



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 02:21 AM UTC

PDB ID : 3J5R / pdb_00003j5r
EMDB ID : EMD-5777
Title : Reconstruction of TRPV1 ion channel in complex with capsaicin by single particle cryo-microscopy
Authors : Liao, M.; Cao, E.; Julius, D.; Cheng, Y.
Deposited on : 2013-10-28
Resolution : 4.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

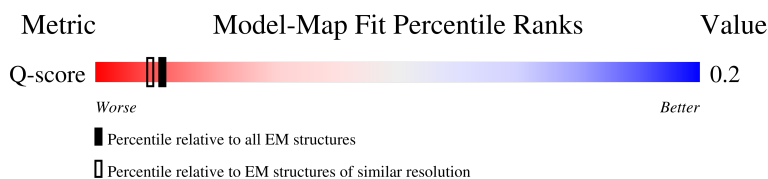
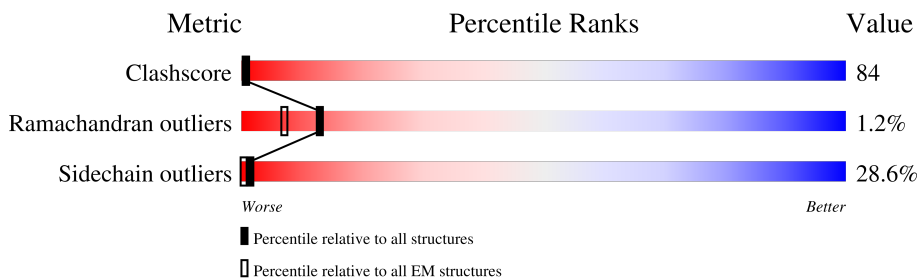
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	598	21% 40% 39% 19% ..
1	B	598	21% 40% 39% 19% ..
1	C	598	22% 40% 39% 19% ..
1	D	598	21% 40% 39% 19% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17564 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.

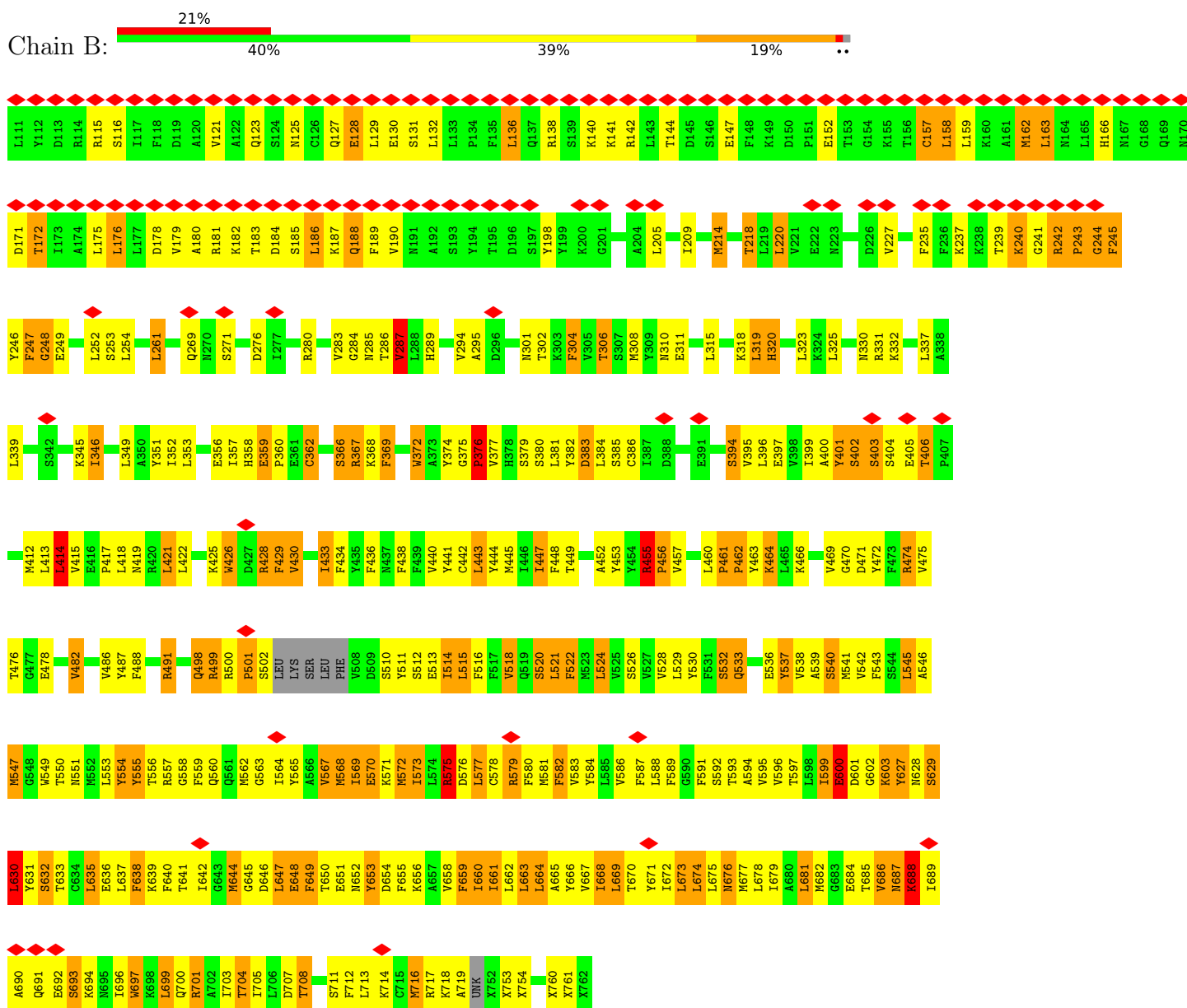
- Molecule 1 is a protein called Transient receptor potential cation channel subfamily V member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	592	Total	C	N	O	S	0	0
			4391	2847	726	798	20		
1	A	592	Total	C	N	O	S	0	0
			4391	2847	726	798	20		
1	C	592	Total	C	N	O	S	0	0
			4391	2847	726	798	20		
1	D	592	Total	C	N	O	S	0	0
			4391	2847	726	798	20		

3 Residue-property plots

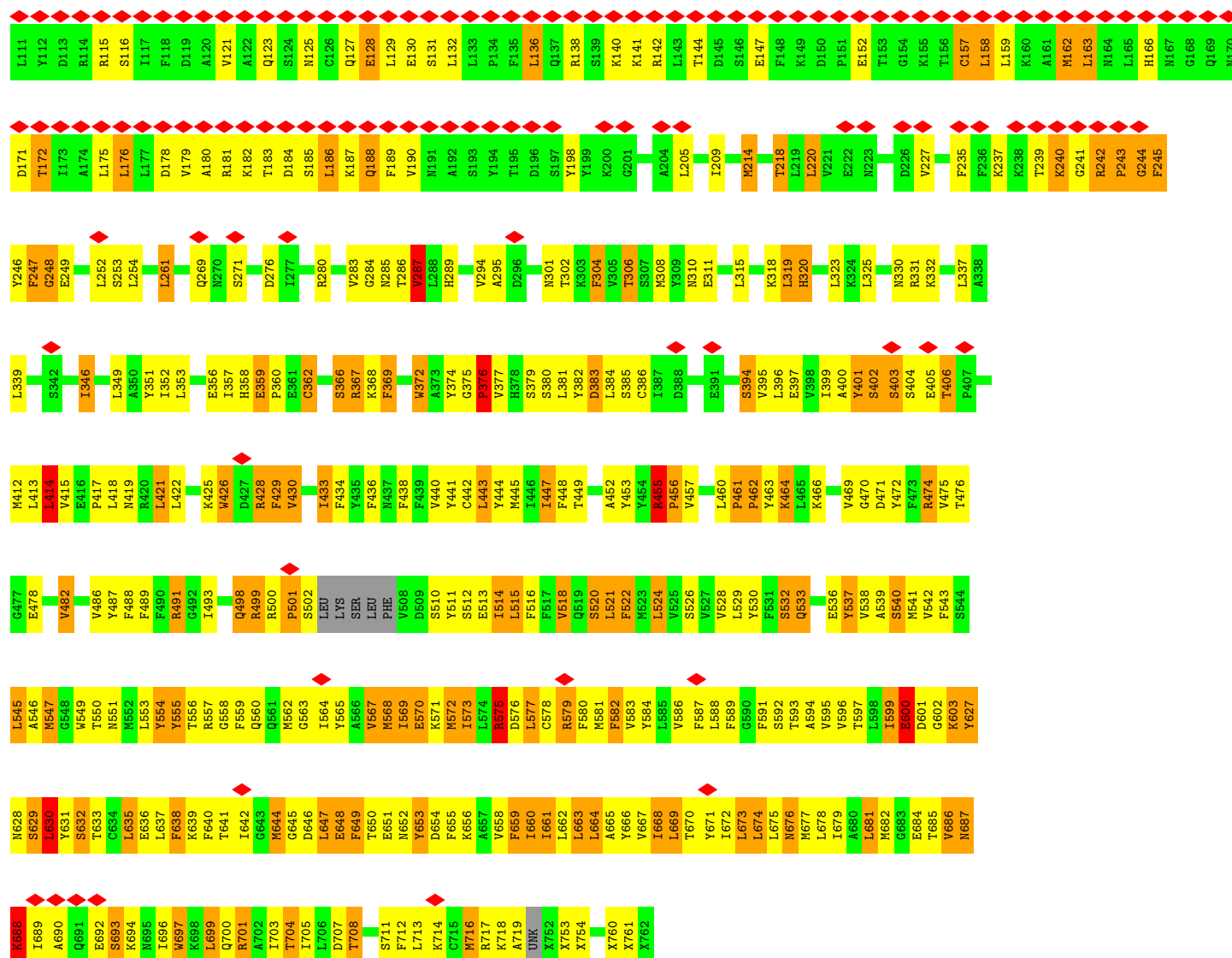
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transient receptor potential cation channel subfamily V member 1



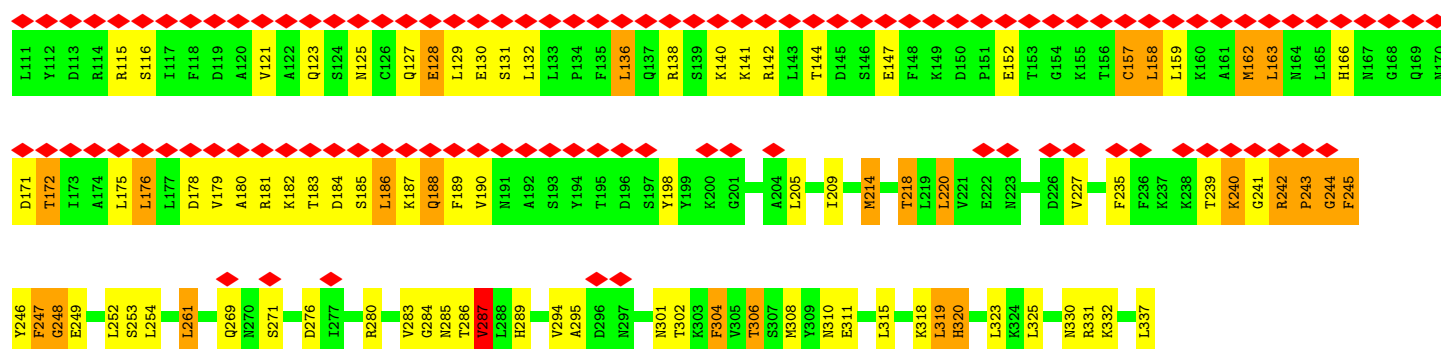
- Molecule 1: Transient receptor potential cation channel subfamily V member 1

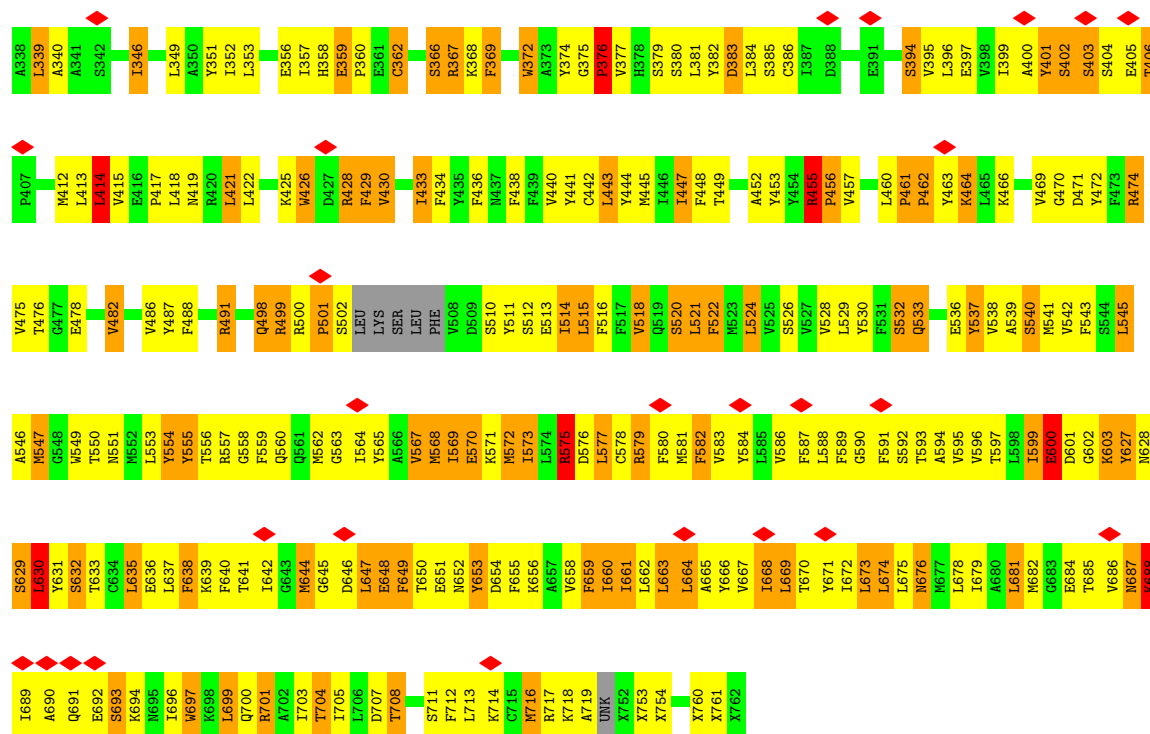
Chain A: 



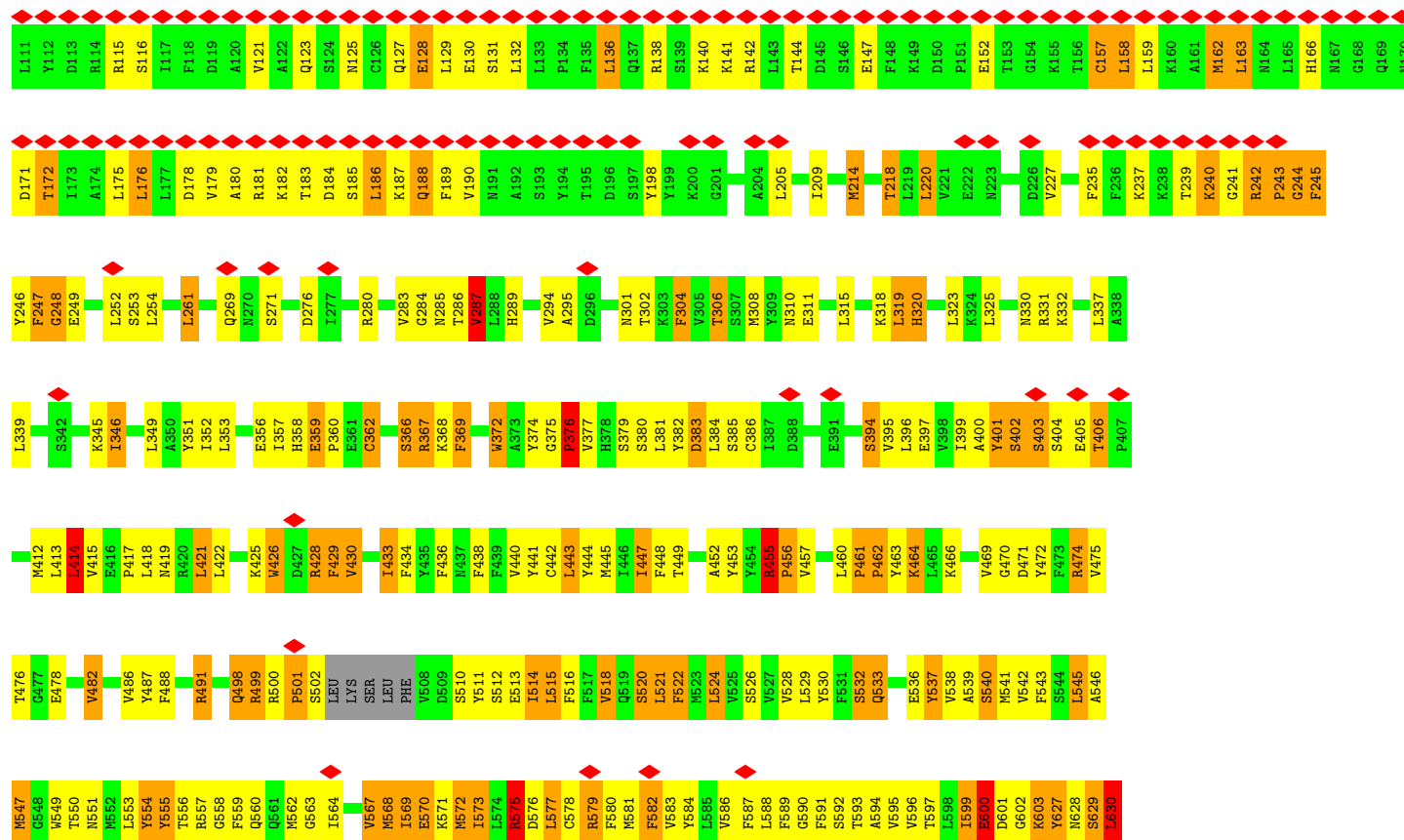
• Molecule 1: Transient receptor potential cation channel subfamily V member 1

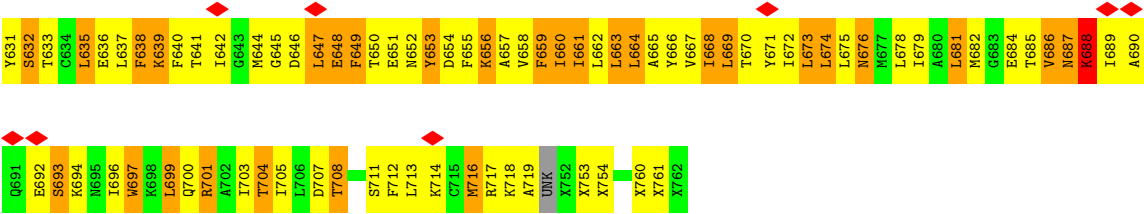
Chain C: 





• Molecule 1: Transient receptor potential potential cation channel subfamily V member 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	33238	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	21	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	22.647	Depositor
Minimum map value	-8.720	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	7	Depositor
Map size ($\text{\AA}$)	311.1936, 311.1936, 311.1936	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2156, 1.2156, 1.2156	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	0.64	12/4425 (0.3%)	1.11	35/6016 (0.6%)
1	B	0.64	12/4425 (0.3%)	1.11	35/6016 (0.6%)
1	C	0.64	12/4425 (0.3%)	1.11	35/6016 (0.6%)
1	D	0.64	12/4425 (0.3%)	1.11	35/6016 (0.6%)
All	All	0.64	48/17700 (0.3%)	1.11	140/24064 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	7
1	C	0	7
1	D	0	7
All	All	0	28

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	MET	CG-SD	8.17	2.01	1.80
1	D	162	MET	CG-SD	8.15	2.01	1.80
1	B	162	MET	CG-SD	8.15	2.01	1.80
1	C	162	MET	CG-SD	8.12	2.01	1.80
1	B	214	MET	CG-SD	6.69	1.97	1.80
1	A	214	MET	CG-SD	6.69	1.97	1.80
1	D	214	MET	CG-SD	6.68	1.97	1.80
1	C	214	MET	CG-SD	6.67	1.97	1.80
1	A	308	MET	SD-CE	6.47	1.95	1.79
1	C	308	MET	SD-CE	6.46	1.95	1.79
1	D	308	MET	SD-CE	6.45	1.95	1.79
1	B	308	MET	SD-CE	6.43	1.95	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	LEU	C-N	6.16	1.41	1.33
1	C	460	LEU	C-N	6.14	1.41	1.33
1	D	460	LEU	C-N	6.14	1.41	1.33
1	B	460	LEU	C-N	6.12	1.41	1.33
1	B	359	GLU	C-N	5.90	1.41	1.33
1	D	359	GLU	C-N	5.87	1.41	1.33
1	A	359	GLU	C-N	5.87	1.41	1.33
1	C	359	GLU	C-N	5.84	1.41	1.33
1	B	455	ARG	C-N	5.72	1.41	1.33
1	D	455	ARG	C-N	5.71	1.41	1.33
1	C	455	ARG	C-N	5.71	1.41	1.33
1	A	455	ARG	C-N	5.66	1.41	1.33
1	B	461	PRO	N-CD	5.46	1.55	1.47
1	C	461	PRO	N-CD	5.46	1.55	1.47
1	D	461	PRO	N-CD	5.45	1.55	1.47
1	A	456	PRO	N-CD	5.43	1.55	1.47
1	A	461	PRO	N-CD	5.42	1.55	1.47
1	D	456	PRO	N-CD	5.42	1.55	1.47
1	C	456	PRO	N-CD	5.41	1.55	1.47
1	B	456	PRO	N-CD	5.39	1.55	1.47
1	A	462	PRO	N-CD	5.19	1.55	1.47
1	C	462	PRO	N-CD	5.19	1.55	1.47
1	D	462	PRO	N-CD	5.18	1.55	1.47
1	A	406	THR	C-N	5.18	1.41	1.34
1	C	406	THR	C-N	5.17	1.41	1.34
1	D	406	THR	C-N	5.17	1.41	1.34
1	B	462	PRO	N-CD	5.13	1.55	1.47
1	B	406	THR	C-N	5.13	1.41	1.34
1	C	376	PRO	N-CD	5.11	1.54	1.47
1	D	376	PRO	N-CD	5.09	1.54	1.47
1	A	376	PRO	N-CD	5.09	1.54	1.47
1	A	360	PRO	N-CD	5.05	1.54	1.47
1	C	360	PRO	N-CD	5.05	1.54	1.47
1	B	376	PRO	N-CD	5.05	1.54	1.47
1	D	360	PRO	N-CD	5.04	1.54	1.47
1	B	360	PRO	N-CD	5.03	1.54	1.47

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	415	VAL	N-CA-C	13.76	124.61	110.72
1	A	415	VAL	N-CA-C	13.75	124.61	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	415	VAL	N-CA-C	13.74	124.60	110.72
1	D	415	VAL	N-CA-C	13.74	124.60	110.72
1	B	383	ASP	N-CA-C	9.97	121.74	111.07
1	A	383	ASP	N-CA-C	9.96	121.73	111.07
1	D	383	ASP	N-CA-C	9.96	121.72	111.07
1	C	383	ASP	N-CA-C	9.94	121.70	111.07
1	A	460	LEU	CA-C-N	-8.99	113.19	119.66
1	A	460	LEU	C-N-CA	-8.99	113.19	119.66
1	B	460	LEU	CA-C-N	-8.98	113.20	119.66
1	B	460	LEU	C-N-CA	-8.98	113.20	119.66
1	D	460	LEU	CA-C-N	-8.97	113.20	119.66
1	D	460	LEU	C-N-CA	-8.97	113.20	119.66
1	C	460	LEU	CA-C-N	-8.91	113.24	119.66
1	C	460	LEU	C-N-CA	-8.91	113.24	119.66
1	B	461	PRO	C-N-CD	8.29	138.84	120.60
1	C	461	PRO	C-N-CD	8.29	138.84	120.60
1	D	461	PRO	C-N-CD	8.28	138.82	120.60
1	A	461	PRO	C-N-CD	8.28	138.81	120.60
1	C	669	LEU	N-CA-C	8.24	120.34	111.36
1	D	669	LEU	N-CA-C	8.23	120.33	111.36
1	B	669	LEU	N-CA-C	8.22	120.32	111.36
1	A	669	LEU	N-CA-C	8.20	120.30	111.36
1	B	693	SER	N-CA-C	7.35	119.30	111.28
1	C	693	SER	N-CA-C	7.34	119.28	111.28
1	D	693	SER	N-CA-C	7.33	119.27	111.28
1	A	693	SER	N-CA-C	7.31	119.25	111.28
1	C	414	LEU	N-CA-C	7.11	125.95	110.80
1	D	414	LEU	N-CA-C	7.10	125.93	110.80
1	B	414	LEU	N-CA-C	7.10	125.92	110.80
1	A	414	LEU	N-CA-C	7.09	125.89	110.80
1	C	359	GLU	CA-C-N	-7.04	112.51	119.76
1	C	359	GLU	C-N-CA	-7.04	112.51	119.76
1	B	359	GLU	CA-C-N	-7.02	112.53	119.76
1	B	359	GLU	C-N-CA	-7.02	112.53	119.76
1	A	359	GLU	CA-C-N	-7.02	112.53	119.76
1	A	359	GLU	C-N-CA	-7.02	112.53	119.76
1	D	359	GLU	CA-C-N	-7.01	112.53	119.76
1	D	359	GLU	C-N-CA	-7.01	112.53	119.76
1	C	430	VAL	N-CA-C	6.78	117.54	110.62
1	D	430	VAL	N-CA-C	6.77	117.53	110.62
1	B	430	VAL	N-CA-C	6.77	117.52	110.62
1	A	430	VAL	N-CA-C	6.76	117.51	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	455	ARG	CA-C-N	-6.47	113.29	119.76
1	D	455	ARG	C-N-CA	-6.47	113.29	119.76
1	B	455	ARG	CA-C-N	-6.47	113.29	119.76
1	B	455	ARG	C-N-CA	-6.47	113.29	119.76
1	A	455	ARG	CA-C-N	-6.46	113.30	119.76
1	A	455	ARG	C-N-CA	-6.46	113.30	119.76
1	C	455	ARG	CA-C-N	-6.44	113.32	119.76
1	C	455	ARG	C-N-CA	-6.44	113.32	119.76
1	A	627	TYR	N-CA-C	-6.43	105.07	113.17
1	B	627	TYR	N-CA-C	-6.42	105.09	113.17
1	D	627	TYR	N-CA-C	-6.41	105.09	113.17
1	C	627	TYR	N-CA-C	-6.41	105.10	113.17
1	C	688	LYS	N-CA-C	6.13	123.86	110.80
1	B	688	LYS	N-CA-C	6.12	123.85	110.80
1	D	688	LYS	N-CA-C	6.12	123.83	110.80
1	A	688	LYS	N-CA-C	6.10	123.79	110.80
1	C	457	VAL	N-CA-C	5.94	116.72	110.72
1	D	457	VAL	N-CA-C	5.91	116.69	110.72
1	A	457	VAL	N-CA-C	5.90	116.68	110.72
1	B	457	VAL	N-CA-C	5.87	116.65	110.72
1	B	320	HIS	CA-C-N	5.84	125.39	119.19
1	B	320	HIS	C-N-CA	5.84	125.39	119.19
1	D	320	HIS	CA-C-N	5.81	125.35	119.19
1	D	320	HIS	C-N-CA	5.81	125.35	119.19
1	A	403	SER	N-CA-C	-5.81	105.03	111.71
1	C	320	HIS	CA-C-N	5.81	125.35	119.19
1	C	320	HIS	C-N-CA	5.81	125.35	119.19
1	D	403	SER	N-CA-C	-5.81	105.03	111.71
1	A	320	HIS	CA-C-N	5.80	125.34	119.19
1	A	320	HIS	C-N-CA	5.80	125.34	119.19
1	C	403	SER	N-CA-C	-5.78	105.06	111.71
1	B	403	SER	N-CA-C	-5.77	105.07	111.71
1	A	575	ARG	N-CA-C	5.62	117.49	111.36
1	D	575	ARG	N-CA-C	5.60	117.46	111.36
1	C	575	ARG	N-CA-C	5.58	117.45	111.36
1	B	575	ARG	N-CA-C	5.57	117.43	111.36
1	C	600	GLU	N-CA-C	5.50	116.96	111.07
1	B	638	PHE	N-CA-C	5.49	117.27	111.28
1	C	638	PHE	N-CA-C	5.49	117.27	111.28
1	D	638	PHE	N-CA-C	5.49	117.26	111.28
1	A	600	GLU	N-CA-C	5.49	116.94	111.07
1	B	600	GLU	N-CA-C	5.48	116.94	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	600	GLU	N-CA-C	5.48	116.93	111.07
1	A	638	PHE	N-CA-C	5.46	117.23	111.28
1	C	405	GLU	N-CA-C	-5.45	102.25	110.70
1	B	249	GLU	N-CA-C	5.44	122.39	110.80
1	B	405	GLU	N-CA-C	-5.44	102.27	110.70
1	D	249	GLU	N-CA-C	5.44	122.38	110.80
1	A	249	GLU	N-CA-C	5.44	122.38	110.80
1	C	249	GLU	N-CA-C	5.43	122.36	110.80
1	D	405	GLU	N-CA-C	-5.43	102.29	110.70
1	A	405	GLU	N-CA-C	-5.42	102.30	110.70
1	B	498	GLN	N-CA-C	5.37	117.21	111.36
1	D	714	LYS	N-CA-C	-5.34	104.28	111.54
1	C	714	LYS	N-CA-C	-5.33	104.29	111.54
1	A	498	GLN	N-CA-C	5.33	117.17	111.36
1	D	498	GLN	N-CA-C	5.32	117.16	111.36
1	A	714	LYS	N-CA-C	-5.32	104.31	111.54
1	B	714	LYS	N-CA-C	-5.30	104.33	111.54
1	C	498	GLN	N-CA-C	5.30	117.14	111.36
1	D	491	ARG	CA-C-N	5.25	125.77	119.94
1	D	491	ARG	C-N-CA	5.25	125.77	119.94
1	C	491	ARG	CA-C-N	5.25	125.77	119.94
1	C	491	ARG	C-N-CA	5.25	125.77	119.94
1	A	461	PRO	CA-C-O	-5.25	116.59	120.73
1	B	491	ARG	CA-C-N	5.24	125.76	119.94
1	B	491	ARG	C-N-CA	5.24	125.76	119.94
1	A	406	THR	CA-C-N	-5.23	113.24	119.05
1	A	406	THR	C-N-CA	-5.23	113.24	119.05
1	B	406	THR	CA-C-N	-5.22	113.26	119.05
1	B	406	THR	C-N-CA	-5.22	113.26	119.05
1	D	406	THR	CA-C-N	-5.19	113.29	119.05
1	D	406	THR	C-N-CA	-5.19	113.29	119.05
1	A	491	ARG	CA-C-N	5.18	125.69	119.94
1	A	491	ARG	C-N-CA	5.18	125.69	119.94
1	D	461	PRO	CA-C-O	-5.18	116.64	120.73
1	B	461	PRO	CA-C-O	-5.17	116.65	120.73
1	C	406	THR	CA-C-N	-5.16	113.32	119.05
1	C	406	THR	C-N-CA	-5.16	113.32	119.05
1	B	287	VAL	CB-CA-C	-5.14	105.20	112.14
1	D	287	VAL	CB-CA-C	-5.14	105.20	112.14
1	A	287	VAL	CB-CA-C	-5.13	105.21	112.14
1	C	461	PRO	CA-C-O	-5.13	116.68	120.73
1	C	287	VAL	CB-CA-C	-5.13	105.22	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	630	LEU	N-CA-C	-5.08	105.74	111.28
1	D	630	LEU	N-CA-C	-5.07	105.75	111.28
1	B	461	PRO	CA-C-N	-5.06	114.85	127.00
1	B	461	PRO	C-N-CA	-5.06	114.85	127.00
1	B	630	LEU	N-CA-C	-5.05	105.78	111.28
1	D	461	PRO	CA-C-N	-5.05	114.89	127.00
1	D	461	PRO	C-N-CA	-5.05	114.89	127.00
1	C	461	PRO	CA-C-N	-5.04	114.91	127.00
1	C	461	PRO	C-N-CA	-5.04	114.91	127.00
1	A	461	PRO	CA-C-N	-5.04	114.92	127.00
1	A	461	PRO	C-N-CA	-5.04	114.92	127.00
1	A	630	LEU	N-CA-C	-5.04	105.79	111.28

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	PRO	Peptide
1	A	244	GLY	Peptide
1	A	247	PHE	Peptide
1	A	248	GLY	Peptide
1	A	376	PRO	Peptide
1	A	686	VAL	Peptide,Mainchain
1	B	243	PRO	Peptide
1	B	244	GLY	Peptide
1	B	247	PHE	Peptide
1	B	248	GLY	Peptide
1	B	376	PRO	Peptide
1	B	686	VAL	Peptide,Mainchain
1	C	243	PRO	Peptide
1	C	244	GLY	Peptide
1	C	247	PHE	Peptide
1	C	248	GLY	Peptide
1	C	376	PRO	Peptide
1	C	686	VAL	Peptide,Mainchain
1	D	243	PRO	Peptide
1	D	244	GLY	Peptide
1	D	247	PHE	Peptide
1	D	248	GLY	Peptide
1	D	376	PRO	Peptide
1	D	686	VAL	Peptide,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	4391	0	4117	765	0
1	B	4391	0	4117	770	0
1	C	4391	0	4117	759	0
1	D	4391	0	4117	771	0
All	All	17564	0	16468	2874	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 84.

All (2874) 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:B:376:PRO:HG3	1:D:245:PHE:CD2	1.23	1.70
1:A:655:PHE:CE2	1:C:536:GLU:HA	1.29	1.66
1:C:655:PHE:CE1	1:D:539:ALA:HB2	1.15	1.64
1:B:539:ALA:HB2	1:D:655:PHE:CE1	1.18	1.62
1:B:376:PRO:CG	1:D:245:PHE:CD2	1.76	1.62
1:B:655:PHE:CD1	1:A:539:ALA:HB2	1.32	1.62
1:B:539:ALA:HB2	1:D:655:PHE:CD1	1.27	1.61
1:A:655:PHE:CE2	1:C:536:GLU:CA	1.84	1.61
1:B:536:GLU:HA	1:D:655:PHE:CE2	1.15	1.61
1:B:655:PHE:CE2	1:A:536:GLU:HA	1.35	1.59
1:A:655:PHE:CZ	1:C:536:GLU:CB	1.80	1.57
1:B:536:GLU:CA	1:D:655:PHE:CZ	1.87	1.57
1:B:539:ALA:CB	1:D:655:PHE:CE1	1.81	1.56
1:B:655:PHE:CE1	1:A:539:ALA:HB2	1.06	1.55
1:C:655:PHE:HE1	1:D:539:ALA:CB	1.18	1.53
1:B:655:PHE:HE1	1:A:539:ALA:CB	1.05	1.52
1:A:396:LEU:CD1	1:A:418:LEU:HD22	1.40	1.51
1:C:396:LEU:CD1	1:C:418:LEU:HD22	1.40	1.48
1:B:655:PHE:CE1	1:A:539:ALA:CB	1.77	1.48
1:D:396:LEU:CD1	1:D:418:LEU:HD22	1.40	1.48
1:A:655:PHE:CE2	1:C:536:GLU:CB	1.96	1.47
1:B:396:LEU:CD1	1:B:418:LEU:HD22	1.40	1.46
1:B:376:PRO:HG2	1:D:245:PHE:CG	1.48	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:539:ALA:CB	1:D:655:PHE:HE1	1.16	1.45
1:A:655:PHE:CZ	1:C:536:GLU:CA	1.96	1.42
1:B:536:GLU:CA	1:D:655:PHE:CE2	1.91	1.42
1:B:655:PHE:CZ	1:A:536:GLU:CA	2.00	1.42
1:B:655:PHE:CZ	1:A:536:GLU:CB	2.04	1.41
1:B:536:GLU:CB	1:D:655:PHE:CZ	2.04	1.40
1:D:426:TRP:HA	1:D:430:VAL:CG1	1.51	1.39
1:B:536:GLU:C	1:D:655:PHE:CZ	2.01	1.37
1:B:376:PRO:HG2	1:D:245:PHE:CB	1.53	1.37
1:A:426:TRP:HA	1:A:430:VAL:CG1	1.51	1.37
1:C:426:TRP:HA	1:C:430:VAL:CG1	1.51	1.37
1:B:426:TRP:HA	1:B:430:VAL:CG1	1.52	1.36
1:B:655:PHE:CE2	1:A:536:GLU:CA	2.07	1.36
1:B:376:PRO:CG	1:D:245:PHE:CG	2.02	1.35
1:B:536:GLU:C	1:D:655:PHE:HZ	1.31	1.35
1:A:337:LEU:HD21	1:A:395:VAL:CG2	1.57	1.34
1:B:337:LEU:HD21	1:B:395:VAL:CG2	1.57	1.33
1:C:655:PHE:CZ	1:D:536:GLU:CB	2.10	1.33
1:C:337:LEU:HD21	1:C:395:VAL:CG2	1.57	1.33
1:D:337:LEU:HD21	1:D:395:VAL:CG2	1.57	1.31
1:D:516:PHE:HE2	1:D:554:TYR:CD2	1.48	1.31
1:C:396:LEU:CD1	1:C:418:LEU:CD2	2.08	1.31
1:B:516:PHE:HE2	1:B:554:TYR:CD2	1.48	1.31
1:C:516:PHE:HE2	1:C:554:TYR:CD2	1.48	1.31
1:D:396:LEU:CD1	1:D:418:LEU:CD2	2.07	1.31
1:A:396:LEU:CD1	1:A:418:LEU:CD2	2.07	1.30
1:A:516:PHE:HE2	1:A:554:TYR:CD2	1.48	1.30
1:B:396:LEU:CD1	1:B:418:LEU:CD2	2.07	1.30
1:C:655:PHE:HZ	1:D:536:GLU:CB	1.39	1.28
1:A:655:PHE:CZ	1:C:536:GLU:C	2.13	1.27
1:C:235:PHE:CZ	1:D:374:TYR:CB	2.17	1.26
1:D:708:THR:O	1:D:712:PHE:CB	1.85	1.24
1:A:708:THR:O	1:A:712:PHE:CB	1.85	1.24
1:B:708:THR:O	1:B:712:PHE:CB	1.86	1.23
1:C:708:THR:O	1:C:712:PHE:CB	1.85	1.23
1:C:655:PHE:CE1	1:D:539:ALA:CB	2.02	1.21
1:C:693:SER:O	1:C:696:ILE:HG22	1.02	1.20
1:C:678:LEU:O	1:C:681:LEU:CD1	1.90	1.20
1:B:516:PHE:CE2	1:B:554:TYR:HD2	1.60	1.20
1:D:678:LEU:O	1:D:681:LEU:CD1	1.90	1.20
1:A:516:PHE:CE2	1:A:554:TYR:HD2	1.60	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:536:GLU:O	1:D:655:PHE:CZ	1.90	1.19
1:D:516:PHE:CE2	1:D:554:TYR:HD2	1.60	1.19
1:D:693:SER:O	1:D:696:ILE:HG22	1.02	1.19
1:C:516:PHE:CE2	1:C:554:TYR:HD2	1.60	1.18
1:B:678:LEU:O	1:B:681:LEU:CD1	1.90	1.18
1:C:655:PHE:CD1	1:D:539:ALA:HB2	1.77	1.18
1:B:560:GLN:NE2	1:B:697:TRP:CZ3	2.12	1.18
1:C:560:GLN:NE2	1:C:697:TRP:CZ3	2.12	1.18
1:A:678:LEU:O	1:A:681:LEU:CD1	1.90	1.18
1:D:664:LEU:O	1:D:668:ILE:HG23	1.44	1.17
1:B:693:SER:O	1:B:696:ILE:CG2	1.93	1.17
1:B:693:SER:O	1:B:696:ILE:HG22	1.02	1.17
1:A:693:SER:O	1:A:696:ILE:CG2	1.93	1.17
1:C:664:LEU:O	1:C:668:ILE:HG23	1.44	1.17
1:A:560:GLN:NE2	1:A:697:TRP:CZ3	2.12	1.17
1:D:560:GLN:NE2	1:D:697:TRP:CZ3	2.12	1.17
1:B:670:THR:O	1:B:674:LEU:HB2	1.44	1.16
1:A:664:LEU:O	1:A:668:ILE:HG23	1.44	1.16
1:B:664:LEU:O	1:B:668:ILE:HG23	1.44	1.16
1:B:655:PHE:HZ	1:A:536:GLU:C	1.54	1.16
1:B:596:VAL:HG22	1:B:633:THR:HG21	1.21	1.16
1:B:655:PHE:HE1	1:A:539:ALA:HB3	0.99	1.16
1:B:516:PHE:CE2	1:B:554:TYR:CD2	2.33	1.15
1:A:693:SER:O	1:A:696:ILE:HG22	1.02	1.15
1:C:461:PRO:O	1:C:533:GLN:OE1	1.65	1.15
1:A:516:PHE:CE2	1:A:554:TYR:CD2	2.33	1.15
1:A:461:PRO:O	1:A:533:GLN:OE1	1.65	1.15
1:A:647:LEU:HD12	1:A:648:GLU:HG3	1.22	1.15
1:D:693:SER:O	1:D:696:ILE:CG2	1.93	1.15
1:B:655:PHE:CZ	1:A:536:GLU:C	2.22	1.14
1:D:461:PRO:O	1:D:533:GLN:OE1	1.65	1.14
1:C:672:ILE:O	1:C:676:ASN:ND2	1.79	1.14
1:C:693:SER:O	1:C:696:ILE:CG2	1.93	1.14
1:B:376:PRO:HG2	1:D:245:PHE:HB3	1.18	1.14
1:A:670:THR:O	1:A:674:LEU:HB2	1.44	1.14
1:C:516:PHE:CE2	1:C:554:TYR:CD2	2.33	1.14
1:B:376:PRO:HG3	1:D:245:PHE:CE2	1.82	1.14
1:D:670:THR:O	1:D:674:LEU:HB2	1.44	1.14
1:B:539:ALA:HB3	1:D:655:PHE:HE1	1.02	1.13
1:C:685:THR:O	1:C:688:LYS:N	1.81	1.13
1:D:516:PHE:CE2	1:D:554:TYR:CD2	2.33	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:645:GLY:O	1:A:644:MET:HG3	1.48	1.13
1:B:359:GLU:H	1:B:362:CYS:CB	1.62	1.13
1:A:359:GLU:H	1:A:362:CYS:CB	1.62	1.13
1:B:678:LEU:O	1:B:681:LEU:HD11	1.49	1.13
1:C:596:VAL:HG22	1:C:633:THR:HG21	1.21	1.13
1:B:430:VAL:O	1:B:433:ILE:HG22	1.48	1.12
1:B:461:PRO:O	1:B:533:GLN:OE1	1.65	1.13
1:A:596:VAL:CG2	1:A:633:THR:HG21	1.80	1.12
1:A:678:LEU:O	1:A:681:LEU:HD11	1.49	1.12
1:C:243:PRO:HB2	1:C:244:GLY:HA3	1.30	1.12
1:D:596:VAL:HG22	1:D:633:THR:HG21	1.21	1.12
1:B:596:VAL:CG2	1:B:633:THR:HG21	1.80	1.12
1:C:670:THR:O	1:C:674:LEU:HB2	1.44	1.12
1:A:243:PRO:HB2	1:A:244:GLY:HA3	1.30	1.11
1:A:645:GLY:O	1:C:644:MET:HG3	1.49	1.11
1:B:645:GLY:O	1:A:644:MET:CG	1.98	1.11
1:D:685:THR:O	1:D:688:LYS:N	1.81	1.11
1:B:681:LEU:HD21	1:B:682:MET:HE2	1.31	1.11
1:B:685:THR:O	1:B:688:LYS:N	1.81	1.11
1:A:685:THR:O	1:A:688:LYS:N	1.81	1.11
1:C:359:GLU:H	1:C:362:CYS:CB	1.62	1.11
1:C:471:ASP:O	1:C:475:VAL:HG23	1.49	1.11
1:C:596:VAL:CG2	1:C:633:THR:HG21	1.80	1.11
1:D:681:LEU:HD21	1:D:682:MET:HE2	1.31	1.11
1:D:359:GLU:H	1:D:362:CYS:CB	1.62	1.11
1:D:596:VAL:CG2	1:D:633:THR:HG21	1.80	1.11
1:D:414:LEU:O	1:D:419:ASN:CB	1.99	1.10
1:D:426:TRP:HA	1:D:430:VAL:HG12	1.28	1.10
1:D:430:VAL:O	1:D:433:ILE:HG22	1.48	1.10
1:A:430:VAL:O	1:A:433:ILE:HG22	1.48	1.10
1:C:414:LEU:O	1:C:419:ASN:CB	1.99	1.10
1:C:430:VAL:O	1:C:433:ILE:HG22	1.48	1.10
1:C:560:GLN:OE1	1:C:564:ILE:HD11	1.52	1.10
1:C:655:PHE:CZ	1:D:536:GLU:CA	2.34	1.10
1:A:471:ASP:O	1:A:475:VAL:HG23	1.49	1.10
1:A:414:LEU:O	1:A:419:ASN:CB	1.99	1.10
1:C:647:LEU:HD12	1:C:648:GLU:HG3	1.22	1.10
1:B:243:PRO:HB2	1:B:244:GLY:HA3	1.29	1.10
1:B:414:LEU:O	1:B:419:ASN:CB	1.99	1.10
1:B:647:LEU:HD12	1:B:648:GLU:HG3	1.22	1.10
1:B:376:PRO:HG2	1:D:245:PHE:CD2	1.60	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:GLN:OE1	1:A:564:ILE:HD11	1.52	1.09
1:B:426:TRP:HA	1:B:430:VAL:HG12	1.28	1.09
1:A:596:VAL:HG22	1:A:633:THR:HG21	1.21	1.09
1:A:426:TRP:HA	1:A:430:VAL:HG12	1.28	1.09
1:D:471:ASP:O	1:D:475:VAL:HG23	1.49	1.09
1:D:596:VAL:HG13	1:D:628:ASN:O	1.52	1.09
1:D:647:LEU:HD12	1:D:648:GLU:HG3	1.22	1.09
1:B:681:LEU:HD13	1:B:682:MET:H	1.16	1.09
1:C:596:VAL:HG13	1:C:628:ASN:O	1.51	1.09
1:B:471:ASP:O	1:B:475:VAL:HG23	1.49	1.08
1:B:560:GLN:OE1	1:B:564:ILE:HD11	1.52	1.08
1:C:678:LEU:O	1:C:681:LEU:HD11	1.49	1.08
1:D:428:ARG:HD2	1:D:429:PHE:CG	1.89	1.08
1:B:596:VAL:HG13	1:B:628:ASN:O	1.51	1.08
1:D:560:GLN:OE1	1:D:564:ILE:HD11	1.52	1.08
1:D:678:LEU:O	1:D:681:LEU:HD11	1.49	1.08
1:B:428:ARG:HD2	1:B:429:PHE:CG	1.89	1.08
1:B:536:GLU:HA	1:D:655:PHE:CZ	1.71	1.08
1:D:243:PRO:HB2	1:D:244:GLY:HA3	1.30	1.08
1:A:428:ARG:HD2	1:A:429:PHE:CG	1.89	1.08
1:A:596:VAL:HG13	1:A:628:ASN:O	1.51	1.08
1:A:396:LEU:HD12	1:A:418:LEU:CD2	1.78	1.07
1:C:681:LEU:HD21	1:C:682:MET:HE2	1.31	1.07
1:A:681:LEU:HD21	1:A:682:MET:HE2	1.31	1.07
1:D:681:LEU:HD13	1:D:682:MET:H	1.16	1.07
1:D:708:THR:O	1:D:712:PHE:N	1.88	1.07
1:C:380:SER:O	1:C:754:UNK:CA	2.03	1.06
1:C:693:SER:C	1:C:696:ILE:HG22	1.80	1.06
1:A:359:GLU:O	1:A:362:CYS:HB3	1.55	1.06
1:D:693:SER:C	1:D:696:ILE:HG22	1.80	1.06
1:A:700:GLN:O	1:A:704:THR:HG23	1.54	1.06
1:C:428:ARG:HD2	1:C:429:PHE:CG	1.89	1.06
1:D:396:LEU:HD12	1:D:418:LEU:CD2	1.78	1.06
1:B:359:GLU:O	1:B:362:CYS:HB3	1.55	1.06
1:C:386:CYS:CB	1:C:395:VAL:HB	1.86	1.06
1:B:700:GLN:O	1:B:704:THR:HG23	1.54	1.06
1:D:359:GLU:O	1:D:362:CYS:HB3	1.55	1.06
1:D:533:GLN:O	1:D:533:GLN:NE2	1.89	1.06
1:A:380:SER:O	1:A:754:UNK:CA	2.03	1.05
1:A:386:CYS:CB	1:A:395:VAL:HB	1.86	1.05
1:C:426:TRP:HA	1:C:430:VAL:HG12	1.28	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:655:PHE:CE2	1:D:536:GLU:HA	1.91	1.05
1:B:533:GLN:NE2	1:B:533:GLN:O	1.89	1.05
1:A:533:GLN:O	1:A:533:GLN:NE2	1.89	1.05
1:A:645:GLY:O	1:C:644:MET:CG	2.03	1.05
1:A:708:THR:O	1:A:712:PHE:N	1.88	1.05
1:D:380:SER:O	1:D:754:UNK:CA	2.03	1.05
1:D:700:GLN:O	1:D:704:THR:HG23	1.54	1.05
1:B:337:LEU:HD21	1:B:395:VAL:HG22	1.33	1.05
1:B:693:SER:C	1:B:696:ILE:HG22	1.80	1.05
1:D:337:LEU:HD21	1:D:395:VAL:HG22	1.33	1.05
1:A:693:SER:C	1:A:696:ILE:HG22	1.80	1.05
1:C:708:THR:O	1:C:712:PHE:N	1.88	1.05
1:B:380:SER:O	1:B:754:UNK:CA	2.03	1.05
1:A:681:LEU:HD13	1:A:682:MET:H	1.16	1.05
1:C:533:GLN:NE2	1:C:533:GLN:O	1.89	1.05
1:C:700:GLN:O	1:C:704:THR:HG23	1.54	1.05
1:A:337:LEU:HD21	1:A:395:VAL:HG22	1.33	1.04
1:C:235:PHE:HZ	1:D:374:TYR:CB	1.60	1.04
1:B:515:LEU:CD2	1:B:551:ASN:OD1	2.05	1.04
1:A:396:LEU:O	1:A:400:ALA:N	1.91	1.04
1:A:515:LEU:CD2	1:A:551:ASN:OD1	2.05	1.04
1:C:359:GLU:O	1:C:362:CYS:HB3	1.55	1.04
1:C:515:LEU:CD2	1:C:551:ASN:OD1	2.05	1.04
1:D:386:CYS:CB	1:D:395:VAL:HB	1.86	1.04
1:C:396:LEU:O	1:C:400:ALA:N	1.91	1.04
1:D:515:LEU:CD2	1:D:551:ASN:OD1	2.05	1.04
1:B:708:THR:O	1:B:712:PHE:N	1.88	1.04
1:B:386:CYS:CB	1:B:395:VAL:HB	1.86	1.03
1:B:655:PHE:CZ	1:A:536:GLU:O	2.10	1.03
1:C:337:LEU:HD21	1:C:395:VAL:HG22	1.33	1.03
1:A:655:PHE:HZ	1:C:536:GLU:C	1.59	1.03
1:D:560:GLN:NE2	1:D:697:TRP:CH2	2.26	1.03
1:B:396:LEU:O	1:B:400:ALA:N	1.91	1.02
1:B:560:GLN:NE2	1:B:697:TRP:CH2	2.26	1.02
1:D:707:ASP:O	1:D:711:SER:HB2	1.59	1.02
1:B:396:LEU:HD12	1:B:418:LEU:CD2	1.78	1.02
1:B:671:TYR:O	1:B:675:LEU:HD23	1.59	1.02
1:C:681:LEU:HD13	1:C:682:MET:H	1.16	1.02
1:D:359:GLU:H	1:D:362:CYS:HB3	1.24	1.02
1:D:671:TYR:O	1:D:675:LEU:HD23	1.59	1.02
1:C:671:TYR:O	1:C:675:LEU:HD23	1.59	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:707:ASP:O	1:C:711:SER:HB2	1.60	1.02
1:C:396:LEU:HD12	1:C:418:LEU:CD2	1.79	1.02
1:C:560:GLN:NE2	1:C:697:TRP:CH2	2.26	1.02
1:D:396:LEU:O	1:D:400:ALA:N	1.91	1.02
1:B:536:GLU:CB	1:D:655:PHE:CE2	2.32	1.02
1:B:353:LEU:HA	1:B:367:ARG:HD3	1.41	1.01
1:A:560:GLN:NE2	1:A:697:TRP:CH2	2.26	1.01
1:B:655:PHE:CE2	1:A:536:GLU:CB	2.35	1.01
1:A:353:LEU:HA	1:A:367:ARG:HD3	1.41	1.01
1:A:681:LEU:HD21	1:A:682:MET:CE	1.89	1.01
1:B:681:LEU:HD21	1:B:682:MET:CE	1.89	1.01
1:A:655:PHE:CZ	1:C:536:GLU:O	2.13	1.01
1:A:658:VAL:HG13	1:C:543:PHE:CZ	1.95	1.01
1:C:681:LEU:HD21	1:C:682:MET:CE	1.89	1.01
1:A:235:PHE:CZ	1:C:374:TYR:CB	2.43	1.01
1:B:239:THR:OG1	1:B:243:PRO:HB3	1.61	1.01
1:D:239:THR:OG1	1:D:243:PRO:HB3	1.61	1.01
1:B:539:ALA:HB2	1:D:655:PHE:HD1	1.27	1.00
1:B:599:ILE:HD11	1:B:628:ASN:CA	1.91	1.00
1:B:644:MET:HG3	1:D:645:GLY:O	1.61	1.00
1:A:676:ASN:HB2	1:C:572:MET:CE	1.91	1.00
1:D:681:LEU:HD21	1:D:682:MET:CE	1.89	1.00
1:B:707:ASP:O	1:B:711:SER:HB2	1.60	1.00
1:A:671:TYR:O	1:A:675:LEU:HD23	1.59	1.00
1:C:239:THR:OG1	1:C:243:PRO:HB3	1.60	1.00
1:C:359:GLU:H	1:C:362:CYS:HB3	1.24	1.00
1:A:346:ILE:HG12	1:A:412:MET:CB	1.92	0.99
1:A:707:ASP:O	1:A:711:SER:HB2	1.59	0.99
1:C:353:LEU:HA	1:C:367:ARG:HD3	1.41	0.99
1:B:426:TRP:HA	1:B:430:VAL:HG13	1.43	0.99
1:D:346:ILE:HG12	1:D:412:MET:CB	1.93	0.99
1:B:235:PHE:CZ	1:A:374:TYR:CB	2.44	0.99
1:B:359:GLU:H	1:B:362:CYS:HB3	1.24	0.99
1:A:599:ILE:HD11	1:A:628:ASN:CA	1.91	0.99
1:C:599:ILE:HD11	1:C:628:ASN:CA	1.91	0.99
1:D:337:LEU:HD21	1:D:395:VAL:HG21	1.44	0.99
1:D:353:LEU:HA	1:D:367:ARG:HD3	1.41	0.99
1:D:599:ILE:HD11	1:D:628:ASN:CA	1.91	0.99
1:A:239:THR:OG1	1:A:243:PRO:HB3	1.61	0.99
1:D:357:ILE:N	1:D:366:SER:OG	1.95	0.99
1:A:357:ILE:N	1:A:366:SER:OG	1.95	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:357:ILE:N	1:C:366:SER:OG	1.95	0.99
1:C:426:TRP:HA	1:C:430:VAL:HG13	1.43	0.99
1:A:426:TRP:HA	1:A:430:VAL:HG13	1.43	0.99
1:C:599:ILE:HD11	1:C:628:ASN:N	1.78	0.98
1:B:346:ILE:HG12	1:B:412:MET:CB	1.93	0.98
1:B:337:LEU:HD21	1:B:395:VAL:HG21	1.44	0.98
1:A:599:ILE:HD11	1:A:628:ASN:N	1.78	0.98
1:C:337:LEU:HD21	1:C:395:VAL:HG21	1.44	0.98
1:C:346:ILE:HG12	1:C:412:MET:CB	1.93	0.98
1:A:337:LEU:HD21	1:A:395:VAL:HG21	1.44	0.98
1:B:357:ILE:N	1:B:366:SER:OG	1.95	0.98
1:B:198:TYR:CE1	1:B:242:ARG:HD2	1.99	0.98
1:B:655:PHE:HZ	1:A:536:GLU:CB	1.59	0.98
1:B:599:ILE:HD11	1:B:628:ASN:N	1.78	0.97
1:A:359:GLU:H	1:A:362:CYS:HB3	1.24	0.97
1:B:539:ALA:CB	1:D:655:PHE:CD1	2.22	0.97
1:B:644:MET:CG	1:D:645:GLY:O	2.13	0.97
1:A:198:TYR:CE1	1:A:242:ARG:HD2	1.99	0.97
1:D:599:ILE:HD11	1:D:628:ASN:N	1.78	0.97
1:D:426:TRP:HA	1:D:430:VAL:HG13	1.43	0.97
1:B:636:GLU:HG2	1:B:649:PHE:CD1	2.00	0.96
1:A:636:GLU:HG2	1:A:649:PHE:CD1	2.00	0.96
1:B:367:ARG:HH22	1:B:385:SER:HB3	1.29	0.96
1:D:198:TYR:CE1	1:D:242:ARG:HD2	1.99	0.96
1:A:560:GLN:O	1:A:564:ILE:HD13	1.66	0.96
1:C:560:GLN:O	1:C:564:ILE:HD13	1.66	0.96
1:A:368:LYS:CB	1:A:381:LEU:O	2.14	0.96
1:D:368:LYS:CB	1:D:381:LEU:O	2.14	0.96
1:B:515:LEU:HD22	1:B:551:ASN:OD1	1.66	0.96
1:D:636:GLU:HG2	1:D:649:PHE:CD1	2.00	0.96
1:B:368:LYS:CB	1:B:381:LEU:O	2.14	0.96
1:B:629:SER:O	1:B:633:THR:HG22	1.66	0.96
1:C:636:GLU:HG2	1:C:649:PHE:CD1	2.00	0.96
1:C:198:TYR:CE1	1:C:242:ARG:HD2	1.99	0.96
1:C:368:LYS:CB	1:C:381:LEU:O	2.14	0.95
1:D:515:LEU:HD22	1:D:551:ASN:OD1	1.66	0.95
1:C:629:SER:O	1:C:633:THR:HG22	1.66	0.95
1:C:655:PHE:HZ	1:D:536:GLU:CA	1.74	0.95
1:C:367:ARG:HH22	1:C:385:SER:HB3	1.29	0.95
1:D:560:GLN:O	1:D:564:ILE:HD13	1.66	0.95
1:D:629:SER:O	1:D:633:THR:HG22	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:GLU:N	1:A:362:CYS:HB3	1.82	0.94
1:B:399:ILE:O	1:B:402:SER:OG	1.85	0.94
1:B:359:GLU:N	1:B:362:CYS:HB3	1.82	0.94
1:D:367:ARG:HH22	1:D:385:SER:HB3	1.29	0.94
1:A:367:ARG:HH22	1:A:385:SER:HB3	1.29	0.94
1:A:386:CYS:O	1:A:394:SER:OG	1.85	0.94
1:C:359:GLU:N	1:C:362:CYS:HB3	1.82	0.94
1:D:399:ILE:O	1:D:402:SER:OG	1.85	0.94
1:B:655:PHE:HZ	1:A:536:GLU:CA	1.54	0.94
1:A:426:TRP:CA	1:A:430:VAL:CG1	2.46	0.94
1:C:515:LEU:HD22	1:C:551:ASN:OD1	1.65	0.94
1:B:707:ASP:O	1:B:711:SER:N	2.01	0.94
1:C:707:ASP:O	1:C:711:SER:N	2.01	0.94
1:D:359:GLU:N	1:D:362:CYS:HB3	1.82	0.94
1:A:707:ASP:O	1:A:711:SER:N	2.01	0.94
1:B:242:ARG:H	1:B:243:PRO:HA	1.33	0.93
1:B:426:TRP:CA	1:B:430:VAL:CG1	2.46	0.93
1:A:655:PHE:HE2	1:C:536:GLU:CA	1.41	0.93
1:C:337:LEU:CD2	1:C:395:VAL:CG2	2.46	0.93
1:D:337:LEU:CD2	1:D:395:VAL:CG2	2.46	0.93
1:A:337:LEU:CD2	1:A:395:VAL:CG2	2.46	0.93
1:A:629:SER:O	1:A:633:THR:HG22	1.66	0.93
1:C:655:PHE:HE1	1:D:539:ALA:HB3	1.33	0.93
1:C:386:CYS:O	1:C:394:SER:OG	1.85	0.93
1:D:684:GLU:O	1:D:687:ASN:HB3	1.69	0.93
1:A:399:ILE:O	1:A:402:SER:OG	1.85	0.93
1:C:399:ILE:O	1:C:402:SER:OG	1.85	0.93
1:B:337:LEU:CD2	1:B:395:VAL:CG2	2.46	0.93
1:C:684:GLU:O	1:C:687:ASN:HB3	1.69	0.93
1:B:376:PRO:CG	1:D:245:PHE:HD2	1.71	0.93
1:B:386:CYS:O	1:B:394:SER:OG	1.85	0.93
1:A:515:LEU:HD22	1:A:551:ASN:OD1	1.66	0.93
1:B:560:GLN:O	1:B:564:ILE:HD13	1.66	0.93
1:D:386:CYS:O	1:D:394:SER:OG	1.85	0.93
1:B:684:GLU:O	1:B:687:ASN:HB3	1.69	0.92
1:D:242:ARG:H	1:D:243:PRO:HA	1.34	0.92
1:D:707:ASP:O	1:D:711:SER:N	2.01	0.92
1:B:652:ASN:O	1:B:653:TYR:HB3	1.70	0.92
1:D:652:ASN:O	1:D:653:TYR:HB3	1.70	0.92
1:A:640:PHE:CD1	1:A:667:VAL:CG2	2.53	0.92
1:A:652:ASN:O	1:A:653:TYR:HB3	1.70	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:684:GLU:O	1:A:687:ASN:HB3	1.69	0.92
1:B:359:GLU:N	1:B:362:CYS:CB	2.33	0.92
1:C:666:TYR:O	1:C:670:THR:HG22	1.69	0.92
1:A:601:ASP:OD1	1:A:602:GLY:N	2.04	0.91
1:C:428:ARG:HG2	1:C:428:ARG:HH11	1.36	0.91
1:C:640:PHE:CD1	1:C:667:VAL:CG2	2.53	0.91
1:D:452:ALA:O	1:D:455:ARG:HG2	1.70	0.91
1:A:242:ARG:H	1:A:243:PRO:HA	1.34	0.91
1:D:426:TRP:CA	1:D:430:VAL:CG1	2.46	0.91
1:A:359:GLU:N	1:A:362:CYS:CB	2.33	0.91
1:D:359:GLU:N	1:D:362:CYS:CB	2.32	0.91
1:D:428:ARG:HG2	1:D:428:ARG:HH11	1.35	0.91
1:D:601:ASP:OD1	1:D:602:GLY:N	2.04	0.91
1:D:666:TYR:O	1:D:670:THR:HG22	1.69	0.91
1:B:428:ARG:HG2	1:B:428:ARG:HH11	1.36	0.91
1:C:242:ARG:H	1:C:243:PRO:HA	1.34	0.91
1:C:426:TRP:CA	1:C:430:VAL:CG1	2.46	0.91
1:C:601:ASP:OD1	1:C:602:GLY:N	2.04	0.91
1:D:640:PHE:CD1	1:D:667:VAL:CG2	2.53	0.90
1:B:640:PHE:CD1	1:B:667:VAL:CG2	2.53	0.90
1:B:666:TYR:O	1:B:670:THR:HG22	1.69	0.90
1:A:452:ALA:O	1:A:455:ARG:HG2	1.70	0.90
1:D:510:SER:OG	1:D:513:GLU:CB	2.19	0.90
1:B:376:PRO:CG	1:D:245:PHE:HB3	2.01	0.90
1:C:452:ALA:O	1:C:455:ARG:HG2	1.70	0.90
1:B:452:ALA:O	1:B:455:ARG:HG2	1.70	0.90
1:D:640:PHE:CD1	1:D:667:VAL:HG22	2.07	0.90
1:B:601:ASP:OD1	1:B:602:GLY:N	2.04	0.90
1:B:640:PHE:CE1	1:B:667:VAL:HG21	2.07	0.90
1:A:666:TYR:O	1:A:670:THR:HG22	1.69	0.90
1:C:510:SER:OG	1:C:513:GLU:CB	2.19	0.90
1:A:510:SER:OG	1:A:513:GLU:CB	2.19	0.90
1:B:510:SER:OG	1:B:513:GLU:CB	2.19	0.89
1:A:640:PHE:CE1	1:A:667:VAL:HG21	2.07	0.89
1:B:547:MET:O	1:B:551:ASN:ND2	2.06	0.89
1:A:428:ARG:HG2	1:A:428:ARG:HH11	1.36	0.89
1:A:640:PHE:CD1	1:A:667:VAL:HG22	2.07	0.89
1:C:640:PHE:CE1	1:C:667:VAL:HG21	2.07	0.89
1:B:704:THR:O	1:B:708:THR:HG23	1.72	0.89
1:A:396:LEU:HD11	1:A:418:LEU:CD2	2.02	0.89
1:D:515:LEU:HD23	1:D:551:ASN:OD1	1.72	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:THR:O	1:A:708:THR:HG23	1.72	0.89
1:C:640:PHE:CD1	1:C:667:VAL:HG22	2.07	0.89
1:A:708:THR:O	1:A:712:PHE:CA	2.21	0.89
1:B:560:GLN:O	1:B:564:ILE:CD1	2.21	0.89
1:D:640:PHE:CE1	1:D:667:VAL:HG21	2.07	0.89
1:A:547:MET:O	1:A:551:ASN:ND2	2.06	0.89
1:C:547:MET:O	1:C:551:ASN:ND2	2.05	0.89
1:C:704:THR:O	1:C:708:THR:HG23	1.72	0.89
1:C:359:GLU:N	1:C:362:CYS:CB	2.32	0.88
1:C:515:LEU:HD23	1:C:551:ASN:OD1	1.72	0.88
1:C:708:THR:O	1:C:712:PHE:CA	2.21	0.88
1:D:396:LEU:HD11	1:D:418:LEU:CD2	2.03	0.88
1:D:704:THR:O	1:D:708:THR:HG23	1.72	0.88
1:C:560:GLN:O	1:C:564:ILE:CD1	2.21	0.88
1:A:515:LEU:HD23	1:A:551:ASN:OD1	1.72	0.88
1:A:560:GLN:O	1:A:564:ILE:CD1	2.21	0.88
1:D:560:GLN:O	1:D:564:ILE:CD1	2.21	0.88
1:C:652:ASN:O	1:C:653:TYR:HB3	1.70	0.88
1:B:708:THR:O	1:B:712:PHE:CA	2.21	0.88
1:A:401:TYR:CA	1:A:402:SER:HB2	2.04	0.88
1:D:693:SER:O	1:D:696:ILE:N	2.07	0.88
1:D:547:MET:O	1:D:551:ASN:ND2	2.06	0.88
1:C:396:LEU:HD11	1:C:418:LEU:CD2	2.03	0.87
1:C:396:LEU:CD1	1:C:418:LEU:HD23	2.05	0.87
1:C:235:PHE:CE2	1:D:374:TYR:CB	2.58	0.87
1:B:401:TYR:CA	1:B:402:SER:HB2	2.04	0.87
1:B:640:PHE:CD1	1:B:667:VAL:HG22	2.07	0.87
1:C:655:PHE:CZ	1:D:536:GLU:HA	2.04	0.87
1:D:367:ARG:HH22	1:D:385:SER:CB	1.88	0.87
1:D:536:GLU:O	1:D:538:VAL:N	2.08	0.87
1:B:536:GLU:O	1:B:538:VAL:N	2.08	0.87
1:B:515:LEU:HD23	1:B:551:ASN:OD1	1.72	0.87
1:D:401:TYR:CA	1:D:402:SER:HB2	2.04	0.87
1:D:708:THR:O	1:D:712:PHE:CA	2.21	0.87
1:B:396:LEU:HD11	1:B:418:LEU:CD2	2.03	0.87
1:C:401:TYR:HA	1:C:402:SER:HB2	1.57	0.87
1:A:396:LEU:CD1	1:A:418:LEU:HD23	2.05	0.87
1:A:658:VAL:HG13	1:C:543:PHE:HZ	1.38	0.87
1:A:693:SER:O	1:A:696:ILE:N	2.07	0.87
1:A:701:ARG:CB	1:A:701:ARG:HH11	1.88	0.87
1:C:367:ARG:HH22	1:C:385:SER:CB	1.88	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:401:TYR:CA	1:C:402:SER:HB2	2.04	0.87
1:C:693:SER:O	1:C:696:ILE:N	2.07	0.87
1:B:693:SER:O	1:B:696:ILE:N	2.07	0.86
1:C:478:GLU:O	1:C:482:VAL:HG23	1.75	0.86
1:D:401:TYR:HA	1:D:402:SER:HB2	1.57	0.86
1:B:701:ARG:CB	1:B:701:ARG:HH11	1.88	0.86
1:A:478:GLU:O	1:A:482:VAL:HG23	1.75	0.86
1:D:426:TRP:CD1	1:D:430:VAL:HG13	2.11	0.86
1:D:560:GLN:HE22	1:D:694:LYS:HD3	1.40	0.86
1:C:560:GLN:HE22	1:C:694:LYS:HD3	1.40	0.86
1:C:337:LEU:CD2	1:C:395:VAL:HG22	2.06	0.86
1:B:367:ARG:HH22	1:B:385:SER:CB	1.88	0.86
1:A:121:VAL:HG22	1:A:172:THR:HG21	1.58	0.86
1:B:560:GLN:NE2	1:B:694:LYS:HD3	1.91	0.86
1:B:655:PHE:HE2	1:A:536:GLU:CA	1.69	0.86
1:C:426:TRP:CD1	1:C:430:VAL:HG13	2.11	0.86
1:D:121:VAL:HG22	1:D:172:THR:HG21	1.58	0.86
1:D:239:THR:CB	1:D:243:PRO:HB3	2.06	0.86
1:D:396:LEU:CD1	1:D:418:LEU:HD23	2.04	0.86
1:B:136:LEU:HD23	1:B:136:LEU:H	1.41	0.86
1:B:478:GLU:O	1:B:482:VAL:HG23	1.75	0.86
1:A:560:GLN:NE2	1:A:694:LYS:HD3	1.90	0.86
1:C:536:GLU:O	1:C:538:VAL:N	2.08	0.86
1:D:681:LEU:HD13	1:D:682:MET:N	1.91	0.86
1:B:681:LEU:HD13	1:B:682:MET:N	1.91	0.86
1:B:655:PHE:CD1	1:A:539:ALA:CB	2.27	0.85
1:A:337:LEU:CD2	1:A:395:VAL:HG22	2.06	0.85
1:A:560:GLN:HE22	1:A:694:LYS:HD3	1.40	0.85
1:A:681:LEU:HD13	1:A:682:MET:N	1.91	0.85
1:C:356:GLU:CB	1:C:368:LYS:O	2.24	0.85
1:D:560:GLN:NE2	1:D:694:LYS:HD3	1.91	0.85
1:D:701:ARG:CB	1:D:701:ARG:HH11	1.88	0.85
1:B:121:VAL:HG22	1:B:172:THR:HG21	1.58	0.85
1:B:239:THR:CB	1:B:243:PRO:HB3	2.06	0.85
1:B:426:TRP:CD1	1:B:430:VAL:HG13	2.11	0.85
1:A:367:ARG:HH22	1:A:385:SER:CB	1.88	0.85
1:C:701:ARG:CB	1:C:701:ARG:HH11	1.88	0.85
1:B:543:PHE:CZ	1:D:658:VAL:HG13	2.12	0.85
1:D:337:LEU:CD2	1:D:395:VAL:HG22	2.06	0.85
1:D:400:ALA:O	1:D:703:ILE:HG12	1.77	0.85
1:A:136:LEU:HD23	1:A:136:LEU:H	1.41	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:GLU:CB	1:A:368:LYS:O	2.24	0.85
1:A:426:TRP:CD1	1:A:430:VAL:HG13	2.11	0.85
1:A:536:GLU:O	1:A:538:VAL:N	2.08	0.85
1:C:560:GLN:NE2	1:C:694:LYS:HD3	1.91	0.85
1:B:396:LEU:CD1	1:B:418:LEU:HD23	2.04	0.85
1:B:645:GLY:O	1:A:644:MET:HG2	1.74	0.85
1:C:400:ALA:O	1:C:703:ILE:HG12	1.77	0.85
1:D:443:LEU:O	1:D:447:ILE:HD13	1.77	0.85
1:D:478:GLU:O	1:D:482:VAL:HG23	1.75	0.85
1:B:536:GLU:CA	1:D:655:PHE:HZ	1.45	0.85
1:A:693:SER:OG	1:A:696:ILE:HG21	1.77	0.85
1:B:337:LEU:CD2	1:B:395:VAL:HG22	2.06	0.85
1:D:356:GLU:CB	1:D:368:LYS:O	2.24	0.85
1:C:121:VAL:HG22	1:C:172:THR:HG21	1.58	0.85
1:D:395:VAL:O	1:D:399:ILE:HG13	1.77	0.85
1:B:356:GLU:CB	1:B:368:LYS:O	2.24	0.84
1:B:386:CYS:CB	1:B:395:VAL:CB	2.55	0.84
1:B:401:TYR:HA	1:B:402:SER:HB2	1.57	0.84
1:A:239:THR:CB	1:A:243:PRO:HB3	2.06	0.84
1:C:395:VAL:O	1:C:399:ILE:HG13	1.77	0.84
1:B:395:VAL:O	1:B:399:ILE:HG13	1.77	0.84
1:C:239:THR:OG1	1:C:241:GLY:HA2	1.77	0.84
1:B:400:ALA:O	1:B:703:ILE:HG12	1.77	0.84
1:B:426:TRP:CA	1:B:430:VAL:HG12	2.07	0.84
1:A:401:TYR:HA	1:A:402:SER:HB2	1.57	0.84
1:C:629:SER:HG	1:C:632:SER:HG	1.16	0.84
1:B:511:TYR:O	1:B:514:ILE:HG22	1.78	0.84
1:A:239:THR:OG1	1:A:241:GLY:HA2	1.77	0.84
1:A:443:LEU:O	1:A:447:ILE:HD13	1.77	0.84
1:C:136:LEU:HD23	1:C:136:LEU:H	1.40	0.84
1:C:655:PHE:CE2	1:D:536:GLU:CB	2.60	0.84
1:C:681:LEU:HD13	1:C:682:MET:N	1.91	0.84
1:D:239:THR:OG1	1:D:241:GLY:HA2	1.77	0.84
1:D:386:CYS:CB	1:D:395:VAL:CB	2.55	0.84
1:B:655:PHE:CZ	1:A:536:GLU:HA	1.81	0.84
1:A:396:LEU:HD12	1:A:418:LEU:HD22	0.84	0.84
1:B:127:GLN:O	1:B:130:GLU:HG3	1.78	0.84
1:B:652:ASN:O	1:B:653:TYR:CB	2.26	0.84
1:A:243:PRO:HB2	1:A:244:GLY:CA	2.08	0.84
1:A:426:TRP:CA	1:A:430:VAL:HG12	2.07	0.84
1:C:426:TRP:CA	1:C:430:VAL:HG12	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:THR:OG1	1:B:241:GLY:HA2	1.77	0.84
1:B:693:SER:OG	1:B:696:ILE:HG21	1.77	0.84
1:C:443:LEU:O	1:C:447:ILE:HD13	1.77	0.84
1:D:426:TRP:CA	1:D:430:VAL:HG12	2.07	0.84
1:D:652:ASN:O	1:D:653:TYR:CB	2.26	0.84
1:A:400:ALA:O	1:A:703:ILE:HG12	1.77	0.84
1:C:239:THR:CB	1:C:243:PRO:HB3	2.05	0.84
1:D:511:TYR:O	1:D:514:ILE:HG22	1.78	0.84
1:B:539:ALA:CA	1:D:655:PHE:CE1	2.61	0.83
1:D:127:GLN:O	1:D:130:GLU:HG3	1.78	0.83
1:D:136:LEU:HD23	1:D:136:LEU:H	1.41	0.83
1:A:386:CYS:CB	1:A:395:VAL:CB	2.55	0.83
1:A:580:PHE:HD2	1:C:565:TYR:HH	0.87	0.83
1:C:127:GLN:O	1:C:130:GLU:HG3	1.78	0.83
1:C:396:LEU:HD12	1:C:418:LEU:HD22	0.84	0.83
1:D:428:ARG:HD3	1:D:429:PHE:N	1.93	0.83
1:B:443:LEU:O	1:B:447:ILE:HD13	1.77	0.83
1:A:652:ASN:O	1:A:653:TYR:CB	2.26	0.83
1:D:386:CYS:CB	1:D:395:VAL:CG2	2.56	0.83
1:B:235:PHE:HZ	1:A:374:TYR:CB	1.92	0.83
1:B:396:LEU:HD12	1:B:418:LEU:HD22	0.84	0.83
1:A:472:TYR:O	1:A:476:THR:HG23	1.78	0.83
1:A:665:ALA:O	1:A:669:LEU:HB2	1.79	0.83
1:C:386:CYS:CB	1:C:395:VAL:CB	2.55	0.83
1:D:669:LEU:O	1:D:673:LEU:HB2	1.79	0.83
1:B:472:TYR:O	1:B:476:THR:HG23	1.78	0.83
1:B:499:ARG:N	1:B:499:ARG:HD2	1.93	0.83
1:A:127:GLN:O	1:A:130:GLU:HG3	1.78	0.83
1:A:395:VAL:O	1:A:399:ILE:HG13	1.77	0.83
1:C:428:ARG:CD	1:C:429:PHE:CG	2.62	0.83
1:C:701:ARG:HH11	1:C:701:ARG:HB2	1.43	0.83
1:D:243:PRO:HB2	1:D:244:GLY:CA	2.08	0.83
1:D:693:SER:OG	1:D:696:ILE:HG21	1.77	0.83
1:A:346:ILE:CG1	1:A:412:MET:CB	2.57	0.83
1:C:664:LEU:O	1:C:668:ILE:CG2	2.27	0.83
1:C:665:ALA:O	1:C:669:LEU:HB2	1.79	0.83
1:C:693:SER:OG	1:C:696:ILE:HG21	1.77	0.83
1:B:374:TYR:CB	1:D:235:PHE:CZ	2.62	0.83
1:B:701:ARG:HH11	1:B:701:ARG:HB2	1.43	0.83
1:A:386:CYS:CB	1:A:395:VAL:CG2	2.56	0.83
1:A:499:ARG:HD2	1:A:499:ARG:N	1.92	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:CYS:CB	1:C:395:VAL:CG2	2.56	0.83
1:C:428:ARG:HD3	1:C:429:PHE:N	1.94	0.83
1:C:669:LEU:O	1:C:669:LEU:HD23	1.78	0.83
1:B:669:LEU:O	1:B:673:LEU:HB2	1.79	0.83
1:D:396:LEU:HD12	1:D:418:LEU:HD22	0.84	0.83
1:D:664:LEU:O	1:D:668:ILE:CG2	2.27	0.83
1:A:676:ASN:HB2	1:C:572:MET:HE1	1.61	0.83
1:B:428:ARG:HD3	1:B:429:PHE:N	1.94	0.82
1:A:701:ARG:HH11	1:A:701:ARG:HB2	1.43	0.82
1:B:386:CYS:CB	1:B:395:VAL:CG2	2.56	0.82
1:A:669:LEU:HD23	1:A:669:LEU:O	1.78	0.82
1:A:669:LEU:O	1:A:673:LEU:HB2	1.79	0.82
1:C:400:ALA:C	1:C:402:SER:HB2	2.05	0.82
1:C:511:TYR:O	1:C:514:ILE:HG22	1.78	0.82
1:B:560:GLN:HE22	1:B:694:LYS:HD3	1.40	0.82
1:C:243:PRO:HB2	1:C:244:GLY:CA	2.08	0.82
1:D:665:ALA:O	1:D:669:LEU:HB2	1.79	0.82
1:B:515:LEU:HD23	1:B:551:ASN:ND2	1.95	0.82
1:B:665:ALA:O	1:B:669:LEU:HB2	1.79	0.82
1:A:400:ALA:C	1:A:402:SER:HB2	2.05	0.82
1:C:499:ARG:N	1:C:499:ARG:HD2	1.92	0.82
1:D:669:LEU:O	1:D:669:LEU:HD23	1.78	0.82
1:C:346:ILE:CG1	1:C:412:MET:CB	2.57	0.82
1:B:243:PRO:HB2	1:B:244:GLY:CA	2.08	0.82
1:B:428:ARG:CD	1:B:429:PHE:CG	2.62	0.82
1:D:629:SER:HG	1:D:632:SER:HG	1.16	0.82
1:A:511:TYR:O	1:A:514:ILE:HG22	1.78	0.82
1:A:629:SER:HG	1:A:632:SER:HG	1.12	0.82
1:B:346:ILE:CG1	1:B:412:MET:CB	2.57	0.82
1:B:669:LEU:O	1:B:669:LEU:HD23	1.78	0.82
1:D:499:ARG:HD2	1:D:499:ARG:N	1.93	0.81
1:B:400:ALA:C	1:B:402:SER:HB2	2.05	0.81
1:B:536:GLU:CB	1:D:655:PHE:HZ	1.67	0.81
1:D:346:ILE:CG1	1:D:412:MET:CB	2.57	0.81
1:D:472:TYR:O	1:D:476:THR:HG23	1.78	0.81
1:C:652:ASN:O	1:C:653:TYR:CB	2.26	0.81
1:D:400:ALA:C	1:D:402:SER:HB2	2.05	0.81
1:D:428:ARG:CD	1:D:429:PHE:CG	2.62	0.81
1:A:428:ARG:CD	1:A:429:PHE:CG	2.62	0.81
1:D:760:UNK:HA	1:D:761:UNK:CB	2.11	0.81
1:A:515:LEU:HD23	1:A:551:ASN:ND2	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:472:TYR:O	1:C:476:THR:HG23	1.78	0.81
1:C:515:LEU:HD23	1:C:551:ASN:ND2	1.95	0.81
1:C:669:LEU:O	1:C:673:LEU:HB2	1.79	0.81
1:D:359:GLU:C	1:D:362:CYS:HB3	2.06	0.81
1:D:701:ARG:HH11	1:D:701:ARG:HB2	1.43	0.81
1:A:428:ARG:HD3	1:A:429:PHE:N	1.94	0.81
1:A:664:LEU:O	1:A:668:ILE:CG2	2.27	0.81
1:A:359:GLU:C	1:A:362:CYS:HB3	2.06	0.81
1:C:655:PHE:CE2	1:D:536:GLU:CA	2.60	0.81
1:D:515:LEU:HD23	1:D:551:ASN:CG	2.06	0.81
1:B:359:GLU:C	1:B:362:CYS:HB3	2.06	0.81
1:B:546:ALA:O	1:B:550:THR:HG23	1.81	0.81
1:B:760:UNK:HA	1:B:761:UNK:CB	2.11	0.80
1:A:563:GLY:O	1:A:567:VAL:HG23	1.82	0.80
1:A:760:UNK:HA	1:A:761:UNK:CB	2.11	0.80
1:C:665:ALA:O	1:C:669:LEU:N	2.13	0.80
1:B:563:GLY:O	1:B:567:VAL:HG23	1.82	0.80
1:D:515:LEU:HD23	1:D:551:ASN:ND2	1.95	0.80
1:C:546:ALA:O	1:C:550:THR:HG23	1.81	0.80
1:C:515:LEU:HD23	1:C:551:ASN:CG	2.06	0.80
1:D:462:PRO:HB2	1:D:464:LYS:N	1.97	0.80
1:C:359:GLU:C	1:C:362:CYS:HB3	2.06	0.80
1:B:664:LEU:O	1:B:668:ILE:CG2	2.27	0.80
1:A:396:LEU:HD13	1:A:418:LEU:CD2	2.12	0.80
1:D:546:ALA:O	1:D:550:THR:HG23	1.81	0.80
1:D:665:ALA:O	1:D:669:LEU:N	2.13	0.80
1:C:462:PRO:HB2	1:C:464:LYS:N	1.97	0.80
1:D:563:GLY:O	1:D:567:VAL:HG23	1.82	0.80
1:A:546:ALA:O	1:A:550:THR:HG23	1.81	0.80
1:B:572:MET:CE	1:D:676:ASN:HB2	2.12	0.79
1:A:515:LEU:HD23	1:A:551:ASN:HD21	1.47	0.79
1:C:760:UNK:HA	1:C:761:UNK:CB	2.11	0.79
1:C:591:PHE:CD2	1:C:666:TYR:HB2	2.18	0.79
1:D:358:HIS:HA	1:D:362:CYS:SG	2.23	0.79
1:B:516:PHE:CE2	1:B:554:TYR:CE2	2.70	0.79
1:B:640:PHE:CD1	1:B:667:VAL:HG21	2.18	0.79
1:A:515:LEU:HD23	1:A:551:ASN:CG	2.06	0.79
1:C:640:PHE:CD1	1:C:667:VAL:HG21	2.17	0.79
1:A:235:PHE:CE2	1:C:374:TYR:CB	2.65	0.79
1:A:665:ALA:O	1:A:669:LEU:N	2.13	0.79
1:B:515:LEU:HD23	1:B:551:ASN:CG	2.06	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:PHE:CE2	1:A:554:TYR:CE2	2.70	0.79
1:B:655:PHE:CE1	1:A:539:ALA:CA	2.66	0.79
1:A:652:ASN:O	1:A:653:TYR:CD2	2.36	0.79
1:C:358:HIS:HA	1:C:362:CYS:SG	2.23	0.79
1:C:396:LEU:HD13	1:C:418:LEU:CD2	2.12	0.79
1:C:652:ASN:O	1:C:653:TYR:CD2	2.36	0.79
1:D:515:LEU:HD23	1:D:551:ASN:HD21	1.47	0.79
1:B:652:ASN:O	1:B:653:TYR:CD2	2.36	0.79
1:A:358:HIS:HA	1:A:362:CYS:SG	2.23	0.79
1:A:640:PHE:CD1	1:A:667:VAL:HG21	2.18	0.79
1:C:563:GLY:O	1:C:567:VAL:HG23	1.82	0.79
1:B:358:HIS:HA	1:B:362:CYS:SG	2.23	0.79
1:D:640:PHE:CD1	1:D:667:VAL:HG21	2.18	0.79
1:B:658:VAL:HG13	1:A:543:PHE:CZ	2.18	0.79
1:C:356:GLU:HA	1:C:366:SER:OG	1.83	0.79
1:C:516:PHE:CE2	1:C:554:TYR:CE2	2.70	0.79
1:B:665:ALA:O	1:B:669:LEU:N	2.13	0.78
1:A:676:ASN:HB2	1:C:572:MET:HE2	1.62	0.78
1:C:661:ILE:O	1:C:661:ILE:HD13	1.83	0.78
1:D:652:ASN:O	1:D:653:TYR:CD2	2.36	0.78
1:B:396:LEU:HD13	1:B:418:LEU:CD2	2.12	0.78
1:B:462:PRO:HB2	1:B:464:LYS:N	1.97	0.78
1:B:515:LEU:HD23	1:B:551:ASN:HD21	1.47	0.78
1:B:591:PHE:CD2	1:B:666:TYR:HB2	2.18	0.78
1:B:658:VAL:O	1:B:661:ILE:HG22	1.84	0.78
1:A:655:PHE:HZ	1:C:536:GLU:CB	1.49	0.78
1:D:658:VAL:O	1:D:661:ILE:HG22	1.84	0.78
1:A:591:PHE:CD2	1:A:666:TYR:HB2	2.18	0.78
1:B:356:GLU:HA	1:B:366:SER:OG	1.83	0.78
1:B:661:ILE:HD13	1:B:661:ILE:O	1.84	0.78
1:A:356:GLU:HA	1:A:366:SER:OG	1.83	0.78
1:C:647:LEU:HG	1:D:639:LYS:HD3	1.64	0.78
1:D:516:PHE:CE2	1:D:554:TYR:CE2	2.70	0.78
1:D:591:PHE:CD2	1:D:666:TYR:HB2	2.18	0.78
1:D:661:ILE:O	1:D:661:ILE:HD13	1.84	0.78
1:A:235:PHE:HZ	1:C:374:TYR:CB	1.94	0.78
1:A:462:PRO:HB2	1:A:464:LYS:N	1.97	0.78
1:B:559:PHE:HB3	1:B:562:MET:H	1.49	0.78
1:A:645:GLY:O	1:C:644:MET:HG2	1.82	0.78
1:A:658:VAL:O	1:A:661:ILE:HG22	1.84	0.78
1:C:694:LYS:C	1:C:694:LYS:HD2	2.10	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:ARG:HD2	1:A:429:PHE:CD2	2.19	0.77
1:D:559:PHE:HB3	1:D:562:MET:H	1.49	0.77
1:B:629:SER:HG	1:B:632:SER:HG	1.13	0.77
1:A:694:LYS:HD2	1:A:694:LYS:C	2.09	0.77
1:C:498:GLN:C	1:C:499:ARG:HD2	2.10	0.77
1:C:402:SER:HB3	1:C:703:ILE:HD11	1.66	0.77
1:C:428:ARG:HD2	1:C:429:PHE:CD2	2.19	0.77
1:C:515:LEU:HD23	1:C:551:ASN:HD21	1.47	0.77
1:C:587:PHE:HE2	1:C:674:LEU:CD2	1.98	0.77
1:B:235:PHE:CE2	1:A:374:TYR:CB	2.67	0.77
1:B:707:ASP:O	1:B:711:SER:CB	2.32	0.77
1:A:402:SER:HB3	1:A:703:ILE:HD11	1.66	0.77
1:A:498:GLN:C	1:A:499:ARG:HD2	2.09	0.77
1:A:587:PHE:HE2	1:A:674:LEU:CD2	1.97	0.77
1:D:498:GLN:C	1:D:499:ARG:HD2	2.09	0.77
1:D:694:LYS:HD2	1:D:694:LYS:C	2.10	0.77
1:B:514:ILE:O	1:B:518:VAL:HG23	1.85	0.77
1:B:587:PHE:HE2	1:B:674:LEU:CD2	1.98	0.77
1:C:707:ASP:O	1:C:711:SER:CB	2.32	0.77
1:D:367:ARG:NH2	1:D:385:SER:HB3	1.99	0.77
1:B:402:SER:HB3	1:B:703:ILE:HD11	1.66	0.77
1:A:242:ARG:N	1:A:243:PRO:HA	1.98	0.77
1:D:356:GLU:HA	1:D:366:SER:OG	1.83	0.77
1:B:488:PHE:HB2	1:B:520:SER:HB3	1.66	0.77
1:C:658:VAL:O	1:C:661:ILE:HG22	1.84	0.77
1:C:559:PHE:HB3	1:C:562:MET:H	1.49	0.77
1:D:587:PHE:HE2	1:D:674:LEU:CD2	1.97	0.77
1:D:707:ASP:O	1:D:711:SER:CB	2.32	0.77
1:B:367:ARG:NH2	1:B:385:SER:HB3	1.99	0.77
1:A:661:ILE:O	1:A:661:ILE:HD13	1.84	0.77
1:B:694:LYS:HD2	1:B:694:LYS:C	2.09	0.76
1:C:488:PHE:HB2	1:C:520:SER:HB3	1.66	0.76
1:B:539:ALA:N	1:D:655:PHE:CE1	2.54	0.76
1:A:707:ASP:O	1:A:711:SER:CB	2.32	0.76
1:D:396:LEU:HD13	1:D:418:LEU:CD2	2.12	0.76
1:B:498:GLN:C	1:B:499:ARG:HD2	2.10	0.76
1:D:514:ILE:O	1:D:518:VAL:HG23	1.85	0.76
1:B:515:LEU:CD2	1:B:551:ASN:CG	2.59	0.76
1:A:559:PHE:HB3	1:A:562:MET:H	1.49	0.76
1:A:682:MET:O	1:A:685:THR:HG22	1.86	0.76
1:C:665:ALA:O	1:C:669:LEU:CB	2.34	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:682:MET:O	1:B:685:THR:HG22	1.86	0.76
1:B:376:PRO:CG	1:D:245:PHE:CB	2.42	0.76
1:A:127:GLN:HG2	1:A:130:GLU:OE2	1.85	0.76
1:C:352:ILE:O	1:C:367:ARG:HD2	1.86	0.76
1:D:352:ILE:O	1:D:367:ARG:HD2	1.86	0.76
1:D:428:ARG:HD2	1:D:429:PHE:CD2	2.19	0.76
1:D:515:LEU:CD2	1:D:551:ASN:CG	2.59	0.76
1:B:428:ARG:HD2	1:B:429:PHE:CD2	2.19	0.76
1:B:647:LEU:HD23	1:A:642:ILE:CD1	2.16	0.76
1:D:488:PHE:HB2	1:D:520:SER:HB3	1.66	0.76
1:A:521:LEU:O	1:A:521:LEU:HD22	1.86	0.76
1:B:352:ILE:O	1:B:367:ARG:HD2	1.86	0.76
1:B:665:ALA:O	1:B:669:LEU:CB	2.34	0.76
1:A:488:PHE:HB2	1:A:520:SER:HB3	1.66	0.76
1:C:514:ILE:O	1:C:518:VAL:HG23	1.85	0.76
1:D:564:ILE:O	1:D:568:MET:HG3	1.86	0.76
1:A:677:MET:N	1:C:572:MET:HE1	2.00	0.76
1:C:367:ARG:NH2	1:C:385:SER:HB3	2.00	0.76
1:C:564:ILE:O	1:C:568:MET:HG3	1.86	0.76
1:D:359:GLU:O	1:D:362:CYS:CB	2.34	0.76
1:D:665:ALA:O	1:D:669:LEU:CB	2.34	0.76
1:C:127:GLN:HG2	1:C:130:GLU:OE2	1.85	0.75
1:D:127:GLN:HG2	1:D:130:GLU:OE2	1.85	0.75
1:D:402:SER:HB3	1:D:703:ILE:HD11	1.66	0.75
1:B:536:GLU:O	1:D:655:PHE:CE1	2.39	0.75
1:A:352:ILE:O	1:A:367:ARG:HD2	1.86	0.75
1:A:367:ARG:NH2	1:A:385:SER:HB3	2.00	0.75
1:A:564:ILE:O	1:A:568:MET:HG3	1.86	0.75
1:C:521:LEU:O	1:C:521:LEU:HD22	1.86	0.75
1:B:487:TYR:HE1	1:B:491:ARG:CD	1.99	0.75
1:D:487:TYR:HE1	1:D:491:ARG:CD	1.99	0.75
1:B:127:GLN:HG2	1:B:130:GLU:OE2	1.85	0.75
1:A:514:ILE:O	1:A:518:VAL:HG23	1.85	0.75
1:A:665:ALA:O	1:A:669:LEU:CB	2.34	0.75
1:D:682:MET:O	1:D:685:THR:HG22	1.86	0.75
1:C:676:ASN:HD22	1:C:676:ASN:H	1.31	0.75
1:B:359:GLU:O	1:B:362:CYS:CB	2.34	0.75
1:B:521:LEU:O	1:B:521:LEU:HD22	1.86	0.75
1:B:572:MET:HE1	1:D:676:ASN:HB2	1.68	0.75
1:A:515:LEU:CD2	1:A:551:ASN:CG	2.59	0.75
1:A:570:GLU:O	1:A:573:ILE:HG22	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:682:MET:O	1:C:685:THR:HG22	1.86	0.75
1:C:515:LEU:CD2	1:C:551:ASN:CG	2.59	0.75
1:B:564:ILE:O	1:B:568:MET:HG3	1.86	0.74
1:B:678:LEU:O	1:B:681:LEU:HD12	1.86	0.74
1:A:461:PRO:HA	1:A:462:PRO:C	2.12	0.74
1:A:658:VAL:CG1	1:C:543:PHE:CZ	2.69	0.74
1:C:461:PRO:HA	1:C:462:PRO:C	2.12	0.74
1:D:668:ILE:HD12	1:D:669:LEU:N	2.02	0.74
1:D:678:LEU:O	1:D:681:LEU:HD12	1.86	0.74
1:C:487:TYR:HE1	1:C:491:ARG:CD	1.99	0.74
1:A:487:TYR:HE1	1:A:491:ARG:CD	1.99	0.74
1:A:572:MET:O	1:A:576:ASP:HB2	1.88	0.74
1:D:243:PRO:CB	1:D:244:GLY:HA3	2.15	0.74
1:D:521:LEU:O	1:D:521:LEU:HD22	1.86	0.74
1:C:570:GLU:O	1:C:573:ILE:HG22	1.87	0.74
1:B:572:MET:O	1:B:576:ASP:HB2	1.87	0.74
1:B:644:MET:HG2	1:D:645:GLY:O	1.87	0.74
1:C:572:MET:O	1:C:576:ASP:HB2	1.87	0.74
1:C:668:ILE:HD12	1:C:669:LEU:N	2.02	0.74
1:D:461:PRO:HA	1:D:462:PRO:C	2.12	0.74
1:D:572:MET:O	1:D:576:ASP:HB2	1.87	0.74
1:C:630:LEU:O	1:C:630:LEU:HD13	1.88	0.74
1:D:649:PHE:H	1:D:649:PHE:HD2	1.36	0.74
1:B:243:PRO:CB	1:B:244:GLY:HA3	2.15	0.74
1:C:649:PHE:H	1:C:649:PHE:HD2	1.36	0.74
1:B:352:ILE:O	1:B:367:ARG:CD	2.36	0.73
1:D:452:ALA:O	1:D:455:ARG:CG	2.36	0.73
1:B:589:PHE:O	1:B:593:THR:HG23	1.88	0.73
1:B:655:PHE:HD1	1:A:539:ALA:HB2	1.38	0.73
1:B:668:ILE:HD12	1:B:669:LEU:N	2.02	0.73
1:A:184:ASP:C	1:A:186:LEU:H	1.96	0.73
1:C:452:ALA:O	1:C:455:ARG:CG	2.36	0.73
1:B:184:ASP:C	1:B:186:LEU:H	1.96	0.73
1:B:452:ALA:O	1:B:455:ARG:CG	2.36	0.73
1:B:461:PRO:HA	1:B:462:PRO:C	2.12	0.73
1:B:647:LEU:CD1	1:B:648:GLU:HG3	2.12	0.73
1:A:452:ALA:O	1:A:455:ARG:CG	2.36	0.73
1:C:352:ILE:O	1:C:367:ARG:CD	2.36	0.73
1:C:647:LEU:HD23	1:D:642:ILE:CD1	2.18	0.73
1:D:570:GLU:O	1:D:573:ILE:HG22	1.87	0.73
1:D:589:PHE:O	1:D:593:THR:HG23	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ILE:O	1:A:367:ARG:CD	2.36	0.73
1:A:630:LEU:HD13	1:A:630:LEU:O	1.88	0.73
1:C:589:PHE:O	1:C:593:THR:HG23	1.88	0.73
1:B:570:GLU:O	1:B:573:ILE:HG22	1.87	0.73
1:D:666:TYR:CE1	1:D:670:THR:HG21	2.24	0.73
1:C:678:LEU:O	1:C:681:LEU:HD12	1.86	0.73
1:D:428:ARG:HD3	1:D:429:PHE:CB	2.19	0.73
1:B:630:LEU:O	1:B:630:LEU:HD13	1.88	0.73
1:C:396:LEU:HD11	1:C:418:LEU:HD22	1.63	0.73
1:B:376:PRO:CB	1:D:245:PHE:CG	2.71	0.73
1:A:678:LEU:O	1:A:681:LEU:HD12	1.86	0.73
1:C:242:ARG:N	1:C:243:PRO:HA	1.98	0.73
1:C:243:PRO:CB	1:C:244:GLY:HA3	2.15	0.73
1:C:359:GLU:O	1:C:362:CYS:CB	2.34	0.73
1:A:511:TYR:CE1	1:A:515:LEU:HD13	2.24	0.73
1:A:668:ILE:HD12	1:A:669:LEU:N	2.02	0.73
1:C:136:LEU:HB2	1:C:141:LYS:O	1.89	0.73
1:D:630:LEU:O	1:D:630:LEU:HD13	1.88	0.73
1:B:428:ARG:HD3	1:B:429:PHE:CB	2.19	0.72
1:A:243:PRO:CB	1:A:244:GLY:HA3	2.15	0.72
1:A:428:ARG:HD3	1:A:429:PHE:CB	2.19	0.72
1:C:666:TYR:CE1	1:C:670:THR:HG21	2.24	0.72
1:B:511:TYR:CE1	1:B:515:LEU:HD13	2.24	0.72
1:B:536:GLU:CA	1:D:655:PHE:HE2	1.55	0.72
1:A:666:TYR:CE1	1:A:670:THR:HG21	2.24	0.72
1:B:666:TYR:CE1	1:B:670:THR:HG21	2.24	0.72
1:B:676:ASN:HB2	1:A:572:MET:CE	2.19	0.72
1:A:580:PHE:CD2	1:A:678:LEU:HD22	2.24	0.72
1:C:428:ARG:HD3	1:C:429:PHE:CB	2.19	0.72
1:C:511:TYR:CE1	1:C:515:LEU:HD13	2.24	0.72
1:C:580:PHE:CD2	1:C:678:LEU:HD22	2.24	0.72
1:A:589:PHE:O	1:A:593:THR:HG23	1.88	0.72
1:D:352:ILE:O	1:D:367:ARG:CD	2.36	0.72
1:A:136:LEU:HB2	1:A:141:LYS:O	1.89	0.72
1:A:567:VAL:O	1:A:571:LYS:HG3	1.90	0.72
1:A:359:GLU:O	1:A:362:CYS:CB	2.34	0.72
1:A:716:MET:SD	1:A:717:ARG:N	2.63	0.72
1:C:567:VAL:O	1:C:571:LYS:HG3	1.90	0.72
1:B:567:VAL:O	1:B:571:LYS:HG3	1.90	0.72
1:A:428:ARG:HD3	1:A:428:ARG:C	2.15	0.72
1:C:428:ARG:HD3	1:C:428:ARG:C	2.15	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:PHE:HE2	1:B:674:LEU:HD21	1.55	0.72
1:B:649:PHE:H	1:B:649:PHE:HD2	1.36	0.72
1:C:184:ASP:C	1:C:186:LEU:H	1.96	0.72
1:D:136:LEU:HB2	1:D:141:LYS:O	1.89	0.72
1:D:567:VAL:O	1:D:571:LYS:HG3	1.90	0.72
1:D:596:VAL:HG22	1:D:633:THR:CG2	2.13	0.72
1:B:515:LEU:O	1:B:518:VAL:N	2.23	0.72
1:A:498:GLN:C	1:A:499:ARG:HH11	1.98	0.72
1:A:515:LEU:O	1:A:518:VAL:N	2.23	0.72
1:C:596:VAL:CG1	1:C:628:ASN:O	2.35	0.72
1:D:580:PHE:CD2	1:D:678:LEU:HD22	2.24	0.72
1:B:428:ARG:HD3	1:B:428:ARG:C	2.15	0.72
1:B:678:LEU:O	1:B:678:LEU:HD12	1.90	0.72
1:C:716:MET:SD	1:C:717:ARG:N	2.63	0.72
1:D:521:LEU:HD13	1:D:521:LEU:C	2.15	0.72
1:D:587:PHE:HE2	1:D:674:LEU:HD21	1.55	0.72
1:B:655:PHE:HE2	1:A:536:GLU:HA	0.94	0.71
1:A:587:PHE:CE2	1:A:674:LEU:CD2	2.73	0.71
1:A:673:LEU:O	1:C:572:MET:SD	2.48	0.71
1:D:428:ARG:HD3	1:D:428:ARG:C	2.15	0.71
1:B:136:LEU:HB2	1:B:141:LYS:O	1.89	0.71
1:A:359:GLU:CA	1:A:362:CYS:HB3	2.20	0.71
1:A:394:SER:O	1:A:397:GLU:N	2.24	0.71
1:A:678:LEU:O	1:A:678:LEU:HD12	1.90	0.71
1:C:515:LEU:O	1:C:518:VAL:N	2.23	0.71
1:D:498:GLN:C	1:D:499:ARG:HH11	1.98	0.71
1:B:521:LEU:HD13	1:B:521:LEU:C	2.15	0.71
1:B:580:PHE:CD2	1:B:678:LEU:HD22	2.24	0.71
1:A:587:PHE:CE2	1:A:674:LEU:HD21	2.25	0.71
1:C:425:LYS:CB	1:C:429:PHE:HE2	2.03	0.71
1:B:394:SER:O	1:B:397:GLU:N	2.24	0.71
1:A:425:LYS:CB	1:A:429:PHE:HE2	2.03	0.71
1:C:587:PHE:CE2	1:C:674:LEU:CD2	2.74	0.71
1:B:636:GLU:HG2	1:B:649:PHE:CE1	2.26	0.71
1:D:425:LYS:CB	1:D:429:PHE:HE2	2.03	0.71
1:B:359:GLU:CA	1:B:362:CYS:HB3	2.20	0.71
1:B:716:MET:SD	1:B:717:ARG:N	2.63	0.71
1:C:498:GLN:C	1:C:499:ARG:HH11	1.98	0.71
1:C:521:LEU:C	1:C:521:LEU:HD13	2.15	0.71
1:C:587:PHE:O	1:C:591:PHE:HD1	1.74	0.71
1:C:678:LEU:O	1:C:678:LEU:HD12	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:TYR:HE1	1:D:242:ARG:HD2	1.55	0.71
1:D:559:PHE:CB	1:D:562:MET:HB2	2.21	0.71
1:D:587:PHE:CE2	1:D:674:LEU:CD2	2.74	0.71
1:B:425:LYS:CB	1:B:429:PHE:HE2	2.03	0.71
1:B:498:GLN:C	1:B:499:ARG:HH11	1.98	0.71
1:D:402:SER:OG	1:D:699:LEU:HD21	1.91	0.71
1:D:515:LEU:O	1:D:518:VAL:N	2.23	0.71
1:A:372:TRP:CZ3	1:A:379:SER:OG	2.44	0.71
1:A:649:PHE:H	1:A:649:PHE:HD2	1.36	0.71
1:C:402:SER:OG	1:C:699:LEU:HD21	1.91	0.71
1:C:587:PHE:HE2	1:C:674:LEU:HD21	1.55	0.71
1:D:487:TYR:CE1	1:D:491:ARG:HG3	2.26	0.71
1:C:414:LEU:C	1:C:419:ASN:CB	2.64	0.71
1:D:394:SER:O	1:D:397:GLU:N	2.24	0.71
1:D:587:PHE:CE2	1:D:674:LEU:HD21	2.25	0.71
1:D:587:PHE:O	1:D:591:PHE:HD1	1.74	0.71
1:A:158:LEU:HD21	1:A:162:MET:HE2	1.73	0.71
1:C:359:GLU:CA	1:C:362:CYS:HB3	2.20	0.71
1:C:587:PHE:CE2	1:C:674:LEU:HD21	2.25	0.71
1:D:184:ASP:C	1:D:186:LEU:H	1.96	0.71
1:D:511:TYR:CE1	1:D:515:LEU:HD13	2.24	0.71
1:D:538:VAL:HG22	1:D:542:VAL:HG23	1.73	0.71
1:D:716:MET:SD	1:D:717:ARG:N	2.63	0.71
1:B:158:LEU:HD21	1:B:162:MET:HE2	1.72	0.70
1:B:402:SER:OG	1:B:699:LEU:HD21	1.91	0.70
1:B:587:PHE:CE2	1:B:674:LEU:CD2	2.74	0.70
1:D:569:ILE:HD13	1:D:569:ILE:C	2.16	0.70
1:A:429:PHE:H	1:A:429:PHE:HD2	1.39	0.70
1:A:587:PHE:HE2	1:A:674:LEU:HD21	1.55	0.70
1:C:538:VAL:HG22	1:C:542:VAL:HG23	1.73	0.70
1:C:569:ILE:C	1:C:569:ILE:HD13	2.16	0.70
1:B:414:LEU:C	1:B:419:ASN:CB	2.64	0.70
1:D:636:GLU:HG2	1:D:649:PHE:CE1	2.26	0.70
1:B:429:PHE:H	1:B:429:PHE:HD2	1.39	0.70
1:A:521:LEU:HD13	1:A:521:LEU:C	2.15	0.70
1:A:587:PHE:O	1:A:591:PHE:HD1	1.74	0.70
1:C:372:TRP:CZ3	1:C:379:SER:OG	2.44	0.70
1:C:487:TYR:CE1	1:C:491:ARG:HG3	2.26	0.70
1:D:678:LEU:O	1:D:678:LEU:HD12	1.90	0.70
1:B:487:TYR:CE1	1:B:491:ARG:HG3	2.26	0.70
1:A:198:TYR:HE1	1:A:242:ARG:HD2	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:636:GLU:HG2	1:A:649:PHE:CE1	2.26	0.70
1:C:647:LEU:HD12	1:C:648:GLU:CG	2.13	0.70
1:D:372:TRP:CZ3	1:D:379:SER:OG	2.44	0.70
1:D:429:PHE:H	1:D:429:PHE:HD2	1.39	0.70
1:A:402:SER:OG	1:A:699:LEU:HD21	1.91	0.70
1:B:306:THR:HG23	1:B:351:TYR:CE1	2.26	0.70
1:A:487:TYR:CE1	1:A:491:ARG:HG3	2.26	0.70
1:A:647:LEU:CD1	1:A:648:GLU:HG3	2.12	0.70
1:C:394:SER:O	1:C:397:GLU:N	2.24	0.70
1:D:306:THR:HG23	1:D:351:TYR:CE1	2.27	0.70
1:D:414:LEU:C	1:D:419:ASN:CB	2.64	0.70
1:B:559:PHE:CB	1:B:562:MET:HB2	2.21	0.70
1:A:414:LEU:C	1:A:419:ASN:CB	2.64	0.70
1:D:158:LEU:HD21	1:D:162:MET:HE2	1.73	0.70
1:B:198:TYR:HE1	1:B:242:ARG:HD2	1.55	0.70
1:B:436:PHE:O	1:B:440:VAL:HG23	1.92	0.70
1:A:559:PHE:CB	1:A:562:MET:HB2	2.21	0.70
1:C:306:THR:HG23	1:C:351:TYR:CE1	2.26	0.70
1:D:359:GLU:CA	1:D:362:CYS:HB3	2.20	0.70
1:B:587:PHE:CE2	1:B:674:LEU:HD21	2.25	0.69
1:A:569:ILE:HD13	1:A:569:ILE:C	2.16	0.69
1:C:559:PHE:CB	1:C:562:MET:HB2	2.21	0.69
1:B:372:TRP:CZ3	1:B:379:SER:OG	2.44	0.69
1:B:569:ILE:C	1:B:569:ILE:HD13	2.16	0.69
1:C:158:LEU:HD21	1:C:162:MET:HE2	1.72	0.69
1:C:685:THR:C	1:C:688:LYS:H	1.97	0.69
1:B:538:VAL:HG22	1:B:542:VAL:HG23	1.73	0.69
1:C:428:ARG:CD	1:C:429:PHE:CD2	2.76	0.69
1:C:681:LEU:HD21	1:C:682:MET:SD	2.32	0.69
1:D:242:ARG:N	1:D:243:PRO:HA	1.98	0.69
1:B:587:PHE:O	1:B:591:PHE:HD1	1.74	0.69
1:A:306:THR:HG23	1:A:351:TYR:CE1	2.26	0.69
1:A:538:VAL:HG22	1:A:542:VAL:HG23	1.73	0.69
1:C:429:PHE:H	1:C:429:PHE:HD2	1.39	0.69
1:C:647:LEU:HD11	1:D:635:LEU:HD11	1.74	0.69
1:C:647:LEU:CD1	1:C:648:GLU:HG3	2.12	0.69
1:D:428:ARG:HD3	1:D:429:PHE:HB3	1.74	0.69
1:C:436:PHE:O	1:C:440:VAL:HG23	1.92	0.69
1:A:436:PHE:O	1:A:440:VAL:HG23	1.92	0.69
1:C:636:GLU:HG2	1:C:649:PHE:CE1	2.26	0.69
1:D:436:PHE:O	1:D:440:VAL:HG23	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:428:ARG:CD	1:B:429:PHE:CD2	2.76	0.69
1:B:681:LEU:HD21	1:B:682:MET:SD	2.32	0.69
1:A:596:VAL:CG1	1:A:628:ASN:O	2.35	0.69
1:A:672:ILE:O	1:A:676:ASN:OD1	2.11	0.69
1:C:668:ILE:HD12	1:C:668:ILE:C	2.18	0.69
1:C:681:LEU:HD22	1:C:682:MET:N	2.08	0.69
1:A:428:ARG:HG2	1:A:428:ARG:NH1	2.07	0.69
1:A:428:ARG:CD	1:A:429:PHE:CD2	2.76	0.69
1:A:668:ILE:HD12	1:A:668:ILE:C	2.18	0.69
1:C:346:ILE:HG12	1:C:412:MET:CA	2.23	0.69
1:C:428:ARG:HD3	1:C:429:PHE:HB3	1.74	0.69
1:B:346:ILE:HG12	1:B:412:MET:CA	2.23	0.69
1:B:681:LEU:HD22	1:B:682:MET:N	2.08	0.69
1:D:681:LEU:HD21	1:D:682:MET:SD	2.32	0.69
1:B:660:ILE:HG13	1:B:661:ILE:N	2.09	0.68
1:A:428:ARG:HD3	1:A:429:PHE:HB3	1.74	0.68
1:A:681:LEU:HD22	1:A:682:MET:N	2.08	0.68
1:D:428:ARG:CD	1:D:429:PHE:CD2	2.76	0.68
1:D:681:LEU:HD22	1:D:682:MET:N	2.08	0.68
1:B:310:ASN:HB2	1:B:351:TYR:OH	1.94	0.68
1:B:642:ILE:CD1	1:D:647:LEU:HD23	2.23	0.68
1:A:647:LEU:HD23	1:C:642:ILE:CD1	2.22	0.68
1:A:647:LEU:HD23	1:C:642:ILE:HD11	1.74	0.68
1:A:660:ILE:HG13	1:A:661:ILE:N	2.09	0.68
1:A:681:LEU:HD21	1:A:682:MET:SD	2.32	0.68
1:C:462:PRO:HB2	1:C:464:LYS:O	1.94	0.68
1:D:668:ILE:HD12	1:D:668:ILE:C	2.18	0.68
1:C:302:THR:O	1:C:306:THR:HB	1.94	0.68
1:B:647:LEU:HD12	1:B:648:GLU:CG	2.13	0.68
1:B:668:ILE:HD12	1:B:668:ILE:C	2.18	0.68
1:A:647:LEU:HD12	1:A:648:GLU:CG	2.13	0.68
1:B:596:VAL:CG1	1:B:628:ASN:O	2.35	0.68
1:A:346:ILE:HG12	1:A:412:MET:CA	2.23	0.68
1:A:462:PRO:HB2	1:A:464:LYS:O	1.93	0.68
1:D:647:LEU:CD1	1:D:648:GLU:HG3	2.12	0.68
1:B:601:ASP:N	1:B:652:ASN:HD21	1.92	0.68
1:A:302:THR:O	1:A:306:THR:HB	1.94	0.68
1:B:672:ILE:O	1:B:676:ASN:OD1	2.12	0.68
1:D:310:ASN:HB2	1:D:351:TYR:OH	1.93	0.68
1:D:596:VAL:CG1	1:D:628:ASN:O	2.35	0.68
1:B:428:ARG:HD3	1:B:429:PHE:HB3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:676:ASN:HB2	1:A:572:MET:HE1	1.74	0.68
1:C:516:PHE:HE2	1:C:554:TYR:HD2	0.76	0.68
1:A:310:ASN:HB2	1:A:351:TYR:OH	1.93	0.67
1:A:374:TYR:O	1:A:377:VAL:N	2.26	0.67
1:A:671:TYR:O	1:A:675:LEU:HB2	1.94	0.67
1:C:428:ARG:HG2	1:C:428:ARG:NH1	2.07	0.67
1:C:310:ASN:HB2	1:C:351:TYR:HH	1.59	0.67
1:C:374:TYR:O	1:C:377:VAL:N	2.26	0.67
1:C:601:ASP:N	1:C:652:ASN:HD21	1.92	0.67
1:D:346:ILE:HG12	1:D:412:MET:CA	2.23	0.67
1:D:462:PRO:HB2	1:D:464:LYS:O	1.94	0.67
1:B:596:VAL:HG22	1:B:633:THR:CG2	2.13	0.67
1:B:601:ASP:H	1:B:652:ASN:HD21	1.42	0.67
1:D:671:TYR:O	1:D:675:LEU:HB2	1.94	0.67
1:A:560:GLN:NE2	1:A:697:TRP:CE3	2.61	0.67
1:D:280:ARG:HG2	1:D:284:GLY:O	1.95	0.67
1:B:685:THR:C	1:B:688:LYS:H	1.97	0.67
1:A:685:THR:C	1:A:688:LYS:H	1.97	0.67
1:D:302:THR:O	1:D:306:THR:HB	1.94	0.67
1:B:718:LYS:O	1:B:719:ALA:HB2	1.95	0.67
1:A:580:PHE:HD2	1:C:565:TYR:OH	1.70	0.67
1:A:601:ASP:H	1:A:652:ASN:HD21	1.42	0.67
1:C:239:THR:HB	1:C:243:PRO:HB3	1.76	0.67
1:C:426:TRP:CD1	1:C:430:VAL:CG1	2.77	0.67
1:C:596:VAL:HG22	1:C:633:THR:CG2	2.13	0.67
1:C:660:ILE:HG13	1:C:661:ILE:N	2.09	0.67
1:B:374:TYR:O	1:B:377:VAL:N	2.26	0.67
1:B:462:PRO:HB2	1:B:464:LYS:O	1.94	0.67
1:B:302:THR:O	1:B:306:THR:HB	1.94	0.67
1:B:498:GLN:CB	1:B:499:ARG:NH1	2.58	0.67
1:A:239:THR:HB	1:A:243:PRO:HB3	1.76	0.67
1:A:601:ASP:N	1:A:652:ASN:HD21	1.92	0.67
1:C:198:TYR:HE1	1:C:242:ARG:HD2	1.56	0.67
1:C:280:ARG:HG2	1:C:284:GLY:O	1.95	0.67
1:C:310:ASN:HB2	1:C:351:TYR:OH	1.94	0.67
1:D:498:GLN:CB	1:D:499:ARG:NH1	2.58	0.66
1:B:539:ALA:HB3	1:D:655:PHE:CE1	1.88	0.66
1:A:426:TRP:CD1	1:A:430:VAL:CG1	2.77	0.66
1:C:462:PRO:HB2	1:C:463:TYR:C	2.20	0.66
1:D:239:THR:HB	1:D:243:PRO:HB3	1.76	0.66
1:D:601:ASP:H	1:D:652:ASN:HD21	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:660:ILE:HG13	1:D:661:ILE:N	2.09	0.66
1:B:374:TYR:CB	1:D:235:PHE:HZ	2.07	0.66
1:B:599:ILE:HD11	1:B:628:ASN:CB	2.25	0.66
1:B:671:TYR:O	1:B:675:LEU:HB2	1.94	0.66
1:D:426:TRP:CD1	1:D:430:VAL:CG1	2.77	0.66
1:A:671:TYR:O	1:A:675:LEU:CD2	2.41	0.66
1:C:669:LEU:HD23	1:C:669:LEU:C	2.21	0.66
1:D:669:LEU:HD23	1:D:669:LEU:C	2.21	0.66
1:B:142:ARG:HD3	1:B:183:THR:HG21	1.78	0.66
1:B:426:TRP:CD1	1:B:430:VAL:CG1	2.78	0.66
1:B:693:SER:OG	1:B:696:ILE:CG2	2.44	0.66
1:A:718:LYS:O	1:A:719:ALA:HB2	1.95	0.66
1:C:428:ARG:HG3	1:C:429:PHE:CD2	2.31	0.66
1:D:142:ARG:HD3	1:D:183:THR:HG21	1.78	0.66
1:D:718:LYS:O	1:D:719:ALA:HB2	1.95	0.66
1:B:397:GLU:HA	1:B:400:ALA:HB3	1.78	0.66
1:B:462:PRO:HB2	1:B:463:TYR:C	2.20	0.66
1:B:528:VAL:O	1:B:532:SER:OG	2.14	0.66
1:B:599:ILE:HD11	1:B:628:ASN:HA	1.77	0.66
1:A:386:CYS:CB	1:A:395:VAL:HG23	2.26	0.66
1:C:671:TYR:O	1:C:675:LEU:HB2	1.94	0.66
1:A:498:GLN:CB	1:A:499:ARG:NH1	2.58	0.66
1:A:693:SER:OG	1:A:696:ILE:CG2	2.44	0.66
1:D:462:PRO:HD2	1:D:464:LYS:H	1.60	0.66
1:A:599:ILE:HD11	1:A:628:ASN:HA	1.78	0.66
1:D:694:LYS:O	1:D:697:TRP:HE3	1.79	0.66
1:B:310:ASN:HB2	1:B:351:TYR:HH	1.59	0.66
1:B:462:PRO:HD2	1:B:464:LYS:H	1.60	0.66
1:A:310:ASN:HB2	1:A:351:TYR:HH	1.59	0.66
1:C:671:TYR:O	1:C:675:LEU:CD2	2.41	0.66
1:C:694:LYS:O	1:C:697:TRP:HE3	1.79	0.66
1:D:462:PRO:HB2	1:D:463:TYR:C	2.20	0.66
1:D:599:ILE:HD11	1:D:628:ASN:CB	2.25	0.66
1:A:599:ILE:HD11	1:A:628:ASN:CB	2.25	0.66
1:A:669:LEU:HD23	1:A:669:LEU:C	2.21	0.66
1:C:386:CYS:CB	1:C:395:VAL:HG23	2.26	0.66
1:C:589:PHE:O	1:C:589:PHE:HD2	1.79	0.66
1:D:428:ARG:HG3	1:D:429:PHE:CD2	2.31	0.66
1:D:516:PHE:HE2	1:D:554:TYR:HD2	0.76	0.66
1:D:589:PHE:O	1:D:589:PHE:HD2	1.79	0.66
1:D:601:ASP:N	1:D:652:ASN:HD21	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:ARG:N	1:B:243:PRO:HA	1.98	0.65
1:A:280:ARG:HG2	1:A:284:GLY:O	1.95	0.65
1:A:372:TRP:CZ3	1:A:379:SER:CB	2.79	0.65
1:A:462:PRO:HB2	1:A:463:TYR:C	2.20	0.65
1:C:397:GLU:HA	1:C:400:ALA:HB3	1.78	0.65
1:C:498:GLN:CB	1:C:499:ARG:NH1	2.58	0.65
1:C:498:GLN:CB	1:C:499:ARG:HH11	2.09	0.65
1:A:356:GLU:CA	1:A:366:SER:OG	2.44	0.65
1:C:599:ILE:HD11	1:C:628:ASN:CB	2.25	0.65
1:D:386:CYS:CB	1:D:395:VAL:HG23	2.26	0.65
1:D:528:VAL:O	1:D:532:SER:OG	2.14	0.65
1:B:400:ALA:O	1:B:402:SER:HB2	1.96	0.65
1:C:462:PRO:HD2	1:C:464:LYS:H	1.60	0.65
1:D:428:ARG:HG2	1:D:428:ARG:NH1	2.07	0.65
1:B:239:THR:CB	1:B:243:PRO:CB	2.75	0.65
1:B:280:ARG:HG2	1:B:284:GLY:O	1.95	0.65
1:A:142:ARG:HD3	1:A:183:THR:HG21	1.78	0.65
1:A:428:ARG:HG3	1:A:429:PHE:CD2	2.31	0.65
1:A:573:ILE:HD13	1:A:577:LEU:HD23	1.78	0.65
1:A:694:LYS:O	1:A:697:TRP:HE3	1.79	0.65
1:C:558:GLY:HA3	1:C:697:TRP:CD1	2.31	0.65
1:C:601:ASP:H	1:C:652:ASN:HD21	1.42	0.65
1:D:498:GLN:CB	1:D:499:ARG:HH11	2.09	0.65
1:B:428:ARG:HG3	1:B:429:PHE:CD2	2.31	0.65
1:B:498:GLN:CB	1:B:499:ARG:HH11	2.09	0.65
1:C:573:ILE:HD13	1:C:577:LEU:HD23	1.78	0.65
1:D:356:GLU:CA	1:D:366:SER:OG	2.44	0.65
1:D:647:LEU:HD12	1:D:648:GLU:CG	2.13	0.65
1:B:239:THR:HB	1:B:243:PRO:HB3	1.76	0.65
1:B:671:TYR:O	1:B:675:LEU:CD2	2.41	0.65
1:B:694:LYS:O	1:B:697:TRP:HE3	1.79	0.65
1:C:142:ARG:HD3	1:C:183:THR:HG21	1.78	0.65
1:C:372:TRP:CZ3	1:C:379:SER:CB	2.80	0.65
1:C:693:SER:OG	1:C:696:ILE:CG2	2.44	0.65
1:C:718:LYS:O	1:C:719:ALA:HB2	1.95	0.65
1:D:372:TRP:CZ3	1:D:379:SER:CB	2.80	0.65
1:B:428:ARG:HG2	1:B:428:ARG:NH1	2.07	0.65
1:B:558:GLY:HA3	1:B:697:TRP:CD1	2.31	0.65
1:A:400:ALA:O	1:A:402:SER:HB2	1.96	0.65
1:B:669:LEU:HD23	1:B:669:LEU:C	2.21	0.65
1:D:158:LEU:HD21	1:D:162:MET:CE	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:239:THR:CB	1:D:243:PRO:CB	2.75	0.65
1:B:356:GLU:CA	1:B:366:SER:OG	2.44	0.65
1:B:386:CYS:CB	1:B:395:VAL:HG23	2.26	0.65
1:A:462:PRO:HD2	1:A:464:LYS:H	1.60	0.65
1:A:498:GLN:CB	1:A:499:ARG:HH11	2.09	0.65
1:D:400:ALA:O	1:D:402:SER:HB2	1.96	0.65
1:D:693:SER:OG	1:D:696:ILE:CG2	2.44	0.65
1:B:158:LEU:HD21	1:B:162:MET:CE	2.27	0.65
1:B:589:PHE:O	1:B:589:PHE:HD2	1.79	0.65
1:C:487:TYR:CD1	1:C:491:ARG:HG3	2.32	0.65
1:C:647:LEU:HD23	1:D:642:ILE:HD12	1.78	0.65
1:B:372:TRP:CZ3	1:B:379:SER:CB	2.80	0.64
1:A:158:LEU:HD21	1:A:162:MET:CE	2.27	0.64
1:A:240:LYS:HZ2	1:A:240:LYS:HB3	1.62	0.64
1:C:400:ALA:O	1:C:402:SER:HB2	1.96	0.64
1:D:653:TYR:HD1	1:D:654:ASP:N	1.95	0.64
1:B:653:TYR:HD1	1:B:654:ASP:N	1.95	0.64
1:A:428:ARG:CD	1:A:429:PHE:CB	2.76	0.64
1:A:528:VAL:O	1:A:532:SER:OG	2.14	0.64
1:C:528:VAL:O	1:C:532:SER:OG	2.14	0.64
1:D:558:GLY:HA3	1:D:697:TRP:CD1	2.31	0.64
1:B:381:LEU:HA	1:B:753:UNK:O	1.98	0.64
1:B:448:PHE:HD2	1:B:448:PHE:O	1.81	0.64
1:A:558:GLY:HA3	1:A:697:TRP:CD1	2.31	0.64
1:A:589:PHE:O	1:A:589:PHE:HD2	1.79	0.64
1:C:239:THR:CB	1:C:243:PRO:CB	2.75	0.64
1:C:448:PHE:HD2	1:C:448:PHE:O	1.80	0.64
1:D:487:TYR:HD1	1:D:487:TYR:O	1.81	0.64
1:B:487:TYR:CD1	1:B:491:ARG:HG3	2.32	0.64
1:A:188:GLN:HE21	1:A:188:GLN:H	1.46	0.64
1:A:381:LEU:HA	1:A:753:UNK:O	1.98	0.64
1:A:653:TYR:HD1	1:A:654:ASP:N	1.95	0.64
1:B:487:TYR:O	1:B:487:TYR:HD1	1.81	0.64
1:A:239:THR:CB	1:A:243:PRO:CB	2.75	0.64
1:C:356:GLU:CA	1:C:366:SER:OG	2.44	0.64
1:C:381:LEU:HA	1:C:753:UNK:O	1.98	0.64
1:C:681:LEU:CD1	1:C:682:MET:HG2	2.28	0.64
1:D:521:LEU:HD13	1:D:522:PHE:N	2.13	0.64
1:D:397:GLU:HA	1:D:400:ALA:HB3	1.78	0.64
1:B:521:LEU:HD13	1:B:522:PHE:N	2.13	0.64
1:B:565:TYR:HH	1:D:580:PHE:HD2	1.46	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:158:LEU:HD21	1:C:162:MET:CE	2.27	0.64
1:B:638:PHE:CE1	1:B:642:ILE:HD11	2.33	0.64
1:A:681:LEU:CD1	1:A:682:MET:HG2	2.28	0.64
1:C:428:ARG:CD	1:C:429:PHE:CB	2.76	0.64
1:B:573:ILE:HD13	1:B:577:LEU:HD23	1.78	0.64
1:A:397:GLU:HA	1:A:400:ALA:HB3	1.78	0.64
1:A:487:TYR:CD1	1:A:491:ARG:HG3	2.32	0.64
1:A:521:LEU:HD13	1:A:522:PHE:N	2.13	0.64
1:D:573:ILE:HD13	1:D:577:LEU:HD23	1.78	0.64
1:D:671:TYR:O	1:D:675:LEU:CD2	2.41	0.64
1:A:394:SER:O	1:A:395:VAL:C	2.41	0.64
1:C:487:TYR:O	1:C:487:TYR:HD1	1.81	0.64
1:C:653:TYR:HD1	1:C:654:ASP:N	1.95	0.64
1:D:188:GLN:HE21	1:D:188:GLN:H	1.46	0.64
1:D:638:PHE:CE1	1:D:642:ILE:HD11	2.33	0.64
1:D:681:LEU:CD1	1:D:682:MET:HG2	2.28	0.64
1:B:188:GLN:HE21	1:B:188:GLN:H	1.46	0.63
1:B:700:GLN:O	1:B:704:THR:CG2	2.41	0.63
1:A:487:TYR:HD1	1:A:487:TYR:O	1.81	0.63
1:C:188:GLN:HE21	1:C:188:GLN:H	1.46	0.63
1:B:240:LYS:HZ2	1:B:240:LYS:HB3	1.63	0.63
1:A:306:THR:O	1:A:351:TYR:CZ	2.52	0.63
1:A:462:PRO:HD2	1:A:463:TYR:CA	2.28	0.63
1:D:374:TYR:O	1:D:377:VAL:N	2.26	0.63
1:D:428:ARG:CD	1:D:429:PHE:CB	2.76	0.63
1:D:487:TYR:CD1	1:D:491:ARG:HG3	2.32	0.63
1:A:448:PHE:O	1:A:448:PHE:HD2	1.81	0.63
1:A:638:PHE:CE1	1:A:642:ILE:HD11	2.33	0.63
1:C:521:LEU:HD13	1:C:522:PHE:N	2.13	0.63
1:C:638:PHE:CE1	1:C:642:ILE:HD11	2.33	0.63
1:B:239:THR:OG1	1:B:241:GLY:CA	2.47	0.63
1:B:394:SER:O	1:B:395:VAL:C	2.41	0.63
1:B:462:PRO:HD2	1:B:463:TYR:CA	2.28	0.63
1:A:142:ARG:CD	1:A:183:THR:HG21	2.29	0.63
1:D:306:THR:O	1:D:351:TYR:CZ	2.52	0.63
1:D:428:ARG:CD	1:D:429:PHE:N	2.62	0.63
1:C:239:THR:HB	1:C:243:PRO:CB	2.29	0.63
1:B:142:ARG:CD	1:B:183:THR:HG21	2.29	0.63
1:A:372:TRP:HZ3	1:A:379:SER:CB	2.12	0.63
1:A:655:PHE:HE2	1:C:536:GLU:HA	0.89	0.63
1:C:372:TRP:HZ3	1:C:379:SER:CB	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ARG:CD	1:D:183:THR:HG21	2.29	0.63
1:D:239:THR:HB	1:D:243:PRO:CB	2.29	0.63
1:D:448:PHE:O	1:D:448:PHE:HD2	1.80	0.63
1:B:573:ILE:HG12	1:B:577:LEU:HD21	1.81	0.63
1:B:694:LYS:HD2	1:B:694:LYS:O	1.99	0.63
1:A:596:VAL:HG22	1:A:633:THR:CG2	2.13	0.63
1:D:381:LEU:HA	1:D:753:UNK:O	1.98	0.63
1:B:214:MET:HE3	1:B:218:THR:OG1	1.99	0.63
1:B:239:THR:HB	1:B:243:PRO:CB	2.29	0.63
1:B:515:LEU:CD2	1:B:551:ASN:ND2	2.62	0.63
1:C:306:THR:O	1:C:351:TYR:CZ	2.52	0.63
1:C:394:SER:O	1:C:395:VAL:C	2.41	0.63
1:D:401:TYR:N	1:D:402:SER:HB2	2.14	0.63
1:D:462:PRO:HD2	1:D:463:TYR:CA	2.28	0.63
1:A:158:LEU:HD22	1:A:158:LEU:O	1.99	0.63
1:C:158:LEU:O	1:C:158:LEU:HD22	1.99	0.63
1:C:462:PRO:HD2	1:C:463:TYR:CA	2.28	0.63
1:C:515:LEU:CD2	1:C:551:ASN:ND2	2.62	0.63
1:D:654:ASP:O	1:D:655:PHE:HB2	1.98	0.63
1:B:158:LEU:O	1:B:158:LEU:HD22	1.98	0.62
1:C:536:GLU:O	1:C:537:TYR:C	2.42	0.62
1:B:253:SER:HA	1:B:287:VAL:HG13	1.81	0.62
1:B:372:TRP:HZ3	1:B:379:SER:CB	2.12	0.62
1:B:654:ASP:O	1:B:655:PHE:HB2	1.98	0.62
1:B:681:LEU:CD1	1:B:682:MET:HG2	2.28	0.62
1:A:655:PHE:HZ	1:C:536:GLU:CA	1.67	0.62
1:C:654:ASP:O	1:C:655:PHE:HB2	1.98	0.62
1:D:158:LEU:O	1:D:158:LEU:HD22	1.99	0.62
1:D:214:MET:HE3	1:D:218:THR:OG1	1.99	0.62
1:D:515:LEU:CD2	1:D:551:ASN:ND2	2.62	0.62
1:D:599:ILE:HD11	1:D:628:ASN:HA	1.77	0.62
1:B:306:THR:O	1:B:351:TYR:CZ	2.52	0.62
1:B:640:PHE:CE1	1:B:667:VAL:CG2	2.80	0.62
1:A:198:TYR:CE1	1:A:242:ARG:CD	2.81	0.62
1:A:694:LYS:HD2	1:A:694:LYS:O	1.99	0.62
1:C:142:ARG:CD	1:C:183:THR:HG21	2.29	0.62
1:C:599:ILE:HD11	1:C:628:ASN:HA	1.77	0.62
1:D:573:ILE:HG12	1:D:577:LEU:HD21	1.81	0.62
1:B:536:GLU:O	1:B:537:TYR:C	2.42	0.62
1:A:536:GLU:O	1:A:537:TYR:C	2.42	0.62
1:D:372:TRP:HZ3	1:D:379:SER:CB	2.12	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:LEU:HD23	1:B:349:LEU:C	2.25	0.62
1:A:239:THR:OG1	1:A:241:GLY:CA	2.47	0.62
1:A:681:LEU:CD2	1:A:682:MET:HE2	2.19	0.62
1:A:428:ARG:CD	1:A:429:PHE:N	2.62	0.62
1:C:253:SER:HA	1:C:287:VAL:HG13	1.81	0.62
1:C:349:LEU:C	1:C:349:LEU:HD23	2.25	0.62
1:A:239:THR:HB	1:A:243:PRO:CB	2.29	0.62
1:A:349:LEU:HD23	1:A:349:LEU:C	2.25	0.62
1:C:214:MET:HE3	1:C:218:THR:OG1	1.99	0.62
1:C:428:ARG:CD	1:C:429:PHE:N	2.62	0.62
1:D:198:TYR:CE1	1:D:242:ARG:CD	2.81	0.62
1:B:320:HIS:HB3	1:B:323:LEU:HD23	1.82	0.62
1:B:401:TYR:N	1:B:402:SER:HB2	2.14	0.62
1:A:320:HIS:HB3	1:A:323:LEU:HD23	1.82	0.62
1:C:401:TYR:N	1:C:402:SER:HB2	2.14	0.62
1:C:461:PRO:O	1:C:533:GLN:CD	2.42	0.62
1:D:239:THR:OG1	1:D:241:GLY:CA	2.47	0.62
1:D:536:GLU:O	1:D:537:TYR:C	2.42	0.62
1:B:428:ARG:CD	1:B:429:PHE:N	2.62	0.62
1:A:401:TYR:N	1:A:402:SER:HB2	2.14	0.62
1:C:320:HIS:HB3	1:C:323:LEU:HD23	1.82	0.62
1:D:394:SER:O	1:D:395:VAL:C	2.41	0.62
1:A:214:MET:HE3	1:A:218:THR:OG1	1.99	0.61
1:A:654:ASP:O	1:A:655:PHE:HB2	1.98	0.61
1:C:198:TYR:CE1	1:C:242:ARG:CD	2.81	0.61
1:C:655:PHE:HE2	1:D:536:GLU:HA	1.60	0.61
1:C:676:ASN:ND2	1:C:676:ASN:H	1.98	0.61
1:C:681:LEU:CD2	1:C:682:MET:HE2	2.19	0.61
1:D:320:HIS:HB3	1:D:323:LEU:HD23	1.82	0.61
1:D:367:ARG:CG	1:D:367:ARG:HH11	2.14	0.61
1:A:418:LEU:O	1:A:422:LEU:HD12	2.00	0.61
1:A:573:ILE:HG12	1:A:577:LEU:HD21	1.81	0.61
1:C:647:LEU:HG	1:D:639:LYS:CD	2.30	0.61
1:D:694:LYS:HD2	1:D:694:LYS:O	1.99	0.61
1:B:428:ARG:CD	1:B:429:PHE:CB	2.76	0.61
1:B:487:TYR:HE1	1:B:491:ARG:CG	2.13	0.61
1:B:559:PHE:HB3	1:B:562:MET:N	2.15	0.61
1:A:665:ALA:HA	1:A:668:ILE:HG13	1.82	0.61
1:C:665:ALA:HA	1:C:668:ILE:HG13	1.82	0.61
1:D:253:SER:HA	1:D:287:VAL:HG13	1.81	0.61
1:D:349:LEU:HD23	1:D:349:LEU:C	2.25	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:665:ALA:HA	1:D:668:ILE:HG13	1.82	0.61
1:B:461:PRO:O	1:B:533:GLN:CD	2.42	0.61
1:A:701:ARG:HH11	1:A:701:ARG:CG	2.14	0.61
1:C:573:ILE:HG12	1:C:577:LEU:HD21	1.81	0.61
1:C:694:LYS:HD2	1:C:694:LYS:O	1.99	0.61
1:B:418:LEU:O	1:B:422:LEU:HD12	2.00	0.61
1:A:579:ARG:CG	1:A:579:ARG:HH11	2.14	0.61
1:C:239:THR:OG1	1:C:241:GLY:CA	2.47	0.61
1:B:374:TYR:CB	1:D:235:PHE:CE2	2.84	0.61
1:A:253:SER:HA	1:A:287:VAL:HG13	1.81	0.61
1:A:515:LEU:CD2	1:A:551:ASN:ND2	2.62	0.61
1:A:487:TYR:HE1	1:A:491:ARG:CG	2.13	0.61
1:A:700:GLN:O	1:A:704:THR:CG2	2.41	0.61
1:D:418:LEU:O	1:D:422:LEU:HD12	2.00	0.61
1:B:579:ARG:HH11	1:B:579:ARG:CG	2.14	0.61
1:C:142:ARG:NE	1:C:183:THR:CG2	2.64	0.61
1:D:142:ARG:NE	1:D:183:THR:CG2	2.64	0.61
1:D:487:TYR:HE1	1:D:491:ARG:CG	2.13	0.61
1:D:579:ARG:CG	1:D:579:ARG:HH11	2.14	0.61
1:A:142:ARG:NE	1:A:183:THR:CG2	2.64	0.61
1:A:367:ARG:CG	1:A:367:ARG:HH11	2.14	0.61
1:C:372:TRP:HZ3	1:C:379:SER:OG	1.84	0.61
1:C:647:LEU:CB	1:D:639:LYS:HE2	2.30	0.61
1:C:700:GLN:O	1:C:704:THR:CG2	2.41	0.61
1:D:242:ARG:HB3	1:D:243:PRO:O	2.01	0.61
1:A:580:PHE:CD2	1:C:565:TYR:OH	2.47	0.60
1:C:418:LEU:O	1:C:422:LEU:HD12	2.01	0.60
1:B:575:ARG:O	1:B:579:ARG:HD3	2.02	0.60
1:B:701:ARG:HH11	1:B:701:ARG:CG	2.14	0.60
1:C:242:ARG:HB3	1:C:243:PRO:O	2.01	0.60
1:C:579:ARG:HH11	1:C:579:ARG:CG	2.14	0.60
1:B:665:ALA:HA	1:B:668:ILE:HG13	1.82	0.60
1:A:421:LEU:HD23	1:A:421:LEU:O	2.01	0.60
1:B:142:ARG:NE	1:B:183:THR:CG2	2.64	0.60
1:B:382:TYR:N	1:B:753:UNK:O	2.33	0.60
1:B:559:PHE:HB2	1:B:562:MET:HB2	1.83	0.60
1:A:242:ARG:HB3	1:A:243:PRO:O	2.01	0.60
1:C:367:ARG:HH11	1:C:367:ARG:CG	2.14	0.60
1:B:367:ARG:HH11	1:B:367:ARG:CG	2.14	0.60
1:A:579:ARG:HA	1:C:562:MET:SD	2.41	0.60
1:C:575:ARG:O	1:C:579:ARG:HD3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:559:PHE:HB2	1:D:562:MET:HB2	1.83	0.60
1:B:184:ASP:C	1:B:186:LEU:N	2.59	0.60
1:B:571:LYS:O	1:B:575:ARG:HG2	2.02	0.60
1:C:487:TYR:HE1	1:C:491:ARG:CG	2.13	0.60
1:C:421:LEU:HD23	1:C:421:LEU:O	2.01	0.60
1:D:685:THR:C	1:D:688:LYS:H	1.97	0.60
1:B:242:ARG:HB3	1:B:243:PRO:O	2.01	0.60
1:B:655:PHE:CE1	1:A:539:ALA:N	2.69	0.60
1:A:571:LYS:O	1:A:575:ARG:HG2	2.02	0.60
1:A:652:ASN:O	1:A:653:TYR:HD2	1.85	0.60
1:A:559:PHE:HB3	1:A:562:MET:N	2.15	0.60
1:C:701:ARG:HH11	1:C:701:ARG:CG	2.14	0.60
1:D:596:VAL:HG21	1:D:630:LEU:HA	1.84	0.60
1:C:571:LYS:O	1:C:575:ARG:HG2	2.02	0.59
1:A:575:ARG:O	1:A:579:ARG:HD3	2.02	0.59
1:C:571:LYS:NZ	1:C:693:SER:OG	2.35	0.59
1:D:421:LEU:HD23	1:D:421:LEU:O	2.01	0.59
1:B:596:VAL:HG21	1:B:630:LEU:HA	1.84	0.59
1:C:652:ASN:O	1:C:653:TYR:CG	2.55	0.59
1:D:184:ASP:C	1:D:186:LEU:N	2.59	0.59
1:D:461:PRO:O	1:D:533:GLN:CD	2.42	0.59
1:B:421:LEU:O	1:B:421:LEU:HD23	2.01	0.59
1:B:658:VAL:HG13	1:A:543:PHE:HZ	1.64	0.59
1:A:426:TRP:HD1	1:A:430:VAL:CG1	2.15	0.59
1:A:652:ASN:O	1:A:653:TYR:CG	2.55	0.59
1:B:198:TYR:CE1	1:B:242:ARG:CD	2.81	0.59
1:A:559:PHE:HB2	1:A:562:MET:HB2	1.83	0.59
1:A:560:GLN:OE1	1:A:564:ILE:CD1	2.41	0.59
1:D:571:LYS:NZ	1:D:693:SER:OG	2.35	0.59
1:D:575:ARG:O	1:D:579:ARG:HD3	2.02	0.59
1:B:560:GLN:NE2	1:B:697:TRP:CE3	2.61	0.59
1:A:461:PRO:O	1:A:533:GLN:CD	2.42	0.59
1:A:596:VAL:HG21	1:A:630:LEU:HA	1.84	0.59
1:C:640:PHE:CE1	1:C:667:VAL:CG2	2.81	0.59
1:D:701:ARG:HH11	1:D:701:ARG:CG	2.14	0.59
1:B:158:LEU:CD2	1:B:162:MET:HE2	2.33	0.59
1:B:462:PRO:HG3	1:B:530:TYR:OH	2.03	0.59
1:B:571:LYS:NZ	1:B:693:SER:OG	2.35	0.59
1:A:571:LYS:NZ	1:A:693:SER:OG	2.35	0.59
1:D:246:TYR:CE1	1:D:248:GLY:CA	2.86	0.59
1:D:382:TYR:N	1:D:753:UNK:O	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:571:LYS:O	1:D:575:ARG:HG2	2.02	0.59
1:B:372:TRP:HZ3	1:B:379:SER:OG	1.84	0.59
1:C:246:TYR:CE1	1:C:248:GLY:CA	2.86	0.59
1:C:559:PHE:HB3	1:C:562:MET:N	2.15	0.59
1:D:372:TRP:HZ3	1:D:379:SER:OG	1.84	0.59
1:D:426:TRP:HD1	1:D:430:VAL:CG1	2.15	0.59
1:D:462:PRO:HG3	1:D:530:TYR:OH	2.03	0.59
1:A:599:ILE:HD11	1:A:628:ASN:HB2	1.85	0.59
1:A:306:THR:OG1	1:A:351:TYR:CD1	2.55	0.58
1:A:571:LYS:HZ3	1:A:693:SER:HB2	1.68	0.58
1:C:596:VAL:HG21	1:C:630:LEU:HA	1.84	0.58
1:D:652:ASN:O	1:D:653:TYR:CG	2.55	0.58
1:B:357:ILE:N	1:B:366:SER:HG	1.99	0.58
1:A:462:PRO:HG3	1:A:530:TYR:OH	2.03	0.58
1:C:399:ILE:HD12	1:C:418:LEU:HD13	1.85	0.58
1:D:559:PHE:HB3	1:D:562:MET:N	2.15	0.58
1:B:599:ILE:HD11	1:B:628:ASN:HB2	1.85	0.58
1:C:396:LEU:HD11	1:C:418:LEU:HD23	1.77	0.58
1:C:560:GLN:NE2	1:C:697:TRP:CE3	2.61	0.58
1:B:246:TYR:CE1	1:B:248:GLY:CA	2.86	0.58
1:C:462:PRO:HG3	1:C:530:TYR:OH	2.03	0.58
1:D:396:LEU:HD11	1:D:418:LEU:HD23	1.77	0.58
1:B:426:TRP:HD1	1:B:430:VAL:CG1	2.16	0.58
1:A:487:TYR:CE1	1:A:491:ARG:CD	2.85	0.58
1:A:537:TYR:O	1:A:540:SER:HB2	2.04	0.58
1:C:428:ARG:CD	1:C:429:PHE:HB3	2.34	0.58
1:C:559:PHE:HB2	1:C:562:MET:HB2	1.83	0.58
1:D:587:PHE:CE2	1:D:674:LEU:HD23	2.39	0.58
1:A:158:LEU:CD2	1:A:162:MET:HE2	2.33	0.58
1:D:357:ILE:N	1:D:366:SER:HG	1.99	0.58
1:B:652:ASN:O	1:B:653:TYR:CG	2.55	0.58
1:B:681:LEU:CD2	1:B:682:MET:HE2	2.19	0.58
1:A:184:ASP:C	1:A:186:LEU:N	2.59	0.58
1:A:246:TYR:CE1	1:A:248:GLY:CA	2.86	0.58
1:A:428:ARG:CD	1:A:429:PHE:HB3	2.34	0.58
1:B:125:ASN:ND2	1:B:128:GLU:HG2	2.18	0.58
1:B:487:TYR:CE1	1:B:491:ARG:CD	2.85	0.58
1:C:125:ASN:ND2	1:C:128:GLU:HG2	2.18	0.58
1:C:158:LEU:CD2	1:C:162:MET:HE2	2.33	0.58
1:C:426:TRP:HD1	1:C:430:VAL:CG1	2.15	0.58
1:D:158:LEU:CD2	1:D:162:MET:HE2	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:399:ILE:HD12	1:D:418:LEU:HD13	1.85	0.58
1:D:487:TYR:CE1	1:D:491:ARG:CD	2.85	0.58
1:B:557:ARG:NH2	1:B:700:GLN:HG3	2.19	0.58
1:A:357:ILE:N	1:A:366:SER:HG	2.02	0.58
1:D:310:ASN:HB2	1:D:351:TYR:HH	1.69	0.58
1:D:560:GLN:NE2	1:D:697:TRP:CE3	2.61	0.58
1:A:125:ASN:ND2	1:A:128:GLU:HG2	2.18	0.58
1:C:557:ARG:NH2	1:C:700:GLN:HG3	2.19	0.58
1:C:564:ILE:HD12	1:C:564:ILE:N	2.19	0.58
1:C:587:PHE:CE2	1:C:674:LEU:HD23	2.39	0.58
1:B:462:PRO:CB	1:B:464:LYS:O	2.52	0.57
1:A:564:ILE:HD12	1:A:564:ILE:N	2.19	0.57
1:C:537:TYR:O	1:C:540:SER:HB2	2.04	0.57
1:D:239:THR:OG1	1:D:243:PRO:CB	2.45	0.57
1:D:462:PRO:CB	1:D:464:LYS:O	2.52	0.57
1:D:537:TYR:O	1:D:540:SER:HB2	2.04	0.57
1:B:587:PHE:CE2	1:B:674:LEU:HD23	2.39	0.57
1:A:557:ARG:NH2	1:A:700:GLN:HG3	2.19	0.57
1:C:175:LEU:O	1:C:179:VAL:HG23	2.04	0.57
1:B:560:GLN:C	1:B:564:ILE:HD13	2.29	0.57
1:A:159:LEU:O	1:A:163:LEU:HD22	2.04	0.57
1:A:462:PRO:CB	1:A:464:LYS:O	2.52	0.57
1:D:125:ASN:ND2	1:D:128:GLU:HG2	2.18	0.57
1:A:245:PHE:CB	1:C:376:PRO:CB	2.67	0.57
1:A:694:LYS:HD3	1:A:697:TRP:CZ3	2.40	0.57
1:C:240:LYS:HZ2	1:C:240:LYS:HB3	1.68	0.57
1:C:352:ILE:O	1:C:367:ARG:HD3	2.05	0.57
1:C:357:ILE:N	1:C:366:SER:HG	1.98	0.57
1:D:557:ARG:NH2	1:D:700:GLN:HG3	2.19	0.57
1:D:700:GLN:O	1:D:704:THR:CG2	2.41	0.57
1:B:537:TYR:O	1:B:540:SER:HB2	2.04	0.57
1:A:382:TYR:N	1:A:753:UNK:O	2.33	0.57
1:A:399:ILE:HD12	1:A:418:LEU:HD13	1.85	0.57
1:C:404:SER:C	1:C:406:THR:H	2.12	0.57
1:C:429:PHE:CD2	1:C:430:VAL:N	2.73	0.57
1:C:560:GLN:OE1	1:C:564:ILE:CD1	2.41	0.57
1:D:159:LEU:O	1:D:163:LEU:HD22	2.04	0.57
1:B:242:ARG:HH11	1:B:242:ARG:CG	2.17	0.57
1:A:404:SER:C	1:A:406:THR:H	2.12	0.57
1:C:159:LEU:O	1:C:163:LEU:HD22	2.04	0.57
1:C:694:LYS:HD3	1:C:697:TRP:CZ3	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:121:VAL:HG22	1:D:172:THR:CG2	2.33	0.57
1:B:536:GLU:HA	1:D:655:PHE:HE2	0.76	0.57
1:B:694:LYS:HD3	1:B:697:TRP:CZ3	2.40	0.57
1:A:429:PHE:N	1:A:429:PHE:CD2	2.73	0.57
1:D:175:LEU:O	1:D:179:VAL:HG23	2.04	0.57
1:D:353:LEU:CA	1:D:367:ARG:HD3	2.26	0.57
1:D:429:PHE:CD2	1:D:430:VAL:N	2.73	0.57
1:B:649:PHE:CD2	1:B:649:PHE:N	2.73	0.57
1:A:429:PHE:CD2	1:A:430:VAL:N	2.73	0.57
1:A:587:PHE:CE2	1:A:674:LEU:HD23	2.39	0.57
1:C:184:ASP:C	1:C:186:LEU:N	2.59	0.57
1:C:592:SER:CB	1:C:637:LEU:HD12	2.35	0.57
1:D:694:LYS:HD3	1:D:697:TRP:CZ3	2.40	0.57
1:B:399:ILE:HD12	1:B:418:LEU:HD13	1.85	0.57
1:C:205:LEU:HA	1:C:220:LEU:HD23	1.86	0.57
1:C:665:ALA:O	1:C:668:ILE:HG13	2.05	0.57
1:D:404:SER:C	1:D:406:THR:H	2.12	0.57
1:D:599:ILE:HD11	1:D:628:ASN:HB2	1.85	0.57
1:D:681:LEU:CD2	1:D:682:MET:HE2	2.19	0.57
1:B:159:LEU:O	1:B:163:LEU:HD22	2.04	0.57
1:A:372:TRP:HZ3	1:A:379:SER:OG	1.84	0.57
1:A:640:PHE:CE1	1:A:667:VAL:CG2	2.81	0.57
1:C:429:PHE:N	1:C:429:PHE:CD2	2.73	0.57
1:C:462:PRO:CB	1:C:464:LYS:O	2.52	0.57
1:C:599:ILE:HD11	1:C:628:ASN:HB2	1.85	0.57
1:C:652:ASN:OD1	1:C:653:TYR:N	2.38	0.57
1:D:560:GLN:C	1:D:564:ILE:HD13	2.29	0.57
1:A:175:LEU:O	1:A:179:VAL:HG23	2.04	0.56
1:A:240:LYS:H	1:A:242:ARG:N	2.03	0.56
1:A:242:ARG:CG	1:A:242:ARG:HH11	2.17	0.56
1:A:673:LEU:HD13	1:C:572:MET:CG	2.35	0.56
1:C:652:ASN:O	1:C:653:TYR:HD2	1.85	0.56
1:B:543:PHE:HZ	1:D:658:VAL:HG13	1.66	0.56
1:B:579:ARG:HG2	1:B:579:ARG:NH1	2.20	0.56
1:B:647:LEU:HD23	1:A:642:ILE:HD11	1.87	0.56
1:A:652:ASN:OD1	1:A:653:TYR:N	2.38	0.56
1:C:240:LYS:HB3	1:C:240:LYS:NZ	2.20	0.56
1:D:247:PHE:CE1	1:D:254:LEU:HD13	2.40	0.56
1:D:429:PHE:N	1:D:429:PHE:CD2	2.73	0.56
1:B:240:LYS:HB3	1:B:240:LYS:NZ	2.20	0.56
1:B:428:ARG:CD	1:B:429:PHE:HB3	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:429:PHE:N	1:B:429:PHE:CD2	2.73	0.56
1:B:429:PHE:CD2	1:B:430:VAL:N	2.73	0.56
1:B:564:ILE:N	1:B:564:ILE:HD12	2.19	0.56
1:A:247:PHE:CE1	1:A:254:LEU:HD13	2.40	0.56
1:A:592:SER:CB	1:A:637:LEU:HD12	2.35	0.56
1:C:247:PHE:CE1	1:C:254:LEU:HD13	2.40	0.56
1:C:681:LEU:HD22	1:C:681:LEU:C	2.30	0.56
1:D:652:ASN:O	1:D:653:TYR:HD2	1.85	0.56
1:D:665:ALA:O	1:D:668:ILE:HG13	2.05	0.56
1:D:681:LEU:HD22	1:D:681:LEU:C	2.30	0.56
1:B:175:LEU:O	1:B:179:VAL:HG23	2.04	0.56
1:B:352:ILE:O	1:B:367:ARG:HD3	2.05	0.56
1:B:447:ILE:HD12	1:B:447:ILE:N	2.21	0.56
1:A:286:THR:H	1:A:289:HIS:CD2	2.24	0.56
1:D:242:ARG:HH11	1:D:242:ARG:CG	2.17	0.56
1:D:306:THR:OG1	1:D:351:TYR:CD1	2.55	0.56
1:D:352:ILE:O	1:D:367:ARG:HD3	2.05	0.56
1:B:180:ALA:O	1:B:185:SER:N	2.39	0.56
1:B:247:PHE:CE1	1:B:254:LEU:HD13	2.40	0.56
1:B:592:SER:CB	1:B:637:LEU:HD12	2.35	0.56
1:C:579:ARG:NH1	1:C:579:ARG:HG2	2.20	0.56
1:D:205:LEU:HA	1:D:220:LEU:HD23	1.86	0.56
1:D:652:ASN:OD1	1:D:653:TYR:N	2.38	0.56
1:B:353:LEU:O	1:B:367:ARG:HG2	2.06	0.56
1:A:240:LYS:HB3	1:A:240:LYS:NZ	2.20	0.56
1:A:579:ARG:NH1	1:A:579:ARG:HG2	2.20	0.56
1:C:655:PHE:CZ	1:D:536:GLU:C	2.83	0.56
1:D:353:LEU:O	1:D:367:ARG:HG2	2.06	0.56
1:B:205:LEU:HA	1:B:220:LEU:HD23	1.86	0.56
1:B:404:SER:C	1:B:406:THR:H	2.12	0.56
1:B:652:ASN:OD1	1:B:653:TYR:N	2.38	0.56
1:B:665:ALA:O	1:B:668:ILE:HG13	2.05	0.56
1:A:352:ILE:O	1:A:367:ARG:HD3	2.05	0.56
1:C:383:ASP:CB	1:C:384:LEU:HA	2.36	0.56
1:D:240:LYS:H	1:D:242:ARG:N	2.03	0.56
1:D:349:LEU:HD23	1:D:353:LEU:HD12	1.88	0.56
1:D:564:ILE:HD12	1:D:564:ILE:N	2.19	0.56
1:B:240:LYS:H	1:B:242:ARG:N	2.03	0.56
1:B:515:LEU:CD2	1:B:551:ASN:HD21	2.18	0.56
1:C:240:LYS:H	1:C:242:ARG:N	2.03	0.56
1:C:286:THR:H	1:C:289:HIS:CD2	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:560:GLN:C	1:C:564:ILE:HD13	2.29	0.56
1:D:592:SER:CB	1:D:637:LEU:HD12	2.35	0.56
1:B:246:TYR:CE1	1:B:248:GLY:HA3	2.41	0.56
1:B:349:LEU:HD23	1:B:353:LEU:HD12	1.88	0.56
1:A:681:LEU:HD22	1:A:681:LEU:C	2.31	0.56
1:C:665:ALA:HA	1:C:668:ILE:CG1	2.35	0.56
1:D:447:ILE:N	1:D:447:ILE:HD12	2.21	0.56
1:B:285:ASN:HA	1:B:289:HIS:CD2	2.41	0.56
1:A:121:VAL:HG22	1:A:172:THR:CG2	2.33	0.56
1:A:246:TYR:CE1	1:A:248:GLY:HA3	2.41	0.56
1:A:401:TYR:HA	1:A:402:SER:CB	2.33	0.56
1:C:180:ALA:O	1:C:185:SER:N	2.39	0.56
1:C:242:ARG:HH11	1:C:242:ARG:CG	2.17	0.56
1:D:240:LYS:NZ	1:D:240:LYS:HB3	2.20	0.56
1:D:367:ARG:NH1	1:D:367:ARG:HG3	2.21	0.56
1:B:396:LEU:HD11	1:B:418:LEU:HD23	1.77	0.55
1:A:205:LEU:HA	1:A:220:LEU:HD23	1.86	0.55
1:A:242:ARG:N	1:A:243:PRO:CA	2.69	0.55
1:A:560:GLN:C	1:A:564:ILE:HD13	2.29	0.55
1:C:401:TYR:HA	1:C:402:SER:CB	2.33	0.55
1:D:285:ASN:HA	1:D:289:HIS:CD2	2.41	0.55
1:D:286:THR:H	1:D:289:HIS:CD2	2.24	0.55
1:D:349:LEU:CD2	1:D:353:LEU:HD12	2.36	0.55
1:D:560:GLN:OE1	1:D:564:ILE:CD1	2.41	0.55
1:D:653:TYR:CD1	1:D:654:ASP:N	2.74	0.55
1:D:665:ALA:HA	1:D:668:ILE:CG1	2.36	0.55
1:B:349:LEU:CD2	1:B:353:LEU:HD12	2.36	0.55
1:C:239:THR:OG1	1:C:243:PRO:CB	2.45	0.55
1:B:396:LEU:O	1:B:400:ALA:CB	2.55	0.55
1:B:652:ASN:O	1:B:653:TYR:HD2	1.85	0.55
1:A:180:ALA:O	1:A:185:SER:N	2.39	0.55
1:C:353:LEU:O	1:C:367:ARG:HG2	2.06	0.55
1:D:180:ALA:O	1:D:185:SER:N	2.39	0.55
1:D:396:LEU:O	1:D:400:ALA:CB	2.55	0.55
1:D:487:TYR:HD1	1:D:487:TYR:C	2.15	0.55
1:B:242:ARG:N	1:B:243:PRO:CA	2.69	0.55
1:B:286:THR:H	1:B:289:HIS:CD2	2.24	0.55
1:B:487:TYR:HD1	1:B:487:TYR:C	2.15	0.55
1:A:181:ARG:C	1:A:184:ASP:H	2.15	0.55
1:A:383:ASP:CB	1:A:384:LEU:HA	2.36	0.55
1:A:665:ALA:O	1:A:668:ILE:HG13	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:246:TYR:CE1	1:D:248:GLY:HA3	2.41	0.55
1:D:579:ARG:NH1	1:D:579:ARG:HG2	2.20	0.55
1:B:181:ARG:C	1:B:184:ASP:H	2.15	0.55
1:B:653:TYR:CD1	1:B:654:ASP:N	2.74	0.55
1:B:681:LEU:HD22	1:B:681:LEU:C	2.30	0.55
1:A:681:LEU:HD11	1:A:682:MET:HG2	1.88	0.55
1:C:367:ARG:HG3	1:C:367:ARG:NH1	2.21	0.55
1:C:382:TYR:N	1:C:753:UNK:O	2.33	0.55
1:C:560:GLN:O	1:C:564:ILE:HD11	2.05	0.55
1:B:413:LEU:O	1:B:414:LEU:O	2.25	0.55
1:B:562:MET:HE1	1:D:579:ARG:O	2.06	0.55
1:A:396:LEU:O	1:A:400:ALA:CB	2.55	0.55
1:C:428:ARG:CG	1:C:429:PHE:CD2	2.90	0.55
1:B:157:CYS:HB2	1:B:176:LEU:HD21	1.89	0.55
1:B:665:ALA:HA	1:B:668:ILE:CG1	2.36	0.55
1:A:285:ASN:HA	1:A:289:HIS:CD2	2.41	0.55
1:A:447:ILE:N	1:A:447:ILE:HD12	2.20	0.55
1:A:653:TYR:CD1	1:A:654:ASP:N	2.74	0.55
1:C:246:TYR:CE1	1:C:248:GLY:HA3	2.41	0.55
1:C:285:ASN:HA	1:C:289:HIS:CD2	2.41	0.55
1:C:681:LEU:HD11	1:C:682:MET:HG2	1.88	0.55
1:B:487:TYR:CE1	1:B:491:ARG:CG	2.90	0.55
1:A:349:LEU:HD23	1:A:353:LEU:HD12	1.88	0.55
1:A:349:LEU:CD2	1:A:353:LEU:HD12	2.36	0.55
1:A:353:LEU:O	1:A:367:ARG:HG2	2.06	0.55
1:A:487:TYR:HD1	1:A:487:TYR:C	2.15	0.55
1:C:181:ARG:C	1:C:184:ASP:H	2.15	0.55
1:C:573:ILE:CD1	1:C:577:LEU:HD23	2.37	0.55
1:D:428:ARG:CD	1:D:429:PHE:HB3	2.34	0.55
1:D:584:TYR:CE2	1:D:641:THR:HG21	2.42	0.55
1:D:640:PHE:CE1	1:D:667:VAL:CG2	2.81	0.55
1:B:367:ARG:HG3	1:B:367:ARG:NH1	2.21	0.55
1:A:584:TYR:CE2	1:A:641:THR:HG21	2.42	0.55
1:C:649:PHE:CD2	1:C:649:PHE:N	2.73	0.55
1:D:383:ASP:CB	1:D:384:LEU:HA	2.36	0.55
1:B:401:TYR:HA	1:B:402:SER:CB	2.33	0.55
1:A:157:CYS:HB2	1:A:176:LEU:HD21	1.89	0.55
1:A:367:ARG:HG3	1:A:367:ARG:NH1	2.21	0.55
1:A:661:ILE:HD13	1:A:661:ILE:C	2.32	0.55
1:C:374:TYR:O	1:C:375:GLY:C	2.50	0.55
1:D:374:TYR:O	1:D:375:GLY:C	2.50	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:631:TYR:CD2	1:D:631:TYR:C	2.85	0.55
1:B:351:TYR:C	1:B:351:TYR:CD2	2.85	0.54
1:B:428:ARG:CG	1:B:429:PHE:CD2	2.90	0.54
1:B:592:SER:CA	1:B:637:LEU:HD12	2.38	0.54
1:A:400:ALA:C	1:A:401:TYR:CD1	2.86	0.54
1:A:592:SER:CA	1:A:637:LEU:HD12	2.38	0.54
1:C:349:LEU:CD2	1:C:353:LEU:HD12	2.36	0.54
1:C:661:ILE:HD13	1:C:661:ILE:C	2.32	0.54
1:C:693:SER:O	1:C:696:ILE:CB	2.55	0.54
1:D:157:CYS:HB2	1:D:176:LEU:HD21	1.89	0.54
1:D:181:ARG:C	1:D:184:ASP:H	2.15	0.54
1:D:401:TYR:HA	1:D:402:SER:CB	2.33	0.54
1:D:448:PHE:C	1:D:448:PHE:CD2	2.86	0.54
1:D:659:PHE:C	1:D:659:PHE:CD1	2.86	0.54
1:B:239:THR:OG1	1:B:243:PRO:CB	2.45	0.54
1:B:374:TYR:O	1:B:375:GLY:C	2.50	0.54
1:B:631:TYR:C	1:B:631:TYR:CD2	2.85	0.54
1:A:554:TYR:C	1:A:554:TYR:CD1	2.86	0.54
1:A:573:ILE:CD1	1:A:577:LEU:HD23	2.37	0.54
1:A:647:LEU:HD11	1:C:635:LEU:HD11	1.87	0.54
1:A:707:ASP:C	1:A:711:SER:HB2	2.31	0.54
1:C:487:TYR:HD1	1:C:487:TYR:C	2.15	0.54
1:C:580:PHE:CE2	1:C:678:LEU:HD22	2.43	0.54
1:D:462:PRO:CD	1:D:463:TYR:CA	2.86	0.54
1:D:487:TYR:CD1	1:D:487:TYR:C	2.85	0.54
1:B:396:LEU:O	1:B:400:ALA:HB2	2.08	0.54
1:A:368:LYS:C	1:A:369:PHE:CD1	2.86	0.54
1:A:413:LEU:O	1:A:414:LEU:O	2.25	0.54
1:A:448:PHE:C	1:A:448:PHE:CD2	2.86	0.54
1:A:665:ALA:HA	1:A:668:ILE:CG1	2.36	0.54
1:C:396:LEU:O	1:C:400:ALA:CB	2.55	0.54
1:C:396:LEU:O	1:C:400:ALA:HB2	2.08	0.54
1:C:413:LEU:O	1:C:414:LEU:O	2.25	0.54
1:C:447:ILE:N	1:C:447:ILE:HD12	2.21	0.54
1:C:584:TYR:CE2	1:C:641:THR:HG21	2.42	0.54
1:D:400:ALA:C	1:D:401:TYR:CD1	2.86	0.54
1:D:511:TYR:C	1:D:511:TYR:CD1	2.85	0.54
1:D:649:PHE:CD2	1:D:649:PHE:N	2.73	0.54
1:D:653:TYR:CD1	1:D:653:TYR:C	2.86	0.54
1:D:681:LEU:HD11	1:D:682:MET:HG2	1.88	0.54
1:B:353:LEU:CA	1:B:367:ARG:HD3	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:ALA:C	1:B:401:TYR:CD1	2.86	0.54
1:B:511:TYR:CD1	1:B:511:TYR:C	2.85	0.54
1:B:560:GLN:OE1	1:B:564:ILE:CD1	2.41	0.54
1:B:564:ILE:HD12	1:B:564:ILE:H	1.73	0.54
1:B:584:TYR:CE2	1:B:641:THR:HG21	2.42	0.54
1:C:320:HIS:CB	1:C:323:LEU:HD23	2.37	0.54
1:C:368:LYS:C	1:C:369:PHE:CD1	2.86	0.54
1:D:368:LYS:C	1:D:369:PHE:CD1	2.86	0.54
1:D:573:ILE:CD1	1:D:577:LEU:HD23	2.37	0.54
1:D:580:PHE:CE2	1:D:678:LEU:HD22	2.43	0.54
1:D:707:ASP:C	1:D:711:SER:HB2	2.30	0.54
1:B:383:ASP:CB	1:B:384:LEU:HA	2.36	0.54
1:B:659:PHE:CD1	1:B:659:PHE:C	2.85	0.54
1:A:676:ASN:C	1:C:572:MET:HE1	2.31	0.54
1:B:214:MET:CE	1:B:218:THR:OG1	2.56	0.54
1:B:368:LYS:C	1:B:369:PHE:CD1	2.86	0.54
1:B:580:PHE:CE2	1:B:678:LEU:HD22	2.42	0.54
1:B:589:PHE:HD2	1:B:589:PHE:C	2.16	0.54
1:C:349:LEU:HD23	1:C:353:LEU:HD12	1.88	0.54
1:C:400:ALA:C	1:C:401:TYR:CD1	2.86	0.54
1:C:678:LEU:HD12	1:C:681:LEU:HD11	1.90	0.54
1:D:396:LEU:O	1:D:400:ALA:HB2	2.08	0.54
1:D:582:PHE:CD1	1:D:582:PHE:C	2.86	0.54
1:B:487:TYR:CD1	1:B:487:TYR:C	2.85	0.54
1:B:571:LYS:HZ3	1:B:693:SER:HB2	1.72	0.54
1:B:582:PHE:C	1:B:582:PHE:CD1	2.86	0.54
1:B:707:ASP:C	1:B:711:SER:HB2	2.30	0.54
1:A:320:HIS:CB	1:A:323:LEU:HD23	2.38	0.54
1:A:580:PHE:CE2	1:A:678:LEU:HD22	2.43	0.54
1:C:353:LEU:CA	1:C:367:ARG:HD3	2.26	0.54
1:C:653:TYR:CD1	1:C:654:ASP:N	2.74	0.54
1:B:121:VAL:HG22	1:B:172:THR:CG2	2.33	0.54
1:B:374:TYR:O	1:B:376:PRO:N	2.41	0.54
1:B:661:ILE:HD13	1:B:661:ILE:C	2.32	0.54
1:B:704:THR:O	1:B:708:THR:CG2	2.52	0.54
1:A:487:TYR:CD1	1:A:487:TYR:C	2.85	0.54
1:A:589:PHE:HD2	1:A:589:PHE:C	2.16	0.54
1:C:157:CYS:HB2	1:C:176:LEU:HD21	1.89	0.54
1:C:462:PRO:CD	1:C:463:TYR:CA	2.86	0.54
1:C:487:TYR:CE1	1:C:491:ARG:CD	2.86	0.54
1:C:521:LEU:HD22	1:C:521:LEU:C	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:428:ARG:CG	1:D:429:PHE:CD2	2.90	0.54
1:D:693:SER:O	1:D:696:ILE:CB	2.55	0.54
1:D:704:THR:O	1:D:708:THR:CG2	2.52	0.54
1:B:448:PHE:C	1:B:448:PHE:CD2	2.86	0.54
1:A:428:ARG:CG	1:A:429:PHE:CD2	2.90	0.54
1:A:462:PRO:CD	1:A:463:TYR:CA	2.86	0.54
1:C:374:TYR:O	1:C:376:PRO:N	2.41	0.54
1:C:511:TYR:CD1	1:C:511:TYR:C	2.85	0.54
1:C:582:PHE:CD1	1:C:582:PHE:C	2.86	0.54
1:C:601:ASP:H	1:C:652:ASN:ND2	2.06	0.54
1:D:589:PHE:HD2	1:D:589:PHE:C	2.16	0.54
1:B:240:LYS:N	1:B:241:GLY:CA	2.71	0.54
1:B:320:HIS:CB	1:B:323:LEU:HD23	2.37	0.54
1:B:678:LEU:HD12	1:B:681:LEU:HD11	1.90	0.54
1:B:681:LEU:HD11	1:B:682:MET:HG2	1.88	0.54
1:A:521:LEU:HD22	1:A:521:LEU:C	2.33	0.54
1:A:582:PHE:CD1	1:A:582:PHE:C	2.86	0.54
1:D:351:TYR:C	1:D:351:TYR:CD2	2.86	0.54
1:D:413:LEU:O	1:D:414:LEU:O	2.25	0.54
1:D:592:SER:CA	1:D:637:LEU:HD12	2.38	0.54
1:B:516:PHE:HE2	1:B:554:TYR:HD2	0.76	0.53
1:B:554:TYR:CD1	1:B:554:TYR:C	2.86	0.53
1:B:560:GLN:O	1:B:564:ILE:HD11	2.05	0.53
1:A:396:LEU:O	1:A:400:ALA:HB2	2.08	0.53
1:A:631:TYR:C	1:A:631:TYR:CD2	2.85	0.53
1:C:592:SER:CA	1:C:637:LEU:HD12	2.38	0.53
1:D:627:TYR:CD2	1:D:650:THR:HB	2.43	0.53
1:B:653:TYR:CD1	1:B:653:TYR:C	2.86	0.53
1:C:631:TYR:C	1:C:631:TYR:CD2	2.86	0.53
1:D:214:MET:CE	1:D:218:THR:OG1	2.56	0.53
1:D:240:LYS:N	1:D:241:GLY:CA	2.71	0.53
1:D:242:ARG:N	1:D:243:PRO:CA	2.69	0.53
1:D:564:ILE:HD12	1:D:564:ILE:H	1.73	0.53
1:A:511:TYR:CD1	1:A:511:TYR:C	2.85	0.53
1:A:538:VAL:C	1:A:540:SER:N	2.66	0.53
1:A:627:TYR:CD2	1:A:650:THR:HB	2.43	0.53
1:A:678:LEU:HD12	1:A:681:LEU:HD11	1.90	0.53
1:C:560:GLN:C	1:C:564:ILE:CD1	2.81	0.53
1:C:653:TYR:CD1	1:C:653:TYR:C	2.86	0.53
1:C:659:PHE:CD1	1:C:659:PHE:C	2.86	0.53
1:D:320:HIS:CB	1:D:323:LEU:HD23	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:374:TYR:O	1:D:376:PRO:N	2.41	0.53
1:B:560:GLN:C	1:B:564:ILE:CD1	2.81	0.53
1:B:682:MET:O	1:B:685:THR:CG2	2.56	0.53
1:A:351:TYR:CD2	1:A:351:TYR:C	2.86	0.53
1:A:374:TYR:O	1:A:375:GLY:C	2.50	0.53
1:A:438:PHE:CD1	1:A:438:PHE:C	2.86	0.53
1:A:653:TYR:CD1	1:A:653:TYR:C	2.86	0.53
1:C:564:ILE:HD12	1:C:564:ILE:H	1.73	0.53
1:D:521:LEU:HD22	1:D:521:LEU:C	2.33	0.53
1:D:662:LEU:C	1:D:662:LEU:HD13	2.34	0.53
1:D:718:LYS:O	1:D:719:ALA:CB	2.57	0.53
1:B:438:PHE:C	1:B:438:PHE:CD1	2.86	0.53
1:B:573:ILE:CD1	1:B:577:LEU:HD23	2.37	0.53
1:A:659:PHE:C	1:A:659:PHE:CD1	2.86	0.53
1:C:536:GLU:O	1:C:539:ALA:N	2.39	0.53
1:C:554:TYR:CD1	1:C:554:TYR:C	2.86	0.53
1:C:589:PHE:HD2	1:C:589:PHE:C	2.16	0.53
1:C:662:LEU:HD13	1:C:662:LEU:C	2.34	0.53
1:D:240:LYS:HB3	1:D:240:LYS:HZ2	1.73	0.53
1:D:661:ILE:HD13	1:D:661:ILE:C	2.32	0.53
1:A:601:ASP:H	1:A:652:ASN:ND2	2.06	0.53
1:A:662:LEU:HD13	1:A:662:LEU:C	2.34	0.53
1:C:240:LYS:N	1:C:241:GLY:CA	2.71	0.53
1:C:627:TYR:CD2	1:C:650:THR:HB	2.43	0.53
1:D:589:PHE:C	1:D:589:PHE:CD2	2.87	0.53
1:D:601:ASP:H	1:D:652:ASN:ND2	2.06	0.53
1:B:286:THR:H	1:B:289:HIS:HD2	1.57	0.53
1:B:462:PRO:CD	1:B:463:TYR:CA	2.85	0.53
1:B:589:PHE:C	1:B:589:PHE:CD2	2.87	0.53
1:B:718:LYS:O	1:B:719:ALA:CB	2.57	0.53
1:A:240:LYS:HE3	1:A:242:ARG:HG2	1.90	0.53
1:A:245:PHE:CD1	1:C:376:PRO:HB3	2.41	0.53
1:A:374:TYR:O	1:A:376:PRO:N	2.41	0.53
1:A:655:PHE:CE1	1:C:536:GLU:O	2.61	0.53
1:A:718:LYS:O	1:A:719:ALA:CB	2.57	0.53
1:C:487:TYR:CE1	1:C:491:ARG:CG	2.90	0.53
1:A:214:MET:CE	1:A:218:THR:OG1	2.56	0.53
1:C:214:MET:CE	1:C:218:THR:OG1	2.56	0.53
1:C:351:TYR:C	1:C:351:TYR:CD2	2.86	0.53
1:D:554:TYR:C	1:D:554:TYR:CD1	2.86	0.53
1:D:559:PHE:CB	1:D:562:MET:CB	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:627:TYR:CD2	1:B:650:THR:HB	2.43	0.53
1:A:142:ARG:CZ	1:A:183:THR:HG22	2.39	0.53
1:A:589:PHE:C	1:A:589:PHE:CD2	2.87	0.53
1:A:596:VAL:HG21	1:A:630:LEU:HD22	1.91	0.53
1:C:374:TYR:C	1:C:376:PRO:CD	2.82	0.53
1:C:487:TYR:CD1	1:C:487:TYR:C	2.85	0.53
1:C:718:LYS:O	1:C:719:ALA:CB	2.57	0.53
1:D:142:ARG:CZ	1:D:183:THR:HG22	2.39	0.53
1:D:678:LEU:HD12	1:D:681:LEU:HD11	1.90	0.53
1:B:559:PHE:CB	1:B:562:MET:CB	2.87	0.53
1:A:564:ILE:HD12	1:A:564:ILE:H	1.73	0.53
1:A:600:GLU:OE1	1:A:653:TYR:HA	2.09	0.53
1:C:121:VAL:HG22	1:C:172:THR:CG2	2.33	0.53
1:C:538:VAL:C	1:C:540:SER:N	2.66	0.53
1:B:240:LYS:HE3	1:B:242:ARG:HG2	1.90	0.52
1:A:374:TYR:C	1:A:376:PRO:CD	2.82	0.52
1:A:560:GLN:O	1:A:564:ILE:HD11	2.05	0.52
1:D:438:PHE:CD1	1:D:438:PHE:C	2.86	0.52
1:D:560:GLN:C	1:D:564:ILE:CD1	2.81	0.52
1:D:659:PHE:O	1:D:662:LEU:HB3	2.09	0.52
1:D:707:ASP:O	1:D:711:SER:CA	2.57	0.52
1:B:659:PHE:O	1:B:662:LEU:HB3	2.09	0.52
1:B:662:LEU:C	1:B:662:LEU:HD13	2.34	0.52
1:A:560:GLN:C	1:A:564:ILE:CD1	2.81	0.52
1:A:647:LEU:CD1	1:C:635:LEU:HD11	2.38	0.52
1:B:640:PHE:HZ	1:B:647:LEU:HA	1.75	0.52
1:A:240:LYS:N	1:A:241:GLY:CA	2.71	0.52
1:A:640:PHE:HZ	1:A:647:LEU:HA	1.75	0.52
1:C:647:LEU:HB3	1:D:639:LYS:HE2	1.91	0.52
1:D:240:LYS:HE3	1:D:242:ARG:HG2	1.90	0.52
1:D:580:PHE:O	1:D:581:MET:C	2.52	0.52
1:C:448:PHE:C	1:C:448:PHE:CD2	2.86	0.52
1:C:584:TYR:HD1	1:C:584:TYR:O	1.93	0.52
1:C:647:LEU:HD12	1:C:648:GLU:H	1.75	0.52
1:D:374:TYR:C	1:D:376:PRO:CD	2.82	0.52
1:D:560:GLN:O	1:D:564:ILE:HD11	2.05	0.52
1:D:596:VAL:HG21	1:D:630:LEU:HD22	1.91	0.52
1:D:640:PHE:HZ	1:D:647:LEU:HA	1.75	0.52
1:B:374:TYR:C	1:B:376:PRO:CD	2.82	0.52
1:B:448:PHE:HD2	1:B:448:PHE:C	2.18	0.52
1:B:449:THR:OG1	1:B:545:LEU:HD21	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:601:ASP:H	1:B:652:ASN:ND2	2.06	0.52
1:C:428:ARG:CG	1:C:429:PHE:N	2.72	0.52
1:C:580:PHE:O	1:C:581:MET:C	2.52	0.52
1:C:600:GLU:OE1	1:C:653:TYR:HA	2.09	0.52
1:C:640:PHE:HZ	1:C:647:LEU:HA	1.75	0.52
1:D:448:PHE:HD2	1:D:448:PHE:C	2.18	0.52
1:B:515:LEU:O	1:B:516:PHE:C	2.53	0.52
1:B:538:VAL:C	1:B:540:SER:N	2.66	0.52
1:B:596:VAL:HG21	1:B:630:LEU:HD22	1.91	0.52
1:B:600:GLU:OE1	1:B:653:TYR:HA	2.09	0.52
1:B:647:LEU:CD1	1:B:648:GLU:N	2.73	0.52
1:B:655:PHE:CE1	1:A:536:GLU:O	2.61	0.52
1:B:707:ASP:O	1:B:711:SER:CA	2.57	0.52
1:A:286:THR:H	1:A:289:HIS:HD2	1.57	0.52
1:A:429:PHE:N	1:A:429:PHE:HD2	2.06	0.52
1:A:659:PHE:O	1:A:662:LEU:HB3	2.09	0.52
1:A:707:ASP:O	1:A:711:SER:CA	2.57	0.52
1:C:142:ARG:CZ	1:C:183:THR:HG22	2.39	0.52
1:C:667:VAL:HG11	1:D:642:ILE:HG12	1.91	0.52
1:A:462:PRO:CD	1:A:464:LYS:H	2.22	0.52
1:A:693:SER:O	1:A:696:ILE:CB	2.55	0.52
1:C:240:LYS:HE3	1:C:242:ARG:HG2	1.90	0.52
1:D:449:THR:OG1	1:D:545:LEU:HD21	2.10	0.52
1:D:647:LEU:HD12	1:D:648:GLU:H	1.75	0.52
1:B:142:ARG:CZ	1:B:183:THR:HG22	2.39	0.52
1:B:428:ARG:CG	1:B:429:PHE:N	2.72	0.52
1:B:647:LEU:HD12	1:B:648:GLU:H	1.75	0.52
1:B:693:SER:O	1:B:696:ILE:CB	2.55	0.52
1:A:448:PHE:HD2	1:A:448:PHE:C	2.18	0.52
1:A:681:LEU:CD1	1:A:681:LEU:N	2.73	0.52
1:D:452:ALA:C	1:D:455:ARG:HG2	2.34	0.52
1:A:449:THR:OG1	1:A:545:LEU:HD21	2.10	0.52
1:A:647:LEU:HD12	1:A:648:GLU:H	1.75	0.52
1:C:447:ILE:N	1:C:447:ILE:CD1	2.73	0.52
1:D:462:PRO:CD	1:D:464:LYS:H	2.22	0.52
1:B:240:LYS:NZ	1:B:240:LYS:CB	2.73	0.52
1:A:447:ILE:N	1:A:447:ILE:CD1	2.73	0.52
1:A:559:PHE:CB	1:A:562:MET:CB	2.87	0.52
1:A:571:LYS:NZ	1:A:693:SER:CB	2.73	0.52
1:C:452:ALA:C	1:C:455:ARG:HG2	2.34	0.52
1:C:559:PHE:CB	1:C:562:MET:CB	2.87	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:647:LEU:CD1	1:C:648:GLU:N	2.73	0.52
1:C:659:PHE:O	1:C:662:LEU:HB3	2.09	0.52
1:D:536:GLU:O	1:D:539:ALA:N	2.39	0.52
1:D:584:TYR:O	1:D:584:TYR:HD1	1.93	0.52
1:A:359:GLU:N	1:A:362:CYS:HB2	2.24	0.51
1:A:516:PHE:HE2	1:A:554:TYR:HD2	0.76	0.51
1:C:245:PHE:CB	1:D:376:PRO:CB	2.75	0.51
1:C:589:PHE:C	1:C:589:PHE:CD2	2.87	0.51
1:C:655:PHE:HZ	1:D:536:GLU:C	2.16	0.51
1:D:286:THR:H	1:D:289:HIS:HD2	1.57	0.51
1:D:428:ARG:CG	1:D:429:PHE:N	2.72	0.51
1:D:600:GLU:OE1	1:D:653:TYR:HA	2.09	0.51
1:D:647:LEU:CD1	1:D:648:GLU:N	2.73	0.51
1:D:668:ILE:CD1	1:D:669:LEU:N	2.73	0.51
1:B:462:PRO:CD	1:B:464:LYS:H	2.22	0.51
1:A:428:ARG:CG	1:A:429:PHE:N	2.72	0.51
1:C:438:PHE:CD1	1:C:438:PHE:C	2.86	0.51
1:C:448:PHE:HD2	1:C:448:PHE:C	2.17	0.51
1:C:647:LEU:CD2	1:D:642:ILE:CD1	2.88	0.51
1:C:707:ASP:O	1:C:711:SER:CA	2.57	0.51
1:D:462:PRO:N	1:D:463:TYR:CA	2.73	0.51
1:D:514:ILE:O	1:D:518:VAL:CG2	2.58	0.51
1:D:571:LYS:NZ	1:D:693:SER:CB	2.73	0.51
1:D:662:LEU:HD13	1:D:662:LEU:O	2.10	0.51
1:B:589:PHE:CE2	1:B:593:THR:CG2	2.94	0.51
1:A:462:PRO:N	1:A:463:TYR:CA	2.73	0.51
1:A:647:LEU:CD1	1:A:648:GLU:N	2.73	0.51
1:C:430:VAL:HG21	1:C:705:ILE:HG12	1.92	0.51
1:C:462:PRO:CD	1:C:464:LYS:H	2.22	0.51
1:C:707:ASP:C	1:C:711:SER:HB2	2.31	0.51
1:D:375:GLY:N	1:D:376:PRO:CD	2.74	0.51
1:D:699:LEU:O	1:D:699:LEU:HD23	2.11	0.51
1:A:402:SER:O	1:A:403:SER:C	2.53	0.51
1:C:449:THR:OG1	1:C:545:LEU:HD21	2.10	0.51
1:C:515:LEU:O	1:C:516:PHE:C	2.53	0.51
1:C:681:LEU:CD1	1:C:681:LEU:N	2.73	0.51
1:B:375:GLY:N	1:B:376:PRO:CD	2.74	0.51
1:B:642:ILE:HD11	1:D:647:LEU:HD23	1.91	0.51
1:B:662:LEU:HD13	1:B:662:LEU:O	2.10	0.51
1:B:699:LEU:O	1:B:699:LEU:HD23	2.11	0.51
1:A:353:LEU:CA	1:A:367:ARG:HD3	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:VAL:HG21	1:A:705:ILE:HG12	1.92	0.51
1:C:242:ARG:HB3	1:C:243:PRO:C	2.36	0.51
1:C:589:PHE:CE2	1:C:593:THR:CG2	2.94	0.51
1:C:662:LEU:HD13	1:C:662:LEU:O	2.10	0.51
1:B:571:LYS:NZ	1:B:693:SER:CB	2.73	0.51
1:B:681:LEU:CD1	1:B:681:LEU:N	2.73	0.51
1:A:673:LEU:HD11	1:C:573:ILE:HB	1.91	0.51
1:C:462:PRO:N	1:C:463:TYR:CA	2.73	0.51
1:C:596:VAL:HG21	1:C:630:LEU:HD22	1.91	0.51
1:D:538:VAL:C	1:D:540:SER:N	2.66	0.51
1:D:665:ALA:CA	1:D:668:ILE:HG13	2.41	0.51
1:B:521:LEU:HD22	1:B:521:LEU:C	2.33	0.51
1:A:239:THR:OG1	1:A:243:PRO:CB	2.45	0.51
1:A:375:GLY:N	1:A:376:PRO:CD	2.74	0.51
1:A:668:ILE:HD12	1:A:669:LEU:CA	2.41	0.51
1:C:242:ARG:N	1:C:243:PRO:CA	2.69	0.51
1:C:367:ARG:CG	1:C:367:ARG:NH1	2.73	0.51
1:C:375:GLY:N	1:C:376:PRO:CD	2.74	0.51
1:D:198:TYR:CD1	1:D:242:ARG:HD2	2.45	0.51
1:D:515:LEU:O	1:D:516:PHE:C	2.53	0.51
1:D:682:MET:O	1:D:685:THR:CG2	2.56	0.51
1:B:178:ASP:O	1:B:182:LYS:HG2	2.11	0.51
1:B:369:PHE:O	1:B:381:LEU:CB	2.59	0.51
1:B:514:ILE:O	1:B:518:VAL:CG2	2.58	0.51
1:B:668:ILE:HD12	1:B:669:LEU:CA	2.41	0.51
1:A:452:ALA:C	1:A:455:ARG:HG2	2.34	0.51
1:A:665:ALA:CA	1:A:668:ILE:HG13	2.41	0.51
1:A:704:THR:O	1:A:708:THR:CG2	2.52	0.51
1:C:178:ASP:O	1:C:182:LYS:HG2	2.11	0.51
1:D:589:PHE:CE2	1:D:593:THR:CG2	2.94	0.51
1:B:430:VAL:HG21	1:B:705:ILE:HG12	1.92	0.51
1:B:447:ILE:N	1:B:447:ILE:CD1	2.73	0.51
1:B:452:ALA:C	1:B:455:ARG:HG2	2.34	0.51
1:A:584:TYR:HD1	1:A:584:TYR:O	1.93	0.51
1:A:699:LEU:O	1:A:699:LEU:HD23	2.11	0.51
1:D:240:LYS:N	1:D:241:GLY:HA2	2.26	0.51
1:D:369:PHE:O	1:D:381:LEU:CB	2.59	0.51
1:D:430:VAL:HG21	1:D:705:ILE:HG12	1.92	0.51
1:B:676:ASN:OD1	1:B:676:ASN:N	2.44	0.51
1:B:716:MET:SD	1:B:716:MET:C	2.94	0.51
1:A:579:ARG:CG	1:A:579:ARG:NH1	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:LEU:HD13	1:A:662:LEU:O	2.10	0.51
1:A:682:MET:O	1:A:685:THR:CG2	2.56	0.51
1:C:571:LYS:NZ	1:C:693:SER:CB	2.73	0.51
1:C:699:LEU:HD23	1:C:699:LEU:O	2.11	0.51
1:D:447:ILE:N	1:D:447:ILE:CD1	2.73	0.51
1:B:462:PRO:N	1:B:463:TYR:CA	2.73	0.50
1:A:242:ARG:HB3	1:A:243:PRO:C	2.36	0.50
1:A:369:PHE:O	1:A:381:LEU:CB	2.59	0.50
1:A:580:PHE:O	1:A:581:MET:C	2.52	0.50
1:A:676:ASN:OD1	1:A:676:ASN:N	2.44	0.50
1:C:286:THR:H	1:C:289:HIS:HD2	1.57	0.50
1:C:704:THR:O	1:C:708:THR:CG2	2.52	0.50
1:B:580:PHE:O	1:B:581:MET:C	2.52	0.50
1:D:359:GLU:N	1:D:362:CYS:HB2	2.24	0.50
1:D:681:LEU:CD1	1:D:681:LEU:N	2.73	0.50
1:B:240:LYS:N	1:B:241:GLY:HA2	2.26	0.50
1:B:584:TYR:O	1:B:584:TYR:HD1	1.93	0.50
1:B:640:PHE:CZ	1:B:647:LEU:HA	2.47	0.50
1:A:136:LEU:H	1:A:136:LEU:CD2	2.19	0.50
1:A:589:PHE:CE2	1:A:593:THR:CG2	2.94	0.50
1:C:682:MET:O	1:C:685:THR:CG2	2.56	0.50
1:C:716:MET:SD	1:C:716:MET:C	2.94	0.50
1:D:242:ARG:HB3	1:D:243:PRO:C	2.36	0.50
1:D:319:LEU:HB3	1:D:320:HIS:CD2	2.47	0.50
1:D:579:ARG:CG	1:D:579:ARG:NH1	2.73	0.50
1:A:396:LEU:HD11	1:A:418:LEU:HD23	1.77	0.50
1:D:640:PHE:CZ	1:D:647:LEU:HA	2.47	0.50
1:D:668:ILE:HD12	1:D:669:LEU:CA	2.41	0.50
1:B:367:ARG:HH22	1:B:385:SER:HB2	1.75	0.50
1:C:198:TYR:CD1	1:C:242:ARG:HD2	2.45	0.50
1:C:640:PHE:CZ	1:C:647:LEU:HA	2.47	0.50
1:D:428:ARG:NH1	1:D:428:ARG:CG	2.73	0.50
1:D:672:ILE:O	1:D:676:ASN:OD1	2.29	0.50
1:D:716:MET:SD	1:D:716:MET:C	2.94	0.50
1:B:536:GLU:O	1:B:539:ALA:N	2.39	0.50
1:A:127:GLN:HA	1:A:130:GLU:HG3	1.94	0.50
1:C:319:LEU:HB3	1:C:320:HIS:CD2	2.47	0.50
1:C:584:TYR:HE2	1:C:641:THR:HG21	1.76	0.50
1:B:242:ARG:HB3	1:B:243:PRO:C	2.36	0.50
1:B:701:ARG:CG	1:B:701:ARG:NH1	2.73	0.50
1:A:356:GLU:C	1:A:366:SER:OG	2.53	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:SER:C	1:A:406:THR:N	2.70	0.50
1:A:462:PRO:CG	1:A:464:LYS:H	2.25	0.50
1:C:359:GLU:N	1:C:362:CYS:HB2	2.24	0.50
1:C:369:PHE:O	1:C:381:LEU:CB	2.59	0.50
1:C:462:PRO:CG	1:C:464:LYS:H	2.25	0.50
1:C:665:ALA:CA	1:C:668:ILE:HG13	2.41	0.50
1:D:356:GLU:C	1:D:366:SER:OG	2.53	0.50
1:D:425:LYS:O	1:D:428:ARG:HG3	2.12	0.50
1:B:136:LEU:H	1:B:136:LEU:CD2	2.19	0.50
1:B:462:PRO:CG	1:B:464:LYS:H	2.25	0.50
1:A:701:ARG:CG	1:A:701:ARG:NH1	2.73	0.50
1:C:240:LYS:N	1:C:241:GLY:HA2	2.26	0.50
1:D:571:LYS:NZ	1:D:693:SER:HB2	2.27	0.50
1:B:127:GLN:HA	1:B:130:GLU:HG3	1.94	0.50
1:B:425:LYS:O	1:B:428:ARG:HG3	2.12	0.50
1:A:515:LEU:O	1:A:516:PHE:C	2.53	0.50
1:C:367:ARG:HH22	1:C:385:SER:HB2	1.75	0.50
1:C:404:SER:C	1:C:406:THR:N	2.70	0.50
1:C:681:LEU:CD2	1:C:682:MET:SD	3.00	0.50
1:D:178:ASP:O	1:D:182:LYS:HG2	2.11	0.50
1:D:396:LEU:HD11	1:D:418:LEU:HD22	1.63	0.50
1:B:158:LEU:HB2	1:B:189:PHE:CZ	2.47	0.49
1:B:571:LYS:NZ	1:B:693:SER:HB2	2.27	0.49
1:A:453:TYR:C	1:A:453:TYR:CD2	2.89	0.49
1:B:444:TYR:CE1	1:B:488:PHE:HE2	2.30	0.49
1:A:178:ASP:O	1:A:182:LYS:HG2	2.11	0.49
1:D:198:TYR:HE1	1:D:242:ARG:CD	2.23	0.49
1:D:247:PHE:CZ	1:D:254:LEU:HD13	2.48	0.49
1:D:584:TYR:HE2	1:D:641:THR:HG21	1.76	0.49
1:D:596:VAL:CG2	1:D:633:THR:CG2	2.73	0.49
1:B:247:PHE:CZ	1:B:254:LEU:HD13	2.48	0.49
1:B:539:ALA:O	1:B:543:PHE:CD2	2.66	0.49
1:A:158:LEU:HB2	1:A:189:PHE:CZ	2.47	0.49
1:A:240:LYS:NZ	1:A:240:LYS:CB	2.73	0.49
1:A:247:PHE:CZ	1:A:254:LEU:HD13	2.48	0.49
1:A:571:LYS:NZ	1:A:693:SER:HB2	2.27	0.49
1:A:599:ILE:CD1	1:A:628:ASN:HB2	2.42	0.49
1:A:649:PHE:CD2	1:A:649:PHE:N	2.73	0.49
1:A:668:ILE:CD1	1:A:669:LEU:N	2.73	0.49
1:A:716:MET:SD	1:A:716:MET:C	2.94	0.49
1:C:444:TYR:CE1	1:C:488:PHE:HE2	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:676:ASN:ND2	1:C:676:ASN:N	2.60	0.49
1:D:428:ARG:HD3	1:D:429:PHE:CA	2.43	0.49
1:D:648:GLU:N	1:D:648:GLU:OE1	2.45	0.49
1:B:428:ARG:HD3	1:B:429:PHE:CA	2.43	0.49
1:C:599:ILE:CD1	1:C:628:ASN:HB2	2.42	0.49
1:D:444:TYR:CE1	1:D:488:PHE:HE2	2.30	0.49
1:B:536:GLU:O	1:B:538:VAL:HG12	2.13	0.49
1:B:655:PHE:CE1	1:A:539:ALA:HB3	1.89	0.49
1:B:669:LEU:C	1:B:669:LEU:CD2	2.86	0.49
1:A:428:ARG:HD3	1:A:429:PHE:CA	2.43	0.49
1:A:584:TYR:HE2	1:A:641:THR:HG21	1.76	0.49
1:A:640:PHE:CZ	1:A:647:LEU:HA	2.47	0.49
1:A:669:LEU:C	1:A:669:LEU:CD2	2.85	0.49
1:C:198:TYR:HE1	1:C:242:ARG:CD	2.23	0.49
1:C:425:LYS:O	1:C:428:ARG:HG3	2.12	0.49
1:C:668:ILE:HD12	1:C:669:LEU:CA	2.41	0.49
1:B:579:ARG:HH11	1:B:579:ARG:HG2	1.77	0.49
1:A:240:LYS:N	1:A:241:GLY:HA2	2.26	0.49
1:C:158:LEU:HB2	1:C:189:PHE:CZ	2.47	0.49
1:C:571:LYS:NZ	1:C:693:SER:HB2	2.27	0.49
1:C:685:THR:O	1:C:688:LYS:CA	2.59	0.49
1:D:462:PRO:CG	1:D:464:LYS:H	2.25	0.49
1:D:571:LYS:HZ3	1:D:693:SER:HB2	1.77	0.49
1:B:319:LEU:HB3	1:B:320:HIS:CD2	2.47	0.49
1:B:579:ARG:CG	1:B:579:ARG:NH1	2.73	0.49
1:B:591:PHE:CD1	1:B:666:TYR:HD1	2.31	0.49
1:B:668:ILE:CD1	1:B:669:LEU:N	2.73	0.49
1:A:462:PRO:HD2	1:A:464:LYS:N	2.28	0.49
1:A:514:ILE:O	1:A:518:VAL:CG2	2.58	0.49
1:C:425:LYS:CB	1:C:429:PHE:CE2	2.92	0.49
1:C:428:ARG:HD3	1:C:429:PHE:CA	2.43	0.49
1:D:404:SER:C	1:D:406:THR:N	2.70	0.49
1:B:367:ARG:HH11	1:B:367:ARG:HG3	1.78	0.49
1:B:665:ALA:CA	1:B:668:ILE:HG13	2.41	0.49
1:A:425:LYS:O	1:A:428:ARG:HG3	2.12	0.49
1:A:515:LEU:CD2	1:A:551:ASN:HD21	2.18	0.49
1:A:630:LEU:HD13	1:A:630:LEU:C	2.37	0.49
1:C:646:ASP:OD2	1:C:649:PHE:HB3	2.12	0.49
1:D:158:LEU:HB2	1:D:189:PHE:CZ	2.47	0.49
1:D:559:PHE:HB3	1:D:562:MET:CB	2.43	0.49
1:B:402:SER:O	1:B:403:SER:C	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:599:ILE:CD1	1:B:628:ASN:HB2	2.42	0.49
1:B:648:GLU:N	1:B:648:GLU:OE1	2.46	0.49
1:A:319:LEU:HB3	1:A:320:HIS:CD2	2.47	0.49
1:A:591:PHE:CD1	1:A:666:TYR:HD1	2.31	0.49
1:A:648:GLU:N	1:A:648:GLU:OE1	2.45	0.49
1:A:673:LEU:HD11	1:C:573:ILE:CB	2.43	0.49
1:C:421:LEU:C	1:C:421:LEU:CD2	2.86	0.49
1:C:536:GLU:O	1:C:538:VAL:HG12	2.13	0.49
1:B:646:ASP:OD2	1:B:649:PHE:HB3	2.12	0.49
1:A:142:ARG:CD	1:A:183:THR:CG2	2.91	0.49
1:C:515:LEU:CD2	1:C:551:ASN:HD21	2.18	0.49
1:D:462:PRO:CB	1:D:464:LYS:N	2.73	0.49
1:D:602:GLY:O	1:D:603:LYS:HD3	2.13	0.49
1:B:158:LEU:O	1:B:158:LEU:CD2	2.61	0.48
1:B:584:TYR:HE2	1:B:641:THR:HG21	1.76	0.48
1:B:602:GLY:O	1:B:603:LYS:HD3	2.13	0.48
1:A:646:ASP:OD2	1:A:649:PHE:HB3	2.12	0.48
1:C:127:GLN:HA	1:C:130:GLU:HG3	1.94	0.48
1:C:239:THR:C	1:C:241:GLY:HA2	2.38	0.48
1:C:240:LYS:NZ	1:C:240:LYS:CB	2.73	0.48
1:C:462:PRO:CB	1:C:464:LYS:N	2.73	0.48
1:D:240:LYS:NZ	1:D:240:LYS:CB	2.73	0.48
1:D:453:TYR:CD2	1:D:453:TYR:C	2.89	0.48
1:D:630:LEU:HD13	1:D:630:LEU:C	2.37	0.48
1:B:198:TYR:CD1	1:B:242:ARG:HD2	2.45	0.48
1:A:367:ARG:CG	1:A:367:ARG:NH1	2.73	0.48
1:A:602:GLY:O	1:A:603:LYS:HD3	2.13	0.48
1:C:247:PHE:CZ	1:C:254:LEU:HD13	2.48	0.48
1:C:356:GLU:C	1:C:366:SER:OG	2.53	0.48
1:C:402:SER:O	1:C:403:SER:C	2.53	0.48
1:D:127:GLN:HA	1:D:130:GLU:HG3	1.94	0.48
1:D:421:LEU:C	1:D:421:LEU:CD2	2.86	0.48
1:D:559:PHE:HB3	1:D:562:MET:HB2	1.94	0.48
1:D:590:GLY:O	1:D:593:THR:OG1	2.31	0.48
1:D:599:ILE:CD1	1:D:628:ASN:HB2	2.42	0.48
1:D:669:LEU:C	1:D:669:LEU:CD2	2.86	0.48
1:B:356:GLU:C	1:B:366:SER:OG	2.53	0.48
1:B:421:LEU:CD2	1:B:421:LEU:C	2.86	0.48
1:A:421:LEU:C	1:A:421:LEU:CD2	2.86	0.48
1:A:444:TYR:CE1	1:A:488:PHE:HE2	2.30	0.48
1:A:559:PHE:HB3	1:A:562:MET:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:655:PHE:HE2	1:C:536:GLU:CB	1.79	0.48
1:A:681:LEU:HD13	1:A:682:MET:HG2	1.95	0.48
1:C:142:ARG:CD	1:C:183:THR:CG2	2.91	0.48
1:C:539:ALA:O	1:C:543:PHE:CD2	2.66	0.48
1:C:559:PHE:HB3	1:C:562:MET:CB	2.43	0.48
1:D:536:GLU:O	1:D:538:VAL:HG12	2.13	0.48
1:D:539:ALA:O	1:D:543:PHE:CD2	2.66	0.48
1:B:559:PHE:HB3	1:B:562:MET:CB	2.43	0.48
1:B:681:LEU:CD2	1:B:682:MET:SD	3.00	0.48
1:A:539:ALA:O	1:A:543:PHE:CD2	2.66	0.48
1:C:158:LEU:O	1:C:158:LEU:CD2	2.61	0.48
1:C:462:PRO:HD2	1:C:464:LYS:N	2.28	0.48
1:C:591:PHE:CD1	1:C:666:TYR:HD1	2.31	0.48
1:C:630:LEU:HD13	1:C:630:LEU:C	2.37	0.48
1:C:668:ILE:CD1	1:C:669:LEU:N	2.73	0.48
1:C:669:LEU:C	1:C:669:LEU:CD2	2.86	0.48
1:D:367:ARG:HH22	1:D:385:SER:HB2	1.75	0.48
1:D:591:PHE:CD1	1:D:666:TYR:HD1	2.31	0.48
1:D:685:THR:O	1:D:688:LYS:CA	2.59	0.48
1:A:198:TYR:HE1	1:A:242:ARG:CD	2.23	0.48
1:C:648:GLU:N	1:C:648:GLU:OE1	2.45	0.48
1:C:694:LYS:C	1:C:694:LYS:CD	2.85	0.48
1:D:136:LEU:H	1:D:136:LEU:CD2	2.19	0.48
1:D:158:LEU:O	1:D:158:LEU:CD2	2.61	0.48
1:D:671:TYR:O	1:D:675:LEU:CB	2.62	0.48
1:A:205:LEU:O	1:A:209:ILE:HG13	2.14	0.48
1:C:346:ILE:HG12	1:C:412:MET:HA	1.95	0.48
1:C:602:GLY:O	1:C:603:LYS:HD3	2.13	0.48
1:C:681:LEU:HD13	1:C:682:MET:HG2	1.95	0.48
1:D:242:ARG:CG	1:D:242:ARG:NH1	2.75	0.48
1:B:158:LEU:HD22	1:B:158:LEU:C	2.38	0.48
1:B:205:LEU:O	1:B:209:ILE:HG13	2.14	0.48
1:A:198:TYR:CD1	1:A:242:ARG:HD2	2.45	0.48
1:A:678:LEU:C	1:A:681:LEU:HD12	2.38	0.48
1:D:239:THR:C	1:D:241:GLY:HA2	2.38	0.48
1:D:668:ILE:O	1:D:672:ILE:HB	2.13	0.48
1:B:596:VAL:CG2	1:B:633:THR:CG2	2.72	0.48
1:A:536:GLU:O	1:A:538:VAL:HG12	2.13	0.48
1:A:559:PHE:HB3	1:A:562:MET:CB	2.43	0.48
1:C:158:LEU:HD22	1:C:158:LEU:C	2.38	0.48
1:C:436:PHE:CE1	1:C:440:VAL:HG21	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:675:LEU:O	1:C:679:ILE:HG13	2.14	0.48
1:C:681:LEU:CD1	1:C:681:LEU:H	2.27	0.48
1:D:665:ALA:C	1:D:668:ILE:HG13	2.39	0.48
1:B:142:ARG:CD	1:B:183:THR:CG2	2.91	0.48
1:B:428:ARG:HD2	1:B:429:PHE:CD1	2.44	0.48
1:B:592:SER:O	1:B:596:VAL:HG23	2.14	0.48
1:B:665:ALA:C	1:B:668:ILE:HG13	2.39	0.48
1:B:678:LEU:C	1:B:681:LEU:HD12	2.38	0.48
1:A:396:LEU:O	1:A:400:ALA:CA	2.62	0.48
1:C:306:THR:HG23	1:C:351:TYR:HE1	1.79	0.48
1:C:330:ASN:O	1:C:331:ARG:C	2.56	0.48
1:C:678:LEU:C	1:C:681:LEU:HD12	2.38	0.48
1:A:668:ILE:O	1:A:672:ILE:HB	2.13	0.48
1:C:245:PHE:HB3	1:D:376:PRO:CB	2.42	0.48
1:C:499:ARG:N	1:C:499:ARG:CD	2.73	0.48
1:D:142:ARG:CD	1:D:183:THR:CG2	2.91	0.48
1:D:681:LEU:CD1	1:D:681:LEU:H	2.27	0.48
1:B:401:TYR:N	1:B:401:TYR:CD1	2.81	0.47
1:B:630:LEU:HD13	1:B:630:LEU:C	2.37	0.47
1:B:668:ILE:O	1:B:672:ILE:HB	2.13	0.47
1:A:396:LEU:HD13	1:A:418:LEU:HD23	1.88	0.47
1:D:436:PHE:CE1	1:D:440:VAL:HG21	2.49	0.47
1:D:646:ASP:OD2	1:D:649:PHE:HB3	2.12	0.47
1:D:675:LEU:O	1:D:679:ILE:HG13	2.14	0.47
1:B:239:THR:C	1:B:241:GLY:HA2	2.39	0.47
1:B:404:SER:C	1:B:406:THR:N	2.70	0.47
1:B:436:PHE:CE1	1:B:440:VAL:HG21	2.49	0.47
1:B:572:MET:HE1	1:D:676:ASN:CB	2.43	0.47
1:A:436:PHE:CE1	1:A:440:VAL:HG21	2.49	0.47
1:A:665:ALA:C	1:A:668:ILE:HG13	2.39	0.47
1:A:668:ILE:HD12	1:A:669:LEU:HA	1.96	0.47
1:C:242:ARG:CG	1:C:242:ARG:NH1	2.75	0.47
1:C:428:ARG:HG3	1:C:429:PHE:H	1.80	0.47
1:C:514:ILE:O	1:C:518:VAL:CG2	2.58	0.47
1:C:592:SER:O	1:C:596:VAL:HG23	2.14	0.47
1:D:330:ASN:O	1:D:331:ARG:C	2.56	0.47
1:D:678:LEU:C	1:D:681:LEU:HD12	2.38	0.47
1:B:539:ALA:CA	1:D:655:PHE:CD1	2.91	0.47
1:B:539:ALA:CA	1:D:655:PHE:HE1	2.02	0.47
1:A:239:THR:C	1:A:241:GLY:HA2	2.39	0.47
1:A:681:LEU:CD2	1:A:682:MET:SD	3.00	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:136:LEU:H	1:C:136:LEU:CD2	2.19	0.47
1:C:665:ALA:C	1:C:668:ILE:HG13	2.39	0.47
1:D:158:LEU:HD22	1:D:158:LEU:C	2.38	0.47
1:D:681:LEU:HD13	1:D:682:MET:HG2	1.95	0.47
1:B:543:PHE:CZ	1:D:658:VAL:CG1	2.93	0.47
1:B:596:VAL:HG23	1:B:633:THR:HG21	1.88	0.47
1:A:239:THR:HA	1:A:243:PRO:HA	1.97	0.47
1:A:367:ARG:HH11	1:A:367:ARG:HG3	1.78	0.47
1:C:239:THR:HA	1:C:243:PRO:HA	1.97	0.47
1:C:367:ARG:HH11	1:C:367:ARG:HG3	1.78	0.47
1:C:559:PHE:HB3	1:C:562:MET:HB2	1.94	0.47
1:D:668:ILE:HD12	1:D:669:LEU:HA	1.96	0.47
1:D:681:LEU:CD1	1:D:682:MET:N	2.73	0.47
1:D:681:LEU:CD2	1:D:682:MET:SD	3.00	0.47
1:A:367:ARG:HH22	1:A:385:SER:HB2	1.75	0.47
1:A:671:TYR:O	1:A:675:LEU:CB	2.62	0.47
1:D:491:ARG:HE	1:D:491:ARG:HB3	1.53	0.47
1:B:428:ARG:HG3	1:B:429:PHE:H	1.80	0.47
1:B:675:LEU:O	1:B:679:ILE:HG13	2.14	0.47
1:B:681:LEU:CD1	1:B:681:LEU:H	2.27	0.47
1:C:205:LEU:O	1:C:209:ILE:HG13	2.14	0.47
1:C:668:ILE:O	1:C:672:ILE:HB	2.13	0.47
1:D:205:LEU:O	1:D:209:ILE:HG13	2.14	0.47
1:D:576:ASP:O	1:D:580:PHE:HB3	2.15	0.47
1:B:129:LEU:HD22	1:B:132:LEU:HD22	1.97	0.47
1:B:239:THR:HA	1:B:243:PRO:HA	1.97	0.47
1:B:242:ARG:CG	1:B:242:ARG:NH1	2.75	0.47
1:B:359:GLU:N	1:B:362:CYS:HB2	2.24	0.47
1:B:396:LEU:O	1:B:400:ALA:CA	2.62	0.47
1:B:589:PHE:HE2	1:B:593:THR:CG2	2.28	0.47
1:B:681:LEU:HD13	1:B:682:MET:HG2	1.95	0.47
1:A:142:ARG:C	1:A:144:THR:H	2.22	0.47
1:A:158:LEU:HD22	1:A:158:LEU:C	2.39	0.47
1:A:428:ARG:HD2	1:A:429:PHE:CD1	2.44	0.47
1:C:129:LEU:HD22	1:C:132:LEU:HD22	1.97	0.47
1:C:687:ASN:ND2	1:C:687:ASN:C	2.73	0.47
1:D:129:LEU:HD22	1:D:132:LEU:HD22	1.97	0.47
1:D:172:THR:O	1:D:176:LEU:HB2	2.15	0.47
1:D:401:TYR:N	1:D:401:TYR:CD1	2.81	0.47
1:D:402:SER:O	1:D:403:SER:C	2.53	0.47
1:B:142:ARG:C	1:B:144:THR:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:462:PRO:CB	1:B:464:LYS:N	2.73	0.47
1:B:538:VAL:HG13	1:B:539:ALA:N	2.30	0.47
1:A:172:THR:O	1:A:176:LEU:HB2	2.15	0.47
1:A:559:PHE:HB2	1:A:562:MET:CB	2.44	0.47
1:A:576:ASP:O	1:A:580:PHE:HB3	2.15	0.47
1:A:592:SER:O	1:A:596:VAL:HG23	2.14	0.47
1:D:499:ARG:N	1:D:499:ARG:CD	2.73	0.47
1:B:594:ALA:O	1:B:597:THR:OG1	2.33	0.47
1:A:536:GLU:O	1:A:539:ALA:N	2.39	0.47
1:A:538:VAL:HG13	1:A:539:ALA:N	2.30	0.47
1:A:675:LEU:O	1:A:679:ILE:HG13	2.14	0.47
1:A:678:LEU:HD12	1:A:678:LEU:C	2.40	0.47
1:C:172:THR:O	1:C:176:LEU:HB2	2.15	0.47
1:C:576:ASP:O	1:C:580:PHE:HB3	2.15	0.47
1:D:239:THR:HA	1:D:243:PRO:HA	1.97	0.47
1:D:469:VAL:O	1:D:472:TYR:N	2.48	0.47
1:D:687:ASN:C	1:D:687:ASN:ND2	2.73	0.47
1:B:245:PHE:HB3	1:A:376:PRO:HG2	1.13	0.47
1:B:559:PHE:HB3	1:B:562:MET:HB2	1.94	0.47
1:B:678:LEU:HD12	1:B:678:LEU:C	2.40	0.47
1:A:330:ASN:O	1:A:331:ARG:C	2.56	0.47
1:A:425:LYS:CB	1:A:429:PHE:CE2	2.92	0.47
1:A:428:ARG:HG3	1:A:429:PHE:H	1.80	0.47
1:A:526:SER:HB2	1:A:540:SER:HB3	1.97	0.47
1:A:594:ALA:O	1:A:597:THR:OG1	2.33	0.47
1:A:673:LEU:HD22	1:A:673:LEU:HA	1.73	0.47
1:C:536:GLU:C	1:C:538:VAL:N	2.73	0.47
1:C:545:LEU:O	1:C:545:LEU:HD23	2.15	0.47
1:C:589:PHE:HE2	1:C:593:THR:CG2	2.28	0.47
1:C:668:ILE:HD12	1:C:669:LEU:HA	1.96	0.47
1:D:536:GLU:C	1:D:538:VAL:N	2.73	0.47
1:D:592:SER:O	1:D:596:VAL:HG23	2.14	0.47
1:B:330:ASN:O	1:B:331:ARG:C	2.56	0.46
1:B:453:TYR:C	1:B:453:TYR:CD2	2.89	0.46
1:B:562:MET:SD	1:D:579:ARG:HA	2.54	0.46
1:A:536:GLU:C	1:A:538:VAL:N	2.73	0.46
1:A:579:ARG:HH11	1:A:579:ARG:HG2	1.77	0.46
1:A:681:LEU:CD1	1:A:681:LEU:H	2.27	0.46
1:C:453:TYR:C	1:C:453:TYR:CD2	2.89	0.46
1:D:115:ARG:O	1:D:115:ARG:HD3	2.15	0.46
1:D:142:ARG:C	1:D:144:THR:H	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:428:ARG:HG3	1:D:429:PHE:H	1.80	0.46
1:B:687:ASN:C	1:B:687:ASN:ND2	2.73	0.46
1:A:589:PHE:HE2	1:A:593:THR:CG2	2.28	0.46
1:A:601:ASP:CG	1:A:602:GLY:N	2.73	0.46
1:A:685:THR:O	1:A:688:LYS:CA	2.59	0.46
1:C:142:ARG:NE	1:C:183:THR:HG22	2.31	0.46
1:C:526:SER:HB2	1:C:540:SER:HB3	1.97	0.46
1:C:627:TYR:HD2	1:C:650:THR:HB	1.80	0.46
1:D:142:ARG:NE	1:D:183:THR:HG22	2.31	0.46
1:D:673:LEU:HD22	1:D:673:LEU:HA	1.73	0.46
1:B:306:THR:O	1:B:351:TYR:OH	2.33	0.46
1:B:402:SER:CB	1:B:703:ILE:HD11	2.41	0.46
1:B:524:LEU:O	1:B:528:VAL:HG23	2.15	0.46
1:B:674:LEU:CD1	1:A:565:TYR:OH	2.63	0.46
1:A:469:VAL:O	1:A:472:TYR:N	2.48	0.46
1:A:637:LEU:HD22	1:A:666:TYR:CE2	2.51	0.46
1:A:673:LEU:HD11	1:C:573:ILE:CA	2.46	0.46
1:A:681:LEU:CD1	1:A:682:MET:N	2.73	0.46
1:C:142:ARG:C	1:C:144:THR:H	2.22	0.46
1:C:469:VAL:O	1:C:472:TYR:N	2.48	0.46
1:C:601:ASP:CG	1:C:602:GLY:N	2.73	0.46
1:D:276:ASP:C	1:D:276:ASP:OD1	2.59	0.46
1:D:601:ASP:CG	1:D:602:GLY:N	2.73	0.46
1:B:276:ASP:C	1:B:276:ASP:OD1	2.59	0.46
1:B:469:VAL:O	1:B:472:TYR:N	2.48	0.46
1:B:577:LEU:O	1:B:581:MET:N	2.48	0.46
1:B:637:LEU:HD22	1:B:666:TYR:CE2	2.51	0.46
1:A:524:LEU:O	1:A:528:VAL:HG23	2.15	0.46
1:A:627:TYR:HD2	1:A:650:THR:HB	1.80	0.46
1:C:559:PHE:HB2	1:C:562:MET:CB	2.45	0.46
1:C:640:PHE:CZ	1:C:663:LEU:HD13	2.51	0.46
1:D:346:ILE:HG12	1:D:412:MET:HA	1.95	0.46
1:D:396:LEU:O	1:D:400:ALA:CA	2.62	0.46
1:D:559:PHE:HB2	1:D:562:MET:CB	2.44	0.46
1:D:591:PHE:CG	1:D:666:TYR:HB2	2.51	0.46
1:D:681:LEU:CD1	1:D:682:MET:H	2.06	0.46
1:B:136:LEU:HD23	1:B:136:LEU:N	2.21	0.46
1:B:188:GLN:H	1:B:188:GLN:NE2	2.13	0.46
1:B:428:ARG:NH1	1:B:428:ARG:CG	2.73	0.46
1:B:591:PHE:CG	1:B:666:TYR:HB2	2.51	0.46
1:A:595:VAL:HG13	1:A:659:PHE:HE2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:ASN:CB	1:C:572:MET:HE1	2.37	0.46
1:A:687:ASN:C	1:A:687:ASN:ND2	2.73	0.46
1:C:596:VAL:CG2	1:C:633:THR:CG2	2.73	0.46
1:D:577:LEU:O	1:D:581:MET:N	2.48	0.46
1:D:701:ARG:HB2	1:D:701:ARG:NH1	2.23	0.46
1:B:245:PHE:CB	1:A:376:PRO:CB	2.78	0.46
1:B:576:ASP:O	1:B:580:PHE:HB3	2.15	0.46
1:B:668:ILE:HD12	1:B:669:LEU:HA	1.96	0.46
1:B:685:THR:O	1:B:688:LYS:CA	2.59	0.46
1:A:115:ARG:O	1:A:115:ARG:HD3	2.15	0.46
1:A:346:ILE:HG12	1:A:412:MET:HA	1.95	0.46
1:A:529:LEU:O	1:A:533:GLN:N	2.49	0.46
1:C:115:ARG:O	1:C:115:ARG:HD3	2.15	0.46
1:C:158:LEU:CD2	1:C:158:LEU:C	2.89	0.46
1:C:428:ARG:HD2	1:C:429:PHE:CD1	2.44	0.46
1:C:591:PHE:CG	1:C:666:TYR:HB2	2.50	0.46
1:D:402:SER:CB	1:D:703:ILE:HD11	2.41	0.46
1:B:198:TYR:HE1	1:B:242:ARG:CD	2.23	0.46
1:B:595:VAL:HG13	1:B:659:PHE:HE2	1.81	0.46
1:B:712:PHE:O	1:B:713:LEU:CB	2.64	0.46
1:A:545:LEU:HD23	1:A:545:LEU:O	2.15	0.46
1:A:640:PHE:CZ	1:A:663:LEU:HD13	2.51	0.46
1:C:577:LEU:O	1:C:581:MET:N	2.48	0.46
1:C:579:ARG:HH11	1:C:579:ARG:CB	2.29	0.46
1:C:637:LEU:HD22	1:C:666:TYR:CE2	2.51	0.46
1:D:400:ALA:O	1:D:703:ILE:CG1	2.57	0.46
1:B:115:ARG:O	1:B:115:ARG:HD3	2.15	0.46
1:B:579:ARG:HH11	1:B:579:ARG:CB	2.29	0.46
1:B:673:LEU:HD22	1:B:673:LEU:HA	1.73	0.46
1:A:129:LEU:HD22	1:A:132:LEU:HD22	1.97	0.46
1:A:681:LEU:HD13	1:A:681:LEU:N	2.31	0.46
1:C:428:ARG:NH1	1:C:428:ARG:CG	2.73	0.46
1:C:529:LEU:O	1:C:533:GLN:N	2.49	0.46
1:C:594:ALA:O	1:C:597:THR:OG1	2.33	0.46
1:D:515:LEU:CD2	1:D:551:ASN:HD21	2.18	0.46
1:D:524:LEU:O	1:D:528:VAL:HG23	2.15	0.46
1:D:589:PHE:HE2	1:D:593:THR:CG2	2.28	0.46
1:B:374:TYR:C	1:B:376:PRO:HD2	2.41	0.46
1:A:577:LEU:O	1:A:581:MET:N	2.49	0.46
1:A:647:LEU:CD1	1:A:648:GLU:H	2.29	0.46
1:C:240:LYS:HD3	1:C:242:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:374:TYR:C	1:C:376:PRO:HD2	2.41	0.46
1:C:401:TYR:N	1:C:401:TYR:CD1	2.81	0.46
1:C:538:VAL:C	1:C:540:SER:H	2.24	0.46
1:C:671:TYR:O	1:C:675:LEU:CB	2.62	0.46
1:C:701:ARG:CG	1:C:701:ARG:NH1	2.73	0.46
1:D:538:VAL:C	1:D:540:SER:H	2.24	0.46
1:D:545:LEU:HD23	1:D:545:LEU:O	2.15	0.46
1:B:142:ARG:NE	1:B:183:THR:HG22	2.31	0.46
1:B:172:THR:O	1:B:176:LEU:HB2	2.15	0.46
1:B:400:ALA:O	1:B:401:TYR:HD1	1.99	0.46
1:B:529:LEU:HA	1:B:532:SER:OG	2.16	0.46
1:B:545:LEU:O	1:B:545:LEU:HD23	2.15	0.46
1:A:142:ARG:NE	1:A:183:THR:HG22	2.31	0.46
1:A:589:PHE:CE2	1:A:593:THR:HG21	2.51	0.46
1:C:712:PHE:O	1:C:713:LEU:CB	2.64	0.46
1:D:538:VAL:HG13	1:D:539:ALA:N	2.30	0.46
1:B:425:LYS:CB	1:B:429:PHE:CE2	2.92	0.45
1:B:441:TYR:CG	1:B:555:TYR:HE1	2.35	0.45
1:C:524:LEU:O	1:C:528:VAL:HG23	2.15	0.45
1:C:589:PHE:CE2	1:C:593:THR:HG21	2.51	0.45
1:D:306:THR:HG23	1:D:351:TYR:HE1	1.79	0.45
1:D:637:LEU:HD22	1:D:666:TYR:CE2	2.51	0.45
1:D:640:PHE:CZ	1:D:663:LEU:HD13	2.51	0.45
1:B:158:LEU:CD2	1:B:158:LEU:C	2.89	0.45
1:B:689:ILE:O	1:B:690:ALA:C	2.60	0.45
1:A:158:LEU:O	1:A:158:LEU:CD2	2.61	0.45
1:A:530:TYR:O	1:A:533:GLN:N	2.50	0.45
1:A:760:UNK:CA	1:A:761:UNK:CB	2.87	0.45
1:C:441:TYR:CG	1:C:555:TYR:HE1	2.34	0.45
1:C:529:LEU:HA	1:C:532:SER:OG	2.16	0.45
1:D:374:TYR:C	1:D:376:PRO:HD2	2.41	0.45
1:D:474:ARG:HE	1:D:474:ARG:HB3	1.55	0.45
1:B:346:ILE:HG12	1:B:412:MET:HA	1.95	0.45
1:B:529:LEU:O	1:B:533:GLN:N	2.49	0.45
1:B:559:PHE:HB2	1:B:562:MET:CB	2.45	0.45
1:B:627:TYR:HD2	1:B:650:THR:HB	1.80	0.45
1:A:579:ARG:HH11	1:A:579:ARG:CB	2.29	0.45
1:A:592:SER:HA	1:A:637:LEU:HD12	1.98	0.45
1:D:441:TYR:CG	1:D:555:TYR:HE1	2.34	0.45
1:D:526:SER:HB2	1:D:540:SER:HB3	1.97	0.45
1:D:529:LEU:HA	1:D:532:SER:OG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:LEU:C	1:B:349:LEU:CD2	2.90	0.45
1:A:557:ARG:HA	1:A:558:GLY:HA2	1.28	0.45
1:B:526:SER:HB2	1:B:540:SER:HB3	1.97	0.45
1:B:640:PHE:CZ	1:B:663:LEU:HD13	2.51	0.45
1:A:240:LYS:HD3	1:A:242:ARG:HG2	1.98	0.45
1:A:276:ASP:C	1:A:276:ASP:OD1	2.59	0.45
1:C:647:LEU:CD1	1:C:648:GLU:H	2.29	0.45
1:D:462:PRO:HD2	1:D:464:LYS:N	2.28	0.45
1:D:629:SER:OG	1:D:632:SER:OG	2.03	0.45
1:D:647:LEU:CD1	1:D:648:GLU:H	2.29	0.45
1:D:678:LEU:HD12	1:D:678:LEU:C	2.40	0.45
1:B:491:ARG:HE	1:B:491:ARG:HB3	1.53	0.45
1:B:647:LEU:CD1	1:B:648:GLU:H	2.29	0.45
1:A:538:VAL:C	1:A:540:SER:H	2.24	0.45
1:A:553:LEU:O	1:A:556:THR:HG22	2.17	0.45
1:A:569:ILE:C	1:A:569:ILE:CD1	2.86	0.45
1:A:681:LEU:CD1	1:A:682:MET:H	2.06	0.45
1:A:760:UNK:HA	1:A:761:UNK:C	2.46	0.45
1:C:429:PHE:HD2	1:C:430:VAL:H	1.64	0.45
1:C:635:LEU:HD22	1:C:635:LEU:HA	1.77	0.45
1:C:760:UNK:HA	1:C:761:UNK:C	2.47	0.45
1:D:240:LYS:HD3	1:D:242:ARG:HG2	1.98	0.45
1:D:579:ARG:HH11	1:D:579:ARG:CB	2.29	0.45
1:B:524:LEU:HD22	1:B:524:LEU:HA	1.81	0.45
1:B:582:PHE:O	1:B:586:VAL:HG23	2.16	0.45
1:B:669:LEU:O	1:B:673:LEU:CB	2.59	0.45
1:B:671:TYR:O	1:B:675:LEU:CB	2.62	0.45
1:A:693:SER:O	1:A:694:LYS:C	2.60	0.45
1:A:712:PHE:O	1:A:713:LEU:CB	2.64	0.45
1:C:553:LEU:O	1:C:556:THR:HG22	2.17	0.45
1:C:647:LEU:HG	1:D:639:LYS:HE2	1.98	0.45
1:D:158:LEU:CD2	1:D:158:LEU:C	2.89	0.45
1:D:594:ALA:O	1:D:597:THR:OG1	2.33	0.45
1:B:240:LYS:HD3	1:B:242:ARG:HG2	1.98	0.45
1:B:400:ALA:C	1:B:402:SER:CB	2.86	0.45
1:B:462:PRO:HD2	1:B:464:LYS:N	2.28	0.45
1:B:530:TYR:O	1:B:533:GLN:N	2.50	0.45
1:B:589:PHE:CE2	1:B:593:THR:HG21	2.51	0.45
1:A:401:TYR:N	1:A:401:TYR:CD1	2.81	0.45
1:A:428:ARG:NH1	1:A:428:ARG:CG	2.73	0.45
1:A:462:PRO:CB	1:A:464:LYS:N	2.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:487:TYR:CE1	1:A:491:ARG:CG	2.90	0.45
1:A:529:LEU:HA	1:A:532:SER:OG	2.16	0.45
1:A:591:PHE:CG	1:A:666:TYR:HB2	2.51	0.45
1:A:689:ILE:O	1:A:690:ALA:C	2.60	0.45
1:D:242:ARG:CB	1:D:243:PRO:CA	2.95	0.45
1:D:349:LEU:C	1:D:349:LEU:CD2	2.90	0.45
1:D:529:LEU:O	1:D:533:GLN:N	2.49	0.45
1:D:582:PHE:O	1:D:586:VAL:HG23	2.16	0.45
1:D:589:PHE:CE2	1:D:593:THR:HG21	2.51	0.45
1:B:376:PRO:CB	1:D:245:PHE:CB	2.93	0.45
1:B:553:LEU:O	1:B:556:THR:HG22	2.17	0.45
1:B:592:SER:HA	1:B:637:LEU:HD12	1.98	0.45
1:B:601:ASP:CG	1:B:602:GLY:N	2.73	0.45
1:B:658:VAL:CG1	1:A:543:PHE:CZ	2.95	0.45
1:A:374:TYR:C	1:A:376:PRO:HD2	2.41	0.45
1:A:453:TYR:CD2	1:A:453:TYR:O	2.70	0.45
1:A:582:PHE:O	1:A:586:VAL:HG23	2.16	0.45
1:A:663:LEU:O	1:A:664:LEU:C	2.60	0.45
1:C:396:LEU:O	1:C:400:ALA:CA	2.62	0.45
1:C:530:TYR:O	1:C:533:GLN:N	2.50	0.45
1:C:595:VAL:HG13	1:C:659:PHE:HE2	1.81	0.45
1:C:647:LEU:CD2	1:D:642:ILE:HD11	2.47	0.45
1:D:346:ILE:HG13	1:D:412:MET:CB	2.45	0.45
1:D:530:TYR:O	1:D:533:GLN:N	2.50	0.45
1:D:573:ILE:O	1:D:577:LEU:CD2	2.65	0.45
1:A:158:LEU:CD2	1:A:158:LEU:C	2.89	0.45
1:A:400:ALA:O	1:A:401:TYR:HD1	2.00	0.45
1:A:635:LEU:HD22	1:A:635:LEU:HA	1.77	0.45
1:C:261:LEU:HD21	1:C:311:GLU:HG2	2.00	0.45
1:C:453:TYR:CD2	1:C:453:TYR:O	2.70	0.45
1:C:538:VAL:HG13	1:C:539:ALA:N	2.30	0.45
1:C:592:SER:HA	1:C:637:LEU:HD12	1.98	0.45
1:D:428:ARG:HD2	1:D:429:PHE:CD1	2.44	0.45
1:D:592:SER:HA	1:D:637:LEU:HD12	1.98	0.45
1:D:595:VAL:HG13	1:D:659:PHE:HE2	1.81	0.45
1:B:237:LYS:HB2	1:B:237:LYS:HE3	1.67	0.44
1:B:554:TYR:CD1	1:B:554:TYR:O	2.70	0.44
1:B:693:SER:O	1:B:694:LYS:C	2.60	0.44
1:A:242:ARG:CG	1:A:242:ARG:NH1	2.75	0.44
1:A:441:TYR:CG	1:A:555:TYR:HE1	2.35	0.44
1:A:573:ILE:CD1	1:A:577:LEU:CD2	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:242:ARG:CB	1:C:243:PRO:CA	2.95	0.44
1:D:421:LEU:HD23	1:D:421:LEU:C	2.42	0.44
1:D:588:LEU:O	1:D:592:SER:HB3	2.18	0.44
1:B:306:THR:HG23	1:B:351:TYR:HE1	1.79	0.44
1:B:573:ILE:O	1:B:577:LEU:CD2	2.65	0.44
1:C:573:ILE:CD1	1:C:577:LEU:CD2	2.96	0.44
1:C:670:THR:O	1:C:674:LEU:CB	2.38	0.44
1:C:681:LEU:CD1	1:C:682:MET:N	2.73	0.44
1:D:453:TYR:CD2	1:D:453:TYR:O	2.70	0.44
1:B:588:LEU:O	1:B:592:SER:HB3	2.18	0.44
1:B:681:LEU:CD1	1:B:682:MET:H	2.06	0.44
1:C:579:ARG:HH11	1:C:579:ARG:HG2	1.77	0.44
1:D:400:ALA:O	1:D:401:TYR:HD1	2.00	0.44
1:D:429:PHE:HD2	1:D:430:VAL:H	1.64	0.44
1:D:701:ARG:CG	1:D:701:ARG:NH1	2.73	0.44
1:D:712:PHE:O	1:D:713:LEU:CB	2.64	0.44
1:B:242:ARG:CB	1:B:243:PRO:CA	2.95	0.44
1:B:584:TYR:CD1	1:B:584:TYR:C	2.95	0.44
1:A:136:LEU:HD23	1:A:136:LEU:N	2.21	0.44
1:A:349:LEU:C	1:A:349:LEU:CD2	2.90	0.44
1:A:568:MET:HA	1:A:571:LYS:CD	2.48	0.44
1:A:694:LYS:C	1:A:694:LYS:CD	2.85	0.44
1:C:568:MET:HA	1:C:571:LYS:CD	2.48	0.44
1:C:582:PHE:O	1:C:586:VAL:HG23	2.16	0.44
1:C:689:ILE:O	1:C:690:ALA:C	2.60	0.44
1:D:579:ARG:HH11	1:D:579:ARG:HG2	1.77	0.44
1:A:554:TYR:CD1	1:A:554:TYR:O	2.70	0.44
1:C:400:ALA:O	1:C:401:TYR:HD1	2.00	0.44
1:D:487:TYR:CE1	1:D:491:ARG:HD3	2.53	0.44
1:D:553:LEU:O	1:D:556:THR:HG22	2.17	0.44
1:D:689:ILE:O	1:D:690:ALA:C	2.60	0.44
1:D:693:SER:O	1:D:694:LYS:C	2.60	0.44
1:B:453:TYR:CD2	1:B:453:TYR:O	2.70	0.44
1:B:584:TYR:O	1:B:584:TYR:CD1	2.70	0.44
1:B:681:LEU:HD13	1:B:681:LEU:N	2.31	0.44
1:A:500:ARG:HA	1:A:501:PRO:HA	1.66	0.44
1:A:664:LEU:O	1:A:668:ILE:CG1	2.66	0.44
1:C:584:TYR:C	1:C:584:TYR:CD1	2.95	0.44
1:C:655:PHE:CD1	1:D:539:ALA:CB	2.70	0.44
1:C:681:LEU:HD13	1:C:681:LEU:N	2.31	0.44
1:D:425:LYS:CB	1:D:429:PHE:CE2	2.92	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:349:LEU:C	1:C:349:LEU:CD2	2.90	0.44
1:D:400:ALA:C	1:D:402:SER:CB	2.86	0.44
1:D:627:TYR:HD2	1:D:650:THR:HB	1.80	0.44
1:D:760:UNK:HA	1:D:761:UNK:C	2.47	0.44
1:B:536:GLU:C	1:B:538:VAL:N	2.72	0.44
1:A:560:GLN:OE1	1:A:560:GLN:HA	2.18	0.44
1:C:276:ASP:C	1:C:276:ASP:OD1	2.59	0.44
1:C:573:ILE:O	1:C:577:LEU:CD2	2.65	0.44
1:D:681:LEU:HD13	1:D:681:LEU:N	2.31	0.44
1:B:568:MET:HA	1:B:571:LYS:CD	2.48	0.44
1:B:573:ILE:CD1	1:B:577:LEU:CD2	2.96	0.44
1:B:689:ILE:HG23	1:B:690:ALA:N	2.33	0.44
1:D:261:LEU:HD21	1:D:311:GLU:HG2	2.00	0.44
1:D:568:MET:HA	1:D:571:LYS:CD	2.48	0.44
1:B:557:ARG:HA	1:B:558:GLY:HA2	1.28	0.43
1:B:568:MET:HA	1:B:571:LYS:HD3	2.00	0.43
1:B:760:UNK:HA	1:B:761:UNK:C	2.47	0.43
1:A:400:ALA:C	1:A:402:SER:CB	2.86	0.43
1:A:402:SER:CB	1:A:703:ILE:HD11	2.41	0.43
1:A:701:ARG:HB2	1:A:701:ARG:NH1	2.23	0.43
1:C:554:TYR:CD1	1:C:554:TYR:O	2.70	0.43
1:C:588:LEU:O	1:C:592:SER:HB3	2.18	0.43
1:D:469:VAL:O	1:D:470:GLY:C	2.61	0.43
1:D:760:UNK:CA	1:D:761:UNK:CB	2.87	0.43
1:A:242:ARG:CB	1:A:243:PRO:CA	2.95	0.43
1:A:524:LEU:HD22	1:A:524:LEU:HA	1.81	0.43
1:A:573:ILE:O	1:A:577:LEU:CD2	2.65	0.43
1:A:584:TYR:O	1:A:584:TYR:CD1	2.70	0.43
1:C:306:THR:O	1:C:351:TYR:OH	2.33	0.43
1:C:678:LEU:HD12	1:C:678:LEU:C	2.40	0.43
1:D:188:GLN:H	1:D:188:GLN:NE2	2.13	0.43
1:D:396:LEU:HD13	1:D:418:LEU:HD23	1.89	0.43
1:D:573:ILE:CD1	1:D:577:LEU:CD2	2.96	0.43
1:D:584:TYR:O	1:D:584:TYR:CD1	2.70	0.43
1:D:664:LEU:O	1:D:668:ILE:CG1	2.66	0.43
1:A:573:ILE:HD13	1:A:573:ILE:O	2.18	0.43
1:A:588:LEU:O	1:A:592:SER:HB3	2.18	0.43
1:C:664:LEU:O	1:C:668:ILE:CG1	2.66	0.43
1:D:426:TRP:HD1	1:D:430:VAL:HG11	1.84	0.43
1:D:560:GLN:OE1	1:D:560:GLN:HA	2.18	0.43
1:D:663:LEU:O	1:D:664:LEU:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:538:VAL:C	1:B:540:SER:H	2.24	0.43
1:B:560:GLN:OE1	1:B:560:GLN:HA	2.18	0.43
1:A:127:GLN:C	1:A:129:LEU:N	2.77	0.43
1:A:269:GLN:HE22	1:A:318:LYS:NZ	2.17	0.43
1:A:673:LEU:CD1	1:C:573:ILE:HB	2.49	0.43
1:C:142:ARG:C	1:C:144:THR:N	2.76	0.43
1:C:421:LEU:HD23	1:C:421:LEU:C	2.42	0.43
1:D:240:LYS:HB2	1:D:241:GLY:C	2.44	0.43
1:D:573:ILE:HD13	1:D:573:ILE:O	2.18	0.43
1:B:487:TYR:CE1	1:B:491:ARG:HD3	2.53	0.43
1:B:573:ILE:HD13	1:B:573:ILE:O	2.18	0.43
1:B:681:LEU:CD1	1:B:682:MET:N	2.73	0.43
1:A:568:MET:HA	1:A:571:LYS:HD3	2.01	0.43
1:C:426:TRP:HD1	1:C:430:VAL:HG11	1.84	0.43
1:B:579:ARG:O	1:B:583:VAL:HG23	2.19	0.43
1:C:240:LYS:N	1:C:242:ARG:N	2.66	0.43
1:C:668:ILE:C	1:C:668:ILE:CD1	2.88	0.43
1:C:669:LEU:O	1:C:673:LEU:CB	2.59	0.43
1:C:687:ASN:HD22	1:C:688:LYS:HB2	1.84	0.43
1:C:689:ILE:HG23	1:C:690:ALA:N	2.33	0.43
1:D:557:ARG:HA	1:D:558:GLY:HA2	1.28	0.43
1:D:661:ILE:C	1:D:661:ILE:CD1	2.92	0.43
1:B:261:LEU:HD21	1:B:311:GLU:HG2	2.00	0.43
1:B:500:ARG:HA	1:B:501:PRO:HA	1.66	0.43
1:A:261:LEU:HD21	1:A:311:GLU:HG2	1.99	0.43
1:A:306:THR:HG23	1:A:351:TYR:HE1	1.79	0.43
1:C:240:LYS:HB2	1:C:241:GLY:C	2.44	0.43
1:C:269:GLN:HE22	1:C:318:LYS:NZ	2.17	0.43
1:C:701:ARG:HB2	1:C:701:ARG:NH1	2.23	0.43
1:D:584:TYR:CD1	1:D:584:TYR:C	2.95	0.43
1:D:669:LEU:O	1:D:673:LEU:CB	2.59	0.43
1:B:474:ARG:HE	1:B:474:ARG:HB3	1.55	0.43
1:B:647:LEU:HD23	1:A:642:ILE:HD12	1.98	0.43
1:B:664:LEU:O	1:B:668:ILE:CG1	2.66	0.43
1:B:687:ASN:HD22	1:B:688:LYS:HB2	1.84	0.43
1:A:237:LYS:HB2	1:A:237:LYS:HE3	1.67	0.43
1:A:295:ALA:HA	1:A:301:ASN:HD21	1.84	0.43
1:A:306:THR:O	1:A:351:TYR:OH	2.33	0.43
1:A:469:VAL:O	1:A:470:GLY:C	2.61	0.43
1:C:127:GLN:C	1:C:129:LEU:N	2.77	0.43
1:C:295:ALA:HA	1:C:301:ASN:HD21	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:237:LYS:HE3	1:D:237:LYS:HB2	1.67	0.43
1:D:500:ARG:HA	1:D:501:PRO:HA	1.66	0.43
1:D:569:ILE:HG23	1:D:570:GLU:N	2.34	0.43
1:B:640:PHE:CZ	1:B:663:LEU:CD1	3.02	0.43
1:B:661:ILE:C	1:B:661:ILE:CD1	2.92	0.43
1:A:579:ARG:O	1:A:583:VAL:HG23	2.19	0.43
1:A:668:ILE:C	1:A:668:ILE:CD1	2.88	0.43
1:C:402:SER:CB	1:C:703:ILE:HD11	2.41	0.43
1:C:592:SER:HA	1:C:637:LEU:CD1	2.49	0.43
1:C:627:TYR:HD2	1:C:650:THR:CB	2.31	0.43
1:B:127:GLN:C	1:B:129:LEU:N	2.77	0.43
1:B:569:ILE:HG23	1:B:570:GLU:N	2.34	0.43
1:B:701:ARG:HB2	1:B:701:ARG:NH1	2.23	0.43
1:A:689:ILE:HG23	1:A:690:ALA:N	2.33	0.43
1:C:438:PHE:CD1	1:C:438:PHE:O	2.72	0.43
1:C:487:TYR:CE1	1:C:491:ARG:HD3	2.53	0.43
1:C:557:ARG:HA	1:C:558:GLY:HA2	1.28	0.43
1:C:560:GLN:OE1	1:C:560:GLN:HA	2.18	0.43
1:C:661:ILE:C	1:C:661:ILE:CD1	2.92	0.43
1:C:681:LEU:HD12	1:C:681:LEU:H	1.84	0.43
1:D:142:ARG:C	1:D:144:THR:N	2.76	0.43
1:D:554:TYR:CD1	1:D:554:TYR:O	2.70	0.43
1:B:240:LYS:HB2	1:B:241:GLY:C	2.44	0.42
1:B:346:ILE:HG13	1:B:412:MET:CB	2.44	0.42
1:B:627:TYR:HD2	1:B:650:THR:CB	2.31	0.42
1:A:142:ARG:C	1:A:144:THR:N	2.76	0.42
1:A:425:LYS:CA	1:A:429:PHE:HE2	2.32	0.42
1:A:584:TYR:CD1	1:A:584:TYR:C	2.95	0.42
1:A:687:ASN:HD22	1:A:688:LYS:HB2	1.84	0.42
1:C:142:ARG:NE	1:C:183:THR:HG21	2.34	0.42
1:C:428:ARG:CD	1:C:428:ARG:C	2.86	0.42
1:C:510:SER:HG	1:C:513:GLU:CB	2.28	0.42
1:B:142:ARG:C	1:B:144:THR:N	2.76	0.42
1:B:592:SER:HA	1:B:637:LEU:CD1	2.49	0.42
1:B:599:ILE:CD1	1:B:628:ASN:N	2.67	0.42
1:B:630:LEU:C	1:B:630:LEU:CD1	2.92	0.42
1:A:421:LEU:HD23	1:A:421:LEU:C	2.43	0.42
1:A:438:PHE:CD1	1:A:438:PHE:O	2.72	0.42
1:A:487:TYR:CE1	1:A:491:ARG:HD3	2.53	0.42
1:C:568:MET:HA	1:C:571:LYS:HD3	2.01	0.42
1:C:693:SER:O	1:C:694:LYS:C	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:687:ASN:HD22	1:D:688:LYS:HB2	1.84	0.42
1:B:295:ALA:HA	1:B:301:ASN:HD21	1.84	0.42
1:B:663:LEU:O	1:B:664:LEU:C	2.60	0.42
1:A:592:SER:HA	1:A:637:LEU:CD1	2.49	0.42
1:C:425:LYS:CA	1:C:429:PHE:HE2	2.32	0.42
1:D:240:LYS:N	1:D:242:ARG:N	2.66	0.42
1:D:640:PHE:CZ	1:D:663:LEU:CD1	3.02	0.42
1:B:240:LYS:N	1:B:242:ARG:N	2.66	0.42
1:B:421:LEU:HD23	1:B:421:LEU:C	2.43	0.42
1:A:487:TYR:HE1	1:A:491:ARG:HD2	1.83	0.42
1:C:579:ARG:O	1:C:583:VAL:HG23	2.19	0.42
1:B:349:LEU:HD23	1:B:349:LEU:O	2.20	0.42
1:B:469:VAL:O	1:B:470:GLY:C	2.61	0.42
1:B:580:PHE:CE2	1:B:678:LEU:CD2	3.03	0.42
1:A:640:PHE:CZ	1:A:663:LEU:CD1	3.02	0.42
1:A:681:LEU:HD12	1:A:681:LEU:H	1.84	0.42
1:C:569:ILE:HG23	1:C:570:GLU:N	2.34	0.42
1:C:584:TYR:O	1:C:584:TYR:CD1	2.70	0.42
1:C:663:LEU:O	1:C:664:LEU:C	2.60	0.42
1:D:569:ILE:C	1:D:569:ILE:CD1	2.86	0.42
1:D:599:ILE:O	1:D:599:ILE:HG13	2.19	0.42
1:B:425:LYS:CA	1:B:429:PHE:HE2	2.32	0.42
1:B:565:TYR:OH	1:D:674:LEU:CD1	2.68	0.42
1:B:599:ILE:O	1:B:599:ILE:HG13	2.19	0.42
1:A:240:LYS:HB2	1:A:241:GLY:C	2.44	0.42
1:A:627:TYR:HD2	1:A:650:THR:CB	2.32	0.42
1:A:661:ILE:C	1:A:661:ILE:CD1	2.92	0.42
1:C:573:ILE:HD13	1:C:573:ILE:O	2.18	0.42
1:D:438:PHE:CD1	1:D:438:PHE:O	2.72	0.42
1:D:511:TYR:CZ	1:D:515:LEU:HD13	2.55	0.42
1:D:627:TYR:HD2	1:D:650:THR:CB	2.32	0.42
1:D:676:ASN:OD1	1:D:676:ASN:N	2.51	0.42
1:B:438:PHE:CD1	1:B:438:PHE:O	2.72	0.42
1:B:647:LEU:CD2	1:A:642:ILE:HD11	2.49	0.42
1:A:580:PHE:CE2	1:A:678:LEU:CD2	3.03	0.42
1:C:188:GLN:H	1:C:188:GLN:NE2	2.13	0.42
1:D:269:GLN:HE22	1:D:318:LYS:NZ	2.17	0.42
1:D:579:ARG:O	1:D:583:VAL:HG23	2.19	0.42
1:D:681:LEU:HD12	1:D:681:LEU:H	1.84	0.42
1:B:681:LEU:HD12	1:B:681:LEU:H	1.84	0.42
1:C:245:PHE:CB	1:D:376:PRO:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:367:ARG:HH11	1:D:367:ARG:HG3	1.78	0.42
1:D:568:MET:HA	1:D:571:LYS:HD3	2.00	0.42
1:B:511:TYR:CZ	1:B:515:LEU:HD13	2.55	0.42
1:B:530:TYR:C	1:B:533:GLN:H	2.28	0.42
1:A:366:SER:HB3	1:A:369:PHE:HE1	1.85	0.42
1:A:530:TYR:C	1:A:533:GLN:H	2.28	0.42
1:A:569:ILE:HG23	1:A:570:GLU:N	2.34	0.42
1:A:701:ARG:HG2	1:A:705:ILE:HD12	2.02	0.42
1:C:434:PHE:HZ	1:C:555:TYR:O	2.03	0.42
1:C:647:LEU:HD23	1:D:642:ILE:HD11	2.01	0.42
1:D:127:GLN:C	1:D:129:LEU:N	2.77	0.42
1:D:689:ILE:HG23	1:D:690:ALA:N	2.33	0.42
1:B:269:GLN:HE22	1:B:318:LYS:NZ	2.17	0.42
1:B:434:PHE:HZ	1:B:555:TYR:O	2.03	0.42
1:C:349:LEU:HD23	1:C:349:LEU:O	2.20	0.42
1:C:366:SER:HB3	1:C:369:PHE:HE1	1.85	0.42
1:D:295:ALA:HA	1:D:301:ASN:HD21	1.84	0.42
1:D:349:LEU:HD23	1:D:349:LEU:O	2.20	0.42
1:D:434:PHE:HZ	1:D:555:TYR:O	2.03	0.42
1:D:530:TYR:C	1:D:533:GLN:H	2.28	0.42
1:D:580:PHE:CE2	1:D:678:LEU:CD2	3.03	0.42
1:D:656:LYS:HB3	1:D:657:ALA:H	1.60	0.42
1:B:242:ARG:CB	1:B:243:PRO:HA	2.50	0.41
1:B:456:PRO:HD3	1:B:474:ARG:NH1	2.35	0.41
1:B:521:LEU:C	1:B:521:LEU:CD1	2.86	0.41
1:B:670:THR:O	1:B:674:LEU:CB	2.38	0.41
1:B:701:ARG:HG2	1:B:705:ILE:HD12	2.02	0.41
1:A:434:PHE:HZ	1:A:555:TYR:O	2.03	0.41
1:A:596:VAL:CG2	1:A:633:THR:CG2	2.73	0.41
1:A:669:LEU:O	1:A:673:LEU:CB	2.59	0.41
1:A:685:THR:HG23	1:A:686:VAL:N	2.35	0.41
1:C:304:PHE:CD1	1:C:304:PHE:C	2.98	0.41
1:C:596:VAL:HG23	1:C:633:THR:HG21	1.88	0.41
1:C:630:LEU:C	1:C:630:LEU:CD1	2.92	0.41
1:C:673:LEU:HD22	1:C:673:LEU:HA	1.73	0.41
1:D:425:LYS:CA	1:D:429:PHE:HE2	2.32	0.41
1:D:456:PRO:HD3	1:D:474:ARG:NH1	2.35	0.41
1:D:545:LEU:CD2	1:D:549:TRP:CD1	3.03	0.41
1:D:592:SER:HA	1:D:637:LEU:CD1	2.49	0.41
1:D:668:ILE:CG1	1:D:669:LEU:N	2.83	0.41
1:D:682:MET:C	1:D:685:THR:HG22	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:ARG:NE	1:A:183:THR:HG21	2.34	0.41
1:A:367:ARG:NH2	1:A:385:SER:CB	2.68	0.41
1:A:589:PHE:HE2	1:A:593:THR:HG21	1.86	0.41
1:A:630:LEU:C	1:A:630:LEU:CD1	2.93	0.41
1:C:545:LEU:CD2	1:C:549:TRP:CD1	3.03	0.41
1:C:668:ILE:CG1	1:C:669:LEU:N	2.83	0.41
1:C:682:MET:C	1:C:685:THR:HG22	2.45	0.41
1:C:701:ARG:HG2	1:C:705:ILE:HD12	2.02	0.41
1:B:366:SER:HB3	1:B:369:PHE:HE1	1.85	0.41
1:B:538:VAL:O	1:B:541:MET:N	2.54	0.41
1:B:564:ILE:CD1	1:B:564:ILE:H	2.33	0.41
1:A:240:LYS:N	1:A:242:ARG:N	2.66	0.41
1:A:560:GLN:NE2	1:A:697:TRP:CZ2	2.84	0.41
1:A:663:LEU:HD23	1:A:663:LEU:HA	1.80	0.41
1:C:245:PHE:CD1	1:D:376:PRO:HB3	2.50	0.41
1:C:640:PHE:CZ	1:C:663:LEU:CD1	3.02	0.41
1:C:689:ILE:C	1:C:691:GLN:N	2.77	0.41
1:D:670:THR:O	1:D:674:LEU:CB	2.38	0.41
1:B:677:MET:N	1:A:572:MET:HE1	2.35	0.41
1:A:245:PHE:CB	1:C:376:PRO:HB2	2.48	0.41
1:A:349:LEU:HD23	1:A:349:LEU:O	2.20	0.41
1:A:456:PRO:HD3	1:A:474:ARG:NH1	2.35	0.41
1:A:689:ILE:HD12	1:A:692:GLU:CB	2.51	0.41
1:C:664:LEU:HD12	1:D:638:PHE:CE1	2.55	0.41
1:D:689:ILE:HD12	1:D:692:GLU:CB	2.51	0.41
1:B:372:TRP:HZ3	1:B:379:SER:HB2	1.86	0.41
1:B:668:ILE:CG1	1:B:669:LEU:N	2.83	0.41
1:B:689:ILE:HD12	1:B:692:GLU:CB	2.51	0.41
1:A:579:ARG:O	1:C:562:MET:HE1	2.21	0.41
1:C:428:ARG:HG3	1:C:429:PHE:N	2.36	0.41
1:C:469:VAL:O	1:C:470:GLY:C	2.61	0.41
1:C:530:TYR:C	1:C:533:GLN:H	2.28	0.41
1:C:538:VAL:O	1:C:541:MET:N	2.53	0.41
1:C:590:GLY:O	1:C:593:THR:OG1	2.31	0.41
1:C:760:UNK:CA	1:C:761:UNK:CB	2.86	0.41
1:D:242:ARG:CB	1:D:243:PRO:HA	2.50	0.41
1:D:630:LEU:C	1:D:630:LEU:CD1	2.92	0.41
1:B:589:PHE:HE2	1:B:593:THR:HG21	1.85	0.41
1:A:127:GLN:C	1:A:129:LEU:H	2.29	0.41
1:A:426:TRP:HD1	1:A:430:VAL:HG11	1.84	0.41
1:A:545:LEU:CD2	1:A:549:TRP:CD1	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:689:ILE:O	1:A:692:GLU:N	2.54	0.41
1:C:571:LYS:HZ3	1:C:693:SER:HB2	1.84	0.41
1:C:573:ILE:HG12	1:C:577:LEU:CD2	2.50	0.41
1:C:599:ILE:O	1:C:599:ILE:HG13	2.20	0.41
1:C:689:ILE:HD12	1:C:692:GLU:CB	2.51	0.41
1:D:136:LEU:HD23	1:D:136:LEU:N	2.21	0.41
1:D:166:HIS:O	1:D:166:HIS:CG	2.74	0.41
1:D:434:PHE:CZ	1:D:555:TYR:O	2.74	0.41
1:B:637:LEU:HD23	1:B:637:LEU:HA	1.96	0.41
1:A:498:GLN:CA	1:A:499:ARG:HH11	2.34	0.41
1:A:599:ILE:O	1:A:599:ILE:HG13	2.20	0.41
1:C:127:GLN:C	1:C:129:LEU:H	2.29	0.41
1:C:346:ILE:HG13	1:C:412:MET:CB	2.45	0.41
1:C:487:TYR:HE1	1:C:491:ARG:HD2	1.84	0.41
1:D:560:GLN:NE2	1:D:697:TRP:CZ2	2.84	0.41
1:D:564:ILE:CD1	1:D:564:ILE:H	2.33	0.41
1:B:295:ALA:HB3	1:B:345:LYS:HD2	2.02	0.41
1:B:498:GLN:CA	1:B:499:ARG:HH11	2.34	0.41
1:B:673:LEU:HD13	1:A:572:MET:CG	2.50	0.41
1:A:242:ARG:CB	1:A:243:PRO:HA	2.50	0.41
1:C:580:PHE:CE2	1:C:678:LEU:CD2	3.03	0.41
1:D:521:LEU:C	1:D:521:LEU:CD1	2.86	0.41
1:B:682:MET:C	1:B:685:THR:HG22	2.45	0.41
1:A:180:ALA:O	1:A:184:ASP:N	2.54	0.41
1:A:400:ALA:O	1:A:703:ILE:CG1	2.57	0.41
1:C:367:ARG:NH2	1:C:385:SER:CB	2.68	0.41
1:C:397:GLU:HA	1:C:400:ALA:CB	2.50	0.41
1:C:400:ALA:O	1:C:703:ILE:CG1	2.57	0.41
1:C:456:PRO:HD3	1:C:474:ARG:NH1	2.35	0.41
1:C:660:ILE:HD13	1:D:631:TYR:OH	2.21	0.41
1:D:304:PHE:CD1	1:D:304:PHE:C	2.98	0.41
1:D:394:SER:C	1:D:396:LEU:N	2.79	0.41
1:D:428:ARG:HG3	1:D:429:PHE:N	2.36	0.41
1:D:538:VAL:O	1:D:541:MET:N	2.53	0.41
1:D:685:THR:HG23	1:D:686:VAL:N	2.35	0.41
1:D:701:ARG:HG2	1:D:705:ILE:HD12	2.02	0.41
1:B:166:HIS:O	1:B:166:HIS:CG	2.74	0.41
1:B:304:PHE:CD1	1:B:304:PHE:C	2.98	0.41
1:A:511:TYR:CZ	1:A:515:LEU:HD13	2.55	0.41
1:A:538:VAL:O	1:A:541:MET:N	2.54	0.41
1:C:242:ARG:CB	1:C:243:PRO:HA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:589:PHE:HE2	1:C:593:THR:HG21	1.86	0.41
1:C:640:PHE:HA	1:C:645:GLY:HA3	2.03	0.41
1:D:640:PHE:HA	1:D:645:GLY:HA3	2.03	0.41
1:B:306:THR:OG1	1:B:351:TYR:CD1	2.55	0.40
1:B:515:LEU:HA	1:B:518:VAL:HG23	2.03	0.40
1:B:640:PHE:HZ	1:B:647:LEU:CA	2.33	0.40
1:B:689:ILE:C	1:B:691:GLN:N	2.77	0.40
1:A:304:PHE:CD1	1:A:304:PHE:C	2.98	0.40
1:C:689:ILE:O	1:C:692:GLU:N	2.54	0.40
1:C:701:ARG:HG2	1:C:705:ILE:CD1	2.52	0.40
1:D:372:TRP:HZ3	1:D:379:SER:HB2	1.85	0.40
1:D:487:TYR:CE1	1:D:491:ARG:CG	2.90	0.40
1:D:701:ARG:HG2	1:D:705:ILE:CD1	2.52	0.40
1:B:545:LEU:CD2	1:B:549:TRP:CD1	3.03	0.40
1:B:635:LEU:HD22	1:B:635:LEU:HA	1.77	0.40
1:A:359:GLU:O	1:A:362:CYS:N	2.48	0.40
1:A:491:ARG:HE	1:A:491:ARG:HB3	1.53	0.40
1:A:564:ILE:CD1	1:A:564:ILE:H	2.33	0.40
1:A:664:LEU:HD12	1:A:664:LEU:HA	1.91	0.40
1:A:668:ILE:CG1	1:A:669:LEU:N	2.83	0.40
1:C:339:LEU:O	1:C:340:ALA:C	2.65	0.40
1:C:394:SER:C	1:C:396:LEU:N	2.79	0.40
1:C:396:LEU:HD13	1:C:418:LEU:HD23	1.88	0.40
1:C:434:PHE:CZ	1:C:555:TYR:O	2.74	0.40
1:C:500:ARG:HA	1:C:501:PRO:HA	1.66	0.40
1:D:125:ASN:HD22	1:D:128:GLU:HG2	1.86	0.40
1:D:142:ARG:NE	1:D:183:THR:HG21	2.34	0.40
1:D:180:ALA:O	1:D:184:ASP:N	2.54	0.40
1:D:366:SER:HB3	1:D:369:PHE:HE1	1.85	0.40
1:D:599:ILE:CD1	1:D:628:ASN:N	2.67	0.40
1:B:579:ARG:O	1:A:562:MET:HE1	2.21	0.40
1:B:689:ILE:O	1:B:692:GLU:N	2.54	0.40
1:A:434:PHE:CZ	1:A:555:TYR:O	2.74	0.40
1:C:125:ASN:HD22	1:C:128:GLU:HG2	1.87	0.40
1:C:498:GLN:CA	1:C:499:ARG:HH11	2.34	0.40
1:D:425:LYS:C	1:D:430:VAL:HG12	2.46	0.40
1:D:461:PRO:HA	1:D:462:PRO:O	2.22	0.40
1:D:640:PHE:HZ	1:D:647:LEU:CA	2.33	0.40
1:B:180:ALA:O	1:B:184:ASP:N	2.54	0.40
1:B:400:ALA:O	1:B:703:ILE:CG1	2.57	0.40
1:B:434:PHE:CZ	1:B:555:TYR:O	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:640:PHE:HA	1:B:645:GLY:HA3	2.03	0.40
1:B:673:LEU:O	1:A:572:MET:SD	2.80	0.40
1:A:188:GLN:H	1:A:188:GLN:NE2	2.13	0.40
1:A:461:PRO:HA	1:A:462:PRO:O	2.22	0.40
1:C:166:HIS:O	1:C:166:HIS:CG	2.74	0.40
1:C:180:ALA:O	1:C:184:ASP:N	2.54	0.40
1:C:372:TRP:HZ3	1:C:379:SER:HB2	1.85	0.40
1:C:647:LEU:HG	1:D:639:LYS:CE	2.51	0.40
1:D:589:PHE:HE2	1:D:593:THR:HG21	1.86	0.40
1:D:664:LEU:O	1:D:668:ILE:HG13	2.21	0.40
1:B:425:LYS:C	1:B:430:VAL:HG12	2.47	0.40
1:B:499:ARG:N	1:B:499:ARG:CD	2.73	0.40
1:B:562:MET:CE	1:D:583:VAL:HG23	2.52	0.40
1:B:685:THR:HG23	1:B:686:VAL:N	2.35	0.40
1:A:166:HIS:O	1:A:166:HIS:CG	2.74	0.40
1:A:394:SER:O	1:A:396:LEU:N	2.54	0.40
1:A:489:PHE:O	1:A:493:ILE:HG13	2.21	0.40
1:A:515:LEU:HA	1:A:518:VAL:HG23	2.03	0.40
1:A:664:LEU:O	1:A:668:ILE:HG13	2.21	0.40
1:A:676:ASN:CB	1:C:572:MET:CE	2.82	0.40
1:C:461:PRO:HA	1:C:462:PRO:O	2.22	0.40
1:D:295:ALA:HB3	1:D:345:LYS:HD2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	577/598 (96%)	525 (91%)	45 (8%)	7 (1%)	10	42
1	B	577/598 (96%)	525 (91%)	45 (8%)	7 (1%)	10	42
1	C	577/598 (96%)	525 (91%)	45 (8%)	7 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	577/598 (96%)	525 (91%)	45 (8%)	7 (1%)	10	42
All	All	2308/2392 (96%)	2100 (91%)	180 (8%)	28 (1%)	13	42

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	414	LEU
1	B	417	PRO
1	B	466	LYS
1	B	537	TYR
1	B	653	TYR
1	A	414	LEU
1	A	417	PRO
1	A	466	LYS
1	A	537	TYR
1	A	653	TYR
1	C	414	LEU
1	C	417	PRO
1	C	466	LYS
1	C	537	TYR
1	C	653	TYR
1	D	414	LEU
1	D	417	PRO
1	D	466	LYS
1	D	537	TYR
1	D	653	TYR
1	B	464	LYS
1	A	464	LYS
1	C	464	LYS
1	D	464	LYS
1	B	501	PRO
1	A	501	PRO
1	C	501	PRO
1	D	501	PRO

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	419/519 (81%)	299 (71%)	120 (29%)	0	2
1	B	419/519 (81%)	299 (71%)	120 (29%)	0	2
1	C	419/519 (81%)	299 (71%)	120 (29%)	0	2
1	D	419/519 (81%)	299 (71%)	120 (29%)	0	2
All	All	1676/2076 (81%)	1196 (71%)	480 (29%)	1	2

All (480) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	116	SER
1	B	123	GLN
1	B	128	GLU
1	B	131	SER
1	B	136	LEU
1	B	138	ARG
1	B	140	LYS
1	B	147	GLU
1	B	152	GLU
1	B	157	CYS
1	B	158	LEU
1	B	163	LEU
1	B	171	ASP
1	B	172	THR
1	B	176	LEU
1	B	186	LEU
1	B	187	LYS
1	B	188	GLN
1	B	190	VAL
1	B	218	THR
1	B	220	LEU
1	B	227	VAL
1	B	240	LYS
1	B	242	ARG
1	B	245	PHE
1	B	252	LEU
1	B	261	LEU
1	B	271	SER
1	B	283	VAL
1	B	287	VAL
1	B	294	VAL

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Mol	Chain	Res	Type
1	B	304	PHE
1	B	306	THR
1	B	315	LEU
1	B	319	LEU
1	B	325	LEU
1	B	332	LYS
1	B	339	LEU
1	B	346	ILE
1	B	362	CYS
1	B	366	SER
1	B	367	ARG
1	B	369	PHE
1	B	372	TRP
1	B	394	SER
1	B	401	TYR
1	B	402	SER
1	B	421	LEU
1	B	426	TRP
1	B	428	ARG
1	B	429	PHE
1	B	433	ILE
1	B	442	CYS
1	B	443	LEU
1	B	445	MET
1	B	447	ILE
1	B	455	ARG
1	B	474	ARG
1	B	482	VAL
1	B	486	VAL
1	B	499	ARG
1	B	502	SER
1	B	512	SER
1	B	514	ILE
1	B	515	LEU
1	B	518	VAL
1	B	520	SER
1	B	521	LEU
1	B	522	PHE
1	B	524	LEU
1	B	532	SER
1	B	533	GLN
1	B	540	SER

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Mol	Chain	Res	Type
1	B	545	LEU
1	B	547	MET
1	B	554	TYR
1	B	555	TYR
1	B	567	VAL
1	B	568	MET
1	B	569	ILE
1	B	570	GLU
1	B	572	MET
1	B	573	ILE
1	B	575	ARG
1	B	577	LEU
1	B	578	CYS
1	B	579	ARG
1	B	582	PHE
1	B	599	ILE
1	B	600	GLU
1	B	603	LYS
1	B	629	SER
1	B	630	LEU
1	B	632	SER
1	B	635	LEU
1	B	639	LYS
1	B	644	MET
1	B	647	LEU
1	B	648	GLU
1	B	649	PHE
1	B	651	GLU
1	B	656	LYS
1	B	659	PHE
1	B	660	ILE
1	B	661	ILE
1	B	663	LEU
1	B	664	LEU
1	B	668	ILE
1	B	673	LEU
1	B	674	LEU
1	B	676	ASN
1	B	681	LEU
1	B	687	ASN
1	B	688	LYS
1	B	697	TRP

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Mol	Chain	Res	Type
1	B	699	LEU
1	B	701	ARG
1	B	704	THR
1	B	708	THR
1	B	716	MET
1	A	116	SER
1	A	123	GLN
1	A	128	GLU
1	A	131	SER
1	A	136	LEU
1	A	138	ARG
1	A	140	LYS
1	A	147	GLU
1	A	152	GLU
1	A	157	CYS
1	A	158	LEU
1	A	163	LEU
1	A	171	ASP
1	A	172	THR
1	A	176	LEU
1	A	186	LEU
1	A	187	LYS
1	A	188	GLN
1	A	190	VAL
1	A	218	THR
1	A	220	LEU
1	A	227	VAL
1	A	240	LYS
1	A	242	ARG
1	A	245	PHE
1	A	252	LEU
1	A	261	LEU
1	A	271	SER
1	A	283	VAL
1	A	287	VAL
1	A	294	VAL
1	A	304	PHE
1	A	306	THR
1	A	315	LEU
1	A	319	LEU
1	A	325	LEU
1	A	332	LYS

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Mol	Chain	Res	Type
1	A	339	LEU
1	A	346	ILE
1	A	362	CYS
1	A	366	SER
1	A	367	ARG
1	A	369	PHE
1	A	372	TRP
1	A	394	SER
1	A	401	TYR
1	A	402	SER
1	A	421	LEU
1	A	426	TRP
1	A	428	ARG
1	A	429	PHE
1	A	433	ILE
1	A	442	CYS
1	A	443	LEU
1	A	445	MET
1	A	447	ILE
1	A	455	ARG
1	A	474	ARG
1	A	482	VAL
1	A	486	VAL
1	A	499	ARG
1	A	502	SER
1	A	512	SER
1	A	514	ILE
1	A	515	LEU
1	A	518	VAL
1	A	520	SER
1	A	521	LEU
1	A	522	PHE
1	A	524	LEU
1	A	532	SER
1	A	533	GLN
1	A	540	SER
1	A	545	LEU
1	A	547	MET
1	A	554	TYR
1	A	555	TYR
1	A	567	VAL
1	A	568	MET

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Mol	Chain	Res	Type
1	A	569	ILE
1	A	570	GLU
1	A	572	MET
1	A	573	ILE
1	A	575	ARG
1	A	577	LEU
1	A	578	CYS
1	A	579	ARG
1	A	582	PHE
1	A	599	ILE
1	A	600	GLU
1	A	603	LYS
1	A	629	SER
1	A	630	LEU
1	A	632	SER
1	A	635	LEU
1	A	639	LYS
1	A	644	MET
1	A	647	LEU
1	A	648	GLU
1	A	649	PHE
1	A	651	GLU
1	A	656	LYS
1	A	659	PHE
1	A	660	ILE
1	A	661	ILE
1	A	663	LEU
1	A	664	LEU
1	A	668	ILE
1	A	673	LEU
1	A	674	LEU
1	A	676	ASN
1	A	681	LEU
1	A	687	ASN
1	A	688	LYS
1	A	697	TRP
1	A	699	LEU
1	A	701	ARG
1	A	704	THR
1	A	708	THR
1	A	716	MET
1	C	116	SER

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Mol	Chain	Res	Type
1	C	123	GLN
1	C	128	GLU
1	C	131	SER
1	C	136	LEU
1	C	138	ARG
1	C	140	LYS
1	C	147	GLU
1	C	152	GLU
1	C	157	CYS
1	C	158	LEU
1	C	163	LEU
1	C	171	ASP
1	C	172	THR
1	C	176	LEU
1	C	186	LEU
1	C	187	LYS
1	C	188	GLN
1	C	190	VAL
1	C	218	THR
1	C	220	LEU
1	C	227	VAL
1	C	240	LYS
1	C	242	ARG
1	C	245	PHE
1	C	252	LEU
1	C	261	LEU
1	C	271	SER
1	C	283	VAL
1	C	287	VAL
1	C	294	VAL
1	C	304	PHE
1	C	306	THR
1	C	315	LEU
1	C	319	LEU
1	C	325	LEU
1	C	332	LYS
1	C	339	LEU
1	C	346	ILE
1	C	362	CYS
1	C	366	SER
1	C	367	ARG
1	C	369	PHE

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Mol	Chain	Res	Type
1	C	372	TRP
1	C	394	SER
1	C	401	TYR
1	C	402	SER
1	C	421	LEU
1	C	426	TRP
1	C	428	ARG
1	C	429	PHE
1	C	433	ILE
1	C	442	CYS
1	C	443	LEU
1	C	445	MET
1	C	447	ILE
1	C	455	ARG
1	C	474	ARG
1	C	482	VAL
1	C	486	VAL
1	C	499	ARG
1	C	502	SER
1	C	512	SER
1	C	514	ILE
1	C	515	LEU
1	C	518	VAL
1	C	520	SER
1	C	521	LEU
1	C	522	PHE
1	C	524	LEU
1	C	532	SER
1	C	533	GLN
1	C	540	SER
1	C	545	LEU
1	C	547	MET
1	C	554	TYR
1	C	555	TYR
1	C	567	VAL
1	C	568	MET
1	C	569	ILE
1	C	570	GLU
1	C	572	MET
1	C	573	ILE
1	C	575	ARG
1	C	577	LEU

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Mol	Chain	Res	Type
1	C	578	CYS
1	C	579	ARG
1	C	582	PHE
1	C	599	ILE
1	C	600	GLU
1	C	603	LYS
1	C	629	SER
1	C	630	LEU
1	C	632	SER
1	C	635	LEU
1	C	639	LYS
1	C	644	MET
1	C	647	LEU
1	C	648	GLU
1	C	649	PHE
1	C	651	GLU
1	C	656	LYS
1	C	659	PHE
1	C	660	ILE
1	C	661	ILE
1	C	663	LEU
1	C	664	LEU
1	C	668	ILE
1	C	673	LEU
1	C	674	LEU
1	C	676	ASN
1	C	681	LEU
1	C	687	ASN
1	C	688	LYS
1	C	697	TRP
1	C	699	LEU
1	C	701	ARG
1	C	704	THR
1	C	708	THR
1	C	716	MET
1	D	116	SER
1	D	123	GLN
1	D	128	GLU
1	D	131	SER
1	D	136	LEU
1	D	138	ARG
1	D	140	LYS

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Mol	Chain	Res	Type
1	D	147	GLU
1	D	152	GLU
1	D	157	CYS
1	D	158	LEU
1	D	163	LEU
1	D	171	ASP
1	D	172	THR
1	D	176	LEU
1	D	186	LEU
1	D	187	LYS
1	D	188	GLN
1	D	190	VAL
1	D	218	THR
1	D	220	LEU
1	D	227	VAL
1	D	240	LYS
1	D	242	ARG
1	D	245	PHE
1	D	252	LEU
1	D	261	LEU
1	D	271	SER
1	D	283	VAL
1	D	287	VAL
1	D	294	VAL
1	D	304	PHE
1	D	306	THR
1	D	315	LEU
1	D	319	LEU
1	D	325	LEU
1	D	332	LYS
1	D	339	LEU
1	D	346	ILE
1	D	362	CYS
1	D	366	SER
1	D	367	ARG
1	D	369	PHE
1	D	372	TRP
1	D	394	SER
1	D	401	TYR
1	D	402	SER
1	D	421	LEU
1	D	426	TRP

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Mol	Chain	Res	Type
1	D	428	ARG
1	D	429	PHE
1	D	433	ILE
1	D	442	CYS
1	D	443	LEU
1	D	445	MET
1	D	447	ILE
1	D	455	ARG
1	D	474	ARG
1	D	482	VAL
1	D	486	VAL
1	D	499	ARG
1	D	502	SER
1	D	512	SER
1	D	514	ILE
1	D	515	LEU
1	D	518	VAL
1	D	520	SER
1	D	521	LEU
1	D	522	PHE
1	D	524	LEU
1	D	532	SER
1	D	533	GLN
1	D	540	SER
1	D	545	LEU
1	D	547	MET
1	D	554	TYR
1	D	555	TYR
1	D	567	VAL
1	D	568	MET
1	D	569	ILE
1	D	570	GLU
1	D	572	MET
1	D	573	ILE
1	D	575	ARG
1	D	577	LEU
1	D	578	CYS
1	D	579	ARG
1	D	582	PHE
1	D	599	ILE
1	D	600	GLU
1	D	603	LYS

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Mol	Chain	Res	Type
1	D	629	SER
1	D	630	LEU
1	D	632	SER
1	D	635	LEU
1	D	639	LYS
1	D	644	MET
1	D	647	LEU
1	D	648	GLU
1	D	649	PHE
1	D	651	GLU
1	D	656	LYS
1	D	659	PHE
1	D	660	ILE
1	D	661	ILE
1	D	663	LEU
1	D	664	LEU
1	D	668	ILE
1	D	673	LEU
1	D	674	LEU
1	D	676	ASN
1	D	681	LEU
1	D	687	ASN
1	D	688	LYS
1	D	697	TRP
1	D	699	LEU
1	D	701	ARG
1	D	704	THR
1	D	708	THR
1	D	716	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	188	GLN
1	B	269	GLN
1	B	289	HIS
1	B	320	HIS
1	B	423	GLN
1	B	687	ASN
1	A	188	GLN
1	A	269	GLN
1	A	289	HIS

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Mol	Chain	Res	Type
1	A	320	HIS
1	A	423	GLN
1	A	687	ASN
1	C	188	GLN
1	C	269	GLN
1	C	289	HIS
1	C	320	HIS
1	C	423	GLN
1	C	676	ASN
1	C	687	ASN
1	D	188	GLN
1	D	269	GLN
1	D	289	HIS
1	D	320	HIS
1	D	423	GLN
1	D	687	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 ⓘ

There are no chain breaks in this entry.

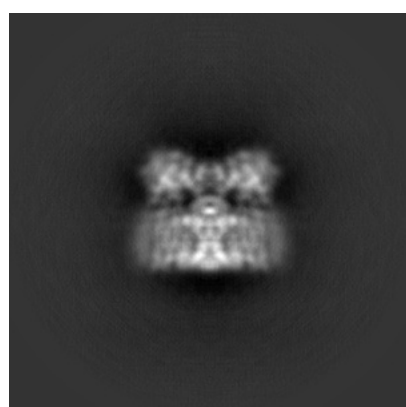
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5777. These allow visual inspection of the internal detail of the map and identification of artifacts.

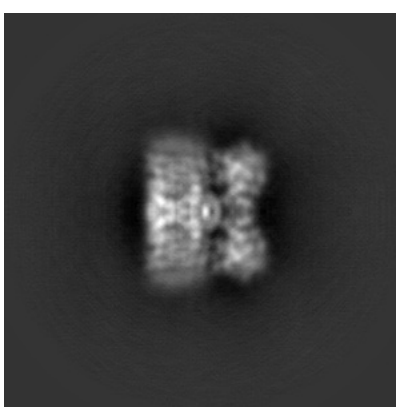
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

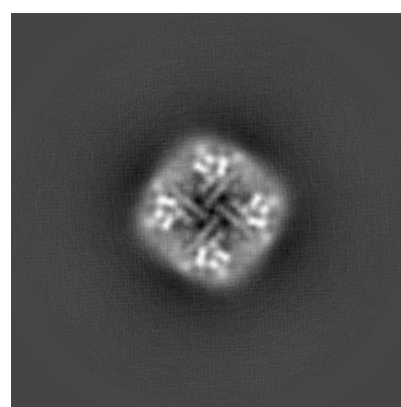
6.1.1 Primary map



X



Y

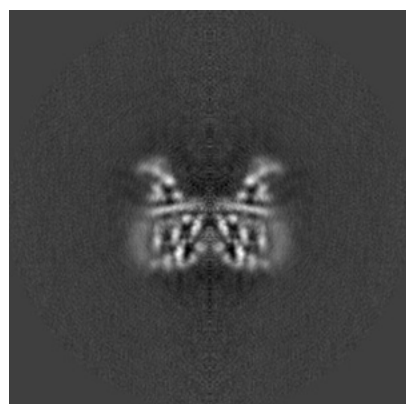


Z

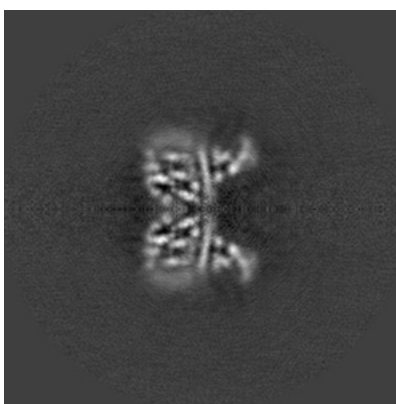
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

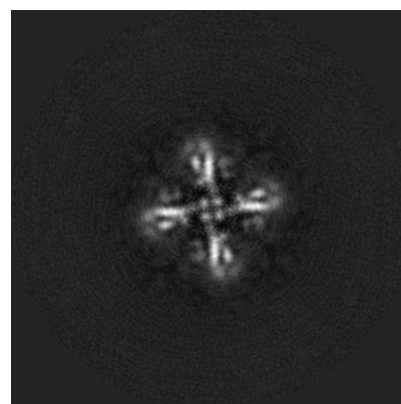
6.2.1 Primary map



X Index: 128



Y Index: 128

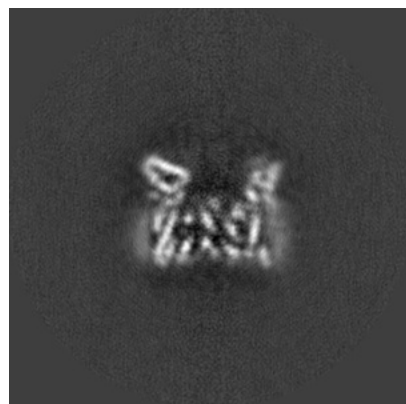


Z Index: 128

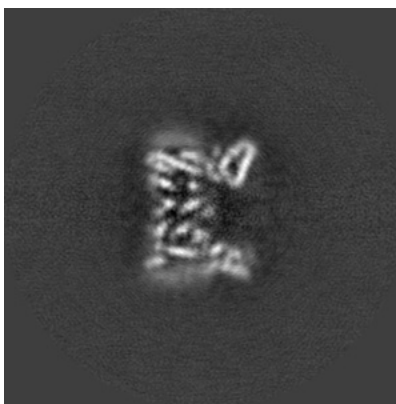
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

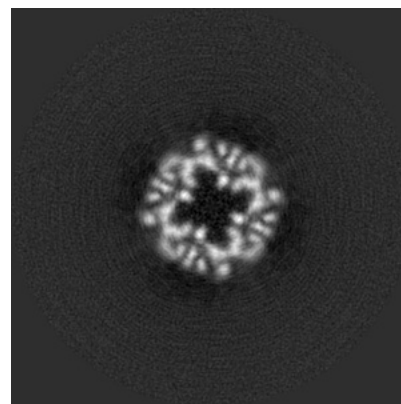
6.3.1 Primary map



X Index: 121



Y Index: 121

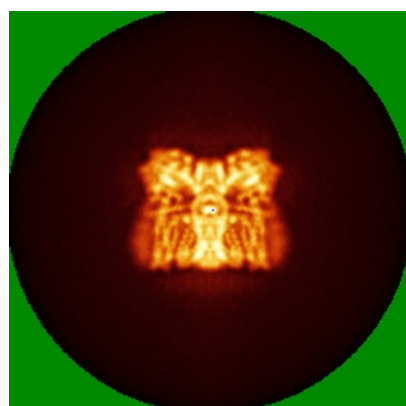


Z Index: 149

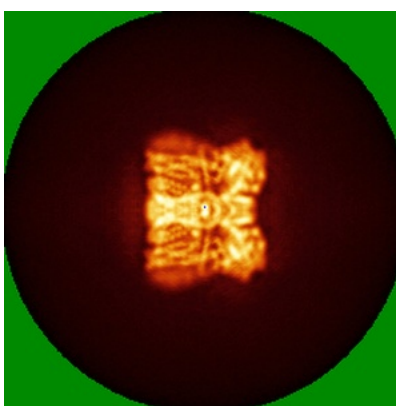
The images above show the largest variance slices of the map in three orthogonal directions.

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

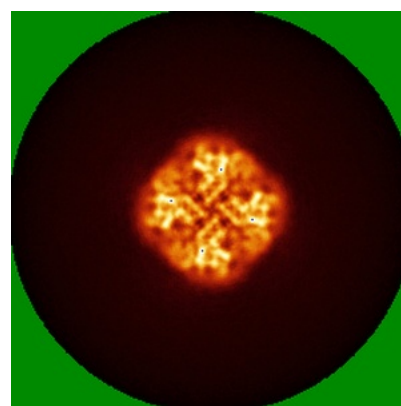
6.4.1 Primary map



X



Y

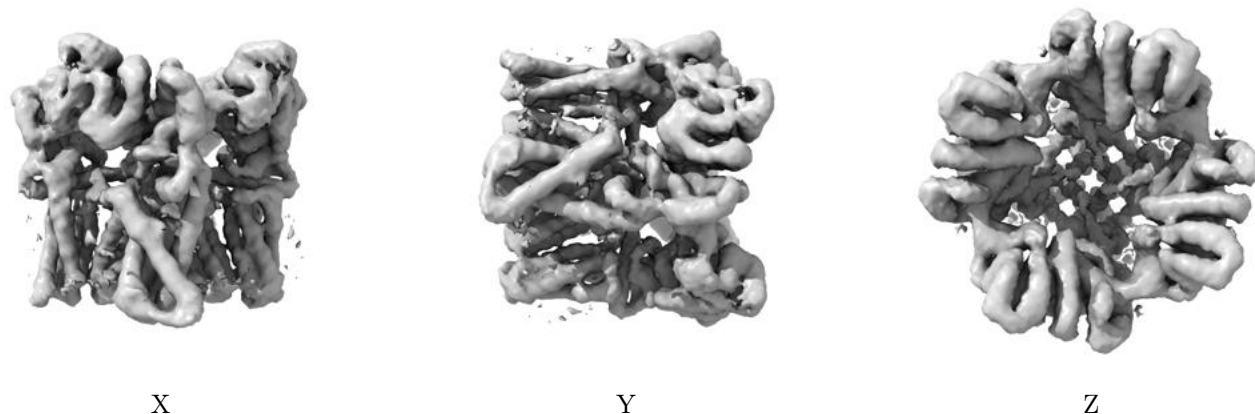


Z

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

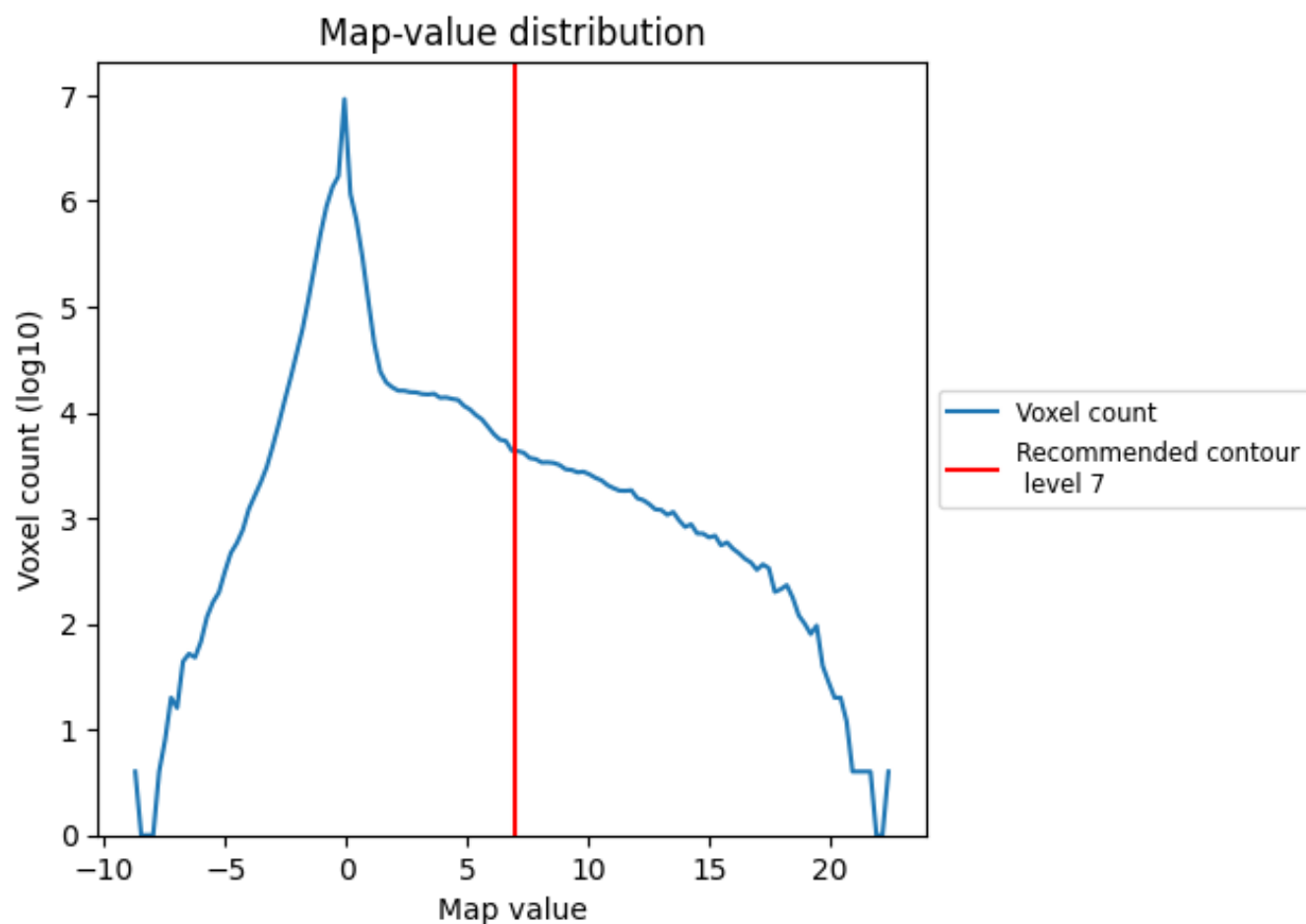
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

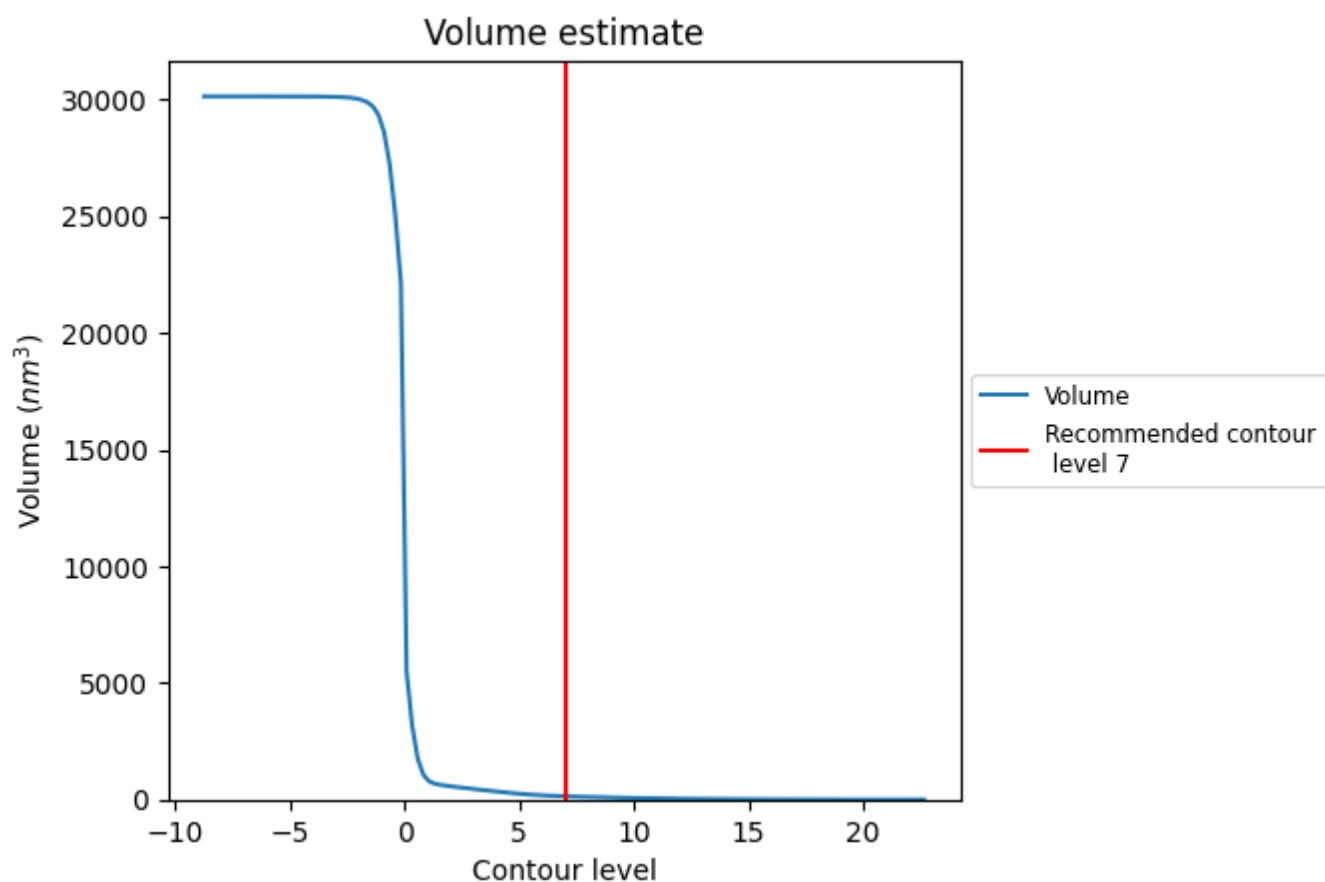
This section contains the results of statistical analysis of the map.

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.

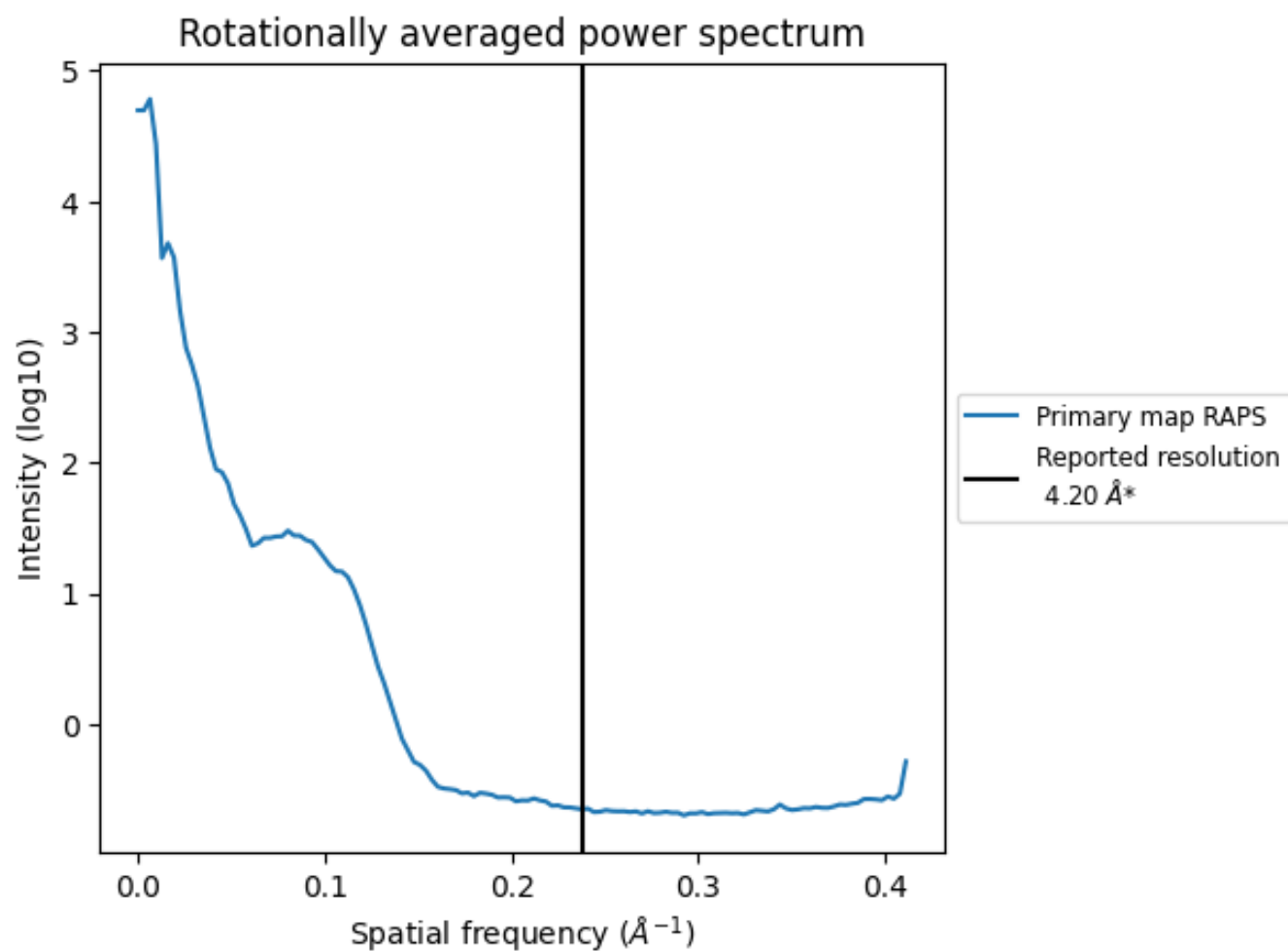
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 140 nm³; this corresponds to an approximate mass of 127 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

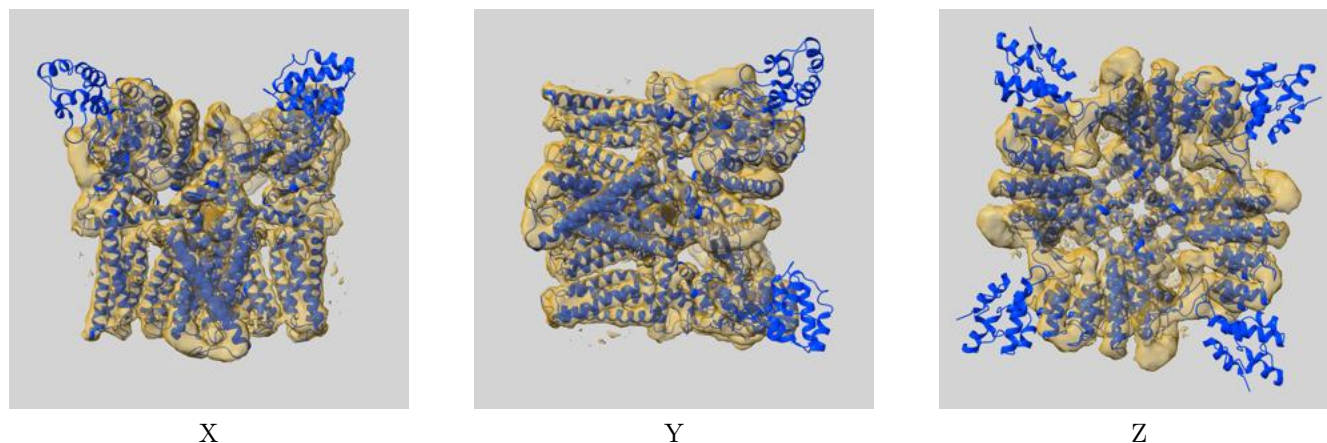
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

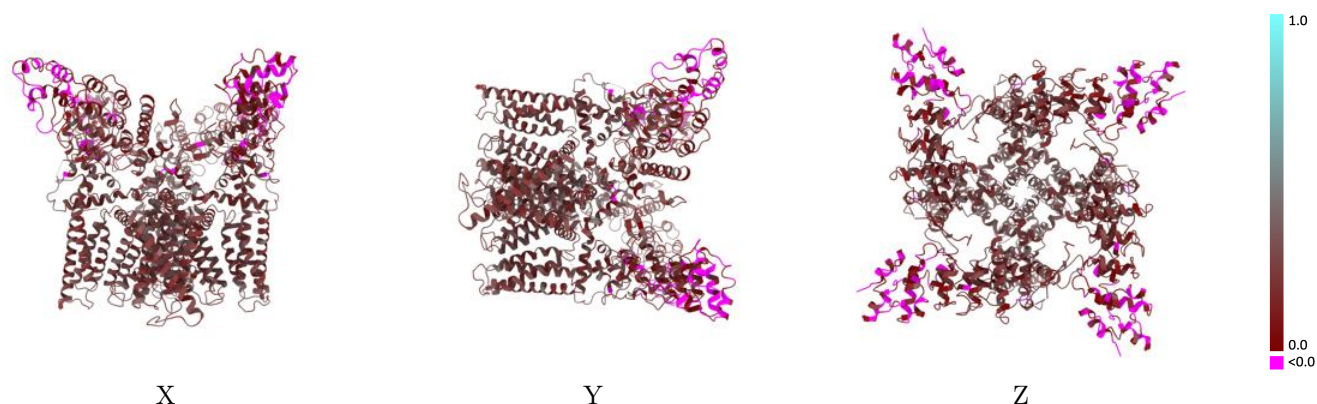
This section contains information regarding the fit between EMDB map EMD-5777 and PDB model 3J5R. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



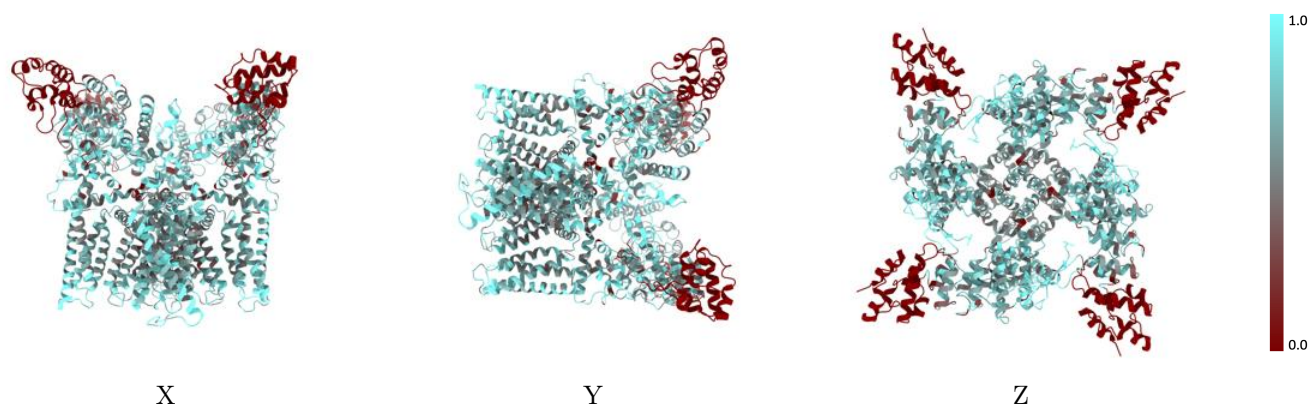
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



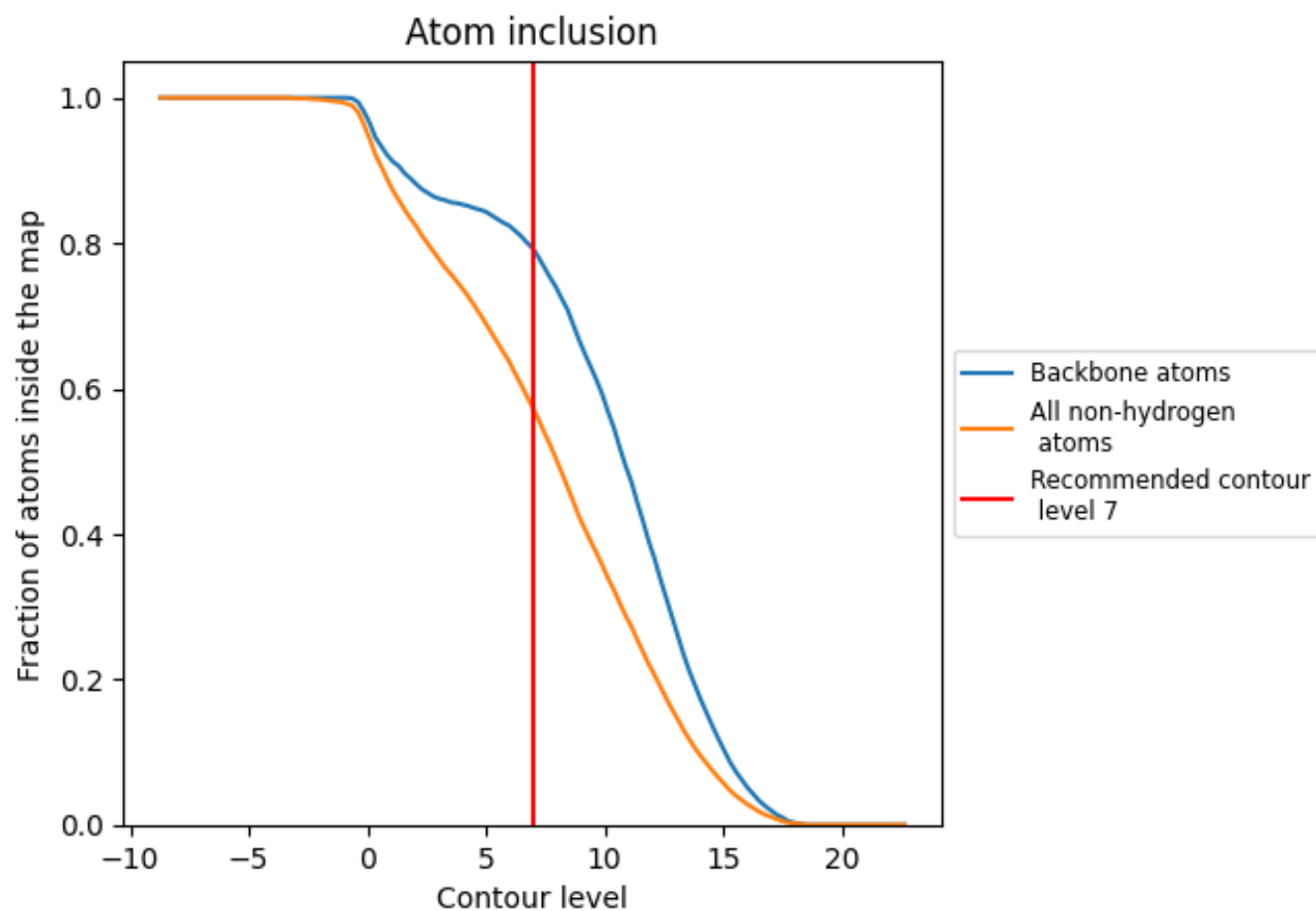
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 57% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5720	0.2000
A	0.5730	0.2020
B	0.5730	0.2010
C	0.5720	0.1980
D	0.5710	0.1990

