



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 08:02 PM UTC

PDB ID : 6RZU / pdb_00006rzu
EMDB ID : EMD-10063
Title : Structure of s-Mgm1 decorating the outer surface of tubulated lipid membranes in the GTPgammaS bound state
Authors : Faelber, K.; Dietrich, L.; Noel, J.K.; Sanchez, R.; Kudryashev, M.; Kuelbrandt, W.; Daumke, O.
Deposited on : 2019-06-13
Resolution : 14.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

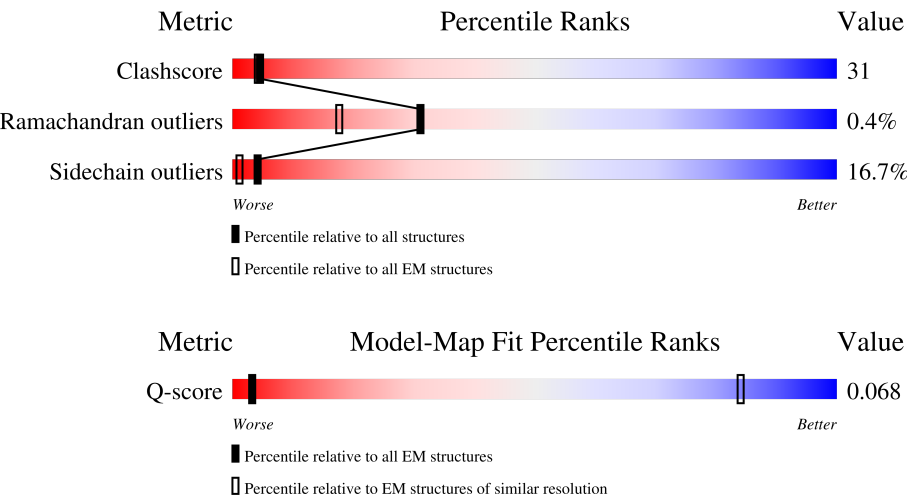
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 14.70 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	31 (14.20 - 15.00)

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	695	33% 42% 34% 15% 5%
1	B	695	22% 49% 33% 12% 5%
1	C	695	19% 49% 35% 9% 5%
1	D	695	34% 43% 33% 16% 5%

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Mol	Chain	Length	Quality of chain
1	E	695	
1	F	695	
1	G	695	
1	H	695	
1	I	695	
1	J	695	
1	K	695	
1	L	695	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 61824 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.

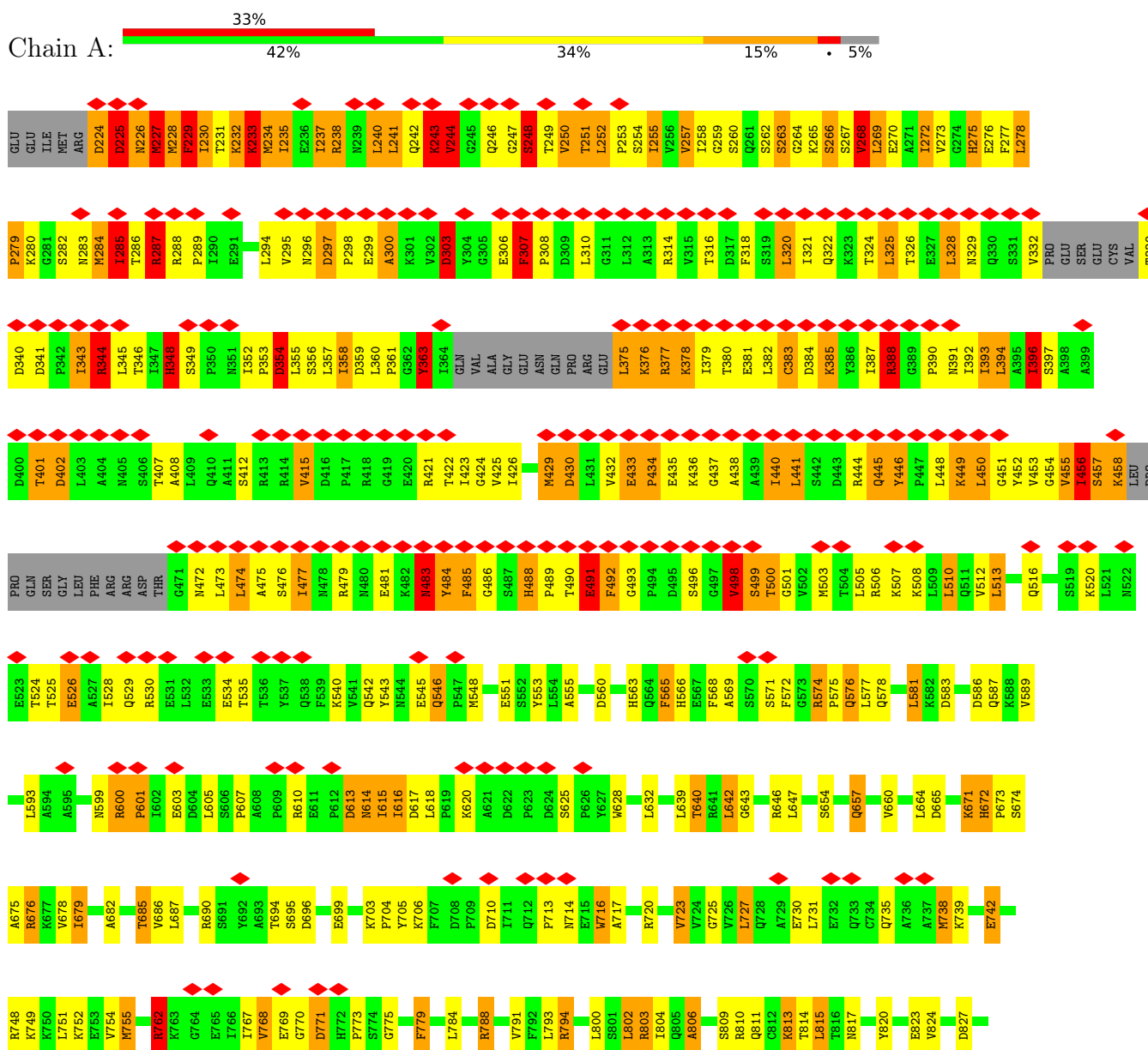
- Molecule 1 is a protein called Putative mitochondrial dynamin protein.

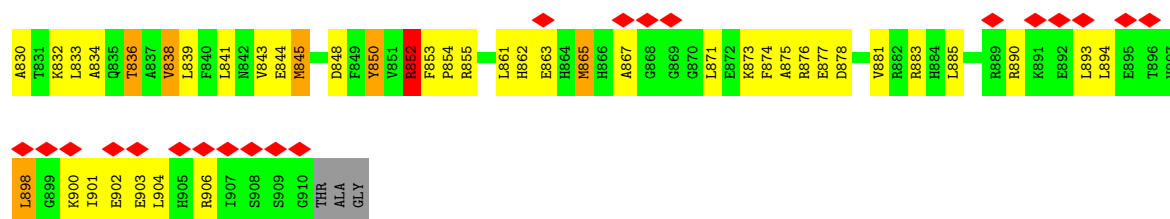
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	B	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	C	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	D	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	E	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	F	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	G	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	H	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	I	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	J	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	K	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	L	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		

3 Residue-property plots

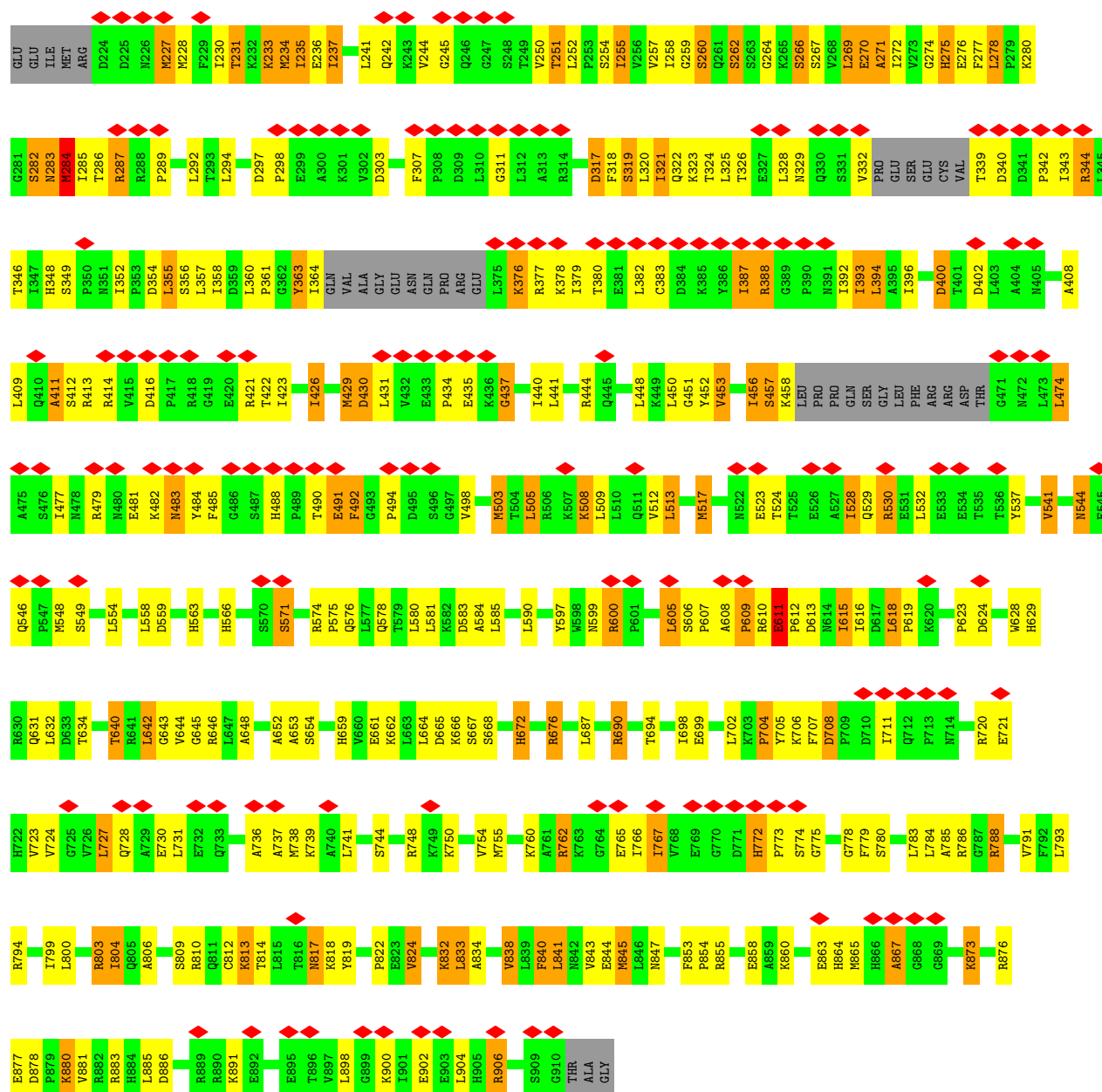
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

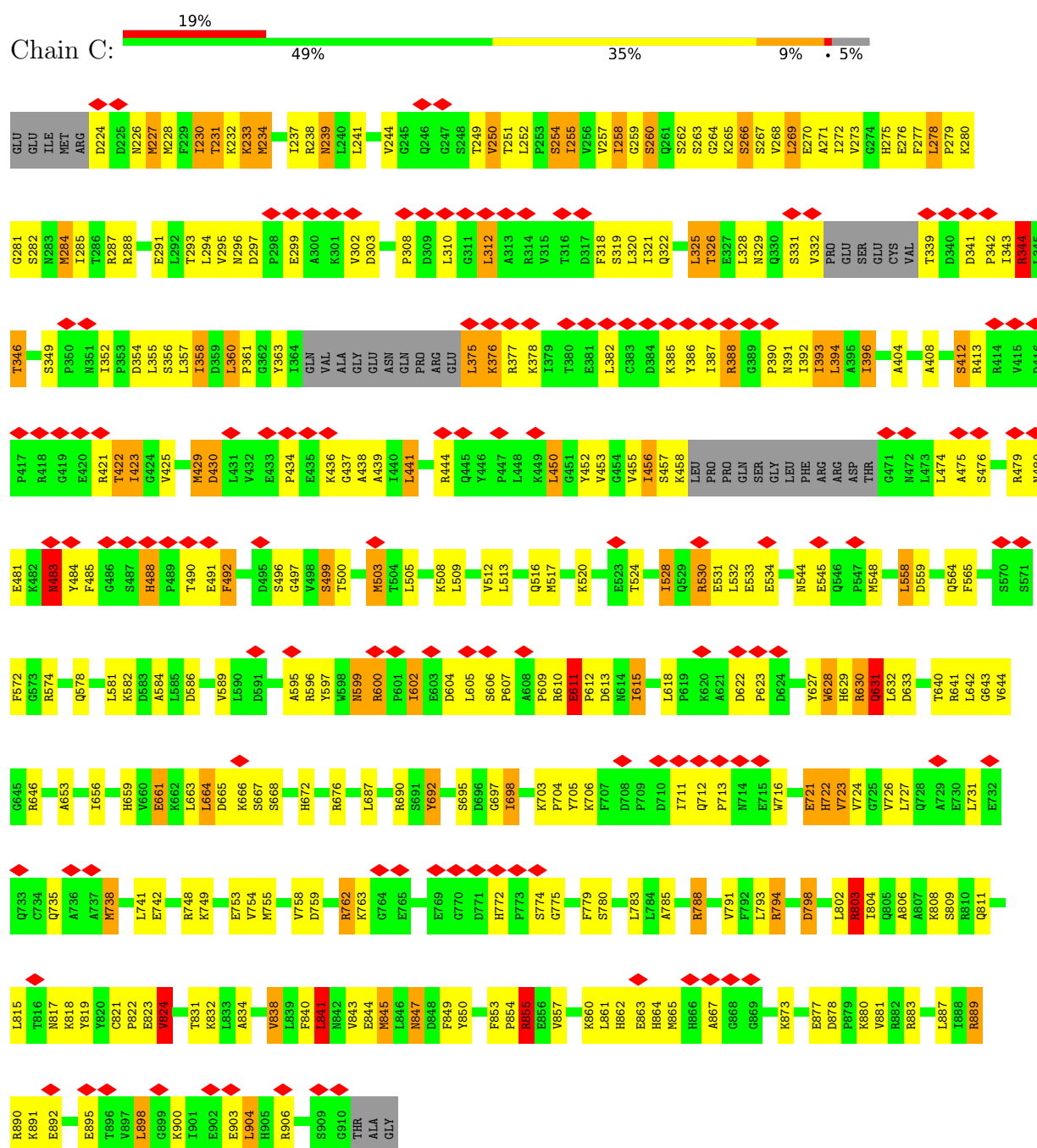




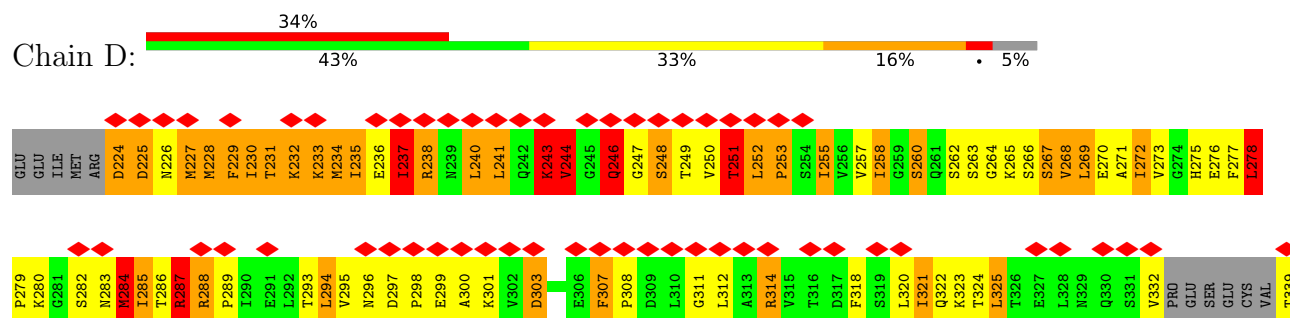
• Molecule 1: Putative mitochondrial dynamin protein

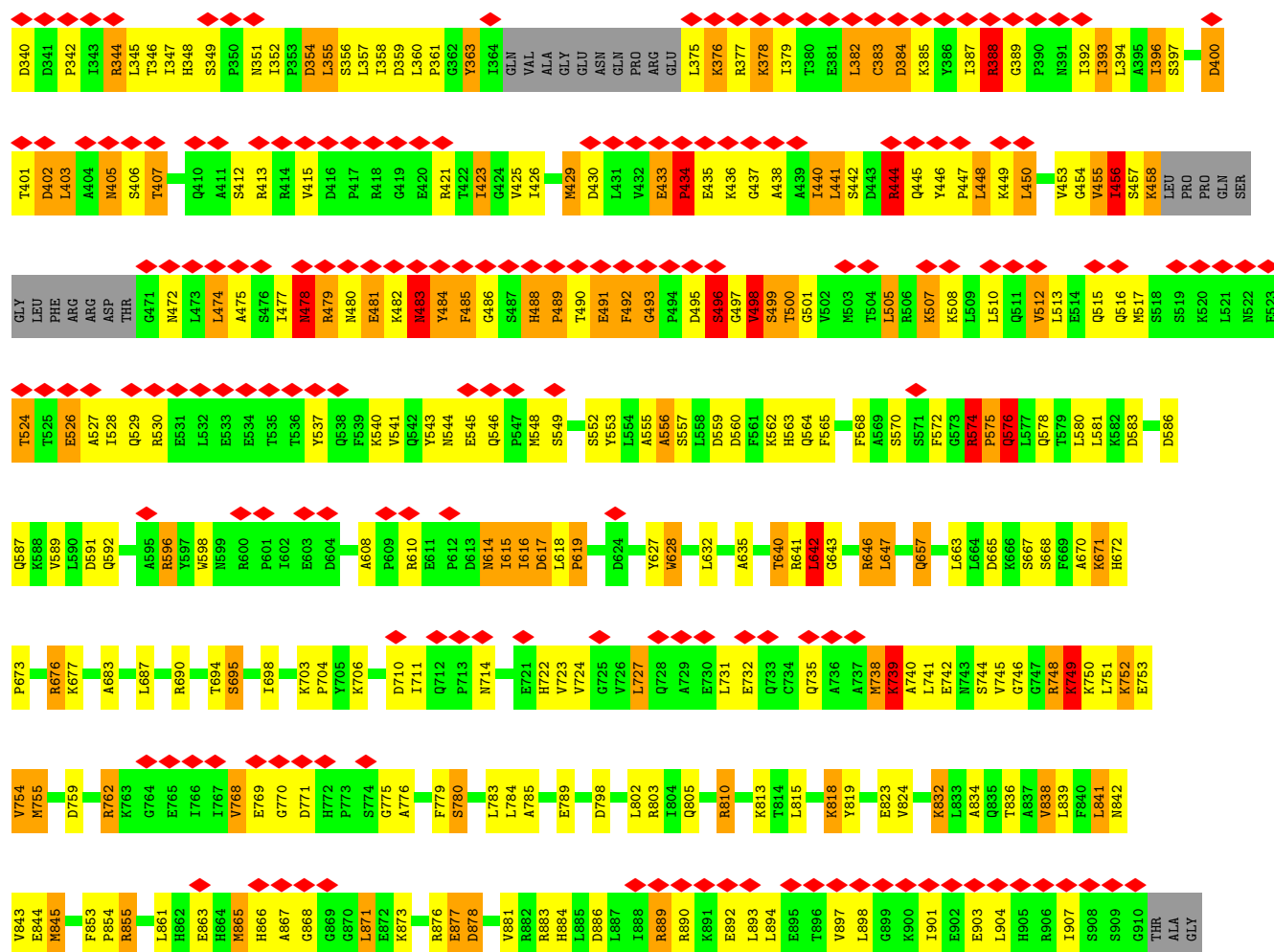


• Molecule 1: Putative mitochondrial dynamin protein

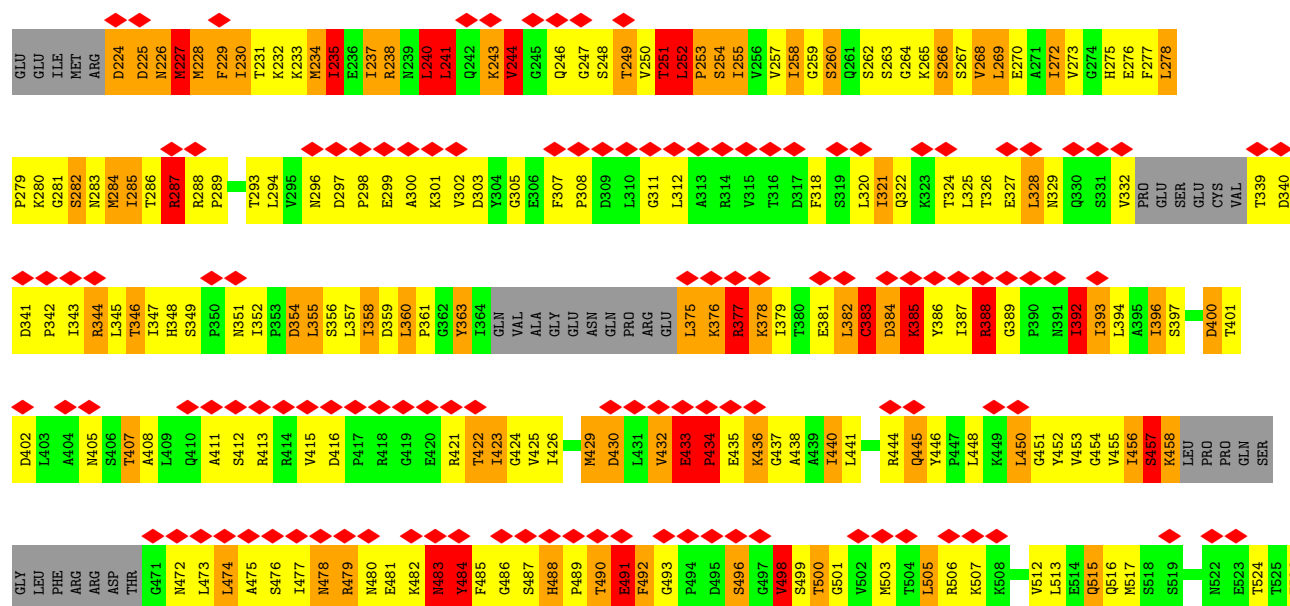


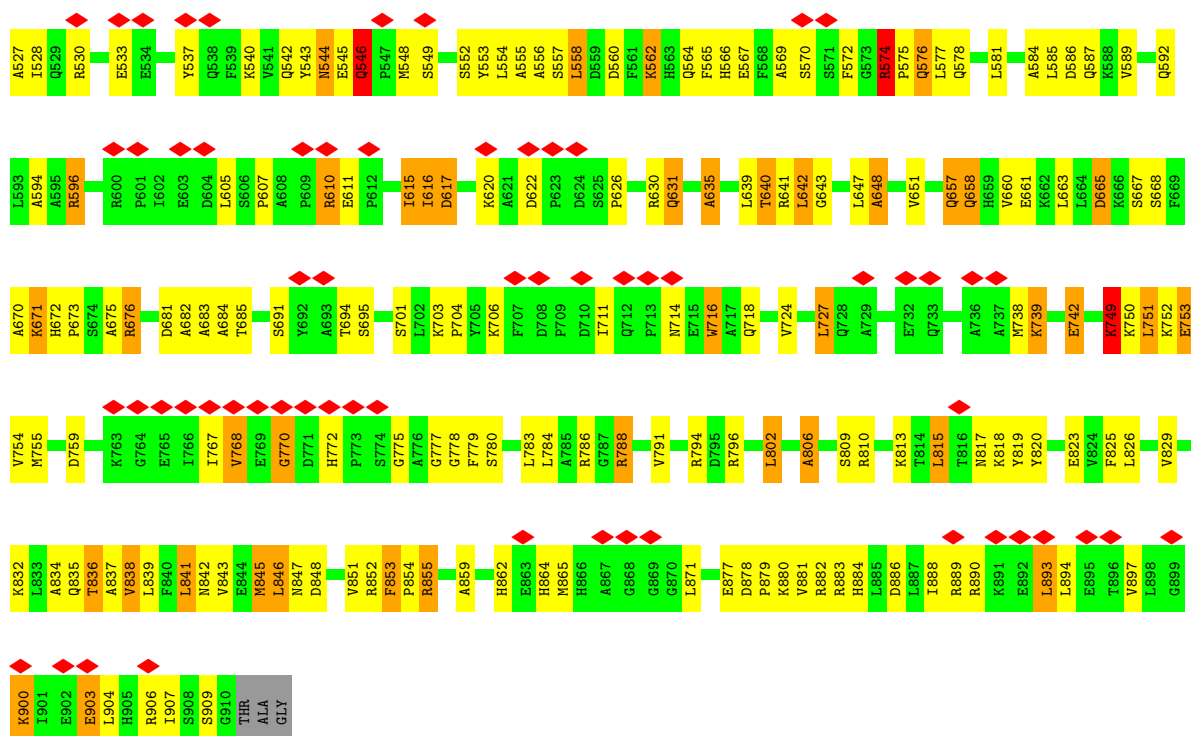
- Molecule 1: Putative mitochondrial dynamin protein



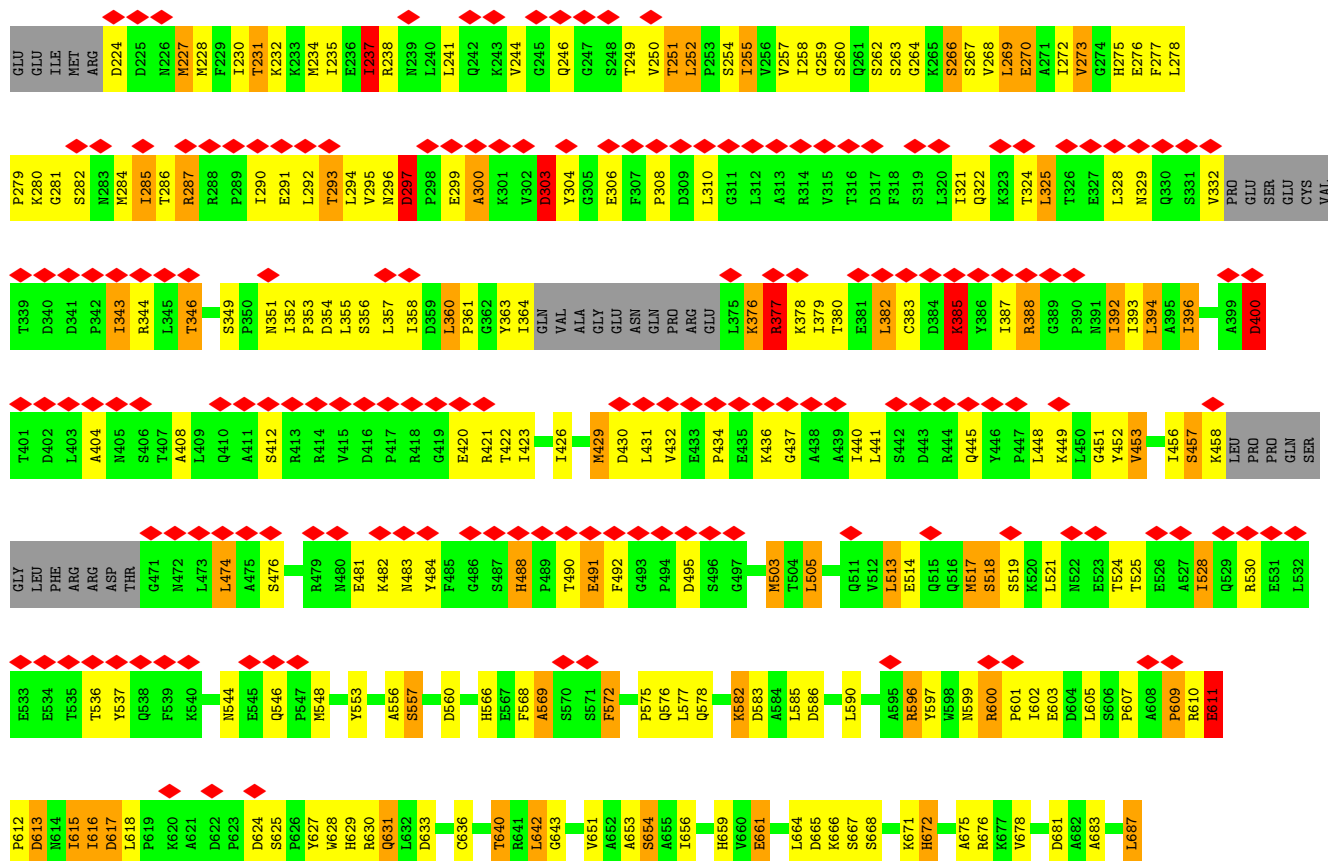


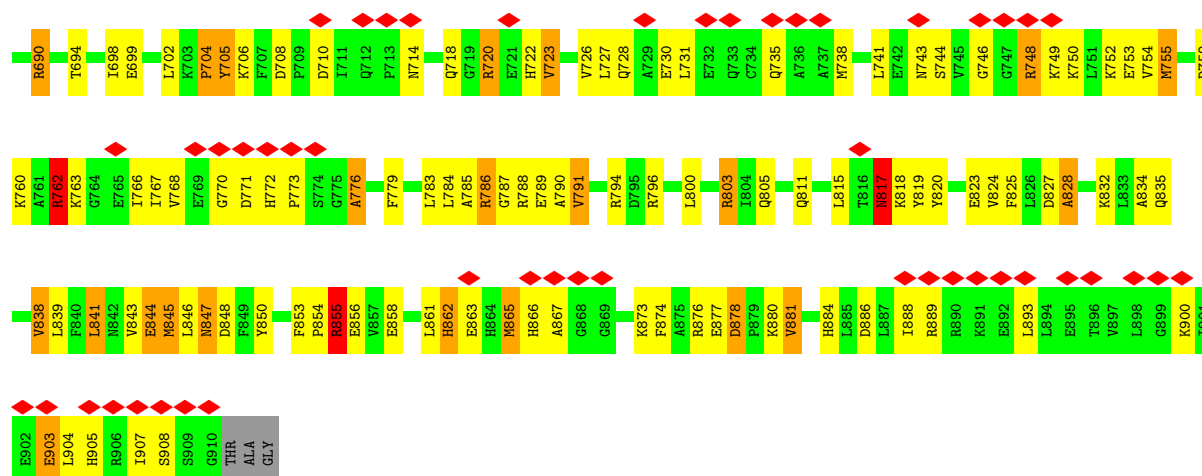
• Molecule 1: Putative mitochondrial dynamin protein



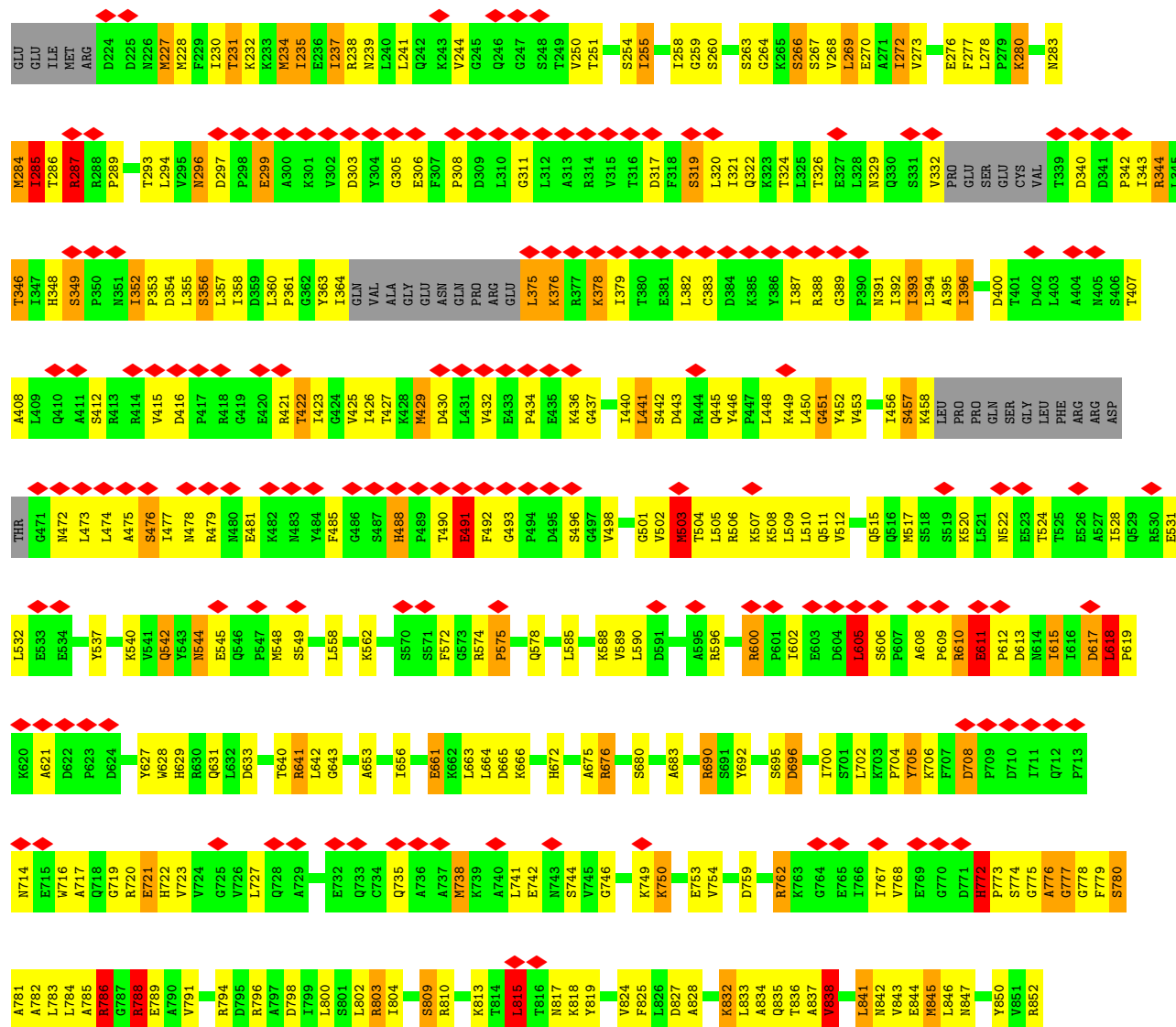


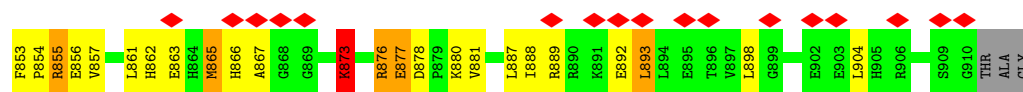
• Molecule 1: Putative mitochondrial dynamin protein



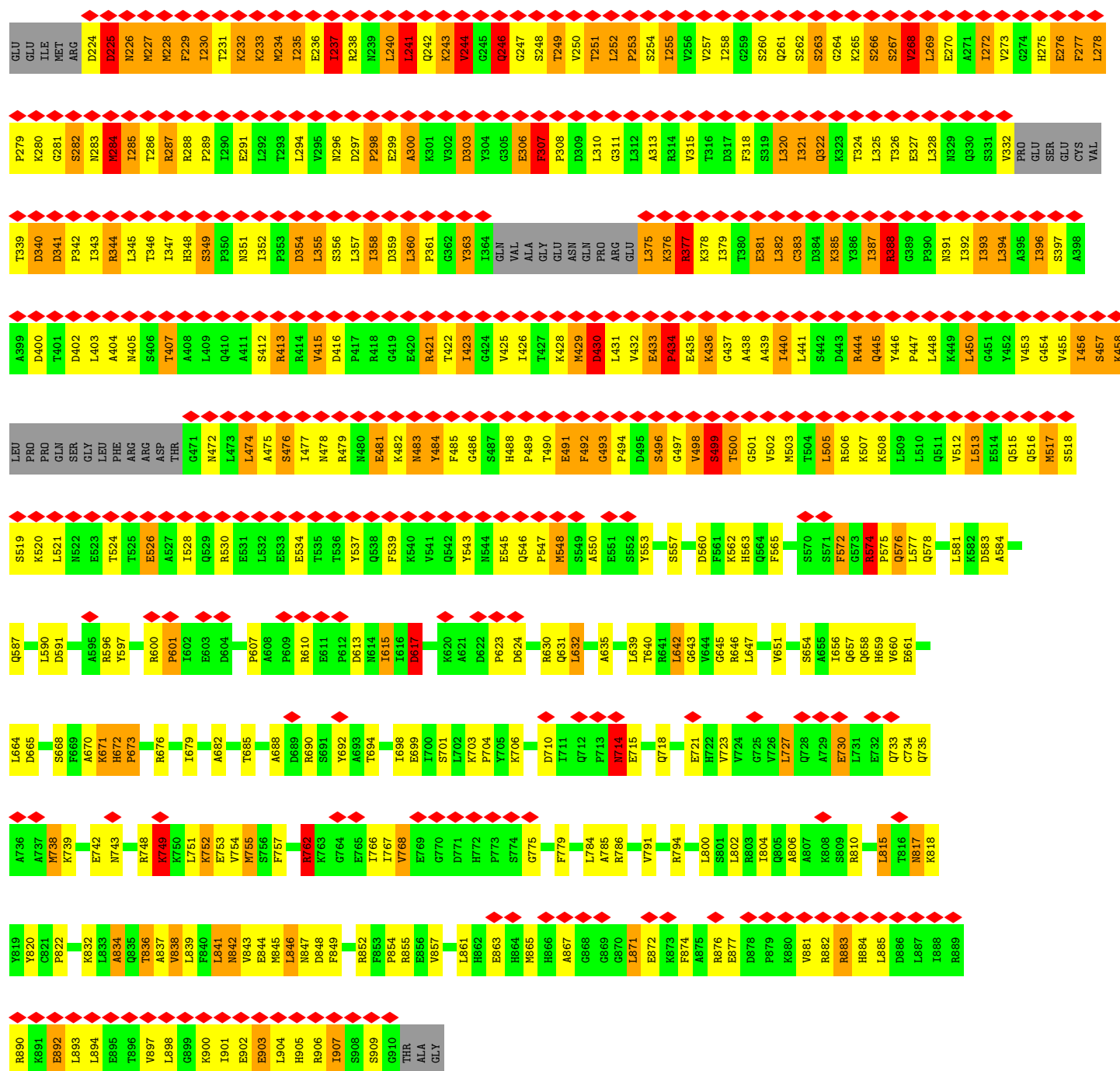


• Molecule 1: Putative mitochondrial dynamin protein



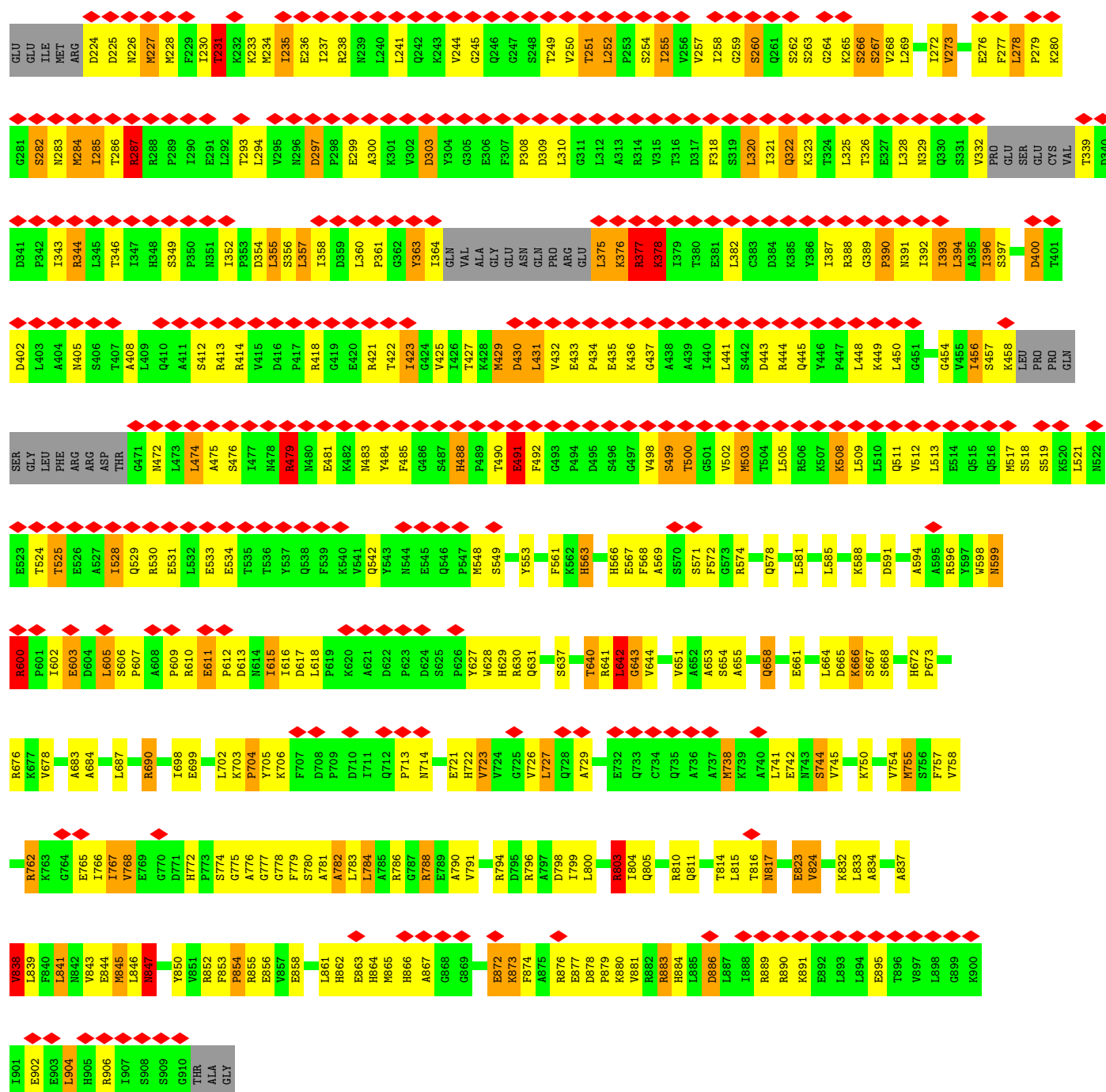


• Molecule 1: Putative mitochondrial dynamin protein



• Molecule 1: Putative mitochondrial dynamin protein

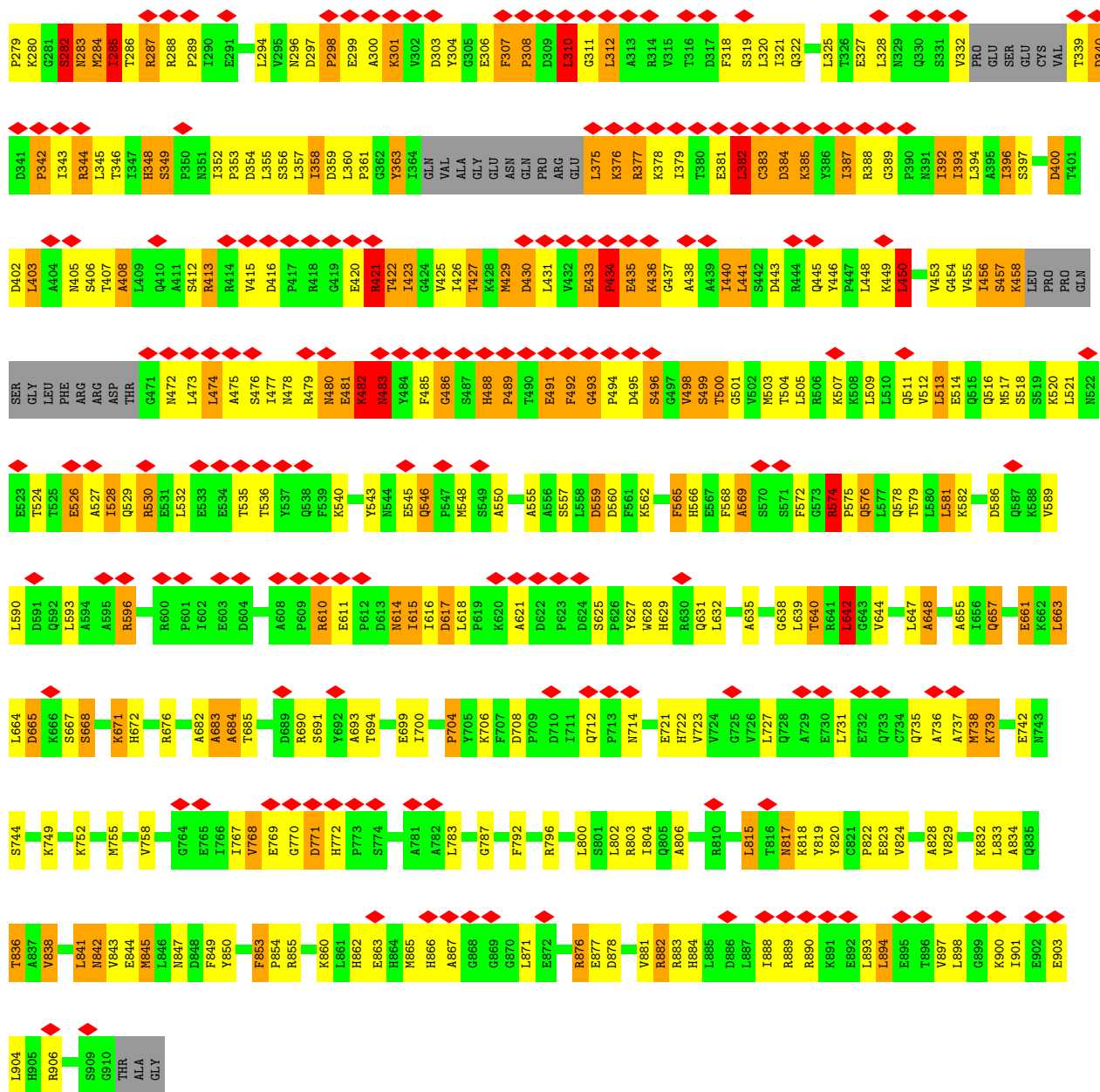
Chain I: 



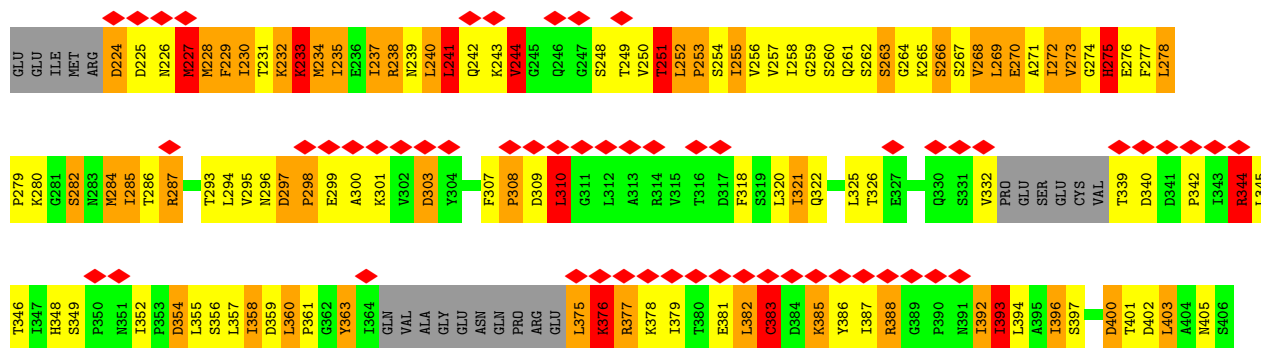
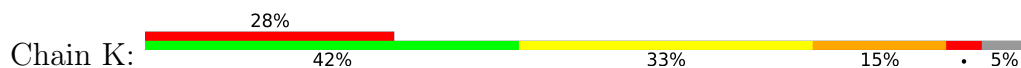
• Molecule 1: Putative mitochondrial dynamin protein

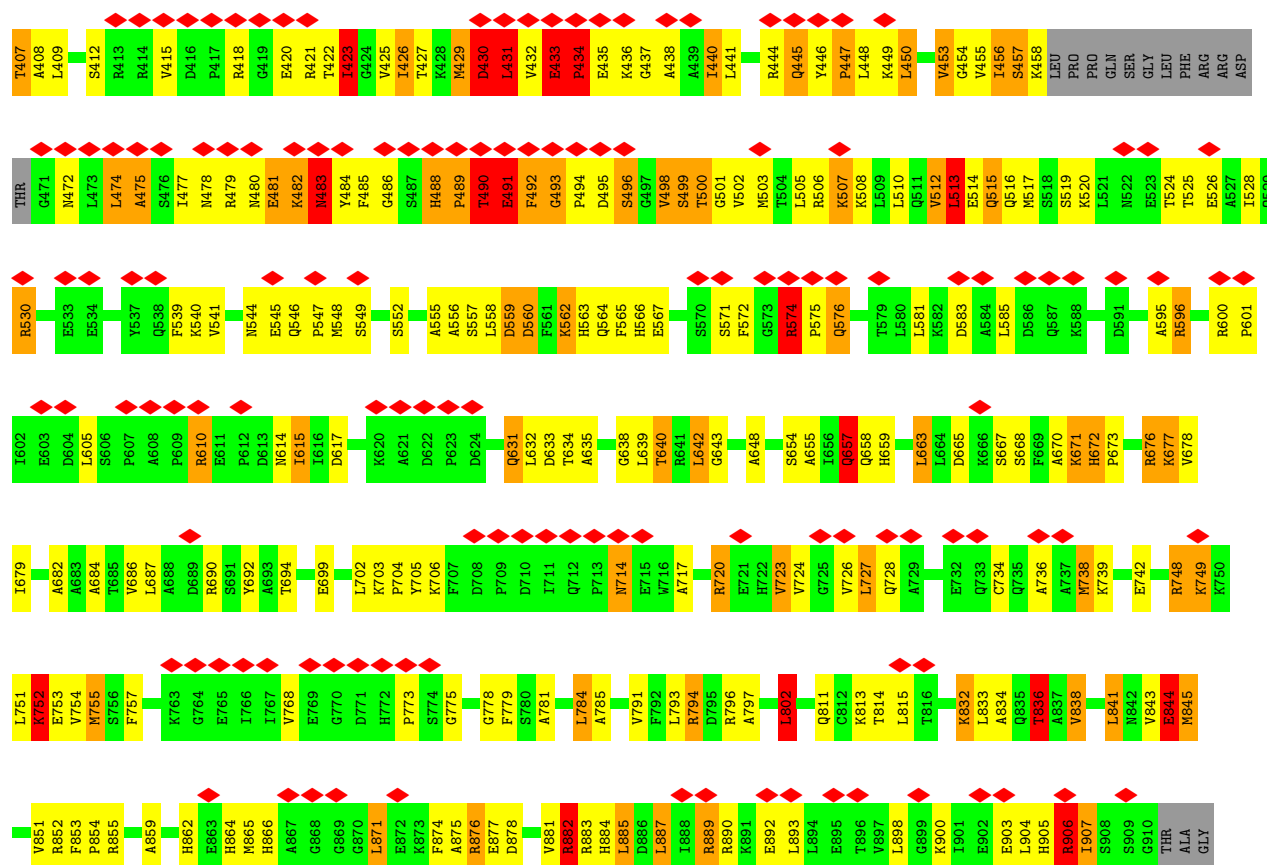
Chain J: 



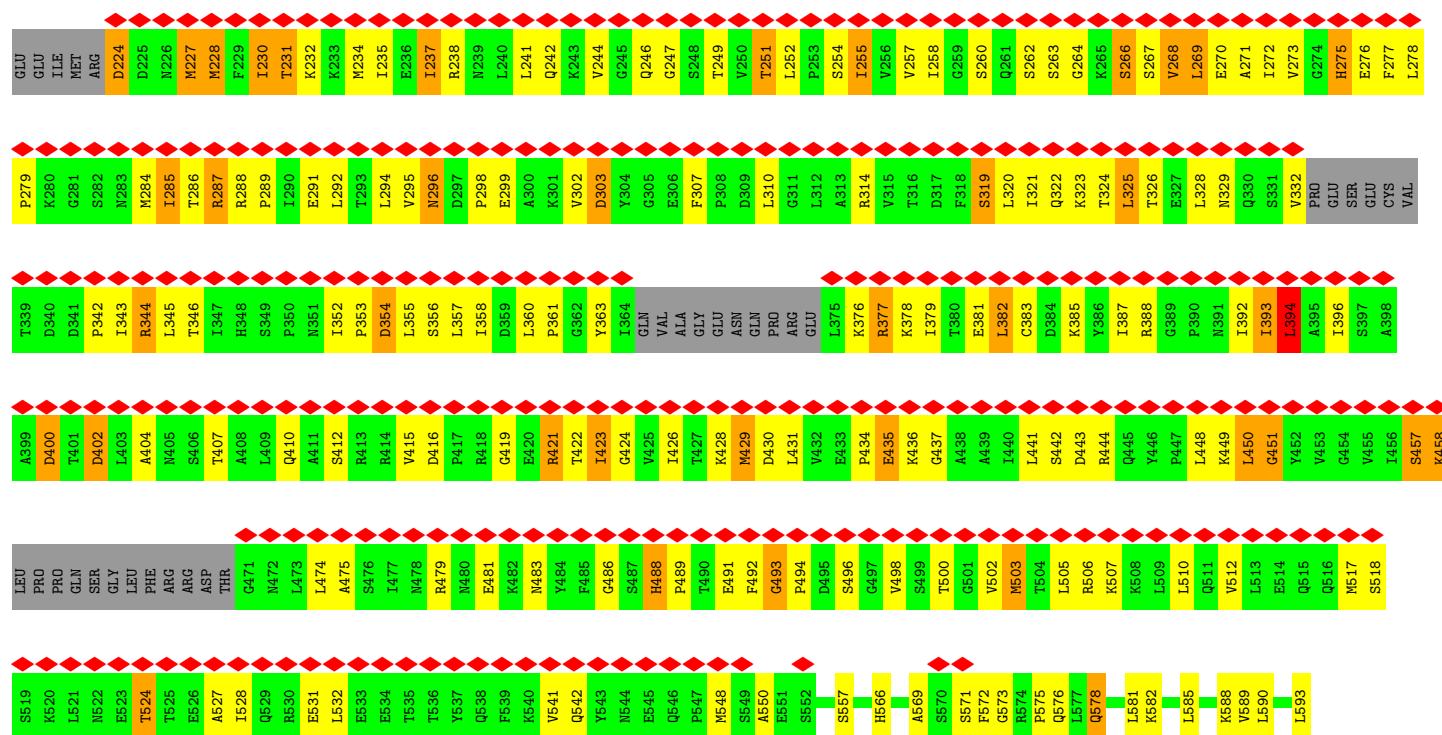


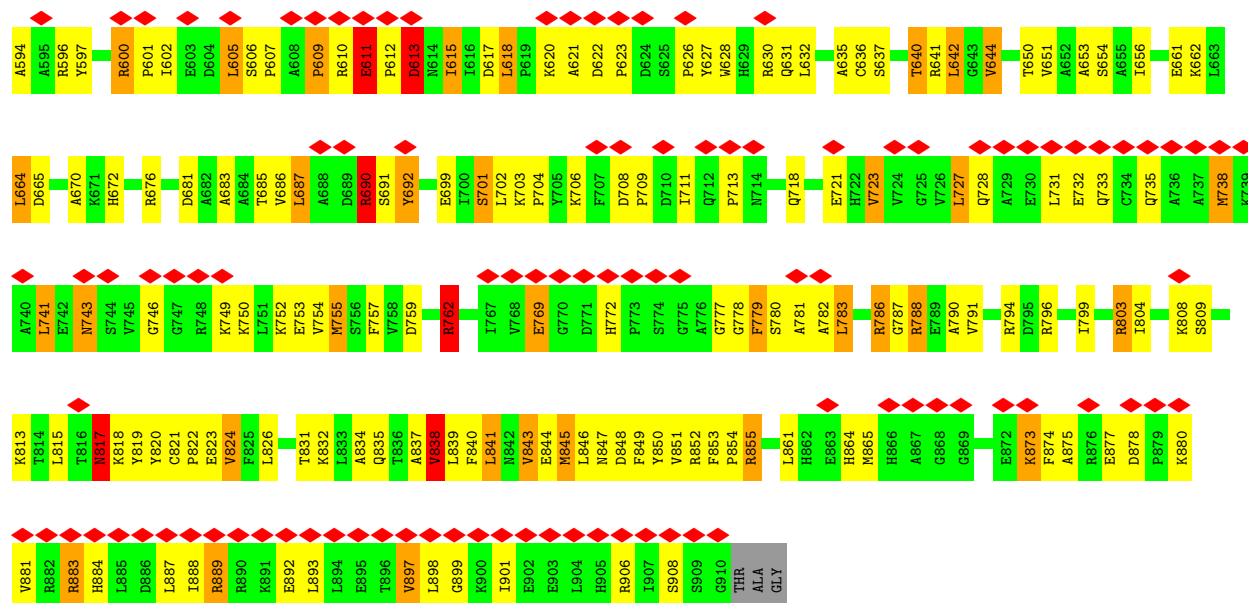
• Molecule 1: Putative mitochondrial dynamin protein





• Molecule 1: Putative mitochondrial dynamin protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	9471	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF determination was done by Gctf and correction was performed by ctfphaseflip from Imod	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	53000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.692	Depositor
Minimum map value	-4.498	Depositor
Average map value	0.207	Depositor
Map value standard deviation	1.019	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	324.0, 324.0, 324.0	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.7, 2.7, 2.7	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	2.05	132/5238 (2.5%)	1.41	39/7075 (0.6%)
1	B	2.00	115/5238 (2.2%)	1.24	7/7075 (0.1%)
1	C	1.97	94/5238 (1.8%)	1.26	5/7075 (0.1%)
1	D	2.04	120/5238 (2.3%)	1.37	37/7075 (0.5%)
1	E	2.04	135/5238 (2.6%)	1.39	38/7075 (0.5%)
1	F	2.02	129/5238 (2.5%)	1.26	12/7075 (0.2%)
1	G	2.08	107/5238 (2.0%)	1.26	3/7075 (0.0%)
1	H	2.07	131/5238 (2.5%)	1.42	49/7075 (0.7%)
1	I	1.99	112/5238 (2.1%)	1.23	2/7075 (0.0%)
1	J	2.06	142/5238 (2.7%)	1.39	39/7075 (0.6%)
1	K	2.07	130/5238 (2.5%)	1.41	39/7075 (0.6%)
1	L	2.03	134/5238 (2.6%)	1.23	9/7075 (0.1%)
All	All	2.03	1481/62856 (2.4%)	1.33	279/84900 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	12
1	B	0	11
1	C	0	12
1	D	0	18
1	E	0	15
1	F	0	16
1	G	0	14
1	H	0	13
1	I	0	19
1	J	0	12
1	K	0	18
1	L	0	12
All	All	0	172

All (1481) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	777	GLY	CA-C	45.48	2.16	1.51
1	K	253	PRO	C-N	-16.44	1.12	1.33
1	D	253	PRO	C-N	-15.70	1.13	1.33
1	H	253	PRO	C-N	-15.68	1.12	1.33
1	J	253	PRO	C-N	-15.08	1.14	1.33
1	E	253	PRO	C-N	-14.07	1.15	1.33
1	A	253	PRO	C-N	-13.38	1.16	1.33
1	K	510	LEU	CA-C	-10.81	1.39	1.52
1	L	779	PHE	CG-CD2	10.72	1.61	1.38
1	L	779	PHE	CG-CD1	10.48	1.60	1.38
1	D	884	HIS	ND1-CE1	-10.24	1.22	1.32
1	L	228	MET	SD-CE	10.23	2.05	1.79
1	K	566	HIS	CB-CG	-9.92	1.36	1.50
1	G	227	MET	CG-SD	9.84	2.05	1.80
1	I	227	MET	SD-CE	9.68	2.03	1.79
1	J	227	MET	SD-CE	9.64	2.03	1.79
1	J	738	MET	SD-CE	9.52	2.03	1.79
1	D	865	MET	SD-CE	9.32	2.02	1.79
1	K	252	LEU	C-N	9.10	1.46	1.33
1	E	234	MET	SD-CE	9.09	2.02	1.79
1	L	779	PHE	CD2-CE2	8.95	1.65	1.38
1	B	906	ARG	NE-CZ	-8.92	1.23	1.33
1	B	234	MET	CG-SD	8.85	2.02	1.80
1	L	779	PHE	CE1-CZ	8.78	1.65	1.38
1	B	659	HIS	CD2-NE2	-8.78	1.28	1.37
1	F	654	SER	C-O	-8.72	1.14	1.24
1	H	320	LEU	C-N	-8.67	1.23	1.34
1	E	252	LEU	C-N	8.56	1.45	1.33
1	G	600	ARG	N-CA	8.54	1.51	1.46
1	C	774	SER	N-CA	8.54	1.57	1.46
1	D	228	MET	SD-CE	8.53	2.00	1.79
1	A	252	LEU	C-N	8.51	1.44	1.33
1	J	550	ALA	CA-C	8.43	1.63	1.52
1	I	511	GLN	C-O	8.42	1.33	1.24
1	G	600	ARG	C-O	8.36	1.30	1.24
1	J	493	GLY	C-O	-8.34	1.12	1.24
1	D	556	ALA	C-O	-8.34	1.14	1.24
1	A	295	VAL	C-O	8.30	1.32	1.24
1	D	498	VAL	C-O	-8.29	1.12	1.24
1	H	385	LYS	CA-C	-8.28	1.42	1.52
1	H	252	LEU	C-N	8.27	1.45	1.33
1	I	865	MET	CG-SD	8.26	2.01	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	429	MET	SD-CE	8.22	2.00	1.79
1	B	435	GLU	C-O	-8.17	1.13	1.24
1	C	258	ILE	CA-C	8.15	1.62	1.52
1	C	341	ASP	N-CA	-8.12	1.34	1.45
1	F	629	HIS	CD2-NE2	-8.12	1.28	1.37
1	H	738	MET	SD-CE	8.09	1.99	1.79
1	A	616	ILE	N-CA	-8.09	1.35	1.46
1	J	845	MET	SD-CE	8.07	1.99	1.79
1	B	845	MET	CG-SD	8.05	2.00	1.80
1	G	234	MET	CG-SD	8.05	2.00	1.80
1	D	388	ARG	C-O	-8.04	1.13	1.24
1	H	900	LYS	C-O	8.04	1.33	1.24
1	L	503	MET	CG-SD	8.01	2.00	1.80
1	G	548	MET	SD-CE	7.99	1.99	1.79
1	K	385	LYS	CA-C	-7.98	1.43	1.52
1	G	865	MET	SD-CE	7.98	1.99	1.79
1	D	314	ARG	C-O	7.97	1.33	1.23
1	D	517	MET	SD-CE	7.96	1.99	1.79
1	H	283	ASN	N-CA	-7.94	1.36	1.46
1	E	228	MET	SD-CE	7.93	1.99	1.79
1	J	227	MET	CG-SD	7.93	2.00	1.80
1	J	548	MET	SD-CE	7.93	1.99	1.79
1	F	445	GLN	N-CA	7.92	1.55	1.46
1	G	832	LYS	C-O	7.90	1.33	1.24
1	L	779	PHE	CD1-CE1	7.90	1.62	1.38
1	I	655	ALA	N-CA	7.89	1.55	1.46
1	K	755	MET	SD-CE	7.89	1.99	1.79
1	C	548	MET	SD-CE	7.89	1.99	1.79
1	D	227	MET	SD-CE	7.87	1.99	1.79
1	F	844	GLU	CA-C	-7.87	1.43	1.52
1	I	525	THR	CA-C	7.86	1.63	1.52
1	H	901	ILE	CA-C	7.84	1.62	1.52
1	C	834	ALA	C-O	-7.83	1.14	1.24
1	B	755	MET	CG-SD	7.82	2.00	1.80
1	L	548	MET	SD-CE	7.79	1.99	1.79
1	L	377	ARG	C-N	-7.78	1.23	1.33
1	K	503	MET	SD-CE	7.78	1.99	1.79
1	E	249	THR	C-N	-7.77	1.25	1.33
1	H	228	MET	CG-SD	7.77	2.00	1.80
1	G	722	HIS	CD2-NE2	7.76	1.46	1.37
1	K	884	HIS	C-O	7.76	1.33	1.24
1	B	245	GLY	C-O	7.75	1.32	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	503	MET	SD-CE	7.74	1.98	1.79
1	F	772	HIS	C-N	-7.73	1.26	1.33
1	L	899	GLY	N-CA	7.73	1.55	1.45
1	F	308	PRO	C-O	-7.72	1.15	1.24
1	A	685	THR	N-CA	-7.71	1.36	1.46
1	A	755	MET	CG-SD	7.71	2.00	1.80
1	E	498	VAL	CA-C	-7.70	1.44	1.53
1	G	828	ALA	C-O	7.70	1.32	1.24
1	H	755	MET	SD-CE	7.69	1.98	1.79
1	D	738	MET	CG-SD	7.64	1.99	1.80
1	J	884	HIS	CG-ND1	7.64	1.46	1.38
1	K	475	ALA	C-O	-7.64	1.15	1.24
1	D	227	MET	CA-C	-7.62	1.43	1.52
1	J	228	MET	SD-CE	7.61	1.98	1.79
1	A	429	MET	SD-CE	7.60	1.98	1.79
1	H	857	VAL	CA-CB	-7.59	1.46	1.54
1	I	629	HIS	CE1-NE2	7.59	1.40	1.32
1	L	690	ARG	C-O	-7.59	1.13	1.24
1	C	724	VAL	C-O	-7.58	1.15	1.24
1	J	308	PRO	N-CD	7.58	1.58	1.47
1	E	517	MET	SD-CE	7.58	1.98	1.79
1	A	227	MET	SD-CE	7.57	1.98	1.79
1	H	518	SER	C-N	7.56	1.43	1.33
1	K	308	PRO	N-CD	7.56	1.58	1.47
1	J	234	MET	SD-CE	7.55	1.98	1.79
1	G	517	MET	CG-SD	7.54	1.99	1.80
1	L	377	ARG	CZ-NH2	7.53	1.43	1.33
1	J	503	MET	SD-CE	7.53	1.98	1.79
1	J	382	LEU	CA-C	-7.53	1.43	1.52
1	F	560	ASP	C-N	7.53	1.43	1.33
1	E	227	MET	SD-CE	7.51	1.98	1.79
1	H	845	MET	CG-SD	7.51	1.99	1.80
1	K	755	MET	CG-SD	7.51	1.99	1.80
1	E	738	MET	SD-CE	7.49	1.98	1.79
1	F	517	MET	SD-CE	7.49	1.98	1.79
1	L	864	HIS	ND1-CE1	-7.49	1.25	1.32
1	D	755	MET	SD-CE	7.48	1.98	1.79
1	B	307	PHE	C-O	-7.47	1.15	1.24
1	B	865	MET	SD-CE	7.46	1.98	1.79
1	H	526	GLU	CA-C	7.46	1.62	1.52
1	H	757	PHE	CA-C	-7.44	1.43	1.52
1	B	453	VAL	C-N	7.42	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	779	PHE	CE2-CZ	7.41	1.60	1.38
1	K	298	PRO	C-O	-7.41	1.15	1.23
1	I	234	MET	CG-SD	7.35	1.99	1.80
1	K	475	ALA	N-CA	-7.35	1.37	1.46
1	E	478	ASN	C-O	7.35	1.32	1.24
1	B	546	GLN	CA-C	-7.33	1.44	1.52
1	C	429	MET	CG-SD	7.33	1.99	1.80
1	A	548	MET	SD-CE	7.32	1.97	1.79
1	B	503	MET	CG-SD	7.32	1.99	1.80
1	F	548	MET	SD-CE	7.32	1.97	1.79
1	E	451	GLY	C-N	-7.30	1.22	1.33
1	H	307	PHE	C-N	7.30	1.43	1.34
1	E	503	MET	CG-SD	7.30	1.99	1.80
1	J	275	HIS	CE1-NE2	7.29	1.39	1.32
1	B	583	ASP	N-CA	7.29	1.55	1.46
1	F	629	HIS	CG-ND1	-7.28	1.30	1.38
1	K	638	GLY	C-O	-7.28	1.15	1.24
1	F	228	MET	CG-SD	7.28	1.99	1.80
1	E	767	ILE	N-CA	-7.27	1.37	1.46
1	H	672	HIS	CA-C	-7.26	1.48	1.53
1	E	548	MET	CG-SD	7.25	1.98	1.80
1	E	865	MET	CG-SD	7.25	1.98	1.80
1	C	265	LYS	C-O	-7.25	1.15	1.24
1	J	238	ARG	NE-CZ	7.24	1.41	1.33
1	A	435	GLU	N-CA	7.22	1.55	1.46
1	I	838	VAL	C-O	-7.21	1.15	1.24
1	J	683	ALA	N-CA	-7.20	1.37	1.46
1	B	508	LYS	N-CA	-7.19	1.37	1.46
1	H	572	PHE	C-N	-7.18	1.24	1.33
1	J	340	ASP	CA-CB	-7.17	1.44	1.54
1	E	386	TYR	C-O	-7.17	1.15	1.24
1	K	738	MET	SD-CE	7.16	1.97	1.79
1	E	620	LYS	CA-C	-7.16	1.46	1.53
1	H	890	ARG	NE-CZ	7.15	1.41	1.33
1	B	548	MET	SD-CE	7.15	1.97	1.79
1	J	865	MET	CG-SD	7.14	1.98	1.80
1	B	517	MET	CG-SD	7.13	1.98	1.80
1	D	845	MET	CG-SD	7.13	1.98	1.80
1	D	406	SER	N-CA	-7.12	1.37	1.46
1	L	759	ASP	CA-C	-7.11	1.43	1.52
1	D	805	GLN	CA-C	-7.10	1.43	1.52
1	A	252	LEU	C-O	-7.09	1.15	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	348	HIS	CE1-NE2	-7.09	1.25	1.32
1	A	613	ASP	CA-CB	-7.09	1.43	1.53
1	F	227	MET	SD-CE	7.09	1.97	1.79
1	L	635	ALA	C-O	-7.08	1.16	1.24
1	A	234	MET	SD-CE	7.08	1.97	1.79
1	E	753	GLU	N-CA	7.08	1.54	1.46
1	A	385	LYS	CA-C	-7.07	1.43	1.52
1	H	892	GLU	CA-CB	7.07	1.64	1.53
1	L	232	LYS	CA-C	7.06	1.61	1.52
1	K	234	MET	CG-SD	7.06	1.98	1.80
1	A	228	MET	SD-CE	7.05	1.97	1.79
1	J	787	GLY	C-N	7.04	1.43	1.33
1	K	517	MET	SD-CE	7.04	1.97	1.79
1	E	488	HIS	CA-CB	-7.04	1.45	1.53
1	C	302	VAL	CA-C	-7.04	1.44	1.52
1	I	234	MET	SD-CE	7.04	1.97	1.79
1	C	698	ILE	C-O	-7.03	1.16	1.24
1	I	517	MET	SD-CE	7.03	1.97	1.79
1	D	570	SER	N-CA	-7.03	1.37	1.46
1	K	738	MET	CG-SD	7.03	1.98	1.80
1	D	746	GLY	C-O	7.02	1.33	1.23
1	H	444	ARG	N-CA	7.02	1.55	1.45
1	E	258	ILE	C-O	7.01	1.31	1.24
1	H	227	MET	CG-SD	7.01	1.98	1.80
1	E	569	ALA	C-O	7.00	1.32	1.24
1	J	517	MET	SD-CE	7.00	1.97	1.79
1	A	396	ILE	CA-C	-7.00	1.44	1.52
1	B	227	MET	SD-CE	7.00	1.97	1.79
1	K	906	ARG	NE-CZ	-7.00	1.25	1.33
1	D	483	ASN	N-CA	7.00	1.55	1.46
1	B	738	MET	CG-SD	6.99	1.98	1.80
1	K	228	MET	CG-SD	6.99	1.98	1.80
1	E	440	ILE	C-O	-6.97	1.16	1.24
1	J	566	HIS	CG-CD2	6.97	1.43	1.35
1	B	699	GLU	CA-CB	6.97	1.64	1.53
1	H	313	ALA	C-O	6.97	1.32	1.24
1	L	548	MET	CG-SD	6.97	1.98	1.80
1	E	546	GLN	CA-C	6.96	1.61	1.53
1	I	642	LEU	C-N	6.95	1.43	1.33
1	C	738	MET	SD-CE	6.94	1.97	1.79
1	L	738	MET	SD-CE	6.94	1.97	1.79
1	F	400	ASP	C-N	-6.94	1.23	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	608	ALA	CA-C	6.93	1.60	1.52
1	H	388	ARG	C-N	-6.93	1.23	1.33
1	L	524	THR	C-N	6.91	1.43	1.33
1	H	591	ASP	N-CA	6.91	1.54	1.46
1	B	271	ALA	N-CA	-6.90	1.38	1.46
1	H	234	MET	SD-CE	6.89	1.96	1.79
1	H	349	SER	C-O	6.89	1.33	1.24
1	K	435	GLU	C-O	-6.87	1.16	1.24
1	G	432	VAL	C-O	6.87	1.31	1.23
1	G	856	GLU	N-CA	-6.87	1.37	1.46
1	K	227	MET	SD-CE	6.87	1.96	1.79
1	A	283	ASN	C-O	-6.87	1.15	1.24
1	A	348	HIS	CG-CD2	-6.87	1.28	1.35
1	J	486	GLY	N-CA	6.86	1.54	1.45
1	H	227	MET	SD-CE	6.86	1.96	1.79
1	D	722	HIS	ND1-CE1	6.85	1.39	1.32
1	E	238	ARG	NE-CZ	6.85	1.40	1.33
1	D	687	LEU	C-O	6.84	1.31	1.24
1	E	438	ALA	CA-C	-6.84	1.43	1.52
1	G	441	LEU	N-CA	6.83	1.54	1.46
1	E	440	ILE	N-CA	-6.83	1.38	1.46
1	F	776	ALA	N-CA	6.83	1.54	1.46
1	D	695	SER	C-O	6.83	1.31	1.24
1	G	845	MET	SD-CE	6.82	1.96	1.79
1	A	432	VAL	CA-C	6.82	1.60	1.52
1	F	866	HIS	C-O	-6.82	1.15	1.24
1	J	421	ARG	CD-NE	6.82	1.55	1.46
1	E	228	MET	CG-SD	6.81	1.97	1.80
1	G	788	ARG	C-O	-6.81	1.16	1.24
1	L	566	HIS	CD2-NE2	-6.81	1.30	1.37
1	K	571	SER	CA-C	6.80	1.61	1.52
1	K	845	MET	SD-CE	6.80	1.96	1.79
1	I	517	MET	CG-SD	6.80	1.97	1.80
1	J	548	MET	CG-SD	6.79	1.97	1.80
1	L	687	LEU	N-CA	6.79	1.54	1.46
1	H	688	ALA	C-O	6.79	1.32	1.24
1	D	868	GLY	C-N	-6.78	1.23	1.33
1	F	888	ILE	C-O	6.77	1.32	1.24
1	K	244	VAL	C-N	-6.77	1.25	1.32
1	E	548	MET	SD-CE	6.76	1.96	1.79
1	I	519	SER	C-O	-6.76	1.16	1.24
1	A	589	VAL	C-O	-6.76	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	310	LEU	N-CA	-6.76	1.38	1.46
1	C	548	MET	CG-SD	6.73	1.97	1.80
1	D	444	ARG	NE-CZ	-6.73	1.25	1.33
1	L	865	MET	SD-CE	6.73	1.96	1.79
1	H	228	MET	SD-CE	6.73	1.96	1.79
1	C	499	SER	C-O	-6.73	1.16	1.23
1	B	767	ILE	C-N	6.72	1.43	1.33
1	F	503	MET	CG-SD	6.72	1.97	1.80
1	A	676	ARG	NE-CZ	-6.72	1.25	1.33
1	E	825	PHE	C-N	-6.72	1.24	1.33
1	K	273	VAL	C-N	-6.72	1.25	1.33
1	H	291	GLU	N-CA	-6.71	1.38	1.46
1	G	759	ASP	C-O	-6.71	1.16	1.24
1	H	583	ASP	CA-C	-6.71	1.44	1.52
1	B	228	MET	SD-CE	6.71	1.96	1.79
1	L	769	GLU	N-CA	-6.70	1.37	1.45
1	F	785	ALA	C-O	6.70	1.31	1.24
1	I	684	ALA	CA-C	-6.70	1.44	1.52
1	I	886	ASP	C-O	6.70	1.32	1.24
1	I	603	GLU	C-O	6.69	1.33	1.23
1	A	738	MET	SD-CE	6.69	1.96	1.79
1	A	503	MET	CG-SD	6.69	1.97	1.80
1	B	730	GLU	C-O	6.69	1.32	1.24
1	I	755	MET	SD-CE	6.68	1.96	1.79
1	J	492	PHE	CA-CB	-6.68	1.45	1.53
1	F	845	MET	CG-SD	6.68	1.97	1.80
1	E	549	SER	C-N	-6.68	1.25	1.33
1	D	744	SER	C-O	-6.67	1.16	1.24
1	D	234	MET	CG-SD	6.67	1.97	1.80
1	A	526	GLU	N-CA	6.67	1.54	1.46
1	B	416	ASP	C-N	6.67	1.42	1.34
1	H	517	MET	SD-CE	6.67	1.96	1.79
1	J	503	MET	CG-SD	6.67	1.97	1.80
1	L	234	MET	SD-CE	6.66	1.96	1.79
1	J	492	PHE	CA-C	-6.66	1.45	1.53
1	L	617	ASP	C-O	-6.66	1.15	1.24
1	D	355	LEU	CA-CB	-6.65	1.45	1.53
1	D	738	MET	SD-CE	6.65	1.96	1.79
1	E	503	MET	SD-CE	6.65	1.96	1.79
1	K	263	SER	C-O	-6.65	1.16	1.24
1	C	865	MET	SD-CE	6.65	1.96	1.79
1	F	281	GLY	C-N	6.65	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	590	LEU	N-CA	6.64	1.54	1.46
1	B	544	ASN	C-N	6.64	1.43	1.33
1	K	513	LEU	CA-C	-6.64	1.44	1.52
1	B	411	ALA	N-CA	6.64	1.54	1.46
1	L	897	VAL	C-O	-6.64	1.16	1.24
1	E	755	MET	CG-SD	6.63	1.97	1.80
1	E	566	HIS	C-O	6.63	1.31	1.24
1	K	376	LYS	CA-C	6.63	1.61	1.52
1	B	804	ILE	C-O	6.63	1.31	1.24
1	B	548	MET	CG-SD	6.62	1.97	1.80
1	A	845	MET	SD-CE	6.61	1.96	1.79
1	J	276	GLU	C-O	6.61	1.31	1.23
1	A	824	VAL	C-N	6.61	1.42	1.33
1	C	503	MET	SD-CE	6.60	1.96	1.79
1	L	651	VAL	CA-CB	6.60	1.62	1.54
1	B	799	ILE	CA-C	-6.60	1.44	1.52
1	G	575	PRO	C-O	6.60	1.32	1.24
1	F	908	SER	CA-C	6.59	1.61	1.52
1	J	429	MET	SD-CE	6.59	1.96	1.79
1	H	547	PRO	N-CA	6.59	1.54	1.47
1	E	616	ILE	C-N	6.58	1.42	1.33
1	A	384	ASP	C-N	-6.57	1.25	1.33
1	F	292	LEU	C-O	-6.57	1.16	1.24
1	J	228	MET	CG-SD	6.57	1.97	1.80
1	B	662	LYS	C-O	-6.57	1.16	1.24
1	F	905	HIS	CA-C	-6.57	1.43	1.52
1	A	613	ASP	C-O	6.57	1.31	1.24
1	L	821	CYS	C-O	6.57	1.32	1.24
1	B	270	GLU	C-O	-6.56	1.16	1.24
1	J	244	VAL	CA-CB	6.56	1.62	1.54
1	F	300	ALA	N-CA	6.56	1.54	1.46
1	H	494	PRO	N-CD	6.55	1.56	1.47
1	L	228	MET	CG-SD	6.55	1.97	1.80
1	B	755	MET	SD-CE	6.55	1.96	1.79
1	K	227	MET	CG-SD	6.55	1.97	1.80
1	H	261	GLN	C-O	-6.54	1.16	1.24
1	I	309	ASP	CA-C	-6.54	1.44	1.52
1	K	686	VAL	CA-CB	6.54	1.62	1.54
1	J	429	MET	CG-SD	6.54	1.97	1.80
1	E	327	GLU	C-O	6.54	1.31	1.24
1	K	663	LEU	C-N	-6.54	1.25	1.33
1	L	503	MET	SD-CE	6.54	1.95	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	864	HIS	CG-ND1	6.54	1.45	1.38
1	G	838	VAL	CA-CB	6.54	1.62	1.54
1	H	672	HIS	CE1-NE2	-6.53	1.26	1.32
1	C	344	ARG	CD-NE	6.52	1.55	1.46
1	D	227	MET	CG-SD	6.52	1.97	1.80
1	D	441	LEU	C-O	-6.52	1.16	1.24
1	A	657	GLN	C-N	6.51	1.42	1.33
1	K	432	VAL	C-O	6.51	1.30	1.23
1	E	691	SER	N-CA	6.51	1.54	1.46
1	A	865	MET	CG-SD	6.50	1.97	1.80
1	L	571	SER	N-CA	6.50	1.54	1.46
1	K	431	LEU	C-N	-6.50	1.24	1.33
1	E	589	VAL	N-CA	6.50	1.54	1.46
1	I	788	ARG	NE-CZ	6.50	1.40	1.33
1	F	536	THR	CA-C	6.49	1.61	1.52
1	K	434	PRO	C-O	-6.49	1.16	1.24
1	L	626	PRO	C-O	6.49	1.32	1.24
1	A	227	MET	CG-SD	6.48	1.97	1.80
1	H	404	ALA	CA-C	-6.48	1.44	1.52
1	H	623	PRO	N-CD	6.47	1.56	1.47
1	I	503	MET	C-O	6.47	1.31	1.24
1	K	865	MET	SD-CE	6.47	1.95	1.79
1	I	252	LEU	N-CA	6.47	1.57	1.45
1	F	227	MET	CG-SD	6.47	1.97	1.80
1	D	754	VAL	N-CA	-6.47	1.38	1.46
1	L	353	PRO	N-CD	6.47	1.56	1.47
1	D	759	ASP	C-O	-6.46	1.16	1.24
1	I	435	GLU	C-O	6.46	1.31	1.24
1	D	517	MET	CG-SD	6.46	1.97	1.80
1	F	672	HIS	C-O	-6.46	1.21	1.23
1	J	406	SER	N-CA	6.46	1.54	1.46
1	H	846	LEU	CA-C	6.46	1.60	1.52
1	E	695	SER	C-N	6.45	1.42	1.33
1	H	768	VAL	N-CA	6.44	1.54	1.46
1	K	726	VAL	C-O	-6.44	1.16	1.24
1	L	817	ASN	CA-C	-6.44	1.46	1.53
1	C	239	ASN	N-CA	6.44	1.54	1.46
1	G	544	ASN	C-O	-6.43	1.14	1.23
1	K	490	THR	C-N	-6.43	1.25	1.33
1	G	446	TYR	CA-CB	-6.42	1.46	1.53
1	H	577	LEU	C-N	-6.42	1.25	1.33
1	A	900	LYS	C-N	6.41	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	566	HIS	CG-CD2	6.41	1.42	1.35
1	J	489	PRO	N-CD	6.40	1.56	1.47
1	B	311	GLY	CA-C	-6.40	1.46	1.52
1	C	429	MET	SD-CE	6.40	1.95	1.79
1	H	659	HIS	N-CA	6.40	1.54	1.46
1	B	541	VAL	CA-CB	6.39	1.62	1.54
1	F	738	MET	SD-CE	6.39	1.95	1.79
1	I	727	LEU	CA-CB	-6.39	1.43	1.53
1	L	310	LEU	C-N	6.39	1.41	1.33
1	K	631	GLN	C-N	6.39	1.42	1.33
1	K	321	ILE	N-CA	6.38	1.54	1.46
1	E	574	ARG	NE-CZ	6.38	1.40	1.33
1	A	343	ILE	CA-CB	6.38	1.60	1.54
1	I	630	ARG	N-CA	6.38	1.54	1.46
1	C	738	MET	CG-SD	6.38	1.96	1.80
1	E	227	MET	CA-C	-6.38	1.44	1.52
1	E	328	LEU	C-N	-6.38	1.25	1.33
1	H	734	CYS	C-O	-6.38	1.16	1.24
1	A	672	HIS	CA-CB	6.38	1.57	1.52
1	L	851	VAL	CA-C	-6.38	1.44	1.52
1	A	344	ARG	N-CA	6.37	1.53	1.45
1	I	666	LYS	N-CA	6.37	1.54	1.46
1	A	865	MET	SD-CE	6.36	1.95	1.79
1	G	520	LYS	C-O	6.36	1.32	1.24
1	E	888	ILE	CB-CG1	6.36	1.66	1.53
1	A	660	VAL	C-O	-6.36	1.16	1.24
1	H	429	MET	N-CA	-6.36	1.38	1.46
1	D	776	ALA	C-N	-6.36	1.25	1.33
1	G	416	ASP	N-CA	6.36	1.53	1.46
1	I	673	PRO	C-O	-6.35	1.16	1.24
1	I	488	HIS	N-CA	6.35	1.53	1.46
1	L	755	MET	SD-CE	6.35	1.95	1.79
1	B	885	LEU	CA-C	-6.34	1.44	1.52
1	G	296	ASN	N-CA	-6.33	1.38	1.46
1	I	378	LYS	CA-C	6.33	1.61	1.52
1	L	227	MET	CG-SD	6.33	1.96	1.80
1	L	642	LEU	N-CA	-6.33	1.38	1.45
1	F	845	MET	SD-CE	6.33	1.95	1.79
1	C	228	MET	SD-CE	6.32	1.95	1.79
1	F	705	TYR	C-N	-6.32	1.25	1.33
1	C	230	ILE	C-O	6.31	1.31	1.24
1	E	738	MET	CG-SD	6.31	1.96	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	704	PRO	CA-CB	6.31	1.62	1.53
1	K	234	MET	SD-CE	6.31	1.95	1.79
1	C	533	GLU	CA-C	6.31	1.60	1.52
1	J	665	ASP	CA-C	-6.31	1.44	1.52
1	K	440	ILE	C-O	-6.31	1.18	1.24
1	I	781	ALA	N-CA	6.30	1.53	1.46
1	A	855	ARG	C-N	6.29	1.42	1.33
1	B	832	LYS	C-N	6.29	1.41	1.33
1	E	626	PRO	CA-C	6.29	1.61	1.52
1	G	506	ARG	NE-CZ	6.29	1.40	1.33
1	H	601	PRO	C-N	6.29	1.44	1.33
1	A	710	ASP	C-N	6.28	1.41	1.33
1	L	713	PRO	C-O	-6.27	1.16	1.24
1	I	866	HIS	CE1-NE2	-6.27	1.26	1.32
1	G	608	ALA	C-O	-6.26	1.16	1.24
1	A	748	ARG	NE-CZ	-6.26	1.26	1.33
1	E	526	GLU	N-CA	-6.25	1.38	1.46
1	I	445	GLN	CA-C	6.25	1.60	1.52
1	J	527	ALA	CA-C	6.25	1.60	1.52
1	A	456	ILE	CA-C	-6.25	1.45	1.52
1	F	865	MET	CA-C	6.25	1.60	1.52
1	H	786	ARG	CZ-NH2	-6.25	1.25	1.33
1	D	429	MET	CG-SD	6.24	1.96	1.80
1	J	234	MET	CG-SD	6.24	1.96	1.80
1	A	390	PRO	CA-CB	-6.24	1.46	1.53
1	B	282	SER	N-CA	6.24	1.54	1.46
1	B	503	MET	SD-CE	6.24	1.95	1.79
1	B	437	GLY	CA-C	6.23	1.59	1.51
1	K	866	HIS	CD2-NE2	-6.23	1.30	1.37
1	I	839	LEU	N-CA	6.23	1.53	1.46
1	F	569	ALA	N-CA	6.23	1.53	1.46
1	K	797	ALA	C-O	6.23	1.31	1.24
1	I	651	VAL	N-CA	6.22	1.53	1.46
1	J	738	MET	CG-SD	6.21	1.96	1.80
1	A	803	ARG	NE-CZ	-6.21	1.26	1.33
1	E	240	LEU	CA-CB	-6.21	1.43	1.53
1	H	565	PHE	C-O	-6.21	1.17	1.24
1	E	577	LEU	N-CA	6.21	1.54	1.46
1	E	829	VAL	N-CA	6.21	1.53	1.46
1	F	388	ARG	NE-CZ	-6.21	1.26	1.33
1	K	752	LYS	C-N	-6.21	1.26	1.33
1	J	684	ALA	CA-CB	6.20	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	695	SER	N-CA	6.19	1.53	1.46
1	H	617	ASP	CA-CB	-6.19	1.44	1.53
1	C	331	SER	C-N	-6.19	1.24	1.33
1	G	705	TYR	N-CA	6.18	1.54	1.46
1	G	501	GLY	N-CA	6.18	1.51	1.45
1	E	837	ALA	C-O	6.18	1.31	1.24
1	B	765	GLU	CA-C	6.17	1.61	1.52
1	I	443	ASP	N-CA	-6.17	1.38	1.46
1	L	550	ALA	CA-CB	-6.17	1.43	1.53
1	E	542	GLN	N-CA	-6.17	1.38	1.46
1	E	558	LEU	CA-CB	6.17	1.63	1.53
1	F	503	MET	SD-CE	6.17	1.95	1.79
1	J	385	LYS	C-O	-6.17	1.17	1.24
1	J	638	GLY	CA-C	-6.17	1.45	1.52
1	H	656	ILE	N-CA	6.17	1.54	1.46
1	B	858	GLU	CA-CB	-6.16	1.43	1.53
1	L	708	ASP	N-CA	6.16	1.53	1.46
1	K	781	ALA	C-O	6.16	1.31	1.24
1	I	322	GLN	N-CA	6.16	1.53	1.46
1	I	297	ASP	CA-CB	-6.16	1.46	1.53
1	E	411	ALA	N-CA	-6.15	1.38	1.46
1	B	275	HIS	CE1-NE2	6.15	1.38	1.32
1	G	873	LYS	C-N	-6.15	1.25	1.33
1	I	782	ALA	C-O	-6.15	1.16	1.24
1	F	513	LEU	C-O	6.15	1.31	1.24
1	G	738	MET	N-CA	-6.15	1.38	1.46
1	F	518	SER	C-O	-6.14	1.16	1.24
1	E	490	THR	N-CA	-6.14	1.39	1.46
1	J	298	PRO	C-N	-6.14	1.25	1.33
1	L	901	ILE	C-N	6.14	1.41	1.33
1	G	865	MET	CG-SD	6.13	1.96	1.80
1	G	548	MET	CG-SD	6.13	1.96	1.80
1	K	884	HIS	CD2-NE2	6.13	1.44	1.37
1	E	517	MET	CG-SD	6.12	1.96	1.80
1	H	227	MET	CA-C	-6.12	1.45	1.52
1	I	762	ARG	C-O	6.12	1.32	1.24
1	B	292	LEU	N-CA	-6.11	1.38	1.46
1	D	878	ASP	CA-C	-6.11	1.46	1.52
1	K	658	GLN	N-CA	-6.10	1.39	1.46
1	A	488	HIS	N-CA	-6.10	1.40	1.46
1	C	628	TRP	C-O	-6.10	1.16	1.24
1	H	692	TYR	N-CA	6.10	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	502	VAL	C-N	-6.10	1.25	1.33
1	K	525	THR	C-O	6.10	1.31	1.24
1	E	484	TYR	N-CA	6.10	1.53	1.46
1	K	773	PRO	C-O	6.10	1.30	1.23
1	A	742	GLU	CA-C	-6.09	1.45	1.52
1	F	865	MET	C-O	-6.09	1.17	1.24
1	A	563	HIS	N-CA	-6.09	1.39	1.46
1	A	452	TYR	CA-C	-6.08	1.45	1.52
1	K	634	THR	C-N	6.08	1.41	1.33
1	I	528	ILE	CA-CB	-6.08	1.47	1.54
1	F	752	LYS	CA-CB	-6.08	1.43	1.53
1	J	796	ARG	N-CA	6.08	1.53	1.46
1	K	426	ILE	N-CA	-6.07	1.39	1.46
1	H	845	MET	SD-CE	6.07	1.94	1.79
1	A	325	LEU	CA-C	6.07	1.60	1.52
1	D	628	TRP	N-CA	6.06	1.53	1.46
1	I	549	SER	C-N	6.06	1.41	1.33
1	E	751	LEU	CA-C	6.06	1.60	1.52
1	F	730	GLU	CA-C	-6.06	1.44	1.52
1	I	596	ARG	NE-CZ	6.06	1.39	1.33
1	D	803	ARG	CD-NE	6.05	1.54	1.46
1	F	293	THR	CA-CB	6.05	1.61	1.53
1	L	755	MET	CG-SD	6.05	1.95	1.80
1	L	840	PHE	N-CA	6.05	1.53	1.46
1	B	298	PRO	C-N	6.05	1.41	1.33
1	D	548	MET	SD-CE	6.05	1.94	1.79
1	C	659	HIS	CE1-NE2	-6.05	1.26	1.32
1	D	246	GLN	C-O	-6.05	1.17	1.24
1	D	429	MET	SD-CE	6.05	1.94	1.79
1	J	529	GLN	C-O	-6.05	1.17	1.24
1	A	297	ASP	CA-C	6.05	1.59	1.53
1	B	554	LEU	C-O	6.05	1.31	1.24
1	D	488	HIS	N-CA	-6.05	1.40	1.46
1	F	865	MET	CG-SD	6.04	1.95	1.80
1	H	268	VAL	CA-CB	-6.04	1.47	1.54
1	E	888	ILE	C-N	-6.04	1.25	1.33
1	K	905	HIS	CG-ND1	-6.04	1.31	1.38
1	F	661	GLU	N-CA	-6.04	1.39	1.46
1	C	631	GLN	N-CA	-6.04	1.39	1.46
1	G	228	MET	SD-CE	6.04	1.94	1.79
1	B	242	GLN	C-O	6.04	1.31	1.24
1	K	271	ALA	C-N	-6.04	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	560	ASP	C-N	6.04	1.42	1.34
1	F	865	MET	SD-CE	6.02	1.94	1.79
1	E	865	MET	N-CA	6.02	1.53	1.46
1	F	760	LYS	N-CA	-6.02	1.39	1.46
1	I	235	ILE	CA-C	6.02	1.60	1.52
1	A	307	PHE	C-N	6.01	1.41	1.34
1	A	696	ASP	CA-C	6.01	1.60	1.52
1	F	762	ARG	CZ-NH2	6.01	1.41	1.33
1	E	581	LEU	N-CA	-6.01	1.39	1.46
1	A	730	GLU	CA-C	6.00	1.60	1.52
1	H	324	THR	C-O	6.00	1.31	1.24
1	G	700	ILE	CA-CB	6.00	1.61	1.54
1	J	862	HIS	CE1-NE2	-6.00	1.26	1.32
1	K	494	PRO	N-CA	6.00	1.54	1.47
1	L	741	LEU	N-CA	6.00	1.53	1.46
1	F	839	LEU	N-CA	-5.99	1.39	1.46
1	H	519	SER	C-N	5.99	1.42	1.33
1	J	353	PRO	C-O	5.99	1.30	1.23
1	B	744	SER	C-N	5.99	1.41	1.33
1	H	563	HIS	CD2-NE2	-5.99	1.31	1.37
1	I	704	PRO	CA-C	5.99	1.60	1.52
1	E	607	PRO	CA-C	5.98	1.60	1.52
1	F	656	ILE	CA-CB	-5.98	1.46	1.54
1	G	810	ARG	CD-NE	5.98	1.54	1.46
1	C	291	GLU	CA-CB	5.98	1.60	1.52
1	L	711	ILE	CA-C	-5.98	1.45	1.52
1	E	250	VAL	N-CA	5.97	1.53	1.46
1	E	882	ARG	C-O	-5.97	1.17	1.24
1	A	503	MET	SD-CE	5.97	1.94	1.79
1	J	385	LYS	C-N	-5.97	1.26	1.33
1	A	625	SER	CA-C	-5.97	1.45	1.52
1	D	526	GLU	CA-C	-5.97	1.44	1.52
1	D	641	ARG	CA-CB	5.96	1.59	1.53
1	K	796	ARG	C-N	5.96	1.41	1.33
1	L	883	ARG	CZ-NH1	5.96	1.41	1.32
1	D	489	PRO	N-CD	5.96	1.56	1.47
1	E	755	MET	SD-CE	5.96	1.94	1.79
1	I	548	MET	SD-CE	5.96	1.94	1.79
1	G	306	GLU	CA-C	5.96	1.59	1.52
1	I	729	ALA	CA-C	-5.96	1.45	1.52
1	H	500	THR	C-N	-5.95	1.25	1.33
1	I	654	SER	N-CA	-5.95	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	504	THR	N-CA	-5.95	1.39	1.46
1	G	272	ILE	N-CA	5.94	1.53	1.46
1	K	293	THR	CA-C	-5.94	1.45	1.52
1	B	429	MET	CG-SD	5.94	1.95	1.80
1	H	493	GLY	C-N	5.94	1.40	1.33
1	C	475	ALA	N-CA	-5.93	1.38	1.46
1	E	234	MET	CG-SD	5.93	1.95	1.80
1	C	376	LYS	N-CA	-5.93	1.38	1.46
1	B	737	ALA	CA-C	-5.93	1.44	1.52
1	D	527	ALA	C-O	-5.93	1.16	1.24
1	H	387	ILE	C-O	-5.93	1.16	1.24
1	E	574	ARG	CZ-NH1	-5.93	1.24	1.32
1	G	621	ALA	CA-C	5.92	1.60	1.52
1	K	814	THR	CA-C	5.92	1.60	1.52
1	D	442	SER	N-CA	5.92	1.53	1.46
1	I	503	MET	SD-CE	5.92	1.94	1.79
1	J	532	LEU	C-N	5.92	1.41	1.33
1	I	755	MET	CG-SD	5.91	1.95	1.80
1	D	342	PRO	N-CD	5.91	1.56	1.47
1	J	755	MET	CG-SD	5.91	1.95	1.80
1	D	435	GLU	N-CA	-5.91	1.39	1.46
1	I	318	PHE	C-O	5.91	1.32	1.24
1	K	548	MET	CG-SD	5.91	1.95	1.80
1	J	888	ILE	CA-CB	5.90	1.61	1.54
1	E	859	ALA	C-O	5.90	1.30	1.24
1	H	439	ALA	CA-C	-5.90	1.45	1.52
1	J	348	HIS	N-CA	-5.90	1.39	1.46
1	L	839	LEU	C-O	5.89	1.30	1.24
1	B	812	CYS	C-O	5.89	1.31	1.24
1	F	900	LYS	C-N	-5.89	1.26	1.33
1	B	711	ILE	CA-C	5.89	1.59	1.52
1	H	738	MET	CG-SD	5.89	1.95	1.80
1	I	889	ARG	CA-C	5.89	1.60	1.52
1	D	614	ASN	C-N	5.88	1.40	1.33
1	D	810	ARG	C-N	-5.88	1.25	1.33
1	D	647	LEU	CA-C	-5.88	1.45	1.52
1	A	806	ALA	C-N	-5.88	1.26	1.34
1	B	891	LYS	C-N	5.88	1.41	1.33
1	G	299	GLU	C-O	-5.88	1.16	1.24
1	G	588	LYS	CA-C	5.88	1.60	1.52
1	I	432	VAL	N-CA	5.87	1.52	1.46
1	B	234	MET	SD-CE	5.87	1.94	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	355	LEU	CA-C	5.87	1.60	1.53
1	L	781	ALA	CA-C	5.87	1.60	1.52
1	E	567	GLU	C-N	5.87	1.41	1.33
1	L	488	HIS	CD2-NE2	-5.86	1.31	1.37
1	J	581	LEU	C-O	5.86	1.30	1.24
1	B	482	LYS	CA-CB	-5.86	1.44	1.53
1	L	686	VAL	CA-C	5.86	1.60	1.52
1	F	855	ARG	N-CA	5.85	1.53	1.46
1	J	514	GLU	C-N	5.85	1.41	1.33
1	K	457	SER	CA-C	-5.85	1.45	1.52
1	J	629	HIS	ND1-CE1	5.85	1.38	1.32
1	C	755	MET	CG-SD	5.85	1.95	1.80
1	I	503	MET	CG-SD	5.85	1.95	1.80
1	A	876	ARG	NE-CZ	5.84	1.39	1.33
1	D	553	TYR	CA-C	5.84	1.60	1.52
1	E	584	ALA	N-CA	-5.84	1.39	1.46
1	F	800	LEU	C-N	5.83	1.41	1.33
1	J	413	ARG	NE-CZ	5.83	1.39	1.33
1	E	883	ARG	CA-CB	5.83	1.62	1.53
1	G	346	THR	CA-C	5.83	1.58	1.52
1	G	750	LYS	CA-CB	5.83	1.62	1.53
1	I	228	MET	SD-CE	5.83	1.94	1.79
1	A	238	ARG	CD-NE	5.83	1.54	1.46
1	H	865	MET	SD-CE	5.83	1.94	1.79
1	F	290	ILE	N-CA	-5.82	1.38	1.46
1	J	635	ALA	C-O	5.82	1.30	1.24
1	C	763	LYS	C-N	-5.81	1.24	1.33
1	A	226	ASN	C-N	-5.81	1.26	1.33
1	A	657	GLN	N-CA	-5.81	1.39	1.46
1	G	522	ASN	N-CA	5.81	1.53	1.46
1	I	713	PRO	C-O	-5.81	1.16	1.24
1	E	886	ASP	C-N	5.80	1.41	1.33
1	L	299	GLU	CA-C	5.80	1.60	1.52
1	C	227	MET	CA-CB	-5.80	1.44	1.53
1	A	553	TYR	C-O	-5.79	1.17	1.24
1	I	823	GLU	N-CA	5.79	1.53	1.46
1	E	806	ALA	C-O	5.79	1.30	1.24
1	I	817	ASN	C-N	-5.79	1.26	1.33
1	I	377	ARG	NE-CZ	5.79	1.39	1.33
1	F	572	PHE	CA-C	-5.79	1.45	1.52
1	E	562	LYS	CA-C	-5.79	1.45	1.52
1	E	846	LEU	CA-C	5.78	1.60	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	711	ILE	CA-CB	-5.78	1.47	1.54
1	L	344	ARG	CD-NE	5.78	1.54	1.46
1	F	557	SER	CA-C	5.78	1.60	1.52
1	F	862	HIS	C-N	5.78	1.41	1.33
1	E	227	MET	C-O	5.78	1.30	1.24
1	L	424	GLY	C-O	-5.78	1.16	1.23
1	C	629	HIS	C-O	-5.78	1.17	1.24
1	J	736	ALA	N-CA	5.78	1.53	1.46
1	C	759	ASP	C-O	5.77	1.30	1.24
1	F	874	PHE	N-CA	5.77	1.53	1.46
1	L	621	ALA	C-O	-5.76	1.16	1.23
1	E	716	TRP	NE1-CE2	5.76	1.43	1.37
1	A	248	SER	CA-C	-5.76	1.45	1.52
1	C	496	SER	CA-CB	5.76	1.63	1.53
1	L	228	MET	C-O	-5.76	1.17	1.24
1	B	289	PRO	N-CA	5.75	1.54	1.47
1	H	806	ALA	C-O	5.75	1.30	1.24
1	J	312	LEU	CA-C	-5.75	1.45	1.52
1	K	841	LEU	C-O	-5.75	1.17	1.24
1	B	528	ILE	C-O	-5.75	1.17	1.24
1	C	599	ASN	CA-C	-5.75	1.45	1.53
1	I	847	ASN	C-O	-5.75	1.17	1.24
1	L	324	THR	N-CA	-5.75	1.39	1.46
1	G	503	MET	CG-SD	5.75	1.95	1.80
1	G	719	GLY	CA-C	-5.75	1.45	1.52
1	H	872	GLU	CA-C	-5.75	1.45	1.52
1	I	429	MET	CG-SD	5.75	1.95	1.80
1	A	449	LYS	CA-C	5.74	1.60	1.53
1	I	563	HIS	CE1-NE2	5.74	1.38	1.32
1	J	482	LYS	N-CA	-5.74	1.39	1.46
1	C	404	ALA	C-O	5.74	1.31	1.24
1	I	228	MET	CG-SD	5.74	1.95	1.80
1	I	323	LYS	CA-C	5.74	1.60	1.52
1	L	884	HIS	C-O	5.74	1.30	1.24
1	H	548	MET	CG-SD	5.74	1.95	1.80
1	I	904	LEU	CA-C	5.74	1.60	1.52
1	A	314	ARG	C-O	5.74	1.31	1.24
1	J	655	ALA	C-O	-5.73	1.17	1.24
1	K	517	MET	CG-SD	5.73	1.95	1.80
1	B	284	MET	N-CA	5.73	1.52	1.46
1	B	704	PRO	C-O	-5.73	1.17	1.24
1	A	244	VAL	C-N	-5.73	1.27	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	906	ARG	C-O	5.73	1.30	1.24
1	D	324	THR	CA-C	5.73	1.59	1.52
1	D	832	LYS	C-N	-5.73	1.26	1.33
1	C	254	SER	N-CA	5.73	1.53	1.46
1	L	746	GLY	C-O	5.72	1.31	1.23
1	G	353	PRO	CA-CB	5.72	1.61	1.53
1	I	698	ILE	CA-CB	-5.72	1.47	1.54
1	L	394	LEU	N-CA	5.72	1.53	1.46
1	A	599	ASN	N-CA	5.72	1.53	1.45
1	I	768	VAL	CA-C	5.72	1.60	1.52
1	G	429	MET	SD-CE	5.72	1.93	1.79
1	C	865	MET	CG-SD	5.71	1.95	1.80
1	K	491	GLU	C-O	-5.71	1.17	1.24
1	L	421	ARG	C-N	5.71	1.41	1.33
1	B	380	THR	CA-C	5.71	1.60	1.52
1	A	455	VAL	CA-CB	5.71	1.61	1.55
1	H	276	GLU	C-O	5.71	1.30	1.23
1	J	579	THR	C-N	-5.71	1.26	1.33
1	L	506	ARG	CZ-NH1	5.71	1.40	1.32
1	C	228	MET	CG-SD	5.71	1.95	1.80
1	A	755	MET	SD-CE	5.71	1.93	1.79
1	D	724	VAL	N-CA	5.71	1.53	1.46
1	A	577	LEU	N-CA	5.71	1.53	1.46
1	L	578	GLN	C-O	-5.71	1.17	1.24
1	E	224	ASP	C-N	-5.70	1.26	1.33
1	F	630	ARG	CD-NE	5.70	1.54	1.46
1	D	455	VAL	C-N	-5.70	1.25	1.33
1	H	848	ASP	CA-CB	-5.70	1.43	1.53
1	I	794	ARG	N-CA	-5.70	1.39	1.46
1	K	757	PHE	N-CA	5.70	1.53	1.46
1	L	620	LYS	CA-C	-5.70	1.47	1.53
1	I	889	ARG	N-CA	5.70	1.53	1.46
1	A	429	MET	CG-SD	5.69	1.95	1.80
1	F	755	MET	CG-SD	5.69	1.95	1.80
1	K	386	TYR	CA-C	-5.69	1.45	1.52
1	K	785	ALA	N-CA	5.69	1.53	1.46
1	B	236	GLU	C-O	-5.69	1.17	1.24
1	E	378	LYS	C-O	5.69	1.30	1.24
1	D	512	VAL	C-O	-5.68	1.17	1.24
1	E	855	ARG	CA-C	-5.68	1.45	1.52
1	D	574	ARG	CA-C	-5.68	1.45	1.52
1	E	416	ASP	C-N	5.68	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	298	PRO	C-O	-5.68	1.17	1.23
1	F	848	ASP	CA-C	5.68	1.60	1.52
1	G	517	MET	SD-CE	5.68	1.93	1.79
1	L	845	MET	CG-SD	5.68	1.95	1.80
1	A	646	ARG	CZ-NH1	5.68	1.40	1.32
1	E	384	ASP	N-CA	-5.68	1.39	1.46
1	D	253	PRO	N-CD	5.67	1.55	1.47
1	E	648	ALA	N-CA	-5.67	1.39	1.46
1	H	415	VAL	C-O	-5.67	1.16	1.24
1	L	849	PHE	CA-CB	-5.67	1.44	1.53
1	D	485	PHE	C-N	-5.67	1.26	1.33
1	D	250	VAL	C-O	-5.67	1.17	1.24
1	K	228	MET	SD-CE	5.67	1.93	1.79
1	A	679	ILE	N-CA	-5.66	1.40	1.46
1	K	262	SER	N-CA	-5.66	1.39	1.46
1	E	845	MET	CG-SD	5.66	1.94	1.80
1	F	738	MET	CG-SD	5.66	1.94	1.80
1	F	566	HIS	CE1-NE2	5.66	1.38	1.32
1	G	680	SER	CA-C	5.66	1.60	1.52
1	D	832	LYS	C-O	5.65	1.30	1.24
1	F	546	GLN	C-O	-5.65	1.16	1.24
1	K	493	GLY	C-N	5.65	1.40	1.33
1	H	434	PRO	N-CA	-5.65	1.40	1.47
1	I	509	LEU	C-O	-5.65	1.17	1.24
1	D	642	LEU	N-CA	5.65	1.52	1.45
1	G	549	SER	CA-C	-5.65	1.45	1.52
1	D	842	ASN	C-O	-5.64	1.17	1.24
1	A	906	ARG	NE-CZ	5.64	1.39	1.33
1	B	275	HIS	N-CA	5.64	1.53	1.46
1	I	794	ARG	CA-C	5.64	1.59	1.52
1	K	512	VAL	N-CA	-5.64	1.40	1.46
1	L	699	GLU	N-CA	-5.64	1.39	1.46
1	B	623	PRO	CA-C	5.64	1.61	1.52
1	L	510	LEU	CA-C	-5.64	1.45	1.52
1	D	258	ILE	C-N	-5.63	1.25	1.33
1	H	225	ASP	N-CA	5.63	1.53	1.46
1	A	779	PHE	CA-C	-5.63	1.46	1.52
1	E	742	GLU	C-N	-5.63	1.26	1.33
1	A	316	THR	C-O	5.63	1.30	1.24
1	H	755	MET	CG-SD	5.63	1.94	1.80
1	I	864	HIS	ND1-CE1	-5.63	1.26	1.32
1	D	252	LEU	N-CA	5.63	1.54	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	813	LYS	C-O	5.62	1.30	1.24
1	H	429	MET	CG-SD	5.62	1.94	1.80
1	J	744	SER	N-CA	-5.62	1.39	1.46
1	A	401	THR	C-O	-5.62	1.17	1.23
1	C	483	ASN	CA-C	-5.62	1.44	1.52
1	F	881	VAL	N-CA	-5.62	1.39	1.46
1	J	663	LEU	CA-C	5.62	1.60	1.52
1	J	842	ASN	N-CA	-5.62	1.39	1.46
1	B	387	ILE	C-O	5.61	1.31	1.24
1	E	227	MET	CG-SD	5.61	1.94	1.80
1	F	517	MET	CG-SD	5.61	1.94	1.80
1	G	815	LEU	C-O	5.61	1.31	1.24
1	A	303	ASP	C-O	-5.61	1.17	1.24
1	F	295	VAL	C-O	5.61	1.29	1.24
1	D	321	ILE	C-N	-5.61	1.26	1.33
1	J	822	PRO	C-N	-5.60	1.27	1.33
1	A	555	ALA	N-CA	5.60	1.53	1.46
1	E	864	HIS	N-CA	-5.60	1.39	1.46
1	J	507	LYS	C-O	-5.60	1.17	1.24
1	J	817	ASN	N-CA	-5.60	1.39	1.46
1	K	657	GLN	N-CA	-5.60	1.39	1.46
1	L	573	GLY	CA-C	-5.60	1.44	1.51
1	C	227	MET	SD-CE	5.60	1.93	1.79
1	C	646	ARG	NE-CZ	-5.60	1.26	1.33
1	G	357	LEU	CA-C	-5.60	1.45	1.52
1	F	828	ALA	C-O	5.59	1.30	1.24
1	A	601	PRO	C-O	5.59	1.30	1.23
1	C	278	LEU	CA-CB	-5.59	1.46	1.53
1	C	589	VAL	C-O	5.59	1.30	1.24
1	J	434	PRO	N-CA	-5.59	1.40	1.47
1	J	228	MET	N-CA	-5.59	1.39	1.46
1	B	773	PRO	CA-C	-5.58	1.47	1.52
1	F	755	MET	C-O	-5.58	1.17	1.24
1	J	737	ALA	N-CA	5.58	1.53	1.46
1	B	804	ILE	CA-CB	-5.58	1.47	1.54
1	L	883	ARG	C-O	5.58	1.30	1.24
1	C	438	ALA	N-CA	-5.58	1.38	1.46
1	D	749	LYS	N-CA	-5.58	1.39	1.46
1	F	303	ASP	CA-CB	5.57	1.59	1.52
1	F	878	ASP	CA-C	5.57	1.59	1.52
1	G	877	GLU	C-O	-5.57	1.16	1.24
1	D	384	ASP	N-CA	-5.57	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	322	GLN	CA-C	-5.57	1.45	1.52
1	J	894	LEU	C-N	5.57	1.41	1.33
1	L	861	LEU	C-N	5.57	1.41	1.33
1	B	571	SER	CA-C	5.57	1.60	1.52
1	C	455	VAL	C-O	-5.57	1.17	1.23
1	G	562	LYS	N-CA	-5.57	1.39	1.46
1	I	456	ILE	CA-CB	5.57	1.60	1.54
1	L	865	MET	CG-SD	5.57	1.94	1.80
1	B	902	GLU	CA-C	5.57	1.60	1.52
1	D	866	HIS	N-CA	-5.56	1.39	1.46
1	J	517	MET	CG-SD	5.56	1.94	1.80
1	L	809	SER	CA-CB	5.56	1.62	1.53
1	H	852	ARG	NE-CZ	5.56	1.39	1.33
1	K	687	LEU	CA-CB	-5.56	1.44	1.53
1	K	862	HIS	C-O	-5.56	1.17	1.24
1	A	394	LEU	CA-CB	5.55	1.61	1.53
1	A	228	MET	CG-SD	5.55	1.94	1.80
1	E	853	PHE	C-N	5.55	1.41	1.34
1	H	284	MET	C-N	-5.55	1.26	1.33
1	J	739	LYS	C-O	5.55	1.30	1.24
1	J	845	MET	N-CA	-5.55	1.39	1.46
1	A	415	VAL	CA-C	5.55	1.60	1.53
1	L	637	SER	C-N	5.55	1.40	1.33
1	F	548	MET	CG-SD	5.54	1.94	1.80
1	A	852	ARG	NE-CZ	5.54	1.39	1.33
1	C	423	ILE	N-CA	-5.54	1.39	1.46
1	F	704	PRO	C-O	-5.54	1.17	1.24
1	K	574	ARG	NE-CZ	5.54	1.39	1.33
1	G	708	ASP	N-CA	-5.54	1.41	1.46
1	H	749	LYS	N-CA	-5.54	1.39	1.46
1	E	909	SER	C-N	-5.54	1.25	1.33
1	L	475	ALA	N-CA	5.54	1.53	1.46
1	H	484	TYR	C-O	5.54	1.30	1.24
1	K	724	VAL	CA-C	-5.54	1.46	1.52
1	B	566	HIS	CA-C	5.54	1.59	1.52
1	F	343	ILE	CA-C	5.54	1.58	1.52
1	B	355	LEU	CA-C	-5.53	1.46	1.53
1	E	711	ILE	N-CA	-5.53	1.39	1.46
1	L	813	LYS	N-CA	-5.53	1.39	1.46
1	F	238	ARG	N-CA	-5.53	1.39	1.46
1	G	683	ALA	N-CA	5.53	1.52	1.46
1	E	718	GLN	C-N	5.52	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	353	PRO	N-CA	5.52	1.53	1.47
1	G	415	VAL	CA-C	5.52	1.58	1.52
1	I	699	GLU	C-O	5.52	1.30	1.24
1	J	589	VAL	CA-C	-5.52	1.46	1.52
1	L	271	ALA	C-N	-5.52	1.26	1.33
1	D	228	MET	CG-SD	5.52	1.94	1.80
1	A	738	MET	CG-SD	5.52	1.94	1.80
1	E	900	LYS	C-N	5.51	1.40	1.33
1	F	568	PHE	C-O	-5.51	1.17	1.24
1	H	340	ASP	CA-CB	5.51	1.60	1.53
1	I	432	VAL	CA-C	-5.51	1.45	1.52
1	J	348	HIS	ND1-CE1	5.51	1.38	1.32
1	E	479	ARG	CZ-NH2	-5.51	1.26	1.33
1	D	472	ASN	C-O	5.51	1.30	1.23
1	J	866	HIS	CE1-NE2	-5.51	1.27	1.32
1	E	788	ARG	NE-CZ	5.51	1.39	1.33
1	H	381	GLU	N-CA	-5.51	1.39	1.46
1	K	342	PRO	N-CD	5.50	1.55	1.47
1	B	321	ILE	CA-CB	5.50	1.61	1.54
1	I	854	PRO	N-CA	5.50	1.54	1.47
1	K	503	MET	CG-SD	5.50	1.94	1.80
1	G	422	THR	CA-C	5.50	1.59	1.52
1	D	564	GLN	C-O	-5.50	1.17	1.24
1	J	238	ARG	CD-NE	5.50	1.53	1.46
1	K	275	HIS	CG-ND1	5.50	1.44	1.38
1	K	677	LYS	C-O	-5.50	1.17	1.24
1	A	257	VAL	CA-CB	5.50	1.60	1.54
1	B	634	THR	C-N	-5.49	1.26	1.33
1	B	772	HIS	C-N	5.49	1.38	1.33
1	E	594	ALA	N-CA	5.49	1.53	1.46
1	H	883	ARG	C-O	-5.49	1.17	1.24
1	K	453	VAL	C-N	5.49	1.39	1.33
1	D	227	MET	N-CA	-5.49	1.39	1.46
1	D	845	MET	SD-CE	5.49	1.93	1.79
1	H	267	SER	C-N	-5.49	1.27	1.33
1	L	314	ARG	NE-CZ	5.49	1.39	1.33
1	B	860	LYS	C-O	-5.49	1.17	1.24
1	F	687	LEU	CA-C	-5.49	1.45	1.52
1	L	410	GLN	CA-C	5.49	1.59	1.52
1	B	474	LEU	N-CA	-5.49	1.40	1.46
1	E	845	MET	SD-CE	5.49	1.93	1.79
1	K	559	ASP	CA-C	-5.49	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	429	MET	SD-CE	5.49	1.93	1.79
1	J	403	LEU	N-CA	-5.49	1.39	1.46
1	J	565	PHE	C-O	-5.49	1.17	1.24
1	J	787	GLY	N-CA	5.49	1.52	1.45
1	K	393	ILE	N-CA	5.49	1.53	1.46
1	B	323	LYS	CA-C	5.48	1.60	1.52
1	F	770	GLY	CA-C	-5.48	1.44	1.51
1	G	348	HIS	CG-CD2	5.48	1.41	1.35
1	C	847	ASN	C-O	5.48	1.30	1.24
1	H	710	ASP	N-CA	-5.48	1.39	1.46
1	I	534	GLU	C-O	-5.48	1.17	1.24
1	J	845	MET	C-O	5.48	1.30	1.23
1	K	885	LEU	N-CA	5.48	1.53	1.46
1	L	527	ALA	C-O	-5.48	1.17	1.24
1	D	249	THR	N-CA	-5.48	1.39	1.46
1	F	324	THR	CA-CB	5.48	1.62	1.53
1	A	535	THR	N-CA	5.48	1.52	1.46
1	E	235	ILE	N-CA	-5.48	1.39	1.46
1	F	528	ILE	CA-C	-5.48	1.45	1.52
1	G	228	MET	CG-SD	5.47	1.94	1.80
1	K	477	ILE	C-N	-5.47	1.26	1.33
1	G	522	ASN	C-N	5.47	1.41	1.33
1	J	264	GLY	C-O	-5.47	1.17	1.23
1	B	233	LYS	N-CA	-5.47	1.39	1.46
1	D	293	THR	C-N	5.47	1.41	1.33
1	A	902	GLU	C-N	5.46	1.41	1.33
1	F	228	MET	SD-CE	5.46	1.93	1.79
1	I	390	PRO	C-O	5.46	1.31	1.24
1	F	270	GLU	N-CA	5.46	1.52	1.46
1	A	793	LEU	N-CA	-5.46	1.39	1.46
1	F	884	HIS	CD2-NE2	-5.46	1.31	1.37
1	K	447	PRO	N-CA	-5.46	1.40	1.46
1	A	353	PRO	CA-CB	-5.46	1.47	1.54
1	G	813	LYS	CA-CB	5.46	1.61	1.53
1	G	661	GLU	CA-CB	-5.46	1.44	1.53
1	E	554	LEU	C-O	-5.45	1.17	1.24
1	B	262	SER	CA-C	-5.45	1.46	1.52
1	J	249	THR	CA-CB	-5.45	1.44	1.53
1	F	484	TYR	N-CA	5.45	1.53	1.46
1	K	429	MET	CG-SD	5.45	1.94	1.80
1	I	862	HIS	C-N	-5.44	1.26	1.33
1	J	700	ILE	N-CA	5.44	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	500	THR	C-O	-5.44	1.17	1.23
1	D	877	GLU	CA-CB	-5.44	1.44	1.53
1	F	903	GLU	CA-C	-5.44	1.45	1.52
1	H	227	MET	N-CA	-5.44	1.39	1.46
1	K	736	ALA	C-O	5.44	1.30	1.24
1	H	499	SER	C-O	-5.44	1.17	1.24
1	D	549	SER	CA-CB	5.44	1.62	1.53
1	F	787	GLY	CA-C	5.44	1.57	1.52
1	J	847	ASN	CA-C	-5.44	1.45	1.52
1	C	661	GLU	CA-C	-5.44	1.45	1.52
1	G	340	ASP	N-CA	5.44	1.52	1.46
1	B	731	LEU	C-N	5.43	1.41	1.33
1	C	341	ASP	C-N	5.43	1.40	1.33
1	J	699	GLU	CA-C	-5.43	1.45	1.52
1	L	493	GLY	N-CA	-5.43	1.37	1.44
1	L	782	ALA	C-N	-5.43	1.26	1.33
1	G	491	GLU	C-O	5.43	1.30	1.24
1	A	253	PRO	N-CD	5.43	1.55	1.47
1	A	363	TYR	C-O	5.43	1.30	1.23
1	A	498	VAL	N-CA	-5.43	1.39	1.46
1	E	302	VAL	CA-C	5.43	1.59	1.52
1	A	898	LEU	N-CA	5.43	1.52	1.46
1	F	783	LEU	N-CA	-5.42	1.39	1.46
1	I	413	ARG	NE-CZ	5.42	1.39	1.33
1	L	692	TYR	N-CA	-5.42	1.39	1.46
1	C	721	GLU	N-CA	-5.42	1.39	1.46
1	G	738	MET	SD-CE	5.42	1.93	1.79
1	A	865	MET	N-CA	5.42	1.52	1.46
1	F	525	THR	C-O	-5.42	1.17	1.24
1	K	549	SER	N-CA	-5.42	1.39	1.45
1	L	594	ALA	CA-C	-5.42	1.46	1.52
1	H	699	GLU	C-N	5.41	1.40	1.33
1	D	740	ALA	CA-CB	5.41	1.61	1.53
1	G	451	GLY	N-CA	5.41	1.52	1.45
1	H	421	ARG	CA-C	-5.41	1.45	1.52
1	L	303	ASP	N-CA	5.41	1.53	1.46
1	J	792	PHE	N-CA	5.40	1.52	1.46
1	K	310	LEU	CA-C	-5.40	1.45	1.52
1	K	429	MET	SD-CE	5.40	1.93	1.79
1	G	429	MET	CG-SD	5.40	1.94	1.80
1	I	561	PHE	N-CA	5.40	1.53	1.46
1	D	575	PRO	CA-CB	5.40	1.61	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	587	GLN	N-CA	-5.40	1.40	1.46
1	A	862	HIS	CD2-NE2	5.40	1.43	1.37
1	F	681	ASP	N-CA	5.40	1.53	1.46
1	F	699	GLU	N-CA	5.40	1.53	1.46
1	G	605	LEU	C-O	-5.40	1.17	1.23
1	J	307	PHE	C-N	5.40	1.41	1.34
1	A	587	GLN	C-O	-5.40	1.17	1.24
1	E	527	ALA	N-CA	-5.40	1.40	1.46
1	F	656	ILE	CA-C	-5.40	1.45	1.52
1	I	310	LEU	CA-CB	5.40	1.59	1.52
1	J	661	GLU	CA-C	-5.40	1.45	1.52
1	G	542	GLN	C-O	-5.39	1.17	1.24
1	H	673	PRO	C-N	5.39	1.40	1.33
1	L	234	MET	CG-SD	5.39	1.94	1.80
1	C	889	ARG	C-O	5.39	1.30	1.24
1	D	234	MET	SD-CE	5.39	1.93	1.79
1	H	734	CYS	CA-C	5.39	1.59	1.52
1	I	738	MET	CG-SD	5.39	1.94	1.80
1	J	272	ILE	CA-C	-5.39	1.46	1.52
1	E	553	TYR	C-N	5.39	1.41	1.33
1	G	478	ASN	CA-C	-5.39	1.46	1.52
1	K	865	MET	CA-C	-5.39	1.46	1.52
1	C	793	LEU	C-O	5.39	1.30	1.24
1	F	237	ILE	CA-C	5.39	1.60	1.52
1	B	482	LYS	N-CA	-5.38	1.39	1.46
1	C	326	THR	N-CA	5.38	1.53	1.46
1	I	233	LYS	C-O	-5.38	1.17	1.24
1	B	576	GLN	C-O	-5.38	1.17	1.24
1	E	594	ALA	CA-CB	-5.38	1.45	1.53
1	F	659	HIS	C-N	-5.38	1.27	1.33
1	J	642	LEU	N-CA	-5.38	1.39	1.45
1	H	646	ARG	C-N	5.38	1.40	1.33
1	J	744	SER	C-O	5.38	1.30	1.24
1	F	844	GLU	N-CA	-5.37	1.40	1.46
1	J	876	ARG	CZ-NH1	5.37	1.40	1.32
1	A	566	HIS	CE1-NE2	-5.37	1.27	1.32
1	J	536	THR	CA-C	-5.37	1.46	1.52
1	F	262	SER	N-CA	-5.37	1.39	1.46
1	F	291	GLU	C-N	5.37	1.41	1.33
1	K	430	ASP	C-N	5.37	1.41	1.33
1	C	633	ASP	CA-C	-5.36	1.46	1.52
1	I	865	MET	SD-CE	5.36	1.93	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	517	MET	SD-CE	5.36	1.93	1.79
1	I	423	ILE	C-O	5.36	1.30	1.24
1	H	394	LEU	C-O	5.36	1.30	1.23
1	H	786	ARG	NE-CZ	5.36	1.39	1.33
1	H	865	MET	CG-SD	5.36	1.94	1.80
1	J	828	ALA	CA-CB	5.36	1.61	1.53
1	L	230	ILE	C-O	5.36	1.30	1.24
1	C	226	ASN	N-CA	-5.35	1.39	1.46
1	D	435	GLU	C-O	-5.35	1.18	1.24
1	E	487	SER	N-CA	-5.35	1.39	1.46
1	E	759	ASP	C-N	-5.35	1.27	1.33
1	I	508	LYS	C-N	5.35	1.40	1.33
1	K	494	PRO	N-CD	5.35	1.55	1.47
1	B	652	ALA	C-O	5.35	1.30	1.24
1	H	355	LEU	CA-C	-5.35	1.46	1.52
1	A	446	TYR	C-N	-5.35	1.26	1.33
1	F	268	VAL	C-O	5.34	1.30	1.24
1	F	325	LEU	N-CA	5.34	1.53	1.46
1	L	733	GLN	CA-C	5.34	1.59	1.52
1	C	584	ALA	C-N	-5.34	1.26	1.33
1	D	646	ARG	C-O	5.34	1.30	1.24
1	L	292	LEU	CA-CB	5.34	1.60	1.53
1	E	862	HIS	CD2-NE2	-5.34	1.31	1.37
1	F	297	ASP	CA-C	-5.34	1.47	1.53
1	E	630	ARG	NE-CZ	-5.33	1.27	1.33
1	H	228	MET	C-O	5.33	1.30	1.24
1	H	291	GLU	CA-C	-5.33	1.46	1.52
1	E	383	CYS	C-O	-5.33	1.17	1.24
1	I	476	SER	C-O	-5.33	1.18	1.24
1	B	451	GLY	C-N	-5.33	1.25	1.33
1	L	887	LEU	C-N	5.33	1.40	1.34
1	F	856	GLU	N-CA	5.33	1.52	1.46
1	A	328	LEU	C-N	-5.33	1.26	1.33
1	B	833	LEU	C-N	-5.33	1.26	1.33
1	F	385	LYS	N-CA	5.32	1.52	1.46
1	G	476	SER	C-N	5.32	1.40	1.33
1	L	488	HIS	CG-ND1	-5.32	1.32	1.38
1	I	245	GLY	CA-C	5.32	1.59	1.51
1	A	287	ARG	C-N	5.32	1.40	1.33
1	J	488	HIS	N-CA	5.32	1.52	1.46
1	F	625	SER	CA-C	-5.32	1.46	1.52
1	H	584	ALA	N-CA	5.32	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	693	ALA	C-O	-5.32	1.17	1.24
1	F	763	LYS	CA-CB	5.32	1.60	1.53
1	C	845	MET	CG-SD	5.31	1.94	1.80
1	J	860	LYS	N-CA	5.31	1.52	1.46
1	D	488	HIS	CE1-NE2	5.31	1.37	1.32
1	H	733	GLN	C-N	-5.31	1.27	1.33
1	J	310	LEU	CA-CB	5.31	1.59	1.52
1	G	506	ARG	CD-NE	-5.31	1.38	1.46
1	J	596	ARG	N-CA	5.31	1.52	1.46
1	J	772	HIS	N-CA	5.31	1.51	1.46
1	D	448	LEU	C-N	-5.31	1.26	1.33
1	H	497	GLY	CA-C	5.31	1.57	1.52
1	I	553	TYR	CA-CB	5.31	1.61	1.53
1	I	355	LEU	CA-C	5.31	1.59	1.52
1	A	560	ASP	CA-C	5.30	1.59	1.52
1	B	865	MET	CG-SD	5.30	1.94	1.80
1	E	772	HIS	CB-CG	5.30	1.57	1.50
1	K	547	PRO	C-N	5.30	1.41	1.33
1	L	709	PRO	C-N	-5.30	1.26	1.33
1	H	547	PRO	CA-C	5.30	1.59	1.53
1	E	452	TYR	C-O	-5.30	1.17	1.23
1	E	506	ARG	C-O	5.30	1.30	1.24
1	I	236	GLU	N-CA	5.30	1.52	1.46
1	D	301	LYS	N-CA	5.30	1.52	1.46
1	H	321	ILE	C-N	5.30	1.41	1.33
1	G	695	SER	CA-CB	-5.29	1.45	1.53
1	F	474	LEU	CA-C	5.29	1.59	1.52
1	K	659	HIS	CG-CD2	-5.29	1.30	1.35
1	A	605	LEU	N-CA	5.28	1.53	1.46
1	E	429	MET	CG-SD	5.28	1.94	1.80
1	B	840	PHE	C-O	-5.28	1.17	1.24
1	G	395	ALA	CA-C	5.28	1.59	1.52
1	L	901	ILE	C-O	5.28	1.30	1.24
1	B	618	LEU	CB-CG	5.28	1.64	1.53
1	B	736	ALA	N-CA	5.28	1.52	1.46
1	H	251	THR	N-CA	5.28	1.52	1.46
1	H	476	SER	N-CA	-5.28	1.40	1.46
1	E	305	GLY	CA-C	-5.28	1.47	1.52
1	C	794	ARG	C-N	5.28	1.40	1.33
1	J	427	THR	CA-CB	5.28	1.61	1.53
1	K	595	ALA	C-O	5.28	1.30	1.24
1	G	450	LEU	N-CA	5.28	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	809	SER	C-N	-5.28	1.26	1.34
1	A	620	LYS	CA-C	5.27	1.59	1.53
1	B	482	LYS	C-O	-5.27	1.17	1.24
1	E	500	THR	C-N	-5.27	1.25	1.33
1	A	830	ALA	N-CA	5.27	1.52	1.46
1	K	253	PRO	CA-C	5.27	1.58	1.53
1	K	841	LEU	N-CA	5.27	1.52	1.46
1	A	687	LEU	C-N	5.27	1.40	1.33
1	F	453	VAL	C-O	-5.27	1.18	1.24
1	B	548	MET	C-O	-5.27	1.17	1.23
1	K	832	LYS	C-O	5.27	1.30	1.24
1	L	246	GLN	C-N	5.27	1.41	1.33
1	L	302	VAL	C-O	-5.27	1.18	1.24
1	A	716	TRP	CA-CB	5.26	1.61	1.53
1	H	236	GLU	CA-C	5.26	1.59	1.52
1	I	231	THR	CA-CB	5.26	1.61	1.53
1	A	477	ILE	CA-C	5.26	1.59	1.52
1	B	580	LEU	C-O	5.26	1.30	1.24
1	J	225	ASP	CA-CB	5.26	1.61	1.53
1	J	648	ALA	C-N	-5.26	1.26	1.33
1	B	640	THR	N-CA	5.26	1.52	1.46
1	G	407	THR	C-O	5.26	1.30	1.24
1	I	723	VAL	N-CA	5.26	1.52	1.46
1	G	343	ILE	CA-CB	5.26	1.60	1.53
1	H	660	VAL	CA-CB	-5.26	1.47	1.54
1	D	731	LEU	C-O	-5.26	1.18	1.24
1	E	347	ILE	N-CA	-5.26	1.39	1.46
1	H	645	GLY	C-N	5.26	1.41	1.34
1	B	755	MET	C-N	-5.25	1.27	1.33
1	I	884	HIS	C-N	5.25	1.41	1.34
1	D	739	LYS	C-N	-5.25	1.27	1.33
1	H	277	PHE	CA-C	5.25	1.59	1.52
1	K	734	CYS	N-CA	-5.25	1.40	1.46
1	J	340	ASP	C-N	5.25	1.40	1.33
1	L	322	GLN	N-CA	5.25	1.52	1.46
1	A	225	ASP	CA-C	5.25	1.59	1.52
1	G	280	LYS	CA-C	-5.25	1.45	1.52
1	K	802	LEU	N-CA	5.25	1.52	1.46
1	K	844	GLU	N-CA	-5.25	1.40	1.46
1	B	728	GLN	CA-C	-5.24	1.45	1.52
1	D	563	HIS	C-O	5.24	1.30	1.24
1	L	379	ILE	CA-C	5.24	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	718	GLN	CA-C	5.24	1.59	1.52
1	B	477	ILE	N-CA	5.24	1.53	1.46
1	J	806	ALA	N-CA	-5.24	1.40	1.46
1	G	285	ILE	CA-CB	-5.24	1.47	1.54
1	A	300	ALA	C-O	-5.24	1.18	1.24
1	B	298	PRO	CA-CB	-5.24	1.46	1.53
1	B	864	HIS	CE1-NE2	5.24	1.37	1.32
1	E	658	GLN	C-O	-5.23	1.18	1.24
1	I	542	GLN	CA-C	5.23	1.59	1.52
1	J	319	SER	N-CA	5.23	1.52	1.46
1	K	793	LEU	N-CA	5.23	1.52	1.46
1	L	224	ASP	C-N	-5.23	1.27	1.33
1	C	890	ARG	NE-CZ	5.23	1.38	1.33
1	J	450	LEU	CA-C	5.23	1.59	1.52
1	H	300	ALA	N-CA	5.23	1.52	1.46
1	J	511	GLN	N-CA	5.23	1.52	1.46
1	J	906	ARG	N-CA	-5.23	1.39	1.46
1	J	758	VAL	C-O	5.23	1.30	1.24
1	B	845	MET	SD-CE	5.22	1.92	1.79
1	H	503	MET	CG-SD	5.22	1.93	1.80
1	L	738	MET	CG-SD	5.22	1.93	1.80
1	L	435	GLU	N-CA	5.22	1.52	1.46
1	A	233	LYS	CA-CB	-5.22	1.44	1.53
1	B	563	HIS	CE1-NE2	-5.22	1.27	1.32
1	C	528	ILE	C-O	5.22	1.30	1.24
1	K	794	ARG	C-N	5.22	1.40	1.33
1	L	268	VAL	C-N	5.22	1.40	1.33
1	B	235	ILE	N-CA	5.21	1.52	1.46
1	C	358	ILE	CA-CB	5.21	1.61	1.54
1	D	237	ILE	CA-CB	5.21	1.61	1.54
1	E	890	ARG	NE-CZ	5.21	1.38	1.33
1	G	746	GLY	C-O	-5.21	1.16	1.23
1	C	604	ASP	N-CA	5.21	1.52	1.46
1	K	686	VAL	C-N	-5.21	1.27	1.33
1	E	401	THR	N-CA	-5.21	1.39	1.46
1	E	724	VAL	CA-C	5.21	1.59	1.52
1	F	553	TYR	CA-C	5.21	1.59	1.52
1	I	566	HIS	CE1-NE2	5.21	1.37	1.32
1	K	256	VAL	C-O	-5.21	1.18	1.24
1	A	883	ARG	CA-C	-5.20	1.46	1.52
1	I	226	ASN	C-O	-5.20	1.17	1.24
1	B	672	HIS	CD2-NE2	5.20	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	260	SER	C-N	5.20	1.41	1.33
1	J	480	ASN	C-N	5.20	1.40	1.33
1	J	528	ILE	CA-CB	-5.20	1.47	1.54
1	K	507	LYS	CA-CB	5.20	1.61	1.53
1	F	596	ARG	CZ-NH1	5.20	1.40	1.32
1	H	757	PHE	C-O	5.20	1.30	1.24
1	G	456	ILE	CA-CB	5.19	1.60	1.53
1	K	655	ALA	C-N	5.19	1.40	1.33
1	L	242	GLN	CA-C	5.19	1.59	1.52
1	E	675	ALA	C-O	5.19	1.30	1.24
1	J	562	LYS	CA-C	5.19	1.59	1.52
1	D	497	GLY	N-CA	-5.19	1.39	1.45
1	E	392	ILE	N-CA	5.19	1.52	1.46
1	J	536	THR	C-N	5.19	1.40	1.33
1	I	637	SER	C-O	5.19	1.30	1.24
1	K	530	ARG	CA-C	5.19	1.59	1.52
1	J	349	SER	C-N	-5.19	1.27	1.33
1	L	319	SER	N-CA	5.19	1.52	1.46
1	L	838	VAL	CA-CB	-5.18	1.47	1.54
1	E	635	ALA	CA-C	-5.18	1.46	1.52
1	F	306	GLU	C-O	-5.18	1.17	1.23
1	H	428	LYS	C-N	5.18	1.40	1.33
1	K	676	ARG	N-CA	-5.18	1.40	1.46
1	C	250	VAL	N-CA	5.18	1.52	1.46
1	G	888	ILE	CA-CB	5.18	1.60	1.54
1	H	306	GLU	C-O	-5.18	1.17	1.23
1	I	784	LEU	C-N	-5.18	1.26	1.33
1	G	329	ASN	CA-C	-5.17	1.46	1.52
1	L	874	PHE	C-O	-5.17	1.18	1.24
1	C	509	LEU	C-O	5.17	1.30	1.24
1	I	803	ARG	C-N	-5.17	1.27	1.33
1	C	530	ARG	NE-CZ	5.17	1.38	1.33
1	E	424	GLY	CA-C	5.17	1.56	1.52
1	G	537	TYR	C-N	5.17	1.41	1.34
1	E	444	ARG	CA-CB	-5.17	1.46	1.53
1	F	773	PRO	CA-C	-5.17	1.45	1.52
1	G	696	ASP	C-N	5.17	1.40	1.33
1	I	397	SER	CA-C	-5.17	1.46	1.52
1	J	532	LEU	N-CA	5.17	1.52	1.46
1	C	887	LEU	C-O	5.17	1.30	1.24
1	F	760	LYS	C-O	5.17	1.30	1.24
1	G	721	GLU	C-O	-5.16	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	834	ALA	C-N	5.16	1.40	1.33
1	G	777	GLY	C-N	5.16	1.41	1.33
1	H	885	LEU	CA-C	5.16	1.59	1.52
1	J	845	MET	CG-SD	5.16	1.93	1.80
1	L	691	SER	CA-CB	-5.16	1.45	1.53
1	A	476	SER	CA-C	-5.16	1.46	1.52
1	A	566	HIS	ND1-CE1	-5.16	1.27	1.32
1	A	827	ASP	CA-C	5.16	1.59	1.52
1	G	852	ARG	CD-NE	5.16	1.53	1.46
1	H	743	ASN	C-O	5.16	1.30	1.24
1	A	354	ASP	N-CA	5.15	1.52	1.46
1	E	880	LYS	CA-C	5.15	1.59	1.52
1	L	788	ARG	CZ-NH1	-5.15	1.25	1.32
1	D	543	TYR	CA-CB	5.15	1.60	1.54
1	J	565	PHE	CA-CB	-5.15	1.45	1.53
1	H	587	GLN	C-O	5.15	1.30	1.24
1	D	741	LEU	C-O	-5.15	1.18	1.24
1	A	424	GLY	CA-C	5.15	1.57	1.52
1	D	258	ILE	N-CA	-5.14	1.40	1.46
1	E	225	ASP	C-N	-5.14	1.27	1.34
1	K	270	GLU	C-N	-5.14	1.27	1.33
1	A	628	TRP	C-N	-5.14	1.27	1.33
1	C	857	VAL	C-O	-5.14	1.18	1.24
1	F	651	VAL	N-CA	-5.14	1.40	1.46
1	L	382	LEU	N-CA	-5.14	1.39	1.46
1	C	692	TYR	N-CA	5.14	1.52	1.46
1	D	755	MET	CG-SD	5.14	1.93	1.80
1	L	701	SER	C-O	5.13	1.30	1.24
1	L	799	ILE	C-O	5.13	1.30	1.24
1	D	563	HIS	CE1-NE2	5.13	1.37	1.32
1	F	304	TYR	N-CA	5.13	1.52	1.46
1	L	429	MET	SD-CE	5.13	1.92	1.79
1	E	457	SER	CA-C	5.13	1.58	1.52
1	J	853	PHE	C-N	5.13	1.40	1.34
1	K	514	GLU	CD-OE2	-5.13	1.15	1.25
1	K	563	HIS	ND1-CE1	-5.13	1.27	1.32
1	E	884	HIS	CA-CB	5.13	1.61	1.53
1	J	574	ARG	C-O	5.13	1.30	1.24
1	C	788	ARG	CA-C	5.12	1.59	1.52
1	E	433	GLU	CA-C	-5.12	1.46	1.53
1	H	574	ARG	CZ-NH1	5.12	1.40	1.32
1	J	443	ASP	C-O	-5.12	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	298	PRO	CA-C	5.12	1.58	1.52
1	L	518	SER	C-O	5.12	1.30	1.24
1	L	908	SER	C-O	5.12	1.30	1.24
1	C	450	LEU	CA-C	5.12	1.59	1.52
1	J	384	ASP	N-CA	-5.12	1.40	1.46
1	L	288	ARG	CA-C	5.12	1.58	1.52
1	J	625	SER	CA-C	-5.12	1.47	1.52
1	F	360	LEU	C-N	5.12	1.40	1.33
1	H	548	MET	SD-CE	5.12	1.92	1.79
1	J	535	THR	CA-CB	5.12	1.61	1.53
1	D	493	GLY	C-O	-5.11	1.17	1.24
1	F	556	ALA	N-CA	-5.11	1.40	1.46
1	G	893	LEU	CB-CG	5.11	1.63	1.53
1	B	793	LEU	C-O	-5.11	1.18	1.24
1	A	695	SER	C-N	5.11	1.40	1.33
1	E	533	GLU	C-O	-5.11	1.18	1.24
1	A	773	PRO	N-CD	5.11	1.54	1.47
1	B	867	ALA	CA-CB	-5.11	1.45	1.53
1	C	558	LEU	CA-CB	-5.11	1.45	1.53
1	G	772	HIS	N-CA	5.11	1.52	1.46
1	L	296	ASN	C-N	5.11	1.40	1.33
1	H	909	SER	N-CA	5.10	1.52	1.46
1	K	717	ALA	CA-C	-5.10	1.46	1.52
1	E	749	LYS	N-CA	-5.10	1.40	1.46
1	I	845	MET	SD-CE	5.10	1.92	1.79
1	J	722	HIS	C-O	5.10	1.30	1.24
1	B	645	GLY	C-N	-5.10	1.26	1.33
1	C	731	LEU	CA-C	5.10	1.59	1.52
1	D	284	MET	N-CA	5.10	1.52	1.46
1	D	583	ASP	C-N	-5.10	1.27	1.33
1	E	254	SER	N-CA	5.10	1.52	1.46
1	E	770	GLY	N-CA	5.10	1.52	1.46
1	G	270	GLU	N-CA	-5.10	1.40	1.46
1	L	875	ALA	C-O	5.10	1.29	1.24
1	C	238	ARG	CD-NE	5.10	1.53	1.46
1	D	238	ARG	CD-NE	5.10	1.53	1.46
1	D	576	GLN	C-O	5.10	1.30	1.24
1	F	805	GLN	C-N	-5.10	1.26	1.33
1	G	789	GLU	CD-OE2	5.10	1.35	1.25
1	J	569	ALA	CA-CB	5.10	1.61	1.53
1	K	507	LYS	CA-C	-5.10	1.46	1.52
1	K	859	ALA	C-O	-5.10	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	901	ILE	N-CA	5.10	1.52	1.46
1	G	457	SER	N-CA	-5.09	1.39	1.46
1	H	651	VAL	C-O	-5.09	1.18	1.24
1	J	408	ALA	C-O	5.09	1.29	1.24
1	K	282	SER	N-CA	5.09	1.53	1.47
1	B	549	SER	N-CA	-5.09	1.39	1.45
1	C	656	ILE	CA-C	-5.09	1.46	1.52
1	C	695	SER	C-O	5.09	1.29	1.24
1	D	403	LEU	C-N	-5.09	1.27	1.33
1	G	319	SER	N-CA	-5.09	1.40	1.46
1	H	300	ALA	C-O	-5.09	1.18	1.24
1	H	834	ALA	C-N	-5.09	1.26	1.33
1	K	845	MET	CG-SD	5.09	1.93	1.80
1	L	874	PHE	C-N	5.09	1.40	1.33
1	D	323	LYS	C-O	5.09	1.30	1.24
1	I	377	ARG	C-O	-5.09	1.18	1.24
1	B	413	ARG	C-N	5.08	1.40	1.33
1	B	450	LEU	N-CA	5.08	1.52	1.46
1	G	675	ALA	CA-C	5.08	1.59	1.52
1	A	310	LEU	CA-C	-5.08	1.47	1.53
1	F	482	LYS	N-CA	5.08	1.52	1.46
1	F	488	HIS	CE1-NE2	5.08	1.37	1.32
1	I	658	GLN	CD-OE1	-5.08	1.13	1.23
1	L	404	ALA	C-N	-5.08	1.25	1.33
1	L	670	ALA	C-O	-5.08	1.18	1.24
1	C	342	PRO	C-N	-5.08	1.25	1.33
1	F	568	PHE	N-CA	5.08	1.52	1.46
1	F	596	ARG	NE-CZ	5.08	1.38	1.33
1	F	624	ASP	CA-C	-5.08	1.48	1.53
1	D	580	LEU	CA-C	-5.08	1.46	1.52
1	G	488	HIS	CB-CG	5.08	1.57	1.50
1	J	483	ASN	C-O	-5.08	1.17	1.24
1	C	798	ASP	C-O	-5.08	1.18	1.24
1	G	311	GLY	C-O	5.08	1.31	1.23
1	H	849	PHE	CA-CB	5.08	1.61	1.53
1	I	320	LEU	C-O	5.08	1.30	1.24
1	F	577	LEU	C-O	-5.07	1.17	1.24
1	H	502	VAL	C-O	5.07	1.30	1.24
1	C	390	PRO	N-CA	5.07	1.53	1.47
1	F	246	GLN	CA-CB	5.07	1.60	1.53
1	G	317	ASP	C-O	5.07	1.30	1.24
1	I	705	TYR	N-CA	-5.07	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	786	ARG	C-N	5.07	1.40	1.33
1	D	780	SER	CA-C	-5.07	1.46	1.53
1	F	865	MET	C-N	-5.07	1.26	1.33
1	G	504	THR	N-CA	5.07	1.52	1.46
1	J	441	LEU	CA-C	-5.07	1.46	1.52
1	L	512	VAL	CA-C	-5.07	1.46	1.52
1	I	872	GLU	N-CA	-5.07	1.40	1.46
1	L	721	GLU	CA-C	-5.07	1.45	1.52
1	B	584	ALA	CA-CB	5.07	1.61	1.53
1	D	294	LEU	N-CA	5.07	1.51	1.45
1	J	476	SER	N-CA	-5.06	1.40	1.46
1	A	268	VAL	C-N	-5.06	1.27	1.33
1	E	324	THR	C-O	-5.06	1.18	1.24
1	F	582	LYS	C-N	5.06	1.40	1.33
1	L	275	HIS	N-CA	5.06	1.52	1.46
1	B	810	ARG	NE-CZ	5.06	1.38	1.33
1	B	494	PRO	N-CD	-5.06	1.40	1.47
1	H	347	ILE	CA-C	5.06	1.58	1.52
1	K	720	ARG	CD-NE	-5.06	1.39	1.46
1	K	438	ALA	CA-CB	-5.06	1.45	1.53
1	A	699	GLU	C-O	5.05	1.30	1.24
1	B	739	LYS	C-O	5.05	1.30	1.24
1	G	810	ARG	CZ-NH1	-5.05	1.25	1.32
1	C	841	LEU	C-O	5.05	1.29	1.24
1	C	711	ILE	CB-CG1	5.05	1.63	1.53
1	E	660	VAL	N-CA	-5.05	1.39	1.46
1	I	491	GLU	N-CA	5.05	1.52	1.46
1	A	542	GLN	N-CA	-5.05	1.39	1.46
1	B	354	ASP	C-N	5.05	1.38	1.33
1	I	703	LYS	C-N	5.05	1.40	1.34
1	L	865	MET	N-CA	-5.05	1.40	1.46
1	D	619	PRO	C-O	-5.04	1.18	1.24
1	A	441	LEU	N-CA	-5.04	1.40	1.46
1	F	404	ALA	C-O	5.04	1.30	1.24
1	F	791	VAL	CA-C	5.04	1.59	1.52
1	I	757	PHE	C-N	5.04	1.40	1.33
1	K	250	VAL	C-O	-5.04	1.18	1.24
1	K	720	ARG	C-O	5.04	1.29	1.24
1	C	862	HIS	CG-CD2	-5.04	1.30	1.35
1	C	233	LYS	C-N	-5.04	1.27	1.33
1	D	231	THR	CA-C	-5.04	1.45	1.52
1	F	440	ILE	C-O	5.04	1.29	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	723	VAL	CA-C	-5.04	1.45	1.52
1	H	403	LEU	C-N	-5.04	1.27	1.33
1	F	304	TYR	C-O	-5.04	1.17	1.24
1	K	308	PRO	C-O	5.04	1.30	1.24
1	K	489	PRO	N-CA	5.04	1.54	1.47
1	K	836	THR	C-O	-5.04	1.17	1.24
1	L	746	GLY	N-CA	5.04	1.52	1.45
1	A	755	MET	C-O	-5.03	1.18	1.24
1	G	589	VAL	CA-C	5.03	1.59	1.52
1	C	755	MET	SD-CE	5.03	1.92	1.79
1	B	342	PRO	CA-C	5.03	1.58	1.52
1	G	618	LEU	C-O	-5.03	1.19	1.24
1	G	690	ARG	NE-CZ	5.03	1.38	1.33
1	D	524	THR	C-N	-5.03	1.27	1.33
1	J	708	ASP	N-CA	5.03	1.52	1.46
1	A	725	GLY	CA-C	5.03	1.57	1.52
1	C	441	LEU	N-CA	5.03	1.52	1.46
1	I	479	ARG	CZ-NH2	-5.03	1.26	1.33
1	K	489	PRO	N-CD	5.03	1.54	1.47
1	C	234	MET	C-O	-5.02	1.18	1.24
1	D	324	THR	C-O	5.02	1.29	1.24
1	I	874	PHE	C-N	-5.02	1.27	1.33
1	C	824	VAL	C-O	5.02	1.30	1.24
1	J	530	ARG	N-CA	5.02	1.52	1.46
1	G	305	GLY	N-CA	5.02	1.51	1.46
1	H	439	ALA	CA-CB	5.02	1.61	1.53
1	H	905	HIS	CE1-NE2	5.02	1.37	1.32
1	K	274	GLY	N-CA	-5.02	1.39	1.45
1	A	862	HIS	C-N	5.02	1.40	1.34
1	H	762	ARG	C-O	-5.02	1.17	1.24
1	I	422	THR	C-O	-5.02	1.18	1.24
1	L	596	ARG	CA-CB	5.02	1.61	1.54
1	A	827	ASP	C-O	-5.02	1.18	1.24
1	C	444	ARG	C-N	5.02	1.40	1.33
1	D	456	ILE	CA-CB	5.01	1.60	1.54
1	D	589	VAL	CA-CB	-5.01	1.48	1.54
1	D	598	TRP	C-N	5.01	1.40	1.33
1	H	430	ASP	C-O	5.01	1.30	1.24
1	H	718	GLN	N-CA	5.01	1.52	1.46
1	A	279	PRO	C-N	5.01	1.39	1.33
1	B	517	MET	SD-CE	5.01	1.92	1.79
1	C	595	ALA	CA-C	5.01	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	746	GLY	C-N	-5.01	1.26	1.33
1	J	234	MET	N-CA	5.01	1.52	1.46
1	K	423	ILE	N-CA	5.01	1.52	1.46
1	C	281	GLY	C-O	5.00	1.31	1.24
1	F	537	TYR	C-O	5.00	1.29	1.24
1	A	225	ASP	CG-OD1	5.00	1.34	1.25
1	A	285	ILE	CA-C	-5.00	1.46	1.52
1	A	850	TYR	N-CA	5.00	1.52	1.46
1	D	347	ILE	N-CA	-5.00	1.40	1.46
1	J	494	PRO	N-CD	5.00	1.54	1.47
1	L	799	ILE	C-N	5.00	1.40	1.33

All (279) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	500	THR	N-CA-C	12.59	127.72	108.96
1	E	440	ILE	N-CA-C	12.54	122.32	110.53
1	H	440	ILE	N-CA-C	11.68	122.54	110.62
1	A	227	MET	N-CA-C	11.62	123.50	111.07
1	K	500	THR	N-CA-C	11.14	124.86	108.60
1	H	500	THR	N-CA-C	11.13	125.82	108.79
1	J	262	SER	N-CA-C	-10.69	99.63	111.07
1	J	500	THR	N-CA-C	10.26	124.49	108.79
1	E	500	THR	N-CA-C	10.19	123.47	108.60
1	A	500	THR	N-CA-C	10.11	124.44	109.07
1	H	445	GLN	CA-C-N	-10.01	111.84	122.85
1	H	445	GLN	C-N-CA	-10.01	111.84	122.85
1	D	440	ILE	N-CA-C	9.99	120.81	110.72
1	K	227	MET	N-CA-C	9.88	122.12	111.36
1	E	244	VAL	CB-CA-C	-9.85	99.13	112.04
1	D	227	MET	N-CA-C	9.70	123.24	111.40
1	K	262	SER	N-CA-C	-9.60	100.90	111.36
1	A	438	ALA	N-CA-C	-9.26	101.27	111.36
1	A	244	VAL	N-CA-C	9.18	119.99	110.36
1	K	440	ILE	N-CA-C	9.17	119.08	110.74
1	H	224	ASP	CA-C-N	9.09	132.46	120.28
1	H	224	ASP	C-N-CA	9.09	132.46	120.28
1	H	244	VAL	CB-CA-C	-9.05	100.39	111.97
1	K	496	SER	N-CA-C	-9.01	97.14	110.48
1	E	227	MET	N-CA-C	8.94	120.79	111.14
1	D	250	VAL	N-CA-C	8.79	122.29	109.63
1	H	244	VAL	N-CA-C	8.77	118.84	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	435	GLU	N-CA-C	-8.75	101.71	111.07
1	A	262	SER	N-CA-C	-8.73	101.71	111.14
1	J	496	SER	N-CA-C	-8.71	98.22	110.50
1	H	496	SER	N-CA-C	-8.60	97.75	110.48
1	A	496	SER	N-CA-C	-8.53	97.85	110.48
1	J	244	VAL	CB-CA-C	-8.52	100.88	112.04
1	J	250	VAL	N-CA-C	8.40	121.72	109.63
1	J	440	ILE	N-CA-C	8.38	119.19	110.72
1	K	244	VAL	N-CA-C	8.34	121.48	111.05
1	A	251	THR	N-CA-C	8.32	119.61	108.38
1	J	224	ASP	CA-C-N	8.30	131.73	120.44
1	J	224	ASP	C-N-CA	8.30	131.73	120.44
1	D	249	THR	N-CA-C	-8.12	102.51	111.36
1	K	244	VAL	CB-CA-C	-8.04	99.70	112.16
1	A	440	ILE	N-CA-C	7.90	118.70	110.72
1	G	777	GLY	O-C-N	-7.83	112.52	122.70
1	H	227	MET	N-CA-C	7.83	119.89	111.36
1	J	438	ALA	N-CA-C	-7.82	102.83	111.36
1	H	484	TYR	N-CA-C	7.78	119.76	111.28
1	A	244	VAL	CB-CA-C	-7.65	102.08	111.88
1	K	882	ARG	NE-CZ-NH1	-7.61	113.89	121.50
1	K	250	VAL	N-CA-C	7.60	120.57	109.63
1	E	262	SER	N-CA-C	-7.58	102.96	111.07
1	E	438	ALA	CA-C-N	-7.56	110.16	120.44
1	E	438	ALA	C-N-CA	-7.56	110.16	120.44
1	D	244	VAL	CB-CA-C	-7.44	100.63	112.16
1	H	228	MET	N-CA-C	-7.40	102.37	111.40
1	A	224	ASP	CA-C-N	7.38	130.16	120.28
1	A	224	ASP	C-N-CA	7.38	130.16	120.28
1	H	234	MET	CB-CG-SD	-7.36	90.62	112.70
1	H	483	ASN	N-CA-C	7.35	120.34	111.82
1	K	249	THR	N-CA-C	-7.28	103.43	111.36
1	D	483	ASN	N-CA-C	7.27	120.63	111.69
1	D	496	SER	N-CA-C	-7.24	99.76	110.48
1	E	228	MET	N-CA-C	-7.09	103.16	111.03
1	K	433	GLU	CA-C-N	7.06	126.55	118.85
1	K	433	GLU	C-N-CA	7.06	126.55	118.85
1	E	249	THR	CA-C-N	6.95	129.81	120.50
1	E	249	THR	C-N-CA	6.95	129.81	120.50
1	K	251	THR	N-CA-C	6.93	118.31	108.74
1	C	604	ASP	N-CA-C	6.91	118.89	111.36
1	K	445	GLN	N-CA-C	-6.89	103.82	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	434	PRO	N-CA-C	-6.88	104.90	113.84
1	A	435	GLU	N-CA-C	-6.87	103.79	111.28
1	E	244	VAL	N-CA-C	6.87	118.45	110.62
1	A	483	ASN	N-CA-C	6.86	120.87	112.23
1	D	238	ARG	N-CA-C	-6.86	103.81	111.28
1	J	227	MET	N-CA-C	6.85	118.74	111.28
1	D	271	ALA	N-CA-C	-6.82	103.85	111.28
1	K	224	ASP	CA-C-N	6.81	129.71	120.38
1	K	224	ASP	C-N-CA	6.81	129.71	120.38
1	J	234	MET	CB-CG-SD	-6.78	92.35	112.70
1	D	226	ASN	N-CA-C	-6.77	103.92	111.71
1	J	228	MET	N-CA-C	-6.76	103.84	111.14
1	J	483	ASN	N-CA-C	6.72	119.96	111.69
1	A	249	THR	N-CA-C	-6.72	104.03	111.36
1	E	241	LEU	N-CA-C	-6.72	103.96	111.28
1	E	253	PRO	N-CA-C	6.71	121.20	110.40
1	A	250	VAL	N-CA-C	6.70	119.28	109.63
1	D	262	SER	N-CA-C	-6.66	103.95	111.14
1	H	311	GLY	N-CA-C	6.66	120.60	111.54
1	A	234	MET	CB-CG-SD	-6.64	92.79	112.70
1	J	488	HIS	CA-C-N	-6.63	112.07	118.97
1	J	488	HIS	C-N-CA	-6.63	112.07	118.97
1	K	238	ARG	N-CA-C	-6.57	104.04	111.07
1	L	238	ARG	NE-CZ-NH2	6.57	125.12	119.20
1	D	405	ASN	N-CA-C	6.55	119.42	111.82
1	E	484	TYR	N-CA-C	6.55	118.50	111.36
1	J	244	VAL	N-CA-C	6.54	118.08	110.62
1	E	251	THR	N-CA-C	6.53	118.06	108.14
1	D	438	ALA	N-CA-C	-6.50	104.27	111.82
1	E	496	SER	N-CA-C	-6.47	100.70	110.28
1	J	493	GLY	CA-C-N	-6.47	113.10	119.76
1	J	493	GLY	C-N-CA	-6.47	113.10	119.76
1	H	246	GLN	N-CA-C	6.47	117.99	111.07
1	E	435	GLU	N-CA-C	-6.45	104.17	111.14
1	D	434	PRO	N-CA-C	-6.43	105.82	113.86
1	A	226	ASN	N-CA-C	-6.38	104.37	111.71
1	K	241	LEU	N-CA-C	-6.32	103.69	111.33
1	L	609	PRO	CA-C-N	6.30	133.04	121.70
1	L	609	PRO	C-N-CA	6.30	133.04	121.70
1	E	250	VAL	N-CA-C	6.25	118.63	109.63
1	E	226	ASN	N-CA-C	-6.24	104.53	111.71
1	A	228	MET	N-CA-C	-6.20	104.58	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	251	THR	N-CA-C	6.19	117.64	108.60
1	D	444	ARG	N-CA-C	-6.19	106.05	113.97
1	H	262	SER	N-CA-C	-6.16	104.49	111.14
1	J	301	LYS	N-CA-C	6.15	120.78	113.16
1	H	433	GLU	O-C-N	6.13	128.40	121.53
1	K	298	PRO	N-CA-C	-6.12	100.86	111.32
1	D	224	ASP	CA-C-N	6.07	128.91	120.29
1	D	224	ASP	C-N-CA	6.07	128.91	120.29
1	H	435	GLU	N-CA-C	-6.06	104.76	111.36
1	K	297	ASP	O-C-N	6.05	126.37	121.05
1	H	405	ASN	N-CA-C	6.04	117.95	111.36
1	A	586	ASP	CA-CB-CG	6.01	118.61	112.60
1	H	249	THR	N-CA-C	-6.01	104.80	111.71
1	K	488	HIS	CA-C-N	-6.01	112.30	118.85
1	K	488	HIS	C-N-CA	-6.01	112.30	118.85
1	H	494	PRO	CB-CA-C	-6.00	104.02	111.64
1	J	434	PRO	N-CA-C	-6.00	105.55	113.65
1	D	484	TYR	N-CA-C	5.99	117.48	111.07
1	B	348	HIS	CA-CB-CG	5.98	119.78	113.80
1	A	485	PHE	CA-C-N	5.94	126.53	120.00
1	A	485	PHE	C-N-CA	5.94	126.53	120.00
1	D	433	GLU	CA-C-N	5.93	125.55	119.56
1	D	433	GLU	C-N-CA	5.93	125.55	119.56
1	H	646	ARG	NE-CZ-NH2	5.92	124.53	119.20
1	B	580	LEU	N-CA-C	5.92	117.42	110.97
1	H	250	VAL	N-CA-C	5.91	118.14	109.63
1	E	483	ASN	N-CA-C	5.90	119.66	112.23
1	H	438	ALA	CA-C-N	-5.88	112.64	120.63
1	H	438	ALA	C-N-CA	-5.88	112.64	120.63
1	J	252	LEU	CA-C-N	-5.88	112.50	119.84
1	J	252	LEU	C-N-CA	-5.88	112.50	119.84
1	K	434	PRO	N-CA-C	-5.83	105.59	113.40
1	D	251	THR	N-CA-C	5.82	117.09	108.60
1	H	233	LYS	N-CA-C	-5.81	105.03	111.36
1	K	228	MET	N-CA-C	-5.81	104.86	111.14
1	A	565	PHE	CA-CB-CG	-5.79	108.01	113.80
1	A	243	LYS	N-CA-C	5.78	120.33	113.16
1	C	855	ARG	NE-CZ-NH1	-5.78	115.72	121.50
1	H	494	PRO	N-CA-C	5.78	120.67	111.26
1	K	887	LEU	N-CA-C	-5.77	105.07	111.36
1	K	252	LEU	CA-C-N	-5.74	114.84	120.98
1	K	252	LEU	C-N-CA	-5.74	114.84	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	477	ILE	N-CA-C	-5.72	105.57	113.00
1	E	238	ARG	N-CA-C	-5.71	104.96	111.07
1	H	298	PRO	N-CA-C	-5.71	102.30	111.38
1	K	493	GLY	CA-C-N	-5.70	113.83	119.93
1	K	493	GLY	C-N-CA	-5.70	113.83	119.93
1	J	494	PRO	N-CA-C	5.69	120.02	111.14
1	C	862	HIS	N-CA-C	-5.67	105.00	111.07
1	B	629	HIS	CA-CB-CG	-5.67	108.13	113.80
1	H	226	ASN	N-CA-C	-5.67	104.47	111.33
1	F	876	ARG	NE-CZ-NH2	5.67	124.30	119.20
1	F	633	ASP	CA-CB-CG	5.66	118.26	112.60
1	H	251	THR	N-CA-C	5.66	116.87	108.60
1	K	484	TYR	N-CA-C	5.64	117.51	111.36
1	A	307	PHE	CA-C-N	-5.64	113.21	119.19
1	A	307	PHE	C-N-CA	-5.64	113.21	119.19
1	J	435	GLU	N-CA-C	-5.63	105.22	111.36
1	A	445	GLN	N-CA-C	-5.63	105.67	112.54
1	I	890	ARG	NE-CZ-NH1	-5.59	115.91	121.50
1	E	574	ARG	NE-CZ-NH1	-5.59	115.91	121.50
1	H	847	ASN	CA-CB-CG	-5.58	107.02	112.60
1	H	252	LEU	CA-C-N	-5.58	115.01	120.98
1	H	252	LEU	C-N-CA	-5.58	115.01	120.98
1	J	526	GLU	CA-C-O	-5.58	114.64	120.55
1	L	494	PRO	CA-C-N	5.56	132.17	121.54
1	L	494	PRO	C-N-CA	5.56	132.17	121.54
1	H	493	GLY	CA-C-N	-5.56	113.98	119.93
1	H	493	GLY	C-N-CA	-5.56	113.98	119.93
1	H	433	GLU	CA-C-N	5.54	125.22	119.56
1	H	433	GLU	C-N-CA	5.54	125.22	119.56
1	F	720	ARG	NE-CZ-NH1	-5.54	115.96	121.50
1	A	813	LYS	N-CA-C	-5.54	105.79	112.54
1	E	405	ASN	N-CA-C	5.53	117.30	111.28
1	H	241	LEU	N-CA-C	-5.51	105.18	111.07
1	J	405	ASN	N-CA-C	5.51	117.28	111.28
1	B	274	GLY	N-CA-C	-5.50	108.11	115.32
1	E	341	ASP	CA-C-N	-5.49	112.98	119.84
1	E	341	ASP	C-N-CA	-5.49	112.98	119.84
1	H	714	ASN	CA-CB-CG	-5.48	107.12	112.60
1	J	691	SER	N-CA-C	5.48	117.69	111.11
1	J	298	PRO	N-CA-C	-5.47	101.96	111.32
1	E	596	ARG	NE-CZ-NH2	5.47	124.12	119.20
1	G	349	SER	CA-C-O	-5.45	113.68	119.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	878	ASP	CA-CB-CG	5.45	118.05	112.60
1	D	278	LEU	O-C-N	5.45	125.20	121.71
1	D	878	ASP	CA-C-O	-5.45	114.91	119.76
1	A	493	GLY	CA-C-N	-5.44	114.15	119.76
1	A	493	GLY	C-N-CA	-5.44	114.15	119.76
1	J	282	SER	CB-CA-C	-5.43	110.30	116.54
1	F	609	PRO	CA-C-N	5.41	131.44	121.70
1	F	609	PRO	C-N-CA	5.41	131.44	121.70
1	D	498	VAL	CB-CA-C	-5.40	105.40	111.45
1	K	234	MET	CB-CG-SD	-5.40	96.51	112.70
1	D	236	GLU	N-CA-C	-5.39	105.49	111.36
1	D	485	PHE	CA-C-N	5.39	126.08	119.99
1	D	485	PHE	C-N-CA	5.39	126.08	119.99
1	E	385	LYS	N-CA-C	-5.39	105.31	111.07
1	K	249	THR	CA-C-N	5.39	127.72	120.50
1	K	249	THR	C-N-CA	5.39	127.72	120.50
1	K	383	CYS	CB-CA-C	-5.38	101.85	110.79
1	J	849	PHE	N-CA-C	-5.37	104.98	112.45
1	K	490	THR	N-CA-C	5.37	116.81	111.07
1	F	796	ARG	NE-CZ-NH1	-5.37	116.13	121.50
1	D	234	MET	CB-CG-SD	-5.37	96.60	112.70
1	E	890	ARG	NE-CZ-NH1	-5.34	116.16	121.50
1	D	771	ASP	CA-CB-CG	5.33	117.93	112.60
1	E	596	ARG	NE-CZ-NH1	-5.33	116.17	121.50
1	E	234	MET	CB-CG-SD	-5.33	96.71	112.70
1	J	433	GLU	CA-C-N	5.33	125.14	119.28
1	J	433	GLU	C-N-CA	5.33	125.14	119.28
1	J	436	LYS	N-CA-C	5.33	117.08	111.28
1	L	889	ARG	N-CA-C	5.31	117.07	111.28
1	K	261	GLN	N-CA-C	5.28	116.72	111.07
1	D	307	PHE	CA-C-N	-5.28	113.09	118.85
1	D	307	PHE	C-N-CA	-5.28	113.09	118.85
1	F	252	LEU	CA-C-N	5.28	125.27	120.21
1	F	252	LEU	C-N-CA	5.28	125.27	120.21
1	D	243	LYS	N-CA-C	5.27	119.69	113.16
1	L	888	ILE	O-C-N	-5.27	116.55	121.87
1	H	624	ASP	CA-CB-CG	5.27	117.87	112.60
1	F	400	ASP	CA-CB-CG	5.26	117.86	112.60
1	L	385	LYS	N-CA-C	5.25	117.00	111.28
1	L	743	ASN	OD1-CG-ND2	-5.25	117.36	122.60
1	D	248	SER	N-CA-C	-5.24	101.76	109.62
1	E	225	ASP	N-CA-C	-5.24	105.65	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	889	ARG	NE-CZ-NH1	-5.24	116.26	121.50
1	K	483	ASN	N-CA-C	5.23	117.06	111.36
1	A	229	PHE	CB-CA-C	-5.20	102.15	110.79
1	J	783	LEU	O-C-N	-5.20	116.61	122.12
1	E	491	GLU	O-C-N	-5.20	116.61	122.12
1	H	377	ARG	N-CA-C	-5.19	105.51	111.07
1	E	445	GLN	N-CA-C	-5.19	106.46	112.89
1	C	488	HIS	CA-C-O	-5.18	116.47	121.34
1	H	341	ASP	CA-C-N	-5.18	113.37	119.84
1	H	341	ASP	C-N-CA	-5.18	113.37	119.84
1	F	708	ASP	CA-CB-CG	5.18	117.78	112.60
1	H	413	ARG	NE-CZ-NH2	-5.16	114.55	119.20
1	I	574	ARG	NE-CZ-NH2	5.14	123.83	119.20
1	J	480	ASN	CA-C-N	-5.14	113.39	120.28
1	J	480	ASN	C-N-CA	-5.14	113.39	120.28
1	A	794	ARG	NE-CZ-NH1	-5.14	116.36	121.50
1	E	433	GLU	CA-C-N	5.14	124.94	119.28
1	E	433	GLU	C-N-CA	5.14	124.94	119.28
1	E	434	PRO	N-CA-C	-5.14	106.71	113.65
1	H	249	THR	CA-C-N	5.13	127.38	120.50
1	H	249	THR	C-N-CA	5.13	127.38	120.50
1	J	888	ILE	N-CA-C	5.13	115.35	110.42
1	E	224	ASP	CA-C-N	5.12	127.56	120.29
1	E	224	ASP	C-N-CA	5.12	127.56	120.29
1	H	237	ILE	N-CA-C	5.12	115.84	110.62
1	D	478	ASN	N-CA-C	-5.10	105.37	112.45
1	C	497	GLY	O-C-N	-5.09	116.93	122.68
1	B	609	PRO	CA-C-N	5.09	130.85	121.70
1	B	609	PRO	C-N-CA	5.09	130.85	121.70
1	A	242	GLN	N-CA-C	-5.08	105.82	111.36
1	A	440	ILE	CB-CA-C	-5.08	105.22	112.22
1	B	708	ASP	O-C-N	5.06	125.32	121.27
1	K	233	LYS	N-CA-C	-5.06	105.95	111.82
1	J	285	ILE	N-CA-CB	5.05	116.46	110.55
1	A	252	LEU	CA-C-N	-5.04	115.37	120.21
1	A	252	LEU	C-N-CA	-5.04	115.37	120.21
1	D	244	VAL	N-CA-C	5.04	117.35	111.05
1	F	576	GLN	N-CA-C	-5.04	105.68	111.07
1	G	641	ARG	NE-CZ-NH2	5.02	123.72	119.20
1	A	566	HIS	CA-CB-CG	-5.01	108.79	113.80
1	A	794	ARG	NE-CZ-NH2	5.01	123.71	119.20
1	A	233	LYS	N-CA-C	-5.00	105.95	111.71

There are no chirality outliers.

All (172) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	388	ARG	Sidechain
1	A	444	ARG	Sidechain
1	A	491	GLU	Sidechain
1	A	583	ASP	Sidechain
1	A	600	ARG	Sidechain
1	A	603	GLU	Sidechain
1	A	613	ASP	Sidechain
1	A	614	ASN	Sidechain
1	A	762	ARG	Sidechain
1	A	788	ARG	Sidechain
1	A	810	ARG	Sidechain
1	A	852	ARG	Sidechain
1	B	283	ASN	Sidechain
1	B	287	ARG	Sidechain
1	B	317	ASP	Sidechain
1	B	388	ARG	Sidechain
1	B	444	ARG	Sidechain
1	B	624	ASP	Sidechain
1	B	646	ARG	Sidechain
1	B	721	GLU	Sidechain
1	B	748	ARG	Sidechain
1	B	788	ARG	Sidechain
1	B	906	ARG	Sidechain
1	C	288	ARG	Sidechain
1	C	299	GLU	Sidechain
1	C	344	ARG	Sidechain
1	C	388	ARG	Sidechain
1	C	413	ARG	Sidechain
1	C	516	GLN	Sidechain
1	C	545	GLU	Sidechain
1	C	586	ASP	Sidechain
1	C	630	ARG	Sidechain
1	C	803	ARG	Sidechain
1	C	855	ARG	Sidechain
1	C	883	ARG	Sidechain
1	D	246	GLN	Sidechain
1	D	253	PRO	Mainchain
1	D	287	ARG	Sidechain
1	D	288	ARG	Sidechain
1	D	314	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	D	444	ARG	Sidechain
1	D	478	ASN	Sidechain
1	D	479	ARG	Sidechain
1	D	574	ARG	Sidechain
1	D	596	ARG	Sidechain
1	D	646	ARG	Sidechain
1	D	676	ARG	Sidechain
1	D	732	GLU	Sidechain
1	D	748	ARG	Sidechain
1	D	762	ARG	Sidechain
1	D	798	ASP	Sidechain
1	D	883	ARG	Sidechain
1	D	892	GLU	Sidechain
1	E	253	PRO	Mainchain
1	E	287	ARG	Sidechain
1	E	377	ARG	Sidechain
1	E	388	ARG	Sidechain
1	E	515	GLN	Sidechain
1	E	530	ARG	Sidechain
1	E	544	ASN	Sidechain
1	E	574	ARG	Sidechain
1	E	658	GLN	Sidechain
1	E	665	ASP	Sidechain
1	E	676	ARG	Sidechain
1	E	681	ASP	Sidechain
1	E	786	ARG	Sidechain
1	E	788	ARG	Sidechain
1	E	796	ARG	Sidechain
1	F	297	ASP	Sidechain
1	F	299	GLU	Sidechain
1	F	377	ARG	Sidechain
1	F	710	ASP	Sidechain
1	F	718	GLN	Sidechain
1	F	720	ARG	Sidechain
1	F	728	GLN	Sidechain
1	F	743	ASN	Sidechain
1	F	748	ARG	Sidechain
1	F	759	ASP	Sidechain
1	F	762	ARG	Sidechain
1	F	789	GLU	Sidechain
1	F	817	ASN	Sidechain
1	F	847	ASN	Sidechain

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Mol	Chain	Res	Type	Group
1	F	855	ARG	Sidechain
1	F	886	ASP	Sidechain
1	G	283	ASN	Sidechain
1	G	287	ARG	Sidechain
1	G	515	GLN	Sidechain
1	G	542	GLN	Sidechain
1	G	610	ARG	Sidechain
1	G	633	ASP	Sidechain
1	G	708	ASP	Sidechain
1	G	735	GLN	Sidechain
1	G	762	ARG	Sidechain
1	G	786	ARG	Sidechain
1	G	788	ARG	Sidechain
1	G	796	ARG	Sidechain
1	G	855	ARG	Sidechain
1	G	876	ARG	Sidechain
1	H	246	GLN	Sidechain
1	H	253	PRO	Mainchain
1	H	388	ARG	Sidechain
1	H	413	ARG	Sidechain
1	H	506	ARG	Sidechain
1	H	574	ARG	Sidechain
1	H	630	ARG	Sidechain
1	H	658	GLN	Sidechain
1	H	661	GLU	Sidechain
1	H	730	GLU	Sidechain
1	H	810	ARG	Sidechain
1	H	817	ASN	Sidechain
1	H	883	ARG	Sidechain
1	I	225	ASP	Sidechain
1	I	287	ARG	Sidechain
1	I	299	GLU	Sidechain
1	I	414	ARG	Sidechain
1	I	418	ARG	Sidechain
1	I	444	ARG	Sidechain
1	I	530	ARG	Sidechain
1	I	600	ARG	Sidechain
1	I	603	GLU	Sidechain
1	I	658	GLN	Sidechain
1	I	765	GLU	Sidechain
1	I	796	ARG	Sidechain
1	I	805	GLN	Sidechain

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Mol	Chain	Res	Type	Group
1	I	847	ASN	Sidechain
1	I	852	ARG	Sidechain
1	I	856	GLU	Sidechain
1	I	872	GLU	Sidechain
1	I	886	ASP	Sidechain
1	I	902	GLU	Sidechain
1	J	253	PRO	Mainchain
1	J	276	GLU	Sidechain
1	J	283	ASN	Sidechain
1	J	306	GLU	Sidechain
1	J	384	ASP	Sidechain
1	J	421	ARG	Sidechain
1	J	445	GLN	Sidechain
1	J	559	ASP	Sidechain
1	J	614	ASN	Sidechain
1	J	712	GLN	Sidechain
1	J	882	ARG	Sidechain
1	J	883	ARG	Sidechain
1	K	253	PRO	Mainchain
1	K	309	ASP	Sidechain
1	K	344	ARG	Sidechain
1	K	405	ASN	Sidechain
1	K	418	ARG	Sidechain
1	K	430	ASP	Sidechain
1	K	515	GLN	Sidechain
1	K	583	ASP	Sidechain
1	K	633	ASP	Sidechain
1	K	699	GLU	Sidechain
1	K	714	ASN	Sidechain
1	K	728	GLN	Sidechain
1	K	748	ARG	Sidechain
1	K	844	GLU	Sidechain
1	K	876	ARG	Sidechain
1	K	882	ARG	Sidechain
1	K	889	ARG	Sidechain
1	K	906	ARG	Sidechain
1	L	287	ARG	Sidechain
1	L	291	GLU	Sidechain
1	L	402	ASP	Sidechain
1	L	443	ASP	Sidechain
1	L	613	ASP	Sidechain
1	L	743	ASN	Sidechain

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Mol	Chain	Res	Type	Group
1	L	762	ARG	Sidechain
1	L	786	ARG	Sidechain
1	L	796	ARG	Sidechain
1	L	855	ARG	Sidechain
1	L	883	ARG	Sidechain
1	L	906	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	5152	0	5222	422	0
1	B	5152	0	5223	212	0
1	C	5152	0	5223	202	0
1	D	5152	0	5222	507	0
1	E	5152	0	5222	471	0
1	F	5152	0	5223	183	0
1	G	5152	0	5223	252	0
1	H	5152	0	5222	452	0
1	I	5152	0	5223	229	0
1	J	5152	0	5222	408	0
1	K	5152	0	5222	465	0
1	L	5152	0	5223	223	0
All	All	61824	0	62670	3864	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 31.

All (3864) 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:441:LEU:HD23	1:E:498:VAL:CB	1.21	1.67
1:D:441:LEU:HD23	1:D:498:VAL:CB	1.25	1.64
1:K:441:LEU:CD2	1:K:498:VAL:HB	1.27	1.64
1:H:426:ILE:CD1	1:H:440:ILE:HG22	1.17	1.61
1:D:426:ILE:CD1	1:D:440:ILE:HG22	1.28	1.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:ILE:CD1	1:A:440:ILE:HG22	1.28	1.59
1:J:426:ILE:CD1	1:J:440:ILE:HG22	1.29	1.59
1:A:441:LEU:HD23	1:A:498:VAL:CB	1.22	1.58
1:H:441:LEU:CD2	1:H:498:VAL:HB	1.21	1.58
1:E:441:LEU:CD2	1:E:498:VAL:HB	1.26	1.58
1:E:426:ILE:CD1	1:E:440:ILE:HG22	1.19	1.57
1:G:777:GLY:CA	1:L:779:PHE:CD1	1.87	1.57
1:H:441:LEU:HD23	1:H:498:VAL:CB	1.09	1.56
1:K:426:ILE:CD1	1:K:440:ILE:HG22	1.23	1.56
1:E:426:ILE:HD13	1:E:440:ILE:CG2	1.34	1.55
1:D:441:LEU:CD2	1:D:498:VAL:HB	1.33	1.53
1:G:777:GLY:CA	1:L:779:PHE:CE1	1.91	1.53
1:G:777:GLY:CA	1:L:779:PHE:CG	1.92	1.53
1:K:441:LEU:HD23	1:K:498:VAL:CB	1.29	1.52
1:J:441:LEU:CD2	1:J:498:VAL:HB	1.40	1.51
1:H:426:ILE:HD13	1:H:440:ILE:CG2	1.32	1.51
1:A:426:ILE:HD13	1:A:440:ILE:CG2	1.40	1.50
1:G:777:GLY:CA	1:L:779:PHE:CD2	1.91	1.49
1:A:441:LEU:HD23	1:A:498:VAL:CG1	1.42	1.49
1:E:426:ILE:CD1	1:E:440:ILE:CG2	1.88	1.49
1:G:777:GLY:C	1:L:779:PHE:CZ	1.91	1.48
1:A:441:LEU:CD2	1:A:498:VAL:HB	1.43	1.48
1:K:426:ILE:HD13	1:K:440:ILE:CG2	1.41	1.48
1:E:234:MET:CE	1:E:234:MET:SD	2.02	1.47
1:D:865:MET:CE	1:D:865:MET:SD	2.02	1.47
1:B:234:MET:SD	1:B:234:MET:CG	2.02	1.46
1:J:738:MET:CE	1:J:738:MET:SD	2.03	1.46
1:G:777:GLY:C	1:L:779:PHE:CE1	1.90	1.46
1:G:777:GLY:CA	1:L:779:PHE:CZ	1.98	1.46
1:G:777:GLY:CA	1:L:779:PHE:CE2	1.99	1.46
1:G:227:MET:CG	1:G:227:MET:SD	2.05	1.45
1:J:227:MET:CE	1:J:227:MET:SD	2.03	1.45
1:I:227:MET:CE	1:I:227:MET:SD	2.03	1.45
1:L:228:MET:CE	1:L:228:MET:SD	2.05	1.44
1:J:441:LEU:HD23	1:J:498:VAL:CB	1.45	1.44
1:D:426:ILE:CD1	1:D:440:ILE:CG2	1.97	1.43
1:G:777:GLY:C	1:L:779:PHE:CE2	1.94	1.43
1:D:478:ASN:ND2	1:D:482:LYS:HZ1	1.18	1.42
1:G:777:GLY:C	1:L:779:PHE:CD1	1.97	1.41
1:J:426:ILE:CD1	1:J:440:ILE:CG2	1.99	1.40
1:G:780:SER:HB3	1:L:778:GLY:CA	1.52	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:777:GLY:C	1:L:779:PHE:CD2	2.01	1.39
1:H:426:ILE:CD1	1:H:440:ILE:CG2	1.94	1.37
1:H:272:ILE:HG23	1:H:278:LEU:CD1	1.55	1.36
1:D:426:ILE:HD13	1:D:440:ILE:CG2	1.51	1.36
1:A:272:ILE:HG23	1:A:278:LEU:CD1	1.56	1.35
1:G:777:GLY:C	1:L:779:PHE:CG	2.05	1.35
1:A:260:SER:O	1:A:264:GLY:N	1.59	1.34
1:D:285:ILE:HD13	1:D:286:THR:N	1.41	1.33
1:H:276:GLU:OE2	1:H:318:PHE:HE2	1.03	1.33
1:H:276:GLU:OE2	1:H:318:PHE:CE2	1.82	1.31
1:K:269:LEU:HD21	1:K:457:SER:OG	1.24	1.31
1:D:276:GLU:OE2	1:D:318:PHE:CE2	1.84	1.30
1:H:269:LEU:CD1	1:H:457:SER:O	1.80	1.30
1:J:426:ILE:HD13	1:J:440:ILE:CG2	1.58	1.29
1:D:260:SER:O	1:D:264:GLY:N	1.64	1.29
1:D:272:ILE:HG23	1:D:278:LEU:CD1	1.63	1.28
1:D:307:PHE:CE1	1:D:345:LEU:HD21	1.66	1.28
1:J:854:PRO:HB2	1:J:855:ARG:NH1	1.45	1.28
1:G:777:GLY:N	1:L:779:PHE:CZ	2.02	1.28
1:D:276:GLU:OE2	1:D:318:PHE:HE2	1.03	1.28
1:G:777:GLY:HA3	1:L:779:PHE:CG	1.59	1.27
1:K:426:ILE:CD1	1:K:440:ILE:CG2	2.02	1.27
1:G:777:GLY:HA3	1:L:779:PHE:CD2	1.56	1.27
1:H:441:LEU:HD23	1:H:498:VAL:CG1	1.62	1.27
1:D:855:ARG:HD2	1:K:555:ALA:CB	1.62	1.27
1:J:272:ILE:HG23	1:J:278:LEU:CD1	1.64	1.27
1:E:269:LEU:HD21	1:E:457:SER:CB	1.63	1.26
1:C:609:PRO:CB	1:C:611:GLU:HB2	1.63	1.26
1:E:269:LEU:HD11	1:E:457:SER:O	1.19	1.25
1:J:260:SER:O	1:J:264:GLY:N	1.70	1.24
1:G:777:GLY:HA2	1:L:779:PHE:CD1	1.52	1.24
1:B:783:LEU:HD12	1:I:777:GLY:CA	1.65	1.24
1:G:778:GLY:N	1:L:779:PHE:CG	2.06	1.24
1:A:441:LEU:CD2	1:A:498:VAL:CB	2.06	1.23
1:K:269:LEU:CD1	1:K:457:SER:O	1.86	1.23
1:J:269:LEU:HD11	1:J:457:SER:O	1.05	1.22
1:J:478:ASN:ND2	1:J:482:LYS:HZ1	1.35	1.22
1:E:441:LEU:HD23	1:E:498:VAL:CG1	1.68	1.22
1:K:269:LEU:CD2	1:K:457:SER:OG	1.89	1.21
1:E:478:ASN:ND2	1:E:482:LYS:HZ1	1.39	1.20
1:K:260:SER:O	1:K:264:GLY:N	1.71	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:441:LEU:HD23	1:D:498:VAL:CG1	1.72	1.20
1:E:272:ILE:HG23	1:E:278:LEU:CD1	1.71	1.20
1:A:426:ILE:CD1	1:A:440:ILE:CG2	2.06	1.19
1:D:269:LEU:HD21	1:D:457:SER:OG	1.38	1.19
1:H:260:SER:O	1:H:264:GLY:N	1.72	1.18
1:D:441:LEU:HG	1:D:498:VAL:HG12	1.23	1.18
1:D:269:LEU:CD1	1:D:457:SER:O	1.90	1.18
1:G:777:GLY:CA	1:G:777:GLY:C	2.16	1.18
1:G:778:GLY:N	1:L:779:PHE:CD2	2.10	1.17
1:H:225:ASP:HB3	1:H:229:PHE:CZ	1.78	1.17
1:H:269:LEU:HD21	1:H:457:SER:CB	1.74	1.17
1:D:269:LEU:CD2	1:D:457:SER:OG	1.92	1.17
1:D:269:LEU:HD11	1:D:457:SER:O	1.01	1.17
1:A:269:LEU:CD1	1:A:457:SER:O	1.93	1.17
1:A:269:LEU:HD11	1:A:457:SER:O	1.01	1.17
1:E:269:LEU:CD2	1:E:457:SER:OG	1.91	1.17
1:J:269:LEU:CD1	1:J:457:SER:O	1.92	1.17
1:K:791:VAL:HG13	1:K:794:ARG:NH2	1.58	1.16
1:J:269:LEU:HD21	1:J:457:SER:CB	1.72	1.16
1:E:426:ILE:HD11	1:E:440:ILE:HG22	1.28	1.16
1:G:777:GLY:O	1:L:779:PHE:CZ	1.98	1.15
1:K:441:LEU:HG	1:K:498:VAL:HG12	1.25	1.15
1:C:609:PRO:HB2	1:C:611:GLU:HB2	1.29	1.14
1:E:285:ILE:HD13	1:E:286:THR:N	1.62	1.14
1:D:441:LEU:CD2	1:D:498:VAL:CB	2.05	1.14
1:H:426:ILE:HD13	1:H:440:ILE:HG21	1.21	1.14
1:K:285:ILE:HD13	1:K:286:THR:H	1.04	1.14
1:K:441:LEU:HD23	1:K:498:VAL:CG1	1.77	1.14
1:G:777:GLY:N	1:L:779:PHE:CE2	2.11	1.13
1:H:488:HIS:HB3	1:H:491:GLU:CG	1.76	1.13
1:G:780:SER:HB3	1:L:778:GLY:HA2	1.19	1.13
1:J:273:VAL:HG11	1:J:457:SER:HB2	1.13	1.12
1:K:272:ILE:HG23	1:K:278:LEU:CD1	1.79	1.13
1:A:273:VAL:HG11	1:A:457:SER:HB2	1.22	1.12
1:J:269:LEU:CD2	1:J:457:SER:OG	1.97	1.12
1:D:478:ASN:ND2	1:D:482:LYS:NZ	1.97	1.12
1:H:285:ILE:HD13	1:H:286:THR:H	1.14	1.12
1:K:269:LEU:HD21	1:K:457:SER:CB	1.78	1.12
1:A:441:LEU:CD2	1:A:498:VAL:CG1	2.23	1.12
1:K:426:ILE:HD13	1:K:440:ILE:HG21	1.23	1.12
1:A:441:LEU:HD21	1:A:499:SER:H	1.15	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:783:LEU:HD12	1:I:777:GLY:HA3	1.24	1.11
1:G:777:GLY:HA2	1:L:779:PHE:CE1	1.71	1.11
1:J:426:ILE:HD11	1:J:440:ILE:CG2	1.69	1.11
1:A:426:ILE:HD11	1:A:440:ILE:HG22	1.28	1.11
1:A:272:ILE:CG2	1:A:278:LEU:HD12	1.81	1.10
1:D:441:LEU:CG	1:D:498:VAL:HG12	1.81	1.10
1:H:426:ILE:HD11	1:H:440:ILE:HG22	1.20	1.10
1:J:285:ILE:HD13	1:J:286:THR:H	1.15	1.10
1:D:426:ILE:HD13	1:D:440:ILE:HG21	1.17	1.10
1:B:609:PRO:HB2	1:B:611:GLU:HB2	1.33	1.10
1:A:441:LEU:HG	1:A:498:VAL:HG12	1.33	1.09
1:D:426:ILE:HD12	1:D:440:ILE:HG22	1.25	1.09
1:E:426:ILE:HD12	1:E:440:ILE:HG22	1.26	1.09
1:J:441:LEU:HG	1:J:498:VAL:HG12	1.16	1.09
1:K:269:LEU:HD11	1:K:457:SER:O	0.94	1.09
1:A:285:ILE:HD13	1:A:286:THR:N	1.67	1.09
1:G:777:GLY:O	1:L:779:PHE:CE1	2.05	1.09
1:H:272:ILE:HG23	1:H:278:LEU:HD13	1.24	1.09
1:E:269:LEU:CD2	1:E:457:SER:CB	2.31	1.09
1:D:855:ARG:HD2	1:K:555:ALA:HB1	1.27	1.09
1:A:269:LEU:CD2	1:A:457:SER:OG	2.01	1.08
1:H:478:ASN:ND2	1:H:482:LYS:HZ1	1.51	1.08
1:J:269:LEU:HA	1:J:272:ILE:HD12	1.31	1.08
1:E:441:LEU:HG	1:E:498:VAL:HG12	1.12	1.08
1:K:269:LEU:HA	1:K:272:ILE:HD12	1.34	1.08
1:L:609:PRO:HB2	1:L:611:GLU:HB2	1.32	1.08
1:A:269:LEU:HD21	1:A:457:SER:CB	1.82	1.08
1:A:278:LEU:HD21	1:A:280:LYS:HD3	1.36	1.07
1:E:272:ILE:HG23	1:E:278:LEU:HD12	1.30	1.07
1:H:441:LEU:HG	1:H:498:VAL:HG12	1.30	1.07
1:I:776:ALA:C	1:I:783:LEU:HD12	1.80	1.07
1:K:278:LEU:HD21	1:K:280:LYS:HD3	1.35	1.07
1:E:273:VAL:HG11	1:E:457:SER:HB2	1.32	1.07
1:A:426:ILE:HD13	1:A:440:ILE:HG21	1.21	1.07
1:D:285:ILE:HD13	1:D:286:THR:H	0.95	1.07
1:K:279:PRO:HG2	1:K:325:LEU:HD21	1.33	1.06
1:K:426:ILE:HD12	1:K:440:ILE:HG22	1.38	1.06
1:H:434:PRO:HB3	1:H:491:GLU:HG3	1.38	1.05
1:A:269:LEU:HD21	1:A:457:SER:OG	1.53	1.05
1:H:272:ILE:HG23	1:H:278:LEU:HD12	1.37	1.05
1:K:307:PHE:CE1	1:K:345:LEU:HD21	1.91	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:426:ILE:HD11	1:K:440:ILE:HG22	1.36	1.05
1:J:426:ILE:HD13	1:J:440:ILE:HG21	1.26	1.05
1:H:269:LEU:HD21	1:H:457:SER:OG	1.55	1.05
1:K:488:HIS:HB3	1:K:491:GLU:HG2	1.36	1.05
1:D:273:VAL:HG11	1:D:457:SER:HB2	1.38	1.04
1:H:269:LEU:HD11	1:H:457:SER:O	0.87	1.04
1:A:441:LEU:CG	1:A:498:VAL:HG12	1.86	1.04
1:C:285:ILE:HD12	1:C:287:ARG:H	1.20	1.04
1:G:780:SER:CB	1:L:778:GLY:CA	2.36	1.04
1:H:251:THR:HG22	1:H:252:LEU:N	1.70	1.04
1:K:273:VAL:HG11	1:K:457:SER:HB2	1.10	1.04
1:E:478:ASN:ND2	1:E:482:LYS:NZ	2.06	1.04
1:L:609:PRO:CB	1:L:611:GLU:HB2	1.88	1.04
1:B:791:VAL:HG13	1:B:794:ARG:NH2	1.73	1.04
1:D:272:ILE:HG23	1:D:278:LEU:HD12	1.05	1.04
1:E:279:PRO:HG2	1:E:325:LEU:HD21	1.39	1.04
1:E:363:TYR:HE1	1:E:383:CYS:SG	1.81	1.04
1:H:441:LEU:HD21	1:H:499:SER:H	1.18	1.04
1:J:478:ASN:ND2	1:J:482:LYS:NZ	2.05	1.03
1:G:780:SER:OG	1:G:783:LEU:HB2	1.57	1.03
1:J:441:LEU:CG	1:J:498:VAL:HG12	1.89	1.03
1:E:286:THR:HB	1:E:361:PRO:HB3	1.36	1.03
1:A:284:MET:HG2	1:A:286:THR:CG2	1.88	1.03
1:A:285:ILE:HD13	1:A:286:THR:H	0.89	1.03
1:D:855:ARG:HD2	1:K:555:ALA:HB3	1.39	1.03
1:H:234:MET:O	1:H:237:ILE:HG22	1.57	1.03
1:K:272:ILE:HG23	1:K:278:LEU:HD12	1.05	1.03
1:H:478:ASN:ND2	1:H:482:LYS:NZ	2.07	1.02
1:E:269:LEU:CD1	1:E:457:SER:O	2.07	1.02
1:E:485:PHE:CD2	1:E:492:PHE:CD1	2.46	1.02
1:K:878:ASP:HB3	1:K:881:VAL:HG22	1.36	1.02
1:E:441:LEU:CG	1:E:498:VAL:HG12	1.88	1.02
1:D:426:ILE:HD11	1:D:440:ILE:HG22	1.35	1.02
1:K:251:THR:HG22	1:K:252:LEU:H	1.23	1.01
1:C:609:PRO:HB2	1:C:611:GLU:CB	1.91	1.01
1:J:272:ILE:HG23	1:J:278:LEU:HD13	1.35	1.01
1:H:232:LYS:HA	1:H:235:ILE:HG22	1.42	1.01
1:J:273:VAL:HG11	1:J:457:SER:CB	1.90	1.01
1:K:376:LYS:NZ	1:K:376:LYS:HA	1.76	1.01
1:E:307:PHE:CE1	1:E:345:LEU:HD21	1.96	1.01
1:E:426:ILE:HD13	1:E:440:ILE:HG21	1.02	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:441:LEU:CD2	1:E:498:VAL:CG1	2.33	1.00
1:D:486:GLY:O	1:D:489:PRO:HD3	1.60	1.00
1:E:285:ILE:HD13	1:E:286:THR:H	0.89	1.00
1:H:441:LEU:CD2	1:H:498:VAL:CB	1.96	1.00
1:H:441:LEU:CG	1:H:498:VAL:HG12	1.90	1.00
1:I:615:ILE:HD11	1:I:803:ARG:HE	1.23	1.00
1:J:307:PHE:CE1	1:J:345:LEU:HD21	1.95	1.00
1:H:441:LEU:HD21	1:H:499:SER:N	1.76	1.00
1:J:297:ASP:CG	1:J:300:ALA:HB3	1.85	1.00
1:K:878:ASP:HB3	1:K:881:VAL:CG2	1.92	1.00
1:H:441:LEU:CD2	1:H:498:VAL:CG1	2.34	0.99
1:A:237:ILE:O	1:A:237:ILE:HD13	1.63	0.99
1:K:285:ILE:HD13	1:K:286:THR:N	1.77	0.99
1:E:269:LEU:HD21	1:E:457:SER:HB2	1.44	0.99
1:L:627:TYR:HE2	1:L:628:TRP:CZ3	1.80	0.99
1:C:609:PRO:HB3	1:C:611:GLU:HB2	1.42	0.99
1:A:251:THR:HG22	1:A:252:LEU:H	1.23	0.98
1:B:783:LEU:CD1	1:I:777:GLY:CA	2.41	0.98
1:C:609:PRO:HB2	1:C:611:GLU:N	1.78	0.98
1:G:772:HIS:CE1	1:L:780:SER:HB3	1.99	0.98
1:D:269:LEU:HD21	1:D:457:SER:CB	1.93	0.98
1:D:270:GLU:O	1:D:273:VAL:HG22	1.63	0.98
1:J:273:VAL:HG21	1:J:457:SER:HB3	1.41	0.98
1:B:609:PRO:CB	1:B:611:GLU:HB2	1.93	0.98
1:E:279:PRO:CB	1:E:322:GLN:HA	1.94	0.98
1:D:278:LEU:CD2	1:D:280:LYS:HD3	1.94	0.98
1:D:441:LEU:CD2	1:D:498:VAL:CG1	2.40	0.98
1:E:429:MET:HE2	1:E:437:GLY:HA2	1.46	0.98
1:E:434:PRO:HG2	1:E:488:HIS:ND1	1.79	0.98
1:H:285:ILE:HG12	1:H:287:ARG:H	1.26	0.97
1:H:429:MET:HE2	1:H:437:GLY:HA2	1.43	0.97
1:B:880:LYS:HG3	1:B:883:ARG:NH2	1.78	0.97
1:D:383:CYS:O	1:D:387:ILE:HG13	1.64	0.97
1:A:286:THR:HB	1:A:361:PRO:HB3	1.44	0.97
1:K:269:LEU:O	1:K:273:VAL:HG13	1.63	0.97
1:J:285:ILE:HG12	1:J:287:ARG:H	1.29	0.97
1:G:774:SER:HB2	1:L:777:GLY:O	1.62	0.97
1:K:276:GLU:OE2	1:K:318:PHE:CE2	2.18	0.97
1:E:453:VAL:HG11	1:E:505:LEU:HB2	1.46	0.97
1:K:441:LEU:CD2	1:K:498:VAL:CB	2.09	0.97
1:J:276:GLU:CD	1:J:318:PHE:HE2	1.70	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:363:TYR:HE1	1:J:383:CYS:SG	1.87	0.97
1:J:854:PRO:HB2	1:J:855:ARG:HH12	1.21	0.97
1:B:780:SER:HB2	1:I:774:SER:OG	1.63	0.96
1:E:434:PRO:CB	1:E:491:GLU:HG3	1.93	0.96
1:K:272:ILE:CG2	1:K:278:LEU:HD12	1.95	0.96
1:D:854:PRO:HB3	1:K:559:ASP:OD2	1.65	0.96
1:H:434:PRO:CB	1:H:491:GLU:HG3	1.94	0.96
1:J:441:LEU:HD23	1:J:498:VAL:CG1	1.94	0.96
1:K:284:MET:HG2	1:K:286:THR:CG2	1.95	0.96
1:E:441:LEU:HG	1:E:498:VAL:CG1	1.95	0.96
1:J:472:ASN:HD21	1:J:475:ALA:HB3	1.30	0.96
1:E:478:ASN:HD21	1:E:482:LYS:NZ	1.61	0.96
1:D:855:ARG:HD3	1:D:855:ARG:N	1.79	0.96
1:J:297:ASP:OD2	1:J:300:ALA:HB3	1.63	0.96
1:K:376:LYS:NZ	1:K:379:ILE:HD12	1.81	0.96
1:B:783:LEU:CD1	1:I:777:GLY:HA2	1.96	0.96
1:K:854:PRO:HB2	1:K:855:ARG:NH1	1.81	0.96
1:K:278:LEU:CD2	1:K:280:LYS:HD3	1.96	0.95
1:D:287:ARG:HH11	1:D:287:ARG:HG3	1.28	0.95
1:E:272:ILE:HG22	1:E:277:PHE:HA	1.46	0.95
1:K:284:MET:HG2	1:K:286:THR:HG22	1.49	0.95
1:D:478:ASN:HD21	1:D:482:LYS:HZ1	1.03	0.95
1:K:453:VAL:HG11	1:K:505:LEU:HB2	1.47	0.95
1:A:269:LEU:HA	1:A:272:ILE:HD12	1.43	0.95
1:G:772:HIS:ND1	1:L:780:SER:HB3	1.81	0.95
1:E:279:PRO:HB3	1:E:322:GLN:HA	1.49	0.95
1:E:556:ALA:HB2	1:J:855:ARG:HH21	1.31	0.95
1:A:441:LEU:CD2	1:A:498:VAL:HG12	1.95	0.95
1:D:269:LEU:O	1:D:273:VAL:HG13	1.65	0.95
1:D:493:GLY:O	1:D:496:SER:HB3	1.66	0.95
1:H:488:HIS:HB3	1:H:491:GLU:HG2	1.46	0.95
1:J:453:VAL:HG11	1:J:505:LEU:HB2	1.47	0.95
1:B:774:SER:O	1:I:774:SER:HB2	1.67	0.95
1:E:441:LEU:CD2	1:E:498:VAL:CB	2.02	0.95
1:E:441:LEU:HD21	1:E:498:VAL:HB	1.49	0.95
1:E:472:ASN:ND2	1:E:475:ALA:HB3	1.82	0.95
1:H:232:LYS:HA	1:H:235:ILE:CG2	1.96	0.94
1:D:485:PHE:CE2	1:D:500:THR:OG1	2.20	0.94
1:J:272:ILE:HG23	1:J:278:LEU:HD12	1.46	0.94
1:A:441:LEU:HD21	1:A:499:SER:N	1.83	0.94
1:A:285:ILE:CD1	1:A:286:THR:H	1.81	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:278:LEU:HB2	1:J:279:PRO:HD2	1.50	0.94
1:K:429:MET:HE2	1:K:437:GLY:HA2	1.48	0.94
1:G:776:ALA:O	1:L:777:GLY:HA3	1.68	0.94
1:A:878:ASP:HB3	1:A:881:VAL:HG22	1.50	0.93
1:A:376:LYS:HA	1:A:376:LYS:NZ	1.84	0.93
1:D:279:PRO:HG2	1:D:325:LEU:HD21	1.50	0.93
1:A:429:MET:HE2	1:A:437:GLY:HA2	1.49	0.93
1:E:234:MET:O	1:E:237:ILE:HG22	1.69	0.93
1:H:453:VAL:HG11	1:H:505:LEU:HB2	1.50	0.93
1:J:488:HIS:HB3	1:J:491:GLU:HG2	1.50	0.93
1:K:383:CYS:O	1:K:387:ILE:HG13	1.68	0.93
1:F:642:LEU:HD22	1:F:643:GLY:H	1.33	0.93
1:G:780:SER:CB	1:L:778:GLY:HA2	1.99	0.93
1:J:269:LEU:HD21	1:J:457:SER:OG	1.58	0.93
1:D:363:TYR:HE1	1:D:383:CYS:SG	1.90	0.93
1:H:269:LEU:CD2	1:H:457:SER:OG	2.16	0.93
1:H:273:VAL:HG11	1:H:457:SER:CB	1.99	0.93
1:K:269:LEU:HD23	1:K:270:GLU:N	1.84	0.93
1:E:377:ARG:HH21	1:E:377:ARG:CG	1.82	0.93
1:K:752:LYS:HG3	1:K:755:MET:HE3	1.48	0.93
1:G:773:PRO:CA	1:G:781:ALA:HB3	1.97	0.92
1:H:441:LEU:HD21	1:H:498:VAL:HB	1.51	0.92
1:K:376:LYS:HZ1	1:K:379:ILE:HD12	1.33	0.92
1:J:272:ILE:HG22	1:J:277:PHE:HA	1.50	0.92
1:D:627:TYR:HE2	1:D:628:TRP:CZ3	1.87	0.92
1:G:780:SER:HB3	1:L:778:GLY:C	1.94	0.92
1:D:855:ARG:HH21	1:K:556:ALA:HA	1.34	0.92
1:B:609:PRO:HB2	1:B:611:GLU:CB	1.99	0.92
1:E:441:LEU:CG	1:E:498:VAL:CG1	2.48	0.92
1:A:441:LEU:HD23	1:A:498:VAL:HB	0.93	0.92
1:D:235:ILE:HD12	1:D:235:ILE:O	1.71	0.91
1:J:269:LEU:CD2	1:J:457:SER:CB	2.46	0.91
1:A:278:LEU:CD2	1:A:280:LYS:HD3	1.98	0.91
1:B:318:PHE:CD1	1:B:321:ILE:HD12	2.05	0.91
1:D:286:THR:CB	1:D:361:PRO:HB3	1.99	0.91
1:H:478:ASN:HD21	1:H:482:LYS:NZ	1.67	0.91
1:H:279:PRO:HB3	1:H:322:GLN:HB2	1.52	0.91
1:J:485:PHE:CD2	1:J:492:PHE:CD1	2.58	0.91
1:B:791:VAL:HG13	1:B:794:ARG:HH21	1.31	0.91
1:J:286:THR:HB	1:J:361:PRO:HB3	1.52	0.91
1:A:279:PRO:HG2	1:A:325:LEU:HD21	1.50	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:434:PRO:HB3	1:E:491:GLU:HG3	1.51	0.91
1:K:441:LEU:HD21	1:K:498:VAL:HB	1.46	0.91
1:D:441:LEU:HD21	1:D:499:SER:H	1.35	0.91
1:A:273:VAL:HG11	1:A:457:SER:CB	2.01	0.91
1:K:273:VAL:CG1	1:K:457:SER:HB2	1.99	0.91
1:E:287:ARG:HH11	1:E:287:ARG:HG3	1.33	0.91
1:H:272:ILE:CG2	1:H:278:LEU:CD1	2.48	0.91
1:A:363:TYR:HE1	1:A:383:CYS:SG	1.94	0.91
1:K:441:LEU:CG	1:K:498:VAL:HG12	1.99	0.91
1:A:272:ILE:HG23	1:A:278:LEU:HD12	0.91	0.90
1:A:285:ILE:HG12	1:A:287:ARG:H	1.35	0.90
1:H:279:PRO:HB3	1:H:322:GLN:CB	2.01	0.90
1:J:485:PHE:HD2	1:J:492:PHE:O	1.53	0.90
1:D:441:LEU:HD21	1:D:499:SER:N	1.86	0.90
1:J:854:PRO:HB2	1:J:855:ARG:HH11	1.32	0.90
1:H:270:GLU:O	1:H:273:VAL:HG22	1.70	0.90
1:H:269:LEU:CD2	1:H:457:SER:CB	2.49	0.90
1:L:615:ILE:HD11	1:L:803:ARG:HE	1.36	0.90
1:D:307:PHE:CD1	1:D:345:LEU:HD21	2.05	0.90
1:I:264:GLY:HA2	1:I:267:SER:HB3	1.54	0.90
1:B:780:SER:HB3	1:I:776:ALA:C	1.97	0.90
1:E:269:LEU:CD2	1:E:457:SER:HB2	1.98	0.90
1:E:552:SER:HA	1:J:855:ARG:HD2	1.54	0.90
1:H:251:THR:HG22	1:H:252:LEU:H	1.27	0.90
1:H:279:PRO:HG2	1:H:325:LEU:HD21	1.54	0.90
1:H:286:THR:CB	1:H:361:PRO:HB3	2.01	0.90
1:K:285:ILE:HG12	1:K:287:ARG:H	1.35	0.90
1:E:854:PRO:HB2	1:E:855:ARG:NH1	1.86	0.89
1:D:285:ILE:CD1	1:D:286:THR:N	2.34	0.89
1:H:273:VAL:HG11	1:H:457:SER:HB2	1.52	0.89
1:K:375:LEU:HD23	1:K:375:LEU:N	1.86	0.89
1:L:791:VAL:HG13	1:L:794:ARG:HH21	1.34	0.89
1:D:752:LYS:HG3	1:D:755:MET:HE3	1.53	0.89
1:J:234:MET:O	1:J:237:ILE:HG22	1.73	0.89
1:H:434:PRO:HG2	1:H:488:HIS:CG	2.08	0.89
1:G:773:PRO:HA	1:G:781:ALA:HB3	1.55	0.89
1:B:260:SER:O	1:B:264:GLY:N	2.05	0.89
1:J:286:THR:CB	1:J:361:PRO:HB3	2.02	0.89
1:A:485:PHE:CE2	1:A:500:THR:OG1	2.24	0.89
1:A:284:MET:HG2	1:A:286:THR:HG23	1.51	0.89
1:A:455:VAL:HG12	1:A:501:GLY:H	1.37	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:273:VAL:CG1	1:J:457:SER:HB2	2.03	0.89
1:E:285:ILE:HG12	1:E:287:ARG:H	1.37	0.89
1:D:279:PRO:HB3	1:D:322:GLN:CB	2.02	0.88
1:D:285:ILE:HG12	1:D:287:ARG:H	1.38	0.88
1:H:363:TYR:HE1	1:H:383:CYS:SG	1.95	0.88
1:H:458:LYS:HD2	1:H:458:LYS:C	1.98	0.88
1:J:233:LYS:HE2	1:J:233:LYS:N	1.87	0.88
1:A:273:VAL:CG1	1:A:457:SER:HB2	2.03	0.88
1:E:363:TYR:CE1	1:E:383:CYS:SG	2.61	0.88
1:B:779:PHE:C	1:I:776:ALA:HB3	1.98	0.88
1:E:273:VAL:HG11	1:E:457:SER:CB	2.03	0.88
1:F:609:PRO:HB2	1:F:611:GLU:HB2	1.54	0.88
1:K:270:GLU:O	1:K:273:VAL:HG22	1.74	0.88
1:K:269:LEU:HD23	1:K:269:LEU:C	1.98	0.88
1:D:272:ILE:CG2	1:D:278:LEU:HD12	1.98	0.87
1:E:272:ILE:HG23	1:E:278:LEU:HD13	1.55	0.87
1:J:429:MET:HE2	1:J:437:GLY:HA2	1.55	0.87
1:K:363:TYR:HE1	1:K:383:CYS:SG	1.97	0.87
1:K:273:VAL:HG11	1:K:457:SER:CB	2.01	0.87
1:E:455:VAL:HG12	1:E:501:GLY:H	1.39	0.87
1:H:339:THR:HG23	1:H:340:ASP:N	1.88	0.87
1:L:791:VAL:HG13	1:L:794:ARG:NH2	1.89	0.87
1:D:441:LEU:CG	1:D:498:VAL:CG1	2.51	0.87
1:D:614:ASN:OD1	1:D:616:ILE:HG22	1.74	0.87
1:J:285:ILE:HD13	1:J:286:THR:N	1.89	0.87
1:D:555:ALA:HB3	1:K:855:ARG:CD	2.04	0.87
1:H:284:MET:HG2	1:H:286:THR:HG22	1.57	0.87
1:J:565:PHE:O	1:J:568:PHE:HB3	1.73	0.87
1:L:778:GLY:C	1:L:779:PHE:HD2	1.82	0.87
1:A:234:MET:O	1:A:237:ILE:HG22	1.74	0.86
1:B:772:HIS:HD2	1:B:775:GLY:O	1.58	0.86
1:D:284:MET:N	1:D:284:MET:SD	2.48	0.86
1:G:862:HIS:CD2	1:G:866:HIS:CD2	2.63	0.86
1:H:478:ASN:HD21	1:H:482:LYS:HZ1	0.87	0.86
1:J:244:VAL:HB	1:J:248:SER:OG	1.74	0.86
1:J:639:LEU:O	1:J:642:LEU:HD23	1.75	0.86
1:K:276:GLU:OE2	1:K:318:PHE:HE2	1.57	0.86
1:K:441:LEU:CD2	1:K:498:VAL:CG1	2.47	0.86
1:K:376:LYS:HA	1:K:376:LYS:HZ3	1.36	0.86
1:D:454:GLY:O	1:D:500:THR:HB	1.76	0.86
1:H:441:LEU:CG	1:H:498:VAL:CG1	2.52	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:776:ALA:O	1:I:783:LEU:HD12	1.72	0.86
1:K:791:VAL:HG13	1:K:794:ARG:HH21	1.36	0.86
1:D:429:MET:HE2	1:D:437:GLY:HA2	1.56	0.86
1:H:383:CYS:O	1:H:387:ILE:HG13	1.75	0.86
1:G:260:SER:O	1:G:264:GLY:N	2.07	0.86
1:D:855:ARG:NH2	1:K:556:ALA:HA	1.91	0.86
1:D:544:ASN:HD22	1:L:641:ARG:HH11	1.21	0.86
1:A:572:PHE:O	1:A:576:GLN:NE2	2.07	0.85
1:D:286:THR:HB	1:D:361:PRO:HB3	1.56	0.85
1:J:278:LEU:HD21	1:J:280:LYS:HD3	1.58	0.85
1:J:486:GLY:O	1:J:489:PRO:HD3	1.75	0.85
1:D:441:LEU:HD21	1:D:498:VAL:HB	1.54	0.85
1:H:434:PRO:HB3	1:H:491:GLU:CG	2.05	0.85
1:D:278:LEU:HB2	1:D:279:PRO:HD2	1.55	0.85
1:A:485:PHE:HD2	1:A:492:PHE:O	1.60	0.85
1:E:285:ILE:CD1	1:E:286:THR:H	1.84	0.85
1:E:441:LEU:HD21	1:E:499:SER:H	1.39	0.85
1:H:269:LEU:O	1:H:273:VAL:HG13	1.75	0.85
1:H:269:LEU:HA	1:H:272:ILE:HD12	1.58	0.85
1:D:307:PHE:HE1	1:D:345:LEU:HD21	1.38	0.85
1:D:855:ARG:HH21	1:K:556:ALA:CA	1.89	0.85
1:E:279:PRO:HB3	1:E:322:GLN:CA	2.07	0.85
1:E:576:GLN:H	1:E:576:GLN:HE21	1.23	0.85
1:H:225:ASP:HB3	1:H:229:PHE:HZ	1.33	0.85
1:D:376:LYS:HA	1:D:376:LYS:NZ	1.92	0.85
1:J:854:PRO:CB	1:J:855:ARG:HH12	1.90	0.85
1:D:279:PRO:HB3	1:D:322:GLN:HB2	1.56	0.85
1:D:485:PHE:CD2	1:D:492:PHE:CD1	2.64	0.84
1:D:572:PHE:O	1:D:576:GLN:NE2	2.10	0.84
1:E:257:VAL:CG2	1:E:359:ASP:HA	2.07	0.84
1:K:485:PHE:CD2	1:K:492:PHE:CD1	2.65	0.84
1:D:285:ILE:HG12	1:D:287:ARG:HB2	1.57	0.84
1:D:753:GLU:CD	1:E:750:LYS:HE2	2.02	0.84
1:F:791:VAL:HG13	1:F:794:ARG:NH2	1.92	0.84
1:K:287:ARG:HG3	1:K:287:ARG:HH11	1.42	0.84
1:J:257:VAL:CG2	1:J:359:ASP:HA	2.07	0.84
1:K:455:VAL:HG12	1:K:501:GLY:H	1.43	0.84
1:A:273:VAL:HG21	1:A:457:SER:HB3	1.59	0.84
1:J:854:PRO:CB	1:J:855:ARG:NH1	2.36	0.84
1:K:752:LYS:HG3	1:K:755:MET:CE	2.07	0.84
1:G:308:PRO:HG3	1:G:344:ARG:HB2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:PRO:CB	1:A:322:GLN:HA	2.08	0.84
1:D:278:LEU:HD21	1:D:280:LYS:HD3	1.59	0.84
1:E:308:PRO:HG3	1:E:344:ARG:HB2	1.60	0.84
1:A:251:THR:HG22	1:A:252:LEU:N	1.93	0.84
1:A:272:ILE:CG2	1:A:278:LEU:CD1	2.48	0.84
1:H:269:LEU:CD2	1:H:457:SER:HB2	2.08	0.84
1:J:426:ILE:HD11	1:J:440:ILE:HG22	0.84	0.84
1:E:273:VAL:CG1	1:E:457:SER:HB2	2.08	0.83
1:K:279:PRO:HG2	1:K:325:LEU:CD2	2.08	0.83
1:D:855:ARG:HH21	1:K:556:ALA:CB	1.90	0.83
1:H:454:GLY:O	1:H:500:THR:HB	1.77	0.83
1:D:229:PHE:HA	1:D:232:LYS:HG2	1.57	0.83
1:D:272:ILE:CG2	1:D:278:LEU:CD1	2.55	0.83
1:A:279:PRO:HB3	1:A:322:GLN:CB	2.08	0.83
1:G:284:MET:N	1:G:284:MET:SD	2.48	0.83
1:H:441:LEU:HB3	1:H:498:VAL:HG11	1.61	0.83
1:J:478:ASN:HD21	1:J:482:LYS:HZ1	1.22	0.83
1:H:272:ILE:CG2	1:H:278:LEU:HD13	2.08	0.83
1:J:278:LEU:CD2	1:J:280:LYS:HD3	2.07	0.83
1:B:488:HIS:HB3	1:B:491:GLU:HG3	1.61	0.83
1:I:611:GLU:N	1:I:612:PRO:HD2	1.94	0.83
1:K:297:ASP:CG	1:K:300:ALA:HB3	2.04	0.83
1:H:287:ARG:HH11	1:H:287:ARG:HG3	1.43	0.83
1:A:453:VAL:HG11	1:A:505:LEU:HB2	1.61	0.83
1:E:576:GLN:H	1:E:576:GLN:NE2	1.76	0.83
1:J:284:MET:N	1:J:284:MET:SD	2.50	0.83
1:L:260:SER:O	1:L:264:GLY:N	2.11	0.83
1:E:377:ARG:HH21	1:E:377:ARG:HG2	1.42	0.83
1:J:251:THR:HG22	1:J:252:LEU:H	1.42	0.83
1:K:485:PHE:HD2	1:K:492:PHE:O	1.60	0.83
1:A:749:LYS:H	1:A:749:LYS:HD2	1.42	0.82
1:E:260:SER:N	1:E:263:SER:HB3	1.94	0.82
1:G:642:LEU:HD22	1:G:643:GLY:H	1.43	0.82
1:H:272:ILE:HG22	1:H:277:PHE:HA	1.59	0.82
1:I:609:PRO:HB2	1:I:611:GLU:N	1.93	0.82
1:A:297:ASP:CG	1:A:300:ALA:HB3	2.04	0.82
1:A:434:PRO:HB3	1:A:491:GLU:HG3	1.60	0.82
1:C:854:PRO:HB2	1:C:855:ARG:CZ	2.09	0.82
1:J:279:PRO:CB	1:J:322:GLN:HA	2.10	0.82
1:K:488:HIS:HB3	1:K:491:GLU:CG	2.09	0.82
1:E:279:PRO:HB3	1:E:322:GLN:CB	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:441:LEU:CG	1:J:498:VAL:CG1	2.57	0.82
1:K:269:LEU:HD11	1:K:457:SER:C	2.02	0.82
1:I:843:VAL:O	1:I:847:ASN:HB2	1.80	0.82
1:E:269:LEU:HD22	1:E:457:SER:OG	1.78	0.82
1:J:441:LEU:HG	1:J:498:VAL:CG1	2.05	0.82
1:K:376:LYS:HE2	1:K:376:LYS:N	1.95	0.82
1:D:284:MET:HG2	1:D:286:THR:CG2	2.10	0.82
1:G:258:ILE:HG22	1:G:360:LEU:HD11	1.59	0.82
1:H:286:THR:OG1	1:H:361:PRO:HB3	1.80	0.82
1:A:286:THR:CB	1:A:361:PRO:HB3	2.09	0.82
1:H:237:ILE:O	1:H:237:ILE:HD13	1.80	0.82
1:H:286:THR:O	1:H:361:PRO:CG	2.28	0.82
1:H:572:PHE:O	1:H:576:GLN:NE2	2.12	0.81
1:A:492:PHE:O	1:A:492:PHE:HD1	1.62	0.81
1:B:615:ILE:HD11	1:B:803:ARG:HE	1.43	0.81
1:A:455:VAL:HG12	1:A:501:GLY:N	1.94	0.81
1:G:285:ILE:HD12	1:G:287:ARG:H	1.46	0.81
1:H:488:HIS:HB3	1:H:491:GLU:HG3	1.61	0.81
1:J:272:ILE:HG21	1:J:277:PHE:CD1	2.15	0.81
1:E:294:LEU:HB3	1:E:352:ILE:HD13	1.62	0.81
1:B:318:PHE:HD1	1:B:321:ILE:HD12	1.43	0.81
1:A:426:ILE:HD12	1:A:440:ILE:HG22	1.60	0.81
1:H:257:VAL:CG2	1:H:359:ASP:HA	2.09	0.81
1:J:441:LEU:CD2	1:J:498:VAL:CB	2.23	0.81
1:A:284:MET:HG2	1:A:286:THR:HG22	1.63	0.81
1:C:609:PRO:CB	1:C:611:GLU:CB	2.52	0.81
1:D:279:PRO:CB	1:D:322:GLN:HA	2.11	0.81
1:E:276:GLU:OE2	1:E:318:PHE:HE2	1.63	0.81
1:K:279:PRO:CB	1:K:322:GLN:HA	2.10	0.81
1:B:843:VAL:O	1:B:847:ASN:HB2	1.80	0.81
1:K:251:THR:HG22	1:K:252:LEU:N	1.94	0.81
1:K:285:ILE:HG13	1:K:332:VAL:HG22	1.63	0.81
1:H:278:LEU:HD22	1:H:280:LYS:HG2	1.62	0.81
1:G:773:PRO:O	1:G:782:ALA:HB2	1.81	0.81
1:H:485:PHE:CE2	1:H:500:THR:OG1	2.34	0.81
1:J:269:LEU:O	1:J:273:VAL:HG13	1.81	0.81
1:L:434:PRO:HG2	1:L:488:HIS:CG	2.15	0.81
1:H:286:THR:O	1:H:361:PRO:HG3	1.81	0.80
1:E:286:THR:CB	1:E:361:PRO:HB3	2.10	0.80
1:H:252:LEU:HD23	1:H:524:THR:HG21	1.64	0.80
1:J:267:SER:HB2	1:J:396:ILE:CD1	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:276:GLU:CD	1:J:318:PHE:CE2	2.60	0.80
1:K:382:LEU:C	1:K:382:LEU:HD12	2.06	0.80
1:D:480:ASN:HA	1:D:483:ASN:OD1	1.80	0.80
1:E:339:THR:HG23	1:E:340:ASP:H	1.46	0.80
1:J:269:LEU:HD21	1:J:457:SER:HB2	1.62	0.80
1:J:376:LYS:HA	1:J:376:LYS:NZ	1.96	0.80
1:A:275:HIS:CD2	1:A:275:HIS:H	2.00	0.80
1:E:376:LYS:NZ	1:E:379:ILE:HD12	1.96	0.80
1:I:260:SER:O	1:I:264:GLY:N	2.14	0.80
1:D:627:TYR:CE2	1:D:628:TRP:CZ3	2.70	0.80
1:F:285:ILE:HD13	1:F:332:VAL:HG22	1.64	0.80
1:L:627:TYR:CE2	1:L:628:TRP:CZ3	2.69	0.80
1:H:285:ILE:HD13	1:H:286:THR:N	1.94	0.80
1:J:456:ILE:HD12	1:J:457:SER:N	1.97	0.80
1:D:855:ARG:CD	1:K:555:ALA:HB3	2.11	0.79
1:E:285:ILE:HG12	1:E:287:ARG:HB2	1.64	0.79
1:J:229:PHE:O	1:J:233:LYS:HG2	1.83	0.79
1:G:862:HIS:CD2	1:G:866:HIS:HD2	1.99	0.79
1:H:434:PRO:HG2	1:H:488:HIS:CD2	2.17	0.79
1:A:257:VAL:CG2	1:A:359:ASP:HA	2.12	0.79
1:B:434:PRO:HG2	1:B:488:HIS:CG	2.18	0.79
1:I:863:GLU:O	1:I:867:ALA:HB3	1.81	0.79
1:K:322:GLN:O	1:K:326:THR:OG1	1.98	0.79
1:K:485:PHE:CE2	1:K:500:THR:OG1	2.35	0.79
1:A:485:PHE:CD2	1:A:492:PHE:CD1	2.70	0.79
1:D:434:PRO:HG2	1:D:488:HIS:CG	2.18	0.79
1:E:854:PRO:HD2	1:E:855:ARG:HH12	1.46	0.79
1:A:376:LYS:HA	1:A:376:LYS:HZ3	1.46	0.79
1:A:576:GLN:NE2	1:A:576:GLN:H	1.80	0.79
1:D:752:LYS:HG3	1:D:755:MET:CE	2.11	0.79
1:E:854:PRO:CD	1:E:855:ARG:HH12	1.96	0.79
1:H:488:HIS:CB	1:H:491:GLU:CG	2.60	0.79
1:E:278:LEU:HB2	1:E:279:PRO:HD2	1.65	0.79
1:B:880:LYS:HG3	1:B:883:ARG:HH21	1.48	0.79
1:C:818:LYS:NZ	1:C:819:TYR:CZ	2.50	0.79
1:J:878:ASP:HB3	1:J:881:VAL:HG22	1.63	0.79
1:L:754:VAL:HG22	1:L:779:PHE:CD1	2.17	0.79
1:A:265:LYS:O	1:A:268:VAL:HG23	1.82	0.79
1:A:383:CYS:O	1:A:387:ILE:HG13	1.81	0.79
1:D:284:MET:HG2	1:D:286:THR:HG22	1.64	0.79
1:E:556:ALA:HB2	1:J:855:ARG:NH2	1.98	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:443:ASP:OD1	1:G:445:GLN:HG3	1.83	0.79
1:H:269:LEU:HD23	1:H:270:GLU:N	1.97	0.79
1:E:854:PRO:CG	1:E:855:ARG:HH12	1.96	0.79
1:H:235:ILE:HD12	1:H:235:ILE:O	1.81	0.79
1:D:269:LEU:HD23	1:D:457:SER:OG	1.82	0.78
1:D:376:LYS:NZ	1:D:379:ILE:HD12	1.98	0.78
1:D:854:PRO:CB	1:K:559:ASP:OD2	2.30	0.78
1:I:772:HIS:HB2	1:I:779:PHE:C	2.07	0.78
1:D:627:TYR:HE2	1:D:628:TRP:CH2	2.01	0.78
1:E:328:LEU:HD13	1:E:343:ILE:HD13	1.63	0.78
1:H:426:ILE:HD12	1:H:440:ILE:HG22	1.55	0.78
1:A:238:ARG:NH2	1:A:356:SER:OG	2.16	0.78
1:D:286:THR:O	1:D:361:PRO:CG	2.31	0.78
1:D:294:LEU:HB3	1:D:352:ILE:HD13	1.65	0.78
1:H:377:ARG:HH21	1:H:377:ARG:CG	1.96	0.78
1:I:776:ALA:C	1:I:783:LEU:CD1	2.56	0.78
1:K:279:PRO:HB3	1:K:322:GLN:CB	2.13	0.78
1:A:388:ARG:O	1:A:421:ARG:NH2	2.15	0.78
1:D:307:PHE:CD1	1:D:345:LEU:CD2	2.66	0.78
1:H:485:PHE:CD2	1:H:492:PHE:CD1	2.70	0.78
1:J:310:LEU:N	1:J:310:LEU:HD23	1.97	0.78
1:E:376:LYS:HZ2	1:E:379:ILE:HD12	1.49	0.78
1:E:485:PHE:CE2	1:E:500:THR:OG1	2.37	0.78
1:E:749:LYS:H	1:E:749:LYS:HD2	1.48	0.78
1:K:441:LEU:HD21	1:K:499:SER:H	1.49	0.78
1:E:388:ARG:O	1:E:421:ARG:NH2	2.17	0.78
1:F:642:LEU:HD22	1:F:643:GLY:N	1.99	0.78
1:K:276:GLU:CD	1:K:318:PHE:HE2	1.91	0.78
1:K:441:LEU:HD21	1:K:499:SER:N	1.98	0.78
1:D:565:PHE:O	1:D:568:PHE:HB3	1.84	0.78
1:H:445:GLN:O	1:H:446:TYR:CD1	2.36	0.78
1:L:843:VAL:O	1:L:847:ASN:HB2	1.82	0.78
1:A:307:PHE:CE1	1:A:345:LEU:HD21	2.19	0.78
1:A:749:LYS:HD2	1:A:749:LYS:N	1.99	0.78
1:D:269:LEU:HA	1:D:272:ILE:HD12	1.65	0.78
1:D:363:TYR:CE1	1:D:383:CYS:SG	2.70	0.78
1:H:339:THR:CG2	1:H:340:ASP:H	1.96	0.78
1:A:238:ARG:HH21	1:A:356:SER:HG	1.32	0.78
1:D:278:LEU:HD22	1:D:280:LYS:HD3	1.66	0.78
1:H:307:PHE:CE1	1:H:345:LEU:HD21	2.18	0.78
1:H:273:VAL:HG21	1:H:457:SER:HB3	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:PRO:HG2	1:A:488:HIS:CG	2.18	0.77
1:C:627:TYR:HE2	1:C:628:TRP:CZ3	2.02	0.77
1:D:445:GLN:O	1:D:446:TYR:CD1	2.37	0.77
1:E:383:CYS:O	1:E:387:ILE:HG13	1.83	0.77
1:I:772:HIS:HB2	1:I:780:SER:HA	1.66	0.77
1:I:777:GLY:O	1:I:783:LEU:CD1	2.32	0.77
1:J:383:CYS:O	1:J:387:ILE:HG13	1.85	0.77
1:K:284:MET:N	1:K:284:MET:SD	2.56	0.77
1:D:544:ASN:HD22	1:L:641:ARG:NH1	1.82	0.77
1:I:772:HIS:O	1:I:780:SER:HA	1.84	0.77
1:D:878:ASP:HB3	1:D:881:VAL:HG22	1.66	0.77
1:E:441:LEU:HD21	1:E:499:SER:N	1.98	0.77
1:J:269:LEU:CA	1:J:272:ILE:HD12	2.12	0.77
1:J:441:LEU:HD21	1:J:498:VAL:HB	1.60	0.77
1:K:234:MET:O	1:K:237:ILE:HG22	1.85	0.77
1:E:276:GLU:OE2	1:E:318:PHE:CE2	2.38	0.77
1:E:455:VAL:HG12	1:E:501:GLY:N	1.98	0.77
1:A:269:LEU:CD2	1:A:457:SER:CB	2.58	0.77
1:G:780:SER:HB3	1:L:778:GLY:HA3	1.65	0.77
1:H:251:THR:CG2	1:H:252:LEU:N	2.47	0.77
1:E:269:LEU:HD21	1:E:457:SER:C	2.08	0.77
1:H:257:VAL:HG22	1:H:359:ASP:HA	1.66	0.77
1:I:609:PRO:HB2	1:I:610:ARG:C	2.10	0.77
1:A:434:PRO:CB	1:A:491:GLU:HG3	2.14	0.77
1:D:297:ASP:CG	1:D:300:ALA:HB3	2.10	0.77
1:J:454:GLY:O	1:J:500:THR:HG22	1.84	0.77
1:K:454:GLY:O	1:K:455:VAL:HG13	1.84	0.77
1:D:243:LYS:O	1:D:243:LYS:HG2	1.84	0.77
1:I:772:HIS:CB	1:I:780:SER:HA	2.15	0.77
1:J:485:PHE:CE2	1:J:500:THR:OG1	2.37	0.77
1:D:307:PHE:CE1	1:D:345:LEU:CD2	2.59	0.76
1:F:285:ILE:HD12	1:F:287:ARG:H	1.48	0.76
1:H:486:GLY:O	1:H:489:PRO:HD3	1.86	0.76
1:K:441:LEU:CG	1:K:498:VAL:CG1	2.62	0.76
1:A:278:LEU:O	1:A:278:LEU:HD13	1.85	0.76
1:D:297:ASP:OD2	1:D:300:ALA:HB3	1.85	0.76
1:E:269:LEU:HD23	1:E:269:LEU:C	2.10	0.76
1:G:780:SER:CB	1:L:778:GLY:HA3	2.14	0.76
1:A:241:LEU:O	1:A:244:VAL:HG23	1.86	0.76
1:C:260:SER:O	1:C:264:GLY:N	2.19	0.76
1:C:843:VAL:O	1:C:847:ASN:HB2	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:578:GLN:HA	1:F:838:VAL:HG21	1.67	0.76
1:K:854:PRO:HB2	1:K:855:ARG:HH12	1.49	0.76
1:D:855:ARG:HE	1:K:556:ALA:N	1.84	0.76
1:E:339:THR:HG23	1:E:340:ASP:N	1.97	0.76
1:H:269:LEU:HD21	1:H:457:SER:HB2	1.61	0.76
1:K:279:PRO:O	1:K:280:LYS:HD2	1.86	0.76
1:F:260:SER:O	1:F:264:GLY:N	2.18	0.76
1:A:486:GLY:O	1:A:489:PRO:HD3	1.85	0.76
1:J:377:ARG:HH21	1:J:377:ARG:HG2	1.51	0.76
1:E:272:ILE:HG23	1:E:278:LEU:H	1.50	0.76
1:H:285:ILE:CD1	1:H:286:THR:H	1.96	0.76
1:A:441:LEU:HD21	1:A:498:VAL:HB	1.63	0.76
1:A:445:GLN:O	1:A:446:TYR:CD1	2.38	0.76
1:E:376:LYS:NZ	1:E:376:LYS:HA	2.00	0.76
1:E:854:PRO:CB	1:E:855:ARG:NH1	2.49	0.76
1:J:441:LEU:CD2	1:J:498:VAL:CG1	2.58	0.76
1:G:615:ILE:HD11	1:G:803:ARG:HE	1.50	0.76
1:F:791:VAL:HG13	1:F:794:ARG:HH21	1.50	0.76
1:H:434:PRO:HB3	1:H:491:GLU:CB	2.16	0.76
1:J:272:ILE:CG2	1:J:277:PHE:HA	2.16	0.76
1:K:272:ILE:HG21	1:K:277:PHE:HD1	1.50	0.76
1:K:279:PRO:HB3	1:K:322:GLN:HA	1.68	0.76
1:A:433:GLU:O	1:A:436:LYS:HB2	1.86	0.75
1:D:270:GLU:HA	1:D:273:VAL:HG22	1.66	0.75
1:F:843:VAL:O	1:F:847:ASN:HB2	1.84	0.75
1:H:339:THR:CG2	1:H:340:ASP:N	2.49	0.75
1:A:260:SER:O	1:A:264:GLY:CA	2.34	0.75
1:I:429:MET:HE2	1:I:437:GLY:HA2	1.67	0.75
1:B:780:SER:HB3	1:I:776:ALA:O	1.86	0.75
1:C:578:GLN:HA	1:C:838:VAL:HG21	1.69	0.75
1:K:275:HIS:H	1:K:275:HIS:CD2	2.03	0.75
1:E:854:PRO:HD2	1:E:855:ARG:NH1	2.01	0.75
1:H:285:ILE:HG13	1:H:332:VAL:HG22	1.68	0.75
1:J:441:LEU:HD21	1:J:499:SER:N	2.01	0.75
1:L:575:PRO:O	1:L:578:GLN:HB3	1.87	0.75
1:E:454:GLY:O	1:E:500:THR:HB	1.86	0.75
1:H:640:THR:HG21	1:H:706:LYS:HA	1.67	0.75
1:J:273:VAL:HG21	1:J:457:SER:CB	2.16	0.75
1:K:441:LEU:HG	1:K:498:VAL:CG1	2.10	0.75
1:F:878:ASP:HB3	1:F:881:VAL:HG12	1.69	0.75
1:H:363:TYR:CE1	1:H:383:CYS:SG	2.77	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:267:SER:HB3	1:K:396:ILE:HG13	1.69	0.75
1:K:434:PRO:CB	1:K:491:GLU:HG3	2.16	0.75
1:A:269:LEU:HA	1:A:272:ILE:CD1	2.17	0.74
1:D:273:VAL:HG21	1:D:457:SER:HB3	1.67	0.74
1:F:524:THR:O	1:F:528:ILE:HG13	1.87	0.74
1:K:279:PRO:HB3	1:K:322:GLN:CA	2.17	0.74
1:A:269:LEU:HD11	1:A:457:SER:C	2.09	0.74
1:A:284:MET:SD	1:A:284:MET:N	2.59	0.74
1:B:665:ASP:OD1	1:B:676:ARG:NH1	2.20	0.74
1:B:772:HIS:CD2	1:B:775:GLY:O	2.40	0.74
1:C:609:PRO:HB2	1:C:611:GLU:CA	2.16	0.74
1:J:279:PRO:HB3	1:J:322:GLN:CB	2.17	0.74
1:J:279:PRO:HB3	1:J:322:GLN:HA	1.69	0.74
1:J:382:LEU:C	1:J:382:LEU:HD12	2.12	0.74
1:J:434:PRO:CB	1:J:491:GLU:HG3	2.16	0.74
1:J:433:GLU:O	1:J:436:LYS:HB2	1.87	0.74
1:D:562:LYS:HE3	1:K:562:LYS:HE2	1.69	0.74
1:D:768:VAL:HG23	1:D:770:GLY:H	1.52	0.74
1:E:272:ILE:CG2	1:E:278:LEU:H	1.99	0.74
1:E:485:PHE:CD2	1:E:492:PHE:CE1	2.76	0.74
1:D:749:LYS:H	1:D:749:LYS:HD2	1.52	0.74
1:E:285:ILE:CD1	1:E:286:THR:N	2.47	0.74
1:J:251:THR:HG22	1:J:252:LEU:N	2.01	0.74
1:B:605:LEU:HD13	1:B:606:SER:O	1.87	0.74
1:G:791:VAL:HG13	1:G:794:ARG:HH21	1.53	0.74
1:H:251:THR:CG2	1:H:252:LEU:H	1.98	0.74
1:K:273:VAL:HG21	1:K:457:SER:HB3	1.70	0.74
1:C:259:GLY:HA2	1:C:408:ALA:HB2	1.70	0.74
1:D:376:LYS:HE2	1:D:376:LYS:N	2.03	0.74
1:F:615:ILE:HD11	1:F:803:ARG:HE	1.51	0.74
1:K:272:ILE:HG22	1:K:277:PHE:HA	1.68	0.74
1:D:244:VAL:HB	1:D:248:SER:OG	1.86	0.74
1:I:775:GLY:HA2	1:I:782:ALA:HB3	1.68	0.74
1:D:555:ALA:HB3	1:K:855:ARG:HD2	1.69	0.74
1:H:749:LYS:H	1:H:749:LYS:HD2	1.52	0.74
1:E:229:PHE:O	1:E:233:LYS:HG2	1.88	0.74
1:J:276:GLU:OE2	1:J:318:PHE:CE2	2.41	0.74
1:K:257:VAL:CG2	1:K:359:ASP:HA	2.17	0.74
1:K:444:ARG:O	1:K:447:PRO:HD3	1.88	0.74
1:D:434:PRO:CB	1:D:491:GLU:HG3	2.18	0.73
1:E:269:LEU:HD21	1:E:457:SER:CA	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:269:LEU:HD23	1:J:457:SER:OG	1.88	0.73
1:H:426:ILE:HD11	1:H:440:ILE:CG2	1.89	0.73
1:K:269:LEU:HA	1:K:272:ILE:CD1	2.15	0.73
1:A:272:ILE:HG22	1:A:277:PHE:HA	1.68	0.73
1:A:279:PRO:O	1:A:280:LYS:HD2	1.87	0.73
1:D:886:ASP:HA	1:D:889:ARG:HG2	1.69	0.73
1:E:434:PRO:HB3	1:E:491:GLU:CG	2.19	0.73
1:H:455:VAL:HG12	1:H:501:GLY:H	1.53	0.73
1:J:308:PRO:HG3	1:J:344:ARG:HB2	1.70	0.73
1:D:455:VAL:HG12	1:D:501:GLY:H	1.51	0.73
1:E:472:ASN:HD21	1:E:475:ALA:HB3	1.54	0.73
1:I:472:ASN:OD1	1:I:475:ALA:HB3	1.88	0.73
1:K:657:GLN:HE22	1:K:684:ALA:HA	1.54	0.73
1:A:811:GLN:O	1:A:814:THR:HG22	1.89	0.73
1:D:251:THR:HG22	1:D:252:LEU:H	1.52	0.73
1:E:279:PRO:O	1:E:280:LYS:HD2	1.88	0.73
1:E:286:THR:O	1:E:361:PRO:HG3	1.89	0.73
1:H:229:PHE:O	1:H:233:LYS:HG2	1.87	0.73
1:L:609:PRO:HB2	1:L:611:GLU:CB	2.14	0.73
1:D:240:LEU:N	1:D:240:LEU:HD23	2.04	0.73
1:F:609:PRO:CB	1:F:611:GLU:HB2	2.18	0.73
1:H:278:LEU:CD2	1:H:280:LYS:HG2	2.19	0.73
1:I:328:LEU:HD13	1:I:343:ILE:HD13	1.71	0.73
1:J:657:GLN:HE22	1:J:684:ALA:HA	1.53	0.73
1:A:273:VAL:HG21	1:A:457:SER:CB	2.18	0.73
1:J:363:TYR:HD2	1:J:407:THR:HB	1.54	0.73
1:K:572:PHE:O	1:K:576:GLN:NE2	2.21	0.73
1:B:863:GLU:O	1:B:867:ALA:HB3	1.88	0.73
1:E:272:ILE:HG21	1:E:277:PHE:HD1	1.54	0.73
1:E:478:ASN:HD21	1:E:482:LYS:HZ1	0.75	0.73
1:F:328:LEU:HD13	1:F:343:ILE:HD13	1.69	0.73
1:H:456:ILE:O	1:H:481:GLU:OE2	2.07	0.73
1:A:671:LYS:N	1:A:671:LYS:HD2	2.04	0.73
1:B:264:GLY:HA2	1:B:267:SER:HB3	1.71	0.73
1:A:485:PHE:HE2	1:A:500:THR:OG1	1.68	0.73
1:D:285:ILE:HG13	1:D:332:VAL:HG22	1.70	0.73
1:K:377:ARG:HG2	1:K:377:ARG:HH21	1.53	0.73
1:K:434:PRO:HG2	1:K:488:HIS:CG	2.23	0.73
1:L:360:LEU:HB2	1:L:361:PRO:HD2	1.71	0.73
1:A:279:PRO:HB3	1:A:322:GLN:CA	2.19	0.72
1:H:269:LEU:HD11	1:H:457:SER:C	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:ILE:CG2	1:A:278:LEU:H	2.02	0.72
1:C:615:ILE:HD11	1:C:803:ARG:HE	1.53	0.72
1:H:237:ILE:HD12	1:H:241:LEU:HD11	1.71	0.72
1:D:267:SER:HB2	1:D:396:ILE:CD1	2.20	0.72
1:D:273:VAL:HG11	1:D:457:SER:CB	2.16	0.72
1:K:843:VAL:HG21	1:L:704:PRO:HA	1.71	0.72
1:D:286:THR:O	1:D:361:PRO:HG3	1.88	0.72
1:K:526:GLU:OE1	1:K:530:ARG:NH1	2.22	0.72
1:A:297:ASP:OD2	1:A:300:ALA:HB3	1.88	0.72
1:H:284:MET:N	1:H:284:MET:SD	2.62	0.72
1:H:671:LYS:H	1:H:671:LYS:HD2	1.53	0.72
1:H:275:HIS:CG	1:H:276:GLU:H	2.08	0.72
1:K:363:TYR:CE1	1:K:383:CYS:SG	2.77	0.72
1:C:853:PHE:HB3	1:C:854:PRO:HD3	1.70	0.72
1:H:240:LEU:HD23	1:H:240:LEU:N	2.05	0.72
1:I:609:PRO:CB	1:I:611:GLU:HB2	2.20	0.72
1:K:639:LEU:O	1:K:642:LEU:HD23	1.90	0.72
1:A:349:SER:HB3	1:A:352:ILE:HG23	1.70	0.72
1:A:441:LEU:CG	1:A:498:VAL:CG1	2.60	0.72
1:A:488:HIS:HB3	1:A:491:GLU:CG	2.19	0.72
1:D:339:THR:HG23	1:D:340:ASP:N	2.03	0.72
1:E:287:ARG:HH11	1:E:287:ARG:CG	2.03	0.72
1:H:339:THR:HG23	1:H:340:ASP:H	1.51	0.72
1:A:246:GLN:HG2	1:A:247:GLY:N	2.04	0.72
1:F:854:PRO:HB2	1:F:855:ARG:CZ	2.19	0.72
1:H:286:THR:HB	1:H:361:PRO:HB3	1.70	0.72
1:E:267:SER:HB2	1:E:396:ILE:CD1	2.20	0.72
1:E:485:PHE:HD2	1:E:492:PHE:O	1.72	0.72
1:G:773:PRO:O	1:G:782:ALA:CB	2.38	0.72
1:E:434:PRO:HB2	1:E:491:GLU:HG3	1.72	0.71
1:E:791:VAL:HG13	1:E:794:ARG:HH21	1.55	0.71
1:K:878:ASP:CB	1:K:881:VAL:HG22	2.19	0.71
1:C:806:ALA:O	1:C:809:SER:HB3	1.89	0.71
1:D:269:LEU:CD2	1:D:457:SER:CB	2.62	0.71
1:H:230:ILE:O	1:H:234:MET:HG3	1.90	0.71
1:J:285:ILE:HG12	1:J:287:ARG:HB2	1.72	0.71
1:J:499:SER:O	1:J:500:THR:HG23	1.90	0.71
1:K:285:ILE:HG12	1:K:287:ARG:HB2	1.72	0.71
1:H:278:LEU:HD21	1:H:280:LYS:HD3	1.70	0.71
1:D:237:ILE:HD11	1:D:897:VAL:HG13	1.73	0.71
1:D:269:LEU:HD11	1:D:457:SER:C	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:THR:O	1:D:361:PRO:HB3	1.91	0.71
1:H:276:GLU:CD	1:H:318:PHE:HE2	1.97	0.71
1:K:229:PHE:O	1:K:233:LYS:HG2	1.91	0.71
1:K:235:ILE:HD12	1:K:235:ILE:O	1.89	0.71
1:D:855:ARG:CD	1:K:555:ALA:CB	2.56	0.71
1:H:238:ARG:HA	1:H:241:LEU:HD12	1.72	0.71
1:H:456:ILE:HD12	1:H:457:SER:N	2.04	0.71
1:C:878:ASP:HB3	1:C:881:VAL:HG12	1.72	0.71
1:J:270:GLU:HA	1:J:273:VAL:HG22	1.71	0.71
1:B:383:CYS:O	1:B:387:ILE:HG13	1.90	0.71
1:B:780:SER:OG	1:B:783:LEU:HB2	1.91	0.71
1:C:284:MET:N	1:C:284:MET:SD	2.63	0.71
1:D:453:VAL:HG11	1:D:505:LEU:HB2	1.72	0.71
1:H:279:PRO:CB	1:H:322:GLN:HA	2.20	0.71
1:K:230:ILE:O	1:K:234:MET:HG3	1.90	0.71
1:B:863:GLU:O	1:B:867:ALA:CB	2.39	0.71
1:H:286:THR:O	1:H:361:PRO:HB3	1.90	0.71
1:H:508:LYS:O	1:H:512:VAL:HG23	1.90	0.71
1:K:286:THR:O	1:K:361:PRO:CG	2.38	0.71
1:K:574:ARG:H	1:K:575:PRO:HD2	1.56	0.71
1:C:326:THR:O	1:C:329:ASN:HB2	1.91	0.71
1:D:871:LEU:O	1:D:871:LEU:HD22	1.91	0.71
1:H:488:HIS:CB	1:H:491:GLU:HG2	2.18	0.71
1:K:229:PHE:CD1	1:K:232:LYS:HD2	2.26	0.71
1:L:285:ILE:HD13	1:L:332:VAL:HG22	1.73	0.71
1:D:229:PHE:O	1:D:233:LYS:HG2	1.90	0.71
1:D:272:ILE:CG2	1:D:278:LEU:H	2.04	0.71
1:D:556:ALA:HB2	1:K:855:ARG:HH21	1.56	0.71
1:J:272:ILE:HG21	1:J:277:PHE:HD1	1.56	0.71
1:B:609:PRO:N	1:B:610:ARG:HA	2.06	0.70
1:D:441:LEU:HB3	1:D:498:VAL:HG11	1.73	0.70
1:E:272:ILE:HG21	1:E:277:PHE:CD1	2.26	0.70
1:G:889:ARG:HH22	1:G:893:LEU:HD12	1.55	0.70
1:B:783:LEU:HD13	1:I:777:GLY:HA2	1.71	0.70
1:D:285:ILE:CD1	1:D:286:THR:H	1.90	0.70
1:E:276:GLU:OE1	1:E:303:ASP:CG	2.35	0.70
1:K:286:THR:O	1:K:361:PRO:HB3	1.92	0.70
1:D:276:GLU:HG2	1:D:277:PHE:N	2.04	0.70
1:D:396:ILE:HG22	1:D:425:VAL:HB	1.73	0.70
1:I:257:VAL:HG12	1:I:394:LEU:HB3	1.71	0.70
1:I:285:ILE:HD13	1:I:332:VAL:HG22	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:441:LEU:HD21	1:J:499:SER:H	1.56	0.70
1:K:478:ASN:ND2	1:K:482:LYS:HZ1	1.90	0.70
1:D:270:GLU:C	1:D:273:VAL:HG22	2.16	0.70
1:E:229:PHE:HA	1:E:232:LYS:HG2	1.74	0.70
1:D:434:PRO:HB3	1:D:491:GLU:HG3	1.71	0.70
1:D:750:LYS:NZ	1:E:779:PHE:CE2	2.60	0.70
1:E:260:SER:H	1:E:263:SER:HB3	1.57	0.70
1:J:252:LEU:HD23	1:J:524:THR:HG21	1.74	0.70
1:K:485:PHE:CZ	1:K:500:THR:OG1	2.42	0.70
1:C:903:GLU:HG3	1:C:906:ARG:NH2	2.07	0.70
1:F:611:GLU:N	1:F:612:PRO:HD2	2.07	0.70
1:H:308:PRO:HG3	1:H:344:ARG:HG3	1.73	0.70
1:H:322:GLN:O	1:H:326:THR:OG1	2.05	0.70
1:A:615:ILE:H	1:A:615:ILE:HD12	1.55	0.70
1:H:263:SER:HA	1:H:266:SER:OG	1.90	0.70
1:H:284:MET:HG2	1:H:286:THR:CG2	2.20	0.70
1:D:339:THR:HG23	1:D:340:ASP:H	1.57	0.70
1:D:855:ARG:HG3	1:K:552:SER:HA	1.74	0.70
1:E:269:LEU:O	1:E:273:VAL:HG13	1.91	0.70
1:E:396:ILE:HG22	1:E:425:VAL:HB	1.74	0.70
1:J:269:LEU:HA	1:J:272:ILE:CD1	2.17	0.70
1:K:269:LEU:CD2	1:K:457:SER:CB	2.62	0.70
1:K:486:GLY:O	1:K:489:PRO:HD3	1.91	0.70
1:D:234:MET:O	1:D:237:ILE:HG22	1.92	0.70
1:E:265:LYS:O	1:E:268:VAL:HG23	1.92	0.70
1:E:267:SER:HB3	1:E:396:ILE:HG13	1.74	0.70
1:K:255:ILE:HD11	1:K:355:LEU:HG	1.74	0.70
1:A:285:ILE:HG13	1:A:332:VAL:HG22	1.72	0.69
1:A:363:TYR:N	1:A:363:TYR:CD1	2.60	0.69
1:D:268:VAL:O	1:D:272:ILE:HG13	1.91	0.69
1:E:286:THR:O	1:E:361:PRO:CG	2.40	0.69
1:E:485:PHE:HD2	1:E:492:PHE:CD1	2.10	0.69
1:E:642:LEU:HD12	1:E:643:GLY:N	2.07	0.69
1:H:863:GLU:O	1:H:867:ALA:HB3	1.92	0.69
1:A:375:LEU:N	1:A:375:LEU:HD23	2.06	0.69
1:B:780:SER:N	1:I:777:GLY:N	2.39	0.69
1:D:441:LEU:HD23	1:D:498:VAL:HB	0.70	0.69
1:E:286:THR:HB	1:E:361:PRO:CB	2.20	0.69
1:E:454:GLY:O	1:E:500:THR:CG2	2.40	0.69
1:H:276:GLU:HG2	1:H:277:PHE:N	2.06	0.69
1:I:665:ASP:OD1	1:I:676:ARG:NH1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:LYS:HD3	1:A:233:LYS:HZ1	1.57	0.69
1:K:272:ILE:CG2	1:K:278:LEU:CD1	2.65	0.69
1:L:627:TYR:OH	1:L:631:GLN:NE2	2.25	0.69
1:C:854:PRO:HB2	1:C:855:ARG:NH2	2.07	0.69
1:E:574:ARG:H	1:E:575:PRO:HD2	1.56	0.69
1:E:854:PRO:CD	1:E:855:ARG:NH1	2.56	0.69
1:I:578:GLN:HA	1:I:838:VAL:HG21	1.74	0.69
1:J:472:ASN:ND2	1:J:475:ALA:HB3	2.05	0.69
1:J:576:GLN:NE2	1:J:576:GLN:H	1.90	0.69
1:K:454:GLY:O	1:K:500:THR:HG22	1.92	0.69
1:A:255:ILE:HA	1:A:392:ILE:O	1.92	0.69
1:C:863:GLU:O	1:C:867:ALA:CB	2.41	0.69
1:D:246:GLN:OE1	1:D:246:GLN:N	2.25	0.69
1:E:272:ILE:CG2	1:E:278:LEU:HD12	2.17	0.69
1:E:878:ASP:HB3	1:E:881:VAL:HG22	1.74	0.69
1:H:287:ARG:HH11	1:H:287:ARG:CG	2.05	0.69
1:K:308:PRO:HG3	1:K:344:ARG:HB2	1.72	0.69
1:B:285:ILE:HD12	1:B:287:ARG:H	1.58	0.69
1:D:279:PRO:HB3	1:D:322:GLN:CA	2.23	0.69
1:I:772:HIS:CD2	1:I:779:PHE:H	2.10	0.69
1:J:272:ILE:CG2	1:J:278:LEU:CD1	2.59	0.69
1:J:297:ASP:OD1	1:J:300:ALA:CB	2.40	0.69
1:L:387:ILE:O	1:L:421:ARG:NH2	2.24	0.69
1:E:276:GLU:CD	1:E:318:PHE:HE2	2.01	0.69
1:E:278:LEU:HD21	1:E:280:LYS:HD3	1.75	0.69
1:G:780:SER:OG	1:L:778:GLY:HA3	1.93	0.69
1:H:225:ASP:CB	1:H:229:PHE:CZ	2.68	0.69
1:H:242:GLN:HE22	1:H:344:ARG:HD2	1.58	0.69
1:H:363:TYR:N	1:H:363:TYR:HD1	1.90	0.69
1:K:272:ILE:HG12	1:K:280:LYS:HG3	1.72	0.69
1:K:704:PRO:HA	1:L:843:VAL:HG21	1.75	0.69
1:B:575:PRO:O	1:B:578:GLN:HB3	1.93	0.69
1:E:269:LEU:HA	1:E:272:ILE:HD12	1.74	0.69
1:E:486:GLY:O	1:E:489:PRO:HD3	1.93	0.69
1:G:775:GLY:O	1:G:776:ALA:CB	2.41	0.69
1:H:294:LEU:HB2	1:H:355:LEU:H	1.56	0.69
1:J:267:SER:HB3	1:J:396:ILE:HG13	1.73	0.69
1:K:257:VAL:HG22	1:K:359:ASP:HA	1.75	0.69
1:L:664:LEU:HD23	1:L:676:ARG:HG3	1.74	0.69
1:L:665:ASP:OD1	1:L:676:ARG:NH1	2.26	0.69
1:A:441:LEU:HD23	1:A:498:VAL:HG11	1.69	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:360:LEU:HB2	1:C:361:PRO:HD2	1.74	0.69
1:E:230:ILE:O	1:E:234:MET:HG3	1.93	0.69
1:E:299:GLU:O	1:E:299:GLU:HG3	1.92	0.69
1:I:777:GLY:O	1:I:783:LEU:HD11	1.92	0.69
1:A:279:PRO:HB3	1:A:322:GLN:HA	1.73	0.68
1:A:456:ILE:HD12	1:A:457:SER:N	2.08	0.68
1:C:609:PRO:HD2	1:C:610:ARG:O	1.93	0.68
1:C:863:GLU:O	1:C:867:ALA:HB3	1.94	0.68
1:D:555:ALA:CB	1:K:855:ARG:HD3	2.24	0.68
1:E:499:SER:O	1:E:500:THR:HG23	1.93	0.68
1:I:569:ALA:HB1	1:I:850:TYR:CE2	2.27	0.68
1:K:310:LEU:N	1:K:310:LEU:HD23	2.07	0.68
1:A:455:VAL:HG12	1:A:501:GLY:CA	2.22	0.68
1:E:268:VAL:O	1:E:272:ILE:HG13	1.93	0.68
1:E:279:PRO:CG	1:E:325:LEU:HD21	2.20	0.68
1:H:269:LEU:HD23	1:H:269:LEU:C	2.18	0.68
1:A:269:LEU:O	1:A:273:VAL:HG13	1.93	0.68
1:D:363:TYR:N	1:D:363:TYR:CD1	2.61	0.68
1:D:434:PRO:HG2	1:D:488:HIS:ND1	2.08	0.68
1:E:278:LEU:CD2	1:E:280:LYS:HD3	2.23	0.68
1:H:272:ILE:CG2	1:H:278:LEU:H	2.06	0.68
1:I:776:ALA:CA	1:I:783:LEU:HD12	2.23	0.68
1:C:224:ASP:CG	1:C:227:MET:HG3	2.18	0.68
1:D:272:ILE:HG23	1:D:278:LEU:HD13	1.70	0.68
1:E:224:ASP:OD2	1:E:227:MET:HB2	1.93	0.68
1:E:279:PRO:O	1:E:280:LYS:CD	2.41	0.68
1:E:854:PRO:CG	1:E:855:ARG:NH1	2.57	0.68
1:I:772:HIS:HB2	1:I:779:PHE:O	1.94	0.68
1:J:269:LEU:HD21	1:J:457:SER:CA	2.23	0.68
1:J:456:ILE:O	1:J:481:GLU:OE2	2.11	0.68
1:K:260:SER:N	1:K:263:SER:HB3	2.08	0.68
1:K:286:THR:CB	1:K:361:PRO:HB3	2.23	0.68
1:H:903:GLU:HG2	1:H:906:ARG:HH21	1.58	0.68
1:J:434:PRO:HB2	1:J:491:GLU:HG3	1.75	0.68
1:J:485:PHE:CD2	1:J:492:PHE:O	2.42	0.68
1:K:255:ILE:HG12	1:K:513:LEU:HD21	1.75	0.68
1:K:287:ARG:HH11	1:K:287:ARG:CG	2.07	0.68
1:K:454:GLY:O	1:K:500:THR:CG2	2.41	0.68
1:A:694:THR:HG21	1:A:845:MET:HB2	1.73	0.68
1:A:878:ASP:HB3	1:A:881:VAL:CG2	2.21	0.68
1:B:319:SER:O	1:B:322:GLN:HB3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:ILE:HD12	1:C:287:ARG:N	2.02	0.68
1:D:478:ASN:CG	1:D:482:LYS:NZ	2.51	0.68
1:D:485:PHE:HA	1:D:492:PHE:HE1	1.58	0.68
1:E:257:VAL:HG22	1:E:359:ASP:HA	1.76	0.68
1:E:434:PRO:HG2	1:E:488:HIS:CG	2.28	0.68
1:J:267:SER:HB2	1:J:396:ILE:HD12	1.74	0.68
1:J:279:PRO:HB3	1:J:322:GLN:CA	2.24	0.68
1:D:508:LYS:O	1:D:512:VAL:HG23	1.92	0.68
1:E:272:ILE:CG2	1:E:278:LEU:CD1	2.63	0.68
1:E:273:VAL:HG21	1:E:457:SER:HB3	1.76	0.68
1:H:376:LYS:NZ	1:H:379:ILE:HD12	2.08	0.68
1:J:272:ILE:HG23	1:J:278:LEU:H	1.59	0.68
1:C:665:ASP:OD1	1:C:676:ARG:NH1	2.26	0.68
1:D:265:LYS:O	1:D:268:VAL:HG23	1.93	0.68
1:G:434:PRO:HG2	1:G:488:HIS:CG	2.29	0.68
1:G:773:PRO:CB	1:G:781:ALA:HB3	2.23	0.68
1:J:269:LEU:CD2	1:J:457:SER:HB2	2.18	0.68
1:A:363:TYR:CE1	1:A:383:CYS:SG	2.78	0.68
1:H:363:TYR:N	1:H:363:TYR:CD1	2.60	0.68
1:J:229:PHE:HA	1:J:232:LYS:HG2	1.75	0.68
1:J:420:GLU:HG3	1:J:449:LYS:HE2	1.76	0.68
1:K:485:PHE:CD2	1:K:492:PHE:O	2.46	0.68
1:A:237:ILE:HD12	1:A:241:LEU:HD11	1.74	0.68
1:E:454:GLY:O	1:E:500:THR:CB	2.42	0.68
1:J:260:SER:O	1:J:264:GLY:CA	2.42	0.68
1:J:818:LYS:HE3	1:J:819:TYR:CZ	2.29	0.68
1:G:775:GLY:O	1:G:776:ALA:HB3	1.93	0.67
1:D:260:SER:O	1:D:264:GLY:CA	2.41	0.67
1:D:556:ALA:HA	1:K:855:ARG:NH2	2.09	0.67
1:E:791:VAL:HG13	1:E:794:ARG:NH2	2.08	0.67
1:J:263:SER:HA	1:J:266:SER:OG	1.94	0.67
1:D:252:LEU:HD23	1:D:524:THR:HG21	1.76	0.67
1:D:278:LEU:HB2	1:D:279:PRO:CD	2.24	0.67
1:D:753:GLU:CG	1:E:750:LYS:HE2	2.24	0.67
1:E:300:ALA:C	1:E:301:LYS:HD3	2.20	0.67
1:F:665:ASP:OD1	1:F:676:ARG:NH1	2.27	0.67
1:J:230:ILE:O	1:J:234:MET:HG3	1.94	0.67
1:J:278:LEU:HB2	1:J:279:PRO:CD	2.24	0.67
1:J:381:GLU:OE1	1:J:381:GLU:HA	1.94	0.67
1:K:286:THR:O	1:K:361:PRO:HG3	1.94	0.67
1:K:434:PRO:HB2	1:K:491:GLU:HG3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:508:LYS:O	1:K:512:VAL:HG23	1.94	0.67
1:D:499:SER:O	1:D:500:THR:CG2	2.42	0.67
1:F:434:PRO:HG2	1:F:488:HIS:CG	2.30	0.67
1:J:276:GLU:HG2	1:J:277:PHE:N	2.10	0.67
1:J:441:LEU:HB3	1:J:498:VAL:HG11	1.77	0.67
1:L:272:ILE:HG23	1:L:277:PHE:HA	1.76	0.67
1:G:383:CYS:O	1:G:387:ILE:HG13	1.95	0.67
1:H:387:ILE:CG2	1:H:415:VAL:HG21	2.24	0.67
1:J:485:PHE:CD2	1:J:492:PHE:HD1	2.11	0.67
1:K:276:GLU:OE2	1:K:318:PHE:CD2	2.47	0.67
1:D:492:PHE:O	1:D:492:PHE:HD1	1.78	0.67
1:A:272:ILE:HG23	1:A:278:LEU:H	1.60	0.67
1:A:339:THR:HG23	1:A:340:ASP:N	2.09	0.67
1:D:225:ASP:OD1	1:D:225:ASP:N	2.28	0.67
1:I:704:PRO:HA	1:J:843:VAL:HG21	1.77	0.67
1:J:363:TYR:CE1	1:J:383:CYS:SG	2.74	0.67
1:K:268:VAL:O	1:K:272:ILE:HG13	1.95	0.67
1:K:272:ILE:HG21	1:K:277:PHE:CD1	2.30	0.67
1:L:854:PRO:HB2	1:L:855:ARG:CZ	2.25	0.67
1:A:308:PRO:HG3	1:A:344:ARG:HB2	1.78	0.66
1:D:854:PRO:HD2	1:D:855:ARG:NH1	2.10	0.66
1:E:472:ASN:HD21	1:E:475:ALA:CB	2.07	0.66
1:H:265:LYS:O	1:H:268:VAL:HG23	1.94	0.66
1:H:434:PRO:CG	1:H:488:HIS:CD2	2.78	0.66
1:E:441:LEU:HD21	1:E:498:VAL:CB	2.16	0.66
1:E:455:VAL:HG12	1:E:501:GLY:CA	2.24	0.66
1:H:307:PHE:N	1:H:307:PHE:HD1	1.93	0.66
1:I:284:MET:SD	1:I:284:MET:N	2.66	0.66
1:I:843:VAL:HG21	1:J:704:PRO:HA	1.78	0.66
1:J:270:GLU:O	1:J:273:VAL:HG22	1.94	0.66
1:J:694:THR:HG21	1:J:845:MET:HE3	1.77	0.66
1:K:270:GLU:HA	1:K:273:VAL:HG22	1.75	0.66
1:A:488:HIS:HB3	1:A:491:GLU:HG2	1.78	0.66
1:E:307:PHE:CE1	1:E:345:LEU:CD2	2.78	0.66
1:E:472:ASN:ND2	1:E:475:ALA:CB	2.57	0.66
1:F:863:GLU:O	1:F:867:ALA:HB3	1.94	0.66
1:J:363:TYR:CD2	1:J:407:THR:HB	2.30	0.66
1:J:441:LEU:HD23	1:J:498:VAL:HB	0.69	0.66
1:K:278:LEU:O	1:K:278:LEU:HD13	1.96	0.66
1:B:608:ALA:C	1:B:610:ARG:HA	2.20	0.66
1:B:642:LEU:HD22	1:B:643:GLY:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:750:LYS:HE2	1:E:753:GLU:OE1	1.94	0.66
1:H:499:SER:O	1:H:500:THR:CG2	2.43	0.66
1:B:355:LEU:HD23	1:B:357:LEU:HD22	1.78	0.66
1:B:723:VAL:HG21	1:B:824:VAL:HA	1.77	0.66
1:D:562:LYS:CE	1:K:562:LYS:HE2	2.24	0.66
1:K:231:THR:O	1:K:235:ILE:HG22	1.95	0.66
1:D:285:ILE:CG1	1:D:287:ARG:H	2.09	0.66
1:D:287:ARG:HH11	1:D:287:ARG:CG	2.05	0.66
1:E:284:MET:HG2	1:E:286:THR:HG22	1.76	0.66
1:H:876:ARG:HB3	1:H:882:ARG:HH21	1.61	0.66
1:J:230:ILE:HG13	1:J:904:LEU:HD11	1.78	0.66
1:E:259:GLY:HA2	1:E:408:ALA:HB2	1.77	0.66
1:E:272:ILE:CG2	1:E:277:PHE:HA	2.24	0.66
1:G:672:HIS:HD2	1:G:877:GLU:HB2	1.61	0.66
1:J:478:ASN:CG	1:J:482:LYS:NZ	2.53	0.66
1:K:307:PHE:CD1	1:K:345:LEU:HD21	2.30	0.66
1:K:480:ASN:HA	1:K:483:ASN:OD1	1.94	0.66
1:A:269:LEU:HD21	1:A:457:SER:CA	2.26	0.66
1:D:441:LEU:HD21	1:D:498:VAL:CB	2.19	0.66
1:D:672:HIS:HA	1:D:877:GLU:CD	2.21	0.66
1:E:393:ILE:HG23	1:E:422:THR:HB	1.78	0.66
1:G:780:SER:CA	1:L:778:GLY:O	2.44	0.66
1:G:863:GLU:O	1:G:867:ALA:HB3	1.96	0.66
1:J:543:TYR:O	1:J:546:GLN:HG2	1.95	0.66
1:L:257:VAL:HG12	1:L:394:LEU:HB3	1.76	0.66
1:A:485:PHE:CD2	1:A:492:PHE:O	2.46	0.66
1:D:363:TYR:N	1:D:363:TYR:HD1	1.94	0.66
1:J:388:ARG:O	1:J:421:ARG:NH2	2.29	0.66
1:J:430:ASP:C	1:J:430:ASP:OD1	2.37	0.66
1:K:276:GLU:OE1	1:K:303:ASP:CG	2.39	0.66
1:K:396:ILE:HG22	1:K:425:VAL:HB	1.78	0.66
1:A:267:SER:HB3	1:A:396:ILE:HG13	1.77	0.66
1:C:664:LEU:HD23	1:C:676:ARG:HG3	1.77	0.66
1:E:454:GLY:O	1:E:500:THR:HG22	1.96	0.66
1:D:270:GLU:O	1:D:273:VAL:CG2	2.42	0.65
1:E:441:LEU:CD2	1:E:498:VAL:HG12	2.15	0.65
1:G:528:ILE:O	1:G:531:GLU:HG2	1.97	0.65
1:H:268:VAL:O	1:H:272:ILE:HG13	1.96	0.65
1:K:433:GLU:O	1:K:436:LYS:HB2	1.95	0.65
1:D:272:ILE:HG22	1:D:277:PHE:HA	1.77	0.65
1:D:441:LEU:CD2	1:D:498:VAL:HG12	2.19	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:478:ASN:HD21	1:D:482:LYS:NZ	1.78	0.65
1:E:818:LYS:HE3	1:E:819:TYR:CZ	2.31	0.65
1:G:322:GLN:O	1:G:326:THR:OG1	2.05	0.65
1:K:275:HIS:CD2	1:K:275:HIS:N	2.63	0.65
1:A:363:TYR:CD2	1:A:407:THR:HB	2.31	0.65
1:E:230:ILE:HG13	1:E:904:LEU:HD11	1.77	0.65
1:G:772:HIS:C	1:G:781:ALA:H	2.03	0.65
1:H:272:ILE:HG21	1:H:277:PHE:HD1	1.61	0.65
1:K:269:LEU:CA	1:K:272:ILE:HD12	2.20	0.65
1:K:285:ILE:CD1	1:K:286:THR:N	2.59	0.65
1:B:360:LEU:HB2	1:B:361:PRO:HD2	1.77	0.65
1:E:299:GLU:O	1:E:299:GLU:CG	2.44	0.65
1:H:434:PRO:CG	1:H:488:HIS:CG	2.79	0.65
1:K:238:ARG:NH2	1:K:356:SER:OG	2.30	0.65
1:A:285:ILE:CD1	1:A:286:THR:N	2.48	0.65
1:D:257:VAL:CG2	1:D:359:ASP:HA	2.26	0.65
1:D:267:SER:HB2	1:D:396:ILE:HD11	1.78	0.65
1:D:434:PRO:CG	1:D:488:HIS:CG	2.80	0.65
1:H:376:LYS:HZ2	1:H:379:ILE:HD12	1.60	0.65
1:J:233:LYS:HE2	1:J:233:LYS:CA	2.26	0.65
1:J:272:ILE:CG2	1:J:278:LEU:H	2.10	0.65
1:A:275:HIS:CG	1:A:276:GLU:H	2.15	0.65
1:B:453:VAL:HG11	1:B:505:LEU:HB2	1.78	0.65
1:E:269:LEU:HD21	1:E:457:SER:O	1.95	0.65
1:G:773:PRO:HB3	1:G:781:ALA:HB3	1.79	0.65
1:K:229:PHE:HA	1:K:232:LYS:HG2	1.79	0.65
1:L:832:LYS:O	1:L:835:GLN:HG2	1.97	0.65
1:A:492:PHE:O	1:A:492:PHE:CD1	2.48	0.65
1:C:227:MET:O	1:C:230:ILE:HG22	1.97	0.65
1:D:270:GLU:CA	1:D:273:VAL:HG22	2.27	0.65
1:D:436:LYS:O	1:D:440:ILE:HG13	1.96	0.65
1:H:286:THR:O	1:H:361:PRO:CB	2.44	0.65
1:H:485:PHE:HE2	1:H:500:THR:OG1	1.80	0.65
1:I:611:GLU:N	1:I:612:PRO:CD	2.60	0.65
1:J:237:ILE:HD13	1:J:237:ILE:O	1.96	0.65
1:K:265:LYS:O	1:K:268:VAL:HG23	1.96	0.65
1:G:227:MET:HA	1:G:230:ILE:HG22	1.78	0.65
1:J:735:GLN:O	1:J:738:MET:HB3	1.97	0.65
1:K:339:THR:HG23	1:K:340:ASP:N	2.12	0.65
1:K:456:ILE:O	1:K:481:GLU:OE2	2.14	0.65
1:A:230:ILE:HG13	1:A:904:LEU:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:GLU:HA	1:A:273:VAL:HG22	1.79	0.65
1:B:585:LEU:HD12	1:B:834:ALA:HB2	1.79	0.65
1:D:683:ALA:HB2	1:D:853:PHE:CE1	2.31	0.65
1:J:269:LEU:HD11	1:J:458:LYS:HB2	1.78	0.65
1:B:254:SER:HB2	1:B:356:SER:O	1.97	0.64
1:D:276:GLU:CD	1:D:318:PHE:HE2	1.99	0.64
1:D:855:ARG:HD3	1:D:855:ARG:H	1.58	0.64
1:E:492:PHE:O	1:E:492:PHE:HD1	1.80	0.64
1:E:574:ARG:HD2	1:E:839:LEU:HD12	1.78	0.64
1:H:454:GLY:O	1:H:500:THR:CB	2.44	0.64
1:I:611:GLU:H	1:I:612:PRO:HD2	1.62	0.64
1:A:275:HIS:CD2	1:A:275:HIS:N	2.65	0.64
1:D:246:GLN:CD	1:D:247:GLY:H	2.05	0.64
1:D:388:ARG:O	1:D:421:ARG:NH2	2.31	0.64
1:E:284:MET:N	1:E:284:MET:SD	2.69	0.64
1:H:423:ILE:HG22	1:H:450:LEU:HD13	1.77	0.64
1:L:254:SER:HB2	1:L:356:SER:O	1.96	0.64
1:H:455:VAL:HG12	1:H:501:GLY:N	2.12	0.64
1:I:755:MET:HE3	1:I:790:ALA:HB1	1.79	0.64
1:J:572:PHE:O	1:J:576:GLN:NE2	2.30	0.64
1:K:279:PRO:O	1:K:280:LYS:CD	2.45	0.64
1:K:388:ARG:O	1:K:421:ARG:NH2	2.29	0.64
1:A:565:PHE:O	1:A:568:PHE:HB3	1.97	0.64
1:H:273:VAL:CG1	1:H:457:SER:HB2	2.26	0.64
1:K:671:LYS:N	1:K:671:LYS:HE3	2.13	0.64
1:A:233:LYS:N	1:A:233:LYS:HE3	2.12	0.64
1:A:269:LEU:HD23	1:A:457:SER:OG	1.95	0.64
1:A:363:TYR:HD2	1:A:407:THR:HB	1.61	0.64
1:I:322:GLN:O	1:I:326:THR:OG1	2.08	0.64
1:J:269:LEU:HD21	1:J:457:SER:O	1.96	0.64
1:K:232:LYS:HG3	1:K:233:LYS:HE3	1.79	0.64
1:E:272:ILE:HG12	1:E:280:LYS:HG3	1.78	0.64
1:G:609:PRO:HB2	1:G:610:ARG:C	2.23	0.64
1:H:376:LYS:NZ	1:H:376:LYS:HA	2.12	0.64
1:J:308:PRO:HG3	1:J:344:ARG:HG3	1.79	0.64
1:K:272:ILE:CG2	1:K:277:PHE:HD1	2.11	0.64
1:L:285:ILE:HD12	1:L:287:ARG:H	1.61	0.64
1:L:778:GLY:C	1:L:779:PHE:CD2	2.71	0.64
1:E:727:LEU:HD21	1:E:823:GLU:HG2	1.80	0.64
1:E:739:LYS:O	1:E:742:GLU:HB2	1.97	0.64
1:G:627:TYR:OH	1:G:631:GLN:NE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:863:GLU:O	1:G:867:ALA:CB	2.46	0.64
1:H:272:ILE:HG21	1:H:277:PHE:CD1	2.33	0.64
1:H:665:ASP:OD1	1:H:676:ARG:NH2	2.31	0.64
1:D:272:ILE:HG21	1:D:277:PHE:HD1	1.62	0.64
1:D:363:TYR:CD2	1:D:407:THR:HB	2.32	0.64
1:D:382:LEU:C	1:D:382:LEU:HD12	2.22	0.64
1:E:441:LEU:HD23	1:E:498:VAL:HB	0.68	0.64
1:F:227:MET:HA	1:F:230:ILE:HG22	1.80	0.64
1:H:881:VAL:O	1:H:884:HIS:HB3	1.97	0.64
1:L:611:GLU:H	1:L:612:PRO:HD2	1.61	0.64
1:A:235:ILE:O	1:A:235:ILE:HD12	1.97	0.64
1:A:363:TYR:N	1:A:363:TYR:HD1	1.95	0.64
1:B:259:GLY:HA2	1:B:408:ALA:HB2	1.78	0.64
1:C:266:SER:HA	1:C:269:LEU:HD22	1.79	0.64
1:C:627:TYR:OH	1:C:631:GLN:NE2	2.30	0.64
1:G:862:HIS:NE2	1:G:866:HIS:CD2	2.66	0.64
1:J:307:PHE:CE1	1:J:345:LEU:CD2	2.79	0.64
1:K:307:PHE:CD1	1:K:345:LEU:CD2	2.80	0.64
1:A:376:LYS:N	1:A:376:LYS:HE2	2.13	0.64
1:D:555:ALA:CB	1:K:855:ARG:CD	2.76	0.64
1:G:297:ASP:HB3	1:G:349:SER:C	2.23	0.64
1:G:627:TYR:HE2	1:G:628:TRP:CZ3	2.15	0.64
1:H:493:GLY:O	1:H:496:SER:HB3	1.97	0.64
1:A:252:LEU:HD23	1:A:524:THR:HG21	1.79	0.63
1:C:429:MET:HE2	1:C:437:GLY:HA2	1.78	0.63
1:D:224:ASP:N	1:D:225:ASP:OD1	2.32	0.63
1:F:754:VAL:HG22	1:F:779:PHE:CD2	2.33	0.63
1:H:307:PHE:N	1:H:307:PHE:CD1	2.66	0.63
1:A:749:LYS:H	1:A:749:LYS:CD	2.11	0.63
1:E:285:ILE:O	1:E:286:THR:OG1	2.14	0.63
1:E:308:PRO:HG3	1:E:344:ARG:HG3	1.80	0.63
1:F:279:PRO:HB3	1:F:322:GLN:HA	1.80	0.63
1:H:298:PRO:O	1:H:299:GLU:HB3	1.97	0.63
1:J:455:VAL:HG12	1:J:501:GLY:N	2.13	0.63
1:J:665:ASP:OD1	1:J:676:ARG:NH2	2.31	0.63
1:D:286:THR:OG1	1:D:361:PRO:HB3	1.98	0.63
1:I:772:HIS:HB2	1:I:780:SER:CA	2.29	0.63
1:A:375:LEU:HB2	1:A:376:LYS:HE2	1.80	0.63
1:G:585:LEU:HD12	1:G:834:ALA:HB2	1.79	0.63
1:H:297:ASP:CG	1:H:300:ALA:HB3	2.24	0.63
1:D:454:GLY:H	1:D:500:THR:HG22	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:672:HIS:HA	1:H:877:GLU:OE2	1.98	0.63
1:K:241:LEU:O	1:K:244:VAL:HG23	1.97	0.63
1:C:627:TYR:CE2	1:C:628:TRP:CZ3	2.86	0.63
1:D:376:LYS:HZ2	1:D:379:ILE:HD12	1.62	0.63
1:E:308:PRO:HG3	1:E:344:ARG:CB	2.29	0.63
1:H:671:LYS:HD2	1:H:671:LYS:N	2.12	0.63
1:H:762:ARG:HG2	1:H:762:ARG:HH11	1.64	0.63
1:K:376:LYS:CA	1:K:376:LYS:CE	2.76	0.63
1:A:269:LEU:CA	1:A:272:ILE:HD12	2.26	0.63
1:B:272:ILE:HG23	1:B:277:PHE:HA	1.80	0.63
1:B:791:VAL:CG1	1:B:794:ARG:HH21	2.08	0.63
1:C:843:VAL:HG21	1:D:704:PRO:HA	1.80	0.63
1:D:286:THR:O	1:D:361:PRO:CB	2.46	0.63
1:F:607:PRO:HD3	1:F:762:ARG:HG3	1.80	0.63
1:J:455:VAL:HG12	1:J:501:GLY:H	1.60	0.63
1:K:308:PRO:HG3	1:K:344:ARG:HG3	1.81	0.63
1:A:672:HIS:HA	1:A:877:GLU:OE2	1.99	0.63
1:D:537:TYR:CE1	1:D:540:LYS:HE3	2.34	0.63
1:J:492:PHE:O	1:J:492:PHE:HD1	1.81	0.63
1:A:243:LYS:O	1:A:243:LYS:HG2	1.96	0.63
1:C:524:THR:O	1:C:528:ILE:HG13	1.99	0.63
1:F:569:ALA:HB1	1:F:850:TYR:CE2	2.34	0.63
1:K:299:GLU:HG3	1:K:299:GLU:O	1.97	0.63
1:B:783:LEU:HD12	1:I:777:GLY:HA2	1.53	0.62
1:D:273:VAL:CG1	1:D:457:SER:HB2	2.22	0.62
1:E:556:ALA:CB	1:J:855:ARG:HH21	2.10	0.62
1:J:413:ARG:NH1	1:J:446:TYR:CE1	2.67	0.62
1:C:224:ASP:HB3	1:C:227:MET:HG3	1.80	0.62
1:E:240:LEU:N	1:E:240:LEU:HD23	2.13	0.62
1:E:818:LYS:HE3	1:E:819:TYR:CE2	2.34	0.62
1:G:360:LEU:HB2	1:G:361:PRO:HD2	1.81	0.62
1:I:800:LEU:O	1:I:804:ILE:HG13	1.99	0.62
1:D:286:THR:HB	1:D:361:PRO:CB	2.29	0.62
1:D:694:THR:HG21	1:D:845:MET:HE3	1.81	0.62
1:I:387:ILE:O	1:I:421:ARG:NH2	2.32	0.62
1:J:269:LEU:HD23	1:J:270:GLU:N	2.13	0.62
1:J:284:MET:HG2	1:J:286:THR:HG22	1.81	0.62
1:J:297:ASP:OD1	1:J:300:ALA:HB3	1.97	0.62
1:J:574:ARG:H	1:J:575:PRO:HD2	1.64	0.62
1:A:640:THR:HG21	1:A:706:LYS:HA	1.79	0.62
1:A:259:GLY:HA2	1:A:408:ALA:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:276:GLU:OE1	1:E:303:ASP:OD1	2.18	0.62
1:H:377:ARG:HH21	1:H:377:ARG:HG2	1.60	0.62
1:D:488:HIS:HB3	1:D:491:GLU:HG2	1.82	0.62
1:E:441:LEU:HB3	1:E:498:VAL:HG11	1.81	0.62
1:E:855:ARG:HD2	1:J:555:ALA:HB3	1.82	0.62
1:F:260:SER:H	1:F:263:SER:HB3	1.64	0.62
1:G:776:ALA:O	1:L:777:GLY:CA	2.47	0.62
1:L:611:GLU:N	1:L:612:PRO:HD2	2.14	0.62
1:G:255:ILE:HD11	1:G:355:LEU:HG	1.81	0.62
1:K:454:GLY:O	1:K:455:VAL:CG1	2.47	0.62
1:K:454:GLY:O	1:K:500:THR:HB	1.99	0.62
1:A:278:LEU:HD13	1:A:278:LEU:C	2.25	0.62
1:D:455:VAL:HG12	1:D:501:GLY:N	2.15	0.62
1:F:569:ALA:HB1	1:F:850:TYR:CD2	2.34	0.62
1:G:665:ASP:OD1	1:G:676:ARG:NH1	2.33	0.62
1:H:488:HIS:CB	1:H:491:GLU:HG3	2.25	0.62
1:J:307:PHE:CD1	1:J:345:LEU:HD21	2.34	0.62
1:J:569:ALA:HA	1:J:850:TYR:CZ	2.35	0.62
1:B:284:MET:N	1:B:284:MET:SD	2.72	0.62
1:B:780:SER:HB2	1:I:774:SER:HG	1.63	0.62
1:J:377:ARG:HH21	1:J:377:ARG:CG	2.12	0.62
1:K:670:ALA:HB3	1:K:671:LYS:NZ	2.14	0.62
1:D:272:ILE:HG23	1:D:278:LEU:H	1.65	0.62
1:E:376:LYS:HA	1:E:376:LYS:HZ1	1.64	0.62
1:G:472:ASN:OD1	1:G:475:ALA:HB3	2.00	0.62
1:K:349:SER:O	1:K:352:ILE:HG13	2.00	0.62
1:K:387:ILE:CG2	1:K:393:ILE:HD12	2.30	0.62
1:A:441:LEU:HB3	1:A:498:VAL:HG11	1.82	0.61
1:A:703:LYS:HE3	1:C:544:ASN:HD22	1.65	0.61
1:E:749:LYS:HD2	1:E:749:LYS:N	2.13	0.61
1:E:832:LYS:O	1:E:836:THR:HG22	2.00	0.61
1:I:690:ARG:NH1	1:I:844:GLU:OE2	2.31	0.61
1:I:863:GLU:O	1:I:867:ALA:CB	2.47	0.61
1:K:272:ILE:CG2	1:K:278:LEU:H	2.13	0.61
1:K:278:LEU:HB2	1:K:279:PRO:HD2	1.81	0.61
1:K:298:PRO:O	1:K:299:GLU:HB3	2.00	0.61
1:A:272:ILE:HG21	1:A:277:PHE:HD1	1.65	0.61
1:D:478:ASN:O	1:D:482:LYS:HG2	2.01	0.61
1:E:640:THR:HG21	1:E:706:LYS:HA	1.82	0.61
1:K:906:ARG:HH22	1:K:907:ILE:HD13	1.64	0.61
1:B:766:ILE:HD12	1:B:767:ILE:H	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:640:THR:HG21	1:D:706:LYS:HA	1.80	0.61
1:H:673:PRO:HD2	1:H:877:GLU:OE1	1.99	0.61
1:J:286:THR:HB	1:J:361:PRO:CB	2.28	0.61
1:J:286:THR:O	1:J:361:PRO:CG	2.48	0.61
1:J:434:PRO:HB3	1:J:491:GLU:HG3	1.80	0.61
1:K:339:THR:HG23	1:K:340:ASP:H	1.64	0.61
1:A:263:SER:OG	1:A:397:SER:HA	1.99	0.61
1:A:349:SER:HB3	1:A:352:ILE:CG2	2.30	0.61
1:D:229:PHE:O	1:D:232:LYS:HG3	2.00	0.61
1:E:665:ASP:OD1	1:E:676:ARG:NH2	2.33	0.61
1:F:683:ALA:HB2	1:F:853:PHE:CE1	2.36	0.61
1:G:791:VAL:HG13	1:G:794:ARG:NH2	2.14	0.61
1:H:238:ARG:NH2	1:H:356:SER:OG	2.34	0.61
1:H:396:ILE:HG22	1:H:425:VAL:HB	1.83	0.61
1:J:225:ASP:N	1:J:225:ASP:OD1	2.32	0.61
1:J:382:LEU:HD12	1:J:382:LEU:O	2.00	0.61
1:A:260:SER:N	1:A:263:SER:HB3	2.15	0.61
1:A:328:LEU:HD13	1:A:343:ILE:HD13	1.82	0.61
1:K:279:PRO:HG3	1:K:321:ILE:HG22	1.83	0.61
1:A:279:PRO:HG2	1:A:325:LEU:CD2	2.27	0.61
1:A:349:SER:O	1:A:352:ILE:HG13	1.99	0.61
1:A:593:LEU:HD21	1:A:823:GLU:HG3	1.82	0.61
1:B:441:LEU:HD23	1:B:498:VAL:HB	1.82	0.61
1:E:258:ILE:HG22	1:E:360:LEU:HD11	1.82	0.61
1:E:377:ARG:CG	1:E:377:ARG:NH2	2.51	0.61
1:H:454:GLY:O	1:H:500:THR:CG2	2.49	0.61
1:I:627:TYR:OH	1:I:631:GLN:NE2	2.34	0.61
1:J:286:THR:OG1	1:J:361:PRO:HB3	1.99	0.61
1:E:269:LEU:HD23	1:E:457:SER:HB2	1.83	0.61
1:G:780:SER:HA	1:L:778:GLY:O	2.00	0.61
1:J:240:LEU:N	1:J:240:LEU:HD23	2.16	0.61
1:J:241:LEU:O	1:J:244:VAL:HG23	2.00	0.61
1:J:434:PRO:HG2	1:J:488:HIS:CG	2.35	0.61
1:K:244:VAL:HB	1:K:248:SER:OG	2.00	0.61
1:K:272:ILE:HG23	1:K:278:LEU:H	1.65	0.61
1:K:403:LEU:N	1:K:403:LEU:HD23	2.14	0.61
1:K:441:LEU:HD23	1:K:498:VAL:HB	0.67	0.61
1:D:423:ILE:HG22	1:D:450:LEU:HD13	1.83	0.61
1:J:278:LEU:HD22	1:J:280:LYS:HG2	1.83	0.61
1:D:260:SER:N	1:D:263:SER:HB3	2.15	0.61
1:G:772:HIS:CD2	1:G:779:PHE:O	2.54	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:773:PRO:HA	1:G:781:ALA:CB	2.29	0.61
1:H:267:SER:HB2	1:H:396:ILE:CD1	2.31	0.61
1:L:400:ASP:N	1:L:400:ASP:OD1	2.34	0.61
1:D:276:GLU:HG2	1:D:277:PHE:H	1.66	0.61
1:G:617:ASP:OD1	1:G:617:ASP:N	2.29	0.61
1:L:381:GLU:HA	1:L:381:GLU:OE1	1.99	0.61
1:G:889:ARG:HA	1:G:892:GLU:HG3	1.83	0.60
1:J:376:LYS:NZ	1:J:379:ILE:HD12	2.16	0.60
1:J:690:ARG:NH1	1:J:844:GLU:OE2	2.34	0.60
1:A:286:THR:O	1:A:361:PRO:CG	2.49	0.60
1:A:297:ASP:CG	1:A:300:ALA:CB	2.74	0.60
1:D:413:ARG:NH1	1:D:446:TYR:CE1	2.69	0.60
1:D:901:ILE:O	1:D:904:LEU:HB3	2.00	0.60
1:F:429:MET:HE1	1:F:441:LEU:HB2	1.83	0.60
1:G:768:VAL:HG11	1:G:784:LEU:HD13	1.83	0.60
1:H:278:LEU:HB2	1:H:279:PRO:HD2	1.83	0.60
1:H:445:GLN:O	1:H:446:TYR:HD1	1.84	0.60
1:H:499:SER:O	1:H:500:THR:HG23	2.01	0.60
1:L:255:ILE:HG23	1:L:392:ILE:HG23	1.83	0.60
1:A:690:ARG:NH1	1:A:844:GLU:OE2	2.33	0.60
1:C:609:PRO:HB2	1:C:610:ARG:C	2.26	0.60
1:H:232:LYS:CA	1:H:235:ILE:HG22	2.25	0.60
1:I:262:SER:O	1:I:266:SER:OG	2.19	0.60
1:J:272:ILE:CG2	1:J:278:LEU:HD13	2.20	0.60
1:J:565:PHE:HA	1:J:663:LEU:HD21	1.81	0.60
1:J:572:PHE:O	1:J:576:GLN:CD	2.44	0.60
1:K:401:THR:HG22	1:K:402:ASP:O	2.00	0.60
1:A:244:VAL:HB	1:A:248:SER:OG	2.01	0.60
1:C:640:THR:HG22	1:C:706:LYS:HG2	1.81	0.60
1:G:772:HIS:O	1:G:781:ALA:N	2.30	0.60
1:H:276:GLU:OE2	1:H:318:PHE:CD2	2.52	0.60
1:K:286:THR:O	1:K:361:PRO:CB	2.50	0.60
1:K:376:LYS:NZ	1:K:376:LYS:CA	2.60	0.60
1:B:285:ILE:HG12	1:B:329:ASN:O	2.01	0.60
1:D:544:ASN:ND2	1:L:641:ARG:HH11	1.96	0.60
1:E:229:PHE:HA	1:E:232:LYS:CG	2.31	0.60
1:F:617:ASP:N	1:F:617:ASP:OD1	2.34	0.60
1:G:364:ILE:HD12	1:G:376:LYS:HZ2	1.66	0.60
1:G:429:MET:HE2	1:G:437:GLY:HA2	1.82	0.60
1:H:472:ASN:ND2	1:H:475:ALA:HB3	2.17	0.60
1:J:434:PRO:HB3	1:J:491:GLU:CG	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:295:VAL:HG12	1:L:296:ASN:O	2.00	0.60
1:C:262:SER:O	1:C:266:SER:OG	2.18	0.60
1:E:232:LYS:O	1:E:235:ILE:HG23	2.01	0.60
1:G:578:GLN:HA	1:G:838:VAL:HG21	1.83	0.60
1:J:279:PRO:HG3	1:J:321:ILE:HG22	1.82	0.60
1:J:287:ARG:HH11	1:J:287:ARG:HG3	1.66	0.60
1:J:727:LEU:HD21	1:J:823:GLU:HG2	1.82	0.60
1:L:607:PRO:HD3	1:L:762:ARG:HG3	1.83	0.60
1:B:429:MET:HE1	1:B:441:LEU:HB2	1.83	0.60
1:B:661:GLU:OE2	1:B:676:ARG:NH2	2.35	0.60
1:B:687:LEU:HD22	1:B:845:MET:HE2	1.83	0.60
1:D:750:LYS:CE	1:E:779:PHE:CE2	2.84	0.60
1:H:458:LYS:C	1:H:458:LYS:CD	2.70	0.60
1:K:564:GLN:O	1:K:567:GLU:HB2	2.01	0.60
1:A:286:THR:O	1:A:361:PRO:HG3	2.02	0.60
1:F:818:LYS:HE3	1:F:819:TYR:CE2	2.36	0.60
1:J:376:LYS:HZ2	1:J:379:ILE:HD12	1.67	0.60
1:K:524:THR:O	1:K:528:ILE:HG13	2.01	0.60
1:L:602:ILE:HB	1:L:788:ARG:HB3	1.83	0.60
1:D:445:GLN:O	1:D:446:TYR:CG	2.54	0.60
1:G:818:LYS:HE3	1:G:819:TYR:CE2	2.36	0.60
1:K:640:THR:HG21	1:K:706:LYS:HA	1.82	0.60
1:A:775:GLY:HA2	1:A:779:PHE:O	2.01	0.60
1:D:627:TYR:CE2	1:D:628:TRP:CE3	2.90	0.60
1:E:363:TYR:CD2	1:E:407:THR:HB	2.37	0.60
1:J:307:PHE:CD1	1:J:345:LEU:CD2	2.84	0.60
1:K:363:TYR:N	1:K:363:TYR:HD1	1.99	0.60
1:D:454:GLY:O	1:D:500:THR:CB	2.49	0.59
1:E:251:THR:HG22	1:E:252:LEU:H	1.66	0.59
1:F:224:ASP:HB3	1:F:227:MET:HG3	1.83	0.59
1:F:449:LYS:C	1:F:451:GLY:H	2.10	0.59
1:H:817:ASN:HB3	1:H:820:TYR:HB2	1.84	0.59
1:K:363:TYR:N	1:K:363:TYR:CD1	2.69	0.59
1:K:690:ARG:O	1:K:690:ARG:HD3	2.02	0.59
1:A:434:PRO:HB3	1:A:491:GLU:CG	2.31	0.59
1:D:275:HIS:H	1:D:275:HIS:CD2	2.20	0.59
1:G:441:LEU:HD23	1:G:498:VAL:HB	1.83	0.59
1:K:276:GLU:OE1	1:K:303:ASP:OD1	2.21	0.59
1:K:376:LYS:HA	1:K:376:LYS:CE	2.32	0.59
1:A:456:ILE:HD12	1:A:456:ILE:C	2.27	0.59
1:A:457:SER:O	1:A:458:LYS:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:800:LEU:O	1:A:804:ILE:HG13	2.02	0.59
1:F:285:ILE:HG12	1:F:329:ASN:O	2.02	0.59
1:H:246:GLN:HG2	1:H:247:GLY:N	2.15	0.59
1:K:307:PHE:CE1	1:K:345:LEU:CD2	2.76	0.59
1:K:455:VAL:CG1	1:K:501:GLY:H	2.15	0.59
1:D:229:PHE:HA	1:D:232:LYS:CG	2.32	0.59
1:D:260:SER:H	1:D:263:SER:HB3	1.66	0.59
1:E:485:PHE:CD2	1:E:492:PHE:HD1	2.18	0.59
1:E:565:PHE:HA	1:E:663:LEU:HD21	1.83	0.59
1:F:755:MET:HE3	1:F:790:ALA:HB1	1.84	0.59
1:G:254:SER:HB2	1:G:356:SER:O	2.02	0.59
1:H:272:ILE:CG2	1:H:277:PHE:HD1	2.15	0.59
1:H:279:PRO:HB3	1:H:322:GLN:CA	2.31	0.59
1:A:832:LYS:O	1:A:836:THR:HG22	2.02	0.59
1:C:227:MET:HA	1:C:230:ILE:HG22	1.84	0.59
1:D:574:ARG:H	1:D:575:PRO:HD2	1.68	0.59
1:E:484:TYR:HE1	1:E:492:PHE:HZ	1.51	0.59
1:H:278:LEU:HD22	1:H:279:PRO:O	2.03	0.59
1:H:441:LEU:HB3	1:H:498:VAL:CG1	2.33	0.59
1:A:392:ILE:HD12	1:A:421:ARG:O	2.02	0.59
1:B:653:ALA:HB2	1:B:845:MET:HE1	1.84	0.59
1:D:297:ASP:OD1	1:D:348:HIS:HB3	2.02	0.59
1:D:575:PRO:O	1:D:578:GLN:HB3	2.02	0.59
1:H:387:ILE:HG22	1:H:415:VAL:HG21	1.83	0.59
1:J:298:PRO:O	1:J:299:GLU:HB3	2.02	0.59
1:J:387:ILE:CG2	1:J:415:VAL:HG21	2.32	0.59
1:K:610:ARG:HA	1:K:610:ARG:HE	1.67	0.59
1:A:456:ILE:O	1:A:481:GLU:OE2	2.20	0.59
1:J:255:ILE:HD12	1:J:357:LEU:HB3	1.84	0.59
1:K:260:SER:H	1:K:263:SER:HB3	1.67	0.59
1:D:745:VAL:O	1:E:778:GLY:CA	2.51	0.59
1:E:499:SER:O	1:E:500:THR:CG2	2.51	0.59
1:I:569:ALA:HB1	1:I:850:TYR:CD2	2.38	0.59
1:A:694:THR:HG21	1:A:845:MET:HE3	1.85	0.59
1:B:272:ILE:HD11	1:B:280:LYS:HB2	1.85	0.59
1:C:294:LEU:HB3	1:C:352:ILE:HD13	1.85	0.59
1:E:671:LYS:N	1:E:671:LYS:HE3	2.17	0.59
1:H:275:HIS:CG	1:H:276:GLU:N	2.70	0.59
1:K:878:ASP:HB3	1:K:881:VAL:HG21	1.84	0.59
1:A:279:PRO:CG	1:A:322:GLN:HA	2.33	0.59
1:B:791:VAL:CG1	1:B:794:ARG:NH2	2.60	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:673:PRO:HD2	1:E:877:GLU:OE1	2.02	0.59
1:F:863:GLU:O	1:F:867:ALA:CB	2.50	0.59
1:G:508:LYS:O	1:G:512:VAL:HG23	2.03	0.59
1:G:878:ASP:HB3	1:G:881:VAL:HG12	1.84	0.59
1:H:505:LEU:O	1:H:505:LEU:HD22	2.02	0.59
1:J:275:HIS:H	1:J:275:HIS:CD2	2.19	0.59
1:A:269:LEU:HD21	1:A:457:SER:HB2	1.83	0.58
1:A:278:LEU:CD2	1:A:280:LYS:CD	2.79	0.58
1:A:279:PRO:HB3	1:A:322:GLN:CG	2.32	0.58
1:C:627:TYR:CZ	1:C:631:GLN:NE2	2.71	0.58
1:D:537:TYR:CD1	1:D:540:LYS:CE	2.86	0.58
1:G:815:LEU:O	1:G:815:LEU:HD12	2.03	0.58
1:K:294:LEU:HB2	1:K:355:LEU:H	1.68	0.58
1:B:488:HIS:HB3	1:B:491:GLU:CG	2.31	0.58
1:C:653:ALA:HB2	1:C:845:MET:HE1	1.85	0.58
1:D:279:PRO:O	1:D:280:LYS:CD	2.51	0.58
1:G:772:HIS:ND1	1:L:780:SER:CB	2.61	0.58
1:H:255:ILE:HG23	1:H:392:ILE:HG23	1.85	0.58
1:I:355:LEU:HD23	1:I:357:LEU:HD22	1.83	0.58
1:K:381:GLU:OE1	1:K:381:GLU:HA	2.03	0.58
1:K:455:VAL:HG12	1:K:501:GLY:N	2.15	0.58
1:B:611:GLU:H	1:B:612:PRO:HD2	1.69	0.58
1:E:272:ILE:CG2	1:E:277:PHE:HD1	2.17	0.58
1:F:279:PRO:CB	1:F:322:GLN:HA	2.33	0.58
1:H:269:LEU:CG	1:H:457:SER:O	2.49	0.58
1:I:588:LYS:O	1:I:591:ASP:HB2	2.03	0.58
1:D:272:ILE:HG21	1:D:277:PHE:CD1	2.39	0.58
1:E:657:GLN:HE22	1:E:684:ALA:HA	1.69	0.58
1:H:441:LEU:CD2	1:H:498:VAL:HG12	2.18	0.58
1:J:279:PRO:HG2	1:J:325:LEU:HD21	1.85	0.58
1:K:387:ILE:CG2	1:K:415:VAL:HG21	2.33	0.58
1:K:672:HIS:HA	1:K:877:GLU:OE2	2.03	0.58
1:A:269:LEU:HD23	1:A:270:GLU:N	2.18	0.58
1:C:297:ASP:HB3	1:C:349:SER:C	2.28	0.58
1:E:484:TYR:HE1	1:E:492:PHE:CZ	2.22	0.58
1:E:672:HIS:HA	1:E:877:GLU:OE2	2.03	0.58
1:H:279:PRO:HB3	1:H:322:GLN:HA	1.83	0.58
1:H:436:LYS:O	1:H:440:ILE:HG13	2.02	0.58
1:J:569:ALA:HB1	1:J:850:TYR:CD2	2.38	0.58
1:J:683:ALA:HB2	1:J:853:PHE:CE1	2.37	0.58
1:K:279:PRO:HB3	1:K:322:GLN:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:SER:HB2	1:C:356:SER:O	2.03	0.58
1:F:575:PRO:HA	1:F:578:GLN:HB3	1.85	0.58
1:J:277:PHE:HD1	1:J:278:LEU:N	2.01	0.58
1:K:230:ILE:HG13	1:K:904:LEU:HD11	1.84	0.58
1:K:294:LEU:HB3	1:K:352:ILE:HD13	1.85	0.58
1:C:611:GLU:N	1:C:612:PRO:HD2	2.18	0.58
1:C:780:SER:OG	1:C:783:LEU:HB2	2.03	0.58
1:D:285:ILE:HD13	1:D:285:ILE:C	2.15	0.58
1:D:562:LYS:CD	1:K:559:ASP:OD1	2.51	0.58
1:E:265:LYS:HA	1:E:268:VAL:CG2	2.34	0.58
1:E:377:ARG:HH21	1:E:377:ARG:HG3	1.65	0.58
1:J:255:ILE:HG12	1:J:513:LEU:HD21	1.85	0.58
1:J:285:ILE:HG12	1:J:287:ARG:N	2.12	0.58
1:J:349:SER:O	1:J:352:ILE:HG13	2.03	0.58
1:K:252:LEU:HD23	1:K:524:THR:HG21	1.86	0.58
1:L:428:LYS:HB3	1:L:431:LEU:HD21	1.85	0.58
1:D:287:ARG:HG3	1:D:287:ARG:NH1	2.06	0.58
1:D:426:ILE:HD12	1:D:440:ILE:CG2	2.01	0.58
1:E:286:THR:O	1:E:361:PRO:HB3	2.02	0.58
1:J:232:LYS:HD2	1:J:233:LYS:HE3	1.84	0.58
1:J:254:SER:HB2	1:J:356:SER:O	2.02	0.58
1:J:278:LEU:CD1	1:J:278:LEU:N	2.66	0.58
1:J:286:THR:O	1:J:361:PRO:HB3	2.04	0.58
1:J:296:ASN:O	1:J:298:PRO:HD3	2.04	0.58
1:K:375:LEU:N	1:K:375:LEU:CD2	2.59	0.58
1:K:434:PRO:HB3	1:K:491:GLU:HG3	1.86	0.58
1:L:640:THR:HG21	1:L:706:LYS:HA	1.84	0.58
1:A:233:LYS:HE3	1:A:233:LYS:CA	2.34	0.58
1:C:224:ASP:HB3	1:C:227:MET:HB2	1.86	0.58
1:E:488:HIS:HB3	1:E:491:GLU:HG2	1.84	0.58
1:H:377:ARG:CG	1:H:377:ARG:NH2	2.60	0.58
1:I:259:GLY:HA2	1:I:408:ALA:HB2	1.84	0.58
1:J:575:PRO:O	1:J:578:GLN:HB3	2.03	0.58
1:E:308:PRO:HD2	1:E:344:ARG:O	2.04	0.58
1:K:269:LEU:HD21	1:K:457:SER:HB2	1.82	0.58
1:K:499:SER:O	1:K:500:THR:HG23	2.04	0.58
1:L:609:PRO:HB3	1:L:611:GLU:HB2	1.83	0.58
1:L:755:MET:HE3	1:L:790:ALA:HB1	1.85	0.58
1:D:257:VAL:HG22	1:D:359:ASP:HA	1.86	0.57
1:E:263:SER:OG	1:E:397:SER:HA	2.04	0.57
1:H:751:LEU:HA	1:H:754:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:430:ASP:HB3	1:I:456:ILE:HG12	1.85	0.57
1:I:642:LEU:HD13	1:I:643:GLY:N	2.19	0.57
1:J:307:PHE:HE1	1:J:345:LEU:HD21	1.60	0.57
1:J:682:ALA:O	1:J:685:THR:HG22	2.03	0.57
1:A:255:ILE:HG13	1:A:357:LEU:HA	1.86	0.57
1:A:270:GLU:O	1:A:273:VAL:HG22	2.04	0.57
1:A:279:PRO:O	1:A:280:LYS:CD	2.51	0.57
1:E:284:MET:HG2	1:E:286:THR:CG2	2.33	0.57
1:H:279:PRO:HG2	1:H:325:LEU:CD2	2.31	0.57
1:H:478:ASN:CG	1:H:482:LYS:NZ	2.62	0.57
1:H:775:GLY:HA2	1:H:779:PHE:O	2.03	0.57
1:I:803:ARG:HD2	1:I:823:GLU:CD	2.29	0.57
1:J:275:HIS:CG	1:J:276:GLU:H	2.22	0.57
1:J:456:ILE:HD12	1:J:456:ILE:C	2.28	0.57
1:A:387:ILE:CG2	1:A:393:ILE:HD12	2.35	0.57
1:C:255:ILE:HD11	1:C:355:LEU:HG	1.85	0.57
1:C:322:GLN:O	1:C:326:THR:OG1	2.10	0.57
1:E:241:LEU:O	1:E:244:VAL:HG23	2.04	0.57
1:E:298:PRO:O	1:E:299:GLU:HB3	2.04	0.57
1:E:339:THR:CG2	1:E:340:ASP:H	2.17	0.57
1:H:441:LEU:HD21	1:H:498:VAL:CB	2.20	0.57
1:K:296:ASN:HB2	1:K:354:ASP:OD2	2.04	0.57
1:K:600:ARG:HB3	1:K:601:PRO:HD2	1.85	0.57
1:A:232:LYS:HD3	1:A:233:LYS:NZ	2.19	0.57
1:A:263:SER:HA	1:A:266:SER:OG	2.05	0.57
1:D:873:LYS:HA	1:D:876:ARG:HB2	1.86	0.57
1:G:779:PHE:CD1	1:L:750:LYS:NZ	2.73	0.57
1:H:485:PHE:HD2	1:H:492:PHE:O	1.87	0.57
1:J:267:SER:CB	1:J:396:ILE:HG13	2.34	0.57
1:J:297:ASP:CG	1:J:300:ALA:CB	2.68	0.57
1:L:662:LYS:O	1:L:665:ASP:HB2	2.04	0.57
1:A:434:PRO:HG2	1:A:488:HIS:ND1	2.18	0.57
1:E:237:ILE:HD12	1:E:241:LEU:HD11	1.86	0.57
1:E:480:ASN:HA	1:E:483:ASN:OD1	2.04	0.57
1:H:670:ALA:HB1	1:H:671:LYS:HZ2	1.69	0.57
1:J:266:SER:HB2	1:J:427:THR:OG1	2.04	0.57
1:A:474:LEU:HG	1:A:475:ALA:H	1.70	0.57
1:D:270:GLU:HA	1:D:273:VAL:CG2	2.33	0.57
1:E:363:TYR:N	1:E:363:TYR:CD1	2.70	0.57
1:F:611:GLU:H	1:F:612:PRO:HD2	1.69	0.57
1:J:263:SER:OG	1:J:397:SER:HA	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:286:THR:OG1	1:K:361:PRO:HB3	2.05	0.57
1:L:627:TYR:CZ	1:L:631:GLN:NE2	2.72	0.57
1:C:224:ASP:CB	1:C:227:MET:HG3	2.34	0.57
1:C:268:VAL:O	1:C:272:ILE:HG13	2.05	0.57
1:D:278:LEU:HD22	1:D:280:LYS:CD	2.34	0.57
1:G:618:LEU:N	1:G:619:PRO:HD2	2.19	0.57
1:H:381:GLU:OE1	1:H:381:GLU:HA	2.05	0.57
1:J:232:LYS:CD	1:J:233:LYS:HE3	2.35	0.57
1:K:454:GLY:N	1:K:500:THR:HG22	2.19	0.57
1:K:751:LEU:O	1:K:754:VAL:HG12	2.05	0.57
1:D:285:ILE:HG12	1:D:287:ARG:N	2.16	0.57
1:D:889:ARG:HG3	1:D:890:ARG:N	2.20	0.57
1:F:258:ILE:HG22	1:F:360:LEU:HD11	1.87	0.57
1:K:270:GLU:C	1:K:273:VAL:HG22	2.30	0.57
1:A:863:GLU:O	1:A:867:ALA:HB3	2.05	0.57
1:D:488:HIS:HB3	1:D:491:GLU:CG	2.35	0.57
1:E:255:ILE:HD11	1:E:355:LEU:HG	1.84	0.57
1:G:473:LEU:HD12	1:G:476:SER:OG	2.05	0.57
1:H:272:ILE:HG23	1:H:278:LEU:H	1.70	0.57
1:H:433:GLU:O	1:H:436:LYS:HB2	2.04	0.57
1:J:387:ILE:HG22	1:J:415:VAL:HG21	1.86	0.57
1:A:387:ILE:HG21	1:A:393:ILE:HD12	1.86	0.57
1:D:308:PRO:HG3	1:D:344:ARG:HG3	1.85	0.57
1:E:279:PRO:HB3	1:E:322:GLN:HB2	1.85	0.57
1:E:704:PRO:HA	1:F:843:VAL:HG21	1.85	0.57
1:H:270:GLU:C	1:H:273:VAL:HG22	2.30	0.57
1:J:294:LEU:HB2	1:J:355:LEU:H	1.69	0.57
1:J:376:LYS:HA	1:J:376:LYS:HZ3	1.68	0.57
1:J:455:VAL:HG12	1:J:501:GLY:CA	2.35	0.57
1:K:382:LEU:HD12	1:K:382:LEU:O	2.05	0.57
1:K:670:ALA:C	1:K:671:LYS:HE3	2.30	0.57
1:L:275:HIS:HB2	1:L:352:ILE:HG21	1.87	0.57
1:A:240:LEU:N	1:A:240:LEU:HD23	2.20	0.56
1:E:477:ILE:O	1:E:477:ILE:HG22	2.05	0.56
1:G:259:GLY:HA2	1:G:408:ALA:HB2	1.87	0.56
1:H:272:ILE:CG2	1:H:278:LEU:HD12	2.22	0.56
1:I:609:PRO:HB2	1:I:611:GLU:HB2	1.85	0.56
1:K:272:ILE:HG12	1:K:278:LEU:CD1	2.34	0.56
1:K:273:VAL:HG21	1:K:457:SER:CB	2.34	0.56
1:C:241:LEU:HD13	1:C:250:VAL:O	2.06	0.56
1:E:363:TYR:N	1:E:363:TYR:HD1	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:556:ALA:CB	1:J:855:ARG:NH2	2.65	0.56
1:J:259:GLY:HA2	1:J:408:ALA:HB2	1.87	0.56
1:J:485:PHE:CE2	1:J:492:PHE:CD1	2.93	0.56
1:L:255:ILE:HD11	1:L:355:LEU:HG	1.87	0.56
1:A:238:ARG:NH2	1:A:356:SER:HG	1.99	0.56
1:A:429:MET:CE	1:A:437:GLY:HA2	2.31	0.56
1:A:543:TYR:O	1:A:546:GLN:HG3	2.06	0.56
1:A:574:ARG:H	1:A:575:PRO:HD2	1.70	0.56
1:C:279:PRO:CB	1:C:322:GLN:HA	2.35	0.56
1:C:640:THR:HG21	1:C:706:LYS:HA	1.87	0.56
1:D:392:ILE:HD12	1:D:421:ARG:O	2.05	0.56
1:D:750:LYS:CE	1:E:753:GLU:OE1	2.52	0.56
1:G:611:GLU:N	1:G:612:PRO:HD2	2.19	0.56
1:I:249:THR:OG1	1:I:531:GLU:OE1	2.23	0.56
1:I:776:ALA:O	1:I:780:SER:HB3	2.05	0.56
1:J:278:LEU:HD13	1:J:278:LEU:H	1.69	0.56
1:J:308:PRO:HG3	1:J:344:ARG:CB	2.35	0.56
1:J:478:ASN:HD21	1:J:482:LYS:NZ	1.88	0.56
1:K:307:PHE:HB2	1:K:310:LEU:HB2	1.86	0.56
1:K:400:ASP:OD1	1:K:400:ASP:N	2.38	0.56
1:K:431:LEU:HD23	1:K:431:LEU:H	1.70	0.56
1:K:694:THR:HG21	1:K:845:MET:HB2	1.86	0.56
1:L:661:GLU:OE2	1:L:676:ARG:NH2	2.39	0.56
1:A:229:PHE:O	1:A:233:LYS:HG2	2.04	0.56
1:B:233:LYS:HE3	1:B:900:LYS:HD2	1.86	0.56
1:C:508:LYS:O	1:C:512:VAL:HG23	2.06	0.56
1:D:855:ARG:N	1:D:855:ARG:CD	2.55	0.56
1:E:246:GLN:HG2	1:E:247:GLY:N	2.20	0.56
1:F:858:GLU:O	1:F:862:HIS:ND1	2.38	0.56
1:G:749:LYS:O	1:G:753:GLU:HG3	2.05	0.56
1:I:738:MET:HE1	1:I:755:MET:HE1	1.86	0.56
1:I:772:HIS:HB2	1:I:780:SER:N	2.20	0.56
1:J:526:GLU:OE1	1:J:530:ARG:NH1	2.39	0.56
1:K:454:GLY:O	1:K:500:THR:CB	2.53	0.56
1:A:454:GLY:O	1:A:500:THR:HB	2.06	0.56
1:A:817:ASN:HB3	1:A:820:TYR:HB2	1.87	0.56
1:C:312:LEU:N	1:C:312:LEU:HD23	2.20	0.56
1:D:246:GLN:CG	1:D:247:GLY:N	2.69	0.56
1:D:263:SER:OG	1:D:397:SER:HA	2.04	0.56
1:D:556:ALA:CB	1:K:855:ARG:HH21	2.19	0.56
1:D:617:ASP:OD1	1:D:617:ASP:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:275:HIS:H	1:E:275:HIS:CD2	2.22	0.56
1:G:276:GLU:HG2	1:G:277:PHE:N	2.20	0.56
1:I:599:ASN:C	1:I:600:ARG:HD2	2.30	0.56
1:I:683:ALA:HB2	1:I:853:PHE:CE1	2.41	0.56
1:L:683:ALA:HB2	1:L:853:PHE:CE1	2.40	0.56
1:B:559:ASP:OD2	1:C:855:ARG:NH2	2.37	0.56
1:D:526:GLU:OE1	1:D:530:ARG:NH1	2.39	0.56
1:E:312:LEU:N	1:E:312:LEU:HD23	2.20	0.56
1:E:524:THR:O	1:E:528:ILE:HG13	2.04	0.56
1:H:260:SER:N	1:H:263:SER:HB3	2.21	0.56
1:H:377:ARG:NH2	1:H:377:ARG:HG3	2.21	0.56
1:K:454:GLY:C	1:K:455:VAL:HG13	2.30	0.56
1:D:694:THR:HG21	1:D:845:MET:HB2	1.86	0.56
1:G:772:HIS:HB3	1:L:780:SER:HA	1.88	0.56
1:I:524:THR:O	1:I:528:ILE:HG13	2.05	0.56
1:K:434:PRO:HG2	1:K:488:HIS:ND1	2.20	0.56
1:K:889:ARG:HG3	1:K:890:ARG:N	2.21	0.56
1:A:834:ALA:O	1:A:838:VAL:HB	2.06	0.56
1:C:257:VAL:HG12	1:C:394:LEU:HB3	1.88	0.56
1:C:690:ARG:NH1	1:C:844:GLU:OE2	2.38	0.56
1:D:231:THR:O	1:D:235:ILE:HG22	2.06	0.56
1:D:492:PHE:CD1	1:D:492:PHE:O	2.58	0.56
1:D:524:THR:O	1:D:528:ILE:HG13	2.06	0.56
1:H:269:LEU:HD21	1:H:457:SER:CA	2.35	0.56
1:H:457:SER:O	1:H:458:LYS:HB2	2.06	0.56
1:J:436:LYS:O	1:J:440:ILE:HG13	2.06	0.56
1:J:863:GLU:O	1:J:867:ALA:HB3	2.04	0.56
1:K:269:LEU:CD2	1:K:269:LEU:C	2.71	0.56
1:K:474:LEU:HG	1:K:475:ALA:H	1.71	0.56
1:A:600:ARG:HB3	1:A:601:PRO:HD2	1.88	0.56
1:C:480:ASN:HA	1:C:483:ASN:OD1	2.06	0.56
1:C:798:ASP:O	1:C:802:LEU:HG	2.05	0.56
1:F:255:ILE:HG12	1:F:513:LEU:HD12	1.87	0.56
1:J:493:GLY:O	1:J:496:SER:HB3	2.05	0.56
1:K:279:PRO:CG	1:K:325:LEU:HD21	2.24	0.56
1:K:286:THR:HB	1:K:361:PRO:HB3	1.88	0.56
1:A:682:ALA:O	1:A:685:THR:HG22	2.06	0.56
1:D:321:ILE:O	1:D:325:LEU:HG	2.06	0.56
1:E:269:LEU:HD23	1:E:457:SER:CB	2.31	0.56
1:H:349:SER:O	1:H:352:ILE:HG13	2.05	0.56
1:H:455:VAL:HG12	1:H:501:GLY:CA	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:269:LEU:HD23	1:K:270:GLU:CA	2.36	0.56
1:A:454:GLY:O	1:A:500:THR:HG22	2.06	0.55
1:A:713:PRO:O	1:A:716:TRP:HB3	2.06	0.55
1:C:607:PRO:HD3	1:C:762:ARG:HG3	1.87	0.55
1:D:529:GLN:HG2	1:D:898:LEU:HD21	1.88	0.55
1:E:297:ASP:HB3	1:E:349:SER:C	2.31	0.55
1:E:671:LYS:HE3	1:E:671:LYS:CA	2.36	0.55
1:F:585:LEU:HD12	1:F:834:ALA:HB2	1.87	0.55
1:H:441:LEU:CB	1:H:498:VAL:CG1	2.84	0.55
1:B:328:LEU:HD13	1:B:343:ILE:HD13	1.88	0.55
1:C:878:ASP:HB3	1:C:881:VAL:CG1	2.34	0.55
1:D:377:ARG:HG2	1:D:377:ARG:HH21	1.70	0.55
1:D:441:LEU:HB3	1:D:498:VAL:CG1	2.36	0.55
1:D:556:ALA:CA	1:K:855:ARG:NH2	2.69	0.55
1:E:854:PRO:HG2	1:E:855:ARG:HH12	1.70	0.55
1:E:855:ARG:HD3	1:E:855:ARG:N	2.21	0.55
1:F:269:LEU:O	1:F:273:VAL:HG13	2.06	0.55
1:F:572:PHE:HB3	1:F:850:TYR:OH	2.06	0.55
1:H:752:LYS:HA	1:H:755:MET:HE2	1.88	0.55
1:J:834:ALA:O	1:J:838:VAL:HB	2.05	0.55
1:K:239:ASN:O	1:K:242:GLN:HB3	2.07	0.55
1:K:278:LEU:HD13	1:K:280:LYS:HG2	1.88	0.55
1:E:264:GLY:O	1:E:268:VAL:HG22	2.05	0.55
1:E:903:GLU:O	1:E:906:ARG:HB3	2.06	0.55
1:H:229:PHE:O	1:H:232:LYS:HG3	2.06	0.55
1:H:276:GLU:OE1	1:H:303:ASP:CG	2.49	0.55
1:H:375:LEU:HD23	1:H:375:LEU:N	2.21	0.55
1:H:477:ILE:O	1:H:477:ILE:HG22	2.06	0.55
1:I:441:LEU:HD23	1:I:498:VAL:HB	1.89	0.55
1:K:376:LYS:NZ	1:K:379:ILE:CD1	2.64	0.55
1:A:257:VAL:HG22	1:A:359:ASP:HA	1.86	0.55
1:A:441:LEU:HD21	1:A:498:VAL:CB	2.24	0.55
1:A:806:ALA:O	1:A:809:SER:HB3	2.07	0.55
1:B:321:ILE:HA	1:B:324:THR:OG1	2.07	0.55
1:D:296:ASN:HB2	1:D:354:ASP:OD2	2.07	0.55
1:D:339:THR:CG2	1:D:340:ASP:H	2.20	0.55
1:D:453:VAL:HG21	1:D:505:LEU:HD23	1.88	0.55
1:D:458:LYS:HD2	1:D:458:LYS:C	2.31	0.55
1:D:485:PHE:HE2	1:D:500:THR:OG1	1.85	0.55
1:D:667:SER:OG	1:D:668:SER:N	2.39	0.55
1:F:611:GLU:N	1:F:612:PRO:CD	2.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:762:ARG:HG2	1:H:762:ARG:NH1	2.18	0.55
1:I:615:ILE:HD11	1:I:803:ARG:NE	2.07	0.55
1:J:241:LEU:HD21	1:J:528:ILE:HD11	1.89	0.55
1:K:259:GLY:HA2	1:K:408:ALA:HB2	1.87	0.55
1:K:690:ARG:NH1	1:K:844:GLU:OE2	2.40	0.55
1:A:269:LEU:HD11	1:A:458:LYS:HB2	1.88	0.55
1:A:526:GLU:OE1	1:A:530:ARG:NH1	2.39	0.55
1:D:235:ILE:HD12	1:D:235:ILE:C	2.31	0.55
1:D:276:GLU:OE2	1:D:318:PHE:CD2	2.53	0.55
1:D:382:LEU:HG	1:D:383:CYS:N	2.22	0.55
1:H:484:TYR:C	1:H:484:TYR:CD1	2.84	0.55
1:H:485:PHE:CZ	1:H:500:THR:OG1	2.52	0.55
1:I:611:GLU:H	1:I:612:PRO:CD	2.18	0.55
1:K:377:ARG:HG2	1:K:377:ARG:NH2	2.21	0.55
1:K:665:ASP:OD1	1:K:676:ARG:NH2	2.40	0.55
1:A:272:ILE:HG21	1:A:277:PHE:CD1	2.41	0.55
1:A:376:LYS:NZ	1:A:379:ILE:HD12	2.22	0.55
1:D:363:TYR:HD2	1:D:407:THR:HB	1.72	0.55
1:E:246:GLN:CD	1:E:246:GLN:H	2.13	0.55
1:G:321:ILE:HA	1:G:324:THR:OG1	2.07	0.55
1:H:263:SER:CA	1:H:266:SER:OG	2.55	0.55
1:I:279:PRO:HG2	1:I:325:LEU:HD21	1.89	0.55
1:I:598:TRP:CD1	1:I:799:ILE:HG21	2.42	0.55
1:J:377:ARG:CG	1:J:377:ARG:NH2	2.70	0.55
1:J:403:LEU:HD23	1:J:403:LEU:N	2.21	0.55
1:J:474:LEU:HG	1:J:475:ALA:H	1.71	0.55
1:K:237:ILE:HD13	1:K:241:LEU:HG	1.88	0.55
1:L:702:LEU:C	1:L:704:PRO:HD2	2.31	0.55
1:C:713:PRO:O	1:C:716:TRP:HB3	2.07	0.55
1:E:454:GLY:N	1:E:500:THR:HG22	2.22	0.55
1:F:266:SER:HA	1:F:269:LEU:HD22	1.87	0.55
1:H:286:THR:HB	1:H:361:PRO:CB	2.37	0.55
1:J:285:ILE:CG1	1:J:287:ARG:HB2	2.36	0.55
1:A:814:THR:HG21	1:A:817:ASN:ND2	2.21	0.55
1:C:791:VAL:HG13	1:C:794:ARG:NH2	2.22	0.55
1:E:382:LEU:HD12	1:E:382:LEU:C	2.31	0.55
1:E:434:PRO:CG	1:E:488:HIS:CG	2.89	0.55
1:F:349:SER:O	1:F:352:ILE:HG13	2.06	0.55
1:H:275:HIS:CD2	1:H:275:HIS:N	2.74	0.55
1:H:842:ASN:O	1:H:846:LEU:HB3	2.06	0.55
1:I:227:MET:O	1:I:231:THR:OG1	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:255:ILE:HD11	1:J:355:LEU:HG	1.89	0.55
1:J:499:SER:O	1:J:500:THR:CG2	2.54	0.55
1:K:264:GLY:O	1:K:268:VAL:HG22	2.07	0.55
1:K:284:MET:SD	1:K:284:MET:O	2.65	0.55
1:B:387:ILE:O	1:B:421:ARG:NH2	2.40	0.55
1:B:672:HIS:HD2	1:B:877:GLU:HB2	1.72	0.55
1:D:255:ILE:HG13	1:D:357:LEU:HA	1.89	0.55
1:D:454:GLY:O	1:D:500:THR:CG2	2.55	0.55
1:D:727:LEU:HD21	1:D:823:GLU:HG2	1.88	0.55
1:E:615:ILE:H	1:E:615:ILE:HD12	1.72	0.55
1:E:848:ASP:HA	1:E:851:VAL:HG22	1.89	0.55
1:F:889:ARG:NH2	1:F:893:LEU:CD1	2.70	0.55
1:G:780:SER:HB3	1:L:778:GLY:O	2.06	0.55
1:H:230:ILE:HG13	1:H:904:LEU:HD11	1.87	0.55
1:H:306:GLU:C	1:H:307:PHE:HD1	2.14	0.55
1:H:485:PHE:HA	1:H:492:PHE:HE1	1.72	0.55
1:I:772:HIS:CB	1:I:780:SER:CA	2.85	0.55
1:A:297:ASP:OD2	1:A:300:ALA:CB	2.55	0.55
1:A:387:ILE:HG22	1:A:415:VAL:HG21	1.89	0.55
1:A:543:TYR:O	1:A:546:GLN:CG	2.55	0.55
1:E:423:ILE:HG22	1:E:450:LEU:HD13	1.89	0.55
1:G:690:ARG:NH1	1:G:844:GLU:OE2	2.40	0.55
1:K:387:ILE:HG22	1:K:415:VAL:HG21	1.89	0.55
1:A:279:PRO:HB3	1:A:322:GLN:HB2	1.87	0.54
1:A:279:PRO:HG3	1:A:322:GLN:HA	1.88	0.54
1:C:532:LEU:HD22	1:C:898:LEU:HD22	1.89	0.54
1:D:279:PRO:O	1:D:280:LYS:HD2	2.07	0.54
1:E:485:PHE:CE2	1:E:492:PHE:CD1	2.93	0.54
1:E:815:LEU:O	1:E:815:LEU:HD22	2.07	0.54
1:G:266:SER:HA	1:G:269:LEU:HD22	1.87	0.54
1:G:289:PRO:HB2	1:G:342:PRO:HB3	1.89	0.54
1:H:229:PHE:HA	1:H:232:LYS:CG	2.37	0.54
1:H:456:ILE:HD12	1:H:456:ILE:C	2.31	0.54
1:K:284:MET:O	1:K:286:THR:HG23	2.07	0.54
1:B:272:ILE:HG12	1:B:278:LEU:HD13	1.89	0.54
1:C:492:PHE:O	1:C:492:PHE:HD1	1.91	0.54
1:F:513:LEU:HD23	1:F:517:MET:HE2	1.90	0.54
1:G:640:THR:HG21	1:G:706:LYS:HA	1.89	0.54
1:H:472:ASN:HD21	1:H:475:ALA:HB3	1.71	0.54
1:H:735:GLN:O	1:H:738:MET:HB3	2.07	0.54
1:A:269:LEU:HD23	1:A:269:LEU:C	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:671:LYS:HD2	1:A:671:LYS:H	1.71	0.54
1:A:673:PRO:HD2	1:A:877:GLU:OE1	2.07	0.54
1:B:234:MET:SD	1:B:234:MET:CB	2.92	0.54
1:D:456:ILE:HD12	1:D:457:SER:N	2.22	0.54
1:D:485:PHE:CD2	1:D:492:PHE:CE1	2.95	0.54
1:E:326:THR:HG22	1:E:329:ASN:HD22	1.72	0.54
1:E:339:THR:CG2	1:E:340:ASP:N	2.68	0.54
1:E:376:LYS:HE2	1:E:376:LYS:N	2.22	0.54
1:G:524:THR:O	1:G:528:ILE:HG13	2.06	0.54
1:I:286:THR:HB	1:I:361:PRO:HB3	1.89	0.54
1:I:777:GLY:O	1:I:783:LEU:HD13	2.06	0.54
1:J:269:LEU:CD1	1:J:458:LYS:HB2	2.36	0.54
1:K:478:ASN:ND2	1:K:482:LYS:NZ	2.55	0.54
1:K:496:SER:OG	1:K:498:VAL:HG22	2.08	0.54
1:L:597:TYR:CE2	1:L:822:PRO:HG3	2.42	0.54
1:L:664:LEU:HB3	1:L:676:ARG:NH1	2.23	0.54
1:A:230:ILE:O	1:A:234:MET:HG3	2.07	0.54
1:A:499:SER:O	1:A:500:THR:CG2	2.55	0.54
1:A:754:VAL:HA	1:A:779:PHE:CE1	2.42	0.54
1:B:705:TYR:CE1	1:B:832:LYS:HD3	2.42	0.54
1:D:496:SER:OG	1:D:498:VAL:HG22	2.07	0.54
1:E:297:ASP:OD1	1:E:348:HIS:HB3	2.08	0.54
1:E:434:PRO:HG2	1:E:488:HIS:CE1	2.41	0.54
1:E:441:LEU:HD23	1:E:498:VAL:HG11	1.82	0.54
1:F:544:ASN:ND2	1:H:703:LYS:HE3	2.22	0.54
1:G:528:ILE:HA	1:G:531:GLU:CD	2.32	0.54
1:G:672:HIS:CD2	1:G:877:GLU:HB2	2.42	0.54
1:K:387:ILE:O	1:K:421:ARG:NH2	2.40	0.54
1:K:720:ARG:CZ	1:K:813:LYS:HG3	2.38	0.54
1:A:614:ASN:OD1	1:A:616:ILE:HG22	2.07	0.54
1:E:254:SER:HB2	1:E:356:SER:O	2.07	0.54
1:F:627:TYR:HE2	1:F:628:TRP:CZ3	2.25	0.54
1:J:363:TYR:CD1	1:J:363:TYR:N	2.75	0.54
1:K:387:ILE:HG23	1:K:393:ILE:HD12	1.88	0.54
1:L:434:PRO:HG2	1:L:488:HIS:CD2	2.43	0.54
1:L:569:ALA:HB1	1:L:850:TYR:CE2	2.43	0.54
1:L:681:ASP:O	1:L:685:THR:HG23	2.08	0.54
1:A:477:ILE:HG22	1:A:477:ILE:O	2.08	0.54
1:A:488:HIS:HB3	1:A:491:GLU:HG3	1.89	0.54
1:B:783:LEU:HG	1:I:772:HIS:CE1	2.43	0.54
1:C:667:SER:OG	1:C:668:SER:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:441:LEU:CB	1:D:498:VAL:CG1	2.86	0.54
1:D:444:ARG:O	1:D:447:PRO:HD3	2.08	0.54
1:D:496:SER:OG	1:D:498:VAL:CG2	2.56	0.54
1:F:599:ASN:C	1:F:600:ARG:HD2	2.33	0.54
1:I:251:THR:HG22	1:I:252:LEU:H	1.73	0.54
1:J:269:LEU:HD21	1:J:457:SER:C	2.32	0.54
1:K:648:ALA:HB1	1:K:841:LEU:HD12	1.89	0.54
1:B:393:ILE:HG23	1:B:422:THR:HB	1.89	0.54
1:B:523:GLU:OE1	1:B:523:GLU:HA	2.07	0.54
1:D:339:THR:CG2	1:D:340:ASP:N	2.70	0.54
1:D:478:ASN:CG	1:D:482:LYS:HZ2	2.16	0.54
1:D:484:TYR:CE1	1:D:492:PHE:HZ	2.26	0.54
1:D:780:SER:OG	1:E:780:SER:HB3	2.08	0.54
1:E:289:PRO:HB2	1:E:342:PRO:HB3	1.88	0.54
1:G:284:MET:HG2	1:G:286:THR:HG23	1.88	0.54
1:G:429:MET:HE1	1:G:441:LEU:HB2	1.90	0.54
1:H:286:THR:HB	1:H:361:PRO:HA	1.89	0.54
1:H:294:LEU:HB2	1:H:355:LEU:N	2.22	0.54
1:J:277:PHE:HD1	1:J:278:LEU:H	1.55	0.54
1:J:279:PRO:HB3	1:J:322:GLN:HB2	1.88	0.54
1:K:441:LEU:HB3	1:K:498:VAL:HG11	1.90	0.54
1:L:249:THR:OG1	1:L:531:GLU:OE1	2.20	0.54
1:L:524:THR:O	1:L:528:ILE:HG13	2.06	0.54
1:A:376:LYS:CA	1:A:376:LYS:CE	2.86	0.54
1:A:441:LEU:CD2	1:A:498:VAL:CA	2.84	0.54
1:A:454:GLY:O	1:A:500:THR:CG2	2.56	0.54
1:B:779:PHE:O	1:I:776:ALA:HB3	2.08	0.54
1:D:376:LYS:CA	1:D:376:LYS:CE	2.86	0.54
1:D:484:TYR:CE1	1:D:492:PHE:CZ	2.96	0.54
1:D:499:SER:O	1:D:500:THR:HG23	2.08	0.54
1:E:445:GLN:O	1:E:446:TYR:CD1	2.61	0.54
1:G:269:LEU:HD11	1:G:457:SER:O	2.08	0.54
1:G:387:ILE:O	1:G:421:ARG:NH2	2.41	0.54
1:G:488:HIS:HB3	1:G:491:GLU:HG3	1.89	0.54
1:G:575:PRO:O	1:G:578:GLN:HB3	2.08	0.54
1:H:376:LYS:HA	1:H:376:LYS:HZ3	1.70	0.54
1:H:543:TYR:CE1	1:H:884:HIS:HB2	2.42	0.54
1:J:257:VAL:HG22	1:J:358:ILE:O	2.06	0.54
1:J:311:GLY:O	1:J:312:LEU:HB2	2.07	0.54
1:J:454:GLY:O	1:J:500:THR:CG2	2.54	0.54
1:A:237:ILE:HD13	1:A:237:ILE:C	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:PHE:CD2	1:A:492:PHE:HD1	2.23	0.54
1:C:258:ILE:HG22	1:C:360:LEU:HD11	1.89	0.54
1:E:275:HIS:CG	1:E:276:GLU:H	2.26	0.54
1:H:441:LEU:HD23	1:H:498:VAL:HB	0.62	0.54
1:K:672:HIS:CD2	1:K:874:PHE:CE2	2.95	0.54
1:K:673:PRO:HD2	1:K:877:GLU:OE1	2.07	0.54
1:L:837:ALA:O	1:L:841:LEU:HB2	2.08	0.54
1:A:499:SER:O	1:A:500:THR:HG23	2.08	0.54
1:B:294:LEU:HB3	1:B:352:ILE:HD13	1.89	0.54
1:D:238:ARG:HA	1:D:241:LEU:HD12	1.90	0.54
1:D:499:SER:O	1:D:500:THR:HG22	2.08	0.54
1:E:387:ILE:O	1:E:421:ARG:NH2	2.40	0.54
1:G:453:VAL:HG11	1:G:505:LEU:HB2	1.90	0.54
1:H:278:LEU:HD21	1:H:280:LYS:CD	2.37	0.54
1:J:285:ILE:CD1	1:J:286:THR:N	2.68	0.54
1:K:376:LYS:HZ3	1:K:379:ILE:HD12	1.69	0.54
1:A:674:SER:O	1:A:678:VAL:HG23	2.07	0.53
1:C:610:ARG:N	1:C:611:GLU:HA	2.23	0.53
1:D:752:LYS:HA	1:D:755:MET:CE	2.38	0.53
1:E:610:ARG:HA	1:E:610:ARG:HE	1.73	0.53
1:G:442:SER:HB2	1:G:498:VAL:HG12	1.89	0.53
1:H:225:ASP:N	1:H:225:ASP:OD1	2.40	0.53
1:I:607:PRO:HG3	1:I:762:ARG:HG3	1.91	0.53
1:J:382:LEU:HG	1:J:383:CYS:N	2.23	0.53
1:L:804:ILE:O	1:L:808:LYS:HG3	2.07	0.53
1:A:387:ILE:CG2	1:A:415:VAL:HG21	2.38	0.53
1:C:224:ASP:O	1:C:227:MET:HB2	2.09	0.53
1:C:279:PRO:HG2	1:C:325:LEU:HD21	1.91	0.53
1:D:433:GLU:O	1:D:436:LYS:HB2	2.08	0.53
1:D:485:PHE:HD2	1:D:492:PHE:O	1.91	0.53
1:D:562:LYS:HE2	1:K:562:LYS:CE	2.38	0.53
1:E:456:ILE:O	1:E:481:GLU:OE2	2.27	0.53
1:G:230:ILE:HG13	1:G:904:LEU:HD11	1.91	0.53
1:G:508:LYS:HD2	1:G:511:GLN:NE2	2.23	0.53
1:G:540:LYS:HA	1:G:545:GLU:HG3	1.90	0.53
1:I:268:VAL:HG12	1:I:280:LYS:HE3	1.89	0.53
1:J:269:LEU:CG	1:J:457:SER:O	2.54	0.53
1:K:775:GLY:HA2	1:K:779:PHE:O	2.07	0.53
1:C:387:ILE:O	1:C:421:ARG:NH2	2.42	0.53
1:D:268:VAL:O	1:D:272:ILE:CD1	2.57	0.53
1:D:376:LYS:HA	1:D:376:LYS:HZ3	1.69	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:672:HIS:HA	1:D:877:GLU:OE2	2.08	0.53
1:F:255:ILE:HA	1:F:392:ILE:O	2.09	0.53
1:J:269:LEU:CD2	1:J:457:SER:O	2.55	0.53
1:J:277:PHE:CD1	1:J:278:LEU:N	2.76	0.53
1:J:480:ASN:C	1:J:480:ASN:OD1	2.51	0.53
1:J:543:TYR:O	1:J:546:GLN:CG	2.56	0.53
1:A:278:LEU:HD22	1:A:279:PRO:O	2.08	0.53
1:A:378:LYS:O	1:A:381:GLU:HB3	2.09	0.53
1:B:642:LEU:HD22	1:B:643:GLY:N	2.23	0.53
1:C:434:PRO:HG2	1:C:488:HIS:CG	2.42	0.53
1:D:671:LYS:HD2	1:D:671:LYS:N	2.24	0.53
1:E:454:GLY:H	1:E:500:THR:HG22	1.74	0.53
1:E:610:ARG:HA	1:E:610:ARG:NE	2.22	0.53
1:J:818:LYS:HE3	1:J:819:TYR:CE2	2.43	0.53
1:A:225:ASP:OD1	1:A:225:ASP:N	2.42	0.53
1:A:434:PRO:CG	1:A:488:HIS:CG	2.90	0.53
1:A:901:ILE:O	1:A:904:LEU:HB3	2.07	0.53
1:C:375:LEU:HD23	1:C:375:LEU:N	2.23	0.53
1:C:642:LEU:HD22	1:C:643:GLY:H	1.72	0.53
1:D:297:ASP:HB3	1:D:349:SER:C	2.34	0.53
1:D:352:ILE:C	1:D:352:ILE:HD12	2.33	0.53
1:D:456:ILE:O	1:D:481:GLU:OE2	2.26	0.53
1:D:458:LYS:C	1:D:458:LYS:CD	2.81	0.53
1:D:676:ARG:HG2	1:D:677:LYS:N	2.22	0.53
1:E:269:LEU:HD21	1:E:457:SER:OG	1.70	0.53
1:G:629:HIS:HA	1:G:819:TYR:CD1	2.44	0.53
1:K:295:VAL:HG12	1:K:296:ASN:O	2.08	0.53
1:A:489:PRO:HG2	1:A:490:THR:H	1.74	0.53
1:B:599:ASN:N	1:B:599:ASN:OD1	2.42	0.53
1:D:264:GLY:O	1:D:268:VAL:HG22	2.09	0.53
1:D:559:ASP:HA	1:K:562:LYS:HE3	1.89	0.53
1:D:745:VAL:O	1:E:778:GLY:HA2	2.09	0.53
1:E:308:PRO:HG3	1:E:344:ARG:CG	2.38	0.53
1:F:273:VAL:HG21	1:F:457:SER:HB3	1.90	0.53
1:G:349:SER:HB3	1:G:352:ILE:HG23	1.90	0.53
1:G:532:LEU:HD22	1:G:898:LEU:HD22	1.91	0.53
1:H:258:ILE:HG22	1:H:360:LEU:HD11	1.91	0.53
1:H:263:SER:OG	1:H:397:SER:HA	2.08	0.53
1:H:278:LEU:CD2	1:H:280:LYS:CG	2.85	0.53
1:J:339:THR:O	1:J:340:ASP:HB3	2.08	0.53
1:K:431:LEU:HD23	1:K:431:LEU:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:780:SER:OG	1:L:783:LEU:HB2	2.09	0.53
1:A:231:THR:O	1:A:235:ILE:HG22	2.09	0.53
1:A:269:LEU:CD2	1:A:457:SER:HB2	2.37	0.53
1:B:855:ARG:NH2	1:C:559:ASP:OD2	2.41	0.53
1:E:285:ILE:HG13	1:E:332:VAL:HG22	1.90	0.53
1:E:287:ARG:HG3	1:E:287:ARG:NH1	2.13	0.53
1:H:232:LYS:O	1:H:235:ILE:HG23	2.08	0.53
1:J:456:ILE:O	1:J:456:ILE:HG23	2.09	0.53
1:J:478:ASN:HD21	1:J:482:LYS:CE	2.21	0.53
1:J:485:PHE:CD2	1:J:492:PHE:CE1	2.97	0.53
1:A:286:THR:HB	1:A:361:PRO:CB	2.28	0.53
1:B:322:GLN:O	1:B:326:THR:OG1	2.12	0.53
1:B:873:LYS:O	1:B:877:GLU:HG3	2.09	0.53
1:C:513:LEU:HD23	1:C:517:MET:HE2	1.89	0.53
1:D:555:ALA:HB1	1:K:855:ARG:HD3	1.90	0.53
1:D:871:LEU:HD22	1:D:871:LEU:C	2.34	0.53
1:F:611:GLU:H	1:F:612:PRO:CD	2.22	0.53
1:H:243:LYS:HG2	1:H:243:LYS:O	2.09	0.53
1:H:485:PHE:N	1:H:485:PHE:CD1	2.77	0.53
1:H:528:ILE:HG23	1:H:894:LEU:HD22	1.91	0.53
1:K:456:ILE:HD12	1:K:457:SER:N	2.24	0.53
1:A:257:VAL:HG22	1:A:358:ILE:O	2.09	0.53
1:C:296:ASN:HB2	1:C:354:ASP:OD2	2.09	0.53
1:E:436:LYS:O	1:E:440:ILE:HG13	2.09	0.53
1:E:671:LYS:HE3	1:E:671:LYS:HA	1.90	0.53
1:H:632:LEU:HD22	1:H:632:LEU:O	2.08	0.53
1:A:298:PRO:O	1:A:299:GLU:HB3	2.08	0.53
1:A:355:LEU:HD23	1:A:357:LEU:HD22	1.91	0.53
1:B:297:ASP:HB3	1:B:349:SER:C	2.34	0.53
1:C:249:THR:OG1	1:C:531:GLU:OE1	2.25	0.53
1:C:268:VAL:HB	1:C:280:LYS:HB3	1.91	0.53
1:C:705:TYR:CE1	1:C:832:LYS:HD3	2.44	0.53
1:D:400:ASP:N	1:D:400:ASP:OD1	2.42	0.53
1:D:753:GLU:HB3	1:E:750:LYS:NZ	2.24	0.53
1:E:237:ILE:HD11	1:E:897:VAL:HG13	1.90	0.53
1:E:275:HIS:HB2	1:E:352:ILE:CG2	2.38	0.53
1:F:259:GLY:HA2	1:F:408:ALA:HB2	1.91	0.53
1:F:722:HIS:O	1:F:726:VAL:HG23	2.08	0.53
1:G:285:ILE:HD13	1:G:332:VAL:HG22	1.90	0.53
1:H:441:LEU:CB	1:H:498:VAL:HG11	2.36	0.53
1:J:540:LYS:HA	1:J:545:GLU:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:270:GLU:CA	1:K:273:VAL:HG22	2.38	0.53
1:K:278:LEU:HD22	1:K:280:LYS:HD3	1.88	0.53
1:A:717:ALA:O	1:A:720:ARG:HB3	2.09	0.52
1:A:754:VAL:HA	1:A:779:PHE:HE1	1.74	0.52
1:D:694:THR:O	1:D:698:ILE:HG13	2.08	0.52
1:E:237:ILE:O	1:E:237:ILE:HD13	2.09	0.52
1:F:260:SER:N	1:F:263:SER:HB3	2.24	0.52
1:F:667:SER:OG	1:F:668:SER:N	2.42	0.52
1:H:308:PRO:HG3	1:H:344:ARG:CG	2.40	0.52
1:I:285:ILE:HD12	1:I:287:ARG:H	1.75	0.52
1:J:257:VAL:HG22	1:J:359:ASP:HA	1.88	0.52
1:K:610:ARG:HA	1:K:610:ARG:NE	2.24	0.52
1:K:906:ARG:NH2	1:K:907:ILE:HD13	2.23	0.52
1:L:873:LYS:O	1:L:877:GLU:HG3	2.09	0.52
1:C:393:ILE:HD11	1:C:412:SER:HB2	1.90	0.52
1:E:229:PHE:CD1	1:E:232:LYS:HD2	2.43	0.52
1:E:478:ASN:O	1:E:482:LYS:HG2	2.08	0.52
1:E:485:PHE:HD2	1:E:492:PHE:HD1	1.53	0.52
1:E:701:SER:O	1:E:704:PRO:HD2	2.08	0.52
1:E:843:VAL:HG21	1:F:704:PRO:HA	1.90	0.52
1:F:687:LEU:HD22	1:F:845:MET:HE2	1.90	0.52
1:F:766:ILE:HD12	1:F:767:ILE:H	1.74	0.52
1:H:902:GLU:OE1	1:H:902:GLU:HA	2.08	0.52
1:I:454:GLY:O	1:I:500:THR:HG22	2.09	0.52
1:B:284:MET:HG2	1:B:286:THR:CG2	2.39	0.52
1:B:640:THR:HG22	1:B:706:LYS:HG2	1.92	0.52
1:B:783:LEU:HG	1:I:772:HIS:HE1	1.74	0.52
1:D:251:THR:HG22	1:D:252:LEU:N	2.22	0.52
1:D:269:LEU:CG	1:D:457:SER:O	2.54	0.52
1:F:257:VAL:HG12	1:F:394:LEU:HB3	1.91	0.52
1:F:723:VAL:HG23	1:F:827:ASP:HB2	1.91	0.52
1:H:279:PRO:CG	1:H:322:GLN:HA	2.39	0.52
1:H:349:SER:HB3	1:H:352:ILE:HG23	1.90	0.52
1:J:450:LEU:HD22	1:J:512:VAL:HG21	1.91	0.52
1:K:738:MET:O	1:K:742:GLU:HG3	2.09	0.52
1:A:568:PHE:O	1:A:571:SER:N	2.40	0.52
1:D:578:GLN:HA	1:D:838:VAL:HG21	1.90	0.52
1:D:854:PRO:HB2	1:D:855:ARG:NH1	2.24	0.52
1:E:232:LYS:HA	1:E:235:ILE:CG2	2.39	0.52
1:H:441:LEU:CD2	1:H:498:VAL:CA	2.82	0.52
1:I:279:PRO:CB	1:I:322:GLN:HA	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:508:LYS:O	1:I:512:VAL:HG23	2.10	0.52
1:J:375:LEU:N	1:J:375:LEU:HD23	2.24	0.52
1:L:687:LEU:HD22	1:L:845:MET:HE2	1.91	0.52
1:A:294:LEU:HB2	1:A:355:LEU:H	1.74	0.52
1:C:260:SER:N	1:C:263:SER:HB3	2.25	0.52
1:D:308:PRO:HD2	1:D:344:ARG:O	2.09	0.52
1:D:434:PRO:HB3	1:D:491:GLU:CG	2.39	0.52
1:E:243:LYS:HG2	1:E:243:LYS:O	2.10	0.52
1:E:400:ASP:N	1:E:400:ASP:OD1	2.41	0.52
1:H:488:HIS:HB3	1:H:491:GLU:CD	2.34	0.52
1:H:607:PRO:HA	1:H:762:ARG:O	2.10	0.52
1:J:270:GLU:CA	1:J:273:VAL:HG22	2.37	0.52
1:J:278:LEU:CD2	1:J:280:LYS:CD	2.86	0.52
1:K:229:PHE:HA	1:K:232:LYS:CG	2.39	0.52
1:K:499:SER:O	1:K:500:THR:CG2	2.58	0.52
1:A:238:ARG:HA	1:A:241:LEU:HD12	1.91	0.52
1:A:272:ILE:CG2	1:A:277:PHE:HD1	2.21	0.52
1:C:319:SER:O	1:C:322:GLN:HB3	2.09	0.52
1:E:387:ILE:CG2	1:E:415:VAL:HG21	2.39	0.52
1:F:596:ARG:HB3	1:F:597:TYR:HD1	1.75	0.52
1:H:229:PHE:HA	1:H:232:LYS:HG2	1.91	0.52
1:H:307:PHE:CE1	1:H:345:LEU:CD2	2.91	0.52
1:H:664:LEU:HD23	1:H:676:ARG:HG3	1.92	0.52
1:I:349:SER:O	1:I:352:ILE:HG13	2.09	0.52
1:L:690:ARG:NH1	1:L:844:GLU:OE2	2.42	0.52
1:A:257:VAL:HG23	1:A:359:ASP:HA	1.88	0.52
1:A:276:GLU:HG2	1:A:277:PHE:H	1.75	0.52
1:A:484:TYR:HE1	1:A:492:PHE:HZ	1.58	0.52
1:A:569:ALA:HA	1:A:850:TYR:CZ	2.44	0.52
1:A:704:PRO:HA	1:B:843:VAL:HG21	1.92	0.52
1:B:524:THR:O	1:B:528:ILE:HG13	2.10	0.52
1:C:269:LEU:O	1:C:272:ILE:HB	2.10	0.52
1:D:673:PRO:HD2	1:D:877:GLU:OE1	2.10	0.52
1:E:682:ALA:O	1:E:685:THR:HG22	2.10	0.52
1:G:255:ILE:HA	1:G:392:ILE:O	2.09	0.52
1:G:269:LEU:CD2	1:G:457:SER:HB2	2.40	0.52
1:G:609:PRO:HB2	1:G:611:GLU:N	2.25	0.52
1:H:267:SER:HB2	1:H:396:ILE:HD11	1.92	0.52
1:H:714:ASN:ND2	1:H:715:GLU:H	2.07	0.52
1:J:232:LYS:O	1:J:235:ILE:HG23	2.10	0.52
1:K:478:ASN:CG	1:K:482:LYS:NZ	2.68	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:694:THR:HG21	1:K:845:MET:HE3	1.91	0.52
1:B:484:TYR:HD1	1:B:485:PHE:CD1	2.27	0.52
1:D:273:VAL:HG21	1:D:457:SER:CB	2.39	0.52
1:D:298:PRO:O	1:D:299:GLU:HB3	2.09	0.52
1:E:301:LYS:HD3	1:E:301:LYS:N	2.25	0.52
1:E:834:ALA:O	1:E:838:VAL:HB	2.10	0.52
1:G:235:ILE:HD13	1:G:356:SER:HB2	1.92	0.52
1:H:276:GLU:OE1	1:H:303:ASP:OD1	2.28	0.52
1:I:572:PHE:HD2	1:I:846:LEU:HD11	1.75	0.52
1:I:854:PRO:HB2	1:I:855:ARG:NH2	2.25	0.52
1:J:264:GLY:O	1:J:268:VAL:HG22	2.10	0.52
1:J:272:ILE:CG2	1:J:277:PHE:HD1	2.22	0.52
1:J:524:THR:O	1:J:528:ILE:HG13	2.10	0.52
1:K:240:LEU:HD23	1:K:240:LEU:N	2.25	0.52
1:K:308:PRO:HD2	1:K:344:ARG:O	2.09	0.52
1:K:791:VAL:HG13	1:K:794:ARG:HH22	1.62	0.52
1:L:285:ILE:HG12	1:L:329:ASN:O	2.08	0.52
1:B:255:ILE:HD11	1:B:355:LEU:HG	1.91	0.52
1:B:779:PHE:HA	1:I:777:GLY:H	1.75	0.52
1:D:376:LYS:HA	1:D:376:LYS:HZ1	1.70	0.52
1:D:562:LYS:CE	1:K:562:LYS:CE	2.87	0.52
1:D:752:LYS:HA	1:D:755:MET:HE2	1.91	0.52
1:D:818:LYS:HE3	1:D:819:TYR:CE2	2.45	0.52
1:E:269:LEU:CD2	1:E:457:SER:O	2.58	0.52
1:F:653:ALA:HB2	1:F:845:MET:HE1	1.92	0.52
1:H:279:PRO:HG3	1:H:322:GLN:HA	1.90	0.52
1:K:299:GLU:O	1:K:299:GLU:CG	2.57	0.52
1:C:430:ASP:HB3	1:C:456:ILE:HG12	1.91	0.52
1:H:815:LEU:O	1:H:815:LEU:HD22	2.10	0.52
1:H:871:LEU:HD13	1:H:871:LEU:C	2.35	0.52
1:I:238:ARG:NH1	1:I:252:LEU:O	2.39	0.52
1:K:278:LEU:O	1:K:280:LYS:HG2	2.10	0.52
1:L:224:ASP:HB3	1:L:227:MET:HB2	1.91	0.52
1:A:307:PHE:N	1:A:307:PHE:HD1	2.08	0.51
1:D:269:LEU:HD21	1:D:457:SER:O	2.10	0.51
1:D:269:LEU:CA	1:D:272:ILE:HD12	2.38	0.51
1:D:723:VAL:O	1:D:727:LEU:HB2	2.10	0.51
1:F:596:ARG:HD2	1:F:631:GLN:HG3	1.91	0.51
1:F:854:PRO:HB2	1:F:855:ARG:NH2	2.25	0.51
1:H:363:TYR:CD2	1:H:407:THR:HB	2.45	0.51
1:I:276:GLU:HG2	1:I:277:PHE:H	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:278:LEU:CD1	1:J:278:LEU:H	2.24	0.51
1:J:423:ILE:HG22	1:J:450:LEU:HD13	1.93	0.51
1:J:723:VAL:HG11	1:J:823:GLU:HB3	1.92	0.51
1:L:627:TYR:CE2	1:L:628:TRP:CE3	2.98	0.51
1:A:483:ASN:C	1:A:483:ASN:ND2	2.68	0.51
1:B:609:PRO:C	1:B:611:GLU:HB2	2.34	0.51
1:C:272:ILE:HG23	1:C:277:PHE:HA	1.92	0.51
1:C:630:ARG:HG2	1:C:630:ARG:HH11	1.74	0.51
1:C:903:GLU:HG3	1:C:906:ARG:HH22	1.74	0.51
1:D:257:VAL:O	1:D:257:VAL:HG23	2.09	0.51
1:D:269:LEU:HD21	1:D:457:SER:CA	2.41	0.51
1:D:537:TYR:CE2	1:D:541:VAL:HG23	2.45	0.51
1:D:671:LYS:HD2	1:D:671:LYS:H	1.75	0.51
1:E:267:SER:HB2	1:E:396:ILE:HD11	1.91	0.51
1:H:578:GLN:HA	1:H:838:VAL:HG21	1.91	0.51
1:H:791:VAL:HG13	1:H:794:ARG:NH2	2.25	0.51
1:J:276:GLU:HG2	1:J:277:PHE:H	1.75	0.51
1:J:478:ASN:CG	1:J:482:LYS:HZ2	2.16	0.51
1:A:455:VAL:CG1	1:A:501:GLY:H	2.16	0.51
1:A:485:PHE:CE2	1:A:492:PHE:CD1	2.98	0.51
1:C:232:LYS:HG3	1:C:354:ASP:OD2	2.09	0.51
1:E:251:THR:HG22	1:E:252:LEU:N	2.26	0.51
1:G:705:TYR:CE1	1:G:832:LYS:HD3	2.46	0.51
1:H:275:HIS:CD2	1:H:275:HIS:H	2.27	0.51
1:I:268:VAL:O	1:I:272:ILE:HG13	2.09	0.51
1:I:776:ALA:HA	1:I:783:LEU:CD1	2.40	0.51
1:J:615:ILE:H	1:J:615:ILE:HD12	1.75	0.51
1:B:600:ARG:HB3	1:B:600:ARG:CZ	2.40	0.51
1:B:690:ARG:NH1	1:B:844:GLU:OE2	2.43	0.51
1:D:426:ILE:CD1	1:D:440:ILE:HG21	1.99	0.51
1:E:260:SER:O	1:E:263:SER:N	2.43	0.51
1:E:267:SER:CB	1:E:396:ILE:HG13	2.39	0.51
1:E:499:SER:C	1:E:500:THR:HG23	2.36	0.51
1:F:255:ILE:HD11	1:F:355:LEU:HG	1.92	0.51
1:F:572:PHE:HD2	1:F:846:LEU:HD11	1.76	0.51
1:F:616:ILE:HD12	1:F:616:ILE:O	2.11	0.51
1:G:376:LYS:HZ3	1:G:379:ILE:HD12	1.76	0.51
1:G:780:SER:CB	1:L:778:GLY:O	2.58	0.51
1:H:600:ARG:HB3	1:H:601:PRO:HD2	1.93	0.51
1:H:723:VAL:O	1:H:727:LEU:HB2	2.11	0.51
1:I:775:GLY:CA	1:I:782:ALA:HB3	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:445:GLN:O	1:K:446:TYR:CD1	2.63	0.51
1:A:339:THR:HG23	1:A:340:ASP:H	1.74	0.51
1:C:318:PHE:CD1	1:C:321:ILE:HD12	2.46	0.51
1:C:564:GLN:HG2	1:C:663:LEU:HG	1.92	0.51
1:E:285:ILE:HG12	1:E:287:ARG:N	2.18	0.51
1:E:683:ALA:HB2	1:E:853:PHE:CE1	2.46	0.51
1:E:775:GLY:HA2	1:E:779:PHE:O	2.10	0.51
1:E:855:ARG:HH11	1:E:855:ARG:H	1.58	0.51
1:F:272:ILE:HD11	1:F:280:LYS:HB2	1.92	0.51
1:F:698:ILE:HD11	1:F:841:LEU:HG	1.93	0.51
1:H:308:PRO:HG3	1:H:344:ARG:HB2	1.93	0.51
1:H:642:LEU:HD12	1:H:643:GLY:N	2.25	0.51
1:J:286:THR:O	1:J:361:PRO:HD3	2.10	0.51
1:L:576:GLN:N	1:L:576:GLN:OE1	2.42	0.51
1:L:703:LYS:N	1:L:704:PRO:HD2	2.25	0.51
1:A:272:ILE:HG23	1:A:278:LEU:HD13	1.72	0.51
1:A:752:LYS:HA	1:A:755:MET:HE2	1.92	0.51
1:B:611:GLU:HG3	1:B:611:GLU:O	2.10	0.51
1:C:904:LEU:C	1:C:904:LEU:HD12	2.36	0.51
1:D:339:THR:O	1:D:340:ASP:HB3	2.11	0.51
1:D:739:LYS:O	1:D:742:GLU:HB2	2.11	0.51
1:E:279:PRO:HG3	1:E:321:ILE:HG22	1.91	0.51
1:E:326:THR:HA	1:E:329:ASN:ND2	2.25	0.51
1:F:453:VAL:HG11	1:F:505:LEU:HB2	1.93	0.51
1:G:230:ILE:O	1:G:234:MET:HG3	2.11	0.51
1:G:496:SER:OG	1:G:498:VAL:HG22	2.10	0.51
1:I:276:GLU:HG2	1:I:277:PHE:N	2.25	0.51
1:K:434:PRO:CG	1:K:488:HIS:CG	2.94	0.51
1:A:224:ASP:CG	1:A:227:MET:HB2	2.36	0.51
1:A:255:ILE:HD11	1:A:355:LEU:HG	1.91	0.51
1:B:780:SER:OG	1:I:777:GLY:HA3	2.10	0.51
1:C:275:HIS:HB2	1:C:352:ILE:HG21	1.91	0.51
1:C:360:LEU:HB2	1:C:361:PRO:CD	2.41	0.51
1:D:246:GLN:HG2	1:D:247:GLY:N	2.24	0.51
1:D:750:LYS:HD2	1:E:779:PHE:HE2	1.76	0.51
1:D:768:VAL:O	1:D:770:GLY:N	2.44	0.51
1:E:842:ASN:O	1:E:846:LEU:HB3	2.11	0.51
1:F:387:ILE:O	1:F:421:ARG:NH2	2.43	0.51
1:H:276:GLU:CG	1:H:277:PHE:N	2.74	0.51
1:H:278:LEU:HD21	1:H:280:LYS:CG	2.40	0.51
1:H:752:LYS:HG3	1:H:755:MET:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:285:ILE:O	1:K:286:THR:OG1	2.24	0.51
1:K:485:PHE:HD2	1:K:492:PHE:CD1	2.26	0.51
1:A:251:THR:CG2	1:A:252:LEU:H	2.09	0.51
1:A:665:ASP:OD1	1:A:676:ARG:NH2	2.44	0.51
1:C:600:ARG:HB3	1:C:600:ARG:CZ	2.41	0.51
1:D:615:ILE:H	1:D:615:ILE:HD12	1.76	0.51
1:D:698:ILE:HD11	1:D:841:LEU:HG	1.91	0.51
1:D:723:VAL:HG21	1:D:824:VAL:HA	1.90	0.51
1:D:753:GLU:HG2	1:E:750:LYS:HE2	1.92	0.51
1:E:279:PRO:CG	1:E:322:GLN:HA	2.38	0.51
1:E:377:ARG:NH2	1:E:377:ARG:HG3	2.24	0.51
1:G:269:LEU:O	1:G:273:VAL:HG13	2.11	0.51
1:J:270:GLU:HA	1:J:273:VAL:CG2	2.38	0.51
1:J:286:THR:O	1:J:361:PRO:HG3	2.10	0.51
1:J:363:TYR:HE1	1:J:383:CYS:HG	0.71	0.51
1:K:670:ALA:HB3	1:K:671:LYS:HZ2	1.75	0.51
1:L:227:MET:HA	1:L:230:ILE:HG22	1.93	0.51
1:A:576:GLN:H	1:A:576:GLN:HE21	1.58	0.51
1:A:861:LEU:O	1:A:865:MET:HG2	2.11	0.51
1:E:278:LEU:HB2	1:E:279:PRO:CD	2.37	0.51
1:E:279:PRO:HB3	1:E:322:GLN:CG	2.41	0.51
1:E:492:PHE:CD1	1:E:492:PHE:O	2.63	0.51
1:F:269:LEU:HA	1:F:272:ILE:HD12	1.93	0.51
1:G:493:GLY:O	1:G:496:SER:HB3	2.11	0.51
1:H:269:LEU:HD11	1:H:458:LYS:HB2	1.93	0.51
1:H:285:ILE:HG12	1:H:287:ARG:HB2	1.92	0.51
1:K:393:ILE:HG23	1:K:422:THR:HB	1.93	0.51
1:K:436:LYS:O	1:K:440:ILE:HG13	2.11	0.51
1:K:876:ARG:HB3	1:K:882:ARG:HH21	1.76	0.51
1:L:258:ILE:HG21	1:L:387:ILE:HD11	1.92	0.51
1:A:815:LEU:HD22	1:A:815:LEU:O	2.11	0.51
1:B:429:MET:HE2	1:B:437:GLY:HA2	1.92	0.51
1:D:275:HIS:CG	1:D:276:GLU:H	2.29	0.51
1:E:806:ALA:O	1:E:809:SER:HB3	2.11	0.51
1:G:364:ILE:HD12	1:G:376:LYS:NZ	2.25	0.51
1:H:307:PHE:CD1	1:H:345:LEU:CD2	2.94	0.51
1:I:434:PRO:HG2	1:I:488:HIS:ND1	2.26	0.51
1:J:308:PRO:HG3	1:J:344:ARG:CG	2.40	0.51
1:K:377:ARG:HH21	1:K:377:ARG:CG	2.19	0.51
1:K:657:GLN:HE22	1:K:684:ALA:CA	2.22	0.51
1:C:722:HIS:O	1:C:726:VAL:HG23	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:ILE:HG12	1:D:278:LEU:CD1	2.40	0.50
1:E:544:ASN:HD22	1:I:641:ARG:NH1	2.09	0.50
1:E:749:LYS:H	1:E:749:LYS:CD	2.19	0.50
1:H:241:LEU:HD21	1:H:528:ILE:HD11	1.92	0.50
1:K:339:THR:CG2	1:K:340:ASP:H	2.24	0.50
1:L:289:PRO:HB2	1:L:342:PRO:HB3	1.93	0.50
1:E:275:HIS:CG	1:E:276:GLU:N	2.79	0.50
1:E:454:GLY:O	1:E:455:VAL:HG13	2.11	0.50
1:E:485:PHE:HE2	1:E:500:THR:OG1	1.93	0.50
1:E:670:ALA:C	1:E:671:LYS:HE3	2.36	0.50
1:H:254:SER:HB2	1:H:356:SER:O	2.11	0.50
1:I:230:ILE:HG13	1:I:904:LEU:HD11	1.93	0.50
1:I:276:GLU:HG3	1:I:474:LEU:HD23	1.93	0.50
1:I:627:TYR:HE2	1:I:628:TRP:CZ3	2.29	0.50
1:I:672:HIS:HA	1:I:877:GLU:OE1	2.12	0.50
1:J:454:GLY:O	1:J:455:VAL:HG13	2.10	0.50
1:K:423:ILE:HG22	1:K:450:LEU:HD13	1.93	0.50
1:A:430:ASP:HB3	1:A:456:ILE:HG12	1.93	0.50
1:B:318:PHE:HD1	1:B:321:ILE:CD1	2.19	0.50
1:E:325:LEU:HA	1:E:328:LEU:HD12	1.93	0.50
1:E:491:GLU:H	1:E:491:GLU:CD	2.17	0.50
1:G:485:PHE:CD2	1:G:492:PHE:CD1	2.98	0.50
1:G:798:ASP:O	1:G:802:LEU:HG	2.11	0.50
1:I:585:LEU:HD12	1:I:834:ALA:HB2	1.93	0.50
1:J:413:ARG:CZ	1:J:446:TYR:CE1	2.95	0.50
1:K:614:ASN:OD1	1:K:615:ILE:HD12	2.11	0.50
1:A:276:GLU:HG2	1:A:277:PHE:N	2.25	0.50
1:A:285:ILE:HG12	1:A:287:ARG:HB2	1.93	0.50
1:B:426:ILE:HG21	1:B:429:MET:HE3	1.93	0.50
1:B:483:ASN:ND2	1:B:483:ASN:C	2.69	0.50
1:E:429:MET:HE2	1:E:437:GLY:CA	2.30	0.50
1:I:231:THR:O	1:I:235:ILE:HG22	2.11	0.50
1:I:258:ILE:HG22	1:I:360:LEU:HD11	1.92	0.50
1:J:569:ALA:HB1	1:J:850:TYR:CE2	2.46	0.50
1:K:278:LEU:HD22	1:K:279:PRO:O	2.11	0.50
1:B:376:LYS:HZ3	1:B:376:LYS:HA	1.77	0.50
1:D:854:PRO:HB2	1:D:855:ARG:HH11	1.76	0.50
1:E:575:PRO:O	1:E:578:GLN:HB3	2.12	0.50
1:F:817:ASN:HB2	1:F:820:TYR:HB2	1.93	0.50
1:G:704:PRO:HA	1:H:843:VAL:HG21	1.92	0.50
1:G:800:LEU:O	1:G:804:ILE:HG13	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:694:THR:O	1:H:698:ILE:HG13	2.10	0.50
1:B:784:LEU:O	1:B:788:ARG:HG3	2.11	0.50
1:C:581:LEU:HD12	1:C:838:VAL:HG23	1.93	0.50
1:C:803:ARG:HD2	1:C:823:GLU:CD	2.37	0.50
1:D:544:ASN:HB2	1:L:641:ARG:HD3	1.94	0.50
1:H:339:THR:O	1:H:340:ASP:HB3	2.10	0.50
1:I:272:ILE:HA	1:I:278:LEU:HD12	1.92	0.50
1:J:393:ILE:HG23	1:J:422:THR:HB	1.93	0.50
1:L:692:TYR:CD2	1:L:692:TYR:C	2.90	0.50
1:A:275:HIS:CG	1:A:276:GLU:N	2.79	0.50
1:A:720:ARG:CZ	1:A:813:LYS:HG3	2.41	0.50
1:A:784:LEU:O	1:A:788:ARG:HG3	2.11	0.50
1:B:257:VAL:HG12	1:B:394:LEU:HB3	1.93	0.50
1:B:610:ARG:N	1:B:611:GLU:HA	2.27	0.50
1:D:272:ILE:HG12	1:D:280:LYS:HG3	1.93	0.50
1:D:441:LEU:CB	1:D:498:VAL:HG12	2.41	0.50
1:D:745:VAL:O	1:E:778:GLY:HA3	2.11	0.50
1:E:457:SER:O	1:E:458:LYS:HB2	2.11	0.50
1:E:483:ASN:ND2	1:E:483:ASN:C	2.70	0.50
1:E:810:ARG:O	1:E:813:LYS:HB2	2.12	0.50
1:E:818:LYS:CE	1:E:819:TYR:CE2	2.94	0.50
1:F:429:MET:HE2	1:F:437:GLY:HA2	1.93	0.50
1:H:387:ILE:HG23	1:H:393:ILE:HD12	1.94	0.50
1:I:255:ILE:HG13	1:I:357:LEU:HA	1.94	0.50
1:L:627:TYR:HE2	1:L:628:TRP:CH2	2.26	0.50
1:B:800:LEU:O	1:B:804:ILE:HG13	2.12	0.50
1:E:544:ASN:HD22	1:I:641:ARG:HH11	1.58	0.50
1:F:227:MET:HA	1:F:230:ILE:CG2	2.42	0.50
1:F:251:THR:HG22	1:F:252:LEU:H	1.77	0.50
1:F:426:ILE:HG21	1:F:429:MET:HE3	1.93	0.50
1:F:514:GLU:O	1:F:518:SER:HB3	2.12	0.50
1:F:575:PRO:O	1:F:578:GLN:HB3	2.11	0.50
1:I:325:LEU:HA	1:I:328:LEU:HD12	1.93	0.50
1:J:768:VAL:HG23	1:J:770:GLY:H	1.76	0.50
1:K:496:SER:OG	1:K:498:VAL:CG2	2.60	0.50
1:A:363:TYR:HE1	1:A:383:CYS:HG	0.76	0.50
1:A:508:LYS:O	1:A:512:VAL:HG23	2.11	0.50
1:D:279:PRO:HG3	1:D:321:ILE:HG22	1.93	0.50
1:D:352:ILE:HD12	1:D:352:ILE:O	2.12	0.50
1:D:376:LYS:HA	1:D:376:LYS:CE	2.41	0.50
1:E:267:SER:HB2	1:E:396:ILE:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:474:LEU:HG	1:E:475:ALA:H	1.77	0.50
1:F:279:PRO:HG2	1:F:325:LEU:HD21	1.93	0.50
1:J:441:LEU:HB3	1:J:498:VAL:CG1	2.41	0.50
1:J:640:THR:HG21	1:J:706:LYS:HA	1.93	0.50
1:C:285:ILE:HD13	1:C:332:VAL:HG22	1.93	0.49
1:C:285:ILE:HG12	1:C:329:ASN:O	2.12	0.49
1:C:328:LEU:HD13	1:C:343:ILE:HD13	1.94	0.49
1:E:768:VAL:HG23	1:E:770:GLY:H	1.76	0.49
1:H:255:ILE:HA	1:H:392:ILE:O	2.12	0.49
1:H:278:LEU:CD2	1:H:280:LYS:HD3	2.40	0.49
1:H:454:GLY:O	1:H:500:THR:HG22	2.11	0.49
1:H:670:ALA:CB	1:H:671:LYS:HZ2	2.25	0.49
1:I:581:LEU:HD12	1:I:838:VAL:HG23	1.94	0.49
1:J:477:ILE:O	1:J:477:ILE:HG22	2.11	0.49
1:B:255:ILE:HA	1:B:392:ILE:O	2.13	0.49
1:D:278:LEU:CD2	1:D:280:LYS:CD	2.78	0.49
1:H:339:THR:HG23	1:H:341:ASP:H	1.76	0.49
1:H:714:ASN:HD22	1:H:715:GLU:N	2.10	0.49
1:K:272:ILE:CG2	1:K:277:PHE:HA	2.41	0.49
1:L:268:VAL:O	1:L:272:ILE:HG13	2.12	0.49
1:A:270:GLU:HA	1:A:273:VAL:CG2	2.41	0.49
1:A:294:LEU:HB3	1:A:352:ILE:HD13	1.94	0.49
1:A:441:LEU:HB3	1:A:498:VAL:CG1	2.41	0.49
1:C:355:LEU:HD23	1:C:357:LEU:HD22	1.94	0.49
1:C:565:PHE:CE2	1:C:853:PHE:HD2	2.30	0.49
1:D:640:THR:C	1:D:642:LEU:H	2.20	0.49
1:D:886:ASP:O	1:D:889:ARG:HG3	2.12	0.49
1:E:355:LEU:HD23	1:E:357:LEU:HD22	1.93	0.49
1:J:275:HIS:CG	1:J:276:GLU:N	2.80	0.49
1:K:297:ASP:OD2	1:K:300:ALA:HB3	2.11	0.49
1:C:712:GLN:HB3	1:C:713:PRO:HD2	1.94	0.49
1:D:307:PHE:CD1	1:D:345:LEU:HD23	2.47	0.49
1:E:455:VAL:CG1	1:E:501:GLY:H	2.16	0.49
1:E:572:PHE:O	1:E:576:GLN:NE2	2.46	0.49
1:H:682:ALA:O	1:H:685:THR:HG22	2.12	0.49
1:I:297:ASP:OD2	1:I:300:ALA:HB3	2.12	0.49
1:J:363:TYR:N	1:J:363:TYR:HD1	2.10	0.49
1:J:441:LEU:CB	1:J:498:VAL:CG1	2.89	0.49
1:K:377:ARG:NH2	1:K:377:ARG:CG	2.73	0.49
1:K:478:ASN:CG	1:K:482:LYS:HZ2	2.20	0.49
1:K:834:ALA:O	1:K:838:VAL:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:GLU:OE1	1:A:551:GLU:N	2.45	0.49
1:D:854:PRO:CD	1:D:855:ARG:NH1	2.76	0.49
1:F:224:ASP:HB3	1:F:227:MET:CG	2.41	0.49
1:F:661:GLU:OE2	1:F:676:ARG:NH2	2.45	0.49
1:G:774:SER:O	1:G:780:SER:HB2	2.12	0.49
1:H:296:ASN:C	1:H:298:PRO:HD3	2.37	0.49
1:I:528:ILE:HA	1:I:531:GLU:HG2	1.95	0.49
1:I:609:PRO:HB2	1:I:611:GLU:CB	2.43	0.49
1:K:300:ALA:C	1:K:301:LYS:HD3	2.37	0.49
1:A:264:GLY:O	1:A:268:VAL:HG22	2.12	0.49
1:A:484:TYR:HE1	1:A:492:PHE:CZ	2.29	0.49
1:A:768:VAL:HG23	1:A:770:GLY:H	1.78	0.49
1:B:780:SER:N	1:I:777:GLY:H	2.09	0.49
1:D:474:LEU:HG	1:D:475:ALA:H	1.78	0.49
1:D:854:PRO:CG	1:D:855:ARG:NH1	2.75	0.49
1:E:605:LEU:HD21	1:E:784:LEU:HD12	1.94	0.49
1:F:610:ARG:HD2	1:F:613:ASP:OD1	2.12	0.49
1:G:510:LEU:HD23	1:G:510:LEU:C	2.38	0.49
1:H:854:PRO:HB2	1:H:855:ARG:NH1	2.27	0.49
1:I:360:LEU:HB2	1:I:361:PRO:HD2	1.95	0.49
1:J:275:HIS:H	1:J:275:HIS:HD2	1.61	0.49
1:J:376:LYS:HA	1:J:376:LYS:HZ1	1.77	0.49
1:A:307:PHE:N	1:A:307:PHE:CD1	2.80	0.49
1:D:387:ILE:CG2	1:D:415:VAL:HG21	2.42	0.49
1:F:903:GLU:O	1:F:907:ILE:HG13	2.12	0.49
1:G:376:LYS:NZ	1:G:379:ILE:HD12	2.26	0.49
1:H:237:ILE:O	1:H:237:ILE:CD1	2.58	0.49
1:H:454:GLY:H	1:H:500:THR:HG22	1.78	0.49
1:J:434:PRO:HB3	1:J:491:GLU:CB	2.43	0.49
1:J:832:LYS:O	1:J:836:THR:HG22	2.11	0.49
1:K:238:ARG:NH2	1:K:356:SER:HG	2.11	0.49
1:K:267:SER:HB3	1:K:396:ILE:CG1	2.42	0.49
1:A:258:ILE:HD13	1:A:387:ILE:HD13	1.95	0.49
1:B:241:LEU:HD13	1:B:250:VAL:O	2.12	0.49
1:E:270:GLU:O	1:E:273:VAL:HG22	2.12	0.49
1:G:227:MET:O	1:G:231:THR:OG1	2.28	0.49
1:G:272:ILE:HG23	1:G:277:PHE:HA	1.95	0.49
1:G:505:LEU:C	1:G:505:LEU:HD13	2.38	0.49
1:H:474:LEU:HG	1:H:475:ALA:H	1.78	0.49
1:J:738:MET:O	1:J:742:GLU:HG3	2.12	0.49
1:L:393:ILE:HG23	1:L:422:THR:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:GLN:CG	1:A:247:GLY:N	2.74	0.49
1:A:339:THR:CG2	1:A:340:ASP:N	2.76	0.49
1:B:702:LEU:HD13	1:B:833:LEU:HD22	1.93	0.49
1:B:780:SER:H	1:I:777:GLY:N	2.09	0.49
1:C:233:LYS:HE3	1:C:900:LYS:HD2	1.95	0.49
1:C:294:LEU:HB3	1:C:352:ILE:CD1	2.42	0.49
1:C:749:LYS:O	1:C:753:GLU:HG3	2.13	0.49
1:C:754:VAL:HG21	1:C:783:LEU:HD22	1.94	0.49
1:D:272:ILE:CG2	1:D:277:PHE:HD1	2.25	0.49
1:D:486:GLY:C	1:D:489:PRO:HD3	2.35	0.49
1:D:562:LYS:HZ1	1:K:558:LEU:CD2	2.26	0.49
1:E:286:THR:O	1:E:361:PRO:CB	2.59	0.49
1:E:307:PHE:CD1	1:E:345:LEU:HD21	2.44	0.49
1:E:564:GLN:HG2	1:E:663:LEU:HD11	1.95	0.49
1:E:817:ASN:HB3	1:E:820:TYR:HB2	1.94	0.49
1:F:275:HIS:CG	1:F:276:GLU:H	2.31	0.49
1:F:275:HIS:HB2	1:F:352:ILE:HG21	1.93	0.49
1:G:441:LEU:HD12	1:G:452:TYR:HB2	1.94	0.49
1:G:653:ALA:HB2	1:G:845:MET:HE1	1.94	0.49
1:H:225:ASP:O	1:H:229:PHE:CG	2.66	0.49
1:J:284:MET:HG2	1:J:286:THR:CG2	2.42	0.49
1:K:258:ILE:HG22	1:K:360:LEU:HD11	1.95	0.49
1:B:235:ILE:HD13	1:B:356:SER:HB2	1.95	0.49
1:C:436:LYS:O	1:C:439:ALA:HB3	2.12	0.49
1:E:225:ASP:N	1:E:225:ASP:OD1	2.43	0.49
1:E:450:LEU:HD22	1:E:512:VAL:CG2	2.43	0.49
1:E:485:PHE:CZ	1:E:500:THR:OG1	2.53	0.49
1:F:227:MET:O	1:F:230:ILE:HG22	2.13	0.49
1:F:835:GLN:O	1:F:838:VAL:HB	2.12	0.49
1:H:392:ILE:HD12	1:H:421:ARG:O	2.13	0.49
1:H:871:LEU:O	1:H:874:PHE:HB3	2.13	0.49
1:I:255:ILE:HD11	1:I:355:LEU:HG	1.95	0.49
1:I:326:THR:HA	1:I:329:ASN:ND2	2.28	0.49
1:J:304:TYR:CE1	1:J:348:HIS:HB2	2.48	0.49
1:J:672:HIS:HA	1:J:877:GLU:OE2	2.13	0.49
1:J:771:ASP:N	1:J:771:ASP:OD1	2.46	0.49
1:K:376:LYS:HE2	1:K:376:LYS:CA	2.42	0.49
1:L:444:ARG:NE	1:L:444:ARG:HA	2.27	0.49
1:A:279:PRO:CG	1:A:325:LEU:HD21	2.33	0.48
1:A:457:SER:O	1:A:458:LYS:CB	2.60	0.48
1:A:703:LYS:HE3	1:C:544:ASN:ND2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:707:PHE:CD2	1:B:708:ASP:HB2	2.48	0.48
1:C:599:ASN:OD1	1:C:599:ASN:N	2.43	0.48
1:C:609:PRO:N	1:C:610:ARG:HA	2.28	0.48
1:G:375:LEU:O	1:G:378:LYS:HB2	2.13	0.48
1:I:396:ILE:HG22	1:I:425:VAL:HB	1.94	0.48
1:I:434:PRO:HG2	1:I:488:HIS:CG	2.48	0.48
1:K:254:SER:HB2	1:K:356:SER:O	2.13	0.48
1:K:270:GLU:HA	1:K:273:VAL:CG2	2.42	0.48
1:K:308:PRO:HG3	1:K:344:ARG:CB	2.42	0.48
1:K:485:PHE:HZ	1:K:500:THR:HG1	1.48	0.48
1:L:383:CYS:O	1:L:387:ILE:HG13	2.12	0.48
1:L:610:ARG:N	1:L:611:GLU:HA	2.28	0.48
1:D:285:ILE:CD1	1:D:287:ARG:H	2.26	0.48
1:E:667:SER:OG	1:E:668:SER:N	2.47	0.48
1:H:834:ALA:O	1:H:838:VAL:HB	2.12	0.48
1:I:272:ILE:HG23	1:I:277:PHE:HA	1.94	0.48
1:I:609:PRO:N	1:I:610:ARG:HA	2.28	0.48
1:J:297:ASP:OD2	1:J:300:ALA:CB	2.50	0.48
1:K:363:TYR:CD2	1:K:407:THR:HB	2.47	0.48
1:A:237:ILE:CD1	1:A:241:LEU:HD11	2.43	0.48
1:A:472:ASN:CG	1:A:472:ASN:O	2.56	0.48
1:B:227:MET:O	1:B:230:ILE:HG22	2.12	0.48
1:C:692:TYR:C	1:C:692:TYR:CD2	2.89	0.48
1:D:483:ASN:C	1:D:483:ASN:ND2	2.72	0.48
1:E:232:LYS:HA	1:E:235:ILE:HG22	1.95	0.48
1:E:257:VAL:HG22	1:E:358:ILE:O	2.14	0.48
1:F:224:ASP:HB3	1:F:227:MET:HB2	1.95	0.48
1:H:377:ARG:HH21	1:H:377:ARG:HG3	1.74	0.48
1:J:286:THR:O	1:J:361:PRO:CB	2.61	0.48
1:J:328:LEU:HD13	1:J:343:ILE:HD13	1.95	0.48
1:J:610:ARG:HD3	1:J:611:GLU:O	2.12	0.48
1:K:257:VAL:HG22	1:K:358:ILE:O	2.14	0.48
1:K:275:HIS:CG	1:K:276:GLU:H	2.31	0.48
1:L:749:LYS:O	1:L:753:GLU:HG3	2.14	0.48
1:L:754:VAL:HG12	1:L:787:GLY:HA3	1.94	0.48
1:L:878:ASP:HB3	1:L:881:VAL:HG12	1.94	0.48
1:A:528:ILE:HG23	1:A:894:LEU:HD22	1.96	0.48
1:D:268:VAL:O	1:D:272:ILE:CG1	2.59	0.48
1:D:387:ILE:CG2	1:D:393:ILE:HD12	2.44	0.48
1:D:574:ARG:N	1:D:575:PRO:HD2	2.29	0.48
1:E:240:LEU:N	1:E:240:LEU:CD2	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:307:PHE:CD1	1:E:345:LEU:CD2	2.96	0.48
1:H:430:ASP:OD1	1:H:431:LEU:HD23	2.13	0.48
1:K:263:SER:HA	1:K:266:SER:OG	2.13	0.48
1:K:392:ILE:HD12	1:K:421:ARG:O	2.12	0.48
1:A:392:ILE:HG21	1:A:513:LEU:HD22	1.96	0.48
1:A:485:PHE:CD2	1:A:492:PHE:CE1	3.00	0.48
1:D:285:ILE:CG1	1:D:287:ARG:HB2	2.38	0.48
1:D:690:ARG:NH1	1:D:844:GLU:OE2	2.47	0.48
1:E:232:LYS:HG3	1:E:233:LYS:HE3	1.94	0.48
1:E:694:THR:HG21	1:E:845:MET:HE3	1.95	0.48
1:G:837:ALA:O	1:G:841:LEU:HB2	2.12	0.48
1:H:257:VAL:HG22	1:H:358:ILE:O	2.13	0.48
1:H:270:GLU:HA	1:H:273:VAL:HG22	1.95	0.48
1:H:307:PHE:CZ	1:H:345:LEU:HD21	2.49	0.48
1:H:574:ARG:H	1:H:575:PRO:HD2	1.79	0.48
1:L:672:HIS:HD2	1:L:877:GLU:HB2	1.78	0.48
1:L:701:SER:O	1:L:704:PRO:HD2	2.13	0.48
1:A:484:TYR:CD1	1:A:484:TYR:C	2.92	0.48
1:D:349:SER:HB3	1:D:352:ILE:HG23	1.95	0.48
1:D:441:LEU:CD2	1:D:498:VAL:CA	2.86	0.48
1:D:556:ALA:CB	1:K:855:ARG:NH2	2.76	0.48
1:D:627:TYR:CD2	1:D:628:TRP:CD2	3.02	0.48
1:E:243:LYS:O	1:E:243:LYS:CG	2.61	0.48
1:F:889:ARG:NH2	1:F:893:LEU:HD12	2.29	0.48
1:G:843:VAL:O	1:G:847:ASN:HB2	2.13	0.48
1:J:441:LEU:CB	1:J:498:VAL:HG12	2.44	0.48
1:J:491:GLU:CD	1:J:491:GLU:N	2.71	0.48
1:J:661:GLU:OE2	1:J:676:ARG:NH1	2.46	0.48
1:K:670:ALA:HB3	1:K:671:LYS:CE	2.44	0.48
1:L:611:GLU:H	1:L:612:PRO:CD	2.27	0.48
1:L:723:VAL:HG21	1:L:824:VAL:HA	1.94	0.48
1:A:286:THR:O	1:A:361:PRO:HB3	2.14	0.48
1:B:252:LEU:HD23	1:B:524:THR:HG21	1.96	0.48
1:C:285:ILE:HD12	1:C:287:ARG:HB2	1.95	0.48
1:H:276:GLU:HG2	1:H:277:PHE:H	1.75	0.48
1:H:429:MET:CE	1:H:437:GLY:HA2	2.31	0.48
1:H:714:ASN:ND2	1:H:715:GLU:N	2.61	0.48
1:I:254:SER:HB2	1:I:356:SER:O	2.13	0.48
1:J:426:ILE:CD1	1:J:440:ILE:HG21	2.00	0.48
1:A:276:GLU:OE1	1:A:303:ASP:CG	2.57	0.48
1:B:269:LEU:HD21	1:B:457:SER:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:PHE:CE1	1:B:321:ILE:HD12	2.47	0.48
1:B:628:TRP:CE3	1:B:628:TRP:HA	2.48	0.48
1:C:273:VAL:HG11	1:C:457:SER:HB3	1.95	0.48
1:D:265:LYS:HA	1:D:268:VAL:CG2	2.44	0.48
1:E:430:ASP:C	1:E:430:ASP:OD1	2.53	0.48
1:E:574:ARG:N	1:E:575:PRO:HD2	2.28	0.48
1:E:818:LYS:CE	1:E:819:TYR:CZ	2.96	0.48
1:F:572:PHE:CD2	1:F:846:LEU:HD11	2.49	0.48
1:G:296:ASN:H	1:G:354:ASP:HB3	1.77	0.48
1:G:889:ARG:HH22	1:G:893:LEU:CD1	2.26	0.48
1:H:382:LEU:C	1:H:382:LEU:HD12	2.39	0.48
1:H:751:LEU:O	1:H:755:MET:HG3	2.14	0.48
1:I:255:ILE:HA	1:I:392:ILE:O	2.14	0.48
1:I:267:SER:OG	1:I:268:VAL:N	2.45	0.48
1:I:672:HIS:HD2	1:I:877:GLU:HB2	1.79	0.48
1:I:723:VAL:HG21	1:I:824:VAL:HA	1.95	0.48
1:I:766:ILE:HG13	1:I:767:ILE:N	2.28	0.48
1:J:492:PHE:CD1	1:J:492:PHE:O	2.64	0.48
1:J:876:ARG:HB3	1:J:882:ARG:HH21	1.78	0.48
1:K:702:LEU:HD13	1:K:833:LEU:HD22	1.96	0.48
1:K:705:TYR:CE1	1:K:832:LYS:HD3	2.49	0.48
1:L:307:PHE:CE1	1:L:345:LEU:HD21	2.49	0.48
1:L:429:MET:HE1	1:L:441:LEU:HB2	1.94	0.48
1:A:258:ILE:HG21	1:A:387:ILE:HD11	1.96	0.48
1:B:667:SER:OG	1:B:668:SER:N	2.45	0.48
1:G:785:ALA:HA	1:G:788:ARG:NH1	2.29	0.48
1:H:308:PRO:CG	1:H:344:ARG:HG3	2.43	0.48
1:A:434:PRO:HB3	1:A:491:GLU:CB	2.44	0.48
1:A:474:LEU:HG	1:A:475:ALA:N	2.29	0.48
1:A:723:VAL:O	1:A:727:LEU:HB2	2.13	0.48
1:B:269:LEU:CD2	1:B:457:SER:HB2	2.44	0.48
1:B:803:ARG:HA	1:B:803:ARG:HD3	1.44	0.48
1:C:268:VAL:HG12	1:C:280:LYS:HE3	1.95	0.48
1:D:246:GLN:CD	1:D:247:GLY:N	2.70	0.48
1:D:477:ILE:HG22	1:D:477:ILE:O	2.13	0.48
1:E:308:PRO:CG	1:E:344:ARG:HG3	2.44	0.48
1:F:273:VAL:HG11	1:F:457:SER:HB3	1.96	0.48
1:F:422:THR:HG23	1:F:422:THR:O	2.13	0.48
1:G:393:ILE:HG23	1:G:422:THR:HB	1.95	0.48
1:G:605:LEU:HD22	1:G:606:SER:N	2.29	0.48
1:H:297:ASP:OD1	1:H:300:ALA:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:599:ASN:OD1	1:I:599:ASN:N	2.40	0.48
1:J:237:ILE:HD12	1:J:241:LEU:HD11	1.96	0.48
1:J:285:ILE:HG13	1:J:332:VAL:HG22	1.95	0.48
1:J:300:ALA:C	1:J:301:LYS:HD3	2.38	0.48
1:J:485:PHE:HA	1:J:492:PHE:HE1	1.79	0.48
1:K:539:PHE:CD2	1:K:545:GLU:HG2	2.49	0.48
1:D:376:LYS:HZ1	1:D:379:ILE:HD12	1.75	0.47
1:E:426:ILE:HD11	1:E:440:ILE:CG2	2.04	0.47
1:F:270:GLU:O	1:F:273:VAL:HG22	2.13	0.47
1:H:285:ILE:CD1	1:H:286:THR:N	2.65	0.47
1:H:742:GLU:CD	1:H:748:ARG:HE	2.22	0.47
1:I:529:GLN:O	1:I:533:GLU:HG3	2.14	0.47
1:J:478:ASN:ND2	1:J:482:LYS:CE	2.76	0.47
1:J:817:ASN:HB3	1:J:820:TYR:HB2	1.96	0.47
1:K:749:LYS:H	1:K:749:LYS:HD2	1.79	0.47
1:L:231:THR:O	1:L:235:ILE:HG22	2.14	0.47
1:L:779:PHE:CD2	1:L:779:PHE:N	2.81	0.47
1:A:225:ASP:O	1:A:226:ASN:C	2.56	0.47
1:A:376:LYS:HA	1:A:376:LYS:CE	2.42	0.47
1:B:760:LYS:HB3	1:B:766:ILE:HG22	1.96	0.47
1:D:240:LEU:N	1:D:240:LEU:CD2	2.74	0.47
1:D:286:THR:O	1:D:361:PRO:CD	2.62	0.47
1:F:286:THR:HB	1:F:361:PRO:HB3	1.97	0.47
1:H:237:ILE:HD11	1:H:897:VAL:HG13	1.94	0.47
1:H:294:LEU:HB3	1:H:352:ILE:HD13	1.96	0.47
1:H:392:ILE:HG21	1:H:513:LEU:HD22	1.96	0.47
1:H:488:HIS:O	1:H:491:GLU:HG2	2.14	0.47
1:H:639:LEU:O	1:H:642:LEU:HD23	2.15	0.47
1:I:364:ILE:HD12	1:I:376:LYS:NZ	2.29	0.47
1:I:878:ASP:HB3	1:I:881:VAL:HG12	1.96	0.47
1:K:229:PHE:O	1:K:232:LYS:HG3	2.14	0.47
1:L:262:SER:O	1:L:266:SER:OG	2.32	0.47
1:L:735:GLN:O	1:L:738:MET:HB3	2.14	0.47
1:A:246:GLN:HE22	1:A:890:ARG:NH1	2.12	0.47
1:A:278:LEU:HB2	1:A:279:PRO:HD2	1.95	0.47
1:A:339:THR:HG23	1:A:341:ASP:H	1.79	0.47
1:B:616:ILE:O	1:B:619:PRO:HD2	2.14	0.47
1:B:878:ASP:HB3	1:B:881:VAL:HG12	1.96	0.47
1:C:849:PHE:O	1:C:853:PHE:HB2	2.13	0.47
1:D:454:GLY:N	1:D:500:THR:HG22	2.29	0.47
1:D:565:PHE:HA	1:D:663:LEU:HD21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:225:ASP:O	1:E:226:ASN:C	2.56	0.47
1:E:275:HIS:CD2	1:E:275:HIS:N	2.82	0.47
1:E:484:TYR:CD1	1:E:484:TYR:C	2.92	0.47
1:G:772:HIS:HD1	1:L:780:SER:HB3	1.74	0.47
1:J:642:LEU:O	1:J:644:VAL:N	2.47	0.47
1:K:255:ILE:HD12	1:K:357:LEU:HB3	1.96	0.47
1:A:278:LEU:CD1	1:A:278:LEU:N	2.77	0.47
1:A:401:THR:HG22	1:A:402:ASP:O	2.15	0.47
1:A:664:LEU:HB3	1:A:676:ARG:NH2	2.29	0.47
1:B:774:SER:O	1:I:774:SER:CB	2.52	0.47
1:C:704:PRO:HA	1:D:843:VAL:HG21	1.96	0.47
1:D:540:LYS:HA	1:D:545:GLU:HG3	1.96	0.47
1:D:665:ASP:OD1	1:D:676:ARG:NH2	2.47	0.47
1:E:296:ASN:HB2	1:E:354:ASP:OD2	2.13	0.47
1:E:441:LEU:CB	1:E:498:VAL:HG11	2.44	0.47
1:E:694:THR:HG21	1:E:845:MET:HB2	1.95	0.47
1:E:847:ASN:O	1:E:851:VAL:HG22	2.13	0.47
1:G:426:ILE:HG21	1:G:429:MET:HE3	1.97	0.47
1:G:842:ASN:O	1:G:846:LEU:HB3	2.14	0.47
1:H:325:LEU:HA	1:H:328:LEU:HD12	1.96	0.47
1:H:387:ILE:CG2	1:H:393:ILE:HD12	2.44	0.47
1:H:432:VAL:HG12	1:H:436:LYS:NZ	2.28	0.47
1:H:615:ILE:H	1:H:615:ILE:HD12	1.79	0.47
1:L:640:THR:HG22	1:L:706:LYS:HG2	1.96	0.47
1:A:376:LYS:NZ	1:A:376:LYS:CA	2.69	0.47
1:A:525:THR:HA	1:A:528:ILE:HD12	1.96	0.47
1:C:429:MET:HE1	1:C:441:LEU:HB2	1.97	0.47
1:F:252:LEU:HD23	1:F:524:THR:HG21	1.96	0.47
1:H:285:ILE:HD13	1:H:285:ILE:N	2.29	0.47
1:H:387:ILE:HG21	1:H:415:VAL:HG21	1.96	0.47
1:H:441:LEU:HD21	1:H:498:VAL:C	2.39	0.47
1:H:492:PHE:O	1:H:492:PHE:HD1	1.97	0.47
1:I:375:LEU:N	1:I:375:LEU:HD23	2.30	0.47
1:I:610:ARG:N	1:I:611:GLU:HA	2.28	0.47
1:J:480:ASN:HA	1:J:483:ASN:OD1	2.14	0.47
1:J:815:LEU:O	1:J:815:LEU:HD22	2.15	0.47
1:L:578:GLN:HA	1:L:838:VAL:HG21	1.95	0.47
1:A:853:PHE:HB3	1:A:854:PRO:HD3	1.96	0.47
1:A:874:PHE:CD1	1:A:874:PHE:C	2.92	0.47
1:B:505:LEU:O	1:B:505:LEU:HD22	2.15	0.47
1:B:720:ARG:NH1	1:B:813:LYS:HA	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:270:GLU:CD	1:E:270:GLU:C	2.82	0.47
1:H:325:LEU:HD12	1:H:326:THR:N	2.30	0.47
1:H:679:ILE:O	1:H:682:ALA:HB3	2.15	0.47
1:J:269:LEU:HD23	1:J:269:LEU:C	2.40	0.47
1:J:294:LEU:HB3	1:J:352:ILE:HD13	1.96	0.47
1:J:376:LYS:HE2	1:J:376:LYS:N	2.29	0.47
1:K:279:PRO:CG	1:K:321:ILE:HG22	2.45	0.47
1:K:883:ARG:O	1:K:887:LEU:HB2	2.14	0.47
1:L:854:PRO:HB2	1:L:855:ARG:NH2	2.30	0.47
1:A:285:ILE:CG1	1:A:286:THR:N	2.77	0.47
1:A:618:LEU:HD23	1:A:803:ARG:HH12	1.79	0.47
1:A:771:ASP:OD1	1:A:771:ASP:N	2.48	0.47
1:B:876:ARG:NH1	1:B:886:ASP:OD1	2.45	0.47
1:D:237:ILE:O	1:D:237:ILE:HD13	2.15	0.47
1:D:286:THR:O	1:D:361:PRO:HD3	2.14	0.47
1:D:384:ASP:O	1:D:385:LYS:C	2.53	0.47
1:D:537:TYR:CE1	1:D:540:LYS:CE	2.98	0.47
1:D:559:ASP:OD2	1:K:562:LYS:CD	2.62	0.47
1:E:231:THR:O	1:E:235:ILE:HG22	2.15	0.47
1:E:279:PRO:HG2	1:E:325:LEU:CD2	2.27	0.47
1:E:754:VAL:HA	1:E:779:PHE:CE1	2.49	0.47
1:F:360:LEU:HB2	1:F:361:PRO:HD2	1.95	0.47
1:G:231:THR:O	1:G:235:ILE:HG22	2.14	0.47
1:G:269:LEU:HD21	1:G:457:SER:HB2	1.97	0.47
1:G:873:LYS:HA	1:G:876:ARG:HB2	1.96	0.47
1:H:238:ARG:CZ	1:H:356:SER:OG	2.63	0.47
1:H:252:LEU:CD2	1:H:524:THR:HG21	2.40	0.47
1:H:273:VAL:HG11	1:H:457:SER:HB3	1.91	0.47
1:H:800:LEU:O	1:H:804:ILE:HG13	2.14	0.47
1:I:297:ASP:HB3	1:I:349:SER:C	2.40	0.47
1:I:687:LEU:HD22	1:I:845:MET:HE2	1.95	0.47
1:K:376:LYS:HA	1:K:376:LYS:HZ2	1.72	0.47
1:K:749:LYS:O	1:K:753:GLU:HG3	2.15	0.47
1:A:499:SER:C	1:A:500:THR:HG23	2.39	0.47
1:D:237:ILE:HD12	1:D:241:LEU:HD11	1.97	0.47
1:D:275:HIS:CD2	1:D:275:HIS:N	2.82	0.47
1:D:361:PRO:HD2	1:D:382:LEU:HD21	1.96	0.47
1:E:278:LEU:CD1	1:E:278:LEU:N	2.78	0.47
1:F:303:ASP:OD1	1:F:349:SER:HB2	2.14	0.47
1:F:723:VAL:HG23	1:F:827:ASP:CB	2.45	0.47
1:H:286:THR:HB	1:H:361:PRO:CA	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:502:VAL:HG13	1:I:503:MET:SD	2.54	0.47
1:I:568:PHE:O	1:I:571:SER:N	2.48	0.47
1:J:270:GLU:C	1:J:273:VAL:HG22	2.39	0.47
1:K:278:LEU:HD13	1:K:278:LEU:C	2.40	0.47
1:K:355:LEU:HD23	1:K:357:LEU:HD22	1.94	0.47
1:L:585:LEU:HD12	1:L:834:ALA:HB2	1.97	0.47
1:A:484:TYR:HD1	1:A:485:PHE:CD1	2.33	0.47
1:A:640:THR:HG23	1:A:833:LEU:HD11	1.96	0.47
1:B:853:PHE:HB3	1:B:854:PRO:HD3	1.97	0.47
1:C:602:ILE:HB	1:C:788:ARG:HB3	1.95	0.47
1:D:785:ALA:O	1:D:789:GLU:HG3	2.15	0.47
1:E:778:GLY:C	1:E:779:PHE:HD2	2.23	0.47
1:G:389:GLY:O	1:G:391:ASN:N	2.42	0.47
1:G:602:ILE:HB	1:G:788:ARG:HB3	1.97	0.47
1:H:260:SER:H	1:H:263:SER:HB3	1.80	0.47
1:H:307:PHE:CD1	1:H:345:LEU:HD21	2.50	0.47
1:H:520:LYS:HD3	1:H:520:LYS:HA	1.56	0.47
1:I:263:SER:OG	1:I:396:ILE:O	2.32	0.47
1:K:297:ASP:OD1	1:K:300:ALA:CB	2.63	0.47
1:A:254:SER:HB2	1:A:356:SER:O	2.15	0.47
1:B:266:SER:HA	1:B:269:LEU:HD22	1.97	0.47
1:B:873:LYS:HB2	1:B:873:LYS:HE3	1.70	0.47
1:D:230:ILE:O	1:D:234:MET:HG3	2.15	0.47
1:D:279:PRO:HG2	1:D:325:LEU:CD2	2.31	0.47
1:D:298:PRO:O	1:D:299:GLU:CB	2.63	0.47
1:D:507:LYS:O	1:D:510:LEU:HB3	2.14	0.47
1:F:294:LEU:HB3	1:F:352:ILE:HD13	1.97	0.47
1:G:285:ILE:HD12	1:G:287:ARG:N	2.24	0.47
1:G:772:HIS:O	1:G:780:SER:HA	2.15	0.47
1:H:670:ALA:CB	1:H:671:LYS:NZ	2.78	0.47
1:I:750:LYS:O	1:I:754:VAL:HG23	2.15	0.47
1:J:648:ALA:HB1	1:J:841:LEU:HD12	1.98	0.47
1:K:310:LEU:N	1:K:310:LEU:CD2	2.78	0.47
1:K:485:PHE:HA	1:K:492:PHE:HE1	1.79	0.47
1:L:605:LEU:HD22	1:L:606:SER:O	2.14	0.47
1:A:593:LEU:CD2	1:A:823:GLU:HG3	2.45	0.46
1:A:751:LEU:HA	1:A:754:VAL:HG12	1.97	0.46
1:B:275:HIS:HB2	1:B:352:ILE:HG21	1.97	0.46
1:D:230:ILE:HG13	1:D:904:LEU:HD11	1.97	0.46
1:D:294:LEU:HB2	1:D:355:LEU:H	1.81	0.46
1:D:457:SER:O	1:D:458:LYS:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:848:ASP:HA	1:E:851:VAL:CG2	2.46	0.46
1:F:241:LEU:HD13	1:F:250:VAL:O	2.15	0.46
1:F:383:CYS:O	1:F:387:ILE:HG13	2.14	0.46
1:F:441:LEU:HD12	1:F:452:TYR:HB2	1.96	0.46
1:G:230:ILE:HG13	1:G:904:LEU:CD1	2.45	0.46
1:H:242:GLN:HE22	1:H:344:ARG:CD	2.27	0.46
1:I:393:ILE:HD11	1:I:412:SER:HB2	1.97	0.46
1:I:434:PRO:HB2	1:I:491:GLU:HG3	1.97	0.46
1:J:321:ILE:O	1:J:325:LEU:HG	2.15	0.46
1:K:285:ILE:HG21	1:K:332:VAL:CG2	2.45	0.46
1:K:690:ARG:O	1:K:694:THR:HG23	2.14	0.46
1:L:754:VAL:HG21	1:L:783:LEU:HD22	1.97	0.46
1:A:320:LEU:O	1:A:324:THR:HG23	2.15	0.46
1:A:456:ILE:O	1:A:456:ILE:HG23	2.14	0.46
1:E:246:GLN:CG	1:E:247:GLY:N	2.78	0.46
1:E:285:ILE:CG1	1:E:287:ARG:HB2	2.42	0.46
1:F:227:MET:CA	1:F:230:ILE:HG22	2.45	0.46
1:G:254:SER:O	1:G:391:ASN:HB3	2.15	0.46
1:G:272:ILE:HD11	1:G:280:LYS:HB2	1.97	0.46
1:G:502:VAL:HG13	1:G:503:MET:N	2.30	0.46
1:H:752:LYS:HG3	1:H:755:MET:CE	2.45	0.46
1:I:429:MET:HE1	1:I:441:LEU:HB2	1.97	0.46
1:K:279:PRO:HG3	1:K:321:ILE:C	2.40	0.46
1:L:605:LEU:HD22	1:L:605:LEU:C	2.41	0.46
1:C:622:ASP:OD1	1:C:623:PRO:HD2	2.15	0.46
1:E:238:ARG:NH2	1:E:356:SER:OG	2.48	0.46
1:G:772:HIS:O	1:G:780:SER:CA	2.64	0.46
1:I:294:LEU:HB3	1:I:352:ILE:HD13	1.96	0.46
1:I:876:ARG:HD3	1:I:876:ARG:HA	1.70	0.46
1:K:229:PHE:CD2	1:K:233:LYS:HD2	2.50	0.46
1:A:297:ASP:HB3	1:A:349:SER:C	2.40	0.46
1:B:400:ASP:N	1:B:400:ASP:OD1	2.46	0.46
1:D:670:ALA:HB1	1:D:671:LYS:HZ1	1.80	0.46
1:E:232:LYS:O	1:E:235:ILE:CG2	2.64	0.46
1:E:269:LEU:CD2	1:E:269:LEU:C	2.82	0.46
1:E:433:GLU:O	1:E:436:LYS:HB2	2.15	0.46
1:F:279:PRO:HG3	1:F:321:ILE:HG22	1.97	0.46
1:F:749:LYS:O	1:F:753:GLU:HG3	2.15	0.46
1:H:474:LEU:HG	1:H:475:ALA:N	2.31	0.46
1:I:303:ASP:OD1	1:I:349:SER:HB2	2.14	0.46
1:I:377:ARG:HG3	1:I:378:LYS:N	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:776:ALA:CA	1:I:783:LEU:CD1	2.90	0.46
1:I:784:LEU:O	1:I:788:ARG:HG3	2.16	0.46
1:J:231:THR:O	1:J:235:ILE:HG22	2.15	0.46
1:J:400:ASP:N	1:J:400:ASP:OD1	2.48	0.46
1:J:667:SER:OG	1:J:668:SER:N	2.49	0.46
1:A:278:LEU:HD13	1:A:280:LYS:HG2	1.96	0.46
1:C:269:LEU:HD23	1:C:270:GLU:N	2.30	0.46
1:D:484:TYR:C	1:D:486:GLY:N	2.71	0.46
1:H:255:ILE:HD12	1:H:357:LEU:HB3	1.97	0.46
1:H:285:ILE:CD1	1:H:285:ILE:H	2.28	0.46
1:H:444:ARG:O	1:H:447:PRO:HD3	2.16	0.46
1:J:565:PHE:CE1	1:J:568:PHE:HD2	2.33	0.46
1:K:224:ASP:O	1:K:227:MET:CB	2.63	0.46
1:A:272:ILE:HG23	1:A:278:LEU:N	2.27	0.46
1:B:863:GLU:O	1:B:867:ALA:HB2	2.15	0.46
1:C:748:ARG:O	1:C:749:LYS:C	2.59	0.46
1:D:618:LEU:HB3	1:D:619:PRO:HD3	1.97	0.46
1:F:224:ASP:O	1:F:227:MET:HB2	2.16	0.46
1:F:434:PRO:HG2	1:F:488:HIS:CD2	2.50	0.46
1:G:716:TRP:HZ3	1:G:825:PHE:HB2	1.80	0.46
1:G:803:ARG:HD3	1:G:803:ARG:HA	1.48	0.46
1:H:289:PRO:HB2	1:H:342:PRO:HB3	1.98	0.46
1:I:308:PRO:HG3	1:I:344:ARG:HB2	1.96	0.46
1:I:326:THR:O	1:I:329:ASN:HB2	2.16	0.46
1:I:661:GLU:OE2	1:I:676:ARG:NH2	2.49	0.46
1:J:485:PHE:HE2	1:J:500:THR:OG1	1.93	0.46
1:K:853:PHE:HB3	1:K:854:PRO:HD3	1.96	0.46
1:L:541:VAL:HG13	1:L:542:GLN:HG3	1.96	0.46
1:A:296:ASN:C	1:A:298:PRO:HD3	2.40	0.46
1:A:823:GLU:H	1:A:823:GLU:CD	2.22	0.46
1:A:843:VAL:HG21	1:B:704:PRO:HA	1.98	0.46
1:C:582:LYS:HE2	1:C:831:THR:HG23	1.97	0.46
1:C:672:HIS:HD2	1:C:877:GLU:HB2	1.79	0.46
1:C:821:CYS:O	1:C:824:VAL:HG13	2.15	0.46
1:E:450:LEU:HD22	1:E:512:VAL:HG22	1.97	0.46
1:F:690:ARG:NH1	1:F:844:GLU:OE2	2.48	0.46
1:G:387:ILE:HG21	1:G:393:ILE:HD12	1.98	0.46
1:H:485:PHE:N	1:H:485:PHE:HD1	2.13	0.46
1:I:433:GLU:O	1:I:436:LYS:HB2	2.16	0.46
1:K:308:PRO:CG	1:K:344:ARG:HG3	2.45	0.46
1:K:339:THR:CG2	1:K:340:ASP:N	2.77	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:387:ILE:O	1:K:388:ARG:C	2.58	0.46
1:K:454:GLY:H	1:K:500:THR:HG22	1.81	0.46
1:L:363:TYR:CD2	1:L:407:THR:HB	2.50	0.46
1:A:285:ILE:O	1:A:286:THR:OG1	2.32	0.46
1:B:227:MET:HA	1:B:230:ILE:HG22	1.97	0.46
1:B:275:HIS:CG	1:B:276:GLU:H	2.34	0.46
1:D:441:LEU:HD21	1:D:498:VAL:CA	2.46	0.46
1:E:540:LYS:HA	1:E:545:GLU:HG3	1.98	0.46
1:G:772:HIS:HD2	1:G:779:PHE:O	1.98	0.46
1:G:889:ARG:O	1:G:892:GLU:HG3	2.15	0.46
1:I:778:GLY:O	1:I:783:LEU:HD13	2.15	0.46
1:J:289:PRO:HB2	1:J:342:PRO:HB3	1.96	0.46
1:J:614:ASN:OD1	1:J:616:ILE:HG22	2.15	0.46
1:L:326:THR:HA	1:L:329:ASN:ND2	2.31	0.46
1:A:286:THR:O	1:A:361:PRO:HD3	2.15	0.46
1:C:425:VAL:HA	1:C:453:VAL:O	2.16	0.46
1:C:873:LYS:O	1:C:877:GLU:HG3	2.16	0.46
1:E:252:LEU:HD23	1:E:524:THR:HG21	1.97	0.46
1:E:269:LEU:HD23	1:E:457:SER:OG	2.02	0.46
1:E:272:ILE:HG23	1:E:278:LEU:N	2.23	0.46
1:E:477:ILE:O	1:E:481:GLU:OE1	2.34	0.46
1:E:672:HIS:HA	1:E:877:GLU:CD	2.41	0.46
1:F:254:SER:HB2	1:F:356:SER:O	2.15	0.46
1:J:257:VAL:HG23	1:J:257:VAL:O	2.16	0.46
1:K:297:ASP:OD1	1:K:300:ALA:HB3	2.14	0.46
1:K:871:LEU:O	1:K:874:PHE:HB3	2.16	0.46
1:L:458:LYS:HD2	1:L:458:LYS:C	2.41	0.46
1:B:766:ILE:HD12	1:B:767:ILE:N	2.31	0.46
1:D:311:GLY:O	1:D:312:LEU:HB2	2.16	0.46
1:E:311:GLY:O	1:E:312:LEU:HB2	2.16	0.46
1:G:832:LYS:O	1:G:835:GLN:HG2	2.16	0.46
1:H:267:SER:CB	1:H:396:ILE:CD1	2.93	0.46
1:I:273:VAL:HG11	1:I:457:SER:HB3	1.98	0.46
1:J:279:PRO:O	1:J:280:LYS:HD2	2.15	0.46
1:J:434:PRO:CG	1:J:488:HIS:CG	2.98	0.46
1:J:889:ARG:HG3	1:J:890:ARG:N	2.29	0.46
1:L:486:GLY:O	1:L:489:PRO:HD3	2.16	0.46
1:A:269:LEU:HD21	1:A:457:SER:C	2.41	0.45
1:B:727:LEU:HB3	1:B:804:ILE:HG12	1.97	0.45
1:B:727:LEU:HD12	1:B:727:LEU:HA	1.82	0.45
1:D:401:THR:HG23	1:D:405:ASN:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:723:VAL:HG11	1:D:823:GLU:HB3	1.98	0.45
1:D:855:ARG:CZ	1:K:556:ALA:HA	2.46	0.45
1:E:426:ILE:HD12	1:E:440:ILE:CG2	2.05	0.45
1:E:555:ALA:HB3	1:J:855:ARG:CD	2.46	0.45
1:F:488:HIS:HB3	1:F:491:GLU:CG	2.46	0.45
1:H:339:THR:HG22	1:H:340:ASP:H	1.80	0.45
1:I:569:ALA:HB1	1:I:850:TYR:CZ	2.51	0.45
1:I:678:VAL:HG11	1:I:861:LEU:HD23	1.99	0.45
1:I:776:ALA:HA	1:I:783:LEU:HD12	1.95	0.45
1:K:375:LEU:HB2	1:K:376:LYS:HE2	1.98	0.45
1:K:907:ILE:HD12	1:K:907:ILE:HA	1.87	0.45
1:L:605:LEU:HD22	1:L:606:SER:N	2.31	0.45
1:L:656:ILE:HD11	1:L:846:LEU:HD12	1.98	0.45
1:A:875:ALA:HB1	1:A:885:LEU:CD1	2.47	0.45
1:B:339:THR:HG23	1:B:340:ASP:N	2.32	0.45
1:B:530:ARG:HD3	1:B:530:ARG:HA	1.54	0.45
1:C:863:GLU:O	1:C:867:ALA:HB2	2.15	0.45
1:D:357:LEU:HD23	1:D:357:LEU:H	1.81	0.45
1:G:235:ILE:HD12	1:G:238:ARG:HD3	1.98	0.45
1:G:319:SER:O	1:G:322:GLN:HB3	2.16	0.45
1:G:776:ALA:O	1:L:757:PHE:CE1	2.69	0.45
1:H:754:VAL:HA	1:H:779:PHE:CE1	2.51	0.45
1:J:234:MET:HE1	1:J:518:SER:OG	2.17	0.45
1:J:246:GLN:HG2	1:J:247:GLY:N	2.30	0.45
1:J:268:VAL:O	1:J:272:ILE:HG13	2.16	0.45
1:J:621:ALA:O	1:J:820:TYR:OH	2.28	0.45
1:K:229:PHE:HA	1:K:232:LYS:HD2	1.97	0.45
1:K:263:SER:OG	1:K:397:SER:HA	2.15	0.45
1:K:275:HIS:CG	1:K:276:GLU:N	2.85	0.45
1:K:376:LYS:HZ2	1:K:376:LYS:HG3	1.33	0.45
1:K:381:GLU:OE1	1:K:381:GLU:CA	2.63	0.45
1:B:750:LYS:O	1:B:754:VAL:HG23	2.16	0.45
1:C:272:ILE:HD11	1:C:280:LYS:HB2	1.98	0.45
1:D:238:ARG:NH2	1:D:356:SER:OG	2.49	0.45
1:D:269:LEU:HD11	1:D:458:LYS:HB2	1.98	0.45
1:D:318:PHE:CD1	1:D:321:ILE:HD12	2.51	0.45
1:D:382:LEU:C	1:D:382:LEU:CD1	2.88	0.45
1:E:282:SER:HB2	1:E:283:ASN:H	1.65	0.45
1:E:375:LEU:N	1:E:375:LEU:HD23	2.31	0.45
1:E:377:ARG:HG2	1:E:377:ARG:NH2	2.21	0.45
1:G:656:ILE:HD11	1:G:846:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:237:ILE:HD13	1:H:237:ILE:C	2.37	0.45
1:H:285:ILE:CD1	1:H:285:ILE:N	2.79	0.45
1:H:360:LEU:HB2	1:H:361:PRO:HD2	1.99	0.45
1:H:550:ALA:O	1:H:553:TYR:HB3	2.17	0.45
1:H:690:ARG:O	1:H:694:THR:HG23	2.17	0.45
1:I:572:PHE:HB3	1:I:850:TYR:OH	2.16	0.45
1:J:279:PRO:O	1:J:280:LYS:CD	2.64	0.45
1:K:387:ILE:HG21	1:K:393:ILE:HD12	1.97	0.45
1:K:670:ALA:CB	1:K:671:LYS:NZ	2.79	0.45
1:A:278:LEU:HD12	1:A:278:LEU:N	2.31	0.45
1:A:540:LYS:HA	1:A:545:GLU:HG3	1.98	0.45
1:B:258:ILE:HG22	1:B:360:LEU:HD11	1.98	0.45
1:E:473:LEU:O	1:E:476:SER:OG	2.32	0.45
1:G:611:GLU:N	1:G:612:PRO:CD	2.79	0.45
1:H:268:VAL:O	1:H:272:ILE:CD1	2.65	0.45
1:I:258:ILE:HG21	1:I:387:ILE:HD11	1.98	0.45
1:L:227:MET:O	1:L:231:THR:OG1	2.31	0.45
1:A:234:MET:C	1:A:237:ILE:HG22	2.42	0.45
1:A:581:LEU:HD12	1:A:838:VAL:HG23	1.98	0.45
1:C:492:PHE:O	1:C:492:PHE:CD1	2.69	0.45
1:C:758:VAL:HB	1:C:791:VAL:HG21	1.97	0.45
1:D:246:GLN:C	1:D:248:SER:H	2.23	0.45
1:D:434:PRO:HG2	1:D:488:HIS:CE1	2.51	0.45
1:D:863:GLU:O	1:D:867:ALA:HB3	2.16	0.45
1:E:639:LEU:O	1:E:642:LEU:HD23	2.16	0.45
1:F:269:LEU:O	1:F:272:ILE:HB	2.16	0.45
1:H:703:LYS:N	1:H:704:PRO:HD2	2.31	0.45
1:H:751:LEU:O	1:H:754:VAL:HG12	2.16	0.45
1:I:738:MET:HE3	1:I:742:GLU:OE2	2.16	0.45
1:I:766:ILE:HG13	1:I:767:ILE:H	1.81	0.45
1:J:232:LYS:HA	1:J:235:ILE:CG2	2.47	0.45
1:J:235:ILE:HD12	1:J:235:ILE:O	2.16	0.45
1:K:272:ILE:HG23	1:K:278:LEU:N	2.30	0.45
1:K:485:PHE:HE2	1:K:500:THR:OG1	1.90	0.45
1:A:376:LYS:HA	1:A:376:LYS:HZ1	1.75	0.45
1:A:429:MET:HE2	1:A:437:GLY:CA	2.32	0.45
1:A:861:LEU:HA	1:A:861:LEU:HD23	1.80	0.45
1:B:529:GLN:HG2	1:B:898:LEU:HD21	1.99	0.45
1:C:698:ILE:HD11	1:C:841:LEU:HG	1.99	0.45
1:C:804:ILE:O	1:C:808:LYS:HG3	2.17	0.45
1:C:903:GLU:HG3	1:C:906:ARG:CZ	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:LEU:HD21	1:D:280:LYS:CD	2.40	0.45
1:D:855:ARG:HE	1:K:556:ALA:CA	2.29	0.45
1:E:294:LEU:HB2	1:E:355:LEU:H	1.82	0.45
1:E:392:ILE:HD11	1:E:423:ILE:HG23	1.97	0.45
1:E:855:ARG:N	1:E:855:ARG:HH11	2.14	0.45
1:F:293:THR:OG1	1:F:346:THR:HG23	2.17	0.45
1:G:294:LEU:HB2	1:G:355:LEU:H	1.81	0.45
1:G:425:VAL:HG12	1:G:427:THR:HG23	1.99	0.45
1:I:349:SER:HB3	1:I:352:ILE:HG12	1.98	0.45
1:K:278:LEU:CD2	1:K:280:LYS:CD	2.83	0.45
1:K:485:PHE:O	1:K:489:PRO:HA	2.17	0.45
1:A:276:GLU:OE1	1:A:303:ASP:OD1	2.35	0.45
1:A:791:VAL:HG13	1:A:794:ARG:NH2	2.30	0.45
1:B:607:PRO:HD3	1:B:762:ARG:HG3	1.98	0.45
1:D:284:MET:O	1:D:286:THR:HG23	2.17	0.45
1:E:275:HIS:HB2	1:E:352:ILE:HG21	1.99	0.45
1:E:889:ARG:HH21	1:E:893:LEU:HG	1.81	0.45
1:H:485:PHE:O	1:H:489:PRO:N	2.50	0.45
1:J:671:LYS:HD2	1:J:671:LYS:N	2.31	0.45
1:A:287:ARG:HH11	1:A:287:ARG:HG3	1.82	0.45
1:A:377:ARG:HG2	1:A:377:ARG:HH21	1.82	0.45
1:A:441:LEU:CB	1:A:498:VAL:CG1	2.95	0.45
1:D:276:GLU:CG	1:D:277:PHE:N	2.78	0.45
1:D:288:ARG:HA	1:D:289:PRO:HD3	1.64	0.45
1:D:775:GLY:HA2	1:D:779:PHE:O	2.17	0.45
1:E:585:LEU:HD12	1:E:834:ALA:HB2	1.98	0.45
1:F:640:THR:HG22	1:F:706:LYS:HG2	1.98	0.45
1:G:750:LYS:O	1:G:754:VAL:HG23	2.17	0.45
1:H:246:GLN:CG	1:H:247:GLY:N	2.80	0.45
1:I:255:ILE:HG12	1:I:513:LEU:HD12	1.99	0.45
1:J:473:LEU:O	1:J:474:LEU:C	2.60	0.45
1:K:670:ALA:CB	1:K:671:LYS:HE3	2.47	0.45
1:L:224:ASP:CG	1:L:227:MET:HG3	2.42	0.45
1:L:326:THR:O	1:L:329:ASN:HB2	2.17	0.45
1:L:728:GLN:O	1:L:732:GLU:HG3	2.16	0.45
1:A:270:GLU:CA	1:A:273:VAL:HG22	2.46	0.45
1:A:285:ILE:CD1	1:A:285:ILE:N	2.79	0.45
1:A:321:ILE:HA	1:A:324:THR:OG1	2.16	0.45
1:A:449:LYS:C	1:A:451:GLY:H	2.25	0.45
1:A:671:LYS:N	1:A:671:LYS:CD	2.77	0.45
1:B:609:PRO:N	1:B:610:ARG:CA	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276:GLU:HG2	1:C:277:PHE:N	2.32	0.45
1:F:272:ILE:HG23	1:F:277:PHE:HA	1.97	0.45
1:G:258:ILE:HG21	1:G:387:ILE:HD11	1.99	0.45
1:H:752:LYS:HA	1:H:755:MET:CE	2.46	0.45
1:H:832:LYS:O	1:H:836:THR:HG22	2.17	0.45
1:J:311:GLY:O	1:J:312:LEU:CB	2.65	0.45
1:K:642:LEU:HD12	1:K:643:GLY:N	2.31	0.45
1:L:582:LYS:HE2	1:L:831:THR:HG23	1.98	0.45
1:A:277:PHE:O	1:A:318:PHE:CD2	2.70	0.45
1:A:376:LYS:HZ2	1:A:379:ILE:HD12	1.81	0.45
1:B:578:GLN:HA	1:B:838:VAL:HG21	1.98	0.45
1:C:772:HIS:HD2	1:C:775:GLY:O	2.00	0.45
1:D:559:ASP:CG	1:K:562:LYS:CD	2.90	0.45
1:E:285:ILE:C	1:E:286:THR:HG1	2.18	0.45
1:E:326:THR:HG22	1:E:329:ASN:ND2	2.32	0.45
1:E:425:VAL:HA	1:E:453:VAL:O	2.16	0.45
1:G:260:SER:H	1:G:263:SER:HB3	1.81	0.45
1:G:505:LEU:HD22	1:G:505:LEU:O	2.16	0.45
1:G:627:TYR:CZ	1:G:631:GLN:NE2	2.83	0.45
1:H:285:ILE:CG1	1:H:286:THR:N	2.79	0.45
1:I:754:VAL:O	1:I:758:VAL:HG23	2.16	0.45
1:I:854:PRO:O	1:I:858:GLU:HG3	2.17	0.45
1:J:267:SER:CB	1:J:396:ILE:CD1	2.89	0.45
1:J:278:LEU:HD22	1:J:279:PRO:O	2.17	0.45
1:J:396:ILE:HG22	1:J:425:VAL:HB	1.99	0.45
1:J:690:ARG:O	1:J:694:THR:HG23	2.17	0.45
1:K:230:ILE:CG2	1:K:231:THR:N	2.79	0.45
1:K:376:LYS:N	1:K:376:LYS:CE	2.74	0.45
1:K:493:GLY:O	1:K:496:SER:HB3	2.16	0.45
1:A:233:LYS:CA	1:A:233:LYS:CE	2.96	0.44
1:B:806:ALA:O	1:B:809:SER:HB3	2.17	0.44
1:C:239:ASN:HD21	1:C:293:THR:HG21	1.82	0.44
1:D:232:LYS:HA	1:D:235:ILE:HG22	1.99	0.44
1:E:269:LEU:HD23	1:E:270:GLU:N	2.31	0.44
1:E:484:TYR:CE1	1:E:492:PHE:HZ	2.33	0.44
1:E:592:GLN:HG2	1:E:635:ALA:O	2.17	0.44
1:E:617:ASP:OD1	1:E:617:ASP:N	2.50	0.44
1:F:279:PRO:HB3	1:F:322:GLN:CA	2.47	0.44
1:I:602:ILE:HB	1:I:788:ARG:HB3	1.99	0.44
1:J:265:LYS:HA	1:J:268:VAL:CG2	2.47	0.44
1:J:453:VAL:HG21	1:J:505:LEU:HD23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:593:LEU:HD21	1:J:823:GLU:HG3	1.99	0.44
1:K:275:HIS:HB2	1:K:352:ILE:HG21	1.99	0.44
1:L:702:LEU:HA	1:L:702:LEU:HD23	1.72	0.44
1:A:607:PRO:HA	1:A:762:ARG:O	2.17	0.44
1:B:720:ARG:O	1:B:724:VAL:HG23	2.17	0.44
1:C:252:LEU:HD23	1:C:524:THR:HG21	1.98	0.44
1:D:275:HIS:CG	1:D:276:GLU:N	2.85	0.44
1:E:345:LEU:HA	1:E:345:LEU:HD23	1.74	0.44
1:J:450:LEU:HD22	1:J:512:VAL:CG2	2.46	0.44
1:A:738:MET:O	1:A:742:GLU:HG3	2.16	0.44
1:D:528:ILE:HG23	1:D:894:LEU:HD22	1.98	0.44
1:E:777:GLY:O	1:E:779:PHE:CE2	2.71	0.44
1:F:227:MET:O	1:F:231:THR:OG1	2.28	0.44
1:F:664:LEU:HB3	1:F:676:ARG:NH1	2.33	0.44
1:H:225:ASP:O	1:H:226:ASN:C	2.58	0.44
1:H:285:ILE:HG12	1:H:287:ARG:N	2.11	0.44
1:H:454:GLY:N	1:H:500:THR:HG22	2.32	0.44
1:I:664:LEU:HD23	1:I:676:ARG:HG3	2.00	0.44
1:J:260:SER:N	1:J:263:SER:HB3	2.32	0.44
1:K:237:ILE:HD12	1:K:241:LEU:HD11	1.99	0.44
1:K:441:LEU:HD21	1:K:498:VAL:CB	2.20	0.44
1:L:442:SER:HB2	1:L:498:VAL:HG12	1.97	0.44
1:D:491:GLU:N	1:D:491:GLU:OE2	2.50	0.44
1:D:907:ILE:HD12	1:D:907:ILE:HA	1.87	0.44
1:E:229:PHE:O	1:E:232:LYS:HG3	2.16	0.44
1:F:297:ASP:CG	1:F:300:ALA:HB3	2.42	0.44
1:F:420:GLU:HG3	1:F:449:LYS:HE2	2.00	0.44
1:F:832:LYS:O	1:F:835:GLN:HG2	2.16	0.44
1:G:241:LEU:HD13	1:G:250:VAL:O	2.17	0.44
1:H:308:PRO:HD2	1:H:344:ARG:O	2.17	0.44
1:H:513:LEU:O	1:H:517:MET:HB2	2.18	0.44
1:H:539:PHE:CD2	1:H:545:GLU:HG2	2.53	0.44
1:J:267:SER:HB2	1:J:396:ILE:HD11	1.97	0.44
1:K:472:ASN:CG	1:K:472:ASN:O	2.58	0.44
1:L:423:ILE:HG22	1:L:450:LEU:HD13	1.98	0.44
1:L:622:ASP:OD1	1:L:623:PRO:HD2	2.18	0.44
1:A:257:VAL:HG21	1:A:359:ASP:HB2	1.99	0.44
1:A:287:ARG:HD2	1:A:332:VAL:CG1	2.48	0.44
1:A:791:VAL:HG13	1:A:794:ARG:HH21	1.83	0.44
1:C:285:ILE:CD1	1:C:287:ARG:HB2	2.47	0.44
1:D:614:ASN:OD1	1:D:616:ILE:CG2	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:690:ARG:O	1:D:694:THR:HG23	2.17	0.44
1:E:269:LEU:CG	1:E:457:SER:O	2.64	0.44
1:E:441:LEU:CD2	1:E:498:VAL:CA	2.89	0.44
1:G:264:GLY:HA2	1:G:267:SER:HB3	1.99	0.44
1:G:642:LEU:HD22	1:G:643:GLY:N	2.22	0.44
1:H:269:LEU:CD2	1:H:269:LEU:C	2.86	0.44
1:H:286:THR:O	1:H:361:PRO:CD	2.65	0.44
1:H:701:SER:O	1:H:704:PRO:HD2	2.16	0.44
1:I:879:PRO:HB2	1:I:883:ARG:HH21	1.81	0.44
1:J:286:THR:O	1:J:361:PRO:CD	2.65	0.44
1:L:429:MET:HE2	1:L:437:GLY:HA2	2.00	0.44
1:L:609:PRO:HB2	1:L:611:GLU:N	2.33	0.44
1:L:650:THR:O	1:L:653:ALA:HB3	2.17	0.44
1:A:272:ILE:H	1:A:272:ILE:HG13	1.61	0.44
1:A:278:LEU:HD21	1:A:280:LYS:CD	2.25	0.44
1:A:306:GLU:C	1:A:307:PHE:HD1	2.26	0.44
1:A:454:GLY:O	1:A:500:THR:CB	2.65	0.44
1:A:576:GLN:NE2	1:A:576:GLN:N	2.59	0.44
1:C:572:PHE:HB3	1:C:850:TYR:OH	2.18	0.44
1:D:269:LEU:HD23	1:D:270:GLU:N	2.33	0.44
1:D:276:GLU:OE1	1:D:303:ASP:CG	2.61	0.44
1:D:278:LEU:HD22	1:D:280:LYS:HG2	1.98	0.44
1:E:233:LYS:HE2	1:E:233:LYS:HA	2.00	0.44
1:E:272:ILE:HG12	1:E:280:LYS:CG	2.47	0.44
1:G:778:GLY:H	1:L:779:PHE:CB	2.27	0.44
1:G:832:LYS:O	1:G:836:THR:HG22	2.17	0.44
1:K:434:PRO:HB3	1:K:491:GLU:CG	2.46	0.44
1:K:875:ALA:HB1	1:K:885:LEU:HD13	1.99	0.44
1:L:458:LYS:C	1:L:458:LYS:HZ3	2.25	0.44
1:A:224:ASP:O	1:A:227:MET:CB	2.66	0.44
1:A:575:PRO:O	1:A:578:GLN:HB3	2.18	0.44
1:B:814:THR:HG23	1:B:817:ASN:OD1	2.17	0.44
1:C:484:TYR:HD1	1:C:485:PHE:CD1	2.35	0.44
1:C:600:ARG:HB3	1:C:600:ARG:NH1	2.33	0.44
1:E:441:LEU:HD21	1:E:498:VAL:CA	2.47	0.44
1:F:364:ILE:HD12	1:F:376:LYS:NZ	2.32	0.44
1:G:321:ILE:HA	1:G:324:THR:HG1	1.82	0.44
1:I:605:LEU:HD13	1:I:606:SER:O	2.17	0.44
1:J:232:LYS:HG3	1:J:233:LYS:CE	2.48	0.44
1:J:388:ARG:O	1:J:389:GLY:C	2.59	0.44
1:J:617:ASP:OD1	1:J:617:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:588:LYS:HD3	1:L:588:LYS:HA	1.74	0.44
1:A:705:TYR:CE1	1:A:832:LYS:HD3	2.53	0.44
1:B:778:GLY:C	1:I:776:ALA:HB1	2.43	0.44
1:C:735:GLN:O	1:C:738:MET:HB3	2.18	0.44
1:D:241:LEU:O	1:D:244:VAL:HG23	2.18	0.44
1:D:295:VAL:O	1:D:352:ILE:HD11	2.17	0.44
1:E:392:ILE:HD12	1:E:421:ARG:O	2.18	0.44
1:F:275:HIS:CG	1:F:276:GLU:N	2.85	0.44
1:F:431:LEU:HD23	1:F:431:LEU:H	1.83	0.44
1:G:473:LEU:O	1:G:477:ILE:HG13	2.18	0.44
1:G:692:TYR:C	1:G:692:TYR:CD2	2.95	0.44
1:H:265:LYS:HA	1:H:268:VAL:CG2	2.48	0.44
1:H:416:ASP:OD2	1:H:422:THR:HG22	2.18	0.44
1:J:664:LEU:HB3	1:J:676:ARG:NH2	2.32	0.44
1:K:307:PHE:CD1	1:K:345:LEU:HD23	2.52	0.44
1:K:778:GLY:C	1:K:779:PHE:HD2	2.26	0.44
1:L:237:ILE:HD11	1:L:897:VAL:HG13	2.00	0.44
1:A:682:ALA:O	1:A:686:VAL:HG23	2.18	0.44
1:B:640:THR:HG21	1:B:706:LYS:HA	2.00	0.44
1:C:357:LEU:HD23	1:C:357:LEU:H	1.83	0.44
1:D:458:LYS:HE2	1:D:458:LYS:O	2.17	0.44
1:D:810:ARG:O	1:D:813:LYS:HB2	2.18	0.44
1:E:244:VAL:HB	1:E:248:SER:OG	2.18	0.44
1:E:387:ILE:HG22	1:E:415:VAL:HG21	1.98	0.44
1:F:596:ARG:HB3	1:F:597:TYR:CD1	2.52	0.44
1:G:609:PRO:HB2	1:G:611:GLU:HB2	2.00	0.44
1:H:296:ASN:HB2	1:H:354:ASP:OD2	2.18	0.44
1:H:749:LYS:O	1:H:753:GLU:HG3	2.18	0.44
1:I:272:ILE:HD11	1:I:280:LYS:HB2	1.99	0.44
1:I:640:THR:HG21	1:I:706:LYS:HA	1.99	0.44
1:J:478:ASN:OD1	1:J:482:LYS:HE3	2.17	0.44
1:J:618:LEU:HD23	1:J:803:ARG:NH1	2.33	0.44
1:J:818:LYS:HG2	1:J:819:TYR:N	2.33	0.44
1:K:266:SER:CB	1:K:427:THR:OG1	2.65	0.44
1:B:285:ILE:HD13	1:B:332:VAL:HG22	2.00	0.43
1:C:293:THR:O	1:C:346:THR:HA	2.18	0.43
1:C:642:LEU:HD13	1:C:643:GLY:N	2.33	0.43
1:C:904:LEU:HD12	1:C:904:LEU:O	2.17	0.43
1:D:272:ILE:HG13	1:D:272:ILE:H	1.55	0.43
1:E:244:VAL:HG11	1:E:894:LEU:HD21	2.00	0.43
1:G:507:LYS:HE3	1:G:507:LYS:HB2	1.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:318:PHE:HD1	1:H:321:ILE:HD12	1.83	0.43
1:I:798:ASP:O	1:I:799:ILE:C	2.61	0.43
1:J:520:LYS:HA	1:J:520:LYS:HD3	1.64	0.43
1:B:321:ILE:O	1:B:322:GLN:C	2.60	0.43
1:B:664:LEU:HD23	1:B:676:ARG:HG3	1.99	0.43
1:C:450:LEU:O	1:C:508:LYS:NZ	2.51	0.43
1:D:278:LEU:CD1	1:D:278:LEU:N	2.81	0.43
1:D:279:PRO:HB2	1:D:322:GLN:HA	1.97	0.43
1:D:559:ASP:OD1	1:K:562:LYS:NZ	2.47	0.43
1:D:754:VAL:HA	1:D:779:PHE:CE1	2.53	0.43
1:E:381:GLU:OE1	1:E:381:GLU:HA	2.18	0.43
1:F:355:LEU:HD23	1:F:357:LEU:HD22	1.98	0.43
1:F:599:ASN:OD1	1:F:599:ASN:N	2.43	0.43
1:F:803:ARG:HD2	1:F:823:GLU:CD	2.44	0.43
1:G:661:GLU:OE2	1:G:676:ARG:NH2	2.51	0.43
1:H:640:THR:HG22	1:H:706:LYS:HG2	2.00	0.43
1:J:454:GLY:H	1:J:500:THR:HG22	1.83	0.43
1:L:441:LEU:HD12	1:L:441:LEU:HA	1.69	0.43
1:A:268:VAL:O	1:A:272:ILE:HG13	2.18	0.43
1:C:279:PRO:HG3	1:C:322:GLN:HA	2.00	0.43
1:D:278:LEU:HD22	1:D:279:PRO:O	2.18	0.43
1:D:559:ASP:OD2	1:K:562:LYS:HD3	2.18	0.43
1:D:735:GLN:O	1:D:738:MET:HB3	2.17	0.43
1:E:478:ASN:CG	1:E:482:LYS:NZ	2.71	0.43
1:E:537:TYR:HE1	1:E:540:LYS:HZ3	1.59	0.43
1:E:832:LYS:O	1:E:835:GLN:HG2	2.19	0.43
1:G:640:THR:HG22	1:G:706:LYS:HG2	2.00	0.43
1:I:400:ASP:OD1	1:I:400:ASP:N	2.51	0.43
1:I:594:ALA:HA	1:I:598:TRP:CE3	2.54	0.43
1:K:269:LEU:CG	1:K:457:SER:O	2.61	0.43
1:K:851:VAL:HG23	1:K:852:ARG:N	2.33	0.43
1:K:875:ALA:HB1	1:K:885:LEU:CD1	2.48	0.43
1:L:449:LYS:C	1:L:451:GLY:H	2.26	0.43
1:L:585:LEU:O	1:L:589:VAL:HG23	2.18	0.43
1:L:618:LEU:CD2	1:L:628:TRP:CE2	3.01	0.43
1:L:630:ARG:HG2	1:L:630:ARG:HH11	1.82	0.43
1:B:609:PRO:HD2	1:B:610:ARG:O	2.18	0.43
1:C:393:ILE:HG23	1:C:422:THR:HB	2.01	0.43
1:D:297:ASP:OD1	1:D:300:ALA:HB3	2.17	0.43
1:D:627:TYR:CE2	1:D:628:TRP:CH2	2.92	0.43
1:E:441:LEU:CB	1:E:498:VAL:CG1	2.96	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:776:ALA:C	1:L:778:GLY:H	2.27	0.43
1:J:457:SER:O	1:J:458:LYS:CB	2.67	0.43
1:K:230:ILE:HG13	1:K:904:LEU:CD1	2.48	0.43
1:K:420:GLU:HG3	1:K:449:LYS:HE2	1.99	0.43
1:L:387:ILE:HG22	1:L:415:VAL:HG21	2.00	0.43
1:A:326:THR:O	1:A:329:ASN:HB2	2.18	0.43
1:A:473:LEU:O	1:A:474:LEU:C	2.62	0.43
1:B:318:PHE:CD1	1:B:321:ILE:CD1	2.91	0.43
1:D:232:LYS:HA	1:D:235:ILE:CG2	2.48	0.43
1:E:576:GLN:NE2	1:E:576:GLN:N	2.57	0.43
1:G:255:ILE:HG23	1:G:392:ILE:HG23	2.00	0.43
1:G:267:SER:CB	1:G:396:ILE:HG13	2.49	0.43
1:G:832:LYS:O	1:G:833:LEU:C	2.61	0.43
1:G:861:LEU:O	1:G:865:MET:HG2	2.19	0.43
1:G:861:LEU:HD23	1:G:861:LEU:HA	1.81	0.43
1:H:285:ILE:C	1:H:286:THR:HG23	2.43	0.43
1:H:328:LEU:HD13	1:H:343:ILE:HD13	2.00	0.43
1:I:873:LYS:O	1:I:877:GLU:HG3	2.18	0.43
1:L:532:LEU:HD22	1:L:898:LEU:HD22	2.00	0.43
1:A:376:LYS:N	1:A:376:LYS:CE	2.81	0.43
1:A:675:ALA:O	1:A:679:ILE:HG13	2.19	0.43
1:A:735:GLN:O	1:A:738:MET:HB3	2.19	0.43
1:C:270:GLU:O	1:C:271:ALA:C	2.62	0.43
1:C:754:VAL:HG22	1:C:779:PHE:CD2	2.53	0.43
1:D:269:LEU:CD2	1:D:457:SER:HB2	2.48	0.43
1:F:530:ARG:HA	1:F:530:ARG:HD3	1.75	0.43
1:H:477:ILE:O	1:H:477:ILE:CG2	2.66	0.43
1:H:490:THR:OG1	1:H:491:GLU:OE2	2.27	0.43
1:H:673:PRO:HA	1:H:676:ARG:HB3	1.99	0.43
1:I:389:GLY:O	1:I:391:ASN:N	2.49	0.43
1:I:758:VAL:HB	1:I:791:VAL:HG21	1.99	0.43
1:J:610:ARG:HA	1:J:610:ARG:NE	2.33	0.43
1:L:264:GLY:HA2	1:L:267:SER:HB3	2.00	0.43
1:A:349:SER:HB3	1:A:352:ILE:HG12	2.00	0.43
1:A:441:LEU:HD21	1:A:498:VAL:CA	2.48	0.43
1:B:344:ARG:H	1:B:344:ARG:HG2	1.63	0.43
1:B:544:ASN:HD22	1:D:703:LYS:HE3	1.83	0.43
1:B:779:PHE:C	1:I:776:ALA:CB	2.83	0.43
1:C:269:LEU:HA	1:C:272:ILE:HD12	2.00	0.43
1:D:387:ILE:HG22	1:D:415:VAL:HG21	1.99	0.43
1:D:396:ILE:HA	1:D:425:VAL:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:861:LEU:HA	1:D:861:LEU:HD23	1.83	0.43
1:E:278:LEU:HD22	1:E:280:LYS:HD3	1.98	0.43
1:E:376:LYS:CA	1:E:376:LYS:CE	2.97	0.43
1:F:363:TYR:N	1:F:363:TYR:CD1	2.86	0.43
1:F:705:TYR:CE1	1:F:832:LYS:HD3	2.53	0.43
1:F:731:LEU:O	1:F:735:GLN:HG3	2.18	0.43
1:G:436:LYS:O	1:G:440:ILE:HG13	2.17	0.43
1:G:744:SER:OG	1:G:786:ARG:NH2	2.51	0.43
1:J:272:ILE:CG2	1:J:277:PHE:CD1	2.96	0.43
1:L:252:LEU:HD23	1:L:524:THR:HG21	2.01	0.43
1:A:272:ILE:CG2	1:A:278:LEU:N	2.77	0.43
1:A:510:LEU:HD13	1:A:510:LEU:C	2.43	0.43
1:A:639:LEU:O	1:A:642:LEU:HD23	2.18	0.43
1:B:285:ILE:HD12	1:B:286:THR:N	2.34	0.43
1:B:653:ALA:HA	1:B:687:LEU:HD13	2.01	0.43
1:C:227:MET:O	1:C:231:THR:OG1	2.36	0.43
1:C:661:GLU:OE2	1:C:676:ARG:NH2	2.52	0.43
1:C:664:LEU:CD2	1:C:676:ARG:HG3	2.47	0.43
1:D:272:ILE:HG12	1:D:278:LEU:HD11	2.01	0.43
1:D:308:PRO:HG3	1:D:344:ARG:HB2	2.00	0.43
1:D:484:TYR:HE1	1:D:492:PHE:CZ	2.35	0.43
1:D:552:SER:HA	1:K:855:ARG:HD2	2.00	0.43
1:D:587:GLN:NE2	1:D:591:ASP:OD1	2.51	0.43
1:D:690:ARG:O	1:D:690:ARG:HD3	2.18	0.43
1:F:449:LYS:C	1:F:451:GLY:N	2.74	0.43
1:F:803:ARG:HD3	1:F:803:ARG:HA	1.62	0.43
1:G:558:LEU:HD12	1:G:861:LEU:HD12	2.00	0.43
1:H:237:ILE:CD1	1:H:237:ILE:C	2.91	0.43
1:H:499:SER:C	1:H:500:THR:HG23	2.43	0.43
1:H:861:LEU:HD23	1:H:861:LEU:HA	1.77	0.43
1:J:900:LYS:HD3	1:J:900:LYS:HA	1.81	0.43
1:K:267:SER:HB2	1:K:396:ILE:CD1	2.49	0.43
1:K:444:ARG:HD2	1:K:444:ARG:HA	1.86	0.43
1:K:640:THR:C	1:K:642:LEU:H	2.27	0.43
1:L:803:ARG:HD2	1:L:823:GLU:CD	2.44	0.43
1:A:233:LYS:HE3	1:A:233:LYS:HA	2.00	0.43
1:A:252:LEU:HD23	1:A:252:LEU:HA	1.79	0.43
1:A:297:ASP:OD1	1:A:348:HIS:HB3	2.19	0.43
1:A:529:GLN:HG2	1:A:898:LEU:HD21	2.01	0.43
1:B:264:GLY:HA2	1:B:267:SER:CB	2.46	0.43
1:B:492:PHE:HD1	1:B:492:PHE:O	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:904:LEU:C	1:B:904:LEU:HD12	2.43	0.43
1:C:230:ILE:O	1:C:234:MET:HG3	2.19	0.43
1:C:267:SER:CB	1:C:396:ILE:HG13	2.49	0.43
1:C:605:LEU:HD13	1:C:606:SER:O	2.19	0.43
1:C:687:LEU:HD22	1:C:845:MET:HE2	2.01	0.43
1:C:891:LYS:HG2	1:C:895:GLU:OE2	2.19	0.43
1:D:345:LEU:HD23	1:D:345:LEU:HA	1.86	0.43
1:D:425:VAL:HA	1:D:453:VAL:O	2.19	0.43
1:E:255:ILE:HD12	1:E:357:LEU:HB3	2.01	0.43
1:E:263:SER:HA	1:E:266:SER:OG	2.19	0.43
1:E:272:ILE:CG2	1:E:278:LEU:HD13	2.39	0.43
1:E:631:GLN:OE1	1:E:631:GLN:HA	2.18	0.43
1:F:279:PRO:O	1:F:280:LYS:HD2	2.19	0.43
1:F:723:VAL:HG11	1:F:823:GLU:HB3	2.01	0.43
1:G:723:VAL:HG23	1:G:827:ASP:CB	2.48	0.43
1:G:853:PHE:O	1:G:857:VAL:HG23	2.18	0.43
1:H:231:THR:O	1:H:235:ILE:HG22	2.18	0.43
1:H:267:SER:CB	1:H:396:ILE:HD11	2.48	0.43
1:H:315:VAL:HG11	1:H:321:ILE:HG13	1.99	0.43
1:I:224:ASP:HB3	1:I:227:MET:HB2	2.00	0.43
1:K:900:LYS:HD3	1:K:900:LYS:HA	1.84	0.43
1:L:279:PRO:HG2	1:L:325:LEU:HD21	2.00	0.43
1:B:508:LYS:O	1:B:509:LEU:C	2.59	0.43
1:D:278:LEU:CB	1:D:279:PRO:CD	2.93	0.43
1:D:339:THR:O	1:D:340:ASP:CB	2.66	0.43
1:D:562:LYS:NZ	1:K:558:LEU:CD2	2.82	0.43
1:D:727:LEU:CD2	1:D:823:GLU:HG2	2.48	0.43
1:E:238:ARG:NE	1:E:356:SER:OG	2.52	0.43
1:E:376:LYS:HZ3	1:E:376:LYS:HG3	1.51	0.43
1:E:854:PRO:HB2	1:E:855:ARG:HH11	1.75	0.43
1:F:385:LYS:HE2	1:F:385:LYS:HB3	1.82	0.43
1:F:664:LEU:HD12	1:F:664:LEU:HA	1.84	0.43
1:H:260:SER:O	1:H:263:SER:N	2.51	0.43
1:I:479:ARG:HH11	1:I:479:ARG:HD2	1.66	0.43
1:I:518:SER:O	1:I:521:LEU:HB3	2.19	0.43
1:I:803:ARG:HD3	1:I:803:ARG:HA	1.66	0.43
1:I:891:LYS:O	1:I:895:GLU:HG3	2.19	0.43
1:J:268:VAL:O	1:J:272:ILE:CD1	2.67	0.43
1:K:269:LEU:HD21	1:K:457:SER:O	2.19	0.43
1:K:269:LEU:CD2	1:K:270:GLU:N	2.69	0.43
1:K:308:PRO:HG3	1:K:344:ARG:CG	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:LEU:HD22	1:A:512:VAL:CG2	2.48	0.42
1:B:270:GLU:O	1:B:271:ALA:C	2.60	0.42
1:C:263:SER:OG	1:C:396:ILE:O	2.36	0.42
1:D:834:ALA:O	1:D:838:VAL:HB	2.19	0.42
1:G:234:MET:O	1:G:237:ILE:HG22	2.19	0.42
1:H:244:VAL:HB	1:H:248:SER:OG	2.19	0.42
1:H:267:SER:HB3	1:H:396:ILE:HG13	2.00	0.42
1:H:288:ARG:HA	1:H:289:PRO:HD3	1.82	0.42
1:H:318:PHE:CD1	1:H:321:ILE:HD12	2.54	0.42
1:H:543:TYR:CD1	1:H:884:HIS:HB2	2.54	0.42
1:I:702:LEU:HD13	1:I:833:LEU:HD22	2.01	0.42
1:J:282:SER:HB2	1:J:283:ASN:H	1.67	0.42
1:J:288:ARG:HA	1:J:289:PRO:HD3	1.79	0.42
1:J:387:ILE:O	1:J:421:ARG:NH2	2.51	0.42
1:J:392:ILE:HG21	1:J:513:LEU:HD22	2.01	0.42
1:J:582:LYS:O	1:J:586:ASP:HB2	2.19	0.42
1:K:670:ALA:HB3	1:K:671:LYS:HE3	2.01	0.42
1:L:260:SER:N	1:L:263:SER:HB3	2.34	0.42
1:L:642:LEU:O	1:L:644:VAL:N	2.49	0.42
1:A:285:ILE:HD13	1:A:285:ILE:N	2.35	0.42
1:B:227:MET:O	1:B:231:THR:OG1	2.34	0.42
1:B:251:THR:HG22	1:B:252:LEU:H	1.83	0.42
1:B:597:TYR:CE2	1:B:822:PRO:HG3	2.55	0.42
1:B:648:ALA:HB1	1:B:841:LEU:HD12	2.00	0.42
1:C:706:LYS:HD2	1:K:544:ASN:HD21	1.84	0.42
1:C:785:ALA:HA	1:C:788:ARG:CZ	2.49	0.42
1:D:244:VAL:HG11	1:D:894:LEU:HD21	2.01	0.42
1:D:269:LEU:CD2	1:D:457:SER:O	2.66	0.42
1:D:375:LEU:O	1:D:378:LYS:N	2.52	0.42
1:E:388:ARG:O	1:E:389:GLY:C	2.61	0.42
1:E:455:VAL:CG1	1:E:501:GLY:N	2.78	0.42
1:E:851:VAL:HG23	1:E:852:ARG:N	2.34	0.42
1:F:263:SER:O	1:F:267:SER:HB3	2.19	0.42
1:F:276:GLU:HG2	1:F:277:PHE:N	2.33	0.42
1:G:664:LEU:HB3	1:G:676:ARG:NH1	2.34	0.42
1:G:690:ARG:HA	1:G:690:ARG:HD3	1.69	0.42
1:H:340:ASP:CG	1:H:340:ASP:O	2.62	0.42
1:H:430:ASP:OD1	1:H:430:ASP:C	2.60	0.42
1:I:722:HIS:O	1:I:726:VAL:HG23	2.19	0.42
1:K:269:LEU:HD21	1:K:457:SER:C	2.44	0.42
1:K:492:PHE:O	1:K:492:PHE:HD1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:258:ILE:HG22	1:L:360:LEU:HD11	2.00	0.42
1:A:233:LYS:CE	1:A:233:LYS:HA	2.49	0.42
1:A:270:GLU:C	1:A:273:VAL:HG22	2.43	0.42
1:B:234:MET:CG	1:B:234:MET:CE	2.96	0.42
1:C:224:ASP:HB3	1:C:227:MET:CG	2.48	0.42
1:D:723:VAL:CG1	1:D:823:GLU:HB3	2.50	0.42
1:D:886:ASP:O	1:D:889:ARG:CG	2.67	0.42
1:E:349:SER:HB3	1:E:352:ILE:HG23	2.01	0.42
1:E:413:ARG:NH1	1:E:446:TYR:CE1	2.88	0.42
1:E:493:GLY:O	1:E:496:SER:HB3	2.19	0.42
1:G:287:ARG:HH11	1:G:287:ARG:HG3	1.85	0.42
1:H:272:ILE:CG2	1:H:277:PHE:HA	2.41	0.42
1:H:907:ILE:HD12	1:H:907:ILE:HA	1.79	0.42
1:I:528:ILE:HA	1:I:531:GLU:CG	2.49	0.42
1:J:499:SER:C	1:J:500:THR:HG23	2.44	0.42
1:J:618:LEU:HD23	1:J:803:ARG:HH12	1.83	0.42
1:K:258:ILE:HD13	1:K:387:ILE:HD13	2.01	0.42
1:K:434:PRO:HG2	1:K:488:HIS:CE1	2.54	0.42
1:K:453:VAL:HG21	1:K:505:LEU:HD23	2.01	0.42
1:L:507:LYS:HB2	1:L:507:LYS:HE3	1.83	0.42
1:B:411:ALA:HA	1:B:414:ARG:HB3	2.01	0.42
1:B:581:LEU:HD23	1:B:581:LEU:HA	1.87	0.42
1:B:615:ILE:HD11	1:B:803:ARG:NE	2.23	0.42
1:B:778:GLY:O	1:I:776:ALA:HB1	2.19	0.42
1:B:783:LEU:CD1	1:I:778:GLY:N	2.82	0.42
1:D:478:ASN:O	1:D:482:LYS:CG	2.66	0.42
1:D:627:TYR:HD2	1:D:628:TRP:CD2	2.37	0.42
1:E:276:GLU:HG2	1:E:277:PHE:H	1.85	0.42
1:E:454:GLY:C	1:E:455:VAL:HG13	2.44	0.42
1:F:231:THR:O	1:F:235:ILE:HG22	2.18	0.42
1:H:243:LYS:O	1:H:243:LYS:CG	2.67	0.42
1:H:247:GLY:O	1:H:249:THR:N	2.48	0.42
1:H:270:GLU:CA	1:H:273:VAL:HG22	2.50	0.42
1:H:297:ASP:OD2	1:H:300:ALA:HB3	2.19	0.42
1:I:235:ILE:HD11	1:I:293:THR:HG22	2.00	0.42
1:I:264:GLY:C	1:I:267:SER:H	2.27	0.42
1:I:667:SER:OG	1:I:668:SER:N	2.53	0.42
1:J:278:LEU:CB	1:J:279:PRO:HD2	2.36	0.42
1:J:382:LEU:C	1:J:382:LEU:CD1	2.76	0.42
1:K:237:ILE:HD13	1:K:237:ILE:O	2.18	0.42
1:K:276:GLU:HG2	1:K:277:PHE:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:596:ARG:HG3	1:K:635:ALA:HB2	2.02	0.42
1:L:296:ASN:HB2	1:L:354:ASP:OD2	2.19	0.42
1:A:288:ARG:HA	1:A:289:PRO:HD3	1.78	0.42
1:B:607:PRO:HG3	1:B:762:ARG:HG3	2.01	0.42
1:B:694:THR:O	1:B:698:ILE:HG13	2.19	0.42
1:F:488:HIS:HB3	1:F:491:GLU:HG3	2.02	0.42
1:F:694:THR:O	1:F:698:ILE:HG13	2.20	0.42
1:G:232:LYS:HE2	1:G:232:LYS:HB3	1.49	0.42
1:G:889:ARG:HA	1:G:892:GLU:CD	2.45	0.42
1:H:269:LEU:HD21	1:H:457:SER:O	2.20	0.42
1:H:281:GLY:O	1:H:282:SER:C	2.63	0.42
1:H:400:ASP:OD1	1:H:400:ASP:N	2.51	0.42
1:H:631:GLN:OE1	1:H:631:GLN:HA	2.18	0.42
1:J:225:ASP:O	1:J:226:ASN:C	2.60	0.42
1:J:238:ARG:HA	1:J:241:LEU:HD12	2.01	0.42
1:J:355:LEU:HD12	1:J:355:LEU:HA	1.85	0.42
1:K:751:LEU:O	1:K:755:MET:HG3	2.19	0.42
1:A:731:LEU:HA	1:A:800:LEU:HD13	2.02	0.42
1:B:241:LEU:HD21	1:B:528:ILE:HD13	2.02	0.42
1:B:690:ARG:HA	1:B:690:ARG:HD3	1.83	0.42
1:C:627:TYR:HE2	1:C:628:TRP:CH2	2.37	0.42
1:E:285:ILE:CD1	1:E:285:ILE:N	2.82	0.42
1:E:543:TYR:O	1:E:546:GLN:HG3	2.19	0.42
1:E:611:GLU:H	1:E:611:GLU:HG2	1.49	0.42
1:F:232:LYS:HG3	1:F:354:ASP:CG	2.44	0.42
1:G:260:SER:N	1:G:263:SER:HB3	2.34	0.42
1:G:596:ARG:HD2	1:G:631:GLN:HG3	2.00	0.42
1:G:611:GLU:H	1:G:612:PRO:HD2	1.85	0.42
1:I:744:SER:OG	1:I:786:ARG:NH2	2.45	0.42
1:K:272:ILE:HG12	1:K:278:LEU:HD11	2.02	0.42
1:K:297:ASP:OD1	1:K:348:HIS:HB3	2.20	0.42
1:K:673:PRO:O	1:K:677:LYS:HB2	2.20	0.42
1:L:251:THR:HG22	1:L:252:LEU:H	1.84	0.42
1:A:229:PHE:HA	1:A:232:LYS:HG2	2.01	0.42
1:A:450:LEU:HD22	1:A:512:VAL:HG21	2.02	0.42
1:B:363:TYR:CD1	1:B:363:TYR:N	2.87	0.42
1:B:532:LEU:HD22	1:B:898:LEU:HD22	2.01	0.42
1:C:308:PRO:HG3	1:C:344:ARG:HB2	2.01	0.42
1:C:889:ARG:O	1:C:892:GLU:HB2	2.20	0.42
1:D:388:ARG:O	1:D:389:GLY:C	2.62	0.42
1:D:657:GLN:HE21	1:D:657:GLN:HB2	1.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:878:ASP:HA	1:E:879:PRO:HD3	1.93	0.42
1:F:904:LEU:C	1:F:904:LEU:HD12	2.44	0.42
1:H:388:ARG:O	1:H:421:ARG:NH2	2.52	0.42
1:I:837:ALA:O	1:I:841:LEU:HB2	2.20	0.42
1:J:376:LYS:CA	1:J:376:LYS:CE	2.97	0.42
1:K:778:GLY:C	1:K:779:PHE:CD2	2.98	0.42
1:K:889:ARG:O	1:K:892:GLU:HB3	2.20	0.42
1:A:396:ILE:HD13	1:A:396:ILE:N	2.35	0.42
1:A:815:LEU:C	1:A:815:LEU:HD13	2.44	0.42
1:B:904:LEU:HD12	1:B:904:LEU:O	2.19	0.42
1:C:484:TYR:HD1	1:C:485:PHE:CE1	2.37	0.42
1:C:530:ARG:HD3	1:C:530:ARG:HA	1.89	0.42
1:D:278:LEU:HD22	1:D:280:LYS:CG	2.49	0.42
1:D:376:LYS:HE2	1:D:376:LYS:CA	2.48	0.42
1:E:272:ILE:HG13	1:E:272:ILE:H	1.55	0.42
1:E:661:GLU:OE2	1:E:676:ARG:NH1	2.53	0.42
1:F:602:ILE:HB	1:F:788:ARG:HB3	2.00	0.42
1:G:780:SER:HG	1:L:778:GLY:HA3	1.80	0.42
1:I:508:LYS:HD2	1:I:508:LYS:HA	1.83	0.42
1:I:803:ARG:HD2	1:I:823:GLU:OE1	2.20	0.42
1:K:275:HIS:H	1:K:275:HIS:HD2	1.60	0.42
1:K:667:SER:OG	1:K:668:SER:N	2.53	0.42
1:L:321:ILE:O	1:L:325:LEU:HG	2.20	0.42
1:A:308:PRO:HD2	1:A:344:ARG:O	2.19	0.42
1:A:875:ALA:O	1:A:881:VAL:HG23	2.19	0.42
1:B:262:SER:O	1:B:266:SER:OG	2.37	0.42
1:B:611:GLU:N	1:B:612:PRO:HD2	2.32	0.42
1:C:861:LEU:HD23	1:C:861:LEU:HA	1.77	0.42
1:D:710:ASP:O	1:D:832:LYS:NZ	2.42	0.42
1:E:716:TRP:CE3	1:E:815:LEU:HD23	2.55	0.42
1:F:585:LEU:HA	1:F:585:LEU:HD23	1.76	0.42
1:F:727:LEU:HD12	1:F:727:LEU:HA	1.93	0.42
1:G:702:LEU:HD23	1:G:702:LEU:HA	1.76	0.42
1:J:627:TYR:HE2	1:J:628:TRP:CZ3	2.38	0.42
1:K:540:LYS:HA	1:K:545:GLU:HG3	2.01	0.42
1:K:565:PHE:HA	1:K:663:LEU:HD21	2.02	0.42
1:L:266:SER:HA	1:L:269:LEU:HD22	2.01	0.42
1:L:275:HIS:CG	1:L:276:GLU:H	2.38	0.42
1:L:582:LYS:HB2	1:L:582:LYS:HE3	1.86	0.42
1:A:232:LYS:HA	1:A:235:ILE:CG2	2.50	0.42
1:A:234:MET:HA	1:A:237:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:LEU:HD12	1:B:326:THR:HG23	2.01	0.42
1:B:426:ILE:HG12	1:B:440:ILE:HG22	2.02	0.42
1:D:258:ILE:HG22	1:D:360:LEU:HD11	2.01	0.42
1:D:401:THR:HG22	1:D:402:ASP:O	2.19	0.42
1:D:703:LYS:N	1:D:704:PRO:HD2	2.35	0.42
1:E:754:VAL:HA	1:E:779:PHE:HE1	1.84	0.42
1:F:267:SER:CB	1:F:396:ILE:HG13	2.50	0.42
1:F:690:ARG:HA	1:F:690:ARG:HD3	1.88	0.42
1:G:887:LEU:HD12	1:G:887:LEU:HA	1.79	0.42
1:H:238:ARG:HG3	1:H:252:LEU:HB2	2.02	0.42
1:I:441:LEU:HD21	1:I:499:SER:O	2.19	0.42
1:J:576:GLN:H	1:J:576:GLN:HE21	1.66	0.42
1:J:616:ILE:HG23	1:J:617:ASP:OD1	2.20	0.42
1:K:260:SER:HG	1:K:407:THR:HG1	1.60	0.42
1:A:224:ASP:O	1:A:227:MET:HB2	2.20	0.41
1:A:441:LEU:CB	1:A:498:VAL:HG12	2.48	0.41
1:A:814:THR:CG2	1:A:817:ASN:ND2	2.82	0.41
1:B:513:LEU:HD23	1:B:517:MET:HE2	2.01	0.41
1:B:818:LYS:HE3	1:B:819:TYR:CE2	2.55	0.41
1:C:255:ILE:HG12	1:C:513:LEU:HD12	2.01	0.41
1:C:441:LEU:HD12	1:C:452:TYR:HB2	2.02	0.41
1:D:855:ARG:HH21	1:K:556:ALA:HB2	1.78	0.41
1:E:749:LYS:O	1:E:753:GLU:HG3	2.19	0.41
1:E:802:LEU:HD22	1:E:802:LEU:HA	1.86	0.41
1:F:234:MET:HA	1:F:237:ILE:HG22	2.02	0.41
1:F:270:GLU:C	1:F:270:GLU:CD	2.87	0.41
1:F:861:LEU:HD23	1:F:861:LEU:HA	1.80	0.41
1:G:779:PHE:HD1	1:L:750:LYS:NZ	2.17	0.41
1:H:232:LYS:O	1:H:235:ILE:CG2	2.68	0.41
1:H:268:VAL:O	1:H:272:ILE:CG1	2.67	0.41
1:H:537:TYR:CD2	1:H:537:TYR:C	2.98	0.41
1:H:664:LEU:HD12	1:H:664:LEU:HA	1.89	0.41
1:I:265:LYS:HD2	1:I:265:LYS:HA	1.79	0.41
1:I:814:THR:OG1	1:I:816:THR:HG23	2.19	0.41
1:K:258:ILE:HG21	1:K:387:ILE:HD11	2.01	0.41
1:L:357:LEU:HD23	1:L:357:LEU:H	1.84	0.41
1:L:593:LEU:CD2	1:L:826:LEU:HD12	2.50	0.41
1:A:873:LYS:O	1:A:873:LYS:HD2	2.19	0.41
1:B:840:PHE:CE1	1:B:844:GLU:HG3	2.55	0.41
1:C:232:LYS:HB3	1:C:232:LYS:HE2	1.68	0.41
1:D:286:THR:HB	1:D:361:PRO:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:537:TYR:CD1	1:D:540:LYS:HE3	2.54	0.41
1:E:275:HIS:HB2	1:E:352:ILE:HG22	2.02	0.41
1:F:825:PHE:O	1:F:828:ALA:HB3	2.20	0.41
1:G:294:LEU:HB3	1:G:352:ILE:HD13	2.02	0.41
1:G:488:HIS:HB3	1:G:491:GLU:CG	2.50	0.41
1:H:277:PHE:HD1	1:H:278:LEU:H	1.68	0.41
1:H:766:ILE:HD12	1:H:766:ILE:HA	1.88	0.41
1:I:241:LEU:HD13	1:I:250:VAL:O	2.20	0.41
1:I:525:THR:O	1:I:529:GLN:HG3	2.21	0.41
1:J:345:LEU:HD23	1:J:345:LEU:HA	1.85	0.41
1:J:593:LEU:CD2	1:J:823:GLU:HG3	2.50	0.41
1:L:284:MET:HG2	1:L:286:THR:CG2	2.50	0.41
1:L:581:LEU:HD23	1:L:581:LEU:HA	1.89	0.41
1:B:508:LYS:O	1:B:512:VAL:HG23	2.20	0.41
1:B:537:TYR:O	1:B:541:VAL:HG12	2.20	0.41
1:B:558:LEU:HD23	1:B:558:LEU:C	2.45	0.41
1:C:565:PHE:CZ	1:C:853:PHE:CD2	3.09	0.41
1:D:278:LEU:CB	1:D:279:PRO:HD2	2.37	0.41
1:D:279:PRO:CG	1:D:322:GLN:HA	2.49	0.41
1:D:285:ILE:CD1	1:D:285:ILE:N	2.83	0.41
1:D:344:ARG:H	1:D:344:ARG:HG2	1.58	0.41
1:D:484:TYR:C	1:D:486:GLY:H	2.27	0.41
1:E:907:ILE:HD12	1:E:907:ILE:HA	1.93	0.41
1:F:377:ARG:HH21	1:F:377:ARG:CG	2.33	0.41
1:G:873:LYS:O	1:G:877:GLU:HG3	2.19	0.41
1:H:229:PHE:CD2	1:H:229:PHE:N	2.87	0.41
1:I:653:ALA:HB2	1:I:845:MET:HE1	2.02	0.41
1:J:731:LEU:HA	1:J:800:LEU:HD13	2.01	0.41
1:K:703:LYS:N	1:K:704:PRO:HD2	2.35	0.41
1:K:742:GLU:HA	1:K:751:LEU:HD13	2.02	0.41
1:L:241:LEU:HD11	1:L:528:ILE:HD11	2.01	0.41
1:L:416:ASP:OD1	1:L:419:GLY:N	2.54	0.41
1:L:572:PHE:HD2	1:L:846:LEU:HD11	1.84	0.41
1:L:808:LYS:HE2	1:L:808:LYS:HB3	1.84	0.41
1:A:254:SER:O	1:A:391:ASN:HB3	2.21	0.41
1:A:393:ILE:HG23	1:A:422:THR:HB	2.01	0.41
1:A:426:ILE:HD11	1:A:440:ILE:CG2	2.12	0.41
1:B:234:MET:HA	1:B:237:ILE:HG22	2.02	0.41
1:B:441:LEU:HD12	1:B:452:TYR:HB2	2.02	0.41
1:C:360:LEU:CB	1:C:361:PRO:HD2	2.47	0.41
1:C:738:MET:O	1:C:742:GLU:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:267:SER:CB	1:D:396:ILE:HG13	2.51	0.41
1:D:382:LEU:CG	1:D:383:CYS:N	2.83	0.41
1:E:458:LYS:HA	1:E:458:LYS:HD2	1.88	0.41
1:F:776:ALA:HB3	1:F:784:LEU:HD11	2.02	0.41
1:G:717:ALA:O	1:G:720:ARG:HB3	2.20	0.41
1:H:393:ILE:HG23	1:H:422:THR:HB	2.02	0.41
1:H:485:PHE:HD1	1:H:485:PHE:H	1.67	0.41
1:H:837:ALA:O	1:H:841:LEU:HB2	2.21	0.41
1:I:568:PHE:C	1:I:571:SER:H	2.28	0.41
1:I:832:LYS:O	1:I:833:LEU:C	2.62	0.41
1:J:224:ASP:N	1:J:225:ASP:OD1	2.53	0.41
1:K:605:LEU:HD21	1:K:784:LEU:HD12	2.00	0.41
1:L:889:ARG:O	1:L:892:GLU:HB2	2.21	0.41
1:A:377:ARG:HH21	1:A:377:ARG:CG	2.33	0.41
1:B:234:MET:HE1	1:B:517:MET:C	2.45	0.41
1:B:376:LYS:NZ	1:B:379:ILE:HD12	2.35	0.41
1:B:409:LEU:HA	1:B:412:SER:HB3	2.03	0.41
1:C:241:LEU:HD23	1:C:241:LEU:HA	1.91	0.41
1:F:377:ARG:HA	1:F:380:THR:OG1	2.20	0.41
1:F:675:ALA:O	1:F:678:VAL:HB	2.20	0.41
1:G:692:TYR:CE2	1:G:696:ASP:HB2	2.56	0.41
1:G:854:PRO:HB2	1:G:855:ARG:CZ	2.50	0.41
1:H:617:ASP:OD1	1:H:617:ASP:N	2.54	0.41
1:I:285:ILE:HG12	1:I:329:ASN:O	2.20	0.41
1:K:279:PRO:HB3	1:K:322:GLN:CG	2.50	0.41
1:K:376:LYS:HZ1	1:K:379:ILE:CD1	2.17	0.41
1:K:490:THR:OG1	1:K:491:GLU:N	2.53	0.41
1:K:692:TYR:CD2	1:K:692:TYR:C	2.98	0.41
1:K:723:VAL:O	1:K:727:LEU:HB2	2.20	0.41
1:K:802:LEU:HA	1:K:802:LEU:HD22	1.72	0.41
1:L:269:LEU:HD11	1:L:457:SER:O	2.21	0.41
1:L:848:ASP:OD2	1:L:852:ARG:HD3	2.20	0.41
1:A:279:PRO:CB	1:A:322:GLN:HG3	2.51	0.41
1:B:269:LEU:HD11	1:B:457:SER:O	2.20	0.41
1:C:241:LEU:HD11	1:C:528:ILE:HD11	2.03	0.41
1:C:703:LYS:N	1:C:704:PRO:HD2	2.35	0.41
1:D:434:PRO:HB3	1:D:491:GLU:CB	2.51	0.41
1:D:499:SER:C	1:D:500:THR:HG23	2.46	0.41
1:G:509:LEU:HD23	1:G:509:LEU:HA	1.87	0.41
1:G:889:ARG:HA	1:G:892:GLU:CG	2.49	0.41
1:G:889:ARG:CA	1:G:892:GLU:HG3	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:270:GLU:O	1:H:273:VAL:CG2	2.55	0.41
1:H:455:VAL:CG1	1:H:501:GLY:H	2.28	0.41
1:H:784:LEU:O	1:H:785:ALA:C	2.64	0.41
1:J:454:GLY:C	1:J:455:VAL:HG13	2.46	0.41
1:K:285:ILE:C	1:K:286:THR:HG23	2.45	0.41
1:K:492:PHE:CD1	1:K:492:PHE:O	2.74	0.41
1:K:576:GLN:NE2	1:K:576:GLN:H	2.18	0.41
1:L:613:ASP:HB3	1:L:627:TYR:OH	2.20	0.41
1:A:574:ARG:N	1:A:575:PRO:HD2	2.35	0.41
1:A:802:LEU:HD22	1:A:802:LEU:HA	1.95	0.41
1:A:848:ASP:O	1:A:852:ARG:HB2	2.20	0.41
1:B:784:LEU:HD23	1:B:784:LEU:HA	1.77	0.41
1:C:528:ILE:O	1:C:531:GLU:HG2	2.20	0.41
1:D:387:ILE:HG23	1:D:393:ILE:HD12	2.03	0.41
1:D:751:LEU:HA	1:D:754:VAL:HG12	2.03	0.41
1:E:288:ARG:HA	1:E:289:PRO:HD3	1.90	0.41
1:E:453:VAL:HG21	1:E:505:LEU:HD23	2.02	0.41
1:F:258:ILE:HG21	1:F:387:ILE:HD11	2.03	0.41
1:F:357:LEU:HD23	1:F:357:LEU:H	1.85	0.41
1:F:640:THR:HG21	1:F:706:LYS:HA	2.03	0.41
1:G:473:LEU:HD12	1:G:473:LEU:HA	1.76	0.41
1:H:441:LEU:CB	1:H:498:VAL:HG12	2.49	0.41
1:H:526:GLU:OE1	1:H:530:ARG:NH1	2.52	0.41
1:J:287:ARG:HD2	1:J:332:VAL:CG1	2.50	0.41
1:K:229:PHE:CG	1:K:232:LYS:HD2	2.54	0.41
1:K:678:VAL:HG21	1:K:864:HIS:CD2	2.55	0.41
1:K:832:LYS:O	1:K:836:THR:HG22	2.21	0.41
1:L:266:SER:O	1:L:270:GLU:HB2	2.21	0.41
1:B:611:GLU:H	1:B:612:PRO:CD	2.34	0.41
1:C:697:GLY:HA3	1:C:840:PHE:CZ	2.56	0.41
1:D:286:THR:HB	1:D:361:PRO:CA	2.51	0.41
1:D:616:ILE:HG22	1:D:616:ILE:H	1.54	0.41
1:D:854:PRO:HD2	1:D:855:ARG:HH12	1.82	0.41
1:E:281:GLY:O	1:E:282:SER:C	2.63	0.41
1:G:738:MET:O	1:G:742:GLU:HG3	2.20	0.41
1:H:279:PRO:HG3	1:H:321:ILE:HG22	2.02	0.41
1:H:730:GLU:O	1:H:730:GLU:HG3	2.21	0.41
1:I:279:PRO:HB3	1:I:322:GLN:CB	2.51	0.41
1:I:605:LEU:HD13	1:I:605:LEU:C	2.45	0.41
1:J:244:VAL:HG11	1:J:894:LEU:HD21	2.02	0.41
1:J:278:LEU:HD21	1:J:280:LYS:CD	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:416:ASP:OD2	1:J:422:THR:HG22	2.21	0.41
1:J:528:ILE:HG21	1:J:528:ILE:HD13	1.86	0.41
1:K:279:PRO:C	1:K:280:LYS:HG2	2.44	0.41
1:K:409:LEU:HD23	1:K:409:LEU:HA	1.90	0.41
1:L:457:SER:O	1:L:458:LYS:HB2	2.20	0.41
1:A:339:THR:CG2	1:A:340:ASP:H	2.34	0.41
1:A:396:ILE:HG22	1:A:425:VAL:HB	2.03	0.41
1:A:543:TYR:O	1:A:546:GLN:HG2	2.20	0.41
1:B:317:ASP:N	1:B:317:ASP:OD1	2.53	0.41
1:B:760:LYS:HB3	1:B:766:ILE:CG2	2.50	0.41
1:B:785:ALA:HA	1:B:788:ARG:CZ	2.51	0.41
1:C:279:PRO:HB3	1:C:322:GLN:HA	2.03	0.41
1:D:444:ARG:NE	1:D:444:ARG:HA	2.35	0.41
1:D:475:ALA:O	1:D:478:ASN:N	2.43	0.41
1:D:562:LYS:HD3	1:K:559:ASP:OD1	2.21	0.41
1:D:754:VAL:HG23	1:D:779:PHE:CD1	2.55	0.41
1:E:294:LEU:HB3	1:E:352:ILE:CD1	2.40	0.41
1:E:384:ASP:O	1:E:385:LYS:C	2.63	0.41
1:E:751:LEU:HA	1:E:754:VAL:HG12	2.03	0.41
1:E:900:LYS:HD3	1:E:900:LYS:HA	1.84	0.41
1:F:227:MET:C	1:F:230:ILE:HG22	2.46	0.41
1:F:286:THR:O	1:F:361:PRO:HD3	2.21	0.41
1:F:382:LEU:C	1:F:382:LEU:HD12	2.46	0.41
1:F:702:LEU:HD23	1:F:702:LEU:HA	1.80	0.41
1:G:239:ASN:HD21	1:G:293:THR:HG21	1.85	0.41
1:G:528:ILE:HA	1:G:531:GLU:HG2	2.02	0.41
1:H:225:ASP:O	1:H:229:PHE:CD2	2.73	0.41
1:H:257:VAL:O	1:H:257:VAL:HG23	2.20	0.41
1:H:272:ILE:HG23	1:H:278:LEU:N	2.35	0.41
1:H:321:ILE:O	1:H:325:LEU:HG	2.21	0.41
1:H:694:THR:HG22	1:H:844:GLU:CG	2.51	0.41
1:H:846:LEU:HD12	1:H:846:LEU:HA	1.92	0.41
1:I:431:LEU:HD23	1:I:431:LEU:H	1.85	0.41
1:I:702:LEU:HD23	1:I:702:LEU:HA	1.76	0.41
1:J:509:LEU:HA	1:J:509:LEU:HD23	1.85	0.41
1:J:723:VAL:CG1	1:J:823:GLU:HB3	2.51	0.41
1:J:800:LEU:O	1:J:804:ILE:HG13	2.20	0.41
1:K:434:PRO:HG2	1:K:488:HIS:CD2	2.56	0.41
1:L:319:SER:O	1:L:323:LYS:HG2	2.21	0.41
1:L:727:LEU:HA	1:L:727:LEU:HD12	1.84	0.41
1:A:520:LYS:HA	1:A:520:LYS:HD3	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:ILE:HD12	1:B:376:LYS:NZ	2.36	0.41
1:C:611:GLU:H	1:C:612:PRO:HD2	1.86	0.41
1:C:754:VAL:O	1:C:758:VAL:HG23	2.21	0.41
1:D:455:VAL:HG12	1:D:501:GLY:CA	2.51	0.41
1:D:592:GLN:HG2	1:D:635:ALA:O	2.21	0.41
1:E:826:LEU:HD23	1:E:826:LEU:HA	1.93	0.41
1:F:249:THR:HG23	1:F:250:VAL:O	2.20	0.41
1:F:296:ASN:H	1:F:354:ASP:HB3	1.85	0.41
1:F:352:ILE:C	1:F:352:ILE:HD12	2.46	0.41
1:F:363:TYR:N	1:F:363:TYR:HD1	2.19	0.41
1:F:583:ASP:O	1:F:586:ASP:HB2	2.21	0.41
1:F:671:LYS:O	1:F:672:HIS:C	2.62	0.41
1:H:492:PHE:CD1	1:H:492:PHE:O	2.74	0.41
1:I:268:VAL:HB	1:I:280:LYS:HB3	2.03	0.41
1:I:727:LEU:HD12	1:I:727:LEU:HA	1.95	0.41
1:J:287:ARG:HH11	1:J:287:ARG:CG	2.33	0.41
1:J:308:PRO:HD2	1:J:344:ARG:O	2.21	0.41
1:K:454:GLY:CA	1:K:500:THR:HG22	2.50	0.41
1:K:488:HIS:CB	1:K:491:GLU:HG2	2.26	0.41
1:K:742:GLU:CD	1:K:748:ARG:HE	2.29	0.41
1:L:392:ILE:HD12	1:L:421:ARG:O	2.21	0.41
1:L:585:LEU:HD23	1:L:585:LEU:HA	1.82	0.41
1:L:611:GLU:N	1:L:612:PRO:CD	2.81	0.41
1:L:817:ASN:HB2	1:L:820:TYR:HB2	2.02	0.41
1:A:279:PRO:HG3	1:A:321:ILE:C	2.46	0.40
1:A:664:LEU:HA	1:A:664:LEU:HD12	1.73	0.40
1:C:326:THR:HA	1:C:329:ASN:ND2	2.36	0.40
1:C:641:ARG:O	1:K:541:VAL:HG13	2.21	0.40
1:D:255:ILE:HA	1:D:392:ILE:O	2.21	0.40
1:D:269:LEU:HD21	1:D:457:SER:C	2.45	0.40
1:D:361:PRO:CG	1:D:382:LEU:HD21	2.50	0.40
1:D:458:LYS:C	1:D:458:LYS:HE2	2.47	0.40
1:E:279:PRO:HG3	1:E:322:GLN:HA	2.03	0.40
1:E:285:ILE:HG21	1:E:332:VAL:CG2	2.51	0.40
1:E:303:ASP:OD1	1:E:349:SER:HB2	2.21	0.40
1:F:861:LEU:O	1:F:865:MET:HG2	2.21	0.40
1:H:254:SER:O	1:H:391:ASN:HB3	2.22	0.40
1:H:276:GLU:CG	1:H:277:PHE:H	2.33	0.40
1:H:597:TYR:CE2	1:H:822:PRO:HG3	2.56	0.40
1:I:364:ILE:HD12	1:I:376:LYS:HZ2	1.86	0.40
1:I:449:LYS:C	1:I:450:LEU:HG	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:363:TYR:HE1	1:K:383:CYS:HG	0.77	0.40
1:K:520:LYS:HA	1:K:520:LYS:HD3	1.80	0.40
1:K:585:LEU:HD23	1:K:585:LEU:HA	1.84	0.40
1:K:679:ILE:O	1:K:682:ALA:HB3	2.21	0.40
1:A:237:ILE:C	1:A:237:ILE:CD1	2.94	0.40
1:A:298:PRO:O	1:A:299:GLU:CB	2.69	0.40
1:A:339:THR:O	1:A:340:ASP:HB3	2.21	0.40
1:B:363:TYR:N	1:B:363:TYR:HD1	2.19	0.40
1:C:260:SER:H	1:C:263:SER:HB3	1.85	0.40
1:C:520:LYS:O	1:C:524:THR:HG23	2.21	0.40
1:C:597:TYR:CE2	1:C:822:PRO:HG3	2.57	0.40
1:D:441:LEU:HD21	1:D:498:VAL:C	2.43	0.40
1:E:235:ILE:HG22	1:E:235:ILE:H	1.60	0.40
1:E:432:VAL:HG12	1:E:436:LYS:NZ	2.36	0.40
1:E:562:LYS:HD2	1:J:559:ASP:CG	2.47	0.40
1:E:648:ALA:HB1	1:E:841:LEU:HD12	2.03	0.40
1:F:672:HIS:HD2	1:F:877:GLU:HB2	1.87	0.40
1:G:572:PHE:HB3	1:G:850:TYR:OH	2.21	0.40
1:G:768:VAL:HG11	1:G:784:LEU:CD1	2.50	0.40
1:H:671:LYS:N	1:H:671:LYS:CD	2.84	0.40
1:I:279:PRO:HB3	1:I:322:GLN:HB2	2.02	0.40
1:I:363:TYR:N	1:I:363:TYR:CD1	2.89	0.40
1:I:484:TYR:HD1	1:I:485:PHE:CD1	2.38	0.40
1:K:875:ALA:O	1:K:881:VAL:HG23	2.21	0.40
1:L:227:MET:HE3	1:L:227:MET:HB3	1.98	0.40
1:L:294:LEU:HB2	1:L:355:LEU:H	1.85	0.40
1:L:328:LEU:HD13	1:L:343:ILE:HD13	2.03	0.40
1:A:296:ASN:HB2	1:A:354:ASP:OD2	2.20	0.40
1:A:485:PHE:O	1:A:489:PRO:HA	2.22	0.40
1:B:491:GLU:H	1:B:491:GLU:HG2	1.56	0.40
1:C:596:ARG:HD2	1:C:631:GLN:HG3	2.01	0.40
1:D:403:LEU:N	1:D:403:LEU:HD23	2.36	0.40
1:E:277:PHE:CD1	1:E:278:LEU:N	2.90	0.40
1:E:528:ILE:HG23	1:E:894:LEU:HD22	2.03	0.40
1:F:400:ASP:OD1	1:F:400:ASP:N	2.54	0.40
1:G:299:GLU:O	1:G:299:GLU:HG2	2.21	0.40
1:G:663:LEU:HD12	1:G:663:LEU:HA	1.86	0.40
1:G:774:SER:O	1:G:780:SER:CB	2.69	0.40
1:H:284:MET:SD	1:H:284:MET:O	2.79	0.40
1:H:287:ARG:CG	1:H:287:ARG:NH1	2.74	0.40
1:H:897:VAL:O	1:H:898:LEU:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:563:HIS:CE1	1:I:567:GLU:OE2	2.74	0.40
1:J:829:VAL:O	1:J:833:LEU:HG	2.21	0.40
1:K:225:ASP:O	1:K:226:ASN:C	2.62	0.40
1:K:267:SER:CB	1:K:396:ILE:CD1	2.99	0.40
1:K:269:LEU:HD21	1:K:457:SER:CA	2.46	0.40
1:L:294:LEU:HB3	1:L:352:ILE:HD13	2.03	0.40
1:L:600:ARG:CB	1:L:601:PRO:CD	2.98	0.40
1:B:275:HIS:CG	1:B:276:GLU:N	2.90	0.40
1:B:430:ASP:HB3	1:B:456:ILE:HG12	2.03	0.40
1:B:615:ILE:O	1:B:615:ILE:HD13	2.22	0.40
1:E:278:LEU:CB	1:E:279:PRO:HD2	2.45	0.40
1:E:285:ILE:HD13	1:E:285:ILE:N	2.36	0.40
1:E:703:LYS:HE3	1:G:544:ASN:ND2	2.36	0.40
1:F:744:SER:OG	1:F:786:ARG:NH2	2.55	0.40
1:F:750:LYS:O	1:F:753:GLU:HB2	2.21	0.40
1:G:268:VAL:HB	1:G:280:LYS:HB3	2.03	0.40
1:G:773:PRO:HA	1:G:781:ALA:CA	2.52	0.40
1:G:778:GLY:HA3	1:L:783:LEU:HD13	2.02	0.40
1:H:279:PRO:HB3	1:H:322:GLN:CG	2.49	0.40
1:H:596:ARG:HG3	1:H:635:ALA:HB2	2.03	0.40
1:I:268:VAL:CG1	1:I:280:LYS:HE3	2.52	0.40
1:J:582:LYS:HA	1:J:582:LYS:HD2	1.91	0.40
1:J:723:VAL:HG21	1:J:824:VAL:HA	2.02	0.40
1:L:387:ILE:O	1:L:387:ILE:HG22	2.21	0.40
1:L:818:LYS:HE3	1:L:819:TYR:CE2	2.56	0.40
1:A:250:VAL:H	1:A:250:VAL:HG23	1.64	0.40
1:A:267:SER:CB	1:A:396:ILE:HG13	2.50	0.40
1:C:227:MET:C	1:C:230:ILE:HG22	2.46	0.40
1:C:254:SER:O	1:C:391:ASN:HB3	2.21	0.40
1:C:295:VAL:HG12	1:C:296:ASN:O	2.22	0.40
1:D:855:ARG:NH2	1:K:556:ALA:CA	2.65	0.40
1:E:293:THR:OG1	1:E:346:THR:HG23	2.21	0.40
1:E:596:ARG:HG3	1:E:635:ALA:HB2	2.03	0.40
1:F:582:LYS:HE3	1:F:582:LYS:HB2	1.90	0.40
1:G:449:LYS:C	1:G:451:GLY:H	2.29	0.40
1:H:267:SER:O	1:H:268:VAL:C	2.64	0.40
1:H:286:THR:O	1:H:361:PRO:HD3	2.22	0.40
1:H:361:PRO:CG	1:H:382:LEU:HD21	2.51	0.40
1:H:670:ALA:HB3	1:H:671:LYS:NZ	2.36	0.40
1:I:441:LEU:CD2	1:I:498:VAL:HB	2.51	0.40
1:I:745:VAL:HG13	1:I:783:LEU:HD21	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:392:ILE:HD11	1:J:423:ILE:HG23	2.03	0.40
1:J:694:THR:HG21	1:J:845:MET:HB2	2.02	0.40
1:L:493:GLY:O	1:L:496:SER:HB3	2.22	0.40
1:L:703:LYS:N	1:L:704:PRO:CD	2.85	0.40
1:L:731:LEU:O	1:L:735:GLN:HG3	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	651/695 (94%)	623 (96%)	26 (4%)	2 (0%)	36	72
1	B	651/695 (94%)	618 (95%)	30 (5%)	3 (0%)	24	63
1	C	651/695 (94%)	619 (95%)	29 (4%)	3 (0%)	24	63
1	D	651/695 (94%)	620 (95%)	29 (4%)	2 (0%)	36	72
1	E	651/695 (94%)	621 (95%)	28 (4%)	2 (0%)	36	72
1	F	651/695 (94%)	624 (96%)	25 (4%)	2 (0%)	36	72
1	G	651/695 (94%)	616 (95%)	31 (5%)	4 (1%)	21	59
1	H	651/695 (94%)	620 (95%)	30 (5%)	1 (0%)	43	78
1	I	651/695 (94%)	608 (93%)	37 (6%)	6 (1%)	14	51
1	J	651/695 (94%)	621 (95%)	27 (4%)	3 (0%)	24	63
1	K	651/695 (94%)	619 (95%)	31 (5%)	1 (0%)	43	78
1	L	651/695 (94%)	614 (94%)	33 (5%)	4 (1%)	21	59
All	All	7812/8340 (94%)	7423 (95%)	356 (5%)	33 (0%)	31	67

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	776	ALA
1	E	388	ARG
1	J	260	SER
1	B	260	SER
1	B	611	GLU
1	D	769	GLU
1	K	574	ARG
1	C	260	SER
1	D	643	GLY
1	F	611	GLU
1	G	356	SER
1	I	260	SER
1	I	282	SER
1	L	611	GLU
1	B	574	ARG
1	E	574	ARG
1	G	611	GLU
1	I	611	GLU
1	J	574	ARG
1	L	843	VAL
1	I	768	VAL
1	A	643	GLY
1	C	574	ARG
1	C	611	GLU
1	I	390	PRO
1	J	342	PRO
1	A	574	ARG
1	F	601	PRO
1	G	574	ARG
1	H	574	ARG
1	I	643	GLY
1	L	247	GLY
1	L	451	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	563/594 (95%)	459 (82%)	104 (18%)	1	8
1	B	563/594 (95%)	489 (87%)	74 (13%)	4	15
1	C	563/594 (95%)	482 (86%)	81 (14%)	3	13
1	D	563/594 (95%)	453 (80%)	110 (20%)	1	7
1	E	563/594 (95%)	454 (81%)	109 (19%)	1	7
1	F	563/594 (95%)	476 (84%)	87 (16%)	2	12
1	G	563/594 (95%)	495 (88%)	68 (12%)	5	17
1	H	563/594 (95%)	448 (80%)	115 (20%)	1	7
1	I	563/594 (95%)	479 (85%)	84 (15%)	3	12
1	J	563/594 (95%)	453 (80%)	110 (20%)	1	7
1	K	563/594 (95%)	452 (80%)	111 (20%)	1	7
1	L	563/594 (95%)	485 (86%)	78 (14%)	3	14
All	All	6756/7128 (95%)	5625 (83%)	1131 (17%)	4	10

All (1131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	ASP
1	A	227	MET
1	A	228	MET
1	A	229	PHE
1	A	230	ILE
1	A	232	LYS
1	A	233	LYS
1	A	235	ILE
1	A	237	ILE
1	A	240	LEU
1	A	241	LEU
1	A	243	LYS
1	A	244	VAL
1	A	248	SER
1	A	255	ILE
1	A	263	SER
1	A	266	SER
1	A	268	VAL
1	A	269	LEU
1	A	272	ILE
1	A	275	HIS
1	A	278	LEU

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Mol	Chain	Res	Type
1	A	282	SER
1	A	284	MET
1	A	285	ILE
1	A	287	ARG
1	A	303	ASP
1	A	307	PHE
1	A	320	LEU
1	A	344	ARG
1	A	346	THR
1	A	348	HIS
1	A	354	ASP
1	A	358	ILE
1	A	360	LEU
1	A	363	TYR
1	A	375	LEU
1	A	376	LYS
1	A	377	ARG
1	A	378	LYS
1	A	380	THR
1	A	382	LEU
1	A	383	CYS
1	A	385	LYS
1	A	388	ARG
1	A	393	ILE
1	A	394	LEU
1	A	396	ILE
1	A	402	ASP
1	A	412	SER
1	A	423	ILE
1	A	430	ASP
1	A	433	GLU
1	A	434	PRO
1	A	448	LEU
1	A	450	LEU
1	A	456	ILE
1	A	457	SER
1	A	458	LYS
1	A	474	LEU
1	A	479	ARG
1	A	483	ASN
1	A	484	TYR
1	A	491	GLU

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Mol	Chain	Res	Type
1	A	492	PHE
1	A	498	VAL
1	A	499	SER
1	A	506	ARG
1	A	507	LYS
1	A	510	LEU
1	A	513	LEU
1	A	516	GLN
1	A	534	GLU
1	A	546	GLN
1	A	576	GLN
1	A	581	LEU
1	A	610	ARG
1	A	615	ILE
1	A	617	ASP
1	A	632	LEU
1	A	640	THR
1	A	642	LEU
1	A	647	LEU
1	A	654	SER
1	A	657	GLN
1	A	671	LYS
1	A	714	ASN
1	A	723	VAL
1	A	727	LEU
1	A	739	LYS
1	A	762	ARG
1	A	767	ILE
1	A	768	VAL
1	A	769	GLU
1	A	771	ASP
1	A	802	LEU
1	A	815	LEU
1	A	836	THR
1	A	838	VAL
1	A	839	LEU
1	A	841	LEU
1	A	871	LEU
1	A	893	LEU
1	A	903	GLU
1	B	231	THR
1	B	237	ILE

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Mol	Chain	Res	Type
1	B	244	VAL
1	B	251	THR
1	B	255	ILE
1	B	266	SER
1	B	269	LEU
1	B	278	LEU
1	B	282	SER
1	B	283	ASN
1	B	284	MET
1	B	303	ASP
1	B	319	SER
1	B	320	LEU
1	B	344	ARG
1	B	346	THR
1	B	358	ILE
1	B	363	TYR
1	B	376	LYS
1	B	377	ARG
1	B	378	LYS
1	B	382	LEU
1	B	388	ARG
1	B	393	ILE
1	B	394	LEU
1	B	396	ILE
1	B	400	ASP
1	B	402	ASP
1	B	423	ILE
1	B	426	ILE
1	B	430	ASP
1	B	431	LEU
1	B	448	LEU
1	B	456	ILE
1	B	457	SER
1	B	458	LYS
1	B	474	LEU
1	B	479	ARG
1	B	481	GLU
1	B	483	ASN
1	B	490	THR
1	B	491	GLU
1	B	492	PHE
1	B	503	MET

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Mol	Chain	Res	Type
1	B	505	LEU
1	B	513	LEU
1	B	530	ARG
1	B	571	SER
1	B	590	LEU
1	B	600	ARG
1	B	605	LEU
1	B	611	GLU
1	B	613	ASP
1	B	615	ILE
1	B	618	LEU
1	B	631	GLN
1	B	632	LEU
1	B	642	LEU
1	B	644	VAL
1	B	654	SER
1	B	666	LYS
1	B	676	ARG
1	B	690	ARG
1	B	727	LEU
1	B	741	LEU
1	B	762	ARG
1	B	786	ARG
1	B	803	ARG
1	B	817	ASN
1	B	824	VAL
1	B	838	VAL
1	B	841	LEU
1	B	873	LYS
1	B	880	LYS
1	C	231	THR
1	C	237	ILE
1	C	244	VAL
1	C	251	THR
1	C	255	ILE
1	C	266	SER
1	C	269	LEU
1	C	278	LEU
1	C	282	SER
1	C	284	MET
1	C	303	ASP
1	C	310	LEU

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Mol	Chain	Res	Type
1	C	312	LEU
1	C	320	LEU
1	C	325	LEU
1	C	339	THR
1	C	344	ARG
1	C	346	THR
1	C	358	ILE
1	C	360	LEU
1	C	363	TYR
1	C	375	LEU
1	C	376	LYS
1	C	377	ARG
1	C	378	LYS
1	C	382	LEU
1	C	385	LYS
1	C	386	TYR
1	C	388	ARG
1	C	392	ILE
1	C	393	ILE
1	C	394	LEU
1	C	396	ILE
1	C	412	SER
1	C	422	THR
1	C	423	ILE
1	C	430	ASP
1	C	456	ILE
1	C	458	LYS
1	C	474	LEU
1	C	476	SER
1	C	479	ARG
1	C	481	GLU
1	C	483	ASN
1	C	490	THR
1	C	491	GLU
1	C	492	PHE
1	C	499	SER
1	C	500	THR
1	C	503	MET
1	C	505	LEU
1	C	534	GLU
1	C	558	LEU
1	C	600	ARG

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Mol	Chain	Res	Type
1	C	602	ILE
1	C	611	GLU
1	C	613	ASP
1	C	615	ILE
1	C	618	LEU
1	C	631	GLN
1	C	632	LEU
1	C	644	VAL
1	C	664	LEU
1	C	666	LYS
1	C	721	GLU
1	C	722	HIS
1	C	723	VAL
1	C	727	LEU
1	C	741	LEU
1	C	762	ARG
1	C	803	ARG
1	C	811	GLN
1	C	815	LEU
1	C	817	ASN
1	C	824	VAL
1	C	838	VAL
1	C	841	LEU
1	C	860	LYS
1	C	880	LYS
1	C	898	LEU
1	C	904	LEU
1	D	225	ASP
1	D	227	MET
1	D	228	MET
1	D	229	PHE
1	D	230	ILE
1	D	232	LYS
1	D	233	LYS
1	D	235	ILE
1	D	237	ILE
1	D	240	LEU
1	D	241	LEU
1	D	243	LYS
1	D	244	VAL
1	D	251	THR
1	D	255	ILE

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Mol	Chain	Res	Type
1	D	266	SER
1	D	267	SER
1	D	268	VAL
1	D	269	LEU
1	D	272	ILE
1	D	278	LEU
1	D	282	SER
1	D	283	ASN
1	D	284	MET
1	D	285	ILE
1	D	287	ARG
1	D	303	ASP
1	D	320	LEU
1	D	325	LEU
1	D	344	ARG
1	D	346	THR
1	D	351	ASN
1	D	354	ASP
1	D	358	ILE
1	D	363	TYR
1	D	376	LYS
1	D	378	LYS
1	D	382	LEU
1	D	383	CYS
1	D	388	ARG
1	D	393	ILE
1	D	394	LEU
1	D	396	ILE
1	D	400	ASP
1	D	402	ASP
1	D	407	THR
1	D	412	SER
1	D	423	ILE
1	D	430	ASP
1	D	434	PRO
1	D	448	LEU
1	D	449	LYS
1	D	450	LEU
1	D	456	ILE
1	D	458	LYS
1	D	474	LEU
1	D	479	ARG

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Mol	Chain	Res	Type
1	D	481	GLU
1	D	483	ASN
1	D	490	THR
1	D	491	GLU
1	D	492	PHE
1	D	495	ASP
1	D	496	SER
1	D	498	VAL
1	D	499	SER
1	D	505	LEU
1	D	507	LYS
1	D	513	LEU
1	D	515	GLN
1	D	516	GLN
1	D	546	GLN
1	D	557	SER
1	D	560	ASP
1	D	576	GLN
1	D	581	LEU
1	D	586	ASP
1	D	596	ARG
1	D	610	ARG
1	D	615	ILE
1	D	616	ILE
1	D	617	ASP
1	D	632	LEU
1	D	640	THR
1	D	642	LEU
1	D	647	LEU
1	D	657	GLN
1	D	671	LYS
1	D	695	SER
1	D	714	ASN
1	D	727	LEU
1	D	739	LYS
1	D	748	ARG
1	D	749	LYS
1	D	752	LYS
1	D	762	ARG
1	D	768	VAL
1	D	783	LEU
1	D	784	LEU

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Mol	Chain	Res	Type
1	D	802	LEU
1	D	815	LEU
1	D	818	LYS
1	D	836	THR
1	D	838	VAL
1	D	839	LEU
1	D	841	LEU
1	D	855	ARG
1	D	871	LEU
1	D	893	LEU
1	D	903	GLU
1	E	227	MET
1	E	228	MET
1	E	229	PHE
1	E	230	ILE
1	E	235	ILE
1	E	237	ILE
1	E	240	LEU
1	E	241	LEU
1	E	243	LYS
1	E	244	VAL
1	E	249	THR
1	E	251	THR
1	E	252	LEU
1	E	255	ILE
1	E	260	SER
1	E	266	SER
1	E	268	VAL
1	E	269	LEU
1	E	272	ILE
1	E	278	LEU
1	E	282	SER
1	E	284	MET
1	E	285	ILE
1	E	287	ARG
1	E	320	LEU
1	E	321	ILE
1	E	344	ARG
1	E	346	THR
1	E	351	ASN
1	E	354	ASP
1	E	358	ILE

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Mol	Chain	Res	Type
1	E	360	LEU
1	E	363	TYR
1	E	375	LEU
1	E	376	LYS
1	E	377	ARG
1	E	378	LYS
1	E	382	LEU
1	E	383	CYS
1	E	385	LYS
1	E	388	ARG
1	E	392	ILE
1	E	393	ILE
1	E	394	LEU
1	E	396	ILE
1	E	400	ASP
1	E	402	ASP
1	E	407	THR
1	E	412	SER
1	E	422	THR
1	E	423	ILE
1	E	430	ASP
1	E	432	VAL
1	E	433	GLU
1	E	434	PRO
1	E	436	LYS
1	E	448	LEU
1	E	450	LEU
1	E	456	ILE
1	E	457	SER
1	E	458	LYS
1	E	474	LEU
1	E	479	ARG
1	E	483	ASN
1	E	484	TYR
1	E	490	THR
1	E	491	GLU
1	E	492	PHE
1	E	498	VAL
1	E	505	LEU
1	E	507	LYS
1	E	513	LEU
1	E	515	GLN

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Mol	Chain	Res	Type
1	E	516	GLN
1	E	546	GLN
1	E	557	SER
1	E	558	LEU
1	E	560	ASP
1	E	570	SER
1	E	576	GLN
1	E	586	ASP
1	E	610	ARG
1	E	615	ILE
1	E	616	ILE
1	E	617	ASP
1	E	622	ASP
1	E	631	GLN
1	E	640	THR
1	E	641	ARG
1	E	642	LEU
1	E	647	LEU
1	E	651	VAL
1	E	657	GLN
1	E	671	LYS
1	E	714	ASN
1	E	727	LEU
1	E	739	LYS
1	E	749	LYS
1	E	752	LYS
1	E	768	VAL
1	E	783	LEU
1	E	802	LEU
1	E	815	LEU
1	E	836	THR
1	E	838	VAL
1	E	841	LEU
1	E	871	LEU
1	E	893	LEU
1	E	903	GLU
1	F	231	THR
1	F	237	ILE
1	F	244	VAL
1	F	251	THR
1	F	255	ILE
1	F	266	SER

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Mol	Chain	Res	Type
1	F	269	LEU
1	F	273	VAL
1	F	278	LEU
1	F	282	SER
1	F	284	MET
1	F	285	ILE
1	F	287	ARG
1	F	303	ASP
1	F	310	LEU
1	F	344	ARG
1	F	346	THR
1	F	351	ASN
1	F	358	ILE
1	F	376	LYS
1	F	377	ARG
1	F	378	LYS
1	F	379	ILE
1	F	382	LEU
1	F	385	LYS
1	F	388	ARG
1	F	392	ILE
1	F	393	ILE
1	F	394	LEU
1	F	396	ILE
1	F	400	ASP
1	F	412	SER
1	F	423	ILE
1	F	430	ASP
1	F	432	VAL
1	F	436	LYS
1	F	448	LEU
1	F	456	ILE
1	F	457	SER
1	F	458	LYS
1	F	474	LEU
1	F	476	SER
1	F	481	GLU
1	F	483	ASN
1	F	490	THR
1	F	491	GLU
1	F	492	PHE
1	F	495	ASP

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Mol	Chain	Res	Type
1	F	503	MET
1	F	505	LEU
1	F	519	SER
1	F	521	LEU
1	F	557	SER
1	F	590	LEU
1	F	600	ARG
1	F	603	GLU
1	F	605	LEU
1	F	611	GLU
1	F	613	ASP
1	F	615	ILE
1	F	616	ILE
1	F	617	ASP
1	F	618	LEU
1	F	631	GLN
1	F	636	CYS
1	F	640	THR
1	F	642	LEU
1	F	654	SER
1	F	666	LYS
1	F	690	ARG
1	F	714	ASN
1	F	723	VAL
1	F	741	LEU
1	F	748	ARG
1	F	762	ARG
1	F	768	VAL
1	F	771	ASP
1	F	786	ARG
1	F	803	ARG
1	F	811	GLN
1	F	815	LEU
1	F	817	ASN
1	F	824	VAL
1	F	838	VAL
1	F	841	LEU
1	F	873	LYS
1	F	880	LYS
1	G	231	THR
1	G	235	ILE
1	G	237	ILE

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Mol	Chain	Res	Type
1	G	244	VAL
1	G	251	THR
1	G	255	ILE
1	G	266	SER
1	G	269	LEU
1	G	278	LEU
1	G	284	MET
1	G	285	ILE
1	G	287	ARG
1	G	303	ASP
1	G	320	LEU
1	G	344	ARG
1	G	346	THR
1	G	352	ILE
1	G	358	ILE
1	G	363	TYR
1	G	375	LEU
1	G	376	LYS
1	G	378	LYS
1	G	382	LEU
1	G	388	ARG
1	G	393	ILE
1	G	394	LEU
1	G	396	ILE
1	G	400	ASP
1	G	412	SER
1	G	423	ILE
1	G	430	ASP
1	G	448	LEU
1	G	458	LYS
1	G	474	LEU
1	G	479	ARG
1	G	481	GLU
1	G	490	THR
1	G	491	GLU
1	G	503	MET
1	G	590	LEU
1	G	600	ARG
1	G	605	LEU
1	G	611	GLU
1	G	613	ASP
1	G	615	ILE

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Mol	Chain	Res	Type
1	G	617	ASP
1	G	618	LEU
1	G	641	ARG
1	G	666	LYS
1	G	676	ARG
1	G	714	ASN
1	G	721	GLU
1	G	727	LEU
1	G	741	LEU
1	G	762	ARG
1	G	767	ILE
1	G	772	HIS
1	G	780	SER
1	G	786	ARG
1	G	803	ARG
1	G	809	SER
1	G	815	LEU
1	G	817	ASN
1	G	824	VAL
1	G	838	VAL
1	G	841	LEU
1	G	873	LYS
1	G	880	LYS
1	H	225	ASP
1	H	227	MET
1	H	228	MET
1	H	229	PHE
1	H	230	ILE
1	H	232	LYS
1	H	235	ILE
1	H	237	ILE
1	H	240	LEU
1	H	241	LEU
1	H	243	LYS
1	H	244	VAL
1	H	255	ILE
1	H	263	SER
1	H	266	SER
1	H	268	VAL
1	H	269	LEU
1	H	272	ILE
1	H	278	LEU

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Mol	Chain	Res	Type
1	H	282	SER
1	H	284	MET
1	H	285	ILE
1	H	287	ARG
1	H	303	ASP
1	H	307	PHE
1	H	320	LEU
1	H	327	GLU
1	H	344	ARG
1	H	346	THR
1	H	348	HIS
1	H	351	ASN
1	H	354	ASP
1	H	358	ILE
1	H	360	LEU
1	H	363	TYR
1	H	375	LEU
1	H	376	LYS
1	H	377	ARG
1	H	378	LYS
1	H	382	LEU
1	H	383	CYS
1	H	385	LYS
1	H	388	ARG
1	H	393	ILE
1	H	394	LEU
1	H	396	ILE
1	H	402	ASP
1	H	407	THR
1	H	412	SER
1	H	423	ILE
1	H	430	ASP
1	H	434	PRO
1	H	436	LYS
1	H	448	LEU
1	H	450	LEU
1	H	456	ILE
1	H	457	SER
1	H	458	LYS
1	H	474	LEU
1	H	476	SER
1	H	479	ARG

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Mol	Chain	Res	Type
1	H	481	GLU
1	H	483	ASN
1	H	491	GLU
1	H	492	PHE
1	H	498	VAL
1	H	499	SER
1	H	505	LEU
1	H	507	LYS
1	H	513	LEU
1	H	515	GLN
1	H	516	GLN
1	H	521	LEU
1	H	534	GLU
1	H	546	GLN
1	H	548	MET
1	H	557	SER
1	H	560	ASP
1	H	562	LYS
1	H	576	GLN
1	H	581	LEU
1	H	590	LEU
1	H	610	ARG
1	H	613	ASP
1	H	615	ILE
1	H	617	ASP
1	H	632	LEU
1	H	642	LEU
1	H	647	LEU
1	H	654	SER
1	H	657	GLN
1	H	668	SER
1	H	671	LYS
1	H	714	ASN
1	H	721	GLU
1	H	727	LEU
1	H	739	LYS
1	H	749	LYS
1	H	752	LYS
1	H	762	ARG
1	H	767	ILE
1	H	768	VAL
1	H	802	LEU

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Mol	Chain	Res	Type
1	H	815	LEU
1	H	818	LYS
1	H	836	THR
1	H	838	VAL
1	H	839	LEU
1	H	841	LEU
1	H	842	ASN
1	H	871	LEU
1	H	892	GLU
1	H	893	LEU
1	H	903	GLU
1	H	907	ILE
1	I	231	THR
1	I	237	ILE
1	I	244	VAL
1	I	251	THR
1	I	255	ILE
1	I	266	SER
1	I	267	SER
1	I	269	LEU
1	I	273	VAL
1	I	278	LEU
1	I	282	SER
1	I	283	ASN
1	I	284	MET
1	I	285	ILE
1	I	287	ARG
1	I	303	ASP
1	I	320	LEU
1	I	321	ILE
1	I	339	THR
1	I	344	ARG
1	I	346	THR
1	I	354	ASP
1	I	357	LEU
1	I	358	ILE
1	I	363	TYR
1	I	375	LEU
1	I	376	LYS
1	I	377	ARG
1	I	378	LYS
1	I	382	LEU

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Mol	Chain	Res	Type
1	I	388	ARG
1	I	393	ILE
1	I	394	LEU
1	I	396	ILE
1	I	400	ASP
1	I	402	ASP
1	I	405	ASN
1	I	423	ILE
1	I	427	THR
1	I	430	ASP
1	I	431	LEU
1	I	448	LEU
1	I	458	LYS
1	I	474	LEU
1	I	479	ARG
1	I	481	GLU
1	I	483	ASN
1	I	490	THR
1	I	491	GLU
1	I	492	PHE
1	I	499	SER
1	I	500	THR
1	I	505	LEU
1	I	599	ASN
1	I	600	ARG
1	I	605	LEU
1	I	613	ASP
1	I	615	ILE
1	I	616	ILE
1	I	617	ASP
1	I	618	LEU
1	I	640	THR
1	I	642	LEU
1	I	644	VAL
1	I	666	LYS
1	I	690	ARG
1	I	714	ASN
1	I	721	GLU
1	I	741	LEU
1	I	744	SER
1	I	767	ILE
1	I	803	ARG

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Mol	Chain	Res	Type
1	I	810	ARG
1	I	811	GLN
1	I	815	LEU
1	I	817	ASN
1	I	824	VAL
1	I	838	VAL
1	I	841	LEU
1	I	847	ASN
1	I	873	LYS
1	I	880	LYS
1	I	883	ARG
1	I	906	ARG
1	J	225	ASP
1	J	227	MET
1	J	228	MET
1	J	230	ILE
1	J	232	LYS
1	J	233	LYS
1	J	235	ILE
1	J	237	ILE
1	J	240	LEU
1	J	241	LEU
1	J	243	LYS
1	J	244	VAL
1	J	251	THR
1	J	255	ILE
1	J	266	SER
1	J	268	VAL
1	J	269	LEU
1	J	272	ILE
1	J	275	HIS
1	J	278	LEU
1	J	282	SER
1	J	284	MET
1	J	285	ILE
1	J	287	ARG
1	J	303	ASP
1	J	310	LEU
1	J	320	LEU
1	J	327	GLU
1	J	344	ARG
1	J	346	THR

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Mol	Chain	Res	Type
1	J	354	ASP
1	J	358	ILE
1	J	360	LEU
1	J	363	TYR
1	J	375	LEU
1	J	376	LYS
1	J	377	ARG
1	J	378	LYS
1	J	382	LEU
1	J	383	CYS
1	J	385	LYS
1	J	387	ILE
1	J	392	ILE
1	J	393	ILE
1	J	394	LEU
1	J	396	ILE
1	J	400	ASP
1	J	402	ASP
1	J	412	SER
1	J	422	THR
1	J	423	ILE
1	J	430	ASP
1	J	431	LEU
1	J	434	PRO
1	J	435	GLU
1	J	448	LEU
1	J	450	LEU
1	J	456	ILE
1	J	457	SER
1	J	458	LYS
1	J	474	LEU
1	J	479	ARG
1	J	481	GLU
1	J	482	LYS
1	J	483	ASN
1	J	491	GLU
1	J	495	ASP
1	J	498	VAL
1	J	499	SER
1	J	513	LEU
1	J	516	GLN
1	J	521	LEU

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Mol	Chain	Res	Type
1	J	546	GLN
1	J	557	SER
1	J	560	ASP
1	J	576	GLN
1	J	581	LEU
1	J	590	LEU
1	J	596	ARG
1	J	610	ARG
1	J	615	ILE
1	J	617	ASP
1	J	631	GLN
1	J	632	LEU
1	J	640	THR
1	J	642	LEU
1	J	647	LEU
1	J	657	GLN
1	J	668	SER
1	J	671	LYS
1	J	714	ASN
1	J	721	GLU
1	J	739	LYS
1	J	749	LYS
1	J	752	LYS
1	J	767	ILE
1	J	768	VAL
1	J	769	GLU
1	J	771	ASP
1	J	802	LEU
1	J	815	LEU
1	J	836	THR
1	J	838	VAL
1	J	841	LEU
1	J	842	ASN
1	J	871	LEU
1	J	893	LEU
1	J	897	VAL
1	J	898	LEU
1	J	903	GLU
1	K	227	MET
1	K	228	MET
1	K	229	PHE
1	K	230	ILE

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Mol	Chain	Res	Type
1	K	232	LYS
1	K	233	LYS
1	K	235	ILE
1	K	237	ILE
1	K	240	LEU
1	K	241	LEU
1	K	243	LYS
1	K	244	VAL
1	K	251	THR
1	K	255	ILE
1	K	266	SER
1	K	268	VAL
1	K	269	LEU
1	K	272	ILE
1	K	275	HIS
1	K	278	LEU
1	K	282	SER
1	K	284	MET
1	K	285	ILE
1	K	287	ARG
1	K	303	ASP
1	K	310	LEU
1	K	320	LEU
1	K	344	ARG
1	K	346	THR
1	K	354	ASP
1	K	358	ILE
1	K	360	LEU
1	K	363	TYR
1	K	375	LEU
1	K	376	LYS
1	K	377	ARG
1	K	378	LYS
1	K	382	LEU
1	K	383	CYS
1	K	385	LYS
1	K	388	ARG
1	K	392	ILE
1	K	393	ILE
1	K	394	LEU
1	K	396	ILE
1	K	400	ASP

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Mol	Chain	Res	Type
1	K	403	LEU
1	K	407	THR
1	K	412	SER
1	K	423	ILE
1	K	430	ASP
1	K	431	LEU
1	K	433	GLU
1	K	434	PRO
1	K	448	LEU
1	K	450	LEU
1	K	456	ILE
1	K	458	LYS
1	K	474	LEU
1	K	479	ARG
1	K	481	GLU
1	K	482	LYS
1	K	483	ASN
1	K	490	THR
1	K	491	GLU
1	K	492	PHE
1	K	495	ASP
1	K	498	VAL
1	K	499	SER
1	K	506	ARG
1	K	507	LYS
1	K	513	LEU
1	K	515	GLN
1	K	516	GLN
1	K	519	SER
1	K	546	GLN
1	K	557	SER
1	K	560	ASP
1	K	562	LYS
1	K	576	GLN
1	K	581	LEU
1	K	596	ARG
1	K	610	ARG
1	K	615	ILE
1	K	617	ASP
1	K	631	GLN
1	K	632	LEU
1	K	640	THR

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Mol	Chain	Res	Type
1	K	642	LEU
1	K	654	SER
1	K	657	GLN
1	K	671	LYS
1	K	672	HIS
1	K	714	ASN
1	K	723	VAL
1	K	727	LEU
1	K	739	LYS
1	K	749	LYS
1	K	752	LYS
1	K	768	VAL
1	K	784	LEU
1	K	802	LEU
1	K	811	GLN
1	K	815	LEU
1	K	836	THR
1	K	838	VAL
1	K	871	LEU
1	K	893	LEU
1	K	898	LEU
1	K	903	GLU
1	K	907	ILE
1	L	231	THR
1	L	237	ILE
1	L	244	VAL
1	L	251	THR
1	L	255	ILE
1	L	266	SER
1	L	269	LEU
1	L	273	VAL
1	L	278	LEU
1	L	285	ILE
1	L	303	ASP
1	L	320	LEU
1	L	325	LEU
1	L	344	ARG
1	L	346	THR
1	L	354	ASP
1	L	358	ILE
1	L	376	LYS
1	L	377	ARG

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Mol	Chain	Res	Type
1	L	378	LYS
1	L	382	LEU
1	L	388	ARG
1	L	393	ILE
1	L	394	LEU
1	L	396	ILE
1	L	400	ASP
1	L	402	ASP
1	L	412	SER
1	L	423	ILE
1	L	426	ILE
1	L	430	ASP
1	L	435	GLU
1	L	436	LYS
1	L	448	LEU
1	L	450	LEU
1	L	457	SER
1	L	458	LYS
1	L	474	LEU
1	L	479	ARG
1	L	481	GLU
1	L	483	ASN
1	L	491	GLU
1	L	492	PHE
1	L	500	THR
1	L	502	VAL
1	L	503	MET
1	L	505	LEU
1	L	557	SER
1	L	600	ARG
1	L	605	LEU
1	L	611	GLU
1	L	613	ASP
1	L	615	ILE
1	L	618	LEU
1	L	632	LEU
1	L	636	CYS
1	L	640	THR
1	L	644	VAL
1	L	654	SER
1	L	664	LEU
1	L	690	ARG

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Mol	Chain	Res	Type
1	L	723	VAL
1	L	727	LEU
1	L	741	LEU
1	L	752	LYS
1	L	762	ARG
1	L	769	GLU
1	L	772	HIS
1	L	783	LEU
1	L	803	ARG
1	L	815	LEU
1	L	817	ASN
1	L	824	VAL
1	L	838	VAL
1	L	841	LEU
1	L	873	LYS
1	L	880	LYS
1	L	893	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (133) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	275	HIS
1	A	488	HIS
1	A	546	GLN
1	A	576	GLN
1	A	712	GLN
1	A	722	HIS
1	A	817	ASN
1	A	847	ASN
1	A	864	HIS
1	A	866	HIS
1	B	483	ASN
1	B	511	GLN
1	B	542	GLN
1	B	563	HIS
1	B	672	HIS
1	B	772	HIS
1	B	811	GLN
1	B	866	HIS
1	C	275	HIS
1	C	283	ASN
1	C	351	ASN

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Mol	Chain	Res	Type
1	C	478	ASN
1	C	511	GLN
1	C	563	HIS
1	C	631	GLN
1	C	672	HIS
1	C	712	GLN
1	C	864	HIS
1	D	242	GLN
1	D	275	HIS
1	D	472	ASN
1	D	478	ASN
1	D	488	HIS
1	D	544	ASN
1	D	576	GLN
1	D	657	GLN
1	D	659	HIS
1	D	722	HIS
1	D	811	GLN
1	D	847	ASN
1	E	242	GLN
1	E	261	GLN
1	E	275	HIS
1	E	329	ASN
1	E	472	ASN
1	E	478	ASN
1	E	488	HIS
1	E	515	GLN
1	E	544	ASN
1	E	546	GLN
1	E	576	GLN
1	E	592	GLN
1	E	614	ASN
1	E	657	GLN
1	E	672	HIS
1	E	722	HIS
1	E	847	ASN
1	E	864	HIS
1	F	239	ASN
1	F	538	GLN
1	F	563	HIS
1	F	614	ASN
1	F	657	GLN

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Mol	Chain	Res	Type
1	F	658	GLN
1	F	659	HIS
1	F	672	HIS
1	F	884	HIS
1	G	329	ASN
1	G	511	GLN
1	G	614	ASN
1	G	631	GLN
1	G	657	GLN
1	G	672	HIS
1	G	862	HIS
1	G	866	HIS
1	H	242	GLN
1	H	275	HIS
1	H	472	ASN
1	H	478	ASN
1	H	488	HIS
1	H	576	GLN
1	H	592	GLN
1	H	659	HIS
1	H	714	ASN
1	H	772	HIS
1	H	811	GLN
1	H	847	ASN
1	H	866	HIS
1	H	884	HIS
1	I	329	ASN
1	I	480	ASN
1	I	483	ASN
1	I	563	HIS
1	I	614	ASN
1	I	631	GLN
1	I	657	GLN
1	I	712	GLN
1	I	772	HIS
1	J	275	HIS
1	J	391	ASN
1	J	472	ASN
1	J	478	ASN
1	J	576	GLN
1	J	592	GLN
1	J	657	GLN

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Mol	Chain	Res	Type
1	J	659	HIS
1	J	722	HIS
1	J	811	GLN
1	K	275	HIS
1	K	445	GLN
1	K	478	ASN
1	K	488	HIS
1	K	544	ASN
1	K	546	GLN
1	K	576	GLN
1	K	657	GLN
1	K	805	GLN
1	K	811	GLN
1	K	842	ASN
1	K	864	HIS
1	K	866	HIS
1	K	884	HIS
1	L	261	GLN
1	L	478	ASN
1	L	483	ASN
1	L	488	HIS
1	L	511	GLN
1	L	563	HIS
1	L	631	GLN
1	L	657	GLN
1	L	672	HIS
1	L	735	GLN
1	L	862	HIS

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	E	1
1	J	1
1	D	1
1	H	1
1	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	253:PRO	C	254:SER	N	1.16
1	E	253:PRO	C	254:SER	N	1.15
1	J	253:PRO	C	254:SER	N	1.14
1	D	253:PRO	C	254:SER	N	1.13
1	H	253:PRO	C	254:SER	N	1.12
1	K	253:PRO	C	254:SER	N	1.12

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10063. These allow visual inspection of the internal detail of the map and identification of artifacts.

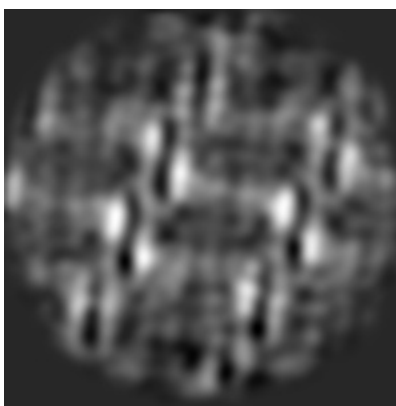
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

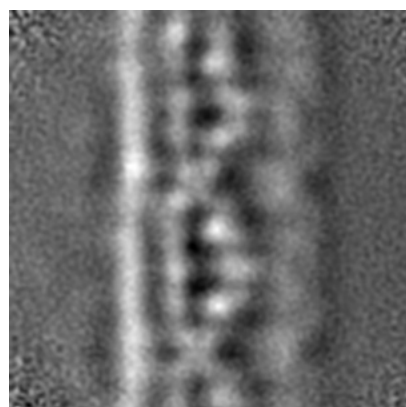


Y

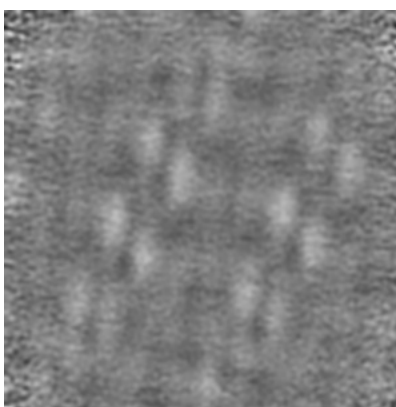


Z

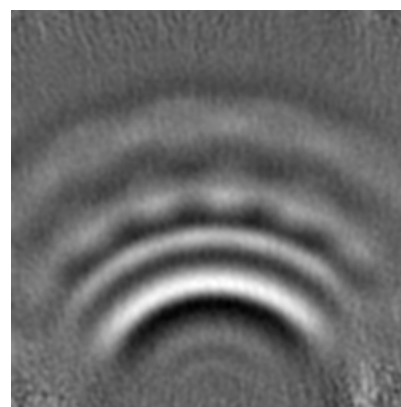
6.1.2 Raw map



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: 60

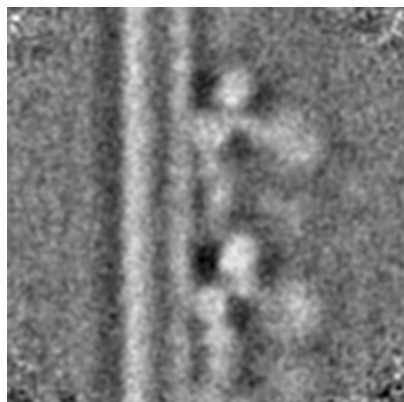


Y Index: 60

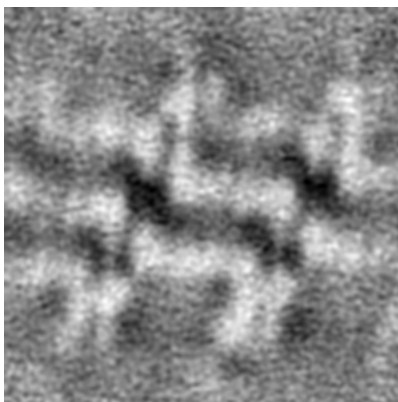


Z Index: 60

6.2.2 Raw map



X Index: 60



Y Index: 60



Z Index: 60

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

6.3 Largest variance slices [i](#)

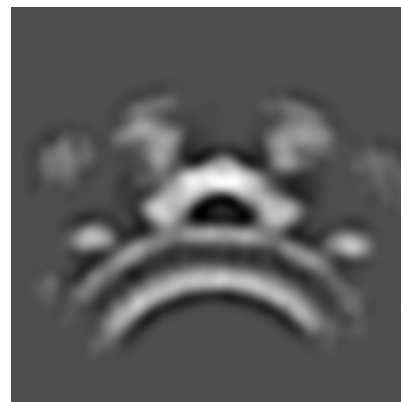
6.3.1 Primary map



X Index: 63

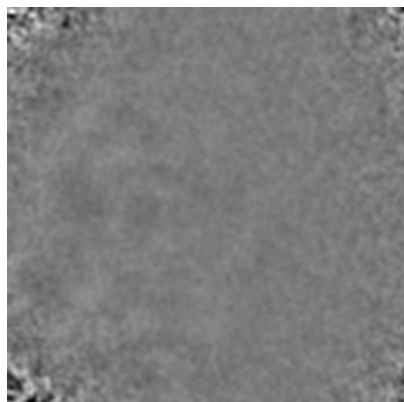


Y Index: 37

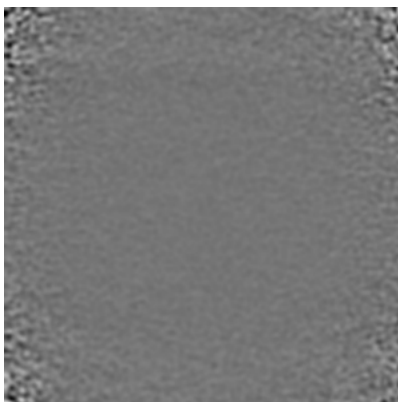


Z Index: 42

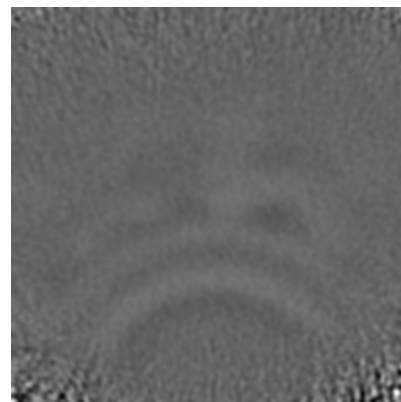
6.3.2 Raw map



X Index: 119



Y Index: 1

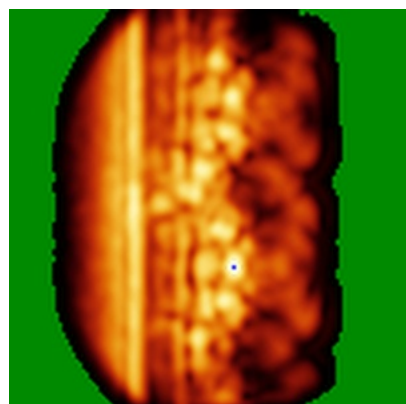


Z Index: 1

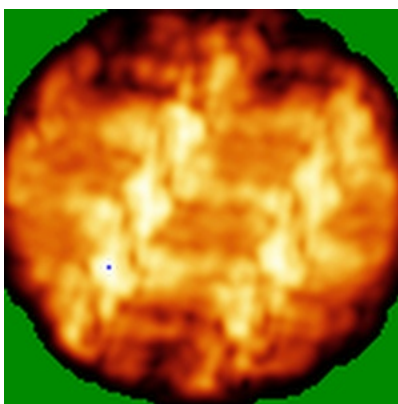
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

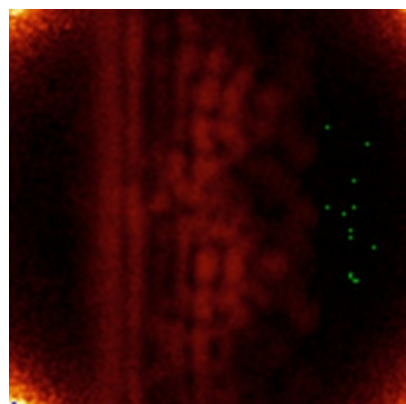


Y

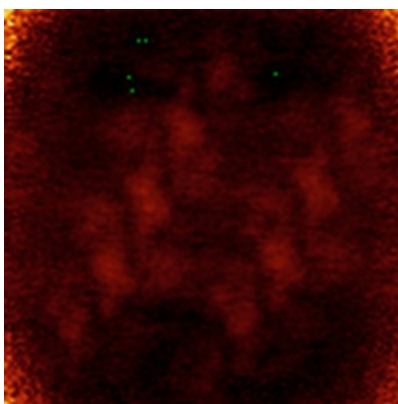


Z

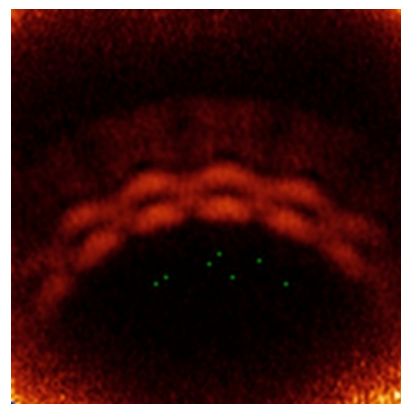
6.4.2 Raw map



X



Y

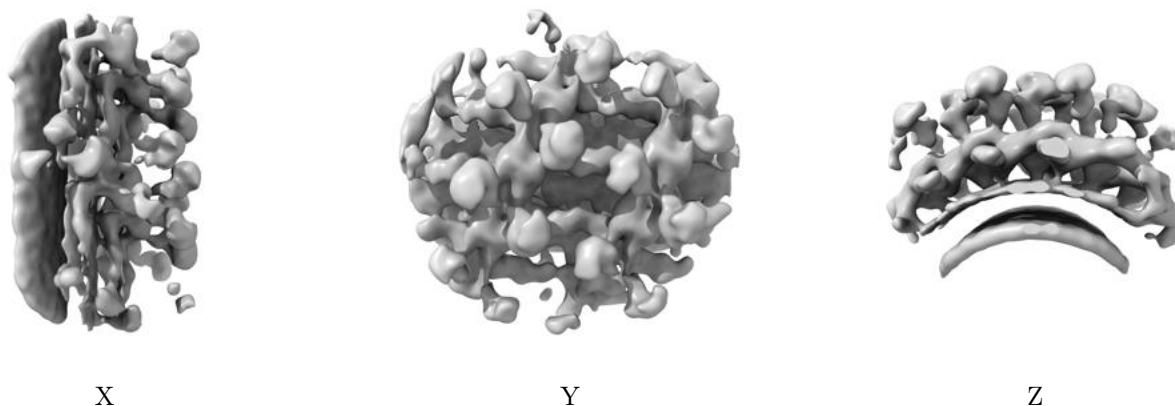


Z

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.

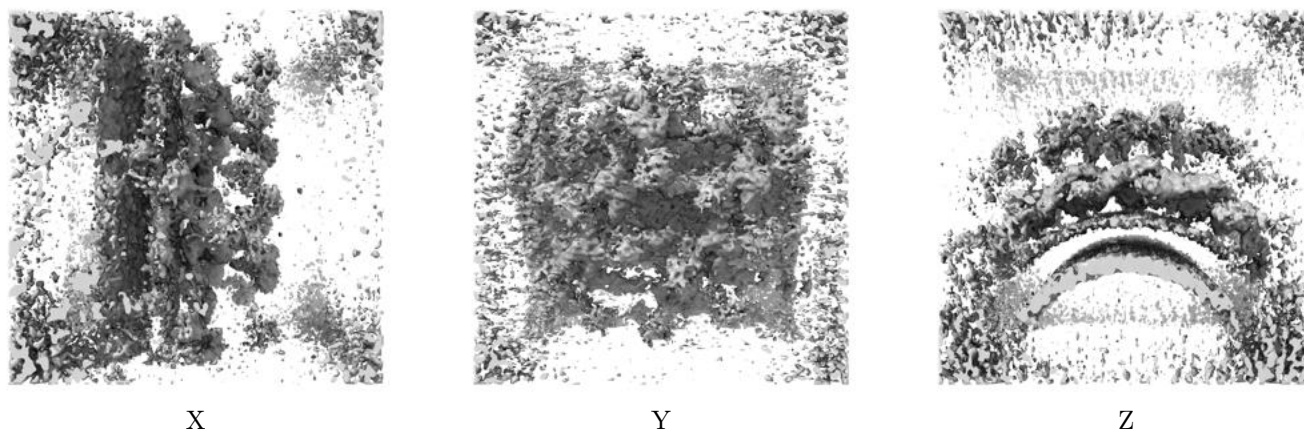
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

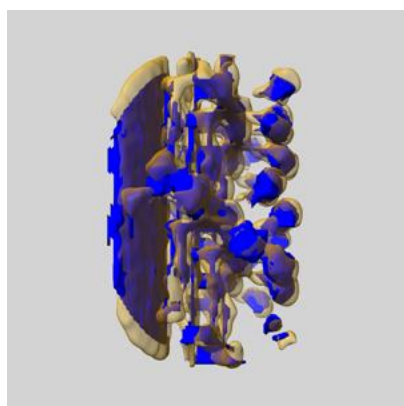
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

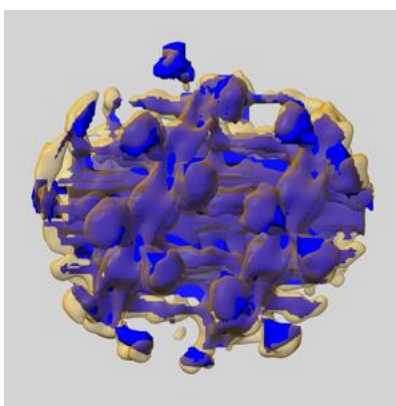
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

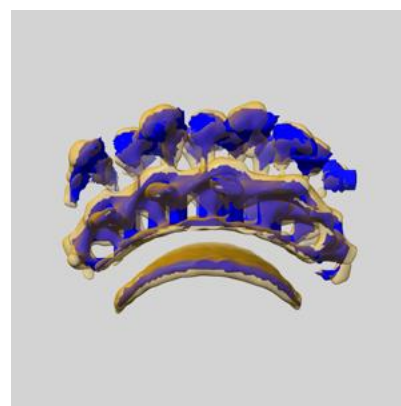
6.6.1 emd_10063_msk_1.map [i](#)



X



Y

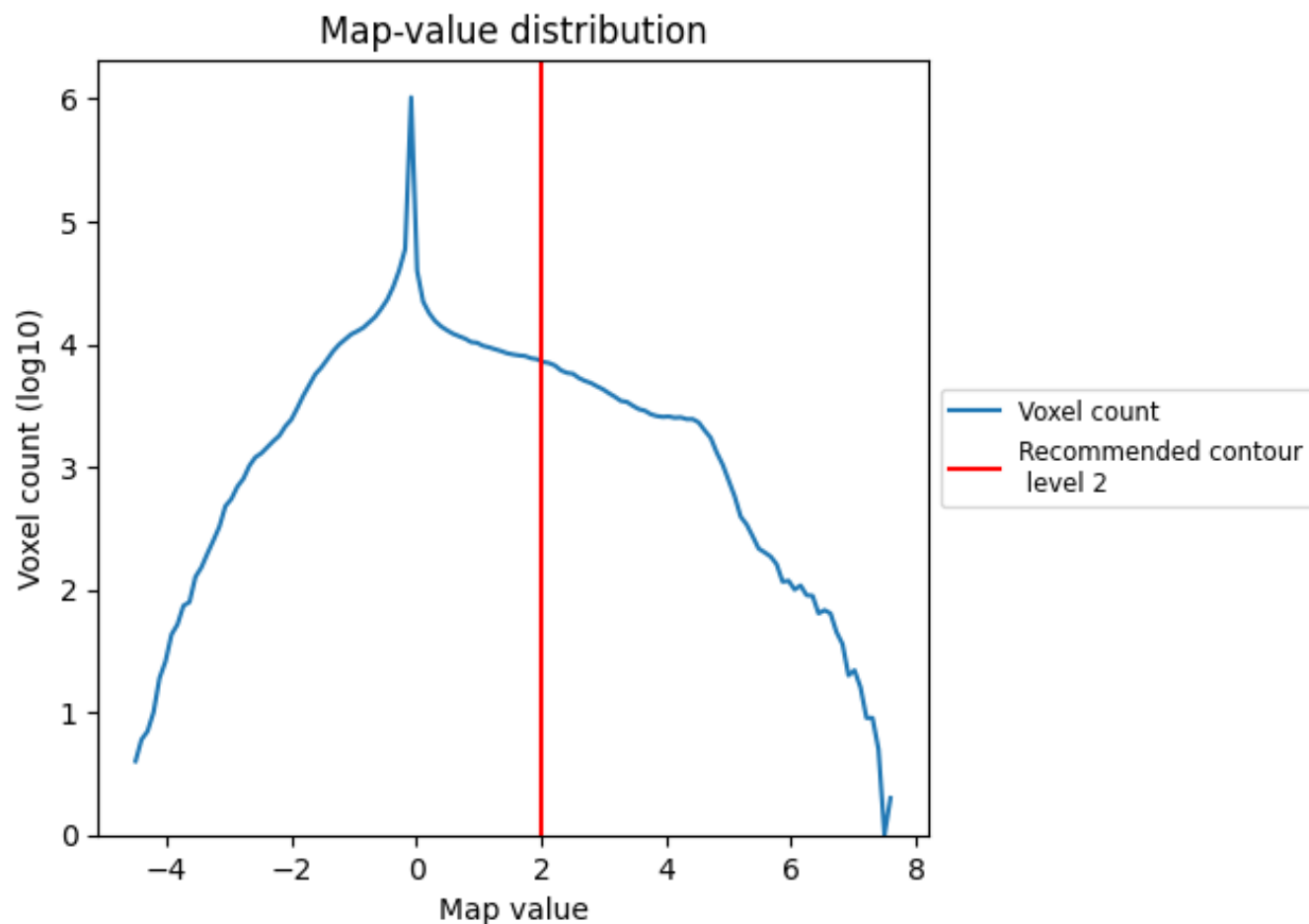


Z

7 Map analysis [i](#)

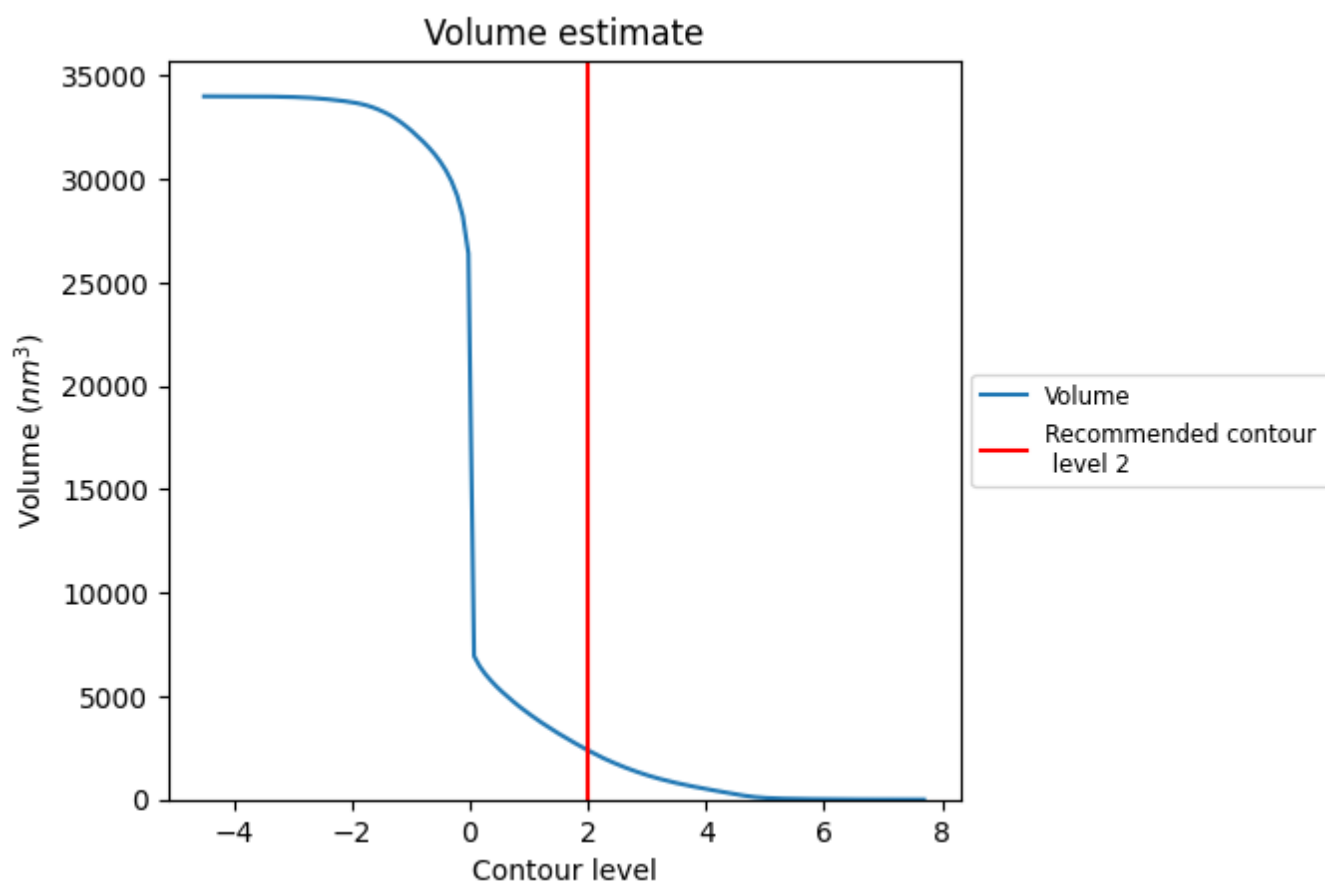
This section contains the results of statistical analysis of the map.

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.

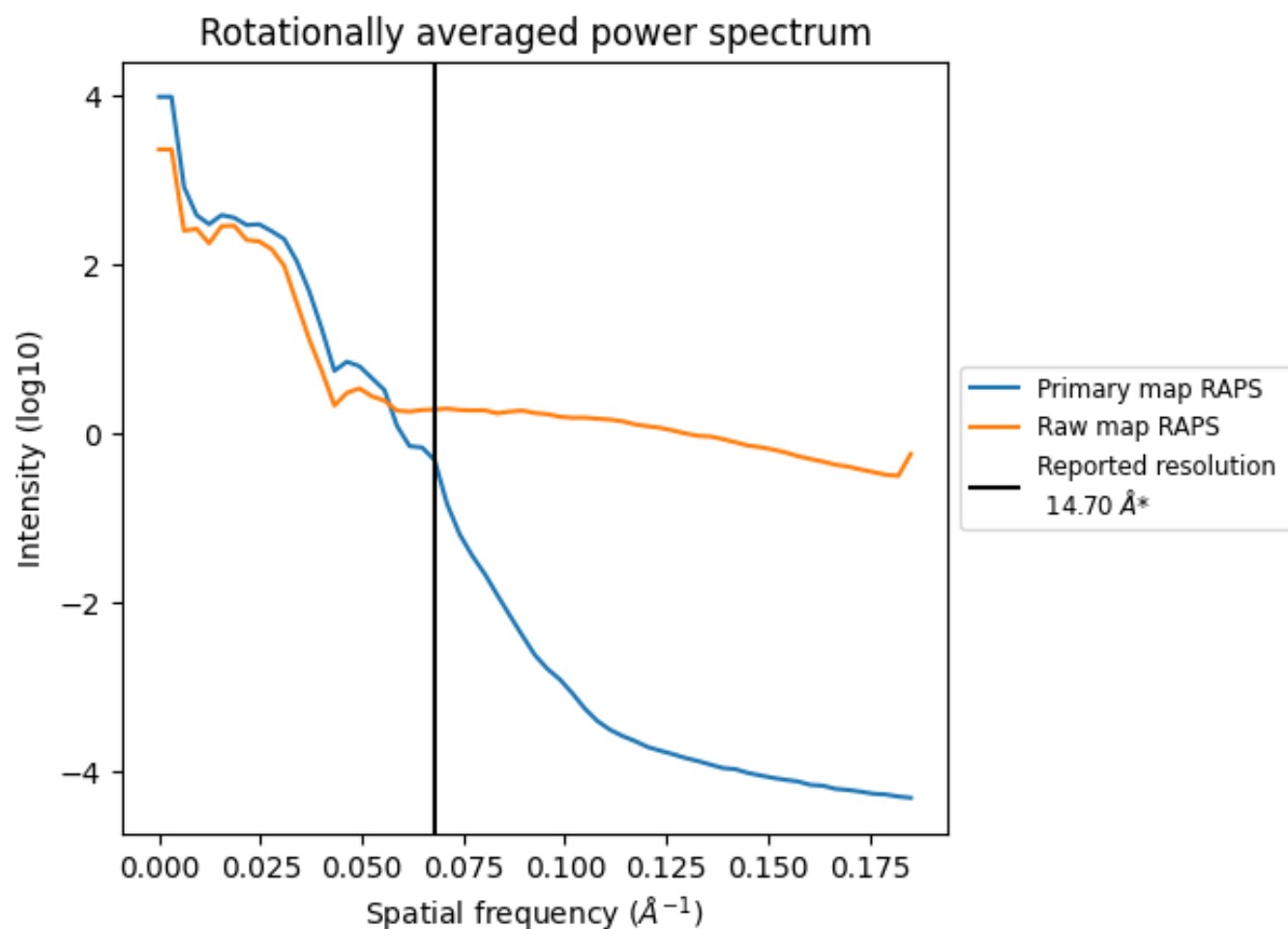
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2386 nm³; this corresponds to an approximate mass of 2155 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 ⓘ

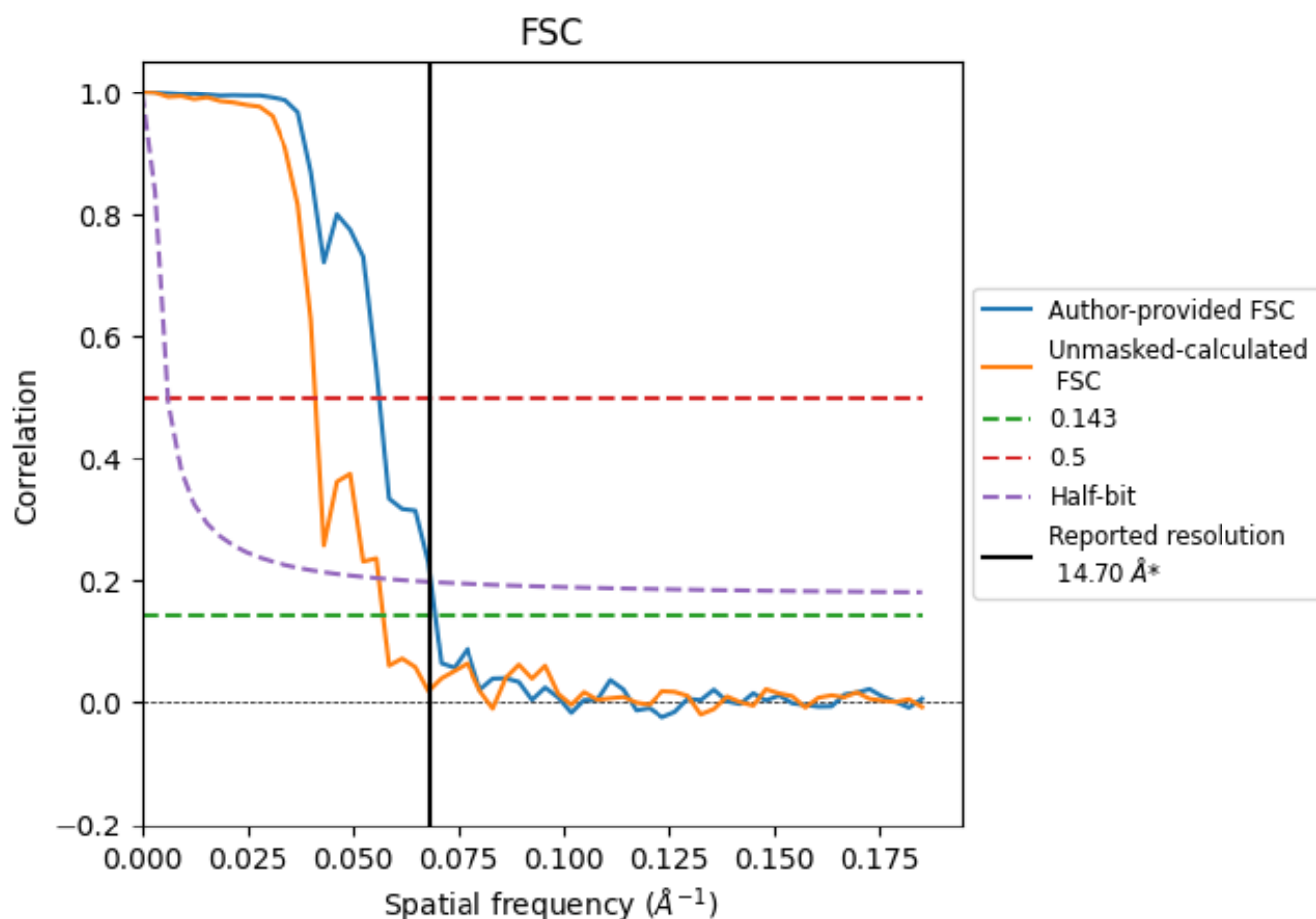


*Reported resolution corresponds to spatial frequency of 0.068 $\text{\AA}^{-1}$

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 0.068 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

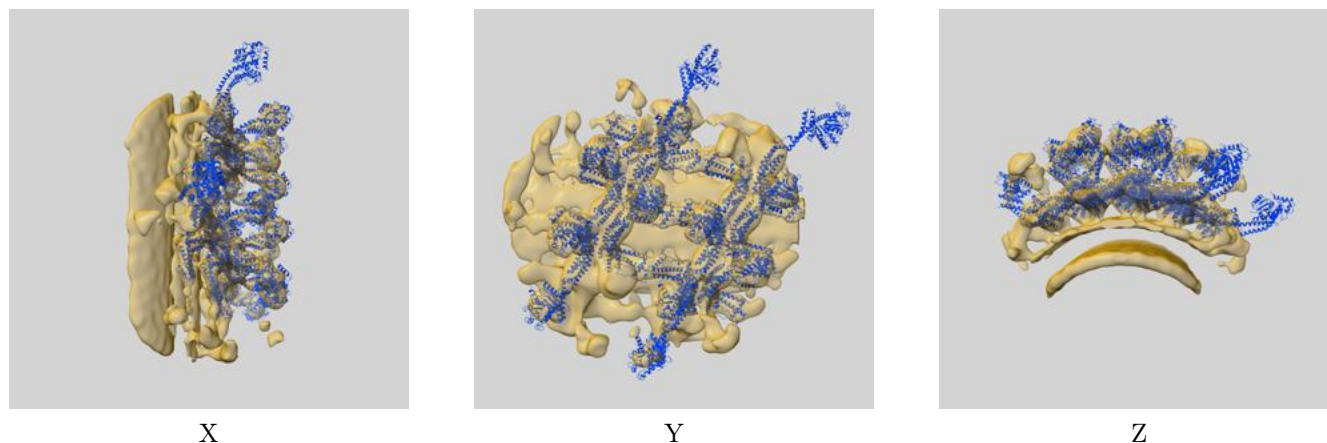
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	14.70	-	-
Author-provided FSC curve	14.39	17.79	14.60
Unmasked-calculated*	17.48	24.27	17.83

*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 17.48 differs from the reported value 14.7 by more than 10 %

9 Map-model fit [i](#)

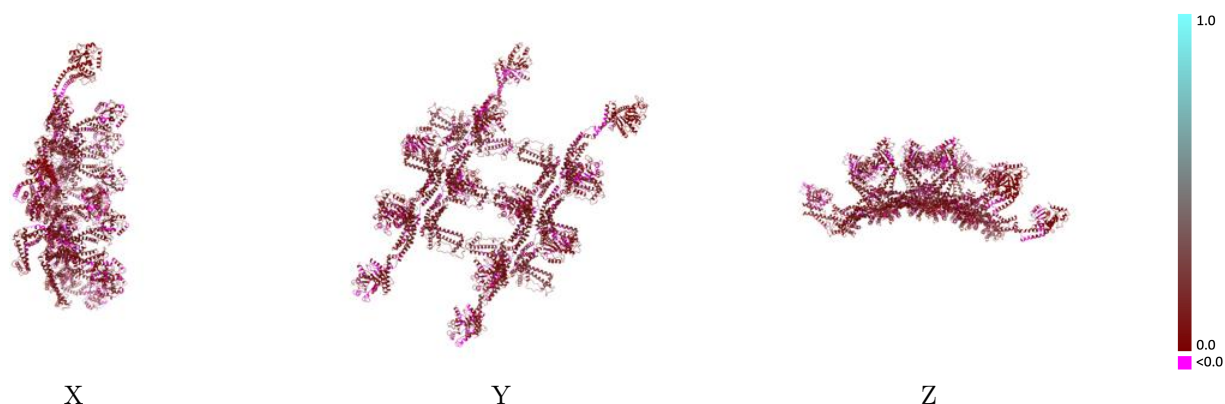
This section contains information regarding the fit between EMDB map EMD-10063 and PDB model 6RZU. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



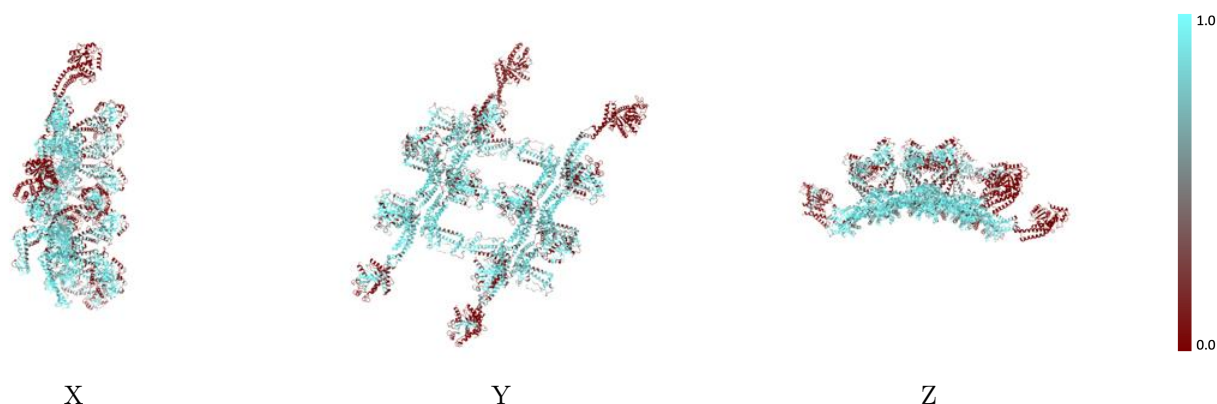
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



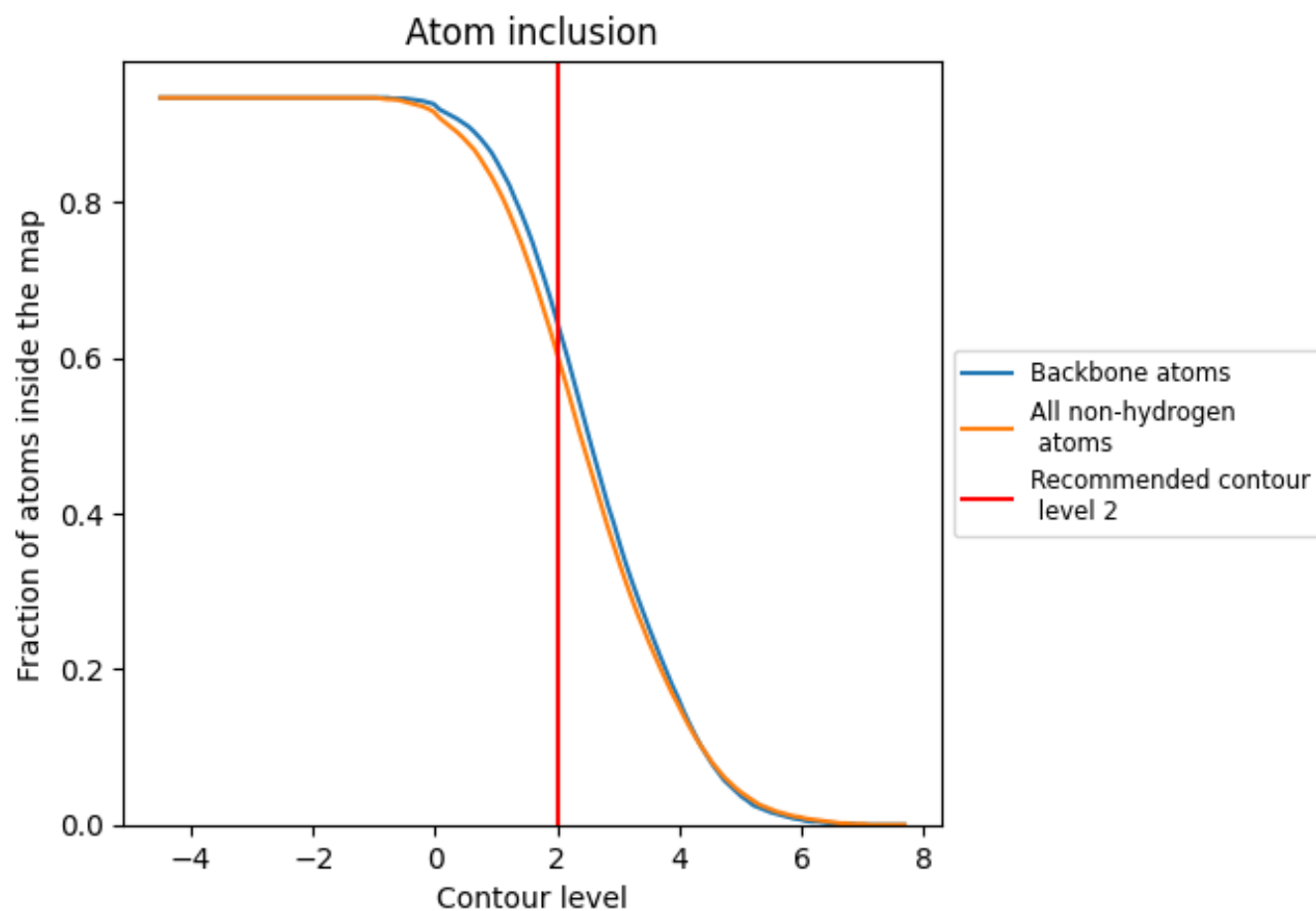
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 60% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6050	0.0680
A	0.6140	0.0690
B	0.7150	0.0760
C	0.7580	0.0750
D	0.5960	0.0770
E	0.6790	0.0720
F	0.6290	0.0760
G	0.6890	0.0760
H	0.3900	0.0400
I	0.4900	0.0680
J	0.6780	0.0750
K	0.6570	0.0710
L	0.3680	0.0430

