



Full wwPDB EM Validation Report ⓘ

Nov 9, 2024 – 01:44 pm GMT

PDB ID : 4AQ5
EMDB ID : EMD-2071
Title : Gating movement in acetylcholine receptor analysed by time-resolved electron cryo-microscopy (closed class)
Authors : Unwin, N.; Fujiyoshi, Y.
Deposited on : 2012-04-12
Resolution : 6.20 Å(reported)
Based on initial model : 2BG9

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

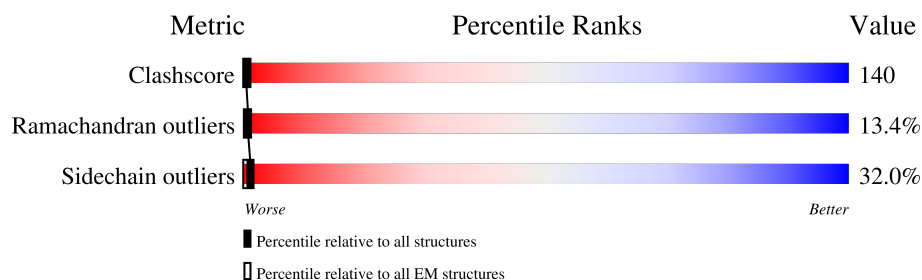
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.20 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	461	<div> <div>31%</div> <div> <div></div> <div>23%</div> <div>28%</div> <div>25%</div> <div>20%</div> </div> </div>
1	D	461	<div> <div>30%</div> <div> <div></div> <div>24%</div> <div>26%</div> <div>26%</div> <div>20%</div> </div> </div>
2	B	493	<div> <div>32%</div> <div> <div></div> <div>22%</div> <div>27%</div> <div>21%</div> <div>25%</div> </div> </div>
3	C	522	<div> <div>31%</div> <div> <div></div> <div>19%</div> <div>28%</div> <div>21%</div> <div>29%</div> </div> </div>
4	E	488	<div> <div>28%</div> <div> <div></div> <div>23%</div> <div>26%</div> <div>24%</div> <div>24%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14924 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 ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		
1	D	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		

- Molecule 2 is a protein called ACETYLCHOLINE RECEPTOR BETA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		

- Molecule 3 is a protein called ACETYLCHOLINE RECEPTOR DELTA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		

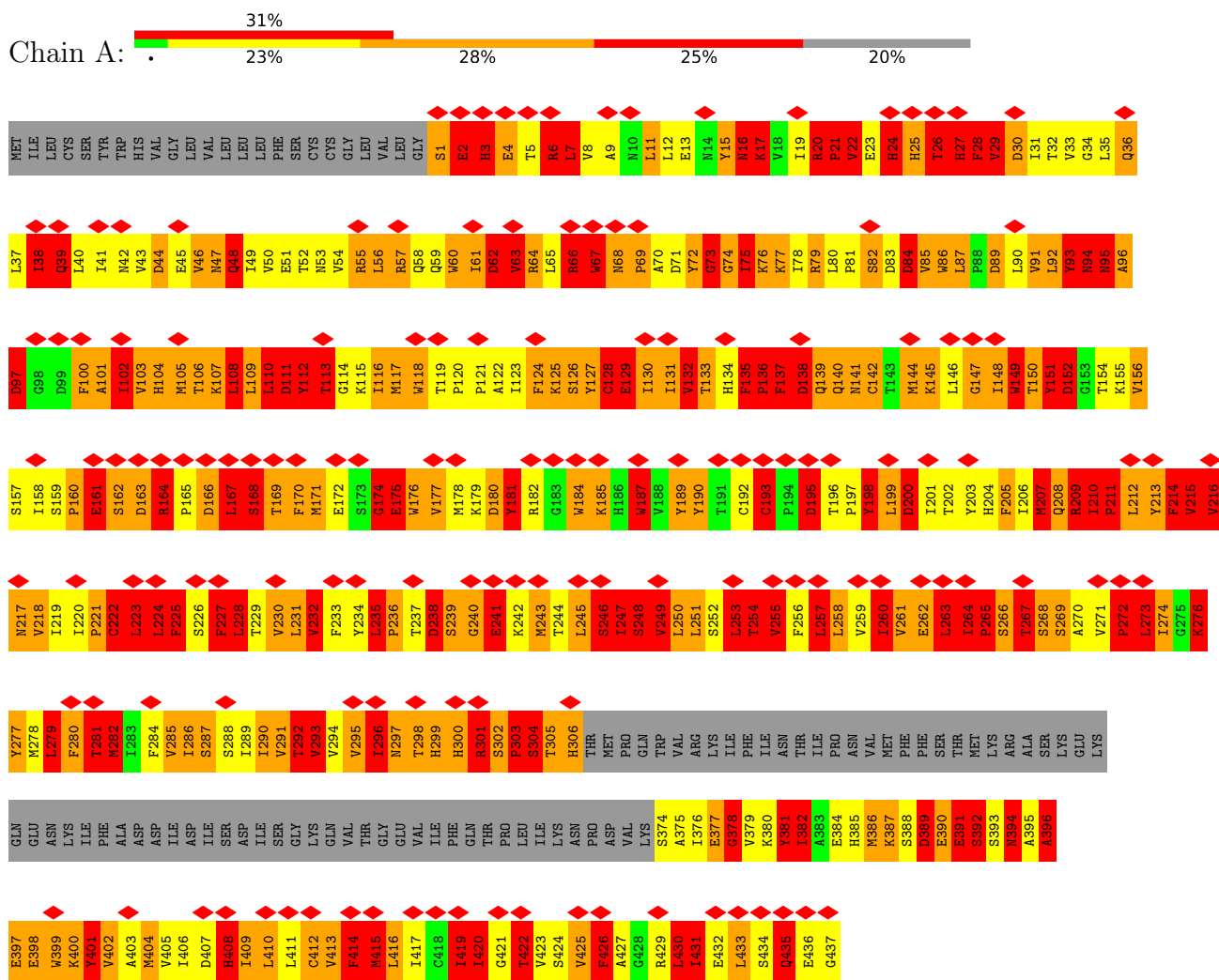
- Molecule 4 is a protein called ACETYLCHOLINE RECEPTOR GAMMA SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	371	Total	C	N	O	S	0	1
			2987	1948	478	551	10		

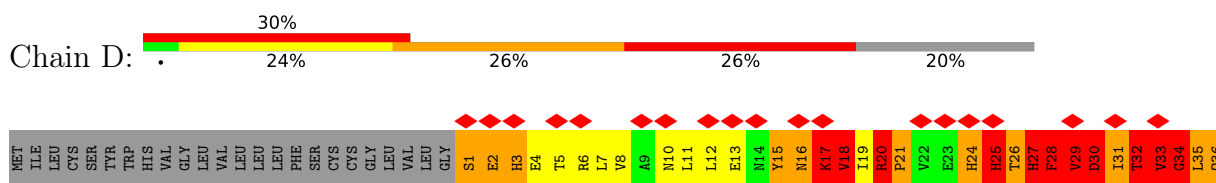
3 Residue-property plots

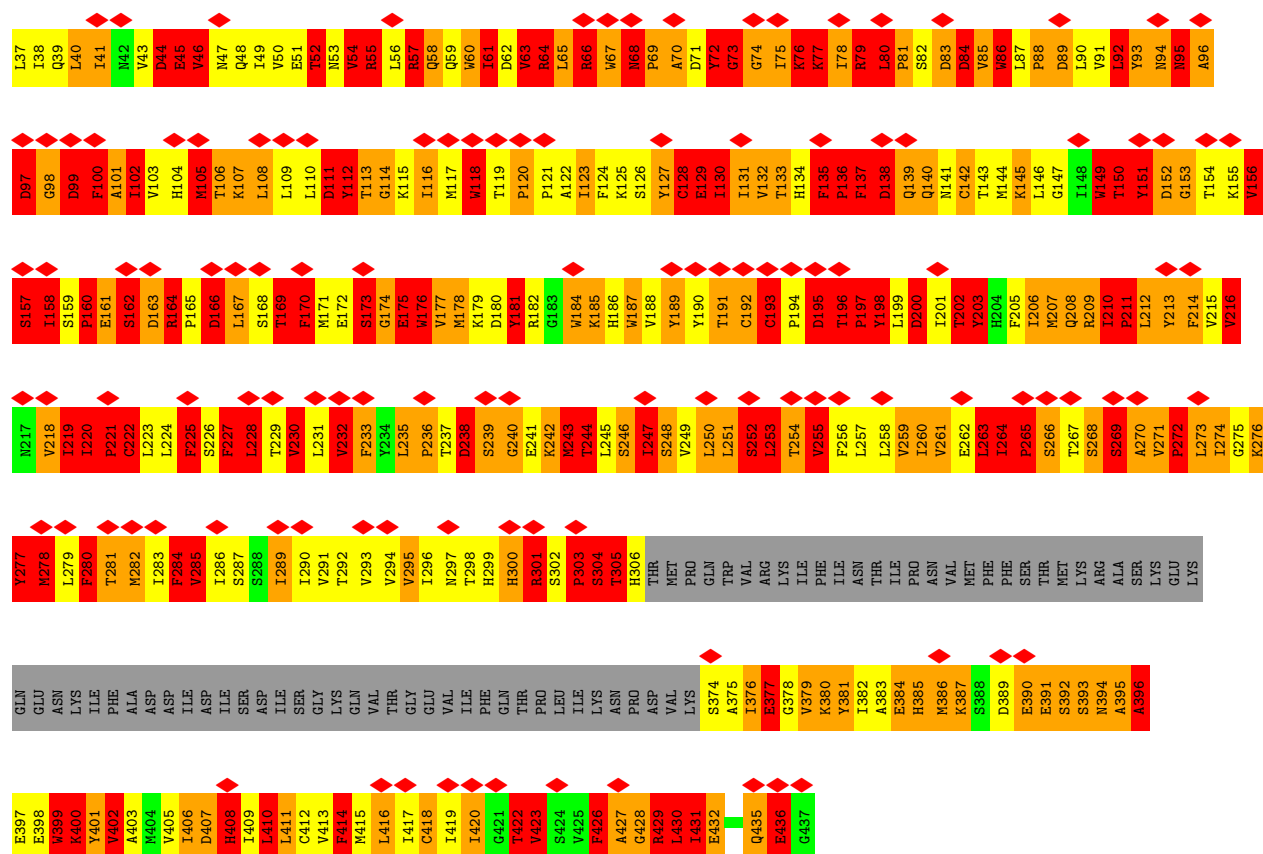
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA

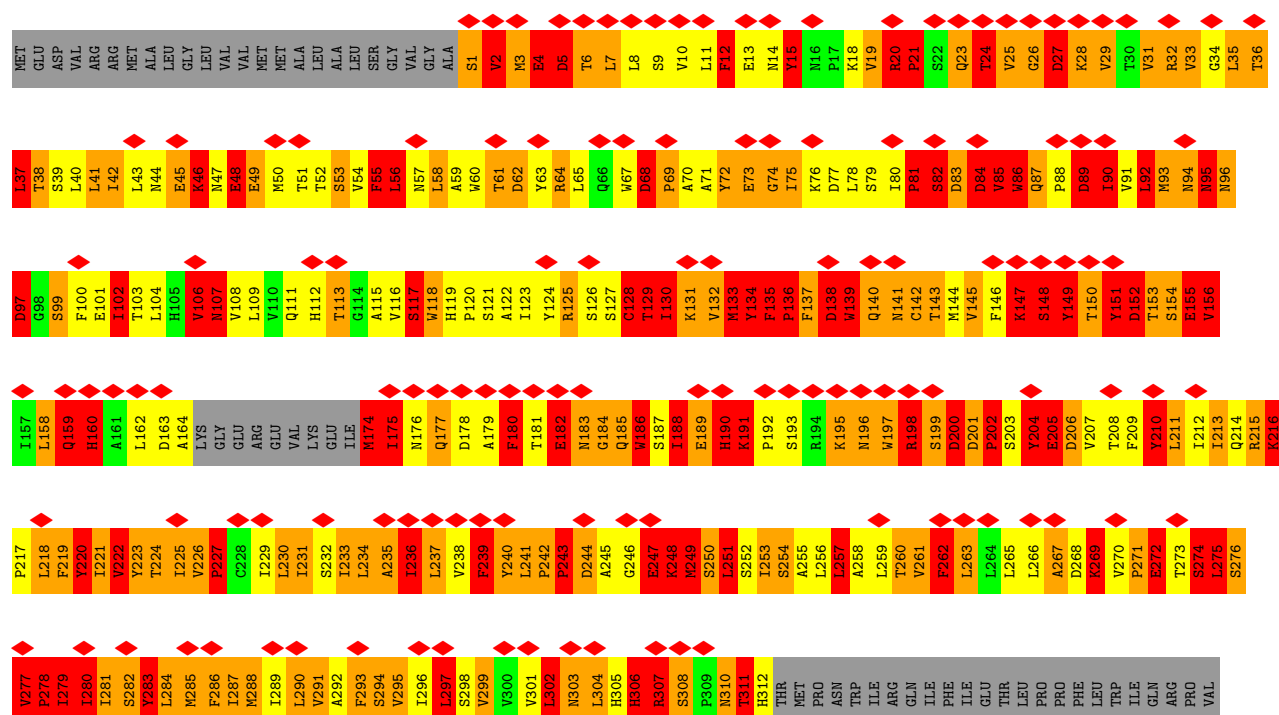
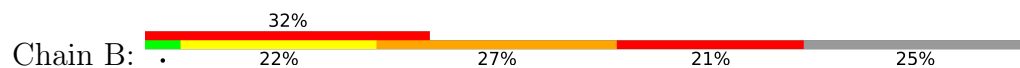


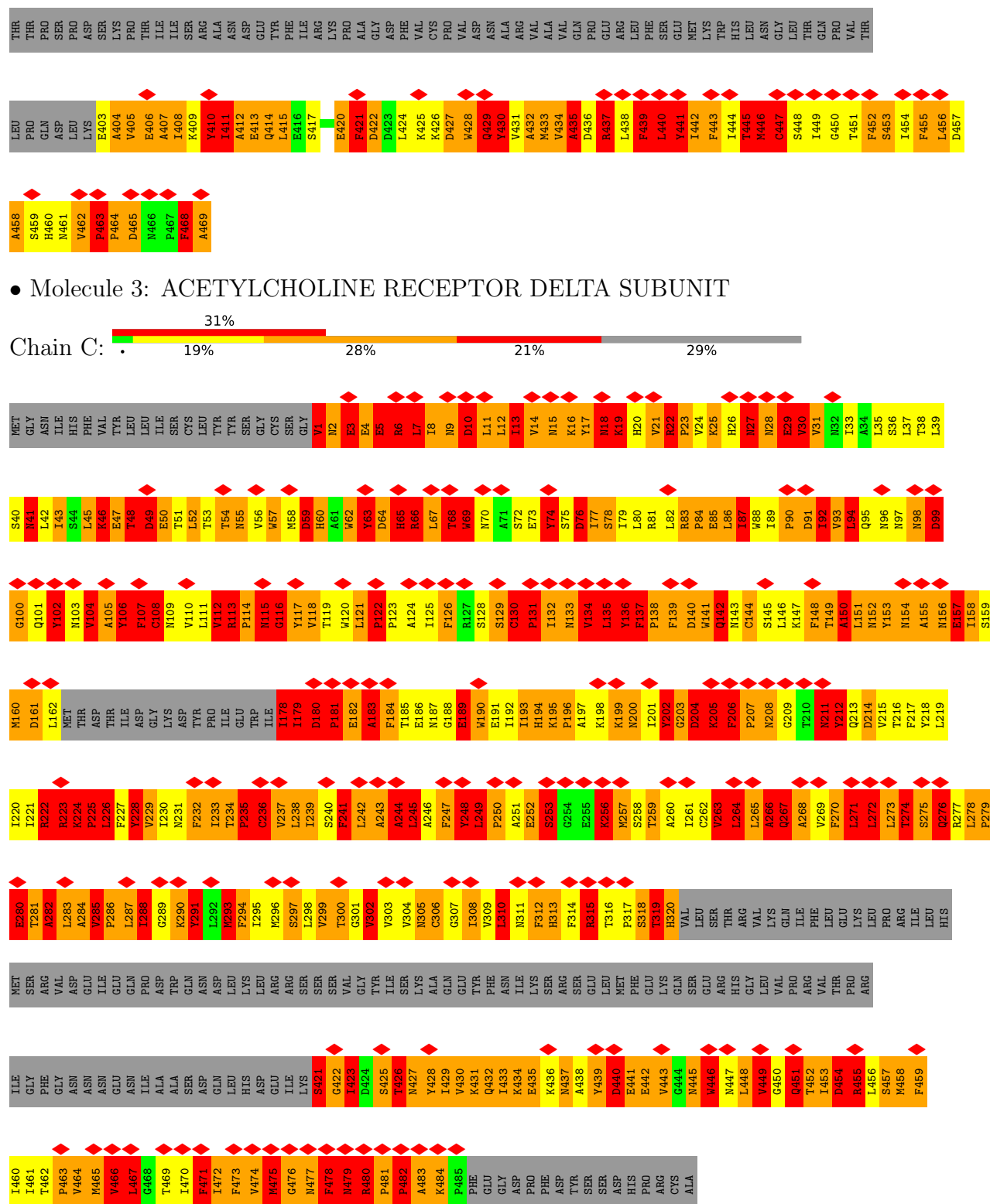
• Molecule 1: ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA



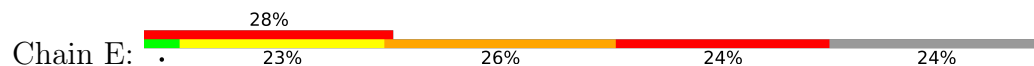


• Molecule 2: ACETYLCHOLINE RECEPTOR BETA SUBUNIT





• Molecule 4: ACETYLCHOLINE RECEPTOR GAMMA SUBUNIT





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	EACH TUBE IMAGE	Depositor
Microscope	JEOL 3000SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	38500	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	4.906	Depositor
Minimum map value	-3.900	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.2	Depositor
Map size (Å)	128.0, 128.0, 168.0	wwPDB
Map dimensions	128, 128, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	1.68	15/3069 (0.5%)	2.70	244/4186 (5.8%)
1	D	1.70	13/3069 (0.4%)	2.80	272/4186 (6.5%)
2	B	1.70	14/3048 (0.5%)	2.78	261/4162 (6.3%)
3	C	1.63	11/3059 (0.4%)	2.83	284/4175 (6.8%)
4	E	1.67	17/3057 (0.6%)	2.80	266/4174 (6.4%)
All	All	1.68	70/15302 (0.5%)	2.78	1327/20883 (6.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	7	116
1	D	6	125
2	B	6	112
3	C	6	125
4	E	12	107
All	All	37	585

All (70) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	129	THR	C-N	-9.22	1.12	1.34
4	E	8	GLU	CB-CG	8.90	1.69	1.52
1	A	118	TRP	CB-CG	8.84	1.66	1.50
1	D	175	GLU	CD-OE1	8.46	1.34	1.25
1	A	222	CYS	CB-SG	-7.49	1.69	1.82
3	C	130	CYS	C-N	7.32	1.48	1.34
4	E	476	GLU	CG-CD	6.93	1.62	1.51
2	B	15	TYR	CB-CG	6.85	1.61	1.51
1	A	118	TRP	CG-CD1	6.61	1.46	1.36
1	D	161	GLU	CD-OE2	6.59	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	126	THR	C-N	-6.53	1.19	1.34
1	D	208	GLN	C-N	6.39	1.48	1.34
4	E	306	VAL	C-N	-6.33	1.19	1.34
1	D	176	TRP	NE1-CE2	-6.26	1.29	1.37
4	E	8	GLU	CG-CD	6.18	1.61	1.51
2	B	406	GLU	CG-CD	-6.16	1.42	1.51
4	E	311	PRO	N-CD	6.15	1.56	1.47
4	E	309	ARG	C-N	-6.13	1.20	1.34
4	E	300	CYS	CB-SG	6.06	1.92	1.82
4	E	224	ASN	C-O	-6.02	1.11	1.23
4	E	123	TYR	CE1-CZ	5.96	1.46	1.38
1	D	176	TRP	CZ3-CH2	-5.86	1.30	1.40
1	D	211	PRO	C-O	5.84	1.34	1.23
3	C	449	VAL	CA-CB	5.83	1.67	1.54
4	E	71	TYR	CB-CG	5.67	1.60	1.51
4	E	62	TYR	CE2-CZ	5.58	1.45	1.38
3	C	280	GLU	CD-OE2	5.57	1.31	1.25
2	B	49	GLU	CD-OE2	5.56	1.31	1.25
1	A	127	TYR	CG-CD1	5.53	1.46	1.39
2	B	413	GLU	CB-CG	5.53	1.62	1.52
2	B	86	TRP	CD1-NE1	5.50	1.47	1.38
3	C	97	ASN	C-O	5.49	1.33	1.23
1	A	205	PHE	C-N	-5.45	1.21	1.34
2	B	225	ILE	CA-CB	5.42	1.67	1.54
1	D	159	SER	CA-CB	5.37	1.61	1.52
1	A	392	SER	CA-CB	5.36	1.60	1.52
1	A	381	TYR	CD1-CE1	-5.33	1.31	1.39
2	B	420	GLU	CD-OE2	-5.32	1.19	1.25
4	E	82	GLU	CD-OE1	5.32	1.31	1.25
2	B	155	GLU	CD-OE1	-5.30	1.19	1.25
1	D	399	TRP	CG-CD1	5.29	1.44	1.36
3	C	129	SER	C-N	5.29	1.46	1.34
1	A	161	GLU	CD-OE2	5.27	1.31	1.25
1	A	211	PRO	CA-C	5.27	1.63	1.52
3	C	315	ARG	NE-CZ	5.26	1.39	1.33
2	B	124	TYR	CG-CD1	5.26	1.46	1.39
1	D	158	ILE	CA-CB	5.24	1.66	1.54
1	D	176	TRP	CD1-NE1	5.23	1.46	1.38
1	A	198	TYR	CE2-CZ	5.22	1.45	1.38
3	C	186	GLU	CD-OE1	-5.20	1.20	1.25
4	E	52	ASN	CB-CG	5.18	1.62	1.51
1	A	381	TYR	CB-CG	5.17	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	280	PHE	CB-CG	-5.15	1.42	1.51
3	C	74	TYR	CG-CD2	5.14	1.45	1.39
2	B	293	PHE	CG-CD2	5.14	1.46	1.38
1	A	126	SER	C-N	-5.13	1.22	1.34
3	C	428	TYR	CG-CD1	5.13	1.45	1.39
1	D	432	GLU	CG-CD	5.13	1.59	1.51
2	B	421	PHE	CE2-CZ	5.10	1.47	1.37
1	D	193	CYS	CB-SG	5.09	1.91	1.82
1	A	227	PHE	CD2-CE2	5.08	1.49	1.39
4	E	240	TYR	CB-CG	5.06	1.59	1.51
4	E	85	TRP	CD2-CE2	5.05	1.47	1.41
4	E	85	TRP	CG-CD1	5.04	1.43	1.36
2	B	294	SER	CA-CB	5.03	1.60	1.52
3	C	202	TYR	CD1-CE1	5.03	1.46	1.39
1	A	136	PRO	N-CA	-5.02	1.38	1.47
1	A	163	ASP	C-N	-5.02	1.22	1.34
2	B	159	GLN	C-N	5.00	1.45	1.34
3	C	206	PHE	CE1-CZ	5.00	1.46	1.37

All (1327) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	309	ARG	NE-CZ-NH1	25.87	133.24	120.30
2	B	307	ARG	NE-CZ-NH2	24.36	132.48	120.30
3	C	277	ARG	NE-CZ-NH2	21.78	131.19	120.30
3	C	17	TYR	CB-CG-CD1	-19.82	109.11	121.00
4	E	17	ARG	NE-CZ-NH2	-18.78	110.91	120.30
2	B	125	ARG	NE-CZ-NH1	18.53	129.56	120.30
1	D	151	TYR	CB-CG-CD1	18.29	131.98	121.00
3	C	113	ARG	NE-CZ-NH2	18.28	129.44	120.30
2	B	20	ARG	NE-CZ-NH2	-18.09	111.26	120.30
1	D	15	TYR	CB-CG-CD1	-17.35	110.59	121.00
1	D	20	ARG	NE-CZ-NH1	17.24	128.92	120.30
4	E	288	PHE	CB-CG-CD2	15.85	131.90	120.80
4	E	62	TYR	CG-CD1-CE1	15.82	133.95	121.30
1	D	209	ARG	NE-CZ-NH1	15.63	128.12	120.30
2	B	215	ARG	NE-CZ-NH1	15.44	128.02	120.30
3	C	113	ARG	NE-CZ-NH1	-15.32	112.64	120.30
4	E	188	ARG	NE-CZ-NH1	15.05	127.82	120.30
1	D	15	TYR	CB-CG-CD2	14.77	129.86	121.00
4	E	63	ARG	NE-CZ-NH1	14.77	127.68	120.30
2	B	307	ARG	NE-CZ-NH1	-14.59	113.01	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	ARG	NE-CZ-NH2	14.23	127.42	120.30
3	C	17	TYR	CB-CG-CD2	14.21	129.53	121.00
1	D	429	ARG	NE-CZ-NH1	-14.00	113.30	120.30
1	A	6	ARG	NE-CZ-NH2	13.85	127.22	120.30
3	C	6	ARG	NE-CZ-NH2	-13.66	113.47	120.30
3	C	63	TYR	CB-CG-CD1	13.63	129.18	121.00
1	D	72	TYR	CB-CG-CD2	13.42	129.05	121.00
1	A	164	ARG	NE-CZ-NH2	-13.29	113.66	120.30
1	A	227	PHE	CB-CG-CD1	13.28	130.10	120.80
2	B	63	TYR	CB-CG-CD1	13.21	128.93	121.00
2	B	64	ARG	NE-CZ-NH1	13.09	126.84	120.30
4	E	71	TYR	CB-CG-CD1	-12.89	113.27	121.00
1	A	177	VAL	CG1-CB-CG2	12.89	131.52	110.90
1	A	209	ARG	NE-CZ-NH2	12.74	126.67	120.30
3	C	139	PHE	CB-CG-CD1	12.63	129.64	120.80
1	D	127	TYR	CG-CD1-CE1	-12.53	111.28	121.30
1	A	151	TYR	CB-CG-CD1	12.48	128.49	121.00
1	D	127	TYR	CB-CG-CD1	-12.45	113.53	121.00
4	E	124	ARG	NE-CZ-NH2	-12.43	114.08	120.30
1	A	64	ARG	NE-CZ-NH1	-12.38	114.11	120.30
3	C	204	ASP	CB-CG-OD2	12.26	129.34	118.30
1	A	135	PHE	CB-CG-CD1	-12.25	112.22	120.80
1	D	111	ASP	CB-CG-OD1	11.96	129.07	118.30
1	A	213	TYR	CB-CG-CD1	-11.93	113.84	121.00
4	E	124	ARG	NE-CZ-NH1	11.84	126.22	120.30
3	C	212	TYR	CB-CG-CD2	11.66	128.00	121.00
2	B	63	TYR	CB-CG-CD2	-11.65	114.01	121.00
2	B	430	TYR	CB-CG-CD2	11.59	127.95	121.00
1	D	79	ARG	NE-CZ-NH1	-11.54	114.53	120.30
3	C	478	PHE	CB-CG-CD1	-11.53	112.73	120.80
2	B	20	ARG	NH1-CZ-NH2	11.53	132.08	119.40
2	B	220	TYR	CD1-CE1-CZ	-11.49	109.46	119.80
4	E	175	GLU	O-C-N	11.40	140.94	122.70
1	A	209	ARG	NE-CZ-NH1	11.28	125.94	120.30
4	E	186	ARG	NE-CZ-NH1	-11.24	114.68	120.30
3	C	232	PHE	CB-CG-CD1	11.22	128.65	120.80
3	C	223	ARG	NE-CZ-NH1	11.20	125.90	120.30
2	B	468	PHE	CB-CG-CD1	11.16	128.61	120.80
1	D	112	TYR	CB-CG-CD1	10.98	127.59	121.00
4	E	5	ARG	NE-CZ-NH1	-10.97	114.81	120.30
4	E	309	ARG	NE-CZ-NH2	-10.96	114.82	120.30
2	B	215	ARG	NH1-CZ-NH2	-10.92	107.39	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	ARG	NH1-CZ-NH2	-10.92	107.39	119.40
4	E	14	TYR	CG-CD1-CE1	-10.90	112.58	121.30
1	A	227	PHE	CB-CG-CD2	-10.88	113.18	120.80
1	D	137	PHE	CB-CG-CD1	10.88	128.41	120.80
1	D	189	TYR	CB-CG-CD1	10.87	127.52	121.00
3	C	139	PHE	CB-CG-CD2	-10.81	113.23	120.80
1	A	20	ARG	NE-CZ-NH1	10.76	125.68	120.30
3	C	439	TYR	CB-CG-CD2	-10.75	114.55	121.00
1	D	72	TYR	CB-CG-CD1	-10.72	114.57	121.00
3	C	222	ARG	NE-CZ-NH1	10.72	125.66	120.30
2	B	134	TYR	CB-CG-CD1	-10.69	114.59	121.00
1	D	408	HIS	N-CA-CB	10.68	129.83	110.60
2	B	198	ARG	NE-CZ-NH2	10.52	125.56	120.30
1	D	250	LEU	CB-CA-C	10.50	130.15	110.20
1	D	401	TYR	CB-CG-CD2	-10.44	114.74	121.00
2	B	220	TYR	CG-CD1-CE1	10.43	129.64	121.30
4	E	309	ARG	CD-NE-CZ	10.42	138.19	123.60
2	B	100	PHE	CB-CG-CD2	-10.41	113.51	120.80
2	B	163	ASP	CB-CG-OD1	10.40	127.66	118.30
1	D	225	PHE	CB-CG-CD1	10.36	128.05	120.80
4	E	201	ASP	CB-CG-OD2	10.22	127.50	118.30
3	C	189	GLU	OE1-CD-OE2	-10.21	111.04	123.30
3	C	277	ARG	NE-CZ-NH1	-10.21	115.20	120.30
3	C	315	ARG	NE-CZ-NH1	10.16	125.38	120.30
1	A	93	TYR	CZ-CE2-CD2	-10.16	110.66	119.80
4	E	240	TYR	CG-CD1-CE1	-10.14	113.19	121.30
3	C	63	TYR	CG-CD2-CE2	10.09	129.37	121.30
3	C	478	PHE	CB-CG-CD2	10.02	127.82	120.80
3	C	151	LEU	CA-CB-CG	10.02	138.34	115.30
4	E	103	TYR	CG-CD1-CE1	10.02	129.31	121.30
4	E	13	ASP	CB-CG-OD1	9.97	127.27	118.30
4	E	116	TYR	CB-CG-CD2	-9.92	115.05	121.00
1	D	149	TRP	CG-CD1-NE1	9.90	120.00	110.10
3	C	266	ALA	N-CA-CB	9.76	123.76	110.10
4	E	435	GLU	OE1-CD-OE2	-9.74	111.61	123.30
1	D	401	TYR	CB-CG-CD1	9.73	126.84	121.00
1	D	138	ASP	CB-CG-OD2	-9.72	109.55	118.30
3	C	313	HIS	CB-CA-C	9.71	129.81	110.40
4	E	61	ASP	CB-CG-OD1	9.66	127.00	118.30
3	C	140	ASP	CB-CG-OD1	9.64	126.98	118.30
1	A	303	PRO	CA-N-CD	-9.62	98.03	111.50
1	D	256	PHE	CB-CG-CD1	9.62	127.53	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	78	ARG	NE-CZ-NH1	-9.60	115.50	120.30
4	E	288	PHE	CG-CD2-CE2	9.60	131.36	120.80
3	C	480	ARG	NE-CZ-NH1	-9.57	115.51	120.30
4	E	177	PHE	CB-CG-CD1	9.55	127.48	120.80
4	E	110	TYR	CG-CD1-CE1	-9.52	113.68	121.30
2	B	139	TRP	CE2-CD2-CG	9.52	114.91	107.30
1	D	238	ASP	CB-CG-OD2	9.51	126.86	118.30
2	B	286	PHE	CB-CG-CD1	-9.48	114.16	120.80
1	A	2	GLU	OE1-CD-OE2	-9.45	111.96	123.30
3	C	66	ARG	NE-CZ-NH1	9.45	125.02	120.30
1	D	181	TYR	CB-CG-CD2	-9.45	115.33	121.00
4	E	186	ARG	NE-CZ-NH2	9.43	125.02	120.30
1	D	30	ASP	CB-CG-OD1	9.43	126.79	118.30
3	C	153	TYR	CD1-CE1-CZ	9.42	128.28	119.80
3	C	141	TRP	CD1-CG-CD2	-9.41	98.78	106.30
1	A	55	ARG	NE-CZ-NH1	9.40	125.00	120.30
4	E	306	VAL	CG1-CB-CG2	9.36	125.88	110.90
1	D	79	ARG	NH1-CZ-NH2	9.36	129.69	119.40
3	C	480	ARG	NE-CZ-NH2	9.35	124.98	120.30
4	E	311	PRO	O-C-N	9.35	137.65	122.70
1	A	412	CYS	CA-CB-SG	9.34	130.81	114.00
3	C	232	PHE	CB-CG-CD2	-9.27	114.31	120.80
4	E	5	ARG	CD-NE-CZ	9.26	136.56	123.60
2	B	89	ASP	CB-CG-OD1	9.26	126.63	118.30
3	C	102	TYR	CD1-CE1-CZ	9.24	128.11	119.80
4	E	136	PHE	CB-CG-CD1	9.22	127.25	120.80
4	E	137	ASP	CB-CG-OD1	9.21	126.59	118.30
1	A	287	SER	N-CA-CB	9.19	124.29	110.50
4	E	458	PHE	CG-CD2-CE2	9.18	130.90	120.80
3	C	184	PHE	CB-CG-CD1	9.16	127.22	120.80
4	E	116	TYR	CB-CG-CD1	9.12	126.47	121.00
2	B	430	TYR	CB-CG-CD1	-9.09	115.55	121.00
3	C	471	PHE	CB-CG-CD2	-9.08	114.44	120.80
1	D	301	ARG	NE-CZ-NH1	9.08	124.84	120.30
3	C	5	GLU	OE1-CD-OE2	-9.07	112.41	123.30
1	A	137	PHE	CB-CG-CD2	9.07	127.15	120.80
4	E	161	ALA	N-CA-CB	9.06	122.78	110.10
2	B	180	PHE	CB-CG-CD1	-9.05	114.47	120.80
1	D	79	ARG	NE-CZ-NH2	-9.05	115.78	120.30
2	B	293	PHE	CB-CG-CD1	9.02	127.12	120.80
4	E	308	LEU	CA-CB-CG	9.02	136.04	115.30
1	D	243	MET	CA-CB-CG	9.00	128.60	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	315	ARG	NE-CZ-NH2	8.98	124.79	120.30
1	A	84	ASP	O-C-N	-8.98	108.33	122.70
2	B	293	PHE	CB-CG-CD2	-8.97	114.52	120.80
1	A	149	TRP	CG-CD2-CE3	-8.93	125.87	133.90
1	D	189	TYR	CZ-CE2-CD2	8.92	127.83	119.80
1	A	390	GLU	OE1-CD-OE2	-8.92	112.60	123.30
2	B	421	PHE	CG-CD1-CE1	-8.91	111.00	120.80
1	A	299	HIS	CA-CB-CG	8.82	128.59	113.60
1	A	181	TYR	CB-CG-CD1	8.82	126.29	121.00
4	E	63	ARG	NH1-CZ-NH2	-8.79	109.73	119.40
4	E	258	LEU	N-CA-CB	8.79	127.97	110.40
1	D	127	TYR	CD1-CG-CD2	8.76	127.53	117.90
1	A	411	LEU	CA-CB-CG	8.72	135.36	115.30
1	A	62	ASP	CB-CG-OD2	8.72	126.15	118.30
1	A	223	LEU	CB-CG-CD2	8.72	125.82	111.00
3	C	137	PHE	CG-CD2-CE2	8.71	130.38	120.80
2	B	441	TYR	CG-CD1-CE1	-8.71	114.33	121.30
1	A	381	TYR	CB-CG-CD2	-8.70	115.78	121.00
3	C	315	ARG	NH1-CZ-NH2	-8.70	109.83	119.40
2	B	457	ASP	CB-CG-OD1	8.69	126.12	118.30
1	D	13	GLU	OE1-CD-OE2	-8.68	112.89	123.30
1	A	137	PHE	CB-CG-CD1	-8.62	114.77	120.80
3	C	202	TYR	CB-CG-CD2	8.62	126.17	121.00
1	D	96	ALA	CB-CA-C	8.62	123.03	110.10
1	D	163	ASP	CB-CG-OD2	8.60	126.04	118.30
2	B	215	ARG	NE-CZ-NH2	8.58	124.59	120.30
3	C	74	TYR	CD1-CE1-CZ	8.56	127.50	119.80
3	C	74	TYR	CG-CD1-CE1	-8.53	114.47	121.30
3	C	141	TRP	CD1-NE1-CE2	-8.53	101.33	109.00
1	A	198	TYR	CD1-CE1-CZ	8.51	127.46	119.80
3	C	129	SER	N-CA-CB	8.51	123.26	110.50
3	C	271	LEU	CB-CG-CD1	-8.49	96.56	111.00
3	C	268	ALA	CB-CA-C	8.49	122.84	110.10
3	C	29	GLU	OE1-CD-OE2	-8.46	113.15	123.30
1	D	66	ARG	NE-CZ-NH2	8.46	124.53	120.30
1	D	426	PHE	CB-CG-CD2	8.46	126.72	120.80
1	D	151	TYR	CD1-CG-CD2	-8.45	108.61	117.90
1	D	300	HIS	O-C-N	8.45	136.21	122.70
1	D	93	TYR	CB-CG-CD1	8.43	126.06	121.00
2	B	410	TYR	CZ-CE2-CD2	8.41	127.37	119.80
1	A	6	ARG	NH1-CZ-NH2	-8.38	110.19	119.40
3	C	76	ASP	CB-CG-OD1	8.37	125.83	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	294	PHE	CZ-CE2-CD2	-8.37	110.06	120.10
3	C	206	PHE	CB-CG-CD1	-8.36	114.95	120.80
4	E	3	GLU	OE1-CD-OE2	-8.31	113.32	123.30
4	E	14	TYR	CB-CG-CD2	-8.31	116.02	121.00
4	E	190	ALA	N-CA-CB	8.30	121.72	110.10
4	E	307	SER	CA-C-N	-8.29	98.96	117.20
1	A	214	PHE	CG-CD1-CE1	-8.28	111.69	120.80
3	C	91	ASP	CB-CG-OD2	8.28	125.75	118.30
1	A	426	PHE	CB-CG-CD2	8.25	126.58	120.80
4	E	285	TYR	CB-CG-CD2	8.24	125.94	121.00
2	B	197	TRP	CH2-CZ2-CE2	-8.23	109.17	117.40
2	B	137	PHE	CB-CG-CD2	8.22	126.56	120.80
1	D	100	PHE	CB-CG-CD2	-8.22	115.05	120.80
1	D	391	GLU	OE1-CD-OE2	8.22	133.16	123.30
2	B	95	ASN	O-C-N	-8.20	109.58	122.70
1	A	86	TRP	CD1-NE1-CE2	-8.20	101.62	109.00
3	C	141	TRP	CG-CD1-NE1	8.20	118.30	110.10
2	B	72	TYR	CB-CG-CD2	8.18	125.91	121.00
2	B	186	TRP	CB-CG-CD1	8.18	137.64	127.00
4	E	82	GLU	OE1-CD-OE2	-8.18	113.48	123.30
2	B	437	ARG	NE-CZ-NH2	-8.18	116.21	120.30
3	C	10	ASP	CB-CG-OD2	8.18	125.66	118.30
1	A	397	GLU	OE1-CD-OE2	8.17	133.11	123.30
2	B	286	PHE	CB-CG-CD2	8.16	126.51	120.80
1	A	429	ARG	NE-CZ-NH2	-8.15	116.23	120.30
2	B	404	ALA	O-C-N	8.11	135.67	122.70
2	B	149	TYR	CG-CD1-CE1	-8.09	114.83	121.30
3	C	247	PHE	CG-CD1-CE1	-8.07	111.92	120.80
1	D	130	ILE	CG1-CB-CG2	8.05	129.12	111.40
1	D	401	TYR	CZ-CE2-CD2	-8.04	112.56	119.80
1	A	257	LEU	CB-CG-CD1	-8.03	97.34	111.00
3	C	300	THR	CA-CB-CG2	-8.04	101.15	112.40
1	A	412	CYS	N-CA-CB	8.00	125.00	110.60
1	D	140	GLN	OE1-CD-NE2	-8.00	103.51	121.90
2	B	286	PHE	CG-CD2-CE2	7.99	129.59	120.80
1	A	93	TYR	CG-CD2-CE2	7.97	127.68	121.30
2	B	200	ASP	CB-CG-OD1	-7.97	111.13	118.30
1	A	241	GLU	OE1-CD-OE2	-7.94	113.78	123.30
2	B	468	PHE	CB-CG-CD2	-7.93	115.25	120.80
1	A	138	ASP	CB-CG-OD2	7.93	125.44	118.30
1	D	176	TRP	CB-CG-CD2	-7.93	116.29	126.60
1	D	6	ARG	NE-CZ-NH2	7.93	124.26	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	66	TRP	CD1-CG-CD2	-7.93	99.96	106.30
3	C	99	ASP	CB-CG-OD1	7.92	125.43	118.30
4	E	99	PHE	CB-CG-CD1	-7.92	115.26	120.80
3	C	83	ARG	NE-CZ-NH1	-7.88	116.36	120.30
4	E	71	TYR	CG-CD1-CE1	-7.87	115.01	121.30
1	D	57	ARG	NE-CZ-NH1	7.86	124.23	120.30
1	A	267	THR	N-CA-CB	7.83	125.18	110.30
4	E	240	TYR	CD1-CE1-CZ	7.82	126.84	119.80
4	E	431	ASP	CB-CG-OD2	-7.82	111.26	118.30
3	C	141	TRP	CB-CG-CD1	7.81	137.15	127.00
4	E	17	ARG	NH1-CZ-NH2	7.81	127.99	119.40
1	D	277	TYR	CB-CG-CD1	-7.80	116.32	121.00
4	E	285	TYR	CG-CD2-CE2	7.80	127.54	121.30
4	E	162	GLU	OE1-CD-OE2	-7.79	113.94	123.30
2	B	133	MET	CA-CB-CG	7.79	126.55	113.30
4	E	198	LEU	CA-CB-CG	7.78	133.20	115.30
4	E	466	PHE	CD1-CE1-CZ	-7.78	110.76	120.10
2	B	19	VAL	C-N-CA	7.78	141.14	121.70
2	B	15	TYR	CB-CG-CD1	7.77	125.66	121.00
1	A	86	TRP	CG-CD1-NE1	7.76	117.86	110.10
3	C	66	ARG	NE-CZ-NH2	-7.75	116.43	120.30
1	A	209	ARG	CD-NE-CZ	7.74	134.43	123.60
3	C	139	PHE	CD1-CE1-CZ	-7.73	110.83	120.10
3	C	104	VAL	CA-CB-CG1	7.72	122.49	110.90
1	D	176	TRP	CA-CB-CG	7.72	128.37	113.70
1	A	248	SER	O-C-N	-7.71	110.36	122.70
1	A	381	TYR	CG-CD2-CE2	-7.71	115.13	121.30
2	B	421	PHE	CD1-CG-CD2	7.71	128.32	118.30
4	E	205	PHE	N-CA-CB	7.71	124.47	110.60
2	B	219	PHE	CB-CG-CD1	7.70	126.19	120.80
2	B	138	ASP	CB-CG-OD2	7.69	125.22	118.30
2	B	62	ASP	CB-CG-OD2	7.69	125.22	118.30
3	C	104	VAL	O-C-N	7.69	135.00	122.70
2	B	437	ARG	CD-NE-CZ	7.68	134.35	123.60
1	D	406	ILE	CG1-CB-CG2	7.65	128.23	111.40
1	D	256	PHE	CG-CD2-CE2	7.64	129.21	120.80
2	B	65	LEU	CA-CB-CG	7.64	132.88	115.30
1	A	232	VAL	CA-CB-CG1	7.64	122.36	110.90
2	B	455	PHE	CG-CD1-CE1	7.64	129.20	120.80
2	B	205	GLU	OE1-CD-OE2	-7.62	114.16	123.30
4	E	46	GLU	OE1-CD-OE2	-7.60	114.18	123.30
1	D	164	ARG	NE-CZ-NH1	-7.60	116.50	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	115	ASN	C-N-CA	7.59	138.25	122.30
1	D	99	ASP	N-CA-CB	7.59	124.26	110.60
3	C	139	PHE	CG-CD1-CE1	7.58	129.14	120.80
1	A	213	TYR	CG-CD2-CE2	-7.58	115.24	121.30
2	B	215	ARG	CA-CB-CG	7.58	130.07	113.40
2	B	297	LEU	CA-CB-CG	-7.57	97.89	115.30
4	E	244	ALA	N-CA-CB	7.57	120.69	110.10
1	A	22	VAL	CA-CB-CG2	7.56	122.25	110.90
4	E	439	TRP	NE1-CE2-CZ2	-7.55	122.09	130.40
1	D	102	ILE	CG1-CB-CG2	-7.55	94.79	111.40
3	C	270	PHE	CB-CG-CD2	7.51	126.06	120.80
4	E	5	ARG	NE-CZ-NH2	7.51	124.06	120.30
3	C	265	LEU	O-C-N	7.51	134.71	122.70
3	C	130	CYS	O-C-N	-7.50	106.85	121.10
3	C	30	VAL	O-C-N	-7.50	110.70	122.70
3	C	312	PHE	CB-CG-CD1	7.49	126.05	120.80
4	E	93	ASN	N-CA-CB	7.49	124.09	110.60
4	E	288	PHE	CB-CG-CD1	-7.49	115.56	120.80
2	B	149	TYR	O-C-N	-7.48	110.73	122.70
3	C	244	ALA	O-C-N	-7.48	110.73	122.70
1	A	28	PHE	CG-CD1-CE1	-7.47	112.58	120.80
1	A	149	TRP	CB-CA-C	7.46	125.33	110.40
1	D	184	TRP	CA-CB-CG	7.46	127.88	113.70
3	C	478	PHE	CG-CD2-CE2	-7.45	112.60	120.80
1	D	163	ASP	CB-CG-OD1	-7.45	111.59	118.30
2	B	293	PHE	CG-CD2-CE2	-7.44	112.62	120.80
1	D	137	PHE	CB-CG-CD2	-7.44	115.59	120.80
4	E	193	ASN	O-C-N	7.44	134.60	122.70
3	C	312	PHE	CB-CG-CD2	-7.44	115.59	120.80
4	E	13	ASP	CB-CG-OD2	-7.43	111.61	118.30
1	A	4	GLU	OE1-CD-OE2	-7.42	114.40	123.30
3	C	117	TYR	CD1-CE1-CZ	-7.40	113.14	119.80
4	E	466	PHE	CG-CD1-CE1	7.40	128.94	120.80
4	E	103	TYR	CD1-CE1-CZ	-7.40	113.14	119.80
1	D	411	LEU	O-C-N	7.39	134.53	122.70
2	B	434	VAL	CG1-CB-CG2	7.39	122.72	110.90
1	D	112	TYR	C-N-CA	7.38	140.15	121.70
2	B	441	TYR	CB-CG-CD2	-7.38	116.57	121.00
3	C	102	TYR	CG-CD1-CE1	-7.38	115.40	121.30
1	A	253	LEU	CA-CB-CG	7.38	132.27	115.30
3	C	136	TYR	CG-CD1-CE1	-7.38	115.40	121.30
1	D	301	ARG	N-CA-C	7.37	130.90	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	291	TYR	CG-CD1-CE1	-7.37	115.41	121.30
2	B	421	PHE	CB-CG-CD1	-7.36	115.65	120.80
3	C	248	TYR	CB-CG-CD1	7.36	125.42	121.00
1	A	432	GLU	O-C-N	-7.35	110.94	122.70
2	B	462	VAL	CB-CA-C	7.35	125.37	111.40
3	C	102	TYR	CB-CG-CD1	-7.35	116.59	121.00
1	D	169	THR	O-C-N	-7.35	110.94	122.70
2	B	283	TYR	CB-CG-CD1	7.34	125.41	121.00
1	D	198	TYR	CB-CG-CD2	-7.34	116.60	121.00
1	D	209	ARG	NH1-CZ-NH2	-7.33	111.34	119.40
1	D	214	PHE	CB-CG-CD2	7.33	125.93	120.80
1	A	181	TYR	CG-CD1-CE1	7.33	127.16	121.30
3	C	49	ASP	O-C-N	-7.33	110.98	122.70
1	A	254	THR	N-CA-CB	7.33	124.22	110.30
1	D	209	ARG	C-N-CA	7.33	140.01	121.70
4	E	62	TYR	CB-CG-CD1	7.32	125.39	121.00
1	A	30	ASP	CB-CG-OD1	7.32	124.89	118.30
1	D	228	LEU	CB-CG-CD2	7.32	123.44	111.00
4	E	164	GLY	CA-C-O	7.31	133.76	120.60
3	C	183	ALA	CB-CA-C	7.31	121.06	110.10
1	D	301	ARG	O-C-N	7.31	134.39	122.70
4	E	454	ALA	CB-CA-C	7.30	121.06	110.10
3	C	190	TRP	O-C-N	7.29	134.37	122.70
1	A	128	CYS	CA-CB-SG	7.29	127.12	114.00
2	B	20	ARG	NE-CZ-NH1	-7.28	116.66	120.30
2	B	134	TYR	CB-CG-CD2	7.27	125.36	121.00
2	B	151	TYR	CB-CG-CD1	7.27	125.36	121.00
3	C	319	THR	O-C-N	-7.27	111.07	122.70
3	C	235	PRO	O-C-N	7.27	134.32	122.70
2	B	152	ASP	CB-CG-OD2	-7.26	111.76	118.30
3	C	19	LYS	N-CA-CB	7.25	123.66	110.60
4	E	154	GLU	OE1-CD-OE2	7.25	132.00	123.30
4	E	458	PHE	CB-CG-CD1	7.23	125.86	120.80
2	B	410	TYR	CG-CD1-CE1	7.22	127.08	121.30
3	C	226	LEU	CB-CG-CD1	-7.22	98.73	111.00
3	C	211	ASN	C-N-CA	7.21	139.73	121.70
1	A	102	ILE	C-N-CA	7.21	139.72	121.70
1	A	175	GLU	OE1-CD-OE2	-7.20	114.67	123.30
1	A	389	ASP	O-C-N	-7.19	111.19	122.70
4	E	439	TRP	CG-CD2-CE3	7.19	140.37	133.90
4	E	66	TRP	CG-CD1-NE1	7.18	117.28	110.10
1	A	413	VAL	CG1-CB-CG2	7.18	122.39	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	64	ASP	CB-CG-OD1	7.17	124.75	118.30
4	E	152	ALA	N-CA-C	7.17	130.36	111.00
4	E	447	ASP	CB-CG-OD2	7.17	124.75	118.30
1	D	227	PHE	CB-CG-CD2	7.17	125.82	120.80
3	C	113	ARG	CD-NE-CZ	7.17	133.63	123.60
1	A	273	LEU	CA-CB-CG	7.16	131.78	115.30
4	E	281	LEU	O-C-N	-7.16	111.25	122.70
4	E	132	THR	C-N-CA	7.15	139.58	121.70
1	A	225	PHE	CB-CG-CD1	7.15	125.80	120.80
2	B	77	ASP	CB-CG-OD2	7.15	124.73	118.30
3	C	440	ASP	CB-CG-OD2	7.15	124.73	118.30
1	D	265	PRO	CA-N-CD	-7.15	101.50	111.50
2	B	97	ASP	CB-CG-OD2	7.15	124.73	118.30
3	C	426	THR	O-C-N	-7.14	111.27	122.70
3	C	157	GLU	N-CA-CB	7.14	123.45	110.60
2	B	219	PHE	CG-CD1-CE1	7.13	128.65	120.80
1	A	96	ALA	N-CA-CB	7.13	120.09	110.10
1	D	427	ALA	N-CA-CB	7.13	120.09	110.10
1	D	149	TRP	CB-CG-CD1	7.13	136.27	127.00
2	B	134	TYR	CG-CD1-CE1	-7.13	115.60	121.30
2	B	12	PHE	O-C-N	-7.13	111.30	122.70
2	B	125	ARG	NE-CZ-NH2	-7.12	116.74	120.30
2	B	82	SER	N-CA-CB	7.12	121.17	110.50
2	B	72	TYR	CA-CB-CG	7.12	126.92	113.40
3	C	228	TYR	CA-CB-CG	7.11	126.91	113.40
2	B	210	TYR	CB-CG-CD1	7.11	125.27	121.00
1	D	381	TYR	CB-CG-CD2	-7.10	116.74	121.00
4	E	452	TRP	CG-CD2-CE3	7.09	140.28	133.90
4	E	421	PHE	N-CA-CB	7.08	123.34	110.60
3	C	57	TRP	CB-CG-CD1	7.08	136.20	127.00
4	E	224	ASN	C-N-CA	7.07	139.37	121.70
1	D	151	TYR	CG-CD1-CE1	7.06	126.95	121.30
2	B	135	PHE	CB-CG-CD1	7.06	125.74	120.80
2	B	285	MET	CA-CB-CG	7.05	125.29	113.30
1	A	232	VAL	CA-CB-CG2	7.05	121.47	110.90
1	A	101	ALA	C-N-CA	7.04	139.29	121.70
4	E	439	TRP	CD1-NE1-CE2	-7.03	102.67	109.00
1	A	60	TRP	CG-CD1-NE1	-7.03	103.07	110.10
3	C	69	TRP	CE3-CZ3-CH2	7.02	128.93	121.20
1	D	200	ASP	CB-CG-OD1	7.02	124.61	118.30
1	D	379	VAL	CB-CA-C	-7.01	98.08	111.40
3	C	59	ASP	CB-CG-OD2	7.01	124.61	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	428	TYR	O-C-N	-7.00	111.50	122.70
1	D	150	THR	N-CA-C	7.00	129.90	111.00
2	B	210	TYR	CZ-CE2-CD2	-6.99	113.51	119.80
4	E	69	SER	N-CA-CB	6.99	120.99	110.50
2	B	4	GLU	OE1-CD-OE2	-6.99	114.91	123.30
1	A	241	GLU	O-C-N	-6.99	111.52	122.70
1	D	221	PRO	N-CD-CG	-6.98	92.72	103.20
3	C	74	TYR	CB-CG-CD2	-6.98	116.81	121.00
1	D	151	TYR	N-CA-CB	6.98	123.16	110.60
4	E	188	ARG	NH1-CZ-NH2	-6.94	111.76	119.40
2	B	148	SER	O-C-N	-6.94	111.59	122.70
3	C	285	VAL	CB-CA-C	-6.93	98.22	111.40
4	E	118	LEU	N-CA-C	6.93	129.71	111.00
4	E	84	LEU	CA-CB-CG	6.93	131.24	115.30
2	B	210	TYR	CG-CD2-CE2	6.93	126.84	121.30
3	C	86	LEU	CB-CG-CD1	6.92	122.77	111.00
3	C	18	ASN	N-CA-CB	-6.92	98.14	110.60
1	D	84	ASP	CB-CG-OD2	6.92	124.53	118.30
1	D	86	TRP	NE1-CE2-CZ2	6.90	137.99	130.40
3	C	136	TYR	CB-CG-CD1	-6.90	116.86	121.00
2	B	190	HIS	CB-CA-C	-6.89	96.61	110.40
4	E	138	TRP	CE2-CD2-CG	-6.89	101.79	107.30
1	A	430	LEU	CA-CB-CG	6.88	131.13	115.30
3	C	83	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	A	238	ASP	CB-CG-OD1	6.88	124.49	118.30
3	C	454	ASP	CB-CG-OD1	-6.88	112.11	118.30
3	C	186	GLU	O-C-N	6.86	133.68	122.70
2	B	132	VAL	C-N-CA	6.86	138.84	121.70
1	D	93	TYR	CG-CD2-CE2	6.86	126.78	121.30
2	B	5	ASP	N-CA-CB	6.85	122.93	110.60
1	D	244	THR	CA-CB-CG2	-6.85	102.81	112.40
2	B	447	CYS	CB-CA-C	6.84	124.08	110.40
2	B	306	HIS	N-CA-CB	6.83	122.90	110.60
4	E	205	PHE	CZ-CE2-CD2	6.83	128.29	120.10
1	D	187	TRP	CD1-NE1-CE2	6.83	115.14	109.00
1	D	162	SER	N-CA-CB	6.82	120.74	110.50
1	D	67	TRP	CB-CG-CD2	6.82	135.47	126.60
2	B	421	PHE	CB-CG-CD2	-6.82	116.03	120.80
1	A	436	GLU	O-C-N	6.82	134.79	123.20
1	A	22	VAL	CG1-CB-CG2	6.80	121.78	110.90
1	A	127	TYR	CB-CG-CD1	6.79	125.08	121.00
4	E	133	TYR	CG-CD1-CE1	-6.79	115.86	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	160	PRO	CA-N-CD	-6.79	101.99	111.50
1	D	401	TYR	CG-CD2-CE2	6.79	126.73	121.30
4	E	173	ASP	CB-CG-OD2	-6.79	112.19	118.30
4	E	130	ALA	CB-CA-C	6.79	120.28	110.10
2	B	198	ARG	CD-NE-CZ	6.78	133.10	123.60
2	B	247	GLU	OE1-CD-OE2	-6.78	115.16	123.30
1	D	86	TRP	CG-CD1-NE1	-6.78	103.32	110.10
4	E	309	ARG	NH1-CZ-NH2	-6.78	111.94	119.40
3	C	116	GLY	N-CA-C	6.77	130.03	113.10
4	E	137	ASP	OD1-CG-OD2	-6.77	110.44	123.30
1	D	28	PHE	CZ-CE2-CD2	-6.76	111.98	120.10
4	E	104	TYR	CZ-CE2-CD2	6.76	125.88	119.80
3	C	206	PHE	CG-CD2-CE2	-6.76	113.37	120.80
4	E	127	CYS	N-CA-CB	6.75	122.76	110.60
4	E	443	GLY	N-CA-C	6.75	129.98	113.10
3	C	428	TYR	CB-CG-CD1	-6.74	116.95	121.00
1	D	99	ASP	O-C-N	-6.73	111.93	122.70
1	A	7	LEU	CA-CB-CG	6.73	130.78	115.30
4	E	77	VAL	C-N-CA	6.73	138.51	121.70
1	A	29	VAL	O-C-N	-6.72	111.94	122.70
3	C	63	TYR	CD1-CE1-CZ	6.72	125.85	119.80
3	C	480	ARG	CD-NE-CZ	6.72	133.00	123.60
2	B	280	ILE	CA-C-N	-6.71	102.43	117.20
3	C	83	ARG	NH1-CZ-NH2	6.71	126.78	119.40
2	B	139	TRP	NE1-CE2-CD2	-6.71	100.59	107.30
3	C	156	ASN	CB-CG-OD1	-6.70	108.19	121.60
1	D	135	PHE	CG-CD1-CE1	-6.70	113.42	120.80
1	A	198	TYR	O-C-N	6.70	133.42	122.70
3	C	479	ASN	C-N-CA	6.69	138.42	121.70
2	B	142	CYS	C-N-CA	6.68	138.41	121.70
4	E	146	ARG	NE-CZ-NH2	6.68	123.64	120.30
3	C	4	GLU	OE1-CD-OE2	-6.68	115.29	123.30
3	C	483	ALA	N-CA-CB	6.68	119.45	110.10
1	A	57	ARG	NE-CZ-NH1	6.66	123.63	120.30
2	B	260	THR	CA-CB-CG2	-6.66	103.07	112.40
2	B	3	MET	O-C-N	6.66	133.36	122.70
2	B	72	TYR	CB-CG-CD1	-6.66	117.00	121.00
2	B	293	PHE	CG-CD1-CE1	6.65	128.12	120.80
1	D	94	ASN	O-C-N	6.65	133.34	122.70
1	A	228	LEU	CB-CG-CD1	-6.65	99.70	111.00
3	C	223	ARG	NH1-CZ-NH2	-6.64	112.09	119.40
3	C	277	ARG	CD-NE-CZ	6.64	132.89	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	98	GLY	CA-C-O	-6.64	108.65	120.60
4	E	131	VAL	O-C-N	-6.63	112.09	122.70
1	A	117	MET	O-C-N	6.62	133.30	122.70
1	D	136	PRO	N-CA-C	6.62	129.32	112.10
2	B	15	TYR	CG-CD1-CE1	6.62	126.59	121.30
2	B	293	PHE	CD1-CE1-CZ	-6.62	112.16	120.10
1	D	265	PRO	N-CA-CB	-6.61	95.33	102.60
1	A	426	PHE	CG-CD1-CE1	6.61	128.07	120.80
2	B	469	ALA	N-CA-CB	-6.61	100.85	110.10
4	E	416	VAL	CA-C-N	-6.61	102.66	117.20
4	E	27	VAL	N-CA-C	6.60	128.82	111.00
2	B	455	PHE	CZ-CE2-CD2	6.60	128.02	120.10
2	B	63	TYR	CG-CD1-CE1	6.60	126.58	121.30
1	A	176	TRP	CD1-NE1-CE2	6.60	114.94	109.00
2	B	197	TRP	CZ3-CH2-CZ2	6.59	129.51	121.60
2	B	197	TRP	CG-CD2-CE3	-6.59	127.97	133.90
1	A	391	GLU	OE1-CD-OE2	-6.58	115.40	123.30
2	B	458	ALA	CB-CA-C	6.58	119.97	110.10
1	A	101	ALA	N-CA-CB	6.58	119.31	110.10
3	C	153	TYR	CB-CG-CD2	-6.58	117.05	121.00
1	D	195	ASP	CB-CG-OD2	6.57	124.21	118.30
1	A	394	ASN	CA-CB-CG	6.57	127.84	113.40
2	B	197	TRP	CE2-CD2-CG	6.57	112.55	107.30
2	B	63	TYR	CD1-CE1-CZ	-6.56	113.90	119.80
1	D	135	PHE	CB-CG-CD1	-6.56	116.21	120.80
1	D	112	TYR	CE1-CZ-CE2	-6.55	109.31	119.80
3	C	92	ILE	C-N-CA	6.55	138.07	121.70
2	B	142	CYS	CB-CA-C	-6.54	97.31	110.40
1	A	238	ASP	O-C-N	-6.54	112.23	122.70
2	B	90	ILE	CA-C-O	6.54	133.84	120.10
3	C	69	TRP	O-C-N	6.54	133.16	122.70
2	B	195	LYS	CA-C-N	6.54	131.58	117.20
4	E	70	GLU	CA-CB-CG	6.54	127.78	113.40
2	B	427	ASP	CB-CG-OD2	6.54	124.18	118.30
4	E	238	LEU	CA-CB-CG	6.54	130.33	115.30
3	C	101	GLN	CG-CD-NE2	6.53	132.37	116.70
1	A	213	TYR	CD1-CE1-CZ	-6.52	113.93	119.80
1	D	149	TRP	CD1-NE1-CE2	-6.52	103.13	109.00
1	D	32	THR	O-C-N	-6.52	112.27	122.70
4	E	118	LEU	CB-CG-CD2	6.52	122.09	111.00
2	B	94	ASN	C-N-CA	6.51	137.97	121.70
3	C	478	PHE	CZ-CE2-CD2	6.51	127.91	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	116	TYR	N-CA-CB	-6.51	98.88	110.60
4	E	260	ALA	O-C-N	-6.51	112.29	122.70
2	B	280	ILE	N-CA-CB	6.50	125.76	110.80
1	D	86	TRP	CD1-NE1-CE2	6.50	114.85	109.00
2	B	62	ASP	OD1-CG-OD2	-6.49	110.97	123.30
1	D	89	ASP	CB-CG-OD1	-6.49	112.46	118.30
3	C	288	ILE	O-C-N	6.49	134.23	123.20
1	D	44	ASP	CB-CG-OD2	-6.48	112.47	118.30
4	E	71	TYR	CA-C-O	6.48	133.71	120.10
3	C	293	MET	N-CA-CB	6.47	122.25	110.60
3	C	67	LEU	CB-CG-CD2	6.47	122.00	111.00
4	E	95	VAL	O-C-N	6.47	133.05	122.70
1	A	175	GLU	C-N-CA	6.46	137.85	121.70
1	A	269	SER	C-N-CA	6.46	137.85	121.70
1	A	149	TRP	CA-CB-CG	6.46	125.97	113.70
1	A	176	TRP	CG-CD2-CE3	6.46	139.71	133.90
2	B	445	THR	CA-CB-CG2	-6.45	103.37	112.40
3	C	136	TYR	CA-CB-CG	6.45	125.66	113.40
2	B	12	PHE	CB-CG-CD2	6.44	125.31	120.80
1	D	73	GLY	C-N-CA	6.44	135.82	122.30
3	C	277	ARG	O-C-N	-6.43	112.40	122.70
4	E	421	PHE	CB-CG-CD2	6.43	125.30	120.80
1	A	67	TRP	CD1-CG-CD2	6.43	111.44	106.30
4	E	291	PHE	CB-CG-CD1	6.43	125.30	120.80
4	E	439	TRP	CE2-CD2-CG	-6.43	102.16	107.30
1	D	176	TRP	N-CA-CB	6.43	122.17	110.60
3	C	248	TYR	CB-CG-CD2	-6.42	117.15	121.00
2	B	441	TYR	CD1-CG-CD2	6.42	124.96	117.90
1	A	20	ARG	NH1-CZ-NH2	-6.41	112.35	119.40
2	B	220	TYR	CZ-CE2-CD2	6.41	125.57	119.80
3	C	224	LYS	N-CA-CB	6.40	122.12	110.60
2	B	55	PHE	CB-CG-CD1	6.40	125.28	120.80
2	B	204	TYR	CA-C-O	-6.38	106.70	120.10
2	B	303	ASN	CB-CA-C	6.38	123.16	110.40
4	E	136	PHE	C-N-CA	6.38	137.65	121.70
1	D	157	SER	O-C-N	-6.38	112.50	122.70
3	C	79	ILE	CB-CA-C	-6.38	98.85	111.60
4	E	238	LEU	CB-CG-CD1	-6.37	100.18	111.00
3	C	471	PHE	CD1-CE1-CZ	-6.36	112.47	120.10
1	D	197	PRO	CA-N-CD	-6.36	102.60	111.50
4	E	76	LEU	CA-CB-CG	6.35	129.91	115.30
1	A	408	HIS	N-CA-CB	6.35	122.03	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	104	VAL	CA-CB-CG2	6.35	120.42	110.90
1	D	176	TRP	CZ3-CH2-CZ2	6.35	129.22	121.60
3	C	264	LEU	CB-CG-CD1	-6.34	100.22	111.00
4	E	106	ASN	CB-CA-C	6.34	123.08	110.40
1	A	401	TYR	CB-CG-CD1	6.33	124.80	121.00
3	C	467	LEU	CA-CB-CG	6.33	129.86	115.30
1	A	213	TYR	CD1-CG-CD2	6.33	124.86	117.90
2	B	7	LEU	CB-CG-CD1	-6.33	100.24	111.00
3	C	464	VAL	CB-CA-C	-6.33	99.38	111.40
2	B	439	PHE	CB-CG-CD2	6.32	125.23	120.80
1	D	272	PRO	CA-N-CD	-6.31	102.67	111.50
2	B	290	LEU	CB-CG-CD2	-6.30	100.28	111.00
4	E	112	ASP	O-C-N	-6.30	112.49	123.20
4	E	25	ASP	CB-CG-OD1	6.29	123.96	118.30
3	C	142	GLN	CG-CD-NE2	6.29	131.80	116.70
1	A	109	LEU	O-C-N	6.29	132.76	122.70
1	A	184	TRP	CZ3-CH2-CZ2	-6.29	114.06	121.60
3	C	1	VAL	C-N-CA	6.29	137.41	121.70
4	E	134	PHE	C-N-CD	6.29	141.60	128.40
3	C	157	GLU	OE1-CD-OE2	6.28	130.84	123.30
2	B	151	TYR	CG-CD1-CE1	6.27	126.31	121.30
4	E	218	PRO	CA-N-CD	-6.27	102.73	111.50
1	A	64	ARG	NE-CZ-NH2	6.26	123.43	120.30
1	A	110	LEU	O-C-N	6.26	132.72	122.70
1	D	112	TYR	CD1-CE1-CZ	6.26	125.43	119.80
2	B	427	ASP	N-CA-CB	6.26	121.86	110.60
3	C	302	VAL	CA-CB-CG2	6.25	120.28	110.90
4	E	238	LEU	N-CA-C	-6.25	94.12	111.00
2	B	45	GLU	OE1-CD-OE2	-6.25	115.80	123.30
2	B	411	ILE	O-C-N	-6.25	112.70	122.70
1	A	224	LEU	CB-CA-C	-6.24	98.34	110.20
3	C	294	PHE	CG-CD2-CE2	6.24	127.66	120.80
4	E	62	TYR	CD1-CG-CD2	-6.24	111.04	117.90
1	A	396	ALA	N-CA-CB	6.24	118.83	110.10
1	D	176	TRP	CB-CG-CD1	6.23	135.09	127.00
2	B	306	HIS	N-CA-C	6.22	127.80	111.00
2	B	182	GLU	OE1-CD-OE2	-6.22	115.84	123.30
2	B	306	HIS	CA-CB-CG	-6.22	103.03	113.60
3	C	19	LYS	CB-CG-CD	6.22	127.77	111.60
1	A	86	TRP	CB-CG-CD1	6.22	135.08	127.00
4	E	98	GLN	CG-CD-NE2	6.22	131.62	116.70
2	B	274	SER	N-CA-CB	6.21	119.82	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	431	ILE	N-CA-CB	6.21	125.09	110.80
3	C	140	ASP	OD1-CG-OD2	-6.21	111.50	123.30
1	A	108	LEU	CA-CB-CG	6.21	129.57	115.30
4	E	215	GLN	CG-CD-NE2	6.21	131.60	116.70
1	D	29	VAL	O-C-N	-6.20	112.78	122.70
1	D	178	MET	CG-SD-CE	6.20	110.12	100.20
1	D	100	PHE	CZ-CE2-CD2	6.20	127.54	120.10
1	D	270	ALA	CB-CA-C	6.20	119.40	110.10
1	D	95	ASN	O-C-N	-6.20	112.79	122.70
4	E	155	VAL	O-C-N	-6.20	112.79	122.70
1	A	57	ARG	NE-CZ-NH2	-6.19	117.20	120.30
3	C	245	LEU	O-C-N	-6.19	112.79	122.70
1	A	151	TYR	CG-CD1-CE1	6.18	126.25	121.30
2	B	404	ALA	C-N-CA	6.18	137.16	121.70
4	E	43	ASN	N-CA-CB	6.18	121.73	110.60
1	D	211	PRO	CB-CA-C	-6.18	96.55	112.00
4	E	414	SER	N-CA-CB	-6.18	101.22	110.50
1	A	209	ARG	N-CA-C	6.17	127.67	111.00
3	C	103	ASN	O-C-N	6.17	132.58	122.70
2	B	48	GLU	OE1-CD-OE2	-6.17	115.89	123.30
4	E	138	TRP	CD1-CG-CD2	6.17	111.24	106.30
3	C	29	GLU	CA-CB-CG	6.17	126.97	113.40
2	B	223	TYR	CB-CG-CD1	-6.17	117.30	121.00
2	B	151	TYR	CD1-CG-CD2	-6.16	111.12	117.90
3	C	46	LYS	N-CA-C	-6.16	94.36	111.00
3	C	466	VAL	CA-CB-CG1	6.16	120.14	110.90
3	C	190	TRP	CG-CD2-CE3	6.16	139.44	133.90
1	D	429	ARG	NH1-CZ-NH2	6.16	126.18	119.40
1	A	63	VAL	CA-CB-CG1	-6.16	101.66	110.90
1	A	171	MET	CB-CA-C	-6.16	98.08	110.40
1	D	198	TYR	CG-CD1-CE1	-6.15	116.38	121.30
3	C	67	LEU	CB-CG-CD1	6.15	121.46	111.00
2	B	186	TRP	CA-CB-CG	6.15	125.38	113.70
2	B	193	SER	N-CA-CB	-6.15	101.28	110.50
2	B	280	ILE	CG1-CB-CG2	6.15	124.92	111.40
1	D	6	ARG	NH1-CZ-NH2	-6.14	112.64	119.40
1	D	295	VAL	CA-C-O	-6.14	107.19	120.10
3	C	94	LEU	CB-CA-C	6.14	121.87	110.20
3	C	455	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	A	257	LEU	CA-CB-CG	6.14	129.42	115.30
4	E	78	ARG	NH1-CZ-NH2	6.13	126.15	119.40
2	B	62	ASP	CB-CG-OD1	6.13	123.81	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	286	PHE	CZ-CE2-CD2	-6.12	112.76	120.10
4	E	85	TRP	CD1-NE1-CE2	6.12	114.50	109.00
1	A	27	HIS	CG-ND1-CE1	6.12	116.76	108.20
2	B	92	LEU	O-C-N	6.11	132.48	122.70
3	C	473	PHE	CD1-CE1-CZ	6.11	127.44	120.10
4	E	198	LEU	CB-CG-CD1	6.11	121.39	111.00
4	E	418	ALA	N-CA-CB	6.11	118.65	110.10
1	D	396	ALA	O-C-N	-6.11	112.93	122.70
3	C	212	TYR	CD1-CE1-CZ	6.10	125.29	119.80
3	C	277	ARG	N-CA-CB	-6.10	99.63	110.60
1	D	414	PHE	CD1-CE1-CZ	6.09	127.41	120.10
1	A	262	GLU	CA-C-N	-6.09	103.80	117.20
1	D	198	TYR	CD1-CG-CD2	6.09	124.60	117.90
1	A	97	ASP	CB-CG-OD2	6.09	123.78	118.30
2	B	72	TYR	CD1-CE1-CZ	6.09	125.28	119.80
3	C	121	LEU	N-CA-C	6.08	127.43	111.00
4	E	83	LEU	N-CA-C	6.08	127.42	111.00
1	A	426	PHE	O-C-N	-6.07	112.99	122.70
1	D	84	ASP	CA-CB-CG	6.06	126.74	113.40
2	B	257	LEU	O-C-N	6.06	132.40	122.70
1	D	273	LEU	CA-CB-CG	6.06	129.24	115.30
1	A	399	TRP	C-N-CA	6.06	136.84	121.70
1	A	86	TRP	NE1-CE2-CZ2	-6.05	123.74	130.40
1	A	103	VAL	CG1-CB-CG2	-6.05	101.21	110.90
1	A	132	VAL	CA-CB-CG2	6.05	119.98	110.90
4	E	476	GLU	OE1-CD-OE2	-6.05	116.03	123.30
2	B	44	ASN	N-CA-C	-6.05	94.67	111.00
3	C	250	PRO	O-C-N	-6.05	113.02	122.70
1	A	24	HIS	CG-ND1-CE1	6.04	116.66	108.20
1	A	28	PHE	CB-CG-CD1	-6.04	116.57	120.80
2	B	275	LEU	CA-C-O	-6.04	107.41	120.10
1	D	393	SER	O-C-N	-6.04	113.03	122.70
4	E	313	THR	N-CA-CB	6.04	121.77	110.30
2	B	44	ASN	O-C-N	6.04	132.36	122.70
3	C	473	PHE	CG-CD2-CE2	6.03	127.44	120.80
4	E	133	TYR	CB-CG-CD2	-6.03	117.38	121.00
1	A	176	TRP	CA-CB-CG	6.03	125.16	113.70
4	E	107	VAL	O-C-N	-6.03	113.05	122.70
2	B	468	PHE	N-CA-CB	6.03	121.45	110.60
3	C	101	GLN	O-C-N	6.03	132.34	122.70
1	D	64	ARG	NE-CZ-NH2	-6.03	117.29	120.30
3	C	275	SER	O-C-N	-6.02	113.06	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	39	LEU	O-C-N	6.02	132.34	122.70
3	C	236	CYS	N-CA-CB	6.02	121.44	110.60
1	A	132	VAL	CG1-CB-CG2	-6.02	101.27	110.90
3	C	88	TRP	CB-CA-C	-6.02	98.36	110.40
3	C	69	TRP	CD2-CE2-CZ2	6.01	129.52	122.30
3	C	432	GLN	OE1-CD-NE2	6.01	135.74	121.90
4	E	104	TYR	CA-CB-CG	6.01	124.83	113.40
3	C	300	THR	C-N-CA	6.01	134.92	122.30
1	D	128	CYS	O-C-N	-6.01	113.08	122.70
2	B	139	TRP	CD2-CE2-CZ2	6.00	129.50	122.30
3	C	223	ARG	CB-CA-C	-6.00	98.40	110.40
3	C	155	ALA	N-CA-CB	6.00	118.50	110.10
3	C	285	VAL	C-N-CD	6.00	140.99	128.40
1	D	19	ILE	O-C-N	-6.00	113.11	122.70
2	B	239	PHE	CD1-CE1-CZ	-5.99	112.91	120.10
3	C	126	PHE	CB-CG-CD2	-5.99	116.61	120.80
1	D	138	ASP	OD1-CG-OD2	5.99	134.68	123.30
1	A	20	ARG	O-C-N	5.98	132.47	121.10
4	E	220	PHE	CG-CD1-CE1	5.98	127.38	120.80
3	C	282	ALA	O-C-N	-5.98	113.14	122.70
4	E	309	ARG	CA-C-N	5.98	130.35	117.20
2	B	219	PHE	CD1-CG-CD2	-5.97	110.54	118.30
2	B	414	GLN	N-CA-CB	5.97	121.35	110.60
4	E	298	THR	N-CA-CB	5.97	121.64	110.30
1	A	60	TRP	CD1-NE1-CE2	5.96	114.37	109.00
3	C	153	TYR	O-C-N	5.96	132.23	122.70
1	A	39	GLN	CG-CD-OE1	-5.96	109.69	121.60
1	D	280	PHE	CB-CG-CD1	-5.95	116.63	120.80
1	D	86	TRP	CD1-CG-CD2	5.95	111.06	106.30
1	A	200	ASP	CB-CG-OD1	5.95	123.65	118.30
2	B	468	PHE	CA-CB-CG	5.95	128.18	113.90
1	D	384	GLU	CG-CD-OE2	5.95	130.20	118.30
1	A	182	ARG	NE-CZ-NH1	5.94	123.27	120.30
4	E	427	LYS	CA-CB-CG	5.94	126.47	113.40
1	A	399	TRP	CD1-NE1-CE2	5.94	114.34	109.00
1	D	57	ARG	NE-CZ-NH2	-5.94	117.33	120.30
3	C	257	MET	CA-CB-CG	5.94	123.39	113.30
1	D	45	GLU	CB-CA-C	5.94	122.28	110.40
2	B	446	MET	N-CA-C	5.94	127.03	111.00
3	C	150	ALA	C-N-CA	5.94	136.54	121.70
1	D	69	PRO	CA-N-CD	-5.93	103.19	111.50
2	B	249	MET	CB-CA-C	5.93	122.26	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	190	TRP	CD2-CE3-CZ3	5.93	126.51	118.80
1	D	203	TYR	CB-CG-CD1	5.93	124.56	121.00
3	C	248	TYR	O-C-N	-5.92	113.22	122.70
1	D	72	TYR	CG-CD1-CE1	5.92	126.04	121.30
2	B	220	TYR	O-C-N	5.92	132.17	122.70
2	B	455	PHE	CG-CD2-CE2	-5.92	114.29	120.80
1	D	127	TYR	N-CA-CB	-5.92	99.95	110.60
1	A	209	ARG	CG-CD-NE	5.92	124.22	111.80
3	C	136	TYR	CG-CD2-CE2	-5.92	116.57	121.30
3	C	29	GLU	CA-C-O	-5.91	107.68	120.10
4	E	254	SER	N-CA-CB	5.91	119.37	110.50
3	C	457	SER	N-CA-CB	-5.91	101.63	110.50
3	C	320	HIS	CG-ND1-CE1	5.91	116.47	108.20
1	D	266	SER	O-C-N	5.91	132.16	122.70
2	B	205	GLU	O-C-N	-5.91	113.25	122.70
1	D	54	VAL	O-C-N	5.90	132.14	122.70
2	B	204	TYR	CZ-CE2-CD2	-5.89	114.50	119.80
2	B	293	PHE	CZ-CE2-CD2	5.89	127.17	120.10
2	B	72	TYR	CG-CD1-CE1	-5.89	116.59	121.30
4	E	237	VAL	CA-CB-CG2	-5.89	102.06	110.90
2	B	190	HIS	CG-ND1-CE1	5.89	116.45	108.20
3	C	184	PHE	CG-CD2-CE2	5.89	127.28	120.80
3	C	459	PHE	O-C-N	5.89	132.12	122.70
4	E	428	GLU	OE1-CD-OE2	5.89	130.37	123.30
1	A	81	PRO	N-CA-CB	-5.89	96.12	102.60
1	A	113	THR	CA-CB-CG2	-5.88	104.16	112.40
2	B	186	TRP	CH2-CZ2-CE2	5.88	123.28	117.40
3	C	248	TYR	CZ-CE2-CD2	-5.88	114.51	119.80
1	D	129	GLU	O-C-N	-5.88	113.29	122.70
3	C	112	VAL	CB-CA-C	-5.88	100.23	111.40
3	C	202	TYR	N-CA-C	5.88	126.87	111.00
3	C	57	TRP	CG-CD1-NE1	5.88	115.98	110.10
1	D	381	TYR	CA-C-O	-5.87	107.76	120.10
2	B	163	ASP	CB-CG-OD2	-5.87	113.02	118.30
3	C	306	CYS	N-CA-C	-5.87	95.15	111.00
1	A	301	ARG	C-N-CA	5.87	136.37	121.70
1	A	111	ASP	N-CA-CB	5.86	121.15	110.60
1	D	2	GLU	OE1-CD-OE2	-5.86	116.26	123.30
1	A	140	GLN	OE1-CD-NE2	-5.86	108.42	121.90
3	C	103	ASN	CA-C-N	-5.86	104.31	117.20
3	C	136	TYR	CD1-CG-CD2	5.86	124.35	117.90
4	E	134	PHE	CB-CG-CD1	5.85	124.90	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	299	VAL	CA-CB-CG2	-5.85	102.12	110.90
1	D	222	CYS	CA-CB-SG	-5.85	103.47	114.00
4	E	14	TYR	CZ-CE2-CD2	-5.85	114.53	119.80
1	D	170	PHE	O-C-N	-5.85	113.34	122.70
1	A	149	TRP	CD1-NE1-CE2	-5.84	103.74	109.00
2	B	178	ASP	CB-CG-OD2	5.84	123.56	118.30
4	E	94	ASN	O-C-N	5.84	132.04	122.70
4	E	117	TRP	CG-CD2-CE3	-5.83	128.65	133.90
1	A	20	ARG	CD-NE-CZ	5.83	131.76	123.60
1	D	381	TYR	CG-CD2-CE2	-5.83	116.64	121.30
1	A	276	LYS	C-N-CA	5.83	136.27	121.70
2	B	159	GLN	C-N-CA	5.83	136.27	121.70
1	A	89	ASP	CB-CG-OD2	-5.83	113.06	118.30
1	D	284	PHE	CB-CG-CD1	5.82	124.88	120.80
1	D	97	ASP	CB-CG-OD2	5.82	123.54	118.30
2	B	410	TYR	CB-CG-CD2	5.82	124.49	121.00
1	D	69	PRO	N-CD-CG	5.82	111.93	103.20
1	A	22	VAL	N-CA-CB	5.81	124.28	111.50
1	A	169	THR	CA-CB-CG2	-5.81	104.27	112.40
1	A	249	VAL	CB-CA-C	-5.81	100.36	111.40
3	C	285	VAL	CA-C-O	-5.81	107.90	120.10
4	E	134	PHE	CG-CD1-CE1	5.81	127.19	120.80
1	A	395	ALA	CB-CA-C	5.81	118.81	110.10
2	B	117	SER	N-CA-CB	-5.80	101.80	110.50
3	C	202	TYR	CG-CD2-CE2	5.80	125.94	121.30
1	D	112	TYR	CG-CD1-CE1	5.80	125.94	121.30
1	D	259	VAL	CA-CB-CG2	-5.80	102.20	110.90
1	D	12	LEU	CB-CG-CD2	-5.80	101.14	111.00
1	D	403	ALA	C-N-CA	5.80	136.19	121.70
1	A	28	PHE	CD1-CG-CD2	5.79	125.83	118.30
1	A	15	TYR	CB-CG-CD1	-5.79	117.53	121.00
4	E	420	ASN	C-N-CA	5.79	136.17	121.70
2	B	458	ALA	C-N-CA	5.79	136.16	121.70
4	E	263	ILE	CG1-CB-CG2	-5.79	98.67	111.40
2	B	186	TRP	CZ3-CH2-CZ2	-5.78	114.66	121.60
1	D	114	GLY	O-C-N	-5.78	113.45	122.70
4	E	289	VAL	CG1-CB-CG2	5.78	120.14	110.90
1	D	100	PHE	CG-CD2-CE2	-5.77	114.45	120.80
1	A	301	ARG	N-CA-C	5.77	126.59	111.00
1	D	429	ARG	O-C-N	-5.77	113.47	122.70
2	B	156	VAL	O-C-N	-5.77	113.47	122.70
4	E	466	PHE	CB-CG-CD2	-5.77	116.76	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	386	MET	CG-SD-CE	5.76	109.42	100.20
1	D	190	TYR	CZ-CE2-CD2	-5.76	114.61	119.80
4	E	154	GLU	C-N-CA	5.76	136.10	121.70
4	E	187	HIS	CG-ND1-CE1	5.76	116.27	108.20
4	E	11	LEU	O-C-N	-5.75	113.42	123.20
1	A	300	HIS	C-N-CA	5.75	136.08	121.70
4	E	219	LEU	O-C-N	5.75	131.90	122.70
3	C	153	TYR	CG-CD1-CE1	-5.75	116.70	121.30
4	E	176	ASP	C-N-CA	5.75	136.07	121.70
1	A	61	ILE	N-CA-CB	5.74	124.00	110.80
1	A	422	THR	O-C-N	-5.74	113.51	122.70
3	C	178	ILE	O-C-N	-5.74	113.52	122.70
4	E	435	GLU	CG-CD-OE1	5.74	129.78	118.30
2	B	164	ALA	N-CA-CB	5.73	118.13	110.10
2	B	278	PRO	CA-N-CD	-5.73	103.47	111.50
1	D	64	ARG	CD-NE-CZ	5.73	131.63	123.60
1	D	270	ALA	N-CA-CB	5.73	118.12	110.10
1	A	399	TRP	CG-CD2-CE3	-5.73	128.75	133.90
1	D	84	ASP	CB-CA-C	5.73	121.85	110.40
2	B	85	VAL	CB-CA-C	-5.72	100.53	111.40
2	B	215	ARG	CB-CA-C	5.72	121.84	110.40
4	E	82	GLU	N-CA-CB	-5.72	100.30	110.60
4	E	421	PHE	CG-CD1-CE1	5.72	127.09	120.80
3	C	476	GLY	CA-C-N	5.72	129.78	117.20
4	E	136	PHE	CG-CD1-CE1	5.71	127.08	120.80
3	C	142	GLN	C-N-CA	5.71	135.97	121.70
1	D	410	LEU	CA-CB-CG	5.71	128.43	115.30
4	E	19	LYS	CA-CB-CG	5.71	125.95	113.40
1	A	216	VAL	O-C-N	-5.70	113.58	122.70
3	C	471	PHE	CE1-CZ-CE2	5.70	130.26	120.00
1	D	198	TYR	CG-CD2-CE2	-5.70	116.74	121.30
1	D	77	LYS	CA-C-N	-5.70	104.66	117.20
3	C	62	TRP	CE3-CZ3-CH2	-5.69	114.94	121.20
1	D	137	PHE	O-C-N	-5.69	113.59	122.70
1	D	149	TRP	CD1-CG-CD2	-5.69	101.75	106.30
2	B	286	PHE	CG-CD1-CE1	-5.69	114.54	120.80
1	D	34	GLY	CA-C-N	-5.69	104.68	117.20
3	C	141	TRP	NE1-CE2-CZ2	-5.69	124.14	130.40
2	B	458	ALA	N-CA-CB	5.69	118.06	110.10
3	C	189	GLU	N-CA-CB	-5.69	100.36	110.60
4	E	78	ARG	N-CA-CB	5.69	120.84	110.60
2	B	89	ASP	C-N-CA	5.69	135.91	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	107	PHE	O-C-N	-5.69	113.60	122.70
4	E	273	PRO	O-C-N	5.68	131.79	122.70
2	B	128	CYS	C-N-CA	5.68	135.91	121.70
2	B	106	VAL	CB-CA-C	-5.68	100.61	111.40
4	E	147	SER	N-CA-C	-5.68	95.66	111.00
1	A	11	LEU	CB-CG-CD2	5.68	120.65	111.00
1	D	130	ILE	C-N-CA	5.68	135.89	121.70
1	A	172	GLU	O-C-N	5.67	131.78	122.70
2	B	219	PHE	O-C-N	5.67	131.78	122.70
3	C	459	PHE	C-N-CA	5.67	135.88	121.70
1	A	198	TYR	CG-CD1-CE1	-5.67	116.76	121.30
2	B	455	PHE	CB-CG-CD2	5.67	124.77	120.80
2	B	118	TRP	CE2-CD2-CG	-5.66	102.77	107.30
1	A	218	VAL	O-C-N	-5.66	113.64	122.70
3	C	22	ARG	CG-CD-NE	-5.66	99.91	111.80
3	C	62	TRP	CD1-NE1-CE2	-5.66	103.91	109.00
1	A	174	GLY	C-N-CA	5.66	135.84	121.70
1	D	88	PRO	O-C-N	5.66	131.75	122.70
1	D	232	VAL	CG1-CB-CG2	5.66	119.95	110.90
1	D	127	TYR	CZ-CE2-CD2	-5.65	114.71	119.80
2	B	465	ASP	CB-CG-OD2	5.64	123.38	118.30
1	D	17	LYS	CA-C-O	-5.64	108.25	120.10
1	D	55	ARG	O-C-N	-5.64	113.67	122.70
1	D	232	VAL	CB-CA-C	-5.64	100.68	111.40
1	D	20	ARG	NH1-CZ-NH2	-5.64	113.19	119.40
1	D	399	TRP	CD1-CG-CD2	-5.64	101.79	106.30
1	A	73	GLY	C-N-CA	5.64	134.15	122.30
4	E	134	PHE	CZ-CE2-CD2	5.64	126.87	120.10
1	D	45	GLU	OE1-CD-OE2	-5.64	116.54	123.30
4	E	439	TRP	O-C-N	5.63	131.71	122.70
1	A	295	VAL	CA-CB-CG1	-5.63	102.45	110.90
1	D	230	VAL	O-C-N	-5.63	113.69	122.70
3	C	263	VAL	CA-CB-CG2	-5.63	102.46	110.90
3	C	276	GLN	CA-C-O	5.63	131.92	120.10
4	E	87	PRO	O-C-N	-5.63	113.70	122.70
1	A	415	MET	CG-SD-CE	5.62	109.19	100.20
1	D	139	GLN	N-CA-C	5.62	126.17	111.00
1	A	97	ASP	O-C-N	-5.62	113.65	123.20
2	B	149	TYR	CZ-CE2-CD2	-5.62	114.75	119.80
2	B	302	LEU	O-C-N	5.62	131.69	122.70
1	A	250	LEU	CB-CA-C	5.61	120.86	110.20
3	C	294	PHE	CG-CD1-CE1	-5.61	114.63	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	189	TYR	CA-CB-CG	5.61	124.06	113.40
1	A	301	ARG	CA-C-O	-5.61	108.32	120.10
4	E	134	PHE	O-C-N	5.61	131.76	121.10
2	B	25	VAL	CA-CB-CG1	5.61	119.31	110.90
4	E	133	TYR	CZ-CE2-CD2	-5.61	114.75	119.80
2	B	94	ASN	O-C-N	5.60	131.67	122.70
1	D	165	PRO	N-CA-CB	5.60	110.03	103.30
1	A	437	GLY	N-CA-C	5.60	127.10	113.10
1	A	436	GLU	OE1-CD-OE2	-5.60	116.58	123.30
2	B	267	ALA	CB-CA-C	5.59	118.49	110.10
3	C	152	ASN	N-CA-CB	-5.59	100.53	110.60
4	E	44	GLU	OE1-CD-OE2	5.59	130.01	123.30
1	D	6	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	D	28	PHE	CG-CD2-CE2	5.59	126.95	120.80
2	B	124	TYR	CA-CB-CG	5.59	124.02	113.40
1	D	5	THR	CA-CB-CG2	-5.59	104.58	112.40
4	E	251	CYS	N-CA-CB	5.59	120.66	110.60
1	A	16	ASN	CB-CG-OD1	-5.59	110.43	121.60
3	C	40	SER	O-C-N	5.59	131.64	122.70
1	D	102	ILE	CB-CG1-CD1	5.58	129.54	113.90
3	C	117	TYR	CE1-CZ-CE2	5.58	128.73	119.80
4	E	237	VAL	O-C-N	-5.58	113.77	122.70
2	B	453	SER	O-C-N	-5.58	113.77	122.70
2	B	307	ARG	N-CA-C	5.58	126.06	111.00
1	D	233	PHE	CB-CG-CD1	-5.58	116.89	120.80
4	E	96	ASP	CB-CG-OD1	-5.58	113.28	118.30
2	B	156	VAL	CA-CB-CG2	5.57	119.26	110.90
3	C	102	TYR	CA-CB-CG	5.57	123.98	113.40
1	A	382	ILE	O-C-N	5.57	131.61	122.70
3	C	286	PRO	CA-N-CD	-5.57	103.70	111.50
4	E	78	ARG	CD-NE-CZ	-5.56	115.81	123.60
4	E	92	GLU	C-N-CA	5.56	135.61	121.70
1	A	30	ASP	CB-CG-OD2	-5.56	113.30	118.30
2	B	55	PHE	CB-CA-C	-5.56	99.29	110.40
3	C	202	TYR	O-C-N	-5.55	113.76	123.20
4	E	138	TRP	NE1-CE2-CD2	5.55	112.86	107.30
2	B	463	PRO	N-CA-C	5.55	126.53	112.10
4	E	471	LEU	C-N-CA	5.55	135.57	121.70
3	C	428	TYR	CB-CG-CD2	5.55	124.33	121.00
2	B	63	TYR	CG-CD2-CE2	-5.55	116.86	121.30
3	C	207	PRO	CA-N-CD	-5.54	103.74	111.50
2	B	180	PHE	CZ-CE2-CD2	-5.54	113.45	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	TRP	CG-CD2-CE3	5.54	138.88	133.90
1	A	176	TRP	CD2-CE3-CZ3	5.54	126.00	118.80
4	E	59	TRP	CE2-CD2-CG	-5.54	102.87	107.30
1	A	281	THR	CA-CB-CG2	-5.53	104.66	112.40
1	D	137	PHE	CB-CA-C	5.53	121.46	110.40
1	D	151	TYR	CG-CD2-CE2	5.53	125.72	121.30
1	D	211	PRO	CA-C-O	-5.52	106.94	120.20
1	D	265	PRO	CA-CB-CG	-5.52	93.51	104.00
1	A	301	ARG	NE-CZ-NH2	5.52	123.06	120.30
2	B	61	THR	O-C-N	-5.52	113.87	122.70
1	D	151	TYR	CA-CB-CG	5.52	123.88	113.40
3	C	65	HIS	N-CA-CB	-5.51	100.68	110.60
3	C	99	ASP	CA-C-N	-5.51	105.18	116.20
2	B	188	ILE	N-CA-C	5.51	125.87	111.00
3	C	144	CYS	CA-CB-SG	5.50	123.91	114.00
4	E	263	ILE	CB-CA-C	-5.50	100.60	111.60
1	A	214	PHE	CB-CG-CD2	-5.50	116.95	120.80
2	B	139	TRP	CB-CG-CD2	5.50	133.75	126.60
1	D	4	GLU	O-C-N	5.50	131.50	122.70
1	D	189	TYR	CD1-CG-CD2	-5.50	111.85	117.90
1	A	255	VAL	C-N-CA	-5.50	107.96	121.70
3	C	455	ARG	CD-NE-CZ	5.49	131.29	123.60
4	E	156	ASN	OD1-CG-ND2	5.49	134.53	121.90
4	E	451	PHE	O-C-N	-5.49	113.91	122.70
1	A	111	ASP	CB-CG-OD2	-5.49	113.36	118.30
3	C	207	PRO	O-C-N	-5.49	113.92	122.70
3	C	225	PRO	CA-N-CD	-5.49	103.81	111.50
4	E	236	VAL	CA-CB-CG1	-5.49	102.67	110.90
4	E	181	GLY	O-C-N	-5.48	113.92	122.70
1	A	414	PHE	O-C-N	5.48	131.47	122.70
3	C	286	PRO	N-CD-CG	5.48	111.42	103.20
3	C	446	TRP	CD1-CG-CD2	-5.48	101.91	106.30
1	D	58	GLN	CG-CD-NE2	5.48	129.85	116.70
1	D	427	ALA	O-C-N	5.48	132.51	123.20
3	C	483	ALA	C-N-CA	5.48	135.40	121.70
1	D	72	TYR	CD1-CE1-CZ	-5.48	114.87	119.80
1	A	60	TRP	CD1-CG-CD2	5.47	110.68	106.30
2	B	277	VAL	CA-CB-CG1	5.47	119.11	110.90
4	E	435	GLU	CA-CB-CG	5.47	125.44	113.40
1	A	89	ASP	CA-CB-CG	-5.47	101.37	113.40
3	C	46	LYS	CA-C-N	-5.47	105.18	117.20
1	D	85	VAL	CA-C-N	-5.47	105.17	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	63	TYR	CD1-CG-CD2	-5.46	111.89	117.90
2	B	150	THR	O-C-N	5.46	131.44	122.70
1	D	111	ASP	CB-CA-C	5.46	121.32	110.40
2	B	95	ASN	C-N-CA	5.46	135.34	121.70
3	C	131	PRO	CA-N-CD	-5.46	103.86	111.50
2	B	138	ASP	OD1-CG-OD2	-5.45	112.94	123.30
3	C	178	ILE	CA-C-O	-5.45	108.65	120.10
1	D	301	ARG	NH1-CZ-NH2	-5.45	113.40	119.40
1	D	301	ARG	CD-NE-CZ	5.45	131.23	123.60
3	C	154	ASN	O-C-N	-5.44	113.99	122.70
1	D	284	PHE	CB-CA-C	-5.44	99.52	110.40
4	E	74	ILE	CA-CB-CG1	5.44	121.34	111.00
4	E	125	SER	O-C-N	-5.44	113.99	122.70
1	D	18	VAL	CB-CA-C	-5.44	101.07	111.40
1	A	132	VAL	CB-CA-C	5.43	121.72	111.40
3	C	23	PRO	N-CA-CB	5.43	109.81	103.30
2	B	422	ASP	CB-CG-OD1	-5.43	113.42	118.30
4	E	16	LYS	C-N-CA	5.42	135.26	121.70
1	D	128	CYS	CB-CA-C	-5.42	99.56	110.40
1	D	408	HIS	O-C-N	-5.42	114.02	122.70
2	B	404	ALA	N-CA-CB	5.42	117.69	110.10
1	D	189	TYR	O-C-N	-5.41	114.04	122.70
1	A	187	TRP	CA-C-O	-5.41	108.73	120.10
3	C	203	GLY	O-C-N	-5.41	114.04	122.70
1	D	422	THR	OG1-CB-CG2	5.41	122.45	110.00
4	E	264	PHE	CB-CG-CD2	5.41	124.59	120.80
3	C	112	VAL	CG1-CB-CG2	5.41	119.55	110.90
1	D	61	ILE	CA-C-O	5.41	131.46	120.10
2	B	303	ASN	O-C-N	-5.41	114.05	122.70
3	C	439	TYR	CD1-CG-CD2	5.41	123.85	117.90
4	E	466	PHE	CB-CG-CD1	5.41	124.58	120.80
1	A	255	VAL	CA-CB-CG2	-5.40	102.80	110.90
1	A	399	TRP	CE2-CD2-CG	5.40	111.62	107.30
2	B	2	VAL	CA-CB-CG1	-5.40	102.80	110.90
1	A	298	THR	CA-CB-CG2	-5.40	104.84	112.40
3	C	75	SER	N-CA-CB	5.40	118.60	110.50
1	D	284	PHE	CZ-CE2-CD2	5.40	126.58	120.10
4	E	263	ILE	C-N-CA	5.40	135.19	121.70
1	A	416	LEU	CB-CG-CD1	-5.39	101.83	111.00
3	C	466	VAL	CA-CB-CG2	5.39	118.99	110.90
1	A	292	THR	OG1-CB-CG2	5.39	122.40	110.00
1	A	279	LEU	CA-CB-CG	5.39	127.69	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	7	LEU	O-C-N	-5.39	114.08	122.70
4	E	26	HIS	N-CA-C	5.38	125.54	111.00
1	A	67	TRP	CG-CD1-NE1	-5.38	104.72	110.10
2	B	6	THR	O-C-N	-5.38	114.09	122.70
1	A	214	PHE	CD1-CG-CD2	5.38	125.29	118.30
1	A	218	VAL	CA-C-O	5.38	131.39	120.10
4	E	280	PRO	CA-C-N	-5.37	105.38	117.20
2	B	89	ASP	CA-C-O	5.37	131.38	120.10
3	C	86	LEU	CB-CG-CD2	-5.37	101.87	111.00
3	C	238	LEU	CB-CA-C	5.37	120.41	110.20
1	D	289	ILE	CG1-CB-CG2	5.37	123.21	111.40
4	E	66	TRP	NE1-CE2-CZ2	-5.37	124.50	130.40
4	E	138	TRP	O-C-N	5.37	131.29	122.70
1	A	258	LEU	CB-CG-CD2	5.37	120.12	111.00
1	A	241	GLU	CG-CD-OE2	5.36	129.03	118.30
3	C	100	GLY	CA-C-O	-5.36	110.95	120.60
3	C	190	TRP	CE2-CD2-CE3	-5.36	112.27	118.70
4	E	29	ASP	CB-CG-OD1	-5.36	113.48	118.30
1	D	27	HIS	O-C-N	5.36	131.27	122.70
1	A	292	THR	CA-CB-CG2	5.35	119.89	112.40
1	D	253	LEU	CA-C-N	-5.35	105.42	117.20
4	E	273	PRO	N-CA-CB	-5.35	96.72	102.60
1	D	225	PHE	CD1-CG-CD2	-5.35	111.35	118.30
1	D	285	VAL	CA-CB-CG1	5.35	118.92	110.90
1	D	380	LYS	CD-CE-NZ	5.35	124.00	111.70
4	E	151	ASN	C-N-CA	5.35	135.06	121.70
1	A	28	PHE	C-N-CA	-5.34	108.35	121.70
2	B	84	ASP	CB-CA-C	5.34	121.08	110.40
4	E	3	GLU	C-N-CA	5.34	133.51	122.30
4	E	297	VAL	N-CA-CB	5.34	123.25	111.50
4	E	439	TRP	NE1-CE2-CD2	5.34	112.64	107.30
4	E	102	ALA	CB-CA-C	-5.34	102.09	110.10
1	D	279	LEU	CB-CG-CD2	-5.33	101.93	111.00
1	A	3	HIS	CB-CA-C	5.33	121.06	110.40
4	E	463	LEU	CA-CB-CG	-5.33	103.04	115.30
1	A	263	LEU	N-CA-C	5.33	125.38	111.00
1	D	401	TYR	CG-CD1-CE1	-5.33	117.04	121.30
3	C	270	PHE	CD1-CG-CD2	-5.33	111.37	118.30
1	D	140	GLN	CG-CD-NE2	5.32	129.47	116.70
1	D	401	TYR	CA-C-O	5.32	131.28	120.10
1	A	164	ARG	CG-CD-NE	5.32	122.97	111.80
4	E	257	VAL	CB-CA-C	-5.32	101.29	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	PHE	CB-CG-CD2	5.32	124.52	120.80
1	D	392	SER	O-C-N	-5.31	114.20	122.70
3	C	280	GLU	O-C-N	-5.31	114.20	122.70
4	E	110	TYR	CZ-CE2-CD2	-5.31	115.02	119.80
1	A	106	THR	O-C-N	-5.31	114.20	122.70
1	D	264	ILE	CB-CA-C	5.31	122.22	111.60
4	E	178	THR	N-CA-C	5.31	125.33	111.00
2	B	428	TRP	CE3-CZ3-CH2	-5.31	115.36	121.20
2	B	3	MET	C-N-CA	5.30	134.96	121.70
4	E	205	PHE	CG-CD2-CE2	-5.30	114.97	120.80
1	A	377	GLU	CA-C-N	5.30	126.79	116.20
2	B	198	ARG	N-CA-CB	5.29	120.13	110.60
1	A	436	GLU	CA-CB-CG	5.29	125.04	113.40
1	D	168	SER	CB-CA-C	5.29	120.16	110.10
1	A	187	TRP	O-C-N	5.29	131.16	122.70
1	A	15	TYR	CG-CD2-CE2	-5.29	117.07	121.30
4	E	183	TRP	C-N-CA	5.28	134.91	121.70
4	E	246	ALA	O-C-N	-5.28	114.22	123.20
2	B	283	TYR	CG-CD2-CE2	5.28	125.52	121.30
2	B	307	ARG	CA-CB-CG	5.28	125.02	113.40
1	D	29	VAL	CA-CB-CG1	5.28	118.82	110.90
4	E	440	VAL	O-C-N	-5.28	114.26	122.70
3	C	108	CYS	O-C-N	-5.28	114.26	122.70
3	C	446	TRP	CB-CG-CD2	5.28	133.46	126.60
1	D	189	TYR	CG-CD1-CE1	5.27	125.52	121.30
4	E	140	ASN	N-CA-CB	-5.27	101.11	110.60
4	E	207	GLU	O-C-N	5.27	131.14	122.70
2	B	180	PHE	CG-CD1-CE1	-5.27	115.00	120.80
4	E	128	PRO	CB-CA-C	5.27	125.18	112.00
1	A	91	VAL	CG1-CB-CG2	-5.27	102.47	110.90
1	A	230	VAL	CG1-CB-CG2	5.27	119.33	110.90
4	E	22	LYS	C-N-CA	5.27	134.86	121.70
1	D	300	HIS	CA-CB-CG	-5.26	104.65	113.60
4	E	117	TRP	N-CA-CB	-5.26	101.12	110.60
4	E	103	TYR	CZ-CE2-CD2	5.26	124.54	119.80
3	C	63	TYR	CZ-CE2-CD2	-5.26	115.06	119.80
3	C	7	LEU	O-C-N	-5.26	114.29	122.70
3	C	277	ARG	NH1-CZ-NH2	-5.26	113.61	119.40
4	E	23	THR	CA-CB-CG2	-5.26	105.04	112.40
4	E	214	ILE	C-N-CA	5.26	134.85	121.70
3	C	93	VAL	CG1-CB-CG2	-5.25	102.49	110.90
4	E	435	GLU	O-C-N	5.25	131.11	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	278	MET	CB-CG-SD	5.25	128.16	112.40
1	A	86	TRP	CD2-CE3-CZ3	-5.25	111.97	118.80
3	C	423	ILE	CA-CB-CG2	5.25	121.41	110.90
4	E	110	TYR	CG-CD2-CE2	5.25	125.50	121.30
4	E	231	LEU	CA-CB-CG	-5.25	103.22	115.30
4	E	232	ILE	CA-CB-CG1	-5.25	101.02	111.00
2	B	410	TYR	O-C-N	-5.25	114.30	122.70
1	A	227	PHE	CG-CD1-CE1	5.25	126.57	120.80
2	B	452	PHE	CB-CG-CD2	-5.25	117.13	120.80
3	C	102	TYR	O-C-N	-5.25	114.31	122.70
4	E	86	LEU	CB-CG-CD1	5.25	119.92	111.00
2	B	86	TRP	O-C-N	-5.25	114.31	122.70
1	D	250	LEU	CB-CG-CD1	5.25	119.92	111.00
1	A	3	HIS	CA-CB-CG	5.24	122.50	113.60
3	C	117	TYR	CZ-CE2-CD2	-5.24	115.08	119.80
1	A	168	SER	O-C-N	-5.24	114.32	122.70
3	C	208	ASN	CB-CA-C	5.24	120.87	110.40
4	E	288	PHE	CD1-CE1-CZ	5.24	126.38	120.10
1	D	305	THR	O-C-N	-5.23	114.33	122.70
4	E	66	TRP	CA-CB-CG	5.23	123.64	113.70
1	A	69	PRO	O-C-N	5.23	131.07	122.70
3	C	68	THR	CB-CA-C	-5.23	97.47	111.60
1	D	252	SER	C-N-CA	5.23	134.78	121.70
2	B	46	LYS	O-C-N	5.23	131.07	122.70
4	E	464	ALA	CB-CA-C	5.23	117.95	110.10
2	B	197	TRP	CD1-CG-CD2	-5.23	102.12	106.30
4	E	285	TYR	O-C-N	5.23	131.06	122.70
3	C	482	PRO	N-CA-CB	5.22	109.57	103.30
3	C	122	PRO	O-C-N	-5.22	111.18	121.10
1	D	166	ASP	O-C-N	-5.22	114.35	122.70
1	A	378	GLY	O-C-N	-5.22	114.35	122.70
3	C	92	ILE	O-C-N	5.22	131.05	122.70
4	E	433	GLY	O-C-N	-5.22	114.35	122.70
2	B	150	THR	CA-CB-CG2	-5.22	105.10	112.40
3	C	104	VAL	C-N-CA	5.21	134.74	121.70
1	D	173	SER	C-N-CA	5.21	133.25	122.30
1	A	272	PRO	O-C-N	-5.21	114.36	122.70
3	C	241	PHE	N-CA-CB	5.21	119.98	110.60
1	A	209	ARG	C-N-CA	5.21	134.72	121.70
1	A	38	ILE	N-CA-CB	5.21	122.77	110.80
2	B	71	ALA	CB-CA-C	-5.20	102.30	110.10
4	E	211	PHE	CB-CG-CD1	5.20	124.44	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	135	PHE	C-N-CD	5.20	139.32	128.40
3	C	446	TRP	CA-C-N	-5.20	105.76	117.20
1	D	63	VAL	CG1-CB-CG2	-5.20	102.58	110.90
2	B	406	GLU	C-N-CA	5.20	134.70	121.70
4	E	71	TYR	CA-C-N	-5.20	105.76	117.20
3	C	137	PHE	CD1-CE1-CZ	5.20	126.34	120.10
1	A	23	GLU	O-C-N	5.20	131.01	122.70
4	E	112	ASP	CA-CB-CG	-5.19	101.97	113.40
2	B	61	THR	CA-CB-CG2	-5.19	105.13	112.40
2	B	272	GLU	N-CA-CB	5.19	119.94	110.60
4	E	137	ASP	CB-CG-OD2	5.19	122.97	118.30
3	C	208	ASN	O-C-N	-5.19	114.38	123.20
2	B	125	ARG	NH1-CZ-NH2	-5.19	113.69	119.40
1	A	152	ASP	CB-CG-OD1	-5.18	113.64	118.30
1	D	304	SER	CB-CA-C	5.18	119.95	110.10
4	E	291	PHE	CB-CA-C	5.18	120.77	110.40
4	E	65	SER	C-N-CA	-5.18	108.74	121.70
3	C	433	ILE	CG1-CB-CG2	-5.18	100.00	111.40
1	A	260	ILE	CA-CB-CG2	5.18	121.26	110.90
1	D	127	TYR	O-C-N	-5.18	114.41	122.70
3	C	287	LEU	CA-CB-CG	5.18	127.21	115.30
1	A	62	ASP	OD1-CG-OD2	-5.18	113.47	123.30
4	E	80	PRO	C-N-CA	5.18	134.64	121.70
4	E	131	VAL	CG1-CB-CG2	5.18	119.18	110.90
3	C	257	MET	CG-SD-CE	5.17	108.48	100.20
1	D	170	PHE	CB-CG-CD1	-5.17	117.18	120.80
3	C	99	ASP	C-N-CA	5.17	133.16	122.30
4	E	284	LYS	CB-CA-C	5.17	120.75	110.40
4	E	62	TYR	CD1-CE1-CZ	-5.17	115.15	119.80
2	B	1	SER	N-CA-C	5.17	124.95	111.00
3	C	448	LEU	CB-CG-CD1	-5.17	102.22	111.00
1	D	118	TRP	CG-CD2-CE3	5.16	138.55	133.90
2	B	262	PHE	CB-CG-CD2	5.16	124.41	120.80
1	D	399	TRP	CE2-CD2-CE3	-5.16	112.51	118.70
2	B	129	THR	O-C-N	5.16	130.96	122.70
2	B	163	ASP	N-CA-C	5.16	124.93	111.00
3	C	212	TYR	CG-CD2-CE2	5.16	125.43	121.30
4	E	68	THR	N-CA-CB	5.16	120.10	110.30
4	E	188	ARG	CA-C-O	5.16	130.93	120.10
4	E	266	PHE	CD1-CE1-CZ	-5.16	113.91	120.10
1	D	67	TRP	O-C-N	5.16	130.95	122.70
1	D	191	THR	N-CA-CB	5.16	120.10	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	159	GLN	N-CA-CB	-5.15	101.32	110.60
1	A	264	ILE	N-CA-C	5.15	124.91	111.00
2	B	49	GLU	N-CA-CB	-5.15	101.33	110.60
4	E	195	ASN	O-C-N	-5.15	114.47	122.70
1	A	23	GLU	OE1-CD-OE2	-5.14	117.13	123.30
2	B	74	GLY	CA-C-O	-5.14	111.34	120.60
2	B	287	ILE	O-C-N	5.14	130.93	122.70
1	D	93	TYR	CA-C-O	-5.14	109.30	120.10
1	D	255	VAL	O-C-N	-5.14	114.47	122.70
1	A	238	ASP	CA-CB-CG	5.14	124.71	113.40
2	B	136	PRO	CA-CB-CG	-5.14	94.23	104.00
1	A	272	PRO	CA-N-CD	-5.14	104.31	111.50
2	B	190	HIS	N-CA-CB	5.14	119.85	110.60
1	D	67	TRP	CE2-CD2-CE3	-5.13	112.54	118.70
1	D	378	GLY	CA-C-O	-5.13	111.36	120.60
1	A	111	ASP	CB-CG-OD1	5.13	122.92	118.30
3	C	291	TYR	CB-CG-CD2	-5.13	117.92	121.00
3	C	437	ASN	CB-CA-C	5.13	120.67	110.40
4	E	111	ASN	O-C-N	-5.13	114.49	122.70
1	A	113	THR	CA-C-N	-5.13	105.94	116.20
1	A	285	VAL	CG1-CB-CG2	5.13	119.11	110.90
3	C	14	VAL	O-C-N	-5.13	114.50	122.70
1	D	196	THR	CA-CB-CG2	5.13	119.58	112.40
1	D	384	GLU	CG-CD-OE1	-5.12	108.06	118.30
2	B	247	GLU	C-N-CA	5.12	134.50	121.70
1	D	253	LEU	CA-C-O	5.12	130.85	120.10
2	B	186	TRP	CB-CG-CD2	-5.12	119.95	126.60
1	D	218	VAL	CA-CB-CG2	5.12	118.58	110.90
4	E	426	THR	N-CA-CB	5.12	120.03	110.30
1	D	29	VAL	CA-CB-CG2	5.12	118.58	110.90
2	B	130	ILE	O-C-N	-5.11	114.52	122.70
4	E	134	PHE	CG-CD2-CE2	-5.11	115.17	120.80
1	A	277	TYR	CA-C-O	5.11	130.82	120.10
2	B	430	TYR	O-C-N	-5.11	114.53	122.70
4	E	458	PHE	CZ-CE2-CD2	-5.11	113.97	120.10
1	D	198	TYR	CE1-CZ-CE2	5.10	127.97	119.80
3	C	101	GLN	OE1-CD-NE2	-5.10	110.17	121.90
1	D	430	LEU	CA-CB-CG	5.10	127.03	115.30
4	E	279	VAL	CA-CB-CG2	-5.10	103.25	110.90
3	C	139	PHE	C-N-CA	5.10	134.45	121.70
1	D	44	ASP	OD1-CG-OD2	5.10	132.99	123.30
4	E	103	TYR	O-C-N	-5.10	114.55	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	272	PRO	O-C-N	-5.09	114.55	122.70
2	B	129	THR	N-CA-C	5.09	124.75	111.00
2	B	299	VAL	CA-CB-CG1	-5.09	103.26	110.90
1	D	129	GLU	CA-C-N	-5.09	106.00	117.20
4	E	312	ASN	CA-C-O	-5.09	109.41	120.10
1	D	118	TRP	CD2-CE2-CZ2	5.09	128.41	122.30
3	C	3	GLU	O-C-N	-5.09	114.56	122.70
1	D	89	ASP	OD1-CG-OD2	5.09	132.97	123.30
1	A	2	GLU	CA-C-N	-5.08	106.02	117.20
1	D	426	PHE	CB-CG-CD1	-5.08	117.24	120.80
4	E	110	TYR	CD1-CE1-CZ	5.08	124.38	119.80
4	E	460	LEU	C-N-CA	5.08	132.97	122.30
1	A	29	VAL	CG1-CB-CG2	-5.08	102.77	110.90
1	D	240	GLY	C-N-CA	5.08	134.40	121.70
3	C	441	GLU	OE1-CD-OE2	5.08	129.39	123.30
4	E	224	ASN	OD1-CG-ND2	5.08	133.58	121.90
1	A	240	GLY	O-C-N	-5.08	114.58	122.70
1	A	394	ASN	CA-C-N	-5.08	106.03	117.20
3	C	478	PHE	N-CA-CB	5.08	119.74	110.60
2	B	149	TYR	CB-CG-CD1	-5.07	117.96	121.00
3	C	135	LEU	CA-CB-CG	5.07	126.96	115.30
3	C	288	ILE	CA-CB-CG2	5.07	121.04	110.90
4	E	205	PHE	CD1-CE1-CZ	-5.07	114.02	120.10
1	A	6	ARG	CD-NE-CZ	5.07	130.70	123.60
2	B	21	PRO	CA-N-CD	-5.07	104.41	111.50
2	B	220	TYR	CA-CB-CG	5.07	123.03	113.40
1	A	129	GLU	O-C-N	5.07	130.80	122.70
2	B	37	LEU	N-CA-CB	-5.07	100.27	110.40
1	D	33	VAL	C-N-CA	-5.07	111.66	122.30
4	E	227	ALA	CA-C-O	-5.07	109.46	120.10
1	A	391	GLU	CG-CD-OE1	5.06	128.43	118.30
2	B	256	LEU	CA-C-O	-5.06	109.47	120.10
1	D	114	GLY	CA-C-N	5.06	128.33	117.20
2	B	1	SER	N-CA-CB	5.06	118.09	110.50
2	B	272	GLU	C-N-CA	5.06	134.35	121.70
3	C	74	TYR	CA-CB-CG	5.06	123.01	113.40
3	C	253	SER	CA-CB-OG	5.06	124.86	111.20
4	E	218	PRO	O-C-N	5.06	130.80	122.70
1	D	374	SER	CB-CA-C	5.05	119.70	110.10
2	B	15	TYR	O-C-N	-5.05	114.61	122.70
4	E	181	GLY	CA-C-O	5.05	129.70	120.60
4	E	24	LEU	N-CA-C	5.05	124.64	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	62	TRP	CE2-CD2-CG	-5.05	103.26	107.30
3	C	198	LYS	CD-CE-NZ	5.05	123.31	111.70
3	C	284	ALA	N-CA-CB	5.05	117.17	110.10
1	A	112	TYR	CD1-CE1-CZ	-5.05	115.26	119.80
1	D	436	GLU	O-C-N	-5.05	114.62	123.20
3	C	238	LEU	CB-CG-CD2	-5.04	102.42	111.00
1	D	399	TRP	NE1-CE2-CZ2	-5.04	124.85	130.40
4	E	308	LEU	C-N-CA	5.04	134.31	121.70
3	C	451	GLN	C-N-CA	5.04	134.30	121.70
2	B	310	ASN	N-CA-CB	5.04	119.66	110.60
4	E	126	THR	O-C-N	5.04	130.76	122.70
4	E	415	CYS	C-N-CA	5.03	134.27	121.70
4	E	423	ALA	O-C-N	5.03	130.75	122.70
1	A	79	ARG	CD-NE-CZ	5.03	130.63	123.60
1	A	265	PRO	O-C-N	-5.03	114.66	122.70
1	A	21	PRO	O-C-N	5.02	130.74	122.70
1	D	219	ILE	O-C-N	-5.02	114.66	122.70
1	D	436	GLU	CB-CA-C	5.02	120.45	110.40
1	A	245	LEU	CB-CA-C	5.02	119.74	110.20
1	A	414	PHE	CB-CG-CD2	-5.02	117.28	120.80
1	D	67	TRP	N-CA-C	5.02	124.56	111.00
3	C	31	VAL	CB-CA-C	-5.02	101.86	111.40
1	D	83	ASP	CB-CG-OD2	-5.02	113.78	118.30
4	E	107	VAL	CG1-CB-CG2	-5.02	102.87	110.90
1	A	95	ASN	CB-CA-C	5.02	120.44	110.40
1	A	149	TRP	CE2-CD2-CE3	5.02	124.72	118.70
3	C	83	ARG	CB-CA-C	-5.01	100.37	110.40
3	C	122	PRO	CA-C-O	5.01	132.24	120.20
4	E	196	TRP	NE1-CE2-CZ2	-5.01	124.88	130.40
3	C	421	SER	O-C-N	-5.01	114.68	123.20
1	D	206	ILE	O-C-N	5.01	130.72	122.70
1	A	234	TYR	CD1-CE1-CZ	5.01	124.31	119.80
3	C	62	TRP	NE1-CE2-CD2	5.01	112.31	107.30
1	D	31	ILE	O-C-N	5.01	130.72	122.70
1	A	166	ASP	N-CA-CB	5.01	119.62	110.60
2	B	227	PRO	N-CD-CG	5.01	110.71	103.20
2	B	271	PRO	O-C-N	5.01	130.72	122.70
4	E	130	ALA	N-CA-CB	5.01	117.11	110.10
2	B	427	ASP	CB-CA-C	-5.01	100.39	110.40
4	E	266	PHE	N-CA-CB	5.01	119.61	110.60
2	B	42	ILE	CA-C-N	-5.00	106.19	117.20
1	D	377	GLU	OE1-CD-OE2	5.00	129.31	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	282	MET	CG-SD-CE	5.00	108.21	100.20
2	B	81	PRO	N-CA-CB	5.00	109.31	103.30
2	B	429	GLN	OE1-CD-NE2	5.00	133.41	121.90
1	D	269	SER	CB-CA-C	5.00	119.61	110.10
4	E	202	ASP	CB-CA-C	5.00	120.40	110.40

All (37) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1	SER	CA
1	A	209	ARG	CA
1	A	267	THR	CB
1	A	292	THR	CB
1	A	304	SER	CA
1	A	305	THR	CB
1	A	374	SER	CA
2	B	1	SER	CA
2	B	84	ASP	CA
2	B	215	ARG	CA
2	B	280	ILE	CA
2	B	307	ARG	CA
2	B	447	CYS	CA
3	C	19	LYS	CA
3	C	48	THR	CA
3	C	129	SER	CA
3	C	180	ASP	CA
3	C	195	LYS	CA
3	C	236	CYS	CA
1	D	45	GLU	CA
1	D	99	ASP	CA
1	D	130	ILE	CB
1	D	136	PRO	CA
1	D	408	HIS	CA
1	D	431	ILE	CA
4	E	26	HIS	CA
4	E	29	ASP	CA
4	E	68	THR	CB,CA
4	E	74	ILE	CB
4	E	93	ASN	CA
4	E	106	ASN	CA
4	E	118	LEU	CA
4	E	130	ALA	CA

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Mol	Chain	Res	Type	Atom
4	E	161	ALA	CA
4	E	173	ASP	CA
4	E	260	ALA	CA

All (585) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	ILE	Mainchain
1	A	104	HIS	Mainchain
1	A	110	LEU	Mainchain
1	A	112	TYR	Mainchain
1	A	113	THR	Mainchain
1	A	115	LYS	Mainchain
1	A	128	CYS	Mainchain
1	A	129	GLU	Mainchain
1	A	132	VAL	Mainchain
1	A	133	THR	Mainchain
1	A	135	PHE	Peptide,Mainchain
1	A	136	PRO	Mainchain
1	A	137	PHE	Mainchain
1	A	138	ASP	Mainchain
1	A	147	GLY	Mainchain
1	A	150	THR	Mainchain
1	A	151	TYR	Mainchain
1	A	152	ASP	Mainchain
1	A	16	ASN	Mainchain
1	A	161	GLU	Peptide,Mainchain
1	A	162	SER	Peptide,Mainchain
1	A	167	LEU	Mainchain
1	A	170	PHE	Mainchain
1	A	174	GLY	Mainchain
1	A	175	GLU	Mainchain
1	A	187	TRP	Mainchain
1	A	193	CYS	Mainchain
1	A	195	ASP	Mainchain
1	A	199	LEU	Mainchain
1	A	207	MET	Mainchain
1	A	208	GLN	Mainchain
1	A	209	ARG	Peptide,Mainchain
1	A	210	ILE	Mainchain
1	A	211	PRO	Mainchain
1	A	215	VAL	Mainchain

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Mol	Chain	Res	Type	Group
1	A	217	ASN	Mainchain
1	A	221	PRO	Mainchain
1	A	222	CYS	Mainchain
1	A	223	LEU	Mainchain
1	A	228	LEU	Mainchain
1	A	231	LEU	Mainchain
1	A	235	LEU	Mainchain
1	A	236	PRO	Mainchain
1	A	238	ASP	Peptide,Mainchain
1	A	24	HIS	Mainchain
1	A	240	GLY	Mainchain
1	A	241	GLU	Mainchain
1	A	246	SER	Mainchain
1	A	248	SER	Mainchain
1	A	25	HIS	Mainchain
1	A	251	LEU	Mainchain
1	A	253	LEU	Mainchain
1	A	255	VAL	Mainchain
1	A	260	ILE	Mainchain
1	A	261	VAL	Mainchain
1	A	264	ILE	Mainchain
1	A	265	PRO	Mainchain
1	A	266	SER	Mainchain
1	A	267	THR	Mainchain
1	A	272	PRO	Mainchain
1	A	273	LEU	Mainchain
1	A	276	LYS	Mainchain
1	A	28	PHE	Mainchain
1	A	281	THR	Mainchain
1	A	286	ILE	Mainchain
1	A	289	ILE	Mainchain
1	A	293	VAL	Mainchain
1	A	296	ILE	Mainchain
1	A	3	HIS	Peptide
1	A	300	HIS	Mainchain
1	A	301	ARG	Mainchain
1	A	302	SER	Mainchain
1	A	303	PRO	Peptide,Mainchain
1	A	304	SER	Peptide,Mainchain
1	A	305	THR	Mainchain
1	A	374	SER	Peptide,Mainchain
1	A	375	ALA	Peptide,Mainchain

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Mol	Chain	Res	Type	Group
1	A	378	GLY	Mainchain
1	A	38	ILE	Mainchain
1	A	389	ASP	Mainchain
1	A	394	ASN	Mainchain
1	A	398	GLU	Mainchain
1	A	400	LYS	Mainchain
1	A	403	ALA	Mainchain
1	A	404	MET	Mainchain
1	A	407	ASP	Mainchain
1	A	408	HIS	Mainchain
1	A	419	ILE	Peptide
1	A	422	THR	Mainchain
1	A	426	PHE	Mainchain
1	A	431	ILE	Mainchain
1	A	435	GLN	Mainchain
1	A	44	ASP	Mainchain
1	A	47	ASN	Mainchain
1	A	48	GLN	Mainchain
1	A	61	ILE	Mainchain
1	A	66	ARG	Mainchain
1	A	67	TRP	Mainchain
1	A	73	GLY	Mainchain
1	A	74	GLY	Mainchain
1	A	77	LYS	Mainchain
1	A	84	ASP	Mainchain
1	A	85	VAL	Mainchain
1	A	94	ASN	Mainchain
1	A	95	ASN	Mainchain
1	A	97	ASP	Peptide,Mainchain
2	B	1	SER	Mainchain
2	B	106	VAL	Mainchain
2	B	107	ASN	Mainchain
2	B	113	THR	Mainchain
2	B	117	SER	Mainchain
2	B	119	HIS	Mainchain
2	B	12	PHE	Mainchain
2	B	130	ILE	Mainchain
2	B	131	LYS	Mainchain
2	B	139	TRP	Mainchain
2	B	14	ASN	Mainchain
2	B	140	GLN	Mainchain
2	B	141	ASN	Mainchain

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Mol	Chain	Res	Type	Group
2	B	143	THR	Mainchain
2	B	147	LYS	Mainchain
2	B	148	SER	Mainchain
2	B	15	TYR	Mainchain
2	B	151	TYR	Mainchain
2	B	152	ASP	Mainchain
2	B	155	GLU	Mainchain
2	B	160	HIS	Mainchain
2	B	174	MET	Mainchain
2	B	175	ILE	Mainchain
2	B	177	GLN	Mainchain
2	B	182	GLU	Mainchain
2	B	184	GLY	Peptide
2	B	186	TRP	Mainchain
2	B	188	ILE	Mainchain
2	B	191	LYS	Mainchain
2	B	199	SER	Mainchain
2	B	202	PRO	Mainchain
2	B	204	TYR	Mainchain
2	B	205	GLU	Mainchain
2	B	210	TYR	Mainchain
2	B	211	LEU	Mainchain
2	B	214	GLN	Mainchain
2	B	216	LYS	Mainchain
2	B	218	LEU	Mainchain
2	B	222	VAL	Mainchain
2	B	224	THR	Mainchain
2	B	226	VAL	Mainchain
2	B	227	PRO	Mainchain
2	B	230	LEU	Mainchain
2	B	231	ILE	Mainchain
2	B	24	THR	Mainchain
2	B	242	PRO	Mainchain
2	B	243	PRO	Mainchain
2	B	244	ASP	Mainchain
2	B	247	GLU	Mainchain
2	B	250	SER	Mainchain
2	B	254	SER	Mainchain
2	B	26	GLY	Peptide
2	B	262	PHE	Mainchain
2	B	269	LYS	Mainchain
2	B	272	GLU	Mainchain

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Mol	Chain	Res	Type	Group
2	B	274	SER	Mainchain
2	B	275	LEU	Mainchain
2	B	276	SER	Peptide
2	B	278	PRO	Mainchain
2	B	279	ILE	Peptide
2	B	280	ILE	Mainchain
2	B	281	ILE	Mainchain
2	B	282	SER	Mainchain
2	B	283	TYR	Peptide,Mainchain
2	B	29	VAL	Mainchain
2	B	294	SER	Mainchain
2	B	297	LEU	Mainchain
2	B	298	SER	Mainchain
2	B	302	LEU	Mainchain
2	B	303	ASN	Mainchain
2	B	306	HIS	Peptide,Mainchain
2	B	311	THR	Peptide,Mainchain
2	B	36	THR	Mainchain
2	B	38	THR	Mainchain
2	B	4	GLU	Mainchain
2	B	405	VAL	Mainchain
2	B	407	ALA	Mainchain
2	B	410	TYR	Mainchain
2	B	412	ALA	Mainchain
2	B	414	GLN	Mainchain
2	B	429	GLN	Mainchain
2	B	430	TYR	Mainchain
2	B	433	MET	Mainchain
2	B	435	ALA	Mainchain
2	B	439	PHE	Mainchain
2	B	440	LEU	Mainchain
2	B	441	TYR	Mainchain
2	B	443	PHE	Mainchain
2	B	445	THR	Mainchain
2	B	446	MET	Mainchain
2	B	447	CYS	Mainchain
2	B	455	PHE	Mainchain
2	B	456	LEU	Mainchain
2	B	461	ASN	Mainchain
2	B	463	PRO	Mainchain
2	B	48	GLU	Mainchain
2	B	56	LEU	Mainchain

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Mol	Chain	Res	Type	Group
2	B	81	PRO	Mainchain
2	B	83	ASP	Mainchain
2	B	84	ASP	Mainchain
2	B	85	VAL	Peptide
2	B	87	GLN	Mainchain
2	B	88	PRO	Mainchain
2	B	92	LEU	Mainchain
2	B	94	ASN	Peptide
2	B	95	ASN	Mainchain
2	B	97	ASP	Peptide,Mainchain
2	B	99	SER	Mainchain
3	C	1	VAL	Peptide
3	C	10	ASP	Mainchain
3	C	105	ALA	Mainchain
3	C	106	TYR	Mainchain
3	C	108	CYS	Mainchain
3	C	11	LEU	Mainchain
3	C	112	VAL	Mainchain
3	C	113	ARG	Mainchain
3	C	118	VAL	Mainchain
3	C	13	ILE	Mainchain
3	C	130	CYS	Mainchain
3	C	133	ASN	Mainchain
3	C	134	VAL	Mainchain
3	C	135	LEU	Mainchain
3	C	152	ASN	Mainchain
3	C	161	ASP	Mainchain
3	C	178	ILE	Mainchain
3	C	179	ILE	Peptide
3	C	18	ASN	Mainchain
3	C	180	ASP	Mainchain
3	C	181	PRO	Mainchain
3	C	182	GLU	Mainchain
3	C	183	ALA	Mainchain
3	C	187	ASN	Peptide
3	C	189	GLU	Mainchain
3	C	193	ILE	Mainchain
3	C	194	HIS	Peptide,Mainchain
3	C	202	TYR	Mainchain
3	C	203	GLY	Mainchain
3	C	204	ASP	Mainchain
3	C	208	ASN	Peptide,Mainchain

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Mol	Chain	Res	Type	Group
3	C	209	GLY	Mainchain
3	C	21	VAL	Mainchain
3	C	211	ASN	Mainchain
3	C	212	TYR	Mainchain
3	C	22	ARG	Mainchain
3	C	222	ARG	Mainchain
3	C	223	ARG	Mainchain
3	C	224	LYS	Mainchain
3	C	225	PRO	Mainchain
3	C	226	LEU	Mainchain
3	C	234	THR	Mainchain
3	C	236	CYS	Mainchain
3	C	237	VAL	Mainchain
3	C	239	ILE	Mainchain
3	C	240	SER	Mainchain
3	C	243	ALA	Mainchain
3	C	244	ALA	Mainchain
3	C	245	LEU	Mainchain
3	C	248	TYR	Mainchain
3	C	249	LEU	Mainchain
3	C	252	GLU	Mainchain
3	C	256	LYS	Peptide
3	C	263	VAL	Mainchain
3	C	266	ALA	Mainchain
3	C	267	GLN	Mainchain
3	C	268	ALA	Mainchain
3	C	27	ASN	Mainchain
3	C	271	LEU	Mainchain
3	C	272	LEU	Mainchain
3	C	273	LEU	Mainchain
3	C	274	THR	Mainchain
3	C	276	GLN	Mainchain
3	C	281	THR	Mainchain
3	C	282	ALA	Mainchain
3	C	283	LEU	Mainchain
3	C	284	ALA	Peptide,Mainchain
3	C	285	VAL	Mainchain
3	C	287	LEU	Mainchain
3	C	29	GLU	Peptide,Mainchain
3	C	290	LYS	Mainchain
3	C	291	TYR	Mainchain
3	C	3	GLU	Mainchain

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Mol	Chain	Res	Type	Group
3	C	30	VAL	Mainchain
3	C	304	VAL	Mainchain
3	C	305	ASN	Mainchain
3	C	310	LEU	Mainchain
3	C	318	SER	Mainchain
3	C	319	THR	Mainchain
3	C	41	ASN	Mainchain
3	C	421	SER	Mainchain
3	C	422	GLY	Peptide
3	C	423	ILE	Mainchain
3	C	425	SER	Mainchain
3	C	426	THR	Mainchain
3	C	427	ASN	Mainchain
3	C	431	LYS	Mainchain
3	C	435	GLU	Mainchain
3	C	440	ASP	Mainchain
3	C	443	VAL	Mainchain
3	C	445	ASN	Mainchain
3	C	451	GLN	Mainchain
3	C	454	ASP	Mainchain
3	C	46	LYS	Mainchain
3	C	463	PRO	Mainchain
3	C	466	VAL	Mainchain
3	C	467	LEU	Mainchain
3	C	47	GLU	Mainchain
3	C	474	VAL	Mainchain
3	C	475	MET	Mainchain
3	C	479	ASN	Mainchain
3	C	48	THR	Mainchain
3	C	481	PRO	Mainchain
3	C	482	PRO	Mainchain
3	C	484	LYS	Mainchain
3	C	49	ASP	Mainchain
3	C	5	GLU	Mainchain
3	C	50	GLU	Mainchain
3	C	68	THR	Mainchain
3	C	74	TYR	Mainchain
3	C	78	SER	Mainchain
3	C	8	ILE	Mainchain
3	C	84	PRO	Mainchain
3	C	85	GLU	Mainchain
3	C	87	ILE	Mainchain

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Mol	Chain	Res	Type	Group
3	C	9	ASN	Mainchain
3	C	90	PRO	Mainchain
3	C	94	LEU	Mainchain
3	C	95	GLN	Mainchain
3	C	98	ASN	Peptide,Mainchain
1	D	1	SER	Mainchain
1	D	100	PHE	Mainchain
1	D	101	ALA	Peptide,Mainchain
1	D	105	MET	Mainchain
1	D	106	THR	Mainchain
1	D	111	ASP	Mainchain
1	D	113	THR	Peptide
1	D	114	GLY	Mainchain
1	D	128	CYS	Mainchain
1	D	129	GLU	Mainchain
1	D	132	VAL	Mainchain
1	D	136	PRO	Mainchain
1	D	137	PHE	Mainchain
1	D	138	ASP	Mainchain
1	D	150	THR	Mainchain
1	D	156	VAL	Mainchain
1	D	157	SER	Mainchain
1	D	16	ASN	Mainchain
1	D	160	PRO	Mainchain
1	D	161	GLU	Peptide
1	D	162	SER	Peptide,Mainchain
1	D	163	ASP	Mainchain
1	D	166	ASP	Mainchain
1	D	169	THR	Mainchain
1	D	17	LYS	Mainchain
1	D	172	GLU	Mainchain
1	D	173	SER	Peptide
1	D	175	GLU	Peptide,Mainchain
1	D	176	TRP	Mainchain
1	D	18	VAL	Mainchain
1	D	181	TYR	Mainchain
1	D	194	PRO	Mainchain
1	D	195	ASP	Mainchain
1	D	197	PRO	Peptide,Mainchain
1	D	20	ARG	Mainchain
1	D	202	THR	Mainchain
1	D	21	PRO	Mainchain

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Mol	Chain	Res	Type	Group
1	D	211	PRO	Mainchain
1	D	213	TYR	Mainchain
1	D	216	VAL	Mainchain
1	D	219	ILE	Mainchain
1	D	221	PRO	Mainchain
1	D	228	LEU	Mainchain
1	D	232	VAL	Mainchain
1	D	238	ASP	Peptide,Mainchain
1	D	24	HIS	Mainchain
1	D	242	LYS	Mainchain
1	D	244	THR	Mainchain
1	D	246	SER	Mainchain
1	D	247	ILE	Mainchain
1	D	248	SER	Mainchain
1	D	25	HIS	Mainchain
1	D	251	LEU	Mainchain
1	D	254	THR	Mainchain
1	D	255	VAL	Mainchain
1	D	260	ILE	Mainchain
1	D	261	VAL	Mainchain
1	D	263	LEU	Mainchain
1	D	264	ILE	Mainchain
1	D	265	PRO	Mainchain
1	D	268	SER	Mainchain
1	D	269	SER	Mainchain
1	D	27	HIS	Mainchain
1	D	275	GLY	Mainchain
1	D	277	TYR	Mainchain
1	D	28	PHE	Mainchain
1	D	284	PHE	Mainchain
1	D	29	VAL	Mainchain
1	D	303	PRO	Mainchain
1	D	304	SER	Mainchain
1	D	305	THR	Mainchain
1	D	32	THR	Mainchain
1	D	33	VAL	Mainchain
1	D	34	GLY	Peptide,Mainchain
1	D	375	ALA	Mainchain
1	D	376	ILE	Mainchain
1	D	385	HIS	Mainchain
1	D	386	MET	Mainchain
1	D	390	GLU	Mainchain

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Mol	Chain	Res	Type	Group
1	D	395	ALA	Mainchain
1	D	396	ALA	Mainchain
1	D	399	TRP	Mainchain
1	D	400	LYS	Mainchain
1	D	402	VAL	Mainchain
1	D	408	HIS	Mainchain
1	D	410	LEU	Mainchain
1	D	414	PHE	Mainchain
1	D	416	LEU	Mainchain
1	D	418	CYS	Mainchain
1	D	422	THR	Peptide
1	D	423	VAL	Mainchain
1	D	428	GLY	Mainchain
1	D	429	ARG	Mainchain
1	D	431	ILE	Mainchain
1	D	44	ASP	Peptide
1	D	46	VAL	Mainchain
1	D	52	THR	Mainchain
1	D	57	ARG	Mainchain
1	D	61	ILE	Mainchain
1	D	63	VAL	Mainchain
1	D	65	LEU	Mainchain
1	D	66	ARG	Mainchain
1	D	68	ASN	Mainchain
1	D	70	ALA	Mainchain
1	D	73	GLY	Mainchain
1	D	74	GLY	Mainchain
1	D	76	LYS	Mainchain
1	D	77	LYS	Mainchain
1	D	79	ARG	Mainchain
1	D	80	LEU	Mainchain
1	D	81	PRO	Mainchain
1	D	82	SER	Mainchain
1	D	83	ASP	Mainchain
1	D	84	ASP	Mainchain
1	D	86	TRP	Mainchain
1	D	92	LEU	Mainchain
1	D	97	ASP	Peptide
1	D	98	GLY	Peptide,Mainchain
4	E	10	LEU	Mainchain
4	E	100	GLU	Mainchain
4	E	101	VAL	Mainchain

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Mol	Chain	Res	Type	Group
4	E	105	ALA	Peptide,Mainchain
4	E	107	VAL	Mainchain
4	E	109	VAL	Peptide
4	E	110	TYR	Peptide
4	E	112	ASP	Mainchain
4	E	118	LEU	Peptide
4	E	127	CYS	Mainchain
4	E	128	PRO	Mainchain
4	E	129	ILE	Mainchain
4	E	131	VAL	Mainchain
4	E	132	THR	Peptide
4	E	137	ASP	Mainchain
4	E	139	GLN	Mainchain
4	E	153	HIS	Mainchain
4	E	159	LEU	Peptide,Mainchain
4	E	160	SER	Peptide
4	E	163	GLU	Mainchain
4	E	17	ARG	Mainchain
4	E	172	ILE	Peptide
4	E	180	ASN	Peptide,Mainchain
4	E	181	GLY	Peptide
4	E	182	GLU	Mainchain
4	E	184	THR	Mainchain
4	E	187	HIS	Mainchain
4	E	189	PRO	Mainchain
4	E	190	ALA	Mainchain
4	E	195	ASN	Mainchain
4	E	196	TRP	Mainchain
4	E	198	LEU	Mainchain
4	E	204	ASP	Mainchain
4	E	215	GLN	Mainchain
4	E	217	LYS	Mainchain
4	E	22	LYS	Mainchain
4	E	221	TYR	Mainchain
4	E	223	ILE	Peptide
4	E	224	ASN	Mainchain
4	E	225	ILE	Mainchain
4	E	226	ILE	Mainchain
4	E	227	ALA	Mainchain
4	E	229	CYS	Mainchain
4	E	232	ILE	Mainchain
4	E	233	SER	Mainchain

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Mol	Chain	Res	Type	Group
4	E	235	LEU	Mainchain
4	E	236	VAL	Mainchain
4	E	237	VAL	Mainchain
4	E	238	LEU	Mainchain
4	E	24	LEU	Mainchain
4	E	250	LYS	Mainchain
4	E	252	THR	Peptide
4	E	255	ILE	Mainchain
4	E	256	SER	Mainchain
4	E	257	VAL	Mainchain
4	E	26	HIS	Mainchain
4	E	260	ALA	Mainchain
4	E	264	PHE	Mainchain
4	E	266	PHE	Mainchain
4	E	267	LEU	Mainchain
4	E	271	LYS	Mainchain
4	E	277	LEU	Mainchain
4	E	278	ASN	Mainchain
4	E	280	PRO	Mainchain
4	E	281	LEU	Mainchain
4	E	289	VAL	Mainchain
4	E	297	VAL	Mainchain
4	E	302	ILE	Mainchain
4	E	304	LEU	Mainchain
4	E	307	SER	Mainchain
4	E	309	ARG	Peptide
4	E	310	THR	Mainchain
4	E	416	VAL	Mainchain
4	E	418	ALA	Mainchain
4	E	422	ILE	Mainchain
4	E	425	SER	Mainchain
4	E	426	THR	Mainchain
4	E	427	LYS	Mainchain
4	E	430	ASN	Mainchain
4	E	441	LEU	Mainchain
4	E	442	ILE	Mainchain
4	E	444	LYS	Mainchain
4	E	460	LEU	Mainchain
4	E	465	ILE	Mainchain
4	E	47	GLU	Mainchain
4	E	5	ARG	Mainchain
4	E	61	ASP	Mainchain

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Mol	Chain	Res	Type	Group
4	E	63	ARG	Mainchain
4	E	65	SER	Mainchain
4	E	69	SER	Mainchain
4	E	70	GLU	Mainchain
4	E	73	GLY	Mainchain
4	E	76	LEU	Mainchain
4	E	79	ILE	Peptide,Mainchain
4	E	81	SER	Mainchain
4	E	83	LEU	Mainchain
4	E	84	LEU	Mainchain
4	E	85	TRP	Mainchain
4	E	88	ASP	Mainchain
4	E	92	GLU	Peptide
4	E	97	GLY	Mainchain
4	E	98	GLN	Mainchain
4	E	99	PHE	Mainchain

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	2991	0	3004	897	0
1	D	2991	0	3005	854	0
2	B	2972	0	2951	830	0
3	C	2983	0	2985	848	0
4	E	2987	0	2988	947	0
All	All	14924	0	14933	4181	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 140.

All (4181) 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:282:MET:CE	1:A:282:MET:SD	2.01	1.46
1:D:86:TRP:CD2	1:D:86:TRP:O	1.71	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:306:HIS:O	2:B:306:HIS:ND1	1.62	1.29
1:A:113:THR:CG2	1:A:113:THR:O	1.76	1.28
1:A:236:PRO:HB3	1:A:299:HIS:CE1	1.69	1.27
2:B:104:LEU:HD12	2:B:118:TRP:CH2	1.71	1.24
3:C:68:THR:HA	3:C:115:ASN:HA	1.22	1.20
3:C:67:LEU:HB3	3:C:116:GLY:CA	1.71	1.19
2:B:87:GLN:HB3	2:B:104:LEU:HD11	1.20	1.18
2:B:31:VAL:HG21	2:B:86:TRP:CZ3	1.77	1.18
3:C:148:PHE:HB2	3:C:215:VAL:CG2	1.73	1.18
2:B:46:LYS:HA	2:B:278:PRO:HD2	1.18	1.17
3:C:67:LEU:CB	3:C:116:GLY:HA2	1.73	1.17
1:D:29:VAL:HG23	1:D:60:TRP:CD1	1.79	1.17
1:D:86:TRP:O	1:D:86:TRP:CG	1.94	1.17
1:A:72:TYR:HB2	1:A:112:TYR:CD2	1.78	1.17
1:A:145:LYS:HG3	1:A:202:THR:HG22	1.26	1.17
4:E:45:LYS:CA	4:E:280:PRO:HA	1.75	1.17
2:B:9:SER:HA	2:B:12:PHE:CE1	1.80	1.17
2:B:132:VAL:HG13	2:B:279:ILE:HA	1.17	1.16
4:E:255:ILE:HD11	4:E:304:LEU:CD2	1.74	1.16
1:D:62:ASP:HB3	1:D:65:LEU:HD13	1.17	1.16
2:B:37:LEU:CA	2:B:54:VAL:HG12	1.73	1.16
4:E:172:ILE:HD12	4:E:188:ARG:HB3	1.22	1.16
4:E:284:LYS:N	4:E:284:LYS:HE3	1.60	1.16
3:C:463:PRO:HA	3:C:466:VAL:HG23	1.24	1.16
3:C:138:PRO:HG3	3:C:288:ILE:HD11	1.19	1.16
1:D:72:TYR:CD1	1:D:72:TYR:C	2.17	1.15
3:C:242:LEU:HD22	3:C:267:GLN:HB3	1.19	1.15
1:A:167:LEU:HD12	1:A:178:MET:HB2	1.26	1.15
1:D:305:THR:HG22	1:D:400:LYS:HB3	1.23	1.15
4:E:138:TRP:HB2	4:E:213:ILE:CG1	1.75	1.14
2:B:176:ASN:HB2	2:B:191:LYS:HB3	1.29	1.14
2:B:248:LYS:CD	2:B:252:SER:HB3	1.78	1.14
3:C:50:GLU:HA	3:C:132:ILE:HD13	1.25	1.13
2:B:191:LYS:O	2:B:191:LYS:CG	1.95	1.13
2:B:236:ILE:HB	2:B:446:MET:HE1	1.24	1.13
1:D:32:THR:HB	1:D:59:GLN:HB3	1.30	1.13
1:D:145:LYS:CG	1:D:202:THR:HG23	1.77	1.13
1:D:198:TYR:N	1:D:198:TYR:HD1	1.44	1.13
2:B:56:LEU:HD22	2:B:120:PRO:CG	1.78	1.13
4:E:44:GLU:HB3	4:E:280:PRO:CG	1.79	1.13
1:A:380:LYS:HB3	2:B:408:ILE:HD13	1.24	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:246:ALA:HB1	4:E:250:LYS:HG3	1.23	1.13
2:B:46:LYS:HE2	2:B:278:PRO:HG3	1.20	1.12
1:D:38:ILE:HA	1:D:169:THR:HG21	1.22	1.12
2:B:133:MET:HG2	2:B:140:GLN:HG3	1.24	1.12
4:E:89:VAL:HG23	4:E:99:PHE:CZ	1.84	1.11
2:B:56:LEU:CD1	2:B:56:LEU:N	2.10	1.11
1:D:48:GLN:HB3	1:D:130:ILE:HD12	1.31	1.11
4:E:66:TRP:NE1	4:E:111:ASN:HA	1.65	1.11
1:A:113:THR:O	1:A:113:THR:HG22	1.31	1.11
2:B:92:LEU:H	2:B:96:ASN:HB2	1.13	1.11
4:E:71:TYR:HA	4:E:111:ASN:HB2	1.25	1.11
1:A:66:ARG:HA	1:A:113:THR:HA	1.24	1.10
1:D:92:LEU:HB3	1:D:95:ASN:HB2	1.29	1.10
2:B:247:GLU:C	2:B:249:MET:HG3	1.72	1.10
1:A:65:LEU:HB3	1:A:110:LEU:HD11	1.24	1.10
2:B:56:LEU:N	2:B:56:LEU:HD13	1.59	1.10
1:A:20:ARG:HG2	1:A:20:ARG:HH11	1.15	1.09
1:D:145:LYS:HG3	1:D:202:THR:CG2	1.81	1.09
1:D:61:ILE:HA	1:D:116:ILE:HD11	1.31	1.09
1:D:131:ILE:HG13	1:D:133:THR:H	1.03	1.09
2:B:48:GLU:HA	2:B:130:ILE:HD11	1.23	1.09
4:E:44:GLU:HB3	4:E:280:PRO:HG3	1.29	1.09
4:E:255:ILE:HD11	4:E:304:LEU:HD22	1.12	1.09
2:B:308:SER:CB	2:B:311:THR:HG22	1.83	1.09
2:B:186:TRP:HB3	2:B:215:ARG:HG3	1.30	1.08
2:B:311:THR:HB	2:B:430:TYR:HD2	1.17	1.08
1:A:38:ILE:HD11	1:A:55:ARG:CG	1.83	1.08
2:B:186:TRP:HB2	2:B:215:ARG:HB2	1.21	1.08
2:B:241:LEU:HD21	2:B:251:LEU:HD11	1.13	1.08
3:C:31:VAL:O	3:C:31:VAL:HG13	1.47	1.08
2:B:23:GLN:HE21	2:B:23:GLN:N	1.52	1.08
1:A:133:THR:HA	1:A:274:ILE:CG2	1.82	1.08
2:B:3:MET:HE3	2:B:69:PRO:HG3	1.23	1.08
2:B:131:LYS:HD3	2:B:132:VAL:H	1.03	1.08
1:D:20:ARG:HG2	1:D:20:ARG:HH11	1.19	1.08
1:D:48:GLN:HB3	1:D:130:ILE:CD1	1.83	1.08
4:E:45:LYS:HA	4:E:280:PRO:HA	1.27	1.08
3:C:278:LEU:C	3:C:278:LEU:HD12	1.73	1.07
1:D:302:SER:HB3	1:D:400:LYS:CG	1.84	1.07
1:D:305:THR:HB	1:D:401:TYR:HD2	1.12	1.07
4:E:136:PHE:CZ	4:E:217:LYS:HD2	1.88	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:189:PRO:HD2	4:E:211:PHE:HB2	1.21	1.07
1:A:97:ASP:HB2	1:A:127:TYR:HB2	1.35	1.07
1:A:380:LYS:CB	2:B:408:ILE:HD13	1.84	1.07
2:B:56:LEU:HD22	2:B:120:PRO:HG2	1.20	1.07
1:D:28:PHE:HD2	1:D:157:SER:HB3	1.17	1.07
1:D:377:GLU:HG3	4:E:415:CYS:HB2	1.14	1.07
1:A:2:GLU:O	1:A:2:GLU:HG2	1.49	1.07
1:A:130:ILE:HD13	1:A:131:ILE:H	1.19	1.07
2:B:308:SER:HB2	2:B:311:THR:HG22	1.07	1.07
4:E:94:ASN:HB3	4:E:125:SER:HB3	1.34	1.07
1:D:35:LEU:HD11	1:D:54:VAL:HG11	1.35	1.07
3:C:59:ASP:HA	3:C:121:LEU:HB3	1.37	1.06
2:B:37:LEU:HA	2:B:54:VAL:CG1	1.83	1.06
2:B:241:LEU:HG	2:B:248:LYS:HE2	1.25	1.06
3:C:445:ASN:HA	3:C:448:LEU:HG	1.37	1.06
4:E:75:ASP:HA	4:E:111:ASN:HD22	1.12	1.06
1:A:38:ILE:CD1	1:A:55:ARG:HG3	1.84	1.06
2:B:248:LYS:HD3	2:B:252:SER:HB3	1.10	1.06
3:C:93:VAL:HG11	3:C:151:LEU:HD13	1.06	1.06
4:E:279:VAL:HB	4:E:280:PRO:HD2	1.13	1.06
1:A:133:THR:HA	1:A:274:ILE:HG22	1.08	1.05
2:B:153:THR:HB	2:B:204:TYR:HB2	1.31	1.05
4:E:19:LYS:HZ3	4:E:154:GLU:HB3	1.19	1.05
4:E:90:VAL:HG22	4:E:95:VAL:CG1	1.86	1.05
2:B:23:GLN:NE2	2:B:23:GLN:H	1.55	1.05
3:C:122:PRO:CB	3:C:123:PRO:HD2	1.82	1.05
1:D:7:LEU:HD21	1:D:70:ALA:HB1	1.36	1.05
1:D:220:ILE:HG21	4:E:294:LEU:HD11	1.33	1.05
4:E:19:LYS:NZ	4:E:154:GLU:HB3	1.70	1.05
4:E:36:LEU:CD2	4:E:51:THR:HG21	1.87	1.05
4:E:235:LEU:HD12	4:E:235:LEU:O	1.55	1.05
4:E:56:GLU:HA	4:E:118:LEU:HB2	1.38	1.05
1:A:148:ILE:HG21	1:A:198:TYR:HB2	1.33	1.04
2:B:130:ILE:HB	2:B:134:TYR:CD2	1.92	1.04
3:C:449:VAL:HG12	3:C:452:THR:HB	1.36	1.04
1:D:129:GLU:OE1	1:D:129:GLU:HA	1.20	1.04
1:D:233:PHE:CZ	1:D:417:ILE:HD12	1.90	1.04
4:E:219:LEU:HB3	4:E:222:ILE:HB	1.37	1.04
4:E:236:VAL:HA	4:E:239:VAL:HG23	1.34	1.04
4:E:129:ILE:HG22	4:E:133:TYR:CD2	1.90	1.04
1:A:2:GLU:CD	1:A:74:GLY:HA2	1.76	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:ASP:HB3	3:C:181:PRO:HD3	1.35	1.04
1:A:277:TYR:HA	1:A:280:PHE:CZ	1.93	1.04
2:B:220:TYR:HB3	2:B:223:TYR:CE2	1.90	1.04
1:D:106:THR:HG22	1:D:107:LYS:H	1.16	1.04
1:A:379:VAL:HG13	4:E:424:LYS:HE2	1.39	1.04
4:E:66:TRP:HE1	4:E:111:ASN:HA	1.21	1.04
4:E:36:LEU:HD23	4:E:51:THR:HG21	1.40	1.03
1:A:64:ARG:HA	1:A:66:ARG:NH1	1.71	1.03
1:A:380:LYS:HB3	2:B:408:ILE:CD1	1.88	1.03
2:B:134:TYR:CE1	2:B:213:ILE:HG13	1.92	1.03
4:E:91:LEU:CD1	4:E:145:PHE:HB3	1.87	1.03
4:E:183:TRP:CB	4:E:216:ARG:HG2	1.88	1.03
1:A:16:ASN:HB2	1:A:19:ILE:HD12	1.36	1.03
2:B:56:LEU:HD13	2:B:56:LEU:H	0.93	1.03
4:E:185:ILE:HG12	4:E:214:ILE:HG22	1.40	1.03
4:E:44:GLU:CD	4:E:129:ILE:HB	1.77	1.03
1:A:57:ARG:HA	1:A:119:THR:HG22	1.05	1.03
1:A:66:ARG:HA	1:A:113:THR:CA	1.87	1.03
1:D:91:VAL:HG22	1:D:96:ALA:HB2	1.38	1.03
1:D:224:LEU:HD21	4:E:297:VAL:HG11	1.36	1.03
3:C:149:THR:HG21	3:C:214:ASP:HB3	1.38	1.02
4:E:47:GLU:HB3	4:E:129:ILE:HG12	1.39	1.02
4:E:91:LEU:HD13	4:E:145:PHE:HB3	1.04	1.02
4:E:279:VAL:CB	4:E:280:PRO:HD2	1.89	1.02
2:B:75:ILE:CD1	2:B:78:LEU:HD13	1.90	1.02
3:C:12:LEU:HB2	3:C:16:LYS:HG2	1.38	1.02
2:B:243:PRO:HB3	2:B:435:ALA:HB1	1.04	1.02
1:D:57:ARG:O	1:D:57:ARG:HG2	1.53	1.02
1:D:302:SER:HB3	1:D:400:LYS:HG2	1.02	1.02
4:E:34:LEU:HD12	4:E:210:PHE:CE2	1.95	1.02
4:E:185:ILE:HG12	4:E:214:ILE:CG2	1.89	1.02
1:A:67:TRP:CD1	1:A:112:TYR:HA	1.93	1.02
2:B:263:LEU:HD22	2:B:291:VAL:HG22	1.36	1.02
3:C:60:HIS:HB3	3:C:62:TRP:HZ3	1.25	1.02
1:D:305:THR:CG2	1:D:400:LYS:HB3	1.90	1.02
3:C:115:ASN:CG	3:C:115:ASN:O	1.94	1.01
2:B:185:GLN:HB3	2:B:219:PHE:HE2	1.20	1.01
3:C:309:VAL:O	3:C:313:HIS:HB3	1.60	1.01
1:D:56:LEU:HG	1:D:120:PRO:HG2	1.38	1.01
4:E:90:VAL:CG2	4:E:95:VAL:HG11	1.90	1.01
4:E:305:ASN:HA	4:E:308:LEU:HD12	1.42	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:THR:O	1:A:133:THR:HG22	1.56	1.01
3:C:113:ARG:HD2	3:C:117:TYR:HB3	1.41	1.01
3:C:159:SER:HA	3:C:213:GLN:HG3	1.36	1.01
4:E:211:PHE:C	4:E:212:LEU:HD12	1.81	1.01
1:A:17:LYS:HE3	1:A:84:ASP:HA	1.39	1.00
2:B:46:LYS:HB2	2:B:277:VAL:N	1.74	1.00
1:D:43:VAL:HG22	1:D:50:VAL:HA	1.37	1.00
1:D:65:LEU:HD23	1:D:110:LEU:HD13	1.42	1.00
2:B:68:ASP:HB3	2:B:69:PRO:CD	1.89	1.00
2:B:243:PRO:CB	2:B:435:ALA:HB1	1.90	1.00
3:C:243:ALA:CB	3:C:302:VAL:HG12	1.90	1.00
1:A:238:ASP:HB3	2:B:306:HIS:NE2	1.76	1.00
1:A:380:LYS:HD3	2:B:408:ILE:CB	1.91	1.00
2:B:242:PRO:HG2	2:B:243:PRO:HD3	1.41	1.00
1:D:92:LEU:CB	1:D:95:ASN:HB2	1.90	1.00
1:D:129:GLU:OE1	1:D:129:GLU:CA	2.06	1.00
4:E:138:TRP:CZ2	4:E:215:GLN:HB2	1.97	1.00
2:B:176:ASN:CB	2:B:191:LYS:HB3	1.91	1.00
3:C:50:GLU:CA	3:C:132:ILE:HD13	1.92	1.00
4:E:235:LEU:HD12	4:E:235:LEU:C	1.82	1.00
2:B:75:ILE:O	2:B:75:ILE:HG13	1.56	1.00
2:B:405:VAL:HG12	2:B:409:LYS:HZ3	1.26	1.00
4:E:240:TYR:CD2	4:E:453:ILE:HD13	1.96	1.00
1:D:252:SER:HB2	4:E:259:LEU:HD13	1.39	1.00
4:E:47:GLU:HA	4:E:129:ILE:HD11	1.41	1.00
4:E:91:LEU:HD13	4:E:145:PHE:CB	1.92	1.00
3:C:115:ASN:O	3:C:115:ASN:ND2	1.94	0.99
1:D:253:LEU:HD23	1:D:254:THR:N	1.77	0.99
4:E:39:LEU:HD23	4:E:183:TRP:HZ2	1.28	0.99
1:D:377:GLU:HG3	4:E:415:CYS:CB	1.92	0.99
4:E:250:LYS:HB3	4:E:253:LEU:HD23	1.43	0.99
2:B:48:GLU:HB2	2:B:130:ILE:HG12	1.45	0.99
3:C:42:LEU:HD22	3:C:190:TRP:CH2	1.97	0.99
1:D:238:ASP:HB3	4:E:308:LEU:CD2	1.91	0.99
3:C:37:LEU:HB2	3:C:217:PHE:CE2	1.97	0.99
3:C:179:ILE:CD1	3:C:195:LYS:HB3	1.93	0.99
4:E:138:TRP:HB2	4:E:213:ILE:HG12	1.42	0.99
1:A:238:ASP:HB3	2:B:306:HIS:CE1	1.97	0.99
4:E:22:LYS:HG3	4:E:23:THR:HB	1.43	0.98
1:A:87:LEU:HD22	1:A:87:LEU:H	1.22	0.98
2:B:311:THR:HB	2:B:430:TYR:CD2	1.98	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:69:TRP:NE1	3:C:114:PRO:HA	1.78	0.98
3:C:122:PRO:HB2	3:C:123:PRO:HD2	1.02	0.98
4:E:79:ILE:HG12	4:E:80:PRO:HD2	1.44	0.98
2:B:306:HIS:HD1	2:B:306:HIS:C	1.65	0.98
4:E:55:ILE:C	4:E:118:LEU:HD13	1.83	0.98
1:A:57:ARG:HD3	1:A:161:GLU:OE2	1.64	0.98
4:E:436:ASN:HA	4:E:439:TRP:HE1	1.29	0.98
2:B:132:VAL:HG13	2:B:279:ILE:CA	1.93	0.98
2:B:133:MET:CG	2:B:140:GLN:HG3	1.93	0.98
3:C:162:LEU:HD11	3:C:217:PHE:CZ	1.99	0.98
3:C:149:THR:CG2	3:C:214:ASP:HB3	1.94	0.97
1:D:35:LEU:HD23	1:D:164:ARG:NH1	1.79	0.97
1:A:57:ARG:HA	1:A:119:THR:CG2	1.93	0.97
2:B:191:LYS:O	2:B:191:LYS:HG3	1.02	0.97
3:C:122:PRO:HB2	3:C:123:PRO:CD	1.92	0.97
1:D:49:ILE:HG21	1:D:125:LYS:NZ	1.78	0.97
4:E:67:ASN:HD22	4:E:67:ASN:H	1.02	0.97
1:A:252:SER:HB3	2:B:257:LEU:HD13	1.46	0.97
3:C:65:HIS:CD2	3:C:65:HIS:H	1.72	0.97
3:C:159:SER:HA	3:C:213:GLN:CG	1.94	0.97
3:C:115:ASN:N	3:C:115:ASN:HD22	1.61	0.97
3:C:426:THR:HG22	3:C:426:THR:O	1.63	0.97
4:E:146:ARG:NH1	4:E:205:PHE:HB3	1.78	0.97
1:D:203:TYR:N	1:D:203:TYR:CD1	2.27	0.97
2:B:142:CYS:HB3	2:B:211:LEU:HG	1.47	0.96
1:D:187:TRP:HB2	1:D:199:LEU:HD23	1.46	0.96
2:B:56:LEU:CD1	2:B:56:LEU:H	1.63	0.96
1:D:7:LEU:CD2	1:D:70:ALA:HB1	1.95	0.96
4:E:187:HIS:CE1	4:E:189:PRO:HG3	1.99	0.96
1:A:38:ILE:HD11	1:A:55:ARG:HG3	0.97	0.96
1:A:64:ARG:HA	1:A:66:ARG:HH11	1.26	0.96
1:A:187:TRP:CH2	1:A:189:TYR:HB3	2.00	0.96
1:D:72:TYR:HB2	1:D:112:TYR:HB2	1.44	0.96
1:A:72:TYR:HB2	1:A:112:TYR:CG	2.01	0.96
4:E:62:TYR:O	4:E:62:TYR:HD1	1.48	0.96
1:A:67:TRP:HD1	1:A:112:TYR:HA	1.30	0.96
1:A:167:LEU:CD1	1:A:178:MET:HB2	1.96	0.96
4:E:138:TRP:HB2	4:E:213:ILE:HG13	1.45	0.96
1:D:304:SER:HB3	1:D:397:GLU:HB2	1.45	0.96
1:D:3:HIS:HB3	1:D:7:LEU:HG	1.46	0.95
1:D:64:ARG:HA	1:D:66:ARG:NH1	1.80	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:TRP:CD1	3:C:221:ILE:HD12	2.00	0.95
3:C:1:VAL:HG22	3:C:4:GLU:OE2	1.67	0.95
1:A:406:ILE:HA	1:A:409:ILE:HD11	1.47	0.95
4:E:183:TRP:HB3	4:E:216:ARG:HG2	1.46	0.95
3:C:93:VAL:HG11	3:C:151:LEU:CD1	1.94	0.95
3:C:316:THR:CG2	3:C:317:PRO:HD2	1.96	0.95
1:D:187:TRP:HB2	1:D:199:LEU:CD2	1.96	0.95
2:B:9:SER:HA	2:B:12:PHE:HE1	1.27	0.95
1:D:107:LYS:CE	4:E:149:THR:HA	1.97	0.95
1:D:408:HIS:O	1:D:412:CYS:HB2	1.67	0.95
4:E:54:TRP:HB3	4:E:118:LEU:HD11	1.45	0.95
4:E:159:LEU:HD12	4:E:192:LYS:CA	1.96	0.95
4:E:236:VAL:HA	4:E:239:VAL:CG2	1.95	0.95
1:D:85:VAL:HG13	1:D:86:TRP:CE3	2.01	0.95
1:A:41:ILE:HD11	1:A:51:GLU:CD	1.88	0.94
1:D:160:PRO:HD3	1:D:185:LYS:HB3	1.47	0.94
2:B:238:VAL:CG2	2:B:255:ALA:HB1	1.97	0.94
1:D:145:LYS:C	1:D:146:LEU:HD12	1.87	0.94
1:A:133:THR:CA	1:A:274:ILE:HG22	1.97	0.94
1:D:198:TYR:N	1:D:198:TYR:CD1	2.15	0.94
1:D:305:THR:HB	1:D:401:TYR:CD2	2.01	0.94
1:A:77:LYS:HG3	1:A:77:LYS:O	1.65	0.94
2:B:46:LYS:HE2	2:B:278:PRO:CG	1.97	0.94
1:D:107:LYS:HD3	1:D:107:LYS:N	1.83	0.94
1:D:169:THR:O	1:D:169:THR:HG22	1.65	0.94
4:E:6:LEU:HD12	4:E:69:SER:HB3	1.47	0.94
3:C:37:LEU:HB2	3:C:217:PHE:HE2	1.31	0.94
1:D:107:LYS:HE3	4:E:149:THR:HA	1.48	0.94
4:E:2:GLU:HA	4:E:5:ARG:HG3	1.46	0.94
1:D:136:PRO:HG3	1:D:274:ILE:CD1	1.96	0.94
4:E:255:ILE:CD1	4:E:304:LEU:HD22	1.96	0.94
1:A:155:LYS:HE3	4:E:76:LEU:HD13	1.49	0.94
2:B:104:LEU:HD12	2:B:118:TRP:HH2	1.20	0.94
1:A:148:ILE:CG2	1:A:198:TYR:HB2	1.96	0.94
3:C:52:LEU:HD21	3:C:130:CYS:HB2	1.47	0.94
4:E:91:LEU:HB2	4:E:95:VAL:H	1.32	0.94
1:A:148:ILE:HD11	1:A:156:VAL:HG13	1.50	0.94
3:C:162:LEU:HD11	3:C:217:PHE:CE1	2.03	0.94
3:C:453:ILE:HG23	3:C:454:ASP:H	1.31	0.94
2:B:270:VAL:HG11	2:B:284:LEU:HD11	1.48	0.93
2:B:436:ASP:O	2:B:440:LEU:HD12	1.66	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:PRO:HG3	1:D:274:ILE:HD11	1.50	0.93
3:C:42:LEU:HG	3:C:54:THR:HG23	1.51	0.93
1:D:40:LEU:HD13	1:D:52:THR:HB	1.49	0.93
1:A:113:THR:O	1:A:113:THR:HG23	1.67	0.93
3:C:179:ILE:HD12	3:C:195:LYS:HB3	1.48	0.93
1:D:426:PHE:HE1	1:D:430:LEU:HD12	1.32	0.93
4:E:162:GLU:HA	4:E:190:ALA:H	1.31	0.93
1:A:43:VAL:HG13	1:A:50:VAL:HG22	1.51	0.93
1:A:250:LEU:CD2	1:A:292:THR:HG22	1.98	0.93
1:A:302:SER:HB2	1:A:306:HIS:C	1.87	0.93
4:E:45:LYS:HE2	4:E:278:ASN:C	1.88	0.92
3:C:279:PRO:HA	3:C:282:ALA:HB3	1.49	0.92
4:E:272:VAL:O	4:E:272:VAL:HG22	1.70	0.92
1:A:380:LYS:HD3	2:B:408:ILE:HB	1.48	0.92
2:B:46:LYS:CA	2:B:278:PRO:HD2	2.00	0.92
2:B:68:ASP:HB3	2:B:69:PRO:HD3	1.48	0.92
2:B:160:HIS:HE2	2:B:209:PHE:HE1	1.16	0.92
3:C:273:LEU:HA	3:C:276:GLN:HG2	1.50	0.92
1:D:171:MET:HG2	1:D:174:GLY:H	1.34	0.92
4:E:27:VAL:HG12	4:E:153:HIS:O	1.70	0.92
1:A:256:PHE:CE1	2:B:261:VAL:HG23	2.04	0.92
4:E:59:TRP:C	4:E:60:ASN:HD22	1.71	0.92
4:E:129:ILE:HG22	4:E:133:TYR:HD2	1.31	0.92
1:A:89:ASP:HB2	1:A:149:TRP:CD1	2.04	0.92
1:A:145:LYS:HG3	1:A:202:THR:CG2	2.00	0.92
2:B:31:VAL:HG21	2:B:86:TRP:HZ3	1.20	0.92
2:B:91:VAL:HG11	2:B:149:TYR:CD1	2.05	0.92
3:C:246:ALA:O	3:C:250:PRO:HD3	1.68	0.92
2:B:297:LEU:O	2:B:297:LEU:HD23	1.69	0.92
3:C:273:LEU:HD23	3:C:276:GLN:CB	1.99	0.92
4:E:94:ASN:HD22	4:E:125:SER:HB2	1.32	0.92
1:A:89:ASP:OD1	1:A:89:ASP:O	1.87	0.91
3:C:42:LEU:HG	3:C:54:THR:CG2	2.00	0.91
4:E:433:GLY:O	4:E:436:ASN:HB2	1.69	0.91
1:A:247:ILE:O	1:A:247:ILE:HD13	1.71	0.91
2:B:9:SER:HA	2:B:12:PHE:CD1	2.05	0.91
3:C:145:SER:C	3:C:146:LEU:HD12	1.89	0.91
2:B:56:LEU:HD21	2:B:103:THR:HA	1.53	0.91
2:B:131:LYS:HD3	2:B:132:VAL:N	1.85	0.91
2:B:186:TRP:HB3	2:B:215:ARG:CG	2.00	0.91
1:D:145:LYS:O	1:D:146:LEU:HD12	1.69	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:66:TRP:CD1	4:E:111:ASN:HA	2.05	0.91
2:B:31:VAL:HG21	2:B:86:TRP:CH2	2.04	0.91
3:C:31:VAL:O	3:C:31:VAL:CG1	2.16	0.91
2:B:67:TRP:HB2	2:B:72:TYR:HB2	1.53	0.91
2:B:241:LEU:CD2	2:B:251:LEU:HD11	2.00	0.91
2:B:134:TYR:HE1	2:B:213:ILE:HG13	1.32	0.91
2:B:405:VAL:HG12	2:B:409:LYS:NZ	1.86	0.91
3:C:241:PHE:O	3:C:245:LEU:HG	1.70	0.91
4:E:79:ILE:HG12	4:E:80:PRO:CD	1.98	0.91
1:A:265:PRO:HA	1:A:268:SER:HB3	1.53	0.91
1:D:302:SER:CB	1:D:400:LYS:HG2	1.98	0.91
2:B:251:LEU:HB2	3:C:261:ILE:HG13	1.51	0.91
2:B:274:SER:HB2	2:B:278:PRO:HB3	1.50	0.91
3:C:279:PRO:HA	3:C:282:ALA:CB	2.00	0.91
4:E:56:GLU:HA	4:E:118:LEU:CB	2.01	0.91
2:B:37:LEU:HA	2:B:54:VAL:HG12	0.92	0.91
3:C:278:LEU:C	3:C:278:LEU:CD1	2.33	0.91
1:D:432:GLU:HG2	1:D:435:GLN:NE2	1.86	0.91
1:A:130:ILE:HD13	1:A:131:ILE:N	1.86	0.91
3:C:191:GLU:CG	3:C:222:ARG:HB3	2.01	0.90
3:C:307:GLY:HA2	3:C:310:LEU:HD23	1.50	0.90
1:D:107:LYS:NZ	4:E:149:THR:HA	1.86	0.90
2:B:81:PRO:HD3	3:C:22:ARG:HH22	1.35	0.90
2:B:186:TRP:HB2	2:B:215:ARG:CB	2.01	0.90
1:A:76:LYS:HG2	1:A:77:LYS:H	1.33	0.90
1:A:142:CYS:HB2	1:A:205:PHE:HB2	1.53	0.90
2:B:270:VAL:CG1	2:B:284:LEU:HD11	2.01	0.90
1:D:48:GLN:CB	1:D:130:ILE:HD12	2.00	0.90
4:E:90:VAL:HG13	4:E:95:VAL:HB	1.51	0.90
2:B:406:GLU:HA	2:B:409:LYS:HD2	1.51	0.90
1:D:28:PHE:CD2	1:D:157:SER:HB3	2.05	0.90
1:D:426:PHE:CE1	1:D:430:LEU:HD12	2.05	0.90
4:E:6:LEU:HD12	4:E:69:SER:CB	2.00	0.90
3:C:1:VAL:HA	3:C:4:GLU:HG2	1.50	0.90
1:A:36:GLN:HA	1:A:164:ARG:NH2	1.87	0.90
1:A:135:PHE:O	1:A:135:PHE:CD1	2.24	0.90
3:C:106:TYR:O	3:C:106:TYR:HD1	1.54	0.90
3:C:434:LYS:HD3	3:C:435:GLU:HG3	1.50	0.90
1:D:160:PRO:HD3	1:D:185:LYS:CB	2.01	0.90
4:E:31:THR:O	4:E:32:LEU:HD23	1.71	0.90
1:D:305:THR:CB	1:D:401:TYR:HD2	1.84	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:216:ARG:O	4:E:217:LYS:HG3	1.72	0.90
1:D:287:SER:HA	1:D:290:ILE:CD1	2.02	0.90
4:E:45:LYS:HD2	4:E:46:GLU:HG2	1.51	0.90
4:E:94:ASN:HB3	4:E:125:SER:CB	2.01	0.90
2:B:46:LYS:CE	2:B:278:PRO:HG3	2.02	0.89
1:D:41:ILE:HD12	1:D:51:GLU:O	1.72	0.89
2:B:131:LYS:CD	2:B:132:VAL:H	1.85	0.89
4:E:32:LEU:O	4:E:33:LYS:HG3	1.71	0.89
2:B:263:LEU:HD22	2:B:291:VAL:CG2	2.03	0.89
3:C:42:LEU:HA	3:C:54:THR:HG22	1.51	0.89
3:C:452:THR:O	3:C:455:ARG:HG2	1.73	0.89
1:D:377:GLU:HB2	4:E:415:CYS:SG	2.13	0.89
2:B:258:ALA:CB	3:C:265:LEU:HD22	2.02	0.89
1:D:46:VAL:HA	1:D:272:PRO:HD3	1.51	0.89
2:B:132:VAL:HG12	2:B:280:ILE:H	1.35	0.89
2:B:142:CYS:HB3	2:B:211:LEU:CG	2.03	0.89
1:D:395:ALA:O	1:D:398:GLU:HG2	1.73	0.89
3:C:138:PRO:HG3	3:C:288:ILE:CD1	2.01	0.89
1:A:102:ILE:O	1:A:102:ILE:HG22	1.72	0.89
1:A:250:LEU:HD11	1:A:296:ILE:HG21	1.55	0.89
3:C:56:VAL:HG13	3:C:126:PHE:HE2	1.35	0.89
4:E:90:VAL:HG22	4:E:95:VAL:HG11	0.94	0.89
4:E:128:PRO:C	4:E:129:ILE:HG23	1.91	0.89
1:D:304:SER:HB3	1:D:397:GLU:CB	2.03	0.89
4:E:271:LYS:C	4:E:273:PRO:HD2	1.91	0.89
1:A:382:ILE:O	1:A:386:MET:HG2	1.72	0.89
1:D:238:ASP:HB3	4:E:308:LEU:HD22	1.54	0.89
2:B:75:ILE:HD11	2:B:78:LEU:HD13	1.55	0.89
3:C:69:TRP:HE1	3:C:114:PRO:HA	1.35	0.89
4:E:135:PRO:HG2	4:E:137:ASP:O	1.73	0.88
4:E:172:ILE:CD1	4:E:188:ARG:HB3	2.02	0.88
4:E:183:TRP:HB3	4:E:216:ARG:CG	2.02	0.88
2:B:34:GLY:C	2:B:35:LEU:HD23	1.94	0.88
3:C:77:ILE:HD12	3:C:80:LEU:HD13	1.53	0.88
1:D:376:ILE:C	1:D:380:LYS:HE2	1.93	0.88
4:E:39:LEU:HD23	4:E:183:TRP:CZ2	2.07	0.88
4:E:67:ASN:HD22	4:E:67:ASN:N	1.71	0.88
1:A:79:ARG:HD2	1:A:107:LYS:HD2	1.55	0.88
1:A:107:LYS:HG2	2:B:150:THR:HG21	1.53	0.88
1:D:160:PRO:HG3	1:D:185:LYS:HB3	1.53	0.88
1:A:406:ILE:HG23	1:A:409:ILE:HD11	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:81:PRO:HD3	3:C:22:ARG:NH2	1.88	0.88
1:A:38:ILE:HG22	1:A:38:ILE:O	1.71	0.88
1:D:56:LEU:HD21	1:D:122:ALA:HB3	1.54	0.88
4:E:71:TYR:HA	4:E:111:ASN:CB	2.04	0.88
4:E:109:VAL:HG12	4:E:110:TYR:O	1.73	0.88
4:E:183:TRP:HB3	4:E:216:ARG:CD	2.04	0.88
4:E:284:LYS:O	4:E:287:ILE:HG23	1.73	0.88
1:A:242:LYS:HB2	1:A:245:LEU:HB2	1.56	0.88
4:E:172:ILE:HD12	4:E:188:ARG:CB	2.02	0.88
3:C:4:GLU:HG3	3:C:5:GLU:H	1.37	0.88
3:C:144:CYS:SG	3:C:146:LEU:HD11	2.13	0.88
2:B:48:GLU:HA	2:B:130:ILE:CD1	2.04	0.87
3:C:16:LYS:HA	3:C:16:LYS:HE3	1.56	0.87
3:C:159:SER:CA	3:C:213:GLN:HG3	2.04	0.87
4:E:144:VAL:HA	4:E:208:ILE:O	1.74	0.87
1:D:303:PRO:HD2	1:D:400:LYS:HD2	1.56	0.87
2:B:241:LEU:CG	2:B:248:LYS:HE2	2.05	0.87
4:E:62:TYR:O	4:E:62:TYR:CD1	2.28	0.87
4:E:136:PHE:CE1	4:E:217:LYS:HG2	2.09	0.87
1:D:49:ILE:HD12	1:D:125:LYS:HE3	1.54	0.87
1:D:131:ILE:HG13	1:D:133:THR:N	1.89	0.87
1:D:160:PRO:CD	1:D:185:LYS:HB3	2.04	0.87
1:A:244:THR:O	1:A:247:ILE:HG22	1.74	0.87
2:B:10:VAL:HG13	2:B:11:LEU:HD22	1.54	0.87
2:B:56:LEU:CD2	2:B:120:PRO:HG2	2.04	0.87
1:D:30:ASP:OD1	1:D:30:ASP:N	2.04	0.87
4:E:31:THR:HB	4:E:58:GLN:HB2	1.57	0.87
4:E:267:LEU:O	4:E:270:GLN:HG3	1.73	0.87
3:C:220:ILE:HG13	3:C:220:ILE:O	1.72	0.87
4:E:132:THR:O	4:E:282:ILE:HD12	1.75	0.87
2:B:185:GLN:HB3	2:B:219:PHE:CE2	2.08	0.87
1:D:106:THR:HG23	1:D:107:LYS:CE	2.03	0.87
4:E:279:VAL:HB	4:E:280:PRO:CD	2.04	0.87
2:B:186:TRP:CB	2:B:215:ARG:HG3	2.03	0.87
2:B:287:ILE:C	2:B:287:ILE:HD12	1.95	0.87
1:D:37:LEU:HD12	1:D:53:ASN:O	1.74	0.87
1:D:167:LEU:CD1	1:D:178:MET:HB2	2.04	0.87
3:C:38:THR:CG2	3:C:57:TRP:CE3	2.58	0.87
3:C:316:THR:HG23	3:C:317:PRO:HD2	1.56	0.87
1:A:41:ILE:HD11	1:A:51:GLU:OE1	1.74	0.86
2:B:104:LEU:HA	2:B:118:TRP:CH2	2.09	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:50:GLU:HB3	3:C:130:CYS:O	1.75	0.86
1:D:87:LEU:HD12	1:D:88:PRO:HD2	1.53	0.86
4:E:6:LEU:CD1	4:E:69:SER:HB3	2.05	0.86
4:E:94:ASN:ND2	4:E:143:LEU:HD23	1.90	0.86
1:A:274:ILE:HG12	1:A:277:TYR:HD1	1.40	0.86
2:B:35:LEU:HD23	2:B:35:LEU:N	1.89	0.86
2:B:132:VAL:O	2:B:279:ILE:HG23	1.73	0.86
3:C:18:ASN:CB	3:C:21:VAL:HB	2.05	0.86
1:D:187:TRP:CZ2	1:D:189:TYR:HB3	2.10	0.86
4:E:140:ASN:C	4:E:140:ASN:HD22	1.77	0.86
1:A:160:PRO:HG3	1:A:185:LYS:HB3	1.55	0.86
1:A:420:ILE:HG13	1:A:421:GLY:N	1.90	0.86
4:E:44:GLU:HG3	4:E:129:ILE:HG13	1.56	0.86
4:E:69:SER:O	4:E:69:SER:OG	1.84	0.86
2:B:185:GLN:CB	2:B:219:PHE:HE2	1.87	0.86
2:B:224:THR:C	2:B:227:PRO:HD2	1.95	0.86
3:C:65:HIS:CD2	3:C:65:HIS:N	2.43	0.86
4:E:91:LEU:H	4:E:95:VAL:CB	1.89	0.86
4:E:271:LYS:HZ3	4:E:271:LYS:HB2	1.40	0.86
4:E:313:THR:HG21	4:E:441:LEU:HA	1.57	0.86
3:C:269:VAL:HG13	3:C:270:PHE:CD1	2.10	0.86
1:D:252:SER:HB2	4:E:259:LEU:CD1	2.05	0.86
2:B:46:LYS:HA	2:B:278:PRO:CD	2.03	0.86
3:C:190:TRP:CB	3:C:223:ARG:HB2	2.04	0.86
4:E:44:GLU:HG3	4:E:129:ILE:CG1	2.06	0.86
4:E:91:LEU:H	4:E:95:VAL:HB	1.41	0.86
2:B:405:VAL:O	2:B:408:ILE:HG22	1.75	0.86
1:A:379:VAL:CG1	4:E:424:LYS:HE2	2.06	0.85
4:E:66:TRP:HB2	4:E:71:TYR:H	1.41	0.85
4:E:146:ARG:CZ	4:E:205:PHE:HB3	2.06	0.85
3:C:137:PHE:CD1	3:C:288:ILE:HB	2.10	0.85
1:A:245:LEU:HD22	2:B:250:SER:HA	1.58	0.85
1:D:203:TYR:H	1:D:203:TYR:HD1	0.85	0.85
3:C:18:ASN:HB3	3:C:21:VAL:HB	1.58	0.85
3:C:83:ARG:O	3:C:87:ILE:HG13	1.74	0.85
4:E:122:ILE:H	4:E:122:ILE:HD13	1.42	0.85
1:A:41:ILE:CG1	1:A:51:GLU:HB3	2.05	0.85
4:E:89:VAL:CG2	4:E:99:PHE:CZ	2.59	0.85
4:E:233:SER:O	4:E:237:VAL:HG23	1.77	0.85
1:A:72:TYR:HB2	1:A:112:TYR:CB	2.06	0.85
2:B:230:LEU:HA	2:B:233:ILE:HG13	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:279:ILE:CG2	2:B:280:ILE:HD13	2.07	0.85
2:B:407:ALA:O	2:B:411:ILE:HG13	1.76	0.85
1:D:46:VAL:HA	1:D:272:PRO:CD	2.06	0.85
4:E:222:ILE:HG23	4:E:223:ILE:H	1.42	0.85
4:E:250:LYS:HA	4:E:253:LEU:HB3	1.57	0.85
2:B:175:ILE:HG12	2:B:176:ASN:H	1.39	0.85
3:C:148:PHE:HB2	3:C:215:VAL:HG22	1.58	0.85
2:B:128:CYS:SG	2:B:144:MET:HG2	2.17	0.85
1:D:75:ILE:HD13	4:E:24:LEU:HD12	1.59	0.85
1:A:242:LYS:HB2	1:A:245:LEU:CB	2.07	0.84
1:D:245:LEU:HD21	4:E:255:ILE:HG13	1.57	0.84
1:A:107:LYS:CE	2:B:150:THR:HB	2.07	0.84
2:B:248:LYS:HD3	2:B:252:SER:CB	2.03	0.84
3:C:110:VAL:HG13	3:C:120:TRP:HB2	1.58	0.84
1:D:398:GLU:HA	1:D:401:TYR:CZ	2.12	0.84
1:A:171:MET:HE3	1:A:176:TRP:CH2	2.12	0.84
1:A:166:ASP:OD1	1:A:166:ASP:O	1.95	0.84
2:B:92:LEU:N	2:B:96:ASN:HB2	1.93	0.84
2:B:142:CYS:CB	2:B:211:LEU:HB2	2.08	0.84
3:C:242:LEU:CD2	3:C:267:GLN:HB3	2.04	0.84
1:D:86:TRP:O	1:D:86:TRP:CE3	2.30	0.84
4:E:292:VAL:O	4:E:296:ILE:HG23	1.77	0.84
4:E:92:GLU:HB3	4:E:144:VAL:HG23	1.60	0.84
1:A:107:LYS:HE2	2:B:150:THR:HB	1.58	0.84
1:A:433:LEU:O	1:A:433:LEU:HD12	1.77	0.84
1:D:118:TRP:HE1	1:D:120:PRO:HB3	1.39	0.84
3:C:50:GLU:HG2	3:C:132:ILE:HB	1.57	0.84
3:C:138:PRO:CG	3:C:288:ILE:HD11	2.07	0.84
1:D:203:TYR:N	1:D:203:TYR:HD1	1.67	0.84
4:E:159:LEU:HD12	4:E:192:LYS:HB2	1.59	0.84
1:D:37:LEU:HD11	1:D:52:THR:OG1	1.78	0.84
4:E:240:TYR:HD2	4:E:453:ILE:HD13	1.39	0.84
1:A:43:VAL:CG1	1:A:50:VAL:HG22	2.08	0.84
1:A:46:VAL:HG23	1:A:271:VAL:N	1.92	0.84
2:B:265:LEU:O	2:B:268:ASP:HB2	1.77	0.84
1:D:106:THR:HG22	1:D:107:LYS:N	1.93	0.84
1:D:176:TRP:CB	1:D:209:ARG:HD2	2.08	0.84
1:D:379:VAL:HA	1:D:382:ILE:HD12	1.60	0.84
4:E:172:ILE:HD11	4:E:187:HIS:C	1.98	0.84
1:A:110:LEU:CD1	1:A:114:GLY:HA2	2.08	0.83
1:A:258:LEU:HD13	4:E:267:LEU:CD2	2.06	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ILE:HG23	1:A:420:ILE:H	1.42	0.83
2:B:176:ASN:HB2	2:B:191:LYS:CB	2.07	0.83
1:D:85:VAL:HG13	1:D:86:TRP:HE3	1.41	0.83
1:D:298:THR:O	1:D:301:ARG:HB3	1.76	0.83
1:A:107:LYS:C	1:A:108:LEU:HD23	1.99	0.83
1:A:145:LYS:C	1:A:146:LEU:HD12	1.98	0.83
2:B:142:CYS:HB3	2:B:211:LEU:HB2	1.60	0.83
2:B:104:LEU:HD12	2:B:118:TRP:CZ3	2.13	0.83
3:C:462:THR:HB	3:C:463:PRO:CD	2.08	0.83
1:A:255:VAL:HG23	1:A:258:LEU:HD12	1.61	0.83
2:B:31:VAL:CG2	2:B:86:TRP:HZ3	1.90	0.83
2:B:297:LEU:HD13	2:B:445:THR:HG21	1.58	0.83
4:E:182:GLU:HG2	4:E:221:TYR:OH	1.77	0.83
2:B:223:TYR:O	2:B:226:VAL:HG22	1.78	0.83
1:D:49:ILE:HG21	1:D:125:LYS:HZ1	1.44	0.83
1:D:111:ASP:OD2	1:D:115:LYS:HD3	1.77	0.83
1:D:259:VAL:HA	1:D:262:GLU:CD	1.98	0.83
1:D:282:MET:HG3	1:D:286:ILE:HD11	1.58	0.83
4:E:227:ALA:N	4:E:228:PRO:HD2	1.93	0.83
1:A:245:LEU:CD2	2:B:250:SER:HA	2.08	0.83
2:B:47:ASN:HB2	2:B:49:GLU:OE1	1.78	0.83
2:B:160:HIS:NE2	2:B:209:PHE:HE1	1.77	0.83
3:C:81:ARG:CZ	3:C:111:LEU:HD13	2.08	0.83
4:E:446:ILE:HG22	4:E:447:ASP:N	1.92	0.83
1:A:33:VAL:CG2	1:A:158:ILE:HG12	2.07	0.83
2:B:38:THR:HG22	2:B:55:PHE:HE1	1.43	0.83
2:B:93:MET:HG3	2:B:206:ASP:CB	2.09	0.83
2:B:242:PRO:CG	2:B:243:PRO:HD3	2.09	0.83
3:C:35:LEU:HD22	3:C:215:VAL:HG11	1.61	0.83
1:D:384:GLU:HG2	4:E:422:ILE:HD12	1.61	0.83
3:C:45:LEU:HD12	3:C:190:TRP:CE3	2.14	0.83
3:C:319:THR:O	3:C:319:THR:CG2	2.27	0.83
1:D:220:ILE:CG2	4:E:294:LEU:HD11	2.09	0.83
4:E:148:GLN:CA	4:E:148:GLN:HE21	1.89	0.83
4:E:283:GLY:O	4:E:287:ILE:HG22	1.78	0.83
1:A:79:ARG:CD	1:A:107:LYS:HD2	2.07	0.83
1:A:171:MET:CE	1:A:176:TRP:CH2	2.62	0.83
1:A:47:ASN:O	1:A:49:ILE:HG13	1.78	0.82
1:D:260:ILE:HG22	1:D:264:ILE:HD11	1.59	0.82
3:C:60:HIS:CD2	3:C:92:ILE:HD13	2.14	0.82
4:E:132:THR:O	4:E:135:PRO:HD3	1.77	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:PRO:HG2	1:A:185:LYS:NZ	1.94	0.82
1:A:423:VAL:O	1:A:426:PHE:HB3	1.79	0.82
1:D:91:VAL:HG22	1:D:96:ALA:CB	2.09	0.82
1:D:109:LEU:O	1:D:116:ILE:HG22	1.80	0.82
4:E:136:PHE:HZ	4:E:217:LYS:HD2	1.40	0.82
4:E:162:GLU:HA	4:E:190:ALA:N	1.94	0.82
1:A:59:GLN:HE22	1:A:117:MET:CG	1.93	0.82
4:E:47:GLU:HB3	4:E:129:ILE:CG1	2.09	0.82
1:A:35:LEU:HD21	1:A:37:LEU:HD23	1.61	0.82
2:B:236:ILE:HB	2:B:446:MET:CE	2.06	0.82
4:E:28:ILE:HD11	4:E:60:ASN:O	1.79	0.82
4:E:159:LEU:HD12	4:E:192:LYS:CB	2.09	0.82
1:A:176:TRP:HB3	1:A:209:ARG:HD2	1.62	0.82
2:B:132:VAL:CG1	2:B:279:ILE:HA	2.07	0.82
3:C:33:ILE:O	3:C:160:MET:HA	1.80	0.82
3:C:56:VAL:HG13	3:C:126:PHE:CE2	2.14	0.82
3:C:77:ILE:CD1	3:C:80:LEU:HD13	2.09	0.82
3:C:190:TRP:HB3	3:C:223:ARG:HB2	1.62	0.82
1:D:176:TRP:HB3	1:D:209:ARG:HD2	1.59	0.82
2:B:218:LEU:HA	2:B:221:ILE:HD11	1.62	0.82
3:C:38:THR:CG2	3:C:57:TRP:HE3	1.92	0.82
4:E:222:ILE:O	4:E:226:ILE:HG13	1.80	0.82
2:B:3:MET:CE	2:B:69:PRO:HG3	2.08	0.82
1:D:176:TRP:CE3	1:D:209:ARG:CZ	2.63	0.82
1:D:296:ILE:HA	1:D:299:HIS:CB	2.10	0.82
4:E:225:ILE:O	4:E:228:PRO:HG2	1.79	0.82
1:A:376:ILE:HG23	1:A:380:LYS:NZ	1.95	0.82
3:C:42:LEU:HD22	3:C:190:TRP:CZ2	2.15	0.82
4:E:47:GLU:O	4:E:126:THR:HG23	1.80	0.82
4:E:183:TRP:HB2	4:E:216:ARG:HG2	1.62	0.82
1:A:60:TRP:HE1	1:A:116:ILE:HD12	1.45	0.81
1:A:65:LEU:HB3	1:A:110:LEU:CD1	2.09	0.81
1:A:148:ILE:CG2	1:A:198:TYR:HD2	1.92	0.81
1:A:216:VAL:HG13	1:A:220:ILE:HD11	1.61	0.81
3:C:263:VAL:HA	1:D:251:LEU:HD11	1.61	0.81
1:D:398:GLU:HA	1:D:401:TYR:CE2	2.15	0.81
4:E:45:LYS:HG2	4:E:279:VAL:C	1.99	0.81
4:E:62:TYR:HD1	4:E:62:TYR:C	1.81	0.81
4:E:236:VAL:CA	4:E:239:VAL:HG23	2.09	0.81
1:A:16:ASN:CB	1:A:19:ILE:HD12	2.10	0.81
1:D:189:TYR:HA	1:D:197:PRO:HD2	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:26:HIS:CG	4:E:26:HIS:O	2.34	0.81
2:B:26:GLY:O	2:B:28:LYS:HE2	1.80	0.81
2:B:247:GLU:O	2:B:249:MET:HG3	1.80	0.81
3:C:113:ARG:HE	3:C:119:THR:HG23	1.46	0.81
3:C:443:VAL:HA	3:C:446:TRP:CD1	2.15	0.81
2:B:45:GLU:HG2	2:B:277:VAL:HB	1.61	0.81
1:D:216:VAL:O	1:D:220:ILE:HG13	1.81	0.81
2:B:409:LYS:HE2	3:C:423:ILE:HG23	1.63	0.81
3:C:1:VAL:HG22	3:C:4:GLU:CD	2.01	0.81
1:D:160:PRO:CG	1:D:185:LYS:HB3	2.08	0.81
1:D:166:ASP:OD2	1:D:181:TYR:HB2	1.81	0.81
1:D:286:ILE:O	1:D:290:ILE:HG23	1.80	0.81
1:A:171:MET:HE3	1:A:176:TRP:CZ2	2.16	0.81
2:B:216:LYS:HD2	2:B:216:LYS:O	1.80	0.81
2:B:243:PRO:HB3	2:B:435:ALA:CB	2.00	0.81
3:C:3:GLU:OE1	3:C:7:LEU:HD12	1.80	0.81
1:D:10:ASN:OD1	1:D:11:LEU:HD23	1.81	0.81
2:B:90:ILE:HG23	2:B:147:LYS:H	1.45	0.81
2:B:142:CYS:O	2:B:210:TYR:HA	1.80	0.81
3:C:93:VAL:CG1	3:C:151:LEU:HD13	2.01	0.81
3:C:110:VAL:CG1	3:C:120:TRP:HB2	2.11	0.81
4:E:91:LEU:H	4:E:95:VAL:CG2	1.94	0.81
4:E:219:LEU:HB3	4:E:222:ILE:CB	2.10	0.81
1:A:236:PRO:HB3	1:A:299:HIS:NE2	1.96	0.80
2:B:186:TRP:CB	2:B:215:ARG:CG	2.59	0.80
1:D:135:PHE:HZ	1:D:273:LEU:HD12	1.45	0.80
1:A:189:TYR:HA	1:A:197:PRO:HD2	1.64	0.80
3:C:135:LEU:O	3:C:138:PRO:HD2	1.82	0.80
3:C:192:ILE:HD12	3:C:219:LEU:HD11	1.63	0.80
3:C:252:GLU:OE2	1:D:301:ARG:HA	1.80	0.80
4:E:63:ARG:HB2	4:E:63:ARG:HH11	1.44	0.80
1:A:110:LEU:HD11	1:A:114:GLY:HA2	1.62	0.80
3:C:42:LEU:HD22	3:C:190:TRP:HH2	1.44	0.80
3:C:463:PRO:HA	3:C:466:VAL:CG2	2.07	0.80
1:D:72:TYR:C	1:D:72:TYR:HD1	1.79	0.80
1:A:167:LEU:HD12	1:A:178:MET:CB	2.09	0.80
2:B:132:VAL:C	2:B:279:ILE:HG23	2.02	0.80
2:B:218:LEU:HD13	2:B:221:ILE:CG1	2.11	0.80
2:B:269:LYS:HE3	2:B:270:VAL:HG22	1.63	0.80
4:E:44:GLU:HA	4:E:129:ILE:CD1	2.12	0.80
1:A:101:ALA:HB3	1:A:123:ILE:O	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:281:ILE:HG22	2:B:285:MET:N	1.96	0.80
1:D:255:VAL:O	1:D:259:VAL:HG23	1.80	0.80
1:D:427:ALA:O	1:D:431:ILE:HG13	1.82	0.80
4:E:172:ILE:HG23	4:E:174:PRO:HD2	1.64	0.80
4:E:262:THR:OG1	4:E:265:LEU:HD12	1.81	0.80
4:E:469:GLY:O	4:E:473:GLN:HB2	1.80	0.80
1:A:2:GLU:CG	1:A:74:GLY:HA2	2.11	0.80
1:A:380:LYS:HD3	2:B:408:ILE:CG2	2.11	0.80
3:C:298:LEU:HD11	3:C:471:PHE:HB2	1.64	0.80
1:A:20:ARG:HG2	1:A:20:ARG:NH1	1.85	0.80
2:B:91:VAL:HA	2:B:96:ASN:ND2	1.97	0.80
2:B:226:VAL:CG2	2:B:227:PRO:HD3	2.11	0.80
1:D:29:VAL:HG23	1:D:60:TRP:HD1	1.46	0.80
1:D:201:ILE:HG22	1:D:203:TYR:CE1	2.16	0.80
4:E:148:GLN:HA	4:E:148:GLN:NE2	1.97	0.80
1:A:108:LEU:HD13	1:A:118:TRP:HB2	1.62	0.80
3:C:47:GLU:HG2	3:C:286:PRO:HD2	1.62	0.80
3:C:279:PRO:O	3:C:282:ALA:HB3	1.81	0.80
1:D:38:ILE:CA	1:D:169:THR:HG21	2.09	0.80
1:D:233:PHE:HZ	1:D:417:ILE:CD1	1.95	0.80
1:D:379:VAL:HA	1:D:382:ILE:CD1	2.12	0.80
4:E:436:ASN:HA	4:E:439:TRP:NE1	1.95	0.80
4:E:55:ILE:HG13	4:E:57:ILE:HG13	1.62	0.80
4:E:141:CYS:SG	4:E:143:LEU:HD11	2.22	0.80
4:E:228:PRO:O	4:E:231:LEU:HD23	1.82	0.80
2:B:27:ASP:C	2:B:28:LYS:HG3	2.02	0.80
3:C:50:GLU:HA	3:C:132:ILE:CD1	2.08	0.80
3:C:466:VAL:O	3:C:470:ILE:HG12	1.82	0.80
1:D:72:TYR:HD1	1:D:72:TYR:O	1.64	0.80
1:A:54:VAL:CG2	1:A:122:ALA:HB3	2.12	0.79
1:A:258:LEU:HD13	4:E:267:LEU:HD23	1.62	0.79
2:B:160:HIS:CE1	2:B:207:VAL:HG11	2.17	0.79
4:E:44:GLU:CB	4:E:280:PRO:HG3	2.12	0.79
4:E:76:LEU:HD23	4:E:77:VAL:H	1.47	0.79
2:B:287:ILE:HA	2:B:290:LEU:HD12	1.63	0.79
3:C:275:SER:O	3:C:279:PRO:HD3	1.82	0.79
1:A:72:TYR:HB2	1:A:112:TYR:HD2	1.44	0.79
1:D:61:ILE:HA	1:D:116:ILE:CD1	2.10	0.79
1:A:3:HIS:HB2	1:A:7:LEU:CD2	2.12	0.79
2:B:133:MET:SD	2:B:140:GLN:HB2	2.22	0.79
3:C:249:LEU:N	3:C:250:PRO:HD2	1.96	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:75:ILE:CD1	1:D:78:ILE:CG2	2.60	0.79
4:E:66:TRP:HB2	4:E:71:TYR:N	1.96	0.79
4:E:463:LEU:HD12	4:E:463:LEU:O	1.82	0.79
1:A:37:LEU:CD2	1:A:54:VAL:HG12	2.12	0.79
1:D:167:LEU:HD11	1:D:178:MET:CB	2.11	0.79
4:E:223:ILE:HA	4:E:226:ILE:HB	1.64	0.79
1:A:62:ASP:HB3	1:A:65:LEU:HD12	1.63	0.79
1:A:133:THR:O	1:A:133:THR:CG2	2.30	0.79
2:B:147:LYS:HB2	2:B:206:ASP:HA	1.65	0.79
1:D:107:LYS:HE3	4:E:149:THR:O	1.83	0.79
1:A:176:TRP:HB3	1:A:209:ARG:CD	2.12	0.79
3:C:299:VAL:O	3:C:303:VAL:HG23	1.82	0.79
4:E:91:LEU:CB	4:E:95:VAL:H	1.96	0.79
1:A:139:GLN:HB2	1:A:207:MET:C	2.04	0.79
3:C:65:HIS:H	3:C:65:HIS:HD2	1.30	0.79
3:C:179:ILE:HG23	3:C:181:PRO:HD2	1.63	0.79
1:D:167:LEU:HD11	1:D:178:MET:HB2	1.65	0.79
2:B:142:CYS:HB3	2:B:211:LEU:CB	2.13	0.79
3:C:155:ALA:HB2	3:C:211:ASN:HA	1.65	0.79
3:C:179:ILE:HG13	3:C:181:PRO:HD2	1.65	0.79
3:C:247:PHE:CE1	3:C:309:VAL:HG22	2.18	0.79
1:A:277:TYR:HA	1:A:280:PHE:CE1	2.17	0.78
2:B:281:ILE:HG23	2:B:284:LEU:HB3	1.65	0.78
3:C:113:ARG:CD	3:C:117:TYR:HB3	2.13	0.78
1:D:7:LEU:HD13	1:D:70:ALA:O	1.82	0.78
1:D:72:TYR:CD1	1:D:72:TYR:O	2.37	0.78
1:D:377:GLU:CG	4:E:415:CYS:HB2	2.05	0.78
2:B:129:THR:HG22	2:B:142:CYS:HA	1.64	0.78
2:B:175:ILE:HG12	2:B:176:ASN:N	1.98	0.78
3:C:457:SER:O	3:C:461:ILE:HG13	1.84	0.78
1:D:32:THR:CB	1:D:59:GLN:HB3	2.11	0.78
1:D:198:TYR:HD1	1:D:198:TYR:H	0.84	0.78
1:A:406:ILE:HA	1:A:409:ILE:CD1	2.14	0.78
2:B:23:GLN:N	2:B:23:GLN:NE2	2.18	0.78
2:B:90:ILE:HG23	2:B:147:LYS:N	1.98	0.78
2:B:226:VAL:O	2:B:230:LEU:HG	1.82	0.78
2:B:439:PHE:HA	2:B:442:ILE:HB	1.63	0.78
3:C:107:PHE:CG	3:C:107:PHE:O	2.37	0.78
3:C:137:PHE:CE1	3:C:288:ILE:HG22	2.18	0.78
1:D:57:ARG:HB2	1:D:119:THR:HG22	1.65	0.78
1:D:78:ILE:HD12	1:D:78:ILE:O	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:TRP:CZ3	1:D:189:TYR:CD1	2.71	0.78
3:C:482:PRO:HG2	3:C:483:ALA:H	1.49	0.78
1:D:29:VAL:HG23	1:D:60:TRP:NE1	1.98	0.78
1:D:31:ILE:HG22	1:D:158:ILE:HG23	1.64	0.78
1:A:166:ASP:HB3	1:A:178:MET:HE2	1.65	0.78
3:C:148:PHE:HB2	3:C:215:VAL:HG21	1.63	0.78
4:E:132:THR:C	4:E:135:PRO:HD3	2.03	0.78
1:A:420:ILE:HG13	1:A:421:GLY:H	1.48	0.78
1:D:75:ILE:HG13	1:D:78:ILE:HG23	1.66	0.78
1:A:218:VAL:HG13	1:A:219:ILE:N	1.99	0.78
1:A:233:PHE:O	1:A:236:PRO:HG2	1.83	0.78
2:B:160:HIS:H	2:B:195:LYS:HZ1	1.30	0.78
2:B:297:LEU:HD13	2:B:445:THR:CG2	2.13	0.78
2:B:408:ILE:HG23	2:B:409:LYS:N	1.96	0.78
3:C:266:ALA:HB1	3:C:270:PHE:CZ	2.18	0.78
3:C:273:LEU:O	3:C:276:GLN:HB2	1.84	0.78
3:C:278:LEU:HD12	3:C:278:LEU:O	1.82	0.78
1:D:48:GLN:OE1	1:D:130:ILE:HD13	1.83	0.78
1:D:296:ILE:HA	1:D:299:HIS:HB2	1.66	0.78
4:E:142:SER:OG	4:E:209:ILE:HD11	1.84	0.78
1:A:66:ARG:HD3	1:A:66:ARG:N	1.97	0.78
2:B:227:PRO:O	2:B:231:ILE:HG12	1.84	0.78
1:D:152:ASP:HB3	1:D:197:PRO:HA	1.64	0.78
1:D:305:THR:HG22	1:D:400:LYS:CB	2.12	0.78
1:A:43:VAL:HG22	1:A:50:VAL:HG13	1.66	0.78
2:B:218:LEU:HD11	2:B:222:VAL:HG22	1.66	0.78
1:D:384:GLU:HG2	4:E:422:ILE:CD1	2.14	0.78
1:A:3:HIS:HB2	1:A:7:LEU:HD21	1.64	0.78
1:A:380:LYS:CD	2:B:408:ILE:HB	2.14	0.78
1:D:62:ASP:HB3	1:D:65:LEU:CD1	2.08	0.78
1:D:271:VAL:HG13	1:D:271:VAL:O	1.84	0.78
4:E:183:TRP:HA	4:E:216:ARG:HA	1.64	0.78
4:E:225:ILE:HD13	4:E:225:ILE:N	1.99	0.78
4:E:249:GLN:NE2	4:E:250:LYS:HE3	1.98	0.78
1:A:66:ARG:HD3	1:A:66:ARG:H	1.46	0.77
2:B:68:ASP:O	2:B:72:TYR:HB3	1.85	0.77
4:E:62:TYR:CD1	4:E:62:TYR:C	2.54	0.77
4:E:100:GLU:HB2	4:E:122:ILE:CD1	2.13	0.77
4:E:229:CYS:HA	4:E:232:ILE:HB	1.65	0.77
3:C:138:PRO:HB3	3:C:290:LYS:HZ2	1.48	0.77
3:C:275:SER:O	3:C:278:LEU:HB3	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:144:VAL:HG12	4:E:209:ILE:HA	1.65	0.77
1:A:413:VAL:HG12	1:A:417:ILE:HD11	1.66	0.77
3:C:93:VAL:CG2	3:C:151:LEU:HD22	2.15	0.77
1:D:292:THR:HA	1:D:295:VAL:HG22	1.67	0.77
4:E:129:ILE:HG22	4:E:133:TYR:CE2	2.18	0.77
4:E:141:CYS:HB3	4:E:212:LEU:HB2	1.66	0.77
1:A:72:TYR:CB	1:A:112:TYR:CD2	2.66	0.77
2:B:238:VAL:HG21	2:B:255:ALA:HB1	1.64	0.77
2:B:270:VAL:HG11	2:B:284:LEU:CD1	2.14	0.77
2:B:287:ILE:HD12	2:B:288:MET:N	1.99	0.77
1:D:72:TYR:HB2	1:D:112:TYR:CB	2.15	0.77
1:D:78:ILE:CD1	1:D:110:LEU:HB3	2.15	0.77
1:D:170:PHE:HE2	1:D:176:TRP:CD1	2.02	0.77
1:D:243:MET:H	1:D:243:MET:HE2	1.50	0.77
1:A:56:LEU:HD23	1:A:57:ARG:N	2.00	0.77
1:A:176:TRP:CE3	1:A:209:ARG:CZ	2.67	0.77
2:B:297:LEU:CD1	2:B:445:THR:HG21	2.14	0.77
2:B:425:LYS:HA	2:B:428:TRP:CD1	2.20	0.77
3:C:6:ARG:O	3:C:9:ASN:HB3	1.84	0.77
1:D:141:ASN:HA	1:D:205:PHE:O	1.85	0.77
1:D:263:LEU:O	1:D:267:THR:HG22	1.85	0.77
2:B:9:SER:CA	2:B:12:PHE:CE1	2.67	0.77
2:B:56:LEU:CD2	2:B:103:THR:HA	2.15	0.77
2:B:141:ASN:HA	2:B:211:LEU:O	1.84	0.77
3:C:38:THR:HG22	3:C:57:TRP:CE3	2.18	0.77
3:C:43:ILE:H	3:C:43:ILE:HD12	1.47	0.77
3:C:316:THR:HG22	3:C:317:PRO:HD2	1.66	0.77
3:C:472:ILE:HB	3:C:475:MET:SD	2.25	0.77
1:D:43:VAL:HG13	1:D:49:ILE:O	1.85	0.77
1:A:224:LEU:HG	1:A:225:PHE:N	1.99	0.77
3:C:68:THR:HA	3:C:115:ASN:CA	2.08	0.77
3:C:472:ILE:HA	3:C:475:MET:HB3	1.66	0.77
3:C:1:VAL:HA	3:C:4:GLU:CG	2.14	0.77
3:C:453:ILE:HG23	3:C:454:ASP:N	1.98	0.77
1:D:55:ARG:HA	1:D:120:PRO:O	1.84	0.77
4:E:313:THR:CB	4:E:441:LEU:HB3	2.15	0.77
2:B:31:VAL:HG12	2:B:158:LEU:HD21	1.67	0.77
2:B:238:VAL:HG22	2:B:255:ALA:HB1	1.66	0.77
3:C:247:PHE:CD2	3:C:460:ILE:HD11	2.19	0.77
1:D:291:VAL:HG11	1:D:413:VAL:HG11	1.66	0.77
4:E:128:PRO:O	4:E:129:ILE:HG12	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ARG:HH11	1:A:20:ARG:CG	1.96	0.76
2:B:35:LEU:HD21	2:B:56:LEU:HA	1.65	0.76
3:C:59:ASP:HA	3:C:121:LEU:CB	2.14	0.76
3:C:216:THR:C	3:C:217:PHE:HD1	1.88	0.76
2:B:20:ARG:HD3	2:B:20:ARG:H	1.48	0.76
3:C:247:PHE:CE2	3:C:460:ILE:HD11	2.20	0.76
1:D:228:LEU:O	1:D:232:VAL:HG23	1.85	0.76
4:E:44:GLU:C	4:E:280:PRO:HB3	2.06	0.76
3:C:90:PRO:HD2	3:C:120:TRP:HZ3	1.50	0.76
3:C:452:THR:O	3:C:456:LEU:HG	1.86	0.76
1:D:243:MET:H	1:D:243:MET:CE	1.98	0.76
4:E:284:LYS:N	4:E:284:LYS:CE	2.44	0.76
3:C:453:ILE:CG2	3:C:454:ASP:H	1.99	0.76
4:E:35:THR:HB	4:E:54:TRP:HE3	1.51	0.76
1:A:90:LEU:CD1	1:A:100:PHE:HE2	1.99	0.76
1:A:413:VAL:O	1:A:417:ILE:HG13	1.84	0.76
2:B:45:GLU:OE1	2:B:277:VAL:HB	1.84	0.76
3:C:7:LEU:HD23	3:C:10:ASP:HB2	1.68	0.76
3:C:113:ARG:HD2	3:C:117:TYR:CB	2.12	0.76
1:D:405:VAL:O	1:D:409:ILE:HG23	1.86	0.76
1:A:52:THR:O	1:A:123:ILE:HG13	1.86	0.76
2:B:31:VAL:CG2	2:B:86:TRP:CZ3	2.64	0.76
3:C:51:THR:HA	3:C:128:SER:O	1.84	0.76
1:D:233:PHE:HZ	1:D:417:ILE:HD12	1.42	0.76
4:E:45:LYS:CA	4:E:280:PRO:CA	2.60	0.76
4:E:45:LYS:HG2	4:E:279:VAL:CA	2.15	0.76
4:E:197:GLN:HG2	4:E:198:LEU:N	2.00	0.76
4:E:219:LEU:CB	4:E:222:ILE:HB	2.14	0.76
2:B:9:SER:CA	2:B:12:PHE:HE1	1.99	0.76
2:B:93:MET:CG	2:B:206:ASP:HB3	2.14	0.76
2:B:104:LEU:HA	2:B:118:TRP:HH2	1.48	0.76
3:C:122:PRO:HB3	1:D:149:TRP:HZ2	1.49	0.76
1:D:60:TRP:CH2	1:D:86:TRP:CZ3	2.74	0.76
1:A:198:TYR:O	1:A:198:TYR:CD1	2.38	0.76
3:C:241:PHE:C	3:C:241:PHE:CD1	2.58	0.76
3:C:271:LEU:HD21	3:C:299:VAL:CG1	2.16	0.76
3:C:431:LYS:HE2	1:D:379:VAL:HG22	1.68	0.76
1:D:36:GLN:HB3	1:D:55:ARG:HG3	1.67	0.76
4:E:209:ILE:HG12	4:E:211:PHE:HE1	1.51	0.76
1:A:290:ILE:O	1:A:293:VAL:HG12	1.86	0.76
2:B:301:VAL:O	2:B:304:LEU:HB3	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2:ASN:HD22	3:C:72:SER:HB3	1.50	0.76
4:E:39:LEU:HD12	4:E:49:LEU:HD13	1.66	0.76
4:E:56:GLU:HB2	4:E:118:LEU:HD22	1.65	0.76
1:A:43:VAL:HG13	1:A:50:VAL:CG2	2.16	0.76
2:B:40:LEU:HD23	2:B:52:THR:OG1	1.86	0.76
3:C:138:PRO:N	3:C:288:ILE:HD12	2.01	0.76
3:C:476:GLY:HA2	3:C:479:ASN:HB3	1.66	0.76
1:D:263:LEU:HD11	4:E:266:PHE:CZ	2.21	0.76
1:D:302:SER:HB2	1:D:305:THR:HG23	1.68	0.76
1:A:102:ILE:O	1:A:102:ILE:CG2	2.34	0.75
1:A:148:ILE:HG22	1:A:198:TYR:HD2	1.51	0.75
2:B:258:ALA:HB2	3:C:265:LEU:HD13	1.67	0.75
1:D:214:PHE:O	1:D:218:VAL:HG23	1.85	0.75
1:D:261:VAL:O	1:D:265:PRO:HD2	1.87	0.75
4:E:172:ILE:HD11	4:E:187:HIS:CA	2.16	0.75
1:A:391:GLU:HA	1:A:394:ASN:ND2	2.01	0.75
1:D:301:ARG:HH12	1:D:406:ILE:HD11	1.49	0.75
1:D:412:CYS:O	1:D:416:LEU:HD23	1.87	0.75
4:E:456:LEU:O	4:E:456:LEU:HD22	1.86	0.75
1:A:135:PHE:N	1:A:136:PRO:HD2	2.02	0.75
4:E:449:ALA:HA	4:E:452:TRP:CD1	2.21	0.75
1:A:89:ASP:OD2	1:A:150:THR:HG22	1.84	0.75
2:B:242:PRO:HG2	2:B:243:PRO:CD	2.16	0.75
3:C:280:GLU:HG3	3:C:281:THR:N	2.00	0.75
1:D:287:SER:O	1:D:290:ILE:HG12	1.86	0.75
1:D:383:ALA:HA	1:D:386:MET:HG2	1.68	0.75
1:A:57:ARG:HD3	1:A:161:GLU:CD	2.07	0.75
1:A:95:ASN:N	1:A:95:ASN:ND2	2.34	0.75
1:D:157:SER:HA	1:D:199:LEU:HD12	1.66	0.75
1:D:379:VAL:HG22	1:D:382:ILE:HD12	1.67	0.75
4:E:27:VAL:HG12	4:E:153:HIS:C	2.07	0.75
4:E:91:LEU:HB3	4:E:94:ASN:H	1.50	0.75
1:A:148:ILE:HG21	1:A:198:TYR:CB	2.15	0.75
3:C:37:LEU:HD12	3:C:217:PHE:CD2	2.22	0.75
3:C:319:THR:HB	3:C:447:ASN:HB3	1.68	0.75
1:A:35:LEU:HD21	1:A:37:LEU:CD2	2.17	0.75
1:A:63:VAL:O	1:A:66:ARG:HD2	1.86	0.75
1:A:156:VAL:HG22	1:A:157:SER:N	2.02	0.75
3:C:8:ILE:HG23	3:C:8:ILE:O	1.86	0.75
1:D:35:LEU:HD11	1:D:54:VAL:CG1	2.15	0.75
1:D:253:LEU:HD23	1:D:254:THR:H	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:55:ILE:N	4:E:118:LEU:HD13	2.02	0.75
4:E:79:ILE:O	4:E:79:ILE:CG2	2.35	0.75
4:E:91:LEU:N	4:E:95:VAL:HB	2.01	0.75
2:B:278:PRO:O	2:B:278:PRO:HG2	1.87	0.75
3:C:299:VAL:O	3:C:302:VAL:HG23	1.87	0.75
3:C:449:VAL:HG12	3:C:452:THR:CB	2.17	0.75
3:C:471:PHE:HD1	3:C:471:PHE:C	1.90	0.75
1:D:244:THR:HG23	1:D:245:LEU:N	2.00	0.75
1:A:46:VAL:HB	1:A:270:ALA:O	1.87	0.75
1:A:145:LYS:HZ2	1:A:202:THR:HG23	1.52	0.75
2:B:31:VAL:HG12	2:B:158:LEU:CD2	2.17	0.75
1:A:36:GLN:C	1:A:36:GLN:OE1	2.25	0.74
3:C:227:PHE:O	3:C:230:ILE:HG12	1.87	0.74
3:C:247:PHE:C	3:C:250:PRO:HD2	2.07	0.74
1:A:151:TYR:O	1:A:198:TYR:HB3	1.86	0.74
1:A:171:MET:HE1	1:A:176:TRP:HH2	1.52	0.74
2:B:58:LEU:HD11	2:B:118:TRP:HE3	1.51	0.74
2:B:236:ILE:CB	2:B:446:MET:HE1	2.11	0.74
3:C:137:PHE:CD1	3:C:137:PHE:C	2.59	0.74
2:B:92:LEU:H	2:B:96:ASN:CB	1.97	0.74
4:E:75:ASP:HA	4:E:111:ASN:ND2	1.95	0.74
2:B:52:THR:HG22	2:B:53:SER:H	1.51	0.74
2:B:70:ALA:O	2:B:74:GLY:HA3	1.87	0.74
1:D:178:MET:HA	1:D:207:MET:CB	2.17	0.74
1:D:271:VAL:O	1:D:271:VAL:CG1	2.35	0.74
4:E:20:PRO:HB3	4:E:61:ASP:OD1	1.88	0.74
4:E:249:GLN:HE22	4:E:250:LYS:HE3	1.52	0.74
1:A:62:ASP:HB3	1:A:65:LEU:CD1	2.17	0.74
1:A:295:VAL:O	1:A:299:HIS:HB2	1.87	0.74
2:B:129:THR:CG2	2:B:142:CYS:HA	2.17	0.74
3:C:194:HIS:CG	3:C:195:LYS:H	2.05	0.74
1:D:130:ILE:HG12	1:D:131:ILE:N	2.01	0.74
1:A:376:ILE:HG23	1:A:380:LYS:HZ1	1.52	0.74
2:B:9:SER:O	2:B:13:GLU:HG3	1.87	0.74
1:D:276:LYS:CD	1:D:276:LYS:H	2.00	0.74
1:A:43:VAL:HG22	1:A:50:VAL:HG22	1.67	0.74
1:A:247:ILE:HG13	4:E:253:LEU:HD12	1.68	0.74
2:B:220:TYR:CB	2:B:223:TYR:CE2	2.71	0.74
2:B:254:SER:C	3:C:265:LEU:HD11	2.08	0.74
3:C:29:GLU:O	3:C:156:ASN:HA	1.88	0.74
3:C:160:MET:H	3:C:213:GLN:HB2	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:161:ASP:HA	3:C:199:LYS:HG2	1.69	0.74
3:C:216:THR:O	3:C:217:PHE:HD1	1.70	0.74
1:D:153:GLY:HA3	1:D:196:THR:HG22	1.69	0.74
1:A:66:ARG:HA	1:A:113:THR:C	2.08	0.74
1:A:67:TRP:HB2	1:A:112:TYR:HB2	1.69	0.74
1:A:239:SER:CB	2:B:312:HIS:HB3	2.17	0.74
1:A:304:SER:HA	1:A:400:LYS:HD3	1.70	0.74
2:B:7:LEU:O	2:B:11:LEU:HD23	1.87	0.74
2:B:46:LYS:HB2	2:B:277:VAL:H	1.50	0.74
2:B:141:ASN:ND2	2:B:212:ILE:HG12	2.02	0.74
3:C:179:ILE:HD12	3:C:195:LYS:CB	2.16	0.74
1:A:106:THR:HG22	1:A:107:LYS:H	1.52	0.74
1:A:388:SER:O	1:A:391:GLU:HB3	1.86	0.74
2:B:20:ARG:HG3	2:B:155:GLU:OE1	1.88	0.74
2:B:91:VAL:C	2:B:92:LEU:HD23	2.08	0.74
2:B:147:LYS:HG3	2:B:148:SER:N	2.03	0.74
3:C:132:ILE:O	3:C:136:TYR:HB2	1.88	0.74
1:D:239:SER:HB2	1:D:242:LYS:HE2	1.69	0.74
4:E:184:THR:CG2	4:E:215:GLN:HG2	2.18	0.74
1:A:92:LEU:HB2	1:A:96:ALA:N	2.03	0.74
1:A:107:LYS:HE3	2:B:150:THR:CG2	2.18	0.74
4:E:140:ASN:HD21	4:E:211:PHE:HA	1.53	0.74
1:D:106:THR:HG23	1:D:107:LYS:HE2	1.69	0.73
1:D:118:TRP:NE1	1:D:120:PRO:HB3	2.03	0.73
1:A:65:LEU:CB	1:A:110:LEU:HD11	2.13	0.73
3:C:52:LEU:HD23	3:C:128:SER:OG	1.88	0.73
3:C:278:LEU:CD1	3:C:278:LEU:O	2.37	0.73
3:C:311:ASN:O	3:C:315:ARG:HB3	1.88	0.73
3:C:427:ASN:HA	3:C:430:VAL:HG23	1.69	0.73
1:D:92:LEU:HD22	1:D:92:LEU:N	2.03	0.73
1:A:141:ASN:HA	1:A:205:PHE:O	1.88	0.73
3:C:137:PHE:CE1	3:C:288:ILE:CG2	2.72	0.73
1:D:56:LEU:HG	1:D:120:PRO:CG	2.15	0.73
4:E:449:ALA:O	4:E:452:TRP:HB2	1.87	0.73
3:C:243:ALA:HB3	3:C:302:VAL:HG12	1.70	0.73
1:D:149:TRP:CE2	1:D:150:THR:HB	2.23	0.73
4:E:27:VAL:HB	4:E:154:GLU:C	2.08	0.73
1:A:43:VAL:CG2	1:A:50:VAL:HG22	2.18	0.73
1:A:187:TRP:CZ2	1:A:189:TYR:HB3	2.24	0.73
1:A:207:MET:H	1:A:207:MET:HE2	1.51	0.73
1:A:406:ILE:CG2	1:A:409:ILE:HD11	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:109:LEU:HB3	2:B:117:SER:HB2	1.68	0.73
2:B:175:ILE:CD1	2:B:190:HIS:HD2	2.02	0.73
3:C:179:ILE:HD11	3:C:195:LYS:HB3	1.69	0.73
1:D:35:LEU:CD1	1:D:54:VAL:HG11	2.16	0.73
4:E:14:TYR:HE2	4:E:16:LYS:HE3	1.53	0.73
1:A:136:PRO:HB3	1:A:277:TYR:OH	1.88	0.73
1:A:278:MET:O	1:A:281:THR:HG22	1.89	0.73
1:A:291:VAL:O	1:A:295:VAL:HG23	1.89	0.73
1:A:397:GLU:O	1:A:400:LYS:HB2	1.88	0.73
2:B:241:LEU:HG	2:B:248:LYS:HB2	1.69	0.73
1:D:3:HIS:HB3	1:D:7:LEU:CG	2.18	0.73
1:D:56:LEU:N	1:D:56:LEU:HD23	2.02	0.73
1:A:166:ASP:OD1	1:A:166:ASP:C	2.27	0.73
1:A:218:VAL:O	1:A:221:PRO:HD2	1.88	0.73
3:C:60:HIS:NE2	3:C:92:ILE:HD13	2.02	0.73
3:C:471:PHE:C	3:C:471:PHE:CD1	2.62	0.73
1:D:135:PHE:C	1:D:135:PHE:CD1	2.60	0.73
4:E:66:TRP:CD1	4:E:111:ASN:CA	2.70	0.73
4:E:127:CYS:SG	4:E:128:PRO:HD2	2.29	0.73
1:A:41:ILE:HD11	1:A:51:GLU:HB3	1.71	0.73
2:B:46:LYS:HB2	2:B:276:SER:C	2.09	0.73
2:B:435:ALA:O	2:B:439:PHE:HB3	1.89	0.73
1:D:247:ILE:HG22	1:D:248:SER:N	2.04	0.73
1:D:419:ILE:HD12	1:D:420:ILE:N	2.04	0.73
4:E:33:LYS:CE	4:E:160:SER:HB2	2.19	0.73
4:E:148:GLN:CA	4:E:148:GLN:NE2	2.50	0.73
3:C:25:LYS:HG3	3:C:25:LYS:O	1.87	0.73
1:D:291:VAL:O	1:D:295:VAL:HG13	1.88	0.73
1:D:379:VAL:HA	1:D:382:ILE:CG1	2.19	0.73
4:E:27:VAL:HB	4:E:154:GLU:O	1.88	0.73
4:E:45:LYS:HE2	4:E:278:ASN:O	1.88	0.73
4:E:65:SER:HA	4:E:112:ASP:HA	1.70	0.73
4:E:448:LYS:N	4:E:448:LYS:HD2	2.02	0.73
1:A:67:TRP:HB2	1:A:112:TYR:O	1.89	0.73
3:C:194:HIS:CG	3:C:195:LYS:N	2.57	0.73
1:D:145:LYS:HG3	1:D:202:THR:HG23	0.85	0.73
1:A:233:PHE:CE1	1:A:413:VAL:HG11	2.23	0.72
1:A:416:LEU:O	1:A:419:ILE:HG22	1.87	0.72
2:B:93:MET:HB2	2:B:145:VAL:CG2	2.19	0.72
3:C:148:PHE:CB	3:C:215:VAL:CG2	2.63	0.72
3:C:196:PRO:HG2	3:C:218:TYR:HB2	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:273:PRO:HG2	4:E:274:GLU:H	1.53	0.72
4:E:431:ASP:O	4:E:435:GLU:HG3	1.88	0.72
2:B:55:PHE:N	2:B:55:PHE:HD1	1.85	0.72
1:D:181:TYR:HE1	1:D:203:TYR:HB3	1.53	0.72
1:D:201:ILE:O	1:D:203:TYR:HE1	1.72	0.72
4:E:42:LEU:HD22	4:E:183:TRP:CZ2	2.23	0.72
4:E:211:PHE:O	4:E:212:LEU:HD12	1.87	0.72
1:A:141:ASN:HB3	1:A:206:ILE:HG13	1.71	0.72
1:A:148:ILE:HD11	1:A:156:VAL:CG1	2.19	0.72
1:D:32:THR:HB	1:D:59:GLN:CB	2.15	0.72
1:D:92:LEU:HD13	1:D:146:LEU:HG	1.71	0.72
1:A:104:HIS:HB2	1:A:105:MET:SD	2.29	0.72
2:B:232:SER:O	2:B:236:ILE:HG22	1.89	0.72
1:D:142:CYS:SG	1:D:144:MET:HG3	2.29	0.72
1:A:77:LYS:O	1:A:77:LYS:CG	2.38	0.72
1:A:245:LEU:HD21	2:B:253:ILE:HB	1.70	0.72
1:A:251:LEU:HD22	4:E:260:ALA:HA	1.70	0.72
2:B:75:ILE:CG2	3:C:27:ASN:HB2	2.19	0.72
4:E:159:LEU:HD12	4:E:192:LYS:N	2.03	0.72
4:E:187:HIS:ND1	4:E:189:PRO:HG3	2.05	0.72
2:B:101:GLU:C	2:B:102:ILE:HG13	2.08	0.72
2:B:226:VAL:HG22	2:B:227:PRO:HD3	1.71	0.72
3:C:111:LEU:HB3	3:C:119:THR:OG1	1.89	0.72
4:E:26:HIS:O	4:E:27:VAL:HG22	1.89	0.72
1:A:110:LEU:HD12	1:A:111:ASP:H	1.55	0.72
1:A:274:ILE:O	1:A:277:TYR:HB2	1.89	0.72
1:A:401:TYR:CD1	1:A:401:TYR:O	2.43	0.72
3:C:201:ILE:HD12	3:C:213:GLN:OE1	1.90	0.72
3:C:257:MET:O	3:C:261:ILE:HG12	1.88	0.72
3:C:306:CYS:O	3:C:309:VAL:HB	1.88	0.72
1:D:64:ARG:HA	1:D:66:ARG:HH11	1.54	0.72
1:A:25:HIS:O	1:A:25:HIS:CG	2.42	0.72
1:A:38:ILE:O	1:A:38:ILE:CG2	2.37	0.72
1:A:56:LEU:O	1:A:119:THR:HA	1.90	0.72
1:A:262:GLU:C	1:A:265:PRO:HD2	2.10	0.72
2:B:220:TYR:HB3	2:B:223:TYR:CZ	2.23	0.72
1:D:43:VAL:HG22	1:D:50:VAL:CA	2.19	0.72
4:E:44:GLU:CG	4:E:129:ILE:HB	2.19	0.72
4:E:172:ILE:HD11	4:E:187:HIS:HA	1.71	0.72
2:B:258:ALA:HB2	3:C:265:LEU:HD22	1.71	0.72
3:C:232:PHE:C	3:C:235:PRO:HD2	2.10	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:250:LEU:HD22	1:D:292:THR:OG1	1.89	0.72
4:E:52:ASN:HD21	4:E:120:PRO:HB2	1.55	0.72
4:E:94:ASN:ND2	4:E:125:SER:HB2	2.03	0.72
2:B:92:LEU:HA	2:B:145:VAL:O	1.90	0.71
3:C:195:LYS:HG3	3:C:195:LYS:O	1.89	0.71
3:C:462:THR:HB	3:C:463:PRO:HD3	1.72	0.71
1:D:250:LEU:HD22	1:D:292:THR:CB	2.19	0.71
4:E:184:THR:O	4:E:214:ILE:HB	1.90	0.71
4:E:240:TYR:HB3	4:E:453:ILE:CD1	2.19	0.71
1:A:39:GLN:O	1:A:53:ASN:HB2	1.89	0.71
1:A:54:VAL:HG23	1:A:122:ALA:HB3	1.71	0.71
1:A:136:PRO:HD3	1:A:274:ILE:HG23	1.70	0.71
2:B:75:ILE:HG22	3:C:27:ASN:HB2	1.71	0.71
2:B:434:VAL:HG13	2:B:438:LEU:HD12	1.71	0.71
3:C:80:LEU:HD11	1:D:20:ARG:HH22	1.54	0.71
3:C:179:ILE:HG13	3:C:181:PRO:CD	2.21	0.71
1:D:7:LEU:O	1:D:11:LEU:HG	1.90	0.71
1:D:276:LYS:H	1:D:276:LYS:HD2	1.54	0.71
4:E:107:VAL:HG13	4:E:117:TRP:HB2	1.70	0.71
1:A:256:PHE:CZ	2:B:261:VAL:HG23	2.25	0.71
2:B:269:LYS:C	2:B:271:PRO:HD2	2.10	0.71
3:C:60:HIS:HB3	3:C:62:TRP:CZ3	2.16	0.71
3:C:293:MET:O	3:C:297:SER:HB3	1.89	0.71
1:D:43:VAL:CG1	1:D:50:VAL:HG22	2.19	0.71
4:E:44:GLU:HB3	4:E:280:PRO:CB	2.20	0.71
1:A:265:PRO:HG2	1:A:266:SER:H	1.55	0.71
2:B:183:ASN:HB2	3:C:50:GLU:OE2	1.90	0.71
2:B:311:THR:CB	2:B:430:TYR:CD2	2.74	0.71
3:C:36:SER:HB3	3:C:59:ASP:CB	2.20	0.71
4:E:48:ALA:HA	4:E:125:SER:O	1.90	0.71
1:A:139:GLN:NE2	1:A:206:ILE:HG23	2.05	0.71
1:A:292:THR:HA	1:A:296:ILE:HD11	1.73	0.71
3:C:35:LEU:HD22	3:C:215:VAL:HG21	1.73	0.71
3:C:143:ASN:OD1	3:C:220:ILE:HB	1.91	0.71
1:D:178:MET:SD	1:D:207:MET:HB3	2.30	0.71
4:E:191:LYS:HB2	4:E:209:ILE:CG2	2.20	0.71
2:B:160:HIS:NE2	2:B:207:VAL:HG11	2.05	0.71
3:C:271:LEU:HD21	3:C:299:VAL:HG11	1.71	0.71
4:E:65:SER:CB	4:E:112:ASP:HA	2.21	0.71
4:E:437:GLU:O	4:E:441:LEU:HG	1.90	0.71
3:C:38:THR:HG21	3:C:57:TRP:CE3	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:458:MET:HA	3:C:461:ILE:HD12	1.73	0.71
4:E:262:THR:HA	4:E:265:LEU:HB2	1.72	0.71
4:E:265:LEU:O	4:E:268:ILE:HG23	1.91	0.71
1:A:95:ASN:HA	1:A:127:TYR:HB3	1.73	0.71
1:A:250:LEU:HD22	1:A:292:THR:HG22	1.72	0.71
2:B:4:GLU:OE1	2:B:8:LEU:HG	1.91	0.71
3:C:80:LEU:O	3:C:112:VAL:HB	1.91	0.71
3:C:316:THR:HG22	3:C:317:PRO:CD	2.20	0.71
1:D:106:THR:C	1:D:107:LYS:HD3	2.09	0.71
1:D:287:SER:HA	1:D:290:ILE:HD13	1.72	0.71
1:A:251:LEU:HD13	4:E:260:ALA:HB3	1.72	0.71
3:C:190:TRP:HD1	3:C:221:ILE:HD12	1.52	0.71
3:C:307:GLY:O	3:C:310:LEU:HB2	1.91	0.71
1:A:72:TYR:CD1	1:A:72:TYR:C	2.63	0.71
2:B:21:PRO:HG2	2:B:85:VAL:CG1	2.21	0.71
3:C:64:ASP:O	3:C:116:GLY:HA3	1.91	0.71
4:E:100:GLU:HB2	4:E:122:ILE:HD11	1.71	0.71
2:B:35:LEU:CD2	2:B:56:LEU:HA	2.20	0.70
2:B:281:ILE:CG2	2:B:284:LEU:HB3	2.19	0.70
4:E:149:THR:HG23	4:E:150:TYR:H	1.55	0.70
2:B:175:ILE:CG1	2:B:176:ASN:H	2.02	0.70
3:C:55:ASN:HA	3:C:124:ALA:O	1.90	0.70
3:C:204:ASP:OD1	3:C:205:LYS:HD3	1.91	0.70
3:C:262:CYS:SG	1:D:251:LEU:CD1	2.78	0.70
4:E:138:TRP:CZ3	4:E:215:GLN:HA	2.26	0.70
4:E:239:VAL:HA	4:E:242:LEU:HD23	1.73	0.70
1:A:279:LEU:HA	1:A:282:MET:HB2	1.71	0.70
2:B:284:LEU:HD23	2:B:287:ILE:HD11	1.74	0.70
2:B:304:LEU:O	2:B:307:ARG:HB3	1.91	0.70
3:C:84:PRO:HG3	3:C:107:PHE:C	2.12	0.70
3:C:479:ASN:ND2	3:C:479:ASN:C	2.44	0.70
1:A:110:LEU:HD12	1:A:111:ASP:N	2.06	0.70
1:A:227:PHE:HA	1:A:230:VAL:HB	1.71	0.70
3:C:7:LEU:HD23	3:C:10:ASP:CB	2.22	0.70
1:D:86:TRP:CD2	1:D:86:TRP:C	2.64	0.70
4:E:44:GLU:OE1	4:E:129:ILE:HD12	1.91	0.70
4:E:235:LEU:C	4:E:235:LEU:CD1	2.53	0.70
1:A:158:ILE:O	1:A:199:LEU:HB2	1.91	0.70
3:C:115:ASN:ND2	3:C:115:ASN:N	2.36	0.70
3:C:206:PHE:C	3:C:206:PHE:CD1	2.64	0.70
3:C:470:ILE:O	3:C:474:VAL:HG23	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:45:LYS:CB	4:E:280:PRO:HA	2.20	0.70
3:C:247:PHE:CD1	3:C:309:VAL:HG22	2.27	0.70
1:D:169:THR:O	1:D:169:THR:CG2	2.36	0.70
4:E:6:LEU:HD12	4:E:69:SER:OG	1.91	0.70
4:E:436:ASN:CA	4:E:439:TRP:HE1	2.02	0.70
1:A:267:THR:O	1:A:271:VAL:HG22	1.90	0.70
1:A:384:GLU:HA	1:A:387:LYS:CG	2.22	0.70
2:B:85:VAL:HG12	2:B:86:TRP:N	2.05	0.70
1:D:60:TRP:CE2	1:D:86:TRP:CH2	2.80	0.70
1:D:229:THR:HA	1:D:232:VAL:HG23	1.73	0.70
1:D:419:ILE:HD12	1:D:420:ILE:CG2	2.22	0.70
4:E:22:LYS:HG3	4:E:23:THR:CB	2.21	0.70
4:E:291:PHE:O	4:E:295:VAL:HG23	1.91	0.70
1:A:66:ARG:CA	1:A:113:THR:HA	2.14	0.70
1:A:76:LYS:HG2	1:A:77:LYS:N	2.06	0.70
2:B:40:LEU:HD13	2:B:41:LEU:N	2.06	0.70
2:B:272:GLU:HG2	2:B:272:GLU:O	1.92	0.70
3:C:245:LEU:O	3:C:249:LEU:HD13	1.92	0.70
3:C:305:ASN:O	3:C:309:VAL:HG23	1.92	0.70
2:B:266:LEU:O	2:B:269:LYS:HG3	1.92	0.70
1:D:72:TYR:CD1	1:D:73:GLY:N	2.60	0.70
4:E:2:GLU:HA	4:E:5:ARG:CG	2.21	0.70
1:A:175:GLU:HB3	1:A:211:PRO:HD3	1.72	0.70
2:B:55:PHE:N	2:B:55:PHE:CD1	2.55	0.70
2:B:108:VAL:HG13	2:B:118:TRP:HB2	1.73	0.70
3:C:162:LEU:CD1	3:C:217:PHE:CE1	2.75	0.70
3:C:180:ASP:CB	3:C:181:PRO:HD3	2.11	0.70
1:D:171:MET:HG2	1:D:171:MET:O	1.92	0.70
1:D:261:VAL:HA	1:D:264:ILE:HD12	1.73	0.70
4:E:197:GLN:HG2	4:E:198:LEU:H	1.56	0.70
4:E:226:ILE:O	4:E:230:VAL:HG23	1.92	0.70
3:C:35:LEU:HD12	3:C:60:HIS:NE2	2.07	0.69
3:C:102:TYR:HE1	3:C:106:TYR:HB3	1.55	0.69
3:C:248:TYR:C	3:C:250:PRO:HD2	2.12	0.69
1:D:146:LEU:HD22	1:D:203:TYR:CZ	2.27	0.69
1:D:167:LEU:CG	1:D:178:MET:HB2	2.21	0.69
1:D:252:SER:O	1:D:255:VAL:HG12	1.92	0.69
1:A:148:ILE:CG2	1:A:198:TYR:CD2	2.74	0.69
2:B:295:VAL:O	2:B:299:VAL:HG23	1.93	0.69
3:C:262:CYS:SG	1:D:251:LEU:HD12	2.32	0.69
3:C:445:ASN:CA	3:C:448:LEU:HG	2.19	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:VAL:C	1:D:274:ILE:HG23	2.12	0.69
1:D:135:PHE:CZ	1:D:273:LEU:HD12	2.27	0.69
1:D:233:PHE:CZ	1:D:417:ILE:CD1	2.68	0.69
1:A:72:TYR:CB	1:A:112:TYR:CB	2.70	0.69
1:A:148:ILE:HG22	1:A:198:TYR:CD2	2.26	0.69
2:B:218:LEU:HD13	2:B:221:ILE:HG13	1.73	0.69
3:C:60:HIS:NE2	3:C:92:ILE:HG21	2.06	0.69
3:C:138:PRO:CD	3:C:288:ILE:HD12	2.22	0.69
1:D:49:ILE:CD1	1:D:125:LYS:HE3	2.22	0.69
1:D:107:LYS:HZ1	4:E:149:THR:HA	1.55	0.69
1:D:137:PHE:CD2	1:D:431:ILE:HB	2.26	0.69
1:D:167:LEU:N	1:D:167:LEU:HD12	2.06	0.69
1:D:245:LEU:HD11	4:E:252:THR:HA	1.74	0.69
4:E:279:VAL:CB	4:E:280:PRO:CD	2.65	0.69
1:A:17:LYS:HB3	1:A:84:ASP:HA	1.73	0.69
1:A:35:LEU:HD23	1:A:35:LEU:C	2.12	0.69
1:A:36:GLN:OE1	1:A:36:GLN:O	2.10	0.69
1:D:7:LEU:HD22	1:D:70:ALA:O	1.91	0.69
1:D:129:GLU:C	1:D:130:ILE:HG23	2.12	0.69
4:E:138:TRP:CE3	4:E:215:GLN:HA	2.28	0.69
4:E:270:GLN:C	4:E:273:PRO:HD2	2.12	0.69
1:A:76:LYS:HG3	1:A:112:TYR:CE2	2.27	0.69
3:C:137:PHE:HZ	3:C:291:TYR:CD2	2.10	0.69
1:D:20:ARG:HH11	1:D:20:ARG:CG	2.03	0.69
1:D:392:SER:O	1:D:395:ALA:HB3	1.91	0.69
4:E:266:PHE:CD1	4:E:266:PHE:O	2.45	0.69
4:E:444:LYS:O	4:E:448:LYS:HG2	1.91	0.69
2:B:2:VAL:HG12	2:B:3:MET:HE3	1.74	0.69
2:B:267:ALA:O	2:B:271:PRO:HD3	1.92	0.69
3:C:19:LYS:O	3:C:19:LYS:CD	2.41	0.69
3:C:42:LEU:HD13	3:C:190:TRP:HZ2	1.56	0.69
4:E:162:GLU:O	4:E:189:PRO:HA	1.91	0.69
1:D:102:ILE:HG23	4:E:98:GLN:HE21	1.57	0.69
1:D:152:ASP:HA	1:D:197:PRO:HA	1.74	0.69
1:D:166:ASP:CG	1:D:178:MET:HE2	2.12	0.69
1:D:178:MET:HA	1:D:207:MET:HB2	1.73	0.69
4:E:44:GLU:HA	4:E:129:ILE:HD11	1.74	0.69
1:A:67:TRP:HA	1:A:67:TRP:CE3	2.27	0.69
1:A:87:LEU:H	1:A:87:LEU:CD2	2.01	0.69
1:A:176:TRP:HA	1:A:209:ARG:HG3	1.74	0.69
1:A:426:PHE:HD1	1:A:427:ALA:N	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:THR:HG23	2:B:129:THR:O	1.93	0.69
2:B:449:ILE:HA	2:B:452:PHE:CD2	2.27	0.69
3:C:106:TYR:C	3:C:107:PHE:HD1	1.95	0.69
1:D:195:ASP:O	1:D:197:PRO:HD3	1.93	0.69
1:A:56:LEU:HD22	1:A:58:GLN:HG3	1.75	0.69
2:B:33:VAL:HG21	2:B:158:LEU:HD13	1.74	0.69
2:B:409:LYS:CE	3:C:423:ILE:HG23	2.23	0.69
3:C:230:ILE:HG13	3:C:231:ASN:ND2	2.07	0.69
1:D:86:TRP:O	1:D:86:TRP:CE2	2.44	0.69
4:E:138:TRP:CB	4:E:213:ILE:HG12	2.21	0.69
2:B:38:THR:HG22	2:B:55:PHE:CE1	2.27	0.69
3:C:137:PHE:CD1	3:C:137:PHE:O	2.46	0.69
3:C:279:PRO:CA	3:C:282:ALA:HB3	2.22	0.69
1:D:60:TRP:CZ2	1:D:86:TRP:CH2	2.80	0.69
1:A:155:LYS:CE	4:E:76:LEU:HD13	2.22	0.68
2:B:241:LEU:HD21	2:B:251:LEU:CD1	2.08	0.68
3:C:102:TYR:CE1	3:C:106:TYR:HB3	2.29	0.68
3:C:179:ILE:CG2	3:C:181:PRO:HD2	2.22	0.68
1:D:239:SER:O	1:D:242:LYS:HG2	1.92	0.68
4:E:217:LYS:N	4:E:218:PRO:HD2	2.08	0.68
4:E:255:ILE:HG22	4:E:256:SER:N	2.06	0.68
1:A:221:PRO:C	1:A:224:LEU:HB3	2.13	0.68
2:B:11:LEU:HD22	2:B:11:LEU:N	2.08	0.68
1:D:245:LEU:HD21	4:E:255:ILE:CG1	2.23	0.68
1:D:257:LEU:HD12	1:D:258:LEU:N	2.09	0.68
4:E:253:LEU:HG	4:E:254:SER:N	2.08	0.68
1:A:41:ILE:CD1	1:A:51:GLU:HB3	2.22	0.68
1:A:261:VAL:O	1:A:261:VAL:CG1	2.42	0.68
1:A:286:ILE:HG22	1:A:286:ILE:O	1.93	0.68
2:B:212:ILE:HG22	2:B:212:ILE:O	1.92	0.68
3:C:269:VAL:HG13	3:C:270:PHE:CE1	2.27	0.68
1:D:215:VAL:O	1:D:219:ILE:HG23	1.93	0.68
4:E:89:VAL:O	4:E:90:VAL:HG23	1.92	0.68
2:B:263:LEU:CD2	2:B:291:VAL:CG2	2.71	0.68
3:C:191:GLU:HG3	3:C:222:ARG:HB3	1.76	0.68
1:D:53:ASN:HB2	1:D:123:ILE:HG12	1.74	0.68
1:D:112:TYR:HD1	1:D:113:THR:H	1.41	0.68
4:E:34:LEU:HD12	4:E:210:PHE:HE2	1.55	0.68
1:A:41:ILE:HG13	1:A:42:ASN:N	2.08	0.68
2:B:56:LEU:O	2:B:120:PRO:HD2	1.93	0.68
2:B:89:ASP:OD1	2:B:148:SER:HB2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:PHE:HE1	1:D:277:TYR:CE2	2.10	0.68
4:E:146:ARG:HD2	4:E:205:PHE:CD2	2.29	0.68
4:E:182:GLU:HA	4:E:218:PRO:CG	2.23	0.68
4:E:313:THR:HB	4:E:441:LEU:HB3	1.73	0.68
2:B:35:LEU:N	2:B:35:LEU:CD2	2.55	0.68
3:C:271:LEU:HD23	3:C:271:LEU:C	2.13	0.68
1:D:140:GLN:HG3	1:D:141:ASN:H	1.58	0.68
1:D:227:PHE:O	1:D:230:VAL:HG12	1.93	0.68
1:A:24:HIS:CD2	1:A:24:HIS:N	2.62	0.68
1:A:247:ILE:O	1:A:247:ILE:CD1	2.42	0.68
3:C:7:LEU:HA	3:C:10:ASP:OD2	1.94	0.68
1:D:78:ILE:O	1:D:78:ILE:CD1	2.40	0.68
1:D:106:THR:CG2	1:D:107:LYS:H	1.98	0.68
1:D:420:ILE:HA	1:D:423:VAL:CG2	2.24	0.68
4:E:42:LEU:HD22	4:E:183:TRP:CE2	2.28	0.68
4:E:45:LYS:HA	4:E:280:PRO:CA	2.16	0.68
4:E:138:TRP:HH2	4:E:215:GLN:NE2	1.91	0.68
4:E:236:VAL:O	4:E:239:VAL:HG23	1.93	0.68
4:E:284:LYS:HE3	4:E:284:LYS:H	1.56	0.68
1:A:29:VAL:HB	1:A:31:ILE:HD12	1.76	0.68
3:C:12:LEU:HB2	3:C:16:LYS:CG	2.20	0.68
1:D:141:ASN:HB3	1:D:206:ILE:CD1	2.24	0.68
1:D:252:SER:OG	4:E:259:LEU:HD22	1.93	0.68
4:E:102:ALA:HB2	4:E:121:ALA:HB2	1.75	0.68
1:A:274:ILE:HG12	1:A:277:TYR:CD1	2.26	0.68
2:B:55:PHE:HA	2:B:120:PRO:O	1.94	0.68
2:B:145:VAL:HA	2:B:207:VAL:O	1.93	0.68
2:B:406:GLU:HG2	2:B:409:LYS:HD2	1.76	0.68
3:C:199:LYS:NZ	3:C:199:LYS:O	2.27	0.68
3:C:270:PHE:CD1	3:C:270:PHE:N	2.60	0.68
3:C:438:ALA:HA	3:C:441:GLU:CD	2.15	0.68
1:D:187:TRP:CH2	1:D:189:TYR:HB3	2.29	0.68
4:E:126:THR:O	4:E:126:THR:HG22	1.92	0.68
1:A:422:THR:O	1:A:425:VAL:HG12	1.93	0.68
2:B:421:PHE:HA	2:B:424:LEU:HB2	1.75	0.68
3:C:242:LEU:HD22	3:C:267:GLN:CB	2.12	0.68
3:C:316:THR:CG2	3:C:317:PRO:CD	2.72	0.68
1:D:92:LEU:CD2	1:D:92:LEU:H	2.06	0.68
1:D:166:ASP:HB3	1:D:167:LEU:HD12	1.75	0.68
1:A:220:ILE:N	1:A:221:PRO:HD2	2.10	0.67
1:D:129:GLU:O	1:D:142:CYS:HB2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:167:LEU:CD1	1:D:178:MET:CB	2.70	0.67
1:D:260:ILE:O	1:D:264:ILE:HG13	1.94	0.67
4:E:172:ILE:CD1	4:E:188:ARG:N	2.58	0.67
4:E:453:ILE:HD12	4:E:454:ALA:N	2.09	0.67
1:A:89:ASP:HB2	1:A:149:TRP:HD1	1.54	0.67
1:A:90:LEU:HD13	1:A:100:PHE:HE2	1.58	0.67
1:A:175:GLU:HB3	1:A:211:PRO:CD	2.23	0.67
1:A:406:ILE:HG23	1:A:409:ILE:CD1	2.24	0.67
3:C:36:SER:HB3	3:C:59:ASP:HB3	1.75	0.67
3:C:138:PRO:CG	3:C:288:ILE:CD1	2.71	0.67
3:C:180:ASP:HB3	3:C:181:PRO:CD	2.21	0.67
1:D:80:LEU:O	1:D:108:LEU:HB3	1.95	0.67
1:D:260:ILE:HG22	1:D:264:ILE:CD1	2.24	0.67
4:E:214:ILE:C	4:E:214:ILE:HD12	2.13	0.67
1:A:139:GLN:OE1	1:A:179:LYS:HG3	1.95	0.67
2:B:58:LEU:HD11	2:B:118:TRP:CE3	2.28	0.67
2:B:439:PHE:O	2:B:442:ILE:HG22	1.95	0.67
3:C:77:ILE:O	3:C:77:ILE:HG13	1.93	0.67
3:C:122:PRO:CB	3:C:123:PRO:CD	2.61	0.67
3:C:462:THR:N	3:C:463:PRO:HD2	2.09	0.67
1:D:76:LYS:HG2	1:D:112:TYR:CD2	2.29	0.67
1:D:287:SER:O	1:D:291:VAL:HG23	1.95	0.67
1:D:395:ALA:HB1	1:D:399:TRP:CZ2	2.29	0.67
4:E:2:GLU:CA	4:E:5:ARG:HG3	2.24	0.67
4:E:20:PRO:HG2	4:E:28:ILE:HD12	1.74	0.67
4:E:47:GLU:CA	4:E:129:ILE:HD11	2.20	0.67
4:E:67:ASN:H	4:E:67:ASN:ND2	1.82	0.67
2:B:40:LEU:HD13	2:B:40:LEU:C	2.15	0.67
3:C:106:TYR:HD1	3:C:106:TYR:C	1.96	0.67
3:C:191:GLU:HG2	3:C:222:ARG:C	2.13	0.67
3:C:220:ILE:O	3:C:220:ILE:CG1	2.42	0.67
3:C:264:LEU:HA	3:C:267:GLN:HG3	1.75	0.67
1:D:296:ILE:HA	1:D:299:HIS:HB3	1.76	0.67
1:D:305:THR:OG1	1:D:305:THR:O	2.12	0.67
1:A:2:GLU:O	1:A:2:GLU:CG	2.34	0.67
1:A:107:LYS:HE3	2:B:150:THR:CB	2.25	0.67
1:A:118:TRP:CD1	1:A:120:PRO:HD3	2.29	0.67
1:A:124:PHE:CD1	1:A:124:PHE:C	2.67	0.67
2:B:143:THR:HG23	2:B:208:THR:HG23	1.77	0.67
2:B:279:ILE:HG22	2:B:280:ILE:N	2.08	0.67
3:C:69:TRP:HE3	3:C:73:GLU:HB3	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:269:VAL:HG13	3:C:270:PHE:HD1	1.55	0.67
1:D:28:PHE:HA	1:D:155:LYS:O	1.93	0.67
1:D:166:ASP:N	1:D:181:TYR:HB3	2.10	0.67
4:E:131:VAL:HG12	4:E:131:VAL:O	1.94	0.67
4:E:188:ARG:HG3	4:E:188:ARG:O	1.94	0.67
1:A:209:ARG:CG	1:A:210:ILE:H	2.07	0.67
1:A:384:GLU:OE2	1:A:387:LYS:HE2	1.95	0.67
3:C:137:PHE:CD1	3:C:288:ILE:CG2	2.77	0.67
3:C:273:LEU:HD23	3:C:276:GLN:HB2	1.75	0.67
1:D:426:PHE:CE1	1:D:430:LEU:CD1	2.78	0.67
4:E:172:ILE:CG2	4:E:174:PRO:HD2	2.24	0.67
4:E:224:ASN:OD1	4:E:224:ASN:O	2.11	0.67
1:A:139:GLN:HB2	1:A:207:MET:O	1.95	0.67
1:A:216:VAL:CG1	1:A:220:ILE:HD11	2.25	0.67
2:B:56:LEU:N	2:B:56:LEU:HD12	2.08	0.67
2:B:101:GLU:O	2:B:102:ILE:HG13	1.94	0.67
2:B:218:LEU:CD1	2:B:221:ILE:CG1	2.72	0.67
1:D:187:TRP:HB2	1:D:199:LEU:HD21	1.77	0.67
1:D:382:ILE:O	1:D:386:MET:HG2	1.94	0.67
4:E:56:GLU:CA	4:E:118:LEU:HB2	2.21	0.67
4:E:83:LEU:HD22	4:E:83:LEU:N	2.10	0.67
4:E:172:ILE:HG23	4:E:174:PRO:CD	2.24	0.67
1:A:79:ARG:HH11	1:A:107:LYS:NZ	1.93	0.67
1:A:148:ILE:CG2	1:A:198:TYR:CB	2.72	0.67
2:B:236:ILE:O	2:B:240:TYR:HB2	1.95	0.67
3:C:30:VAL:HG13	3:C:31:VAL:C	2.16	0.67
3:C:226:LEU:H	3:C:227:PHE:HD1	1.40	0.67
1:D:259:VAL:HG13	1:D:262:GLU:OE1	1.95	0.67
4:E:77:VAL:CG1	4:E:78:ARG:H	2.07	0.67
4:E:146:ARG:HB3	4:E:207:GLU:HA	1.77	0.67
1:A:238:ASP:CB	2:B:306:HIS:CE1	2.75	0.67
2:B:40:LEU:HD22	2:B:51:THR:O	1.94	0.67
2:B:112:HIS:CG	2:B:113:THR:H	2.12	0.67
2:B:279:ILE:CG2	2:B:280:ILE:N	2.58	0.67
3:C:199:LYS:HD2	3:C:200:ASN:N	2.10	0.67
1:D:62:ASP:CB	1:D:65:LEU:HD13	2.11	0.67
1:A:34:GLY:CA	1:A:57:ARG:HG2	2.25	0.67
1:A:34:GLY:HA3	1:A:57:ARG:HG2	1.77	0.67
1:A:76:LYS:HA	1:A:112:TYR:CD2	2.29	0.67
1:A:176:TRP:CE3	1:A:209:ARG:NH2	2.63	0.67
2:B:259:LEU:HD23	2:B:259:LEU:O	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:ILE:HG22	2:B:293:PHE:CZ	2.29	0.67
1:D:60:TRP:CZ2	1:D:86:TRP:CZ3	2.83	0.67
1:A:168:SER:OG	1:A:169:THR:HG23	1.95	0.66
2:B:48:GLU:HB2	2:B:130:ILE:CG1	2.22	0.66
1:D:35:LEU:CD2	1:D:164:ARG:NH1	2.56	0.66
1:D:287:SER:HA	1:D:290:ILE:HG12	1.77	0.66
4:E:54:TRP:CB	4:E:118:LEU:HD11	2.21	0.66
1:A:108:LEU:CD1	1:A:118:TRP:HB2	2.24	0.66
1:A:136:PRO:HA	1:A:277:TYR:OH	1.95	0.66
1:A:216:VAL:HG12	1:A:220:ILE:HD12	1.75	0.66
2:B:270:VAL:HG11	2:B:284:LEU:CG	2.25	0.66
1:D:7:LEU:HA	1:D:10:ASN:ND2	2.10	0.66
4:E:33:LYS:HE3	4:E:160:SER:HB2	1.78	0.66
4:E:44:GLU:HB3	4:E:280:PRO:CD	2.26	0.66
4:E:75:ASP:HB3	4:E:110:TYR:CZ	2.31	0.66
1:A:156:VAL:CG2	1:A:157:SER:N	2.57	0.66
1:A:209:ARG:HG2	1:A:210:ILE:H	1.59	0.66
2:B:93:MET:HG3	2:B:206:ASP:CG	2.15	0.66
2:B:160:HIS:H	2:B:195:LYS:NZ	1.93	0.66
2:B:297:LEU:CD1	2:B:445:THR:CG2	2.72	0.66
2:B:304:LEU:O	2:B:304:LEU:HD23	1.96	0.66
1:D:109:LEU:HD12	1:D:117:MET:HB3	1.77	0.66
1:D:129:GLU:O	1:D:130:ILE:HG23	1.95	0.66
1:D:229:THR:HA	1:D:232:VAL:CG2	2.25	0.66
1:D:254:THR:HG23	1:D:255:VAL:N	2.09	0.66
1:D:292:THR:HA	1:D:295:VAL:CG2	2.25	0.66
1:A:145:LYS:NZ	1:A:202:THR:CG2	2.58	0.66
2:B:296:ILE:O	2:B:296:ILE:HG22	1.96	0.66
3:C:270:PHE:N	3:C:270:PHE:HD1	1.92	0.66
1:D:104:HIS:HB2	1:D:105:MET:SD	2.35	0.66
4:E:44:GLU:CD	4:E:129:ILE:CB	2.60	0.66
1:A:29:VAL:HG21	1:A:86:TRP:CZ3	2.31	0.66
1:A:107:LYS:O	1:A:108:LEU:HD23	1.96	0.66
1:A:155:LYS:HG3	4:E:78:ARG:HE	1.60	0.66
1:A:216:VAL:CG1	1:A:220:ILE:CD1	2.74	0.66
1:A:389:ASP:O	1:A:392:SER:HB3	1.94	0.66
1:D:110:LEU:HD12	1:D:111:ASP:H	1.60	0.66
2:B:92:LEU:HD22	2:B:146:PHE:CD1	2.30	0.66
2:B:261:VAL:HG12	2:B:262:PHE:HD1	1.60	0.66
2:B:269:LYS:HE3	2:B:270:VAL:CG2	2.25	0.66
3:C:138:PRO:HB3	3:C:290:LYS:NZ	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:177:VAL:HG12	1:D:208:GLN:HG2	1.77	0.66
1:D:257:LEU:HD12	1:D:257:LEU:C	2.15	0.66
4:E:71:TYR:HD1	4:E:111:ASN:ND2	1.92	0.66
1:A:35:LEU:HD23	1:A:36:GLN:N	2.09	0.66
1:A:201:ILE:HG21	1:A:203:TYR:HE1	1.60	0.66
1:A:218:VAL:CG1	1:A:219:ILE:N	2.59	0.66
1:A:239:SER:HB2	2:B:312:HIS:HB3	1.76	0.66
1:A:265:PRO:CA	1:A:268:SER:HB3	2.25	0.66
2:B:429:GLN:HA	2:B:429:GLN:HE21	1.60	0.66
3:C:233:ILE:HD13	3:C:233:ILE:N	2.10	0.66
1:D:137:PHE:O	1:D:435:GLN:HA	1.96	0.66
2:B:82:SER:O	2:B:83:ASP:HB3	1.94	0.66
2:B:176:ASN:HD22	2:B:188:ILE:HG21	1.61	0.66
3:C:138:PRO:HB2	3:C:140:ASP:OD1	1.96	0.66
3:C:195:LYS:HE3	3:C:217:PHE:HB3	1.78	0.66
3:C:199:LYS:HZ2	3:C:199:LYS:C	1.99	0.66
3:C:243:ALA:CB	3:C:302:VAL:CG1	2.72	0.66
1:D:249:VAL:O	1:D:253:LEU:HB3	1.95	0.66
1:A:134:HIS:CD2	1:A:207:MET:CE	2.79	0.66
1:A:384:GLU:CD	2:B:411:ILE:HG21	2.16	0.66
1:D:107:LYS:HB3	4:E:150:TYR:HE1	1.61	0.66
1:D:220:ILE:HG21	4:E:294:LEU:CD1	2.19	0.66
4:E:103:TYR:CG	4:E:104:TYR:N	2.61	0.66
1:A:187:TRP:CH2	1:A:189:TYR:CB	2.78	0.66
2:B:56:LEU:HD23	2:B:103:THR:HG23	1.78	0.66
2:B:290:LEU:HD21	2:B:453:SER:CB	2.26	0.66
1:D:289:ILE:HG22	1:D:290:ILE:N	2.11	0.66
4:E:309:ARG:HD2	4:E:310:THR:OG1	1.96	0.66
1:A:380:LYS:HD3	2:B:408:ILE:HG21	1.76	0.65
2:B:440:LEU:O	2:B:443:PHE:HB3	1.96	0.65
3:C:482:PRO:HG2	3:C:483:ALA:N	2.10	0.65
1:D:132:VAL:HB	1:D:274:ILE:HA	1.76	0.65
4:E:77:VAL:CG1	4:E:78:ARG:N	2.59	0.65
1:A:139:GLN:NE2	1:A:206:ILE:CG2	2.59	0.65
3:C:42:LEU:CD2	3:C:190:TRP:CH2	2.77	0.65
3:C:98:ASN:C	3:C:100:GLY:H	2.00	0.65
3:C:274:THR:HG22	3:C:275:SER:N	2.11	0.65
3:C:455:ARG:O	3:C:459:PHE:HD1	1.80	0.65
1:D:177:VAL:O	1:D:207:MET:HB2	1.96	0.65
4:E:56:GLU:N	4:E:118:LEU:HD13	2.12	0.65
4:E:237:VAL:CG2	4:E:457:LEU:HD21	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:HIS:NE2	1:A:207:MET:HE3	2.10	0.65
3:C:18:ASN:HB2	3:C:21:VAL:HB	1.78	0.65
3:C:80:LEU:CD1	1:D:20:ARG:HH22	2.08	0.65
3:C:153:TYR:O	3:C:212:TYR:HB3	1.96	0.65
1:D:40:LEU:CD1	1:D:52:THR:HB	2.24	0.65
1:D:176:TRP:HB3	1:D:209:ARG:CD	2.24	0.65
1:D:287:SER:HA	1:D:290:ILE:CG1	2.25	0.65
1:D:393:SER:O	1:D:396:ALA:HB3	1.97	0.65
4:E:144:VAL:HG12	4:E:209:ILE:CA	2.26	0.65
4:E:221:TYR:N	4:E:221:TYR:CD1	2.63	0.65
4:E:252:THR:O	4:E:255:ILE:HB	1.96	0.65
3:C:69:TRP:CD1	3:C:114:PRO:C	2.69	0.65
4:E:39:LEU:CD1	4:E:49:LEU:HD13	2.25	0.65
3:C:223:ARG:HG2	3:C:224:LYS:N	2.12	0.65
3:C:230:ILE:HG13	3:C:231:ASN:N	2.11	0.65
1:D:37:LEU:CD1	1:D:54:VAL:HG13	2.25	0.65
4:E:183:TRP:HB3	4:E:216:ARG:NE	2.11	0.65
4:E:262:THR:O	4:E:262:THR:HG22	1.95	0.65
1:A:34:GLY:HA3	1:A:57:ARG:HD3	1.79	0.65
3:C:19:LYS:O	3:C:19:LYS:HD2	1.96	0.65
3:C:38:THR:OG1	3:C:178:ILE:HD13	1.97	0.65
3:C:447:ASN:O	3:C:449:VAL:HG23	1.96	0.65
1:D:92:LEU:N	1:D:92:LEU:CD2	2.58	0.65
1:D:178:MET:SD	1:D:207:MET:CB	2.85	0.65
4:E:235:LEU:HA	4:E:238:LEU:HG	1.77	0.65
1:A:190:TYR:HB2	1:A:192:CYS:SG	2.36	0.65
1:D:75:ILE:HG13	1:D:78:ILE:CG2	2.27	0.65
1:D:379:VAL:O	1:D:379:VAL:HG12	1.96	0.65
4:E:9:LYS:HG3	4:E:10:LEU:N	2.11	0.65
4:E:152:ALA:HB3	4:E:204:ASP:O	1.96	0.65
4:E:182:GLU:HG3	4:E:218:PRO:O	1.96	0.65
1:A:224:LEU:CG	1:A:225:PHE:N	2.58	0.65
1:A:235:LEU:HB3	1:A:236:PRO:CD	2.27	0.65
3:C:11:LEU:O	3:C:16:LYS:HB2	1.97	0.65
3:C:60:HIS:CD2	3:C:92:ILE:CD1	2.80	0.65
3:C:434:LYS:HD3	3:C:435:GLU:CG	2.25	0.65
1:D:107:LYS:HB3	4:E:150:TYR:CE1	2.31	0.65
1:D:152:ASP:CA	1:D:197:PRO:HA	2.26	0.65
1:A:17:LYS:HE3	1:A:84:ASP:CA	2.22	0.65
1:A:68:ASN:CG	1:A:69:PRO:HD2	2.18	0.65
1:A:160:PRO:HG3	1:A:185:LYS:HE2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:GLU:HA	1:A:400:LYS:HD2	1.78	0.65
2:B:46:LYS:HB2	2:B:278:PRO:HD3	1.79	0.65
3:C:106:TYR:C	3:C:106:TYR:CD1	2.69	0.65
3:C:247:PHE:CE1	3:C:309:VAL:CG2	2.80	0.65
3:C:319:THR:O	3:C:319:THR:HG22	1.97	0.65
3:C:443:VAL:HA	3:C:446:TRP:HD1	1.61	0.65
1:D:21:PRO:HB3	1:D:62:ASP:OD2	1.96	0.65
4:E:159:LEU:CD1	4:E:192:LYS:HB2	2.27	0.65
4:E:284:LYS:HE3	4:E:284:LYS:CA	2.27	0.65
1:A:41:ILE:HD11	1:A:51:GLU:CB	2.26	0.65
2:B:111:GLN:HB2	2:B:115:ALA:HB3	1.78	0.65
2:B:438:LEU:HA	2:B:441:TYR:HB3	1.78	0.65
3:C:33:ILE:HG22	3:C:160:MET:SD	2.37	0.65
3:C:205:LYS:HD3	3:C:205:LYS:H	1.61	0.65
1:D:302:SER:CB	1:D:305:THR:HG23	2.26	0.65
4:E:76:LEU:HD23	4:E:77:VAL:N	2.12	0.65
4:E:148:GLN:HE21	4:E:148:GLN:N	1.94	0.65
1:A:45:GLU:OE1	1:A:271:VAL:HB	1.97	0.64
2:B:198:ARG:HH11	2:B:198:ARG:HG3	1.62	0.64
3:C:63:TYR:CE1	3:C:116:GLY:HA3	2.32	0.64
3:C:69:TRP:HB2	3:C:74:TYR:N	2.12	0.64
3:C:102:TYR:HD1	3:C:102:TYR:O	1.79	0.64
1:D:219:ILE:HD12	1:D:219:ILE:O	1.97	0.64
4:E:293:SER:O	4:E:296:ILE:HG12	1.97	0.64
1:A:137:PHE:CE1	1:A:210:ILE:HD12	2.33	0.64
1:A:301:ARG:HH11	1:A:301:ARG:HG2	1.61	0.64
1:A:394:ASN:O	1:A:398:GLU:HG3	1.97	0.64
3:C:137:PHE:CZ	3:C:291:TYR:CE2	2.86	0.64
1:D:167:LEU:CD1	1:D:167:LEU:N	2.60	0.64
4:E:191:LYS:O	4:E:209:ILE:HG22	1.96	0.64
4:E:272:VAL:O	4:E:272:VAL:CG2	2.42	0.64
1:A:52:THR:O	1:A:123:ILE:HA	1.96	0.64
2:B:132:VAL:HG12	2:B:280:ILE:N	2.10	0.64
2:B:252:SER:O	2:B:255:ALA:HB3	1.98	0.64
3:C:4:GLU:HG3	3:C:5:GLU:N	2.09	0.64
1:D:213:TYR:O	1:D:216:VAL:HG23	1.97	0.64
1:A:179:LYS:HE2	1:A:208:GLN:CD	2.17	0.64
2:B:276:SER:OG	2:B:277:VAL:HG13	1.98	0.64
1:D:379:VAL:HA	1:D:382:ILE:HG13	1.79	0.64
4:E:131:VAL:HA	4:E:281:LEU:O	1.97	0.64
4:E:184:THR:HG23	4:E:215:GLN:HG2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:189:PRO:HD2	4:E:211:PHE:CB	2.12	0.64
4:E:267:LEU:HD12	4:E:270:GLN:OE1	1.96	0.64
4:E:276:SER:HB3	4:E:281:LEU:HD13	1.78	0.64
1:A:31:ILE:CG1	1:A:60:TRP:HB3	2.27	0.64
1:A:92:LEU:HB2	1:A:96:ALA:H	1.60	0.64
1:A:108:LEU:HB3	1:A:117:MET:O	1.97	0.64
2:B:138:ASP:HB3	2:B:464:PRO:O	1.98	0.64
1:D:20:ARG:HG2	1:D:20:ARG:NH1	1.92	0.64
4:E:172:ILE:CD1	4:E:187:HIS:HA	2.28	0.64
1:A:245:LEU:HD13	2:B:250:SER:HB2	1.79	0.64
1:D:58:GLN:NE2	1:D:88:PRO:HG3	2.13	0.64
4:E:227:ALA:N	4:E:228:PRO:CD	2.61	0.64
4:E:237:VAL:HG21	4:E:457:LEU:HD21	1.80	0.64
2:B:142:CYS:O	2:B:210:TYR:HD1	1.80	0.64
2:B:150:THR:O	2:B:150:THR:HG22	1.97	0.64
3:C:30:VAL:HG22	3:C:157:GLU:C	2.18	0.64
3:C:42:LEU:HA	3:C:54:THR:CG2	2.26	0.64
3:C:58:MET:SD	3:C:92:ILE:CD1	2.86	0.64
1:D:78:ILE:HD11	1:D:110:LEU:HG	1.80	0.64
1:D:92:LEU:HB2	1:D:95:ASN:HB2	1.80	0.64
4:E:38:ASN:O	4:E:51:THR:HA	1.96	0.64
4:E:215:GLN:HG3	4:E:216:ARG:N	2.13	0.64
1:A:15:TYR:CE2	1:A:84:ASP:HB3	2.32	0.64
1:A:20:ARG:HB3	1:A:86:TRP:CD2	2.33	0.64
1:A:106:THR:HG22	1:A:107:LYS:N	2.12	0.64
1:A:171:MET:HE1	1:A:176:TRP:CH2	2.31	0.64
2:B:3:MET:O	2:B:7:LEU:HG	1.98	0.64
2:B:278:PRO:CG	2:B:278:PRO:O	2.45	0.64
3:C:429:ILE:O	3:C:433:ILE:HG13	1.98	0.64
1:A:212:LEU:HA	1:A:215:VAL:HG23	1.79	0.64
3:C:137:PHE:CZ	3:C:291:TYR:CD2	2.86	0.64
3:C:273:LEU:HD23	3:C:276:GLN:CG	2.28	0.64
1:D:77:LYS:HB2	1:D:111:ASP:OD1	1.98	0.64
1:D:134:HIS:C	1:D:134:HIS:ND1	2.50	0.64
2:B:92:LEU:HD13	2:B:146:PHE:CE1	2.32	0.64
3:C:110:VAL:HG13	3:C:120:TRP:CB	2.27	0.64
1:D:92:LEU:HD13	1:D:146:LEU:CG	2.28	0.64
1:D:164:ARG:HH11	1:D:181:TYR:HE2	1.45	0.64
1:D:211:PRO:HB3	1:D:213:TYR:HD2	1.62	0.64
4:E:52:ASN:HA	4:E:121:ALA:O	1.97	0.64
1:A:20:ARG:NH1	1:A:20:ARG:CG	2.58	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:HD13	1:A:118:TRP:CB	2.28	0.63
1:A:239:SER:HB2	2:B:312:HIS:CB	2.29	0.63
2:B:175:ILE:HG12	2:B:177:GLN:H	1.63	0.63
2:B:254:SER:O	3:C:265:LEU:HD11	1.98	0.63
3:C:435:GLU:O	3:C:438:ALA:HB3	1.98	0.63
1:D:263:LEU:HD11	4:E:266:PHE:CE2	2.33	0.63
4:E:89:VAL:HG23	4:E:99:PHE:CE1	2.33	0.63
1:A:139:GLN:HE21	1:A:206:ILE:HG23	1.62	0.63
1:A:414:PHE:HA	1:A:417:ILE:HD12	1.80	0.63
2:B:56:LEU:HD13	2:B:120:PRO:O	1.98	0.63
2:B:138:ASP:HA	2:B:464:PRO:O	1.98	0.63
1:D:152:ASP:CB	1:D:197:PRO:HA	2.27	0.63
4:E:269:ALA:O	4:E:273:PRO:HD3	1.98	0.63
1:A:146:LEU:HD12	1:A:146:LEU:N	2.13	0.63
2:B:128:CYS:SG	2:B:144:MET:CG	2.86	0.63
2:B:296:ILE:O	2:B:296:ILE:CG2	2.46	0.63
2:B:415:LEU:HD13	2:B:415:LEU:C	2.18	0.63
3:C:155:ALA:CB	3:C:211:ASN:HA	2.28	0.63
3:C:199:LYS:HZ3	3:C:200:ASN:HA	1.63	0.63
3:C:234:THR:N	3:C:235:PRO:HD2	2.13	0.63
1:D:167:LEU:HG	1:D:178:MET:HB2	1.79	0.63
4:E:82:GLU:C	4:E:83:LEU:HD22	2.18	0.63
1:A:34:GLY:HA3	1:A:57:ARG:CG	2.29	0.63
1:D:282:MET:HG3	1:D:286:ILE:CD1	2.27	0.63
2:B:141:ASN:HD21	2:B:212:ILE:HG12	1.64	0.63
2:B:155:GLU:O	2:B:156:VAL:HB	1.99	0.63
2:B:218:LEU:HD13	2:B:221:ILE:HD11	1.79	0.63
1:D:176:TRP:CE3	1:D:209:ARG:NE	2.66	0.63
1:D:391:GLU:HA	1:D:394:ASN:OD1	1.98	0.63
1:A:54:VAL:HG22	1:A:122:ALA:HB3	1.81	0.63
1:A:136:PRO:HG3	1:A:274:ILE:CG2	2.28	0.63
1:A:305:THR:O	1:A:306:HIS:HB3	1.97	0.63
3:C:113:ARG:HG3	3:C:117:TYR:O	1.97	0.63
3:C:158:ILE:HG23	3:C:159:SER:N	2.14	0.63
3:C:426:THR:O	3:C:426:THR:CG2	2.33	0.63
1:D:253:LEU:HD23	1:D:254:THR:CA	2.27	0.63
4:E:34:LEU:HB2	4:E:210:PHE:HZ	1.64	0.63
1:A:72:TYR:CB	1:A:112:TYR:HB2	2.28	0.63
1:A:144:MET:HB2	1:A:203:TYR:HB2	1.78	0.63
1:A:160:PRO:HG2	1:A:185:LYS:HZ3	1.64	0.63
1:A:265:PRO:HG2	1:A:266:SER:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ILE:CG2	1:A:420:ILE:H	2.12	0.63
1:D:231:LEU:O	1:D:235:LEU:HG	1.98	0.63
1:A:176:TRP:CA	1:A:209:ARG:HG3	2.28	0.63
1:A:212:LEU:HA	1:A:215:VAL:CG2	2.29	0.63
1:A:243:MET:HG2	1:A:244:THR:H	1.63	0.63
2:B:186:TRP:CB	2:B:215:ARG:HB2	2.12	0.63
3:C:266:ALA:CB	1:D:251:LEU:HD13	2.28	0.63
1:D:135:PHE:C	1:D:135:PHE:HD1	2.01	0.63
1:D:176:TRP:CZ3	1:D:209:ARG:CZ	2.82	0.63
1:D:253:LEU:HD23	1:D:254:THR:HB	1.79	0.63
2:B:112:HIS:CG	2:B:113:THR:N	2.66	0.63
2:B:242:PRO:HB3	2:B:305:HIS:HE1	1.63	0.63
3:C:179:ILE:CD1	3:C:195:LYS:CB	2.72	0.63
3:C:259:THR:O	3:C:263:VAL:HG23	1.98	0.63
1:D:387:LYS:O	1:D:391:GLU:HG3	1.99	0.63
4:E:55:ILE:N	4:E:118:LEU:CD1	2.61	0.63
4:E:136:PHE:HA	4:E:138:TRP:CZ3	2.33	0.63
4:E:212:LEU:O	4:E:214:ILE:HG23	1.98	0.63
1:A:306:HIS:O	1:A:306:HIS:CD2	2.51	0.62
2:B:134:TYR:HE1	2:B:213:ILE:CG1	2.09	0.62
2:B:218:LEU:HD13	2:B:221:ILE:CD1	2.28	0.62
1:D:75:ILE:HD12	1:D:78:ILE:HG22	1.81	0.62
1:D:171:MET:SD	1:D:176:TRP:CH2	2.92	0.62
4:E:77:VAL:HG13	4:E:78:ARG:H	1.63	0.62
1:A:60:TRP:NE1	1:A:116:ILE:HD12	2.13	0.62
2:B:93:MET:HG3	2:B:206:ASP:HB3	1.77	0.62
2:B:175:ILE:HD12	2:B:190:HIS:HD2	1.64	0.62
3:C:59:ASP:CG	3:C:121:LEU:HD22	2.19	0.62
3:C:137:PHE:CD1	3:C:288:ILE:CB	2.83	0.62
3:C:206:PHE:CD1	3:C:206:PHE:O	2.52	0.62
1:D:296:ILE:HG22	1:D:299:HIS:ND1	2.14	0.62
1:D:398:GLU:HG3	1:D:399:TRP:CE3	2.34	0.62
4:E:19:LYS:HZ1	4:E:154:GLU:HB3	1.64	0.62
4:E:33:LYS:NZ	4:E:160:SER:HB2	2.14	0.62
4:E:54:TRP:C	4:E:118:LEU:CD1	2.67	0.62
4:E:453:ILE:O	4:E:457:LEU:HB2	1.99	0.62
1:A:34:GLY:HA3	1:A:57:ARG:CD	2.30	0.62
2:B:11:LEU:HD22	2:B:11:LEU:H	1.64	0.62
2:B:242:PRO:CB	2:B:243:PRO:HD3	2.29	0.62
3:C:431:LYS:HE2	1:D:379:VAL:CG2	2.29	0.62
1:D:292:THR:O	1:D:296:ILE:HG12	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:384:GLU:OE1	1:D:384:GLU:HA	1.99	0.62
1:A:37:LEU:HA	1:A:53:ASN:O	1.99	0.62
1:A:133:THR:O	1:A:136:PRO:HG2	2.00	0.62
1:A:156:VAL:CG2	1:A:157:SER:H	2.12	0.62
2:B:85:VAL:O	2:B:87:GLN:HG3	1.99	0.62
1:D:75:ILE:CD1	1:D:78:ILE:HG22	2.28	0.62
1:D:280:PHE:N	1:D:280:PHE:CD1	2.63	0.62
4:E:182:GLU:CD	4:E:220:PHE:HE2	2.02	0.62
2:B:45:GLU:CG	2:B:277:VAL:HB	2.27	0.62
1:D:36:GLN:HE21	1:D:38:ILE:HG13	1.64	0.62
2:B:270:VAL:N	2:B:271:PRO:HD2	2.15	0.62
2:B:408:ILE:CG2	2:B:409:LYS:N	2.61	0.62
3:C:33:ILE:HG12	3:C:62:TRP:HB3	1.81	0.62
3:C:113:ARG:HB3	3:C:114:PRO:HD2	1.81	0.62
3:C:160:MET:H	3:C:213:GLN:CB	2.12	0.62
4:E:246:ALA:HB1	4:E:250:LYS:CG	2.16	0.62
1:A:46:VAL:HA	1:A:272:PRO:HD2	1.82	0.62
1:A:252:SER:OG	2:B:257:LEU:HD22	1.99	0.62
1:A:286:ILE:O	1:A:286:ILE:CG2	2.47	0.62
3:C:191:GLU:CD	3:C:222:ARG:HB3	2.19	0.62
1:D:92:LEU:HD21	1:D:124:PHE:CZ	2.35	0.62
1:D:111:ASP:OD2	1:D:115:LYS:HB3	1.98	0.62
4:E:32:LEU:HD12	4:E:208:ILE:HD11	1.81	0.62
1:A:291:VAL:O	1:A:294:VAL:HG12	2.00	0.62
4:E:32:LEU:HD12	4:E:157:LEU:HD13	1.81	0.62
4:E:33:LYS:HE3	4:E:160:SER:CB	2.29	0.62
4:E:79:ILE:O	4:E:79:ILE:HG22	1.99	0.62
4:E:140:ASN:OD1	4:E:211:PHE:HB3	2.00	0.62
1:A:75:ILE:HG13	1:A:78:ILE:CG2	2.29	0.62
1:A:235:LEU:HB3	1:A:236:PRO:HD3	1.80	0.62
1:A:282:MET:O	1:A:285:VAL:HG12	2.00	0.62
2:B:283:TYR:HA	2:B:286:PHE:CZ	2.35	0.62
3:C:58:MET:O	3:C:58:MET:HG2	2.00	0.62
3:C:147:LYS:HE2	3:C:216:THR:HG23	1.81	0.62
3:C:319:THR:O	3:C:319:THR:HG23	1.98	0.62
1:D:282:MET:CE	1:D:286:ILE:HD11	2.30	0.62
4:E:61:ASP:OD1	4:E:63:ARG:HB3	1.99	0.62
1:A:41:ILE:CD1	1:A:51:GLU:CD	2.66	0.62
1:A:67:TRP:CG	1:A:71:ASP:HB3	2.34	0.62
1:A:121:PRO:HB2	2:B:149:TYR:CZ	2.34	0.62
1:A:245:LEU:HD13	2:B:250:SER:CB	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:408:ILE:HG13	2:B:408:ILE:O	1.97	0.62
3:C:279:PRO:HA	3:C:282:ALA:HB2	1.80	0.62
3:C:422:GLY:O	3:C:425:SER:HB2	2.00	0.62
3:C:478:PHE:C	3:C:478:PHE:HD1	2.03	0.62
4:E:213:ILE:HG23	4:E:213:ILE:O	2.00	0.62
4:E:219:LEU:HB3	4:E:222:ILE:CG2	2.30	0.62
1:A:105:MET:O	1:A:105:MET:HG2	1.99	0.61
1:A:132:VAL:O	1:A:274:ILE:HG22	2.00	0.61
2:B:195:LYS:HA	2:B:207:VAL:HG13	1.82	0.61
2:B:261:VAL:HG12	2:B:262:PHE:CD1	2.34	0.61
2:B:283:TYR:HD1	2:B:283:TYR:H	1.48	0.61
2:B:287:ILE:HA	2:B:290:LEU:CD1	2.29	0.61
2:B:438:LEU:O	2:B:442:ILE:HB	2.00	0.61
3:C:11:LEU:C	3:C:16:LYS:HG3	2.20	0.61
3:C:52:LEU:HD22	3:C:52:LEU:N	2.14	0.61
3:C:81:ARG:NH1	3:C:111:LEU:HB2	2.14	0.61
1:D:102:ILE:O	1:D:102:ILE:HG22	2.00	0.61
4:E:159:LEU:CD1	4:E:191:LYS:C	2.69	0.61
4:E:238:LEU:C	4:E:242:LEU:HD23	2.21	0.61
1:A:274:ILE:HD13	1:A:277:TYR:HE1	1.64	0.61
2:B:11:LEU:H	2:B:11:LEU:CD2	2.13	0.61
2:B:47:ASN:HB2	2:B:49:GLU:CD	2.19	0.61
2:B:58:LEU:CD1	2:B:118:TRP:HB3	2.29	0.61
3:C:63:TYR:HD1	3:C:64:ASP:N	1.98	0.61
3:C:263:VAL:CA	1:D:251:LEU:HD11	2.31	0.61
1:A:379:VAL:HA	1:A:382:ILE:HD11	1.81	0.61
2:B:274:SER:HB2	2:B:278:PRO:CB	2.29	0.61
3:C:146:LEU:HD12	3:C:146:LEU:N	2.15	0.61
3:C:180:ASP:OD2	3:C:192:ILE:HG21	1.99	0.61
3:C:193:ILE:HD11	3:C:222:ARG:HB2	1.82	0.61
1:D:48:GLN:CB	1:D:130:ILE:CD1	2.65	0.61
1:D:138:ASP:OD1	1:D:138:ASP:N	2.33	0.61
4:E:32:LEU:HA	4:E:56:GLU:O	2.01	0.61
4:E:44:GLU:HA	4:E:129:ILE:HD12	1.81	0.61
4:E:284:LYS:CE	4:E:284:LYS:H	2.12	0.61
1:A:148:ILE:CG2	1:A:148:ILE:O	2.49	0.61
1:A:416:LEU:O	1:A:420:ILE:HG23	2.01	0.61
2:B:35:LEU:HD22	2:B:55:PHE:O	2.01	0.61
2:B:270:VAL:N	2:B:271:PRO:CD	2.64	0.61
3:C:69:TRP:HZ2	3:C:112:VAL:HG12	1.66	0.61
3:C:243:ALA:HB3	3:C:302:VAL:CG1	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:475:MET:HA	3:C:478:PHE:CZ	2.35	0.61
1:D:106:THR:CG2	1:D:107:LYS:HE2	2.30	0.61
4:E:14:TYR:CE1	4:E:84:LEU:CD1	2.83	0.61
4:E:55:ILE:O	4:E:118:LEU:HB2	2.01	0.61
4:E:55:ILE:HG23	4:E:119:PRO:CD	2.29	0.61
1:A:62:ASP:HB3	1:A:65:LEU:HG	1.81	0.61
1:A:108:LEU:HD22	1:A:118:TRP:HA	1.82	0.61
2:B:160:HIS:NE2	2:B:209:PHE:CE1	2.58	0.61
3:C:160:MET:H	3:C:213:GLN:CG	2.13	0.61
3:C:228:TYR:CD1	3:C:229:VAL:N	2.68	0.61
4:E:59:TRP:CD2	4:E:115:MET:HB2	2.36	0.61
1:A:201:ILE:CG2	1:A:203:TYR:HE1	2.14	0.61
2:B:285:MET:O	2:B:289:ILE:HG12	1.99	0.61
3:C:50:GLU:CG	3:C:132:ILE:HB	2.27	0.61
3:C:106:TYR:CE1	3:C:107:PHE:HE1	2.19	0.61
1:D:260:ILE:CG2	1:D:264:ILE:HD11	2.30	0.61
1:D:419:ILE:HD12	1:D:420:ILE:HG22	1.83	0.61
4:E:14:TYR:HE1	4:E:84:LEU:CD1	2.12	0.61
4:E:22:LYS:HG3	4:E:23:THR:N	2.16	0.61
4:E:185:ILE:HG12	4:E:214:ILE:HG21	1.82	0.61
4:E:414:SER:N	4:E:416:VAL:HG13	2.15	0.61
1:A:17:LYS:CE	1:A:84:ASP:HA	2.25	0.61
1:A:34:GLY:HA3	1:A:161:GLU:CD	2.21	0.61
1:A:46:VAL:CG2	1:A:270:ALA:C	2.69	0.61
1:A:233:PHE:HE1	1:A:413:VAL:HG11	1.63	0.61
2:B:3:MET:O	2:B:6:THR:HB	2.01	0.61
2:B:108:VAL:HG22	2:B:118:TRP:CG	2.36	0.61
2:B:108:VAL:HG22	2:B:118:TRP:HB2	1.83	0.61
2:B:270:VAL:CG1	2:B:284:LEU:CD1	2.74	0.61
3:C:90:PRO:HD2	3:C:120:TRP:CZ3	2.34	0.61
3:C:316:THR:HG22	3:C:317:PRO:N	2.14	0.61
1:D:381:TYR:CE1	4:E:419:CYS:SG	2.93	0.61
1:A:37:LEU:HD23	1:A:54:VAL:HG12	1.82	0.61
2:B:40:LEU:HA	2:B:52:THR:HG23	1.81	0.61
2:B:187:SER:OG	2:B:216:LYS:HE2	2.01	0.61
2:B:226:VAL:HG23	2:B:227:PRO:HD3	1.82	0.61
2:B:244:ASP:CG	3:C:314:PHE:HE1	2.04	0.61
3:C:66:ARG:HG2	3:C:66:ARG:HH11	1.65	0.61
3:C:93:VAL:CB	3:C:151:LEU:HD22	2.31	0.61
3:C:147:LYS:HE2	3:C:216:THR:CG2	2.31	0.61
3:C:241:PHE:HA	3:C:244:ALA:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:102:ILE:HG12	4:E:98:GLN:HE21	1.66	0.61
1:D:106:THR:CG2	1:D:107:LYS:HD3	2.31	0.61
4:E:56:GLU:CB	4:E:118:LEU:HD22	2.29	0.61
4:E:305:ASN:HA	4:E:308:LEU:CD1	2.25	0.61
1:A:207:MET:O	1:A:207:MET:CE	2.49	0.61
2:B:56:LEU:CD2	2:B:103:THR:HG23	2.31	0.61
2:B:176:ASN:ND2	2:B:188:ILE:HD12	2.15	0.61
2:B:439:PHE:O	2:B:439:PHE:CD1	2.54	0.61
3:C:93:VAL:HG21	3:C:151:LEU:HD22	1.82	0.61
1:D:60:TRP:CZ3	1:D:116:ILE:HG13	2.36	0.61
1:D:257:LEU:HA	1:D:260:ILE:CG1	2.31	0.61
4:E:61:ASP:O	4:E:113:GLY:HA2	2.00	0.61
4:E:91:LEU:HB2	4:E:95:VAL:HG23	1.83	0.61
4:E:138:TRP:CH2	4:E:215:GLN:CG	2.84	0.61
4:E:159:LEU:HD12	4:E:191:LYS:C	2.21	0.61
2:B:134:TYR:CE1	2:B:213:ILE:CG1	2.77	0.61
2:B:189:GLU:HG3	2:B:468:PHE:CB	2.30	0.61
2:B:442:ILE:O	2:B:446:MET:HG2	2.01	0.61
3:C:69:TRP:CE3	3:C:73:GLU:HB3	2.36	0.61
3:C:190:TRP:HB2	3:C:223:ARG:HB2	1.82	0.61
3:C:200:ASN:ND2	3:C:201:ILE:H	1.98	0.61
3:C:247:PHE:HA	3:C:250:PRO:HG3	1.81	0.61
3:C:319:THR:CB	3:C:447:ASN:HB3	2.31	0.61
4:E:31:THR:HA	4:E:158:GLN:HG3	1.83	0.61
4:E:74:ILE:HG12	4:E:76:LEU:O	2.01	0.61
4:E:195:ASN:OD1	4:E:204:ASP:HA	2.01	0.61
1:A:27:HIS:C	1:A:28:PHE:CG	2.74	0.60
2:B:35:LEU:HD13	2:B:55:PHE:O	2.01	0.60
2:B:87:GLN:CB	2:B:104:LEU:HD11	2.13	0.60
3:C:269:VAL:HA	3:C:272:LEU:HD11	1.81	0.60
1:D:222:CYS:SG	1:D:225:PHE:CZ	2.92	0.60
4:E:20:PRO:HG3	4:E:61:ASP:CG	2.21	0.60
4:E:209:ILE:HG12	4:E:211:PHE:CE1	2.35	0.60
1:A:58:GLN:HB3	1:A:60:TRP:CZ3	2.36	0.60
1:A:100:PHE:HB3	1:A:103:VAL:HG21	1.82	0.60
1:A:175:GLU:OE1	1:A:175:GLU:HA	2.01	0.60
2:B:58:LEU:HD11	2:B:118:TRP:HB3	1.83	0.60
3:C:81:ARG:NH1	3:C:111:LEU:HD13	2.14	0.60
4:E:50:THR:HA	4:E:123:TYR:O	2.00	0.60
4:E:250:LYS:HD2	4:E:253:LEU:HD22	1.83	0.60
1:A:134:HIS:CD2	1:A:207:MET:HE3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LYS:HZ2	1:A:202:THR:CG2	2.13	0.60
2:B:37:LEU:HD23	2:B:179:ALA:HB3	1.83	0.60
2:B:197:TRP:CD1	2:B:204:TYR:HB3	2.36	0.60
1:D:44:ASP:OD2	1:D:46:VAL:HG23	2.01	0.60
1:D:175:GLU:HB3	1:D:211:PRO:HG3	1.81	0.60
4:E:138:TRP:CH2	4:E:215:GLN:CD	2.75	0.60
4:E:173:ASP:OD1	4:E:173:ASP:O	2.19	0.60
1:A:174:GLY:HA2	1:A:176:TRP:CZ3	2.36	0.60
1:A:207:MET:O	1:A:207:MET:HE3	2.01	0.60
2:B:32:ARG:HE	2:B:59:ALA:C	2.04	0.60
2:B:69:PRO:O	2:B:73:GLU:HB2	2.01	0.60
3:C:238:LEU:HA	3:C:241:PHE:CE2	2.36	0.60
1:D:36:GLN:HE21	1:D:38:ILE:CG1	2.15	0.60
1:D:107:LYS:HE3	4:E:149:THR:CA	2.29	0.60
1:D:381:TYR:O	1:D:385:HIS:HB2	2.00	0.60
2:B:145:VAL:CG1	2:B:206:ASP:HB2	2.32	0.60
2:B:153:THR:HG23	2:B:156:VAL:O	2.01	0.60
3:C:58:MET:HE1	3:C:120:TRP:CZ2	2.36	0.60
3:C:78:SER:C	3:C:114:PRO:HB3	2.21	0.60
1:D:187:TRP:CZ3	1:D:189:TYR:HD1	2.16	0.60
1:D:379:VAL:CA	1:D:382:ILE:HD12	2.30	0.60
4:E:182:GLU:HA	4:E:218:PRO:HG3	1.83	0.60
4:E:214:ILE:HD12	4:E:215:GLN:N	2.16	0.60
4:E:222:ILE:HG23	4:E:223:ILE:N	2.15	0.60
1:A:58:GLN:NE2	1:A:90:LEU:HD11	2.16	0.60
1:A:100:PHE:HB3	1:A:103:VAL:CG2	2.30	0.60
2:B:34:GLY:C	2:B:35:LEU:CD2	2.69	0.60
2:B:111:GLN:CD	2:B:115:ALA:HB3	2.21	0.60
4:E:140:ASN:C	4:E:140:ASN:ND2	2.53	0.60
1:A:93:TYR:CD2	1:A:145:LYS:HB3	2.37	0.60
1:A:135:PHE:N	1:A:136:PRO:CD	2.63	0.60
1:A:250:LEU:CD2	1:A:292:THR:CG2	2.78	0.60
1:A:305:THR:HB	1:A:400:LYS:HB2	1.83	0.60
2:B:75:ILE:HG22	3:C:27:ASN:CB	2.32	0.60
3:C:43:ILE:HD12	3:C:43:ILE:N	2.17	0.60
3:C:247:PHE:CE1	3:C:309:VAL:HA	2.37	0.60
1:D:56:LEU:N	1:D:120:PRO:HD2	2.17	0.60
1:D:91:VAL:CG2	1:D:96:ALA:CB	2.80	0.60
1:D:137:PHE:HD2	1:D:431:ILE:HB	1.67	0.60
1:D:192:CYS:SG	1:D:193:CYS:N	2.75	0.60
1:D:259:VAL:HA	1:D:262:GLU:OE2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:301:ARG:HH12	1:D:406:ILE:CD1	2.15	0.60
1:D:432:GLU:HG2	1:D:435:GLN:HE21	1.65	0.60
4:E:14:TYR:HE2	4:E:16:LYS:CE	2.12	0.60
4:E:36:LEU:CD2	4:E:51:THR:CG2	2.74	0.60
4:E:101:VAL:CG2	4:E:101:VAL:O	2.50	0.60
1:A:74:GLY:O	1:A:75:ILE:HG23	2.01	0.60
1:A:76:LYS:HG3	1:A:112:TYR:CZ	2.37	0.60
2:B:187:SER:C	2:B:188:ILE:HG12	2.20	0.60
2:B:239:PHE:HB3	2:B:442:ILE:HG12	1.83	0.60
3:C:460:ILE:HG22	3:C:461:ILE:N	2.15	0.60
1:D:414:PHE:HE1	1:D:418:CYS:HG	1.50	0.60
4:E:182:GLU:OE1	4:E:220:PHE:HE2	1.84	0.60
1:A:75:ILE:HG13	1:A:78:ILE:HG21	1.83	0.60
3:C:129:SER:O	3:C:129:SER:OG	2.20	0.60
1:D:43:VAL:HG11	1:D:50:VAL:HG22	1.83	0.60
1:D:75:ILE:HD11	1:D:78:ILE:CG2	2.32	0.60
1:D:103:VAL:HG13	1:D:118:TRP:CZ2	2.37	0.60
1:D:141:ASN:HB3	1:D:206:ILE:HD11	1.83	0.60
4:E:49:LEU:O	4:E:124:ARG:HD2	2.02	0.60
4:E:75:ASP:HB3	4:E:110:TYR:CE1	2.37	0.60
4:E:146:ARG:NH1	4:E:205:PHE:CB	2.60	0.60
1:A:242:LYS:HB2	1:A:245:LEU:HB3	1.83	0.60
2:B:46:LYS:HB3	2:B:276:SER:O	2.02	0.60
2:B:104:LEU:CD1	2:B:118:TRP:HH2	2.06	0.60
3:C:58:MET:SD	3:C:92:ILE:HD11	2.42	0.60
3:C:247:PHE:C	3:C:250:PRO:CD	2.70	0.60
3:C:276:GLN:C	3:C:279:PRO:HD2	2.22	0.60
3:C:463:PRO:O	3:C:467:LEU:HD23	2.02	0.60
1:D:145:LYS:C	1:D:146:LEU:CD1	2.66	0.60
1:D:379:VAL:HG22	1:D:382:ILE:CD1	2.32	0.60
1:D:409:ILE:HG13	1:D:410:LEU:N	2.16	0.60
1:A:72:TYR:CB	1:A:112:TYR:HD2	2.09	0.59
1:A:157:SER:HB2	1:A:199:LEU:CD1	2.32	0.59
2:B:82:SER:C	2:B:84:ASP:H	2.05	0.59
3:C:76:ASP:C	3:C:77:ILE:HG23	2.21	0.59
4:E:31:THR:CB	4:E:58:GLN:HB2	2.31	0.59
4:E:86:LEU:HD13	4:E:103:TYR:CE1	2.37	0.59
1:A:66:ARG:O	1:A:66:ARG:CD	2.50	0.59
1:A:107:LYS:HE3	2:B:150:THR:HG22	1.82	0.59
2:B:56:LEU:HD22	2:B:120:PRO:HG3	1.82	0.59
3:C:135:LEU:C	3:C:137:PHE:H	2.06	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:247:PHE:CD2	3:C:460:ILE:CD1	2.84	0.59
1:D:49:ILE:HG21	1:D:125:LYS:HZ2	1.65	0.59
4:E:47:GLU:HB3	4:E:129:ILE:CD1	2.31	0.59
2:B:46:LYS:CB	2:B:278:PRO:HD3	2.32	0.59
2:B:238:VAL:HG22	2:B:255:ALA:CB	2.31	0.59
2:B:450:GLY:O	2:B:454:ILE:HG13	2.01	0.59
3:C:234:THR:O	3:C:238:LEU:HD13	2.02	0.59
1:D:409:ILE:O	1:D:412:CYS:HB3	2.02	0.59
4:E:289:VAL:HG12	4:E:290:MET:N	2.18	0.59
2:B:188:ILE:CG2	2:B:190:HIS:H	2.14	0.59
1:D:65:LEU:HD23	1:D:110:LEU:CD1	2.25	0.59
1:D:419:ILE:CD1	1:D:420:ILE:CG2	2.80	0.59
1:D:420:ILE:HA	1:D:423:VAL:HG23	1.84	0.59
1:A:80:LEU:CD2	1:A:110:LEU:HB2	2.32	0.59
1:A:148:ILE:O	1:A:148:ILE:HG23	2.00	0.59
2:B:153:THR:CB	2:B:204:TYR:HB2	2.20	0.59
3:C:67:LEU:HD11	3:C:112:VAL:HG13	1.84	0.59
1:D:187:TRP:CB	1:D:199:LEU:HD23	2.27	0.59
4:E:55:ILE:CG2	4:E:119:PRO:HG2	2.31	0.59
4:E:83:LEU:N	4:E:83:LEU:CD2	2.64	0.59
4:E:271:LYS:HB2	4:E:271:LYS:NZ	2.14	0.59
1:A:32:THR:HG23	1:A:159:SER:O	2.02	0.59
1:A:245:LEU:CD2	2:B:253:ILE:HB	2.32	0.59
3:C:67:LEU:HD11	3:C:112:VAL:CG1	2.32	0.59
4:E:468:THR:HG22	4:E:468:THR:O	2.03	0.59
1:A:1:SER:N	1:A:4:GLU:HB2	2.18	0.59
1:A:243:MET:HG2	1:A:244:THR:N	2.16	0.59
1:A:296:ILE:HD13	1:A:296:ILE:N	2.17	0.59
1:D:45:GLU:OE2	1:D:271:VAL:HG22	2.03	0.59
1:D:171:MET:HG2	1:D:174:GLY:N	2.13	0.59
1:D:409:ILE:HA	1:D:412:CYS:HB2	1.85	0.59
4:E:41:SER:O	4:E:49:LEU:HA	2.03	0.59
4:E:250:LYS:HB3	4:E:253:LEU:CD2	2.27	0.59
1:A:3:HIS:O	1:A:7:LEU:HG	2.02	0.59
1:A:41:ILE:HD11	1:A:51:GLU:CG	2.32	0.59
1:A:93:TYR:N	1:A:93:TYR:CD1	2.63	0.59
2:B:28:LYS:HD3	2:B:154:SER:O	2.03	0.59
3:C:84:PRO:HG3	3:C:107:PHE:O	2.03	0.59
3:C:219:LEU:HD11	3:C:221:ILE:HG22	1.83	0.59
3:C:249:LEU:N	3:C:250:PRO:CD	2.64	0.59
1:D:134:HIS:C	1:D:134:HIS:HD1	2.06	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:PHE:N	1:D:136:PRO:CD	2.66	0.59
4:E:14:TYR:CE1	4:E:84:LEU:HD12	2.38	0.59
4:E:80:PRO:HB2	4:E:83:LEU:HD23	1.85	0.59
4:E:138:TRP:CB	4:E:213:ILE:CG1	2.68	0.59
1:A:7:LEU:HD22	1:A:70:ALA:O	2.02	0.59
2:B:33:VAL:HG11	2:B:158:LEU:HD11	1.85	0.59
2:B:135:PHE:HD2	2:B:283:TYR:CE1	2.20	0.59
2:B:184:GLY:C	2:B:186:TRP:H	2.06	0.59
2:B:265:LEU:HA	2:B:268:ASP:OD2	2.02	0.59
3:C:84:PRO:HD2	3:C:85:GLU:OE1	2.02	0.59
3:C:225:PRO:O	3:C:226:LEU:HD23	2.03	0.59
3:C:461:ILE:O	3:C:464:VAL:HG12	2.03	0.59
1:D:223:LEU:HD23	1:D:223:LEU:C	2.23	0.59
4:E:432:SER:O	4:E:435:GLU:HB2	2.03	0.59
1:A:59:GLN:HE22	1:A:117:MET:HG3	1.66	0.59
1:A:90:LEU:O	1:A:91:VAL:HG23	2.03	0.59
1:A:108:LEU:HD21	1:A:118:TRP:CD1	2.38	0.59
2:B:258:ALA:HB2	3:C:265:LEU:CD1	2.33	0.59
2:B:308:SER:HB2	2:B:311:THR:CG2	2.04	0.59
1:D:390:GLU:O	1:D:393:SER:HB2	2.03	0.59
4:E:44:GLU:OE2	4:E:129:ILE:HB	2.00	0.59
4:E:138:TRP:CD1	4:E:213:ILE:HG12	2.38	0.59
4:E:182:GLU:HA	4:E:218:PRO:HG2	1.84	0.59
4:E:416:VAL:HG22	4:E:417:GLU:H	1.68	0.59
1:A:145:LYS:NZ	1:A:202:THR:HG23	2.17	0.58
2:B:153:THR:O	2:B:204:TYR:HD2	1.84	0.58
2:B:248:LYS:NZ	2:B:252:SER:CB	2.66	0.58
3:C:270:PHE:CE1	1:D:255:VAL:CG2	2.86	0.58
1:D:261:VAL:O	1:D:261:VAL:CG1	2.51	0.58
4:E:45:LYS:N	4:E:280:PRO:CA	2.66	0.58
4:E:135:PRO:HB2	4:E:137:ASP:OD1	2.03	0.58
4:E:313:THR:HG21	4:E:441:LEU:CA	2.32	0.58
1:A:35:LEU:HD13	1:A:203:TYR:OH	2.03	0.58
2:B:285:MET:O	2:B:288:MET:HB3	2.03	0.58
3:C:93:VAL:HG21	3:C:151:LEU:CD2	2.33	0.58
3:C:104:VAL:O	3:C:123:PRO:HG2	2.03	0.58
1:D:33:VAL:HA	1:D:57:ARG:O	2.04	0.58
4:E:35:THR:HB	4:E:54:TRP:CE3	2.37	0.58
4:E:71:TYR:HD1	4:E:111:ASN:CG	2.05	0.58
4:E:77:VAL:HB	4:E:109:VAL:O	2.02	0.58
1:A:187:TRP:HD1	1:A:199:LEU:HD23	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ILE:CD1	1:A:247:ILE:C	2.72	0.58
3:C:35:LEU:HD21	3:C:37:LEU:CD2	2.33	0.58
4:E:287:ILE:HG13	4:E:291:PHE:CD2	2.38	0.58
1:A:89:ASP:OD1	1:A:89:ASP:C	2.40	0.58
1:A:90:LEU:HD12	1:A:100:PHE:HE2	1.68	0.58
1:A:148:ILE:CD1	1:A:156:VAL:HG13	2.29	0.58
1:A:236:PRO:HG3	1:A:299:HIS:NE2	2.18	0.58
2:B:49:GLU:HA	2:B:127:SER:HA	1.86	0.58
2:B:95:ASN:HB3	2:B:127:SER:H	1.67	0.58
2:B:290:LEU:HD21	2:B:453:SER:HB3	1.83	0.58
3:C:33:ILE:CG2	3:C:160:MET:SD	2.90	0.58
3:C:204:ASP:H	3:C:207:PRO:HG2	1.68	0.58
4:E:36:LEU:HD23	4:E:51:THR:CG2	2.26	0.58
4:E:45:LYS:HG2	4:E:279:VAL:HA	1.85	0.58
4:E:212:LEU:HD12	4:E:212:LEU:N	2.18	0.58
1:A:216:VAL:HG13	1:A:220:ILE:CD1	2.34	0.58
2:B:10:VAL:CG1	2:B:11:LEU:HD22	2.30	0.58
2:B:278:PRO:C	2:B:279:ILE:HG13	2.24	0.58
2:B:291:VAL:HG12	2:B:292:ALA:N	2.18	0.58
3:C:482:PRO:CG	3:C:483:ALA:H	2.15	0.58
1:D:166:ASP:CB	1:D:181:TYR:HB2	2.33	0.58
1:D:187:TRP:CH2	1:D:189:TYR:CD1	2.91	0.58
1:D:243:MET:HE2	1:D:243:MET:N	2.19	0.58
1:D:291:VAL:O	1:D:295:VAL:HG22	2.04	0.58
4:E:9:LYS:O	4:E:9:LYS:HD2	2.03	0.58
4:E:103:TYR:C	4:E:104:TYR:CD1	2.77	0.58
1:A:43:VAL:HG22	1:A:50:VAL:CG1	2.33	0.58
1:A:50:VAL:HG12	1:A:51:GLU:N	2.17	0.58
1:A:52:THR:C	1:A:123:ILE:HG13	2.23	0.58
1:A:107:LYS:HG2	2:B:150:THR:CG2	2.31	0.58
2:B:186:TRP:CE3	2:B:215:ARG:CZ	2.87	0.58
1:D:30:ASP:O	1:D:60:TRP:HB2	2.02	0.58
1:D:45:GLU:CD	1:D:271:VAL:HG22	2.23	0.58
1:D:62:ASP:O	1:D:65:LEU:HB2	2.04	0.58
4:E:27:VAL:CG1	4:E:153:HIS:C	2.71	0.58
1:A:148:ILE:HG23	1:A:198:TYR:HD2	1.68	0.58
1:A:419:ILE:HG23	1:A:420:ILE:N	2.16	0.58
2:B:185:GLN:CD	2:B:219:PHE:CE2	2.77	0.58
2:B:241:LEU:N	2:B:242:PRO:HD2	2.19	0.58
3:C:42:LEU:CA	3:C:54:THR:HG22	2.30	0.58
3:C:452:THR:O	3:C:452:THR:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:34:LEU:HB2	4:E:210:PHE:CZ	2.38	0.58
4:E:242:LEU:C	4:E:242:LEU:HD12	2.24	0.58
2:B:91:VAL:HA	2:B:96:ASN:CG	2.24	0.58
2:B:230:LEU:CA	2:B:233:ILE:HG13	2.29	0.58
2:B:279:ILE:HG22	2:B:280:ILE:HD13	1.84	0.58
3:C:3:GLU:O	3:C:7:LEU:HB2	2.04	0.58
3:C:228:TYR:HD1	3:C:229:VAL:H	1.52	0.58
3:C:426:THR:HA	3:C:429:ILE:HG23	1.85	0.58
1:D:76:LYS:HD2	1:D:112:TYR:HE2	1.68	0.58
1:D:106:THR:HG23	1:D:107:LYS:CD	2.32	0.58
1:D:228:LEU:HD11	4:E:258:LEU:HD21	1.84	0.58
4:E:416:VAL:CG2	4:E:417:GLU:N	2.65	0.58
1:A:6:ARG:HB3	1:A:6:ARG:HH11	1.67	0.58
1:A:64:ARG:CA	1:A:66:ARG:HH11	2.11	0.58
1:A:107:LYS:HE3	2:B:150:THR:HB	1.80	0.58
1:A:255:VAL:CG2	1:A:258:LEU:HD12	2.30	0.58
2:B:130:ILE:O	2:B:134:TYR:HB2	2.04	0.58
2:B:185:GLN:CG	2:B:219:PHE:HE2	2.16	0.58
3:C:59:ASP:OD1	3:C:121:LEU:HD13	2.03	0.58
3:C:142:GLN:HG3	3:C:143:ASN:H	1.69	0.58
3:C:262:CYS:SG	1:D:251:LEU:HD11	2.44	0.58
1:D:244:THR:HG23	1:D:245:LEU:H	1.69	0.58
4:E:140:ASN:HD22	4:E:141:CYS:N	2.02	0.58
1:A:59:GLN:NE2	1:A:117:MET:SD	2.77	0.58
1:A:133:THR:C	1:A:136:PRO:HG2	2.24	0.58
2:B:132:VAL:CG1	2:B:280:ILE:H	2.11	0.58
2:B:279:ILE:HG21	2:B:280:ILE:HD13	1.85	0.58
1:D:35:LEU:CD1	1:D:54:VAL:CG1	2.79	0.58
1:D:54:VAL:O	1:D:56:LEU:HD23	2.04	0.58
1:D:105:MET:HG2	1:D:105:MET:O	2.03	0.58
1:D:133:THR:HG22	1:D:136:PRO:HG2	1.85	0.58
4:E:89:VAL:CG2	4:E:99:PHE:CE2	2.87	0.58
4:E:117:TRP:CD1	4:E:119:PRO:HD3	2.39	0.58
4:E:297:VAL:O	4:E:301:VAL:HG22	2.03	0.58
4:E:304:LEU:HG	4:E:304:LEU:O	2.04	0.58
4:E:416:VAL:HG22	4:E:417:GLU:N	2.19	0.58
1:A:29:VAL:HB	1:A:31:ILE:CD1	2.32	0.57
1:A:207:MET:H	1:A:207:MET:CE	2.16	0.57
2:B:33:VAL:HG22	2:B:158:LEU:HD22	1.85	0.57
3:C:429:ILE:HG13	3:C:430:VAL:N	2.19	0.57
1:D:76:LYS:HE3	1:D:112:TYR:CE2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:407:ASP:OD1	1:D:408:HIS:HD2	1.87	0.57
4:E:273:PRO:HG2	4:E:274:GLU:N	2.19	0.57
1:A:107:LYS:CE	2:B:150:THR:CB	2.81	0.57
1:A:176:TRP:CE3	1:A:209:ARG:NH1	2.72	0.57
1:A:294:VAL:HG13	1:A:295:VAL:N	2.19	0.57
2:B:2:VAL:HG12	2:B:69:PRO:HG3	1.86	0.57
2:B:144:MET:CE	2:B:211:LEU:HD21	2.34	0.57
3:C:154:ASN:HB3	3:C:211:ASN:HB3	1.86	0.57
1:D:166:ASP:CG	1:D:178:MET:CE	2.72	0.57
1:D:280:PHE:HB3	1:D:284:PHE:CZ	2.40	0.57
1:A:46:VAL:HG21	1:A:269:SER:O	2.04	0.57
1:A:139:GLN:CB	1:A:207:MET:C	2.72	0.57
2:B:56:LEU:HD21	2:B:103:THR:CA	2.31	0.57
2:B:270:VAL:HG12	2:B:284:LEU:HD11	1.87	0.57
3:C:319:THR:HG22	3:C:320:HIS:N	2.18	0.57
4:E:159:LEU:CG	4:E:192:LYS:HB2	2.34	0.57
1:A:378:GLY:O	1:A:382:ILE:HG12	2.04	0.57
2:B:59:ALA:HA	2:B:116:VAL:O	2.05	0.57
3:C:70:ASN:O	3:C:74:TYR:HB3	2.04	0.57
1:D:167:LEU:HD11	1:D:178:MET:HB3	1.84	0.57
1:D:281:THR:O	1:D:285:VAL:HB	2.04	0.57
4:E:14:TYR:CZ	4:E:84:LEU:HD12	2.40	0.57
3:C:104:VAL:HA	3:C:106:TYR:CE1	2.40	0.57
3:C:106:TYR:C	3:C:107:PHE:CD1	2.76	0.57
3:C:271:LEU:HD21	3:C:299:VAL:HG12	1.87	0.57
3:C:449:VAL:O	3:C:452:THR:HG22	2.03	0.57
3:C:469:THR:O	3:C:473:PHE:HB2	2.04	0.57
1:D:28:PHE:HB3	1:D:156:VAL:C	2.23	0.57
4:E:34:LEU:HD12	4:E:210:PHE:CZ	2.40	0.57
4:E:34:LEU:CD2	4:E:55:ILE:HA	2.35	0.57
4:E:436:ASN:CA	4:E:439:TRP:NE1	2.63	0.57
2:B:28:LYS:HB3	2:B:155:GLU:HA	1.87	0.57
2:B:68:ASP:CB	2:B:69:PRO:CD	2.73	0.57
2:B:274:SER:CB	2:B:278:PRO:HB3	2.29	0.57
3:C:193:ILE:CD1	3:C:222:ARG:HB2	2.33	0.57
3:C:478:PHE:C	3:C:478:PHE:CD1	2.78	0.57
4:E:30:VAL:O	4:E:158:GLN:HG3	2.05	0.57
4:E:172:ILE:HD11	4:E:188:ARG:N	2.19	0.57
1:A:92:LEU:HB3	1:A:95:ASN:HB2	1.86	0.57
1:A:263:LEU:N	1:A:263:LEU:HD23	2.19	0.57
3:C:243:ALA:HB2	3:C:302:VAL:HG12	1.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:110:LEU:HD12	1:D:111:ASP:N	2.20	0.57
1:D:136:PRO:CG	1:D:274:ILE:HD11	2.32	0.57
1:D:144:MET:HE3	1:D:205:PHE:CE1	2.40	0.57
1:D:419:ILE:CD1	1:D:420:ILE:HG22	2.35	0.57
4:E:67:ASN:N	4:E:67:ASN:ND2	2.42	0.57
1:A:41:ILE:HG12	1:A:51:GLU:HB3	1.84	0.57
1:A:286:ILE:O	1:A:290:ILE:HG12	2.04	0.57
2:B:10:VAL:O	2:B:13:GLU:HB2	2.05	0.57
2:B:145:VAL:HG12	2:B:206:ASP:HB2	1.86	0.57
2:B:281:ILE:HG22	2:B:285:MET:H	1.66	0.57
2:B:444:ILE:HG23	2:B:445:THR:N	2.20	0.57
3:C:16:LYS:HA	3:C:16:LYS:CE	2.33	0.57
3:C:291:TYR:N	3:C:291:TYR:CD1	2.71	0.57
1:D:88:PRO:HG2	1:D:88:PRO:O	2.05	0.57
4:E:235:LEU:O	4:E:235:LEU:CD1	2.43	0.57
1:A:31:ILE:HG13	1:A:60:TRP:HB3	1.87	0.57
1:A:56:LEU:CD2	1:A:57:ARG:N	2.68	0.57
1:A:80:LEU:HD23	1:A:110:LEU:HB2	1.87	0.57
1:A:147:GLY:HA2	1:A:158:ILE:HG21	1.87	0.57
1:A:160:PRO:CG	1:A:185:LYS:NZ	2.68	0.57
2:B:222:VAL:O	2:B:225:ILE:HB	2.05	0.57
3:C:63:TYR:HB2	3:C:117:TYR:CE1	2.39	0.57
3:C:190:TRP:CD1	3:C:221:ILE:CD1	2.84	0.57
4:E:134:PHE:N	4:E:135:PRO:CD	2.68	0.57
4:E:184:THR:HG21	4:E:215:GLN:HG2	1.85	0.57
4:E:224:ASN:O	4:E:228:PRO:HG3	2.04	0.57
1:A:2:GLU:O	1:A:7:LEU:HD21	2.05	0.57
1:A:107:LYS:NZ	2:B:151:TYR:CD2	2.73	0.57
1:A:198:TYR:CD1	1:A:198:TYR:C	2.76	0.57
1:A:406:ILE:HA	1:A:409:ILE:CG1	2.34	0.57
2:B:281:ILE:H	2:B:281:ILE:HD12	1.70	0.57
3:C:36:SER:HB3	3:C:59:ASP:HB2	1.86	0.57
3:C:247:PHE:HE1	3:C:309:VAL:CG2	2.18	0.57
1:D:274:ILE:HB	1:D:276:LYS:HD3	1.87	0.57
4:E:32:LEU:CD1	4:E:157:LEU:HD13	2.33	0.57
4:E:138:TRP:CZ2	4:E:215:GLN:CB	2.82	0.57
2:B:36:THR:O	2:B:54:VAL:HB	2.05	0.56
2:B:91:VAL:HG12	2:B:147:LYS:O	2.05	0.56
2:B:147:LYS:CG	2:B:148:SER:N	2.68	0.56
3:C:42:LEU:CD2	3:C:190:TRP:CZ2	2.86	0.56
3:C:472:ILE:CA	3:C:475:MET:HB3	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:ILE:O	1:D:203:TYR:CE1	2.56	0.56
1:A:175:GLU:OE1	1:A:211:PRO:HG3	2.04	0.56
1:A:209:ARG:CG	1:A:210:ILE:N	2.68	0.56
1:A:220:ILE:N	1:A:221:PRO:CD	2.68	0.56
1:A:227:PHE:CD2	2:B:299:VAL:HG11	2.41	0.56
1:A:247:ILE:HD13	1:A:247:ILE:C	2.20	0.56
1:A:258:LEU:HD13	4:E:267:LEU:HD22	1.86	0.56
2:B:175:ILE:CG1	2:B:176:ASN:N	2.62	0.56
2:B:223:TYR:O	2:B:227:PRO:HD3	2.05	0.56
2:B:232:SER:O	2:B:235:ALA:HB3	2.05	0.56
2:B:287:ILE:CA	2:B:290:LEU:HD12	2.35	0.56
3:C:35:LEU:HD22	3:C:215:VAL:CG1	2.33	0.56
3:C:93:VAL:HB	3:C:151:LEU:HD22	1.85	0.56
3:C:139:PHE:O	3:C:222:ARG:HG2	2.05	0.56
1:D:15:TYR:CE2	1:D:84:ASP:HB3	2.40	0.56
1:A:160:PRO:HG2	1:A:185:LYS:HZ1	1.68	0.56
1:A:256:PHE:N	1:A:256:PHE:CD1	2.70	0.56
2:B:40:LEU:HB2	2:B:52:THR:HG23	1.87	0.56
2:B:72:TYR:O	2:B:76:LYS:HG2	2.05	0.56
2:B:230:LEU:HA	2:B:233:ILE:CG1	2.34	0.56
3:C:137:PHE:H	3:C:138:PRO:CD	2.18	0.56
3:C:241:PHE:C	3:C:241:PHE:HD1	2.09	0.56
3:C:475:MET:O	3:C:478:PHE:CE1	2.59	0.56
1:D:37:LEU:CA	1:D:54:VAL:HG13	2.35	0.56
2:B:92:LEU:N	2:B:92:LEU:HD23	2.20	0.56
2:B:108:VAL:CG1	2:B:118:TRP:HB2	2.35	0.56
3:C:25:LYS:O	3:C:25:LYS:CG	2.52	0.56
3:C:434:LYS:CE	3:C:435:GLU:HG2	2.35	0.56
4:E:79:ILE:CG1	4:E:80:PRO:CD	2.79	0.56
4:E:247:GLY:H	4:E:250:LYS:NZ	2.02	0.56
4:E:273:PRO:CG	4:E:274:GLU:H	2.18	0.56
2:B:84:ASP:C	2:B:85:VAL:CG2	2.73	0.56
2:B:425:LYS:HA	2:B:428:TRP:HD1	1.67	0.56
3:C:59:ASP:OD1	3:C:121:LEU:HB2	2.06	0.56
3:C:271:LEU:C	3:C:271:LEU:CD2	2.73	0.56
4:E:55:ILE:CA	4:E:118:LEU:HD13	2.35	0.56
4:E:76:LEU:CD2	4:E:77:VAL:N	2.68	0.56
4:E:103:TYR:CD2	4:E:104:TYR:HD1	2.22	0.56
4:E:257:VAL:O	4:E:257:VAL:HG12	2.06	0.56
1:A:36:GLN:O	1:A:38:ILE:HD12	2.03	0.56
1:A:43:VAL:HG22	1:A:50:VAL:CG2	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ILE:CG2	1:A:261:VAL:N	2.67	0.56
1:A:306:HIS:C	1:A:306:HIS:CD2	2.79	0.56
1:A:384:GLU:HA	1:A:387:LYS:HG3	1.87	0.56
1:A:426:PHE:CD1	1:A:426:PHE:C	2.79	0.56
2:B:431:VAL:HG23	2:B:433:MET:H	1.71	0.56
2:B:431:VAL:O	2:B:432:ALA:HB3	2.05	0.56
3:C:216:THR:C	3:C:217:PHE:CD1	2.77	0.56
1:D:253:LEU:CD2	1:D:254:THR:N	2.59	0.56
1:A:134:HIS:CD2	1:A:207:MET:HE1	2.39	0.56
1:A:135:PHE:CD1	1:A:135:PHE:C	2.78	0.56
2:B:93:MET:HG2	2:B:206:ASP:HB3	1.88	0.56
3:C:33:ILE:HG12	3:C:62:TRP:CB	2.36	0.56
1:D:239:SER:CB	1:D:242:LYS:HE2	2.34	0.56
4:E:158:GLN:O	4:E:159:LEU:HD23	2.05	0.56
1:A:67:TRP:HA	1:A:67:TRP:HE3	1.66	0.56
1:A:213:TYR:CG	1:A:214:PHE:N	2.73	0.56
1:A:236:PRO:CB	1:A:299:HIS:NE2	2.68	0.56
2:B:46:LYS:HE2	2:B:278:PRO:CD	2.36	0.56
2:B:248:LYS:CD	2:B:252:SER:CB	2.69	0.56
3:C:30:VAL:HG21	3:C:158:ILE:O	2.05	0.56
3:C:120:TRP:CD1	3:C:122:PRO:HD3	2.41	0.56
3:C:437:ASN:O	3:C:441:GLU:HG3	2.06	0.56
1:D:75:ILE:HD11	1:D:78:ILE:HG21	1.86	0.56
4:E:92:GLU:OE1	4:E:144:VAL:HG21	2.05	0.56
3:C:3:GLU:OE1	3:C:3:GLU:O	2.23	0.56
1:D:11:LEU:O	1:D:15:TYR:HB2	2.06	0.56
4:E:27:VAL:HG12	4:E:154:GLU:HA	1.88	0.56
4:E:59:TRP:CZ2	4:E:115:MET:HB3	2.41	0.56
4:E:452:TRP:CE3	4:E:452:TRP:HA	2.40	0.56
1:A:177:VAL:O	1:A:207:MET:HB2	2.06	0.56
2:B:54:VAL:O	2:B:121:SER:HA	2.06	0.56
2:B:205:GLU:HB3	2:B:206:ASP:OD1	2.05	0.56
2:B:283:TYR:O	2:B:287:ILE:HG23	2.06	0.56
3:C:215:VAL:HG23	3:C:215:VAL:O	2.06	0.56
3:C:256:LYS:HB2	3:C:259:THR:HG22	1.87	0.56
1:D:106:THR:CG2	1:D:107:LYS:N	2.60	0.56
1:D:260:ILE:HA	1:D:263:LEU:HD12	1.88	0.56
4:E:138:TRP:CH2	4:E:215:GLN:CB	2.89	0.56
4:E:146:ARG:HD2	4:E:206:GLN:O	2.06	0.56
1:A:293:VAL:HG23	4:E:238:LEU:HD11	1.88	0.55
1:A:380:LYS:CG	2:B:408:ILE:HD13	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:GLU:HA	1:A:393:SER:OG	2.06	0.55
3:C:12:LEU:C	3:C:13:ILE:HG13	2.24	0.55
3:C:30:VAL:HG22	3:C:158:ILE:CA	2.36	0.55
3:C:475:MET:HA	3:C:478:PHE:CE2	2.41	0.55
4:E:44:GLU:HG3	4:E:129:ILE:CB	2.35	0.55
4:E:283:GLY:C	4:E:284:LYS:HE3	2.23	0.55
1:A:20:ARG:HG3	1:A:22:VAL:HG22	1.87	0.55
2:B:136:PRO:HD3	2:B:280:ILE:HD11	1.87	0.55
2:B:239:PHE:N	2:B:239:PHE:CD1	2.73	0.55
3:C:37:LEU:HD12	3:C:217:PHE:CE2	2.41	0.55
3:C:74:TYR:O	3:C:78:SER:HA	2.06	0.55
3:C:431:LYS:CE	1:D:379:VAL:HG22	2.34	0.55
1:D:37:LEU:HD13	1:D:54:VAL:HG13	1.87	0.55
1:D:78:ILE:HD13	1:D:110:LEU:HB3	1.89	0.55
1:A:118:TRP:NE1	1:A:120:PRO:HG3	2.22	0.55
1:A:284:PHE:CD1	1:A:284:PHE:N	2.73	0.55
2:B:284:LEU:O	2:B:288:MET:HB2	2.07	0.55
3:C:69:TRP:HB2	3:C:74:TYR:H	1.71	0.55
3:C:229:VAL:O	3:C:233:ILE:HG12	2.06	0.55
1:D:134:HIS:NE2	1:D:207:MET:CE	2.69	0.55
1:D:141:ASN:HB3	1:D:206:ILE:HG12	1.89	0.55
1:D:166:ASP:HB2	1:D:181:TYR:HB2	1.87	0.55
4:E:448:LYS:N	4:E:448:LYS:CD	2.63	0.55
1:A:2:GLU:O	1:A:7:LEU:HD11	2.06	0.55
1:A:20:ARG:HG3	1:A:20:ARG:O	2.05	0.55
2:B:37:LEU:CB	2:B:54:VAL:HG12	2.35	0.55
2:B:67:TRP:HB2	2:B:72:TYR:CB	2.33	0.55
2:B:266:LEU:O	2:B:270:VAL:HG23	2.05	0.55
3:C:7:LEU:HD13	3:C:73:GLU:CD	2.26	0.55
3:C:237:VAL:HG23	3:C:238:LEU:HD12	1.87	0.55
4:E:91:LEU:HB2	4:E:95:VAL:N	2.12	0.55
1:A:43:VAL:CB	1:A:50:VAL:HG22	2.36	0.55
1:A:292:THR:O	1:A:296:ILE:HG12	2.05	0.55
1:A:426:PHE:HD1	1:A:426:PHE:C	2.09	0.55
2:B:21:PRO:CG	2:B:85:VAL:CG1	2.84	0.55
2:B:185:GLN:CG	2:B:219:PHE:CE2	2.89	0.55
2:B:220:TYR:CG	2:B:223:TYR:HE2	2.25	0.55
3:C:35:LEU:HD12	3:C:92:ILE:HG21	1.87	0.55
3:C:443:VAL:O	3:C:443:VAL:HG12	2.05	0.55
1:D:43:VAL:CG2	1:D:50:VAL:HG13	2.36	0.55
1:D:76:LYS:CD	1:D:112:TYR:CE2	2.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:429:ARG:N	1:D:429:ARG:HE	2.04	0.55
4:E:44:GLU:HB3	4:E:280:PRO:HB3	1.87	0.55
4:E:268:ILE:HG13	4:E:269:ALA:N	2.22	0.55
1:A:31:ILE:HG12	1:A:60:TRP:HB3	1.88	0.55
1:A:301:ARG:HA	4:E:245:GLN:HB3	1.89	0.55
1:A:410:LEU:HD13	1:A:414:PHE:HD2	1.72	0.55
2:B:130:ILE:HD12	2:B:134:TYR:HE2	1.71	0.55
2:B:248:LYS:HZ3	2:B:252:SER:HA	1.72	0.55
2:B:248:LYS:CE	2:B:252:SER:HB3	2.35	0.55
3:C:63:TYR:HA	3:C:117:TYR:HA	1.88	0.55
3:C:77:ILE:HD11	3:C:80:LEU:HD22	1.89	0.55
3:C:107:PHE:O	3:C:107:PHE:CD2	2.59	0.55
3:C:460:ILE:O	3:C:463:PRO:HG2	2.07	0.55
1:D:107:LYS:HE3	4:E:149:THR:C	2.27	0.55
4:E:227:ALA:H	4:E:228:PRO:HD2	1.72	0.55
1:A:15:TYR:HE2	1:A:84:ASP:HB3	1.71	0.55
1:A:285:VAL:O	1:A:288:SER:HB3	2.07	0.55
2:B:15:TYR:O	2:B:15:TYR:CD1	2.60	0.55
2:B:21:PRO:HG2	2:B:85:VAL:HG11	1.89	0.55
2:B:95:ASN:HB3	2:B:126:SER:HB2	1.88	0.55
2:B:197:TRP:HB3	2:B:204:TYR:HD1	1.72	0.55
3:C:38:THR:HG21	3:C:57:TRP:CZ3	2.41	0.55
3:C:42:LEU:CD1	3:C:190:TRP:HZ2	2.18	0.55
1:D:253:LEU:HD23	1:D:254:THR:CB	2.36	0.55
1:D:401:TYR:O	1:D:401:TYR:CD1	2.60	0.55
4:E:144:VAL:HG23	4:E:144:VAL:O	2.07	0.55
4:E:191:LYS:HB2	4:E:209:ILE:HG21	1.87	0.55
4:E:441:LEU:C	4:E:441:LEU:HD12	2.27	0.55
1:A:15:TYR:HE2	1:A:84:ASP:OD2	1.89	0.55
1:A:132:VAL:C	1:A:274:ILE:HG22	2.25	0.55
1:A:166:ASP:HB3	1:A:178:MET:CE	2.35	0.55
1:A:207:MET:O	1:A:207:MET:HG2	2.06	0.55
2:B:67:TRP:CB	2:B:72:TYR:HB2	2.34	0.55
3:C:38:THR:CG2	3:C:57:TRP:CZ3	2.90	0.55
3:C:270:PHE:CE1	1:D:255:VAL:HG21	2.42	0.55
4:E:239:VAL:O	4:E:243:PRO:HD3	2.07	0.55
1:A:104:HIS:C	1:A:105:MET:SD	2.85	0.55
1:A:124:PHE:C	1:A:124:PHE:HD1	2.09	0.55
1:A:200:ASP:OD1	1:A:200:ASP:N	2.40	0.55
1:A:280:PHE:HB3	1:A:284:PHE:CE2	2.41	0.55
3:C:225:PRO:HG2	3:C:228:TYR:CD1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:249:LEU:HB3	3:C:256:LYS:NZ	2.22	0.55
3:C:289:GLY:O	3:C:293:MET:HE2	2.07	0.55
1:D:7:LEU:HD22	1:D:70:ALA:HB1	1.86	0.55
1:D:78:ILE:HD11	1:D:110:LEU:CG	2.37	0.55
1:D:149:TRP:CG	1:D:150:THR:N	2.74	0.55
1:D:191:THR:O	1:D:191:THR:HG22	2.06	0.55
4:E:63:ARG:O	4:E:64:LEU:HG	2.07	0.55
4:E:255:ILE:HD11	4:E:304:LEU:HD21	1.80	0.55
4:E:289:VAL:HG12	4:E:290:MET:CG	2.36	0.55
1:A:9:ALA:O	1:A:13:GLU:HG3	2.06	0.55
1:A:238:ASP:O	1:A:239:SER:HB2	2.07	0.55
1:A:252:SER:O	1:A:256:PHE:CD1	2.60	0.55
3:C:184:PHE:CD1	3:C:185:THR:N	2.75	0.55
4:E:54:TRP:C	4:E:118:LEU:HD13	2.27	0.55
4:E:147:SER:O	4:E:205:PHE:CE2	2.60	0.55
4:E:240:TYR:HB3	4:E:453:ILE:HD11	1.88	0.55
2:B:135:PHE:N	2:B:136:PRO:CD	2.70	0.54
3:C:83:ARG:HB3	3:C:84:PRO:HD2	1.89	0.54
3:C:291:TYR:N	3:C:291:TYR:HD1	2.06	0.54
3:C:438:ALA:HA	3:C:441:GLU:OE1	2.07	0.54
1:D:21:PRO:HD2	1:D:86:TRP:CG	2.42	0.54
1:D:106:THR:HG23	1:D:107:LYS:HD3	1.88	0.54
1:D:120:PRO:HG2	1:D:120:PRO:O	2.07	0.54
1:D:152:ASP:HB3	1:D:197:PRO:CA	2.37	0.54
1:D:250:LEU:HA	1:D:253:LEU:HD22	1.87	0.54
4:E:40:ILE:HB	4:E:50:THR:HB	1.88	0.54
4:E:138:TRP:CH2	4:E:215:GLN:NE2	2.73	0.54
4:E:242:LEU:N	4:E:243:PRO:HD2	2.21	0.54
1:A:79:ARG:HH11	1:A:107:LYS:HZ2	1.55	0.54
1:A:85:VAL:CG1	1:A:86:TRP:N	2.69	0.54
2:B:291:VAL:HG12	2:B:292:ALA:H	1.71	0.54
2:B:441:TYR:O	2:B:444:ILE:HG22	2.07	0.54
3:C:9:ASN:O	3:C:12:LEU:HG	2.07	0.54
3:C:26:HIS:ND1	3:C:26:HIS:N	2.51	0.54
1:D:103:VAL:HG13	1:D:118:TRP:HZ2	1.71	0.54
1:D:395:ALA:HB1	1:D:399:TRP:CE2	2.41	0.54
4:E:34:LEU:HD23	4:E:55:ILE:HA	1.89	0.54
4:E:44:GLU:HG3	4:E:129:ILE:HB	1.89	0.54
4:E:45:LYS:HB3	4:E:280:PRO:HA	1.87	0.54
1:A:258:LEU:O	1:A:261:VAL:HB	2.07	0.54
1:A:417:ILE:HA	1:A:420:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:12:LEU:HB3	3:C:15:ASN:HB3	1.90	0.54
1:D:75:ILE:HD13	4:E:24:LEU:CD1	2.34	0.54
1:D:75:ILE:CG1	1:D:78:ILE:CG2	2.85	0.54
1:D:102:ILE:HG12	4:E:98:GLN:NE2	2.21	0.54
4:E:34:LEU:HA	4:E:54:TRP:O	2.07	0.54
4:E:49:LEU:HD12	4:E:50:THR:N	2.21	0.54
4:E:100:GLU:HB2	4:E:122:ILE:CG1	2.38	0.54
2:B:84:ASP:C	2:B:85:VAL:HG23	2.28	0.54
2:B:216:LYS:HE3	2:B:216:LYS:H	1.72	0.54
2:B:258:ALA:O	2:B:262:PHE:CD1	2.60	0.54
2:B:258:ALA:HB1	3:C:265:LEU:HD22	1.89	0.54
2:B:409:LYS:O	2:B:412:ALA:HB3	2.07	0.54
1:D:92:LEU:HD13	1:D:146:LEU:CD1	2.37	0.54
1:D:92:LEU:HB2	1:D:96:ALA:N	2.22	0.54
1:A:37:LEU:HD22	1:A:54:VAL:HG12	1.88	0.54
2:B:247:GLU:CA	2:B:249:MET:HG3	2.37	0.54
2:B:287:ILE:C	2:B:287:ILE:CD1	2.68	0.54
3:C:65:HIS:N	3:C:65:HIS:HD2	1.96	0.54
3:C:266:ALA:HB3	1:D:251:LEU:HD13	1.89	0.54
1:D:414:PHE:O	1:D:414:PHE:HD1	1.90	0.54
4:E:289:VAL:HG12	4:E:290:MET:HG3	1.90	0.54
1:A:36:GLN:HG2	1:A:164:ARG:HH21	1.72	0.54
2:B:46:LYS:CB	2:B:278:PRO:CD	2.85	0.54
2:B:133:MET:SD	2:B:140:GLN:CB	2.94	0.54
2:B:147:LYS:HG3	2:B:148:SER:H	1.73	0.54
1:D:37:LEU:CB	1:D:54:VAL:HG13	2.37	0.54
1:D:76:LYS:HD2	1:D:112:TYR:CE2	2.43	0.54
1:D:85:VAL:HG13	1:D:86:TRP:N	2.22	0.54
1:A:87:LEU:HD22	1:A:87:LEU:N	2.04	0.54
2:B:142:CYS:SG	2:B:143:THR:N	2.81	0.54
2:B:258:ALA:HB2	3:C:265:LEU:CD2	2.35	0.54
3:C:22:ARG:O	3:C:24:VAL:HG23	2.07	0.54
3:C:63:TYR:HE1	3:C:116:GLY:HA3	1.70	0.54
3:C:182:GLU:O	3:C:183:ALA:HB2	2.08	0.54
3:C:201:ILE:O	3:C:202:TYR:CG	2.60	0.54
1:D:79:ARG:NH1	4:E:154:GLU:CD	2.61	0.54
4:E:136:PHE:CZ	4:E:217:LYS:CD	2.79	0.54
4:E:233:SER:O	4:E:236:VAL:HG23	2.07	0.54
1:A:217:ASN:O	1:A:221:PRO:HD3	2.08	0.54
1:A:239:SER:CB	2:B:312:HIS:CB	2.84	0.54
1:A:406:ILE:CG2	1:A:409:ILE:CD1	2.84	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:104:LEU:HA	2:B:118:TRP:CZ2	2.42	0.54
2:B:220:TYR:HD2	2:B:223:TYR:HH	1.55	0.54
3:C:160:MET:N	3:C:213:GLN:HG3	2.23	0.54
3:C:272:LEU:O	3:C:276:GLN:HG2	2.07	0.54
1:D:38:ILE:O	1:D:39:GLN:HG3	2.08	0.54
1:D:101:ALA:C	1:D:102:ILE:HD12	2.28	0.54
1:D:240:GLY:C	1:D:242:LYS:H	2.12	0.54
4:E:138:TRP:CH2	4:E:215:GLN:HB2	2.42	0.54
1:A:93:TYR:H	1:A:93:TYR:HD1	1.52	0.54
1:A:147:GLY:HA2	1:A:158:ILE:HD13	1.90	0.54
1:A:236:PRO:CG	1:A:299:HIS:NE2	2.71	0.54
1:A:293:VAL:CG2	4:E:238:LEU:HD11	2.38	0.54
1:A:435:GLN:HG2	1:A:435:GLN:O	2.08	0.54
2:B:132:VAL:CG1	2:B:280:ILE:N	2.71	0.54
2:B:290:LEU:HD21	2:B:453:SER:OG	2.08	0.54
2:B:404:ALA:O	2:B:407:ALA:HB3	2.08	0.54
3:C:190:TRP:HB2	3:C:222:ARG:O	2.07	0.54
3:C:436:LYS:O	3:C:439:TYR:HB2	2.07	0.54
1:D:43:VAL:HG13	1:D:50:VAL:HG22	1.89	0.54
4:E:59:TRP:HH2	4:E:107:VAL:CG1	2.21	0.54
4:E:259:LEU:N	4:E:259:LEU:HD23	2.23	0.54
1:A:255:VAL:O	1:A:259:VAL:HG23	2.08	0.53
2:B:251:LEU:C	2:B:251:LEU:HD12	2.29	0.53
3:C:263:VAL:HA	1:D:251:LEU:CD1	2.35	0.53
1:D:102:ILE:CG2	4:E:98:GLN:HE21	2.21	0.53
1:D:135:PHE:CE1	1:D:277:TYR:CE2	2.95	0.53
1:D:376:ILE:HG22	1:D:380:LYS:NZ	2.22	0.53
4:E:68:THR:HB	4:E:72:GLU:OE1	2.08	0.53
1:A:46:VAL:CG2	1:A:271:VAL:N	2.68	0.53
1:A:66:ARG:H	1:A:66:ARG:CD	2.18	0.53
3:C:35:LEU:CD2	3:C:215:VAL:HG11	2.35	0.53
3:C:92:ILE:HA	3:C:149:THR:O	2.08	0.53
3:C:230:ILE:HG13	3:C:231:ASN:HD22	1.74	0.53
1:D:27:HIS:O	1:D:28:PHE:HB2	2.08	0.53
1:D:49:ILE:CG2	1:D:125:LYS:HE3	2.38	0.53
1:D:170:PHE:CE2	1:D:176:TRP:CD1	2.91	0.53
1:A:38:ILE:HD12	1:A:38:ILE:N	2.23	0.53
2:B:226:VAL:C	2:B:230:LEU:HG	2.29	0.53
2:B:270:VAL:HG11	2:B:284:LEU:HD21	1.90	0.53
3:C:69:TRP:CD1	3:C:114:PRO:HA	2.43	0.53
3:C:72:SER:HA	3:C:76:ASP:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:114:PRO:O	3:C:115:ASN:HB3	2.09	0.53
3:C:137:PHE:CE1	3:C:291:TYR:CE2	2.96	0.53
3:C:252:GLU:HG3	1:D:300:HIS:C	2.29	0.53
3:C:305:ASN:O	3:C:308:ILE:HG22	2.08	0.53
1:D:239:SER:HB3	1:D:242:LYS:HD3	1.90	0.53
4:E:129:ILE:CG2	4:E:133:TYR:HD2	2.11	0.53
4:E:143:LEU:HD12	4:E:210:PHE:O	2.07	0.53
4:E:159:LEU:HB2	4:E:192:LYS:HB2	1.89	0.53
4:E:239:VAL:HA	4:E:242:LEU:CD2	2.38	0.53
1:A:201:ILE:CG2	1:A:203:TYR:CE1	2.91	0.53
2:B:201:ASP:OD1	2:B:202:PRO:HD2	2.09	0.53
2:B:304:LEU:O	2:B:307:ARG:HD3	2.08	0.53
3:C:148:PHE:HB2	3:C:215:VAL:HG23	1.83	0.53
1:D:233:PHE:CE2	1:D:413:VAL:HG11	2.44	0.53
4:E:313:THR:HB	4:E:440:VAL:HG12	1.90	0.53
1:A:131:ILE:HD11	1:A:140:GLN:CD	2.28	0.53
1:A:160:PRO:HG3	1:A:185:LYS:CE	2.37	0.53
2:B:35:LEU:HD13	2:B:55:PHE:C	2.28	0.53
2:B:46:LYS:CB	2:B:276:SER:O	2.56	0.53
3:C:47:GLU:CD	3:C:285:VAL:HB	2.29	0.53
3:C:82:LEU:HG	3:C:86:LEU:HB2	1.91	0.53
3:C:228:TYR:CD1	3:C:229:VAL:HG22	2.44	0.53
3:C:475:MET:O	3:C:478:PHE:CD1	2.62	0.53
4:E:91:LEU:HA	4:E:145:PHE:CB	2.37	0.53
4:E:283:GLY:O	4:E:286:LEU:HB2	2.08	0.53
1:A:391:GLU:HA	1:A:394:ASN:HD21	1.73	0.53
1:A:419:ILE:O	1:A:423:VAL:HG23	2.08	0.53
2:B:28:LYS:HB3	2:B:155:GLU:CA	2.39	0.53
2:B:186:TRP:CB	2:B:215:ARG:CB	2.78	0.53
2:B:218:LEU:HD11	2:B:222:VAL:CG2	2.36	0.53
3:C:115:ASN:ND2	3:C:115:ASN:C	2.52	0.53
3:C:228:TYR:CE1	3:C:229:VAL:HG22	2.43	0.53
3:C:273:LEU:HD23	3:C:276:GLN:HB3	1.88	0.53
1:D:29:VAL:CG2	1:D:60:TRP:NE1	2.70	0.53
1:D:179:LYS:HB2	1:D:206:ILE:HG22	1.90	0.53
1:D:376:ILE:O	1:D:380:LYS:HG3	2.08	0.53
4:E:38:ASN:O	4:E:51:THR:HG23	2.09	0.53
4:E:65:SER:CA	4:E:112:ASP:HA	2.38	0.53
4:E:83:LEU:O	4:E:84:LEU:HB2	2.07	0.53
4:E:237:VAL:HG22	4:E:457:LEU:CD2	2.39	0.53
4:E:296:ILE:CG1	4:E:297:VAL:N	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HG22	1:A:158:ILE:HG12	1.87	0.53
1:A:178:MET:SD	1:A:207:MET:HB3	2.48	0.53
1:A:257:LEU:O	1:A:260:ILE:HG22	2.07	0.53
1:A:294:VAL:CG1	1:A:295:VAL:N	2.72	0.53
1:A:397:GLU:HA	1:A:400:LYS:CD	2.38	0.53
2:B:459:SER:HA	2:B:463:PRO:HD2	1.89	0.53
3:C:247:PHE:O	3:C:250:PRO:CG	2.57	0.53
3:C:300:THR:HG22	3:C:300:THR:O	2.09	0.53
1:D:235:LEU:HD23	1:D:235:LEU:N	2.23	0.53
1:D:254:THR:CG2	1:D:255:VAL:N	2.71	0.53
4:E:100:GLU:HB2	4:E:122:ILE:HG12	1.91	0.53
4:E:152:ALA:HA	4:E:155:VAL:O	2.08	0.53
1:A:3:HIS:HB2	1:A:7:LEU:HD23	1.87	0.53
1:A:195:ASP:OD1	1:A:197:PRO:HG3	2.09	0.53
2:B:45:GLU:HG2	2:B:277:VAL:HA	1.91	0.53
1:D:222:CYS:O	1:D:225:PHE:CD1	2.61	0.53
1:D:412:CYS:HB3	1:D:413:VAL:HG23	1.90	0.53
4:E:2:GLU:HB3	4:E:6:LEU:HG	1.91	0.53
4:E:37:THR:OG1	4:E:54:TRP:CZ3	2.60	0.53
4:E:123:TYR:N	4:E:123:TYR:CD1	2.77	0.53
4:E:223:ILE:HG12	4:E:226:ILE:HD12	1.91	0.53
4:E:302:ILE:O	4:E:305:ASN:HB3	2.09	0.53
4:E:313:THR:OG1	4:E:441:LEU:HB3	2.09	0.53
2:B:449:ILE:HA	2:B:452:PHE:HD2	1.73	0.53
3:C:56:VAL:CG2	3:C:124:ALA:HB3	2.39	0.53
3:C:113:ARG:HB2	3:C:117:TYR:O	2.07	0.53
1:D:130:ILE:O	1:D:134:HIS:HB2	2.07	0.53
1:A:171:MET:HG2	1:A:174:GLY:N	2.24	0.53
2:B:11:LEU:N	2:B:11:LEU:CD2	2.71	0.53
2:B:135:PHE:H	2:B:136:PRO:CD	2.22	0.53
3:C:465:MET:O	3:C:465:MET:HG2	2.07	0.53
1:D:63:VAL:O	1:D:63:VAL:HG22	2.08	0.53
1:D:250:LEU:O	1:D:254:THR:HG22	2.09	0.53
1:A:251:LEU:HD22	4:E:260:ALA:CA	2.39	0.52
1:A:261:VAL:O	1:A:265:PRO:HD3	2.09	0.52
1:A:410:LEU:O	1:A:414:PHE:HB2	2.09	0.52
2:B:97:ASP:HB3	2:B:125:ARG:HG3	1.91	0.52
2:B:247:GLU:O	2:B:249:MET:CG	2.56	0.52
3:C:159:SER:HA	3:C:213:GLN:HG2	1.88	0.52
1:D:426:PHE:CG	1:D:427:ALA:N	2.77	0.52
4:E:44:GLU:CA	4:E:129:ILE:HD12	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:182:GLU:CD	4:E:220:PHE:CE2	2.82	0.52
1:A:134:HIS:C	1:A:136:PRO:HD2	2.29	0.52
1:A:247:ILE:CG1	4:E:253:LEU:HD12	2.38	0.52
1:A:380:LYS:O	1:A:384:GLU:HB2	2.09	0.52
2:B:53:SER:HA	2:B:122:ALA:O	2.09	0.52
2:B:438:LEU:HD23	2:B:441:TYR:CB	2.38	0.52
3:C:201:ILE:HB	3:C:213:GLN:OE1	2.09	0.52
1:D:85:VAL:CG1	1:D:86:TRP:N	2.72	0.52
1:D:301:ARG:HH22	1:D:406:ILE:CD1	2.21	0.52
4:E:178:THR:HG22	4:E:180:ASN:H	1.74	0.52
1:A:49:ILE:HG12	1:A:97:ASP:OD2	2.09	0.52
1:A:66:ARG:HD3	1:A:66:ARG:O	2.09	0.52
2:B:37:LEU:HD12	2:B:54:VAL:HG11	1.91	0.52
2:B:108:VAL:CG2	2:B:118:TRP:HB2	2.40	0.52
2:B:409:LYS:HE2	3:C:423:ILE:CG2	2.37	0.52
3:C:180:ASP:CB	3:C:181:PRO:CD	2.84	0.52
3:C:266:ALA:HB2	1:D:251:LEU:HD13	1.91	0.52
1:D:20:ARG:CG	1:D:20:ARG:NH1	2.66	0.52
1:D:181:TYR:CE1	1:D:203:TYR:HB3	2.40	0.52
1:D:186:HIS:CE1	1:D:187:TRP:O	2.63	0.52
4:E:94:ASN:CG	4:E:143:LEU:HD23	2.29	0.52
4:E:215:GLN:HG3	4:E:216:ARG:H	1.74	0.52
4:E:455:LEU:HD12	4:E:455:LEU:O	2.09	0.52
1:A:261:VAL:O	1:A:261:VAL:HG12	2.08	0.52
3:C:106:TYR:CD1	3:C:107:PHE:CD1	2.96	0.52
3:C:190:TRP:HA	3:C:223:ARG:HA	1.92	0.52
1:D:167:LEU:CD1	1:D:167:LEU:H	2.23	0.52
4:E:44:GLU:CB	4:E:280:PRO:HB3	2.39	0.52
4:E:264:PHE:O	4:E:267:LEU:HB3	2.09	0.52
1:A:66:ARG:CA	1:A:113:THR:C	2.78	0.52
1:A:89:ASP:O	1:A:149:TRP:HB3	2.10	0.52
1:A:93:TYR:N	1:A:93:TYR:HD1	2.06	0.52
1:A:171:MET:CE	1:A:176:TRP:CZ2	2.87	0.52
2:B:93:MET:HB2	2:B:145:VAL:CB	2.40	0.52
2:B:175:ILE:HD12	2:B:190:HIS:CD2	2.43	0.52
3:C:426:THR:CA	3:C:429:ILE:HG23	2.39	0.52
4:E:88:ASP:O	4:E:88:ASP:CG	2.47	0.52
1:A:79:ARG:HD3	1:A:107:LYS:HD2	1.90	0.52
1:A:251:LEU:HD11	4:E:256:SER:O	2.08	0.52
2:B:280:ILE:C	2:B:282:SER:H	2.11	0.52
3:C:81:ARG:HA	3:C:112:VAL:HG23	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:135:LEU:C	3:C:138:PRO:HD2	2.30	0.52
3:C:234:THR:N	3:C:235:PRO:CD	2.72	0.52
3:C:464:VAL:O	3:C:464:VAL:HG22	2.09	0.52
1:D:233:PHE:CE1	1:D:417:ILE:HD12	2.43	0.52
4:E:454:ALA:O	4:E:457:LEU:HB3	2.09	0.52
1:A:117:MET:CG	1:A:119:THR:HG23	2.40	0.52
2:B:186:TRP:HB3	2:B:215:ARG:CD	2.39	0.52
2:B:444:ILE:O	2:B:448:SER:HB2	2.08	0.52
3:C:314:PHE:CD1	3:C:314:PHE:O	2.62	0.52
3:C:452:THR:C	3:C:455:ARG:HG2	2.28	0.52
1:D:93:TYR:CE2	1:D:198:TYR:CE2	2.98	0.52
1:D:224:LEU:O	1:D:228:LEU:HD23	2.10	0.52
1:D:302:SER:CB	1:D:400:LYS:CG	2.75	0.52
4:E:83:LEU:O	4:E:84:LEU:HD13	2.09	0.52
4:E:444:LYS:HA	4:E:444:LYS:HE3	1.91	0.52
1:A:95:ASN:HA	1:A:127:TYR:O	2.08	0.52
1:A:136:PRO:HG3	1:A:274:ILE:HG23	1.91	0.52
1:A:196:THR:HG22	1:A:196:THR:O	2.10	0.52
1:A:287:SER:HA	1:A:290:ILE:HG13	1.92	0.52
1:A:293:VAL:O	1:A:297:ASN:HB3	2.10	0.52
2:B:103:THR:OG1	2:B:122:ALA:CB	2.57	0.52
2:B:290:LEU:HD11	2:B:453:SER:HB2	1.92	0.52
3:C:132:ILE:HG22	3:C:133:ASN:N	2.25	0.52
3:C:162:LEU:CD1	3:C:217:PHE:CZ	2.84	0.52
1:D:226:SER:O	1:D:230:VAL:HB	2.10	0.52
1:D:305:THR:CB	1:D:401:TYR:CD2	2.76	0.52
4:E:58:GLN:HA	4:E:59:TRP:HE3	1.75	0.52
1:A:72:TYR:HB2	1:A:112:TYR:HB2	1.86	0.52
1:A:176:TRP:CZ3	1:A:209:ARG:NH2	2.78	0.52
2:B:227:PRO:C	2:B:231:ILE:HG12	2.30	0.52
3:C:63:TYR:CD1	3:C:64:ASP:N	2.77	0.52
1:D:28:PHE:CZ	1:D:153:GLY:O	2.63	0.52
1:D:289:ILE:O	1:D:293:VAL:HG23	2.09	0.52
4:E:182:GLU:CA	4:E:218:PRO:CG	2.88	0.52
1:A:108:LEU:CD2	1:A:118:TRP:CD1	2.93	0.52
1:A:231:LEU:C	1:A:233:PHE:N	2.64	0.52
1:A:379:VAL:CG1	4:E:424:LYS:CE	2.86	0.52
1:A:385:HIS:HD1	1:A:385:HIS:C	2.13	0.52
2:B:284:LEU:HA	2:B:287:ILE:HG13	1.90	0.52
3:C:42:LEU:CD2	3:C:190:TRP:HH2	2.17	0.52
3:C:42:LEU:CG	3:C:54:THR:CG2	2.83	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:67:LEU:HB3	3:C:116:GLY:HA2	0.78	0.52
3:C:482:PRO:CG	3:C:483:ALA:N	2.73	0.52
4:E:452:TRP:HA	4:E:452:TRP:HE3	1.75	0.52
1:A:237:THR:HB	1:A:406:ILE:CG2	2.40	0.51
3:C:93:VAL:CG1	3:C:151:LEU:HB2	2.40	0.51
3:C:222:ARG:NH2	3:C:223:ARG:C	2.64	0.51
3:C:223:ARG:CG	3:C:224:LYS:N	2.73	0.51
3:C:308:ILE:CG2	3:C:309:VAL:N	2.73	0.51
1:D:242:LYS:HB2	1:D:245:LEU:CD1	2.40	0.51
1:D:298:THR:O	1:D:301:ARG:HD3	2.09	0.51
4:E:55:ILE:HG13	4:E:57:ILE:CG1	2.35	0.51
1:A:45:GLU:CD	1:A:271:VAL:HB	2.30	0.51
1:A:134:HIS:NE2	1:A:207:MET:CE	2.73	0.51
1:A:151:TYR:HB2	1:A:156:VAL:HG13	1.92	0.51
2:B:145:VAL:HG13	2:B:208:THR:HA	1.93	0.51
2:B:409:LYS:CE	3:C:423:ILE:CG2	2.88	0.51
3:C:438:ALA:O	3:C:442:GLU:HB2	2.10	0.51
4:E:60:ASN:HD22	4:E:60:ASN:N	2.07	0.51
4:E:133:TYR:C	4:E:135:PRO:HD2	2.30	0.51
4:E:173:ASP:OD2	4:E:185:ILE:HD13	2.10	0.51
1:A:47:ASN:O	1:A:48:GLN:HG2	2.09	0.51
1:A:142:CYS:CB	1:A:205:PHE:HB2	2.35	0.51
1:A:227:PHE:CD1	1:A:227:PHE:O	2.63	0.51
2:B:85:VAL:HG12	2:B:86:TRP:CA	2.39	0.51
2:B:135:PHE:CD2	2:B:283:TYR:CE1	2.98	0.51
1:D:36:GLN:NE2	1:D:38:ILE:CG1	2.73	0.51
1:D:49:ILE:CG1	1:D:125:LYS:HE3	2.40	0.51
1:D:92:LEU:HG	1:D:124:PHE:CE1	2.46	0.51
4:E:143:LEU:O	4:E:210:PHE:HB2	2.10	0.51
4:E:217:LYS:N	4:E:218:PRO:CD	2.72	0.51
4:E:283:GLY:HA3	4:E:284:LYS:NZ	2.25	0.51
4:E:296:ILE:HG13	4:E:297:VAL:N	2.24	0.51
4:E:453:ILE:HD12	4:E:453:ILE:C	2.31	0.51
1:A:41:ILE:CG2	1:A:123:ILE:HD11	2.41	0.51
1:A:106:THR:HG21	1:A:120:PRO:HB3	1.92	0.51
1:A:133:THR:C	1:A:136:PRO:HD2	2.30	0.51
1:A:254:THR:O	1:A:258:LEU:HG	2.10	0.51
1:D:76:LYS:HG2	1:D:112:TYR:HD2	1.75	0.51
1:D:78:ILE:HD12	1:D:78:ILE:H	1.76	0.51
1:D:97:ASP:OD1	1:D:97:ASP:O	2.27	0.51
4:E:145:PHE:O	4:E:208:ILE:HD12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:159:LEU:HD12	4:E:192:LYS:HA	1.91	0.51
4:E:173:ASP:CB	4:E:185:ILE:HG21	2.40	0.51
4:E:231:LEU:HG	4:E:232:ILE:N	2.17	0.51
4:E:463:LEU:O	4:E:463:LEU:CD1	2.57	0.51
1:A:50:VAL:HG12	1:A:52:THR:HG23	1.90	0.51
1:A:54:VAL:HG22	1:A:122:ALA:CB	2.41	0.51
2:B:10:VAL:CG1	2:B:11:LEU:CD2	2.88	0.51
2:B:189:GLU:O	2:B:190:HIS:CG	2.63	0.51
2:B:218:LEU:CD1	2:B:221:ILE:HD11	2.40	0.51
2:B:291:VAL:CG1	2:B:292:ALA:N	2.72	0.51
3:C:80:LEU:HG	3:C:81:ARG:N	2.26	0.51
3:C:106:TYR:CD1	3:C:107:PHE:CE1	2.98	0.51
1:D:244:THR:CG2	1:D:245:LEU:N	2.70	0.51
1:D:250:LEU:HD23	1:D:253:LEU:HD22	1.91	0.51
4:E:173:ASP:CG	4:E:185:ILE:HD13	2.31	0.51
1:A:107:LYS:O	1:A:108:LEU:CD2	2.59	0.51
1:A:218:VAL:CG1	1:A:219:ILE:H	2.23	0.51
1:A:413:VAL:O	1:A:416:LEU:HB3	2.09	0.51
2:B:258:ALA:CB	3:C:265:LEU:CD2	2.85	0.51
3:C:94:LEU:N	3:C:94:LEU:HD23	2.26	0.51
1:D:38:ILE:O	1:D:38:ILE:HG22	2.11	0.51
1:D:56:LEU:CG	1:D:120:PRO:CG	2.88	0.51
1:D:225:PHE:HD1	1:D:226:SER:N	2.08	0.51
1:D:249:VAL:HA	1:D:252:SER:HB3	1.92	0.51
1:D:305:THR:CG2	1:D:400:LYS:CB	2.78	0.51
1:A:131:ILE:CD1	1:A:133:THR:HB	2.41	0.51
2:B:32:ARG:HH21	2:B:60:TRP:C	2.13	0.51
2:B:112:HIS:NE2	2:B:113:THR:HG23	2.26	0.51
2:B:269:LYS:HD2	2:B:270:VAL:N	2.25	0.51
3:C:69:TRP:HB2	3:C:74:TYR:HB2	1.92	0.51
3:C:110:VAL:HG13	3:C:120:TRP:CA	2.41	0.51
3:C:289:GLY:O	3:C:293:MET:CE	2.59	0.51
1:D:280:PHE:O	1:D:284:PHE:CD1	2.64	0.51
1:D:283:ILE:N	1:D:286:ILE:HD12	2.25	0.51
4:E:58:GLN:HA	4:E:59:TRP:CE3	2.45	0.51
4:E:109:VAL:HG13	4:E:115:MET:HE1	1.93	0.51
1:A:15:TYR:OH	1:A:84:ASP:HB3	2.10	0.51
1:A:111:ASP:C	1:A:113:THR:N	2.64	0.51
1:A:129:GLU:HG2	1:A:130:ILE:N	2.24	0.51
1:A:385:HIS:C	1:A:385:HIS:ND1	2.64	0.51
2:B:132:VAL:HA	2:B:279:ILE:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:307:ARG:NH1	2:B:434:VAL:HG21	2.25	0.51
3:C:201:ILE:O	3:C:202:TYR:CD1	2.64	0.51
1:D:107:LYS:NZ	4:E:149:THR:CA	2.68	0.51
4:E:58:GLN:CA	4:E:59:TRP:HE3	2.24	0.51
4:E:143:LEU:HD12	4:E:143:LEU:H	1.75	0.51
4:E:192:LYS:HZ2	4:E:206:GLN:HE22	1.58	0.51
4:E:242:LEU:HD12	4:E:242:LEU:O	2.11	0.51
1:A:136:PRO:CB	1:A:138:ASP:OD1	2.59	0.51
1:A:139:GLN:HG3	1:A:207:MET:N	2.26	0.51
1:A:384:GLU:CD	2:B:411:ILE:CG2	2.79	0.51
1:A:431:ILE:HG22	1:A:431:ILE:O	2.10	0.51
2:B:40:LEU:CA	2:B:52:THR:HG23	2.40	0.51
2:B:54:VAL:C	2:B:55:PHE:HD1	2.14	0.51
2:B:185:GLN:CB	2:B:219:PHE:CE2	2.78	0.51
3:C:192:ILE:HD13	3:C:221:ILE:CG2	2.40	0.51
3:C:318:SER:HB2	3:C:447:ASN:ND2	2.26	0.51
1:D:57:ARG:CB	1:D:119:THR:HG22	2.37	0.51
4:E:77:VAL:HG12	4:E:78:ARG:N	2.26	0.51
4:E:258:LEU:HG	4:E:258:LEU:O	2.10	0.51
4:E:270:GLN:C	4:E:273:PRO:CD	2.80	0.51
1:A:50:VAL:HG12	1:A:52:THR:CG2	2.41	0.51
1:A:137:PHE:O	1:A:208:GLN:HB2	2.11	0.51
1:A:250:LEU:HD21	1:A:292:THR:HG22	1.88	0.51
2:B:248:LYS:NZ	2:B:252:SER:HB3	2.25	0.51
3:C:30:VAL:HG22	3:C:158:ILE:N	2.26	0.51
3:C:221:ILE:HG13	3:C:222:ARG:N	2.25	0.51
3:C:298:LEU:CD1	3:C:471:PHE:HD2	2.24	0.51
1:D:212:LEU:O	1:D:215:VAL:HB	2.11	0.51
1:D:377:GLU:CB	4:E:415:CYS:SG	2.95	0.51
1:D:398:GLU:CA	1:D:401:TYR:CZ	2.92	0.51
1:D:419:ILE:CD1	1:D:420:ILE:HG23	2.41	0.51
4:E:14:TYR:CE2	4:E:16:LYS:CE	2.93	0.51
4:E:37:THR:OG1	4:E:54:TRP:CE3	2.63	0.51
4:E:59:TRP:CE3	4:E:59:TRP:N	2.79	0.51
4:E:262:THR:CA	4:E:265:LEU:HB2	2.40	0.51
1:A:35:LEU:C	1:A:35:LEU:CD2	2.77	0.50
1:A:187:TRP:HD1	1:A:199:LEU:CD2	2.24	0.50
2:B:40:LEU:CB	2:B:52:THR:HG23	2.40	0.50
2:B:69:PRO:O	2:B:73:GLU:CB	2.59	0.50
2:B:138:ASP:CA	2:B:464:PRO:O	2.59	0.50
2:B:263:LEU:CD2	2:B:291:VAL:HG23	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:406:GLU:HG2	2:B:409:LYS:CD	2.41	0.50
3:C:260:ALA:HB1	3:C:313:HIS:NE2	2.26	0.50
1:D:58:GLN:NE2	1:D:88:PRO:CG	2.74	0.50
1:D:100:PHE:N	1:D:100:PHE:CD1	2.78	0.50
1:D:261:VAL:O	1:D:261:VAL:HG12	2.11	0.50
1:D:295:VAL:O	1:D:299:HIS:HB2	2.10	0.50
1:D:410:LEU:O	1:D:414:PHE:HB2	2.11	0.50
4:E:75:ASP:HB3	4:E:110:TYR:OH	2.11	0.50
1:A:20:ARG:CG	1:A:20:ARG:O	2.59	0.50
1:A:41:ILE:HG12	1:A:51:GLU:O	2.11	0.50
1:A:57:ARG:HD3	1:A:161:GLU:OE1	2.10	0.50
2:B:210:TYR:C	2:B:211:LEU:HD23	2.31	0.50
2:B:223:TYR:O	2:B:223:TYR:HD1	1.93	0.50
3:C:30:VAL:HG23	3:C:157:GLU:H	1.76	0.50
3:C:74:TYR:HD1	3:C:114:PRO:HB2	1.75	0.50
3:C:179:ILE:CG1	3:C:181:PRO:HD2	2.38	0.50
1:D:25:HIS:CD2	1:D:155:LYS:HZ1	2.29	0.50
1:D:56:LEU:HD12	1:D:120:PRO:HG3	1.93	0.50
1:D:257:LEU:HA	1:D:260:ILE:HG13	1.92	0.50
4:E:138:TRP:HD1	4:E:213:ILE:CD1	2.24	0.50
4:E:173:ASP:HB2	4:E:185:ILE:HG21	1.93	0.50
4:E:240:TYR:O	4:E:243:PRO:CG	2.60	0.50
4:E:425:SER:O	4:E:429:GLN:HB3	2.12	0.50
1:A:2:GLU:HG3	1:A:74:GLY:HA2	1.93	0.50
2:B:58:LEU:HD21	2:B:118:TRP:CE3	2.46	0.50
2:B:220:TYR:CG	2:B:223:TYR:CE2	2.99	0.50
2:B:277:VAL:H	2:B:278:PRO:HD3	1.75	0.50
3:C:63:TYR:CE1	3:C:65:HIS:HA	2.46	0.50
3:C:80:LEU:CD1	1:D:20:ARG:NH2	2.73	0.50
1:D:50:VAL:HB	1:D:126:SER:OG	2.11	0.50
4:E:48:ALA:HA	4:E:126:THR:HA	1.94	0.50
4:E:79:ILE:O	4:E:79:ILE:HG23	2.09	0.50
4:E:90:VAL:HA	4:E:99:PHE:HE1	1.77	0.50
4:E:138:TRP:CE2	4:E:215:GLN:HB2	2.44	0.50
4:E:152:ALA:H	4:E:205:PHE:HD1	1.59	0.50
4:E:309:ARG:HD2	4:E:310:THR:HG23	1.91	0.50
1:A:401:TYR:O	1:A:401:TYR:CG	2.65	0.50
3:C:7:LEU:CD2	3:C:10:ASP:HB2	2.39	0.50
3:C:30:VAL:HG22	3:C:158:ILE:HA	1.93	0.50
3:C:35:LEU:CD2	3:C:37:LEU:HG	2.42	0.50
3:C:69:TRP:HD1	3:C:114:PRO:O	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:252:GLU:CG	1:D:300:HIS:C	2.80	0.50
3:C:426:THR:HA	3:C:429:ILE:CG2	2.41	0.50
1:D:37:LEU:HA	1:D:54:VAL:HG13	1.92	0.50
1:D:398:GLU:OE2	1:D:399:TRP:CZ3	2.64	0.50
1:D:432:GLU:O	1:D:436:GLU:HG3	2.11	0.50
4:E:239:VAL:CA	4:E:242:LEU:HD23	2.41	0.50
4:E:473:GLN:HA	4:E:476:GLU:HB2	1.92	0.50
1:A:56:LEU:HD23	1:A:57:ARG:H	1.77	0.50
1:A:209:ARG:C	1:A:210:ILE:CG1	2.79	0.50
2:B:28:LYS:HD3	2:B:154:SER:C	2.31	0.50
2:B:46:LYS:CB	2:B:276:SER:C	2.77	0.50
2:B:175:ILE:CD1	2:B:190:HIS:CD2	2.90	0.50
3:C:54:THR:O	3:C:126:PHE:CD2	2.65	0.50
3:C:219:LEU:HG	3:C:221:ILE:HG23	1.94	0.50
1:D:11:LEU:HD11	1:D:71:ASP:OD2	2.11	0.50
1:D:16:ASN:C	1:D:17:LYS:HG3	2.31	0.50
1:D:63:VAL:O	1:D:66:ARG:HD3	2.12	0.50
1:D:176:TRP:HB3	1:D:209:ARG:HG3	1.94	0.50
1:D:407:ASP:OD1	1:D:408:HIS:CD2	2.64	0.50
4:E:104:TYR:N	4:E:104:TYR:CD1	2.79	0.50
1:A:287:SER:O	1:A:291:VAL:HG23	2.11	0.50
1:A:380:LYS:CA	2:B:408:ILE:HD13	2.38	0.50
2:B:4:GLU:O	2:B:8:LEU:HG	2.11	0.50
2:B:185:GLN:O	2:B:217:PRO:HB3	2.11	0.50
3:C:102:TYR:O	3:C:102:TYR:CD1	2.62	0.50
3:C:161:ASP:OD1	3:C:199:LYS:HD3	2.11	0.50
3:C:258:SER:O	3:C:261:ILE:HB	2.12	0.50
1:D:54:VAL:O	1:D:56:LEU:CD2	2.60	0.50
4:E:122:ILE:HG12	4:E:122:ILE:O	2.10	0.50
4:E:147:SER:O	4:E:205:PHE:HE2	1.94	0.50
1:A:20:ARG:HB2	1:A:86:TRP:CE3	2.46	0.50
1:A:151:TYR:HB2	1:A:156:VAL:CG1	2.41	0.50
1:A:161:GLU:HG3	1:A:162:SER:N	2.27	0.50
1:A:227:PHE:CE2	2:B:299:VAL:CG1	2.94	0.50
2:B:2:VAL:HG12	2:B:3:MET:CE	2.41	0.50
2:B:85:VAL:CG1	2:B:86:TRP:N	2.74	0.50
2:B:146:PHE:O	2:B:147:LYS:HB2	2.11	0.50
3:C:68:THR:CA	3:C:115:ASN:HA	2.16	0.50
3:C:132:ILE:CG2	3:C:133:ASN:N	2.75	0.50
3:C:160:MET:N	3:C:213:GLN:HB2	2.25	0.50
1:D:18:VAL:O	1:D:18:VAL:HG12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:GLN:HE21	1:D:88:PRO:HG3	1.75	0.50
1:D:134:HIS:NE2	1:D:207:MET:HE3	2.27	0.50
1:D:176:TRP:HE3	1:D:209:ARG:NE	2.08	0.50
1:D:398:GLU:HA	1:D:401:TYR:CD2	2.47	0.50
4:E:103:TYR:CD2	4:E:104:TYR:CD1	3.00	0.50
4:E:128:PRO:HD2	4:E:141:CYS:HA	1.93	0.50
4:E:282:ILE:HG23	4:E:282:ILE:O	2.11	0.50
1:A:36:GLN:HA	1:A:164:ARG:CZ	2.41	0.50
1:A:50:VAL:CG1	1:A:51:GLU:N	2.75	0.50
1:A:249:VAL:HG12	1:A:250:LEU:N	2.27	0.50
2:B:112:HIS:CD2	2:B:113:THR:HG23	2.47	0.50
2:B:284:LEU:HA	2:B:287:ILE:CG1	2.42	0.50
1:D:259:VAL:HG22	1:D:262:GLU:OE2	2.11	0.50
1:D:289:ILE:O	1:D:292:THR:HG22	2.12	0.50
1:D:298:THR:O	1:D:301:ARG:CB	2.56	0.50
1:D:415:MET:O	1:D:419:ILE:HG23	2.12	0.50
4:E:58:GLN:C	4:E:59:TRP:HE3	2.14	0.50
4:E:86:LEU:CD1	4:E:103:TYR:OH	2.60	0.50
4:E:174:PRO:HA	4:E:177:PHE:CB	2.42	0.50
1:A:3:HIS:CB	1:A:7:LEU:HD23	2.42	0.50
1:A:58:GLN:HE21	1:A:90:LEU:HD21	1.76	0.50
1:A:92:LEU:CB	1:A:95:ASN:HB2	2.42	0.50
1:A:178:MET:HA	1:A:207:MET:CB	2.42	0.50
1:A:179:LYS:HB2	1:A:206:ILE:HG22	1.93	0.50
1:A:251:LEU:HD22	4:E:260:ALA:CB	2.42	0.50
1:A:379:VAL:CG2	4:E:424:LYS:HE3	2.40	0.50
2:B:130:ILE:HB	2:B:134:TYR:CE2	2.43	0.50
2:B:439:PHE:CA	2:B:442:ILE:HB	2.37	0.50
3:C:122:PRO:CB	1:D:149:TRP:HZ2	2.20	0.50
3:C:122:PRO:HB3	1:D:149:TRP:CZ2	2.38	0.50
3:C:263:VAL:O	3:C:267:GLN:HG2	2.12	0.50
1:D:66:ARG:O	1:D:67:TRP:CE3	2.65	0.50
1:D:76:LYS:HG2	1:D:112:TYR:CE2	2.47	0.50
4:E:14:TYR:OH	4:E:84:LEU:HD12	2.11	0.50
4:E:123:TYR:HD1	4:E:123:TYR:H	1.60	0.50
1:A:90:LEU:HD12	1:A:100:PHE:CE2	2.47	0.49
2:B:229:ILE:O	2:B:233:ILE:HG12	2.11	0.49
3:C:63:TYR:O	3:C:65:HIS:CD2	2.65	0.49
1:D:229:THR:O	1:D:232:VAL:HB	2.12	0.49
1:D:414:PHE:O	1:D:414:PHE:CD1	2.64	0.49
4:E:33:LYS:HG2	4:E:160:SER:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:123:TYR:N	4:E:123:TYR:HD1	2.10	0.49
4:E:313:THR:OG1	4:E:313:THR:O	2.24	0.49
1:A:56:LEU:HD12	1:A:90:LEU:HD13	1.93	0.49
1:A:95:ASN:OD1	1:A:144:MET:CG	2.59	0.49
1:A:274:ILE:HD13	1:A:277:TYR:CE1	2.47	0.49
1:A:293:VAL:CG1	1:A:294:VAL:N	2.76	0.49
2:B:286:PHE:CE1	2:B:287:ILE:HG23	2.46	0.49
3:C:141:TRP:CH2	3:C:223:ARG:HD3	2.48	0.49
3:C:462:THR:N	3:C:463:PRO:CD	2.73	0.49
1:D:32:THR:HG21	1:D:59:GLN:HE21	1.76	0.49
1:D:137:PHE:CE2	1:D:277:TYR:HE1	2.30	0.49
4:E:27:VAL:HB	4:E:154:GLU:CA	2.42	0.49
4:E:45:LYS:CE	4:E:278:ASN:C	2.72	0.49
1:A:233:PHE:CE1	1:A:413:VAL:CG1	2.94	0.49
1:A:304:SER:HB2	1:A:397:GLU:HG2	1.94	0.49
1:A:385:HIS:ND1	1:A:385:HIS:O	2.46	0.49
2:B:75:ILE:HG21	3:C:27:ASN:HB2	1.93	0.49
2:B:147:LYS:CG	2:B:148:SER:H	2.25	0.49
2:B:223:TYR:O	2:B:223:TYR:CD1	2.66	0.49
3:C:110:VAL:CG2	3:C:120:TRP:HB2	2.42	0.49
3:C:308:ILE:HG22	3:C:309:VAL:N	2.27	0.49
1:D:106:THR:CG2	1:D:107:LYS:CD	2.90	0.49
1:D:140:GLN:HG3	1:D:141:ASN:N	2.25	0.49
1:D:152:ASP:CB	1:D:196:THR:O	2.60	0.49
4:E:140:ASN:HD21	4:E:211:PHE:CA	2.22	0.49
1:A:136:PRO:CD	1:A:274:ILE:HG23	2.38	0.49
1:A:136:PRO:CA	1:A:277:TYR:OH	2.60	0.49
1:A:214:PHE:CD1	1:A:214:PHE:C	2.83	0.49
1:A:276:LYS:N	1:A:276:LYS:HD2	2.27	0.49
1:A:284:PHE:N	1:A:284:PHE:HD1	2.10	0.49
2:B:137:PHE:CD1	2:B:137:PHE:N	2.79	0.49
2:B:159:GLN:HA	2:B:195:LYS:HZ3	1.78	0.49
2:B:304:LEU:HD23	2:B:304:LEU:C	2.32	0.49
3:C:58:MET:HE1	3:C:105:ALA:O	2.13	0.49
3:C:192:ILE:CD1	3:C:221:ILE:CG2	2.90	0.49
3:C:427:ASN:HA	3:C:430:VAL:CG2	2.40	0.49
1:D:26:THR:C	1:D:28:PHE:H	2.15	0.49
1:D:93:TYR:OH	1:D:198:TYR:CD2	2.66	0.49
1:D:157:SER:CA	1:D:199:LEU:HD12	2.40	0.49
1:D:291:VAL:HG12	1:D:295:VAL:HG11	1.94	0.49
4:E:133:TYR:C	4:E:135:PRO:CD	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:192:LYS:NZ	4:E:206:GLN:HE22	2.10	0.49
4:E:250:LYS:CA	4:E:253:LEU:HB3	2.34	0.49
1:A:207:MET:N	1:A:207:MET:SD	2.86	0.49
1:A:379:VAL:HG22	4:E:424:LYS:HE3	1.94	0.49
2:B:185:GLN:O	2:B:217:PRO:CA	2.60	0.49
2:B:302:LEU:O	2:B:305:HIS:HB2	2.12	0.49
3:C:51:THR:C	3:C:52:LEU:HD13	2.32	0.49
3:C:249:LEU:N	3:C:249:LEU:CD1	2.75	0.49
3:C:464:VAL:CG1	3:C:465:MET:N	2.76	0.49
1:D:32:THR:O	1:D:58:GLN:HA	2.12	0.49
1:D:49:ILE:HG21	1:D:125:LYS:CE	2.42	0.49
1:D:53:ASN:HD21	1:D:121:PRO:C	2.14	0.49
1:D:432:GLU:HG2	1:D:435:GLN:HE22	1.74	0.49
4:E:35:THR:CB	4:E:54:TRP:HE3	2.22	0.49
4:E:44:GLU:CG	4:E:129:ILE:HD12	2.42	0.49
4:E:107:VAL:CG1	4:E:117:TRP:HB2	2.39	0.49
4:E:258:LEU:HD13	4:E:301:VAL:HG13	1.93	0.49
4:E:289:VAL:O	4:E:293:SER:HB3	2.12	0.49
1:A:170:PHE:HZ	1:A:176:TRP:O	1.94	0.49
2:B:35:LEU:CD1	2:B:56:LEU:HD12	2.41	0.49
2:B:50:MET:HB3	2:B:126:SER:OG	2.12	0.49
2:B:92:LEU:HD12	2:B:95:ASN:HB2	1.95	0.49
2:B:103:THR:OG1	2:B:122:ALA:HB1	2.12	0.49
2:B:132:VAL:HG13	2:B:279:ILE:C	2.32	0.49
2:B:269:LYS:O	2:B:273:THR:HG23	2.13	0.49
1:D:135:PHE:CZ	1:D:273:LEU:CD1	2.96	0.49
1:D:191:THR:O	1:D:191:THR:CG2	2.61	0.49
1:D:419:ILE:HD12	1:D:420:ILE:HG23	1.95	0.49
2:B:133:MET:CB	2:B:140:GLN:HG3	2.43	0.49
3:C:63:TYR:CD1	3:C:116:GLY:HA3	2.48	0.49
3:C:148:PHE:CB	3:C:215:VAL:HG22	2.39	0.49
3:C:158:ILE:CG2	3:C:159:SER:N	2.75	0.49
3:C:185:THR:O	3:C:185:THR:HG22	2.11	0.49
3:C:222:ARG:NH2	3:C:224:LYS:N	2.61	0.49
3:C:298:LEU:CD1	3:C:471:PHE:CD2	2.95	0.49
3:C:434:LYS:HE2	3:C:435:GLU:HG2	1.94	0.49
1:D:289:ILE:CG2	1:D:290:ILE:N	2.76	0.49
4:E:138:TRP:CD1	4:E:213:ILE:CD1	2.96	0.49
4:E:284:LYS:H	4:E:284:LYS:CD	2.26	0.49
1:A:7:LEU:O	1:A:11:LEU:HG	2.13	0.49
1:A:171:MET:HG2	1:A:174:GLY:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ILE:CG2	1:A:420:ILE:N	2.74	0.49
2:B:46:LYS:HD2	2:B:275:LEU:C	2.33	0.49
2:B:185:GLN:NE2	2:B:219:PHE:CD2	2.81	0.49
2:B:192:PRO:HD2	2:B:210:TYR:O	2.13	0.49
2:B:279:ILE:HG22	2:B:280:ILE:CA	2.42	0.49
3:C:252:GLU:HG3	1:D:300:HIS:CB	2.43	0.49
1:D:28:PHE:HB3	1:D:156:VAL:CA	2.43	0.49
1:D:29:VAL:CG2	1:D:60:TRP:CD1	2.73	0.49
4:E:183:TRP:HB2	4:E:215:GLN:O	2.13	0.49
4:E:247:GLY:H	4:E:250:LYS:HZ2	1.61	0.49
1:A:175:GLU:C	1:A:211:PRO:HD3	2.33	0.49
2:B:92:LEU:HD22	2:B:146:PHE:CG	2.48	0.49
2:B:93:MET:HB2	2:B:145:VAL:HB	1.95	0.49
2:B:141:ASN:HA	2:B:211:LEU:C	2.33	0.49
2:B:444:ILE:CG2	2:B:445:THR:N	2.76	0.49
2:B:468:PHE:O	2:B:469:ALA:HB2	2.13	0.49
3:C:21:VAL:O	3:C:23:PRO:HD3	2.13	0.49
1:D:405:VAL:O	1:D:405:VAL:HG12	2.11	0.49
1:D:420:ILE:HA	1:D:423:VAL:HB	1.95	0.49
4:E:14:TYR:HE1	4:E:84:LEU:HD11	1.77	0.49
4:E:140:ASN:CG	4:E:211:PHE:HB3	2.34	0.49
4:E:161:ALA:O	4:E:190:ALA:HB3	2.12	0.49
2:B:238:VAL:CG2	2:B:255:ALA:CB	2.82	0.49
3:C:141:TRP:HB2	3:C:222:ARG:HA	1.95	0.49
3:C:235:PRO:HG2	3:C:236:CYS:H	1.78	0.49
3:C:252:GLU:CD	1:D:301:ARG:HA	2.33	0.49
1:D:35:LEU:HD23	1:D:164:ARG:HH11	1.70	0.49
1:D:72:TYR:CG	1:D:73:GLY:N	2.78	0.49
1:D:134:HIS:NE2	1:D:207:MET:HE2	2.28	0.49
4:E:9:LYS:HD2	4:E:9:LYS:C	2.32	0.49
4:E:66:TRP:NE1	4:E:111:ASN:CA	2.56	0.49
4:E:86:LEU:HD13	4:E:103:TYR:OH	2.12	0.49
1:A:62:ASP:CB	1:A:65:LEU:HD12	2.37	0.48
1:A:227:PHE:CE2	2:B:299:VAL:HG12	2.48	0.48
4:E:215:GLN:CG	4:E:216:ARG:N	2.76	0.48
4:E:240:TYR:CD2	4:E:453:ILE:CD1	2.83	0.48
1:A:256:PHE:N	1:A:256:PHE:HD1	2.10	0.48
3:C:136:TYR:CD1	3:C:142:GLN:HB3	2.48	0.48
3:C:314:PHE:O	3:C:314:PHE:HD1	1.96	0.48
3:C:315:ARG:H	3:C:315:ARG:CD	2.25	0.48
3:C:431:LYS:HA	3:C:434:LYS:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:THR:O	1:D:247:ILE:HB	2.13	0.48
1:D:283:ILE:HA	1:D:286:ILE:HD12	1.94	0.48
1:D:298:THR:C	1:D:301:ARG:HB3	2.34	0.48
4:E:44:GLU:CG	4:E:129:ILE:CG1	2.86	0.48
4:E:59:TRP:CE2	4:E:115:MET:HB2	2.48	0.48
4:E:187:HIS:ND1	4:E:189:PRO:CG	2.74	0.48
4:E:262:THR:CB	4:E:265:LEU:HD12	2.42	0.48
4:E:302:ILE:O	4:E:306:VAL:HG23	2.13	0.48
1:A:67:TRP:HB2	1:A:112:TYR:CB	2.41	0.48
2:B:188:ILE:CG2	2:B:189:GLU:N	2.74	0.48
1:D:63:VAL:O	1:D:63:VAL:CG2	2.61	0.48
1:D:86:TRP:CE3	1:D:86:TRP:C	2.87	0.48
1:D:228:LEU:CD1	4:E:258:LEU:HD21	2.43	0.48
4:E:182:GLU:CA	4:E:218:PRO:HG2	2.42	0.48
4:E:303:VAL:O	4:E:306:VAL:HB	2.13	0.48
1:A:136:PRO:CB	1:A:277:TYR:OH	2.58	0.48
2:B:139:TRP:CZ2	2:B:215:ARG:O	2.66	0.48
3:C:12:LEU:HD12	3:C:16:LYS:HD2	1.96	0.48
3:C:30:VAL:HG13	3:C:31:VAL:O	2.12	0.48
3:C:59:ASP:OD2	3:C:121:LEU:HD22	2.13	0.48
3:C:80:LEU:O	3:C:112:VAL:CB	2.60	0.48
3:C:113:ARG:CG	3:C:117:TYR:O	2.62	0.48
3:C:179:ILE:HG23	3:C:181:PRO:CD	2.41	0.48
3:C:264:LEU:HA	3:C:267:GLN:CG	2.40	0.48
1:D:48:GLN:HB3	1:D:130:ILE:HD13	1.83	0.48
4:E:38:ASN:O	4:E:51:THR:CA	2.61	0.48
4:E:79:ILE:CG1	4:E:80:PRO:HD3	2.44	0.48
4:E:138:TRP:O	4:E:213:ILE:HG13	2.13	0.48
1:A:181:TYR:HB2	1:A:204:HIS:O	2.13	0.48
1:A:249:VAL:HG13	1:A:253:LEU:HD23	1.94	0.48
2:B:138:ASP:CB	2:B:464:PRO:O	2.61	0.48
2:B:221:ILE:HA	2:B:224:THR:HB	1.94	0.48
2:B:241:LEU:HD12	2:B:241:LEU:O	2.14	0.48
3:C:39:LEU:HD12	3:C:39:LEU:N	2.28	0.48
3:C:471:PHE:CD1	3:C:472:ILE:N	2.82	0.48
1:D:112:TYR:HD1	1:D:113:THR:N	2.07	0.48
1:D:166:ASP:CG	1:D:181:TYR:HB2	2.32	0.48
4:E:95:VAL:HG22	4:E:123:TYR:CD2	2.49	0.48
4:E:184:THR:HG23	4:E:215:GLN:CG	2.44	0.48
4:E:232:ILE:HG22	4:E:233:SER:N	2.29	0.48
4:E:237:VAL:HG22	4:E:457:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:239:VAL:N	4:E:242:LEU:HD23	2.28	0.48
4:E:264:PHE:N	4:E:264:PHE:HD1	2.12	0.48
1:A:51:GLU:HA	1:A:124:PHE:O	2.14	0.48
3:C:25:LYS:HA	3:C:25:LYS:NZ	2.29	0.48
3:C:290:LYS:O	3:C:294:PHE:CE2	2.66	0.48
1:D:47:ASN:O	1:D:49:ILE:HG12	2.14	0.48
1:D:201:ILE:CG2	1:D:203:TYR:CE1	2.94	0.48
1:D:245:LEU:CD1	4:E:252:THR:HA	2.42	0.48
4:E:56:GLU:HA	4:E:118:LEU:CG	2.43	0.48
4:E:143:LEU:HD12	4:E:143:LEU:N	2.29	0.48
4:E:266:PHE:HD1	4:E:269:ALA:HB3	1.79	0.48
1:A:17:LYS:HB3	1:A:84:ASP:O	2.13	0.48
1:A:133:THR:O	1:A:140:GLN:HB2	2.13	0.48
1:A:136:PRO:HB3	1:A:138:ASP:OD1	2.14	0.48
2:B:129:THR:HG22	2:B:142:CYS:CA	2.39	0.48
2:B:130:ILE:HD12	2:B:134:TYR:CE2	2.48	0.48
3:C:30:VAL:HG21	3:C:158:ILE:C	2.34	0.48
3:C:69:TRP:HE1	3:C:114:PRO:CA	2.15	0.48
3:C:69:TRP:HD1	3:C:114:PRO:C	2.15	0.48
1:D:141:ASN:HB3	1:D:206:ILE:CG1	2.43	0.48
4:E:240:TYR:HB3	4:E:453:ILE:HG12	1.95	0.48
4:E:261:GLN:HG3	4:E:262:THR:N	2.29	0.48
1:A:276:LYS:HD2	1:A:276:LYS:H	1.78	0.48
2:B:32:ARG:HG3	2:B:59:ALA:O	2.13	0.48
2:B:101:GLU:OE1	2:B:123:ILE:HG21	2.14	0.48
2:B:186:TRP:CZ3	2:B:215:ARG:CZ	2.96	0.48
2:B:187:SER:O	2:B:188:ILE:HG12	2.14	0.48
2:B:218:LEU:CD1	2:B:221:ILE:HG12	2.44	0.48
2:B:280:ILE:C	2:B:282:SER:N	2.67	0.48
3:C:125:ILE:O	3:C:125:ILE:HG22	2.13	0.48
3:C:184:PHE:CE1	3:C:185:THR:O	2.66	0.48
1:D:93:TYR:CZ	1:D:198:TYR:CE2	3.01	0.48
1:D:112:TYR:HE1	1:D:113:THR:HG1	1.57	0.48
1:D:146:LEU:HD22	1:D:203:TYR:OH	2.14	0.48
1:D:291:VAL:HG12	1:D:295:VAL:CG1	2.43	0.48
4:E:44:GLU:OE1	4:E:129:ILE:CD1	2.61	0.48
4:E:153:HIS:C	4:E:154:GLU:HG3	2.33	0.48
4:E:293:SER:O	4:E:297:VAL:HG23	2.14	0.48
1:A:33:VAL:O	1:A:161:GLU:HG2	2.14	0.48
1:A:112:TYR:N	1:A:112:TYR:CD1	2.79	0.48
1:A:247:ILE:CG2	1:A:248:SER:N	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:SER:O	1:A:396:ALA:HB3	2.13	0.48
2:B:185:GLN:HB3	2:B:217:PRO:HB3	1.94	0.48
2:B:438:LEU:O	2:B:442:ILE:CD1	2.61	0.48
3:C:56:VAL:HG22	3:C:124:ALA:HB3	1.96	0.48
3:C:60:HIS:HE1	3:C:160:MET:CE	2.26	0.48
3:C:194:HIS:ND1	3:C:195:LYS:N	2.62	0.48
3:C:278:LEU:HD12	3:C:279:PRO:N	2.27	0.48
4:E:29:ASP:N	4:E:29:ASP:OD1	2.46	0.48
4:E:79:ILE:HG12	4:E:80:PRO:HD3	1.88	0.48
4:E:299:ASN:ND2	4:E:456:LEU:HG	2.28	0.48
3:C:160:MET:H	3:C:213:GLN:HG3	1.78	0.48
3:C:271:LEU:HD23	3:C:271:LEU:O	2.13	0.48
3:C:275:SER:O	3:C:279:PRO:CD	2.58	0.48
1:D:36:GLN:NE2	1:D:38:ILE:HG12	2.29	0.48
1:D:100:PHE:N	1:D:100:PHE:HD1	2.11	0.48
4:E:91:LEU:HB3	4:E:94:ASN:N	2.22	0.48
4:E:294:LEU:HA	4:E:297:VAL:HG23	1.96	0.48
1:A:62:ASP:OD1	1:A:64:ARG:HB2	2.13	0.47
1:A:145:LYS:CG	1:A:202:THR:HG22	2.19	0.47
2:B:186:TRP:CG	2:B:215:ARG:HD2	2.48	0.47
3:C:204:ASP:H	3:C:207:PRO:CG	2.26	0.47
1:D:60:TRP:O	1:D:61:ILE:HG23	2.14	0.47
1:D:107:LYS:HZ2	4:E:149:THR:CB	2.27	0.47
1:D:376:ILE:O	1:D:380:LYS:HE2	2.13	0.47
4:E:94:ASN:ND2	4:E:143:LEU:CD2	2.72	0.47
4:E:304:LEU:O	4:E:308:LEU:HB2	2.13	0.47
1:A:251:LEU:HD11	4:E:256:SER:C	2.35	0.47
1:A:252:SER:O	1:A:256:PHE:CE1	2.67	0.47
1:A:422:THR:HA	1:A:425:VAL:HG12	1.96	0.47
2:B:20:ARG:H	2:B:20:ARG:CD	2.23	0.47
2:B:92:LEU:HD22	2:B:146:PHE:HA	1.96	0.47
2:B:135:PHE:N	2:B:136:PRO:HD2	2.29	0.47
3:C:137:PHE:O	3:C:137:PHE:CG	2.66	0.47
3:C:233:ILE:N	3:C:233:ILE:CD1	2.77	0.47
1:D:106:THR:HG23	1:D:107:LYS:NZ	2.28	0.47
1:D:390:GLU:O	1:D:393:SER:CB	2.61	0.47
1:D:419:ILE:O	1:D:422:THR:HG22	2.13	0.47
4:E:262:THR:HG23	4:E:265:LEU:HB2	1.96	0.47
1:A:133:THR:C	1:A:136:PRO:CG	2.82	0.47
2:B:75:ILE:HD11	2:B:78:LEU:CD1	2.36	0.47
2:B:176:ASN:HB3	2:B:191:LYS:HB3	1.87	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:192:PRO:HB2	2:B:210:TYR:HB2	1.95	0.47
3:C:3:GLU:OE1	3:C:7:LEU:CD1	2.58	0.47
3:C:185:THR:HG22	3:C:188:GLY:H	1.79	0.47
1:D:35:LEU:HB3	1:D:164:ARG:CZ	2.44	0.47
1:D:60:TRP:O	1:D:116:ILE:HG12	2.14	0.47
1:D:130:ILE:CA	1:D:134:HIS:HB2	2.44	0.47
4:E:81:SER:O	4:E:86:LEU:HD11	2.15	0.47
4:E:177:PHE:CE1	4:E:178:THR:O	2.67	0.47
4:E:463:LEU:HD12	4:E:463:LEU:C	2.30	0.47
2:B:223:TYR:CD1	2:B:223:TYR:C	2.88	0.47
2:B:239:PHE:HB3	2:B:442:ILE:CG1	2.42	0.47
2:B:299:VAL:O	2:B:302:LEU:HB3	2.13	0.47
3:C:16:LYS:HE3	3:C:16:LYS:CA	2.35	0.47
3:C:150:ALA:HB3	3:C:158:ILE:CD1	2.44	0.47
3:C:185:THR:HG22	3:C:188:GLY:N	2.29	0.47
3:C:270:PHE:CZ	1:D:255:VAL:HB	2.49	0.47
1:D:37:LEU:CD1	1:D:54:VAL:HG22	2.44	0.47
1:D:233:PHE:O	1:D:236:PRO:HG2	2.13	0.47
1:D:250:LEU:CD2	1:D:292:THR:CB	2.91	0.47
4:E:116:TYR:CD1	4:E:116:TYR:C	2.88	0.47
4:E:117:TRP:O	4:E:118:LEU:CB	2.59	0.47
4:E:209:ILE:CG1	4:E:211:PHE:CE1	2.97	0.47
4:E:240:TYR:CB	4:E:453:ILE:CD1	2.91	0.47
1:A:29:VAL:HG21	1:A:86:TRP:HZ3	1.78	0.47
1:A:43:VAL:CG1	1:A:50:VAL:CG2	2.85	0.47
1:A:108:LEU:HD13	1:A:118:TRP:CA	2.44	0.47
2:B:91:VAL:HG22	2:B:92:LEU:N	2.29	0.47
2:B:184:GLY:C	2:B:186:TRP:N	2.68	0.47
3:C:113:ARG:NE	3:C:119:THR:HG23	2.24	0.47
3:C:156:ASN:O	3:C:157:GLU:HG3	2.15	0.47
3:C:429:ILE:C	3:C:429:ILE:HD12	2.34	0.47
1:D:379:VAL:CG2	1:D:382:ILE:HD12	2.39	0.47
1:A:33:VAL:HG23	1:A:158:ILE:HG12	1.91	0.47
1:A:176:TRP:HB3	1:A:209:ARG:CG	2.44	0.47
1:A:201:ILE:HG22	1:A:203:TYR:CE1	2.50	0.47
2:B:21:PRO:CG	2:B:85:VAL:HG13	2.44	0.47
2:B:56:LEU:C	2:B:120:PRO:HD2	2.34	0.47
2:B:234:LEU:HD11	2:B:262:PHE:CE2	2.50	0.47
3:C:312:PHE:O	3:C:315:ARG:HD2	2.15	0.47
3:C:429:ILE:CG1	3:C:430:VAL:N	2.77	0.47
3:C:464:VAL:HG13	3:C:465:MET:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:TRP:CZ3	1:D:209:ARG:NH2	2.82	0.47
1:D:236:PRO:HB3	1:D:299:HIS:NE2	2.29	0.47
4:E:157:LEU:CD1	4:E:208:ILE:HD11	2.44	0.47
4:E:185:ILE:CG1	4:E:214:ILE:CG2	2.79	0.47
4:E:238:LEU:O	4:E:242:LEU:HB3	2.15	0.47
4:E:262:THR:HG23	4:E:265:LEU:HD12	1.96	0.47
1:A:39:GLN:C	1:A:40:LEU:HD23	2.35	0.47
1:A:41:ILE:HG13	1:A:51:GLU:HB3	1.94	0.47
1:A:130:ILE:O	1:A:134:HIS:HB2	2.14	0.47
1:A:192:CYS:SG	1:A:193:CYS:N	2.87	0.47
1:A:259:VAL:HG13	1:A:262:GLU:OE1	2.15	0.47
2:B:45:GLU:CD	2:B:277:VAL:HB	2.34	0.47
2:B:81:PRO:HA	2:B:107:ASN:HA	1.96	0.47
2:B:196:ASN:C	2:B:196:ASN:OD1	2.53	0.47
3:C:35:LEU:HD21	3:C:37:LEU:HD21	1.97	0.47
3:C:110:VAL:HG12	3:C:111:LEU:N	2.29	0.47
3:C:211:ASN:ND2	3:C:212:TYR:CE1	2.82	0.47
3:C:253:SER:HB2	1:D:306:HIS:HB3	1.96	0.47
3:C:439:TYR:O	3:C:443:VAL:HG23	2.14	0.47
3:C:449:VAL:CG1	3:C:452:THR:HB	2.25	0.47
1:D:49:ILE:CG2	1:D:125:LYS:CE	2.93	0.47
1:D:92:LEU:HD13	1:D:146:LEU:HD11	1.95	0.47
1:D:137:PHE:HB3	1:D:431:ILE:O	2.14	0.47
1:D:420:ILE:HA	1:D:423:VAL:CB	2.44	0.47
4:E:20:PRO:CB	4:E:61:ASP:OD1	2.60	0.47
4:E:62:TYR:C	4:E:64:LEU:H	2.18	0.47
4:E:116:TYR:HD1	4:E:117:TRP:N	2.13	0.47
4:E:131:VAL:HA	4:E:282:ILE:HA	1.96	0.47
4:E:174:PRO:HA	4:E:177:PHE:HB3	1.96	0.47
4:E:219:LEU:HD13	4:E:222:ILE:HB	1.95	0.47
4:E:232:ILE:O	4:E:236:VAL:HG22	2.14	0.47
4:E:262:THR:O	4:E:262:THR:CG2	2.62	0.47
1:A:215:VAL:O	1:A:218:VAL:HG12	2.15	0.47
1:A:281:THR:O	1:A:285:VAL:HG12	2.14	0.47
2:B:152:ASP:OD1	2:B:203:SER:CB	2.63	0.47
3:C:122:PRO:HA	1:D:149:TRP:CH2	2.50	0.47
3:C:179:ILE:HD12	3:C:179:ILE:HA	1.79	0.47
3:C:252:GLU:HG3	1:D:300:HIS:HB3	1.96	0.47
3:C:452:THR:HG23	3:C:456:LEU:HG	1.97	0.47
1:D:34:GLY:C	1:D:57:ARG:HD2	2.34	0.47
1:D:43:VAL:HG21	1:D:50:VAL:HG13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:112:TYR:CD1	1:D:112:TYR:N	2.83	0.47
1:D:135:PHE:CD2	1:D:210:ILE:HG12	2.50	0.47
4:E:264:PHE:N	4:E:264:PHE:CD1	2.82	0.47
1:A:76:LYS:O	1:A:112:TYR:CD2	2.68	0.47
1:A:166:ASP:CB	1:A:178:MET:CE	2.93	0.47
1:A:270:ALA:C	1:A:271:VAL:HG13	2.36	0.47
2:B:15:TYR:O	2:B:15:TYR:HD1	1.97	0.47
2:B:69:PRO:HG2	2:B:70:ALA:H	1.80	0.47
2:B:92:LEU:HB2	2:B:95:ASN:HB2	1.97	0.47
2:B:233:ILE:O	2:B:237:LEU:HD22	2.15	0.47
3:C:19:LYS:O	3:C:19:LYS:CE	2.63	0.47
3:C:143:ASN:OD1	3:C:220:ILE:CB	2.62	0.47
1:D:384:GLU:HG2	4:E:422:ILE:HD11	1.93	0.47
4:E:90:VAL:HG13	4:E:95:VAL:CB	2.36	0.47
4:E:100:GLU:HG3	4:E:122:ILE:O	2.14	0.47
4:E:116:TYR:C	4:E:116:TYR:HD1	2.19	0.47
4:E:417:GLU:O	4:E:421:PHE:CG	2.68	0.47
1:A:236:PRO:CB	1:A:299:HIS:CE1	2.65	0.47
1:A:405:VAL:HG23	1:A:405:VAL:O	2.15	0.47
2:B:78:LEU:HD23	2:B:80:ILE:HD11	1.96	0.47
2:B:240:TYR:O	2:B:244:ASP:HB2	2.15	0.47
3:C:41:ASN:HD22	3:C:41:ASN:HA	1.23	0.47
3:C:66:ARG:HH11	3:C:66:ARG:CG	2.27	0.47
3:C:113:ARG:NE	3:C:117:TYR:HB3	2.30	0.47
3:C:137:PHE:N	3:C:138:PRO:CD	2.76	0.47
3:C:138:PRO:CD	3:C:288:ILE:CD1	2.91	0.47
3:C:148:PHE:CD1	3:C:148:PHE:N	2.83	0.47
3:C:179:ILE:HD12	3:C:195:LYS:CG	2.44	0.47
3:C:427:ASN:O	3:C:431:LYS:HG3	2.14	0.47
1:D:66:ARG:HA	1:D:113:THR:O	2.15	0.47
1:D:129:GLU:C	1:D:130:ILE:CG2	2.80	0.47
1:D:242:LYS:HA	1:D:243:MET:HE2	1.96	0.47
4:E:45:LYS:HZ1	4:E:278:ASN:HA	1.79	0.47
4:E:71:TYR:CG	4:E:72:GLU:N	2.83	0.47
4:E:107:VAL:HG13	4:E:117:TRP:CB	2.43	0.47
4:E:146:ARG:CD	4:E:205:PHE:CD2	2.97	0.47
4:E:172:ILE:HD12	4:E:188:ARG:CA	2.44	0.47
4:E:206:GLN:HE21	4:E:206:GLN:HB3	1.36	0.47
1:A:223:LEU:HA	1:A:226:SER:OG	2.15	0.46
1:D:157:SER:HB2	1:D:199:LEU:CD1	2.44	0.46
4:E:110:TYR:HB3	4:E:112:ASP:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:263:ILE:HG21	4:E:263:ILE:HD13	1.55	0.46
1:A:129:GLU:O	1:A:142:CYS:SG	2.74	0.46
1:A:187:TRP:CD1	1:A:199:LEU:CD2	2.98	0.46
1:A:233:PHE:CZ	1:A:413:VAL:HG11	2.49	0.46
2:B:10:VAL:HG13	2:B:11:LEU:CD2	2.33	0.46
3:C:38:THR:OG1	3:C:178:ILE:HG21	2.14	0.46
3:C:232:PHE:O	3:C:235:PRO:CG	2.63	0.46
3:C:289:GLY:O	3:C:293:MET:SD	2.73	0.46
1:D:377:GLU:N	1:D:380:LYS:HE2	2.29	0.46
4:E:30:VAL:O	4:E:157:LEU:HA	2.15	0.46
4:E:138:TRP:CG	4:E:213:ILE:HG12	2.50	0.46
4:E:247:GLY:N	4:E:250:LYS:HZ2	2.14	0.46
1:A:56:LEU:CD2	1:A:56:LEU:C	2.83	0.46
1:A:72:TYR:HB3	1:A:112:TYR:HB2	1.97	0.46
1:A:227:PHE:O	1:A:230:VAL:HB	2.15	0.46
2:B:196:ASN:O	2:B:197:TRP:CD1	2.68	0.46
2:B:245:ALA:O	2:B:248:LYS:HB3	2.16	0.46
2:B:268:ASP:O	2:B:271:PRO:HD2	2.15	0.46
3:C:63:TYR:HD1	3:C:64:ASP:H	1.61	0.46
3:C:63:TYR:HB2	3:C:117:TYR:CZ	2.51	0.46
1:A:176:TRP:CB	1:A:209:ARG:HG3	2.46	0.46
1:A:241:GLU:HG2	1:A:241:GLU:O	2.15	0.46
1:A:280:PHE:O	1:A:284:PHE:CG	2.68	0.46
2:B:7:LEU:HD11	2:B:69:PRO:HD2	1.97	0.46
2:B:188:ILE:HG22	2:B:190:HIS:N	2.29	0.46
2:B:306:HIS:ND1	2:B:306:HIS:C	2.30	0.46
3:C:77:ILE:HD12	3:C:80:LEU:CD1	2.36	0.46
3:C:84:PRO:CG	3:C:107:PHE:O	2.63	0.46
3:C:111:LEU:O	3:C:118:VAL:HG13	2.16	0.46
3:C:113:ARG:CB	3:C:117:TYR:O	2.64	0.46
3:C:266:ALA:HB3	1:D:251:LEU:HD22	1.98	0.46
1:D:44:ASP:O	1:D:48:GLN:HA	2.15	0.46
1:D:111:ASP:OD2	1:D:115:LYS:CD	2.58	0.46
1:D:151:TYR:O	1:D:198:TYR:HB3	2.16	0.46
1:D:177:VAL:HG12	1:D:208:GLN:CG	2.43	0.46
1:D:377:GLU:HA	1:D:380:LYS:CE	2.46	0.46
4:E:55:ILE:HG23	4:E:119:PRO:HD2	1.97	0.46
4:E:59:TRP:HH2	4:E:107:VAL:HG12	1.81	0.46
4:E:93:ASN:CG	4:E:93:ASN:O	2.54	0.46
4:E:216:ARG:C	4:E:218:PRO:HD2	2.35	0.46
4:E:270:GLN:O	4:E:273:PRO:CG	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ASN:ND2	1:A:94:ASN:C	2.69	0.46
1:A:285:VAL:HG13	1:A:286:ILE:HG13	1.98	0.46
1:A:376:ILE:CG2	1:A:380:LYS:HZ1	2.25	0.46
1:A:379:VAL:HG13	4:E:424:LYS:CE	2.28	0.46
2:B:252:SER:O	2:B:255:ALA:CB	2.63	0.46
3:C:80:LEU:HG	3:C:81:ARG:H	1.81	0.46
3:C:115:ASN:HD22	3:C:115:ASN:H	1.51	0.46
3:C:122:PRO:CB	1:D:149:TRP:CZ2	2.98	0.46
1:D:176:TRP:CB	1:D:209:ARG:HG3	2.46	0.46
4:E:172:ILE:HG13	4:E:173:ASP:HA	1.98	0.46
4:E:232:ILE:HA	4:E:232:ILE:HD13	1.51	0.46
4:E:256:SER:O	4:E:259:LEU:HB2	2.16	0.46
2:B:109:LEU:HB3	2:B:117:SER:CB	2.40	0.46
3:C:35:LEU:HD22	3:C:215:VAL:CG2	2.43	0.46
3:C:462:THR:O	3:C:466:VAL:HG22	2.16	0.46
1:D:78:ILE:CD1	1:D:110:LEU:CB	2.91	0.46
1:D:170:PHE:CZ	1:D:171:MET:O	2.68	0.46
1:D:264:ILE:HG13	1:D:264:ILE:H	1.39	0.46
4:E:444:LYS:HA	4:E:444:LYS:CE	2.45	0.46
4:E:470:HIS:CE1	4:E:474:VAL:HG23	2.50	0.46
1:A:75:ILE:O	1:A:78:ILE:HG23	2.16	0.46
1:A:262:GLU:O	1:A:265:PRO:HD2	2.15	0.46
1:A:415:MET:HA	1:A:415:MET:CE	2.46	0.46
3:C:206:PHE:O	3:C:206:PHE:HD1	1.98	0.46
3:C:269:VAL:HA	3:C:272:LEU:CD1	2.45	0.46
3:C:310:LEU:O	3:C:314:PHE:CD2	2.69	0.46
1:D:35:LEU:HD12	1:D:36:GLN:N	2.31	0.46
1:D:51:GLU:HA	1:D:124:PHE:O	2.16	0.46
1:D:68:ASN:HB2	1:D:69:PRO:CD	2.44	0.46
1:D:144:MET:CE	1:D:205:PHE:CE1	2.99	0.46
1:D:412:CYS:O	1:D:415:MET:HE2	2.16	0.46
4:E:76:LEU:C	4:E:77:VAL:HG23	2.36	0.46
4:E:287:ILE:HG13	4:E:291:PHE:CE2	2.51	0.46
1:A:28:PHE:HD1	1:A:154:THR:O	1.99	0.46
1:A:409:ILE:H	1:A:409:ILE:HG13	1.46	0.46
2:B:35:LEU:HD22	2:B:35:LEU:HA	1.55	0.46
2:B:239:PHE:CB	2:B:442:ILE:HG12	2.45	0.46
2:B:242:PRO:CG	2:B:243:PRO:CD	2.88	0.46
2:B:284:LEU:O	2:B:288:MET:CB	2.64	0.46
3:C:52:LEU:HD22	3:C:52:LEU:H	1.80	0.46
3:C:216:THR:O	3:C:217:PHE:CD1	2.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:245:LEU:HA	3:C:248:TYR:HD2	1.80	0.46
3:C:279:PRO:C	3:C:282:ALA:HB3	2.35	0.46
3:C:294:PHE:CE1	3:C:474:VAL:HG11	2.50	0.46
1:D:21:PRO:CB	1:D:62:ASP:OD2	2.63	0.46
1:D:28:PHE:CE1	1:D:153:GLY:O	2.69	0.46
1:D:38:ILE:C	1:D:39:GLN:HG3	2.36	0.46
1:D:394:ASN:C	1:D:396:ALA:N	2.66	0.46
4:E:182:GLU:CG	4:E:221:TYR:OH	2.59	0.46
4:E:217:LYS:NZ	4:E:219:LEU:HD12	2.30	0.46
1:A:26:THR:O	1:A:28:PHE:CD1	2.69	0.46
1:A:31:ILE:HG23	1:A:60:TRP:HE3	1.81	0.46
1:A:34:GLY:CA	1:A:161:GLU:CD	2.85	0.46
1:A:46:VAL:HG23	1:A:270:ALA:C	2.30	0.46
1:A:48:GLN:HB2	1:A:128:CYS:O	2.15	0.46
1:A:137:PHE:CE1	1:A:210:ILE:CD1	2.98	0.46
1:A:258:LEU:HB3	4:E:267:LEU:HD21	1.98	0.46
2:B:56:LEU:CG	2:B:120:PRO:HG2	2.45	0.46
2:B:136:PRO:O	2:B:136:PRO:HG2	2.16	0.46
2:B:283:TYR:CD1	2:B:283:TYR:N	2.82	0.46
2:B:431:VAL:O	2:B:432:ALA:CB	2.63	0.46
3:C:22:ARG:CD	3:C:22:ARG:H	2.29	0.46
3:C:276:GLN:O	3:C:279:PRO:HD2	2.16	0.46
1:D:95:ASN:ND2	1:D:127:TYR:C	2.69	0.46
1:D:282:MET:C	1:D:286:ILE:HD12	2.37	0.46
1:D:287:SER:CA	1:D:290:ILE:HG12	2.46	0.46
1:D:379:VAL:O	1:D:379:VAL:CG1	2.61	0.46
4:E:272:VAL:N	4:E:273:PRO:HD2	2.29	0.46
1:A:79:ARG:HH11	1:A:107:LYS:HZ1	1.63	0.46
1:A:152:ASP:HA	1:A:198:TYR:H	1.81	0.46
1:A:255:VAL:CG1	1:A:256:PHE:N	2.78	0.46
1:A:377:GLU:N	1:A:380:LYS:HE2	2.31	0.46
2:B:160:HIS:HE2	2:B:207:VAL:HG11	1.80	0.46
2:B:218:LEU:C	2:B:219:PHE:CD1	2.89	0.46
3:C:230:ILE:CD1	3:C:231:ASN:ND2	2.79	0.46
1:D:33:VAL:HG13	1:D:201:ILE:HD11	1.98	0.46
1:D:53:ASN:HD22	1:D:123:ILE:HG13	1.81	0.46
1:D:252:SER:CB	4:E:259:LEU:HD22	2.46	0.46
4:E:86:LEU:HD13	4:E:103:TYR:HE1	1.78	0.46
4:E:93:ASN:HB3	4:E:143:LEU:HA	1.98	0.46
4:E:133:TYR:CZ	4:E:139:GLN:O	2.69	0.46
4:E:207:GLU:C	4:E:208:ILE:HG13	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LYS:NZ	2:B:151:TYR:CG	2.80	0.45
1:A:145:LYS:HZ3	1:A:202:THR:HG21	1.81	0.45
1:A:160:PRO:CG	1:A:185:LYS:CE	2.94	0.45
1:A:256:PHE:CE1	2:B:261:VAL:CG2	2.89	0.45
2:B:10:VAL:HG13	2:B:11:LEU:N	2.31	0.45
2:B:46:LYS:CB	2:B:277:VAL:N	2.63	0.45
2:B:90:ILE:HA	2:B:148:SER:HA	1.97	0.45
3:C:47:GLU:O	3:C:132:ILE:HG21	2.16	0.45
3:C:271:LEU:CD2	3:C:299:VAL:CG1	2.92	0.45
3:C:298:LEU:CD1	3:C:471:PHE:HB2	2.39	0.45
3:C:443:VAL:O	3:C:443:VAL:CG1	2.64	0.45
1:D:25:HIS:CD2	1:D:155:LYS:NZ	2.84	0.45
1:D:57:ARG:HA	1:D:119:THR:HG22	1.97	0.45
1:D:286:ILE:O	1:D:286:ILE:HG22	2.16	0.45
4:E:101:VAL:O	4:E:101:VAL:HG23	2.15	0.45
4:E:232:ILE:O	4:E:235:LEU:HB3	2.16	0.45
4:E:245:GLN:H	4:E:245:GLN:HG3	1.44	0.45
1:A:260:ILE:HG23	1:A:261:VAL:N	2.31	0.45
2:B:142:CYS:CB	2:B:211:LEU:CB	2.81	0.45
2:B:270:VAL:HG11	2:B:284:LEU:CD2	2.45	0.45
3:C:148:PHE:C	3:C:149:THR:HG22	2.36	0.45
3:C:234:THR:HB	3:C:235:PRO:HD3	1.99	0.45
3:C:431:LYS:O	3:C:434:LYS:HB3	2.15	0.45
1:D:63:VAL:C	1:D:65:LEU:H	2.20	0.45
1:D:246:SER:O	1:D:250:LEU:HD12	2.15	0.45
4:E:20:PRO:HG3	4:E:61:ASP:CB	2.46	0.45
4:E:30:VAL:HG22	4:E:59:TRP:HB3	1.97	0.45
4:E:159:LEU:CB	4:E:192:LYS:HB2	2.46	0.45
4:E:184:THR:HG23	4:E:215:GLN:CB	2.46	0.45
4:E:209:ILE:CG1	4:E:211:PHE:HE1	2.24	0.45
4:E:240:TYR:CD2	4:E:453:ILE:HB	2.51	0.45
4:E:240:TYR:C	4:E:243:PRO:HD2	2.36	0.45
1:A:65:LEU:HD13	1:A:110:LEU:HD13	1.98	0.45
1:A:163:ASP:O	1:A:164:ARG:HG3	2.17	0.45
1:A:176:TRP:HB3	1:A:209:ARG:HG3	1.98	0.45
2:B:37:LEU:CA	2:B:54:VAL:CG1	2.66	0.45
2:B:108:VAL:HG22	2:B:118:TRP:CB	2.46	0.45
2:B:130:ILE:CB	2:B:134:TYR:CD2	2.82	0.45
2:B:147:LYS:CB	2:B:206:ASP:HA	2.41	0.45
2:B:199:SER:C	2:B:201:ASP:N	2.69	0.45
2:B:422:ASP:O	2:B:425:LYS:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:424:LEU:O	2:B:427:ASP:HB3	2.16	0.45
3:C:426:THR:C	3:C:429:ILE:HG23	2.37	0.45
3:C:471:PHE:HD1	3:C:471:PHE:O	1.99	0.45
1:D:300:HIS:O	1:D:306:HIS:HA	2.16	0.45
1:D:413:VAL:HA	1:D:416:LEU:HB2	1.99	0.45
4:E:250:LYS:CB	4:E:253:LEU:HD23	2.32	0.45
1:A:6:ARG:NH1	1:A:6:ARG:CB	2.80	0.45
1:A:67:TRP:CD1	1:A:71:ASP:HB3	2.51	0.45
1:A:246:SER:C	1:A:248:SER:N	2.67	0.45
1:A:305:THR:HB	1:A:400:LYS:CB	2.46	0.45
3:C:25:LYS:HB3	3:C:28:ASN:HD21	1.80	0.45
3:C:50:GLU:CB	3:C:132:ILE:HD13	2.43	0.45
3:C:296:MET:HA	3:C:296:MET:CE	2.46	0.45
3:C:478:PHE:O	3:C:482:PRO:HD3	2.16	0.45
1:D:280:PHE:N	1:D:280:PHE:HD1	2.13	0.45
4:E:140:ASN:OD1	4:E:211:PHE:CD2	2.70	0.45
4:E:453:ILE:HD12	4:E:454:ALA:CA	2.47	0.45
1:A:46:VAL:HG23	1:A:271:VAL:CA	2.47	0.45
1:A:65:LEU:CB	1:A:114:GLY:HA2	2.47	0.45
1:A:176:TRP:CD2	1:A:209:ARG:NH1	2.85	0.45
1:A:292:THR:CA	1:A:296:ILE:HD11	2.44	0.45
2:B:101:GLU:HB2	2:B:123:ILE:HG22	1.98	0.45
2:B:186:TRP:HB2	2:B:215:ARG:CG	2.32	0.45
2:B:289:ILE:HG22	2:B:293:PHE:CE2	2.51	0.45
2:B:442:ILE:HG22	2:B:443:PHE:N	2.29	0.45
3:C:37:LEU:HD21	3:C:148:PHE:CD2	2.51	0.45
3:C:233:ILE:C	3:C:235:PRO:HD2	2.37	0.45
3:C:247:PHE:HE1	3:C:309:VAL:HA	1.81	0.45
3:C:278:LEU:O	3:C:278:LEU:HD13	2.13	0.45
1:D:187:TRP:HZ2	1:D:196:THR:HA	1.81	0.45
1:D:382:ILE:O	1:D:385:HIS:HB3	2.16	0.45
1:D:419:ILE:O	1:D:423:VAL:HG23	2.17	0.45
4:E:71:TYR:CD1	4:E:111:ASN:ND2	2.81	0.45
4:E:91:LEU:HD13	4:E:145:PHE:CA	2.45	0.45
4:E:93:ASN:HB3	4:E:144:VAL:H	1.82	0.45
4:E:222:ILE:CG2	4:E:223:ILE:H	2.22	0.45
4:E:222:ILE:HG12	4:E:226:ILE:CD1	2.45	0.45
4:E:235:LEU:O	4:E:238:LEU:HB2	2.17	0.45
1:A:20:ARG:CB	1:A:86:TRP:CD2	3.00	0.45
1:A:46:VAL:HG12	1:A:47:ASN:CG	2.36	0.45
1:A:110:LEU:HG	1:A:111:ASP:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:GLY:HA2	1:A:176:TRP:CE3	2.52	0.45
1:A:410:LEU:HD13	1:A:410:LEU:C	2.37	0.45
2:B:137:PHE:H	2:B:137:PHE:HD1	1.61	0.45
2:B:233:ILE:HG12	2:B:233:ILE:H	1.63	0.45
3:C:46:LYS:HG3	3:C:49:ASP:OD1	2.17	0.45
3:C:98:ASN:C	3:C:100:GLY:N	2.69	0.45
3:C:431:LYS:CE	1:D:379:VAL:CG2	2.95	0.45
1:D:7:LEU:HD13	1:D:70:ALA:C	2.37	0.45
1:D:178:MET:HA	1:D:207:MET:HB3	1.96	0.45
1:D:286:ILE:HG22	1:D:290:ILE:HG23	1.98	0.45
1:D:398:GLU:HA	1:D:401:TYR:CE1	2.52	0.45
4:E:221:TYR:O	4:E:224:ASN:HB3	2.16	0.45
4:E:240:TYR:CG	4:E:453:ILE:HD13	2.49	0.45
4:E:262:THR:HA	4:E:265:LEU:CB	2.45	0.45
4:E:273:PRO:CG	4:E:274:GLU:N	2.78	0.45
4:E:472:ASN:ND2	4:E:472:ASN:O	2.50	0.45
1:A:170:PHE:HE1	1:A:176:TRP:CD1	2.35	0.45
2:B:92:LEU:HB2	2:B:96:ASN:H	1.82	0.45
3:C:30:VAL:HG13	3:C:31:VAL:N	2.31	0.45
3:C:137:PHE:CE1	3:C:288:ILE:HG21	2.50	0.45
3:C:149:THR:HG22	3:C:214:ASP:HB3	1.92	0.45
3:C:179:ILE:HG13	3:C:181:PRO:HD3	1.96	0.45
3:C:288:ILE:HG21	3:C:288:ILE:HD13	1.77	0.45
1:D:38:ILE:O	1:D:39:GLN:CG	2.65	0.45
1:D:130:ILE:O	1:D:131:ILE:HG12	2.15	0.45
1:D:283:ILE:O	1:D:287:SER:HB2	2.17	0.45
4:E:54:TRP:C	4:E:118:LEU:HD11	2.36	0.45
4:E:127:CYS:SG	4:E:128:PRO:CD	3.04	0.45
4:E:140:ASN:OD1	4:E:211:PHE:CG	2.70	0.45
4:E:240:TYR:HB3	4:E:453:ILE:CG1	2.47	0.45
1:A:3:HIS:CB	1:A:7:LEU:CD2	2.89	0.45
1:A:37:LEU:O	1:A:169:THR:HG21	2.16	0.45
1:A:111:ASP:C	1:A:113:THR:H	2.19	0.45
1:A:251:LEU:CD2	4:E:260:ALA:HA	2.42	0.45
2:B:45:GLU:OE1	2:B:277:VAL:CB	2.60	0.45
2:B:75:ILE:HD11	2:B:78:LEU:HB2	1.98	0.45
2:B:132:VAL:CG1	2:B:279:ILE:CA	2.81	0.45
2:B:296:ILE:HD13	2:B:296:ILE:HA	1.82	0.45
3:C:20:HIS:O	3:C:20:HIS:CG	2.69	0.45
3:C:48:THR:H	3:C:285:VAL:HA	1.82	0.45
3:C:106:TYR:O	3:C:106:TYR:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:150:ALA:HB3	3:C:158:ILE:HD13	1.98	0.45
3:C:200:ASN:OD1	3:C:202:TYR:CE2	2.70	0.45
1:D:43:VAL:HA	1:D:49:ILE:O	2.16	0.45
1:D:176:TRP:CG	1:D:209:ARG:HD2	2.52	0.45
1:D:265:PRO:O	1:D:269:SER:HB2	2.16	0.45
4:E:44:GLU:CB	4:E:129:ILE:HD12	2.46	0.45
4:E:55:ILE:HG21	4:E:119:PRO:HG2	1.97	0.45
4:E:138:TRP:HB3	4:E:214:ILE:O	2.17	0.45
4:E:159:LEU:HD23	4:E:159:LEU:HA	1.59	0.45
4:E:270:GLN:O	4:E:273:PRO:HD2	2.16	0.45
1:A:28:PHE:CD1	1:A:154:THR:O	2.70	0.45
1:A:175:GLU:CD	1:A:211:PRO:HG3	2.37	0.45
1:A:227:PHE:O	1:A:227:PHE:HD1	2.00	0.45
1:A:396:ALA:O	1:A:400:LYS:HG3	2.16	0.45
2:B:35:LEU:HA	2:B:55:PHE:O	2.16	0.45
2:B:45:GLU:HG2	2:B:277:VAL:CB	2.40	0.45
2:B:141:ASN:CA	2:B:211:LEU:O	2.62	0.45
1:D:61:ILE:HG22	1:D:116:ILE:HD13	1.98	0.45
1:D:130:ILE:HG22	1:D:134:HIS:HD2	1.82	0.45
4:E:44:GLU:O	4:E:129:ILE:HG13	2.16	0.45
4:E:135:PRO:CG	4:E:137:ASP:OD1	2.65	0.45
1:A:35:LEU:CD1	1:A:203:TYR:OH	2.65	0.45
1:A:106:THR:CG2	1:A:107:LYS:N	2.79	0.45
1:A:148:ILE:O	1:A:198:TYR:HD2	1.98	0.45
1:A:293:VAL:HG22	4:E:238:LEU:HD21	1.98	0.45
2:B:101:GLU:OE1	2:B:123:ILE:CG2	2.65	0.45
2:B:439:PHE:HA	2:B:442:ILE:CB	2.41	0.45
3:C:23:PRO:HB3	3:C:66:ARG:NH1	2.32	0.45
3:C:219:LEU:HG	3:C:221:ILE:CG2	2.46	0.45
3:C:298:LEU:HD13	3:C:471:PHE:HD2	1.82	0.45
1:D:56:LEU:CG	1:D:120:PRO:HG2	2.27	0.45
1:D:105:MET:O	1:D:105:MET:CG	2.63	0.45
1:A:221:PRO:O	1:A:224:LEU:HB3	2.16	0.44
3:C:191:GLU:OE2	3:C:222:ARG:HB3	2.18	0.44
1:D:218:VAL:O	1:D:221:PRO:HG2	2.17	0.44
1:D:409:ILE:CA	1:D:412:CYS:HB2	2.47	0.44
4:E:30:VAL:HG12	4:E:157:LEU:HD22	1.99	0.44
4:E:172:ILE:HD12	4:E:188:ARG:N	2.30	0.44
4:E:242:LEU:HG	4:E:243:PRO:CD	2.48	0.44
1:A:72:TYR:HA	1:A:112:TYR:HB3	1.98	0.44
1:A:222:CYS:HA	1:A:225:PHE:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:PHE:CD1	1:A:225:PHE:C	2.89	0.44
2:B:61:THR:HG22	2:B:62:ASP:N	2.32	0.44
2:B:118:TRP:CD1	2:B:120:PRO:HD3	2.52	0.44
2:B:189:GLU:HG3	2:B:468:PHE:HB2	1.98	0.44
3:C:109:ASN:OD1	1:D:150:THR:HG21	2.18	0.44
1:D:60:TRP:HZ3	1:D:116:ILE:HG13	1.81	0.44
1:D:88:PRO:O	1:D:88:PRO:CG	2.65	0.44
1:D:242:LYS:CA	1:D:243:MET:HE2	2.48	0.44
4:E:146:ARG:CD	4:E:206:GLN:O	2.65	0.44
4:E:146:ARG:HG3	4:E:147:SER:O	2.16	0.44
1:A:6:ARG:HH11	1:A:6:ARG:CB	2.29	0.44
1:A:64:ARG:HH11	1:A:64:ARG:HD2	1.47	0.44
1:A:111:ASP:N	1:A:111:ASP:OD1	2.51	0.44
1:A:276:LYS:H	1:A:276:LYS:CD	2.30	0.44
2:B:297:LEU:HD11	2:B:445:THR:CG2	2.48	0.44
3:C:56:VAL:CG1	3:C:126:PHE:HE2	2.19	0.44
3:C:98:ASN:CG	3:C:98:ASN:O	2.55	0.44
3:C:480:ARG:HB2	3:C:481:PRO:HD3	1.99	0.44
1:D:90:LEU:HA	1:D:90:LEU:HD23	1.74	0.44
1:D:178:MET:HE3	1:D:207:MET:HB3	1.99	0.44
4:E:175:GLU:HG2	4:E:176:ASP:N	2.33	0.44
4:E:269:ALA:O	4:E:273:PRO:CD	2.64	0.44
1:A:57:ARG:CG	1:A:57:ARG:O	2.65	0.44
1:A:92:LEU:HB3	1:A:95:ASN:ND2	2.33	0.44
1:A:304:SER:CB	1:A:400:LYS:HZ2	2.30	0.44
1:A:306:HIS:O	1:A:306:HIS:CG	2.70	0.44
2:B:34:GLY:O	2:B:35:LEU:CD2	2.65	0.44
2:B:53:SER:O	2:B:54:VAL:HG13	2.17	0.44
2:B:75:ILE:CD1	2:B:78:LEU:CD1	2.79	0.44
2:B:112:HIS:N	2:B:112:HIS:ND1	2.65	0.44
2:B:251:LEU:HD12	2:B:251:LEU:O	2.16	0.44
3:C:17:TYR:OH	3:C:19:LYS:HD2	2.17	0.44
3:C:106:TYR:CD1	3:C:107:PHE:HD1	2.36	0.44
3:C:118:VAL:HG12	3:C:119:THR:N	2.33	0.44
3:C:231:ASN:O	3:C:235:PRO:HD3	2.17	0.44
3:C:266:ALA:O	3:C:270:PHE:CD1	2.70	0.44
1:D:46:VAL:HG22	1:D:270:ALA:O	2.17	0.44
1:D:426:PHE:HE1	1:D:430:LEU:CD1	2.13	0.44
4:E:59:TRP:CZ2	4:E:115:MET:CB	3.01	0.44
4:E:281:LEU:HA	4:E:281:LEU:HD12	1.61	0.44
3:C:247:PHE:O	3:C:250:PRO:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:LYS:HA	1:D:111:ASP:HA	2.00	0.44
1:D:245:LEU:HD21	4:E:255:ILE:HG21	2.00	0.44
1:D:277:TYR:HA	1:D:280:PHE:CZ	2.52	0.44
4:E:47:GLU:CB	4:E:129:ILE:HG12	2.29	0.44
4:E:135:PRO:C	4:E:136:PHE:HD1	2.20	0.44
4:E:173:ASP:HA	4:E:174:PRO:HD2	1.84	0.44
4:E:304:LEU:O	4:E:304:LEU:CG	2.65	0.44
1:A:27:HIS:O	1:A:28:PHE:CD2	2.71	0.44
1:A:95:ASN:HB3	1:A:144:MET:SD	2.58	0.44
1:A:110:LEU:HD12	1:A:114:GLY:HA2	1.96	0.44
1:A:271:VAL:HG23	1:A:271:VAL:O	2.18	0.44
1:A:376:ILE:HG23	1:A:380:LYS:HZ3	1.82	0.44
2:B:28:LYS:HB3	2:B:155:GLU:C	2.38	0.44
2:B:46:LYS:CA	2:B:278:PRO:CD	2.78	0.44
2:B:101:GLU:CD	2:B:123:ILE:HG22	2.38	0.44
2:B:146:PHE:O	2:B:206:ASP:HA	2.17	0.44
2:B:212:ILE:O	2:B:212:ILE:CG2	2.64	0.44
3:C:53:THR:HA	3:C:126:PHE:O	2.17	0.44
3:C:230:ILE:CG1	3:C:231:ASN:ND2	2.77	0.44
3:C:288:ILE:HD13	3:C:290:LYS:HD2	2.00	0.44
3:C:315:ARG:H	3:C:315:ARG:HD3	1.82	0.44
1:D:149:TRP:CD2	1:D:150:THR:N	2.85	0.44
1:D:176:TRP:HB3	1:D:209:ARG:CG	2.48	0.44
1:D:278:MET:O	1:D:278:MET:CE	2.66	0.44
1:D:381:TYR:CD1	4:E:419:CYS:SG	3.06	0.44
4:E:1:ASN:C	4:E:3:GLU:N	2.71	0.44
4:E:75:ASP:CB	4:E:110:TYR:CZ	3.00	0.44
4:E:131:VAL:O	4:E:131:VAL:CG1	2.63	0.44
4:E:302:ILE:HG21	4:E:302:ILE:HD13	1.73	0.44
1:A:41:ILE:HG21	1:A:123:ILE:HD11	1.99	0.44
1:A:152:ASP:N	1:A:152:ASP:OD1	2.50	0.44
1:A:185:LYS:HB3	1:A:185:LYS:HE2	1.82	0.44
2:B:56:LEU:CD2	2:B:103:THR:CA	2.91	0.44
2:B:85:VAL:HG12	2:B:86:TRP:HB3	2.00	0.44
2:B:189:GLU:HG3	2:B:468:PHE:HB3	2.00	0.44
3:C:130:CYS:HA	3:C:131:PRO:HD2	1.58	0.44
3:C:137:PHE:HD1	3:C:288:ILE:CD1	2.31	0.44
3:C:219:LEU:CD1	3:C:221:ILE:HG22	2.47	0.44
3:C:319:THR:CB	3:C:447:ASN:CB	2.96	0.44
1:D:93:TYR:OH	1:D:198:TYR:HD2	2.00	0.44
1:D:187:TRP:CH2	1:D:189:TYR:CG	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:210:ILE:HG22	1:D:211:PRO:O	2.18	0.44
4:E:1:ASN:O	4:E:69:SER:HB2	2.18	0.44
4:E:104:TYR:N	4:E:104:TYR:HD1	2.15	0.44
4:E:183:TRP:HB2	4:E:214:ILE:HD13	1.99	0.44
1:A:89:ASP:OD2	1:A:151:TYR:CE1	2.71	0.44
1:A:95:ASN:ND2	1:A:95:ASN:H	2.12	0.44
1:A:219:ILE:O	1:A:222:CYS:HB2	2.16	0.44
1:A:252:SER:CB	2:B:257:LEU:HD13	2.31	0.44
2:B:59:ALA:CB	2:B:116:VAL:O	2.66	0.44
2:B:129:THR:CG2	2:B:129:THR:O	2.62	0.44
2:B:140:GLN:HB3	2:B:141:ASN:H	1.64	0.44
3:C:48:THR:N	3:C:285:VAL:HA	2.33	0.44
3:C:153:TYR:HB2	3:C:158:ILE:HB	2.00	0.44
3:C:279:PRO:O	3:C:282:ALA:CB	2.59	0.44
1:D:37:LEU:HD13	1:D:54:VAL:HG22	1.99	0.44
1:D:130:ILE:HA	1:D:134:HIS:HB2	1.99	0.44
1:D:167:LEU:HD21	1:D:178:MET:O	2.18	0.44
1:D:186:HIS:CG	1:D:187:TRP:N	2.85	0.44
1:D:409:ILE:HA	1:D:412:CYS:CB	2.47	0.44
4:E:108:LEU:O	4:E:115:MET:HA	2.18	0.44
1:A:12:LEU:HG	1:A:13:GLU:N	2.32	0.44
1:A:50:VAL:CG1	1:A:52:THR:CG2	2.96	0.44
1:A:104:HIS:CB	1:A:105:MET:SD	3.03	0.44
1:A:130:ILE:O	1:A:134:HIS:CB	2.66	0.44
1:A:235:LEU:N	1:A:236:PRO:HD2	2.32	0.44
2:B:55:PHE:C	2:B:56:LEU:HD13	2.33	0.44
2:B:68:ASP:HB3	2:B:69:PRO:HD2	1.88	0.44
2:B:135:PHE:CD2	2:B:283:TYR:CZ	3.06	0.44
2:B:202:PRO:HG2	2:B:203:SER:N	2.33	0.44
2:B:302:LEU:HD12	2:B:302:LEU:HA	1.87	0.44
2:B:422:ASP:C	2:B:422:ASP:OD1	2.55	0.44
2:B:429:GLN:HA	2:B:429:GLN:NE2	2.29	0.44
1:D:107:LYS:NZ	4:E:149:THR:CB	2.81	0.44
1:D:247:ILE:CG2	1:D:248:SER:N	2.70	0.44
1:D:278:MET:O	1:D:278:MET:HE3	2.18	0.44
1:D:282:MET:HE2	1:D:286:ILE:HD11	2.00	0.44
1:D:377:GLU:HA	1:D:380:LYS:HD2	2.00	0.44
4:E:267:LEU:HA	4:E:270:GLN:CG	2.48	0.44
4:E:447:ASP:O	4:E:450:CYS:HB2	2.18	0.44
1:A:15:TYR:CZ	1:A:84:ASP:HB3	2.53	0.43
1:A:120:PRO:HA	1:A:121:PRO:HD3	1.68	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:GLN:CB	2:B:115:ALA:HB3	2.47	0.43
2:B:281:ILE:HG22	2:B:284:LEU:HB3	1.99	0.43
2:B:408:ILE:CG2	2:B:409:LYS:H	2.29	0.43
1:D:7:LEU:CD1	1:D:70:ALA:O	2.60	0.43
1:D:53:ASN:HD22	1:D:123:ILE:CG1	2.31	0.43
1:D:76:LYS:HE2	1:D:76:LYS:HB3	1.83	0.43
1:D:178:MET:SD	1:D:207:MET:CG	3.06	0.43
1:D:274:ILE:HG13	1:D:277:TYR:CD2	2.53	0.43
1:D:283:ILE:CA	1:D:286:ILE:HD12	2.48	0.43
1:D:429:ARG:CA	1:D:429:ARG:NE	2.81	0.43
4:E:109:VAL:HG13	4:E:115:MET:CE	2.48	0.43
4:E:242:LEU:HA	4:E:245:GLN:OE1	2.18	0.43
4:E:281:LEU:HD11	4:E:286:LEU:HD11	1.98	0.43
1:A:27:HIS:C	1:A:28:PHE:CD2	2.92	0.43
1:A:100:PHE:CB	1:A:103:VAL:HG21	2.46	0.43
1:A:224:LEU:HG	1:A:225:PHE:CA	2.49	0.43
2:B:46:LYS:HE2	2:B:278:PRO:HD3	1.99	0.43
2:B:142:CYS:N	2:B:211:LEU:HB2	2.32	0.43
2:B:297:LEU:CD1	2:B:445:THR:HG23	2.46	0.43
2:B:406:GLU:CG	2:B:409:LYS:HD2	2.46	0.43
3:C:247:PHE:C	3:C:250:PRO:CG	2.86	0.43
1:D:66:ARG:HD3	1:D:66:ARG:H	1.83	0.43
1:D:225:PHE:CD1	1:D:225:PHE:C	2.91	0.43
1:D:245:LEU:O	1:D:249:VAL:HG23	2.19	0.43
4:E:13:ASP:C	4:E:13:ASP:OD1	2.57	0.43
4:E:173:ASP:CB	4:E:185:ILE:HD13	2.47	0.43
1:A:66:ARG:O	1:A:66:ARG:CG	2.65	0.43
2:B:92:LEU:CA	2:B:145:VAL:O	2.65	0.43
2:B:93:MET:CG	2:B:206:ASP:CB	2.77	0.43
2:B:101:GLU:CD	2:B:123:ILE:CG2	2.87	0.43
2:B:104:LEU:CD1	2:B:118:TRP:CZ3	2.93	0.43
3:C:69:TRP:HB3	3:C:73:GLU:CB	2.48	0.43
4:E:22:LYS:CG	4:E:23:THR:N	2.78	0.43
4:E:91:LEU:HA	4:E:145:PHE:HA	1.99	0.43
4:E:187:HIS:ND1	4:E:188:ARG:N	2.67	0.43
4:E:227:ALA:O	4:E:231:LEU:HB3	2.18	0.43
1:A:80:LEU:HD21	1:A:110:LEU:HB2	2.00	0.43
1:A:146:LEU:N	1:A:146:LEU:CD1	2.79	0.43
1:A:189:TYR:HA	1:A:197:PRO:CD	2.42	0.43
1:A:255:VAL:HA	1:A:258:LEU:HD12	1.99	0.43
1:A:431:ILE:O	1:A:431:ILE:CG2	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:THR:HG22	2:B:25:VAL:H	1.84	0.43
3:C:64:ASP:CB	3:C:116:GLY:O	2.65	0.43
1:D:141:ASN:ND2	1:D:182:ARG:HH22	2.17	0.43
1:D:212:LEU:O	1:D:216:VAL:HG22	2.17	0.43
1:D:257:LEU:HA	1:D:260:ILE:HB	2.00	0.43
4:E:44:GLU:CG	4:E:129:ILE:CB	2.91	0.43
4:E:45:LYS:NZ	4:E:278:ASN:HA	2.33	0.43
4:E:294:LEU:CA	4:E:297:VAL:HG23	2.48	0.43
1:A:15:TYR:CD1	1:A:15:TYR:C	2.85	0.43
1:A:134:HIS:N	1:A:136:PRO:HD2	2.34	0.43
1:A:237:THR:HB	1:A:406:ILE:HG22	2.00	0.43
1:A:243:MET:SD	4:E:249:GLN:OE1	2.77	0.43
1:A:244:THR:HG23	1:A:245:LEU:N	2.34	0.43
1:A:298:THR:HG23	1:A:301:ARG:HD3	1.99	0.43
2:B:93:MET:CG	2:B:145:VAL:HB	2.49	0.43
3:C:252:GLU:HG3	1:D:300:HIS:O	2.18	0.43
3:C:295:ILE:O	3:C:299:VAL:HG23	2.18	0.43
1:D:106:THR:HG23	1:D:107:LYS:HZ3	1.84	0.43
4:E:19:LYS:NZ	4:E:154:GLU:CB	2.62	0.43
4:E:83:LEU:O	4:E:84:LEU:CD1	2.67	0.43
4:E:191:LYS:HB2	4:E:191:LYS:HE2	1.49	0.43
4:E:210:PHE:O	4:E:212:LEU:CD1	2.67	0.43
4:E:236:VAL:C	4:E:239:VAL:HG23	2.38	0.43
4:E:271:LYS:HZ2	4:E:271:LYS:HG3	1.42	0.43
1:A:5:THR:HA	1:A:8:VAL:HG22	2.00	0.43
1:A:41:ILE:O	1:A:42:ASN:CG	2.56	0.43
1:A:92:LEU:CD2	1:A:92:LEU:N	2.82	0.43
1:A:163:ASP:C	1:A:164:ARG:HG3	2.39	0.43
1:A:221:PRO:CA	1:A:224:LEU:HB3	2.48	0.43
1:A:228:LEU:HD12	1:A:253:LEU:CD2	2.49	0.43
2:B:11:LEU:HD13	2:B:11:LEU:HA	1.88	0.43
2:B:158:LEU:HD23	2:B:158:LEU:HA	1.59	0.43
2:B:218:LEU:CD1	2:B:222:VAL:CG2	2.96	0.43
2:B:284:LEU:O	2:B:287:ILE:HG13	2.18	0.43
2:B:434:VAL:CG1	2:B:438:LEU:HD12	2.42	0.43
3:C:19:LYS:O	3:C:19:LYS:CG	2.67	0.43
3:C:77:ILE:CD1	3:C:80:LEU:HB2	2.49	0.43
3:C:106:TYR:CE1	3:C:107:PHE:CE1	3.03	0.43
1:D:75:ILE:CG1	1:D:78:ILE:HG23	2.43	0.43
1:D:416:LEU:HA	1:D:419:ILE:HG13	2.00	0.43
4:E:14:TYR:CE2	4:E:16:LYS:NZ	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:159:LEU:CD1	4:E:192:LYS:CA	2.83	0.43
1:A:135:PHE:CD1	1:A:273:LEU:HB2	2.53	0.43
1:A:187:TRP:CZ3	1:A:189:TYR:HB3	2.52	0.43
1:A:224:LEU:C	1:A:224:LEU:HD12	2.38	0.43
1:A:301:ARG:HG2	1:A:301:ARG:NH1	2.33	0.43
2:B:93:MET:HB2	2:B:145:VAL:HG23	2.00	0.43
3:C:13:ILE:HB	3:C:14:VAL:H	1.64	0.43
3:C:80:LEU:HD12	1:D:20:ARG:NH2	2.33	0.43
3:C:142:GLN:CG	3:C:143:ASN:H	2.29	0.43
3:C:148:PHE:O	3:C:215:VAL:HG22	2.18	0.43
1:D:34:GLY:CA	1:D:57:ARG:HD2	2.48	0.43
1:D:95:ASN:HD21	1:D:128:CYS:HB3	1.83	0.43
1:D:170:PHE:CG	1:D:171:MET:N	2.87	0.43
4:E:39:LEU:CD2	4:E:183:TRP:CZ2	2.92	0.43
4:E:44:GLU:HB3	4:E:280:PRO:HD3	1.96	0.43
4:E:94:ASN:ND2	4:E:126:THR:H	2.17	0.43
1:A:305:THR:O	1:A:305:THR:HG22	2.19	0.43
2:B:35:LEU:O	2:B:174:MET:CE	2.66	0.43
3:C:12:LEU:HD23	3:C:12:LEU:HA	1.96	0.43
3:C:82:LEU:HB2	3:C:112:VAL:HG21	2.00	0.43
3:C:137:PHE:HD1	3:C:288:ILE:HD12	1.84	0.43
3:C:269:VAL:CG1	3:C:270:PHE:CE1	3.01	0.43
1:D:80:LEU:CB	1:D:81:PRO:HD2	2.48	0.43
1:D:189:TYR:HA	1:D:197:PRO:CD	2.39	0.43
1:D:216:VAL:O	1:D:220:ILE:CG1	2.58	0.43
4:E:22:LYS:HZ1	4:E:26:HIS:HB3	1.84	0.43
4:E:27:VAL:HG12	4:E:154:GLU:CA	2.49	0.43
4:E:47:GLU:HB3	4:E:128:PRO:O	2.19	0.43
4:E:113:GLY:C	4:E:115:MET:SD	2.97	0.43
4:E:145:PHE:O	4:E:208:ILE:CG1	2.66	0.43
4:E:262:THR:HG23	4:E:265:LEU:CD1	2.49	0.43
4:E:288:PHE:O	4:E:292:VAL:HG23	2.19	0.43
1:A:68:ASN:ND2	1:A:69:PRO:HD2	2.33	0.43
3:C:60:HIS:NE2	3:C:92:ILE:CG2	2.81	0.43
3:C:308:ILE:HG22	3:C:309:VAL:H	1.84	0.43
1:D:293:VAL:HG12	1:D:294:VAL:N	2.33	0.43
4:E:55:ILE:HG13	4:E:55:ILE:O	2.18	0.43
1:A:65:LEU:HB2	1:A:114:GLY:CA	2.48	0.43
1:A:106:THR:CG2	1:A:107:LYS:H	2.25	0.43
1:A:131:ILE:HD11	1:A:140:GLN:NE2	2.34	0.43
1:A:258:LEU:HB3	4:E:267:LEU:CD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:428:TRP:O	2:B:431:VAL:HG13	2.19	0.43
3:C:45:LEU:HD23	3:C:52:LEU:HD12	2.01	0.43
3:C:108:CYS:SG	3:C:109:ASN:N	2.91	0.43
3:C:135:LEU:C	3:C:137:PHE:N	2.70	0.43
3:C:195:LYS:HA	3:C:196:PRO:HD2	1.82	0.43
1:D:29:VAL:HG13	1:D:156:VAL:HG12	2.00	0.43
1:D:44:ASP:CG	1:D:46:VAL:HG23	2.39	0.43
1:D:92:LEU:H	1:D:92:LEU:HD23	1.81	0.43
1:D:199:LEU:C	1:D:200:ASP:OD1	2.56	0.43
1:D:263:LEU:CD1	4:E:266:PHE:CZ	2.99	0.43
1:D:305:THR:C	1:D:306:HIS:CG	2.91	0.43
4:E:42:LEU:HD22	4:E:183:TRP:CH2	2.52	0.43
4:E:95:VAL:O	4:E:95:VAL:HG12	2.19	0.43
4:E:456:LEU:C	4:E:456:LEU:HD13	2.39	0.43
1:A:136:PRO:HB2	1:A:138:ASP:OD1	2.18	0.42
1:A:137:PHE:HE1	1:A:210:ILE:HG13	1.84	0.42
1:A:145:LYS:NZ	1:A:202:THR:HG21	2.32	0.42
1:A:187:TRP:CD1	1:A:197:PRO:O	2.73	0.42
1:A:279:LEU:HD13	1:A:282:MET:HB3	2.01	0.42
1:A:305:THR:OG1	1:A:400:LYS:HB3	2.19	0.42
1:A:416:LEU:C	1:A:419:ILE:HG22	2.40	0.42
1:A:419:ILE:HD13	1:A:423:VAL:CG2	2.49	0.42
3:C:191:GLU:HG3	3:C:222:ARG:CB	2.48	0.42
3:C:222:ARG:NH2	3:C:224:LYS:CA	2.82	0.42
3:C:251:ALA:C	3:C:253:SER:H	2.23	0.42
1:D:233:PHE:HE2	1:D:413:VAL:HG11	1.84	0.42
1:D:419:ILE:HD12	1:D:419:ILE:C	2.39	0.42
4:E:94:ASN:CG	4:E:126:THR:H	2.22	0.42
4:E:219:LEU:HD23	4:E:221:TYR:CE2	2.54	0.42
4:E:269:ALA:O	4:E:273:PRO:HG3	2.18	0.42
1:A:66:ARG:O	1:A:67:TRP:CE3	2.72	0.42
1:A:92:LEU:C	1:A:95:ASN:HD22	2.23	0.42
1:A:228:LEU:CD1	1:A:253:LEU:HD23	2.49	0.42
2:B:133:MET:CE	2:B:140:GLN:HB3	2.49	0.42
2:B:185:GLN:O	2:B:217:PRO:CB	2.67	0.42
3:C:42:LEU:HD23	3:C:42:LEU:C	2.40	0.42
3:C:162:LEU:CD1	3:C:217:PHE:HE1	2.29	0.42
4:E:100:GLU:CD	4:E:122:ILE:HG12	2.39	0.42
4:E:159:LEU:HD21	4:E:208:ILE:HG23	2.01	0.42
4:E:200:LYS:O	4:E:200:LYS:CG	2.67	0.42
1:A:148:ILE:O	1:A:198:TYR:CD2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:THR:HA	1:A:270:ALA:HB3	2.02	0.42
1:A:376:ILE:O	1:A:380:LYS:HG3	2.20	0.42
2:B:233:ILE:O	2:B:237:LEU:HB2	2.19	0.42
1:D:57:ARG:HA	1:D:119:THR:HA	2.02	0.42
1:D:80:LEU:HB2	1:D:108:LEU:CD2	2.49	0.42
1:D:260:ILE:O	1:D:263:LEU:HB2	2.19	0.42
4:E:76:LEU:O	4:E:77:VAL:CG2	2.67	0.42
1:A:15:TYR:CE2	1:A:84:ASP:OD2	2.71	0.42
1:A:95:ASN:OD1	1:A:144:MET:CB	2.68	0.42
1:A:229:THR:HG21	1:A:291:VAL:HG11	2.02	0.42
1:A:402:VAL:CG1	1:A:404:MET:HG2	2.50	0.42
2:B:187:SER:CB	2:B:216:LYS:HE2	2.50	0.42
1:D:53:ASN:CB	1:D:123:ILE:HG12	2.47	0.42
1:D:242:LYS:HB2	1:D:245:LEU:HD13	2.01	0.42
1:D:411:LEU:HD23	1:D:411:LEU:HA	1.66	0.42
4:E:55:ILE:HG23	4:E:119:PRO:N	2.35	0.42
4:E:66:TRP:C	4:E:71:TYR:HB3	2.39	0.42
4:E:147:SER:O	4:E:205:PHE:CD2	2.72	0.42
4:E:242:LEU:HG	4:E:243:PRO:HD3	2.01	0.42
4:E:271:LYS:C	4:E:273:PRO:CD	2.77	0.42
1:A:54:VAL:CG2	1:A:122:ALA:CB	2.91	0.42
1:A:76:LYS:CG	1:A:77:LYS:N	2.81	0.42
1:A:261:VAL:O	1:A:265:PRO:HG3	2.19	0.42
1:A:274:ILE:O	1:A:277:TYR:CB	2.64	0.42
1:A:279:LEU:HD13	1:A:282:MET:CB	2.49	0.42
1:A:306:HIS:O	1:A:306:HIS:HD2	1.99	0.42
2:B:142:CYS:CB	2:B:211:LEU:HD12	2.49	0.42
2:B:254:SER:O	3:C:265:LEU:CD1	2.67	0.42
3:C:247:PHE:HE1	3:C:309:VAL:HG23	1.84	0.42
3:C:270:PHE:CE1	1:D:255:VAL:HG23	2.53	0.42
3:C:271:LEU:CD2	3:C:299:VAL:HG11	2.44	0.42
3:C:422:GLY:H	3:C:423:ILE:HG13	1.85	0.42
1:D:35:LEU:HD12	1:D:36:GLN:H	1.84	0.42
1:D:93:TYR:OH	1:D:147:GLY:HA3	2.19	0.42
1:D:133:THR:O	1:D:136:PRO:HD2	2.19	0.42
4:E:59:TRP:CE3	4:E:115:MET:HB2	2.54	0.42
4:E:66:TRP:CD1	4:E:111:ASN:HB2	2.54	0.42
1:A:31:ILE:HA	1:A:59:GLN:O	2.20	0.42
1:A:95:ASN:OD1	1:A:144:MET:SD	2.78	0.42
1:A:117:MET:HG3	1:A:119:THR:HG23	2.02	0.42
1:A:184:TRP:CE3	1:A:185:LYS:O	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:GLU:OE2	2:B:404:ALA:HB3	2.20	0.42
1:A:379:VAL:HG22	4:E:424:LYS:CE	2.49	0.42
2:B:69:PRO:HG2	2:B:70:ALA:N	2.34	0.42
2:B:272:GLU:O	2:B:272:GLU:CG	2.58	0.42
3:C:7:LEU:HD13	3:C:73:GLU:CG	2.49	0.42
3:C:76:ASP:C	3:C:77:ILE:CG2	2.86	0.42
3:C:303:VAL:O	3:C:306:CYS:HB2	2.19	0.42
1:D:60:TRP:O	1:D:61:ILE:CG2	2.67	0.42
1:D:80:LEU:HD12	1:D:80:LEU:HA	1.72	0.42
1:D:89:ASP:OD1	1:D:89:ASP:O	2.37	0.42
1:D:227:PHE:HE1	1:D:231:LEU:HD21	1.84	0.42
1:D:381:TYR:O	1:D:385:HIS:CB	2.67	0.42
4:E:453:ILE:O	4:E:457:LEU:CB	2.67	0.42
1:A:54:VAL:O	1:A:122:ALA:HB3	2.20	0.42
1:A:95:ASN:H	1:A:95:ASN:HD22	1.68	0.42
1:A:136:PRO:CG	1:A:274:ILE:HG23	2.50	0.42
1:A:216:VAL:O	1:A:217:ASN:C	2.58	0.42
1:A:261:VAL:O	1:A:265:PRO:CD	2.67	0.42
1:A:291:VAL:HG12	1:A:292:THR:N	2.35	0.42
1:A:384:GLU:OE1	2:B:411:ILE:CG2	2.68	0.42
2:B:424:LEU:HD22	2:B:428:TRP:CZ2	2.55	0.42
3:C:215:VAL:HB	3:C:217:PHE:CE1	2.55	0.42
1:D:92:LEU:HB2	1:D:96:ALA:H	1.85	0.42
4:E:74:ILE:CG1	4:E:74:ILE:O	2.68	0.42
4:E:80:PRO:HB2	4:E:83:LEU:CD2	2.50	0.42
4:E:149:THR:HG23	4:E:150:TYR:N	2.30	0.42
1:A:58:GLN:HB2	1:A:118:TRP:HB3	2.00	0.42
2:B:92:LEU:HG	2:B:96:ASN:HD22	1.83	0.42
2:B:199:SER:C	2:B:201:ASP:H	2.21	0.42
2:B:223:TYR:C	2:B:226:VAL:HG22	2.37	0.42
2:B:262:PHE:CD1	2:B:262:PHE:N	2.86	0.42
3:C:161:ASP:HA	3:C:199:LYS:CG	2.45	0.42
3:C:434:LYS:CG	3:C:435:GLU:N	2.81	0.42
1:D:47:ASN:C	1:D:48:GLN:HG2	2.40	0.42
1:D:152:ASP:HB2	1:D:196:THR:O	2.20	0.42
1:D:377:GLU:HA	1:D:380:LYS:HE3	2.00	0.42
4:E:183:TRP:C	4:E:184:THR:HG22	2.40	0.42
4:E:200:LYS:O	4:E:200:LYS:HG3	2.19	0.42
4:E:242:LEU:N	4:E:243:PRO:CD	2.83	0.42
4:E:419:CYS:HA	4:E:422:ILE:HG12	2.02	0.42
1:A:146:LEU:HD22	1:A:203:TYR:OH	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:LYS:N	1:A:276:LYS:CD	2.83	0.42
1:A:281:THR:HG23	1:A:282:MET:N	2.34	0.42
2:B:27:ASP:C	2:B:28:LYS:CG	2.79	0.42
2:B:45:GLU:HG2	2:B:277:VAL:CA	2.48	0.42
2:B:130:ILE:CB	2:B:134:TYR:CE2	3.03	0.42
2:B:147:LYS:HE2	2:B:148:SER:OG	2.20	0.42
2:B:460:HIS:C	2:B:464:PRO:HD2	2.40	0.42
3:C:30:VAL:CG2	3:C:157:GLU:H	2.32	0.42
3:C:149:THR:HB	3:C:214:ASP:HA	2.02	0.42
3:C:199:LYS:NZ	3:C:200:ASN:HA	2.33	0.42
3:C:447:ASN:O	3:C:448:LEU:C	2.58	0.42
1:D:26:THR:O	1:D:28:PHE:HD1	2.03	0.42
1:D:37:LEU:HD13	1:D:54:VAL:CG1	2.50	0.42
1:D:238:ASP:HB3	4:E:308:LEU:HD23	1.91	0.42
1:D:245:LEU:HD12	4:E:252:THR:HB	2.01	0.42
1:D:264:ILE:HA	1:D:267:THR:HG23	2.02	0.42
1:D:377:GLU:CG	4:E:415:CYS:CB	2.81	0.42
4:E:83:LEU:O	4:E:84:LEU:CB	2.67	0.42
4:E:261:GLN:HE22	4:E:296:ILE:HD11	1.84	0.42
1:A:21:PRO:HB3	1:A:62:ASP:OD2	2.20	0.42
1:A:51:GLU:HG3	1:A:125:LYS:HD2	2.01	0.42
1:A:203:TYR:HB3	1:A:205:PHE:HE1	1.84	0.42
1:A:229:THR:O	1:A:232:VAL:N	2.53	0.42
2:B:31:VAL:HG12	2:B:158:LEU:HD23	1.96	0.42
2:B:133:MET:CE	2:B:140:GLN:CB	2.98	0.42
2:B:140:GLN:O	2:B:213:ILE:HD13	2.20	0.42
2:B:180:PHE:CZ	2:B:186:TRP:O	2.72	0.42
2:B:191:LYS:HA	2:B:210:TYR:O	2.20	0.42
2:B:254:SER:OG	3:C:261:ILE:CG2	2.67	0.42
2:B:288:MET:O	2:B:291:VAL:HG12	2.20	0.42
3:C:296:MET:HA	3:C:296:MET:HE3	2.01	0.42
1:D:78:ILE:CD1	1:D:78:ILE:C	2.88	0.42
1:D:85:VAL:HG13	1:D:86:TRP:C	2.40	0.42
4:E:145:PHE:O	4:E:208:ILE:HG13	2.20	0.42
4:E:212:LEU:N	4:E:212:LEU:CD1	2.83	0.42
1:A:72:TYR:CD1	1:A:72:TYR:O	2.72	0.41
1:A:80:LEU:HD23	1:A:110:LEU:CB	2.49	0.41
1:A:108:LEU:O	1:A:109:LEU:HD23	2.20	0.41
1:A:167:LEU:HA	1:A:170:PHE:HB2	2.02	0.41
1:A:187:TRP:CD1	1:A:199:LEU:HD23	2.51	0.41
1:A:243:MET:CG	4:E:249:GLN:OE1	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:GLU:CD	1:A:390:GLU:C	2.78	0.41
1:A:406:ILE:HD13	1:A:406:ILE:N	2.35	0.41
3:C:150:ALA:CB	3:C:158:ILE:CD1	2.98	0.41
4:E:70:GLU:O	4:E:74:ILE:HD13	2.20	0.41
4:E:216:ARG:C	4:E:217:LYS:HG3	2.38	0.41
4:E:252:THR:O	4:E:253:LEU:C	2.58	0.41
2:B:82:SER:C	2:B:84:ASP:N	2.71	0.41
2:B:203:SER:O	2:B:205:GLU:HG2	2.20	0.41
3:C:130:CYS:SG	3:C:146:LEU:HD11	2.59	0.41
3:C:139:PHE:CE1	3:C:291:TYR:OH	2.61	0.41
1:D:135:PHE:HD1	1:D:136:PRO:N	2.18	0.41
1:D:137:PHE:HD2	1:D:431:ILE:CB	2.32	0.41
1:D:212:LEU:O	1:D:216:VAL:CG2	2.68	0.41
1:D:305:THR:C	1:D:306:HIS:ND1	2.74	0.41
1:D:398:GLU:C	1:D:400:LYS:N	2.73	0.41
1:D:402:VAL:H	1:D:402:VAL:HG23	1.32	0.41
1:D:416:LEU:HA	1:D:419:ILE:CG1	2.50	0.41
4:E:267:LEU:HD12	4:E:270:GLN:CD	2.40	0.41
1:A:176:TRP:HE3	1:A:209:ARG:CZ	2.27	0.41
2:B:188:ILE:HG23	2:B:189:GLU:N	2.34	0.41
3:C:29:GLU:O	3:C:156:ASN:CA	2.64	0.41
3:C:67:LEU:CG	3:C:116:GLY:HA2	2.46	0.41
3:C:110:VAL:HG22	3:C:120:TRP:HB2	2.02	0.41
3:C:479:ASN:C	3:C:479:ASN:HD22	2.20	0.41
1:D:250:LEU:HD23	1:D:253:LEU:HD13	2.03	0.41
4:E:54:TRP:CA	4:E:118:LEU:HD11	2.49	0.41
4:E:63:ARG:HB2	4:E:63:ARG:NH1	2.24	0.41
4:E:89:VAL:O	4:E:99:PHE:CE1	2.73	0.41
4:E:133:TYR:CG	4:E:139:GLN:HB3	2.55	0.41
4:E:159:LEU:HB3	4:E:160:SER:H	1.57	0.41
4:E:195:ASN:HB3	4:E:205:PHE:H	1.85	0.41
4:E:451:PHE:HA	4:E:454:ALA:HB3	2.02	0.41
1:A:123:ILE:O	1:A:123:ILE:HG23	2.19	0.41
1:A:130:ILE:CD1	1:A:131:ILE:N	2.71	0.41
1:A:245:LEU:CD1	2:B:250:SER:HB2	2.49	0.41
1:A:387:LYS:H	1:A:387:LYS:HG2	1.54	0.41
3:C:110:VAL:HG22	3:C:120:TRP:CG	2.56	0.41
3:C:134:VAL:HG12	3:C:134:VAL:O	2.20	0.41
3:C:283:LEU:C	3:C:285:VAL:H	2.22	0.41
1:D:255:VAL:O	1:D:259:VAL:CG2	2.61	0.41
4:E:103:TYR:CD2	4:E:104:TYR:N	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:261:GLN:HE21	4:E:265:LEU:HD11	1.84	0.41
4:E:266:PHE:CD1	4:E:266:PHE:C	2.91	0.41
4:E:276:SER:HB3	4:E:281:LEU:CD1	2.47	0.41
4:E:436:ASN:HA	4:E:439:TRP:CD1	2.52	0.41
1:A:27:HIS:O	1:A:28:PHE:CB	2.69	0.41
1:A:155:LYS:HD3	1:A:155:LYS:HA	1.50	0.41
1:A:198:TYR:O	1:A:198:TYR:HD1	1.99	0.41
2:B:144:MET:O	2:B:209:PHE:CD2	2.73	0.41
2:B:159:GLN:O	2:B:159:GLN:HG3	2.19	0.41
2:B:192:PRO:HD2	2:B:210:TYR:CB	2.51	0.41
2:B:221:ILE:O	2:B:224:THR:HB	2.21	0.41
2:B:249:MET:CE	2:B:250:SER:HB3	2.50	0.41
2:B:250:SER:C	2:B:252:SER:N	2.74	0.41
2:B:282:SER:O	2:B:286:PHE:CD2	2.74	0.41
2:B:409:LYS:NZ	3:C:423:ILE:HG23	2.35	0.41
3:C:35:LEU:CD2	3:C:215:VAL:HG21	2.46	0.41
3:C:162:LEU:HD11	3:C:197:ALA:HB1	2.01	0.41
3:C:189:GLU:C	3:C:223:ARG:HG3	2.40	0.41
3:C:316:THR:HB	3:C:320:HIS:H	1.85	0.41
1:D:31:ILE:O	1:D:158:ILE:HA	2.21	0.41
1:D:49:ILE:CG2	1:D:125:LYS:NZ	2.66	0.41
1:D:166:ASP:CB	1:D:178:MET:HE2	2.51	0.41
1:D:195:ASP:C	1:D:197:PRO:HD3	2.41	0.41
4:E:182:GLU:HG3	4:E:218:PRO:HG2	2.02	0.41
4:E:214:ILE:C	4:E:214:ILE:CD1	2.79	0.41
4:E:266:PHE:CZ	4:E:270:GLN:HB3	2.55	0.41
1:A:166:ASP:CB	1:A:178:MET:HE2	2.44	0.41
1:A:203:TYR:CD1	1:A:203:TYR:N	2.89	0.41
1:A:381:TYR:CD1	1:A:381:TYR:N	2.89	0.41
2:B:57:ASN:HA	2:B:118:TRP:O	2.20	0.41
2:B:136:PRO:HD3	2:B:280:ILE:CD1	2.51	0.41
2:B:427:ASP:OD1	2:B:427:ASP:C	2.59	0.41
3:C:25:LYS:HA	3:C:25:LYS:HZ2	1.84	0.41
4:E:74:ILE:O	4:E:74:ILE:HD13	2.21	0.41
4:E:140:ASN:ND2	4:E:212:LEU:H	2.18	0.41
4:E:213:ILE:O	4:E:213:ILE:CG2	2.68	0.41
1:A:148:ILE:HG23	1:A:198:TYR:CD2	2.51	0.41
1:A:218:VAL:C	1:A:221:PRO:HD2	2.41	0.41
1:A:265:PRO:CG	1:A:266:SER:N	2.80	0.41
1:A:406:ILE:O	1:A:409:ILE:HG13	2.20	0.41
2:B:46:LYS:HB2	2:B:278:PRO:CD	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:52:THR:HG22	2:B:53:SER:N	2.28	0.41
2:B:61:THR:CG2	2:B:62:ASP:N	2.81	0.41
2:B:420:GLU:O	2:B:424:LEU:N	2.53	0.41
2:B:456:LEU:N	2:B:456:LEU:CD2	2.84	0.41
3:C:3:GLU:CD	3:C:7:LEU:HG	2.41	0.41
3:C:143:ASN:HA	3:C:220:ILE:HA	2.02	0.41
3:C:278:LEU:N	3:C:279:PRO:HD2	2.35	0.41
1:D:235:LEU:HD13	1:D:242:LYS:HE3	2.01	0.41
1:D:264:ILE:HB	1:D:265:PRO:CD	2.50	0.41
4:E:6:LEU:HD11	4:E:69:SER:HB3	1.96	0.41
4:E:20:PRO:HG3	4:E:61:ASP:HB2	2.01	0.41
4:E:42:LEU:HA	4:E:42:LEU:HD12	1.84	0.41
4:E:47:GLU:CB	4:E:128:PRO:O	2.69	0.41
4:E:92:GLU:HB3	4:E:93:ASN:H	1.67	0.41
4:E:435:GLU:HB3	4:E:439:TRP:CZ2	2.55	0.41
1:A:175:GLU:CB	1:A:211:PRO:HG3	2.50	0.41
1:A:303:PRO:HB2	1:A:304:SER:H	1.73	0.41
1:A:379:VAL:HA	1:A:382:ILE:CG1	2.50	0.41
2:B:248:LYS:HE2	2:B:248:LYS:HB2	1.82	0.41
2:B:261:VAL:O	2:B:265:LEU:HG	2.21	0.41
2:B:282:SER:HB3	2:B:283:TYR:HD1	1.85	0.41
3:C:58:MET:SD	3:C:92:ILE:HD12	2.58	0.41
3:C:199:LYS:NZ	3:C:199:LYS:C	2.72	0.41
3:C:462:THR:H	3:C:463:PRO:HD2	1.82	0.41
1:D:3:HIS:HB3	1:D:7:LEU:CD2	2.51	0.41
1:D:26:THR:O	1:D:28:PHE:CD1	2.73	0.41
1:D:76:LYS:CE	1:D:112:TYR:CE2	3.03	0.41
1:D:251:LEU:HA	1:D:251:LEU:HD23	1.70	0.41
1:D:282:MET:HE3	1:D:286:ILE:HD11	2.01	0.41
4:E:66:TRP:CD1	4:E:66:TRP:N	2.89	0.41
4:E:138:TRP:HH2	4:E:215:GLN:HE21	1.64	0.41
4:E:138:TRP:CD1	4:E:213:ILE:HD11	2.56	0.41
4:E:255:ILE:C	4:E:257:VAL:N	2.73	0.41
4:E:283:GLY:C	4:E:287:ILE:HG22	2.40	0.41
1:A:46:VAL:HG12	1:A:47:ASN:ND2	2.35	0.41
1:A:146:LEU:HD22	1:A:203:TYR:CZ	2.55	0.41
1:A:209:ARG:C	1:A:210:ILE:HG12	2.37	0.41
1:A:235:LEU:CB	1:A:236:PRO:CD	2.96	0.41
1:A:277:TYR:O	1:A:280:PHE:CG	2.74	0.41
2:B:2:VAL:CG1	2:B:69:PRO:HG3	2.50	0.41
2:B:35:LEU:HD11	2:B:56:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:182:GLU:C	2:B:184:GLY:H	2.23	0.41
2:B:248:LYS:HZ2	2:B:252:SER:HB2	1.86	0.41
2:B:281:ILE:O	2:B:282:SER:C	2.59	0.41
2:B:417:SER:O	2:B:421:PHE:CE2	2.74	0.41
3:C:37:LEU:HD11	3:C:148:PHE:CG	2.56	0.41
3:C:43:ILE:H	3:C:43:ILE:CD1	2.22	0.41
3:C:84:PRO:CG	3:C:107:PHE:C	2.85	0.41
3:C:86:LEU:HD23	3:C:86:LEU:HA	1.83	0.41
3:C:89:ILE:HD13	3:C:89:ILE:HG21	1.64	0.41
3:C:137:PHE:CD1	3:C:288:ILE:HG21	2.55	0.41
3:C:142:GLN:HG3	3:C:143:ASN:N	2.35	0.41
3:C:154:ASN:HA	3:C:211:ASN:HB2	2.02	0.41
3:C:180:ASP:HB3	3:C:192:ILE:HG21	2.03	0.41
3:C:247:PHE:CD1	3:C:309:VAL:CG2	3.00	0.41
1:D:38:ILE:C	1:D:169:THR:HG21	2.40	0.41
1:D:93:TYR:CD1	1:D:93:TYR:N	2.88	0.41
1:D:184:TRP:HE3	1:D:185:LYS:O	2.03	0.41
1:D:377:GLU:HA	1:D:380:LYS:CD	2.51	0.41
1:D:429:ARG:NE	1:D:429:ARG:HA	2.36	0.41
4:E:33:LYS:CE	4:E:160:SER:CB	2.89	0.41
4:E:45:LYS:CG	4:E:279:VAL:C	2.81	0.41
4:E:273:PRO:O	4:E:277:LEU:HG	2.21	0.41
4:E:297:VAL:HB	4:E:298:THR:H	1.56	0.41
1:A:206:ILE:HD12	1:A:206:ILE:N	2.36	0.41
1:A:226:SER:O	1:A:230:VAL:HG23	2.21	0.41
1:A:265:PRO:CG	1:A:266:SER:H	2.28	0.41
2:B:180:PHE:HZ	2:B:186:TRP:O	2.04	0.41
3:C:58:MET:CG	3:C:92:ILE:HD12	2.50	0.41
3:C:280:GLU:HG3	3:C:281:THR:H	1.79	0.41
1:D:133:THR:HG23	1:D:274:ILE:HG21	2.02	0.41
1:D:155:LYS:HA	1:D:155:LYS:HD3	1.88	0.41
1:D:175:GLU:HB3	1:D:211:PRO:CG	2.50	0.41
4:E:283:GLY:HA3	4:E:284:LYS:HZ2	1.86	0.41
1:A:259:VAL:O	1:A:263:LEU:HG	2.21	0.40
2:B:108:VAL:HG13	2:B:117:SER:O	2.20	0.40
2:B:147:LYS:CD	2:B:148:SER:H	2.34	0.40
2:B:150:THR:CG2	2:B:150:THR:O	2.67	0.40
2:B:162:LEU:C	2:B:174:MET:N	2.74	0.40
2:B:185:GLN:CD	2:B:219:PHE:CD2	2.94	0.40
2:B:248:LYS:HZ3	2:B:252:SER:CB	2.33	0.40
2:B:248:LYS:O	2:B:249:MET:C	2.59	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:148:PHE:N	3:C:148:PHE:HD1	2.19	0.40
3:C:474:VAL:HA	3:C:477:ASN:ND2	2.36	0.40
1:D:225:PHE:HD1	1:D:225:PHE:C	2.24	0.40
4:E:1:ASN:HD22	4:E:69:SER:HA	1.86	0.40
4:E:45:LYS:N	4:E:280:PRO:HB3	2.37	0.40
4:E:59:TRP:CE2	4:E:115:MET:CB	3.03	0.40
4:E:136:PHE:HB3	4:E:475:PRO:CB	2.51	0.40
4:E:294:LEU:C	4:E:297:VAL:HG23	2.41	0.40
1:A:3:HIS:C	1:A:7:LEU:HG	2.42	0.40
1:A:46:VAL:CB	1:A:270:ALA:O	2.62	0.40
1:A:95:ASN:OD1	1:A:144:MET:HA	2.21	0.40
1:A:305:THR:CB	1:A:400:LYS:HB2	2.50	0.40
3:C:116:GLY:O	3:C:118:VAL:HG23	2.21	0.40
1:D:56:LEU:CA	1:D:120:PRO:HD2	2.51	0.40
1:D:137:PHE:HB2	1:D:431:ILE:HG22	2.02	0.40
1:D:410:LEU:O	1:D:414:PHE:CB	2.69	0.40
4:E:217:LYS:HE3	4:E:217:LYS:HB2	1.84	0.40
4:E:222:ILE:O	4:E:225:ILE:HB	2.20	0.40
4:E:294:LEU:O	4:E:297:VAL:HG23	2.21	0.40
1:A:72:TYR:CG	1:A:73:GLY:N	2.89	0.40
1:A:165:PRO:O	1:A:168:SER:HB3	2.21	0.40
1:A:251:LEU:CD1	4:E:256:SER:O	2.70	0.40
1:A:379:VAL:HA	1:A:382:ILE:CD1	2.49	0.40
2:B:10:VAL:CG1	2:B:11:LEU:N	2.84	0.40
2:B:218:LEU:CD1	2:B:221:ILE:HG13	2.43	0.40
2:B:459:SER:O	2:B:463:PRO:HB2	2.22	0.40
3:C:28:ASN:HB2	3:C:29:GLU:H	1.48	0.40
3:C:43:ILE:N	3:C:43:ILE:CD1	2.80	0.40
3:C:60:HIS:CE1	3:C:160:MET:CE	3.04	0.40
3:C:230:ILE:CG1	3:C:231:ASN:N	2.82	0.40
1:D:34:GLY:N	1:D:57:ARG:HD2	2.37	0.40
1:D:43:VAL:HG13	1:D:49:ILE:C	2.39	0.40
1:D:92:LEU:CD1	1:D:146:LEU:HD11	2.51	0.40
1:D:423:VAL:CA	1:D:426:PHE:HB3	2.51	0.40
4:E:66:TRP:HB2	4:E:71:TYR:CB	2.51	0.40
4:E:66:TRP:CE3	4:E:70:GLU:CG	3.05	0.40
4:E:91:LEU:HA	4:E:145:PHE:CA	2.52	0.40
4:E:182:GLU:HA	4:E:182:GLU:OE1	2.21	0.40
4:E:187:HIS:HE1	4:E:189:PRO:HG3	1.69	0.40
4:E:195:ASN:HB3	4:E:205:PHE:N	2.36	0.40
4:E:269:ALA:O	4:E:273:PRO:CG	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:283:GLY:O	4:E:287:ILE:CG2	2.61	0.40
4:E:306:VAL:O	4:E:309:ARG:CG	2.69	0.40
1:A:56:LEU:CD1	1:A:90:LEU:HD13	2.51	0.40
1:A:82:SER:O	1:A:84:ASP:N	2.54	0.40
1:A:148:ILE:N	1:A:158:ILE:HD12	2.36	0.40
1:A:227:PHE:CE2	2:B:299:VAL:HG11	2.56	0.40
1:A:397:GLU:HG2	1:A:400:LYS:HD2	2.04	0.40
1:A:426:PHE:CD1	1:A:427:ALA:N	2.78	0.40
2:B:262:PHE:HA	2:B:265:LEU:HD12	2.03	0.40
2:B:438:LEU:HD23	2:B:441:TYR:HB3	2.03	0.40
3:C:47:GLU:HG2	3:C:286:PRO:CD	2.43	0.40
3:C:58:MET:HG3	3:C:92:ILE:HD12	2.03	0.40
3:C:452:THR:CG2	3:C:453:ILE:N	2.77	0.40
1:D:253:LEU:CD2	1:D:254:THR:HB	2.50	0.40
4:E:38:ASN:ND2	4:E:40:ILE:HG12	2.37	0.40
4:E:173:ASP:HB3	4:E:185:ILE:HG21	2.03	0.40
4:E:306:VAL:O	4:E:309:ARG:HG2	2.22	0.40
4:E:448:LYS:HD2	4:E:448:LYS:HA	1.68	0.40
1:A:43:VAL:HG12	1:A:44:ASP:N	2.36	0.40
1:A:52:THR:O	1:A:123:ILE:CG1	2.64	0.40
1:A:91:VAL:HB	1:A:149:TRP:HB2	2.04	0.40
1:A:175:GLU:HB3	1:A:211:PRO:HG3	2.03	0.40
1:A:260:ILE:O	1:A:264:ILE:HG23	2.22	0.40
2:B:46:LYS:CB	2:B:278:PRO:HD2	2.49	0.40
2:B:248:LYS:HZ3	2:B:252:SER:CA	2.34	0.40
2:B:271:PRO:O	2:B:275:LEU:HD23	2.22	0.40
2:B:437:ARG:HD2	2:B:437:ARG:HA	1.72	0.40
2:B:451:THR:HA	2:B:454:ILE:HD12	2.04	0.40
3:C:54:THR:O	3:C:126:PHE:CE2	2.75	0.40
3:C:194:HIS:HB3	3:C:220:ILE:HG12	2.02	0.40
3:C:439:TYR:CD1	3:C:439:TYR:N	2.90	0.40
3:C:450:GLY:O	3:C:453:ILE:HG22	2.22	0.40
3:C:470:ILE:HD13	3:C:470:ILE:HA	1.80	0.40
1:D:41:ILE:HG21	4:E:96:ASP:OD2	2.21	0.40
1:D:44:ASP:O	1:D:48:GLN:CA	2.70	0.40
1:D:178:MET:CE	1:D:207:MET:HB3	2.51	0.40
1:D:415:MET:HE2	1:D:415:MET:HB2	1.87	0.40
4:E:188:ARG:N	4:E:189:PRO:HD3	2.33	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	366/461 (79%)	260 (71%)	58 (16%)	48 (13%)	0	4
1	D	366/461 (79%)	264 (72%)	56 (15%)	46 (13%)	0	4
2	B	364/493 (74%)	243 (67%)	65 (18%)	56 (15%)	0	3
3	C	364/522 (70%)	252 (69%)	68 (19%)	44 (12%)	0	4
4	E	365/488 (75%)	234 (64%)	80 (22%)	51 (14%)	0	3
All	All	1825/2425 (75%)	1253 (69%)	327 (18%)	245 (13%)	0	4

All (245) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	PRO
1	A	24	HIS
1	A	27	HIS
1	A	48	GLN
1	A	76	LYS
1	A	83	ASP
1	A	93	TYR
1	A	97	ASP
1	A	102	ILE
1	A	112	TYR
1	A	131	ILE
1	A	212	LEU
1	A	215	VAL
1	A	216	VAL
1	A	282	MET
1	A	292	THR
1	A	301	ARG
1	A	303	PRO
1	A	304	SER
1	A	420	ILE
2	B	27	ASP

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Mol	Chain	Res	Type
2	B	48	GLU
2	B	68	ASP
2	B	81	PRO
2	B	90	ILE
2	B	93	MET
2	B	96	ASN
2	B	99	SER
2	B	102	ILE
2	B	107	ASN
2	B	129	THR
2	B	139	TRP
2	B	185	GLN
2	B	206	ASP
2	B	222	VAL
2	B	235	ALA
2	B	249	MET
2	B	251	LEU
2	B	277	VAL
2	B	280	ILE
2	B	283	TYR
2	B	284	LEU
2	B	306	HIS
2	B	307	ARG
2	B	410	TYR
3	C	2	ASN
3	C	5	GLU
3	C	30	VAL
3	C	48	THR
3	C	99	ASP
3	C	115	ASN
3	C	116	GLY
3	C	131	PRO
3	C	180	ASP
3	C	212	TYR
3	C	224	LYS
3	C	253	SER
3	C	310	LEU
3	C	423	ILE
3	C	453	ILE
3	C	484	LYS
1	D	2	GLU
1	D	24	HIS

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Mol	Chain	Res	Type
1	D	30	ASP
1	D	45	GLU
1	D	64	ARG
1	D	74	GLY
1	D	75	ILE
1	D	84	ASP
1	D	102	ILE
1	D	130	ILE
1	D	131	ILE
1	D	136	PRO
1	D	153	GLY
1	D	210	ILE
1	D	239	SER
1	D	241	GLU
1	D	269	SER
1	D	282	MET
1	D	301	ARG
1	D	423	VAL
1	D	426	PHE
1	D	435	GLN
1	D	436	GLU
4	E	16	LYS
4	E	27	VAL
4	E	84	LEU
4	E	93	ASN
4	E	95	VAL
4	E	106	ASN
4	E	111	ASN
4	E	128	PRO
4	E	129	ILE
4	E	152	ALA
4	E	173	ASP
4	E	217	LYS
4	E	253	LEU
4	E	271	LYS
4	E	280	PRO
4	E	298	THR
4	E	309	ARG
4	E	443	GLY
1	A	2	GLU
1	A	7	LEU
1	A	17	LYS

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Mol	Chain	Res	Type
1	A	75	ILE
1	A	232	VAL
1	A	239	SER
1	A	265	PRO
1	A	293	VAL
1	A	392	SER
2	B	2	VAL
2	B	4	GLU
2	B	86	TRP
2	B	156	VAL
2	B	190	HIS
2	B	236	ILE
2	B	246	GLY
2	B	279	ILE
2	B	304	LEU
2	B	415	LEU
3	C	13	ILE
3	C	132	ILE
3	C	136	TYR
3	C	157	GLU
3	C	301	GLY
3	C	434	LYS
3	C	449	VAL
3	C	471	PHE
1	D	73	GLY
1	D	76	LYS
1	D	174	GLY
1	D	220	ILE
1	D	276	LYS
1	D	280	PHE
1	D	428	GLY
4	E	2	GLU
4	E	47	GLU
4	E	63	ARG
4	E	64	LEU
4	E	74	ILE
4	E	92	GLU
4	E	98	GLN
4	E	101	VAL
4	E	112	ASP
4	E	132	THR
4	E	196	TRP

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Mol	Chain	Res	Type
4	E	249	GLN
1	A	28	PHE
1	A	82	SER
1	A	180	ASP
1	A	210	ILE
1	A	419	ILE
1	A	426	PHE
2	B	39	SER
2	B	147	LYS
2	B	198	ARG
2	B	200	ASP
2	B	432	ALA
2	B	458	ALA
3	C	6	ARG
3	C	12	LEU
3	C	205	LYS
3	C	482	PRO
1	D	139	GLN
1	D	192	CYS
1	D	235	LEU
4	E	22	LYS
4	E	135	PRO
4	E	184	THR
4	E	198	LEU
4	E	246	ALA
4	E	297	VAL
1	A	26	THR
1	A	135	PHE
1	A	198	TYR
1	A	248	SER
1	A	396	ALA
2	B	5	ASP
2	B	153	THR
2	B	183	ASN
2	B	291	VAL
2	B	413	GLU
2	B	435	ALA
3	C	225	PRO
3	C	440	ASP
1	D	162	SER
1	D	268	SER
1	D	303	PRO

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Mol	Chain	Res	Type
4	E	149	THR
4	E	161	ALA
4	E	177	PHE
4	E	231	LEU
4	E	272	VAL
1	A	148	ILE
1	A	291	VAL
1	A	430	LEU
2	B	154	SER
2	B	248	LYS
2	B	411	ILE
3	C	19	LYS
3	C	76	ASP
3	C	137	PHE
3	C	138	PRO
3	C	150	ALA
3	C	195	LYS
3	C	235	PRO
1	D	25	HIS
1	D	95	ASN
1	D	97	ASP
1	D	99	ASP
1	D	252	SER
1	D	263	LEU
4	E	85	TRP
4	E	120	PRO
4	E	200	LYS
4	E	222	ILE
1	A	214	PHE
2	B	24	THR
3	C	77	ILE
3	C	142	GLN
3	C	477	ASN
1	D	68	ASN
1	D	236	PRO
4	E	7	ILE
4	E	203	ILE
4	E	256	SER
1	A	160	PRO
2	B	135	PHE
3	C	122	PRO
3	C	239	ILE

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Mol	Chain	Res	Type
1	D	264	ILE
4	E	134	PHE
1	A	264	ILE
2	B	75	ILE
2	B	243	PRO
1	A	249	VAL
2	B	175	ILE
3	C	134	VAL
4	E	119	PRO
2	B	295	VAL
3	C	181	PRO
1	A	247	ILE
1	D	196	THR
4	E	416	VAL

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	343/427 (80%)	231 (67%)	112 (33%)	0	2
1	D	343/427 (80%)	230 (67%)	113 (33%)	0	2
2	B	340/449 (76%)	235 (69%)	105 (31%)	0	2
3	C	335/475 (70%)	235 (70%)	100 (30%)	0	2
4	E	337/447 (75%)	224 (66%)	113 (34%)	0	1
All	All	1698/2225 (76%)	1155 (68%)	543 (32%)	1	2

All (543) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	2	GLU
1	A	3	HIS
1	A	6	ARG
1	A	17	LYS

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Mol	Chain	Res	Type
1	A	20	ARG
1	A	22	VAL
1	A	24	HIS
1	A	26	THR
1	A	29	VAL
1	A	30	ASP
1	A	36	GLN
1	A	39	GLN
1	A	46	VAL
1	A	56	LEU
1	A	62	ASP
1	A	63	VAL
1	A	66	ARG
1	A	67	TRP
1	A	68	ASN
1	A	72	TYR
1	A	75	ILE
1	A	87	LEU
1	A	92	LEU
1	A	93	TYR
1	A	94	ASN
1	A	95	ASN
1	A	100	PHE
1	A	105	MET
1	A	107	LYS
1	A	108	LEU
1	A	111	ASP
1	A	112	TYR
1	A	116	ILE
1	A	124	PHE
1	A	125	LYS
1	A	126	SER
1	A	129	GLU
1	A	130	ILE
1	A	137	PHE
1	A	139	GLN
1	A	141	ASN
1	A	142	CYS
1	A	144	MET
1	A	145	LYS
1	A	149	TRP
1	A	151	TYR

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Mol	Chain	Res	Type
1	A	156	VAL
1	A	164	ARG
1	A	167	LEU
1	A	168	SER
1	A	180	ASP
1	A	181	TYR
1	A	185	LYS
1	A	189	TYR
1	A	190	TYR
1	A	193	CYS
1	A	195	ASP
1	A	198	TYR
1	A	200	ASP
1	A	207	MET
1	A	210	ILE
1	A	224	LEU
1	A	225	PHE
1	A	227	PHE
1	A	235	LEU
1	A	243	MET
1	A	246	SER
1	A	247	ILE
1	A	254	THR
1	A	255	VAL
1	A	257	LEU
1	A	260	ILE
1	A	263	LEU
1	A	264	ILE
1	A	267	THR
1	A	268	SER
1	A	273	LEU
1	A	274	ILE
1	A	279	LEU
1	A	280	PHE
1	A	282	MET
1	A	290	ILE
1	A	293	VAL
1	A	296	ILE
1	A	297	ASN
1	A	304	SER
1	A	306	HIS
1	A	381	TYR

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Mol	Chain	Res	Type
1	A	382	ILE
1	A	387	LYS
1	A	389	ASP
1	A	391	GLU
1	A	399	TRP
1	A	401	TYR
1	A	402	VAL
1	A	408	HIS
1	A	409	ILE
1	A	410	LEU
1	A	412	CYS
1	A	414	PHE
1	A	415	MET
1	A	419	ILE
1	A	420	ILE
1	A	424	SER
1	A	425	VAL
1	A	426	PHE
1	A	430	LEU
1	A	431	ILE
1	A	433	LEU
1	A	434	SER
1	A	435	GLN
2	B	5	ASP
2	B	15	TYR
2	B	18	LYS
2	B	19	VAL
2	B	20	ARG
2	B	21	PRO
2	B	23	GLN
2	B	27	ASP
2	B	28	LYS
2	B	29	VAL
2	B	31	VAL
2	B	32	ARG
2	B	33	VAL
2	B	35	LEU
2	B	37	LEU
2	B	41	LEU
2	B	42	ILE
2	B	43	LEU
2	B	46	LYS

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Mol	Chain	Res	Type
2	B	53	SER
2	B	55	PHE
2	B	56	LEU
2	B	58	LEU
2	B	64	ARG
2	B	68	ASP
2	B	69	PRO
2	B	73	GLU
2	B	79	SER
2	B	82	SER
2	B	89	ASP
2	B	95	ASN
2	B	97	ASP
2	B	102	ILE
2	B	106	VAL
2	B	107	ASN
2	B	117	SER
2	B	128	CYS
2	B	129	THR
2	B	133	MET
2	B	134	TYR
2	B	135	PHE
2	B	136	PRO
2	B	138	ASP
2	B	145	VAL
2	B	149	TYR
2	B	158	LEU
2	B	159	GLN
2	B	160	HIS
2	B	174	MET
2	B	180	PHE
2	B	181	THR
2	B	188	ILE
2	B	189	GLU
2	B	191	LYS
2	B	196	ASN
2	B	200	ASP
2	B	201	ASP
2	B	202	PRO
2	B	213	ILE
2	B	216	LYS
2	B	220	TYR

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Mol	Chain	Res	Type
2	B	221	ILE
2	B	222	VAL
2	B	233	ILE
2	B	234	LEU
2	B	236	ILE
2	B	237	LEU
2	B	239	PHE
2	B	240	TYR
2	B	241	LEU
2	B	248	LYS
2	B	251	LEU
2	B	253	ILE
2	B	257	LEU
2	B	260	THR
2	B	261	VAL
2	B	263	LEU
2	B	269	LYS
2	B	275	LEU
2	B	277	VAL
2	B	278	PRO
2	B	280	ILE
2	B	283	TYR
2	B	288	MET
2	B	297	LEU
2	B	306	HIS
2	B	307	ARG
2	B	308	SER
2	B	310	ASN
2	B	311	THR
2	B	403	GLU
2	B	408	ILE
2	B	421	PHE
2	B	426	LYS
2	B	429	GLN
2	B	437	ARG
2	B	439	PHE
2	B	440	LEU
2	B	442	ILE
2	B	447	CYS
2	B	462	VAL
2	B	463	PRO
2	B	464	PRO

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Mol	Chain	Res	Type
2	B	465	ASP
2	B	468	PHE
3	C	3	GLU
3	C	7	LEU
3	C	13	ILE
3	C	15	ASN
3	C	16	LYS
3	C	19	LYS
3	C	22	ARG
3	C	25	LYS
3	C	27	ASN
3	C	28	ASN
3	C	30	VAL
3	C	41	ASN
3	C	43	ILE
3	C	45	LEU
3	C	46	LYS
3	C	52	LEU
3	C	54	THR
3	C	55	ASN
3	C	59	ASP
3	C	60	HIS
3	C	63	TYR
3	C	65	HIS
3	C	66	ARG
3	C	69	TRP
3	C	87	ILE
3	C	91	ASP
3	C	92	ILE
3	C	96	ASN
3	C	99	ASP
3	C	102	TYR
3	C	104	VAL
3	C	106	TYR
3	C	107	PHE
3	C	114	PRO
3	C	115	ASN
3	C	130	CYS
3	C	148	PHE
3	C	149	THR
3	C	158	ILE
3	C	160	MET

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Mol	Chain	Res	Type
3	C	179	ILE
3	C	180	ASP
3	C	196	PRO
3	C	199	LYS
3	C	200	ASN
3	C	202	TYR
3	C	205	LYS
3	C	206	PHE
3	C	211	ASN
3	C	214	ASP
3	C	222	ARG
3	C	224	LYS
3	C	225	PRO
3	C	228	TYR
3	C	229	VAL
3	C	233	ILE
3	C	241	PHE
3	C	242	LEU
3	C	249	LEU
3	C	256	LYS
3	C	259	THR
3	C	264	LEU
3	C	267	GLN
3	C	271	LEU
3	C	272	LEU
3	C	274	THR
3	C	276	GLN
3	C	278	LEU
3	C	279	PRO
3	C	280	GLU
3	C	285	VAL
3	C	288	ILE
3	C	291	TYR
3	C	293	MET
3	C	297	SER
3	C	302	VAL
3	C	308	ILE
3	C	310	LEU
3	C	315	ARG
3	C	319	THR
3	C	421	SER
3	C	423	ILE

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Mol	Chain	Res	Type
3	C	428	TYR
3	C	429	ILE
3	C	430	VAL
3	C	432	GLN
3	C	442	GLU
3	C	446	TRP
3	C	451	GLN
3	C	452	THR
3	C	455	ARG
3	C	458	MET
3	C	465	MET
3	C	467	LEU
3	C	471	PHE
3	C	472	ILE
3	C	475	MET
3	C	478	PHE
3	C	479	ASN
3	C	480	ARG
1	D	1	SER
1	D	3	HIS
1	D	8	VAL
1	D	20	ARG
1	D	26	THR
1	D	27	HIS
1	D	30	ASP
1	D	35	LEU
1	D	36	GLN
1	D	40	LEU
1	D	41	ILE
1	D	46	VAL
1	D	52	THR
1	D	54	VAL
1	D	55	ARG
1	D	57	ARG
1	D	60	TRP
1	D	61	ILE
1	D	66	ARG
1	D	72	TYR
1	D	76	LYS
1	D	78	ILE
1	D	79	ARG
1	D	80	LEU

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Mol	Chain	Res	Type
1	D	84	ASP
1	D	86	TRP
1	D	92	LEU
1	D	94	ASN
1	D	99	ASP
1	D	105	MET
1	D	107	LYS
1	D	108	LEU
1	D	112	TYR
1	D	116	ILE
1	D	118	TRP
1	D	120	PRO
1	D	123	ILE
1	D	129	GLU
1	D	130	ILE
1	D	133	THR
1	D	135	PHE
1	D	138	ASP
1	D	142	CYS
1	D	143	THR
1	D	145	LYS
1	D	149	TRP
1	D	151	TYR
1	D	152	ASP
1	D	154	THR
1	D	156	VAL
1	D	158	ILE
1	D	160	PRO
1	D	164	ARG
1	D	166	ASP
1	D	167	LEU
1	D	170	PHE
1	D	173	SER
1	D	176	TRP
1	D	177	VAL
1	D	180	ASP
1	D	185	LYS
1	D	188	VAL
1	D	193	CYS
1	D	198	TYR
1	D	200	ASP
1	D	202	THR

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Mol	Chain	Res	Type
1	D	203	TYR
1	D	207	MET
1	D	210	ILE
1	D	212	LEU
1	D	216	VAL
1	D	219	ILE
1	D	220	ILE
1	D	222	CYS
1	D	225	PHE
1	D	227	PHE
1	D	230	VAL
1	D	237	THR
1	D	238	ASP
1	D	243	MET
1	D	244	THR
1	D	247	ILE
1	D	253	LEU
1	D	265	PRO
1	D	266	SER
1	D	271	VAL
1	D	272	PRO
1	D	274	ILE
1	D	278	MET
1	D	280	PHE
1	D	281	THR
1	D	285	VAL
1	D	297	ASN
1	D	301	ARG
1	D	303	PRO
1	D	305	THR
1	D	377	GLU
1	D	387	LYS
1	D	389	ASP
1	D	394	ASN
1	D	399	TRP
1	D	400	LYS
1	D	402	VAL
1	D	407	ASP
1	D	408	HIS
1	D	410	LEU
1	D	414	PHE
1	D	420	ILE

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Mol	Chain	Res	Type
1	D	422	THR
1	D	426	PHE
1	D	430	LEU
1	D	431	ILE
1	D	436	GLU
4	E	5	ARG
4	E	10	LEU
4	E	13	ASP
4	E	17	ARG
4	E	18	ILE
4	E	19	LYS
4	E	25	ASP
4	E	27	VAL
4	E	29	ASP
4	E	31	THR
4	E	44	GLU
4	E	45	LYS
4	E	47	GLU
4	E	49	LEU
4	E	52	ASN
4	E	60	ASN
4	E	62	TYR
4	E	63	ARG
4	E	66	TRP
4	E	67	ASN
4	E	69	SER
4	E	70	GLU
4	E	71	TYR
4	E	74	ILE
4	E	75	ASP
4	E	79	ILE
4	E	82	GLU
4	E	83	LEU
4	E	86	LEU
4	E	89	VAL
4	E	90	VAL
4	E	93	ASN
4	E	96	ASP
4	E	101	VAL
4	E	104	TYR
4	E	106	ASN
4	E	110	TYR

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Mol	Chain	Res	Type
4	E	111	ASN
4	E	116	TYR
4	E	122	ILE
4	E	123	TYR
4	E	124	ARG
4	E	125	SER
4	E	127	CYS
4	E	135	PRO
4	E	138	TRP
4	E	140	ASN
4	E	143	LEU
4	E	147	SER
4	E	148	GLN
4	E	151	ASN
4	E	156	ASN
4	E	158	GLN
4	E	160	SER
4	E	163	GLU
4	E	172	ILE
4	E	175	GLU
4	E	176	ASP
4	E	177	PHE
4	E	179	GLU
4	E	182	GLU
4	E	184	THR
4	E	188	ARG
4	E	191	LYS
4	E	195	ASN
4	E	196	TRP
4	E	198	LEU
4	E	206	GLN
4	E	210	PHE
4	E	213	ILE
4	E	214	ILE
4	E	217	LYS
4	E	221	TYR
4	E	225	ILE
4	E	231	LEU
4	E	232	ILE
4	E	235	LEU
4	E	237	VAL
4	E	238	LEU

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Mol	Chain	Res	Type
4	E	239	VAL
4	E	242	LEU
4	E	252	THR
4	E	255	ILE
4	E	258	LEU
4	E	268	ILE
4	E	270	GLN
4	E	271	LYS
4	E	276	SER
4	E	277	LEU
4	E	279	VAL
4	E	284	LYS
4	E	286	LEU
4	E	287	ILE
4	E	291	PHE
4	E	293	SER
4	E	294	LEU
4	E	296	ILE
4	E	301	VAL
4	E	303	VAL
4	E	308	LEU
4	E	309	ARG
4	E	310	THR
4	E	416	VAL
4	E	419	CYS
4	E	439	TRP
4	E	444	LYS
4	E	446	ILE
4	E	452	TRP
4	E	455	LEU
4	E	456	LEU
4	E	465	ILE
4	E	471	LEU
4	E	473	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	HIS
1	A	58	GLN
1	A	59	GLN
1	A	306	HIS

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Mol	Chain	Res	Type
1	A	435	GLN
2	B	23	GLN
2	B	47	ASN
2	B	96	ASN
2	B	111	GLN
2	B	176	ASN
2	B	185	GLN
2	B	190	HIS
2	B	305	HIS
2	B	310	ASN
2	B	429	GLN
2	B	460	HIS
3	C	2	ASN
3	C	15	ASN
3	C	41	ASN
3	C	55	ASN
3	C	65	HIS
3	C	97	ASN
3	C	103	ASN
3	C	115	ASN
3	C	200	ASN
3	C	231	ASN
3	C	267	GLN
3	C	447	ASN
3	C	479	ASN
1	D	16	ASN
1	D	36	GLN
1	D	53	ASN
1	D	58	GLN
1	D	59	GLN
1	D	141	ASN
1	D	408	HIS
1	D	435	GLN
4	E	1	ASN
4	E	26	HIS
4	E	52	ASN
4	E	60	ASN
4	E	67	ASN
4	E	93	ASN
4	E	94	ASN
4	E	98	GLN
4	E	106	ASN

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Mol	Chain	Res	Type
4	E	111	ASN
4	E	140	ASN
4	E	148	GLN
4	E	156	ASN
4	E	197	GLN
4	E	206	GLN
4	E	215	GLN
4	E	261	GLN
4	E	299	ASN
4	E	472	ASN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	E	3
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	126:THR	C	127:CYS	N	1.19
1	E	306:VAL	C	307:SER	N	1.19
1	E	309:ARG	C	310:THR	N	1.19
1	B	129:THR	C	130:ILE	N	1.12

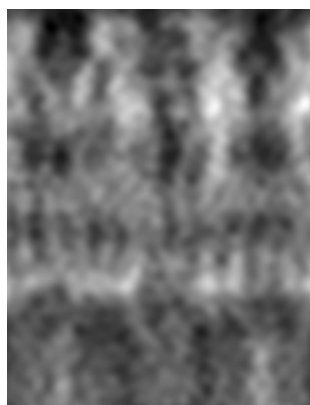
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2071. These allow visual inspection of the internal detail of the map and identification of artifacts.

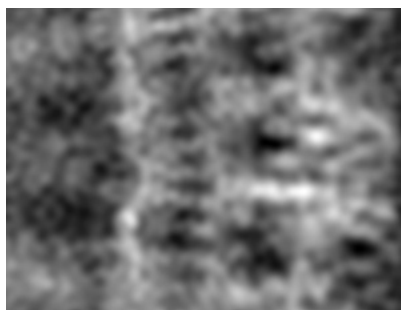
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

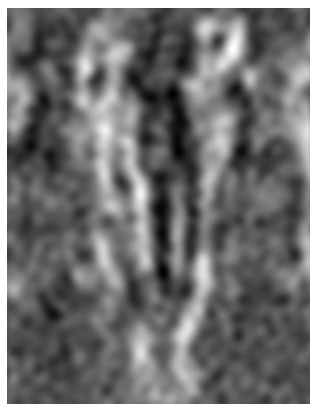


Z

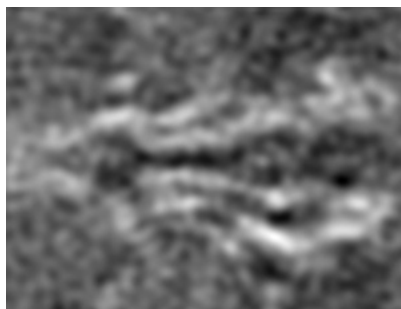
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

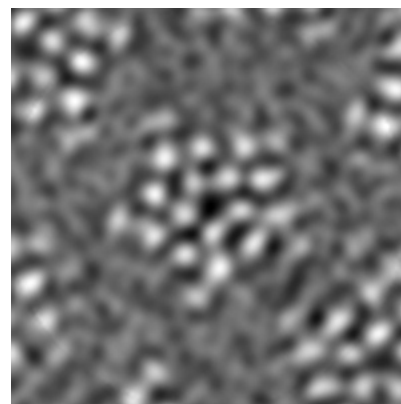
6.2.1 Primary map



X Index: 64



Y Index: 64

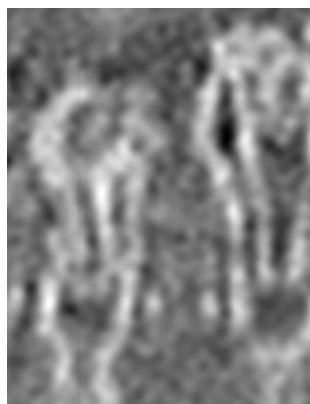


Z Index: 84

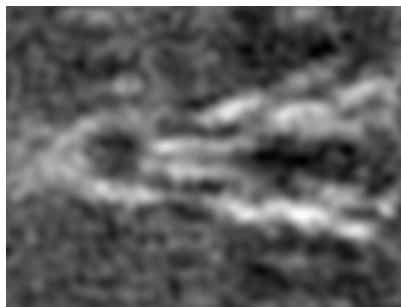
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

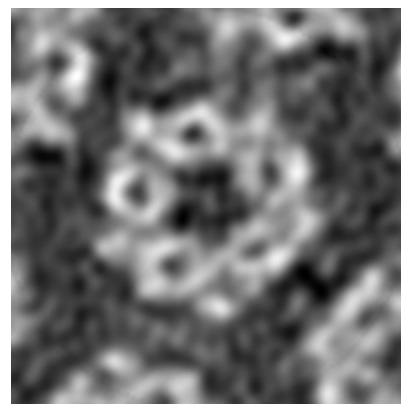
6.3.1 Primary map



X Index: 7



Y Index: 71

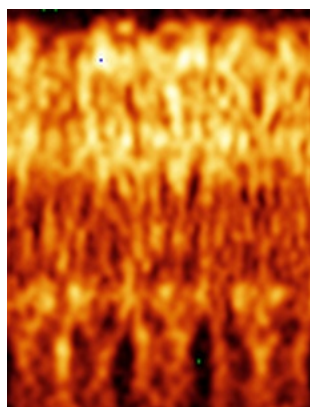


Z Index: 145

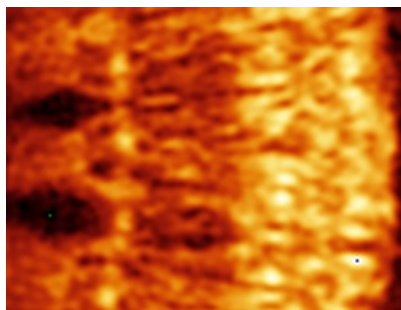
The images above show the largest variance slices of the map in three orthogonal directions.

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

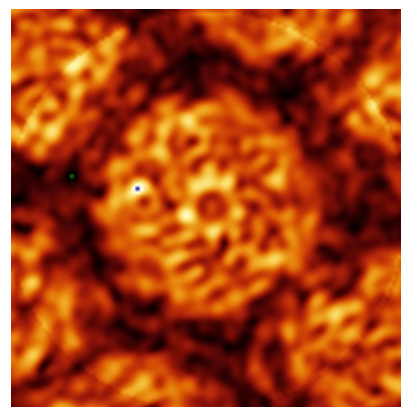
6.4.1 Primary map



X



Y

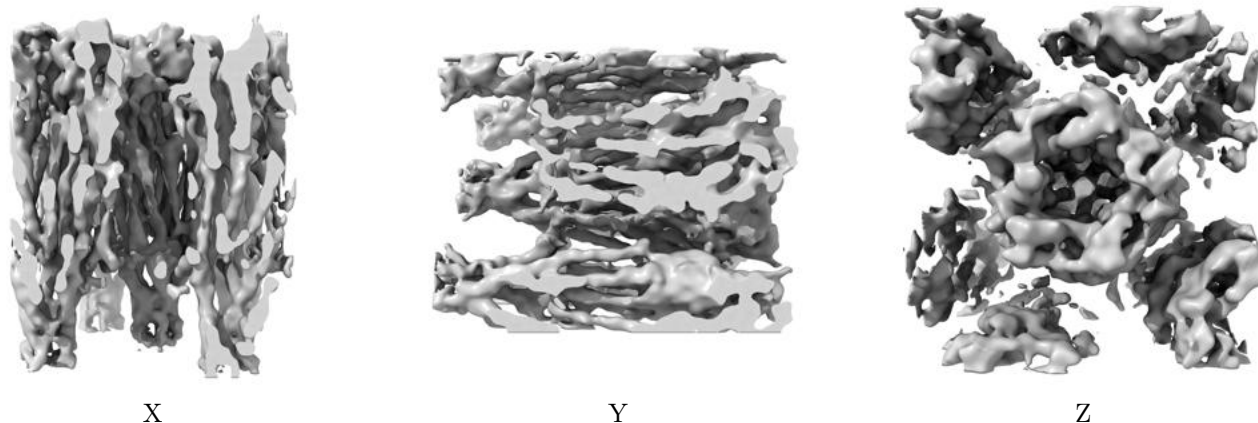


Z

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 1.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

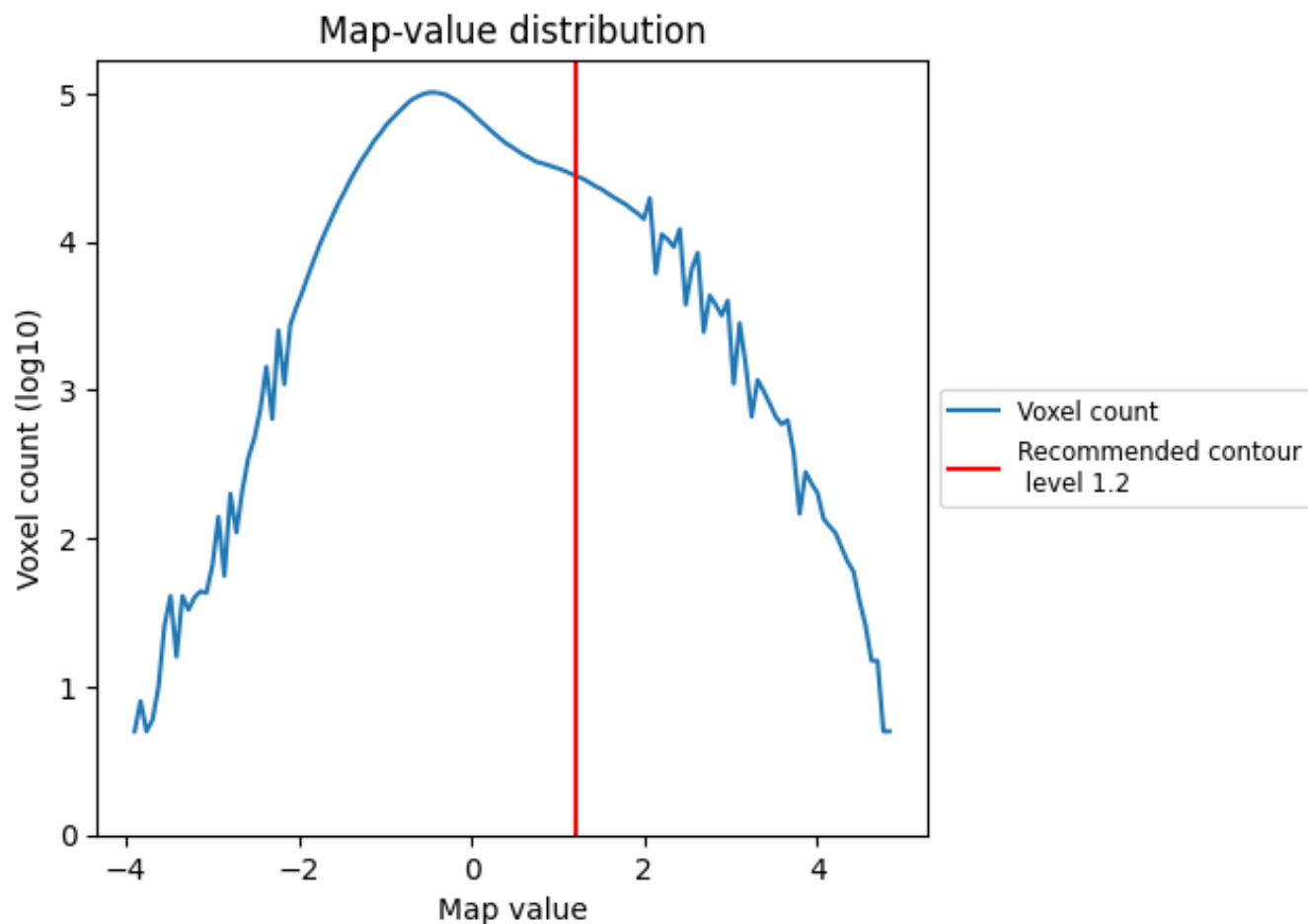
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

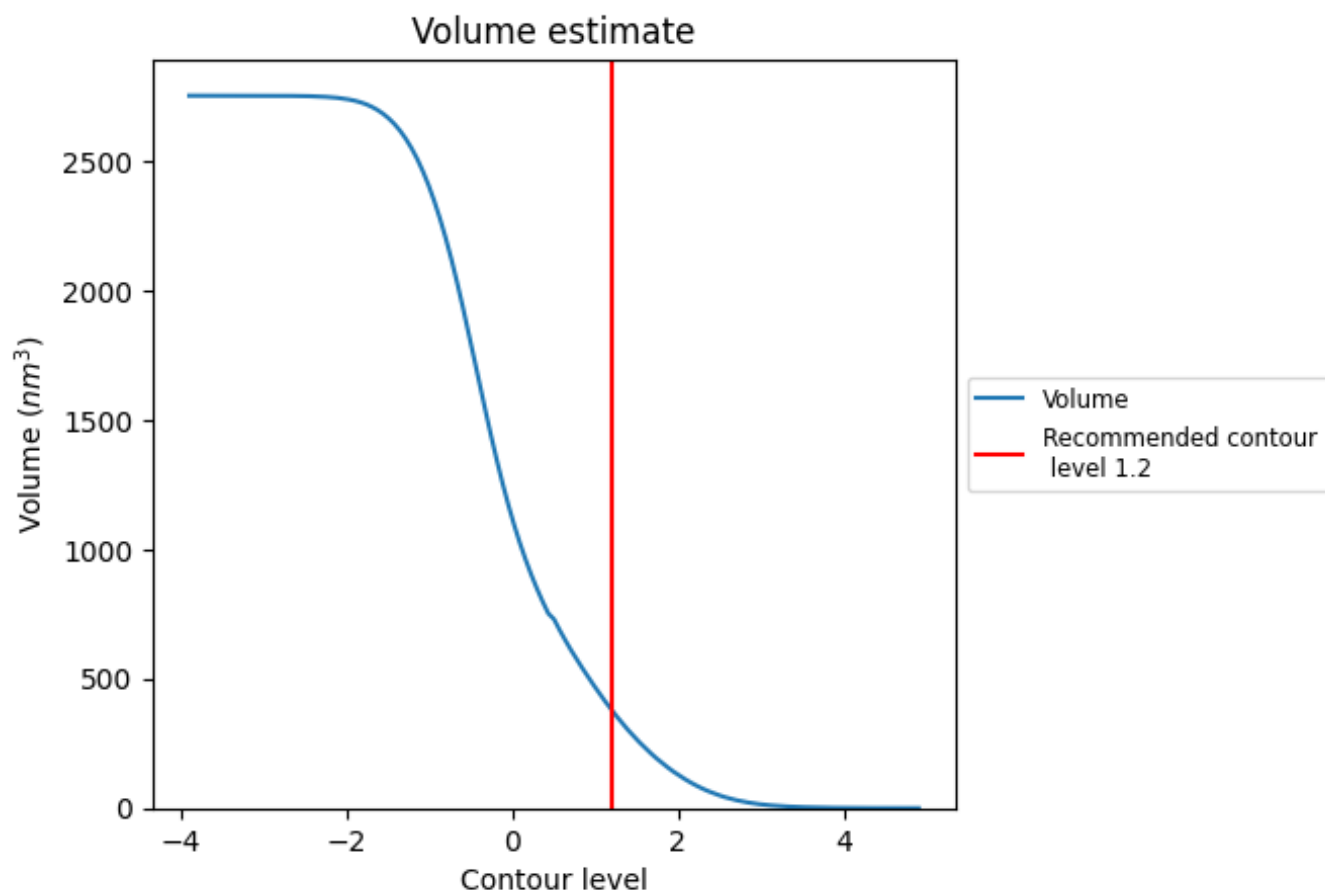
This section contains the results of statistical analysis of the map.

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 379 nm³; this corresponds to an approximate mass of 342 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

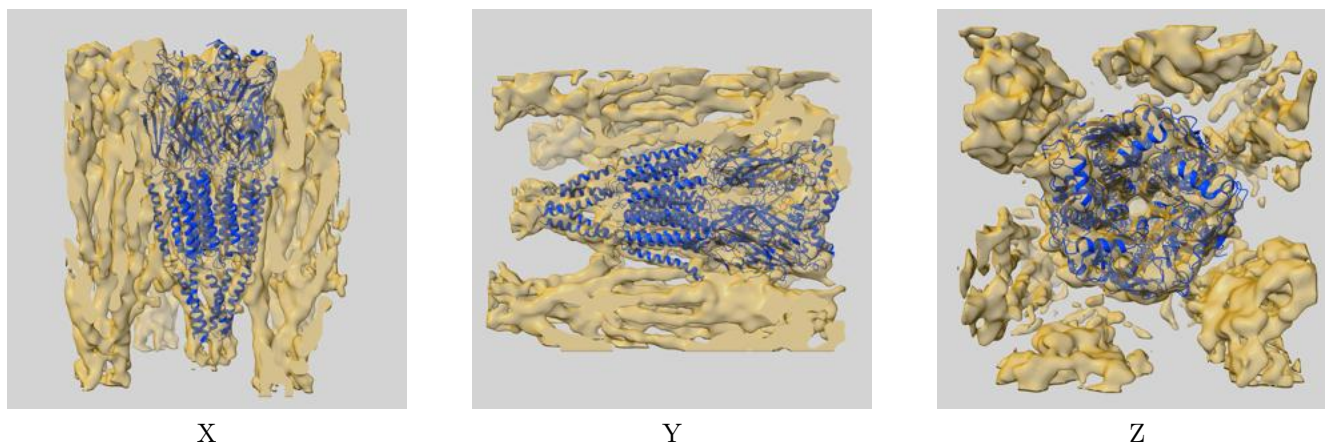
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

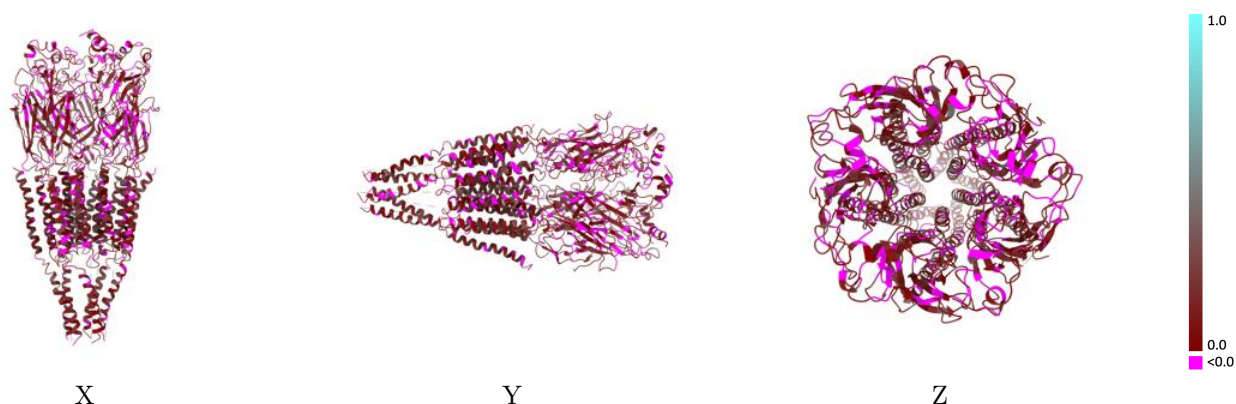
This section contains information regarding the fit between EMDB map EMD-2071 and PDB model 4AQ5. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



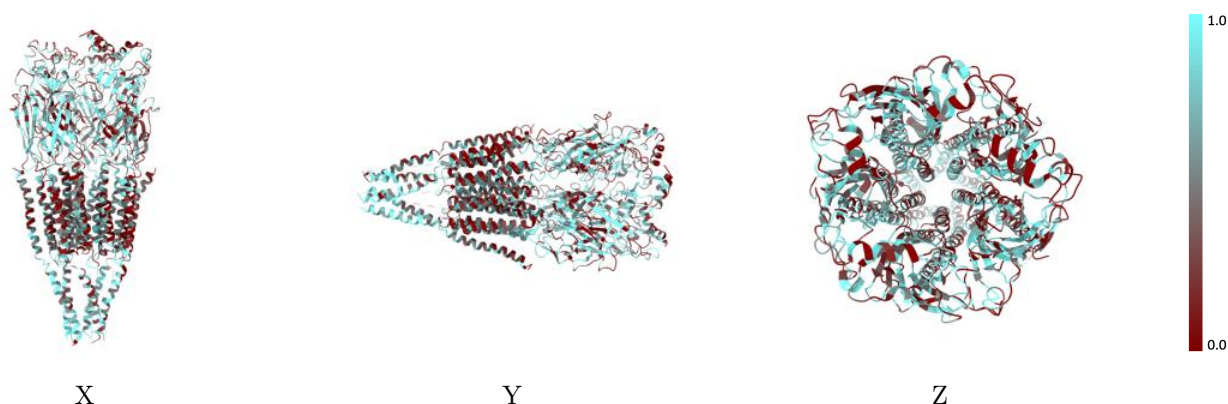
The images above show the 3D surface view of the map at the recommended contour level 1.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



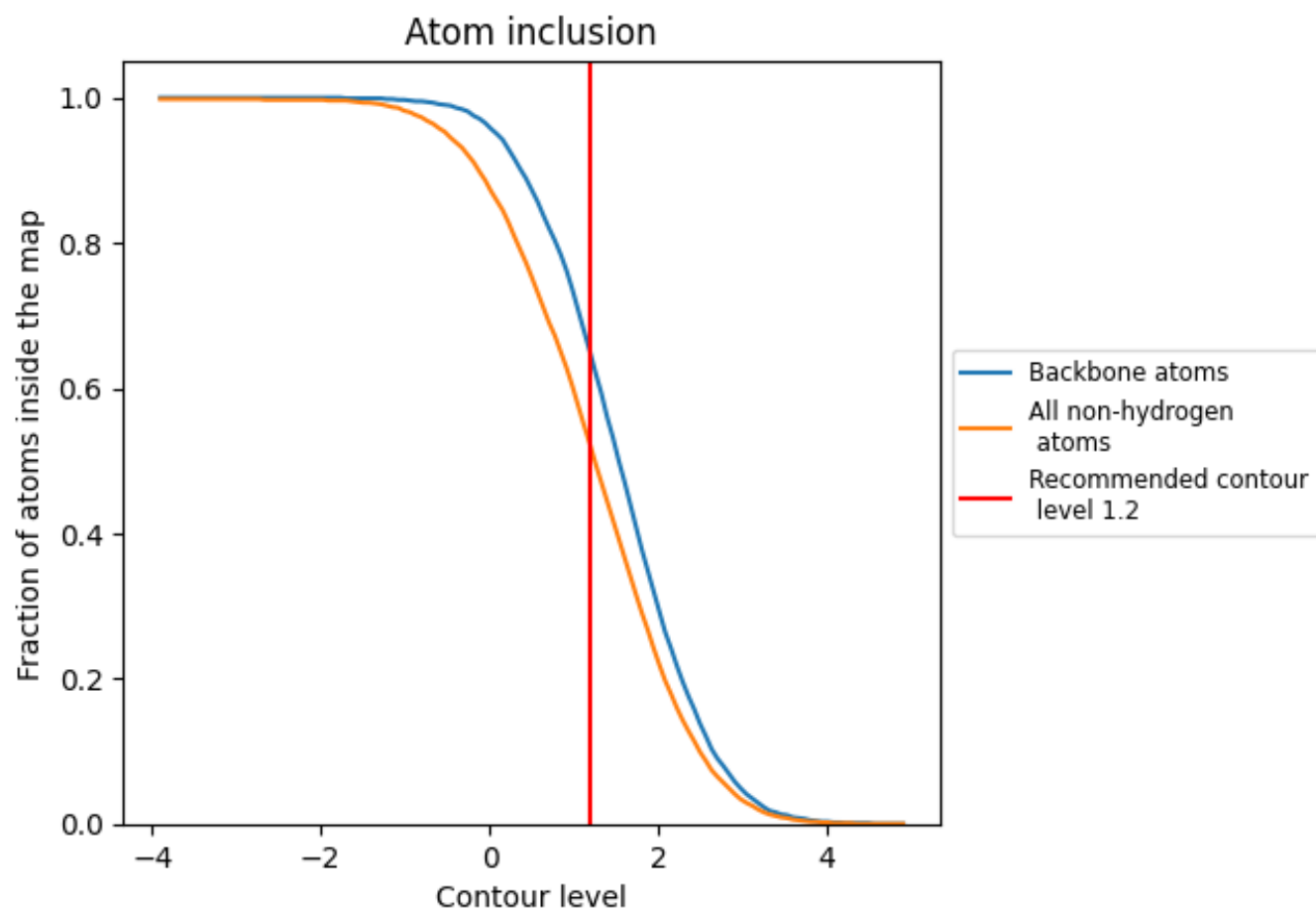
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 52% 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 (1.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5200	<div></div> 0.1050
A	<div></div> 0.5320	<div></div> 0.1070
B	<div></div> 0.4930	<div></div> 0.0950
C	<div></div> 0.4880	<div></div> 0.0980
D	<div></div> 0.5340	<div></div> 0.1100
E	<div></div> 0.5530	<div></div> 0.1160

