



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:36 AM UTC

PDB ID : 1KPK / pdb_00001kpk
Title : Crystal Structure of the ClC Chloride Channel from E. coli
Authors : Dutzler, R.; Campbell, E.B.; Cadene, M.; Chait, B.T.; MacKinnon, R.
Deposited on : 2001-12-31
Resolution : 3.50 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

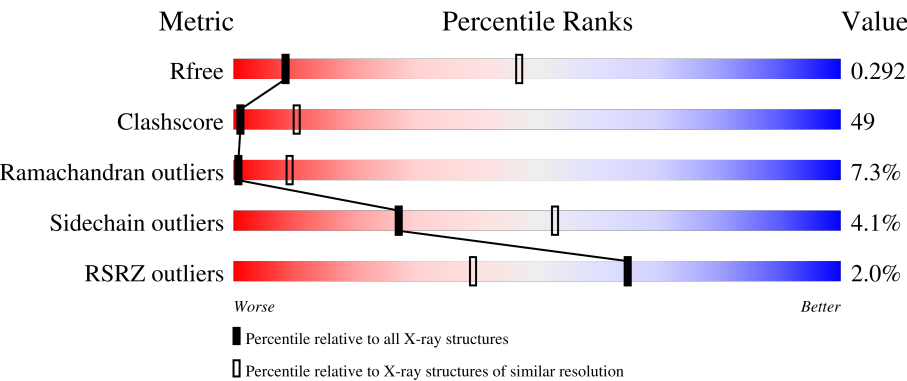
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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

Mol	Chain	Length	Quality of chain
1	A	473	2% 35% 50% 9% • 5%
1	B	473	3% 35% 50% 9% • 5%
1	C	473	2% 35% 50% 9% • 5%
1	D	473	% 37% 49% 9% • 5%
1	E	473	2% 35% 50% 9% • 5%

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Mol	Chain	Length	Quality of chain
1	F	473	2% 36% 49% 9% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 20274 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.

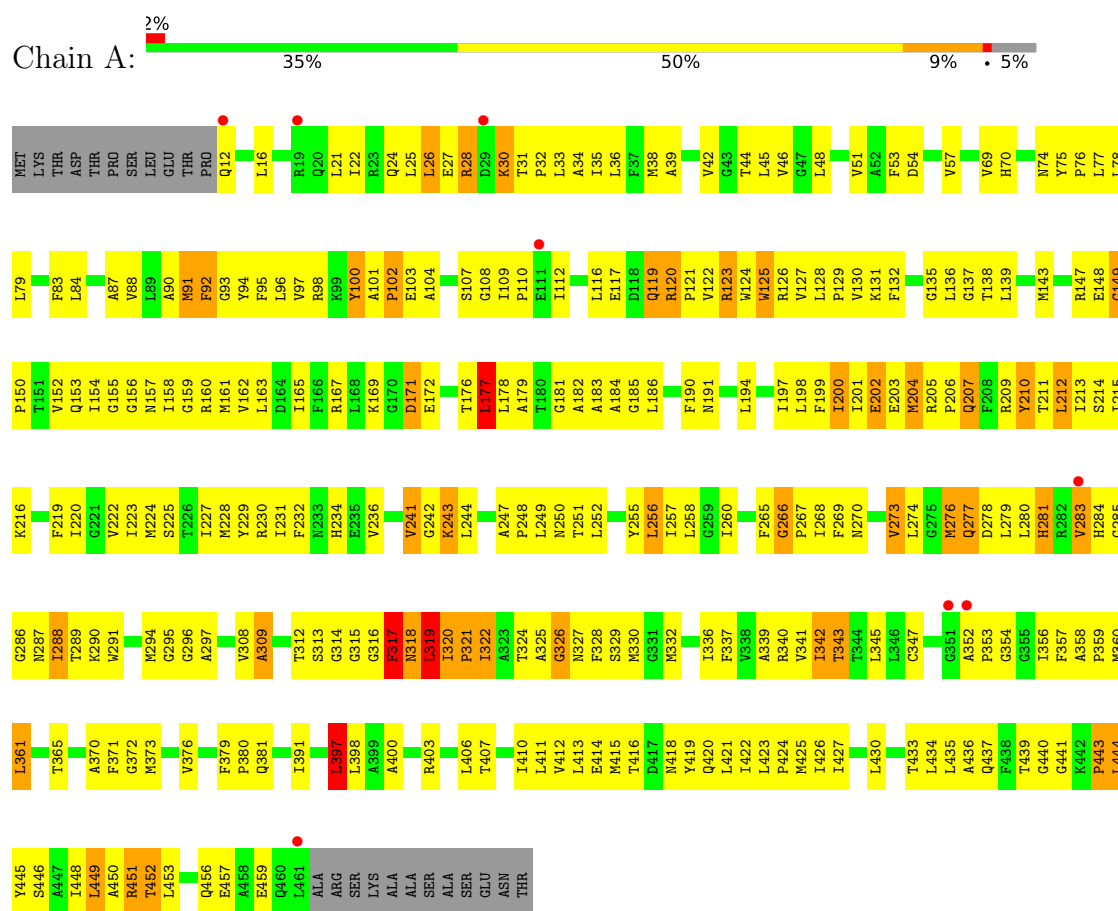
- Molecule 1 is a protein called putative channel transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			
1	B	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			
1	C	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			
1	D	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			
1	E	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			
1	F	450	Total	C	N	O	S	0	0	0
			3379	2219	570	570	20			

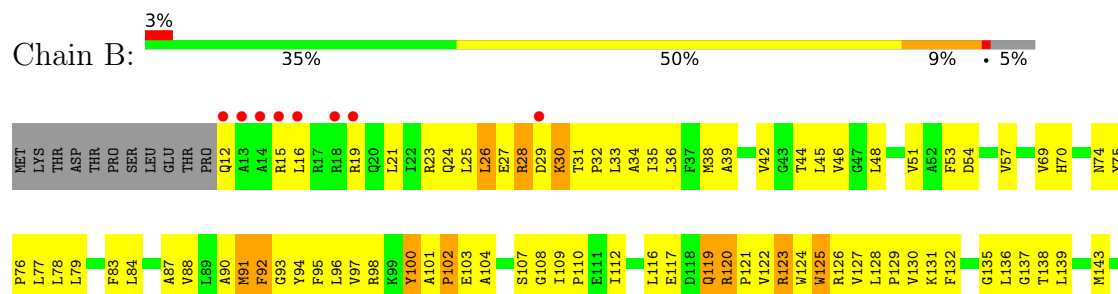
3 Residue-property plots

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.

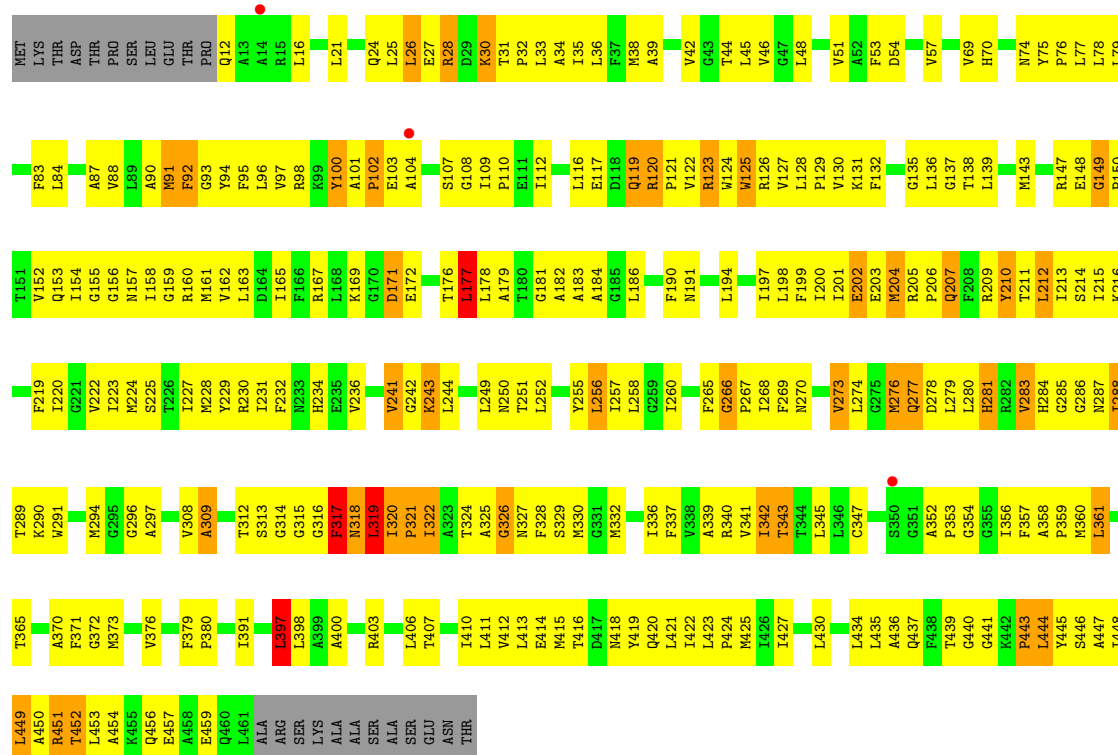
- Molecule 1: putative channel transporter



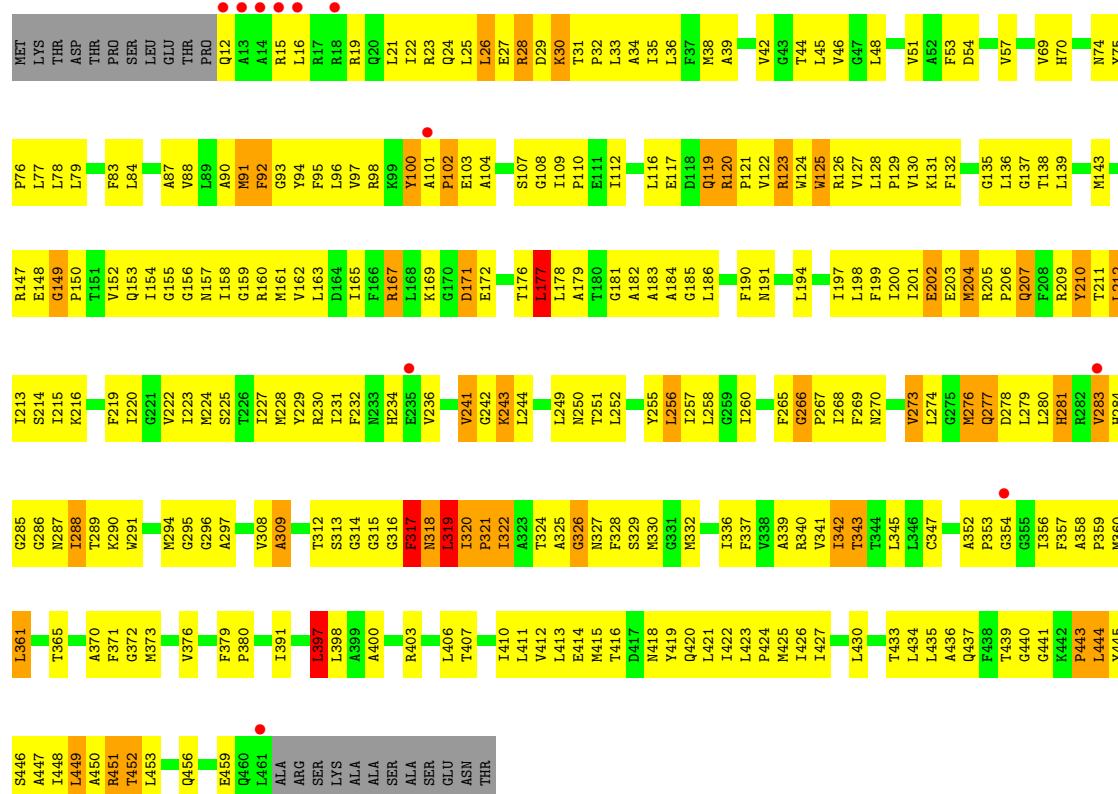
- Molecule 1: putative channel transporter



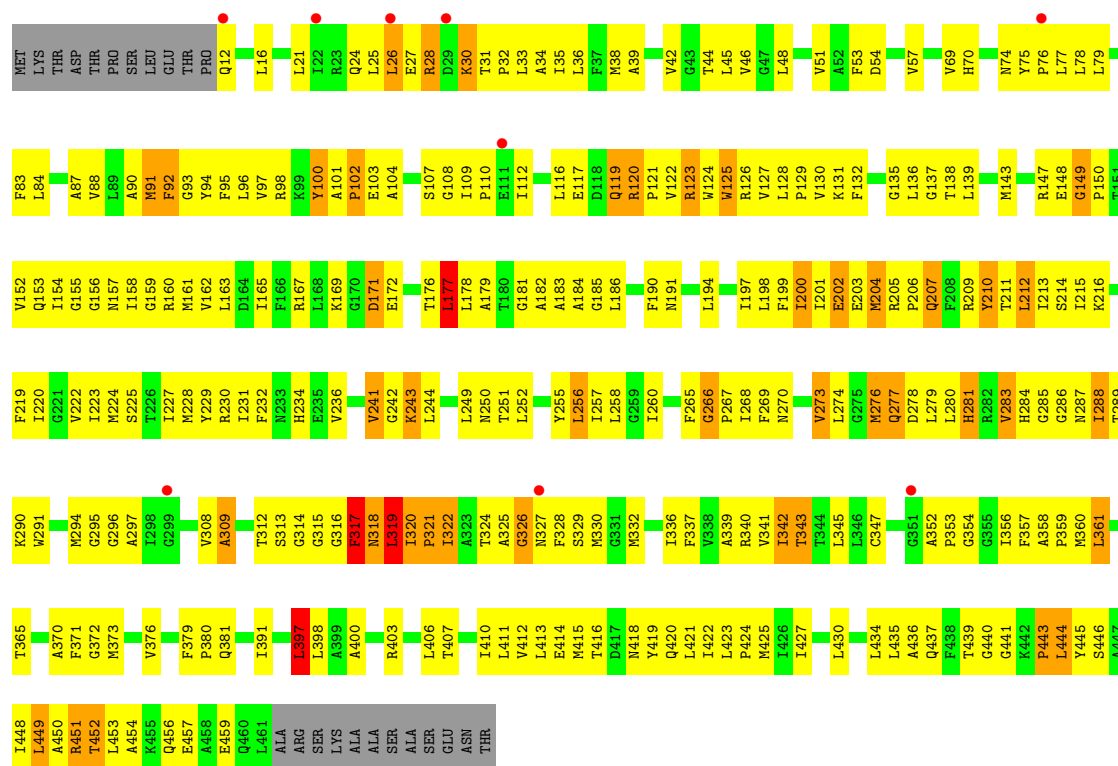




• Molecule 1: putative channel transporter



● Molecule 1: putative channel transporter



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.66Å 152.53Å 263.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.50 20.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-3.50) 98.8 (20.00-3.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 3.52Å)	Xtriage
Refinement program	CNS 0.3	Depositor
R, R_{free}	0.290 , 0.301 0.285 , 0.292	Depositor DCC
R_{free} test set	5321 reflections (9.90%)	wwPDB-VP
Wilson B-factor (Å ²)	125.9	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	20274	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.85% 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 i

5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
1	B	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
1	C	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
1	D	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
1	E	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
1	F	0.62	1/3451 (0.0%)	1.16	30/4683 (0.6%)
All	All	0.62	6/20706 (0.0%)	1.16	180/28098 (0.6%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	276	MET	SD-CE	5.45	1.93	1.79
1	C	276	MET	SD-CE	5.43	1.93	1.79
1	E	276	MET	SD-CE	5.42	1.93	1.79
1	F	276	MET	SD-CE	5.42	1.93	1.79
1	A	276	MET	SD-CE	5.42	1.93	1.79
1	B	276	MET	SD-CE	5.39	1.93	1.79

All (180) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	456	GLN	N-CA-C	-8.81	103.04	113.88
1	F	456	GLN	N-CA-C	-8.80	103.06	113.88
1	A	456	GLN	N-CA-C	-8.77	103.10	113.88
1	C	456	GLN	N-CA-C	-8.75	103.12	113.88
1	B	456	GLN	N-CA-C	-8.74	103.13	113.88
1	D	456	GLN	N-CA-C	-8.74	103.13	113.88
1	C	277	GLN	N-CA-C	-8.65	102.64	113.02
1	E	277	GLN	N-CA-C	-8.65	102.64	113.02
1	A	277	GLN	N-CA-C	-8.63	102.66	113.02
1	B	277	GLN	N-CA-C	-8.62	102.68	113.02
1	D	277	GLN	N-CA-C	-8.62	102.68	113.02
1	F	277	GLN	N-CA-C	-8.61	102.69	113.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	202	GLU	N-CA-C	-8.50	104.03	114.75
1	A	202	GLU	N-CA-C	-8.49	104.05	114.75
1	B	202	GLU	N-CA-C	-8.48	104.06	114.75
1	D	202	GLU	N-CA-C	-8.48	104.07	114.75
1	E	202	GLU	N-CA-C	-8.48	104.07	114.75
1	C	202	GLU	N-CA-C	-8.44	104.12	114.75
1	D	320	ILE	N-CA-C	8.44	127.11	108.88
1	F	320	ILE	N-CA-C	8.44	127.11	108.88
1	A	320	ILE	N-CA-C	8.44	127.10	108.88
1	C	320	ILE	N-CA-C	8.42	127.06	108.88
1	B	320	ILE	N-CA-C	8.41	127.06	108.88
1	E	320	ILE	N-CA-C	8.41	127.05	108.88
1	F	327	ASN	N-CA-C	7.55	126.87	110.80
1	B	327	ASN	N-CA-C	7.54	126.87	110.80
1	A	327	ASN	N-CA-C	7.54	126.85	110.80
1	C	327	ASN	N-CA-C	7.54	126.85	110.80
1	E	327	ASN	N-CA-C	7.53	126.84	110.80
1	D	327	ASN	N-CA-C	7.52	126.82	110.80
1	D	70	HIS	N-CA-C	-7.48	102.05	112.45
1	C	70	HIS	N-CA-C	-7.47	102.07	112.45
1	E	70	HIS	N-CA-C	-7.47	102.07	112.45
1	B	70	HIS	N-CA-C	-7.45	102.09	112.45
1	F	70	HIS	N-CA-C	-7.45	102.09	112.45
1	A	70	HIS	N-CA-C	-7.45	102.10	112.45
1	C	309	ALA	CA-C-N	7.32	126.95	119.56
1	C	309	ALA	C-N-CA	7.32	126.95	119.56
1	E	309	ALA	CA-C-N	7.29	126.92	119.56
1	E	309	ALA	C-N-CA	7.29	126.92	119.56
1	D	309	ALA	CA-C-N	7.29	126.92	119.56
1	D	309	ALA	C-N-CA	7.29	126.92	119.56
1	B	309	ALA	CA-C-N	7.28	126.92	119.56
1	B	309	ALA	C-N-CA	7.28	126.92	119.56
1	A	309	ALA	CA-C-N	7.28	126.91	119.56
1	A	309	ALA	C-N-CA	7.28	126.91	119.56
1	F	309	ALA	CA-C-N	7.24	126.88	119.56
1	F	309	ALA	C-N-CA	7.24	126.88	119.56
1	E	100	TYR	N-CA-C	7.15	122.10	113.23
1	B	100	TYR	N-CA-C	7.13	122.08	113.23
1	C	100	TYR	N-CA-C	7.13	122.07	113.23
1	A	100	TYR	N-CA-C	7.12	122.06	113.23
1	F	100	TYR	N-CA-C	7.11	122.05	113.23
1	D	100	TYR	N-CA-C	7.09	122.02	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	241	VAL	N-CA-C	-6.75	98.46	108.85
1	A	241	VAL	N-CA-C	-6.74	98.47	108.85
1	E	241	VAL	N-CA-C	-6.74	98.47	108.85
1	C	241	VAL	N-CA-C	-6.72	98.49	108.85
1	F	437	GLN	N-CA-C	-6.72	103.99	112.93
1	D	437	GLN	N-CA-C	-6.72	103.99	112.93
1	D	241	VAL	N-CA-C	-6.72	98.51	108.85
1	B	437	GLN	N-CA-C	-6.71	104.00	112.93
1	B	241	VAL	N-CA-C	-6.71	98.52	108.85
1	A	437	GLN	N-CA-C	-6.71	104.01	112.93
1	E	437	GLN	N-CA-C	-6.69	104.03	112.93
1	C	437	GLN	N-CA-C	-6.69	104.03	112.93
1	D	243	LYS	N-CA-C	-6.62	98.92	109.59
1	F	243	LYS	N-CA-C	-6.62	98.92	109.59
1	E	243	LYS	N-CA-C	-6.62	98.93	109.59
1	A	243	LYS	N-CA-C	-6.62	98.94	109.59
1	B	243	LYS	N-CA-C	-6.62	98.94	109.59
1	C	243	LYS	N-CA-C	-6.60	98.96	109.59
1	F	207	GLN	N-CA-C	6.53	121.39	113.17
1	C	207	GLN	N-CA-C	6.51	121.38	113.17
1	B	207	GLN	N-CA-C	6.50	121.36	113.17
1	E	207	GLN	N-CA-C	6.50	121.36	113.17
1	A	207	GLN	N-CA-C	6.50	121.36	113.17
1	D	207	GLN	N-CA-C	6.49	121.34	113.17
1	F	28	ARG	N-CA-C	6.38	118.54	110.24
1	A	28	ARG	N-CA-C	6.35	118.49	110.24
1	B	28	ARG	N-CA-C	6.35	118.49	110.24
1	E	28	ARG	N-CA-C	6.34	118.49	110.24
1	D	28	ARG	N-CA-C	6.34	118.48	110.24
1	C	28	ARG	N-CA-C	6.34	118.48	110.24
1	D	171	ASP	N-CA-C	-6.33	104.25	112.23
1	B	171	ASP	N-CA-C	-6.32	104.26	112.23
1	C	171	ASP	N-CA-C	-6.32	104.27	112.23
1	A	171	ASP	N-CA-C	-6.32	104.27	112.23
1	E	171	ASP	N-CA-C	-6.31	104.28	112.23
1	F	171	ASP	N-CA-C	-6.30	104.29	112.23
1	C	256	LEU	N-CA-C	-6.04	104.62	111.14
1	A	256	LEU	N-CA-C	-6.00	104.66	111.14
1	E	256	LEU	N-CA-C	-5.99	104.67	111.14
1	B	256	LEU	N-CA-C	-5.98	104.68	111.14
1	F	256	LEU	N-CA-C	-5.96	104.70	111.14
1	D	256	LEU	N-CA-C	-5.96	104.70	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	361	LEU	N-CA-C	-5.83	104.29	111.40
1	F	163	LEU	N-CA-C	-5.82	104.53	111.69
1	D	361	LEU	N-CA-C	-5.81	104.31	111.40
1	F	361	LEU	N-CA-C	-5.81	104.31	111.40
1	E	361	LEU	N-CA-C	-5.81	104.31	111.40
1	A	361	LEU	N-CA-C	-5.81	104.32	111.40
1	C	163	LEU	N-CA-C	-5.81	104.55	111.69
1	A	163	LEU	N-CA-C	-5.80	104.56	111.69
1	D	163	LEU	N-CA-C	-5.79	104.56	111.69
1	E	163	LEU	N-CA-C	-5.78	104.58	111.69
1	B	163	LEU	N-CA-C	-5.78	104.58	111.69
1	B	361	LEU	N-CA-C	-5.77	104.36	111.40
1	B	397	LEU	N-CA-C	-5.72	104.96	111.14
1	D	397	LEU	N-CA-C	-5.71	104.97	111.14
1	C	397	LEU	N-CA-C	-5.71	104.97	111.14
1	A	397	LEU	N-CA-C	-5.71	104.98	111.14
1	E	397	LEU	N-CA-C	-5.69	105.00	111.14
1	F	397	LEU	N-CA-C	-5.68	105.01	111.14
1	D	449	LEU	N-CA-C	-5.65	105.04	111.14
1	F	449	LEU	N-CA-C	-5.64	105.05	111.14
1	E	449	LEU	N-CA-C	-5.62	105.07	111.14
1	A	449	LEU	N-CA-C	-5.62	105.07	111.14
1	C	449	LEU	N-CA-C	-5.61	105.08	111.14
1	B	449	LEU	N-CA-C	-5.61	105.08	111.14
1	C	380	PRO	N-CA-C	-5.40	107.72	114.20
1	F	117	GLU	N-CA-C	-5.40	106.70	113.72
1	B	380	PRO	N-CA-C	-5.39	107.73	114.20
1	A	380	PRO	N-CA-C	-5.39	107.73	114.20
1	D	380	PRO	N-CA-C	-5.39	107.73	114.20
1	E	380	PRO	N-CA-C	-5.38	107.75	114.20
1	F	380	PRO	N-CA-C	-5.36	107.76	114.20
1	C	117	GLU	N-CA-C	-5.36	106.75	113.72
1	A	117	GLU	N-CA-C	-5.36	106.75	113.72
1	B	117	GLU	N-CA-C	-5.35	106.76	113.72
1	C	439	THR	N-CA-C	-5.35	105.40	112.94
1	D	117	GLU	N-CA-C	-5.35	106.77	113.72
1	E	439	THR	N-CA-C	-5.35	105.40	112.94
1	A	439	THR	N-CA-C	-5.34	105.41	112.94
1	E	117	GLU	N-CA-C	-5.34	106.78	113.72
1	E	169	LYS	N-CA-C	5.33	117.98	110.14
1	A	169	LYS	N-CA-C	5.33	117.97	110.14
1	C	169	LYS	N-CA-C	5.32	117.97	110.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	169	LYS	N-CA-C	5.32	117.97	110.14
1	B	439	THR	N-CA-C	-5.32	105.44	112.94
1	D	439	THR	N-CA-C	-5.32	105.44	112.94
1	F	169	LYS	N-CA-C	5.32	117.96	110.14
1	F	439	THR	N-CA-C	-5.32	105.44	112.94
1	B	169	LYS	N-CA-C	5.30	117.93	110.14
1	F	266	GLY	CA-C-N	5.25	124.43	118.97
1	F	266	GLY	C-N-CA	5.25	124.43	118.97
1	E	266	GLY	CA-C-N	5.24	124.42	118.97
1	E	266	GLY	C-N-CA	5.24	124.42	118.97
1	C	266	GLY	CA-C-N	5.21	124.39	118.97
1	C	266	GLY	C-N-CA	5.21	124.39	118.97
1	A	266	GLY	CA-C-N	5.21	124.39	118.97
1	A	266	GLY	C-N-CA	5.21	124.39	118.97
1	B	266	GLY	CA-C-N	5.20	124.38	118.97
1	B	266	GLY	C-N-CA	5.20	124.38	118.97
1	E	403	ARG	N-CA-C	5.17	118.46	111.17
1	D	403	ARG	N-CA-C	5.16	118.44	111.17
1	D	266	GLY	CA-C-N	5.15	124.33	118.97
1	D	266	GLY	C-N-CA	5.15	124.33	118.97
1	E	441	GLY	N-CA-C	-5.15	103.50	112.06
1	C	403	ARG	N-CA-C	5.15	118.43	111.17
1	A	403	ARG	N-CA-C	5.15	118.43	111.17
1	B	403	ARG	N-CA-C	5.14	118.42	111.17
1	D	39	ALA	N-CA-C	-5.14	105.80	111.71
1	A	441	GLY	N-CA-C	-5.14	103.53	112.06
1	B	441	GLY	N-CA-C	-5.13	103.54	112.06
1	A	39	ALA	N-CA-C	-5.13	105.81	111.71
1	C	39	ALA	N-CA-C	-5.13	105.81	111.71
1	F	403	ARG	N-CA-C	5.13	118.40	111.17
1	F	441	GLY	N-CA-C	-5.12	103.56	112.06
1	D	441	GLY	N-CA-C	-5.12	103.56	112.06
1	C	441	GLY	N-CA-C	-5.11	103.57	112.06
1	E	39	ALA	N-CA-C	-5.11	105.83	111.71
1	B	39	ALA	N-CA-C	-5.11	105.84	111.71
1	F	39	ALA	N-CA-C	-5.11	105.84	111.71
1	D	281	HIS	N-CA-C	-5.10	106.91	113.23
1	C	281	HIS	N-CA-C	-5.08	106.94	113.23
1	F	281	HIS	N-CA-C	-5.06	106.95	113.23
1	E	281	HIS	N-CA-C	-5.06	106.96	113.23
1	A	281	HIS	N-CA-C	-5.05	106.97	113.23
1	B	281	HIS	N-CA-C	-5.02	107.01	113.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3379	0	3537	369	0
1	B	3379	0	3537	374	52
1	C	3379	0	3537	371	1
1	D	3379	0	3537	374	4
1	E	3379	0	3537	364	49
1	F	3379	0	3537	369	0
All	All	20274	0	21222	2048	53

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 49.

All (2048) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:THR:HG23	1:D:228:MET:HE3	1.37	1.07
1:B:44:THR:HG23	1:B:228:MET:HE3	1.37	1.06
1:D:200:ILE:HD13	1:D:204:MET:HG3	1.38	1.06
1:B:200:ILE:HD13	1:B:204:MET:HG3	1.38	1.05
1:F:200:ILE:HD13	1:F:204:MET:HG3	1.38	1.05
1:E:200:ILE:HD13	1:E:204:MET:HG3	1.38	1.05
1:E:44:THR:HG23	1:E:228:MET:HE3	1.37	1.05
1:A:44:THR:HG23	1:A:228:MET:HE3	1.37	1.03
1:F:322:ILE:N	1:F:322:ILE:HD12	1.74	1.03
1:C:44:THR:HG23	1:C:228:MET:HE3	1.37	1.02
1:C:322:ILE:N	1:C:322:ILE:HD12	1.74	1.02
1:A:200:ILE:HD13	1:A:204:MET:HG3	1.38	1.01
1:A:322:ILE:N	1:A:322:ILE:HD12	1.74	1.01
1:D:322:ILE:HD12	1:D:322:ILE:N	1.74	1.01
1:B:322:ILE:HD12	1:B:322:ILE:N	1.74	1.01
1:E:322:ILE:HD12	1:E:322:ILE:N	1.74	1.01
1:C:200:ILE:HD13	1:C:204:MET:HG3	1.38	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:44:THR:HG23	1:F:228:MET:HE3	1.37	1.00
1:A:120:ARG:NH1	1:A:120:ARG:HB3	1.80	0.96
1:E:120:ARG:HB3	1:E:120:ARG:NH1	1.80	0.96
1:F:322:ILE:HD12	1:F:322:ILE:H	1.30	0.96
1:C:120:ARG:NH1	1:C:120:ARG:HB3	1.80	0.96
1:F:120:ARG:HB3	1:F:120:ARG:HH11	1.31	0.95
1:B:120:ARG:HB3	1:B:120:ARG:NH1	1.80	0.95
1:D:120:ARG:HB3	1:D:120:ARG:NH1	1.80	0.95
1:F:120:ARG:HB3	1:F:120:ARG:NH1	1.80	0.95
1:B:322:ILE:HD12	1:B:322:ILE:H	1.29	0.94
1:E:430:LEU:HD21	1:F:220:ILE:HG12	1.48	0.94
1:C:322:ILE:HD12	1:C:322:ILE:H	1.29	0.93
1:C:430:LEU:HD21	1:D:220:ILE:HG12	1.48	0.93
1:D:322:ILE:HD12	1:D:322:ILE:H	1.30	0.93
1:E:120:ARG:HB3	1:E:120:ARG:HH11	1.31	0.93
1:B:120:ARG:HB3	1:B:120:ARG:HH11	1.31	0.93
1:A:430:LEU:HD21	1:B:220:ILE:HG12	1.48	0.93
1:D:120:ARG:HB3	1:D:120:ARG:HH11	1.31	0.93
1:A:322:ILE:HD12	1:A:322:ILE:H	1.29	0.92
1:A:120:ARG:HB3	1:A:120:ARG:HH11	1.31	0.92
1:E:104:ALA:HB1	1:E:131:LYS:HD3	1.52	0.92
1:C:104:ALA:HB1	1:C:131:LYS:HD3	1.52	0.91
1:F:104:ALA:HB1	1:F:131:LYS:HD3	1.52	0.91
1:D:123:ARG:HH11	1:D:123:ARG:H	0.91	0.91
1:C:120:ARG:HB3	1:C:120:ARG:HH11	1.31	0.91
1:A:104:ALA:HB1	1:A:131:LYS:HD3	1.52	0.91
1:B:123:ARG:HH11	1:B:123:ARG:H	0.91	0.91
1:B:104:ALA:HB1	1:B:131:LYS:HD3	1.52	0.90
1:D:104:ALA:HB1	1:D:131:LYS:HD3	1.52	0.89
1:E:322:ILE:HD12	1:E:322:ILE:H	1.29	0.89
1:F:451:ARG:HB3	1:F:451:ARG:HH11	1.38	0.89
1:B:451:ARG:HB3	1:B:451:ARG:HH11	1.38	0.88
1:F:123:ARG:HH11	1:F:123:ARG:H	0.91	0.88
1:D:451:ARG:HB3	1:D:451:ARG:HH11	1.38	0.88
1:C:317:PHE:HA	1:C:321:PRO:CD	2.03	0.88
1:C:451:ARG:HB3	1:C:451:ARG:HH11	1.38	0.88
1:E:337:PHE:O	1:E:341:VAL:HG23	1.74	0.88
1:A:317:PHE:HA	1:A:321:PRO:CD	2.04	0.88
1:C:123:ARG:HH11	1:C:123:ARG:H	0.91	0.88
1:A:123:ARG:HH11	1:A:123:ARG:H	0.91	0.87
1:C:337:PHE:O	1:C:341:VAL:HG23	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:PHE:HA	1:F:321:PRO:CD	2.04	0.87
1:A:451:ARG:HB3	1:A:451:ARG:HH11	1.38	0.87
1:D:317:PHE:HA	1:D:321:PRO:CD	2.04	0.87
1:A:337:PHE:O	1:A:341:VAL:HG23	1.74	0.87
1:B:317:PHE:HA	1:B:321:PRO:CD	2.04	0.87
1:F:337:PHE:O	1:F:341:VAL:HG23	1.74	0.87
1:E:123:ARG:HH11	1:E:123:ARG:H	0.91	0.86
1:E:317:PHE:HA	1:E:321:PRO:CD	2.04	0.86
1:E:451:ARG:HB3	1:E:451:ARG:HH11	1.38	0.86
1:E:31:THR:HG21	1:E:36:LEU:HD21	1.58	0.86
1:F:87:ALA:O	1:F:91:MET:HG2	1.76	0.86
1:D:337:PHE:O	1:D:341:VAL:HG23	1.74	0.86
1:B:337:PHE:O	1:B:341:VAL:HG23	1.74	0.85
1:D:87:ALA:O	1:D:91:MET:HG2	1.76	0.85
1:A:31:THR:HG21	1:A:36:LEU:HD21	1.58	0.85
1:C:87:ALA:O	1:C:91:MET:HG2	1.76	0.85
1:E:87:ALA:O	1:E:91:MET:HG2	1.76	0.85
1:E:183:ALA:HB2	1:E:200:ILE:HG13	1.59	0.85
1:F:31:THR:HG21	1:F:36:LEU:HD21	1.58	0.85
1:F:183:ALA:HB2	1:F:200:ILE:HG13	1.59	0.85
1:B:87:ALA:O	1:B:91:MET:HG2	1.76	0.85
1:C:31:THR:HG21	1:C:36:LEU:HD21	1.58	0.84
1:E:317:PHE:HA	1:E:321:PRO:HD3	1.60	0.84
1:A:87:ALA:O	1:A:91:MET:HG2	1.76	0.84
1:D:421:LEU:O	1:D:425:MET:HG3	1.77	0.84
1:F:421:LEU:O	1:F:425:MET:HG3	1.77	0.84
1:B:421:LEU:O	1:B:425:MET:HG3	1.77	0.84
1:A:183:ALA:HB2	1:A:200:ILE:HG13	1.59	0.84
1:E:421:LEU:O	1:E:425:MET:HG3	1.77	0.84
1:C:183:ALA:HB2	1:C:200:ILE:HG13	1.59	0.84
1:C:421:LEU:O	1:C:425:MET:HG3	1.77	0.84
1:F:317:PHE:HA	1:F:321:PRO:HD3	1.60	0.83
1:A:421:LEU:O	1:A:425:MET:HG3	1.77	0.83
1:C:317:PHE:HA	1:C:321:PRO:HD3	1.60	0.83
1:B:183:ALA:HB2	1:B:200:ILE:HG13	1.59	0.83
1:D:183:ALA:HB2	1:D:200:ILE:HG13	1.59	0.83
1:A:317:PHE:HA	1:A:321:PRO:HD3	1.60	0.83
1:D:31:THR:HG21	1:D:36:LEU:HD21	1.58	0.83
1:E:336:ILE:O	1:E:340:ARG:HG3	1.79	0.82
1:B:31:THR:HG21	1:B:36:LEU:HD21	1.58	0.82
1:D:336:ILE:O	1:D:340:ARG:HG3	1.79	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:123:ARG:HH11	1:E:123:ARG:N	1.76	0.82
1:F:336:ILE:O	1:F:340:ARG:HG3	1.79	0.82
1:B:336:ILE:O	1:B:340:ARG:HG3	1.79	0.82
1:C:211:THR:HG22	1:C:212:LEU:H	1.44	0.82
1:A:211:THR:HG22	1:A:212:LEU:H	1.45	0.81
1:C:336:ILE:O	1:C:340:ARG:HG3	1.79	0.81
1:D:317:PHE:HA	1:D:321:PRO:HD3	1.60	0.81
1:A:336:ILE:O	1:A:340:ARG:HG3	1.79	0.81
1:E:211:THR:HG22	1:E:212:LEU:H	1.45	0.81
1:A:324:THR:C	1:A:326:GLY:H	1.89	0.81
1:B:317:PHE:HA	1:B:321:PRO:HD3	1.60	0.81
1:B:211:THR:HG22	1:B:212:LEU:H	1.45	0.81
1:E:324:THR:C	1:E:326:GLY:H	1.89	0.80
1:B:98:ARG:HH21	1:B:102:PRO:HB3	1.46	0.80
1:D:98:ARG:HH21	1:D:102:PRO:HB3	1.46	0.80
1:D:211:THR:HG22	1:D:212:LEU:H	1.45	0.80
1:F:98:ARG:HH21	1:F:102:PRO:HB3	1.46	0.80
1:C:324:THR:C	1:C:326:GLY:H	1.89	0.80
1:B:123:ARG:H	1:B:123:ARG:NH1	1.77	0.80
1:A:123:ARG:HH11	1:A:123:ARG:N	1.76	0.80
1:F:211:THR:HG22	1:F:212:LEU:H	1.44	0.80
1:C:98:ARG:HH21	1:C:102:PRO:HB3	1.46	0.79
1:D:123:ARG:H	1:D:123:ARG:NH1	1.77	0.79
1:A:98:ARG:HH21	1:A:102:PRO:HB3	1.46	0.79
1:C:123:ARG:HH11	1:C:123:ARG:N	1.76	0.79
1:B:324:THR:C	1:B:326:GLY:H	1.89	0.79
1:E:123:ARG:H	1:E:123:ARG:NH1	1.77	0.79
1:A:322:ILE:H	1:A:322:ILE:CD1	1.96	0.78
1:D:324:THR:C	1:D:326:GLY:H	1.89	0.78
1:E:98:ARG:HH21	1:E:102:PRO:HB3	1.46	0.78
1:F:324:THR:C	1:F:326:GLY:H	1.89	0.78
1:A:227:ILE:O	1:A:231:ILE:HG12	1.84	0.78
1:C:322:ILE:H	1:C:322:ILE:CD1	1.96	0.78
1:E:227:ILE:O	1:E:231:ILE:HG12	1.84	0.78
1:C:227:ILE:O	1:C:231:ILE:HG12	1.84	0.78
1:D:227:ILE:O	1:D:231:ILE:HG12	1.84	0.78
1:F:123:ARG:HH11	1:F:123:ARG:N	1.76	0.78
1:B:227:ILE:O	1:B:231:ILE:HG12	1.84	0.78
1:B:123:ARG:HH11	1:B:123:ARG:N	1.76	0.77
1:E:322:ILE:H	1:E:322:ILE:CD1	1.96	0.77
1:E:430:LEU:HD22	1:F:223:ILE:HD12	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:123:ARG:H	1:F:123:ARG:NH1	1.77	0.77
1:F:227:ILE:O	1:F:231:ILE:HG12	1.84	0.77
1:D:138:THR:HG21	1:D:352:ALA:HB1	1.65	0.77
1:B:322:ILE:H	1:B:322:ILE:CD1	1.96	0.77
1:C:430:LEU:HD22	1:D:223:ILE:HD12	1.66	0.77
1:D:322:ILE:H	1:D:322:ILE:CD1	1.96	0.77
1:A:138:THR:HG21	1:A:352:ALA:HB1	1.65	0.77
1:C:138:THR:HG21	1:C:352:ALA:HB1	1.65	0.77
1:D:123:ARG:HH11	1:D:123:ARG:N	1.76	0.77
1:B:138:THR:HG21	1:B:352:ALA:HB1	1.65	0.76
1:F:322:ILE:H	1:F:322:ILE:CD1	1.96	0.76
1:F:138:THR:HG21	1:F:352:ALA:HB1	1.65	0.76
1:A:430:LEU:HD22	1:B:223:ILE:HD12	1.66	0.76
1:C:103:GLU:HB3	1:C:123:ARG:HH21	1.51	0.76
1:A:103:GLU:HB3	1:A:123:ARG:HH21	1.51	0.76
1:E:116:LEU:HD23	1:E:178:LEU:HD23	1.68	0.76
1:E:138:THR:HG21	1:E:352:ALA:HB1	1.65	0.76
1:B:116:LEU:HD23	1:B:178:LEU:HD23	1.68	0.76
1:B:103:GLU:HB3	1:B:123:ARG:HH21	1.51	0.75
1:F:260:ILE:HG23	1:F:435:LEU:HG	1.68	0.75
1:A:260:ILE:HG23	1:A:435:LEU:HG	1.68	0.75
1:E:103:GLU:HB3	1:E:123:ARG:HH21	1.51	0.75
1:D:103:GLU:HB3	1:D:123:ARG:HH21	1.51	0.75
1:D:260:ILE:HG23	1:D:435:LEU:HG	1.68	0.75
1:D:116:LEU:HD23	1:D:178:LEU:HD23	1.68	0.75
1:C:123:ARG:H	1:C:123:ARG:NH1	1.77	0.75
1:C:260:ILE:HG23	1:C:435:LEU:HG	1.69	0.75
1:E:260:ILE:HG23	1:E:435:LEU:HG	1.69	0.75
1:F:116:LEU:HD23	1:F:178:LEU:HD23	1.68	0.75
1:B:260:ILE:HG23	1:B:435:LEU:HG	1.68	0.75
1:C:270:ASN:CG	1:C:444:LEU:HD23	2.12	0.75
1:A:270:ASN:CG	1:A:444:LEU:HD23	2.12	0.75
1:B:98:ARG:HA	1:B:98:ARG:HE	1.52	0.75
1:C:200:ILE:CD1	1:C:204:MET:HG3	2.17	0.75
1:D:98:ARG:HA	1:D:98:ARG:HE	1.52	0.74
1:F:103:GLU:HB3	1:F:123:ARG:HH21	1.51	0.74
1:A:116:LEU:HD23	1:A:178:LEU:HD23	1.68	0.74
1:A:317:PHE:C	1:A:319:LEU:H	1.96	0.74
1:E:270:ASN:CG	1:E:444:LEU:HD23	2.12	0.74
1:C:220:ILE:HG12	1:D:430:LEU:HD21	1.69	0.74
1:C:28:ARG:CZ	1:D:207:GLN:HE22	2.01	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:LEU:HD23	1:C:178:LEU:HD23	1.68	0.74
1:C:317:PHE:C	1:C:319:LEU:H	1.96	0.74
1:C:450:ALA:CB	1:D:26:LEU:HD21	2.17	0.74
1:D:270:ASN:CG	1:D:444:LEU:HD23	2.12	0.74
1:E:28:ARG:CZ	1:F:207:GLN:HE22	2.01	0.74
1:A:220:ILE:HG12	1:B:430:LEU:HD21	1.69	0.74
1:E:98:ARG:HA	1:E:98:ARG:HE	1.52	0.74
1:E:223:ILE:HD12	1:F:430:LEU:HD22	1.69	0.74
1:E:450:ALA:CB	1:F:26:LEU:HD21	2.17	0.74
1:F:98:ARG:HA	1:F:98:ARG:HE	1.52	0.74
1:A:28:ARG:CZ	1:B:207:GLN:HE22	2.01	0.74
1:A:123:ARG:H	1:A:123:ARG:NH1	1.77	0.74
1:A:450:ALA:CB	1:B:26:LEU:HD21	2.17	0.74
1:E:220:ILE:HG12	1:F:430:LEU:HD21	1.69	0.74
1:B:270:ASN:CG	1:B:444:LEU:HD23	2.12	0.74
1:F:270:ASN:CG	1:F:444:LEU:HD23	2.12	0.74
1:D:322:ILE:N	1:D:322:ILE:CD1	2.42	0.74
1:A:98:ARG:HA	1:A:98:ARG:HE	1.52	0.73
1:C:98:ARG:HA	1:C:98:ARG:HE	1.52	0.73
1:F:92:PHE:O	1:F:96:LEU:HD23	1.88	0.73
1:F:317:PHE:C	1:F:319:LEU:H	1.96	0.73
1:D:92:PHE:O	1:D:96:LEU:HD23	1.88	0.73
1:B:92:PHE:O	1:B:96:LEU:HD23	1.88	0.73
1:A:92:PHE:O	1:A:96:LEU:HD23	1.88	0.73
1:E:92:PHE:O	1:E:96:LEU:HD23	1.88	0.73
1:A:223:ILE:CD1	1:B:430:LEU:HD22	2.19	0.73
1:C:223:ILE:CD1	1:D:430:LEU:HD22	2.19	0.72
1:D:317:PHE:C	1:D:319:LEU:H	1.96	0.72
1:E:223:ILE:CD1	1:F:430:LEU:HD22	2.19	0.72
1:A:223:ILE:HD12	1:B:430:LEU:HD22	1.69	0.72
1:C:92:PHE:O	1:C:96:LEU:HD23	1.88	0.72
1:C:223:ILE:HD12	1:D:430:LEU:HD22	1.69	0.72
1:E:317:PHE:C	1:E:319:LEU:H	1.96	0.72
1:C:207:GLN:HE22	1:D:28:ARG:CZ	2.01	0.72
1:E:207:GLN:HE22	1:F:28:ARG:CZ	2.01	0.72
1:A:207:GLN:HE22	1:B:28:ARG:CZ	2.01	0.72
1:F:200:ILE:CD1	1:F:204:MET:HG3	2.17	0.72
1:E:200:ILE:CD1	1:E:204:MET:HG3	2.17	0.71
1:B:317:PHE:C	1:B:319:LEU:H	1.96	0.71
1:E:211:THR:CG2	1:E:213:ILE:HG13	2.20	0.71
1:B:44:THR:O	1:B:48:LEU:HB2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:44:THR:O	1:E:48:LEU:HB2	1.91	0.71
1:F:148:GLU:OE1	1:F:357:PHE:HB3	1.91	0.71
1:D:211:THR:CG2	1:D:213:ILE:HG13	2.20	0.71
1:E:430:LEU:HD22	1:F:223:ILE:CD1	2.21	0.71
1:F:211:THR:CG2	1:F:213:ILE:HG13	2.20	0.71
1:A:148:GLU:OE1	1:A:357:PHE:HB3	1.91	0.71
1:D:44:THR:O	1:D:48:LEU:HB2	1.90	0.71
1:B:148:GLU:OE1	1:B:357:PHE:HB3	1.91	0.71
1:B:211:THR:CG2	1:B:213:ILE:HG13	2.20	0.71
1:C:148:GLU:OE1	1:C:357:PHE:HB3	1.91	0.71
1:A:44:THR:O	1:A:48:LEU:HB2	1.90	0.70
1:F:448:ILE:O	1:F:452:THR:HG22	1.91	0.70
1:C:430:LEU:HD22	1:D:223:ILE:CD1	2.21	0.70
1:F:44:THR:O	1:F:48:LEU:HB2	1.91	0.70
1:D:148:GLU:OE1	1:D:357:PHE:HB3	1.91	0.70
1:A:84:LEU:O	1:A:88:VAL:HG23	1.92	0.70
1:C:211:THR:CG2	1:C:213:ILE:HG13	2.20	0.70
1:A:211:THR:CG2	1:A:213:ILE:HG13	2.20	0.70
1:C:44:THR:O	1:C:48:LEU:HB2	1.91	0.70
1:C:84:LEU:O	1:C:88:VAL:HG23	1.92	0.70
1:E:148:GLU:OE1	1:E:357:PHE:HB3	1.91	0.70
1:A:430:LEU:HD22	1:B:223:ILE:CD1	2.21	0.70
1:E:448:ILE:O	1:E:452:THR:HG22	1.91	0.70
1:A:200:ILE:CD1	1:A:204:MET:HG3	2.17	0.70
1:D:448:ILE:O	1:D:452:THR:HG22	1.91	0.70
1:E:451:ARG:HH11	1:E:451:ARG:CB	2.06	0.69
1:B:84:LEU:O	1:B:88:VAL:HG23	1.92	0.69
1:B:244:LEU:HD12	1:B:244:LEU:N	2.08	0.69
1:B:448:ILE:O	1:B:452:THR:HG22	1.91	0.69
1:C:244:LEU:HD12	1:C:244:LEU:N	2.08	0.69
1:F:84:LEU:O	1:F:88:VAL:HG23	1.92	0.69
1:A:448:ILE:O	1:A:452:THR:HG22	1.91	0.69
1:C:448:ILE:O	1:C:452:THR:HG22	1.91	0.69
1:A:75:TYR:N	1:A:76:PRO:HD2	2.08	0.69
1:C:75:TYR:N	1:C:76:PRO:HD2	2.08	0.69
1:E:84:LEU:O	1:E:88:VAL:HG23	1.92	0.69
1:E:198:LEU:HD21	1:F:198:LEU:HD21	1.75	0.69
1:B:75:TYR:N	1:B:76:PRO:HD2	2.08	0.69
1:B:109:ILE:HD11	1:B:152:VAL:HG21	1.74	0.69
1:D:75:TYR:N	1:D:76:PRO:HD2	2.08	0.69
1:D:84:LEU:O	1:D:88:VAL:HG23	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:LEU:N	1:D:244:LEU:HD12	2.08	0.69
1:A:244:LEU:N	1:A:244:LEU:HD12	2.08	0.69
1:F:75:TYR:N	1:F:76:PRO:HD2	2.08	0.69
1:F:109:ILE:HD11	1:F:152:VAL:HG21	1.73	0.69
1:F:244:LEU:N	1:F:244:LEU:HD12	2.08	0.69
1:C:109:ILE:HD11	1:C:152:VAL:HG21	1.74	0.69
1:D:109:ILE:HD11	1:D:152:VAL:HG21	1.74	0.69
1:E:281:HIS:HA	1:E:284:HIS:NE2	2.09	0.68
1:A:281:HIS:HA	1:A:284:HIS:NE2	2.09	0.68
1:A:451:ARG:HH11	1:A:451:ARG:CB	2.05	0.68
1:C:451:ARG:HH11	1:C:451:ARG:CB	2.05	0.68
1:D:281:HIS:HA	1:D:284:HIS:NE2	2.09	0.68
1:A:109:ILE:HD11	1:A:152:VAL:HG21	1.74	0.68
1:B:281:HIS:HA	1:B:284:HIS:NE2	2.09	0.68
1:F:281:HIS:HA	1:F:284:HIS:NE2	2.09	0.68
1:E:75:TYR:N	1:E:76:PRO:HD2	2.08	0.68
1:C:281:HIS:HA	1:C:284:HIS:NE2	2.09	0.68
1:D:200:ILE:CD1	1:D:204:MET:HG3	2.17	0.68
1:D:251:THR:HG22	1:D:255:TYR:HE1	1.59	0.68
1:D:451:ARG:HH11	1:D:451:ARG:CB	2.06	0.68
1:E:98:ARG:HH21	1:E:102:PRO:CB	2.07	0.68
1:B:451:ARG:HH11	1:B:451:ARG:CB	2.05	0.68
1:C:30:LYS:NZ	1:C:30:LYS:HB3	2.09	0.68
1:C:251:THR:HG22	1:C:255:TYR:HE1	1.59	0.68
1:E:244:LEU:HD12	1:E:244:LEU:N	2.08	0.68
1:F:451:ARG:HH11	1:F:451:ARG:CB	2.05	0.68
1:A:30:LYS:NZ	1:A:30:LYS:HB3	2.09	0.68
1:A:98:ARG:HH21	1:A:102:PRO:CB	2.07	0.68
1:B:200:ILE:CD1	1:B:204:MET:HG3	2.17	0.68
1:B:30:LYS:HB3	1:B:30:LYS:NZ	2.09	0.68
1:B:98:ARG:HH21	1:B:102:PRO:CB	2.07	0.68
1:C:98:ARG:HH21	1:C:102:PRO:CB	2.07	0.68
1:D:98:ARG:HH21	1:D:102:PRO:CB	2.07	0.68
1:E:30:LYS:NZ	1:E:30:LYS:HB3	2.09	0.68
1:F:98:ARG:HH21	1:F:102:PRO:CB	2.07	0.68
1:D:30:LYS:NZ	1:D:30:LYS:HB3	2.09	0.68
1:E:251:THR:HG22	1:E:255:TYR:HE1	1.59	0.68
1:B:251:THR:HG22	1:B:255:TYR:HE1	1.59	0.67
1:E:109:ILE:HD11	1:E:152:VAL:HG21	1.74	0.67
1:F:30:LYS:NZ	1:F:30:LYS:HB3	2.09	0.67
1:F:278:ASP:C	1:F:280:LEU:H	2.03	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:198:LEU:HD21	1:D:198:LEU:HD21	1.75	0.67
1:A:251:THR:HG22	1:A:255:TYR:HE1	1.59	0.67
1:A:198:LEU:HD21	1:B:198:LEU:HD21	1.75	0.67
1:F:251:THR:HG22	1:F:255:TYR:HE1	1.59	0.67
1:D:211:THR:HG22	1:D:212:LEU:N	2.11	0.67
1:B:211:THR:HG22	1:B:212:LEU:N	2.11	0.66
1:C:120:ARG:HH11	1:C:120:ARG:CB	2.07	0.66
1:A:278:ASP:C	1:A:280:LEU:H	2.03	0.66
1:D:161:MET:HE2	1:D:165:ILE:HD11	1.78	0.66
1:F:161:MET:HE2	1:F:165:ILE:HD11	1.78	0.66
1:A:120:ARG:HH11	1:A:120:ARG:CB	2.07	0.66
1:B:161:MET:HE2	1:B:165:ILE:HD11	1.78	0.66
1:D:211:THR:HG22	1:D:213:ILE:HG13	1.78	0.66
1:E:161:MET:HE2	1:E:165:ILE:HD11	1.78	0.66
1:F:317:PHE:O	1:F:319:LEU:N	2.29	0.66
1:E:223:ILE:O	1:E:227:ILE:HG13	1.96	0.66
1:E:211:THR:HG22	1:E:213:ILE:HG13	1.78	0.66
1:E:211:THR:HG22	1:E:212:LEU:N	2.11	0.66
1:B:211:THR:HG22	1:B:213:ILE:HG13	1.78	0.66
1:E:203:GLU:CD	1:F:28:ARG:HH22	2.05	0.66
1:A:203:GLU:CD	1:B:28:ARG:HH22	2.04	0.65
1:A:211:THR:HG22	1:A:212:LEU:N	2.10	0.65
1:C:203:GLU:CD	1:D:28:ARG:HH22	2.05	0.65
1:E:317:PHE:O	1:E:319:LEU:N	2.29	0.65
1:F:273:VAL:HA	1:F:345:LEU:HD22	1.78	0.65
1:C:211:THR:HG22	1:C:212:LEU:N	2.10	0.65
1:E:278:ASP:C	1:E:280:LEU:H	2.03	0.65
1:D:212:LEU:N	1:D:212:LEU:HD12	2.11	0.65
1:C:278:ASP:C	1:C:280:LEU:H	2.03	0.65
1:F:223:ILE:O	1:F:227:ILE:HG13	1.96	0.65
1:A:161:MET:HE2	1:A:165:ILE:HD11	1.78	0.65
1:B:32:PRO:HD2	1:B:35:ILE:HD12	1.79	0.65
1:B:278:ASP:C	1:B:280:LEU:H	2.03	0.65
1:C:273:VAL:HA	1:C:345:LEU:HD22	1.78	0.65
1:D:32:PRO:HD2	1:D:35:ILE:HD12	1.79	0.65
1:D:317:PHE:O	1:D:319:LEU:N	2.29	0.65
1:F:120:ARG:HH11	1:F:120:ARG:CB	2.07	0.65
1:F:411:LEU:HG	1:F:415:MET:HE2	1.79	0.65
1:B:223:ILE:O	1:B:227:ILE:HG13	1.96	0.65
1:B:317:PHE:O	1:B:319:LEU:N	2.29	0.65
1:E:32:PRO:HD2	1:E:35:ILE:HD12	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:212:LEU:HD12	1:F:212:LEU:N	2.11	0.65
1:A:223:ILE:O	1:A:227:ILE:HG13	1.96	0.65
1:C:223:ILE:O	1:C:227:ILE:HG13	1.96	0.65
1:B:212:LEU:N	1:B:212:LEU:HD12	2.11	0.65
1:C:161:MET:HE2	1:C:165:ILE:HD11	1.78	0.65
1:E:317:PHE:HA	1:E:321:PRO:HD2	1.79	0.65
1:A:126:ARG:O	1:A:130:VAL:HG23	1.97	0.65
1:A:212:LEU:N	1:A:212:LEU:HD12	2.11	0.65
1:B:273:VAL:HA	1:B:345:LEU:HD22	1.78	0.65
1:C:126:ARG:O	1:C:130:VAL:HG23	1.97	0.65
1:F:211:THR:HG22	1:F:213:ILE:HG13	1.78	0.65
1:D:223:ILE:O	1:D:227:ILE:HG13	1.96	0.64
1:D:273:VAL:HA	1:D:345:LEU:HD22	1.78	0.64
1:D:278:ASP:C	1:D:280:LEU:H	2.03	0.64
1:D:317:PHE:HA	1:D:321:PRO:HD2	1.79	0.64
1:A:273:VAL:HA	1:A:345:LEU:HD22	1.79	0.64
1:A:317:PHE:O	1:A:319:LEU:N	2.29	0.64
1:B:317:PHE:HA	1:B:321:PRO:HD2	1.79	0.64
1:C:194:LEU:HD13	1:D:410:ILE:HD11	1.79	0.64
1:C:211:THR:HG22	1:C:213:ILE:HG13	1.78	0.64
1:C:212:LEU:N	1:C:212:LEU:HD12	2.11	0.64
1:C:317:PHE:O	1:C:319:LEU:N	2.29	0.64
1:C:324:THR:HG22	1:C:328:PHE:CE2	2.32	0.64
1:D:324:THR:HG22	1:D:328:PHE:CE2	2.33	0.64
1:D:411:LEU:HG	1:D:415:MET:HE2	1.79	0.64
1:E:450:ALA:HB3	1:F:26:LEU:HD21	1.79	0.64
1:A:211:THR:HG22	1:A:213:ILE:HG13	1.78	0.64
1:B:324:THR:HG22	1:B:328:PHE:CE2	2.32	0.64
1:E:411:LEU:HG	1:E:415:MET:HE2	1.79	0.64
1:A:32:PRO:HD2	1:A:35:ILE:HD12	1.79	0.64
1:A:207:GLN:NE2	1:B:28:ARG:CZ	2.61	0.64
1:A:324:THR:HG22	1:A:328:PHE:CE2	2.33	0.64
1:A:411:LEU:HG	1:A:415:MET:HE2	1.79	0.64
1:B:120:ARG:HH11	1:B:120:ARG:CB	2.07	0.64
1:E:120:ARG:HH11	1:E:120:ARG:CB	2.08	0.64
1:F:211:THR:HG22	1:F:212:LEU:N	2.10	0.64
1:A:317:PHE:HA	1:A:321:PRO:HD2	1.79	0.64
1:B:411:LEU:HG	1:B:415:MET:HE2	1.79	0.64
1:C:207:GLN:NE2	1:D:28:ARG:CZ	2.61	0.64
1:C:317:PHE:HA	1:C:321:PRO:HD2	1.79	0.64
1:C:411:LEU:HG	1:C:415:MET:HE2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:32:PRO:HD2	1:F:35:ILE:HD12	1.79	0.64
1:C:32:PRO:HD2	1:C:35:ILE:HD12	1.79	0.64
1:E:212:LEU:N	1:E:212:LEU:HD12	2.11	0.64
1:E:28:ARG:CZ	1:F:207:GLN:NE2	2.61	0.64
1:E:273:VAL:HA	1:E:345:LEU:HD22	1.79	0.64
1:F:324:THR:HG22	1:F:328:PHE:CE2	2.33	0.64
1:A:194:LEU:HD13	1:B:410:ILE:HD11	1.80	0.64
1:E:126:ARG:O	1:E:130:VAL:HG23	1.97	0.64
1:F:126:ARG:O	1:F:130:VAL:HG23	1.97	0.64
1:D:123:ARG:N	1:D:123:ARG:HD3	2.13	0.64
1:B:123:ARG:N	1:B:123:ARG:HD3	2.13	0.63
1:C:154:ILE:O	1:C:158:ILE:HG12	1.98	0.63
1:D:120:ARG:HH11	1:D:120:ARG:CB	2.07	0.63
1:F:317:PHE:HA	1:F:321:PRO:HD2	1.79	0.63
1:A:123:ARG:N	1:A:123:ARG:HD3	2.13	0.63
1:A:450:ALA:HB3	1:B:26:LEU:HD21	1.79	0.63
1:E:324:THR:HG22	1:E:328:PHE:CE2	2.33	0.63
1:A:154:ILE:O	1:A:158:ILE:HG12	1.98	0.63
1:E:123:ARG:N	1:E:123:ARG:HD3	2.13	0.63
1:E:434:LEU:HD23	1:F:216:LYS:HD3	1.81	0.63
1:F:123:ARG:N	1:F:123:ARG:HD3	2.13	0.63
1:F:148:GLU:H	1:F:148:GLU:CD	2.07	0.63
1:C:123:ARG:N	1:C:123:ARG:HD3	2.13	0.63
1:E:194:LEU:HD13	1:F:410:ILE:HD11	1.79	0.63
1:A:148:GLU:CD	1:A:148:GLU:H	2.07	0.63
1:C:434:LEU:HD23	1:D:216:LYS:HD3	1.81	0.63
1:C:450:ALA:HB3	1:D:26:LEU:HD21	1.79	0.63
1:E:154:ILE:O	1:E:158:ILE:HG12	1.98	0.63
1:F:154:ILE:O	1:F:158:ILE:HG12	1.98	0.63
1:B:324:THR:C	1:B:326:GLY:N	2.56	0.63
1:E:148:GLU:H	1:E:148:GLU:CD	2.07	0.63
1:A:434:LEU:HD23	1:B:216:LYS:HD3	1.81	0.63
1:F:324:THR:C	1:F:326:GLY:N	2.56	0.63
1:B:126:ARG:O	1:B:130:VAL:HG23	1.97	0.62
1:D:126:ARG:O	1:D:130:VAL:HG23	1.97	0.62
1:E:207:GLN:NE2	1:F:28:ARG:CZ	2.61	0.62
1:C:148:GLU:H	1:C:148:GLU:CD	2.07	0.62
1:A:320:ILE:O	1:A:324:THR:HG23	1.99	0.62
1:B:320:ILE:O	1:B:324:THR:HG23	1.99	0.62
1:D:320:ILE:O	1:D:324:THR:HG23	1.99	0.62
1:B:148:GLU:H	1:B:148:GLU:CD	2.07	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:ILE:O	1:C:324:THR:HG23	1.99	0.62
1:D:154:ILE:O	1:D:158:ILE:HG12	1.98	0.62
1:A:30:LYS:HB3	1:A:30:LYS:HZ3	1.64	0.62
1:A:244:LEU:HD12	1:A:418:ASN:HD21	1.65	0.62
1:B:154:ILE:O	1:B:158:ILE:HG12	1.98	0.62
1:B:244:LEU:HD12	1:B:418:ASN:HD21	1.65	0.62
1:D:46:VAL:HG21	1:D:181:GLY:HA2	1.81	0.62
1:C:244:LEU:HD12	1:C:418:ASN:HD21	1.65	0.62
1:A:28:ARG:CZ	1:B:207:GLN:NE2	2.61	0.62
1:A:276:MET:O	1:A:280:LEU:HD23	2.00	0.62
1:C:28:ARG:CZ	1:D:207:GLN:NE2	2.61	0.62
1:C:324:THR:C	1:C:326:GLY:N	2.56	0.62
1:D:244:LEU:HD12	1:D:418:ASN:HD21	1.65	0.62
1:F:46:VAL:HG21	1:F:181:GLY:HA2	1.81	0.62
1:F:157:ASN:C	1:F:159:GLY:N	2.56	0.62
1:F:276:MET:O	1:F:280:LEU:HD23	2.00	0.62
1:C:276:MET:O	1:C:280:LEU:HD23	2.00	0.62
1:E:320:ILE:O	1:E:324:THR:HG23	2.00	0.62
1:D:148:GLU:CD	1:D:148:GLU:H	2.07	0.62
1:E:276:MET:O	1:E:280:LEU:HD23	1.99	0.62
1:C:46:VAL:HG21	1:C:181:GLY:HA2	1.81	0.61
1:C:131:LYS:NZ	1:C:153:GLN:NE2	2.48	0.61
1:B:46:VAL:HG21	1:B:181:GLY:HA2	1.81	0.61
1:B:131:LYS:NZ	1:B:153:GLN:NE2	2.48	0.61
1:A:324:THR:C	1:A:326:GLY:N	2.56	0.61
1:D:131:LYS:NZ	1:D:153:GLN:NE2	2.48	0.61
1:D:276:MET:O	1:D:280:LEU:HD23	2.00	0.61
1:E:131:LYS:NZ	1:E:153:GLN:NE2	2.48	0.61
1:E:317:PHE:C	1:E:319:LEU:N	2.59	0.61
1:F:200:ILE:O	1:F:200:ILE:HG22	2.00	0.61
1:B:313:SER:OG	1:B:314:GLY:N	2.32	0.61
1:C:200:ILE:O	1:C:200:ILE:HG22	2.00	0.61
1:A:131:LYS:NZ	1:A:153:GLN:NE2	2.48	0.61
1:E:46:VAL:HG21	1:E:181:GLY:HA2	1.81	0.61
1:F:320:ILE:O	1:F:324:THR:HG23	1.99	0.61
1:F:244:LEU:HD12	1:F:418:ASN:HD21	1.65	0.61
1:F:317:PHE:C	1:F:319:LEU:N	2.58	0.61
1:A:83:PHE:C	1:A:83:PHE:CD1	2.79	0.61
1:B:200:ILE:HG22	1:B:200:ILE:O	2.00	0.61
1:B:276:MET:O	1:B:280:LEU:HD23	2.00	0.61
1:D:313:SER:OG	1:D:314:GLY:N	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:VAL:HG21	1:A:181:GLY:HA2	1.81	0.61
1:A:372:GLY:O	1:A:376:VAL:HG23	2.01	0.61
1:C:83:PHE:CD1	1:C:83:PHE:C	2.79	0.61
1:D:200:ILE:O	1:D:200:ILE:HG22	2.00	0.61
1:E:420:GLN:HG3	1:E:421:LEU:HG	1.83	0.61
1:A:103:GLU:CB	1:A:123:ARG:HH21	2.14	0.61
1:A:200:ILE:O	1:A:200:ILE:HG22	2.00	0.61
1:C:103:GLU:CB	1:C:123:ARG:HH21	2.14	0.61
1:C:372:GLY:O	1:C:376:VAL:HG23	2.01	0.60
1:F:103:GLU:CB	1:F:123:ARG:HH21	2.14	0.60
1:F:182:ALA:HB1	1:F:204:MET:HE2	1.83	0.60
1:F:420:GLN:HG3	1:F:421:LEU:HG	1.83	0.60
1:B:317:PHE:C	1:B:319:LEU:N	2.59	0.60
1:F:131:LYS:NZ	1:F:153:GLN:NE2	2.48	0.60
1:A:182:ALA:HB1	1:A:204:MET:HE2	1.83	0.60
1:B:83:PHE:CD1	1:B:83:PHE:C	2.79	0.60
1:D:83:PHE:C	1:D:83:PHE:CD1	2.79	0.60
1:E:200:ILE:HG22	1:E:200:ILE:O	2.00	0.60
1:C:182:ALA:HB1	1:C:204:MET:HE2	1.83	0.60
1:E:103:GLU:CB	1:E:123:ARG:HH21	2.14	0.60
1:B:103:GLU:CB	1:B:123:ARG:HH21	2.14	0.60
1:D:420:GLN:HG3	1:D:421:LEU:HG	1.83	0.60
1:D:103:GLU:CB	1:D:123:ARG:HH21	2.14	0.60
1:E:372:GLY:O	1:E:376:VAL:HG23	2.01	0.60
1:B:420:GLN:HG3	1:B:421:LEU:HG	1.83	0.60
1:E:433:THR:HG22	1:F:216:LYS:NZ	2.16	0.60
1:A:157:ASN:C	1:A:159:GLY:N	2.56	0.60
1:A:420:GLN:HG3	1:A:421:LEU:HG	1.83	0.60
1:B:372:GLY:O	1:B:376:VAL:HG23	2.01	0.60
1:D:317:PHE:C	1:D:319:LEU:N	2.58	0.60
1:E:182:ALA:HB1	1:E:204:MET:HE2	1.83	0.60
1:A:433:THR:HG22	1:B:216:LYS:NZ	2.16	0.60
1:C:420:GLN:HG3	1:C:421:LEU:HG	1.83	0.60
1:E:198:LEU:HD21	1:F:198:LEU:CD2	2.32	0.60
1:A:313:SER:OG	1:A:314:GLY:N	2.32	0.60
1:C:433:THR:HG22	1:D:216:LYS:NZ	2.16	0.60
1:D:372:GLY:O	1:D:376:VAL:HG23	2.01	0.60
1:E:244:LEU:HD12	1:E:418:ASN:HD21	1.65	0.60
1:A:75:TYR:O	1:A:79:LEU:HG	2.03	0.59
1:F:83:PHE:CD1	1:F:83:PHE:C	2.79	0.59
1:F:313:SER:OG	1:F:314:GLY:N	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:372:GLY:O	1:F:376:VAL:HG23	2.01	0.59
1:C:75:TYR:O	1:C:79:LEU:HG	2.03	0.59
1:C:157:ASN:C	1:C:159:GLY:N	2.56	0.59
1:E:419:TYR:CE1	1:F:414:GLU:OE1	2.56	0.59
1:C:313:SER:OG	1:C:314:GLY:N	2.32	0.59
1:E:83:PHE:CD1	1:E:83:PHE:C	2.79	0.59
1:F:423:LEU:HB3	1:F:424:PRO:HD3	1.85	0.59
1:A:356:ILE:HG13	1:A:360:MET:HE2	1.85	0.59
1:E:157:ASN:C	1:E:159:GLY:N	2.56	0.59
1:D:182:ALA:HB1	1:D:204:MET:HE2	1.83	0.59
1:E:97:VAL:HG21	1:E:353:PRO:HD3	1.85	0.59
1:C:198:LEU:HD21	1:D:198:LEU:CD2	2.32	0.59
1:A:317:PHE:C	1:A:319:LEU:N	2.58	0.59
1:C:356:ILE:HG13	1:C:360:MET:HE2	1.84	0.59
1:D:97:VAL:HG21	1:D:353:PRO:HD3	1.85	0.59
1:E:423:LEU:HB3	1:E:424:PRO:HD3	1.85	0.58
1:F:75:TYR:O	1:F:79:LEU:HG	2.03	0.58
1:B:75:TYR:O	1:B:79:LEU:HG	2.03	0.58
1:B:423:LEU:HB3	1:B:424:PRO:HD3	1.85	0.58
1:C:419:TYR:CE1	1:D:414:GLU:OE1	2.56	0.58
1:C:423:LEU:HB3	1:C:424:PRO:HD3	1.85	0.58
1:A:159:GLY:O	1:A:162:VAL:HG22	2.04	0.58
1:B:159:GLY:O	1:B:162:VAL:HG22	2.04	0.58
1:C:159:GLY:O	1:C:162:VAL:HG22	2.04	0.58
1:D:159:GLY:O	1:D:162:VAL:HG22	2.04	0.58
1:D:423:LEU:HB3	1:D:424:PRO:HD3	1.85	0.58
1:F:97:VAL:HG21	1:F:353:PRO:HD3	1.85	0.58
1:A:198:LEU:HD21	1:B:198:LEU:CD2	2.32	0.58
1:A:419:TYR:CE1	1:B:414:GLU:OE1	2.56	0.58
1:C:317:PHE:C	1:C:319:LEU:N	2.58	0.58
1:D:75:TYR:O	1:D:79:LEU:HG	2.03	0.58
1:E:198:LEU:CD2	1:F:198:LEU:HD21	2.33	0.58
1:A:203:GLU:OE1	1:B:28:ARG:NH2	2.36	0.58
1:C:21:LEU:O	1:C:25:LEU:N	2.34	0.58
1:E:75:TYR:O	1:E:79:LEU:HG	2.03	0.58
1:B:97:VAL:HG21	1:B:353:PRO:HD3	1.85	0.58
1:B:182:ALA:HB1	1:B:204:MET:HE2	1.83	0.58
1:C:270:ASN:HA	1:C:273:VAL:CG1	2.34	0.58
1:A:423:LEU:HB3	1:A:424:PRO:HD3	1.85	0.58
1:B:234:HIS:O	1:B:236:VAL:HG23	2.04	0.58
1:B:356:ILE:HG13	1:B:360:MET:HE2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:198:LEU:CD2	1:D:198:LEU:HD21	2.33	0.58
1:C:203:GLU:OE1	1:D:28:ARG:NH2	2.36	0.58
1:D:234:HIS:O	1:D:236:VAL:HG23	2.04	0.58
1:D:324:THR:C	1:D:326:GLY:N	2.56	0.58
1:A:198:LEU:CD2	1:B:198:LEU:HD21	2.33	0.58
1:A:270:ASN:HA	1:A:273:VAL:CG1	2.34	0.58
1:F:356:ILE:HG13	1:F:360:MET:HE2	1.84	0.58
1:C:97:VAL:HG21	1:C:353:PRO:HD3	1.85	0.58
1:E:203:GLU:OE1	1:F:28:ARG:NH2	2.36	0.58
1:A:184:ALA:HB1	1:A:225:SER:HB2	1.86	0.58
1:D:332:MET:O	1:D:336:ILE:HG13	2.04	0.58
1:E:356:ILE:HG13	1:E:360:MET:HE2	1.85	0.58
1:E:419:TYR:OH	1:F:414:GLU:OE1	2.19	0.58
1:F:159:GLY:O	1:F:162:VAL:HG22	2.04	0.58
1:F:270:ASN:HA	1:F:273:VAL:CG1	2.34	0.58
1:E:270:ASN:HA	1:E:273:VAL:CG1	2.34	0.57
1:A:88:VAL:O	1:A:91:MET:HB2	2.04	0.57
1:B:332:MET:O	1:B:336:ILE:HG13	2.04	0.57
1:C:184:ALA:HB1	1:C:225:SER:HB2	1.86	0.57
1:E:159:GLY:O	1:E:162:VAL:HG22	2.04	0.57
1:E:234:HIS:O	1:E:236:VAL:HG23	2.04	0.57
1:F:34:ALA:O	1:F:38:MET:HB2	2.05	0.57
1:D:157:ASN:C	1:D:159:GLY:N	2.56	0.57
1:A:97:VAL:HG21	1:A:353:PRO:HD3	1.85	0.57
1:A:148:GLU:O	1:A:149:GLY:C	2.48	0.57
1:A:332:MET:O	1:A:336:ILE:HG13	2.04	0.57
1:B:148:GLU:O	1:B:149:GLY:C	2.48	0.57
1:C:88:VAL:O	1:C:91:MET:HB2	2.04	0.57
1:C:430:LEU:HD13	1:D:219:PHE:CD2	2.39	0.57
1:E:34:ALA:O	1:E:38:MET:HB2	2.05	0.57
1:A:430:LEU:HD13	1:B:219:PHE:CD2	2.39	0.57
1:C:148:GLU:O	1:C:149:GLY:C	2.48	0.57
1:C:332:MET:O	1:C:336:ILE:HG13	2.04	0.57
1:D:131:LYS:HZ2	1:D:153:GLN:NE2	2.02	0.57
1:D:356:ILE:HG13	1:D:360:MET:HE2	1.85	0.57
1:F:148:GLU:O	1:F:149:GLY:C	2.48	0.57
1:A:446:SER:O	1:A:449:LEU:N	2.38	0.57
1:B:128:LEU:HB2	1:B:129:PRO:CD	2.35	0.57
1:B:446:SER:O	1:B:449:LEU:N	2.38	0.57
1:C:128:LEU:HB2	1:C:129:PRO:CD	2.35	0.57
1:C:446:SER:O	1:C:449:LEU:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:GLU:O	1:D:149:GLY:C	2.48	0.57
1:D:446:SER:O	1:D:449:LEU:N	2.38	0.57
1:E:132:PHE:O	1:E:136:LEU:HB2	2.05	0.57
1:F:128:LEU:HB2	1:F:129:PRO:CD	2.35	0.57
1:F:184:ALA:HB1	1:F:225:SER:HB2	1.86	0.57
1:A:128:LEU:HB2	1:A:129:PRO:CD	2.35	0.57
1:B:157:ASN:C	1:B:159:GLY:N	2.56	0.57
1:B:184:ALA:HB1	1:B:225:SER:HB2	1.86	0.57
1:D:184:ALA:HB1	1:D:225:SER:HB2	1.86	0.57
1:D:270:ASN:HA	1:D:273:VAL:CG1	2.34	0.57
1:E:313:SER:OG	1:E:314:GLY:N	2.32	0.57
1:E:430:LEU:HD13	1:F:219:PHE:CD2	2.39	0.57
1:F:446:SER:O	1:F:449:LEU:N	2.38	0.57
1:A:426:ILE:HG22	1:B:223:ILE:HD11	1.87	0.57
1:B:88:VAL:O	1:B:91:MET:HB2	2.04	0.57
1:C:234:HIS:O	1:C:236:VAL:HG23	2.04	0.57
1:D:98:ARG:HA	1:D:98:ARG:NE	2.20	0.57
1:D:127:VAL:HB	1:D:157:ASN:ND2	2.20	0.57
1:D:128:LEU:HB2	1:D:129:PRO:CD	2.35	0.57
1:F:88:VAL:O	1:F:91:MET:HB2	2.04	0.57
1:A:132:PHE:O	1:A:136:LEU:HB2	2.05	0.57
1:B:127:VAL:HB	1:B:157:ASN:ND2	2.20	0.57
1:B:132:PHE:O	1:B:136:LEU:HB2	2.05	0.57
1:B:270:ASN:HA	1:B:273:VAL:CG1	2.34	0.57
1:E:127:VAL:HB	1:E:157:ASN:ND2	2.20	0.57
1:A:234:HIS:O	1:A:236:VAL:HG23	2.04	0.57
1:C:270:ASN:ND2	1:C:444:LEU:HD23	2.20	0.57
1:C:360:MET:HE3	1:C:398:LEU:HD23	1.87	0.57
1:D:360:MET:HE3	1:D:398:LEU:HD23	1.87	0.57
1:F:332:MET:O	1:F:336:ILE:HG13	2.04	0.57
1:A:360:MET:HE3	1:A:398:LEU:HD23	1.87	0.56
1:B:211:THR:HG21	1:B:213:ILE:HG13	1.87	0.56
1:B:330:MET:HE1	1:B:370:ALA:HB1	1.87	0.56
1:C:132:PHE:O	1:C:136:LEU:HB2	2.05	0.56
1:C:324:THR:HG22	1:C:328:PHE:CD2	2.40	0.56
1:C:426:ILE:HG22	1:D:223:ILE:HD11	1.87	0.56
1:E:128:LEU:HB2	1:E:129:PRO:CD	2.35	0.56
1:A:270:ASN:ND2	1:A:444:LEU:HD23	2.20	0.56
1:A:324:THR:HG22	1:A:328:PHE:CD2	2.40	0.56
1:B:98:ARG:HA	1:B:98:ARG:NE	2.20	0.56
1:B:360:MET:HE3	1:B:398:LEU:HD23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:ALA:O	1:C:38:MET:HB2	2.05	0.56
1:C:211:THR:HG21	1:C:213:ILE:HG13	1.87	0.56
1:D:88:VAL:O	1:D:91:MET:HB2	2.04	0.56
1:E:88:VAL:O	1:E:91:MET:HB2	2.04	0.56
1:E:270:ASN:ND2	1:E:444:LEU:HD23	2.20	0.56
1:E:324:THR:HG22	1:E:328:PHE:CD2	2.40	0.56
1:E:332:MET:O	1:E:336:ILE:HG13	2.04	0.56
1:F:234:HIS:O	1:F:236:VAL:HG23	2.04	0.56
1:F:270:ASN:ND2	1:F:444:LEU:HD23	2.20	0.56
1:A:127:VAL:HB	1:A:157:ASN:ND2	2.20	0.56
1:A:211:THR:HG21	1:A:213:ILE:HG13	1.87	0.56
1:B:324:THR:HG22	1:B:328:PHE:CD2	2.40	0.56
1:D:132:PHE:O	1:D:136:LEU:HB2	2.05	0.56
1:D:211:THR:HG21	1:D:213:ILE:HG13	1.87	0.56
1:D:330:MET:HE1	1:D:370:ALA:HB1	1.87	0.56
1:E:184:ALA:HB1	1:E:225:SER:HB2	1.86	0.56
1:F:330:MET:HE1	1:F:370:ALA:HB1	1.87	0.56
1:E:360:MET:HE3	1:E:398:LEU:HD23	1.87	0.56
1:A:34:ALA:O	1:A:38:MET:HB2	2.05	0.56
1:C:127:VAL:HB	1:C:157:ASN:ND2	2.20	0.56
1:D:34:ALA:O	1:D:38:MET:HB2	2.05	0.56
1:E:330:MET:HE1	1:E:370:ALA:HB1	1.88	0.56
1:F:324:THR:HG22	1:F:328:PHE:CD2	2.41	0.56
1:D:324:THR:HG22	1:D:328:PHE:CD2	2.41	0.56
1:E:21:LEU:O	1:E:25:LEU:N	2.34	0.56
1:E:148:GLU:O	1:E:149:GLY:C	2.48	0.56
1:E:426:ILE:HG22	1:F:223:ILE:HD11	1.87	0.56
1:D:116:LEU:CD2	1:D:178:LEU:HD23	2.36	0.56
1:F:127:VAL:HB	1:F:157:ASN:ND2	2.20	0.56
1:F:360:MET:SD	1:F:397:LEU:HD12	2.46	0.56
1:B:34:ALA:O	1:B:38:MET:HB2	2.05	0.56
1:B:131:LYS:HZ2	1:B:153:GLN:NE2	2.04	0.56
1:B:360:MET:SD	1:B:397:LEU:HD12	2.46	0.56
1:D:360:MET:SD	1:D:397:LEU:HD12	2.46	0.56
1:F:132:PHE:O	1:F:136:LEU:HB2	2.05	0.56
1:F:312:THR:HG22	1:F:339:ALA:CB	2.36	0.56
1:F:360:MET:HE3	1:F:398:LEU:HD23	1.88	0.56
1:A:122:VAL:HB	1:A:160:ARG:CD	2.36	0.56
1:C:322:ILE:N	1:C:322:ILE:CD1	2.42	0.56
1:E:122:VAL:HB	1:E:160:ARG:CD	2.36	0.56
1:E:360:MET:SD	1:E:397:LEU:HD12	2.46	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:VAL:HB	1:F:160:ARG:CD	2.36	0.56
1:A:312:THR:HG22	1:A:339:ALA:CB	2.36	0.56
1:A:360:MET:SD	1:A:397:LEU:HD12	2.46	0.56
1:B:116:LEU:CD2	1:B:178:LEU:HD23	2.36	0.56
1:C:122:VAL:HB	1:C:160:ARG:CD	2.36	0.56
1:D:270:ASN:ND2	1:D:444:LEU:HD23	2.20	0.56
1:F:30:LYS:HB3	1:F:30:LYS:HZ2	1.70	0.56
1:C:360:MET:SD	1:C:397:LEU:HD12	2.46	0.55
1:D:312:THR:HG22	1:D:339:ALA:CB	2.36	0.55
1:E:446:SER:O	1:E:449:LEU:N	2.38	0.55
1:A:116:LEU:CD2	1:A:178:LEU:HD23	2.36	0.55
1:B:288:ILE:O	1:B:288:ILE:HG22	2.07	0.55
1:C:312:THR:HG22	1:C:339:ALA:CB	2.36	0.55
1:E:312:THR:HG22	1:E:339:ALA:CB	2.36	0.55
1:F:116:LEU:CD2	1:F:178:LEU:HD23	2.36	0.55
1:D:288:ILE:HG22	1:D:288:ILE:O	2.06	0.55
1:F:321:PRO:N	1:F:322:ILE:HD12	2.22	0.55
1:A:210:TYR:H	1:B:210:TYR:HB2	1.70	0.55
1:C:210:TYR:H	1:D:210:TYR:HB2	1.70	0.55
1:C:330:MET:HE1	1:C:370:ALA:HB1	1.87	0.55
1:F:320:ILE:O	1:F:322:ILE:N	2.39	0.55
1:B:312:THR:HG22	1:B:339:ALA:CB	2.36	0.55
1:E:320:ILE:O	1:E:322:ILE:N	2.39	0.55
1:A:320:ILE:O	1:A:322:ILE:N	2.39	0.55
1:B:270:ASN:ND2	1:B:444:LEU:HD23	2.20	0.55
1:C:116:LEU:CD2	1:C:178:LEU:HD23	2.35	0.55
1:C:320:ILE:O	1:C:322:ILE:N	2.39	0.55
1:D:21:LEU:O	1:D:25:LEU:N	2.34	0.55
1:D:211:THR:C	1:D:212:LEU:HD12	2.32	0.55
1:E:258:LEU:HD13	1:E:371:PHE:CG	2.42	0.55
1:A:210:TYR:HB2	1:B:210:TYR:H	1.71	0.55
1:A:330:MET:HE1	1:A:370:ALA:HB1	1.87	0.55
1:E:210:TYR:HB2	1:F:210:TYR:H	1.71	0.55
1:F:258:LEU:HD13	1:F:371:PHE:CG	2.42	0.55
1:A:211:THR:C	1:A:212:LEU:HD12	2.32	0.55
1:A:249:LEU:C	1:A:251:THR:H	2.15	0.55
1:B:98:ARG:NH2	1:B:102:PRO:HB3	2.21	0.55
1:B:211:THR:C	1:B:212:LEU:HD12	2.32	0.55
1:C:171:ASP:HB2	1:C:212:LEU:HD22	1.89	0.55
1:D:249:LEU:C	1:D:251:THR:H	2.15	0.55
1:E:210:TYR:H	1:F:210:TYR:HB2	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:211:THR:HG21	1:E:213:ILE:HG13	1.87	0.55
1:E:321:PRO:N	1:E:322:ILE:HD12	2.22	0.55
1:E:370:ALA:O	1:E:373:MET:HB2	2.07	0.55
1:B:122:VAL:HB	1:B:160:ARG:CD	2.36	0.55
1:B:249:LEU:C	1:B:251:THR:H	2.15	0.55
1:C:258:LEU:HD13	1:C:371:PHE:CG	2.42	0.55
1:D:98:ARG:NH2	1:D:102:PRO:HB3	2.21	0.55
1:E:74:ASN:HD21	1:E:77:LEU:CB	2.20	0.55
1:E:249:LEU:C	1:E:251:THR:H	2.15	0.55
1:F:131:LYS:HZ2	1:F:153:GLN:NE2	2.05	0.55
1:F:171:ASP:HB2	1:F:212:LEU:HD22	1.89	0.55
1:F:211:THR:HG21	1:F:213:ILE:HG13	1.87	0.55
1:A:258:LEU:HD13	1:A:371:PHE:CG	2.42	0.55
1:B:74:ASN:HD21	1:B:77:LEU:CB	2.20	0.55
1:B:320:ILE:O	1:B:322:ILE:N	2.39	0.55
1:E:211:THR:C	1:E:212:LEU:HD12	2.32	0.55
1:F:370:ALA:O	1:F:373:MET:HB2	2.07	0.55
1:C:74:ASN:HD21	1:C:77:LEU:CB	2.20	0.54
1:C:135:GLY:HA2	1:C:138:THR:OG1	2.08	0.54
1:D:122:VAL:HB	1:D:160:ARG:CD	2.36	0.54
1:D:320:ILE:O	1:D:322:ILE:N	2.39	0.54
1:A:74:ASN:HD21	1:A:77:LEU:CB	2.20	0.54
1:A:135:GLY:HA2	1:A:138:THR:OG1	2.08	0.54
1:C:211:THR:C	1:C:212:LEU:HD12	2.32	0.54
1:D:74:ASN:HD21	1:D:77:LEU:CB	2.20	0.54
1:D:258:LEU:HD13	1:D:371:PHE:CG	2.42	0.54
1:E:116:LEU:CD2	1:E:178:LEU:HD23	2.36	0.54
1:F:244:LEU:CD1	1:F:418:ASN:ND2	2.70	0.54
1:A:74:ASN:HD21	1:A:77:LEU:HB2	1.73	0.54
1:A:171:ASP:HB2	1:A:212:LEU:HD22	1.89	0.54
1:A:370:ALA:O	1:A:373:MET:HB2	2.07	0.54
1:B:258:LEU:HD13	1:B:371:PHE:CG	2.42	0.54
1:C:74:ASN:HD21	1:C:77:LEU:HB2	1.73	0.54
1:D:171:ASP:HB2	1:D:212:LEU:HD22	1.89	0.54
1:E:216:LYS:HD3	1:F:434:LEU:HD23	1.89	0.54
1:F:249:LEU:C	1:F:251:THR:H	2.15	0.54
1:A:288:ILE:HG22	1:A:288:ILE:O	2.07	0.54
1:A:321:PRO:N	1:A:322:ILE:HD12	2.22	0.54
1:C:210:TYR:HB2	1:D:210:TYR:H	1.71	0.54
1:D:135:GLY:HA2	1:D:138:THR:OG1	2.08	0.54
1:E:410:ILE:HD11	1:F:194:LEU:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ASP:OD1	1:A:147:ARG:NH1	2.40	0.54
1:B:21:LEU:O	1:B:25:LEU:N	2.34	0.54
1:B:54:ASP:OD1	1:B:147:ARG:NH1	2.40	0.54
1:C:98:ARG:HA	1:C:98:ARG:NE	2.20	0.54
1:C:321:PRO:N	1:C:322:ILE:HD12	2.22	0.54
1:F:211:THR:C	1:F:212:LEU:HD12	2.32	0.54
1:C:433:THR:HG22	1:D:216:LYS:HZ3	1.73	0.54
1:D:321:PRO:N	1:D:322:ILE:HD12	2.22	0.54
1:D:370:ALA:O	1:D:373:MET:HB2	2.07	0.54
1:F:74:ASN:HD21	1:F:77:LEU:CB	2.20	0.54
1:F:135:GLY:HA2	1:F:138:THR:OG1	2.08	0.54
1:F:322:ILE:N	1:F:322:ILE:CD1	2.42	0.54
1:B:135:GLY:HA2	1:B:138:THR:OG1	2.08	0.54
1:C:288:ILE:O	1:C:288:ILE:HG22	2.06	0.54
1:C:370:ALA:O	1:C:373:MET:HB2	2.07	0.54
1:D:54:ASP:OD1	1:D:147:ARG:NH1	2.40	0.54
1:F:54:ASP:OD1	1:F:147:ARG:NH1	2.40	0.54
1:B:321:PRO:N	1:B:322:ILE:HD12	2.22	0.54
1:C:249:LEU:C	1:C:251:THR:H	2.15	0.54
1:E:171:ASP:HB2	1:E:212:LEU:HD22	1.89	0.54
1:E:244:LEU:CD1	1:E:418:ASN:ND2	2.70	0.54
1:A:224:MET:O	1:A:228:MET:HG2	2.08	0.54
1:B:244:LEU:CD1	1:B:418:ASN:ND2	2.70	0.54
1:A:244:LEU:CD1	1:A:418:ASN:ND2	2.70	0.54
1:B:171:ASP:HB2	1:B:212:LEU:HD22	1.89	0.54
1:C:54:ASP:OD1	1:C:147:ARG:NH1	2.40	0.54
1:C:244:LEU:CD1	1:C:418:ASN:ND2	2.70	0.54
1:D:224:MET:O	1:D:228:MET:HG2	2.08	0.54
1:D:244:LEU:CD1	1:D:418:ASN:ND2	2.70	0.54
1:E:54:ASP:OD1	1:E:147:ARG:NH1	2.40	0.54
1:E:135:GLY:HA2	1:E:138:THR:OG1	2.08	0.54
1:A:216:LYS:HD3	1:B:434:LEU:HD23	1.89	0.53
1:A:28:ARG:NH2	1:B:207:GLN:HE22	2.05	0.53
1:B:224:MET:O	1:B:228:MET:HG2	2.08	0.53
1:B:370:ALA:O	1:B:373:MET:HB2	2.07	0.53
1:C:28:ARG:NH2	1:D:207:GLN:HE22	2.05	0.53
1:C:224:MET:O	1:C:228:MET:HG2	2.08	0.53
1:F:98:ARG:HA	1:F:98:ARG:NE	2.20	0.53
1:A:98:ARG:HA	1:A:98:ARG:NE	2.20	0.53
1:B:74:ASN:HD21	1:B:77:LEU:HB2	1.73	0.53
1:E:74:ASN:HD21	1:E:77:LEU:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:446:SER:OG	1:F:28:ARG:NH1	2.41	0.53
1:F:288:ILE:HG22	1:F:288:ILE:O	2.07	0.53
1:A:449:LEU:O	1:A:453:LEU:HB2	2.09	0.53
1:B:449:LEU:O	1:B:453:LEU:HB2	2.09	0.53
1:C:198:LEU:HD13	1:C:406:LEU:HG	1.89	0.53
1:C:410:ILE:HD11	1:D:194:LEU:HD13	1.89	0.53
1:A:410:ILE:HD11	1:B:194:LEU:HD13	1.89	0.53
1:A:446:SER:OG	1:B:28:ARG:NH1	2.41	0.53
1:C:28:ARG:NH1	1:D:446:SER:OG	2.42	0.53
1:C:219:PHE:CD2	1:D:430:LEU:HD13	2.44	0.53
1:C:446:SER:OG	1:D:28:ARG:NH1	2.41	0.53
1:D:74:ASN:HD21	1:D:77:LEU:HB2	1.73	0.53
1:F:74:ASN:HD21	1:F:77:LEU:HB2	1.73	0.53
1:A:219:PHE:CD2	1:B:430:LEU:HD13	2.44	0.53
1:A:433:THR:HG22	1:B:216:LYS:HZ3	1.74	0.53
1:C:216:LYS:HD3	1:D:434:LEU:HD23	1.89	0.53
1:C:244:LEU:HD13	1:C:418:ASN:ND2	2.24	0.53
1:C:449:LEU:O	1:C:453:LEU:HB2	2.09	0.53
1:D:449:LEU:O	1:D:453:LEU:HB2	2.09	0.53
1:E:98:ARG:HA	1:E:98:ARG:NE	2.20	0.53
1:F:198:LEU:HD13	1:F:406:LEU:HG	1.89	0.53
1:F:224:MET:O	1:F:228:MET:HG2	2.08	0.53
1:A:28:ARG:NH1	1:B:446:SER:OG	2.42	0.53
1:A:244:LEU:HD13	1:A:418:ASN:ND2	2.24	0.53
1:B:198:LEU:HD13	1:B:406:LEU:HG	1.89	0.53
1:E:109:ILE:N	1:E:110:PRO:HD2	2.24	0.53
1:E:219:PHE:CD2	1:F:430:LEU:HD13	2.44	0.53
1:E:288:ILE:O	1:E:288:ILE:HG22	2.07	0.53
1:A:198:LEU:HD13	1:A:406:LEU:HG	1.89	0.53
1:C:110:PRO:O	1:C:449:LEU:HD13	2.09	0.53
1:C:157:ASN:C	1:C:159:GLY:H	2.16	0.53
1:C:288:ILE:N	1:C:288:ILE:HD12	2.24	0.53
1:F:109:ILE:N	1:F:110:PRO:HD2	2.24	0.53
1:F:191:ASN:HB2	1:F:229:TYR:CE2	2.44	0.53
1:A:419:TYR:OH	1:B:414:GLU:OE1	2.19	0.53
1:B:98:ARG:NH1	1:B:291:TRP:CZ3	2.77	0.53
1:B:157:ASN:C	1:B:159:GLY:H	2.16	0.53
1:D:98:ARG:NH1	1:D:291:TRP:CZ3	2.77	0.53
1:E:244:LEU:HD13	1:E:418:ASN:ND2	2.24	0.53
1:E:449:LEU:O	1:E:453:LEU:HB2	2.09	0.53
1:F:244:LEU:HD13	1:F:418:ASN:ND2	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ILE:N	1:A:110:PRO:HD2	2.24	0.52
1:A:110:PRO:O	1:A:449:LEU:HD13	2.09	0.52
1:C:109:ILE:N	1:C:110:PRO:HD2	2.24	0.52
1:E:198:LEU:HD13	1:E:406:LEU:HG	1.89	0.52
1:E:274:LEU:HD12	1:E:277:GLN:HE21	1.74	0.52
1:A:288:ILE:HD12	1:A:288:ILE:N	2.24	0.52
1:B:284:HIS:O	1:B:286:GLY:N	2.42	0.52
1:E:28:ARG:NH1	1:F:446:SER:OG	2.42	0.52
1:E:28:ARG:NH2	1:F:207:GLN:HE22	2.05	0.52
1:E:98:ARG:NH1	1:E:291:TRP:CZ3	2.77	0.52
1:F:288:ILE:HD12	1:F:288:ILE:N	2.24	0.52
1:D:109:ILE:N	1:D:110:PRO:HD2	2.24	0.52
1:D:198:LEU:HD13	1:D:406:LEU:HG	1.89	0.52
1:D:209:ARG:O	1:D:210:TYR:C	2.52	0.52
1:D:244:LEU:HD13	1:D:418:ASN:ND2	2.24	0.52
1:D:284:HIS:O	1:D:286:GLY:N	2.43	0.52
1:F:21:LEU:O	1:F:25:LEU:N	2.34	0.52
1:A:157:ASN:C	1:A:159:GLY:H	2.16	0.52
1:B:110:PRO:O	1:B:449:LEU:HD13	2.09	0.52
1:B:209:ARG:O	1:B:210:TYR:C	2.52	0.52
1:D:191:ASN:HB2	1:D:229:TYR:CE2	2.44	0.52
1:E:209:ARG:O	1:E:210:TYR:C	2.52	0.52
1:E:224:MET:O	1:E:228:MET:HG2	2.08	0.52
1:F:110:PRO:O	1:F:449:LEU:HD13	2.09	0.52
1:A:284:HIS:O	1:A:286:GLY:N	2.43	0.52
1:B:109:ILE:N	1:B:110:PRO:HD2	2.24	0.52
1:C:98:ARG:NH1	1:C:291:TRP:CZ3	2.77	0.52
1:C:191:ASN:HB2	1:C:229:TYR:CE2	2.44	0.52
1:D:288:ILE:HD12	1:D:288:ILE:N	2.24	0.52
1:F:90:ALA:O	1:F:94:TYR:HD1	1.93	0.52
1:A:209:ARG:O	1:A:210:TYR:C	2.52	0.52
1:B:191:ASN:HB2	1:B:229:TYR:CE2	2.44	0.52
1:B:244:LEU:HD13	1:B:418:ASN:ND2	2.24	0.52
1:B:288:ILE:HD12	1:B:288:ILE:N	2.24	0.52
1:C:419:TYR:OH	1:D:414:GLU:OE1	2.19	0.52
1:D:444:LEU:HD13	1:D:444:LEU:O	2.10	0.52
1:A:98:ARG:NH1	1:A:291:TRP:CZ3	2.77	0.52
1:B:444:LEU:O	1:B:444:LEU:HD13	2.10	0.52
1:C:209:ARG:O	1:C:210:TYR:C	2.52	0.52
1:C:274:LEU:HD12	1:C:277:GLN:HE21	1.74	0.52
1:C:284:HIS:O	1:C:286:GLY:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:157:ASN:C	1:D:159:GLY:H	2.16	0.52
1:D:274:LEU:HD12	1:D:277:GLN:HE21	1.75	0.52
1:E:98:ARG:NH2	1:E:102:PRO:HB3	2.21	0.52
1:E:110:PRO:O	1:E:449:LEU:HD13	2.09	0.52
1:E:191:ASN:HB2	1:E:229:TYR:CE2	2.44	0.52
1:F:444:LEU:O	1:F:444:LEU:HD13	2.10	0.52
1:A:444:LEU:O	1:A:444:LEU:HD13	2.10	0.52
1:B:200:ILE:HA	1:B:204:MET:HB2	1.92	0.52
1:E:90:ALA:O	1:E:94:TYR:HD1	1.93	0.52
1:E:284:HIS:O	1:E:286:GLY:N	2.43	0.52
1:E:451:ARG:C	1:E:453:LEU:H	2.18	0.52
1:F:98:ARG:NH2	1:F:102:PRO:HB3	2.21	0.52
1:F:284:HIS:O	1:F:286:GLY:N	2.43	0.52
1:A:90:ALA:O	1:A:94:TYR:HD1	1.93	0.52
1:B:314:GLY:C	1:B:316:GLY:H	2.18	0.52
1:D:109:ILE:HG21	1:D:445:TYR:CD1	2.45	0.52
1:D:110:PRO:O	1:D:449:LEU:HD13	2.09	0.52
1:A:191:ASN:HB2	1:A:229:TYR:CE2	2.44	0.52
1:A:200:ILE:HA	1:A:204:MET:HB2	1.92	0.52
1:A:274:LEU:HD12	1:A:277:GLN:HE21	1.74	0.52
1:C:444:LEU:O	1:C:444:LEU:HD13	2.10	0.52
1:E:314:GLY:C	1:E:316:GLY:H	2.18	0.52
1:E:444:LEU:O	1:E:444:LEU:HD13	2.10	0.52
1:F:157:ASN:C	1:F:159:GLY:H	2.16	0.52
1:F:314:GLY:C	1:F:316:GLY:H	2.18	0.52
1:B:109:ILE:HG21	1:B:445:TYR:CD1	2.45	0.51
1:B:451:ARG:C	1:B:453:LEU:H	2.18	0.51
1:C:314:GLY:C	1:C:316:GLY:H	2.18	0.51
1:C:451:ARG:C	1:C:453:LEU:H	2.18	0.51
1:D:200:ILE:HA	1:D:204:MET:HB2	1.92	0.51
1:D:314:GLY:C	1:D:316:GLY:H	2.18	0.51
1:E:288:ILE:N	1:E:288:ILE:HD12	2.24	0.51
1:F:98:ARG:NH1	1:F:291:TRP:CZ3	2.77	0.51
1:A:314:GLY:C	1:A:316:GLY:H	2.18	0.51
1:A:321:PRO:HA	1:A:365:THR:HG21	1.92	0.51
1:A:451:ARG:C	1:A:453:LEU:H	2.18	0.51
1:B:132:PHE:C	1:B:132:PHE:CD2	2.88	0.51
1:E:321:PRO:HA	1:E:365:THR:HG21	1.92	0.51
1:F:209:ARG:O	1:F:210:TYR:C	2.52	0.51
1:F:274:LEU:HD12	1:F:277:GLN:HE21	1.74	0.51
1:B:274:LEU:HD12	1:B:277:GLN:HE21	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:ILE:HA	1:C:204:MET:HB2	1.92	0.51
1:D:451:ARG:C	1:D:453:LEU:H	2.18	0.51
1:C:321:PRO:HA	1:C:365:THR:HG21	1.93	0.51
1:D:132:PHE:C	1:D:132:PHE:CD2	2.88	0.51
1:E:109:ILE:HG21	1:E:445:TYR:CD1	2.45	0.51
1:E:203:GLU:O	1:E:204:MET:C	2.54	0.51
1:E:430:LEU:CD1	1:F:219:PHE:HB3	2.40	0.51
1:A:203:GLU:O	1:A:204:MET:C	2.54	0.51
1:C:90:ALA:O	1:C:94:TYR:HD1	1.93	0.51
1:E:200:ILE:HA	1:E:204:MET:HB2	1.92	0.51
1:F:449:LEU:O	1:F:453:LEU:HB2	2.09	0.51
1:E:157:ASN:C	1:E:159:GLY:H	2.16	0.51
1:C:132:PHE:C	1:C:132:PHE:CD2	2.88	0.51
1:C:419:TYR:CZ	1:D:414:GLU:OE1	2.64	0.51
1:D:90:ALA:O	1:D:94:TYR:HD1	1.93	0.51
1:E:101:ALA:C	1:E:103:GLU:H	2.19	0.51
1:F:176:THR:HG22	1:F:177:LEU:N	2.26	0.51
1:F:200:ILE:HA	1:F:204:MET:HB2	1.92	0.51
1:F:321:PRO:HA	1:F:365:THR:HG21	1.92	0.51
1:F:451:ARG:C	1:F:453:LEU:H	2.18	0.51
1:A:176:THR:HG22	1:A:177:LEU:N	2.26	0.51
1:B:101:ALA:C	1:B:103:GLU:H	2.19	0.51
1:C:203:GLU:O	1:C:204:MET:C	2.54	0.51
1:A:132:PHE:C	1:A:132:PHE:CD2	2.88	0.51
1:F:101:ALA:C	1:F:103:GLU:H	2.19	0.51
1:F:449:LEU:HA	1:F:452:THR:HG22	1.93	0.51
1:A:101:ALA:C	1:A:103:GLU:H	2.19	0.51
1:A:109:ILE:HG21	1:A:445:TYR:CD1	2.45	0.51
1:B:308:VAL:O	1:B:309:ALA:HB3	2.11	0.51
1:C:249:LEU:HD11	1:D:230:ARG:HB3	1.93	0.51
1:D:101:ALA:C	1:D:103:GLU:H	2.19	0.51
1:D:321:PRO:HA	1:D:365:THR:HG21	1.92	0.51
1:A:419:TYR:CZ	1:B:414:GLU:OE1	2.64	0.50
1:B:176:THR:HG22	1:B:177:LEU:N	2.26	0.50
1:C:176:THR:HG22	1:C:177:LEU:N	2.26	0.50
1:E:419:TYR:CZ	1:F:414:GLU:OE1	2.64	0.50
1:F:109:ILE:HG21	1:F:445:TYR:CD1	2.45	0.50
1:F:132:PHE:C	1:F:132:PHE:CD2	2.88	0.50
1:A:249:LEU:HD11	1:B:230:ARG:HB3	1.93	0.50
1:B:42:VAL:HG21	1:B:177:LEU:HD13	1.94	0.50
1:B:90:ALA:O	1:B:94:TYR:HD1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:308:VAL:O	1:D:309:ALA:HB3	2.11	0.50
1:D:176:THR:HG22	1:D:177:LEU:N	2.26	0.50
1:E:176:THR:HG22	1:E:177:LEU:N	2.26	0.50
1:E:244:LEU:CD1	1:E:418:ASN:HD21	2.25	0.50
1:E:249:LEU:HD11	1:F:230:ARG:HB3	1.94	0.50
1:F:203:GLU:O	1:F:204:MET:C	2.54	0.50
1:F:308:VAL:O	1:F:309:ALA:HB3	2.12	0.50
1:C:101:ALA:C	1:C:103:GLU:H	2.19	0.50
1:C:109:ILE:HG21	1:C:445:TYR:CD1	2.45	0.50
1:C:449:LEU:HA	1:C:452:THR:HG22	1.93	0.50
1:D:148:GLU:HG2	1:D:357:PHE:HD2	1.77	0.50
1:E:449:LEU:HA	1:E:452:THR:HG22	1.93	0.50
1:F:318:ASN:O	1:F:319:LEU:HD13	2.12	0.50
1:A:434:LEU:C	1:A:436:ALA:N	2.70	0.50
1:B:148:GLU:HG2	1:B:357:PHE:HD2	1.77	0.50
1:C:148:GLU:HG2	1:C:357:PHE:HD2	1.77	0.50
1:C:434:LEU:C	1:C:436:ALA:N	2.70	0.50
1:D:42:VAL:HG21	1:D:177:LEU:HD13	1.94	0.50
1:F:112:ILE:HD12	1:F:156:GLY:HA3	1.94	0.50
1:A:148:GLU:HG2	1:A:357:PHE:HD2	1.77	0.50
1:A:430:LEU:CD1	1:B:219:PHE:HB3	2.40	0.50
1:B:30:LYS:HB3	1:B:30:LYS:HZ3	1.74	0.50
1:E:132:PHE:C	1:E:132:PHE:CD2	2.88	0.50
1:A:112:ILE:HD12	1:A:156:GLY:HA3	1.94	0.50
1:B:321:PRO:HA	1:B:365:THR:HG21	1.93	0.50
1:C:372:GLY:O	1:C:373:MET:C	2.55	0.50
1:C:430:LEU:CD1	1:D:219:PHE:HB3	2.41	0.50
1:D:122:VAL:HB	1:D:160:ARG:HD2	1.94	0.50
1:E:318:ASN:O	1:E:319:LEU:HD13	2.12	0.50
1:E:372:GLY:O	1:E:373:MET:C	2.55	0.50
1:F:321:PRO:C	1:F:322:ILE:HD12	2.36	0.50
1:B:122:VAL:HB	1:B:160:ARG:HD2	1.94	0.50
1:E:112:ILE:HD12	1:E:156:GLY:HA3	1.94	0.50
1:E:324:THR:C	1:E:326:GLY:N	2.56	0.50
1:F:372:GLY:O	1:F:373:MET:C	2.55	0.50
1:A:21:LEU:O	1:A:25:LEU:N	2.34	0.50
1:A:372:GLY:O	1:A:373:MET:C	2.55	0.50
1:A:449:LEU:HA	1:A:452:THR:HG22	1.93	0.50
1:C:321:PRO:C	1:C:322:ILE:HD12	2.36	0.50
1:E:294:MET:O	1:E:297:ALA:HB3	2.12	0.50
1:C:42:VAL:HG21	1:C:177:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:ILE:HD12	1:C:156:GLY:HA3	1.94	0.49
1:C:269:PHE:O	1:C:273:VAL:HG12	2.12	0.49
1:C:308:VAL:O	1:C:309:ALA:HB3	2.12	0.49
1:D:449:LEU:HA	1:D:452:THR:HG22	1.93	0.49
1:E:42:VAL:HG21	1:E:177:LEU:HD13	1.94	0.49
1:B:203:GLU:O	1:B:204:MET:C	2.54	0.49
1:D:203:GLU:O	1:D:204:MET:C	2.54	0.49
1:E:269:PHE:O	1:E:273:VAL:HG12	2.12	0.49
1:E:459:GLU:O	1:E:459:GLU:HG2	2.12	0.49
1:F:148:GLU:HG2	1:F:357:PHE:CD2	2.48	0.49
1:F:269:PHE:O	1:F:273:VAL:HG12	2.12	0.49
1:F:459:GLU:O	1:F:459:GLU:HG2	2.12	0.49
1:A:269:PHE:O	1:A:273:VAL:HG12	2.12	0.49
1:A:430:LEU:CD2	1:B:223:ILE:HD12	2.40	0.49
1:D:434:LEU:C	1:D:436:ALA:H	2.20	0.49
1:E:308:VAL:O	1:E:309:ALA:HB3	2.11	0.49
1:A:315:GLY:H	1:A:318:ASN:ND2	2.10	0.49
1:B:434:LEU:C	1:B:436:ALA:H	2.21	0.49
1:D:278:ASP:C	1:D:280:LEU:N	2.71	0.49
1:D:443:PRO:O	1:D:446:SER:N	2.41	0.49
1:E:30:LYS:O	1:E:30:LYS:HG2	2.12	0.49
1:E:434:LEU:C	1:E:436:ALA:H	2.21	0.49
1:F:358:ALA:O	1:F:361:LEU:HB2	2.13	0.49
1:A:42:VAL:HG21	1:A:177:LEU:HD13	1.94	0.49
1:A:153:GLN:C	1:A:155:GLY:N	2.69	0.49
1:B:322:ILE:N	1:B:322:ILE:CD1	2.42	0.49
1:B:449:LEU:HA	1:B:452:THR:HG22	1.93	0.49
1:D:269:PHE:O	1:D:273:VAL:HG12	2.12	0.49
1:D:288:ILE:HD12	1:D:288:ILE:H	1.77	0.49
1:D:294:MET:O	1:D:297:ALA:HB3	2.12	0.49
1:E:198:LEU:HD13	1:E:406:LEU:CD2	2.43	0.49
1:F:288:ILE:HD12	1:F:288:ILE:H	1.77	0.49
1:F:320:ILE:C	1:F:322:ILE:H	2.21	0.49
1:A:294:MET:O	1:A:297:ALA:HB3	2.12	0.49
1:A:459:GLU:O	1:A:459:GLU:HG2	2.12	0.49
1:B:288:ILE:HD12	1:B:288:ILE:H	1.77	0.49
1:B:318:ASN:O	1:B:319:LEU:HD13	2.12	0.49
1:C:288:ILE:HD12	1:C:288:ILE:H	1.77	0.49
1:C:315:GLY:H	1:C:318:ASN:ND2	2.10	0.49
1:C:459:GLU:O	1:C:459:GLU:HG2	2.12	0.49
1:D:30:LYS:HB3	1:D:30:LYS:HZ3	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:LEU:HD13	1:D:406:LEU:CD2	2.43	0.49
1:A:30:LYS:HG2	1:A:30:LYS:O	2.12	0.49
1:A:288:ILE:HD12	1:A:288:ILE:H	1.77	0.49
1:A:318:ASN:O	1:A:319:LEU:HD13	2.12	0.49
1:A:321:PRO:C	1:A:322:ILE:HD12	2.36	0.49
1:B:294:MET:O	1:B:297:ALA:HB3	2.12	0.49
1:B:443:PRO:O	1:B:446:SER:N	2.41	0.49
1:C:122:VAL:HB	1:C:160:ARG:HD2	1.94	0.49
1:C:131:LYS:HZ2	1:C:153:GLN:NE2	2.09	0.49
1:C:148:GLU:HG2	1:C:357:PHE:CD2	2.48	0.49
1:C:294:MET:O	1:C:297:ALA:HB3	2.12	0.49
1:E:148:GLU:HG2	1:E:357:PHE:CD2	2.48	0.49
1:F:123:ARG:CZ	1:F:127:VAL:HG21	2.43	0.49
1:F:148:GLU:HG2	1:F:357:PHE:HD2	1.77	0.49
1:A:122:VAL:HB	1:A:160:ARG:HD2	1.94	0.49
1:A:148:GLU:HG2	1:A:357:PHE:CD2	2.48	0.49
1:A:198:LEU:HD13	1:A:406:LEU:CD2	2.43	0.49
1:B:112:ILE:HD12	1:B:156:GLY:HA3	1.94	0.49
1:B:269:PHE:O	1:B:273:VAL:HG12	2.12	0.49
1:C:198:LEU:HD13	1:C:406:LEU:CD2	2.43	0.49
1:E:209:ARG:O	1:E:209:ARG:HG3	2.13	0.49
1:E:358:ALA:O	1:E:361:LEU:HB2	2.13	0.49
1:F:30:LYS:HG2	1:F:30:LYS:O	2.12	0.49
1:F:315:GLY:H	1:F:318:ASN:ND2	2.10	0.49
1:F:434:LEU:C	1:F:436:ALA:H	2.21	0.49
1:A:308:VAL:O	1:A:309:ALA:HB3	2.11	0.49
1:C:153:GLN:C	1:C:155:GLY:N	2.69	0.49
1:C:318:ASN:O	1:C:319:LEU:HD13	2.12	0.49
1:C:430:LEU:CD2	1:D:223:ILE:HD12	2.40	0.49
1:D:112:ILE:HD12	1:D:156:GLY:HA3	1.94	0.49
1:F:42:VAL:HG21	1:F:177:LEU:HD13	1.94	0.49
1:A:358:ALA:O	1:A:361:LEU:HB2	2.13	0.49
1:B:124:TRP:HA	1:B:157:ASN:HD22	1.78	0.49
1:B:148:GLU:HG2	1:B:357:PHE:CD2	2.48	0.49
1:C:30:LYS:O	1:C:30:LYS:HG2	2.12	0.49
1:D:30:LYS:HG2	1:D:30:LYS:O	2.12	0.49
1:D:318:ASN:O	1:D:319:LEU:HD13	2.12	0.49
1:E:26:LEU:HD21	1:F:450:ALA:CB	2.43	0.49
1:E:216:LYS:O	1:E:220:ILE:HG13	2.13	0.49
1:A:278:ASP:C	1:A:280:LEU:N	2.71	0.48
1:B:30:LYS:O	1:B:30:LYS:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:GLU:HG2	1:B:459:GLU:O	2.12	0.48
1:C:30:LYS:HB3	1:C:30:LYS:HZ2	1.78	0.48
1:D:124:TRP:HA	1:D:157:ASN:HD22	1.78	0.48
1:D:148:GLU:HG2	1:D:357:PHE:CD2	2.48	0.48
1:D:216:LYS:O	1:D:220:ILE:HG13	2.13	0.48
1:F:122:VAL:HB	1:F:160:ARG:HD2	1.94	0.48
1:F:216:LYS:O	1:F:220:ILE:HG13	2.13	0.48
1:D:123:ARG:CZ	1:D:127:VAL:HG21	2.43	0.48
1:D:153:GLN:C	1:D:155:GLY:N	2.69	0.48
1:D:244:LEU:CD1	1:D:418:ASN:HD21	2.25	0.48
1:E:123:ARG:CZ	1:E:127:VAL:HG21	2.43	0.48
1:E:124:TRP:HA	1:E:157:ASN:HD22	1.78	0.48
1:E:132:PHE:C	1:E:132:PHE:HD2	2.22	0.48
1:F:198:LEU:HD13	1:F:406:LEU:CD2	2.43	0.48
1:A:26:LEU:HD21	1:B:450:ALA:CB	2.43	0.48
1:A:124:TRP:HA	1:A:157:ASN:HD22	1.78	0.48
1:A:223:ILE:HD11	1:B:430:LEU:HD22	1.93	0.48
1:B:198:LEU:HD13	1:B:406:LEU:CD2	2.43	0.48
1:C:223:ILE:HD11	1:D:430:LEU:HD22	1.93	0.48
1:E:288:ILE:HD12	1:E:288:ILE:H	1.77	0.48
1:E:430:LEU:HD21	1:F:220:ILE:CG1	2.32	0.48
1:F:294:MET:O	1:F:297:ALA:HB3	2.12	0.48
1:F:443:PRO:O	1:F:446:SER:N	2.41	0.48
1:A:108:GLY:HA2	1:A:153:GLN:NE2	2.29	0.48
1:B:128:LEU:HB2	1:B:129:PRO:HD2	1.96	0.48
1:B:216:LYS:O	1:B:220:ILE:HG13	2.13	0.48
1:B:244:LEU:CD1	1:B:418:ASN:HD21	2.25	0.48
1:C:108:GLY:HA2	1:C:153:GLN:NE2	2.29	0.48
1:C:109:ILE:HD11	1:C:152:VAL:CG2	2.43	0.48
1:E:122:VAL:HB	1:E:160:ARG:HD2	1.94	0.48
1:E:278:ASP:C	1:E:280:LEU:N	2.71	0.48
1:F:132:PHE:C	1:F:132:PHE:HD2	2.22	0.48
1:B:153:GLN:C	1:B:155:GLY:N	2.69	0.48
1:C:26:LEU:HD21	1:D:450:ALA:CB	2.43	0.48
1:C:123:ARG:CZ	1:C:127:VAL:HG21	2.43	0.48
1:C:278:ASP:C	1:C:280:LEU:N	2.71	0.48
1:D:128:LEU:HB2	1:D:129:PRO:HD2	1.96	0.48
1:E:148:GLU:HG2	1:E:357:PHE:HD2	1.77	0.48
1:E:153:GLN:O	1:E:154:ILE:C	2.57	0.48
1:A:131:LYS:HZ2	1:A:153:GLN:NE2	2.10	0.48
1:A:434:LEU:C	1:A:436:ALA:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:LYS:HB3	1:C:30:LYS:HZ3	1.78	0.48
1:C:98:ARG:NH2	1:C:102:PRO:HB3	2.21	0.48
1:C:358:ALA:O	1:C:361:LEU:HB2	2.13	0.48
1:C:434:LEU:C	1:C:436:ALA:H	2.21	0.48
1:D:459:GLU:HG2	1:D:459:GLU:O	2.12	0.48
1:E:433:THR:HG22	1:F:216:LYS:HZ3	1.77	0.48
1:F:124:TRP:HA	1:F:157:ASN:HD22	1.78	0.48
1:F:434:LEU:C	1:F:436:ALA:N	2.70	0.48
1:A:132:PHE:C	1:A:132:PHE:HD2	2.22	0.48
1:A:267:PRO:O	1:A:270:ASN:HB2	2.14	0.48
1:A:312:THR:HG22	1:A:339:ALA:HB1	1.96	0.48
1:B:123:ARG:CZ	1:B:127:VAL:HG21	2.43	0.48
1:B:209:ARG:O	1:B:209:ARG:HG3	2.13	0.48
1:B:372:GLY:O	1:B:373:MET:C	2.55	0.48
1:C:124:TRP:HA	1:C:157:ASN:HD22	1.78	0.48
1:D:91:MET:O	1:D:93:GLY:N	2.47	0.48
1:D:315:GLY:H	1:D:318:ASN:ND2	2.10	0.48
1:D:358:ALA:O	1:D:361:LEU:HB2	2.13	0.48
1:E:91:MET:O	1:E:93:GLY:N	2.47	0.48
1:B:91:MET:O	1:B:93:GLY:N	2.47	0.48
1:B:108:GLY:HA2	1:B:153:GLN:NE2	2.29	0.48
1:C:128:LEU:HB2	1:C:129:PRO:HD2	1.96	0.48
1:C:216:LYS:O	1:C:220:ILE:HG13	2.13	0.48
1:C:312:THR:HG22	1:C:339:ALA:HB1	1.96	0.48
1:D:209:ARG:O	1:D:209:ARG:HG3	2.13	0.48
1:E:434:LEU:C	1:E:436:ALA:N	2.70	0.48
1:F:267:PRO:O	1:F:270:ASN:HB2	2.14	0.48
1:A:320:ILE:C	1:A:322:ILE:H	2.21	0.48
1:A:422:ILE:HD12	1:A:425:MET:HE2	1.96	0.48
1:B:312:THR:HG22	1:B:339:ALA:HB1	1.96	0.48
1:B:320:ILE:C	1:B:322:ILE:H	2.21	0.48
1:B:422:ILE:HD12	1:B:425:MET:HE2	1.95	0.48
1:C:267:PRO:O	1:C:270:ASN:HB2	2.14	0.48
1:C:433:THR:CG2	1:D:216:LYS:HE2	2.44	0.48
1:D:312:THR:HG22	1:D:339:ALA:HB1	1.96	0.48
1:D:372:GLY:O	1:D:373:MET:C	2.55	0.48
1:A:123:ARG:CZ	1:A:127:VAL:HG21	2.43	0.48
1:A:128:LEU:HB2	1:A:129:PRO:HD2	1.96	0.48
1:B:315:GLY:H	1:B:318:ASN:ND2	2.10	0.48
1:D:179:ALA:HB1	1:D:200:ILE:HG21	1.96	0.48
1:D:320:ILE:C	1:D:322:ILE:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:108:GLY:HA2	1:E:153:GLN:NE2	2.29	0.48
1:E:131:LYS:HZ2	1:E:153:GLN:NE2	2.10	0.48
1:E:148:GLU:CD	1:E:357:PHE:HB3	2.39	0.48
1:E:179:ALA:HB1	1:E:200:ILE:HG21	1.96	0.48
1:E:430:LEU:CD2	1:F:223:ILE:HD12	2.40	0.48
1:F:91:MET:O	1:F:93:GLY:N	2.47	0.48
1:A:433:THR:CG2	1:B:216:LYS:HE2	2.44	0.47
1:B:179:ALA:HB1	1:B:200:ILE:HG21	1.96	0.47
1:C:132:PHE:C	1:C:132:PHE:HD2	2.21	0.47
1:D:434:LEU:C	1:D:436:ALA:N	2.70	0.47
1:E:91:MET:C	1:E:93:GLY:N	2.70	0.47
1:E:443:PRO:O	1:E:446:SER:N	2.41	0.47
1:F:153:GLN:C	1:F:155:GLY:N	2.69	0.47
1:D:42:VAL:HG22	1:D:162:VAL:HG21	1.96	0.47
1:B:267:PRO:O	1:B:270:ASN:HB2	2.14	0.47
1:B:321:PRO:C	1:B:322:ILE:HD12	2.36	0.47
1:B:358:ALA:O	1:B:361:LEU:HB2	2.13	0.47
1:D:91:MET:C	1:D:93:GLY:N	2.70	0.47
1:D:108:GLY:HA2	1:D:153:GLN:NE2	2.29	0.47
1:D:132:PHE:C	1:D:132:PHE:HD2	2.21	0.47
1:E:153:GLN:C	1:E:155:GLY:N	2.69	0.47
1:E:267:PRO:O	1:E:270:ASN:HB2	2.14	0.47
1:F:266:GLY:HA3	1:F:400:ALA:HB1	1.97	0.47
1:A:216:LYS:O	1:A:220:ILE:HG13	2.13	0.47
1:B:91:MET:C	1:B:93:GLY:N	2.70	0.47
1:C:244:LEU:CD1	1:C:418:ASN:HD21	2.25	0.47
1:C:320:ILE:C	1:C:322:ILE:H	2.21	0.47
1:C:422:ILE:HD12	1:C:425:MET:HE2	1.96	0.47
1:D:422:ILE:HD12	1:D:425:MET:HE2	1.95	0.47
1:A:91:MET:O	1:A:93:GLY:N	2.47	0.47
1:A:98:ARG:NH2	1:A:102:PRO:HB3	2.21	0.47
1:B:42:VAL:HG22	1:B:162:VAL:HG21	1.97	0.47
1:C:266:GLY:HA3	1:C:400:ALA:HB1	1.97	0.47
1:E:315:GLY:H	1:E:318:ASN:ND2	2.10	0.47
1:F:108:GLY:HA2	1:F:153:GLN:NE2	2.29	0.47
1:F:209:ARG:O	1:F:209:ARG:HG3	2.13	0.47
1:A:148:GLU:CD	1:A:357:PHE:HB3	2.39	0.47
1:B:132:PHE:C	1:B:132:PHE:HD2	2.22	0.47
1:E:320:ILE:C	1:E:322:ILE:H	2.21	0.47
1:F:148:GLU:CD	1:F:357:PHE:HB3	2.39	0.47
1:A:244:LEU:CD1	1:A:418:ASN:HD21	2.25	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:GLY:HA3	1:A:400:ALA:HB1	1.97	0.47
1:B:153:GLN:O	1:B:154:ILE:C	2.57	0.47
1:C:74:ASN:ND2	1:C:77:LEU:HB3	2.29	0.47
1:C:91:MET:O	1:C:93:GLY:N	2.47	0.47
1:C:287:ASN:HB3	1:C:290:LYS:HB2	1.97	0.47
1:D:148:GLU:CD	1:D:357:PHE:HB3	2.39	0.47
1:D:153:GLN:O	1:D:154:ILE:C	2.57	0.47
1:D:267:PRO:O	1:D:270:ASN:HB2	2.14	0.47
1:E:266:GLY:HA3	1:E:400:ALA:HB1	1.97	0.47
1:E:433:THR:CG2	1:F:216:LYS:HE2	2.44	0.47
1:F:74:ASN:ND2	1:F:77:LEU:HB3	2.29	0.47
1:F:109:ILE:HD11	1:F:152:VAL:CG2	2.43	0.47
1:F:287:ASN:HB3	1:F:290:LYS:HB2	1.97	0.47
1:F:422:ILE:HD12	1:F:425:MET:HE2	1.95	0.47
1:C:153:GLN:O	1:C:154:ILE:C	2.57	0.47
1:C:433:THR:HG21	1:D:216:LYS:HE2	1.97	0.47
1:E:183:ALA:HB2	1:E:200:ILE:CG1	2.39	0.47
1:E:223:ILE:HD11	1:F:430:LEU:HD22	1.93	0.47
1:E:287:ASN:HB3	1:E:290:LYS:HB2	1.97	0.47
1:F:128:LEU:HB2	1:F:129:PRO:HD2	1.96	0.47
1:A:91:MET:C	1:A:93:GLY:N	2.70	0.47
1:A:179:ALA:HB1	1:A:200:ILE:HG21	1.96	0.47
1:A:287:ASN:HB3	1:A:290:LYS:HB2	1.97	0.47
1:B:74:ASN:ND2	1:B:77:LEU:HB3	2.29	0.47
1:B:148:GLU:CD	1:B:357:PHE:HB3	2.39	0.47
1:B:287:ASN:HB3	1:B:290:LYS:HB2	1.97	0.47
1:C:91:MET:C	1:C:93:GLY:N	2.70	0.47
1:E:249:LEU:HD11	1:F:230:ARG:CB	2.45	0.47
1:F:153:GLN:O	1:F:154:ILE:C	2.57	0.47
1:A:74:ASN:ND2	1:A:77:LEU:HB3	2.29	0.47
1:A:209:ARG:O	1:A:209:ARG:HG3	2.13	0.47
1:A:433:THR:HG21	1:B:216:LYS:HE2	1.97	0.47
1:B:266:GLY:HA3	1:B:400:ALA:HB1	1.97	0.47
1:C:148:GLU:CD	1:C:357:PHE:HB3	2.39	0.47
1:E:42:VAL:HG22	1:E:162:VAL:HG21	1.97	0.47
1:E:74:ASN:ND2	1:E:77:LEU:HB3	2.29	0.47
1:E:312:THR:HG22	1:E:339:ALA:HB1	1.96	0.47
1:F:312:THR:HG22	1:F:339:ALA:HB1	1.96	0.47
1:A:12:GLN:O	1:A:16:LEU:HB2	2.16	0.46
1:A:153:GLN:O	1:A:154:ILE:C	2.57	0.46
1:B:434:LEU:C	1:B:436:ALA:N	2.70	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:GLN:O	1:C:16:LEU:HB2	2.16	0.46
1:C:179:ALA:HB1	1:C:200:ILE:HG21	1.96	0.46
1:E:30:LYS:HB3	1:E:30:LYS:HZ3	1.79	0.46
1:E:216:LYS:HD3	1:F:434:LEU:CD2	2.45	0.46
1:A:430:LEU:HD21	1:B:220:ILE:CG1	2.32	0.46
1:C:42:VAL:HG22	1:C:162:VAL:HG21	1.97	0.46
1:E:108:GLY:HA3	1:E:153:GLN:HE21	1.81	0.46
1:E:422:ILE:HD12	1:E:425:MET:HE2	1.96	0.46
1:C:274:LEU:O	1:C:277:GLN:HG2	2.15	0.46
1:E:109:ILE:HD11	1:E:152:VAL:CG2	2.43	0.46
1:F:12:GLN:O	1:F:16:LEU:HB2	2.16	0.46
1:F:179:ALA:HB1	1:F:200:ILE:HG21	1.96	0.46
1:A:274:LEU:O	1:A:277:GLN:HG2	2.15	0.46
1:D:74:ASN:ND2	1:D:77:LEU:HB3	2.29	0.46
1:D:287:ASN:HB3	1:D:290:LYS:HB2	1.97	0.46
1:D:321:PRO:C	1:D:322:ILE:HD12	2.36	0.46
1:E:128:LEU:HB2	1:E:129:PRO:HD2	1.96	0.46
1:E:321:PRO:C	1:E:322:ILE:HD12	2.36	0.46
1:E:358:ALA:HB3	1:E:359:PRO:CD	2.46	0.46
1:F:244:LEU:CD1	1:F:418:ASN:HD21	2.25	0.46
1:A:74:ASN:ND2	1:A:77:LEU:CB	2.79	0.46
1:B:74:ASN:ND2	1:B:77:LEU:CB	2.79	0.46
1:C:209:ARG:O	1:C:209:ARG:HG3	2.13	0.46
1:C:216:LYS:HD3	1:D:434:LEU:CD2	2.45	0.46
1:D:74:ASN:ND2	1:D:77:LEU:CB	2.79	0.46
1:D:266:GLY:HA3	1:D:400:ALA:HB1	1.97	0.46
1:D:274:LEU:O	1:D:277:GLN:HG2	2.15	0.46
1:E:135:GLY:C	1:E:137:GLY:N	2.73	0.46
1:A:320:ILE:C	1:A:322:ILE:N	2.74	0.46
1:B:12:GLN:O	1:B:16:LEU:HB2	2.16	0.46
1:C:320:ILE:C	1:C:322:ILE:N	2.74	0.46
1:E:74:ASN:ND2	1:E:77:LEU:CB	2.79	0.46
1:E:255:TYR:CG	1:E:424:PRO:HB3	2.51	0.46
1:E:320:ILE:C	1:E:322:ILE:N	2.74	0.46
1:A:249:LEU:HD11	1:B:230:ARG:CB	2.45	0.46
1:C:74:ASN:ND2	1:C:77:LEU:CB	2.79	0.46
1:C:108:GLY:HA3	1:C:153:GLN:HE21	1.81	0.46
1:E:12:GLN:O	1:E:16:LEU:HB2	2.16	0.46
1:E:22:ILE:HD13	1:F:454:ALA:HB2	1.98	0.46
1:E:30:LYS:HB3	1:E:30:LYS:HZ2	1.78	0.46
1:A:42:VAL:HG22	1:A:162:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:LEU:H	1:A:418:ASN:ND2	2.14	0.46
1:C:249:LEU:HD11	1:D:230:ARG:CB	2.45	0.46
1:C:255:TYR:CG	1:C:424:PRO:HB3	2.51	0.46
1:D:94:TYR:CZ	1:D:352:ALA:HB2	2.51	0.46
1:F:274:LEU:O	1:F:277:GLN:HG2	2.15	0.46
1:F:358:ALA:HB3	1:F:359:PRO:CD	2.46	0.46
1:A:109:ILE:HD11	1:A:152:VAL:CG2	2.43	0.46
1:A:216:LYS:HD3	1:B:434:LEU:CD2	2.45	0.46
1:A:255:TYR:CG	1:A:424:PRO:HB3	2.51	0.46
1:B:94:TYR:CZ	1:B:352:ALA:HB2	2.51	0.46
1:B:274:LEU:O	1:B:277:GLN:HG2	2.15	0.46
1:C:391:ILE:HD12	1:C:391:ILE:N	2.31	0.46
1:C:430:LEU:HD21	1:D:220:ILE:CG1	2.32	0.46
1:E:94:TYR:CZ	1:E:352:ALA:HB2	2.51	0.46
1:F:255:TYR:CG	1:F:424:PRO:HB3	2.51	0.46
1:A:108:GLY:HA3	1:A:153:GLN:HE21	1.81	0.46
1:B:358:ALA:HB3	1:B:359:PRO:CD	2.46	0.46
1:D:12:GLN:O	1:D:16:LEU:HB2	2.16	0.46
1:E:127:VAL:HB	1:E:157:ASN:HD21	1.81	0.46
1:F:74:ASN:ND2	1:F:77:LEU:CB	2.79	0.46
1:C:244:LEU:H	1:C:418:ASN:ND2	2.14	0.45
1:C:284:HIS:CE1	1:C:291:TRP:CD2	3.04	0.45
1:D:283:VAL:O	1:D:283:VAL:HG12	2.16	0.45
1:D:358:ALA:HB3	1:D:359:PRO:CD	2.46	0.45
1:E:433:THR:HG21	1:F:216:LYS:HE2	1.97	0.45
1:F:284:HIS:C	1:F:286:GLY:H	2.25	0.45
1:F:391:ILE:N	1:F:391:ILE:HD12	2.31	0.45
1:A:391:ILE:N	1:A:391:ILE:HD12	2.31	0.45
1:C:128:LEU:CB	1:C:129:PRO:CD	2.95	0.45
1:D:244:LEU:H	1:D:418:ASN:ND2	2.14	0.45
1:D:256:LEU:O	1:D:257:ILE:C	2.59	0.45
1:D:276:MET:HG2	1:D:280:LEU:HD23	1.98	0.45
1:F:42:VAL:HG22	1:F:162:VAL:HG21	1.97	0.45
1:F:108:GLY:HA3	1:F:153:GLN:HE21	1.81	0.45
1:B:95:PHE:O	1:B:96:LEU:C	2.60	0.45
1:B:255:TYR:CG	1:B:424:PRO:HB3	2.51	0.45
1:D:95:PHE:O	1:D:96:LEU:C	2.60	0.45
1:D:128:LEU:CB	1:D:129:PRO:CD	2.95	0.45
1:D:255:TYR:CG	1:D:424:PRO:HB3	2.51	0.45
1:D:284:HIS:CE1	1:D:291:TRP:CD2	3.04	0.45
1:E:276:MET:HG2	1:E:280:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:VAL:HB	1:A:157:ASN:HD21	1.81	0.45
1:A:284:HIS:CE1	1:A:291:TRP:CD2	3.04	0.45
1:A:316:GLY:HA2	1:A:340:ARG:NH2	2.32	0.45
1:B:256:LEU:O	1:B:257:ILE:C	2.59	0.45
1:B:276:MET:HG2	1:B:280:LEU:HD23	1.98	0.45
1:C:94:TYR:CZ	1:C:352:ALA:HB2	2.51	0.45
1:E:284:HIS:C	1:E:286:GLY:H	2.25	0.45
1:E:286:GLY:O	1:E:288:ILE:HD12	2.17	0.45
1:E:391:ILE:HD12	1:E:391:ILE:N	2.31	0.45
1:F:94:TYR:CZ	1:F:352:ALA:HB2	2.51	0.45
1:A:94:TYR:CZ	1:A:352:ALA:HB2	2.51	0.45
1:A:128:LEU:CB	1:A:129:PRO:CD	2.95	0.45
1:A:244:LEU:N	1:A:244:LEU:CD1	2.79	0.45
1:A:316:GLY:C	1:A:318:ASN:H	2.25	0.45
1:A:430:LEU:HD11	1:B:219:PHE:HB3	1.99	0.45
1:B:186:LEU:HD22	1:B:199:PHE:CD2	2.52	0.45
1:B:283:VAL:O	1:B:283:VAL:HG12	2.16	0.45
1:C:316:GLY:HA2	1:C:340:ARG:NH2	2.32	0.45
1:C:430:LEU:HD11	1:D:219:PHE:HB3	1.99	0.45
1:D:391:ILE:N	1:D:391:ILE:HD12	2.31	0.45
1:E:316:GLY:HA2	1:E:340:ARG:NH2	2.32	0.45
1:F:91:MET:C	1:F:93:GLY:N	2.70	0.45
1:F:283:VAL:O	1:F:283:VAL:HG12	2.16	0.45
1:F:286:GLY:O	1:F:288:ILE:HD12	2.17	0.45
1:A:284:HIS:C	1:A:286:GLY:H	2.25	0.45
1:A:317:PHE:C	1:A:317:PHE:CD1	2.95	0.45
1:B:317:PHE:C	1:B:317:PHE:CD1	2.95	0.45
1:B:320:ILE:C	1:B:322:ILE:N	2.74	0.45
1:C:316:GLY:C	1:C:318:ASN:H	2.25	0.45
1:D:127:VAL:HB	1:D:157:ASN:HD21	1.81	0.45
1:D:316:GLY:C	1:D:318:ASN:H	2.25	0.45
1:E:128:LEU:CB	1:E:129:PRO:CD	2.95	0.45
1:E:274:LEU:O	1:E:277:GLN:HG2	2.15	0.45
1:E:444:LEU:O	1:E:448:ILE:HG13	2.17	0.45
1:A:358:ALA:HB3	1:A:359:PRO:CD	2.46	0.45
1:B:127:VAL:HB	1:B:157:ASN:HD21	1.81	0.45
1:B:244:LEU:H	1:B:418:ASN:ND2	2.14	0.45
1:B:316:GLY:C	1:B:318:ASN:H	2.25	0.45
1:C:135:GLY:C	1:C:137:GLY:N	2.73	0.45
1:C:244:LEU:N	1:C:244:LEU:CD1	2.79	0.45
1:C:317:PHE:C	1:C:317:PHE:CD1	2.95	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:LEU:HD22	1:D:199:PHE:CD2	2.52	0.45
1:D:320:ILE:C	1:D:322:ILE:N	2.74	0.45
1:E:186:LEU:HD22	1:E:199:PHE:CD2	2.52	0.45
1:E:244:LEU:H	1:E:418:ASN:ND2	2.14	0.45
1:F:244:LEU:H	1:F:418:ASN:ND2	2.14	0.45
1:F:258:LEU:HD13	1:F:371:PHE:CB	2.47	0.45
1:F:284:HIS:CE1	1:F:291:TRP:CD2	3.04	0.45
1:F:316:GLY:HA2	1:F:340:ARG:NH2	2.32	0.45
1:F:444:LEU:O	1:F:448:ILE:HG13	2.17	0.45
1:A:22:ILE:HD13	1:B:454:ALA:HB2	1.98	0.45
1:A:251:THR:HG22	1:A:255:TYR:CE1	2.47	0.45
1:B:108:GLY:HA3	1:B:153:GLN:HE21	1.81	0.45
1:B:284:HIS:CE1	1:B:291:TRP:CD2	3.04	0.45
1:B:391:ILE:HD12	1:B:391:ILE:N	2.31	0.45
1:C:256:LEU:O	1:C:257:ILE:C	2.59	0.45
1:C:284:HIS:C	1:C:286:GLY:H	2.24	0.45
1:D:286:GLY:O	1:D:288:ILE:HD12	2.17	0.45
1:F:135:GLY:C	1:F:137:GLY:N	2.73	0.45
1:F:317:PHE:C	1:F:317:PHE:CD1	2.95	0.45
1:F:423:LEU:HD12	1:F:423:LEU:HA	1.81	0.45
1:A:258:LEU:HD13	1:A:371:PHE:CB	2.47	0.45
1:B:42:VAL:O	1:B:46:VAL:HG23	2.17	0.45
1:B:51:VAL:HG21	1:B:232:PHE:CG	2.52	0.45
1:B:258:LEU:HD13	1:B:371:PHE:CB	2.47	0.45
1:B:286:GLY:O	1:B:288:ILE:HD12	2.17	0.45
1:C:127:VAL:HB	1:C:157:ASN:HD21	1.81	0.45
1:D:51:VAL:HG21	1:D:232:PHE:CG	2.52	0.45
1:D:258:LEU:HD13	1:D:371:PHE:CB	2.47	0.45
1:E:316:GLY:C	1:E:318:ASN:H	2.25	0.45
1:F:186:LEU:HD22	1:F:199:PHE:CD2	2.52	0.45
1:F:256:LEU:O	1:F:257:ILE:C	2.59	0.45
1:A:75:TYR:N	1:A:76:PRO:CD	2.80	0.45
1:A:135:GLY:C	1:A:137:GLY:N	2.73	0.45
1:C:22:ILE:HD13	1:D:454:ALA:HB2	1.98	0.45
1:C:413:LEU:HB2	1:C:425:MET:HE1	1.99	0.45
1:D:108:GLY:HA3	1:D:153:GLN:HE21	1.81	0.45
1:D:243:LYS:HD2	1:D:243:LYS:O	2.17	0.45
1:E:258:LEU:HD13	1:E:371:PHE:CB	2.47	0.45
1:F:30:LYS:O	1:F:30:LYS:CG	2.65	0.45
1:F:127:VAL:HB	1:F:157:ASN:HD21	1.81	0.45
1:F:276:MET:HG2	1:F:280:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:316:GLY:C	1:F:318:ASN:H	2.25	0.45
1:A:256:LEU:O	1:A:257:ILE:C	2.59	0.44
1:A:283:VAL:HG12	1:A:283:VAL:O	2.16	0.44
1:A:413:LEU:HB2	1:A:425:MET:HE1	1.99	0.44
1:B:128:LEU:CB	1:B:129:PRO:CD	2.95	0.44
1:B:243:LYS:O	1:B:243:LYS:HD2	2.17	0.44
1:C:358:ALA:HB3	1:C:359:PRO:CD	2.46	0.44
1:D:30:LYS:HB3	1:D:30:LYS:HZ2	1.81	0.44
1:D:42:VAL:O	1:D:46:VAL:HG23	2.17	0.44
1:D:122:VAL:HB	1:D:160:ARG:HD3	1.99	0.44
1:D:244:LEU:N	1:D:244:LEU:CD1	2.79	0.44
1:E:256:LEU:O	1:E:257:ILE:C	2.60	0.44
1:E:284:HIS:CE1	1:E:291:TRP:CD2	3.04	0.44
1:E:317:PHE:C	1:E:317:PHE:CD1	2.95	0.44
1:F:128:LEU:CB	1:F:129:PRO:CD	2.95	0.44
1:F:252:LEU:HD22	1:F:427:ILE:HD12	1.99	0.44
1:A:51:VAL:HG21	1:A:232:PHE:CG	2.52	0.44
1:A:444:LEU:O	1:A:448:ILE:HG13	2.17	0.44
1:C:258:LEU:HD13	1:C:371:PHE:CB	2.47	0.44
1:E:104:ALA:HB2	1:E:127:VAL:HG13	1.99	0.44
1:F:122:VAL:HB	1:F:160:ARG:HD3	1.98	0.44
1:F:243:LYS:HD2	1:F:243:LYS:O	2.17	0.44
1:F:413:LEU:HB2	1:F:425:MET:HE1	1.99	0.44
1:A:30:LYS:O	1:A:30:LYS:CG	2.65	0.44
1:B:316:GLY:HA2	1:B:340:ARG:NH2	2.32	0.44
1:C:95:PHE:O	1:C:96:LEU:C	2.59	0.44
1:C:286:GLY:O	1:C:288:ILE:HD12	2.17	0.44
1:C:444:LEU:O	1:C:448:ILE:HG13	2.17	0.44
1:E:51:VAL:HG21	1:E:232:PHE:CG	2.52	0.44
1:E:243:LYS:O	1:E:243:LYS:HD2	2.17	0.44
1:E:267:PRO:HG2	1:E:268:ILE:H	1.82	0.44
1:E:340:ARG:HB3	1:E:340:ARG:HH11	1.82	0.44
1:E:413:LEU:HB2	1:E:425:MET:HE1	1.99	0.44
1:F:251:THR:HG22	1:F:255:TYR:CE1	2.47	0.44
1:A:186:LEU:HD22	1:A:199:PHE:CD2	2.52	0.44
1:B:444:LEU:O	1:B:448:ILE:HG13	2.17	0.44
1:C:51:VAL:HG21	1:C:232:PHE:CG	2.52	0.44
1:C:186:LEU:HD22	1:C:199:PHE:CD2	2.52	0.44
1:C:252:LEU:HD22	1:C:427:ILE:HD12	1.99	0.44
1:D:135:GLY:C	1:D:137:GLY:N	2.73	0.44
1:D:316:GLY:HA2	1:D:340:ARG:NH2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:444:LEU:O	1:D:448:ILE:HG13	2.17	0.44
1:E:75:TYR:N	1:E:76:PRO:CD	2.80	0.44
1:E:283:VAL:O	1:E:283:VAL:HG12	2.16	0.44
1:E:406:LEU:HD21	1:F:198:LEU:HD21	2.00	0.44
1:F:340:ARG:HB3	1:F:340:ARG:HH11	1.83	0.44
1:A:95:PHE:O	1:A:96:LEU:C	2.60	0.44
1:A:276:MET:HG2	1:A:280:LEU:HD23	1.98	0.44
1:B:284:HIS:C	1:B:286:GLY:H	2.25	0.44
1:C:75:TYR:N	1:C:76:PRO:CD	2.80	0.44
1:D:340:ARG:HB3	1:D:340:ARG:HH11	1.83	0.44
1:E:122:VAL:HB	1:E:160:ARG:HD3	1.99	0.44
1:E:252:LEU:HD22	1:E:427:ILE:HD12	1.99	0.44
1:F:42:VAL:O	1:F:46:VAL:HG23	2.17	0.44
1:A:122:VAL:HB	1:A:160:ARG:HD3	1.99	0.44
1:A:124:TRP:HB2	1:A:128:LEU:HG	2.00	0.44
1:A:198:LEU:HD21	1:B:406:LEU:HD21	2.00	0.44
1:A:286:GLY:O	1:A:288:ILE:HD12	2.17	0.44
1:B:329:SER:O	1:B:330:MET:C	2.61	0.44
1:B:340:ARG:HB3	1:B:340:ARG:HH11	1.83	0.44
1:C:198:LEU:HD21	1:D:406:LEU:HD21	2.00	0.44
1:C:283:VAL:O	1:C:283:VAL:HG12	2.16	0.44
1:E:124:TRP:HB2	1:E:128:LEU:HG	2.00	0.44
1:E:207:GLN:HE22	1:F:28:ARG:NH2	2.15	0.44
1:F:104:ALA:HB2	1:F:127:VAL:HG13	1.99	0.44
1:A:42:VAL:O	1:A:46:VAL:HG23	2.17	0.44
1:A:340:ARG:HB3	1:A:340:ARG:HH11	1.83	0.44
1:B:122:VAL:HB	1:B:160:ARG:HD3	1.99	0.44
1:B:244:LEU:N	1:B:244:LEU:CD1	2.79	0.44
1:B:314:GLY:C	1:B:316:GLY:N	2.76	0.44
1:C:124:TRP:HB2	1:C:128:LEU:HG	2.00	0.44
1:C:243:LYS:HD2	1:C:243:LYS:O	2.17	0.44
1:D:288:ILE:O	1:D:288:ILE:CG2	2.66	0.44
1:E:95:PHE:O	1:E:96:LEU:C	2.59	0.44
1:E:434:LEU:CD2	1:F:216:LYS:HD3	2.46	0.44
1:A:243:LYS:HD2	1:A:243:LYS:O	2.17	0.44
1:B:108:GLY:CA	1:B:153:GLN:NE2	2.81	0.44
1:B:252:LEU:HD22	1:B:427:ILE:HD12	1.99	0.44
1:B:267:PRO:HG2	1:B:268:ILE:H	1.82	0.44
1:C:30:LYS:O	1:C:30:LYS:CG	2.65	0.44
1:C:42:VAL:O	1:C:46:VAL:HG23	2.17	0.44
1:C:251:THR:HG22	1:C:255:TYR:CE1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:340:ARG:HB3	1:C:340:ARG:HH11	1.83	0.44
1:D:109:ILE:HD11	1:D:152:VAL:CG2	2.43	0.44
1:D:284:HIS:C	1:D:286:GLY:H	2.25	0.44
1:D:314:GLY:C	1:D:316:GLY:N	2.76	0.44
1:D:329:SER:O	1:D:330:MET:C	2.61	0.44
1:E:198:LEU:HD21	1:F:406:LEU:HD21	2.00	0.44
1:E:288:ILE:O	1:E:288:ILE:CG2	2.66	0.44
1:E:430:LEU:HD11	1:F:219:PHE:HB3	1.99	0.44
1:F:379:PHE:CD1	1:F:379:PHE:N	2.86	0.44
1:A:252:LEU:HD22	1:A:427:ILE:HD12	1.99	0.44
1:B:30:LYS:HB3	1:B:30:LYS:HZ2	1.83	0.44
1:C:122:VAL:HB	1:C:160:ARG:HD3	1.99	0.44
1:C:157:ASN:O	1:C:158:ILE:C	2.61	0.44
1:C:276:MET:HG2	1:C:280:LEU:HD23	1.98	0.44
1:E:30:LYS:O	1:E:30:LYS:CG	2.65	0.44
1:E:42:VAL:O	1:E:46:VAL:HG23	2.17	0.44
1:E:329:SER:O	1:E:330:MET:C	2.61	0.44
1:E:449:LEU:O	1:E:450:ALA:C	2.61	0.44
1:F:90:ALA:HB3	1:F:296:GLY:HA2	2.00	0.44
1:B:21:LEU:O	1:B:24:GLN:N	2.52	0.43
1:C:91:MET:O	1:C:92:PHE:C	2.61	0.43
1:D:122:VAL:HA	1:D:123:ARG:NH1	2.33	0.43
1:D:317:PHE:C	1:D:317:PHE:CD1	2.95	0.43
1:E:90:ALA:HB3	1:E:296:GLY:HA2	2.00	0.43
1:E:98:ARG:NH2	1:E:102:PRO:CB	2.79	0.43
1:F:122:VAL:HA	1:F:123:ARG:NH1	2.34	0.43
1:F:124:TRP:HB2	1:F:128:LEU:HG	2.00	0.43
1:A:91:MET:O	1:A:92:PHE:C	2.61	0.43
1:A:104:ALA:HB2	1:A:127:VAL:HG13	1.99	0.43
1:A:157:ASN:O	1:A:158:ILE:C	2.61	0.43
1:A:450:ALA:CB	1:B:26:LEU:CD2	2.94	0.43
1:B:91:MET:O	1:B:92:PHE:C	2.61	0.43
1:B:122:VAL:HA	1:B:123:ARG:NH1	2.34	0.43
1:B:135:GLY:C	1:B:137:GLY:N	2.73	0.43
1:B:288:ILE:O	1:B:288:ILE:CG2	2.66	0.43
1:C:104:ALA:HB2	1:C:127:VAL:HG13	1.99	0.43
1:C:207:GLN:HE22	1:D:28:ARG:NH2	2.15	0.43
1:D:108:GLY:CA	1:D:153:GLN:NE2	2.81	0.43
1:D:252:LEU:HD22	1:D:427:ILE:HD12	1.99	0.43
1:E:108:GLY:CA	1:E:153:GLN:NE2	2.81	0.43
1:F:267:PRO:HG2	1:F:268:ILE:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:VAL:HA	1:A:123:ARG:NH1	2.34	0.43
1:A:314:GLY:C	1:A:316:GLY:N	2.76	0.43
1:B:379:PHE:CD1	1:B:379:PHE:N	2.86	0.43
1:C:288:ILE:O	1:C:288:ILE:CG2	2.66	0.43
1:D:21:LEU:O	1:D:24:GLN:N	2.52	0.43
1:D:91:MET:O	1:D:92:PHE:C	2.61	0.43
1:F:21:LEU:O	1:F:24:GLN:N	2.51	0.43
1:F:278:ASP:C	1:F:280:LEU:N	2.71	0.43
1:F:288:ILE:O	1:F:288:ILE:CG2	2.66	0.43
1:B:30:LYS:O	1:B:30:LYS:CG	2.65	0.43
1:B:100:TYR:O	1:B:126:ARG:HD3	2.18	0.43
1:C:131:LYS:NZ	1:C:153:GLN:HE21	2.16	0.43
1:C:434:LEU:CD2	1:D:216:LYS:HD3	2.46	0.43
1:D:100:TYR:O	1:D:126:ARG:HD3	2.18	0.43
1:D:183:ALA:HB2	1:D:200:ILE:CG1	2.39	0.43
1:D:449:LEU:O	1:D:450:ALA:C	2.61	0.43
1:E:28:ARG:NE	1:F:443:PRO:HG2	2.33	0.43
1:F:51:VAL:HG21	1:F:232:PHE:CG	2.52	0.43
1:F:199:PHE:C	1:F:201:ILE:H	2.26	0.43
1:A:148:GLU:CD	1:A:148:GLU:N	2.76	0.43
1:A:207:GLN:HE22	1:B:28:ARG:NH2	2.15	0.43
1:A:288:ILE:O	1:A:288:ILE:CG2	2.66	0.43
1:B:109:ILE:HD11	1:B:152:VAL:CG2	2.43	0.43
1:C:108:GLY:CA	1:C:153:GLN:NE2	2.81	0.43
1:C:122:VAL:HA	1:C:123:ARG:NH1	2.34	0.43
1:C:124:TRP:CG	1:C:125:TRP:N	2.86	0.43
1:C:148:GLU:CD	1:C:148:GLU:N	2.76	0.43
1:D:267:PRO:HG2	1:D:268:ILE:H	1.82	0.43
1:E:122:VAL:HA	1:E:123:ARG:NH1	2.34	0.43
1:F:100:TYR:O	1:F:126:ARG:HD3	2.18	0.43
1:F:148:GLU:CD	1:F:148:GLU:N	2.76	0.43
1:F:191:ASN:OD1	1:F:230:ARG:NH1	2.52	0.43
1:F:199:PHE:CD1	1:F:407:THR:HG21	2.54	0.43
1:A:90:ALA:HB3	1:A:296:GLY:HA2	2.00	0.43
1:A:124:TRP:CG	1:A:125:TRP:N	2.86	0.43
1:A:265:PHE:CE2	1:A:269:PHE:HB2	2.54	0.43
1:B:104:ALA:HB2	1:B:127:VAL:HG13	1.99	0.43
1:B:116:LEU:HB3	1:B:206:PRO:HD3	2.01	0.43
1:B:199:PHE:CD1	1:B:407:THR:HG21	2.54	0.43
1:B:266:GLY:N	1:B:267:PRO:HD2	2.33	0.43
1:B:315:GLY:N	1:B:318:ASN:ND2	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:ASP:OD1	1:C:216:LYS:NZ	2.51	0.43
1:C:90:ALA:HB3	1:C:296:GLY:HA2	2.00	0.43
1:C:199:PHE:CD1	1:C:407:THR:HG21	2.54	0.43
1:C:267:PRO:HG2	1:C:268:ILE:H	1.82	0.43
1:D:104:ALA:HB2	1:D:127:VAL:HG13	1.99	0.43
1:D:116:LEU:HB3	1:D:206:PRO:HD3	2.01	0.43
1:D:315:GLY:N	1:D:318:ASN:ND2	2.67	0.43
1:D:321:PRO:HD2	1:D:322:ILE:CD1	2.49	0.43
1:D:379:PHE:N	1:D:379:PHE:CD1	2.86	0.43
1:E:116:LEU:HB3	1:E:206:PRO:HD3	2.01	0.43
1:E:124:TRP:CG	1:E:125:TRP:N	2.86	0.43
1:E:244:LEU:H	1:E:418:ASN:HD21	1.67	0.43
1:F:98:ARG:NH2	1:F:102:PRO:CB	2.80	0.43
1:F:124:TRP:CG	1:F:125:TRP:N	2.86	0.43
1:A:131:LYS:NZ	1:A:153:GLN:HE21	2.16	0.43
1:A:199:PHE:C	1:A:201:ILE:H	2.26	0.43
1:A:321:PRO:HD2	1:A:322:ILE:CD1	2.49	0.43
1:B:449:LEU:O	1:B:450:ALA:C	2.61	0.43
1:C:100:TYR:O	1:C:126:ARG:HD3	2.18	0.43
1:C:209:ARG:HG2	1:C:209:ARG:HH11	1.84	0.43
1:C:265:PHE:CE2	1:C:269:PHE:HB2	2.54	0.43
1:C:314:GLY:C	1:C:316:GLY:N	2.76	0.43
1:D:199:PHE:CD1	1:D:407:THR:HG21	2.54	0.43
1:E:157:ASN:O	1:E:158:ILE:C	2.61	0.43
1:E:191:ASN:OD1	1:E:230:ARG:NH1	2.52	0.43
1:E:315:GLY:N	1:E:318:ASN:ND2	2.67	0.43
1:E:379:PHE:CD1	1:E:379:PHE:N	2.86	0.43
1:F:183:ALA:HB2	1:F:200:ILE:CG1	2.39	0.43
1:F:266:GLY:N	1:F:267:PRO:HD2	2.34	0.43
1:F:322:ILE:C	1:F:324:THR:N	2.77	0.43
1:A:209:ARG:HG2	1:A:209:ARG:HH11	1.84	0.43
1:A:267:PRO:HG2	1:A:268:ILE:H	1.82	0.43
1:A:274:LEU:HD12	1:A:277:GLN:NE2	2.34	0.43
1:A:288:ILE:H	1:A:288:ILE:CD1	2.32	0.43
1:B:413:LEU:HB2	1:B:425:MET:HE1	1.99	0.43
1:C:28:ARG:NE	1:D:443:PRO:HG2	2.33	0.43
1:C:266:GLY:N	1:C:267:PRO:HD2	2.34	0.43
1:D:30:LYS:O	1:D:30:LYS:CG	2.65	0.43
1:E:266:GLY:N	1:E:267:PRO:HD2	2.33	0.43
1:F:95:PHE:O	1:F:96:LEU:C	2.60	0.43
1:F:131:LYS:NZ	1:F:153:GLN:HE21	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:288:ILE:H	1:F:288:ILE:CD1	2.32	0.43
1:A:100:TYR:O	1:A:126:ARG:HD3	2.18	0.43
1:A:108:GLY:CA	1:A:153:GLN:NE2	2.81	0.43
1:A:266:GLY:N	1:A:267:PRO:HD2	2.34	0.43
1:A:321:PRO:CA	1:A:322:ILE:HD12	2.49	0.43
1:A:406:LEU:HD21	1:B:198:LEU:HD21	2.00	0.43
1:B:191:ASN:OD1	1:B:230:ARG:NH1	2.52	0.43
1:B:244:LEU:H	1:B:418:ASN:HD21	1.67	0.43
1:B:273:VAL:HG13	1:B:274:LEU:N	2.34	0.43
1:C:143:MET:HE2	1:C:347:CYS:HB3	2.01	0.43
1:C:191:ASN:OD1	1:C:230:ARG:NH1	2.52	0.43
1:C:199:PHE:C	1:C:201:ILE:H	2.26	0.43
1:C:274:LEU:HD12	1:C:277:GLN:NE2	2.34	0.43
1:C:288:ILE:H	1:C:288:ILE:CD1	2.32	0.43
1:E:199:PHE:CD1	1:E:407:THR:HG21	2.54	0.43
1:E:273:VAL:HG13	1:E:274:LEU:N	2.34	0.43
1:F:119:GLN:O	1:F:120:ARG:C	2.62	0.43
1:F:270:ASN:HA	1:F:273:VAL:HG12	2.01	0.43
1:A:45:LEU:O	1:A:46:VAL:C	2.62	0.43
1:A:329:SER:O	1:A:330:MET:C	2.61	0.43
1:A:379:PHE:N	1:A:379:PHE:CD1	2.86	0.43
1:B:57:VAL:HG22	1:B:136:LEU:HD12	2.01	0.43
1:B:78:LEU:C	1:B:78:LEU:HD13	2.44	0.43
1:B:124:TRP:CG	1:B:125:TRP:N	2.86	0.43
1:B:265:PHE:CE2	1:B:269:PHE:HB2	2.54	0.43
1:B:321:PRO:HD2	1:B:322:ILE:CD1	2.49	0.43
1:D:57:VAL:HG22	1:D:136:LEU:HD12	2.01	0.43
1:D:191:ASN:OD1	1:D:230:ARG:NH1	2.52	0.43
1:D:423:LEU:HD12	1:D:423:LEU:HA	1.81	0.43
1:E:21:LEU:O	1:E:24:GLN:N	2.52	0.43
1:E:29:ASP:OD1	1:E:216:LYS:NZ	2.51	0.43
1:E:202:GLU:HG2	1:E:202:GLU:O	2.19	0.43
1:F:91:MET:O	1:F:92:PHE:C	2.61	0.43
1:F:215:ILE:HG22	1:F:216:LYS:N	2.34	0.43
1:F:321:PRO:HD2	1:F:322:ILE:CD1	2.49	0.43
1:A:28:ARG:NE	1:B:443:PRO:HG2	2.33	0.42
1:A:69:VAL:O	1:A:69:VAL:HG12	2.19	0.42
1:A:116:LEU:HB3	1:A:206:PRO:HD3	2.01	0.42
1:A:143:MET:HE2	1:A:347:CYS:HB3	2.01	0.42
1:A:191:ASN:OD1	1:A:230:ARG:NH1	2.52	0.42
1:A:194:LEU:HD13	1:B:410:ILE:CD1	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:LYS:NZ	1:B:153:GLN:HE21	2.16	0.42
1:B:150:PRO:CD	1:B:354:GLY:HA2	2.49	0.42
1:B:288:ILE:H	1:B:288:ILE:CD1	2.32	0.42
1:C:69:VAL:O	1:C:69:VAL:HG12	2.19	0.42
1:C:321:PRO:CA	1:C:322:ILE:HD12	2.49	0.42
1:C:322:ILE:C	1:C:324:THR:N	2.77	0.42
1:C:406:LEU:HD21	1:D:198:LEU:HD21	2.00	0.42
1:D:25:LEU:C	1:D:27:GLU:H	2.27	0.42
1:D:78:LEU:C	1:D:78:LEU:HD13	2.44	0.42
1:D:124:TRP:CG	1:D:125:TRP:N	2.86	0.42
1:D:265:PHE:CE2	1:D:269:PHE:HB2	2.54	0.42
1:E:100:TYR:O	1:E:126:ARG:HD3	2.18	0.42
1:F:273:VAL:HG13	1:F:274:LEU:N	2.34	0.42
1:F:449:LEU:O	1:F:450:ALA:C	2.61	0.42
1:A:434:LEU:CD2	1:B:216:LYS:HD3	2.46	0.42
1:A:449:LEU:O	1:A:450:ALA:C	2.61	0.42
1:B:148:GLU:CD	1:B:148:GLU:N	2.76	0.42
1:B:202:GLU:O	1:B:202:GLU:HG2	2.19	0.42
1:B:209:ARG:HG2	1:B:209:ARG:HH11	1.84	0.42
1:B:214:SER:O	1:B:215:ILE:C	2.63	0.42
1:C:379:PHE:N	1:C:379:PHE:CD1	2.86	0.42
1:D:124:TRP:HB2	1:D:128:LEU:HG	2.00	0.42
1:D:266:GLY:N	1:D:267:PRO:HD2	2.34	0.42
1:D:273:VAL:HG13	1:D:274:LEU:N	2.34	0.42
1:D:288:ILE:H	1:D:288:ILE:CD1	2.32	0.42
1:D:413:LEU:HB2	1:D:425:MET:HE1	1.99	0.42
1:E:46:VAL:HG11	1:E:181:GLY:O	2.19	0.42
1:E:199:PHE:C	1:E:201:ILE:H	2.26	0.42
1:E:214:SER:O	1:E:215:ILE:C	2.63	0.42
1:E:215:ILE:HG22	1:E:216:LYS:N	2.34	0.42
1:F:25:LEU:C	1:F:27:GLU:H	2.27	0.42
1:F:69:VAL:O	1:F:69:VAL:HG12	2.19	0.42
1:F:108:GLY:CA	1:F:153:GLN:NE2	2.81	0.42
1:F:209:ARG:HG2	1:F:209:ARG:HH11	1.84	0.42
1:A:21:LEU:O	1:A:24:GLN:N	2.52	0.42
1:A:199:PHE:CD1	1:A:407:THR:HG21	2.54	0.42
1:B:199:PHE:C	1:B:201:ILE:H	2.26	0.42
1:B:322:ILE:C	1:B:324:THR:N	2.77	0.42
1:C:21:LEU:O	1:C:24:GLN:N	2.52	0.42
1:C:119:GLN:O	1:C:120:ARG:C	2.62	0.42
1:C:273:VAL:HG13	1:C:274:LEU:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:321:PRO:HD2	1:C:322:ILE:CD1	2.49	0.42
1:C:329:SER:O	1:C:330:MET:C	2.61	0.42
1:D:150:PRO:CD	1:D:354:GLY:HA2	2.49	0.42
1:D:324:THR:O	1:D:326:GLY:N	2.53	0.42
1:E:119:GLN:O	1:E:120:ARG:C	2.62	0.42
1:E:150:PRO:CD	1:E:354:GLY:HA2	2.49	0.42
1:E:176:THR:HA	1:E:213:ILE:HG23	2.01	0.42
1:E:414:GLU:OE1	1:F:419:TYR:CE1	2.73	0.42
1:F:176:THR:HA	1:F:213:ILE:HG23	2.01	0.42
1:F:252:LEU:HD13	1:F:427:ILE:HD11	2.01	0.42
1:A:25:LEU:C	1:A:27:GLU:H	2.27	0.42
1:A:183:ALA:C	1:A:185:GLY:N	2.77	0.42
1:A:252:LEU:HD13	1:A:427:ILE:HD11	2.01	0.42
1:A:270:ASN:HA	1:A:273:VAL:HG12	2.01	0.42
1:A:287:ASN:C	1:A:289:THR:H	2.28	0.42
1:A:322:ILE:C	1:A:324:THR:N	2.77	0.42
1:B:183:ALA:HB2	1:B:200:ILE:CG1	2.39	0.42
1:B:324:THR:O	1:B:326:GLY:N	2.53	0.42
1:B:342:ILE:O	1:B:343:THR:C	2.63	0.42
1:C:45:LEU:O	1:C:46:VAL:C	2.62	0.42
1:C:150:PRO:CD	1:C:354:GLY:HA2	2.49	0.42
1:C:194:LEU:HD13	1:D:410:ILE:CD1	2.47	0.42
1:C:449:LEU:O	1:C:450:ALA:C	2.61	0.42
1:D:176:THR:HA	1:D:213:ILE:HG23	2.01	0.42
1:D:252:LEU:HD13	1:D:427:ILE:HD11	2.01	0.42
1:D:322:ILE:C	1:D:324:THR:N	2.77	0.42
1:D:342:ILE:O	1:D:343:THR:C	2.63	0.42
1:E:91:MET:O	1:E:92:PHE:C	2.61	0.42
1:E:274:LEU:HD12	1:E:277:GLN:NE2	2.34	0.42
1:E:312:THR:CG2	1:E:339:ALA:HB1	2.50	0.42
1:E:321:PRO:CA	1:E:322:ILE:HD12	2.49	0.42
1:F:116:LEU:HB3	1:F:206:PRO:HD3	2.01	0.42
1:F:244:LEU:H	1:F:418:ASN:HD21	1.67	0.42
1:F:329:SER:O	1:F:330:MET:C	2.61	0.42
1:A:57:VAL:HG22	1:A:136:LEU:HD12	2.01	0.42
1:A:78:LEU:HD13	1:A:78:LEU:C	2.44	0.42
1:B:25:LEU:C	1:B:27:GLU:H	2.27	0.42
1:B:90:ALA:HB3	1:B:296:GLY:HA2	2.00	0.42
1:B:252:LEU:HD13	1:B:427:ILE:HD11	2.01	0.42
1:C:287:ASN:C	1:C:289:THR:H	2.28	0.42
1:C:324:THR:O	1:C:326:GLY:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:414:GLU:OE1	1:D:419:TYR:CE1	2.73	0.42
1:C:446:SER:C	1:C:448:ILE:N	2.78	0.42
1:D:90:ALA:HB3	1:D:296:GLY:HA2	2.00	0.42
1:D:214:SER:O	1:D:215:ILE:C	2.63	0.42
1:D:244:LEU:H	1:D:418:ASN:HD21	1.67	0.42
1:D:412:VAL:O	1:D:413:LEU:C	2.63	0.42
1:E:288:ILE:H	1:E:288:ILE:CD1	2.32	0.42
1:F:46:VAL:HG11	1:F:181:GLY:O	2.19	0.42
1:F:157:ASN:O	1:F:158:ILE:C	2.61	0.42
1:F:202:GLU:O	1:F:202:GLU:HG2	2.19	0.42
1:F:315:GLY:N	1:F:318:ASN:ND2	2.67	0.42
1:A:119:GLN:O	1:A:120:ARG:C	2.62	0.42
1:A:150:PRO:CD	1:A:354:GLY:HA2	2.49	0.42
1:B:321:PRO:CA	1:B:322:ILE:HD12	2.49	0.42
1:B:412:VAL:O	1:B:413:LEU:C	2.63	0.42
1:C:25:LEU:C	1:C:27:GLU:H	2.27	0.42
1:C:116:LEU:HB3	1:C:206:PRO:HD3	2.01	0.42
1:C:176:THR:HA	1:C:213:ILE:HG23	2.01	0.42
1:C:215:ILE:HG22	1:C:216:LYS:N	2.34	0.42
1:C:412:VAL:O	1:C:413:LEU:C	2.63	0.42
1:D:209:ARG:HG2	1:D:209:ARG:HH11	1.84	0.42
1:D:312:THR:CG2	1:D:339:ALA:HB1	2.50	0.42
1:E:78:LEU:C	1:E:78:LEU:HD13	2.44	0.42
1:E:321:PRO:HD2	1:E:322:ILE:CD1	2.49	0.42
1:F:265:PHE:CE2	1:F:269:PHE:HB2	2.54	0.42
1:F:342:ILE:O	1:F:343:THR:C	2.63	0.42
1:F:421:LEU:O	1:F:424:PRO:HD2	2.20	0.42
1:A:157:ASN:O	1:A:159:GLY:N	2.52	0.42
1:A:202:GLU:O	1:A:202:GLU:HG2	2.19	0.42
1:A:324:THR:O	1:A:326:GLY:N	2.53	0.42
1:A:414:GLU:OE1	1:B:419:TYR:CE1	2.73	0.42
1:A:446:SER:C	1:A:448:ILE:N	2.78	0.42
1:B:212:LEU:N	1:B:212:LEU:CD1	2.81	0.42
1:B:287:ASN:C	1:B:289:THR:H	2.28	0.42
1:B:312:THR:CG2	1:B:339:ALA:HB1	2.50	0.42
1:C:223:ILE:HD12	1:D:430:LEU:CD2	2.45	0.42
1:C:252:LEU:HD13	1:C:427:ILE:HD11	2.01	0.42
1:C:315:GLY:N	1:C:318:ASN:ND2	2.67	0.42
1:D:119:GLN:O	1:D:120:ARG:C	2.62	0.42
1:D:202:GLU:O	1:D:202:GLU:HG2	2.19	0.42
1:D:287:ASN:C	1:D:289:THR:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:ASN:O	1:E:159:GLY:N	2.52	0.42
1:E:251:THR:HG22	1:E:255:TYR:CE1	2.47	0.42
1:E:426:ILE:O	1:E:427:ILE:C	2.62	0.42
1:F:150:PRO:CD	1:F:354:GLY:HA2	2.49	0.42
1:A:273:VAL:HG13	1:A:274:LEU:N	2.34	0.42
1:A:412:VAL:O	1:A:413:LEU:C	2.63	0.42
1:B:46:VAL:HG11	1:B:181:GLY:O	2.19	0.42
1:B:124:TRP:HB2	1:B:128:LEU:HG	2.00	0.42
1:C:78:LEU:HD13	1:C:78:LEU:C	2.44	0.42
1:C:157:ASN:O	1:C:159:GLY:N	2.52	0.42
1:C:244:LEU:H	1:C:418:ASN:HD21	1.67	0.42
1:C:270:ASN:HA	1:C:273:VAL:HG12	2.01	0.42
1:D:148:GLU:CD	1:D:148:GLU:N	2.76	0.42
1:D:199:PHE:C	1:D:201:ILE:H	2.26	0.42
1:E:25:LEU:C	1:E:27:GLU:H	2.27	0.42
1:E:45:LEU:O	1:E:46:VAL:C	2.62	0.42
1:E:265:PHE:CE2	1:E:269:PHE:HB2	2.54	0.42
1:E:287:ASN:C	1:E:289:THR:H	2.28	0.42
1:E:314:GLY:C	1:E:316:GLY:N	2.76	0.42
1:E:324:THR:O	1:E:326:GLY:N	2.53	0.42
1:F:45:LEU:O	1:F:46:VAL:C	2.62	0.42
1:F:75:TYR:N	1:F:76:PRO:CD	2.79	0.42
1:F:244:LEU:N	1:F:244:LEU:CD1	2.79	0.42
1:F:324:THR:O	1:F:326:GLY:N	2.52	0.42
1:A:190:PHE:HE1	1:A:357:PHE:CE2	2.38	0.42
1:A:201:ILE:HA	1:A:205:ARG:HG2	2.01	0.42
1:A:244:LEU:H	1:A:418:ASN:HD21	1.67	0.42
1:A:312:THR:CG2	1:A:339:ALA:HB1	2.50	0.42
1:B:100:TYR:N	1:B:100:TYR:CD1	2.88	0.42
1:C:57:VAL:HG22	1:C:136:LEU:HD12	2.01	0.42
1:D:270:ASN:HA	1:D:273:VAL:HG12	2.01	0.42
1:E:342:ILE:O	1:E:343:THR:C	2.63	0.42
1:E:421:LEU:O	1:E:424:PRO:HD2	2.20	0.42
1:F:24:GLN:O	1:F:25:LEU:C	2.63	0.42
1:F:100:TYR:CD1	1:F:100:TYR:N	2.88	0.42
1:A:53:PHE:CZ	1:A:139:LEU:HD12	2.55	0.42
1:A:176:THR:HA	1:A:213:ILE:HG23	2.01	0.42
1:A:214:SER:O	1:A:215:ILE:C	2.63	0.42
1:A:315:GLY:N	1:A:318:ASN:ND2	2.67	0.42
1:B:176:THR:HA	1:B:213:ILE:HG23	2.01	0.42
1:C:183:ALA:C	1:C:185:GLY:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:202:GLU:O	1:C:202:GLU:HG2	2.19	0.42
1:D:53:PHE:CZ	1:D:139:LEU:HD12	2.55	0.42
1:D:100:TYR:N	1:D:100:TYR:CD1	2.88	0.42
1:D:190:PHE:HE1	1:D:357:PHE:CE2	2.38	0.42
1:D:421:LEU:C	1:D:425:MET:HG3	2.44	0.42
1:E:100:TYR:N	1:E:100:TYR:CD1	2.88	0.42
1:E:143:MET:HE2	1:E:347:CYS:HB3	2.01	0.42
1:F:78:LEU:HD13	1:F:78:LEU:C	2.44	0.42
1:F:190:PHE:HE1	1:F:357:PHE:CE2	2.38	0.42
1:F:201:ILE:HA	1:F:205:ARG:HG2	2.01	0.42
1:F:287:ASN:C	1:F:289:THR:H	2.28	0.42
1:A:223:ILE:HD12	1:B:430:LEU:CD2	2.45	0.41
1:B:201:ILE:HA	1:B:205:ARG:HG2	2.01	0.41
1:C:190:PHE:HE1	1:C:357:PHE:CE2	2.38	0.41
1:C:197:ILE:HG12	1:C:222:VAL:HG21	2.02	0.41
1:C:379:PHE:C	1:C:381:GLN:H	2.28	0.41
1:D:321:PRO:CA	1:D:322:ILE:HD12	2.49	0.41
1:D:446:SER:C	1:D:448:ILE:N	2.78	0.41
1:E:57:VAL:HG22	1:E:136:LEU:HD12	2.01	0.41
1:E:69:VAL:O	1:E:69:VAL:HG12	2.19	0.41
1:E:412:VAL:O	1:E:413:LEU:C	2.63	0.41
1:F:53:PHE:CZ	1:F:139:LEU:HD12	2.55	0.41
1:F:143:MET:HE2	1:F:347:CYS:HB3	2.01	0.41
1:F:197:ILE:HG12	1:F:222:VAL:HG21	2.02	0.41
1:F:214:SER:O	1:F:215:ILE:C	2.63	0.41
1:A:421:LEU:O	1:A:424:PRO:HD2	2.20	0.41
1:B:53:PHE:CZ	1:B:139:LEU:HD12	2.55	0.41
1:B:69:VAL:O	1:B:69:VAL:HG12	2.19	0.41
1:B:119:GLN:O	1:B:120:ARG:C	2.62	0.41
1:B:190:PHE:HE1	1:B:357:PHE:CE2	2.38	0.41
1:C:53:PHE:CZ	1:C:139:LEU:HD12	2.55	0.41
1:C:197:ILE:CG1	1:C:222:VAL:HG21	2.51	0.41
1:D:46:VAL:HG11	1:D:181:GLY:O	2.19	0.41
1:D:131:LYS:NZ	1:D:153:GLN:HE21	2.16	0.41
1:F:57:VAL:HG22	1:F:136:LEU:HD12	2.01	0.41
1:F:183:ALA:C	1:F:185:GLY:N	2.77	0.41
1:F:278:ASP:O	1:F:280:LEU:N	2.53	0.41
1:F:446:SER:C	1:F:448:ILE:N	2.78	0.41
1:A:46:VAL:HG11	1:A:181:GLY:O	2.19	0.41
1:A:197:ILE:CG1	1:A:222:VAL:HG21	2.51	0.41
1:B:157:ASN:O	1:B:159:GLY:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:ILE:HG22	1:B:216:LYS:N	2.34	0.41
1:B:270:ASN:HA	1:B:273:VAL:HG12	2.01	0.41
1:B:274:LEU:HD12	1:B:277:GLN:NE2	2.34	0.41
1:B:421:LEU:O	1:B:424:PRO:HD2	2.20	0.41
1:C:46:VAL:HG11	1:C:181:GLY:O	2.19	0.41
1:C:201:ILE:HA	1:C:205:ARG:HG2	2.01	0.41
1:C:214:SER:O	1:C:215:ILE:C	2.63	0.41
1:C:247:ALA:HA	1:C:248:PRO:HD2	1.93	0.41
1:C:312:THR:CG2	1:C:339:ALA:HB1	2.50	0.41
1:C:342:ILE:O	1:C:343:THR:C	2.63	0.41
1:E:194:LEU:HD13	1:F:410:ILE:CD1	2.47	0.41
1:E:201:ILE:HA	1:E:205:ARG:HG2	2.01	0.41
1:E:209:ARG:HG2	1:E:209:ARG:HH11	1.84	0.41
1:E:223:ILE:HD12	1:F:430:LEU:CD2	2.45	0.41
1:E:252:LEU:HD13	1:E:427:ILE:HD11	2.01	0.41
1:F:103:GLU:HG3	1:F:123:ARG:HE	1.85	0.41
1:F:412:VAL:O	1:F:413:LEU:C	2.63	0.41
1:B:103:GLU:HG3	1:B:123:ARG:HE	1.84	0.41
1:B:143:MET:HE2	1:B:347:CYS:HB3	2.01	0.41
1:B:197:ILE:CG1	1:B:222:VAL:HG21	2.51	0.41
1:B:278:ASP:C	1:B:280:LEU:N	2.71	0.41
1:B:421:LEU:C	1:B:425:MET:HG3	2.44	0.41
1:C:278:ASP:O	1:C:280:LEU:N	2.53	0.41
1:C:421:LEU:O	1:C:424:PRO:HD2	2.20	0.41
1:D:69:VAL:O	1:D:69:VAL:HG12	2.19	0.41
1:E:103:GLU:HG3	1:E:123:ARG:HE	1.84	0.41
1:E:322:ILE:C	1:E:324:THR:N	2.77	0.41
1:E:430:LEU:HD13	1:F:219:PHE:HD2	1.85	0.41
1:A:215:ILE:HG22	1:A:216:LYS:N	2.34	0.41
1:B:124:TRP:O	1:B:126:ARG:N	2.53	0.41
1:B:183:ALA:C	1:B:185:GLY:N	2.77	0.41
1:B:190:PHE:CD1	1:B:411:LEU:HD11	2.56	0.41
1:D:103:GLU:HG3	1:D:123:ARG:HE	1.84	0.41
1:D:274:LEU:HD12	1:D:277:GLN:NE2	2.34	0.41
1:E:53:PHE:CZ	1:E:139:LEU:HD12	2.55	0.41
1:E:197:ILE:CG1	1:E:222:VAL:HG21	2.51	0.41
1:F:190:PHE:CD1	1:F:411:LEU:HD11	2.56	0.41
1:A:197:ILE:HG12	1:A:222:VAL:HG21	2.02	0.41
1:A:379:PHE:C	1:A:381:GLN:H	2.29	0.41
1:B:249:LEU:C	1:B:251:THR:N	2.79	0.41
1:B:421:LEU:C	1:B:424:PRO:HD2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:446:SER:O	1:B:447:ALA:C	2.64	0.41
1:C:411:LEU:O	1:C:415:MET:HG2	2.21	0.41
1:D:24:GLN:O	1:D:25:LEU:C	2.62	0.41
1:D:190:PHE:CD1	1:D:411:LEU:HD11	2.56	0.41
1:D:212:LEU:N	1:D:212:LEU:CD1	2.81	0.41
1:D:421:LEU:C	1:D:424:PRO:HD2	2.46	0.41
1:D:446:SER:O	1:D:447:ALA:C	2.64	0.41
1:E:124:TRP:O	1:E:126:ARG:N	2.53	0.41
1:E:190:PHE:CD1	1:E:411:LEU:HD11	2.56	0.41
1:E:197:ILE:HG12	1:E:222:VAL:HG21	2.02	0.41
1:F:124:TRP:CD1	1:F:161:MET:HG3	2.56	0.41
1:A:342:ILE:O	1:A:343:THR:C	2.63	0.41
1:C:124:TRP:O	1:C:126:ARG:N	2.53	0.41
1:D:124:TRP:CD1	1:D:125:TRP:N	2.89	0.41
1:D:197:ILE:CG1	1:D:222:VAL:HG21	2.51	0.41
1:D:249:LEU:C	1:D:251:THR:N	2.79	0.41
1:E:190:PHE:HE1	1:E:357:PHE:CE2	2.38	0.41
1:E:421:LEU:C	1:E:424:PRO:HD2	2.46	0.41
1:F:274:LEU:HD12	1:F:277:GLN:NE2	2.34	0.41
1:F:276:MET:C	1:F:278:ASP:H	2.29	0.41
1:A:28:ARG:HH22	1:B:203:GLU:CD	2.29	0.41
1:A:103:GLU:HG3	1:A:123:ARG:HE	1.84	0.41
1:A:356:ILE:HA	1:A:359:PRO:CG	2.51	0.41
1:A:411:LEU:O	1:A:415:MET:HG2	2.21	0.41
1:A:443:PRO:O	1:A:446:SER:N	2.41	0.41
1:C:356:ILE:HA	1:C:359:PRO:CG	2.51	0.41
1:D:45:LEU:O	1:D:46:VAL:C	2.62	0.41
1:D:157:ASN:O	1:D:158:ILE:C	2.61	0.41
1:D:157:ASN:O	1:D:159:GLY:N	2.52	0.41
1:D:200:ILE:O	1:D:200:ILE:CG2	2.68	0.41
1:D:201:ILE:HA	1:D:205:ARG:HG2	2.01	0.41
1:D:251:THR:HG22	1:D:255:TYR:CE1	2.46	0.41
1:D:421:LEU:O	1:D:424:PRO:HD2	2.20	0.41
1:E:24:GLN:O	1:E:25:LEU:C	2.62	0.41
1:F:124:TRP:O	1:F:126:ARG:N	2.53	0.41
1:F:197:ILE:CG1	1:F:222:VAL:HG21	2.51	0.41
1:F:284:HIS:CE1	1:F:291:TRP:CE3	3.09	0.41
1:F:321:PRO:CA	1:F:322:ILE:HD12	2.49	0.41
1:A:24:GLN:O	1:A:25:LEU:C	2.63	0.41
1:A:124:TRP:O	1:A:126:ARG:N	2.53	0.41
1:A:179:ALA:HB1	1:A:200:ILE:CG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ALA:HA	1:A:248:PRO:HD2	1.93	0.41
1:A:278:ASP:O	1:A:280:LEU:N	2.53	0.41
1:A:317:PHE:CA	1:A:321:PRO:HD2	2.50	0.41
1:B:124:TRP:CD1	1:B:125:TRP:N	2.89	0.41
1:B:124:TRP:CD1	1:B:161:MET:HG3	2.56	0.41
1:B:176:THR:C	1:B:178:LEU:N	2.79	0.41
1:B:200:ILE:O	1:B:200:ILE:CG2	2.68	0.41
1:B:411:LEU:O	1:B:415:MET:HG2	2.21	0.41
1:B:446:SER:C	1:B:448:ILE:N	2.78	0.41
1:C:28:ARG:HH22	1:D:203:GLU:CD	2.29	0.41
1:C:98:ARG:NH2	1:C:102:PRO:CB	2.79	0.41
1:C:103:GLU:HG3	1:C:123:ARG:HE	1.84	0.41
1:C:179:ALA:HB1	1:C:200:ILE:CG2	2.51	0.41
1:C:190:PHE:CD1	1:C:411:LEU:HD11	2.56	0.41
1:C:249:LEU:C	1:C:251:THR:N	2.79	0.41
1:C:317:PHE:CA	1:C:321:PRO:HD2	2.50	0.41
1:D:124:TRP:O	1:D:126:ARG:N	2.53	0.41
1:D:278:ASP:O	1:D:280:LEU:N	2.53	0.41
1:E:28:ARG:HH22	1:F:203:GLU:CD	2.29	0.41
1:E:179:ALA:HB1	1:E:200:ILE:CG2	2.51	0.41
1:E:183:ALA:C	1:E:185:GLY:N	2.77	0.41
1:E:249:LEU:C	1:E:251:THR:N	2.79	0.41
1:E:278:ASP:O	1:E:280:LEU:N	2.53	0.41
1:E:316:GLY:O	1:E:318:ASN:N	2.54	0.41
1:E:423:LEU:HD12	1:E:423:LEU:HA	1.81	0.41
1:E:446:SER:O	1:E:447:ALA:C	2.64	0.41
1:F:312:THR:CG2	1:F:339:ALA:HB1	2.50	0.41
1:F:314:GLY:C	1:F:316:GLY:N	2.76	0.41
1:A:443:PRO:HG2	1:B:28:ARG:NE	2.36	0.41
1:B:29:ASP:OD1	1:B:216:LYS:NZ	2.51	0.41
1:B:93:GLY:C	1:B:95:PHE:N	2.79	0.41
1:B:157:ASN:O	1:B:158:ILE:C	2.61	0.41
1:B:423:LEU:HD12	1:B:423:LEU:HA	1.81	0.41
1:C:123:ARG:N	1:C:123:ARG:CD	2.81	0.41
1:C:200:ILE:O	1:C:200:ILE:CG2	2.68	0.41
1:C:201:ILE:HD13	1:C:201:ILE:HG21	1.87	0.41
1:C:443:PRO:HG2	1:D:28:ARG:NE	2.36	0.41
1:D:143:MET:HE2	1:D:347:CYS:HB3	2.01	0.41
1:D:215:ILE:HG22	1:D:216:LYS:N	2.34	0.41
1:D:341:VAL:O	1:D:345:LEU:HG	2.21	0.41
1:F:157:ASN:O	1:F:159:GLY:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:320:ILE:C	1:F:322:ILE:N	2.74	0.41
1:F:421:LEU:C	1:F:424:PRO:HD2	2.46	0.41
1:A:124:TRP:CD1	1:A:125:TRP:N	2.89	0.40
1:A:190:PHE:CD1	1:A:411:LEU:HD11	2.56	0.40
1:A:249:LEU:C	1:A:251:THR:N	2.79	0.40
1:A:423:LEU:HD12	1:A:423:LEU:HA	1.81	0.40
1:B:24:GLN:O	1:B:25:LEU:C	2.63	0.40
1:C:284:HIS:CE1	1:C:291:TRP:CE3	3.09	0.40
1:D:356:ILE:HA	1:D:359:PRO:CG	2.51	0.40
1:E:443:PRO:HG2	1:F:28:ARG:NE	2.36	0.40
1:F:124:TRP:CD1	1:F:125:TRP:N	2.89	0.40
1:F:176:THR:C	1:F:178:LEU:N	2.79	0.40
1:F:341:VAL:O	1:F:345:LEU:HG	2.21	0.40
1:F:379:PHE:C	1:F:381:GLN:H	2.28	0.40
1:A:100:TYR:N	1:A:100:TYR:CD1	2.88	0.40
1:A:201:ILE:HD13	1:A:201:ILE:HG21	1.87	0.40
1:A:295:GLY:C	1:A:297:ALA:N	2.79	0.40
1:B:197:ILE:HG12	1:B:222:VAL:HG21	2.02	0.40
1:B:278:ASP:O	1:B:280:LEU:N	2.53	0.40
1:B:457:GLU:C	1:B:459:GLU:H	2.30	0.40
1:C:100:TYR:CD1	1:C:100:TYR:N	2.88	0.40
1:C:124:TRP:CD1	1:C:125:TRP:N	2.89	0.40
1:D:124:TRP:CD1	1:D:161:MET:HG3	2.56	0.40
1:D:176:THR:C	1:D:178:LEU:N	2.79	0.40
1:D:197:ILE:HG12	1:D:222:VAL:HG21	2.02	0.40
1:D:211:THR:CG2	1:D:212:LEU:H	2.26	0.40
1:D:273:VAL:CA	1:D:345:LEU:HD22	2.49	0.40
1:D:411:LEU:O	1:D:415:MET:HG2	2.21	0.40
1:D:457:GLU:C	1:D:459:GLU:H	2.30	0.40
1:E:124:TRP:CD1	1:E:125:TRP:N	2.89	0.40
1:E:131:LYS:NZ	1:E:153:GLN:HE21	2.16	0.40
1:E:411:LEU:O	1:E:415:MET:HG2	2.21	0.40
1:F:295:GLY:C	1:F:297:ALA:N	2.79	0.40
1:A:98:ARG:NH2	1:A:102:PRO:CB	2.80	0.40
1:A:200:ILE:O	1:A:200:ILE:CG2	2.68	0.40
1:B:356:ILE:HA	1:B:359:PRO:CG	2.51	0.40
1:C:426:ILE:O	1:C:427:ILE:C	2.62	0.40
1:D:123:ARG:N	1:D:123:ARG:CD	2.81	0.40
1:E:426:ILE:HG22	1:F:223:ILE:CD1	2.51	0.40
1:F:356:ILE:HA	1:F:359:PRO:CG	2.51	0.40
1:A:420:GLN:H	1:A:420:GLN:HG2	1.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:THR:HG22	1:B:255:TYR:CE1	2.47	0.40
1:B:341:VAL:O	1:B:345:LEU:HG	2.22	0.40
1:B:361:LEU:HD23	1:B:361:LEU:HA	1.95	0.40
1:B:379:PHE:C	1:B:381:GLN:H	2.29	0.40
1:C:295:GLY:C	1:C:297:ALA:N	2.79	0.40
1:C:421:LEU:C	1:C:424:PRO:HD2	2.46	0.40
1:C:450:ALA:CB	1:D:26:LEU:CD2	2.94	0.40
1:D:93:GLY:C	1:D:95:PHE:N	2.79	0.40
1:E:284:HIS:CE1	1:E:291:TRP:CE3	3.09	0.40
1:A:183:ALA:HB2	1:A:200:ILE:CG1	2.39	0.40
1:A:426:ILE:O	1:A:427:ILE:C	2.62	0.40
1:A:457:GLU:C	1:A:459:GLU:H	2.30	0.40
1:B:45:LEU:O	1:B:46:VAL:C	2.62	0.40
1:B:75:TYR:N	1:B:76:PRO:CD	2.80	0.40
1:B:360:MET:HE3	1:B:398:LEU:CD2	2.52	0.40
1:C:24:GLN:O	1:C:25:LEU:C	2.62	0.40
1:C:430:LEU:HD13	1:D:219:PHE:HD2	1.85	0.40
1:D:223:ILE:HG22	1:D:227:ILE:HD11	2.04	0.40
1:D:360:MET:HE3	1:D:398:LEU:CD2	2.52	0.40
1:E:295:GLY:C	1:E:297:ALA:N	2.79	0.40
1:F:316:GLY:O	1:F:318:ASN:N	2.54	0.40
1:F:457:GLU:C	1:F:459:GLU:H	2.30	0.40

All (53) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:ARG:CA	1:E:12:GLN:NE2[4_455]	0.70	1.50
1:B:16:LEU:CG	1:E:19:ARG:CZ[4_455]	0.73	1.47
1:B:19:ARG:NH1	1:E:16:LEU:CB[4_455]	0.88	1.32
1:B:12:GLN:CD	1:E:15:ARG:CB[4_455]	0.91	1.29
1:B:19:ARG:NH1	1:E:16:LEU:CG[4_455]	0.96	1.24
1:B:16:LEU:CD2	1:E:19:ARG:NH2[4_455]	1.03	1.17
1:B:19:ARG:CD	1:E:16:LEU:CD1[4_455]	1.05	1.15
1:B:12:GLN:NE2	1:E:15:ARG:CB[4_455]	1.07	1.13
1:B:167:ARG:NH1	1:D:12:GLN:OE1[2_554]	1.15	1.05
1:B:15:ARG:CB	1:E:12:GLN:NE2[4_455]	1.18	1.02
1:B:19:ARG:CZ	1:E:16:LEU:CG[4_455]	1.18	1.02
1:B:12:GLN:OE1	1:E:15:ARG:CB[4_455]	1.26	0.94
1:B:19:ARG:CZ	1:E:16:LEU:CB[4_455]	1.28	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:19:ARG:NE	1:E:16:LEU:CD2[4_455]	1.31	0.89
1:B:19:ARG:CZ	1:E:16:LEU:CD2[4_455]	1.34	0.86
1:B:12:GLN:N	1:E:15:ARG:NH2[4_455]	1.35	0.85
1:B:16:LEU:CD2	1:E:19:ARG:CZ[4_455]	1.35	0.85
1:B:16:LEU:CG	1:E:19:ARG:NH2[4_455]	1.38	0.82
1:B:15:ARG:C	1:E:12:GLN:NE2[4_455]	1.39	0.81
1:B:15:ARG:O	1:E:12:GLN:OE1[4_455]	1.40	0.80
1:B:16:LEU:CG	1:E:19:ARG:NH1[4_455]	1.52	0.68
1:B:12:GLN:NE2	1:E:15:ARG:CG[4_455]	1.57	0.63
1:B:15:ARG:CB	1:E:12:GLN:CD[4_455]	1.57	0.63
1:C:12:GLN:OE1	1:E:167:ARG:NH2[3_645]	1.58	0.62
1:B:16:LEU:CD1	1:E:19:ARG:NE[4_455]	1.59	0.61
1:B:19:ARG:NE	1:E:16:LEU:CG[4_455]	1.61	0.59
1:B:16:LEU:CD2	1:E:19:ARG:NE[4_455]	1.64	0.56
1:B:16:LEU:CG	1:E:19:ARG:NE[4_455]	1.66	0.54
1:B:167:ARG:CZ	1:D:12:GLN:OE1[2_554]	1.66	0.54
1:B:15:ARG:O	1:E:12:GLN:CD[4_455]	1.70	0.50
1:B:12:GLN:NE2	1:E:15:ARG:CA[4_455]	1.74	0.46
1:B:15:ARG:C	1:E:12:GLN:CD[4_455]	1.80	0.40
1:B:19:ARG:NH1	1:E:16:LEU:CA[4_455]	1.81	0.39
1:B:16:LEU:CD1	1:E:19:ARG:CZ[4_455]	1.85	0.35
1:B:19:ARG:NE	1:E:16:LEU:CD1[4_455]	1.85	0.35
1:B:167:ARG:NH1	1:D:12:GLN:CD[2_554]	1.87	0.33
1:B:23:ARG:NH1	1:E:23:ARG:CD[4_455]	1.89	0.31
1:B:12:GLN:NE2	1:E:15:ARG:N[4_455]	1.91	0.29
1:B:12:GLN:CD	1:E:15:ARG:CG[4_455]	1.93	0.27
1:B:16:LEU:CD1	1:E:19:ARG:CD[4_455]	1.93	0.27
1:B:16:LEU:CB	1:E:19:ARG:NH2[4_455]	1.93	0.27
1:B:15:ARG:N	1:E:12:GLN:NE2[4_455]	1.96	0.24
1:B:19:ARG:NH2	1:E:16:LEU:CB[4_455]	1.97	0.23
1:B:19:ARG:CD	1:E:16:LEU:CG[4_455]	1.98	0.22
1:B:15:ARG:CA	1:E:12:GLN:CD[4_455]	2.00	0.20
1:B:167:ARG:NH2	1:D:12:GLN:OE1[2_554]	2.03	0.17
1:B:19:ARG:NH2	1:E:16:LEU:CD2[4_455]	2.06	0.14
1:B:15:ARG:O	1:E:12:GLN:NE2[4_455]	2.09	0.11
1:B:12:GLN:N	1:E:15:ARG:CZ[4_455]	2.14	0.06
1:B:16:LEU:O	1:E:19:ARG:NH1[4_455]	2.17	0.03
1:B:12:GLN:CG	1:E:15:ARG:NE[4_455]	2.18	0.02
1:B:19:ARG:NH1	1:E:16:LEU:CD2[4_455]	2.18	0.02
1:B:16:LEU:CB	1:E:19:ARG:CZ[4_455]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	448/473 (95%)	340 (76%)	75 (17%)	33 (7%)	1	9
1	B	448/473 (95%)	340 (76%)	75 (17%)	33 (7%)	1	9
1	C	448/473 (95%)	340 (76%)	75 (17%)	33 (7%)	1	9
1	D	448/473 (95%)	340 (76%)	76 (17%)	32 (7%)	1	10
1	E	448/473 (95%)	340 (76%)	76 (17%)	32 (7%)	1	10
1	F	448/473 (95%)	340 (76%)	75 (17%)	33 (7%)	1	9
All	All	2688/2838 (95%)	2040 (76%)	452 (17%)	196 (7%)	1	9

All (196) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	LEU
1	B	319	LEU
1	C	319	LEU
1	D	319	LEU
1	E	319	LEU
1	F	319	LEU
1	A	33	LEU
1	A	167	ARG
1	A	204	MET
1	A	285	GLY
1	A	318	ASN
1	B	33	LEU
1	B	167	ARG
1	B	204	MET
1	B	285	GLY
1	B	318	ASN
1	C	33	LEU
1	C	167	ARG
1	C	204	MET
1	C	285	GLY

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Mol	Chain	Res	Type
1	C	318	ASN
1	D	33	LEU
1	D	167	ARG
1	D	204	MET
1	D	285	GLY
1	D	318	ASN
1	E	33	LEU
1	E	167	ARG
1	E	204	MET
1	E	285	GLY
1	E	318	ASN
1	F	33	LEU
1	F	167	ARG
1	F	204	MET
1	F	285	GLY
1	F	318	ASN
1	A	92	PHE
1	A	107	SER
1	A	125	TRP
1	A	172	GLU
1	A	210	TYR
1	A	250	ASN
1	A	279	LEU
1	A	325	ALA
1	A	444	LEU
1	B	92	PHE
1	B	107	SER
1	B	125	TRP
1	B	172	GLU
1	B	210	TYR
1	B	250	ASN
1	B	279	LEU
1	B	325	ALA
1	B	444	LEU
1	C	92	PHE
1	C	107	SER
1	C	125	TRP
1	C	172	GLU
1	C	210	TYR
1	C	250	ASN
1	C	279	LEU
1	C	325	ALA

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Mol	Chain	Res	Type
1	C	444	LEU
1	D	92	PHE
1	D	107	SER
1	D	125	TRP
1	D	172	GLU
1	D	210	TYR
1	D	250	ASN
1	D	279	LEU
1	D	325	ALA
1	D	444	LEU
1	E	92	PHE
1	E	107	SER
1	E	125	TRP
1	E	172	GLU
1	E	210	TYR
1	E	250	ASN
1	E	279	LEU
1	E	325	ALA
1	E	444	LEU
1	F	92	PHE
1	F	107	SER
1	F	125	TRP
1	F	172	GLU
1	F	210	TYR
1	F	250	ASN
1	F	279	LEU
1	F	325	ALA
1	F	444	LEU
1	A	91	MET
1	A	121	PRO
1	A	177	LEU
1	A	242	GLY
1	A	283	VAL
1	A	342	ILE
1	A	343	THR
1	A	452	THR
1	B	91	MET
1	B	121	PRO
1	B	177	LEU
1	B	242	GLY
1	B	283	VAL
1	B	342	ILE

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Mol	Chain	Res	Type
1	B	343	THR
1	B	452	THR
1	C	91	MET
1	C	121	PRO
1	C	177	LEU
1	C	242	GLY
1	C	283	VAL
1	C	342	ILE
1	C	343	THR
1	C	452	THR
1	D	91	MET
1	D	121	PRO
1	D	177	LEU
1	D	242	GLY
1	D	283	VAL
1	D	342	ILE
1	D	343	THR
1	D	452	THR
1	E	91	MET
1	E	121	PRO
1	E	177	LEU
1	E	242	GLY
1	E	283	VAL
1	E	342	ILE
1	E	343	THR
1	E	452	THR
1	F	91	MET
1	F	121	PRO
1	F	177	LEU
1	F	242	GLY
1	F	283	VAL
1	F	342	ILE
1	F	343	THR
1	F	452	THR
1	A	102	PRO
1	A	317	PHE
1	A	326	GLY
1	B	102	PRO
1	B	317	PHE
1	B	326	GLY
1	C	102	PRO
1	C	317	PHE

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Mol	Chain	Res	Type
1	C	326	GLY
1	D	102	PRO
1	D	317	PHE
1	D	326	GLY
1	E	102	PRO
1	E	317	PHE
1	E	326	GLY
1	F	102	PRO
1	F	317	PHE
1	F	326	GLY
1	A	26	LEU
1	A	443	PRO
1	B	26	LEU
1	B	443	PRO
1	C	26	LEU
1	C	443	PRO
1	D	26	LEU
1	D	443	PRO
1	E	26	LEU
1	E	443	PRO
1	F	26	LEU
1	F	443	PRO
1	A	149	GLY
1	A	288	ILE
1	B	149	GLY
1	B	288	ILE
1	C	149	GLY
1	C	288	ILE
1	D	149	GLY
1	D	288	ILE
1	E	149	GLY
1	E	288	ILE
1	F	149	GLY
1	F	288	ILE
1	A	321	PRO
1	A	440	GLY
1	B	321	PRO
1	B	440	GLY
1	C	321	PRO
1	C	440	GLY
1	D	321	PRO
1	D	440	GLY

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Mol	Chain	Res	Type
1	E	321	PRO
1	E	440	GLY
1	F	321	PRO
1	F	440	GLY
1	A	200	ILE
1	B	200	ILE
1	C	200	ILE
1	F	200	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	339/358 (95%)	325 (96%)	14 (4%)	27	53
1	B	339/358 (95%)	325 (96%)	14 (4%)	27	53
1	C	339/358 (95%)	325 (96%)	14 (4%)	27	53
1	D	339/358 (95%)	325 (96%)	14 (4%)	27	53
1	E	339/358 (95%)	325 (96%)	14 (4%)	27	53
1	F	339/358 (95%)	325 (96%)	14 (4%)	27	53
All	All	2034/2148 (95%)	1950 (96%)	84 (4%)	27	53

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LYS
1	A	119	GLN
1	A	120	ARG
1	A	123	ARG
1	A	177	LEU
1	A	212	LEU
1	A	241	VAL
1	A	273	VAL
1	A	317	PHE
1	A	319	LEU

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Mol	Chain	Res	Type
1	A	322	ILE
1	A	397	LEU
1	A	416	THR
1	A	451	ARG
1	B	30	LYS
1	B	119	GLN
1	B	120	ARG
1	B	123	ARG
1	B	177	LEU
1	B	212	LEU
1	B	241	VAL
1	B	273	VAL
1	B	317	PHE
1	B	319	LEU
1	B	322	ILE
1	B	397	LEU
1	B	416	THR
1	B	451	ARG
1	C	30	LYS
1	C	119	GLN
1	C	120	ARG
1	C	123	ARG
1	C	177	LEU
1	C	212	LEU
1	C	241	VAL
1	C	273	VAL
1	C	317	PHE
1	C	319	LEU
1	C	322	ILE
1	C	397	LEU
1	C	416	THR
1	C	451	ARG
1	D	30	LYS
1	D	119	GLN
1	D	120	ARG
1	D	123	ARG
1	D	177	LEU
1	D	212	LEU
1	D	241	VAL
1	D	273	VAL
1	D	317	PHE
1	D	319	LEU

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Mol	Chain	Res	Type
1	D	322	ILE
1	D	397	LEU
1	D	416	THR
1	D	451	ARG
1	E	30	LYS
1	E	119	GLN
1	E	120	ARG
1	E	123	ARG
1	E	177	LEU
1	E	212	LEU
1	E	241	VAL
1	E	273	VAL
1	E	317	PHE
1	E	319	LEU
1	E	322	ILE
1	E	397	LEU
1	E	416	THR
1	E	451	ARG
1	F	30	LYS
1	F	119	GLN
1	F	120	ARG
1	F	123	ARG
1	F	177	LEU
1	F	212	LEU
1	F	241	VAL
1	F	273	VAL
1	F	317	PHE
1	F	319	LEU
1	F	322	ILE
1	F	397	LEU
1	F	416	THR
1	F	451	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	74	ASN
1	A	153	GLN
1	A	157	ASN
1	A	207	GLN
1	A	270	ASN

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Mol	Chain	Res	Type
1	A	277	GLN
1	A	318	ASN
1	A	327	ASN
1	A	418	ASN
1	A	420	GLN
1	A	437	GLN
1	B	62	ASN
1	B	74	ASN
1	B	153	GLN
1	B	157	ASN
1	B	207	GLN
1	B	270	ASN
1	B	277	GLN
1	B	318	ASN
1	B	327	ASN
1	B	418	ASN
1	B	420	GLN
1	B	437	GLN
1	C	62	ASN
1	C	74	ASN
1	C	153	GLN
1	C	157	ASN
1	C	207	GLN
1	C	250	ASN
1	C	270	ASN
1	C	277	GLN
1	C	318	ASN
1	C	327	ASN
1	C	418	ASN
1	C	420	GLN
1	C	437	GLN
1	D	62	ASN
1	D	74	ASN
1	D	153	GLN
1	D	157	ASN
1	D	207	GLN
1	D	270	ASN
1	D	277	GLN
1	D	318	ASN
1	D	327	ASN
1	D	418	ASN
1	D	420	GLN

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Mol	Chain	Res	Type
1	D	437	GLN
1	E	62	ASN
1	E	74	ASN
1	E	153	GLN
1	E	157	ASN
1	E	207	GLN
1	E	250	ASN
1	E	270	ASN
1	E	277	GLN
1	E	318	ASN
1	E	327	ASN
1	E	418	ASN
1	E	420	GLN
1	E	437	GLN
1	F	62	ASN
1	F	74	ASN
1	F	153	GLN
1	F	157	ASN
1	F	207	GLN
1	F	270	ASN
1	F	277	GLN
1	F	318	ASN
1	F	327	ASN
1	F	418	ASN
1	F	420	GLN
1	F	437	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	450/473 (95%)	0.04	8 (1%) 67 42	51, 100, 147, 151	0
1	B	450/473 (95%)	0.10	12 (2%) 56 33	51, 100, 147, 151	0
1	C	450/473 (95%)	0.11	11 (2%) 59 35	51, 100, 147, 151	0
1	D	450/473 (95%)	0.10	3 (0%) 84 63	51, 100, 147, 151	0
1	E	450/473 (95%)	0.13	11 (2%) 59 35	51, 100, 147, 151	0
1	F	450/473 (95%)	0.17	9 (2%) 65 39	51, 100, 147, 151	0
All	All	2700/2838 (95%)	0.11	54 (2%) 65 39	51, 100, 147, 151	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	GLN	6.8
1	E	12	GLN	5.9
1	C	104	ALA	5.2
1	A	12	GLN	4.2
1	E	354	GLY	4.1
1	F	26	LEU	4.0
1	E	15	ARG	3.9
1	B	283	VAL	3.5
1	A	29	ASP	3.2
1	C	90	ALA	3.0
1	B	18	ARG	3.0
1	C	188	ALA	3.0
1	E	14	ALA	2.9
1	E	235	GLU	2.8
1	B	29	ASP	2.7
1	C	290	LYS	2.7
1	B	15	ARG	2.7
1	C	354	GLY	2.7
1	B	401	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	18	ARG	2.6
1	A	461	LEU	2.6
1	D	14	ALA	2.6
1	B	167	ARG	2.5
1	B	396	ALA	2.5
1	F	12	GLN	2.5
1	A	352	ALA	2.5
1	F	29	ASP	2.4
1	B	19	ARG	2.4
1	E	283	VAL	2.4
1	B	13	ALA	2.4
1	F	111	GLU	2.3
1	A	283	VAL	2.3
1	C	447	ALA	2.3
1	E	16	LEU	2.3
1	F	351	GLY	2.3
1	F	299	GLY	2.2
1	F	76	PRO	2.2
1	C	286	GLY	2.2
1	C	347	CYS	2.1
1	B	14	ALA	2.1
1	D	104	ALA	2.1
1	A	19	ARG	2.1
1	E	13	ALA	2.1
1	E	101	ALA	2.1
1	A	351	GLY	2.1
1	F	22	ILE	2.1
1	C	12	GLN	2.1
1	C	287	ASN	2.1
1	A	111	GLU	2.0
1	D	350	SER	2.0
1	E	461	LEU	2.0
1	F	327	ASN	2.0
1	B	16	LEU	2.0
1	C	325	ALA	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.