



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 08:05 PM UTC

PDB ID : 4BIJ / pdb_00004bij
EMDB ID : EMD-2355
Title : Threading model of T7 large terminase
Authors : Dauden, M.I.; Martin-Benito, J.; Sanchez-Ferrero, J.C.; Pulido-Cid, M.;
Valpuesta, J.M.; Carrascosa, J.L.
Deposited on : 2013-04-10
Resolution : 16.00 Å(reported)
Based on initial model : 3CPE

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

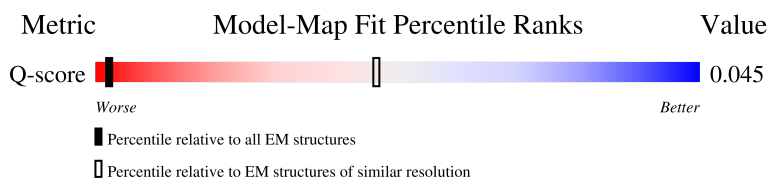
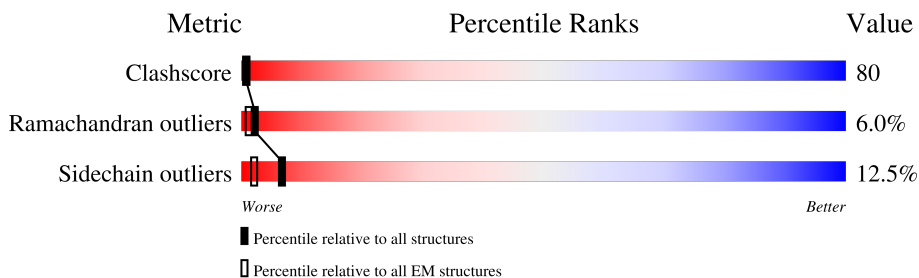
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 16.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	41 (15.50 - 16.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	476	
1	B	476	
1	C	476	
1	D	476	

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Mol	Chain	Length	Quality of chain
1	E	476	22% 31% 45% 17% 7%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18855 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

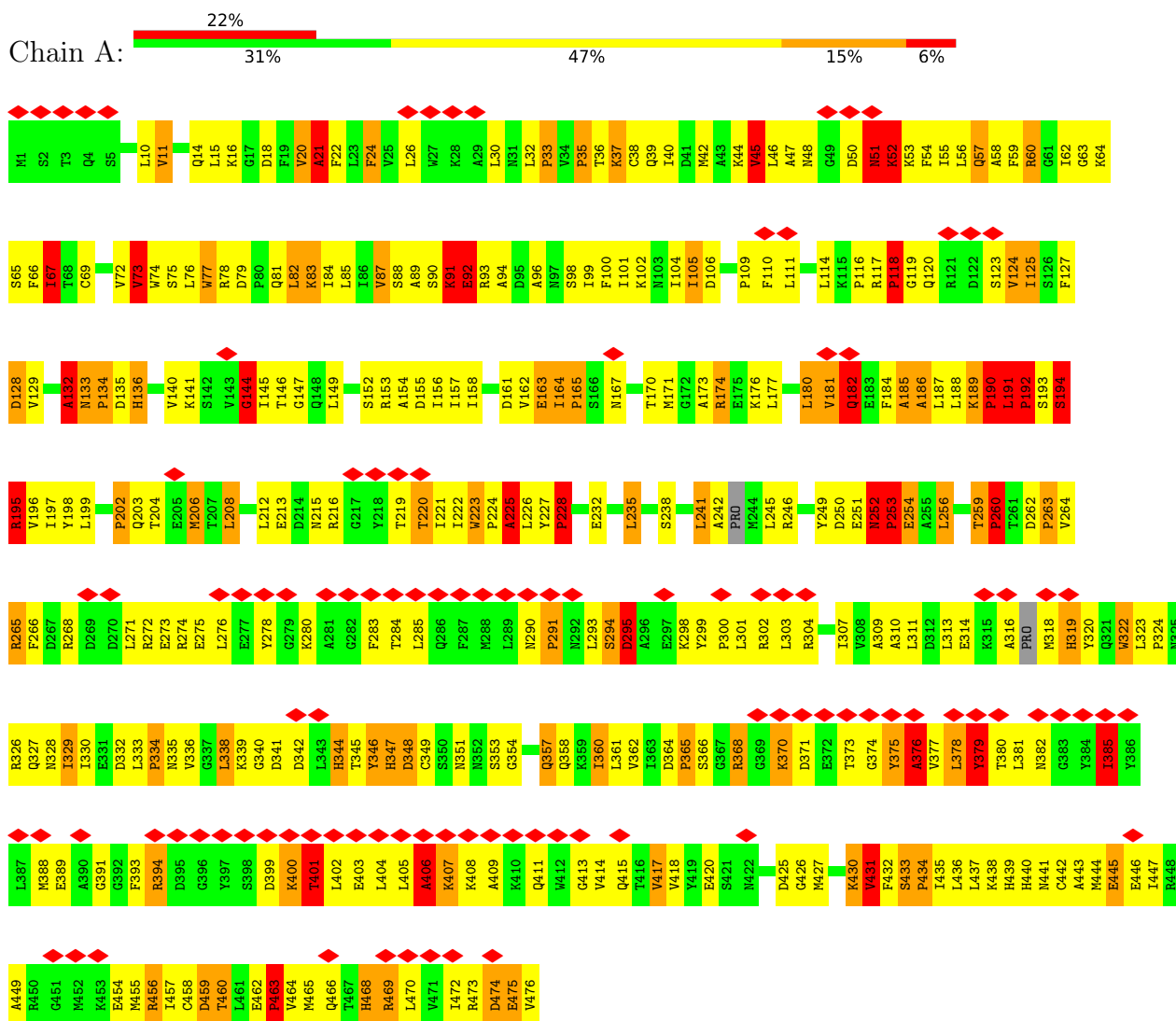
- Molecule 1 is a protein called DNA MATURASE B.

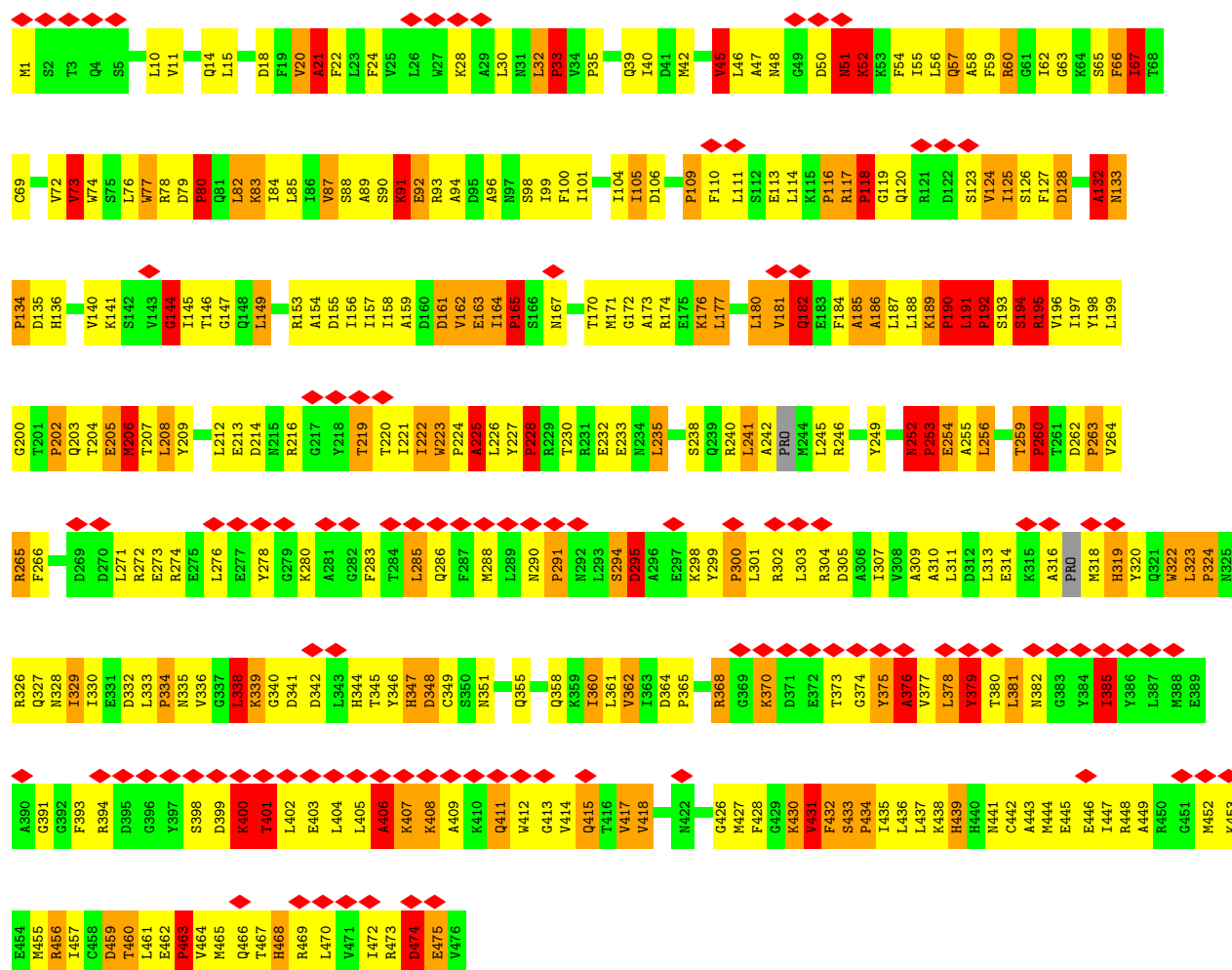
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	474	Total 3771	C 2402	N 648	O 703	S 18	0	0
1	B	474	Total 3771	C 2402	N 648	O 703	S 18	0	0
1	C	474	Total 3771	C 2402	N 648	O 703	S 18	0	0
1	D	474	Total 3771	C 2402	N 648	O 703	S 18	0	0
1	E	474	Total 3771	C 2402	N 648	O 703	S 18	0	0

3 Residue-property plots

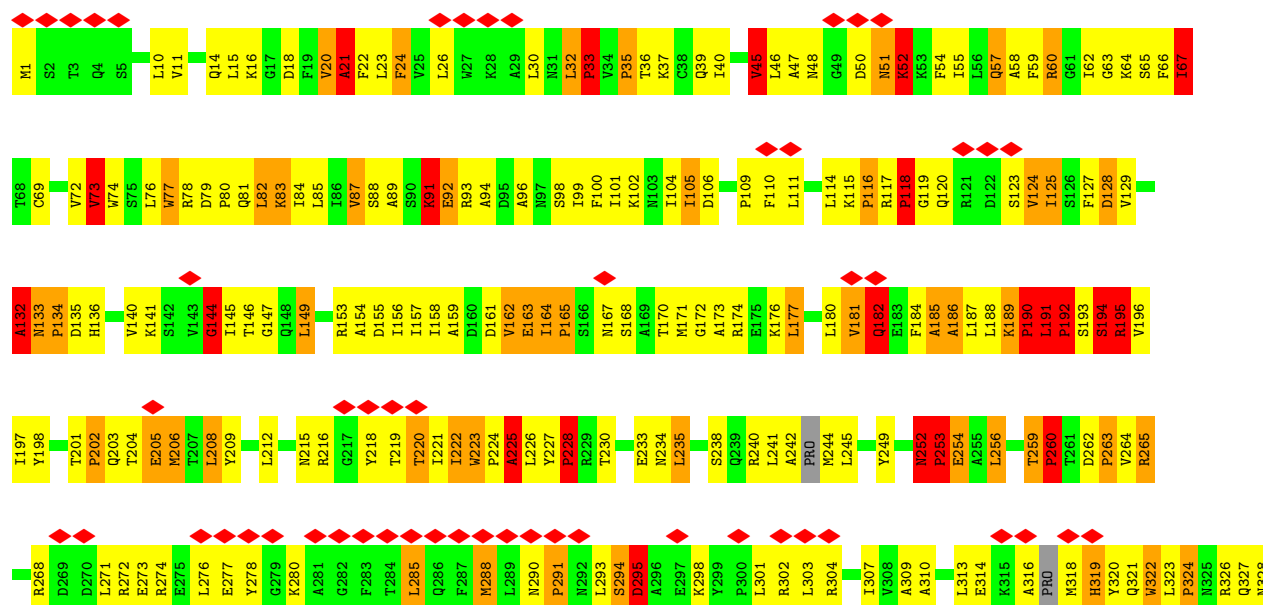
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

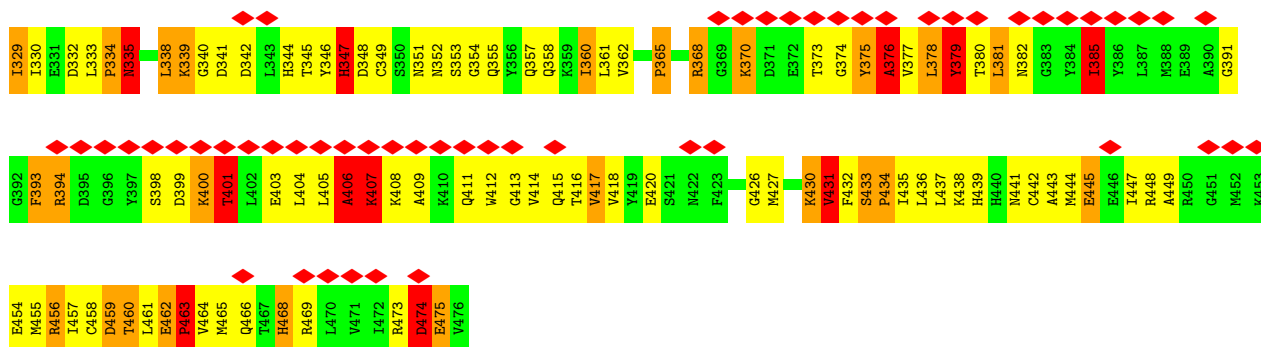
• Molecule 1: DNA MATURASE B



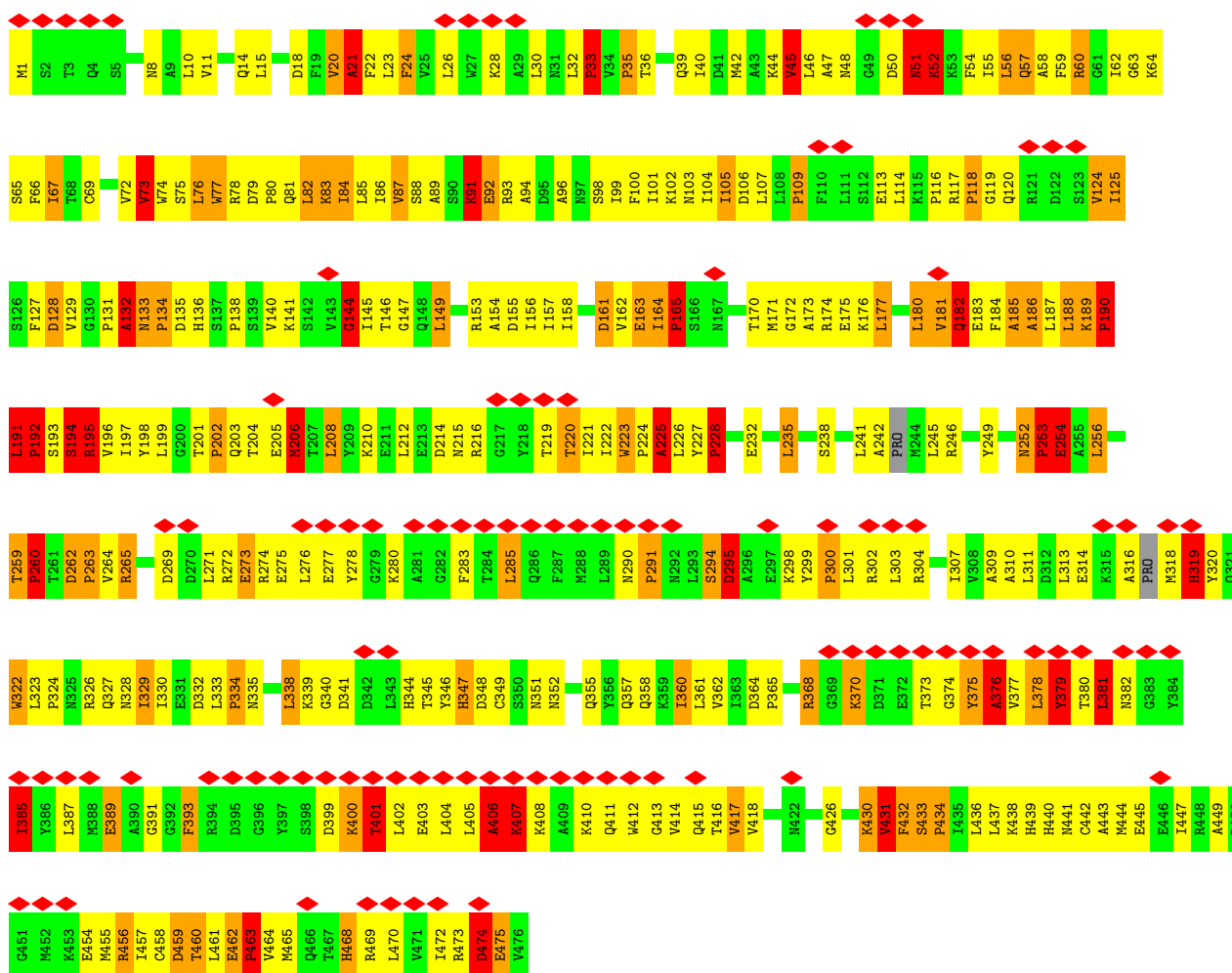


• Molecule 1: DNA MATURASE B



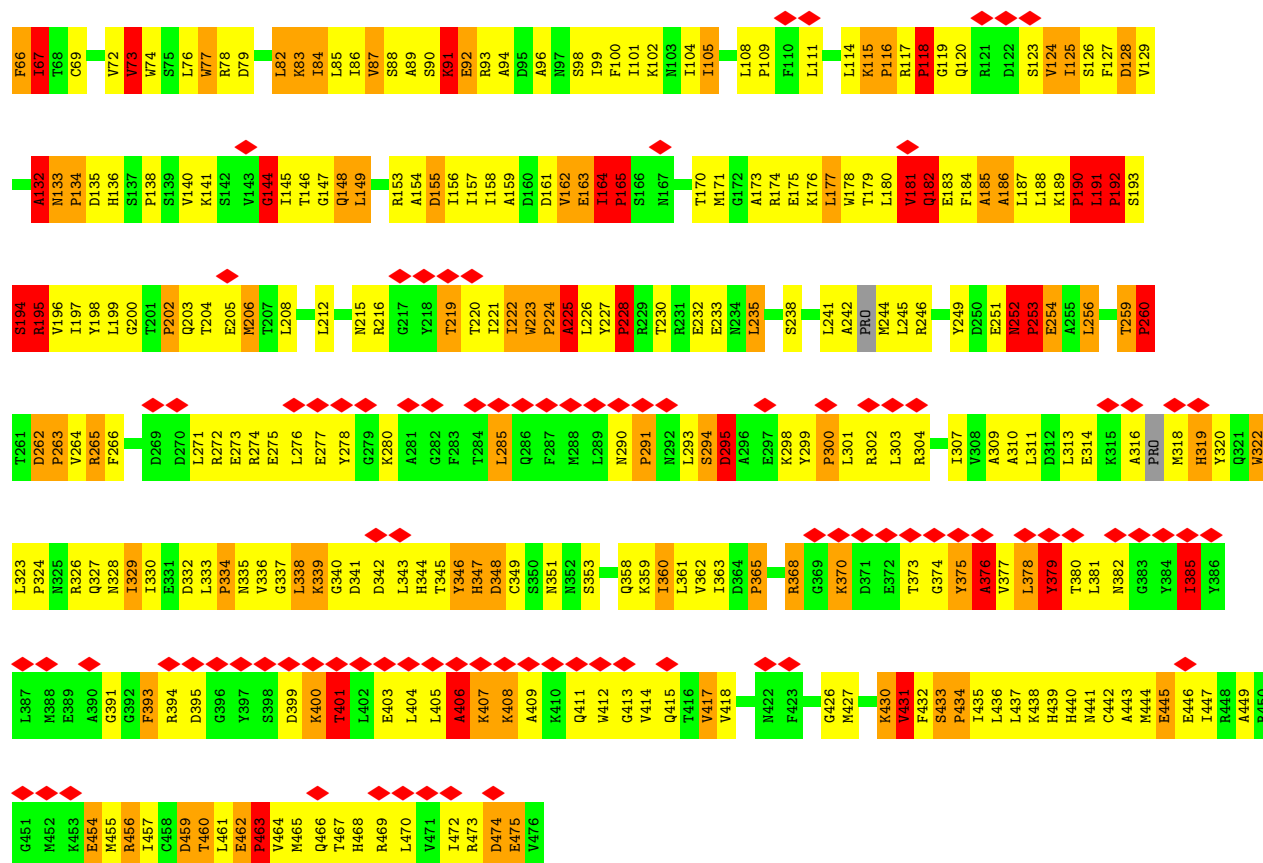


• Molecule 1: DNA MATURASE B



• Molecule 1: DNA MATURASE B





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	3650	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PLATE	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	100	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	67000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	0.094	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0383	Depositor
Map size ($\text{\AA}$)	352.0, 352.0, 352.0	wwPDB
Map dimensions	80, 80, 80	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	4.4, 4.4, 4.4	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.25	32/3850 (0.8%)	1.86	133/5212 (2.6%)
1	B	1.24	30/3850 (0.8%)	1.85	136/5212 (2.6%)
1	C	1.23	32/3850 (0.8%)	1.84	130/5212 (2.5%)
1	D	1.21	34/3850 (0.9%)	1.84	131/5212 (2.5%)
1	E	1.27	31/3850 (0.8%)	1.84	134/5212 (2.6%)
All	All	1.24	159/19250 (0.8%)	1.85	664/26060 (2.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	13
1	B	0	14
1	C	0	14
1	D	0	14
1	E	0	13
All	All	0	68

All (159) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	291	PRO	N-CD	-23.70	1.14	1.47
1	B	134	PRO	N-CD	20.22	1.76	1.47
1	E	300	PRO	N-CD	19.52	1.75	1.47
1	C	291	PRO	N-CD	-19.37	1.20	1.47
1	B	291	PRO	N-CD	-19.12	1.21	1.47
1	E	134	PRO	N-CD	19.09	1.74	1.47
1	A	291	PRO	N-CD	-17.49	1.23	1.47
1	A	134	PRO	N-CD	17.26	1.72	1.47
1	D	291	PRO	N-CD	-16.80	1.24	1.47
1	C	134	PRO	N-CD	16.20	1.70	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	434	PRO	N-CD	15.72	1.69	1.47
1	D	300	PRO	N-CD	15.61	1.69	1.47
1	B	434	PRO	N-CD	15.26	1.69	1.47
1	D	434	PRO	N-CD	14.55	1.68	1.47
1	A	434	PRO	N-CD	14.48	1.68	1.47
1	E	116	PRO	N-CD	14.08	1.67	1.47
1	E	434	PRO	N-CD	13.71	1.67	1.47
1	B	116	PRO	N-CD	12.98	1.66	1.47
1	A	300	PRO	N-CD	12.96	1.65	1.47
1	D	202	PRO	N-CD	12.84	1.65	1.47
1	C	116	PRO	N-CD	12.41	1.65	1.47
1	D	134	PRO	N-CD	12.09	1.64	1.47
1	C	202	PRO	N-CD	11.92	1.64	1.47
1	E	365	PRO	N-CD	11.86	1.64	1.47
1	A	190	PRO	N-CD	11.58	1.64	1.47
1	B	260	PRO	N-CD	11.50	1.63	1.47
1	B	300	PRO	N-CD	11.45	1.63	1.47
1	B	202	PRO	N-CD	11.43	1.63	1.47
1	A	202	PRO	N-CD	11.42	1.63	1.47
1	C	190	PRO	N-CD	11.39	1.63	1.47
1	E	33	PRO	N-CD	-10.92	1.32	1.47
1	A	260	PRO	N-CD	10.73	1.62	1.47
1	D	260	PRO	N-CD	10.23	1.62	1.47
1	A	365	PRO	N-CD	10.23	1.62	1.47
1	D	253	PRO	N-CD	10.20	1.62	1.47
1	E	253	PRO	N-CD	9.91	1.61	1.47
1	D	80	PRO	N-CD	-9.91	1.33	1.47
1	C	253	PRO	N-CD	9.82	1.61	1.47
1	C	365	PRO	N-CD	9.72	1.61	1.47
1	A	33	PRO	N-CD	-9.63	1.34	1.47
1	B	118	PRO	N-CD	9.42	1.60	1.47
1	A	253	PRO	N-CD	9.39	1.60	1.47
1	B	253	PRO	N-CD	9.34	1.60	1.47
1	B	190	PRO	N-CD	8.88	1.60	1.47
1	C	223	TRP	NE1-CE2	-8.45	1.28	1.37
1	B	223	TRP	NE1-CE2	-8.35	1.28	1.37
1	D	223	TRP	NE1-CE2	-8.27	1.28	1.37
1	E	223	TRP	NE1-CE2	-8.27	1.28	1.37
1	A	223	TRP	NE1-CE2	-8.22	1.28	1.37
1	D	190	PRO	N-CD	8.10	1.59	1.47
1	A	35	PRO	N-CD	7.50	1.58	1.47
1	C	165	PRO	N-CD	-7.43	1.37	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	77	TRP	NE1-CE2	-7.11	1.29	1.37
1	C	77	TRP	NE1-CE2	-7.10	1.29	1.37
1	A	77	TRP	NE1-CE2	-7.06	1.29	1.37
1	D	77	TRP	NE1-CE2	-7.03	1.29	1.37
1	B	77	TRP	NE1-CE2	-7.00	1.29	1.37
1	D	376	ALA	N-CA	-6.99	1.37	1.46
1	C	376	ALA	N-CA	-6.99	1.37	1.46
1	C	192	PRO	N-CA	-6.96	1.38	1.47
1	E	376	ALA	N-CA	-6.96	1.37	1.46
1	A	376	ALA	N-CA	-6.96	1.37	1.46
1	B	376	ALA	N-CA	-6.93	1.37	1.46
1	D	192	PRO	N-CA	-6.90	1.38	1.47
1	E	192	PRO	N-CA	-6.89	1.38	1.47
1	A	192	PRO	N-CA	-6.87	1.38	1.47
1	B	192	PRO	N-CA	-6.85	1.38	1.47
1	C	319	HIS	CG-ND1	-6.80	1.30	1.38
1	A	319	HIS	CG-ND1	-6.78	1.30	1.38
1	D	319	HIS	CG-ND1	-6.75	1.30	1.38
1	B	319	HIS	CG-ND1	-6.74	1.30	1.38
1	B	463	PRO	N-CD	-6.60	1.38	1.47
1	C	260	PRO	N-CD	6.51	1.56	1.47
1	A	136	HIS	CG-ND1	-6.38	1.31	1.38
1	E	463	PRO	N-CD	-6.28	1.39	1.47
1	C	439	HIS	CG-ND1	-6.21	1.31	1.38
1	D	186	ALA	C-O	-6.16	1.17	1.24
1	E	439	HIS	CG-ND1	-6.16	1.31	1.38
1	D	439	HIS	CG-ND1	-6.14	1.31	1.38
1	E	322	TRP	NE1-CE2	-6.12	1.30	1.37
1	A	439	HIS	CG-ND1	-6.12	1.31	1.38
1	D	322	TRP	NE1-CE2	-6.11	1.30	1.37
1	B	322	TRP	NE1-CE2	-6.11	1.30	1.37
1	B	439	HIS	CG-ND1	-6.10	1.31	1.38
1	A	186	ALA	C-O	-6.09	1.17	1.24
1	D	463	PRO	N-CD	-6.07	1.39	1.47
1	B	186	ALA	C-O	-6.06	1.17	1.24
1	C	322	TRP	NE1-CE2	-6.05	1.30	1.37
1	C	186	ALA	C-O	-6.04	1.17	1.24
1	A	322	TRP	NE1-CE2	-6.04	1.30	1.37
1	E	186	ALA	C-O	-5.98	1.17	1.24
1	B	468	HIS	CD2-NE2	-5.96	1.31	1.37
1	C	468	HIS	CD2-NE2	-5.95	1.31	1.37
1	D	468	HIS	CD2-NE2	-5.94	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	468	HIS	CD2-NE2	-5.91	1.31	1.37
1	E	468	HIS	CD2-NE2	-5.86	1.31	1.37
1	E	440	HIS	CG-ND1	-5.79	1.31	1.38
1	A	440	HIS	CG-ND1	-5.73	1.31	1.38
1	C	35	PRO	N-CD	5.72	1.55	1.47
1	D	440	HIS	CG-ND1	-5.67	1.32	1.38
1	D	35	PRO	N-CD	5.62	1.55	1.47
1	C	194	SER	CA-CB	-5.59	1.44	1.53
1	E	194	SER	CA-CB	-5.56	1.44	1.53
1	A	194	SER	CA-CB	-5.55	1.44	1.53
1	B	194	SER	CA-CB	-5.54	1.44	1.53
1	D	194	SER	CA-CB	-5.53	1.44	1.53
1	E	138	PRO	N-CD	5.48	1.55	1.47
1	C	463	PRO	N-CD	-5.45	1.40	1.47
1	E	260	PRO	N-CD	5.44	1.55	1.47
1	C	319	HIS	CA-CB	-5.43	1.45	1.53
1	B	319	HIS	CA-CB	-5.39	1.45	1.53
1	D	319	HIS	CA-CB	-5.39	1.45	1.53
1	A	319	HIS	CA-CB	-5.38	1.45	1.53
1	B	319	HIS	CD2-NE2	-5.38	1.31	1.37
1	D	319	HIS	CD2-NE2	-5.38	1.31	1.37
1	E	35	PRO	N-CD	5.36	1.55	1.47
1	E	319	HIS	CA-CB	-5.33	1.46	1.53
1	C	109	PRO	N-CD	-5.30	1.40	1.47
1	C	319	HIS	CD2-NE2	-5.29	1.32	1.37
1	A	319	HIS	CD2-NE2	-5.27	1.32	1.37
1	B	324	PRO	N-CD	5.27	1.55	1.47
1	E	344	HIS	CG-ND1	-5.26	1.32	1.38
1	D	344	HIS	CG-ND1	-5.25	1.32	1.38
1	E	440	HIS	CD2-NE2	-5.23	1.32	1.37
1	C	344	HIS	CG-ND1	-5.23	1.32	1.38
1	D	131	PRO	N-CD	-5.22	1.40	1.47
1	E	45	VAL	C-O	-5.22	1.17	1.24
1	A	45	VAL	C-O	-5.21	1.17	1.24
1	B	45	VAL	C-O	-5.21	1.17	1.24
1	A	468	HIS	CG-ND1	-5.20	1.32	1.38
1	A	440	HIS	CD2-NE2	-5.20	1.32	1.37
1	D	45	VAL	C-O	-5.20	1.17	1.24
1	B	344	HIS	CG-ND1	-5.17	1.32	1.38
1	C	439	HIS	CD2-NE2	-5.17	1.32	1.37
1	C	468	HIS	CG-ND1	-5.17	1.32	1.38
1	D	440	HIS	CD2-NE2	-5.16	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	344	HIS	CG-ND1	-5.15	1.32	1.38
1	B	468	HIS	CG-ND1	-5.14	1.32	1.38
1	E	256	LEU	C-O	-5.12	1.18	1.24
1	C	256	LEU	C-O	-5.12	1.18	1.24
1	B	256	LEU	C-O	-5.11	1.18	1.24
1	C	45	VAL	C-O	-5.10	1.18	1.24
1	D	440	HIS	CG-CD2	-5.08	1.30	1.35
1	A	256	LEU	C-O	-5.08	1.18	1.24
1	B	439	HIS	CD2-NE2	-5.07	1.32	1.37
1	D	439	HIS	CD2-NE2	-5.07	1.32	1.37
1	C	376	ALA	C-N	-5.07	1.26	1.33
1	B	376	ALA	C-N	-5.06	1.26	1.33
1	D	256	LEU	C-O	-5.06	1.18	1.24
1	D	468	HIS	CG-ND1	-5.06	1.32	1.38
1	A	376	ALA	C-N	-5.06	1.26	1.33
1	E	439	HIS	CD2-NE2	-5.05	1.32	1.37
1	E	440	HIS	CG-CD2	-5.05	1.30	1.35
1	D	344	HIS	CD2-NE2	-5.03	1.32	1.37
1	E	376	ALA	C-N	-5.02	1.26	1.33
1	A	439	HIS	CD2-NE2	-5.02	1.32	1.37
1	E	468	HIS	CG-ND1	-5.02	1.32	1.38
1	D	376	ALA	C-N	-5.01	1.26	1.33
1	C	344	HIS	CD2-NE2	-5.00	1.32	1.37

All (664) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	291	PRO	N-CD-CG	15.74	126.81	103.20
1	A	291	PRO	N-CD-CG	15.70	126.75	103.20
1	E	186	ALA	CA-C-O	-15.31	104.93	120.70
1	A	186	ALA	CA-C-O	-15.30	104.94	120.70
1	C	186	ALA	CA-C-O	-15.27	104.97	120.70
1	B	186	ALA	CA-C-O	-15.20	105.04	120.70
1	D	186	ALA	CA-C-O	-15.17	105.08	120.70
1	A	259	THR	O-C-N	-15.08	106.53	120.71
1	D	259	THR	O-C-N	-15.07	106.54	120.71
1	E	259	THR	O-C-N	-15.05	106.56	120.71
1	B	259	THR	O-C-N	-15.01	106.60	120.71
1	C	259	THR	O-C-N	-15.01	106.60	120.71
1	C	291	PRO	N-CD-CG	14.42	124.83	103.20
1	E	192	PRO	N-CD-CG	13.94	124.12	103.20
1	A	192	PRO	N-CD-CG	13.92	124.09	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	192	PRO	N-CD-CG	13.34	123.21	103.20
1	E	291	PRO	N-CD-CG	13.25	123.07	103.20
1	C	192	PRO	N-CD-CG	12.53	121.99	103.20
1	D	291	PRO	N-CD-CG	12.13	121.39	103.20
1	D	192	PRO	N-CD-CG	12.12	121.39	103.20
1	D	463	PRO	N-CD-CG	12.02	121.22	103.20
1	B	463	PRO	N-CD-CG	11.94	121.11	103.20
1	E	463	PRO	N-CD-CG	11.93	121.09	103.20
1	C	463	PRO	N-CD-CG	11.82	120.93	103.20
1	E	192	PRO	CA-N-CD	-11.72	95.59	112.00
1	A	192	PRO	CA-N-CD	-11.66	95.67	112.00
1	B	77	TRP	CZ3-CH2-CZ2	-11.62	106.39	121.50
1	A	77	TRP	CZ3-CH2-CZ2	-11.62	106.40	121.50
1	D	77	TRP	CZ3-CH2-CZ2	-11.62	106.40	121.50
1	A	463	PRO	N-CD-CG	11.60	120.60	103.20
1	E	77	TRP	CZ3-CH2-CZ2	-11.58	106.44	121.50
1	C	77	TRP	CZ3-CH2-CZ2	-11.56	106.47	121.50
1	B	192	PRO	CA-N-CD	-11.27	96.22	112.00
1	E	77	TRP	CH2-CZ2-CE2	11.26	132.13	117.50
1	A	77	TRP	CH2-CZ2-CE2	11.24	132.12	117.50
1	B	77	TRP	CH2-CZ2-CE2	11.23	132.10	117.50
1	C	462	GLU	CA-C-N	11.22	130.64	118.97
1	C	462	GLU	C-N-CA	11.22	130.64	118.97
1	D	77	TRP	CH2-CZ2-CE2	11.22	132.09	117.50
1	C	77	TRP	CH2-CZ2-CE2	11.18	132.04	117.50
1	D	462	GLU	CA-C-N	11.18	130.59	118.97
1	D	462	GLU	C-N-CA	11.18	130.59	118.97
1	B	462	GLU	CA-C-N	11.16	130.58	118.97
1	B	462	GLU	C-N-CA	11.16	130.58	118.97
1	A	462	GLU	CA-C-N	11.13	130.55	118.97
1	A	462	GLU	C-N-CA	11.13	130.55	118.97
1	A	189	LYS	CA-C-N	11.12	130.91	119.56
1	A	189	LYS	C-N-CA	11.12	130.91	119.56
1	E	189	LYS	CA-C-N	11.12	130.91	119.56
1	E	189	LYS	C-N-CA	11.12	130.91	119.56
1	C	189	LYS	CA-C-N	11.12	130.90	119.56
1	C	189	LYS	C-N-CA	11.12	130.90	119.56
1	B	189	LYS	CA-C-N	11.12	130.90	119.56
1	B	189	LYS	C-N-CA	11.12	130.90	119.56
1	E	462	GLU	CA-C-N	11.12	130.53	118.97
1	E	462	GLU	C-N-CA	11.12	130.53	118.97
1	D	189	LYS	CA-C-N	11.11	130.89	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	189	LYS	C-N-CA	11.11	130.89	119.56
1	D	192	PRO	CA-N-CD	-10.99	96.61	112.00
1	C	192	PRO	CA-N-CD	-10.84	96.82	112.00
1	C	319	HIS	CA-CB-CG	10.76	124.56	113.80
1	D	319	HIS	CA-CB-CG	10.74	124.55	113.80
1	B	319	HIS	CA-CB-CG	10.72	124.52	113.80
1	A	319	HIS	CA-CB-CG	10.70	124.50	113.80
1	D	433	SER	CA-C-N	10.55	130.38	119.19
1	D	433	SER	C-N-CA	10.55	130.38	119.19
1	C	433	SER	CA-C-N	10.54	130.37	119.19
1	C	433	SER	C-N-CA	10.54	130.37	119.19
1	E	433	SER	CA-C-N	10.52	130.34	119.19
1	E	433	SER	C-N-CA	10.52	130.34	119.19
1	B	433	SER	CA-C-N	10.52	130.34	119.19
1	B	433	SER	C-N-CA	10.52	130.34	119.19
1	A	433	SER	CA-C-N	10.50	130.32	119.19
1	A	433	SER	C-N-CA	10.50	130.32	119.19
1	C	256	LEU	CA-C-O	-10.42	109.51	120.55
1	E	256	LEU	CA-C-O	-10.41	109.52	120.55
1	D	256	LEU	CA-C-O	-10.38	109.55	120.55
1	A	256	LEU	CA-C-O	-10.37	109.56	120.55
1	B	256	LEU	CA-C-O	-10.33	109.60	120.55
1	D	463	PRO	CA-N-CD	-9.94	98.08	112.00
1	E	190	PRO	N-CD-CG	9.90	118.05	103.20
1	C	463	PRO	CA-N-CD	-9.90	98.14	112.00
1	A	463	PRO	CA-N-CD	-9.81	98.27	112.00
1	B	21	ALA	CA-C-O	-9.76	109.26	120.58
1	A	21	ALA	CA-C-O	-9.72	109.30	120.58
1	A	165	PRO	N-CD-CG	9.72	117.78	103.20
1	E	21	ALA	CA-C-O	-9.72	109.30	120.58
1	C	21	ALA	CA-C-O	-9.72	109.31	120.58
1	D	21	ALA	CA-C-O	-9.71	109.32	120.58
1	E	463	PRO	CA-N-CD	-9.71	98.41	112.00
1	B	463	PRO	CA-N-CD	-9.44	98.78	112.00
1	E	259	THR	CA-C-O	9.44	127.49	118.34
1	D	259	THR	CA-C-O	9.43	127.49	118.34
1	C	259	THR	CA-C-O	9.42	127.48	118.34
1	A	259	THR	CA-C-O	9.42	127.48	118.34
1	B	259	THR	CA-C-O	9.40	127.46	118.34
1	E	190	PRO	CA-N-CD	-9.40	98.84	112.00
1	C	51	ASN	OD1-CG-ND2	-9.29	113.31	122.60
1	A	291	PRO	CA-N-CD	-9.28	99.01	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	51	ASN	OD1-CG-ND2	-9.25	113.35	122.60
1	A	51	ASN	OD1-CG-ND2	-9.24	113.36	122.60
1	B	165	PRO	CA-N-CD	-9.22	99.09	112.00
1	D	51	ASN	OD1-CG-ND2	-9.21	113.39	122.60
1	E	51	ASN	OD1-CG-ND2	-9.16	113.44	122.60
1	D	165	PRO	N-CD-CG	9.10	116.86	103.20
1	B	165	PRO	N-CD-CG	9.10	116.84	103.20
1	D	165	PRO	CA-N-CD	-9.07	99.30	112.00
1	E	165	PRO	CA-N-CD	-9.06	99.31	112.00
1	D	290	ASN	CA-C-N	9.02	131.12	119.84
1	D	290	ASN	C-N-CA	9.02	131.12	119.84
1	A	290	ASN	CA-C-N	9.00	131.09	119.84
1	A	290	ASN	C-N-CA	9.00	131.09	119.84
1	A	118	PRO	N-CD-CG	-8.97	89.74	103.20
1	E	290	ASN	CA-C-N	8.96	131.03	119.84
1	E	290	ASN	C-N-CA	8.96	131.03	119.84
1	B	290	ASN	CA-C-N	8.95	131.03	119.84
1	B	290	ASN	C-N-CA	8.95	131.03	119.84
1	C	290	ASN	CA-C-N	8.94	131.01	119.84
1	C	290	ASN	C-N-CA	8.94	131.01	119.84
1	B	295	ASP	O-C-N	-8.86	112.12	123.02
1	E	295	ASP	O-C-N	-8.86	112.12	123.02
1	D	295	ASP	O-C-N	-8.85	112.14	123.02
1	A	295	ASP	O-C-N	-8.84	112.14	123.02
1	E	165	PRO	N-CD-CG	8.81	116.41	103.20
1	C	295	ASP	O-C-N	-8.80	112.20	123.02
1	A	32	LEU	CA-C-N	8.58	129.09	119.83
1	A	32	LEU	C-N-CA	8.58	129.09	119.83
1	B	291	PRO	CA-N-CD	-8.58	99.99	112.00
1	B	32	LEU	CA-C-N	8.52	129.03	119.83
1	B	32	LEU	C-N-CA	8.52	129.03	119.83
1	D	32	LEU	CA-C-N	8.51	129.03	119.83
1	D	32	LEU	C-N-CA	8.51	129.03	119.83
1	E	32	LEU	CA-C-N	8.51	129.02	119.83
1	E	32	LEU	C-N-CA	8.51	129.02	119.83
1	C	32	LEU	CA-C-N	8.51	129.02	119.83
1	C	32	LEU	C-N-CA	8.51	129.02	119.83
1	C	163	GLU	CB-CG-CD	8.48	127.01	112.60
1	C	190	PRO	CA-N-CD	-8.47	100.14	112.00
1	B	163	GLU	CB-CG-CD	8.47	127.00	112.60
1	B	182	GLN	N-CA-CB	8.46	124.88	110.50
1	E	163	GLU	CB-CG-CD	8.46	126.98	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	163	GLU	CB-CG-CD	8.45	126.97	112.60
1	C	182	GLN	N-CA-CB	8.45	124.87	110.50
1	A	163	GLU	CB-CG-CD	8.45	126.97	112.60
1	A	190	PRO	CA-N-CD	-8.44	100.18	112.00
1	D	182	GLN	N-CA-CB	8.44	124.84	110.50
1	E	182	GLN	N-CA-CB	8.43	124.83	110.50
1	A	182	GLN	N-CA-CB	8.43	124.83	110.50
1	D	228	PRO	CA-N-CD	-8.33	100.34	112.00
1	C	228	PRO	CA-N-CD	-8.33	100.34	112.00
1	E	228	PRO	CA-N-CD	-8.32	100.35	112.00
1	A	186	ALA	O-C-N	8.31	131.07	122.09
1	A	228	PRO	CA-N-CD	-8.31	100.37	112.00
1	C	165	PRO	N-CD-CG	8.30	115.66	103.20
1	B	228	PRO	CA-N-CD	-8.29	100.39	112.00
1	E	186	ALA	O-C-N	8.28	131.03	122.09
1	A	417	VAL	O-C-N	8.25	130.19	121.94
1	B	417	VAL	O-C-N	8.25	130.19	121.94
1	C	186	ALA	O-C-N	8.24	130.99	122.09
1	D	186	ALA	O-C-N	8.22	130.97	122.09
1	B	186	ALA	O-C-N	8.21	130.96	122.09
1	D	190	PRO	CA-N-CD	-8.21	100.50	112.00
1	E	417	VAL	O-C-N	8.21	130.15	121.94
1	C	417	VAL	O-C-N	8.20	130.14	121.94
1	A	165	PRO	CA-N-CD	-8.18	100.54	112.00
1	B	33	PRO	CA-N-CD	-8.17	100.56	112.00
1	B	190	PRO	CA-N-CD	-8.15	100.59	112.00
1	C	225	ALA	N-CA-CB	8.11	123.22	111.05
1	D	417	VAL	O-C-N	8.11	130.05	121.94
1	B	225	ALA	N-CA-CB	8.11	123.22	111.05
1	A	225	ALA	N-CA-CB	8.11	123.21	111.05
1	E	225	ALA	N-CA-CB	8.09	123.18	111.05
1	D	225	ALA	N-CA-CB	8.09	123.18	111.05
1	C	118	PRO	N-CD-CG	-8.02	91.17	103.20
1	B	430	LYS	CA-C-O	-8.01	111.56	120.69
1	A	430	LYS	CA-C-O	-7.97	111.61	120.69
1	E	430	LYS	CA-C-O	-7.97	111.61	120.69
1	E	300	PRO	N-CD-CG	-7.96	91.26	103.20
1	C	430	LYS	CA-C-O	-7.95	111.63	120.69
1	D	430	LYS	CA-C-O	-7.95	111.63	120.69
1	E	118	PRO	N-CD-CG	-7.94	91.29	103.20
1	C	459	ASP	CA-C-O	-7.88	110.91	119.97
1	D	459	ASP	CA-C-O	-7.88	110.91	119.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	459	ASP	CA-C-O	-7.86	110.93	119.97
1	A	459	ASP	CA-C-O	-7.86	110.94	119.97
1	B	459	ASP	CA-C-O	-7.86	110.94	119.97
1	E	365	PRO	N-CD-CG	-7.82	91.48	103.20
1	E	57	GLN	CG-CD-NE2	7.75	128.03	116.40
1	E	360	ILE	O-C-N	7.74	129.69	121.87
1	E	360	ILE	CA-C-O	-7.71	112.32	120.57
1	A	360	ILE	O-C-N	7.70	129.65	121.87
1	A	360	ILE	CA-C-O	-7.70	112.33	120.57
1	B	57	GLN	CG-CD-NE2	7.69	127.94	116.40
1	D	57	GLN	CG-CD-NE2	7.69	127.93	116.40
1	B	360	ILE	CA-C-O	-7.68	112.35	120.57
1	D	360	ILE	O-C-N	7.68	129.63	121.87
1	A	57	GLN	CG-CD-NE2	7.68	127.92	116.40
1	C	57	GLN	CG-CD-NE2	7.66	127.90	116.40
1	C	360	ILE	O-C-N	7.66	129.61	121.87
1	D	360	ILE	CA-C-O	-7.66	112.37	120.57
1	E	376	ALA	CA-C-O	7.66	131.46	120.51
1	B	360	ILE	O-C-N	7.65	129.60	121.87
1	C	360	ILE	CA-C-O	-7.65	112.39	120.57
1	E	225	ALA	O-C-N	-7.64	112.01	122.94
1	D	376	ALA	CA-C-O	7.63	131.43	120.51
1	A	376	ALA	CA-C-O	7.63	131.42	120.51
1	B	376	ALA	CA-C-O	7.62	131.41	120.51
1	C	376	ALA	CA-C-O	7.61	131.39	120.51
1	A	225	ALA	O-C-N	-7.59	112.08	122.94
1	D	235	LEU	CD1-CG-CD2	7.58	127.48	110.80
1	B	225	ALA	O-C-N	-7.58	112.10	122.94
1	C	225	ALA	O-C-N	-7.57	112.11	122.94
1	D	225	ALA	O-C-N	-7.57	112.11	122.94
1	A	235	LEU	CD1-CG-CD2	7.56	127.44	110.80
1	C	235	LEU	CD1-CG-CD2	7.56	127.43	110.80
1	E	235	LEU	CD1-CG-CD2	7.56	127.43	110.80
1	B	235	LEU	CD1-CG-CD2	7.54	127.39	110.80
1	E	33	PRO	N-CD-CG	7.51	114.47	103.20
1	A	33	PRO	N-CD-CG	7.42	114.33	103.20
1	C	291	PRO	CA-N-CD	-7.41	101.63	112.00
1	C	469	ARG	CB-CA-C	-7.40	96.46	110.67
1	D	469	ARG	CB-CA-C	-7.40	96.47	110.67
1	E	469	ARG	CB-CA-C	-7.40	96.47	110.67
1	A	469	ARG	CB-CA-C	-7.39	96.49	110.67
1	B	469	ARG	CB-CA-C	-7.38	96.49	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	365	PRO	N-CD-CG	-7.35	92.18	103.20
1	A	401	THR	OG1-CB-CG2	7.29	123.88	109.30
1	E	73	VAL	CG1-CB-CG2	-7.28	94.79	110.80
1	E	401	THR	OG1-CB-CG2	7.28	123.85	109.30
1	D	225	ALA	N-CA-C	7.26	120.92	109.81
1	A	73	VAL	CG1-CB-CG2	-7.26	94.83	110.80
1	B	401	THR	OG1-CB-CG2	7.26	123.82	109.30
1	D	401	THR	OG1-CB-CG2	7.26	123.82	109.30
1	D	73	VAL	CG1-CB-CG2	-7.26	94.84	110.80
1	C	401	THR	OG1-CB-CG2	7.25	123.81	109.30
1	A	225	ALA	N-CA-C	7.25	120.90	109.81
1	B	225	ALA	N-CA-C	7.25	120.90	109.81
1	B	73	VAL	CG1-CB-CG2	-7.24	94.86	110.80
1	C	225	ALA	N-CA-C	7.24	120.89	109.81
1	E	225	ALA	N-CA-C	7.24	120.89	109.81
1	C	73	VAL	CG1-CB-CG2	-7.23	94.89	110.80
1	E	431	VAL	N-CA-C	7.21	117.98	110.62
1	E	376	ALA	O-C-N	-7.21	113.00	122.59
1	A	376	ALA	O-C-N	-7.21	113.00	122.59
1	A	431	VAL	N-CA-C	7.21	117.97	110.62
1	B	376	ALA	O-C-N	-7.20	113.01	122.59
1	D	431	VAL	N-CA-C	7.20	117.96	110.62
1	C	376	ALA	O-C-N	-7.20	113.02	122.59
1	A	194	SER	CB-CA-C	7.19	124.72	110.42
1	E	194	SER	CB-CA-C	7.18	124.72	110.42
1	D	376	ALA	O-C-N	-7.18	113.04	122.59
1	C	194	SER	CB-CA-C	7.18	124.70	110.42
1	A	67	ILE	CA-CB-CG2	-7.17	98.32	110.50
1	A	259	THR	CA-C-N	7.17	126.79	119.19
1	A	259	THR	C-N-CA	7.17	126.79	119.19
1	B	194	SER	CB-CA-C	7.16	124.67	110.42
1	E	259	THR	CA-C-N	7.15	126.77	119.19
1	E	259	THR	C-N-CA	7.15	126.77	119.19
1	D	259	THR	CA-C-N	7.15	126.77	119.19
1	D	259	THR	C-N-CA	7.15	126.77	119.19
1	D	67	ILE	CA-CB-CG2	-7.15	98.35	110.50
1	C	259	THR	CA-C-N	7.15	126.77	119.19
1	C	259	THR	C-N-CA	7.15	126.77	119.19
1	E	67	ILE	CA-CB-CG2	-7.14	98.35	110.50
1	C	431	VAL	N-CA-C	7.14	117.90	110.62
1	B	431	VAL	N-CA-C	7.14	117.90	110.62
1	B	324	PRO	CA-N-CD	-7.13	102.01	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	67	ILE	CA-CB-CG2	-7.13	98.38	110.50
1	D	194	SER	CB-CA-C	7.13	124.61	110.42
1	C	67	ILE	CA-CB-CG2	-7.13	98.39	110.50
1	B	259	THR	CA-C-N	7.12	126.74	119.19
1	B	259	THR	C-N-CA	7.12	126.74	119.19
1	A	379	TYR	CZ-CE2-CD2	7.06	132.31	119.60
1	C	365	PRO	N-CD-CG	-7.04	92.64	103.20
1	B	379	TYR	CZ-CE2-CD2	7.03	132.25	119.60
1	E	379	TYR	CZ-CE2-CD2	7.02	132.23	119.60
1	A	319	HIS	N-CA-CB	-7.01	95.31	110.88
1	D	319	HIS	N-CA-CB	-7.01	95.31	110.88
1	C	319	HIS	N-CA-CB	-7.01	95.33	110.88
1	E	319	HIS	N-CA-CB	-7.00	95.33	110.88
1	A	319	HIS	CE1-NE2-CD2	-6.99	102.01	109.00
1	B	319	HIS	N-CA-CB	-6.99	95.37	110.88
1	C	379	TYR	CZ-CE2-CD2	6.99	132.18	119.60
1	D	379	TYR	CZ-CE2-CD2	6.98	132.16	119.60
1	A	368	ARG	CA-C-O	6.97	128.03	120.43
1	B	294	SER	N-CA-CB	-6.97	99.90	110.91
1	D	294	SER	N-CA-CB	-6.97	99.90	110.91
1	E	294	SER	N-CA-CB	-6.97	99.90	110.91
1	C	319	HIS	CE1-NE2-CD2	-6.95	102.05	109.00
1	D	291	PRO	CA-N-CD	-6.95	102.27	112.00
1	C	294	SER	N-CA-CB	-6.95	99.93	110.91
1	A	294	SER	N-CA-CB	-6.95	99.94	110.91
1	C	368	ARG	CA-C-O	6.95	128.00	120.43
1	D	368	ARG	CA-C-O	6.95	128.00	120.43
1	D	319	HIS	CE1-NE2-CD2	-6.94	102.06	109.00
1	C	33	PRO	N-CD-CG	6.93	113.59	103.20
1	D	33	PRO	N-CD-CG	6.92	113.58	103.20
1	E	368	ARG	CA-C-O	6.91	127.96	120.43
1	C	33	PRO	CA-N-CD	-6.90	102.33	112.00
1	B	368	ARG	CA-C-O	6.89	127.94	120.43
1	A	182	GLN	CB-CA-C	-6.89	97.02	110.10
1	B	182	GLN	CB-CA-C	-6.88	97.02	110.10
1	D	182	GLN	CB-CA-C	-6.88	97.02	110.10
1	E	182	GLN	CB-CA-C	-6.88	97.03	110.10
1	C	324	PRO	CA-N-CD	-6.87	102.39	112.00
1	B	319	HIS	CE1-NE2-CD2	-6.86	102.14	109.00
1	C	182	GLN	CB-CA-C	-6.86	97.08	110.10
1	D	324	PRO	CA-N-CD	-6.84	102.43	112.00
1	B	431	VAL	CG1-CB-CG2	-6.78	95.88	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	431	VAL	CG1-CB-CG2	-6.76	95.92	110.80
1	C	431	VAL	CG1-CB-CG2	-6.76	95.92	110.80
1	E	431	VAL	CG1-CB-CG2	-6.76	95.93	110.80
1	D	431	VAL	CG1-CB-CG2	-6.74	95.98	110.80
1	A	319	HIS	CG-CD2-NE2	6.69	113.89	107.20
1	C	319	HIS	CG-CD2-NE2	6.69	113.89	107.20
1	D	440	HIS	CG-CD2-NE2	6.68	113.88	107.20
1	D	319	HIS	CG-CD2-NE2	6.68	113.88	107.20
1	A	202	PRO	CB-CA-C	-6.68	102.20	110.95
1	B	202	PRO	CB-CA-C	-6.68	102.20	110.95
1	A	440	HIS	CG-CD2-NE2	6.66	113.86	107.20
1	D	202	PRO	CB-CA-C	-6.66	102.22	110.95
1	E	202	PRO	CB-CA-C	-6.66	102.22	110.95
1	C	227	TYR	CA-C-N	6.66	127.19	119.47
1	C	227	TYR	C-N-CA	6.66	127.19	119.47
1	E	440	HIS	CG-CD2-NE2	6.66	113.86	107.20
1	D	33	PRO	CA-N-CD	-6.65	102.69	112.00
1	B	118	PRO	N-CD-CG	-6.64	93.24	103.20
1	D	227	TYR	CA-C-N	6.63	127.16	119.47
1	D	227	TYR	C-N-CA	6.63	127.16	119.47
1	B	319	HIS	CG-CD2-NE2	6.63	113.83	107.20
1	E	227	TYR	CA-C-N	6.63	127.16	119.47
1	E	227	TYR	C-N-CA	6.63	127.16	119.47
1	C	202	PRO	CB-CA-C	-6.62	102.27	110.95
1	A	227	TYR	CA-C-N	6.62	127.15	119.47
1	A	227	TYR	C-N-CA	6.62	127.15	119.47
1	B	227	TYR	CA-C-N	6.62	127.14	119.47
1	B	227	TYR	C-N-CA	6.62	127.14	119.47
1	D	300	PRO	N-CD-CG	-6.60	93.31	103.20
1	E	417	VAL	N-CA-C	6.59	117.28	110.36
1	C	417	VAL	N-CA-C	6.58	117.27	110.36
1	B	417	VAL	N-CA-C	6.57	117.26	110.36
1	D	417	VAL	N-CA-C	6.56	117.25	110.36
1	A	417	VAL	N-CA-C	6.53	117.22	110.36
1	B	368	ARG	O-C-N	-6.50	115.92	123.27
1	C	368	ARG	O-C-N	-6.50	115.92	123.27
1	D	368	ARG	O-C-N	-6.49	115.93	123.27
1	A	368	ARG	O-C-N	-6.49	115.94	123.27
1	B	381	LEU	CD1-CG-CD2	-6.48	96.54	110.80
1	D	381	LEU	CD1-CG-CD2	-6.48	96.55	110.80
1	E	381	LEU	CD1-CG-CD2	-6.47	96.57	110.80
1	E	368	ARG	O-C-N	-6.46	115.96	123.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	191	LEU	CA-C-N	6.46	127.92	119.84
1	C	191	LEU	C-N-CA	6.46	127.92	119.84
1	A	381	LEU	CD1-CG-CD2	-6.46	96.59	110.80
1	C	381	LEU	CD1-CG-CD2	-6.45	96.62	110.80
1	D	195	ARG	CD-NE-CZ	-6.43	115.40	124.40
1	E	191	LEU	CA-C-N	6.41	127.86	119.84
1	E	191	LEU	C-N-CA	6.41	127.86	119.84
1	A	195	ARG	CD-NE-CZ	-6.41	115.42	124.40
1	C	195	ARG	CD-NE-CZ	-6.41	115.42	124.40
1	B	33	PRO	N-CD-CG	6.39	112.79	103.20
1	E	195	ARG	CD-NE-CZ	-6.39	115.46	124.40
1	B	195	ARG	CD-NE-CZ	-6.38	115.46	124.40
1	B	191	LEU	CA-C-N	6.38	127.81	119.84
1	B	191	LEU	C-N-CA	6.38	127.81	119.84
1	A	191	LEU	CA-C-N	6.34	127.77	119.84
1	A	191	LEU	C-N-CA	6.34	127.77	119.84
1	D	191	LEU	CA-C-N	6.34	127.77	119.84
1	D	191	LEU	C-N-CA	6.34	127.77	119.84
1	E	291	PRO	CA-N-CD	-6.30	103.17	112.00
1	E	52	LYS	N-CA-CB	-6.29	99.86	110.49
1	A	195	ARG	N-CA-CB	6.29	121.18	110.50
1	A	52	LYS	N-CA-CB	-6.28	99.87	110.49
1	C	52	LYS	N-CA-CB	-6.27	99.89	110.49
1	D	195	ARG	N-CA-CB	6.27	121.16	110.50
1	B	52	LYS	N-CA-CB	-6.27	99.90	110.49
1	D	52	LYS	N-CA-CB	-6.26	99.90	110.49
1	B	195	ARG	N-CA-CB	6.26	121.14	110.50
1	E	376	ALA	CB-CA-C	6.26	122.88	110.42
1	D	132	ALA	CB-CA-C	-6.26	97.97	110.42
1	E	195	ARG	N-CA-CB	6.26	121.14	110.50
1	C	195	ARG	N-CA-CB	6.25	121.13	110.50
1	E	368	ARG	NE-CZ-NH2	6.25	124.83	119.20
1	A	132	ALA	CB-CA-C	-6.25	97.98	110.42
1	A	368	ARG	NE-CZ-NH2	6.25	124.82	119.20
1	E	132	ALA	CB-CA-C	-6.25	97.99	110.42
1	E	385	ILE	CA-C-O	-6.24	112.98	120.78
1	D	376	ALA	CB-CA-C	6.24	122.83	110.42
1	B	376	ALA	CB-CA-C	6.23	122.82	110.42
1	C	376	ALA	CB-CA-C	6.23	122.82	110.42
1	A	385	ILE	CA-C-O	-6.22	113.00	120.78
1	B	385	ILE	CA-C-O	-6.22	113.00	120.78
1	A	376	ALA	CB-CA-C	6.22	122.79	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	385	ILE	CA-C-O	-6.21	113.02	120.78
1	C	132	ALA	CB-CA-C	-6.21	98.06	110.42
1	B	132	ALA	CB-CA-C	-6.21	98.06	110.42
1	D	385	ILE	CA-C-O	-6.21	113.02	120.78
1	B	134	PRO	N-CD-CG	-6.19	93.91	103.20
1	C	368	ARG	NE-CZ-NH2	6.19	124.77	119.20
1	D	338	LEU	CD1-CG-CD2	-6.19	97.17	110.80
1	C	109	PRO	N-CD-CG	6.19	112.48	103.20
1	E	338	LEU	CD1-CG-CD2	-6.18	97.21	110.80
1	B	368	ARG	NE-CZ-NH2	6.18	124.76	119.20
1	A	338	LEU	CD1-CG-CD2	-6.17	97.22	110.80
1	C	338	LEU	CD1-CG-CD2	-6.17	97.22	110.80
1	D	368	ARG	NE-CZ-NH2	6.17	124.75	119.20
1	B	338	LEU	CD1-CG-CD2	-6.16	97.25	110.80
1	E	324	PRO	N-CD-CG	6.12	112.38	103.20
1	C	400	LYS	CA-C-O	-6.04	114.35	122.44
1	D	144	GLY	CA-C-O	-6.04	110.06	120.57
1	E	400	LYS	CA-C-O	-6.04	114.35	122.44
1	B	400	LYS	CA-C-O	-6.04	114.35	122.44
1	E	144	GLY	CA-C-O	-6.02	110.10	120.57
1	A	144	GLY	CA-C-O	-6.02	110.10	120.57
1	B	182	GLN	CG-CD-OE1	6.01	132.82	120.80
1	D	182	GLN	CG-CD-OE1	6.00	132.81	120.80
1	A	324	PRO	CA-N-CD	-6.00	103.60	112.00
1	C	144	GLY	CA-C-O	-6.00	110.14	120.57
1	C	182	GLN	CG-CD-OE1	5.99	132.79	120.80
1	A	400	LYS	CA-C-O	-5.99	114.41	122.44
1	B	144	GLY	CA-C-O	-5.99	110.15	120.57
1	A	182	GLN	CG-CD-OE1	5.99	132.77	120.80
1	E	324	PRO	CA-N-CD	-5.97	103.64	112.00
1	D	400	LYS	CA-C-O	-5.96	114.45	122.44
1	E	182	GLN	CG-CD-OE1	5.94	132.69	120.80
1	E	319	HIS	N-CA-C	5.93	119.62	108.65
1	C	407	LYS	CA-C-N	5.92	128.22	120.28
1	C	407	LYS	C-N-CA	5.92	128.22	120.28
1	E	407	LYS	CA-C-N	5.92	128.22	120.28
1	E	407	LYS	C-N-CA	5.92	128.22	120.28
1	A	319	HIS	N-CA-C	5.92	119.60	108.65
1	A	407	LYS	CA-C-N	5.92	128.21	120.28
1	A	407	LYS	C-N-CA	5.92	128.21	120.28
1	B	319	HIS	N-CA-C	5.90	119.56	108.65
1	B	407	LYS	CA-C-N	5.89	128.18	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	407	LYS	C-N-CA	5.89	128.18	120.28
1	D	407	LYS	CA-C-N	5.89	128.18	120.28
1	D	407	LYS	C-N-CA	5.89	128.18	120.28
1	C	319	HIS	N-CA-C	5.89	119.55	108.65
1	D	77	TRP	CE3-CZ3-CH2	5.89	128.76	121.10
1	D	319	HIS	N-CA-C	5.89	119.55	108.65
1	D	190	PRO	N-CD-CG	5.88	112.02	103.20
1	A	92	GLU	CA-C-N	5.87	128.42	120.44
1	A	92	GLU	C-N-CA	5.87	128.42	120.44
1	C	77	TRP	CE3-CZ3-CH2	5.86	128.72	121.10
1	B	92	GLU	CA-C-N	5.86	128.40	120.44
1	B	92	GLU	C-N-CA	5.86	128.40	120.44
1	B	77	TRP	CE3-CZ3-CH2	5.85	128.71	121.10
1	E	77	TRP	CE3-CZ3-CH2	5.84	128.70	121.10
1	D	439	HIS	ND1-CG-CD2	5.84	111.94	106.10
1	E	109	PRO	N-CD-CG	5.84	111.96	103.20
1	C	92	GLU	CA-C-N	5.83	128.36	120.44
1	C	92	GLU	C-N-CA	5.83	128.36	120.44
1	B	48	ASN	OD1-CG-ND2	-5.82	116.78	122.60
1	A	77	TRP	CE3-CZ3-CH2	5.81	128.65	121.10
1	E	378	LEU	N-CA-C	5.81	118.11	111.02
1	A	439	HIS	ND1-CG-CD2	5.80	111.91	106.10
1	D	92	GLU	CA-C-N	5.80	128.33	120.44
1	D	92	GLU	C-N-CA	5.80	128.33	120.44
1	C	434	PRO	CA-N-CD	-5.80	103.88	112.00
1	D	378	LEU	N-CA-C	5.80	118.09	111.02
1	A	378	LEU	N-CA-C	5.79	118.09	111.02
1	C	48	ASN	OD1-CG-ND2	-5.79	116.81	122.60
1	C	378	LEU	N-CA-C	5.79	118.08	111.02
1	B	439	HIS	ND1-CG-CD2	5.78	111.88	106.10
1	E	92	GLU	CA-C-N	5.78	128.30	120.44
1	E	92	GLU	C-N-CA	5.78	128.30	120.44
1	B	378	LEU	N-CA-C	5.78	118.07	111.02
1	E	439	HIS	ND1-CG-CD2	5.77	111.87	106.10
1	B	439	HIS	CA-CB-CG	5.76	119.56	113.80
1	D	324	PRO	N-CD-CG	5.74	111.82	103.20
1	A	105	ILE	CG1-CB-CG2	5.74	127.92	110.70
1	B	434	PRO	CA-N-CD	-5.73	103.98	112.00
1	D	48	ASN	OD1-CG-ND2	-5.73	116.87	122.60
1	C	439	HIS	CA-CB-CG	5.72	119.52	113.80
1	C	439	HIS	ND1-CG-CD2	5.72	111.82	106.10
1	E	105	ILE	CG1-CB-CG2	5.72	127.86	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	PRO	N-CD-CG	5.71	111.77	103.20
1	C	105	ILE	CG1-CB-CG2	5.71	127.84	110.70
1	B	105	ILE	CG1-CB-CG2	5.71	127.83	110.70
1	D	105	ILE	CG1-CB-CG2	5.71	127.83	110.70
1	E	52	LYS	CA-CB-CG	5.71	125.51	114.10
1	B	52	LYS	CA-CB-CG	5.70	125.49	114.10
1	A	48	ASN	OD1-CG-ND2	-5.69	116.91	122.60
1	A	52	LYS	CA-CB-CG	5.69	125.47	114.10
1	E	439	HIS	CA-CB-CG	5.69	119.49	113.80
1	D	439	HIS	CA-CB-CG	5.68	119.48	113.80
1	E	48	ASN	OD1-CG-ND2	-5.68	116.92	122.60
1	C	52	LYS	CA-CB-CG	5.67	125.45	114.10
1	E	134	PRO	N-CD-CG	-5.67	94.69	103.20
1	D	52	LYS	CA-CB-CG	5.67	125.43	114.10
1	A	434	PRO	CA-N-CD	-5.66	104.08	112.00
1	D	434	PRO	CA-N-CD	-5.66	104.08	112.00
1	A	439	HIS	CA-CB-CG	5.65	119.45	113.80
1	D	109	PRO	CA-N-CD	-5.65	104.09	112.00
1	B	80	PRO	CA-N-CD	-5.64	104.10	112.00
1	D	60	ARG	O-C-N	-5.63	116.09	122.68
1	A	379	TYR	CG-CD2-CE2	-5.63	112.76	121.20
1	B	60	ARG	O-C-N	-5.61	116.12	122.68
1	A	60	ARG	O-C-N	-5.60	116.13	122.68
1	E	379	TYR	CG-CD2-CE2	-5.59	112.81	121.20
1	A	300	PRO	N-CD-CG	-5.58	94.82	103.20
1	C	60	ARG	O-C-N	-5.58	116.15	122.68
1	E	60	ARG	O-C-N	-5.57	116.16	122.68
1	E	434	PRO	CA-N-CD	-5.57	104.20	112.00
1	B	324	PRO	N-CD-CG	5.56	111.54	103.20
1	C	379	TYR	CG-CD2-CE2	-5.56	112.86	121.20
1	A	322	TRP	CG-CD1-NE1	5.55	117.42	110.20
1	B	379	TYR	CG-CD2-CE2	-5.55	112.87	121.20
1	D	322	TRP	CG-CD1-NE1	5.55	117.41	110.20
1	D	379	TYR	CG-CD2-CE2	-5.54	112.89	121.20
1	C	322	TRP	CG-CD1-NE1	5.54	117.40	110.20
1	D	335	ASN	OD1-CG-ND2	5.53	128.13	122.60
1	C	324	PRO	N-CD-CG	5.53	111.49	103.20
1	D	15	LEU	CD1-CG-CD2	-5.52	98.65	110.80
1	B	322	TRP	CG-CD1-NE1	5.51	117.37	110.20
1	C	335	ASN	OD1-CG-ND2	5.51	128.11	122.60
1	E	15	LEU	CD1-CG-CD2	-5.50	98.69	110.80
1	B	109	PRO	N-CD-CG	5.50	111.45	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	LEU	CD1-CG-CD2	-5.50	98.70	110.80
1	B	335	ASN	OD1-CG-ND2	5.50	128.10	122.60
1	C	15	LEU	CD1-CG-CD2	-5.50	98.70	110.80
1	E	322	TRP	CG-CD1-NE1	5.50	117.35	110.20
1	A	15	LEU	CD1-CG-CD2	-5.50	98.71	110.80
1	C	375	TYR	O-C-N	5.49	127.94	122.12
1	E	335	ASN	OD1-CG-ND2	5.49	128.09	122.60
1	A	335	ASN	OD1-CG-ND2	5.48	128.08	122.60
1	A	417	VAL	N-CA-CB	5.46	116.58	110.51
1	B	260	PRO	CA-N-CD	-5.45	104.36	112.00
1	E	417	VAL	N-CA-CB	5.43	116.54	110.51
1	A	375	TYR	O-C-N	5.43	127.87	122.12
1	B	375	TYR	O-C-N	5.42	127.87	122.12
1	B	190	PRO	N-CD-CG	5.42	111.33	103.20
1	B	417	VAL	N-CA-CB	5.41	116.52	110.51
1	D	417	VAL	N-CA-CB	5.41	116.51	110.51
1	D	375	TYR	O-C-N	5.40	127.84	122.12
1	D	260	PRO	CA-N-CD	-5.39	104.46	112.00
1	B	460	THR	CA-CB-OG1	5.38	117.67	109.60
1	C	417	VAL	N-CA-CB	5.38	116.48	110.51
1	A	188	LEU	CB-CG-CD1	-5.38	94.56	110.70
1	B	188	LEU	CB-CG-CD1	-5.38	94.57	110.70
1	E	460	THR	CA-CB-OG1	5.38	117.67	109.60
1	A	460	THR	CA-CB-OG1	5.38	117.66	109.60
1	D	188	LEU	CB-CG-CD1	-5.38	94.57	110.70
1	A	185	ALA	CB-CA-C	-5.37	101.87	110.79
1	C	185	ALA	CB-CA-C	-5.37	101.87	110.79
1	E	375	TYR	O-C-N	5.37	127.81	122.12
1	D	460	THR	CA-CB-OG1	5.37	117.65	109.60
1	B	185	ALA	CB-CA-C	-5.37	101.89	110.79
1	C	188	LEU	CB-CG-CD1	-5.36	94.61	110.70
1	C	460	THR	CA-CB-OG1	5.36	117.65	109.60
1	E	188	LEU	CB-CG-CD1	-5.36	94.61	110.70
1	D	185	ALA	CB-CA-C	-5.36	101.90	110.79
1	A	439	HIS	CB-CG-CD2	-5.36	124.24	131.20
1	C	439	HIS	CB-CG-CD2	-5.34	124.26	131.20
1	E	185	ALA	CB-CA-C	-5.33	101.94	110.79
1	D	439	HIS	CB-CG-CD2	-5.32	124.28	131.20
1	B	439	HIS	CB-CG-CD2	-5.32	124.29	131.20
1	D	109	PRO	N-CD-CG	5.30	111.15	103.20
1	E	439	HIS	CB-CG-CD2	-5.30	124.31	131.20
1	A	206	MET	CG-SD-CE	-5.28	89.28	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	206	MET	CG-SD-CE	-5.27	89.30	100.90
1	D	206	MET	CG-SD-CE	-5.27	89.30	100.90
1	C	206	MET	CG-SD-CE	-5.27	89.31	100.90
1	E	206	MET	CG-SD-CE	-5.27	89.31	100.90
1	C	124	VAL	CA-C-O	-5.26	116.09	121.67
1	A	128	ASP	CA-C-N	5.25	127.54	120.50
1	A	128	ASP	C-N-CA	5.25	127.54	120.50
1	E	128	ASP	CA-C-N	5.25	127.54	120.50
1	E	128	ASP	C-N-CA	5.25	127.54	120.50
1	A	109	PRO	CA-N-CD	-5.25	104.65	112.00
1	A	439	HIS	N-CA-C	5.24	120.33	112.94
1	E	439	HIS	N-CA-C	5.23	120.32	112.94
1	B	181	VAL	CB-CA-C	5.23	119.86	111.29
1	C	128	ASP	CA-C-N	5.22	127.50	120.50
1	C	128	ASP	C-N-CA	5.22	127.50	120.50
1	D	128	ASP	CA-C-N	5.22	127.50	120.50
1	D	128	ASP	C-N-CA	5.22	127.50	120.50
1	B	456	ARG	CD-NE-CZ	5.22	131.71	124.40
1	D	181	VAL	CB-CA-C	5.21	119.84	111.29
1	B	128	ASP	CA-C-N	5.21	127.48	120.50
1	B	128	ASP	C-N-CA	5.21	127.48	120.50
1	C	181	VAL	CB-CA-C	5.21	119.83	111.29
1	A	181	VAL	CB-CA-C	5.20	119.81	111.29
1	B	439	HIS	N-CA-C	5.20	120.27	112.94
1	C	124	VAL	CA-C-N	5.20	131.05	121.70
1	C	124	VAL	C-N-CA	5.20	131.05	121.70
1	D	265	ARG	CD-NE-CZ	5.19	131.67	124.40
1	C	265	ARG	CD-NE-CZ	5.19	131.66	124.40
1	E	181	VAL	CB-CA-C	5.19	119.80	111.29
1	D	439	HIS	N-CA-C	5.19	120.25	112.94
1	A	260	PRO	CA-N-CD	-5.18	104.74	112.00
1	A	182	GLN	OE1-CD-NE2	-5.18	117.42	122.60
1	C	190	PRO	N-CA-C	-5.18	107.11	113.84
1	A	124	VAL	CA-C-O	-5.18	116.18	121.67
1	C	439	HIS	N-CA-C	5.18	120.24	112.94
1	C	456	ARG	CD-NE-CZ	5.18	131.65	124.40
1	B	202	PRO	CA-N-CD	-5.17	104.76	112.00
1	B	265	ARG	CD-NE-CZ	5.17	131.64	124.40
1	A	265	ARG	CD-NE-CZ	5.17	131.63	124.40
1	C	379	TYR	O-C-N	-5.16	116.75	122.07
1	A	379	TYR	O-C-N	-5.16	116.75	122.07
1	D	379	TYR	O-C-N	-5.16	116.76	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	124	VAL	CA-C-O	-5.16	116.20	121.67
1	A	124	VAL	CA-C-N	5.16	130.99	121.70
1	A	124	VAL	C-N-CA	5.16	130.99	121.70
1	E	265	ARG	CD-NE-CZ	5.16	131.62	124.40
1	A	190	PRO	N-CA-C	-5.15	107.14	113.84
1	B	190	PRO	N-CA-C	-5.15	107.14	113.84
1	D	124	VAL	CA-C-O	-5.15	116.21	121.67
1	D	456	ARG	CD-NE-CZ	5.15	131.61	124.40
1	C	252	ASN	C-N-CD	-5.15	103.90	125.00
1	B	124	VAL	CA-C-O	-5.14	116.22	121.67
1	E	124	VAL	CA-C-N	5.14	130.96	121.70
1	E	124	VAL	C-N-CA	5.14	130.96	121.70
1	E	456	ARG	CD-NE-CZ	5.14	131.60	124.40
1	B	124	VAL	CA-C-N	5.14	130.95	121.70
1	B	124	VAL	C-N-CA	5.14	130.95	121.70
1	A	456	ARG	CD-NE-CZ	5.14	131.59	124.40
1	D	124	VAL	CA-C-N	5.14	130.95	121.70
1	D	124	VAL	C-N-CA	5.14	130.95	121.70
1	D	182	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	B	182	GLN	OE1-CD-NE2	-5.12	117.48	122.60
1	B	379	TYR	O-C-N	-5.12	116.80	122.07
1	E	252	ASN	C-N-CD	-5.12	104.02	125.00
1	E	190	PRO	N-CA-C	-5.11	107.19	113.84
1	A	91	LYS	N-CA-CB	-5.10	102.93	111.20
1	E	379	TYR	O-C-N	-5.10	116.81	122.07
1	B	252	ASN	C-N-CD	-5.10	104.09	125.00
1	D	91	LYS	N-CA-CB	-5.09	102.95	111.20
1	D	190	PRO	N-CA-C	-5.09	107.22	113.84
1	C	194	SER	CA-C-O	-5.09	113.24	120.51
1	D	194	SER	CA-C-O	-5.08	113.24	120.51
1	E	91	LYS	N-CA-CB	-5.08	102.96	111.20
1	E	256	LEU	O-C-N	5.08	127.50	122.12
1	A	252	ASN	C-N-CD	-5.08	104.19	125.00
1	A	194	SER	CA-C-O	-5.07	113.25	120.51
1	C	347	HIS	CB-CG-CD2	-5.07	124.61	131.20
1	B	194	SER	CA-C-O	-5.07	113.26	120.51
1	C	256	LEU	O-C-N	5.07	127.49	122.12
1	E	194	SER	CA-C-O	-5.06	113.28	120.51
1	B	295	ASP	CA-C-O	5.05	126.35	120.49
1	B	404	LEU	CD1-CG-CD2	-5.05	99.68	110.80
1	C	91	LYS	N-CA-CB	-5.05	103.01	111.20
1	A	404	LEU	CD1-CG-CD2	-5.05	99.69	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	182	GLN	OE1-CD-NE2	-5.05	117.55	122.60
1	D	404	LEU	CD1-CG-CD2	-5.05	99.70	110.80
1	B	91	LYS	N-CA-CB	-5.04	103.04	111.20
1	B	117	ARG	C-N-CD	-5.04	104.35	125.00
1	B	109	PRO	CA-N-CD	-5.03	104.95	112.00
1	E	404	LEU	CD1-CG-CD2	-5.03	99.73	110.80
1	E	182	GLN	OE1-CD-NE2	-5.03	117.57	122.60
1	A	256	LEU	O-C-N	5.03	127.45	122.12
1	C	295	ASP	CA-C-O	5.03	126.32	120.49
1	A	378	LEU	CD1-CG-CD2	-5.02	99.75	110.80
1	E	155	ASP	CA-C-O	-5.02	113.66	119.64
1	C	404	LEU	CD1-CG-CD2	-5.02	99.76	110.80
1	E	57	GLN	CG-CD-OE1	-5.02	110.76	120.80
1	E	116	PRO	N-CD-CG	-5.02	95.67	103.20
1	D	295	ASP	CA-C-O	5.01	126.31	120.49
1	A	295	ASP	CA-C-O	5.01	126.30	120.49
1	E	454	GLU	CG-CD-OE1	-5.01	106.89	118.40
1	B	439	HIS	N-CA-CB	-5.00	102.72	110.98
1	E	439	HIS	N-CA-CB	-5.00	102.72	110.98

There are no chirality outliers.

All (68) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	144	GLY	Peptide
1	A	194	SER	Mainchain
1	A	21	ALA	Mainchain
1	A	225	ALA	Mainchain
1	A	295	ASP	Mainchain
1	A	319	HIS	Sidechain
1	A	347	HIS	Peptide
1	A	379	TYR	Sidechain
1	A	406	ALA	Peptide,Mainchain
1	A	474	ASP	Peptide
1	A	82	LEU	Peptide
1	A	91	LYS	Peptide
1	B	144	GLY	Peptide
1	B	194	SER	Mainchain
1	B	21	ALA	Mainchain
1	B	225	ALA	Mainchain
1	B	295	ASP	Mainchain
1	B	319	HIS	Sidechain

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Mol	Chain	Res	Type	Group
1	B	347	HIS	Peptide
1	B	379	TYR	Sidechain
1	B	406	ALA	Peptide,Mainchain
1	B	474	ASP	Peptide,Mainchain
1	B	82	LEU	Peptide
1	B	91	LYS	Peptide
1	C	144	GLY	Peptide
1	C	194	SER	Mainchain
1	C	21	ALA	Mainchain
1	C	225	ALA	Mainchain
1	C	295	ASP	Mainchain
1	C	319	HIS	Sidechain
1	C	347	HIS	Peptide
1	C	379	TYR	Sidechain
1	C	406	ALA	Peptide,Mainchain
1	C	474	ASP	Peptide,Mainchain
1	C	82	LEU	Peptide
1	C	91	LYS	Peptide
1	D	144	GLY	Peptide
1	D	194	SER	Mainchain
1	D	21	ALA	Mainchain
1	D	225	ALA	Mainchain
1	D	295	ASP	Mainchain
1	D	319	HIS	Sidechain
1	D	347	HIS	Peptide
1	D	379	TYR	Sidechain
1	D	406	ALA	Peptide,Mainchain
1	D	474	ASP	Peptide,Mainchain
1	D	82	LEU	Peptide
1	D	91	LYS	Peptide
1	E	144	GLY	Peptide
1	E	194	SER	Mainchain
1	E	21	ALA	Mainchain
1	E	225	ALA	Mainchain
1	E	295	ASP	Mainchain
1	E	347	HIS	Peptide
1	E	379	TYR	Sidechain
1	E	406	ALA	Peptide,Mainchain
1	E	474	ASP	Peptide,Mainchain
1	E	82	LEU	Peptide
1	E	91	LYS	Peptide

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	3771	0	3778	677	0
1	B	3771	0	3776	671	0
1	C	3771	0	3778	697	0
1	D	3771	0	3778	706	0
1	E	3771	0	3778	692	0
All	All	18855	0	18888	3028	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 80.

All (3028) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:TYR:N	1:E:173:ALA:CB	1.69	1.56
1:D:173:ALA:CB	1:E:346:TYR:N	1.69	1.54
1:D:346:TYR:CE1	1:D:349:CYS:HB3	1.41	1.52
1:B:173:ALA:CB	1:C:346:TYR:N	1.69	1.52
1:C:173:ALA:CB	1:D:346:TYR:N	1.69	1.51
1:A:177:LEU:HA	1:B:347:HIS:CD2	1.46	1.51
1:A:173:ALA:CB	1:B:346:TYR:N	1.69	1.50
1:C:177:LEU:HB3	1:D:347:HIS:CD2	1.46	1.48
1:C:346:TYR:CE2	1:C:349:CYS:HB3	1.47	1.48
1:C:173:ALA:HB1	1:D:345:THR:C	1.41	1.44
1:A:401:THR:CG2	1:A:402:LEU:H	1.18	1.44
1:B:173:ALA:HB1	1:C:345:THR:C	1.41	1.44
1:D:173:ALA:HB1	1:E:345:THR:C	1.41	1.42
1:A:173:ALA:HB1	1:B:345:THR:C	1.41	1.42
1:D:173:ALA:HA	1:E:346:TYR:CB	1.50	1.42
1:A:345:THR:C	1:E:173:ALA:HB1	1.41	1.41
1:A:347:HIS:ND1	1:E:177:LEU:CB	1.82	1.41
1:B:173:ALA:HA	1:C:346:TYR:CB	1.50	1.39
1:C:173:ALA:CA	1:D:346:TYR:HA	1.51	1.39
1:A:346:TYR:CB	1:E:173:ALA:HA	1.50	1.39
1:E:116:PRO:CD	1:E:116:PRO:N	1.67	1.39
1:D:173:ALA:CA	1:E:346:TYR:HA	1.51	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:ALA:HA	1:B:346:TYR:CB	1.50	1.38
1:B:173:ALA:CA	1:C:346:TYR:HA	1.51	1.38
1:E:300:PRO:CD	1:E:300:PRO:N	1.75	1.38
1:A:173:ALA:CA	1:B:346:TYR:HA	1.51	1.38
1:B:173:ALA:CA	1:C:346:TYR:CA	2.02	1.38
1:C:173:ALA:CA	1:D:346:TYR:CA	2.02	1.38
1:C:173:ALA:HA	1:D:346:TYR:CB	1.50	1.38
1:A:346:TYR:HA	1:E:173:ALA:CA	1.50	1.37
1:A:173:ALA:CA	1:B:346:TYR:CA	2.02	1.37
1:B:134:PRO:CD	1:B:134:PRO:N	1.76	1.36
1:D:173:ALA:CA	1:E:346:TYR:CA	2.02	1.35
1:A:134:PRO:N	1:A:134:PRO:CD	1.71	1.35
1:A:346:TYR:CA	1:E:173:ALA:CA	2.02	1.35
1:E:134:PRO:CD	1:E:134:PRO:N	1.74	1.35
1:B:434:PRO:CD	1:B:434:PRO:N	1.69	1.35
1:C:434:PRO:N	1:C:434:PRO:CD	1.69	1.34
1:D:434:PRO:CD	1:D:434:PRO:N	1.68	1.33
1:D:300:PRO:CD	1:D:300:PRO:N	1.69	1.32
1:A:434:PRO:CD	1:A:434:PRO:N	1.68	1.32
1:A:346:TYR:CA	1:E:173:ALA:HA	1.60	1.32
1:D:176:LYS:HB3	1:E:347:HIS:CB	1.60	1.31
1:B:436:LEU:HA	1:B:439:HIS:CE1	1.65	1.30
1:A:401:THR:CG2	1:A:402:LEU:N	1.77	1.30
1:C:177:LEU:CB	1:D:347:HIS:CD2	2.13	1.30
1:E:182:GLN:NE2	1:E:185:ALA:HB2	1.44	1.29
1:A:173:ALA:HA	1:B:346:TYR:CA	1.61	1.29
1:A:235:LEU:CD2	1:A:245:LEU:HB3	1.61	1.29
1:C:378:LEU:HD22	1:C:400:LYS:O	1.28	1.29
1:D:173:ALA:C	1:E:346:TYR:HA	1.57	1.29
1:E:378:LEU:HD22	1:E:400:LYS:O	1.29	1.29
1:A:173:ALA:C	1:B:346:TYR:HA	1.57	1.28
1:C:134:PRO:CD	1:C:134:PRO:N	1.70	1.28
1:B:173:ALA:C	1:C:346:TYR:HA	1.57	1.28
1:C:173:ALA:HA	1:D:346:TYR:CA	1.61	1.28
1:B:235:LEU:CD2	1:B:245:LEU:HB3	1.64	1.27
1:D:401:THR:CG2	1:D:402:LEU:H	1.10	1.27
1:D:378:LEU:HD22	1:D:400:LYS:O	1.25	1.27
1:C:346:TYR:CE2	1:C:349:CYS:CB	2.18	1.26
1:E:163:GLU:OE1	1:E:208:LEU:HB3	1.34	1.26
1:E:235:LEU:CD2	1:E:245:LEU:HB3	1.64	1.26
1:A:235:LEU:CD1	1:A:241:LEU:HD22	1.66	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:TYR:HA	1:E:173:ALA:C	1.57	1.26
1:C:173:ALA:C	1:D:346:TYR:HA	1.57	1.26
1:D:173:ALA:HA	1:E:346:TYR:CA	1.60	1.25
1:D:98:SER:HB3	1:D:136:HIS:CE1	1.71	1.25
1:D:177:LEU:HA	1:E:347:HIS:ND1	1.50	1.25
1:B:378:LEU:HD22	1:B:400:LYS:O	1.37	1.25
1:B:173:ALA:HA	1:C:346:TYR:CA	1.60	1.25
1:C:235:LEU:CD2	1:C:245:LEU:HB3	1.69	1.23
1:D:182:GLN:NE2	1:D:185:ALA:HB2	1.51	1.22
1:D:346:TYR:CE1	1:D:349:CYS:CB	2.20	1.22
1:A:274:ARG:HD3	1:A:414:VAL:CG1	1.68	1.21
1:A:182:GLN:NE2	1:A:185:ALA:HB2	1.55	1.21
1:B:182:GLN:NE2	1:B:185:ALA:HB2	1.51	1.21
1:A:437:LEU:HD23	1:A:458:CYS:SG	1.80	1.21
1:B:173:ALA:HA	1:C:346:TYR:HB3	1.22	1.21
1:C:182:GLN:NE2	1:C:185:ALA:HB2	1.55	1.20
1:A:376:ALA:HB2	1:E:181:VAL:O	1.40	1.20
1:A:347:HIS:ND1	1:E:177:LEU:CA	2.04	1.20
1:D:256:LEU:O	1:D:260:PRO:HD2	1.42	1.20
1:A:220:THR:HG22	1:A:445:GLU:O	1.41	1.19
1:A:417:VAL:HB	1:A:465:MET:HG3	1.24	1.19
1:B:163:GLU:OE1	1:B:208:LEU:HB2	1.42	1.19
1:A:181:VAL:O	1:B:376:ALA:HB2	1.40	1.19
1:B:256:LEU:O	1:B:260:PRO:HD2	1.42	1.19
1:C:235:LEU:HD21	1:C:245:LEU:HB3	1.24	1.19
1:D:181:VAL:O	1:E:376:ALA:HB2	1.40	1.19
1:D:346:TYR:CZ	1:D:349:CYS:HB3	1.76	1.19
1:D:401:THR:CG2	1:D:402:LEU:N	1.75	1.19
1:B:181:VAL:O	1:C:376:ALA:HB2	1.40	1.18
1:D:173:ALA:CB	1:E:346:TYR:CA	2.21	1.18
1:D:235:LEU:HD11	1:D:241:LEU:CD2	1.73	1.18
1:A:430:LYS:O	1:A:434:PRO:HD3	1.43	1.18
1:C:181:VAL:O	1:D:376:ALA:HB2	1.40	1.18
1:A:346:TYR:CA	1:E:173:ALA:CB	2.21	1.17
1:C:430:LYS:O	1:C:434:PRO:HD3	1.44	1.17
1:A:220:THR:HG21	1:A:446:GLU:CG	1.74	1.17
1:C:176:LYS:HE3	1:D:348:ASP:CG	1.67	1.17
1:B:430:LYS:O	1:B:434:PRO:HD3	1.43	1.17
1:D:417:VAL:HB	1:D:465:MET:HG3	1.20	1.17
1:A:345:THR:OG1	1:E:173:ALA:HB3	1.42	1.17
1:C:117:ARG:HB3	1:C:118:PRO:HD3	1.26	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:417:VAL:HB	1:C:465:MET:HG3	1.26	1.17
1:A:52:LYS:HB2	1:A:184:PHE:HZ	1.00	1.17
1:A:56:LEU:HG	1:A:222:ILE:CG2	1.74	1.16
1:A:256:LEU:O	1:A:260:PRO:HD2	1.44	1.16
1:B:272:ARG:HB2	1:B:441:ASN:HB2	1.27	1.16
1:D:52:LYS:HB2	1:D:184:PHE:CZ	1.80	1.16
1:D:437:LEU:HD23	1:D:458:CYS:SG	1.85	1.16
1:A:235:LEU:HD21	1:A:245:LEU:HB3	1.17	1.16
1:C:176:LYS:CE	1:D:348:ASP:OD2	1.93	1.16
1:B:52:LYS:HB2	1:B:184:PHE:CZ	1.80	1.16
1:C:173:ALA:CB	1:D:346:TYR:CA	2.21	1.16
1:E:52:LYS:HB2	1:E:184:PHE:CZ	1.80	1.16
1:E:52:LYS:HB2	1:E:184:PHE:HZ	1.02	1.16
1:C:52:LYS:HB2	1:C:184:PHE:CZ	1.80	1.16
1:A:274:ARG:CD	1:A:414:VAL:HG13	1.75	1.15
1:D:313:LEU:HD12	1:D:374:GLY:HA2	1.28	1.15
1:C:174:ARG:NH1	1:D:345:THR:OG1	1.78	1.15
1:D:430:LYS:O	1:D:434:PRO:HD3	1.45	1.15
1:A:52:LYS:HB2	1:A:184:PHE:CZ	1.80	1.15
1:C:159:ALA:HB3	1:C:198:TYR:CD1	1.82	1.15
1:D:370:LYS:HE2	1:D:399:ASP:HB3	1.27	1.15
1:E:313:LEU:HD12	1:E:374:GLY:HA2	1.29	1.14
1:A:124:VAL:HB	1:A:125:ILE:HB	1.23	1.14
1:A:173:ALA:CB	1:B:346:TYR:CA	2.21	1.14
1:B:417:VAL:HB	1:B:465:MET:HG3	1.15	1.14
1:E:417:VAL:HB	1:E:465:MET:HG3	1.18	1.14
1:A:313:LEU:HD12	1:A:374:GLY:HA2	1.29	1.14
1:E:430:LYS:O	1:E:434:PRO:HD3	1.44	1.14
1:B:173:ALA:CB	1:C:346:TYR:CA	2.21	1.13
1:B:176:LYS:HB3	1:C:347:HIS:CB	1.78	1.13
1:A:83:LYS:HG3	1:A:155:ASP:CB	1.77	1.13
1:E:256:LEU:O	1:E:260:PRO:HD2	1.47	1.13
1:C:176:LYS:HB2	1:D:347:HIS:H	1.14	1.13
1:A:173:ALA:HB1	1:B:346:TYR:CA	1.78	1.13
1:A:347:HIS:N	1:E:176:LYS:HB2	1.64	1.13
1:D:56:LEU:HG	1:D:222:ILE:HG23	1.22	1.13
1:A:322:TRP:HD1	1:A:456:ARG:HB3	0.98	1.12
1:A:176:LYS:HB2	1:B:347:HIS:N	1.64	1.12
1:A:346:TYR:CA	1:E:173:ALA:HB1	1.78	1.12
1:D:56:LEU:HG	1:D:222:ILE:CG2	1.79	1.12
1:E:124:VAL:HB	1:E:125:ILE:HB	1.22	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ALA:HB1	1:C:346:TYR:CA	1.78	1.12
1:C:77:TRP:HE1	1:C:105:ILE:HG12	0.98	1.12
1:C:173:ALA:HB3	1:D:345:THR:HG23	1.26	1.12
1:A:235:LEU:HD11	1:A:241:LEU:CD2	1.79	1.12
1:C:173:ALA:CB	1:D:345:THR:C	2.13	1.12
1:A:177:LEU:CA	1:B:347:HIS:CD2	2.32	1.11
1:B:173:ALA:CB	1:C:345:THR:C	2.14	1.11
1:C:52:LYS:HB2	1:C:184:PHE:HZ	1.03	1.11
1:C:124:VAL:HB	1:C:125:ILE:HB	1.21	1.11
1:C:83:LYS:HE2	1:C:192:PRO:HA	1.17	1.11
1:C:173:ALA:CB	1:D:345:THR:HG23	1.80	1.11
1:C:173:ALA:HB1	1:D:346:TYR:CA	1.78	1.11
1:A:117:ARG:HB3	1:A:118:PRO:HD3	1.27	1.11
1:B:176:LYS:HB3	1:C:347:HIS:HB3	1.16	1.11
1:C:181:VAL:HA	1:C:182:GLN:HG2	1.32	1.11
1:D:173:ALA:HB1	1:E:346:TYR:CA	1.78	1.11
1:D:173:ALA:O	1:E:346:TYR:HA	1.50	1.11
1:A:83:LYS:HG3	1:A:155:ASP:HB2	1.23	1.10
1:A:163:GLU:OE1	1:A:208:LEU:HB2	1.49	1.10
1:A:235:LEU:HD11	1:A:241:LEU:HD22	1.22	1.10
1:B:77:TRP:HE1	1:B:105:ILE:HG12	0.97	1.10
1:B:235:LEU:HD21	1:B:245:LEU:HB3	1.18	1.10
1:E:322:TRP:HD1	1:E:456:ARG:HB3	1.03	1.10
1:B:313:LEU:HD12	1:B:374:GLY:HA2	1.29	1.10
1:C:173:ALA:HA	1:D:346:TYR:HB3	1.21	1.10
1:C:176:LYS:HB3	1:D:347:HIS:HB3	1.24	1.10
1:A:173:ALA:CA	1:B:346:TYR:HB3	1.81	1.10
1:A:401:THR:HG22	1:A:402:LEU:N	1.63	1.10
1:B:173:ALA:O	1:C:346:TYR:HA	1.50	1.10
1:E:117:ARG:HB3	1:E:118:PRO:HD3	1.13	1.10
1:B:18:ASP:OD1	1:B:35:PRO:HG3	1.47	1.09
1:B:173:ALA:CA	1:C:346:TYR:HB3	1.82	1.09
1:D:201:THR:CG2	1:D:202:PRO:HD2	1.83	1.09
1:A:173:ALA:HA	1:B:346:TYR:HB3	1.17	1.09
1:B:322:TRP:HD1	1:B:456:ARG:HB3	0.99	1.09
1:D:124:VAL:HB	1:D:125:ILE:HB	1.23	1.09
1:A:173:ALA:O	1:B:346:TYR:HA	1.50	1.09
1:A:285:LEU:HD11	1:A:434:PRO:HG2	1.23	1.09
1:A:347:HIS:H	1:E:176:LYS:HB2	1.13	1.09
1:B:52:LYS:HB2	1:B:184:PHE:HZ	1.01	1.09
1:B:181:VAL:HA	1:B:182:GLN:HG2	1.34	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:181:VAL:HA	1:D:182:GLN:HG2	1.34	1.09
1:D:322:TRP:HD1	1:D:456:ARG:HB3	1.04	1.09
1:C:173:ALA:CA	1:D:346:TYR:HB3	1.82	1.09
1:C:173:ALA:CA	1:D:346:TYR:CB	2.29	1.09
1:C:322:TRP:HD1	1:C:456:ARG:HB3	0.94	1.09
1:B:124:VAL:HB	1:B:125:ILE:HB	1.23	1.08
1:B:173:ALA:HB1	1:C:346:TYR:N	0.76	1.08
1:E:235:LEU:HD21	1:E:245:LEU:HB3	1.18	1.08
1:A:173:ALA:HB1	1:B:346:TYR:N	0.76	1.08
1:A:181:VAL:HA	1:A:182:GLN:HG2	1.32	1.08
1:A:401:THR:HG23	1:A:402:LEU:N	1.31	1.08
1:C:173:ALA:O	1:D:346:TYR:HA	1.50	1.08
1:C:322:TRP:CD1	1:C:456:ARG:HB3	1.86	1.08
1:D:52:LYS:HB2	1:D:184:PHE:HZ	1.03	1.08
1:D:273:GLU:HG2	1:D:280:LYS:HZ1	1.16	1.08
1:C:173:ALA:HB1	1:D:346:TYR:N	0.75	1.08
1:C:176:LYS:HB2	1:D:347:HIS:N	1.69	1.08
1:C:256:LEU:O	1:C:260:PRO:HD2	1.51	1.08
1:E:262:ASP:CB	1:E:263:PRO:HD3	1.82	1.08
1:A:346:TYR:N	1:E:173:ALA:HB1	0.76	1.07
1:C:368:ARG:O	1:C:401:THR:HB	1.54	1.07
1:E:273:GLU:HG2	1:E:280:LYS:HZ1	1.13	1.07
1:E:368:ARG:O	1:E:401:THR:HB	1.54	1.07
1:A:89:ALA:O	1:A:140:VAL:HA	1.55	1.07
1:A:176:LYS:HB2	1:B:347:HIS:H	1.13	1.07
1:A:347:HIS:HB3	1:E:176:LYS:CB	1.84	1.07
1:A:220:THR:CG2	1:A:446:GLU:HG2	1.85	1.07
1:A:376:ALA:HA	1:E:181:VAL:HB	1.35	1.07
1:D:173:ALA:CA	1:E:346:TYR:HB3	1.85	1.07
1:D:272:ARG:HB2	1:D:441:ASN:HB2	1.36	1.07
1:E:148:GLN:HE21	1:E:175:GLU:HG3	1.19	1.07
1:A:346:TYR:HA	1:E:173:ALA:O	1.50	1.07
1:D:235:LEU:CD1	1:D:241:LEU:HD22	1.83	1.07
1:D:291:PRO:HG2	1:D:295:ASP:HB3	1.33	1.07
1:A:345:THR:C	1:E:173:ALA:CB	2.14	1.06
1:A:347:HIS:ND1	1:E:177:LEU:HA	1.67	1.06
1:A:347:HIS:ND1	1:E:177:LEU:HB2	1.64	1.06
1:B:176:LYS:HE2	1:C:348:ASP:CG	1.80	1.06
1:D:173:ALA:HB1	1:E:346:TYR:N	0.75	1.06
1:E:77:TRP:HE1	1:E:105:ILE:HG12	0.96	1.06
1:A:182:GLN:HE21	1:A:185:ALA:CB	1.68	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:TRP:CD1	1:A:456:ARG:HB3	1.90	1.06
1:C:202:PRO:HD3	1:C:265:ARG:HD2	1.09	1.06
1:D:89:ALA:O	1:D:140:VAL:HA	1.55	1.06
1:E:181:VAL:HA	1:E:182:GLN:HG2	1.36	1.06
1:E:182:GLN:HE21	1:E:185:ALA:CB	1.69	1.06
1:A:346:TYR:HB3	1:E:173:ALA:HA	1.07	1.06
1:B:59:PHE:CE2	1:B:60:ARG:O	2.09	1.06
1:D:182:GLN:HE21	1:D:185:ALA:CB	1.68	1.06
1:C:176:LYS:HE3	1:D:348:ASP:OD2	1.53	1.06
1:D:173:ALA:HB3	1:E:345:THR:HG23	1.39	1.05
1:A:346:TYR:HB3	1:E:173:ALA:CA	1.86	1.05
1:C:182:GLN:HE21	1:C:185:ALA:CB	1.68	1.05
1:C:262:ASP:CB	1:C:263:PRO:HD3	1.84	1.05
1:B:368:ARG:HH21	1:B:381:LEU:HD12	1.16	1.05
1:D:173:ALA:HB2	1:E:346:TYR:CD2	1.91	1.05
1:D:176:LYS:HB3	1:E:347:HIS:HB3	1.32	1.05
1:B:89:ALA:O	1:B:140:VAL:HA	1.55	1.05
1:B:368:ARG:O	1:B:401:THR:HB	1.54	1.05
1:C:272:ARG:HB2	1:C:441:ASN:HB2	1.36	1.05
1:D:18:ASP:OD1	1:D:35:PRO:HG3	1.57	1.05
1:D:401:THR:HG22	1:D:402:LEU:N	1.39	1.05
1:C:89:ALA:O	1:C:140:VAL:HA	1.55	1.04
1:B:182:GLN:HE21	1:B:185:ALA:CB	1.68	1.04
1:D:173:ALA:CA	1:E:346:TYR:CB	2.29	1.04
1:D:262:ASP:HB3	1:D:263:PRO:HD3	1.39	1.04
1:E:89:ALA:O	1:E:140:VAL:HA	1.55	1.04
1:A:58:ALA:O	1:A:265:ARG:HD3	1.57	1.04
1:B:202:PRO:CD	1:B:265:ARG:HD2	1.87	1.04
1:C:73:VAL:CG2	1:C:105:ILE:HG13	1.86	1.04
1:E:220:THR:HG21	1:E:446:GLU:HG3	1.09	1.04
1:B:176:LYS:HB2	1:C:347:HIS:H	1.20	1.04
1:B:322:TRP:CD1	1:B:456:ARG:HB3	1.92	1.04
1:D:56:LEU:CG	1:D:222:ILE:HG23	1.87	1.04
1:D:176:LYS:HB3	1:E:347:HIS:CA	1.87	1.04
1:B:77:TRP:NE1	1:B:105:ILE:HG12	1.72	1.03
1:B:220:THR:CG2	1:B:446:GLU:HG3	1.88	1.03
1:B:280:LYS:HE2	1:B:438:LYS:HA	1.36	1.03
1:C:51:ASN:HB2	1:C:54:PHE:CZ	1.94	1.03
1:C:346:TYR:CD2	1:C:349:CYS:N	2.26	1.03
1:E:73:VAL:CG2	1:E:105:ILE:HG13	1.87	1.03
1:E:83:LYS:HG2	1:E:155:ASP:HB2	1.33	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:ALA:CA	1:B:346:TYR:CB	2.29	1.03
1:B:262:ASP:CB	1:B:263:PRO:HD3	1.84	1.03
1:D:235:LEU:HD11	1:D:241:LEU:HD22	1.09	1.03
1:E:77:TRP:NE1	1:E:105:ILE:HG12	1.71	1.03
1:B:73:VAL:CG2	1:B:105:ILE:HG13	1.87	1.03
1:B:173:ALA:CB	1:C:345:THR:HG23	1.89	1.03
1:B:202:PRO:HD3	1:B:265:ARG:CD	1.88	1.03
1:E:18:ASP:OD1	1:E:35:PRO:HG3	1.57	1.03
1:C:346:TYR:HD2	1:C:349:CYS:N	1.57	1.03
1:A:346:TYR:N	1:A:346:TYR:HD1	1.54	1.03
1:C:176:LYS:CB	1:D:347:HIS:HB3	1.88	1.03
1:E:51:ASN:HB2	1:E:54:PHE:CZ	1.93	1.03
1:E:235:LEU:HD11	1:E:241:LEU:CD2	1.89	1.03
1:A:173:ALA:HB3	1:B:345:THR:HG23	1.39	1.02
1:B:220:THR:HG21	1:B:446:GLU:HG3	1.07	1.02
1:B:378:LEU:HD11	1:B:401:THR:OG1	1.58	1.02
1:C:77:TRP:NE1	1:C:105:ILE:HG12	1.72	1.02
1:A:56:LEU:HG	1:A:222:ILE:HG23	1.40	1.02
1:C:170:THR:HA	1:D:345:THR:HG21	1.37	1.02
1:D:202:PRO:HD3	1:D:265:ARG:HD2	1.03	1.02
1:A:202:PRO:HD3	1:A:265:ARG:CD	1.88	1.02
1:A:280:LYS:HE2	1:A:438:LYS:HA	1.37	1.02
1:A:345:THR:HB	1:E:174:ARG:NH1	1.73	1.02
1:B:177:LEU:HA	1:C:347:HIS:CD2	1.95	1.02
1:D:173:ALA:CB	1:E:345:THR:HG23	1.89	1.02
1:D:262:ASP:CB	1:D:263:PRO:HD3	1.87	1.02
1:A:256:LEU:O	1:A:260:PRO:CD	2.08	1.02
1:A:370:LYS:HE2	1:A:399:ASP:HB3	1.42	1.02
1:C:18:ASP:OD1	1:C:35:PRO:HG3	1.58	1.02
1:A:173:ALA:CB	1:B:345:THR:HG23	1.89	1.02
1:A:322:TRP:HD1	1:A:456:ARG:CB	1.72	1.02
1:B:55:ILE:HG22	1:B:57:GLN:OE1	1.58	1.02
1:B:173:ALA:HB3	1:C:345:THR:HG23	1.39	1.02
1:C:83:LYS:NZ	1:C:193:SER:H	1.54	1.01
1:E:194:SER:HA	1:E:195:ARG:HB2	1.41	1.01
1:A:347:HIS:ND1	1:E:177:LEU:HB3	1.76	1.01
1:C:60:ARG:CG	1:C:201:THR:HG21	1.88	1.01
1:D:133:ASN:H	1:D:134:PRO:HD2	1.25	1.01
1:D:173:ALA:HA	1:E:346:TYR:HB3	1.07	1.01
1:A:173:ALA:CB	1:B:345:THR:C	2.13	1.01
1:A:194:SER:HA	1:A:195:ARG:HB2	1.41	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:LEU:N	1:C:347:HIS:CB	2.24	1.01
1:D:322:TRP:HD1	1:D:456:ARG:CB	1.72	1.01
1:B:67:ILE:N	1:B:67:ILE:HD12	1.75	1.01
1:B:254:GLU:HG3	1:B:255:ALA:H	0.89	1.01
1:C:176:LYS:CE	1:D:348:ASP:CG	2.28	1.01
1:C:177:LEU:N	1:D:347:HIS:CB	2.24	1.01
1:E:220:THR:CG2	1:E:446:GLU:HG3	1.90	1.01
1:E:322:TRP:HD1	1:E:456:ARG:CB	1.73	1.01
1:C:262:ASP:HB3	1:C:263:PRO:HD3	1.40	1.01
1:D:173:ALA:CB	1:E:345:THR:C	2.13	1.01
1:A:75:SER:HB3	1:A:83:LYS:HZ3	1.26	1.00
1:A:262:ASP:CB	1:A:263:PRO:HD3	1.84	1.00
1:B:173:ALA:CA	1:C:346:TYR:CB	2.29	1.00
1:C:322:TRP:HD1	1:C:456:ARG:CB	1.72	1.00
1:D:58:ALA:O	1:D:265:ARG:HD3	1.60	1.00
1:D:177:LEU:N	1:E:347:HIS:CB	2.24	1.00
1:A:202:PRO:CD	1:A:265:ARG:HD2	1.90	1.00
1:D:73:VAL:HG22	1:D:105:ILE:HG12	1.43	1.00
1:E:265:ARG:O	1:E:265:ARG:HD3	1.61	1.00
1:A:347:HIS:CB	1:E:177:LEU:N	2.24	1.00
1:B:58:ALA:O	1:B:265:ARG:HD3	1.61	1.00
1:B:176:LYS:HB2	1:C:347:HIS:N	1.75	1.00
1:C:163:GLU:OE1	1:C:208:LEU:HB2	1.61	1.00
1:D:176:LYS:CB	1:E:347:HIS:HB3	1.91	1.00
1:D:201:THR:HG22	1:D:202:PRO:HD2	1.44	1.00
1:D:83:LYS:HE3	1:D:156:ILE:HG22	1.42	1.00
1:D:204:THR:HG22	1:D:205:GLU:H	1.24	1.00
1:E:322:TRP:CD1	1:E:456:ARG:HB3	1.96	1.00
1:E:223:TRP:HE1	1:E:265:ARG:HB3	1.23	1.00
1:A:73:VAL:HG22	1:A:105:ILE:HG12	1.42	1.00
1:B:21:ALA:O	1:B:33:PRO:HD3	1.60	1.00
1:B:170:THR:HA	1:C:345:THR:HG21	1.44	1.00
1:B:322:TRP:HD1	1:B:456:ARG:CB	1.74	1.00
1:C:370:LYS:HE2	1:C:399:ASP:CB	1.91	1.00
1:A:177:LEU:N	1:B:347:HIS:CB	2.24	0.99
1:C:346:TYR:CZ	1:C:349:CYS:HB3	1.96	0.99
1:E:64:LYS:O	1:E:67:ILE:HG13	1.61	0.99
1:D:194:SER:HA	1:D:195:ARG:HB2	1.41	0.99
1:B:254:GLU:CG	1:B:255:ALA:H	1.75	0.99
1:B:256:LEU:O	1:B:260:PRO:CD	2.08	0.99
1:D:313:LEU:CD1	1:D:374:GLY:HA2	1.92	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:PHE:CD2	1:B:60:ARG:O	2.15	0.99
1:C:256:LEU:O	1:C:260:PRO:CD	2.10	0.99
1:D:322:TRP:CD1	1:D:456:ARG:HB3	1.97	0.99
1:E:291:PRO:HG2	1:E:295:ASP:HB3	1.45	0.99
1:B:176:LYS:CB	1:C:347:HIS:HB3	1.92	0.99
1:C:194:SER:HA	1:C:195:ARG:HB2	1.41	0.99
1:D:85:LEU:HD22	1:D:136:HIS:CD2	1.98	0.99
1:E:313:LEU:CD1	1:E:374:GLY:HA2	1.92	0.99
1:C:176:LYS:HB3	1:D:347:HIS:CB	1.92	0.99
1:B:194:SER:HA	1:B:195:ARG:HB2	1.41	0.99
1:C:176:LYS:HE2	1:D:348:ASP:OD2	1.59	0.99
1:D:170:THR:HA	1:E:345:THR:HG21	1.44	0.99
1:A:291:PRO:HG2	1:A:295:ASP:HB3	1.44	0.99
1:B:291:PRO:HG2	1:B:295:ASP:HB3	1.44	0.99
1:D:256:LEU:O	1:D:260:PRO:CD	2.10	0.99
1:B:85:LEU:HB3	1:B:136:HIS:HD2	1.27	0.98
1:C:370:LYS:HE2	1:C:399:ASP:HB3	1.00	0.98
1:D:378:LEU:CD2	1:D:400:LYS:O	2.11	0.98
1:A:176:LYS:CB	1:B:347:HIS:HB3	1.93	0.98
1:C:235:LEU:HD11	1:C:241:LEU:CD2	1.94	0.98
1:A:18:ASP:OD1	1:A:35:PRO:HG3	1.61	0.98
1:B:159:ALA:HB3	1:B:198:TYR:CD1	1.99	0.98
1:B:194:SER:HA	1:B:195:ARG:CB	1.93	0.98
1:D:194:SER:HA	1:D:195:ARG:CB	1.93	0.98
1:A:313:LEU:CD1	1:A:374:GLY:HA2	1.93	0.98
1:A:170:THR:HA	1:B:345:THR:HG21	1.44	0.97
1:D:401:THR:HG23	1:D:402:LEU:N	1.52	0.97
1:E:370:LYS:HE2	1:E:375:TYR:CE1	1.99	0.97
1:C:83:LYS:HZ3	1:C:193:SER:N	1.60	0.97
1:E:417:VAL:CB	1:E:465:MET:HG3	1.93	0.97
1:B:205:GLU:HG2	1:B:209:TYR:CD2	1.99	0.97
1:D:436:LEU:HD22	1:D:457:ILE:HG22	1.46	0.97
1:B:59:PHE:CE1	1:B:62:ILE:HB	1.98	0.97
1:D:202:PRO:HD3	1:D:265:ARG:CD	1.94	0.97
1:C:156:ILE:HB	1:C:194:SER:OG	1.65	0.96
1:C:133:ASN:H	1:C:134:PRO:HD2	1.30	0.96
1:D:98:SER:HB3	1:D:136:HIS:HE1	1.18	0.96
1:A:436:LEU:HD22	1:A:457:ILE:HG22	1.47	0.96
1:D:83:LYS:HE3	1:D:156:ILE:CG2	1.94	0.96
1:A:235:LEU:HD22	1:A:245:LEU:HB3	1.48	0.96
1:D:98:SER:CB	1:D:136:HIS:CE1	2.47	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:GLY:O	1:A:378:LEU:HG	1.65	0.96
1:B:220:THR:HG21	1:B:446:GLU:CG	1.94	0.96
1:C:313:LEU:HD12	1:C:374:GLY:HA2	1.47	0.96
1:D:176:LYS:HB3	1:E:347:HIS:N	1.79	0.96
1:A:332:ASP:O	1:A:334:PRO:HD3	1.65	0.96
1:A:194:SER:HA	1:A:195:ARG:CB	1.93	0.96
1:B:254:GLU:HG3	1:B:255:ALA:N	1.71	0.96
1:D:57:GLN:OE1	1:D:265:ARG:NH2	1.98	0.95
1:E:256:LEU:O	1:E:260:PRO:CD	2.14	0.95
1:C:202:PRO:HB3	1:C:265:ARG:NH1	1.80	0.95
1:D:401:THR:HG23	1:D:402:LEU:H	0.83	0.95
1:C:291:PRO:HG2	1:C:295:ASP:HB3	1.46	0.95
1:B:177:LEU:HB3	1:C:347:HIS:ND1	1.81	0.95
1:C:163:GLU:HG3	1:C:203:GLN:HB2	1.47	0.95
1:E:329:ILE:HG23	1:E:330:ILE:H	1.31	0.95
1:A:346:TYR:CB	1:E:173:ALA:CA	2.29	0.95
1:B:436:LEU:HD22	1:B:457:ILE:HG22	1.45	0.95
1:D:156:ILE:HB	1:D:194:SER:OG	1.67	0.95
1:D:176:LYS:CG	1:E:347:HIS:C	2.39	0.95
1:E:220:THR:HG21	1:E:446:GLU:CG	1.96	0.95
1:A:156:ILE:HB	1:A:194:SER:OG	1.66	0.95
1:E:332:ASP:O	1:E:334:PRO:HD3	1.66	0.95
1:A:83:LYS:HD2	1:A:193:SER:O	1.66	0.95
1:A:329:ILE:HG23	1:A:330:ILE:H	1.31	0.95
1:D:124:VAL:CB	1:D:125:ILE:HB	1.97	0.95
1:B:163:GLU:HG3	1:B:203:GLN:HB2	1.48	0.95
1:E:194:SER:HA	1:E:195:ARG:CB	1.93	0.95
1:E:370:LYS:HE3	1:E:399:ASP:HB3	1.46	0.95
1:B:368:ARG:NH2	1:B:381:LEU:HD12	1.81	0.95
1:A:163:GLU:HG3	1:A:203:GLN:HB2	1.48	0.94
1:A:274:ARG:HD3	1:A:414:VAL:HG13	0.96	0.94
1:B:262:ASP:HB3	1:B:263:PRO:HD3	1.48	0.94
1:B:117:ARG:HB3	1:B:118:PRO:HD3	1.49	0.94
1:B:313:LEU:CD1	1:B:374:GLY:HA2	1.96	0.94
1:C:159:ALA:HB3	1:C:198:TYR:HD1	1.20	0.94
1:D:280:LYS:HZ2	1:D:438:LYS:HA	1.31	0.94
1:C:124:VAL:CB	1:C:125:ILE:HB	1.97	0.94
1:A:202:PRO:HD3	1:A:265:ARG:HD2	0.95	0.94
1:B:177:LEU:N	1:C:347:HIS:HB2	1.82	0.94
1:D:177:LEU:N	1:E:347:HIS:HB2	1.82	0.94
1:A:163:GLU:OE1	1:A:208:LEU:CB	2.14	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:TRP:HZ2	1:A:105:ILE:HG23	1.33	0.94
1:A:177:LEU:HA	1:B:347:HIS:HD2	1.28	0.94
1:C:220:THR:O	1:C:445:GLU:OE1	1.86	0.94
1:C:436:LEU:HD22	1:C:457:ILE:HG22	1.50	0.94
1:B:156:ILE:HB	1:B:194:SER:OG	1.67	0.94
1:B:332:ASP:O	1:B:334:PRO:HD3	1.66	0.94
1:C:378:LEU:CD2	1:C:400:LYS:O	2.14	0.94
1:D:273:GLU:HG2	1:D:280:LYS:NZ	1.81	0.94
1:E:55:ILE:HG22	1:E:57:GLN:HE21	1.30	0.94
1:E:163:GLU:OE1	1:E:208:LEU:CB	2.16	0.94
1:A:124:VAL:CB	1:A:125:ILE:HB	1.97	0.94
1:C:332:ASP:O	1:C:334:PRO:HD3	1.66	0.94
1:E:59:PHE:CE1	1:E:62:ILE:HB	2.03	0.94
1:E:124:VAL:CB	1:E:125:ILE:HB	1.97	0.94
1:E:156:ILE:HB	1:E:194:SER:OG	1.68	0.94
1:E:208:LEU:HD21	1:E:265:ARG:NH2	1.83	0.94
1:E:77:TRP:CZ3	1:E:114:LEU:N	2.36	0.94
1:E:235:LEU:HD11	1:E:241:LEU:HD22	1.49	0.94
1:A:91:LYS:HB2	1:A:93:ARG:HB2	1.47	0.93
1:A:101:ILE:O	1:A:105:ILE:HG13	1.66	0.93
1:A:417:VAL:CB	1:A:465:MET:HG3	1.97	0.93
1:B:124:VAL:CB	1:B:125:ILE:HB	1.97	0.93
1:C:59:PHE:CE1	1:C:62:ILE:HB	2.03	0.93
1:D:77:TRP:HZ2	1:D:105:ILE:HG23	1.33	0.93
1:A:177:LEU:N	1:B:347:HIS:HB2	1.82	0.93
1:A:347:HIS:HB3	1:E:176:LYS:HB3	1.47	0.93
1:B:173:ALA:HB1	1:C:346:TYR:H	1.14	0.93
1:C:173:ALA:HB1	1:D:346:TYR:H	1.14	0.93
1:D:163:GLU:OE1	1:D:208:LEU:HB2	1.67	0.93
1:B:77:TRP:CZ3	1:B:114:LEU:N	2.37	0.93
1:D:235:LEU:HD22	1:D:245:LEU:HB3	1.49	0.93
1:E:378:LEU:CD2	1:E:400:LYS:O	2.15	0.93
1:D:332:ASP:O	1:D:334:PRO:HD3	1.67	0.93
1:D:202:PRO:CD	1:D:265:ARG:HD2	1.97	0.93
1:B:329:ILE:HG23	1:B:330:ILE:H	1.31	0.93
1:D:101:ILE:O	1:D:105:ILE:HG13	1.69	0.93
1:E:83:LYS:CG	1:E:155:ASP:HB2	1.97	0.93
1:C:177:LEU:N	1:D:347:HIS:HB2	1.84	0.92
1:E:436:LEU:HD22	1:E:457:ILE:HG22	1.49	0.92
1:D:176:LYS:CB	1:E:347:HIS:CB	2.48	0.92
1:D:346:TYR:CD1	1:D:349:CYS:N	2.37	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:VAL:HB	1:B:376:ALA:HA	1.51	0.92
1:A:347:HIS:HB3	1:E:176:LYS:C	1.94	0.92
1:D:235:LEU:CD2	1:D:245:LEU:HB3	1.98	0.92
1:A:173:ALA:HA	1:B:346:TYR:HA	1.25	0.92
1:A:176:LYS:CB	1:B:347:HIS:CB	2.48	0.92
1:B:176:LYS:CB	1:C:347:HIS:CB	2.48	0.92
1:C:430:LYS:O	1:C:434:PRO:CD	2.17	0.92
1:D:329:ILE:HG23	1:D:330:ILE:H	1.32	0.92
1:E:273:GLU:HG2	1:E:280:LYS:NZ	1.83	0.92
1:A:59:PHE:CE1	1:A:62:ILE:HB	2.04	0.92
1:A:430:LYS:O	1:A:434:PRO:CD	2.18	0.92
1:C:417:VAL:CB	1:C:465:MET:HG3	1.98	0.92
1:B:67:ILE:HD12	1:B:67:ILE:H	1.32	0.92
1:C:117:ARG:CB	1:C:118:PRO:HD3	2.00	0.92
1:A:347:HIS:CB	1:E:176:LYS:CB	2.48	0.91
1:C:181:VAL:HB	1:D:376:ALA:HA	1.52	0.91
1:E:235:LEU:CD1	1:E:241:LEU:HD22	2.00	0.91
1:B:83:LYS:HZ3	1:B:193:SER:H	0.99	0.91
1:C:329:ILE:HG23	1:C:330:ILE:H	1.32	0.91
1:D:430:LYS:O	1:D:434:PRO:CD	2.18	0.91
1:B:132:ALA:N	1:B:133:ASN:HA	1.86	0.91
1:C:194:SER:HA	1:C:195:ARG:CB	1.94	0.91
1:C:370:LYS:CE	1:C:399:ASP:HB3	1.96	0.91
1:B:430:LYS:O	1:B:434:PRO:CD	2.17	0.91
1:D:173:ALA:HB1	1:E:346:TYR:H	1.14	0.91
1:E:133:ASN:H	1:E:134:PRO:HD2	1.34	0.91
1:A:39:GLN:HB3	1:A:67:ILE:HG12	1.53	0.91
1:B:181:VAL:HB	1:C:376:ALA:HA	1.53	0.91
1:E:117:ARG:CB	1:E:118:PRO:HD3	1.99	0.91
1:E:163:GLU:HG3	1:E:203:GLN:HB2	1.53	0.91
1:B:177:LEU:CA	1:C:347:HIS:CG	2.53	0.91
1:D:329:ILE:HG23	1:D:330:ILE:N	1.83	0.91
1:C:329:ILE:HG23	1:C:330:ILE:N	1.85	0.91
1:D:163:GLU:HG3	1:D:203:GLN:HB2	1.50	0.91
1:D:322:TRP:CD1	1:D:456:ARG:CB	2.53	0.91
1:D:379:TYR:O	1:D:385:ILE:HB	1.70	0.91
1:E:262:ASP:HB3	1:E:263:PRO:HD3	1.52	0.91
1:A:220:THR:HG21	1:A:446:GLU:HG2	0.94	0.91
1:A:468:HIS:HA	1:A:473:ARG:HD3	1.53	0.91
1:C:235:LEU:HD11	1:C:241:LEU:HD22	1.49	0.91
1:B:177:LEU:HA	1:C:347:HIS:CG	2.05	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:379:TYR:O	1:C:385:ILE:HB	1.70	0.91
1:D:461:LEU:O	1:D:465:MET:HG2	1.71	0.91
1:C:22:PHE:HA	1:C:33:PRO:HD3	1.53	0.91
1:C:132:ALA:N	1:C:133:ASN:HA	1.86	0.91
1:D:132:ALA:N	1:D:133:ASN:HA	1.86	0.90
1:C:77:TRP:CZ3	1:C:114:LEU:N	2.38	0.90
1:D:118:PRO:HD2	1:D:128:ASP:HA	1.54	0.90
1:E:379:TYR:O	1:E:385:ILE:HB	1.70	0.90
1:B:133:ASN:H	1:B:134:PRO:HD2	1.36	0.90
1:C:57:GLN:HE21	1:C:265:ARG:NH2	1.68	0.90
1:C:60:ARG:HG2	1:C:201:THR:HG21	1.51	0.90
1:A:345:THR:OG1	1:E:173:ALA:CB	2.19	0.90
1:B:120:GLN:O	1:B:120:GLN:HG2	1.69	0.90
1:D:163:GLU:OE1	1:D:208:LEU:CB	2.19	0.90
1:E:382:ASN:HB3	1:E:385:ILE:HG12	1.54	0.90
1:A:347:HIS:HB2	1:E:177:LEU:N	1.86	0.90
1:C:176:LYS:C	1:D:347:HIS:HB3	1.96	0.90
1:D:468:HIS:HA	1:D:473:ARG:HD3	1.53	0.90
1:A:132:ALA:N	1:A:133:ASN:HA	1.86	0.90
1:A:379:TYR:O	1:A:385:ILE:HB	1.70	0.90
1:B:378:LEU:CD2	1:B:400:LYS:O	2.20	0.90
1:B:117:ARG:CB	1:B:118:PRO:HD3	2.02	0.90
1:C:382:ASN:HB3	1:C:385:ILE:HG12	1.54	0.90
1:D:39:GLN:HB3	1:D:67:ILE:HG12	1.54	0.90
1:A:347:HIS:CG	1:E:177:LEU:HA	2.06	0.90
1:A:329:ILE:HG23	1:A:330:ILE:N	1.85	0.90
1:B:202:PRO:HD3	1:B:265:ARG:HD2	0.95	0.90
1:C:58:ALA:O	1:C:265:ARG:HD3	1.70	0.90
1:E:322:TRP:CD1	1:E:456:ARG:CB	2.53	0.90
1:E:329:ILE:HG23	1:E:330:ILE:N	1.84	0.90
1:A:346:TYR:H	1:E:173:ALA:HB1	1.14	0.89
1:A:91:LYS:HB3	1:A:93:ARG:H	1.37	0.89
1:A:173:ALA:HB1	1:B:346:TYR:H	1.14	0.89
1:A:235:LEU:HD12	1:A:241:LEU:HD22	1.49	0.89
1:C:57:GLN:NE2	1:C:265:ARG:NH2	2.20	0.89
1:C:76:LEU:HB2	1:C:136:HIS:CE1	2.06	0.89
1:D:177:LEU:CA	1:E:347:HIS:CG	2.56	0.89
1:A:177:LEU:CA	1:B:347:HIS:CG	2.55	0.89
1:B:379:TYR:O	1:B:385:ILE:HB	1.71	0.89
1:E:430:LYS:O	1:E:434:PRO:CD	2.19	0.89
1:B:176:LYS:HE2	1:C:348:ASP:OD2	1.71	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:LEU:CD1	1:C:241:LEU:HD22	2.02	0.89
1:D:56:LEU:CD2	1:D:222:ILE:HG23	2.03	0.89
1:D:176:LYS:C	1:E:347:HIS:HB3	1.98	0.89
1:B:220:THR:HG22	1:B:445:GLU:O	1.72	0.89
1:E:117:ARG:HB3	1:E:118:PRO:CD	2.00	0.89
1:C:174:ARG:NH1	1:D:345:THR:CB	2.36	0.89
1:C:176:LYS:CB	1:D:347:HIS:CB	2.48	0.89
1:D:22:PHE:HA	1:D:33:PRO:HD3	1.51	0.89
1:A:144:GLY:HA2	1:A:146:THR:N	1.88	0.88
1:C:144:GLY:HA2	1:C:146:THR:N	1.88	0.88
1:D:370:LYS:CE	1:D:399:ASP:HB3	2.02	0.88
1:E:132:ALA:N	1:E:133:ASN:HA	1.86	0.88
1:A:176:LYS:HB3	1:B:347:HIS:HB3	1.52	0.88
1:A:345:THR:HA	1:E:174:ARG:HH12	1.38	0.88
1:C:177:LEU:HA	1:D:347:HIS:CG	2.07	0.88
1:C:202:PRO:HD3	1:C:265:ARG:CD	2.02	0.88
1:B:144:GLY:HA2	1:B:146:THR:N	1.88	0.88
1:B:368:ARG:NH2	1:B:381:LEU:CD1	2.37	0.88
1:A:176:LYS:C	1:B:347:HIS:HB3	1.99	0.88
1:A:280:LYS:NZ	1:A:437:LEU:HB2	1.89	0.88
1:B:176:LYS:C	1:C:347:HIS:HB3	1.99	0.88
1:D:177:LEU:HA	1:E:347:HIS:CG	2.07	0.88
1:E:144:GLY:HA2	1:E:146:THR:N	1.88	0.88
1:E:235:LEU:HD22	1:E:245:LEU:HB3	1.55	0.88
1:A:176:LYS:HB2	1:B:347:HIS:CB	2.03	0.88
1:D:173:ALA:HA	1:E:346:TYR:HA	1.25	0.88
1:A:73:VAL:CG2	1:A:105:ILE:HG12	2.03	0.88
1:B:98:SER:HA	1:B:101:ILE:HD12	1.56	0.88
1:C:301:LEU:HD21	1:C:362:VAL:HG23	1.55	0.88
1:D:202:PRO:HB3	1:D:265:ARG:NH1	1.87	0.88
1:A:347:HIS:CB	1:E:176:LYS:HB2	2.04	0.88
1:B:329:ILE:HG23	1:B:330:ILE:N	1.87	0.88
1:E:83:LYS:CG	1:E:155:ASP:CB	2.53	0.87
1:E:368:ARG:HB2	1:E:401:THR:HG21	1.56	0.87
1:A:414:VAL:HG11	1:A:447:ILE:HD13	1.55	0.87
1:C:322:TRP:CD1	1:C:456:ARG:CB	2.53	0.87
1:D:144:GLY:HA2	1:D:146:THR:N	1.88	0.87
1:B:235:LEU:HD22	1:B:245:LEU:HB3	1.54	0.87
1:C:378:LEU:HD21	1:C:401:THR:CG2	2.05	0.87
1:C:468:HIS:HA	1:C:473:ARG:HD3	1.54	0.87
1:A:417:VAL:HB	1:A:465:MET:CG	2.02	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:ARG:HG3	1:C:201:THR:HG21	1.53	0.87
1:C:177:LEU:CA	1:D:347:HIS:CG	2.56	0.87
1:C:177:LEU:CA	1:D:347:HIS:CD2	2.57	0.87
1:D:181:VAL:HB	1:E:376:ALA:HA	1.57	0.87
1:E:148:GLN:NE2	1:E:175:GLU:HG3	1.89	0.87
1:B:176:LYS:CE	1:C:348:ASP:OD2	2.22	0.87
1:A:117:ARG:CB	1:A:118:PRO:HD3	2.04	0.87
1:B:461:LEU:O	1:B:465:MET:HG2	1.75	0.87
1:E:370:LYS:HE3	1:E:399:ASP:CB	2.03	0.87
1:A:177:LEU:HA	1:B:347:HIS:CG	2.08	0.86
1:C:437:LEU:CD2	1:C:458:CYS:SG	2.63	0.86
1:C:417:VAL:HB	1:C:465:MET:CG	2.04	0.86
1:A:301:LEU:HD21	1:A:362:VAL:HG23	1.57	0.86
1:D:120:GLN:O	1:D:120:GLN:HG2	1.72	0.86
1:E:182:GLN:HE21	1:E:185:ALA:HB2	0.76	0.86
1:B:351:ASN:HD21	1:B:377:VAL:HA	1.38	0.86
1:A:98:SER:HA	1:A:101:ILE:HD12	1.58	0.86
1:D:21:ALA:O	1:D:33:PRO:HD2	1.75	0.86
1:D:370:LYS:HB3	1:D:375:TYR:CZ	2.11	0.86
1:B:378:LEU:HD21	1:B:401:THR:CG2	2.06	0.86
1:C:177:LEU:HB3	1:D:347:HIS:HD2	0.86	0.86
1:D:301:LEU:HD21	1:D:362:VAL:HG23	1.58	0.86
1:E:370:LYS:HB3	1:E:375:TYR:CZ	2.10	0.86
1:B:417:VAL:CB	1:B:465:MET:HG3	2.03	0.86
1:E:39:GLN:HB3	1:E:67:ILE:HG21	1.57	0.86
1:C:98:SER:HA	1:C:101:ILE:HD12	1.57	0.86
1:D:201:THR:HG23	1:D:202:PRO:HD2	1.55	0.86
1:D:346:TYR:HD1	1:D:349:CYS:H	0.96	0.86
1:D:351:ASN:HD21	1:D:377:VAL:HA	1.40	0.86
1:C:173:ALA:HB3	1:D:345:THR:CG2	2.04	0.85
1:C:235:LEU:HD22	1:C:245:LEU:HB3	1.57	0.85
1:B:322:TRP:CD1	1:B:456:ARG:CB	2.56	0.85
1:D:378:LEU:HD21	1:D:401:THR:OG1	1.76	0.85
1:A:132:ALA:N	1:A:133:ASN:OD1	2.10	0.85
1:A:347:HIS:CE1	1:E:177:LEU:HB2	2.11	0.85
1:B:173:ALA:HA	1:C:346:TYR:HA	1.25	0.85
1:C:21:ALA:O	1:C:33:PRO:HD2	1.76	0.85
1:D:436:LEU:CD2	1:D:457:ILE:HG22	2.06	0.85
1:E:83:LYS:HG3	1:E:155:ASP:CB	2.06	0.85
1:D:156:ILE:HB	1:D:194:SER:CB	2.06	0.85
1:C:132:ALA:N	1:C:133:ASN:OD1	2.09	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:ALA:N	1:B:133:ASN:OD1	2.09	0.85
1:C:351:ASN:HD21	1:C:377:VAL:HA	1.39	0.85
1:A:347:HIS:CG	1:E:177:LEU:CA	2.59	0.85
1:C:120:GLN:HG2	1:C:120:GLN:O	1.75	0.85
1:C:274:ARG:HD3	1:C:414:VAL:CG1	2.05	0.85
1:C:414:VAL:HG11	1:C:447:ILE:HD13	1.58	0.85
1:E:156:ILE:HB	1:E:194:SER:CB	2.06	0.85
1:B:176:LYS:HB3	1:C:347:HIS:CA	2.07	0.85
1:E:91:LYS:HB3	1:E:93:ARG:H	1.42	0.85
1:A:156:ILE:HB	1:A:194:SER:CB	2.07	0.84
1:E:59:PHE:CD2	1:E:60:ARG:O	2.30	0.84
1:A:322:TRP:CD1	1:A:456:ARG:CB	2.53	0.84
1:A:351:ASN:HD21	1:A:377:VAL:HA	1.42	0.84
1:E:148:GLN:NE2	1:E:175:GLU:CG	2.39	0.84
1:B:368:ARG:HB2	1:B:401:THR:HG21	1.59	0.84
1:B:378:LEU:HD21	1:B:401:THR:HG21	1.60	0.84
1:B:156:ILE:HB	1:B:194:SER:CB	2.07	0.84
1:A:59:PHE:CD2	1:A:60:ARG:O	2.30	0.84
1:C:346:TYR:CD2	1:C:349:CYS:CB	2.60	0.84
1:D:280:LYS:NZ	1:D:438:LYS:HA	1.91	0.84
1:D:98:SER:HA	1:D:101:ILE:HD12	1.57	0.84
1:E:280:LYS:NZ	1:E:438:LYS:HA	1.93	0.84
1:A:370:LYS:HB3	1:A:375:TYR:CZ	2.12	0.84
1:A:417:VAL:CA	1:A:465:MET:HG3	2.07	0.84
1:E:73:VAL:HG22	1:E:105:ILE:HG13	1.58	0.84
1:C:378:LEU:HD11	1:C:401:THR:OG1	1.78	0.84
1:E:220:THR:HG22	1:E:445:GLU:O	1.77	0.84
1:E:378:LEU:HD21	1:E:401:THR:CG2	2.06	0.84
1:C:39:GLN:HB3	1:C:67:ILE:HG12	1.59	0.84
1:D:177:LEU:HB3	1:E:347:HIS:CD2	2.13	0.84
1:B:73:VAL:HG22	1:B:105:ILE:HG13	1.58	0.83
1:C:174:ARG:HH12	1:D:345:THR:HA	1.42	0.83
1:D:59:PHE:CD1	1:D:225:ALA:HA	2.12	0.83
1:E:132:ALA:N	1:E:133:ASN:OD1	2.11	0.83
1:C:173:ALA:HA	1:D:346:TYR:HA	1.25	0.83
1:B:235:LEU:HD21	1:B:245:LEU:CB	2.06	0.83
1:C:202:PRO:CD	1:C:265:ARG:HD2	2.03	0.83
1:C:274:ARG:HD3	1:C:414:VAL:HG12	1.59	0.83
1:D:132:ALA:N	1:D:133:ASN:OD1	2.10	0.83
1:E:436:LEU:CD2	1:E:457:ILE:HG22	2.08	0.83
1:B:417:VAL:HG23	1:B:465:MET:HE3	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:378:LEU:HD21	1:C:401:THR:HG21	1.60	0.83
1:E:98:SER:HA	1:E:101:ILE:HD12	1.60	0.83
1:C:59:PHE:CD2	1:C:60:ARG:O	2.31	0.83
1:C:156:ILE:HB	1:C:194:SER:CB	2.07	0.83
1:A:346:TYR:CD1	1:E:173:ALA:HB2	2.14	0.83
1:A:235:LEU:HD21	1:A:245:LEU:CB	2.04	0.83
1:B:280:LYS:NZ	1:B:437:LEU:HB2	1.92	0.83
1:C:313:LEU:CD1	1:C:374:GLY:HA2	2.09	0.83
1:E:221:ILE:HB	1:E:222:ILE:HG12	1.59	0.83
1:E:382:ASN:CB	1:E:385:ILE:HG12	2.09	0.83
1:C:173:ALA:CB	1:D:346:TYR:CB	2.57	0.83
1:E:378:LEU:HD11	1:E:401:THR:OG1	1.78	0.83
1:A:56:LEU:CG	1:A:222:ILE:HG23	2.07	0.83
1:C:181:VAL:HA	1:C:182:GLN:CG	2.08	0.83
1:D:436:LEU:HD22	1:D:457:ILE:CG2	2.09	0.83
1:E:301:LEU:HD21	1:E:362:VAL:HG23	1.60	0.83
1:A:120:GLN:O	1:A:120:GLN:HG2	1.78	0.83
1:A:220:THR:HG22	1:A:445:GLU:C	2.04	0.83
1:C:382:ASN:CB	1:C:385:ILE:HG12	2.08	0.83
1:C:417:VAL:CA	1:C:465:MET:HG3	2.08	0.83
1:E:414:VAL:HG11	1:E:447:ILE:HD13	1.58	0.83
1:D:118:PRO:CG	1:D:129:VAL:H	1.91	0.82
1:D:73:VAL:CG2	1:D:105:ILE:HG12	2.08	0.82
1:D:173:ALA:CB	1:E:346:TYR:CB	2.57	0.82
1:A:75:SER:HB3	1:A:83:LYS:NZ	1.94	0.82
1:B:176:LYS:CB	1:C:347:HIS:N	2.42	0.82
1:C:22:PHE:HA	1:C:33:PRO:CD	2.10	0.82
1:D:375:TYR:HA	1:D:378:LEU:HD12	1.61	0.82
1:B:177:LEU:HB3	1:C:347:HIS:CG	2.14	0.82
1:E:252:ASN:HB3	1:E:253:PRO:HD3	1.61	0.82
1:A:56:LEU:CG	1:A:222:ILE:CG2	2.57	0.82
1:A:181:VAL:HA	1:A:182:GLN:CG	2.08	0.82
1:C:176:LYS:CB	1:D:347:HIS:N	2.42	0.82
1:E:77:TRP:HZ3	1:E:114:LEU:N	1.77	0.82
1:E:362:VAL:O	1:E:362:VAL:HG12	1.79	0.82
1:A:346:TYR:CG	1:E:173:ALA:HB2	2.15	0.82
1:D:176:LYS:CB	1:E:347:HIS:N	2.42	0.82
1:E:235:LEU:HD11	1:E:241:LEU:HD23	1.61	0.82
1:A:87:VAL:HB	1:A:158:ILE:HG13	1.62	0.82
1:A:133:ASN:H	1:A:134:PRO:HD3	1.44	0.82
1:A:176:LYS:CB	1:B:347:HIS:N	2.42	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:LYS:CB	1:E:184:PHE:HZ	1.91	0.82
1:B:173:ALA:CB	1:C:346:TYR:CB	2.57	0.82
1:A:346:TYR:CB	1:E:173:ALA:CB	2.57	0.82
1:B:173:ALA:C	1:C:346:TYR:CA	2.44	0.82
1:C:370:LYS:HB3	1:C:375:TYR:CZ	2.15	0.82
1:B:87:VAL:HB	1:B:158:ILE:HG13	1.62	0.81
1:E:57:GLN:HB3	1:E:265:ARG:NE	1.94	0.81
1:A:10:LEU:HD23	1:A:11:VAL:HG13	1.62	0.81
1:A:223:TRP:CE3	1:A:444:MET:HB2	2.14	0.81
1:E:85:LEU:HB3	1:E:136:HIS:ND1	1.94	0.81
1:A:347:HIS:N	1:E:176:LYS:CB	2.42	0.81
1:B:252:ASN:HB3	1:B:253:PRO:HD3	1.63	0.81
1:E:378:LEU:HD21	1:E:401:THR:HG21	1.60	0.81
1:E:417:VAL:HB	1:E:465:MET:CG	2.06	0.81
1:A:370:LYS:CE	1:A:399:ASP:HB3	2.10	0.81
1:B:181:VAL:HA	1:B:182:GLN:CG	2.10	0.81
1:C:285:LEU:HD22	1:C:431:VAL:HG13	1.62	0.81
1:E:400:LYS:O	1:E:401:THR:HG23	1.80	0.81
1:A:73:VAL:CG2	1:A:105:ILE:CG1	2.58	0.81
1:A:77:TRP:CZ2	1:A:105:ILE:HG23	2.16	0.81
1:A:77:TRP:HZ3	1:A:114:LEU:HB2	1.46	0.81
1:C:73:VAL:HG22	1:C:105:ILE:HG13	1.61	0.81
1:E:351:ASN:HD21	1:E:377:VAL:HA	1.45	0.81
1:B:177:LEU:H	1:C:347:HIS:HB2	1.44	0.81
1:D:73:VAL:CG2	1:D:105:ILE:CG1	2.58	0.81
1:A:163:GLU:HB2	1:A:208:LEU:HD12	1.62	0.81
1:A:173:ALA:CB	1:B:346:TYR:CB	2.57	0.81
1:A:362:VAL:O	1:A:362:VAL:HG12	1.80	0.81
1:C:252:ASN:HB3	1:C:253:PRO:HD3	1.62	0.81
1:B:223:TRP:CE3	1:B:444:MET:HB2	2.16	0.81
1:C:173:ALA:C	1:D:345:THR:O	2.24	0.81
1:C:400:LYS:O	1:C:401:THR:HG23	1.80	0.81
1:D:77:TRP:HZ3	1:D:114:LEU:HB2	1.45	0.81
1:C:362:VAL:O	1:C:362:VAL:HG12	1.80	0.81
1:E:375:TYR:HA	1:E:378:LEU:HD12	1.62	0.81
1:C:83:LYS:CE	1:C:192:PRO:HA	2.05	0.81
1:E:87:VAL:HB	1:E:158:ILE:HG13	1.62	0.81
1:A:167:ASN:O	1:A:171:MET:SD	2.38	0.80
1:D:177:LEU:CA	1:E:347:HIS:ND1	2.39	0.80
1:E:73:VAL:HG22	1:E:105:ILE:CG1	2.10	0.80
1:E:445:GLU:OE1	1:E:445:GLU:N	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ARG:HB3	1:A:118:PRO:CD	2.10	0.80
1:A:414:VAL:HA	1:A:417:VAL:HG12	1.61	0.80
1:B:77:TRP:HZ3	1:B:114:LEU:N	1.80	0.80
1:B:173:ALA:C	1:C:345:THR:O	2.24	0.80
1:C:163:GLU:HG2	1:C:203:GLN:N	1.97	0.80
1:C:173:ALA:O	1:D:346:TYR:CA	2.29	0.80
1:D:52:LYS:CB	1:D:184:PHE:HZ	1.91	0.80
1:D:173:ALA:C	1:E:345:THR:O	2.24	0.80
1:E:235:LEU:HD21	1:E:245:LEU:CB	2.06	0.80
1:B:436:LEU:CD2	1:B:457:ILE:HG22	2.11	0.80
1:C:170:THR:HA	1:D:345:THR:CG2	2.10	0.80
1:C:346:TYR:CE2	1:C:349:CYS:CA	2.65	0.80
1:E:83:LYS:HG3	1:E:155:ASP:HB3	1.61	0.80
1:B:316:ALA:HB3	1:B:318:MET:HE2	1.63	0.80
1:C:52:LYS:CB	1:C:184:PHE:HZ	1.90	0.80
1:A:173:ALA:C	1:B:345:THR:O	2.24	0.80
1:C:436:LEU:CD2	1:C:457:ILE:HG22	2.10	0.80
1:A:85:LEU:HB3	1:A:136:HIS:ND1	1.97	0.80
1:A:346:TYR:CA	1:E:173:ALA:O	2.30	0.80
1:A:346:TYR:CD1	1:E:173:ALA:CB	2.65	0.80
1:D:22:PHE:HA	1:D:33:PRO:CD	2.10	0.80
1:D:362:VAL:HG12	1:D:362:VAL:O	1.79	0.80
1:A:91:LYS:HB3	1:A:93:ARG:N	1.96	0.80
1:A:345:THR:CB	1:E:174:ARG:NH1	2.44	0.80
1:B:378:LEU:HD11	1:B:401:THR:HG1	1.42	0.80
1:C:87:VAL:HB	1:C:158:ILE:HG13	1.63	0.80
1:C:375:TYR:HA	1:C:378:LEU:HD12	1.62	0.80
1:E:10:LEU:HD23	1:E:11:VAL:HG13	1.63	0.80
1:E:186:ALA:O	1:E:190:PRO:HD2	1.82	0.80
1:A:345:THR:HA	1:E:174:ARG:NH1	1.97	0.80
1:A:379:TYR:HA	1:A:385:ILE:HG13	1.64	0.80
1:C:156:ILE:CA	1:C:194:SER:HB3	2.12	0.80
1:D:87:VAL:HB	1:D:158:ILE:HG13	1.62	0.80
1:D:118:PRO:HG3	1:D:129:VAL:H	1.46	0.80
1:E:148:GLN:HE21	1:E:175:GLU:CG	1.93	0.80
1:E:163:GLU:CD	1:E:208:LEU:HB3	2.07	0.80
1:E:436:LEU:HD22	1:E:457:ILE:CG2	2.11	0.80
1:A:252:ASN:HB3	1:A:253:PRO:HD3	1.63	0.80
1:C:73:VAL:HG23	1:C:105:ILE:HG13	1.64	0.80
1:C:117:ARG:HB3	1:C:118:PRO:CD	2.09	0.80
1:A:262:ASP:HB3	1:A:263:PRO:HD3	1.62	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:THR:O	1:E:173:ALA:C	2.24	0.79
1:B:163:GLU:HG2	1:B:203:GLN:N	1.97	0.79
1:D:163:GLU:HG2	1:D:203:GLN:N	1.97	0.79
1:D:181:VAL:HA	1:D:182:GLN:CG	2.10	0.79
1:E:120:GLN:O	1:E:120:GLN:HG2	1.82	0.79
1:C:163:GLU:HB2	1:C:208:LEU:HD12	1.63	0.79
1:D:77:TRP:CZ2	1:D:105:ILE:HG23	2.16	0.79
1:D:156:ILE:CA	1:D:194:SER:HB3	2.12	0.79
1:D:379:TYR:HA	1:D:385:ILE:HG13	1.64	0.79
1:A:83:LYS:CG	1:A:155:ASP:HB2	2.10	0.79
1:A:177:LEU:H	1:B:347:HIS:HB2	1.44	0.79
1:C:436:LEU:HD22	1:C:457:ILE:CG2	2.12	0.79
1:B:73:VAL:HG22	1:B:105:ILE:CG1	2.11	0.79
1:B:436:LEU:HD22	1:B:457:ILE:CG2	2.12	0.79
1:C:177:LEU:H	1:D:347:HIS:HB2	1.46	0.79
1:D:468:HIS:HA	1:D:473:ARG:CD	2.12	0.79
1:E:291:PRO:HG2	1:E:295:ASP:CB	2.12	0.79
1:A:163:GLU:HG2	1:A:203:GLN:N	1.97	0.79
1:A:272:ARG:HB2	1:A:441:ASN:HB2	1.65	0.79
1:B:173:ALA:HB3	1:C:345:THR:CG2	2.13	0.79
1:C:57:GLN:HG3	1:C:212:LEU:HD13	1.65	0.79
1:D:85:LEU:CD2	1:D:136:HIS:CD2	2.65	0.79
1:B:362:VAL:HG13	1:B:362:VAL:O	1.81	0.79
1:C:159:ALA:CB	1:C:198:TYR:CD1	2.65	0.79
1:E:156:ILE:CA	1:E:194:SER:HB3	2.12	0.79
1:E:274:ARG:HD3	1:E:414:VAL:HG12	1.64	0.79
1:A:186:ALA:O	1:A:190:PRO:CD	2.31	0.79
1:A:379:TYR:HB2	1:E:181:VAL:HG21	1.65	0.79
1:A:468:HIS:HA	1:A:473:ARG:CD	2.12	0.79
1:C:73:VAL:HG22	1:C:105:ILE:CG1	2.13	0.79
1:C:174:ARG:HH12	1:D:345:THR:CB	1.96	0.79
1:E:294:SER:HB2	1:E:340:GLY:O	1.83	0.79
1:A:173:ALA:O	1:B:346:TYR:CA	2.29	0.78
1:D:177:LEU:H	1:E:347:HIS:HB2	1.45	0.78
1:A:156:ILE:CA	1:A:194:SER:HB3	2.12	0.78
1:A:173:ALA:HB3	1:B:345:THR:CG2	2.13	0.78
1:C:414:VAL:HA	1:C:417:VAL:HG12	1.63	0.78
1:D:190:PRO:HB2	1:D:192:PRO:HD2	1.64	0.78
1:D:346:TYR:CE1	1:D:349:CYS:CA	2.66	0.78
1:D:77:TRP:CZ3	1:D:114:LEU:HB2	2.17	0.78
1:D:85:LEU:HD22	1:D:136:HIS:HD2	1.45	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:294:SER:HB2	1:D:340:GLY:O	1.83	0.78
1:A:21:ALA:O	1:A:33:PRO:HD3	1.83	0.78
1:A:57:GLN:HG3	1:A:212:LEU:HD13	1.65	0.78
1:B:128:ASP:HB3	1:B:134:PRO:O	1.84	0.78
1:B:156:ILE:CA	1:B:194:SER:HB3	2.12	0.78
1:B:285:LEU:HD22	1:B:431:VAL:HG13	1.65	0.78
1:D:382:ASN:HB3	1:D:385:ILE:HG12	1.64	0.78
1:B:205:GLU:HG2	1:B:209:TYR:HD2	1.45	0.78
1:C:186:ALA:O	1:C:190:PRO:CD	2.32	0.78
1:D:201:THR:CG2	1:D:202:PRO:CD	2.62	0.78
1:A:436:LEU:CD2	1:A:457:ILE:HG22	2.13	0.78
1:C:84:ILE:HG23	1:C:154:ALA:HA	1.65	0.78
1:A:346:TYR:CA	1:E:173:ALA:C	2.44	0.78
1:D:417:VAL:CB	1:D:465:MET:HG3	2.09	0.78
1:B:162:VAL:HB	1:B:208:LEU:HD21	1.66	0.78
1:A:57:GLN:OE1	1:A:265:ARG:NH2	2.17	0.78
1:A:294:SER:HB2	1:A:340:GLY:O	1.83	0.78
1:A:437:LEU:CD2	1:A:458:CYS:SG	2.68	0.78
1:B:167:ASN:O	1:B:171:MET:SD	2.42	0.78
1:B:382:ASN:HB3	1:B:385:ILE:HG12	1.66	0.78
1:D:220:THR:OG1	1:D:445:GLU:HB2	1.83	0.78
1:E:414:VAL:HA	1:E:417:VAL:HG12	1.66	0.78
1:A:144:GLY:HA2	1:A:147:GLY:H	1.48	0.77
1:B:436:LEU:HA	1:B:439:HIS:HE1	1.46	0.77
1:E:85:LEU:HD12	1:E:156:ILE:HG21	1.65	0.77
1:E:417:VAL:CA	1:E:465:MET:HG3	2.14	0.77
1:E:467:THR:HG22	1:E:473:ARG:HG3	1.66	0.77
1:A:177:LEU:HB3	1:B:347:HIS:CG	2.19	0.77
1:A:368:ARG:HB2	1:A:378:LEU:HD21	1.66	0.77
1:C:144:GLY:HA2	1:C:147:GLY:H	1.48	0.77
1:C:346:TYR:HD2	1:C:349:CYS:H	0.81	0.77
1:D:144:GLY:HA2	1:D:147:GLY:H	1.48	0.77
1:E:144:GLY:HA2	1:E:147:GLY:H	1.48	0.77
1:E:163:GLU:HB2	1:E:208:LEU:HD13	1.64	0.77
1:B:173:ALA:O	1:C:346:TYR:CA	2.29	0.77
1:E:163:GLU:HG2	1:E:203:GLN:N	1.99	0.77
1:E:272:ARG:HB2	1:E:441:ASN:HB2	1.67	0.77
1:B:84:ILE:HG23	1:B:154:ALA:HA	1.66	0.77
1:E:370:LYS:HE2	1:E:375:TYR:HE1	1.46	0.77
1:A:84:ILE:HG23	1:A:154:ALA:HA	1.65	0.77
1:A:382:ASN:HB3	1:A:385:ILE:HG12	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:467:THR:HG22	1:B:473:ARG:HG3	1.65	0.77
1:D:173:ALA:HB3	1:E:345:THR:CG2	2.13	0.77
1:A:379:TYR:HB3	1:A:385:ILE:HG21	1.65	0.77
1:B:45:VAL:O	1:B:54:PHE:CE2	2.38	0.77
1:C:10:LEU:HD12	1:C:78:ARG:HD2	1.65	0.77
1:D:173:ALA:O	1:E:346:TYR:CA	2.29	0.77
1:A:262:ASP:HB2	1:A:263:PRO:HD3	1.66	0.77
1:C:235:LEU:HD21	1:C:245:LEU:CB	2.11	0.77
1:E:77:TRP:HE1	1:E:105:ILE:CG1	1.90	0.77
1:C:45:VAL:O	1:C:54:PHE:CE2	2.38	0.77
1:C:174:ARG:NH1	1:D:345:THR:HA	1.99	0.77
1:D:182:GLN:HE21	1:D:185:ALA:HB2	0.73	0.77
1:B:144:GLY:HA2	1:B:147:GLY:H	1.48	0.76
1:A:77:TRP:CZ3	1:A:114:LEU:HB2	2.20	0.76
1:B:73:VAL:HG23	1:B:105:ILE:HG13	1.67	0.76
1:B:294:SER:HB2	1:B:340:GLY:O	1.83	0.76
1:B:400:LYS:O	1:B:401:THR:HG23	1.84	0.76
1:D:56:LEU:CG	1:D:222:ILE:CG2	2.57	0.76
1:D:59:PHE:CZ	1:D:62:ILE:HB	2.20	0.76
1:E:59:PHE:CE2	1:E:60:ARG:O	2.38	0.76
1:B:91:LYS:CB	1:B:93:ARG:H	1.99	0.76
1:B:170:THR:HA	1:C:345:THR:CG2	2.14	0.76
1:C:368:ARG:HB2	1:C:401:THR:HG21	1.67	0.76
1:D:45:VAL:O	1:D:54:PHE:CE2	2.39	0.76
1:A:170:THR:HA	1:B:345:THR:CG2	2.14	0.76
1:A:280:LYS:HZ1	1:A:437:LEU:HB2	1.49	0.76
1:A:347:HIS:HB2	1:E:177:LEU:H	1.49	0.76
1:C:190:PRO:HB2	1:C:192:PRO:HD2	1.67	0.76
1:D:173:ALA:HB2	1:E:346:TYR:CG	2.20	0.76
1:E:91:LYS:HB3	1:E:93:ARG:N	2.00	0.76
1:B:414:VAL:HA	1:B:417:VAL:HG12	1.66	0.76
1:C:182:GLN:HE21	1:C:185:ALA:HB2	0.73	0.76
1:C:294:SER:HB2	1:C:340:GLY:O	1.85	0.76
1:D:128:ASP:HB3	1:D:134:PRO:O	1.84	0.76
1:D:252:ASN:HB3	1:D:253:PRO:HD3	1.67	0.76
1:E:252:ASN:HB3	1:E:253:PRO:CD	2.16	0.76
1:E:470:LEU:HD21	1:E:472:ILE:HD12	1.68	0.76
1:A:77:TRP:HZ2	1:A:105:ILE:CG2	1.99	0.76
1:A:436:LEU:HD22	1:A:457:ILE:CG2	2.15	0.76
1:E:181:VAL:HA	1:E:182:GLN:CG	2.13	0.76
1:E:280:LYS:HZ2	1:E:438:LYS:HA	1.48	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:LEU:HG	1:A:222:ILE:HG22	1.67	0.76
1:B:280:LYS:CE	1:B:438:LYS:HA	2.16	0.76
1:C:77:TRP:HZ3	1:C:114:LEU:N	1.82	0.76
1:E:57:GLN:OE1	1:E:265:ARG:NH2	2.18	0.76
1:E:57:GLN:O	1:E:223:TRP:CD1	2.39	0.76
1:A:59:PHE:CE2	1:A:60:ARG:O	2.39	0.76
1:C:220:THR:O	1:C:220:THR:OG1	1.97	0.76
1:D:285:LEU:HD22	1:D:431:VAL:HG13	1.68	0.76
1:D:313:LEU:HD12	1:D:374:GLY:CA	2.11	0.76
1:C:216:ARG:O	1:C:411:GLN:OE1	2.03	0.76
1:D:56:LEU:HD13	1:D:199:LEU:HD12	1.68	0.76
1:D:170:THR:HA	1:E:345:THR:CG2	2.14	0.76
1:D:414:VAL:HA	1:D:417:VAL:HG12	1.68	0.76
1:A:133:ASN:H	1:A:134:PRO:CD	2.00	0.75
1:D:177:LEU:HB3	1:E:347:HIS:CG	2.19	0.75
1:D:470:LEU:HD21	1:D:472:ILE:HD12	1.68	0.75
1:A:176:LYS:HB2	1:B:347:HIS:CA	2.15	0.75
1:B:67:ILE:H	1:B:67:ILE:CD1	1.98	0.75
1:B:368:ARG:H	1:B:401:THR:CG2	1.99	0.75
1:C:91:LYS:CB	1:C:93:ARG:H	1.99	0.75
1:E:45:VAL:O	1:E:54:PHE:CE2	2.39	0.75
1:E:291:PRO:HD3	1:E:295:ASP:O	1.85	0.75
1:A:182:GLN:HE21	1:A:185:ALA:HB2	0.73	0.75
1:B:186:ALA:O	1:B:190:PRO:CD	2.34	0.75
1:B:252:ASN:HB3	1:B:253:PRO:CD	2.17	0.75
1:C:220:THR:CA	1:C:445:GLU:HB2	2.17	0.75
1:D:196:VAL:HG13	1:D:198:TYR:CE1	2.21	0.75
1:D:216:ARG:O	1:D:411:GLN:OE1	2.04	0.75
1:D:346:TYR:CD1	1:D:349:CYS:CB	2.69	0.75
1:E:190:PRO:HB2	1:E:192:PRO:HD2	1.68	0.75
1:B:91:LYS:HB3	1:B:93:ARG:H	1.52	0.75
1:C:128:ASP:HB3	1:C:134:PRO:O	1.86	0.75
1:D:173:ALA:C	1:E:346:TYR:CA	2.44	0.75
1:E:128:ASP:HB3	1:E:134:PRO:O	1.87	0.75
1:D:77:TRP:HZ2	1:D:105:ILE:CG2	2.00	0.75
1:D:144:GLY:O	1:D:171:MET:HG2	1.87	0.75
1:E:221:ILE:CB	1:E:222:ILE:HG12	2.17	0.75
1:A:91:LYS:CB	1:A:93:ARG:H	1.99	0.75
1:A:202:PRO:HB3	1:A:265:ARG:NH1	2.02	0.75
1:A:252:ASN:HB3	1:A:253:PRO:CD	2.17	0.75
1:C:59:PHE:CE2	1:C:60:ARG:O	2.40	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:PRO:HB2	1:A:192:PRO:HD2	1.69	0.74
1:A:313:LEU:HD12	1:A:374:GLY:CA	2.13	0.74
1:A:347:HIS:CA	1:E:176:LYS:HB2	2.16	0.74
1:C:45:VAL:O	1:C:54:PHE:CZ	2.40	0.74
1:D:437:LEU:CD2	1:D:458:CYS:SG	2.71	0.74
1:E:59:PHE:CZ	1:E:62:ILE:HB	2.22	0.74
1:D:186:ALA:O	1:D:190:PRO:CD	2.35	0.74
1:E:115:LYS:C	1:E:116:PRO:CD	2.57	0.74
1:A:45:VAL:O	1:A:54:PHE:CE2	2.40	0.74
1:C:59:PHE:CZ	1:C:62:ILE:HB	2.21	0.74
1:C:162:VAL:O	1:C:165:PRO:HD2	1.88	0.74
1:E:202:PRO:HD3	1:E:265:ARG:HG2	1.70	0.74
1:B:45:VAL:O	1:B:54:PHE:CZ	2.40	0.74
1:B:176:LYS:HB3	1:C:347:HIS:C	2.12	0.74
1:B:190:PRO:HB2	1:B:192:PRO:HD2	1.67	0.74
1:C:176:LYS:HB3	1:D:347:HIS:C	2.12	0.74
1:A:52:LYS:CB	1:A:184:PHE:HZ	1.91	0.74
1:A:59:PHE:CZ	1:A:62:ILE:HB	2.21	0.74
1:B:156:ILE:HA	1:B:194:SER:HB3	1.69	0.74
1:D:45:VAL:O	1:D:54:PHE:CZ	2.40	0.74
1:D:91:LYS:CB	1:D:93:ARG:H	1.99	0.74
1:E:45:VAL:O	1:E:54:PHE:CZ	2.40	0.74
1:E:91:LYS:CB	1:E:93:ARG:H	1.99	0.74
1:E:220:THR:CA	1:E:445:GLU:HB2	2.17	0.74
1:B:182:GLN:HE21	1:B:185:ALA:HB2	0.73	0.74
1:D:133:ASN:H	1:D:134:PRO:CD	1.99	0.74
1:D:176:LYS:HB3	1:E:347:HIS:H	1.48	0.74
1:D:177:LEU:HA	1:E:347:HIS:HD1	1.51	0.74
1:E:55:ILE:CG2	1:E:57:GLN:HE21	1.99	0.74
1:B:85:LEU:HB3	1:B:136:HIS:CD2	2.19	0.74
1:D:252:ASN:HB3	1:D:253:PRO:CD	2.18	0.74
1:E:272:ARG:HB3	1:E:442:CYS:H	1.53	0.74
1:E:379:TYR:HA	1:E:385:ILE:HG13	1.68	0.74
1:C:174:ARG:NH1	1:D:345:THR:CA	2.51	0.74
1:C:177:LEU:CB	1:D:347:HIS:HD2	1.72	0.74
1:B:379:TYR:HA	1:B:385:ILE:HG13	1.69	0.74
1:C:252:ASN:HB3	1:C:253:PRO:CD	2.17	0.74
1:B:159:ALA:HB3	1:B:198:TYR:HD1	1.50	0.74
1:A:45:VAL:O	1:A:54:PHE:CZ	2.40	0.73
1:C:174:ARG:HH12	1:D:345:THR:CA	2.00	0.73
1:D:346:TYR:HD1	1:D:349:CYS:N	1.78	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:370:LYS:HG3	1:E:401:THR:OG1	1.88	0.73
1:A:72:VAL:HG13	1:A:85:LEU:HD13	1.70	0.73
1:A:144:GLY:CA	1:A:147:GLY:H	2.01	0.73
1:C:235:LEU:HD11	1:C:241:LEU:HD23	1.69	0.73
1:C:368:ARG:H	1:C:401:THR:CG2	2.01	0.73
1:C:468:HIS:HA	1:C:473:ARG:CD	2.17	0.73
1:E:73:VAL:HG23	1:E:105:ILE:HG13	1.69	0.73
1:A:345:THR:CA	1:E:174:ARG:HH12	2.01	0.73
1:D:156:ILE:HA	1:D:194:SER:HB3	1.69	0.73
1:D:412:TRP:CZ3	1:D:416:THR:OG1	2.41	0.73
1:A:128:ASP:HB3	1:A:134:PRO:O	1.87	0.73
1:C:176:LYS:HB3	1:D:347:HIS:CA	2.17	0.73
1:D:144:GLY:CA	1:D:147:GLY:H	2.01	0.73
1:A:76:LEU:HG	1:A:134:PRO:HB2	1.69	0.73
1:B:85:LEU:CB	1:B:136:HIS:HD2	2.01	0.73
1:D:373:THR:O	1:D:376:ALA:HB3	1.89	0.73
1:A:91:LYS:CB	1:A:93:ARG:HB2	2.19	0.73
1:E:128:ASP:O	1:E:135:ASP:HB3	1.88	0.73
1:B:144:GLY:CA	1:B:147:GLY:H	2.01	0.73
1:D:51:ASN:HB2	1:D:54:PHE:CZ	2.24	0.73
1:E:21:ALA:O	1:E:33:PRO:HD3	1.88	0.73
1:E:156:ILE:HA	1:E:194:SER:HB3	1.69	0.73
1:C:186:ALA:O	1:C:190:PRO:HD2	1.88	0.73
1:C:373:THR:O	1:C:376:ALA:HB3	1.89	0.73
1:E:144:GLY:CA	1:E:147:GLY:H	2.01	0.73
1:E:313:LEU:HD12	1:E:374:GLY:CA	2.13	0.73
1:E:368:ARG:H	1:E:401:THR:CG2	2.01	0.73
1:A:156:ILE:HA	1:A:194:SER:HB3	1.69	0.72
1:B:181:VAL:CB	1:C:376:ALA:HA	2.19	0.72
1:D:132:ALA:H	1:D:133:ASN:HA	1.54	0.72
1:A:181:VAL:CB	1:B:376:ALA:HA	2.19	0.72
1:A:345:THR:CA	1:E:174:ARG:NH1	2.52	0.72
1:A:346:TYR:N	1:A:346:TYR:CD1	2.31	0.72
1:B:442:CYS:HA	1:B:447:ILE:HD13	1.69	0.72
1:C:163:GLU:OE1	1:C:208:LEU:CB	2.35	0.72
1:A:186:ALA:O	1:A:190:PRO:HD2	1.88	0.72
1:A:220:THR:CA	1:A:445:GLU:HB3	2.18	0.72
1:B:373:THR:O	1:B:376:ALA:HB3	1.89	0.72
1:C:144:GLY:CA	1:C:147:GLY:H	2.01	0.72
1:C:149:LEU:HD23	1:C:174:ARG:HD2	1.71	0.72
1:D:10:LEU:HD23	1:D:11:VAL:HG13	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:LEU:HD23	1:C:11:VAL:HG13	1.69	0.72
1:D:186:ALA:O	1:D:190:PRO:HD2	1.89	0.72
1:E:373:THR:O	1:E:376:ALA:HB3	1.89	0.72
1:A:21:ALA:O	1:A:33:PRO:CD	2.38	0.72
1:B:132:ALA:H	1:B:133:ASN:HA	1.55	0.72
1:C:72:VAL:HG13	1:C:85:LEU:HD13	1.70	0.72
1:C:379:TYR:HA	1:C:385:ILE:HG13	1.71	0.72
1:E:21:ALA:O	1:E:33:PRO:CD	2.38	0.72
1:B:177:LEU:CB	1:C:347:HIS:CG	2.72	0.72
1:E:181:VAL:N	1:E:182:GLN:HB3	2.05	0.72
1:E:272:ARG:CB	1:E:441:ASN:HB2	2.20	0.72
1:D:57:GLN:HG3	1:D:212:LEU:HD13	1.71	0.72
1:D:181:VAL:CB	1:E:376:ALA:HA	2.19	0.72
1:A:204:THR:HG22	1:A:268:ARG:HD3	1.71	0.72
1:A:373:THR:O	1:A:376:ALA:HB3	1.89	0.72
1:B:368:ARG:H	1:B:401:THR:HG22	1.55	0.72
1:A:220:THR:HA	1:A:445:GLU:HB3	1.71	0.72
1:D:329:ILE:CG2	1:D:330:ILE:H	2.03	0.72
1:C:161:ASP:O	1:C:165:PRO:HD3	1.90	0.71
1:C:177:LEU:HA	1:D:347:HIS:CD2	2.24	0.71
1:D:118:PRO:HG3	1:D:129:VAL:N	2.05	0.71
1:A:177:LEU:CB	1:B:347:HIS:CG	2.74	0.71
1:B:313:LEU:HD12	1:B:374:GLY:CA	2.14	0.71
1:C:156:ILE:HA	1:C:194:SER:HB3	1.69	0.71
1:D:291:PRO:HD3	1:D:295:ASP:O	1.90	0.71
1:B:52:LYS:CB	1:B:184:PHE:HZ	1.91	0.71
1:B:55:ILE:CG2	1:B:57:GLN:OE1	2.38	0.71
1:B:117:ARG:CB	1:B:118:PRO:CD	2.68	0.71
1:C:181:VAL:CB	1:D:376:ALA:HA	2.19	0.71
1:E:149:LEU:HD23	1:E:174:ARG:HD2	1.71	0.71
1:E:379:TYR:HB3	1:E:385:ILE:HG21	1.71	0.71
1:A:272:ARG:HB3	1:A:442:CYS:H	1.55	0.71
1:E:91:LYS:C	1:E:93:ARG:H	1.98	0.71
1:D:91:LYS:C	1:D:93:ARG:H	1.98	0.71
1:D:223:TRP:CE3	1:D:444:MET:HB2	2.26	0.71
1:D:338:LEU:HD22	1:D:430:LYS:HG3	1.71	0.71
1:E:132:ALA:H	1:E:133:ASN:HA	1.55	0.71
1:E:370:LYS:CE	1:E:399:ASP:HB3	2.20	0.71
1:B:83:LYS:NZ	1:B:193:SER:H	1.85	0.71
1:B:91:LYS:C	1:B:93:ARG:H	1.98	0.71
1:B:186:ALA:O	1:B:190:PRO:HD2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:LYS:C	1:C:93:ARG:H	1.98	0.71
1:D:220:THR:C	1:D:445:GLU:HB2	2.16	0.71
1:E:368:ARG:H	1:E:401:THR:HG22	1.56	0.71
1:A:91:LYS:C	1:A:93:ARG:H	1.98	0.71
1:C:91:LYS:HB2	1:C:93:ARG:HB2	1.73	0.71
1:D:177:LEU:HA	1:E:347:HIS:CE1	2.26	0.71
1:D:128:ASP:O	1:D:135:ASP:HB3	1.90	0.71
1:A:51:ASN:HB2	1:A:54:PHE:CZ	2.25	0.70
1:B:382:ASN:CB	1:B:385:ILE:HG12	2.21	0.70
1:C:338:LEU:HD22	1:C:430:LYS:HG3	1.71	0.70
1:D:83:LYS:HD2	1:D:193:SER:O	1.90	0.70
1:E:55:ILE:CG2	1:E:57:GLN:NE2	2.54	0.70
1:B:77:TRP:HE1	1:B:105:ILE:CG1	1.91	0.70
1:C:173:ALA:C	1:D:346:TYR:CA	2.44	0.70
1:C:272:ARG:CB	1:C:441:ASN:HB2	2.20	0.70
1:E:285:LEU:HD22	1:E:431:VAL:HG13	1.73	0.70
1:D:379:TYR:HB3	1:D:385:ILE:HG21	1.71	0.70
1:D:442:CYS:HA	1:D:447:ILE:HD13	1.73	0.70
1:A:346:TYR:CG	1:E:173:ALA:CB	2.73	0.70
1:C:159:ALA:CB	1:C:198:TYR:CE1	2.74	0.70
1:D:181:VAL:N	1:D:182:GLN:HB3	2.07	0.70
1:A:379:TYR:CB	1:E:181:VAL:HG21	2.21	0.70
1:B:220:THR:HA	1:B:445:GLU:HB3	1.74	0.70
1:C:57:GLN:HE21	1:C:265:ARG:HH22	1.36	0.70
1:C:69:CYS:HA	1:C:101:ILE:HG12	1.74	0.70
1:C:145:ILE:HB	1:C:174:ARG:HG3	1.73	0.70
1:B:51:ASN:HB2	1:B:54:PHE:CZ	2.26	0.70
1:A:235:LEU:HD11	1:A:241:LEU:HD23	1.72	0.70
1:A:301:LEU:HD22	1:A:360:ILE:O	1.92	0.70
1:A:347:HIS:HB3	1:E:177:LEU:N	2.02	0.70
1:B:181:VAL:N	1:B:182:GLN:HB3	2.07	0.70
1:E:69:CYS:HA	1:E:101:ILE:HG12	1.72	0.70
1:B:176:LYS:CB	1:C:347:HIS:CA	2.70	0.70
1:D:133:ASN:N	1:D:134:PRO:HD2	2.04	0.70
1:E:220:THR:C	1:E:445:GLU:HB2	2.17	0.70
1:A:176:LYS:CB	1:B:347:HIS:CA	2.70	0.70
1:C:132:ALA:H	1:C:133:ASN:HA	1.55	0.70
1:C:285:LEU:HB2	1:C:431:VAL:HG22	1.74	0.70
1:D:72:VAL:HG13	1:D:85:LEU:HD13	1.73	0.70
1:E:301:LEU:HD22	1:E:360:ILE:O	1.92	0.70
1:E:370:LYS:HB3	1:E:375:TYR:CE1	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:VAL:CA	1:D:125:ILE:HB	2.22	0.69
1:D:201:THR:HG22	1:D:202:PRO:CD	2.20	0.69
1:A:216:ARG:HA	1:A:219:THR:O	1.92	0.69
1:A:347:HIS:CA	1:E:176:LYS:CB	2.70	0.69
1:C:55:ILE:HG22	1:C:57:GLN:OE1	1.92	0.69
1:C:176:LYS:CB	1:D:347:HIS:CA	2.70	0.69
1:C:181:VAL:HG21	1:D:379:TYR:CB	2.23	0.69
1:D:382:ASN:CB	1:D:385:ILE:HG12	2.21	0.69
1:E:39:GLN:HB3	1:E:67:ILE:CG2	2.22	0.69
1:E:208:LEU:HD21	1:E:265:ARG:HH22	1.57	0.69
1:E:216:ARG:HA	1:E:219:THR:O	1.92	0.69
1:A:124:VAL:CA	1:A:125:ILE:HB	2.22	0.69
1:A:401:THR:HG23	1:A:402:LEU:H	0.54	0.69
1:B:72:VAL:HG11	1:B:101:ILE:HD13	1.75	0.69
1:D:91:LYS:HB2	1:D:93:ARG:HB2	1.74	0.69
1:D:216:ARG:HA	1:D:219:THR:O	1.92	0.69
1:A:132:ALA:H	1:A:133:ASN:CG	2.01	0.69
1:A:382:ASN:CB	1:A:385:ILE:HG12	2.22	0.69
1:B:124:VAL:CA	1:B:125:ILE:HB	2.22	0.69
1:B:285:LEU:HB2	1:B:431:VAL:HG22	1.75	0.69
1:B:436:LEU:CA	1:B:439:HIS:CE1	2.61	0.69
1:C:220:THR:C	1:C:445:GLU:HB2	2.17	0.69
1:E:55:ILE:HG22	1:E:57:GLN:NE2	2.05	0.69
1:A:132:ALA:H	1:A:133:ASN:HA	1.55	0.69
1:A:176:LYS:HB3	1:B:347:HIS:C	2.18	0.69
1:B:216:ARG:HA	1:B:219:THR:O	1.92	0.69
1:C:133:ASN:H	1:C:134:PRO:CD	2.05	0.69
1:D:91:LYS:HB2	1:D:93:ARG:CB	2.22	0.69
1:E:221:ILE:CA	1:E:445:GLU:HG2	2.22	0.69
1:A:347:HIS:C	1:E:176:LYS:HB3	2.17	0.69
1:C:132:ALA:H	1:C:133:ASN:CG	2.01	0.69
1:A:51:ASN:O	1:A:52:LYS:HB3	1.92	0.69
1:A:176:LYS:HG3	1:B:346:TYR:HB2	1.73	0.69
1:A:334:PRO:HB3	1:A:427:MET:HE3	1.73	0.69
1:B:69:CYS:HA	1:B:101:ILE:HG12	1.74	0.69
1:B:132:ALA:H	1:B:133:ASN:CG	2.01	0.69
1:D:285:LEU:HB2	1:D:431:VAL:HG22	1.75	0.69
1:A:285:LEU:HG	1:A:431:VAL:HA	1.74	0.69
1:C:216:ARG:HA	1:C:219:THR:O	1.92	0.69
1:E:39:GLN:CB	1:E:67:ILE:HG21	2.23	0.69
1:E:76:LEU:HG	1:E:134:PRO:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:VAL:CA	1:E:125:ILE:HB	2.22	0.69
1:A:181:VAL:HG21	1:B:379:TYR:CB	2.22	0.69
1:C:91:LYS:HB3	1:C:93:ARG:H	1.57	0.69
1:C:368:ARG:H	1:C:401:THR:HG22	1.56	0.69
1:D:163:GLU:OE1	1:D:208:LEU:HB3	1.93	0.69
1:A:329:ILE:CG2	1:A:330:ILE:H	2.04	0.68
1:B:52:LYS:HA	1:B:195:ARG:HG2	1.75	0.68
1:D:69:CYS:HA	1:D:101:ILE:HG12	1.75	0.68
1:E:57:GLN:HG3	1:E:212:LEU:HD13	1.73	0.68
1:A:346:TYR:HA	1:E:173:ALA:HA	1.25	0.68
1:B:181:VAL:HG21	1:C:379:TYR:CB	2.23	0.68
1:C:173:ALA:CB	1:D:345:THR:CG2	2.66	0.68
1:C:181:VAL:N	1:C:182:GLN:HB3	2.08	0.68
1:C:301:LEU:HD22	1:C:360:ILE:O	1.92	0.68
1:D:301:LEU:HD22	1:D:360:ILE:O	1.92	0.68
1:A:345:THR:CB	1:E:174:ARG:HH12	2.05	0.68
1:E:329:ILE:CG2	1:E:330:ILE:H	2.03	0.68
1:C:91:LYS:HB2	1:C:93:ARG:CB	2.23	0.68
1:D:132:ALA:H	1:D:133:ASN:CG	2.02	0.68
1:E:164:ILE:HG22	1:E:203:GLN:HG3	1.74	0.68
1:C:173:ALA:CB	1:D:346:TYR:HB3	2.23	0.68
1:C:221:ILE:HB	1:C:222:ILE:HG13	1.74	0.68
1:D:72:VAL:HG11	1:D:101:ILE:HD13	1.75	0.68
1:D:322:TRP:CD1	1:D:456:ARG:HB2	2.29	0.68
1:A:52:LYS:HA	1:A:195:ARG:HG2	1.75	0.68
1:B:72:VAL:HG13	1:B:85:LEU:HD13	1.74	0.68
1:D:56:LEU:CD2	1:D:222:ILE:CG2	2.72	0.68
1:E:52:LYS:HA	1:E:195:ARG:HG2	1.76	0.68
1:E:311:LEU:HD23	1:E:368:ARG:HG2	1.76	0.68
1:A:69:CYS:HA	1:A:101:ILE:HG12	1.74	0.68
1:B:301:LEU:HD22	1:B:360:ILE:O	1.92	0.68
1:D:82:LEU:O	1:D:83:LYS:HB3	1.93	0.68
1:E:221:ILE:HB	1:E:222:ILE:CG1	2.22	0.68
1:A:272:ARG:CB	1:A:441:ASN:HB2	2.24	0.68
1:C:370:LYS:HG2	1:C:401:THR:OG1	1.94	0.68
1:D:83:LYS:HE3	1:D:156:ILE:HG21	1.76	0.68
1:D:181:VAL:HG21	1:E:379:TYR:CB	2.24	0.68
1:D:204:THR:CG2	1:D:205:GLU:H	2.02	0.68
1:D:415:GLN:O	1:D:418:VAL:HG12	1.93	0.68
1:E:132:ALA:H	1:E:133:ASN:CG	2.02	0.68
1:D:177:LEU:CB	1:E:347:HIS:CG	2.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:ILE:HB	1:E:194:SER:HB3	1.76	0.67
1:A:181:VAL:N	1:A:182:GLN:HB3	2.08	0.67
1:A:368:ARG:HB2	1:A:378:LEU:CD2	2.24	0.67
1:B:173:ALA:CB	1:C:346:TYR:HB3	2.21	0.67
1:C:84:ILE:CG2	1:C:154:ALA:HA	2.24	0.67
1:C:221:ILE:CA	1:C:445:GLU:HG2	2.25	0.67
1:C:379:TYR:HB3	1:C:385:ILE:HG21	1.76	0.67
1:C:415:GLN:O	1:C:418:VAL:HG12	1.94	0.67
1:C:334:PRO:HB3	1:C:427:MET:HE3	1.76	0.67
1:E:314:GLU:HG2	1:E:314:GLU:O	1.93	0.67
1:C:83:LYS:HZ3	1:C:193:SER:H	0.74	0.67
1:D:39:GLN:CB	1:D:67:ILE:HG12	2.24	0.67
1:A:314:GLU:O	1:A:314:GLU:HG2	1.94	0.67
1:C:437:LEU:HD23	1:C:458:CYS:SG	2.33	0.67
1:A:173:ALA:C	1:B:346:TYR:CA	2.44	0.67
1:A:376:ALA:HA	1:E:181:VAL:CB	2.19	0.67
1:D:73:VAL:CG2	1:D:105:ILE:HG13	2.25	0.67
1:E:285:LEU:HB2	1:E:431:VAL:HG22	1.75	0.67
1:C:124:VAL:CA	1:C:125:ILE:HB	2.24	0.67
1:D:91:LYS:HB3	1:D:93:ARG:H	1.59	0.67
1:D:173:ALA:CB	1:E:346:TYR:CG	2.78	0.67
1:D:417:VAL:HG23	1:D:465:MET:HE3	1.75	0.67
1:B:91:LYS:HB3	1:B:93:ARG:N	2.10	0.67
1:B:314:GLU:HG2	1:B:314:GLU:O	1.94	0.67
1:B:334:PRO:HB3	1:B:427:MET:HE3	1.75	0.67
1:C:118:PRO:HD2	1:C:128:ASP:HA	1.77	0.67
1:E:190:PRO:C	1:E:192:PRO:HD2	2.20	0.67
1:A:84:ILE:CG2	1:A:154:ALA:HA	2.24	0.67
1:B:329:ILE:CG2	1:B:330:ILE:H	2.06	0.67
1:C:52:LYS:HA	1:C:195:ARG:HG2	1.75	0.67
1:C:77:TRP:HE1	1:C:105:ILE:CG1	1.91	0.67
1:D:314:GLU:O	1:D:314:GLU:HG2	1.93	0.67
1:E:20:VAL:O	1:E:22:PHE:CD2	2.48	0.67
1:E:72:VAL:HG11	1:E:101:ILE:HD13	1.75	0.67
1:A:329:ILE:CG2	1:A:330:ILE:N	2.58	0.66
1:B:254:GLU:CG	1:B:255:ALA:N	2.45	0.66
1:B:280:LYS:NZ	1:B:437:LEU:CB	2.58	0.66
1:B:370:LYS:HG3	1:B:401:THR:OG1	1.95	0.66
1:C:291:PRO:HG2	1:C:295:ASP:CB	2.24	0.66
1:E:415:GLN:O	1:E:418:VAL:HG12	1.94	0.66
1:A:415:GLN:O	1:A:418:VAL:HG12	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:ILE:HB	1:D:194:SER:HB3	1.77	0.66
1:A:39:GLN:CB	1:A:67:ILE:HG12	2.24	0.66
1:D:222:ILE:HA	1:D:445:GLU:OE2	1.96	0.66
1:E:378:LEU:HD11	1:E:401:THR:HG1	1.60	0.66
1:D:273:GLU:CG	1:D:280:LYS:HZ1	1.99	0.66
1:E:370:LYS:HZ2	1:E:403:GLU:HA	1.58	0.66
1:C:83:LYS:HE2	1:C:192:PRO:CA	2.10	0.66
1:C:85:LEU:HD12	1:C:156:ILE:HG21	1.77	0.66
1:C:181:VAL:HG21	1:D:379:TYR:HB2	1.78	0.66
1:A:20:VAL:O	1:A:22:PHE:CD2	2.48	0.66
1:A:190:PRO:C	1:A:192:PRO:HD2	2.20	0.66
1:A:348:ASP:C	1:A:348:ASP:OD1	2.38	0.66
1:A:414:VAL:CA	1:A:417:VAL:HG12	2.25	0.66
1:C:14:GLN:NE2	1:C:40:ILE:HG12	2.11	0.66
1:E:145:ILE:HB	1:E:174:ARG:HG3	1.76	0.66
1:A:14:GLN:NE2	1:A:40:ILE:HG12	2.10	0.66
1:C:51:ASN:O	1:C:52:LYS:HB3	1.95	0.66
1:C:329:ILE:CG2	1:C:330:ILE:H	2.05	0.66
1:E:118:PRO:HD2	1:E:128:ASP:HA	1.78	0.66
1:E:91:LYS:HB2	1:E:93:ARG:HB2	1.78	0.66
1:C:346:TYR:CD2	1:C:349:CYS:HB2	2.31	0.66
1:E:322:TRP:CD1	1:E:456:ARG:HB2	2.30	0.66
1:A:72:VAL:HG11	1:A:101:ILE:HD13	1.78	0.65
1:A:118:PRO:HD2	1:A:128:ASP:HA	1.77	0.65
1:A:298:LYS:HZ2	1:A:430:LYS:HA	1.59	0.65
1:C:351:ASN:ND2	1:C:377:VAL:HA	2.12	0.65
1:C:437:LEU:HD22	1:C:458:CYS:SG	2.35	0.65
1:D:51:ASN:O	1:D:52:LYS:HB3	1.95	0.65
1:E:291:PRO:CG	1:E:295:ASP:HB3	2.23	0.65
1:A:291:PRO:HD2	1:A:295:ASP:O	1.96	0.65
1:B:51:ASN:O	1:B:52:LYS:HB3	1.93	0.65
1:B:220:THR:CA	1:B:445:GLU:HB3	2.27	0.65
1:C:314:GLU:O	1:C:314:GLU:HG2	1.94	0.65
1:D:220:THR:CA	1:D:445:GLU:HB2	2.27	0.65
1:A:280:LYS:NZ	1:A:437:LEU:CB	2.60	0.65
1:D:145:ILE:HB	1:D:174:ARG:HG3	1.77	0.65
1:D:181:VAL:CG1	1:E:376:ALA:HA	2.26	0.65
1:E:51:ASN:O	1:E:52:LYS:HB3	1.95	0.65
1:E:348:ASP:C	1:E:348:ASP:OD1	2.37	0.65
1:A:132:ALA:N	1:A:133:ASN:CA	2.59	0.65
1:D:362:VAL:O	1:D:362:VAL:CG1	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:348:ASP:OD1	1:E:349:CYS:N	2.30	0.65
1:A:85:LEU:HD12	1:A:156:ILE:HG21	1.78	0.65
1:A:235:LEU:CD2	1:A:245:LEU:CB	2.57	0.65
1:E:84:ILE:CG2	1:E:153:ARG:O	2.44	0.65
1:A:56:LEU:CD2	1:A:222:ILE:HG23	2.26	0.65
1:A:73:VAL:HG23	1:A:105:ILE:CG1	2.27	0.65
1:B:159:ALA:CB	1:B:198:TYR:CD1	2.79	0.65
1:B:274:ARG:HE	1:B:414:VAL:CG1	2.10	0.65
1:B:375:TYR:O	1:B:378:LEU:HB2	1.97	0.65
1:C:132:ALA:H	1:C:133:ASN:CA	2.10	0.65
1:D:176:LYS:CB	1:E:347:HIS:H	2.06	0.65
1:C:76:LEU:HB2	1:C:136:HIS:HE1	1.60	0.65
1:A:351:ASN:ND2	1:A:377:VAL:HA	2.11	0.65
1:B:84:ILE:CG2	1:B:154:ALA:HA	2.26	0.65
1:B:91:LYS:HB2	1:B:93:ARG:CB	2.26	0.65
1:B:149:LEU:HD23	1:B:174:ARG:HG3	1.79	0.65
1:B:156:ILE:HB	1:B:194:SER:HB3	1.78	0.65
1:C:159:ALA:HB3	1:C:198:TYR:CE1	2.32	0.65
1:D:190:PRO:HB2	1:D:192:PRO:CD	2.25	0.65
1:E:57:GLN:O	1:E:223:TRP:HD1	1.78	0.65
1:C:132:ALA:N	1:C:133:ASN:CA	2.59	0.65
1:C:375:TYR:O	1:C:378:LEU:HB2	1.97	0.65
1:B:323:LEU:HB3	1:B:339:LYS:HB2	1.79	0.64
1:B:329:ILE:CG2	1:B:330:ILE:N	2.60	0.64
1:C:172:GLY:O	1:C:176:LYS:HD3	1.97	0.64
1:E:133:ASN:H	1:E:134:PRO:CD	2.07	0.64
1:B:128:ASP:O	1:B:135:ASP:HB3	1.97	0.64
1:B:181:VAL:HG21	1:C:379:TYR:HB2	1.79	0.64
1:D:117:ARG:HB3	1:D:118:PRO:HD3	1.79	0.64
1:E:132:ALA:N	1:E:133:ASN:CA	2.59	0.64
1:A:83:LYS:CD	1:A:193:SER:O	2.44	0.64
1:B:378:LEU:CD1	1:B:401:THR:OG1	2.42	0.64
1:D:272:ARG:CB	1:D:441:ASN:HB2	2.22	0.64
1:D:375:TYR:O	1:D:378:LEU:HB2	1.97	0.64
1:E:119:GLY:HA2	1:E:127:PHE:CD2	2.32	0.64
1:A:309:ALA:CB	1:A:358:GLN:HE22	2.11	0.64
1:C:176:LYS:C	1:D:347:HIS:CB	2.66	0.64
1:D:132:ALA:H	1:D:133:ASN:CA	2.10	0.64
1:D:181:VAL:O	1:D:181:VAL:HG12	1.96	0.64
1:D:347:HIS:HE1	1:D:376:ALA:CB	2.09	0.64
1:C:190:PRO:HB2	1:C:192:PRO:CD	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:362:VAL:O	1:C:362:VAL:CG1	2.45	0.64
1:E:10:LEU:HD12	1:E:78:ARG:HD2	1.80	0.64
1:E:309:ALA:CB	1:E:358:GLN:HE22	2.11	0.64
1:E:362:VAL:O	1:E:362:VAL:CG1	2.45	0.64
1:E:375:TYR:O	1:E:378:LEU:HB2	1.98	0.64
1:A:181:VAL:HG21	1:B:379:TYR:HB2	1.80	0.64
1:C:159:ALA:HB2	1:C:198:TYR:HE1	1.62	0.64
1:C:370:LYS:HB3	1:C:375:TYR:CE1	2.32	0.64
1:C:382:ASN:HB3	1:C:385:ILE:CG1	2.27	0.64
1:E:417:VAL:HG23	1:E:465:MET:HE3	1.80	0.64
1:B:10:LEU:HD12	1:B:78:ARG:HD2	1.80	0.64
1:D:235:LEU:HD11	1:D:241:LEU:HD23	1.75	0.64
1:E:132:ALA:H	1:E:133:ASN:CA	2.10	0.64
1:E:382:ASN:HB3	1:E:385:ILE:CG1	2.27	0.64
1:A:370:LYS:HG3	1:A:378:LEU:HD11	1.80	0.64
1:B:91:LYS:HB2	1:B:93:ARG:HB2	1.79	0.64
1:C:177:LEU:N	1:D:347:HIS:HB3	2.05	0.64
1:C:414:VAL:CA	1:C:417:VAL:HG12	2.28	0.64
1:E:351:ASN:ND2	1:E:377:VAL:HA	2.12	0.64
1:B:132:ALA:H	1:B:133:ASN:CA	2.10	0.64
1:A:347:HIS:CB	1:E:176:LYS:HB3	2.20	0.63
1:E:223:TRP:NE1	1:E:265:ARG:HB3	2.05	0.63
1:B:303:LEU:HG	1:B:304:ARG:HG3	1.79	0.63
1:E:226:LEU:HD13	1:E:263:PRO:HB3	1.79	0.63
1:B:132:ALA:N	1:B:133:ASN:CA	2.59	0.63
1:A:347:HIS:CE1	1:E:177:LEU:HA	2.34	0.63
1:D:176:LYS:CB	1:E:347:HIS:CA	2.70	0.63
1:D:433:SER:C	1:D:434:PRO:CD	2.65	0.63
1:E:223:TRP:HE1	1:E:265:ARG:CB	2.06	0.63
1:A:132:ALA:H	1:A:133:ASN:CA	2.10	0.63
1:A:382:ASN:HB3	1:A:385:ILE:CG1	2.27	0.63
1:D:351:ASN:ND2	1:D:377:VAL:HA	2.11	0.63
1:E:182:GLN:NE2	1:E:185:ALA:CB	2.40	0.63
1:A:10:LEU:HD12	1:A:78:ARG:HD2	1.81	0.63
1:A:362:VAL:O	1:A:362:VAL:CG1	2.46	0.63
1:D:382:ASN:HB3	1:D:385:ILE:CG1	2.28	0.63
1:A:280:LYS:HE2	1:A:438:LYS:CA	2.20	0.63
1:B:294:SER:HB3	1:B:341:ASP:HB3	1.81	0.63
1:C:72:VAL:HG11	1:C:101:ILE:HD13	1.80	0.63
1:E:208:LEU:HD21	1:E:265:ARG:HH21	1.63	0.63
1:A:83:LYS:HG3	1:A:155:ASP:HB3	1.76	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:ASN:H	1:B:134:PRO:CD	2.08	0.62
1:D:117:ARG:HB3	1:D:118:PRO:CD	2.29	0.62
1:D:226:LEU:HB2	1:D:263:PRO:HB3	1.81	0.62
1:E:196:VAL:CG1	1:E:198:TYR:CE1	2.82	0.62
1:B:351:ASN:ND2	1:B:377:VAL:HA	2.11	0.62
1:E:262:ASP:HB2	1:E:263:PRO:HD3	1.76	0.62
1:E:265:ARG:HD3	1:E:265:ARG:C	2.23	0.62
1:A:348:ASP:OD1	1:A:349:CYS:N	2.33	0.62
1:C:161:ASP:HB3	1:C:164:ILE:HG22	1.82	0.62
1:A:346:TYR:HB2	1:E:176:LYS:HG3	1.81	0.62
1:D:162:VAL:HG21	1:D:198:TYR:HB3	1.81	0.62
1:A:226:LEU:HB2	1:A:263:PRO:HB3	1.81	0.62
1:B:362:VAL:O	1:B:362:VAL:CG1	2.47	0.62
1:C:173:ALA:O	1:D:345:THR:O	2.17	0.62
1:C:346:TYR:HE2	1:C:349:CYS:HB3	1.51	0.62
1:D:132:ALA:N	1:D:133:ASN:CA	2.59	0.62
1:A:156:ILE:HB	1:A:194:SER:HB3	1.79	0.62
1:B:73:VAL:CG2	1:B:105:ILE:CG1	2.68	0.62
1:B:226:LEU:HB2	1:B:263:PRO:HB3	1.82	0.62
1:B:346:TYR:HD1	1:B:349:CYS:H	1.42	0.62
1:B:379:TYR:HB3	1:B:385:ILE:HG21	1.82	0.62
1:C:252:ASN:CB	1:C:253:PRO:CD	2.78	0.62
1:D:124:VAL:HB	1:D:125:ILE:CB	2.15	0.62
1:E:272:ARG:HB3	1:E:442:CYS:N	2.14	0.62
1:A:285:LEU:HD22	1:A:285:LEU:N	2.14	0.62
1:B:433:SER:HA	1:B:457:ILE:HD13	1.82	0.62
1:D:173:ALA:O	1:E:345:THR:O	2.18	0.62
1:D:181:VAL:HG21	1:E:379:TYR:HB2	1.81	0.62
1:B:163:GLU:CG	1:B:203:GLN:HB2	2.27	0.62
1:B:348:ASP:C	1:B:348:ASP:OD1	2.43	0.62
1:C:77:TRP:CZ3	1:C:114:LEU:HB2	2.35	0.62
1:E:20:VAL:O	1:E:22:PHE:CE2	2.52	0.62
1:E:72:VAL:HG13	1:E:85:LEU:HD13	1.81	0.62
1:C:309:ALA:CB	1:C:358:GLN:HE22	2.13	0.62
1:B:328:ASN:HA	1:B:333:LEU:HD22	1.81	0.62
1:D:73:VAL:HG23	1:D:105:ILE:CG1	2.30	0.62
1:E:252:ASN:CB	1:E:253:PRO:CD	2.78	0.62
1:E:414:VAL:CA	1:E:417:VAL:HG12	2.30	0.62
1:A:20:VAL:O	1:A:22:PHE:CE2	2.53	0.61
1:B:190:PRO:C	1:B:192:PRO:HD2	2.25	0.61
1:C:91:LYS:HB3	1:C:93:ARG:N	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:159:ALA:HB2	1:C:198:TYR:CE1	2.34	0.61
1:C:378:LEU:CD2	1:C:401:THR:CG2	2.78	0.61
1:A:417:VAL:HA	1:A:465:MET:HG3	1.82	0.61
1:B:77:TRP:CZ3	1:B:114:LEU:HB2	2.35	0.61
1:B:173:ALA:CB	1:C:345:THR:CG2	2.73	0.61
1:B:190:PRO:HB2	1:B:192:PRO:CD	2.31	0.61
1:C:163:GLU:CG	1:C:203:GLN:HB2	2.25	0.61
1:B:311:LEU:HB3	1:B:368:ARG:HG2	1.82	0.61
1:B:414:VAL:CA	1:B:417:VAL:HG12	2.30	0.61
1:C:226:LEU:HB2	1:C:263:PRO:HB3	1.83	0.61
1:C:309:ALA:HB3	1:C:358:GLN:HE22	1.66	0.61
1:D:75:SER:HB3	1:D:83:LYS:NZ	2.16	0.61
1:D:201:THR:HG23	1:D:202:PRO:CD	2.26	0.61
1:D:320:TYR:H	1:D:456:ARG:HG3	1.65	0.61
1:B:124:VAL:HB	1:B:125:ILE:CB	2.16	0.61
1:C:433:SER:C	1:C:434:PRO:CD	2.66	0.61
1:A:345:THR:O	1:E:173:ALA:O	2.18	0.61
1:B:39:GLN:HB3	1:B:67:ILE:HG13	1.82	0.61
1:D:79:ASP:HB3	1:D:82:LEU:O	2.00	0.61
1:E:164:ILE:HG13	1:E:165:PRO:HD3	1.82	0.61
1:A:173:ALA:CB	1:B:346:TYR:HB3	2.27	0.61
1:A:285:LEU:HB3	1:A:431:VAL:HG22	1.83	0.61
1:B:176:LYS:C	1:C:347:HIS:CB	2.66	0.61
1:D:173:ALA:CB	1:E:345:THR:CG2	2.73	0.61
1:E:259:THR:HB	1:E:260:PRO:HD3	1.82	0.61
1:E:303:LEU:HG	1:E:304:ARG:HG3	1.82	0.61
1:A:79:ASP:HB3	1:A:82:LEU:O	2.01	0.61
1:B:85:LEU:HD12	1:B:156:ILE:HG21	1.82	0.61
1:B:96:ALA:HA	1:B:99:ILE:HD12	1.82	0.61
1:B:173:ALA:O	1:C:345:THR:O	2.17	0.61
1:C:120:GLN:HA	1:C:124:VAL:O	2.01	0.61
1:E:274:ARG:HD3	1:E:414:VAL:CG1	2.30	0.61
1:A:347:HIS:HB3	1:E:176:LYS:CA	2.31	0.61
1:B:173:ALA:HB2	1:C:345:THR:HG23	1.81	0.61
1:B:460:THR:HA	1:B:463:PRO:HG2	1.83	0.61
1:D:173:ALA:HB2	1:E:345:THR:HG23	1.81	0.61
1:E:320:TYR:H	1:E:456:ARG:HG3	1.66	0.61
1:A:73:VAL:HG23	1:A:105:ILE:HG13	1.83	0.61
1:A:173:ALA:O	1:B:345:THR:O	2.18	0.61
1:A:252:ASN:CB	1:A:253:PRO:CD	2.78	0.61
1:C:156:ILE:HB	1:C:194:SER:HB3	1.79	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:105:ILE:HA	1:E:108:LEU:HD12	1.81	0.61
1:A:120:GLN:HA	1:A:124:VAL:O	2.01	0.61
1:C:259:THR:HB	1:C:260:PRO:HD3	1.82	0.61
1:C:323:LEU:HB3	1:C:339:LYS:HB2	1.83	0.61
1:D:84:ILE:CG2	1:D:153:ARG:O	2.49	0.61
1:E:235:LEU:HD12	1:E:241:LEU:HD22	1.80	0.61
1:E:328:ASN:HA	1:E:333:LEU:HD22	1.82	0.61
1:A:309:ALA:HB3	1:A:358:GLN:HE22	1.66	0.60
1:A:346:TYR:CD1	1:E:173:ALA:HB1	2.34	0.60
1:B:77:TRP:HZ3	1:B:114:LEU:CA	2.14	0.60
1:A:181:VAL:O	1:B:376:ALA:CB	2.33	0.60
1:B:252:ASN:CB	1:B:253:PRO:CD	2.78	0.60
1:B:280:LYS:HZ1	1:B:437:LEU:HB2	1.65	0.60
1:B:434:PRO:HA	1:B:437:LEU:HD12	1.84	0.60
1:C:91:LYS:C	1:C:93:ARG:N	2.59	0.60
1:D:118:PRO:CG	1:D:129:VAL:N	2.62	0.60
1:E:148:GLN:NE2	1:E:175:GLU:HG2	2.15	0.60
1:C:346:TYR:HE2	1:C:349:CYS:C	2.08	0.60
1:D:459:ASP:O	1:D:463:PRO:HD2	2.01	0.60
1:A:196:VAL:HG13	1:A:198:TYR:CE1	2.35	0.60
1:C:230:THR:HA	1:C:233:GLU:HG3	1.83	0.60
1:D:120:GLN:HA	1:D:124:VAL:O	2.01	0.60
1:D:303:LEU:HG	1:D:304:ARG:HG3	1.84	0.60
1:D:309:ALA:CB	1:D:358:GLN:HE22	2.14	0.60
1:E:14:GLN:NE2	1:E:40:ILE:HG12	2.16	0.60
1:A:459:ASP:O	1:A:463:PRO:CD	2.49	0.60
1:B:368:ARG:NH2	1:B:381:LEU:HD13	2.17	0.60
1:C:96:ALA:HA	1:C:99:ILE:HD12	1.83	0.60
1:E:301:LEU:HB2	1:E:361:LEU:HD23	1.83	0.60
1:A:119:GLY:HA2	1:A:127:PHE:CD1	2.37	0.60
1:A:370:LYS:O	1:A:375:TYR:CE1	2.54	0.60
1:B:172:GLY:O	1:B:176:LYS:HD2	2.02	0.60
1:E:56:LEU:HD23	1:E:222:ILE:HB	1.83	0.60
1:E:79:ASP:HB3	1:E:82:LEU:O	2.00	0.60
1:E:235:LEU:CD1	1:E:241:LEU:CD2	2.65	0.60
1:A:56:LEU:CD2	1:A:222:ILE:CG2	2.80	0.60
1:A:73:VAL:CG2	1:A:105:ILE:HG13	2.30	0.60
1:A:173:ALA:HB2	1:B:345:THR:HG23	1.81	0.60
1:B:120:GLN:HA	1:B:124:VAL:O	2.01	0.60
1:B:272:ARG:HB3	1:B:442:CYS:HB2	1.82	0.60
1:D:156:ILE:CB	1:D:194:SER:HB3	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:ILE:CB	1:E:194:SER:HB3	2.31	0.60
1:A:370:LYS:C	1:A:375:TYR:CE1	2.79	0.60
1:C:417:VAL:HA	1:C:465:MET:HG3	1.83	0.60
1:E:329:ILE:CG2	1:E:330:ILE:N	2.57	0.60
1:E:459:ASP:O	1:E:463:PRO:CD	2.50	0.60
1:C:459:ASP:O	1:C:463:PRO:HD2	2.02	0.60
1:D:252:ASN:CB	1:D:253:PRO:CD	2.80	0.60
1:B:84:ILE:HG13	1:B:135:ASP:OD1	2.02	0.59
1:B:91:LYS:C	1:B:93:ARG:N	2.59	0.59
1:D:118:PRO:HG2	1:D:129:VAL:H	1.67	0.59
1:D:414:VAL:O	1:D:417:VAL:HG12	2.01	0.59
1:A:163:GLU:CG	1:A:203:GLN:HB2	2.27	0.59
1:C:346:TYR:CE2	1:C:349:CYS:N	2.70	0.59
1:D:73:VAL:HG23	1:D:105:ILE:HG13	1.82	0.59
1:D:91:LYS:C	1:D:93:ARG:N	2.59	0.59
1:D:221:ILE:CA	1:D:445:GLU:HG2	2.33	0.59
1:D:414:VAL:CA	1:D:417:VAL:HG12	2.32	0.59
1:E:187:LEU:HB3	1:E:192:PRO:HB2	1.84	0.59
1:A:177:LEU:CB	1:B:347:HIS:CD2	2.85	0.59
1:C:77:TRP:HZ3	1:C:114:LEU:CA	2.15	0.59
1:C:459:ASP:O	1:C:463:PRO:CD	2.49	0.59
1:D:235:LEU:HD21	1:D:245:LEU:HB3	1.84	0.59
1:E:378:LEU:CD2	1:E:401:THR:CG2	2.78	0.59
1:A:56:LEU:HD13	1:A:199:LEU:HD12	1.84	0.59
1:A:177:LEU:N	1:B:347:HIS:CG	2.70	0.59
1:A:272:ARG:HB3	1:A:442:CYS:N	2.16	0.59
1:B:459:ASP:O	1:B:463:PRO:CD	2.50	0.59
1:C:187:LEU:HB3	1:C:192:PRO:HB2	1.83	0.59
1:D:91:LYS:HB3	1:D:93:ARG:N	2.16	0.59
1:E:77:TRP:HZ3	1:E:114:LEU:CA	2.15	0.59
1:A:433:SER:C	1:A:434:PRO:CD	2.65	0.59
1:B:221:ILE:C	1:B:445:GLU:HG3	2.28	0.59
1:B:414:VAL:O	1:B:417:VAL:HG12	2.02	0.59
1:C:84:ILE:HG22	1:C:153:ARG:O	2.03	0.59
1:D:460:THR:HA	1:D:463:PRO:HG2	1.84	0.59
1:B:280:LYS:HZ3	1:B:437:LEU:CB	2.13	0.59
1:E:120:GLN:HA	1:E:124:VAL:O	2.01	0.59
1:A:176:LYS:CG	1:B:346:TYR:HB2	2.33	0.59
1:A:376:ALA:CB	1:E:181:VAL:O	2.33	0.59
1:B:84:ILE:HG22	1:B:153:ARG:O	2.03	0.59
1:B:181:VAL:O	1:C:376:ALA:CB	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LEU:HB3	1:B:192:PRO:HB2	1.84	0.59
1:C:100:PHE:O	1:C:104:ILE:HG12	2.03	0.59
1:A:322:TRP:CD1	1:A:456:ARG:HB2	2.36	0.59
1:B:51:ASN:CB	1:B:54:PHE:CZ	2.86	0.59
1:C:46:LEU:HD22	1:C:197:ILE:HG12	1.84	0.59
1:C:79:ASP:HB3	1:C:82:LEU:O	2.03	0.59
1:C:173:ALA:HB2	1:D:345:THR:HG23	1.77	0.59
1:D:163:GLU:CG	1:D:203:GLN:HB2	2.28	0.59
1:E:414:VAL:O	1:E:417:VAL:HG12	2.02	0.59
1:A:176:LYS:HB3	1:B:347:HIS:CB	2.21	0.59
1:C:66:PHE:O	1:C:69:CYS:SG	2.61	0.59
1:D:459:ASP:O	1:D:463:PRO:CD	2.50	0.59
1:E:226:LEU:HB2	1:E:263:PRO:HB3	1.85	0.59
1:A:89:ALA:HB3	1:A:94:ALA:HB2	1.84	0.59
1:B:433:SER:C	1:B:434:PRO:CD	2.66	0.59
1:C:187:LEU:O	1:C:192:PRO:HD2	2.02	0.59
1:D:59:PHE:CD2	1:D:60:ARG:O	2.56	0.59
1:E:89:ALA:HB3	1:E:94:ALA:HB2	1.84	0.59
1:E:96:ALA:HA	1:E:99:ILE:HD12	1.84	0.59
1:E:326:ARG:HD3	1:E:333:LEU:HB3	1.84	0.59
1:A:414:VAL:HA	1:A:417:VAL:CG1	2.31	0.58
1:B:14:GLN:NE2	1:B:40:ILE:HG12	2.18	0.58
1:B:156:ILE:CB	1:B:194:SER:HB3	2.32	0.58
1:B:181:VAL:O	1:B:181:VAL:HG12	2.03	0.58
1:D:173:ALA:HB3	1:E:345:THR:C	2.22	0.58
1:D:196:VAL:CG1	1:D:198:TYR:CZ	2.86	0.58
1:D:346:TYR:CE1	1:D:349:CYS:N	2.71	0.58
1:A:259:THR:HB	1:A:260:PRO:HD3	1.84	0.58
1:A:303:LEU:HG	1:A:304:ARG:HG3	1.85	0.58
1:A:459:ASP:O	1:A:463:PRO:HD2	2.02	0.58
1:C:73:VAL:CG2	1:C:105:ILE:CG1	2.68	0.58
1:C:89:ALA:HB3	1:C:94:ALA:HB2	1.84	0.58
1:E:221:ILE:CA	1:E:222:ILE:HG12	2.32	0.58
1:A:84:ILE:HG22	1:A:153:ARG:O	2.03	0.58
1:B:272:ARG:CB	1:B:441:ASN:HB2	2.18	0.58
1:C:172:GLY:O	1:C:176:LYS:CD	2.51	0.58
1:C:177:LEU:HB3	1:D:347:HIS:CG	2.23	0.58
1:D:85:LEU:HD12	1:D:156:ILE:HG21	1.84	0.58
1:B:100:PHE:O	1:B:104:ILE:HG12	2.03	0.58
1:B:181:VAL:CG1	1:C:376:ALA:HA	2.33	0.58
1:B:291:PRO:HD2	1:B:295:ASP:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:ARG:HB2	1:B:378:LEU:HD21	1.85	0.58
1:B:382:ASN:HB3	1:B:385:ILE:CG1	2.33	0.58
1:C:87:VAL:HA	1:C:158:ILE:O	2.04	0.58
1:C:156:ILE:CB	1:C:194:SER:HB3	2.33	0.58
1:D:84:ILE:HG12	1:D:154:ALA:HA	1.85	0.58
1:E:459:ASP:O	1:E:463:PRO:HD2	2.03	0.58
1:B:10:LEU:HD23	1:B:11:VAL:HG13	1.85	0.58
1:B:378:LEU:HD13	1:B:400:LYS:O	2.04	0.58
1:C:173:ALA:HB3	1:D:345:THR:C	2.22	0.58
1:D:177:LEU:N	1:E:347:HIS:CG	2.71	0.58
1:D:187:LEU:HB3	1:D:192:PRO:HB2	1.84	0.58
1:A:82:LEU:O	1:A:134:PRO:HG3	2.04	0.58
1:A:187:LEU:HB3	1:A:192:PRO:HB2	1.83	0.58
1:B:89:ALA:HB3	1:B:94:ALA:HB2	1.84	0.58
1:B:232:GLU:HB3	1:B:246:ARG:HG2	1.85	0.58
1:B:368:ARG:CB	1:B:401:THR:HG21	2.33	0.58
1:D:346:TYR:HE1	1:D:349:CYS:C	2.12	0.58
1:E:434:PRO:HA	1:E:437:LEU:HD12	1.86	0.58
1:A:256:LEU:O	1:A:260:PRO:HD3	2.03	0.58
1:B:79:ASP:HB3	1:B:82:LEU:O	2.04	0.58
1:D:196:VAL:CG1	1:D:198:TYR:CE1	2.86	0.58
1:E:66:PHE:O	1:E:69:CYS:SG	2.61	0.58
1:E:141:LYS:HZ3	1:E:171:MET:HB2	1.69	0.58
1:A:189:LYS:HB2	1:A:190:PRO:HD3	1.86	0.58
1:A:320:TYR:H	1:A:456:ARG:HG3	1.69	0.58
1:A:347:HIS:CG	1:E:177:LEU:N	2.72	0.58
1:B:59:PHE:CZ	1:B:62:ILE:HB	2.37	0.58
1:B:87:VAL:HA	1:B:158:ILE:O	2.04	0.58
1:B:259:THR:HB	1:B:260:PRO:HD3	1.86	0.58
1:C:285:LEU:CB	1:C:431:VAL:HG22	2.34	0.58
1:C:294:SER:HB2	1:C:340:GLY:C	2.29	0.58
1:D:87:VAL:HA	1:D:158:ILE:O	2.04	0.58
1:D:89:ALA:HB3	1:D:94:ALA:HB2	1.84	0.58
1:D:176:LYS:HB3	1:E:347:HIS:HB2	1.71	0.58
1:D:187:LEU:O	1:D:192:PRO:HD2	2.03	0.58
1:D:223:TRP:N	1:D:445:GLU:OE2	2.37	0.58
1:D:323:LEU:HB3	1:D:339:LYS:HB2	1.84	0.58
1:E:91:LYS:C	1:E:93:ARG:N	2.59	0.58
1:E:460:THR:HA	1:E:463:PRO:HG2	1.84	0.58
1:A:51:ASN:CB	1:A:54:PHE:CZ	2.87	0.58
1:A:294:SER:HB2	1:A:340:GLY:C	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:PHE:O	1:B:69:CYS:SG	2.61	0.58
1:D:10:LEU:HD12	1:D:78:ARG:HD2	1.85	0.58
1:D:449:ALA:HB2	1:D:455:MET:HB3	1.86	0.58
1:B:57:GLN:HG2	1:B:212:LEU:HD13	1.85	0.58
1:C:55:ILE:CG2	1:C:57:GLN:OE1	2.52	0.58
1:C:133:ASN:N	1:C:134:PRO:HD2	2.12	0.58
1:C:346:TYR:CD2	1:C:349:CYS:CA	2.87	0.58
1:D:204:THR:HG22	1:D:205:GLU:N	2.08	0.58
1:E:87:VAL:HA	1:E:158:ILE:O	2.04	0.58
1:C:417:VAL:HG23	1:C:465:MET:HE3	1.85	0.57
1:D:77:TRP:HE1	1:D:105:ILE:HG12	1.69	0.57
1:E:46:LEU:HD22	1:E:197:ILE:HG12	1.85	0.57
1:A:345:THR:C	1:E:173:ALA:HB3	2.22	0.57
1:B:177:LEU:N	1:C:347:HIS:CG	2.70	0.57
1:C:368:ARG:CB	1:C:401:THR:HG21	2.34	0.57
1:D:84:ILE:HG23	1:D:153:ARG:O	2.04	0.57
1:D:272:ARG:HB3	1:D:442:CYS:HB2	1.85	0.57
1:D:370:LYS:O	1:D:375:TYR:CE1	2.57	0.57
1:D:441:ASN:C	1:D:447:ILE:HG23	2.28	0.57
1:A:87:VAL:HA	1:A:158:ILE:O	2.04	0.57
1:A:173:ALA:HB3	1:B:345:THR:C	2.22	0.57
1:D:66:PHE:O	1:D:69:CYS:SG	2.61	0.57
1:D:346:TYR:HB2	1:D:348:ASP:HB3	1.87	0.57
1:E:294:SER:HB2	1:E:340:GLY:C	2.29	0.57
1:B:230:THR:HA	1:B:233:GLU:HG3	1.85	0.57
1:B:320:TYR:H	1:B:456:ARG:HG3	1.69	0.57
1:C:181:VAL:CG1	1:D:376:ALA:HA	2.34	0.57
1:C:460:THR:HA	1:C:463:PRO:HG2	1.86	0.57
1:D:259:THR:HB	1:D:260:PRO:HD3	1.85	0.57
1:E:83:LYS:HG2	1:E:155:ASP:CB	2.14	0.57
1:E:220:THR:HB	1:E:445:GLU:HB2	1.86	0.57
1:A:156:ILE:CB	1:A:194:SER:HB3	2.33	0.57
1:A:181:VAL:O	1:A:181:VAL:HG12	2.05	0.57
1:C:119:GLY:HA2	1:C:127:PHE:CD1	2.39	0.57
1:C:177:LEU:N	1:D:347:HIS:CG	2.71	0.57
1:E:42:MET:HE2	1:E:224:PRO:HG2	1.86	0.57
1:A:77:TRP:HE1	1:A:105:ILE:HG12	1.69	0.57
1:A:468:HIS:CA	1:A:473:ARG:HD3	2.31	0.57
1:B:21:ALA:O	1:B:33:PRO:CD	2.45	0.57
1:B:280:LYS:HE2	1:B:438:LYS:CA	2.25	0.57
1:B:285:LEU:CB	1:B:431:VAL:HG22	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:SER:HB2	1:B:340:GLY:C	2.29	0.57
1:B:375:TYR:HA	1:B:378:LEU:HD12	1.86	0.57
1:B:470:LEU:HD21	1:B:472:ILE:HD12	1.85	0.57
1:D:51:ASN:CB	1:D:54:PHE:CZ	2.88	0.57
1:A:186:ALA:O	1:A:190:PRO:HD3	2.05	0.57
1:B:348:ASP:OD1	1:B:349:CYS:N	2.38	0.57
1:C:220:THR:CB	1:C:445:GLU:HB2	2.35	0.57
1:C:276:LEU:HD23	1:C:278:TYR:HB2	1.87	0.57
1:C:414:VAL:O	1:C:417:VAL:HG12	2.04	0.57
1:D:468:HIS:CA	1:D:473:ARG:HD3	2.32	0.57
1:A:66:PHE:O	1:A:69:CYS:SG	2.61	0.57
1:A:193:SER:O	1:A:194:SER:HB2	2.05	0.57
1:B:176:LYS:CD	1:C:348:ASP:OD2	2.49	0.57
1:B:262:ASP:HB2	1:B:263:PRO:HD3	1.80	0.57
1:C:64:LYS:HA	1:C:67:ILE:HD12	1.87	0.57
1:D:85:LEU:HD12	1:D:156:ILE:HD13	1.86	0.57
1:D:291:PRO:CD	1:D:295:ASP:O	2.53	0.57
1:D:291:PRO:CG	1:D:295:ASP:HB3	2.20	0.57
1:E:190:PRO:HB2	1:E:192:PRO:CD	2.34	0.57
1:E:368:ARG:HB2	1:E:378:LEU:HD21	1.85	0.57
1:E:449:ALA:HB2	1:E:455:MET:HB3	1.87	0.57
1:A:181:VAL:CG1	1:B:376:ALA:HA	2.35	0.57
1:A:388:MET:HE1	1:E:412:TRP:CH2	2.40	0.57
1:B:173:ALA:HB3	1:C:345:THR:C	2.23	0.57
1:B:435:ILE:HA	1:B:438:LYS:HG3	1.87	0.57
1:B:449:ALA:HB2	1:B:455:MET:HB3	1.86	0.57
1:C:76:LEU:CB	1:C:136:HIS:CE1	2.85	0.57
1:C:190:PRO:C	1:C:192:PRO:HD2	2.30	0.57
1:E:220:THR:CB	1:E:445:GLU:HB2	2.35	0.57
1:E:365:PRO:HA	1:E:391:GLY:O	2.05	0.57
1:A:96:ALA:HA	1:A:99:ILE:HD12	1.85	0.57
1:A:274:ARG:HD2	1:A:417:VAL:HG13	1.85	0.57
1:A:414:VAL:C	1:A:417:VAL:HG12	2.29	0.57
1:A:449:ALA:HB2	1:A:455:MET:HB3	1.87	0.57
1:B:83:LYS:HE2	1:B:192:PRO:HA	1.86	0.57
1:D:59:PHE:CE1	1:D:225:ALA:O	2.57	0.57
1:D:294:SER:HB2	1:D:340:GLY:C	2.29	0.57
1:D:311:LEU:HD23	1:D:368:ARG:HD3	1.86	0.57
1:D:319:HIS:CB	1:D:456:ARG:HE	2.18	0.57
1:A:232:GLU:HB3	1:A:246:ARG:HG2	1.86	0.56
1:B:42:MET:HG3	1:B:56:LEU:HD21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:ILE:CG2	1:B:153:ARG:O	2.52	0.56
1:D:285:LEU:CB	1:D:431:VAL:HG22	2.34	0.56
1:A:42:MET:HG3	1:A:56:LEU:HD21	1.85	0.56
1:A:378:LEU:HD13	1:A:400:LYS:O	2.06	0.56
1:B:163:GLU:OE1	1:B:208:LEU:CB	2.35	0.56
1:B:368:ARG:HH22	1:B:381:LEU:HD13	1.68	0.56
1:E:26:LEU:HD23	1:E:26:LEU:H	1.70	0.56
1:A:365:PRO:HA	1:A:391:GLY:O	2.05	0.56
1:A:470:LEU:HD21	1:A:472:ILE:HD12	1.87	0.56
1:B:365:PRO:HA	1:B:391:GLY:O	2.05	0.56
1:C:365:PRO:HA	1:C:391:GLY:O	2.05	0.56
1:C:449:ALA:HB2	1:C:455:MET:HB3	1.87	0.56
1:D:196:VAL:HG11	1:D:198:TYR:CZ	2.40	0.56
1:B:322:TRP:CD1	1:B:456:ARG:HB2	2.40	0.56
1:C:181:VAL:O	1:D:376:ALA:CB	2.33	0.56
1:D:156:ILE:CB	1:D:194:SER:CB	2.83	0.56
1:C:162:VAL:C	1:C:165:PRO:HD2	2.30	0.56
1:C:414:VAL:C	1:C:417:VAL:HG12	2.30	0.56
1:D:181:VAL:O	1:E:376:ALA:CB	2.33	0.56
1:E:115:LYS:HA	1:E:116:PRO:HD3	1.88	0.56
1:B:156:ILE:CB	1:B:194:SER:CB	2.83	0.56
1:D:365:PRO:HA	1:D:391:GLY:O	2.05	0.56
1:D:370:LYS:C	1:D:375:TYR:CE1	2.84	0.56
1:E:85:LEU:HD12	1:E:156:ILE:HD13	1.86	0.56
1:E:196:VAL:HG13	1:E:198:TYR:CE1	2.41	0.56
1:A:460:THR:HA	1:A:463:PRO:HG2	1.87	0.56
1:C:193:SER:O	1:C:194:SER:HB2	2.05	0.56
1:C:322:TRP:CD1	1:C:456:ARG:HB2	2.40	0.56
1:E:91:LYS:HB2	1:E:93:ARG:CB	2.35	0.56
1:A:156:ILE:CB	1:A:194:SER:CB	2.83	0.56
1:C:368:ARG:HB2	1:C:378:LEU:HD21	1.88	0.56
1:E:156:ILE:CB	1:E:194:SER:CB	2.83	0.56
1:A:120:GLN:O	1:A:120:GLN:CG	2.52	0.56
1:A:434:PRO:HA	1:A:437:LEU:HD12	1.87	0.56
1:B:414:VAL:C	1:B:417:VAL:HG12	2.31	0.56
1:B:441:ASN:C	1:B:447:ILE:HG23	2.31	0.56
1:C:156:ILE:CB	1:C:194:SER:CB	2.83	0.56
1:C:176:LYS:CA	1:D:347:HIS:HB3	2.36	0.56
1:C:346:TYR:HE2	1:C:349:CYS:CA	2.17	0.56
1:C:376:ALA:O	1:C:377:VAL:C	2.47	0.56
1:E:77:TRP:CZ3	1:E:114:LEU:HB2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:PHE:O	1:A:104:ILE:HG12	2.06	0.56
1:B:163:GLU:HG3	1:B:203:GLN:CB	2.29	0.56
1:C:26:LEU:HD23	1:C:26:LEU:H	1.70	0.56
1:C:370:LYS:CG	1:C:401:THR:OG1	2.54	0.56
1:B:176:LYS:CE	1:C:348:ASP:CG	2.48	0.55
1:B:193:SER:O	1:B:194:SER:HB2	2.05	0.55
1:B:298:LYS:NZ	1:B:430:LYS:HA	2.21	0.55
1:B:309:ALA:CB	1:B:358:GLN:HE22	2.18	0.55
1:D:193:SER:O	1:D:194:SER:HB2	2.06	0.55
1:A:326:ARG:O	1:A:328:ASN:OD1	2.25	0.55
1:A:469:ARG:O	1:A:469:ARG:HG2	2.05	0.55
1:C:85:LEU:HD12	1:C:156:ILE:HD13	1.88	0.55
1:C:181:VAL:O	1:C:181:VAL:HG12	2.04	0.55
1:D:190:PRO:C	1:D:192:PRO:HD2	2.31	0.55
1:E:115:LYS:HA	1:E:116:PRO:CD	2.36	0.55
1:E:144:GLY:O	1:E:171:MET:HG2	2.07	0.55
1:E:368:ARG:CB	1:E:401:THR:HG21	2.34	0.55
1:B:159:ALA:CB	1:B:198:TYR:CE1	2.90	0.55
1:D:52:LYS:HA	1:D:195:ARG:HG2	1.88	0.55
1:D:118:PRO:HG2	1:D:128:ASP:N	2.21	0.55
1:D:417:VAL:HA	1:D:465:MET:SD	2.46	0.55
1:E:64:LYS:HB2	1:E:199:LEU:HD21	1.88	0.55
1:E:177:LEU:C	1:E:177:LEU:HD12	2.31	0.55
1:C:85:LEU:HB3	1:C:136:HIS:HD1	1.71	0.55
1:C:141:LYS:HZ3	1:C:171:MET:HB2	1.70	0.55
1:C:202:PRO:HB3	1:C:265:ARG:HH12	1.71	0.55
1:D:26:LEU:H	1:D:26:LEU:HD23	1.70	0.55
1:D:347:HIS:HE1	1:D:376:ALA:HB1	1.69	0.55
1:D:381:LEU:HD23	1:D:387:LEU:HB2	1.89	0.55
1:E:376:ALA:O	1:E:377:VAL:C	2.47	0.55
1:E:414:VAL:C	1:E:417:VAL:HG12	2.31	0.55
1:A:190:PRO:HB2	1:A:192:PRO:CD	2.35	0.55
1:A:322:TRP:CH2	1:A:457:ILE:HD12	2.42	0.55
1:D:23:LEU:HG	1:D:33:PRO:HG3	1.88	0.55
1:D:181:VAL:HG21	1:E:379:TYR:CG	2.41	0.55
1:E:322:TRP:CH2	1:E:457:ILE:HD12	2.42	0.55
1:A:91:LYS:C	1:A:93:ARG:N	2.59	0.55
1:B:73:VAL:HG22	1:B:105:ILE:HG12	1.87	0.55
1:B:274:ARG:NE	1:B:414:VAL:CG1	2.69	0.55
1:C:117:ARG:CB	1:C:118:PRO:CD	2.79	0.55
1:C:346:TYR:HB2	1:C:348:ASP:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:TRP:HA	1:D:77:TRP:CE3	2.41	0.55
1:A:173:ALA:CB	1:B:345:THR:CG2	2.73	0.55
1:B:346:TYR:CD1	1:B:349:CYS:N	2.72	0.55
1:B:459:ASP:O	1:B:463:PRO:HD2	2.07	0.55
1:C:190:PRO:C	1:C:192:PRO:CD	2.80	0.55
1:D:24:PHE:CD2	1:D:30:LEU:HD13	2.42	0.55
1:D:368:ARG:HB2	1:D:378:LEU:HD21	1.89	0.55
1:E:51:ASN:HB2	1:E:54:PHE:HZ	1.64	0.55
1:E:196:VAL:CG1	1:E:198:TYR:CZ	2.90	0.55
1:E:319:HIS:HB3	1:E:456:ARG:HE	1.71	0.55
1:A:414:VAL:O	1:A:417:VAL:HG12	2.07	0.55
1:D:322:TRP:CZ3	1:D:457:ILE:HD12	2.42	0.55
1:D:414:VAL:C	1:D:417:VAL:HG12	2.32	0.55
1:D:417:VAL:HB	1:D:465:MET:CG	2.13	0.55
1:A:376:ALA:O	1:A:377:VAL:C	2.47	0.55
1:C:186:ALA:O	1:C:190:PRO:HD3	2.06	0.55
1:C:235:LEU:HD12	1:C:241:LEU:HD22	1.84	0.55
1:C:303:LEU:HG	1:C:304:ARG:HG3	1.89	0.55
1:D:262:ASP:CB	1:D:263:PRO:CD	2.76	0.55
1:A:274:ARG:CD	1:A:414:VAL:CG1	2.57	0.54
1:B:189:LYS:HB2	1:B:190:PRO:HD3	1.90	0.54
1:C:84:ILE:CG2	1:C:153:ARG:O	2.54	0.54
1:C:322:TRP:CH2	1:C:457:ILE:HD12	2.41	0.54
1:D:100:PHE:O	1:D:104:ILE:HG12	2.06	0.54
1:B:256:LEU:O	1:B:260:PRO:HD3	2.05	0.54
1:C:177:LEU:HB2	1:D:347:HIS:CD2	2.31	0.54
1:E:73:VAL:HG22	1:E:105:ILE:HG12	1.87	0.54
1:D:58:ALA:C	1:D:265:ARG:HD3	2.30	0.54
1:A:26:LEU:HD23	1:A:26:LEU:H	1.72	0.54
1:A:83:LYS:O	1:A:134:PRO:HA	2.08	0.54
1:A:235:LEU:CD1	1:A:241:LEU:CD2	2.51	0.54
1:A:328:ASN:HA	1:A:333:LEU:HD22	1.90	0.54
1:B:10:LEU:HG	1:B:78:ARG:HB3	1.90	0.54
1:B:186:ALA:O	1:B:190:PRO:HD3	2.08	0.54
1:B:301:LEU:HD13	1:B:361:LEU:HA	1.90	0.54
1:C:320:TYR:H	1:C:456:ARG:HG3	1.71	0.54
1:C:414:VAL:HA	1:C:417:VAL:CG1	2.35	0.54
1:D:73:VAL:HG13	1:D:77:TRP:HD1	1.72	0.54
1:D:190:PRO:C	1:D:192:PRO:CD	2.80	0.54
1:D:322:TRP:CH2	1:D:457:ILE:HD12	2.42	0.54
1:A:280:LYS:HZ3	1:A:437:LEU:CB	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:LEU:HD12	1:B:156:ILE:HD13	1.88	0.54
1:C:163:GLU:HG3	1:C:203:GLN:CB	2.29	0.54
1:C:328:ASN:HA	1:C:333:LEU:HD22	1.89	0.54
1:D:55:ILE:HG22	1:D:57:GLN:HE21	1.73	0.54
1:A:163:GLU:OE1	1:A:208:LEU:HB3	2.02	0.54
1:B:83:LYS:O	1:B:134:PRO:HA	2.08	0.54
1:C:120:GLN:O	1:C:120:GLN:CG	2.54	0.54
1:D:370:LYS:NZ	1:D:375:TYR:CE2	2.75	0.54
1:A:58:ALA:C	1:A:265:ARG:HD3	2.31	0.54
1:A:84:ILE:CG2	1:A:153:ARG:O	2.54	0.54
1:A:368:ARG:CB	1:A:378:LEU:HD21	2.36	0.54
1:A:375:TYR:HA	1:A:378:LEU:HD12	1.89	0.54
1:C:301:LEU:HD13	1:C:361:LEU:HA	1.90	0.54
1:E:298:LYS:NZ	1:E:430:LYS:HA	2.23	0.54
1:A:141:LYS:O	1:A:144:GLY:O	2.26	0.54
1:B:141:LYS:O	1:B:144:GLY:O	2.26	0.54
1:C:216:ARG:HH12	1:C:444:MET:HE2	1.73	0.54
1:D:301:LEU:HD13	1:D:361:LEU:HA	1.90	0.54
1:E:193:SER:O	1:E:194:SER:HB2	2.08	0.54
1:E:323:LEU:HB3	1:E:339:LYS:HB2	1.89	0.54
1:B:307:ILE:C	1:B:364:ASP:OD1	2.51	0.54
1:B:406:ALA:O	1:B:408:LYS:N	2.41	0.54
1:C:124:VAL:HB	1:C:125:ILE:CB	2.16	0.54
1:C:291:PRO:CD	1:C:295:ASP:O	2.56	0.54
1:D:311:LEU:HB3	1:D:368:ARG:HG2	1.90	0.54
1:E:57:GLN:C	1:E:265:ARG:HG3	2.33	0.54
1:E:83:LYS:O	1:E:134:PRO:HA	2.08	0.54
1:E:406:ALA:O	1:E:408:LYS:N	2.41	0.54
1:A:57:GLN:HB3	1:A:265:ARG:CZ	2.37	0.54
1:B:10:LEU:O	1:B:74:TRP:CZ2	2.61	0.54
1:B:415:GLN:O	1:B:418:VAL:HG12	2.07	0.54
1:C:39:GLN:CB	1:C:67:ILE:HG12	2.35	0.54
1:D:83:LYS:O	1:D:134:PRO:HA	2.08	0.54
1:D:141:LYS:O	1:D:144:GLY:O	2.26	0.54
1:E:16:LYS:C	1:E:16:LYS:HD2	2.33	0.54
1:A:73:VAL:HG13	1:A:77:TRP:HD1	1.73	0.53
1:A:162:VAL:C	1:A:165:PRO:HD2	2.33	0.53
1:B:46:LEU:HD22	1:B:197:ILE:HG12	1.89	0.53
1:C:45:VAL:HG22	1:C:54:PHE:CE1	2.44	0.53
1:C:57:GLN:HB3	1:C:265:ARG:CZ	2.38	0.53
1:C:141:LYS:O	1:C:144:GLY:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:LYS:CA	1:E:347:HIS:HB3	2.38	0.53
1:B:57:GLN:CD	1:B:57:GLN:N	2.66	0.53
1:C:378:LEU:CD1	1:C:401:THR:OG1	2.54	0.53
1:D:59:PHE:HD1	1:D:225:ALA:HA	1.69	0.53
1:D:225:ALA:O	1:D:228:PRO:HD2	2.09	0.53
1:D:298:LYS:NZ	1:D:430:LYS:HA	2.23	0.53
1:B:433:SER:HB2	1:B:457:ILE:CD1	2.38	0.53
1:C:225:ALA:O	1:C:228:PRO:HD2	2.09	0.53
1:C:272:ARG:HB3	1:C:442:CYS:HB2	1.89	0.53
1:D:173:ALA:C	1:E:345:THR:C	2.77	0.53
1:D:272:ARG:HB2	1:D:441:ASN:CB	2.26	0.53
1:E:162:VAL:C	1:E:165:PRO:HD2	2.34	0.53
1:E:285:LEU:CB	1:E:431:VAL:HG22	2.38	0.53
1:E:301:LEU:HG	1:E:302:ARG:N	2.24	0.53
1:E:301:LEU:HD13	1:E:361:LEU:HA	1.90	0.53
1:E:359:LYS:HD2	1:E:363:ILE:HD13	1.90	0.53
1:A:10:LEU:O	1:A:74:TRP:CZ2	2.61	0.53
1:A:64:LYS:HA	1:A:67:ILE:HD12	1.91	0.53
1:A:133:ASN:N	1:A:134:PRO:CD	2.71	0.53
1:B:45:VAL:HG22	1:B:54:PHE:CE1	2.44	0.53
1:C:73:VAL:HG22	1:C:105:ILE:HG12	1.88	0.53
1:C:83:LYS:O	1:C:134:PRO:HA	2.08	0.53
1:C:155:ASP:O	1:C:194:SER:C	2.52	0.53
1:C:164:ILE:N	1:C:165:PRO:CD	2.72	0.53
1:D:136:HIS:ND1	1:D:138:PRO:HD3	2.22	0.53
1:D:299:TYR:C	1:D:300:PRO:CD	2.68	0.53
1:E:141:LYS:O	1:E:144:GLY:O	2.26	0.53
1:A:366:SER:HB3	1:A:368:ARG:HE	1.72	0.53
1:B:235:LEU:HD12	1:B:241:LEU:HG	1.90	0.53
1:D:155:ASP:O	1:D:194:SER:C	2.52	0.53
1:E:378:LEU:CD1	1:E:401:THR:OG1	2.54	0.53
1:B:39:GLN:HB3	1:B:67:ILE:CG1	2.38	0.53
1:B:173:ALA:C	1:C:345:THR:C	2.77	0.53
1:B:173:ALA:HB2	1:C:346:TYR:HD1	1.73	0.53
1:C:256:LEU:O	1:C:260:PRO:HD3	2.02	0.53
1:C:339:LYS:HZ1	1:C:353:SER:HB2	1.74	0.53
1:D:310:ALA:HB2	1:D:464:VAL:HG23	1.91	0.53
1:E:100:PHE:O	1:E:104:ILE:HG12	2.09	0.53
1:E:124:VAL:HB	1:E:125:ILE:CB	2.16	0.53
1:E:155:ASP:O	1:E:194:SER:C	2.52	0.53
1:E:186:ALA:O	1:E:190:PRO:CD	2.54	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:225:ALA:O	1:E:228:PRO:HD2	2.09	0.53
1:E:310:ALA:HB2	1:E:464:VAL:HG23	1.91	0.53
1:A:77:TRP:HA	1:A:77:TRP:CE3	2.42	0.53
1:A:173:ALA:HB2	1:B:346:TYR:CD2	2.44	0.53
1:A:301:LEU:HD13	1:A:361:LEU:HA	1.90	0.53
1:A:406:ALA:O	1:A:408:LYS:N	2.41	0.53
1:B:173:ALA:HB3	1:C:345:THR:CB	2.39	0.53
1:B:376:ALA:O	1:B:377:VAL:C	2.47	0.53
1:C:174:ARG:CZ	1:D:345:THR:OG1	2.53	0.53
1:C:176:LYS:HG2	1:D:346:TYR:HB2	1.90	0.53
1:C:298:LYS:NZ	1:C:430:LYS:HA	2.24	0.53
1:C:406:ALA:O	1:C:408:LYS:N	2.41	0.53
1:D:21:ALA:C	1:D:33:PRO:HD2	2.34	0.53
1:D:376:ALA:O	1:D:377:VAL:C	2.47	0.53
1:A:128:ASP:O	1:A:135:ASP:HB3	2.09	0.53
1:B:155:ASP:O	1:B:194:SER:C	2.52	0.53
1:B:202:PRO:HB3	1:B:265:ARG:NH1	2.23	0.53
1:C:82:LEU:C	1:C:83:LYS:HG3	2.34	0.53
1:D:173:ALA:HB3	1:E:345:THR:CB	2.39	0.53
1:E:161:ASP:O	1:E:165:PRO:CD	2.57	0.53
1:E:190:PRO:HB2	1:E:192:PRO:HG2	1.91	0.53
1:A:314:GLU:O	1:A:314:GLU:CG	2.57	0.53
1:A:347:HIS:CA	1:E:176:LYS:HB3	2.39	0.53
1:B:225:ALA:O	1:B:228:PRO:HD2	2.08	0.53
1:C:322:TRP:CZ3	1:C:457:ILE:HD12	2.44	0.53
1:D:189:LYS:HB2	1:D:190:PRO:HD3	1.90	0.53
1:D:274:ARG:HD3	1:D:417:VAL:HG13	1.90	0.53
1:D:314:GLU:O	1:D:314:GLU:CG	2.57	0.53
1:E:230:THR:HA	1:E:233:GLU:HG3	1.90	0.53
1:A:345:THR:C	1:E:173:ALA:C	2.77	0.53
1:C:265:ARG:O	1:C:265:ARG:HG3	2.08	0.53
1:C:310:ALA:HB2	1:C:464:VAL:HG23	1.91	0.53
1:C:313:LEU:HD11	1:C:377:VAL:HB	1.90	0.53
1:D:406:ALA:O	1:D:408:LYS:N	2.41	0.53
1:A:117:ARG:CB	1:A:118:PRO:CD	2.81	0.52
1:B:73:VAL:HG21	1:B:104:ILE:HB	1.90	0.52
1:B:190:PRO:C	1:B:192:PRO:CD	2.82	0.52
1:C:173:ALA:HB3	1:D:345:THR:CB	2.39	0.52
1:E:368:ARG:HD2	1:E:378:LEU:HD23	1.90	0.52
1:A:176:LYS:HB2	1:B:347:HIS:HB2	1.90	0.52
1:B:56:LEU:HB2	1:B:199:LEU:HG	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:307:ILE:HD13	1:B:327:GLN:HA	1.91	0.52
1:C:77:TRP:HZ3	1:C:114:LEU:HB2	1.73	0.52
1:D:161:ASP:HB3	1:D:164:ILE:HG22	1.91	0.52
1:A:280:LYS:CE	1:A:438:LYS:HA	2.24	0.52
1:B:310:ALA:HB2	1:B:464:VAL:HG23	1.91	0.52
1:C:21:ALA:C	1:C:33:PRO:HD2	2.34	0.52
1:C:202:PRO:CB	1:C:265:ARG:NH1	2.66	0.52
1:C:382:ASN:CG	1:C:385:ILE:HG12	2.34	0.52
1:E:19:PHE:O	1:E:32:LEU:HD21	2.10	0.52
1:E:84:ILE:HG23	1:E:153:ARG:O	2.08	0.52
1:E:181:VAL:N	1:E:182:GLN:CB	2.73	0.52
1:E:266:PHE:CE1	1:E:272:ARG:HG3	2.44	0.52
1:E:334:PRO:HB3	1:E:427:MET:HE3	1.90	0.52
1:A:14:GLN:OE1	1:A:40:ILE:HG23	2.09	0.52
1:A:155:ASP:O	1:A:194:SER:C	2.52	0.52
1:A:173:ALA:C	1:B:345:THR:C	2.77	0.52
1:A:190:PRO:HB2	1:A:192:PRO:HG2	1.91	0.52
1:A:196:VAL:HG13	1:A:198:TYR:HE1	1.73	0.52
1:C:170:THR:CA	1:D:345:THR:HG21	2.27	0.52
1:C:193:SER:HB2	1:C:195:ARG:NH2	2.25	0.52
1:B:274:ARG:NE	1:B:414:VAL:HG12	2.24	0.52
1:C:173:ALA:C	1:D:345:THR:C	2.77	0.52
1:E:414:VAL:HA	1:E:417:VAL:CG1	2.38	0.52
1:A:225:ALA:O	1:A:228:PRO:HD2	2.09	0.52
1:A:310:ALA:HB2	1:A:464:VAL:HG23	1.91	0.52
1:C:51:ASN:HB2	1:C:54:PHE:HZ	1.66	0.52
1:C:235:LEU:CD1	1:C:241:LEU:CD2	2.70	0.52
1:C:262:ASP:CB	1:C:263:PRO:CD	2.74	0.52
1:C:272:ARG:HB3	1:C:442:CYS:H	1.74	0.52
1:E:14:GLN:OE1	1:E:40:ILE:HG23	2.10	0.52
1:C:57:GLN:NE2	1:C:265:ARG:HH21	2.03	0.52
1:C:468:HIS:HD2	1:C:468:HIS:O	1.92	0.52
1:E:116:PRO:HB3	1:E:127:PHE:CZ	2.45	0.52
1:E:119:GLY:HA2	1:E:127:PHE:HD2	1.74	0.52
1:E:221:ILE:HA	1:E:445:GLU:HG2	1.88	0.52
1:A:191:LEU:N	1:A:192:PRO:HD2	2.25	0.52
1:A:298:LYS:NZ	1:A:430:LYS:HA	2.25	0.52
1:A:311:LEU:HB3	1:A:368:ARG:HG3	1.92	0.52
1:B:77:TRP:HZ3	1:B:114:LEU:HB2	1.75	0.52
1:B:394:ARG:HB3	1:B:400:LYS:HD3	1.91	0.52
1:C:181:VAL:N	1:C:182:GLN:CB	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:PRO:HD3	1:C:295:ASP:O	2.10	0.52
1:D:125:ILE:O	1:D:125:ILE:CG2	2.58	0.52
1:D:220:THR:CB	1:D:445:GLU:HB2	2.39	0.52
1:E:196:VAL:HG11	1:E:198:TYR:CZ	2.45	0.52
1:A:144:GLY:O	1:A:171:MET:HG2	2.10	0.52
1:A:176:LYS:HB3	1:B:347:HIS:CA	2.40	0.52
1:B:300:PRO:HB2	1:B:302:ARG:HH12	1.75	0.52
1:C:14:GLN:OE1	1:C:40:ILE:HG23	2.09	0.52
1:C:119:GLY:HA2	1:C:127:PHE:HD1	1.74	0.52
1:C:216:ARG:NH1	1:C:444:MET:HE2	2.25	0.52
1:E:125:ILE:CG2	1:E:125:ILE:O	2.58	0.52
1:E:208:LEU:CD2	1:E:265:ARG:HH22	2.23	0.52
1:E:314:GLU:O	1:E:314:GLU:CG	2.57	0.52
1:A:173:ALA:HB3	1:B:345:THR:CB	2.39	0.52
1:A:176:LYS:CA	1:B:347:HIS:HB3	2.40	0.52
1:B:220:THR:HG23	1:B:411:GLN:CD	2.35	0.52
1:D:319:HIS:HB3	1:D:456:ARG:HE	1.75	0.52
1:B:21:ALA:HB3	1:B:33:PRO:HG3	1.92	0.51
1:B:161:ASP:O	1:B:165:PRO:CD	2.58	0.51
1:C:128:ASP:O	1:C:135:ASP:HB3	2.09	0.51
1:C:294:SER:OG	1:C:341:ASP:HB2	2.10	0.51
1:D:193:SER:HB2	1:D:195:ARG:NH2	2.25	0.51
1:A:345:THR:OG1	1:E:170:THR:HA	2.09	0.51
1:B:280:LYS:NZ	1:B:437:LEU:C	2.69	0.51
1:B:291:PRO:HG2	1:B:295:ASP:CB	2.28	0.51
1:B:294:SER:CB	1:B:341:ASP:HB3	2.41	0.51
1:B:414:VAL:HA	1:B:417:VAL:CG1	2.38	0.51
1:D:161:ASP:O	1:D:165:PRO:CD	2.58	0.51
1:A:181:VAL:N	1:A:182:GLN:CB	2.73	0.51
1:A:322:TRP:CZ3	1:A:457:ILE:HD12	2.45	0.51
1:B:125:ILE:O	1:B:125:ILE:CG2	2.58	0.51
1:B:176:LYS:CA	1:C:347:HIS:HB3	2.39	0.51
1:E:76:LEU:HB2	1:E:136:HIS:CE1	2.46	0.51
1:E:313:LEU:CD1	1:E:374:GLY:CA	2.79	0.51
1:D:59:PHE:CD1	1:D:225:ALA:CA	2.89	0.51
1:D:59:PHE:CE1	1:D:225:ALA:C	2.89	0.51
1:C:378:LEU:HD11	1:C:401:THR:HG1	1.75	0.51
1:E:417:VAL:HA	1:E:465:MET:HG3	1.92	0.51
1:A:24:PHE:CD2	1:A:30:LEU:HD13	2.46	0.51
1:A:53:LYS:HD3	1:A:196:VAL:HB	1.91	0.51
1:A:124:VAL:HB	1:A:125:ILE:CB	2.16	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:VAL:N	1:B:182:GLN:CB	2.73	0.51
1:E:191:LEU:N	1:E:192:PRO:HD2	2.25	0.51
1:E:370:LYS:CG	1:E:401:THR:OG1	2.56	0.51
1:D:355:GLN:HB2	1:D:381:LEU:HD21	1.92	0.51
1:E:24:PHE:CD2	1:E:30:LEU:HD13	2.46	0.51
1:E:117:ARG:HD3	1:E:118:PRO:HD3	1.93	0.51
1:A:85:LEU:CB	1:A:136:HIS:ND1	2.72	0.51
1:A:301:LEU:HG	1:A:302:ARG:N	2.24	0.51
1:A:323:LEU:HB3	1:A:339:LYS:HB2	1.92	0.51
1:A:417:VAL:HG23	1:A:465:MET:HE3	1.93	0.51
1:B:272:ARG:HB3	1:B:442:CYS:CB	2.41	0.51
1:C:176:LYS:HB2	1:D:347:HIS:CB	2.33	0.51
1:D:83:LYS:HG3	1:D:155:ASP:HB2	1.91	0.51
1:D:468:HIS:HA	1:D:473:ARG:NE	2.26	0.51
1:E:19:PHE:C	1:E:32:LEU:HD21	2.36	0.51
1:E:319:HIS:CB	1:E:456:ARG:HE	2.24	0.51
1:B:52:LYS:CB	1:B:184:PHE:CZ	2.74	0.51
1:C:24:PHE:CD2	1:C:30:LEU:HD13	2.46	0.51
1:C:314:GLU:O	1:C:314:GLU:CG	2.57	0.51
1:D:370:LYS:HE3	1:D:403:GLU:HA	1.93	0.51
1:D:432:PHE:N	1:D:432:PHE:HD1	2.09	0.51
1:E:322:TRP:CZ3	1:E:457:ILE:HD12	2.46	0.51
1:C:73:VAL:HG21	1:C:104:ILE:HB	1.92	0.51
1:C:76:LEU:HG	1:C:134:PRO:HB2	1.92	0.51
1:D:370:LYS:HG3	1:D:378:LEU:HD11	1.91	0.51
1:E:73:VAL:HG21	1:E:104:ILE:HB	1.93	0.51
1:E:435:ILE:HA	1:E:438:LYS:HG3	1.92	0.51
1:A:125:ILE:CG2	1:A:125:ILE:O	2.58	0.50
1:B:301:LEU:HG	1:B:302:ARG:N	2.25	0.50
1:B:314:GLU:O	1:B:314:GLU:CG	2.57	0.50
1:C:10:LEU:O	1:C:74:TRP:CZ2	2.64	0.50
1:D:14:GLN:NE2	1:D:40:ILE:HG12	2.26	0.50
1:E:45:VAL:HG22	1:E:54:PHE:CE1	2.45	0.50
1:E:85:LEU:HD12	1:E:156:ILE:CG2	2.37	0.50
1:E:85:LEU:HA	1:E:156:ILE:HG23	1.92	0.50
1:A:177:LEU:HB3	1:B:347:HIS:ND1	2.27	0.50
1:A:313:LEU:CD1	1:A:374:GLY:CA	2.80	0.50
1:C:181:VAL:HG21	1:D:379:TYR:CG	2.46	0.50
1:C:189:LYS:HB2	1:C:190:PRO:HD3	1.93	0.50
1:D:162:VAL:C	1:D:165:PRO:HD2	2.36	0.50
1:E:111:LEU:HD23	1:E:111:LEU:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:LYS:HZ1	1:B:438:LYS:N	2.09	0.50
1:B:432:PHE:N	1:B:432:PHE:HD1	2.09	0.50
1:A:285:LEU:CB	1:A:431:VAL:HG22	2.40	0.50
1:B:117:ARG:HB2	1:B:118:PRO:CD	2.40	0.50
1:C:176:LYS:HD2	1:C:176:LYS:N	2.25	0.50
1:D:85:LEU:HA	1:D:156:ILE:HG23	1.93	0.50
1:E:45:VAL:HG21	1:E:222:ILE:HD11	1.93	0.50
1:A:54:PHE:HD1	1:A:221:ILE:HD13	1.77	0.50
1:B:10:LEU:O	1:B:74:TRP:HZ2	1.94	0.50
1:B:59:PHE:CD2	1:B:263:PRO:HA	2.47	0.50
1:C:88:SER:HB3	1:C:141:LYS:CG	2.41	0.50
1:C:378:LEU:CD2	1:C:401:THR:HG23	2.41	0.50
1:D:163:GLU:HG3	1:D:203:GLN:CB	2.34	0.50
1:D:180:LEU:HD21	1:E:380:THR:OG1	2.11	0.50
1:D:181:VAL:N	1:D:182:GLN:CB	2.73	0.50
1:E:190:PRO:C	1:E:192:PRO:CD	2.84	0.50
1:E:370:LYS:CE	1:E:375:TYR:CE1	2.86	0.50
1:C:125:ILE:CG2	1:C:125:ILE:O	2.59	0.50
1:D:73:VAL:HG21	1:D:104:ILE:HB	1.93	0.50
1:B:313:LEU:HD11	1:B:377:VAL:HB	1.92	0.50
1:C:301:LEU:HG	1:C:302:ARG:N	2.25	0.50
1:C:468:HIS:CA	1:C:473:ARG:HD3	2.35	0.50
1:D:96:ALA:HA	1:D:99:ILE:HD12	1.93	0.50
1:D:220:THR:O	1:D:220:THR:HG23	2.09	0.50
1:B:191:LEU:N	1:B:192:PRO:HD2	2.26	0.50
1:B:291:PRO:CD	1:B:295:ASP:O	2.60	0.50
1:B:433:SER:CA	1:B:457:ILE:HD13	2.42	0.50
1:D:10:LEU:O	1:D:74:TRP:CZ2	2.64	0.50
1:D:59:PHE:HD2	1:D:60:ARG:O	1.95	0.50
1:D:141:LYS:HZ3	1:D:171:MET:HB2	1.76	0.50
1:D:221:ILE:C	1:D:445:GLU:HG2	2.36	0.50
1:D:272:ARG:HB3	1:D:442:CYS:CB	2.42	0.50
1:A:116:PRO:HB3	1:A:127:PHE:CZ	2.47	0.50
1:A:311:LEU:HD23	1:A:368:ARG:HG2	1.94	0.50
1:C:85:LEU:HB3	1:C:136:HIS:ND1	2.27	0.50
1:C:435:ILE:HA	1:C:438:LYS:HG3	1.94	0.50
1:E:309:ALA:HB2	1:E:358:GLN:HE22	1.77	0.50
1:E:417:VAL:HA	1:E:465:MET:SD	2.51	0.50
1:A:311:LEU:HB2	1:A:323:LEU:HD12	1.93	0.49
1:D:21:ALA:O	1:D:22:PHE:CD1	2.65	0.49
1:E:73:VAL:HG22	1:E:77:TRP:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:LEU:CG	1:E:134:PRO:HB2	2.42	0.49
1:E:280:LYS:HZ3	1:E:438:LYS:HA	1.73	0.49
1:E:382:ASN:CG	1:E:385:ILE:HG12	2.36	0.49
1:A:163:GLU:HG3	1:A:203:GLN:CB	2.33	0.49
1:A:190:PRO:C	1:A:192:PRO:CD	2.84	0.49
1:B:326:ARG:HD3	1:B:333:LEU:HB3	1.92	0.49
1:C:144:GLY:O	1:C:171:MET:HG2	2.12	0.49
1:C:415:GLN:O	1:C:418:VAL:CG1	2.60	0.49
1:D:136:HIS:CE1	1:D:138:PRO:HD3	2.46	0.49
1:E:415:GLN:O	1:E:418:VAL:CG1	2.60	0.49
1:A:375:TYR:O	1:A:378:LEU:HB2	2.12	0.49
1:A:415:GLN:O	1:A:418:VAL:CG1	2.60	0.49
1:C:173:ALA:HB2	1:D:346:TYR:CD2	2.47	0.49
1:D:125:ILE:O	1:D:138:PRO:HD2	2.12	0.49
1:E:190:PRO:CB	1:E:192:PRO:HD2	2.41	0.49
1:A:10:LEU:O	1:A:74:TRP:HZ2	1.94	0.49
1:A:52:LYS:CB	1:A:184:PHE:CZ	2.73	0.49
1:A:161:ASP:O	1:A:165:PRO:CD	2.60	0.49
1:B:76:LEU:HB3	1:B:136:HIS:CE1	2.47	0.49
1:B:173:ALA:HB2	1:C:346:TYR:CD1	2.47	0.49
1:B:187:LEU:O	1:B:192:PRO:HD2	2.12	0.49
1:C:173:ALA:HB1	1:D:345:THR:CA	2.36	0.49
1:D:55:ILE:CG2	1:D:57:GLN:HE21	2.25	0.49
1:D:256:LEU:O	1:D:260:PRO:HD3	2.09	0.49
1:E:144:GLY:HA2	1:E:147:GLY:N	2.23	0.49
1:E:309:ALA:HB3	1:E:358:GLN:HE22	1.77	0.49
1:A:468:HIS:HA	1:A:473:ARG:NE	2.26	0.49
1:B:190:PRO:HB2	1:B:192:PRO:HG2	1.94	0.49
1:C:157:ILE:HB	1:C:196:VAL:HG22	1.94	0.49
1:D:98:SER:HB2	1:D:136:HIS:CE1	2.44	0.49
1:D:172:GLY:HA2	1:D:175:GLU:OE1	2.12	0.49
1:D:301:LEU:HG	1:D:302:ARG:N	2.24	0.49
1:E:221:ILE:N	1:E:445:GLU:HG2	2.27	0.49
1:E:378:LEU:CD2	1:E:401:THR:HG23	2.42	0.49
1:A:313:LEU:HD11	1:A:377:VAL:HB	1.94	0.49
1:B:177:LEU:CB	1:C:347:HIS:ND1	2.66	0.49
1:C:73:VAL:HG22	1:C:77:TRP:HE1	1.76	0.49
1:D:299:TYR:HA	1:D:300:PRO:CD	2.42	0.49
1:E:54:PHE:HD1	1:E:221:ILE:HD13	1.78	0.49
1:E:118:PRO:HG2	1:E:129:VAL:HB	1.95	0.49
1:E:293:LEU:HD13	1:E:353:SER:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:LEU:O	1:A:116:PRO:HD3	2.12	0.49
1:A:119:GLY:HA2	1:A:127:PHE:HD1	1.73	0.49
1:C:23:LEU:HG	1:C:33:PRO:HG3	1.95	0.49
1:C:249:TYR:O	1:C:253:PRO:HD2	2.13	0.49
1:D:149:LEU:HG	1:D:174:ARG:HH11	1.78	0.49
1:D:157:ILE:HB	1:D:196:VAL:HG22	1.94	0.49
1:D:173:ALA:HB2	1:E:346:TYR:HD2	1.68	0.49
1:E:202:PRO:HB3	1:E:265:ARG:CZ	2.43	0.49
1:B:159:ALA:HB2	1:B:198:TYR:CE1	2.47	0.49
1:E:161:ASP:HB3	1:E:164:ILE:HG12	1.93	0.49
1:A:226:LEU:HD13	1:A:263:PRO:HB3	1.94	0.49
1:B:57:GLN:CD	1:B:212:LEU:HD13	2.38	0.49
1:B:162:VAL:C	1:B:165:PRO:HD2	2.37	0.49
1:B:262:ASP:CB	1:B:263:PRO:CD	2.73	0.49
1:E:57:GLN:CG	1:E:212:LEU:HD13	2.40	0.49
1:E:163:GLU:CG	1:E:203:GLN:HB2	2.35	0.49
1:E:190:PRO:HB2	1:E:192:PRO:CG	2.43	0.49
1:A:144:GLY:HA2	1:A:147:GLY:N	2.23	0.49
1:A:266:PHE:CE1	1:A:272:ARG:HG3	2.48	0.49
1:B:190:PRO:HB2	1:B:192:PRO:CG	2.43	0.49
1:C:111:LEU:HD23	1:C:111:LEU:H	1.77	0.49
1:C:368:ARG:H	1:C:401:THR:HG21	1.77	0.49
1:D:54:PHE:HD1	1:D:221:ILE:HD13	1.78	0.49
1:D:414:VAL:HA	1:D:417:VAL:CG1	2.41	0.49
1:E:294:SER:OG	1:E:341:ASP:HB2	2.13	0.49
1:A:141:LYS:HZ3	1:A:171:MET:HB2	1.78	0.48
1:A:157:ILE:HB	1:A:196:VAL:HG22	1.94	0.48
1:A:307:ILE:HD13	1:A:327:GLN:HA	1.95	0.48
1:B:21:ALA:O	1:B:22:PHE:CD1	2.66	0.48
1:B:190:PRO:CB	1:B:192:PRO:HD2	2.41	0.48
1:B:443:ALA:HB1	1:B:448:ARG:NH2	2.27	0.48
1:C:221:ILE:HA	1:C:445:GLU:HG2	1.95	0.48
1:C:273:GLU:HA	1:C:441:ASN:HA	1.95	0.48
1:B:119:GLY:HA2	1:B:127:PHE:CD2	2.48	0.48
1:B:159:ALA:HB3	1:B:198:TYR:CE1	2.47	0.48
1:B:378:LEU:CD2	1:B:401:THR:CG2	2.84	0.48
1:C:21:ALA:O	1:C:22:PHE:CD1	2.66	0.48
1:C:54:PHE:HD1	1:C:221:ILE:HD13	1.78	0.48
1:C:191:LEU:N	1:C:192:PRO:HD2	2.28	0.48
1:C:288:MET:HE2	1:C:288:MET:HA	1.95	0.48
1:E:313:LEU:HD11	1:E:377:VAL:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:PRO:HB2	1:A:192:PRO:CG	2.44	0.48
1:A:291:PRO:CD	1:A:295:ASP:O	2.61	0.48
1:B:111:LEU:H	1:B:111:LEU:HD23	1.77	0.48
1:C:181:VAL:CA	1:C:182:GLN:CG	2.88	0.48
1:D:88:SER:HB3	1:D:141:LYS:CG	2.42	0.48
1:D:273:GLU:HA	1:D:441:ASN:HA	1.95	0.48
1:D:322:TRP:HB3	1:D:460:THR:HG21	1.96	0.48
1:B:73:VAL:HG22	1:B:77:TRP:HE1	1.79	0.48
1:C:164:ILE:N	1:C:165:PRO:HD3	2.28	0.48
1:D:144:GLY:HA2	1:D:147:GLY:N	2.23	0.48
1:D:176:LYS:CB	1:E:347:HIS:C	2.86	0.48
1:A:57:GLN:CG	1:A:212:LEU:HD13	2.41	0.48
1:A:284:THR:C	1:A:285:LEU:HD22	2.38	0.48
1:A:441:ASN:C	1:A:447:ILE:HG23	2.38	0.48
1:B:157:ILE:HB	1:B:196:VAL:HG22	1.94	0.48
1:B:368:ARG:H	1:B:401:THR:HG21	1.74	0.48
1:C:10:LEU:O	1:C:74:TRP:HZ2	1.96	0.48
1:C:322:TRP:HB3	1:C:460:THR:HG21	1.96	0.48
1:C:400:LYS:O	1:C:401:THR:CG2	2.58	0.48
1:D:10:LEU:O	1:D:74:TRP:HZ2	1.96	0.48
1:D:45:VAL:HG22	1:D:54:PHE:CE1	2.48	0.48
1:D:313:LEU:HD11	1:D:377:VAL:HB	1.95	0.48
1:D:415:GLN:O	1:D:418:VAL:CG1	2.60	0.48
1:D:434:PRO:HA	1:D:437:LEU:HD12	1.94	0.48
1:A:190:PRO:CB	1:A:192:PRO:HD2	2.41	0.48
1:A:322:TRP:HB3	1:A:460:THR:HG21	1.96	0.48
1:A:382:ASN:CB	1:A:385:ILE:CG1	2.90	0.48
1:B:465:MET:O	1:B:468:HIS:HB3	2.14	0.48
1:C:85:LEU:HA	1:C:156:ILE:HG23	1.95	0.48
1:C:403:GLU:HG2	1:C:405:LEU:H	1.78	0.48
1:D:73:VAL:HG13	1:D:77:TRP:CD1	2.47	0.48
1:D:338:LEU:HD23	1:D:457:ILE:HD11	1.95	0.48
1:E:299:TYR:C	1:E:300:PRO:CD	2.74	0.48
1:E:307:ILE:HD13	1:E:327:GLN:HA	1.95	0.48
1:A:46:LEU:CD2	1:A:54:PHE:HB2	2.43	0.48
1:B:439:HIS:CD2	1:B:453:LYS:HB3	2.49	0.48
1:C:58:ALA:C	1:C:265:ARG:HD3	2.37	0.48
1:C:190:PRO:CB	1:C:192:PRO:HD2	2.42	0.48
1:E:161:ASP:O	1:E:165:PRO:HD3	2.14	0.48
1:E:249:TYR:O	1:E:253:PRO:HD2	2.13	0.48
1:E:400:LYS:O	1:E:401:THR:CG2	2.58	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LYS:CA	1:A:93:ARG:H	2.27	0.48
1:B:181:VAL:HG21	1:C:379:TYR:CG	2.48	0.48
1:C:91:LYS:CA	1:C:93:ARG:H	2.27	0.48
1:D:91:LYS:CA	1:D:93:ARG:H	2.27	0.48
1:D:176:LYS:CG	1:E:347:HIS:HB3	2.42	0.48
1:A:380:THR:OG1	1:E:180:LEU:HD21	2.14	0.48
1:B:432:PHE:N	1:B:432:PHE:CD1	2.81	0.48
1:C:77:TRP:HZ3	1:C:114:LEU:CB	2.26	0.48
1:C:226:LEU:HD13	1:C:263:PRO:HB3	1.95	0.48
1:C:432:PHE:N	1:C:432:PHE:HD1	2.11	0.48
1:C:291:PRO:CG	1:C:295:ASP:HB3	2.32	0.48
1:D:294:SER:OG	1:D:341:ASP:HB2	2.13	0.48
1:E:77:TRP:CE2	1:E:105:ILE:HG12	2.45	0.48
1:A:294:SER:OG	1:A:341:ASP:HB2	2.14	0.47
1:B:76:LEU:HD11	1:B:128:ASP:OD2	2.14	0.47
1:B:161:ASP:O	1:B:165:PRO:HD2	2.14	0.47
1:C:118:PRO:HD2	1:C:128:ASP:CA	2.43	0.47
1:D:309:ALA:HB2	1:D:358:GLN:HE22	1.78	0.47
1:E:115:LYS:CA	1:E:116:PRO:CD	2.91	0.47
1:E:275:GLU:OE2	1:E:437:LEU:HD22	2.14	0.47
1:E:326:ARG:O	1:E:328:ASN:OD1	2.32	0.47
1:A:433:SER:CA	1:A:434:PRO:CD	2.92	0.47
1:B:259:THR:O	1:B:264:VAL:HG23	2.14	0.47
1:B:322:TRP:HB3	1:B:460:THR:HG21	1.97	0.47
1:C:307:ILE:HD13	1:C:327:GLN:HA	1.95	0.47
1:D:55:ILE:CG2	1:D:57:GLN:NE2	2.77	0.47
1:D:117:ARG:CB	1:D:118:PRO:HD3	2.43	0.47
1:E:88:SER:HB3	1:E:141:LYS:CG	2.44	0.47
1:E:322:TRP:HB3	1:E:460:THR:HG21	1.96	0.47
1:B:91:LYS:CA	1:B:93:ARG:H	2.27	0.47
1:B:176:LYS:CB	1:C:347:HIS:C	2.86	0.47
1:B:286:GLN:HG2	1:B:288:MET:HE2	1.97	0.47
1:C:190:PRO:HB2	1:C:192:PRO:HG2	1.96	0.47
1:C:338:LEU:HD23	1:C:457:ILE:HD11	1.97	0.47
1:E:91:LYS:CA	1:E:93:ARG:H	2.27	0.47
1:A:45:VAL:HG22	1:A:54:PHE:CE1	2.49	0.47
1:A:249:TYR:O	1:A:253:PRO:HD2	2.14	0.47
1:B:88:SER:HB3	1:B:141:LYS:CG	2.45	0.47
1:A:56:LEU:HB2	1:A:199:LEU:HG	1.96	0.47
1:C:190:PRO:HB2	1:C:192:PRO:CG	2.44	0.47
1:C:223:TRP:O	1:C:223:TRP:CE3	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:ASN:OD1	1:C:240:ARG:HD3	2.14	0.47
1:D:155:ASP:C	1:D:194:SER:CB	2.87	0.47
1:D:265:ARG:HG3	1:D:265:ARG:O	2.15	0.47
1:E:232:GLU:HB3	1:E:246:ARG:HG2	1.97	0.47
1:E:338:LEU:HD23	1:E:457:ILE:HD11	1.96	0.47
1:A:73:VAL:HG21	1:A:104:ILE:HB	1.95	0.47
1:A:262:ASP:CB	1:A:263:PRO:CD	2.74	0.47
1:B:173:ALA:HB1	1:C:345:THR:CA	2.36	0.47
1:B:316:ALA:O	1:B:318:MET:HB2	2.13	0.47
1:C:83:LYS:CE	1:C:193:SER:H	2.23	0.47
1:E:46:LEU:HD22	1:E:197:ILE:CG1	2.45	0.47
1:E:444:MET:HA	1:E:445:GLU:HA	1.56	0.47
1:A:417:VAL:N	1:A:465:MET:HG3	2.28	0.47
1:B:57:GLN:O	1:B:223:TRP:HD1	1.98	0.47
1:B:77:TRP:HZ3	1:B:114:LEU:CB	2.27	0.47
1:B:77:TRP:CE2	1:B:105:ILE:HG12	2.47	0.47
1:B:161:ASP:HB3	1:B:164:ILE:HG22	1.96	0.47
1:B:433:SER:CA	1:B:434:PRO:CD	2.93	0.47
1:C:52:LYS:CB	1:C:184:PHE:CZ	2.73	0.47
1:C:173:ALA:HB2	1:D:346:TYR:HD2	1.79	0.47
1:D:20:VAL:HA	1:D:22:PHE:CZ	2.49	0.47
1:D:76:LEU:HD11	1:D:128:ASP:OD2	2.14	0.47
1:D:368:ARG:NH2	1:D:381:LEU:HB3	2.29	0.47
1:D:432:PHE:N	1:D:432:PHE:CD1	2.81	0.47
1:D:433:SER:CA	1:D:434:PRO:CD	2.92	0.47
1:E:155:ASP:C	1:E:194:SER:CB	2.88	0.47
1:A:155:ASP:C	1:A:194:SER:CB	2.88	0.47
1:A:220:THR:C	1:A:445:GLU:CB	2.88	0.47
1:A:326:ARG:HD3	1:A:333:LEU:HB3	1.96	0.47
1:A:465:MET:O	1:A:468:HIS:HB3	2.14	0.47
1:B:182:GLN:NE2	1:B:185:ALA:CB	2.46	0.47
1:B:273:GLU:HA	1:B:441:ASN:HA	1.95	0.47
1:C:176:LYS:CB	1:D:347:HIS:C	2.86	0.47
1:C:241:LEU:HG	1:C:244:MET:HB2	1.97	0.47
1:E:208:LEU:CD2	1:E:265:ARG:NH2	2.67	0.47
1:E:273:GLU:HA	1:E:441:ASN:HA	1.95	0.47
1:A:161:ASP:O	1:A:165:PRO:HD3	2.14	0.47
1:A:235:LEU:HA	1:A:235:LEU:HD23	1.52	0.47
1:A:273:GLU:HA	1:A:441:ASN:HA	1.95	0.47
1:A:347:HIS:HE2	1:A:376:ALA:CB	2.28	0.47
1:B:76:LEU:CB	1:B:136:HIS:CE1	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:ASP:C	1:B:194:SER:CB	2.88	0.47
1:B:235:LEU:HD23	1:B:235:LEU:HA	1.50	0.47
1:B:249:TYR:O	1:B:253:PRO:HD2	2.14	0.47
1:B:265:ARG:HH11	1:B:265:ARG:HG3	1.80	0.47
1:C:272:ARG:HB3	1:C:442:CYS:CB	2.44	0.47
1:C:313:LEU:CD2	1:C:377:VAL:HG21	2.45	0.47
1:C:316:ALA:O	1:C:318:MET:HB2	2.14	0.47
1:C:370:LYS:O	1:C:375:TYR:CE2	2.68	0.47
1:D:59:PHE:HB2	1:D:263:PRO:HA	1.96	0.47
1:D:75:SER:HB3	1:D:83:LYS:HZ3	1.79	0.47
1:D:119:GLY:HA2	1:D:127:PHE:CD2	2.49	0.47
1:D:202:PRO:CB	1:D:265:ARG:NH1	2.71	0.47
1:A:54:PHE:O	1:A:55:ILE:HD13	2.15	0.47
1:A:382:ASN:CG	1:A:385:ILE:HG12	2.40	0.47
1:C:155:ASP:C	1:C:194:SER:CB	2.88	0.47
1:C:346:TYR:HE2	1:C:349:CYS:CB	2.12	0.47
1:D:1:MET:O	1:D:1:MET:HE3	2.14	0.47
1:D:272:ARG:HB3	1:D:442:CYS:H	1.78	0.47
1:A:73:VAL:HG13	1:A:77:TRP:CD1	2.49	0.46
1:B:309:ALA:HB3	1:B:358:GLN:HE22	1.78	0.46
1:C:252:ASN:C	1:C:254:GLU:N	2.73	0.46
1:C:417:VAL:N	1:C:465:MET:HG3	2.30	0.46
1:D:232:GLU:HB3	1:D:246:ARG:HG2	1.96	0.46
1:E:57:GLN:HB3	1:E:265:ARG:CZ	2.44	0.46
1:E:220:THR:C	1:E:445:GLU:CB	2.87	0.46
1:A:57:GLN:O	1:A:223:TRP:HD1	1.99	0.46
1:A:85:LEU:HA	1:A:156:ILE:HG23	1.97	0.46
1:B:220:THR:C	1:B:445:GLU:CB	2.88	0.46
1:B:252:ASN:C	1:B:254:GLU:N	2.73	0.46
1:C:176:LYS:HB2	1:D:347:HIS:CA	2.37	0.46
1:C:433:SER:CA	1:C:434:PRO:CD	2.93	0.46
1:D:114:LEU:O	1:D:116:PRO:HD3	2.15	0.46
1:D:307:ILE:HD13	1:D:327:GLN:HA	1.97	0.46
1:E:252:ASN:C	1:E:254:GLU:N	2.73	0.46
1:A:118:PRO:HD2	1:A:128:ASP:CA	2.42	0.46
1:B:45:VAL:HG12	1:B:46:LEU:HG	1.98	0.46
1:B:280:LYS:HZ3	1:B:437:LEU:HB3	1.81	0.46
1:B:428:PHE:HE1	1:B:461:LEU:HD22	1.79	0.46
1:B:432:PHE:O	1:B:436:LEU:HD13	2.16	0.46
1:C:46:LEU:HD22	1:C:197:ILE:CG1	2.45	0.46
1:C:441:ASN:C	1:C:447:ILE:HG23	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:PRO:CB	1:D:192:PRO:HD2	2.40	0.46
1:E:221:ILE:HA	1:E:222:ILE:HG12	1.96	0.46
1:E:346:TYR:CE1	1:E:349:CYS:HB3	2.51	0.46
1:E:441:ASN:C	1:E:447:ILE:HG23	2.40	0.46
1:A:85:LEU:HD12	1:A:156:ILE:HD13	1.96	0.46
1:A:293:LEU:HD13	1:A:353:SER:HB2	1.97	0.46
1:B:144:GLY:HA2	1:B:147:GLY:N	2.23	0.46
1:B:235:LEU:CD1	1:B:241:LEU:HG	2.44	0.46
1:C:259:THR:O	1:C:264:VAL:HG23	2.15	0.46
1:D:117:ARG:CB	1:D:118:PRO:CD	2.93	0.46
1:D:412:TRP:CE3	1:D:416:THR:OG1	2.66	0.46
1:E:45:VAL:HG12	1:E:46:LEU:HG	1.98	0.46
1:E:241:LEU:HG	1:E:244:MET:HB2	1.96	0.46
1:A:181:VAL:CA	1:A:182:GLN:CG	2.88	0.46
1:C:116:PRO:HB3	1:C:127:PHE:CZ	2.50	0.46
1:C:118:PRO:HG2	1:C:129:VAL:HB	1.97	0.46
1:D:57:GLN:HB3	1:D:265:ARG:CZ	2.44	0.46
1:D:91:LYS:CB	1:D:93:ARG:N	2.74	0.46
1:D:193:SER:HB2	1:D:195:ARG:HH22	1.80	0.46
1:D:252:ASN:C	1:D:254:GLU:N	2.73	0.46
1:E:22:PHE:HA	1:E:33:PRO:HD3	1.97	0.46
1:B:85:LEU:HA	1:B:156:ILE:HG23	1.96	0.46
1:B:173:ALA:HB2	1:C:346:TYR:HB3	1.96	0.46
1:C:144:GLY:HA2	1:C:147:GLY:N	2.23	0.46
1:C:168:SER:HA	1:C:171:MET:SD	2.55	0.46
1:C:274:ARG:CD	1:C:414:VAL:CG1	2.86	0.46
1:C:444:MET:HA	1:C:445:GLU:HA	1.56	0.46
1:D:56:LEU:HD21	1:D:222:ILE:CG2	2.45	0.46
1:E:73:VAL:HG13	1:E:77:TRP:CD1	2.51	0.46
1:B:20:VAL:HA	1:B:22:PHE:CZ	2.51	0.46
1:B:298:LYS:HZ2	1:B:430:LYS:HA	1.81	0.46
1:C:355:GLN:HB2	1:C:381:LEU:HD21	1.97	0.46
1:C:432:PHE:N	1:C:432:PHE:CD1	2.83	0.46
1:D:191:LEU:N	1:D:192:PRO:HD2	2.31	0.46
1:E:162:VAL:HG23	1:E:208:LEU:HD12	1.98	0.46
1:E:222:ILE:HA	1:E:445:GLU:OE2	2.16	0.46
1:A:55:ILE:HG22	1:A:57:GLN:NE2	2.31	0.46
1:D:57:GLN:CG	1:D:212:LEU:HD13	2.41	0.46
1:D:259:THR:O	1:D:264:VAL:HG23	2.16	0.46
1:D:378:LEU:CD2	1:D:401:THR:OG1	2.55	0.46
1:E:55:ILE:HD13	1:E:215:ASN:CG	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LEU:HB2	1:A:136:HIS:CE1	2.51	0.46
1:A:323:LEU:O	1:A:338:LEU:HA	2.16	0.46
1:B:76:LEU:HG	1:B:134:PRO:HB2	1.96	0.46
1:B:206:MET:HE2	1:B:207:THR:H	1.80	0.46
1:B:280:LYS:HZ1	1:B:437:LEU:C	2.24	0.46
1:B:378:LEU:CD2	1:B:401:THR:HG23	2.46	0.46
1:D:181:VAL:CA	1:D:182:GLN:CG	2.90	0.46
1:D:190:PRO:HB2	1:D:192:PRO:CG	2.45	0.46
1:D:193:SER:O	1:D:194:SER:CB	2.64	0.46
1:D:444:MET:HA	1:D:445:GLU:HA	1.56	0.46
1:E:118:PRO:HD2	1:E:128:ASP:CA	2.44	0.46
1:A:176:LYS:CB	1:B:347:HIS:C	2.86	0.46
1:A:291:PRO:HG2	1:A:295:ASP:CB	2.32	0.46
1:A:345:THR:CB	1:E:173:ALA:HB3	2.39	0.46
1:C:351:ASN:CG	1:C:380:THR:HB	2.41	0.46
1:D:441:ASN:O	1:D:447:ILE:HG23	2.15	0.46
1:E:85:LEU:CB	1:E:136:HIS:ND1	2.73	0.46
1:A:252:ASN:C	1:A:254:GLU:N	2.73	0.45
1:B:274:ARG:HE	1:B:414:VAL:HG11	1.81	0.45
1:B:327:GLN:HG2	1:B:329:ILE:HG22	1.97	0.45
1:C:45:VAL:HG12	1:C:46:LEU:HG	1.98	0.45
1:C:145:ILE:CB	1:C:174:ARG:HG3	2.46	0.45
1:C:420:GLU:CD	1:C:465:MET:HE1	2.41	0.45
1:D:46:LEU:CD2	1:D:54:PHE:HB2	2.46	0.45
1:A:193:SER:O	1:A:194:SER:CB	2.64	0.45
1:B:82:LEU:O	1:B:83:LYS:HB2	2.17	0.45
1:B:173:ALA:HB2	1:C:346:TYR:CB	2.45	0.45
1:B:351:ASN:HB3	1:B:381:LEU:HG	1.98	0.45
1:B:441:ASN:O	1:B:447:ILE:HG23	2.15	0.45
1:C:57:GLN:CG	1:C:212:LEU:HD13	2.41	0.45
1:C:158:ILE:HG22	1:C:197:ILE:HB	1.99	0.45
1:D:161:ASP:O	1:D:165:PRO:HD2	2.16	0.45
1:D:382:ASN:CG	1:D:385:ILE:HG12	2.41	0.45
1:E:156:ILE:HD11	1:E:197:ILE:HD13	1.98	0.45
1:E:259:THR:O	1:E:264:VAL:HG23	2.15	0.45
1:A:46:LEU:HD22	1:A:197:ILE:CG1	2.47	0.45
1:A:259:THR:O	1:A:264:VAL:HG23	2.16	0.45
1:B:159:ALA:HB1	1:B:162:VAL:CG1	2.47	0.45
1:B:355:GLN:HB2	1:B:381:LEU:HD21	1.99	0.45
1:B:370:LYS:NZ	1:B:399:ASP:HA	2.32	0.45
1:C:76:LEU:HD11	1:C:128:ASP:OD2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:403:GLU:HG2	1:D:405:LEU:H	1.81	0.45
1:A:276:LEU:HD23	1:A:278:TYR:HB2	1.97	0.45
1:B:57:GLN:CG	1:B:212:LEU:HD13	2.47	0.45
1:B:144:GLY:O	1:B:171:MET:HG2	2.16	0.45
1:B:221:ILE:HB	1:B:222:ILE:HG13	1.98	0.45
1:B:323:LEU:O	1:B:338:LEU:HA	2.16	0.45
1:B:382:ASN:CG	1:B:385:ILE:HG12	2.41	0.45
1:C:72:VAL:HG13	1:C:85:LEU:CD1	2.42	0.45
1:C:159:ALA:HB1	1:C:162:VAL:CG1	2.46	0.45
1:C:323:LEU:O	1:C:338:LEU:HA	2.16	0.45
1:D:158:ILE:HG22	1:D:197:ILE:HB	1.99	0.45
1:D:161:ASP:O	1:D:164:ILE:HG22	2.16	0.45
1:D:174:ARG:HD3	1:D:174:ARG:HA	1.77	0.45
1:D:309:ALA:HB3	1:D:358:GLN:HE22	1.80	0.45
1:D:328:ASN:CG	1:D:328:ASN:O	2.59	0.45
1:E:84:ILE:HG12	1:E:154:ALA:HA	1.99	0.45
1:E:298:LYS:HZ2	1:E:430:LYS:HA	1.82	0.45
1:A:161:ASP:O	1:A:164:ILE:HG22	2.17	0.45
1:D:36:THR:HB	1:D:39:GLN:HG3	1.97	0.45
1:D:79:ASP:CB	1:D:82:LEU:O	2.65	0.45
1:D:202:PRO:HD3	1:D:265:ARG:HA	1.98	0.45
1:D:323:LEU:O	1:D:338:LEU:HA	2.16	0.45
1:E:368:ARG:H	1:E:401:THR:HG21	1.77	0.45
1:E:379:TYR:O	1:E:385:ILE:CB	2.55	0.45
1:E:415:GLN:C	1:E:418:VAL:HG12	2.41	0.45
1:C:156:ILE:HD11	1:C:197:ILE:HD13	1.98	0.45
1:C:220:THR:C	1:C:445:GLU:CB	2.87	0.45
1:D:364:ASP:C	1:D:364:ASP:OD1	2.59	0.45
1:E:21:ALA:C	1:E:33:PRO:HG3	2.42	0.45
1:E:158:ILE:HG22	1:E:197:ILE:HB	1.99	0.45
1:E:159:ALA:HB1	1:E:162:VAL:CG1	2.46	0.45
1:E:190:PRO:O	1:E:191:LEU:HB2	2.17	0.45
1:E:193:SER:O	1:E:194:SER:CB	2.64	0.45
1:E:323:LEU:O	1:E:338:LEU:HA	2.16	0.45
1:B:73:VAL:HG13	1:B:77:TRP:CD1	2.52	0.45
1:B:77:TRP:CH2	1:B:113:GLU:HG3	2.52	0.45
1:B:299:TYR:HD2	1:B:336:VAL:HG12	1.81	0.45
1:B:351:ASN:CG	1:B:380:THR:HB	2.42	0.45
1:B:456:ARG:HD3	1:B:456:ARG:HA	1.78	0.45
1:D:186:ALA:O	1:D:190:PRO:HD3	2.13	0.45
1:D:415:GLN:C	1:D:418:VAL:HG12	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:465:MET:O	1:D:468:HIS:HB3	2.16	0.45
1:E:252:ASN:C	1:E:254:GLU:H	2.25	0.45
1:A:85:LEU:HD13	1:A:136:HIS:CE1	2.51	0.45
1:A:118:PRO:HG2	1:A:129:VAL:HB	1.98	0.45
1:A:235:LEU:HD22	1:A:245:LEU:CB	2.32	0.45
1:B:226:LEU:HD13	1:B:263:PRO:HB3	1.99	0.45
1:B:394:ARG:O	1:B:394:ARG:HG2	2.17	0.45
1:C:79:ASP:CB	1:C:82:LEU:O	2.65	0.45
1:C:313:LEU:HD21	1:C:377:VAL:HG21	1.98	0.45
1:D:136:HIS:HD1	1:D:138:PRO:HD3	1.81	0.45
1:D:252:ASN:C	1:D:254:GLU:H	2.25	0.45
1:E:163:GLU:HG3	1:E:203:GLN:CB	2.37	0.45
1:A:39:GLN:HG2	1:A:67:ILE:HD11	1.97	0.45
1:A:110:PHE:CG	1:A:111:LEU:N	2.85	0.45
1:A:173:ALA:HB2	1:B:346:TYR:CB	2.45	0.45
1:A:347:HIS:C	1:E:176:LYS:CB	2.86	0.45
1:C:191:LEU:N	1:C:192:PRO:CD	2.80	0.45
1:C:221:ILE:N	1:C:445:GLU:HG2	2.32	0.45
1:D:220:THR:C	1:D:445:GLU:CB	2.87	0.45
1:E:77:TRP:HZ3	1:E:114:LEU:HB2	1.81	0.45
1:E:299:TYR:HA	1:E:300:PRO:CD	2.47	0.45
1:E:394:ARG:HB3	1:E:400:LYS:HA	1.98	0.45
1:A:181:VAL:HG21	1:B:379:TYR:CD2	2.51	0.45
1:A:221:ILE:C	1:A:445:GLU:HG3	2.41	0.45
1:B:79:ASP:CB	1:B:82:LEU:O	2.65	0.45
1:B:158:ILE:HG22	1:B:197:ILE:HB	1.99	0.45
1:B:378:LEU:HD21	1:B:401:THR:HG23	1.97	0.45
1:C:252:ASN:C	1:C:254:GLU:H	2.25	0.45
1:C:468:HIS:HA	1:C:473:ARG:NE	2.31	0.45
1:D:177:LEU:CB	1:E:347:HIS:CD2	2.91	0.45
1:D:202:PRO:HB3	1:D:265:ARG:HH12	1.79	0.45
1:B:57:GLN:HG3	1:B:265:ARG:NH2	2.32	0.44
1:B:145:ILE:N	1:B:171:MET:HG3	2.32	0.44
1:C:144:GLY:HA2	1:C:146:THR:H	1.79	0.44
1:C:173:ALA:HB2	1:D:346:TYR:CB	2.45	0.44
1:D:182:GLN:NE2	1:D:185:ALA:CB	2.46	0.44
1:A:79:ASP:CB	1:A:82:LEU:O	2.65	0.44
1:A:294:SER:CB	1:A:341:ASP:HB2	2.48	0.44
1:A:347:HIS:CB	1:E:176:LYS:C	2.66	0.44
1:A:370:LYS:HE3	1:A:403:GLU:HA	1.98	0.44
1:A:370:LYS:HG2	1:A:375:TYR:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:VAL:HG13	1:B:77:TRP:HD1	1.82	0.44
1:B:180:LEU:HD13	1:B:180:LEU:HA	1.77	0.44
1:B:252:ASN:C	1:B:254:GLU:H	2.25	0.44
1:B:346:TYR:C	1:B:348:ASP:H	2.25	0.44
1:C:220:THR:O	1:C:445:GLU:CD	2.58	0.44
1:C:415:GLN:C	1:C:418:VAL:HG12	2.41	0.44
1:D:173:ALA:HB1	1:E:345:THR:CA	2.36	0.44
1:D:316:ALA:O	1:D:318:MET:HB2	2.17	0.44
1:E:461:LEU:O	1:E:465:MET:HG2	2.17	0.44
1:A:220:THR:C	1:A:445:GLU:HB3	2.41	0.44
1:C:83:LYS:HD3	1:C:193:SER:O	2.17	0.44
1:C:193:SER:O	1:C:194:SER:CB	2.64	0.44
1:C:272:ARG:HB3	1:C:442:CYS:N	2.32	0.44
1:D:161:ASP:O	1:D:165:PRO:HD3	2.18	0.44
1:E:16:LYS:HE2	1:E:74:TRP:HB2	1.99	0.44
1:A:55:ILE:HG22	1:A:57:GLN:HE21	1.81	0.44
1:A:316:ALA:O	1:A:318:MET:HB2	2.17	0.44
1:A:394:ARG:HD3	1:A:394:ARG:N	2.31	0.44
1:B:193:SER:O	1:B:194:SER:CB	2.64	0.44
1:B:266:PHE:CZ	1:B:272:ARG:HG2	2.52	0.44
1:C:221:ILE:CB	1:C:222:ILE:HG13	2.46	0.44
1:C:448:ARG:HG2	1:C:455:MET:SD	2.57	0.44
1:E:10:LEU:HB2	1:E:78:ARG:HD2	2.00	0.44
1:A:190:PRO:O	1:A:191:LEU:HB2	2.17	0.44
1:A:252:ASN:C	1:A:254:GLU:H	2.25	0.44
1:A:415:GLN:C	1:A:418:VAL:HG12	2.41	0.44
1:A:435:ILE:HA	1:A:438:LYS:HG3	1.99	0.44
1:B:30:LEU:HD12	1:B:30:LEU:HA	1.84	0.44
1:B:190:PRO:O	1:B:191:LEU:HB2	2.17	0.44
1:B:403:GLU:HG2	1:B:405:LEU:H	1.82	0.44
1:C:83:LYS:NZ	1:C:193:SER:N	2.39	0.44
1:C:161:ASP:O	1:C:164:ILE:HG22	2.18	0.44
1:D:176:LYS:HG3	1:E:347:HIS:C	2.39	0.44
1:D:226:LEU:HD13	1:D:263:PRO:HB3	1.98	0.44
1:D:346:TYR:CD1	1:D:349:CYS:CA	2.97	0.44
1:E:276:LEU:HD23	1:E:278:TYR:HB2	1.98	0.44
1:E:320:TYR:CD2	1:E:342:ASP:HB3	2.53	0.44
1:E:403:GLU:HG2	1:E:405:LEU:H	1.83	0.44
1:A:37:LYS:HG2	1:A:38:CYS:N	2.33	0.44
1:A:73:VAL:HG22	1:A:77:TRP:HE1	1.83	0.44
1:A:181:VAL:HG21	1:B:379:TYR:CG	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:ARG:HG3	1:A:265:ARG:O	2.17	0.44
1:B:124:VAL:HA	1:B:125:ILE:HB	1.98	0.44
1:D:176:LYS:HB2	1:E:347:HIS:N	2.28	0.44
1:E:161:ASP:O	1:E:165:PRO:HD2	2.18	0.44
1:A:173:ALA:HB1	1:B:345:THR:CA	2.36	0.44
1:A:346:TYR:CD2	1:A:349:CYS:HB2	2.53	0.44
1:C:155:ASP:C	1:C:194:SER:HB3	2.43	0.44
1:C:190:PRO:O	1:C:191:LEU:HB2	2.17	0.44
1:C:346:TYR:C	1:C:348:ASP:H	2.26	0.44
1:C:370:LYS:HG2	1:C:378:LEU:HD11	2.00	0.44
1:E:73:VAL:HG13	1:E:77:TRP:HD1	1.83	0.44
1:E:409:ALA:HB1	1:E:466:GLN:OE1	2.17	0.44
1:A:170:THR:CA	1:B:345:THR:HG21	2.33	0.44
1:A:456:ARG:HD3	1:A:456:ARG:HA	1.80	0.44
1:B:311:LEU:HD13	1:B:323:LEU:HD12	2.00	0.44
1:D:285:LEU:H	1:D:285:LEU:HG	1.49	0.44
1:D:379:TYR:O	1:D:385:ILE:CB	2.55	0.44
1:E:413:GLY:O	1:E:465:MET:CB	2.66	0.44
1:E:441:ASN:O	1:E:447:ILE:HG23	2.18	0.44
1:A:72:VAL:HG13	1:A:85:LEU:CD1	2.44	0.44
1:A:235:LEU:HD22	1:A:245:LEU:HD23	1.99	0.44
1:A:374:GLY:C	1:A:378:LEU:HG	2.38	0.44
1:B:202:PRO:HD3	1:B:265:ARG:HA	2.00	0.44
1:B:241:LEU:O	1:B:242:ALA:C	2.61	0.44
1:C:125:ILE:O	1:C:125:ILE:HG22	2.17	0.44
1:D:21:ALA:C	1:D:33:PRO:HG2	2.42	0.44
1:D:190:PRO:O	1:D:191:LEU:HB2	2.18	0.44
1:E:370:LYS:CE	1:E:375:TYR:HE1	2.25	0.44
1:E:456:ARG:HD3	1:E:456:ARG:HA	1.79	0.44
1:A:241:LEU:O	1:A:242:ALA:C	2.61	0.43
1:A:275:GLU:OE1	1:A:437:LEU:HD13	2.18	0.43
1:A:370:LYS:HB3	1:A:375:TYR:CE1	2.51	0.43
1:B:79:ASP:OD1	1:B:83:LYS:HD2	2.18	0.43
1:C:1:MET:O	1:C:1:MET:HE3	2.18	0.43
1:C:21:ALA:C	1:C:33:PRO:HG2	2.43	0.43
1:C:215:ASN:O	1:C:219:THR:HG22	2.18	0.43
1:C:294:SER:CB	1:C:341:ASP:HB2	2.48	0.43
1:C:413:GLY:O	1:C:465:MET:CB	2.66	0.43
1:D:176:LYS:CE	1:D:180:LEU:HD22	2.48	0.43
1:D:413:GLY:O	1:D:465:MET:CB	2.66	0.43
1:E:346:TYR:C	1:E:348:ASP:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:446:GLU:HB3	1:E:447:ILE:H	1.66	0.43
1:A:158:ILE:HG22	1:A:197:ILE:HB	1.99	0.43
1:A:371:ASP:O	1:A:375:TYR:HD1	2.01	0.43
1:A:441:ASN:O	1:A:447:ILE:HG23	2.17	0.43
1:B:235:LEU:CD2	1:B:245:LEU:CB	2.61	0.43
1:C:202:PRO:HD3	1:C:265:ARG:HA	1.99	0.43
1:D:191:LEU:N	1:D:192:PRO:CD	2.81	0.43
1:D:215:ASN:O	1:D:219:THR:HG22	2.19	0.43
1:D:407:LYS:O	1:D:411:GLN:HG2	2.18	0.43
1:A:155:ASP:C	1:A:194:SER:HB3	2.43	0.43
1:A:403:GLU:HG2	1:A:405:LEU:H	1.83	0.43
1:E:79:ASP:CB	1:E:82:LEU:O	2.65	0.43
1:E:177:LEU:HG	1:E:178:TRP:N	2.33	0.43
1:A:88:SER:HB3	1:A:141:LYS:CG	2.49	0.43
1:A:125:ILE:O	1:A:125:ILE:HG22	2.19	0.43
1:B:46:LEU:HD22	1:B:197:ILE:CG1	2.48	0.43
1:B:119:GLY:HA2	1:B:127:PHE:HD2	1.83	0.43
1:B:156:ILE:HD11	1:B:197:ILE:HD13	1.99	0.43
1:B:378:LEU:HD13	1:B:400:LYS:C	2.43	0.43
1:C:47:ALA:O	1:C:50:ASP:O	2.37	0.43
1:C:241:LEU:O	1:C:242:ALA:C	2.61	0.43
1:C:329:ILE:HG23	1:C:330:ILE:HG12	2.00	0.43
1:C:379:TYR:O	1:C:385:ILE:CB	2.55	0.43
1:C:394:ARG:O	1:C:394:ARG:HG2	2.16	0.43
1:D:101:ILE:HG22	1:D:105:ILE:HD11	2.00	0.43
1:E:18:ASP:O	1:E:32:LEU:HD13	2.18	0.43
1:E:220:THR:C	1:E:445:GLU:HG2	2.43	0.43
1:A:47:ALA:O	1:A:50:ASP:O	2.37	0.43
1:A:413:GLY:O	1:A:465:MET:CB	2.66	0.43
1:B:32:LEU:HD12	1:B:32:LEU:H	1.84	0.43
1:D:194:SER:H	1:D:195:ARG:HG3	1.83	0.43
1:D:346:TYR:C	1:D:348:ASP:H	2.25	0.43
1:D:351:ASN:CG	1:D:380:THR:HB	2.43	0.43
1:E:125:ILE:O	1:E:125:ILE:HG22	2.18	0.43
1:A:215:ASN:O	1:A:219:THR:HG22	2.18	0.43
1:B:33:PRO:CD	1:B:33:PRO:O	2.66	0.43
1:D:10:LEU:HG	1:D:78:ARG:HB3	2.01	0.43
1:D:76:LEU:HD12	1:D:134:PRO:HB2	2.00	0.43
1:D:76:LEU:HG	1:D:134:PRO:HB2	2.00	0.43
1:D:176:LYS:HE3	1:D:180:LEU:HD13	1.99	0.43
1:D:410:LYS:O	1:D:414:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:241:LEU:O	1:E:242:ALA:C	2.61	0.43
1:E:431:VAL:C	1:E:434:PRO:HD2	2.44	0.43
1:A:202:PRO:HD3	1:A:265:ARG:HA	2.01	0.43
1:A:346:TYR:C	1:A:348:ASP:H	2.25	0.43
1:B:155:ASP:C	1:B:194:SER:HB3	2.44	0.43
1:B:413:GLY:O	1:B:465:MET:CB	2.66	0.43
1:B:417:VAL:HA	1:B:465:MET:SD	2.59	0.43
1:C:32:LEU:H	1:C:32:LEU:HD12	1.84	0.43
1:C:88:SER:HB3	1:C:141:LYS:HD2	2.01	0.43
1:C:162:VAL:HA	1:C:165:PRO:HG2	2.00	0.43
1:D:47:ALA:O	1:D:50:ASP:O	2.37	0.43
1:D:347:HIS:CE1	1:D:376:ALA:HB1	2.52	0.43
1:D:432:PHE:O	1:D:436:LEU:HD13	2.19	0.43
1:E:220:THR:HA	1:E:445:GLU:HB2	1.99	0.43
1:E:294:SER:CB	1:E:341:ASP:HB2	2.48	0.43
1:A:82:LEU:O	1:A:83:LYS:HB3	2.18	0.43
1:A:265:ARG:HG3	1:A:265:ARG:HH11	1.84	0.43
1:A:299:TYR:HD2	1:A:336:VAL:HG12	1.84	0.43
1:B:1:MET:O	1:B:1:MET:HE3	2.19	0.43
1:B:57:GLN:HB3	1:B:265:ARG:CZ	2.49	0.43
1:B:159:ALA:CB	1:B:162:VAL:CG1	2.97	0.43
1:B:428:PHE:CE1	1:B:461:LEU:HD22	2.54	0.43
1:C:220:THR:HA	1:C:445:GLU:HB2	1.98	0.43
1:C:370:LYS:C	1:C:375:TYR:CE2	2.97	0.43
1:D:273:GLU:OE2	1:D:441:ASN:HB3	2.19	0.43
1:D:346:TYR:C	1:D:348:ASP:N	2.77	0.43
1:E:299:TYR:CE2	1:E:427:MET:HE1	2.54	0.43
1:E:432:PHE:O	1:E:436:LEU:HD13	2.19	0.43
1:A:161:ASP:HB3	1:A:164:ILE:HG22	2.00	0.43
1:A:346:TYR:C	1:A:348:ASP:N	2.77	0.43
1:A:431:VAL:C	1:A:434:PRO:HD2	2.44	0.43
1:B:91:LYS:CB	1:B:93:ARG:N	2.74	0.43
1:B:307:ILE:O	1:B:364:ASP:OD1	2.36	0.43
1:B:446:GLU:HB3	1:B:447:ILE:H	1.66	0.43
1:B:459:ASP:O	1:B:463:PRO:HD3	2.19	0.43
1:C:144:GLY:HA2	1:C:145:ILE:C	2.43	0.43
1:C:285:LEU:CD2	1:C:431:VAL:HG13	2.40	0.43
1:C:326:ARG:HD2	1:C:335:ASN:HA	2.01	0.43
1:C:436:LEU:HG	1:C:454:GLU:O	2.19	0.43
1:C:456:ARG:HD3	1:C:456:ARG:HA	1.80	0.43
1:D:190:PRO:HB2	1:D:192:PRO:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:381:LEU:HD22	1:D:389:GLU:HB2	2.01	0.43
1:D:436:LEU:HG	1:D:454:GLU:O	2.19	0.43
1:E:77:TRP:HZ3	1:E:114:LEU:CB	2.32	0.43
1:E:199:LEU:HD12	1:E:200:GLY:N	2.34	0.43
1:E:346:TYR:HB2	1:E:348:ASP:OD1	2.19	0.43
1:A:144:GLY:HA2	1:A:146:THR:H	1.79	0.43
1:A:162:VAL:HG21	1:A:198:TYR:HD2	1.84	0.43
1:A:345:THR:CA	1:E:173:ALA:HB1	2.36	0.43
1:B:47:ALA:O	1:B:50:ASP:O	2.37	0.43
1:B:57:GLN:C	1:B:265:ARG:HG2	2.44	0.43
1:B:77:TRP:CZ3	1:B:114:LEU:CB	3.02	0.43
1:B:161:ASP:O	1:B:165:PRO:HD3	2.19	0.43
1:C:338:LEU:HD22	1:C:430:LYS:CG	2.47	0.43
1:C:354:GLY:O	1:C:358:GLN:HG2	2.18	0.43
1:C:368:ARG:HD3	1:C:377:VAL:HG12	1.99	0.43
1:C:368:ARG:N	1:C:401:THR:CG2	2.79	0.43
1:D:346:TYR:CD1	1:D:349:CYS:HB2	2.54	0.43
1:D:381:LEU:HD23	1:D:381:LEU:HA	1.79	0.43
1:E:159:ALA:CB	1:E:162:VAL:CG1	2.97	0.43
1:E:159:ALA:HB3	1:E:198:TYR:CD1	2.53	0.43
1:E:274:ARG:CD	1:E:414:VAL:CG1	2.97	0.43
1:A:145:ILE:HB	1:A:174:ARG:HD2	2.00	0.42
1:B:76:LEU:HA	1:B:79:ASP:OD2	2.19	0.42
1:B:199:LEU:HD23	1:B:200:GLY:N	2.34	0.42
1:B:274:ARG:HD2	1:B:418:VAL:HB	2.00	0.42
1:B:305:ASP:O	1:B:362:VAL:HG11	2.19	0.42
1:C:36:THR:HB	1:C:39:GLN:HG3	2.00	0.42
1:D:64:LYS:HA	1:D:67:ILE:HD12	2.00	0.42
1:D:116:PRO:HB3	1:D:127:PHE:CZ	2.54	0.42
1:D:285:LEU:CD2	1:D:431:VAL:HG13	2.45	0.42
1:E:21:ALA:C	1:E:33:PRO:HD3	2.45	0.42
1:E:133:ASN:N	1:E:134:PRO:CD	2.80	0.42
1:E:144:GLY:HA2	1:E:145:ILE:C	2.43	0.42
1:E:155:ASP:C	1:E:194:SER:HB2	2.44	0.42
1:A:51:ASN:HB3	1:A:52:LYS:H	1.73	0.42
1:A:309:ALA:HB2	1:A:364:ASP:OD2	2.19	0.42
1:B:125:ILE:O	1:B:125:ILE:HG22	2.19	0.42
1:B:145:ILE:H	1:B:171:MET:HG3	1.84	0.42
1:B:163:GLU:HG2	1:B:202:PRO:C	2.44	0.42
1:C:73:VAL:HG13	1:C:77:TRP:HD1	1.84	0.42
1:C:77:TRP:CE2	1:C:105:ILE:HG12	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:406:ALA:C	1:C:408:LYS:H	2.28	0.42
1:D:241:LEU:O	1:D:242:ALA:C	2.61	0.42
1:D:370:LYS:NZ	1:D:375:TYR:HE2	2.15	0.42
1:D:378:LEU:HD11	1:D:401:THR:HB	2.02	0.42
1:D:406:ALA:C	1:D:408:LYS:H	2.28	0.42
1:E:346:TYR:C	1:E:348:ASP:N	2.77	0.42
1:A:21:ALA:C	1:A:33:PRO:HD3	2.43	0.42
1:A:344:HIS:HA	1:A:346:TYR:CE1	2.55	0.42
1:A:413:GLY:O	1:A:465:MET:HB3	2.18	0.42
1:B:368:ARG:N	1:B:401:THR:CG2	2.76	0.42
1:B:473:ARG:C	1:B:475:GLU:H	2.27	0.42
1:C:20:VAL:HA	1:C:22:PHE:CZ	2.54	0.42
1:C:167:ASN:O	1:C:171:MET:HE3	2.19	0.42
1:C:346:TYR:C	1:C:348:ASP:N	2.77	0.42
1:C:473:ARG:C	1:C:475:GLU:H	2.28	0.42
1:D:163:GLU:HG2	1:D:202:PRO:C	2.44	0.42
1:D:181:VAL:CG1	1:E:376:ALA:CA	2.95	0.42
1:E:291:PRO:CD	1:E:295:ASP:O	2.61	0.42
1:A:36:THR:HB	1:A:39:GLN:HG3	2.01	0.42
1:A:163:GLU:HG2	1:A:202:PRO:C	2.45	0.42
1:A:351:ASN:CG	1:A:380:THR:HB	2.44	0.42
1:B:346:TYR:C	1:B:348:ASP:N	2.76	0.42
1:B:400:LYS:O	1:B:401:THR:CG2	2.60	0.42
1:C:83:LYS:CE	1:C:193:SER:N	2.82	0.42
1:C:173:ALA:HB2	1:D:346:TYR:HB3	1.99	0.42
1:D:176:LYS:HB3	1:E:347:HIS:C	2.44	0.42
1:E:15:LEU:HG	1:E:19:PHE:CD2	2.54	0.42
1:E:47:ALA:O	1:E:50:ASP:O	2.37	0.42
1:E:181:VAL:CA	1:E:182:GLN:CG	2.93	0.42
1:A:46:LEU:HD23	1:A:54:PHE:CD2	2.55	0.42
1:A:144:GLY:HA2	1:A:145:ILE:C	2.43	0.42
1:B:220:THR:O	1:B:445:GLU:HB2	2.20	0.42
1:B:338:LEU:HD13	1:B:430:LYS:CG	2.50	0.42
1:B:444:MET:HA	1:B:445:GLU:HA	1.56	0.42
1:C:79:ASP:OD1	1:C:83:LYS:HD2	2.19	0.42
1:C:413:GLY:O	1:C:465:MET:HB3	2.19	0.42
1:D:57:GLN:O	1:D:223:TRP:HD1	2.02	0.42
1:D:382:ASN:CB	1:D:385:ILE:CG1	2.90	0.42
1:E:436:LEU:HG	1:E:454:GLU:O	2.19	0.42
1:A:30:LEU:HD12	1:A:30:LEU:HA	1.87	0.42
1:B:51:ASN:HB2	1:B:54:PHE:HZ	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:LEU:HB2	1:B:136:HIS:NE2	2.34	0.42
1:B:320:TYR:CD1	1:B:342:ASP:HB3	2.54	0.42
1:B:406:ALA:C	1:B:408:LYS:H	2.28	0.42
1:C:141:LYS:NZ	1:C:171:MET:HB2	2.34	0.42
1:C:370:LYS:HG2	1:C:401:THR:HG1	1.83	0.42
1:C:432:PHE:O	1:C:436:LEU:HD13	2.19	0.42
1:C:433:SER:HA	1:C:457:ILE:HG21	2.02	0.42
1:D:313:LEU:HD22	1:D:377:VAL:HG21	2.01	0.42
1:E:406:ALA:C	1:E:408:LYS:H	2.28	0.42
1:A:329:ILE:HG23	1:A:330:ILE:HG12	2.01	0.42
1:B:10:LEU:HA	1:B:78:ARG:HG3	2.01	0.42
1:C:30:LEU:HD12	1:C:30:LEU:HA	1.88	0.42
1:D:52:LYS:CB	1:D:184:PHE:CZ	2.73	0.42
1:E:225:ALA:O	1:E:228:PRO:CD	2.68	0.42
1:E:285:LEU:H	1:E:285:LEU:HG	1.47	0.42
1:E:379:TYR:CA	1:E:385:ILE:HG13	2.45	0.42
1:A:21:ALA:C	1:A:33:PRO:HG3	2.45	0.42
1:A:124:VAL:HA	1:A:125:ILE:HB	1.98	0.42
1:A:351:ASN:ND2	1:A:380:THR:HB	2.34	0.42
1:B:88:SER:HB3	1:B:141:LYS:HB2	2.01	0.42
1:C:441:ASN:O	1:C:447:ILE:HG23	2.19	0.42
1:D:144:GLY:HA2	1:D:146:THR:H	1.80	0.42
1:D:155:ASP:O	1:D:194:SER:CB	2.68	0.42
1:D:294:SER:CB	1:D:341:ASP:HB2	2.49	0.42
1:D:313:LEU:CD1	1:D:374:GLY:CA	2.79	0.42
1:D:346:TYR:CZ	1:D:349:CYS:CB	2.71	0.42
1:E:223:TRP:CZ2	1:E:225:ALA:HB2	2.55	0.42
1:E:235:LEU:CD2	1:E:245:LEU:CB	2.61	0.42
1:E:273:GLU:CG	1:E:280:LYS:HZ1	2.04	0.42
1:E:351:ASN:CG	1:E:380:THR:HB	2.45	0.42
1:E:413:GLY:O	1:E:465:MET:HB3	2.20	0.42
1:A:21:ALA:HB3	1:A:33:PRO:HG3	2.01	0.42
1:A:357:GLN:HE22	1:A:361:LEU:HD11	1.85	0.42
1:B:191:LEU:N	1:B:192:PRO:CD	2.82	0.42
1:B:433:SER:HB2	1:B:457:ILE:HD13	2.02	0.42
1:D:85:LEU:CD2	1:D:136:HIS:HD2	2.17	0.42
1:D:155:ASP:C	1:D:194:SER:HB2	2.45	0.42
1:D:193:SER:HB2	1:D:195:ARG:CZ	2.50	0.42
1:D:473:ARG:C	1:D:475:GLU:H	2.28	0.42
1:E:155:ASP:O	1:E:194:SER:CB	2.68	0.42
1:E:225:ALA:O	1:E:226:LEU:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:299:TYR:HD2	1:E:336:VAL:HG12	1.85	0.42
1:A:333:LEU:O	1:A:426:GLY:HA2	2.20	0.42
1:B:80:PRO:HD2	1:B:83:LYS:NZ	2.35	0.42
1:B:155:ASP:O	1:B:194:SER:CB	2.68	0.42
1:B:468:HIS:HA	1:B:473:ARG:HE	1.85	0.42
1:C:39:GLN:HG2	1:C:67:ILE:HD11	2.02	0.42
1:C:73:VAL:HG13	1:C:77:TRP:CD1	2.55	0.42
1:D:103:ASN:O	1:D:107:LEU:HG	2.20	0.42
1:D:173:ALA:CB	1:E:346:TYR:H	1.92	0.42
1:D:265:ARG:HG3	1:D:265:ARG:HH11	1.84	0.42
1:D:443:ALA:O	1:D:444:MET:C	2.63	0.42
1:E:307:ILE:HG21	1:E:361:LEU:HD13	2.01	0.42
1:A:84:ILE:HB	1:A:135:ASP:OD2	2.20	0.41
1:A:225:ALA:O	1:A:226:LEU:C	2.62	0.41
1:A:225:ALA:O	1:A:228:PRO:CD	2.68	0.41
1:A:354:GLY:O	1:A:358:GLN:HG2	2.20	0.41
1:A:364:ASP:HA	1:A:365:PRO:HD3	1.97	0.41
1:A:473:ARG:C	1:A:475:GLU:H	2.28	0.41
1:B:174:ARG:HD2	1:B:174:ARG:HA	1.87	0.41
1:C:88:SER:CB	1:C:141:LYS:HD2	2.50	0.41
1:C:155:ASP:O	1:C:194:SER:CB	2.68	0.41
1:C:163:GLU:HG2	1:C:202:PRO:C	2.44	0.41
1:C:393:PHE:O	1:C:401:THR:HA	2.20	0.41
1:C:443:ALA:O	1:C:444:MET:C	2.63	0.41
1:D:145:ILE:HG21	1:D:170:THR:HB	2.02	0.41
1:D:206:MET:HE2	1:D:206:MET:HB3	1.83	0.41
1:D:370:LYS:HG2	1:D:375:TYR:CD2	2.55	0.41
1:E:393:PHE:O	1:E:401:THR:HA	2.20	0.41
1:A:173:ALA:O	1:B:347:HIS:N	2.53	0.41
1:A:393:PHE:O	1:A:401:THR:HA	2.20	0.41
1:B:409:ALA:HB1	1:B:466:GLN:OE1	2.20	0.41
1:C:159:ALA:CB	1:C:162:VAL:CG1	2.98	0.41
1:C:225:ALA:O	1:C:228:PRO:CD	2.68	0.41
1:D:225:ALA:O	1:D:228:PRO:CD	2.68	0.41
1:D:370:LYS:HB3	1:D:375:TYR:CE1	2.53	0.41
1:E:16:LYS:HD2	1:E:16:LYS:O	2.20	0.41
1:E:63:GLY:O	1:E:66:PHE:HB2	2.21	0.41
1:E:251:GLU:C	1:E:252:ASN:O	2.63	0.41
1:A:10:LEU:HA	1:A:78:ARG:HG3	2.02	0.41
1:A:145:ILE:HG21	1:A:170:THR:HB	2.02	0.41
1:B:159:ALA:HB2	1:B:198:TYR:HE1	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ALA:O	1:C:347:HIS:N	2.53	0.41
1:B:220:THR:C	1:B:445:GLU:HB2	2.46	0.41
1:C:60:ARG:HG2	1:C:201:THR:CG2	2.35	0.41
1:C:110:PHE:CG	1:C:111:LEU:N	2.89	0.41
1:D:36:THR:C	1:D:40:ILE:HD12	2.46	0.41
1:D:56:LEU:HB2	1:D:199:LEU:HG	2.02	0.41
1:D:56:LEU:HD23	1:D:222:ILE:HG23	1.93	0.41
1:D:118:PRO:HG3	1:D:129:VAL:HB	2.02	0.41
1:D:125:ILE:O	1:D:125:ILE:HG22	2.19	0.41
1:D:173:ALA:O	1:E:347:HIS:N	2.53	0.41
1:D:393:PHE:O	1:D:401:THR:HA	2.20	0.41
1:E:316:ALA:O	1:E:318:MET:HB2	2.20	0.41
1:E:473:ARG:C	1:E:475:GLU:H	2.28	0.41
1:A:63:GLY:O	1:A:66:PHE:HB2	2.20	0.41
1:A:193:SER:HB2	1:A:195:ARG:NH2	2.35	0.41
1:A:280:LYS:HA	1:A:283:PHE:CD2	2.55	0.41
1:A:432:PHE:O	1:A:436:LEU:HD13	2.20	0.41
1:A:436:LEU:HG	1:A:454:GLU:O	2.21	0.41
1:B:110:PHE:CG	1:B:111:LEU:N	2.88	0.41
1:B:433:SER:HB2	1:B:457:ILE:HD11	2.03	0.41
1:C:84:ILE:HB	1:C:135:ASP:OD2	2.21	0.41
1:C:173:ALA:O	1:D:347:HIS:N	2.53	0.41
1:D:118:PRO:HG3	1:D:129:VAL:CB	2.51	0.41
1:D:188:LEU:HD23	1:D:188:LEU:HA	1.91	0.41
1:D:333:LEU:O	1:D:426:GLY:HA2	2.21	0.41
1:E:272:ARG:HB3	1:E:441:ASN:HB2	2.02	0.41
1:A:81:GLN:C	1:A:82:LEU:HG	2.45	0.41
1:A:156:ILE:HD11	1:A:197:ILE:HD13	2.02	0.41
1:A:173:ALA:CB	1:B:346:TYR:H	1.92	0.41
1:A:327:GLN:HG2	1:A:329:ILE:HG22	2.01	0.41
1:B:161:ASP:O	1:B:164:ILE:HG22	2.20	0.41
1:B:225:ALA:O	1:B:228:PRO:CD	2.68	0.41
1:B:333:LEU:O	1:B:426:GLY:HA2	2.21	0.41
1:B:402:LEU:HD22	1:B:466:GLN:NE2	2.35	0.41
1:B:443:ALA:O	1:B:444:MET:C	2.63	0.41
1:C:205:GLU:HG2	1:C:209:TYR:CD2	2.55	0.41
1:D:63:GLY:O	1:D:66:PHE:HB2	2.20	0.41
1:D:272:ARG:HB3	1:D:442:CYS:N	2.35	0.41
1:D:326:ARG:NH2	1:D:333:LEU:HD22	2.35	0.41
1:E:51:ASN:HB2	1:E:54:PHE:CE2	2.51	0.41
1:A:443:ALA:O	1:A:444:MET:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:GLY:O	1:B:66:PHE:HB2	2.21	0.41
1:B:220:THR:HG21	1:B:446:GLU:CD	2.44	0.41
1:B:223:TRP:CE3	1:B:444:MET:CB	2.97	0.41
1:C:235:LEU:HA	1:C:235:LEU:HD23	1.49	0.41
1:D:149:LEU:HG	1:D:174:ARG:NH1	2.36	0.41
1:E:443:ALA:O	1:E:444:MET:C	2.63	0.41
1:A:16:LYS:HD2	1:A:16:LYS:C	2.45	0.41
1:A:59:PHE:HB2	1:A:263:PRO:HA	2.03	0.41
1:B:276:LEU:HG	1:B:278:TYR:H	1.85	0.41
1:C:333:LEU:O	1:C:426:GLY:HA2	2.20	0.41
1:C:357:GLN:NE2	1:C:361:LEU:HD11	2.36	0.41
1:D:46:LEU:HD22	1:D:197:ILE:CG1	2.50	0.41
1:D:88:SER:HB3	1:D:141:LYS:HB2	2.02	0.41
1:D:187:LEU:C	1:D:192:PRO:HB2	2.46	0.41
1:A:56:LEU:HD23	1:A:222:ILE:HG23	2.01	0.41
1:A:155:ASP:O	1:A:194:SER:CB	2.68	0.41
1:A:174:ARG:NE	1:A:174:ARG:HA	2.35	0.41
1:B:299:TYR:HE2	1:B:427:MET:HE1	1.85	0.41
1:B:347:HIS:CE1	1:B:373:THR:HA	2.56	0.41
1:B:470:LEU:HG	1:B:472:ILE:H	1.86	0.41
1:C:167:ASN:O	1:C:171:MET:CE	2.68	0.41
1:C:218:TYR:O	1:C:408:LYS:HD3	2.21	0.41
1:D:72:VAL:HG13	1:D:85:LEU:CD1	2.48	0.41
1:D:276:LEU:HD23	1:D:278:TYR:HB2	2.02	0.41
1:E:351:ASN:ND2	1:E:380:THR:HB	2.36	0.41
1:A:320:TYR:CD1	1:A:342:ASP:HB3	2.56	0.41
1:A:345:THR:CA	1:E:173:ALA:CB	2.95	0.41
1:A:347:HIS:N	1:E:173:ALA:O	2.53	0.41
1:A:370:LYS:HE3	1:A:403:GLU:CA	2.50	0.41
1:A:370:LYS:HG2	1:A:375:TYR:CE2	2.56	0.41
1:A:409:ALA:HA	1:A:466:GLN:NE2	2.36	0.41
1:B:141:LYS:HZ3	1:B:171:MET:HB2	1.85	0.41
1:B:225:ALA:O	1:B:226:LEU:C	2.62	0.41
1:B:265:ARG:HG3	1:B:265:ARG:O	2.21	0.41
1:B:272:ARG:HD3	1:B:442:CYS:HB2	2.02	0.41
1:B:431:VAL:C	1:B:434:PRO:HD2	2.46	0.41
1:C:124:VAL:HA	1:C:125:ILE:HB	2.00	0.41
1:C:225:ALA:O	1:C:226:LEU:C	2.62	0.41
1:D:249:TYR:O	1:D:253:PRO:HD2	2.21	0.41
1:D:313:LEU:CD2	1:D:377:VAL:HG21	2.51	0.41
1:E:36:THR:C	1:E:40:ILE:HD12	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:LYS:CB	1:E:184:PHE:CZ	2.74	0.41
1:E:59:PHE:HB2	1:E:263:PRO:HA	2.03	0.41
1:E:86:ILE:O	1:E:157:ILE:HA	2.21	0.41
1:E:271:LEU:HD13	1:E:271:LEU:HA	1.90	0.41
1:E:333:LEU:O	1:E:426:GLY:HA2	2.21	0.41
1:E:370:LYS:O	1:E:375:TYR:CE2	2.73	0.41
1:E:374:GLY:O	1:E:378:LEU:HG	2.21	0.41
1:A:459:ASP:O	1:A:463:PRO:HD3	2.20	0.41
1:B:83:LYS:CE	1:B:192:PRO:HA	2.50	0.41
1:B:182:GLN:HG3	1:B:185:ALA:H	1.86	0.41
1:C:133:ASN:N	1:C:134:PRO:CD	2.77	0.41
1:C:314:GLU:OE1	1:C:321:GLN:HB2	2.21	0.41
1:C:409:ALA:HA	1:C:466:GLN:OE1	2.21	0.41
1:D:81:GLN:C	1:D:82:LEU:HG	2.46	0.41
1:D:182:GLN:HG3	1:D:185:ALA:H	1.86	0.41
1:E:20:VAL:CG1	1:E:108:LEU:HD23	2.51	0.41
1:E:433:SER:HA	1:E:457:ILE:HD13	2.03	0.41
1:E:473:ARG:C	1:E:475:GLU:N	2.79	0.41
1:A:55:ILE:HD12	1:A:198:TYR:HB2	2.03	0.40
1:A:88:SER:HB3	1:A:141:LYS:HB2	2.02	0.40
1:A:173:ALA:CB	1:B:345:THR:CA	2.95	0.40
1:B:116:PRO:HB3	1:B:127:PHE:CZ	2.56	0.40
1:B:379:TYR:CB	1:B:385:ILE:HG21	2.49	0.40
1:B:433:SER:HA	1:B:457:ILE:HG21	2.03	0.40
1:C:99:ILE:O	1:C:102:LYS:HB2	2.21	0.40
1:C:407:LYS:O	1:C:411:GLN:HG2	2.20	0.40
1:D:124:VAL:HA	1:D:125:ILE:HB	1.97	0.40
1:D:155:ASP:C	1:D:194:SER:HB3	2.45	0.40
1:D:378:LEU:HD21	1:D:401:THR:HG1	1.83	0.40
1:E:30:LEU:HD12	1:E:30:LEU:HA	1.87	0.40
1:E:235:LEU:HA	1:E:235:LEU:HD23	1.49	0.40
1:E:330:ILE:HG13	1:E:332:ASP:O	2.21	0.40
1:A:22:PHE:HA	1:A:33:PRO:HD3	2.03	0.40
1:A:406:ALA:C	1:A:408:LYS:H	2.28	0.40
1:C:416:THR:HB	1:C:465:MET:HB3	2.03	0.40
1:D:86:ILE:O	1:D:157:ILE:HA	2.21	0.40
1:D:91:LYS:HB2	1:D:93:ARG:HB3	2.01	0.40
1:D:280:LYS:HA	1:D:283:PHE:CD2	2.56	0.40
1:E:145:ILE:HG22	1:E:170:THR:C	2.46	0.40
1:E:182:GLN:HG3	1:E:185:ALA:H	1.85	0.40
1:E:382:ASN:CB	1:E:385:ILE:CG1	2.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ARG:HA	1:A:174:ARG:HE	1.86	0.40
1:A:382:ASN:ND2	1:A:400:LYS:HD3	2.37	0.40
1:A:433:SER:HA	1:A:457:ILE:HG21	2.02	0.40
1:B:373:THR:C	1:B:376:ALA:HB3	2.46	0.40
1:C:59:PHE:HB2	1:C:263:PRO:HA	2.03	0.40
1:C:63:GLY:O	1:C:66:PHE:HB2	2.21	0.40
1:C:461:LEU:O	1:C:465:MET:HG2	2.22	0.40
1:D:275:GLU:OE1	1:D:437:LEU:HD13	2.21	0.40
1:D:378:LEU:CD2	1:D:401:THR:HG1	2.35	0.40
1:E:99:ILE:O	1:E:102:LYS:HB2	2.21	0.40
1:A:14:GLN:CD	1:A:40:ILE:HG12	2.45	0.40
1:A:56:LEU:HD21	1:A:222:ILE:HG21	2.04	0.40
1:A:79:ASP:OD2	1:A:83:LYS:HE2	2.21	0.40
1:A:91:LYS:HD3	1:A:92:GLU:HB2	2.04	0.40
1:A:145:ILE:H	1:A:145:ILE:HG23	1.67	0.40
1:A:145:ILE:HG22	1:A:170:THR:C	2.46	0.40
1:A:163:GLU:CG	1:A:203:GLN:N	2.78	0.40
1:A:180:LEU:HD13	1:A:180:LEU:HA	1.76	0.40
1:A:187:LEU:C	1:A:192:PRO:HB2	2.47	0.40
1:A:251:GLU:C	1:A:252:ASN:O	2.63	0.40
1:B:20:VAL:CG1	1:B:109:PRO:HD2	2.51	0.40
1:B:54:PHE:CD1	1:B:221:ILE:HD12	2.57	0.40
1:B:54:PHE:HD1	1:B:221:ILE:HD12	1.86	0.40
1:B:133:ASN:N	1:B:134:PRO:CD	2.81	0.40
1:B:187:LEU:C	1:B:192:PRO:HB2	2.47	0.40
1:B:272:ARG:HB3	1:B:442:CYS:H	1.86	0.40
1:B:457:ILE:O	1:B:460:THR:HG22	2.22	0.40
1:C:187:LEU:C	1:C:192:PRO:HB2	2.47	0.40
1:C:320:TYR:CD1	1:C:342:ASP:HB3	2.56	0.40
1:C:417:VAL:HG23	1:C:465:MET:CE	2.51	0.40
1:D:99:ILE:O	1:D:102:LYS:HB2	2.21	0.40
1:D:173:ALA:CB	1:E:345:THR:CA	2.95	0.40
1:D:431:VAL:C	1:D:434:PRO:HD2	2.46	0.40
1:E:21:ALA:HB3	1:E:33:PRO:HG3	2.03	0.40
1:E:73:VAL:CG2	1:E:105:ILE:CG1	2.69	0.40
1:E:124:VAL:HA	1:E:125:ILE:HB	1.98	0.40
1:E:187:LEU:C	1:E:192:PRO:HB2	2.47	0.40
1:E:187:LEU:O	1:E:192:PRO:HD2	2.21	0.40
1:E:370:LYS:HE3	1:E:399:ASP:CG	2.46	0.40
1:E:376:ALA:C	1:E:378:LEU:N	2.80	0.40
1:A:84:ILE:HG13	1:A:135:ASP:OD1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ILE:O	1:A:102:LYS:HB2	2.21	0.40
1:A:370:LYS:NZ	1:A:399:ASP:HB3	2.34	0.40
1:A:379:TYR:CA	1:A:385:ILE:HG13	2.43	0.40
1:A:473:ARG:C	1:A:475:GLU:N	2.79	0.40
1:B:311:LEU:HB2	1:B:323:LEU:HD12	2.03	0.40
1:B:338:LEU:HD13	1:B:430:LYS:HB2	2.03	0.40
1:B:473:ARG:C	1:B:475:GLU:N	2.79	0.40
1:C:14:GLN:CD	1:C:40:ILE:HG12	2.46	0.40
1:C:81:GLN:C	1:C:82:LEU:HG	2.47	0.40
1:C:145:ILE:HG22	1:C:170:THR:C	2.47	0.40
1:E:163:GLU:HG2	1:E:203:GLN:H	1.82	0.40
1:E:191:LEU:N	1:E:192:PRO:CD	2.85	0.40
1:E:337:GLY:C	1:E:338:LEU:HD12	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	468/476 (98%)	394 (84%)	46 (10%)	28 (6%)	1	13
1	B	468/476 (98%)	394 (84%)	46 (10%)	28 (6%)	1	13
1	C	468/476 (98%)	394 (84%)	46 (10%)	28 (6%)	1	13
1	D	468/476 (98%)	394 (84%)	46 (10%)	28 (6%)	1	13
1	E	468/476 (98%)	394 (84%)	46 (10%)	28 (6%)	1	13
All	All	2340/2380 (98%)	1970 (84%)	230 (10%)	140 (6%)	2	13

All (140) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	LYS

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Mol	Chain	Res	Type
1	A	92	GLU
1	A	125	ILE
1	A	132	ALA
1	A	182	GLN
1	A	191	LEU
1	A	194	SER
1	A	195	ARG
1	A	252	ASN
1	A	253	PRO
1	A	376	ALA
1	A	401	THR
1	A	407	LYS
1	A	475	GLU
1	B	83	LYS
1	B	92	GLU
1	B	125	ILE
1	B	132	ALA
1	B	182	GLN
1	B	191	LEU
1	B	194	SER
1	B	195	ARG
1	B	252	ASN
1	B	253	PRO
1	B	376	ALA
1	B	401	THR
1	B	407	LYS
1	B	475	GLU
1	C	83	LYS
1	C	92	GLU
1	C	125	ILE
1	C	132	ALA
1	C	182	GLN
1	C	191	LEU
1	C	194	SER
1	C	195	ARG
1	C	252	ASN
1	C	253	PRO
1	C	376	ALA
1	C	401	THR
1	C	407	LYS
1	C	475	GLU
1	D	83	LYS

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Mol	Chain	Res	Type
1	D	92	GLU
1	D	125	ILE
1	D	132	ALA
1	D	182	GLN
1	D	191	LEU
1	D	194	SER
1	D	195	ARG
1	D	252	ASN
1	D	253	PRO
1	D	376	ALA
1	D	401	THR
1	D	407	LYS
1	D	475	GLU
1	E	83	LYS
1	E	92	GLU
1	E	125	ILE
1	E	132	ALA
1	E	182	GLN
1	E	191	LEU
1	E	194	SER
1	E	195	ARG
1	E	252	ASN
1	E	253	PRO
1	E	376	ALA
1	E	401	THR
1	E	407	LYS
1	E	475	GLU
1	A	52	LYS
1	A	474	ASP
1	B	52	LYS
1	B	474	ASP
1	C	52	LYS
1	C	474	ASP
1	D	52	LYS
1	D	474	ASP
1	E	52	LYS
1	E	474	ASP
1	A	192	PRO
1	B	192	PRO
1	C	192	PRO
1	D	192	PRO
1	E	192	PRO

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Mol	Chain	Res	Type
1	A	133	ASN
1	A	206	MET
1	A	224	PRO
1	A	254	GLU
1	B	133	ASN
1	B	206	MET
1	B	224	PRO
1	B	254	GLU
1	C	133	ASN
1	C	206	MET
1	C	224	PRO
1	C	254	GLU
1	D	133	ASN
1	D	206	MET
1	D	224	PRO
1	D	254	GLU
1	E	133	ASN
1	E	206	MET
1	E	224	PRO
1	E	254	GLU
1	A	164	ILE
1	A	385	ILE
1	A	406	ALA
1	B	164	ILE
1	B	385	ILE
1	B	406	ALA
1	C	164	ILE
1	C	385	ILE
1	C	406	ALA
1	D	164	ILE
1	D	385	ILE
1	D	406	ALA
1	E	164	ILE
1	E	385	ILE
1	E	406	ALA
1	A	334	PRO
1	B	334	PRO
1	C	334	PRO
1	D	334	PRO
1	E	334	PRO
1	A	118	PRO
1	A	329	ILE

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Mol	Chain	Res	Type
1	B	118	PRO
1	B	329	ILE
1	C	118	PRO
1	C	329	ILE
1	D	118	PRO
1	D	329	ILE
1	E	118	PRO
1	E	329	ILE
1	A	263	PRO
1	B	263	PRO
1	C	263	PRO
1	D	263	PRO
1	E	263	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	409/411 (100%)	366 (90%)	43 (10%)	6	21
1	B	409/411 (100%)	348 (85%)	61 (15%)	3	12
1	C	409/411 (100%)	360 (88%)	49 (12%)	5	17
1	D	409/411 (100%)	357 (87%)	52 (13%)	4	16
1	E	409/411 (100%)	359 (88%)	50 (12%)	5	17
All	All	2045/2055 (100%)	1790 (88%)	255 (12%)	7	16

All (255) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	VAL
1	A	20	VAL
1	A	24	PHE
1	A	37	LYS
1	A	44	LYS
1	A	45	VAL

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Mol	Chain	Res	Type
1	A	51	ASN
1	A	65	SER
1	A	67	ILE
1	A	73	VAL
1	A	87	VAL
1	A	90	SER
1	A	106	ASP
1	A	123	SER
1	A	149	LEU
1	A	152	SER
1	A	174	ARG
1	A	180	LEU
1	A	190	PRO
1	A	192	PRO
1	A	208	LEU
1	A	213	GLU
1	A	220	THR
1	A	228	PRO
1	A	238	SER
1	A	241	LEU
1	A	250	ASP
1	A	260	PRO
1	A	271	LEU
1	A	346	TYR
1	A	348	ASP
1	A	357	GLN
1	A	370	LYS
1	A	389	GLU
1	A	394	ARG
1	A	401	THR
1	A	411	GLN
1	A	420	GLU
1	A	425	ASP
1	A	431	VAL
1	A	445	GLU
1	A	463	PRO
1	A	476	VAL
1	B	20	VAL
1	B	24	PHE
1	B	28	LYS
1	B	33	PRO
1	B	45	VAL

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Mol	Chain	Res	Type
1	B	51	ASN
1	B	65	SER
1	B	66	PHE
1	B	67	ILE
1	B	73	VAL
1	B	80	PRO
1	B	87	VAL
1	B	90	SER
1	B	106	ASP
1	B	123	SER
1	B	126	SER
1	B	149	LEU
1	B	161	ASP
1	B	162	VAL
1	B	165	PRO
1	B	176	LYS
1	B	177	LEU
1	B	180	LEU
1	B	190	PRO
1	B	192	PRO
1	B	204	THR
1	B	205	GLU
1	B	206	MET
1	B	208	LEU
1	B	213	GLU
1	B	214	ASP
1	B	219	THR
1	B	222	ILE
1	B	228	PRO
1	B	238	SER
1	B	240	ARG
1	B	241	LEU
1	B	260	PRO
1	B	271	LEU
1	B	283	PHE
1	B	285	LEU
1	B	323	LEU
1	B	324	PRO
1	B	338	LEU
1	B	339	LYS
1	B	348	ASP
1	B	362	VAL

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Mol	Chain	Res	Type
1	B	370	LYS
1	B	393	PHE
1	B	398	SER
1	B	400	LYS
1	B	408	LYS
1	B	411	GLN
1	B	412	TRP
1	B	415	GLN
1	B	418	VAL
1	B	431	VAL
1	B	432	PHE
1	B	452	MET
1	B	463	PRO
1	B	474	ASP
1	C	16	LYS
1	C	20	VAL
1	C	24	PHE
1	C	33	PRO
1	C	37	LYS
1	C	45	VAL
1	C	65	SER
1	C	67	ILE
1	C	73	VAL
1	C	80	PRO
1	C	87	VAL
1	C	106	ASP
1	C	115	LYS
1	C	123	SER
1	C	149	LEU
1	C	162	VAL
1	C	177	LEU
1	C	180	LEU
1	C	190	PRO
1	C	192	PRO
1	C	204	THR
1	C	205	GLU
1	C	208	LEU
1	C	220	THR
1	C	222	ILE
1	C	228	PRO
1	C	238	SER
1	C	260	PRO

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Mol	Chain	Res	Type
1	C	268	ARG
1	C	271	LEU
1	C	277	GLU
1	C	280	LYS
1	C	285	LEU
1	C	288	MET
1	C	293	LEU
1	C	324	PRO
1	C	335	ASN
1	C	339	LYS
1	C	352	ASN
1	C	370	LYS
1	C	393	PHE
1	C	394	ARG
1	C	398	SER
1	C	412	TRP
1	C	431	VAL
1	C	445	GLU
1	C	462	GLU
1	C	463	PRO
1	C	474	ASP
1	D	8	ASN
1	D	20	VAL
1	D	24	PHE
1	D	28	LYS
1	D	33	PRO
1	D	42	MET
1	D	44	LYS
1	D	45	VAL
1	D	51	ASN
1	D	56	LEU
1	D	65	SER
1	D	73	VAL
1	D	76	LEU
1	D	84	ILE
1	D	87	VAL
1	D	106	ASP
1	D	109	PRO
1	D	113	GLU
1	D	149	LEU
1	D	161	ASP
1	D	165	PRO

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Mol	Chain	Res	Type
1	D	177	LEU
1	D	180	LEU
1	D	183	GLU
1	D	190	PRO
1	D	192	PRO
1	D	208	LEU
1	D	210	LYS
1	D	214	ASP
1	D	220	THR
1	D	228	PRO
1	D	238	SER
1	D	254	GLU
1	D	260	PRO
1	D	262	ASP
1	D	269	ASP
1	D	271	LEU
1	D	273	GLU
1	D	277	GLU
1	D	285	LEU
1	D	352	ASN
1	D	357	GLN
1	D	370	LYS
1	D	381	LEU
1	D	389	GLU
1	D	393	PHE
1	D	401	THR
1	D	431	VAL
1	D	432	PHE
1	D	462	GLU
1	D	463	PRO
1	D	474	ASP
1	E	11	VAL
1	E	20	VAL
1	E	24	PHE
1	E	28	LYS
1	E	44	LYS
1	E	45	VAL
1	E	65	SER
1	E	66	PHE
1	E	67	ILE
1	E	73	VAL
1	E	84	ILE

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Mol	Chain	Res	Type
1	E	87	VAL
1	E	90	SER
1	E	115	LYS
1	E	123	SER
1	E	126	SER
1	E	148	GLN
1	E	149	LEU
1	E	162	VAL
1	E	164	ILE
1	E	165	PRO
1	E	177	LEU
1	E	179	THR
1	E	181	VAL
1	E	183	GLU
1	E	190	PRO
1	E	192	PRO
1	E	204	THR
1	E	205	GLU
1	E	219	THR
1	E	222	ILE
1	E	228	PRO
1	E	238	SER
1	E	260	PRO
1	E	262	ASP
1	E	277	GLU
1	E	285	LEU
1	E	339	LYS
1	E	343	LEU
1	E	346	TYR
1	E	348	ASP
1	E	370	LYS
1	E	393	PHE
1	E	395	ASP
1	E	408	LYS
1	E	411	GLN
1	E	431	VAL
1	E	445	GLU
1	E	462	GLU
1	E	463	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	182	GLN
1	A	325	ASN
1	A	351	ASN
1	A	357	GLN
1	A	358	GLN
1	A	440	HIS
1	B	97	ASN
1	B	136	HIS
1	B	182	GLN
1	B	286	GLN
1	B	325	ASN
1	B	347	HIS
1	B	351	ASN
1	B	358	GLN
1	C	57	GLN
1	C	97	ASN
1	C	182	GLN
1	C	325	ASN
1	C	335	ASN
1	C	351	ASN
1	C	357	GLN
1	C	358	GLN
1	C	411	GLN
1	C	415	GLN
1	D	136	HIS
1	D	182	GLN
1	D	325	ASN
1	D	347	HIS
1	D	351	ASN
1	D	352	ASN
1	D	358	GLN
1	D	411	GLN
1	D	440	HIS
1	E	97	ASN
1	E	148	GLN
1	E	182	GLN
1	E	321	GLN
1	E	325	ASN
1	E	335	ASN
1	E	351	ASN
1	E	357	GLN
1	E	358	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

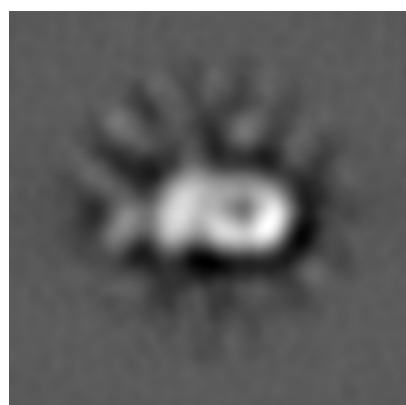
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2355. These allow visual inspection of the internal detail of the map and identification of artifacts.

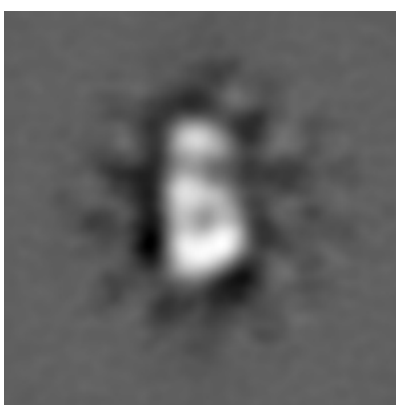
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

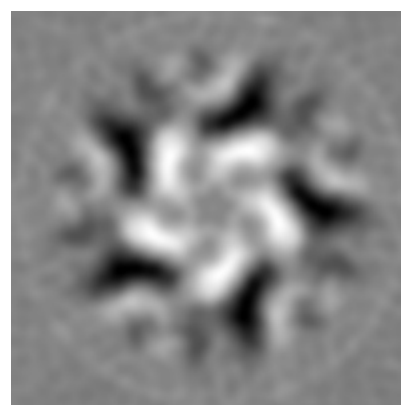
6.1.1 Primary map



X



Y

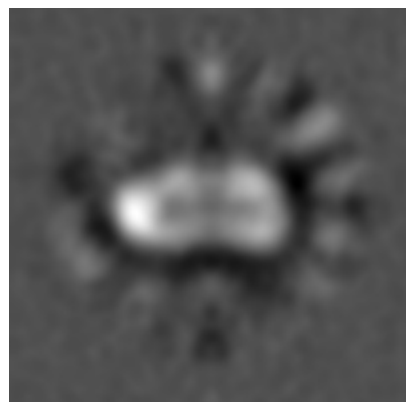


Z

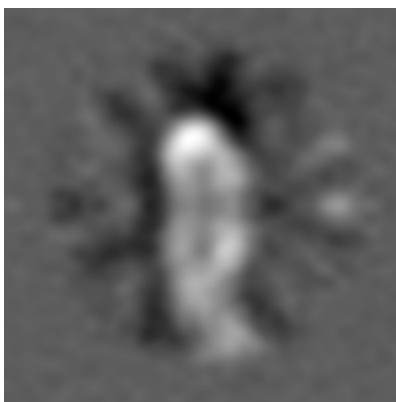
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

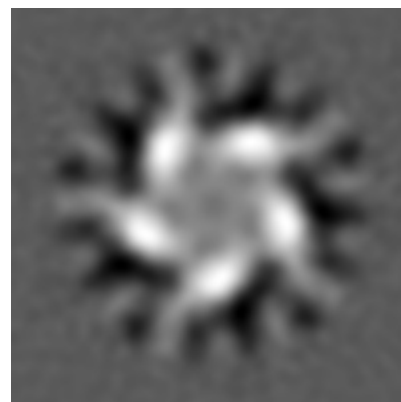
6.2.1 Primary map



X Index: 40



Y Index: 40

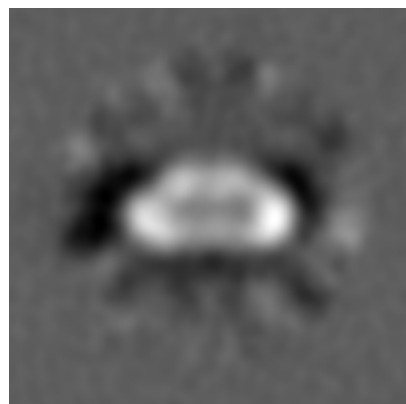


Z Index: 40

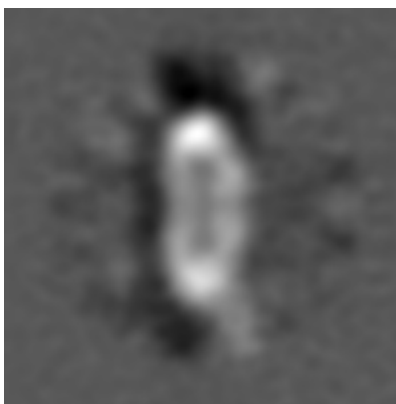
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

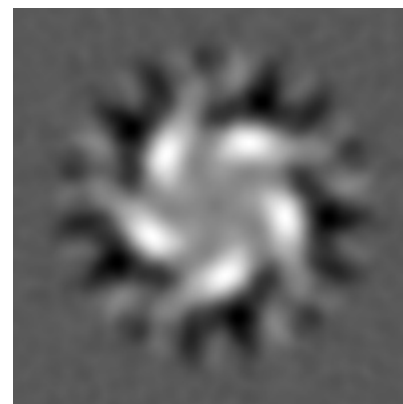
6.3.1 Primary map



X Index: 45



Y Index: 37

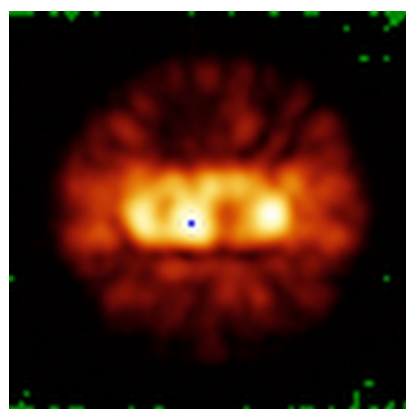


Z Index: 37

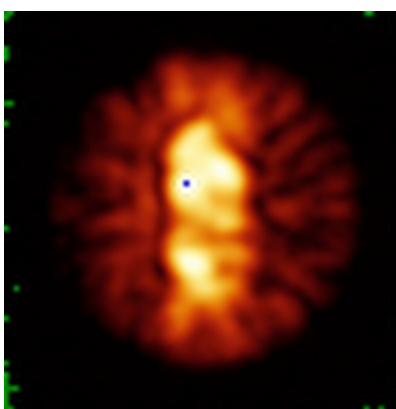
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

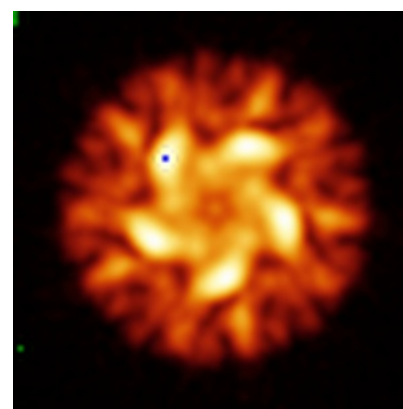
6.4.1 Primary map



X



Y

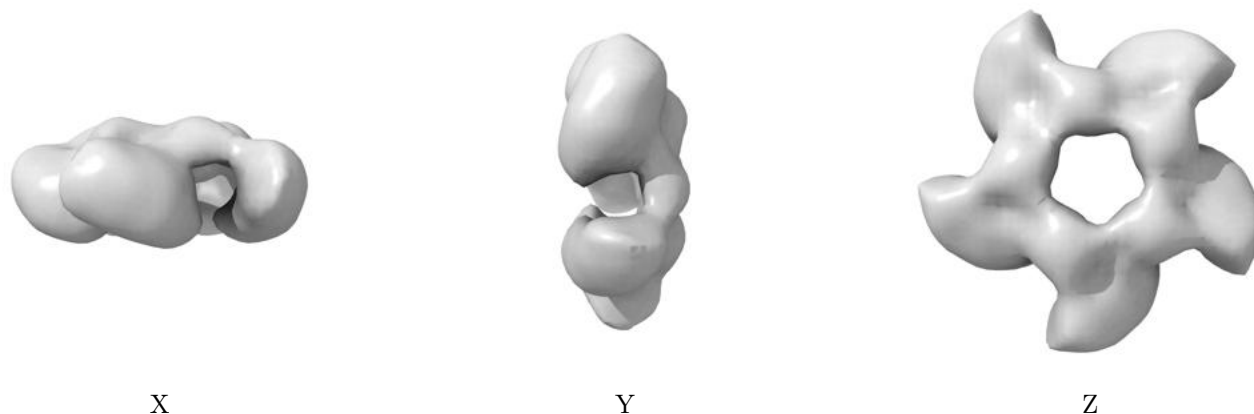


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0383. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

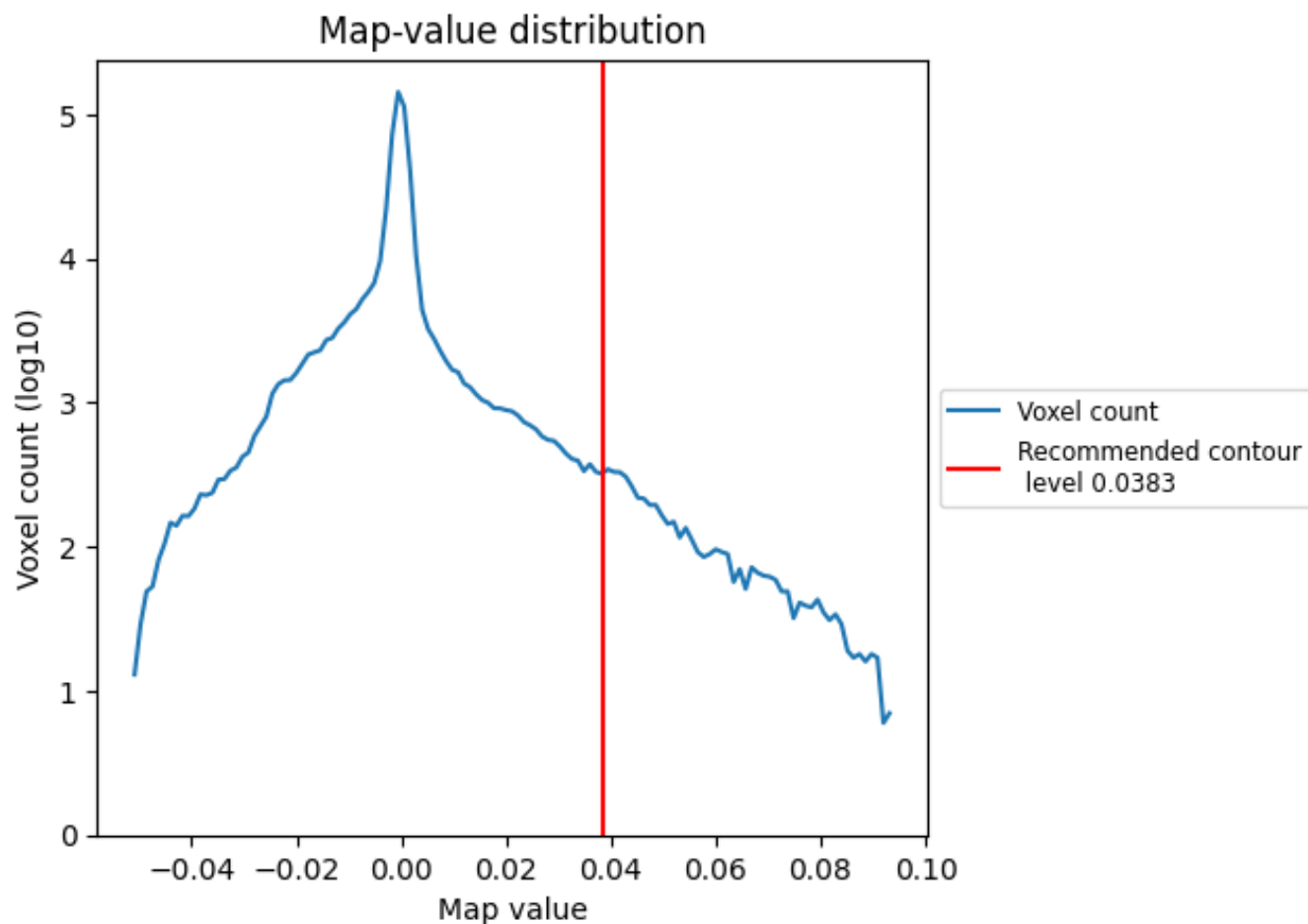
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

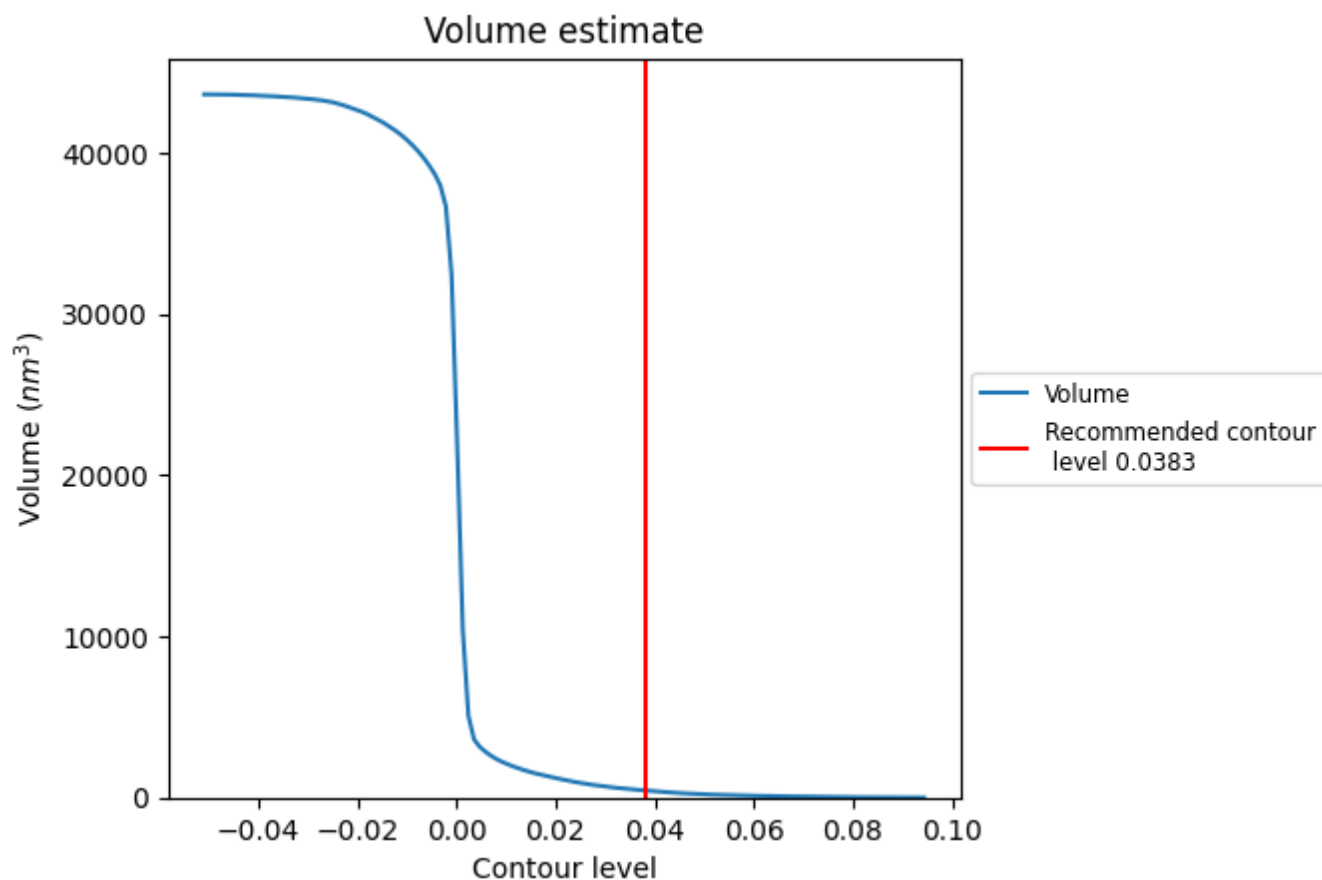
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

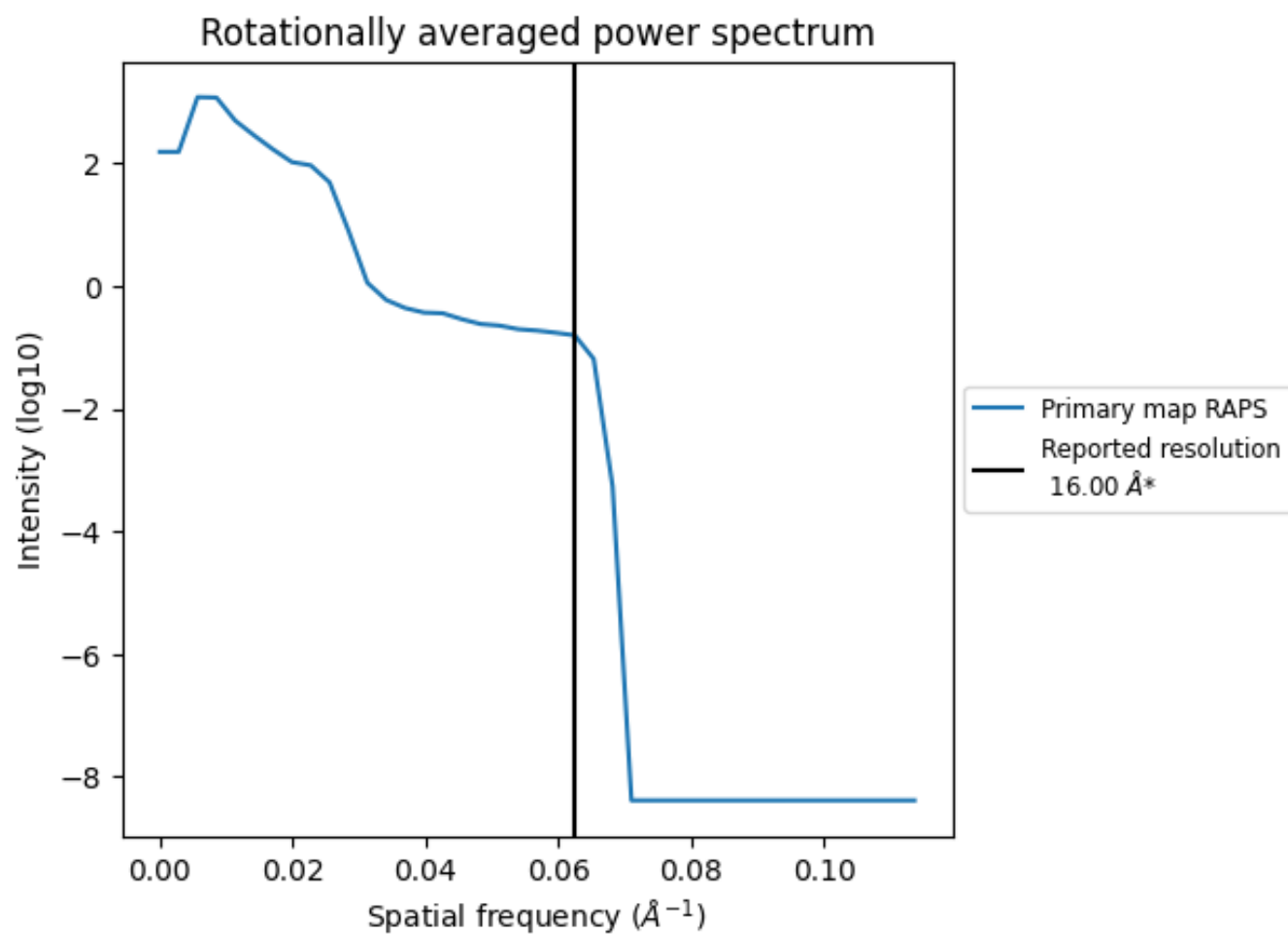
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 435 nm³; this corresponds to an approximate mass of 393 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.062 Å⁻¹

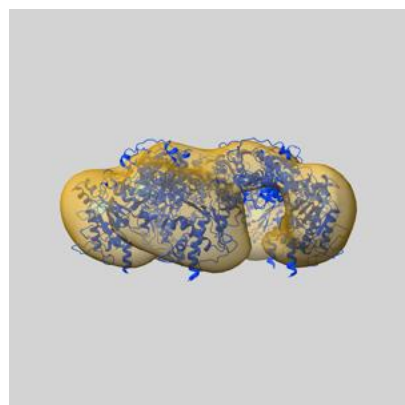
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

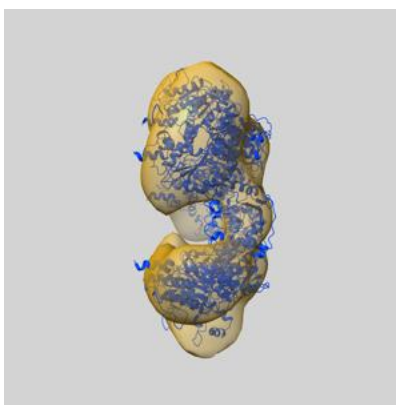
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2355 and PDB model 4BIJ. Per-residue inclusion information can be found in section 3 on page 5.

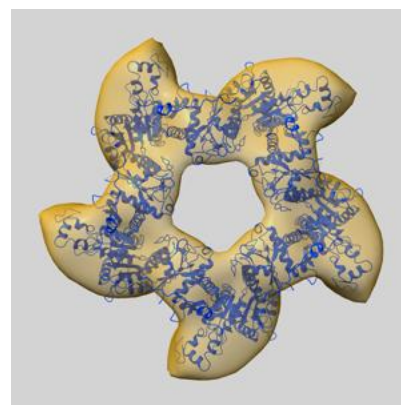
9.1 Map-model overlay [i](#)



X



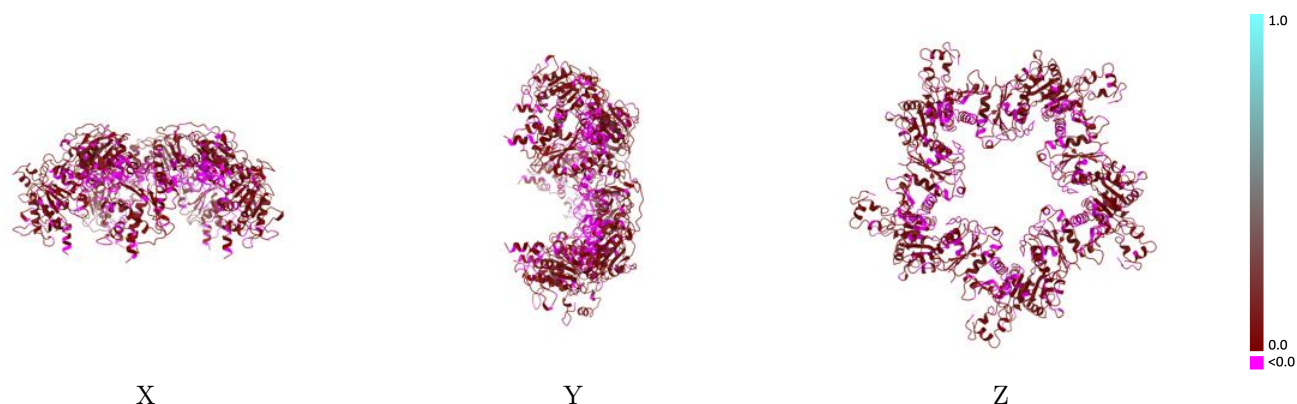
Y



Z

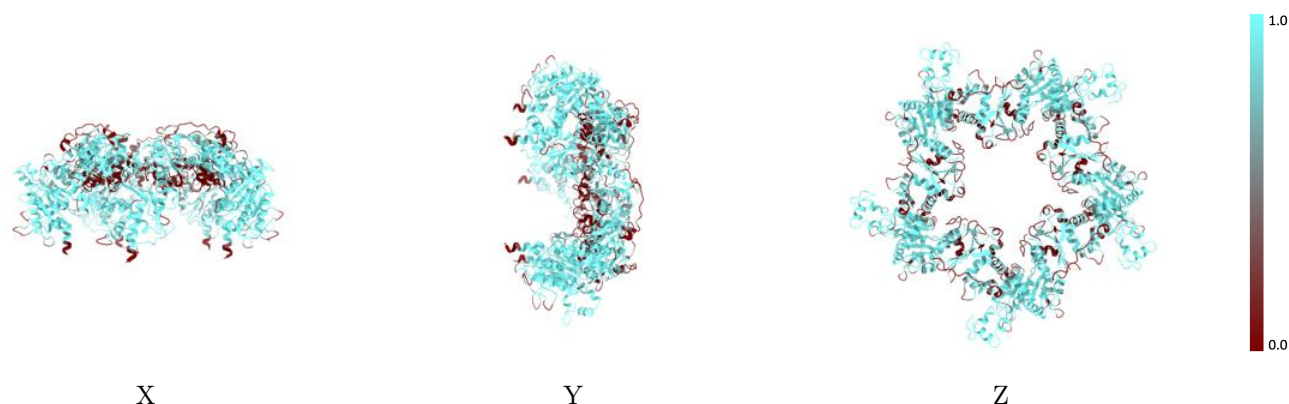
The images above show the 3D surface view of the map at the recommended contour level 0.0383 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



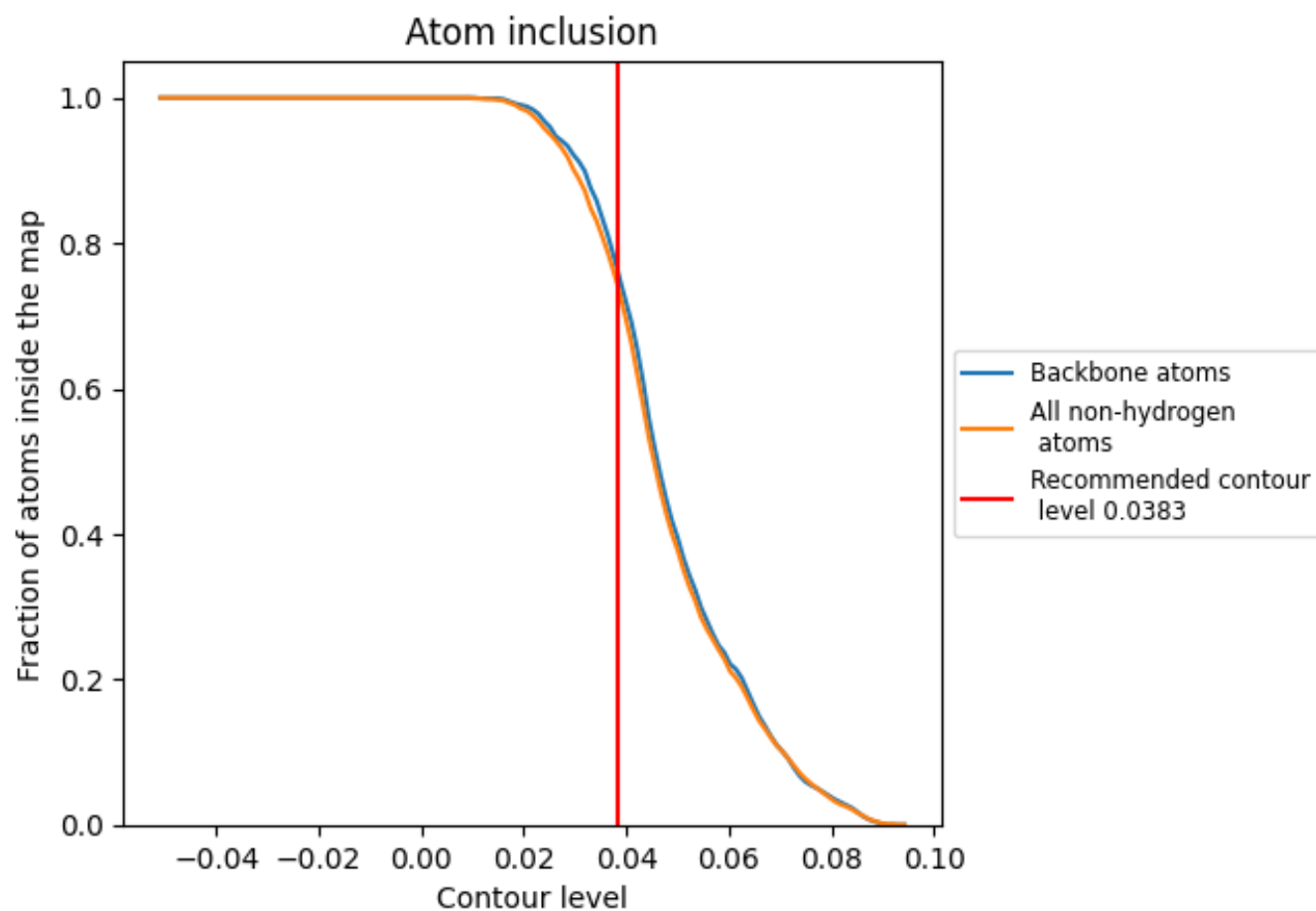
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0383).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0383) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7430	0.0450
A	0.7440	0.0410
B	0.7420	0.0440
C	0.7420	0.0480
D	0.7430	0.0460
E	0.7430	0.0440

