Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 06:00 am GMT

PDB ID	:	6RZT
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:

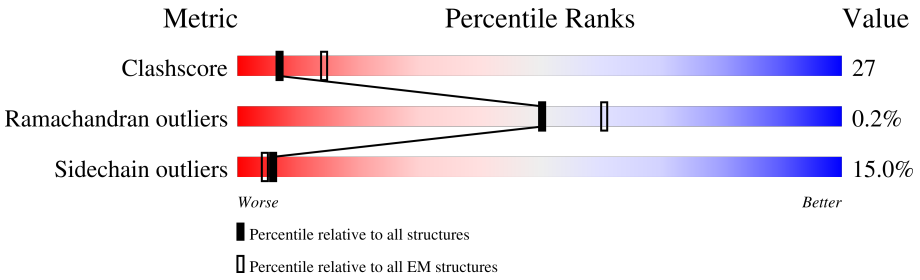
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 14.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	24% 55% 29% 10% 5%
1	B	695	24% 64% 26% • 5%
1	C	695	23% 63% 27% • 5%
1	D	695	24% 52% 31% 11% 5%
1	E	695	61% 54% 30% 10% • 5%
1	F	695	26% 64% 26% • 5%
1	G	695	27% 64% 26% 5% 5%
1	H	695	23% 53% 32% 10% 5%

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Mol	Chain	Length	Quality of chain
1	I	695	25% 55% 29% 10% • 5%
1	J	695	54% 66% 24% • 5%
1	K	695	26% 55% 30% 10% 5%
1	L	695	28% 64% 26% • 5%

2 Entry composition (i)

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.

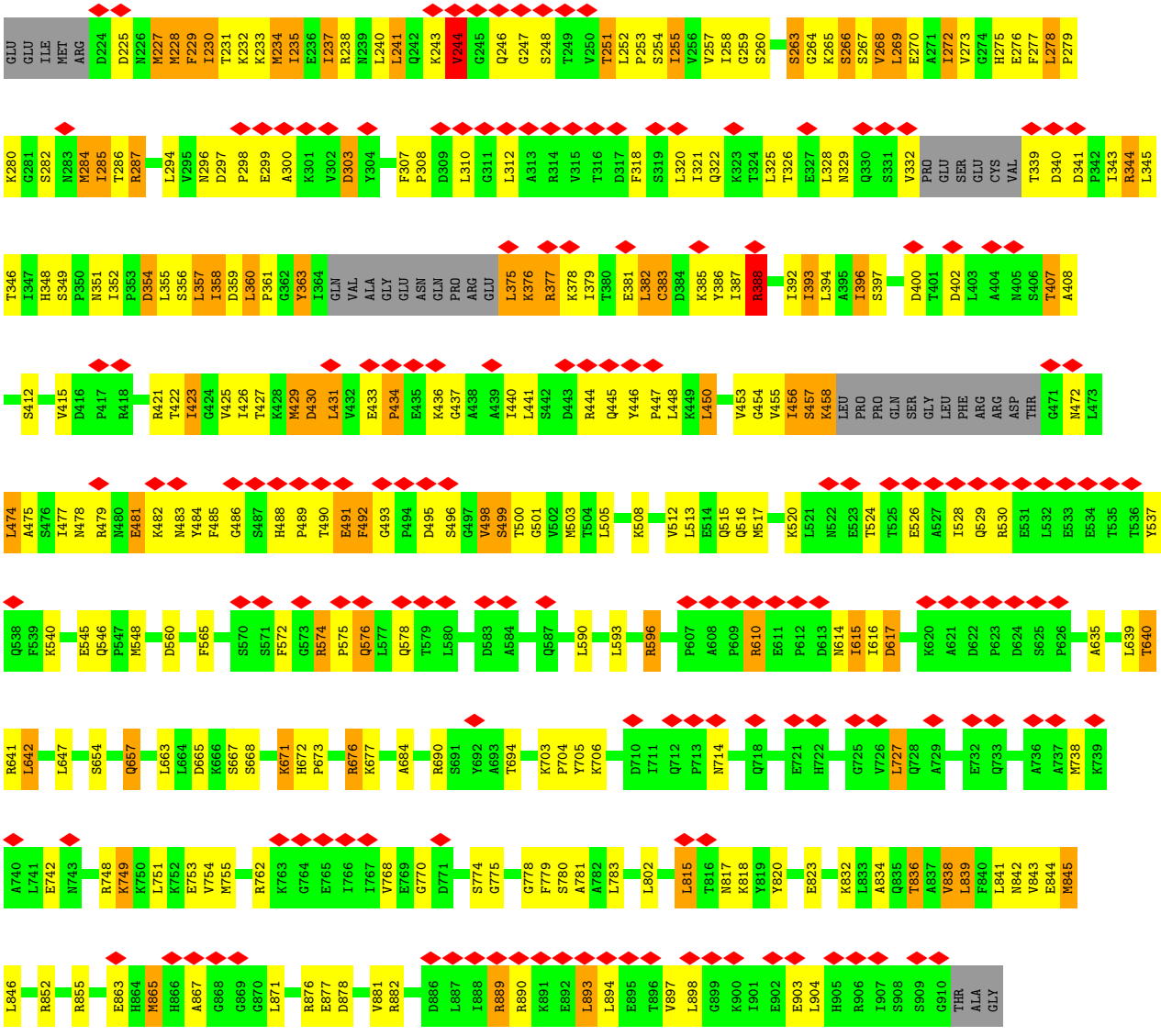
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	B	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	C	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	D	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	E	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
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 (i)

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.

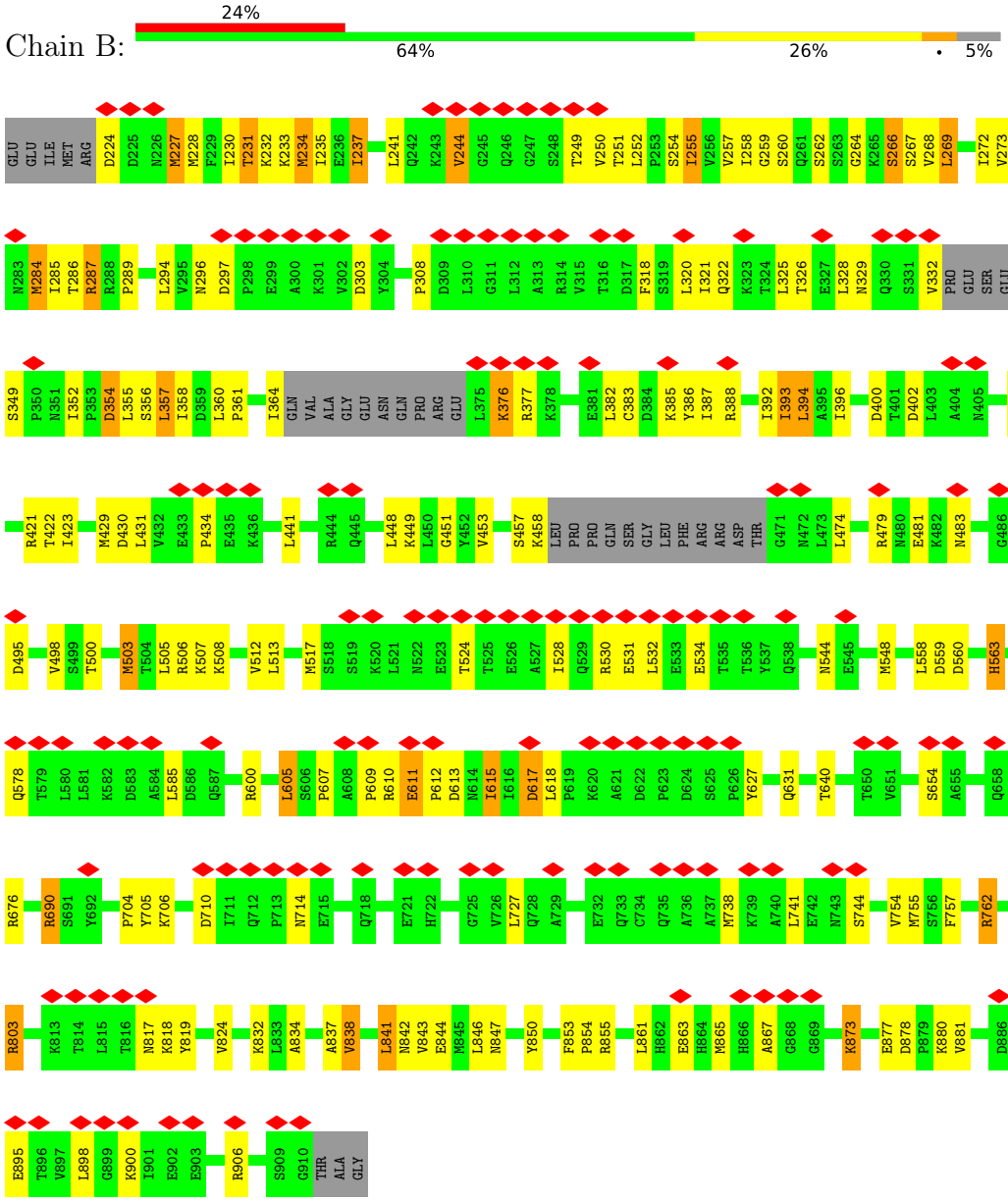
• Molecule 1: Putative mitochondrial dynamin protein

Chain A:



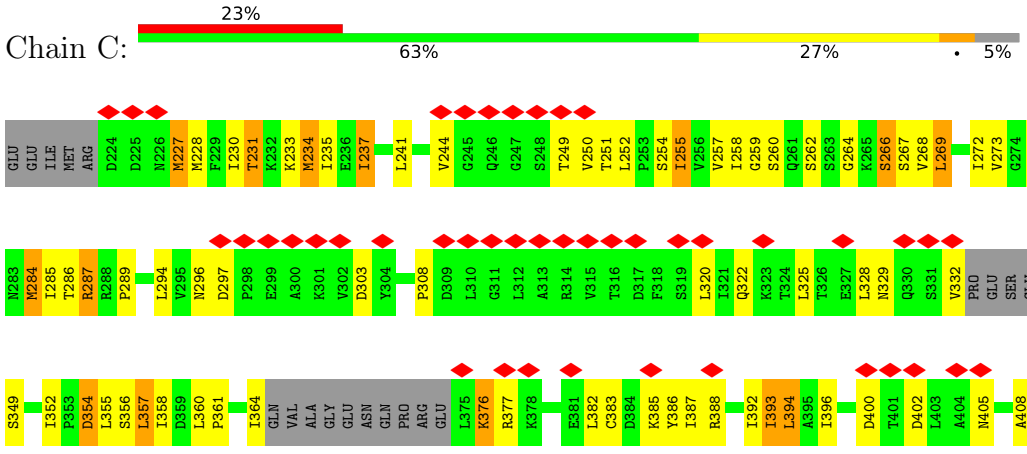
• Molecule 1: Putative mitochondrial dynamin protein

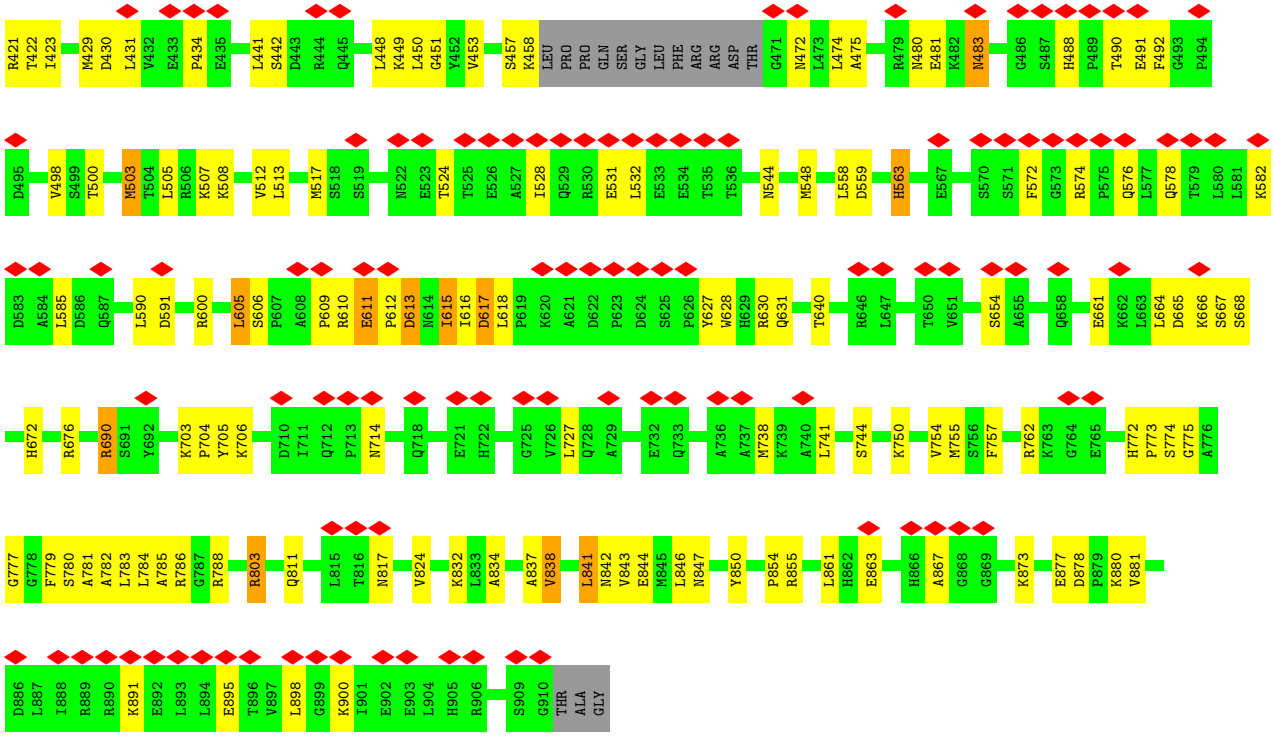
Chain B:



• Molecule 1: Putative mitochondrial dynamin protein

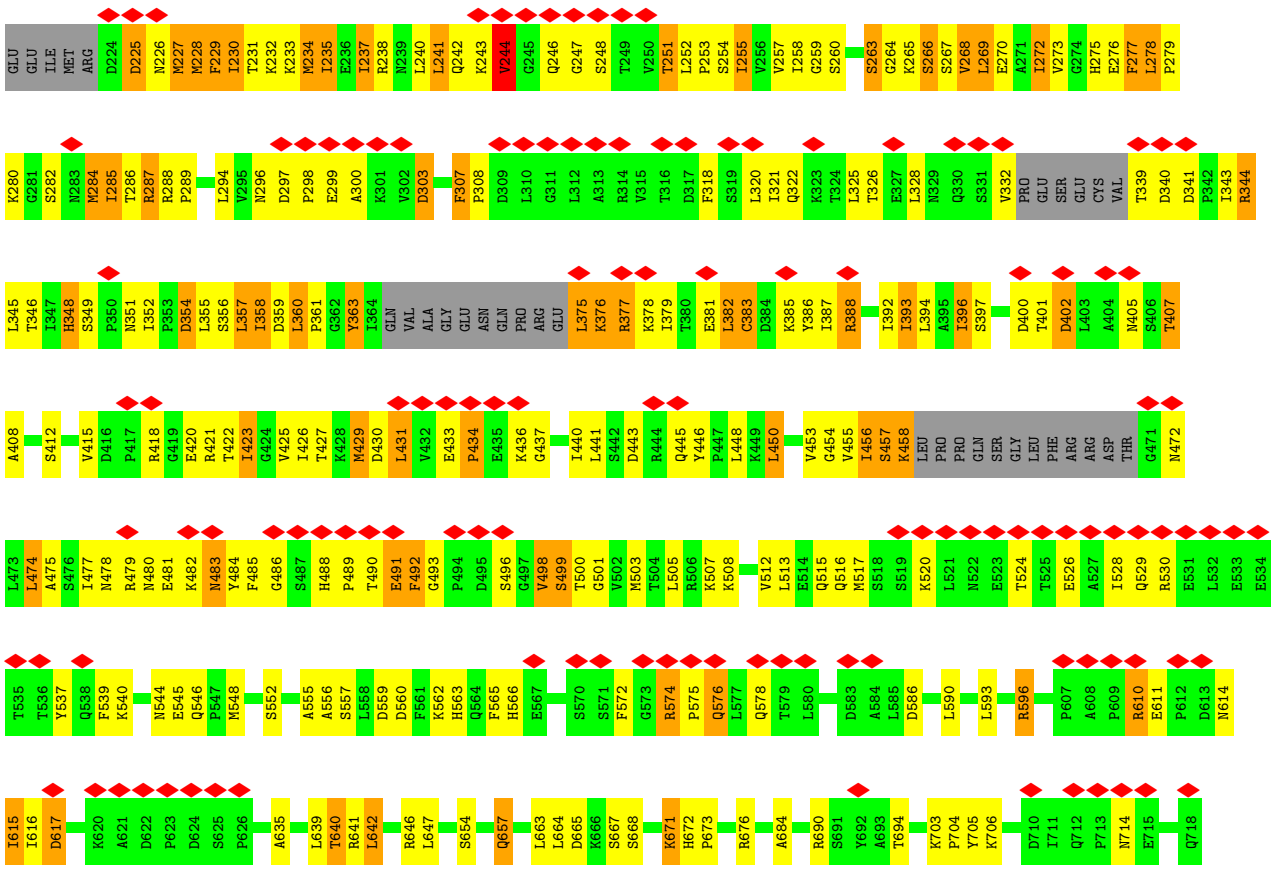
Chain C:

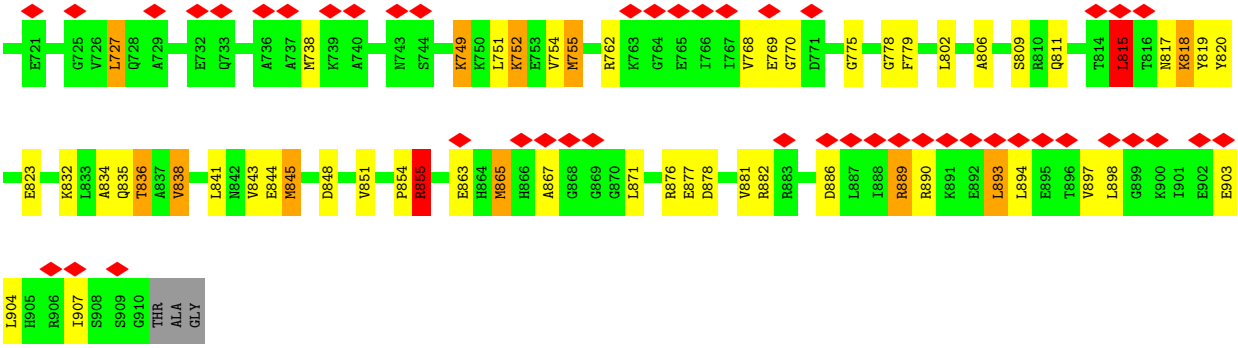




• Molecule 1: Putative mitochondrial dynamin protein

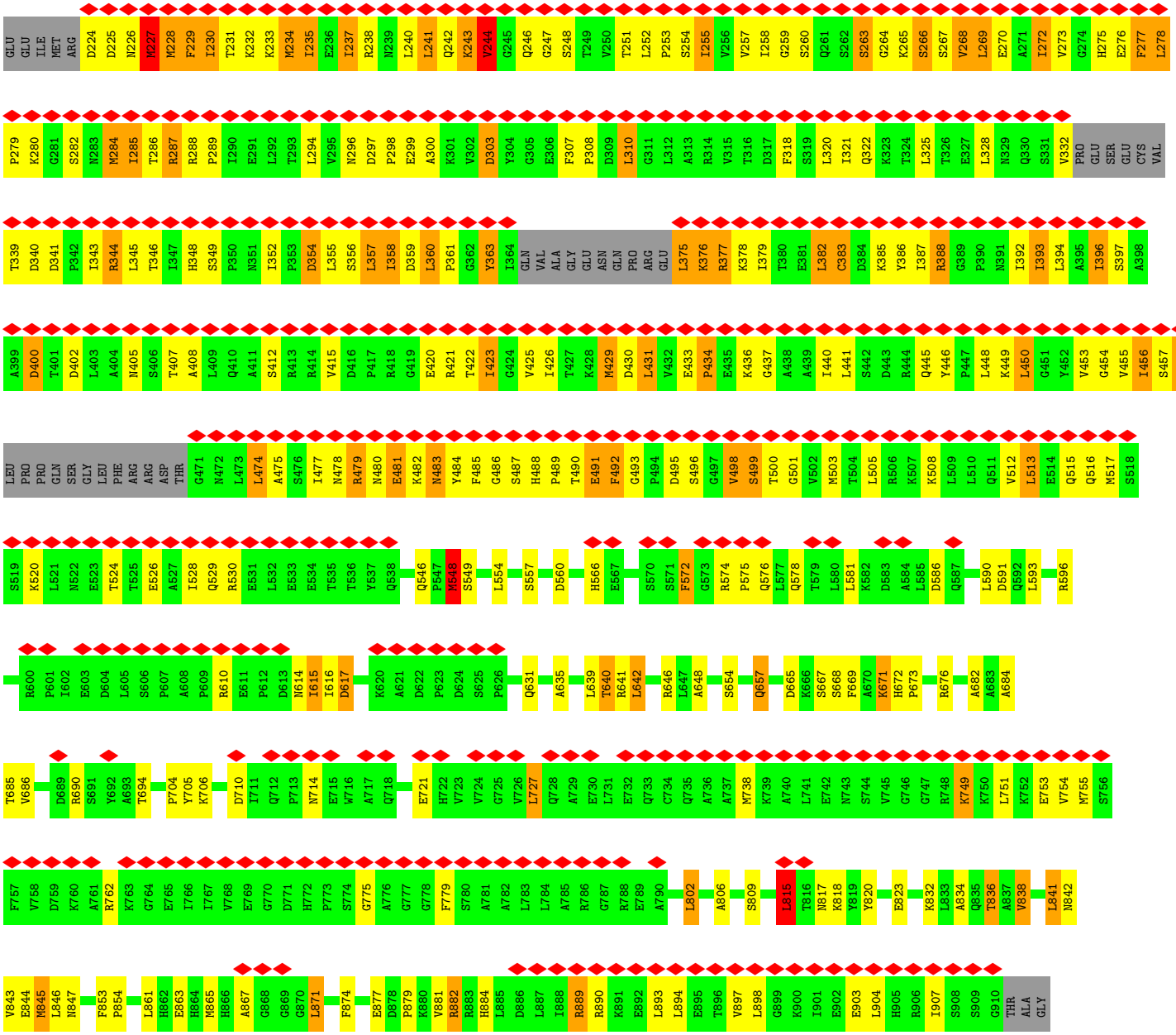
Chain D:





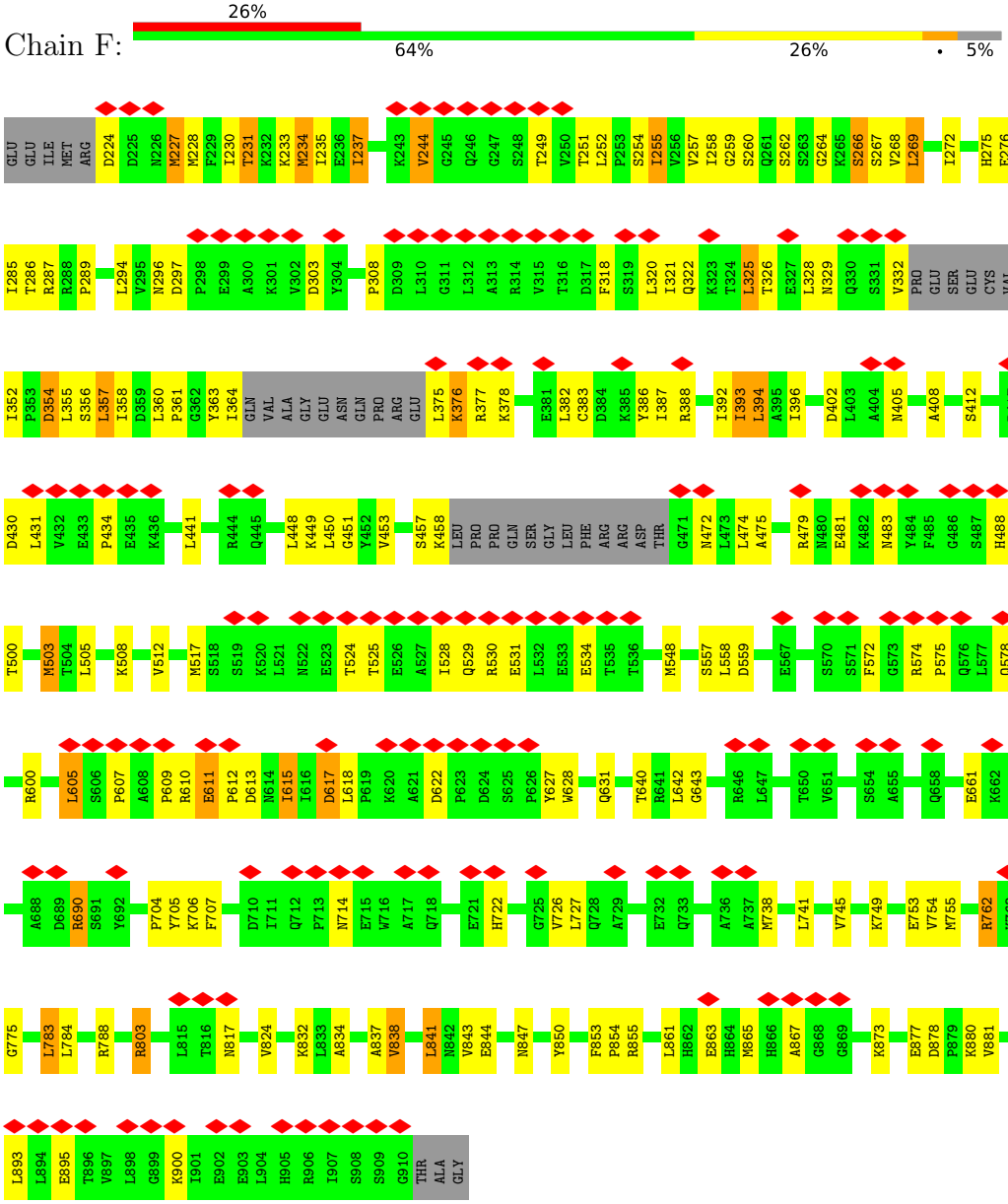
• Molecule 1: Putative mitochondrial dynamin protein

Chain E:



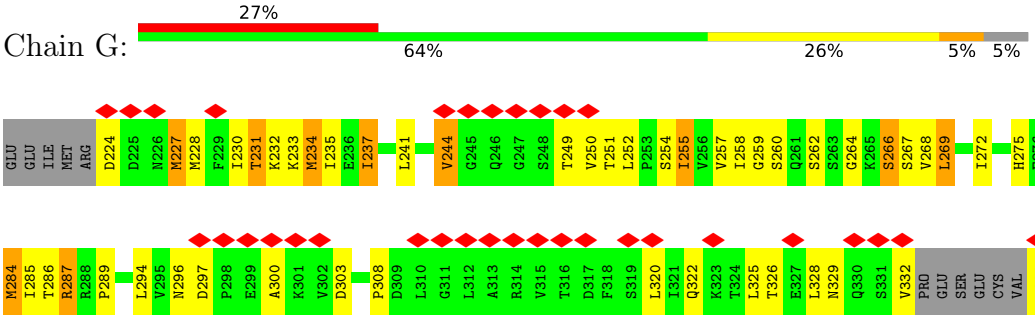
• Molecule 1: Putative mitochondrial dynamin protein

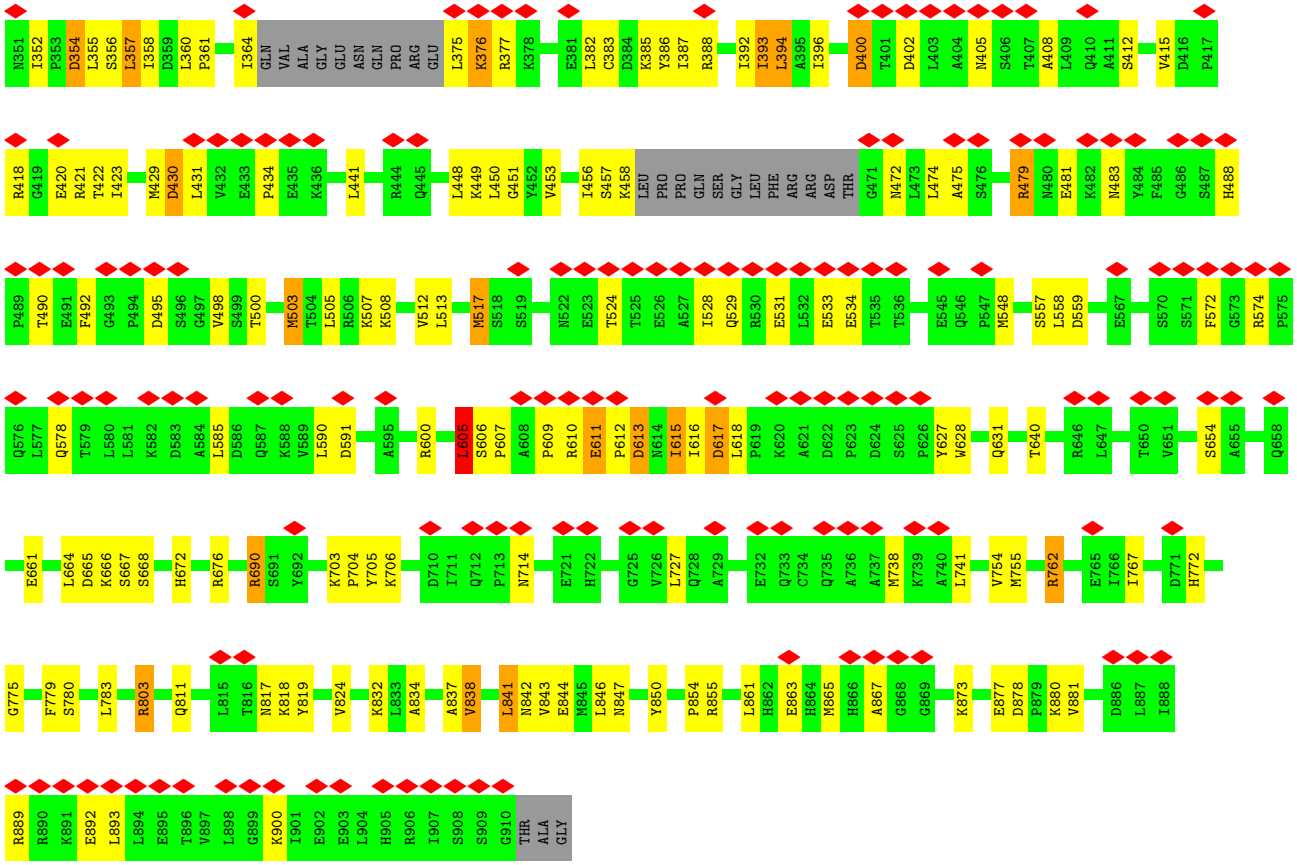
Chain F:



• Molecule 1: Putative mitochondrial dynamin protein

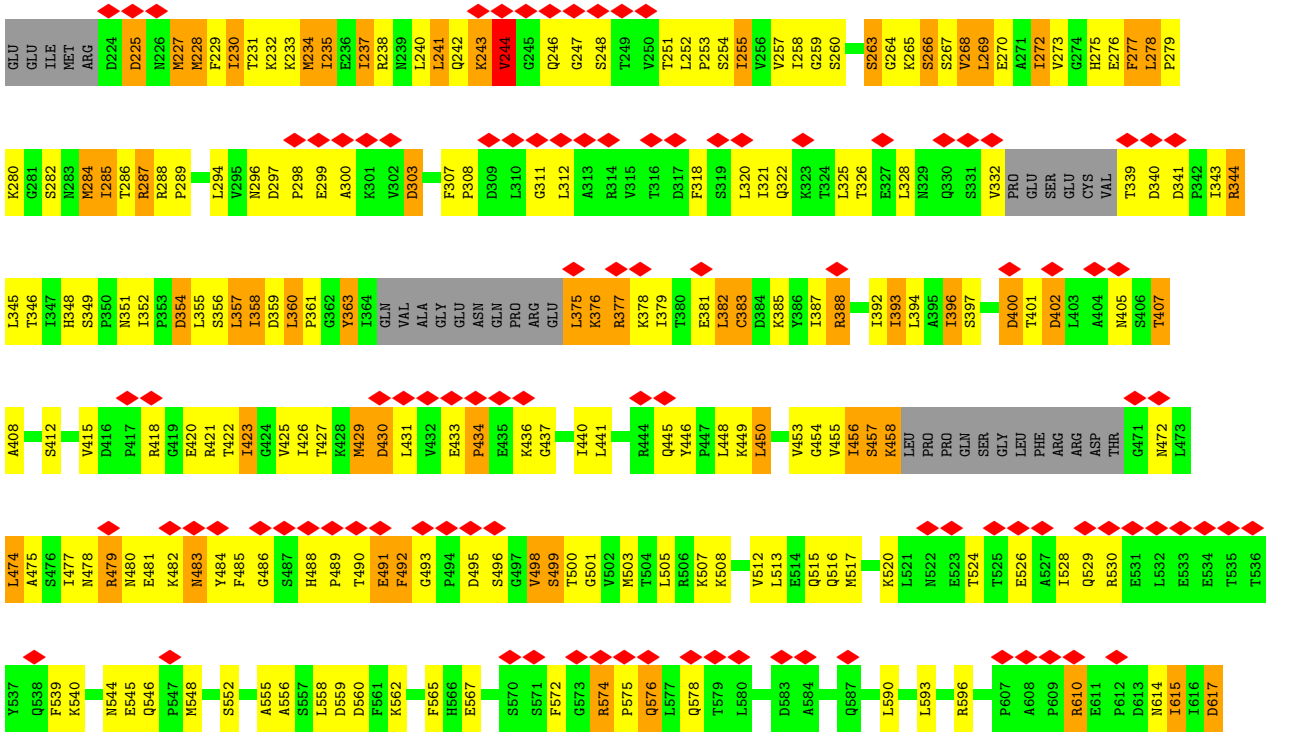
Chain G:

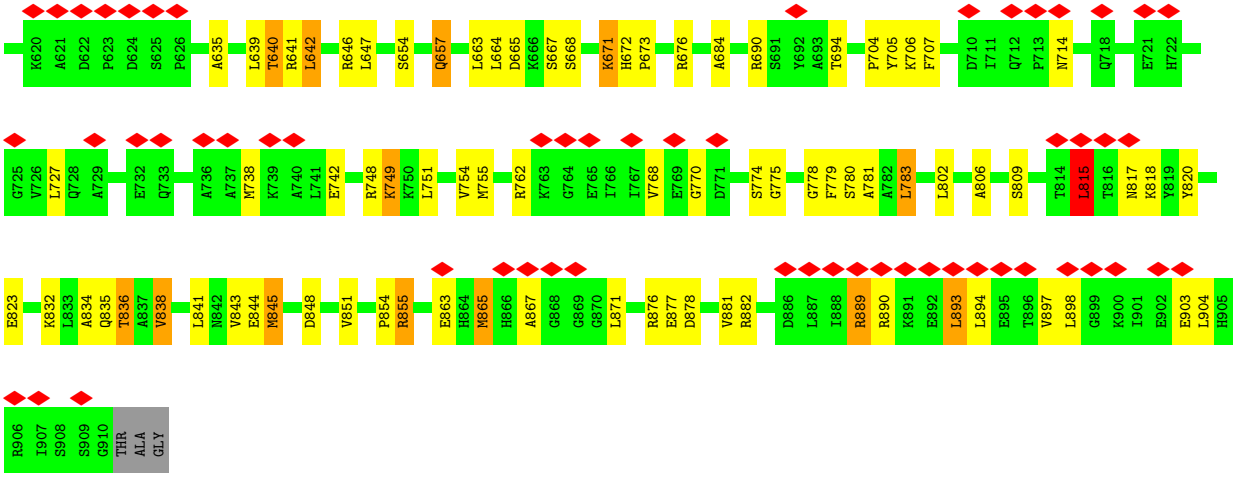




• Molecule 1: Putative mitochondrial dynamin protein

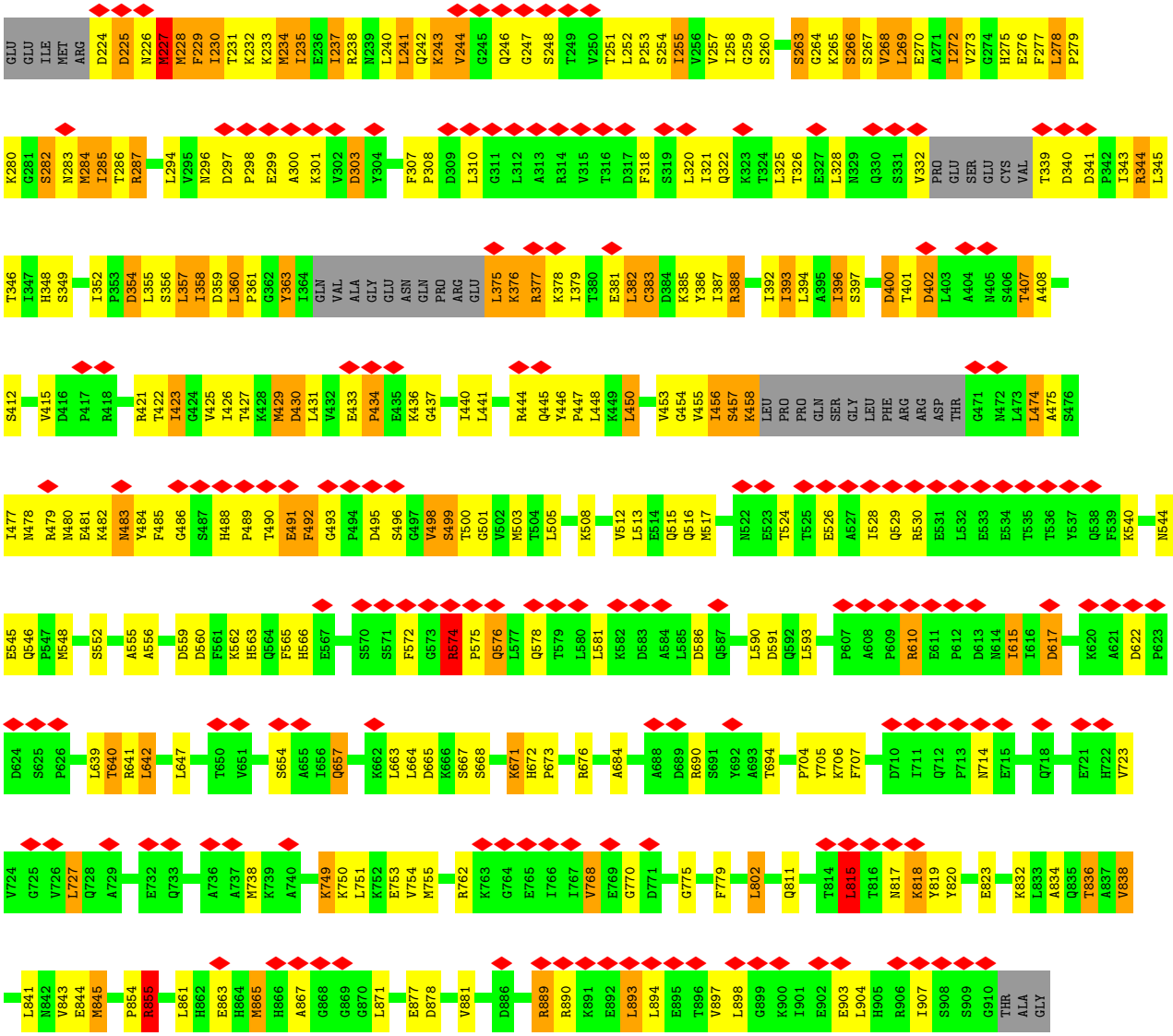
Chain H:





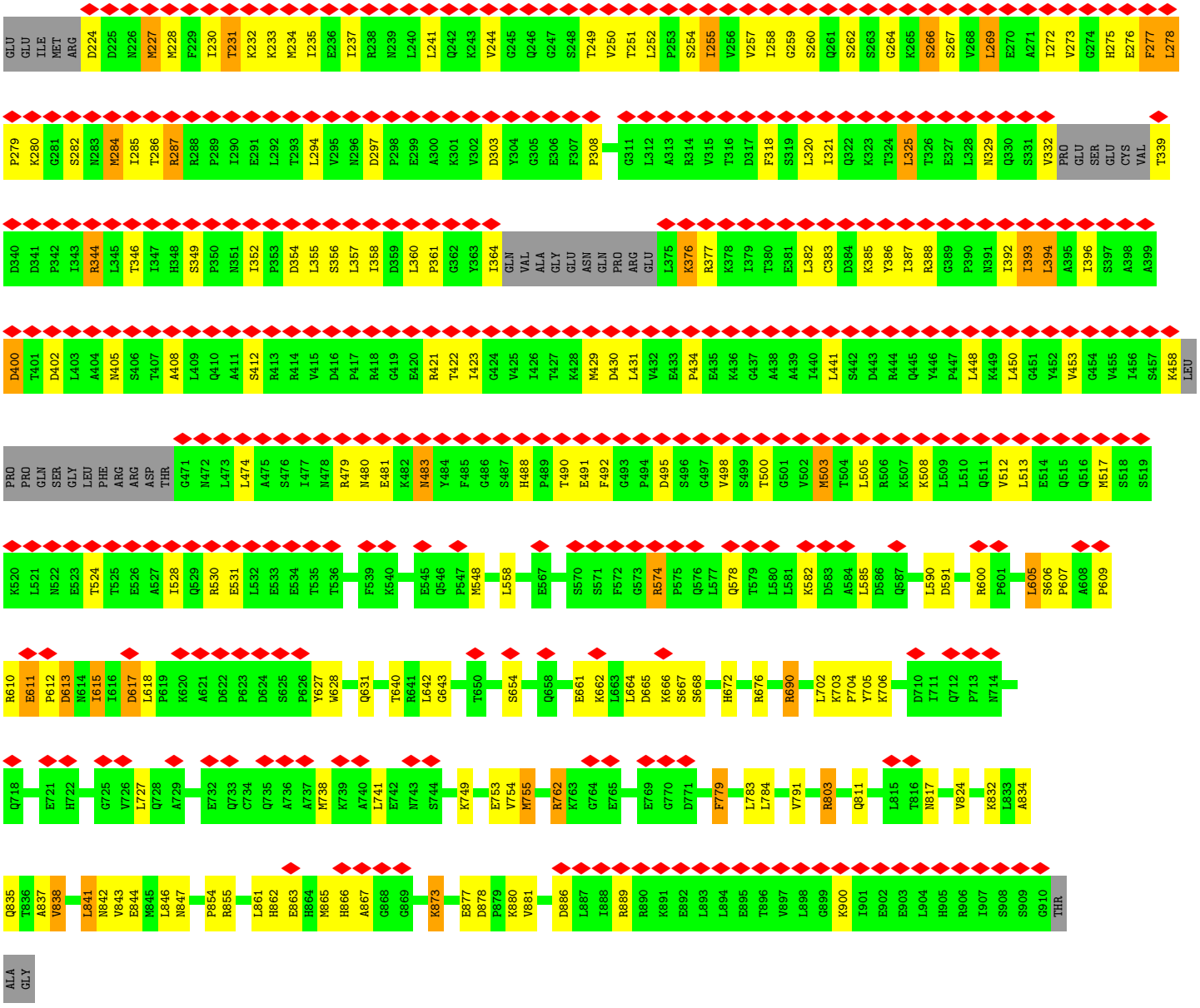
• Molecule 1: Putative mitochondrial dynamin protein

Chain I:



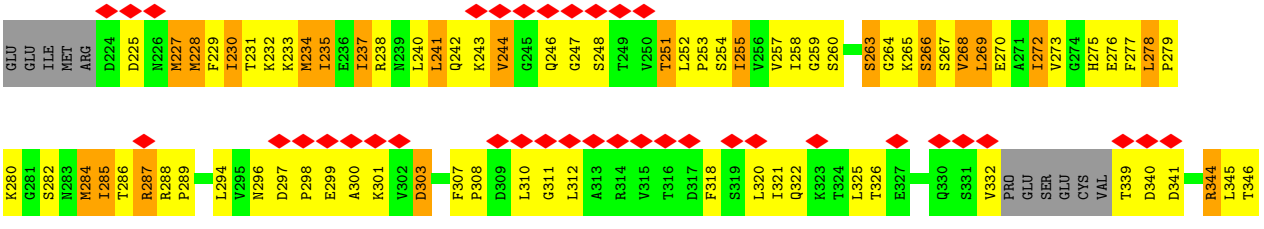
• Molecule 1: Putative mitochondrial dynamin protein

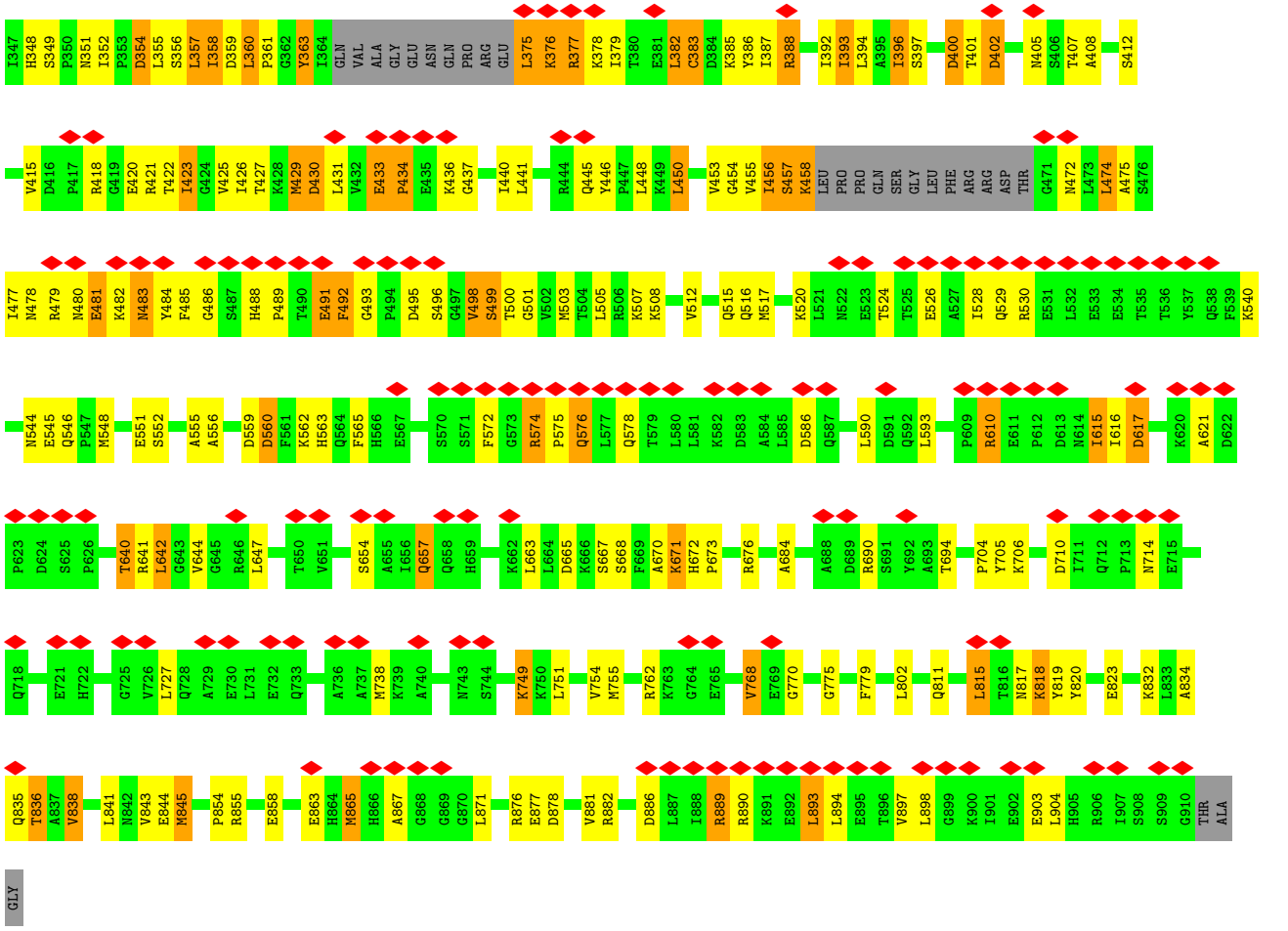
Chain J:



• Molecule 1: Putative mitochondrial dynamin protein

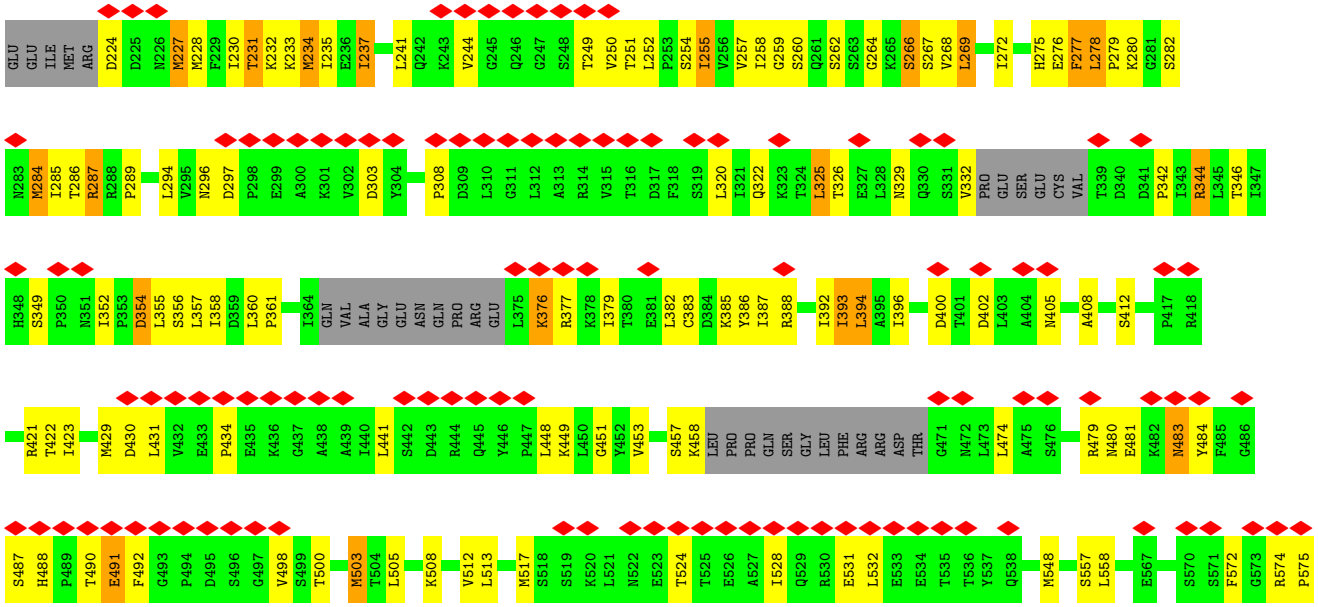
Chain K:

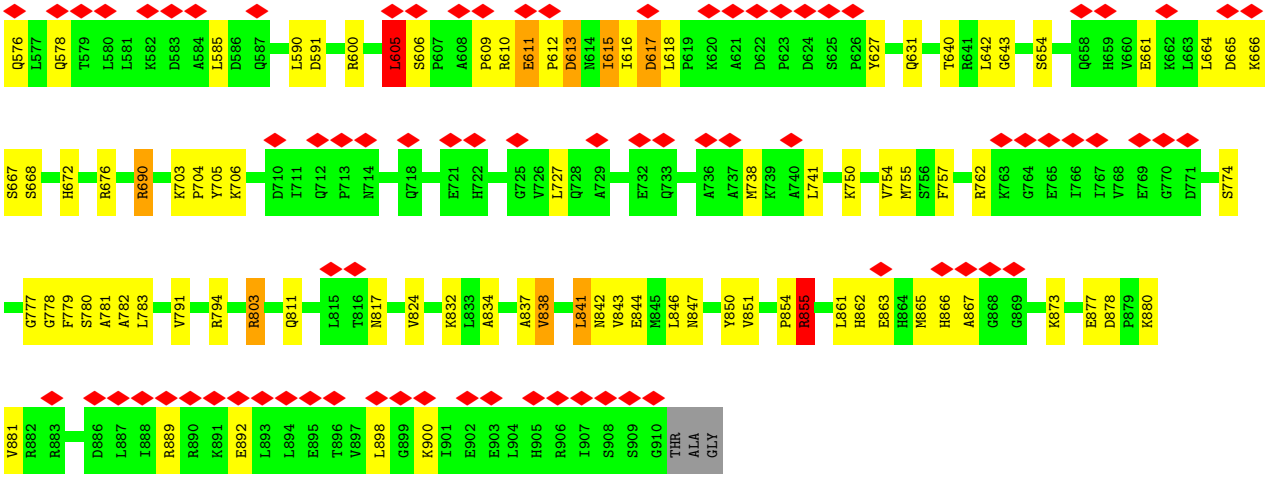




• Molecule 1: Putative mitochondrial dynamin protein

Chain L:




Q576 L577 Q578 T579 L580 L581 K582 D583 A584 L585 D586 Q587 L590 D591 R600 L605 S606 P607 A608 P609 R610 E611 P612 D613 N614 I615 I616 D617 L618 P619 K620 A621 D622 P623 D624 S625 P626 Y627 Q631 T640 R641 L642 G643 S654 Q658 H659 V660 E661 K662 L663 L664 D665 K666
S667 S668 H672 R676 R690 K703 P704 Y705 K706 D710 I711 Q712 F713 N714 Q718 E721 H722 G725 V726 L727 Q728 A729 E732 Q733 A736 A737 M738 K739 A740 L741 K750 V754 M755 S756 F757 R762 K763 G764 E765 I766 I767 V768 E769 G770 D771 S774
G777 G778 F779 S780 A781 A782 L783 V791 R794 R803 Q811 L815 T816 N817 V824 K832 L833 A834 A837 V838 L841 N842 V843 E844 M845 L846 N847 Y850 V851 P854 R855 L861 H862 E863 H864 M865 H866 A867 G868 G869 K873 E877 D878 P879 K880
V881 R882 R883 D886 L887 I888 R889 R890 K891 E892 L893 L894 E895 T896 V897 L898 G899 K900 I901 E902 E903 L904 H905 R906 I907 S908 S909 G910 THR ALA GLY

4 Experimental information (i)

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 ($e^-/Å^2$)	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 (i)

5.1 Standard geometry (i)

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	0.57	11/5238 (0.2%)	0.62	4/7075 (0.1%)
1	B	0.47	10/5238 (0.2%)	0.51	2/7075 (0.0%)
1	C	0.46	9/5238 (0.2%)	0.51	2/7075 (0.0%)
1	D	0.56	11/5238 (0.2%)	0.62	5/7075 (0.1%)
1	E	0.57	11/5238 (0.2%)	0.62	4/7075 (0.1%)
1	F	0.46	10/5238 (0.2%)	0.51	3/7075 (0.0%)
1	G	0.47	10/5238 (0.2%)	0.51	2/7075 (0.0%)
1	H	0.56	11/5238 (0.2%)	0.62	4/7075 (0.1%)
1	I	0.56	11/5238 (0.2%)	0.62	4/7075 (0.1%)
1	J	0.67	16/5238 (0.3%)	0.50	3/7075 (0.0%)
1	K	0.56	11/5238 (0.2%)	0.62	4/7075 (0.1%)
1	L	0.47	10/5238 (0.2%)	0.51	3/7075 (0.0%)
All	All	0.54	131/62856 (0.2%)	0.57	40/84900 (0.0%)

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 (131) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	779	PHE	CG-CD2	16.89	1.64	1.38
1	J	779	PHE	CG-CD1	16.11	1.62	1.38
1	J	779	PHE	CE1-CZ	14.66	1.65	1.37
1	J	779	PHE	CE2-CZ	12.79	1.61	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	779	PHE	CD1-CE1	11.57	1.62	1.39
1	J	779	PHE	CD2-CE2	11.24	1.61	1.39
1	K	253	PRO	C-N	-9.22	1.12	1.34
1	I	253	PRO	C-N	-8.88	1.13	1.34
1	E	253	PRO	C-N	-8.75	1.14	1.34
1	H	253	PRO	C-N	-8.70	1.14	1.34
1	A	253	PRO	C-N	-8.65	1.14	1.34
1	D	253	PRO	C-N	-8.35	1.14	1.34
1	K	227	MET	CG-SD	6.14	1.97	1.81
1	H	227	MET	CG-SD	6.10	1.97	1.81
1	I	227	MET	CG-SD	6.10	1.97	1.81
1	I	845	MET	CG-SD	6.03	1.96	1.81
1	A	227	MET	CG-SD	6.03	1.96	1.81
1	E	227	MET	CG-SD	6.01	1.96	1.81
1	D	845	MET	CG-SD	5.98	1.96	1.81
1	D	227	MET	CG-SD	5.88	1.96	1.81
1	G	738	MET	CG-SD	5.87	1.96	1.81
1	K	738	MET	CG-SD	5.86	1.96	1.81
1	H	738	MET	CG-SD	5.84	1.96	1.81
1	H	429	MET	CG-SD	5.83	1.96	1.81
1	J	429	MET	CG-SD	5.83	1.96	1.81
1	B	228	MET	CG-SD	5.82	1.96	1.81
1	I	738	MET	CG-SD	5.82	1.96	1.81
1	I	429	MET	CG-SD	5.80	1.96	1.81
1	D	738	MET	CG-SD	5.80	1.96	1.81
1	J	548	MET	CG-SD	5.79	1.96	1.81
1	B	755	MET	CG-SD	5.78	1.96	1.81
1	H	845	MET	CG-SD	5.78	1.96	1.81
1	B	503	MET	CG-SD	5.78	1.96	1.81
1	D	517	MET	CG-SD	5.77	1.96	1.81
1	A	738	MET	CG-SD	5.76	1.96	1.81
1	F	429	MET	CG-SD	5.74	1.96	1.81
1	E	845	MET	CG-SD	5.74	1.96	1.81
1	I	548	MET	CG-SD	5.71	1.96	1.81
1	A	517	MET	CG-SD	5.69	1.96	1.81
1	H	548	MET	CG-SD	5.68	1.96	1.81
1	E	738	MET	CG-SD	5.68	1.96	1.81
1	F	738	MET	CG-SD	5.68	1.96	1.81
1	K	845	MET	CG-SD	5.66	1.95	1.81
1	E	755	MET	CG-SD	5.66	1.95	1.81
1	G	865	MET	CG-SD	5.65	1.95	1.81
1	F	755	MET	CG-SD	5.65	1.95	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	429	MET	CG-SD	5.64	1.95	1.81
1	I	517	MET	CG-SD	5.64	1.95	1.81
1	B	738	MET	CG-SD	5.64	1.95	1.81
1	L	503	MET	CG-SD	5.64	1.95	1.81
1	G	429	MET	CG-SD	5.63	1.95	1.81
1	K	429	MET	CG-SD	5.63	1.95	1.81
1	A	429	MET	CG-SD	5.62	1.95	1.81
1	D	429	MET	CG-SD	5.62	1.95	1.81
1	L	228	MET	CG-SD	5.62	1.95	1.81
1	H	517	MET	CG-SD	5.61	1.95	1.81
1	J	234	MET	CG-SD	5.60	1.95	1.81
1	K	548	MET	CG-SD	5.58	1.95	1.81
1	K	228	MET	CG-SD	5.57	1.95	1.81
1	E	517	MET	CG-SD	5.56	1.95	1.81
1	D	228	MET	CG-SD	5.56	1.95	1.81
1	C	503	MET	CG-SD	5.56	1.95	1.81
1	G	755	MET	CG-SD	5.55	1.95	1.81
1	L	429	MET	CG-SD	5.54	1.95	1.81
1	L	548	MET	CG-SD	5.54	1.95	1.81
1	A	228	MET	CG-SD	5.54	1.95	1.81
1	G	548	MET	CG-SD	5.54	1.95	1.81
1	E	548	MET	CG-SD	5.53	1.95	1.81
1	I	865	MET	CG-SD	5.53	1.95	1.81
1	L	738	MET	CG-SD	5.52	1.95	1.81
1	J	228	MET	CG-SD	5.50	1.95	1.81
1	F	503	MET	CG-SD	5.50	1.95	1.81
1	L	865	MET	CG-SD	5.49	1.95	1.81
1	A	865	MET	CG-SD	5.48	1.95	1.81
1	B	227	MET	CG-SD	5.47	1.95	1.81
1	J	503	MET	CG-SD	5.47	1.95	1.81
1	D	503	MET	CG-SD	5.47	1.95	1.81
1	G	234	MET	CG-SD	5.47	1.95	1.81
1	A	845	MET	CG-SD	5.46	1.95	1.81
1	C	548	MET	CG-SD	5.46	1.95	1.81
1	H	228	MET	CG-SD	5.46	1.95	1.81
1	J	738	MET	CG-SD	5.45	1.95	1.81
1	C	228	MET	CG-SD	5.45	1.95	1.81
1	J	755	MET	CG-SD	5.43	1.95	1.81
1	K	755	MET	CG-SD	5.43	1.95	1.81
1	C	738	MET	CG-SD	5.43	1.95	1.81
1	G	517	MET	CG-SD	5.42	1.95	1.81
1	H	865	MET	CG-SD	5.42	1.95	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	755	MET	CG-SD	5.42	1.95	1.81
1	D	755	MET	CG-SD	5.41	1.95	1.81
1	F	228	MET	CG-SD	5.41	1.95	1.81
1	F	865	MET	CG-SD	5.40	1.95	1.81
1	A	548	MET	CG-SD	5.40	1.95	1.81
1	B	429	MET	CG-SD	5.40	1.95	1.81
1	L	755	MET	CG-SD	5.40	1.95	1.81
1	G	503	MET	CG-SD	5.40	1.95	1.81
1	B	517	MET	CG-SD	5.38	1.95	1.81
1	K	503	MET	CG-SD	5.38	1.95	1.81
1	L	227	MET	CG-SD	5.38	1.95	1.81
1	E	228	MET	CG-SD	5.36	1.95	1.81
1	K	865	MET	CG-SD	5.36	1.95	1.81
1	E	503	MET	CG-SD	5.35	1.95	1.81
1	D	548	MET	CG-SD	5.34	1.95	1.81
1	F	517	MET	CG-SD	5.34	1.95	1.81
1	J	517	MET	CG-SD	5.34	1.95	1.81
1	F	234	MET	CG-SD	5.34	1.95	1.81
1	K	517	MET	CG-SD	5.34	1.95	1.81
1	I	228	MET	CG-SD	5.33	1.95	1.81
1	I	503	MET	CG-SD	5.32	1.95	1.81
1	J	227	MET	CG-SD	5.32	1.95	1.81
1	B	234	MET	CG-SD	5.31	1.95	1.81
1	G	228	MET	CG-SD	5.29	1.95	1.81
1	H	503	MET	CG-SD	5.29	1.95	1.81
1	C	755	MET	CG-SD	5.28	1.94	1.81
1	B	548	MET	CG-SD	5.28	1.94	1.81
1	A	503	MET	CG-SD	5.27	1.94	1.81
1	A	755	MET	CG-SD	5.26	1.94	1.81
1	D	865	MET	CG-SD	5.22	1.94	1.81
1	C	429	MET	CG-SD	5.22	1.94	1.81
1	F	548	MET	CG-SD	5.21	1.94	1.81
1	H	755	MET	CG-SD	5.21	1.94	1.81
1	J	865	MET	CG-SD	5.20	1.94	1.81
1	C	227	MET	CG-SD	5.15	1.94	1.81
1	C	517	MET	CG-SD	5.15	1.94	1.81
1	E	865	MET	CG-SD	5.14	1.94	1.81
1	B	865	MET	CG-SD	5.13	1.94	1.81
1	C	234	MET	CG-SD	5.12	1.94	1.81
1	G	227	MET	CG-SD	5.11	1.94	1.81
1	L	234	MET	CG-SD	5.11	1.94	1.81
1	F	227	MET	CG-SD	5.10	1.94	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	517	MET	CG-SD	5.02	1.94	1.81

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	K	234	MET	CB-CG-SD	-6.21	93.78	112.40
1	A	244	VAL	CB-CA-C	-6.17	99.69	111.40
1	A	234	MET	CB-CG-SD	-6.13	94.00	112.40
1	D	234	MET	CB-CG-SD	-6.11	94.06	112.40
1	I	244	VAL	CB-CA-C	-6.11	99.80	111.40
1	I	234	MET	CB-CG-SD	-6.10	94.11	112.40
1	E	234	MET	CB-CG-SD	-6.00	94.40	112.40
1	H	244	VAL	CB-CA-C	-5.98	100.04	111.40
1	D	244	VAL	CB-CA-C	-5.92	100.14	111.40
1	H	234	MET	CB-CG-SD	-5.90	94.69	112.40
1	E	244	VAL	CB-CA-C	-5.78	100.42	111.40
1	D	815	LEU	CA-CB-CG	5.78	128.59	115.30
1	K	244	VAL	CB-CA-C	-5.74	100.50	111.40
1	A	815	LEU	CA-CB-CG	5.66	128.32	115.30
1	K	815	LEU	CA-CB-CG	5.64	128.28	115.30
1	F	278	LEU	CA-CB-CG	5.50	127.96	115.30
1	G	605	LEU	CA-CB-CG	5.48	127.91	115.30
1	F	605	LEU	CA-CB-CG	5.48	127.90	115.30
1	C	278	LEU	CA-CB-CG	5.44	127.82	115.30
1	B	278	LEU	CA-CB-CG	5.43	127.79	115.30
1	J	325	LEU	CA-CB-CG	5.41	127.74	115.30
1	B	605	LEU	CA-CB-CG	5.39	127.69	115.30
1	I	815	LEU	CA-CB-CG	5.39	127.69	115.30
1	E	815	LEU	CA-CB-CG	5.35	127.59	115.30
1	H	815	LEU	CA-CB-CG	5.34	127.57	115.30
1	I	341	ASP	C-N-CD	5.30	139.53	128.40
1	D	341	ASP	C-N-CD	5.29	139.50	128.40
1	L	325	LEU	CA-CB-CG	5.22	127.32	115.30
1	G	278	LEU	CA-CB-CG	5.21	127.29	115.30
1	L	278	LEU	CA-CB-CG	5.20	127.27	115.30
1	J	605	LEU	CA-CB-CG	5.19	127.23	115.30
1	F	325	LEU	CA-CB-CG	5.17	127.20	115.30
1	K	341	ASP	C-N-CD	5.17	139.26	128.40
1	L	605	LEU	CA-CB-CG	5.14	127.13	115.30
1	A	341	ASP	C-N-CD	5.14	139.19	128.40
1	E	341	ASP	C-N-CD	5.13	139.17	128.40
1	C	605	LEU	CA-CB-CG	5.10	127.03	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	307	PHE	C-N-CD	5.10	139.11	128.40
1	J	278	LEU	CA-CB-CG	5.08	126.98	115.30
1	H	341	ASP	C-N-CD	5.07	139.05	128.40

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	472	0
1	B	5152	0	5223	117	0
1	C	5152	0	5223	195	0
1	D	5152	0	5221	471	0
1	E	5152	0	5221	398	0
1	F	5152	0	5223	124	0
1	G	5152	0	5223	133	0
1	H	5152	0	5221	546	0
1	I	5152	0	5221	454	0
1	J	5152	0	5223	113	0
1	K	5152	0	5221	450	0
1	L	5152	0	5223	186	0
All	All	61824	0	62664	3373	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 27.

All (3373) 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
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:E:478:ASN:ND2	1:E:482:LYS:HZ1	1.13	1.46
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:A:783:LEU:HD12	1:H:778:GLY:C	1.81	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
1:D:426:ILE:HD12	1:D:440:ILE:HG22	1.46	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: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:I:225:ASP:C	1:I:229:PHE:CE1	2.38	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:A:778:GLY:C	1:H:783:LEU:HD12	1.85	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:A:286:THR:HB	1:A:361:PRO:HB3	1.49	0.94
1:D:225:ASP:C	1:D:229:PHE:HE1	1.70	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: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:225:ASP:C	1:E:229:PHE:CE1	2.42	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:225:ASP:C	1:D:229:PHE:CE1	2.41	0.92
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
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:E:272:ILE:CG2	1:E:278:LEU:HD12	1.99	0.89
1:E:478:ASN:HD21	1:E:482:LYS:HZ1	1.16	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
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:276:GLU:CD	1:A:318:PHE:HE2	1.77	0.86
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
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:H:276:GLU:CD	1:H:318:PHE:HE2	1.80	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:780:SER:C	1:L:780:SER:HB3	1.96	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
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: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: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:K:276:GLU:CD	1:K:318:PHE:HE2	1.80	0.83
1:A:775:GLY:C	1:H:780:SER:HB2	1.97	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:D:276:GLU:CD	1:D:318:PHE:HE2	1.82	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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: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:D:297:ASP:CG	1:D:300:ALA:HB3	2.01	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:276:GLU:CD	1:I:318:PHE:HE2	1.85	0.80
1:I:284:MET:HG2	1:I:286:THR:CG2	2.12	0.80
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:276:GLU:CD	1:E:318:PHE:HE2	1.84	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: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:I:297:ASP:CG	1:I:300:ALA:HB3	2.01	0.78
1:E:485:PHE:CE2	1:E:500:THR:OG1	2.34	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:I:251:THR:HG22	1:I:252:LEU:N	1.98	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
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:251:THR:HG22	1:A:252:LEU:N	1.98	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:C:780:SER:HB2	1:L:779:PHE:C	2.04	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
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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:SER:HB2	1:H:775:GLY:C	2.07	0.75
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:E:297:ASP:CG	1:E:300:ALA:HB3	2.08	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:609:PRO:HB2	1:C:610:ARG:C	2.09	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
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:E:235:ILE:HD12	1:E:235:ILE:O	1.88	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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:781:ALA:HB2	1:H:774:SER:HG	1.54	0.71
1:E:286:THR:O	1:E:361:PRO:CG	2.38	0.71
1:H:284:MET:HG2	1:H:286:THR:HG23	1.71	0.71
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:K:297:ASP:CG	1:K:300:ALA:HB3	2.10	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:272:ILE:HG21	1:H:277:PHE:HD1	1.53	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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: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:E:225:ASP:C	1:E:229:PHE:HE1	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:C:774:SER:HA	1:L:774:SER:C	2.12	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:H:297:ASP:CG	1:H:300:ALA:HB3	2.13	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: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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:E:478:ASN:CG	1:E:482:LYS:NZ	2.47	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: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:269:LEU:HD23	1:D:269:LEU:C	2.15	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:D:235:ILE:HD12	1:D:235:ILE:O	1.94	0.67
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:K:229:PHE:HA	1:K:232:LYS:HG2	1.76	0.67
1:A:478:ASN:CG	1:A:482:LYS:NZ	2.47	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:I:276:GLU:OE2	1:I:318:PHE:HE2	1.66	0.67
1:E:615:ILE:H	1:E:615:ILE:HD12	1.59	0.67
1:I:478:ASN:CG	1:I:482:LYS:NZ	2.47	0.67
1:K:235:ILE:HD12	1:K:235:ILE:O	1.95	0.67
1:G:609:PRO:HB2	1:G:610:ARG:C	2.15	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: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: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:269:LEU:HD23	1:H:269:LEU:C	2.16	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
1:I:240:LEU:N	1:I:240:LEU:HD23	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:H:478:ASN:CG	1:H:482:LYS:NZ	2.49	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: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: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
1:K:322:GLN:O	1:K:326:THR:OG1	2.11	0.65
1:C:434:PRO:HG2	1:C:488:HIS:CG	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:D:478:ASN:CG	1:D:482:LYS:NZ	2.50	0.64
1:E:269:LEU:CD2	1:E:457:SER:HB2	2.24	0.64
1:E:269:LEU:HD23	1:E:269:LEU:C	2.17	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:K:478:ASN:CG	1:K:482:LYS:NZ	2.50	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
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:A:478:ASN:CG	1:A:482:LYS:HZ2	2.01	0.64
1:C:611:GLU:N	1:C:612:PRO:HD2	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:774:SER:HA	1:H:774:SER:HG	1.63	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: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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:PRO:HB3	1:D:491:GLU:CG	2.27	0.63
1:H:430:ASP:C	1:H:430:ASP:OD1	2.35	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: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: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:269:LEU:HD23	1:A:269:LEU:C	2.20	0.63
1:A:272:ILE:CG2	1:A:277:PHE:HA	2.24	0.63
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:H:265:LYS:O	1:H:268:VAL:HG23	1.98	0.62
1:I:225:ASP:C	1:I:229:PHE:HE1	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
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:D:499:SER:O	1:D:500:THR:CG2	2.48	0.61
1:K:430:ASP:OD1	1:K:430:ASP:C	2.38	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
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: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:I:269:LEU:HD23	1:I:269:LEU:C	2.21	0.61
1:C:854:PRO:HB2	1:C:855:ARG:NH2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:269:LEU:HD23	1:K:269:LEU:C	2.21	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
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:K:478:ASN:CG	1:K:482:LYS:HZ2	2.03	0.61
1:L:224:ASP:HB3	1:L:227:MET:HB2	1.82	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:E:485:PHE:HA	1:E:492:PHE:HE1	1.66	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:E:226:ASN:N	1:E:229:PHE:HE1	1.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:ASP:CG	1:A:300:ALA:HB3	2.20	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:H:230:ILE:HG13	1:H:904:LEU:HD11	1.84	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
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:474:LEU:HG	1:I:475:ALA:H	1.67	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: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
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:G:703:LYS:HE3	1:K:544:ASN:CG	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:E:298:PRO:O	1:E:299:GLU:HB3	2.03	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: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:D:544:ASN:CG	1:J:703:LYS:HE3	2.23	0.59
1:E:286:THR:O	1:E:361:PRO:CB	2.51	0.59
1:G:878:ASP:HB3	1:G:881:VAL:HG12	1.85	0.59
1:I:226:ASN:N	1:I:229:PHE:HE1	2.01	0.59
1:I:454:GLY:O	1:I:500:THR:CG2	2.50	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
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:H:322:GLN:O	1:H:326:THR:OG1	2.13	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:G:847:ASN:ND2	1:H:707:PHE:CZ	2.72	0.58
1:I:269:LEU:HD11	1:I:457:SER:C	2.11	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: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:249:THR:OG1	1:J:531:GLU:OE1	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:249:THR:OG1	1:B:531:GLU:OE1	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: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
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:F:609:PRO:HB2	1:F:610:ARG:C	2.24	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:423:ILE:HG22	1:H:450:LEU:HD13	1.86	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:A:430:ASP:C	1:A:430:ASP:OD1	2.43	0.57
1:E:423:ILE:HG22	1:E:450:LEU:HD13	1.86	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:C:779:PHE:C	1:L:783:LEU:HD12	2.24	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:376:LYS:HA	1:K:376:LYS:HZ1	1.66	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:E:237:ILE:HD12	1:E:241:LEU:HD11	1.87	0.56
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: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:L:609:PRO:HB2	1:L:610:ARG:C	2.26	0.56
1:A:376:LYS:HA	1:A:376:LYS:CE	2.35	0.56
1:A:382:LEU:C	1:A:382:LEU:HD12	2.26	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:780:SER:HB3	1:L:779:PHE:CA	2.26	0.55
1:D:322:GLN:O	1:D:326:THR:OG1	2.14	0.55
1:E:269:LEU:HD21	1:E:457:SER:CA	2.36	0.55
1:H:297:ASP:HB3	1:H:349:SER:C	2.27	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:I:297:ASP:HB3	1:I:349:SER:C	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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: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:K:267:SER:CB	1:K:396:ILE:HG13	2.35	0.55
1:A:297:ASP:HB3	1:A:349:SER:C	2.26	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: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:276:GLU:CD	1:D:318:PHE:CE2	2.72	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:382:LEU:C	1:I:382:LEU:HD12	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:772:HIS:HD2	1:F:775:GLY:O	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
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:H:559:ASP:CG	1:K:854:PRO:CB	2.76	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:I:429:MET:CE	1:I:437:GLY:HA2	2.37	0.54
1:I:478:ASN:CG	1:I:482:LYS:HZ2	2.11	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:H:478:ASN:CG	1:H:482:LYS:HZ2	2.10	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:D:889:ARG:HG3	1:D:890:ARG:N	2.23	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:D:276:GLU:HG2	1:D:277:PHE:N	2.23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:I:267:SER:HB2	1:I:396:ILE:CD1	2.38	0.54
1:K:297:ASP:HB3	1:K:349:SER:C	2.29	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:H:382:LEU:C	1:H:382:LEU:HD12	2.29	0.53
1:H:429:MET:CE	1:H:437:GLY:HA2	2.39	0.53
1:H:559:ASP:CG	1:K:854:PRO:HB2	2.28	0.53
1:B:854:PRO:HB2	1:B:855:ARG:CZ	2.39	0.53
1:D:834:ALA:O	1:D:838:VAL:HB	2.08	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:774:SER:HG	1:H:781:ALA:HB2	1.70	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
1:D:429:MET:CE	1:D:437:GLY:HA2	2.39	0.53
1:E:297:ASP:HB3	1:E:349:SER:C	2.29	0.53
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:D:768:VAL:HG23	1:D:770:GLY:H	1.74	0.52
1:E:429:MET:CE	1:E:437:GLY:HA2	2.38	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:276:GLU:OE1	1:K:303:ASP:OD1	2.27	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: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:H:296:ASN:C	1:H:298:PRO:HD3	2.29	0.52
1:J:585:LEU:HD12	1:J:834:ALA:HB2	1.90	0.52
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:375:LEU:N	1:A:375:LEU:HD23	2.23	0.52
1:A:429:MET:CE	1:A:437:GLY:HA2	2.39	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:296:ASN:C	1:I:298:PRO:HD3	2.30	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:I:430:ASP:C	1:I:430:ASP:OD1	2.48	0.52
1:K:276:GLU:OE1	1:K:303:ASP:CG	2.48	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:774:SER:C	1:L:781:ALA:H	2.12	0.52
1:D:382:LEU:C	1:D:382:LEU:HD12	2.30	0.52
1:D:478:ASN:CG	1:D:482:LYS:HZ2	2.11	0.52
1:E:255:ILE:HA	1:E:392:ILE:O	2.10	0.52
1:E:276:GLU:OE1	1:E:303:ASP:CG	2.48	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:382:LEU:C	1:K:382:LEU:HD12	2.30	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
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:300:ALA:C	1:K:301:LYS:HD3	2.30	0.52
1:K:485:PHE:CE2	1:K:492:PHE:CD1	2.98	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:H:276:GLU:OE1	1:H:303:ASP:CG	2.47	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:297:ASP:HB3	1:D:349:SER:C	2.30	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:429:MET:HE1	1:H:437:GLY:HA2	1.92	0.51
1:H:434:PRO:HG2	1:H:488:HIS:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:K:429:MET:CE	1:K:437:GLY:HA2	2.40	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
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:275:HIS:CG	1:E:276:GLU:N	2.78	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:SER:HB2	1:C:356:SER:O	2.10	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
1:D:615:ILE:H	1:D:615:ILE:HD12	1.75	0.50
1:D:778:GLY:C	1:D:779:PHE:CD2	2.85	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:458:LYS:HD2	1:D:458:LYS:C	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:562:LYS:HZ1	1:I:562:LYS:HZ1	1.60	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:G:297:ASP:HB3	1:G:349:SER:C	2.32	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:J:662:LYS:O	1:J:665:ASP:HB2	2.11	0.50
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:HG22	1:E:415:VAL:HG21	1.92	0.50
1:E:387:ILE:O	1:E:421:ARG:NH2	2.45	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:238:ARG:NH2	1:H:356:SER:HG	2.10	0.50
1:H:555:ALA:CB	1:K:855:ARG:HG2	2.42	0.50
1:I:225:ASP:OD1	1:I:225:ASP:N	2.45	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: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
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:225:ASP:OD1	1:D:225:ASP:N	2.44	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:562:LYS:NZ	1:I:562:LYS:HZ1	2.09	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ASN:HB2	1:A:354:ASP:OD2	2.12	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:275:HIS:CG	1:K:276:GLU:N	2.78	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
1:B:297:ASP:HB3	1:B:349:SER:C	2.33	0.49
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: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: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:D:778:GLY:C	1:D:779:PHE:HD2	2.16	0.48
1:E:328:LEU:HD13	1:E:343:ILE:HD13	1.95	0.48
1:F:297:ASP:HB3	1:F:349:SER:C	2.33	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:H:225:ASP:N	1:H:225:ASP:OD1	2.47	0.48
1:I:705:TYR:CE1	1:I:832:LYS:HD3	2.49	0.48
1:J:609:PRO:HB2	1:J:610:ARG:C	2.33	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
1:E:478:ASN:HD21	1:E:482:LYS:CE	2.27	0.48
1:G:449:LYS:C	1:G:451:GLY:H	2.17	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:I:243:LYS:O	1:I:243:LYS:HG2	2.14	0.48
1:I:300:ALA:C	1:I:301:LYS:HD3	2.34	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: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:A:774:SER:HG	1:H:774:SER:HA	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:375:LEU:HB2	1:D:376:LYS:HE2	1.94	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: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
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:D:296:ASN:C	1:D:298:PRO:HD3	2.34	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:L:297:ASP:HB3	1:L:349:SER:C	2.33	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:276:GLU:OE1	1:A:303:ASP:CG	2.52	0.47
1:D:260:SER:O	1:D:264:GLY:CA	2.56	0.47
1:D:339:THR:O	1:D:340:ASP:HB3	2.14	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
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:J:297:ASP:HB3	1:J:349:SER:C	2.35	0.47
1:C:297:ASP:HB3	1:C:349:SER:C	2.33	0.47
1:D:477:ILE:HG22	1:D:477:ILE:O	2.13	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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:318:PHE:HD1	1:A:321:ILE:HD12	1.80	0.47
1:A:477:ILE:HG22	1:A:477:ILE:O	2.13	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:429:MET:HE1	1:E:437:GLY:HA2	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:I:429:MET:HE2	1:I:437:GLY:HA2	1.96	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: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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:276:GLU:CD	1:I:318:PHE:CE2	2.68	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: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
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: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: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:429:MET:HE2	1:D:437:GLY:HA2	1.96	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: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: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:E:382:LEU:HD12	1:E:382:LEU:C	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:456:ILE:O	1:K:456:ILE:HG23	2.15	0.46
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:B:449:LYS:C	1:B:451:GLY:H	2.19	0.46
1:C:773:PRO:C	1:L:774:SER:HB2	2.35	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: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:278:LEU:HD13	1:H:278:LEU:C	2.35	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: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:H:400:ASP:OD1	1:H:400:ASP:N	2.49	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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:D:752:LYS:HG3	1:D:755:MET:HE3	1.97	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:I:226:ASN:CA	1:I:229:PHE:CE1	2.99	0.45
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: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: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: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: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:449:LYS:C	1:L:451:GLY:H	2.20	0.45
1:L:508:LYS:O	1:L:512:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:LYS:N	1:A:376:LYS:HE2	2.32	0.45
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: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: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:I:269:LEU:HD21	1:I:457:SER:C	2.37	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:E:296:ASN:C	1:E:298:PRO:HD3	2.37	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
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:278:LEU:HD13	1:D:278:LEU:C	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:D:562:LYS:HZ1	1:I:562:LYS:NZ	2.15	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
1:D:269:LEU:HD21	1:D:457:SER:C	2.37	0.44
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:K:296:ASN:C	1:K:298:PRO:HD3	2.38	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:C:780:SER:CB	1:L:779:PHE:C	2.77	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:429:MET:HE2	1:A:437:GLY:HA2	1.99	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:E:269:LEU:HD21	1:E:457:SER:C	2.38	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:G:703:LYS:CG	1:K:544:ASN:HD21	2.24	0.43
1:I:429:MET:HE1	1:I:437:GLY:HA2	2.00	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:CG	1:I:299:GLU:O	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: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:C:782:ALA:HB3	1:L:778:GLY:C	2.38	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:K:429:MET:HE2	1:K:437:GLY:HA2	1.99	0.43
1:L:279:PRO:CB	1:L:322:GLN:HA	2.48	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:499:SER:C	1:D:500:THR:HG23	2.39	0.43
1:E:671:LYS:C	1:E:672:HIS:CD2	2.91	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
1:H:225:ASP:O	1:H:229:PHE:CD1	2.72	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:I:499:SER:C	1:I:500:THR:HG23	2.39	0.43
1:J:294:LEU:HB3	1:J:352:ILE:HD13	1.99	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:A:429:MET:HE1	1:A:437:GLY:HA2	2.01	0.43
1:D:286:THR:O	1:D:361:PRO:HD3	2.19	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: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
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: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:A:676:ARG:HG2	1:A:677:LYS:N	2.34	0.43
1:D:485:PHE:CD2	1:D:492:PHE:O	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:K:429:MET:HE1	1:K:437:GLY:HA2	2.01	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:269:LEU:HD21	1:A:457:SER:C	2.39	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:562:LYS:HD2	1:I:559:ASP:CG	2.39	0.42
1:E:478:ASN:ND2	1:E:482:LYS:CE	2.79	0.42
1:E:710:ASP:O	1:E:832:LYS:NZ	2.43	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
1:H:311:GLY:O	1:H:312:LEU:HB2	2.18	0.42
1:H:499:SER:C	1:H:500:THR:HG23	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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: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
1:A:326:THR:HA	1:A:329:ASN:ND2	2.34	0.42
1:A:499:SER:C	1:A:500:THR:HG23	2.40	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:458:LYS:HA	1:I:458:LYS:HD2	1.94	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:I:255:ILE:HG13	1:I:357:LEU:HA	2.00	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:E:278:LEU:HD13	1:E:278:LEU:C	2.40	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
1:I:265:LYS:HA	1:I:268:VAL:CG2	2.49	0.42
1:I:276:GLU:OE1	1:I:303:ASP:CG	2.58	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:690:ARG:O	1:D:694:THR:HG23	2.20	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: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
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:559:ASP:CG	1:K:854:PRO:HB3	2.40	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:A:296:ASN:C	1:A:298:PRO:HD3	2.41	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:429:MET:HE2	1:E:437:GLY:HA2	2.01	0.41
1:E:560:ASP:OD2	1:E:668:SER:OG	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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
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:382:LEU:HD12	1:I:382:LEU:O	2.21	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:K:499:SER:C	1:K:500:THR:HG23	2.40	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:456:ILE:HD12	1:E:456:ILE:C	2.40	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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:F:449:LYS:C	1:F:451:GLY:H	2.23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:483:ASN:HD22	1:K:483:ASN:C	2.23	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:B:609:PRO:HB2	1:B:610:ARG:C	2.41	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
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: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:449:LYS:C	1:C:451:GLY:H	2.25	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:478:ASN:CG	1:E:482:LYS:HZ2	2.22	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:246:GLN:H	1:H:246:GLN:CD	2.24	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:269:LEU:HD21	1:K:457:SER:C	2.41	0.41
1:K:276:GLU:CD	1:K:318:PHE:CE2	2.69	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: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:G:269:LEU:HD11	1:G:457:SER:O	2.20	0.41
1:I:268:VAL:O	1:I:272:ILE:CG1	2.69	0.41
1:I:456:ILE:HD12	1:I:456:ILE:C	2.40	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: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:K:491:GLU:CD	1:K:491:GLU:H	2.24	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: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:C:231:THR:O	1:C:235:ILE:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:458:LYS:HD2	1:I:458:LYS:C	2.40	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
1:J:530:ARG:HA	1:J:530:ARG:HD3	1.80	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:484:TYR:CD1	1:A:484:TYR:C	2.95	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: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:710:ASP:O	1:K:832:LYS:NZ	2.44	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:A:456:ILE:HD12	1:A:456:ILE:C	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:H:484:TYR:CD1	1:H:484:TYR:C	2.94	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
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:G:234:MET:HE2	1:G:517:MET:HB3	2.04	0.40
1:H:456:ILE:HD12	1:H:456:ILE:C	2.41	0.40
1:H:664:LEU:HB3	1:H:676:ARG:NH2	2.36	0.40
1:H:742:GLU:CD	1:H:748:ARG:HE	2.25	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:484:TYR:CD1	1:K:484:TYR:C	2.94	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:A:742:GLU:CD	1:A:748:ARG:HE	2.25	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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 (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	41	77
1	B	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	41	77
1	C	651/695 (94%)	624 (96%)	25 (4%)	2 (0%)	41	77
1	D	651/695 (94%)	631 (97%)	19 (3%)	1 (0%)	47	81
1	E	651/695 (94%)	625 (96%)	26 (4%)	0	100	100
1	F	651/695 (94%)	623 (96%)	26 (4%)	2 (0%)	41	77
1	G	651/695 (94%)	625 (96%)	24 (4%)	2 (0%)	41	77
1	H	651/695 (94%)	630 (97%)	20 (3%)	1 (0%)	47	81
1	I	651/695 (94%)	625 (96%)	25 (4%)	1 (0%)	47	81
1	J	651/695 (94%)	623 (96%)	26 (4%)	2 (0%)	41	77
1	K	651/695 (94%)	627 (96%)	23 (4%)	1 (0%)	47	81
1	L	651/695 (94%)	627 (96%)	22 (3%)	2 (0%)	41	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	7812/8340 (94%)	7510 (96%)	284 (4%)	18 (0%)	50 81

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 (i)

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%)	465 (83%)	98 (17%)	2 11
1	B	563/594 (95%)	494 (88%)	69 (12%)	4 19
1	C	563/594 (95%)	496 (88%)	67 (12%)	5 20
1	D	563/594 (95%)	459 (82%)	104 (18%)	1 9
1	E	563/594 (95%)	461 (82%)	102 (18%)	1 10
1	F	563/594 (95%)	494 (88%)	69 (12%)	4 19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	563/594 (95%)	491 (87%)	72 (13%)	4 18
1	H	563/594 (95%)	464 (82%)	99 (18%)	2 11
1	I	563/594 (95%)	463 (82%)	100 (18%)	2 10
1	J	563/594 (95%)	495 (88%)	68 (12%)	5 20
1	K	563/594 (95%)	465 (83%)	98 (17%)	2 11
1	L	563/594 (95%)	496 (88%)	67 (12%)	5 20
All	All	6756/7128 (95%)	5743 (85%)	1013 (15%)	6 15

All (1013) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
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	241	LEU
1	A	243	LYS
1	A	244	VAL
1	A	251	THR
1	A	255	ILE
1	A	263	SER
1	A	266	SER
1	A	268	VAL
1	A	269	LEU
1	A	272	ILE
1	A	278	LEU
1	A	282	SER
1	A	284	MET
1	A	285	ILE
1	A	287	ARG
1	A	303	ASP
1	A	320	LEU
1	A	344	ARG
1	A	346	THR
1	A	348	HIS
1	A	351	ASN
1	A	354	ASP
1	A	357	LEU

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Mol	Chain	Res	Type
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	386	TYR
1	A	388	ARG
1	A	393	ILE
1	A	394	LEU
1	A	396	ILE
1	A	402	ASP
1	A	407	THR
1	A	412	SER
1	A	423	ILE
1	A	430	ASP
1	A	431	LEU
1	A	434	PRO
1	A	448	LEU
1	A	450	LEU
1	A	456	ILE
1	A	457	SER
1	A	458	LYS
1	A	474	LEU
1	A	479	ARG
1	A	481	GLU
1	A	483	ASN
1	A	490	THR
1	A	491	GLU
1	A	492	PHE
1	A	495	ASP
1	A	498	VAL
1	A	499	SER
1	A	515	GLN
1	A	516	GLN
1	A	546	GLN
1	A	560	ASP
1	A	576	GLN

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Mol	Chain	Res	Type
1	A	590	LEU
1	A	596	ARG
1	A	610	ARG
1	A	615	ILE
1	A	617	ASP
1	A	640	THR
1	A	641	ARG
1	A	642	LEU
1	A	647	LEU
1	A	654	SER
1	A	657	GLN
1	A	671	LYS
1	A	676	ARG
1	A	714	ASN
1	A	727	LEU
1	A	749	LYS
1	A	762	ARG
1	A	802	LEU
1	A	815	LEU
1	A	818	LYS
1	A	836	THR
1	A	838	VAL
1	A	839	LEU
1	A	841	LEU
1	A	889	ARG
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	277	PHE
1	B	278	LEU
1	B	282	SER
1	B	284	MET
1	B	287	ARG
1	B	303	ASP
1	B	320	LEU
1	B	339	THR

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Mol	Chain	Res	Type
1	B	344	ARG
1	B	346	THR
1	B	354	ASP
1	B	357	LEU
1	B	358	ILE
1	B	376	LYS
1	B	377	ARG
1	B	382	LEU
1	B	385	LYS
1	B	386	TYR
1	B	388	ARG
1	B	393	ILE
1	B	394	LEU
1	B	396	ILE
1	B	402	ASP
1	B	412	SER
1	B	423	ILE
1	B	430	ASP
1	B	431	LEU
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
1	B	491	GLU
1	B	492	PHE
1	B	495	ASP
1	B	500	THR
1	B	503	MET
1	B	563	HIS
1	B	600	ARG
1	B	605	LEU
1	B	613	ASP
1	B	615	ILE
1	B	617	ASP
1	B	618	LEU
1	B	654	SER
1	B	666	LYS
1	B	690	ARG
1	B	710	ASP

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Mol	Chain	Res	Type
1	B	714	ASN
1	B	727	LEU
1	B	741	LEU
1	B	762	ARG
1	B	803	ARG
1	B	817	ASN
1	B	824	VAL
1	B	838	VAL
1	B	841	LEU
1	B	873	LYS
1	B	880	LYS
1	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	277	PHE
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	354	ASP
1	C	357	LEU
1	C	358	ILE
1	C	376	LYS
1	C	377	ARG
1	C	382	LEU
1	C	385	LYS
1	C	386	TYR
1	C	388	ARG
1	C	393	ILE
1	C	394	LEU
1	C	396	ILE
1	C	402	ASP

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Mol	Chain	Res	Type
1	C	405	ASN
1	C	412	SER
1	C	423	ILE
1	C	430	ASP
1	C	431	LEU
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	591	ASP
1	C	600	ARG
1	C	613	ASP
1	C	615	ILE
1	C	617	ASP
1	C	618	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	762	ARG
1	C	803	ARG
1	C	811	GLN
1	C	817	ASN
1	C	824	VAL
1	C	838	VAL
1	C	841	LEU
1	C	880	LYS
1	D	225	ASP
1	D	227	MET
1	D	228	MET
1	D	229	PHE
1	D	230	ILE

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Mol	Chain	Res	Type
1	D	235	ILE
1	D	237	ILE
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	277	PHE
1	D	278	LEU
1	D	282	SER
1	D	284	MET
1	D	285	ILE
1	D	287	ARG
1	D	303	ASP
1	D	320	LEU
1	D	344	ARG
1	D	346	THR
1	D	348	HIS
1	D	351	ASN
1	D	354	ASP
1	D	357	LEU
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	386	TYR
1	D	388	ARG
1	D	393	ILE
1	D	394	LEU
1	D	396	ILE
1	D	402	ASP

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Mol	Chain	Res	Type
1	D	405	ASN
1	D	407	THR
1	D	412	SER
1	D	423	ILE
1	D	430	ASP
1	D	431	LEU
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	483	ASN
1	D	490	THR
1	D	491	GLU
1	D	492	PHE
1	D	498	VAL
1	D	499	SER
1	D	507	LYS
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	586	ASP
1	D	590	LEU
1	D	596	ARG
1	D	610	ARG
1	D	615	ILE
1	D	617	ASP
1	D	640	THR
1	D	641	ARG
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

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Mol	Chain	Res	Type
1	D	749	LYS
1	D	752	LYS
1	D	762	ARG
1	D	769	GLU
1	D	802	LEU
1	D	811	GLN
1	D	815	LEU
1	D	818	LYS
1	D	836	THR
1	D	838	VAL
1	D	841	LEU
1	D	855	ARG
1	D	889	ARG
1	D	893	LEU
1	D	903	GLU
1	E	227	MET
1	E	228	MET
1	E	229	PHE
1	E	230	ILE
1	E	235	ILE
1	E	237	ILE
1	E	241	LEU
1	E	243	LYS
1	E	244	VAL
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	277	PHE
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	348	HIS

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Mol	Chain	Res	Type
1	E	354	ASP
1	E	357	LEU
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	386	TYR
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	405	ASN
1	E	412	SER
1	E	423	ILE
1	E	430	ASP
1	E	431	LEU
1	E	434	PRO
1	E	448	LEU
1	E	450	LEU
1	E	456	ILE
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	492	PHE
1	E	495	ASP
1	E	498	VAL
1	E	499	SER
1	E	513	LEU
1	E	515	GLN
1	E	516	GLN

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Mol	Chain	Res	Type
1	E	546	GLN
1	E	548	MET
1	E	566	HIS
1	E	572	PHE
1	E	586	ASP
1	E	590	LEU
1	E	591	ASP
1	E	610	ARG
1	E	615	ILE
1	E	617	ASP
1	E	631	GLN
1	E	640	THR
1	E	641	ARG
1	E	642	LEU
1	E	654	SER
1	E	657	GLN
1	E	671	LYS
1	E	714	ASN
1	E	721	GLU
1	E	727	LEU
1	E	749	LYS
1	E	762	ARG
1	E	802	LEU
1	E	815	LEU
1	E	818	LYS
1	E	836	THR
1	E	838	VAL
1	E	841	LEU
1	E	871	LEU
1	E	882	ARG
1	E	889	ARG
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

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Mol	Chain	Res	Type
1	F	282	SER
1	F	284	MET
1	F	303	ASP
1	F	320	LEU
1	F	339	THR
1	F	344	ARG
1	F	346	THR
1	F	354	ASP
1	F	357	LEU
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	386	TYR
1	F	388	ARG
1	F	393	ILE
1	F	394	LEU
1	F	396	ILE
1	F	402	ASP
1	F	405	ASN
1	F	412	SER
1	F	423	ILE
1	F	430	ASP
1	F	431	LEU
1	F	448	LEU
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	591	ASP
1	F	600	ARG
1	F	605	LEU

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Mol	Chain	Res	Type
1	F	613	ASP
1	F	615	ILE
1	F	617	ASP
1	F	618	LEU
1	F	622	ASP
1	F	666	LYS
1	F	690	ARG
1	F	714	ASN
1	F	727	LEU
1	F	741	LEU
1	F	762	ARG
1	F	783	LEU
1	F	803	ARG
1	F	817	ASN
1	F	824	VAL
1	F	838	VAL
1	F	841	LEU
1	F	880	LYS
1	G	231	THR
1	G	237	ILE
1	G	244	VAL
1	G	251	THR
1	G	255	ILE
1	G	266	SER
1	G	269	LEU
1	G	277	PHE
1	G	278	LEU
1	G	282	SER
1	G	284	MET
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	354	ASP
1	G	357	LEU
1	G	358	ILE
1	G	375	LEU
1	G	376	LYS
1	G	377	ARG
1	G	382	LEU

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Mol	Chain	Res	Type
1	G	385	LYS
1	G	386	TYR
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	405	ASN
1	G	412	SER
1	G	423	ILE
1	G	430	ASP
1	G	431	LEU
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	492	PHE
1	G	495	ASP
1	G	500	THR
1	G	503	MET
1	G	557	SER
1	G	590	LEU
1	G	591	ASP
1	G	600	ARG
1	G	605	LEU
1	G	613	ASP
1	G	615	ILE
1	G	617	ASP
1	G	618	LEU
1	G	654	SER
1	G	666	LYS
1	G	690	ARG
1	G	714	ASN
1	G	727	LEU
1	G	741	LEU
1	G	762	ARG
1	G	767	ILE
1	G	803	ARG

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Mol	Chain	Res	Type
1	G	811	GLN
1	G	817	ASN
1	G	824	VAL
1	G	838	VAL
1	G	841	LEU
1	G	880	LYS
1	H	225	ASP
1	H	227	MET
1	H	228	MET
1	H	230	ILE
1	H	235	ILE
1	H	237	ILE
1	H	241	LEU
1	H	243	LYS
1	H	244	VAL
1	H	255	ILE
1	H	263	SER
1	H	266	SER
1	H	268	VAL
1	H	269	LEU
1	H	272	ILE
1	H	277	PHE
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	348	HIS
1	H	351	ASN
1	H	354	ASP
1	H	357	LEU
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

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Mol	Chain	Res	Type
1	H	382	LEU
1	H	383	CYS
1	H	385	LYS
1	H	388	ARG
1	H	393	ILE
1	H	394	LEU
1	H	396	ILE
1	H	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	431	LEU
1	H	434	PRO
1	H	448	LEU
1	H	450	LEU
1	H	456	ILE
1	H	457	SER
1	H	458	LYS
1	H	474	LEU
1	H	479	ARG
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	507	LYS
1	H	515	GLN
1	H	516	GLN
1	H	546	GLN
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	640	THR

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Mol	Chain	Res	Type
1	H	641	ARG
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	749	LYS
1	H	762	ARG
1	H	783	LEU
1	H	802	LEU
1	H	815	LEU
1	H	818	LYS
1	H	836	THR
1	H	838	VAL
1	H	841	LEU
1	H	855	ARG
1	H	889	ARG
1	H	893	LEU
1	H	903	GLU
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	241	LEU
1	I	243	LYS
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

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Mol	Chain	Res	Type
1	I	320	LEU
1	I	344	ARG
1	I	346	THR
1	I	348	HIS
1	I	354	ASP
1	I	357	LEU
1	I	358	ILE
1	I	360	LEU
1	I	363	TYR
1	I	375	LEU
1	I	376	LYS
1	I	377	ARG
1	I	378	LYS
1	I	382	LEU
1	I	383	CYS
1	I	385	LYS
1	I	386	TYR
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	431	LEU
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	483	ASN
1	I	490	THR
1	I	491	GLU
1	I	492	PHE
1	I	495	ASP
1	I	498	VAL

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Mol	Chain	Res	Type
1	I	499	SER
1	I	515	GLN
1	I	516	GLN
1	I	546	GLN
1	I	560	ASP
1	I	576	GLN
1	I	581	LEU
1	I	586	ASP
1	I	590	LEU
1	I	591	ASP
1	I	610	ARG
1	I	615	ILE
1	I	617	ASP
1	I	622	ASP
1	I	640	THR
1	I	641	ARG
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	749	LYS
1	I	762	ARG
1	I	768	VAL
1	I	802	LEU
1	I	811	GLN
1	I	815	LEU
1	I	818	LYS
1	I	836	THR
1	I	838	VAL
1	I	841	LEU
1	I	855	ARG
1	I	889	ARG
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

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Mol	Chain	Res	Type
1	J	266	SER
1	J	269	LEU
1	J	277	PHE
1	J	278	LEU
1	J	282	SER
1	J	284	MET
1	J	287	ARG
1	J	303	ASP
1	J	320	LEU
1	J	339	THR
1	J	344	ARG
1	J	346	THR
1	J	354	ASP
1	J	358	ILE
1	J	376	LYS
1	J	377	ARG
1	J	382	LEU
1	J	385	LYS
1	J	386	TYR
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	405	ASN
1	J	412	SER
1	J	423	ILE
1	J	430	ASP
1	J	431	LEU
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

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Mol	Chain	Res	Type
1	J	590	LEU
1	J	591	ASP
1	J	600	ARG
1	J	613	ASP
1	J	615	ILE
1	J	617	ASP
1	J	618	LEU
1	J	654	SER
1	J	666	LYS
1	J	690	ARG
1	J	727	LEU
1	J	741	LEU
1	J	762	ARG
1	J	803	ARG
1	J	811	GLN
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	235	ILE
1	K	237	ILE
1	K	241	LEU
1	K	243	LYS
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	320	LEU

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Mol	Chain	Res	Type
1	K	344	ARG
1	K	346	THR
1	K	348	HIS
1	K	351	ASN
1	K	354	ASP
1	K	357	LEU
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	386	TYR
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	405	ASN
1	K	412	SER
1	K	423	ILE
1	K	430	ASP
1	K	431	LEU
1	K	433	GLU
1	K	434	PRO
1	K	448	LEU
1	K	450	LEU
1	K	456	ILE
1	K	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	495	ASP

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Mol	Chain	Res	Type
1	K	498	VAL
1	K	499	SER
1	K	507	LYS
1	K	515	GLN
1	K	516	GLN
1	K	546	GLN
1	K	560	ASP
1	K	576	GLN
1	K	586	ASP
1	K	590	LEU
1	K	610	ARG
1	K	615	ILE
1	K	617	ASP
1	K	640	THR
1	K	641	ARG
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	749	LYS
1	K	762	ARG
1	K	768	VAL
1	K	802	LEU
1	K	811	GLN
1	K	815	LEU
1	K	818	LYS
1	K	836	THR
1	K	838	VAL
1	K	841	LEU
1	K	889	ARG
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

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Mol	Chain	Res	Type
1	L	277	PHE
1	L	278	LEU
1	L	282	SER
1	L	284	MET
1	L	287	ARG
1	L	303	ASP
1	L	320	LEU
1	L	344	ARG
1	L	346	THR
1	L	354	ASP
1	L	358	ILE
1	L	376	LYS
1	L	377	ARG
1	L	382	LEU
1	L	385	LYS
1	L	386	TYR
1	L	388	ARG
1	L	393	ILE
1	L	394	LEU
1	L	396	ILE
1	L	402	ASP
1	L	405	ASN
1	L	412	SER
1	L	423	ILE
1	L	430	ASP
1	L	431	LEU
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	591	ASP
1	L	600	ARG
1	L	605	LEU

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Mol	Chain	Res	Type
1	L	613	ASP
1	L	615	ILE
1	L	617	ASP
1	L	618	LEU
1	L	654	SER
1	L	666	LYS
1	L	690	ARG
1	L	727	LEU
1	L	741	LEU
1	L	762	ARG
1	L	803	ARG
1	L	811	GLN
1	L	817	ASN
1	L	824	VAL
1	L	838	VAL
1	L	841	LEU
1	L	855	ARG
1	L	880	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	A	275	HIS
1	A	472	ASN
1	A	478	ASN
1	A	576	GLN
1	A	657	GLN
1	B	631	GLN
1	B	672	HIS
1	C	631	GLN
1	C	672	HIS
1	C	772	HIS
1	D	242	GLN
1	D	275	HIS
1	D	472	ASN
1	D	478	ASN
1	D	488	HIS
1	D	544	ASN
1	D	563	HIS
1	D	566	HIS
1	D	576	GLN

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Mol	Chain	Res	Type
1	D	657	GLN
1	D	866	HIS
1	E	242	GLN
1	E	275	HIS
1	E	472	ASN
1	E	478	ASN
1	E	488	HIS
1	E	576	GLN
1	E	657	GLN
1	E	672	HIS
1	F	563	HIS
1	F	631	GLN
1	F	672	HIS
1	F	772	HIS
1	G	563	HIS
1	G	631	GLN
1	G	672	HIS
1	G	772	HIS
1	H	242	GLN
1	H	275	HIS
1	H	472	ASN
1	H	478	ASN
1	H	488	HIS
1	H	544	ASN
1	H	576	GLN
1	H	657	GLN
1	I	242	GLN
1	I	275	HIS
1	I	478	ASN
1	I	488	HIS
1	I	544	ASN
1	I	566	HIS
1	I	576	GLN
1	I	657	GLN
1	J	631	GLN
1	J	672	HIS
1	J	866	HIS
1	K	242	GLN
1	K	275	HIS
1	K	472	ASN
1	K	478	ASN
1	K	483	ASN

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Mol	Chain	Res	Type
1	K	488	HIS
1	K	544	ASN
1	K	576	GLN
1	K	657	GLN
1	L	631	GLN
1	L	672	HIS
1	L	866	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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

Continued on next page...

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Mol	Chain	Number of breaks
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

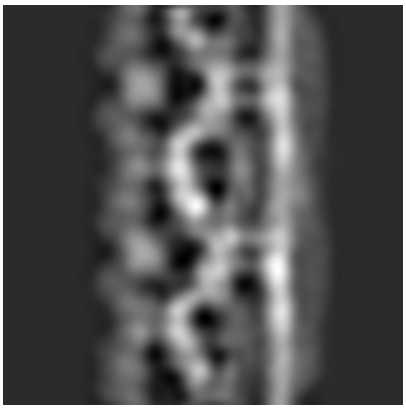
6 Map visualisation

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.

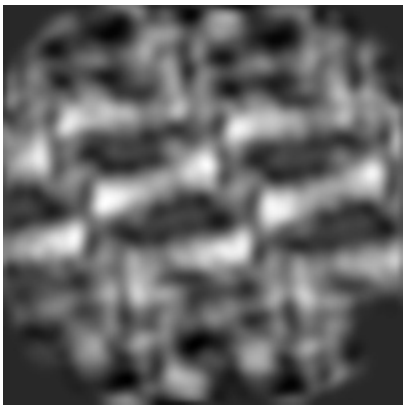
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

6.1.1 Primary map



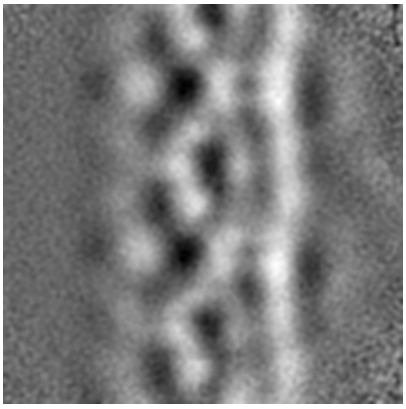
X



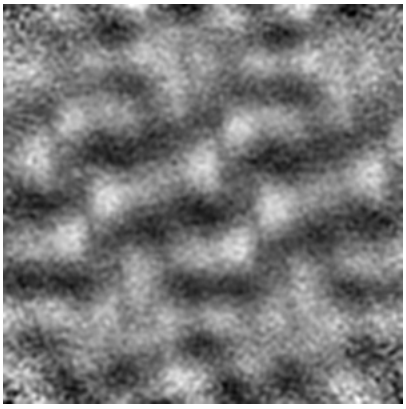
Y

Z

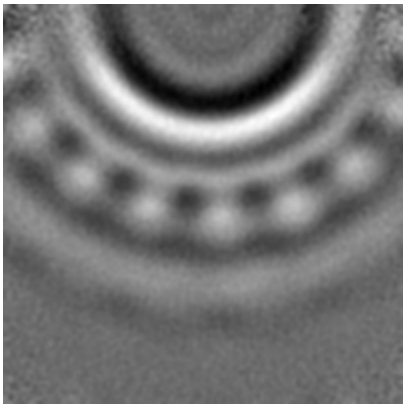
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

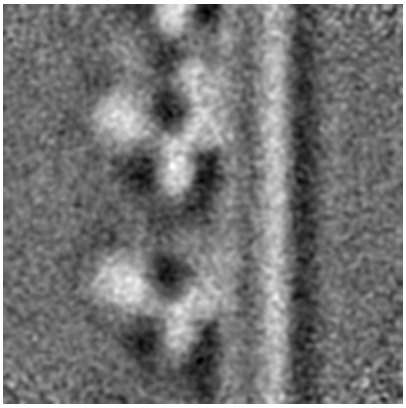
6.2.1 Primary map

X Index: 60

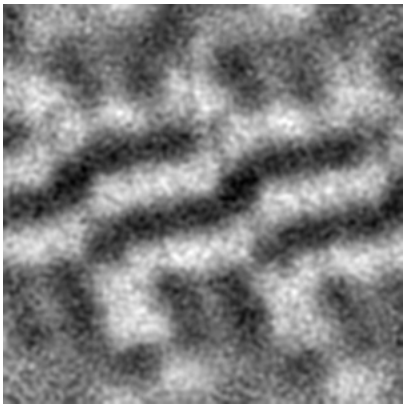
Y Index: 60

Z Index: 60

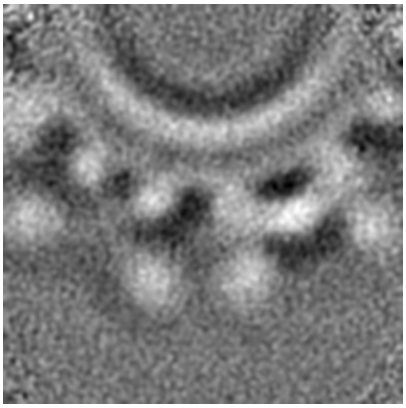
6.2.2 Raw map



X Index: 60



Y Index: 60



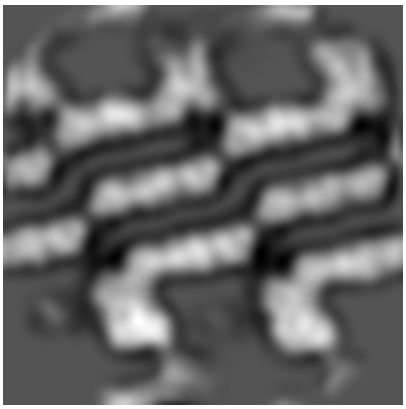
Z Index: 60

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

6.3 Largest variance slices (i)

6.3.1 Primary map

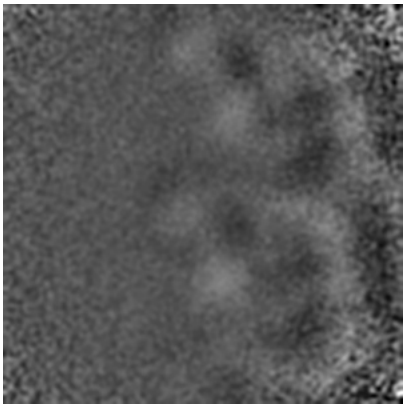
X Index: 86



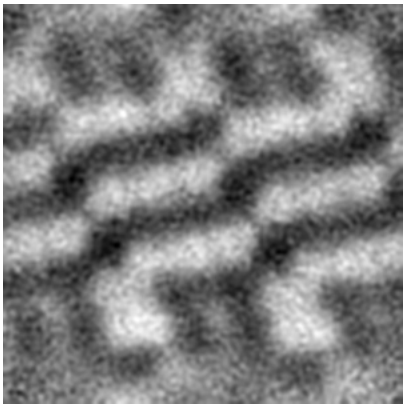
Y Index: 62

Z Index: 48

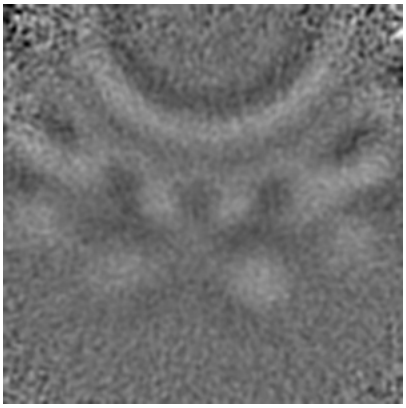
6.3.2 Raw map



X Index: 0



Y Index: 62

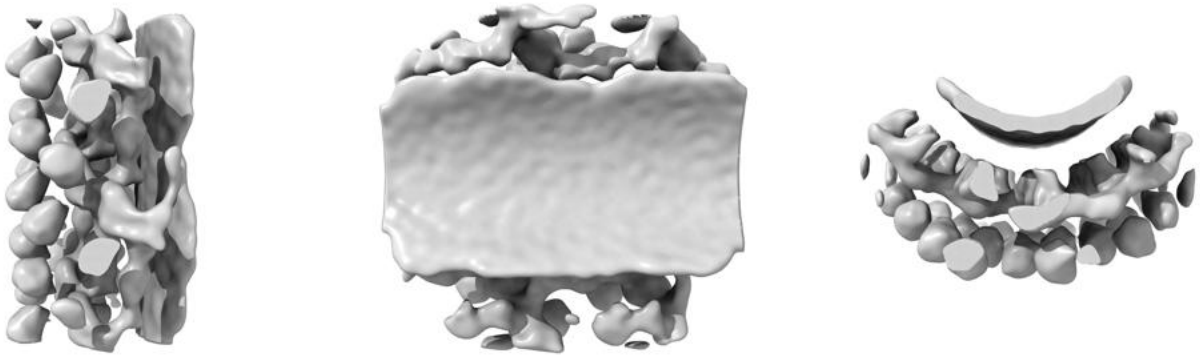


Z Index: 1

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

6.4 Orthogonal surface views (i)

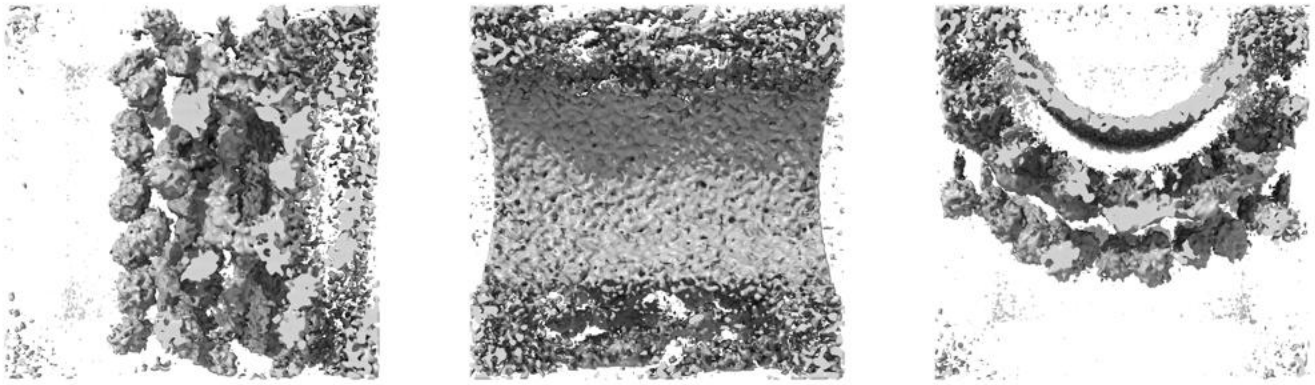
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X Y Z

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

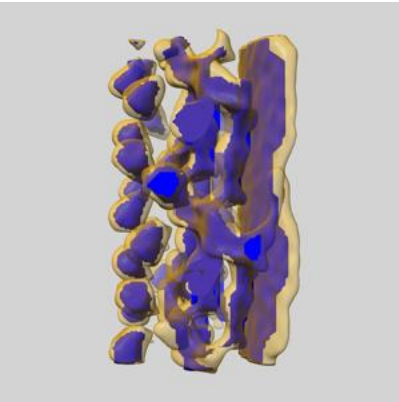
6.5 Mask visualisation (i)

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

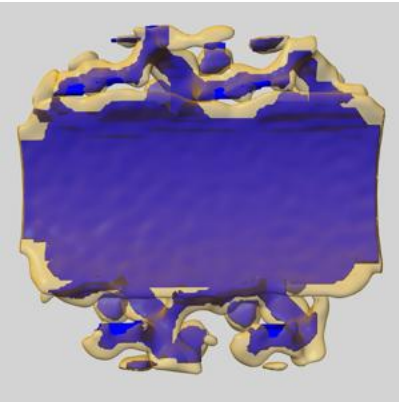
A mask typically either:

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

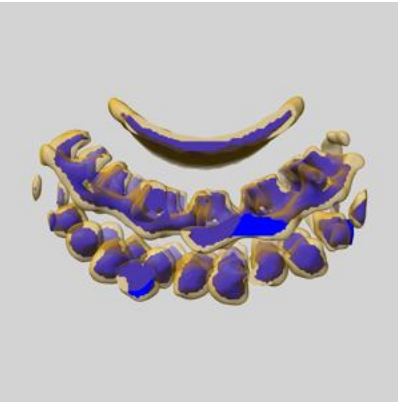
6.5.1 emd_10062_msk_1.map (i)



X



Y

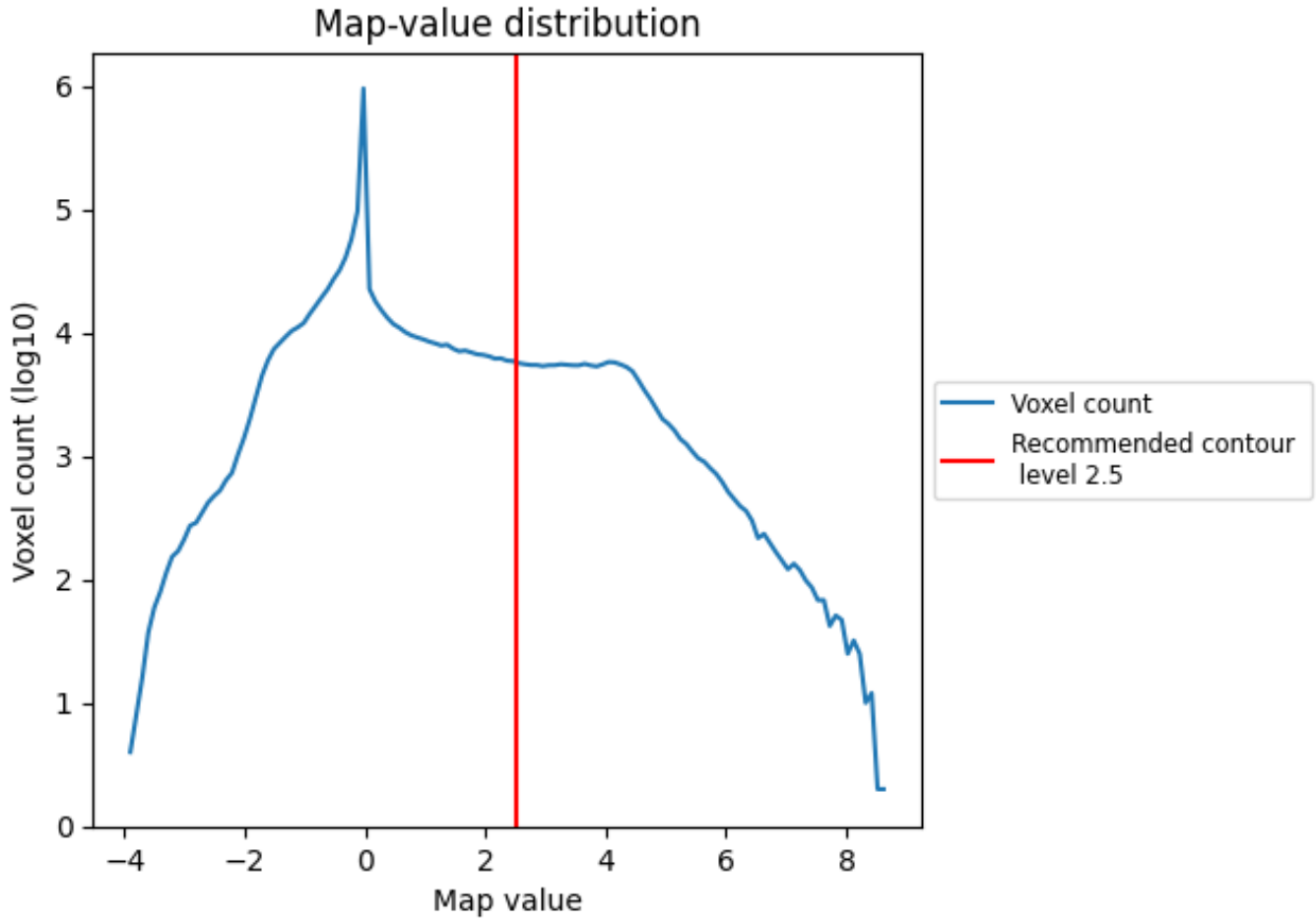


Z

7 Map analysis

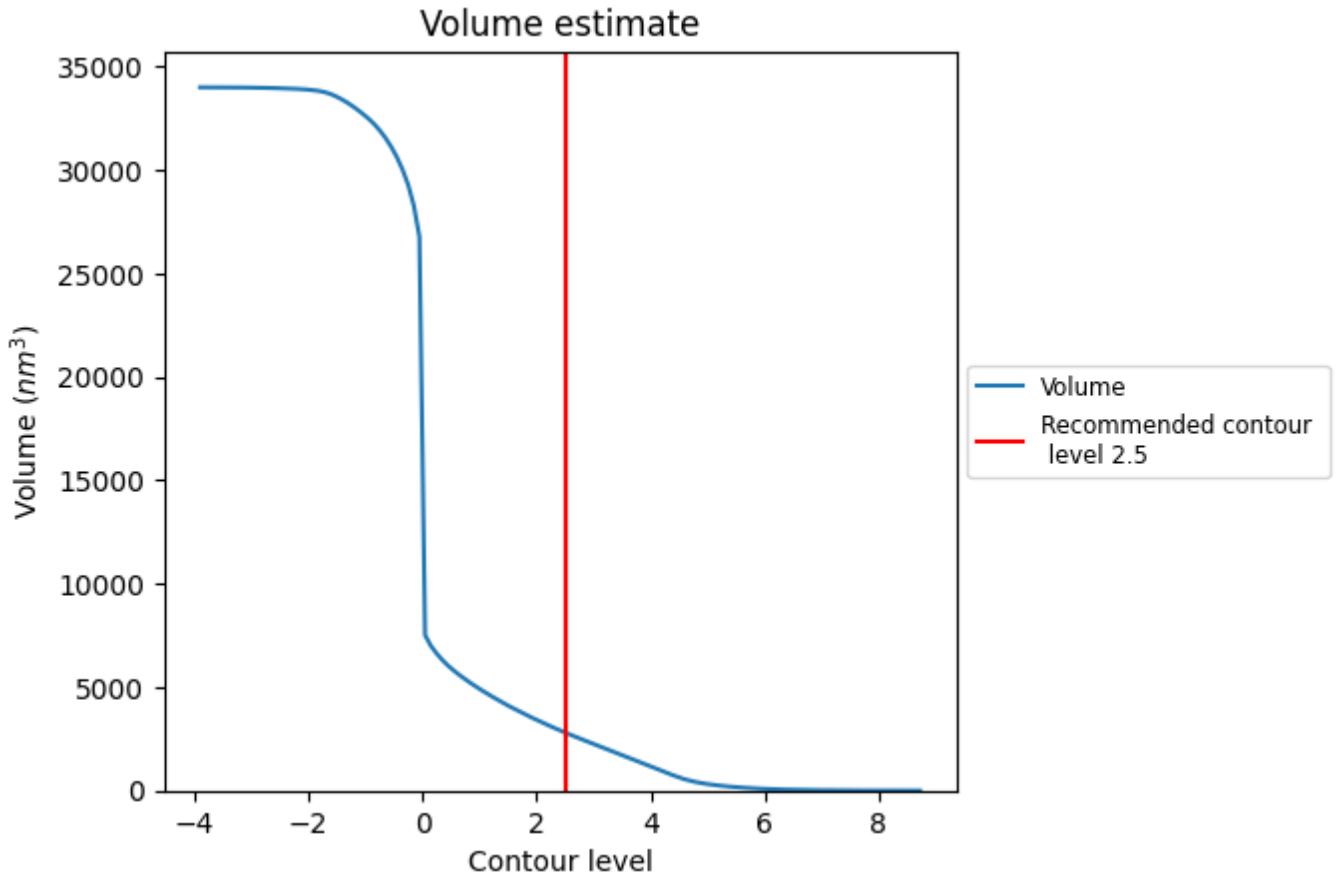
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

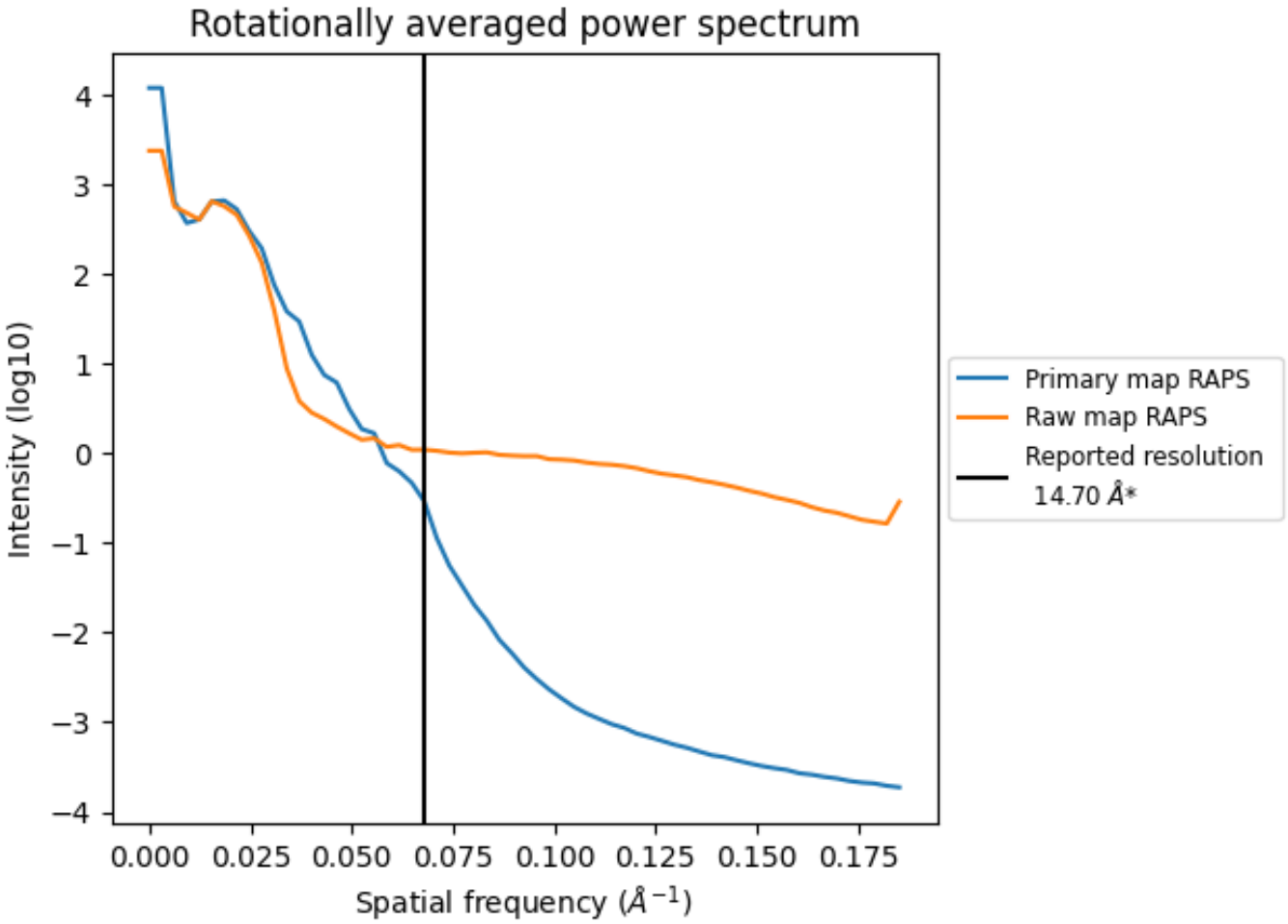
7.2 Volume estimate



The volume at the recommended contour level is 2804 nm^3; 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 (i)

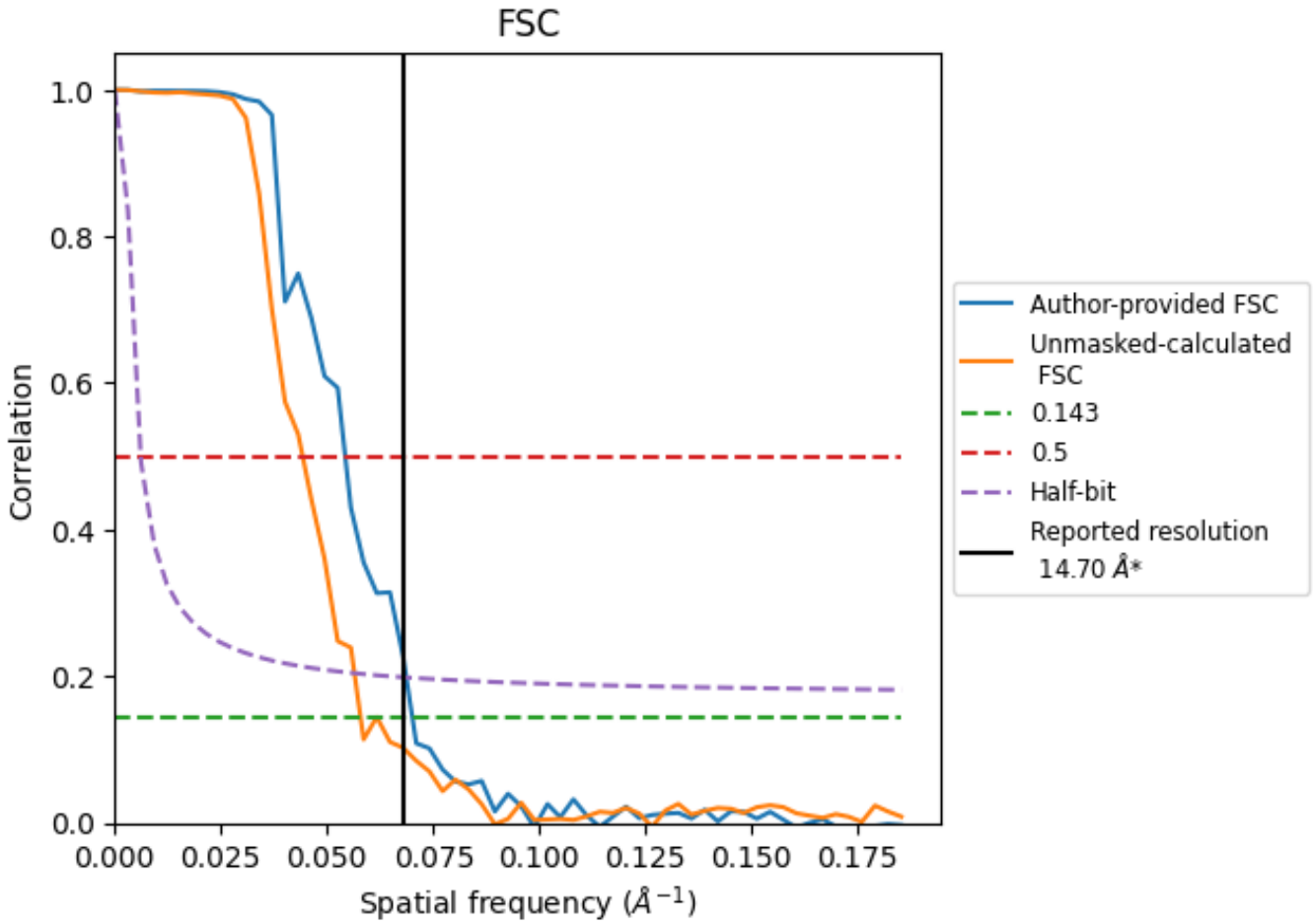


*Reported resolution corresponds to spatial frequency of 0.068 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.068 Å^{-1}

8.2 Resolution estimates (i)

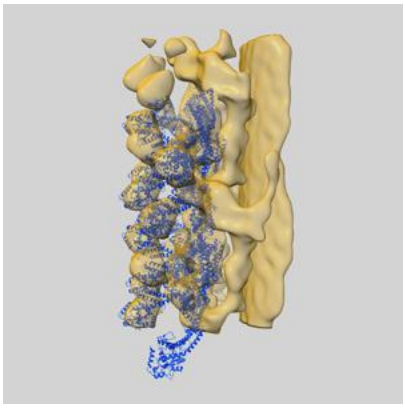
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	14.70	-	-
Author-provided FSC curve	14.27	18.45	14.56
Unmasked-calculated*	17.27	22.57	17.73

*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 %

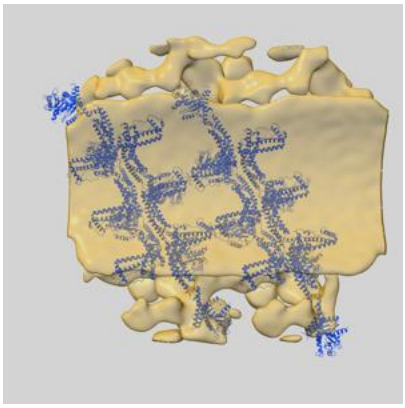
9 Map-model fit

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.

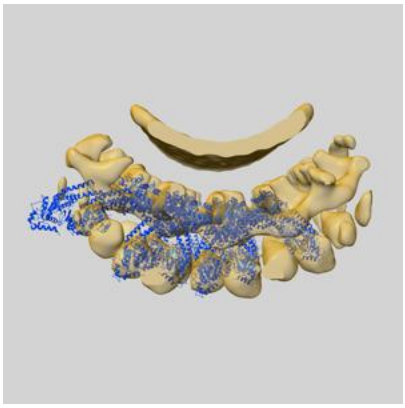
9.1 Map-model overlay



X



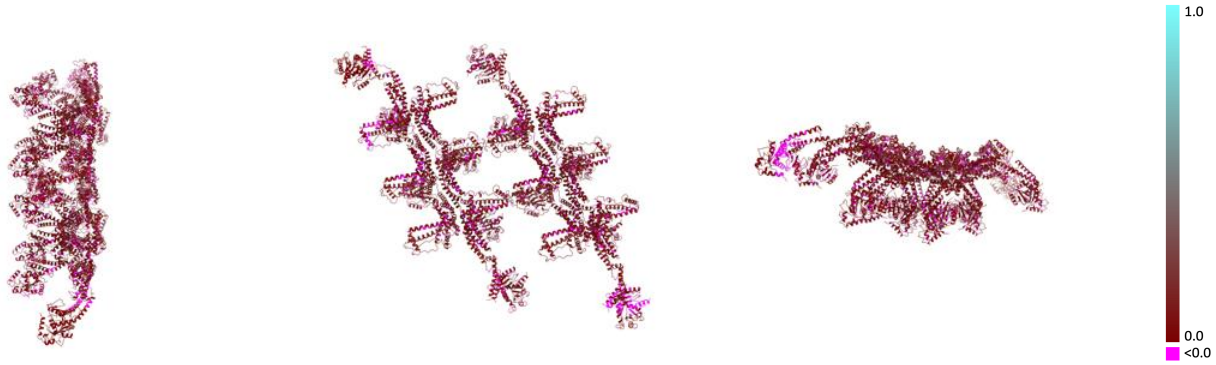
Y



Z

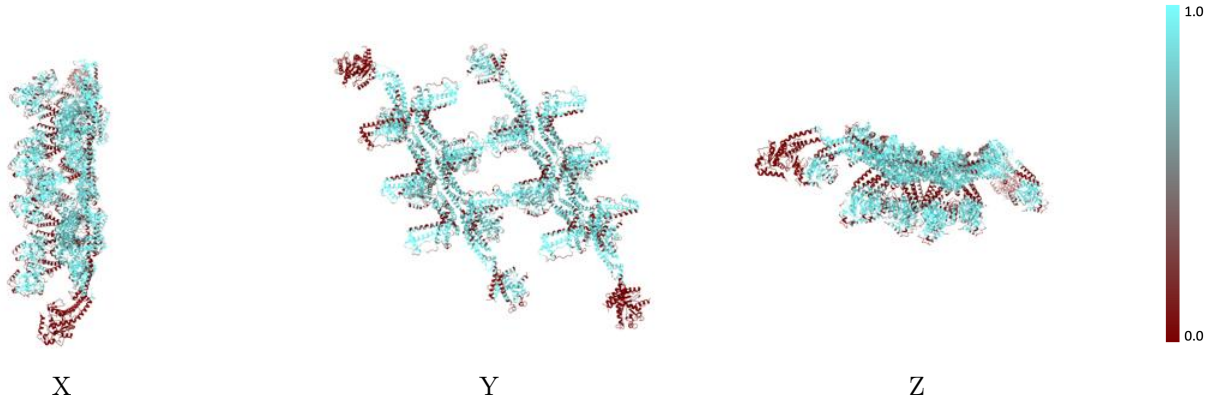
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



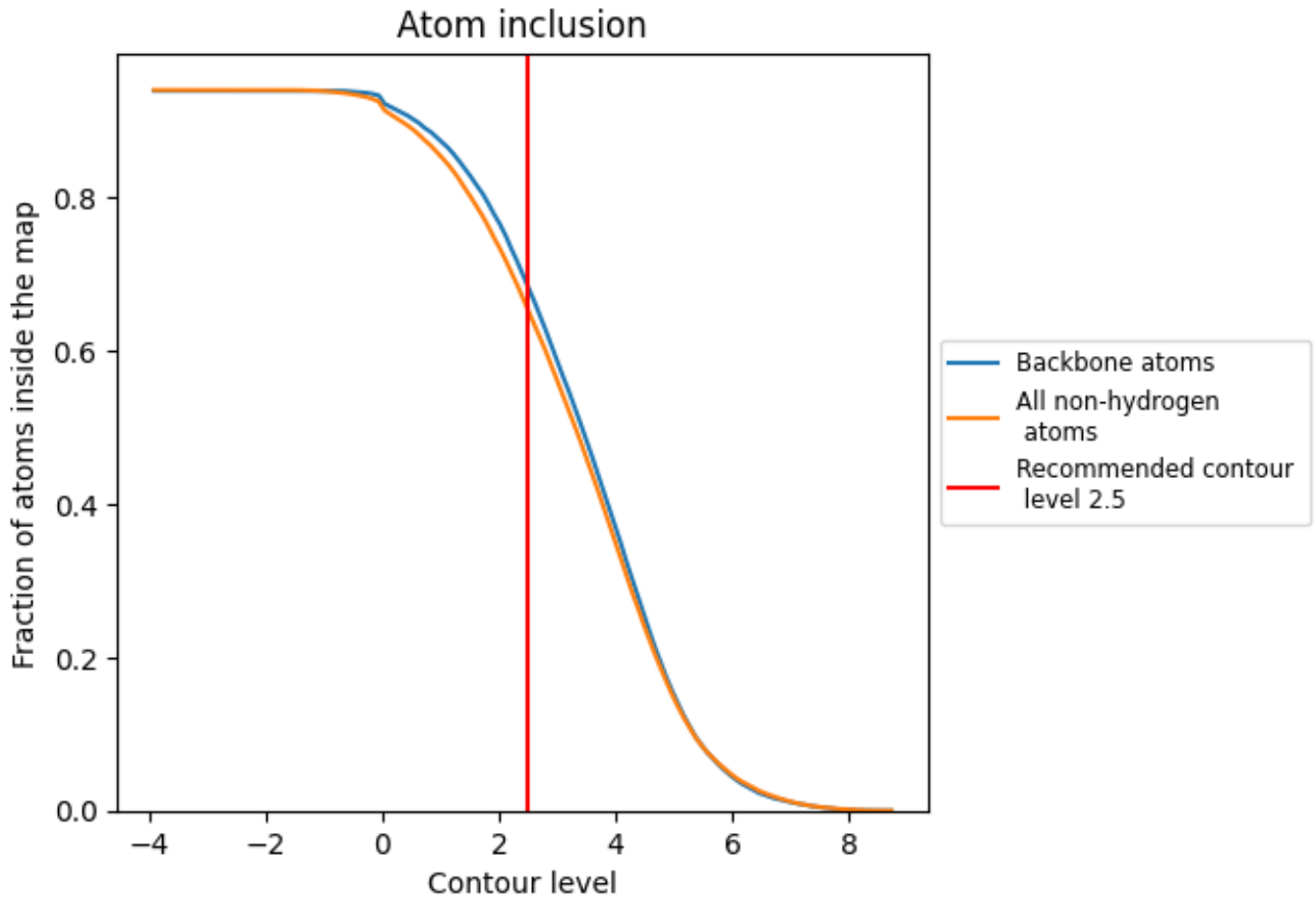
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.6529	0.0650
A	0.7179	0.0740
B	0.7238	0.0690
C	0.7284	0.0740
D	0.7133	0.0730
E	0.3482	0.0320
F	0.6987	0.0710
G	0.6848	0.0690
H	0.7228	0.0740
I	0.7139	0.0720
J	0.4051	0.0340
K	0.7050	0.0710
L	0.6727	0.0700