	2:G:218:VAL:HG22	2.43	0.53
3:A:34:PHE:C	3:A:35:VAL:HG13	2.32	0.53
3:B:77:VAL:HG12	3:B:78:GLY:H	1.71	0.53
3:B:281:MET:HB3	3:B:355:PHE:O	2.07	0.53
1:H:459:THR:HB	1:H:460:PRO:HD2	1.91	0.53
2:I:134:VAL:C	2:I:136:SER:N	2.66	0.53
2:I:187:SER:O	2:I:188:LEU:C	2.50	0.53
2:I:239:ASP:O	2:I:243:TYR:CE2	2.61	0.53
3:C:15:GLU:O	3:C:17:VAL:HG23	2.08	0.53
3:C:120:VAL:C	3:C:122:GLN:H	2.16	0.53
3:C:180:HIS:HA	3:C:187:MET:HE1	1.90	0.53
3:D:12:ALA:CB	3:D:17:VAL:HA	2.38	0.53
3:D:32:VAL:O	3:D:33:VAL:HG12	2.08	0.53
3:D:268:LEU:HD12	3:D:270:VAL:HG22	1.87	0.53
3:D:334:VAL:O	3:D:335:VAL:CG2	2.56	0.53
2:G:3:MET:HG2	2:G:4:VAL:H	1.73	0.53
2:G:178:LYS:O	2:G:181:PHE:HB2	2.08	0.53
3:A:120:VAL:C	3:A:122:GLN:H	2.16	0.53
3:A:260:MET:HB2	3:A:261:PRO:HD2	1.90	0.53
1:H:336:PHE:HA	1:H:339:LEU:HD12	1.89	0.53
1:H:415:PHE:O	1:H:420:PRO:HD3	2.08	0.53
3:D:163:ASN:O	3:D:164:LEU:HG	2.07	0.53
1:F:422:LEU:HA	1:F:425:PRO:CG	2.38	0.53
2:G:174:VAL:O	2:G:177:ILE:HG22	2.09	0.53
3:A:107:LYS:HB2	3:A:107:LYS:NZ	2.24	0.53
3:A:120:VAL:HG23	3:A:121:LEU:N	2.23	0.53
3:B:272:SER:O	3:B:273:ARG:C	2.51	0.53
1:H:99:GLN:HE22	2:I:146:ARG:NH1	1.93	0.53
1:H:345:GLY:C	1:H:347:ILE:H	2.15	0.53
1:H:373:ILE:HG13	1:H:374:ILE:HG23	1.89	0.53
1:H:408:ALA:HB1	1:H:412:GLN:CB	2.38	0.53
1:H:419:LEU:C	1:H:421:LEU:N	2.59	0.53
2:I:17:HIS:O	2:I:20:LEU:HB3	2.08	0.53
3:C:298:VAL:HG21	3:C:347:LEU:O	2.08	0.53
1:F:439:ASN:CB	2:G:132:PRO:HB2	2.39	0.53
3:A:180:HIS:HA	3:A:187:MET:HE1	1.90	0.53
3:A:298:VAL:HG21	3:A:347:LEU:O	2.08	0.53
3:B:260:MET:HB2	3:B:261:PRO:CD	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:88:ALA:O	1:H:89:ILE:C	2.49	0.53
1:H:496:LEU:O	1:H:496:LEU:HD12	2.08	0.53
2:I:28:MET:CA	2:I:31:LEU:HD21	2.33	0.53
2:I:81:VAL:O	2:I:84:TRP:HB2	2.09	0.53
2:I:198:THR:OG1	2:I:199:PRO:CD	2.56	0.53
3:C:188:ILE:HG22	3:C:189:TYR:H	1.73	0.53
3:D:20:LYS:HG2	3:D:211:ARG:HD3	1.90	0.53
3:D:22:ILE:O	3:D:23:ASN:CG	2.51	0.53
3:D:309:GLN:C	3:D:311:GLY:H	2.17	0.53
3:D:334:VAL:C	3:D:335:VAL:CG2	2.82	0.53
1:F:83:LEU:HD11	2:G:131:PHE:HD1	1.73	0.53
1:F:344:PHE:CZ	2:G:257:ASN:CB	2.92	0.53
1:F:345:GLY:C	1:F:347:ILE:H	2.15	0.53
2:G:17:HIS:O	2:G:20:LEU:HB3	2.08	0.53
3:A:10:THR:CB	3:A:57:SER:HB3	2.37	0.53
3:A:23:ASN:O	3:A:24:LEU:HD23	2.09	0.53
3:B:12:ALA:CB	3:B:17:VAL:HA	2.38	0.53
3:B:45:LEU:HD12	3:B:207:LEU:HD11	1.90	0.53
1:H:383:TYR:CE2	1:H:384:MET:HE2	2.43	0.53
1:H:398:ASP:O	1:H:399:LEU:C	2.49	0.53
2:I:31:LEU:H	2:I:31:LEU:CD2	2.01	0.53
2:I:147:LEU:HD21	2:I:154:ILE:HD11	1.90	0.53
3:C:60:LEU:C	3:C:61:PHE:CD1	2.87	0.53
3:D:186:THR:O	3:D:187:MET:CG	2.55	0.53
1:F:76:GLY:HA2	1:F:80:LEU:HD22	1.90	0.53
1:F:366:THR:HG23	1:F:367:THR:N	2.23	0.53
1:F:415:PHE:O	1:F:420:PRO:HD3	2.08	0.53
3:A:9:VAL:HG22	3:A:59:ASP:O	2.08	0.53
3:A:182:ARG:NH2	3:A:183:LEU:HG	2.24	0.53
3:B:191:THR:OG1	3:B:192:HIS:N	2.39	0.53
3:C:120:VAL:HG23	3:C:121:LEU:N	2.23	0.53
3:C:182:ARG:NH2	3:C:183:LEU:HG	2.24	0.53
3:D:177:SER:O	3:D:181:LYS:HG2	2.09	0.53
3:D:250:ALA:O	3:D:252:ASP:N	2.42	0.53
1:F:93:ASN:O	1:F:95:SER:N	2.40	0.53
1:F:423:ILE:CG1	1:F:424:LYS:H	2.22	0.53
2:G:124:GLY:O	2:G:128:PHE:HB2	2.09	0.53
3:A:128:ASP:O	3:A:129:ARG:O	2.27	0.53
1:H:280:ILE:HG13	1:H:467:LEU:CD2	2.39	0.53
3:D:38:SER:C	3:D:40:CYS:H	2.15	0.53
3:D:190:VAL:CG1	3:D:191:THR:N	2.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:96:SER:C	1:F:97:THR:HG23	2.34	0.53
1:F:281:PHE:HA	1:F:467:LEU:CD2	2.36	0.53
1:F:373:ILE:HG13	1:F:374:ILE:HG23	1.89	0.53
2:G:230:VAL:HG12	2:G:231:PRO:N	2.23	0.53
3:B:329:TYR:OH	3:B:331:GLN:NE2	2.42	0.53
1:H:344:PHE:CZ	2:I:257:ASN:CB	2.92	0.53
1:H:422:LEU:HA	1:H:425:PRO:CG	2.38	0.53
2:I:24:ILE:HD12	2:I:25:ALA:CA	2.38	0.53
2:I:92:ALA:CB	2:I:227:ILE:HD13	2.34	0.53
3:C:204:ILE:HD12	3:C:221:LEU:HD12	1.91	0.53
3:C:353:HIS:CE1	3:C:364:ARG:HD3	2.44	0.53
3:C:369:PRO:O	3:C:370:GLY:C	2.52	0.53
3:C:371:VAL:O	3:C:371:VAL:HG12	2.08	0.53
2:G:81:VAL:O	2:G:84:TRP:HB2	2.09	0.53
3:A:253:GLN:HB2	3:A:267:TRP:HE3	1.74	0.53
3:A:291:LEU:HB3	3:A:292:PRO:CD	2.39	0.53
3:B:96:MET:HE2	3:B:114:VAL:HG13	1.91	0.53
1:H:96:SER:C	1:H:97:THR:HG23	2.33	0.53
1:H:423:ILE:CG1	1:H:424:LYS:H	2.22	0.53
1:H:439:ASN:CB	2:I:132:PRO:HB2	2.39	0.53
2:I:173:HIS:CD2	2:I:218:VAL:HG22	2.43	0.53
3:C:332:ASN:O	3:C:333:ASP:O	2.27	0.53
3:D:228:ARG:HG2	3:D:228:ARG:HH11	1.73	0.53
1:F:450:GLY:HA3	1:F:465:ASP:CG	2.34	0.53
2:G:174:VAL:HA	2:G:177:ILE:CG2	2.39	0.53
2:G:190:GLU:CD	3:A:52:LEU:HD13	2.34	0.53
2:G:198:THR:OG1	2:G:199:PRO:CD	2.56	0.53
3:A:43:SER:O	3:A:46:LEU:HB2	2.08	0.53
3:A:349:PRO:HA	3:A:352:CYS:SG	2.49	0.53
3:B:228:ARG:HG2	3:B:228:ARG:HH11	1.73	0.53
3:B:334:VAL:C	3:B:335:VAL:CG2	2.82	0.53
1:H:380:GLY:C	1:H:382:PRO:HD2	2.34	0.53
3:C:46:LEU:CD1	3:C:190:VAL:HG23	2.39	0.53
3:C:291:LEU:HB3	3:C:292:PRO:CD	2.39	0.53
3:D:328:VAL:HG12	3:D:329:TYR:N	2.23	0.53
1:F:77:LEU:O	1:F:82:PRO:HD3	2.09	0.52
1:F:457:THR:HB	1:F:461:ALA:HB3	1.89	0.52
2:G:104:THR:HG22	2:G:105:THR:N	2.24	0.52
3:A:5:GLN:O	3:A:6:LEU:HD12	2.09	0.52
3:A:145:GLY:HA2	3:A:148:LEU:CD1	2.35	0.52
3:A:332:ASN:O	3:A:333:ASP:O	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:83:SER:O	3:B:84:TYR:CD2	2.62	0.52
3:B:177:SER:O	3:B:181:LYS:HG2	2.09	0.52
3:B:298:VAL:HB	3:B:347:LEU:N	2.23	0.52
3:C:128:ASP:O	3:C:129:ARG:O	2.27	0.52
3:C:160:PRO:O	3:C:161:LEU:HG	2.09	0.52
3:D:76:GLY:O	3:D:152:PRO:O	2.27	0.52
2:G:244:THR:HG1	2:G:246:ALA:HB3	1.71	0.52
3:A:9:VAL:O	3:A:21:ASP:HA	2.09	0.52
3:A:84:TYR:CE1	3:A:140:GLN:NE2	2.77	0.52
3:A:140:GLN:OE1	3:A:164:LEU:HD11	2.09	0.52
3:A:191:THR:O	3:A:192:HIS:CD2	2.63	0.52
3:A:204:ILE:HD12	3:A:221:LEU:HD12	1.91	0.52
3:B:76:GLY:O	3:B:152:PRO:O	2.27	0.52
3:B:188:ILE:CD1	3:B:188:ILE:H	2.19	0.52
3:B:190:VAL:CG1	3:B:191:THR:N	2.71	0.52
3:B:328:VAL:HG12	3:B:329:TYR:N	2.23	0.52
1:H:45:THR:HG23	1:H:46:THR:N	2.24	0.52
1:H:366:THR:HG23	1:H:367:THR:N	2.23	0.52
2:I:124:GLY:O	2:I:128:PHE:HB2	2.09	0.52
3:C:285:ILE:HD12	3:C:286:ARG:N	2.16	0.52
3:D:188:ILE:CD1	3:D:188:ILE:H	2.19	0.52
3:A:353:HIS:CE1	3:A:364:ARG:HD3	2.44	0.52
3:B:125:HIS:NE2	3:B:126:LEU:HG	2.24	0.52
3:B:369:PRO:C	3:B:371:VAL:H	2.17	0.52
1:H:450:GLY:HA3	1:H:465:ASP:CG	2.34	0.52
2:I:245:LEU:CG	2:I:249:MET:HE2	2.30	0.52
3:C:8:ASN:O	3:C:58:GLY:HA3	2.10	0.52
3:C:140:GLN:OE1	3:C:164:LEU:HD11	2.10	0.52
1:F:280:ILE:HG13	1:F:467:LEU:CD2	2.39	0.52
1:F:280:ILE:HD11	1:F:467:LEU:HD13	1.91	0.52
1:F:296:VAL:HG21	1:F:426:LEU:HD21	1.91	0.52
1:F:380:GLY:C	1:F:382:PRO:HD2	2.34	0.52
3:A:186:THR:HG22	3:A:187:MET:H	1.73	0.52
3:A:190:VAL:O	3:A:191:THR:HB	2.07	0.52
3:B:11:LYS:N	3:B:19:SER:HB2	2.24	0.52
1:H:77:LEU:O	1:H:82:PRO:HD3	2.09	0.52
1:H:375:VAL:HG11	1:H:443:LEU:HD11	1.91	0.52
2:I:190:GLU:CD	3:C:52:LEU:HD13	2.34	0.52
3:C:5:GLN:O	3:C:6:LEU:HD12	2.09	0.52
3:C:9:VAL:O	3:C:21:ASP:HA	2.09	0.52
3:D:125:HIS:NE2	3:D:126:LEU:HG	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:45:THR:HG23	1:F:46:THR:N	2.24	0.52
1:F:501:LEU:CD1	2:G:127:ILE:HG23	2.39	0.52
3:A:60:LEU:C	3:A:61:PHE:CD1	2.87	0.52
3:A:188:ILE:H	3:A:188:ILE:CD1	2.20	0.52
3:A:371:VAL:HG12	3:A:371:VAL:O	2.08	0.52
1:H:501:LEU:CD1	2:I:127:ILE:HG23	2.39	0.52
2:I:109:ALA:HA	2:I:113:MET:HE3	1.90	0.52
2:I:174:VAL:O	2:I:177:ILE:HG22	2.09	0.52
2:I:230:VAL:HG12	2:I:231:PRO:CD	2.40	0.52
3:C:9:VAL:HG12	3:C:10:THR:H	1.74	0.52
3:C:107:LYS:HB2	3:C:107:LYS:NZ	2.24	0.52
3:C:349:PRO:HA	3:C:352:CYS:SG	2.49	0.52
3:D:232:GLY:CA	3:D:238:LYS:HE2	2.39	0.52
3:D:275:VAL:HG23	3:D:275:VAL:O	2.10	0.52
3:D:311:GLY:O	3:D:313:GLU:N	2.42	0.52
1:F:306:VAL:HG11	1:F:318:ARG:HD3	1.92	0.52
1:F:446:LEU:HD11	2:G:250:GLN:OE1	2.08	0.52
1:F:459:THR:HB	1:F:460:PRO:HD2	1.91	0.52
2:G:230:VAL:HG12	2:G:231:PRO:CD	2.40	0.52
3:A:160:PRO:O	3:A:161:LEU:HG	2.09	0.52
3:A:243:PRO:C	3:A:244:VAL:CG2	2.83	0.52
3:B:100:LEU:HD13	3:B:110:ILE:CG1	2.40	0.52
3:B:268:LEU:HD12	3:B:270:VAL:HG22	1.87	0.52
1:H:306:VAL:HG11	1:H:318:ARG:HD3	1.92	0.52
2:I:36:ALA:O	2:I:37:ILE:HG12	2.09	0.52
3:C:122:GLN:O	3:C:123:LEU:HD12	2.10	0.52
3:C:260:MET:HB2	3:C:261:PRO:HD2	1.90	0.52
3:D:55:ILE:HG21	3:D:68:ASN:ND2	2.25	0.52
3:D:83:SER:O	3:D:84:TYR:CD2	2.62	0.52
3:D:96:MET:HE2	3:D:114:VAL:HG13	1.91	0.52
3:D:335:VAL:HG12	3:D:337:VAL:HG23	1.92	0.52
3:D:354:LEU:C	3:D:355:PHE:CG	2.88	0.52
1:F:78:PHE:O	1:F:82:PRO:HG2	2.10	0.52
1:F:96:SER:O	1:F:97:THR:CG2	2.57	0.52
3:A:356:ARG:HG3	3:A:356:ARG:HH11	1.74	0.52
3:B:311:GLY:O	3:B:313:GLU:N	2.42	0.52
1:H:76:GLY:HA2	1:H:80:LEU:HD22	1.90	0.52
1:H:90:ALA:HB1	1:H:490:ILE:HD12	1.92	0.52
1:H:280:ILE:HD11	1:H:467:LEU:HD13	1.91	0.52
1:H:284:THR:CG2	1:H:466:LEU:CA	2.74	0.52
2:I:95:SER:O	2:I:99:ILE:HG13	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:VAL:CG1	3:C:191:THR:N	2.73	0.52
3:C:191:THR:O	3:C:192:HIS:CD2	2.63	0.52
3:C:243:PRO:C	3:C:244:VAL:CG2	2.83	0.52
3:C:260:MET:HB2	3:C:261:PRO:CD	2.39	0.52
3:D:329:TYR:OH	3:D:331:GLN:NE2	2.42	0.52
2:G:91:VAL:O	2:G:95:SER:HB2	2.10	0.52
2:G:174:VAL:CA	2:G:177:ILE:HG22	2.40	0.52
3:A:46:LEU:CD1	3:A:190:VAL:HG23	2.39	0.52
3:A:190:VAL:CG1	3:A:191:THR:N	2.73	0.52
3:C:84:TYR:CE1	3:C:140:GLN:NE2	2.77	0.52
3:D:369:PRO:C	3:D:371:VAL:H	2.17	0.52
1:F:376:ASN:O	1:F:377:THR:C	2.53	0.52
3:A:41:GLY:O	3:A:44:THR:HB	2.10	0.52
3:D:11:LYS:N	3:D:19:SER:HB2	2.24	0.52
1:F:92:THR:HG23	1:F:93:ASN:N	2.19	0.52
1:F:265:THR:HG23	1:F:266:ARG:N	2.25	0.52
1:F:293:PHE:C	1:F:293:PHE:CD2	2.88	0.52
1:F:364:ASP:HB3	1:F:367:THR:CG2	2.40	0.52
1:F:381:TYR:CD1	1:F:382:PRO:N	2.62	0.52
3:A:307:VAL:HA	3:A:316:ILE:HG12	1.92	0.52
3:B:247:THR:HG21	3:B:265:GLN:OE1	2.10	0.52
3:B:250:ALA:O	3:B:252:ASP:N	2.42	0.52
3:C:40:CYS:HB3	3:C:42:LYS:HZ1	1.74	0.52
1:F:295:THR:HG23	1:F:380:GLY:C	2.35	0.51
3:A:145:GLY:HA2	3:A:148:LEU:HB2	1.92	0.51
3:A:260:MET:HB2	3:A:261:PRO:CD	2.39	0.51
3:B:275:VAL:HG23	3:B:275:VAL:O	2.10	0.51
3:B:323:ILE:HG12	3:B:324:ARG:N	2.25	0.51
1:H:295:THR:HG23	1:H:380:GLY:C	2.35	0.51
2:I:104:THR:HG22	2:I:105:THR:N	2.24	0.51
3:C:91:SER:CB	3:C:129:ARG:O	2.58	0.51
3:C:96:MET:HE3	3:C:142:VAL:HG12	1.90	0.51
3:C:303:GLU:O	3:C:318:ILE:HG23	2.10	0.51
3:D:55:ILE:HD12	3:D:55:ILE:H	1.75	0.51
3:D:100:LEU:HD13	3:D:110:ILE:CG1	2.40	0.51
3:D:120:VAL:CG2	3:D:121:LEU:N	2.73	0.51
3:D:246:VAL:HG23	3:D:279:ALA:O	2.10	0.51
3:D:323:ILE:HG12	3:D:324:ARG:N	2.25	0.51
1:F:375:VAL:HG11	1:F:443:LEU:HD11	1.91	0.51
3:A:9:VAL:HG12	3:A:10:THR:H	1.74	0.51
3:A:122:GLN:O	3:A:123:LEU:HD12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:354:LEU:C	3:B:355:PHE:CG	2.88	0.51
1:H:78:PHE:O	1:H:82:PRO:HG2	2.10	0.51
1:H:96:SER:O	1:H:97:THR:CG2	2.57	0.51
1:H:267:VAL:HG13	1:H:488:ALA:CB	2.40	0.51
1:H:364:ASP:HB3	1:H:367:THR:CG2	2.40	0.51
2:I:107:ALA:O	2:I:110:PHE:HB2	2.10	0.51
2:I:174:VAL:HA	2:I:177:ILE:CG2	2.39	0.51
3:C:23:ASN:O	3:C:24:LEU:HD23	2.09	0.51
3:C:145:GLY:HA2	3:C:148:LEU:HB2	1.92	0.51
3:C:155:PHE:HB2	3:C:187:MET:CG	2.40	0.51
3:C:253:GLN:HB2	3:C:267:TRP:HE3	1.74	0.51
3:C:356:ARG:HH11	3:C:356:ARG:HG3	1.74	0.51
3:D:34:PHE:O	3:D:35:VAL:CG1	2.48	0.51
2:G:107:ALA:O	2:G:110:PHE:HB2	2.11	0.51
1:H:270:ASP:HB3	1:H:274:GLN:HB2	1.92	0.51
2:I:227:ILE:HG22	2:I:228:THR:N	2.25	0.51
3:C:143:ALA:O	3:C:144:ILE:C	2.54	0.51
3:D:313:GLU:CD	3:D:330:ARG:HH21	2.18	0.51
1:F:454:ARG:HB2	1:F:457:THR:HG21	1.93	0.51
1:F:503:ILE:HG22	1:F:507:LYS:NZ	2.24	0.51
3:A:8:ASN:O	3:A:58:GLY:HA3	2.10	0.51
3:A:40:CYS:HB3	3:A:42:LYS:HZ1	1.75	0.51
3:A:62:ILE:HG22	3:A:63:GLY:N	2.25	0.51
3:A:301:GLU:CA	3:A:344:ALA:HB2	2.35	0.51
3:B:55:ILE:HD12	3:B:55:ILE:H	1.75	0.51
3:B:232:GLY:CA	3:B:238:LYS:HE2	2.39	0.51
3:B:368:GLU:CB	3:B:369:PRO:HD2	2.28	0.51
1:H:83:LEU:HD11	2:I:131:PHE:HD1	1.74	0.51
1:H:376:ASN:O	1:H:377:THR:C	2.53	0.51
3:C:291:LEU:O	3:C:345:ILE:HB	2.10	0.51
3:D:236:SER:CB	3:D:237:PRO:HD3	2.35	0.51
1:F:267:VAL:HG13	1:F:488:ALA:CB	2.40	0.51
1:F:483:ASP:O	1:F:485:GLY:N	2.44	0.51
2:G:36:ALA:O	2:G:37:ILE:HG12	2.10	0.51
3:A:55:ILE:HD13	3:A:68:ASN:CB	2.41	0.51
3:A:310:LEU:O	3:A:312:ASN:N	2.44	0.51
3:B:120:VAL:CG2	3:B:121:LEU:N	2.73	0.51
3:B:309:GLN:C	3:B:311:GLY:H	2.17	0.51
3:B:313:GLU:CD	3:B:330:ARG:HH21	2.18	0.51
3:B:335:VAL:HG12	3:B:337:VAL:HG23	1.92	0.51
1:H:293:PHE:CD2	1:H:293:PHE:C	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:296:VAL:HG21	1:H:426:LEU:HD21	1.91	0.51
1:H:303:ALA:CA	1:H:385:MET:HE1	2.28	0.51
1:H:317:TYR:OH	2:I:17:HIS:CD2	2.64	0.51
1:H:396:PRO:HB2	1:H:398:ASP:OD1	2.11	0.51
1:H:444:ILE:HG21	1:H:469:ASN:OD1	2.10	0.51
1:H:449:ASN:C	1:H:451:GLY:H	2.19	0.51
2:I:167:LEU:C	2:I:169:GLY:H	2.18	0.51
3:C:6:LEU:CG	3:C:9:VAL:HG21	2.41	0.51
3:C:156:LEU:N	3:C:156:LEU:HD23	2.24	0.51
3:C:294:ASP:OD1	3:C:295:ILE:N	2.44	0.51
3:D:247:THR:HG21	3:D:265:GLN:OE1	2.10	0.51
1:F:396:PRO:HB2	1:F:398:ASP:OD1	2.11	0.51
2:G:227:ILE:HG22	2:G:228:THR:N	2.25	0.51
3:A:4:VAL:CG2	3:A:5:GLN:N	2.74	0.51
3:A:291:LEU:O	3:A:345:ILE:HB	2.10	0.51
3:B:55:ILE:HG21	3:B:68:ASN:ND2	2.25	0.51
3:B:164:LEU:HD13	3:B:168:LEU:CD2	2.38	0.51
3:B:172:MET:O	3:B:176:ILE:HG12	2.11	0.51
2:I:225:ALA:HA	2:I:228:THR:CG2	2.41	0.51
3:D:214:GLN:HG2	3:D:215:VAL:N	2.26	0.51
3:D:309:GLN:O	3:D:311:GLY:N	2.39	0.51
2:G:4:VAL:HG11	3:B:72:PRO:HD3	1.93	0.51
3:A:369:PRO:O	3:A:370:GLY:C	2.52	0.51
3:B:311:GLY:C	3:B:313:GLU:N	2.65	0.51
1:H:87:ILE:O	1:H:90:ALA:CB	2.58	0.51
1:H:92:THR:HA	1:H:263:ASN:HA	1.93	0.51
1:H:265:THR:HG23	1:H:266:ARG:N	2.25	0.51
2:I:227:ILE:O	2:I:229:GLU:N	2.43	0.51
3:C:219:LEU:O	3:C:220:GLU:C	2.54	0.51
3:C:307:VAL:HA	3:C:316:ILE:HG12	1.92	0.51
1:F:270:ASP:HB3	1:F:274:GLN:HB2	1.92	0.51
2:G:95:SER:O	2:G:99:ILE:HG13	2.10	0.51
2:G:132:PRO:O	2:G:134:VAL:HG12	2.11	0.51
2:G:225:ALA:HA	2:G:228:THR:CG2	2.41	0.51
3:A:294:ASP:OD1	3:A:295:ILE:N	2.44	0.51
3:A:334:VAL:CG1	3:A:335:VAL:H	2.17	0.51
3:B:18:VAL:CG1	3:B:19:SER:H	2.20	0.51
3:D:120:VAL:HG23	3:D:121:LEU:N	2.25	0.51
3:D:186:THR:C	3:D:187:MET:HG3	2.35	0.51
3:D:350:GLU:N	3:D:350:GLU:OE2	2.44	0.51
3:A:6:LEU:CG	3:A:9:VAL:HG21	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:156:LEU:HD23	3:A:156:LEU:N	2.24	0.51
3:A:210:GLY:O	3:A:211:ARG:HG2	2.11	0.51
3:B:186:THR:C	3:B:187:MET:HG3	2.35	0.51
2:I:4:VAL:HG11	3:D:72:PRO:HD3	1.93	0.51
3:C:145:GLY:HA2	3:C:148:LEU:CD1	2.35	0.51
3:C:214:GLN:CG	3:C:215:VAL:N	2.59	0.51
3:C:306:VAL:CG2	3:C:317:HIS:ND1	2.74	0.51
3:C:310:LEU:O	3:C:312:ASN:N	2.44	0.51
3:D:243:PRO:O	3:D:244:VAL:HG22	2.11	0.51
2:G:147:LEU:CD2	2:G:154:ILE:HD11	2.41	0.51
2:G:197:ALA:HB1	2:G:202:ALA:N	2.26	0.51
3:B:92:VAL:HG11	3:B:126:LEU:O	2.11	0.51
3:B:246:VAL:HG23	3:B:279:ALA:O	2.10	0.51
1:H:302:LEU:CD2	1:H:321:LEU:HD13	2.41	0.51
3:C:41:GLY:O	3:C:44:THR:HB	2.10	0.51
3:C:62:ILE:HG22	3:C:63:GLY:N	2.25	0.51
3:D:92:VAL:HG11	3:D:126:LEU:O	2.11	0.51
1:F:99:GLN:HG3	1:F:100:LEU:N	2.26	0.50
1:F:302:LEU:CD2	1:F:321:LEU:HD13	2.41	0.50
1:F:306:VAL:CG1	1:F:318:ARG:HD3	2.40	0.50
1:F:449:ASN:C	1:F:451:GLY:H	2.19	0.50
3:A:155:PHE:HB2	3:A:187:MET:CG	2.40	0.50
3:A:303:GLU:O	3:A:318:ILE:HG23	2.10	0.50
3:B:96:MET:C	3:B:98:PHE:N	2.67	0.50
1:H:421:LEU:O	1:H:422:LEU:HG	2.11	0.50
1:H:498:VAL:HA	1:H:501:LEU:CD1	2.40	0.50
2:I:174:VAL:CA	2:I:177:ILE:HG22	2.40	0.50
1:F:92:THR:HA	1:F:263:ASN:HA	1.93	0.50
2:G:211:SER:C	2:G:213:PRO:HD2	2.36	0.50
3:A:306:VAL:CG2	3:A:317:HIS:ND1	2.74	0.50
3:B:169:ARG:CB	3:B:169:ARG:HH11	2.24	0.50
1:H:377:THR:HG22	1:H:378:TRP:N	2.25	0.50
1:H:396:PRO:O	1:H:399:LEU:HB2	2.11	0.50
1:H:441:PHE:CE1	1:H:445:GLN:HG3	2.47	0.50
2:I:91:VAL:O	2:I:95:SER:HB2	2.10	0.50
2:I:132:PRO:O	2:I:134:VAL:HG12	2.11	0.50
3:C:210:GLY:O	3:C:211:ARG:HG2	2.11	0.50
3:C:246:VAL:HG13	3:C:255:GLN:O	2.11	0.50
3:D:197:ALA:O	3:D:201:ALA:HB2	2.10	0.50
3:D:323:ILE:HG12	3:D:324:ARG:H	1.76	0.50
1:F:87:ILE:O	1:F:90:ALA:CB	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:167:LEU:C	2:G:169:GLY:H	2.18	0.50
3:A:203:LYS:HG2	3:A:204:ILE:H	1.76	0.50
3:B:120:VAL:HG23	3:B:121:LEU:N	2.25	0.50
3:B:350:GLU:CB	3:B:366:HIS:CE1	2.95	0.50
1:H:306:VAL:CG1	1:H:318:ARG:HD3	2.40	0.50
2:I:197:ALA:HB1	2:I:202:ALA:N	2.26	0.50
3:C:4:VAL:CG2	3:C:5:GLN:N	2.74	0.50
3:C:34:PHE:O	3:C:35:VAL:HG12	2.11	0.50
3:A:80:VAL:CG2	3:A:160:PRO:HB3	2.41	0.50
3:B:350:GLU:N	3:B:350:GLU:OE2	2.44	0.50
1:H:486:LEU:HB2	1:H:489:ALA:HB3	1.93	0.50
2:I:114:ARG:HG2	2:I:118:LYS:HZ1	1.75	0.50
2:I:147:LEU:CD2	2:I:154:ILE:HD11	2.41	0.50
3:C:258:LEU:N	3:C:258:LEU:CD2	2.75	0.50
3:C:354:LEU:C	3:C:355:PHE:CG	2.89	0.50
3:D:55:ILE:HG21	3:D:68:ASN:OD1	2.12	0.50
3:D:169:ARG:CB	3:D:169:ARG:HH11	2.24	0.50
1:F:90:ALA:HB1	1:F:490:ILE:HD12	1.92	0.50
1:F:317:TYR:OH	2:G:17:HIS:CD2	2.64	0.50
1:F:396:PRO:O	1:F:399:LEU:HB2	2.11	0.50
2:G:227:ILE:O	2:G:229:GLU:N	2.43	0.50
3:A:34:PHE:C	3:A:35:VAL:CG1	2.84	0.50
3:A:66:ARG:O	3:A:67:MET:CG	2.49	0.50
3:A:357:GLU:C	3:A:359:GLY:N	2.68	0.50
3:B:214:GLN:CG	3:B:215:VAL:N	2.75	0.50
3:B:253:GLN:CB	3:B:267:TRP:CE3	2.95	0.50
3:B:276:GLN:HE21	3:B:277:VAL:H	1.60	0.50
1:H:454:ARG:HG3	1:H:462:GLY:C	2.37	0.50
1:H:503:ILE:HG22	1:H:507:LYS:NZ	2.25	0.50
2:I:244:THR:H	2:I:247:VAL:HG23	1.76	0.50
2:I:244:THR:HG1	2:I:246:ALA:HB3	1.76	0.50
3:C:45:LEU:O	3:C:46:LEU:C	2.54	0.50
3:C:203:LYS:HG2	3:C:204:ILE:H	1.76	0.50
3:C:334:VAL:CG1	3:C:335:VAL:H	2.16	0.50
3:D:9:VAL:O	3:D:21:ASP:HA	2.12	0.50
3:D:188:ILE:HG22	3:D:189:TYR:H	1.76	0.50
3:D:276:GLN:HE21	3:D:277:VAL:H	1.60	0.50
1:F:425:PRO:HG2	1:F:426:LEU:H	1.77	0.50
2:G:209:PRO:HA	2:G:212:VAL:HG23	1.93	0.50
3:A:143:ALA:O	3:A:144:ILE:C	2.54	0.50
3:B:235:GLY:O	3:B:236:SER:O	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:256:VAL:O	3:B:265:GLN:HA	2.12	0.50
3:C:110:ILE:O	3:C:114:VAL:CG2	2.55	0.50
3:D:291:LEU:HB3	3:D:292:PRO:CD	2.42	0.50
2:G:262:ASP:O	2:G:265:ALA:HB3	2.12	0.50
3:A:91:SER:CB	3:A:129:ARG:O	2.59	0.50
3:A:246:VAL:HG13	3:A:255:GLN:O	2.11	0.50
3:B:7:GLN:HA	3:B:23:ASN:OD1	2.12	0.50
3:B:214:GLN:HG2	3:B:215:VAL:N	2.26	0.50
3:B:276:GLN:HG3	3:B:277:VAL:O	2.11	0.50
1:H:498:VAL:HG22	1:H:501:LEU:HD12	1.94	0.50
2:I:229:GLU:CD	2:I:230:VAL:N	2.64	0.50
3:C:55:ILE:HD13	3:C:68:ASN:CB	2.41	0.50
3:C:80:VAL:CG2	3:C:160:PRO:HB3	2.41	0.50
3:D:349:PRO:O	3:D:352:CYS:CB	2.55	0.50
1:F:421:LEU:O	1:F:422:LEU:HG	2.11	0.50
1:F:454:ARG:HG3	1:F:462:GLY:C	2.37	0.50
3:B:290:LEU:HD22	3:B:345:ILE:HD13	1.93	0.50
3:B:299:ILE:HG22	3:B:300:LEU:N	2.27	0.50
1:H:99:GLN:HG3	1:H:100:LEU:N	2.26	0.50
1:H:280:ILE:CD1	1:H:467:LEU:HD13	2.41	0.50
1:H:425:PRO:HG2	1:H:426:LEU:H	1.77	0.50
2:I:29:PHE:HB3	2:I:30:PRO:CD	2.33	0.50
3:C:204:ILE:HB	3:C:221:LEU:HD11	1.93	0.50
3:C:252:ASP:O	3:C:270:VAL:O	2.30	0.50
3:D:236:SER:CB	3:D:237:PRO:CD	2.90	0.50
3:D:276:GLN:HG3	3:D:277:VAL:O	2.11	0.50
1:F:280:ILE:CD1	1:F:467:LEU:HD13	2.41	0.50
1:F:414:PHE:HA	1:F:418:THR:HG23	1.93	0.50
2:G:4:VAL:HG22	2:G:5:GLN:N	2.27	0.50
3:A:222:TYR:OH	3:A:288:GLU:OE2	2.22	0.50
3:A:314:THR:HG22	3:A:315:GLN:N	2.27	0.50
3:B:197:ALA:O	3:B:201:ALA:HB2	2.10	0.50
2:I:209:PRO:HA	2:I:212:VAL:HG23	1.93	0.50
2:I:262:ASP:O	2:I:265:ALA:HB3	2.12	0.50
3:C:204:ILE:CG2	3:C:205:VAL:N	2.61	0.50
3:D:214:GLN:OE1	3:D:230:VAL:HG11	2.12	0.50
1:F:444:ILE:HG21	1:F:469:ASN:OD1	2.10	0.49
2:G:88:SER:HB3	2:G:227:ILE:CD1	2.42	0.49
3:A:198:MET:HE1	3:A:234:ILE:HG22	1.94	0.49
3:A:204:ILE:HB	3:A:221:LEU:HD11	1.93	0.49
3:B:188:ILE:HG22	3:B:189:TYR:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:193:ASP:C	3:B:195:VAL:N	2.69	0.49
3:B:255:GLN:HE21	3:B:267:TRP:NE1	2.10	0.49
3:B:323:ILE:HG12	3:B:324:ARG:H	1.76	0.49
1:H:76:GLY:HA2	1:H:80:LEU:HB2	1.94	0.49
1:H:454:ARG:HB2	1:H:457:THR:HG21	1.93	0.49
3:C:34:PHE:C	3:C:35:VAL:CG1	2.84	0.49
3:D:134:LEU:HD22	3:D:138:GLN:OE1	2.12	0.49
3:D:172:MET:O	3:D:176:ILE:HG12	2.11	0.49
3:D:243:PRO:CB	3:D:259:PRO:HG3	2.31	0.49
1:F:263:ASN:OD1	1:F:264:PHE:N	2.45	0.49
1:F:312:ARG:CG	1:F:313:GLY:N	2.75	0.49
1:F:427:THR:O	1:F:431:ILE:HG12	2.13	0.49
1:F:441:PHE:CE1	1:F:445:GLN:HG3	2.47	0.49
1:F:490:ILE:CG1	2:G:135:LEU:HD23	2.23	0.49
1:F:498:VAL:HG22	1:F:501:LEU:HD12	1.94	0.49
3:A:34:PHE:O	3:A:35:VAL:HG12	2.11	0.49
3:B:132:LYS:HG3	3:B:133:ALA:N	2.26	0.49
3:B:236:SER:CB	3:B:237:PRO:CD	2.90	0.49
3:B:291:LEU:HB3	3:B:292:PRO:CD	2.42	0.49
3:D:7:GLN:HA	3:D:23:ASN:OD1	2.12	0.49
3:D:253:GLN:CB	3:D:267:TRP:CE3	2.95	0.49
3:D:362:CYS:O	3:D:363:ARG:C	2.55	0.49
1:F:76:GLY:HA2	1:F:80:LEU:HB2	1.94	0.49
1:F:377:THR:HG22	1:F:378:TRP:N	2.25	0.49
1:F:486:LEU:HB2	1:F:489:ALA:HB3	1.93	0.49
2:G:244:THR:H	2:G:247:VAL:HG23	1.76	0.49
3:A:46:LEU:O	3:A:49:ILE:HB	2.12	0.49
3:A:258:LEU:N	3:A:258:LEU:CD2	2.75	0.49
3:A:319:GLN:O	3:A:319:GLN:HG2	2.13	0.49
3:B:84:TYR:O	3:B:85:ALA:HB3	2.12	0.49
1:H:409:GLY:HA2	1:H:412:GLN:N	2.27	0.49
2:I:208:LEU:C	2:I:210:LEU:N	2.69	0.49
3:C:88:PRO:CA	3:C:131:PRO:HG2	2.42	0.49
3:C:91:SER:O	3:C:95:ASN:HB2	2.12	0.49
3:C:314:THR:HG22	3:C:315:GLN:N	2.27	0.49
3:D:132:LYS:HG3	3:D:133:ALA:N	2.26	0.49
3:D:164:LEU:CD1	3:D:168:LEU:HD23	2.38	0.49
3:D:235:GLY:O	3:D:236:SER:O	2.30	0.49
3:D:311:GLY:C	3:D:313:GLU:N	2.65	0.49
1:F:409:GLY:HA2	1:F:412:GLN:N	2.27	0.49
3:A:227:ASP:OD1	3:A:230:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:134:LEU:HD22	3:B:138:GLN:OE1	2.12	0.49
3:B:227:ASP:HA	3:B:361:ALA:HB2	1.93	0.49
1:H:288:SER:OG	1:H:438:PHE:CA	2.60	0.49
1:H:330:PHE:HA	1:H:333:ILE:HD11	1.94	0.49
1:H:372:LEU:HD13	1:H:447:LEU:HD12	1.94	0.49
3:C:205:VAL:HG12	3:C:207:LEU:HD23	1.95	0.49
3:C:222:TYR:OH	3:C:288:GLU:OE2	2.22	0.49
3:C:342:THR:O	3:C:343:PHE:HB2	2.11	0.49
3:D:77:VAL:CG1	3:D:78:GLY:H	2.25	0.49
3:D:227:ASP:HA	3:D:361:ALA:HB2	1.93	0.49
3:D:240:ASN:ND2	3:D:287:PRO:HG3	2.28	0.49
3:A:301:GLU:HG2	3:A:302:GLY:N	2.28	0.49
3:B:9:VAL:O	3:B:21:ASP:HA	2.12	0.49
1:H:263:ASN:OD1	1:H:264:PHE:N	2.45	0.49
1:H:358:LYS:O	1:H:358:LYS:CG	2.58	0.49
1:H:432:ALA:O	1:H:435:ALA:HB3	2.13	0.49
2:I:93:GLY:CA	2:I:223:PHE:HE1	2.21	0.49
3:C:20:LYS:O	3:C:211:ARG:NE	2.46	0.49
3:C:222:TYR:OH	3:D:312:ASN:HB3	2.12	0.49
3:D:214:GLN:CG	3:D:215:VAL:N	2.75	0.49
1:F:87:ILE:HG13	1:F:490:ILE:HG22	1.93	0.49
1:F:346:GLU:HA	1:F:349:MET:CG	2.32	0.49
1:F:501:LEU:HB3	2:G:127:ILE:CG2	2.36	0.49
2:G:172:LEU:CD2	2:G:173:HIS:N	2.73	0.49
2:G:194:LEU:CA	3:A:73:ALA:HB2	2.41	0.49
3:A:45:LEU:O	3:A:46:LEU:C	2.54	0.49
3:A:339:GLU:O	3:A:341:ALA:N	2.43	0.49
3:B:49:ILE:O	3:B:75:ARG:NH1	2.46	0.49
3:B:243:PRO:O	3:B:244:VAL:HG22	2.11	0.49
3:B:334:VAL:C	3:B:335:VAL:HG23	2.38	0.49
1:H:87:ILE:HG13	1:H:490:ILE:HG22	1.93	0.49
1:H:296:VAL:HG12	1:H:297:ALA:N	2.28	0.49
1:H:414:PHE:HA	1:H:418:THR:HG23	1.93	0.49
1:H:465:ASP:CG	1:H:473:ARG:NH2	2.68	0.49
2:I:85:LEU:CA	2:I:245:LEU:HD13	2.43	0.49
3:C:163:ASN:O	3:C:164:LEU:HG	2.13	0.49
3:C:227:ASP:OD1	3:C:230:VAL:HG23	2.13	0.49
3:C:319:GLN:O	3:C:319:GLN:HG2	2.12	0.49
3:D:271:GLU:HB2	3:D:363:ARG:HB3	1.94	0.49
3:D:290:LEU:HD22	3:D:345:ILE:HD13	1.93	0.49
3:D:299:ILE:HG22	3:D:300:LEU:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:126:LEU:HD23	2:G:126:LEU:C	2.38	0.49
3:A:219:LEU:O	3:A:220:GLU:C	2.54	0.49
3:A:328:VAL:HG12	3:A:329:TYR:H	1.78	0.49
3:A:354:LEU:C	3:A:355:PHE:CG	2.89	0.49
3:B:32:VAL:O	3:B:33:VAL:CG1	2.61	0.49
1:H:312:ARG:CG	1:H:313:GLY:N	2.75	0.49
2:I:211:SER:C	2:I:213:PRO:HD2	2.36	0.49
3:D:83:SER:C	3:D:84:TYR:CG	2.91	0.49
3:D:164:LEU:HD13	3:D:168:LEU:CD2	2.38	0.49
3:D:267:TRP:O	3:D:268:LEU:HD23	2.12	0.49
1:F:401:GLU:O	1:F:404:ALA:HB3	2.13	0.49
2:G:208:LEU:C	2:G:210:LEU:N	2.69	0.49
3:A:91:SER:O	3:A:95:ASN:HB2	2.12	0.49
3:A:222:TYR:OH	3:B:312:ASN:HB3	2.12	0.49
3:A:228:ARG:HD2	3:A:228:ARG:O	2.13	0.49
3:B:12:ALA:HA	3:B:17:VAL:HA	1.95	0.49
3:B:214:GLN:OE1	3:B:230:VAL:HG11	2.12	0.49
1:H:372:LEU:HD12	1:H:443:LEU:CG	2.43	0.49
2:I:4:VAL:HG22	2:I:5:GLN:N	2.27	0.49
3:C:328:VAL:HG12	3:C:329:TYR:H	1.78	0.49
3:D:334:VAL:C	3:D:335:VAL:HG23	2.38	0.49
1:F:376:ASN:O	1:F:380:GLY:N	2.32	0.49
2:G:85:LEU:CA	2:G:245:LEU:HD13	2.43	0.49
3:A:225:PRO:CD	3:A:353:HIS:NE2	2.64	0.49
3:B:164:LEU:CD1	3:B:168:LEU:HD23	2.38	0.49
1:H:271:GLU:HG2	1:H:272:GLY:N	2.28	0.49
3:C:301:GLU:HG2	3:C:302:GLY:N	2.28	0.49
1:F:271:GLU:HG2	1:F:272:GLY:N	2.28	0.49
2:G:255:PRO:O	2:G:259:LEU:CB	2.60	0.49
1:H:89:ILE:O	1:H:90:ALA:C	2.56	0.49
1:H:264:PHE:O	1:H:267:VAL:N	2.46	0.49
2:I:88:SER:HB3	2:I:227:ILE:CD1	2.42	0.49
3:C:10:THR:CG2	3:C:11:LYS:N	2.74	0.49
3:C:100:LEU:HD13	3:C:110:ILE:HG12	1.94	0.49
3:C:329:TYR:CE2	3:C:343:PHE:HE2	2.31	0.49
3:C:350:GLU:OE2	3:C:351:ARG:N	2.44	0.49
1:F:97:THR:O	1:F:98:ASN:CB	2.61	0.48
1:F:288:SER:OG	1:F:438:PHE:CA	2.60	0.48
1:F:465:ASP:CG	1:F:473:ARG:NH2	2.68	0.48
2:G:126:LEU:CD2	2:G:127:ILE:N	2.77	0.48
2:G:203:PHE:O	2:G:207:LEU:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:88:PRO:CA	3:A:131:PRO:HG2	2.42	0.48
3:A:125:HIS:C	3:A:127:LEU:H	2.21	0.48
3:A:189:TYR:CD2	3:A:190:VAL:O	2.66	0.48
3:A:329:TYR:CE2	3:A:343:PHE:HE2	2.31	0.48
3:B:297:ASP:O	3:B:299:ILE:N	2.45	0.48
3:B:314:THR:CG2	3:B:315:GLN:N	2.76	0.48
2:I:203:PHE:O	2:I:207:LEU:HB3	2.13	0.48
3:C:47:ARG:O	3:C:48:MET:C	2.56	0.48
3:D:84:TYR:O	3:D:85:ALA:HB3	2.12	0.48
3:D:256:VAL:O	3:D:265:GLN:HA	2.12	0.48
2:G:110:PHE:HD1	2:G:174:VAL:HG11	1.78	0.48
3:B:351:ARG:NE	3:B:368:GLU:OE1	2.38	0.48
1:H:337:LYS:NZ	2:I:253:LEU:HA	2.28	0.48
1:H:376:ASN:ND2	1:H:379:LEU:HD23	2.28	0.48
3:C:52:LEU:O	3:C:53:GLU:HB2	2.13	0.48
3:C:185:ARG:HG2	3:C:185:ARG:HH11	1.78	0.48
3:D:168:LEU:CD1	3:D:172:MET:HE3	2.44	0.48
1:F:438:PHE:CD1	1:F:439:ASN:OD1	2.64	0.48
1:F:501:LEU:CD2	2:G:130:MET:SD	3.01	0.48
2:G:185:ASP:C	2:G:188:LEU:HD13	2.37	0.48
3:A:82:GLN:O	3:A:83:SER:O	2.32	0.48
3:A:350:GLU:OE2	3:A:351:ARG:N	2.44	0.48
3:B:168:LEU:CD1	3:B:172:MET:HE3	2.44	0.48
1:H:303:ALA:HA	1:H:306:VAL:HG23	1.96	0.48
2:I:126:LEU:HD23	2:I:126:LEU:C	2.38	0.48
2:I:255:PRO:O	2:I:259:LEU:CB	2.60	0.48
3:C:198:MET:HE1	3:C:234:ILE:HG22	1.94	0.48
3:C:256:VAL:CG1	3:C:268:LEU:HD21	2.38	0.48
3:D:32:VAL:O	3:D:33:VAL:CG1	2.61	0.48
3:D:169:ARG:NH1	3:D:169:ARG:CB	2.75	0.48
3:D:193:ASP:C	3:D:195:VAL:N	2.68	0.48
1:F:303:ALA:HA	1:F:306:VAL:HG23	1.96	0.48
1:F:341:ASN:HB3	1:F:344:PHE:C	2.38	0.48
1:F:383:TYR:CE2	1:F:387:LEU:HD22	2.49	0.48
2:G:225:ALA:HA	2:G:228:THR:HG22	1.95	0.48
3:A:222:TYR:OH	3:B:312:ASN:CB	2.61	0.48
3:A:236:SER:CB	3:A:237:PRO:CD	2.88	0.48
3:B:85:ALA:O	3:B:146:ARG:NH1	2.46	0.48
3:B:218:PRO:O	3:B:221:LEU:HB2	2.13	0.48
3:B:240:ASN:ND2	3:B:287:PRO:HG3	2.28	0.48
1:H:97:THR:O	1:H:98:ASN:CB	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:427:THR:O	1:H:431:ILE:HG12	2.13	0.48
2:I:110:PHE:HD1	2:I:174:VAL:HG11	1.78	0.48
2:I:129:GLN:C	2:I:131:PHE:N	2.70	0.48
3:C:66:ARG:O	3:C:67:MET:CG	2.50	0.48
3:C:222:TYR:OH	3:D:312:ASN:CB	2.61	0.48
3:D:13:TRP:HH2	3:D:53:GLU:CD	2.21	0.48
1:F:376:ASN:ND2	1:F:379:LEU:HD23	2.28	0.48
1:F:432:ALA:O	1:F:435:ALA:HB3	2.13	0.48
3:A:73:ALA:HB3	3:A:74:GLU:OE2	2.14	0.48
3:A:100:LEU:HD13	3:A:110:ILE:HG12	1.94	0.48
3:A:256:VAL:HG22	3:A:266:VAL:O	2.13	0.48
3:A:256:VAL:CG1	3:A:268:LEU:HD21	2.38	0.48
3:B:13:TRP:HH2	3:B:53:GLU:CD	2.21	0.48
3:B:156:LEU:HD22	3:B:188:ILE:HB	1.95	0.48
1:H:401:GLU:O	1:H:404:ALA:HB3	2.13	0.48
1:H:448:THR:C	1:H:450:GLY:N	2.71	0.48
1:H:501:LEU:CD2	2:I:130:MET:SD	3.01	0.48
2:I:92:ALA:HA	2:I:226:ALA:HB1	1.96	0.48
2:I:245:LEU:HG	2:I:249:MET:CE	2.33	0.48
2:I:250:GLN:O	2:I:253:LEU:HD13	2.13	0.48
3:D:61:PHE:HB3	3:D:65:LYS:O	2.13	0.48
3:D:198:MET:HE2	3:D:234:ILE:HG22	1.94	0.48
3:D:255:GLN:HE21	3:D:267:TRP:NE1	2.10	0.48
3:D:297:ASP:O	3:D:299:ILE:N	2.45	0.48
3:D:314:THR:CG2	3:D:315:GLN:N	2.76	0.48
1:F:88:ALA:C	1:F:90:ALA:N	2.70	0.48
1:F:89:ILE:O	1:F:90:ALA:C	2.56	0.48
3:A:20:LYS:O	3:A:211:ARG:NE	2.46	0.48
3:A:205:VAL:HG12	3:A:207:LEU:HD23	1.95	0.48
3:A:252:ASP:O	3:A:270:VAL:O	2.30	0.48
3:A:342:THR:O	3:A:343:PHE:HB2	2.11	0.48
3:B:11:LYS:HG3	3:B:12:ALA:N	2.27	0.48
3:B:61:PHE:HB3	3:B:65:LYS:O	2.13	0.48
3:B:77:VAL:CG1	3:B:78:GLY:H	2.25	0.48
1:H:88:ALA:C	1:H:90:ALA:N	2.70	0.48
1:H:471:THR:HG21	2:I:135:LEU:HD22	1.96	0.48
3:C:152:PRO:HD2	3:C:155:PHE:CZ	2.49	0.48
3:C:300:LEU:HD12	3:C:347:LEU:HD23	1.94	0.48
3:D:12:ALA:HA	3:D:17:VAL:HA	1.95	0.48
1:F:330:PHE:HA	1:F:333:ILE:HD11	1.94	0.48
3:A:40:CYS:CB	3:A:42:LYS:HZ3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:185:ARG:HG2	3:A:185:ARG:HH11	1.78	0.48
3:A:191:THR:OG1	3:A:192:HIS:N	2.46	0.48
3:B:83:SER:C	3:B:84:TYR:CG	2.91	0.48
3:B:89:HIS:CG	3:B:90:LEU:H	2.32	0.48
3:B:156:LEU:O	3:B:157:LEU:HD12	2.12	0.48
3:B:240:ASN:O	3:B:241:PHE:CD1	2.67	0.48
3:B:255:GLN:O	3:B:256:VAL:CG1	2.62	0.48
3:B:267:TRP:O	3:B:268:LEU:HD23	2.12	0.48
3:C:125:HIS:CE1	3:C:126:LEU:HG	2.49	0.48
3:C:174:ILE:O	3:C:178:ARG:HG3	2.14	0.48
3:D:293:SER:HA	3:D:345:ILE:HA	1.95	0.48
1:F:293:PHE:C	1:F:293:PHE:HD2	2.22	0.48
1:F:296:VAL:O	1:F:297:ALA:C	2.57	0.48
1:F:372:LEU:HD13	1:F:447:LEU:HD12	1.94	0.48
1:F:383:TYR:CD2	1:F:383:TYR:C	2.92	0.48
2:G:250:GLN:O	2:G:253:LEU:HD13	2.13	0.48
3:A:123:LEU:HD21	3:A:142:VAL:HG22	1.96	0.48
3:A:174:ILE:O	3:A:178:ARG:HG3	2.14	0.48
3:B:55:ILE:HG21	3:B:68:ASN:OD1	2.12	0.48
3:B:168:LEU:O	3:B:169:ARG:C	2.56	0.48
1:H:352:SER:HB3	1:H:358:LYS:CB	2.43	0.48
2:I:37:ILE:HG13	2:I:264:ALA:CB	2.44	0.48
3:C:9:VAL:HG12	3:C:10:THR:N	2.29	0.48
3:C:40:CYS:CB	3:C:42:LYS:NZ	2.76	0.48
3:C:82:GLN:O	3:C:83:SER:O	2.32	0.48
3:C:122:GLN:O	3:C:123:LEU:CD1	2.61	0.48
3:C:246:VAL:O	3:C:246:VAL:HG12	2.14	0.48
3:D:61:PHE:N	3:D:61:PHE:CD1	2.82	0.48
3:D:85:ALA:O	3:D:146:ARG:NH1	2.46	0.48
3:D:178:ARG:O	3:D:182:ARG:HB2	2.14	0.48
1:F:41:LEU:HD12	1:F:89:ILE:CD1	2.38	0.48
3:B:291:LEU:HD23	3:B:292:PRO:HD3	1.96	0.48
3:B:293:SER:HA	3:B:345:ILE:HA	1.95	0.48
1:H:346:GLU:O	1:H:349:MET:HB2	2.14	0.48
1:H:383:TYR:CD2	1:H:383:TYR:C	2.92	0.48
1:H:383:TYR:CE2	1:H:387:LEU:HD22	2.49	0.48
2:I:126:LEU:CD2	2:I:127:ILE:N	2.77	0.48
3:C:28:GLU:CG	3:C:29:GLY:N	2.77	0.48
3:C:132:LYS:O	3:C:134:LEU:N	2.45	0.48
3:C:191:THR:OG1	3:C:192:HIS:N	2.46	0.48
3:C:228:ARG:HD2	3:C:228:ARG:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:89:HIS:CG	3:D:90:LEU:H	2.32	0.48
3:D:125:HIS:CD2	3:D:126:LEU:HG	2.49	0.48
3:D:240:ASN:O	3:D:241:PHE:CD1	2.67	0.48
3:D:255:GLN:O	3:D:256:VAL:CG1	2.62	0.48
1:F:448:THR:C	1:F:450:GLY:N	2.71	0.48
2:G:37:ILE:HG13	2:G:264:ALA:CB	2.44	0.48
2:G:212:VAL:HG22	2:G:215:LEU:CD1	2.42	0.48
3:A:85:ALA:C	3:A:146:ARG:HH22	2.21	0.48
3:A:152:PRO:HG2	3:A:153:SER:H	1.79	0.48
3:A:152:PRO:HD2	3:A:155:PHE:CZ	2.49	0.48
3:A:201:ALA:HB1	3:A:203:LYS:O	2.14	0.48
3:A:334:VAL:CG1	3:A:335:VAL:N	2.77	0.48
3:B:232:GLY:HA3	3:B:238:LYS:HE2	1.96	0.48
3:B:349:PRO:HG2	3:B:350:GLU:H	1.79	0.48
1:H:87:ILE:H	1:H:87:ILE:HD12	1.78	0.48
1:H:342:GLN:HE22	1:H:363:SER:H	1.62	0.48
2:I:212:VAL:N	2:I:213:PRO:CD	2.77	0.48
2:I:225:ALA:HA	2:I:228:THR:HG22	1.95	0.48
3:C:46:LEU:O	3:C:49:ILE:HB	2.12	0.48
3:C:125:HIS:C	3:C:127:LEU:H	2.21	0.48
3:C:189:TYR:CD2	3:C:190:VAL:O	2.66	0.48
3:C:256:VAL:HG22	3:C:266:VAL:O	2.13	0.48
3:D:218:PRO:O	3:D:221:LEU:HB2	2.13	0.48
3:D:298:VAL:HB	3:D:347:LEU:N	2.23	0.48
3:D:350:GLU:CB	3:D:366:HIS:CE1	2.95	0.48
1:F:288:SER:OG	1:F:438:PHE:HA	2.14	0.47
1:F:296:VAL:CG2	1:F:384:MET:SD	3.02	0.47
1:F:333:ILE:HA	1:F:336:PHE:CD1	2.47	0.47
3:A:122:GLN:O	3:A:123:LEU:CD1	2.61	0.47
3:A:164:LEU:HD13	3:A:168:LEU:CG	2.43	0.47
3:A:288:GLU:H	3:A:288:GLU:CD	2.21	0.47
3:B:12:ALA:C	3:B:14:GLY:N	2.72	0.47
3:B:291:LEU:HB3	3:B:292:PRO:HD2	1.96	0.47
1:H:341:ASN:HB3	1:H:344:PHE:C	2.38	0.47
1:H:503:ILE:CG2	1:H:507:LYS:NZ	2.77	0.47
3:C:201:ALA:HB1	3:C:203:LYS:O	2.14	0.47
3:D:271:GLU:O	3:D:272:SER:HB3	2.14	0.47
3:D:306:VAL:CG1	3:D:307:VAL:H	2.25	0.47
3:D:349:PRO:HG2	3:D:350:GLU:H	1.79	0.47
1:F:471:THR:HG21	2:G:135:LEU:HD22	1.95	0.47
3:A:110:ILE:O	3:A:114:VAL:CG2	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:125:HIS:CE1	3:A:126:LEU:HG	2.49	0.47
3:A:361:ALA:O	3:A:363:ARG:N	2.47	0.47
3:B:287:PRO:CB	3:B:330:ARG:H	2.27	0.47
1:H:288:SER:OG	1:H:438:PHE:HA	2.14	0.47
1:H:293:PHE:C	1:H:293:PHE:HD2	2.22	0.47
1:H:296:VAL:O	1:H:297:ALA:C	2.57	0.47
3:C:357:GLU:C	3:C:359:GLY:N	2.68	0.47
3:D:291:LEU:HD23	3:D:292:PRO:HD3	1.96	0.47
1:F:342:GLN:HE22	1:F:363:SER:H	1.62	0.47
1:F:372:LEU:HD12	1:F:443:LEU:CG	2.43	0.47
2:G:88:SER:HG	2:G:245:LEU:H	1.60	0.47
2:G:229:GLU:CD	2:G:230:VAL:N	2.64	0.47
3:A:59:ASP:OD1	3:A:66:ARG:NH2	2.47	0.47
3:A:163:ASN:O	3:A:164:LEU:HG	2.13	0.47
3:B:40:CYS:CB	3:B:42:LYS:HG3	2.45	0.47
3:B:90:LEU:O	3:B:131:PRO:CG	2.62	0.47
3:B:125:HIS:CD2	3:B:126:LEU:HG	2.49	0.47
1:H:96:SER:CB	1:H:481:GLY:HA3	2.44	0.47
1:H:333:ILE:HA	1:H:336:PHE:CD1	2.47	0.47
1:H:385:MET:HE3	1:H:389:MET:HB2	1.96	0.47
3:C:97:SER:HA	3:C:100:LEU:HD11	1.96	0.47
3:D:12:ALA:C	3:D:14:GLY:N	2.72	0.47
3:D:277:VAL:C	3:D:279:ALA:H	2.22	0.47
3:D:291:LEU:HD12	3:D:348:PRO:HG3	1.97	0.47
1:F:44:ILE:O	1:F:47:LEU:HB3	2.14	0.47
2:G:137:LEU:HA	2:G:140:LEU:HB2	1.96	0.47
3:A:52:LEU:O	3:A:53:GLU:HB2	2.13	0.47
3:A:180:HIS:O	3:A:184:GLY:HA2	2.14	0.47
3:B:45:LEU:HA	3:B:48:MET:HE3	1.96	0.47
3:B:178:ARG:O	3:B:182:ARG:HB2	2.14	0.47
3:B:198:MET:HE2	3:B:234:ILE:HG22	1.94	0.47
3:B:306:VAL:CG1	3:B:307:VAL:H	2.25	0.47
1:H:438:PHE:CD1	1:H:439:ASN:OD1	2.64	0.47
1:H:483:ASP:O	1:H:485:GLY:N	2.44	0.47
2:I:4:VAL:HG22	2:I:5:GLN:H	1.80	0.47
3:C:85:ALA:C	3:C:146:ARG:HH22	2.21	0.47
3:C:310:LEU:O	3:C:310:LEU:CD2	2.63	0.47
1:F:87:ILE:HD12	1:F:87:ILE:H	1.78	0.47
3:A:10:THR:CG2	3:A:11:LYS:N	2.74	0.47
3:B:271:GLU:O	3:B:272:SER:HB3	2.14	0.47
3:B:271:GLU:HB2	3:B:363:ARG:HB3	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:312:ARG:HD2	1:H:313:GLY:N	2.23	0.47
2:I:33:MET:O	2:I:36:ALA:N	2.47	0.47
3:C:73:ALA:HB3	3:C:74:GLU:OE2	2.14	0.47
3:D:11:LYS:HG3	3:D:12:ALA:N	2.28	0.47
3:D:156:LEU:O	3:D:157:LEU:HD12	2.13	0.47
3:D:168:LEU:O	3:D:169:ARG:C	2.56	0.47
1:F:307:GLN:C	1:F:309:GLU:N	2.71	0.47
1:F:352:SER:HB3	1:F:358:LYS:CB	2.43	0.47
2:G:212:VAL:N	2:G:213:PRO:CD	2.77	0.47
3:A:9:VAL:HG12	3:A:10:THR:N	2.29	0.47
3:A:80:VAL:O	3:A:80:VAL:HG13	2.15	0.47
3:A:310:LEU:O	3:A:310:LEU:CD2	2.62	0.47
3:B:123:LEU:CD1	3:B:141:ARG:NH2	2.77	0.47
3:C:8:ASN:H	3:C:23:ASN:ND2	2.13	0.47
3:C:12:ALA:C	3:C:14:GLY:N	2.73	0.47
3:C:124:ALA:O	3:C:127:LEU:HD22	2.15	0.47
3:D:28:GLU:CG	3:D:29:GLY:N	2.78	0.47
3:D:192:HIS:O	3:D:194:GLN:N	2.48	0.47
1:F:337:LYS:NZ	2:G:253:LEU:HA	2.29	0.47
1:F:498:VAL:HA	1:F:501:LEU:CD1	2.40	0.47
2:G:33:MET:O	2:G:36:ALA:N	2.47	0.47
2:G:129:GLN:C	2:G:131:PHE:N	2.70	0.47
3:A:6:LEU:HB3	3:A:9:VAL:HG23	1.97	0.47
3:A:40:CYS:CB	3:A:42:LYS:NZ	2.76	0.47
3:A:47:ARG:O	3:A:48:MET:C	2.56	0.47
3:A:214:GLN:HB2	3:A:226:ALA:CB	2.45	0.47
3:A:246:VAL:O	3:A:246:VAL:HG12	2.14	0.47
3:A:287:PRO:CG	3:A:328:VAL:HB	2.45	0.47
3:B:7:GLN:NE2	3:B:61:PHE:CE1	2.83	0.47
3:B:32:VAL:C	3:B:33:VAL:CG1	2.88	0.47
3:B:79:MET:HA	3:B:147:THR:HG21	1.97	0.47
3:B:190:VAL:HG12	3:B:191:THR:N	2.29	0.47
3:B:276:GLN:NE2	3:B:277:VAL:H	2.13	0.47
3:B:314:THR:CG2	3:B:315:GLN:H	2.27	0.47
1:H:288:SER:HB2	1:H:434:PHE:CE2	2.49	0.47
2:I:137:LEU:HA	2:I:140:LEU:HB2	1.96	0.47
2:I:208:LEU:O	2:I:210:LEU:N	2.47	0.47
3:C:40:CYS:CB	3:C:42:LYS:HZ3	2.28	0.47
3:C:55:ILE:HG12	3:C:68:ASN:CG	2.39	0.47
3:C:59:ASP:OD1	3:C:66:ARG:NH2	2.47	0.47
3:C:152:PRO:HG2	3:C:153:SER:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:287:PRO:CG	3:C:328:VAL:HB	2.45	0.47
3:C:339:GLU:O	3:C:341:ALA:N	2.43	0.47
3:C:361:ALA:O	3:C:363:ARG:N	2.47	0.47
3:D:37:PRO:O	3:D:40:CYS:HB3	2.15	0.47
3:D:123:LEU:CD1	3:D:141:ARG:NH2	2.77	0.47
3:D:276:GLN:NE2	3:D:277:VAL:H	2.13	0.47
3:D:291:LEU:HB3	3:D:292:PRO:HD2	1.96	0.47
1:F:296:VAL:HG12	1:F:297:ALA:N	2.28	0.47
1:F:503:ILE:CG2	1:F:507:LYS:NZ	2.77	0.47
2:G:4:VAL:HG22	2:G:5:GLN:H	1.80	0.47
3:A:12:ALA:C	3:A:14:GLY:N	2.72	0.47
3:A:55:ILE:HG12	3:A:68:ASN:CG	2.39	0.47
3:A:97:SER:HA	3:A:100:LEU:HD11	1.96	0.47
3:A:100:LEU:HD21	3:A:149:VAL:HG12	1.97	0.47
3:A:300:LEU:HD12	3:A:347:LEU:HD23	1.94	0.47
3:B:362:CYS:O	3:B:363:ARG:C	2.55	0.47
1:H:327:VAL:N	2:I:274:ILE:HG21	2.29	0.47
1:H:414:PHE:HE1	1:H:419:LEU:HD12	1.78	0.47
3:C:8:ASN:CG	3:C:23:ASN:HD21	2.22	0.47
3:C:42:LYS:HD2	3:C:190:VAL:HG13	1.97	0.47
3:C:80:VAL:HG13	3:C:80:VAL:O	2.15	0.47
3:C:123:LEU:HD21	3:C:142:VAL:HG22	1.96	0.47
3:C:356:ARG:HG3	3:C:356:ARG:NH1	2.30	0.47
3:D:79:MET:HA	3:D:147:THR:HG21	1.97	0.47
3:D:124:ALA:O	3:D:127:LEU:HD22	2.15	0.47
1:F:96:SER:CB	1:F:481:GLY:HA3	2.44	0.47
1:F:264:PHE:O	1:F:267:VAL:N	2.46	0.47
2:G:208:LEU:O	2:G:210:LEU:N	2.47	0.47
2:G:257:ASN:C	2:G:258:TYR:CD2	2.93	0.47
3:A:20:LYS:HB3	3:A:211:ARG:HD3	1.97	0.47
3:B:28:GLU:CG	3:B:29:GLY:N	2.78	0.47
1:H:271:GLU:N	1:H:271:GLU:CD	2.73	0.47
2:I:148:GLY:CA	2:I:155:GLY:CA	2.89	0.47
3:C:101:LYS:O	3:C:103:ALA:N	2.48	0.47
3:D:156:LEU:HD22	3:D:188:ILE:HB	1.95	0.47
3:D:232:GLY:HA3	3:D:238:LYS:HE2	1.96	0.47
3:A:28:GLU:CG	3:A:29:GLY:N	2.77	0.47
3:A:75:ARG:HB3	3:A:77:VAL:HG23	1.97	0.47
3:A:80:VAL:HG11	3:A:160:PRO:HG3	1.97	0.47
3:A:180:HIS:O	3:A:184:GLY:CA	2.63	0.47
3:B:61:PHE:N	3:B:61:PHE:CD1	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:80:VAL:HG13	3:B:80:VAL:O	2.15	0.47
3:B:89:HIS:CG	3:B:90:LEU:N	2.83	0.47
3:B:91:SER:O	3:B:95:ASN:HB2	2.14	0.47
3:B:124:ALA:O	3:B:127:LEU:HD22	2.15	0.47
1:H:326:ALA:O	2:I:274:ILE:HG23	2.15	0.47
1:H:372:LEU:CD1	1:H:447:LEU:HD12	2.45	0.47
1:H:490:ILE:CG1	2:I:135:LEU:HD23	2.23	0.47
3:C:164:LEU:HD13	3:C:168:LEU:CG	2.43	0.47
3:D:32:VAL:C	3:D:33:VAL:CG1	2.88	0.47
3:D:45:LEU:HA	3:D:48:MET:HE3	1.96	0.47
3:D:89:HIS:CG	3:D:90:LEU:N	2.83	0.47
3:D:169:ARG:HB2	3:D:169:ARG:HH11	1.80	0.47
3:D:289:HIS:CE1	3:D:351:ARG:NH1	2.83	0.47
1:F:348:ASN:O	1:F:351:LEU:HB2	2.16	0.46
1:F:358:LYS:O	1:F:358:LYS:CG	2.58	0.46
1:F:414:PHE:HE1	1:F:419:LEU:HD12	1.78	0.46
2:G:208:LEU:O	2:G:211:SER:N	2.48	0.46
3:A:42:LYS:HD2	3:A:190:VAL:HG13	1.97	0.46
3:A:366:HIS:O	3:A:366:HIS:CG	2.69	0.46
3:B:273:ARG:HH11	3:B:273:ARG:HG2	1.80	0.46
3:B:354:LEU:CD1	3:B:355:PHE:H	2.28	0.46
1:H:87:ILE:HD12	1:H:87:ILE:N	2.30	0.46
1:H:296:VAL:CG2	1:H:384:MET:SD	3.02	0.46
2:I:32:LEU:O	2:I:35:VAL:CB	2.60	0.46
2:I:35:VAL:C	2:I:37:ILE:N	2.56	0.46
2:I:79:PHE:HB2	2:I:252:TYR:OH	2.15	0.46
2:I:257:ASN:C	2:I:258:TYR:CD2	2.93	0.46
3:C:20:LYS:HB3	3:C:211:ARG:HD3	1.97	0.46
3:C:222:TYR:O	3:C:286:ARG:NH2	2.44	0.46
3:C:236:SER:CB	3:C:237:PRO:CD	2.88	0.46
3:C:239:MET:SD	3:C:241:PHE:CE1	3.08	0.46
3:D:85:ALA:C	3:D:86:LEU:HD23	2.40	0.46
3:D:168:LEU:HD11	3:D:172:MET:HE3	1.97	0.46
3:D:317:HIS:O	3:D:318:ILE:CG1	2.62	0.46
1:F:372:LEU:CD1	1:F:447:LEU:HD12	2.45	0.46
1:F:454:ARG:C	1:F:455:LEU:HG	2.40	0.46
2:G:79:PHE:HB2	2:G:252:TYR:OH	2.15	0.46
3:A:101:LYS:O	3:A:103:ALA:N	2.47	0.46
3:A:124:ALA:O	3:A:127:LEU:HD22	2.15	0.46
3:A:256:VAL:O	3:A:265:GLN:HA	2.14	0.46
3:B:98:PHE:CE1	3:B:102:LEU:HD11	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:374:ILE:CD1	1:H:375:VAL:N	2.76	0.46
1:H:501:LEU:HB3	2:I:127:ILE:CG2	2.37	0.46
2:I:255:PRO:O	2:I:259:LEU:CG	2.63	0.46
3:C:80:VAL:HG11	3:C:160:PRO:HG3	1.97	0.46
3:C:214:GLN:HB2	3:C:226:ALA:CB	2.45	0.46
3:D:40:CYS:CB	3:D:42:LYS:HG3	2.45	0.46
3:D:191:THR:O	3:D:192:HIS:CG	2.68	0.46
1:F:288:SER:HB2	1:F:434:PHE:CE2	2.49	0.46
1:F:346:GLU:O	1:F:349:MET:HB2	2.14	0.46
3:A:8:ASN:H	3:A:23:ASN:ND2	2.13	0.46
3:B:85:ALA:C	3:B:86:LEU:HD23	2.40	0.46
3:B:166:ALA:O	3:B:170:VAL:HG23	2.15	0.46
3:B:267:TRP:C	3:B:268:LEU:HD23	2.40	0.46
3:B:277:VAL:C	3:B:279:ALA:H	2.22	0.46
3:B:291:LEU:HD12	3:B:348:PRO:HG3	1.96	0.46
3:B:313:GLU:OE1	3:B:330:ARG:NH2	2.47	0.46
1:H:348:ASN:O	1:H:351:LEU:HB2	2.16	0.46
3:C:180:HIS:O	3:C:184:GLY:CA	2.63	0.46
3:C:256:VAL:O	3:C:265:GLN:HA	2.14	0.46
3:D:12:ALA:HA	3:D:16:VAL:O	2.15	0.46
3:D:96:MET:C	3:D:98:PHE:N	2.67	0.46
3:D:98:PHE:CE1	3:D:102:LEU:HD11	2.50	0.46
3:D:155:PHE:HD1	3:D:155:PHE:H	1.64	0.46
1:F:465:ASP:OD2	1:F:473:ARG:NH2	2.48	0.46
1:F:473:ARG:C	1:F:475:ALA:N	2.73	0.46
2:G:93:GLY:CA	2:G:223:PHE:HE1	2.21	0.46
2:G:255:PRO:O	2:G:259:LEU:CG	2.63	0.46
3:A:40:CYS:C	3:A:42:LYS:H	2.23	0.46
3:B:157:LEU:HB3	3:B:160:PRO:CD	2.46	0.46
3:B:243:PRO:C	3:B:244:VAL:CG2	2.89	0.46
1:H:368:ALA:O	1:H:371:MET:CB	2.64	0.46
1:H:376:ASN:O	1:H:380:GLY:N	2.32	0.46
3:C:52:LEU:HD23	3:C:72:PRO:HG2	1.97	0.46
3:C:254:VAL:HG21	3:C:270:VAL:HG12	1.98	0.46
3:D:7:GLN:NE2	3:D:61:PHE:CE1	2.83	0.46
3:D:83:SER:O	3:D:84:TYR:CD1	2.68	0.46
3:D:90:LEU:O	3:D:131:PRO:CG	2.62	0.46
1:F:271:GLU:CD	1:F:271:GLU:N	2.73	0.46
1:F:304:CYS:SG	1:F:305:LEU:HD23	2.56	0.46
3:A:239:MET:SD	3:A:241:PHE:CE1	3.08	0.46
3:A:368:GLU:HG2	3:A:369:PRO:CD	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:118:ALA:HB1	3:B:123:LEU:O	2.16	0.46
3:B:243:PRO:CB	3:B:259:PRO:HG3	2.31	0.46
3:B:289:HIS:CE1	3:B:351:ARG:NH1	2.83	0.46
3:C:100:LEU:HD21	3:C:149:VAL:HG12	1.97	0.46
3:C:320:ILE:HG23	3:C:321:PRO:HD2	1.97	0.46
3:D:11:LYS:CG	3:D:12:ALA:N	2.79	0.46
3:D:49:ILE:O	3:D:75:ARG:NH1	2.46	0.46
3:D:77:VAL:C	3:D:152:PRO:HB2	2.40	0.46
3:D:91:SER:O	3:D:95:ASN:HB2	2.14	0.46
3:D:157:LEU:HB3	3:D:160:PRO:CD	2.46	0.46
3:D:273:ARG:HG2	3:D:273:ARG:HH11	1.80	0.46
3:D:314:THR:CG2	3:D:315:GLN:H	2.27	0.46
3:D:315:GLN:HG2	3:D:330:ARG:HG2	1.98	0.46
3:D:323:ILE:HG23	3:D:325:GLN:O	2.15	0.46
1:F:330:PHE:O	1:F:333:ILE:CD1	2.63	0.46
1:F:497:LEU:HD23	1:F:501:LEU:HG	1.97	0.46
2:G:245:LEU:HG	2:G:249:MET:CE	2.33	0.46
2:G:252:TYR:N	2:G:252:TYR:HD1	2.13	0.46
3:A:8:ASN:CG	3:A:23:ASN:HD21	2.22	0.46
3:A:356:ARG:HG3	3:A:356:ARG:NH1	2.30	0.46
3:B:191:THR:O	3:B:192:HIS:CG	2.68	0.46
3:B:366:HIS:O	3:B:368:GLU:N	2.48	0.46
1:H:44:ILE:O	1:H:47:LEU:HB3	2.14	0.46
1:H:308:TRP:HD1	1:H:310:ALA:HB3	1.81	0.46
1:H:471:THR:HG22	2:I:135:LEU:CD1	2.46	0.46
3:C:6:LEU:HB3	3:C:9:VAL:CG2	2.46	0.46
3:C:180:HIS:O	3:C:184:GLY:HA2	2.14	0.46
3:D:206:VAL:HG21	3:D:230:VAL:HG13	1.96	0.46
3:D:294:ASP:OD2	3:D:295:ILE:HG13	2.15	0.46
1:F:87:ILE:HD12	1:F:87:ILE:N	2.30	0.46
1:F:327:VAL:N	2:G:274:ILE:HG21	2.29	0.46
1:F:471:THR:HG22	2:G:135:LEU:CD1	2.46	0.46
3:A:24:LEU:HD13	3:A:26:ILE:HD11	1.97	0.46
3:A:155:PHE:HB2	3:A:187:MET:HG2	1.98	0.46
3:A:161:LEU:HD12	3:A:189:TYR:OH	2.16	0.46
3:B:349:PRO:O	3:B:352:CYS:CB	2.55	0.46
1:H:304:CYS:SG	1:H:305:LEU:HD23	2.56	0.46
2:I:114:ARG:O	2:I:115:PHE:HB3	2.16	0.46
3:C:24:LEU:HD13	3:C:26:ILE:HD11	1.97	0.46
3:C:97:SER:O	3:C:100:LEU:HD12	2.16	0.46
3:C:272:SER:O	3:C:275:VAL:HB	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:96:MET:CE	3:D:114:VAL:HG13	2.46	0.46
3:D:155:PHE:O	3:D:157:LEU:HD12	2.15	0.46
3:D:190:VAL:HG12	3:D:191:THR:N	2.29	0.46
3:D:267:TRP:C	3:D:268:LEU:HD23	2.40	0.46
1:F:292:VAL:HG21	1:F:434:PHE:HB2	1.97	0.46
1:F:368:ALA:O	1:F:371:MET:CB	2.64	0.46
1:F:497:LEU:HD13	2:G:132:PRO:CD	2.31	0.46
2:G:148:GLY:CA	2:G:155:GLY:CA	2.89	0.46
3:A:10:THR:C	3:A:56:THR:HB	2.40	0.46
3:A:272:SER:O	3:A:275:VAL:HB	2.16	0.46
3:B:37:PRO:O	3:B:40:CYS:HB3	2.15	0.46
3:B:266:VAL:HG22	3:B:267:TRP:N	2.28	0.46
1:H:267:VAL:HG13	1:H:488:ALA:CA	2.42	0.46
1:H:292:VAL:HG21	1:H:434:PHE:HB2	1.97	0.46
1:H:437:ASN:O	1:H:440:ASN:HB2	2.16	0.46
2:I:159:HIS:NE2	2:I:242:SER:HB2	2.31	0.46
2:I:172:LEU:CD2	2:I:173:HIS:N	2.73	0.46
3:C:266:VAL:O	3:C:268:LEU:HD23	2.16	0.46
3:C:368:GLU:HG2	3:C:369:PRO:CD	2.32	0.46
3:D:306:VAL:CG1	3:D:307:VAL:N	2.78	0.46
1:F:267:VAL:HG13	1:F:488:ALA:CA	2.42	0.46
1:F:308:TRP:CD1	1:F:310:ALA:HB3	2.51	0.46
1:F:425:PRO:O	1:F:428:PRO:HD2	2.16	0.46
3:A:6:LEU:HB3	3:A:9:VAL:CG2	2.46	0.46
3:A:250:ALA:O	3:A:272:SER:OG	2.25	0.46
3:B:155:PHE:O	3:B:157:LEU:HD12	2.15	0.46
3:B:192:HIS:O	3:B:194:GLN:N	2.48	0.46
3:B:206:VAL:HG21	3:B:230:VAL:HG13	1.96	0.46
1:H:454:ARG:C	1:H:455:LEU:HG	2.40	0.46
2:I:260:TRP:O	2:I:263:PHE:HB3	2.16	0.46
3:C:10:THR:C	3:C:56:THR:HB	2.40	0.46
3:C:301:GLU:CA	3:C:344:ALA:HB2	2.35	0.46
3:C:303:GLU:C	3:C:318:ILE:HG23	2.41	0.46
3:C:366:HIS:O	3:C:366:HIS:CG	2.69	0.46
3:D:304:VAL:HG13	3:D:316:ILE:CG2	2.46	0.46
1:F:88:ALA:O	1:F:90:ALA:N	2.49	0.46
1:F:385:MET:HE3	1:F:389:MET:HB2	1.96	0.46
2:G:31:LEU:H	2:G:31:LEU:CD2	2.01	0.46
3:A:6:LEU:CD2	3:A:9:VAL:HG21	2.45	0.46
3:A:120:VAL:CG2	3:A:121:LEU:N	2.79	0.46
3:A:303:GLU:C	3:A:318:ILE:HG23	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:320:ILE:HG23	3:A:321:PRO:HD2	1.97	0.46
3:B:83:SER:O	3:B:84:TYR:CD1	2.68	0.46
3:B:83:SER:C	3:B:84:TYR:CD2	2.94	0.46
3:B:214:GLN:CG	3:B:215:VAL:H	2.29	0.46
3:B:294:ASP:OD2	3:B:295:ILE:HG13	2.15	0.46
1:H:88:ALA:O	1:H:90:ALA:N	2.49	0.46
1:H:317:TYR:HE2	2:I:20:LEU:CG	2.22	0.46
1:H:330:PHE:CG	1:H:331:ILE:N	2.83	0.46
2:I:18:LEU:CD2	2:I:19:LEU:N	2.77	0.46
2:I:251:GLN:O	2:I:253:LEU:N	2.40	0.46
3:C:75:ARG:HB3	3:C:77:VAL:HG23	1.97	0.46
3:C:354:LEU:C	3:C:355:PHE:CD1	2.94	0.46
1:F:324:PRO:HA	1:F:378:TRP:CH2	2.51	0.45
1:F:326:ALA:O	2:G:274:ILE:HG23	2.15	0.45
2:G:114:ARG:O	2:G:115:PHE:HB3	2.16	0.45
3:A:97:SER:O	3:A:100:LEU:HD12	2.16	0.45
3:A:106:LYS:O	3:A:110:ILE:HG13	2.16	0.45
3:A:352:CYS:O	3:A:364:ARG:HD2	2.16	0.45
3:A:368:GLU:CB	3:A:369:PRO:HD2	2.46	0.45
3:B:11:LYS:CG	3:B:12:ALA:N	2.79	0.45
3:B:342:THR:OG1	3:B:343:PHE:N	2.50	0.45
2:I:208:LEU:O	2:I:211:SER:N	2.48	0.45
3:C:120:VAL:CG2	3:C:121:LEU:N	2.79	0.45
3:C:161:LEU:HD12	3:C:189:TYR:OH	2.16	0.45
3:C:199:THR:OG1	3:C:200:LEU:N	2.49	0.45
3:C:214:GLN:NE2	3:C:226:ALA:HB2	2.31	0.45
3:D:96:MET:HG3	3:D:142:VAL:HG12	1.98	0.45
3:D:155:PHE:HB2	3:D:187:MET:HG2	1.98	0.45
3:D:244:VAL:O	3:D:245:LYS:HG2	2.16	0.45
3:D:366:HIS:O	3:D:368:GLU:N	2.48	0.45
1:F:280:ILE:HG13	1:F:467:LEU:HD22	1.98	0.45
2:G:159:HIS:NE2	2:G:242:SER:HB2	2.31	0.45
3:A:169:ARG:HB2	3:A:169:ARG:CZ	2.46	0.45
3:B:12:ALA:HA	3:B:16:VAL:O	2.15	0.45
3:B:309:GLN:O	3:B:311:GLY:N	2.39	0.45
3:B:323:ILE:HG23	3:B:325:GLN:O	2.15	0.45
3:B:355:PHE:N	3:B:355:PHE:CD1	2.85	0.45
2:I:194:LEU:CA	3:C:73:ALA:HB2	2.41	0.45
3:C:189:TYR:HD2	3:C:190:VAL:O	1.99	0.45
3:C:302:GLY:HA2	3:C:321:PRO:HD3	1.97	0.45
3:D:24:LEU:CD1	3:D:26:ILE:HD11	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:42:LYS:CE	3:D:190:VAL:HG13	2.47	0.45
3:D:51:GLY:O	3:D:53:GLU:N	2.39	0.45
3:D:62:ILE:CD1	3:D:75:ARG:HB3	2.47	0.45
1:F:383:TYR:C	1:F:383:TYR:HD2	2.24	0.45
1:F:437:ASN:O	1:F:440:ASN:HB2	2.16	0.45
3:A:49:ILE:O	3:A:75:ARG:NH1	2.49	0.45
3:A:224:TYR:HE2	3:A:371:VAL:CG1	2.30	0.45
3:A:266:VAL:O	3:A:268:LEU:HD23	2.16	0.45
3:B:77:VAL:C	3:B:152:PRO:HB2	2.40	0.45
3:B:315:GLN:HG2	3:B:330:ARG:HG2	1.98	0.45
1:H:76:GLY:O	1:H:80:LEU:HB2	2.17	0.45
1:H:308:TRP:CD1	1:H:310:ALA:HB3	2.51	0.45
3:C:57:SER:OG	3:C:58:GLY:N	2.50	0.45
3:C:344:ALA:O	3:C:345:ILE:CG2	2.63	0.45
3:D:80:VAL:O	3:D:80:VAL:HG13	2.15	0.45
3:D:166:ALA:O	3:D:170:VAL:HG23	2.15	0.45
3:D:214:GLN:CG	3:D:215:VAL:H	2.29	0.45
1:F:76:GLY:O	1:F:80:LEU:HB2	2.17	0.45
1:F:308:TRP:HD1	1:F:310:ALA:HB3	1.81	0.45
1:F:335:ILE:HD12	1:F:339:LEU:CD1	2.40	0.45
1:F:509:THR:C	1:F:510:ARG:O	2.57	0.45
3:A:348:PRO:HA	3:A:349:PRO:HD2	1.88	0.45
3:B:96:MET:CE	3:B:114:VAL:HG13	2.46	0.45
3:B:168:LEU:HD11	3:B:172:MET:HE3	1.97	0.45
1:H:280:ILE:HG13	1:H:467:LEU:HD22	1.98	0.45
1:H:333:ILE:CA	1:H:336:PHE:HB2	2.46	0.45
1:H:497:LEU:CD2	2:I:131:PHE:HD2	2.28	0.45
3:C:6:LEU:CD2	3:C:9:VAL:HG21	2.45	0.45
3:C:10:THR:CG2	3:C:11:LYS:H	2.26	0.45
3:C:44:THR:HG22	3:C:48:MET:CE	2.41	0.45
3:C:169:ARG:HB2	3:C:169:ARG:CZ	2.46	0.45
3:C:186:THR:CG2	3:C:187:MET:N	2.79	0.45
3:D:91:SER:HB2	3:D:129:ARG:O	2.16	0.45
1:F:348:ASN:HA	1:F:351:LEU:HD22	1.99	0.45
1:F:374:ILE:CD1	1:F:375:VAL:N	2.76	0.45
3:A:215:VAL:HG12	3:A:216:GLY:N	2.31	0.45
3:A:302:GLY:HA2	3:A:321:PRO:HD3	1.97	0.45
3:A:335:VAL:O	3:A:337:VAL:HG23	2.17	0.45
3:A:354:LEU:O	3:A:355:PHE:CG	2.70	0.45
3:B:62:ILE:CD1	3:B:75:ARG:HB3	2.46	0.45
3:B:219:LEU:O	3:B:220:GLU:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:263:ASN:OD1	1:H:263:ASN:C	2.60	0.45
1:H:270:ASP:C	1:H:271:GLU:CD	2.85	0.45
1:H:330:PHE:O	1:H:333:ILE:CD1	2.63	0.45
1:H:383:TYR:C	1:H:383:TYR:HD2	2.24	0.45
1:H:425:PRO:O	1:H:428:PRO:HD2	2.16	0.45
2:I:19:LEU:HA	2:I:22:LEU:HD23	1.98	0.45
2:I:191:ALA:O	2:I:194:LEU:CB	2.65	0.45
2:I:198:THR:O	2:I:199:PRO:C	2.59	0.45
3:C:6:LEU:HB3	3:C:9:VAL:HG23	1.97	0.45
3:C:155:PHE:HB2	3:C:187:MET:HG2	1.98	0.45
3:C:215:VAL:HG12	3:C:216:GLY:N	2.31	0.45
3:D:83:SER:C	3:D:84:TYR:CD2	2.94	0.45
3:D:159:GLU:HG2	3:D:191:THR:HA	1.98	0.45
3:D:243:PRO:C	3:D:244:VAL:CG2	2.89	0.45
1:F:99:GLN:HG3	1:F:100:LEU:HD23	1.98	0.45
1:F:263:ASN:OD1	1:F:263:ASN:C	2.60	0.45
2:G:92:ALA:HA	2:G:226:ALA:HB1	1.96	0.45
3:A:109:VAL:O	3:A:113:ARG:HG2	2.17	0.45
3:A:123:LEU:CD1	3:A:141:ARG:NH2	2.77	0.45
3:B:155:PHE:H	3:B:155:PHE:HD1	1.64	0.45
3:B:270:VAL:HG12	3:B:271:GLU:H	1.80	0.45
3:D:301:GLU:HA	3:D:344:ALA:HB1	1.92	0.45
1:F:428:PRO:HG2	1:F:429:LEU:H	1.82	0.45
2:G:19:LEU:HA	2:G:22:LEU:HD23	1.98	0.45
2:G:32:LEU:O	2:G:35:VAL:CB	2.60	0.45
2:G:37:ILE:O	2:G:38:SER:HB2	2.16	0.45
2:G:260:TRP:O	2:G:263:PHE:HB3	2.16	0.45
2:G:264:ALA:O	2:G:267:ALA:HB3	2.16	0.45
3:A:57:SER:OG	3:A:58:GLY:N	2.50	0.45
3:A:117:VAL:O	3:A:118:ALA:C	2.59	0.45
3:A:254:VAL:HG21	3:A:270:VAL:HG12	1.98	0.45
3:B:38:SER:C	3:B:40:CYS:N	2.75	0.45
3:B:62:ILE:HD12	3:B:75:ARG:HB3	1.99	0.45
3:B:66:ARG:HG2	3:B:66:ARG:O	2.17	0.45
3:B:96:MET:HG3	3:B:142:VAL:HG12	1.98	0.45
3:B:312:ASN:O	3:B:313:GLU:HB3	2.17	0.45
3:B:317:HIS:O	3:B:318:ILE:CG1	2.62	0.45
1:H:322:ILE:HG21	2:I:278:PHE:CZ	2.52	0.45
1:H:324:PRO:HA	1:H:378:TRP:CH2	2.51	0.45
3:C:49:ILE:O	3:C:75:ARG:NH1	2.49	0.45
3:C:106:LYS:O	3:C:110:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:155:PHE:O	3:C:157:LEU:CD1	2.65	0.45
3:D:27:HIS:ND1	3:D:27:HIS:N	2.63	0.45
3:D:219:LEU:O	3:D:220:GLU:C	2.60	0.45
3:D:320:ILE:CG2	3:D:321:PRO:HD2	2.35	0.45
1:F:330:PHE:CG	1:F:331:ILE:N	2.83	0.45
1:F:505:ASN:HB2	2:G:127:ILE:HD11	1.99	0.45
3:A:44:THR:HG22	3:A:48:MET:CE	2.41	0.45
3:A:121:LEU:HD11	3:A:148:LEU:CD1	2.47	0.45
3:A:155:PHE:O	3:A:157:LEU:CD1	2.65	0.45
3:A:222:TYR:O	3:A:286:ARG:NH2	2.44	0.45
3:A:354:LEU:C	3:A:355:PHE:CD1	2.94	0.45
3:B:42:LYS:HE2	3:B:190:VAL:HG11	1.98	0.45
1:H:41:LEU:HD12	1:H:89:ILE:CD1	2.38	0.45
1:H:110:LEU:C	1:H:110:LEU:CD2	2.90	0.45
2:I:37:ILE:O	2:I:38:SER:HB2	2.16	0.45
2:I:185:ASP:C	2:I:188:LEU:HD13	2.37	0.45
2:I:264:ALA:O	2:I:267:ALA:HB3	2.16	0.45
3:C:109:VAL:O	3:C:113:ARG:HG2	2.17	0.45
3:C:352:CYS:O	3:C:364:ARG:HD2	2.16	0.45
3:D:2:ALA:O	3:D:4:VAL:N	2.48	0.45
3:D:45:LEU:HD11	3:D:207:LEU:HD11	1.98	0.45
3:D:66:ARG:HG2	3:D:66:ARG:O	2.17	0.45
3:D:118:ALA:HB1	3:D:123:LEU:O	2.16	0.45
3:D:169:ARG:HB2	3:D:169:ARG:CZ	2.47	0.45
1:F:305:LEU:HD13	2:G:16:THR:HG23	1.99	0.45
2:G:110:PHE:CD1	2:G:174:VAL:HG11	2.52	0.45
3:A:52:LEU:HD23	3:A:72:PRO:HG2	1.97	0.45
3:A:186:THR:CG2	3:A:187:MET:N	2.79	0.45
3:A:214:GLN:NE2	3:A:226:ALA:HB2	2.31	0.45
3:B:36:GLY:HA2	3:B:233:PHE:CE2	2.52	0.45
3:B:91:SER:HB2	3:B:129:ARG:O	2.16	0.45
3:B:244:VAL:O	3:B:245:LYS:HG2	2.16	0.45
3:B:372:ALA:O	3:B:373:SER:HB2	2.17	0.45
1:H:93:ASN:OD1	1:H:98:ASN:ND2	2.50	0.45
1:H:308:TRP:CZ2	1:H:410:PRO:HB3	2.52	0.45
2:I:88:SER:HG	2:I:245:LEU:H	1.60	0.45
2:I:110:PHE:CD1	2:I:174:VAL:HG11	2.52	0.45
3:C:117:VAL:O	3:C:118:ALA:C	2.59	0.45
3:C:254:VAL:CG2	3:C:270:VAL:HG12	2.47	0.45
3:D:36:GLY:HA2	3:D:233:PHE:CE2	2.52	0.45
3:D:123:LEU:HG	3:D:126:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:125:HIS:C	3:D:127:LEU:H	2.25	0.45
3:D:276:GLN:HG3	3:D:277:VAL:N	2.32	0.45
3:D:317:HIS:C	3:D:318:ILE:HG13	2.41	0.45
1:F:322:ILE:HG21	2:G:278:PHE:CZ	2.52	0.45
1:F:322:ILE:HG22	1:F:323:LEU:N	2.32	0.45
1:F:326:ALA:C	2:G:274:ILE:CG2	2.90	0.45
1:F:433:SER:O	1:F:436:PHE:HB3	2.17	0.45
2:G:84:TRP:HB2	2:G:245:LEU:HD12	1.98	0.45
2:G:198:THR:O	2:G:199:PRO:C	2.59	0.45
3:A:31:PHE:N	3:A:202:ASP:OD2	2.50	0.45
3:A:199:THR:OG1	3:A:200:LEU:N	2.49	0.45
3:A:232:GLY:O	3:A:238:LYS:HG3	2.17	0.45
3:B:24:LEU:CD1	3:B:26:ILE:HD11	2.47	0.45
3:B:169:ARG:NH1	3:B:169:ARG:CB	2.75	0.45
3:B:304:VAL:HG13	3:B:316:ILE:CG2	2.46	0.45
1:H:100:LEU:O	1:H:101:THR:HG23	2.17	0.45
1:H:284:THR:O	1:H:287:PHE:HB3	2.17	0.45
1:H:348:ASN:HA	1:H:351:LEU:HD22	1.98	0.45
1:H:374:ILE:C	1:H:374:ILE:CD1	2.82	0.45
1:H:439:ASN:ND2	2:I:132:PRO:CB	2.80	0.45
2:I:139:ALA:O	2:I:142:ALA:HB3	2.17	0.45
3:C:40:CYS:C	3:C:42:LYS:N	2.74	0.45
3:C:46:LEU:HD13	3:C:190:VAL:CG2	2.47	0.45
3:C:121:LEU:HD11	3:C:148:LEU:CD1	2.47	0.45
3:D:31:PHE:HB3	3:D:202:ASP:OD2	2.17	0.45
3:D:266:VAL:HG22	3:D:267:TRP:N	2.28	0.45
3:D:349:PRO:HD2	3:D:350:GLU:OE1	2.17	0.45
1:F:310:ALA:O	1:F:312:ARG:N	2.50	0.44
1:F:348:ASN:HD21	1:F:361:TRP:HD1	1.65	0.44
1:F:400:TYR:O	1:F:401:GLU:C	2.60	0.44
2:G:94:ILE:CD1	2:G:163:ILE:HG21	2.47	0.44
3:B:27:HIS:ND1	3:B:27:HIS:N	2.63	0.44
3:B:31:PHE:HB3	3:B:202:ASP:OD2	2.17	0.44
3:B:155:PHE:HB2	3:B:187:MET:HG2	1.98	0.44
3:B:169:ARG:HB2	3:B:169:ARG:CZ	2.47	0.44
3:B:317:HIS:C	3:B:318:ILE:HG13	2.41	0.44
3:B:320:ILE:CG2	3:B:321:PRO:HD2	2.35	0.44
3:B:351:ARG:HE	3:B:368:GLU:CD	2.23	0.44
1:H:99:GLN:HG3	1:H:100:LEU:HD23	1.99	0.44
1:H:326:ALA:C	2:I:274:ILE:CG2	2.90	0.44
3:C:335:VAL:O	3:C:337:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:270:VAL:HG12	3:D:271:GLU:H	1.80	0.44
1:F:326:ALA:C	2:G:274:ILE:HG23	2.42	0.44
2:G:88:SER:HB3	2:G:227:ILE:HD11	1.99	0.44
3:B:12:ALA:HB2	3:B:17:VAL:HA	2.00	0.44
3:B:42:LYS:CE	3:B:190:VAL:HG13	2.47	0.44
3:B:60:LEU:HD12	3:B:61:PHE:H	1.79	0.44
1:H:86:THR:C	1:H:490:ILE:HG21	2.42	0.44
1:H:90:ALA:HA	1:H:490:ILE:HD12	1.99	0.44
1:H:346:GLU:HA	1:H:349:MET:CG	2.32	0.44
1:H:497:LEU:HD23	1:H:501:LEU:HG	1.98	0.44
1:H:497:LEU:CD1	2:I:132:PRO:HD3	2.31	0.44
2:I:229:GLU:CG	2:I:230:VAL:N	2.80	0.44
3:C:368:GLU:CB	3:C:369:PRO:HD2	2.46	0.44
3:D:62:ILE:HD12	3:D:75:ARG:HB3	1.99	0.44
1:F:306:VAL:HG21	1:F:385:MET:HE1	1.99	0.44
1:F:497:LEU:CD2	2:G:131:PHE:HD2	2.28	0.44
2:G:6:PRO:O	2:G:8:SER:N	2.51	0.44
2:G:181:PHE:HZ	2:G:203:PHE:CE2	2.35	0.44
3:A:10:THR:CG2	3:A:11:LYS:H	2.26	0.44
3:A:50:ALA:O	3:A:75:ARG:CZ	2.66	0.44
3:A:239:MET:HE3	3:A:286:ARG:CZ	2.48	0.44
1:H:284:THR:CB	1:H:467:LEU:HD23	2.47	0.44
1:H:306:VAL:HG21	1:H:385:MET:HE1	1.99	0.44
1:H:310:ALA:O	1:H:312:ARG:N	2.50	0.44
1:H:331:ILE:HD13	1:H:331:ILE:O	2.17	0.44
2:I:18:LEU:O	2:I:22:LEU:HD23	2.18	0.44
2:I:88:SER:HB3	2:I:227:ILE:HD11	1.99	0.44
3:C:195:VAL:O	3:C:196:GLU:C	2.61	0.44
3:C:232:GLY:O	3:C:238:LYS:HG3	2.17	0.44
3:D:162:SER:OG	3:D:163:ASN:N	2.50	0.44
3:D:283:LEU:HD12	3:D:353:HIS:O	2.17	0.44
1:F:73:ALA:O	1:F:77:LEU:HB2	2.17	0.44
2:G:191:ALA:O	2:G:194:LEU:CB	2.65	0.44
3:A:24:LEU:CD1	3:A:26:ILE:HD11	2.48	0.44
3:A:46:LEU:HD13	3:A:190:VAL:CG2	2.47	0.44
3:A:195:VAL:O	3:A:196:GLU:C	2.61	0.44
3:A:217:LYS:HB3	3:A:218:PRO:CD	2.48	0.44
3:B:42:LYS:O	3:B:43:SER:C	2.60	0.44
1:H:428:PRO:HG2	1:H:429:LEU:H	1.82	0.44
2:I:94:ILE:CD1	2:I:163:ILE:HG21	2.47	0.44
3:C:50:ALA:O	3:C:75:ARG:CZ	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:139:ARG:O	3:C:140:GLN:C	2.60	0.44
3:D:123:LEU:CD1	3:D:141:ARG:HH21	2.31	0.44
3:D:351:ARG:NE	3:D:368:GLU:OE1	2.38	0.44
3:D:368:GLU:OE1	3:D:369:PRO:HD2	2.17	0.44
1:F:110:LEU:C	1:F:110:LEU:CD2	2.90	0.44
1:F:270:ASP:C	1:F:271:GLU:CD	2.85	0.44
1:F:322:ILE:CG2	2:G:278:PHE:CE1	3.00	0.44
1:F:357:VAL:HG11	1:F:359:PRO:HG3	1.99	0.44
1:F:439:ASN:ND2	2:G:132:PRO:CB	2.80	0.44
2:G:18:LEU:O	2:G:22:LEU:HD23	2.18	0.44
3:A:189:TYR:HD2	3:A:190:VAL:O	1.99	0.44
3:B:276:GLN:HG3	3:B:277:VAL:N	2.32	0.44
3:B:327:LEU:HD12	3:B:327:LEU:HA	1.83	0.44
3:B:349:PRO:HD2	3:B:350:GLU:OE1	2.17	0.44
3:B:368:GLU:OE1	3:B:369:PRO:HD2	2.17	0.44
1:H:305:LEU:HD13	2:I:16:THR:HG23	1.99	0.44
1:H:341:ASN:HB3	1:H:344:PHE:CB	2.48	0.44
1:H:433:SER:O	1:H:436:PHE:HB3	2.17	0.44
1:H:509:THR:C	1:H:510:ARG:O	2.57	0.44
2:I:245:LEU:HA	2:I:245:LEU:HD12	1.79	0.44
3:C:31:PHE:N	3:C:202:ASP:OD2	2.50	0.44
3:C:299:ILE:CG2	3:C:300:LEU:H	2.26	0.44
3:D:74:GLU:C	3:D:76:GLY:H	2.26	0.44
2:G:18:LEU:CD2	2:G:19:LEU:N	2.77	0.44
2:G:221:LEU:O	2:G:224:ILE:HG13	2.18	0.44
3:A:179:LEU:O	3:A:182:ARG:HB3	2.18	0.44
3:A:254:VAL:CG2	3:A:270:VAL:HG12	2.47	0.44
3:B:4:VAL:CG2	3:B:5:GLN:H	2.31	0.44
3:B:159:GLU:HG2	3:B:191:THR:HA	1.98	0.44
3:B:301:GLU:HA	3:B:344:ALA:HB1	1.92	0.44
1:H:90:ALA:O	1:H:487:ALA:HB2	2.17	0.44
1:H:267:VAL:CA	1:H:488:ALA:HB2	2.38	0.44
1:H:276:PRO:HG2	1:H:277:PHE:H	1.83	0.44
1:H:375:VAL:HG12	1:H:376:ASN:N	2.33	0.44
2:I:6:PRO:O	2:I:8:SER:N	2.51	0.44
2:I:221:LEU:O	2:I:224:ILE:HG13	2.18	0.44
3:C:87:TYR:HB2	3:C:95:ASN:ND2	2.33	0.44
3:C:217:LYS:HB3	3:C:218:PRO:CD	2.48	0.44
3:C:354:LEU:O	3:C:355:PHE:CG	2.70	0.44
3:D:42:LYS:HE2	3:D:190:VAL:HG11	1.98	0.44
3:D:194:GLN:H	3:D:194:GLN:NE2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:273:ARG:HG2	3:D:273:ARG:NH1	2.33	0.44
3:D:312:ASN:O	3:D:313:GLU:HB3	2.17	0.44
3:D:346:GLY:O	3:D:348:PRO:HD2	2.18	0.44
1:F:284:THR:O	1:F:287:PHE:HB3	2.17	0.44
2:G:27:ILE:O	2:G:28:MET:HG2	2.18	0.44
2:G:139:ALA:O	2:G:142:ALA:HB3	2.17	0.44
2:G:244:THR:H	2:G:247:VAL:CG2	2.31	0.44
3:A:204:ILE:HD12	3:A:221:LEU:CD1	2.48	0.44
3:A:283:LEU:O	3:A:283:LEU:HG	2.17	0.44
3:B:123:LEU:HG	3:B:126:LEU:HD12	1.99	0.44
3:B:273:ARG:HG2	3:B:273:ARG:NH1	2.33	0.44
3:B:307:VAL:CG1	3:B:309:GLN:NE2	2.77	0.44
1:H:92:THR:HG23	1:H:93:ASN:N	2.19	0.44
1:H:326:ALA:C	2:I:274:ILE:HG23	2.42	0.44
1:H:376:ASN:HA	1:H:379:LEU:HB3	1.99	0.44
1:H:413:ASN:O	1:H:417:ILE:HB	2.17	0.44
1:H:505:ASN:HB2	2:I:127:ILE:HD11	1.99	0.44
2:I:27:ILE:O	2:I:28:MET:HG2	2.18	0.44
3:C:285:ILE:CG1	3:C:286:ARG:N	2.81	0.44
3:D:260:MET:CE	3:D:320:ILE:HG21	2.48	0.44
3:D:274:ASP:O	3:D:275:VAL:HG13	2.18	0.44
1:F:100:LEU:O	1:F:101:THR:HG23	2.17	0.44
1:F:413:ASN:O	1:F:417:ILE:HB	2.17	0.44
2:G:24:ILE:CG1	2:G:25:ALA:N	2.81	0.44
3:A:74:GLU:CD	3:A:74:GLU:H	2.26	0.44
3:B:162:SER:OG	3:B:163:ASN:N	2.50	0.44
3:B:298:VAL:HG21	3:B:347:LEU:C	2.43	0.44
2:I:120:THR:HG23	2:I:121:LEU:N	2.33	0.44
2:I:252:TYR:N	2:I:252:TYR:HD1	2.14	0.44
3:D:42:LYS:O	3:D:43:SER:C	2.60	0.44
3:D:100:LEU:HD13	3:D:110:ILE:CD1	2.48	0.44
3:D:342:THR:OG1	3:D:343:PHE:N	2.50	0.44
1:F:375:VAL:HG12	1:F:376:ASN:N	2.32	0.44
1:F:376:ASN:HA	1:F:379:LEU:HB3	1.99	0.44
2:G:102:LEU:HD23	2:G:102:LEU:N	2.33	0.44
2:G:120:THR:HG23	2:G:121:LEU:N	2.33	0.44
3:B:45:LEU:HD11	3:B:207:LEU:HD11	1.98	0.44
3:B:251:ILE:O	3:B:252:ASP:OD1	2.36	0.44
1:H:357:VAL:HG11	1:H:359:PRO:HG3	1.99	0.44
1:H:497:LEU:HD13	2:I:132:PRO:CD	2.31	0.44
2:I:84:TRP:HB2	2:I:245:LEU:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:192:ALA:O	2:I:193:ALA:C	2.60	0.44
2:I:203:PHE:O	2:I:208:LEU:N	2.47	0.44
1:F:276:PRO:HG2	1:F:277:PHE:H	1.83	0.43
3:B:79:MET:SD	3:B:81:PHE:CZ	3.11	0.43
3:B:346:GLY:O	3:B:348:PRO:HD2	2.18	0.43
1:H:82:PRO:HB3	2:I:139:ALA:HB3	2.00	0.43
2:I:102:LEU:N	2:I:102:LEU:HD23	2.33	0.43
3:C:40:CYS:C	3:C:42:LYS:H	2.23	0.43
3:C:246:VAL:HG21	3:C:281:MET:HG3	2.00	0.43
1:F:284:THR:CB	1:F:467:LEU:HD23	2.47	0.43
1:F:399:LEU:CD2	3:B:87:TYR:CE2	3.01	0.43
1:F:497:LEU:CD1	2:G:132:PRO:HD3	2.31	0.43
2:G:157:ASN:O	2:G:157:ASN:CG	2.61	0.43
3:A:132:LYS:O	3:A:134:LEU:N	2.45	0.43
3:A:139:ARG:O	3:A:140:GLN:C	2.60	0.43
3:A:222:TYR:CE1	3:A:286:ARG:CZ	3.01	0.43
3:B:28:GLU:HG3	3:B:29:GLY:H	1.82	0.43
3:B:82:GLN:O	3:B:83:SER:O	2.36	0.43
3:B:125:HIS:C	3:B:127:LEU:H	2.25	0.43
1:H:91:PHE:CB	1:H:485:GLY:CA	2.96	0.43
1:H:470:TYR:O	1:H:474:ILE:HG12	2.18	0.43
3:D:11:LYS:CG	3:D:12:ALA:H	2.29	0.43
3:D:79:MET:SD	3:D:81:PHE:CZ	3.11	0.43
1:F:82:PRO:HA	2:G:139:ALA:HB1	1.99	0.43
1:F:91:PHE:CB	1:F:485:GLY:CA	2.96	0.43
1:F:331:ILE:HD13	1:F:331:ILE:O	2.17	0.43
1:F:395:ILE:HG23	1:F:396:PRO:HD2	2.01	0.43
1:F:449:ASN:C	1:F:451:GLY:N	2.77	0.43
1:F:454:ARG:HB2	1:F:457:THR:HG23	2.00	0.43
2:G:229:GLU:CG	2:G:230:VAL:N	2.81	0.43
3:A:32:VAL:C	3:A:33:VAL:HG13	2.44	0.43
3:A:50:ALA:HB2	3:A:156:LEU:HD12	2.00	0.43
3:A:217:LYS:HB3	3:A:218:PRO:HD2	2.00	0.43
1:H:94:TYR:H	1:H:94:TYR:HD1	1.66	0.43
3:C:24:LEU:CD1	3:C:26:ILE:HD11	2.48	0.43
3:C:155:PHE:HB2	3:C:187:MET:HG3	2.00	0.43
3:C:253:GLN:H	3:C:253:GLN:HG2	1.65	0.43
3:C:347:LEU:O	3:C:349:PRO:CD	2.66	0.43
3:D:355:PHE:N	3:D:355:PHE:CD1	2.85	0.43
1:F:290:ILE:HG13	1:F:291:THR:N	2.33	0.43
1:F:329:SER:O	1:F:333:ILE:CG1	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:470:TYR:O	1:F:474:ILE:HG12	2.18	0.43
2:G:167:LEU:C	2:G:169:GLY:N	2.77	0.43
2:G:251:GLN:O	2:G:253:LEU:N	2.40	0.43
3:A:18:VAL:O	3:A:18:VAL:CG1	2.57	0.43
3:A:28:GLU:O	3:A:30:GLU:N	2.52	0.43
3:A:195:VAL:HG13	3:B:310:LEU:CD2	2.48	0.43
3:A:299:ILE:CG2	3:A:300:LEU:H	2.26	0.43
3:B:74:GLU:C	3:B:76:GLY:H	2.26	0.43
3:B:240:ASN:O	3:B:241:PHE:CG	2.71	0.43
1:H:307:GLN:C	1:H:309:GLU:N	2.72	0.43
1:H:322:ILE:HG22	1:H:323:LEU:N	2.32	0.43
1:H:399:LEU:CD2	3:D:87:TYR:CE2	3.01	0.43
2:I:24:ILE:CG1	2:I:25:ALA:N	2.81	0.43
3:C:283:LEU:O	3:C:283:LEU:HG	2.17	0.43
3:D:12:ALA:HB2	3:D:17:VAL:HA	2.00	0.43
3:D:171:GLN:O	3:D:175:GLU:HG2	2.19	0.43
3:D:240:ASN:O	3:D:241:PHE:CG	2.71	0.43
2:G:91:VAL:O	2:G:95:SER:CB	2.67	0.43
2:G:208:LEU:HD23	2:G:208:LEU:HA	1.84	0.43
3:B:51:GLY:O	3:B:53:GLU:N	2.39	0.43
3:B:269:PRO:O	3:B:365:LEU:HG	2.19	0.43
3:B:283:LEU:HD12	3:B:353:HIS:O	2.17	0.43
1:H:345:GLY:O	1:H:347:ILE:N	2.51	0.43
1:H:468:VAL:CG1	1:H:469:ASN:N	2.81	0.43
3:C:32:VAL:C	3:C:33:VAL:HG13	2.44	0.43
3:C:50:ALA:HB2	3:C:156:LEU:HD12	2.00	0.43
3:C:195:VAL:HG13	3:D:310:LEU:CD2	2.47	0.43
3:C:222:TYR:CE1	3:C:286:ARG:CZ	3.01	0.43
3:C:223:HIS:O	3:C:353:HIS:CE1	2.72	0.43
3:C:311:GLY:O	3:C:313:GLU:N	2.46	0.43
3:D:269:PRO:O	3:D:365:LEU:HG	2.19	0.43
3:D:298:VAL:HG21	3:D:347:LEU:C	2.43	0.43
1:F:93:ASN:OD1	1:F:98:ASN:ND2	2.50	0.43
1:F:399:LEU:HD21	3:B:87:TYR:CD2	2.53	0.43
2:G:88:SER:O	2:G:227:ILE:HD11	2.18	0.43
2:G:245:LEU:HA	2:G:245:LEU:HD12	1.79	0.43
3:A:174:ILE:O	3:A:178:ARG:N	2.38	0.43
3:A:344:ALA:O	3:A:345:ILE:CG2	2.63	0.43
3:B:123:LEU:CD1	3:B:141:ARG:HH21	2.31	0.43
3:B:222:TYR:HE1	3:B:286:ARG:NE	2.16	0.43
3:B:274:ASP:O	3:B:275:VAL:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:322:ILE:CG2	2:I:278:PHE:CE1	3.00	0.43
1:H:408:ALA:HB1	1:H:412:GLN:HB2	2.00	0.43
2:I:244:THR:H	2:I:247:VAL:CG2	2.31	0.43
3:D:28:GLU:HG3	3:D:29:GLY:H	1.82	0.43
3:D:79:MET:HG2	3:D:80:VAL:N	2.34	0.43
3:D:160:PRO:C	3:D:162:SER:H	2.26	0.43
3:D:255:GLN:NE2	3:D:267:TRP:CE2	2.86	0.43
3:D:372:ALA:O	3:D:373:SER:HB2	2.17	0.43
1:F:90:ALA:HA	1:F:490:ILE:HD12	1.99	0.43
1:F:390:GLY:O	1:F:393:LYS:HB2	2.19	0.43
3:A:268:LEU:HA	3:A:269:PRO:HD2	1.75	0.43
3:B:194:GLN:H	3:B:194:GLN:NE2	2.16	0.43
3:B:255:GLN:NE2	3:B:267:TRP:CE2	2.86	0.43
3:B:356:ARG:HH11	3:B:360:THR:CB	2.32	0.43
1:H:390:GLY:O	1:H:393:LYS:HB2	2.19	0.43
1:H:399:LEU:HD21	3:D:87:TYR:CD2	2.54	0.43
1:H:465:ASP:OD2	1:H:473:ARG:NH2	2.48	0.43
1:H:509:THR:O	1:H:509:THR:HG23	2.19	0.43
2:I:85:LEU:N	2:I:245:LEU:HD13	2.33	0.43
2:I:212:VAL:O	2:I:213:PRO:C	2.61	0.43
3:D:92:VAL:HB	3:D:127:LEU:O	2.19	0.43
3:D:297:ASP:O	3:D:299:ILE:HG12	2.19	0.43
1:F:280:ILE:CG1	1:F:467:LEU:HD22	2.48	0.43
1:F:468:VAL:CG1	1:F:469:ASN:N	2.81	0.43
3:B:240:ASN:HD21	3:B:328:VAL:CB	2.24	0.43
1:H:73:ALA:O	1:H:77:LEU:HB2	2.17	0.43
1:H:82:PRO:HA	2:I:139:ALA:HB1	1.99	0.43
1:H:473:ARG:C	1:H:475:ALA:N	2.73	0.43
2:I:88:SER:C	2:I:227:ILE:HD11	2.44	0.43
2:I:91:VAL:O	2:I:95:SER:CB	2.67	0.43
2:I:96:ALA:HA	2:I:222:SER:HB3	2.01	0.43
3:C:204:ILE:HD12	3:C:221:LEU:CD1	2.48	0.43
3:C:215:VAL:CG1	3:C:216:GLY:N	2.81	0.43
3:C:224:TYR:HE2	3:C:371:VAL:CG1	2.29	0.43
3:C:239:MET:HE3	3:C:286:ARG:CZ	2.48	0.43
3:D:150:ALA:O	3:D:151:GLU:HB2	2.19	0.43
3:D:283:LEU:HD12	3:D:283:LEU:C	2.44	0.43
1:F:341:ASN:HB3	1:F:344:PHE:CB	2.48	0.43
2:G:96:ALA:HA	2:G:222:SER:HB3	2.01	0.43
2:G:192:ALA:O	2:G:193:ALA:C	2.60	0.43
2:G:230:VAL:HG12	2:G:231:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:240:ASN:ND2	3:A:287:PRO:HG3	2.34	0.43
3:A:246:VAL:HG21	3:A:281:MET:HG3	2.00	0.43
3:A:253:GLN:O	3:A:254:VAL:HG23	2.19	0.43
3:A:285:ILE:CG1	3:A:286:ARG:N	2.81	0.43
3:A:289:HIS:O	3:A:291:LEU:N	2.52	0.43
3:B:28:GLU:CG	3:B:29:GLY:H	2.32	0.43
3:B:116:GLN:CD	3:B:116:GLN:C	2.86	0.43
3:B:148:LEU:O	3:B:149:VAL:C	2.62	0.43
3:B:160:PRO:C	3:B:162:SER:H	2.26	0.43
3:B:171:GLN:O	3:B:175:GLU:HG2	2.19	0.43
2:I:146:ARG:O	2:I:149:GLU:CG	2.66	0.43
3:C:123:LEU:CD1	3:C:141:ARG:NH2	2.77	0.43
3:C:363:ARG:O	3:C:363:ARG:CG	2.66	0.43
3:D:116:GLN:C	3:D:116:GLN:CD	2.87	0.43
3:D:313:GLU:OE1	3:D:330:ARG:NH2	2.47	0.43
3:D:363:ARG:CG	3:D:364:ARG:N	2.81	0.43
2:G:18:LEU:CG	2:G:19:LEU:N	2.82	0.43
2:G:88:SER:C	2:G:227:ILE:HD11	2.44	0.43
3:A:155:PHE:HB2	3:A:187:MET:HG3	2.00	0.43
3:B:100:LEU:HD13	3:B:110:ILE:CD1	2.48	0.43
2:I:167:LEU:C	2:I:169:GLY:N	2.77	0.43
3:C:11:LYS:HB2	3:C:48:MET:HE1	2.01	0.43
3:C:217:LYS:HB3	3:C:218:PRO:HD2	2.00	0.43
3:C:291:LEU:HD23	3:C:292:PRO:HD3	2.01	0.43
3:D:82:GLN:O	3:D:83:SER:O	2.36	0.43
3:D:257:GLU:HB2	3:D:265:GLN:HA	2.01	0.43
3:D:258:LEU:N	3:D:258:LEU:CD2	2.80	0.43
1:F:376:ASN:HD21	1:F:379:LEU:HD23	1.84	0.42
1:F:387:LEU:HD12	1:F:387:LEU:HA	1.94	0.42
3:A:234:ILE:CG2	3:A:235:GLY:H	2.27	0.42
3:B:2:ALA:O	3:B:4:VAL:N	2.48	0.42
3:B:180:HIS:HB2	3:B:187:MET:SD	2.59	0.42
1:H:280:ILE:CG1	1:H:467:LEU:HD22	2.48	0.42
1:H:290:ILE:HG13	1:H:291:THR:N	2.33	0.42
1:H:314:LYS:H	1:H:314:LYS:CD	2.27	0.42
1:H:439:ASN:CB	2:I:132:PRO:CB	2.97	0.42
2:I:103:SER:O	2:I:107:ALA:CB	2.67	0.42
2:I:244:THR:HG1	2:I:247:VAL:HG23	1.83	0.42
3:C:74:GLU:H	3:C:74:GLU:CD	2.26	0.42
3:C:289:HIS:O	3:C:291:LEU:N	2.52	0.42
3:C:351:ARG:HG3	3:C:351:ARG:NH1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:90:ALA:O	1:F:487:ALA:HB2	2.17	0.42
1:F:400:TYR:O	1:F:403:SER:HB2	2.20	0.42
1:F:408:ALA:HB1	1:F:412:GLN:HB2	2.00	0.42
2:G:88:SER:OG	2:G:245:LEU:N	2.34	0.42
2:G:103:SER:O	2:G:107:ALA:CB	2.67	0.42
3:A:87:TYR:HB2	3:A:95:ASN:ND2	2.33	0.42
3:A:152:PRO:CG	3:A:153:SER:H	2.32	0.42
3:A:298:VAL:HG21	3:A:349:PRO:HD3	2.01	0.42
1:H:348:ASN:HD21	1:H:361:TRP:HD1	1.65	0.42
1:H:459:THR:HB	1:H:474:ILE:CG2	2.49	0.42
2:I:99:ILE:HD12	2:I:222:SER:OG	2.19	0.42
3:C:179:LEU:O	3:C:182:ARG:HB3	2.18	0.42
1:F:86:THR:C	1:F:490:ILE:HG21	2.42	0.42
1:F:342:GLN:H	1:F:342:GLN:HG2	1.44	0.42
1:F:345:GLY:O	1:F:347:ILE:N	2.52	0.42
2:G:85:LEU:N	2:G:245:LEU:HD13	2.33	0.42
3:A:84:TYR:CE1	3:A:140:GLN:HG3	2.55	0.42
3:A:194:GLN:CD	3:A:194:GLN:H	2.26	0.42
3:A:242:LEU:HB2	3:A:243:PRO:CD	2.49	0.42
3:A:289:HIS:O	3:A:291:LEU:HG	2.19	0.42
3:A:345:ILE:O	3:A:345:ILE:HD12	2.19	0.42
3:B:150:ALA:O	3:B:151:GLU:HB2	2.19	0.42
3:B:208:ASP:O	3:B:209:ALA:HB3	2.20	0.42
3:B:283:LEU:HD12	3:B:283:LEU:C	2.44	0.42
3:B:363:ARG:CG	3:B:364:ARG:N	2.81	0.42
1:H:83:LEU:HD13	1:H:83:LEU:HA	1.91	0.42
1:H:92:THR:CG2	1:H:93:ASN:H	2.17	0.42
1:H:454:ARG:HB2	1:H:457:THR:HG23	2.00	0.42
1:H:471:THR:CG2	2:I:135:LEU:HD22	2.50	0.42
3:C:253:GLN:O	3:C:254:VAL:HG23	2.19	0.42
3:C:289:HIS:O	3:C:291:LEU:HG	2.19	0.42
3:C:291:LEU:HB3	3:C:292:PRO:HD2	2.01	0.42
3:D:4:VAL:CG2	3:D:5:GLN:H	2.31	0.42
1:F:82:PRO:HB3	2:G:139:ALA:HB3	2.00	0.42
1:F:94:TYR:CE2	1:F:99:GLN:HA	2.54	0.42
1:F:333:ILE:CA	1:F:336:PHE:HB2	2.46	0.42
1:F:405:MET:O	3:B:73:ALA:CB	2.68	0.42
2:G:99:ILE:HD12	2:G:222:SER:OG	2.19	0.42
3:A:215:VAL:CG1	3:A:216:GLY:N	2.81	0.42
3:A:291:LEU:HB3	3:A:292:PRO:HD2	2.01	0.42
3:A:347:LEU:O	3:A:349:PRO:CD	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:32:VAL:C	3:B:33:VAL:HG13	2.45	0.42
3:B:180:HIS:HA	3:B:187:MET:SD	2.59	0.42
1:H:284:THR:CG2	1:H:467:LEU:N	2.75	0.42
1:H:395:ILE:HG23	1:H:396:PRO:HD2	2.01	0.42
2:I:18:LEU:CG	2:I:19:LEU:N	2.82	0.42
3:C:159:GLU:O	3:C:161:LEU:N	2.48	0.42
3:C:308:GLU:C	3:C:309:GLN:O	2.60	0.42
3:D:208:ASP:O	3:D:209:ALA:HB3	2.20	0.42
3:D:240:ASN:HD21	3:D:328:VAL:CB	2.25	0.42
3:D:251:ILE:O	3:D:252:ASP:OD1	2.36	0.42
1:F:41:LEU:CD2	1:F:44:ILE:HD12	2.50	0.42
1:F:330:PHE:HZ	2:G:249:MET:HE3	1.83	0.42
1:F:459:THR:HB	1:F:474:ILE:CG2	2.49	0.42
2:G:216:ALA:O	2:G:220:ILE:HG23	2.19	0.42
3:A:54:THR:HA	3:A:55:ILE:HD12	2.02	0.42
3:A:223:HIS:O	3:A:353:HIS:CE1	2.72	0.42
3:A:311:GLY:O	3:A:313:GLU:N	2.46	0.42
3:B:23:ASN:O	3:B:24:LEU:CD2	2.66	0.42
3:B:42:LYS:CE	3:B:190:VAL:CG1	2.98	0.42
3:B:335:VAL:C	3:B:336:LEU:O	2.59	0.42
1:H:300:MET:HB2	1:H:388:CYS:SG	2.59	0.42
1:H:400:TYR:O	1:H:401:GLU:C	2.60	0.42
2:I:88:SER:O	2:I:227:ILE:HD11	2.18	0.42
2:I:216:ALA:O	2:I:220:ILE:HG23	2.19	0.42
2:I:254:ASN:CB	2:I:255:PRO:CD	2.82	0.42
3:C:194:GLN:H	3:C:194:GLN:CD	2.26	0.42
3:C:242:LEU:HB2	3:C:243:PRO:CD	2.49	0.42
3:C:312:ASN:O	3:C:313:GLU:CB	2.67	0.42
2:G:100:VAL:HG22	2:G:218:VAL:CG1	2.49	0.42
2:G:146:ARG:O	2:G:149:GLU:CG	2.66	0.42
3:A:11:LYS:HB2	3:A:48:MET:HE1	2.01	0.42
3:A:26:ILE:HG23	3:A:32:VAL:CG2	2.50	0.42
3:A:242:LEU:N	3:A:242:LEU:HD12	2.35	0.42
3:A:286:ARG:HG2	3:A:286:ARG:HH11	1.84	0.42
3:B:260:MET:CE	3:B:320:ILE:HG21	2.48	0.42
1:H:419:LEU:HB3	1:H:420:PRO:HD3	2.02	0.42
1:H:486:LEU:CB	1:H:489:ALA:HB3	2.50	0.42
2:I:230:VAL:HG12	2:I:231:PRO:HD3	2.01	0.42
3:C:28:GLU:O	3:C:30:GLU:N	2.52	0.42
3:C:51:GLY:CA	3:C:72:PRO:HG3	2.50	0.42
3:C:284:GLY:O	3:C:353:HIS:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:52:LEU:HD23	3:D:72:PRO:CG	2.50	0.42
1:F:295:THR:HG23	1:F:381:TYR:HA	2.02	0.42
1:F:337:LYS:NZ	2:G:253:LEU:HD12	2.35	0.42
2:G:212:VAL:O	2:G:213:PRO:C	2.61	0.42
3:B:92:VAL:HB	3:B:127:LEU:O	2.19	0.42
1:H:41:LEU:CD2	1:H:44:ILE:HD12	2.50	0.42
1:H:423:ILE:HD13	1:H:423:ILE:N	2.34	0.42
2:I:94:ILE:CG1	2:I:163:ILE:HG21	2.49	0.42
3:C:240:ASN:ND2	3:C:287:PRO:HG3	2.34	0.42
3:C:298:VAL:HG21	3:C:349:PRO:HD3	2.01	0.42
3:C:345:ILE:O	3:C:345:ILE:HD12	2.19	0.42
3:C:357:GLU:O	3:C:359:GLY:N	2.52	0.42
3:D:89:HIS:NE2	3:D:90:LEU:HG	2.34	0.42
3:D:287:PRO:CB	3:D:330:ARG:H	2.27	0.42
1:F:300:MET:HB2	1:F:388:CYS:SG	2.59	0.42
1:F:419:LEU:HB3	1:F:420:PRO:HD3	2.02	0.42
1:F:439:ASN:CB	2:G:132:PRO:CB	2.97	0.42
2:G:230:VAL:CG1	2:G:231:PRO:HD3	2.50	0.42
3:A:31:PHE:HD2	3:A:180:HIS:CG	2.37	0.42
3:A:34:PHE:CD2	3:A:34:PHE:N	2.88	0.42
3:A:40:CYS:C	3:A:42:LYS:N	2.74	0.42
3:A:291:LEU:HD23	3:A:292:PRO:HD3	2.01	0.42
3:A:312:ASN:O	3:A:313:GLU:CB	2.67	0.42
1:H:337:LYS:NZ	2:I:253:LEU:HD12	2.35	0.42
1:H:440:ASN:OD1	1:H:443:LEU:HB3	2.20	0.42
2:I:100:VAL:HG22	2:I:218:VAL:CG1	2.49	0.42
2:I:157:ASN:O	2:I:157:ASN:CG	2.62	0.42
3:D:32:VAL:C	3:D:33:VAL:HG13	2.45	0.42
3:D:356:ARG:HH11	3:D:360:THR:CB	2.32	0.42
1:F:438:PHE:O	1:F:466:LEU:HD13	2.20	0.42
1:F:471:THR:CG2	2:G:135:LEU:HD22	2.49	0.42
3:B:197:ALA:O	3:B:201:ALA:CB	2.68	0.42
1:H:48:ILE:HG13	1:H:49:LEU:H	1.85	0.42
2:I:197:ALA:C	2:I:198:THR:O	2.63	0.42
3:C:225:PRO:CD	3:C:353:HIS:NE2	2.64	0.42
3:D:28:GLU:CG	3:D:29:GLY:H	2.32	0.42
3:D:148:LEU:O	3:D:149:VAL:C	2.62	0.42
3:D:180:HIS:HB2	3:D:187:MET:SD	2.59	0.42
1:F:279:ALA:HB1	1:F:454:ARG:CZ	2.50	0.42
1:F:283:TRP:NE1	1:F:466:LEU:HD23	2.35	0.42
1:F:306:VAL:HG12	1:F:318:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:334:LEU:O	1:F:335:ILE:C	2.60	0.42
1:F:391:LEU:CD2	1:F:425:PRO:HB2	2.32	0.42
1:F:400:TYR:CE2	1:F:413:ASN:HB3	2.55	0.42
3:A:259:PRO:O	3:A:263:ARG:NH1	2.53	0.42
3:A:357:GLU:O	3:A:359:GLY:N	2.52	0.42
3:B:242:LEU:HD12	3:B:283:LEU:O	2.19	0.42
3:B:297:ASP:O	3:B:299:ILE:HG12	2.19	0.42
3:B:369:PRO:O	3:B:371:VAL:HG23	2.20	0.42
1:H:283:TRP:NE1	1:H:466:LEU:HD23	2.35	0.42
1:H:376:ASN:HD21	1:H:379:LEU:HD23	1.84	0.42
2:I:84:TRP:CB	2:I:245:LEU:HD12	2.50	0.42
2:I:212:VAL:HG22	2:I:215:LEU:CD1	2.42	0.42
2:I:255:PRO:C	2:I:256:GLN:O	2.63	0.42
3:C:242:LEU:N	3:C:242:LEU:HD12	2.35	0.42
3:C:248:ALA:O	3:C:249:THR:HG23	2.20	0.42
3:C:259:PRO:O	3:C:263:ARG:NH1	2.53	0.42
3:C:291:LEU:CB	3:C:292:PRO:CD	2.98	0.42
3:D:42:LYS:CE	3:D:190:VAL:CG1	2.98	0.42
3:D:253:GLN:C	3:D:254:VAL:HG23	2.45	0.42
3:D:274:ASP:C	3:D:275:VAL:HG13	2.45	0.42
3:D:308:GLU:O	3:D:310:LEU:N	2.50	0.42
1:F:90:ALA:CA	1:F:490:ILE:HD12	2.49	0.41
1:F:97:THR:O	1:F:98:ASN:HB2	2.20	0.41
1:F:364:ASP:HA	1:F:365:PRO:HD3	1.91	0.41
1:F:423:ILE:HD13	1:F:423:ILE:N	2.34	0.41
2:G:24:ILE:HD12	2:G:24:ILE:C	2.45	0.41
2:G:214:ILE:HA	2:G:214:ILE:HD12	1.83	0.41
2:G:227:ILE:HD12	2:G:227:ILE:HA	1.82	0.41
3:A:40:CYS:HB3	3:A:42:LYS:HZ3	1.83	0.41
3:B:74:GLU:O	3:B:76:GLY:N	2.53	0.41
3:B:249:THR:O	3:B:250:ALA:HB2	2.20	0.41
1:H:306:VAL:HG12	1:H:318:ARG:HH11	1.85	0.41
1:H:405:MET:O	3:D:73:ALA:CB	2.68	0.41
2:I:94:ILE:HD11	2:I:163:ILE:HD13	2.02	0.41
2:I:104:THR:CG2	2:I:105:THR:N	2.83	0.41
3:C:31:PHE:HD2	3:C:180:HIS:CG	2.37	0.41
3:C:286:ARG:HG2	3:C:286:ARG:HH11	1.84	0.41
3:D:52:LEU:O	3:D:53:GLU:HB2	2.20	0.41
3:D:155:PHE:N	3:D:155:PHE:HD1	2.16	0.41
3:D:197:ALA:O	3:D:201:ALA:CB	2.68	0.41
3:D:222:TYR:HE1	3:D:286:ARG:NE	2.16	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:242:LEU:HD12	3:D:283:LEU:O	2.19	0.41
1:F:89:ILE:C	1:F:91:PHE:N	2.77	0.41
1:F:280:ILE:HG13	1:F:467:LEU:HD21	2.02	0.41
1:F:352:SER:HB3	1:F:358:LYS:HB2	2.02	0.41
1:F:446:LEU:N	1:F:446:LEU:CD1	2.83	0.41
3:A:32:VAL:CG1	3:A:33:VAL:H	2.31	0.41
3:A:143:ALA:C	3:A:145:GLY:N	2.74	0.41
3:A:284:GLY:O	3:A:353:HIS:HB2	2.20	0.41
3:A:339:GLU:C	3:A:341:ALA:N	2.78	0.41
3:B:316:ILE:HG22	3:B:318:ILE:HG13	2.03	0.41
1:H:334:LEU:O	1:H:335:ILE:C	2.60	0.41
1:H:338:GLY:HA3	2:I:260:TRP:NE1	2.35	0.41
2:I:130:MET:HE2	2:I:130:MET:HB2	2.00	0.41
3:C:32:VAL:CG1	3:C:33:VAL:H	2.31	0.41
3:C:335:VAL:O	3:C:336:LEU:C	2.62	0.41
1:F:440:ASN:OD1	1:F:443:LEU:HB3	2.20	0.41
1:F:486:LEU:CB	1:F:489:ALA:HB3	2.50	0.41
1:F:509:THR:O	1:F:509:THR:HG23	2.19	0.41
2:G:237:LEU:HD13	2:G:242:SER:O	2.20	0.41
3:A:248:ALA:O	3:A:249:THR:HG23	2.20	0.41
3:A:272:SER:C	3:A:273:ARG:O	2.58	0.41
3:A:291:LEU:CB	3:A:292:PRO:CD	2.98	0.41
3:B:51:GLY:HA2	3:B:75:ARG:CZ	2.50	0.41
3:B:79:MET:HG2	3:B:80:VAL:N	2.34	0.41
3:B:113:ARG:NE	3:B:149:VAL:O	2.51	0.41
1:H:400:TYR:O	1:H:403:SER:HB2	2.20	0.41
1:H:446:LEU:N	1:H:446:LEU:CD1	2.83	0.41
1:H:460:PRO:HD3	1:H:482:GLN:HG2	2.02	0.41
3:C:18:VAL:O	3:C:19:SER:OG	2.34	0.41
3:C:67:MET:O	3:C:68:ASN:C	2.62	0.41
3:C:301:GLU:CG	3:C:302:GLY:N	2.84	0.41
3:C:355:PHE:HD2	3:C:361:ALA:HA	1.85	0.41
3:D:186:THR:CG2	3:D:187:MET:N	2.83	0.41
3:D:286:ARG:HH11	3:D:286:ARG:HG2	1.85	0.41
3:D:369:PRO:O	3:D:371:VAL:N	2.41	0.41
1:F:111:ASP:O	1:F:113:SER:N	2.53	0.41
1:F:308:TRP:CZ2	1:F:410:PRO:HB3	2.52	0.41
1:F:331:ILE:HG21	2:G:270:SER:OG	2.21	0.41
1:F:486:LEU:HD13	1:F:490:ILE:HG13	2.03	0.41
1:F:486:LEU:O	1:F:490:ILE:CG1	2.57	0.41
2:G:212:VAL:HA	2:G:215:LEU:CG	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:67:MET:O	3:A:68:ASN:C	2.62	0.41
3:A:102:LEU:HA	3:A:102:LEU:HD12	1.84	0.41
3:A:245:LYS:HE2	3:A:280:ASN:OD1	2.20	0.41
3:A:300:LEU:HD22	3:A:320:ILE:CD1	2.51	0.41
3:B:180:HIS:O	3:B:184:GLY:N	2.45	0.41
1:H:90:ALA:CA	1:H:490:ILE:HD12	2.49	0.41
1:H:97:THR:O	1:H:98:ASN:HB2	2.20	0.41
3:C:6:LEU:HG	3:C:9:VAL:HG21	2.03	0.41
3:C:84:TYR:CE1	3:C:140:GLN:HG3	2.55	0.41
3:C:277:VAL:C	3:C:279:ALA:H	2.28	0.41
3:D:32:VAL:CG1	3:D:33:VAL:N	2.83	0.41
3:D:180:HIS:HA	3:D:187:MET:SD	2.59	0.41
1:F:267:VAL:CA	1:F:488:ALA:HB2	2.38	0.41
2:G:84:TRP:CB	2:G:245:LEU:HD12	2.50	0.41
2:G:104:THR:CG2	2:G:105:THR:N	2.83	0.41
3:A:35:VAL:C	3:A:42:LYS:HD3	2.46	0.41
3:A:159:GLU:O	3:A:161:LEU:N	2.48	0.41
3:A:354:LEU:HG	3:A:355:PHE:N	2.35	0.41
3:B:306:VAL:CG1	3:B:307:VAL:N	2.78	0.41
1:H:331:ILE:HG21	2:I:270:SER:OG	2.21	0.41
1:H:400:TYR:CE2	1:H:413:ASN:HB3	2.55	0.41
1:H:454:ARG:NH1	1:H:463:TYR:HA	2.35	0.41
1:H:471:THR:CG2	2:I:135:LEU:CD2	2.99	0.41
1:H:498:VAL:HA	1:H:501:LEU:CG	2.51	0.41
2:I:103:SER:O	2:I:107:ALA:HB2	2.21	0.41
3:D:270:VAL:O	3:D:365:LEU:HD11	2.21	0.41
3:D:354:LEU:CD1	3:D:355:PHE:H	2.28	0.41
1:F:94:TYR:HD1	1:F:94:TYR:H	1.66	0.41
1:F:278:LEU:H	1:F:278:LEU:CD2	2.33	0.41
1:F:338:GLY:HA3	2:G:260:TRP:NE1	2.35	0.41
1:F:358:LYS:N	1:F:359:PRO:CD	2.83	0.41
1:F:498:VAL:HA	1:F:501:LEU:CG	2.51	0.41
2:G:255:PRO:C	2:G:256:GLN:O	2.63	0.41
3:A:34:PHE:CE2	3:A:188:ILE:HG23	2.56	0.41
3:A:335:VAL:O	3:A:336:LEU:C	2.62	0.41
3:B:10:THR:O	3:B:56:THR:HB	2.20	0.41
3:B:52:LEU:HD23	3:B:72:PRO:CG	2.50	0.41
3:B:253:GLN:C	3:B:254:VAL:HG23	2.45	0.41
3:C:26:ILE:HG23	3:C:32:VAL:CG2	2.50	0.41
3:C:268:LEU:HA	3:C:269:PRO:HD2	1.75	0.41
3:C:300:LEU:HD22	3:C:320:ILE:CD1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:320:ILE:HD11	3:C:327:LEU:HD22	2.03	0.41
3:D:175:GLU:O	3:D:176:ILE:C	2.63	0.41
1:F:328:PRO:HD2	1:F:331:ILE:CG2	2.51	0.41
1:F:460:PRO:HD3	1:F:482:GLN:HG2	2.01	0.41
2:G:94:ILE:CG1	2:G:163:ILE:HG21	2.49	0.41
3:A:81:PHE:CD1	3:A:85:ALA:HB2	2.55	0.41
3:A:240:ASN:HD21	3:A:328:VAL:N	2.18	0.41
3:B:225:PRO:HD2	3:B:353:HIS:CD2	2.56	0.41
3:B:257:GLU:HB2	3:B:265:GLN:HA	2.01	0.41
3:B:286:ARG:HH11	3:B:286:ARG:HG2	1.85	0.41
3:B:329:TYR:CE2	3:B:343:PHE:HE2	2.37	0.41
3:B:366:HIS:O	3:B:368:GLU:HG2	2.21	0.41
1:H:287:PHE:CE2	1:H:437:ASN:O	2.70	0.41
1:H:326:ALA:O	2:I:274:ILE:CG2	2.69	0.41
1:H:424:LYS:NZ	1:H:511:MET:CE	2.77	0.41
2:I:230:VAL:CG1	2:I:231:PRO:HD3	2.50	0.41
3:C:354:LEU:HG	3:C:355:PHE:N	2.35	0.41
3:D:51:GLY:HA2	3:D:75:ARG:CZ	2.50	0.41
3:D:345:ILE:O	3:D:345:ILE:HD12	2.21	0.41
1:F:283:TRP:CH2	1:F:369:ARG:HB3	2.55	0.41
1:F:337:LYS:NZ	2:G:253:LEU:CD1	2.80	0.41
2:G:93:GLY:CA	2:G:223:PHE:CE1	3.01	0.41
2:G:94:ILE:HD11	2:G:163:ILE:HD13	2.02	0.41
2:G:280:LEU:HD23	2:G:280:LEU:C	2.46	0.41
3:A:210:GLY:O	3:A:211:ARG:CG	2.69	0.41
3:A:299:ILE:O	3:A:300:LEU:HG	2.20	0.41
3:A:314:THR:HG22	3:A:315:GLN:H	1.86	0.41
3:B:41:GLY:O	3:B:42:LYS:C	2.63	0.41
3:B:52:LEU:O	3:B:53:GLU:HB2	2.20	0.41
3:B:224:TYR:CE2	3:B:371:VAL:HG11	2.56	0.41
3:B:274:ASP:C	3:B:275:VAL:HG13	2.45	0.41
3:B:298:VAL:O	3:B:346:GLY:HA2	2.21	0.41
3:B:345:ILE:O	3:B:345:ILE:HD12	2.21	0.41
1:H:337:LYS:NZ	2:I:253:LEU:CG	2.81	0.41
1:H:352:SER:HB3	1:H:358:LYS:HB2	2.02	0.41
1:H:446:LEU:N	1:H:446:LEU:HD12	2.36	0.41
1:H:449:ASN:C	1:H:451:GLY:N	2.77	0.41
3:C:34:PHE:CD2	3:C:34:PHE:N	2.88	0.41
3:C:34:PHE:CE2	3:C:188:ILE:HG23	2.56	0.41
3:C:164:LEU:HD13	3:C:168:LEU:CD2	2.51	0.41
3:D:10:THR:O	3:D:56:THR:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:23:ASN:O	3:D:24:LEU:CD2	2.66	0.41
1:F:81:PHE:CZ	1:F:85:CYS:SG	3.14	0.41
1:F:306:VAL:CG1	1:F:318:ARG:HH11	2.34	0.41
1:F:326:ALA:O	2:G:274:ILE:CG2	2.69	0.41
1:F:470:TYR:CE2	1:F:474:ILE:HD13	2.56	0.41
2:G:22:LEU:HD22	2:G:22:LEU:N	2.36	0.41
2:G:100:VAL:CG2	2:G:218:VAL:HG12	2.51	0.41
2:G:160:GLY:HA2	2:G:163:ILE:HG12	2.03	0.41
2:G:187:SER:HA	2:G:190:GLU:OE1	2.21	0.41
3:A:32:VAL:CG1	3:A:33:VAL:N	2.82	0.41
3:A:43:SER:O	3:A:46:LEU:N	2.54	0.41
3:A:51:GLY:CA	3:A:72:PRO:HG3	2.50	0.41
3:A:153:SER:O	3:A:185:ARG:CB	2.65	0.41
3:A:285:ILE:CD1	3:A:286:ARG:N	2.81	0.41
3:A:351:ARG:HG3	3:A:351:ARG:NH1	2.33	0.41
3:B:26:ILE:H	3:B:26:ILE:CD1	2.14	0.41
3:B:155:PHE:N	3:B:155:PHE:HD1	2.16	0.41
3:B:168:LEU:CD1	3:B:172:MET:HG2	2.51	0.41
3:B:169:ARG:HD3	3:B:193:ASP:OD1	2.21	0.41
3:B:175:GLU:O	3:B:176:ILE:C	2.63	0.41
3:B:242:LEU:CD1	3:B:283:LEU:O	2.69	0.41
3:B:270:VAL:O	3:B:365:LEU:HD11	2.21	0.41
3:B:299:ILE:O	3:B:300:LEU:CG	2.69	0.41
1:H:271:GLU:HG2	1:H:272:GLY:H	1.85	0.41
1:H:283:TRP:CH2	1:H:369:ARG:HB3	2.55	0.41
1:H:347:ILE:CG2	1:H:348:ASN:N	2.47	0.41
1:H:427:THR:O	1:H:428:PRO:C	2.64	0.41
1:H:492:THR:HG23	1:H:493:LEU:N	2.36	0.41
2:I:100:VAL:CG2	2:I:218:VAL:HG12	2.51	0.41
2:I:237:LEU:HD13	2:I:242:SER:O	2.20	0.41
3:C:35:VAL:C	3:C:42:LYS:HD3	2.46	0.41
3:C:54:THR:HA	3:C:55:ILE:HD12	2.02	0.41
3:C:84:TYR:O	3:C:85:ALA:HB3	2.21	0.41
3:C:240:ASN:HD21	3:C:328:VAL:N	2.18	0.41
3:C:248:ALA:C	3:C:249:THR:HG23	2.46	0.41
3:D:38:SER:C	3:D:40:CYS:N	2.75	0.41
3:D:85:ALA:O	3:D:146:ARG:CZ	2.69	0.41
3:D:168:LEU:CD1	3:D:172:MET:HG2	2.51	0.41
3:D:249:THR:O	3:D:250:ALA:HB2	2.20	0.41
3:D:276:GLN:HE21	3:D:277:VAL:N	2.19	0.41
3:D:299:ILE:C	3:D:300:LEU:HG	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:307:VAL:CG1	3:D:309:GLN:NE2	2.77	0.41
3:D:329:TYR:CE2	3:D:343:PHE:HE2	2.38	0.41
3:D:351:ARG:HE	3:D:368:GLU:CD	2.23	0.41
3:D:366:HIS:O	3:D:368:GLU:HG2	2.21	0.41
3:D:369:PRO:O	3:D:371:VAL:HG23	2.20	0.41
1:F:271:GLU:HG2	1:F:272:GLY:H	1.85	0.41
1:F:454:ARG:NH1	1:F:463:TYR:HA	2.35	0.41
3:A:36:GLY:C	3:A:37:PRO:O	2.63	0.41
3:A:90:LEU:O	3:A:131:PRO:HD3	2.21	0.41
3:A:164:LEU:HD13	3:A:168:LEU:CD2	2.51	0.41
3:A:244:VAL:HG23	3:A:281:MET:C	2.47	0.41
3:A:277:VAL:C	3:A:279:ALA:H	2.29	0.41
3:B:190:VAL:C	3:B:191:THR:HG22	2.46	0.41
3:B:207:LEU:HD23	3:B:207:LEU:HA	1.85	0.41
1:H:94:TYR:CE2	1:H:99:GLN:HA	2.54	0.41
1:H:280:ILE:HG13	1:H:467:LEU:HD21	2.02	0.41
1:H:328:PRO:HD2	1:H:331:ILE:CG2	2.51	0.41
2:I:148:GLY:HA3	2:I:155:GLY:HA3	2.01	0.41
3:C:36:GLY:C	3:C:37:PRO:O	2.63	0.41
3:C:102:LEU:HA	3:C:102:LEU:HD12	1.84	0.41
3:C:210:GLY:O	3:C:211:ARG:CG	2.69	0.41
3:C:222:TYR:CE1	3:C:286:ARG:NE	2.89	0.41
3:C:239:MET:SD	3:C:241:PHE:HE1	2.44	0.41
3:C:245:LYS:HE2	3:C:280:ASN:OD1	2.20	0.41
3:C:337:VAL:O	3:C:338:GLU:C	2.64	0.41
3:D:11:LYS:CA	3:D:56:THR:HB	2.39	0.41
3:D:224:TYR:CE2	3:D:371:VAL:HG11	2.56	0.41
3:D:316:ILE:HG22	3:D:318:ILE:HG13	2.03	0.41
1:F:277:PHE:HZ	1:F:492:THR:HG21	1.86	0.40
1:F:295:THR:HG22	1:F:384:MET:CG	2.51	0.40
1:F:312:ARG:HD2	1:F:313:GLY:N	2.23	0.40
1:F:447:LEU:HD23	1:F:447:LEU:HA	1.90	0.40
3:A:2:ALA:C	3:A:3:SER:O	2.64	0.40
3:A:186:THR:CG2	3:A:187:MET:H	2.34	0.40
3:B:11:LYS:CA	3:B:56:THR:HB	2.39	0.40
3:B:55:ILE:N	3:B:55:ILE:CD1	2.83	0.40
3:B:100:LEU:CD1	3:B:101:LYS:N	2.72	0.40
3:B:107:LYS:NZ	3:B:107:LYS:HB2	2.37	0.40
3:B:174:ILE:O	3:B:177:SER:CB	2.66	0.40
1:H:279:ALA:HB1	1:H:454:ARG:CZ	2.50	0.40
1:H:438:PHE:O	1:H:466:LEU:HD13	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:181:PHE:HZ	2:I:203:PHE:CE2	2.35	0.40
3:C:8:ASN:HA	3:C:22:ILE:O	2.21	0.40
3:C:188:ILE:O	3:C:189:TYR:HB2	2.21	0.40
3:C:299:ILE:O	3:C:300:LEU:HG	2.20	0.40
3:D:74:GLU:O	3:D:76:GLY:N	2.53	0.40
3:D:222:TYR:HE1	3:D:286:ARG:CD	2.34	0.40
1:F:348:ASN:HA	1:F:351:LEU:CD2	2.51	0.40
1:F:492:THR:HG23	1:F:493:LEU:N	2.36	0.40
2:G:131:PHE:HD2	2:G:131:PHE:HA	1.81	0.40
3:A:8:ASN:HA	3:A:22:ILE:O	2.21	0.40
3:A:22:ILE:O	3:A:23:ASN:ND2	2.54	0.40
3:A:84:TYR:O	3:A:85:ALA:HB3	2.21	0.40
3:A:200:LEU:HD23	3:A:200:LEU:HA	1.75	0.40
3:A:267:TRP:O	3:A:268:LEU:HD23	2.20	0.40
3:A:355:PHE:HD2	3:A:361:ALA:HA	1.85	0.40
3:B:97:SER:O	3:B:101:LYS:HD3	2.22	0.40
3:B:226:ALA:O	3:B:361:ALA:CB	2.70	0.40
3:B:276:GLN:HE21	3:B:277:VAL:N	2.19	0.40
3:B:310:LEU:O	3:B:312:ASN:N	2.54	0.40
1:H:265:THR:O	1:H:266:ARG:C	2.64	0.40
1:H:297:ALA:O	1:H:301:VAL:HB	2.21	0.40
1:H:323:LEU:HA	1:H:326:ALA:CB	2.52	0.40
2:I:177:ILE:HG23	2:I:178:LYS:N	2.36	0.40
2:I:199:PRO:O	2:I:203:PHE:HB2	2.21	0.40
2:I:214:ILE:HD12	2:I:214:ILE:HA	1.83	0.40
2:I:280:LEU:HD23	2:I:280:LEU:C	2.46	0.40
3:C:43:SER:O	3:C:46:LEU:N	2.54	0.40
3:C:81:PHE:CD1	3:C:85:ALA:HB2	2.55	0.40
3:C:90:LEU:O	3:C:131:PRO:HD3	2.21	0.40
3:C:159:GLU:O	3:C:162:SER:OG	2.39	0.40
3:C:267:TRP:O	3:C:268:LEU:HD23	2.20	0.40
3:C:272:SER:C	3:C:273:ARG:O	2.58	0.40
3:D:41:GLY:O	3:D:42:LYS:C	2.63	0.40
3:D:51:GLY:C	3:D:53:GLU:H	2.26	0.40
3:D:81:PHE:N	3:D:81:PHE:CD1	2.89	0.40
3:D:87:TYR:HB2	3:D:95:ASN:ND2	2.37	0.40
3:D:310:LEU:O	3:D:312:ASN:N	2.54	0.40
1:F:348:ASN:HD21	1:F:361:TRP:CD1	2.39	0.40
1:F:470:TYR:O	1:F:470:TYR:HD2	2.04	0.40
1:F:471:THR:CG2	2:G:135:LEU:CD2	2.99	0.40
3:A:26:ILE:HG23	3:A:32:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:121:LEU:HD11	3:A:148:LEU:HD12	2.03	0.40
3:A:133:ALA:O	3:A:134:LEU:CG	2.68	0.40
3:A:222:TYR:CE1	3:A:286:ARG:NE	2.89	0.40
3:A:239:MET:SD	3:A:241:PHE:HE1	2.44	0.40
3:A:301:GLU:CG	3:A:302:GLY:N	2.84	0.40
3:B:85:ALA:O	3:B:146:ARG:CZ	2.69	0.40
3:B:130:LYS:HA	3:B:131:PRO:HD3	1.90	0.40
1:H:81:PHE:CZ	1:H:85:CYS:SG	3.14	0.40
1:H:295:THR:HG23	1:H:381:TYR:HA	2.02	0.40
1:H:348:ASN:HA	1:H:351:LEU:CD2	2.51	0.40
1:H:441:PHE:CD2	1:H:468:VAL:HG22	2.54	0.40
1:H:486:LEU:HD13	1:H:490:ILE:HG13	2.03	0.40
2:I:100:VAL:O	2:I:104:THR:HB	2.21	0.40
2:I:172:LEU:HD21	2:I:173:HIS:CD2	2.57	0.40
2:I:174:VAL:C	2:I:177:ILE:HG22	2.46	0.40
3:C:121:LEU:HD11	3:C:148:LEU:HD12	2.03	0.40
3:C:345:ILE:HD12	3:C:345:ILE:C	2.46	0.40
3:D:169:ARG:HD3	3:D:193:ASP:OD1	2.21	0.40
3:D:225:PRO:HD2	3:D:353:HIS:CD2	2.56	0.40
1:F:265:THR:HG23	1:F:266:ARG:H	1.86	0.40
1:F:486:LEU:H	1:F:486:LEU:CD1	2.10	0.40
2:G:174:VAL:C	2:G:177:ILE:HG22	2.46	0.40
3:A:22:ILE:H	3:A:22:ILE:HG12	1.64	0.40
3:A:35:VAL:CG2	3:A:233:PHE:HE2	2.34	0.40
3:A:320:ILE:HD11	3:A:327:LEU:HD22	2.03	0.40
3:A:345:ILE:HD12	3:A:345:ILE:C	2.46	0.40
3:B:87:TYR:HB2	3:B:95:ASN:ND2	2.37	0.40
3:B:168:LEU:HD12	3:B:168:LEU:HA	1.89	0.40
3:B:235:GLY:O	3:B:236:SER:C	2.64	0.40
1:H:295:THR:HG22	1:H:384:MET:CG	2.51	0.40
1:H:330:PHE:HZ	2:I:249:MET:HE3	1.83	0.40
1:H:387:LEU:HD12	1:H:387:LEU:HA	1.94	0.40
1:H:470:TYR:O	1:H:470:TYR:HD2	2.04	0.40
2:I:160:GLY:O	2:I:163:ILE:HG12	2.22	0.40
3:C:336:LEU:C	3:C:337:VAL:CG2	2.94	0.40
2:G:4:VAL:O	2:G:5:GLN:CB	2.69	0.40
2:G:199:PRO:O	2:G:203:PHE:HB2	2.21	0.40
3:A:126:LEU:HD22	3:A:134:LEU:HD23	2.04	0.40
3:A:159:GLU:O	3:A:162:SER:OG	2.39	0.40
3:A:160:PRO:O	3:A:161:LEU:CG	2.70	0.40
3:B:10:THR:CG2	3:B:11:LYS:N	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:61:PHE:CD2	3:B:65:LYS:O	2.75	0.40
3:B:281:MET:HB3	3:B:354:LEU:CD1	2.49	0.40
1:H:277:PHE:HZ	1:H:492:THR:HG21	1.86	0.40
1:H:316:VAL:O	1:H:319:VAL:HG23	2.22	0.40
2:I:187:SER:HA	2:I:190:GLU:OE1	2.21	0.40
2:I:249:MET:HB3	2:I:263:PHE:HE1	1.86	0.40
3:C:80:VAL:CG1	3:C:160:PRO:HG3	2.52	0.40
3:C:182:ARG:HH21	3:C:183:LEU:CD2	2.35	0.40
3:C:312:ASN:O	3:C:312:ASN:CG	2.63	0.40
3:C:314:THR:HG22	3:C:315:GLN:H	1.86	0.40
3:C:351:ARG:HD3	3:C:351:ARG:HA	1.91	0.40
3:D:97:SER:O	3:D:101:LYS:HD3	2.22	0.40
3:D:123:LEU:CD1	3:D:126:LEU:HD12	2.52	0.40

All (31) 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)
3:A:182:ARG:O	3:B:324:ARG:NH1[2_565]	0.90	1.30
3:C:267:TRP:NE1	3:C:267:TRP:NE1[3_555]	1.15	1.05
3:B:340:GLY:O	3:B:340:GLY:O[2_565]	1.19	1.01
3:B:276:GLN:OE1	3:D:274:ASP:N[2_565]	1.26	0.94
3:A:119:GLU:CG	3:A:119:GLU:CD[2_565]	1.27	0.93
3:A:119:GLU:CG	3:A:119:GLU:CG[2_565]	1.28	0.92
3:C:253:GLN:NE2	3:C:265:GLN:NE2[3_555]	1.40	0.80
3:A:182:ARG:O	3:B:324:ARG:CZ[2_565]	1.43	0.77
3:A:119:GLU:OE1	3:A:119:GLU:OE1[2_565]	1.51	0.69
3:B:247:THR:O	3:D:251:ILE:CD1[2_565]	1.56	0.64
3:B:276:GLN:OE1	3:D:274:ASP:CA[2_565]	1.61	0.59
3:A:182:ARG:C	3:B:324:ARG:NH1[2_565]	1.77	0.43
3:A:119:GLU:CD	3:A:119:GLU:CD[2_565]	1.86	0.34
3:C:255:GLN:NE2	3:C:267:TRP:CE2[3_555]	1.88	0.32
3:A:119:GLU:CB	3:A:119:GLU:CD[2_565]	1.90	0.30
3:C:297:ASP:OD2	3:C:297:ASP:OD2[3_555]	1.91	0.29
3:A:119:GLU:CG	3:A:119:GLU:OE2[2_565]	1.92	0.28
3:C:255:GLN:NE2	3:C:267:TRP:NE1[3_555]	1.93	0.27
3:C:253:GLN:NE2	3:C:265:GLN:CD[3_555]	1.99	0.21
3:C:253:GLN:CD	3:C:265:GLN:NE2[3_555]	2.01	0.19
3:A:119:GLU:CD	3:A:119:GLU:OE1[2_565]	2.03	0.17
3:C:267:TRP:CD1	3:C:267:TRP:NE1[3_555]	2.04	0.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:274:ASP:N	3:D:276:GLN:OE1[2_565]	2.05	0.15
3:A:182:ARG:O	3:B:324:ARG:NH2[2_565]	2.07	0.13
3:B:276:GLN:CD	3:D:274:ASP:N[2_565]	2.09	0.11
3:A:119:GLU:CG	3:A:119:GLU:OE1[2_565]	2.10	0.10
3:B:340:GLY:C	3:B:340:GLY:O[2_565]	2.10	0.10
3:A:119:GLU:CB	3:A:119:GLU:OE1[2_565]	2.12	0.08
3:A:119:GLU:CB	3:A:119:GLU:OE2[2_565]	2.13	0.07
3:A:182:ARG:C	3:B:324:ARG:NH2[2_565]	2.14	0.06
3:C:267:TRP:NE1	3:C:267:TRP:CE2[3_555]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	310/480 (65%)	209 (67%)	61 (20%)	40 (13%)	0	4
1	H	310/480 (65%)	209 (67%)	61 (20%)	40 (13%)	0	4
2	G	250/296 (84%)	179 (72%)	38 (15%)	33 (13%)	0	3
2	I	250/296 (84%)	179 (72%)	38 (15%)	33 (13%)	0	3
3	A	369/381 (97%)	198 (54%)	97 (26%)	74 (20%)	0	1
3	B	370/381 (97%)	203 (55%)	95 (26%)	72 (20%)	0	2
3	C	369/381 (97%)	198 (54%)	96 (26%)	75 (20%)	0	1
3	D	370/381 (97%)	203 (55%)	95 (26%)	72 (20%)	0	2
All	All	2598/3076 (84%)	1578 (61%)	581 (22%)	439 (17%)	0	2

All (439) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	90	ALA
1	F	92	THR
1	F	94	TYR

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Mol	Chain	Res	Type
1	F	96	SER
1	F	98	ASN
1	F	269	THR
1	F	275	LYS
1	F	309	GLU
1	F	357	VAL
1	F	422	LEU
1	F	449	ASN
1	F	509	THR
1	F	512	LYS
2	G	7	LYS
2	G	36	ALA
2	G	38	SER
2	G	74	ILE
2	G	76	PRO
2	G	77	PRO
2	G	78	PRO
2	G	133	ALA
2	G	230	VAL
2	G	285	LEU
3	A	13	TRP
3	A	16	VAL
3	A	83	SER
3	A	102	LEU
3	A	103	ALA
3	A	129	ARG
3	A	152	PRO
3	A	224	TYR
3	A	236	SER
3	A	240	ASN
3	A	246	VAL
3	A	290	LEU
3	A	298	VAL
3	A	310	LEU
3	A	313	GLU
3	A	333	ASP
3	A	335	VAL
3	A	337	VAL
3	A	347	LEU
3	A	352	CYS
3	A	363	ARG
3	A	366	HIS

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Mol	Chain	Res	Type
3	A	371	VAL
3	B	13	TRP
3	B	16	VAL
3	B	52	LEU
3	B	75	ARG
3	B	153	SER
3	B	191	THR
3	B	224	TYR
3	B	236	SER
3	B	246	VAL
3	B	251	ILE
3	B	264	GLN
3	B	280	ASN
3	B	290	LEU
3	B	298	VAL
3	B	333	ASP
3	B	335	VAL
3	B	337	VAL
3	B	347	LEU
3	B	366	HIS
3	B	367	LYS
3	B	372	ALA
1	H	90	ALA
1	H	92	THR
1	H	94	TYR
1	H	96	SER
1	H	98	ASN
1	H	269	THR
1	H	275	LYS
1	H	309	GLU
1	H	357	VAL
1	H	422	LEU
1	H	449	ASN
1	H	509	THR
1	H	512	LYS
2	I	7	LYS
2	I	36	ALA
2	I	38	SER
2	I	74	ILE
2	I	76	PRO
2	I	77	PRO
2	I	78	PRO

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Mol	Chain	Res	Type
2	I	133	ALA
2	I	230	VAL
2	I	285	LEU
3	C	13	TRP
3	C	16	VAL
3	C	83	SER
3	C	102	LEU
3	C	103	ALA
3	C	129	ARG
3	C	152	PRO
3	C	224	TYR
3	C	236	SER
3	C	240	ASN
3	C	246	VAL
3	C	290	LEU
3	C	298	VAL
3	C	310	LEU
3	C	313	GLU
3	C	333	ASP
3	C	335	VAL
3	C	337	VAL
3	C	347	LEU
3	C	352	CYS
3	C	363	ARG
3	C	366	HIS
3	C	371	VAL
3	D	13	TRP
3	D	16	VAL
3	D	52	LEU
3	D	75	ARG
3	D	153	SER
3	D	191	THR
3	D	224	TYR
3	D	236	SER
3	D	246	VAL
3	D	251	ILE
3	D	264	GLN
3	D	280	ASN
3	D	290	LEU
3	D	298	VAL
3	D	333	ASP
3	D	335	VAL

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Mol	Chain	Res	Type
3	D	337	VAL
3	D	347	LEU
3	D	366	HIS
3	D	367	LYS
3	D	372	ALA
1	F	263	ASN
1	F	267	VAL
1	F	271	GLU
1	F	312	ARG
1	F	347	ILE
1	F	417	ILE
1	F	465	ASP
1	F	474	ILE
1	F	480	GLY
1	F	481	GLY
1	F	484	PHE
2	G	37	ILE
2	G	80	PRO
2	G	130	MET
2	G	135	LEU
2	G	152	PRO
2	G	252	TYR
3	A	19	SER
3	A	29	GLY
3	A	63	GLY
3	A	64	GLU
3	A	84	TYR
3	A	104	GLY
3	A	105	ALA
3	A	133	ALA
3	A	153	SER
3	A	191	THR
3	A	193	ASP
3	A	237	PRO
3	A	278	GLY
3	A	295	ILE
3	A	299	ILE
3	A	300	LEU
3	A	307	VAL
3	A	311	GLY
3	A	312	ASN
3	A	318	ILE

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Mol	Chain	Res	Type
3	A	319	GLN
3	A	359	GLY
3	B	3	SER
3	B	64	GLU
3	B	84	TYR
3	B	97	SER
3	B	192	HIS
3	B	193	ASP
3	B	201	ALA
3	B	208	ASP
3	B	244	VAL
3	B	295	ILE
3	B	311	GLY
3	B	312	ASN
3	B	370	GLY
1	H	263	ASN
1	H	267	VAL
1	H	271	GLU
1	H	312	ARG
1	H	347	ILE
1	H	417	ILE
1	H	465	ASP
1	H	474	ILE
1	H	480	GLY
1	H	481	GLY
1	H	484	PHE
2	I	37	ILE
2	I	80	PRO
2	I	130	MET
2	I	135	LEU
2	I	152	PRO
2	I	252	TYR
3	C	19	SER
3	C	29	GLY
3	C	63	GLY
3	C	64	GLU
3	C	84	TYR
3	C	104	GLY
3	C	105	ALA
3	C	133	ALA
3	C	153	SER
3	C	191	THR

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Mol	Chain	Res	Type
3	C	193	ASP
3	C	237	PRO
3	C	278	GLY
3	C	295	ILE
3	C	299	ILE
3	C	300	LEU
3	C	307	VAL
3	C	311	GLY
3	C	312	ASN
3	C	318	ILE
3	C	319	GLN
3	C	359	GLY
3	D	3	SER
3	D	84	TYR
3	D	97	SER
3	D	192	HIS
3	D	193	ASP
3	D	201	ALA
3	D	208	ASP
3	D	244	VAL
3	D	295	ILE
3	D	311	GLY
3	D	312	ASN
3	D	370	GLY
1	F	340	PHE
1	F	344	PHE
1	F	345	GLY
1	F	421	LEU
1	F	455	LEU
1	F	466	LEU
1	F	479	GLY
2	G	40	ARG
2	G	153	PHE
2	G	228	THR
2	G	256	GLN
2	G	259	LEU
3	A	52	LEU
3	A	53	GLU
3	A	126	LEU
3	A	161	LEU
3	A	275	VAL
3	A	331	GLN

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Mol	Chain	Res	Type
3	A	358	ASP
3	A	367	LYS
3	B	83	SER
3	B	161	LEU
3	B	275	VAL
3	B	292	PRO
3	B	308	GLU
3	B	309	GLN
3	B	310	LEU
3	B	313	GLU
3	B	371	VAL
1	H	340	PHE
1	H	344	PHE
1	H	345	GLY
1	H	421	LEU
1	H	455	LEU
1	H	466	LEU
1	H	479	GLY
2	I	40	ARG
2	I	153	PHE
2	I	228	THR
2	I	256	GLN
2	I	259	LEU
3	C	52	LEU
3	C	53	GLU
3	C	126	LEU
3	C	161	LEU
3	C	275	VAL
3	C	331	GLN
3	C	358	ASP
3	C	367	LYS
3	D	64	GLU
3	D	83	SER
3	D	161	LEU
3	D	275	VAL
3	D	292	PRO
3	D	309	GLN
3	D	310	LEU
3	D	313	GLU
3	D	371	VAL
1	F	97	THR
1	F	111	ASP

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Mol	Chain	Res	Type
1	F	311	LEU
1	F	363	SER
1	F	483	ASP
2	G	5	GLN
2	G	28	MET
2	G	151	ILE
2	G	237	LEU
2	G	284	TRP
3	A	197	ALA
3	A	269	PRO
3	B	12	ALA
3	B	104	GLY
3	B	126	LEU
3	B	158	ASP
3	B	300	LEU
3	B	318	ILE
3	B	324	ARG
3	B	358	ASP
1	H	97	THR
1	H	111	ASP
1	H	311	LEU
1	H	363	SER
1	H	483	ASP
2	I	5	GLN
2	I	28	MET
2	I	151	ILE
2	I	237	LEU
2	I	284	TRP
3	C	197	ALA
3	C	269	PRO
3	D	12	ALA
3	D	104	GLY
3	D	126	LEU
3	D	158	ASP
3	D	300	LEU
3	D	308	GLU
3	D	318	ILE
3	D	324	ARG
3	D	358	ASP
1	F	476	PHE
2	G	113	MET
2	G	167	LEU

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Mol	Chain	Res	Type
2	G	168	GLY
3	A	30	GLU
3	A	67	MET
3	A	80	VAL
3	A	281	MET
3	A	362	CYS
3	B	62	ILE
3	B	67	MET
3	B	266	VAL
3	B	322	SER
3	B	329	TYR
3	B	331	GLN
3	B	349	PRO
1	H	476	PHE
2	I	113	MET
2	I	167	LEU
2	I	168	GLY
3	C	30	GLU
3	C	67	MET
3	C	80	VAL
3	C	281	MET
3	C	362	CYS
3	D	62	ILE
3	D	67	MET
3	D	266	VAL
3	D	322	SER
3	D	329	TYR
3	D	331	GLN
3	D	349	PRO
1	F	456	GLY
1	F	460	PRO
2	G	155	GLY
2	G	198	THR
3	A	206	VAL
3	A	254	VAL
3	A	340	GLY
3	A	361	ALA
3	B	17	VAL
3	B	35	VAL
3	B	307	VAL
1	H	456	GLY
1	H	460	PRO

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Mol	Chain	Res	Type
2	I	155	GLY
2	I	198	THR
3	C	12	ALA
3	C	206	VAL
3	C	254	VAL
3	C	340	GLY
3	C	361	ALA
3	D	17	VAL
3	D	35	VAL
3	D	307	VAL
1	F	356	GLY
2	G	27	ILE
3	A	266	VAL
3	B	29	GLY
3	B	256	VAL
3	B	285	ILE
3	B	359	GLY
1	H	356	GLY
2	I	27	ILE
3	C	266	VAL
3	D	29	GLY
3	D	256	VAL
3	D	285	ILE
3	D	359	GLY
3	A	205	VAL
3	A	260	MET
3	A	348	PRO
3	B	204	ILE
3	C	205	VAL
3	C	260	MET
3	C	348	PRO
3	D	204	ILE
2	G	115	PHE
3	A	17	VAL
3	A	18	VAL
3	B	87	TYR
3	B	254	VAL
2	I	115	PHE
3	C	17	VAL
3	C	18	VAL
3	D	87	TYR
3	D	254	VAL

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Mol	Chain	Res	Type
3	A	77	VAL
3	A	212	VAL
3	A	244	VAL
3	B	210	GLY
3	B	368	GLU
3	C	77	VAL
3	C	212	VAL
3	C	244	VAL
3	D	210	GLY
3	D	368	GLU
3	A	195	VAL
3	B	131	PRO
3	B	260	MET
3	C	195	VAL
3	D	131	PRO
3	D	260	MET

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	F	253/394 (64%)	200 (79%)	53 (21%)	1	7
1	H	253/394 (64%)	200 (79%)	53 (21%)	1	7
2	G	198/237 (84%)	160 (81%)	38 (19%)	1	8
2	I	198/237 (84%)	160 (81%)	38 (19%)	1	8
3	A	314/323 (97%)	265 (84%)	49 (16%)	2	13
3	B	315/323 (98%)	270 (86%)	45 (14%)	3	15
3	C	314/323 (97%)	265 (84%)	49 (16%)	2	13
3	D	315/323 (98%)	270 (86%)	45 (14%)	3	15
All	All	2160/2554 (85%)	1790 (83%)	370 (17%)	2	11

All (370) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	41	LEU
1	F	51	SER
1	F	54	LEU
1	F	83	LEU
1	F	92	THR
1	F	98	ASN
1	F	99	GLN
1	F	110	LEU
1	F	271	GLU
1	F	285	VAL
1	F	293	PHE
1	F	296	VAL
1	F	304	CYS
1	F	309	GLU
1	F	311	LEU
1	F	314	LYS
1	F	319	VAL
1	F	322	ILE
1	F	325	TYR
1	F	330	PHE
1	F	331	ILE
1	F	333	ILE
1	F	336	PHE
1	F	342	GLN
1	F	346	GLU
1	F	349	MET
1	F	351	LEU
1	F	366	THR
1	F	367	THR
1	F	370	THR
1	F	371	MET
1	F	373	ILE
1	F	374	ILE
1	F	375	VAL
1	F	376	ASN
1	F	377	THR
1	F	381	TYR
1	F	383	TYR
1	F	388	CYS
1	F	391	LEU
1	F	397	ASP
1	F	398	ASP
1	F	399	LEU

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Mol	Chain	Res	Type
1	F	411	PHE
1	F	423	ILE
1	F	430	MET
1	F	434	PHE
1	F	447	LEU
1	F	453	ASP
1	F	477	GLU
1	F	486	LEU
1	F	505	ASN
1	F	513	PHE
2	G	5	GLN
2	G	9	GLN
2	G	18	LEU
2	G	21	LEU
2	G	30	PRO
2	G	31	LEU
2	G	37	ILE
2	G	81	VAL
2	G	83	LEU
2	G	84	TRP
2	G	85	LEU
2	G	91	VAL
2	G	104	THR
2	G	125	MET
2	G	126	LEU
2	G	128	PHE
2	G	130	MET
2	G	131	PHE
2	G	135	LEU
2	G	147	LEU
2	G	156	LEU
2	G	172	LEU
2	G	175	TRP
2	G	181	PHE
2	G	183	THR
2	G	199	PRO
2	G	214	ILE
2	G	224	ILE
2	G	227	ILE
2	G	235	LEU
2	G	247	VAL
2	G	252	TYR

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Mol	Chain	Res	Type
2	G	259	LEU
2	G	268	VAL
2	G	272	LEU
2	G	277	VAL
2	G	278	PHE
2	G	284	TRP
3	A	4	VAL
3	A	16	VAL
3	A	22	ILE
3	A	31	PHE
3	A	43	SER
3	A	45	LEU
3	A	46	LEU
3	A	48	MET
3	A	55	ILE
3	A	60	LEU
3	A	64	GLU
3	A	65	LYS
3	A	67	MET
3	A	69	ASP
3	A	70	THR
3	A	72	PRO
3	A	81	PHE
3	A	82	GLN
3	A	83	SER
3	A	86	LEU
3	A	100	LEU
3	A	101	LYS
3	A	102	LEU
3	A	107	LYS
3	A	116	GLN
3	A	123	LEU
3	A	127	LEU
3	A	147	THR
3	A	162	SER
3	A	176	ILE
3	A	188	ILE
3	A	189	TYR
3	A	193	ASP
3	A	194	GLN
3	A	198	MET
3	A	234	ILE

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Mol	Chain	Res	Type
3	A	237	PRO
3	A	242	LEU
3	A	244	VAL
3	A	258	LEU
3	A	268	LEU
3	A	270	VAL
3	A	273	ARG
3	A	280	ASN
3	A	297	ASP
3	A	298	VAL
3	A	342	THR
3	A	347	LEU
3	A	350	GLU
3	B	4	VAL
3	B	16	VAL
3	B	25	ASP
3	B	26	ILE
3	B	27	HIS
3	B	33	VAL
3	B	34	PHE
3	B	35	VAL
3	B	43	SER
3	B	55	ILE
3	B	60	LEU
3	B	61	PHE
3	B	64	GLU
3	B	79	MET
3	B	86	LEU
3	B	107	LYS
3	B	115	ASN
3	B	123	LEU
3	B	127	LEU
3	B	142	VAL
3	B	147	THR
3	B	155	PHE
3	B	188	ILE
3	B	189	TYR
3	B	194	GLN
3	B	198	MET
3	B	234	ILE
3	B	242	LEU
3	B	244	VAL

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Mol	Chain	Res	Type
3	B	249	THR
3	B	257	GLU
3	B	258	LEU
3	B	260	MET
3	B	266	VAL
3	B	268	LEU
3	B	297	ASP
3	B	298	VAL
3	B	301	GLU
3	B	307	VAL
3	B	321	PRO
3	B	345	ILE
3	B	347	LEU
3	B	350	GLU
3	B	354	LEU
3	B	355	PHE
1	H	41	LEU
1	H	51	SER
1	H	54	LEU
1	H	83	LEU
1	H	92	THR
1	H	98	ASN
1	H	99	GLN
1	H	110	LEU
1	H	271	GLU
1	H	285	VAL
1	H	293	PHE
1	H	296	VAL
1	H	304	CYS
1	H	309	GLU
1	H	311	LEU
1	H	314	LYS
1	H	319	VAL
1	H	322	ILE
1	H	325	TYR
1	H	330	PHE
1	H	331	ILE
1	H	333	ILE
1	H	336	PHE
1	H	342	GLN
1	H	346	GLU
1	H	349	MET

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Mol	Chain	Res	Type
1	H	351	LEU
1	H	366	THR
1	H	367	THR
1	H	370	THR
1	H	371	MET
1	H	373	ILE
1	H	374	ILE
1	H	375	VAL
1	H	376	ASN
1	H	377	THR
1	H	381	TYR
1	H	383	TYR
1	H	388	CYS
1	H	391	LEU
1	H	397	ASP
1	H	398	ASP
1	H	399	LEU
1	H	411	PHE
1	H	423	ILE
1	H	430	MET
1	H	434	PHE
1	H	447	LEU
1	H	453	ASP
1	H	477	GLU
1	H	486	LEU
1	H	505	ASN
1	H	513	PHE
2	I	5	GLN
2	I	9	GLN
2	I	18	LEU
2	I	21	LEU
2	I	30	PRO
2	I	31	LEU
2	I	37	ILE
2	I	81	VAL
2	I	83	LEU
2	I	84	TRP
2	I	85	LEU
2	I	91	VAL
2	I	104	THR
2	I	125	MET
2	I	126	LEU

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Mol	Chain	Res	Type
2	I	128	PHE
2	I	130	MET
2	I	131	PHE
2	I	135	LEU
2	I	147	LEU
2	I	156	LEU
2	I	172	LEU
2	I	175	TRP
2	I	181	PHE
2	I	183	THR
2	I	199	PRO
2	I	214	ILE
2	I	224	ILE
2	I	227	ILE
2	I	235	LEU
2	I	247	VAL
2	I	252	TYR
2	I	259	LEU
2	I	268	VAL
2	I	272	LEU
2	I	277	VAL
2	I	278	PHE
2	I	284	TRP
3	C	4	VAL
3	C	16	VAL
3	C	22	ILE
3	C	31	PHE
3	C	43	SER
3	C	45	LEU
3	C	46	LEU
3	C	48	MET
3	C	55	ILE
3	C	60	LEU
3	C	64	GLU
3	C	65	LYS
3	C	67	MET
3	C	69	ASP
3	C	70	THR
3	C	72	PRO
3	C	81	PHE
3	C	82	GLN
3	C	83	SER

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Mol	Chain	Res	Type
3	C	86	LEU
3	C	100	LEU
3	C	101	LYS
3	C	102	LEU
3	C	107	LYS
3	C	116	GLN
3	C	123	LEU
3	C	127	LEU
3	C	147	THR
3	C	162	SER
3	C	176	ILE
3	C	188	ILE
3	C	189	TYR
3	C	193	ASP
3	C	194	GLN
3	C	198	MET
3	C	234	ILE
3	C	237	PRO
3	C	242	LEU
3	C	244	VAL
3	C	258	LEU
3	C	268	LEU
3	C	270	VAL
3	C	273	ARG
3	C	280	ASN
3	C	297	ASP
3	C	298	VAL
3	C	342	THR
3	C	347	LEU
3	C	350	GLU
3	D	4	VAL
3	D	16	VAL
3	D	25	ASP
3	D	26	ILE
3	D	27	HIS
3	D	33	VAL
3	D	34	PHE
3	D	35	VAL
3	D	43	SER
3	D	55	ILE
3	D	60	LEU
3	D	61	PHE

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Mol	Chain	Res	Type
3	D	64	GLU
3	D	79	MET
3	D	86	LEU
3	D	107	LYS
3	D	115	ASN
3	D	123	LEU
3	D	127	LEU
3	D	142	VAL
3	D	147	THR
3	D	155	PHE
3	D	188	ILE
3	D	189	TYR
3	D	194	GLN
3	D	198	MET
3	D	234	ILE
3	D	242	LEU
3	D	244	VAL
3	D	249	THR
3	D	257	GLU
3	D	258	LEU
3	D	260	MET
3	D	266	VAL
3	D	268	LEU
3	D	297	ASP
3	D	298	VAL
3	D	301	GLU
3	D	307	VAL
3	D	321	PRO
3	D	345	ILE
3	D	347	LEU
3	D	350	GLU
3	D	354	LEU
3	D	355	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	98	ASN
1	F	99	GLN
1	F	106	GLN
1	F	341	ASN
1	F	376	ASN

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Mol	Chain	Res	Type
1	F	413	ASN
1	F	439	ASN
1	F	445	GLN
2	G	17	HIS
2	G	87	ASN
2	G	157	ASN
2	G	173	HIS
2	G	256	GLN
3	A	8	ASN
3	A	23	ASN
3	A	82	GLN
3	A	95	ASN
3	A	125	HIS
3	A	192	HIS
3	A	214	GLN
3	A	240	ASN
3	A	253	GLN
3	A	305	GLN
3	A	315	GLN
3	A	319	GLN
3	A	366	HIS
3	B	89	HIS
3	B	111	ASN
3	B	138	GLN
3	B	171	GLN
3	B	194	GLN
3	B	255	GLN
3	B	264	GLN
3	B	276	GLN
3	B	309	GLN
3	B	315	GLN
3	B	319	GLN
3	B	326	ASN
3	B	331	GLN
1	H	98	ASN
1	H	99	GLN
1	H	106	GLN
1	H	341	ASN
1	H	342	GLN
1	H	376	ASN
1	H	413	ASN
1	H	439	ASN

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Mol	Chain	Res	Type
2	I	17	HIS
2	I	87	ASN
2	I	157	ASN
2	I	173	HIS
2	I	256	GLN
3	C	8	ASN
3	C	23	ASN
3	C	82	GLN
3	C	95	ASN
3	C	125	HIS
3	C	192	HIS
3	C	214	GLN
3	C	240	ASN
3	C	253	GLN
3	C	305	GLN
3	C	315	GLN
3	C	319	GLN
3	C	366	HIS
3	D	89	HIS
3	D	111	ASN
3	D	138	GLN
3	D	171	GLN
3	D	194	GLN
3	D	255	GLN
3	D	264	GLN
3	D	276	GLN
3	D	315	GLN
3	D	319	GLN
3	D	326	ASN
3	D	331	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	F	316/480 (65%)	0.70	37 (11%)	9 13	187, 310, 422, 493	0
1	H	316/480 (65%)	0.60	27 (8%)	16 20	187, 310, 422, 493	0
2	G	254/296 (85%)	0.51	20 (7%)	18 21	204, 296, 401, 510	0
2	I	254/296 (85%)	0.66	28 (11%)	10 15	204, 296, 401, 510	0
3	A	371/381 (97%)	0.88	56 (15%)	5 10	195, 296, 384, 474	0
3	B	372/381 (97%)	0.68	51 (13%)	6 11	150, 281, 361, 454	0
3	C	371/381 (97%)	0.71	42 (11%)	10 14	195, 296, 384, 474	0
3	D	372/381 (97%)	0.63	38 (10%)	12 16	150, 281, 361, 454	0
All	All	2626/3076 (85%)	0.68	299 (11%)	10 14	150, 294, 398, 510	0

All (299) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	158	ASP	9.1
3	D	363	ARG	8.5
2	I	132	PRO	7.8
3	A	251	ILE	6.5
3	A	274	ASP	6.3
3	B	271	GLU	6.2
3	A	252	ASP	6.1
1	F	472	TYR	6.0
2	I	166	TYR	5.5
2	G	128	PHE	5.5
1	H	336	PHE	5.3
1	F	355	PHE	5.2
2	I	6	PRO	5.1
1	F	475	ALA	5.1
3	C	249	THR	5.0
1	H	380	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
3	D	290	LEU	4.9
3	C	52	LEU	4.9
3	D	347	LEU	4.9
1	F	436	PHE	4.8
3	D	158	ASP	4.8
3	B	269	PRO	4.7
3	C	143	ALA	4.7
2	I	200	TRP	4.7
2	G	121	LEU	4.6
2	G	200	TRP	4.6
1	H	370	THR	4.5
1	F	329	SER	4.5
3	A	273	ARG	4.5
3	B	365	LEU	4.5
1	H	355	PHE	4.5
3	D	96	MET	4.5
3	B	46	LEU	4.5
3	D	46	LEU	4.5
3	A	206	VAL	4.4
1	F	442	VAL	4.3
3	A	272	SER	4.3
3	D	309	GLN	4.2
3	D	239	MET	4.2
3	C	350	GLU	4.2
3	C	269	PRO	4.2
2	I	95	SER	4.1
1	F	380	GLY	4.1
3	A	322	SER	4.0
3	A	96	MET	4.0
3	A	347	LEU	4.0
3	C	332	ASN	4.0
1	F	94	TYR	4.0
3	C	144	ILE	3.9
3	A	148	LEU	3.9
3	D	156	LEU	3.9
3	A	329	TYR	3.9
2	I	217	VAL	3.8
3	B	99	GLY	3.8
3	A	47	ARG	3.7
3	D	155	PHE	3.7
3	C	281	MET	3.7
3	D	198	MET	3.7

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Mol	Chain	Res	Type	RSRZ
2	G	175	TRP	3.7
3	D	101	LYS	3.7
1	H	351	LEU	3.7
3	C	297	ASP	3.7
1	F	383	TYR	3.6
1	H	415	PHE	3.6
3	A	125	HIS	3.6
3	B	154	VAL	3.6
3	D	83	SER	3.6
3	D	349	PRO	3.5
3	D	157	LEU	3.5
3	A	43	SER	3.5
2	I	76	PRO	3.5
2	G	83	LEU	3.5
3	C	248	ALA	3.5
3	C	251	ILE	3.4
3	A	275	VAL	3.4
3	B	89	HIS	3.4
3	C	289	HIS	3.4
1	F	72	MET	3.4
1	F	471	THR	3.4
2	G	189	GLU	3.4
3	C	276	GLN	3.4
1	F	308	TRP	3.3
1	H	70	PRO	3.3
1	F	302	LEU	3.3
3	B	49	ILE	3.3
1	F	411	PHE	3.3
3	B	81	PHE	3.3
3	A	209	ALA	3.3
1	F	433	SER	3.3
3	A	97	SER	3.3
1	H	309	GLU	3.2
3	B	245	LYS	3.2
3	C	283	LEU	3.2
3	A	25	ASP	3.2
3	D	312	ASN	3.2
2	G	132	PRO	3.2
3	C	176	ILE	3.2
3	A	158	ASP	3.2
3	C	244	VAL	3.2
2	G	167	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
3	D	332	ASN	3.1
1	F	430	MET	3.1
3	C	53	GLU	3.1
3	D	220	GLU	3.1
1	F	441	PHE	3.1
3	A	14	GLY	3.1
1	F	421	LEU	3.1
3	D	54	THR	3.1
2	I	284	TRP	3.1
3	A	46	LEU	3.1
3	B	283	LEU	3.0
3	B	291	LEU	3.0
2	I	131	PHE	3.0
3	C	146	ARG	3.0
2	I	78	PRO	3.0
2	I	73	ARG	3.0
3	A	352	CYS	3.0
3	B	126	LEU	3.0
2	I	75	THR	3.0
2	G	233	ALA	3.0
3	D	271	GLU	3.0
3	A	276	GLN	3.0
3	C	235	GLY	2.9
2	I	159	HIS	2.9
2	G	241	ASN	2.9
3	A	93	ALA	2.9
2	I	224	ILE	2.9
3	A	254	VAL	2.9
1	F	384	MET	2.9
3	C	301	GLU	2.9
3	D	310	LEU	2.9
1	F	406	ASP	2.9
3	B	252	ASP	2.9
3	C	257	GLU	2.9
3	C	288	GLU	2.9
3	D	74	GLU	2.8
3	B	82	GLN	2.8
2	G	192	ALA	2.8
3	A	221	LEU	2.8
1	F	42	PHE	2.8
3	C	194	GLN	2.8
3	A	149	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
3	A	198	MET	2.7
2	I	193	ALA	2.7
1	H	42	PHE	2.7
3	B	206	VAL	2.7
3	B	363	ARG	2.7
3	A	290	LEU	2.7
3	A	117	VAL	2.7
3	B	350	GLU	2.6
3	B	92	VAL	2.6
1	F	446	LEU	2.6
3	C	79	MET	2.6
1	F	439	ASN	2.6
1	F	274	GLN	2.6
2	I	128	PHE	2.6
3	A	170	VAL	2.6
3	B	293	SER	2.6
3	B	340	GLY	2.6
3	B	213	ALA	2.6
1	F	325	TYR	2.6
1	H	329	SER	2.6
3	B	123	LEU	2.6
3	C	261	PRO	2.6
3	D	89	HIS	2.5
1	H	483	ASP	2.5
3	B	212	VAL	2.5
3	A	229	PHE	2.5
3	C	186	THR	2.5
3	C	267	TRP	2.5
3	C	295	ILE	2.5
3	B	308	GLU	2.5
1	H	340	PHE	2.5
2	G	203	PHE	2.5
3	D	236	SER	2.5
3	A	308	GLU	2.5
2	I	7	LYS	2.5
1	F	278	LEU	2.5
3	B	45	LEU	2.5
3	D	342	THR	2.5
1	F	470	TYR	2.5
2	I	133	ALA	2.5
3	C	279	ALA	2.5
1	F	102	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	H	411	PHE	2.4
3	B	214	GLN	2.4
2	G	204	ARG	2.4
2	I	112	ARG	2.4
3	A	353	HIS	2.4
1	F	382	PRO	2.4
2	I	192	ALA	2.4
3	C	2	ALA	2.4
3	D	50	ALA	2.4
3	D	125	HIS	2.4
3	A	92	VAL	2.4
3	A	336	LEU	2.4
3	C	202	ASP	2.4
3	D	69	ASP	2.4
1	H	350	MET	2.4
3	A	82	GLN	2.4
3	C	122	GLN	2.4
3	A	268	LEU	2.4
3	B	207	LEU	2.4
1	H	369	ARG	2.4
3	D	80	VAL	2.4
1	H	376	ASN	2.3
2	G	41	GLN	2.3
1	F	304	CYS	2.3
2	I	225	ALA	2.3
3	A	151	GLU	2.3
3	A	249	THR	2.3
3	B	79	MET	2.3
3	C	349	PRO	2.3
3	A	50	ALA	2.3
1	H	449	ASN	2.3
3	B	156	LEU	2.3
3	C	173	ARG	2.3
3	A	266	VAL	2.3
1	H	514	ASP	2.3
3	C	185	ARG	2.3
2	I	5	GLN	2.3
3	A	259	PRO	2.2
2	G	232	VAL	2.2
2	G	120	THR	2.2
3	A	2	ALA	2.2
3	B	88	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
3	A	44	THR	2.2
3	B	273	ARG	2.2
2	G	220	ILE	2.2
3	A	299	ILE	2.2
1	H	356	GLY	2.2
2	G	176	THR	2.2
3	B	101	LYS	2.2
3	A	114	VAL	2.2
3	D	302	GLY	2.2
1	H	373	ILE	2.2
1	F	474	ILE	2.2
3	C	299	ILE	2.2
3	B	28	GLU	2.2
3	D	339	GLU	2.2
1	F	372	LEU	2.1
1	H	492	THR	2.1
3	C	247	THR	2.1
3	B	27	HIS	2.1
1	F	309	GLU	2.1
3	A	271	GLU	2.1
1	F	395	ILE	2.1
2	G	206	VAL	2.1
3	A	122	GLN	2.1
2	G	202	ALA	2.1
3	B	210	GLY	2.1
3	B	303	GLU	2.1
3	B	121	LEU	2.1
3	B	362	CYS	2.1
3	C	179	LEU	2.1
3	D	241	PHE	2.1
2	I	205	LEU	2.1
3	A	270	VAL	2.1
2	I	254	ASN	2.1
2	I	182	GLU	2.1
3	C	175	GLU	2.1
1	F	437	ASN	2.1
1	H	354	LEU	2.1
1	H	451	GLY	2.1
3	A	179	LEU	2.1
3	A	300	LEU	2.1
3	B	77	VAL	2.1
3	B	286	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	325	TYR	2.1
3	A	126	LEU	2.1
3	B	181	LYS	2.1
3	B	217	LYS	2.1
3	B	192	HIS	2.1
2	I	37	ILE	2.1
3	C	250	ALA	2.1
3	D	13	TRP	2.1
2	I	136	SER	2.1
3	D	330	ARG	2.0
2	I	285	LEU	2.0
3	A	285	ILE	2.0
3	B	353	HIS	2.0
1	F	449	ASN	2.0
3	D	280	ASN	2.0
1	H	292	VAL	2.0
1	H	319	VAL	2.0
3	A	52	LEU	2.0
3	C	195	VAL	2.0
3	A	100	LEU	2.0
1	H	400	TYR	2.0
3	B	34	PHE	2.0
3	D	144	ILE	2.0
3	B	289	HIS	2.0
3	B	348	PRO	2.0
3	C	218	PRO	2.0
1	F	307	GLN	2.0
3	B	96	MET	2.0
3	B	264	GLN	2.0
3	D	275	VAL	2.0
3	D	307	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no 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.