



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:36 AM UTC

PDB ID : 6RZT / pdb_00006rzt
EMDB ID : EMD-10062
Title : Structure of s-Mgm1 decorating the outer surface of tubulated lipid membranes
Authors : Faelber, K.; Dietrich, L.; Noel, J.K.; Sanchez, R.; Kudryashev, M.; Kuehlbrandt, 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

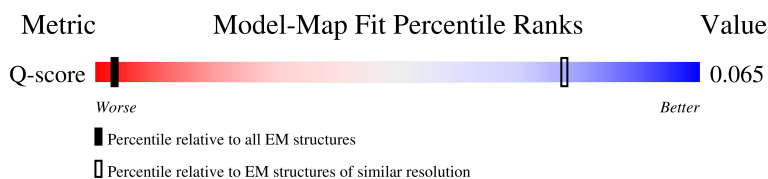
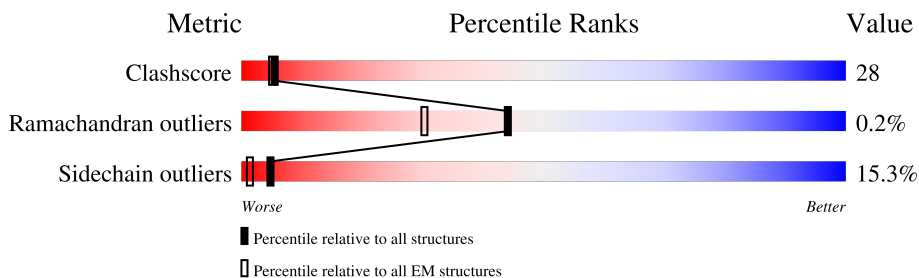
1 Overall quality at a glance

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	
1	B	695	
1	C	695	
1	D	695	

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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.

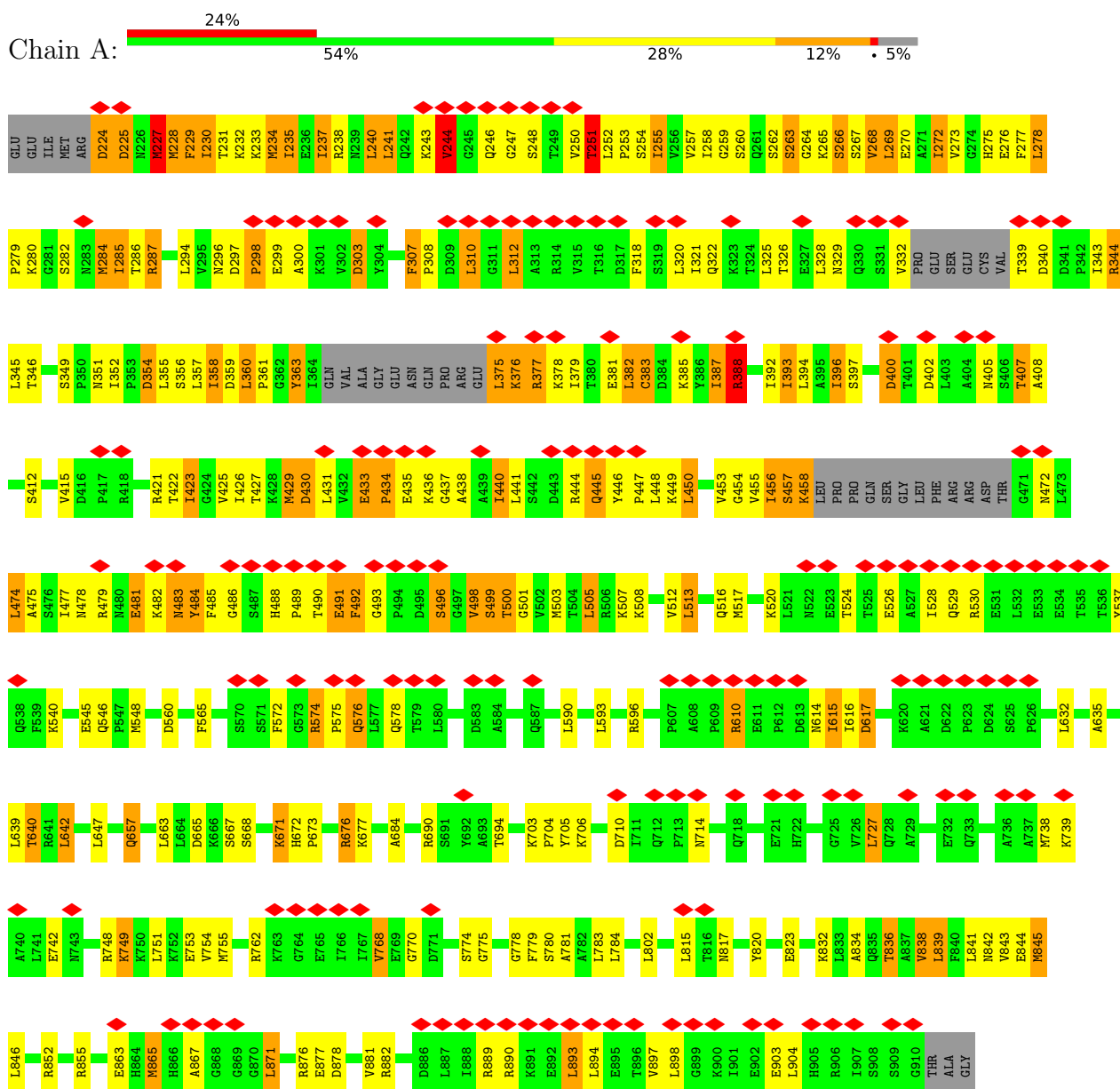
- Molecule 1 is a protein called Putative mitochondrial dynamin protein.

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

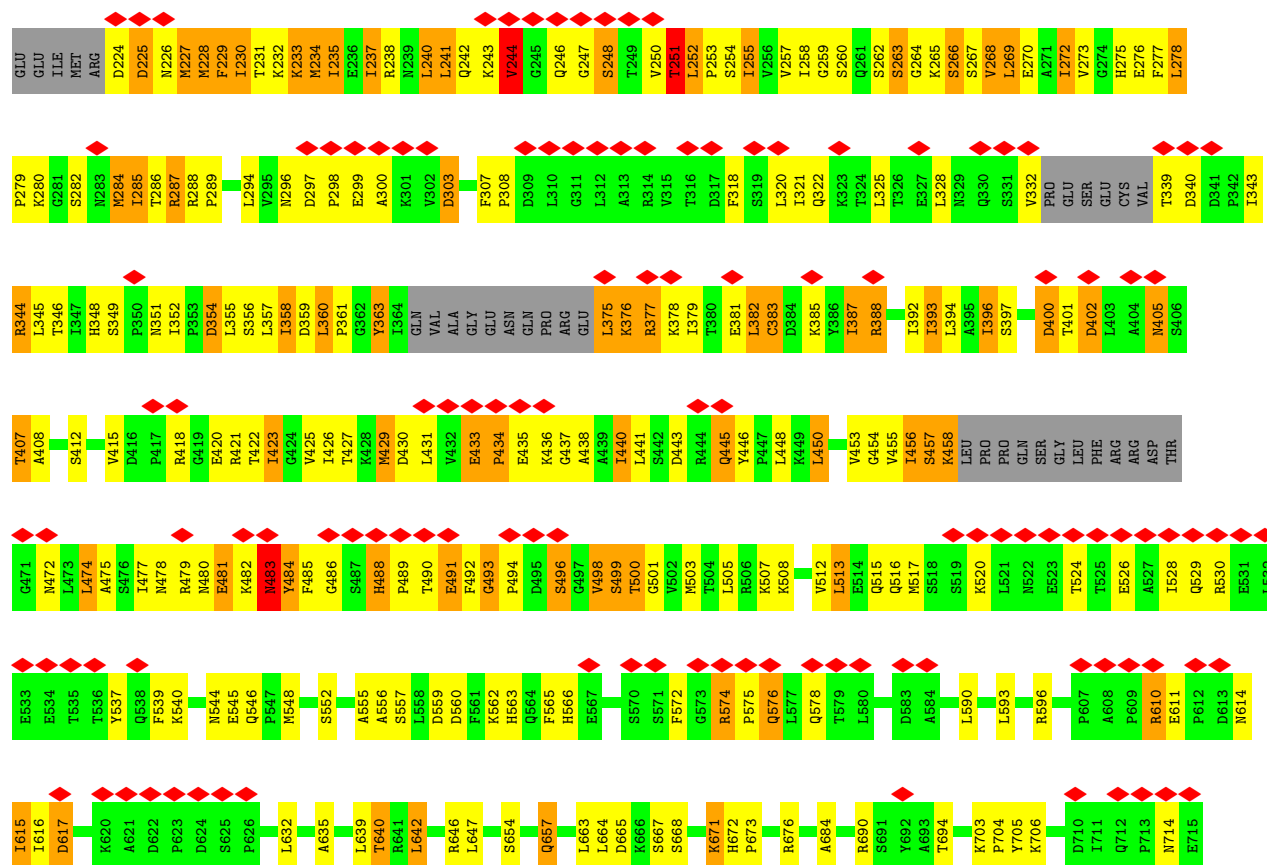
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

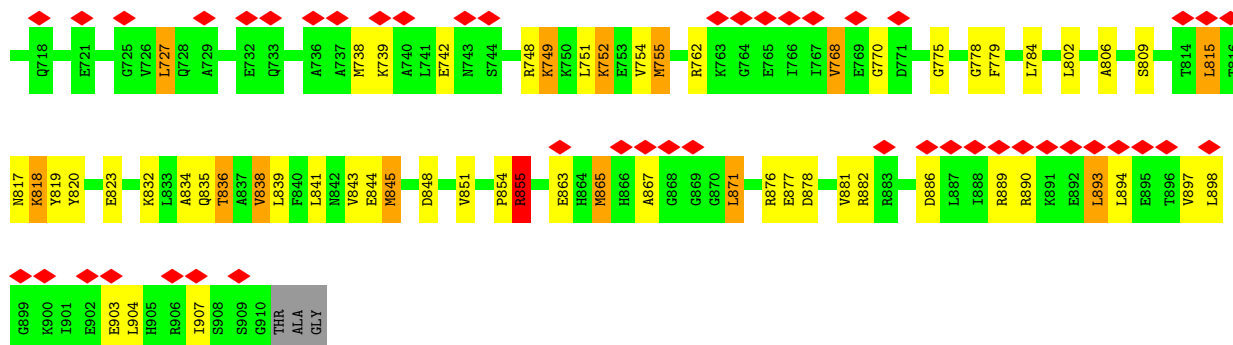
- Molecule 1: Putative mitochondrial dynamin protein



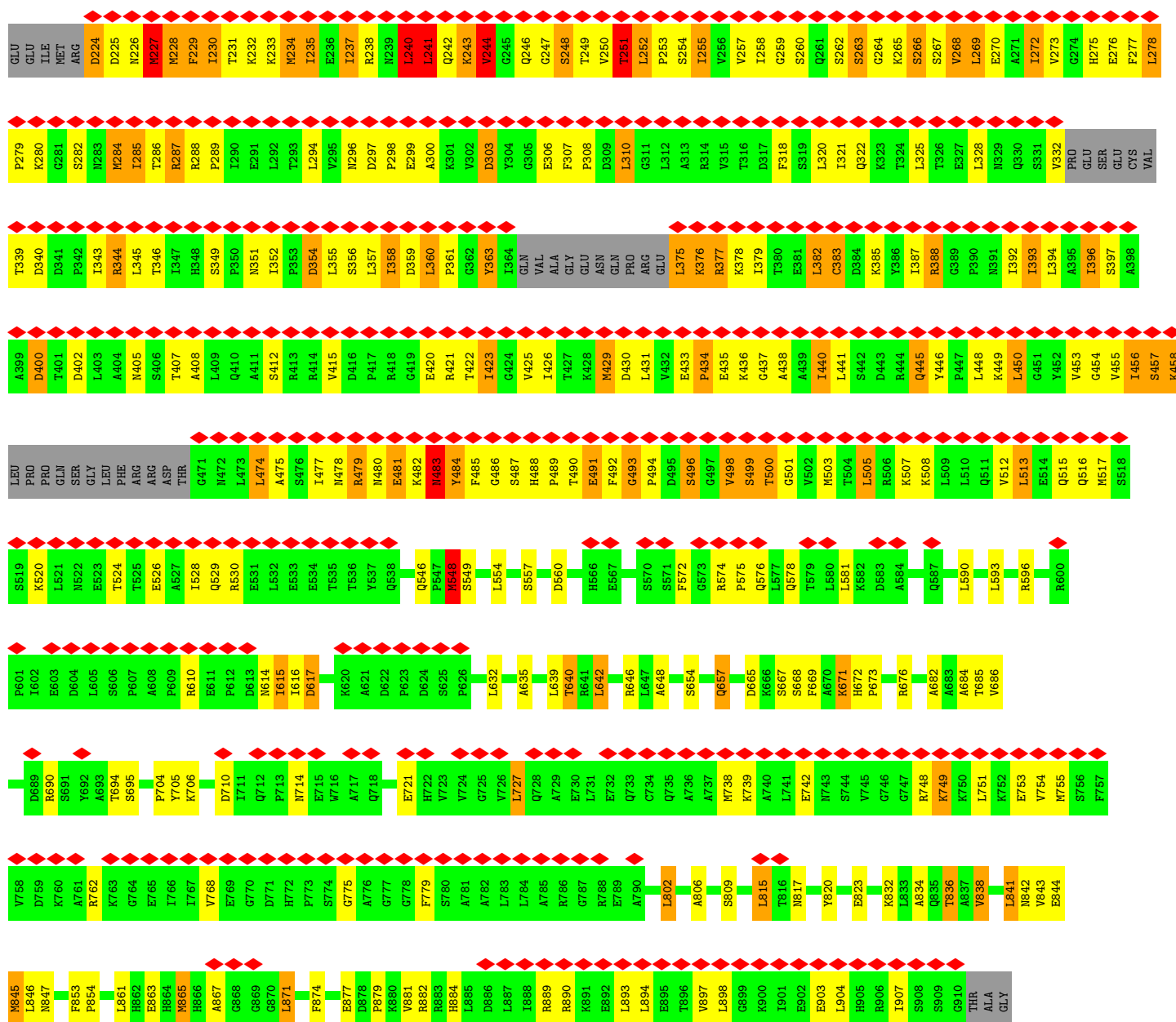
- Molecule 1: Putative mitochondrial dynamin protein



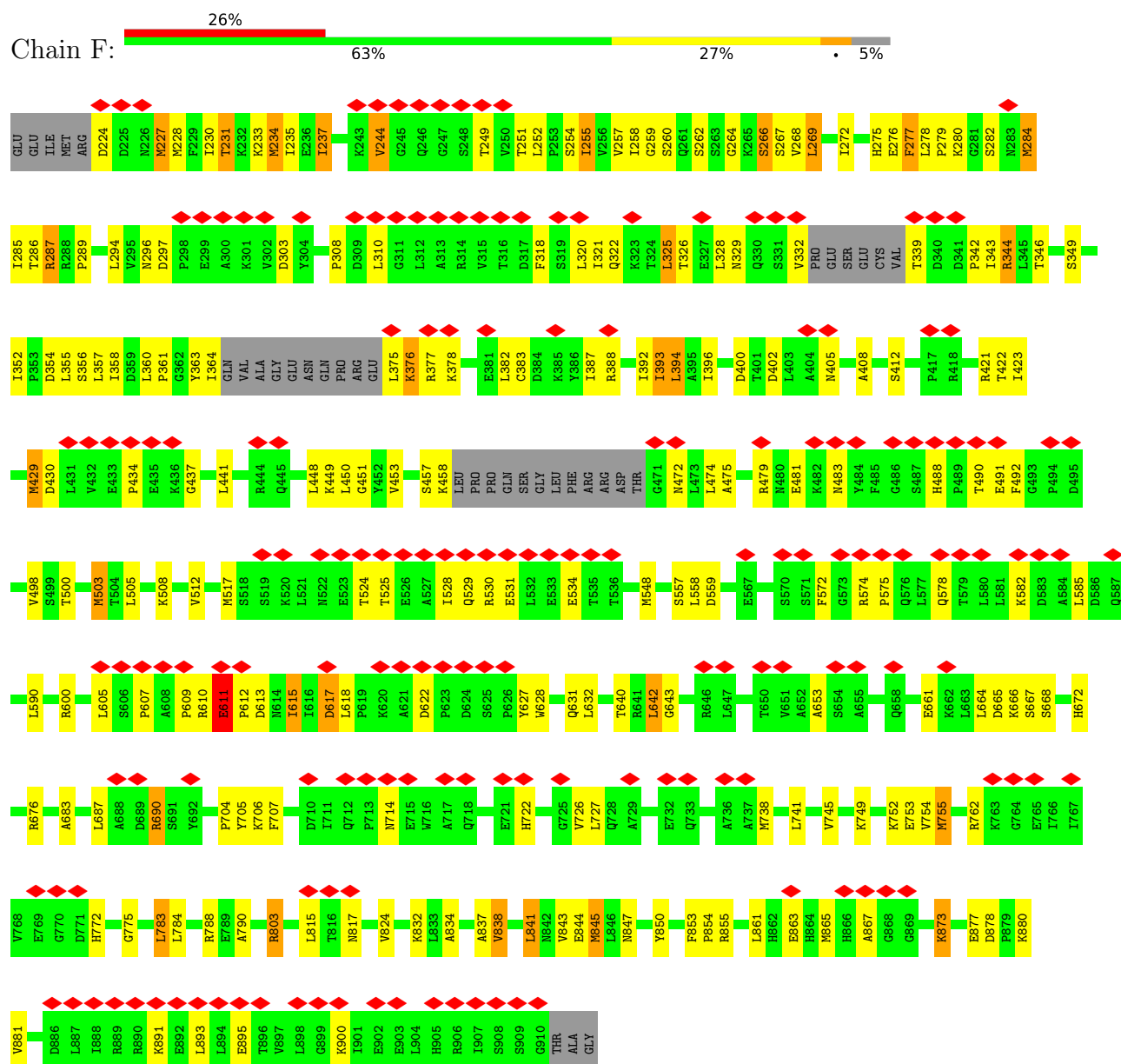




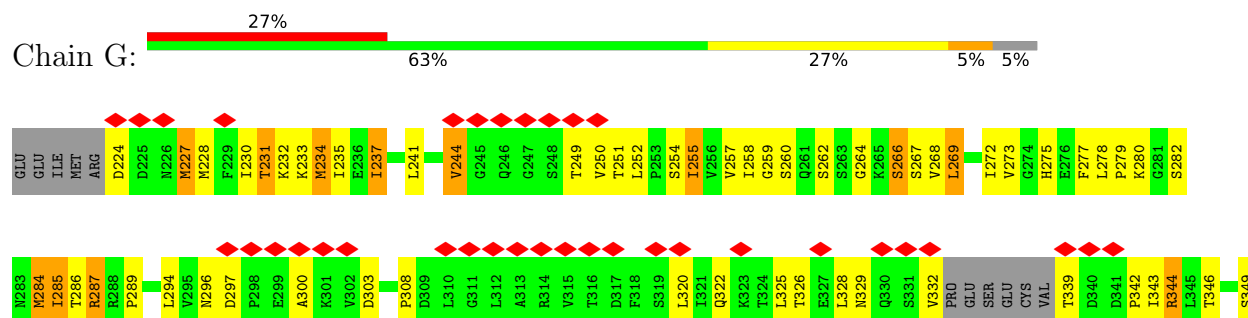
• Molecule 1: Putative mitochondrial dynamin protein

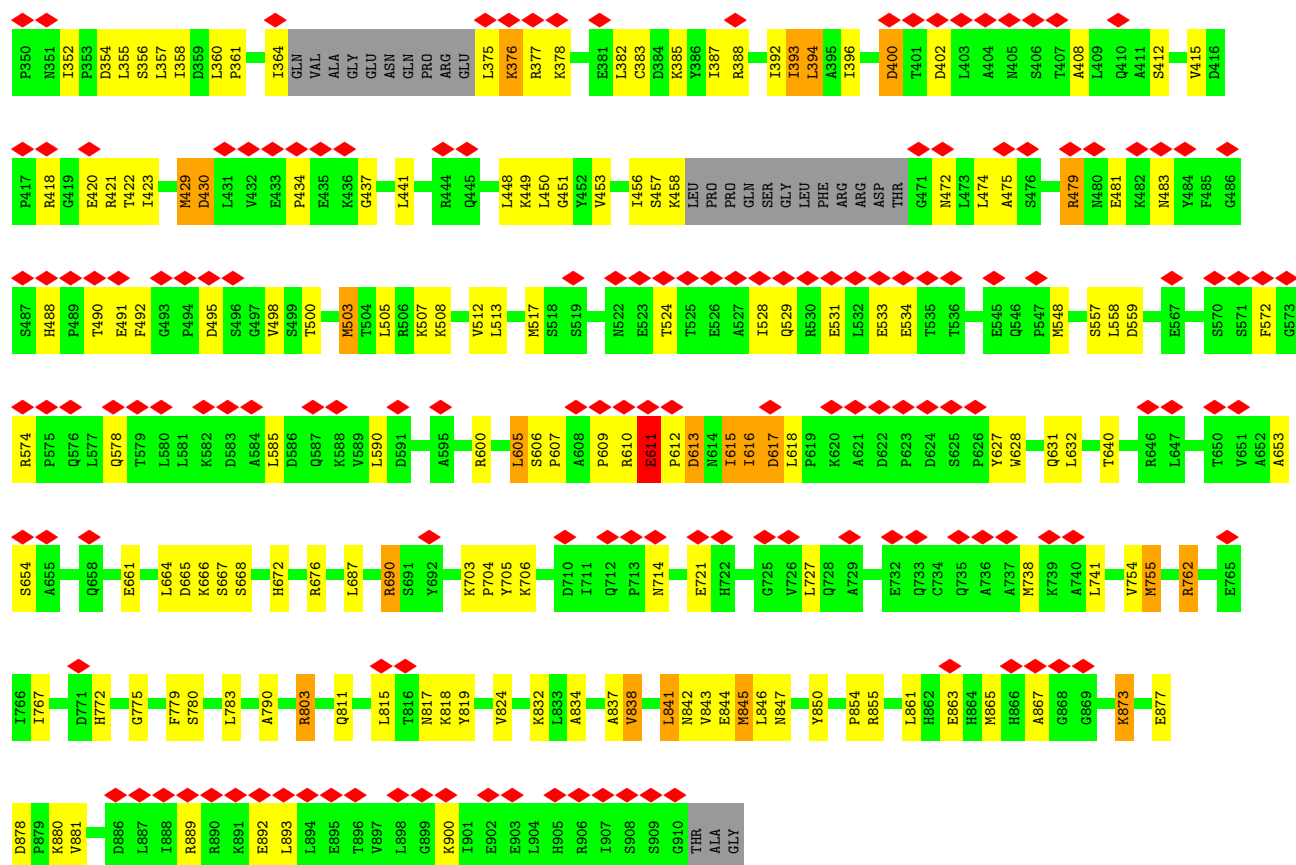


• Molecule 1: Putative mitochondrial dynamin protein

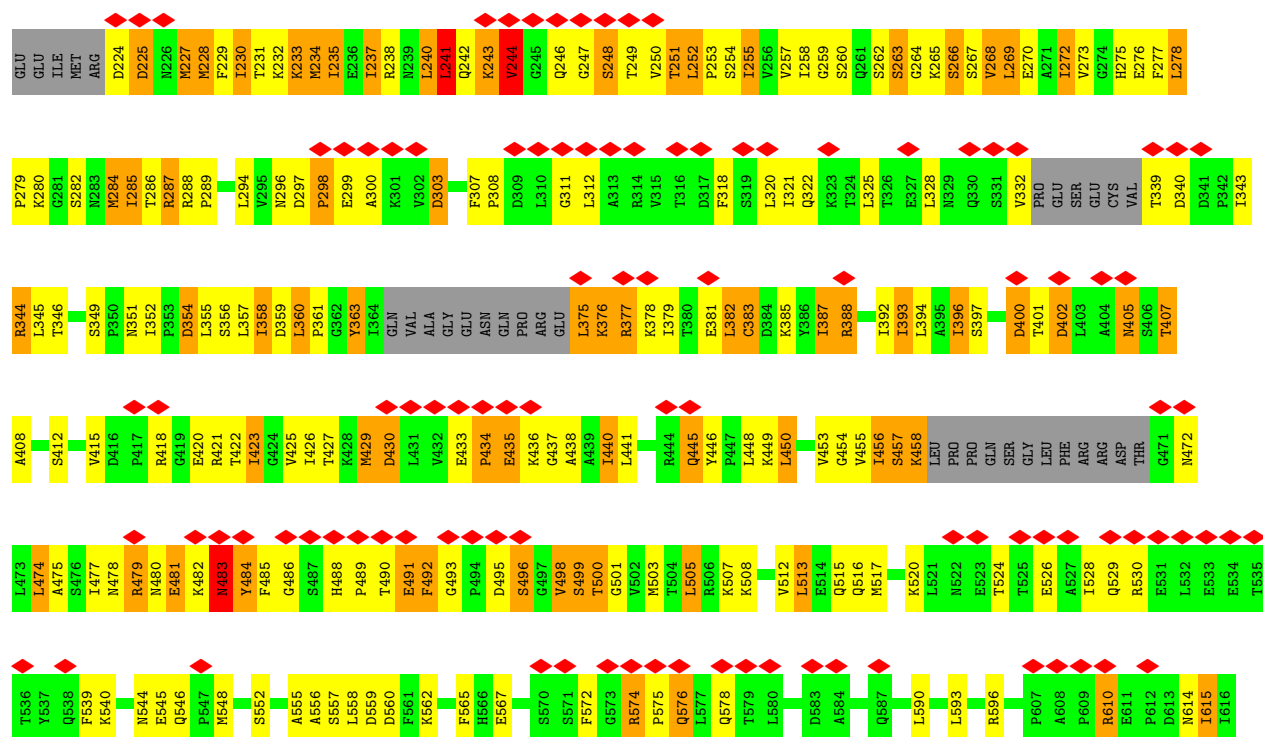


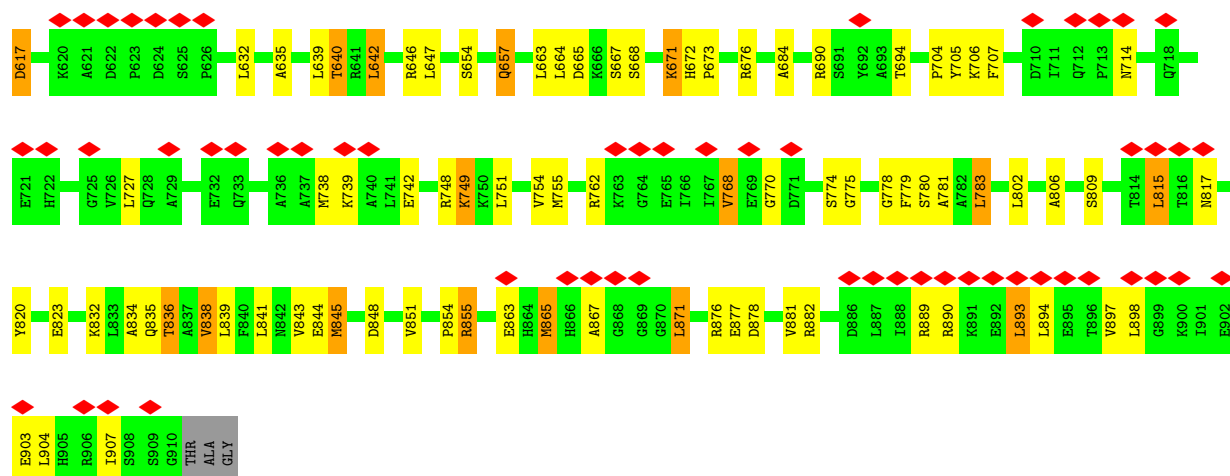
• Molecule 1: Putative mitochondrial dynamin protein



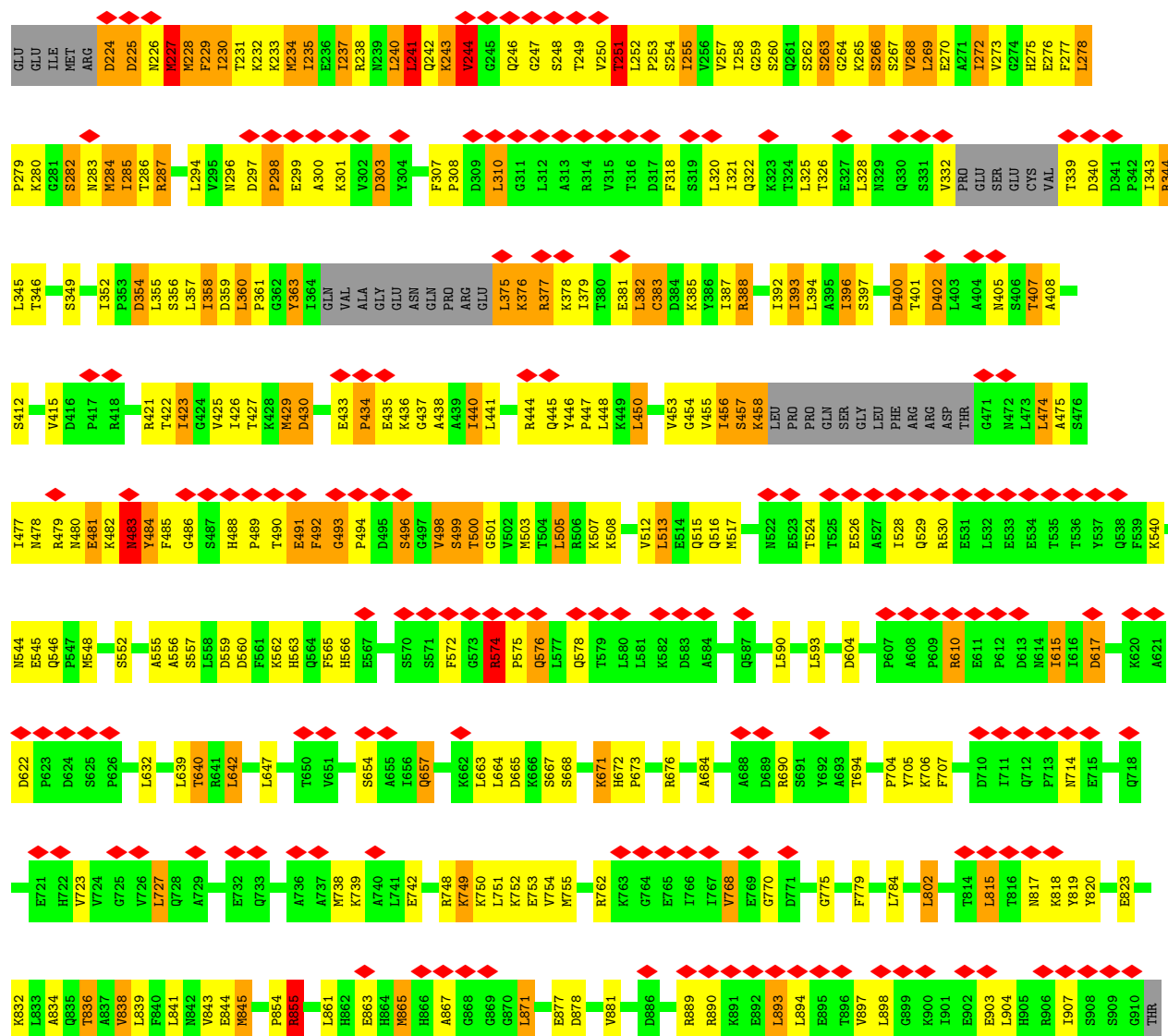


• Molecule 1: Putative mitochondrial dynamin protein



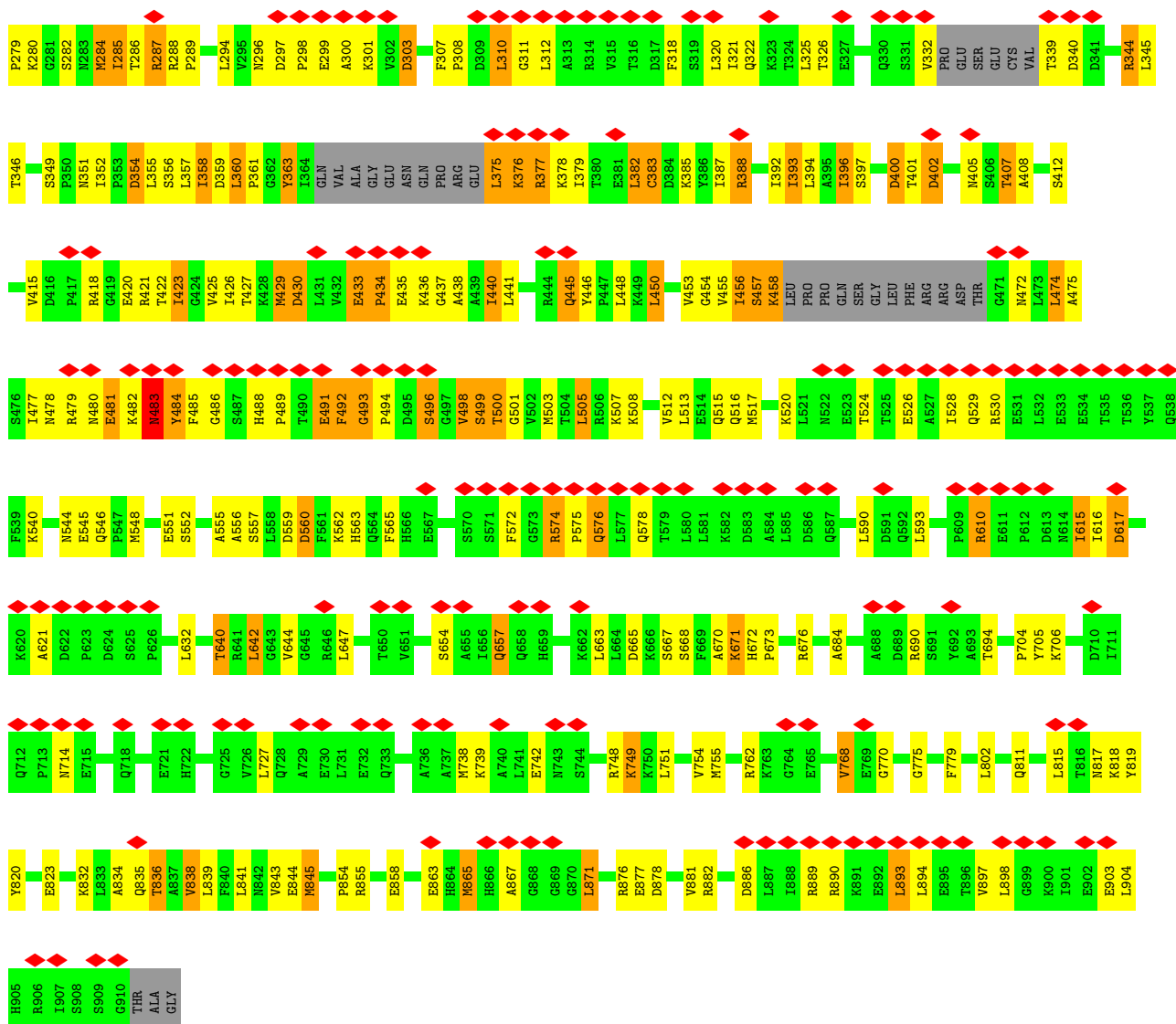


• Molecule 1: Putative mitochondrial dynamin protein

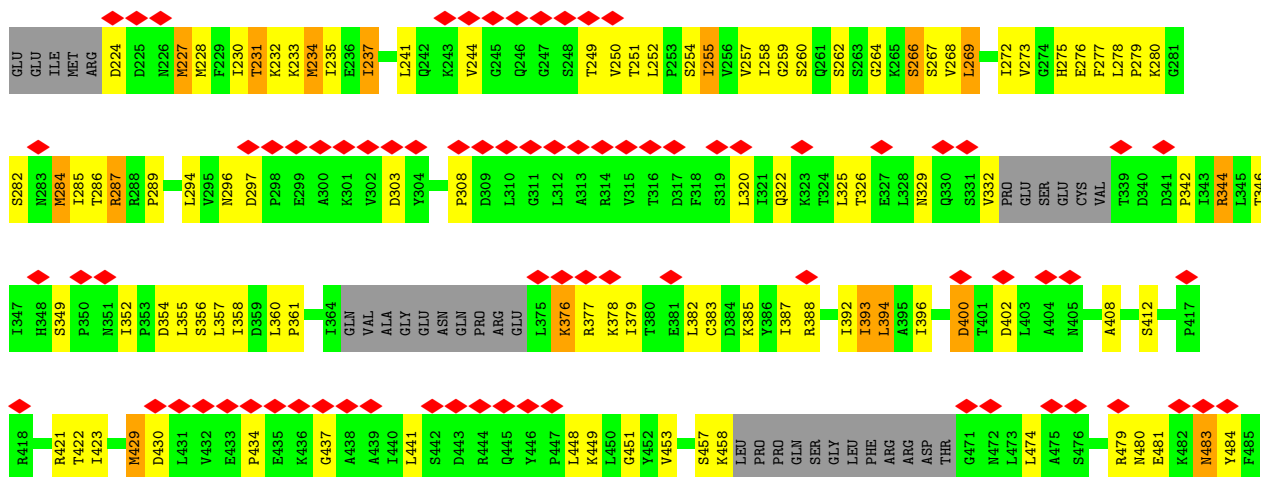


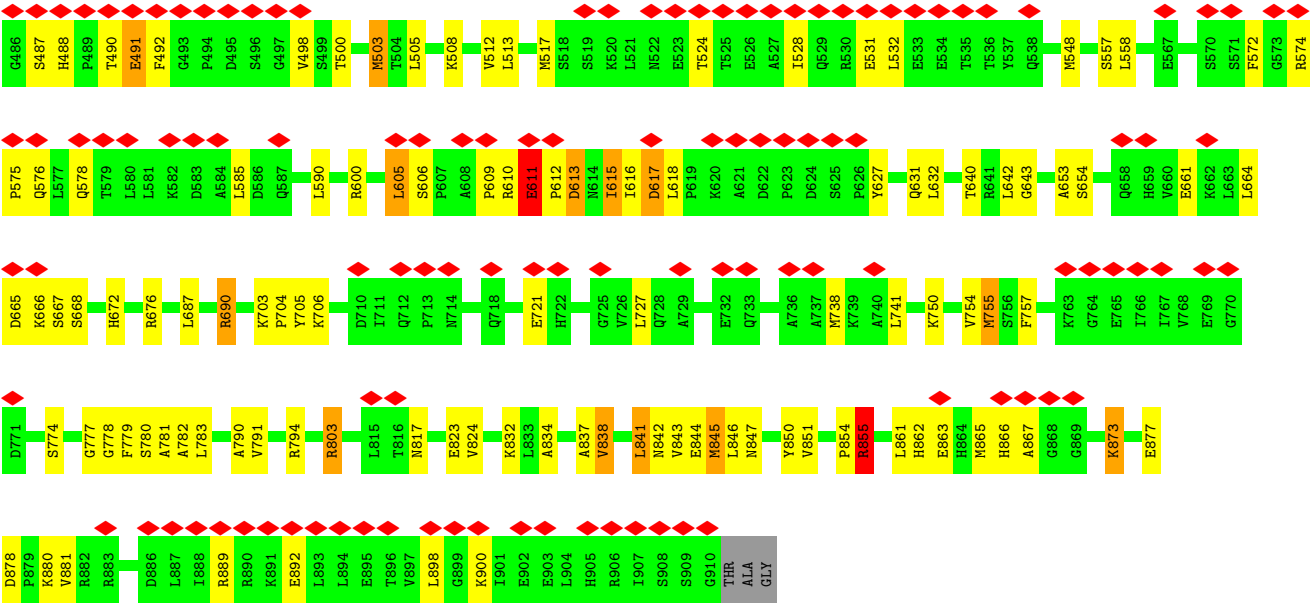
Group	Percentage
Top Group (Red)	54%
Bottom Group (Green)	65%





• 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	11474	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	8.722	Depositor
Minimum map value	-3.902	Depositor
Average map value	0.334	Depositor
Map value standard deviation	1.242	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.75	23/5238 (0.4%)	0.83	24/7075 (0.3%)
1	B	0.56	22/5238 (0.4%)	0.49	0/7075
1	C	0.55	22/5238 (0.4%)	0.48	0/7075
1	D	0.74	26/5238 (0.5%)	0.84	28/7075 (0.4%)
1	E	0.76	23/5238 (0.4%)	0.84	30/7075 (0.4%)
1	F	0.56	22/5238 (0.4%)	0.48	0/7075
1	G	0.58	22/5238 (0.4%)	0.48	0/7075
1	H	0.75	23/5238 (0.4%)	0.83	28/7075 (0.4%)
1	I	0.74	23/5238 (0.4%)	0.81	25/7075 (0.4%)
1	J	0.66	28/5238 (0.5%)	0.48	0/7075
1	K	0.75	24/5238 (0.5%)	0.83	30/7075 (0.4%)
1	L	0.56	22/5238 (0.4%)	0.48	0/7075
All	All	0.67	280/62856 (0.4%)	0.68	165/84900 (0.2%)

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	D	0	1
1	I	0	2
1	J	0	1
1	L	0	1
All	All	0	5

All (280) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	253	PRO	C-N	-16.37	1.12	1.33
1	I	253	PRO	C-N	-15.74	1.13	1.33
1	E	253	PRO	C-N	-15.50	1.14	1.33
1	H	253	PRO	C-N	-15.40	1.14	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	253	PRO	C-N	-15.32	1.14	1.33
1	D	253	PRO	C-N	-14.78	1.14	1.33
1	J	779	PHE	CG-CD2	12.02	1.64	1.38
1	J	779	PHE	CG-CD1	11.46	1.62	1.38
1	J	779	PHE	CE1-CZ	8.85	1.65	1.38
1	J	779	PHE	CD1-CE1	7.91	1.62	1.38
1	J	779	PHE	CD2-CE2	7.69	1.61	1.38
1	J	779	PHE	CE2-CZ	7.67	1.61	1.38
1	I	228	MET	SD-CE	7.34	1.98	1.79
1	K	227	MET	SD-CE	7.33	1.97	1.79
1	D	227	MET	SD-CE	7.32	1.97	1.79
1	I	227	MET	SD-CE	7.21	1.97	1.79
1	A	227	MET	SD-CE	7.13	1.97	1.79
1	A	228	MET	SD-CE	7.05	1.97	1.79
1	E	228	MET	SD-CE	7.04	1.97	1.79
1	H	227	MET	SD-CE	7.04	1.97	1.79
1	E	227	MET	SD-CE	6.99	1.97	1.79
1	H	228	MET	SD-CE	6.97	1.97	1.79
1	K	228	MET	SD-CE	6.89	1.96	1.79
1	H	548	MET	SD-CE	6.82	1.96	1.79
1	D	228	MET	SD-CE	6.82	1.96	1.79
1	H	738	MET	SD-CE	6.80	1.96	1.79
1	A	738	MET	SD-CE	6.72	1.96	1.79
1	B	429	MET	SD-CE	6.70	1.96	1.79
1	K	234	MET	SD-CE	6.67	1.96	1.79
1	G	738	MET	SD-CE	6.67	1.96	1.79
1	K	429	MET	SD-CE	6.66	1.96	1.79
1	J	429	MET	SD-CE	6.62	1.96	1.79
1	D	429	MET	SD-CE	6.61	1.96	1.79
1	I	503	MET	SD-CE	6.60	1.96	1.79
1	H	845	MET	SD-CE	6.59	1.96	1.79
1	L	503	MET	SD-CE	6.59	1.96	1.79
1	A	234	MET	SD-CE	6.59	1.96	1.79
1	I	517	MET	SD-CE	6.58	1.96	1.79
1	B	738	MET	SD-CE	6.58	1.96	1.79
1	F	738	MET	SD-CE	6.58	1.96	1.79
1	L	548	MET	SD-CE	6.57	1.96	1.79
1	B	845	MET	SD-CE	6.56	1.96	1.79
1	C	503	MET	SD-CE	6.55	1.96	1.79
1	K	227	MET	CG-SD	6.55	1.97	1.80
1	D	738	MET	SD-CE	6.55	1.96	1.79
1	J	517	MET	SD-CE	6.54	1.96	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	234	MET	SD-CE	6.54	1.96	1.79
1	A	517	MET	SD-CE	6.54	1.95	1.79
1	G	755	MET	SD-CE	6.52	1.95	1.79
1	H	227	MET	CG-SD	6.50	1.97	1.80
1	I	227	MET	CG-SD	6.50	1.97	1.80
1	E	429	MET	SD-CE	6.50	1.95	1.79
1	G	845	MET	SD-CE	6.50	1.95	1.79
1	E	234	MET	SD-CE	6.48	1.95	1.79
1	G	865	MET	SD-CE	6.48	1.95	1.79
1	I	429	MET	SD-CE	6.47	1.95	1.79
1	A	548	MET	SD-CE	6.46	1.95	1.79
1	E	548	MET	SD-CE	6.46	1.95	1.79
1	E	503	MET	SD-CE	6.45	1.95	1.79
1	H	234	MET	SD-CE	6.44	1.95	1.79
1	I	845	MET	CG-SD	6.43	1.96	1.80
1	A	227	MET	CG-SD	6.43	1.96	1.80
1	J	738	MET	SD-CE	6.42	1.95	1.79
1	K	548	MET	SD-CE	6.42	1.95	1.79
1	D	503	MET	SD-CE	6.42	1.95	1.79
1	A	429	MET	SD-CE	6.42	1.95	1.79
1	E	227	MET	CG-SD	6.41	1.96	1.80
1	F	503	MET	SD-CE	6.41	1.95	1.79
1	E	738	MET	SD-CE	6.40	1.95	1.79
1	K	755	MET	SD-CE	6.39	1.95	1.79
1	E	517	MET	SD-CE	6.39	1.95	1.79
1	K	503	MET	SD-CE	6.39	1.95	1.79
1	D	845	MET	CG-SD	6.38	1.96	1.80
1	I	548	MET	SD-CE	6.38	1.95	1.79
1	K	517	MET	SD-CE	6.38	1.95	1.79
1	D	517	MET	SD-CE	6.37	1.95	1.79
1	D	845	MET	SD-CE	6.37	1.95	1.79
1	K	845	MET	SD-CE	6.37	1.95	1.79
1	C	228	MET	SD-CE	6.37	1.95	1.79
1	J	503	MET	SD-CE	6.36	1.95	1.79
1	L	738	MET	SD-CE	6.36	1.95	1.79
1	D	755	MET	SD-CE	6.35	1.95	1.79
1	H	755	MET	SD-CE	6.35	1.95	1.79
1	A	845	MET	SD-CE	6.34	1.95	1.79
1	G	548	MET	SD-CE	6.34	1.95	1.79
1	J	234	MET	SD-CE	6.34	1.95	1.79
1	C	548	MET	SD-CE	6.34	1.95	1.79
1	E	252	LEU	C-N	6.34	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	503	MET	SD-CE	6.33	1.95	1.79
1	C	429	MET	SD-CE	6.33	1.95	1.79
1	F	429	MET	SD-CE	6.33	1.95	1.79
1	I	755	MET	SD-CE	6.32	1.95	1.79
1	G	429	MET	SD-CE	6.32	1.95	1.79
1	H	503	MET	SD-CE	6.32	1.95	1.79
1	K	738	MET	SD-CE	6.32	1.95	1.79
1	A	755	MET	SD-CE	6.31	1.95	1.79
1	C	738	MET	SD-CE	6.30	1.95	1.79
1	L	228	MET	SD-CE	6.30	1.95	1.79
1	F	517	MET	SD-CE	6.29	1.95	1.79
1	G	503	MET	SD-CE	6.29	1.95	1.79
1	D	865	MET	SD-CE	6.28	1.95	1.79
1	J	845	MET	SD-CE	6.28	1.95	1.79
1	D	227	MET	CG-SD	6.28	1.96	1.80
1	L	845	MET	SD-CE	6.27	1.95	1.79
1	G	738	MET	CG-SD	6.27	1.96	1.80
1	D	548	MET	SD-CE	6.26	1.95	1.79
1	A	865	MET	SD-CE	6.26	1.95	1.79
1	K	738	MET	CG-SD	6.26	1.96	1.80
1	B	234	MET	SD-CE	6.25	1.95	1.79
1	F	234	MET	SD-CE	6.25	1.95	1.79
1	C	517	MET	SD-CE	6.25	1.95	1.79
1	I	845	MET	SD-CE	6.25	1.95	1.79
1	B	865	MET	SD-CE	6.25	1.95	1.79
1	G	228	MET	SD-CE	6.24	1.95	1.79
1	H	517	MET	SD-CE	6.24	1.95	1.79
1	I	738	MET	SD-CE	6.24	1.95	1.79
1	D	234	MET	SD-CE	6.23	1.95	1.79
1	I	865	MET	SD-CE	6.23	1.95	1.79
1	H	738	MET	CG-SD	6.23	1.96	1.80
1	J	228	MET	SD-CE	6.23	1.95	1.79
1	J	548	MET	SD-CE	6.23	1.95	1.79
1	H	429	MET	CG-SD	6.22	1.96	1.80
1	J	429	MET	CG-SD	6.22	1.96	1.80
1	A	503	MET	SD-CE	6.22	1.95	1.79
1	F	548	MET	SD-CE	6.22	1.95	1.79
1	G	234	MET	SD-CE	6.22	1.95	1.79
1	J	865	MET	SD-CE	6.22	1.95	1.79
1	B	228	MET	CG-SD	6.21	1.96	1.80
1	I	738	MET	CG-SD	6.21	1.96	1.80
1	I	429	MET	CG-SD	6.19	1.96	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	738	MET	CG-SD	6.19	1.96	1.80
1	L	755	MET	SD-CE	6.19	1.95	1.79
1	E	845	MET	SD-CE	6.19	1.95	1.79
1	C	755	MET	SD-CE	6.18	1.95	1.79
1	J	548	MET	CG-SD	6.18	1.96	1.80
1	G	227	MET	SD-CE	6.18	1.95	1.79
1	L	227	MET	SD-CE	6.18	1.95	1.79
1	B	548	MET	SD-CE	6.17	1.95	1.79
1	B	755	MET	CG-SD	6.17	1.96	1.80
1	H	845	MET	CG-SD	6.17	1.96	1.80
1	F	755	MET	SD-CE	6.17	1.95	1.79
1	B	503	MET	CG-SD	6.17	1.96	1.80
1	C	845	MET	SD-CE	6.17	1.95	1.79
1	C	865	MET	SD-CE	6.17	1.95	1.79
1	F	227	MET	SD-CE	6.17	1.95	1.79
1	L	517	MET	SD-CE	6.17	1.95	1.79
1	D	517	MET	CG-SD	6.16	1.96	1.80
1	A	738	MET	CG-SD	6.15	1.96	1.80
1	E	755	MET	SD-CE	6.14	1.94	1.79
1	F	429	MET	CG-SD	6.13	1.96	1.80
1	F	865	MET	SD-CE	6.13	1.94	1.79
1	L	865	MET	SD-CE	6.13	1.94	1.79
1	E	845	MET	CG-SD	6.13	1.96	1.80
1	G	517	MET	SD-CE	6.12	1.94	1.79
1	C	227	MET	SD-CE	6.12	1.94	1.79
1	L	429	MET	SD-CE	6.12	1.94	1.79
1	B	517	MET	SD-CE	6.11	1.94	1.79
1	H	429	MET	SD-CE	6.11	1.94	1.79
1	I	548	MET	CG-SD	6.09	1.96	1.80
1	J	755	MET	SD-CE	6.09	1.94	1.79
1	B	228	MET	SD-CE	6.09	1.94	1.79
1	C	234	MET	SD-CE	6.08	1.94	1.79
1	K	252	LEU	C-N	6.08	1.41	1.33
1	A	517	MET	CG-SD	6.08	1.96	1.80
1	B	227	MET	SD-CE	6.07	1.94	1.79
1	H	548	MET	CG-SD	6.07	1.96	1.80
1	E	738	MET	CG-SD	6.07	1.96	1.80
1	F	738	MET	CG-SD	6.06	1.96	1.80
1	J	227	MET	SD-CE	6.06	1.94	1.79
1	K	845	MET	CG-SD	6.05	1.95	1.80
1	E	755	MET	CG-SD	6.04	1.95	1.80
1	G	865	MET	CG-SD	6.04	1.95	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	755	MET	CG-SD	6.03	1.95	1.80
1	F	845	MET	SD-CE	6.03	1.94	1.79
1	K	865	MET	SD-CE	6.03	1.94	1.79
1	E	429	MET	CG-SD	6.03	1.95	1.80
1	I	517	MET	CG-SD	6.03	1.95	1.80
1	H	865	MET	SD-CE	6.03	1.94	1.79
1	B	738	MET	CG-SD	6.02	1.95	1.80
1	L	503	MET	CG-SD	6.02	1.95	1.80
1	G	429	MET	CG-SD	6.01	1.95	1.80
1	K	429	MET	CG-SD	6.01	1.95	1.80
1	A	429	MET	CG-SD	6.00	1.95	1.80
1	D	429	MET	CG-SD	6.00	1.95	1.80
1	L	228	MET	CG-SD	6.00	1.95	1.80
1	H	517	MET	CG-SD	6.00	1.95	1.80
1	J	234	MET	CG-SD	5.99	1.95	1.80
1	K	548	MET	CG-SD	5.96	1.95	1.80
1	K	228	MET	CG-SD	5.96	1.95	1.80
1	E	517	MET	CG-SD	5.95	1.95	1.80
1	L	234	MET	SD-CE	5.95	1.94	1.79
1	D	228	MET	CG-SD	5.94	1.95	1.80
1	F	228	MET	SD-CE	5.94	1.94	1.79
1	C	503	MET	CG-SD	5.94	1.95	1.80
1	G	755	MET	CG-SD	5.93	1.95	1.80
1	L	429	MET	CG-SD	5.92	1.95	1.80
1	L	548	MET	CG-SD	5.92	1.95	1.80
1	A	228	MET	CG-SD	5.92	1.95	1.80
1	G	548	MET	CG-SD	5.92	1.95	1.80
1	E	548	MET	CG-SD	5.91	1.95	1.80
1	I	865	MET	CG-SD	5.91	1.95	1.80
1	L	738	MET	CG-SD	5.90	1.95	1.80
1	J	228	MET	CG-SD	5.88	1.95	1.80
1	F	503	MET	CG-SD	5.88	1.95	1.80
1	L	865	MET	CG-SD	5.87	1.95	1.80
1	B	755	MET	SD-CE	5.86	1.94	1.79
1	D	252	LEU	C-N	5.86	1.40	1.33
1	A	865	MET	CG-SD	5.86	1.95	1.80
1	B	227	MET	CG-SD	5.85	1.95	1.80
1	J	503	MET	CG-SD	5.85	1.95	1.80
1	D	503	MET	CG-SD	5.85	1.95	1.80
1	G	234	MET	CG-SD	5.85	1.95	1.80
1	A	845	MET	CG-SD	5.84	1.95	1.80
1	C	548	MET	CG-SD	5.84	1.95	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	228	MET	CG-SD	5.83	1.95	1.80
1	J	738	MET	CG-SD	5.83	1.95	1.80
1	C	228	MET	CG-SD	5.83	1.95	1.80
1	J	755	MET	CG-SD	5.81	1.95	1.80
1	K	755	MET	CG-SD	5.81	1.95	1.80
1	C	738	MET	CG-SD	5.80	1.95	1.80
1	G	517	MET	CG-SD	5.80	1.95	1.80
1	E	865	MET	SD-CE	5.80	1.94	1.79
1	H	865	MET	CG-SD	5.80	1.95	1.80
1	I	755	MET	CG-SD	5.80	1.95	1.80
1	D	755	MET	CG-SD	5.79	1.95	1.80
1	F	228	MET	CG-SD	5.79	1.95	1.80
1	F	865	MET	CG-SD	5.78	1.95	1.80
1	A	548	MET	CG-SD	5.78	1.95	1.80
1	B	429	MET	CG-SD	5.78	1.95	1.80
1	L	755	MET	CG-SD	5.78	1.95	1.80
1	G	503	MET	CG-SD	5.78	1.95	1.80
1	B	517	MET	CG-SD	5.75	1.95	1.80
1	K	503	MET	CG-SD	5.75	1.95	1.80
1	L	227	MET	CG-SD	5.75	1.95	1.80
1	E	228	MET	CG-SD	5.73	1.95	1.80
1	K	865	MET	CG-SD	5.73	1.95	1.80
1	E	503	MET	CG-SD	5.72	1.95	1.80
1	D	548	MET	CG-SD	5.72	1.95	1.80
1	J	517	MET	CG-SD	5.72	1.95	1.80
1	F	517	MET	CG-SD	5.71	1.95	1.80
1	F	234	MET	CG-SD	5.71	1.95	1.80
1	K	517	MET	CG-SD	5.71	1.95	1.80
1	I	228	MET	CG-SD	5.70	1.95	1.80
1	I	503	MET	CG-SD	5.69	1.95	1.80
1	J	227	MET	CG-SD	5.69	1.95	1.80
1	B	234	MET	CG-SD	5.68	1.95	1.80
1	G	228	MET	CG-SD	5.67	1.95	1.80
1	H	503	MET	CG-SD	5.66	1.95	1.80
1	C	755	MET	CG-SD	5.65	1.94	1.80
1	B	548	MET	CG-SD	5.65	1.94	1.80
1	A	503	MET	CG-SD	5.64	1.94	1.80
1	A	755	MET	CG-SD	5.63	1.94	1.80
1	D	865	MET	CG-SD	5.59	1.94	1.80
1	C	429	MET	CG-SD	5.59	1.94	1.80
1	F	548	MET	CG-SD	5.58	1.94	1.80
1	H	755	MET	CG-SD	5.58	1.94	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	865	MET	CG-SD	5.57	1.94	1.80
1	C	517	MET	CG-SD	5.52	1.94	1.80
1	C	227	MET	CG-SD	5.52	1.94	1.80
1	E	865	MET	CG-SD	5.51	1.94	1.80
1	B	865	MET	CG-SD	5.50	1.94	1.80
1	C	234	MET	CG-SD	5.49	1.94	1.80
1	G	227	MET	CG-SD	5.47	1.94	1.80
1	L	234	MET	CG-SD	5.47	1.94	1.80
1	F	227	MET	CG-SD	5.46	1.94	1.80
1	L	517	MET	CG-SD	5.38	1.94	1.80
1	F	845	MET	CG-SD	5.35	1.94	1.80
1	C	865	MET	CG-SD	5.34	1.94	1.80
1	K	234	MET	CG-SD	5.31	1.94	1.80
1	J	845	MET	CG-SD	5.29	1.94	1.80
1	A	307	PHE	C-N	5.26	1.40	1.34
1	B	845	MET	CG-SD	5.22	1.93	1.80
1	H	252	LEU	C-N	5.17	1.40	1.33
1	C	845	MET	CG-SD	5.14	1.93	1.80
1	L	845	MET	CG-SD	5.13	1.93	1.80
1	G	845	MET	CG-SD	5.12	1.93	1.80
1	D	493	GLY	C-N	5.12	1.39	1.33
1	D	488	HIS	C-N	5.03	1.40	1.34
1	D	234	MET	CG-SD	5.03	1.93	1.80
1	I	234	MET	CG-SD	5.02	1.93	1.80

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	445	GLN	CA-C-N	-10.72	112.40	122.37
1	K	445	GLN	C-N-CA	-10.72	112.40	122.37
1	E	445	GLN	CA-C-N	-10.65	112.47	122.37
1	E	445	GLN	C-N-CA	-10.65	112.47	122.37
1	D	445	GLN	CA-C-N	-10.38	112.72	122.37
1	D	445	GLN	C-N-CA	-10.38	112.72	122.37
1	A	445	GLN	CA-C-N	-10.35	112.75	122.37
1	A	445	GLN	C-N-CA	-10.35	112.75	122.37
1	H	445	GLN	CA-C-N	-10.27	112.82	122.37
1	H	445	GLN	C-N-CA	-10.27	112.82	122.37
1	E	440	ILE	N-CA-C	10.11	120.03	110.53
1	I	500	THR	N-CA-C	10.00	124.09	108.79
1	A	500	THR	N-CA-C	9.99	124.08	108.79
1	A	440	ILE	N-CA-C	9.92	119.86	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	500	THR	N-CA-C	9.92	123.97	108.79
1	D	440	ILE	N-CA-C	9.74	119.69	110.53
1	K	500	THR	N-CA-C	9.71	123.64	108.79
1	H	440	ILE	N-CA-C	9.66	119.61	110.53
1	K	440	ILE	N-CA-C	9.51	119.47	110.53
1	E	500	THR	N-CA-C	9.42	123.39	109.07
1	H	483	ASN	N-CA-C	9.38	121.58	111.36
1	D	500	THR	N-CA-C	9.38	123.13	108.79
1	E	483	ASN	N-CA-C	9.35	121.55	111.36
1	A	244	VAL	CB-CA-C	-9.22	99.69	112.14
1	A	483	ASN	N-CA-C	9.22	121.42	111.36
1	H	227	MET	N-CA-C	9.17	121.04	111.14
1	I	483	ASN	N-CA-C	9.16	121.35	111.36
1	I	244	VAL	CB-CA-C	-9.14	99.80	112.14
1	D	483	ASN	N-CA-C	8.97	121.14	111.36
1	K	483	ASN	N-CA-C	8.97	121.14	111.36
1	H	244	VAL	CB-CA-C	-8.97	100.04	112.14
1	D	227	MET	N-CA-C	8.95	121.11	111.36
1	D	244	VAL	CB-CA-C	-8.89	100.14	112.14
1	D	496	SER	N-CA-C	-8.76	98.14	110.50
1	E	244	VAL	CB-CA-C	-8.68	100.42	112.14
1	K	244	VAL	CB-CA-C	-8.62	100.50	112.14
1	I	440	ILE	N-CA-C	8.60	119.40	110.72
1	A	244	VAL	N-CA-C	8.57	119.36	110.62
1	D	244	VAL	N-CA-C	8.54	119.33	110.62
1	I	244	VAL	N-CA-C	8.54	119.33	110.62
1	E	227	MET	N-CA-C	8.53	120.66	111.36
1	H	496	SER	N-CA-C	-8.47	98.56	110.50
1	H	244	VAL	N-CA-C	8.35	119.14	110.62
1	A	227	MET	N-CA-C	8.28	120.39	111.36
1	K	227	MET	N-CA-C	8.28	120.38	111.36
1	K	244	VAL	N-CA-C	8.26	119.05	110.62
1	I	227	MET	N-CA-C	8.03	119.82	111.14
1	E	244	VAL	N-CA-C	7.85	118.63	110.62
1	I	496	SER	N-CA-C	-7.79	99.52	110.50
1	E	262	SER	N-CA-C	-7.75	102.77	111.14
1	A	496	SER	N-CA-C	-7.63	99.18	110.48
1	A	262	SER	N-CA-C	-7.60	103.08	111.36
1	D	262	SER	N-CA-C	-7.59	102.94	111.14
1	K	262	SER	N-CA-C	-7.57	102.97	111.14
1	K	496	SER	N-CA-C	-7.53	99.33	110.48
1	I	262	SER	N-CA-C	-7.53	103.16	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	262	SER	N-CA-C	-7.52	103.02	111.14
1	E	496	SER	N-CA-C	-7.34	99.61	110.48
1	K	224	ASP	CA-C-N	7.16	129.87	120.28
1	K	224	ASP	C-N-CA	7.16	129.87	120.28
1	E	435	GLU	N-CA-C	-7.13	103.51	111.28
1	E	250	VAL	N-CA-C	7.10	119.86	109.63
1	K	250	VAL	N-CA-C	7.10	119.85	109.63
1	I	251	THR	N-CA-C	7.09	118.95	108.60
1	A	251	THR	N-CA-C	7.08	118.94	108.60
1	H	224	ASP	CA-C-N	7.07	130.33	120.29
1	H	224	ASP	C-N-CA	7.07	130.33	120.29
1	D	224	ASP	CA-C-N	7.06	130.04	120.44
1	D	224	ASP	C-N-CA	7.06	130.04	120.44
1	I	435	GLU	N-CA-C	-7.05	103.68	111.36
1	H	250	VAL	N-CA-C	7.01	119.72	109.63
1	E	251	THR	N-CA-C	7.00	118.82	108.60
1	D	251	THR	N-CA-C	6.98	118.79	108.60
1	A	250	VAL	N-CA-C	6.94	119.62	109.63
1	K	251	THR	N-CA-C	6.88	118.64	108.60
1	H	251	THR	N-CA-C	6.79	118.52	108.60
1	I	250	VAL	N-CA-C	6.79	119.41	109.63
1	D	250	VAL	N-CA-C	6.76	119.37	109.63
1	A	224	ASP	CA-C-N	6.73	129.85	120.29
1	A	224	ASP	C-N-CA	6.73	129.85	120.29
1	A	435	GLU	N-CA-C	-6.68	104.08	111.36
1	D	435	GLU	N-CA-C	-6.67	104.00	111.28
1	H	435	GLU	N-CA-C	-6.60	104.16	111.36
1	K	435	GLU	N-CA-C	-6.58	104.19	111.36
1	K	234	MET	CB-CG-SD	-6.31	93.78	112.70
1	I	224	ASP	CA-C-N	6.30	129.01	120.44
1	I	224	ASP	C-N-CA	6.30	129.01	120.44
1	D	484	TYR	N-CA-C	6.27	118.11	111.28
1	A	234	MET	CB-CG-SD	-6.23	94.00	112.70
1	D	234	MET	CB-CG-SD	-6.21	94.06	112.70
1	I	234	MET	CB-CG-SD	-6.20	94.11	112.70
1	A	228	MET	N-CA-C	-6.18	104.62	111.36
1	I	438	ALA	CA-C-N	-6.17	112.05	120.44
1	I	438	ALA	C-N-CA	-6.17	112.05	120.44
1	E	234	MET	CB-CG-SD	-6.10	94.40	112.70
1	E	224	ASP	CA-C-N	6.05	128.88	120.29
1	E	224	ASP	C-N-CA	6.05	128.88	120.29
1	H	234	MET	CB-CG-SD	-6.00	94.69	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	438	ALA	CA-C-N	-5.99	112.30	120.44
1	E	438	ALA	C-N-CA	-5.99	112.30	120.44
1	K	228	MET	N-CA-C	-5.99	104.67	111.07
1	K	484	TYR	N-CA-C	5.97	117.87	111.36
1	H	484	TYR	N-CA-C	5.93	117.74	111.28
1	E	249	THR	N-CA-C	-5.91	104.84	111.28
1	A	484	TYR	N-CA-C	5.86	117.67	111.28
1	E	405	ASN	N-CA-C	5.79	117.68	111.36
1	A	438	ALA	CA-C-N	-5.79	112.56	120.44
1	A	438	ALA	C-N-CA	-5.79	112.56	120.44
1	H	438	ALA	CA-C-N	-5.67	112.73	120.44
1	H	438	ALA	C-N-CA	-5.67	112.73	120.44
1	E	484	TYR	N-CA-C	5.66	117.45	111.28
1	D	405	ASN	N-CA-C	5.62	117.41	111.28
1	D	494	PRO	N-CA-C	5.62	119.69	111.03
1	D	438	ALA	CA-C-N	-5.61	112.81	120.44
1	D	438	ALA	C-N-CA	-5.61	112.81	120.44
1	H	405	ASN	N-CA-C	5.61	117.39	111.28
1	A	405	ASN	N-CA-C	5.58	117.37	111.28
1	H	249	THR	N-CA-C	-5.58	105.28	111.36
1	K	252	LEU	CA-C-N	-5.47	114.96	120.21
1	K	252	LEU	C-N-CA	-5.47	114.96	120.21
1	I	405	ASN	N-CA-C	5.45	117.22	111.28
1	K	249	THR	N-CA-C	-5.40	105.48	111.36
1	I	298	PRO	N-CA-C	-5.40	102.72	111.19
1	I	484	TYR	N-CA-C	5.37	117.13	111.28
1	K	438	ALA	CA-C-N	-5.32	113.21	120.44
1	K	438	ALA	C-N-CA	-5.32	113.21	120.44
1	E	248	SER	N-CA-C	-5.29	101.69	109.62
1	I	241	LEU	N-CA-C	-5.29	105.59	111.36
1	D	248	SER	N-CA-C	-5.28	101.70	109.62
1	K	405	ASN	N-CA-C	5.28	117.03	111.28
1	D	252	LEU	CA-C-N	-5.25	115.32	120.52
1	D	252	LEU	C-N-CA	-5.25	115.32	120.52
1	D	493	GLY	CA-C-N	-5.25	114.17	119.83
1	D	493	GLY	C-N-CA	-5.25	114.17	119.83
1	E	253	PRO	N-CA-C	5.24	118.56	111.22
1	A	298	PRO	N-CA-C	-5.23	102.98	111.19
1	I	494	PRO	N-CA-C	5.22	119.07	111.03
1	K	493	GLY	CA-C-N	-5.22	114.19	119.83
1	K	493	GLY	C-N-CA	-5.22	114.19	119.83
1	K	253	PRO	N-CA-C	5.21	118.51	111.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	494	PRO	N-CA-C	5.20	119.04	111.03
1	D	433	GLU	CA-C-N	5.19	124.99	119.28
1	D	433	GLU	C-N-CA	5.19	124.99	119.28
1	H	253	PRO	N-CA-C	5.19	118.49	111.22
1	I	249	THR	N-CA-C	-5.19	105.70	111.36
1	K	241	LEU	N-CA-C	-5.13	105.77	111.36
1	K	248	SER	N-CA-C	-5.12	101.94	109.62
1	E	252	LEU	CA-C-N	-5.12	115.30	120.21
1	E	252	LEU	C-N-CA	-5.12	115.30	120.21
1	E	493	GLY	CA-C-N	-5.09	114.34	119.83
1	E	493	GLY	C-N-CA	-5.09	114.34	119.83
1	E	240	LEU	N-CA-C	5.08	116.82	111.28
1	E	494	PRO	N-CA-C	5.08	118.85	111.03
1	I	228	MET	N-CA-C	-5.08	105.65	111.14
1	A	433	GLU	CA-C-N	5.08	124.86	119.28
1	A	433	GLU	C-N-CA	5.08	124.86	119.28
1	E	241	LEU	N-CA-C	-5.08	105.75	111.28
1	H	248	SER	N-CA-C	-5.07	102.01	109.62
1	H	241	LEU	N-CA-C	-5.07	105.83	111.36
1	H	252	LEU	CA-C-N	-5.04	115.37	120.21
1	H	252	LEU	C-N-CA	-5.04	115.37	120.21
1	H	298	PRO	N-CA-C	-5.04	102.70	111.32
1	H	228	MET	N-CA-C	-5.02	105.72	111.14
1	I	493	GLY	CA-C-N	-5.01	114.42	119.83
1	I	493	GLY	C-N-CA	-5.01	114.42	119.83

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	855	ARG	Sidechain
1	I	574	ARG	Sidechain
1	I	855	ARG	Sidechain
1	J	574	ARG	Sidechain
1	L	855	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	5221	480	0
1	B	5152	0	5223	123	0
1	C	5152	0	5223	201	0
1	D	5152	0	5222	480	0
1	E	5152	0	5221	408	0
1	F	5152	0	5223	130	0
1	G	5152	0	5223	137	0
1	H	5152	0	5221	549	0
1	I	5152	0	5221	462	0
1	J	5152	0	5223	122	0
1	K	5152	0	5221	456	0
1	L	5152	0	5223	192	0
All	All	61824	0	62665	3454	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 28.

All (3454) 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:K:426:ILE:CD1	1:K:440:ILE:HG22	1.24	1.64
1:D:426:ILE:CD1	1:D:440:ILE:HG22	1.20	1.64
1:E:441:LEU:HD23	1:E:498:VAL:CB	1.17	1.63
1:H:426:ILE:CD1	1:H:440:ILE:HG22	1.20	1.62
1:K:441:LEU:CD2	1:K:498:VAL:HB	1.29	1.61
1:A:426:ILE:CD1	1:A:440:ILE:HG22	1.20	1.61
1:K:441:LEU:HD23	1:K:498:VAL:CB	1.16	1.60
1:H:441:LEU:HD23	1:H:498:VAL:CB	1.17	1.60
1:I:441:LEU:CD2	1:I:498:VAL:HB	1.28	1.59
1:D:441:LEU:HD23	1:D:498:VAL:CB	1.18	1.58
1:E:426:ILE:HD13	1:E:440:ILE:CG2	1.35	1.57
1:I:426:ILE:CD1	1:I:440:ILE:HG22	1.20	1.56
1:E:426:ILE:CD1	1:E:440:ILE:HG22	1.20	1.56
1:I:441:LEU:HD23	1:I:498:VAL:CB	1.15	1.56
1:A:441:LEU:HD23	1:A:498:VAL:CB	1.16	1.55
1:H:441:LEU:CD2	1:H:498:VAL:HB	1.30	1.55
1:A:426:ILE:HD13	1:A:440:ILE:CG2	1.33	1.55
1:A:441:LEU:CD2	1:A:498:VAL:HB	1.33	1.54
1:H:426:ILE:HD13	1:H:440:ILE:CG2	1.36	1.53
1:D:426:ILE:HD13	1:D:440:ILE:CG2	1.36	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:441:LEU:CD2	1:D:498:VAL:HB	1.35	1.52
1:E:441:LEU:CD2	1:E:498:VAL:HB	1.34	1.52
1:I:426:ILE:HD13	1:I:440:ILE:CG2	1.37	1.49
1:K:426:ILE:HD13	1:K:440:ILE:CG2	1.40	1.48
1:I:478:ASN:ND2	1:I:482:LYS:HZ1	1.18	1.39
1:A:775:GLY:CA	1:H:780:SER:HB2	1.51	1.39
1:A:780:SER:HB2	1:H:775:GLY:CA	1.50	1.38
1:C:780:SER:CB	1:L:779:PHE:HA	1.53	1.36
1:H:855:ARG:CD	1:K:555:ALA:HB3	1.53	1.35
1:H:260:SER:O	1:H:264:GLY:N	1.58	1.35
1:E:478:ASN:ND2	1:E:482:LYS:HZ1	1.23	1.34
1:K:260:SER:O	1:K:264:GLY:N	1.60	1.34
1:I:260:SER:O	1:I:264:GLY:N	1.60	1.34
1:A:478:ASN:ND2	1:A:482:LYS:HZ1	1.24	1.33
1:D:478:ASN:ND2	1:D:482:LYS:HZ1	1.19	1.33
1:D:260:SER:O	1:D:264:GLY:N	1.59	1.33
1:K:478:ASN:ND2	1:K:482:LYS:HZ1	1.27	1.33
1:E:260:SER:O	1:E:264:GLY:N	1.59	1.32
1:H:426:ILE:CD1	1:H:440:ILE:CG2	1.96	1.31
1:D:854:PRO:HB2	1:D:855:ARG:NH1	1.45	1.31
1:A:260:SER:O	1:A:264:GLY:N	1.60	1.30
1:A:426:ILE:CD1	1:A:440:ILE:CG2	1.97	1.29
1:K:426:ILE:CD1	1:K:440:ILE:CG2	1.99	1.29
1:D:426:ILE:CD1	1:D:440:ILE:CG2	1.96	1.28
1:A:276:GLU:OE2	1:A:318:PHE:CE2	1.85	1.28
1:I:441:LEU:HD23	1:I:498:VAL:CG1	1.64	1.28
1:D:441:LEU:HD23	1:D:498:VAL:CG1	1.63	1.28
1:E:426:ILE:CD1	1:E:440:ILE:CG2	1.97	1.28
1:I:426:ILE:CD1	1:I:440:ILE:CG2	1.97	1.28
1:E:441:LEU:HD23	1:E:498:VAL:CG1	1.64	1.26
1:D:225:ASP:O	1:D:229:PHE:CE1	1.87	1.26
1:H:855:ARG:HD3	1:K:555:ALA:CB	1.66	1.26
1:A:441:LEU:HD23	1:A:498:VAL:CG1	1.65	1.25
1:I:272:ILE:HG23	1:I:278:LEU:CD1	1.65	1.25
1:K:272:ILE:HG23	1:K:278:LEU:CD1	1.65	1.25
1:K:441:LEU:HD23	1:K:498:VAL:CG1	1.67	1.25
1:H:441:LEU:HD23	1:H:498:VAL:CG1	1.66	1.25
1:I:854:PRO:HB2	1:I:855:ARG:NH1	1.50	1.24
1:A:272:ILE:HG23	1:A:278:LEU:CD1	1.66	1.24
1:E:269:LEU:HD11	1:E:457:SER:O	1.07	1.23
1:H:854:PRO:HB2	1:H:855:ARG:NH1	1.51	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:272:ILE:HG23	1:E:278:LEU:CD1	1.67	1.23
1:H:478:ASN:ND2	1:H:482:LYS:HZ1	1.34	1.23
1:D:272:ILE:HG23	1:D:278:LEU:CD1	1.67	1.23
1:E:276:GLU:OE2	1:E:318:PHE:HE2	1.16	1.22
1:E:276:GLU:OE2	1:E:318:PHE:CE2	1.92	1.22
1:A:276:GLU:OE2	1:A:318:PHE:HE2	1.11	1.22
1:A:269:LEU:HD11	1:A:457:SER:O	1.07	1.21
1:I:269:LEU:HD11	1:I:457:SER:O	1.07	1.20
1:K:269:LEU:HD11	1:K:457:SER:O	1.04	1.19
1:H:272:ILE:HG23	1:H:278:LEU:CD1	1.70	1.19
1:D:269:LEU:HD11	1:D:457:SER:O	1.04	1.18
1:D:855:ARG:CD	1:I:555:ALA:HB3	1.72	1.18
1:C:780:SER:HB2	1:L:779:PHE:CA	1.72	1.17
1:H:269:LEU:HD11	1:H:457:SER:O	1.04	1.17
1:I:269:LEU:HD21	1:I:457:SER:CB	1.74	1.16
1:H:269:LEU:HD21	1:H:457:SER:CB	1.74	1.16
1:K:269:LEU:HD21	1:K:457:SER:CB	1.73	1.16
1:E:269:LEU:HD21	1:E:457:SER:CB	1.75	1.16
1:H:426:ILE:HD11	1:H:440:ILE:HG22	1.24	1.16
1:D:269:LEU:HD21	1:D:457:SER:CB	1.75	1.15
1:D:854:PRO:HB3	1:I:559:ASP:OD2	1.42	1.15
1:I:478:ASN:ND2	1:I:482:LYS:NZ	1.94	1.15
1:A:269:LEU:HD21	1:A:457:SER:CB	1.75	1.15
1:A:783:LEU:HD12	1:H:778:GLY:O	1.47	1.15
1:H:269:LEU:HD21	1:H:457:SER:OG	1.46	1.15
1:D:269:LEU:CD1	1:D:457:SER:O	1.95	1.14
1:A:478:ASN:ND2	1:A:482:LYS:NZ	1.95	1.14
1:D:478:ASN:ND2	1:D:482:LYS:NZ	1.94	1.14
1:E:478:ASN:ND2	1:E:482:LYS:NZ	1.95	1.14
1:K:426:ILE:HD11	1:K:440:ILE:HG22	1.26	1.14
1:H:269:LEU:CD1	1:H:457:SER:O	1.95	1.14
1:K:269:LEU:HD21	1:K:457:SER:OG	1.48	1.14
1:K:269:LEU:CD1	1:K:457:SER:O	1.96	1.14
1:D:269:LEU:HD21	1:D:457:SER:OG	1.48	1.13
1:D:555:ALA:HB3	1:I:855:ARG:HD3	1.15	1.13
1:E:269:LEU:HD21	1:E:457:SER:OG	1.48	1.13
1:A:426:ILE:HD13	1:A:440:ILE:HG21	1.14	1.13
1:C:774:SER:HB2	1:L:781:ALA:HB2	1.28	1.13
1:I:426:ILE:HD13	1:I:440:ILE:HG21	1.13	1.13
1:D:855:ARG:HD3	1:I:555:ALA:CB	1.78	1.13
1:H:278:LEU:HD21	1:H:280:LYS:HD3	1.20	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:269:LEU:HA	1:K:272:ILE:HD12	1.27	1.12
1:C:774:SER:CB	1:L:774:SER:HA	1.79	1.12
1:H:478:ASN:ND2	1:H:482:LYS:NZ	1.96	1.12
1:K:478:ASN:ND2	1:K:482:LYS:NZ	1.97	1.12
1:A:441:LEU:HG	1:A:498:VAL:HG12	1.31	1.11
1:D:559:ASP:OD2	1:I:854:PRO:HB3	1.48	1.11
1:I:269:LEU:CD1	1:I:457:SER:O	1.97	1.11
1:A:426:ILE:HD11	1:A:440:ILE:HG22	1.31	1.11
1:I:269:LEU:HD21	1:I:457:SER:OG	1.50	1.11
1:A:269:LEU:CD1	1:A:457:SER:O	1.97	1.11
1:A:285:ILE:HD13	1:A:286:THR:H	1.10	1.11
1:A:269:LEU:HD21	1:A:457:SER:OG	1.49	1.11
1:E:426:ILE:HD13	1:E:440:ILE:HG21	1.14	1.11
1:H:273:VAL:HG11	1:H:457:SER:HB2	1.33	1.11
1:H:285:ILE:HD13	1:H:286:THR:H	1.06	1.11
1:K:441:LEU:HG	1:K:498:VAL:HG12	1.32	1.10
1:D:441:LEU:HG	1:D:498:VAL:HG12	1.31	1.10
1:H:426:ILE:HD13	1:H:440:ILE:HG21	1.13	1.10
1:A:778:GLY:CA	1:H:783:LEU:HD12	1.81	1.10
1:D:426:ILE:HD13	1:D:440:ILE:HG21	1.12	1.10
1:E:269:LEU:CD1	1:E:457:SER:O	1.98	1.10
1:H:556:ALA:HB2	1:K:855:ARG:NE	1.66	1.10
1:K:269:LEU:CD2	1:K:457:SER:OG	2.00	1.10
1:H:441:LEU:HG	1:H:498:VAL:HG12	1.32	1.09
1:E:269:LEU:CD2	1:E:457:SER:OG	2.01	1.09
1:H:269:LEU:CD2	1:H:457:SER:OG	2.00	1.09
1:H:276:GLU:OE2	1:H:318:PHE:CE2	2.03	1.09
1:C:774:SER:HB2	1:L:781:ALA:CB	1.81	1.09
1:E:225:ASP:O	1:E:229:PHE:CE1	2.06	1.08
1:I:426:ILE:HD11	1:I:440:ILE:HG22	1.18	1.08
1:A:783:LEU:HD12	1:H:778:GLY:CA	1.82	1.08
1:E:441:LEU:HG	1:E:498:VAL:HG12	1.36	1.08
1:K:278:LEU:HD21	1:K:280:LYS:HD3	1.21	1.08
1:K:488:HIS:HB3	1:K:491:GLU:CG	1.83	1.08
1:A:269:LEU:CD2	1:A:457:SER:OG	2.02	1.08
1:A:780:SER:HB2	1:H:775:GLY:HA3	1.14	1.08
1:D:278:LEU:HD21	1:D:280:LYS:HD3	1.28	1.07
1:D:441:LEU:CD2	1:D:498:VAL:CB	2.07	1.07
1:E:285:ILE:HD13	1:E:286:THR:H	1.13	1.07
1:D:269:LEU:CD2	1:D:457:SER:OG	2.02	1.07
1:D:426:ILE:HD11	1:D:440:ILE:HG22	1.22	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:556:ALA:HB2	1:K:855:ARG:HE	1.06	1.07
1:I:269:LEU:CD2	1:I:457:SER:OG	2.01	1.07
1:I:278:LEU:HD21	1:I:280:LYS:HD3	1.31	1.07
1:I:441:LEU:HG	1:I:498:VAL:HG12	1.35	1.07
1:E:441:LEU:CD2	1:E:498:VAL:CB	2.07	1.07
1:E:272:ILE:HG23	1:E:278:LEU:HD12	1.07	1.07
1:A:778:GLY:O	1:H:783:LEU:HD12	1.55	1.06
1:A:780:SER:CB	1:H:775:GLY:CA	2.33	1.06
1:K:426:ILE:HD13	1:K:440:ILE:HG21	1.15	1.06
1:E:426:ILE:HD11	1:E:440:ILE:HG22	1.19	1.06
1:D:555:ALA:HB3	1:I:855:ARG:CD	1.84	1.06
1:A:778:GLY:HA3	1:H:783:LEU:HD12	1.38	1.06
1:D:555:ALA:CB	1:I:855:ARG:HD3	1.85	1.06
1:D:855:ARG:HD3	1:I:555:ALA:HB3	1.06	1.06
1:D:269:LEU:HA	1:D:272:ILE:HD12	1.34	1.05
1:D:307:PHE:CE1	1:D:345:LEU:HD21	1.90	1.05
1:K:285:ILE:HD13	1:K:286:THR:H	1.14	1.05
1:D:285:ILE:HD13	1:D:286:THR:H	1.08	1.05
1:D:854:PRO:HB2	1:D:855:ARG:HH12	0.93	1.05
1:E:279:PRO:HG2	1:E:325:LEU:HD21	1.37	1.05
1:K:307:PHE:CE1	1:K:345:LEU:HD21	1.91	1.05
1:D:273:VAL:HG11	1:D:457:SER:HB2	1.37	1.05
1:L:855:ARG:H	1:L:855:ARG:HD2	1.22	1.05
1:I:854:PRO:HB2	1:I:855:ARG:HH12	0.93	1.05
1:H:441:LEU:CD2	1:H:498:VAL:CB	2.06	1.04
1:A:778:GLY:HA3	1:H:783:LEU:CD1	1.88	1.04
1:A:279:PRO:HG2	1:A:325:LEU:HD21	1.37	1.03
1:E:273:VAL:HG11	1:E:457:SER:HB2	1.36	1.03
1:H:272:ILE:HG23	1:H:278:LEU:HD12	1.05	1.03
1:A:272:ILE:HG23	1:A:278:LEU:HD12	1.07	1.03
1:D:441:LEU:CG	1:D:498:VAL:HG12	1.88	1.03
1:A:783:LEU:HD12	1:H:778:GLY:C	1.81	1.03
1:K:273:VAL:HG11	1:K:457:SER:HB2	1.36	1.03
1:I:269:LEU:HA	1:I:272:ILE:HD12	1.36	1.03
1:D:284:MET:HG2	1:D:286:THR:CG2	1.88	1.02
1:I:272:ILE:HG23	1:I:278:LEU:HD12	1.07	1.02
1:I:285:ILE:HD13	1:I:286:THR:H	1.16	1.02
1:K:273:VAL:HG21	1:K:457:SER:HB3	1.39	1.02
1:A:278:LEU:HD21	1:A:280:LYS:HD3	1.34	1.02
1:H:279:PRO:HG2	1:H:325:LEU:HD21	1.41	1.02
1:H:285:ILE:HD13	1:H:286:THR:N	1.72	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:441:LEU:HD21	1:H:499:SER:H	1.24	1.02
1:K:272:ILE:HG23	1:K:278:LEU:HD12	1.03	1.02
1:D:273:VAL:HG21	1:D:457:SER:HB3	1.41	1.02
1:H:307:PHE:CE1	1:H:345:LEU:HD21	1.94	1.02
1:I:225:ASP:C	1:I:229:PHE:CE1	2.38	1.02
1:I:273:VAL:HG11	1:I:457:SER:HB2	1.38	1.02
1:A:273:VAL:HG11	1:A:457:SER:HB2	1.38	1.01
1:A:441:LEU:CD2	1:A:498:VAL:CB	2.06	1.01
1:A:307:PHE:CE1	1:A:345:LEU:HD21	1.95	1.01
1:A:775:GLY:HA2	1:H:780:SER:HB2	1.40	1.01
1:K:441:LEU:CD2	1:K:498:VAL:CB	2.05	1.01
1:H:562:LYS:HE2	1:K:562:LYS:NZ	1.74	1.01
1:I:276:GLU:OE2	1:I:318:PHE:CE2	2.14	1.01
1:K:279:PRO:HG2	1:K:325:LEU:HD21	1.41	1.01
1:A:775:GLY:HA3	1:H:780:SER:HB2	1.39	1.01
1:C:775:GLY:HA3	1:L:782:ALA:H	1.24	1.01
1:A:273:VAL:HG21	1:A:457:SER:HB3	1.39	1.01
1:A:778:GLY:C	1:H:783:LEU:HD12	1.85	1.01
1:A:781:ALA:HB2	1:H:774:SER:OG	1.62	1.00
1:C:781:ALA:N	1:L:780:SER:HB3	1.76	1.00
1:K:272:ILE:HG22	1:K:277:PHE:HA	1.43	1.00
1:C:774:SER:HB3	1:L:774:SER:HA	1.04	1.00
1:H:269:LEU:HA	1:H:272:ILE:HD12	1.38	1.00
1:E:488:HIS:HB3	1:E:491:GLU:HG2	1.44	1.00
1:D:285:ILE:HD13	1:D:286:THR:N	1.77	1.00
1:A:441:LEU:CG	1:A:498:VAL:HG12	1.90	1.00
1:C:780:SER:HB2	1:L:779:PHE:HA	1.03	0.99
1:D:225:ASP:C	1:D:229:PHE:HE1	1.70	0.99
1:E:278:LEU:HD21	1:E:280:LYS:HD3	1.44	0.99
1:D:279:PRO:HG2	1:D:325:LEU:HD21	1.41	0.99
1:H:273:VAL:HG21	1:H:457:SER:HB3	1.43	0.99
1:H:426:ILE:HD12	1:H:440:ILE:HG22	1.44	0.99
1:A:426:ILE:HD12	1:A:440:ILE:HG22	1.41	0.98
1:H:278:LEU:CD2	1:H:280:LYS:HD3	1.92	0.98
1:I:273:VAL:HG21	1:I:457:SER:HB3	1.42	0.98
1:A:269:LEU:HA	1:A:272:ILE:HD12	1.42	0.98
1:I:441:LEU:HD21	1:I:499:SER:H	1.27	0.98
1:H:363:TYR:HE1	1:H:383:CYS:SG	1.86	0.98
1:E:225:ASP:C	1:E:229:PHE:CE1	2.42	0.98
1:E:273:VAL:HG21	1:E:457:SER:HB3	1.45	0.98
1:K:278:LEU:CD2	1:K:280:LYS:HD3	1.92	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:426:ILE:HD12	1:D:440:ILE:HG22	1.46	0.98
1:I:429:MET:HE2	1:I:437:GLY:HA2	1.45	0.98
1:D:441:LEU:HD21	1:D:499:SER:H	1.25	0.98
1:I:307:PHE:CE1	1:I:345:LEU:HD21	1.98	0.98
1:K:441:LEU:HD21	1:K:499:SER:H	1.24	0.98
1:D:272:ILE:CG2	1:D:278:LEU:HD12	1.91	0.98
1:H:441:LEU:CG	1:H:498:VAL:HG12	1.93	0.98
1:H:855:ARG:HD3	1:K:555:ALA:HB3	0.99	0.98
1:K:441:LEU:CG	1:K:498:VAL:HG12	1.94	0.98
1:H:276:GLU:OE2	1:H:318:PHE:HE2	1.38	0.97
1:A:441:LEU:CD2	1:A:498:VAL:CG1	2.40	0.97
1:D:562:LYS:CE	1:I:562:LYS:CE	2.43	0.97
1:K:426:ILE:HD12	1:K:440:ILE:HG22	1.46	0.97
1:D:225:ASP:C	1:D:229:PHE:CE1	2.41	0.97
1:E:307:PHE:CE1	1:E:345:LEU:HD21	1.99	0.97
1:H:854:PRO:HB2	1:H:855:ARG:HH12	1.16	0.97
1:K:272:ILE:CG2	1:K:278:LEU:HD12	1.95	0.97
1:D:363:TYR:HE1	1:D:383:CYS:SG	1.88	0.97
1:I:272:ILE:HG22	1:I:277:PHE:HA	1.44	0.97
1:A:429:MET:HE2	1:A:437:GLY:HA2	1.47	0.96
1:A:441:LEU:HD21	1:A:499:SER:H	1.27	0.96
1:I:279:PRO:HG2	1:I:325:LEU:HD21	1.43	0.96
1:I:363:TYR:HE1	1:I:383:CYS:SG	1.88	0.96
1:A:775:GLY:CA	1:H:780:SER:CB	2.43	0.96
1:E:441:LEU:CG	1:E:498:VAL:HG12	1.94	0.96
1:A:363:TYR:HE1	1:A:383:CYS:SG	1.87	0.96
1:E:429:MET:HE2	1:E:437:GLY:HA2	1.46	0.96
1:D:272:ILE:HG23	1:D:278:LEU:HD12	1.00	0.96
1:K:376:LYS:NZ	1:K:376:LYS:HA	1.80	0.96
1:C:780:SER:CB	1:L:779:PHE:CA	2.38	0.96
1:D:556:ALA:HA	1:I:855:ARG:NH2	1.81	0.96
1:D:562:LYS:HE3	1:I:562:LYS:HE2	1.48	0.96
1:A:285:ILE:HD13	1:A:286:THR:N	1.81	0.95
1:A:376:LYS:HA	1:A:376:LYS:NZ	1.82	0.95
1:K:363:TYR:HE1	1:K:383:CYS:SG	1.88	0.95
1:A:251:THR:HG22	1:A:252:LEU:H	1.31	0.95
1:H:429:MET:HE2	1:H:437:GLY:HA2	1.48	0.95
1:E:363:TYR:HE1	1:E:383:CYS:SG	1.88	0.95
1:I:434:PRO:CB	1:I:491:GLU:HG3	1.96	0.95
1:D:284:MET:HG2	1:D:286:THR:HG22	1.48	0.95
1:C:780:SER:N	1:L:783:LEU:HD12	1.82	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:ILE:HG22	1:D:277:PHE:HA	1.47	0.95
1:H:441:LEU:HD21	1:H:499:SER:N	1.81	0.95
1:I:441:LEU:CG	1:I:498:VAL:HG12	1.95	0.95
1:K:488:HIS:HB3	1:K:491:GLU:HG2	1.47	0.95
1:A:783:LEU:CD1	1:H:778:GLY:HA3	1.97	0.95
1:D:429:MET:HE2	1:D:437:GLY:HA2	1.49	0.95
1:A:286:THR:HB	1:A:361:PRO:HB3	1.49	0.94
1:H:272:ILE:CG2	1:H:278:LEU:HD12	1.95	0.94
1:E:441:LEU:HD21	1:E:499:SER:H	1.30	0.94
1:H:272:ILE:HG22	1:H:277:PHE:HA	1.49	0.94
1:H:488:HIS:HB3	1:H:491:GLU:HG2	1.46	0.94
1:A:441:LEU:HD21	1:A:499:SER:N	1.83	0.94
1:K:429:MET:HE2	1:K:437:GLY:HA2	1.50	0.94
1:K:441:LEU:HD21	1:K:499:SER:N	1.82	0.94
1:E:251:THR:HG22	1:E:252:LEU:H	1.31	0.94
1:A:376:LYS:HA	1:A:376:LYS:HZ3	1.30	0.94
1:D:441:LEU:HD21	1:D:499:SER:N	1.81	0.94
1:C:774:SER:O	1:L:780:SER:HB2	1.67	0.93
1:D:286:THR:HB	1:D:361:PRO:HB3	1.50	0.93
1:E:434:PRO:CB	1:E:491:GLU:HG3	1.97	0.93
1:L:854:PRO:HB2	1:L:855:ARG:NH2	1.82	0.93
1:A:272:ILE:HG22	1:A:277:PHE:HA	1.47	0.93
1:E:269:LEU:HA	1:E:272:ILE:HD12	1.50	0.93
1:E:441:LEU:CD2	1:E:498:VAL:CG1	2.40	0.93
1:A:434:PRO:HB3	1:A:491:GLU:HG3	1.48	0.93
1:D:278:LEU:CD2	1:D:280:LYS:HD3	1.97	0.93
1:D:376:LYS:HA	1:D:376:LYS:NZ	1.83	0.93
1:K:485:PHE:CD2	1:K:492:PHE:CD1	2.57	0.93
1:A:434:PRO:CB	1:A:491:GLU:HG3	1.98	0.93
1:E:426:ILE:HD12	1:E:440:ILE:HG22	1.51	0.93
1:H:286:THR:HB	1:H:361:PRO:HB3	1.51	0.93
1:C:780:SER:HA	1:L:780:SER:H	1.33	0.93
1:H:556:ALA:CB	1:K:855:ARG:HE	1.82	0.93
1:I:272:ILE:CG2	1:I:278:LEU:HD12	1.98	0.92
1:D:441:LEU:CD2	1:D:498:VAL:CG1	2.39	0.92
1:C:780:SER:CA	1:L:780:SER:H	1.81	0.92
1:E:285:ILE:HD13	1:E:286:THR:N	1.84	0.92
1:E:441:LEU:HD21	1:E:499:SER:N	1.84	0.92
1:H:562:LYS:HE2	1:K:562:LYS:HZ1	1.33	0.92
1:A:272:ILE:CG2	1:A:278:LEU:HD12	1.99	0.92
1:H:285:ILE:HG12	1:H:287:ARG:H	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:PHE:CD2	1:A:492:PHE:CD1	2.58	0.92
1:K:234:MET:O	1:K:237:ILE:HG22	1.70	0.92
1:D:485:PHE:CD2	1:D:492:PHE:CD1	2.57	0.91
1:K:285:ILE:HD13	1:K:286:THR:N	1.85	0.91
1:E:286:THR:HB	1:E:361:PRO:HB3	1.52	0.91
1:H:376:LYS:HA	1:H:376:LYS:NZ	1.83	0.91
1:I:441:LEU:HD21	1:I:499:SER:N	1.84	0.91
1:A:276:GLU:CD	1:A:318:PHE:HE2	1.77	0.91
1:C:780:SER:CB	1:L:780:SER:H	1.84	0.91
1:H:251:THR:HG22	1:H:252:LEU:H	1.33	0.91
1:I:286:THR:HB	1:I:361:PRO:HB3	1.49	0.91
1:I:854:PRO:CB	1:I:855:ARG:HH12	1.83	0.91
1:A:285:ILE:HG12	1:A:287:ARG:H	1.35	0.91
1:A:488:HIS:HB3	1:A:491:GLU:CG	2.00	0.91
1:E:488:HIS:HB3	1:E:491:GLU:CG	2.01	0.91
1:K:276:GLU:OE2	1:K:318:PHE:CE2	2.24	0.91
1:K:434:PRO:CB	1:K:491:GLU:HG3	2.01	0.91
1:H:855:ARG:HH11	1:K:555:ALA:HB1	1.37	0.90
1:H:376:LYS:HA	1:H:376:LYS:HZ3	1.34	0.90
1:I:485:PHE:CD2	1:I:492:PHE:CD1	2.59	0.90
1:H:276:GLU:CD	1:H:318:PHE:HE2	1.80	0.90
1:H:441:LEU:CD2	1:H:498:VAL:CG1	2.41	0.90
1:J:754:VAL:HA	1:J:779:PHE:HE1	1.35	0.90
1:D:854:PRO:CB	1:D:855:ARG:HH12	1.81	0.90
1:K:478:ASN:HD21	1:K:482:LYS:HZ1	0.91	0.90
1:I:251:THR:HG22	1:I:252:LEU:H	1.34	0.90
1:I:285:ILE:HD13	1:I:286:THR:N	1.87	0.90
1:A:284:MET:HG2	1:A:286:THR:CG2	2.01	0.90
1:H:284:MET:HG2	1:H:286:THR:CG2	2.02	0.90
1:I:426:ILE:HD12	1:I:440:ILE:HG22	1.51	0.90
1:K:269:LEU:CD2	1:K:457:SER:CB	2.50	0.90
1:G:703:LYS:HG3	1:K:544:ASN:ND2	1.85	0.90
1:A:780:SER:CB	1:H:775:GLY:HA2	2.02	0.90
1:C:780:SER:C	1:L:780:SER:HB3	1.96	0.89
1:E:272:ILE:CG2	1:E:278:LEU:HD12	1.99	0.89
1:I:278:LEU:CD2	1:I:280:LYS:HD3	2.01	0.89
1:H:485:PHE:CD2	1:H:492:PHE:CD1	2.59	0.89
1:H:287:ARG:HH11	1:H:287:ARG:HG3	1.36	0.89
1:I:376:LYS:HA	1:I:376:LYS:NZ	1.87	0.89
1:D:251:THR:HG22	1:D:252:LEU:H	1.35	0.89
1:E:877:GLU:HA	1:E:882:ARG:HE	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:278:LEU:HD21	1:K:280:LYS:CD	2.03	0.89
1:E:455:VAL:HG12	1:E:501:GLY:H	1.38	0.89
1:H:478:ASN:HD21	1:H:482:LYS:NZ	1.61	0.89
1:A:780:SER:CB	1:H:775:GLY:HA3	2.00	0.89
1:D:279:PRO:HB3	1:D:322:GLN:CB	2.03	0.89
1:L:285:ILE:HD12	1:L:287:ARG:H	1.37	0.88
1:A:269:LEU:CD2	1:A:457:SER:CB	2.52	0.88
1:H:485:PHE:HD2	1:H:492:PHE:O	1.57	0.88
1:I:455:VAL:HG12	1:I:501:GLY:H	1.38	0.88
1:K:276:GLU:CD	1:K:318:PHE:HE2	1.80	0.88
1:A:775:GLY:C	1:H:780:SER:HB2	1.97	0.88
1:C:774:SER:HA	1:L:774:SER:O	1.72	0.88
1:I:453:VAL:HG11	1:I:505:LEU:HB2	1.55	0.88
1:D:276:GLU:CD	1:D:318:PHE:HE2	1.82	0.88
1:D:562:LYS:HE2	1:I:562:LYS:HE3	1.55	0.88
1:D:855:ARG:NH2	1:I:556:ALA:HA	1.88	0.88
1:C:285:ILE:HD12	1:C:287:ARG:H	1.38	0.88
1:D:285:ILE:HG12	1:D:287:ARG:H	1.36	0.88
1:H:854:PRO:CB	1:H:855:ARG:HH12	1.87	0.88
1:D:478:ASN:HD21	1:D:482:LYS:HZ1	0.91	0.88
1:I:441:LEU:CD2	1:I:498:VAL:CG1	2.40	0.88
1:A:778:GLY:HA2	1:H:783:LEU:HB2	1.54	0.88
1:D:455:VAL:HG12	1:D:501:GLY:H	1.38	0.87
1:A:783:LEU:HD12	1:H:778:GLY:HA3	1.54	0.87
1:H:562:LYS:HE3	1:K:562:LYS:HE2	1.54	0.87
1:K:441:LEU:CD2	1:K:498:VAL:CG1	2.41	0.87
1:I:269:LEU:CD2	1:I:457:SER:CB	2.50	0.87
1:D:376:LYS:HA	1:D:376:LYS:HZ3	1.39	0.87
1:A:783:LEU:CD1	1:H:778:GLY:CA	2.50	0.87
1:E:269:LEU:O	1:E:273:VAL:HG13	1.74	0.87
1:K:472:ASN:HD21	1:K:475:ALA:HB3	1.38	0.87
1:A:453:VAL:HG11	1:A:505:LEU:HB2	1.57	0.87
1:E:272:ILE:HG22	1:E:277:PHE:HA	1.57	0.87
1:E:485:PHE:CD2	1:E:492:PHE:CD1	2.63	0.87
1:K:434:PRO:HB3	1:K:491:GLU:HG3	1.53	0.87
1:K:485:PHE:CE2	1:K:500:THR:OG1	2.25	0.87
1:H:279:PRO:HB3	1:H:322:GLN:CB	2.05	0.86
1:I:269:LEU:O	1:I:273:VAL:HG13	1.74	0.86
1:A:279:PRO:HB3	1:A:322:GLN:CB	2.05	0.86
1:E:434:PRO:HG2	1:E:488:HIS:CG	2.09	0.86
1:A:478:ASN:HD21	1:A:482:LYS:NZ	1.67	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:434:PRO:CB	1:H:491:GLU:HG3	2.04	0.86
1:A:269:LEU:O	1:A:273:VAL:HG13	1.76	0.86
1:D:269:LEU:O	1:D:273:VAL:HG13	1.75	0.86
1:H:278:LEU:HD21	1:H:280:LYS:CD	2.04	0.86
1:K:455:VAL:HG12	1:K:501:GLY:H	1.38	0.86
1:E:453:VAL:HG11	1:E:505:LEU:HB2	1.56	0.86
1:H:434:PRO:HG2	1:H:488:HIS:CG	2.11	0.86
1:I:225:ASP:O	1:I:229:PHE:CE1	2.28	0.86
1:K:453:VAL:HG11	1:K:505:LEU:HB2	1.57	0.86
1:D:269:LEU:CD2	1:D:457:SER:CB	2.52	0.86
1:F:285:ILE:HD12	1:F:287:ARG:H	1.41	0.86
1:H:269:LEU:O	1:H:273:VAL:HG13	1.74	0.86
1:B:285:ILE:HD12	1:B:287:ARG:H	1.39	0.86
1:E:234:MET:O	1:E:237:ILE:HG22	1.76	0.86
1:A:455:VAL:HG12	1:A:501:GLY:H	1.38	0.86
1:K:284:MET:HG2	1:K:286:THR:HG22	1.58	0.86
1:E:376:LYS:NZ	1:E:379:ILE:HD12	1.90	0.85
1:I:441:LEU:CD2	1:I:498:VAL:CB	2.04	0.85
1:K:286:THR:HB	1:K:361:PRO:HB3	1.54	0.85
1:K:383:CYS:O	1:K:387:ILE:HG13	1.76	0.85
1:H:455:VAL:HG12	1:H:501:GLY:H	1.39	0.85
1:K:434:PRO:HG2	1:K:488:HIS:CG	2.12	0.85
1:A:278:LEU:CD2	1:A:280:LYS:HD3	2.06	0.85
1:A:488:HIS:HB3	1:A:491:GLU:HG2	1.59	0.85
1:D:434:PRO:CB	1:D:491:GLU:HG3	2.06	0.85
1:H:453:VAL:HG11	1:H:505:LEU:HB2	1.58	0.85
1:I:488:HIS:HB3	1:I:491:GLU:HG2	1.56	0.85
1:H:562:LYS:CE	1:K:562:LYS:NZ	2.39	0.85
1:K:251:THR:HG22	1:K:252:LEU:H	1.39	0.85
1:A:286:THR:CB	1:A:361:PRO:HB3	2.06	0.85
1:E:279:PRO:HB3	1:E:322:GLN:CB	2.07	0.85
1:E:383:CYS:O	1:E:387:ILE:HG13	1.75	0.85
1:A:775:GLY:HA2	1:H:780:SER:CB	2.05	0.85
1:A:779:PHE:N	1:H:780:SER:HB3	1.92	0.85
1:C:780:SER:HA	1:L:780:SER:CB	2.06	0.85
1:D:297:ASP:CG	1:D:300:ALA:HB3	2.01	0.85
1:I:434:PRO:HB3	1:I:491:GLU:HG3	1.56	0.85
1:I:485:PHE:CE2	1:I:500:THR:OG1	2.28	0.85
1:A:485:PHE:CE2	1:A:500:THR:OG1	2.29	0.85
1:H:269:LEU:CD2	1:H:457:SER:CB	2.52	0.85
1:I:383:CYS:O	1:I:387:ILE:HG13	1.77	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:THR:CB	1:D:361:PRO:HB3	2.06	0.84
1:D:485:PHE:CE2	1:D:500:THR:OG1	2.28	0.84
1:E:269:LEU:CD2	1:E:457:SER:CB	2.52	0.84
1:A:774:SER:OG	1:H:781:ALA:HB2	1.76	0.84
1:E:478:ASN:HD21	1:E:482:LYS:HZ1	1.22	0.84
1:I:276:GLU:CD	1:I:318:PHE:HE2	1.85	0.84
1:I:279:PRO:HB3	1:I:322:GLN:CB	2.07	0.84
1:K:269:LEU:O	1:K:273:VAL:HG13	1.76	0.84
1:D:453:VAL:HG11	1:D:505:LEU:HB2	1.59	0.84
1:A:383:CYS:O	1:A:387:ILE:HG13	1.77	0.84
1:C:774:SER:HB3	1:L:774:SER:CA	2.00	0.84
1:D:383:CYS:O	1:D:387:ILE:HG13	1.78	0.84
1:E:376:LYS:HZ1	1:E:379:ILE:HD12	1.39	0.84
1:D:234:MET:O	1:D:237:ILE:HG22	1.75	0.84
1:E:276:GLU:CD	1:E:318:PHE:HE2	1.84	0.84
1:E:284:MET:N	1:E:284:MET:SD	2.49	0.84
1:E:434:PRO:HB3	1:E:491:GLU:HG3	1.56	0.84
1:J:754:VAL:HA	1:J:779:PHE:CE1	2.13	0.84
1:I:488:HIS:HB3	1:I:491:GLU:CG	2.08	0.84
1:A:284:MET:SD	1:A:284:MET:N	2.51	0.83
1:H:485:PHE:CE2	1:H:500:THR:OG1	2.29	0.83
1:C:774:SER:CB	1:L:781:ALA:CB	2.56	0.83
1:A:478:ASN:HD21	1:A:482:LYS:HZ1	0.85	0.83
1:A:486:GLY:O	1:A:489:PRO:HD3	1.79	0.83
1:H:286:THR:CB	1:H:361:PRO:HB3	2.08	0.83
1:A:308:PRO:HG3	1:A:344:ARG:HB2	1.57	0.83
1:H:488:HIS:HB3	1:H:491:GLU:CG	2.07	0.83
1:D:418:ARG:HH21	1:D:420:GLU:HB3	1.42	0.83
1:E:286:THR:CB	1:E:361:PRO:HB3	2.08	0.83
1:I:297:ASP:CG	1:I:300:ALA:HB3	2.01	0.83
1:H:279:PRO:CB	1:H:322:GLN:HA	2.09	0.83
1:E:285:ILE:HG12	1:E:287:ARG:H	1.44	0.83
1:D:562:LYS:HE2	1:I:562:LYS:CE	2.05	0.83
1:E:376:LYS:NZ	1:E:376:LYS:HA	1.94	0.83
1:A:778:GLY:CA	1:H:783:LEU:CD1	2.52	0.83
1:I:287:ARG:HH11	1:I:287:ARG:HG3	1.43	0.83
1:H:434:PRO:HB3	1:H:491:GLU:HG3	1.61	0.82
1:K:279:PRO:HB3	1:K:322:GLN:CB	2.09	0.82
1:D:488:HIS:HB3	1:D:491:GLU:HG2	1.61	0.82
1:H:562:LYS:HE3	1:K:562:LYS:CE	2.08	0.82
1:C:780:SER:CB	1:L:780:SER:N	2.42	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:781:ALA:H	1:L:780:SER:CA	1.93	0.82
1:H:284:MET:N	1:H:284:MET:SD	2.53	0.82
1:C:780:SER:HB3	1:L:779:PHE:HA	1.59	0.82
1:D:279:PRO:CB	1:D:322:GLN:HA	2.10	0.82
1:I:286:THR:CB	1:I:361:PRO:HB3	2.08	0.82
1:K:488:HIS:HB3	1:K:491:GLU:HG3	1.60	0.82
1:I:297:ASP:OD2	1:I:300:ALA:HB3	1.79	0.81
1:C:780:SER:HB2	1:L:779:PHE:C	2.04	0.81
1:K:297:ASP:OD2	1:K:300:ALA:HB3	1.81	0.81
1:A:775:GLY:HA3	1:H:781:ALA:H	1.46	0.81
1:D:441:LEU:CG	1:D:498:VAL:CG1	2.59	0.81
1:E:485:PHE:HD2	1:E:492:PHE:O	1.63	0.81
1:A:441:LEU:CG	1:A:498:VAL:CG1	2.59	0.81
1:K:480:ASN:HA	1:K:483:ASN:OD1	1.79	0.81
1:A:434:PRO:HG2	1:A:488:HIS:CG	2.16	0.81
1:A:775:GLY:HA3	1:H:781:ALA:N	1.95	0.81
1:D:272:ILE:CG2	1:D:278:LEU:CD1	2.56	0.81
1:G:285:ILE:HD12	1:G:287:ARG:H	1.44	0.81
1:G:615:ILE:HD11	1:G:803:ARG:HE	1.46	0.81
1:H:383:CYS:O	1:H:387:ILE:HG13	1.80	0.81
1:K:572:PHE:O	1:K:576:GLN:NE2	2.14	0.81
1:I:285:ILE:HG12	1:I:287:ARG:H	1.46	0.81
1:K:273:VAL:HG11	1:K:457:SER:CB	2.10	0.81
1:D:278:LEU:HD21	1:D:280:LYS:CD	2.10	0.80
1:K:441:LEU:CG	1:K:498:VAL:CG1	2.60	0.80
1:K:472:ASN:ND2	1:K:475:ALA:HB3	1.96	0.80
1:C:774:SER:CB	1:L:781:ALA:HB3	2.11	0.80
1:D:244:VAL:HB	1:D:248:SER:OG	1.82	0.80
1:H:285:ILE:HG12	1:H:287:ARG:HB2	1.63	0.80
1:I:272:ILE:CG2	1:I:278:LEU:CD1	2.55	0.80
1:K:285:ILE:HG12	1:K:287:ARG:H	1.42	0.80
1:D:226:ASN:HA	1:D:229:PHE:CE1	2.14	0.80
1:A:780:SER:HB2	1:H:775:GLY:C	2.07	0.80
1:I:478:ASN:HD21	1:I:482:LYS:HZ1	0.81	0.80
1:H:273:VAL:HG11	1:H:457:SER:CB	2.11	0.80
1:I:485:PHE:HD2	1:I:492:PHE:O	1.64	0.80
1:H:234:MET:O	1:H:237:ILE:HG22	1.81	0.80
1:K:269:LEU:HA	1:K:272:ILE:CD1	2.11	0.80
1:D:562:LYS:CE	1:I:562:LYS:HE2	2.09	0.80
1:K:485:PHE:HD2	1:K:492:PHE:O	1.65	0.80
1:I:284:MET:HG2	1:I:286:THR:CG2	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:572:PHE:O	1:I:576:GLN:NE2	2.14	0.80
1:A:267:SER:HB3	1:A:396:ILE:HG13	1.64	0.80
1:A:878:ASP:HB3	1:A:881:VAL:HG22	1.63	0.79
1:H:441:LEU:CG	1:H:498:VAL:CG1	2.60	0.79
1:H:855:ARG:NE	1:K:555:ALA:HB3	1.97	0.79
1:K:286:THR:CB	1:K:361:PRO:HB3	2.10	0.79
1:J:260:SER:O	1:J:264:GLY:N	2.16	0.79
1:E:433:GLU:O	1:E:436:LYS:HB2	1.82	0.79
1:A:234:MET:O	1:A:237:ILE:HG22	1.82	0.79
1:K:486:GLY:O	1:K:489:PRO:HD3	1.81	0.79
1:D:572:PHE:O	1:D:576:GLN:NE2	2.15	0.79
1:G:260:SER:O	1:G:264:GLY:N	2.16	0.79
1:I:434:PRO:HG2	1:I:488:HIS:CG	2.18	0.79
1:I:441:LEU:CG	1:I:498:VAL:CG1	2.61	0.79
1:A:363:TYR:CE1	1:A:383:CYS:SG	2.70	0.79
1:C:284:MET:HG2	1:C:286:THR:CG2	2.13	0.79
1:D:544:ASN:ND2	1:J:703:LYS:HE3	1.98	0.79
1:E:272:ILE:CG2	1:E:278:LEU:CD1	2.56	0.79
1:E:251:THR:HG22	1:E:252:LEU:N	1.96	0.79
1:F:642:LEU:HD22	1:F:643:GLY:H	1.47	0.79
1:D:229:PHE:HA	1:D:232:LYS:HG2	1.65	0.79
1:H:567:GLU:HG3	1:K:563:HIS:CE1	2.18	0.79
1:H:572:PHE:O	1:H:576:GLN:NE2	2.15	0.79
1:A:572:PHE:O	1:A:576:GLN:NE2	2.16	0.78
1:E:297:ASP:CG	1:E:300:ALA:HB3	2.08	0.78
1:K:257:VAL:CG2	1:K:359:ASP:HA	2.13	0.78
1:K:272:ILE:HG21	1:K:277:PHE:CD1	2.18	0.78
1:D:434:PRO:HG2	1:D:488:HIS:CG	2.17	0.78
1:F:260:SER:O	1:F:264:GLY:N	2.16	0.78
1:I:478:ASN:HD21	1:I:482:LYS:NZ	1.66	0.78
1:E:485:PHE:CE2	1:E:500:THR:OG1	2.34	0.78
1:H:855:ARG:HH11	1:K:555:ALA:CB	1.95	0.78
1:I:284:MET:SD	1:I:284:MET:N	2.56	0.78
1:I:486:GLY:O	1:I:489:PRO:HD3	1.84	0.78
1:A:257:VAL:CG2	1:A:359:ASP:HA	2.14	0.78
1:A:279:PRO:CB	1:A:322:GLN:HA	2.13	0.78
1:A:272:ILE:CG2	1:A:278:LEU:CD1	2.56	0.78
1:D:855:ARG:HD2	1:I:552:SER:HA	1.64	0.78
1:H:556:ALA:CB	1:K:855:ARG:HH21	1.97	0.78
1:H:610:ARG:HA	1:H:610:ARG:HE	1.49	0.78
1:I:257:VAL:CG2	1:I:359:ASP:HA	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:267:SER:HB3	1:I:396:ILE:HG13	1.65	0.78
1:K:269:LEU:CA	1:K:272:ILE:HD12	2.11	0.78
1:A:285:ILE:HG13	1:A:332:VAL:HG22	1.66	0.78
1:H:251:THR:HG22	1:H:252:LEU:N	1.97	0.78
1:L:260:SER:O	1:L:264:GLY:N	2.17	0.78
1:C:609:PRO:HB2	1:C:610:ARG:C	2.09	0.78
1:C:782:ALA:HB3	1:L:778:GLY:HA2	1.66	0.78
1:E:285:ILE:HG13	1:E:332:VAL:HG22	1.66	0.77
1:I:273:VAL:HG11	1:I:457:SER:CB	2.13	0.77
1:A:278:LEU:HD21	1:A:280:LYS:CD	2.14	0.77
1:B:260:SER:O	1:B:264:GLY:N	2.16	0.77
1:D:287:ARG:HH11	1:D:287:ARG:HG3	1.49	0.77
1:F:843:VAL:O	1:F:847:ASN:HB2	1.84	0.77
1:I:229:PHE:HA	1:I:232:LYS:HG2	1.66	0.77
1:A:273:VAL:HG11	1:A:457:SER:CB	2.14	0.77
1:E:614:ASN:OD1	1:E:616:ILE:HG22	1.84	0.77
1:I:441:LEU:HB3	1:I:498:VAL:HG11	1.67	0.77
1:K:267:SER:HB3	1:K:396:ILE:HG13	1.66	0.77
1:D:434:PRO:HB3	1:D:491:GLU:HG3	1.63	0.77
1:A:774:SER:OG	1:H:774:SER:HA	1.84	0.77
1:G:703:LYS:HG3	1:K:544:ASN:HD21	1.50	0.77
1:F:615:ILE:HD11	1:F:803:ARG:HE	1.49	0.77
1:H:556:ALA:HB2	1:K:855:ARG:CZ	2.15	0.77
1:I:225:ASP:O	1:I:229:PHE:CD1	2.37	0.77
1:K:441:LEU:HB3	1:K:498:VAL:HG11	1.67	0.77
1:C:260:SER:O	1:C:264:GLY:N	2.17	0.77
1:D:285:ILE:HG12	1:D:287:ARG:HB2	1.67	0.77
1:E:572:PHE:O	1:E:576:GLN:NE2	2.18	0.77
1:I:279:PRO:CB	1:I:322:GLN:HA	2.14	0.77
1:K:272:ILE:CG2	1:K:278:LEU:CD1	2.55	0.77
1:K:285:ILE:HG13	1:K:332:VAL:HG22	1.66	0.77
1:L:854:PRO:HB2	1:L:855:ARG:CZ	2.15	0.77
1:D:556:ALA:HA	1:I:855:ARG:CZ	2.15	0.77
1:E:267:SER:HB3	1:E:396:ILE:HG13	1.66	0.77
1:I:298:PRO:O	1:I:299:GLU:HB3	1.84	0.77
1:K:297:ASP:CG	1:K:300:ALA:HB3	2.10	0.77
1:E:279:PRO:CB	1:E:322:GLN:HA	2.15	0.77
1:C:775:GLY:HA3	1:L:782:ALA:N	2.00	0.77
1:F:854:PRO:HB2	1:F:855:ARG:NH2	1.99	0.77
1:H:878:ASP:HB3	1:H:881:VAL:HG22	1.66	0.77
1:I:234:MET:O	1:I:237:ILE:HG22	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:THR:HG22	1:D:252:LEU:N	2.00	0.76
1:H:267:SER:HB3	1:H:396:ILE:HG13	1.67	0.76
1:H:285:ILE:HG13	1:H:332:VAL:HG22	1.66	0.76
1:A:774:SER:HA	1:H:774:SER:OG	1.85	0.76
1:D:485:PHE:HD2	1:D:492:PHE:O	1.68	0.76
1:E:278:LEU:CD2	1:E:280:LYS:HD3	2.13	0.76
1:E:284:MET:HG2	1:E:286:THR:CG2	2.15	0.76
1:I:285:ILE:HG13	1:I:332:VAL:HG22	1.67	0.76
1:A:783:LEU:CD1	1:H:778:GLY:O	2.33	0.76
1:C:780:SER:CA	1:L:780:SER:N	2.48	0.76
1:D:376:LYS:NZ	1:D:379:ILE:HD12	2.01	0.76
1:E:225:ASP:C	1:E:229:PHE:HE1	1.93	0.76
1:H:257:VAL:CG2	1:H:359:ASP:HA	2.15	0.76
1:I:363:TYR:CE1	1:I:383:CYS:SG	2.71	0.76
1:D:257:VAL:CG2	1:D:359:ASP:HA	2.15	0.76
1:D:267:SER:HB3	1:D:396:ILE:HG13	1.67	0.76
1:E:269:LEU:HD23	1:E:270:GLU:N	2.01	0.76
1:H:244:VAL:HB	1:H:248:SER:OG	1.85	0.76
1:I:272:ILE:HG21	1:I:277:PHE:CD1	2.20	0.76
1:K:363:TYR:CE1	1:K:383:CYS:SG	2.72	0.76
1:B:615:ILE:HD11	1:B:803:ARG:HE	1.50	0.76
1:H:269:LEU:HD21	1:H:457:SER:HB2	1.68	0.76
1:I:251:THR:HG22	1:I:252:LEU:N	1.98	0.76
1:D:273:VAL:HG21	1:D:457:SER:CB	2.16	0.76
1:E:226:ASN:HA	1:E:229:PHE:CE1	2.21	0.76
1:E:273:VAL:HG11	1:E:457:SER:CB	2.14	0.76
1:K:273:VAL:CG1	1:K:457:SER:HB2	2.15	0.76
1:K:279:PRO:CB	1:K:322:GLN:HA	2.16	0.76
1:L:878:ASP:HB3	1:L:881:VAL:HG12	1.67	0.76
1:A:251:THR:HG22	1:A:252:LEU:N	1.98	0.76
1:D:486:GLY:O	1:D:489:PRO:HD3	1.85	0.76
1:A:434:PRO:HB3	1:A:491:GLU:CG	2.15	0.76
1:K:276:GLU:OE2	1:K:318:PHE:HE2	1.65	0.76
1:D:272:ILE:HG21	1:D:277:PHE:CD1	2.22	0.75
1:E:388:ARG:O	1:E:421:ARG:NH2	2.18	0.75
1:E:441:LEU:CG	1:E:498:VAL:CG1	2.62	0.75
1:H:273:VAL:CG1	1:H:457:SER:HB2	2.14	0.75
1:C:780:SER:HA	1:L:780:SER:N	2.01	0.75
1:E:257:VAL:CG2	1:E:359:ASP:HA	2.16	0.75
1:H:279:PRO:HB3	1:H:322:GLN:HA	1.68	0.75
1:I:375:LEU:N	1:I:375:LEU:HD23	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:843:VAL:O	1:L:847:ASN:HB2	1.87	0.75
1:D:269:LEU:HD23	1:D:270:GLU:N	2.00	0.75
1:D:285:ILE:HG13	1:D:332:VAL:HG22	1.67	0.75
1:G:284:MET:HG2	1:G:286:THR:CG2	2.15	0.75
1:H:441:LEU:HD21	1:H:498:VAL:HB	1.62	0.75
1:K:433:GLU:O	1:K:436:LYS:HB2	1.86	0.75
1:B:843:VAL:O	1:B:847:ASN:HB2	1.86	0.75
1:I:244:VAL:HB	1:I:248:SER:OG	1.86	0.75
1:C:615:ILE:HD11	1:C:803:ARG:HE	1.51	0.75
1:E:225:ASP:O	1:E:229:PHE:CD1	2.39	0.75
1:H:854:PRO:CB	1:H:855:ARG:NH1	2.41	0.75
1:K:284:MET:HG2	1:K:286:THR:CG2	2.17	0.75
1:A:377:ARG:HG2	1:A:377:ARG:HH21	1.51	0.75
1:A:441:LEU:HB3	1:A:498:VAL:HG11	1.68	0.75
1:A:778:GLY:O	1:H:783:LEU:CD1	2.35	0.75
1:E:308:PRO:HG3	1:E:344:ARG:HB2	1.67	0.75
1:K:474:LEU:HG	1:K:475:ALA:H	1.52	0.75
1:D:279:PRO:HB3	1:D:322:GLN:HB2	1.69	0.75
1:K:376:LYS:HA	1:K:376:LYS:HZ3	1.48	0.75
1:I:878:ASP:HB3	1:I:881:VAL:HG22	1.69	0.74
1:D:279:PRO:HB3	1:D:322:GLN:CA	2.17	0.74
1:E:244:VAL:HB	1:E:248:SER:OG	1.88	0.74
1:G:224:ASP:HB3	1:G:227:MET:HB2	1.68	0.74
1:H:269:LEU:HD23	1:H:270:GLU:N	2.02	0.74
1:I:388:ARG:O	1:I:421:ARG:NH2	2.20	0.74
1:K:308:PRO:HG3	1:K:344:ARG:HB2	1.68	0.74
1:A:286:THR:O	1:A:361:PRO:CG	2.35	0.74
1:D:562:LYS:HE3	1:I:562:LYS:CE	2.09	0.74
1:I:278:LEU:HD21	1:I:280:LYS:CD	2.14	0.74
1:I:434:PRO:HB3	1:I:491:GLU:CG	2.17	0.74
1:D:273:VAL:HG11	1:D:457:SER:CB	2.15	0.74
1:H:279:PRO:HB3	1:H:322:GLN:CA	2.18	0.74
1:A:388:ARG:O	1:A:421:ARG:NH2	2.20	0.74
1:C:780:SER:OG	1:C:783:LEU:HB2	1.87	0.74
1:D:284:MET:N	1:D:284:MET:SD	2.60	0.74
1:E:434:PRO:HB3	1:E:491:GLU:CG	2.17	0.74
1:H:273:VAL:HG21	1:H:457:SER:CB	2.17	0.74
1:H:441:LEU:HB3	1:H:498:VAL:HG11	1.69	0.74
1:I:286:THR:O	1:I:361:PRO:CG	2.36	0.74
1:J:843:VAL:O	1:J:847:ASN:HB2	1.88	0.74
1:L:615:ILE:HD11	1:L:803:ARG:HE	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:855:ARG:HD2	1:L:855:ARG:N	1.98	0.74
1:D:418:ARG:NH2	1:D:420:GLU:HB3	2.02	0.74
1:E:229:PHE:HA	1:E:232:LYS:HG2	1.70	0.74
1:H:562:LYS:HD2	1:K:559:ASP:OD1	1.88	0.74
1:A:778:GLY:CA	1:H:783:LEU:CG	2.66	0.74
1:K:478:ASN:HD21	1:K:482:LYS:NZ	1.71	0.74
1:D:269:LEU:HD21	1:D:457:SER:HB2	1.68	0.74
1:I:284:MET:HG2	1:I:286:THR:HG22	1.67	0.74
1:K:269:LEU:HD21	1:K:457:SER:HB2	1.67	0.74
1:C:774:SER:HA	1:L:774:SER:C	2.12	0.74
1:H:297:ASP:CG	1:H:300:ALA:HB3	2.13	0.74
1:L:610:ARG:HB3	1:L:613:ASP:OD1	1.88	0.74
1:E:310:LEU:N	1:E:310:LEU:HD23	2.02	0.73
1:D:286:THR:O	1:D:361:PRO:CG	2.36	0.73
1:H:278:LEU:HD22	1:H:279:PRO:O	1.89	0.73
1:I:273:VAL:CG1	1:I:457:SER:HB2	2.18	0.73
1:A:272:ILE:HG21	1:A:277:PHE:CD1	2.24	0.73
1:E:441:LEU:HB3	1:E:498:VAL:HG11	1.69	0.73
1:I:376:LYS:NZ	1:I:379:ILE:HD12	2.03	0.73
1:K:284:MET:N	1:K:284:MET:SD	2.59	0.73
1:A:455:VAL:HG12	1:A:501:GLY:N	2.04	0.73
1:D:308:PRO:HG3	1:D:344:ARG:HB2	1.68	0.73
1:C:775:GLY:HA2	1:L:780:SER:HB2	1.70	0.73
1:C:781:ALA:N	1:L:780:SER:CB	2.50	0.73
1:C:843:VAL:O	1:C:847:ASN:HB2	1.88	0.73
1:E:279:PRO:HB3	1:E:322:GLN:HB2	1.69	0.73
1:E:297:ASP:OD2	1:E:300:ALA:HB3	1.87	0.73
1:I:269:LEU:HD21	1:I:457:SER:HB2	1.66	0.73
1:I:455:VAL:HG12	1:I:501:GLY:N	2.03	0.73
1:D:279:PRO:HB3	1:D:322:GLN:HA	1.69	0.73
1:D:363:TYR:CE1	1:D:383:CYS:SG	2.71	0.73
1:D:610:ARG:HA	1:D:610:ARG:HE	1.54	0.73
1:E:273:VAL:CG1	1:E:457:SER:HB2	2.16	0.73
1:K:878:ASP:HB3	1:K:881:VAL:HG22	1.70	0.73
1:A:273:VAL:HG21	1:A:457:SER:CB	2.16	0.73
1:D:544:ASN:HD21	1:J:703:LYS:HG3	1.53	0.73
1:E:441:LEU:CD2	1:E:498:VAL:HG12	2.16	0.73
1:A:778:GLY:HA2	1:H:783:LEU:CB	2.19	0.73
1:C:774:SER:HB2	1:L:781:ALA:HB3	1.68	0.73
1:C:878:ASP:HB3	1:C:881:VAL:HG12	1.71	0.73
1:D:297:ASP:OD2	1:D:300:ALA:HB3	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:285:ILE:HG12	1:K:287:ARG:HB2	1.70	0.73
1:D:273:VAL:CG1	1:D:457:SER:HB2	2.16	0.73
1:D:455:VAL:HG12	1:D:501:GLY:N	2.04	0.73
1:E:455:VAL:HG12	1:E:501:GLY:N	2.03	0.73
1:K:251:THR:HG22	1:K:252:LEU:N	2.04	0.73
1:A:817:ASN:HB3	1:A:820:TYR:HB2	1.70	0.72
1:C:774:SER:CA	1:L:774:SER:O	2.37	0.72
1:D:284:MET:HG2	1:D:286:THR:HG23	1.70	0.72
1:D:441:LEU:CD2	1:D:498:VAL:HG12	2.14	0.72
1:H:455:VAL:HG12	1:H:501:GLY:N	2.04	0.72
1:L:611:GLU:H	1:L:612:PRO:HD2	1.53	0.72
1:I:269:LEU:HD11	1:I:457:SER:C	2.11	0.72
1:E:235:ILE:HD12	1:E:235:ILE:O	1.88	0.72
1:E:478:ASN:CG	1:E:482:LYS:NZ	2.47	0.72
1:H:286:THR:O	1:H:361:PRO:CG	2.36	0.72
1:K:244:VAL:HB	1:K:248:SER:OG	1.89	0.72
1:B:434:PRO:HG2	1:B:488:HIS:CG	2.24	0.72
1:D:441:LEU:HB3	1:D:498:VAL:HG11	1.71	0.72
1:I:225:ASP:C	1:I:229:PHE:HE1	1.98	0.72
1:I:269:LEU:HD23	1:I:270:GLU:N	2.03	0.72
1:I:308:PRO:HG3	1:I:344:ARG:HB2	1.70	0.72
1:K:272:ILE:HG21	1:K:277:PHE:HD1	1.53	0.72
1:A:269:LEU:HD23	1:A:270:GLU:N	2.04	0.72
1:A:286:THR:O	1:A:361:PRO:HG3	1.89	0.72
1:A:783:LEU:CG	1:H:778:GLY:HA2	2.20	0.72
1:D:269:LEU:HD23	1:D:269:LEU:C	2.15	0.72
1:K:434:PRO:HB3	1:K:491:GLU:CG	2.18	0.72
1:A:279:PRO:HB3	1:A:322:GLN:HB2	1.70	0.72
1:D:433:GLU:O	1:D:436:LYS:HB2	1.89	0.72
1:E:881:VAL:O	1:E:884:HIS:HB3	1.90	0.72
1:D:488:HIS:HB3	1:D:491:GLU:CG	2.20	0.72
1:E:287:ARG:HH11	1:E:287:ARG:HG3	1.54	0.72
1:G:843:VAL:O	1:G:847:ASN:HB2	1.90	0.72
1:A:478:ASN:CG	1:A:482:LYS:NZ	2.47	0.72
1:I:478:ASN:CG	1:I:482:LYS:NZ	2.47	0.72
1:E:269:LEU:HD21	1:E:457:SER:HB2	1.69	0.72
1:H:286:THR:O	1:H:361:PRO:HB3	1.90	0.72
1:J:615:ILE:HD11	1:J:803:ARG:HE	1.53	0.72
1:E:286:THR:O	1:E:361:PRO:CG	2.38	0.71
1:G:609:PRO:HB2	1:G:610:ARG:C	2.15	0.71
1:H:284:MET:HG2	1:H:286:THR:HG23	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:ILE:CG2	1:D:278:LEU:H	2.03	0.71
1:I:272:ILE:HG23	1:I:278:LEU:HD13	1.70	0.71
1:K:273:VAL:HG21	1:K:457:SER:CB	2.17	0.71
1:D:388:ARG:O	1:D:421:ARG:NH2	2.24	0.71
1:H:272:ILE:HG23	1:H:278:LEU:H	1.56	0.71
1:K:388:ARG:O	1:K:421:ARG:NH2	2.20	0.71
1:A:278:LEU:HD22	1:A:279:PRO:O	1.90	0.71
1:C:780:SER:HB2	1:L:780:SER:N	2.05	0.71
1:D:778:GLY:O	1:D:779:PHE:HD2	1.73	0.71
1:H:279:PRO:HB3	1:H:322:GLN:HB2	1.73	0.71
1:J:642:LEU:HD22	1:J:643:GLY:H	1.54	0.71
1:A:269:LEU:HD21	1:A:457:SER:HB2	1.68	0.71
1:D:225:ASP:O	1:D:229:PHE:CD1	2.41	0.71
1:E:272:ILE:HG23	1:E:278:LEU:HD13	1.72	0.71
1:I:286:THR:O	1:I:361:PRO:HG3	1.90	0.71
1:K:418:ARG:HE	1:K:420:GLU:HB3	1.55	0.71
1:K:455:VAL:HG12	1:K:501:GLY:N	2.05	0.71
1:A:485:PHE:HD2	1:A:492:PHE:O	1.72	0.71
1:H:269:LEU:HD23	1:H:269:LEU:C	2.16	0.71
1:H:272:ILE:HG21	1:H:277:PHE:HD1	1.53	0.71
1:H:478:ASN:CG	1:H:482:LYS:NZ	2.49	0.71
1:J:285:ILE:HD12	1:J:287:ARG:H	1.56	0.71
1:K:286:THR:O	1:K:361:PRO:CG	2.39	0.71
1:A:493:GLY:O	1:A:496:SER:HB3	1.90	0.71
1:A:778:GLY:HA3	1:H:783:LEU:CG	2.20	0.71
1:E:877:GLU:HA	1:E:882:ARG:NE	2.05	0.71
1:H:388:ARG:O	1:H:421:ARG:NH2	2.22	0.71
1:H:478:ASN:HD21	1:H:482:LYS:HZ1	0.75	0.71
1:I:272:ILE:CG2	1:I:278:LEU:H	2.02	0.71
1:K:269:LEU:HD23	1:K:270:GLU:N	2.06	0.71
1:K:454:GLY:O	1:K:500:THR:HB	1.91	0.71
1:A:229:PHE:O	1:A:233:LYS:HG2	1.90	0.70
1:A:273:VAL:CG1	1:A:457:SER:HB2	2.17	0.70
1:D:272:ILE:HG23	1:D:278:LEU:H	1.56	0.70
1:E:273:VAL:HG21	1:E:457:SER:CB	2.19	0.70
1:I:286:THR:O	1:I:361:PRO:HB3	1.91	0.70
1:I:454:GLY:O	1:I:500:THR:HB	1.91	0.70
1:F:611:GLU:H	1:F:612:PRO:HD2	1.56	0.70
1:H:567:GLU:CG	1:K:563:HIS:HE1	2.04	0.70
1:K:286:THR:O	1:K:361:PRO:HB3	1.91	0.70
1:A:278:LEU:HB2	1:A:279:PRO:HD2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:LEU:CD2	1:A:498:VAL:HG12	2.17	0.70
1:C:611:GLU:H	1:C:612:PRO:HD2	1.56	0.70
1:D:226:ASN:N	1:D:229:PHE:HE1	1.89	0.70
1:H:272:ILE:CG2	1:H:278:LEU:CD1	2.58	0.70
1:K:229:PHE:O	1:K:233:LYS:HG2	1.91	0.70
1:G:687:LEU:HD22	1:G:845:MET:HE2	1.74	0.70
1:K:237:ILE:O	1:K:237:ILE:HD13	1.92	0.70
1:H:474:LEU:HG	1:H:475:ALA:H	1.56	0.70
1:K:272:ILE:CG2	1:K:278:LEU:H	2.03	0.70
1:H:272:ILE:CG2	1:H:278:LEU:H	2.04	0.70
1:K:272:ILE:HG23	1:K:278:LEU:H	1.55	0.70
1:A:272:ILE:HG23	1:A:278:LEU:HD13	1.71	0.70
1:C:472:ASN:OD1	1:C:475:ALA:HB3	1.91	0.70
1:H:308:PRO:HG3	1:H:344:ARG:HG3	1.73	0.70
1:K:441:LEU:HD21	1:K:498:VAL:HB	1.62	0.70
1:E:237:ILE:O	1:E:237:ILE:HD13	1.92	0.70
1:I:272:ILE:HG23	1:I:278:LEU:H	1.55	0.70
1:A:287:ARG:HH11	1:A:287:ARG:HG3	1.57	0.69
1:A:488:HIS:HB3	1:A:491:GLU:HG3	1.74	0.69
1:H:272:ILE:HG21	1:H:277:PHE:CD1	2.27	0.69
1:H:287:ARG:HH11	1:H:287:ARG:CG	2.04	0.69
1:I:279:PRO:HB3	1:I:322:GLN:CA	2.22	0.69
1:I:279:PRO:HB3	1:I:322:GLN:HA	1.73	0.69
1:I:441:LEU:HD21	1:I:498:VAL:HB	1.61	0.69
1:A:272:ILE:CG2	1:A:278:LEU:H	2.05	0.69
1:H:472:ASN:ND2	1:H:475:ALA:HB3	2.07	0.69
1:B:878:ASP:HB3	1:B:881:VAL:HG12	1.73	0.69
1:E:272:ILE:HG21	1:E:277:PHE:HD1	1.58	0.69
1:E:286:THR:O	1:E:361:PRO:HB3	1.93	0.69
1:A:279:PRO:HB3	1:A:322:GLN:CA	2.23	0.69
1:E:278:LEU:HD21	1:E:280:LYS:CD	2.20	0.69
1:E:363:TYR:CE1	1:E:383:CYS:SG	2.72	0.69
1:F:284:MET:SD	1:F:284:MET:N	2.65	0.69
1:G:854:PRO:HB2	1:G:855:ARG:NH2	2.08	0.69
1:H:278:LEU:O	1:H:278:LEU:HD13	1.93	0.69
1:H:375:LEU:HD23	1:H:375:LEU:N	2.07	0.69
1:I:273:VAL:HG21	1:I:457:SER:CB	2.20	0.69
1:K:269:LEU:CD2	1:K:457:SER:HB2	2.20	0.69
1:K:278:LEU:HD22	1:K:279:PRO:O	1.92	0.69
1:A:279:PRO:HB3	1:A:322:GLN:HA	1.74	0.69
1:D:307:PHE:CE1	1:D:345:LEU:CD2	2.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:478:ASN:CG	1:D:482:LYS:NZ	2.50	0.69
1:H:297:ASP:OD2	1:H:300:ALA:HB3	1.93	0.69
1:A:244:VAL:HB	1:A:248:SER:OG	1.91	0.69
1:A:272:ILE:HG21	1:A:277:PHE:HD1	1.58	0.69
1:A:286:THR:O	1:A:361:PRO:HB3	1.93	0.69
1:D:226:ASN:CA	1:D:229:PHE:CE1	2.75	0.69
1:D:226:ASN:CA	1:D:229:PHE:HE1	2.05	0.69
1:E:269:LEU:HD23	1:E:269:LEU:C	2.17	0.69
1:K:478:ASN:CG	1:K:482:LYS:NZ	2.50	0.69
1:H:377:ARG:HG2	1:H:377:ARG:HH21	1.57	0.69
1:I:269:LEU:CD2	1:I:457:SER:HB2	2.19	0.69
1:I:376:LYS:HA	1:I:376:LYS:HZ3	1.54	0.69
1:A:272:ILE:HG23	1:A:278:LEU:H	1.58	0.69
1:D:272:ILE:HG21	1:D:277:PHE:HD1	1.56	0.69
1:E:286:THR:O	1:E:361:PRO:HG3	1.92	0.69
1:H:229:PHE:O	1:H:233:LYS:HG2	1.93	0.69
1:I:279:PRO:HB3	1:I:322:GLN:HB2	1.73	0.69
1:K:225:ASP:O	1:K:229:PHE:HD1	1.76	0.69
1:D:229:PHE:O	1:D:233:LYS:HG2	1.93	0.69
1:A:297:ASP:OD2	1:A:300:ALA:HB3	1.93	0.69
1:A:307:PHE:CE1	1:A:345:LEU:CD2	2.75	0.69
1:D:286:THR:O	1:D:361:PRO:HG3	1.92	0.69
1:D:855:ARG:HH11	1:I:555:ALA:HB1	1.58	0.69
1:H:237:ILE:O	1:H:237:ILE:HD13	1.93	0.69
1:H:472:ASN:HD21	1:H:475:ALA:HB3	1.57	0.69
1:I:270:GLU:O	1:I:273:VAL:HG22	1.92	0.69
1:D:441:LEU:HD23	1:D:498:VAL:HB	0.69	0.68
1:E:339:THR:HG23	1:E:340:ASP:N	2.08	0.68
1:F:687:LEU:HD22	1:F:845:MET:HE2	1.76	0.68
1:H:339:THR:HG23	1:H:340:ASP:N	2.08	0.68
1:D:478:ASN:HD21	1:D:482:LYS:NZ	1.73	0.68
1:E:278:LEU:HD22	1:E:279:PRO:O	1.94	0.68
1:G:434:PRO:HG2	1:G:488:HIS:CG	2.28	0.68
1:I:272:ILE:HG21	1:I:277:PHE:HD1	1.58	0.68
1:A:339:THR:HG23	1:A:340:ASP:H	1.59	0.68
1:A:478:ASN:CG	1:A:482:LYS:HZ2	2.01	0.68
1:B:687:LEU:HD22	1:B:845:MET:HE2	1.76	0.68
1:D:269:LEU:CD2	1:D:457:SER:HB2	2.23	0.68
1:I:237:ILE:O	1:I:237:ILE:HD13	1.94	0.68
1:I:576:GLN:NE2	1:I:576:GLN:H	1.91	0.68
1:K:272:ILE:HG23	1:K:278:LEU:HD13	1.72	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:MET:HG2	1:A:286:THR:HG23	1.76	0.68
1:C:780:SER:HA	1:L:780:SER:OG	1.93	0.68
1:D:278:LEU:HB2	1:D:279:PRO:HD2	1.76	0.68
1:D:445:GLN:O	1:D:446:TYR:CD1	2.45	0.68
1:H:430:ASP:C	1:H:430:ASP:OD1	2.35	0.68
1:I:493:GLY:O	1:I:496:SER:HB3	1.93	0.68
1:A:269:LEU:CD2	1:A:457:SER:HB2	2.22	0.68
1:D:237:ILE:O	1:D:237:ILE:HD13	1.93	0.68
1:E:229:PHE:O	1:E:233:LYS:HG2	1.94	0.68
1:E:441:LEU:HD23	1:E:498:VAL:HB	0.68	0.68
1:H:286:THR:O	1:H:361:PRO:HG3	1.93	0.68
1:D:339:THR:HG23	1:D:340:ASP:N	2.09	0.68
1:D:485:PHE:CD2	1:D:492:PHE:HD1	2.12	0.68
1:E:284:MET:HG2	1:E:286:THR:HG22	1.75	0.68
1:I:433:GLU:O	1:I:436:LYS:HB2	1.93	0.68
1:K:272:ILE:CG2	1:K:277:PHE:HA	2.19	0.68
1:K:704:PRO:HA	1:L:843:VAL:HG21	1.75	0.68
1:H:433:GLU:O	1:H:436:LYS:HB2	1.94	0.68
1:H:434:PRO:HB3	1:H:491:GLU:CG	2.23	0.68
1:H:562:LYS:CE	1:K:562:LYS:CE	2.72	0.68
1:K:307:PHE:CE1	1:K:345:LEU:CD2	2.72	0.68
1:A:310:LEU:HD23	1:A:310:LEU:N	2.08	0.68
1:H:363:TYR:CE1	1:H:383:CYS:SG	2.71	0.68
1:H:855:ARG:HD2	1:K:552:SER:HA	1.75	0.68
1:L:434:PRO:HG2	1:L:488:HIS:CG	2.29	0.68
1:A:783:LEU:CG	1:H:778:GLY:CA	2.71	0.68
1:D:556:ALA:CA	1:I:855:ARG:CZ	2.72	0.68
1:H:270:GLU:O	1:H:273:VAL:HG22	1.94	0.68
1:H:279:PRO:HG2	1:H:325:LEU:CD2	2.23	0.68
1:I:434:PRO:HB3	1:I:491:GLU:CB	2.24	0.68
1:A:269:LEU:HD23	1:A:269:LEU:C	2.20	0.67
1:D:441:LEU:HD21	1:D:498:VAL:HB	1.65	0.67
1:E:260:SER:N	1:E:263:SER:HB3	2.09	0.67
1:H:268:VAL:O	1:H:272:ILE:HG13	1.94	0.67
1:I:260:SER:N	1:I:263:SER:HB3	2.08	0.67
1:D:286:THR:O	1:D:361:PRO:HB3	1.93	0.67
1:E:640:THR:HG21	1:E:706:LYS:HA	1.75	0.67
1:L:284:MET:N	1:L:284:MET:SD	2.66	0.67
1:A:235:ILE:O	1:A:235:ILE:HD12	1.93	0.67
1:C:687:LEU:HD22	1:C:845:MET:HE2	1.76	0.67
1:D:235:ILE:HD12	1:D:235:ILE:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:610:ARG:HD2	1:J:613:ASP:OD1	1.94	0.67
1:K:286:THR:O	1:K:361:PRO:HG3	1.94	0.67
1:A:284:MET:HG2	1:A:286:THR:HG22	1.75	0.67
1:D:694:THR:HG21	1:D:845:MET:HB2	1.75	0.67
1:I:229:PHE:O	1:I:233:LYS:HG2	1.93	0.67
1:I:276:GLU:CD	1:I:318:PHE:CE2	2.68	0.67
1:K:229:PHE:HA	1:K:232:LYS:HG2	1.76	0.67
1:D:278:LEU:O	1:D:278:LEU:HD13	1.94	0.67
1:H:454:GLY:O	1:H:500:THR:HB	1.95	0.67
1:E:615:ILE:H	1:E:615:ILE:HD12	1.59	0.67
1:K:235:ILE:HD12	1:K:235:ILE:O	1.95	0.67
1:I:278:LEU:HB2	1:I:279:PRO:HD2	1.77	0.67
1:K:278:LEU:HB2	1:K:279:PRO:HD2	1.77	0.67
1:A:783:LEU:HG	1:H:778:GLY:HA2	1.76	0.67
1:C:774:SER:OG	1:L:781:ALA:HB3	1.92	0.67
1:D:233:LYS:HE2	1:D:233:LYS:HA	1.75	0.67
1:E:279:PRO:HB3	1:E:322:GLN:CA	2.25	0.67
1:H:567:GLU:HG3	1:K:563:HIS:HE1	1.59	0.67
1:K:279:PRO:HB3	1:K:322:GLN:HA	1.77	0.67
1:H:276:GLU:OE2	1:H:318:PHE:CD2	2.48	0.67
1:H:855:ARG:NH1	1:K:555:ALA:HB1	2.09	0.67
1:A:230:ILE:O	1:A:234:MET:HG3	1.95	0.67
1:D:260:SER:N	1:D:263:SER:HB3	2.10	0.67
1:H:278:LEU:HB2	1:H:279:PRO:HD2	1.77	0.67
1:L:687:LEU:HD22	1:L:845:MET:HE2	1.77	0.67
1:A:445:GLN:O	1:A:446:TYR:CD1	2.47	0.66
1:H:230:ILE:O	1:H:234:MET:HG3	1.96	0.66
1:D:278:LEU:HD22	1:D:279:PRO:O	1.95	0.66
1:D:562:LYS:CE	1:I:562:LYS:HE3	2.16	0.66
1:E:279:PRO:HG2	1:E:325:LEU:CD2	2.22	0.66
1:G:578:GLN:HA	1:G:838:VAL:HG21	1.76	0.66
1:H:269:LEU:CD2	1:H:457:SER:HB2	2.23	0.66
1:K:279:PRO:HB3	1:K:322:GLN:HB2	1.75	0.66
1:E:270:GLU:O	1:E:273:VAL:HG22	1.95	0.66
1:H:694:THR:HG21	1:H:845:MET:HB2	1.77	0.66
1:K:430:ASP:OD1	1:K:430:ASP:C	2.38	0.66
1:A:270:GLU:O	1:A:273:VAL:HG22	1.96	0.66
1:E:279:PRO:HB3	1:E:322:GLN:HA	1.77	0.66
1:E:375:LEU:N	1:E:375:LEU:HD23	2.10	0.66
1:H:493:GLY:O	1:H:496:SER:HB3	1.96	0.66
1:H:855:ARG:NH1	1:K:555:ALA:CB	2.57	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:240:LEU:N	1:I:240:LEU:HD23	2.10	0.66
1:I:456:ILE:O	1:I:481:GLU:OE2	2.13	0.66
1:A:694:THR:HG21	1:A:845:MET:HB2	1.76	0.66
1:D:308:PRO:HG3	1:D:344:ARG:HG3	1.77	0.66
1:E:445:GLN:O	1:E:446:TYR:CD1	2.49	0.66
1:H:441:LEU:CD2	1:H:498:VAL:HG12	2.19	0.66
1:I:285:ILE:HG12	1:I:287:ARG:HB2	1.77	0.66
1:A:260:SER:N	1:A:263:SER:HB3	2.10	0.66
1:C:782:ALA:CB	1:L:778:GLY:HA2	2.26	0.66
1:E:434:PRO:CG	1:E:488:HIS:CG	2.78	0.66
1:H:272:ILE:CG2	1:H:277:PHE:HA	2.25	0.66
1:I:269:LEU:HD23	1:I:269:LEU:C	2.21	0.66
1:K:279:PRO:HB3	1:K:322:GLN:CA	2.26	0.66
1:A:237:ILE:O	1:A:237:ILE:HD13	1.95	0.66
1:A:441:LEU:HD21	1:A:498:VAL:HB	1.66	0.66
1:D:230:ILE:O	1:D:234:MET:HG3	1.95	0.66
1:E:434:PRO:HB3	1:E:491:GLU:CB	2.26	0.66
1:H:485:PHE:CD2	1:H:492:PHE:O	2.46	0.66
1:B:284:MET:N	1:B:284:MET:SD	2.69	0.66
1:E:230:ILE:O	1:E:234:MET:HG3	1.96	0.66
1:E:272:ILE:HG23	1:E:278:LEU:H	1.61	0.66
1:K:279:PRO:HG2	1:K:325:LEU:CD2	2.23	0.66
1:K:434:PRO:CG	1:K:488:HIS:CG	2.79	0.66
1:C:610:ARG:HB3	1:C:613:ASP:OD1	1.95	0.66
1:C:775:GLY:CA	1:L:782:ALA:H	2.05	0.66
1:D:493:GLY:O	1:D:496:SER:HB3	1.96	0.66
1:I:225:ASP:HB3	1:I:229:PHE:CZ	2.31	0.66
1:I:272:ILE:CG2	1:I:277:PHE:HA	2.22	0.66
1:K:230:ILE:O	1:K:234:MET:HG3	1.95	0.66
1:K:269:LEU:HD23	1:K:269:LEU:C	2.21	0.66
1:A:339:THR:HG23	1:A:340:ASP:N	2.09	0.66
1:A:441:LEU:HD23	1:A:498:VAL:HB	0.66	0.66
1:A:852:ARG:HA	1:A:855:ARG:CZ	2.26	0.66
1:D:552:SER:HA	1:I:855:ARG:HD2	1.78	0.66
1:E:240:LEU:N	1:E:240:LEU:HD23	2.10	0.66
1:H:307:PHE:CE1	1:H:345:LEU:CD2	2.76	0.66
1:H:492:PHE:O	1:H:492:PHE:HD1	1.78	0.66
1:I:278:LEU:HD22	1:I:279:PRO:O	1.96	0.66
1:K:268:VAL:O	1:K:272:ILE:HG13	1.96	0.66
1:E:272:ILE:CG2	1:E:278:LEU:H	2.09	0.65
1:I:230:ILE:O	1:I:234:MET:HG3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:322:GLN:O	1:K:326:THR:OG1	2.11	0.65
1:L:429:MET:HE2	1:L:437:GLY:HA2	1.78	0.65
1:B:429:MET:HE2	1:B:437:GLY:HA2	1.79	0.65
1:C:429:MET:HE2	1:C:437:GLY:HA2	1.78	0.65
1:C:434:PRO:HG2	1:C:488:HIS:CG	2.32	0.65
1:E:231:THR:O	1:E:235:ILE:HG22	1.97	0.65
1:H:285:ILE:CD1	1:H:286:THR:N	2.57	0.65
1:I:235:ILE:O	1:I:235:ILE:HD12	1.96	0.65
1:L:863:GLU:O	1:L:867:ALA:HB3	1.96	0.65
1:E:285:ILE:HG12	1:E:287:ARG:HB2	1.79	0.65
1:H:376:LYS:NZ	1:H:379:ILE:HD12	2.12	0.65
1:H:485:PHE:HE2	1:H:500:THR:OG1	1.80	0.65
1:K:233:LYS:HE2	1:K:233:LYS:HA	1.78	0.65
1:K:252:LEU:HD23	1:K:524:THR:HG21	1.77	0.65
1:D:240:LEU:N	1:D:240:LEU:HD23	2.10	0.65
1:E:272:ILE:HG21	1:E:277:PHE:CD1	2.32	0.65
1:H:396:ILE:HG22	1:H:425:VAL:HB	1.78	0.65
1:I:640:THR:HG21	1:I:706:LYS:HA	1.77	0.65
1:K:493:GLY:O	1:K:496:SER:HB3	1.96	0.65
1:D:257:VAL:HG22	1:D:359:ASP:HA	1.79	0.65
1:D:307:PHE:CD1	1:D:345:LEU:HD21	2.31	0.65
1:E:454:GLY:O	1:E:500:THR:HB	1.96	0.65
1:F:429:MET:HE2	1:F:437:GLY:HA2	1.78	0.65
1:H:339:THR:HG23	1:H:340:ASP:H	1.61	0.65
1:I:339:THR:HG23	1:I:340:ASP:N	2.11	0.65
1:K:275:HIS:CG	1:K:276:GLU:H	2.14	0.65
1:A:285:ILE:HG12	1:A:287:ARG:HB2	1.77	0.65
1:D:640:THR:HG21	1:D:706:LYS:HA	1.76	0.65
1:D:665:ASP:OD1	1:D:676:ARG:NH2	2.30	0.65
1:G:284:MET:HG2	1:G:286:THR:HG22	1.78	0.65
1:G:429:MET:HE2	1:G:437:GLY:HA2	1.77	0.65
1:H:485:PHE:CD2	1:H:492:PHE:HD1	2.15	0.65
1:H:567:GLU:CG	1:K:563:HIS:CE1	2.80	0.65
1:I:226:ASN:HA	1:I:229:PHE:CD1	2.32	0.65
1:J:429:MET:HE2	1:J:437:GLY:HA2	1.79	0.65
1:K:260:SER:N	1:K:263:SER:HB3	2.11	0.65
1:K:265:LYS:O	1:K:268:VAL:HG23	1.96	0.65
1:A:454:GLY:O	1:A:500:THR:HB	1.97	0.65
1:D:499:SER:O	1:D:500:THR:HG23	1.95	0.65
1:D:526:GLU:OE1	1:D:530:ARG:NH1	2.30	0.65
1:E:441:LEU:HD21	1:E:498:VAL:HB	1.68	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:524:THR:O	1:G:528:ILE:HG13	1.97	0.65
1:H:257:VAL:HG22	1:H:359:ASP:HA	1.79	0.65
1:I:363:TYR:CD2	1:I:407:THR:HB	2.31	0.65
1:A:396:ILE:HG22	1:A:425:VAL:HB	1.77	0.65
1:C:360:LEU:HB2	1:C:361:PRO:HD2	1.78	0.65
1:D:878:ASP:HB3	1:D:881:VAL:HG22	1.79	0.65
1:I:694:THR:HG21	1:I:845:MET:HB2	1.77	0.65
1:K:434:PRO:HG2	1:K:488:HIS:ND1	2.12	0.65
1:K:665:ASP:OD1	1:K:676:ARG:NH2	2.30	0.65
1:H:235:ILE:HD12	1:H:235:ILE:O	1.96	0.65
1:H:260:SER:N	1:H:263:SER:HB3	2.12	0.65
1:K:478:ASN:CG	1:K:482:LYS:HZ2	2.03	0.65
1:A:297:ASP:CG	1:A:300:ALA:HB3	2.20	0.65
1:A:363:TYR:CD2	1:A:407:THR:HB	2.32	0.65
1:H:308:PRO:HG3	1:H:344:ARG:HB2	1.79	0.65
1:I:376:LYS:HZ2	1:I:379:ILE:HD12	1.61	0.65
1:K:240:LEU:HD23	1:K:240:LEU:N	2.11	0.65
1:C:863:GLU:O	1:C:867:ALA:HB3	1.97	0.64
1:E:269:LEU:CD2	1:E:457:SER:HB2	2.24	0.64
1:F:863:GLU:O	1:F:867:ALA:HB3	1.97	0.64
1:I:238:ARG:NH2	1:I:356:SER:OG	2.30	0.64
1:I:257:VAL:HG22	1:I:359:ASP:HA	1.79	0.64
1:I:704:PRO:HA	1:J:843:VAL:HG21	1.78	0.64
1:C:284:MET:HG2	1:C:286:THR:HG23	1.78	0.64
1:D:231:THR:O	1:D:235:ILE:HG22	1.97	0.64
1:D:269:LEU:CA	1:D:272:ILE:HD12	2.20	0.64
1:D:270:GLU:O	1:D:273:VAL:HG22	1.97	0.64
1:G:665:ASP:OD1	1:G:676:ARG:NH1	2.31	0.64
1:J:578:GLN:HA	1:J:838:VAL:HG21	1.79	0.64
1:F:284:MET:HG2	1:F:286:THR:CG2	2.28	0.64
1:H:240:LEU:HD23	1:H:240:LEU:N	2.12	0.64
1:K:376:LYS:NZ	1:K:379:ILE:HD12	2.12	0.64
1:B:578:GLN:HA	1:B:838:VAL:HG21	1.80	0.64
1:D:854:PRO:HG2	1:D:855:ARG:HH22	1.62	0.64
1:E:226:ASN:HA	1:E:229:PHE:CD1	2.32	0.64
1:I:275:HIS:CG	1:I:276:GLU:H	2.16	0.64
1:K:257:VAL:HG22	1:K:359:ASP:HA	1.79	0.64
1:A:657:GLN:HE22	1:A:684:ALA:HA	1.62	0.64
1:D:363:TYR:CD2	1:D:407:THR:HB	2.31	0.64
1:E:456:ILE:O	1:E:481:GLU:OE2	2.16	0.64
1:H:238:ARG:NH2	1:H:356:SER:OG	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:610:ARG:HA	1:H:610:ARG:NE	2.12	0.64
1:I:287:ARG:HH11	1:I:287:ARG:CG	2.10	0.64
1:I:526:GLU:OE1	1:I:530:ARG:NH1	2.31	0.64
1:J:284:MET:N	1:J:284:MET:SD	2.68	0.64
1:A:238:ARG:NH2	1:A:356:SER:OG	2.30	0.64
1:C:611:GLU:N	1:C:612:PRO:HD2	2.12	0.64
1:G:843:VAL:HG21	1:H:704:PRO:HA	1.78	0.64
1:H:456:ILE:O	1:H:481:GLU:OE2	2.15	0.64
1:A:690:ARG:NH1	1:A:844:GLU:OE2	2.31	0.64
1:A:778:GLY:HA2	1:H:783:LEU:CG	2.28	0.64
1:G:854:PRO:HB2	1:G:855:ARG:CZ	2.27	0.64
1:H:272:ILE:HG12	1:H:278:LEU:CD1	2.28	0.64
1:H:526:GLU:OE1	1:H:530:ARG:NH1	2.31	0.64
1:H:665:ASP:OD1	1:H:676:ARG:NH2	2.31	0.64
1:H:855:ARG:HH21	1:K:556:ALA:HB2	1.62	0.64
1:D:268:VAL:O	1:D:272:ILE:HG13	1.98	0.64
1:D:279:PRO:O	1:D:280:LYS:HD2	1.98	0.64
1:D:286:THR:HB	1:D:361:PRO:CB	2.26	0.64
1:D:396:ILE:HG22	1:D:425:VAL:HB	1.79	0.64
1:D:690:ARG:NH1	1:D:844:GLU:OE2	2.31	0.64
1:E:275:HIS:CG	1:E:276:GLU:H	2.16	0.64
1:G:703:LYS:HE3	1:K:544:ASN:CG	2.22	0.64
1:I:252:LEU:HD23	1:I:524:THR:HG21	1.80	0.64
1:I:499:SER:O	1:I:500:THR:HG23	1.98	0.64
1:K:278:LEU:CD2	1:K:280:LYS:CD	2.67	0.64
1:K:574:ARG:H	1:K:575:PRO:HD2	1.62	0.64
1:A:257:VAL:HG22	1:A:359:ASP:HA	1.80	0.64
1:A:779:PHE:H	1:H:780:SER:HB3	1.63	0.64
1:D:252:LEU:HD23	1:D:524:THR:HG21	1.80	0.64
1:D:269:LEU:HD11	1:D:458:LYS:HB2	1.80	0.64
1:D:276:GLU:CD	1:D:318:PHE:CE2	2.72	0.64
1:E:278:LEU:HD13	1:E:278:LEU:O	1.97	0.64
1:E:843:VAL:HG21	1:F:704:PRO:HA	1.79	0.64
1:H:279:PRO:O	1:H:280:LYS:HD2	1.97	0.64
1:K:238:ARG:NH2	1:K:356:SER:OG	2.31	0.64
1:K:278:LEU:HD13	1:K:278:LEU:O	1.97	0.64
1:K:363:TYR:CD2	1:K:407:THR:HB	2.33	0.64
1:A:298:PRO:O	1:A:299:GLU:HB3	1.97	0.64
1:D:544:ASN:CG	1:J:703:LYS:HE3	2.23	0.64
1:H:486:GLY:O	1:H:489:PRO:HD3	1.98	0.64
1:H:499:SER:O	1:H:500:THR:HG23	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:526:GLU:OE1	1:K:530:ARG:NH1	2.31	0.64
1:D:855:ARG:NH2	1:I:556:ALA:CA	2.60	0.63
1:E:276:GLU:HG2	1:E:277:PHE:N	2.13	0.63
1:E:485:PHE:CD2	1:E:492:PHE:HD1	2.12	0.63
1:I:485:PHE:HE2	1:I:500:THR:OG1	1.77	0.63
1:A:434:PRO:HB3	1:A:491:GLU:CB	2.28	0.63
1:D:272:ILE:HG12	1:D:278:LEU:CD1	2.28	0.63
1:D:339:THR:HG23	1:D:340:ASP:H	1.62	0.63
1:D:434:PRO:HB3	1:D:491:GLU:CG	2.27	0.63
1:I:396:ILE:HG22	1:I:425:VAL:HB	1.79	0.63
1:A:775:GLY:CA	1:H:781:ALA:H	2.10	0.63
1:D:272:ILE:CG2	1:D:277:PHE:HA	2.25	0.63
1:E:339:THR:HG23	1:E:340:ASP:H	1.62	0.63
1:I:276:GLU:OE2	1:I:318:PHE:CD2	2.50	0.63
1:J:687:LEU:HD22	1:J:845:MET:HE2	1.80	0.63
1:K:310:LEU:N	1:K:310:LEU:HD23	2.12	0.63
1:K:694:THR:HG21	1:K:845:MET:HB2	1.79	0.63
1:E:278:LEU:HB2	1:E:279:PRO:HD2	1.80	0.63
1:E:478:ASN:CG	1:E:482:LYS:HZ2	2.07	0.63
1:I:308:PRO:HG3	1:I:344:ARG:HG3	1.80	0.63
1:A:363:TYR:N	1:A:363:TYR:CD1	2.66	0.63
1:A:665:ASP:OD1	1:A:676:ARG:NH2	2.31	0.63
1:E:238:ARG:NH2	1:E:356:SER:OG	2.32	0.63
1:E:276:GLU:OE2	1:E:318:PHE:CD2	2.48	0.63
1:E:690:ARG:NH1	1:E:844:GLU:OE2	2.32	0.63
1:H:445:GLN:O	1:H:446:TYR:CD1	2.51	0.63
1:H:806:ALA:O	1:H:809:SER:HB3	1.98	0.63
1:I:690:ARG:NH1	1:I:844:GLU:OE2	2.30	0.63
1:A:574:ARG:H	1:A:575:PRO:HD2	1.63	0.63
1:D:456:ILE:O	1:D:481:GLU:OE2	2.17	0.63
1:I:279:PRO:HG2	1:I:325:LEU:CD2	2.24	0.63
1:K:396:ILE:HG22	1:K:425:VAL:HB	1.80	0.63
1:K:485:PHE:HE2	1:K:500:THR:OG1	1.77	0.63
1:H:690:ARG:NH1	1:H:844:GLU:OE2	2.32	0.63
1:K:230:ILE:HG13	1:K:904:LEU:HD11	1.81	0.63
1:A:499:SER:O	1:A:500:THR:HG23	1.99	0.63
1:C:843:VAL:HG21	1:D:704:PRO:HA	1.80	0.63
1:I:485:PHE:CD2	1:I:492:PHE:HD1	2.17	0.63
1:I:665:ASP:OD1	1:I:676:ARG:NH2	2.32	0.63
1:K:492:PHE:O	1:K:492:PHE:HD1	1.81	0.63
1:A:272:ILE:CG2	1:A:277:PHE:HA	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:258:ILE:HG22	1:F:360:LEU:HD11	1.81	0.63
1:F:524:THR:O	1:F:528:ILE:HG13	1.98	0.63
1:F:878:ASP:HB3	1:F:881:VAL:HG12	1.80	0.63
1:H:363:TYR:CD2	1:H:407:THR:HB	2.34	0.63
1:H:640:THR:HG21	1:H:706:LYS:HA	1.81	0.63
1:I:268:VAL:O	1:I:272:ILE:HG13	1.98	0.63
1:L:524:THR:O	1:L:528:ILE:HG13	1.99	0.63
1:A:230:ILE:HG13	1:A:904:LEU:HD11	1.81	0.62
1:A:231:THR:O	1:A:235:ILE:HG22	1.98	0.62
1:J:863:GLU:O	1:J:867:ALA:HB3	1.99	0.62
1:A:286:THR:HB	1:A:361:PRO:CB	2.26	0.62
1:A:783:LEU:HG	1:H:778:GLY:CA	2.28	0.62
1:H:278:LEU:CD2	1:H:280:LYS:CD	2.69	0.62
1:I:231:THR:O	1:I:235:ILE:HG22	1.99	0.62
1:K:499:SER:O	1:K:500:THR:HG23	1.99	0.62
1:A:275:HIS:CG	1:A:276:GLU:H	2.17	0.62
1:A:640:THR:HG21	1:A:706:LYS:HA	1.79	0.62
1:D:559:ASP:OD2	1:I:854:PRO:CB	2.37	0.62
1:K:456:ILE:O	1:K:481:GLU:OE2	2.17	0.62
1:L:642:LEU:HD22	1:L:643:GLY:H	1.64	0.62
1:A:526:GLU:OE1	1:A:530:ARG:NH1	2.33	0.62
1:E:834:ALA:O	1:E:838:VAL:HB	1.99	0.62
1:F:429:MET:HE1	1:F:441:LEU:HB2	1.81	0.62
1:H:265:LYS:O	1:H:268:VAL:HG23	1.98	0.62
1:I:230:ILE:HG13	1:I:904:LEU:HD11	1.80	0.62
1:I:445:GLN:O	1:I:446:TYR:CD1	2.52	0.62
1:I:499:SER:O	1:I:500:THR:CG2	2.47	0.62
1:K:886:ASP:HA	1:K:889:ARG:HG2	1.81	0.62
1:A:376:LYS:NZ	1:A:379:ILE:HD12	2.14	0.62
1:B:308:PRO:HG3	1:B:344:ARG:HB2	1.81	0.62
1:F:308:PRO:HG3	1:F:344:ARG:HB2	1.82	0.62
1:F:360:LEU:HB2	1:F:361:PRO:HD2	1.80	0.62
1:G:472:ASN:OD1	1:G:475:ALA:HB3	1.99	0.62
1:H:307:PHE:CD1	1:H:345:LEU:HD21	2.34	0.62
1:I:307:PHE:CE1	1:I:345:LEU:CD2	2.77	0.62
1:I:339:THR:HG23	1:I:340:ASP:H	1.63	0.62
1:K:231:THR:O	1:K:235:ILE:HG22	1.98	0.62
1:K:423:ILE:HG22	1:K:450:LEU:HD13	1.81	0.62
1:B:665:ASP:OD1	1:B:676:ARG:NH1	2.33	0.62
1:F:434:PRO:HG2	1:F:488:HIS:CG	2.35	0.62
1:H:499:SER:O	1:H:500:THR:CG2	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:387:ILE:O	1:L:421:ARG:NH2	2.32	0.62
1:A:778:GLY:CA	1:H:783:LEU:HG	2.30	0.62
1:C:429:MET:HE1	1:C:441:LEU:HB2	1.81	0.62
1:D:574:ARG:H	1:D:575:PRO:HD2	1.65	0.62
1:E:230:ILE:HG13	1:E:904:LEU:HD11	1.82	0.62
1:F:611:GLU:N	1:F:612:PRO:HD2	2.14	0.62
1:F:854:PRO:HB2	1:F:855:ARG:CZ	2.30	0.62
1:G:863:GLU:O	1:G:867:ALA:HB3	2.00	0.62
1:H:231:THR:O	1:H:235:ILE:HG22	1.99	0.62
1:J:754:VAL:HG13	1:J:779:PHE:HD1	1.64	0.62
1:L:258:ILE:HG22	1:L:360:LEU:HD11	1.80	0.62
1:A:268:VAL:O	1:A:272:ILE:HG13	2.00	0.62
1:A:279:PRO:HG2	1:A:325:LEU:CD2	2.23	0.62
1:A:704:PRO:HA	1:B:843:VAL:HG21	1.80	0.62
1:F:387:ILE:O	1:F:421:ARG:NH2	2.33	0.62
1:F:609:PRO:HB2	1:F:610:ARG:C	2.24	0.62
1:K:339:THR:HG23	1:K:340:ASP:N	2.15	0.62
1:K:445:GLN:O	1:K:446:TYR:CD1	2.52	0.62
1:H:246:GLN:HG2	1:H:247:GLY:N	2.15	0.62
1:I:441:LEU:HD23	1:I:498:VAL:HB	0.63	0.62
1:K:238:ARG:HA	1:K:241:LEU:HD12	1.82	0.62
1:A:285:ILE:CD1	1:A:286:THR:N	2.62	0.62
1:E:294:LEU:HB3	1:E:352:ILE:HD13	1.80	0.62
1:G:258:ILE:HG22	1:G:360:LEU:HD11	1.82	0.62
1:K:499:SER:O	1:K:500:THR:CG2	2.48	0.62
1:K:690:ARG:NH1	1:K:844:GLU:OE2	2.33	0.62
1:A:430:ASP:C	1:A:430:ASP:OD1	2.43	0.61
1:B:429:MET:HE1	1:B:441:LEU:HB2	1.82	0.61
1:D:499:SER:O	1:D:500:THR:CG2	2.48	0.61
1:L:249:THR:OG1	1:L:531:GLU:OE1	2.17	0.61
1:A:265:LYS:O	1:A:268:VAL:HG23	2.00	0.61
1:A:328:LEU:HD13	1:A:343:ILE:HD13	1.82	0.61
1:A:456:ILE:O	1:A:481:GLU:OE2	2.18	0.61
1:B:258:ILE:HG22	1:B:360:LEU:HD11	1.82	0.61
1:D:454:GLY:O	1:D:500:THR:HG22	2.00	0.61
1:D:610:ARG:HA	1:D:610:ARG:NE	2.13	0.61
1:E:265:LYS:O	1:E:268:VAL:HG23	2.00	0.61
1:F:227:MET:HA	1:F:230:ILE:HG22	1.83	0.61
1:I:278:LEU:CD2	1:I:280:LYS:CD	2.78	0.61
1:K:488:HIS:CB	1:K:491:GLU:HG2	2.26	0.61
1:D:238:ARG:NH2	1:D:356:SER:OG	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:434:PRO:HB2	1:E:491:GLU:HG3	1.80	0.61
1:G:387:ILE:O	1:G:421:ARG:NH2	2.34	0.61
1:I:574:ARG:H	1:I:575:PRO:HD2	1.66	0.61
1:K:270:GLU:O	1:K:273:VAL:HG22	2.00	0.61
1:B:863:GLU:O	1:B:867:ALA:HB3	2.01	0.61
1:C:779:PHE:C	1:L:783:LEU:HD12	2.24	0.61
1:D:556:ALA:CA	1:I:855:ARG:NH2	2.61	0.61
1:E:257:VAL:HG22	1:E:359:ASP:HA	1.82	0.61
1:E:665:ASP:OD1	1:E:676:ARG:NH2	2.34	0.61
1:F:665:ASP:OD1	1:F:676:ARG:NH1	2.34	0.61
1:C:854:PRO:HB2	1:C:855:ARG:NH2	2.15	0.61
1:H:269:LEU:CA	1:H:272:ILE:HD12	2.24	0.61
1:H:284:MET:HG2	1:H:286:THR:HG22	1.80	0.61
1:H:434:PRO:HB3	1:H:491:GLU:CB	2.30	0.61
1:H:562:LYS:CE	1:K:562:LYS:HZ3	2.11	0.61
1:J:429:MET:HE1	1:J:441:LEU:HB2	1.81	0.61
1:L:665:ASP:OD1	1:L:676:ARG:NH1	2.33	0.61
1:A:456:ILE:HD12	1:A:457:SER:N	2.14	0.61
1:D:230:ILE:HG13	1:D:904:LEU:HD11	1.81	0.61
1:D:269:LEU:HA	1:D:272:ILE:CD1	2.20	0.61
1:H:286:THR:O	1:H:361:PRO:CB	2.48	0.61
1:I:286:THR:O	1:I:361:PRO:CB	2.49	0.61
1:A:278:LEU:HD13	1:A:278:LEU:O	2.00	0.61
1:A:775:GLY:HA3	1:H:780:SER:CB	2.19	0.61
1:C:387:ILE:O	1:C:421:ARG:NH2	2.34	0.61
1:D:279:PRO:O	1:D:280:LYS:CD	2.49	0.61
1:E:396:ILE:HG22	1:E:425:VAL:HB	1.83	0.61
1:E:486:GLY:O	1:E:489:PRO:HD3	2.00	0.61
1:E:526:GLU:OE1	1:E:530:ARG:NH1	2.33	0.61
1:J:387:ILE:O	1:J:421:ARG:NH2	2.34	0.61
1:K:276:GLU:CD	1:K:318:PHE:CE2	2.69	0.61
1:L:360:LEU:HB2	1:L:361:PRO:HD2	1.83	0.61
1:A:308:PRO:HG3	1:A:344:ARG:CB	2.30	0.61
1:D:285:ILE:CD1	1:D:286:THR:N	2.60	0.61
1:D:563:HIS:CD2	1:I:566:HIS:CD2	2.88	0.61
1:E:307:PHE:CE1	1:E:345:LEU:CD2	2.78	0.61
1:G:360:LEU:HB2	1:G:361:PRO:HD2	1.81	0.61
1:H:275:HIS:CG	1:H:276:GLU:H	2.18	0.61
1:H:294:LEU:HB3	1:H:352:ILE:HD13	1.81	0.61
1:H:556:ALA:HB3	1:K:855:ARG:HH21	1.65	0.61
1:I:269:LEU:CA	1:I:272:ILE:HD12	2.21	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:272:ILE:CG2	1:K:277:PHE:HD1	2.14	0.61
1:K:434:PRO:HB3	1:K:491:GLU:CB	2.31	0.61
1:C:782:ALA:HB3	1:L:778:GLY:CA	2.31	0.61
1:D:229:PHE:HA	1:D:232:LYS:CG	2.31	0.61
1:D:441:LEU:HB3	1:D:498:VAL:CG1	2.30	0.61
1:I:278:LEU:HD13	1:I:278:LEU:O	1.99	0.61
1:L:224:ASP:HB3	1:L:227:MET:HB2	1.82	0.61
1:L:429:MET:HE1	1:L:441:LEU:HB2	1.81	0.61
1:L:609:PRO:HB2	1:L:610:ARG:C	2.26	0.61
1:A:382:LEU:C	1:A:382:LEU:HD12	2.26	0.61
1:A:778:GLY:HA2	1:H:780:SER:OG	2.00	0.61
1:E:226:ASN:CA	1:E:229:PHE:CE1	2.84	0.61
1:E:308:PRO:HG3	1:E:344:ARG:HG3	1.83	0.61
1:E:657:GLN:HE22	1:E:684:ALA:HA	1.65	0.61
1:H:252:LEU:HD23	1:H:524:THR:HG21	1.83	0.61
1:H:255:ILE:HD11	1:H:355:LEU:HG	1.83	0.61
1:I:854:PRO:HB2	1:I:855:ARG:CZ	2.28	0.61
1:A:286:THR:O	1:A:361:PRO:CB	2.49	0.60
1:B:524:THR:O	1:B:528:ILE:HG13	2.01	0.60
1:C:524:THR:O	1:C:528:ILE:HG13	2.01	0.60
1:C:781:ALA:H	1:L:780:SER:N	1.97	0.60
1:A:441:LEU:HB3	1:A:498:VAL:CG1	2.30	0.60
1:D:307:PHE:CD1	1:D:345:LEU:CD2	2.84	0.60
1:D:454:GLY:O	1:D:500:THR:HB	2.01	0.60
1:E:499:SER:O	1:E:500:THR:HG23	2.01	0.60
1:E:574:ARG:H	1:E:575:PRO:HD2	1.66	0.60
1:H:270:GLU:HA	1:H:273:VAL:HG22	1.83	0.60
1:H:562:LYS:HE2	1:K:562:LYS:HZ3	1.63	0.60
1:H:854:PRO:HB3	1:K:559:ASP:OD2	2.00	0.60
1:I:277:PHE:HD1	1:I:278:LEU:H	1.48	0.60
1:C:665:ASP:OD1	1:C:676:ARG:NH1	2.34	0.60
1:C:774:SER:CA	1:L:774:SER:HA	2.31	0.60
1:D:363:TYR:N	1:D:363:TYR:CD1	2.68	0.60
1:D:434:PRO:CG	1:D:488:HIS:CG	2.83	0.60
1:D:454:GLY:O	1:D:500:THR:CG2	2.49	0.60
1:G:611:GLU:N	1:G:612:PRO:HD2	2.16	0.60
1:H:264:GLY:O	1:H:268:VAL:HG22	2.02	0.60
1:H:272:ILE:HG12	1:H:278:LEU:HD11	1.84	0.60
1:H:363:TYR:N	1:H:363:TYR:CD1	2.68	0.60
1:A:781:ALA:N	1:H:775:GLY:HA3	2.17	0.60
1:D:275:HIS:CG	1:D:276:GLU:H	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:485:PHE:HA	1:E:492:PHE:HE1	1.66	0.60
1:G:429:MET:HE1	1:G:441:LEU:HB2	1.82	0.60
1:H:276:GLU:HG2	1:H:277:PHE:N	2.16	0.60
1:H:556:ALA:HB2	1:K:855:ARG:NH2	2.16	0.60
1:K:363:TYR:N	1:K:363:TYR:CD1	2.68	0.60
1:A:272:ILE:HG12	1:A:278:LEU:CD1	2.32	0.60
1:A:433:GLU:O	1:A:436:LYS:HB2	2.00	0.60
1:A:454:GLY:O	1:A:500:THR:CG2	2.50	0.60
1:A:499:SER:O	1:A:500:THR:CG2	2.49	0.60
1:D:265:LYS:O	1:D:268:VAL:HG23	2.00	0.60
1:D:434:PRO:HB3	1:D:491:GLU:CB	2.30	0.60
1:D:854:PRO:HB2	1:D:855:ARG:CZ	2.25	0.60
1:H:574:ARG:H	1:H:575:PRO:HD2	1.66	0.60
1:L:575:PRO:O	1:L:578:GLN:HB3	2.01	0.60
1:B:611:GLU:N	1:B:612:PRO:HD2	2.16	0.60
1:D:272:ILE:HG12	1:D:278:LEU:HD11	1.84	0.60
1:D:480:ASN:HA	1:D:483:ASN:OD1	2.01	0.60
1:D:749:LYS:H	1:D:749:LYS:HD2	1.67	0.60
1:E:226:ASN:N	1:E:229:PHE:HE1	1.98	0.60
1:H:230:ILE:HG13	1:H:904:LEU:HD11	1.84	0.60
1:H:297:ASP:HB3	1:H:349:SER:C	2.27	0.60
1:H:576:GLN:NE2	1:H:576:GLN:H	2.00	0.60
1:I:265:LYS:O	1:I:268:VAL:HG23	2.01	0.60
1:I:363:TYR:N	1:I:363:TYR:CD1	2.69	0.60
1:J:524:THR:O	1:J:528:ILE:HG13	2.02	0.60
1:K:308:PRO:HG3	1:K:344:ARG:HG3	1.84	0.60
1:A:276:GLU:OE2	1:A:318:PHE:CD2	2.51	0.60
1:H:272:ILE:CG2	1:H:277:PHE:HD1	2.14	0.60
1:H:279:PRO:O	1:H:280:LYS:CD	2.50	0.60
1:J:285:ILE:HD13	1:J:332:VAL:HG22	1.84	0.60
1:K:376:LYS:HZ2	1:K:379:ILE:HD12	1.65	0.60
1:C:578:GLN:HA	1:C:838:VAL:HG21	1.82	0.60
1:D:423:ILE:HG22	1:D:450:LEU:HD13	1.83	0.60
1:I:269:LEU:HA	1:I:272:ILE:CD1	2.22	0.60
1:I:615:ILE:H	1:I:615:ILE:HD12	1.66	0.60
1:K:279:PRO:O	1:K:280:LYS:HD2	2.01	0.60
1:K:294:LEU:HB3	1:K:352:ILE:HD13	1.83	0.60
1:K:441:LEU:HD23	1:K:498:VAL:HB	0.62	0.60
1:K:454:GLY:O	1:K:500:THR:CG2	2.50	0.60
1:C:774:SER:CB	1:L:774:SER:CA	2.67	0.60
1:H:387:ILE:CG2	1:H:415:VAL:HG21	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:277:PHE:HD1	1:I:278:LEU:N	2.00	0.60
1:I:434:PRO:HB2	1:I:491:GLU:HG3	1.82	0.60
1:A:252:LEU:HD23	1:A:524:THR:HG21	1.83	0.60
1:A:297:ASP:HB3	1:A:349:SER:C	2.26	0.60
1:B:249:THR:OG1	1:B:531:GLU:OE1	2.19	0.60
1:C:854:PRO:HB2	1:C:855:ARG:CZ	2.32	0.60
1:D:246:GLN:HG2	1:D:247:GLY:N	2.16	0.60
1:H:434:PRO:CG	1:H:488:HIS:CG	2.84	0.60
1:I:246:GLN:HG2	1:I:247:GLY:N	2.16	0.60
1:K:264:GLY:O	1:K:268:VAL:HG22	2.02	0.60
1:C:249:THR:OG1	1:C:531:GLU:OE1	2.18	0.59
1:H:441:LEU:HD23	1:H:498:VAL:HB	0.64	0.59
1:H:556:ALA:CB	1:K:855:ARG:NH2	2.65	0.59
1:I:286:THR:HB	1:I:361:PRO:CB	2.26	0.59
1:J:360:LEU:HB2	1:J:361:PRO:HD2	1.84	0.59
1:L:611:GLU:N	1:L:612:PRO:HD2	2.16	0.59
1:C:627:TYR:OH	1:C:631:GLN:NE2	2.35	0.59
1:D:363:TYR:N	1:D:363:TYR:HD1	2.00	0.59
1:H:454:GLY:O	1:H:500:THR:CG2	2.50	0.59
1:H:889:ARG:HG3	1:H:890:ARG:N	2.17	0.59
1:I:297:ASP:HB3	1:I:349:SER:C	2.27	0.59
1:K:286:THR:O	1:K:361:PRO:CB	2.50	0.59
1:A:240:LEU:N	1:A:240:LEU:HD23	2.17	0.59
1:A:778:GLY:HA3	1:H:783:LEU:HG	1.84	0.59
1:D:255:ILE:HD11	1:D:355:LEU:HG	1.85	0.59
1:D:286:THR:O	1:D:361:PRO:CB	2.50	0.59
1:E:441:LEU:HB3	1:E:498:VAL:CG1	2.32	0.59
1:F:705:TYR:CE1	1:F:832:LYS:HD3	2.38	0.59
1:I:382:LEU:C	1:I:382:LEU:HD12	2.27	0.59
1:I:474:LEU:HG	1:I:475:ALA:H	1.67	0.59
1:I:478:ASN:CG	1:I:482:LYS:HZ2	2.11	0.59
1:K:232:LYS:HA	1:K:235:ILE:CG2	2.32	0.59
1:L:851:VAL:O	1:L:855:ARG:HD3	2.02	0.59
1:C:284:MET:N	1:C:284:MET:SD	2.74	0.59
1:E:363:TYR:N	1:E:363:TYR:CD1	2.68	0.59
1:H:441:LEU:HB3	1:H:498:VAL:CG1	2.32	0.59
1:H:478:ASN:CG	1:H:482:LYS:HZ2	2.10	0.59
1:I:485:PHE:CZ	1:I:500:THR:OG1	2.52	0.59
1:J:863:GLU:O	1:J:867:ALA:CB	2.50	0.59
1:K:456:ILE:HD12	1:K:457:SER:N	2.17	0.59
1:L:308:PRO:HG3	1:L:344:ARG:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:PHE:HA	1:A:232:LYS:HG2	1.84	0.59
1:B:387:ILE:O	1:B:421:ARG:NH2	2.35	0.59
1:D:264:GLY:O	1:D:268:VAL:HG22	2.02	0.59
1:D:272:ILE:CG2	1:D:277:PHE:HD1	2.15	0.59
1:D:278:LEU:CD2	1:D:280:LYS:CD	2.74	0.59
1:D:294:LEU:HB3	1:D:352:ILE:HD13	1.84	0.59
1:E:226:ASN:HA	1:E:229:PHE:HE1	1.67	0.59
1:J:665:ASP:OD1	1:J:676:ARG:NH1	2.35	0.59
1:K:377:ARG:HG2	1:K:377:ARG:HH21	1.68	0.59
1:A:363:TYR:N	1:A:363:TYR:HD1	1.99	0.59
1:A:843:VAL:HG21	1:B:704:PRO:HA	1.84	0.59
1:B:360:LEU:HB2	1:B:361:PRO:HD2	1.84	0.59
1:H:229:PHE:HA	1:H:232:LYS:HG2	1.83	0.59
1:H:377:ARG:HH21	1:H:377:ARG:CG	2.16	0.59
1:H:657:GLN:HE22	1:H:684:ALA:HA	1.66	0.59
1:I:229:PHE:HA	1:I:232:LYS:CG	2.32	0.59
1:L:627:TYR:OH	1:L:631:GLN:NE2	2.35	0.59
1:C:258:ILE:HG22	1:C:360:LEU:HD11	1.84	0.59
1:C:780:SER:CA	1:L:780:SER:HB3	2.31	0.59
1:D:232:LYS:HA	1:D:235:ILE:CG2	2.33	0.59
1:D:552:SER:O	1:I:855:ARG:HD2	2.03	0.59
1:D:855:ARG:CZ	1:I:556:ALA:HA	2.32	0.59
1:E:286:THR:HB	1:E:361:PRO:CB	2.28	0.59
1:F:578:GLN:HA	1:F:838:VAL:HG21	1.85	0.59
1:G:259:GLY:HA2	1:G:408:ALA:HB2	1.85	0.59
1:H:559:ASP:CG	1:K:854:PRO:CB	2.76	0.59
1:A:294:LEU:HB3	1:A:352:ILE:HD13	1.84	0.59
1:A:423:ILE:HG22	1:A:450:LEU:HD13	1.84	0.59
1:E:286:THR:O	1:E:361:PRO:CB	2.51	0.59
1:E:298:PRO:O	1:E:299:GLU:HB3	2.03	0.59
1:G:878:ASP:HB3	1:G:881:VAL:HG12	1.85	0.59
1:H:559:ASP:CG	1:K:854:PRO:HB2	2.28	0.59
1:I:454:GLY:O	1:I:500:THR:CG2	2.50	0.59
1:J:249:THR:OG1	1:J:531:GLU:OE1	2.17	0.59
1:A:279:PRO:CG	1:A:325:LEU:HD21	2.23	0.59
1:D:375:LEU:N	1:D:375:LEU:HD23	2.18	0.59
1:E:454:GLY:O	1:E:500:THR:CG2	2.50	0.59
1:H:456:ILE:HD12	1:H:457:SER:N	2.18	0.59
1:K:441:LEU:HB3	1:K:498:VAL:CG1	2.31	0.59
1:E:832:LYS:O	1:E:836:THR:HG22	2.02	0.59
1:H:286:THR:HB	1:H:361:PRO:CB	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:605:LEU:HD13	1:J:606:SER:O	2.03	0.59
1:A:264:GLY:O	1:A:268:VAL:HG22	2.02	0.58
1:E:889:ARG:HG3	1:E:890:ARG:N	2.17	0.58
1:H:263:SER:OG	1:H:397:SER:HA	2.03	0.58
1:I:263:SER:OG	1:I:397:SER:HA	2.02	0.58
1:I:264:GLY:O	1:I:268:VAL:HG22	2.03	0.58
1:I:322:GLN:O	1:I:326:THR:OG1	2.13	0.58
1:J:878:ASP:HB3	1:J:881:VAL:HG12	1.85	0.58
1:K:387:ILE:CG2	1:K:415:VAL:HG21	2.33	0.58
1:L:863:GLU:O	1:L:867:ALA:CB	2.51	0.58
1:A:434:PRO:CG	1:A:488:HIS:CG	2.84	0.58
1:D:263:SER:OG	1:D:397:SER:HA	2.03	0.58
1:E:575:PRO:O	1:E:578:GLN:HB3	2.03	0.58
1:I:269:LEU:HD21	1:I:457:SER:CA	2.33	0.58
1:H:307:PHE:CD1	1:H:345:LEU:CD2	2.86	0.58
1:A:639:LEU:O	1:A:642:LEU:HD23	2.03	0.58
1:D:376:LYS:HZ2	1:D:379:ILE:HD12	1.67	0.58
1:D:855:ARG:CZ	1:I:556:ALA:CA	2.81	0.58
1:E:499:SER:O	1:E:500:THR:CG2	2.52	0.58
1:H:267:SER:HB2	1:H:396:ILE:CD1	2.33	0.58
1:K:297:ASP:HB3	1:K:349:SER:C	2.29	0.58
1:C:690:ARG:NH1	1:C:844:GLU:OE2	2.36	0.58
1:E:226:ASN:CA	1:E:229:PHE:HE1	2.17	0.58
1:I:441:LEU:HB3	1:I:498:VAL:CG1	2.32	0.58
1:I:818:LYS:HE3	1:I:819:TYR:CZ	2.37	0.58
1:K:524:THR:O	1:K:528:ILE:HG13	2.04	0.58
1:A:454:GLY:O	1:A:500:THR:HG22	2.04	0.58
1:D:279:PRO:HG2	1:D:325:LEU:CD2	2.25	0.58
1:E:272:ILE:HG12	1:E:278:LEU:CD1	2.34	0.58
1:E:456:ILE:HD12	1:E:457:SER:N	2.18	0.58
1:E:871:LEU:O	1:E:874:PHE:HB3	2.02	0.58
1:I:485:PHE:CD2	1:I:492:PHE:O	2.53	0.58
1:B:854:PRO:HB2	1:B:855:ARG:NH2	2.19	0.58
1:E:524:THR:O	1:E:528:ILE:HG13	2.03	0.58
1:H:480:ASN:HA	1:H:483:ASN:OD1	2.03	0.58
1:I:226:ASN:N	1:I:229:PHE:HE1	2.01	0.58
1:I:454:GLY:O	1:I:500:THR:CB	2.52	0.58
1:K:363:TYR:N	1:K:363:TYR:HD1	2.01	0.58
1:K:454:GLY:O	1:K:500:THR:CB	2.52	0.58
1:L:690:ARG:NH1	1:L:844:GLU:OE2	2.37	0.58
1:G:255:ILE:HD11	1:G:355:LEU:HG	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:847:ASN:ND2	1:H:707:PHE:CZ	2.72	0.58
1:K:263:SER:OG	1:K:397:SER:HA	2.03	0.58
1:K:363:TYR:HD2	1:K:407:THR:HB	1.69	0.58
1:C:863:GLU:O	1:C:867:ALA:CB	2.52	0.58
1:D:272:ILE:HG23	1:D:278:LEU:HD13	1.79	0.58
1:E:232:LYS:HA	1:E:235:ILE:CG2	2.34	0.58
1:E:241:LEU:O	1:E:244:VAL:HG23	2.03	0.58
1:E:246:GLN:HG2	1:E:247:GLY:N	2.19	0.58
1:E:268:VAL:O	1:E:272:ILE:HG13	2.03	0.58
1:E:363:TYR:N	1:E:363:TYR:HD1	2.02	0.58
1:E:485:PHE:HE2	1:E:500:THR:OG1	1.84	0.58
1:H:298:PRO:O	1:H:299:GLU:HB3	2.03	0.58
1:I:610:ARG:HA	1:I:610:ARG:HE	1.69	0.58
1:J:611:GLU:N	1:J:612:PRO:HD2	2.18	0.58
1:K:269:LEU:HD21	1:K:457:SER:CA	2.34	0.58
1:D:376:LYS:HZ1	1:D:379:ILE:HD12	1.69	0.58
1:H:275:HIS:H	1:H:275:HIS:CD2	2.21	0.58
1:H:382:LEU:C	1:H:382:LEU:HD12	2.29	0.58
1:H:524:THR:O	1:H:528:ILE:HG13	2.04	0.58
1:I:272:ILE:CG2	1:I:277:PHE:HD1	2.17	0.58
1:I:294:LEU:HB3	1:I:352:ILE:HD13	1.85	0.58
1:J:611:GLU:HG3	1:J:611:GLU:O	2.04	0.58
1:A:272:ILE:CG2	1:A:277:PHE:HD1	2.17	0.57
1:A:377:ARG:HH21	1:A:377:ARG:CG	2.17	0.57
1:E:279:PRO:CG	1:E:325:LEU:HD21	2.25	0.57
1:E:454:GLY:O	1:E:500:THR:HG22	2.04	0.57
1:I:363:TYR:N	1:I:363:TYR:HD1	2.02	0.57
1:A:263:SER:OG	1:A:397:SER:HA	2.03	0.57
1:A:780:SER:HB3	1:H:779:PHE:N	2.19	0.57
1:B:863:GLU:O	1:B:867:ALA:CB	2.52	0.57
1:D:363:TYR:HD2	1:D:407:THR:HB	1.69	0.57
1:D:387:ILE:CG2	1:D:415:VAL:HG21	2.33	0.57
1:D:456:ILE:HD12	1:D:457:SER:N	2.20	0.57
1:E:363:TYR:CD2	1:E:407:THR:HB	2.39	0.57
1:G:690:ARG:NH1	1:G:844:GLU:OE2	2.37	0.57
1:K:287:ARG:HG3	1:K:287:ARG:HH11	1.69	0.57
1:D:657:GLN:HE22	1:D:684:ALA:HA	1.68	0.57
1:E:278:LEU:HD22	1:E:280:LYS:HG2	1.84	0.57
1:E:297:ASP:HB3	1:E:349:SER:C	2.29	0.57
1:E:436:LYS:O	1:E:440:ILE:HG13	2.04	0.57
1:E:704:PRO:HA	1:F:843:VAL:HG21	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:363:TYR:HD2	1:I:407:THR:HB	1.69	0.57
1:K:349:SER:O	1:K:352:ILE:HG13	2.05	0.57
1:K:485:PHE:CD2	1:K:492:PHE:HD1	2.18	0.57
1:A:774:SER:CA	1:H:774:SER:OG	2.52	0.57
1:C:781:ALA:N	1:L:780:SER:CA	2.65	0.57
1:F:690:ARG:NH1	1:F:844:GLU:OE2	2.37	0.57
1:K:225:ASP:O	1:K:229:PHE:CD1	2.57	0.57
1:C:703:LYS:HG3	1:I:544:ASN:HD21	1.69	0.57
1:D:855:ARG:CZ	1:I:556:ALA:N	2.67	0.57
1:H:376:LYS:HA	1:H:376:LYS:CE	2.34	0.57
1:I:456:ILE:HD12	1:I:457:SER:N	2.19	0.57
1:K:232:LYS:HG3	1:K:233:LYS:HE3	1.86	0.57
1:K:307:PHE:CD1	1:K:345:LEU:CD2	2.88	0.57
1:A:255:ILE:HD11	1:A:355:LEU:HG	1.85	0.57
1:A:279:PRO:O	1:A:280:LYS:HD2	2.04	0.57
1:A:474:LEU:HG	1:A:475:ALA:H	1.70	0.57
1:A:779:PHE:O	1:H:780:SER:HA	2.04	0.57
1:D:267:SER:HB2	1:D:396:ILE:CD1	2.34	0.57
1:D:478:ASN:CG	1:D:482:LYS:HZ2	2.11	0.57
1:E:387:ILE:CG2	1:E:415:VAL:HG21	2.35	0.57
1:E:548:MET:HG3	1:E:549:SER:N	2.19	0.57
1:H:454:GLY:O	1:H:500:THR:HG22	2.04	0.57
1:I:275:HIS:CD2	1:I:275:HIS:H	2.23	0.57
1:K:339:THR:HG23	1:K:340:ASP:H	1.68	0.57
1:A:258:ILE:HG22	1:A:360:LEU:HD11	1.87	0.57
1:A:363:TYR:HD2	1:A:407:THR:HB	1.68	0.57
1:B:259:GLY:HA2	1:B:408:ALA:HB2	1.87	0.57
1:F:863:GLU:O	1:F:867:ALA:CB	2.53	0.57
1:G:227:MET:HA	1:G:230:ILE:HG22	1.87	0.57
1:G:383:CYS:O	1:G:387:ILE:HG13	2.04	0.57
1:I:279:PRO:O	1:I:280:LYS:HD2	2.04	0.57
1:K:298:PRO:O	1:K:299:GLU:HB3	2.03	0.57
1:E:252:LEU:HD23	1:E:524:THR:HG21	1.86	0.57
1:F:259:GLY:HA2	1:F:408:ALA:HB2	1.86	0.57
1:H:296:ASN:C	1:H:298:PRO:HD3	2.29	0.57
1:H:423:ILE:HG22	1:H:450:LEU:HD13	1.86	0.57
1:I:296:ASN:C	1:I:298:PRO:HD3	2.30	0.57
1:K:276:GLU:OE1	1:K:303:ASP:CG	2.48	0.57
1:A:267:SER:CB	1:A:396:ILE:HG13	2.35	0.57
1:A:267:SER:HB2	1:A:396:ILE:CD1	2.35	0.57
1:C:774:SER:C	1:L:781:ALA:H	2.12	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:423:ILE:HG22	1:E:450:LEU:HD13	1.86	0.57
1:I:430:ASP:C	1:I:430:ASP:OD1	2.48	0.57
1:L:285:ILE:HD13	1:L:332:VAL:HG22	1.87	0.57
1:A:279:PRO:O	1:A:280:LYS:CD	2.53	0.57
1:A:387:ILE:CG2	1:A:415:VAL:HG21	2.34	0.57
1:A:524:THR:O	1:A:528:ILE:HG13	2.04	0.57
1:B:690:ARG:NH1	1:B:844:GLU:OE2	2.38	0.57
1:E:263:SER:HA	1:E:266:SER:OG	2.05	0.57
1:G:285:ILE:HD13	1:G:332:VAL:HG22	1.87	0.57
1:G:627:TYR:OH	1:G:631:GLN:NE2	2.38	0.57
1:H:552:SER:O	1:K:855:ARG:NE	2.38	0.57
1:H:855:ARG:CD	1:K:552:SER:HA	2.35	0.57
1:J:383:CYS:O	1:J:387:ILE:HG13	2.05	0.57
1:K:307:PHE:CD1	1:K:345:LEU:HD21	2.36	0.57
1:D:382:LEU:C	1:D:382:LEU:HD12	2.30	0.56
1:D:485:PHE:HE2	1:D:500:THR:OG1	1.84	0.56
1:E:224:ASP:OD2	1:E:227:MET:HB2	2.03	0.56
1:E:276:GLU:OE1	1:E:303:ASP:CG	2.48	0.56
1:F:249:THR:OG1	1:F:531:GLU:OE1	2.19	0.56
1:H:363:TYR:N	1:H:363:TYR:HD1	2.02	0.56
1:K:382:LEU:C	1:K:382:LEU:HD12	2.30	0.56
1:C:272:ILE:HG23	1:C:277:PHE:HA	1.87	0.56
1:D:492:PHE:O	1:D:492:PHE:HD1	1.87	0.56
1:E:671:LYS:N	1:E:671:LYS:HD2	2.20	0.56
1:H:363:TYR:HD2	1:H:407:THR:HB	1.68	0.56
1:A:278:LEU:HD22	1:A:280:LYS:HG2	1.88	0.56
1:A:441:LEU:CD2	1:A:498:VAL:CA	2.83	0.56
1:G:308:PRO:HG3	1:G:344:ARG:HB2	1.87	0.56
1:H:232:LYS:HA	1:H:235:ILE:CG2	2.35	0.56
1:H:276:GLU:OE1	1:H:303:ASP:CG	2.47	0.56
1:K:255:ILE:HD11	1:K:355:LEU:HG	1.86	0.56
1:K:272:ILE:HG12	1:K:278:LEU:CD1	2.34	0.56
1:K:275:HIS:H	1:K:275:HIS:CD2	2.24	0.56
1:K:278:LEU:HD22	1:K:280:LYS:HG2	1.87	0.56
1:K:300:ALA:C	1:K:301:LYS:HD3	2.30	0.56
1:K:376:LYS:HA	1:K:376:LYS:HZ1	1.66	0.56
1:B:755:MET:HE3	1:B:790:ALA:HB1	1.88	0.56
1:D:238:ARG:HA	1:D:241:LEU:HD12	1.87	0.56
1:D:436:LYS:O	1:D:440:ILE:HG13	2.05	0.56
1:D:562:LYS:HZ1	1:I:562:LYS:HZ1	1.54	0.56
1:E:237:ILE:HD12	1:E:241:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:754:VAL:HG13	1:J:779:PHE:CD1	2.40	0.56
1:K:237:ILE:HD12	1:K:241:LEU:HD11	1.86	0.56
1:K:277:PHE:HD1	1:K:278:LEU:H	1.52	0.56
1:K:640:THR:HG21	1:K:706:LYS:HA	1.88	0.56
1:D:297:ASP:HB3	1:D:349:SER:C	2.30	0.56
1:F:284:MET:HG2	1:F:286:THR:HG23	1.88	0.56
1:J:272:ILE:HG23	1:J:277:PHE:HA	1.87	0.56
1:J:627:TYR:HE2	1:J:628:TRP:CZ3	2.23	0.56
1:K:267:SER:HB2	1:K:396:ILE:CD1	2.34	0.56
1:K:276:GLU:OE2	1:K:318:PHE:CD2	2.59	0.56
1:A:376:LYS:HA	1:A:376:LYS:CE	2.35	0.56
1:B:285:ILE:HD13	1:B:332:VAL:HG22	1.86	0.56
1:D:308:PRO:HG3	1:D:344:ARG:CB	2.36	0.56
1:E:272:ILE:CG2	1:E:277:PHE:HD1	2.18	0.56
1:E:278:LEU:CD2	1:E:280:LYS:HG2	2.36	0.56
1:H:349:SER:O	1:H:352:ILE:HG13	2.06	0.56
1:I:232:LYS:HA	1:I:235:ILE:CG2	2.35	0.56
1:A:241:LEU:O	1:A:244:VAL:HG23	2.06	0.56
1:A:278:LEU:CD2	1:A:280:LYS:CD	2.79	0.56
1:D:576:GLN:NE2	1:D:576:GLN:H	2.04	0.56
1:G:863:GLU:O	1:G:867:ALA:CB	2.53	0.56
1:H:269:LEU:HA	1:H:272:ILE:CD1	2.25	0.56
1:J:653:ALA:HB2	1:J:845:MET:HE1	1.87	0.56
1:L:755:MET:HE3	1:L:790:ALA:HB1	1.88	0.56
1:C:774:SER:O	1:L:780:SER:CB	2.49	0.56
1:E:272:ILE:HG12	1:E:278:LEU:HD11	1.88	0.56
1:I:441:LEU:CD2	1:I:498:VAL:HG12	2.19	0.56
1:L:255:ILE:HD11	1:L:355:LEU:HG	1.88	0.56
1:L:272:ILE:HG23	1:L:277:PHE:HA	1.88	0.56
1:E:264:GLY:O	1:E:268:VAL:HG22	2.06	0.56
1:F:640:THR:HG21	1:F:706:LYS:HA	1.88	0.56
1:H:232:LYS:HG3	1:H:233:LYS:HE3	1.88	0.56
1:H:287:ARG:CG	1:H:287:ARG:NH1	2.68	0.56
1:I:310:LEU:HD23	1:I:310:LEU:N	2.20	0.56
1:K:279:PRO:O	1:K:280:LYS:CD	2.53	0.56
1:K:843:VAL:HG21	1:L:704:PRO:HA	1.86	0.56
1:A:308:PRO:HG3	1:A:344:ARG:HG3	1.88	0.56
1:C:383:CYS:O	1:C:387:ILE:HG13	2.06	0.56
1:D:441:LEU:CD2	1:D:498:VAL:CA	2.83	0.56
1:H:241:LEU:O	1:H:244:VAL:HG23	2.05	0.56
1:H:855:ARG:NH2	1:K:556:ALA:HA	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:272:ILE:HG12	1:I:278:LEU:CD1	2.36	0.56
1:K:241:LEU:O	1:K:244:VAL:HG23	2.05	0.56
1:D:226:ASN:HA	1:D:229:PHE:CD1	2.41	0.55
1:E:847:ASN:OD1	1:F:707:PHE:CE2	2.59	0.55
1:G:272:ILE:HG23	1:G:277:PHE:HA	1.88	0.55
1:I:434:PRO:CG	1:I:488:HIS:CG	2.87	0.55
1:C:611:GLU:O	1:C:611:GLU:HG3	2.05	0.55
1:C:755:MET:HE3	1:C:790:ALA:HB1	1.89	0.55
1:C:780:SER:HB3	1:L:779:PHE:CA	2.26	0.55
1:E:269:LEU:HD21	1:E:457:SER:CA	2.36	0.55
1:H:387:ILE:HG22	1:H:415:VAL:HG21	1.89	0.55
1:H:454:GLY:O	1:H:500:THR:CB	2.54	0.55
1:H:492:PHE:CD1	1:H:492:PHE:O	2.59	0.55
1:L:862:HIS:CD2	1:L:866:HIS:CD2	2.94	0.55
1:A:277:PHE:HD1	1:A:278:LEU:H	1.53	0.55
1:A:774:SER:OG	1:H:774:SER:CA	2.53	0.55
1:H:485:PHE:HA	1:H:492:PHE:HE1	1.72	0.55
1:K:375:LEU:HD23	1:K:375:LEU:N	2.22	0.55
1:K:454:GLY:O	1:K:500:THR:HG22	2.06	0.55
1:D:297:ASP:OD1	1:D:300:ALA:HB3	2.06	0.55
1:E:229:PHE:HA	1:E:232:LYS:CG	2.35	0.55
1:E:263:SER:OG	1:E:397:SER:HA	2.06	0.55
1:E:363:TYR:HD2	1:E:407:THR:HB	1.71	0.55
1:I:387:ILE:CG2	1:I:415:VAL:HG21	2.36	0.55
1:L:259:GLY:HA2	1:L:408:ALA:HB2	1.89	0.55
1:L:284:MET:HG2	1:L:286:THR:CG2	2.36	0.55
1:A:272:ILE:HG12	1:A:278:LEU:HD11	1.88	0.55
1:B:705:TYR:CE1	1:B:832:LYS:HD3	2.42	0.55
1:E:260:SER:H	1:E:263:SER:HB3	1.71	0.55
1:E:454:GLY:O	1:E:500:THR:CB	2.55	0.55
1:F:627:TYR:OH	1:F:631:GLN:NE2	2.38	0.55
1:J:854:PRO:HB2	1:J:855:ARG:NH2	2.21	0.55
1:K:246:GLN:HG2	1:K:247:GLY:N	2.21	0.55
1:A:780:SER:OG	1:A:783:LEU:HB2	2.07	0.55
1:D:298:PRO:O	1:D:299:GLU:HB3	2.06	0.55
1:D:308:PRO:HD2	1:D:344:ARG:O	2.06	0.55
1:E:269:LEU:HD11	1:E:457:SER:C	2.14	0.55
1:E:308:PRO:HG3	1:E:344:ARG:CB	2.37	0.55
1:E:441:LEU:CD2	1:E:498:VAL:CA	2.84	0.55
1:J:258:ILE:HG22	1:J:360:LEU:HD11	1.88	0.55
1:J:690:ARG:NH1	1:J:844:GLU:OE2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:610:ARG:HA	1:A:610:ARG:HE	1.70	0.55
1:B:255:ILE:HD11	1:B:355:LEU:HG	1.89	0.55
1:B:488:HIS:HB3	1:B:491:GLU:HG3	1.87	0.55
1:D:778:GLY:C	1:D:779:PHE:CD2	2.85	0.55
1:E:255:ILE:HD11	1:E:355:LEU:HG	1.87	0.55
1:E:279:PRO:HG3	1:E:321:ILE:HG22	1.88	0.55
1:F:255:ILE:HD11	1:F:355:LEU:HG	1.89	0.55
1:F:383:CYS:O	1:F:387:ILE:HG13	2.05	0.55
1:F:755:MET:HE3	1:F:790:ALA:HB1	1.89	0.55
1:G:297:ASP:HB3	1:G:349:SER:C	2.32	0.55
1:K:267:SER:CB	1:K:396:ILE:HG13	2.35	0.55
1:A:783:LEU:HB2	1:H:778:GLY:HA2	1.89	0.55
1:C:255:ILE:HD11	1:C:355:LEU:HG	1.88	0.55
1:D:275:HIS:H	1:D:275:HIS:CD2	2.24	0.55
1:D:458:LYS:HD2	1:D:458:LYS:C	2.31	0.55
1:E:694:THR:HG21	1:E:845:MET:HB2	1.87	0.55
1:H:434:PRO:HB2	1:H:491:GLU:HG3	1.86	0.55
1:I:307:PHE:CD1	1:I:345:LEU:CD2	2.90	0.55
1:J:284:MET:HG2	1:J:286:THR:CG2	2.37	0.55
1:K:474:LEU:HG	1:K:475:ALA:N	2.21	0.55
1:A:257:VAL:HG22	1:A:358:ILE:O	2.07	0.55
1:A:275:HIS:CD2	1:A:275:HIS:H	2.25	0.55
1:A:485:PHE:HE2	1:A:500:THR:OG1	1.82	0.55
1:C:704:PRO:HA	1:D:843:VAL:HG21	1.88	0.55
1:D:434:PRO:HB2	1:D:491:GLU:HG3	1.88	0.55
1:E:847:ASN:OD1	1:F:707:PHE:HE2	1.90	0.55
1:G:284:MET:N	1:G:284:MET:SD	2.76	0.55
1:H:565:PHE:HA	1:H:663:LEU:HD21	1.89	0.55
1:I:423:ILE:HG22	1:I:450:LEU:HD13	1.89	0.55
1:K:259:GLY:HA2	1:K:408:ALA:HB2	1.89	0.55
1:E:287:ARG:HH11	1:E:287:ARG:CG	2.20	0.55
1:E:377:ARG:HH21	1:E:377:ARG:HG2	1.71	0.55
1:F:772:HIS:HD2	1:F:775:GLY:O	1.89	0.55
1:G:653:ALA:HB2	1:G:845:MET:HE1	1.89	0.55
1:H:237:ILE:HD12	1:H:241:LEU:HD11	1.89	0.55
1:I:225:ASP:HB3	1:I:229:PHE:HZ	1.70	0.55
1:I:238:ARG:HA	1:I:241:LEU:HD12	1.89	0.55
1:I:258:ILE:HG22	1:I:360:LEU:HD11	1.89	0.55
1:I:279:PRO:O	1:I:280:LYS:CD	2.55	0.55
1:I:339:THR:O	1:I:340:ASP:HB3	2.07	0.55
1:I:454:GLY:H	1:I:500:THR:HG22	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:524:THR:O	1:I:528:ILE:HG13	2.07	0.55
1:K:485:PHE:CD2	1:K:492:PHE:O	2.54	0.55
1:L:322:GLN:O	1:L:326:THR:OG1	2.16	0.55
1:D:387:ILE:HG22	1:D:415:VAL:HG21	1.89	0.54
1:H:267:SER:CB	1:H:396:ILE:HG13	2.36	0.54
1:I:673:PRO:HD2	1:I:877:GLU:OE1	2.07	0.54
1:K:308:PRO:HD2	1:K:344:ARG:O	2.07	0.54
1:C:308:PRO:HG3	1:C:344:ARG:HB2	1.88	0.54
1:E:485:PHE:CD2	1:E:492:PHE:O	2.53	0.54
1:F:257:VAL:HG12	1:F:394:LEU:HB3	1.89	0.54
1:G:585:LEU:HD12	1:G:834:ALA:HB2	1.87	0.54
1:H:254:SER:HB2	1:H:356:SER:O	2.06	0.54
1:I:436:LYS:O	1:I:440:ILE:HG13	2.07	0.54
1:I:488:HIS:HB3	1:I:491:GLU:HG3	1.89	0.54
1:J:259:GLY:HA2	1:J:408:ALA:HB2	1.89	0.54
1:A:308:PRO:HD2	1:A:344:ARG:O	2.07	0.54
1:D:255:ILE:HA	1:D:392:ILE:O	2.07	0.54
1:G:264:GLY:HA2	1:G:267:SER:HB3	1.90	0.54
1:I:226:ASN:HA	1:I:229:PHE:CE1	2.42	0.54
1:I:277:PHE:CD1	1:I:278:LEU:N	2.75	0.54
1:J:627:TYR:OH	1:J:631:GLN:NE2	2.40	0.54
1:K:278:LEU:CD2	1:K:280:LYS:HG2	2.38	0.54
1:K:485:PHE:CD2	1:K:492:PHE:CE1	2.95	0.54
1:A:269:LEU:HD21	1:A:457:SER:CA	2.35	0.54
1:A:307:PHE:CD1	1:A:345:LEU:CD2	2.90	0.54
1:B:272:ILE:HG23	1:B:277:PHE:HA	1.90	0.54
1:D:556:ALA:N	1:I:855:ARG:CZ	2.71	0.54
1:K:576:GLN:NE2	1:K:576:GLN:H	2.06	0.54
1:K:657:GLN:HE22	1:K:684:ALA:HA	1.73	0.54
1:A:780:SER:HB3	1:H:779:PHE:O	2.07	0.54
1:B:488:HIS:HB3	1:B:491:GLU:CG	2.38	0.54
1:B:627:TYR:OH	1:B:631:GLN:NE2	2.41	0.54
1:C:227:MET:HA	1:C:230:ILE:HG22	1.88	0.54
1:C:285:ILE:HG12	1:C:329:ASN:O	2.08	0.54
1:D:457:SER:O	1:D:458:LYS:HB2	2.08	0.54
1:G:661:GLU:OE2	1:G:676:ARG:NH2	2.40	0.54
1:G:755:MET:HE3	1:G:790:ALA:HB1	1.90	0.54
1:I:226:ASN:N	1:I:229:PHE:CE1	2.76	0.54
1:J:233:LYS:HE3	1:J:900:LYS:HD2	1.90	0.54
1:L:383:CYS:O	1:L:387:ILE:HG13	2.07	0.54
1:A:276:GLU:OE1	1:A:303:ASP:OD1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:ILE:HD13	1:C:332:VAL:HG22	1.89	0.54
1:C:781:ALA:H	1:L:780:SER:HA	1.71	0.54
1:H:243:LYS:HG2	1:H:243:LYS:O	2.08	0.54
1:H:855:ARG:NH2	1:K:556:ALA:CA	2.70	0.54
1:K:233:LYS:HE3	1:K:233:LYS:N	2.23	0.54
1:K:454:GLY:H	1:K:500:THR:HG22	1.73	0.54
1:A:485:PHE:CD2	1:A:492:PHE:HD1	2.21	0.54
1:D:237:ILE:HD12	1:D:241:LEU:HD11	1.89	0.54
1:F:297:ASP:HB3	1:F:349:SER:C	2.33	0.54
1:I:454:GLY:O	1:I:500:THR:HG22	2.07	0.54
1:I:639:LEU:O	1:I:642:LEU:HD23	2.08	0.54
1:I:657:GLN:HE22	1:I:684:ALA:HA	1.73	0.54
1:B:383:CYS:O	1:B:387:ILE:HG13	2.07	0.54
1:D:257:VAL:HG22	1:D:358:ILE:O	2.08	0.54
1:D:276:GLU:OE1	1:D:303:ASP:OD1	2.24	0.54
1:E:480:ASN:HA	1:E:483:ASN:OD1	2.08	0.54
1:H:318:PHE:HD1	1:H:321:ILE:HD12	1.72	0.54
1:I:307:PHE:CD1	1:I:345:LEU:HD21	2.41	0.54
1:L:257:VAL:HG12	1:L:394:LEU:HB3	1.90	0.54
1:A:254:SER:HB2	1:A:356:SER:O	2.08	0.54
1:A:441:LEU:CB	1:A:498:VAL:CG1	2.86	0.54
1:C:259:GLY:HA2	1:C:408:ALA:HB2	1.89	0.54
1:C:441:LEU:HD23	1:C:498:VAL:HB	1.90	0.54
1:C:775:GLY:HA3	1:L:782:ALA:CB	2.38	0.54
1:D:441:LEU:CB	1:D:498:VAL:HG12	2.38	0.54
1:G:284:MET:HG2	1:G:286:THR:HG23	1.89	0.54
1:H:376:LYS:CE	1:H:376:LYS:CA	2.86	0.54
1:H:436:LYS:O	1:H:440:ILE:HG13	2.07	0.54
1:I:255:ILE:HD11	1:I:355:LEU:HG	1.90	0.54
1:K:278:LEU:CD2	1:K:280:LYS:CG	2.85	0.54
1:K:279:PRO:CG	1:K:325:LEU:HD21	2.28	0.54
1:L:227:MET:HA	1:L:230:ILE:HG22	1.89	0.54
1:A:485:PHE:CZ	1:A:500:THR:OG1	2.52	0.54
1:A:705:TYR:CE1	1:A:832:LYS:HD3	2.43	0.54
1:D:267:SER:CB	1:D:396:ILE:HG13	2.37	0.54
1:D:754:VAL:HA	1:D:779:PHE:CE1	2.43	0.54
1:D:889:ARG:HG3	1:D:890:ARG:N	2.23	0.54
1:F:575:PRO:O	1:F:578:GLN:HB3	2.08	0.54
1:F:754:VAL:HG21	1:F:783:LEU:HD22	1.89	0.54
1:G:257:VAL:HG12	1:G:394:LEU:HB3	1.90	0.54
1:G:705:TYR:CE1	1:G:832:LYS:HD3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:267:SER:HB2	1:I:396:ILE:CD1	2.38	0.54
1:A:277:PHE:HD1	1:A:278:LEU:N	2.06	0.53
1:B:257:VAL:HG12	1:B:394:LEU:HB3	1.89	0.53
1:D:269:LEU:HD11	1:D:457:SER:C	2.13	0.53
1:D:308:PRO:CG	1:D:344:ARG:HG3	2.38	0.53
1:D:441:LEU:CB	1:D:498:VAL:CG1	2.86	0.53
1:D:453:VAL:HG21	1:D:505:LEU:HD23	1.89	0.53
1:D:524:THR:O	1:D:528:ILE:HG13	2.09	0.53
1:E:671:LYS:O	1:E:672:HIS:CD2	2.61	0.53
1:K:308:PRO:HG3	1:K:344:ARG:CB	2.38	0.53
1:K:441:LEU:CD2	1:K:498:VAL:HG12	2.21	0.53
1:A:434:PRO:HG2	1:A:488:HIS:ND1	2.23	0.53
1:B:297:ASP:HB3	1:B:349:SER:C	2.33	0.53
1:E:272:ILE:CG2	1:E:277:PHE:HA	2.32	0.53
1:E:493:GLY:O	1:E:496:SER:HB3	2.08	0.53
1:F:264:GLY:HA2	1:F:267:SER:HB3	1.90	0.53
1:F:642:LEU:HD22	1:F:643:GLY:N	2.22	0.53
1:H:259:GLY:HA2	1:H:408:ALA:HB2	1.90	0.53
1:H:318:PHE:CD1	1:H:321:ILE:HD12	2.43	0.53
1:H:508:LYS:O	1:H:512:VAL:HG23	2.07	0.53
1:I:492:PHE:O	1:I:492:PHE:HD1	1.89	0.53
1:I:529:GLN:HG2	1:I:898:LEU:HD21	1.90	0.53
1:A:312:LEU:HD23	1:A:312:LEU:N	2.22	0.53
1:C:780:SER:CA	1:L:780:SER:CB	2.81	0.53
1:E:237:ILE:HD11	1:E:897:VAL:HG13	1.89	0.53
1:E:238:ARG:HA	1:E:241:LEU:HD12	1.89	0.53
1:E:307:PHE:CD1	1:E:345:LEU:CD2	2.91	0.53
1:E:492:PHE:O	1:E:492:PHE:HD1	1.92	0.53
1:H:855:ARG:CZ	1:K:556:ALA:N	2.71	0.53
1:J:607:PRO:HG3	1:J:762:ARG:HG3	1.89	0.53
1:K:889:ARG:HG3	1:K:890:ARG:N	2.22	0.53
1:A:339:THR:O	1:A:340:ASP:HB3	2.07	0.53
1:B:227:MET:HA	1:B:230:ILE:HG22	1.90	0.53
1:C:257:VAL:HG12	1:C:394:LEU:HB3	1.89	0.53
1:D:673:PRO:HD2	1:D:877:GLU:OE1	2.09	0.53
1:D:778:GLY:C	1:D:779:PHE:HD2	2.16	0.53
1:E:278:LEU:CD2	1:E:280:LYS:CD	2.85	0.53
1:E:393:ILE:HG23	1:E:422:THR:HB	1.91	0.53
1:H:376:LYS:HE2	1:H:376:LYS:N	2.24	0.53
1:K:270:GLU:HA	1:K:273:VAL:HG22	1.89	0.53
1:K:615:ILE:HD12	1:K:615:ILE:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:GLY:O	1:A:500:THR:CB	2.56	0.53
1:A:508:LYS:O	1:A:512:VAL:HG23	2.08	0.53
1:D:269:LEU:HD21	1:D:457:SER:CA	2.35	0.53
1:D:426:ILE:HD11	1:D:440:ILE:CG2	2.01	0.53
1:D:454:GLY:O	1:D:500:THR:CB	2.56	0.53
1:D:485:PHE:HA	1:D:492:PHE:HE1	1.73	0.53
1:E:257:VAL:HG22	1:E:358:ILE:O	2.08	0.53
1:E:488:HIS:HB3	1:E:491:GLU:HG3	1.88	0.53
1:H:296:ASN:HB2	1:H:354:ASP:OD2	2.09	0.53
1:I:485:PHE:HA	1:I:492:PHE:HE1	1.73	0.53
1:K:254:SER:HB2	1:K:356:SER:O	2.09	0.53
1:K:277:PHE:HD1	1:K:278:LEU:N	2.06	0.53
1:K:876:ARG:HB3	1:K:882:ARG:HH21	1.73	0.53
1:A:779:PHE:O	1:H:780:SER:HB3	2.08	0.53
1:D:376:LYS:HE2	1:D:376:LYS:N	2.23	0.53
1:E:259:GLY:HA2	1:E:408:ALA:HB2	1.90	0.53
1:J:755:MET:HE3	1:J:790:ALA:HB1	1.91	0.53
1:B:854:PRO:HB2	1:B:855:ARG:CZ	2.39	0.53
1:D:276:GLU:HG2	1:D:277:PHE:N	2.23	0.53
1:D:834:ALA:O	1:D:838:VAL:HB	2.08	0.53
1:G:449:LYS:C	1:G:451:GLY:H	2.17	0.53
1:G:607:PRO:HG3	1:G:762:ARG:HG3	1.91	0.53
1:I:237:ILE:HD12	1:I:241:LEU:HD11	1.90	0.53
1:I:300:ALA:C	1:I:301:LYS:HD3	2.34	0.53
1:I:308:PRO:HG3	1:I:344:ARG:CB	2.38	0.53
1:I:308:PRO:HD2	1:I:344:ARG:O	2.09	0.53
1:I:401:THR:HG22	1:I:402:ASP:O	2.07	0.53
1:I:508:LYS:O	1:I:512:VAL:HG23	2.09	0.53
1:J:609:PRO:HB2	1:J:610:ARG:C	2.33	0.53
1:K:387:ILE:HG22	1:K:415:VAL:HG21	1.90	0.53
1:L:480:ASN:HA	1:L:483:ASN:OD1	2.08	0.53
1:A:376:LYS:HZ1	1:A:379:ILE:HD12	1.74	0.53
1:E:270:GLU:HA	1:E:273:VAL:HG22	1.91	0.53
1:F:855:ARG:NH2	1:G:559:ASP:OD2	2.42	0.53
1:H:238:ARG:HA	1:H:241:LEU:HD12	1.90	0.53
1:I:889:ARG:HG3	1:I:890:ARG:N	2.23	0.53
1:K:257:VAL:HG22	1:K:358:ILE:O	2.08	0.53
1:A:387:ILE:HG22	1:A:415:VAL:HG21	1.90	0.53
1:A:485:PHE:HA	1:A:492:PHE:HE1	1.74	0.53
1:D:258:ILE:HG22	1:D:360:LEU:HD11	1.91	0.53
1:D:277:PHE:HD1	1:D:278:LEU:H	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:272:ILE:HG23	1:H:278:LEU:HD13	1.78	0.53
1:H:453:VAL:HG21	1:H:505:LEU:HD23	1.90	0.53
1:H:544:ASN:ND2	1:L:703:LYS:HE3	2.24	0.53
1:I:270:GLU:HA	1:I:273:VAL:HG22	1.89	0.53
1:K:258:ILE:HG22	1:K:360:LEU:HD11	1.91	0.53
1:A:237:ILE:HD12	1:A:241:LEU:HD11	1.91	0.53
1:D:259:GLY:HA2	1:D:408:ALA:HB2	1.91	0.53
1:D:279:PRO:HG3	1:D:321:ILE:HG22	1.91	0.53
1:E:308:PRO:HD2	1:E:344:ARG:O	2.09	0.53
1:F:640:THR:HG22	1:F:706:LYS:HG2	1.91	0.53
1:F:672:HIS:HD2	1:F:877:GLU:HB2	1.74	0.53
1:H:257:VAL:HG22	1:H:358:ILE:O	2.09	0.53
1:H:258:ILE:HG22	1:H:360:LEU:HD11	1.90	0.53
1:L:254:SER:HB2	1:L:356:SER:O	2.09	0.53
1:L:672:HIS:HD2	1:L:877:GLU:HB2	1.74	0.53
1:A:774:SER:HG	1:H:774:SER:HA	1.74	0.52
1:D:768:VAL:HG23	1:D:770:GLY:H	1.74	0.52
1:E:453:VAL:HG21	1:E:505:LEU:HD23	1.92	0.52
1:E:775:GLY:HA2	1:E:779:PHE:O	2.08	0.52
1:F:441:LEU:HD23	1:F:498:VAL:HB	1.91	0.52
1:G:672:HIS:HD2	1:G:877:GLU:HB2	1.73	0.52
1:K:508:LYS:O	1:K:512:VAL:HG23	2.09	0.52
1:A:484:TYR:HD1	1:A:485:PHE:CD1	2.27	0.52
1:A:781:ALA:H	1:H:775:GLY:HA3	1.75	0.52
1:A:889:ARG:HG3	1:A:890:ARG:N	2.23	0.52
1:C:672:HIS:HD2	1:C:877:GLU:HB2	1.75	0.52
1:E:485:PHE:CZ	1:E:500:THR:OG1	2.54	0.52
1:H:269:LEU:HD21	1:H:457:SER:CA	2.37	0.52
1:I:257:VAL:HG22	1:I:358:ILE:O	2.09	0.52
1:I:269:LEU:HD23	1:I:457:SER:OG	2.04	0.52
1:I:441:LEU:CD2	1:I:498:VAL:CA	2.85	0.52
1:K:276:GLU:OE1	1:K:303:ASP:OD1	2.27	0.52
1:L:297:ASP:HB3	1:L:349:SER:C	2.33	0.52
1:C:705:TYR:CE1	1:C:832:LYS:HD3	2.45	0.52
1:D:254:SER:HB2	1:D:356:SER:O	2.09	0.52
1:D:279:PRO:CG	1:D:325:LEU:HD21	2.27	0.52
1:D:296:ASN:C	1:D:298:PRO:HD3	2.34	0.52
1:E:307:PHE:CD1	1:E:345:LEU:HD21	2.43	0.52
1:G:441:LEU:HD23	1:G:498:VAL:HB	1.90	0.52
1:H:279:PRO:CG	1:H:325:LEU:HD21	2.28	0.52
1:J:585:LEU:HD12	1:J:834:ALA:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:255:ILE:HA	1:K:392:ILE:O	2.08	0.52
1:K:272:ILE:HG12	1:K:278:LEU:HD11	1.90	0.52
1:K:441:LEU:CB	1:K:498:VAL:CG1	2.87	0.52
1:A:263:SER:HA	1:A:266:SER:OG	2.09	0.52
1:A:270:GLU:HA	1:A:273:VAL:HG22	1.90	0.52
1:A:276:GLU:OE1	1:A:303:ASP:CG	2.52	0.52
1:A:375:LEU:N	1:A:375:LEU:HD23	2.23	0.52
1:A:672:HIS:HA	1:A:877:GLU:OE2	2.09	0.52
1:H:426:ILE:HD11	1:H:440:ILE:CG2	2.04	0.52
1:I:279:PRO:CG	1:I:325:LEU:HD21	2.29	0.52
1:I:381:GLU:HA	1:I:381:GLU:OE1	2.10	0.52
1:K:453:VAL:HG21	1:K:505:LEU:HD23	1.91	0.52
1:E:669:PHE:CD2	1:E:669:PHE:N	2.78	0.52
1:G:285:ILE:HG12	1:G:329:ASN:O	2.10	0.52
1:H:276:GLU:OE1	1:H:303:ASP:OD1	2.28	0.52
1:H:308:PRO:HD2	1:H:344:ARG:O	2.09	0.52
1:I:254:SER:HB2	1:I:356:SER:O	2.09	0.52
1:J:297:ASP:HB3	1:J:349:SER:C	2.35	0.52
1:K:286:THR:HB	1:K:361:PRO:CB	2.31	0.52
1:K:671:LYS:N	1:K:671:LYS:HD2	2.24	0.52
1:A:269:LEU:HD11	1:A:458:LYS:HB2	1.91	0.52
1:A:278:LEU:CD2	1:A:280:LYS:HG2	2.40	0.52
1:A:436:LYS:O	1:A:440:ILE:HG13	2.10	0.52
1:C:297:ASP:HB3	1:C:349:SER:C	2.33	0.52
1:C:585:LEU:HD12	1:C:834:ALA:HB2	1.91	0.52
1:C:774:SER:HA	1:L:774:SER:CA	2.40	0.52
1:E:646:ARG:NH2	1:G:534:GLU:OE2	2.43	0.52
1:I:276:GLU:OE1	1:I:303:ASP:OD1	2.27	0.52
1:I:376:LYS:HA	1:I:376:LYS:CE	2.39	0.52
1:A:246:GLN:HG2	1:A:247:GLY:N	2.24	0.52
1:A:614:ASN:OD1	1:A:616:ILE:HG22	2.09	0.52
1:E:255:ILE:HA	1:E:392:ILE:O	2.10	0.52
1:E:426:ILE:HD11	1:E:440:ILE:CG2	2.02	0.52
1:F:285:ILE:HG12	1:F:329:ASN:O	2.09	0.52
1:G:627:TYR:HE2	1:G:628:TRP:CZ3	2.28	0.52
1:I:453:VAL:HG21	1:I:505:LEU:HD23	1.90	0.52
1:I:854:PRO:HG2	1:I:855:ARG:HH22	1.73	0.52
1:K:269:LEU:HD23	1:K:457:SER:OG	2.03	0.52
1:K:492:PHE:CD1	1:K:492:PHE:O	2.61	0.52
1:D:508:LYS:O	1:D:512:VAL:HG23	2.09	0.52
1:H:308:PRO:CG	1:H:344:ARG:HG3	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:272:ILE:HG12	1:I:278:LEU:HD11	1.91	0.52
1:J:254:SER:HB2	1:J:356:SER:O	2.10	0.52
1:K:277:PHE:CD1	1:K:278:LEU:N	2.78	0.52
1:A:276:GLU:HG2	1:A:277:PHE:N	2.25	0.52
1:A:529:GLN:HG2	1:A:898:LEU:HD21	1.92	0.52
1:A:852:ARG:CG	1:A:855:ARG:HH21	2.22	0.52
1:D:529:GLN:HG2	1:D:898:LEU:HD21	1.92	0.52
1:E:285:ILE:CD1	1:E:286:THR:N	2.66	0.52
1:K:485:PHE:CE2	1:K:492:PHE:CD1	2.98	0.52
1:L:653:ALA:HB2	1:L:845:MET:HE1	1.91	0.52
1:A:307:PHE:CD1	1:A:345:LEU:HD21	2.42	0.52
1:E:246:GLN:CG	1:E:247:GLY:N	2.73	0.52
1:I:441:LEU:CB	1:I:498:VAL:CG1	2.88	0.52
1:J:705:TYR:CE1	1:J:832:LYS:HD3	2.45	0.52
1:K:276:GLU:HG2	1:K:277:PHE:N	2.25	0.52
1:K:376:LYS:HA	1:K:376:LYS:CE	2.40	0.52
1:K:775:GLY:HA2	1:K:779:PHE:O	2.09	0.52
1:A:472:ASN:HD21	1:A:475:ALA:HB3	1.74	0.51
1:A:779:PHE:O	1:H:780:SER:CB	2.58	0.51
1:D:434:PRO:HG2	1:D:488:HIS:ND1	2.25	0.51
1:E:441:LEU:CB	1:E:498:VAL:CG1	2.89	0.51
1:E:554:LEU:HA	1:E:557:SER:OG	2.10	0.51
1:H:434:PRO:HG2	1:H:488:HIS:CD2	2.45	0.51
1:H:441:LEU:CD2	1:H:498:VAL:CA	2.84	0.51
1:I:296:ASN:HB2	1:I:354:ASP:OD2	2.10	0.51
1:A:852:ARG:HG3	1:A:855:ARG:HH21	1.75	0.51
1:C:774:SER:CA	1:L:774:SER:CA	2.88	0.51
1:E:276:GLU:HG2	1:E:277:PHE:H	1.75	0.51
1:E:529:GLN:HG2	1:E:898:LEU:HD21	1.93	0.51
1:G:873:LYS:O	1:G:877:GLU:HG3	2.10	0.51
1:H:615:ILE:H	1:H:615:ILE:HD12	1.75	0.51
1:A:780:SER:HA	1:H:779:PHE:O	2.10	0.51
1:D:308:PRO:HG3	1:D:344:ARG:CG	2.41	0.51
1:D:376:LYS:HA	1:D:376:LYS:CE	2.40	0.51
1:H:339:THR:O	1:H:340:ASP:HB3	2.09	0.51
1:H:754:VAL:HA	1:H:779:PHE:CE1	2.46	0.51
1:J:617:ASP:OD1	1:J:617:ASP:N	2.44	0.51
1:A:269:LEU:CA	1:A:272:ILE:HD12	2.27	0.51
1:A:277:PHE:CD1	1:A:278:LEU:N	2.79	0.51
1:A:779:PHE:O	1:H:780:SER:CA	2.58	0.51
1:B:264:GLY:HA2	1:B:267:SER:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:653:ALA:HB2	1:C:845:MET:HE1	1.92	0.51
1:D:287:ARG:HH11	1:D:287:ARG:CG	2.17	0.51
1:D:817:ASN:HB3	1:D:820:TYR:HB2	1.93	0.51
1:E:296:ASN:HB2	1:E:354:ASP:OD2	2.11	0.51
1:F:254:SER:HB2	1:F:356:SER:O	2.09	0.51
1:F:269:LEU:HA	1:F:272:ILE:HD12	1.92	0.51
1:F:661:GLU:OE2	1:F:676:ARG:NH2	2.44	0.51
1:I:272:ILE:HG12	1:I:280:LYS:HG3	1.92	0.51
1:I:355:LEU:HD23	1:I:357:LEU:HD22	1.93	0.51
1:J:264:GLY:HA2	1:J:267:SER:HB3	1.93	0.51
1:K:285:ILE:N	1:K:285:ILE:CD1	2.74	0.51
1:L:661:GLU:OE2	1:L:676:ARG:NH2	2.43	0.51
1:A:376:LYS:CE	1:A:376:LYS:CA	2.89	0.51
1:A:783:LEU:CB	1:H:778:GLY:HA2	2.41	0.51
1:C:264:GLY:HA2	1:C:267:SER:HB3	1.91	0.51
1:C:873:LYS:O	1:C:877:GLU:HG3	2.11	0.51
1:D:855:ARG:HH11	1:I:555:ALA:CB	2.23	0.51
1:E:376:LYS:HA	1:E:376:LYS:HZ2	1.72	0.51
1:E:376:LYS:HA	1:E:376:LYS:HZ3	1.70	0.51
1:F:262:SER:O	1:F:266:SER:OG	2.29	0.51
1:F:653:ALA:HB2	1:F:845:MET:HE1	1.92	0.51
1:G:254:SER:HB2	1:G:356:SER:O	2.10	0.51
1:H:279:PRO:HG3	1:H:321:ILE:HG22	1.92	0.51
1:I:233:LYS:HE2	1:I:233:LYS:HA	1.93	0.51
1:I:259:GLY:HA2	1:I:408:ALA:HB2	1.92	0.51
1:I:275:HIS:CG	1:I:276:GLU:N	2.78	0.51
1:I:308:PRO:CG	1:I:344:ARG:HG3	2.41	0.51
1:I:387:ILE:HG22	1:I:415:VAL:HG21	1.92	0.51
1:L:640:THR:HG21	1:L:706:LYS:HA	1.93	0.51
1:B:441:LEU:HD23	1:B:498:VAL:HB	1.93	0.51
1:E:478:ASN:HD21	1:E:482:LYS:NZ	1.88	0.51
1:I:278:LEU:HD22	1:I:280:LYS:HG2	1.93	0.51
1:J:886:ASP:O	1:J:889:ARG:HB3	2.10	0.51
1:K:284:MET:O	1:K:286:THR:HG23	2.11	0.51
1:L:585:LEU:HD12	1:L:834:ALA:HB2	1.91	0.51
1:H:855:ARG:CD	1:K:555:ALA:CB	2.44	0.51
1:I:285:ILE:N	1:I:285:ILE:CD1	2.73	0.51
1:I:287:ARG:CG	1:I:287:ARG:NH1	2.70	0.51
1:I:480:ASN:HA	1:I:483:ASN:OD1	2.10	0.51
1:K:237:ILE:HD11	1:K:897:VAL:HG13	1.93	0.51
1:K:339:THR:O	1:K:340:ASP:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:565:PHE:HA	1:K:663:LEU:HD21	1.93	0.51
1:L:279:PRO:HG2	1:L:325:LEU:HD21	1.93	0.51
1:A:349:SER:O	1:A:352:ILE:HG13	2.11	0.51
1:B:254:SER:HB2	1:B:356:SER:O	2.09	0.51
1:D:318:PHE:HD1	1:D:321:ILE:HD12	1.76	0.51
1:F:272:ILE:HG23	1:F:277:PHE:HA	1.93	0.51
1:H:272:ILE:HG23	1:H:278:LEU:N	2.23	0.51
1:H:441:LEU:CB	1:H:498:VAL:CG1	2.88	0.51
1:H:562:LYS:HB2	1:K:562:LYS:HE3	1.91	0.51
1:I:272:ILE:HG23	1:I:278:LEU:N	2.25	0.51
1:K:672:HIS:HA	1:K:877:GLU:OE2	2.10	0.51
1:L:441:LEU:HD23	1:L:498:VAL:HB	1.93	0.51
1:A:441:LEU:CB	1:A:498:VAL:HG12	2.41	0.51
1:A:780:SER:OG	1:H:778:GLY:HA2	2.11	0.51
1:B:449:LYS:C	1:B:451:GLY:H	2.19	0.51
1:B:661:GLU:OE2	1:B:676:ARG:NH2	2.44	0.51
1:B:672:HIS:HD2	1:B:877:GLU:HB2	1.74	0.51
1:C:640:THR:HG22	1:C:706:LYS:HG2	1.92	0.51
1:C:757:PHE:CE1	1:C:777:GLY:HA3	2.45	0.51
1:E:382:LEU:HD12	1:E:382:LEU:C	2.35	0.51
1:H:263:SER:HA	1:H:266:SER:OG	2.10	0.51
1:H:817:ASN:HB3	1:H:820:TYR:HB2	1.93	0.51
1:J:262:SER:O	1:J:266:SER:OG	2.29	0.51
1:J:640:THR:HG22	1:J:706:LYS:HG2	1.93	0.51
1:K:441:LEU:CD2	1:K:498:VAL:CA	2.85	0.51
1:C:254:SER:HB2	1:C:356:SER:O	2.10	0.51
1:E:376:LYS:HZ3	1:E:379:ILE:HD12	1.76	0.51
1:H:457:SER:O	1:H:458:LYS:HB2	2.11	0.51
1:H:815:LEU:O	1:H:815:LEU:HD22	2.11	0.51
1:H:855:ARG:NH2	1:K:556:ALA:HB2	2.25	0.51
1:K:376:LYS:CE	1:K:376:LYS:CA	2.89	0.51
1:K:376:LYS:HE2	1:K:376:LYS:N	2.26	0.51
1:K:393:ILE:HG23	1:K:422:THR:HB	1.93	0.51
1:K:401:THR:HG22	1:K:402:ASP:O	2.10	0.51
1:L:640:THR:HG22	1:L:706:LYS:HG2	1.93	0.51
1:A:232:LYS:HG3	1:A:233:LYS:HE3	1.94	0.50
1:A:834:ALA:O	1:A:838:VAL:HB	2.11	0.50
1:B:585:LEU:HD12	1:B:834:ALA:HB2	1.92	0.50
1:D:233:LYS:CA	1:D:233:LYS:CE	2.89	0.50
1:D:277:PHE:HD1	1:D:278:LEU:N	2.09	0.50
1:D:418:ARG:HH21	1:D:420:GLU:CB	2.18	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:615:ILE:H	1:D:615:ILE:HD12	1.75	0.50
1:E:258:ILE:HG22	1:E:360:LEU:HD11	1.93	0.50
1:E:508:LYS:O	1:E:512:VAL:HG23	2.11	0.50
1:H:260:SER:H	1:H:263:SER:HB3	1.76	0.50
1:H:278:LEU:HD22	1:H:280:LYS:HG2	1.93	0.50
1:I:754:VAL:HA	1:I:779:PHE:CE1	2.46	0.50
1:L:558:LEU:HD12	1:L:861:LEU:HD12	1.93	0.50
1:A:673:PRO:HD2	1:A:877:GLU:OE1	2.11	0.50
1:C:605:LEU:HD13	1:C:606:SER:O	2.12	0.50
1:D:537:TYR:CD1	1:D:540:LYS:HE2	2.46	0.50
1:E:275:HIS:H	1:E:275:HIS:CD2	2.30	0.50
1:F:285:ILE:HD13	1:F:332:VAL:HG22	1.92	0.50
1:H:255:ILE:HA	1:H:392:ILE:O	2.11	0.50
1:I:817:ASN:HB3	1:I:820:TYR:HB2	1.93	0.50
1:K:233:LYS:CA	1:K:233:LYS:CE	2.89	0.50
1:L:578:GLN:HA	1:L:838:VAL:HG21	1.93	0.50
1:A:259:GLY:HA2	1:A:408:ALA:HB2	1.93	0.50
1:A:453:VAL:HG21	1:A:505:LEU:HD23	1.93	0.50
1:D:349:SER:HB3	1:D:352:ILE:HG23	1.92	0.50
1:I:434:PRO:HG2	1:I:488:HIS:ND1	2.26	0.50
1:J:661:GLU:OE2	1:J:676:ARG:NH2	2.44	0.50
1:A:537:TYR:CD1	1:A:540:LYS:HE2	2.46	0.50
1:A:576:GLN:NE2	1:A:576:GLN:H	2.10	0.50
1:C:773:PRO:C	1:L:774:SER:HB2	2.35	0.50
1:D:241:LEU:O	1:D:244:VAL:HG23	2.12	0.50
1:D:272:ILE:HG23	1:D:278:LEU:N	2.24	0.50
1:E:246:GLN:HE22	1:E:890:ARG:HH12	1.58	0.50
1:E:478:ASN:O	1:E:482:LYS:HG2	2.11	0.50
1:F:252:LEU:HD23	1:F:524:THR:HG21	1.93	0.50
1:G:279:PRO:HG2	1:G:325:LEU:HD21	1.93	0.50
1:H:278:LEU:HD13	1:H:278:LEU:C	2.35	0.50
1:H:454:GLY:H	1:H:500:THR:HG22	1.75	0.50
1:I:434:PRO:HB3	1:I:491:GLU:HB2	1.93	0.50
1:J:279:PRO:HG2	1:J:325:LEU:HD21	1.93	0.50
1:J:441:LEU:HD23	1:J:498:VAL:HB	1.92	0.50
1:A:232:LYS:HA	1:A:235:ILE:CG2	2.41	0.50
1:C:774:SER:CB	1:L:774:SER:O	2.60	0.50
1:D:278:LEU:HD22	1:D:280:LYS:HG2	1.94	0.50
1:D:562:LYS:NZ	1:I:562:LYS:HZ1	2.09	0.50
1:E:694:THR:HG21	1:E:845:MET:HE3	1.94	0.50
1:J:662:LYS:O	1:J:665:ASP:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:285:ILE:CD1	1:K:286:THR:N	2.67	0.50
1:L:285:ILE:HG12	1:L:329:ASN:O	2.12	0.50
1:L:605:LEU:HD22	1:L:606:SER:N	2.27	0.50
1:A:778:GLY:CA	1:H:783:LEU:HB2	2.35	0.50
1:B:617:ASP:OD1	1:B:617:ASP:N	2.45	0.50
1:D:296:ASN:HB2	1:D:354:ASP:OD2	2.12	0.50
1:E:387:ILE:O	1:E:421:ARG:NH2	2.45	0.50
1:E:387:ILE:HG22	1:E:415:VAL:HG21	1.92	0.50
1:I:285:ILE:HD13	1:I:285:ILE:N	2.26	0.50
1:A:238:ARG:HA	1:A:241:LEU:HD12	1.93	0.50
1:C:661:GLU:OE2	1:C:676:ARG:NH2	2.45	0.50
1:H:639:LEU:O	1:H:642:LEU:HD23	2.12	0.50
1:K:610:ARG:HA	1:K:610:ARG:HE	1.77	0.50
1:L:449:LYS:C	1:L:451:GLY:H	2.20	0.50
1:L:837:ALA:O	1:L:841:LEU:HB2	2.12	0.50
1:B:262:SER:O	1:B:266:SER:OG	2.30	0.50
1:B:285:ILE:HG12	1:B:329:ASN:O	2.11	0.50
1:D:672:HIS:HA	1:D:877:GLU:OE2	2.11	0.50
1:E:254:SER:HB2	1:E:356:SER:O	2.11	0.50
1:E:279:PRO:O	1:E:280:LYS:CD	2.59	0.50
1:E:318:PHE:HD1	1:E:321:ILE:HD12	1.77	0.50
1:F:873:LYS:O	1:F:877:GLU:HG3	2.11	0.50
1:H:488:HIS:HB3	1:H:491:GLU:HG3	1.93	0.50
1:I:843:VAL:HG21	1:J:704:PRO:HA	1.92	0.50
1:L:262:SER:O	1:L:266:SER:OG	2.29	0.50
1:D:376:LYS:CE	1:D:376:LYS:CA	2.89	0.50
1:H:555:ALA:CB	1:K:855:ARG:HG2	2.42	0.50
1:K:272:ILE:HG23	1:K:278:LEU:N	2.25	0.50
1:A:457:SER:O	1:A:458:LYS:HB2	2.13	0.49
1:A:754:VAL:HA	1:A:779:PHE:CE1	2.47	0.49
1:B:279:PRO:HG2	1:B:325:LEU:HD21	1.94	0.49
1:D:269:LEU:HD21	1:D:457:SER:O	2.12	0.49
1:E:349:SER:O	1:E:352:ILE:HG13	2.12	0.49
1:G:262:SER:O	1:G:266:SER:OG	2.30	0.49
1:H:376:LYS:HZ1	1:H:379:ILE:HD12	1.76	0.49
1:H:474:LEU:HG	1:H:475:ALA:N	2.25	0.49
1:I:226:ASN:HA	1:I:229:PHE:HD1	1.74	0.49
1:I:269:LEU:HD21	1:I:457:SER:C	2.37	0.49
1:I:349:SER:O	1:I:352:ILE:HG13	2.12	0.49
1:K:263:SER:HA	1:K:266:SER:OG	2.12	0.49
1:B:855:ARG:NH2	1:C:559:ASP:OD2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:PRO:HG2	1:C:325:LEU:HD21	1.93	0.49
1:D:232:LYS:HA	1:D:235:ILE:HG22	1.94	0.49
1:D:269:LEU:CD1	1:D:458:LYS:HB2	2.42	0.49
1:E:434:PRO:HG2	1:E:488:HIS:ND1	2.26	0.49
1:J:252:LEU:HD23	1:J:524:THR:HG21	1.95	0.49
1:K:232:LYS:HA	1:K:235:ILE:HG22	1.93	0.49
1:L:611:GLU:HG3	1:L:611:GLU:O	2.13	0.49
1:A:454:GLY:H	1:A:500:THR:HG22	1.76	0.49
1:A:783:LEU:CG	1:H:778:GLY:HA3	2.40	0.49
1:B:255:ILE:HA	1:B:392:ILE:O	2.12	0.49
1:C:262:SER:O	1:C:266:SER:OG	2.30	0.49
1:D:233:LYS:N	1:D:233:LYS:HE3	2.27	0.49
1:E:276:GLU:OE1	1:E:303:ASP:OD1	2.29	0.49
1:E:296:ASN:C	1:E:298:PRO:HD3	2.37	0.49
1:E:817:ASN:HB3	1:E:820:TYR:HB2	1.93	0.49
1:H:393:ILE:HG23	1:H:422:THR:HB	1.93	0.49
1:J:257:VAL:HG12	1:J:394:LEU:HB3	1.94	0.49
1:J:272:ILE:HD11	1:J:280:LYS:HB2	1.94	0.49
1:J:672:HIS:HD2	1:J:877:GLU:HB2	1.76	0.49
1:K:285:ILE:HD13	1:K:285:ILE:N	2.27	0.49
1:K:484:TYR:HE1	1:K:492:PHE:CZ	2.30	0.49
1:K:751:LEU:HA	1:K:754:VAL:HG12	1.93	0.49
1:A:565:PHE:HA	1:A:663:LEU:HD21	1.94	0.49
1:A:615:ILE:H	1:A:615:ILE:HD12	1.76	0.49
1:B:640:THR:HG22	1:B:706:LYS:HG2	1.95	0.49
1:D:225:ASP:OD1	1:D:225:ASP:N	2.44	0.49
1:D:297:ASP:OD1	1:D:300:ALA:CB	2.60	0.49
1:D:705:TYR:CE1	1:D:832:LYS:HD3	2.47	0.49
1:E:260:SER:O	1:E:264:GLY:CA	2.55	0.49
1:J:255:ILE:HD11	1:J:355:LEU:HG	1.93	0.49
1:J:308:PRO:HG3	1:J:344:ARG:HB2	1.94	0.49
1:K:673:PRO:HD2	1:K:877:GLU:OE1	2.11	0.49
1:A:393:ILE:HG23	1:A:422:THR:HB	1.94	0.49
1:D:269:LEU:CG	1:D:457:SER:O	2.60	0.49
1:D:339:THR:CG2	1:D:340:ASP:H	2.25	0.49
1:D:671:LYS:HD2	1:D:671:LYS:N	2.26	0.49
1:I:455:VAL:HG12	1:I:501:GLY:CA	2.41	0.49
1:I:484:TYR:HD1	1:I:485:PHE:CD1	2.30	0.49
1:K:387:ILE:O	1:K:421:ARG:NH2	2.46	0.49
1:K:834:ALA:O	1:K:838:VAL:HB	2.13	0.49
1:A:237:ILE:HD11	1:A:897:VAL:HG13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:611:GLU:H	1:B:612:PRO:HD2	1.78	0.49
1:C:255:ILE:HA	1:C:392:ILE:O	2.12	0.49
1:C:664:LEU:HD23	1:C:676:ARG:HG3	1.94	0.49
1:D:339:THR:CG2	1:D:340:ASP:N	2.75	0.49
1:D:886:ASP:HA	1:D:889:ARG:HG2	1.94	0.49
1:E:278:LEU:CD2	1:E:280:LYS:CG	2.89	0.49
1:E:339:THR:CG2	1:E:340:ASP:H	2.25	0.49
1:E:671:LYS:HG2	1:E:879:PRO:HG3	1.93	0.49
1:G:244:VAL:HA	1:G:893:LEU:HD13	1.95	0.49
1:G:704:PRO:HA	1:H:843:VAL:HG21	1.94	0.49
1:H:278:LEU:CD2	1:H:280:LYS:CG	2.90	0.49
1:H:672:HIS:HA	1:H:877:GLU:OE2	2.12	0.49
1:J:349:SER:HB3	1:J:352:ILE:HG12	1.93	0.49
1:A:275:HIS:CG	1:A:276:GLU:N	2.79	0.49
1:E:267:SER:HB2	1:E:396:ILE:CD1	2.42	0.49
1:E:454:GLY:H	1:E:500:THR:HG22	1.77	0.49
1:F:268:VAL:HB	1:F:280:LYS:HB3	1.94	0.49
1:F:322:GLN:O	1:F:326:THR:OG1	2.12	0.49
1:G:640:THR:HG22	1:G:706:LYS:HG2	1.94	0.49
1:I:255:ILE:HA	1:I:392:ILE:O	2.12	0.49
1:I:387:ILE:O	1:I:421:ARG:NH2	2.46	0.49
1:I:477:ILE:HG22	1:I:477:ILE:O	2.13	0.49
1:I:672:HIS:HA	1:I:877:GLU:OE2	2.13	0.49
1:I:834:ALA:O	1:I:838:VAL:HB	2.13	0.49
1:K:296:ASN:HB2	1:K:354:ASP:OD2	2.13	0.49
1:A:296:ASN:HB2	1:A:354:ASP:OD2	2.12	0.49
1:B:653:ALA:HB2	1:B:845:MET:HE1	1.93	0.49
1:D:269:LEU:HD21	1:D:457:SER:C	2.37	0.49
1:E:673:PRO:HD2	1:E:877:GLU:OE1	2.11	0.49
1:E:751:LEU:HA	1:E:754:VAL:HG12	1.95	0.49
1:F:279:PRO:HG2	1:F:325:LEU:HD21	1.95	0.49
1:L:873:LYS:O	1:L:877:GLU:HG3	2.12	0.49
1:B:559:ASP:OD2	1:C:855:ARG:NH2	2.45	0.49
1:C:873:LYS:HB2	1:C:873:LYS:HE3	1.63	0.49
1:H:260:SER:O	1:H:264:GLY:CA	2.53	0.49
1:H:308:PRO:HG3	1:H:344:ARG:CG	2.40	0.49
1:K:296:ASN:C	1:K:298:PRO:HD3	2.38	0.49
1:K:301:LYS:HD3	1:K:301:LYS:N	2.28	0.49
1:K:349:SER:HB3	1:K:352:ILE:HG23	1.95	0.49
1:K:454:GLY:N	1:K:500:THR:HG22	2.28	0.49
1:A:269:LEU:HD23	1:A:457:SER:OG	2.05	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276:GLU:HG2	1:C:277:PHE:N	2.28	0.49
1:C:775:GLY:HA2	1:L:780:SER:CB	2.41	0.49
1:C:780:SER:CB	1:L:779:PHE:C	2.77	0.49
1:E:528:ILE:HG23	1:E:894:LEU:HD22	1.95	0.49
1:F:227:MET:O	1:F:230:ILE:HG22	2.12	0.49
1:H:673:PRO:HD2	1:H:877:GLU:OE1	2.12	0.49
1:I:376:LYS:CE	1:I:376:LYS:CA	2.91	0.49
1:K:279:PRO:HG3	1:K:321:ILE:HG22	1.95	0.49
1:A:255:ILE:HA	1:A:392:ILE:O	2.13	0.48
1:A:269:LEU:HD21	1:A:457:SER:O	2.13	0.48
1:D:278:LEU:HD13	1:D:278:LEU:C	2.35	0.48
1:E:269:LEU:HD21	1:E:457:SER:C	2.38	0.48
1:F:559:ASP:OD2	1:G:855:ARG:NH2	2.46	0.48
1:F:837:ALA:O	1:F:841:LEU:HB2	2.13	0.48
1:H:232:LYS:O	1:H:235:ILE:HG23	2.13	0.48
1:I:297:ASP:OD1	1:I:300:ALA:HB3	2.13	0.48
1:I:376:LYS:HA	1:I:376:LYS:HZ1	1.76	0.48
1:K:454:GLY:O	1:K:455:VAL:HG13	2.12	0.48
1:E:328:LEU:HD13	1:E:343:ILE:HD13	1.95	0.48
1:G:255:ILE:HA	1:G:392:ILE:O	2.13	0.48
1:G:508:LYS:O	1:G:512:VAL:HG23	2.13	0.48
1:I:269:LEU:HD21	1:I:457:SER:O	2.13	0.48
1:K:485:PHE:HA	1:K:492:PHE:HE1	1.78	0.48
1:E:455:VAL:HG12	1:E:501:GLY:CA	2.42	0.48
1:E:639:LEU:O	1:E:642:LEU:HD23	2.13	0.48
1:H:876:ARG:HB3	1:H:882:ARG:HH21	1.78	0.48
1:I:224:ASP:OD2	1:I:227:MET:HB2	2.13	0.48
1:I:768:VAL:HG23	1:I:770:GLY:H	1.78	0.48
1:A:377:ARG:CG	1:A:377:ARG:NH2	2.74	0.48
1:B:393:ILE:HG23	1:B:422:THR:HB	1.96	0.48
1:C:611:GLU:H	1:C:612:PRO:CD	2.24	0.48
1:D:260:SER:H	1:D:263:SER:HB3	1.76	0.48
1:D:278:LEU:CD2	1:D:280:LYS:CG	2.92	0.48
1:D:751:LEU:HA	1:D:754:VAL:HG12	1.96	0.48
1:F:255:ILE:HA	1:F:392:ILE:O	2.13	0.48
1:G:322:GLN:O	1:G:326:THR:OG1	2.14	0.48
1:G:605:LEU:HD22	1:G:606:SER:N	2.29	0.48
1:I:705:TYR:CE1	1:I:832:LYS:HD3	2.49	0.48
1:A:272:ILE:HG23	1:A:278:LEU:N	2.26	0.48
1:A:434:PRO:HB2	1:A:491:GLU:HG3	1.92	0.48
1:E:285:ILE:HD13	1:E:285:ILE:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:478:ASN:HD21	1:E:482:LYS:CE	2.27	0.48
1:H:854:PRO:CG	1:H:855:ARG:HH12	2.27	0.48
1:A:225:ASP:OD1	1:A:225:ASP:N	2.46	0.48
1:D:270:GLU:HA	1:D:273:VAL:HG22	1.96	0.48
1:D:285:ILE:CD1	1:D:285:ILE:N	2.77	0.48
1:D:556:ALA:HB2	1:I:855:ARG:HE	1.78	0.48
1:D:775:GLY:HA2	1:D:779:PHE:O	2.14	0.48
1:E:376:LYS:HA	1:E:376:LYS:CE	2.43	0.48
1:E:671:LYS:C	1:E:672:HIS:CD2	2.91	0.48
1:I:243:LYS:O	1:I:243:LYS:HG2	2.14	0.48
1:I:775:GLY:HA2	1:I:779:PHE:O	2.14	0.48
1:K:477:ILE:O	1:K:477:ILE:HG22	2.13	0.48
1:A:279:PRO:HB3	1:A:322:GLN:CG	2.44	0.48
1:B:266:SER:HA	1:B:269:LEU:HD22	1.94	0.48
1:C:782:ALA:HB3	1:L:778:GLY:C	2.38	0.48
1:D:455:VAL:HG12	1:D:501:GLY:CA	2.44	0.48
1:D:855:ARG:HD2	1:I:555:ALA:HB3	1.81	0.48
1:G:664:LEU:HD23	1:G:676:ARG:HG3	1.96	0.48
1:H:237:ILE:HD11	1:H:897:VAL:HG13	1.96	0.48
1:I:232:LYS:HA	1:I:235:ILE:HG22	1.96	0.48
1:I:393:ILE:HG23	1:I:422:THR:HB	1.95	0.48
1:I:610:ARG:HA	1:I:610:ARG:NE	2.29	0.48
1:L:705:TYR:CE1	1:L:832:LYS:HD3	2.49	0.48
1:A:278:LEU:CD2	1:A:280:LYS:CG	2.91	0.48
1:D:375:LEU:HB2	1:D:376:LYS:HE2	1.94	0.48
1:D:499:SER:C	1:D:500:THR:HG23	2.39	0.48
1:E:285:ILE:CD1	1:E:285:ILE:N	2.76	0.48
1:E:477:ILE:O	1:E:477:ILE:HG22	2.13	0.48
1:E:863:GLU:O	1:E:867:ALA:HB3	2.13	0.48
1:F:328:LEU:HD13	1:F:343:ILE:HD13	1.94	0.48
1:F:664:LEU:HD23	1:F:676:ARG:HG3	1.95	0.48
1:H:275:HIS:CG	1:H:276:GLU:N	2.81	0.48
1:H:705:TYR:CE1	1:H:832:LYS:HD3	2.49	0.48
1:H:855:ARG:HD2	1:K:551:GLU:O	2.14	0.48
1:I:499:SER:C	1:I:500:THR:HG23	2.39	0.48
1:B:664:LEU:HD23	1:B:676:ARG:HG3	1.96	0.48
1:D:275:HIS:CG	1:D:276:GLU:N	2.82	0.48
1:D:387:ILE:O	1:D:421:ARG:NH2	2.47	0.48
1:D:393:ILE:HG23	1:D:422:THR:HB	1.95	0.48
1:D:431:LEU:HD23	1:D:431:LEU:H	1.79	0.48
1:E:881:VAL:HA	1:E:884:HIS:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:453:VAL:HG11	1:F:505:LEU:HB2	1.96	0.48
1:H:308:PRO:HG3	1:H:344:ARG:CB	2.43	0.48
1:I:241:LEU:O	1:I:244:VAL:HG23	2.13	0.48
1:J:224:ASP:HB3	1:J:227:MET:HB2	1.96	0.48
1:K:278:LEU:HD21	1:K:280:LYS:CG	2.44	0.48
1:K:529:GLN:HG2	1:K:898:LEU:HD21	1.96	0.48
1:B:534:GLU:OE2	1:D:646:ARG:NH2	2.47	0.48
1:C:294:LEU:HB3	1:C:352:ILE:HD13	1.96	0.48
1:E:308:PRO:CG	1:E:344:ARG:HG3	2.44	0.48
1:I:667:SER:OG	1:I:668:SER:N	2.47	0.48
1:J:558:LEU:HD12	1:J:861:LEU:HD12	1.96	0.48
1:K:266:SER:HB2	1:K:427:THR:OG1	2.14	0.48
1:A:667:SER:OG	1:A:668:SER:N	2.46	0.47
1:B:667:SER:OG	1:B:668:SER:N	2.47	0.47
1:C:393:ILE:HG23	1:C:422:THR:HB	1.96	0.47
1:D:318:PHE:CD1	1:D:321:ILE:HD12	2.49	0.47
1:D:562:LYS:HZ1	1:I:562:LYS:NZ	2.12	0.47
1:D:832:LYS:O	1:D:836:THR:HG22	2.14	0.47
1:E:339:THR:CG2	1:E:340:ASP:N	2.75	0.47
1:F:294:LEU:HB3	1:F:352:ILE:HD13	1.95	0.47
1:F:585:LEU:HD12	1:F:834:ALA:HB2	1.95	0.47
1:H:455:VAL:HG12	1:H:501:GLY:CA	2.44	0.47
1:I:565:PHE:HA	1:I:663:LEU:HD21	1.96	0.47
1:I:578:GLN:HA	1:I:838:VAL:HG21	1.94	0.47
1:I:671:LYS:N	1:I:671:LYS:HD2	2.29	0.47
1:I:727:LEU:HD21	1:I:823:GLU:HG2	1.95	0.47
1:K:260:SER:O	1:K:264:GLY:CA	2.57	0.47
1:K:308:PRO:CG	1:K:344:ARG:HG3	2.44	0.47
1:K:436:LYS:O	1:K:440:ILE:HG13	2.14	0.47
1:A:246:GLN:CG	1:A:247:GLY:N	2.77	0.47
1:D:260:SER:O	1:D:264:GLY:CA	2.56	0.47
1:D:639:LEU:O	1:D:642:LEU:HD23	2.15	0.47
1:F:667:SER:OG	1:F:668:SER:N	2.47	0.47
1:G:249:THR:OG1	1:G:531:GLU:OE1	2.19	0.47
1:H:275:HIS:CD2	1:H:275:HIS:N	2.82	0.47
1:I:328:LEU:HD13	1:I:343:ILE:HD13	1.97	0.47
1:A:260:SER:O	1:A:264:GLY:CA	2.56	0.47
1:D:263:SER:HA	1:D:266:SER:OG	2.14	0.47
1:D:355:LEU:HD23	1:D:357:LEU:HD22	1.96	0.47
1:D:377:ARG:HG2	1:D:377:ARG:HH21	1.79	0.47
1:F:534:GLU:OE2	1:H:646:ARG:NH2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:297:ASP:OD2	1:G:300:ALA:HB3	2.14	0.47
1:H:269:LEU:HD23	1:H:457:SER:OG	2.08	0.47
1:I:260:SER:H	1:I:263:SER:HB3	1.76	0.47
1:I:454:GLY:N	1:I:500:THR:HG22	2.29	0.47
1:A:269:LEU:HD21	1:A:457:SER:C	2.39	0.47
1:D:339:THR:O	1:D:340:ASP:HB3	2.14	0.47
1:E:284:MET:O	1:E:286:THR:HG23	2.14	0.47
1:E:815:LEU:O	1:E:815:LEU:HD22	2.13	0.47
1:G:393:ILE:HG23	1:G:422:THR:HB	1.96	0.47
1:H:233:LYS:HE2	1:H:233:LYS:HA	1.95	0.47
1:H:285:ILE:CG1	1:H:287:ARG:HB2	2.37	0.47
1:H:499:SER:C	1:H:500:THR:HG23	2.39	0.47
1:H:558:LEU:CD2	1:K:858:GLU:OE2	2.63	0.47
1:I:276:GLU:HG2	1:I:277:PHE:N	2.28	0.47
1:K:272:ILE:HG12	1:K:280:LYS:HG3	1.95	0.47
1:K:275:HIS:CG	1:K:276:GLU:N	2.78	0.47
1:K:578:GLN:HA	1:K:838:VAL:HG21	1.96	0.47
1:B:224:ASP:HB3	1:B:227:MET:HB2	1.96	0.47
1:D:279:PRO:HB3	1:D:322:GLN:CG	2.45	0.47
1:D:287:ARG:CG	1:D:287:ARG:NH1	2.76	0.47
1:D:472:ASN:ND2	1:D:475:ALA:HB3	2.29	0.47
1:D:562:LYS:HD2	1:I:559:ASP:CG	2.39	0.47
1:E:246:GLN:HE22	1:E:890:ARG:NH1	2.13	0.47
1:H:278:LEU:CD2	1:H:280:LYS:HG2	2.44	0.47
1:K:485:PHE:CZ	1:K:500:THR:OG1	2.52	0.47
1:A:279:PRO:HG3	1:A:321:ILE:HG22	1.95	0.47
1:A:444:ARG:HD3	1:A:444:ARG:HA	1.67	0.47
1:B:252:LEU:HD23	1:B:524:THR:HG21	1.96	0.47
1:B:508:LYS:O	1:B:512:VAL:HG23	2.15	0.47
1:C:284:MET:HG2	1:C:286:THR:HG22	1.94	0.47
1:D:555:ALA:HB1	1:I:855:ARG:HH11	1.79	0.47
1:D:863:GLU:O	1:D:867:ALA:HB3	2.14	0.47
1:E:233:LYS:HE2	1:E:233:LYS:HA	1.95	0.47
1:E:376:LYS:HE2	1:E:376:LYS:N	2.29	0.47
1:E:671:LYS:HD3	1:E:879:PRO:HG3	1.97	0.47
1:F:233:LYS:HE3	1:F:900:LYS:HD2	1.97	0.47
1:F:558:LEU:HD12	1:F:861:LEU:HD12	1.97	0.47
1:H:667:SER:OG	1:H:668:SER:N	2.48	0.47
1:H:854:PRO:CB	1:K:559:ASP:OD2	2.63	0.47
1:J:285:ILE:HG12	1:J:329:ASN:O	2.14	0.47
1:L:252:LEU:HD23	1:L:524:THR:HG21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:PHE:HD1	1:A:321:ILE:HD12	1.80	0.47
1:A:456:ILE:HD12	1:A:456:ILE:C	2.39	0.47
1:A:477:ILE:HG22	1:A:477:ILE:O	2.13	0.47
1:A:499:SER:C	1:A:500:THR:HG23	2.40	0.47
1:A:863:GLU:O	1:A:867:ALA:HB3	2.14	0.47
1:B:611:GLU:HG3	1:B:611:GLU:O	2.15	0.47
1:B:873:LYS:O	1:B:877:GLU:HG3	2.15	0.47
1:C:227:MET:O	1:C:230:ILE:HG22	2.15	0.47
1:D:278:LEU:CD2	1:D:280:LYS:HG2	2.44	0.47
1:D:484:TYR:HD1	1:D:485:PHE:CD1	2.33	0.47
1:D:566:HIS:HB3	1:I:563:HIS:CG	2.50	0.47
1:E:376:LYS:CE	1:E:376:LYS:CA	2.93	0.47
1:E:487:SER:OG	1:E:488:HIS:CD2	2.68	0.47
1:G:617:ASP:OD1	1:G:617:ASP:N	2.48	0.47
1:H:269:LEU:CG	1:H:457:SER:O	2.61	0.47
1:H:339:THR:CG2	1:H:340:ASP:H	2.27	0.47
1:H:454:GLY:O	1:H:455:VAL:HG13	2.14	0.47
1:H:555:ALA:HB3	1:K:855:ARG:HG2	1.96	0.47
1:H:578:GLN:HA	1:H:838:VAL:HG21	1.97	0.47
1:I:285:ILE:CD1	1:I:285:ILE:H	2.28	0.47
1:J:664:LEU:HD23	1:J:676:ARG:HG3	1.95	0.47
1:L:611:GLU:H	1:L:612:PRO:CD	2.26	0.47
1:L:667:SER:OG	1:L:668:SER:N	2.48	0.47
1:L:873:LYS:HB2	1:L:873:LYS:HE3	1.63	0.47
1:A:472:ASN:ND2	1:A:475:ALA:HB3	2.30	0.47
1:D:578:GLN:HA	1:D:838:VAL:HG21	1.97	0.47
1:J:508:LYS:O	1:J:512:VAL:HG23	2.15	0.47
1:D:246:GLN:CG	1:D:247:GLY:N	2.77	0.47
1:E:278:LEU:HD21	1:E:280:LYS:CG	2.44	0.47
1:E:279:PRO:O	1:E:280:LYS:HD2	2.14	0.47
1:E:307:PHE:CD1	1:E:307:PHE:N	2.83	0.47
1:H:285:ILE:HG12	1:H:287:ARG:N	2.16	0.47
1:I:275:HIS:CD2	1:I:275:HIS:N	2.83	0.47
1:K:441:LEU:CB	1:K:498:VAL:HG12	2.45	0.47
1:K:667:SER:OG	1:K:668:SER:N	2.48	0.47
1:A:387:ILE:O	1:A:421:ARG:NH2	2.48	0.47
1:C:617:ASP:OD1	1:C:617:ASP:N	2.48	0.47
1:C:750:LYS:NZ	1:L:750:LYS:HG2	2.30	0.47
1:C:837:ALA:O	1:C:841:LEU:HB2	2.15	0.47
1:D:477:ILE:O	1:D:477:ILE:HG22	2.13	0.47
1:E:278:LEU:HD13	1:E:278:LEU:C	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:THR:O	1:E:340:ASP:HB3	2.15	0.47
1:E:727:LEU:HD21	1:E:823:GLU:HG2	1.97	0.47
1:F:749:LYS:O	1:F:753:GLU:HG3	2.14	0.47
1:H:485:PHE:CE2	1:H:492:PHE:CD1	3.03	0.47
1:I:260:SER:O	1:I:264:GLY:CA	2.57	0.47
1:I:276:GLU:OE1	1:I:303:ASP:CG	2.58	0.47
1:J:611:GLU:N	1:J:612:PRO:CD	2.78	0.47
1:A:285:ILE:CD1	1:A:285:ILE:N	2.77	0.46
1:A:455:VAL:HG12	1:A:501:GLY:CA	2.44	0.46
1:B:328:LEU:HD13	1:B:343:ILE:HD13	1.96	0.46
1:B:560:ASP:HA	1:B:563:HIS:HD2	1.81	0.46
1:D:277:PHE:CD1	1:D:278:LEU:N	2.82	0.46
1:G:873:LYS:HB2	1:G:873:LYS:HE3	1.59	0.46
1:I:279:PRO:HB3	1:I:322:GLN:CG	2.44	0.46
1:K:278:LEU:HD13	1:K:280:LYS:HG2	1.97	0.46
1:A:266:SER:HB2	1:A:427:THR:OG1	2.15	0.46
1:A:596:ARG:HG3	1:A:635:ALA:HB2	1.97	0.46
1:A:671:LYS:N	1:A:671:LYS:HD2	2.30	0.46
1:D:752:LYS:HG3	1:D:755:MET:HE3	1.97	0.46
1:D:818:LYS:HE3	1:D:819:TYR:CZ	2.50	0.46
1:E:242:GLN:HE22	1:E:344:ARG:CD	2.27	0.46
1:E:318:PHE:CD1	1:E:321:ILE:HD12	2.50	0.46
1:E:456:ILE:HD12	1:E:456:ILE:C	2.40	0.46
1:E:475:ALA:O	1:E:479:ARG:HG2	2.14	0.46
1:F:508:LYS:O	1:F:512:VAL:HG23	2.15	0.46
1:G:818:LYS:HE3	1:G:819:TYR:CE2	2.51	0.46
1:H:279:PRO:HB3	1:H:322:GLN:CG	2.45	0.46
1:H:441:LEU:HD21	1:H:498:VAL:CB	2.31	0.46
1:H:454:GLY:N	1:H:500:THR:HG22	2.30	0.46
1:H:751:LEU:HA	1:H:754:VAL:HG12	1.96	0.46
1:K:244:VAL:HG11	1:K:894:LEU:HD21	1.97	0.46
1:L:255:ILE:HA	1:L:392:ILE:O	2.15	0.46
1:A:694:THR:HG21	1:A:845:MET:HE3	1.97	0.46
1:A:774:SER:OG	1:H:774:SER:CB	2.63	0.46
1:A:780:SER:CA	1:H:779:PHE:O	2.63	0.46
1:C:508:LYS:O	1:C:512:VAL:HG23	2.15	0.46
1:D:285:ILE:HD13	1:D:285:ILE:N	2.30	0.46
1:D:485:PHE:CD2	1:D:492:PHE:CE1	3.03	0.46
1:E:269:LEU:HD21	1:E:457:SER:O	2.15	0.46
1:E:434:PRO:HB3	1:E:491:GLU:HB2	1.96	0.46
1:H:276:GLU:HG2	1:H:277:PHE:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:277:PHE:HD1	1:H:278:LEU:H	1.63	0.46
1:H:529:GLN:HG2	1:H:898:LEU:HD21	1.96	0.46
1:I:694:THR:HG21	1:I:845:MET:HE3	1.97	0.46
1:J:227:MET:HA	1:J:230:ILE:HG22	1.98	0.46
1:K:418:ARG:HE	1:K:420:GLU:CB	2.26	0.46
1:K:754:VAL:HA	1:K:779:PHE:CE1	2.49	0.46
1:L:264:GLY:HA2	1:L:267:SER:HB3	1.97	0.46
1:A:296:ASN:C	1:A:298:PRO:HD3	2.41	0.46
1:A:349:SER:HB3	1:A:352:ILE:HG23	1.97	0.46
1:A:355:LEU:HD23	1:A:357:LEU:HD22	1.96	0.46
1:A:377:ARG:HG2	1:A:377:ARG:NH2	2.26	0.46
1:A:852:ARG:HG3	1:A:855:ARG:NH2	2.30	0.46
1:B:572:PHE:HB3	1:B:850:TYR:OH	2.15	0.46
1:D:237:ILE:HD11	1:D:897:VAL:HG13	1.97	0.46
1:D:454:GLY:H	1:D:500:THR:HG22	1.79	0.46
1:D:848:ASP:HA	1:D:851:VAL:HG22	1.97	0.46
1:E:297:ASP:OD1	1:E:300:ALA:HB3	2.16	0.46
1:E:400:ASP:N	1:E:400:ASP:OD1	2.47	0.46
1:E:474:LEU:HG	1:E:475:ALA:H	1.80	0.46
1:G:328:LEU:HD13	1:G:343:ILE:HD13	1.97	0.46
1:I:225:ASP:OD1	1:I:225:ASP:N	2.45	0.46
1:I:263:SER:HA	1:I:266:SER:OG	2.16	0.46
1:J:837:ALA:O	1:J:841:LEU:HB2	2.16	0.46
1:K:400:ASP:OD1	1:K:400:ASP:N	2.47	0.46
1:K:455:VAL:HG12	1:K:501:GLY:CA	2.44	0.46
1:K:484:TYR:HD1	1:K:485:PHE:CD1	2.34	0.46
1:K:694:THR:HG21	1:K:845:MET:HE3	1.97	0.46
1:A:260:SER:H	1:A:263:SER:HB3	1.77	0.46
1:C:268:VAL:HB	1:C:280:LYS:HB3	1.97	0.46
1:E:232:LYS:HA	1:E:235:ILE:HG22	1.97	0.46
1:F:227:MET:O	1:F:231:THR:OG1	2.32	0.46
1:H:279:PRO:CG	1:H:322:GLN:HA	2.45	0.46
1:H:288:ARG:HA	1:H:289:PRO:HD3	1.78	0.46
1:H:387:ILE:O	1:H:421:ARG:NH2	2.48	0.46
1:I:285:ILE:CD1	1:I:286:THR:N	2.68	0.46
1:I:376:LYS:N	1:I:376:LYS:HE2	2.31	0.46
1:I:377:ARG:HG2	1:I:377:ARG:HH21	1.78	0.46
1:I:485:PHE:CE2	1:I:492:PHE:CD1	3.02	0.46
1:K:229:PHE:HA	1:K:232:LYS:CG	2.43	0.46
1:K:278:LEU:HD11	1:K:280:LYS:HG3	1.98	0.46
1:K:499:SER:C	1:K:500:THR:HG23	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:616:ILE:HG23	1:L:617:ASP:OD1	2.15	0.46
1:L:664:LEU:HD23	1:L:676:ARG:HG3	1.96	0.46
1:E:232:LYS:O	1:E:235:ILE:HG23	2.15	0.46
1:E:308:PRO:HG3	1:E:344:ARG:CG	2.45	0.46
1:E:499:SER:C	1:E:500:THR:HG23	2.41	0.46
1:F:286:THR:HB	1:F:361:PRO:HB3	1.98	0.46
1:H:232:LYS:HA	1:H:235:ILE:HG22	1.97	0.46
1:H:297:ASP:OD1	1:H:300:ALA:HB3	2.14	0.46
1:H:339:THR:CG2	1:H:340:ASP:N	2.77	0.46
1:H:477:ILE:O	1:H:477:ILE:HG22	2.14	0.46
1:H:889:ARG:HH21	1:H:893:LEU:HG	1.81	0.46
1:K:418:ARG:NE	1:K:420:GLU:HB3	2.27	0.46
1:K:670:ALA:HB1	1:K:671:LYS:NZ	2.31	0.46
1:A:339:THR:CG2	1:A:340:ASP:N	2.78	0.46
1:A:484:TYR:HE1	1:A:492:PHE:CZ	2.34	0.46
1:A:749:LYS:O	1:A:753:GLU:HG3	2.16	0.46
1:B:284:MET:HG2	1:B:286:THR:CG2	2.45	0.46
1:C:252:LEU:HD23	1:C:524:THR:HG21	1.97	0.46
1:C:453:VAL:HG11	1:C:505:LEU:HB2	1.96	0.46
1:D:242:GLN:HE22	1:D:344:ARG:CD	2.29	0.46
1:D:266:SER:HB2	1:D:427:THR:OG1	2.16	0.46
1:D:454:GLY:O	1:D:455:VAL:HG13	2.15	0.46
1:D:544:ASN:ND2	1:J:703:LYS:HG3	2.27	0.46
1:E:275:HIS:CG	1:E:276:GLU:N	2.78	0.46
1:E:593:LEU:HD21	1:E:823:GLU:HG3	1.97	0.46
1:H:272:ILE:HG12	1:H:280:LYS:HG3	1.98	0.46
1:H:377:ARG:CG	1:H:377:ARG:NH2	2.75	0.46
1:K:279:PRO:HB3	1:K:322:GLN:CG	2.45	0.46
1:K:426:ILE:HD11	1:K:440:ILE:CG2	2.05	0.46
1:K:818:LYS:HE3	1:K:819:TYR:CZ	2.50	0.46
1:A:308:PRO:HG3	1:A:344:ARG:CG	2.45	0.46
1:B:234:MET:HA	1:B:237:ILE:HG22	1.97	0.46
1:C:667:SER:OG	1:C:668:SER:N	2.48	0.46
1:C:780:SER:H	1:L:783:LEU:HD12	1.75	0.46
1:D:381:GLU:OE1	1:D:381:GLU:HA	2.15	0.46
1:D:485:PHE:CE2	1:D:492:PHE:CD1	3.02	0.46
1:D:492:PHE:CD1	1:D:492:PHE:O	2.68	0.46
1:E:272:ILE:HG23	1:E:278:LEU:N	2.30	0.46
1:E:574:ARG:N	1:E:575:PRO:HD2	2.28	0.46
1:F:269:LEU:O	1:F:272:ILE:HB	2.16	0.46
1:F:449:LYS:C	1:F:451:GLY:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:456:ILE:HD12	1:H:456:ILE:C	2.41	0.46
1:I:818:LYS:HE3	1:I:819:TYR:CE2	2.51	0.46
1:L:268:VAL:HB	1:L:280:LYS:HB3	1.98	0.46
1:B:269:LEU:HD21	1:B:457:SER:HB2	1.97	0.46
1:D:272:ILE:CG1	1:D:278:LEU:HD11	2.46	0.46
1:D:284:MET:O	1:D:286:THR:HG23	2.15	0.46
1:D:815:LEU:O	1:D:815:LEU:HD22	2.16	0.46
1:E:667:SER:OG	1:E:668:SER:N	2.49	0.46
1:E:671:LYS:CD	1:E:879:PRO:HG3	2.46	0.46
1:H:855:ARG:CZ	1:K:555:ALA:HB3	2.44	0.46
1:I:832:LYS:O	1:I:836:THR:HG22	2.16	0.46
1:K:376:LYS:NZ	1:K:376:LYS:CA	2.68	0.46
1:K:483:ASN:HD22	1:K:483:ASN:C	2.23	0.46
1:K:593:LEU:HD21	1:K:823:GLU:HG3	1.98	0.46
1:A:285:ILE:HD13	1:A:285:ILE:N	2.29	0.46
1:A:610:ARG:HA	1:A:610:ARG:NE	2.29	0.46
1:B:609:PRO:HB2	1:B:610:ARG:C	2.41	0.46
1:B:889:ARG:O	1:B:892:GLU:HB2	2.16	0.46
1:C:272:ILE:HD11	1:C:280:LYS:HB2	1.96	0.46
1:E:648:ALA:HB1	1:E:841:LEU:HD12	1.98	0.46
1:F:276:GLU:HG2	1:F:277:PHE:N	2.30	0.46
1:F:355:LEU:HD23	1:F:357:LEU:HD22	1.97	0.46
1:F:873:LYS:HB2	1:F:873:LYS:HE3	1.63	0.46
1:G:227:MET:O	1:G:230:ILE:HG22	2.16	0.46
1:H:376:LYS:HZ2	1:H:379:ILE:HD12	1.78	0.46
1:I:266:SER:HB2	1:I:427:THR:OG1	2.16	0.46
1:I:269:LEU:HD11	1:I:458:LYS:HB2	1.98	0.46
1:I:454:GLY:O	1:I:455:VAL:HG13	2.16	0.46
1:I:456:ILE:HD12	1:I:456:ILE:C	2.40	0.46
1:I:457:SER:O	1:I:458:LYS:HB2	2.16	0.46
1:J:667:SER:OG	1:J:668:SER:N	2.49	0.46
1:K:278:LEU:CD1	1:K:278:LEU:N	2.79	0.46
1:B:227:MET:O	1:B:231:THR:OG1	2.33	0.45
1:B:355:LEU:HD23	1:B:357:LEU:HD22	1.98	0.45
1:C:233:LYS:HE3	1:C:900:LYS:HD2	1.98	0.45
1:D:593:LEU:HD21	1:D:823:GLU:HG3	1.98	0.45
1:E:267:SER:CB	1:E:396:ILE:HG13	2.43	0.45
1:G:611:GLU:N	1:G:612:PRO:CD	2.79	0.45
1:H:225:ASP:N	1:H:225:ASP:OD1	2.47	0.45
1:H:246:GLN:H	1:H:246:GLN:CD	2.24	0.45
1:I:226:ASN:CA	1:I:229:PHE:CE1	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:278:LEU:CD1	1:I:278:LEU:N	2.78	0.45
1:I:308:PRO:HG3	1:I:344:ARG:CG	2.44	0.45
1:K:269:LEU:HD21	1:K:457:SER:C	2.41	0.45
1:L:233:LYS:HE3	1:L:900:LYS:HD2	1.98	0.45
1:L:272:ILE:HD11	1:L:280:LYS:HB2	1.98	0.45
1:A:278:LEU:CD1	1:A:278:LEU:N	2.79	0.45
1:C:449:LYS:C	1:C:451:GLY:H	2.25	0.45
1:C:558:LEU:HD12	1:C:861:LEU:HD12	1.97	0.45
1:E:441:LEU:CB	1:E:498:VAL:HG12	2.46	0.45
1:E:484:TYR:HE1	1:E:492:PHE:CZ	2.34	0.45
1:G:268:VAL:HB	1:G:280:LYS:HB3	1.98	0.45
1:H:559:ASP:OD1	1:K:854:PRO:HB2	2.16	0.45
1:A:269:LEU:HD11	1:A:457:SER:C	2.15	0.45
1:A:780:SER:CA	1:H:775:GLY:CA	2.94	0.45
1:B:566:HIS:CD2	1:C:563:HIS:CD2	3.04	0.45
1:D:474:LEU:HG	1:D:475:ALA:H	1.81	0.45
1:G:453:VAL:HG11	1:G:505:LEU:HB2	1.99	0.45
1:G:861:LEU:HD23	1:G:861:LEU:HA	1.81	0.45
1:H:225:ASP:O	1:H:229:PHE:HD1	1.98	0.45
1:H:242:GLN:HE22	1:H:344:ARG:CD	2.30	0.45
1:H:269:LEU:HD11	1:H:458:LYS:HB2	1.99	0.45
1:I:282:SER:HB2	1:I:283:ASN:H	1.64	0.45
1:J:357:LEU:H	1:J:357:LEU:HD23	1.82	0.45
1:J:873:LYS:O	1:J:877:GLU:HG3	2.17	0.45
1:A:484:TYR:CD1	1:A:484:TYR:C	2.95	0.45
1:B:294:LEU:HB3	1:B:352:ILE:HD13	1.97	0.45
1:B:453:VAL:HG11	1:B:505:LEU:HB2	1.98	0.45
1:C:703:LYS:HG3	1:I:544:ASN:ND2	2.31	0.45
1:C:855:ARG:NE	1:C:855:ARG:HA	2.31	0.45
1:D:275:HIS:CD2	1:D:275:HIS:N	2.85	0.45
1:D:454:GLY:N	1:D:500:THR:HG22	2.31	0.45
1:D:667:SER:OG	1:D:668:SER:N	2.50	0.45
1:D:854:PRO:HG2	1:D:855:ARG:NH2	2.31	0.45
1:E:671:LYS:O	1:E:672:HIS:HD2	1.98	0.45
1:F:393:ILE:HG23	1:F:422:THR:HB	1.97	0.45
1:G:234:MET:HA	1:G:237:ILE:HG22	1.98	0.45
1:G:616:ILE:HG23	1:G:617:ASP:OD1	2.17	0.45
1:I:426:ILE:HD11	1:I:440:ILE:CG2	2.02	0.45
1:J:854:PRO:HB2	1:J:855:ARG:CZ	2.46	0.45
1:L:508:LYS:O	1:L:512:VAL:HG23	2.16	0.45
1:A:376:LYS:N	1:A:376:LYS:HE2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:GLY:O	1:A:455:VAL:HG13	2.16	0.45
1:A:768:VAL:HG23	1:A:770:GLY:H	1.81	0.45
1:B:322:GLN:O	1:B:326:THR:OG1	2.13	0.45
1:C:328:LEU:HD13	1:C:343:ILE:HD13	1.99	0.45
1:C:480:ASN:HA	1:C:483:ASN:OD1	2.17	0.45
1:C:780:SER:HA	1:L:780:SER:CA	2.47	0.45
1:E:377:ARG:HH21	1:E:377:ARG:CG	2.30	0.45
1:E:554:LEU:HD13	1:E:865:MET:HE3	1.97	0.45
1:H:834:ALA:O	1:H:838:VAL:HB	2.17	0.45
1:I:287:ARG:HG3	1:I:287:ARG:NH1	2.21	0.45
1:I:863:GLU:O	1:I:867:ALA:HB3	2.17	0.45
1:J:453:VAL:HG11	1:J:505:LEU:HB2	1.99	0.45
1:J:610:ARG:HB2	1:J:611:GLU:HA	1.99	0.45
1:K:269:LEU:HD21	1:K:457:SER:O	2.16	0.45
1:K:491:GLU:H	1:K:491:GLU:CD	2.24	0.45
1:L:791:VAL:HG13	1:L:794:ARG:HH21	1.80	0.45
1:A:279:PRO:CG	1:A:322:GLN:HA	2.46	0.45
1:A:387:ILE:CG2	1:A:393:ILE:HD12	2.47	0.45
1:B:318:PHE:CD1	1:B:321:ILE:HD12	2.51	0.45
1:B:744:SER:OG	1:B:786:ARG:NH2	2.49	0.45
1:C:703:LYS:HE3	1:I:544:ASN:ND2	2.31	0.45
1:D:400:ASP:N	1:D:400:ASP:OD1	2.50	0.45
1:D:778:GLY:O	1:D:779:PHE:CD2	2.63	0.45
1:E:287:ARG:CG	1:E:287:ARG:NH1	2.78	0.45
1:E:344:ARG:H	1:E:344:ARG:HG2	1.59	0.45
1:E:454:GLY:O	1:E:455:VAL:HG13	2.17	0.45
1:H:272:ILE:CG1	1:H:278:LEU:HD11	2.47	0.45
1:H:484:TYR:C	1:H:484:TYR:CD1	2.94	0.45
1:I:279:PRO:HG3	1:I:321:ILE:HG22	1.97	0.45
1:J:255:ILE:HA	1:J:392:ILE:O	2.16	0.45
1:A:454:GLY:N	1:A:500:THR:HG22	2.32	0.45
1:B:640:THR:HG21	1:B:706:LYS:HA	1.99	0.45
1:F:234:MET:HA	1:F:237:ILE:HG22	1.97	0.45
1:G:667:SER:OG	1:G:668:SER:N	2.49	0.45
1:H:266:SER:HB2	1:H:427:THR:OG1	2.17	0.45
1:H:742:GLU:CD	1:H:748:ARG:HE	2.25	0.45
1:K:484:TYR:C	1:K:484:TYR:CD1	2.94	0.45
1:L:289:PRO:HB2	1:L:342:PRO:HB3	1.99	0.45
1:L:488:HIS:HB3	1:L:491:GLU:CG	2.47	0.45
1:L:488:HIS:HB3	1:L:491:GLU:HG3	1.98	0.45
1:L:610:ARG:N	1:L:611:GLU:HA	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:GLU:CD	1:A:748:ARG:HE	2.25	0.45
1:A:832:LYS:O	1:A:836:THR:HG22	2.17	0.45
1:C:234:MET:HA	1:C:237:ILE:HG22	1.99	0.45
1:D:232:LYS:HG3	1:D:233:LYS:HE3	1.98	0.45
1:D:278:LEU:HD13	1:D:280:LYS:HG2	1.98	0.45
1:D:349:SER:O	1:D:352:ILE:HG13	2.16	0.45
1:H:285:ILE:CD1	1:H:285:ILE:N	2.79	0.45
1:H:434:PRO:HB3	1:H:491:GLU:HB2	1.99	0.45
1:H:559:ASP:CG	1:K:854:PRO:HB3	2.40	0.45
1:H:863:GLU:O	1:H:867:ALA:HB3	2.17	0.45
1:I:241:LEU:HD21	1:I:528:ILE:HD11	1.98	0.45
1:I:400:ASP:OD1	1:I:400:ASP:N	2.48	0.45
1:I:750:LYS:O	1:I:753:GLU:HB2	2.16	0.45
1:J:231:THR:O	1:J:235:ILE:HG22	2.17	0.45
1:J:275:HIS:HB2	1:J:352:ILE:HG21	1.98	0.45
1:J:276:GLU:HG2	1:J:277:PHE:N	2.31	0.45
1:J:434:PRO:HG2	1:J:488:HIS:CG	2.51	0.45
1:K:278:LEU:CD1	1:K:280:LYS:HG2	2.46	0.45
1:L:234:MET:HA	1:L:237:ILE:HG22	1.99	0.45
1:A:381:GLU:HA	1:A:381:GLU:OE1	2.17	0.45
1:B:269:LEU:CD2	1:B:457:SER:HB2	2.47	0.45
1:B:272:ILE:HD11	1:B:280:LYS:HB2	1.99	0.45
1:B:611:GLU:N	1:B:612:PRO:CD	2.80	0.45
1:C:754:VAL:HG21	1:C:783:LEU:HD22	1.99	0.45
1:C:785:ALA:HA	1:C:788:ARG:CZ	2.47	0.45
1:G:224:ASP:HB3	1:G:227:MET:CB	2.41	0.45
1:G:224:ASP:HB3	1:G:227:MET:HG3	1.99	0.45
1:H:269:LEU:HD21	1:H:457:SER:O	2.17	0.45
1:H:485:PHE:CD2	1:H:492:PHE:CE1	3.05	0.45
1:H:596:ARG:HG3	1:H:635:ALA:HB2	1.99	0.45
1:I:278:LEU:CD2	1:I:280:LYS:HG2	2.47	0.45
1:I:441:LEU:CB	1:I:498:VAL:HG12	2.47	0.45
1:I:492:PHE:CD1	1:I:492:PHE:O	2.69	0.45
1:K:269:LEU:CG	1:K:457:SER:O	2.63	0.45
1:C:241:LEU:HD13	1:C:250:VAL:O	2.17	0.45
1:F:607:PRO:HG3	1:F:762:ARG:HG3	1.98	0.45
1:G:233:LYS:HE3	1:G:900:LYS:HD2	1.99	0.45
1:H:420:GLU:HG3	1:H:449:LYS:HE2	1.99	0.45
1:H:832:LYS:O	1:H:836:THR:HG22	2.17	0.45
1:J:400:ASP:N	1:J:400:ASP:OD1	2.50	0.45
1:K:865:MET:HB3	1:K:871:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:GLN:HA	1:A:838:VAL:HG21	1.98	0.44
1:C:773:PRO:HG2	1:L:774:SER:HB3	1.99	0.44
1:D:232:LYS:O	1:D:235:ILE:HG23	2.17	0.44
1:D:328:LEU:HD13	1:D:343:ILE:HD13	1.99	0.44
1:E:225:ASP:N	1:E:225:ASP:OD1	2.50	0.44
1:E:229:PHE:O	1:E:232:LYS:HG3	2.16	0.44
1:E:842:ASN:O	1:E:846:LEU:HB3	2.17	0.44
1:G:558:LEU:HD12	1:G:861:LEU:HD12	1.98	0.44
1:H:854:PRO:HB2	1:H:855:ARG:HH11	1.63	0.44
1:I:267:SER:CB	1:I:396:ILE:HG13	2.40	0.44
1:I:865:MET:HB3	1:I:871:LEU:HB2	1.98	0.44
1:K:294:LEU:HB2	1:K:355:LEU:H	1.82	0.44
1:A:344:ARG:H	1:A:344:ARG:HG2	1.64	0.44
1:A:727:LEU:HD21	1:A:823:GLU:HG2	1.98	0.44
1:A:778:GLY:C	1:H:780:SER:H	2.24	0.44
1:B:268:VAL:HB	1:B:280:LYS:HB3	1.99	0.44
1:D:889:ARG:HH21	1:D:893:LEU:HG	1.82	0.44
1:E:243:LYS:HG2	1:E:243:LYS:O	2.17	0.44
1:E:307:PHE:N	1:E:307:PHE:HD1	2.15	0.44
1:E:420:GLU:HG3	1:E:449:LYS:HE2	1.98	0.44
1:I:593:LEU:HD21	1:I:823:GLU:HG3	2.00	0.44
1:B:530:ARG:HD3	1:B:530:ARG:HA	1.78	0.44
1:B:757:PHE:CE1	1:B:777:GLY:HA3	2.53	0.44
1:C:355:LEU:HD23	1:C:357:LEU:HD22	2.00	0.44
1:D:279:PRO:CG	1:D:322:GLN:HA	2.47	0.44
1:D:443:ASP:OD1	1:D:445:GLN:HG3	2.17	0.44
1:G:232:LYS:HB3	1:G:232:LYS:HE2	1.78	0.44
1:G:326:THR:HA	1:G:329:ASN:ND2	2.32	0.44
1:G:889:ARG:O	1:G:892:GLU:HB2	2.17	0.44
1:H:251:THR:CG2	1:H:252:LEU:H	2.17	0.44
1:H:349:SER:HB3	1:H:352:ILE:HG23	1.99	0.44
1:H:617:ASP:N	1:H:617:ASP:OD1	2.50	0.44
1:I:484:TYR:HE1	1:I:492:PHE:CZ	2.35	0.44
1:J:255:ILE:HG12	1:J:513:LEU:HD12	2.00	0.44
1:J:393:ILE:HG23	1:J:422:THR:HB	1.97	0.44
1:K:434:PRO:HB3	1:K:491:GLU:HB2	1.99	0.44
1:K:520:LYS:HA	1:K:520:LYS:HD3	1.73	0.44
1:A:251:THR:CG2	1:A:252:LEU:H	2.16	0.44
1:B:400:ASP:N	1:B:400:ASP:OD1	2.50	0.44
1:D:229:PHE:O	1:D:232:LYS:HG3	2.17	0.44
1:D:241:LEU:HD21	1:D:528:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:ILE:HG12	1:D:280:LYS:HG3	1.99	0.44
1:E:278:LEU:CD1	1:E:278:LEU:N	2.80	0.44
1:E:488:HIS:CB	1:E:491:GLU:HG2	2.29	0.44
1:H:277:PHE:CD1	1:H:278:LEU:N	2.86	0.44
1:H:520:LYS:HA	1:H:520:LYS:HD3	1.79	0.44
1:H:567:GLU:HG2	1:K:563:HIS:HE1	1.79	0.44
1:I:458:LYS:C	1:I:458:LYS:HD2	2.40	0.44
1:K:288:ARG:HA	1:K:289:PRO:HD3	1.79	0.44
1:K:434:PRO:HB2	1:K:491:GLU:HG3	1.96	0.44
1:K:768:VAL:HG23	1:K:770:GLY:H	1.81	0.44
1:K:832:LYS:O	1:K:836:THR:HG22	2.17	0.44
1:L:878:ASP:HB3	1:L:881:VAL:CG1	2.40	0.44
1:A:339:THR:CG2	1:A:340:ASP:H	2.27	0.44
1:A:444:ARG:O	1:A:447:PRO:HD3	2.18	0.44
1:B:891:LYS:HG2	1:B:895:GLU:OE2	2.18	0.44
1:C:255:ILE:HG12	1:C:513:LEU:HD12	1.98	0.44
1:D:458:LYS:C	1:D:458:LYS:CD	2.90	0.44
1:E:265:LYS:HA	1:E:268:VAL:CG2	2.48	0.44
1:F:745:VAL:HG13	1:F:783:LEU:HD21	1.99	0.44
1:G:507:LYS:HE3	1:G:507:LYS:HB2	1.82	0.44
1:G:572:PHE:HB3	1:G:850:TYR:OH	2.18	0.44
1:H:269:LEU:HD21	1:H:457:SER:C	2.43	0.44
1:K:456:ILE:O	1:K:456:ILE:HG23	2.15	0.44
1:L:842:ASN:O	1:L:846:LEU:HB3	2.17	0.44
1:A:617:ASP:OD1	1:A:617:ASP:N	2.51	0.44
1:B:784:LEU:HD23	1:B:784:LEU:HA	1.79	0.44
1:D:540:LYS:HA	1:D:545:GLU:HG3	2.00	0.44
1:G:289:PRO:HB2	1:G:342:PRO:HB3	2.00	0.44
1:H:671:LYS:N	1:H:671:LYS:HD2	2.33	0.44
1:J:276:GLU:HG2	1:J:277:PHE:H	1.81	0.44
1:K:246:GLN:CG	1:K:247:GLY:N	2.81	0.44
1:L:453:VAL:HG11	1:L:505:LEU:HB2	1.99	0.44
1:A:224:ASP:CG	1:A:227:MET:HB2	2.43	0.44
1:A:278:LEU:HD13	1:A:278:LEU:C	2.41	0.44
1:A:889:ARG:HH21	1:A:893:LEU:HG	1.82	0.44
1:B:837:ALA:O	1:B:841:LEU:HB2	2.17	0.44
1:G:272:ILE:HD11	1:G:280:LYS:HB2	1.98	0.44
1:H:229:PHE:HA	1:H:232:LYS:CG	2.48	0.44
1:H:265:LYS:HA	1:H:268:VAL:CG2	2.48	0.44
1:H:278:LEU:CD1	1:H:278:LEU:N	2.81	0.44
1:H:279:PRO:O	1:H:280:LYS:CG	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:233:LYS:HE2	1:K:233:LYS:CA	2.46	0.44
1:L:296:ASN:H	1:L:354:ASP:HB3	1.83	0.44
1:A:278:LEU:HD21	1:A:280:LYS:CG	2.47	0.44
1:A:287:ARG:HG3	1:A:287:ARG:NH1	2.29	0.44
1:A:778:GLY:CA	1:H:780:SER:OG	2.64	0.44
1:B:233:LYS:HE3	1:B:900:LYS:HD2	1.99	0.44
1:B:607:PRO:HG3	1:B:762:ARG:HG3	1.98	0.44
1:C:227:MET:O	1:C:231:THR:OG1	2.35	0.44
1:C:442:SER:HB2	1:C:498:VAL:HG12	2.00	0.44
1:D:269:LEU:HD23	1:D:270:GLU:CA	2.47	0.44
1:F:269:LEU:CD2	1:F:457:SER:HB2	2.48	0.44
1:F:803:ARG:HD3	1:F:803:ARG:HA	1.74	0.44
1:H:294:LEU:HB2	1:H:355:LEU:H	1.82	0.44
1:H:387:ILE:CG2	1:H:393:ILE:HD12	2.48	0.44
1:I:339:THR:CG2	1:I:340:ASP:H	2.30	0.44
1:J:890:ARG:C	1:J:892:GLU:N	2.76	0.44
1:K:255:ILE:HG13	1:K:357:LEU:HA	1.99	0.44
1:K:285:ILE:CD1	1:K:285:ILE:H	2.31	0.44
1:K:308:PRO:HG3	1:K:344:ARG:CG	2.46	0.44
1:K:616:ILE:HG23	1:K:617:ASP:OD1	2.18	0.44
1:K:817:ASN:HB3	1:K:820:TYR:HB2	2.00	0.44
1:C:773:PRO:HG2	1:L:774:SER:CB	2.47	0.44
1:C:861:LEU:HD23	1:C:861:LEU:HA	1.76	0.44
1:D:278:LEU:CD1	1:D:280:LYS:HG2	2.48	0.44
1:D:565:PHE:HA	1:D:663:LEU:HD21	1.99	0.44
1:D:614:ASN:OD1	1:D:616:ILE:HG22	2.18	0.44
1:E:279:PRO:HB3	1:E:322:GLN:CG	2.47	0.44
1:G:611:GLU:H	1:G:612:PRO:HD2	1.83	0.44
1:H:269:LEU:CD2	1:H:269:LEU:C	2.86	0.44
1:H:285:ILE:HD13	1:H:285:ILE:N	2.33	0.44
1:I:278:LEU:CD2	1:I:280:LYS:CG	2.95	0.44
1:K:260:SER:H	1:K:263:SER:HB3	1.78	0.44
1:A:275:HIS:CD2	1:A:275:HIS:N	2.86	0.43
1:A:780:SER:HB3	1:H:779:PHE:H	1.82	0.43
1:D:286:THR:OG1	1:D:361:PRO:HB3	2.16	0.43
1:D:456:ILE:HD12	1:D:456:ILE:C	2.42	0.43
1:G:703:LYS:CG	1:K:544:ASN:HD21	2.24	0.43
1:I:278:LEU:HD13	1:I:278:LEU:C	2.41	0.43
1:L:357:LEU:HD23	1:L:357:LEU:H	1.83	0.43
1:A:780:SER:CA	1:H:775:GLY:HA2	2.47	0.43
1:D:742:GLU:CD	1:D:748:ARG:HE	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:266:SER:HA	1:F:269:LEU:HD22	2.00	0.43
1:F:269:LEU:HD21	1:F:457:SER:HB2	2.00	0.43
1:H:278:LEU:HD21	1:H:280:LYS:CG	2.48	0.43
1:H:878:ASP:HB3	1:H:881:VAL:CG2	2.43	0.43
1:K:574:ARG:N	1:K:575:PRO:HD2	2.29	0.43
1:K:889:ARG:HH21	1:K:893:LEU:HG	1.82	0.43
1:L:854:PRO:HG2	1:L:855:ARG:NH1	2.32	0.43
1:A:325:LEU:HA	1:A:328:LEU:HD12	1.99	0.43
1:B:818:LYS:HE3	1:B:819:TYR:CE2	2.53	0.43
1:B:861:LEU:HD23	1:B:861:LEU:HA	1.79	0.43
1:D:276:GLU:OE1	1:D:303:ASP:CG	2.60	0.43
1:D:288:ARG:HA	1:D:289:PRO:HD3	1.78	0.43
1:E:454:GLY:N	1:E:500:THR:HG22	2.33	0.43
1:E:682:ALA:O	1:E:685:THR:HG22	2.19	0.43
1:H:775:GLY:HA2	1:H:779:PHE:O	2.18	0.43
1:I:299:GLU:O	1:I:299:GLU:CG	2.66	0.43
1:I:861:LEU:HD23	1:I:861:LEU:HA	1.90	0.43
1:K:418:ARG:HH21	1:K:420:GLU:HB3	1.83	0.43
1:K:456:ILE:HD12	1:K:456:ILE:C	2.42	0.43
1:K:457:SER:O	1:K:458:LYS:HB2	2.18	0.43
1:L:393:ILE:HG23	1:L:422:THR:HB	2.00	0.43
1:C:400:ASP:OD1	1:C:400:ASP:N	2.51	0.43
1:D:611:GLU:H	1:D:611:GLU:HG2	1.66	0.43
1:E:434:PRO:HG2	1:E:488:HIS:CD2	2.52	0.43
1:E:457:SER:O	1:E:458:LYS:HB2	2.18	0.43
1:G:780:SER:OG	1:G:783:LEU:HB2	2.18	0.43
1:I:617:ASP:OD1	1:I:617:ASP:N	2.50	0.43
1:J:241:LEU:HD13	1:J:250:VAL:O	2.19	0.43
1:K:232:LYS:O	1:K:235:ILE:HG23	2.19	0.43
1:L:279:PRO:CB	1:L:322:GLN:HA	2.48	0.43
1:A:269:LEU:CD2	1:A:269:LEU:C	2.88	0.43
1:A:269:LEU:CG	1:A:457:SER:O	2.64	0.43
1:A:278:LEU:HB2	1:A:279:PRO:CD	2.46	0.43
1:A:488:HIS:CB	1:A:491:GLU:HG2	2.38	0.43
1:A:842:ASN:O	1:A:846:LEU:HB3	2.18	0.43
1:C:364:ILE:HD12	1:C:376:LYS:NZ	2.33	0.43
1:D:456:ILE:O	1:D:456:ILE:HG23	2.18	0.43
1:D:457:SER:O	1:D:458:LYS:CB	2.67	0.43
1:D:752:LYS:HA	1:D:755:MET:HE2	2.00	0.43
1:F:272:ILE:HD11	1:F:280:LYS:HB2	2.00	0.43
1:G:294:LEU:HB3	1:G:352:ILE:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:225:ASP:O	1:H:229:PHE:CD1	2.72	0.43
1:H:454:GLY:C	1:H:455:VAL:HG13	2.44	0.43
1:I:229:PHE:O	1:I:232:LYS:HG3	2.18	0.43
1:I:237:ILE:HD11	1:I:897:VAL:HG13	2.01	0.43
1:I:345:LEU:HD23	1:I:345:LEU:HA	1.86	0.43
1:I:528:ILE:HG23	1:I:894:LEU:HD22	2.01	0.43
1:J:364:ILE:HD12	1:J:376:LYS:NZ	2.33	0.43
1:L:241:LEU:HD13	1:L:250:VAL:O	2.19	0.43
1:B:853:PHE:HB3	1:B:854:PRO:HD3	2.01	0.43
1:C:279:PRO:CB	1:C:322:GLN:HA	2.49	0.43
1:D:563:HIS:CG	1:I:566:HIS:HB3	2.54	0.43
1:D:694:THR:HG21	1:D:845:MET:HE3	1.99	0.43
1:E:272:ILE:CG1	1:E:278:LEU:HD11	2.48	0.43
1:E:881:VAL:HA	1:E:884:HIS:CB	2.48	0.43
1:F:231:THR:O	1:F:235:ILE:HG22	2.18	0.43
1:G:610:ARG:HD2	1:G:613:ASP:OD1	2.19	0.43
1:I:339:THR:CG2	1:I:340:ASP:N	2.79	0.43
1:J:294:LEU:HB3	1:J:352:ILE:HD13	1.99	0.43
1:K:278:LEU:HD13	1:K:278:LEU:C	2.41	0.43
1:K:430:ASP:OD1	1:K:430:ASP:O	2.37	0.43
1:L:576:GLN:OE1	1:L:576:GLN:N	2.51	0.43
1:A:272:ILE:CG1	1:A:278:LEU:HD11	2.49	0.43
1:D:286:THR:O	1:D:361:PRO:HD3	2.19	0.43
1:E:484:TYR:CD1	1:E:484:TYR:C	2.96	0.43
1:E:581:LEU:HD12	1:E:838:VAL:HG23	2.01	0.43
1:F:472:ASN:OD1	1:F:475:ALA:HB3	2.19	0.43
1:F:861:LEU:HD23	1:F:861:LEU:HA	1.80	0.43
1:G:296:ASN:H	1:G:354:ASP:HB3	1.83	0.43
1:G:664:LEU:HB3	1:G:676:ARG:NH1	2.34	0.43
1:I:232:LYS:O	1:I:235:ILE:HG23	2.18	0.43
1:J:642:LEU:HD22	1:J:643:GLY:N	2.27	0.43
1:J:778:GLY:C	1:J:779:PHE:HD2	2.27	0.43
1:A:528:ILE:HG23	1:A:894:LEU:HD22	2.00	0.43
1:A:778:GLY:CA	1:H:783:LEU:CB	2.94	0.43
1:B:803:ARG:HA	1:B:803:ARG:HD3	1.74	0.43
1:D:233:LYS:HE2	1:D:233:LYS:CA	2.45	0.43
1:D:286:THR:O	1:D:361:PRO:CD	2.67	0.43
1:D:574:ARG:N	1:D:575:PRO:HD2	2.34	0.43
1:D:907:ILE:HD12	1:D:907:ILE:HA	1.92	0.43
1:E:269:LEU:HD23	1:E:270:GLU:CA	2.48	0.43
1:E:672:HIS:HA	1:E:877:GLU:OE2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:611:GLU:H	1:F:612:PRO:CD	2.26	0.43
1:G:275:HIS:HB2	1:G:352:ILE:HG21	2.01	0.43
1:H:576:GLN:H	1:H:576:GLN:HE21	1.66	0.43
1:I:225:ASP:CB	1:I:229:PHE:CZ	3.01	0.43
1:I:284:MET:O	1:I:286:THR:HG23	2.18	0.43
1:J:449:LYS:C	1:J:451:GLY:H	2.27	0.43
1:L:617:ASP:OD1	1:L:617:ASP:N	2.51	0.43
1:A:279:PRO:O	1:A:280:LYS:CG	2.67	0.43
1:A:287:ARG:NH1	1:A:287:ARG:CG	2.82	0.43
1:A:574:ARG:N	1:A:575:PRO:HD2	2.32	0.43
1:D:485:PHE:CD2	1:D:492:PHE:O	2.59	0.43
1:D:617:ASP:OD1	1:D:617:ASP:N	2.52	0.43
1:G:754:VAL:HG21	1:G:783:LEU:HD22	2.00	0.43
1:H:344:ARG:H	1:H:344:ARG:HG2	1.65	0.43
1:H:694:THR:HG21	1:H:845:MET:HE3	2.00	0.43
1:I:279:PRO:CG	1:I:322:GLN:HA	2.47	0.43
1:I:387:ILE:CG2	1:I:393:ILE:HD12	2.49	0.43
1:J:842:ASN:O	1:J:846:LEU:HB3	2.19	0.43
1:K:377:ARG:HH21	1:K:377:ARG:CG	2.31	0.43
1:L:400:ASP:N	1:L:400:ASP:OD1	2.52	0.43
1:A:294:LEU:HB2	1:A:355:LEU:H	1.83	0.43
1:B:544:ASN:HB3	1:D:703:LYS:HE3	2.01	0.43
1:C:582:LYS:HB2	1:C:582:LYS:HE3	1.85	0.43
1:C:891:LYS:HG2	1:C:895:GLU:OE2	2.18	0.43
1:D:255:ILE:HG13	1:D:357:LEU:HA	2.01	0.43
1:D:278:LEU:HB2	1:D:279:PRO:CD	2.47	0.43
1:D:556:ALA:N	1:I:855:ARG:NE	2.67	0.43
1:D:566:HIS:CD2	1:I:563:HIS:CD2	3.06	0.43
1:E:286:THR:OG1	1:E:361:PRO:HB3	2.17	0.43
1:E:345:LEU:HD23	1:E:345:LEU:HA	1.90	0.43
1:G:269:LEU:CD2	1:G:457:SER:HB2	2.49	0.43
1:H:401:THR:HG22	1:H:402:ASP:O	2.18	0.43
1:L:294:LEU:HB3	1:L:352:ILE:HD13	2.00	0.43
1:A:255:ILE:HG12	1:A:513:LEU:HD21	2.00	0.42
1:A:778:GLY:HA2	1:H:783:LEU:HG	1.96	0.42
1:A:780:SER:CB	1:H:779:PHE:O	2.67	0.42
1:C:780:SER:HB3	1:L:780:SER:H	1.78	0.42
1:D:450:LEU:O	1:D:508:LYS:NZ	2.49	0.42
1:E:478:ASN:ND2	1:E:482:LYS:CE	2.79	0.42
1:F:784:LEU:HD23	1:F:784:LEU:HA	1.86	0.42
1:G:364:ILE:HD12	1:G:376:LYS:NZ	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:311:GLY:O	1:H:312:LEU:HB2	2.18	0.42
1:I:742:GLU:CD	1:I:748:ARG:HE	2.26	0.42
1:K:275:HIS:CD2	1:K:275:HIS:N	2.85	0.42
1:K:832:LYS:O	1:K:835:GLN:HG2	2.19	0.42
1:L:269:LEU:HA	1:L:272:ILE:HD12	2.01	0.42
1:A:232:LYS:HA	1:A:235:ILE:HG22	2.01	0.42
1:A:272:ILE:CG2	1:A:277:PHE:CD1	2.97	0.42
1:A:540:LYS:HA	1:A:545:GLU:HG3	2.01	0.42
1:A:703:LYS:HE3	1:C:544:ASN:HB3	2.01	0.42
1:A:852:ARG:CG	1:A:855:ARG:NH2	2.82	0.42
1:B:754:VAL:HG22	1:B:779:PHE:CD2	2.54	0.42
1:C:376:LYS:HA	1:C:376:LYS:HZ3	1.84	0.42
1:D:297:ASP:OD1	1:D:348:HIS:HB3	2.19	0.42
1:D:450:LEU:HD22	1:D:512:VAL:CG2	2.49	0.42
1:E:387:ILE:CG2	1:E:393:ILE:HD12	2.49	0.42
1:E:454:GLY:C	1:E:455:VAL:HG13	2.44	0.42
1:F:891:LYS:HG2	1:F:895:GLU:OE2	2.19	0.42
1:G:400:ASP:N	1:G:400:ASP:OD1	2.49	0.42
1:H:269:LEU:HD23	1:H:270:GLU:CA	2.48	0.42
1:I:297:ASP:OD1	1:I:300:ALA:CB	2.67	0.42
1:I:723:VAL:O	1:I:727:LEU:HB2	2.20	0.42
1:J:227:MET:O	1:J:231:THR:OG1	2.33	0.42
1:J:284:MET:HG2	1:J:286:THR:HG23	2.00	0.42
1:L:255:ILE:HG12	1:L:513:LEU:HD12	2.01	0.42
1:A:246:GLN:HE22	1:A:890:ARG:NH1	2.17	0.42
1:A:454:GLY:C	1:A:455:VAL:HG13	2.44	0.42
1:B:232:LYS:HE2	1:B:232:LYS:HB3	1.80	0.42
1:E:279:PRO:O	1:E:280:LYS:HG2	2.19	0.42
1:G:430:ASP:HB3	1:G:456:ILE:HG12	2.01	0.42
1:H:441:LEU:CB	1:H:498:VAL:HG12	2.44	0.42
1:I:454:GLY:C	1:I:455:VAL:HG13	2.44	0.42
1:I:802:LEU:HD22	1:I:802:LEU:HA	1.92	0.42
1:J:754:VAL:HG21	1:J:783:LEU:HD22	2.01	0.42
1:J:755:MET:HG2	1:J:791:VAL:HG22	2.01	0.42
1:K:307:PHE:CD1	1:K:307:PHE:N	2.86	0.42
1:K:318:PHE:HD1	1:K:321:ILE:HD12	1.85	0.42
1:K:450:LEU:O	1:K:508:LYS:NZ	2.49	0.42
1:K:705:TYR:CE1	1:K:832:LYS:HD3	2.54	0.42
1:L:294:LEU:HB2	1:L:355:LEU:H	1.84	0.42
1:A:255:ILE:HG13	1:A:357:LEU:HA	2.00	0.42
1:A:318:PHE:CD1	1:A:321:ILE:HD12	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:THR:HA	1:A:329:ASN:ND2	2.34	0.42
1:A:657:GLN:HE21	1:A:657:GLN:HB2	1.49	0.42
1:B:296:ASN:H	1:B:354:ASP:HB3	1.83	0.42
1:C:627:TYR:CD1	1:C:630:ARG:NH2	2.87	0.42
1:C:784:LEU:O	1:C:788:ARG:HG3	2.20	0.42
1:D:278:LEU:CD1	1:D:278:LEU:N	2.82	0.42
1:D:401:THR:HG22	1:D:402:ASP:O	2.19	0.42
1:I:429:MET:HE2	1:I:437:GLY:CA	2.33	0.42
1:I:458:LYS:HD2	1:I:458:LYS:HA	1.94	0.42
1:I:491:GLU:CD	1:I:491:GLU:H	2.26	0.42
1:J:861:LEU:HA	1:J:861:LEU:HD23	1.80	0.42
1:A:307:PHE:CD1	1:A:307:PHE:N	2.87	0.42
1:A:774:SER:CB	1:H:774:SER:OG	2.68	0.42
1:C:289:PRO:HB2	1:C:342:PRO:HB3	2.01	0.42
1:D:278:LEU:HD11	1:D:280:LYS:HG3	2.00	0.42
1:D:392:ILE:HD12	1:D:421:ARG:O	2.19	0.42
1:D:450:LEU:HD22	1:D:512:VAL:HG22	2.01	0.42
1:D:539:PHE:CD2	1:D:545:GLU:HG2	2.55	0.42
1:D:555:ALA:HB3	1:I:855:ARG:HD2	1.88	0.42
1:D:865:MET:HB3	1:D:871:LEU:HB2	2.00	0.42
1:F:275:HIS:HB2	1:F:352:ILE:HG21	2.00	0.42
1:H:294:LEU:HB3	1:H:352:ILE:CD1	2.49	0.42
1:I:255:ILE:HG12	1:I:513:LEU:HD21	2.01	0.42
1:I:294:LEU:HB2	1:I:355:LEU:H	1.84	0.42
1:K:429:MET:HE2	1:K:437:GLY:CA	2.34	0.42
1:K:742:GLU:CD	1:K:748:ARG:HE	2.26	0.42
1:L:275:HIS:HB2	1:L:352:ILE:HG21	2.00	0.42
1:A:286:THR:O	1:A:361:PRO:CD	2.68	0.42
1:A:308:PRO:CG	1:A:344:ARG:HG3	2.49	0.42
1:A:520:LYS:HA	1:A:520:LYS:HD3	1.73	0.42
1:B:244:VAL:HA	1:B:893:LEU:HD13	2.02	0.42
1:C:611:GLU:N	1:C:612:PRO:CD	2.80	0.42
1:D:269:LEU:HD23	1:D:457:SER:OG	2.08	0.42
1:E:269:LEU:HD23	1:E:457:SER:OG	2.06	0.42
1:F:279:PRO:CB	1:F:322:GLN:HA	2.50	0.42
1:G:357:LEU:H	1:G:357:LEU:HD23	1.85	0.42
1:H:400:ASP:OD1	1:H:400:ASP:N	2.49	0.42
1:I:255:ILE:HG13	1:I:357:LEU:HA	2.00	0.42
1:I:270:GLU:C	1:I:273:VAL:HG22	2.45	0.42
1:I:657:GLN:HE21	1:I:657:GLN:HB2	1.60	0.42
1:I:707:PHE:CZ	1:J:847:ASN:ND2	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:270:GLU:C	1:K:270:GLU:CD	2.88	0.42
1:K:318:PHE:CD1	1:K:321:ILE:HD12	2.54	0.42
1:K:392:ILE:HD12	1:K:421:ARG:O	2.19	0.42
1:K:454:GLY:O	1:K:455:VAL:CG1	2.68	0.42
1:K:560:ASP:OD2	1:K:668:SER:OG	2.32	0.42
1:K:690:ARG:O	1:K:694:THR:HG23	2.20	0.42
1:K:863:GLU:O	1:K:867:ALA:HB3	2.20	0.42
1:L:572:PHE:HB3	1:L:850:TYR:OH	2.20	0.42
1:L:889:ARG:O	1:L:892:GLU:HB2	2.19	0.42
1:B:231:THR:O	1:B:235:ILE:HG22	2.20	0.42
1:B:255:ILE:HG12	1:B:513:LEU:HD12	2.01	0.42
1:B:532:LEU:HD22	1:B:898:LEU:HD22	2.01	0.42
1:C:640:THR:HG21	1:C:706:LYS:HA	2.02	0.42
1:C:772:HIS:CD2	1:C:772:HIS:O	2.73	0.42
1:D:596:ARG:HG3	1:D:635:ALA:HB2	2.01	0.42
1:E:279:PRO:O	1:E:280:LYS:CG	2.68	0.42
1:F:357:LEU:HD23	1:F:357:LEU:H	1.84	0.42
1:G:241:LEU:HD13	1:G:250:VAL:O	2.20	0.42
1:G:252:LEU:HD23	1:G:524:THR:HG21	2.01	0.42
1:G:269:LEU:HA	1:G:272:ILE:HD12	2.01	0.42
1:H:484:TYR:HE1	1:H:492:PHE:CZ	2.38	0.42
1:I:307:PHE:CD1	1:I:307:PHE:N	2.86	0.42
1:I:392:ILE:HD12	1:I:421:ARG:O	2.19	0.42
1:I:749:LYS:O	1:I:753:GLU:HG3	2.19	0.42
1:K:454:GLY:C	1:K:455:VAL:HG13	2.44	0.42
1:L:232:LYS:HB3	1:L:232:LYS:HE2	1.81	0.42
1:L:532:LEU:HD22	1:L:898:LEU:HD22	2.02	0.42
1:A:392:ILE:HD12	1:A:421:ARG:O	2.19	0.42
1:A:676:ARG:HG2	1:A:677:LYS:N	2.34	0.42
1:B:289:PRO:HB2	1:B:342:PRO:HB3	2.01	0.42
1:B:558:LEU:HD12	1:B:861:LEU:HD12	2.02	0.42
1:D:279:PRO:O	1:D:280:LYS:CG	2.68	0.42
1:D:294:LEU:HB2	1:D:355:LEU:H	1.83	0.42
1:D:434:PRO:HB3	1:D:491:GLU:HB2	2.00	0.42
1:D:485:PHE:HD2	1:D:492:PHE:HD1	1.64	0.42
1:F:269:LEU:HD11	1:F:457:SER:O	2.20	0.42
1:F:607:PRO:HD3	1:F:762:ARG:HG3	2.01	0.42
1:F:617:ASP:OD1	1:F:617:ASP:N	2.45	0.42
1:G:279:PRO:CB	1:G:322:GLN:HA	2.50	0.42
1:G:690:ARG:HA	1:G:690:ARG:HD3	1.86	0.42
1:H:392:ILE:HD12	1:H:421:ARG:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:265:LYS:HA	1:I:268:VAL:CG2	2.49	0.42
1:K:242:GLN:HE22	1:K:344:ARG:CD	2.33	0.42
1:K:272:ILE:CG1	1:K:278:LEU:HD11	2.50	0.42
1:A:431:LEU:H	1:A:431:LEU:HD23	1.85	0.42
1:C:357:LEU:HD23	1:C:357:LEU:H	1.85	0.42
1:C:744:SER:OG	1:C:786:ARG:NH2	2.52	0.42
1:E:596:ARG:HG3	1:E:635:ALA:HB2	2.01	0.42
1:E:705:TYR:CE1	1:E:832:LYS:HD3	2.55	0.42
1:F:289:PRO:HB2	1:F:342:PRO:HB3	2.02	0.42
1:F:349:SER:HB3	1:F:352:ILE:HG23	2.01	0.42
1:F:582:LYS:HB2	1:F:582:LYS:HE3	1.81	0.42
1:G:475:ALA:O	1:G:479:ARG:HG2	2.20	0.42
1:G:837:ALA:O	1:G:841:LEU:HB2	2.20	0.42
1:H:229:PHE:O	1:H:232:LYS:HG3	2.18	0.42
1:I:272:ILE:HG13	1:I:272:ILE:H	1.65	0.42
1:I:484:TYR:CD1	1:I:484:TYR:C	2.98	0.42
1:I:485:PHE:CD2	1:I:492:PHE:CE1	3.07	0.42
1:L:757:PHE:CE1	1:L:777:GLY:HA3	2.54	0.42
1:C:294:LEU:HB2	1:C:355:LEU:H	1.85	0.42
1:C:781:ALA:N	1:L:780:SER:N	2.64	0.42
1:D:690:ARG:O	1:D:694:THR:HG23	2.20	0.42
1:D:876:ARG:HB3	1:D:882:ARG:HH21	1.85	0.42
1:E:754:VAL:HA	1:E:779:PHE:HE1	1.85	0.42
1:E:853:PHE:HB3	1:E:854:PRO:HD3	2.01	0.42
1:F:854:PRO:CB	1:F:855:ARG:NH2	2.76	0.42
1:G:842:ASN:O	1:G:846:LEU:HB3	2.20	0.42
1:H:240:LEU:N	1:H:240:LEU:CD2	2.80	0.42
1:H:355:LEU:HD23	1:H:357:LEU:HD22	2.02	0.42
1:H:865:MET:HB3	1:H:871:LEU:HB2	2.01	0.42
1:I:815:LEU:O	1:I:815:LEU:HD22	2.20	0.42
1:I:889:ARG:HH21	1:I:893:LEU:HG	1.84	0.42
1:K:754:VAL:HA	1:K:779:PHE:HE1	1.84	0.42
1:L:276:GLU:HG2	1:L:277:PHE:N	2.34	0.42
1:A:246:GLN:OE1	1:A:246:GLN:N	2.51	0.41
1:A:450:LEU:O	1:A:508:LYS:NZ	2.49	0.41
1:A:593:LEU:HD21	1:A:823:GLU:HG3	2.02	0.41
1:B:241:LEU:HD13	1:B:250:VAL:O	2.19	0.41
1:B:507:LYS:HB2	1:B:507:LYS:HE3	1.82	0.41
1:C:275:HIS:HB2	1:C:352:ILE:HG21	2.01	0.41
1:D:272:ILE:CG1	1:D:278:LEU:CD1	2.98	0.41
1:D:664:LEU:HB3	1:D:676:ARG:NH2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:226:ASN:CA	1:E:229:PHE:CD1	3.00	0.41
1:H:307:PHE:CD1	1:H:307:PHE:N	2.87	0.41
1:H:780:SER:OG	1:H:783:LEU:HB2	2.20	0.41
1:I:244:VAL:HG11	1:I:894:LEU:HD21	2.02	0.41
1:I:444:ARG:O	1:I:447:PRO:HD3	2.19	0.41
1:K:238:ARG:CZ	1:K:356:SER:OG	2.68	0.41
1:L:224:ASP:HB3	1:L:227:MET:CB	2.49	0.41
1:L:376:LYS:NZ	1:L:379:ILE:HD12	2.35	0.41
1:C:627:TYR:HE2	1:C:628:TRP:CZ3	2.39	0.41
1:C:780:SER:HA	1:L:780:SER:HB3	1.86	0.41
1:D:240:LEU:N	1:D:240:LEU:CD2	2.79	0.41
1:E:560:ASP:OD2	1:E:668:SER:OG	2.31	0.41
1:E:871:LEU:C	1:E:871:LEU:HD22	2.45	0.41
1:F:285:ILE:HD12	1:F:287:ARG:N	2.22	0.41
1:F:363:TYR:N	1:F:363:TYR:CD1	2.89	0.41
1:F:611:GLU:N	1:F:612:PRO:CD	2.82	0.41
1:H:286:THR:O	1:H:361:PRO:HD3	2.20	0.41
1:H:381:GLU:OE1	1:H:381:GLU:HA	2.20	0.41
1:I:272:ILE:CG2	1:I:277:PHE:CD1	2.95	0.41
1:J:862:HIS:CD2	1:J:866:HIS:CD2	3.08	0.41
1:K:387:ILE:CG2	1:K:393:ILE:HD12	2.50	0.41
1:A:270:GLU:C	1:A:270:GLU:CD	2.89	0.41
1:D:441:LEU:HD21	1:D:498:VAL:CB	2.31	0.41
1:E:285:ILE:CD1	1:E:285:ILE:H	2.33	0.41
1:E:861:LEU:HD23	1:E:861:LEU:HA	1.86	0.41
1:F:244:VAL:HA	1:F:893:LEU:HD13	2.01	0.41
1:F:321:ILE:O	1:F:325:LEU:HG	2.20	0.41
1:F:364:ILE:HD12	1:F:376:LYS:NZ	2.35	0.41
1:F:784:LEU:O	1:F:788:ARG:HG3	2.21	0.41
1:G:255:ILE:HG12	1:G:513:LEU:HD12	2.03	0.41
1:G:284:MET:O	1:G:286:THR:HG23	2.20	0.41
1:H:539:PHE:CD2	1:H:545:GLU:HG2	2.55	0.41
1:J:640:THR:HG21	1:J:706:LYS:HA	2.02	0.41
1:K:377:ARG:CG	1:K:377:ARG:NH2	2.84	0.41
1:K:450:LEU:HD22	1:K:512:VAL:CG2	2.50	0.41
1:K:483:ASN:C	1:K:483:ASN:ND2	2.78	0.41
1:A:241:LEU:HD21	1:A:528:ILE:HD11	2.01	0.41
1:C:269:LEU:CD2	1:C:457:SER:HB2	2.51	0.41
1:D:528:ILE:HG23	1:D:894:LEU:HD22	2.03	0.41
1:E:269:LEU:CG	1:E:457:SER:O	2.66	0.41
1:E:279:PRO:CG	1:E:322:GLN:HA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:710:ASP:O	1:E:832:LYS:NZ	2.43	0.41
1:F:525:THR:O	1:F:529:GLN:HG3	2.20	0.41
1:H:286:THR:O	1:H:361:PRO:CD	2.68	0.41
1:H:848:ASP:HA	1:H:851:VAL:HG22	2.03	0.41
1:I:540:LYS:HA	1:I:545:GLU:HG3	2.03	0.41
1:I:751:LEU:HA	1:I:754:VAL:HG12	2.02	0.41
1:K:285:ILE:CG1	1:K:287:ARG:HB2	2.46	0.41
1:K:307:PHE:N	1:K:307:PHE:HD1	2.17	0.41
1:L:227:MET:O	1:L:231:THR:OG1	2.34	0.41
1:A:269:LEU:HD23	1:A:270:GLU:CA	2.51	0.41
1:A:400:ASP:OD1	1:A:400:ASP:N	2.52	0.41
1:A:751:LEU:HA	1:A:754:VAL:HG12	2.02	0.41
1:A:878:ASP:HB3	1:A:881:VAL:CG2	2.43	0.41
1:C:532:LEU:HD22	1:C:898:LEU:HD22	2.03	0.41
1:D:226:ASN:CA	1:D:229:PHE:CD1	3.02	0.41
1:E:306:GLU:C	1:E:307:PHE:HD1	2.28	0.41
1:H:238:ARG:CZ	1:H:356:SER:OG	2.68	0.41
1:H:255:ILE:HG13	1:H:357:LEU:HA	2.02	0.41
1:H:278:LEU:HD13	1:H:280:LYS:HG2	2.02	0.41
1:H:345:LEU:HD23	1:H:345:LEU:HA	1.89	0.41
1:J:749:LYS:O	1:J:753:GLU:HG3	2.20	0.41
1:K:278:LEU:CD1	1:K:280:LYS:CG	2.98	0.41
1:K:458:LYS:HA	1:K:458:LYS:HD2	1.91	0.41
1:A:265:LYS:HA	1:A:268:VAL:CG2	2.49	0.41
1:A:286:THR:O	1:A:361:PRO:HD3	2.21	0.41
1:A:574:ARG:CZ	1:A:839:LEU:HD11	2.51	0.41
1:C:576:GLN:OE1	1:C:576:GLN:N	2.53	0.41
1:C:842:ASN:O	1:C:846:LEU:HB3	2.21	0.41
1:D:454:GLY:C	1:D:455:VAL:HG13	2.46	0.41
1:D:478:ASN:O	1:D:482:LYS:HG2	2.21	0.41
1:D:832:LYS:O	1:D:835:GLN:HG2	2.20	0.41
1:E:235:ILE:HD12	1:E:235:ILE:C	2.45	0.41
1:E:377:ARG:CG	1:E:377:ARG:NH2	2.82	0.41
1:E:431:LEU:H	1:E:431:LEU:HD23	1.86	0.41
1:E:617:ASP:OD1	1:E:617:ASP:N	2.51	0.41
1:E:754:VAL:HA	1:E:779:PHE:CE1	2.56	0.41
1:G:294:LEU:HB2	1:G:355:LEU:H	1.86	0.41
1:H:255:ILE:HG12	1:H:513:LEU:HD21	2.01	0.41
1:H:285:ILE:CG1	1:H:287:ARG:H	2.19	0.41
1:H:286:THR:OG1	1:H:361:PRO:HB3	2.21	0.41
1:H:450:LEU:O	1:H:508:LYS:NZ	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:475:ALA:O	1:H:479:ARG:HG2	2.21	0.41
1:H:528:ILE:HG23	1:H:894:LEU:HD22	2.01	0.41
1:H:540:LYS:HA	1:H:545:GLU:HG3	2.01	0.41
1:I:268:VAL:O	1:I:272:ILE:CD1	2.69	0.41
1:I:301:LYS:HD3	1:I:301:LYS:N	2.35	0.41
1:J:832:LYS:O	1:J:835:GLN:HG2	2.20	0.41
1:J:873:LYS:HB2	1:J:873:LYS:HE3	1.61	0.41
1:L:754:VAL:HG21	1:L:783:LEU:HD22	2.03	0.41
1:A:268:VAL:O	1:A:272:ILE:CD1	2.69	0.41
1:A:537:TYR:CE1	1:A:540:LYS:HE2	2.55	0.41
1:A:690:ARG:O	1:A:694:THR:HG23	2.21	0.41
1:A:876:ARG:HB3	1:A:882:ARG:HH21	1.84	0.41
1:B:364:ILE:HD12	1:B:376:LYS:NZ	2.35	0.41
1:C:258:ILE:HG21	1:C:387:ILE:HD11	2.01	0.41
1:D:458:LYS:HD2	1:D:458:LYS:HA	1.94	0.41
1:D:552:SER:CA	1:I:855:ARG:HD2	2.50	0.41
1:D:562:LYS:CE	1:I:562:LYS:NZ	2.82	0.41
1:D:727:LEU:HD21	1:D:823:GLU:HG2	2.02	0.41
1:F:318:PHE:CD1	1:F:321:ILE:HD12	2.56	0.41
1:G:224:ASP:O	1:G:227:MET:HB2	2.21	0.41
1:G:387:ILE:HG22	1:G:415:VAL:HG21	2.03	0.41
1:G:772:HIS:HD2	1:G:775:GLY:O	2.04	0.41
1:H:456:ILE:O	1:H:456:ILE:HG23	2.21	0.41
1:H:749:LYS:HD2	1:H:749:LYS:H	1.86	0.41
1:H:768:VAL:HG23	1:H:770:GLY:H	1.85	0.41
1:I:226:ASN:CA	1:I:229:PHE:CD1	3.01	0.41
1:I:349:SER:HB3	1:I:352:ILE:HG23	2.03	0.41
1:J:269:LEU:O	1:J:273:VAL:HG13	2.21	0.41
1:K:344:ARG:H	1:K:344:ARG:HG2	1.61	0.41
1:K:621:ALA:O	1:K:820:TYR:OH	2.36	0.41
1:L:284:MET:HG2	1:L:286:THR:HG22	2.02	0.41
1:L:611:GLU:N	1:L:612:PRO:CD	2.84	0.41
1:L:664:LEU:HB3	1:L:676:ARG:NH1	2.35	0.41
1:A:275:HIS:HB2	1:A:352:ILE:CG2	2.50	0.41
1:A:657:GLN:HE22	1:A:684:ALA:CA	2.33	0.41
1:A:781:ALA:H	1:H:775:GLY:CA	2.33	0.41
1:C:803:ARG:HD2	1:C:823:GLU:CD	2.46	0.41
1:D:285:ILE:O	1:D:286:THR:OG1	2.32	0.41
1:E:355:LEU:HD23	1:E:357:LEU:HD22	2.03	0.41
1:F:224:ASP:HB3	1:F:227:MET:HB2	2.01	0.41
1:F:450:LEU:O	1:F:508:LYS:NZ	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:231:THR:O	1:G:235:ILE:HG22	2.20	0.41
1:G:450:LEU:O	1:G:508:LYS:NZ	2.54	0.41
1:H:241:LEU:HD21	1:H:528:ILE:HD11	2.02	0.41
1:H:272:ILE:CG1	1:H:278:LEU:CD1	2.98	0.41
1:J:803:ARG:HD3	1:J:803:ARG:HA	1.71	0.41
1:K:576:GLN:H	1:K:576:GLN:HE21	1.68	0.41
1:L:231:THR:O	1:L:235:ILE:HG22	2.21	0.41
1:A:450:LEU:HD22	1:A:512:VAL:CG2	2.51	0.41
1:A:491:GLU:CD	1:A:491:GLU:H	2.29	0.41
1:A:774:SER:HG	1:H:781:ALA:HB2	1.79	0.41
1:A:783:LEU:HG	1:H:778:GLY:HA3	2.00	0.41
1:A:783:LEU:HD23	1:A:783:LEU:HA	1.92	0.41
1:B:842:ASN:O	1:B:846:LEU:HB3	2.20	0.41
1:C:392:ILE:HD12	1:C:421:ARG:O	2.21	0.41
1:C:507:LYS:HB2	1:C:507:LYS:HE3	1.84	0.41
1:C:572:PHE:HB3	1:C:850:TYR:OH	2.20	0.41
1:C:779:PHE:HA	1:L:783:LEU:CD1	2.50	0.41
1:D:387:ILE:CG2	1:D:393:ILE:HD12	2.51	0.41
1:D:855:ARG:NH1	1:I:555:ALA:C	2.79	0.41
1:E:246:GLN:CD	1:E:247:GLY:H	2.29	0.41
1:E:255:ILE:HG12	1:E:513:LEU:HD21	2.03	0.41
1:E:288:ARG:HA	1:E:289:PRO:HD3	1.80	0.41
1:E:294:LEU:HB2	1:E:355:LEU:H	1.86	0.41
1:E:392:ILE:HD12	1:E:421:ARG:O	2.20	0.41
1:E:802:LEU:HD22	1:E:802:LEU:HA	1.96	0.41
1:E:806:ALA:O	1:E:809:SER:HB3	2.21	0.41
1:F:530:ARG:HD3	1:F:530:ARG:HA	1.81	0.41
1:F:683:ALA:HB2	1:F:853:PHE:CE1	2.56	0.41
1:G:224:ASP:HB3	1:G:227:MET:CG	2.51	0.41
1:G:227:MET:O	1:G:231:THR:OG1	2.32	0.41
1:G:269:LEU:HD21	1:G:457:SER:HB2	2.03	0.41
1:H:278:LEU:HD11	1:H:280:LYS:HG3	2.02	0.41
1:H:298:PRO:O	1:H:299:GLU:CB	2.69	0.41
1:H:593:LEU:HD21	1:H:823:GLU:HG3	2.03	0.41
1:H:855:ARG:NH1	1:K:555:ALA:HB3	2.34	0.41
1:I:240:LEU:N	1:I:240:LEU:CD2	2.78	0.41
1:K:339:THR:CG2	1:K:340:ASP:N	2.82	0.41
1:K:642:LEU:O	1:K:644:VAL:N	2.53	0.41
1:K:671:LYS:N	1:K:671:LYS:CD	2.84	0.41
1:L:484:TYR:O	1:L:487:SER:HB3	2.21	0.41
1:A:429:MET:HE2	1:A:437:GLY:CA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:607:PRO:HD2	1:B:762:ARG:O	2.22	0.41
1:B:754:VAL:HG21	1:B:783:LEU:HD22	2.03	0.41
1:C:450:LEU:O	1:C:508:LYS:NZ	2.54	0.41
1:E:275:HIS:CD2	1:E:275:HIS:N	2.90	0.41
1:E:672:HIS:HA	1:E:877:GLU:CD	2.46	0.41
1:G:269:LEU:HD11	1:G:457:SER:O	2.20	0.41
1:H:279:PRO:C	1:H:280:LYS:HG2	2.46	0.41
1:I:268:VAL:O	1:I:272:ILE:CG1	2.69	0.41
1:I:382:LEU:HD12	1:I:382:LEU:O	2.21	0.41
1:I:458:LYS:C	1:I:458:LYS:CD	2.92	0.41
1:J:450:LEU:O	1:J:508:LYS:NZ	2.53	0.41
1:J:784:LEU:HD23	1:J:784:LEU:HA	1.84	0.41
1:J:890:ARG:C	1:J:892:GLU:H	2.29	0.41
1:K:268:VAL:O	1:K:272:ILE:CD1	2.69	0.41
1:K:311:GLY:O	1:K:312:LEU:HB2	2.20	0.41
1:L:269:LEU:CD2	1:L:457:SER:HB2	2.51	0.41
1:L:355:LEU:HD23	1:L:357:LEU:HD22	2.03	0.41
1:A:286:THR:OG1	1:A:361:PRO:HB3	2.19	0.40
1:A:710:ASP:O	1:A:832:LYS:NZ	2.43	0.40
1:A:775:GLY:HA2	1:A:779:PHE:O	2.21	0.40
1:A:780:SER:CA	1:H:775:GLY:HA3	2.50	0.40
1:B:269:LEU:HA	1:B:272:ILE:HD12	2.03	0.40
1:B:387:ILE:HG22	1:B:415:VAL:HG21	2.03	0.40
1:B:611:GLU:H	1:B:612:PRO:CD	2.34	0.40
1:B:778:GLY:C	1:B:779:PHE:CD1	2.99	0.40
1:C:231:THR:O	1:C:235:ILE:HG22	2.21	0.40
1:C:276:GLU:HG2	1:C:277:PHE:H	1.87	0.40
1:C:616:ILE:HG23	1:C:617:ASP:OD1	2.22	0.40
1:C:784:LEU:HD23	1:C:784:LEU:HA	1.93	0.40
1:D:255:ILE:HG12	1:D:513:LEU:HD21	2.03	0.40
1:E:742:GLU:CD	1:E:748:ARG:HE	2.29	0.40
1:G:266:SER:HA	1:G:269:LEU:HD22	2.03	0.40
1:G:349:SER:HB3	1:G:352:ILE:HG12	2.02	0.40
1:H:270:GLU:C	1:H:273:VAL:HG22	2.45	0.40
1:H:832:LYS:O	1:H:835:GLN:HG2	2.20	0.40
1:I:242:GLN:HE22	1:I:344:ARG:CD	2.34	0.40
1:I:269:LEU:CD2	1:I:269:LEU:C	2.90	0.40
1:I:690:ARG:O	1:I:694:THR:HG23	2.20	0.40
1:I:907:ILE:HD12	1:I:907:ILE:HA	1.92	0.40
1:J:232:LYS:HE2	1:J:232:LYS:HB3	1.84	0.40
1:J:258:ILE:HG21	1:J:387:ILE:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:530:ARG:HA	1:J:530:ARG:HD3	1.80	0.40
1:L:803:ARG:HD2	1:L:823:GLU:CD	2.46	0.40
1:L:861:LEU:HD23	1:L:861:LEU:HA	1.76	0.40
1:A:279:PRO:HG3	1:A:322:GLN:HA	2.03	0.40
1:A:307:PHE:N	1:A:307:PHE:HD1	2.18	0.40
1:A:775:GLY:HA2	1:H:780:SER:CA	2.50	0.40
1:C:269:LEU:O	1:C:273:VAL:HG13	2.21	0.40
1:C:296:ASN:H	1:C:354:ASP:HB3	1.86	0.40
1:D:270:GLU:C	1:D:270:GLU:CD	2.89	0.40
1:D:382:LEU:HD12	1:D:382:LEU:O	2.21	0.40
1:D:806:ALA:O	1:D:809:SER:HB3	2.22	0.40
1:E:615:ILE:H	1:E:615:ILE:CD1	2.25	0.40
1:E:907:ILE:HD12	1:E:907:ILE:HA	1.95	0.40
1:F:628:TRP:CE3	1:F:628:TRP:HA	2.55	0.40
1:H:252:LEU:HD23	1:H:252:LEU:HA	1.91	0.40
1:H:277:PHE:HD1	1:H:278:LEU:N	2.19	0.40
1:H:450:LEU:HD22	1:H:512:VAL:CG2	2.51	0.40
1:H:454:GLY:O	1:H:455:VAL:CG1	2.69	0.40
1:I:474:LEU:HG	1:I:475:ALA:N	2.35	0.40
1:I:664:LEU:HD23	1:I:676:ARG:HG3	2.04	0.40
1:J:318:PHE:CD1	1:J:321:ILE:HD12	2.57	0.40
1:K:749:LYS:H	1:K:749:LYS:HD2	1.86	0.40
1:A:240:LEU:N	1:A:240:LEU:CD2	2.84	0.40
1:A:454:GLY:O	1:A:455:VAL:CG1	2.70	0.40
1:B:227:MET:O	1:B:230:ILE:HG22	2.21	0.40
1:D:657:GLN:HE21	1:D:657:GLN:HB2	1.57	0.40
1:E:520:LYS:HA	1:E:520:LYS:HD3	1.79	0.40
1:F:296:ASN:H	1:F:354:ASP:HB3	1.86	0.40
1:F:572:PHE:HB3	1:F:850:TYR:OH	2.22	0.40
1:G:387:ILE:HG21	1:G:393:ILE:HD12	2.04	0.40
1:G:529:GLN:O	1:G:533:GLU:HG3	2.21	0.40
1:H:270:GLU:CA	1:H:273:VAL:HG22	2.50	0.40
1:H:279:PRO:O	1:H:280:LYS:HG2	2.22	0.40
1:I:243:LYS:O	1:I:243:LYS:CG	2.70	0.40
1:I:450:LEU:HD22	1:I:512:VAL:CG2	2.51	0.40
1:I:478:ASN:O	1:I:482:LYS:HG2	2.21	0.40
1:J:582:LYS:HE3	1:J:582:LYS:HB2	1.83	0.40
1:J:702:LEU:HD23	1:J:702:LEU:HA	1.89	0.40
1:K:272:ILE:CG2	1:K:277:PHE:CD1	2.93	0.40
1:A:246:GLN:HE22	1:A:890:ARG:HH12	1.69	0.40
1:A:865:MET:HB3	1:A:871:LEU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:GLY:O	1:B:506:ARG:HD2	2.21	0.40
1:B:387:ILE:HG21	1:B:393:ILE:HD12	2.02	0.40
1:C:387:ILE:HG22	1:C:415:VAL:HG21	2.03	0.40
1:D:272:ILE:CG2	1:D:278:LEU:N	2.78	0.40
1:F:722:HIS:O	1:F:726:VAL:HG23	2.22	0.40
1:H:664:LEU:HB3	1:H:676:ARG:NH2	2.36	0.40
1:I:376:LYS:HZ1	1:I:379:ILE:HD12	1.79	0.40
1:I:664:LEU:HB3	1:I:676:ARG:NH2	2.36	0.40
1:J:294:LEU:HB2	1:J:355:LEU:H	1.86	0.40
1:J:480:ASN:HA	1:J:483:ASN:OD1	2.22	0.40
1:K:240:LEU:N	1:K:240:LEU:CD2	2.79	0.40
1:K:474:LEU:CG	1:K:475:ALA:N	2.84	0.40
1:K:488:HIS:O	1:K:491:GLU:HG2	2.22	0.40
1:K:540:LYS:HA	1:K:545:GLU:HG3	2.03	0.40
1:A:574:ARG:HD2	1:A:839:LEU:HD12	2.03	0.40
1:B:269:LEU:O	1:B:273:VAL:HG13	2.21	0.40
1:C:269:LEU:HD11	1:C:457:SER:O	2.21	0.40
1:D:269:LEU:CD2	1:D:457:SER:O	2.70	0.40
1:D:520:LYS:HA	1:D:520:LYS:HD3	1.79	0.40
1:E:682:ALA:O	1:E:686:VAL:HG23	2.21	0.40
1:E:749:LYS:O	1:E:753:GLU:HG3	2.20	0.40
1:F:611:GLU:O	1:F:611:GLU:HG3	2.22	0.40
1:G:418:ARG:HH21	1:G:420:GLU:HB3	1.86	0.40
1:G:754:VAL:HG22	1:G:779:PHE:CD2	2.56	0.40
1:G:855:ARG:HA	1:G:855:ARG:NE	2.37	0.40
1:H:246:GLN:CG	1:H:247:GLY:N	2.84	0.40
1:H:328:LEU:HD13	1:H:343:ILE:HD13	2.03	0.40
1:H:418:ARG:HH21	1:H:420:GLU:HB3	1.86	0.40
1:K:339:THR:CG2	1:K:340:ASP:H	2.34	0.40
1:L:269:LEU:HD21	1:L:457:SER:HB2	2.04	0.40
1:L:387:ILE:HG21	1:L:393:ILE:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	36	72
1	B	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	36	72
1	C	651/695 (94%)	624 (96%)	25 (4%)	2 (0%)	36	72
1	D	651/695 (94%)	631 (97%)	19 (3%)	1 (0%)	43	78
1	E	651/695 (94%)	625 (96%)	26 (4%)	0	100	100
1	F	651/695 (94%)	623 (96%)	26 (4%)	2 (0%)	36	72
1	G	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	36	72
1	H	651/695 (94%)	630 (97%)	20 (3%)	1 (0%)	43	78
1	I	651/695 (94%)	625 (96%)	25 (4%)	1 (0%)	43	78
1	J	651/695 (94%)	623 (96%)	26 (4%)	2 (0%)	36	72
1	K	651/695 (94%)	627 (96%)	23 (4%)	1 (0%)	43	78
1	L	651/695 (94%)	627 (96%)	22 (3%)	2 (0%)	36	72
All	All	7812/8340 (94%)	7510 (96%)	284 (4%)	18 (0%)	44	78

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	611	GLU
1	F	611	GLU
1	L	611	GLU
1	A	388	ARG
1	B	611	GLU
1	G	611	GLU
1	I	574	ARG
1	J	611	GLU
1	A	574	ARG
1	D	574	ARG
1	B	574	ARG
1	F	574	ARG
1	H	574	ARG
1	L	574	ARG
1	C	574	ARG
1	G	574	ARG
1	J	574	ARG
1	K	574	ARG

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%)	461 (82%)	102 (18%)	2	9
1	B	563/594 (95%)	491 (87%)	72 (13%)	4	15
1	C	563/594 (95%)	496 (88%)	67 (12%)	5	18
1	D	563/594 (95%)	459 (82%)	104 (18%)	1	8
1	E	563/594 (95%)	468 (83%)	95 (17%)	2	10
1	F	563/594 (95%)	490 (87%)	73 (13%)	4	15
1	G	563/594 (95%)	488 (87%)	75 (13%)	4	14
1	H	563/594 (95%)	457 (81%)	106 (19%)	1	8
1	I	563/594 (95%)	459 (82%)	104 (18%)	1	8
1	J	563/594 (95%)	493 (88%)	70 (12%)	4	17
1	K	563/594 (95%)	463 (82%)	100 (18%)	2	9
1	L	563/594 (95%)	497 (88%)	66 (12%)	5	18
All	All	6756/7128 (95%)	5722 (85%)	1034 (15%)	5	12

All (1034) 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	235	ILE
1	A	237	ILE
1	A	240	LEU
1	A	241	LEU
1	A	243	LYS
1	A	244	VAL
1	A	251	THR
1	A	255	ILE
1	A	263	SER

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Mol	Chain	Res	Type
1	A	266	SER
1	A	268	VAL
1	A	269	LEU
1	A	272	ILE
1	A	278	LEU
1	A	282	SER
1	A	284	MET
1	A	285	ILE
1	A	287	ARG
1	A	303	ASP
1	A	310	LEU
1	A	312	LEU
1	A	320	LEU
1	A	344	ARG
1	A	346	THR
1	A	351	ASN
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	382	LEU
1	A	383	CYS
1	A	385	LYS
1	A	387	ILE
1	A	388	ARG
1	A	393	ILE
1	A	394	LEU
1	A	396	ILE
1	A	400	ASP
1	A	402	ASP
1	A	407	THR
1	A	412	SER
1	A	423	ILE
1	A	430	ASP
1	A	434	PRO
1	A	448	LEU
1	A	449	LYS
1	A	450	LEU

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Mol	Chain	Res	Type
1	A	456	ILE
1	A	457	SER
1	A	458	LYS
1	A	474	LEU
1	A	479	ARG
1	A	481	GLU
1	A	483	ASN
1	A	490	THR
1	A	491	GLU
1	A	492	PHE
1	A	498	VAL
1	A	499	SER
1	A	505	LEU
1	A	507	LYS
1	A	513	LEU
1	A	516	GLN
1	A	546	GLN
1	A	560	ASP
1	A	576	GLN
1	A	590	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	657	GLN
1	A	671	LYS
1	A	676	ARG
1	A	714	ASN
1	A	727	LEU
1	A	739	LYS
1	A	749	LYS
1	A	762	ARG
1	A	768	VAL
1	A	784	LEU
1	A	802	LEU
1	A	815	LEU
1	A	836	THR
1	A	838	VAL
1	A	839	LEU

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Mol	Chain	Res	Type
1	A	841	LEU
1	A	871	LEU
1	A	893	LEU
1	A	903	GLU
1	B	231	THR
1	B	237	ILE
1	B	244	VAL
1	B	251	THR
1	B	255	ILE
1	B	266	SER
1	B	269	LEU
1	B	273	VAL
1	B	278	LEU
1	B	282	SER
1	B	284	MET
1	B	303	ASP
1	B	320	LEU
1	B	339	THR
1	B	344	ARG
1	B	346	THR
1	B	358	ILE
1	B	376	LYS
1	B	377	ARG
1	B	378	LYS
1	B	382	LEU
1	B	385	LYS
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	412	SER
1	B	423	ILE
1	B	430	ASP
1	B	448	LEU
1	B	458	LYS
1	B	474	LEU
1	B	479	ARG
1	B	481	GLU
1	B	483	ASN
1	B	490	THR

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Mol	Chain	Res	Type
1	B	491	GLU
1	B	492	PHE
1	B	495	ASP
1	B	500	THR
1	B	503	MET
1	B	557	SER
1	B	563	HIS
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	616	ILE
1	B	617	ASP
1	B	618	LEU
1	B	632	LEU
1	B	654	SER
1	B	666	LYS
1	B	690	ARG
1	B	710	ASP
1	B	714	ASN
1	B	721	GLU
1	B	727	LEU
1	B	741	LEU
1	B	803	ARG
1	B	815	LEU
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	B	906	ARG
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	273	VAL

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Mol	Chain	Res	Type
1	C	278	LEU
1	C	282	SER
1	C	284	MET
1	C	287	ARG
1	C	303	ASP
1	C	320	LEU
1	C	339	THR
1	C	344	ARG
1	C	346	THR
1	C	358	ILE
1	C	376	LYS
1	C	377	ARG
1	C	382	LEU
1	C	385	LYS
1	C	388	ARG
1	C	393	ILE
1	C	394	LEU
1	C	396	ILE
1	C	400	ASP
1	C	402	ASP
1	C	423	ILE
1	C	430	ASP
1	C	448	LEU
1	C	458	LYS
1	C	474	LEU
1	C	481	GLU
1	C	483	ASN
1	C	490	THR
1	C	491	GLU
1	C	492	PHE
1	C	500	THR
1	C	503	MET
1	C	563	HIS
1	C	590	LEU
1	C	600	ARG
1	C	603	GLU
1	C	605	LEU
1	C	611	GLU
1	C	613	ASP
1	C	615	ILE
1	C	616	ILE
1	C	617	ASP

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Mol	Chain	Res	Type
1	C	618	LEU
1	C	632	LEU
1	C	654	SER
1	C	666	LYS
1	C	690	ARG
1	C	714	ASN
1	C	727	LEU
1	C	741	LEU
1	C	752	LYS
1	C	803	ARG
1	C	815	LEU
1	C	817	ASN
1	C	824	VAL
1	C	838	VAL
1	C	841	LEU
1	C	873	LYS
1	C	880	LYS
1	D	225	ASP
1	D	227	MET
1	D	228	MET
1	D	229	PHE
1	D	230	ILE
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
1	D	263	SER
1	D	266	SER
1	D	268	VAL
1	D	269	LEU
1	D	272	ILE
1	D	278	LEU
1	D	282	SER
1	D	284	MET
1	D	285	ILE
1	D	287	ARG
1	D	303	ASP

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Mol	Chain	Res	Type
1	D	320	LEU
1	D	344	ARG
1	D	346	THR
1	D	351	ASN
1	D	354	ASP
1	D	358	ILE
1	D	360	LEU
1	D	363	TYR
1	D	375	LEU
1	D	376	LYS
1	D	377	ARG
1	D	378	LYS
1	D	382	LEU
1	D	383	CYS
1	D	385	LYS
1	D	387	ILE
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	405	ASN
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	450	LEU
1	D	456	ILE
1	D	457	SER
1	D	458	LYS
1	D	474	LEU
1	D	479	ARG
1	D	481	GLU
1	D	483	ASN
1	D	490	THR
1	D	491	GLU
1	D	498	VAL
1	D	499	SER
1	D	507	LYS

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Mol	Chain	Res	Type
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	590	LEU
1	D	610	ARG
1	D	615	ILE
1	D	617	ASP
1	D	632	LEU
1	D	640	THR
1	D	642	LEU
1	D	647	LEU
1	D	654	SER
1	D	657	GLN
1	D	671	LYS
1	D	714	ASN
1	D	727	LEU
1	D	739	LYS
1	D	749	LYS
1	D	752	LYS
1	D	762	ARG
1	D	768	VAL
1	D	784	LEU
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

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Mol	Chain	Res	Type
1	E	237	ILE
1	E	240	LEU
1	E	241	LEU
1	E	243	LYS
1	E	244	VAL
1	E	251	THR
1	E	255	ILE
1	E	263	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	303	ASP
1	E	310	LEU
1	E	320	LEU
1	E	344	ARG
1	E	346	THR
1	E	351	ASN
1	E	354	ASP
1	E	358	ILE
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	393	ILE
1	E	394	LEU
1	E	396	ILE
1	E	400	ASP
1	E	402	ASP
1	E	412	SER
1	E	423	ILE

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Mol	Chain	Res	Type
1	E	430	ASP
1	E	434	PRO
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	481	GLU
1	E	483	ASN
1	E	490	THR
1	E	491	GLU
1	E	498	VAL
1	E	499	SER
1	E	505	LEU
1	E	507	LYS
1	E	513	LEU
1	E	515	GLN
1	E	516	GLN
1	E	546	GLN
1	E	548	MET
1	E	590	LEU
1	E	610	ARG
1	E	615	ILE
1	E	617	ASP
1	E	632	LEU
1	E	640	THR
1	E	642	LEU
1	E	654	SER
1	E	657	GLN
1	E	671	LYS
1	E	695	SER
1	E	714	ASN
1	E	721	GLU
1	E	727	LEU
1	E	739	LYS
1	E	749	LYS
1	E	762	ARG
1	E	768	VAL
1	E	802	LEU
1	E	815	LEU

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Mol	Chain	Res	Type
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
1	F	269	LEU
1	F	277	PHE
1	F	278	LEU
1	F	282	SER
1	F	284	MET
1	F	287	ARG
1	F	303	ASP
1	F	310	LEU
1	F	320	LEU
1	F	325	LEU
1	F	339	THR
1	F	344	ARG
1	F	346	THR
1	F	358	ILE
1	F	375	LEU
1	F	376	LYS
1	F	377	ARG
1	F	378	LYS
1	F	382	LEU
1	F	388	ARG
1	F	393	ILE
1	F	394	LEU
1	F	396	ILE
1	F	400	ASP
1	F	402	ASP
1	F	405	ASN
1	F	412	SER
1	F	423	ILE
1	F	430	ASP
1	F	448	LEU

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Mol	Chain	Res	Type
1	F	458	LYS
1	F	474	LEU
1	F	479	ARG
1	F	481	GLU
1	F	483	ASN
1	F	490	THR
1	F	491	GLU
1	F	492	PHE
1	F	500	THR
1	F	503	MET
1	F	557	SER
1	F	590	LEU
1	F	600	ARG
1	F	605	LEU
1	F	611	GLU
1	F	613	ASP
1	F	615	ILE
1	F	617	ASP
1	F	618	LEU
1	F	622	ASP
1	F	632	LEU
1	F	642	LEU
1	F	666	LYS
1	F	690	ARG
1	F	714	ASN
1	F	727	LEU
1	F	741	LEU
1	F	752	LYS
1	F	783	LEU
1	F	803	ARG
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	237	ILE
1	G	244	VAL
1	G	251	THR
1	G	255	ILE

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Mol	Chain	Res	Type
1	G	266	SER
1	G	269	LEU
1	G	273	VAL
1	G	278	LEU
1	G	282	SER
1	G	284	MET
1	G	285	ILE
1	G	287	ARG
1	G	303	ASP
1	G	320	LEU
1	G	339	THR
1	G	344	ARG
1	G	346	THR
1	G	358	ILE
1	G	375	LEU
1	G	376	LYS
1	G	377	ARG
1	G	378	LYS
1	G	382	LEU
1	G	385	LYS
1	G	388	ARG
1	G	393	ILE
1	G	394	LEU
1	G	396	ILE
1	G	400	ASP
1	G	402	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	483	ASN
1	G	490	THR
1	G	491	GLU
1	G	492	PHE
1	G	495	ASP
1	G	500	THR
1	G	503	MET
1	G	557	SER

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Mol	Chain	Res	Type
1	G	590	LEU
1	G	600	ARG
1	G	605	LEU
1	G	611	GLU
1	G	613	ASP
1	G	615	ILE
1	G	616	ILE
1	G	617	ASP
1	G	618	LEU
1	G	632	LEU
1	G	654	SER
1	G	666	LYS
1	G	690	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	803	ARG
1	G	811	GLN
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	230	ILE
1	H	233	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

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Mol	Chain	Res	Type
1	H	268	VAL
1	H	269	LEU
1	H	272	ILE
1	H	278	LEU
1	H	282	SER
1	H	284	MET
1	H	285	ILE
1	H	287	ARG
1	H	303	ASP
1	H	320	LEU
1	H	344	ARG
1	H	346	THR
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	387	ILE
1	H	388	ARG
1	H	393	ILE
1	H	394	LEU
1	H	396	ILE
1	H	400	ASP
1	H	402	ASP
1	H	405	ASN
1	H	407	THR
1	H	412	SER
1	H	423	ILE
1	H	430	ASP
1	H	434	PRO
1	H	435	GLU
1	H	448	LEU
1	H	450	LEU
1	H	456	ILE
1	H	457	SER

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Mol	Chain	Res	Type
1	H	458	LYS
1	H	474	LEU
1	H	479	ARG
1	H	481	GLU
1	H	483	ASN
1	H	490	THR
1	H	491	GLU
1	H	492	PHE
1	H	495	ASP
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	546	GLN
1	H	557	SER
1	H	560	ASP
1	H	576	GLN
1	H	590	LEU
1	H	610	ARG
1	H	614	ASN
1	H	615	ILE
1	H	617	ASP
1	H	632	LEU
1	H	640	THR
1	H	642	LEU
1	H	647	LEU
1	H	654	SER
1	H	657	GLN
1	H	671	LYS
1	H	714	ASN
1	H	727	LEU
1	H	739	LYS
1	H	749	LYS
1	H	762	ARG
1	H	768	VAL
1	H	783	LEU
1	H	802	LEU
1	H	815	LEU
1	H	836	THR

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Mol	Chain	Res	Type
1	H	838	VAL
1	H	839	LEU
1	H	841	LEU
1	H	855	ARG
1	H	871	LEU
1	H	893	LEU
1	H	903	GLU
1	H	907	ILE
1	I	225	ASP
1	I	227	MET
1	I	228	MET
1	I	229	PHE
1	I	230	ILE
1	I	235	ILE
1	I	237	ILE
1	I	240	LEU
1	I	241	LEU
1	I	243	LYS
1	I	244	VAL
1	I	251	THR
1	I	255	ILE
1	I	263	SER
1	I	266	SER
1	I	268	VAL
1	I	269	LEU
1	I	272	ILE
1	I	278	LEU
1	I	282	SER
1	I	284	MET
1	I	285	ILE
1	I	287	ARG
1	I	303	ASP
1	I	310	LEU
1	I	320	LEU
1	I	344	ARG
1	I	346	THR
1	I	354	ASP
1	I	358	ILE
1	I	360	LEU
1	I	363	TYR
1	I	375	LEU
1	I	376	LYS

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Mol	Chain	Res	Type
1	I	377	ARG
1	I	378	LYS
1	I	382	LEU
1	I	383	CYS
1	I	385	LYS
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	407	THR
1	I	412	SER
1	I	423	ILE
1	I	430	ASP
1	I	434	PRO
1	I	448	LEU
1	I	450	LEU
1	I	456	ILE
1	I	457	SER
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	498	VAL
1	I	499	SER
1	I	505	LEU
1	I	507	LYS
1	I	513	LEU
1	I	515	GLN
1	I	516	GLN
1	I	546	GLN
1	I	557	SER
1	I	560	ASP
1	I	576	GLN
1	I	590	LEU
1	I	604	ASP
1	I	610	ARG

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Mol	Chain	Res	Type
1	I	615	ILE
1	I	617	ASP
1	I	622	ASP
1	I	632	LEU
1	I	640	THR
1	I	642	LEU
1	I	647	LEU
1	I	654	SER
1	I	657	GLN
1	I	671	LYS
1	I	714	ASN
1	I	727	LEU
1	I	739	LYS
1	I	749	LYS
1	I	752	LYS
1	I	762	ARG
1	I	768	VAL
1	I	784	LEU
1	I	802	LEU
1	I	815	LEU
1	I	836	THR
1	I	838	VAL
1	I	839	LEU
1	I	841	LEU
1	I	855	ARG
1	I	871	LEU
1	I	893	LEU
1	I	903	GLU
1	J	231	THR
1	J	237	ILE
1	J	244	VAL
1	J	251	THR
1	J	255	ILE
1	J	266	SER
1	J	269	LEU
1	J	273	VAL
1	J	278	LEU
1	J	282	SER
1	J	284	MET
1	J	285	ILE
1	J	287	ARG
1	J	303	ASP

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Mol	Chain	Res	Type
1	J	320	LEU
1	J	339	THR
1	J	344	ARG
1	J	346	THR
1	J	358	ILE
1	J	376	LYS
1	J	377	ARG
1	J	378	LYS
1	J	382	LEU
1	J	385	LYS
1	J	388	ARG
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	423	ILE
1	J	430	ASP
1	J	448	LEU
1	J	458	LYS
1	J	474	LEU
1	J	479	ARG
1	J	481	GLU
1	J	483	ASN
1	J	490	THR
1	J	491	GLU
1	J	492	PHE
1	J	495	ASP
1	J	500	THR
1	J	503	MET
1	J	557	SER
1	J	590	LEU
1	J	600	ARG
1	J	611	GLU
1	J	613	ASP
1	J	615	ILE
1	J	616	ILE
1	J	617	ASP
1	J	618	LEU
1	J	632	LEU
1	J	642	LEU

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Mol	Chain	Res	Type
1	J	654	SER
1	J	666	LYS
1	J	690	ARG
1	J	727	LEU
1	J	741	LEU
1	J	803	ARG
1	J	811	GLN
1	J	815	LEU
1	J	817	ASN
1	J	824	VAL
1	J	838	VAL
1	J	841	LEU
1	J	873	LYS
1	J	880	LYS
1	K	227	MET
1	K	228	MET
1	K	230	ILE
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	263	SER
1	K	266	SER
1	K	268	VAL
1	K	269	LEU
1	K	272	ILE
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	351	ASN

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Mol	Chain	Res	Type
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	393	ILE
1	K	394	LEU
1	K	396	ILE
1	K	400	ASP
1	K	402	ASP
1	K	407	THR
1	K	412	SER
1	K	423	ILE
1	K	430	ASP
1	K	433	GLU
1	K	434	PRO
1	K	448	LEU
1	K	450	LEU
1	K	456	ILE
1	K	457	SER
1	K	458	LYS
1	K	474	LEU
1	K	479	ARG
1	K	481	GLU
1	K	483	ASN
1	K	491	GLU
1	K	492	PHE
1	K	498	VAL
1	K	499	SER
1	K	505	LEU
1	K	507	LYS
1	K	513	LEU
1	K	515	GLN
1	K	516	GLN
1	K	546	GLN

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Mol	Chain	Res	Type
1	K	557	SER
1	K	560	ASP
1	K	576	GLN
1	K	590	LEU
1	K	610	ARG
1	K	615	ILE
1	K	617	ASP
1	K	632	LEU
1	K	640	THR
1	K	642	LEU
1	K	647	LEU
1	K	654	SER
1	K	657	GLN
1	K	671	LYS
1	K	714	ASN
1	K	727	LEU
1	K	739	LYS
1	K	749	LYS
1	K	762	ARG
1	K	768	VAL
1	K	802	LEU
1	K	811	GLN
1	K	815	LEU
1	K	836	THR
1	K	838	VAL
1	K	839	LEU
1	K	841	LEU
1	K	871	LEU
1	K	893	LEU
1	K	903	GLU
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	282	SER
1	L	284	MET
1	L	287	ARG

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Mol	Chain	Res	Type
1	L	303	ASP
1	L	320	LEU
1	L	344	ARG
1	L	346	THR
1	L	358	ILE
1	L	376	LYS
1	L	377	ARG
1	L	378	LYS
1	L	382	LEU
1	L	385	LYS
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	430	ASP
1	L	448	LEU
1	L	458	LYS
1	L	474	LEU
1	L	479	ARG
1	L	481	GLU
1	L	483	ASN
1	L	490	THR
1	L	491	GLU
1	L	492	PHE
1	L	500	THR
1	L	503	MET
1	L	557	SER
1	L	590	LEU
1	L	600	ARG
1	L	605	LEU
1	L	611	GLU
1	L	613	ASP
1	L	615	ILE
1	L	617	ASP
1	L	618	LEU
1	L	632	LEU
1	L	654	SER
1	L	666	LYS

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Mol	Chain	Res	Type
1	L	690	ARG
1	L	721	GLU
1	L	727	LEU
1	L	741	LEU
1	L	803	ARG
1	L	817	ASN
1	L	824	VAL
1	L	838	VAL
1	L	841	LEU
1	L	855	ARG
1	L	873	LYS
1	L	880	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (122) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	A	261	GLN
1	A	275	HIS
1	A	472	ASN
1	A	478	ASN
1	A	576	GLN
1	A	657	GLN
1	B	563	HIS
1	B	631	GLN
1	B	657	GLN
1	B	658	GLN
1	B	672	HIS
1	B	712	GLN
1	B	772	HIS
1	C	488	HIS
1	C	563	HIS
1	C	631	GLN
1	C	657	GLN
1	C	658	GLN
1	C	672	HIS
1	C	712	GLN
1	C	772	HIS
1	D	242	GLN
1	D	261	GLN
1	D	275	HIS
1	D	472	ASN

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Mol	Chain	Res	Type
1	D	478	ASN
1	D	488	HIS
1	D	544	ASN
1	D	563	HIS
1	D	566	HIS
1	D	576	GLN
1	D	592	GLN
1	D	657	GLN
1	D	659	HIS
1	D	847	ASN
1	D	866	HIS
1	E	242	GLN
1	E	261	GLN
1	E	275	HIS
1	E	472	ASN
1	E	478	ASN
1	E	488	HIS
1	E	576	GLN
1	E	592	GLN
1	E	657	GLN
1	E	659	HIS
1	E	672	HIS
1	E	811	GLN
1	E	842	ASN
1	E	864	HIS
1	E	866	HIS
1	F	529	GLN
1	F	563	HIS
1	F	631	GLN
1	F	657	GLN
1	F	672	HIS
1	F	772	HIS
1	G	563	HIS
1	G	614	ASN
1	G	631	GLN
1	G	658	GLN
1	G	672	HIS
1	G	712	GLN
1	G	772	HIS
1	H	242	GLN
1	H	261	GLN
1	H	275	HIS

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Mol	Chain	Res	Type
1	H	472	ASN
1	H	478	ASN
1	H	488	HIS
1	H	544	ASN
1	H	546	GLN
1	H	576	GLN
1	H	592	GLN
1	H	657	GLN
1	H	811	GLN
1	H	847	ASN
1	H	864	HIS
1	H	866	HIS
1	I	242	GLN
1	I	261	GLN
1	I	275	HIS
1	I	478	ASN
1	I	488	HIS
1	I	515	GLN
1	I	544	ASN
1	I	566	HIS
1	I	576	GLN
1	I	592	GLN
1	I	657	GLN
1	I	659	HIS
1	I	772	HIS
1	I	847	ASN
1	I	864	HIS
1	I	866	HIS
1	J	488	HIS
1	J	631	GLN
1	J	672	HIS
1	J	864	HIS
1	K	242	GLN
1	K	261	GLN
1	K	275	HIS
1	K	472	ASN
1	K	478	ASN
1	K	483	ASN
1	K	488	HIS
1	K	515	GLN
1	K	544	ASN
1	K	546	GLN

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Mol	Chain	Res	Type
1	K	576	GLN
1	K	657	GLN
1	K	659	HIS
1	K	772	HIS
1	K	811	GLN
1	K	847	ASN
1	L	329	ASN
1	L	563	HIS
1	L	631	GLN
1	L	657	GLN
1	L	672	HIS
1	L	712	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	D	1
1	H	1
1	E	1
1	I	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	1.14
1	D	253:PRO	C	254:SER	N	1.14
1	H	253:PRO	C	254:SER	N	1.14
1	E	253:PRO	C	254:SER	N	1.13
1	I	253:PRO	C	254:SER	N	1.13
1	K	253:PRO	C	254:SER	N	1.12

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10062. These allow visual inspection of the internal detail of the map and identification of artifacts.

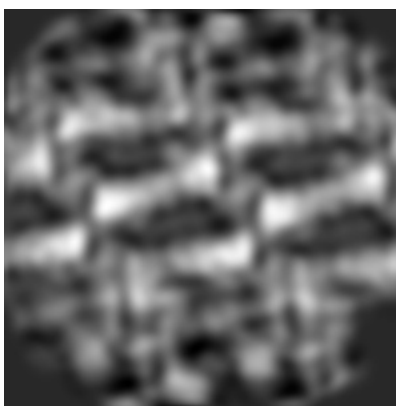
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

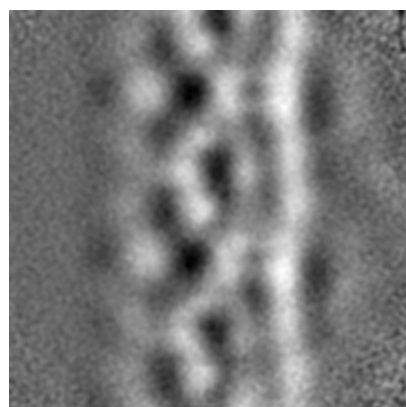


Y

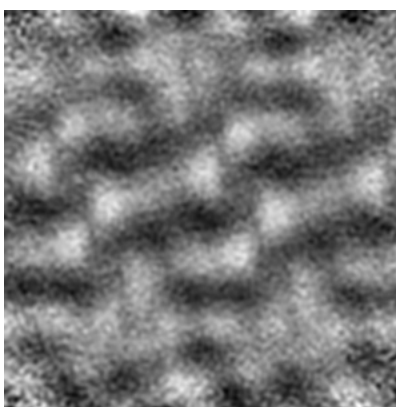


Z

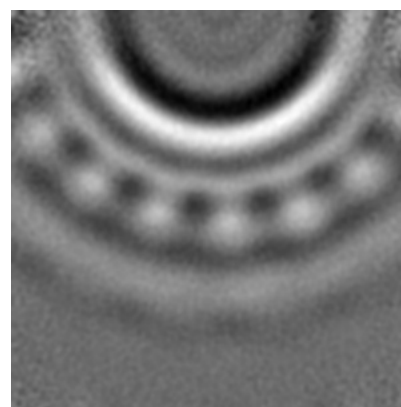
6.1.2 Raw map



X



Y



Z

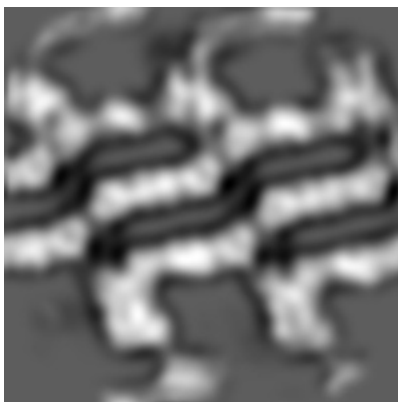
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 60

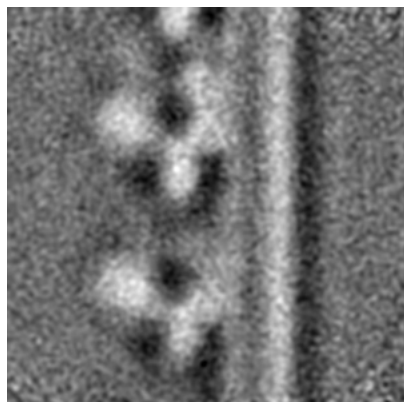


Y Index: 60

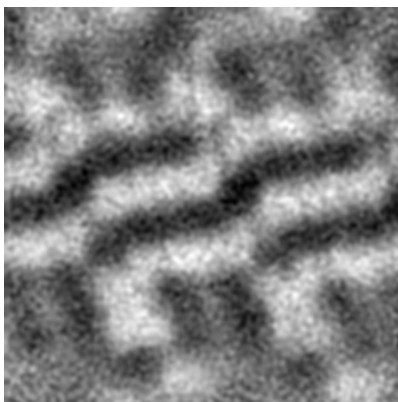


Z Index: 60

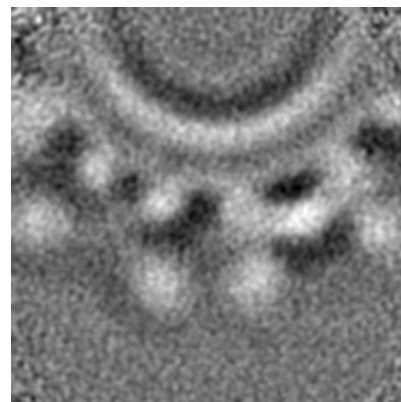
6.2.2 Raw map



X Index: 60



Y Index: 60

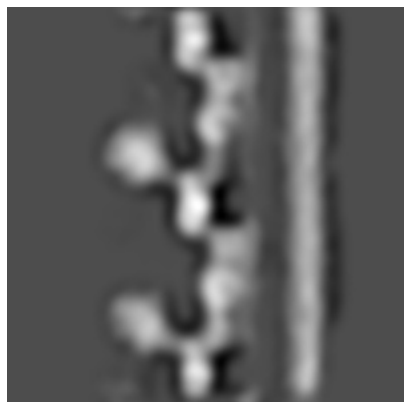


Z Index: 60

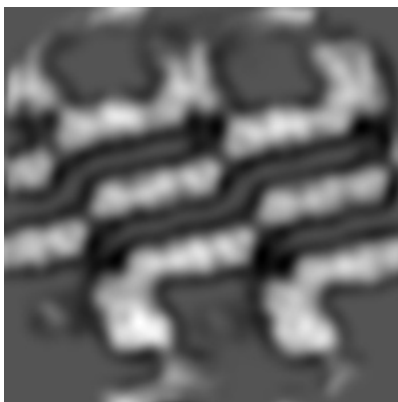
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 86

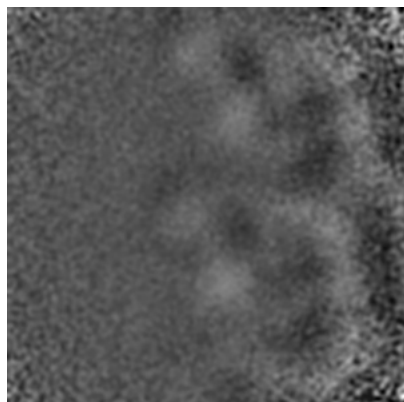


Y Index: 62

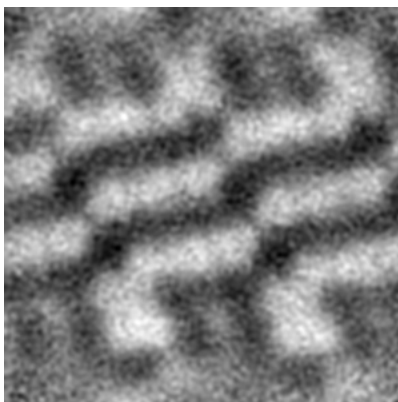


Z Index: 48

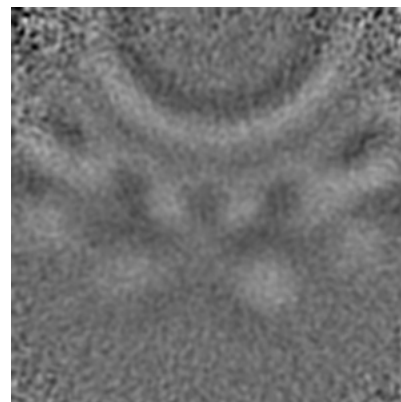
6.3.2 Raw map



X Index: 0



Y Index: 62

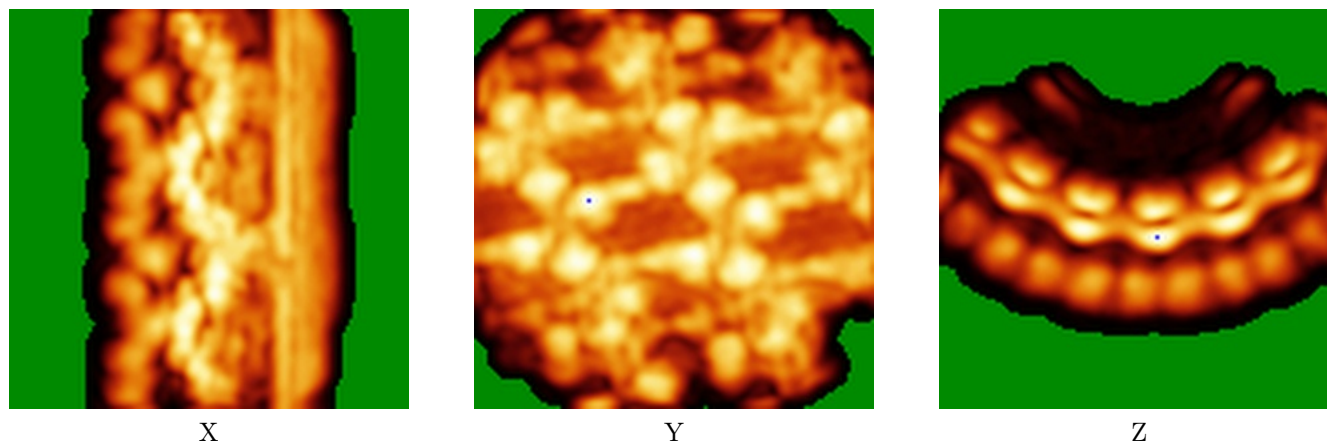


Z Index: 1

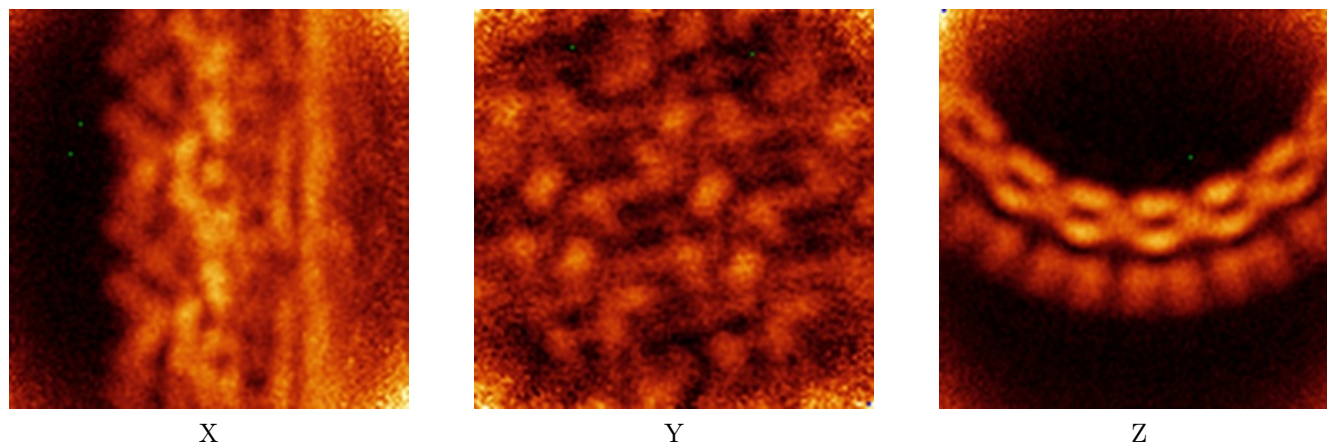
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

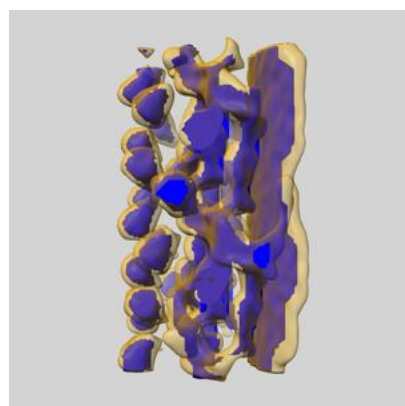
6.6 Mask visualisation [i](#)

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

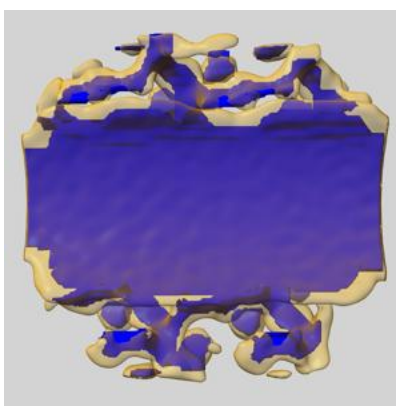
A mask typically either:

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

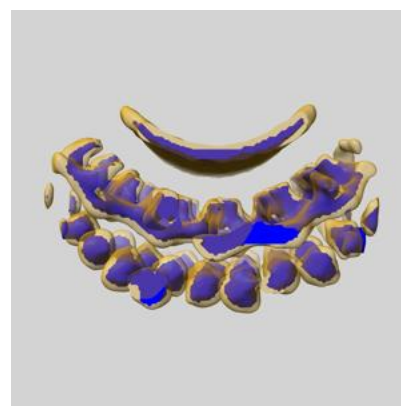
6.6.1 emd_10062_msk_1.map [i](#)



X



Y

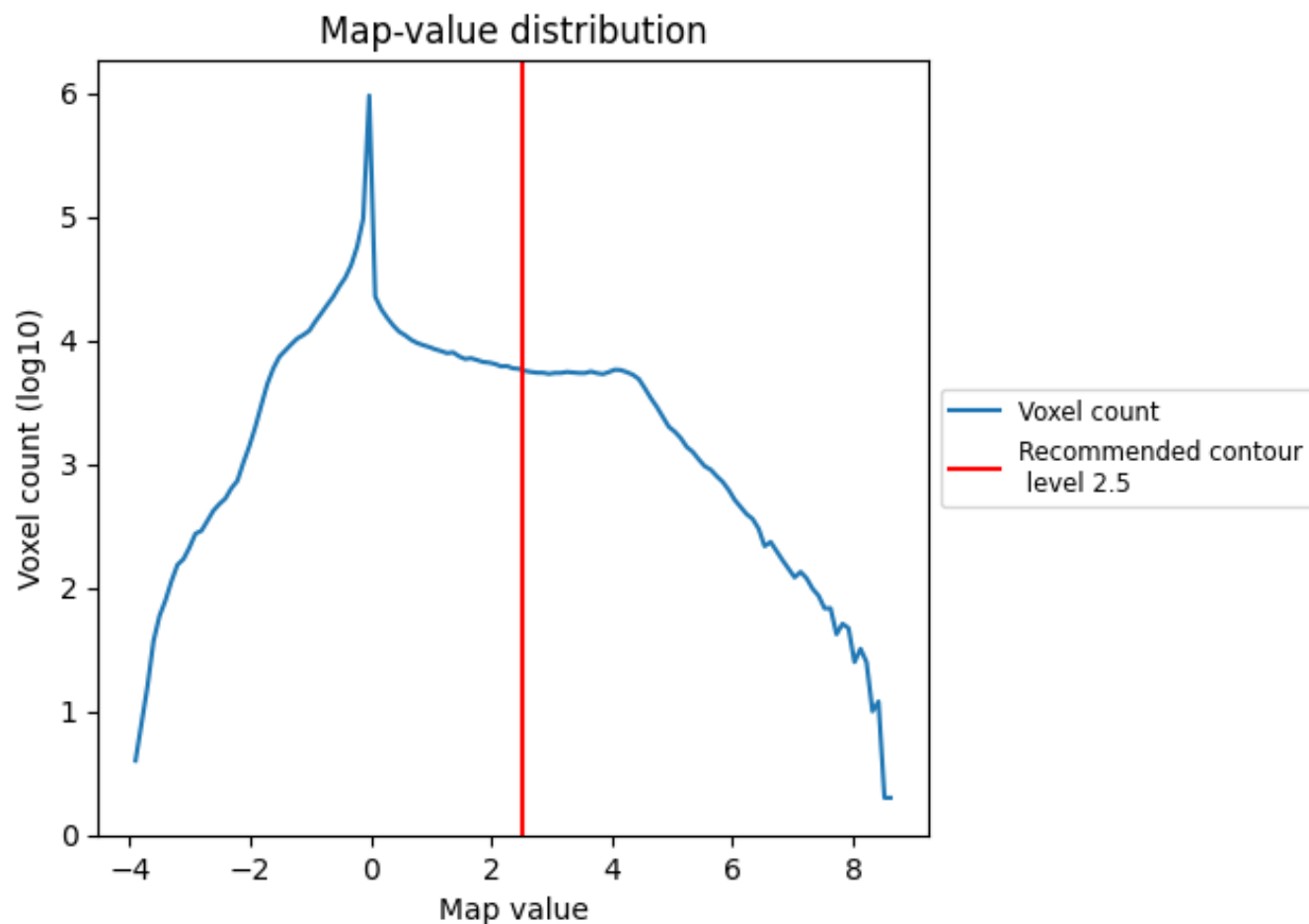


Z

7 Map analysis [i](#)

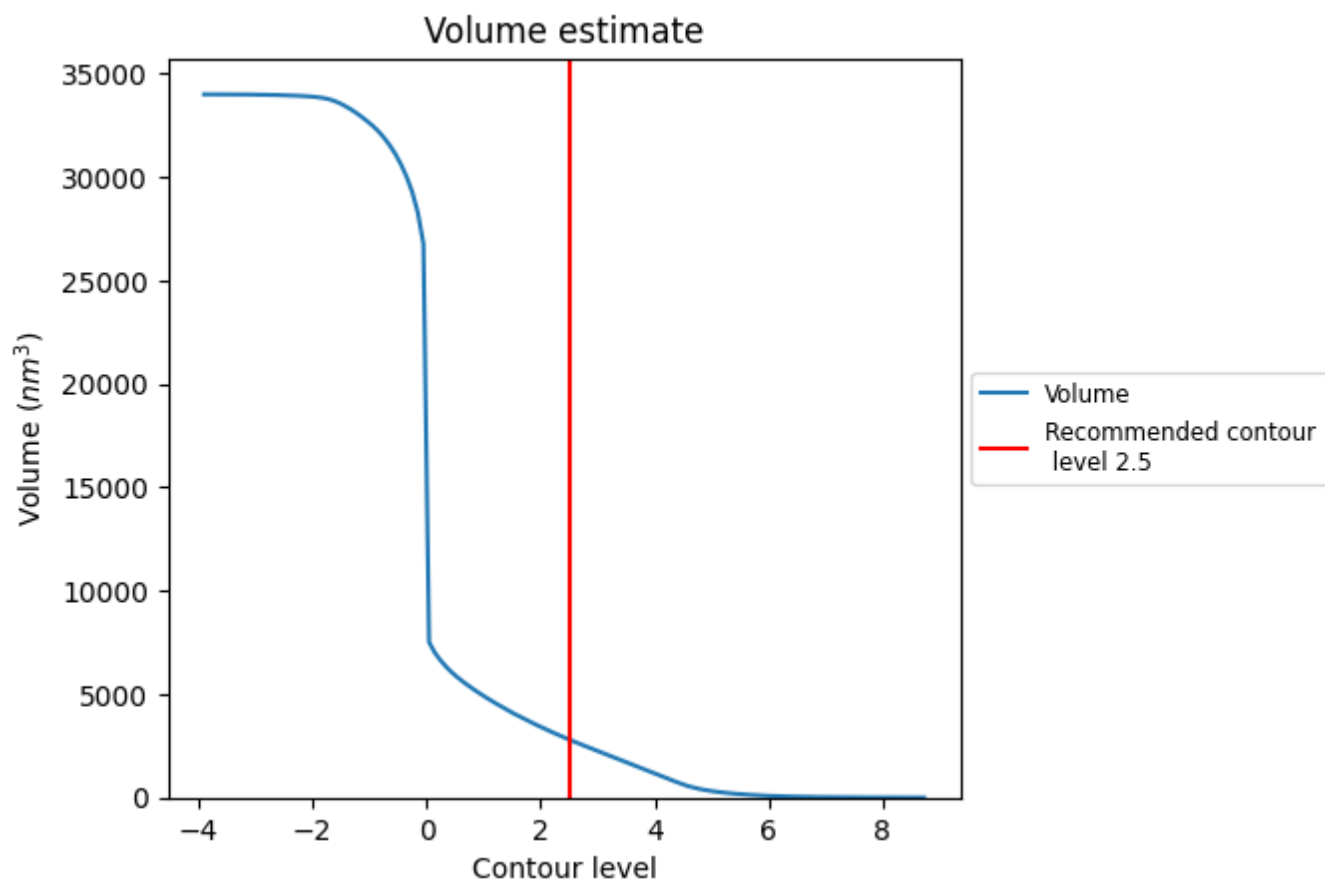
This section contains the results of statistical analysis of the map.

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.

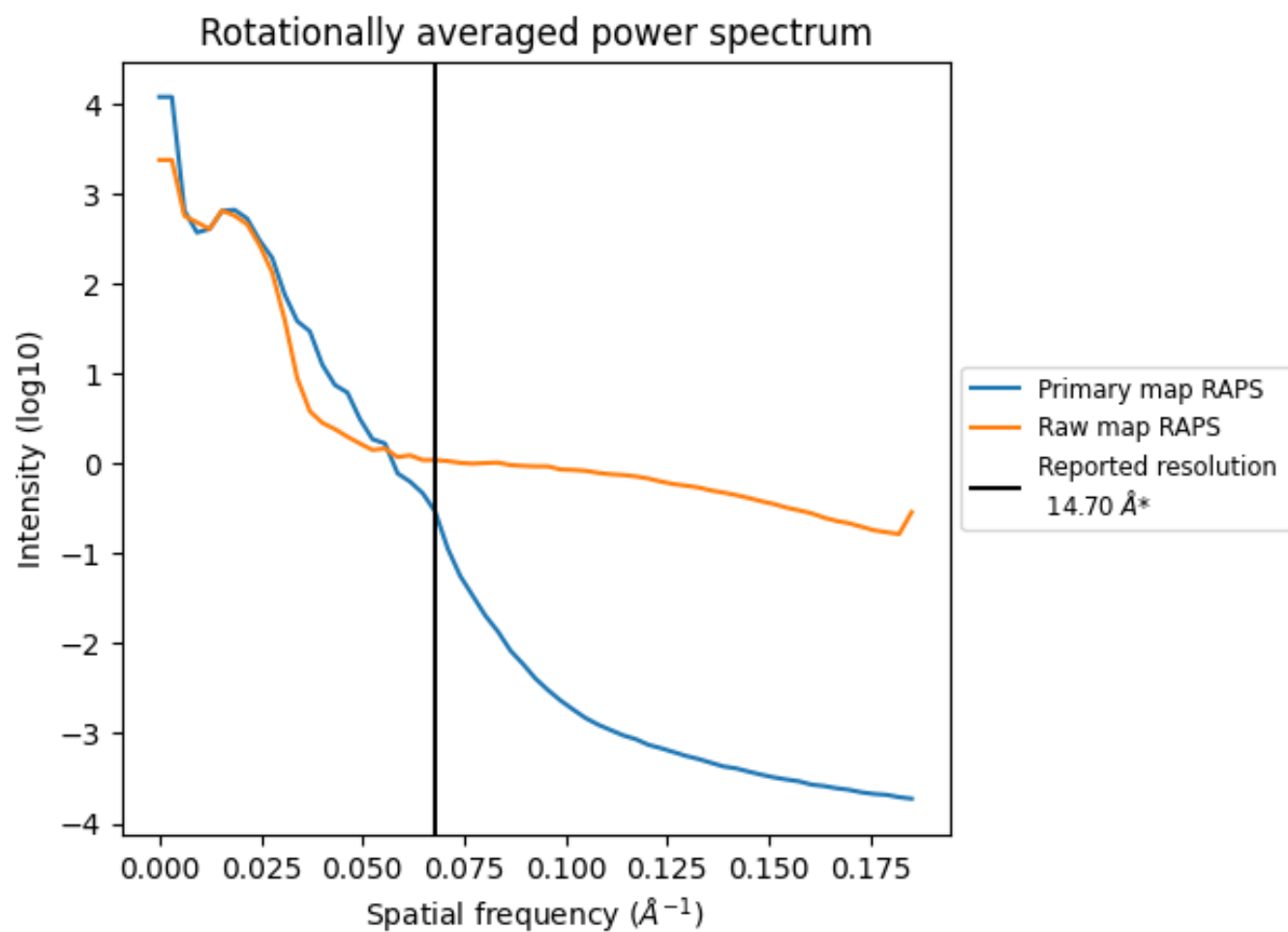
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2804 nm³; this corresponds to an approximate mass of 2533 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 ⓘ

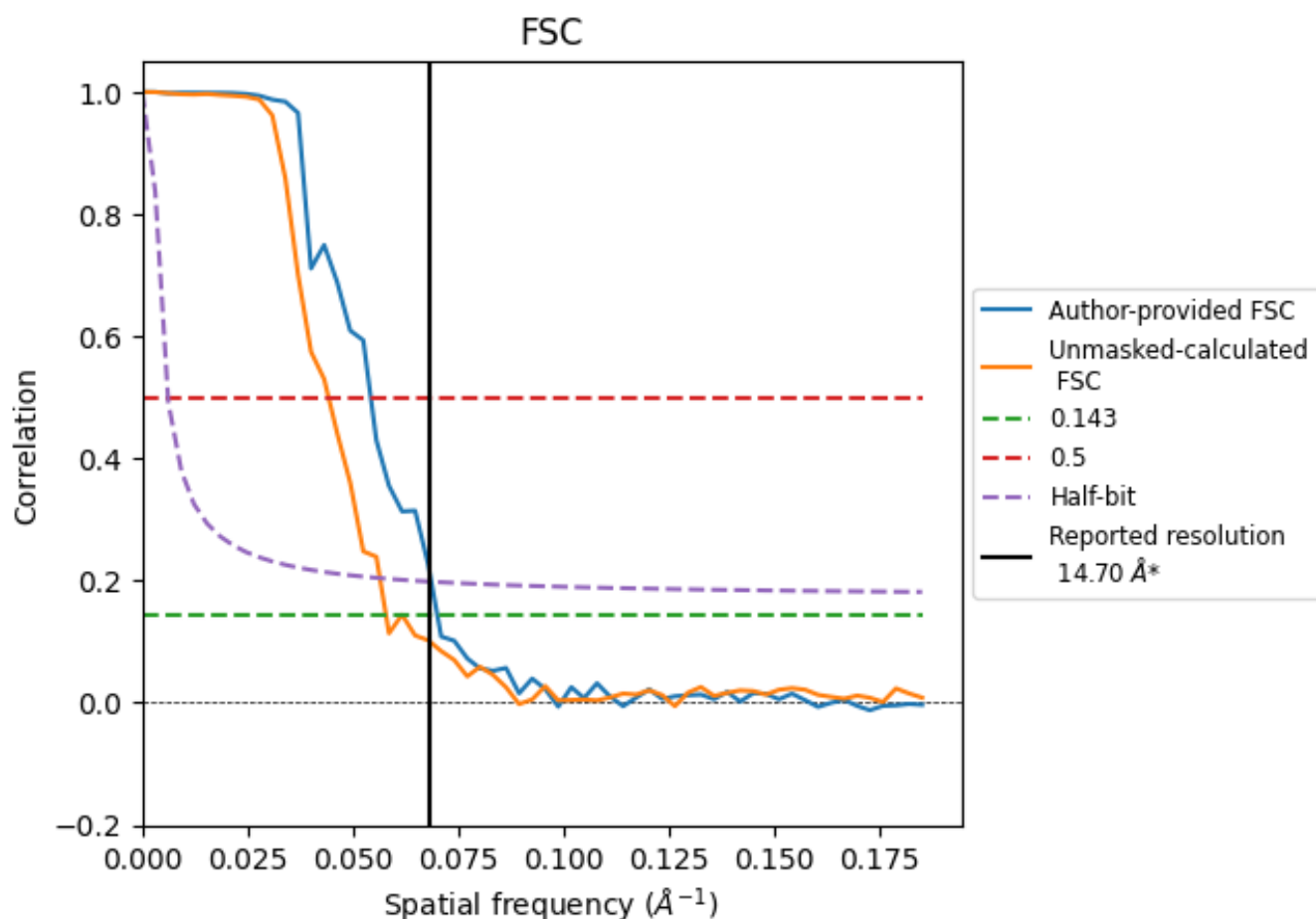


*Reported resolution corresponds to spatial frequency of 0.068 $\text{\AA}^{-1}$

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	14.27	18.45	14.56
Unmasked-calculated*	17.27	22.57	17.73

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

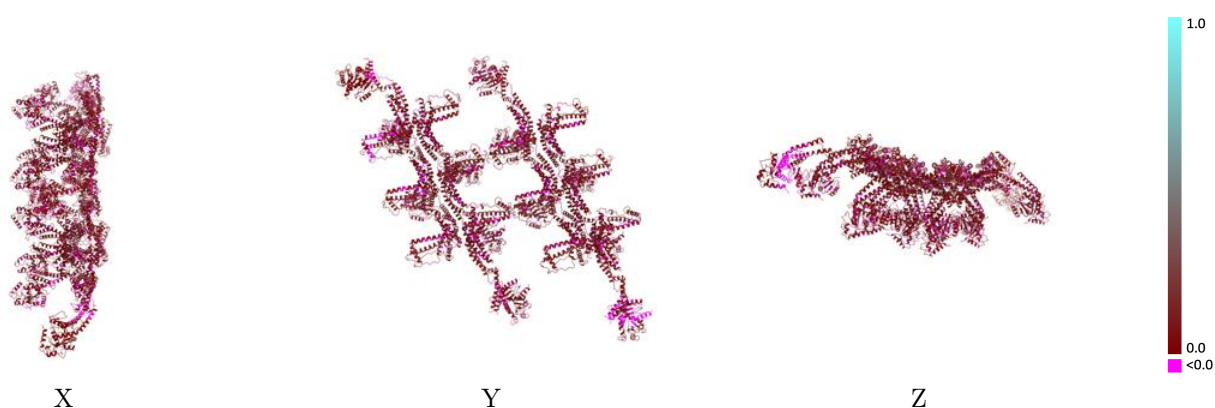
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10062 and PDB model 6RZT. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

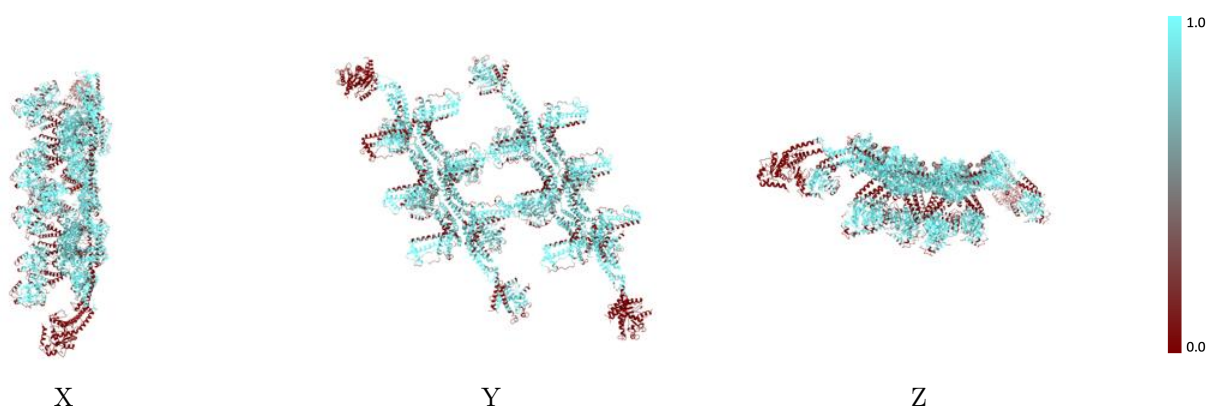
This section was not generated.

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



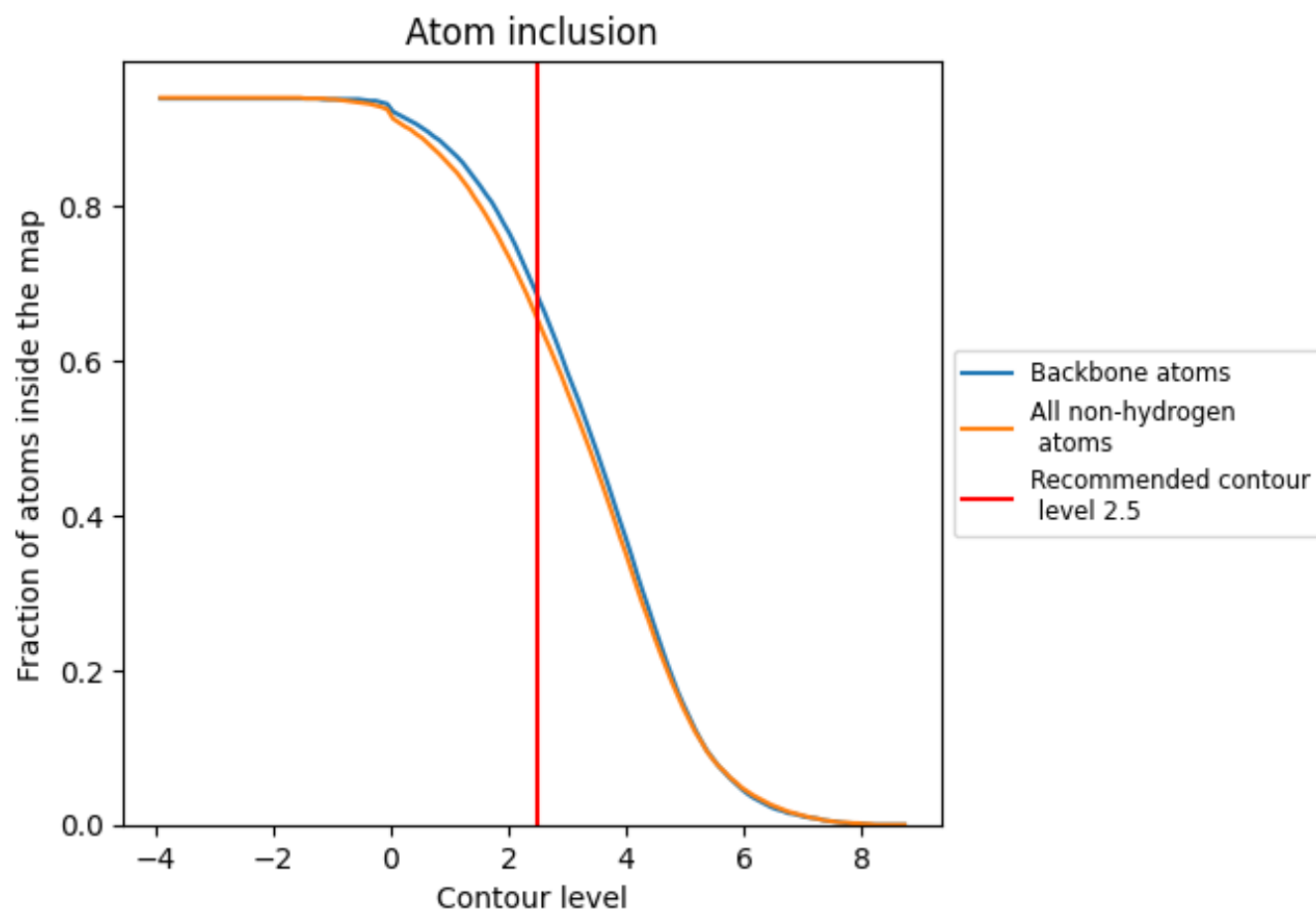
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 65% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6530	0.0650
A	0.7180	0.0740
B	0.7240	0.0690
C	0.7280	0.0740
D	0.7130	0.0730
E	0.3480	0.0320
F	0.6990	0.0710
G	0.6850	0.0690
H	0.7230	0.0740
I	0.7140	0.0720
J	0.4050	0.0340
K	0.7050	0.0710
L	0.6730	0.0700

