



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:43 PM UTC

PDB ID : 8JFL / pdb_00008jfl
EMDB ID : EMD-36213
Title : PhK holoenzyme in active state, muscle isoform
Authors : Yang, X.K.; Xiao, J.Y.
Deposited on : 2023-05-18
Resolution : 2.90 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

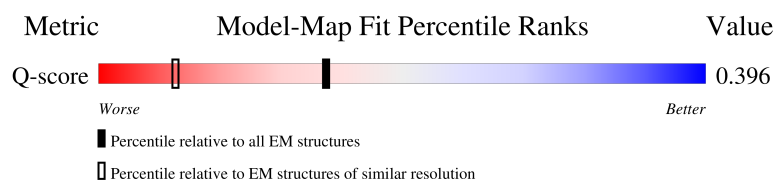
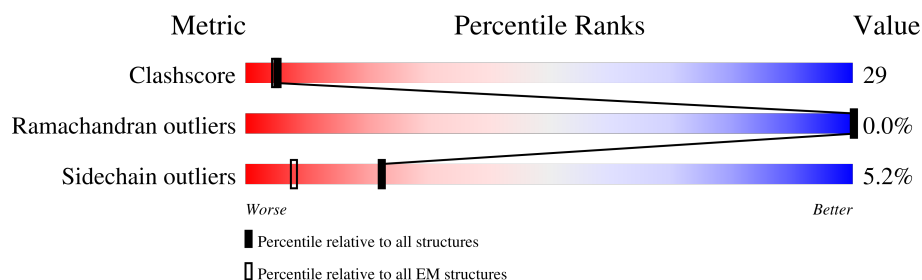
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



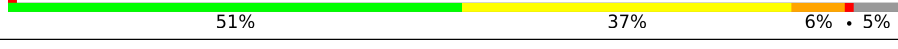
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1223	
1	E	1223	
1	I	1223	
1	M	1223	

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Mol	Chain	Length	Quality of chain
2	C	387	 88%
2	G	387	 88%
2	K	387	 88%
2	O	387	 88%
3	B	1093	 51% 37% 6% • 5%
3	F	1093	 51% 36% 6% • 5%
3	J	1093	 52% 36% 6% • 5%
3	N	1093	 51% 37% 6% • 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FAR	A	1301	-	-	X	-
4	FAR	B	1101	-	-	X	-
4	FAR	E	1301	-	-	X	-
4	FAR	F	1101	-	-	X	-
4	FAR	F	1103	-	-	X	-
4	FAR	I	1301	-	-	X	-
4	FAR	M	1301	-	-	X	-
4	FAR	N	1101	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 65884 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 Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	970	Total	C	N	O	S	0	0
			7673	4891	1295	1442	45		
1	E	970	Total	C	N	O	S	0	0
			7673	4891	1295	1442	45		
1	M	970	Total	C	N	O	S	0	0
			7673	4891	1295	1442	45		
1	I	970	Total	C	N	O	S	0	0
			7673	4891	1295	1442	45		

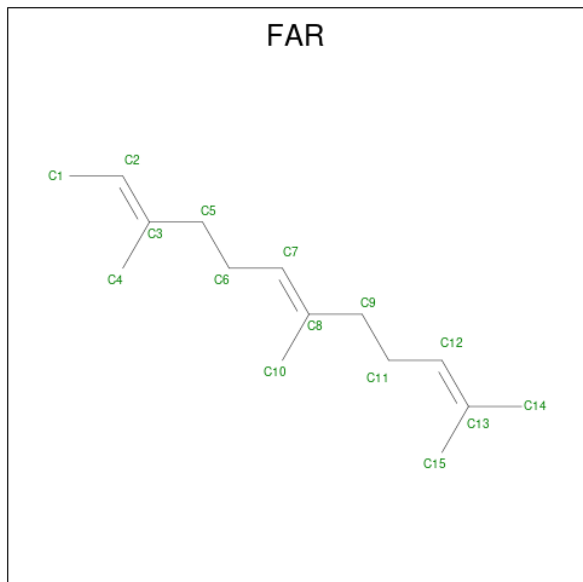
- Molecule 2 is a protein called Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	48	Total	C	N	O	0	0
			402	263	75	64		
2	G	48	Total	C	N	O	0	0
			402	263	75	64		
2	O	48	Total	C	N	O	0	0
			402	263	75	64		
2	K	48	Total	C	N	O	0	0
			402	263	75	64		

- Molecule 3 is a protein called Phosphorylase b kinase regulatory subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	1033	Total	C	N	O	S	0	0
			8339	5338	1423	1541	37		
3	F	1033	Total	C	N	O	S	0	0
			8339	5338	1423	1541	37		
3	J	1033	Total	C	N	O	S	0	0
			8339	5338	1423	1541	37		
3	N	1033	Total	C	N	O	S	0	0
			8339	5338	1423	1541	37		

- Molecule 4 is FARNESYL (CCD ID: FAR) (formula: $C_{15}H_{26}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
4	A	1	Total C 15 15	0
4	E	1	Total C 15 15	0
4	M	1	Total C 15 15	0
4	I	1	Total C 15 15	0
4	B	1	Total C 15 15	0
4	F	1	Total C 15 15	0
4	F	1	Total C 15 15	0
4	N	1	Total C 15 15	0

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

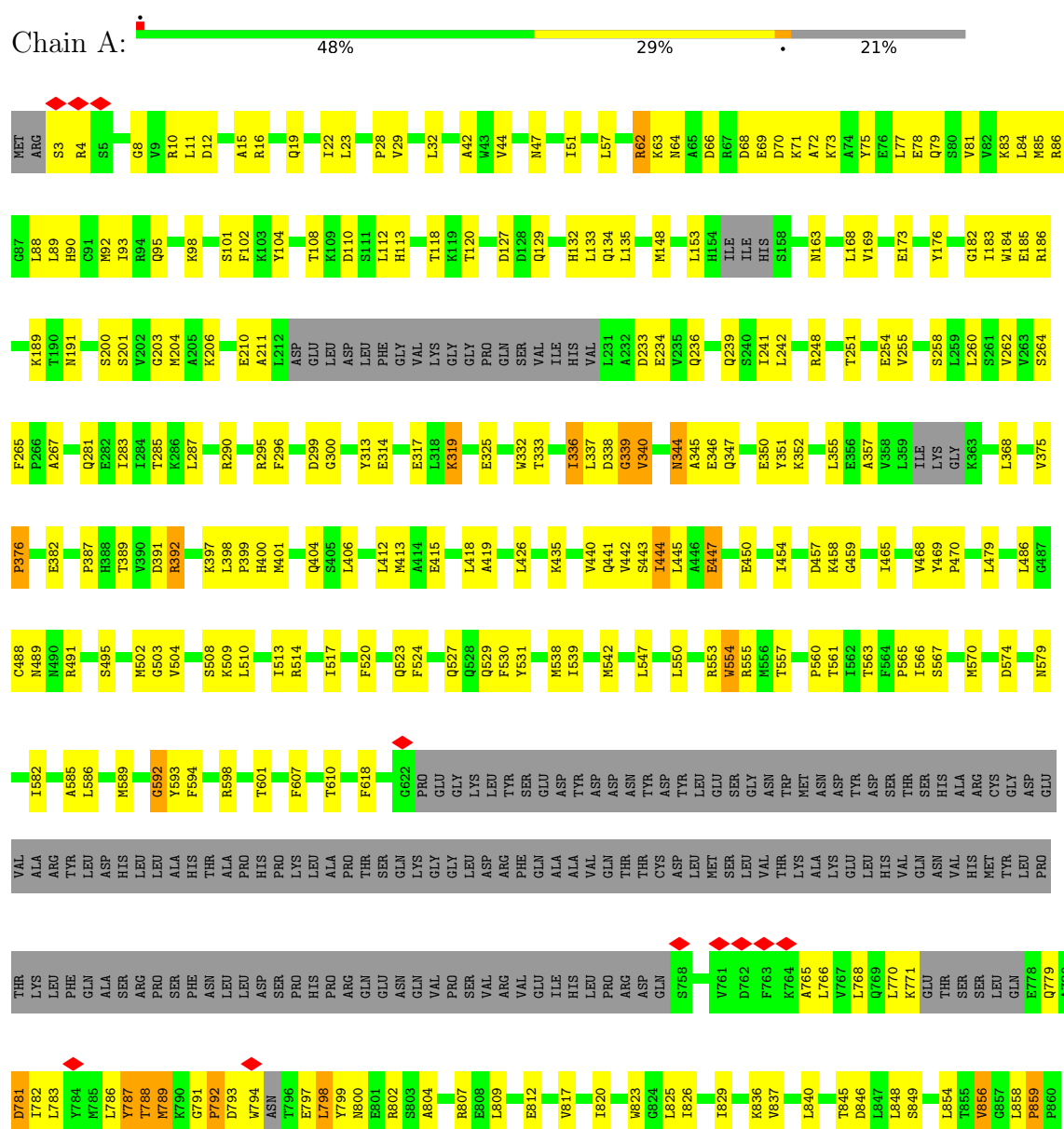


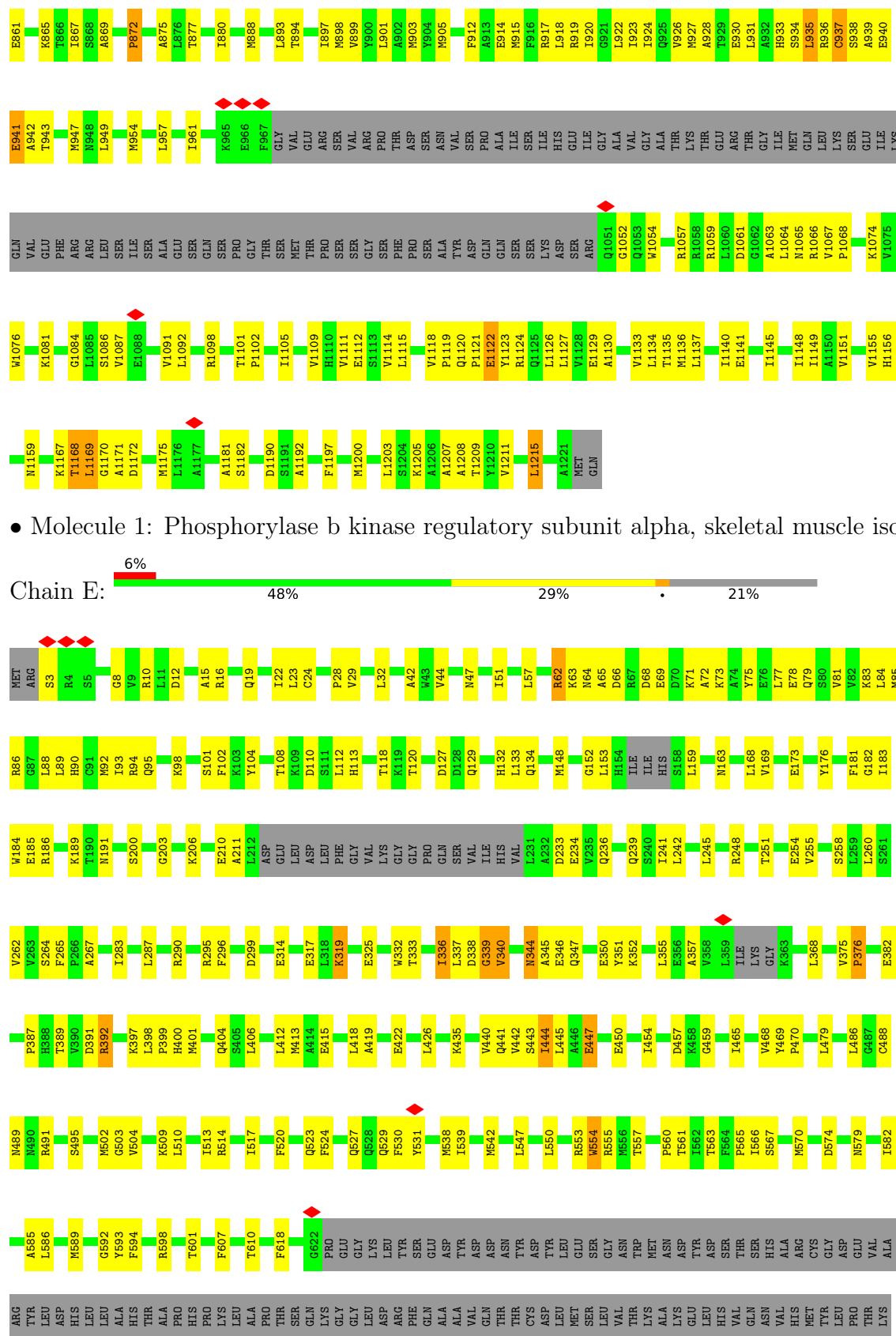
Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
5	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
5	J	1	Total	C	N	O	P	0
			27	10	5	10	2	
5	N	1	Total	C	N	O	P	0
			27	10	5	10	2	

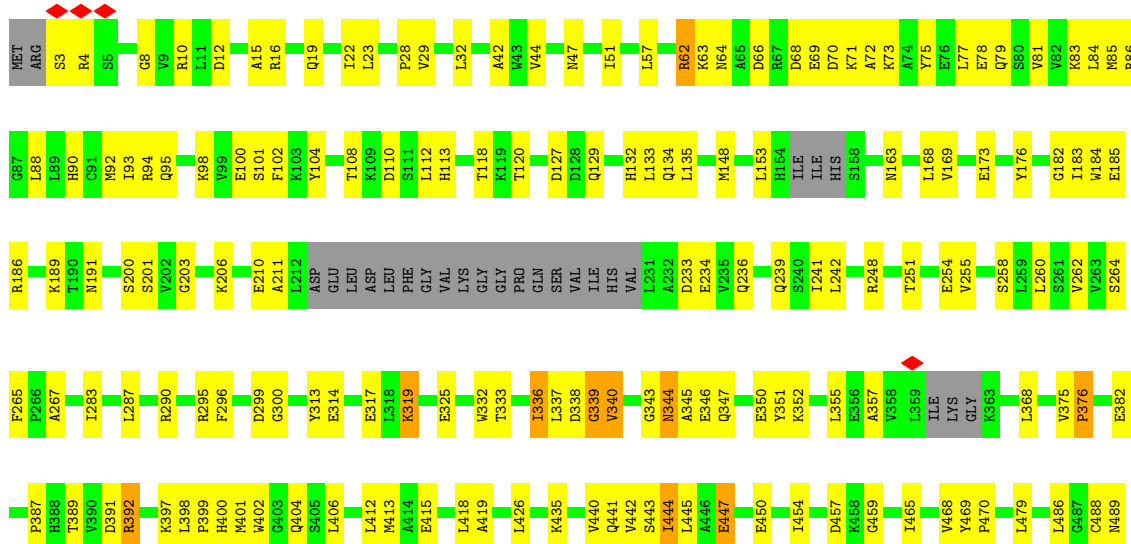
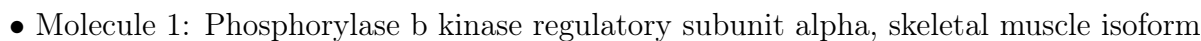
3 Residue-property plots

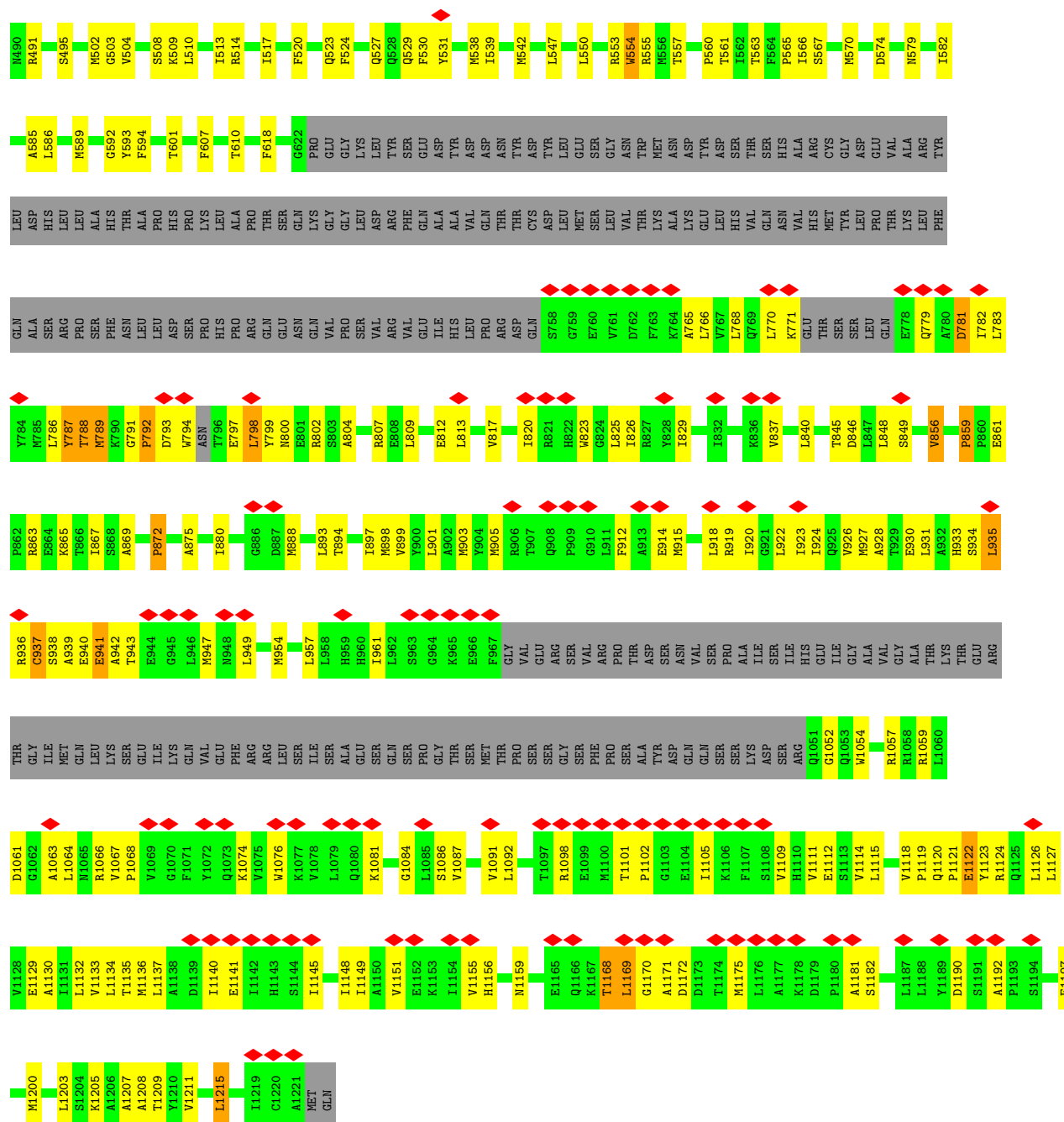
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform

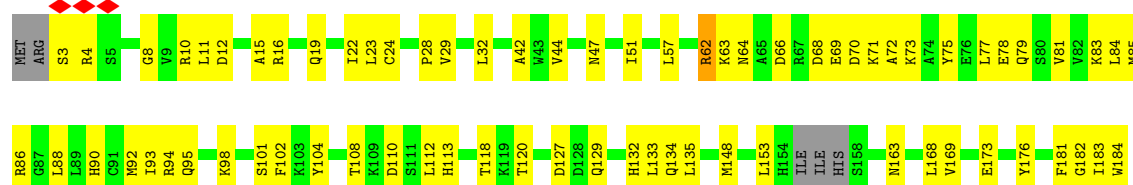


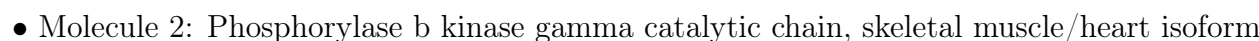






- Molecule 1: Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform



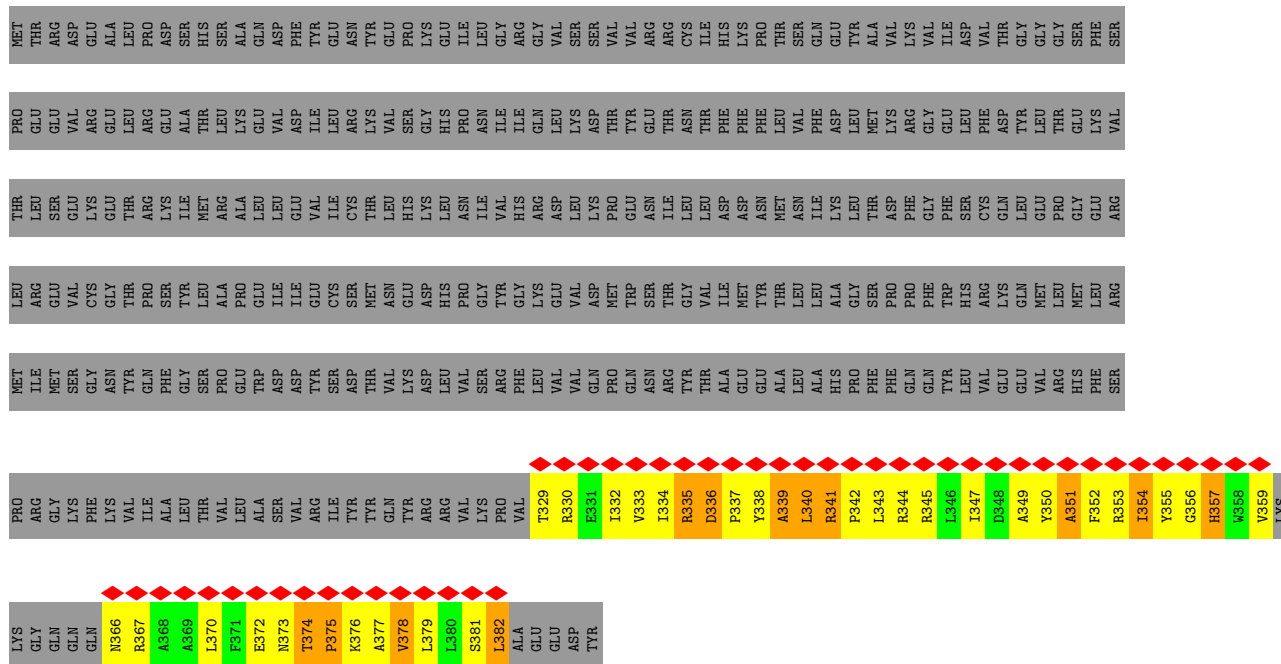


- Molecule 2: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform

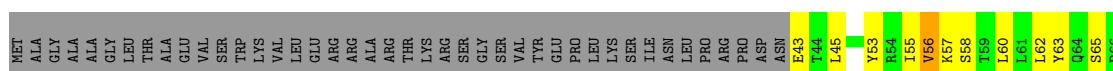
- Molecule 2: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform

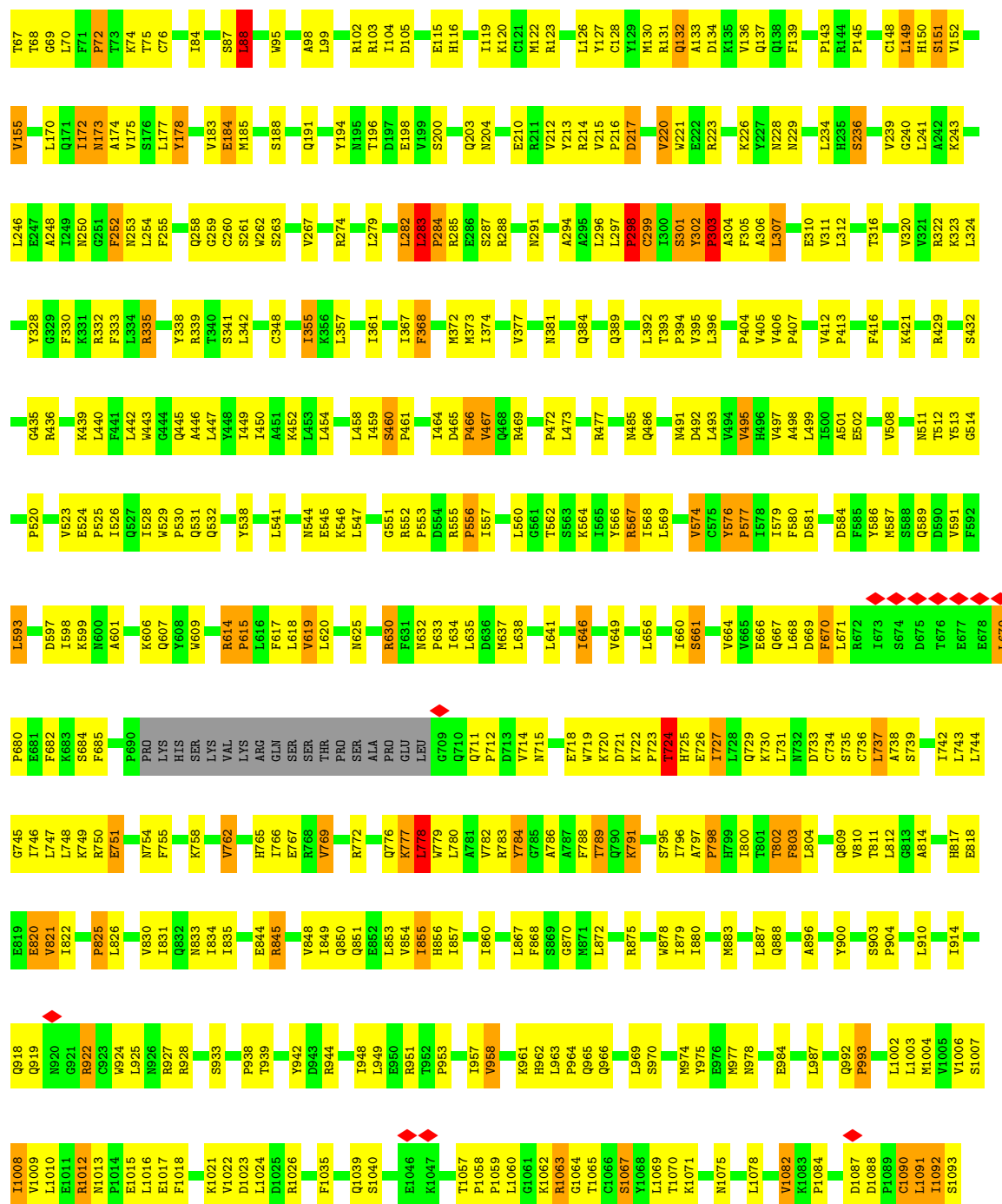


- Molecule 2: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform



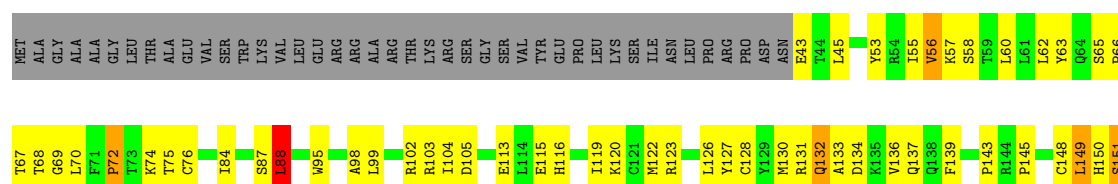
- Molecule 3: Phosphorylase b kinase regulatory subunit beta

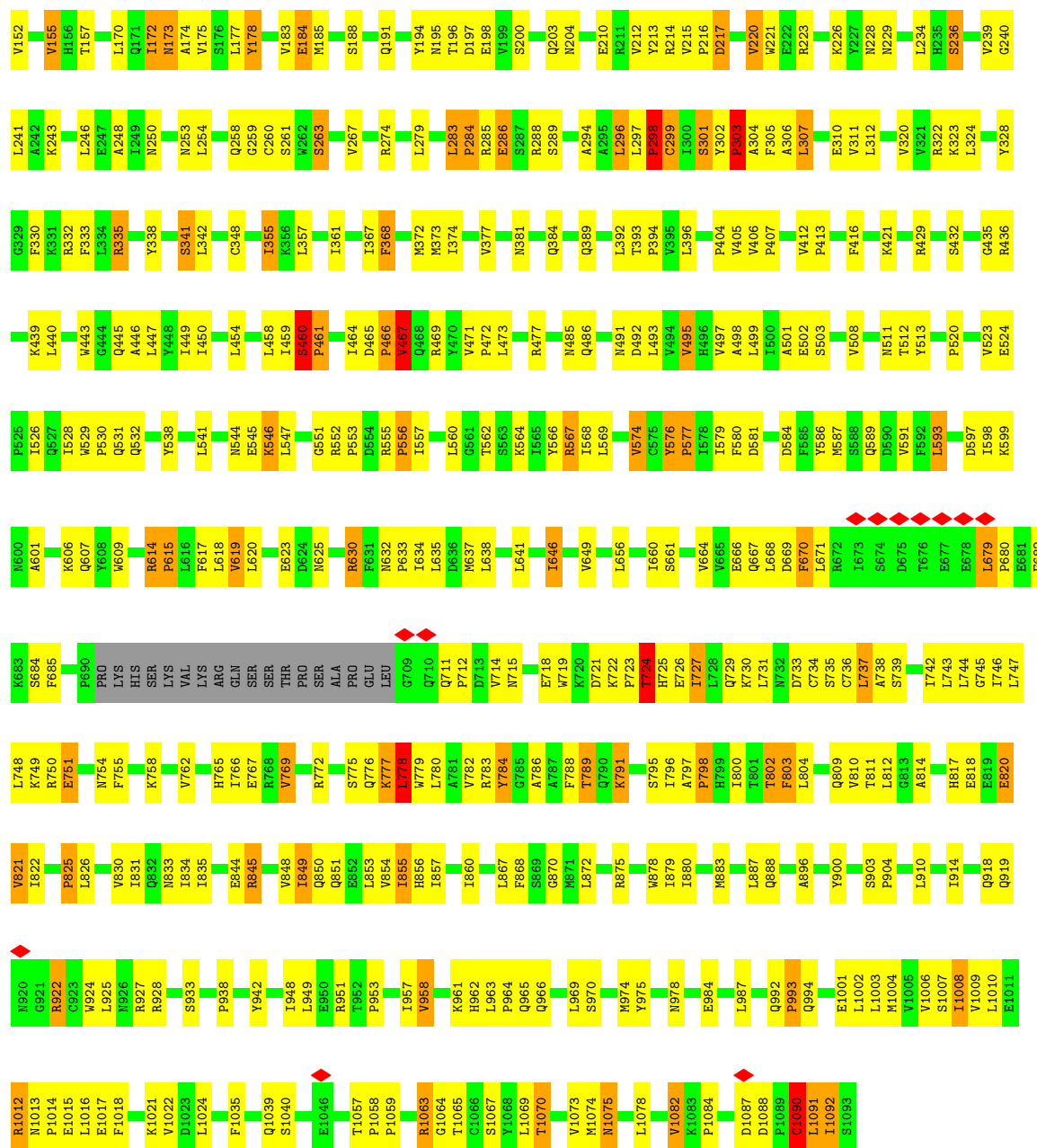




• Molecule 3: Phosphorylase b kinase regulatory subunit beta

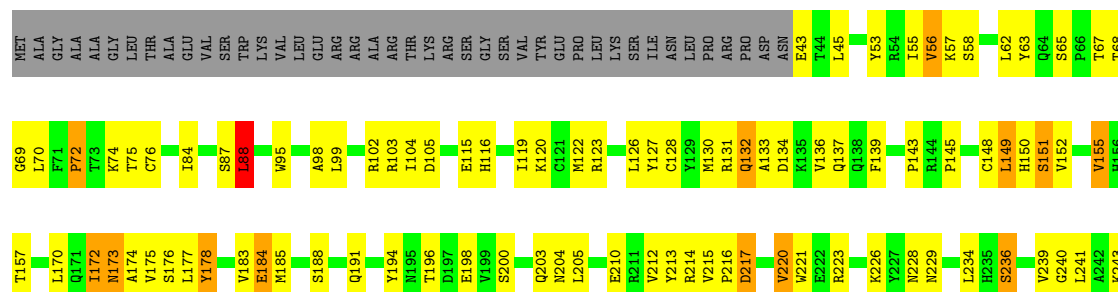
Chain F: 51% 36% 6% • 5%

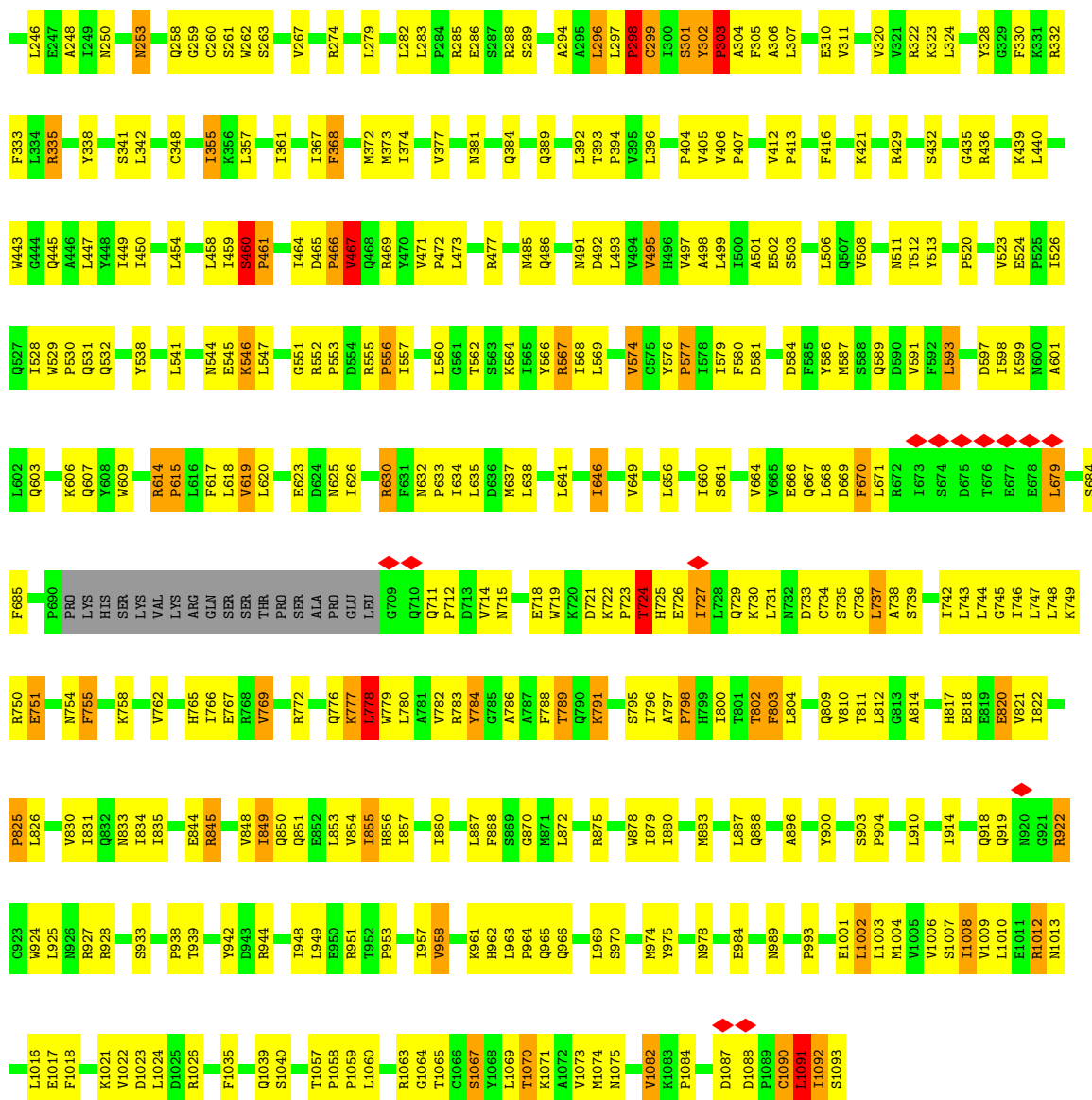




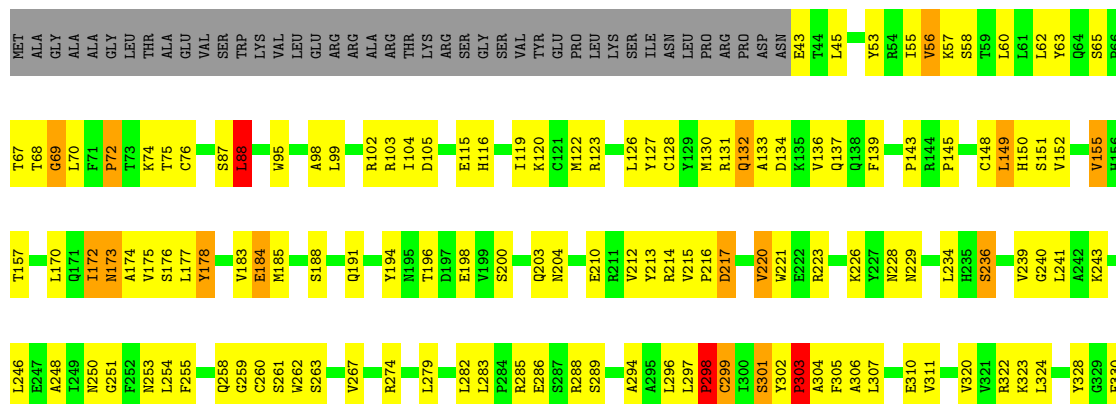
• Molecule 3: Phosphorylase b kinase regulatory subunit beta

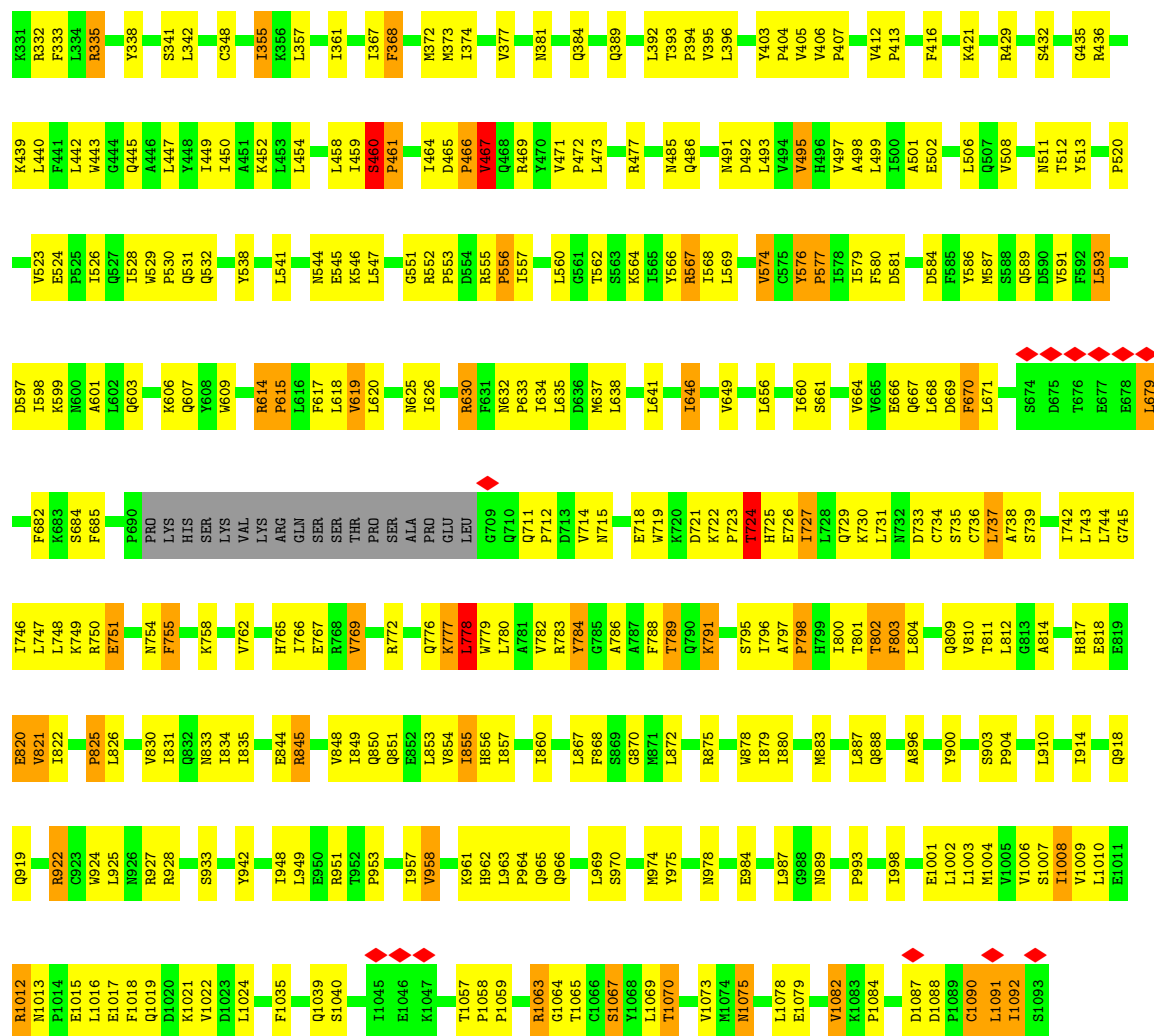
Chain J: 52% 36% 6% • 5%





• Molecule 3: Phosphorylase b kinase regulatory subunit beta





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	432047	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.761	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	481.50003, 481.50003, 481.50003	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FAR, ADP

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	0.79	19/7826 (0.2%)	0.82	43/10595 (0.4%)
1	E	0.79	19/7826 (0.2%)	0.82	38/10595 (0.4%)
1	I	0.79	18/7826 (0.2%)	0.82	43/10595 (0.4%)
1	M	0.79	20/7826 (0.3%)	0.82	42/10595 (0.4%)
2	C	1.46	4/411 (1.0%)	1.62	12/557 (2.2%)
2	G	1.44	4/411 (1.0%)	1.61	12/557 (2.2%)
2	K	1.43	4/411 (1.0%)	1.61	12/557 (2.2%)
2	O	1.43	4/411 (1.0%)	1.61	12/557 (2.2%)
3	B	1.21	31/8527 (0.4%)	1.65	119/11556 (1.0%)
3	F	1.20	30/8527 (0.4%)	1.65	124/11556 (1.1%)
3	J	1.20	28/8527 (0.3%)	1.63	113/11556 (1.0%)
3	N	1.20	29/8527 (0.3%)	1.64	119/11556 (1.0%)
All	All	1.04	210/67056 (0.3%)	1.32	689/90832 (0.8%)

All (210) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	284	PRO	N-CD	9.55	1.61	1.47
1	E	376	PRO	CA-C	-8.04	1.47	1.51
1	M	376	PRO	CA-C	-7.97	1.47	1.51
1	A	376	PRO	CA-C	-7.89	1.47	1.51
1	I	376	PRO	CA-C	-7.81	1.47	1.51
3	J	615	PRO	C-O	-7.79	1.15	1.23
3	F	615	PRO	C-O	-7.79	1.15	1.23
3	B	615	PRO	C-O	-7.77	1.15	1.23
1	E	593	TYR	CA-C	-7.75	1.43	1.52
1	I	593	TYR	CA-C	-7.74	1.43	1.52
3	N	615	PRO	C-O	-7.72	1.15	1.23
1	A	593	TYR	CA-C	-7.70	1.43	1.52
1	M	593	TYR	CA-C	-7.67	1.43	1.52
3	N	301	SER	CA-CB	-7.31	1.42	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	301	SER	CA-CB	-7.28	1.42	1.53
3	B	301	SER	CA-CB	-7.27	1.42	1.53
3	J	301	SER	CA-CB	-7.24	1.42	1.53
3	F	472	PRO	C-O	-7.02	1.15	1.23
3	N	472	PRO	C-O	-6.98	1.15	1.23
3	J	472	PRO	C-O	-6.96	1.15	1.23
3	B	472	PRO	C-O	-6.93	1.15	1.23
2	O	341	ARG	CA-C	-6.83	1.44	1.52
2	C	341	ARG	CA-C	-6.83	1.44	1.52
2	G	341	ARG	CA-C	-6.83	1.44	1.52
2	K	341	ARG	CA-C	-6.75	1.44	1.52
3	B	263	SER	CA-CB	-6.67	1.43	1.53
3	J	263	SER	CA-CB	-6.65	1.43	1.53
3	F	263	SER	CA-CB	-6.64	1.43	1.53
3	B	253	ASN	CA-C	-6.64	1.44	1.52
3	N	263	SER	CA-CB	-6.63	1.43	1.53
3	F	253	ASN	CA-C	-6.23	1.44	1.52
3	J	1075	ASN	C-O	6.15	1.31	1.24
1	M	376	PRO	CA-CB	-6.14	1.48	1.53
3	B	1075	ASN	C-O	6.12	1.31	1.24
1	A	376	PRO	CA-CB	-6.11	1.48	1.53
3	F	1075	ASN	C-O	6.10	1.31	1.24
1	I	376	PRO	CA-CB	-6.08	1.48	1.53
3	N	1075	ASN	C-O	6.07	1.31	1.24
1	E	376	PRO	CA-CB	-6.06	1.48	1.53
1	E	375	VAL	CA-C	-6.04	1.47	1.53
1	I	375	VAL	CA-C	-6.02	1.47	1.53
1	A	375	VAL	CA-C	-5.99	1.47	1.53
3	B	283	LEU	CA-C	-5.97	1.45	1.52
2	C	336	ASP	CA-C	-5.95	1.44	1.52
2	G	336	ASP	CA-C	-5.94	1.44	1.52
1	I	554	TRP	CA-C	-5.93	1.45	1.52
1	M	375	VAL	CA-C	-5.93	1.47	1.53
2	K	336	ASP	CA-C	-5.91	1.44	1.52
2	O	336	ASP	CA-C	-5.91	1.44	1.52
1	A	781	ASP	CA-C	-5.90	1.46	1.52
1	M	781	ASP	CA-C	-5.90	1.46	1.52
1	A	554	TRP	CA-C	-5.90	1.45	1.52
1	E	781	ASP	CA-C	-5.90	1.46	1.52
1	E	554	TRP	CA-C	-5.88	1.45	1.52
1	M	554	TRP	CA-C	-5.87	1.45	1.52
1	A	447	GLU	CA-C	-5.86	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	447	GLU	CA-C	-5.85	1.45	1.52
1	M	447	GLU	CA-C	-5.85	1.45	1.52
1	I	781	ASP	CA-C	-5.82	1.46	1.52
1	E	447	GLU	CA-C	-5.81	1.45	1.52
1	A	594	PHE	N-CA	-5.80	1.38	1.46
1	I	594	PHE	N-CA	-5.79	1.38	1.46
1	E	594	PHE	N-CA	-5.79	1.38	1.46
1	M	594	PHE	N-CA	-5.77	1.38	1.46
2	G	339	ALA	CA-C	-5.73	1.45	1.52
2	C	339	ALA	CA-C	-5.71	1.45	1.52
3	B	72	PRO	C-O	-5.70	1.18	1.23
2	O	339	ALA	CA-C	-5.69	1.45	1.52
2	K	339	ALA	CA-C	-5.69	1.45	1.52
3	N	253	ASN	CA-C	-5.61	1.45	1.52
1	I	1168	THR	CA-C	-5.60	1.45	1.52
3	F	407	PRO	C-O	-5.59	1.17	1.23
1	A	1168	THR	CA-C	-5.57	1.45	1.52
3	N	65	SER	CA-CB	-5.56	1.44	1.53
3	B	65	SER	CA-CB	-5.56	1.44	1.53
3	B	407	PRO	C-O	-5.55	1.17	1.23
3	J	65	SER	CA-CB	-5.55	1.44	1.53
1	E	937	CYS	CA-C	-5.55	1.46	1.53
1	M	792	PRO	N-CD	-5.54	1.40	1.47
3	J	407	PRO	C-O	-5.54	1.17	1.23
3	F	58	SER	CA-CB	-5.53	1.44	1.53
1	M	1168	THR	CA-C	-5.53	1.45	1.52
3	F	65	SER	CA-CB	-5.53	1.44	1.53
1	A	792	PRO	N-CD	-5.52	1.40	1.47
3	N	407	PRO	C-O	-5.52	1.17	1.23
1	E	1168	THR	CA-C	-5.52	1.45	1.52
1	I	935	LEU	CA-C	-5.52	1.48	1.53
1	E	792	PRO	N-CD	-5.50	1.40	1.47
1	A	937	CYS	CA-C	-5.50	1.46	1.53
1	I	792	PRO	N-CD	-5.50	1.40	1.47
3	B	58	SER	CA-CB	-5.50	1.44	1.53
3	N	58	SER	CA-CB	-5.49	1.44	1.53
3	J	58	SER	CA-CB	-5.48	1.44	1.53
3	N	661	SER	CA-CB	-5.47	1.44	1.53
3	J	661	SER	CA-CB	-5.46	1.44	1.53
1	I	937	CYS	CA-C	-5.46	1.46	1.53
1	M	937	CYS	CA-C	-5.45	1.46	1.53
3	B	200	SER	CA-CB	-5.45	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	661	SER	CA-CB	-5.45	1.45	1.53
3	J	200	SER	CA-CB	-5.45	1.44	1.53
1	M	935	LEU	CA-C	-5.45	1.48	1.53
3	B	661	SER	CA-CB	-5.44	1.45	1.53
3	F	200	SER	CA-CB	-5.44	1.44	1.53
1	I	443	SER	CA-C	-5.43	1.46	1.52
3	N	200	SER	CA-CB	-5.43	1.44	1.53
3	N	461	PRO	N-CA	-5.43	1.40	1.47
1	A	443	SER	CA-C	-5.40	1.46	1.52
1	A	935	LEU	CA-C	-5.40	1.48	1.53
1	A	786	LEU	CA-C	-5.39	1.45	1.52
3	B	461	PRO	N-CA	-5.39	1.40	1.47
1	E	786	LEU	CA-C	-5.38	1.45	1.52
3	F	461	PRO	N-CA	-5.38	1.40	1.47
3	J	461	PRO	N-CA	-5.38	1.40	1.47
1	M	786	LEU	CA-C	-5.37	1.45	1.52
3	F	432	SER	CA-CB	-5.37	1.45	1.53
1	M	443	SER	CA-C	-5.37	1.46	1.52
1	E	935	LEU	CA-C	-5.37	1.48	1.53
3	B	432	SER	CA-CB	-5.37	1.45	1.53
3	N	282	LEU	CA-C	-5.35	1.45	1.52
3	N	432	SER	CA-CB	-5.35	1.45	1.53
1	E	443	SER	CA-C	-5.35	1.46	1.52
1	E	1122	GLU	CA-C	-5.35	1.46	1.52
1	I	1122	GLU	CA-C	-5.34	1.46	1.52
1	I	786	LEU	CA-C	-5.34	1.45	1.52
3	F	1058	PRO	C-O	-5.34	1.18	1.24
3	J	432	SER	CA-CB	-5.32	1.45	1.53
1	A	1122	GLU	CA-C	-5.30	1.46	1.52
3	J	1058	PRO	C-O	-5.30	1.18	1.24
3	J	530	PRO	C-O	-5.29	1.17	1.23
1	M	1122	GLU	CA-C	-5.29	1.46	1.52
3	B	1058	PRO	C-O	-5.28	1.18	1.24
3	N	145	PRO	C-O	-5.28	1.17	1.24
3	F	530	PRO	C-O	-5.28	1.17	1.23
3	N	1058	PRO	C-O	-5.28	1.18	1.24
3	N	530	PRO	C-O	-5.27	1.17	1.23
3	N	809	GLN	C-O	-5.25	1.18	1.24
2	K	351	ALA	CA-C	-5.25	1.46	1.52
3	J	993	PRO	C-O	-5.25	1.18	1.24
2	C	351	ALA	CA-C	-5.25	1.46	1.52
3	F	87	SER	CA-CB	-5.25	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	87	SER	CA-CB	-5.25	1.45	1.53
3	B	993	PRO	C-O	-5.24	1.18	1.24
3	F	809	GLN	C-O	-5.24	1.18	1.24
3	B	809	GLN	C-O	-5.24	1.18	1.24
3	F	145	PRO	C-O	-5.24	1.17	1.24
3	B	530	PRO	C-O	-5.23	1.17	1.23
3	J	809	GLN	C-O	-5.23	1.18	1.24
3	N	993	PRO	C-O	-5.23	1.18	1.24
2	O	351	ALA	CA-C	-5.23	1.46	1.52
3	J	87	SER	CA-CB	-5.23	1.45	1.53
3	F	993	PRO	C-O	-5.23	1.18	1.24
2	G	351	ALA	CA-C	-5.22	1.46	1.52
3	B	145	PRO	C-O	-5.22	1.17	1.24
3	N	577	PRO	C-O	-5.21	1.17	1.23
3	N	72	PRO	C-O	-5.20	1.18	1.23
3	B	87	SER	CA-CB	-5.19	1.45	1.53
1	I	440	VAL	CA-C	-5.19	1.47	1.53
3	J	145	PRO	C-O	-5.18	1.17	1.24
3	J	577	PRO	C-O	-5.18	1.17	1.23
3	F	254	LEU	N-CA	-5.18	1.39	1.46
1	M	579	ASN	CA-C	-5.17	1.46	1.52
3	F	784	TYR	C-O	-5.17	1.18	1.24
3	J	798	PRO	C-O	-5.17	1.17	1.24
3	N	798	PRO	C-O	-5.17	1.17	1.24
3	F	577	PRO	C-O	-5.16	1.17	1.23
1	E	579	ASN	CA-C	-5.16	1.46	1.52
3	B	577	PRO	C-O	-5.16	1.17	1.23
3	B	798	PRO	C-O	-5.16	1.17	1.24
3	B	252	PHE	N-CA	-5.15	1.39	1.46
1	A	579	ASN	CA-C	-5.15	1.46	1.52
1	E	440	VAL	CA-C	-5.15	1.47	1.53
3	J	784	TYR	C-O	-5.14	1.18	1.24
1	A	440	VAL	CA-C	-5.14	1.47	1.53
3	B	784	TYR	C-O	-5.14	1.18	1.24
3	J	203	GLN	C-O	-5.13	1.18	1.24
3	J	72	PRO	C-O	-5.12	1.18	1.23
1	I	579	ASN	CA-C	-5.11	1.46	1.52
3	J	460	SER	CA-CB	-5.10	1.46	1.53
3	F	460	SER	CA-CB	-5.10	1.46	1.53
3	B	203	GLN	C-O	-5.10	1.18	1.24
1	M	440	VAL	CA-C	-5.10	1.47	1.53
3	F	495	VAL	C-O	-5.10	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	72	PRO	C-O	-5.09	1.18	1.23
3	N	460	SER	CA-CB	-5.09	1.46	1.53
3	N	784	TYR	C-O	-5.08	1.18	1.24
3	F	798	PRO	C-O	-5.08	1.17	1.24
3	F	203	GLN	C-O	-5.08	1.18	1.24
3	N	203	GLN	C-O	-5.08	1.18	1.24
3	B	460	SER	CA-CB	-5.07	1.46	1.53
1	I	319	LYS	CA-C	-5.07	1.46	1.52
3	J	495	VAL	C-O	-5.06	1.18	1.24
1	E	319	LYS	CA-C	-5.06	1.46	1.52
3	B	282	LEU	CA-C	-5.05	1.46	1.52
1	A	319	LYS	CA-C	-5.04	1.46	1.52
1	E	538	MET	CA-C	-5.04	1.46	1.52
1	M	319	LYS	CA-C	-5.04	1.46	1.52
3	N	176	SER	CA-CB	-5.03	1.45	1.53
1	M	538	MET	CA-C	-5.03	1.46	1.52
3	F	341	SER	CA-CB	-5.03	1.45	1.53
3	N	495	VAL	C-O	-5.02	1.18	1.24
3	B	495	VAL	C-O	-5.02	1.18	1.24
3	J	176	SER	CA-CB	-5.02	1.45	1.53
3	J	188	SER	CA-CB	-5.02	1.44	1.53
1	M	592	GLY	CA-C	-5.01	1.45	1.51
3	J	849	ILE	C-O	-5.01	1.18	1.24
3	B	188	SER	CA-CB	-5.01	1.44	1.53
3	F	188	SER	CA-CB	-5.01	1.44	1.53
1	A	538	MET	CA-C	-5.00	1.46	1.52
3	F	849	ILE	C-O	-5.00	1.18	1.24
3	N	188	SER	CA-CB	-5.00	1.44	1.53

All (689) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	347	GLN	N-CA-C	-14.94	91.88	112.94
1	E	347	GLN	N-CA-C	-14.93	91.89	112.94
1	A	347	GLN	N-CA-C	-14.90	91.93	112.94
1	M	347	GLN	N-CA-C	-14.89	91.94	112.94
3	F	283	LEU	N-CA-C	14.63	133.94	113.16
1	E	859	PRO	N-CA-C	14.63	128.55	110.70
1	I	859	PRO	N-CA-C	14.62	128.54	110.70
1	A	859	PRO	N-CA-C	14.62	128.54	110.70
1	M	859	PRO	N-CA-C	14.60	128.51	110.70
1	E	340	VAL	N-CA-C	-13.87	100.67	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	340	VAL	N-CA-C	-13.86	100.68	111.90
1	A	340	VAL	N-CA-C	-13.85	100.69	111.90
1	M	340	VAL	N-CA-C	-13.83	100.70	111.90
1	E	856	VAL	N-CA-C	13.19	129.44	113.22
1	A	856	VAL	N-CA-C	13.17	129.42	113.22
1	M	856	VAL	N-CA-C	13.17	129.42	113.22
1	I	856	VAL	N-CA-C	13.17	129.41	113.22
3	N	253	ASN	N-CA-C	-13.12	89.18	109.25
3	B	283	LEU	CA-C-N	-12.09	104.73	119.84
3	B	283	LEU	C-N-CA	-12.09	104.73	119.84
3	B	284	PRO	N-CA-C	-11.72	88.32	112.47
1	E	344	ASN	N-CA-C	11.29	125.08	108.60
1	I	344	ASN	N-CA-C	11.26	125.04	108.60
1	A	344	ASN	N-CA-C	11.26	125.03	108.60
1	M	1169	LEU	N-CA-C	-11.25	98.65	112.38
1	M	344	ASN	N-CA-C	11.25	125.03	108.60
1	A	1169	LEU	N-CA-C	-11.24	98.67	112.38
1	I	1169	LEU	N-CA-C	-11.23	98.68	112.38
1	E	1169	LEU	N-CA-C	-11.21	98.70	112.38
1	E	935	LEU	N-CA-C	-10.88	98.18	110.91
1	A	935	LEU	N-CA-C	-10.87	98.19	110.91
1	M	935	LEU	N-CA-C	-10.87	98.19	110.91
1	I	935	LEU	N-CA-C	-10.85	98.22	110.91
3	F	1091	LEU	N-CA-C	-10.60	100.35	113.28
2	C	381	SER	N-CA-C	-10.46	100.82	114.31
2	G	381	SER	N-CA-C	-10.43	100.85	114.31
2	K	381	SER	N-CA-C	-10.43	100.86	114.31
2	O	381	SER	N-CA-C	-10.10	101.28	114.31
2	K	375	PRO	N-CA-C	-10.04	95.42	111.38
2	C	375	PRO	N-CA-C	-10.03	95.43	111.38
2	O	375	PRO	N-CA-C	-10.02	95.45	111.38
2	G	375	PRO	N-CA-C	-10.00	95.48	111.38
1	M	861	GLU	N-CA-C	9.95	126.29	112.75
1	E	861	GLU	N-CA-C	9.95	126.29	112.75
1	I	861	GLU	N-CA-C	9.95	126.28	112.75
1	A	861	GLU	N-CA-C	9.94	126.27	112.75
3	B	725	HIS	N-CA-C	-9.93	101.38	113.19
3	J	725	HIS	N-CA-C	-9.92	101.38	113.19
3	N	725	HIS	N-CA-C	-9.92	101.38	113.19
3	F	725	HIS	N-CA-C	-9.91	101.40	113.19
3	B	303	PRO	N-CA-CB	-9.73	91.90	102.60
3	J	303	PRO	N-CA-CB	-9.72	91.91	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	303	PRO	N-CA-CB	-9.72	91.91	102.60
3	N	303	PRO	N-CA-CB	-9.67	91.96	102.60
3	B	867	LEU	N-CA-C	-9.63	101.53	113.18
3	N	867	LEU	N-CA-C	-9.63	101.53	113.18
3	J	867	LEU	N-CA-C	-9.62	101.55	113.18
3	F	867	LEU	N-CA-C	-9.57	101.61	113.18
3	B	777	LYS	CB-CA-C	9.07	124.61	111.73
3	F	284	PRO	N-CA-C	-9.07	101.41	113.65
3	J	777	LYS	CB-CA-C	9.06	124.60	111.73
3	F	777	LYS	CB-CA-C	9.04	124.57	111.73
3	N	777	LYS	CB-CA-C	8.77	124.61	111.80
3	B	384	GLN	N-CA-C	-8.59	102.93	113.41
3	F	384	GLN	N-CA-C	-8.58	102.94	113.41
3	N	384	GLN	N-CA-C	-8.58	102.95	113.41
1	E	799	TYR	N-CA-C	8.56	121.84	110.53
3	J	384	GLN	N-CA-C	-8.56	102.97	113.41
1	A	799	TYR	N-CA-C	8.54	121.80	110.53
1	I	799	TYR	N-CA-C	8.54	121.80	110.53
1	M	799	TYR	N-CA-C	8.52	121.78	110.53
1	M	444	ILE	N-CA-C	-8.45	96.34	108.17
3	B	283	LEU	N-CA-C	8.45	128.49	109.81
1	A	444	ILE	N-CA-C	-8.45	96.34	108.17
1	E	444	ILE	N-CA-C	-8.43	96.37	108.17
1	I	444	ILE	N-CA-C	-8.43	96.36	108.17
3	F	661	SER	N-CA-C	8.37	120.02	111.07
3	N	661	SER	N-CA-C	8.35	120.00	111.07
3	B	661	SER	N-CA-C	8.34	119.99	111.07
3	J	661	SER	N-CA-C	8.33	119.98	111.07
3	J	306	ALA	N-CA-C	8.31	120.12	111.14
3	F	306	ALA	N-CA-C	8.29	120.09	111.14
3	B	306	ALA	N-CA-C	8.27	120.08	111.14
3	N	306	ALA	N-CA-C	8.27	120.07	111.14
1	A	789	MET	N-CA-C	-8.22	102.40	111.36
1	I	789	MET	N-CA-C	-8.22	102.40	111.36
3	N	254	LEU	N-CA-C	-8.22	102.97	113.16
1	E	789	MET	N-CA-C	-8.21	102.41	111.36
1	M	789	MET	N-CA-C	-8.19	102.43	111.36
1	E	129	GLN	N-CA-C	8.11	123.21	113.16
1	A	129	GLN	N-CA-C	8.07	123.17	113.16
1	I	129	GLN	N-CA-C	8.06	123.16	113.16
1	M	129	GLN	N-CA-C	8.03	123.12	113.16
3	B	467	VAL	N-CA-C	-7.95	99.36	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	467	VAL	N-CA-C	-7.95	99.36	109.30
3	F	467	VAL	N-CA-C	-7.95	99.37	109.30
3	J	467	VAL	N-CA-C	-7.93	99.38	109.30
3	J	253	ASN	N-CA-C	-7.93	97.12	109.25
3	F	1091	LEU	CB-CA-C	7.90	124.89	109.72
1	M	872	PRO	CA-N-CD	-7.84	101.02	112.00
2	K	341	ARG	CA-C-N	-7.83	110.36	119.05
2	K	341	ARG	C-N-CA	-7.83	110.36	119.05
1	I	872	PRO	CA-N-CD	-7.82	101.06	112.00
2	G	341	ARG	CA-C-N	-7.81	110.38	119.05
2	G	341	ARG	C-N-CA	-7.81	110.38	119.05
1	E	872	PRO	CA-N-CD	-7.81	101.07	112.00
1	A	872	PRO	CA-N-CD	-7.81	101.07	112.00
1	A	940	GLU	N-CA-C	7.80	119.42	111.07
2	C	341	ARG	CA-C-N	-7.80	110.40	119.05
2	C	341	ARG	C-N-CA	-7.80	110.40	119.05
3	N	746	ILE	N-CA-C	-7.79	102.67	110.62
2	O	341	ARG	CA-C-N	-7.79	110.41	119.05
2	O	341	ARG	C-N-CA	-7.79	110.41	119.05
3	B	746	ILE	N-CA-C	-7.78	102.69	110.62
3	J	746	ILE	N-CA-C	-7.77	102.69	110.62
3	F	746	ILE	N-CA-C	-7.76	102.71	110.62
3	F	556	PRO	CB-CA-C	-7.70	102.10	111.11
1	I	940	GLU	N-CA-C	7.70	119.45	111.14
3	J	556	PRO	CB-CA-C	-7.70	102.10	111.11
1	M	940	GLU	N-CA-C	7.69	119.45	111.14
3	B	556	PRO	CB-CA-C	-7.69	102.11	111.11
3	F	283	LEU	CA-C-N	-7.69	110.82	119.28
3	F	283	LEU	C-N-CA	-7.69	110.82	119.28
3	N	556	PRO	CB-CA-C	-7.69	102.11	111.11
1	E	940	GLU	N-CA-C	7.69	119.44	111.14
1	E	336	ILE	N-CA-C	-7.62	105.26	111.81
1	A	336	ILE	N-CA-C	-7.60	105.27	111.81
1	I	336	ILE	N-CA-C	-7.59	105.28	111.81
3	J	614	ARG	CB-CA-C	7.59	120.50	109.11
3	F	614	ARG	CB-CA-C	7.58	120.47	109.11
3	N	553	PRO	CB-CA-C	7.55	120.90	111.23
3	N	1091	LEU	N-CA-C	-7.55	104.04	113.18
3	B	614	ARG	CB-CA-C	7.55	120.43	109.11
1	M	345	ALA	N-CA-C	-7.54	103.39	112.59
3	N	614	ARG	CB-CA-C	7.54	120.42	109.11
3	J	553	PRO	CB-CA-C	7.54	120.88	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	336	ILE	N-CA-C	-7.53	105.33	111.81
1	A	345	ALA	N-CA-C	-7.53	103.41	112.59
1	I	345	ALA	N-CA-C	-7.53	103.41	112.59
3	N	303	PRO	N-CA-C	7.53	131.67	112.10
3	B	303	PRO	N-CA-C	7.52	131.64	112.10
3	F	303	PRO	N-CA-C	7.52	131.64	112.10
3	B	553	PRO	CB-CA-C	7.51	120.85	111.23
1	E	345	ALA	N-CA-C	-7.51	103.42	112.59
3	F	553	PRO	CB-CA-C	7.51	120.85	111.23
3	J	303	PRO	N-CA-C	7.51	131.63	112.10
3	F	302	TYR	CB-CA-C	-7.38	95.62	110.17
3	B	302	TYR	CB-CA-C	-7.37	95.66	110.17
3	N	302	TYR	CB-CA-C	-7.36	95.68	110.17
3	J	302	TYR	CB-CA-C	-7.35	95.69	110.17
3	F	134	ASP	N-CA-C	-7.32	103.38	111.36
3	B	134	ASP	N-CA-C	-7.32	103.39	111.36
3	N	134	ASP	N-CA-C	-7.31	103.39	111.36
3	J	134	ASP	N-CA-C	-7.31	103.39	111.36
2	O	335	ARG	N-CA-C	7.21	118.93	111.14
3	N	723	PRO	N-CA-C	-7.20	104.47	114.98
2	G	335	ARG	N-CA-C	7.18	118.90	111.14
2	C	335	ARG	N-CA-C	7.18	118.89	111.14
3	J	723	PRO	N-CA-C	-7.18	104.50	114.98
3	B	723	PRO	N-CA-C	-7.18	104.50	114.98
3	B	253	ASN	N-CA-C	-7.17	98.35	109.76
2	K	335	ARG	N-CA-C	7.15	118.86	111.14
3	F	723	PRO	N-CA-C	-7.14	104.55	114.98
3	F	789	THR	CB-CA-C	-7.04	97.84	110.37
3	F	870	GLY	N-CA-C	-7.04	105.50	115.43
3	B	789	THR	CB-CA-C	-7.04	97.84	110.37
3	B	870	GLY	N-CA-C	-7.02	105.53	115.43
3	J	789	THR	CB-CA-C	-7.02	97.87	110.37
3	N	789	THR	CB-CA-C	-7.02	97.88	110.37
3	N	870	GLY	N-CA-C	-7.01	105.55	115.43
3	J	870	GLY	N-CA-C	-7.01	105.55	115.43
3	B	927	ARG	N-CA-C	-6.97	103.61	111.14
3	N	927	ARG	N-CA-C	-6.97	103.61	111.14
3	F	927	ARG	N-CA-C	-6.96	103.62	111.14
1	M	781	ASP	N-CA-C	-6.95	103.44	112.68
3	N	335	ARG	CB-CA-C	6.95	121.59	111.73
3	J	335	ARG	CB-CA-C	6.94	121.58	111.73
3	B	335	ARG	CB-CA-C	6.93	121.58	111.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	781	ASP	N-CA-C	-6.93	103.46	112.68
1	A	781	ASP	N-CA-C	-6.93	103.47	112.68
3	F	381	ASN	CB-CA-C	-6.92	104.21	110.44
3	J	927	ARG	N-CA-C	-6.91	103.67	111.14
1	E	781	ASP	N-CA-C	-6.89	103.51	112.68
3	F	335	ARG	CB-CA-C	6.88	121.50	111.73
3	B	381	ASN	CB-CA-C	-6.88	104.25	110.44
3	N	381	ASN	CB-CA-C	-6.87	104.25	110.44
3	J	381	ASN	CB-CA-C	-6.86	104.26	110.44
3	F	513	TYR	CB-CA-C	6.85	122.56	110.37
3	J	513	TYR	CB-CA-C	6.83	122.53	110.37
3	B	513	TYR	CB-CA-C	6.83	122.52	110.37
3	J	546	LYS	N-CA-C	-6.83	103.63	112.23
3	B	546	LYS	N-CA-C	-6.81	103.65	112.23
3	N	513	TYR	CB-CA-C	6.81	122.49	110.37
3	F	546	LYS	N-CA-C	-6.81	103.65	112.23
3	N	546	LYS	N-CA-C	-6.77	103.70	112.23
3	N	333	PHE	CA-CB-CG	6.76	120.56	113.80
1	E	346	GLU	N-CA-C	-6.75	98.65	109.39
1	A	346	GLU	N-CA-C	-6.72	98.70	109.39
3	F	333	PHE	CA-CB-CG	6.72	120.52	113.80
1	M	346	GLU	N-CA-C	-6.72	98.71	109.39
3	B	333	PHE	CA-CB-CG	6.71	120.51	113.80
1	I	376	PRO	N-CA-C	-6.70	104.04	110.47
3	F	285	ARG	N-CA-C	6.70	120.37	110.46
1	I	346	GLU	N-CA-C	-6.69	98.75	109.39
3	B	458	LEU	N-CA-C	-6.69	105.15	113.38
3	N	458	LEU	N-CA-C	-6.69	105.16	113.38
3	J	458	LEU	N-CA-C	-6.69	105.16	113.38
3	J	333	PHE	CA-CB-CG	6.68	120.48	113.80
1	A	376	PRO	N-CA-C	-6.67	104.06	110.47
3	F	560	LEU	N-CA-C	-6.67	104.36	113.30
3	J	562	THR	N-CA-C	-6.67	104.89	113.16
3	B	560	LEU	N-CA-C	-6.66	104.38	113.30
1	E	376	PRO	N-CA-C	-6.66	104.08	110.47
3	J	560	LEU	N-CA-C	-6.66	104.38	113.30
3	F	562	THR	N-CA-C	-6.65	104.91	113.16
3	F	458	LEU	N-CA-C	-6.65	105.20	113.38
3	N	562	THR	N-CA-C	-6.65	104.91	113.16
1	M	376	PRO	N-CA-C	-6.65	104.09	110.47
3	B	562	THR	N-CA-C	-6.64	104.93	113.16
3	F	466	PRO	N-CA-C	-6.63	103.99	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	560	LEU	N-CA-C	-6.63	104.42	113.30
3	B	466	PRO	N-CA-C	-6.62	104.00	113.47
3	J	466	PRO	N-CA-C	-6.60	104.03	113.47
3	N	466	PRO	N-CA-C	-6.59	104.04	113.47
3	J	724	THR	N-CA-C	6.57	119.28	110.35
1	M	338	ASP	N-CA-C	-6.56	98.58	109.46
1	A	338	ASP	N-CA-C	-6.55	98.59	109.46
3	N	724	THR	N-CA-C	6.55	119.26	110.35
1	E	338	ASP	N-CA-C	-6.55	98.59	109.46
1	I	338	ASP	N-CA-C	-6.54	98.60	109.46
3	B	724	THR	N-CA-C	6.54	119.25	110.35
3	J	721	ASP	N-CA-C	-6.54	104.19	111.71
3	F	724	THR	N-CA-C	6.53	119.24	110.35
3	J	723	PRO	CB-CA-C	-6.53	101.86	109.89
3	F	723	PRO	CB-CA-C	-6.52	101.87	109.89
3	B	723	PRO	CB-CA-C	-6.52	101.88	109.89
3	N	723	PRO	CB-CA-C	-6.50	101.90	109.89
3	B	721	ASP	N-CA-C	-6.50	104.24	111.71
3	N	721	ASP	N-CA-C	-6.49	104.24	111.71
1	M	488	CYS	N-CA-C	6.48	119.30	108.73
1	E	488	CYS	N-CA-C	6.48	119.29	108.73
1	A	488	CYS	N-CA-C	6.46	119.27	108.73
3	F	721	ASP	N-CA-C	-6.46	104.28	111.71
1	I	488	CYS	N-CA-C	6.45	119.24	108.73
3	F	204	ASN	CB-CA-C	6.44	122.55	110.63
3	N	204	ASN	CB-CA-C	6.44	122.54	110.63
3	B	204	ASN	CB-CA-C	6.43	122.53	110.63
3	J	204	ASN	CB-CA-C	6.42	122.51	110.63
2	O	355	TYR	N-CA-C	6.41	120.91	111.87
2	K	355	TYR	N-CA-C	6.40	120.89	111.87
2	C	355	TYR	N-CA-C	6.39	120.88	111.87
2	G	355	TYR	N-CA-C	6.38	120.87	111.87
3	B	255	PHE	N-CA-C	-6.38	105.53	113.38
3	F	368	PHE	CB-CA-C	6.36	123.74	110.32
3	J	173	ASN	N-CA-C	-6.36	104.43	111.36
3	B	368	PHE	CB-CA-C	6.35	123.72	110.32
3	N	368	PHE	CB-CA-C	6.34	123.70	110.32
3	B	173	ASN	N-CA-C	-6.33	104.46	111.36
3	J	368	PHE	CB-CA-C	6.33	123.68	110.32
3	F	173	ASN	N-CA-C	-6.33	104.46	111.36
1	M	788	THR	N-CA-C	-6.31	105.74	113.50
1	A	788	THR	N-CA-C	-6.30	105.75	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	788	THR	N-CA-C	-6.29	105.76	113.50
1	I	788	THR	N-CA-C	-6.29	105.76	113.50
3	N	173	ASN	N-CA-C	-6.29	104.50	111.36
3	N	619	VAL	CA-C-O	-6.28	117.17	122.63
3	B	461	PRO	N-CA-CB	-6.28	96.43	103.33
3	J	461	PRO	N-CA-CB	-6.28	96.43	103.33
3	F	461	PRO	N-CA-CB	-6.27	96.44	103.33
3	N	818	GLU	O-C-N	6.26	131.34	123.01
1	E	798	LEU	N-CA-C	6.26	118.60	110.53
3	N	461	PRO	N-CA-CB	-6.26	96.45	103.33
1	A	787	TYR	N-CA-C	6.26	120.63	113.19
3	J	818	GLU	O-C-N	6.26	131.33	123.01
1	M	787	TYR	N-CA-C	6.25	120.63	113.19
3	F	845	ARG	N-CA-C	-6.25	104.91	112.54
1	A	798	LEU	N-CA-C	6.25	118.59	110.53
1	I	798	LEU	N-CA-C	6.25	118.60	110.53
1	I	787	TYR	N-CA-C	6.25	120.63	113.19
3	B	332	ARG	CB-CG-CD	-6.25	96.93	111.30
3	J	619	VAL	CA-C-O	-6.25	117.19	122.63
3	J	332	ARG	CB-CG-CD	-6.24	96.95	111.30
3	F	332	ARG	CB-CG-CD	-6.24	96.95	111.30
3	F	818	GLU	O-C-N	6.24	131.31	123.01
3	F	619	VAL	CA-C-O	-6.24	117.20	122.63
3	N	332	ARG	CB-CG-CD	-6.24	96.96	111.30
3	B	619	VAL	CA-C-O	-6.23	117.21	122.63
3	B	818	GLU	O-C-N	6.23	131.30	123.01
3	N	845	ARG	N-CA-C	-6.23	104.94	112.54
1	M	798	LEU	N-CA-C	6.23	118.56	110.53
3	B	845	ARG	N-CA-C	-6.20	104.97	112.54
3	J	845	ARG	N-CA-C	-6.20	104.97	112.54
3	N	727	ILE	N-CA-C	-6.19	103.86	110.36
3	F	727	ILE	N-CA-C	-6.18	103.87	110.36
3	B	727	ILE	N-CA-C	-6.17	103.88	110.36
1	M	941	GLU	N-CA-C	-6.14	104.70	111.82
3	J	727	ILE	N-CA-C	-6.12	103.93	110.36
1	A	941	GLU	N-CA-C	-6.12	104.72	111.82
1	E	392	ARG	N-CA-C	6.12	118.61	110.53
1	A	392	ARG	N-CA-C	6.11	118.60	110.53
1	I	941	GLU	N-CA-C	-6.11	104.73	111.82
1	M	392	ARG	N-CA-C	6.11	118.59	110.53
1	I	392	ARG	N-CA-C	6.09	118.58	110.53
1	E	457	ASP	N-CA-C	-6.08	104.66	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	457	ASP	N-CA-C	-6.07	104.66	111.28
2	G	354	ILE	CB-CA-C	-6.07	103.84	112.22
1	A	457	ASP	N-CA-C	-6.07	104.67	111.28
1	I	457	ASP	N-CA-C	-6.07	104.67	111.28
3	B	900	TYR	CB-CA-C	6.06	121.16	110.85
1	E	941	GLU	N-CA-C	-6.06	104.80	111.82
3	N	900	TYR	CB-CA-C	6.05	121.14	110.85
2	C	354	ILE	CB-CA-C	-6.03	103.89	112.22
3	F	900	TYR	CB-CA-C	6.03	121.11	110.85
3	J	900	TYR	CB-CA-C	6.03	121.09	110.85
2	O	354	ILE	CB-CA-C	-6.02	103.91	112.22
2	K	354	ILE	CB-CA-C	-6.01	103.92	112.22
3	B	287	SER	N-CA-C	6.01	116.18	108.24
3	F	236	SER	N-CA-C	-6.01	104.80	111.71
3	J	236	SER	N-CA-C	-5.99	104.82	111.71
2	K	357	HIS	N-CA-C	-5.99	105.74	113.16
3	B	236	SER	N-CA-C	-5.98	104.83	111.71
3	N	236	SER	N-CA-C	-5.98	104.84	111.71
2	C	357	HIS	N-CA-C	-5.96	105.77	113.16
2	O	357	HIS	N-CA-C	-5.96	105.77	113.16
2	G	357	HIS	N-CA-C	-5.94	105.79	113.16
2	O	345	ARG	N-CA-C	-5.93	104.82	111.28
2	C	345	ARG	N-CA-C	-5.91	104.84	111.28
2	G	345	ARG	N-CA-C	-5.90	104.85	111.28
3	J	299	CYS	CB-CA-C	-5.89	98.69	110.42
3	B	459	ILE	N-CA-C	-5.89	99.12	108.90
1	I	459	GLY	N-CA-C	5.89	122.57	114.92
3	B	299	CYS	CB-CA-C	-5.88	98.71	110.42
3	N	299	CYS	CB-CA-C	-5.88	98.71	110.42
2	K	345	ARG	N-CA-C	-5.88	104.87	111.28
3	F	459	ILE	N-CA-C	-5.88	99.14	108.90
1	A	459	GLY	N-CA-C	5.88	122.56	114.92
3	N	459	ILE	N-CA-C	-5.88	99.14	108.90
1	M	459	GLY	N-CA-C	5.87	122.56	114.92
3	J	459	ILE	N-CA-C	-5.87	99.15	108.90
3	F	299	CYS	CB-CA-C	-5.86	98.76	110.42
1	E	459	GLY	N-CA-C	5.85	122.52	114.92
3	B	250	ASN	CB-CA-C	-5.84	101.80	110.67
3	N	250	ASN	CB-CA-C	-5.83	101.81	110.67
3	N	251	GLY	N-CA-C	5.83	121.63	114.69
3	F	1090	CYS	CA-C-N	-5.82	111.23	122.06
3	F	1090	CYS	C-N-CA	-5.82	111.23	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	557	ILE	N-CA-C	-5.81	102.07	109.80
1	M	869	ALA	CA-C-N	-5.78	113.82	119.78
1	M	869	ALA	C-N-CA	-5.78	113.82	119.78
3	F	557	ILE	N-CA-C	-5.78	102.11	109.80
3	N	576	TYR	CB-CA-C	5.77	118.56	109.27
3	J	557	ILE	N-CA-C	-5.77	102.13	109.80
3	J	576	TYR	CB-CA-C	5.76	118.55	109.27
3	N	557	ILE	N-CA-C	-5.76	102.14	109.80
3	B	576	TYR	CB-CA-C	5.75	118.53	109.27
3	F	576	TYR	CB-CA-C	5.74	118.52	109.27
1	A	869	ALA	CA-C-N	-5.74	113.87	119.78
1	A	869	ALA	C-N-CA	-5.74	113.87	119.78
3	F	133	ALA	N-CA-C	-5.73	105.63	113.30
3	B	133	ALA	N-CA-C	-5.72	105.63	113.30
3	J	961	LYS	CA-C-O	-5.72	114.94	121.58
3	F	298	PRO	N-CA-CB	-5.72	96.74	103.26
3	J	133	ALA	N-CA-C	-5.72	105.64	113.30
3	B	1091	LEU	N-CA-C	-5.72	104.50	112.45
3	F	737	LEU	N-CA-C	-5.72	106.28	113.20
3	N	737	LEU	N-CA-C	-5.72	106.28	113.20
3	N	294	ALA	N-CA-C	-5.71	106.07	113.16
1	I	869	ALA	CA-C-N	-5.71	113.90	119.78
1	I	869	ALA	C-N-CA	-5.71	113.90	119.78
1	E	869	ALA	CA-C-N	-5.71	113.90	119.78
1	E	869	ALA	C-N-CA	-5.71	113.90	119.78
3	B	737	LEU	N-CA-C	-5.71	106.29	113.20
3	J	294	ALA	N-CA-C	-5.70	106.09	113.16
3	J	298	PRO	N-CA-CB	-5.70	96.76	103.26
3	B	812	LEU	N-CA-C	-5.70	101.30	110.14
3	F	961	LYS	CA-C-O	-5.70	114.97	121.58
3	B	961	LYS	CA-C-O	-5.70	114.97	121.58
3	F	294	ALA	N-CA-C	-5.70	106.10	113.16
3	B	294	ALA	N-CA-C	-5.69	106.10	113.16
3	J	1091	LEU	N-CA-C	-5.69	104.54	112.45
3	N	133	ALA	N-CA-C	-5.69	105.67	113.30
3	B	298	PRO	N-CA-CB	-5.69	96.77	103.26
3	F	254	LEU	N-CA-C	-5.69	106.10	113.16
3	J	776	GLN	N-CA-C	-5.69	106.31	113.20
3	N	298	PRO	N-CA-CB	-5.68	96.78	103.26
3	N	776	GLN	N-CA-C	-5.68	106.33	113.20
3	J	737	LEU	N-CA-C	-5.68	106.33	113.20
3	F	286	GLU	N-CA-C	5.68	120.34	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	776	GLN	N-CA-C	-5.67	106.33	113.20
3	F	574	VAL	N-CA-C	-5.67	100.32	108.48
3	J	812	LEU	N-CA-C	-5.67	101.36	110.14
3	N	229	ASN	CB-CA-C	-5.67	99.34	110.11
3	J	229	ASN	CB-CA-C	-5.66	99.35	110.11
3	N	961	LYS	CA-C-O	-5.66	115.02	121.58
1	M	389	THR	CB-CA-C	-5.66	100.75	109.29
3	J	574	VAL	N-CA-C	-5.66	100.33	108.48
3	N	812	LEU	N-CA-C	-5.66	101.37	110.14
3	B	229	ASN	CB-CA-C	-5.65	99.37	110.11
3	F	253	ASN	N-CA-C	-5.65	100.78	109.76
1	M	339	GLY	N-CA-C	-5.65	99.79	113.18
3	J	250	ASN	CB-CA-C	-5.65	101.79	110.26
1	A	339	GLY	N-CA-C	-5.64	99.81	113.18
1	E	389	THR	CB-CA-C	-5.64	100.77	109.29
3	B	574	VAL	N-CA-C	-5.64	100.36	108.48
3	F	776	GLN	N-CA-C	-5.64	106.37	113.20
3	F	812	LEU	N-CA-C	-5.64	101.39	110.14
3	F	229	ASN	CB-CA-C	-5.64	99.40	110.11
1	I	339	GLY	N-CA-C	-5.63	99.84	113.18
1	I	389	THR	CB-CA-C	-5.63	100.79	109.29
1	E	339	GLY	N-CA-C	-5.63	99.84	113.18
1	A	389	THR	CB-CA-C	-5.62	100.80	109.29
3	N	289	SER	N-CA-C	5.61	117.48	111.36
1	M	592	GLY	CA-C-N	-5.61	114.10	122.74
1	M	592	GLY	C-N-CA	-5.61	114.10	122.74
3	F	289	SER	N-CA-C	5.61	117.47	111.36
3	J	748	LEU	N-CA-C	-5.61	105.70	112.54
3	N	574	VAL	N-CA-C	-5.60	100.42	108.48
1	I	592	GLY	CA-C-N	-5.59	114.12	122.74
1	I	592	GLY	C-N-CA	-5.59	114.12	122.74
3	J	289	SER	N-CA-C	5.59	117.45	111.36
3	N	748	LEU	N-CA-C	-5.59	105.72	112.54
3	B	925	LEU	N-CA-C	-5.59	104.68	112.45
1	A	592	GLY	CA-C-N	-5.58	114.14	122.74
1	A	592	GLY	C-N-CA	-5.58	114.14	122.74
3	N	925	LEU	N-CA-C	-5.58	104.69	112.45
3	F	748	LEU	N-CA-C	-5.58	105.74	112.54
3	N	184	GLU	CB-CA-C	5.57	120.31	110.85
3	J	925	LEU	N-CA-C	-5.56	104.72	112.45
3	B	172	ILE	N-CA-C	-5.55	106.41	112.80
3	B	748	LEU	N-CA-C	-5.55	105.76	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	172	ILE	N-CA-C	-5.55	106.41	112.80
3	B	993	PRO	CB-CA-C	-5.55	104.01	112.11
3	N	993	PRO	CB-CA-C	-5.55	104.01	112.11
3	F	925	LEU	N-CA-C	-5.55	104.74	112.45
3	J	184	GLU	CB-CA-C	5.55	120.28	110.85
3	F	993	PRO	CB-CA-C	-5.54	104.02	112.11
3	B	184	GLU	CB-CA-C	5.54	120.26	110.85
3	J	993	PRO	CB-CA-C	-5.54	104.03	112.11
3	B	301	SER	CB-CA-C	-5.53	100.51	111.91
3	F	184	GLU	CB-CA-C	5.53	120.25	110.85
3	J	137	GLN	CB-CG-CD	-5.53	103.20	112.60
3	J	172	ILE	N-CA-C	-5.53	106.44	112.80
3	J	301	SER	CB-CA-C	-5.53	100.52	111.91
3	N	172	ILE	N-CA-C	-5.52	106.45	112.80
3	N	255	PHE	N-CA-C	-5.52	106.38	113.23
3	J	305	PHE	CB-CA-C	5.52	119.73	111.89
3	J	459	ILE	CA-C-O	-5.52	116.17	121.63
1	I	375	VAL	N-CA-C	-5.52	103.54	108.95
3	N	137	GLN	CB-CG-CD	-5.52	103.22	112.60
3	B	137	GLN	CB-CG-CD	-5.52	103.22	112.60
3	F	301	SER	CB-CA-C	-5.52	100.55	111.91
1	I	786	LEU	N-CA-C	-5.51	105.27	111.28
3	B	305	PHE	CB-CA-C	5.51	119.72	111.89
3	F	305	PHE	CB-CA-C	5.51	119.72	111.89
3	J	1070	THR	N-CA-C	-5.50	105.28	111.28
3	N	305	PHE	CB-CA-C	5.50	119.70	111.89
3	N	132	GLN	CB-CA-C	-5.50	104.13	111.88
3	N	301	SER	CB-CA-C	-5.50	100.58	111.91
3	J	132	GLN	CB-CA-C	-5.50	104.13	111.88
3	B	459	ILE	CA-C-O	-5.49	116.19	121.63
3	F	459	ILE	CA-C-O	-5.49	116.19	121.63
3	N	459	ILE	CA-C-O	-5.49	116.19	121.63
3	B	132	GLN	CB-CA-C	-5.49	104.14	111.88
3	F	137	GLN	CB-CG-CD	-5.49	103.27	112.60
3	F	132	GLN	CB-CA-C	-5.49	104.15	111.88
1	A	375	VAL	N-CA-C	-5.48	103.58	108.95
3	N	1070	THR	N-CA-C	-5.48	105.31	111.28
1	A	786	LEU	N-CA-C	-5.47	105.31	111.28
3	B	1070	THR	N-CA-C	-5.47	105.31	111.28
3	F	1070	THR	N-CA-C	-5.47	105.32	111.28
1	M	375	VAL	N-CA-C	-5.46	103.60	108.95
1	E	375	VAL	N-CA-C	-5.45	103.61	108.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	786	LEU	N-CA-C	-5.45	105.34	111.28
3	F	123	ARG	N-CA-C	-5.45	106.41	113.16
1	A	1215	LEU	CA-C-N	-5.44	112.92	118.85
1	A	1215	LEU	C-N-CA	-5.44	112.92	118.85
1	E	1215	LEU	CA-C-N	-5.44	112.92	118.85
1	E	1215	LEU	C-N-CA	-5.44	112.92	118.85
1	M	1215	LEU	CA-C-N	-5.44	112.92	118.85
1	M	1215	LEU	C-N-CA	-5.44	112.92	118.85
3	B	123	ARG	N-CA-C	-5.43	106.43	113.16
3	J	123	ARG	N-CA-C	-5.42	106.44	113.16
3	N	123	ARG	N-CA-C	-5.42	106.45	113.16
1	M	786	LEU	N-CA-C	-5.41	105.39	111.28
1	E	1126	LEU	N-CA-C	-5.41	104.93	112.45
1	I	1215	LEU	CA-C-N	-5.40	112.96	118.85
1	I	1215	LEU	C-N-CA	-5.40	112.96	118.85
3	B	758	LYS	N-CA-C	-5.40	104.64	111.11
3	J	155	VAL	N-CA-C	-5.38	105.13	110.62
3	J	758	LYS	N-CA-C	-5.38	104.65	111.11
3	N	758	LYS	N-CA-C	-5.38	104.65	111.11
1	M	1126	LEU	N-CA-C	-5.38	104.97	112.45
1	I	1126	LEU	N-CA-C	-5.38	104.97	112.45
1	A	1126	LEU	N-CA-C	-5.38	104.97	112.45
3	F	758	LYS	N-CA-C	-5.37	104.66	111.11
3	B	155	VAL	N-CA-C	-5.36	105.16	110.62
3	F	825	PRO	CB-CA-C	5.36	118.37	111.46
3	N	155	VAL	N-CA-C	-5.36	105.16	110.62
3	B	1012	ARG	N-CA-C	-5.35	105.53	111.36
1	M	62	ARG	N-CA-C	5.35	117.11	111.28
3	F	1012	ARG	N-CA-C	-5.34	105.54	111.36
1	E	387	PRO	N-CA-C	5.34	119.57	111.19
3	J	178	TYR	N-CA-C	-5.34	105.36	111.07
1	A	387	PRO	N-CA-C	5.33	119.56	111.19
3	N	825	PRO	CB-CA-C	5.33	118.34	111.46
3	J	825	PRO	CB-CA-C	5.33	118.33	111.46
1	M	387	PRO	N-CA-C	5.33	119.55	111.19
3	B	825	PRO	CB-CA-C	5.33	118.33	111.46
3	J	243	LYS	N-CA-C	-5.33	105.47	111.28
3	J	1012	ARG	N-CA-C	-5.33	105.55	111.36
2	K	340	LEU	N-CA-C	-5.32	102.03	109.96
3	B	1075	ASN	CB-CA-C	5.32	119.24	110.88
3	F	155	VAL	N-CA-C	-5.32	105.19	110.62
2	C	340	LEU	N-CA-C	-5.32	102.03	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	1012	ARG	N-CA-C	-5.32	105.56	111.36
3	F	178	TYR	N-CA-C	-5.32	105.38	111.07
3	J	670	PHE	CA-CB-CG	5.32	119.12	113.80
3	N	1075	ASN	CB-CA-C	5.32	119.23	110.88
3	B	226	LYS	N-CA-C	-5.32	105.48	111.28
3	J	1075	ASN	CB-CA-C	5.32	119.22	110.88
3	B	178	TYR	N-CA-C	-5.31	105.38	111.07
3	J	226	LYS	N-CA-C	-5.31	105.49	111.28
1	I	387	PRO	N-CA-C	5.31	119.52	111.19
3	F	1075	ASN	CB-CA-C	5.31	119.21	110.88
3	N	226	LYS	N-CA-C	-5.31	105.50	111.28
2	O	340	LEU	N-CA-C	-5.30	102.06	109.96
3	N	178	TYR	N-CA-C	-5.30	105.40	111.07
1	A	62	ARG	N-CA-C	5.30	117.05	111.28
2	G	340	LEU	N-CA-C	-5.30	102.07	109.96
3	N	1084	PRO	N-CA-C	-5.29	102.88	111.03
3	F	243	LYS	N-CA-C	-5.29	105.51	111.28
3	F	175	VAL	N-CA-C	-5.29	105.38	110.72
3	B	243	LYS	N-CA-C	-5.28	105.52	111.28
3	F	1084	PRO	N-CA-C	-5.28	102.90	111.03
3	N	243	LYS	N-CA-C	-5.28	105.53	111.28
3	N	670	PHE	CA-CB-CG	5.28	119.08	113.80
3	F	226	LYS	N-CA-C	-5.27	105.53	111.28
3	B	1084	PRO	N-CA-C	-5.27	102.92	111.03
3	J	751	GLU	CB-CA-C	5.27	118.46	109.24
3	F	751	GLU	CB-CA-C	5.26	118.45	109.24
3	J	1084	PRO	N-CA-C	-5.26	102.92	111.03
3	B	670	PHE	CA-CB-CG	5.26	119.06	113.80
3	B	751	GLU	CB-CA-C	5.25	118.44	109.24
3	N	751	GLU	CB-CA-C	5.25	118.44	109.24
3	B	175	VAL	N-CA-C	-5.25	105.42	110.72
3	J	389	GLN	N-CA-C	-5.25	105.64	111.36
3	N	175	VAL	N-CA-C	-5.25	105.42	110.72
3	N	389	GLN	N-CA-C	-5.25	105.64	111.36
3	J	175	VAL	N-CA-C	-5.24	105.42	110.72
3	N	301	SER	CA-C-O	-5.24	115.70	121.31
2	K	336	ASP	CA-C-N	-5.24	113.52	119.28
2	K	336	ASP	C-N-CA	-5.24	113.52	119.28
3	F	783	ARG	N-CA-C	-5.24	107.02	113.41
2	C	336	ASP	CA-C-N	-5.23	113.52	119.28
2	C	336	ASP	C-N-CA	-5.23	113.52	119.28
3	B	116	HIS	CB-CA-C	5.23	121.24	110.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	116	HIS	CB-CA-C	5.23	121.23	110.31
3	F	670	PHE	CA-CB-CG	5.22	119.03	113.80
1	I	62	ARG	N-CA-C	5.22	117.05	111.36
3	J	116	HIS	CB-CA-C	5.22	121.22	110.31
3	J	301	SER	CA-C-O	-5.22	115.72	121.31
2	O	336	ASP	CA-C-N	-5.22	113.54	119.28
2	O	336	ASP	C-N-CA	-5.22	113.54	119.28
3	N	116	HIS	CB-CA-C	5.22	121.22	110.31
3	B	301	SER	CA-C-O	-5.22	115.73	121.31
3	J	749	LYS	CB-CA-C	-5.22	101.27	111.03
3	F	749	LYS	CB-CA-C	-5.21	101.29	111.03
3	B	749	LYS	CB-CA-C	-5.21	101.30	111.03
3	N	465	ASP	CB-CA-C	-5.20	103.03	111.14
3	B	783	ARG	N-CA-C	-5.20	107.07	113.41
3	N	749	LYS	CB-CA-C	-5.20	101.31	111.03
3	B	389	GLN	N-CA-C	-5.20	105.69	111.36
3	B	465	ASP	CB-CA-C	-5.20	103.03	111.14
3	F	301	SER	CA-C-O	-5.20	115.75	121.31
3	B	282	LEU	N-CA-C	-5.20	99.73	110.80
3	F	389	GLN	N-CA-C	-5.20	105.70	111.36
1	E	62	ARG	N-CA-C	5.19	117.02	111.36
3	J	465	ASP	CB-CA-C	-5.19	103.04	111.14
3	J	436	ARG	N-CA-C	-5.19	105.74	111.71
2	G	336	ASP	CA-C-N	-5.18	113.58	119.28
2	G	336	ASP	C-N-CA	-5.18	113.58	119.28
3	F	465	ASP	CB-CA-C	-5.18	103.05	111.14
3	N	783	ARG	N-CA-C	-5.18	107.09	113.41
3	J	738	ALA	N-CA-C	-5.18	106.64	113.12
3	F	436	ARG	N-CA-C	-5.17	105.76	111.71
3	B	436	ARG	N-CA-C	-5.17	105.77	111.71
3	B	778	LEU	CA-C-O	-5.17	116.29	122.13
3	F	778	LEU	CA-C-O	-5.17	116.29	122.13
3	N	436	ARG	N-CA-C	-5.16	105.77	111.71
3	J	783	ARG	N-CA-C	-5.16	107.11	113.41
3	B	738	ALA	N-CA-C	-5.15	106.68	113.12
3	N	88	LEU	CA-C-N	-5.15	112.48	120.31
3	N	88	LEU	C-N-CA	-5.15	112.48	120.31
3	F	217	ASP	CA-CB-CG	5.15	117.75	112.60
3	J	88	LEU	CA-C-N	-5.15	112.48	120.31
3	J	88	LEU	C-N-CA	-5.15	112.48	120.31
3	J	778	LEU	CA-C-O	-5.15	116.31	122.13
3	N	738	ALA	N-CA-C	-5.15	106.69	113.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	149	LEU	N-CA-C	-5.14	102.67	110.28
3	J	217	ASP	CA-CB-CG	5.14	117.74	112.60
3	B	88	LEU	CA-C-N	-5.14	112.50	120.31
3	B	88	LEU	C-N-CA	-5.14	112.50	120.31
3	J	802	THR	N-CA-C	-5.14	105.68	111.28
3	N	149	LEU	N-CA-C	-5.14	102.67	110.28
3	F	311	VAL	CA-C-O	-5.14	115.61	120.95
3	B	630	ARG	N-CA-C	-5.14	106.27	112.54
3	N	630	ARG	N-CA-C	-5.14	106.27	112.54
3	F	88	LEU	CA-C-N	-5.13	112.51	120.31
3	F	88	LEU	C-N-CA	-5.13	112.51	120.31
3	J	149	LEU	N-CA-C	-5.13	102.68	110.28
3	J	311	VAL	CA-C-O	-5.13	115.61	120.95
3	B	217	ASP	CA-CB-CG	5.13	117.73	112.60
3	F	844	GLU	N-CA-C	-5.13	106.71	113.17
3	B	149	LEU	N-CA-C	-5.12	102.69	110.28
3	N	1088	ASP	O-C-N	5.12	125.98	121.37
3	F	738	ALA	N-CA-C	-5.12	106.72	113.12
3	N	217	ASP	CA-CB-CG	5.12	117.72	112.60
3	B	311	VAL	CA-C-O	-5.12	115.63	120.95
3	N	778	LEU	CA-C-O	-5.11	116.35	122.13
3	N	844	GLU	N-CA-C	-5.11	106.74	113.17
3	F	1088	ASP	O-C-N	5.10	125.96	121.37
3	F	630	ARG	N-CA-C	-5.10	106.32	112.54
3	J	1088	ASP	O-C-N	5.10	125.96	121.37
3	B	802	THR	N-CA-C	-5.10	105.72	111.28
3	J	630	ARG	N-CA-C	-5.10	106.32	112.54
3	N	311	VAL	CA-C-O	-5.10	115.65	120.95
3	J	844	GLU	N-CA-C	-5.09	106.75	113.17
3	N	555	ARG	CB-CA-C	-5.09	100.14	110.17
3	N	802	THR	N-CA-C	-5.09	105.73	111.28
3	B	844	GLU	N-CA-C	-5.09	106.76	113.17
3	F	802	THR	N-CA-C	-5.09	105.73	111.28
3	B	1088	ASP	O-C-N	5.09	125.95	121.37
3	N	1063	ARG	CA-C-N	-5.09	117.06	122.30
3	N	1063	ARG	C-N-CA	-5.09	117.06	122.30
3	F	735	SER	N-CA-C	-5.09	107.08	113.28
3	J	1063	ARG	CA-C-N	-5.08	117.07	122.30
3	J	1063	ARG	C-N-CA	-5.08	117.07	122.30
3	N	735	SER	N-CA-C	-5.08	107.08	113.28
3	N	803	PHE	N-CA-C	-5.08	105.65	111.14
3	F	711	GLN	N-CA-C	-5.08	100.00	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	555	ARG	CB-CA-C	-5.08	100.17	110.17
3	J	555	ARG	CB-CA-C	-5.08	100.17	110.17
3	J	711	GLN	N-CA-C	-5.08	100.01	108.23
3	B	555	ARG	CB-CA-C	-5.08	100.17	110.17
3	J	735	SER	N-CA-C	-5.07	107.09	113.28
3	B	1063	ARG	CA-C-N	-5.07	117.08	122.30
3	B	1063	ARG	C-N-CA	-5.07	117.08	122.30
3	F	1063	ARG	CA-C-N	-5.07	117.08	122.30
3	F	1063	ARG	C-N-CA	-5.07	117.08	122.30
3	B	711	GLN	N-CA-C	-5.07	100.02	108.23
3	B	735	SER	N-CA-C	-5.07	107.10	113.28
3	B	803	PHE	N-CA-C	-5.07	105.67	111.14
3	N	711	GLN	N-CA-C	-5.07	100.02	108.23
3	F	250	ASN	CB-CA-C	-5.06	101.80	109.89
3	F	803	PHE	N-CA-C	-5.05	105.69	111.14
3	N	679	LEU	CA-C-O	-5.05	115.44	120.64
3	F	577	PRO	N-CA-CB	-5.05	98.65	103.39
3	F	784	TYR	N-CA-C	-5.05	105.86	111.36
3	B	679	LEU	CA-C-O	-5.04	115.44	120.64
3	J	784	TYR	N-CA-C	-5.04	105.86	111.36
3	N	821	VAL	CA-C-N	-5.04	116.18	122.48
3	N	821	VAL	C-N-CA	-5.04	116.18	122.48
3	F	679	LEU	CA-C-O	-5.04	115.45	120.64
3	J	577	PRO	N-CA-CB	-5.04	98.66	103.39
1	A	859	PRO	CA-C-N	-5.04	114.57	119.76
1	A	859	PRO	C-N-CA	-5.04	114.57	119.76
1	I	859	PRO	CA-C-N	-5.04	114.57	119.76
1	I	859	PRO	C-N-CA	-5.04	114.57	119.76
3	N	784	TYR	N-CA-C	-5.04	105.87	111.36
3	B	784	TYR	N-CA-C	-5.03	105.87	111.36
3	J	803	PHE	N-CA-C	-5.03	105.70	111.14
3	N	801	THR	N-CA-C	-5.03	106.99	113.23
3	B	821	VAL	CA-C-N	-5.03	116.19	122.48
3	B	821	VAL	C-N-CA	-5.03	116.19	122.48
3	F	987	LEU	N-CA-C	-5.03	106.99	113.02
3	J	679	LEU	CA-C-O	-5.03	115.46	120.64
3	F	821	VAL	CA-C-N	-5.02	116.20	122.48
3	F	821	VAL	C-N-CA	-5.02	116.20	122.48
3	B	987	LEU	N-CA-C	-5.02	107.00	113.02
3	J	1002	LEU	N-CA-C	-5.02	105.70	111.07
1	M	343	GLY	N-CA-C	5.01	117.22	111.36
3	J	755	PHE	N-CA-CB	5.01	117.25	109.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	577	PRO	N-CA-CB	-5.01	98.68	103.39
3	N	987	LEU	N-CA-C	-5.00	107.01	113.02
3	B	762	VAL	N-CA-C	-5.00	105.52	110.62
3	J	296	LEU	N-CA-C	-5.00	106.02	111.82
3	N	755	PHE	N-CA-CB	5.00	117.24	109.48
3	F	296	LEU	N-CA-C	-5.00	106.02	111.82
3	N	69	GLY	N-CA-C	-5.00	108.42	114.92

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7673	0	7689	417	0
1	E	7673	0	7689	456	0
1	I	7673	0	7689	421	0
1	M	7673	0	7689	408	0
2	C	402	0	417	68	0
2	G	402	0	417	68	0
2	K	402	0	417	70	0
2	O	402	0	417	69	0
3	B	8339	0	8330	617	0
3	F	8339	0	8328	658	0
3	J	8339	0	8330	595	0
3	N	8339	0	8329	565	0
4	A	15	0	23	18	0
4	B	15	0	23	19	0
4	E	15	0	23	17	0
4	F	30	0	49	66	0
4	I	15	0	23	18	0
4	M	15	0	23	17	0
4	N	15	0	24	40	0
5	B	27	0	12	3	0
5	F	27	0	12	2	0
5	J	27	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	27	0	12	2	0
All	All	65884	0	65977	3760	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 29.

All (3760) 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:E:28:PRO:HG2	3:F:547:LEU:CD2	1.26	1.64
3:B:974:MET:HE3	3:B:975:TYR:CZ	1.20	1.64
3:N:974:MET:CE	3:N:975:TYR:CZ	1.82	1.63
3:J:974:MET:HE3	3:J:975:TYR:CZ	1.20	1.63
3:N:974:MET:HE3	3:N:975:TYR:CZ	1.20	1.63
4:F:1101:FAR:C15	3:J:1013:ASN:HD21	1.04	1.61
3:F:974:MET:HE3	3:F:975:TYR:CZ	1.20	1.61
1:E:28:PRO:CG	3:F:547:LEU:HD21	1.14	1.60
3:B:974:MET:CE	3:B:975:TYR:CZ	1.82	1.59
3:F:965:GLN:HG2	3:F:969:LEU:CD1	1.14	1.59
3:N:965:GLN:HG2	3:N:969:LEU:CD1	1.14	1.58
1:I:1211:VAL:CG2	4:I:1301:FAR:H101	1.33	1.58
3:F:974:MET:CE	3:F:975:TYR:CZ	1.82	1.55
3:B:965:GLN:HG2	3:B:969:LEU:CD1	1.14	1.55
3:J:965:GLN:HG2	3:J:969:LEU:CD1	1.14	1.55
3:F:1013:ASN:HD21	4:F:1103:FAR:C15	0.97	1.54
3:J:974:MET:CE	3:J:975:TYR:CZ	1.82	1.54
1:E:1211:VAL:CG2	4:E:1301:FAR:H101	1.33	1.53
1:A:1211:VAL:CG2	4:A:1301:FAR:H101	1.33	1.52
1:I:28:PRO:CG	3:J:547:LEU:HD21	1.36	1.52
3:B:1092:ILE:HD11	3:N:1001:GLU:CG	1.08	1.51
3:F:1009:VAL:HA	4:F:1103:FAR:C14	1.38	1.51
1:M:1211:VAL:CG2	4:M:1301:FAR:H101	1.33	1.50
3:J:965:GLN:CG	3:J:969:LEU:HD11	1.40	1.50
2:G:332:ILE:HD13	2:G:340:LEU:CD1	1.41	1.49
2:C:332:ILE:HD13	2:C:340:LEU:CD1	1.41	1.49
4:F:1101:FAR:C14	3:J:1009:VAL:HA	1.42	1.49
1:I:28:PRO:HG2	3:J:547:LEU:CD2	1.42	1.48
3:B:965:GLN:CG	3:B:969:LEU:CD1	1.89	1.47
3:F:965:GLN:CG	3:F:969:LEU:CD1	1.89	1.47
3:B:965:GLN:CG	3:B:969:LEU:HD11	1.40	1.47
3:J:744:LEU:HD22	3:J:765:HIS:CD2	1.50	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:332:ILE:HD13	2:O:340:LEU:CD1	1.41	1.45
2:K:332:ILE:HD13	2:K:340:LEU:CD1	1.41	1.45
3:F:744:LEU:HD22	3:F:765:HIS:CD2	1.50	1.45
3:J:965:GLN:CG	3:J:969:LEU:CD1	1.89	1.45
1:E:120:THR:HG22	3:F:131:ARG:CZ	1.44	1.43
3:B:744:LEU:HD22	3:B:765:HIS:CD2	1.50	1.43
3:N:965:GLN:CG	3:N:969:LEU:HD11	1.40	1.43
3:F:965:GLN:CG	3:F:969:LEU:HD11	1.40	1.43
3:N:744:LEU:HD22	3:N:765:HIS:CD2	1.50	1.42
1:E:28:PRO:CG	3:F:547:LEU:CD2	1.87	1.41
1:A:788:THR:O	1:A:792:PRO:CD	1.69	1.41
3:B:1092:ILE:CD1	3:N:1001:GLU:HG2	0.93	1.41
1:M:788:THR:O	1:M:792:PRO:CD	1.69	1.40
3:N:965:GLN:CG	3:N:969:LEU:CD1	1.89	1.40
1:E:66:ASP:CB	3:B:667:GLN:HE22	1.32	1.40
1:M:28:PRO:CG	3:N:547:LEU:HD21	1.49	1.39
4:F:1101:FAR:H151	3:J:1013:ASN:ND2	1.07	1.39
1:A:28:PRO:CG	3:B:547:LEU:HD21	1.50	1.39
1:I:28:PRO:CG	3:J:547:LEU:CD2	1.96	1.37
1:I:788:THR:O	1:I:792:PRO:CD	1.69	1.37
1:E:788:THR:O	1:E:792:PRO:CD	1.69	1.37
3:F:1001:GLU:HG2	3:J:1092:ILE:CD1	0.88	1.35
3:J:974:MET:HE3	3:J:975:TYR:CE1	1.62	1.35
3:N:974:MET:HE3	3:N:975:TYR:CE1	1.62	1.35
3:B:974:MET:HE3	3:B:975:TYR:CE1	1.62	1.33
3:F:1001:GLU:CG	3:J:1092:ILE:HD11	0.86	1.33
1:E:93:ILE:HG22	3:F:67:THR:CG2	1.57	1.32
1:M:28:PRO:HG2	3:N:547:LEU:CD2	1.58	1.32
3:F:974:MET:HE3	3:F:975:TYR:CE1	1.62	1.32
3:J:361:ILE:HD11	3:J:421:LYS:CE	1.60	1.31
1:I:788:THR:O	1:I:792:PRO:HD2	1.23	1.31
1:E:63:LYS:C	3:B:567:ARG:HH22	1.37	1.31
1:E:788:THR:O	1:E:792:PRO:HD2	1.23	1.31
1:A:28:PRO:CG	3:B:547:LEU:CD2	2.07	1.30
1:M:28:PRO:CG	3:N:547:LEU:CD2	2.07	1.29
3:B:361:ILE:HD11	3:B:421:LYS:CE	1.60	1.29
3:F:361:ILE:HD11	3:F:421:LYS:CE	1.60	1.29
3:B:223:ARG:HD3	3:B:228:ASN:OD1	1.30	1.29
4:F:1101:FAR:H143	3:J:1009:VAL:CA	1.60	1.29
3:N:361:ILE:HD11	3:N:421:LYS:CE	1.60	1.28
3:N:223:ARG:HD3	3:N:228:ASN:OD1	1.30	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1101:FAR:C15	3:N:1013:ASN:HD21	1.46	1.27
1:M:788:THR:O	1:M:792:PRO:HD2	1.23	1.26
3:B:1013:ASN:HD21	4:N:1101:FAR:C15	1.47	1.26
1:I:93:ILE:HG22	3:J:67:THR:CG2	1.65	1.26
3:B:579:ILE:CD1	3:B:601:ALA:HB2	1.65	1.26
3:F:579:ILE:CD1	3:F:601:ALA:HB2	1.65	1.25
3:J:579:ILE:CD1	3:J:601:ALA:HB2	1.65	1.25
3:B:1093:SER:O	3:N:924:TRP:CH2	1.89	1.25
3:B:1092:ILE:HD11	3:N:1001:GLU:CD	1.60	1.25
3:F:223:ARG:HD3	3:F:228:ASN:OD1	1.30	1.25
1:A:557:THR:HG23	3:F:511:ASN:OD1	1.34	1.25
3:F:1001:GLU:HG2	3:J:1092:ILE:CG1	1.67	1.25
3:F:1013:ASN:ND2	4:F:1103:FAR:H151	0.95	1.25
3:N:579:ILE:CD1	3:N:601:ALA:HB2	1.65	1.25
3:J:223:ARG:HD3	3:J:228:ASN:OD1	1.30	1.25
1:I:28:PRO:CB	3:J:547:LEU:HD21	1.66	1.24
1:A:28:PRO:CB	3:B:547:LEU:HD21	1.68	1.23
1:E:66:ASP:CB	3:B:667:GLN:NE2	2.00	1.23
1:I:557:THR:HG23	3:N:511:ASN:OD1	1.38	1.23
1:A:28:PRO:HG2	3:B:547:LEU:CD2	1.62	1.23
1:A:788:THR:O	1:A:792:PRO:HD2	1.23	1.23
3:B:974:MET:CE	3:B:975:TYR:CE2	2.23	1.22
3:J:974:MET:CE	3:J:975:TYR:CE2	2.23	1.22
1:M:557:THR:HG23	3:J:511:ASN:OD1	1.38	1.22
3:N:974:MET:CE	3:N:975:TYR:CE2	2.23	1.22
1:M:28:PRO:CB	3:N:547:LEU:HD21	1.70	1.22
3:B:74:LYS:HD3	3:B:439:LYS:NZ	1.53	1.22
3:B:1013:ASN:ND2	4:N:1101:FAR:H151	1.51	1.22
3:F:744:LEU:CD2	3:F:765:HIS:CD2	2.23	1.21
3:J:74:LYS:HD3	3:J:439:LYS:NZ	1.53	1.21
1:M:768:LEU:HD23	1:M:802:ARG:NH2	1.55	1.21
3:B:744:LEU:CD2	3:B:765:HIS:CD2	2.23	1.21
3:J:744:LEU:CD2	3:J:765:HIS:CD2	2.23	1.21
3:F:1009:VAL:CA	4:F:1103:FAR:H143	1.70	1.21
1:E:768:LEU:HD23	1:E:802:ARG:NH2	1.54	1.21
1:A:768:LEU:HD23	1:A:802:ARG:NH2	1.55	1.20
3:F:974:MET:CE	3:F:975:TYR:CE2	2.23	1.20
3:N:744:LEU:CD2	3:N:765:HIS:CD2	2.23	1.20
3:F:74:LYS:HD3	3:F:439:LYS:NZ	1.53	1.20
3:F:1001:GLU:CB	3:J:1092:ILE:HD11	1.70	1.20
3:N:74:LYS:HD3	3:N:439:LYS:NZ	1.53	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:768:LEU:HD23	1:I:802:ARG:NH2	1.55	1.19
1:A:1211:VAL:CG2	4:A:1301:FAR:C10	2.20	1.19
1:M:1211:VAL:CG2	4:M:1301:FAR:C10	2.20	1.19
2:K:332:ILE:CD1	2:K:340:LEU:CD1	2.21	1.18
2:C:332:ILE:CD1	2:C:340:LEU:CD1	2.21	1.18
1:I:1211:VAL:CG2	4:I:1301:FAR:C10	2.20	1.18
1:E:1211:VAL:CG2	4:E:1301:FAR:C10	2.20	1.18
2:O:332:ILE:CD1	2:O:340:LEU:CD1	2.21	1.17
1:E:120:THR:CG2	3:F:131:ARG:CZ	2.21	1.17
3:F:974:MET:HE1	3:F:975:TYR:OH	1.45	1.16
1:A:768:LEU:CD2	1:A:802:ARG:HH21	1.58	1.16
3:B:974:MET:HE1	3:B:975:TYR:OH	1.45	1.16
2:G:332:ILE:CD1	2:G:340:LEU:CD1	2.21	1.16
3:B:261:SER:HB2	3:B:669:ASP:OD2	1.44	1.16
3:B:1090:CYS:SG	4:B:1101:FAR:C1	1.07	1.16
3:J:261:SER:HB2	3:J:669:ASP:OD2	1.44	1.16
3:B:1092:ILE:CD1	3:N:1001:GLU:CG	1.83	1.15
3:F:261:SER:HB2	3:F:669:ASP:OD2	1.44	1.15
1:E:768:LEU:CD2	1:E:802:ARG:HH21	1.58	1.15
1:I:768:LEU:CD2	1:I:802:ARG:HH21	1.59	1.15
3:F:924:TRP:CH2	3:J:1093:SER:O	2.00	1.15
1:M:93:ILE:HG22	3:N:67:THR:CG2	1.75	1.14
3:J:974:MET:HE1	3:J:975:TYR:OH	1.45	1.14
3:N:974:MET:HE1	3:N:975:TYR:OH	1.45	1.14
1:E:28:PRO:CB	3:F:547:LEU:HD21	1.77	1.14
2:C:332:ILE:HB	2:C:340:LEU:HD11	1.18	1.14
1:M:768:LEU:CD2	1:M:802:ARG:HH21	1.59	1.14
3:N:261:SER:HB2	3:N:669:ASP:OD2	1.44	1.14
1:E:28:PRO:HB2	3:F:130:MET:CE	1.77	1.13
1:E:62:ARG:NH1	3:F:258:GLN:OE1	1.78	1.13
2:O:332:ILE:CD1	2:O:340:LEU:HD13	1.78	1.13
1:I:120:THR:HG22	3:J:131:ARG:CZ	1.77	1.13
2:G:332:ILE:HB	2:G:340:LEU:HD11	1.18	1.12
3:B:579:ILE:HD11	3:B:601:ALA:HB2	1.23	1.12
3:F:361:ILE:CD1	3:F:421:LYS:HE3	1.78	1.12
2:G:332:ILE:CD1	2:G:340:LEU:HD13	1.79	1.12
2:K:332:ILE:CD1	2:K:340:LEU:HD13	1.78	1.12
1:A:93:ILE:HG22	3:B:67:THR:HG22	1.20	1.12
3:B:1009:VAL:HA	4:N:1101:FAR:C14	1.78	1.12
3:B:1090:CYS:SG	4:B:1101:FAR:H13	0.88	1.12
3:J:143:PRO:HB2	3:J:215:VAL:HG21	1.31	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:120:THR:HG22	3:F:131:ARG:NE	1.62	1.12
4:F:1101:FAR:H151	3:J:1013:ASN:CG	1.74	1.12
2:O:332:ILE:HB	2:O:340:LEU:HD11	1.19	1.11
1:I:66:ASP:CB	3:N:667:GLN:HE22	1.61	1.11
3:N:361:ILE:CD1	3:N:421:LYS:HE3	1.79	1.11
3:B:361:ILE:CD1	3:B:421:LYS:HE3	1.78	1.11
3:F:1090:CYS:SG	4:F:1101:FAR:C1	1.01	1.11
4:F:1103:FAR:C1	3:J:1090:CYS:SG	1.01	1.11
3:J:361:ILE:CD1	3:J:421:LYS:HE3	1.79	1.11
3:N:1090:CYS:SG	4:N:1101:FAR:C1	1.01	1.11
1:A:62:ARG:NH1	3:B:258:GLN:OE1	1.82	1.10
1:I:28:PRO:HG2	3:J:547:LEU:HD23	1.23	1.10
1:M:93:ILE:HG22	3:N:67:THR:HG22	1.11	1.10
3:F:965:GLN:HG3	3:F:969:LEU:HD11	1.24	1.10
3:F:143:PRO:HB2	3:F:215:VAL:HG21	1.32	1.10
1:A:768:LEU:CD2	1:A:802:ARG:NH2	2.15	1.10
3:B:965:GLN:HG3	3:B:969:LEU:HD11	1.24	1.10
1:A:28:PRO:HG2	3:B:547:LEU:HD23	1.33	1.09
2:C:332:ILE:CD1	2:C:340:LEU:HD13	1.78	1.09
1:M:768:LEU:CD2	1:M:802:ARG:NH2	2.15	1.09
2:G:332:ILE:HD13	2:G:340:LEU:HD12	1.34	1.09
1:M:66:ASP:CB	3:J:667:GLN:HE22	1.65	1.09
3:B:1009:VAL:HA	4:N:1101:FAR:H143	1.14	1.09
3:F:974:MET:HE2	3:F:975:TYR:CE2	1.88	1.09
1:E:28:PRO:HG2	3:F:547:LEU:HD23	1.34	1.09
1:E:491:ARG:HG2	3:F:62:LEU:HD11	1.32	1.09
4:F:1103:FAR:H13	3:J:1090:CYS:SG	0.83	1.09
3:N:579:ILE:HD11	3:N:601:ALA:HB2	1.23	1.09
3:N:965:GLN:HG3	3:N:969:LEU:HD11	1.24	1.09
1:I:93:ILE:CG2	3:J:67:THR:HG22	1.81	1.09
3:N:526:ILE:HD13	3:N:660:ILE:HD12	1.16	1.09
1:E:93:ILE:HG22	3:F:67:THR:HG22	1.12	1.08
3:J:579:ILE:HD11	3:J:601:ALA:HB2	1.23	1.08
3:N:143:PRO:HB2	3:N:215:VAL:HG21	1.32	1.08
3:F:579:ILE:HD11	3:F:601:ALA:HB2	1.23	1.08
3:F:526:ILE:HD13	3:F:660:ILE:CD1	1.83	1.08
3:F:526:ILE:HD13	3:F:660:ILE:HD12	1.16	1.08
3:J:526:ILE:HD13	3:J:660:ILE:HD12	1.16	1.08
3:J:974:MET:CE	3:J:975:TYR:OH	1.99	1.08
1:M:28:PRO:HG2	3:N:547:LEU:HD23	1.31	1.08
1:I:768:LEU:CD2	1:I:802:ARG:NH2	2.15	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:974:MET:CE	3:F:975:TYR:OH	2.00	1.08
1:A:788:THR:O	1:A:792:PRO:CG	2.01	1.08
1:E:28:PRO:HB2	3:F:130:MET:HE1	1.20	1.07
1:I:62:ARG:NH1	3:J:258:GLN:OE1	1.86	1.07
1:I:788:THR:O	1:I:792:PRO:CG	2.01	1.07
3:B:526:ILE:HD13	3:B:660:ILE:CD1	1.83	1.07
3:B:1092:ILE:HD12	3:N:1001:GLU:HG2	1.11	1.07
1:A:1137:LEU:HD13	4:A:1301:FAR:H61	1.29	1.07
1:E:768:LEU:CD2	1:E:802:ARG:NH2	2.15	1.07
1:M:788:THR:O	1:M:792:PRO:CG	2.01	1.07
3:B:526:ILE:HD13	3:B:660:ILE:HD12	1.16	1.07
1:A:93:ILE:HG22	3:B:67:THR:CG2	1.84	1.07
1:E:120:THR:HG21	3:F:131:ARG:NH2	1.68	1.07
1:E:1137:LEU:HD13	4:E:1301:FAR:H61	1.29	1.07
1:M:1120:GLN:HE21	1:M:1181:ALA:CB	1.68	1.07
3:F:1001:GLU:HA	3:J:1092:ILE:HD12	1.18	1.07
1:A:1120:GLN:HE21	1:A:1181:ALA:CB	1.68	1.07
1:I:1137:LEU:HD13	4:I:1301:FAR:H61	1.29	1.07
3:J:526:ILE:HD13	3:J:660:ILE:CD1	1.83	1.07
3:N:526:ILE:HD13	3:N:660:ILE:CD1	1.84	1.06
2:K:332:ILE:HB	2:K:340:LEU:HD11	1.18	1.06
3:N:965:GLN:CG	3:N:969:LEU:HD12	1.69	1.06
1:M:1137:LEU:HD13	4:M:1301:FAR:H61	1.29	1.06
4:B:1101:FAR:C14	3:N:1009:VAL:HA	1.85	1.06
1:E:491:ARG:HG3	3:F:62:LEU:CD1	1.85	1.06
1:E:788:THR:O	1:E:792:PRO:CG	2.01	1.06
3:B:143:PRO:HB2	3:B:215:VAL:HG21	1.32	1.06
3:N:1015:GLU:OE1	4:N:1101:FAR:H62	1.56	1.06
1:A:435:LYS:HD3	1:A:555:ARG:HD2	1.38	1.05
1:A:1211:VAL:HG21	4:A:1301:FAR:C10	1.85	1.05
3:J:965:GLN:HG3	3:J:969:LEU:HD11	1.24	1.05
1:M:120:THR:HG22	3:N:131:ARG:CZ	1.86	1.05
4:F:1103:FAR:C2	3:J:1090:CYS:SG	2.44	1.05
3:N:1090:CYS:SG	4:N:1101:FAR:C2	2.44	1.05
1:A:1120:GLN:NE2	1:A:1181:ALA:HB3	1.72	1.05
1:E:120:THR:CG2	3:F:131:ARG:NH2	2.19	1.05
1:E:1120:GLN:HE21	1:E:1181:ALA:CB	1.68	1.05
1:M:1120:GLN:NE2	1:M:1181:ALA:HB3	1.72	1.05
1:I:1120:GLN:HE21	1:I:1181:ALA:CB	1.68	1.05
1:E:63:LYS:C	3:B:567:ARG:NH2	2.14	1.05
3:B:974:MET:HE2	3:B:975:TYR:CE2	1.88	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:974:MET:HE2	3:N:975:TYR:CE2	1.88	1.05
1:A:66:ASP:CB	3:F:667:GLN:HE22	1.69	1.05
3:B:1015:GLU:OE1	3:N:1012:ARG:NH1	1.90	1.05
3:J:853:LEU:CD1	3:J:880:ILE:HG13	1.87	1.05
3:F:1001:GLU:CB	3:J:1092:ILE:CD1	2.32	1.04
1:I:1120:GLN:NE2	1:I:1181:ALA:HB3	1.72	1.04
3:B:853:LEU:CD1	3:B:880:ILE:HG13	1.87	1.04
1:A:68:ASP:OD1	3:B:259:GLY:O	1.75	1.04
3:F:853:LEU:CD1	3:F:880:ILE:HG13	1.87	1.04
3:N:853:LEU:CD1	3:N:880:ILE:HG13	1.87	1.04
1:E:435:LYS:HD3	1:E:555:ARG:HD2	1.38	1.04
1:E:1120:GLN:NE2	1:E:1181:ALA:HB3	1.72	1.04
1:M:435:LYS:HD3	1:M:555:ARG:HD2	1.38	1.04
1:E:1120:GLN:NE2	1:E:1181:ALA:CB	2.21	1.04
3:J:223:ARG:HD3	3:J:228:ASN:CG	1.83	1.04
3:J:974:MET:HE2	3:J:975:TYR:CE2	1.88	1.04
1:A:1120:GLN:OE1	1:A:1182:SER:HB3	1.58	1.03
1:M:93:ILE:CG2	3:N:67:THR:HG22	1.88	1.03
1:M:1120:GLN:OE1	1:M:1182:SER:HB3	1.58	1.03
1:I:435:LYS:HD3	1:I:555:ARG:HD2	1.38	1.03
1:A:28:PRO:HB2	3:B:547:LEU:HD21	1.40	1.03
1:I:1120:GLN:NE2	1:I:1181:ALA:CB	2.21	1.03
2:K:332:ILE:HD13	2:K:340:LEU:HD12	1.34	1.03
3:B:223:ARG:HD3	3:B:228:ASN:CG	1.83	1.03
2:C:332:ILE:HD13	2:C:340:LEU:HD12	1.34	1.03
3:N:74:LYS:HD3	3:N:439:LYS:HZ1	1.08	1.03
1:A:1120:GLN:NE2	1:A:1181:ALA:CB	2.21	1.03
3:F:223:ARG:HD3	3:F:228:ASN:CG	1.84	1.03
1:E:75:TYR:OH	3:F:191:GLN:CG	2.07	1.03
1:M:1120:GLN:NE2	1:M:1181:ALA:CB	2.21	1.03
3:N:1090:CYS:SG	4:N:1101:FAR:H13	0.83	1.03
1:E:66:ASP:HB3	3:B:667:GLN:HE22	0.87	1.02
1:E:491:ARG:CG	3:F:62:LEU:HD11	1.89	1.02
1:E:491:ARG:CG	3:F:62:LEU:CD1	2.36	1.02
2:O:332:ILE:HD13	2:O:340:LEU:HD12	1.34	1.02
4:B:1101:FAR:H143	3:N:1009:VAL:HA	1.37	1.02
3:J:625:ASN:O	3:J:634:ILE:HD12	1.60	1.02
3:B:965:GLN:CG	3:B:969:LEU:HD12	1.69	1.02
3:J:143:PRO:HB2	3:J:215:VAL:CG2	1.89	1.02
3:J:173:ASN:OD1	3:J:174:ALA:N	1.92	1.02
3:N:173:ASN:OD1	3:N:174:ALA:N	1.92	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1093:SER:O	3:N:924:TRP:CZ2	2.12	1.02
1:I:113:HIS:NE2	1:I:127:ASP:OD1	1.92	1.02
3:F:143:PRO:HB2	3:F:215:VAL:CG2	1.89	1.02
3:N:143:PRO:HB2	3:N:215:VAL:CG2	1.89	1.02
3:N:974:MET:CE	3:N:975:TYR:OH	2.00	1.02
1:A:113:HIS:NE2	1:A:127:ASP:OD1	1.92	1.02
2:C:332:ILE:HB	2:C:340:LEU:CD1	1.89	1.02
1:E:1120:GLN:OE1	1:E:1182:SER:HB3	1.58	1.02
2:G:332:ILE:HB	2:G:340:LEU:CD1	1.89	1.02
1:M:783:LEU:O	1:M:787:TYR:HD2	1.43	1.02
1:I:1211:VAL:HG21	4:I:1301:FAR:C10	1.85	1.02
3:B:974:MET:CE	3:B:975:TYR:OH	2.00	1.02
1:M:28:PRO:HB2	3:N:547:LEU:HD21	1.42	1.01
2:K:332:ILE:HB	2:K:340:LEU:CD1	1.89	1.01
3:B:625:ASN:O	3:B:634:ILE:HD12	1.60	1.01
3:N:223:ARG:HD3	3:N:228:ASN:CG	1.84	1.01
1:M:113:HIS:NE2	1:M:127:ASP:OD1	1.92	1.01
1:I:783:LEU:O	1:I:787:TYR:HD2	1.42	1.01
3:B:173:ASN:OD1	3:B:174:ALA:N	1.92	1.01
1:E:28:PRO:HG3	3:F:547:LEU:CD2	1.84	1.01
1:I:63:LYS:C	3:N:567:ARG:HH22	1.67	1.01
1:I:66:ASP:HB3	3:N:667:GLN:HE22	1.21	1.01
3:B:143:PRO:HB2	3:B:215:VAL:CG2	1.89	1.01
3:F:173:ASN:OD1	3:F:174:ALA:N	1.92	1.01
3:F:625:ASN:O	3:F:634:ILE:HD12	1.60	1.01
3:N:1015:GLU:OE2	4:N:1101:FAR:H41	1.60	1.01
1:A:1211:VAL:HG23	4:A:1301:FAR:H101	1.43	1.01
3:F:1013:ASN:CG	4:F:1103:FAR:H151	1.86	1.01
1:E:783:LEU:O	1:E:787:TYR:HD2	1.42	1.01
3:F:1015:GLU:OE2	4:F:1101:FAR:C4	2.09	1.01
3:N:625:ASN:O	3:N:634:ILE:HD12	1.59	1.01
2:O:332:ILE:HB	2:O:340:LEU:CD1	1.89	1.00
1:M:1211:VAL:HG21	4:M:1301:FAR:C10	1.85	1.00
1:M:1211:VAL:HG23	4:M:1301:FAR:H101	1.43	1.00
3:B:744:LEU:HD21	3:B:765:HIS:HB3	1.40	1.00
3:F:1090:CYS:SG	4:F:1101:FAR:C2	2.49	1.00
1:A:783:LEU:O	1:A:787:TYR:HD2	1.42	1.00
3:F:744:LEU:HD21	3:F:765:HIS:HB3	1.40	1.00
3:F:1009:VAL:HA	4:F:1103:FAR:H141	1.40	1.00
1:I:1120:GLN:OE1	1:I:1182:SER:HB3	1.58	1.00
1:E:113:HIS:NE2	1:E:127:ASP:OD1	1.92	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1015:GLU:OE1	4:F:1101:FAR:H62	1.60	1.00
3:F:1001:GLU:CD	3:J:1092:ILE:HD11	1.87	0.99
3:B:485:ASN:ND2	3:F:105:ASP:OD1	1.95	0.99
3:F:1015:GLU:OE2	4:F:1101:FAR:H41	1.59	0.99
3:N:744:LEU:HD21	3:N:765:HIS:HB3	1.40	0.99
3:N:744:LEU:CD2	3:N:765:HIS:CG	2.46	0.99
3:F:1082:VAL:HG21	3:J:1060:LEU:HD23	1.45	0.99
1:A:783:LEU:O	1:A:787:TYR:CD2	2.16	0.99
1:I:93:ILE:HG22	3:J:67:THR:HG22	1.01	0.99
3:F:283:LEU:HD21	3:F:307:LEU:HG	1.44	0.99
1:E:491:ARG:HG3	3:F:62:LEU:HD12	1.41	0.98
3:B:744:LEU:CD2	3:B:765:HIS:CG	2.46	0.98
3:F:74:LYS:HD3	3:F:439:LYS:HZ3	1.28	0.98
3:J:485:ASN:ND2	3:N:105:ASP:OD1	1.96	0.98
1:M:783:LEU:O	1:M:787:TYR:CD2	2.16	0.98
3:N:1015:GLU:OE2	4:N:1101:FAR:C4	2.10	0.98
1:A:66:ASP:HB3	3:F:667:GLN:HE22	1.29	0.98
1:E:872:PRO:HD2	1:E:875:ALA:HB3	1.45	0.98
1:I:1211:VAL:HG23	4:I:1301:FAR:H101	1.43	0.98
1:E:783:LEU:O	1:E:787:TYR:CD2	2.16	0.98
3:J:744:LEU:CD2	3:J:765:HIS:CG	2.46	0.98
4:F:1101:FAR:C15	3:J:1013:ASN:ND2	1.82	0.98
3:F:1001:GLU:HG2	3:J:1092:ILE:HD12	1.46	0.98
1:E:66:ASP:HB2	3:B:667:GLN:NE2	1.78	0.98
1:E:93:ILE:HG22	3:F:67:THR:HG23	1.46	0.98
1:I:783:LEU:O	1:I:787:TYR:CD2	2.16	0.98
3:F:965:GLN:CG	3:F:969:LEU:HD12	1.69	0.98
3:J:744:LEU:HD21	3:J:765:HIS:HB3	1.40	0.98
2:O:332:ILE:HD13	2:O:340:LEU:HD13	0.98	0.98
3:F:1013:ASN:HD21	4:F:1103:FAR:H152	1.29	0.98
2:C:332:ILE:HD13	2:C:340:LEU:HD13	0.98	0.98
1:A:93:ILE:CG2	3:B:67:THR:HG22	1.94	0.97
2:G:332:ILE:HD13	2:G:340:LEU:HD13	0.98	0.97
3:B:1090:CYS:SG	4:B:1101:FAR:C2	2.50	0.97
1:A:872:PRO:HD2	1:A:875:ALA:HB3	1.45	0.97
2:C:332:ILE:CB	2:C:340:LEU:HD11	1.95	0.97
1:E:1211:VAL:HG23	4:E:1301:FAR:C10	1.93	0.97
3:B:744:LEU:HD22	3:B:765:HIS:HD2	1.29	0.97
3:F:1004:MET:CB	3:J:1092:ILE:HG21	1.94	0.97
3:N:744:LEU:HD22	3:N:765:HIS:HD2	1.29	0.97
3:B:74:LYS:HD3	3:B:439:LYS:HZ1	1.23	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:625:ASN:O	3:N:634:ILE:CD1	2.12	0.97
3:F:1001:GLU:CA	3:J:1092:ILE:HD12	1.94	0.97
2:O:332:ILE:CB	2:O:340:LEU:HD11	1.95	0.97
3:F:1090:CYS:SG	4:F:1101:FAR:H13	0.96	0.97
1:M:1211:VAL:HG23	4:M:1301:FAR:C10	1.93	0.97
3:B:625:ASN:O	3:B:634:ILE:CD1	2.12	0.97
3:B:1012:ARG:NH1	4:N:1101:FAR:H7	1.78	0.97
3:F:744:LEU:CD2	3:F:765:HIS:CG	2.46	0.97
1:E:79:GLN:NE2	3:F:194:TYR:CE1	2.32	0.97
2:K:332:ILE:HD13	2:K:340:LEU:HD13	0.98	0.97
1:I:872:PRO:HD2	1:I:875:ALA:HB3	1.45	0.96
3:F:625:ASN:O	3:F:634:ILE:CD1	2.12	0.96
3:F:1009:VAL:CA	4:F:1103:FAR:C14	2.34	0.96
1:E:1211:VAL:HG23	4:E:1301:FAR:H101	1.43	0.96
1:M:441:GLN:NE2	1:M:607:PHE:HB3	1.80	0.96
3:B:413:PRO:HG2	3:B:416:PHE:HD2	1.27	0.96
1:E:83:LYS:HE3	3:F:198:GLU:OE1	1.65	0.96
1:I:441:GLN:NE2	1:I:607:PHE:HB3	1.80	0.96
2:K:332:ILE:CB	2:K:340:LEU:HD11	1.94	0.96
1:A:441:GLN:NE2	1:A:607:PHE:HB3	1.80	0.96
1:M:771:LYS:HG3	1:M:802:ARG:NH1	1.81	0.96
1:E:419:ALA:HB1	3:B:524:GLU:OE1	1.64	0.96
1:E:1211:VAL:HG21	4:E:1301:FAR:C10	1.85	0.96
1:A:771:LYS:HG3	1:A:802:ARG:NH1	1.81	0.96
1:E:441:GLN:NE2	1:E:607:PHE:HB3	1.80	0.96
1:I:28:PRO:HB2	3:J:547:LEU:HD21	1.45	0.96
3:N:413:PRO:HG2	3:N:416:PHE:HD2	1.27	0.96
1:I:771:LYS:HG3	1:I:802:ARG:NH1	1.81	0.96
1:E:83:LYS:HD2	3:F:198:GLU:OE1	1.65	0.96
2:G:332:ILE:CB	2:G:340:LEU:HD11	1.94	0.96
3:F:413:PRO:HG2	3:F:416:PHE:HD2	1.27	0.96
3:J:625:ASN:O	3:J:634:ILE:CD1	2.12	0.96
3:B:1013:ASN:HD21	4:N:1101:FAR:H151	1.04	0.96
1:A:120:THR:HG22	3:B:131:ARG:CZ	1.94	0.95
1:A:63:LYS:C	3:F:567:ARG:HH22	1.72	0.95
1:M:62:ARG:NH1	3:N:258:GLN:OE1	1.98	0.95
3:J:965:GLN:CG	3:J:969:LEU:HD12	1.69	0.95
3:N:261:SER:CB	3:N:669:ASP:OD2	2.15	0.95
1:E:93:ILE:CG2	3:F:67:THR:HG22	1.96	0.95
1:I:28:PRO:HG3	3:J:547:LEU:CD2	1.95	0.95
3:J:261:SER:CB	3:J:669:ASP:OD2	2.15	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:771:LYS:HG3	1:E:802:ARG:NH1	1.81	0.95
4:B:1101:FAR:C15	3:N:1013:ASN:ND2	2.28	0.95
3:J:413:PRO:HG2	3:J:416:PHE:HD2	1.27	0.95
3:N:974:MET:HE1	3:N:975:TYR:CZ	1.96	0.95
3:B:1092:ILE:CG1	3:N:1001:GLU:HG2	1.96	0.95
3:J:105:ASP:OD1	3:N:485:ASN:ND2	1.99	0.94
3:F:261:SER:CB	3:F:669:ASP:OD2	2.15	0.94
1:A:1211:VAL:HG23	4:A:1301:FAR:C10	1.93	0.94
3:B:261:SER:CB	3:B:669:ASP:OD2	2.15	0.94
3:J:974:MET:HE3	3:J:975:TYR:CE2	1.97	0.94
1:A:75:TYR:OH	3:B:191:GLN:HB3	1.68	0.94
3:B:579:ILE:CD1	3:B:601:ALA:CB	2.46	0.94
1:E:1211:VAL:HG21	4:E:1301:FAR:H101	0.95	0.93
1:M:872:PRO:HD2	1:M:875:ALA:HB3	1.45	0.93
3:F:283:LEU:HD23	3:F:307:LEU:HD21	1.50	0.93
3:J:579:ILE:CD1	3:J:601:ALA:CB	2.46	0.93
3:B:103:ARG:NH2	3:F:477:ARG:CZ	2.31	0.93
1:M:66:ASP:HB3	3:J:667:GLN:HE22	1.32	0.93
3:F:579:ILE:CD1	3:F:601:ALA:CB	2.46	0.93
3:J:223:ARG:CD	3:J:228:ASN:OD1	2.17	0.93
3:J:744:LEU:HD22	3:J:765:HIS:HD2	1.29	0.93
1:M:1211:VAL:HG21	4:M:1301:FAR:H101	0.95	0.93
3:B:1015:GLU:CD	3:N:1012:ARG:HH12	1.76	0.93
3:N:223:ARG:CD	3:N:228:ASN:OD1	2.17	0.93
3:F:1001:GLU:HA	3:J:1092:ILE:CD1	1.99	0.92
3:N:579:ILE:CD1	3:N:601:ALA:CB	2.46	0.92
3:F:974:MET:HE1	3:F:975:TYR:HH	1.25	0.92
3:B:1093:SER:O	3:N:1059:PRO:HG3	1.69	0.92
3:F:223:ARG:CD	3:F:228:ASN:OD1	2.17	0.92
1:A:68:ASP:CG	3:B:259:GLY:O	2.13	0.92
3:F:744:LEU:HD22	3:F:765:HIS:HD2	1.29	0.92
1:A:1211:VAL:HG21	4:A:1301:FAR:H101	0.95	0.92
1:I:1211:VAL:HG21	4:I:1301:FAR:H101	0.95	0.92
3:B:1009:VAL:CA	4:N:1101:FAR:H143	1.99	0.92
1:E:28:PRO:HG3	3:F:547:LEU:HD21	1.46	0.91
1:I:66:ASP:CB	3:N:667:GLN:NE2	2.33	0.91
3:B:803:PHE:CD2	3:B:810:VAL:HG22	2.05	0.91
1:E:93:ILE:CG2	3:F:67:THR:CG2	2.47	0.91
3:F:744:LEU:HD21	3:F:765:HIS:CB	2.00	0.91
1:E:66:ASP:HB3	3:B:667:GLN:NE2	1.73	0.91
3:F:803:PHE:CD2	3:F:810:VAL:HG22	2.05	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:744:LEU:HD21	3:B:765:HIS:CB	2.00	0.91
3:J:74:LYS:HD3	3:J:439:LYS:HZ1	1.13	0.91
3:J:803:PHE:CD2	3:J:810:VAL:HG22	2.05	0.91
3:N:744:LEU:HD21	3:N:765:HIS:CB	2.00	0.91
1:I:93:ILE:CG2	3:J:67:THR:CG2	2.45	0.91
3:B:223:ARG:CD	3:B:228:ASN:OD1	2.17	0.91
3:B:942:TYR:OH	3:B:984:GLU:OE2	1.88	0.91
3:F:75:THR:HG21	3:F:440:LEU:HB2	1.52	0.91
1:I:1211:VAL:HG23	4:I:1301:FAR:C10	1.92	0.91
3:F:361:ILE:CD1	3:F:421:LYS:CE	2.44	0.91
3:F:74:LYS:HD3	3:F:439:LYS:HZ1	1.29	0.91
3:N:361:ILE:CD1	3:N:421:LYS:CE	2.44	0.91
3:B:795:SER:OG	3:B:855:ILE:CD1	2.19	0.90
3:F:1004:MET:HG3	3:J:1092:ILE:CG2	2.02	0.90
3:N:942:TYR:OH	3:N:984:GLU:OE2	1.88	0.90
3:F:942:TYR:OH	3:F:984:GLU:OE2	1.88	0.90
3:J:75:THR:HG21	3:J:440:LEU:HB2	1.52	0.90
3:N:803:PHE:CD2	3:N:810:VAL:HG22	2.05	0.90
3:J:103:ARG:NH2	3:N:477:ARG:CZ	2.34	0.90
3:F:795:SER:OG	3:F:855:ILE:CD1	2.19	0.90
3:B:477:ARG:CZ	3:F:103:ARG:NH2	2.35	0.90
3:J:744:LEU:HD21	3:J:765:HIS:CB	2.00	0.90
3:J:942:TYR:OH	3:J:984:GLU:OE2	1.88	0.90
1:A:445:LEU:HD12	1:A:563:THR:HG23	1.54	0.89
3:N:795:SER:OG	3:N:855:ILE:CD1	2.19	0.89
1:A:28:PRO:HG3	3:B:547:LEU:CD2	1.98	0.89
1:I:68:ASP:OD1	3:J:259:GLY:O	1.90	0.89
3:F:1004:MET:HB2	3:J:1092:ILE:HG21	1.52	0.89
1:A:29:VAL:HG11	3:B:131:ARG:CG	2.02	0.89
1:M:63:LYS:C	3:J:567:ARG:HH22	1.80	0.89
3:B:361:ILE:CD1	3:B:421:LYS:CE	2.44	0.89
3:N:1090:CYS:HG	4:N:1101:FAR:C1	0.72	0.89
1:I:1137:LEU:CD1	4:I:1301:FAR:H61	2.03	0.89
3:N:822:ILE:HG23	3:N:826:LEU:HD12	1.55	0.89
1:I:445:LEU:HD12	1:I:563:THR:HG23	1.54	0.89
1:M:1137:LEU:CD1	4:M:1301:FAR:H61	2.02	0.89
3:B:75:THR:HG21	3:B:440:LEU:HB2	1.52	0.89
1:A:1137:LEU:CD1	4:A:1301:FAR:H61	2.03	0.89
1:I:28:PRO:HB2	3:J:130:MET:CE	2.04	0.88
3:J:795:SER:OG	3:J:855:ILE:CD1	2.19	0.88
3:B:1008:ILE:CG2	3:B:1012:ARG:NE	2.36	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:587:MET:HE1	3:J:855:ILE:HG13	1.55	0.88
1:M:445:LEU:HD12	1:M:563:THR:HG23	1.54	0.88
1:I:79:GLN:NE2	3:J:194:TYR:CE1	2.41	0.88
3:N:75:THR:HG21	3:N:440:LEU:HB2	1.52	0.88
1:M:28:PRO:HG3	3:N:547:LEU:CD2	2.01	0.88
3:J:477:ARG:CZ	3:N:103:ARG:NH2	2.36	0.88
1:A:29:VAL:HG11	3:B:131:ARG:HG3	1.55	0.88
1:E:1137:LEU:CD1	4:E:1301:FAR:H61	2.03	0.88
3:B:74:LYS:HD3	3:B:439:LYS:HZ3	1.35	0.88
3:N:587:MET:HE1	3:N:855:ILE:HG13	1.55	0.88
1:E:445:LEU:HD12	1:E:563:THR:HG23	1.54	0.88
3:B:105:ASP:OD1	3:F:485:ASN:ND2	2.07	0.88
1:A:79:GLN:NE2	3:B:194:TYR:CE1	2.42	0.88
1:E:75:TYR:OH	3:F:191:GLN:CD	2.16	0.88
3:F:587:MET:HE1	3:F:855:ILE:HG13	1.56	0.88
3:J:822:ILE:HG23	3:J:826:LEU:HD12	1.55	0.88
1:E:75:TYR:OH	3:F:191:GLN:OE1	1.90	0.88
3:B:822:ILE:HG23	3:B:826:LEU:HD12	1.55	0.88
1:E:83:LYS:CD	3:F:198:GLU:OE1	2.22	0.87
3:B:1012:ARG:HH12	4:N:1101:FAR:H7	1.35	0.87
3:F:1009:VAL:HA	4:F:1103:FAR:H143	0.88	0.87
3:J:361:ILE:CD1	3:J:421:LYS:CE	2.44	0.87
3:B:587:MET:HE1	3:B:855:ILE:HG13	1.55	0.87
3:F:1004:MET:CB	3:J:1092:ILE:CG2	2.52	0.87
3:N:361:ILE:HD11	3:N:421:LYS:HE3	0.88	0.87
1:M:68:ASP:OD1	3:N:259:GLY:O	1.93	0.87
1:I:28:PRO:HB2	3:J:130:MET:HE1	1.54	0.87
2:K:332:ILE:CD1	2:K:340:LEU:HD12	1.99	0.87
3:B:361:ILE:HD11	3:B:421:LYS:HE3	0.88	0.87
3:B:656:LEU:HG	3:B:660:ILE:HD11	1.57	0.87
3:N:335:ARG:HB3	3:N:355:ILE:HG23	1.56	0.87
3:N:656:LEU:HG	3:N:660:ILE:HD11	1.57	0.87
3:B:1090:CYS:SG	4:B:1101:FAR:H11	1.16	0.86
3:B:974:MET:HE1	3:B:975:TYR:HH	1.33	0.86
3:F:853:LEU:HD11	3:F:880:ILE:HG13	1.57	0.86
3:F:361:ILE:HD11	3:F:421:LYS:HE3	0.88	0.86
1:A:1172:ASP:HB3	1:A:1175:MET:HB2	1.55	0.86
2:C:359:VAL:HG21	2:C:367:ARG:HG2	1.58	0.86
1:E:1120:GLN:HE21	1:E:1181:ALA:HB3	1.31	0.86
1:I:75:TYR:OH	3:J:191:GLN:HB3	1.76	0.86
3:J:361:ILE:HD11	3:J:421:LYS:HE3	0.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:656:LEU:HG	3:J:660:ILE:HD11	1.57	0.86
3:B:1012:ARG:HD2	4:N:1101:FAR:H142	1.58	0.86
3:F:335:ARG:HB3	3:F:355:ILE:HG23	1.56	0.86
3:B:798:PRO:HA	5:B:1102:ADP:O2B	1.75	0.85
2:O:359:VAL:HG21	2:O:367:ARG:HG2	1.58	0.85
3:F:822:ILE:HG23	3:F:826:LEU:HD12	1.55	0.85
1:A:557:THR:CG2	3:F:511:ASN:OD1	2.22	0.85
1:E:83:LYS:CE	3:F:198:GLU:OE1	2.24	0.85
1:M:441:GLN:HE22	1:M:607:PHE:HB3	1.41	0.85
3:F:656:LEU:HG	3:F:660:ILE:HD11	1.57	0.85
1:E:94:ARG:NH1	3:F:157:THR:HA	1.92	0.85
1:M:66:ASP:CB	3:J:667:GLN:NE2	2.40	0.85
3:B:335:ARG:HB3	3:B:355:ILE:HG23	1.56	0.85
3:J:335:ARG:HB3	3:J:355:ILE:HG23	1.56	0.85
1:I:771:LYS:HG3	1:I:802:ARG:HH12	1.41	0.85
2:K:359:VAL:HG21	2:K:367:ARG:HG2	1.58	0.85
3:J:853:LEU:HD11	3:J:880:ILE:HG13	1.57	0.85
1:I:771:LYS:CG	1:I:802:ARG:NH1	2.40	0.85
1:A:441:GLN:HE22	1:A:607:PHE:HB3	1.41	0.85
3:F:1013:ASN:ND2	4:F:1103:FAR:C15	1.80	0.85
1:A:771:LYS:CG	1:A:802:ARG:NH1	2.40	0.84
1:M:771:LYS:CG	1:M:802:ARG:NH1	2.40	0.84
1:E:29:VAL:HG11	3:F:131:ARG:HG3	1.58	0.84
1:M:771:LYS:HD2	1:M:802:ARG:NH1	1.93	0.84
3:B:574:VAL:HG21	3:B:656:LEU:HD21	1.60	0.84
1:A:771:LYS:HG3	1:A:802:ARG:HH12	1.41	0.84
1:M:29:VAL:HG11	3:N:131:ARG:HG3	1.59	0.84
3:J:587:MET:HE1	3:J:855:ILE:CG1	2.08	0.84
3:F:1001:GLU:CG	3:J:1092:ILE:CD1	1.74	0.84
4:F:1103:FAR:H11	3:J:1090:CYS:SG	1.15	0.84
1:E:441:GLN:HE22	1:E:607:PHE:HB3	1.41	0.84
1:E:1172:ASP:HB3	1:E:1175:MET:HB2	1.57	0.84
2:O:332:ILE:CD1	2:O:340:LEU:HD12	1.99	0.84
1:I:771:LYS:HD2	1:I:802:ARG:NH1	1.93	0.84
1:E:788:THR:C	1:E:792:PRO:HD2	2.03	0.84
3:N:853:LEU:HD11	3:N:880:ILE:HG13	1.57	0.84
1:M:771:LYS:HG3	1:M:802:ARG:HH12	1.41	0.84
1:A:771:LYS:HD2	1:A:802:ARG:NH1	1.93	0.84
1:E:28:PRO:CB	3:F:130:MET:HE1	2.07	0.84
1:I:441:GLN:HE22	1:I:607:PHE:HB3	1.41	0.84
3:F:1013:ASN:HD21	4:F:1101:FAR:C15	1.90	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:1103:FAR:H12A	3:J:1090:CYS:SG	1.46	0.84
3:J:526:ILE:CD1	3:J:660:ILE:HD12	2.06	0.84
3:N:1090:CYS:SG	4:N:1101:FAR:H11	1.14	0.84
1:M:29:VAL:HG11	3:N:131:ARG:CG	2.08	0.84
3:F:283:LEU:CD2	3:F:307:LEU:HG	2.07	0.84
3:F:587:MET:HE1	3:F:855:ILE:CG1	2.08	0.84
3:F:1070:THR:HG21	4:F:1103:FAR:H91	1.60	0.84
1:M:93:ILE:CG2	3:N:67:THR:CG2	2.53	0.83
1:I:788:THR:C	1:I:792:PRO:HD2	2.03	0.83
1:E:771:LYS:CG	1:E:802:ARG:NH1	2.40	0.83
3:B:587:MET:HE1	3:B:855:ILE:CG1	2.08	0.83
3:B:853:LEU:HD11	3:B:880:ILE:HG13	1.57	0.83
3:F:526:ILE:CD1	3:F:660:ILE:HD12	2.06	0.83
3:N:587:MET:HE1	3:N:855:ILE:CG1	2.08	0.83
1:E:771:LYS:HD2	1:E:802:ARG:NH1	1.93	0.83
2:G:332:ILE:CD1	2:G:340:LEU:HD12	1.99	0.83
3:N:172:ILE:HG21	3:N:212:VAL:CG2	2.08	0.83
3:N:574:VAL:HG21	3:N:656:LEU:HD21	1.60	0.83
3:J:172:ILE:HG21	3:J:212:VAL:CG2	2.08	0.83
1:I:1120:GLN:HE21	1:I:1181:ALA:HB3	1.30	0.83
3:B:172:ILE:HG21	3:B:212:VAL:CG2	2.08	0.83
4:F:1101:FAR:C14	3:J:1009:VAL:CA	2.37	0.83
1:A:788:THR:C	1:A:792:PRO:HD2	2.03	0.83
1:M:788:THR:C	1:M:792:PRO:HD2	2.03	0.83
3:J:413:PRO:HG2	3:J:416:PHE:CD2	2.13	0.83
1:M:75:TYR:OH	3:N:191:GLN:HB3	1.79	0.83
3:F:172:ILE:HG21	3:F:212:VAL:CG2	2.08	0.83
3:J:965:GLN:HG2	3:J:969:LEU:HD12	0.83	0.83
3:B:965:GLN:HG2	3:B:969:LEU:HD12	0.83	0.83
3:N:413:PRO:HG2	3:N:416:PHE:CD2	2.13	0.83
3:N:526:ILE:CD1	3:N:660:ILE:HD12	2.06	0.83
1:I:29:VAL:HG11	3:J:131:ARG:HG3	1.61	0.82
1:I:79:GLN:NE2	3:J:194:TYR:CD1	2.46	0.82
1:A:79:GLN:HB3	3:B:194:TYR:HB3	1.61	0.82
1:A:419:ALA:HB1	3:F:524:GLU:OE1	1.79	0.82
1:I:83:LYS:HD2	3:J:198:GLU:OE1	1.77	0.82
3:F:574:VAL:HG21	3:F:656:LEU:HD21	1.59	0.82
1:M:1120:GLN:HE21	1:M:1181:ALA:HB1	1.44	0.82
3:F:1004:MET:CG	3:J:1092:ILE:HG21	2.09	0.82
3:F:1059:PRO:HG3	3:J:1093:SER:O	1.80	0.82
3:B:143:PRO:CB	3:B:215:VAL:HG21	2.10	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:965:GLN:HG2	3:N:969:LEU:HD12	0.83	0.82
3:B:413:PRO:HG2	3:B:416:PHE:CD2	2.13	0.82
3:B:1013:ASN:CG	4:N:1101:FAR:H151	2.05	0.82
3:J:656:LEU:HG	3:J:660:ILE:CD1	2.10	0.82
2:G:359:VAL:HG21	2:G:367:ARG:HG2	1.58	0.82
1:I:120:THR:CG2	3:J:131:ARG:NH2	2.43	0.82
3:F:413:PRO:HG2	3:F:416:PHE:CD2	2.13	0.82
3:J:574:VAL:HG21	3:J:656:LEU:HD21	1.60	0.82
1:A:1120:GLN:HE21	1:A:1181:ALA:HB1	1.43	0.82
3:F:965:GLN:HG2	3:F:969:LEU:HD12	0.83	0.82
1:A:66:ASP:CB	3:F:667:GLN:NE2	2.41	0.81
3:F:744:LEU:HD21	3:F:765:HIS:CG	2.14	0.81
1:A:29:VAL:CG1	3:B:131:ARG:HG3	2.10	0.81
2:C:332:ILE:CD1	2:C:340:LEU:HD12	1.99	0.81
3:B:656:LEU:HG	3:B:660:ILE:CD1	2.10	0.81
1:E:28:PRO:HG3	3:F:547:LEU:CG	2.11	0.81
1:E:75:TYR:OH	3:F:191:GLN:HB3	1.81	0.81
1:E:1120:GLN:HE21	1:E:1181:ALA:HB1	1.43	0.81
1:M:771:LYS:CD	1:M:802:ARG:NH1	2.44	0.81
1:M:1211:VAL:CB	4:M:1301:FAR:H101	2.10	0.81
1:I:1211:VAL:CB	4:I:1301:FAR:H101	2.10	0.81
3:N:143:PRO:CB	3:N:215:VAL:HG21	2.10	0.81
3:N:579:ILE:HD11	3:N:601:ALA:CB	2.09	0.81
1:E:804:ALA:HB1	1:E:809:LEU:HD11	1.62	0.81
1:M:804:ALA:HB1	1:M:809:LEU:HD11	1.62	0.81
3:B:712:PRO:HD3	3:B:780:LEU:HD23	1.62	0.81
3:B:744:LEU:HD21	3:B:765:HIS:CG	2.14	0.81
1:I:804:ALA:HB1	1:I:809:LEU:HD11	1.62	0.81
3:J:486:GLN:HE22	3:J:492:ASP:C	1.89	0.81
3:N:656:LEU:HG	3:N:660:ILE:CD1	2.10	0.81
1:A:290:ARG:O	1:A:352:LYS:NZ	2.14	0.81
3:B:974:MET:HE3	3:B:975:TYR:CE2	1.97	0.81
3:B:1008:ILE:HG21	3:B:1012:ARG:CZ	2.10	0.81
1:E:771:LYS:CD	1:E:802:ARG:NH1	2.44	0.81
1:I:771:LYS:CD	1:I:802:ARG:NH1	2.44	0.81
3:F:486:GLN:HE22	3:F:492:ASP:C	1.89	0.81
1:A:804:ALA:HB1	1:A:809:LEU:HD11	1.62	0.81
1:E:290:ARG:O	1:E:352:LYS:NZ	2.14	0.81
1:I:290:ARG:O	1:I:352:LYS:NZ	2.14	0.81
1:I:1120:GLN:HE21	1:I:1181:ALA:HB1	1.44	0.81
3:F:1001:GLU:CA	3:J:1092:ILE:CD1	2.56	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:1103:FAR:H12A	3:J:1090:CYS:HG	0.83	0.81
3:N:712:PRO:HD3	3:N:780:LEU:HD23	1.62	0.81
1:A:771:LYS:CD	1:A:802:ARG:NH1	2.44	0.81
1:A:1211:VAL:CB	4:A:1301:FAR:H101	2.10	0.81
3:J:803:PHE:CD2	3:J:810:VAL:CG2	2.64	0.81
3:N:486:GLN:HE22	3:N:492:ASP:C	1.89	0.81
1:E:79:GLN:NE2	3:F:194:TYR:CD1	2.46	0.80
3:F:656:LEU:HG	3:F:660:ILE:CD1	2.10	0.80
3:B:486:GLN:HE22	3:B:492:ASP:C	1.89	0.80
3:F:803:PHE:CD2	3:F:810:VAL:CG2	2.64	0.80
3:J:712:PRO:HD3	3:J:780:LEU:HD23	1.62	0.80
1:A:79:GLN:NE2	3:B:194:TYR:CD1	2.49	0.80
1:M:290:ARG:O	1:M:352:LYS:NZ	2.14	0.80
3:B:1090:CYS:HG	4:B:1101:FAR:C1	1.01	0.80
1:M:435:LYS:HD3	1:M:555:ARG:CD	2.12	0.80
3:N:803:PHE:CD2	3:N:810:VAL:CG2	2.64	0.80
4:F:1101:FAR:H141	3:J:1009:VAL:HA	1.62	0.80
3:J:143:PRO:CB	3:J:215:VAL:HG21	2.10	0.80
1:E:771:LYS:HG3	1:E:802:ARG:HH12	1.41	0.80
3:F:1015:GLU:CD	4:F:1101:FAR:H41	2.05	0.80
3:J:744:LEU:HD21	3:J:765:HIS:CG	2.14	0.80
1:M:557:THR:CG2	3:J:511:ASN:OD1	2.28	0.80
3:F:1004:MET:HG3	3:J:1092:ILE:HG21	1.62	0.80
1:A:1120:GLN:HE21	1:A:1181:ALA:HB3	1.30	0.80
1:E:1211:VAL:CB	4:E:1301:FAR:H101	2.11	0.80
1:I:435:LYS:HD3	1:I:555:ARG:CD	2.12	0.80
3:B:803:PHE:CD2	3:B:810:VAL:CG2	2.64	0.80
3:F:143:PRO:CB	3:F:215:VAL:HG21	2.10	0.79
1:A:435:LYS:HD3	1:A:555:ARG:CD	2.12	0.79
1:E:64:ASN:CA	3:B:567:ARG:NH2	2.46	0.79
1:I:29:VAL:HG11	3:J:131:ARG:CG	2.12	0.79
3:N:974:MET:HE3	3:N:975:TYR:CE2	1.97	0.79
1:A:1209:THR:HG23	2:C:334:ILE:HD13	1.65	0.79
1:M:79:GLN:NE2	3:N:194:TYR:CE1	2.50	0.79
3:B:714:VAL:HG11	3:B:743:LEU:HG	1.64	0.79
3:F:712:PRO:HD3	3:F:780:LEU:HD23	1.62	0.79
3:N:1090:CYS:HG	4:N:1101:FAR:C2	1.89	0.79
1:E:64:ASN:N	3:B:567:ARG:NH2	2.29	0.79
1:A:771:LYS:CG	1:A:802:ARG:HH12	1.96	0.79
3:F:579:ILE:HD11	3:F:601:ALA:CB	2.10	0.79
3:N:714:VAL:HG11	3:N:743:LEU:HG	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:826:LEU:HD22	3:F:830:VAL:HG11	1.65	0.79
3:N:826:LEU:HD22	3:N:830:VAL:HG11	1.65	0.79
1:E:75:TYR:OH	3:F:191:GLN:CB	2.31	0.79
3:B:826:LEU:HD22	3:B:830:VAL:HG11	1.65	0.79
3:J:74:LYS:HD3	3:J:439:LYS:HZ3	1.45	0.79
3:J:826:LEU:HD22	3:J:830:VAL:HG11	1.65	0.78
1:M:79:GLN:HB3	3:N:194:TYR:HB3	1.66	0.78
1:E:435:LYS:HD3	1:E:555:ARG:CD	2.12	0.78
1:M:771:LYS:CG	1:M:802:ARG:HH12	1.96	0.78
1:I:66:ASP:HB2	3:N:667:GLN:NE2	1.99	0.78
1:I:557:THR:CG2	3:N:511:ASN:OD1	2.28	0.78
1:E:63:LYS:O	3:B:567:ARG:NH2	2.09	0.78
1:A:28:PRO:HB2	3:B:130:MET:CE	2.14	0.78
3:F:714:VAL:HG11	3:F:743:LEU:HG	1.64	0.78
1:E:771:LYS:CG	1:E:802:ARG:HH12	1.96	0.78
1:E:1209:THR:HG23	2:G:334:ILE:HD13	1.65	0.78
1:M:1209:THR:HG23	2:O:334:ILE:HD13	1.65	0.78
1:I:419:ALA:HB1	3:N:524:GLU:OE1	1.83	0.78
3:B:965:GLN:CD	3:B:969:LEU:CD1	2.56	0.78
3:B:1092:ILE:CD1	3:N:1001:GLU:CB	2.62	0.78
1:E:64:ASN:N	3:B:567:ARG:HH22	1.80	0.77
3:F:965:GLN:CD	3:F:969:LEU:CD1	2.56	0.77
3:J:714:VAL:HG11	3:J:743:LEU:HG	1.64	0.77
3:B:486:GLN:NE2	3:B:492:ASP:OD1	2.18	0.77
3:N:486:GLN:NE2	3:N:492:ASP:OD1	2.18	0.77
3:N:965:GLN:CD	3:N:969:LEU:CD1	2.56	0.77
1:M:28:PRO:HB2	3:N:130:MET:CE	2.15	0.77
1:I:79:GLN:HB3	3:J:194:TYR:HB3	1.67	0.77
1:I:771:LYS:CG	1:I:802:ARG:HH12	1.96	0.77
3:F:283:LEU:CD2	3:F:307:LEU:CG	2.63	0.77
3:J:965:GLN:CD	3:J:969:LEU:CD1	2.56	0.77
3:N:744:LEU:HD21	3:N:765:HIS:CG	2.14	0.77
1:M:441:GLN:NE2	1:M:561:THR:OG1	2.17	0.77
1:A:28:PRO:CG	3:B:547:LEU:HD23	1.96	0.77
3:F:223:ARG:HH22	3:F:338:TYR:HA	1.50	0.77
1:M:66:ASP:HB2	3:J:667:GLN:HE22	1.48	0.77
2:O:332:ILE:CB	2:O:340:LEU:CD1	2.61	0.77
3:F:486:GLN:NE2	3:F:492:ASP:OD1	2.18	0.77
3:F:1082:VAL:HG21	3:J:1060:LEU:CD2	2.15	0.77
1:M:419:ALA:HB1	3:J:524:GLU:OE1	1.84	0.76
1:I:163:ASN:HB2	1:I:489:ASN:ND2	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:579:ILE:HD11	3:J:601:ALA:CB	2.10	0.76
3:F:1004:MET:CG	3:J:1092:ILE:CG2	2.64	0.76
1:I:120:THR:CG2	3:J:131:ARG:CZ	2.61	0.76
3:B:1092:ILE:HD12	3:N:1001:GLU:HA	1.67	0.76
3:J:486:GLN:NE2	3:J:492:ASP:OD1	2.18	0.76
3:N:74:LYS:CD	3:N:439:LYS:HZ1	1.93	0.76
3:B:1008:ILE:CG2	3:B:1012:ARG:CZ	2.62	0.76
3:J:223:ARG:HH22	3:J:338:TYR:HA	1.50	0.76
3:N:223:ARG:HH22	3:N:338:TYR:HA	1.50	0.76
1:M:66:ASP:HB2	3:J:667:GLN:NE2	2.00	0.76
3:B:579:ILE:HD11	3:B:601:ALA:CB	2.10	0.76
3:F:924:TRP:HH2	3:J:1093:SER:O	1.67	0.76
1:E:163:ASN:HB2	1:E:489:ASN:ND2	2.00	0.76
1:M:794:TRP:O	1:M:798:LEU:HD12	1.86	0.76
1:I:794:TRP:O	1:I:798:LEU:HD12	1.86	0.76
1:E:794:TRP:O	1:E:798:LEU:HD12	1.86	0.76
3:B:1012:ARG:HH22	4:N:1101:FAR:H41	1.48	0.76
3:B:1013:ASN:HD21	4:B:1101:FAR:C15	1.98	0.76
3:B:1013:ASN:ND2	4:N:1101:FAR:C15	2.23	0.76
3:B:1090:CYS:HG	4:B:1101:FAR:H12A	0.62	0.76
1:E:66:ASP:CA	3:B:667:GLN:NE2	2.48	0.76
1:M:28:PRO:HB2	3:N:130:MET:HE1	1.67	0.76
3:B:1008:ILE:HG22	3:B:1012:ARG:NE	2.00	0.76
4:F:1103:FAR:H13	3:J:1090:CYS:CB	2.14	0.76
1:I:1209:THR:HG23	2:K:334:ILE:HD13	1.65	0.76
1:I:75:TYR:OH	3:J:191:GLN:CG	2.33	0.76
3:B:223:ARG:HH22	3:B:338:TYR:HA	1.50	0.75
1:E:66:ASP:HB2	3:B:667:GLN:CD	2.10	0.75
1:A:163:ASN:HB2	1:A:489:ASN:ND2	2.00	0.75
2:O:332:ILE:CG1	2:O:340:LEU:CD1	2.64	0.75
3:F:184:GLU:HG2	3:F:466:PRO:HD2	1.68	0.75
1:I:120:THR:HG22	3:J:131:ARG:NE	2.00	0.75
3:J:523:VAL:HG23	3:J:523:VAL:O	1.85	0.75
3:J:853:LEU:HD12	3:J:880:ILE:HG13	1.69	0.75
1:M:163:ASN:HB2	1:M:489:ASN:ND2	2.00	0.75
1:I:63:LYS:C	3:N:567:ARG:NH2	2.44	0.75
1:A:93:ILE:CG2	3:B:67:THR:CG2	2.60	0.75
2:C:332:ILE:CG1	2:C:340:LEU:CD1	2.64	0.75
1:I:68:ASP:CG	3:J:259:GLY:O	2.28	0.75
1:M:68:ASP:CG	3:N:259:GLY:O	2.28	0.75
2:K:332:ILE:CG1	2:K:340:LEU:CD1	2.64	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:853:LEU:CD1	3:B:880:ILE:CG1	2.64	0.75
3:N:74:LYS:HD3	3:N:439:LYS:HZ3	1.51	0.75
1:E:382:GLU:OE1	1:E:382:GLU:N	2.20	0.75
2:G:332:ILE:CG1	2:G:340:LEU:CD1	2.64	0.75
1:M:29:VAL:CG1	3:N:131:ARG:HG3	2.15	0.75
3:B:526:ILE:CD1	3:B:660:ILE:HD12	2.06	0.75
1:E:28:PRO:HG3	3:F:547:LEU:HG	1.69	0.74
1:E:441:GLN:NE2	1:E:561:THR:OG1	2.17	0.74
1:M:1120:GLN:HE21	1:M:1181:ALA:HB3	1.31	0.74
1:I:120:THR:HG22	3:J:131:ARG:NH2	2.01	0.74
3:B:566:TYR:HE1	3:B:666:GLU:OE1	1.70	0.74
3:F:523:VAL:HG23	3:F:523:VAL:O	1.85	0.74
3:F:523:VAL:HG21	3:F:528:ILE:HD11	1.69	0.74
1:A:68:ASP:OD2	3:B:259:GLY:O	2.04	0.74
1:E:422:GLU:OE2	3:B:525:PRO:HG3	1.86	0.74
1:A:794:TRP:O	1:A:798:LEU:HD12	1.86	0.74
1:M:120:THR:CG2	3:N:131:ARG:NH2	2.51	0.74
3:J:853:LEU:CD1	3:J:880:ILE:CG1	2.64	0.74
3:N:184:GLU:HG2	3:N:466:PRO:HD2	1.68	0.74
1:M:382:GLU:OE1	1:M:382:GLU:N	2.20	0.74
2:O:375:PRO:HD2	2:O:378:VAL:HG13	1.70	0.74
3:B:523:VAL:HG21	3:B:528:ILE:HD11	1.69	0.74
3:B:523:VAL:HG23	3:B:523:VAL:O	1.85	0.74
4:F:1103:FAR:C15	3:J:1013:ASN:HD21	2.00	0.74
3:N:172:ILE:HG21	3:N:212:VAL:HG22	1.69	0.74
3:J:184:GLU:HG2	3:J:466:PRO:HD2	1.68	0.74
3:N:853:LEU:CD1	3:N:880:ILE:CG1	2.64	0.74
1:A:441:GLN:NE2	1:A:561:THR:OG1	2.17	0.74
2:C:375:PRO:HD2	2:C:378:VAL:HG13	1.70	0.74
3:B:948:ILE:HD11	3:B:1007:SER:HA	1.70	0.74
3:F:283:LEU:HD21	3:F:307:LEU:CG	2.17	0.74
3:F:1018:PHE:CD2	3:F:1022:VAL:HG22	2.23	0.74
3:J:1018:PHE:CD2	3:J:1022:VAL:HG22	2.23	0.74
3:N:948:ILE:HD11	3:N:1007:SER:HA	1.70	0.74
3:N:1013:ASN:HD21	4:N:1101:FAR:C15	2.00	0.74
3:B:853:LEU:HD12	3:B:880:ILE:HG13	1.69	0.74
3:J:74:LYS:CD	3:J:439:LYS:HZ1	1.98	0.74
3:B:184:GLU:HG2	3:B:466:PRO:HD2	1.68	0.74
3:F:1002:LEU:HD23	3:F:1024:LEU:HD22	1.70	0.74
3:J:566:TYR:HE1	3:J:666:GLU:OE1	1.70	0.74
3:F:974:MET:HE3	3:F:975:TYR:CE2	1.97	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:1018:PHE:CD2	3:N:1022:VAL:HG22	2.23	0.74
1:A:28:PRO:HB2	3:B:130:MET:HE1	1.68	0.73
2:K:375:PRO:HD2	2:K:378:VAL:HG13	1.70	0.73
3:F:498:ALA:HB3	3:F:618:LEU:HD23	1.70	0.73
3:F:853:LEU:CD1	3:F:880:ILE:CG1	2.64	0.73
3:J:523:VAL:HG21	3:J:528:ILE:HD11	1.69	0.73
3:N:523:VAL:HG23	3:N:523:VAL:O	1.85	0.73
3:F:566:TYR:HE1	3:F:666:GLU:OE1	1.69	0.73
1:A:75:TYR:OH	3:B:191:GLN:CB	2.34	0.73
3:N:523:VAL:HG21	3:N:528:ILE:HD11	1.69	0.73
1:E:68:ASP:OD1	3:F:259:GLY:O	2.07	0.73
1:I:382:GLU:N	1:I:382:GLU:OE1	2.20	0.73
3:J:1002:LEU:HD23	3:J:1024:LEU:HD22	1.70	0.73
1:M:79:GLN:NE2	3:N:194:TYR:CD1	2.55	0.73
3:F:579:ILE:HD13	3:F:601:ALA:HB2	1.69	0.73
3:J:795:SER:OG	3:J:855:ILE:HD13	1.87	0.73
3:B:172:ILE:HG21	3:B:212:VAL:HG22	1.69	0.73
3:B:1018:PHE:CD2	3:B:1022:VAL:HG22	2.23	0.73
1:A:75:TYR:OH	3:B:191:GLN:CG	2.37	0.73
1:A:901:LEU:HD22	1:A:912:PHE:HZ	1.53	0.73
1:E:893:LEU:HD22	1:E:954:MET:HE1	1.71	0.73
3:B:795:SER:OG	3:B:855:ILE:HD13	1.87	0.73
3:J:498:ALA:HB3	3:J:618:LEU:HD23	1.70	0.73
3:N:566:TYR:HE1	3:N:666:GLU:OE1	1.70	0.73
1:A:382:GLU:N	1:A:382:GLU:OE1	2.20	0.73
1:A:1208:ALA:HB3	2:C:334:ILE:HG12	1.71	0.73
4:B:1101:FAR:H141	3:N:1009:VAL:HA	1.66	0.73
3:F:172:ILE:HG21	3:F:212:VAL:HG22	1.69	0.73
1:E:1208:ALA:HB3	2:G:334:ILE:HG12	1.71	0.73
3:J:948:ILE:HD11	3:J:1007:SER:HA	1.70	0.73
3:F:795:SER:OG	3:F:855:ILE:HD13	1.87	0.72
1:E:75:TYR:HH	3:F:191:GLN:CD	1.94	0.72
2:G:375:PRO:HD2	2:G:378:VAL:HG13	1.70	0.72
3:B:1002:LEU:HD23	3:B:1024:LEU:HD22	1.70	0.72
3:F:853:LEU:HD12	3:F:880:ILE:HG13	1.69	0.72
3:J:508:VAL:O	3:J:512:THR:HG23	1.89	0.72
1:A:79:GLN:HB3	3:B:194:TYR:CB	2.18	0.72
3:F:173:ASN:ND2	3:F:220:VAL:HA	2.04	0.72
3:N:173:ASN:ND2	3:N:220:VAL:HA	2.04	0.72
2:C:332:ILE:CB	2:C:340:LEU:CD1	2.61	0.72
1:M:901:LEU:HD22	1:M:912:PHE:HZ	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:283:LEU:HD23	3:F:307:LEU:CD2	2.18	0.72
3:N:795:SER:OG	3:N:855:ILE:HD13	1.87	0.72
3:N:1002:LEU:HD23	3:N:1024:LEU:HD22	1.70	0.72
2:G:332:ILE:CB	2:G:340:LEU:CD1	2.61	0.72
2:K:332:ILE:CB	2:K:340:LEU:CD1	2.61	0.72
3:F:508:VAL:O	3:F:512:THR:HG23	1.89	0.72
3:F:1090:CYS:SG	4:F:1101:FAR:H11	1.17	0.72
3:N:853:LEU:HD12	3:N:880:ILE:HG13	1.69	0.72
1:E:901:LEU:HD22	1:E:912:PHE:HZ	1.53	0.72
1:I:29:VAL:CG1	3:J:131:ARG:HG3	2.18	0.72
1:I:901:LEU:HD22	1:I:912:PHE:HZ	1.53	0.72
3:F:948:ILE:HD11	3:F:1007:SER:HA	1.70	0.72
3:N:1090:CYS:CB	4:N:1101:FAR:H13	2.14	0.72
1:A:1209:THR:CG2	2:C:334:ILE:HD13	2.20	0.72
1:M:1081:LYS:HB3	4:M:1301:FAR:H143	1.72	0.72
3:B:498:ALA:HB3	3:B:618:LEU:HD23	1.70	0.72
3:J:173:ASN:ND2	3:J:220:VAL:HA	2.04	0.72
1:A:1081:LYS:HB3	4:A:1301:FAR:H143	1.72	0.72
1:M:120:THR:HG22	3:N:131:ARG:NH2	2.05	0.72
3:B:223:ARG:HD3	3:B:228:ASN:ND2	2.05	0.72
3:B:508:VAL:O	3:B:512:THR:HG23	1.89	0.72
1:E:94:ARG:HH12	3:F:157:THR:CA	2.03	0.72
1:M:893:LEU:HD22	1:M:954:MET:HE1	1.71	0.72
1:I:1081:LYS:HB3	4:I:1301:FAR:H143	1.72	0.72
3:B:173:ASN:ND2	3:B:220:VAL:HA	2.04	0.72
1:A:893:LEU:HD22	1:A:954:MET:HE1	1.71	0.72
1:M:1209:THR:CG2	2:O:334:ILE:HD13	2.20	0.72
1:I:893:LEU:HD22	1:I:954:MET:HE1	1.71	0.72
3:J:172:ILE:HG21	3:J:212:VAL:HG22	1.69	0.72
3:J:579:ILE:HD13	3:J:601:ALA:HB2	1.69	0.72
1:E:1209:THR:CG2	2:G:334:ILE:HD13	2.20	0.71
1:M:83:LYS:HD2	3:N:198:GLU:OE1	1.90	0.71
1:M:872:PRO:CD	1:M:875:ALA:HB3	2.20	0.71
1:I:441:GLN:NE2	1:I:561:THR:OG1	2.17	0.71
3:N:508:VAL:O	3:N:512:THR:HG23	1.89	0.71
1:A:779:GLN:HB3	1:A:782:ILE:HG12	1.73	0.71
1:E:64:ASN:HA	3:B:567:ARG:NH2	2.05	0.71
1:E:75:TYR:OH	3:F:191:GLN:HG3	1.88	0.71
1:I:1209:THR:CG2	2:K:334:ILE:HD13	2.20	0.71
3:F:495:VAL:HG13	3:F:615:PRO:HB2	1.72	0.71
3:J:322:ARG:HH11	3:J:323:LYS:HE2	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:724:THR:C	3:J:726:GLU:H	1.98	0.71
1:A:66:ASP:HB2	3:F:667:GLN:NE2	2.05	0.71
3:B:495:VAL:HG13	3:B:615:PRO:HB2	1.72	0.71
1:M:779:GLN:HB3	1:M:782:ILE:HG12	1.73	0.71
1:I:28:PRO:HG2	3:J:547:LEU:HD21	1.12	0.71
3:J:223:ARG:HD3	3:J:228:ASN:ND2	2.05	0.71
3:N:1015:GLU:CD	4:N:1101:FAR:H41	2.16	0.71
1:M:290:ARG:NH2	1:M:391:ASP:OD1	2.23	0.71
1:I:1208:ALA:HB3	2:K:334:ILE:HG12	1.71	0.71
3:N:498:ALA:HB3	3:N:618:LEU:HD23	1.70	0.71
3:F:172:ILE:HD13	3:F:212:VAL:HG22	1.73	0.71
4:F:1101:FAR:C10	3:J:1070:THR:OG1	2.38	0.71
3:N:853:LEU:CD2	3:N:883:MET:HE1	2.21	0.71
1:E:779:GLN:HB3	1:E:782:ILE:HG12	1.73	0.71
3:B:172:ILE:HD13	3:B:212:VAL:HG22	1.73	0.71
3:F:965:GLN:HG2	3:F:969:LEU:CG	2.18	0.71
1:A:83:LYS:HD2	3:B:198:GLU:OE1	1.91	0.70
1:E:422:GLU:OE2	3:B:525:PRO:CG	2.38	0.70
3:J:495:VAL:HG13	3:J:615:PRO:HB2	1.72	0.70
1:A:524:PHE:HE1	1:A:539:ILE:HG23	1.56	0.70
1:E:66:ASP:HA	3:B:667:GLN:NE2	2.06	0.70
1:E:491:ARG:HD3	3:F:62:LEU:HG	1.73	0.70
1:M:1172:ASP:HB3	1:M:1175:MET:HB2	1.73	0.70
1:I:75:TYR:OH	3:J:191:GLN:CB	2.39	0.70
1:I:120:THR:HG21	3:J:131:ARG:NH2	2.06	0.70
3:B:566:TYR:CE1	3:B:666:GLU:OE1	2.45	0.70
3:F:223:ARG:HD3	3:F:228:ASN:ND2	2.05	0.70
3:F:1013:ASN:HA	3:J:1012:ARG:HD3	1.73	0.70
1:M:1208:ALA:HB3	2:O:334:ILE:HG12	1.71	0.70
1:I:779:GLN:HB3	1:I:782:ILE:HG12	1.73	0.70
3:B:853:LEU:CD2	3:B:883:MET:HE1	2.21	0.70
3:F:724:THR:C	3:F:726:GLU:H	1.98	0.70
3:J:566:TYR:CE1	3:J:666:GLU:OE1	2.44	0.70
3:N:495:VAL:HG13	3:N:615:PRO:HB2	1.72	0.70
3:N:566:TYR:CE1	3:N:666:GLU:OE1	2.45	0.70
1:E:1081:LYS:HB3	4:E:1301:FAR:H143	1.72	0.70
3:F:322:ARG:HH11	3:F:323:LYS:HE2	1.56	0.70
3:F:1090:CYS:SG	4:F:1101:FAR:H12A	1.29	0.70
3:N:223:ARG:HD3	3:N:228:ASN:ND2	2.05	0.70
1:E:872:PRO:CD	1:E:875:ALA:HB3	2.20	0.70
3:J:172:ILE:HD13	3:J:212:VAL:HG22	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:274:ARG:HH22	3:J:802:THR:HA	1.57	0.70
3:J:491:ASN:HD21	3:J:607:GLN:HA	1.57	0.70
3:J:853:LEU:CD2	3:J:883:MET:HE1	2.21	0.70
3:N:322:ARG:HH11	3:N:323:LYS:HE2	1.56	0.70
3:N:593:LEU:HD21	3:N:856:HIS:HE1	1.57	0.70
1:A:78:GLU:HB3	1:A:153:LEU:HD21	1.74	0.70
1:A:1120:GLN:NE2	1:A:1181:ALA:HB1	2.03	0.70
1:I:79:GLN:HB3	3:J:194:TYR:CB	2.21	0.70
3:B:593:LEU:HD21	3:B:856:HIS:HE1	1.57	0.70
3:B:1012:ARG:HB2	4:N:1101:FAR:C14	2.21	0.70
3:J:593:LEU:HD21	3:J:856:HIS:HE1	1.57	0.70
1:E:768:LEU:HD22	1:E:802:ARG:NH2	2.07	0.70
3:B:491:ASN:HD21	3:B:607:GLN:HA	1.57	0.70
3:F:491:ASN:HD21	3:F:607:GLN:HA	1.57	0.70
1:A:69:GLU:HG3	3:B:262:TRP:CZ3	2.26	0.70
1:M:1200:MET:HA	1:M:1203:LEU:HD12	1.74	0.70
3:B:322:ARG:HH11	3:B:323:LYS:HE2	1.56	0.70
3:N:172:ILE:HD13	3:N:212:VAL:HG22	1.73	0.70
1:E:94:ARG:NH2	3:F:157:THR:O	2.23	0.70
1:E:557:THR:HG23	3:B:511:ASN:OD1	1.92	0.70
1:E:1200:MET:HA	1:E:1203:LEU:HD12	1.74	0.70
1:M:524:PHE:HE1	1:M:539:ILE:HG23	1.57	0.70
1:M:768:LEU:HD22	1:M:802:ARG:NH2	2.07	0.70
3:N:724:THR:C	3:N:726:GLU:H	1.98	0.70
1:E:28:PRO:HG2	3:F:547:LEU:HD21	0.79	0.69
3:B:1092:ILE:HD11	3:N:1001:GLU:CB	2.13	0.69
3:F:1015:GLU:HG3	3:J:1012:ARG:HH22	1.56	0.69
1:A:872:PRO:CD	1:A:875:ALA:HB3	2.20	0.69
1:I:1200:MET:HA	1:I:1203:LEU:HD12	1.74	0.69
3:B:724:THR:C	3:B:726:GLU:H	1.98	0.69
4:F:1101:FAR:H91	3:J:1070:THR:HG21	1.74	0.69
1:A:1200:MET:HA	1:A:1203:LEU:HD12	1.74	0.69
3:B:274:ARG:HH22	3:B:802:THR:HA	1.57	0.69
1:E:524:PHE:HE1	1:E:539:ILE:HG23	1.57	0.69
3:F:274:ARG:HH22	3:F:802:THR:HA	1.57	0.69
1:A:68:ASP:OD2	3:B:260:CYS:HA	1.92	0.69
1:I:163:ASN:CB	1:I:489:ASN:ND2	2.56	0.69
3:F:566:TYR:CE1	3:F:666:GLU:OE1	2.44	0.69
3:N:274:ARG:HH22	3:N:802:THR:HA	1.57	0.69
1:A:163:ASN:CB	1:A:489:ASN:ND2	2.56	0.69
3:B:1093:SER:O	3:N:924:TRP:HH2	1.67	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1004:MET:CE	3:J:1091:LEU:HB2	2.23	0.69
3:J:214:ARG:HA	3:J:825:PRO:HG2	1.75	0.69
1:E:290:ARG:NH2	1:E:391:ASP:OD1	2.23	0.69
1:M:78:GLU:HB3	1:M:153:LEU:HD21	1.74	0.69
1:M:254:GLU:OE1	1:M:1101:THR:OG1	2.11	0.69
1:I:524:PHE:HE1	1:I:539:ILE:HG23	1.56	0.69
3:B:88:LEU:HD21	3:B:178:TYR:HA	1.75	0.69
3:B:214:ARG:NH2	5:B:1102:ADP:O3B	2.25	0.69
3:F:214:ARG:HA	3:F:825:PRO:HG2	1.75	0.69
3:F:853:LEU:CD2	3:F:883:MET:HE1	2.21	0.69
3:F:1082:VAL:CG2	3:J:1060:LEU:CD2	2.71	0.69
3:N:214:ARG:HA	3:N:825:PRO:HG2	1.75	0.69
1:M:163:ASN:CB	1:M:489:ASN:ND2	2.56	0.69
3:B:579:ILE:HD13	3:B:601:ALA:HB2	1.69	0.69
1:E:1136:MET:HE1	2:G:347:ILE:HA	1.76	0.69
1:M:1136:MET:HE1	2:O:347:ILE:HA	1.75	0.69
1:I:872:PRO:CD	1:I:875:ALA:HB3	2.20	0.69
3:J:591:VAL:HG21	3:J:634:ILE:HG13	1.75	0.69
3:N:88:LEU:HD21	3:N:178:TYR:HA	1.75	0.69
1:A:1136:MET:HE1	2:C:347:ILE:HA	1.76	0.68
3:J:965:GLN:HG2	3:J:969:LEU:CG	2.18	0.68
3:N:491:ASN:HD21	3:N:607:GLN:HA	1.57	0.68
1:A:63:LYS:C	3:F:567:ARG:NH2	2.49	0.68
1:I:1136:MET:HE1	2:K:347:ILE:HA	1.76	0.68
3:B:965:GLN:HG2	3:B:969:LEU:CG	2.18	0.68
3:B:1013:ASN:OD1	4:B:1101:FAR:C13	2.41	0.68
3:B:1090:CYS:SG	4:B:1101:FAR:H12A	1.50	0.68
3:F:593:LEU:HD21	3:F:856:HIS:HE1	1.57	0.68
1:M:413:MET:HG2	1:M:418:LEU:HB3	1.76	0.68
3:B:1008:ILE:HG22	3:B:1012:ARG:CD	2.23	0.68
3:F:591:VAL:HG21	3:F:634:ILE:HG13	1.75	0.68
1:A:69:GLU:HG3	3:B:262:TRP:HZ3	1.58	0.68
3:F:744:LEU:O	3:F:766:ILE:HD11	1.94	0.68
3:N:786:ALA:HB3	3:N:848:VAL:HG11	1.76	0.68
1:A:445:LEU:HD12	1:A:563:THR:CG2	2.24	0.68
1:A:923:ILE:O	1:A:927:MET:HG3	1.94	0.68
1:E:78:GLU:HB3	1:E:153:LEU:HD21	1.74	0.68
1:M:28:PRO:HG2	3:N:547:LEU:HD21	1.29	0.68
1:M:1109:VAL:HA	1:M:1112:GLU:HG2	1.75	0.68
3:F:1074:MET:HG3	3:J:1074:MET:HE2	1.75	0.68
3:B:786:ALA:HB3	3:B:848:VAL:HG11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:THR:HG22	3:B:131:ARG:NH2	2.09	0.68
1:A:447:GLU:OE1	1:A:567:SER:HA	1.94	0.68
1:E:163:ASN:CB	1:E:489:ASN:ND2	2.56	0.68
1:E:445:LEU:HD12	1:E:563:THR:CG2	2.24	0.68
3:B:214:ARG:HA	3:B:825:PRO:HG2	1.75	0.68
3:J:786:ALA:HB3	3:J:848:VAL:HG11	1.75	0.68
3:N:744:LEU:O	3:N:766:ILE:HD11	1.94	0.68
1:A:254:GLU:OE1	1:A:1101:THR:OG1	2.11	0.68
1:A:1109:VAL:HA	1:A:1112:GLU:HG2	1.75	0.68
1:M:68:ASP:OD2	3:N:259:GLY:O	2.11	0.68
1:M:445:LEU:HD12	1:M:563:THR:CG2	2.24	0.68
1:I:78:GLU:HB3	1:I:153:LEU:HD21	1.74	0.68
3:F:406:VAL:H	3:F:445:GLN:HE22	1.42	0.68
4:F:1101:FAR:H143	3:J:1009:VAL:HA	0.71	0.68
3:N:1013:ASN:OD1	4:N:1101:FAR:C13	2.41	0.68
1:A:290:ARG:NH2	1:A:391:ASP:OD1	2.23	0.68
1:M:447:GLU:OE1	1:M:567:SER:HA	1.94	0.68
3:F:938:PRO:HG2	3:J:1092:ILE:HB	1.76	0.68
3:N:965:GLN:HG2	3:N:969:LEU:CG	2.18	0.68
1:A:66:ASP:HB2	3:F:667:GLN:HE22	1.56	0.68
1:A:413:MET:HG2	1:A:418:LEU:HB3	1.76	0.68
1:E:254:GLU:OE1	1:E:1101:THR:OG1	2.11	0.68
1:E:1120:GLN:NE2	1:E:1181:ALA:HB1	2.03	0.68
3:N:591:VAL:HG21	3:N:634:ILE:HG13	1.75	0.68
1:A:768:LEU:HD22	1:A:802:ARG:NH2	2.07	0.67
1:E:447:GLU:OE1	1:E:567:SER:HA	1.94	0.67
1:I:413:MET:HG2	1:I:418:LEU:HB3	1.76	0.67
1:I:447:GLU:OE1	1:I:567:SER:HA	1.94	0.67
3:J:88:LEU:HD21	3:J:178:TYR:HA	1.75	0.67
1:A:1209:THR:HG23	2:C:334:ILE:CG2	2.25	0.67
1:E:1109:VAL:HA	1:E:1112:GLU:HG2	1.75	0.67
1:I:1092:LEU:HB2	1:I:1114:VAL:HG11	1.76	0.67
3:J:744:LEU:O	3:J:766:ILE:HD11	1.94	0.67
1:E:1092:LEU:HB2	1:E:1114:VAL:HG11	1.76	0.67
4:F:1103:FAR:C13	3:J:1013:ASN:OD1	2.42	0.67
1:E:29:VAL:HG11	3:F:131:ARG:CG	2.22	0.67
1:E:442:VAL:HG21	1:E:589:MET:HE2	1.77	0.67
1:M:1209:THR:HG23	2:O:334:ILE:CG2	2.25	0.67
3:F:405:VAL:HG21	3:F:435:GLY:HA3	1.77	0.67
4:F:1101:FAR:H142	3:J:1012:ARG:HB2	1.76	0.67
3:J:405:VAL:HG21	3:J:435:GLY:HA3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:579:ILE:HD13	3:N:601:ALA:HB2	1.69	0.67
1:A:10:ARG:NH1	1:A:415:GLU:OE1	2.28	0.67
1:E:28:PRO:HB2	3:F:547:LEU:HD21	1.73	0.67
1:I:254:GLU:OE1	1:I:1101:THR:OG1	2.11	0.67
1:I:290:ARG:NH2	1:I:391:ASP:OD1	2.23	0.67
1:I:1209:THR:HG23	2:K:334:ILE:CG2	2.25	0.67
1:I:442:VAL:HG21	1:I:589:MET:HE2	1.77	0.67
1:I:1109:VAL:HA	1:I:1112:GLU:HG2	1.75	0.67
3:B:591:VAL:HG21	3:B:634:ILE:HG13	1.75	0.67
3:B:853:LEU:HD11	3:B:880:ILE:CG1	2.24	0.67
3:F:88:LEU:HD21	3:F:178:TYR:HA	1.75	0.67
3:F:875:ARG:HB2	3:F:878:TRP:HB2	1.77	0.67
1:E:10:ARG:NH1	1:E:415:GLU:OE1	2.28	0.67
1:E:923:ILE:O	1:E:927:MET:HG3	1.94	0.67
1:M:923:ILE:O	1:M:927:MET:HG3	1.94	0.67
1:M:1092:LEU:HB2	1:M:1114:VAL:HG11	1.76	0.67
3:B:744:LEU:O	3:B:766:ILE:HD11	1.94	0.67
3:F:786:ALA:HB3	3:F:848:VAL:HG11	1.75	0.67
1:E:1209:THR:HG23	2:G:334:ILE:CG2	2.25	0.67
3:J:406:VAL:H	3:J:445:GLN:HE22	1.42	0.67
1:E:29:VAL:CG1	3:F:131:ARG:HG3	2.25	0.67
1:M:10:ARG:NH1	1:M:415:GLU:OE1	2.28	0.67
3:J:853:LEU:HD11	3:J:880:ILE:CG1	2.24	0.67
3:N:405:VAL:HG21	3:N:435:GLY:HA3	1.77	0.67
1:M:79:GLN:HB3	3:N:194:TYR:CB	2.25	0.67
1:I:923:ILE:O	1:I:927:MET:HG3	1.94	0.67
3:N:406:VAL:H	3:N:445:GLN:HE22	1.42	0.67
1:M:1120:GLN:NE2	1:M:1181:ALA:HB1	2.03	0.66
1:I:10:ARG:NH1	1:I:415:GLU:OE1	2.27	0.66
3:B:777:LYS:HG2	3:B:779:TRP:CZ2	2.30	0.66
3:F:1090:CYS:HG	4:F:1101:FAR:C2	2.01	0.66
3:J:875:ARG:HB2	3:J:878:TRP:HB2	1.77	0.66
1:E:413:MET:HG2	1:E:418:LEU:HB3	1.76	0.66
3:B:493:LEU:HD21	3:B:615:PRO:HG2	1.77	0.66
3:F:586:TYR:HB3	3:F:782:VAL:HG12	1.78	0.66
1:M:75:TYR:OH	3:N:191:GLN:CG	2.43	0.66
1:M:442:VAL:HG21	1:M:589:MET:HE2	1.77	0.66
3:J:777:LYS:HG2	3:J:779:TRP:CZ2	2.30	0.66
3:N:586:TYR:HB3	3:N:782:VAL:HG12	1.77	0.66
1:I:93:ILE:HG22	3:J:67:THR:HG23	1.70	0.66
1:I:445:LEU:HD12	1:I:563:THR:CG2	2.24	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:143:PRO:CB	3:B:215:VAL:CG2	2.71	0.66
3:F:777:LYS:HG2	3:F:779:TRP:CZ2	2.30	0.66
3:B:405:VAL:HG21	3:B:435:GLY:HA3	1.77	0.66
3:J:586:TYR:HB3	3:J:782:VAL:HG12	1.78	0.66
1:A:120:THR:CG2	3:B:131:ARG:NH2	2.58	0.66
1:I:28:PRO:CG	3:J:547:LEU:HD23	1.93	0.66
1:I:75:TYR:OH	3:J:191:GLN:OE1	2.13	0.66
3:B:279:LEU:HG	3:B:283:LEU:HD22	1.76	0.66
3:B:586:TYR:HB3	3:B:782:VAL:HG12	1.78	0.66
3:N:875:ARG:HB2	3:N:878:TRP:HB2	1.77	0.66
1:M:859:PRO:HB2	1:M:1119:PRO:HA	1.78	0.66
2:C:335:ARG:O	2:C:336:ASP:OD1	2.14	0.66
1:E:93:ILE:HG21	3:F:66:PRO:C	2.21	0.66
1:M:120:THR:CG2	3:N:131:ARG:CZ	2.71	0.66
1:I:28:PRO:HG3	3:J:547:LEU:CG	2.25	0.66
4:F:1101:FAR:H51	3:J:1008:ILE:HG21	1.76	0.66
3:N:777:LYS:HG2	3:N:779:TRP:CZ2	2.30	0.66
1:A:859:PRO:HB2	1:A:1119:PRO:HA	1.78	0.65
1:A:1200:MET:HE1	2:C:351:ALA:HA	1.78	0.65
2:G:335:ARG:O	2:G:336:ASP:OD1	2.14	0.65
2:O:335:ARG:O	2:O:336:ASP:OD1	2.14	0.65
3:F:593:LEU:HD21	3:F:856:HIS:CE1	2.31	0.65
1:A:1092:LEU:HB2	1:A:1114:VAL:HG11	1.76	0.65
3:B:724:THR:HB	3:B:726:GLU:H	1.61	0.65
1:E:1200:MET:HE1	2:G:351:ALA:HA	1.79	0.65
2:K:335:ARG:O	2:K:336:ASP:OD1	2.14	0.65
4:B:1101:FAR:H143	3:N:1009:VAL:CA	2.20	0.65
3:J:724:THR:HB	3:J:726:GLU:H	1.61	0.65
1:A:442:VAL:HG21	1:A:589:MET:HE2	1.77	0.65
1:I:768:LEU:HD22	1:I:802:ARG:NH2	2.07	0.65
3:N:724:THR:C	3:N:726:GLU:N	2.54	0.65
1:M:1200:MET:HE1	2:O:351:ALA:HA	1.79	0.65
3:B:1090:CYS:CB	4:B:1101:FAR:H13	2.19	0.65
3:N:724:THR:HB	3:N:726:GLU:H	1.61	0.65
1:M:771:LYS:CD	1:M:802:ARG:HH11	2.10	0.65
1:I:1200:MET:HE1	2:K:351:ALA:HA	1.78	0.65
3:B:406:VAL:H	3:B:445:GLN:HE22	1.42	0.65
4:F:1101:FAR:H102	3:J:1070:THR:OG1	1.97	0.65
3:J:493:LEU:HD21	3:J:615:PRO:HG2	1.77	0.65
3:J:853:LEU:HD12	3:J:880:ILE:CG1	2.26	0.65
3:N:853:LEU:HD11	3:N:880:ILE:CG1	2.24	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:445:LEU:O	1:I:565:PRO:HA	1.97	0.65
3:B:460:SER:HB2	3:F:477:ARG:NH2	2.11	0.65
3:B:1009:VAL:HA	4:N:1101:FAR:H141	1.77	0.65
1:A:29:VAL:HG11	3:B:131:ARG:HG2	1.79	0.65
1:A:163:ASN:HB2	1:A:489:ASN:HD21	1.62	0.65
1:M:872:PRO:HD2	1:M:872:PRO:O	1.97	0.65
3:B:724:THR:C	3:B:726:GLU:N	2.54	0.65
3:B:875:ARG:HB2	3:B:878:TRP:HB2	1.77	0.65
1:M:445:LEU:O	1:M:565:PRO:HA	1.97	0.65
1:I:859:PRO:HB2	1:I:1119:PRO:HA	1.79	0.65
3:F:143:PRO:HB2	3:F:215:VAL:HG22	1.79	0.65
1:E:872:PRO:HD2	1:E:872:PRO:O	1.97	0.65
1:M:113:HIS:HA	1:M:132:HIS:HB3	1.79	0.65
1:M:1168:THR:C	1:M:1170:GLY:N	2.52	0.65
1:I:83:LYS:CD	3:J:198:GLU:OE1	2.45	0.65
3:F:625:ASN:HB3	3:F:634:ILE:CD1	2.27	0.65
3:J:593:LEU:HD21	3:J:856:HIS:CE1	2.31	0.65
1:E:79:GLN:HB3	3:F:194:TYR:CB	2.28	0.64
1:I:771:LYS:CD	1:I:802:ARG:HH11	2.10	0.64
3:B:593:LEU:HD21	3:B:856:HIS:CE1	2.31	0.64
3:B:625:ASN:HB3	3:B:634:ILE:CD1	2.27	0.64
3:F:853:LEU:HD12	3:F:880:ILE:CG1	2.26	0.64
3:N:853:LEU:HD22	3:N:883:MET:HE1	1.79	0.64
1:A:445:LEU:O	1:A:565:PRO:HA	1.97	0.64
1:A:1137:LEU:HD13	4:A:1301:FAR:C6	2.19	0.64
1:E:62:ARG:CZ	3:F:258:GLN:OE1	2.44	0.64
1:E:113:HIS:HA	1:E:132:HIS:HB3	1.79	0.64
1:E:445:LEU:O	1:E:565:PRO:HA	1.97	0.64
1:E:768:LEU:HD23	1:E:802:ARG:HH21	1.24	0.64
1:M:75:TYR:OH	3:N:191:GLN:CB	2.45	0.64
1:I:113:HIS:HA	1:I:132:HIS:HB3	1.79	0.64
3:B:853:LEU:HD12	3:B:880:ILE:CG1	2.26	0.64
3:F:724:THR:HB	3:F:726:GLU:H	1.61	0.64
1:M:28:PRO:CG	3:N:547:LEU:HD23	1.98	0.64
1:M:163:ASN:HB2	1:M:489:ASN:HD21	1.62	0.64
3:N:493:LEU:HD21	3:N:615:PRO:HG2	1.77	0.64
3:N:625:ASN:HB3	3:N:634:ILE:CD1	2.27	0.64
3:F:493:LEU:HD21	3:F:615:PRO:HG2	1.77	0.64
3:N:593:LEU:HD21	3:N:856:HIS:CE1	2.31	0.64
3:J:625:ASN:HB3	3:J:634:ILE:CD1	2.27	0.64
1:A:113:HIS:HA	1:A:132:HIS:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1168:THR:C	1:E:1170:GLY:N	2.52	0.64
1:M:68:ASP:OD2	3:N:260:CYS:HA	1.98	0.64
1:M:69:GLU:HG3	3:N:262:TRP:CZ3	2.33	0.64
1:M:69:GLU:HG3	3:N:262:TRP:HZ3	1.61	0.64
1:I:931:LEU:HD11	1:I:949:LEU:HD11	1.80	0.64
3:J:223:ARG:HB3	3:J:228:ASN:OD1	1.98	0.64
3:N:172:ILE:HG21	3:N:212:VAL:HG21	1.80	0.64
3:N:853:LEU:HD12	3:N:880:ILE:CG1	2.26	0.64
1:I:768:LEU:HD23	1:I:802:ARG:HH21	1.24	0.64
3:F:625:ASN:O	3:F:634:ILE:HD11	1.98	0.64
3:F:1070:THR:OG1	4:F:1103:FAR:H102	1.97	0.64
1:E:859:PRO:HB2	1:E:1119:PRO:HA	1.78	0.64
1:E:931:LEU:HD11	1:E:949:LEU:HD11	1.80	0.63
3:B:223:ARG:HB3	3:B:228:ASN:OD1	1.98	0.63
3:B:853:LEU:HD22	3:B:883:MET:HE1	1.79	0.63
2:O:332:ILE:CG1	2:O:340:LEU:HD13	2.28	0.63
1:I:28:PRO:HG3	3:J:547:LEU:HG	1.79	0.63
1:I:176:TYR:HB2	1:I:241:ILE:HD13	1.81	0.63
3:F:924:TRP:CZ2	3:J:1093:SER:O	2.51	0.63
1:A:872:PRO:HD2	1:A:872:PRO:O	1.97	0.63
1:M:176:TYR:HB2	1:M:241:ILE:HD13	1.81	0.63
3:B:800:ILE:O	3:B:804:LEU:HG	1.99	0.63
3:F:467:VAL:HG12	3:F:469:ARG:HG2	1.81	0.63
3:F:853:LEU:HD22	3:F:883:MET:HE1	1.79	0.63
3:J:556:PRO:HD2	5:J:1101:ADP:O1A	1.99	0.63
3:J:800:ILE:O	3:J:804:LEU:HG	1.99	0.63
1:A:817:VAL:HA	1:A:820:ILE:HG12	1.81	0.63
3:N:223:ARG:HB3	3:N:228:ASN:OD1	1.98	0.63
1:A:69:GLU:CG	3:B:262:TRP:CZ3	2.82	0.63
1:A:176:TYR:HB2	1:A:241:ILE:HD13	1.81	0.63
2:G:349:ALA:O	2:G:353:ARG:HG3	1.99	0.63
3:F:223:ARG:HB3	3:F:228:ASN:OD1	1.98	0.63
1:E:24:CYS:O	3:F:546:LYS:HD3	1.99	0.63
1:I:817:VAL:HA	1:I:820:ILE:HG12	1.81	0.63
1:I:872:PRO:HD2	1:I:872:PRO:O	1.97	0.63
1:I:930:GLU:HA	1:I:933:HIS:CD2	2.34	0.63
3:B:467:VAL:HG12	3:B:469:ARG:HG2	1.81	0.63
3:F:556:PRO:HD2	5:F:1102:ADP:O2A	1.99	0.63
3:N:467:VAL:HG12	3:N:469:ARG:HG2	1.81	0.63
3:J:467:VAL:HG12	3:J:469:ARG:HG2	1.81	0.63
3:J:853:LEU:HD22	3:J:883:MET:HE1	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:556:PRO:HD2	5:N:1102:ADP:O1A	1.99	0.63
3:N:800:ILE:O	3:N:804:LEU:HG	1.99	0.63
1:A:19:GLN:HA	1:A:23:LEU:HB2	1.81	0.63
1:M:19:GLN:HA	1:M:23:LEU:HB2	1.81	0.63
1:I:163:ASN:HB2	1:I:489:ASN:HD21	1.61	0.63
3:N:625:ASN:O	3:N:634:ILE:HD11	1.98	0.63
1:A:771:LYS:CD	1:A:802:ARG:HH11	2.10	0.63
1:E:72:ALA:HB2	3:F:260:CYS:HB2	1.80	0.63
1:E:120:THR:CG2	3:F:131:ARG:NE	2.50	0.63
1:E:163:ASN:HB2	1:E:489:ASN:HD21	1.62	0.63
1:E:771:LYS:CD	1:E:802:ARG:HH11	2.10	0.63
1:M:450:GLU:O	1:M:454:ILE:HG13	1.99	0.63
1:M:931:LEU:HD11	1:M:949:LEU:HD11	1.80	0.63
2:O:349:ALA:O	2:O:353:ARG:HG3	1.99	0.63
3:F:853:LEU:HD11	3:F:880:ILE:CG1	2.24	0.63
3:N:143:PRO:CB	3:N:215:VAL:CG2	2.71	0.63
1:E:817:VAL:HA	1:E:820:ILE:HG12	1.81	0.62
3:B:143:PRO:HB2	3:B:215:VAL:HG22	1.79	0.62
3:B:172:ILE:HG21	3:B:212:VAL:HG21	1.80	0.62
3:J:724:THR:C	3:J:726:GLU:N	2.54	0.62
1:E:450:GLU:O	1:E:454:ILE:HG13	1.99	0.62
1:M:817:VAL:HA	1:M:820:ILE:HG12	1.81	0.62
2:K:349:ALA:O	2:K:353:ARG:HG3	1.99	0.62
3:B:1012:ARG:HB2	4:N:1101:FAR:H141	1.81	0.62
3:F:800:ILE:O	3:F:804:LEU:HG	1.99	0.62
3:J:172:ILE:HG21	3:J:212:VAL:HG21	1.80	0.62
3:N:283:LEU:HA	3:N:285:ARG:H	1.64	0.62
2:C:349:ALA:O	2:C:353:ARG:HG3	1.99	0.62
2:G:332:ILE:CG1	2:G:340:LEU:HD13	2.28	0.62
3:F:223:ARG:NH2	3:F:338:TYR:HA	2.14	0.62
3:F:279:LEU:O	3:F:283:LEU:HB2	2.00	0.62
3:N:173:ASN:OD1	3:N:173:ASN:C	2.42	0.62
1:A:768:LEU:HD23	1:A:802:ARG:HH21	1.24	0.62
1:M:444:ILE:HG12	1:M:586:LEU:HD22	1.82	0.62
1:I:68:ASP:OD2	3:J:259:GLY:O	2.16	0.62
1:I:444:ILE:HG12	1:I:586:LEU:HD22	1.81	0.62
1:I:1137:LEU:HD13	4:I:1301:FAR:C6	2.19	0.62
1:I:1168:THR:C	1:I:1170:GLY:N	2.52	0.62
3:F:143:PRO:CB	3:F:215:VAL:CG2	2.71	0.62
3:F:173:ASN:OD1	3:F:173:ASN:C	2.42	0.62
3:J:625:ASN:O	3:J:634:ILE:HD11	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:223:ARG:NH2	3:N:338:TYR:HA	2.14	0.62
3:N:288:ARG:HH11	3:N:978:ASN:HD21	1.48	0.62
3:F:172:ILE:HG21	3:F:212:VAL:HG21	1.80	0.62
3:J:288:ARG:HH11	3:J:978:ASN:HD21	1.48	0.62
1:A:899:VAL:O	1:A:903:MET:HG3	2.00	0.62
1:A:930:GLU:HA	1:A:933:HIS:CD2	2.34	0.62
1:E:28:PRO:CG	3:F:547:LEU:HD23	2.02	0.62
1:I:19:GLN:HA	1:I:23:LEU:HB2	1.81	0.62
1:I:450:GLU:O	1:I:454:ILE:HG13	1.99	0.62
1:E:444:ILE:HG12	1:E:586:LEU:HD22	1.81	0.62
1:E:930:GLU:HA	1:E:933:HIS:CD2	2.34	0.62
1:M:491:ARG:HG3	3:N:62:LEU:CD1	2.30	0.62
1:I:72:ALA:HB2	3:J:260:CYS:HB2	1.81	0.62
1:I:83:LYS:HE3	3:J:198:GLU:OE1	2.00	0.62
1:I:899:VAL:O	1:I:903:MET:HG3	2.00	0.62
3:B:223:ARG:NH2	3:B:338:TYR:HA	2.14	0.62
3:F:625:ASN:C	3:F:634:ILE:CD1	2.73	0.62
3:N:625:ASN:C	3:N:634:ILE:CD1	2.73	0.62
1:A:450:GLU:O	1:A:454:ILE:HG13	1.99	0.62
1:E:176:TYR:HB2	1:E:241:ILE:HD13	1.81	0.62
1:M:930:GLU:HA	1:M:933:HIS:CD2	2.34	0.62
1:I:491:ARG:HG3	3:J:62:LEU:CD1	2.29	0.62
1:I:1127:LEU:HD22	1:I:1151:VAL:HG12	1.81	0.62
3:J:173:ASN:OD1	3:J:173:ASN:C	2.42	0.62
3:J:625:ASN:C	3:J:634:ILE:CD1	2.73	0.62
3:N:1015:GLU:OE2	4:N:1101:FAR:H42	1.99	0.62
1:A:444:ILE:HG12	1:A:586:LEU:HD22	1.81	0.62
1:E:899:VAL:O	1:E:903:MET:HG3	2.00	0.62
3:B:1060:LEU:HD23	3:N:1082:VAL:HG21	1.80	0.62
1:A:1200:MET:HE2	2:C:354:ILE:HD12	1.82	0.62
3:B:173:ASN:OD1	3:B:173:ASN:C	2.42	0.62
1:A:69:GLU:CG	3:B:262:TRP:HZ3	2.13	0.61
1:A:1086:SER:OG	1:A:1148:ILE:HG22	2.00	0.61
1:A:1127:LEU:HD22	1:A:1151:VAL:HG12	1.81	0.61
1:E:1127:LEU:HD22	1:E:1151:VAL:HG12	1.81	0.61
1:M:899:VAL:O	1:M:903:MET:HG3	2.00	0.61
3:B:310:GLU:OE2	3:B:473:LEU:HB2	2.00	0.61
1:E:791:GLY:H	1:E:792:PRO:HD2	1.66	0.61
3:J:143:PRO:CB	3:J:215:VAL:CG2	2.71	0.61
3:J:172:ILE:O	3:J:172:ILE:HG22	2.00	0.61
1:E:19:GLN:HA	1:E:23:LEU:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:288:ARG:HH11	3:F:978:ASN:HD21	1.48	0.61
1:I:791:GLY:H	1:I:792:PRO:HD2	1.66	0.61
3:J:223:ARG:NH2	3:J:338:TYR:HA	2.14	0.61
1:E:94:ARG:HH12	3:F:157:THR:HA	1.60	0.61
1:E:1086:SER:OG	1:E:1148:ILE:HG22	2.00	0.61
1:I:1086:SER:OG	1:I:1148:ILE:HG22	2.00	0.61
3:J:310:GLU:OE2	3:J:473:LEU:HB2	2.00	0.61
1:A:931:LEU:HD11	1:A:949:LEU:HD11	1.80	0.61
1:M:1086:SER:OG	1:M:1148:ILE:HG22	2.00	0.61
1:I:1200:MET:HE2	2:K:354:ILE:HD12	1.82	0.61
3:F:172:ILE:HG22	3:F:172:ILE:O	2.00	0.61
3:F:724:THR:C	3:F:726:GLU:N	2.54	0.61
1:M:768:LEU:HD22	1:M:802:ARG:HH21	1.60	0.61
3:B:460:SER:CB	3:F:477:ARG:HH22	2.14	0.61
3:B:625:ASN:C	3:B:634:ILE:CD1	2.73	0.61
3:F:283:LEU:HD23	3:F:307:LEU:CG	2.31	0.61
3:F:1070:THR:OG1	4:F:1103:FAR:C10	2.48	0.61
4:F:1103:FAR:C1	3:J:1090:CYS:HG	1.10	0.61
3:J:872:LEU:HB3	3:J:984:GLU:OE2	2.01	0.61
1:M:1200:MET:HE2	2:O:354:ILE:HD12	1.82	0.61
3:N:1090:CYS:HG	4:N:1101:FAR:H12A	0.44	0.61
1:I:491:ARG:HG3	3:J:62:LEU:HD12	1.83	0.61
3:J:727:ILE:HG22	3:J:747:LEU:HD11	1.83	0.61
3:J:974:MET:HE1	3:J:975:TYR:HH	1.64	0.61
3:N:310:GLU:OE2	3:N:473:LEU:HB2	2.00	0.61
1:M:791:GLY:H	1:M:792:PRO:HD2	1.66	0.60
1:A:28:PRO:HG2	3:B:547:LEU:HD21	1.34	0.60
1:E:72:ALA:CB	3:F:260:CYS:HB2	2.31	0.60
1:E:1200:MET:HE2	2:G:354:ILE:HD12	1.82	0.60
1:E:1208:ALA:CB	2:G:334:ILE:HG12	2.32	0.60
1:M:926:VAL:HG23	1:M:1059:ARG:HG2	1.83	0.60
4:M:1301:FAR:H2	2:O:330:ARG:HG3	1.83	0.60
3:N:172:ILE:HG22	3:N:172:ILE:O	2.00	0.60
1:A:95:GLN:HE22	1:A:113:HIS:CG	2.19	0.60
1:M:1127:LEU:HD22	1:M:1151:VAL:HG12	1.81	0.60
3:B:811:THR:OG1	3:B:875:ARG:HA	2.02	0.60
3:N:727:ILE:HG22	3:N:747:LEU:HD11	1.83	0.60
1:A:961:ILE:HG22	1:A:1064:LEU:HD21	1.84	0.60
1:M:961:ILE:HG22	1:M:1064:LEU:HD21	1.84	0.60
3:B:477:ARG:NH1	3:F:103:ARG:NH2	2.49	0.60
1:A:75:TYR:HH	3:B:191:GLN:HB3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:68:ASP:CG	3:F:259:GLY:O	2.45	0.60
2:K:332:ILE:CG1	2:K:340:LEU:HD13	2.28	0.60
1:I:928:ALA:HB1	1:I:943:THR:HG22	1.84	0.60
4:I:1301:FAR:H2	2:K:330:ARG:HG3	1.83	0.60
3:F:811:THR:OG1	3:F:875:ARG:HA	2.02	0.60
3:F:965:GLN:CD	3:F:969:LEU:HD11	2.22	0.60
1:I:961:ILE:HG22	1:I:1064:LEU:HD21	1.84	0.60
1:I:1120:GLN:NE2	1:I:1181:ALA:HB1	2.03	0.60
3:B:172:ILE:O	3:B:172:ILE:HG22	2.00	0.60
3:F:1004:MET:HB3	3:J:1092:ILE:CG2	2.32	0.60
4:F:1101:FAR:H101	3:J:1070:THR:OG1	2.01	0.60
1:A:926:VAL:HG23	1:A:1059:ARG:HG2	1.83	0.60
1:E:547:LEU:HD11	1:E:589:MET:HE3	1.84	0.60
1:M:120:THR:HG22	3:N:131:ARG:NE	2.15	0.60
1:M:928:ALA:HB1	1:M:943:THR:HG22	1.84	0.60
1:I:547:LEU:HD11	1:I:589:MET:HE3	1.84	0.60
3:F:283:LEU:HB3	3:F:312:LEU:HD13	1.83	0.60
3:F:310:GLU:OE2	3:F:473:LEU:HB2	2.01	0.60
1:M:95:GLN:HE22	1:M:113:HIS:CG	2.19	0.60
3:F:1013:ASN:ND2	4:F:1101:FAR:C15	2.59	0.60
1:E:928:ALA:HB1	1:E:943:THR:HG22	1.84	0.60
1:I:491:ARG:HG2	3:J:62:LEU:HD11	1.84	0.60
3:F:1013:ASN:OD1	4:F:1101:FAR:C13	2.50	0.60
1:A:928:ALA:HB1	1:A:943:THR:HG22	1.84	0.59
1:E:926:VAL:HG23	1:E:1059:ARG:HG2	1.83	0.59
1:M:63:LYS:C	3:J:567:ARG:NH2	2.57	0.59
1:I:491:ARG:CG	3:J:62:LEU:HD11	2.32	0.59
3:B:625:ASN:O	3:B:634:ILE:HD11	1.98	0.59
3:B:625:ASN:HB3	3:B:634:ILE:HD13	1.84	0.59
3:N:143:PRO:HB2	3:N:215:VAL:HG22	1.79	0.59
3:N:795:SER:OG	3:N:855:ILE:HD11	2.02	0.59
1:M:547:LEU:HD11	1:M:589:MET:HE3	1.84	0.59
1:I:95:GLN:HE22	1:I:113:HIS:CG	2.19	0.59
3:N:811:THR:OG1	3:N:875:ARG:HA	2.02	0.59
1:A:791:GLY:H	1:A:792:PRO:HD2	1.66	0.59
1:E:28:PRO:CG	3:F:547:LEU:CG	2.70	0.59
1:M:120:THR:HG21	3:N:131:ARG:NH2	2.16	0.59
1:I:1208:ALA:CB	2:K:334:ILE:HG12	2.32	0.59
3:J:177:LEU:HD11	3:J:303:PRO:HG3	1.84	0.59
3:N:803:PHE:CG	3:N:810:VAL:CG2	2.86	0.59
1:A:1208:ALA:CB	2:C:334:ILE:HG12	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1215:LEU:HB3	2:K:330:ARG:HH22	1.67	0.59
3:B:872:LEU:HB3	3:B:984:GLU:OE2	2.01	0.59
3:F:177:LEU:HD11	3:F:303:PRO:HG3	1.84	0.59
3:F:795:SER:OG	3:F:855:ILE:HD11	2.02	0.59
3:F:872:LEU:HB3	3:F:984:GLU:OE2	2.01	0.59
3:J:803:PHE:CG	3:J:810:VAL:CG2	2.85	0.59
3:N:872:LEU:HB3	3:N:984:GLU:OE2	2.01	0.59
4:A:1301:FAR:H2	2:C:330:ARG:HG3	1.83	0.59
1:E:95:GLN:HE22	1:E:113:HIS:CG	2.19	0.59
3:F:727:ILE:HG22	3:F:747:LEU:HD11	1.83	0.59
2:C:332:ILE:CG1	2:C:340:LEU:HD13	2.28	0.59
1:E:1081:LYS:CB	4:E:1301:FAR:H143	2.33	0.59
2:K:356:GLY:O	2:K:359:VAL:HG12	2.03	0.59
3:F:803:PHE:CG	3:F:810:VAL:CG2	2.86	0.59
3:F:1091:LEU:HB2	3:J:1004:MET:CE	2.32	0.59
3:J:132:GLN:HE22	3:J:150:HIS:CG	2.20	0.59
3:N:342:LEU:HD22	3:N:421:LYS:HZ1	1.67	0.59
3:N:625:ASN:HB3	3:N:634:ILE:HD13	1.84	0.59
1:A:547:LEU:HD11	1:A:589:MET:HE3	1.84	0.59
1:E:352:LYS:HD2	1:E:352:LYS:O	2.03	0.59
1:E:445:LEU:CD1	1:E:563:THR:HG23	2.30	0.59
1:E:1215:LEU:HB3	2:G:330:ARG:HH22	1.67	0.59
1:M:491:ARG:CG	3:N:62:LEU:HD11	2.32	0.59
2:O:356:GLY:O	2:O:359:VAL:HG12	2.03	0.59
1:I:445:LEU:CD1	1:I:563:THR:HG23	2.30	0.59
3:F:1059:PRO:HG3	3:J:1093:SER:C	2.27	0.59
1:E:961:ILE:HG22	1:E:1064:LEU:HD21	1.84	0.59
1:I:926:VAL:HG23	1:I:1059:ARG:HG2	1.83	0.59
3:B:803:PHE:CG	3:B:810:VAL:CG2	2.86	0.59
3:F:1015:GLU:CG	3:J:1012:ARG:HH22	2.15	0.59
1:M:352:LYS:HD2	1:M:352:LYS:O	2.03	0.59
3:B:283:LEU:HB3	3:B:312:LEU:HD13	1.84	0.59
1:M:491:ARG:HG3	3:N:62:LEU:HD12	1.84	0.59
1:I:1081:LYS:CB	4:I:1301:FAR:H143	2.32	0.59
3:J:493:LEU:HD21	3:J:615:PRO:CG	2.33	0.59
1:A:1081:LYS:CB	4:A:1301:FAR:H143	2.32	0.58
1:M:1208:ALA:CB	2:O:334:ILE:HG12	2.32	0.58
3:B:529:TRP:CD1	3:B:684:SER:HB3	2.39	0.58
3:B:727:ILE:HG22	3:B:747:LEU:HD11	1.83	0.58
3:J:811:THR:OG1	3:J:875:ARG:HA	2.02	0.58
3:N:132:GLN:HE22	3:N:150:HIS:CG	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:501:ALA:O	3:N:520:PRO:HD3	2.03	0.58
2:C:356:GLY:O	2:C:359:VAL:HG12	2.03	0.58
1:M:930:GLU:OE2	1:M:933:HIS:NE2	2.36	0.58
3:F:68:THR:HB	3:F:70:LEU:HD12	1.86	0.58
3:F:501:ALA:O	3:F:520:PRO:HD3	2.03	0.58
3:F:1004:MET:HG3	3:J:1092:ILE:HG22	1.84	0.58
3:F:1015:GLU:CD	3:J:1012:ARG:HH22	2.11	0.58
3:J:460:SER:HB2	3:N:477:ARG:NH2	2.18	0.58
1:A:894:THR:HA	1:A:920:ILE:HG21	1.85	0.58
1:E:75:TYR:CD1	3:F:258:GLN:HB2	2.38	0.58
1:M:768:LEU:HD23	1:M:802:ARG:HH21	1.24	0.58
1:M:1215:LEU:HB3	2:O:330:ARG:HH22	1.67	0.58
1:I:352:LYS:HD2	1:I:352:LYS:O	2.03	0.58
3:B:132:GLN:HE22	3:B:150:HIS:CG	2.20	0.58
3:N:53:TYR:CZ	3:N:57:LYS:HG3	2.39	0.58
3:N:177:LEU:HD11	3:N:303:PRO:HG3	1.84	0.58
1:A:332:TRP:HH2	1:A:352:LYS:HZ2	1.50	0.58
1:A:1120:GLN:HE22	1:A:1182:SER:N	2.02	0.58
1:E:509:LYS:HG2	1:E:554:TRP:HH2	1.69	0.58
1:E:926:VAL:HG13	1:E:961:ILE:HD12	1.86	0.58
1:E:930:GLU:OE2	1:E:933:HIS:NE2	2.36	0.58
4:E:1301:FAR:H2	2:G:330:ARG:HG3	1.83	0.58
1:M:1081:LYS:CB	4:M:1301:FAR:H143	2.33	0.58
1:I:163:ASN:CB	1:I:489:ASN:HD21	2.16	0.58
3:F:132:GLN:HE22	3:F:150:HIS:CG	2.20	0.58
3:F:283:LEU:O	3:F:284:PRO:C	2.45	0.58
3:J:53:TYR:CZ	3:J:57:LYS:HG3	2.39	0.58
3:N:586:TYR:CB	3:N:782:VAL:HG12	2.33	0.58
1:A:352:LYS:O	1:A:352:LYS:HD2	2.03	0.58
1:A:930:GLU:OE2	1:A:933:HIS:NE2	2.35	0.58
2:G:356:GLY:O	2:G:359:VAL:HG12	2.03	0.58
3:B:493:LEU:HD21	3:B:615:PRO:CG	2.33	0.58
3:B:795:SER:OG	3:B:855:ILE:HD11	2.02	0.58
3:F:625:ASN:HB3	3:F:634:ILE:HD13	1.84	0.58
3:J:68:THR:HB	3:J:70:LEU:HD12	1.86	0.58
3:N:493:LEU:HD21	3:N:615:PRO:CG	2.33	0.58
3:N:529:TRP:CD1	3:N:684:SER:HB3	2.39	0.58
1:E:888:MET:HA	1:E:888:MET:HE3	1.86	0.58
1:E:1120:GLN:HE22	1:E:1182:SER:N	2.02	0.58
1:I:1209:THR:HG23	2:K:334:ILE:HG23	1.86	0.58
3:B:501:ALA:O	3:B:520:PRO:HD3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:148:CYS:HB3	3:F:170:LEU:HD13	1.86	0.58
3:F:734:CYS:SG	3:F:743:LEU:HD12	2.44	0.58
3:F:780:LEU:HG	3:F:784:TYR:CE2	2.39	0.58
3:J:143:PRO:HB2	3:J:215:VAL:HG22	1.79	0.58
3:J:501:ALA:O	3:J:520:PRO:HD3	2.03	0.58
3:N:734:CYS:SG	3:N:743:LEU:HD12	2.44	0.58
1:A:1215:LEU:HB3	2:C:330:ARG:HH22	1.67	0.58
2:C:359:VAL:HG21	2:C:367:ARG:CG	2.32	0.58
1:M:894:THR:HA	1:M:920:ILE:HG21	1.85	0.58
1:I:930:GLU:OE2	1:I:933:HIS:NE2	2.35	0.58
3:B:1012:ARG:HB2	4:N:1101:FAR:H142	1.85	0.58
3:J:586:TYR:CB	3:J:782:VAL:HG12	2.34	0.58
3:J:625:ASN:HB3	3:J:634:ILE:HD13	1.84	0.58
3:J:630:ARG:HE	3:J:777:LYS:HE3	1.68	0.58
1:M:509:LYS:HG2	1:M:554:TRP:HH2	1.69	0.58
1:I:926:VAL:HG13	1:I:961:ILE:HD12	1.86	0.58
3:B:126:LEU:HB2	3:B:178:TYR:OH	2.03	0.58
3:B:328:TYR:CD2	3:B:429:ARG:HD2	2.39	0.58
3:F:126:LEU:HB2	3:F:178:TYR:OH	2.04	0.58
3:F:493:LEU:HD21	3:F:615:PRO:CG	2.33	0.58
3:F:731:LEU:HD21	3:F:744:LEU:HB2	1.86	0.58
1:A:509:LYS:HG2	1:A:554:TRP:HH2	1.69	0.58
1:A:1168:THR:C	1:A:1170:GLY:N	2.52	0.58
1:E:75:TYR:CD1	3:F:258:GLN:CB	2.87	0.58
1:M:265:PHE:CD2	1:M:337:LEU:HD13	2.39	0.58
1:M:445:LEU:CD1	1:M:563:THR:HG23	2.30	0.58
1:M:1209:THR:HG23	2:O:334:ILE:HG23	1.86	0.58
3:B:279:LEU:O	3:B:283:LEU:HB2	2.04	0.58
3:J:328:TYR:CD2	3:J:429:ARG:HD2	2.39	0.58
3:N:126:LEU:HB2	3:N:178:TYR:OH	2.03	0.58
1:A:163:ASN:CB	1:A:489:ASN:HD21	2.16	0.58
1:A:926:VAL:HG13	1:A:961:ILE:HD12	1.86	0.58
1:E:65:ALA:N	3:B:567:ARG:HH21	2.01	0.58
1:E:93:ILE:CG2	3:F:67:THR:HG23	2.23	0.58
1:E:206:LYS:NZ	1:E:210:GLU:OE2	2.37	0.58
1:E:265:PHE:CD2	1:E:337:LEU:HD13	2.39	0.58
1:M:926:VAL:HG13	1:M:961:ILE:HD12	1.86	0.58
3:F:630:ARG:HE	3:F:777:LYS:HE3	1.68	0.58
3:J:98:ALA:HB1	3:J:115:GLU:HG3	1.86	0.58
3:J:731:LEU:HD21	3:J:744:LEU:HB2	1.86	0.58
3:J:780:LEU:HG	3:J:784:TYR:CE2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:328:TYR:CD2	3:N:429:ARG:HD2	2.39	0.58
1:A:265:PHE:CD2	1:A:337:LEU:HD13	2.39	0.57
1:E:251:THR:HA	1:E:1105:ILE:HG13	1.86	0.57
1:I:888:MET:HA	1:I:888:MET:HE3	1.86	0.57
2:K:359:VAL:HG21	2:K:367:ARG:CG	2.32	0.57
3:B:53:TYR:CZ	3:B:57:LYS:HG3	2.39	0.57
3:B:148:CYS:HB3	3:B:170:LEU:HD13	1.86	0.57
3:B:477:ARG:NH2	3:F:460:SER:HB2	2.18	0.57
3:B:1060:LEU:HB3	3:N:1082:VAL:HG23	1.85	0.57
3:F:586:TYR:CB	3:F:782:VAL:HG12	2.33	0.57
3:J:45:LEU:HD23	3:J:104:ILE:HG13	1.86	0.57
1:M:206:LYS:NZ	1:M:210:GLU:OE2	2.37	0.57
1:I:509:LYS:HG2	1:I:554:TRP:HH2	1.69	0.57
3:B:586:TYR:CB	3:B:782:VAL:HG12	2.33	0.57
3:F:53:TYR:CZ	3:F:57:LYS:HG3	2.39	0.57
3:J:965:GLN:CD	3:J:969:LEU:HD11	2.22	0.57
3:N:780:LEU:HG	3:N:784:TYR:CE2	2.39	0.57
1:E:1137:LEU:HD13	4:E:1301:FAR:C6	2.19	0.57
1:E:1140:ILE:H	1:E:1140:ILE:HD12	1.70	0.57
1:M:922:LEU:HD22	1:M:1121:PRO:HG3	1.86	0.57
1:M:1120:GLN:HE22	1:M:1182:SER:N	2.02	0.57
1:I:1081:LYS:HB3	4:I:1301:FAR:C14	2.35	0.57
1:I:1140:ILE:HD12	1:I:1140:ILE:H	1.69	0.57
3:B:734:CYS:SG	3:B:743:LEU:HD12	2.44	0.57
3:N:45:LEU:HD23	3:N:104:ILE:HG13	1.87	0.57
3:N:98:ALA:HB1	3:N:115:GLU:HG3	1.86	0.57
1:E:75:TYR:CZ	3:F:191:GLN:OE1	2.57	0.57
1:M:1137:LEU:HD13	4:M:1301:FAR:C6	2.19	0.57
1:I:1120:GLN:HE22	1:I:1182:SER:N	2.02	0.57
3:B:74:LYS:CD	3:B:439:LYS:HZ1	2.07	0.57
3:F:328:TYR:CD2	3:F:429:ARG:HD2	2.39	0.57
3:J:529:TRP:CD1	3:J:684:SER:HB3	2.39	0.57
3:N:630:ARG:HE	3:N:777:LYS:HE3	1.68	0.57
3:N:731:LEU:HD21	3:N:744:LEU:HB2	1.86	0.57
3:N:965:GLN:CD	3:N:969:LEU:HD11	2.22	0.57
1:A:206:LYS:NZ	1:A:210:GLU:OE2	2.37	0.57
1:I:265:PHE:CD2	1:I:337:LEU:HD13	2.39	0.57
2:K:350:TYR:O	2:K:354:ILE:HG13	2.05	0.57
3:B:45:LEU:HD23	3:B:104:ILE:HG13	1.86	0.57
3:B:68:THR:HB	3:B:70:LEU:HD12	1.86	0.57
3:B:853:LEU:HD12	3:B:880:ILE:CD1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:45:LEU:HD23	3:F:104:ILE:HG13	1.86	0.57
3:F:98:ALA:HB1	3:F:115:GLU:HG3	1.86	0.57
3:J:63:TYR:O	3:J:72:PRO:HD3	2.05	0.57
1:E:1208:ALA:HB1	2:G:334:ILE:HG13	1.86	0.57
1:M:1140:ILE:H	1:M:1140:ILE:HD12	1.69	0.57
2:O:359:VAL:HG21	2:O:367:ARG:CG	2.32	0.57
1:I:922:LEU:HD22	1:I:1121:PRO:HG3	1.87	0.57
3:J:126:LEU:HB2	3:J:178:TYR:OH	2.03	0.57
3:N:68:THR:HB	3:N:70:LEU:HD12	1.86	0.57
3:N:342:LEU:CD2	3:N:421:LYS:HZ1	2.18	0.57
1:I:93:ILE:CG2	3:J:67:THR:HG23	2.31	0.57
1:I:1208:ALA:HB1	2:K:334:ILE:HG13	1.86	0.57
3:B:392:LEU:HG	3:B:396:LEU:HG	1.87	0.57
3:F:361:ILE:CD1	3:F:421:LYS:HE2	2.35	0.57
3:N:853:LEU:HD12	3:N:880:ILE:CD1	2.35	0.57
1:A:1208:ALA:HB1	2:C:334:ILE:HG13	1.86	0.57
1:A:1209:THR:HG23	2:C:334:ILE:HG23	1.86	0.57
1:M:1200:MET:CE	2:O:351:ALA:HA	2.35	0.57
1:I:75:TYR:OH	3:J:191:GLN:CD	2.47	0.57
3:B:98:ALA:HB1	3:B:115:GLU:HG3	1.86	0.57
3:B:177:LEU:HD11	3:B:303:PRO:HG3	1.84	0.57
3:B:630:ARG:HE	3:B:777:LYS:HE3	1.68	0.57
3:B:742:ILE:HA	3:B:788:PHE:HE2	1.70	0.57
3:B:1093:SER:C	3:N:1059:PRO:HG3	2.28	0.57
3:F:948:ILE:HD11	3:F:1007:SER:CA	2.35	0.57
1:A:72:ALA:HB2	3:B:260:CYS:HB2	1.87	0.57
3:B:965:GLN:CD	3:B:969:LEU:HD11	2.22	0.57
3:F:392:LEU:HG	3:F:396:LEU:HG	1.87	0.57
3:F:938:PRO:CG	3:J:1092:ILE:HB	2.35	0.57
3:J:586:TYR:HA	3:J:589:GLN:HE22	1.70	0.57
3:J:853:LEU:HD12	3:J:880:ILE:CD1	2.35	0.57
3:N:63:TYR:O	3:N:72:PRO:HD3	2.05	0.57
1:A:445:LEU:CD1	1:A:563:THR:HG23	2.30	0.57
1:A:768:LEU:HD22	1:A:802:ARG:HH21	1.60	0.57
1:E:28:PRO:HB2	3:F:130:MET:HE2	1.77	0.57
1:E:1209:THR:HG23	2:G:334:ILE:HG23	1.86	0.57
2:O:350:TYR:O	2:O:354:ILE:HG13	2.05	0.57
3:B:780:LEU:HG	3:B:784:TYR:CE2	2.39	0.57
3:F:63:TYR:O	3:F:72:PRO:HD3	2.05	0.57
3:J:734:CYS:SG	3:J:743:LEU:HD12	2.44	0.57
3:N:392:LEU:HG	3:N:396:LEU:HG	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:MET:HA	1:A:888:MET:HE3	1.86	0.56
2:C:350:TYR:O	2:C:354:ILE:HG13	2.05	0.56
1:E:163:ASN:CB	1:E:489:ASN:HD21	2.16	0.56
3:J:148:CYS:HB3	3:J:170:LEU:HD13	1.86	0.56
3:J:574:VAL:HG23	3:J:618:LEU:HD11	1.87	0.56
1:A:51:ILE:HD13	1:A:84:LEU:HD13	1.87	0.56
1:A:251:THR:HA	1:A:1105:ILE:HG13	1.86	0.56
1:A:491:ARG:HG3	3:B:62:LEU:CD1	2.36	0.56
1:A:922:LEU:HD22	1:A:1121:PRO:HG3	1.87	0.56
1:A:1205:LYS:HG3	2:C:337:PRO:HG2	1.87	0.56
1:E:29:VAL:HG13	3:F:130:MET:HB2	1.87	0.56
1:E:29:VAL:HG22	3:F:130:MET:HB3	1.87	0.56
1:E:90:HIS:HD2	3:F:67:THR:O	1.88	0.56
1:E:1200:MET:CE	2:G:351:ALA:HA	2.35	0.56
2:G:359:VAL:HG21	2:G:367:ARG:CG	2.32	0.56
1:M:29:VAL:HG11	3:N:131:ARG:HG2	1.87	0.56
1:M:888:MET:HA	1:M:888:MET:HE3	1.86	0.56
1:M:1205:LYS:HG3	2:O:337:PRO:HG2	1.87	0.56
1:I:75:TYR:HH	3:J:191:GLN:HB3	1.70	0.56
1:I:894:THR:HA	1:I:920:ILE:HG21	1.85	0.56
3:B:236:SER:HB2	3:B:296:LEU:HD21	1.87	0.56
3:B:784:TYR:CD1	3:B:845:ARG:HD3	2.41	0.56
1:A:1200:MET:CE	2:C:351:ALA:HA	2.35	0.56
1:E:894:THR:HA	1:E:920:ILE:HG21	1.85	0.56
1:M:51:ILE:HD13	1:M:84:LEU:HD13	1.87	0.56
1:M:163:ASN:CB	1:M:489:ASN:HD21	2.16	0.56
1:M:251:THR:HA	1:M:1105:ILE:HG13	1.86	0.56
1:M:1208:ALA:HB2	4:M:1301:FAR:H51	1.88	0.56
1:M:1208:ALA:HB1	2:O:334:ILE:HG13	1.86	0.56
1:I:206:LYS:NZ	1:I:210:GLU:OE2	2.37	0.56
1:I:251:THR:HA	1:I:1105:ILE:HG13	1.85	0.56
1:I:1200:MET:CE	2:K:351:ALA:HA	2.35	0.56
3:B:393:THR:HB	3:B:394:PRO:HD3	1.87	0.56
3:B:731:LEU:HD21	3:B:744:LEU:HB2	1.86	0.56
3:B:1063:ARG:NH1	3:N:1079:GLU:HG2	2.19	0.56
3:B:1078:LEU:HD22	3:N:1067:SER:HB2	1.85	0.56
3:F:393:THR:HB	3:F:394:PRO:HD3	1.87	0.56
3:F:529:TRP:CD1	3:F:684:SER:HB3	2.38	0.56
3:F:586:TYR:HA	3:F:589:GLN:HE22	1.70	0.56
3:F:742:ILE:HA	3:F:788:PHE:HE2	1.70	0.56
3:F:853:LEU:HD12	3:F:880:ILE:CD1	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1002:LEU:CD2	3:F:1024:LEU:HD22	2.35	0.56
3:N:148:CYS:HB3	3:N:170:LEU:HD13	1.86	0.56
3:N:668:LEU:HG	3:N:670:PHE:CE2	2.41	0.56
1:A:1081:LYS:HB3	4:A:1301:FAR:C14	2.35	0.56
1:A:1208:ALA:HB2	4:A:1301:FAR:H51	1.88	0.56
1:E:922:LEU:HD22	1:E:1121:PRO:HG3	1.86	0.56
3:B:63:TYR:O	3:B:72:PRO:HD3	2.05	0.56
3:B:726:GLU:C	3:B:729:GLN:H	2.14	0.56
3:J:392:LEU:HG	3:J:396:LEU:HG	1.87	0.56
3:J:784:TYR:CD1	3:J:845:ARG:HD3	2.40	0.56
3:N:586:TYR:HA	3:N:589:GLN:HE22	1.70	0.56
3:N:742:ILE:HA	3:N:788:PHE:HE2	1.70	0.56
3:B:574:VAL:HG23	3:B:618:LEU:HD11	1.87	0.56
3:B:730:LYS:HB2	3:B:743:LEU:HD13	1.88	0.56
3:B:948:ILE:HD11	3:B:1007:SER:CA	2.35	0.56
3:F:574:VAL:HG23	3:F:618:LEU:HD11	1.87	0.56
3:F:850:GLN:HG3	3:F:880:ILE:CD1	2.36	0.56
3:F:1004:MET:HE2	3:J:1091:LEU:HB2	1.85	0.56
3:N:393:THR:HB	3:N:394:PRO:HD3	1.88	0.56
1:A:397:LYS:HE3	1:A:400:HIS:HD2	1.71	0.56
1:M:1081:LYS:HB3	4:M:1301:FAR:C14	2.35	0.56
1:I:51:ILE:HD13	1:I:84:LEU:HD13	1.87	0.56
1:I:893:LEU:HD11	1:I:947:MET:HE1	1.88	0.56
1:I:1208:ALA:HB2	4:I:1301:FAR:H51	1.88	0.56
3:J:236:SER:HB2	3:J:296:LEU:HD21	1.87	0.56
3:J:393:THR:HB	3:J:394:PRO:HD3	1.88	0.56
3:J:668:LEU:HG	3:J:670:PHE:CE2	2.40	0.56
3:N:574:VAL:HG23	3:N:618:LEU:HD11	1.87	0.56
3:N:726:GLU:C	3:N:729:GLN:H	2.14	0.56
1:A:1140:ILE:HD12	1:A:1140:ILE:H	1.69	0.56
1:E:893:LEU:HD11	1:E:947:MET:HE1	1.88	0.56
3:F:730:LYS:HB2	3:F:743:LEU:HD13	1.88	0.56
3:F:784:TYR:CD1	3:F:845:ARG:HD3	2.41	0.56
3:F:918:GLN:HE22	3:F:922:ARG:HH11	1.54	0.56
3:J:298:PRO:O	3:J:301:SER:O	2.24	0.56
3:J:948:ILE:HD11	3:J:1007:SER:CA	2.35	0.56
1:E:79:GLN:HB3	3:F:194:TYR:HB3	1.87	0.56
1:M:574:ASP:OD1	1:M:574:ASP:N	2.39	0.56
3:B:668:LEU:HG	3:B:670:PHE:CE2	2.41	0.56
3:F:668:LEU:HG	3:F:670:PHE:CE2	2.40	0.56
3:J:730:LYS:HB2	3:J:743:LEU:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:730:LYS:HB2	3:N:743:LEU:HD13	1.88	0.56
3:N:850:GLN:HG3	3:N:880:ILE:CD1	2.36	0.56
3:N:1002:LEU:CD2	3:N:1024:LEU:HD22	2.35	0.56
1:A:788:THR:O	1:A:792:PRO:HG2	2.03	0.56
1:A:893:LEU:HD11	1:A:947:MET:HE1	1.88	0.56
1:E:86:ARG:HH22	3:F:120:LYS:HG3	1.69	0.56
1:E:419:ALA:CB	3:B:524:GLU:OE1	2.47	0.56
1:E:491:ARG:CD	3:F:62:LEU:HG	2.36	0.56
1:E:846:ASP:O	1:E:849:SER:OG	2.23	0.56
3:B:1092:ILE:HD12	3:N:1001:GLU:CA	2.35	0.56
3:B:1092:ILE:HD12	3:N:1001:GLU:CG	1.94	0.56
3:F:298:PRO:O	3:F:301:SER:O	2.24	0.56
3:F:726:GLU:C	3:F:729:GLN:H	2.14	0.56
3:J:477:ARG:NH2	3:N:460:SER:HB2	2.21	0.56
3:J:742:ILE:HA	3:J:788:PHE:HE2	1.70	0.56
3:J:751:GLU:HB3	3:J:755:PHE:CG	2.41	0.56
3:J:953:PRO:HD2	3:J:1018:PHE:O	2.06	0.56
3:N:953:PRO:HD2	3:N:1018:PHE:O	2.06	0.56
1:M:75:TYR:HH	3:N:191:GLN:HB3	1.70	0.56
3:B:283:LEU:O	3:B:316:THR:OG1	2.24	0.56
3:B:598:ILE:CD1	3:B:637:MET:SD	2.94	0.56
3:B:918:GLN:HE22	3:B:922:ARG:HH11	1.54	0.56
3:F:115:GLU:O	3:F:119:ILE:HD12	2.06	0.56
3:F:236:SER:HB2	3:F:296:LEU:HD21	1.87	0.56
3:F:283:LEU:CD2	3:F:307:LEU:HD21	2.31	0.56
3:F:953:PRO:HD2	3:F:1018:PHE:O	2.06	0.56
3:J:1002:LEU:CD2	3:J:1024:LEU:HD22	2.35	0.56
3:N:236:SER:HB2	3:N:296:LEU:HD21	1.87	0.56
3:N:598:ILE:CD1	3:N:637:MET:SD	2.94	0.56
1:M:397:LYS:HE3	1:M:400:HIS:HD2	1.71	0.55
1:I:332:TRP:HH2	1:I:352:LYS:HZ2	1.51	0.55
3:B:586:TYR:HA	3:B:589:GLN:HE22	1.70	0.55
3:B:850:GLN:HG3	3:B:880:ILE:CD1	2.36	0.55
3:F:598:ILE:CD1	3:F:637:MET:SD	2.94	0.55
3:F:751:GLU:HB3	3:F:755:PHE:CG	2.41	0.55
3:J:115:GLU:O	3:J:119:ILE:HD12	2.06	0.55
3:J:598:ILE:CD1	3:J:637:MET:SD	2.94	0.55
3:N:298:PRO:O	3:N:301:SER:O	2.24	0.55
3:N:784:TYR:CD1	3:N:845:ARG:HD3	2.41	0.55
1:A:339:GLY:HA2	1:A:344:ASN:HB2	1.89	0.55
1:A:919:ARG:HE	1:A:922:LEU:HD12	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:893:LEU:HD11	1:M:947:MET:HE1	1.88	0.55
1:M:919:ARG:HE	1:M:922:LEU:HD12	1.70	0.55
1:I:397:LYS:HE3	1:I:400:HIS:HD2	1.71	0.55
1:I:880:ILE:HD11	1:I:898:MET:HE1	1.89	0.55
3:B:298:PRO:O	3:B:301:SER:O	2.24	0.55
3:B:1018:PHE:CD2	3:B:1022:VAL:CG2	2.90	0.55
3:F:1082:VAL:CG2	3:J:1060:LEU:HD22	2.36	0.55
3:F:1091:LEU:HD23	3:J:944:ARG:NH1	2.22	0.55
4:F:1101:FAR:C14	3:J:1012:ARG:HB2	2.36	0.55
3:J:795:SER:OG	3:J:855:ILE:HD11	2.02	0.55
3:J:948:ILE:HD12	3:J:1010:LEU:HD12	1.89	0.55
1:E:51:ILE:HD13	1:E:84:LEU:HD13	1.87	0.55
1:M:339:GLY:HA2	1:M:344:ASN:HB2	1.89	0.55
1:M:880:ILE:HD11	1:M:898:MET:HE1	1.89	0.55
1:I:1205:LYS:HG3	2:K:337:PRO:HG2	1.87	0.55
3:B:751:GLU:HB3	3:B:755:PHE:CG	2.41	0.55
1:E:880:ILE:HD11	1:E:898:MET:HE1	1.88	0.55
2:G:350:TYR:O	2:G:354:ILE:HG13	2.05	0.55
3:B:949:LEU:HD22	3:B:963:LEU:CD2	2.37	0.55
3:B:953:PRO:HD2	3:B:1018:PHE:O	2.06	0.55
3:J:853:LEU:HD21	3:J:883:MET:HE1	1.89	0.55
3:N:115:GLU:O	3:N:119:ILE:HD12	2.06	0.55
1:E:919:ARG:HE	1:E:922:LEU:HD12	1.70	0.55
3:J:850:GLN:HG3	3:J:880:ILE:CD1	2.36	0.55
1:I:339:GLY:HA2	1:I:344:ASN:HB2	1.89	0.55
3:F:283:LEU:CD2	3:F:307:LEU:CD2	2.83	0.55
3:F:503:SER:OG	3:F:623:GLU:OE1	2.23	0.55
1:A:610:THR:HG22	3:F:635:LEU:CD2	2.37	0.55
1:E:397:LYS:HE3	1:E:400:HIS:HD2	1.71	0.55
1:E:1197:PHE:HE2	2:G:373:ASN:O	1.90	0.55
1:M:491:ARG:HG2	3:N:62:LEU:HD11	1.88	0.55
1:I:919:ARG:HE	1:I:922:LEU:HD12	1.70	0.55
3:B:367:ILE:HD11	3:B:447:LEU:HD12	1.89	0.55
3:B:477:ARG:HH22	3:F:460:SER:CB	2.20	0.55
3:F:213:TYR:O	3:F:234:LEU:HD21	2.07	0.55
3:F:569:LEU:HD13	3:F:679:LEU:HB3	1.89	0.55
3:F:948:ILE:HD12	3:F:1010:LEU:HD12	1.89	0.55
3:J:918:GLN:HE22	3:J:922:ARG:HH11	1.54	0.55
3:N:853:LEU:HD21	3:N:883:MET:HE1	1.89	0.55
1:A:574:ASP:N	1:A:574:ASP:OD1	2.39	0.55
1:E:152:GLY:HA3	3:B:661:SER:OG	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:809:LEU:HA	1:E:812:GLU:HB3	1.89	0.55
1:I:809:LEU:HA	1:I:812:GLU:HB3	1.89	0.55
1:I:1171:ALA:HB2	2:K:377:ALA:HB2	1.88	0.55
3:B:115:GLU:O	3:B:119:ILE:HD12	2.06	0.55
3:F:751:GLU:HB3	3:F:755:PHE:CB	2.37	0.55
3:F:1018:PHE:CD2	3:F:1022:VAL:CG2	2.90	0.55
3:N:948:ILE:HD12	3:N:1010:LEU:HD12	1.89	0.55
1:A:1197:PHE:HE2	2:C:373:ASN:O	1.90	0.55
1:E:788:THR:O	1:E:792:PRO:HG2	2.03	0.55
1:I:1208:ALA:CB	2:K:334:ILE:CG1	2.85	0.55
3:N:361:ILE:CD1	3:N:421:LYS:HE2	2.35	0.55
3:N:949:LEU:HD22	3:N:963:LEU:CD2	2.37	0.55
1:E:64:ASN:CA	3:B:567:ARG:HH21	2.19	0.55
1:M:1087:VAL:HG21	1:M:1115:LEU:HD12	1.89	0.55
1:M:1122:GLU:O	1:M:1123:TYR:C	2.48	0.55
1:M:1197:PHE:HE2	2:O:373:ASN:O	1.90	0.55
3:F:853:LEU:HD21	3:F:883:MET:HE1	1.89	0.55
3:J:726:GLU:C	3:J:729:GLN:H	2.14	0.55
3:N:751:GLU:HB3	3:N:755:PHE:CB	2.37	0.55
3:N:751:GLU:HB3	3:N:755:PHE:CG	2.41	0.55
3:N:948:ILE:HD11	3:N:1007:SER:CA	2.35	0.55
1:A:880:ILE:HD11	1:A:898:MET:HE1	1.89	0.54
1:E:1208:ALA:HB2	4:E:1301:FAR:H51	1.88	0.54
1:M:1074:LYS:HE2	2:O:353:ARG:NH2	2.23	0.54
3:F:949:LEU:HD22	3:F:963:LEU:CD2	2.37	0.54
1:A:71:LYS:HD2	3:B:258:GLN:NE2	2.22	0.54
1:A:75:TYR:HH	3:B:191:GLN:CD	2.13	0.54
1:A:1087:VAL:HG21	1:A:1115:LEU:HD12	1.89	0.54
1:E:29:VAL:HG13	3:F:130:MET:CB	2.37	0.54
3:B:853:LEU:HD21	3:B:883:MET:HE1	1.89	0.54
3:F:949:LEU:HD22	3:F:963:LEU:HD21	1.90	0.54
3:J:45:LEU:HD23	3:J:104:ILE:CG1	2.37	0.54
3:J:949:LEU:HD22	3:J:963:LEU:CD2	2.37	0.54
1:E:610:THR:HG22	3:B:635:LEU:CD2	2.38	0.54
1:E:936:ARG:H	1:E:936:ARG:HD2	1.72	0.54
1:E:1087:VAL:HG21	1:E:1115:LEU:HD12	1.89	0.54
1:E:1208:ALA:CB	2:G:334:ILE:CG1	2.85	0.54
1:I:574:ASP:N	1:I:574:ASP:OD1	2.39	0.54
3:F:1091:LEU:C	3:J:938:PRO:HB3	2.33	0.54
3:N:213:TYR:O	3:N:234:LEU:HD21	2.07	0.54
3:N:367:ILE:HD11	3:N:447:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:PRO:HB2	3:B:130:MET:HE2	1.90	0.54
1:E:1081:LYS:HB3	4:E:1301:FAR:C14	2.35	0.54
1:M:809:LEU:HA	1:M:812:GLU:HB3	1.89	0.54
1:I:69:GLU:HG3	3:J:262:TRP:CZ3	2.43	0.54
1:I:1087:VAL:HG21	1:I:1115:LEU:HD12	1.89	0.54
3:J:569:LEU:HD13	3:J:679:LEU:HB3	1.89	0.54
1:E:1122:GLU:O	1:E:1123:TYR:C	2.48	0.54
1:I:1074:LYS:HE2	2:K:353:ARG:NH2	2.23	0.54
3:B:213:TYR:O	3:B:234:LEU:HD21	2.07	0.54
3:B:361:ILE:CD1	3:B:421:LYS:HE2	2.35	0.54
3:F:965:GLN:O	3:F:969:LEU:HG	2.08	0.54
3:J:949:LEU:HD22	3:J:963:LEU:HD21	1.90	0.54
1:A:491:ARG:CG	3:B:62:LEU:HD11	2.38	0.54
1:A:846:ASP:O	1:A:849:SER:OG	2.23	0.54
1:A:1171:ALA:HB2	2:C:377:ALA:HB2	1.88	0.54
1:E:1205:LYS:HG3	2:G:337:PRO:HG2	1.87	0.54
1:M:1171:ALA:HB2	2:O:377:ALA:HB2	1.88	0.54
1:M:1208:ALA:CB	2:O:334:ILE:CG1	2.85	0.54
3:B:751:GLU:HB3	3:B:755:PHE:CB	2.37	0.54
3:F:45:LEU:HD23	3:F:104:ILE:CG1	2.37	0.54
3:J:751:GLU:HB3	3:J:755:PHE:CB	2.37	0.54
3:J:1018:PHE:CD2	3:J:1022:VAL:CG2	2.90	0.54
3:N:737:LEU:HD21	3:N:772:ARG:NH2	2.23	0.54
1:A:1074:LYS:HE2	2:C:353:ARG:NH2	2.23	0.54
1:A:1208:ALA:CB	2:C:334:ILE:CG1	2.85	0.54
1:I:491:ARG:CG	3:J:62:LEU:CD1	2.85	0.54
1:I:936:ARG:H	1:I:936:ARG:HD2	1.72	0.54
3:B:45:LEU:HD23	3:B:104:ILE:CG1	2.37	0.54
3:B:948:ILE:HD12	3:B:1010:LEU:HD12	1.89	0.54
3:F:1092:ILE:HG21	3:J:1001:GLU:HG2	1.89	0.54
3:J:965:GLN:O	3:J:969:LEU:HG	2.08	0.54
3:N:965:GLN:O	3:N:969:LEU:HG	2.07	0.54
1:E:1120:GLN:HE22	1:E:1181:ALA:C	2.16	0.54
1:E:1200:MET:CE	2:G:354:ILE:HD12	2.38	0.54
1:M:1127:LEU:CD2	1:M:1151:VAL:HG12	2.38	0.54
2:K:359:VAL:CG2	2:K:367:ARG:HG2	2.36	0.54
3:J:213:TYR:O	3:J:234:LEU:HD21	2.07	0.54
1:A:809:LEU:HA	1:A:812:GLU:HB3	1.89	0.54
1:E:339:GLY:HA2	1:E:344:ASN:HB2	1.89	0.54
1:E:1171:ALA:HB2	2:G:377:ALA:HB2	1.88	0.54
1:I:1122:GLU:O	1:I:1123:TYR:C	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1197:PHE:HE2	2:K:373:ASN:O	1.90	0.54
3:B:737:LEU:HD21	3:B:772:ARG:NH2	2.23	0.54
3:B:1002:LEU:CD2	3:B:1024:LEU:HD22	2.35	0.54
3:B:1092:ILE:HG21	3:N:1004:MET:CB	2.38	0.54
3:F:374:ILE:HG23	3:F:454:LEU:HD12	1.89	0.54
1:A:1127:LEU:CD2	1:A:1151:VAL:HG12	2.38	0.54
1:E:574:ASP:OD1	1:E:574:ASP:N	2.39	0.54
1:E:1074:LYS:HE2	2:G:353:ARG:NH2	2.23	0.54
1:M:936:ARG:H	1:M:936:ARG:HD2	1.72	0.54
3:F:1015:GLU:HG3	3:J:1012:ARG:NH2	2.23	0.54
3:N:569:LEU:HD13	3:N:679:LEU:HB3	1.89	0.54
3:N:918:GLN:HE22	3:N:922:ARG:HH11	1.54	0.54
3:N:949:LEU:HD22	3:N:963:LEU:HD21	1.90	0.54
1:I:68:ASP:OD2	3:J:260:CYS:HA	2.08	0.53
1:I:1120:GLN:HE22	1:I:1181:ALA:C	2.16	0.53
3:B:342:LEU:CD2	3:B:421:LYS:NZ	2.72	0.53
3:B:374:ILE:HG23	3:B:454:LEU:HD12	1.89	0.53
3:B:965:GLN:O	3:B:969:LEU:HG	2.08	0.53
3:F:367:ILE:HD11	3:F:447:LEU:HD12	1.89	0.53
1:A:783:LEU:O	1:A:787:TYR:CE2	2.61	0.53
1:A:936:ARG:H	1:A:936:ARG:HD2	1.72	0.53
1:A:1122:GLU:O	1:A:1123:TYR:C	2.48	0.53
2:C:329:THR:O	2:C:332:ILE:HG13	2.09	0.53
1:E:939:ALA:O	1:E:943:THR:HG23	2.09	0.53
1:M:823:TRP:CE3	1:M:826:ILE:HD12	2.43	0.53
2:K:329:THR:O	2:K:332:ILE:HG13	2.09	0.53
3:J:374:ILE:HG23	3:J:454:LEU:HD12	1.89	0.53
3:N:45:LEU:HD23	3:N:104:ILE:CG1	2.38	0.53
3:N:374:ILE:HG23	3:N:454:LEU:HD12	1.89	0.53
1:E:376:PRO:HD3	1:E:392:ARG:HA	1.91	0.53
1:E:783:LEU:O	1:E:787:TYR:CE2	2.61	0.53
1:E:915:MET:HE3	1:E:1064:LEU:HB3	1.91	0.53
1:M:783:LEU:O	1:M:787:TYR:CE2	2.61	0.53
3:F:342:LEU:CD2	3:F:421:LYS:NZ	2.72	0.53
3:N:1018:PHE:CD2	3:N:1022:VAL:CG2	2.90	0.53
2:O:329:THR:O	2:O:332:ILE:HG13	2.09	0.53
1:I:376:PRO:HD3	1:I:392:ARG:HA	1.91	0.53
3:J:477:ARG:NH1	3:N:103:ARG:NH2	2.57	0.53
3:N:568:ILE:HG12	3:N:668:LEU:HD22	1.91	0.53
1:A:51:ILE:HG13	1:A:81:VAL:HG22	1.91	0.53
1:E:491:ARG:CG	3:F:62:LEU:HD12	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:768:LEU:HD22	1:E:802:ARG:HH21	1.60	0.53
1:M:939:ALA:O	1:M:943:THR:HG23	2.09	0.53
1:I:915:MET:HE3	1:I:1064:LEU:HB3	1.91	0.53
3:B:288:ARG:HH11	3:B:978:ASN:HD21	1.57	0.53
3:B:568:ILE:HG12	3:B:668:LEU:HD22	1.91	0.53
3:F:737:LEU:HD21	3:F:772:ARG:NH2	2.23	0.53
3:F:1015:GLU:OE2	4:F:1101:FAR:H42	2.05	0.53
3:J:460:SER:CB	3:N:477:ARG:HH22	2.21	0.53
1:A:791:GLY:N	1:A:792:PRO:HD2	2.24	0.53
1:A:939:ALA:O	1:A:943:THR:HG23	2.09	0.53
2:G:375:PRO:HD2	2:G:378:VAL:CG1	2.38	0.53
1:M:51:ILE:HG13	1:M:81:VAL:HG22	1.91	0.53
1:I:823:TRP:CE3	1:I:826:ILE:HD12	2.43	0.53
1:I:1200:MET:CE	2:K:354:ILE:HD12	2.38	0.53
2:K:338:TYR:CE1	2:K:344:ARG:HG3	2.44	0.53
3:B:850:GLN:O	3:B:854:VAL:HG23	2.09	0.53
3:F:1004:MET:CG	3:J:1092:ILE:HG22	2.37	0.53
3:N:342:LEU:CD2	3:N:421:LYS:NZ	2.72	0.53
1:E:823:TRP:CE3	1:E:826:ILE:HD12	2.43	0.53
1:E:1127:LEU:CD2	1:E:1151:VAL:HG12	2.38	0.53
1:M:1120:GLN:HE22	1:M:1181:ALA:C	2.16	0.53
1:I:783:LEU:O	1:I:787:TYR:CE2	2.61	0.53
3:B:949:LEU:HD22	3:B:963:LEU:HD21	1.90	0.53
3:J:367:ILE:HD11	3:J:447:LEU:HD12	1.89	0.53
1:A:823:TRP:CE3	1:A:826:ILE:HD12	2.43	0.53
2:G:329:THR:O	2:G:332:ILE:HG13	2.09	0.53
1:M:93:ILE:HG22	3:N:67:THR:HG23	1.78	0.53
1:I:69:GLU:HG3	3:J:262:TRP:HZ3	1.74	0.53
1:I:1127:LEU:CD2	1:I:1151:VAL:HG12	2.38	0.53
3:F:1091:LEU:HD12	3:J:939:THR:CG2	2.39	0.53
3:J:361:ILE:CD1	3:J:421:LYS:HE2	2.35	0.53
1:A:915:MET:HE3	1:A:1064:LEU:HB3	1.91	0.53
1:M:57:LEU:HB3	1:M:77:LEU:HD13	1.91	0.53
1:M:314:GLU:N	1:M:317:GLU:OE2	2.40	0.53
1:M:791:GLY:N	1:M:792:PRO:HD2	2.24	0.53
3:B:279:LEU:O	3:B:283:LEU:HD22	2.09	0.53
3:F:1082:VAL:HG23	3:J:1060:LEU:HB3	1.91	0.53
3:J:320:VAL:O	3:J:324:LEU:HB2	2.09	0.53
3:N:850:GLN:O	3:N:854:VAL:HG23	2.09	0.53
1:A:75:TYR:OH	3:B:191:GLN:OE1	2.21	0.52
1:A:1200:MET:CE	2:C:354:ILE:HD12	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:69:GLU:CG	3:N:262:TRP:CZ3	2.92	0.52
1:I:101:SER:OG	1:I:110:ASP:OD2	2.27	0.52
1:I:189:LYS:HG3	1:I:296:PHE:HE2	1.74	0.52
3:B:569:LEU:HD13	3:B:679:LEU:HB3	1.89	0.52
3:B:1013:ASN:ND2	4:B:1101:FAR:C15	2.68	0.52
1:A:57:LEU:HB3	1:A:77:LEU:HD13	1.91	0.52
1:E:101:SER:OG	1:E:110:ASP:OD2	2.27	0.52
1:E:189:LYS:HG3	1:E:296:PHE:HE2	1.74	0.52
3:F:320:VAL:O	3:F:324:LEU:HB2	2.10	0.52
3:F:564:LYS:HE3	3:F:666:GLU:OE1	2.10	0.52
3:J:342:LEU:CD2	3:J:421:LYS:NZ	2.72	0.52
3:J:737:LEU:HD21	3:J:772:ARG:NH2	2.23	0.52
1:M:376:PRO:HD3	1:M:392:ARG:HA	1.91	0.52
1:I:939:ALA:O	1:I:943:THR:HG23	2.09	0.52
3:N:320:VAL:O	3:N:324:LEU:HB2	2.09	0.52
1:A:1169:LEU:HD12	2:C:375:PRO:HG2	1.92	0.52
1:E:422:GLU:CD	3:B:525:PRO:HG3	2.34	0.52
1:M:1169:LEU:HD12	2:O:375:PRO:HG2	1.92	0.52
3:F:486:GLN:NE2	3:F:492:ASP:O	2.41	0.52
3:F:574:VAL:CG2	3:F:618:LEU:HD11	2.40	0.52
3:F:1014:PRO:HD2	3:J:1012:ARG:CZ	2.39	0.52
3:F:1015:GLU:OE1	4:F:1101:FAR:C6	2.47	0.52
3:J:564:LYS:HE3	3:J:666:GLU:OE1	2.09	0.52
3:N:127:TYR:CZ	3:N:131:ARG:HD2	2.44	0.52
3:N:564:LYS:HE3	3:N:666:GLU:OE1	2.10	0.52
3:N:1013:ASN:ND2	4:N:1101:FAR:C15	2.68	0.52
1:A:781:ASP:HA	1:A:825:LEU:HD21	1.91	0.52
1:E:422:GLU:OE2	3:B:525:PRO:HB3	2.10	0.52
1:M:69:GLU:CG	3:N:262:TRP:HZ3	2.23	0.52
1:M:300:GLY:O	1:M:313:TYR:OH	2.21	0.52
2:O:338:TYR:CE1	2:O:344:ARG:HG3	2.44	0.52
1:I:504:VAL:O	1:I:508:SER:OG	2.20	0.52
3:B:814:ALA:HB3	3:B:817:HIS:HB2	1.92	0.52
3:F:568:ILE:HG12	3:F:668:LEU:HD22	1.91	0.52
3:F:1082:VAL:CG2	3:J:1060:LEU:HD23	2.25	0.52
3:J:127:TYR:CZ	3:J:131:ARG:HD2	2.44	0.52
3:J:568:ILE:HG12	3:J:668:LEU:HD22	1.91	0.52
3:N:751:GLU:HB3	3:N:755:PHE:HB2	1.91	0.52
1:E:51:ILE:HG13	1:E:81:VAL:HG22	1.91	0.52
2:G:338:TYR:CE1	2:G:344:ARG:HG3	2.44	0.52
1:M:72:ALA:HB2	3:N:260:CYS:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1200:MET:CE	2:O:354:ILE:HD12	2.38	0.52
3:B:751:GLU:HB3	3:B:755:PHE:HB2	1.91	0.52
3:J:850:GLN:O	3:J:854:VAL:HG23	2.09	0.52
1:M:42:ALA:HB1	1:M:47:ASN:HD21	1.75	0.52
1:I:781:ASP:HA	1:I:825:LEU:HD21	1.91	0.52
3:B:127:TYR:CZ	3:B:131:ARG:HD2	2.44	0.52
3:B:1008:ILE:HG21	4:N:1101:FAR:H51	1.92	0.52
3:B:1062:LYS:HE2	3:N:1019:GLN:HE22	1.74	0.52
3:F:70:LEU:HD11	3:F:128:CYS:SG	2.50	0.52
3:J:751:GLU:HB3	3:J:755:PHE:HB2	1.91	0.52
3:N:70:LEU:HD11	3:N:128:CYS:SG	2.50	0.52
1:E:893:LEU:HD21	1:E:947:MET:HE1	1.92	0.52
1:M:491:ARG:CG	3:N:62:LEU:CD1	2.87	0.52
1:M:1120:GLN:HE22	1:M:1181:ALA:HB3	1.71	0.52
1:M:1192:ALA:HB3	2:O:372:GLU:HB2	1.92	0.52
3:F:850:GLN:O	3:F:854:VAL:HG23	2.09	0.52
3:F:853:LEU:HD12	3:F:880:ILE:HD11	1.92	0.52
3:J:103:ARG:NH2	3:N:477:ARG:NH1	2.57	0.52
1:A:42:ALA:HB1	1:A:47:ASN:HD21	1.75	0.52
2:C:338:TYR:CE1	2:C:344:ARG:HG3	2.44	0.52
1:E:781:ASP:HA	1:E:825:LEU:HD21	1.91	0.52
2:G:359:VAL:CG2	2:G:367:ARG:HG2	2.36	0.52
1:M:28:PRO:HG3	3:N:547:LEU:CG	2.40	0.52
1:M:75:TYR:OH	3:N:191:GLN:OE1	2.27	0.52
1:M:189:LYS:HG3	1:M:296:PHE:HE2	1.74	0.52
1:M:781:ASP:HA	1:M:825:LEU:HD21	1.91	0.52
3:B:460:SER:CB	3:F:477:ARG:NH2	2.72	0.52
3:B:784:TYR:CE1	3:B:845:ARG:HD3	2.45	0.52
3:F:962:HIS:HE1	3:F:1021:LYS:HD3	1.75	0.52
3:J:625:ASN:C	3:J:634:ILE:HD12	2.34	0.52
3:N:814:ALA:HB3	3:N:817:HIS:HB2	1.92	0.52
3:N:1015:GLU:OE1	4:N:1101:FAR:C6	2.45	0.52
1:A:1120:GLN:HE22	1:A:1181:ALA:C	2.16	0.52
1:A:1192:ALA:HB3	2:C:372:GLU:HB2	1.92	0.52
1:I:791:GLY:N	1:I:792:PRO:HD2	2.24	0.52
1:I:893:LEU:HD21	1:I:947:MET:HE1	1.92	0.52
3:B:69:GLY:HA3	3:B:120:LYS:HG2	1.92	0.52
3:B:962:HIS:HE1	3:B:1021:LYS:HD3	1.75	0.52
3:N:574:VAL:CG2	3:N:618:LEU:HD11	2.40	0.52
1:A:893:LEU:HD21	1:A:947:MET:HE1	1.92	0.51
1:A:1205:LYS:HG3	2:C:337:PRO:CG	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:90:HIS:CD2	3:F:67:THR:O	2.62	0.51
1:E:1169:LEU:HD12	2:G:375:PRO:HG2	1.91	0.51
1:M:915:MET:HE3	1:M:1064:LEU:HB3	1.91	0.51
1:M:1205:LYS:HG3	2:O:337:PRO:CG	2.40	0.51
3:B:591:VAL:CG2	3:B:634:ILE:HG13	2.40	0.51
3:F:69:GLY:HA3	3:F:120:LYS:HG2	1.92	0.51
3:J:70:LEU:HD11	3:J:128:CYS:SG	2.50	0.51
3:J:853:LEU:HD12	3:J:880:ILE:HD11	1.92	0.51
3:N:69:GLY:HA3	3:N:120:LYS:HG2	1.92	0.51
1:E:94:ARG:HH12	3:F:157:THR:HB	1.74	0.51
1:E:486:LEU:HD13	1:E:618:PHE:CD1	2.46	0.51
1:M:486:LEU:HD13	1:M:618:PHE:CD1	2.46	0.51
1:I:42:ALA:HB1	1:I:47:ASN:HD21	1.75	0.51
1:I:51:ILE:HG13	1:I:81:VAL:HG22	1.91	0.51
1:I:486:LEU:HD13	1:I:618:PHE:CD1	2.46	0.51
3:B:800:ILE:HD12	3:B:831:ILE:HD13	1.93	0.51
3:F:127:TYR:CZ	3:F:131:ARG:HD2	2.44	0.51
3:J:274:ARG:HH22	3:J:802:THR:CA	2.22	0.51
3:J:503:SER:OG	3:J:623:GLU:OE1	2.23	0.51
3:J:574:VAL:CG2	3:J:618:LEU:HD11	2.40	0.51
3:J:962:HIS:CE1	3:J:1021:LYS:HD3	2.45	0.51
3:N:274:ARG:HH22	3:N:802:THR:CA	2.22	0.51
1:I:57:LEU:HB3	1:I:77:LEU:HD13	1.91	0.51
3:B:564:LYS:HE3	3:B:666:GLU:OE1	2.09	0.51
3:B:574:VAL:CG2	3:B:618:LEU:HD11	2.40	0.51
3:B:962:HIS:CE1	3:B:1021:LYS:HD3	2.45	0.51
3:F:274:ARG:HH22	3:F:802:THR:CA	2.22	0.51
3:F:342:LEU:CD2	3:F:421:LYS:HZ1	2.24	0.51
3:F:544:ASN:HD22	3:F:547:LEU:HG	1.76	0.51
3:F:625:ASN:C	3:F:634:ILE:HD12	2.34	0.51
3:J:183:VAL:HG11	3:J:248:ALA:HB1	1.92	0.51
1:E:42:ALA:HB1	1:E:47:ASN:HD21	1.75	0.51
1:I:69:GLU:O	1:I:73:LYS:HG3	2.11	0.51
3:F:210:GLU:HA	3:F:246:LEU:HD11	1.93	0.51
3:F:962:HIS:CE1	3:F:1021:LYS:HD3	2.45	0.51
3:F:1074:MET:HE2	3:J:1074:MET:HG3	1.92	0.51
1:A:376:PRO:HD3	1:A:392:ARG:HA	1.91	0.51
1:E:817:VAL:HG23	1:E:826:ILE:HG12	1.92	0.51
1:I:1169:LEU:HD12	2:K:375:PRO:HG2	1.91	0.51
3:B:70:LEU:HD11	3:B:128:CYS:SG	2.50	0.51
3:B:320:VAL:O	3:B:324:LEU:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:632:ASN:HB2	3:B:633:PRO:HD3	1.93	0.51
3:F:1074:MET:HE2	3:J:1074:MET:HE2	1.92	0.51
3:F:1091:LEU:HB2	3:J:1004:MET:HE2	1.93	0.51
3:N:183:VAL:HG11	3:N:248:ALA:HB1	1.92	0.51
1:A:163:ASN:CG	1:A:489:ASN:HD21	2.18	0.51
1:A:314:GLU:N	1:A:317:GLU:OE2	2.40	0.51
3:B:210:GLU:HA	3:B:246:LEU:HD11	1.93	0.51
3:B:577:PRO:HD2	3:B:580:PHE:HD2	1.76	0.51
3:F:183:VAL:HG11	3:F:248:ALA:HB1	1.92	0.51
3:F:724:THR:HB	3:F:726:GLU:HB2	1.92	0.51
3:J:69:GLY:HA3	3:J:120:LYS:HG2	1.92	0.51
3:J:830:VAL:O	3:J:834:ILE:HG13	2.11	0.51
3:J:962:HIS:HE1	3:J:1021:LYS:HD3	1.75	0.51
3:N:849:ILE:HG23	3:N:880:ILE:HD13	1.92	0.51
1:A:90:HIS:HA	1:A:93:ILE:HB	1.93	0.51
1:M:872:PRO:CD	1:M:872:PRO:O	2.58	0.51
2:O:375:PRO:HD2	2:O:378:VAL:CG1	2.38	0.51
1:I:357:ALA:HB2	1:I:398:LEU:HD11	1.93	0.51
3:J:210:GLU:HA	3:J:246:LEU:HD11	1.93	0.51
3:J:849:ILE:HG23	3:J:880:ILE:HD13	1.92	0.51
3:N:210:GLU:HA	3:N:246:LEU:HD11	1.93	0.51
1:E:57:LEU:HB3	1:E:77:LEU:HD13	1.91	0.51
1:E:69:GLU:O	1:E:73:LYS:HG3	2.11	0.51
1:E:357:ALA:HB2	1:E:398:LEU:HD11	1.93	0.51
1:E:848:LEU:HD11	1:E:867:ILE:HG22	1.93	0.51
1:I:872:PRO:CD	1:I:872:PRO:O	2.58	0.51
3:B:283:LEU:HD23	3:B:307:LEU:HD21	1.92	0.51
3:B:486:GLN:NE2	3:B:492:ASP:O	2.41	0.51
1:E:163:ASN:CG	1:E:489:ASN:HD21	2.18	0.51
1:M:90:HIS:HA	1:M:93:ILE:HB	1.93	0.51
1:I:1156:HIS:O	1:I:1159:ASN:N	2.44	0.51
1:I:1192:ALA:HB3	2:K:372:GLU:HB2	1.92	0.51
1:I:1205:LYS:HG3	2:K:337:PRO:CG	2.40	0.51
3:F:523:VAL:O	3:F:523:VAL:CG2	2.56	0.51
3:F:745:GLY:HA2	3:F:766:ILE:HD11	1.93	0.51
3:F:751:GLU:HB3	3:F:755:PHE:HB2	1.91	0.51
3:F:814:ALA:HB3	3:F:817:HIS:HB2	1.92	0.51
3:J:598:ILE:HD13	3:J:637:MET:SD	2.51	0.51
3:J:784:TYR:CE1	3:J:845:ARG:HD3	2.45	0.51
3:N:486:GLN:NE2	3:N:492:ASP:O	2.41	0.51
3:N:784:TYR:CE1	3:N:845:ARG:HD3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:853:LEU:HD12	3:N:880:ILE:HD11	1.92	0.51
3:N:962:HIS:HE1	3:N:1021:LYS:HD3	1.75	0.51
1:A:189:LYS:HG3	1:A:296:PHE:HE2	1.74	0.51
1:A:486:LEU:HD13	1:A:618:PHE:CD1	2.46	0.51
1:A:1156:HIS:O	1:A:1159:ASN:N	2.44	0.51
1:M:846:ASP:O	1:M:849:SER:OG	2.23	0.51
3:B:183:VAL:HG11	3:B:248:ALA:HB1	1.92	0.51
3:B:556:PRO:HB2	5:B:1102:ADP:C8	2.46	0.51
3:B:830:VAL:O	3:B:834:ILE:HG13	2.11	0.51
3:F:74:LYS:CD	3:F:439:LYS:HZ1	2.14	0.51
3:F:342:LEU:HD22	3:F:421:LYS:NZ	2.26	0.51
3:J:342:LEU:HD23	3:J:357:LEU:HB3	1.93	0.51
3:J:591:VAL:CG2	3:J:634:ILE:HG13	2.40	0.51
3:J:724:THR:HB	3:J:726:GLU:HB2	1.93	0.51
3:N:598:ILE:HD12	3:N:637:MET:SD	2.51	0.51
3:N:632:ASN:HB2	3:N:633:PRO:HD3	1.93	0.51
1:E:314:GLU:N	1:E:317:GLU:OE2	2.40	0.50
1:E:1156:HIS:O	1:E:1159:ASN:N	2.44	0.50
1:E:1172:ASP:HB3	1:E:1175:MET:CB	2.35	0.50
1:M:441:GLN:OE1	1:M:607:PHE:CD1	2.64	0.50
1:I:848:LEU:HD11	1:I:867:ILE:HG22	1.93	0.50
3:F:283:LEU:CD2	3:F:307:LEU:HD11	2.42	0.50
3:N:577:PRO:HD2	3:N:580:PHE:HD2	1.76	0.50
3:N:830:VAL:O	3:N:834:ILE:HG13	2.11	0.50
1:M:163:ASN:CG	1:M:489:ASN:HD21	2.18	0.50
1:M:1086:SER:OG	1:M:1148:ILE:CG2	2.60	0.50
1:I:441:GLN:OE1	1:I:607:PHE:CD1	2.64	0.50
3:B:1060:LEU:CD2	3:N:1082:VAL:HG21	2.41	0.50
3:F:784:TYR:CE1	3:F:845:ARG:HD3	2.45	0.50
3:F:830:VAL:O	3:F:834:ILE:HG13	2.11	0.50
3:F:1009:VAL:CA	4:F:1103:FAR:H141	2.25	0.50
3:J:477:ARG:HH22	3:N:460:SER:CB	2.23	0.50
3:J:544:ASN:HD22	3:J:547:LEU:HG	1.75	0.50
3:J:577:PRO:HD2	3:J:580:PHE:HD2	1.76	0.50
3:J:625:ASN:HB3	3:J:634:ILE:HD11	1.94	0.50
3:N:800:ILE:HD12	3:N:831:ILE:HD13	1.93	0.50
1:M:1156:HIS:O	1:M:1159:ASN:N	2.43	0.50
1:I:1208:ALA:HB1	2:K:334:ILE:CG1	2.42	0.50
3:B:849:ILE:HG23	3:B:880:ILE:HD13	1.92	0.50
3:F:598:ILE:HD12	3:F:637:MET:SD	2.51	0.50
3:J:715:ASN:HB3	3:J:718:GLU:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1023:ASP:HB3	3:J:1026:ARG:HB2	1.92	0.50
3:J:1090:CYS:HB3	3:J:1093:SER:HB2	1.94	0.50
3:N:342:LEU:HD23	3:N:357:LEU:HB3	1.94	0.50
1:A:441:GLN:OE1	1:A:607:PHE:CD1	2.64	0.50
1:A:1209:THR:HG23	2:C:334:ILE:HG21	1.93	0.50
1:E:1192:ALA:HB3	2:G:372:GLU:HB2	1.92	0.50
1:E:1205:LYS:HG3	2:G:337:PRO:CG	2.41	0.50
1:M:69:GLU:O	1:M:73:LYS:HG3	2.11	0.50
1:I:83:LYS:CE	3:J:198:GLU:OE1	2.59	0.50
1:I:264:SER:OG	1:I:265:PHE:N	2.44	0.50
2:K:375:PRO:HD2	2:K:378:VAL:CG1	2.38	0.50
3:B:724:THR:HB	3:B:726:GLU:HB2	1.92	0.50
3:B:853:LEU:HD12	3:B:880:ILE:HD11	1.92	0.50
3:B:1023:ASP:HB3	3:B:1026:ARG:HB2	1.92	0.50
3:B:1090:CYS:HB3	3:B:1093:SER:HB2	1.94	0.50
3:F:577:PRO:HD2	3:F:580:PHE:HD2	1.76	0.50
3:F:719:TRP:CE3	3:F:722:LYS:HE2	2.47	0.50
3:N:962:HIS:CE1	3:N:1021:LYS:HD3	2.45	0.50
1:A:69:GLU:O	1:A:73:LYS:HG3	2.11	0.50
1:A:491:ARG:HG3	3:B:62:LEU:HD12	1.92	0.50
1:A:817:VAL:HG23	1:A:826:ILE:HG12	1.92	0.50
1:E:791:GLY:N	1:E:792:PRO:HD2	2.24	0.50
1:E:1208:ALA:HB1	2:G:334:ILE:CG1	2.42	0.50
1:M:101:SER:OG	1:M:110:ASP:OD2	2.27	0.50
1:M:357:ALA:HB2	1:M:398:LEU:HD11	1.93	0.50
1:M:893:LEU:HD21	1:M:947:MET:HE1	1.92	0.50
1:I:90:HIS:HA	1:I:93:ILE:HB	1.93	0.50
1:I:817:VAL:HG23	1:I:826:ILE:HG12	1.92	0.50
3:B:544:ASN:HD22	3:B:547:LEU:HG	1.76	0.50
3:J:579:ILE:HD12	3:J:601:ALA:CB	2.41	0.50
3:J:598:ILE:HD12	3:J:637:MET:SD	2.51	0.50
3:J:800:ILE:HD12	3:J:831:ILE:HD13	1.93	0.50
3:J:814:ALA:HB3	3:J:817:HIS:HB2	1.92	0.50
3:N:715:ASN:HB3	3:N:718:GLU:HG2	1.94	0.50
1:A:319:LYS:HE3	1:A:1098:ARG:HA	1.94	0.50
1:A:937:CYS:SG	1:A:942:ALA:HB2	2.52	0.50
2:C:375:PRO:HD2	2:C:378:VAL:CG1	2.38	0.50
1:M:1209:THR:HG23	2:O:334:ILE:HG21	1.93	0.50
3:B:274:ARG:HH22	3:B:802:THR:CA	2.22	0.50
3:B:342:LEU:HD22	3:B:421:LYS:NZ	2.26	0.50
3:B:944:ARG:NH1	3:N:1091:LEU:HD23	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:342:LEU:HD23	3:F:357:LEU:HB3	1.94	0.50
3:F:579:ILE:HD12	3:F:601:ALA:CB	2.41	0.50
3:F:625:ASN:HB3	3:F:634:ILE:HD11	1.94	0.50
3:F:715:ASN:HB3	3:F:718:GLU:HG2	1.94	0.50
3:F:1004:MET:HB2	3:J:1092:ILE:CG2	2.28	0.50
3:J:719:TRP:CE3	3:J:722:LYS:HE2	2.47	0.50
3:N:1004:MET:O	3:N:1008:ILE:HG12	2.12	0.50
1:E:93:ILE:HG21	3:F:67:THR:N	2.27	0.50
1:I:163:ASN:CG	1:I:489:ASN:HD21	2.18	0.50
3:F:499:LEU:HD23	3:F:619:VAL:HB	1.94	0.50
1:A:92:MET:HG2	1:A:112:LEU:HD13	1.94	0.50
1:A:300:GLY:O	1:A:313:TYR:OH	2.21	0.50
1:E:1129:GLU:O	1:E:1133:VAL:HG13	2.12	0.50
3:B:103:ARG:NH2	3:F:477:ARG:NE	2.60	0.50
3:B:406:VAL:H	3:B:445:GLN:NE2	2.10	0.50
3:B:625:ASN:HB3	3:B:634:ILE:HD11	1.94	0.50
3:F:591:VAL:CG2	3:F:634:ILE:HG13	2.40	0.50
3:F:632:ASN:HB2	3:F:633:PRO:HD3	1.93	0.50
3:F:849:ILE:HG23	3:F:880:ILE:HD13	1.92	0.50
3:N:598:ILE:HD13	3:N:637:MET:SD	2.51	0.50
1:E:92:MET:HG2	1:E:112:LEU:HD13	1.94	0.50
1:E:845:THR:O	1:E:849:SER:HB3	2.12	0.50
1:E:937:CYS:SG	1:E:942:ALA:HB2	2.52	0.50
1:M:937:CYS:SG	1:M:942:ALA:HB2	2.52	0.50
1:I:22:ILE:HG12	1:I:401:MET:HG2	1.94	0.50
3:F:579:ILE:HG23	3:F:597:ASP:HB3	1.94	0.50
3:F:598:ILE:HD13	3:F:637:MET:SD	2.51	0.50
3:F:800:ILE:HD12	3:F:831:ILE:HD13	1.93	0.50
3:J:342:LEU:HD22	3:J:421:LYS:NZ	2.26	0.50
3:N:342:LEU:HD22	3:N:421:LYS:NZ	2.26	0.50
3:N:625:ASN:HB3	3:N:634:ILE:HD11	1.94	0.50
1:A:28:PRO:HG3	3:B:547:LEU:CG	2.42	0.49
1:A:101:SER:OG	1:A:110:ASP:OD2	2.27	0.49
1:E:299:ASP:H	1:E:325:GLU:HG2	1.77	0.49
1:M:22:ILE:HG12	1:M:401:MET:HG2	1.94	0.49
3:B:413:PRO:CG	3:B:416:PHE:HD2	2.13	0.49
3:B:598:ILE:HD12	3:B:637:MET:SD	2.51	0.49
3:B:598:ILE:HD13	3:B:637:MET:SD	2.51	0.49
3:B:857:ILE:HG12	3:B:868:PHE:HZ	1.77	0.49
3:J:499:LEU:HD23	3:J:619:VAL:HB	1.94	0.49
3:J:856:HIS:O	3:J:860:ILE:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:TYR:OH	3:B:191:GLN:CD	2.56	0.49
1:A:872:PRO:CD	1:A:872:PRO:O	2.58	0.49
1:E:94:ARG:HH12	3:F:157:THR:CB	2.24	0.49
1:E:441:GLN:OE1	1:E:607:PHE:CD1	2.64	0.49
1:M:817:VAL:HG23	1:M:826:ILE:HG12	1.92	0.49
1:M:848:LEU:HD11	1:M:867:ILE:HG22	1.93	0.49
1:I:92:MET:HG2	1:I:112:LEU:HD13	1.94	0.49
1:I:94:ARG:HH12	3:J:157:THR:HB	1.76	0.49
3:J:745:GLY:HA2	3:J:766:ILE:HD11	1.93	0.49
3:N:724:THR:HB	3:N:726:GLU:HB2	1.93	0.49
1:E:90:HIS:HA	1:E:93:ILE:HB	1.93	0.49
1:E:186:ARG:HE	1:E:191:ASN:HD21	1.60	0.49
1:E:264:SER:OG	1:E:265:PHE:N	2.44	0.49
1:E:1086:SER:OG	1:E:1148:ILE:CG2	2.60	0.49
1:M:845:THR:O	1:M:849:SER:HB3	2.12	0.49
1:I:937:CYS:SG	1:I:942:ALA:HB2	2.52	0.49
3:B:342:LEU:HD23	3:B:357:LEU:HB3	1.93	0.49
3:B:811:THR:HG22	3:B:821:VAL:HG22	1.95	0.49
3:B:856:HIS:O	3:B:860:ILE:HG12	2.12	0.49
3:J:903:SER:O	3:J:904:PRO:C	2.56	0.49
3:N:903:SER:O	3:N:904:PRO:C	2.56	0.49
1:A:357:ALA:HB2	1:A:398:LEU:HD11	1.93	0.49
1:A:848:LEU:HD11	1:A:867:ILE:HG22	1.93	0.49
1:A:897:ILE:O	1:A:901:LEU:HG	2.13	0.49
1:A:1086:SER:OG	1:A:1148:ILE:CG2	2.60	0.49
1:M:28:PRO:HG3	3:N:547:LEU:HG	1.95	0.49
1:M:319:LYS:HE3	1:M:1098:ARG:HA	1.94	0.49
1:I:28:PRO:HB2	3:J:130:MET:HE2	1.88	0.49
1:I:1209:THR:HG23	2:K:334:ILE:HG21	1.93	0.49
3:B:719:TRP:CE3	3:B:722:LYS:HE2	2.47	0.49
3:F:797:ALA:HB3	3:F:798:PRO:HD3	1.94	0.49
3:F:857:ILE:HG12	3:F:868:PHE:HZ	1.77	0.49
3:J:632:ASN:HB2	3:J:633:PRO:HD3	1.93	0.49
3:J:951:ARG:O	3:J:1017:GLU:HG3	2.13	0.49
3:N:745:GLY:HA2	3:N:766:ILE:HD11	1.93	0.49
1:E:22:ILE:HG12	1:E:401:MET:HG2	1.94	0.49
1:M:1208:ALA:HB1	2:O:334:ILE:CG1	2.42	0.49
1:I:314:GLU:N	1:I:317:GLU:OE2	2.40	0.49
1:I:845:THR:O	1:I:849:SER:HB3	2.12	0.49
3:B:103:ARG:NH2	3:F:477:ARG:NH1	2.58	0.49
3:F:730:LYS:HB2	3:F:743:LEU:CD1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1090:CYS:CB	4:F:1101:FAR:H13	2.24	0.49
3:N:406:VAL:H	3:N:445:GLN:NE2	2.10	0.49
3:N:413:PRO:CG	3:N:416:PHE:HD2	2.13	0.49
3:N:544:ASN:HD22	3:N:547:LEU:HG	1.76	0.49
3:N:951:ARG:O	3:N:1017:GLU:HG3	2.13	0.49
1:A:83:LYS:CD	3:B:198:GLU:OE1	2.60	0.49
1:A:120:THR:HG21	3:B:131:ARG:NH2	2.27	0.49
3:F:541:LEU:HD13	3:F:670:PHE:CD2	2.48	0.49
3:J:730:LYS:HB2	3:J:743:LEU:CD1	2.43	0.49
3:J:797:ALA:HB3	3:J:798:PRO:HD3	1.94	0.49
3:J:857:ILE:HG12	3:J:868:PHE:HZ	1.77	0.49
1:A:22:ILE:HG12	1:A:401:MET:HG2	1.94	0.49
1:M:93:ILE:CG2	3:N:67:THR:HG23	2.39	0.49
1:M:504:VAL:O	1:M:508:SER:OG	2.20	0.49
2:O:359:VAL:CG2	2:O:367:ARG:HG2	2.36	0.49
1:I:72:ALA:CB	3:J:260:CYS:HB2	2.41	0.49
1:I:1129:GLU:O	1:I:1133:VAL:HG13	2.12	0.49
3:B:285:ARG:HH22	3:B:977:MET:HB2	1.76	0.49
3:B:734:CYS:SG	3:B:743:LEU:CD1	3.01	0.49
3:B:951:ARG:O	3:B:1017:GLU:HG3	2.13	0.49
3:F:856:HIS:O	3:F:860:ILE:HG12	2.12	0.49
3:F:1004:MET:O	3:F:1008:ILE:HG12	2.12	0.49
3:J:579:ILE:HG23	3:J:597:ASP:HB3	1.94	0.49
3:N:719:TRP:CE3	3:N:722:LYS:HE2	2.47	0.49
1:I:1086:SER:OG	1:I:1148:ILE:CG2	2.60	0.49
3:B:183:VAL:CG1	3:B:467:VAL:HG21	2.43	0.49
3:B:283:LEU:HD21	3:B:307:LEU:HG	1.95	0.49
3:B:526:ILE:HG21	3:B:660:ILE:CD1	2.43	0.49
3:B:730:LYS:HB2	3:B:743:LEU:CD1	2.43	0.49
3:B:745:GLY:HA2	3:B:766:ILE:HD11	1.93	0.49
3:B:835:ILE:HD13	3:B:851:GLN:HG3	1.95	0.49
3:B:1092:ILE:HG21	3:N:1004:MET:HG3	1.95	0.49
3:F:173:ASN:HD21	3:F:220:VAL:HA	1.77	0.49
3:F:1015:GLU:OE1	4:F:1101:FAR:H41	2.12	0.49
3:J:795:SER:C	3:J:798:PRO:HD2	2.38	0.49
3:N:734:CYS:SG	3:N:743:LEU:CD1	3.01	0.49
3:N:811:THR:HG22	3:N:821:VAL:HG22	1.95	0.49
1:M:264:SER:OG	1:M:265:PHE:N	2.44	0.49
1:M:1129:GLU:O	1:M:1133:VAL:HG13	2.12	0.49
1:I:846:ASP:O	1:I:849:SER:OG	2.23	0.49
1:I:1054:TRP:CZ2	2:K:370:LEU:HA	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1120:GLN:HE22	1:I:1181:ALA:HB3	1.71	0.49
3:B:715:ASN:HB3	3:B:718:GLU:HG2	1.94	0.49
3:B:888:GLN:HA	3:B:896:ALA:HB2	1.95	0.49
3:B:1004:MET:O	3:B:1008:ILE:HG12	2.12	0.49
3:F:330:PHE:HB2	3:F:368:PHE:HB2	1.95	0.49
3:J:1004:MET:O	3:J:1008:ILE:HG12	2.12	0.49
3:N:183:VAL:CG1	3:N:467:VAL:HG21	2.43	0.49
3:N:541:LEU:HD13	3:N:670:PHE:CD2	2.48	0.49
3:N:591:VAL:CG2	3:N:634:ILE:HG13	2.40	0.49
3:N:857:ILE:HG12	3:N:868:PHE:HZ	1.76	0.49
1:A:264:SER:OG	1:A:265:PHE:N	2.44	0.49
1:E:75:TYR:HH	3:F:191:GLN:HB3	1.73	0.49
1:M:83:LYS:CD	3:N:198:GLU:OE1	2.60	0.49
1:M:897:ILE:O	1:M:901:LEU:HG	2.13	0.49
1:M:1120:GLN:HE22	1:M:1181:ALA:CB	2.21	0.49
1:I:71:LYS:HD2	3:J:258:GLN:NE2	2.28	0.49
1:I:585:ALA:O	1:I:589:MET:HG3	2.13	0.49
3:B:1009:VAL:CA	4:N:1101:FAR:C14	2.71	0.49
3:F:795:SER:C	3:F:798:PRO:HD2	2.38	0.49
3:J:132:GLN:HE22	3:J:150:HIS:HB2	1.78	0.49
3:J:486:GLN:NE2	3:J:492:ASP:O	2.41	0.49
3:N:330:PHE:HB2	3:N:368:PHE:HB2	1.95	0.49
3:N:499:LEU:HD23	3:N:619:VAL:HB	1.94	0.49
3:N:835:ILE:HD13	3:N:851:GLN:HG3	1.95	0.49
3:N:856:HIS:O	3:N:860:ILE:HG12	2.12	0.49
1:A:95:GLN:HE22	1:A:113:HIS:CD2	2.32	0.48
1:A:299:ASP:H	1:A:325:GLU:HG2	1.77	0.48
1:A:585:ALA:O	1:A:589:MET:HG3	2.13	0.48
1:A:1129:GLU:O	1:A:1133:VAL:HG13	2.12	0.48
1:E:1092:LEU:HD21	1:E:1111:VAL:HG22	1.95	0.48
3:B:132:GLN:HE22	3:B:150:HIS:HB2	1.78	0.48
3:F:74:LYS:CD	3:F:439:LYS:HZ3	2.13	0.48
3:F:183:VAL:CG1	3:F:467:VAL:HG21	2.43	0.48
3:F:283:LEU:HD23	3:F:307:LEU:HD11	1.94	0.48
3:F:526:ILE:HG21	3:F:660:ILE:CD1	2.43	0.48
3:J:223:ARG:NE	3:J:228:ASN:HD21	2.11	0.48
3:J:526:ILE:HG21	3:J:660:ILE:CD1	2.43	0.48
3:J:734:CYS:SG	3:J:743:LEU:CD1	3.01	0.48
3:N:577:PRO:HD2	3:N:580:PHE:CD2	2.48	0.48
1:A:186:ARG:NE	1:A:191:ASN:HD21	2.12	0.48
1:A:340:VAL:HG11	1:A:413:MET:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:610:THR:HG22	3:F:635:LEU:HD21	1.95	0.48
1:E:15:ALA:HA	1:E:57:LEU:HD21	1.95	0.48
1:E:893:LEU:HD13	1:E:924:ILE:HD12	1.95	0.48
2:G:352:PHE:O	2:G:353:ARG:C	2.55	0.48
1:M:585:ALA:O	1:M:589:MET:HG3	2.13	0.48
1:M:788:THR:O	1:M:792:PRO:HG2	2.03	0.48
1:I:299:ASP:H	1:I:325:GLU:HG2	1.77	0.48
1:I:788:THR:O	1:I:792:PRO:HG2	2.03	0.48
3:B:499:LEU:HD23	3:B:619:VAL:HB	1.94	0.48
3:B:579:ILE:HG23	3:B:597:ASP:HB3	1.94	0.48
3:F:413:PRO:CG	3:F:416:PHE:HD2	2.13	0.48
3:J:330:PHE:HB2	3:J:368:PHE:HB2	1.95	0.48
3:J:888:GLN:HA	3:J:896:ALA:HB2	1.95	0.48
3:N:579:ILE:HG23	3:N:597:ASP:HB3	1.94	0.48
3:N:795:SER:C	3:N:798:PRO:HD2	2.38	0.48
1:A:1091:VAL:HG13	1:A:1148:ILE:HG21	1.95	0.48
1:M:186:ARG:NE	1:M:191:ASN:HD21	2.12	0.48
1:M:299:ASP:H	1:M:325:GLU:HG2	1.77	0.48
1:I:186:ARG:HE	1:I:191:ASN:HD21	1.60	0.48
1:I:340:VAL:HG11	1:I:413:MET:HB3	1.95	0.48
3:B:223:ARG:HD3	3:B:228:ASN:HD21	1.78	0.48
3:B:564:LYS:HG2	3:B:609:TRP:HH2	1.79	0.48
3:B:795:SER:C	3:B:798:PRO:HD2	2.38	0.48
3:F:132:GLN:HE22	3:F:150:HIS:HB2	1.78	0.48
3:F:586:TYR:HB2	3:F:782:VAL:HG11	1.95	0.48
3:F:1091:LEU:HB2	3:J:1004:MET:HE1	1.94	0.48
3:J:577:PRO:HD2	3:J:580:PHE:CD2	2.48	0.48
3:J:586:TYR:HB2	3:J:782:VAL:HG11	1.95	0.48
3:N:962:HIS:CD2	3:N:964:PRO:HB3	2.49	0.48
1:A:44:VAL:HG22	1:A:88:LEU:HD22	1.95	0.48
1:A:845:THR:O	1:A:849:SER:HB3	2.12	0.48
1:A:1208:ALA:HB1	2:C:334:ILE:CG1	2.42	0.48
1:I:893:LEU:HD13	1:I:924:ILE:HD12	1.95	0.48
3:B:223:ARG:NE	3:B:228:ASN:HD21	2.11	0.48
3:F:577:PRO:HD2	3:F:580:PHE:CD2	2.48	0.48
3:F:919:GLN:N	3:F:919:GLN:OE1	2.47	0.48
3:J:406:VAL:H	3:J:445:GLN:NE2	2.10	0.48
3:N:888:GLN:HA	3:N:896:ALA:HB2	1.95	0.48
3:N:1013:ASN:OD1	4:N:1101:FAR:C15	2.61	0.48
1:A:186:ARG:HE	1:A:191:ASN:HD21	1.60	0.48
2:C:352:PHE:O	2:C:353:ARG:C	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:340:VAL:HG11	1:E:413:MET:HB3	1.95	0.48
1:E:872:PRO:CD	1:E:872:PRO:O	2.58	0.48
1:E:1091:VAL:HG13	1:E:1148:ILE:HG21	1.95	0.48
1:E:1209:THR:HG23	2:G:334:ILE:HG21	1.93	0.48
1:M:83:LYS:HE3	3:N:198:GLU:OE1	2.12	0.48
3:B:577:PRO:HD2	3:B:580:PHE:CD2	2.48	0.48
3:B:903:SER:O	3:B:904:PRO:C	2.56	0.48
3:B:939:THR:HG23	3:N:1091:LEU:HD12	1.95	0.48
3:F:223:ARG:NE	3:F:228:ASN:HD21	2.11	0.48
3:F:887:LEU:HG	3:F:910:LEU:HD21	1.95	0.48
3:F:888:GLN:HA	3:F:896:ALA:HB2	1.95	0.48
3:F:951:ARG:O	3:F:1017:GLU:HG3	2.13	0.48
3:J:1008:ILE:HG22	3:J:1012:ARG:HD2	1.96	0.48
1:A:1208:ALA:O	2:C:330:ARG:HD3	2.14	0.48
1:E:68:ASP:OD2	3:F:259:GLY:O	2.32	0.48
1:M:92:MET:HG2	1:M:112:LEU:HD13	1.94	0.48
1:M:95:GLN:HE22	1:M:113:HIS:CD2	2.32	0.48
1:M:186:ARG:HE	1:M:191:ASN:HD21	1.60	0.48
1:I:1092:LEU:HD21	1:I:1111:VAL:HG22	1.95	0.48
3:B:285:ARG:HG2	3:B:291:ASN:HA	1.96	0.48
3:B:541:LEU:HD13	3:B:670:PHE:CD2	2.48	0.48
3:F:903:SER:O	3:F:904:PRO:C	2.56	0.48
3:F:962:HIS:CD2	3:F:964:PRO:HB3	2.49	0.48
3:N:526:ILE:HG21	3:N:660:ILE:CD1	2.43	0.48
3:N:797:ALA:HB3	3:N:798:PRO:HD3	1.94	0.48
1:E:290:ARG:NH1	1:E:391:ASP:OD1	2.47	0.48
1:M:340:VAL:HG11	1:M:413:MET:HB3	1.95	0.48
3:B:105:ASP:O	3:F:614:ARG:NH2	2.46	0.48
3:B:330:PHE:HB2	3:B:368:PHE:HB2	1.95	0.48
3:B:1016:LEU:HD23	3:B:1082:VAL:HG12	1.96	0.48
3:F:734:CYS:SG	3:F:743:LEU:CD1	3.01	0.48
3:F:1008:ILE:HG22	3:F:1012:ARG:HD2	1.96	0.48
3:J:811:THR:HG22	3:J:821:VAL:HG22	1.95	0.48
3:J:962:HIS:CD2	3:J:964:PRO:HB3	2.49	0.48
3:N:1016:LEU:HD23	3:N:1082:VAL:HG12	1.96	0.48
1:E:186:ARG:NE	1:E:191:ASN:HD21	2.12	0.48
1:E:1054:TRP:CZ2	2:G:370:LEU:HA	2.48	0.48
1:E:1208:ALA:O	2:G:330:ARG:HD3	2.14	0.48
1:M:1208:ALA:O	2:O:330:ARG:HD3	2.14	0.48
2:O:352:PHE:CD1	2:O:352:PHE:C	2.92	0.48
1:I:1091:VAL:HG11	1:I:1148:ILE:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:797:ALA:HB3	3:B:798:PRO:HD3	1.94	0.48
3:F:136:VAL:HG23	3:F:149:LEU:HD21	1.96	0.48
3:F:564:LYS:HG2	3:F:609:TRP:HH2	1.78	0.48
3:N:730:LYS:HB2	3:N:743:LEU:CD1	2.43	0.48
1:A:1054:TRP:CZ2	2:C:370:LEU:HA	2.48	0.48
1:E:236:GLN:HA	1:E:239:GLN:HB3	1.95	0.48
1:E:1091:VAL:HG11	1:E:1148:ILE:HD13	1.96	0.48
1:I:186:ARG:NE	1:I:191:ASN:HD21	2.12	0.48
1:I:897:ILE:O	1:I:901:LEU:HG	2.13	0.48
3:B:919:GLN:OE1	3:B:919:GLN:N	2.47	0.48
3:N:586:TYR:HB2	3:N:782:VAL:HG11	1.95	0.48
3:N:1002:LEU:HD13	3:N:1069:LEU:HD22	1.96	0.48
1:A:236:GLN:HA	1:A:239:GLN:HB3	1.95	0.48
1:E:319:LYS:HE3	1:E:1098:ARG:HA	1.94	0.48
1:E:809:LEU:O	1:E:813:LEU:N	2.37	0.48
1:E:1127:LEU:HD23	1:E:1155:VAL:HG21	1.96	0.48
1:M:1054:TRP:CZ2	2:O:370:LEU:HA	2.48	0.48
1:M:1091:VAL:HG13	1:M:1148:ILE:HG21	1.95	0.48
1:I:75:TYR:OH	3:J:191:GLN:HG3	2.12	0.48
1:I:524:PHE:HB2	1:I:542:MET:SD	2.54	0.48
3:B:173:ASN:HD21	3:B:220:VAL:HA	1.77	0.48
3:B:962:HIS:CD2	3:B:964:PRO:HB3	2.49	0.48
3:J:541:LEU:HD13	3:J:670:PHE:CD2	2.48	0.48
3:J:1002:LEU:HD13	3:J:1069:LEU:HD22	1.96	0.48
3:N:523:VAL:O	3:N:523:VAL:CG2	2.56	0.48
3:N:712:PRO:HD3	3:N:780:LEU:CD2	2.40	0.48
1:A:15:ALA:HA	1:A:57:LEU:HD21	1.95	0.47
1:E:28:PRO:HB3	3:F:197:ASP:HB3	1.95	0.47
1:E:897:ILE:O	1:E:901:LEU:HG	2.13	0.47
1:M:236:GLN:HA	1:M:239:GLN:HB3	1.95	0.47
2:O:352:PHE:O	2:O:353:ARG:C	2.55	0.47
1:I:15:ALA:HA	1:I:57:LEU:HD21	1.95	0.47
1:I:236:GLN:HA	1:I:239:GLN:HB3	1.95	0.47
3:B:477:ARG:CZ	3:F:103:ARG:HH21	2.22	0.47
3:B:778:LEU:O	3:B:782:VAL:HG23	2.14	0.47
3:B:1008:ILE:HG22	3:B:1012:ARG:HD2	1.94	0.47
3:F:778:LEU:O	3:F:782:VAL:HG23	2.14	0.47
4:F:1103:FAR:C15	3:J:1013:ASN:OD1	2.62	0.47
3:J:183:VAL:CG1	3:J:467:VAL:HG21	2.43	0.47
3:J:523:VAL:O	3:J:523:VAL:CG2	2.56	0.47
3:J:835:ILE:HD13	3:J:851:GLN:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:887:LEU:HG	3:J:910:LEU:HD21	1.95	0.47
3:N:173:ASN:HD21	3:N:220:VAL:HA	1.77	0.47
3:N:564:LYS:HG2	3:N:609:TRP:HH2	1.78	0.47
1:A:85:MET:HE2	1:A:148:MET:SD	2.55	0.47
1:E:422:GLU:OE2	3:B:525:PRO:CB	2.62	0.47
1:I:69:GLU:CG	3:J:262:TRP:CZ3	2.97	0.47
1:I:319:LYS:HE3	1:I:1098:ARG:HA	1.94	0.47
1:I:1054:TRP:HZ2	2:K:370:LEU:HA	1.80	0.47
1:I:1091:VAL:HG13	1:I:1148:ILE:HG21	1.95	0.47
3:B:887:LEU:HG	3:B:910:LEU:HD21	1.95	0.47
3:N:136:VAL:HG23	3:N:149:LEU:HD21	1.96	0.47
3:N:223:ARG:NE	3:N:228:ASN:HD21	2.11	0.47
3:N:835:ILE:HG21	3:N:851:GLN:HE21	1.79	0.47
1:A:771:LYS:HG3	1:A:802:ARG:HH11	1.75	0.47
1:A:1120:GLN:HE22	1:A:1181:ALA:HB3	1.71	0.47
1:E:1068:PRO:HG3	2:G:354:ILE:HG23	1.96	0.47
1:M:71:LYS:HD2	3:N:258:GLN:NE2	2.28	0.47
1:M:1054:TRP:HZ2	2:O:370:LEU:HA	1.80	0.47
3:B:221:TRP:CH2	3:B:368:PHE:HZ	2.32	0.47
3:B:367:ILE:HD11	3:B:443:TRP:CD1	2.49	0.47
3:B:1002:LEU:HD13	3:B:1069:LEU:HD22	1.96	0.47
3:F:373:MET:O	3:F:377:VAL:HG23	2.15	0.47
3:F:811:THR:HG22	3:F:821:VAL:HG22	1.95	0.47
3:J:297:LEU:HD21	3:J:372:MET:HG2	1.96	0.47
3:J:564:LYS:HG2	3:J:609:TRP:HH2	1.79	0.47
3:J:835:ILE:HG21	3:J:851:GLN:HE21	1.79	0.47
3:J:919:GLN:OE1	3:J:919:GLN:N	2.47	0.47
3:J:1016:LEU:HD23	3:J:1082:VAL:HG12	1.96	0.47
3:N:878:TRP:HE3	3:N:933:SER:HA	1.79	0.47
1:E:44:VAL:HG22	1:E:88:LEU:HD22	1.95	0.47
1:E:75:TYR:HB2	3:F:258:GLN:HB3	1.95	0.47
1:E:85:MET:HE2	1:E:148:MET:SD	2.55	0.47
1:M:524:PHE:HB2	1:M:542:MET:SD	2.54	0.47
3:B:136:VAL:HG23	3:B:149:LEU:HD21	1.96	0.47
3:B:373:MET:O	3:B:377:VAL:HG23	2.15	0.47
3:F:342:LEU:HD21	3:F:421:LYS:HZ1	1.79	0.47
3:F:367:ILE:HD11	3:F:443:TRP:CD1	2.49	0.47
3:J:136:VAL:HG23	3:J:149:LEU:HD21	1.96	0.47
3:J:223:ARG:HD3	3:J:228:ASN:HD21	1.78	0.47
3:J:803:PHE:CE2	3:J:810:VAL:HG22	2.49	0.47
3:N:132:GLN:HE22	3:N:150:HIS:HB2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:177:LEU:CD1	3:N:303:PRO:HG3	2.45	0.47
3:N:283:LEU:HA	3:N:285:ARG:N	2.29	0.47
3:N:367:ILE:HD11	3:N:443:TRP:CD1	2.49	0.47
1:A:893:LEU:HD13	1:A:924:ILE:HD12	1.95	0.47
1:A:1054:TRP:HZ2	2:C:370:LEU:HA	1.79	0.47
1:M:1091:VAL:HG11	1:M:1148:ILE:HD13	1.96	0.47
1:M:1092:LEU:HD21	1:M:1111:VAL:HG22	1.95	0.47
1:I:794:TRP:O	1:I:798:LEU:CD1	2.61	0.47
3:B:297:LEU:HD21	3:B:372:MET:HG2	1.96	0.47
3:F:297:LEU:HD21	3:F:372:MET:HG2	1.96	0.47
3:F:835:ILE:HG21	3:F:851:GLN:HE21	1.79	0.47
3:F:878:TRP:HE3	3:F:933:SER:HA	1.79	0.47
3:J:173:ASN:HD21	3:J:220:VAL:HA	1.77	0.47
1:A:1092:LEU:HD21	1:A:1111:VAL:HG22	1.95	0.47
1:E:585:ALA:O	1:E:589:MET:HG3	2.13	0.47
1:M:44:VAL:HG22	1:M:88:LEU:HD22	1.95	0.47
1:M:1061:ASP:OD2	2:O:357:HIS:CE1	2.68	0.47
1:I:63:LYS:O	3:N:567:ARG:NH2	2.30	0.47
1:I:69:GLU:CG	3:J:262:TRP:HZ3	2.28	0.47
2:K:352:PHE:C	2:K:352:PHE:CD1	2.92	0.47
3:B:586:TYR:HB2	3:B:782:VAL:HG11	1.95	0.47
3:F:283:LEU:CD2	3:F:307:LEU:CD1	2.92	0.47
3:F:1002:LEU:HD13	3:F:1069:LEU:HD22	1.96	0.47
3:F:1091:LEU:HG	3:J:939:THR:O	2.14	0.47
3:N:887:LEU:HG	3:N:910:LEU:HD21	1.95	0.47
1:A:504:VAL:O	1:A:508:SER:OG	2.20	0.47
1:A:1068:PRO:HG3	2:C:354:ILE:HG23	1.96	0.47
2:C:352:PHE:C	2:C:352:PHE:CD1	2.92	0.47
1:E:32:LEU:HD12	1:E:118:THR:HA	1.96	0.47
1:E:93:ILE:HG21	3:F:67:THR:CA	2.45	0.47
1:E:1054:TRP:HZ2	2:G:370:LEU:HA	1.79	0.47
1:M:15:ALA:HA	1:M:57:LEU:HD21	1.95	0.47
1:M:893:LEU:HD13	1:M:924:ILE:HD12	1.95	0.47
1:M:923:ILE:O	1:M:926:VAL:HG12	2.15	0.47
1:I:32:LEU:HD12	1:I:118:THR:HA	1.96	0.47
1:I:95:GLN:HE22	1:I:113:HIS:CD2	2.32	0.47
1:I:290:ARG:NH1	1:I:391:ASP:OD1	2.47	0.47
1:I:923:ILE:O	1:I:926:VAL:HG12	2.15	0.47
1:I:1061:ASP:OD2	2:K:357:HIS:CE1	2.68	0.47
1:I:1208:ALA:O	2:K:330:ARG:HD3	2.14	0.47
2:K:352:PHE:O	2:K:353:ARG:C	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:526:ILE:HD13	3:B:660:ILE:HD13	1.90	0.47
3:F:177:LEU:CD1	3:F:303:PRO:HG3	2.45	0.47
3:F:221:TRP:CH2	3:F:368:PHE:HZ	2.32	0.47
3:F:406:VAL:H	3:F:445:GLN:NE2	2.10	0.47
3:J:172:ILE:O	3:J:172:ILE:CG2	2.62	0.47
3:J:177:LEU:CD1	3:J:303:PRO:HG3	2.45	0.47
3:J:221:TRP:CH2	3:J:368:PHE:HZ	2.32	0.47
3:J:586:TYR:HB2	3:J:782:VAL:CG1	2.45	0.47
3:J:789:THR:HG22	3:J:789:THR:O	2.15	0.47
3:N:172:ILE:O	3:N:172:ILE:CG2	2.62	0.47
3:N:373:MET:O	3:N:377:VAL:HG23	2.15	0.47
3:N:374:ILE:HG23	3:N:454:LEU:CD1	2.45	0.47
3:N:538:TYR:HB3	3:N:552:ARG:HD3	1.97	0.47
3:N:545:GLU:HG2	3:N:545:GLU:O	2.15	0.47
3:N:586:TYR:HB2	3:N:782:VAL:CG1	2.45	0.47
3:N:587:MET:HE1	3:N:855:ILE:CD1	2.45	0.47
3:N:1008:ILE:HG22	3:N:1012:ARG:HD2	1.96	0.47
1:A:524:PHE:HB2	1:A:542:MET:SD	2.54	0.47
1:A:938:SER:OG	1:A:941:GLU:CG	2.63	0.47
1:M:32:LEU:HD12	1:M:118:THR:HA	1.96	0.47
1:M:248:ARG:HA	1:M:254:GLU:O	2.15	0.47
1:M:938:SER:OG	1:M:941:GLU:CG	2.63	0.47
1:I:44:VAL:HG22	1:I:88:LEU:HD22	1.95	0.47
3:B:177:LEU:CD1	3:B:303:PRO:HG3	2.45	0.47
3:B:523:VAL:O	3:B:523:VAL:CG2	2.56	0.47
3:B:538:TYR:HB3	3:B:552:ARG:HD3	1.97	0.47
3:B:878:TRP:HE3	3:B:933:SER:HA	1.79	0.47
3:F:726:GLU:HA	3:F:729:GLN:CB	2.45	0.47
3:F:835:ILE:HD13	3:F:851:GLN:HG3	1.95	0.47
3:F:1091:LEU:HD23	3:J:944:ARG:HH11	1.80	0.47
1:A:1061:ASP:OD2	2:C:357:HIS:CE1	2.68	0.47
1:E:524:PHE:HB2	1:E:542:MET:SD	2.54	0.47
1:E:788:THR:O	1:E:792:PRO:HG3	2.09	0.47
1:M:290:ARG:NH1	1:M:391:ASP:OD1	2.47	0.47
3:B:374:ILE:HG23	3:B:454:LEU:CD1	2.45	0.47
3:B:545:GLU:O	3:B:545:GLU:HG2	2.15	0.47
3:J:727:ILE:HG21	3:J:747:LEU:HG	1.97	0.47
3:N:778:LEU:O	3:N:782:VAL:HG23	2.14	0.47
1:A:83:LYS:HE3	3:B:198:GLU:OE1	2.15	0.47
1:A:290:ARG:NH1	1:A:391:ASP:OD1	2.47	0.47
1:A:923:ILE:O	1:A:926:VAL:HG12	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1120:GLN:HE22	1:A:1181:ALA:CB	2.21	0.47
1:A:1127:LEU:HD23	1:A:1155:VAL:HG21	1.96	0.47
1:M:333:THR:O	1:M:337:LEU:HG	2.15	0.47
1:M:817:VAL:HG21	1:M:829:ILE:HD12	1.97	0.47
1:I:1068:PRO:HG3	2:K:354:ILE:HG23	1.96	0.47
3:B:532:GLN:H	3:B:532:GLN:HG3	1.51	0.47
3:B:586:TYR:CB	3:B:782:VAL:CG1	2.93	0.47
3:B:1002:LEU:O	3:B:1006:VAL:HG23	2.15	0.47
3:B:1008:ILE:HG21	3:B:1012:ARG:NH2	2.29	0.47
3:F:172:ILE:O	3:F:172:ILE:CG2	2.62	0.47
3:F:545:GLU:HG2	3:F:545:GLU:O	2.15	0.47
3:J:586:TYR:CB	3:J:782:VAL:CG1	2.93	0.47
3:J:726:GLU:HA	3:J:729:GLN:CB	2.45	0.47
3:N:1002:LEU:O	3:N:1006:VAL:HG23	2.15	0.47
1:E:510:LEU:HD23	1:E:517:ILE:HG21	1.97	0.46
1:M:85:MET:HE2	1:M:148:MET:SD	2.55	0.46
1:M:1127:LEU:HD22	1:M:1151:VAL:CG1	2.45	0.46
3:B:726:GLU:HA	3:B:729:GLN:CB	2.45	0.46
3:B:1071:LYS:HE2	3:N:1075:ASN:HA	1.96	0.46
3:F:587:MET:HE1	3:F:855:ILE:CD1	2.45	0.46
3:F:1002:LEU:O	3:F:1006:VAL:HG23	2.15	0.46
3:F:1016:LEU:HD23	3:F:1082:VAL:HG12	1.96	0.46
3:J:367:ILE:HD11	3:J:443:TRP:CD1	2.49	0.46
3:N:726:GLU:HA	3:N:729:GLN:CB	2.45	0.46
3:N:789:THR:O	3:N:789:THR:HG22	2.15	0.46
1:A:817:VAL:HG21	1:A:829:ILE:HD12	1.97	0.46
1:E:260:LEU:HG	1:E:283:ILE:HD13	1.98	0.46
1:M:332:TRP:HH2	1:M:352:LYS:HZ2	1.60	0.46
1:M:771:LYS:HG3	1:M:802:ARG:HH11	1.75	0.46
1:M:794:TRP:O	1:M:798:LEU:CD1	2.61	0.46
1:I:333:THR:O	1:I:337:LEU:HG	2.15	0.46
3:B:586:TYR:HB2	3:B:782:VAL:CG1	2.45	0.46
3:B:835:ILE:HG21	3:B:851:GLN:HE21	1.79	0.46
3:B:1092:ILE:HG21	3:N:1004:MET:HB2	1.97	0.46
3:F:586:TYR:CB	3:F:782:VAL:CG1	2.93	0.46
3:J:283:LEU:HA	3:J:285:ARG:H	1.80	0.46
3:J:373:MET:O	3:J:377:VAL:HG23	2.15	0.46
3:J:965:GLN:CD	3:J:969:LEU:HD12	2.31	0.46
3:N:221:TRP:CH2	3:N:368:PHE:HZ	2.32	0.46
3:N:335:ARG:NH1	3:N:970:SER:O	2.48	0.46
3:N:586:TYR:CB	3:N:782:VAL:CG1	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:1090:CYS:SG	4:N:1101:FAR:H12A	1.46	0.46
1:A:914:GLU:HG3	1:A:1066:ARG:HG3	1.98	0.46
4:A:1301:FAR:H43	2:C:333:VAL:HG21	1.98	0.46
1:E:95:GLN:HE22	1:E:113:HIS:CD2	2.31	0.46
1:E:248:ARG:HA	1:E:254:GLU:O	2.15	0.46
1:E:923:ILE:O	1:E:926:VAL:HG12	2.15	0.46
2:G:352:PHE:CD1	2:G:352:PHE:C	2.92	0.46
1:I:531:TYR:HB2	1:I:823:TRP:HZ3	1.81	0.46
1:I:1127:LEU:HD22	1:I:1151:VAL:CG1	2.45	0.46
3:F:223:ARG:HD3	3:F:228:ASN:HD21	1.78	0.46
3:F:374:ILE:HG23	3:F:454:LEU:CD1	2.45	0.46
3:F:450:ILE:HG23	3:F:464:ILE:CD1	2.46	0.46
3:F:538:TYR:HB3	3:F:552:ARG:HD3	1.97	0.46
3:F:1001:GLU:CG	3:J:1092:ILE:CG1	2.57	0.46
3:F:1078:LEU:HD22	3:J:1067:SER:HA	1.97	0.46
3:J:374:ILE:HG23	3:J:454:LEU:CD1	2.45	0.46
3:J:545:GLU:O	3:J:545:GLU:HG2	2.15	0.46
3:J:778:LEU:O	3:J:782:VAL:HG23	2.14	0.46
1:A:69:GLU:HG2	3:B:262:TRP:CH2	2.50	0.46
1:A:531:TYR:HB2	1:A:823:TRP:HZ3	1.81	0.46
1:E:333:THR:O	1:E:337:LEU:HG	2.15	0.46
1:M:914:GLU:HG3	1:M:1066:ARG:HG3	1.98	0.46
1:I:85:MET:HE2	1:I:148:MET:SD	2.55	0.46
1:I:397:LYS:HE3	1:I:400:HIS:CD2	2.51	0.46
3:B:1004:MET:CE	3:N:1091:LEU:HB2	2.45	0.46
3:J:538:TYR:HB3	3:J:552:ARG:HD3	1.97	0.46
3:J:878:TRP:HE3	3:J:933:SER:HA	1.79	0.46
3:J:1002:LEU:O	3:J:1006:VAL:HG23	2.15	0.46
3:N:727:ILE:HG21	3:N:747:LEU:HG	1.97	0.46
1:A:914:GLU:HB2	1:A:1067:VAL:O	2.16	0.46
1:E:938:SER:OG	1:E:941:GLU:CG	2.63	0.46
1:E:1061:ASP:OD2	2:G:357:HIS:CE1	2.68	0.46
1:M:94:ARG:HH12	3:N:157:THR:HB	1.81	0.46
1:I:66:ASP:HB2	3:N:667:GLN:HE22	1.52	0.46
1:I:260:LEU:HG	1:I:283:ILE:HD13	1.98	0.46
3:B:45:LEU:CD2	3:B:104:ILE:HG13	2.46	0.46
3:B:1015:GLU:CD	3:N:1012:ARG:NH1	2.38	0.46
3:F:803:PHE:CE2	3:F:810:VAL:HG22	2.49	0.46
3:N:297:LEU:HD21	3:N:372:MET:HG2	1.96	0.46
3:N:396:LEU:HD21	3:N:406:VAL:HG22	1.97	0.46
3:N:450:ILE:HG23	3:N:464:ILE:CD1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:919:GLN:N	3:N:919:GLN:OE1	2.47	0.46
1:A:32:LEU:HD12	1:A:118:THR:HA	1.96	0.46
1:A:68:ASP:O	1:A:69:GLU:C	2.58	0.46
1:A:104:TYR:OH	1:A:495:SER:O	2.31	0.46
1:A:1091:VAL:HG11	1:A:1148:ILE:HD13	1.96	0.46
1:E:771:LYS:HG3	1:E:802:ARG:HH11	1.75	0.46
1:M:531:TYR:HB2	1:M:823:TRP:HZ3	1.81	0.46
3:B:335:ARG:NH1	3:B:970:SER:O	2.48	0.46
3:B:396:LEU:HD21	3:B:406:VAL:HG22	1.97	0.46
3:B:450:ILE:HG23	3:B:464:ILE:CD1	2.46	0.46
3:B:789:THR:HG22	3:B:789:THR:O	2.15	0.46
3:F:586:TYR:HB2	3:F:782:VAL:CG1	2.45	0.46
3:F:727:ILE:HG21	3:F:747:LEU:HG	1.97	0.46
3:N:1035:PHE:CZ	3:N:1039:GLN:HG3	2.51	0.46
1:A:333:THR:O	1:A:337:LEU:HG	2.15	0.46
1:M:901:LEU:HD22	1:M:912:PHE:CZ	2.43	0.46
1:I:79:GLN:HB2	3:J:194:TYR:O	2.15	0.46
1:I:510:LEU:HD23	1:I:517:ILE:HG21	1.97	0.46
1:I:938:SER:OG	1:I:941:GLU:CG	2.63	0.46
1:I:1127:LEU:HD23	1:I:1155:VAL:HG21	1.96	0.46
3:B:172:ILE:O	3:B:172:ILE:CG2	2.62	0.46
3:B:1057:THR:CG2	3:B:1064:GLY:HA2	2.46	0.46
3:B:1092:ILE:HD12	3:N:1001:GLU:CB	2.40	0.46
3:F:789:THR:O	3:F:789:THR:HG22	2.15	0.46
3:N:584:ASP:HB2	3:N:791:LYS:HE3	1.98	0.46
1:A:10:ARG:NH1	1:A:10:ARG:HB3	2.31	0.46
1:A:79:GLN:NE2	3:B:194:TYR:CZ	2.82	0.46
1:A:200:SER:HA	1:A:262:VAL:HG21	1.98	0.46
1:M:397:LYS:HE3	1:M:400:HIS:CD2	2.51	0.46
1:I:248:ARG:HA	1:I:254:GLU:O	2.15	0.46
2:K:341:ARG:O	2:K:342:PRO:C	2.57	0.46
3:B:587:MET:HE1	3:B:855:ILE:CD1	2.45	0.46
3:F:335:ARG:NH1	3:F:970:SER:O	2.49	0.46
3:F:1035:PHE:CZ	3:F:1039:GLN:HG3	2.51	0.46
4:F:1101:FAR:C5	3:J:1008:ILE:HG13	2.46	0.46
3:J:335:ARG:NH1	3:J:970:SER:O	2.48	0.46
3:J:584:ASP:HB2	3:J:791:LYS:HE3	1.98	0.46
3:J:587:MET:HE1	3:J:855:ILE:CD1	2.45	0.46
1:A:248:ARG:HA	1:A:254:GLU:O	2.15	0.46
1:A:1081:LYS:CB	4:A:1301:FAR:C14	2.94	0.46
1:E:64:ASN:C	3:B:567:ARG:HH21	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:184:TRP:O	1:E:185:GLU:HG2	2.16	0.46
1:E:771:LYS:NZ	1:E:802:ARG:HD3	2.31	0.46
1:E:1127:LEU:HD22	1:E:1151:VAL:CG1	2.45	0.46
1:I:817:VAL:HG21	1:I:829:ILE:HD12	1.97	0.46
1:I:914:GLU:HG3	1:I:1066:ARG:HG3	1.98	0.46
3:B:826:LEU:HD22	3:B:830:VAL:CG1	2.43	0.46
3:B:1013:ASN:OD1	4:B:1101:FAR:C15	2.64	0.46
1:M:72:ALA:CB	3:N:262:TRP:CZ2	2.99	0.46
1:M:184:TRP:O	1:M:185:GLU:HG2	2.16	0.46
1:M:1068:PRO:HG3	2:O:354:ILE:HG23	1.96	0.46
1:I:189:LYS:C	1:I:191:ASN:N	2.71	0.46
1:I:914:GLU:HB2	1:I:1067:VAL:O	2.16	0.46
3:F:584:ASP:HB2	3:F:791:LYS:HE3	1.98	0.46
3:J:95:TRP:CE3	3:J:185:MET:HE2	2.51	0.46
3:J:1057:THR:CG2	3:J:1064:GLY:HA2	2.46	0.46
3:N:625:ASN:C	3:N:634:ILE:HD12	2.34	0.46
3:N:736:CYS:HB3	3:N:739:SER:H	1.81	0.46
1:A:108:THR:HG22	1:A:133:LEU:HD23	1.98	0.45
1:A:211:ALA:HB1	1:A:426:LEU:HD13	1.99	0.45
1:A:1207:ALA:O	1:A:1211:VAL:HG23	2.17	0.45
1:E:68:ASP:O	1:E:69:GLU:C	2.58	0.45
1:E:817:VAL:HG21	1:E:829:ILE:HD12	1.97	0.45
1:M:72:ALA:HB3	3:N:262:TRP:CZ2	2.51	0.45
1:M:809:LEU:O	1:M:813:LEU:N	2.37	0.45
4:M:1301:FAR:H43	2:O:333:VAL:HG21	1.98	0.45
1:I:184:TRP:O	1:I:185:GLU:HG2	2.16	0.45
1:I:400:HIS:O	1:I:404:GLN:N	2.43	0.45
3:B:584:ASP:HB2	3:B:791:LYS:HE3	1.98	0.45
3:B:849:ILE:HG23	3:B:880:ILE:CD1	2.46	0.45
3:F:76:CYS:O	3:F:76:CYS:SG	2.74	0.45
3:F:298:PRO:O	3:F:303:PRO:HD2	2.16	0.45
3:J:76:CYS:O	3:J:76:CYS:SG	2.74	0.45
3:J:342:LEU:CD2	3:J:421:LYS:HZ1	2.29	0.45
1:A:510:LEU:HD23	1:A:517:ILE:HG21	1.97	0.45
1:M:922:LEU:HD23	1:M:922:LEU:HA	1.81	0.45
3:B:76:CYS:O	3:B:76:CYS:SG	2.74	0.45
3:B:223:ARG:CZ	3:B:228:ASN:HD21	2.29	0.45
3:B:939:THR:CG2	3:N:1091:LEU:HD12	2.45	0.45
3:B:1035:PHE:CZ	3:B:1039:GLN:HG3	2.51	0.45
3:F:714:VAL:HG11	3:F:743:LEU:CG	2.41	0.45
3:F:857:ILE:HG12	3:F:868:PHE:CZ	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:736:CYS:HB3	3:J:739:SER:H	1.81	0.45
3:J:754:ASN:O	3:J:755:PHE:C	2.59	0.45
3:J:857:ILE:HG12	3:J:868:PHE:CZ	2.52	0.45
3:J:1035:PHE:CZ	3:J:1039:GLN:HG3	2.51	0.45
3:N:803:PHE:CE2	3:N:810:VAL:HG22	2.49	0.45
1:A:1127:LEU:HD22	1:A:1151:VAL:CG1	2.45	0.45
1:E:531:TYR:HB2	1:E:823:TRP:HZ3	1.81	0.45
1:E:1134:LEU:HD11	1:E:1149:ILE:HG21	1.99	0.45
1:M:200:SER:HA	1:M:262:VAL:HG21	1.98	0.45
1:M:510:LEU:HD23	1:M:517:ILE:HG21	1.97	0.45
1:M:1127:LEU:HD23	1:M:1155:VAL:HG21	1.96	0.45
4:I:1301:FAR:H43	2:K:333:VAL:HG21	1.98	0.45
3:B:298:PRO:O	3:B:303:PRO:HD2	2.16	0.45
3:B:477:ARG:NH1	3:F:103:ARG:HH22	2.14	0.45
3:F:95:TRP:CE3	3:F:185:MET:HE2	2.52	0.45
3:F:796:ILE:HD11	3:F:851:GLN:O	2.17	0.45
3:F:1091:LEU:O	3:J:938:PRO:HB3	2.16	0.45
3:J:450:ILE:HG23	3:J:464:ILE:CD1	2.46	0.45
3:N:95:TRP:CE3	3:N:185:MET:HE2	2.52	0.45
1:E:112:LEU:HD11	1:E:168:LEU:HD21	1.98	0.45
1:E:794:TRP:O	1:E:798:LEU:CD1	2.61	0.45
1:M:10:ARG:NH1	1:M:10:ARG:HB3	2.31	0.45
1:M:788:THR:O	1:M:792:PRO:HG3	2.09	0.45
1:M:927:MET:HE3	1:M:957:LEU:HB3	1.98	0.45
3:B:95:TRP:CE3	3:B:185:MET:HE2	2.52	0.45
3:B:122:MET:HE3	3:B:178:TYR:CE1	2.52	0.45
3:B:355:ILE:HD13	3:B:355:ILE:HA	1.77	0.45
3:B:625:ASN:C	3:B:634:ILE:HD12	2.34	0.45
3:B:883:MET:HG3	3:B:914:ILE:HD13	1.99	0.45
3:B:1093:SER:C	3:N:924:TRP:CZ2	2.90	0.45
3:F:396:LEU:HD21	3:F:406:VAL:HG22	1.97	0.45
3:F:800:ILE:HD13	3:F:822:ILE:HD12	1.99	0.45
3:J:45:LEU:CD2	3:J:104:ILE:HG13	2.46	0.45
3:J:849:ILE:HG23	3:J:880:ILE:CD1	2.46	0.45
3:J:857:ILE:HG23	3:J:868:PHE:CZ	2.51	0.45
3:N:883:MET:HG3	3:N:914:ILE:HD13	1.99	0.45
1:A:491:ARG:HG2	3:B:62:LEU:HD11	1.97	0.45
1:E:914:GLU:HB2	1:E:1067:VAL:O	2.16	0.45
1:M:504:VAL:HG22	1:M:550:LEU:HG	1.98	0.45
1:M:914:GLU:HB2	1:M:1067:VAL:O	2.16	0.45
1:I:435:LYS:HE2	1:I:435:LYS:HB3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1052:GLY:HA2	1:I:1190:ASP:OD2	2.16	0.45
3:B:523:VAL:HG21	3:B:528:ILE:CD1	2.43	0.45
3:F:122:MET:HE3	3:F:178:TYR:CE1	2.52	0.45
3:F:223:ARG:CZ	3:F:228:ASN:HD21	2.29	0.45
3:J:342:LEU:HD22	3:J:421:LYS:HZ1	1.80	0.45
3:J:413:PRO:CG	3:J:416:PHE:HD2	2.13	0.45
3:J:826:LEU:HD22	3:J:830:VAL:CG1	2.43	0.45
3:J:879:ILE:HG22	3:J:883:MET:HE3	1.99	0.45
3:N:122:MET:HE3	3:N:178:TYR:CE1	2.52	0.45
3:N:942:TYR:CZ	3:N:984:GLU:OE2	2.69	0.45
1:A:441:GLN:CD	1:A:607:PHE:CG	2.95	0.45
1:A:794:TRP:O	1:A:798:LEU:CD1	2.61	0.45
1:A:934:SER:O	1:A:935:LEU:HB2	2.17	0.45
2:C:359:VAL:CG2	2:C:367:ARG:HG2	2.36	0.45
1:E:104:TYR:OH	1:E:495:SER:O	2.31	0.45
1:E:108:THR:HG22	1:E:133:LEU:HD23	1.98	0.45
1:E:938:SER:OG	1:E:941:GLU:HG3	2.17	0.45
1:E:1081:LYS:CB	4:E:1301:FAR:C14	2.94	0.45
1:M:211:ALA:HB1	1:M:426:LEU:HD13	1.99	0.45
1:M:260:LEU:HG	1:M:283:ILE:HD13	1.98	0.45
2:O:374:THR:OG1	2:O:379:LEU:HB2	2.16	0.45
1:I:10:ARG:NH1	1:I:10:ARG:HB3	2.31	0.45
1:I:68:ASP:O	1:I:69:GLU:C	2.58	0.45
1:I:788:THR:C	1:I:792:PRO:CD	2.70	0.45
3:B:727:ILE:HG21	3:B:747:LEU:HG	1.97	0.45
3:B:803:PHE:CE2	3:B:810:VAL:HG22	2.49	0.45
3:F:45:LEU:CD2	3:F:104:ILE:HG13	2.46	0.45
3:F:1092:ILE:HG13	4:F:1101:FAR:H11	1.97	0.45
3:N:45:LEU:CD2	3:N:104:ILE:HG13	2.46	0.45
3:N:526:ILE:HD13	3:N:660:ILE:HD13	1.90	0.45
3:N:796:ILE:HD11	3:N:851:GLN:O	2.17	0.45
3:N:857:ILE:HG12	3:N:868:PHE:CZ	2.52	0.45
1:A:93:ILE:HG22	3:B:67:THR:HG23	1.86	0.45
1:A:938:SER:OG	1:A:941:GLU:HG3	2.17	0.45
1:A:1052:GLY:HA2	1:A:1190:ASP:OD2	2.16	0.45
1:E:64:ASN:CA	3:B:567:ARG:HH22	2.21	0.45
1:E:200:SER:HA	1:E:262:VAL:HG21	1.98	0.45
1:E:491:ARG:HD3	3:F:62:LEU:CG	2.45	0.45
1:E:504:VAL:HG22	1:E:550:LEU:HG	1.98	0.45
1:M:435:LYS:HE2	1:M:435:LYS:HB3	1.80	0.45
3:B:634:ILE:HG22	3:B:638:LEU:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:736:CYS:HB3	3:B:739:SER:H	1.81	0.45
3:B:1012:ARG:NH2	4:N:1101:FAR:H41	2.26	0.45
3:F:223:ARG:CD	3:F:228:ASN:ND2	2.79	0.45
3:F:712:PRO:HD3	3:F:780:LEU:CD2	2.41	0.45
3:F:879:ILE:HG22	3:F:883:MET:HE3	1.99	0.45
3:J:69:GLY:CA	3:J:120:LYS:HG2	2.47	0.45
3:J:396:LEU:HD21	3:J:406:VAL:HG22	1.97	0.45
3:N:76:CYS:O	3:N:76:CYS:SG	2.74	0.45
3:N:298:PRO:O	3:N:303:PRO:HD2	2.16	0.45
3:N:849:ILE:HG23	3:N:880:ILE:CD1	2.46	0.45
3:N:1057:THR:CG2	3:N:1064:GLY:HA2	2.46	0.45
1:A:57:LEU:HD13	1:A:412:LEU:HD11	1.99	0.45
1:A:184:TRP:O	1:A:185:GLU:HG2	2.16	0.45
1:A:479:LEU:HB2	1:A:520:PHE:CD2	2.52	0.45
1:E:337:LEU:CD1	1:E:406:LEU:HD22	2.47	0.45
1:E:479:LEU:HB2	1:E:520:PHE:CD2	2.52	0.45
1:E:1052:GLY:HA2	1:E:1190:ASP:OD2	2.16	0.45
1:M:771:LYS:NZ	1:M:802:ARG:HD3	2.31	0.45
1:I:112:LEU:HD11	1:I:168:LEU:HD21	1.98	0.45
1:I:200:SER:HA	1:I:262:VAL:HG21	1.98	0.45
1:I:504:VAL:HG22	1:I:550:LEU:HG	1.98	0.45
1:I:1120:GLN:HA	1:I:1121:PRO:HD3	1.89	0.45
3:B:69:GLY:CA	3:B:120:LYS:HG2	2.47	0.45
3:B:279:LEU:HG	3:B:283:LEU:CD2	2.44	0.45
3:B:742:ILE:HD11	3:B:784:TYR:CZ	2.52	0.45
3:B:857:ILE:HG23	3:B:868:PHE:CZ	2.51	0.45
3:B:958:VAL:HG22	3:B:1024:LEU:HD12	1.99	0.45
3:F:742:ILE:HD11	3:F:784:TYR:CZ	2.52	0.45
3:J:98:ALA:O	3:J:102:ARG:HG3	2.17	0.45
3:J:223:ARG:CZ	3:J:228:ASN:HD21	2.29	0.45
3:N:742:ILE:HD11	3:N:784:TYR:CZ	2.52	0.45
3:N:958:VAL:HG22	3:N:1024:LEU:HD12	1.99	0.45
1:A:86:ARG:O	1:A:90:HIS:ND1	2.50	0.45
1:A:765:ALA:HB1	1:A:768:LEU:CD1	2.47	0.45
1:E:10:ARG:NH1	1:E:10:ARG:HB3	2.31	0.45
1:E:400:HIS:O	1:E:404:GLN:N	2.43	0.45
1:E:435:LYS:HB3	1:E:435:LYS:HE2	1.80	0.45
1:E:441:GLN:CD	1:E:607:PHE:CG	2.95	0.45
1:E:914:GLU:HG3	1:E:1066:ARG:HG3	1.98	0.45
1:E:934:SER:O	1:E:935:LEU:HB2	2.17	0.45
2:G:341:ARG:O	2:G:342:PRO:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:342:LEU:CD2	3:B:421:LYS:HZ1	2.29	0.45
3:B:464:ILE:C	3:B:466:PRO:HD3	2.42	0.45
3:F:849:ILE:HG23	3:F:880:ILE:CD1	2.46	0.45
3:F:1057:THR:CG2	3:F:1064:GLY:HA2	2.46	0.45
3:J:742:ILE:HD11	3:J:784:TYR:CZ	2.52	0.45
3:J:989:ASN:HD22	3:J:989:ASN:HA	1.63	0.45
3:N:69:GLY:CA	3:N:120:LYS:HG2	2.47	0.45
3:N:98:ALA:O	3:N:102:ARG:HG3	2.17	0.45
3:N:223:ARG:CZ	3:N:228:ASN:HD21	2.29	0.45
3:N:857:ILE:HG23	3:N:868:PHE:CZ	2.51	0.45
1:A:28:PRO:HG3	3:B:547:LEU:HG	1.99	0.45
1:E:211:ALA:HB1	1:E:426:LEU:HD13	1.98	0.45
1:M:112:LEU:HD11	1:M:168:LEU:HD21	1.98	0.45
1:M:1052:GLY:HA2	1:M:1190:ASP:OD2	2.16	0.45
2:O:382:LEU:HD13	2:O:382:LEU:HA	1.76	0.45
1:I:108:THR:HG22	1:I:133:LEU:HD23	1.98	0.45
1:I:441:GLN:CD	1:I:607:PHE:CG	2.95	0.45
1:I:1134:LEU:HD11	1:I:1149:ILE:HG21	1.99	0.45
3:B:216:PRO:HG3	3:B:234:LEU:HD11	1.99	0.45
3:B:779:TRP:HA	3:B:782:VAL:HG23	1.99	0.45
3:F:240:GLY:HA3	3:F:299:CYS:SG	2.57	0.45
3:F:857:ILE:HG23	3:F:868:PHE:CZ	2.51	0.45
3:N:452:LYS:HD2	3:N:452:LYS:HA	1.72	0.45
1:A:72:ALA:HB3	3:B:262:TRP:CZ2	2.52	0.44
1:A:337:LEU:CD1	1:A:406:LEU:HD22	2.47	0.44
1:A:1197:PHE:CZ	2:C:375:PRO:HG3	2.53	0.44
1:E:66:ASP:HA	3:B:667:GLN:HE21	1.82	0.44
1:E:189:LYS:C	1:E:191:ASN:N	2.71	0.44
1:E:1084:GLY:C	1:E:1148:ILE:HG23	2.42	0.44
1:E:1207:ALA:O	1:E:1211:VAL:HG23	2.17	0.44
1:M:1081:LYS:CB	4:M:1301:FAR:C14	2.94	0.44
1:M:1084:GLY:C	1:M:1148:ILE:HG23	2.42	0.44
1:I:233:ASP:OD2	1:I:503:GLY:N	2.50	0.44
1:I:771:LYS:NZ	1:I:802:ARG:HD3	2.31	0.44
1:I:927:MET:HE3	1:I:957:LEU:HB3	1.98	0.44
1:I:1207:ALA:O	1:I:1211:VAL:HG23	2.17	0.44
3:B:342:LEU:HD21	3:B:421:LYS:HZ1	1.82	0.44
3:B:754:ASN:O	3:B:755:PHE:C	2.59	0.44
3:B:857:ILE:HG12	3:B:868:PHE:CZ	2.52	0.44
3:J:298:PRO:O	3:J:303:PRO:HD2	2.16	0.44
3:J:634:ILE:HG22	3:J:638:LEU:CD1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:HG	1:A:283:ILE:HD13	1.97	0.44
1:A:927:MET:HE3	1:A:957:LEU:HB3	1.98	0.44
1:E:765:ALA:HB1	1:E:768:LEU:CD1	2.47	0.44
1:E:927:MET:HE3	1:E:957:LEU:HB3	1.98	0.44
4:E:1301:FAR:H43	2:G:333:VAL:HG21	1.98	0.44
1:M:108:THR:HG22	1:M:133:LEU:HD23	1.98	0.44
1:M:938:SER:OG	1:M:941:GLU:HG3	2.17	0.44
1:I:479:LEU:HB2	1:I:520:PHE:CD2	2.52	0.44
1:I:788:THR:O	1:I:792:PRO:HG3	2.09	0.44
3:B:98:ALA:O	3:B:102:ARG:HG3	2.17	0.44
3:B:284:PRO:HD3	3:B:312:LEU:HD21	2.00	0.44
3:B:477:ARG:NH2	3:F:460:SER:CB	2.80	0.44
3:F:754:ASN:O	3:F:755:PHE:C	2.59	0.44
3:J:103:ARG:HH21	3:N:477:ARG:CZ	2.28	0.44
3:J:122:MET:HE3	3:J:178:TYR:CE1	2.52	0.44
3:J:240:GLY:HA3	3:J:299:CYS:SG	2.57	0.44
3:J:497:VAL:HA	3:J:617:PHE:O	2.17	0.44
3:J:796:ILE:HD11	3:J:851:GLN:O	2.17	0.44
3:J:883:MET:HG3	3:J:914:ILE:HD13	1.99	0.44
3:N:464:ILE:C	3:N:466:PRO:HD3	2.42	0.44
3:N:497:VAL:HA	3:N:617:PHE:O	2.17	0.44
3:N:556:PRO:HB2	5:N:1102:ADP:C8	2.52	0.44
3:N:779:TRP:HA	3:N:782:VAL:HG23	1.99	0.44
1:A:69:GLU:HG2	3:B:262:TRP:CZ3	2.51	0.44
2:C:382:LEU:HD13	2:C:382:LEU:HA	1.76	0.44
1:E:169:VAL:O	1:E:173:GLU:HB2	2.17	0.44
1:E:502:MET:HE3	1:E:502:MET:HB3	1.83	0.44
1:E:1074:LYS:HG2	1:E:1135:THR:HG21	1.99	0.44
1:E:1120:GLN:HE22	1:E:1181:ALA:CB	2.21	0.44
1:M:57:LEU:HD13	1:M:412:LEU:HD11	1.99	0.44
1:M:262:VAL:HA	1:M:267:ALA:HB3	2.00	0.44
1:M:1207:ALA:O	1:M:1211:VAL:HG23	2.17	0.44
1:I:337:LEU:CD1	1:I:406:LEU:HD22	2.47	0.44
3:B:780:LEU:HD12	3:B:780:LEU:HA	1.84	0.44
3:F:98:ALA:O	3:F:102:ARG:HG3	2.17	0.44
3:F:883:MET:HG3	3:F:914:ILE:HD13	1.99	0.44
3:F:1090:CYS:C	3:F:1091:LEU:HD13	2.42	0.44
3:J:958:VAL:HG22	3:J:1024:LEU:HD12	1.99	0.44
3:N:811:THR:HA	3:N:820:GLU:O	2.18	0.44
1:A:112:LEU:HD11	1:A:168:LEU:HD21	1.98	0.44
1:A:234:GLU:H	1:A:234:GLU:CD	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1084:GLY:C	1:A:1148:ILE:HG23	2.42	0.44
1:A:1130:ALA:HA	1:A:1133:VAL:HG22	2.00	0.44
1:E:1054:TRP:HA	1:E:1057:ARG:HG3	2.00	0.44
2:G:374:THR:OG1	2:G:379:LEU:HB2	2.17	0.44
1:M:98:LYS:HE3	1:M:127:ASP:OD1	2.18	0.44
1:M:234:GLU:H	1:M:234:GLU:CD	2.26	0.44
1:M:337:LEU:CD1	1:M:406:LEU:HD22	2.47	0.44
1:M:1130:ALA:HA	1:M:1133:VAL:HG22	2.00	0.44
1:I:465:ILE:O	1:I:468:VAL:HG12	2.18	0.44
3:B:103:ARG:HH21	3:F:477:ARG:CZ	2.26	0.44
3:B:477:ARG:HD3	3:F:103:ARG:CZ	2.48	0.44
3:B:497:VAL:HA	3:B:617:PHE:O	2.17	0.44
3:B:796:ILE:HD11	3:B:851:GLN:O	2.17	0.44
3:F:139:PHE:CD1	3:F:143:PRO:HA	2.53	0.44
3:F:223:ARG:CD	3:F:228:ASN:HD21	2.31	0.44
3:F:587:MET:HE1	3:F:855:ILE:CB	2.48	0.44
3:J:223:ARG:CD	3:J:228:ASN:HD21	2.31	0.44
3:J:304:ALA:O	3:J:469:ARG:HB3	2.18	0.44
3:J:942:TYR:CZ	3:J:984:GLU:OE2	2.70	0.44
3:J:1059:PRO:HA	3:J:1065:THR:OG1	2.17	0.44
3:N:304:ALA:O	3:N:469:ARG:HB3	2.18	0.44
3:N:879:ILE:HG22	3:N:883:MET:HE3	1.99	0.44
1:A:169:VAL:O	1:A:173:GLU:HB2	2.17	0.44
1:A:771:LYS:NZ	1:A:802:ARG:HD3	2.31	0.44
1:E:86:ARG:O	1:E:90:HIS:ND1	2.50	0.44
1:M:86:ARG:O	1:M:90:HIS:ND1	2.50	0.44
1:I:262:VAL:HA	1:I:267:ALA:HB3	2.00	0.44
1:I:1081:LYS:CB	4:I:1301:FAR:C14	2.94	0.44
3:B:223:ARG:CD	3:B:228:ASN:HD21	2.31	0.44
3:B:730:LYS:O	3:B:733:ASP:N	2.46	0.44
3:F:69:GLY:CA	3:F:120:LYS:HG2	2.47	0.44
3:F:737:LEU:HD22	3:F:769:VAL:HG22	2.00	0.44
4:F:1103:FAR:C15	3:J:1013:ASN:ND2	2.69	0.44
3:J:737:LEU:HD22	3:J:769:VAL:HG22	2.00	0.44
3:J:811:THR:HA	3:J:820:GLU:O	2.18	0.44
3:N:240:GLY:HA3	3:N:299:CYS:SG	2.57	0.44
3:N:998:ILE:HD13	3:N:998:ILE:HA	1.84	0.44
1:A:93:ILE:CG2	3:B:67:THR:HG23	2.45	0.44
1:A:504:VAL:HG22	1:A:550:LEU:HG	1.98	0.44
1:E:98:LYS:HE3	1:E:127:ASP:OD1	2.18	0.44
1:M:934:SER:O	1:M:935:LEU:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:86:ARG:O	1:I:90:HIS:ND1	2.50	0.44
1:I:809:LEU:O	1:I:813:LEU:N	2.38	0.44
1:I:938:SER:OG	1:I:941:GLU:HG3	2.17	0.44
3:B:304:ALA:O	3:B:469:ARG:HB3	2.18	0.44
3:B:452:LYS:HD2	3:B:452:LYS:HA	1.72	0.44
3:F:216:PRO:HG3	3:F:234:LEU:HD11	1.99	0.44
3:F:958:VAL:HG22	3:F:1024:LEU:HD12	1.99	0.44
3:F:1063:ARG:HD2	3:F:1063:ARG:HA	1.82	0.44
3:J:800:ILE:HD13	3:J:822:ILE:HD12	1.99	0.44
3:N:216:PRO:HG3	3:N:234:LEU:HD11	1.99	0.44
3:N:634:ILE:HG22	3:N:638:LEU:CD1	2.47	0.44
1:A:3:SER:O	1:A:8:GLY:N	2.51	0.44
1:A:788:THR:O	1:A:792:PRO:HG3	2.09	0.44
1:M:169:VAL:O	1:M:173:GLU:HB2	2.17	0.44
1:M:479:LEU:HB2	1:M:520:PHE:CD2	2.52	0.44
1:M:1134:LEU:HD11	1:M:1149:ILE:HG21	1.99	0.44
1:M:1197:PHE:CZ	2:O:375:PRO:HG3	2.52	0.44
1:I:858:LEU:HD23	1:I:858:LEU:HA	1.80	0.44
1:I:934:SER:O	1:I:935:LEU:HB2	2.17	0.44
3:B:240:GLY:HA3	3:B:299:CYS:SG	2.57	0.44
3:B:714:VAL:HG11	3:B:743:LEU:CG	2.41	0.44
3:B:1059:PRO:HA	3:B:1065:THR:OG1	2.17	0.44
3:F:736:CYS:HB3	3:F:739:SER:H	1.82	0.44
3:F:1090:CYS:HG	4:F:1101:FAR:C1	1.13	0.44
3:F:1091:LEU:HD12	3:J:939:THR:HG23	1.98	0.44
3:J:361:ILE:CG1	3:J:421:LYS:CE	2.96	0.44
3:N:373:MET:HE2	3:N:373:MET:HB3	1.87	0.44
3:N:569:LEU:HD22	3:N:679:LEU:HD22	2.00	0.44
3:N:1059:PRO:HA	3:N:1065:THR:OG1	2.18	0.44
1:A:98:LYS:HE3	1:A:127:ASP:OD1	2.18	0.44
2:C:333:VAL:O	2:C:337:PRO:HG3	2.18	0.44
1:E:62:ARG:NH2	3:F:258:GLN:OE1	2.50	0.44
1:E:1067:VAL:HG12	1:E:1124:ARG:NH2	2.33	0.44
1:M:3:SER:O	1:M:8:GLY:N	2.51	0.44
1:M:441:GLN:CD	1:M:607:PHE:CG	2.95	0.44
1:I:98:LYS:HE3	1:I:127:ASP:OD1	2.18	0.44
1:I:901:LEU:HD22	1:I:912:PHE:CZ	2.43	0.44
1:I:1074:LYS:HG2	1:I:1135:THR:HG21	1.99	0.44
1:I:1084:GLY:C	1:I:1148:ILE:HG23	2.42	0.44
3:B:139:PHE:CD1	3:B:143:PRO:HA	2.53	0.44
3:B:1092:ILE:CG2	3:N:1004:MET:HG3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1075:ASN:HA	3:J:1071:LYS:HE2	2.00	0.44
3:J:105:ASP:O	3:N:614:ARG:NH2	2.51	0.44
3:J:464:ILE:C	3:J:466:PRO:HD3	2.42	0.44
3:J:556:PRO:HB2	5:J:1101:ADP:C8	2.52	0.44
1:A:233:ASP:OD2	1:A:503:GLY:N	2.50	0.44
1:A:262:VAL:HA	1:A:267:ALA:HB3	2.00	0.44
1:A:550:LEU:HD23	1:A:550:LEU:HA	1.88	0.44
1:A:1134:LEU:HD11	1:A:1149:ILE:HG21	1.99	0.44
1:M:441:GLN:CD	1:M:607:PHE:HB3	2.42	0.44
1:M:765:ALA:HB1	1:M:768:LEU:CD1	2.47	0.44
1:I:337:LEU:HD11	1:I:406:LEU:HD22	2.00	0.44
1:I:765:ALA:HB1	1:I:768:LEU:CD1	2.47	0.44
3:B:755:PHE:O	3:B:762:VAL:HG13	2.18	0.44
3:F:373:MET:HE2	3:F:373:MET:HB3	1.87	0.44
3:F:744:LEU:HD21	3:F:765:HIS:CD2	2.32	0.44
3:F:1059:PRO:HA	3:F:1065:THR:OG1	2.17	0.44
3:J:587:MET:HE1	3:J:855:ILE:CB	2.48	0.44
3:N:223:ARG:CD	3:N:228:ASN:ND2	2.79	0.44
1:A:75:TYR:HH	3:B:191:GLN:CG	2.31	0.43
1:A:1074:LYS:HG2	1:A:1135:THR:HG21	1.99	0.43
1:E:66:ASP:HB2	3:B:667:GLN:OE1	2.16	0.43
1:E:234:GLU:H	1:E:234:GLU:CD	2.26	0.43
1:E:527:GLN:HB3	1:E:529:GLN:HE22	1.83	0.43
1:E:1197:PHE:CZ	2:G:375:PRO:HG3	2.53	0.43
2:G:333:VAL:O	2:G:337:PRO:HG3	2.18	0.43
1:M:465:ILE:O	1:M:468:VAL:HG12	2.18	0.43
2:O:341:ARG:O	2:O:342:PRO:C	2.57	0.43
1:I:24:CYS:O	3:J:546:LYS:HD3	2.18	0.43
1:I:768:LEU:HD22	1:I:802:ARG:HH21	1.60	0.43
1:I:1197:PHE:CZ	2:K:375:PRO:HG3	2.52	0.43
2:K:333:VAL:O	2:K:337:PRO:HG3	2.18	0.43
3:B:800:ILE:HD13	3:B:822:ILE:HD12	1.99	0.43
3:B:879:ILE:HG22	3:B:883:MET:HE3	1.99	0.43
4:B:1101:FAR:H91	3:N:1070:THR:HG21	2.00	0.43
3:F:497:VAL:HA	3:F:617:PHE:O	2.17	0.43
3:F:556:PRO:HB2	5:F:1102:ADP:C8	2.52	0.43
3:F:1012:ARG:HD3	3:J:1013:ASN:HA	2.00	0.43
3:J:139:PHE:CD1	3:J:143:PRO:HA	2.53	0.43
3:J:183:VAL:HG12	3:J:467:VAL:HG21	2.00	0.43
3:J:569:LEU:HD22	3:J:679:LEU:HD22	2.00	0.43
3:J:587:MET:CE	3:J:855:ILE:HG13	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:223:ARG:CD	3:N:228:ASN:HD21	2.31	0.43
3:N:1092:ILE:HG23	4:N:1101:FAR:H11	2.00	0.43
1:A:79:GLN:HB2	3:B:194:TYR:O	2.19	0.43
1:A:491:ARG:CG	3:B:62:LEU:CD1	2.96	0.43
1:E:337:LEU:HD11	1:E:406:LEU:HD22	2.00	0.43
1:E:397:LYS:HE3	1:E:400:HIS:CD2	2.51	0.43
1:E:465:ILE:O	1:E:468:VAL:HG12	2.18	0.43
1:E:1215:LEU:O	2:G:330:ARG:NH2	2.52	0.43
2:G:333:VAL:HG13	2:G:343:LEU:HD21	2.00	0.43
1:M:100:GLU:OE2	1:M:495:SER:OG	2.30	0.43
1:M:527:GLN:HB3	1:M:529:GLN:HE22	1.83	0.43
1:I:3:SER:O	1:I:8:GLY:N	2.51	0.43
1:I:211:ALA:HB1	1:I:426:LEU:HD13	1.99	0.43
1:I:441:GLN:HG2	1:I:560:PRO:O	2.18	0.43
3:B:599:LYS:HG2	3:B:646:ILE:HG12	2.00	0.43
3:B:811:THR:HA	3:B:820:GLU:O	2.18	0.43
3:F:304:ALA:O	3:F:469:ARG:HB3	2.18	0.43
3:F:464:ILE:C	3:F:466:PRO:HD3	2.42	0.43
3:F:780:LEU:HD12	3:F:780:LEU:HA	1.84	0.43
3:J:714:VAL:HG11	3:J:743:LEU:CG	2.41	0.43
3:J:924:TRP:CE2	3:J:1059:PRO:HD3	2.53	0.43
3:N:139:PHE:CD1	3:N:143:PRO:HA	2.53	0.43
3:N:523:VAL:HG21	3:N:528:ILE:CD1	2.43	0.43
1:A:1054:TRP:HA	1:A:1057:ARG:HG3	2.00	0.43
1:E:469:TYR:CG	1:E:470:PRO:HA	2.54	0.43
1:E:1130:ALA:HA	1:E:1133:VAL:HG22	2.00	0.43
1:M:441:GLN:HG2	1:M:560:PRO:O	2.18	0.43
1:M:1215:LEU:O	2:O:330:ARG:NH2	2.51	0.43
1:I:57:LEU:HD13	1:I:412:LEU:HD11	1.99	0.43
1:I:169:VAL:O	1:I:173:GLU:HB2	2.17	0.43
1:I:1054:TRP:HA	1:I:1057:ARG:HG3	2.00	0.43
1:I:1130:ALA:HA	1:I:1133:VAL:HG22	2.00	0.43
2:K:374:THR:OG1	2:K:379:LEU:HB2	2.17	0.43
3:F:132:GLN:HE22	3:F:150:HIS:CB	2.32	0.43
3:F:634:ILE:HG22	3:F:638:LEU:CD1	2.47	0.43
3:F:942:TYR:CZ	3:F:984:GLU:OE2	2.69	0.43
3:F:1004:MET:HE2	3:J:1092:ILE:HG22	2.00	0.43
3:N:170:LEU:O	3:N:217:ASP:HB2	2.19	0.43
3:N:924:TRP:CE2	3:N:1059:PRO:HD3	2.53	0.43
1:A:441:GLN:CD	1:A:607:PHE:HB3	2.42	0.43
1:A:825:LEU:O	1:A:829:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:513:ILE:HG22	1:E:514:ARG:HG3	2.01	0.43
1:E:797:GLU:HG2	1:E:807:ARG:HD2	2.00	0.43
1:E:840:LEU:HD11	1:E:898:MET:HE3	2.00	0.43
1:E:1120:GLN:HE22	1:E:1181:ALA:HB3	1.71	0.43
1:M:337:LEU:HD11	1:M:406:LEU:HD22	2.00	0.43
1:M:1054:TRP:HA	1:M:1057:ARG:HG3	2.00	0.43
1:I:797:GLU:HG2	1:I:807:ARG:HD2	2.01	0.43
1:I:1067:VAL:HG12	1:I:1124:ARG:NH2	2.33	0.43
2:K:333:VAL:HG13	2:K:343:LEU:HD21	2.01	0.43
3:B:103:ARG:HH22	3:F:477:ARG:NH1	2.16	0.43
3:B:361:ILE:CG1	3:B:421:LYS:CE	2.96	0.43
3:J:279:LEU:HG	3:J:283:LEU:HD12	2.00	0.43
3:N:587:MET:HE1	3:N:855:ILE:CB	2.48	0.43
3:N:599:LYS:HG2	3:N:646:ILE:HG12	2.00	0.43
1:E:3:SER:O	1:E:8:GLY:N	2.51	0.43
1:E:93:ILE:HG21	3:F:67:THR:HA	2.00	0.43
1:E:134:GLN:HG2	1:E:182:GLY:O	2.19	0.43
1:E:262:VAL:HA	1:E:267:ALA:HB3	2.00	0.43
1:M:189:LYS:C	1:M:191:ASN:N	2.71	0.43
1:I:57:LEU:HD12	1:I:57:LEU:HA	1.79	0.43
1:I:66:ASP:HA	3:N:667:GLN:NE2	2.34	0.43
1:I:458:LYS:HD3	1:I:458:LYS:HA	1.76	0.43
1:I:840:LEU:HD11	1:I:898:MET:HE3	2.00	0.43
1:I:1215:LEU:O	2:K:330:ARG:NH2	2.52	0.43
2:K:382:LEU:HD13	2:K:382:LEU:HA	1.76	0.43
3:B:569:LEU:HD22	3:B:679:LEU:HD22	2.00	0.43
3:B:587:MET:CE	3:B:855:ILE:HG13	2.38	0.43
3:B:737:LEU:HD22	3:B:769:VAL:HG22	2.00	0.43
3:F:568:ILE:HG23	3:F:671:LEU:CD1	2.49	0.43
3:F:811:THR:HA	3:F:820:GLU:O	2.18	0.43
3:F:1001:GLU:HG2	3:J:1092:ILE:HG13	1.85	0.43
3:J:132:GLN:HE22	3:J:150:HIS:CB	2.31	0.43
3:N:183:VAL:HG12	3:N:467:VAL:HG21	2.00	0.43
3:N:1057:THR:HG22	3:N:1064:GLY:HA2	2.00	0.43
1:A:120:THR:HG22	3:B:131:ARG:NE	2.28	0.43
1:A:184:TRP:CD2	1:A:295:ARG:HD2	2.54	0.43
1:A:465:ILE:O	1:A:468:VAL:HG12	2.18	0.43
1:A:513:ILE:HG22	1:A:514:ARG:HG3	2.01	0.43
1:A:854:LEU:O	1:A:867:ILE:N	2.38	0.43
1:E:57:LEU:HD13	1:E:412:LEU:HD11	1.99	0.43
1:E:557:THR:HG22	3:B:514:GLY:HA2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:566:ILE:HA	1:E:570:MET:SD	2.59	0.43
1:E:825:LEU:O	1:E:829:ILE:HG13	2.19	0.43
1:M:1067:VAL:HG12	1:M:1124:ARG:NH2	2.33	0.43
1:I:924:ILE:HD13	1:I:924:ILE:HA	1.89	0.43
3:B:170:LEU:O	3:B:217:ASP:HB2	2.19	0.43
3:B:587:MET:HE1	3:B:855:ILE:CB	2.48	0.43
3:B:924:TRP:CE2	3:B:1059:PRO:HD3	2.53	0.43
3:J:779:TRP:HA	3:J:782:VAL:HG23	2.00	0.43
3:N:714:VAL:HG13	3:N:719:TRP:CD1	2.54	0.43
3:N:744:LEU:HG	3:N:766:ILE:HG13	2.01	0.43
3:N:949:LEU:CD2	3:N:963:LEU:HG	2.49	0.43
1:A:901:LEU:HD22	1:A:912:PHE:CZ	2.43	0.43
1:E:62:ARG:C	1:E:64:ASN:H	2.27	0.43
1:M:184:TRP:CD2	1:M:295:ARG:HD2	2.54	0.43
1:M:797:GLU:HG2	1:M:807:ARG:HD2	2.00	0.43
1:M:918:LEU:HD13	1:M:918:LEU:HA	1.91	0.43
1:M:1074:LYS:HG2	1:M:1135:THR:HG21	1.99	0.43
1:I:62:ARG:C	1:I:64:ASN:N	2.76	0.43
1:I:104:TYR:OH	1:I:495:SER:O	2.31	0.43
3:B:1057:THR:HG22	3:B:1064:GLY:HA2	2.00	0.43
3:N:800:ILE:HD13	3:N:822:ILE:HD12	1.99	0.43
1:A:72:ALA:CB	3:B:260:CYS:HB2	2.49	0.43
1:A:75:TYR:OH	3:B:191:GLN:HG3	2.17	0.43
1:A:79:GLN:HB3	3:B:194:TYR:CG	2.54	0.43
1:A:89:LEU:O	1:A:93:ILE:N	2.43	0.43
1:A:441:GLN:HG2	1:A:560:PRO:O	2.18	0.43
1:A:1168:THR:C	1:A:1170:GLY:H	2.24	0.43
1:E:203:GLY:HA2	1:E:242:LEU:HD11	2.01	0.43
1:E:523:GLN:O	1:E:527:GLN:HG3	2.19	0.43
1:M:28:PRO:HB2	3:N:130:MET:HE2	1.94	0.43
1:M:68:ASP:O	1:M:69:GLU:C	2.58	0.43
1:M:75:TYR:OH	3:N:191:GLN:CD	2.61	0.43
1:M:203:GLY:HA2	1:M:242:LEU:HD11	2.01	0.43
1:M:825:LEU:O	1:M:829:ILE:HG13	2.19	0.43
1:M:1132:LEU:O	1:M:1136:MET:N	2.46	0.43
1:I:28:PRO:CB	3:J:130:MET:HE1	2.39	0.43
1:I:184:TRP:CE2	1:I:295:ARG:HD2	2.54	0.43
1:I:523:GLN:O	1:I:527:GLN:HG3	2.19	0.43
3:B:223:ARG:CD	3:B:228:ASN:ND2	2.79	0.43
3:B:714:VAL:HG13	3:B:719:TRP:CD1	2.54	0.43
3:B:744:LEU:HG	3:B:766:ILE:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:938:PRO:HB3	3:N:1091:LEU:O	2.18	0.43
3:B:949:LEU:CD2	3:B:963:LEU:HG	2.49	0.43
3:F:744:LEU:HG	3:F:766:ILE:HG13	2.01	0.43
3:F:924:TRP:CE2	3:F:1059:PRO:HD3	2.53	0.43
3:F:949:LEU:CD2	3:F:963:LEU:HG	2.49	0.43
3:J:744:LEU:HG	3:J:766:ILE:HG13	2.01	0.43
3:N:279:LEU:HG	3:N:283:LEU:CD1	2.49	0.43
1:A:71:LYS:HD2	3:B:258:GLN:HE22	1.83	0.43
1:A:183:ILE:HD13	1:A:258:SER:HB2	2.00	0.43
1:A:397:LYS:HE3	1:A:400:HIS:CD2	2.51	0.43
1:A:1208:ALA:HB3	2:C:334:ILE:CG1	2.46	0.43
2:G:382:LEU:HD13	2:G:382:LEU:HA	1.76	0.43
1:M:183:ILE:HD13	1:M:258:SER:HB2	2.00	0.43
1:M:840:LEU:HD11	1:M:898:MET:HE3	2.00	0.43
1:M:1067:VAL:HG12	1:M:1124:ARG:HH22	1.84	0.43
1:I:134:GLN:HG2	1:I:182:GLY:O	2.19	0.43
1:I:469:TYR:CG	1:I:470:PRO:HA	2.54	0.43
1:I:1067:VAL:HG12	1:I:1124:ARG:HH22	1.84	0.43
1:I:1118:VAL:HG21	1:I:1127:LEU:HD12	2.01	0.43
3:B:132:GLN:HE22	3:B:150:HIS:CB	2.31	0.43
3:F:214:ARG:HB2	3:F:825:PRO:HB2	2.01	0.43
3:F:576:TYR:HA	3:F:577:PRO:HD3	1.84	0.43
3:F:1014:PRO:HD2	3:J:1012:ARG:NE	2.34	0.43
3:J:216:PRO:HG3	3:J:234:LEU:HD11	1.99	0.43
3:J:477:ARG:CZ	3:N:103:ARG:HH21	2.28	0.43
3:J:714:VAL:HG13	3:J:719:TRP:CD1	2.54	0.43
3:J:755:PHE:O	3:J:762:VAL:HG13	2.18	0.43
3:J:1057:THR:HG22	3:J:1064:GLY:HA2	2.00	0.43
3:N:568:ILE:HG23	3:N:671:LEU:CD1	2.49	0.43
3:N:737:LEU:HD22	3:N:769:VAL:HG22	2.00	0.43
1:A:62:ARG:C	1:A:64:ASN:H	2.27	0.43
1:A:62:ARG:C	1:A:64:ASN:N	2.76	0.43
1:A:797:GLU:HG2	1:A:807:ARG:HD2	2.00	0.43
1:E:184:TRP:CE2	1:E:295:ARG:HD2	2.54	0.43
1:E:441:GLN:HG2	1:E:560:PRO:O	2.18	0.43
1:M:523:GLN:O	1:M:527:GLN:HG3	2.19	0.43
1:M:1208:ALA:C	2:O:334:ILE:HD11	2.44	0.43
2:O:333:VAL:HG13	2:O:343:LEU:HD21	2.00	0.43
1:I:610:THR:HG22	3:N:635:LEU:CD2	2.48	0.43
1:I:770:LEU:HD22	1:I:787:TYR:CE2	2.54	0.43
1:I:1172:ASP:O	1:I:1175:MET:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1092:ILE:CD1	3:N:1001:GLU:CD	2.54	0.43
3:F:1004:MET:CB	3:J:1092:ILE:HG22	2.44	0.43
3:F:1009:VAL:CB	4:F:1103:FAR:H143	2.42	0.43
3:N:714:VAL:HG11	3:N:743:LEU:CG	2.41	0.43
1:A:337:LEU:HD11	1:A:406:LEU:HD22	2.00	0.42
1:A:770:LEU:HD22	1:A:787:TYR:CE2	2.54	0.42
1:A:1215:LEU:O	2:C:330:ARG:NH2	2.52	0.42
2:G:339:ALA:O	2:G:340:LEU:C	2.62	0.42
1:M:184:TRP:CE2	1:M:295:ARG:HD2	2.54	0.42
1:M:441:GLN:HG3	1:M:561:THR:HG23	2.01	0.42
1:M:469:TYR:CG	1:M:470:PRO:HA	2.54	0.42
1:I:203:GLY:HA2	1:I:242:LEU:HD11	2.01	0.42
1:I:441:GLN:CD	1:I:607:PHE:HB3	2.42	0.42
1:I:1141:GLU:OE2	1:I:1215:LEU:HD21	2.19	0.42
3:B:568:ILE:HG23	3:B:671:LEU:CD1	2.49	0.42
3:B:992:GLN:HA	3:B:993:PRO:HD3	1.89	0.42
3:F:532:GLN:H	3:F:532:GLN:HG3	1.51	0.42
3:F:569:LEU:HD22	3:F:679:LEU:HD22	2.00	0.42
3:F:593:LEU:HD12	3:F:593:LEU:HA	1.86	0.42
3:F:606:LYS:HD3	3:F:649:VAL:HG22	2.01	0.42
3:F:714:VAL:HG13	3:F:719:TRP:CD1	2.54	0.42
3:J:214:ARG:HB2	3:J:825:PRO:HB2	2.01	0.42
3:J:789:THR:HG21	3:J:791:LYS:NZ	2.34	0.42
3:N:355:ILE:HD13	3:N:355:ILE:HA	1.78	0.42
3:N:630:ARG:HE	3:N:777:LYS:CE	2.32	0.42
3:N:755:PHE:O	3:N:762:VAL:HG13	2.18	0.42
1:A:203:GLY:HA2	1:A:242:LEU:HD11	2.01	0.42
1:A:840:LEU:HD11	1:A:898:MET:HE3	2.00	0.42
1:A:1067:VAL:HG12	1:A:1124:ARG:NH2	2.33	0.42
1:E:102:PHE:HB2	1:E:110:ASP:O	2.19	0.42
1:E:184:TRP:CD2	1:E:295:ARG:HD2	2.54	0.42
1:E:441:GLN:HG3	1:E:561:THR:HG23	2.01	0.42
1:E:442:VAL:HG22	1:E:601:THR:HG22	2.02	0.42
1:E:800:ASN:ND2	1:E:809:LEU:HD13	2.34	0.42
1:M:62:ARG:C	1:M:64:ASN:N	2.76	0.42
1:M:71:LYS:HD2	3:N:258:GLN:HE22	1.83	0.42
1:M:770:LEU:HD22	1:M:787:TYR:CE2	2.54	0.42
2:O:333:VAL:O	2:O:337:PRO:HG3	2.18	0.42
1:I:94:ARG:NH1	3:J:157:THR:HA	2.34	0.42
1:I:102:PHE:HB2	1:I:110:ASP:O	2.19	0.42
3:B:497:VAL:HG21	3:B:641:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:726:GLU:HA	3:F:729:GLN:HB2	2.01	0.42
3:F:755:PHE:O	3:F:762:VAL:HG13	2.18	0.42
3:F:779:TRP:HA	3:F:782:VAL:HG23	1.99	0.42
3:F:786:ALA:CB	3:F:848:VAL:HG11	2.47	0.42
3:F:1078:LEU:HD11	3:J:1070:THR:CG2	2.48	0.42
3:J:460:SER:CB	3:N:477:ARG:NH2	2.79	0.42
3:J:599:LYS:HG2	3:J:646:ILE:HG12	2.00	0.42
3:J:928:ARG:HH12	3:J:1065:THR:HG21	1.84	0.42
3:J:949:LEU:CD2	3:J:963:LEU:HG	2.49	0.42
3:N:214:ARG:HB2	3:N:825:PRO:HB2	2.00	0.42
3:N:789:THR:HG21	3:N:791:LYS:NZ	2.35	0.42
1:A:442:VAL:HG22	1:A:601:THR:HG22	2.02	0.42
1:A:469:TYR:CG	1:A:470:PRO:HA	2.54	0.42
1:A:566:ILE:HA	1:A:570:MET:SD	2.59	0.42
1:A:1208:ALA:C	2:C:334:ILE:HD11	2.44	0.42
1:M:102:PHE:HB2	1:M:110:ASP:O	2.19	0.42
1:M:368:LEU:HA	1:M:399:PRO:HB3	2.01	0.42
1:M:1118:VAL:HG21	1:M:1127:LEU:HD12	2.01	0.42
1:M:1141:GLU:OE2	1:M:1215:LEU:HD21	2.19	0.42
1:M:1168:THR:C	1:M:1170:GLY:H	2.24	0.42
1:I:441:GLN:HG3	1:I:561:THR:HG23	2.01	0.42
1:I:442:VAL:HG22	1:I:601:THR:HG22	2.02	0.42
1:I:527:GLN:HB3	1:I:529:GLN:HE22	1.83	0.42
1:I:856:VAL:HG22	1:I:865:LYS:O	2.20	0.42
1:I:905:MET:HG2	1:I:912:PHE:CD2	2.55	0.42
3:B:216:PRO:HG3	3:B:234:LEU:CD1	2.50	0.42
3:J:95:TRP:CE2	3:J:99:LEU:HD11	2.55	0.42
3:N:60:LEU:HD23	3:N:60:LEU:HA	1.90	0.42
3:N:754:ASN:O	3:N:755:PHE:C	2.59	0.42
1:E:233:ASP:OD2	1:E:503:GLY:N	2.50	0.42
1:E:1120:GLN:HA	1:E:1121:PRO:HD3	1.89	0.42
1:M:442:VAL:HG22	1:M:601:THR:HG22	2.02	0.42
1:I:566:ILE:HA	1:I:570:MET:SD	2.59	0.42
1:I:1208:ALA:C	2:K:334:ILE:HD11	2.44	0.42
3:B:361:ILE:CG1	3:B:421:LYS:HE3	2.44	0.42
3:F:95:TRP:CE2	3:F:99:LEU:HD11	2.55	0.42
3:F:599:LYS:HG2	3:F:646:ILE:HG12	2.00	0.42
3:J:122:MET:HE3	3:J:122:MET:HB3	1.84	0.42
3:J:282:LEU:HD23	3:J:282:LEU:HA	1.91	0.42
3:J:568:ILE:HG23	3:J:671:LEU:CD1	2.49	0.42
3:J:630:ARG:HE	3:J:777:LYS:CE	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:132:GLN:HE22	3:N:150:HIS:CB	2.32	0.42
1:A:441:GLN:O	1:A:561:THR:HA	2.20	0.42
1:A:527:GLN:HB3	1:A:529:GLN:HE22	1.83	0.42
1:A:856:VAL:HG22	1:A:865:LYS:O	2.20	0.42
1:A:1141:GLU:OE2	1:A:1215:LEU:HD21	2.19	0.42
1:E:1208:ALA:C	2:G:334:ILE:HD11	2.44	0.42
1:M:255:VAL:HG13	1:M:287:LEU:HD11	2.02	0.42
1:M:419:ALA:CB	3:J:524:GLU:OE1	2.63	0.42
1:M:513:ILE:HG22	1:M:514:ARG:HG3	2.01	0.42
2:O:340:LEU:HA	2:O:340:LEU:HD23	1.85	0.42
1:I:62:ARG:C	1:I:64:ASN:H	2.27	0.42
1:I:184:TRP:CD2	1:I:295:ARG:HD2	2.54	0.42
1:I:234:GLU:H	1:I:234:GLU:CD	2.26	0.42
1:I:513:ILE:HG22	1:I:514:ARG:HG3	2.01	0.42
1:I:582:ILE:O	1:I:586:LEU:HG	2.20	0.42
1:I:800:ASN:ND2	1:I:809:LEU:HD13	2.34	0.42
1:I:825:LEU:O	1:I:829:ILE:HG13	2.19	0.42
1:I:1076:TRP:CZ2	1:I:1102:PRO:HD3	2.55	0.42
3:B:214:ARG:HB2	3:B:825:PRO:HB2	2.01	0.42
3:B:579:ILE:HD12	3:B:601:ALA:CB	2.41	0.42
3:B:614:ARG:HA	3:B:615:PRO:HD3	1.92	0.42
3:B:928:ARG:HH12	3:B:1065:THR:HG21	1.85	0.42
3:F:183:VAL:HG12	3:F:467:VAL:HG21	2.00	0.42
3:F:789:THR:HG21	3:F:791:LYS:NZ	2.35	0.42
3:F:928:ARG:HH12	3:F:1065:THR:HG21	1.84	0.42
3:J:216:PRO:HG3	3:J:234:LEU:CD1	2.50	0.42
3:J:580:PHE:CZ	3:J:598:ILE:HG12	2.55	0.42
3:J:872:LEU:HB3	3:J:984:GLU:CD	2.45	0.42
1:A:189:LYS:C	1:A:191:ASN:N	2.71	0.42
1:E:582:ILE:O	1:E:586:LEU:HG	2.20	0.42
1:E:1076:TRP:CZ2	1:E:1102:PRO:HD3	2.55	0.42
1:E:1118:VAL:HG21	1:E:1127:LEU:HD12	2.01	0.42
1:I:66:ASP:CA	3:N:667:GLN:NE2	2.81	0.42
1:I:183:ILE:HD13	1:I:258:SER:HB2	2.00	0.42
3:B:103:ARG:CZ	3:F:477:ARG:CD	2.98	0.42
3:B:580:PHE:CZ	3:B:598:ILE:HG12	2.55	0.42
3:B:942:TYR:CZ	3:B:984:GLU:OE2	2.70	0.42
3:B:957:ILE:CG1	3:B:962:HIS:ND1	2.83	0.42
3:F:1004:MET:HE1	3:J:1091:LEU:HB2	2.00	0.42
3:F:1057:THR:HG22	3:F:1064:GLY:HA2	2.00	0.42
3:J:205:LEU:HD23	3:J:205:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:587:MET:CE	3:N:855:ILE:HG13	2.38	0.42
1:A:184:TRP:CE2	1:A:295:ARG:HD2	2.54	0.42
1:A:236:GLN:HG3	1:A:553:ARG:HB3	2.02	0.42
1:A:400:HIS:O	1:A:404:GLN:N	2.43	0.42
1:A:441:GLN:HG3	1:A:561:THR:HG23	2.01	0.42
1:E:183:ILE:HD13	1:E:258:SER:HB2	2.00	0.42
1:E:856:VAL:HG22	1:E:865:LYS:O	2.20	0.42
1:M:502:MET:HE3	1:M:502:MET:HB3	1.83	0.42
1:M:1076:TRP:CZ2	1:M:1102:PRO:HD3	2.55	0.42
1:I:1205:LYS:O	1:I:1209:THR:OG1	2.31	0.42
3:B:872:LEU:HB3	3:B:984:GLU:CD	2.45	0.42
3:F:580:PHE:CZ	3:F:598:ILE:HG12	2.55	0.42
3:J:170:LEU:O	3:J:217:ASP:HB2	2.19	0.42
3:J:523:VAL:HG21	3:J:528:ILE:CD1	2.43	0.42
3:J:606:LYS:HD3	3:J:649:VAL:HG22	2.02	0.42
3:N:95:TRP:CE2	3:N:99:LEU:HD11	2.55	0.42
3:N:497:VAL:HG21	3:N:641:LEU:HD22	2.01	0.42
3:N:502:GLU:HG3	3:N:685:PHE:HZ	1.85	0.42
1:A:134:GLN:HG2	1:A:182:GLY:O	2.19	0.42
1:A:435:LYS:HE2	1:A:435:LYS:HB3	1.80	0.42
1:A:1118:VAL:HG21	1:A:1127:LEU:HD12	2.01	0.42
1:E:854:LEU:O	1:E:867:ILE:N	2.38	0.42
1:M:441:GLN:O	1:M:561:THR:HA	2.20	0.42
1:M:566:ILE:HA	1:M:570:MET:SD	2.59	0.42
1:I:66:ASP:HB2	3:N:667:GLN:CD	2.44	0.42
1:I:922:LEU:HD13	1:I:1063:ALA:HA	2.02	0.42
1:I:1122:GLU:C	1:I:1124:ARG:N	2.78	0.42
3:B:630:ARG:HE	3:B:777:LYS:CE	2.32	0.42
3:F:992:GLN:HA	3:F:993:PRO:HD3	1.89	0.42
3:J:103:ARG:NH2	3:N:477:ARG:NE	2.67	0.42
3:J:212:VAL:HG12	3:J:239:VAL:HG22	2.01	0.42
3:J:957:ILE:CG1	3:J:962:HIS:ND1	2.83	0.42
3:N:965:GLN:CD	3:N:969:LEU:HD12	2.31	0.42
1:A:789:MET:O	1:A:793:ASP:HB2	2.20	0.42
1:A:1076:TRP:CZ2	1:A:1102:PRO:HD3	2.55	0.42
1:E:905:MET:HG2	1:E:912:PHE:CD2	2.55	0.42
1:M:104:TYR:OH	1:M:495:SER:O	2.31	0.42
1:M:794:TRP:C	1:M:798:LEU:HD12	2.43	0.42
1:M:856:VAL:HG22	1:M:865:LYS:O	2.20	0.42
1:I:771:LYS:HG3	1:I:802:ARG:HH11	1.75	0.42
3:B:88:LEU:CD2	3:B:178:TYR:HA	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:618:LEU:HD21	3:B:656:LEU:HD11	2.02	0.42
3:F:216:PRO:HG3	3:F:234:LEU:CD1	2.49	0.42
3:F:361:ILE:CG1	3:F:421:LYS:CE	2.96	0.42
3:F:957:ILE:CG1	3:F:962:HIS:ND1	2.83	0.42
3:F:1013:ASN:OD1	4:F:1101:FAR:C15	2.68	0.42
3:J:412:VAL:HG22	3:J:429:ARG:HG2	2.02	0.42
3:N:412:VAL:HG22	3:N:429:ARG:HG2	2.02	0.42
3:N:579:ILE:HD12	3:N:601:ALA:CB	2.41	0.42
3:N:614:ARG:HA	3:N:615:PRO:HD3	1.92	0.42
3:N:989:ASN:HD22	3:N:989:ASN:HA	1.63	0.42
1:A:794:TRP:C	1:A:798:LEU:HD12	2.43	0.42
1:A:858:LEU:HD23	1:A:858:LEU:HA	1.80	0.42
1:A:1067:VAL:HG12	1:A:1124:ARG:HH22	1.84	0.42
2:C:333:VAL:HG13	2:C:343:LEU:HD21	2.01	0.42
1:E:71:LYS:HD2	3:F:258:GLN:NE2	2.35	0.42
1:E:79:GLN:HB3	3:F:194:TYR:CG	2.55	0.42
1:E:236:GLN:HE21	1:E:553:ARG:HB3	1.85	0.42
1:E:441:GLN:O	1:E:561:THR:HA	2.20	0.42
1:E:1057:ARG:H	1:E:1057:ARG:HG2	1.61	0.42
1:E:1205:LYS:O	1:E:1209:THR:OG1	2.31	0.42
1:M:236:GLN:HG3	1:M:553:ARG:HB3	2.02	0.42
1:M:400:HIS:O	1:M:404:GLN:N	2.43	0.42
1:M:905:MET:HG2	1:M:912:PHE:CD2	2.55	0.42
1:I:368:LEU:HA	1:I:399:PRO:HB3	2.01	0.42
1:I:502:MET:O	1:I:523:GLN:NE2	2.50	0.42
3:B:212:VAL:HG12	3:B:239:VAL:HG22	2.01	0.42
3:B:637:MET:HG3	3:B:646:ILE:CD1	2.50	0.42
3:F:173:ASN:ND2	3:F:220:VAL:CA	2.80	0.42
3:F:1006:VAL:HG22	3:F:1073:VAL:HG21	2.02	0.42
3:F:1016:LEU:HD11	4:F:1101:FAR:H92	2.02	0.42
3:J:618:LEU:HD21	3:J:656:LEU:HD11	2.02	0.42
3:N:361:ILE:CG1	3:N:421:LYS:CE	2.96	0.42
3:N:580:PHE:CZ	3:N:598:ILE:HG12	2.55	0.42
3:N:606:LYS:HD3	3:N:649:VAL:HG22	2.02	0.42
1:E:1141:GLU:OE2	1:E:1215:LEU:HD21	2.19	0.41
1:M:134:GLN:HG2	1:M:182:GLY:O	2.19	0.41
1:M:332:TRP:HZ3	1:M:355:LEU:HD21	1.85	0.41
1:I:236:GLN:HG3	1:I:553:ARG:HB3	2.02	0.41
1:I:236:GLN:HE21	1:I:553:ARG:HB3	1.85	0.41
3:B:541:LEU:O	3:B:551:GLY:HA2	2.21	0.41
3:B:726:GLU:HA	3:B:729:GLN:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:170:LEU:O	3:F:217:ASP:HB2	2.19	0.41
3:F:173:ASN:HD22	3:F:220:VAL:CA	2.33	0.41
3:F:618:LEU:HD21	3:F:656:LEU:HD11	2.02	0.41
3:J:103:ARG:HH22	3:N:477:ARG:NH1	2.18	0.41
3:J:355:ILE:HD13	3:J:355:ILE:HA	1.78	0.41
3:N:216:PRO:HG3	3:N:234:LEU:CD1	2.50	0.41
3:N:618:LEU:HD21	3:N:656:LEU:HD11	2.02	0.41
3:N:957:ILE:CG1	3:N:962:HIS:ND1	2.83	0.41
1:A:11:LEU:HA	1:A:11:LEU:HD23	1.81	0.41
1:A:368:LEU:HA	1:A:399:PRO:HB3	2.01	0.41
1:A:523:GLN:O	1:A:527:GLN:HG3	2.19	0.41
1:E:441:GLN:CD	1:E:607:PHE:HB3	2.42	0.41
1:E:765:ALA:O	1:E:766:LEU:HD23	2.20	0.41
2:G:333:VAL:HG13	2:G:343:LEU:CD2	2.50	0.41
1:M:800:ASN:ND2	1:M:809:LEU:HD13	2.34	0.41
3:B:173:ASN:HD22	3:B:220:VAL:CA	2.33	0.41
3:B:502:GLU:HG3	3:B:685:PHE:HZ	1.85	0.41
3:B:789:THR:HG21	3:B:791:LYS:NZ	2.35	0.41
3:B:1063:ARG:HA	3:B:1063:ARG:HD2	1.82	0.41
3:B:1067:SER:HB2	3:N:1078:LEU:HD22	2.02	0.41
3:F:283:LEU:HD23	3:F:307:LEU:CD1	2.51	0.41
3:F:541:LEU:O	3:F:551:GLY:HA2	2.21	0.41
3:F:872:LEU:HB3	3:F:984:GLU:CD	2.45	0.41
3:F:924:TRP:CH2	3:J:1093:SER:C	2.92	0.41
3:F:994:GLN:H	3:F:994:GLN:HG2	1.53	0.41
3:J:1006:VAL:HG22	3:J:1073:VAL:HG21	2.02	0.41
3:N:56:VAL:CG2	3:N:449:ILE:HG13	2.51	0.41
3:N:212:VAL:HG12	3:N:239:VAL:HG22	2.01	0.41
3:N:637:MET:HG3	3:N:646:ILE:CD1	2.50	0.41
3:N:826:LEU:HD22	3:N:830:VAL:CG1	2.43	0.41
3:N:1063:ARG:HD2	3:N:1063:ARG:HA	1.82	0.41
1:A:102:PHE:HB2	1:A:110:ASP:O	2.19	0.41
1:E:368:LEU:HA	1:E:399:PRO:HB3	2.01	0.41
1:E:530:PHE:CD2	1:E:837:VAL:HG22	2.55	0.41
1:E:770:LEU:HD22	1:E:787:TYR:CE2	2.54	0.41
1:E:922:LEU:HD13	1:E:1063:ALA:HA	2.02	0.41
1:E:1145:ILE:HG23	1:E:1215:LEU:HD13	2.03	0.41
1:M:530:PHE:CD2	1:M:837:VAL:HG22	2.55	0.41
1:M:1120:GLN:HA	1:M:1121:PRO:HD3	1.89	0.41
1:I:1208:ALA:CB	4:I:1301:FAR:H51	2.50	0.41
3:B:454:LEU:HD23	3:B:454:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1003:LEU:HD21	3:B:1024:LEU:HD11	2.01	0.41
3:F:405:VAL:HA	3:F:445:GLN:HE22	1.86	0.41
3:F:413:PRO:CG	3:F:416:PHE:CD2	2.95	0.41
3:F:1015:GLU:CD	4:F:1101:FAR:C4	2.81	0.41
3:J:246:LEU:HB3	3:J:267:VAL:HG11	2.02	0.41
3:J:497:VAL:HG21	3:J:641:LEU:HD22	2.02	0.41
3:N:223:ARG:CB	3:N:228:ASN:OD1	2.68	0.41
3:N:246:LEU:HB3	3:N:267:VAL:HG11	2.02	0.41
3:N:413:PRO:CG	3:N:416:PHE:CD2	2.95	0.41
3:N:928:ARG:HH12	3:N:1065:THR:HG21	1.84	0.41
2:C:341:ARG:O	2:C:342:PRO:C	2.57	0.41
1:E:89:LEU:O	1:E:93:ILE:N	2.43	0.41
1:E:94:ARG:HG3	3:F:67:THR:HG21	2.03	0.41
1:E:153:LEU:HD23	1:E:153:LEU:HA	1.94	0.41
1:M:1134:LEU:HD23	1:M:1134:LEU:HA	1.90	0.41
1:I:62:ARG:CZ	3:J:258:GLN:OE1	2.62	0.41
1:I:255:VAL:HG13	1:I:287:LEU:HD11	2.02	0.41
1:I:441:GLN:O	1:I:561:THR:HA	2.20	0.41
1:I:502:MET:HE3	1:I:502:MET:HB3	1.83	0.41
1:I:765:ALA:O	1:I:766:LEU:HD23	2.20	0.41
1:I:1208:ALA:O	2:K:334:ILE:HD11	2.21	0.41
3:B:95:TRP:CE2	3:B:99:LEU:HD11	2.55	0.41
3:B:183:VAL:HG12	3:B:467:VAL:HG21	2.00	0.41
3:F:212:VAL:HG12	3:F:239:VAL:HG22	2.01	0.41
3:F:637:MET:HG3	3:F:646:ILE:CD1	2.50	0.41
3:F:646:ILE:O	3:F:646:ILE:HG23	2.21	0.41
3:F:737:LEU:HD21	3:F:772:ARG:CZ	2.51	0.41
3:F:878:TRP:CE3	3:F:933:SER:HA	2.55	0.41
3:F:965:GLN:CD	3:F:969:LEU:HD12	2.31	0.41
3:F:1004:MET:CE	3:J:1092:ILE:HG22	2.50	0.41
3:N:361:ILE:CG1	3:N:421:LYS:HE3	2.44	0.41
3:N:541:LEU:O	3:N:551:GLY:HA2	2.20	0.41
3:N:872:LEU:HB3	3:N:984:GLU:CD	2.45	0.41
1:A:204:MET:HE2	1:A:204:MET:HB2	1.84	0.41
1:A:905:MET:HG2	1:A:912:PHE:CD2	2.55	0.41
1:A:1145:ILE:HD11	1:A:1149:ILE:HD11	2.03	0.41
2:C:366:ASN:O	2:C:367:ARG:HB2	2.21	0.41
1:E:159:LEU:HD22	3:F:113:GLU:OE1	2.21	0.41
1:E:332:TRP:HZ3	1:E:355:LEU:HD21	1.84	0.41
1:E:928:ALA:CB	1:E:943:THR:HG22	2.50	0.41
1:E:1067:VAL:HG12	1:E:1124:ARG:HH22	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:332:TRP:O	1:M:336:ILE:HG13	2.21	0.41
1:M:922:LEU:HD13	1:M:1063:ALA:HA	2.02	0.41
1:M:1208:ALA:O	2:O:334:ILE:HD11	2.21	0.41
2:O:333:VAL:HG13	2:O:343:LEU:CD2	2.50	0.41
1:I:789:MET:O	1:I:793:ASP:HB2	2.20	0.41
3:B:342:LEU:HD22	3:B:421:LYS:HZ3	1.86	0.41
3:B:413:PRO:CG	3:B:416:PHE:CD2	2.95	0.41
3:F:56:VAL:CG2	3:F:449:ILE:HG13	2.51	0.41
3:J:55:ILE:HD13	3:J:404:PRO:HD2	2.03	0.41
3:J:56:VAL:CG2	3:J:449:ILE:HG13	2.51	0.41
3:J:223:ARG:CD	3:J:228:ASN:ND2	2.79	0.41
3:J:502:GLU:HG3	3:J:685:PHE:HZ	1.85	0.41
3:J:646:ILE:HG23	3:J:646:ILE:O	2.21	0.41
3:J:726:GLU:HA	3:J:729:GLN:HB2	2.01	0.41
3:J:737:LEU:HD21	3:J:772:ARG:CZ	2.51	0.41
3:J:1010:LEU:HD23	3:J:1010:LEU:HA	1.90	0.41
3:N:223:ARG:HD3	3:N:228:ASN:HD21	1.78	0.41
1:A:765:ALA:O	1:A:766:LEU:HD23	2.20	0.41
1:E:83:LYS:HD3	3:F:195:ASN:OD1	2.21	0.41
1:E:236:GLN:HG3	1:E:553:ARG:HB3	2.02	0.41
2:G:359:VAL:HG21	2:G:367:ARG:CD	2.51	0.41
1:M:765:ALA:O	1:M:766:LEU:HD23	2.20	0.41
1:M:928:ALA:CB	1:M:943:THR:HG22	2.50	0.41
1:I:64:ASN:N	3:N:567:ARG:NH2	2.68	0.41
3:B:56:VAL:CG2	3:B:449:ILE:HG13	2.51	0.41
3:B:246:LEU:HB3	3:B:267:VAL:HG11	2.02	0.41
3:F:45:LEU:HG	3:F:104:ILE:HD11	2.02	0.41
3:F:1003:LEU:HD21	3:F:1024:LEU:HD11	2.02	0.41
3:J:603:GLN:HA	3:J:649:VAL:HG21	2.03	0.41
3:J:712:PRO:HD3	3:J:780:LEU:CD2	2.41	0.41
3:N:576:TYR:HA	3:N:577:PRO:HD3	1.84	0.41
1:A:458:LYS:HD3	1:A:458:LYS:HA	1.76	0.41
1:A:582:ILE:O	1:A:586:LEU:HG	2.20	0.41
1:E:163:ASN:CG	1:E:489:ASN:ND2	2.79	0.41
1:I:332:TRP:HZ3	1:I:355:LEU:HD21	1.85	0.41
1:I:530:PHE:CD2	1:I:837:VAL:HG22	2.55	0.41
3:B:938:PRO:HB3	3:N:1091:LEU:C	2.46	0.41
3:F:614:ARG:HA	3:F:615:PRO:HD3	1.92	0.41
3:F:656:LEU:HD12	3:F:656:LEU:HA	1.92	0.41
3:F:796:ILE:O	3:F:800:ILE:HG13	2.21	0.41
3:J:173:ASN:HD22	3:J:220:VAL:CA	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:614:ARG:HA	3:J:615:PRO:HD3	1.92	0.41
3:N:591:VAL:HG21	3:N:634:ILE:CG1	2.49	0.41
3:N:603:GLN:HA	3:N:649:VAL:HG21	2.03	0.41
1:A:255:VAL:HG13	1:A:287:LEU:HD11	2.02	0.41
1:A:332:TRP:HZ3	1:A:355:LEU:HD21	1.85	0.41
1:A:530:PHE:CD2	1:A:837:VAL:HG22	2.55	0.41
1:A:779:GLN:C	1:A:781:ASP:H	2.29	0.41
1:A:1208:ALA:CB	4:A:1301:FAR:H51	2.51	0.41
1:A:1208:ALA:O	2:C:334:ILE:HD11	2.21	0.41
1:E:12:ASP:O	1:E:16:ARG:HG3	2.21	0.41
1:M:12:ASP:O	1:M:16:ARG:HG3	2.21	0.41
1:M:62:ARG:C	1:M:64:ASN:H	2.27	0.41
1:I:402:TRP:CD1	1:I:402:TRP:C	2.99	0.41
3:B:45:LEU:HG	3:B:104:ILE:HD11	2.02	0.41
3:B:55:ILE:HD13	3:B:404:PRO:HD2	2.03	0.41
3:B:412:VAL:HG22	3:B:429:ARG:HG2	2.02	0.41
3:B:606:LYS:HD3	3:B:649:VAL:HG22	2.01	0.41
3:B:796:ILE:O	3:B:800:ILE:HG13	2.21	0.41
3:F:55:ILE:HD13	3:F:404:PRO:HD2	2.03	0.41
3:F:60:LEU:HD23	3:F:60:LEU:HA	1.90	0.41
3:F:279:LEU:HG	3:F:283:LEU:HD22	2.02	0.41
3:F:630:ARG:HE	3:F:777:LYS:CE	2.32	0.41
3:J:45:LEU:HG	3:J:104:ILE:HD11	2.02	0.41
3:J:173:ASN:ND2	3:J:220:VAL:CA	2.80	0.41
3:J:730:LYS:O	3:J:733:ASP:N	2.46	0.41
3:J:796:ILE:HD13	3:J:796:ILE:HA	1.87	0.41
3:N:55:ILE:HD13	3:N:404:PRO:HD2	2.03	0.41
3:N:173:ASN:HD22	3:N:220:VAL:CA	2.33	0.41
1:A:4:ARG:NH2	1:A:70:ASP:OD2	2.54	0.41
1:A:12:ASP:O	1:A:16:ARG:HG3	2.21	0.41
1:A:72:ALA:CB	3:B:262:TRP:CZ2	3.04	0.41
1:A:75:TYR:HH	3:B:191:GLN:CB	2.27	0.41
1:A:419:ALA:CB	3:F:524:GLU:OE1	2.61	0.41
1:A:502:MET:HB3	1:A:502:MET:HE3	1.83	0.41
1:A:800:ASN:ND2	1:A:809:LEU:HD13	2.34	0.41
1:A:836:LYS:HD3	1:A:877:THR:HG21	2.03	0.41
1:A:922:LEU:HD13	1:A:1063:ALA:HA	2.02	0.41
1:A:1145:ILE:HG23	1:A:1215:LEU:HD13	2.03	0.41
2:C:333:VAL:HG13	2:C:343:LEU:CD2	2.50	0.41
1:E:592:GLY:O	1:E:598:ARG:HA	2.21	0.41
1:E:1208:ALA:O	2:G:334:ILE:HD11	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:135:LEU:HB2	1:M:201:SER:HB3	2.03	0.41
1:M:173:GLU:HG2	1:M:234:GLU:HG2	2.03	0.41
1:M:236:GLN:HE21	1:M:553:ARG:HB3	1.85	0.41
1:M:582:ILE:O	1:M:586:LEU:HG	2.20	0.41
1:M:789:MET:O	1:M:793:ASP:HB2	2.20	0.41
1:I:12:ASP:O	1:I:16:ARG:HG3	2.21	0.41
1:I:28:PRO:CG	3:J:547:LEU:CG	2.81	0.41
1:I:314:GLU:O	1:I:317:GLU:HG2	2.21	0.41
3:B:529:TRP:CZ2	3:B:682:PHE:HB3	2.56	0.41
3:B:576:TYR:HA	3:B:577:PRO:HD3	1.84	0.41
3:B:957:ILE:HG12	3:B:962:HIS:ND1	2.36	0.41
3:B:965:GLN:CD	3:B:969:LEU:HD12	2.31	0.41
3:B:1012:ARG:CD	4:N:1101:FAR:H142	2.41	0.41
3:F:246:LEU:HB3	3:F:267:VAL:HG11	2.02	0.41
3:F:279:LEU:CD1	3:F:283:LEU:HD13	2.51	0.41
3:F:412:VAL:HG22	3:F:429:ARG:HG2	2.02	0.41
3:F:497:VAL:HG21	3:F:641:LEU:HD22	2.01	0.41
3:F:730:LYS:O	3:F:733:ASP:N	2.46	0.41
3:J:532:GLN:H	3:J:532:GLN:HG3	1.51	0.41
3:J:1003:LEU:HD21	3:J:1024:LEU:HD11	2.02	0.41
3:N:529:TRP:CZ2	3:N:682:PHE:HB3	2.56	0.41
3:N:722:LYS:HB3	3:N:724:THR:OG1	2.21	0.41
3:N:796:ILE:O	3:N:800:ILE:HG13	2.21	0.41
3:N:878:TRP:CE3	3:N:933:SER:HA	2.55	0.41
3:N:1003:LEU:HD21	3:N:1024:LEU:HD11	2.01	0.41
1:A:135:LEU:HB2	1:A:201:SER:HB3	2.03	0.41
1:A:592:GLY:O	1:A:598:ARG:HA	2.21	0.41
1:A:917:ARG:HB3	1:A:1065:ASN:HD22	1.86	0.41
1:E:79:GLN:HB3	3:F:194:TYR:CA	2.51	0.41
1:E:332:TRP:O	1:E:336:ILE:HG13	2.21	0.41
1:E:924:ILE:HD13	1:E:924:ILE:HA	1.90	0.41
1:M:233:ASP:OD2	1:M:503:GLY:N	2.50	0.41
1:M:610:THR:HG22	3:J:635:LEU:CD2	2.51	0.41
1:M:1145:ILE:HD11	1:M:1149:ILE:HD11	2.03	0.41
1:I:11:LEU:HD23	1:I:11:LEU:HA	1.81	0.41
1:I:71:LYS:HD2	3:J:258:GLN:HE22	1.85	0.41
1:I:163:ASN:CG	1:I:489:ASN:ND2	2.79	0.41
1:I:779:GLN:C	1:I:781:ASP:H	2.29	0.41
1:I:1145:ILE:HG23	1:I:1215:LEU:HD13	2.03	0.41
2:K:339:ALA:O	2:K:340:LEU:C	2.62	0.41
2:K:359:VAL:HG21	2:K:367:ARG:CD	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:103:ARG:CZ	3:F:477:ARG:HD3	2.50	0.41
3:F:523:VAL:HG21	3:F:528:ILE:CD1	2.43	0.41
3:J:405:VAL:HA	3:J:445:GLN:HE22	1.86	0.41
3:J:526:ILE:HD13	3:J:660:ILE:HD13	1.90	0.41
3:J:541:LEU:O	3:J:551:GLY:HA2	2.20	0.41
3:N:60:LEU:HD23	3:N:442:LEU:HD22	2.03	0.41
3:N:714:VAL:HG21	3:N:743:LEU:HD11	2.03	0.41
2:C:340:LEU:HD23	2:C:340:LEU:HA	1.85	0.40
1:E:79:GLN:HB2	3:F:194:TYR:O	2.21	0.40
1:E:255:VAL:HG13	1:E:287:LEU:HD11	2.02	0.40
1:E:779:GLN:C	1:E:781:ASP:H	2.29	0.40
1:E:798:LEU:O	1:E:806:VAL:HG23	2.21	0.40
1:M:314:GLU:O	1:M:317:GLU:HG2	2.21	0.40
1:M:402:TRP:CD1	1:M:402:TRP:C	2.99	0.40
1:M:779:GLN:C	1:M:781:ASP:H	2.29	0.40
1:I:4:ARG:NH2	1:I:70:ASP:OD2	2.54	0.40
1:I:64:ASN:CA	3:N:567:ARG:NH2	2.84	0.40
1:I:592:GLY:O	1:I:598:ARG:HA	2.21	0.40
1:I:1145:ILE:HD11	1:I:1149:ILE:HD11	2.03	0.40
3:B:84:ILE:HG12	3:B:151:SER:O	2.22	0.40
3:B:338:TYR:O	3:B:339:ARG:C	2.64	0.40
3:B:405:VAL:HA	3:B:445:GLN:HE22	1.86	0.40
3:B:714:VAL:HG21	3:B:743:LEU:HD11	2.03	0.40
3:B:878:TRP:CE3	3:B:933:SER:HA	2.55	0.40
3:F:60:LEU:HD11	3:F:446:ALA:HB2	2.03	0.40
3:F:263:SER:O	3:F:263:SER:OG	2.39	0.40
3:F:283:LEU:HD21	3:F:307:LEU:CD1	2.51	0.40
3:F:1091:LEU:N	3:F:1091:LEU:HD22	2.36	0.40
3:J:279:LEU:HD11	3:J:283:LEU:HD11	2.01	0.40
3:J:413:PRO:CG	3:J:416:PHE:CD2	2.95	0.40
3:J:637:MET:HG3	3:J:646:ILE:CD1	2.50	0.40
3:N:392:LEU:HA	3:N:395:VAL:HG22	2.03	0.40
3:N:730:LYS:O	3:N:733:ASP:N	2.46	0.40
1:A:350:GLU:HG2	1:A:351:TYR:N	2.37	0.40
1:A:918:LEU:HD13	1:A:918:LEU:HA	1.91	0.40
1:E:51:ILE:HG12	1:E:81:VAL:HA	2.03	0.40
1:E:314:GLU:O	1:E:317:GLU:HG2	2.21	0.40
1:E:804:ALA:HB1	1:E:809:LEU:CD1	2.43	0.40
1:E:918:LEU:HD13	1:E:918:LEU:HA	1.91	0.40
1:E:929:THR:HG21	1:E:1059:ARG:HD2	2.03	0.40
1:M:1205:LYS:CG	2:O:337:PRO:CG	3.00	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:135:LEU:HB2	1:I:201:SER:HB3	2.03	0.40
1:I:332:TRP:O	1:I:336:ILE:HG13	2.21	0.40
1:I:794:TRP:C	1:I:798:LEU:HD12	2.43	0.40
2:K:333:VAL:HG13	2:K:343:LEU:CD2	2.50	0.40
3:B:60:LEU:HD11	3:B:446:ALA:HB2	2.03	0.40
3:B:252:PHE:HD2	3:B:254:LEU:HD23	1.86	0.40
3:B:302:TYR:OH	3:B:464:ILE:HD11	2.21	0.40
3:B:392:LEU:HA	3:B:395:VAL:HG22	2.03	0.40
3:B:722:LYS:HB3	3:B:724:THR:OG1	2.21	0.40
3:B:737:LEU:HD21	3:B:772:ARG:CZ	2.51	0.40
3:F:173:ASN:HD22	3:F:220:VAL:HA	1.84	0.40
3:F:724:THR:CB	3:F:726:GLU:HB2	2.51	0.40
3:J:84:ILE:HG12	3:J:151:SER:O	2.22	0.40
3:J:302:TYR:OH	3:J:464:ILE:HD11	2.21	0.40
3:J:722:LYS:HB3	3:J:724:THR:OG1	2.21	0.40
3:N:45:LEU:HG	3:N:104:ILE:HD11	2.02	0.40
3:N:403:TYR:HA	3:N:404:PRO:HD3	1.95	0.40
3:N:405:VAL:HA	3:N:445:GLN:HE22	1.86	0.40
3:N:724:THR:CB	3:N:726:GLU:HB2	2.51	0.40
3:N:737:LEU:HD21	3:N:772:ARG:CZ	2.51	0.40
1:A:281:GLN:O	1:A:285:THR:OG1	2.33	0.40
2:C:339:ALA:O	2:C:340:LEU:C	2.62	0.40
1:E:1209:THR:CG2	2:G:334:ILE:HG21	2.52	0.40
1:M:51:ILE:HG12	1:M:81:VAL:HA	2.03	0.40
1:M:350:GLU:HG2	1:M:351:TYR:N	2.37	0.40
1:M:550:LEU:HD23	1:M:550:LEU:HA	1.88	0.40
1:M:863:ARG:H	1:M:863:ARG:HG3	1.52	0.40
1:I:173:GLU:HG2	1:I:234:GLU:HG2	2.03	0.40
2:K:376:LYS:HA	2:K:379:LEU:HB3	2.04	0.40
3:B:60:LEU:HD23	3:B:442:LEU:HD22	2.03	0.40
3:B:283:LEU:HB3	3:B:312:LEU:CD1	2.48	0.40
3:B:646:ILE:HG23	3:B:646:ILE:O	2.21	0.40
3:B:720:LYS:HE3	3:B:720:LYS:HB2	1.92	0.40
3:F:502:GLU:HG3	3:F:685:PHE:HZ	1.85	0.40
3:F:587:MET:CE	3:F:855:ILE:HG13	2.38	0.40
3:F:671:LEU:HD22	3:F:680:PRO:HG3	2.02	0.40
3:F:722:LYS:HB3	3:F:724:THR:OG1	2.21	0.40
3:J:556:PRO:HB2	5:J:1101:ADP:H8	1.87	0.40
3:N:646:ILE:HG23	3:N:646:ILE:O	2.21	0.40
3:N:726:GLU:HA	3:N:729:GLN:HB2	2.02	0.40
3:N:1006:VAL:HG22	3:N:1073:VAL:HG21	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ILE:HG12	1:A:81:VAL:HA	2.03	0.40
1:A:89:LEU:HD12	1:A:89:LEU:HA	1.94	0.40
1:A:332:TRP:O	1:A:336:ILE:HG13	2.21	0.40
1:E:28:PRO:O	3:F:130:MET:SD	2.79	0.40
1:E:133:LEU:O	1:E:181:PHE:HB2	2.22	0.40
1:E:173:GLU:HG2	1:E:234:GLU:HG2	2.03	0.40
1:E:245:LEU:HG	1:E:851:GLN:CD	2.47	0.40
1:M:163:ASN:CG	1:M:489:ASN:ND2	2.79	0.40
1:M:1145:ILE:HG23	1:M:1215:LEU:HD13	2.02	0.40
2:O:359:VAL:HG21	2:O:367:ARG:CD	2.51	0.40
1:I:133:LEU:O	1:I:181:PHE:HB2	2.22	0.40
1:I:798:LEU:O	1:I:806:VAL:HG23	2.22	0.40
1:I:1167:LYS:O	1:I:1170:GLY:HA2	2.21	0.40
2:K:366:ASN:O	2:K:367:ARG:HB2	2.21	0.40
3:B:671:LEU:HD22	3:B:680:PRO:HG3	2.02	0.40
3:F:84:ILE:HG12	3:F:151:SER:O	2.22	0.40
3:F:223:ARG:CB	3:F:228:ASN:OD1	2.68	0.40
3:J:506:LEU:CD1	3:J:626:ILE:HG12	2.51	0.40
3:J:786:ALA:CB	3:J:848:VAL:HG11	2.47	0.40
3:N:506:LEU:CD1	3:N:626:ILE:HG12	2.51	0.40
1:A:176:TYR:HB2	1:A:241:ILE:CD1	2.50	0.40
1:A:1167:LYS:O	1:A:1170:GLY:HA2	2.21	0.40
1:E:350:GLU:HG2	1:E:351:TYR:N	2.37	0.40
1:E:1065:ASN:ND2	1:E:1116:ASN:HD22	2.20	0.40
1:E:1167:LYS:O	1:E:1170:GLY:HA2	2.21	0.40
1:M:4:ARG:NH2	1:M:70:ASP:OD2	2.54	0.40
1:M:933:HIS:O	1:M:936:ARG:HG3	2.22	0.40
2:O:376:LYS:HA	2:O:379:LEU:HB3	2.04	0.40
1:I:355:LEU:HD12	1:I:355:LEU:O	2.22	0.40
1:I:922:LEU:HD23	1:I:922:LEU:HA	1.81	0.40
1:I:1209:THR:CG2	2:K:334:ILE:HG21	2.52	0.40
3:B:373:MET:HE2	3:B:373:MET:HB3	1.87	0.40
3:F:454:LEU:HD23	3:F:454:LEU:HA	1.90	0.40
3:F:529:TRP:CZ2	3:F:682:PHE:HB3	2.56	0.40
3:F:775:SER:C	3:F:777:LYS:H	2.29	0.40
3:J:260:CYS:SG	3:J:261:SER:N	2.94	0.40
3:J:477:ARG:NH2	3:N:460:SER:CB	2.82	0.40
3:N:532:GLN:H	3:N:532:GLN:HG3	1.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	954/1223 (78%)	912 (96%)	42 (4%)	0	100	100
1	E	954/1223 (78%)	914 (96%)	40 (4%)	0	100	100
1	I	954/1223 (78%)	912 (96%)	42 (4%)	0	100	100
1	M	954/1223 (78%)	913 (96%)	41 (4%)	0	100	100
2	C	44/387 (11%)	43 (98%)	1 (2%)	0	100	100
2	G	44/387 (11%)	42 (96%)	2 (4%)	0	100	100
2	K	44/387 (11%)	42 (96%)	2 (4%)	0	100	100
2	O	44/387 (11%)	42 (96%)	2 (4%)	0	100	100
3	B	1029/1093 (94%)	992 (96%)	36 (4%)	1 (0%)	48	77
3	F	1029/1093 (94%)	995 (97%)	34 (3%)	0	100	100
3	J	1029/1093 (94%)	994 (97%)	35 (3%)	0	100	100
3	N	1029/1093 (94%)	993 (96%)	36 (4%)	0	100	100
All	All	8108/10812 (75%)	7794 (96%)	313 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	283	LEU

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	
2	K	10/349 (3%)	7 (70%)	3 (30%)	0	1
3	B	816/975 (84%)	773 (95%)	43 (5%)	20	52
3	F	924/975 (95%)	878 (95%)	46 (5%)	22	53
3	J	924/975 (95%)	876 (95%)	48 (5%)	21	52
3	N	924/975 (95%)	878 (95%)	46 (5%)	22	53
All	All	3598/4249 (85%)	3412 (95%)	186 (5%)	22	52

All (186) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	374	THR
2	K	378	VAL
2	K	382	LEU
3	B	43	GLU
3	B	56	VAL
3	B	88	LEU
3	B	151	SER
3	B	152	VAL
3	B	155	VAL
3	B	196	THR
3	B	220	VAL
3	B	241	LEU
3	B	282	LEU
3	B	298	PRO
3	B	303	PRO
3	B	307	LEU
3	B	341	SER
3	B	348	CYS
3	B	355	ILE
3	B	531	GLN
3	B	567	ARG
3	B	581	ASP
3	B	593	LEU
3	B	620	LEU
3	B	646	ILE
3	B	664	VAL
3	B	724	THR
3	B	750	ARG
3	B	767	GLU
3	B	769	VAL
3	B	778	LEU

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Mol	Chain	Res	Type
3	B	791	LYS
3	B	820	GLU
3	B	833	ASN
3	B	855	ILE
3	B	922	ARG
3	B	958	VAL
3	B	966	GLN
3	B	1008	ILE
3	B	1040	SER
3	B	1067	SER
3	B	1082	VAL
3	B	1087	ASP
3	B	1090	CYS
3	B	1091	LEU
3	B	1092	ILE
3	F	43	GLU
3	F	56	VAL
3	F	88	LEU
3	F	151	SER
3	F	152	VAL
3	F	155	VAL
3	F	196	THR
3	F	220	VAL
3	F	241	LEU
3	F	286	GLU
3	F	298	PRO
3	F	303	PRO
3	F	307	LEU
3	F	341	SER
3	F	348	CYS
3	F	355	ILE
3	F	460	SER
3	F	461	PRO
3	F	467	VAL
3	F	471	VAL
3	F	531	GLN
3	F	567	ARG
3	F	581	ASP
3	F	593	LEU
3	F	620	LEU
3	F	646	ILE
3	F	664	VAL

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Mol	Chain	Res	Type
3	F	724	THR
3	F	750	ARG
3	F	767	GLU
3	F	769	VAL
3	F	778	LEU
3	F	791	LYS
3	F	820	GLU
3	F	833	ASN
3	F	855	ILE
3	F	922	ARG
3	F	958	VAL
3	F	966	GLN
3	F	1008	ILE
3	F	1040	SER
3	F	1067	SER
3	F	1082	VAL
3	F	1087	ASP
3	F	1090	CYS
3	F	1092	ILE
3	J	43	GLU
3	J	56	VAL
3	J	88	LEU
3	J	151	SER
3	J	152	VAL
3	J	155	VAL
3	J	196	THR
3	J	220	VAL
3	J	241	LEU
3	J	253	ASN
3	J	286	GLU
3	J	298	PRO
3	J	303	PRO
3	J	307	LEU
3	J	341	SER
3	J	348	CYS
3	J	355	ILE
3	J	460	SER
3	J	461	PRO
3	J	467	VAL
3	J	471	VAL
3	J	531	GLN
3	J	567	ARG

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Mol	Chain	Res	Type
3	J	581	ASP
3	J	593	LEU
3	J	620	LEU
3	J	646	ILE
3	J	664	VAL
3	J	724	THR
3	J	750	ARG
3	J	767	GLU
3	J	769	VAL
3	J	778	LEU
3	J	791	LYS
3	J	820	GLU
3	J	833	ASN
3	J	855	ILE
3	J	922	ARG
3	J	958	VAL
3	J	966	GLN
3	J	1008	ILE
3	J	1040	SER
3	J	1067	SER
3	J	1082	VAL
3	J	1087	ASP
3	J	1090	CYS
3	J	1091	LEU
3	J	1092	ILE
3	N	43	GLU
3	N	56	VAL
3	N	88	LEU
3	N	151	SER
3	N	152	VAL
3	N	155	VAL
3	N	196	THR
3	N	220	VAL
3	N	241	LEU
3	N	286	GLU
3	N	298	PRO
3	N	303	PRO
3	N	307	LEU
3	N	341	SER
3	N	348	CYS
3	N	355	ILE
3	N	460	SER

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Mol	Chain	Res	Type
3	N	461	PRO
3	N	467	VAL
3	N	471	VAL
3	N	531	GLN
3	N	567	ARG
3	N	581	ASP
3	N	593	LEU
3	N	620	LEU
3	N	646	ILE
3	N	664	VAL
3	N	724	THR
3	N	750	ARG
3	N	767	GLU
3	N	769	VAL
3	N	778	LEU
3	N	791	LYS
3	N	820	GLU
3	N	833	ASN
3	N	855	ILE
3	N	922	ARG
3	N	958	VAL
3	N	966	GLN
3	N	1008	ILE
3	N	1040	SER
3	N	1067	SER
3	N	1082	VAL
3	N	1087	ASP
3	N	1090	CYS
3	N	1092	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	51	HIS
3	B	132	GLN
3	B	315	GLN
3	B	516	GLN
3	B	589	GLN
3	B	607	GLN
3	B	625	ASN
3	B	652	HIS
3	B	667	GLN

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Mol	Chain	Res	Type
3	B	710	GLN
3	B	711	GLN
3	B	740	GLN
3	B	765	HIS
3	B	809	GLN
3	B	824	ASN
3	B	856	HIS
3	B	901	GLN
3	B	909	GLN
3	B	916	GLN
3	B	918	GLN
3	B	954	ASN
3	B	978	ASN
3	B	989	ASN
3	B	1019	GLN
3	B	1048	GLN
3	B	1085	ASN
3	F	51	HIS
3	F	132	GLN
3	F	171	GLN
3	F	315	GLN
3	F	346	ASN
3	F	398	HIS
3	F	445	GLN
3	F	491	ASN
3	F	516	GLN
3	F	589	GLN
3	F	607	GLN
3	F	625	ASN
3	F	652	HIS
3	F	667	GLN
3	F	710	GLN
3	F	711	GLN
3	F	740	GLN
3	F	765	HIS
3	F	809	GLN
3	F	824	ASN
3	F	856	HIS
3	F	901	GLN
3	F	909	GLN
3	F	916	GLN
3	F	918	GLN

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Mol	Chain	Res	Type
3	F	935	ASN
3	F	954	ASN
3	F	978	ASN
3	F	989	ASN
3	F	1019	GLN
3	F	1048	GLN
3	F	1085	ASN
3	J	51	HIS
3	J	132	GLN
3	J	315	GLN
3	J	386	GLN
3	J	398	HIS
3	J	445	GLN
3	J	491	ASN
3	J	516	GLN
3	J	589	GLN
3	J	607	GLN
3	J	625	ASN
3	J	667	GLN
3	J	710	GLN
3	J	711	GLN
3	J	740	GLN
3	J	765	HIS
3	J	809	GLN
3	J	824	ASN
3	J	856	HIS
3	J	901	GLN
3	J	909	GLN
3	J	916	GLN
3	J	918	GLN
3	J	935	ASN
3	J	954	ASN
3	J	978	ASN
3	J	989	ASN
3	J	1013	ASN
3	J	1019	GLN
3	J	1039	GLN
3	J	1048	GLN
3	J	1085	ASN
3	N	51	HIS
3	N	132	GLN
3	N	315	GLN

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Mol	Chain	Res	Type
3	N	386	GLN
3	N	398	HIS
3	N	445	GLN
3	N	491	ASN
3	N	516	GLN
3	N	589	GLN
3	N	607	GLN
3	N	625	ASN
3	N	652	HIS
3	N	667	GLN
3	N	710	GLN
3	N	711	GLN
3	N	740	GLN
3	N	765	HIS
3	N	809	GLN
3	N	824	ASN
3	N	856	HIS
3	N	901	GLN
3	N	909	GLN
3	N	916	GLN
3	N	918	GLN
3	N	935	ASN
3	N	954	ASN
3	N	978	ASN
3	N	989	ASN
3	N	1019	GLN
3	N	1048	GLN
3	N	1085	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FAR	E	1301	-	14,14,14	0.36	0	15,16,16	1.60	4 (26%)
4	FAR	A	1301	-	14,14,14	0.36	0	15,16,16	1.59	4 (26%)
5	ADP	J	1101	-	28,29,29	0.46	0	43,45,45	0.46	0
4	FAR	F	1101	-	14,14,14	0.30	0	15,16,16	0.31	0
4	FAR	M	1301	-	14,14,14	0.36	0	15,16,16	1.59	4 (26%)
4	FAR	N	1101	4	14,14,14	0.31	0	15,16,16	0.31	0
5	ADP	B	1102	-	28,29,29	0.47	0	43,45,45	0.45	0
4	FAR	F	1103	-	14,14,14	0.31	0	15,16,16	0.31	0
5	ADP	N	1102	-	28,29,29	0.47	0	43,45,45	0.46	0
4	FAR	I	1301	-	14,14,14	0.36	0	15,16,16	1.60	4 (26%)
5	ADP	F	1102	-	28,29,29	0.46	0	43,45,45	0.44	0
4	FAR	B	1101	4	14,14,14	0.31	0	15,16,16	0.31	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FAR	E	1301	-	-	2/14/14/14	-
4	FAR	A	1301	-	-	2/14/14/14	-
5	ADP	J	1101	-	-	2/16/32/32	0/3/3/3
4	FAR	F	1101	-	-	4/14/14/14	-
4	FAR	M	1301	-	-	2/14/14/14	-
4	FAR	N	1101	4	-	4/14/14/14	-
5	ADP	B	1102	-	-	2/16/32/32	0/3/3/3
4	FAR	F	1103	-	-	4/14/14/14	-
5	ADP	N	1102	-	-	2/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FAR	I	1301	-	-	2/14/14/14	-
5	ADP	F	1102	-	-	2/16/32/32	0/3/3/3
4	FAR	B	1101	4	-	4/14/14/14	-

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	1301	FAR	C4-C3-C5	3.19	120.77	115.23
4	E	1301	FAR	C4-C3-C5	3.18	120.76	115.23
4	A	1301	FAR	C4-C3-C5	3.17	120.74	115.23
4	M	1301	FAR	C4-C3-C5	3.14	120.68	115.23
4	M	1301	FAR	C1-C2-C3	-2.63	120.46	126.44
4	I	1301	FAR	C1-C2-C3	-2.62	120.47	126.44
4	A	1301	FAR	C1-C2-C3	-2.62	120.47	126.44
4	E	1301	FAR	C1-C2-C3	-2.62	120.47	126.44
4	E	1301	FAR	C6-C7-C8	-2.48	121.96	127.62
4	I	1301	FAR	C6-C7-C8	-2.47	121.97	127.62
4	M	1301	FAR	C6-C7-C8	-2.47	121.97	127.62
4	A	1301	FAR	C6-C7-C8	-2.46	122.00	127.62
4	I	1301	FAR	C15-C13-C14	2.27	119.80	114.59
4	E	1301	FAR	C15-C13-C14	2.26	119.80	114.59
4	M	1301	FAR	C15-C13-C14	2.26	119.80	114.59
4	A	1301	FAR	C15-C13-C14	2.25	119.77	114.59

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1102	ADP	O4'-C4'-C5'-O5'
5	F	1102	ADP	O4'-C4'-C5'-O5'
5	J	1101	ADP	O4'-C4'-C5'-O5'
5	N	1102	ADP	O4'-C4'-C5'-O5'
4	B	1101	FAR	C3-C5-C6-C7
4	F	1101	FAR	C3-C5-C6-C7
4	F	1103	FAR	C3-C5-C6-C7
4	N	1101	FAR	C3-C5-C6-C7
5	B	1102	ADP	C3'-C4'-C5'-O5'
5	F	1102	ADP	C3'-C4'-C5'-O5'
5	J	1101	ADP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
5	N	1102	ADP	C3'-C4'-C5'-O5'
4	A	1301	FAR	C10-C8-C9-C11
4	E	1301	FAR	C10-C8-C9-C11
4	M	1301	FAR	C10-C8-C9-C11
4	I	1301	FAR	C10-C8-C9-C11
4	A	1301	FAR	C7-C8-C9-C11
4	E	1301	FAR	C7-C8-C9-C11
4	M	1301	FAR	C7-C8-C9-C11
4	I	1301	FAR	C7-C8-C9-C11
4	B	1101	FAR	C10-C8-C9-C11
4	F	1101	FAR	C10-C8-C9-C11
4	F	1103	FAR	C10-C8-C9-C11
4	N	1101	FAR	C10-C8-C9-C11
4	F	1101	FAR	C7-C8-C9-C11
4	N	1101	FAR	C7-C8-C9-C11
4	B	1101	FAR	C7-C8-C9-C11
4	F	1103	FAR	C7-C8-C9-C11
4	B	1101	FAR	C9-C11-C12-C13
4	F	1101	FAR	C9-C11-C12-C13
4	F	1103	FAR	C9-C11-C12-C13
4	N	1101	FAR	C9-C11-C12-C13

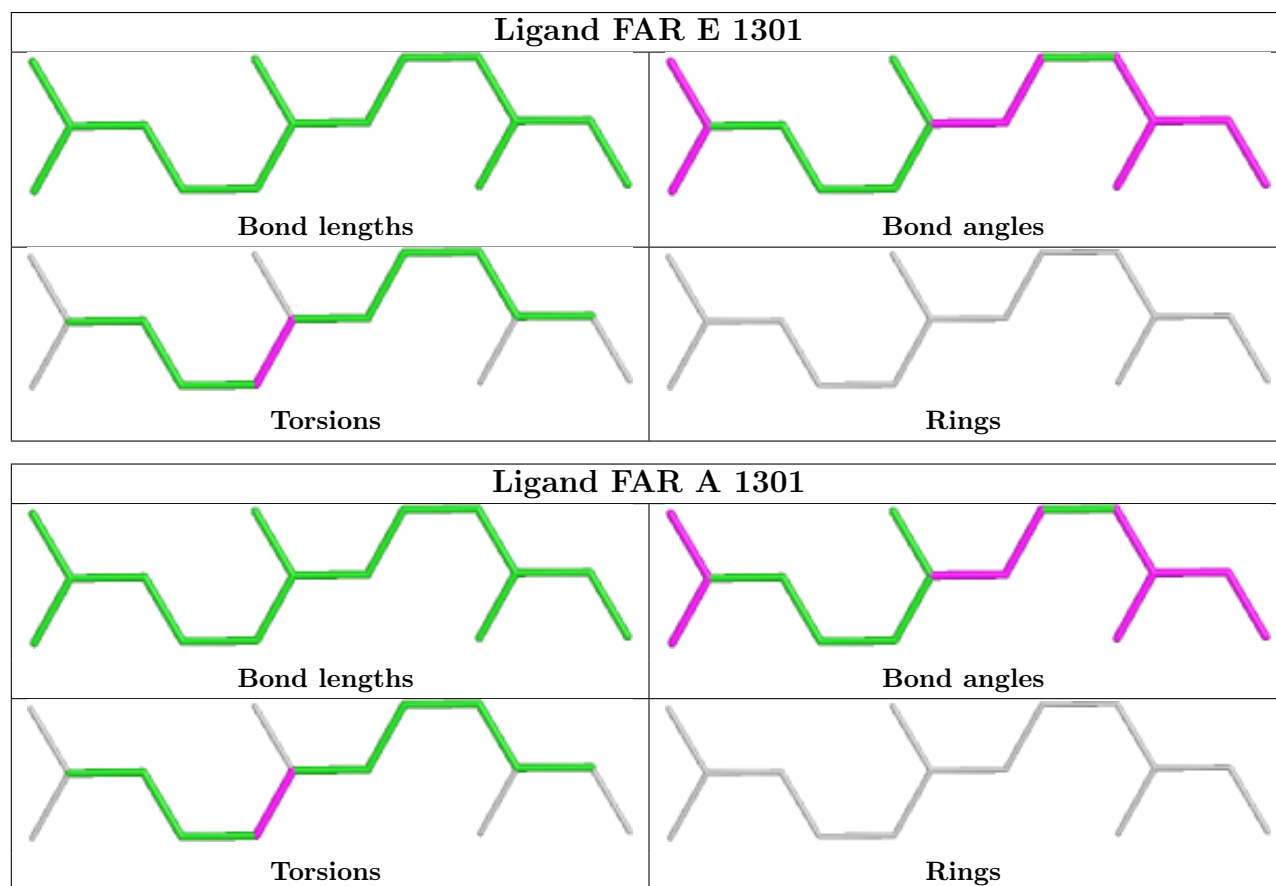
There are no ring outliers.

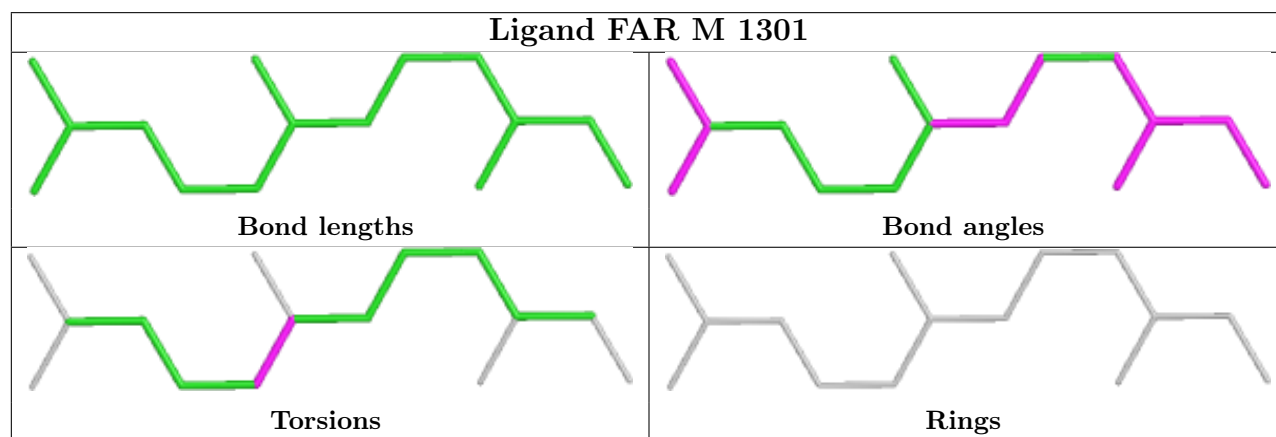
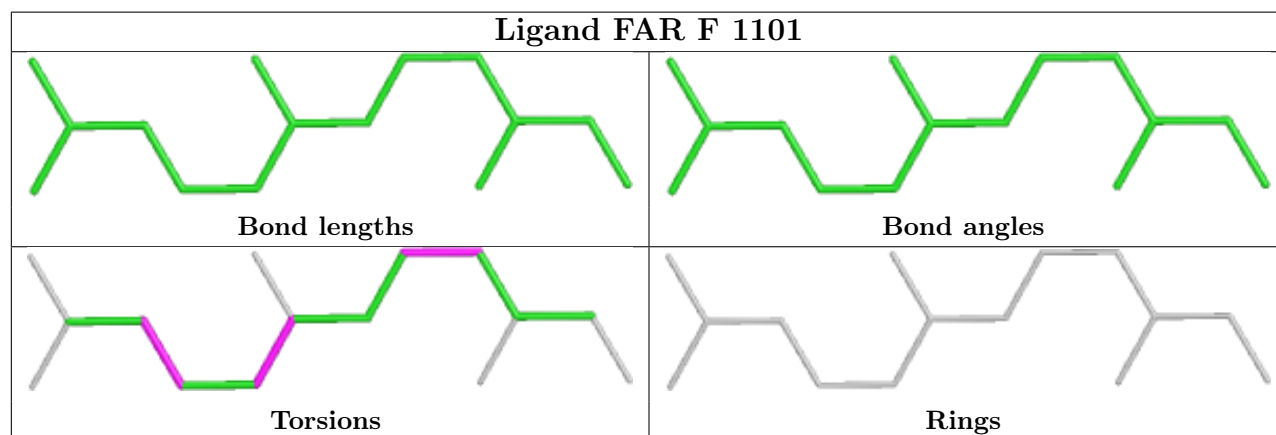
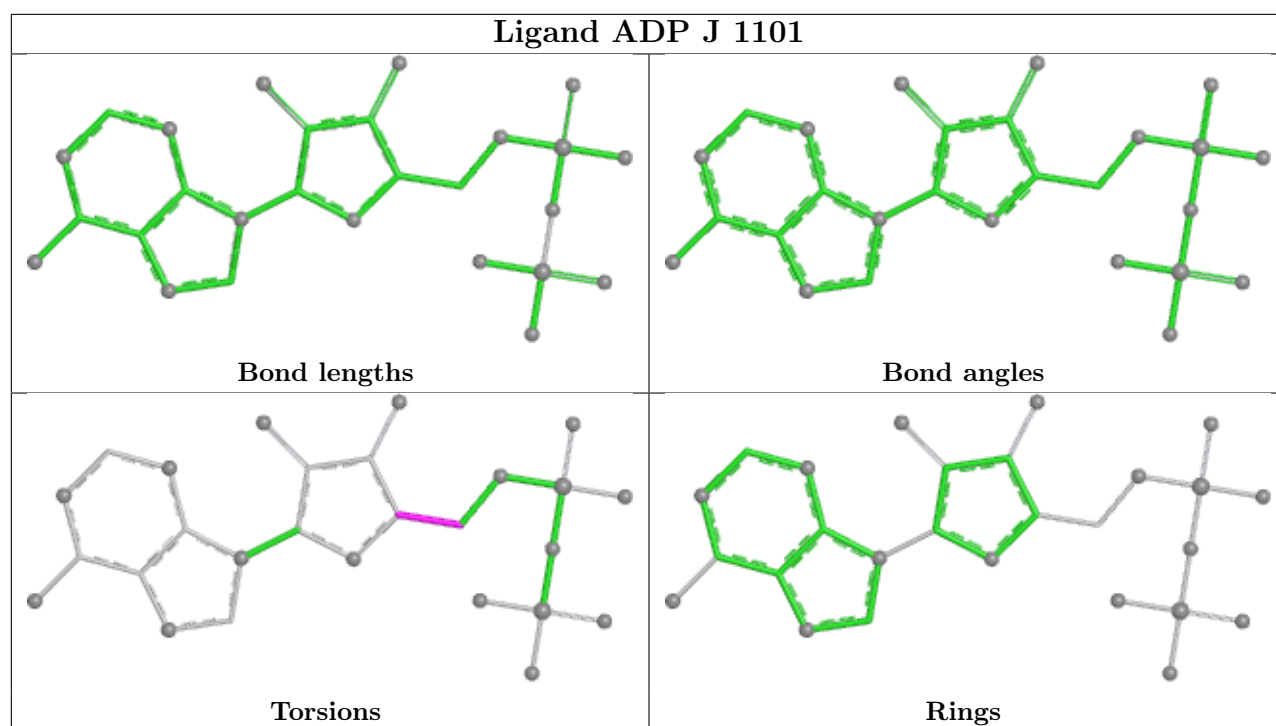
12 monomers are involved in 205 short contacts:

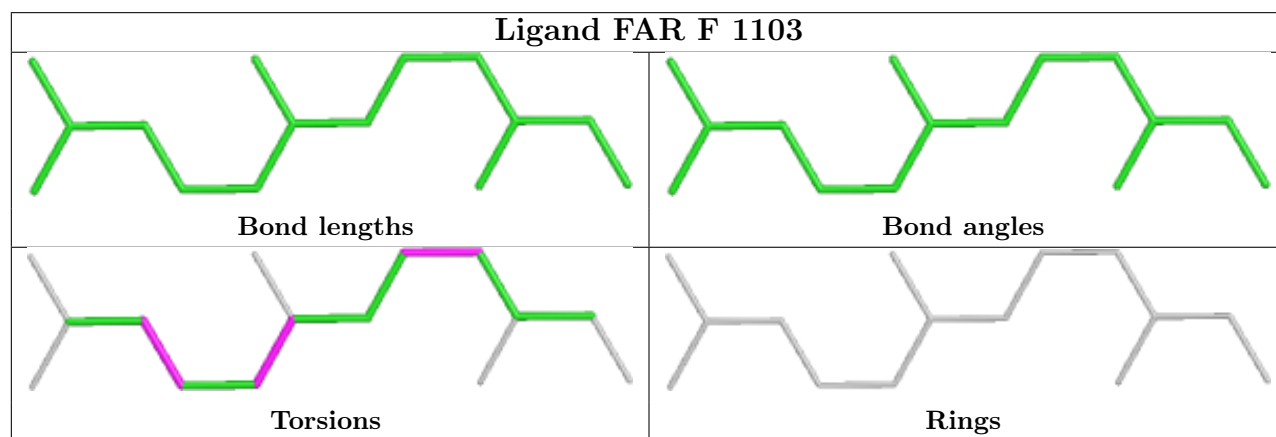
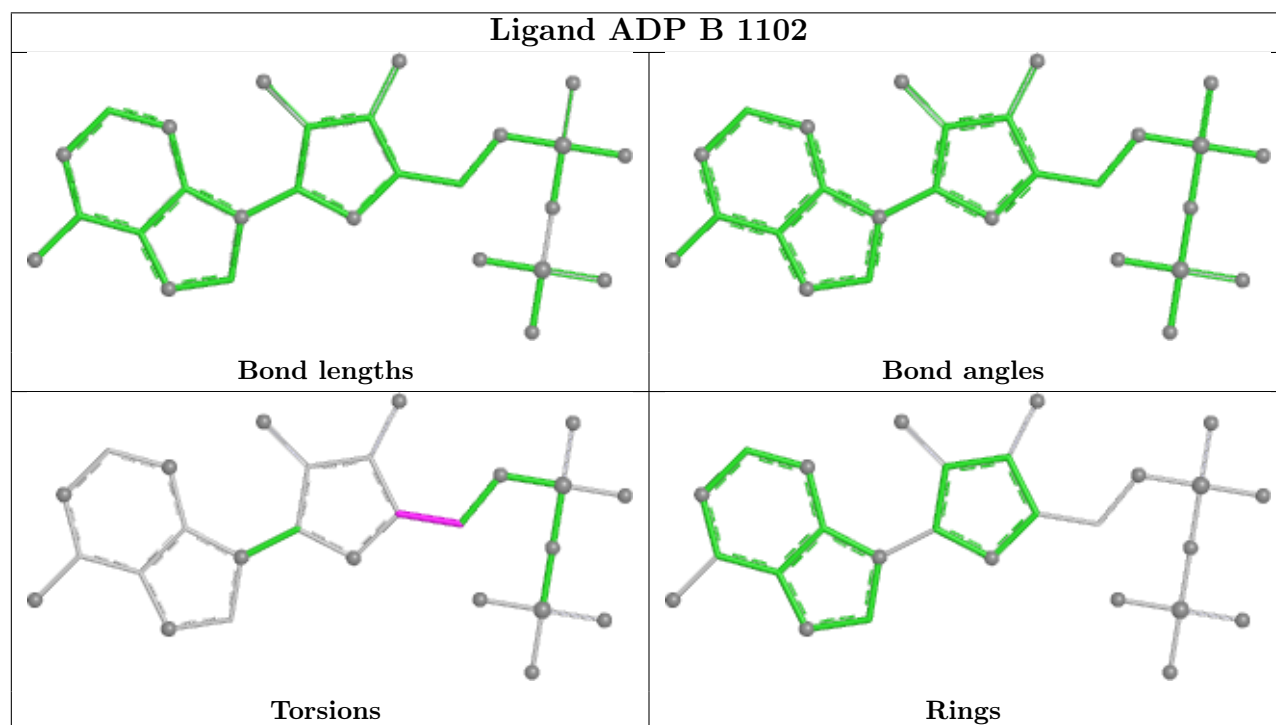
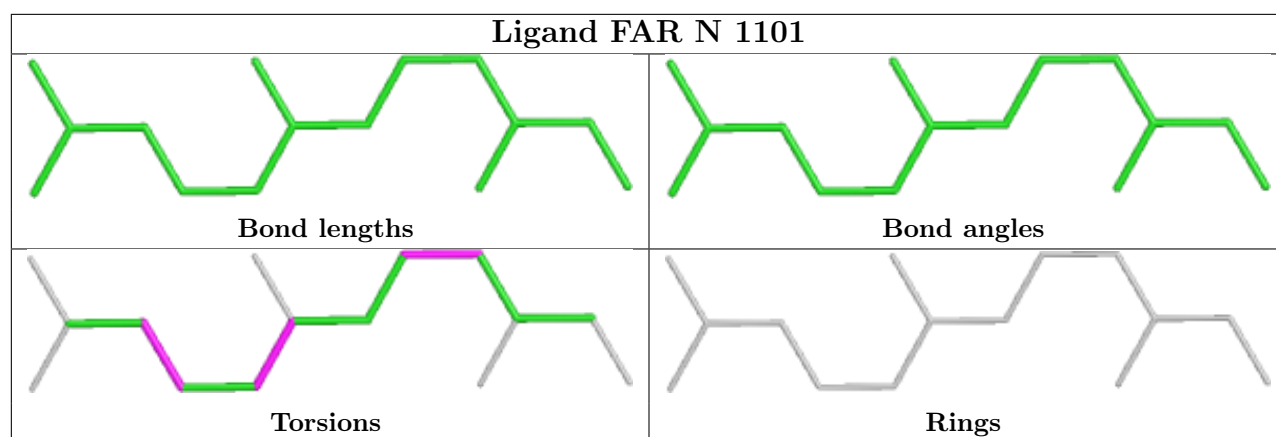
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1301	FAR	17	0
4	A	1301	FAR	18	0
5	J	1101	ADP	3	0
4	F	1101	FAR	39	0
4	M	1301	FAR	17	0
4	N	1101	FAR	40	0
5	B	1102	ADP	3	0
4	F	1103	FAR	27	0
5	N	1102	ADP	2	0
4	I	1301	FAR	18	0
5	F	1102	ADP	2	0
4	B	1101	FAR	19	0

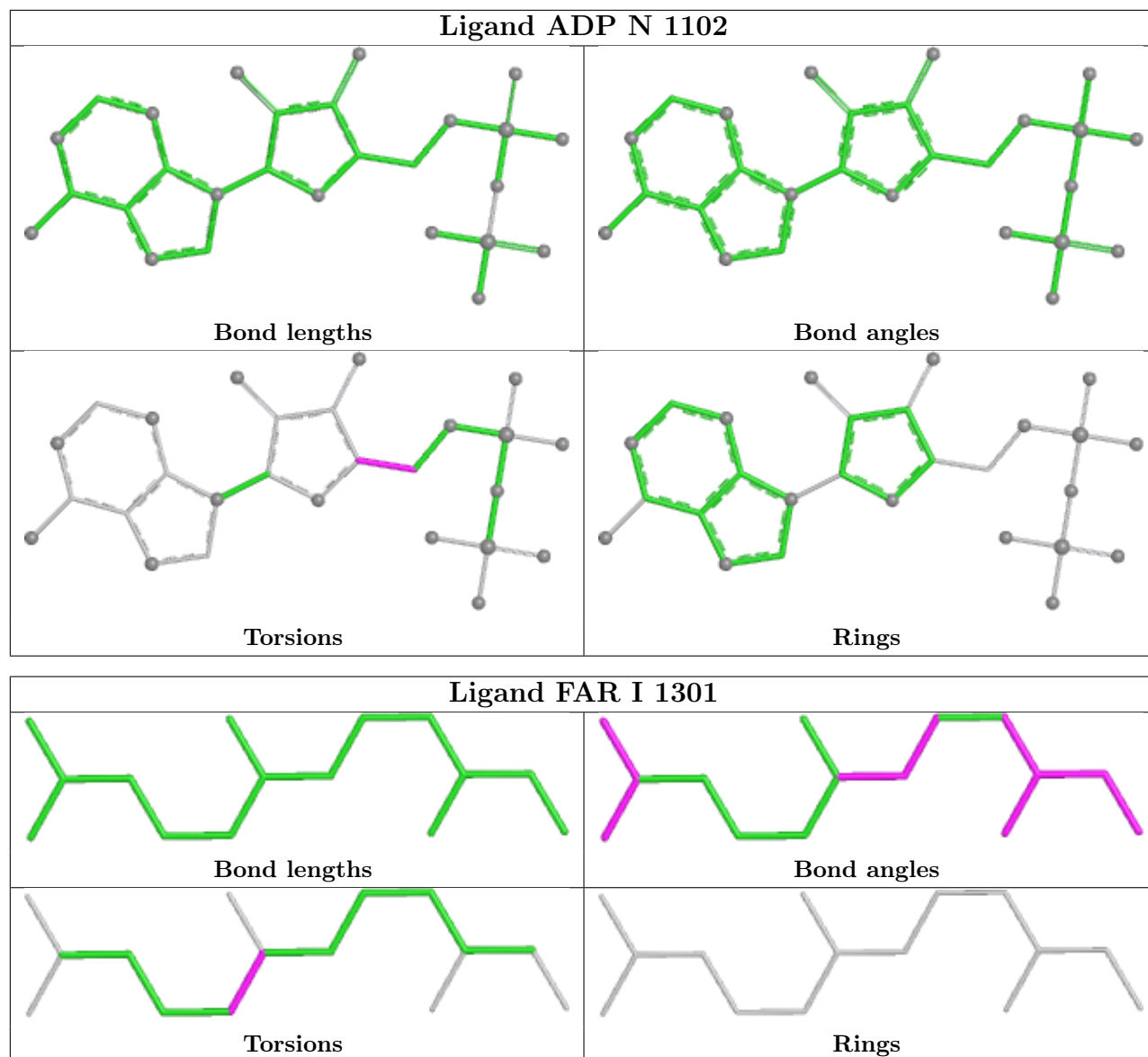
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

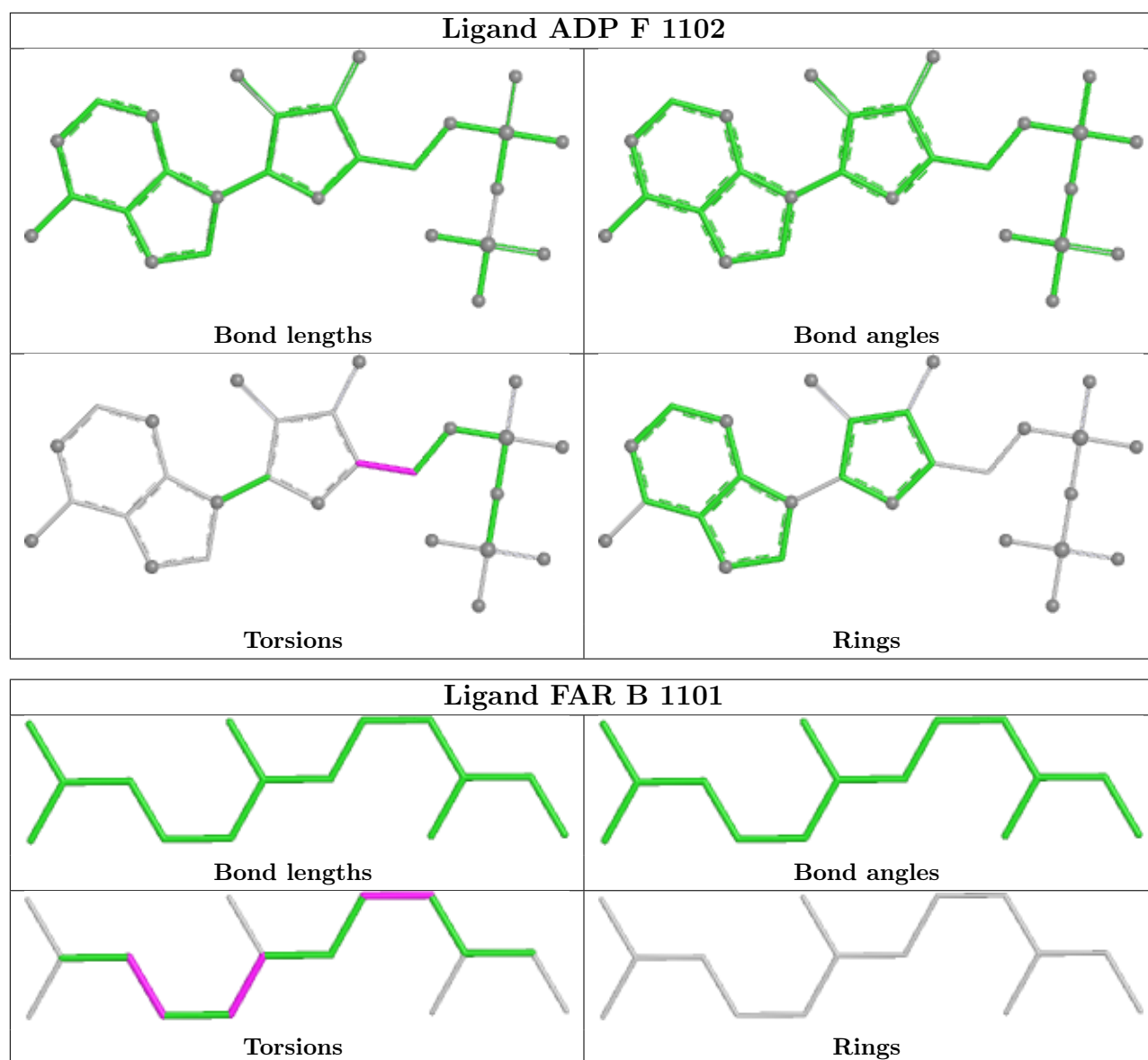
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

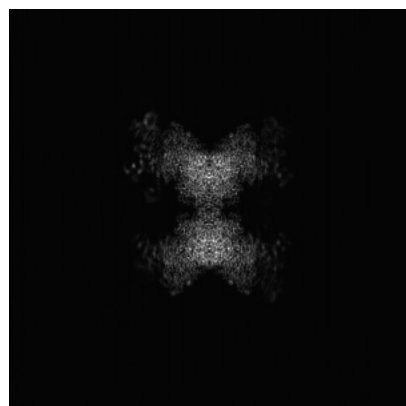
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36213. These allow visual inspection of the internal detail of the map and identification of artifacts.

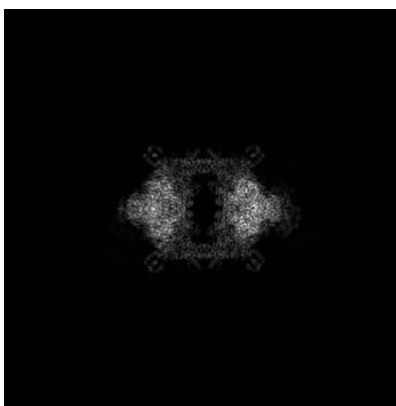
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

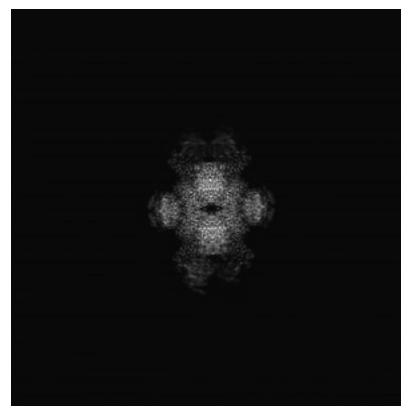
6.1.1 Primary map



X

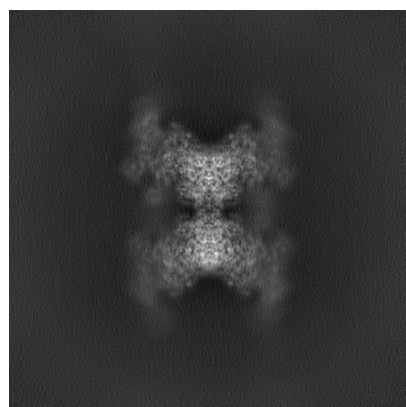


Y

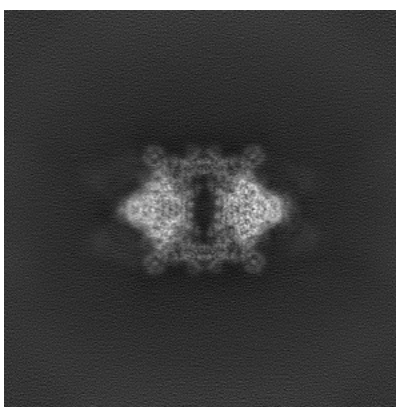


Z

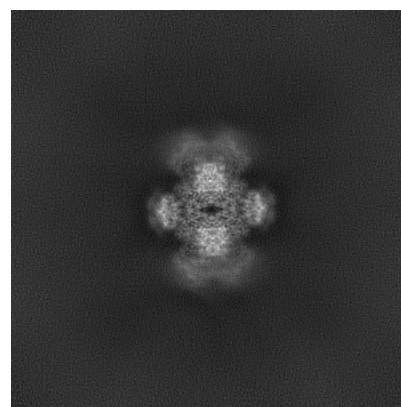
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

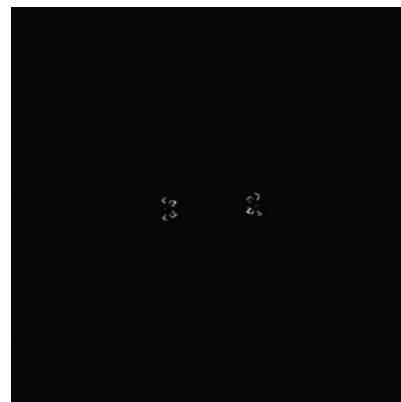
6.2.1 Primary map



X Index: 225

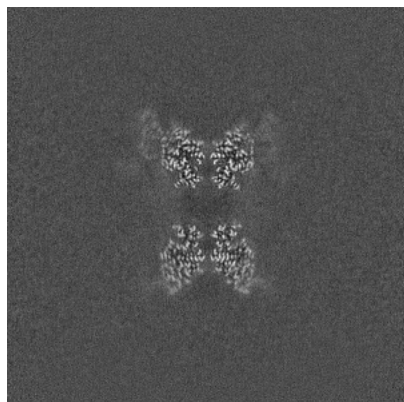


Y Index: 225

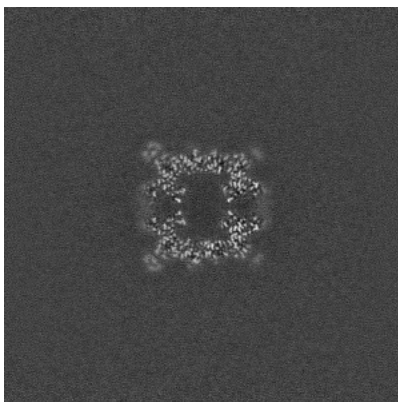


Z Index: 225

6.2.2 Raw map



X Index: 225



Y Index: 225



Z Index: 225

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: 225

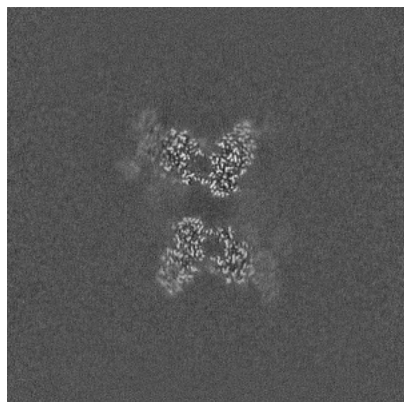


Y Index: 233

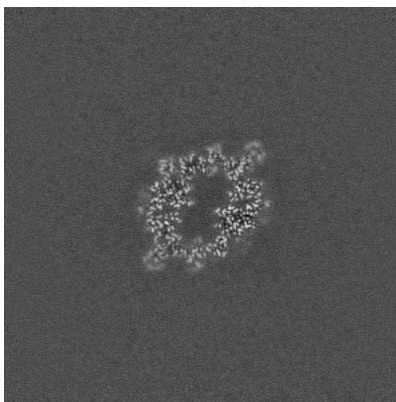


Z Index: 269

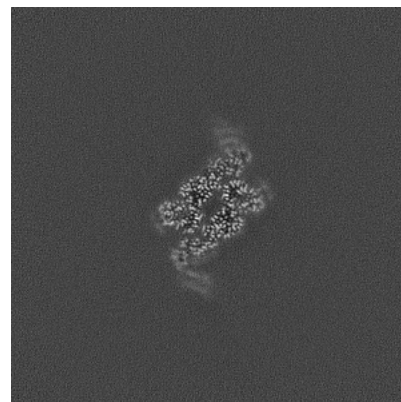
6.3.2 Raw map



X Index: 219



Y Index: 233

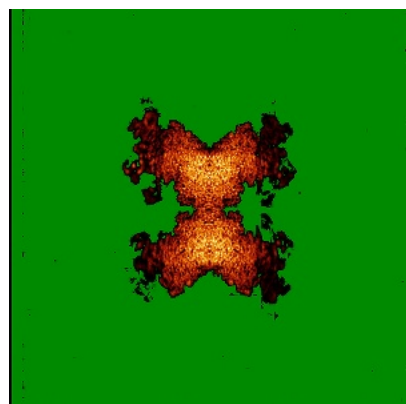


Z Index: 269

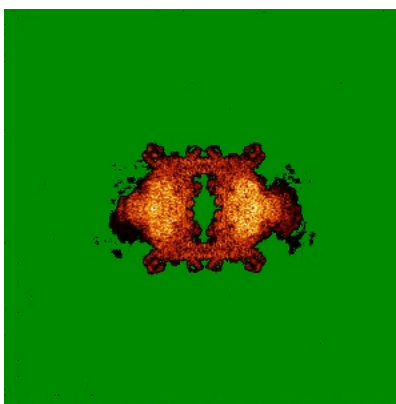
The images above show the largest variance slices of the map in three orthogonal directions.

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

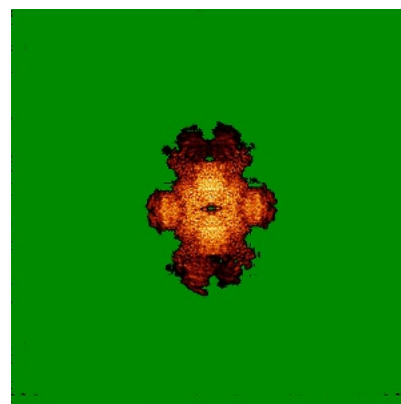
6.4.1 Primary map



X

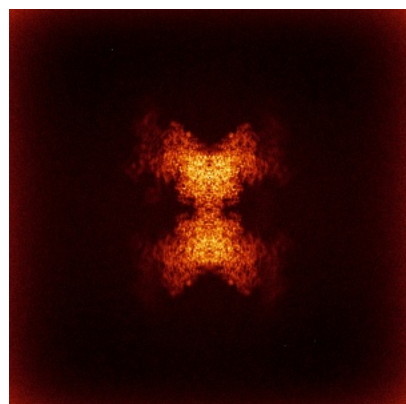


Y

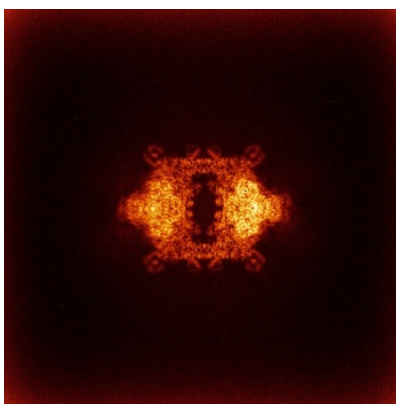


Z

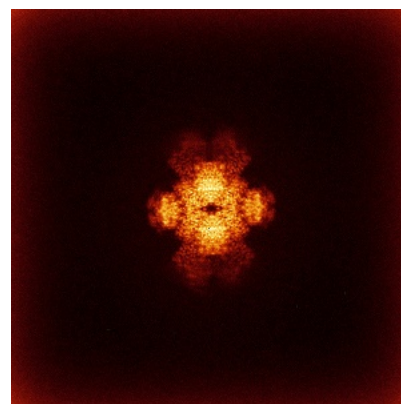
6.4.2 Raw map



X



Y

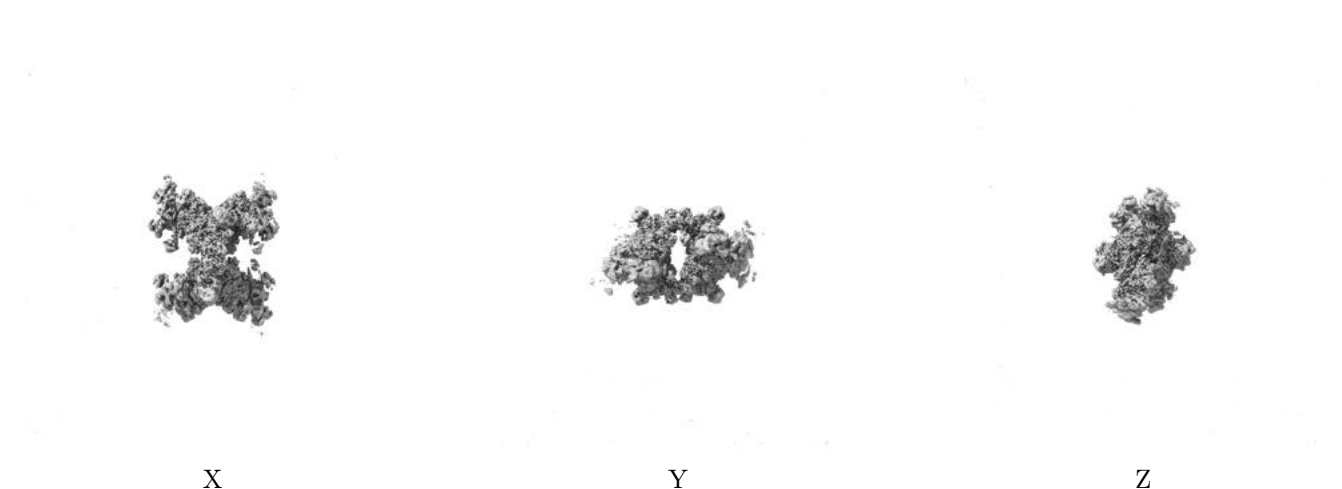


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

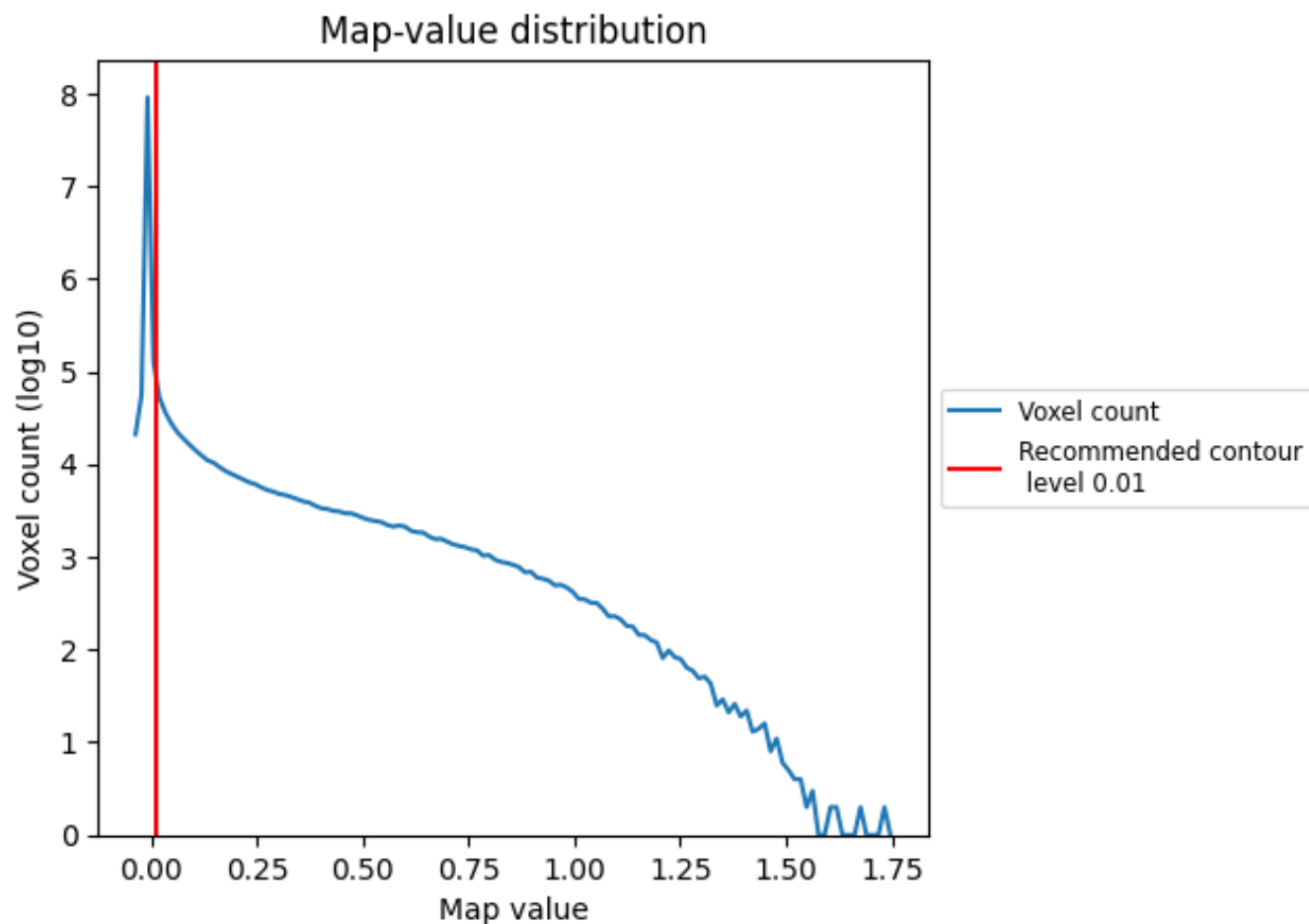
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

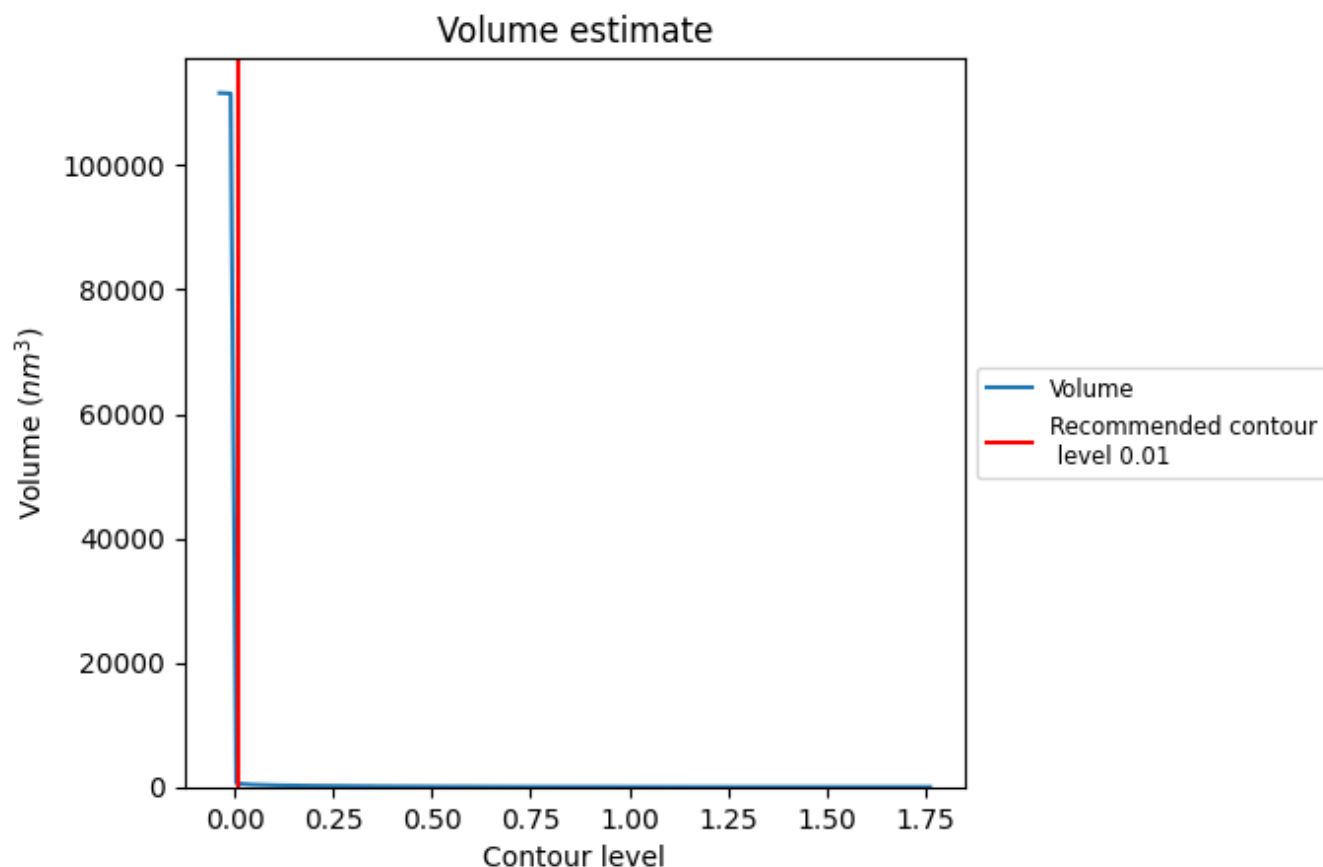
This section contains the results of statistical analysis of the map.

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.

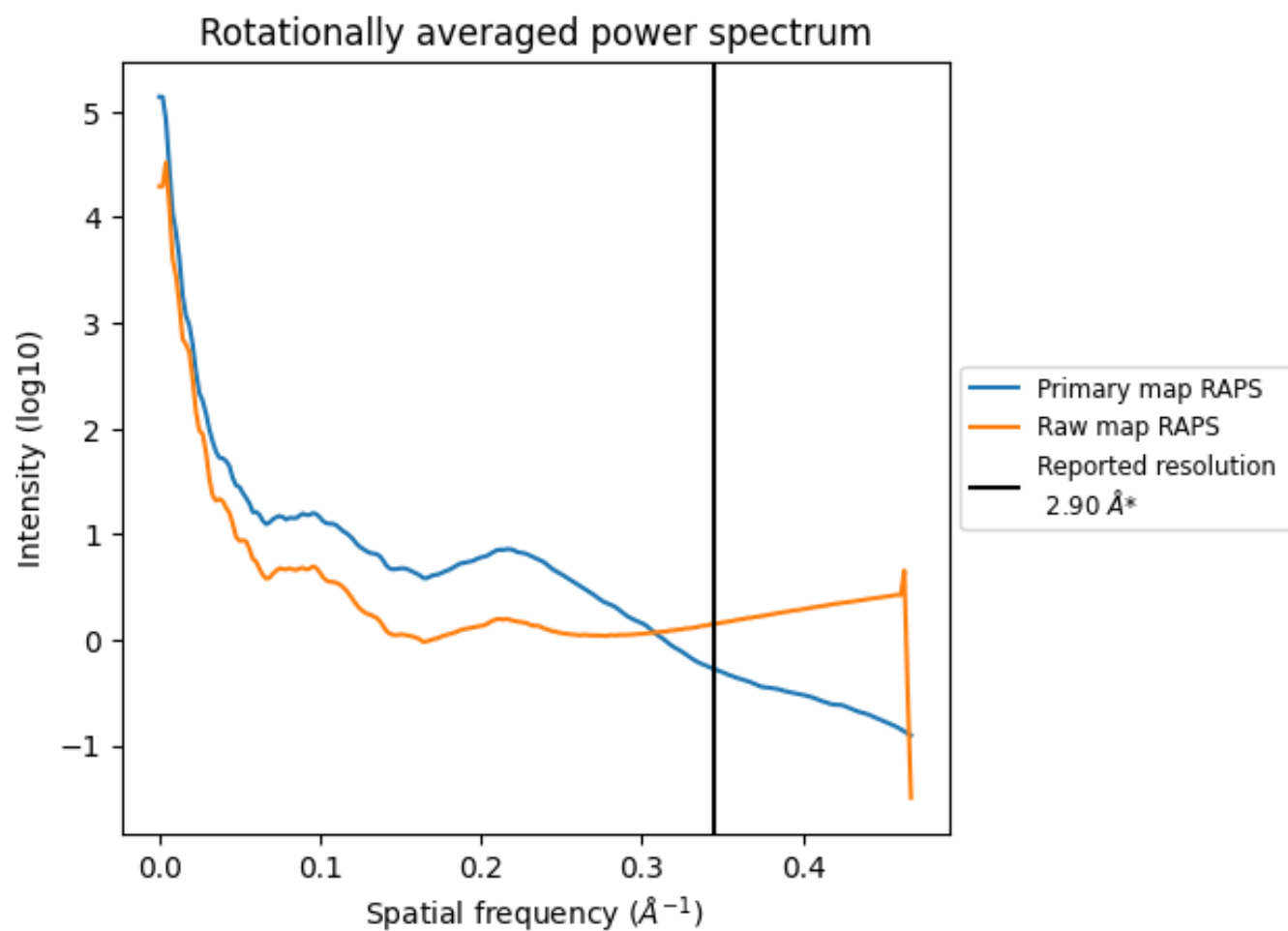
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 587 nm³; this corresponds to an approximate mass of 531 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 ⓘ

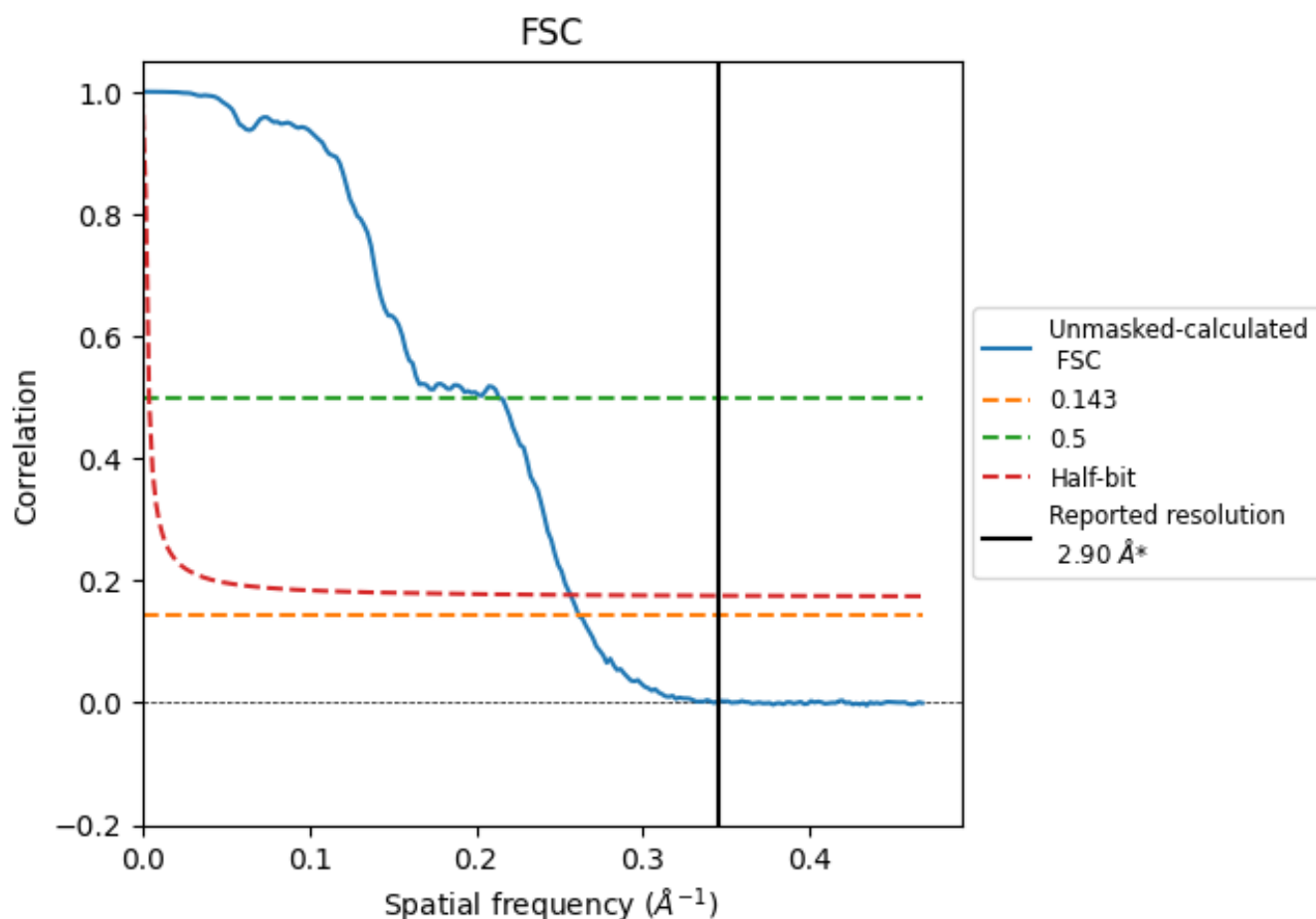


*Reported resolution corresponds to spatial frequency of $0.345 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

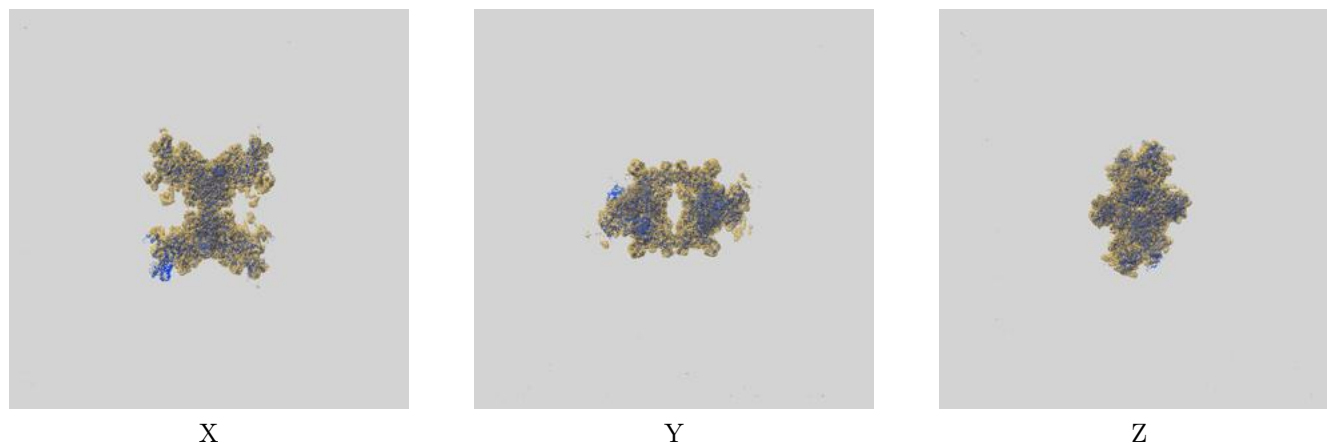
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	4.68	3.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.82 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

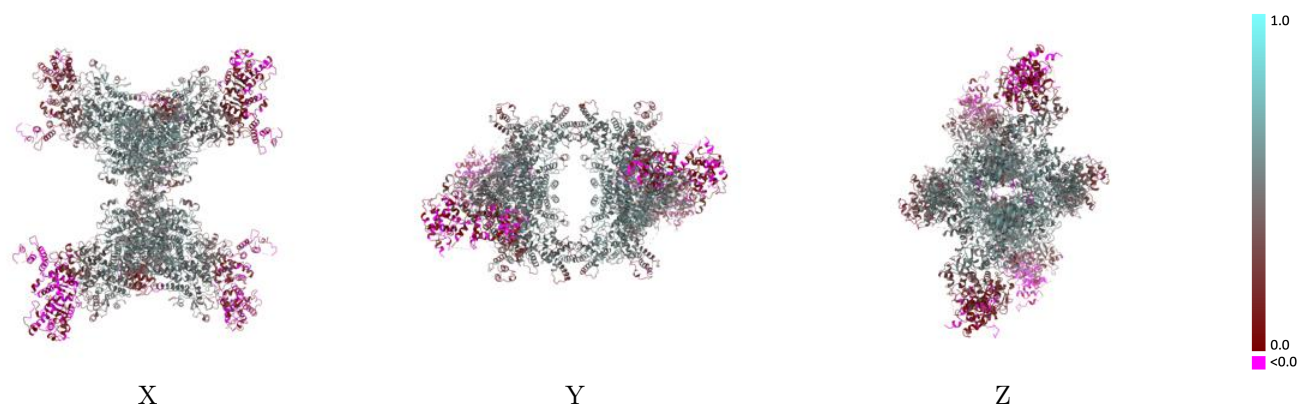
This section contains information regarding the fit between EMDB map EMD-36213 and PDB model 8JFL. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



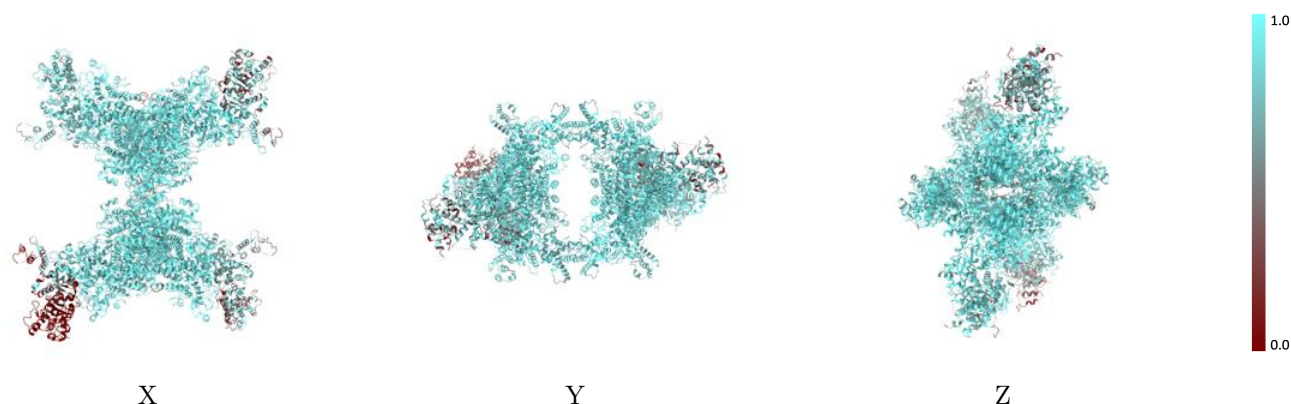
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



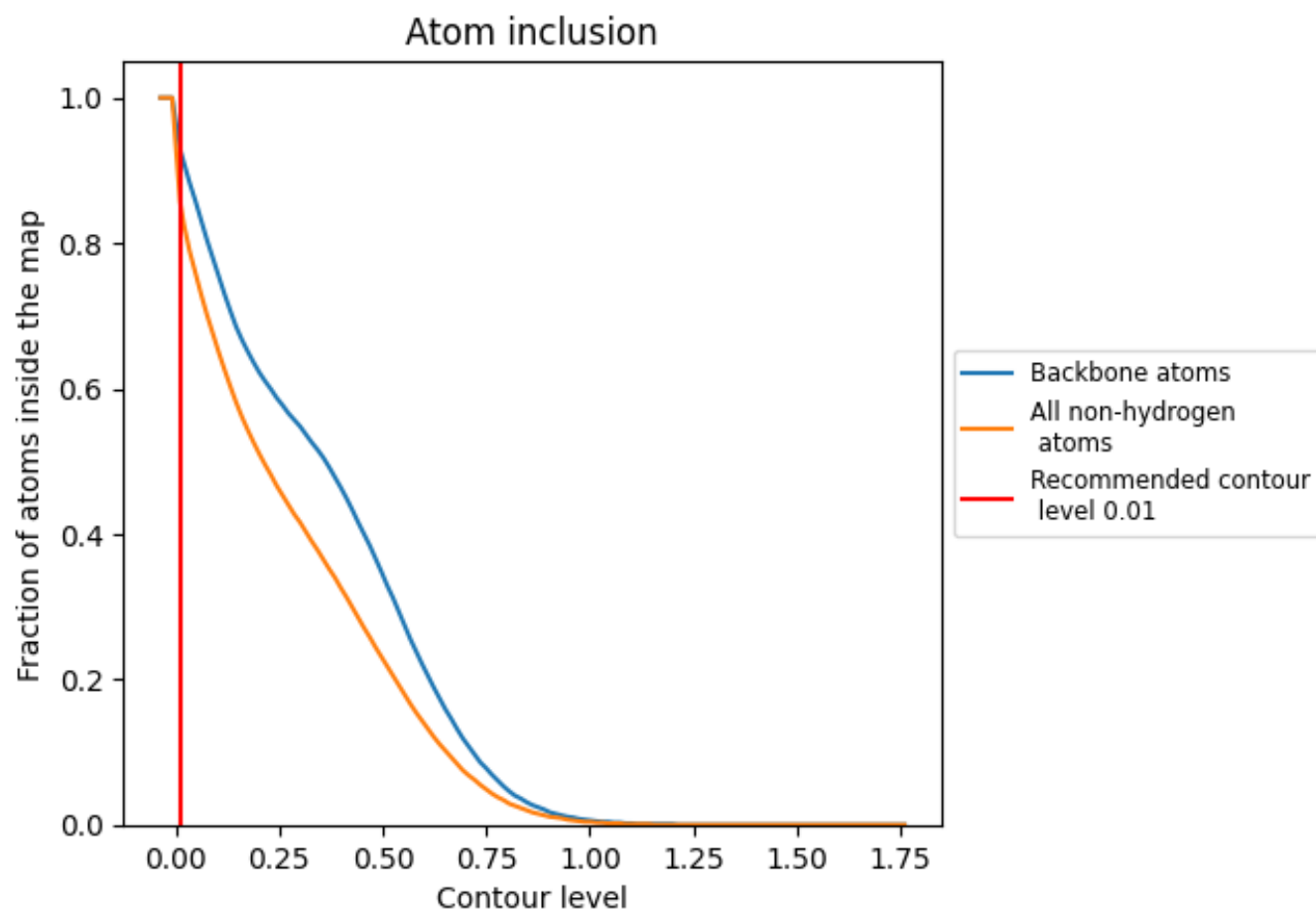
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8570	0.3960
A	0.8740	0.3650
B	0.9460	0.5160
C	0.7660	0.1280
E	0.8190	0.3100
F	0.9430	0.5030
G	0.5570	0.0650
I	0.6550	0.2370
J	0.9420	0.4910
K	0.0100	0.0640
M	0.7910	0.2870
N	0.9390	0.4870
O	0.4480	0.0450

