



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 03:22 AM UTC

PDB ID : 6RZW / pdb_00006rzw
EMDB ID : EMD-10065
Title : Structure of s-Mgm1 decorating the inner surface of tubulated lipid membranes in the GTPgammaS bound state
Authors : Faelber, K.; Dietrich, L.; Noel, J.K.; Sanchez, R.; Kudryashev, M.; Kuelbrandt, W.; Daumke, O.
Deposited on : 2019-06-13
Resolution : 18.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

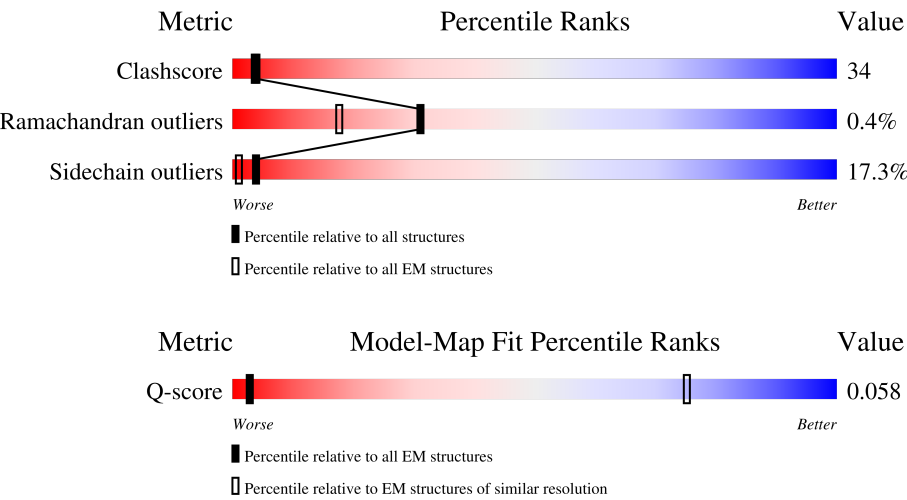
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 18.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	16 (18.30 - 19.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	695	
1	B	695	
1	C	695	
1	D	695	

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Mol	Chain	Length	Quality of chain
1	E	695	11% 41% 34% 17% • 5%
1	F	695	12% 48% 35% 11% • 5%
1	G	695	9% 48% 35% 12% • 5%
1	H	695	19% 39% 35% 17% • 5%
1	I	695	12% 49% 35% 10% • 5%
1	J	695	11% 39% 36% 17% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 51520 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.

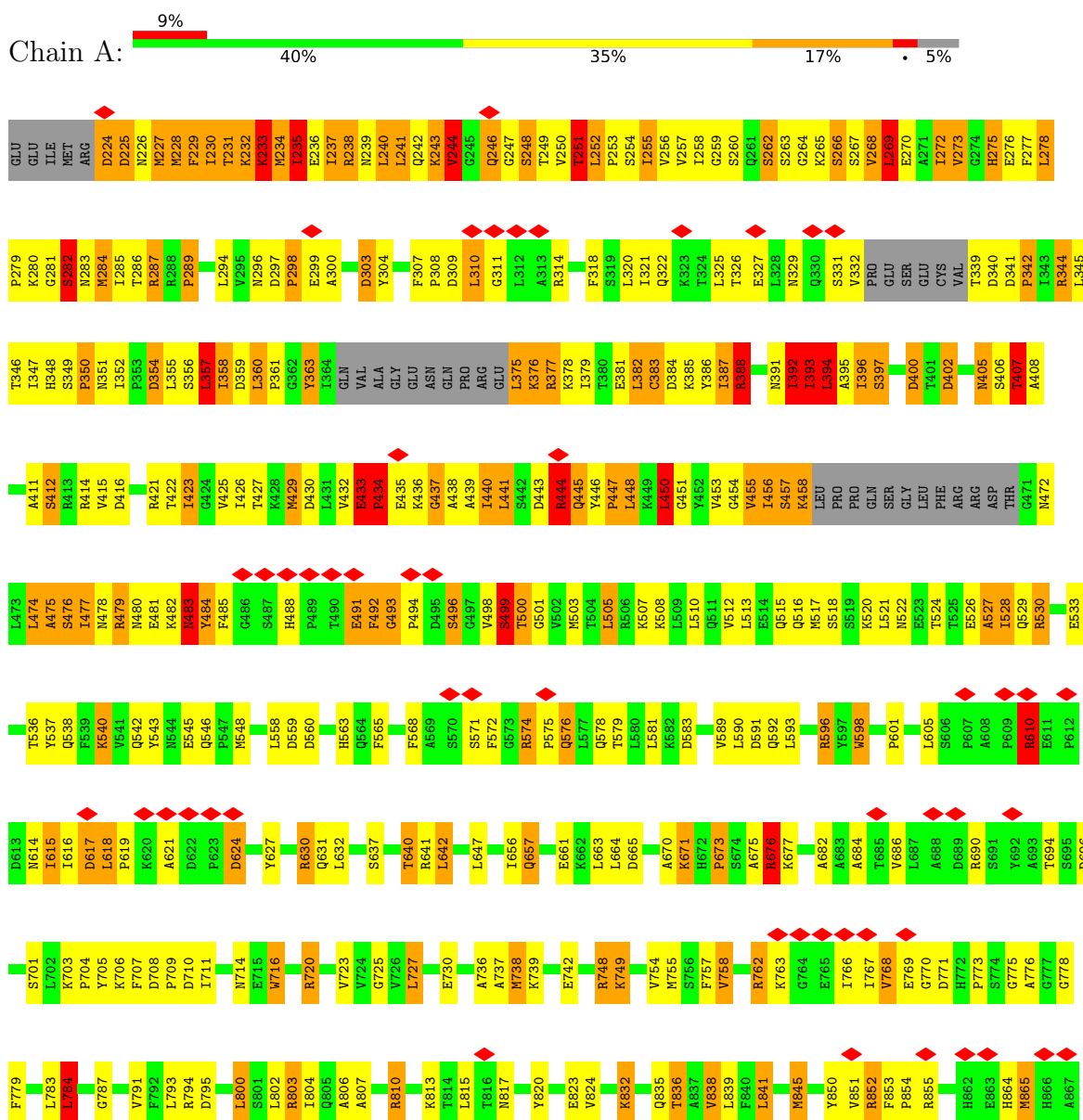
- Molecule 1 is a protein called Putative mitochondrial dynamin protein.

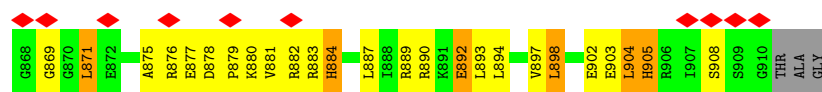
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	B	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	C	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	D	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17		
1	E	659	Total	C	N	O	S	0	0
			5152	3243	910	982	17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

3 Residue-property plots

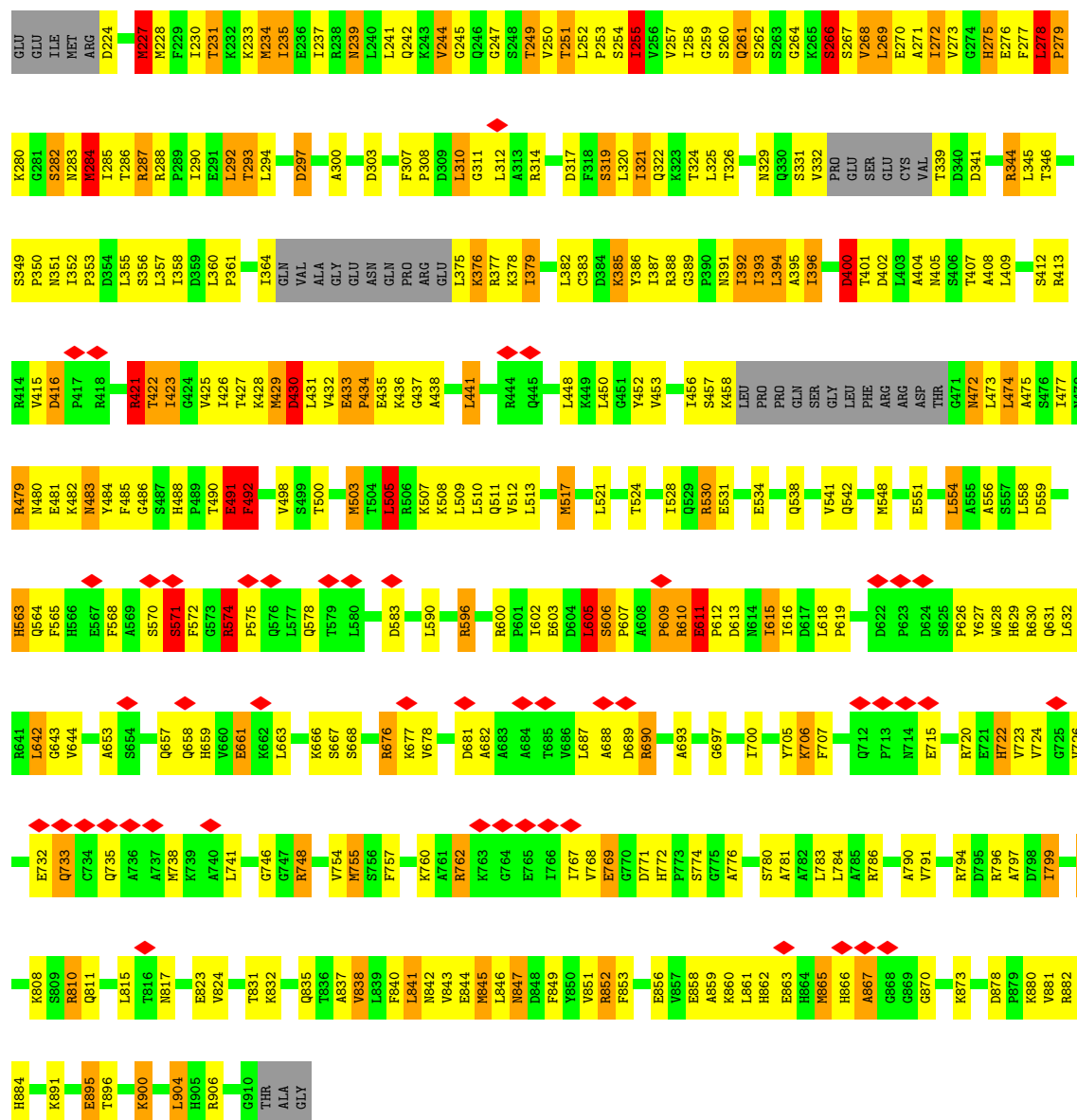
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Putative mitochondrial dynamin protein



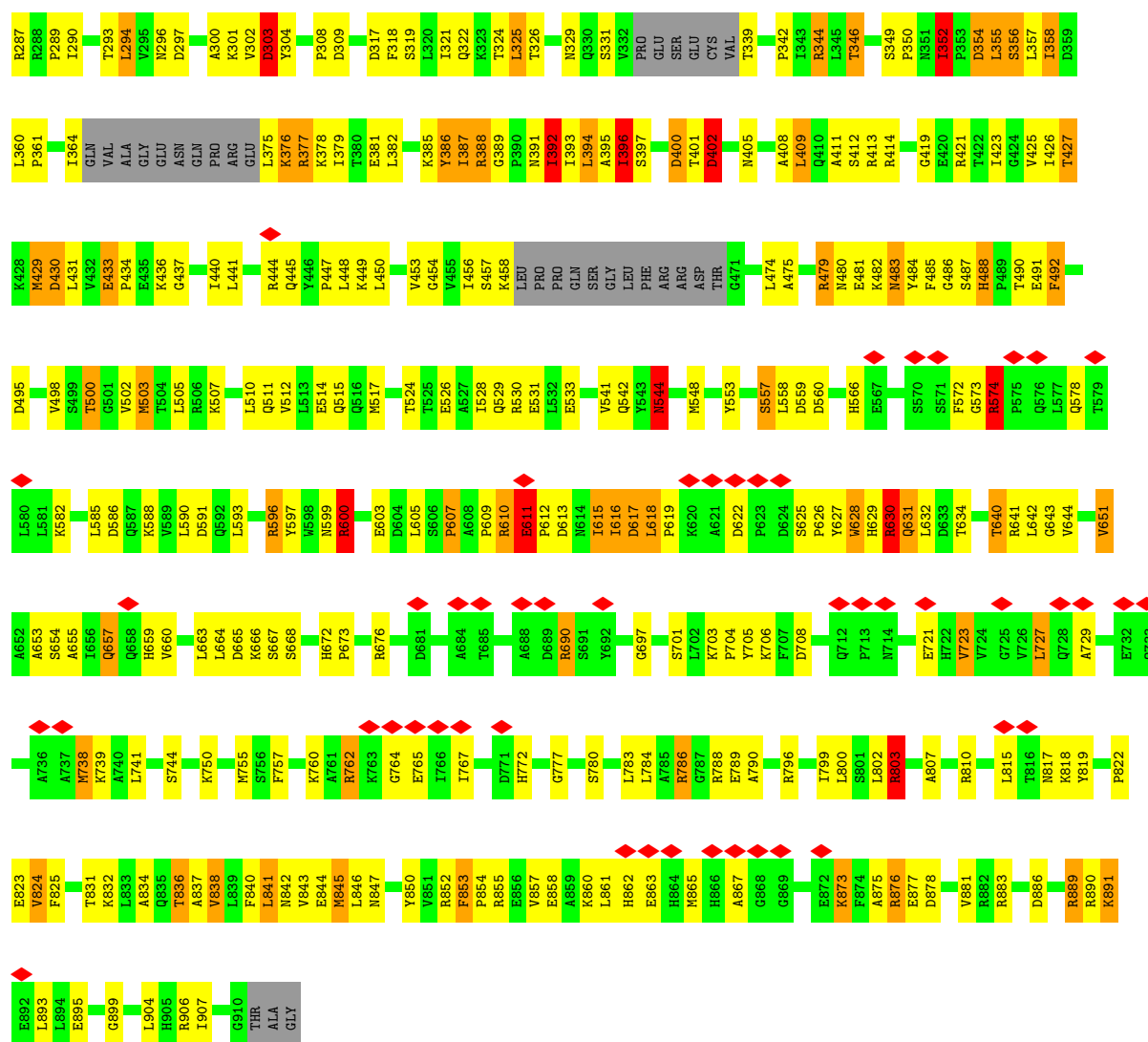


• Molecule 1: Putative mitochondrial dynamin protein

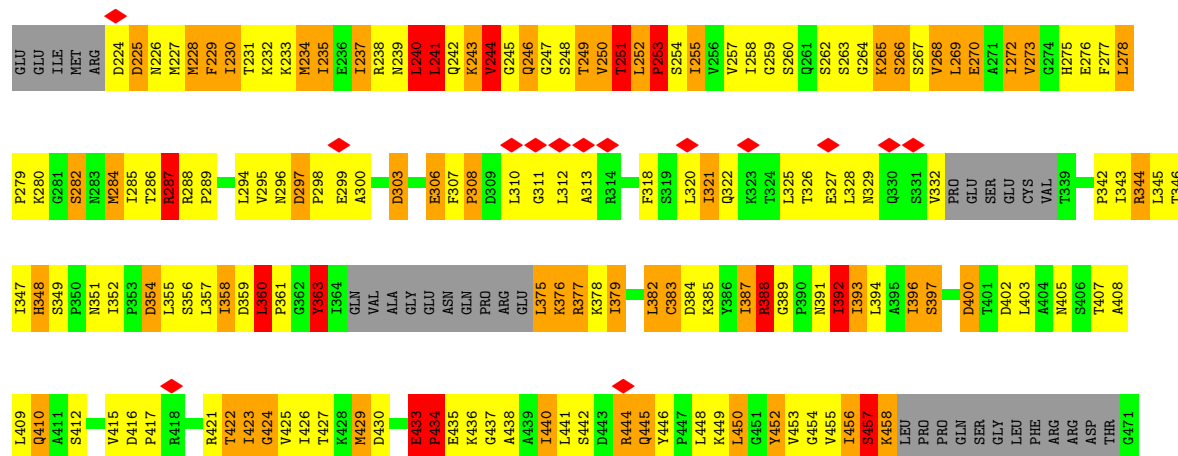
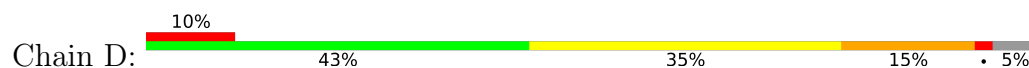


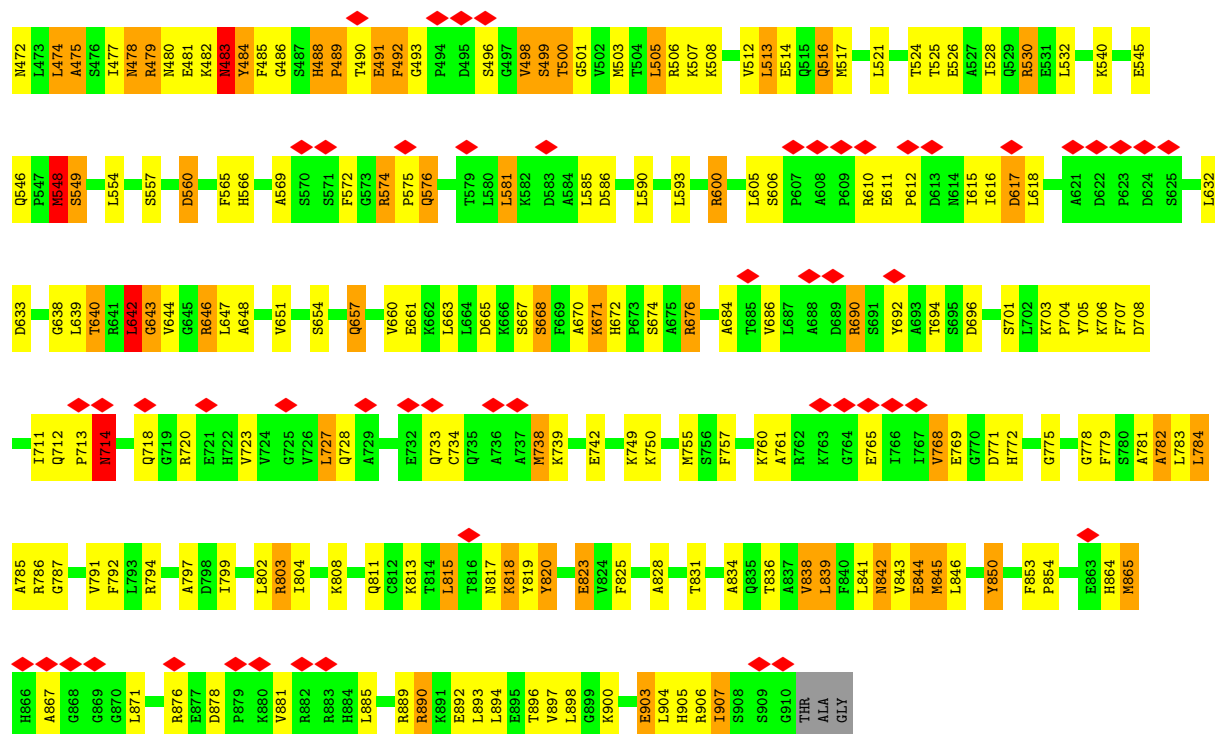
• Molecule 1: Putative mitochondrial dynamin protein



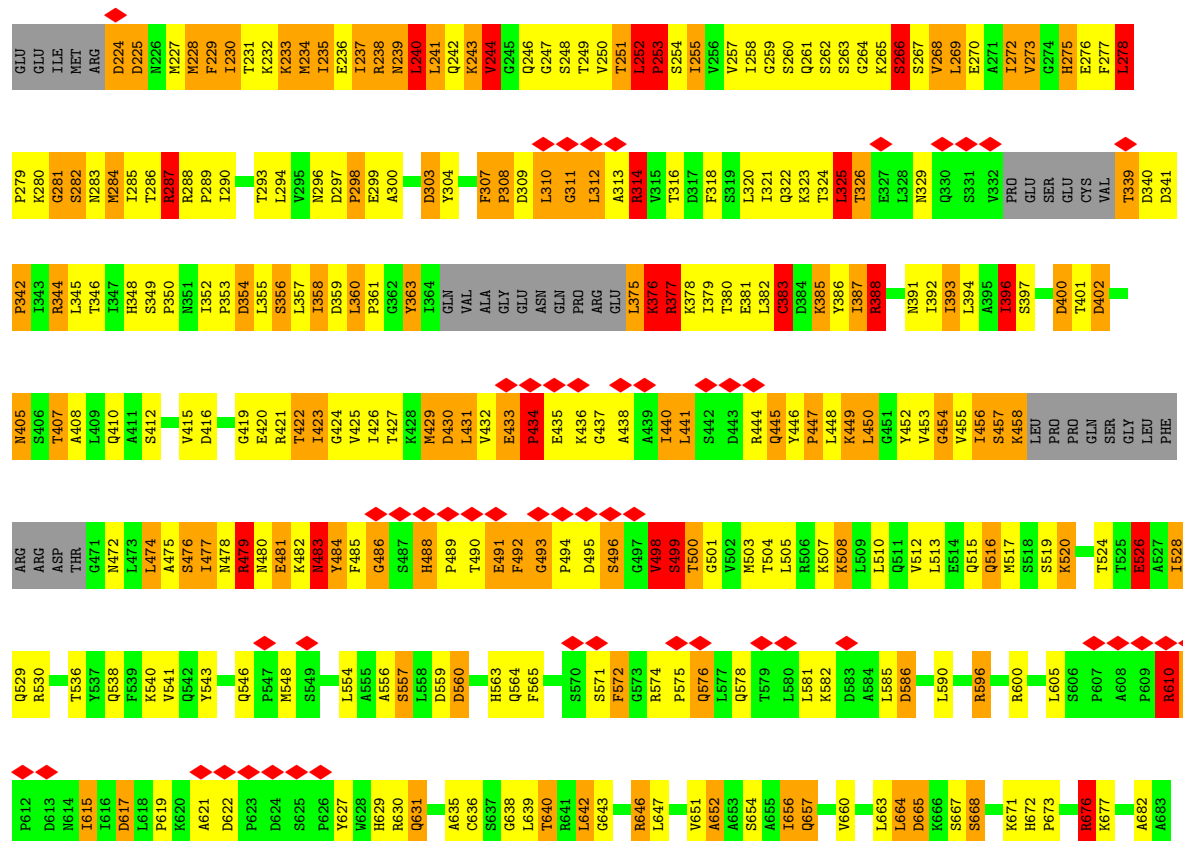


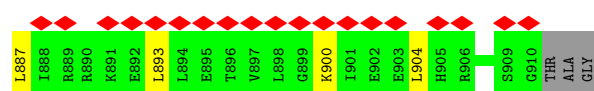
• Molecule 1: Putative mitochondrial dynamin protein





• Molecule 1: Putative mitochondrial dynamin protein

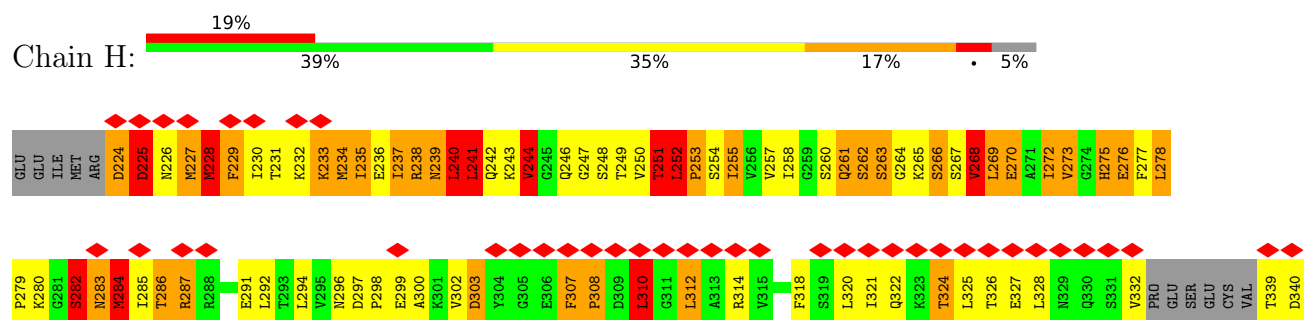


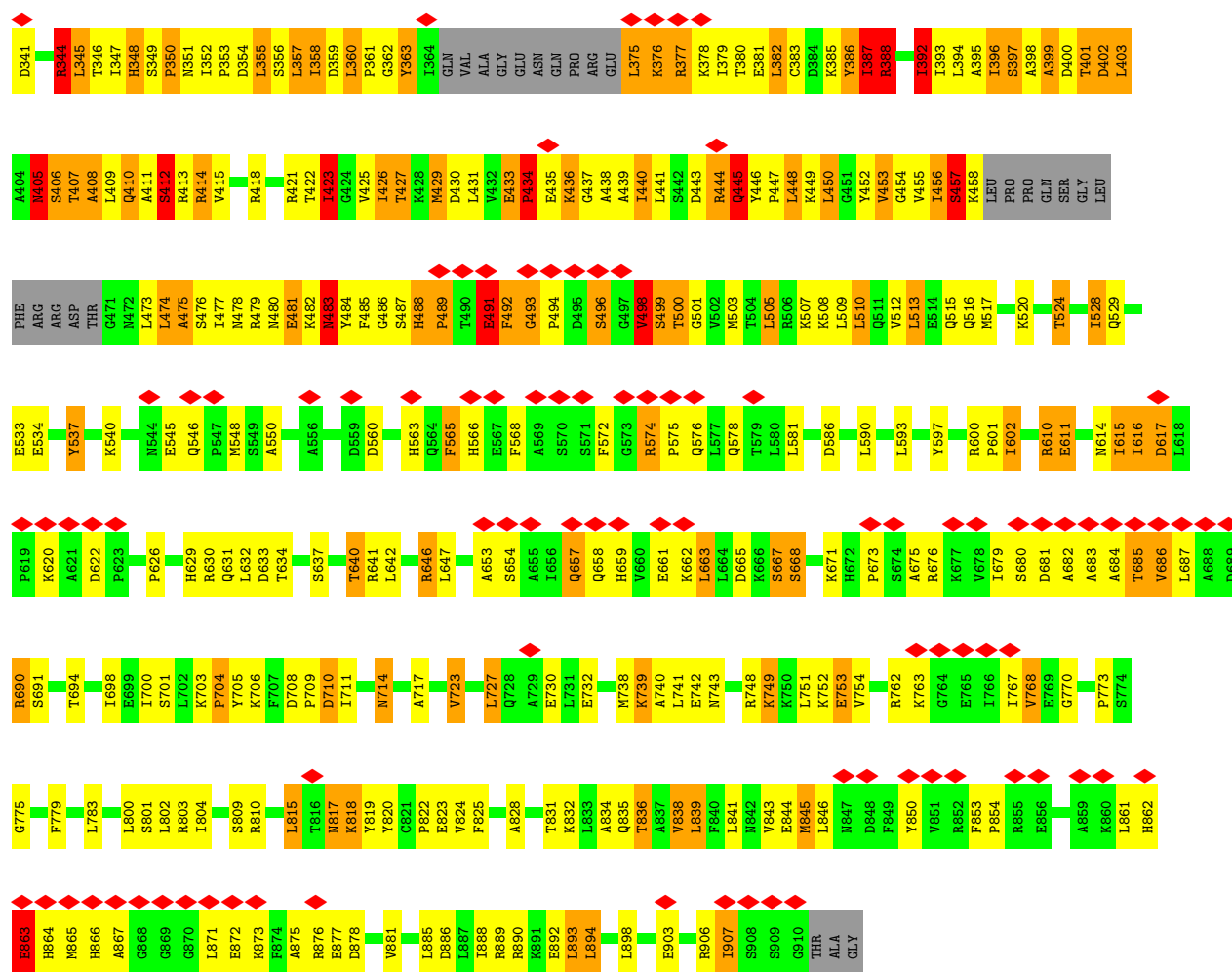


• Molecule 1: Putative mitochondrial dynamin protein

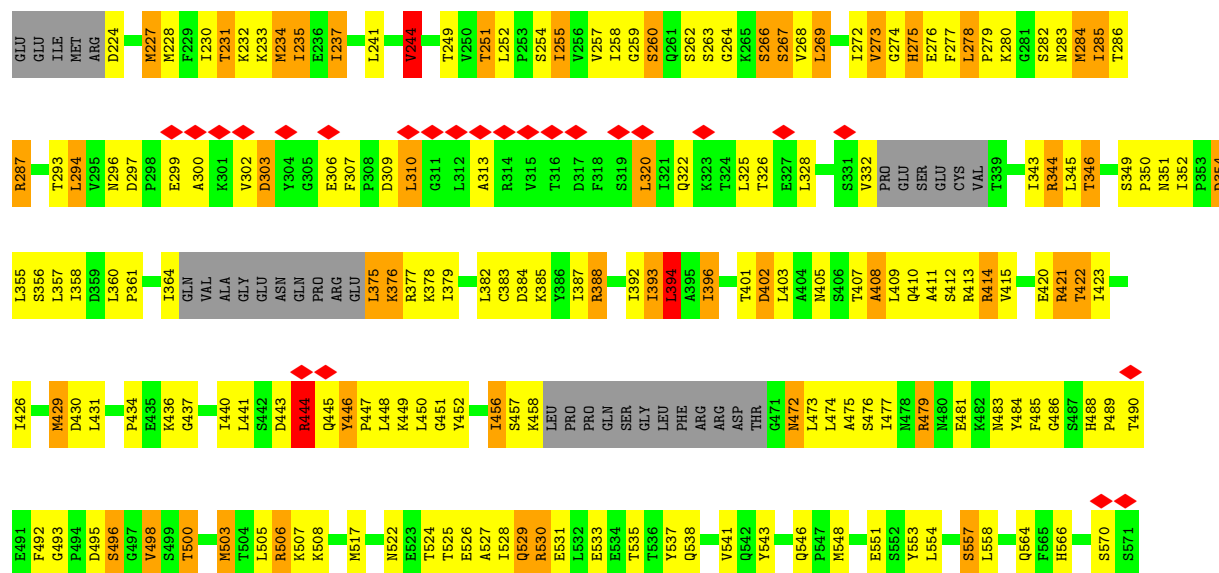


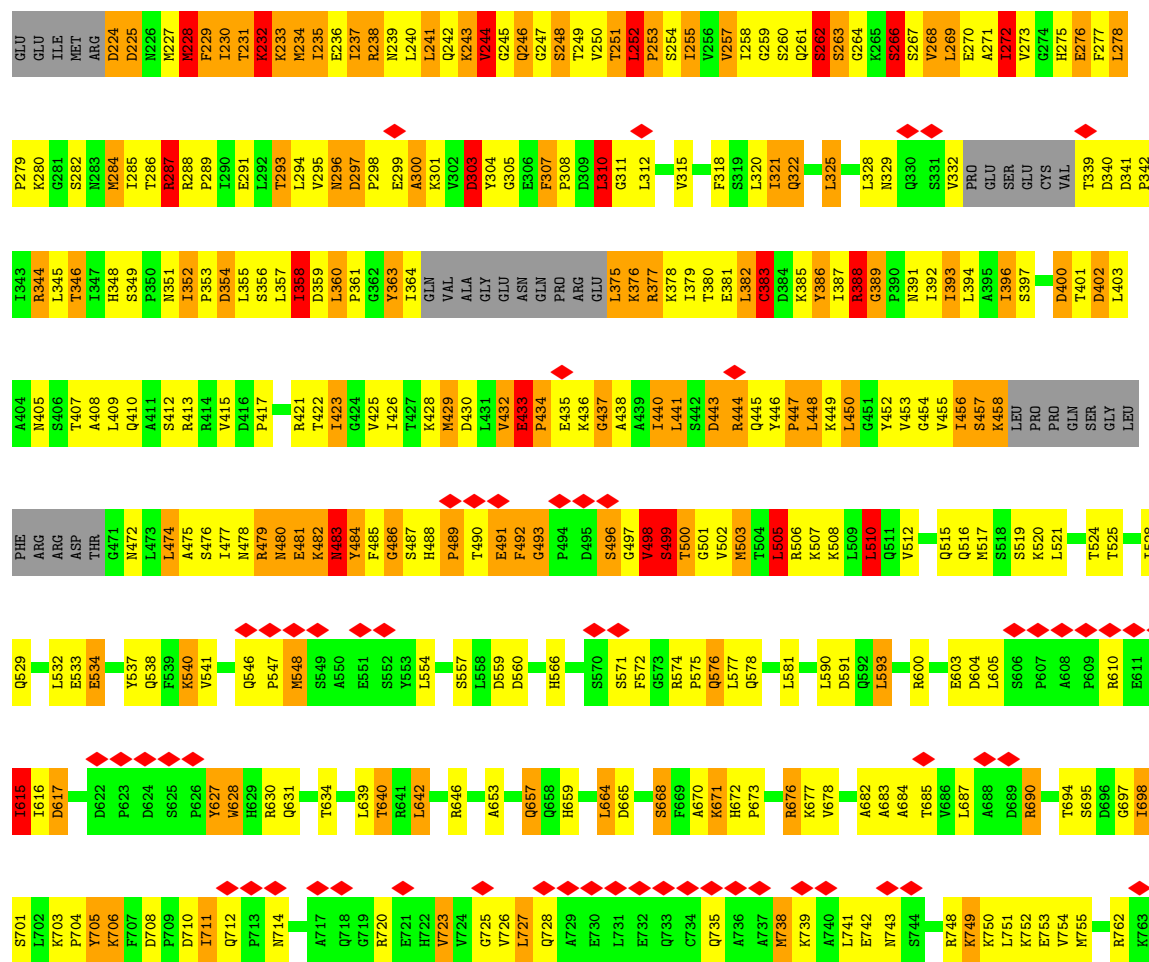
• Molecule 1: Putative mitochondrial dynamin protein

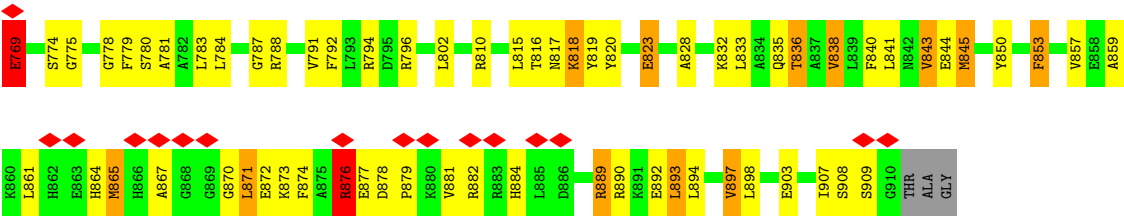




• Molecule 1: Putative mitochondrial dynamin protein







4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1820	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF determination was done by Gctf and correction was performed by ctfphaseflip from IMOD	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	53000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.290	Depositor
Minimum map value	-1.812	Depositor
Average map value	0.127	Depositor
Map value standard deviation	0.496	Depositor
Recommended contour level	0.67	Depositor
Map size (Å)	432.0, 432.0, 432.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7, 2.7, 2.7	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	2.08	131/5238 (2.5%)	1.44	50/7075 (0.7%)
1	B	2.02	137/5238 (2.6%)	1.24	1/7075 (0.0%)
1	C	1.98	98/5238 (1.9%)	1.25	8/7075 (0.1%)
1	D	2.06	141/5238 (2.7%)	1.42	34/7075 (0.5%)
1	E	2.06	133/5238 (2.5%)	1.43	44/7075 (0.6%)
1	F	2.00	119/5238 (2.3%)	1.25	7/7075 (0.1%)
1	G	2.00	114/5238 (2.2%)	1.23	5/7075 (0.1%)
1	H	2.08	150/5238 (2.9%)	1.42	47/7075 (0.7%)
1	I	2.08	104/5238 (2.0%)	1.25	2/7075 (0.0%)
1	J	2.07	127/5238 (2.4%)	1.42	45/7075 (0.6%)
All	All	2.04	1254/52380 (2.4%)	1.34	243/70750 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	15
1	B	0	10
1	C	0	17
1	D	0	7
1	E	0	17
1	F	0	21
1	G	0	12
1	H	0	14
1	I	0	20
1	J	0	18
All	All	0	151

All (1254) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	626	PRO	N-CA	24.86	1.80	1.47
1	A	540	LYS	CD-CE	22.09	2.18	1.52
1	I	626	PRO	CA-CB	20.21	1.86	1.53
1	I	626	PRO	N-CD	20.20	1.76	1.47
1	E	253	PRO	C-N	-19.97	1.08	1.33
1	D	253	PRO	C-N	-16.99	1.11	1.33
1	H	253	PRO	C-N	-16.91	1.11	1.33
1	J	253	PRO	C-N	-16.70	1.12	1.33
1	A	253	PRO	C-N	-14.18	1.15	1.33
1	H	865	MET	N-CA	-11.89	1.32	1.46
1	D	383	CYS	C-O	-10.35	1.12	1.24
1	B	407	THR	C-N	10.00	1.46	1.33
1	J	498	VAL	C-O	-9.91	1.11	1.24
1	A	479	ARG	NE-CZ	9.54	1.43	1.33
1	F	882	ARG	NE-CZ	-9.50	1.22	1.33
1	A	348	HIS	CG-ND1	9.14	1.48	1.38
1	B	350	PRO	C-O	9.10	1.35	1.24
1	H	228	MET	SD-CE	9.05	2.02	1.79
1	C	392	ILE	CA-CB	9.03	1.62	1.53
1	G	503	MET	SD-CE	8.96	2.02	1.79
1	B	571	SER	N-CA	8.94	1.57	1.46
1	E	388	ARG	C-O	-8.80	1.12	1.24
1	I	631	GLN	N-CA	-8.78	1.35	1.46
1	E	227	MET	CA-C	-8.76	1.41	1.52
1	J	228	MET	SD-CE	8.72	2.01	1.79
1	I	503	MET	SD-CE	8.71	2.01	1.79
1	H	681	ASP	C-O	-8.67	1.13	1.24
1	J	738	MET	CG-SD	8.66	2.02	1.80
1	I	626	PRO	CG-CD	8.62	1.80	1.50
1	A	738	MET	CG-SD	8.59	2.02	1.80
1	H	503	MET	SD-CE	8.59	2.01	1.79
1	B	883	ARG	C-O	8.56	1.34	1.24
1	D	548	MET	SD-CE	8.52	2.00	1.79
1	C	750	LYS	N-CA	-8.50	1.36	1.46
1	I	429	MET	CG-SD	8.43	2.01	1.80
1	C	772	HIS	CA-C	8.37	1.62	1.52
1	D	585	LEU	C-N	8.35	1.44	1.33
1	B	845	MET	SD-CE	8.32	2.00	1.79
1	G	228	MET	SD-CE	8.29	2.00	1.79
1	D	760	LYS	C-O	8.28	1.33	1.24
1	I	845	MET	CG-SD	8.27	2.01	1.80
1	J	307	PHE	C-N	8.25	1.45	1.34
1	F	227	MET	SD-CE	8.25	2.00	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	HIS	N-CA	-8.23	1.38	1.46
1	E	314	ARG	NE-CZ	8.19	1.42	1.33
1	A	758	VAL	CA-CB	8.18	1.64	1.54
1	J	391	ASN	N-CA	-8.13	1.35	1.45
1	B	602	ILE	CA-CB	-8.12	1.44	1.54
1	G	865	MET	SD-CE	8.09	1.99	1.79
1	E	227	MET	SD-CE	8.06	1.99	1.79
1	J	547	PRO	CA-C	8.04	1.62	1.52
1	A	451	GLY	N-CA	-8.02	1.33	1.45
1	D	672	HIS	C-O	8.01	1.27	1.23
1	D	718	GLN	C-O	8.00	1.33	1.24
1	H	418	ARG	NE-CZ	7.99	1.41	1.33
1	J	440	ILE	C-O	-7.97	1.15	1.24
1	H	347	ILE	CA-C	7.92	1.62	1.52
1	C	227	MET	CG-SD	7.91	2.00	1.80
1	C	228	MET	CG-SD	7.89	2.00	1.80
1	D	227	MET	SD-CE	7.88	1.99	1.79
1	I	638	GLY	C-N	7.87	1.44	1.33
1	J	503	MET	CG-SD	7.85	2.00	1.80
1	C	574	ARG	NE-CZ	7.83	1.41	1.33
1	G	227	MET	SD-CE	7.83	1.99	1.79
1	A	583	ASP	N-CA	7.83	1.55	1.46
1	E	307	PHE	C-N	7.82	1.43	1.34
1	D	249	THR	C-O	-7.74	1.14	1.24
1	I	865	MET	SD-CE	7.74	1.98	1.79
1	E	724	VAL	C-N	7.73	1.43	1.33
1	D	803	ARG	N-CA	7.73	1.56	1.46
1	H	489	PRO	N-CD	7.73	1.58	1.47
1	I	693	ALA	N-CA	7.71	1.55	1.46
1	H	392	ILE	C-O	7.70	1.33	1.23
1	E	536	THR	C-O	7.67	1.33	1.24
1	H	503	MET	CG-SD	7.65	1.99	1.80
1	B	548	MET	SD-CE	7.64	1.98	1.79
1	D	234	MET	SD-CE	7.63	1.98	1.79
1	C	586	ASP	N-CA	7.63	1.55	1.46
1	G	672	HIS	C-N	-7.63	1.24	1.33
1	I	703	LYS	C-O	-7.61	1.17	1.24
1	D	287	ARG	CA-C	-7.60	1.42	1.52
1	D	738	MET	SD-CE	7.60	1.98	1.79
1	I	244	VAL	C-N	7.60	1.43	1.33
1	F	751	LEU	N-CA	-7.58	1.36	1.46
1	E	853	PHE	C-O	-7.58	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	728	GLN	C-O	7.58	1.32	1.24
1	H	817	ASN	N-CA	-7.56	1.36	1.46
1	G	695	SER	C-O	-7.55	1.15	1.24
1	F	297	ASP	CA-CB	-7.53	1.45	1.53
1	G	429	MET	SD-CE	7.53	1.98	1.79
1	A	250	VAL	C-O	-7.48	1.16	1.24
1	D	479	ARG	NE-CZ	-7.46	1.24	1.33
1	E	629	HIS	CG-CD2	7.46	1.44	1.35
1	B	859	ALA	CA-C	7.45	1.62	1.52
1	C	548	MET	SD-CE	7.44	1.98	1.79
1	B	227	MET	SD-CE	7.43	1.98	1.79
1	H	429	MET	SD-CE	7.43	1.98	1.79
1	E	387	ILE	C-O	-7.42	1.15	1.24
1	F	234	MET	SD-CE	7.42	1.98	1.79
1	A	503	MET	SD-CE	7.38	1.98	1.79
1	E	528	ILE	CA-C	-7.38	1.43	1.52
1	A	832	LYS	C-O	7.37	1.32	1.24
1	I	804	ILE	N-CA	7.37	1.55	1.46
1	B	255	ILE	C-O	-7.37	1.15	1.24
1	J	823	GLU	C-O	7.37	1.32	1.24
1	B	379	ILE	N-CA	7.36	1.55	1.46
1	H	453	VAL	C-N	7.36	1.38	1.33
1	E	342	PRO	N-CD	7.32	1.57	1.47
1	H	476	SER	C-N	7.31	1.41	1.33
1	E	631	GLN	C-O	-7.30	1.15	1.24
1	B	353	PRO	C-N	7.29	1.43	1.33
1	D	905	HIS	CD2-NE2	7.29	1.45	1.37
1	J	272	ILE	C-N	-7.28	1.25	1.34
1	J	566	HIS	C-O	7.28	1.32	1.24
1	C	352	ILE	CA-CB	-7.27	1.44	1.54
1	C	738	MET	CG-SD	7.25	1.98	1.80
1	D	503	MET	CG-SD	7.24	1.98	1.80
1	J	845	MET	SD-CE	7.24	1.97	1.79
1	H	227	MET	N-CA	-7.23	1.37	1.46
1	H	659	HIS	C-N	-7.23	1.24	1.34
1	H	401	THR	N-CA	7.23	1.54	1.46
1	B	429	MET	SD-CE	7.22	1.97	1.79
1	A	227	MET	SD-CE	7.21	1.97	1.79
1	I	698	ILE	C-N	7.20	1.43	1.33
1	C	227	MET	SD-CE	7.20	1.97	1.79
1	F	563	HIS	C-N	-7.20	1.24	1.33
1	H	434	PRO	C-N	-7.18	1.24	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	429	MET	CG-SD	7.18	1.98	1.80
1	D	660	VAL	CA-CB	-7.15	1.45	1.54
1	A	475	ALA	N-CA	-7.13	1.37	1.46
1	H	510	LEU	N-CA	7.13	1.55	1.46
1	I	668	SER	C-O	-7.13	1.14	1.24
1	G	313	ALA	N-CA	7.13	1.54	1.46
1	H	452	TYR	N-CA	7.12	1.54	1.45
1	B	409	LEU	C-O	7.12	1.32	1.24
1	E	800	LEU	C-N	7.12	1.43	1.33
1	E	688	ALA	CA-C	7.12	1.62	1.52
1	B	688	ALA	C-N	7.11	1.42	1.33
1	I	300	ALA	CA-CB	7.10	1.64	1.53
1	G	845	MET	SD-CE	7.09	1.97	1.79
1	J	437	GLY	CA-C	-7.08	1.44	1.52
1	D	387	ILE	CA-C	-7.07	1.42	1.52
1	D	782	ALA	CA-C	7.06	1.62	1.52
1	E	636	CYS	CA-C	7.05	1.61	1.52
1	G	381	GLU	CA-CB	7.05	1.64	1.53
1	G	566	HIS	CG-ND1	7.05	1.46	1.38
1	J	482	LYS	N-CA	-7.04	1.38	1.46
1	B	275	HIS	CE1-NE2	7.03	1.39	1.32
1	G	349	SER	CA-C	-7.03	1.45	1.52
1	C	603	GLU	C-O	-7.01	1.14	1.23
1	C	628	TRP	CA-C	7.00	1.61	1.52
1	F	843	VAL	C-O	6.99	1.31	1.24
1	C	387	ILE	C-O	6.99	1.33	1.24
1	D	392	ILE	N-CA	6.99	1.55	1.46
1	I	548	MET	SD-CE	6.99	1.97	1.79
1	C	862	HIS	CG-ND1	6.99	1.46	1.38
1	J	677	LYS	CA-C	-6.98	1.43	1.52
1	E	785	ALA	C-O	-6.97	1.16	1.24
1	H	620	LYS	CA-C	6.97	1.61	1.53
1	J	305	GLY	CA-C	6.97	1.57	1.52
1	D	517	MET	SD-CE	6.96	1.97	1.79
1	E	622	ASP	CA-C	6.96	1.60	1.53
1	I	228	MET	CG-SD	6.96	1.98	1.80
1	D	493	GLY	C-N	6.95	1.42	1.33
1	F	548	MET	SD-CE	6.94	1.97	1.79
1	A	763	LYS	CA-C	6.93	1.62	1.53
1	F	548	MET	CG-SD	6.93	1.98	1.80
1	B	429	MET	CG-SD	6.93	1.98	1.80
1	F	506	ARG	NE-CZ	6.92	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	475	ALA	C-O	-6.92	1.16	1.24
1	F	290	ILE	C-O	6.92	1.31	1.24
1	B	738	MET	SD-CE	6.92	1.96	1.79
1	E	253	PRO	N-CD	6.91	1.57	1.47
1	I	627	TYR	N-CA	-6.91	1.36	1.46
1	H	439	ALA	N-CA	-6.91	1.38	1.46
1	I	703	LYS	CA-C	6.90	1.61	1.52
1	G	767	ILE	CA-C	6.89	1.60	1.52
1	A	675	ALA	N-CA	6.89	1.54	1.46
1	C	573	GLY	CA-C	6.88	1.61	1.52
1	B	870	GLY	C-N	-6.88	1.25	1.33
1	F	778	GLY	C-O	6.88	1.33	1.23
1	G	722	HIS	ND1-CE1	6.88	1.39	1.32
1	A	455	VAL	CA-CB	6.88	1.62	1.55
1	J	755	MET	CG-SD	6.88	1.98	1.80
1	E	227	MET	CG-SD	6.88	1.98	1.80
1	G	417	PRO	CA-CB	-6.88	1.44	1.53
1	C	655	ALA	C-N	-6.87	1.25	1.33
1	H	865	MET	SD-CE	6.86	1.96	1.79
1	I	727	LEU	C-N	6.86	1.43	1.33
1	C	738	MET	SD-CE	6.85	1.96	1.79
1	C	304	TYR	C-N	6.84	1.42	1.32
1	I	496	SER	C-O	6.84	1.32	1.23
1	E	447	PRO	C-O	6.84	1.31	1.23
1	F	727	LEU	N-CA	6.84	1.54	1.46
1	J	227	MET	CG-SD	6.84	1.97	1.80
1	E	548	MET	SD-CE	6.83	1.96	1.79
1	E	234	MET	SD-CE	6.83	1.96	1.79
1	A	776	ALA	N-CA	6.83	1.54	1.46
1	J	833	LEU	C-N	-6.83	1.24	1.33
1	F	845	MET	SD-CE	6.83	1.96	1.79
1	C	228	MET	SD-CE	6.82	1.96	1.79
1	D	321	ILE	CA-C	-6.82	1.44	1.52
1	H	244	VAL	CA-CB	-6.82	1.46	1.54
1	I	738	MET	SD-CE	6.81	1.96	1.79
1	D	227	MET	CG-SD	6.81	1.97	1.80
1	D	797	ALA	C-O	6.81	1.32	1.24
1	J	497	GLY	C-O	-6.81	1.15	1.23
1	A	563	HIS	CE1-NE2	6.80	1.39	1.32
1	H	496	SER	C-O	-6.80	1.15	1.23
1	D	506	ARG	C-N	6.80	1.42	1.33
1	F	711	ILE	C-O	-6.80	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	234	MET	SD-CE	6.80	1.96	1.79
1	G	807	ALA	C-N	6.80	1.43	1.33
1	A	503	MET	CG-SD	6.79	1.97	1.80
1	C	600	ARG	CZ-NH2	6.79	1.42	1.33
1	H	307	PHE	C-N	6.79	1.42	1.34
1	C	596	ARG	NE-CZ	6.79	1.40	1.33
1	H	809	SER	N-CA	6.79	1.54	1.45
1	B	266	SER	N-CA	-6.77	1.38	1.46
1	F	502	VAL	N-CA	-6.77	1.37	1.46
1	A	548	MET	CG-SD	6.77	1.97	1.80
1	J	566	HIS	CG-ND1	-6.77	1.30	1.38
1	G	738	MET	CG-SD	6.76	1.97	1.80
1	D	803	ARG	CD-NE	6.76	1.55	1.46
1	B	896	THR	C-N	-6.76	1.25	1.33
1	J	245	GLY	N-CA	-6.76	1.37	1.45
1	H	292	LEU	CA-CB	-6.75	1.43	1.53
1	A	441	LEU	C-O	-6.75	1.16	1.24
1	I	889	ARG	N-CA	6.75	1.54	1.46
1	E	845	MET	SD-CE	6.75	1.96	1.79
1	F	740	ALA	N-CA	6.74	1.54	1.46
1	D	438	ALA	C-N	-6.74	1.25	1.33
1	E	266	SER	C-O	-6.72	1.16	1.24
1	A	784	LEU	N-CA	-6.72	1.38	1.46
1	F	525	THR	N-CA	6.71	1.54	1.46
1	J	631	GLN	CA-C	-6.71	1.44	1.52
1	J	695	SER	C-N	-6.70	1.25	1.33
1	D	517	MET	CG-SD	6.70	1.97	1.80
1	A	803	ARG	NE-CZ	-6.69	1.25	1.33
1	J	893	LEU	C-N	6.69	1.42	1.33
1	H	408	ALA	CA-C	-6.68	1.44	1.52
1	G	267	SER	C-N	6.68	1.42	1.33
1	G	672	HIS	CG-ND1	6.68	1.45	1.38
1	H	517	MET	CG-SD	6.67	1.97	1.80
1	I	759	ASP	C-N	6.67	1.42	1.33
1	J	872	GLU	CA-C	6.67	1.61	1.52
1	E	339	THR	CB-OG1	-6.66	1.33	1.43
1	I	708	ASP	C-O	-6.66	1.17	1.24
1	E	526	GLU	C-O	6.66	1.31	1.24
1	D	638	GLY	CA-C	-6.66	1.44	1.52
1	J	538	GLN	N-CA	6.66	1.54	1.46
1	H	845	MET	SD-CE	6.65	1.96	1.79
1	D	384	ASP	CA-C	-6.65	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	503	MET	SD-CE	6.65	1.96	1.79
1	D	765	GLU	N-CA	6.65	1.54	1.46
1	B	503	MET	SD-CE	6.64	1.96	1.79
1	C	629	HIS	CG-CD2	-6.64	1.28	1.35
1	E	517	MET	CG-SD	6.64	1.97	1.80
1	D	785	ALA	N-CA	-6.61	1.38	1.46
1	G	862	HIS	CE1-NE2	6.61	1.39	1.32
1	A	499	SER	C-N	6.61	1.41	1.33
1	H	738	MET	CG-SD	6.61	1.97	1.80
1	A	762	ARG	NE-CZ	6.60	1.40	1.33
1	I	414	ARG	C-N	-6.60	1.26	1.33
1	D	864	HIS	CG-CD2	6.59	1.43	1.35
1	G	517	MET	SD-CE	6.59	1.96	1.79
1	D	612	PRO	N-CD	6.58	1.56	1.47
1	I	517	MET	SD-CE	6.58	1.96	1.79
1	B	707	PHE	C-N	-6.58	1.27	1.33
1	B	799	ILE	CA-CB	6.58	1.62	1.54
1	J	245	GLY	CA-C	-6.57	1.44	1.51
1	E	488	HIS	C-N	6.57	1.42	1.34
1	A	248	SER	CA-C	-6.57	1.46	1.53
1	D	865	MET	CG-SD	6.57	1.97	1.80
1	G	322	GLN	C-O	6.57	1.31	1.24
1	A	491	GLU	CA-C	6.56	1.61	1.52
1	F	553	TYR	C-O	6.56	1.31	1.24
1	E	796	ARG	CA-C	6.56	1.61	1.52
1	B	786	ARG	CA-C	6.55	1.61	1.52
1	H	663	LEU	C-O	-6.55	1.16	1.24
1	F	234	MET	CG-SD	6.55	1.97	1.80
1	F	517	MET	SD-CE	6.54	1.96	1.79
1	H	665	ASP	CG-OD1	-6.54	1.12	1.25
1	A	429	MET	SD-CE	6.54	1.96	1.79
1	J	884	HIS	CE1-NE2	6.54	1.39	1.32
1	J	796	ARG	NE-CZ	6.54	1.40	1.33
1	C	290	ILE	C-O	6.53	1.31	1.24
1	J	227	MET	SD-CE	6.53	1.95	1.79
1	H	661	GLU	N-CA	6.53	1.54	1.46
1	G	565	PHE	N-CA	-6.53	1.38	1.46
1	F	629	HIS	CG-CD2	6.53	1.43	1.35
1	B	227	MET	CG-SD	6.53	1.97	1.80
1	F	503	MET	SD-CE	6.52	1.95	1.79
1	H	537	TYR	N-CA	6.52	1.53	1.46
1	J	517	MET	CG-SD	6.52	1.97	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	661	GLU	CA-C	-6.52	1.44	1.52
1	B	900	LYS	C-N	6.51	1.42	1.33
1	J	499	SER	C-O	-6.51	1.15	1.24
1	F	808	LYS	CA-C	6.51	1.61	1.52
1	A	767	ILE	N-CA	-6.50	1.38	1.46
1	H	700	ILE	C-O	6.50	1.31	1.24
1	J	634	THR	C-O	-6.50	1.15	1.24
1	D	772	HIS	CA-C	-6.50	1.46	1.52
1	B	228	MET	SD-CE	6.50	1.95	1.79
1	E	454	GLY	CA-C	6.50	1.56	1.52
1	E	630	ARG	CD-NE	6.49	1.55	1.46
1	E	496	SER	C-N	-6.49	1.25	1.33
1	B	849	PHE	C-O	6.48	1.31	1.24
1	F	227	MET	CG-SD	6.48	1.97	1.80
1	I	706	LYS	CA-C	-6.48	1.44	1.52
1	J	738	MET	SD-CE	6.47	1.95	1.79
1	A	624	ASP	N-CA	-6.47	1.39	1.46
1	I	852	ARG	CZ-NH1	-6.47	1.23	1.32
1	D	251	THR	C-O	-6.47	1.16	1.23
1	E	849	PHE	C-O	-6.47	1.16	1.24
1	B	386	TYR	C-O	-6.46	1.16	1.24
1	C	876	ARG	CZ-NH1	6.46	1.41	1.32
1	D	445	GLN	N-CA	-6.46	1.38	1.46
1	G	902	GLU	C-O	6.45	1.32	1.24
1	G	832	LYS	C-N	6.45	1.42	1.33
1	J	703	LYS	CA-C	6.45	1.59	1.52
1	J	548	MET	CG-SD	6.44	1.96	1.80
1	H	392	ILE	CA-C	-6.44	1.46	1.53
1	I	306	GLU	CA-C	6.43	1.60	1.52
1	I	755	MET	CA-C	6.42	1.61	1.52
1	A	407	THR	N-CA	6.42	1.54	1.46
1	D	429	MET	CG-SD	6.42	1.96	1.80
1	D	844	GLU	N-CA	6.41	1.54	1.46
1	A	477	ILE	C-O	-6.41	1.16	1.24
1	E	652	ALA	CA-CB	-6.40	1.43	1.53
1	A	850	TYR	C-O	6.40	1.31	1.24
1	J	257	VAL	C-O	6.40	1.31	1.24
1	A	238	ARG	NE-CZ	6.40	1.40	1.33
1	H	251	THR	CA-C	6.40	1.60	1.52
1	B	629	HIS	CE1-NE2	6.39	1.39	1.32
1	B	865	MET	SD-CE	6.39	1.95	1.79
1	G	447	PRO	C-O	6.39	1.30	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	548	MET	SD-CE	6.39	1.95	1.79
1	D	818	LYS	N-CA	6.39	1.54	1.46
1	A	771	ASP	C-N	-6.38	1.28	1.33
1	D	379	ILE	N-CA	-6.38	1.39	1.46
1	D	661	GLU	N-CA	6.38	1.54	1.46
1	A	807	ALA	C-O	-6.38	1.16	1.24
1	F	676	ARG	NE-CZ	6.38	1.40	1.33
1	J	857	VAL	C-O	6.38	1.31	1.24
1	B	252	LEU	CA-C	-6.37	1.44	1.52
1	E	843	VAL	CA-C	-6.37	1.45	1.52
1	I	525	THR	C-O	-6.37	1.16	1.24
1	C	358	ILE	C-O	-6.37	1.17	1.24
1	E	610	ARG	C-O	-6.37	1.16	1.24
1	I	477	ILE	N-CA	-6.37	1.39	1.46
1	H	423	ILE	N-CA	6.37	1.53	1.46
1	I	762	ARG	C-O	-6.37	1.16	1.24
1	D	818	LYS	C-O	6.36	1.31	1.24
1	H	738	MET	SD-CE	6.36	1.95	1.79
1	E	503	MET	CG-SD	6.35	1.96	1.80
1	A	381	GLU	N-CA	-6.35	1.38	1.46
1	A	610	ARG	NE-CZ	6.35	1.40	1.33
1	F	503	MET	CG-SD	6.35	1.96	1.80
1	E	239	ASN	C-O	-6.34	1.16	1.24
1	J	559	ASP	N-CA	-6.34	1.38	1.46
1	E	388	ARG	NE-CZ	-6.33	1.26	1.33
1	G	876	ARG	CZ-NH2	6.33	1.41	1.33
1	F	887	LEU	C-O	6.32	1.31	1.24
1	I	320	LEU	C-O	6.32	1.31	1.24
1	F	852	ARG	CA-C	6.32	1.61	1.52
1	I	755	MET	SD-CE	6.32	1.95	1.79
1	J	231	THR	CA-C	-6.32	1.44	1.52
1	D	618	LEU	CA-C	6.31	1.59	1.52
1	I	853	PHE	CA-C	6.31	1.60	1.52
1	F	725	GLY	CA-C	6.31	1.58	1.52
1	H	493	GLY	C-N	6.31	1.41	1.33
1	G	636	CYS	C-O	6.30	1.31	1.24
1	B	554	LEU	C-N	6.30	1.41	1.33
1	J	249	THR	N-CA	-6.30	1.38	1.46
1	C	397	SER	CA-C	6.30	1.59	1.52
1	E	851	VAL	CA-C	6.30	1.59	1.52
1	C	409	LEU	N-CA	6.30	1.54	1.46
1	F	738	MET	CG-SD	6.29	1.96	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	686	VAL	C-O	6.29	1.31	1.24
1	H	876	ARG	CA-C	-6.29	1.43	1.52
1	E	738	MET	CA-C	-6.29	1.44	1.52
1	B	755	MET	CG-SD	6.29	1.96	1.80
1	D	273	VAL	C-N	-6.29	1.26	1.33
1	B	738	MET	CG-SD	6.28	1.96	1.80
1	F	272	ILE	CA-C	-6.28	1.45	1.52
1	A	475	ALA	CA-C	-6.28	1.44	1.52
1	C	429	MET	SD-CE	6.28	1.95	1.79
1	E	755	MET	CG-SD	6.27	1.96	1.80
1	H	513	LEU	C-O	6.27	1.31	1.24
1	B	769	GLU	N-CA	6.26	1.53	1.45
1	B	297	ASP	CA-C	6.26	1.60	1.53
1	E	278	LEU	CA-C	6.26	1.58	1.52
1	G	755	MET	SD-CE	6.26	1.95	1.79
1	B	858	GLU	C-O	-6.26	1.17	1.24
1	E	694	THR	C-N	6.26	1.41	1.33
1	H	308	PRO	N-CD	6.25	1.56	1.47
1	F	622	ASP	C-O	6.25	1.32	1.24
1	F	696	ASP	N-CA	6.25	1.53	1.46
1	B	831	THR	CA-C	6.25	1.60	1.52
1	E	416	ASP	CA-C	-6.25	1.46	1.52
1	A	601	PRO	N-CA	6.24	1.54	1.47
1	F	764	GLY	C-O	6.24	1.30	1.24
1	E	499	SER	C-O	-6.24	1.16	1.24
1	A	228	MET	SD-CE	6.24	1.95	1.79
1	G	865	MET	CG-SD	6.23	1.96	1.80
1	H	622	ASP	C-N	6.23	1.41	1.33
1	D	475	ALA	C-O	-6.23	1.16	1.24
1	E	435	GLU	C-O	-6.23	1.16	1.24
1	A	253	PRO	N-CD	6.22	1.56	1.47
1	I	845	MET	SD-CE	6.22	1.95	1.79
1	D	738	MET	CG-SD	6.22	1.96	1.80
1	D	489	PRO	N-CD	6.22	1.56	1.47
1	H	548	MET	CG-SD	6.21	1.96	1.80
1	D	228	MET	SD-CE	6.21	1.95	1.79
1	H	426	ILE	CA-CB	-6.21	1.46	1.53
1	E	314	ARG	CA-C	-6.21	1.45	1.52
1	C	331	SER	C-O	6.21	1.31	1.24
1	I	736	ALA	C-O	6.21	1.31	1.24
1	E	540	LYS	CA-CB	6.20	1.63	1.53
1	B	404	ALA	N-CA	6.20	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	503	MET	CA-C	6.20	1.60	1.52
1	H	717	ALA	N-CA	6.20	1.53	1.46
1	A	845	MET	SD-CE	6.19	1.95	1.79
1	G	446	TYR	CA-C	6.19	1.59	1.53
1	I	759	ASP	N-CA	6.19	1.53	1.46
1	D	600	ARG	NE-CZ	6.19	1.39	1.33
1	A	476	SER	CA-C	-6.18	1.44	1.52
1	J	871	LEU	CA-CB	6.18	1.63	1.53
1	A	755	MET	CG-SD	6.17	1.96	1.80
1	E	876	ARG	C-O	6.17	1.31	1.24
1	G	503	MET	CA-C	-6.17	1.44	1.52
1	H	438	ALA	C-O	-6.16	1.16	1.24
1	B	866	HIS	N-CA	6.16	1.54	1.46
1	D	549	SER	C-O	-6.16	1.15	1.23
1	F	403	LEU	N-CA	-6.15	1.38	1.46
1	C	703	LYS	C-O	-6.15	1.18	1.24
1	I	538	GLN	C-O	6.15	1.31	1.24
1	H	395	ALA	C-O	-6.14	1.16	1.23
1	C	626	PRO	C-N	6.14	1.41	1.33
1	E	410	GLN	CA-C	6.14	1.60	1.52
1	E	508	LYS	CA-C	6.14	1.60	1.52
1	C	586	ASP	C-O	6.14	1.31	1.24
1	E	701	SER	C-O	-6.14	1.16	1.24
1	I	842	ASN	N-CA	-6.14	1.39	1.46
1	J	892	GLU	C-N	-6.13	1.26	1.33
1	B	312	LEU	N-CA	6.13	1.53	1.46
1	H	310	LEU	CA-CB	6.13	1.60	1.52
1	I	299	GLU	CA-CB	6.13	1.63	1.53
1	G	853	PHE	N-CA	6.13	1.52	1.46
1	C	842	ASN	C-O	-6.13	1.17	1.24
1	E	228	MET	CG-SD	6.13	1.96	1.80
1	I	716	TRP	N-CA	-6.12	1.39	1.46
1	A	256	VAL	C-O	6.12	1.31	1.24
1	F	555	ALA	CA-CB	-6.12	1.43	1.53
1	G	439	ALA	C-N	6.12	1.41	1.33
1	C	414	ARG	NE-CZ	6.12	1.39	1.33
1	J	443	ASP	CA-C	-6.12	1.45	1.52
1	A	289	PRO	CA-CB	6.12	1.61	1.53
1	B	847	ASN	C-O	-6.11	1.17	1.24
1	B	452	TYR	C-O	6.11	1.31	1.23
1	E	429	MET	SD-CE	6.11	1.94	1.79
1	I	616	ILE	N-CA	6.11	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	325	LEU	CA-C	6.10	1.60	1.52
1	C	429	MET	CG-SD	6.10	1.96	1.80
1	F	738	MET	SD-CE	6.10	1.94	1.79
1	H	685	THR	N-CA	6.10	1.53	1.46
1	F	608	ALA	CA-C	-6.10	1.45	1.53
1	D	282	SER	C-O	-6.10	1.18	1.24
1	D	244	VAL	C-N	-6.09	1.27	1.33
1	J	865	MET	CG-SD	6.09	1.96	1.80
1	A	357	LEU	C-N	6.09	1.42	1.33
1	G	444	ARG	C-O	6.09	1.31	1.23
1	G	738	MET	N-CA	6.09	1.53	1.46
1	B	755	MET	SD-CE	6.09	1.94	1.79
1	B	657	GLN	N-CA	-6.09	1.38	1.46
1	H	602	ILE	N-CA	6.09	1.53	1.46
1	C	657	GLN	N-CA	-6.08	1.39	1.46
1	B	570	SER	C-N	6.08	1.42	1.33
1	J	310	LEU	N-CA	-6.08	1.39	1.46
1	E	827	ASP	CA-C	6.07	1.60	1.52
1	A	865	MET	CG-SD	6.07	1.96	1.80
1	D	503	MET	SD-CE	6.07	1.94	1.79
1	E	288	ARG	C-O	-6.07	1.17	1.24
1	J	864	HIS	CG-CD2	-6.07	1.29	1.35
1	B	700	ILE	N-CA	6.06	1.53	1.46
1	E	504	THR	C-O	6.06	1.31	1.24
1	D	733	GLN	N-CA	-6.06	1.39	1.46
1	H	831	THR	N-CA	6.06	1.53	1.46
1	I	503	MET	CG-SD	6.05	1.95	1.80
1	G	633	ASP	CA-C	6.05	1.60	1.52
1	C	845	MET	SD-CE	6.05	1.94	1.79
1	J	297	ASP	C-N	-6.05	1.25	1.33
1	E	517	MET	CA-C	6.05	1.60	1.52
1	G	357	LEU	N-CA	6.05	1.53	1.45
1	B	884	HIS	CG-ND1	-6.04	1.31	1.38
1	D	249	THR	N-CA	-6.04	1.39	1.46
1	C	891	LYS	C-N	-6.04	1.26	1.33
1	J	447	PRO	C-N	-6.04	1.26	1.33
1	F	574	ARG	C-N	-6.04	1.26	1.33
1	G	828	ALA	C-O	6.04	1.31	1.24
1	H	380	THR	N-CA	6.04	1.53	1.46
1	J	781	ALA	CA-C	6.04	1.60	1.52
1	C	427	THR	N-CA	6.03	1.52	1.45
1	F	514	GLU	CA-C	-6.03	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	558	LEU	C-O	6.03	1.31	1.24
1	E	353	PRO	N-CA	6.03	1.53	1.46
1	D	593	LEU	C-O	6.02	1.31	1.24
1	J	659	HIS	N-CA	6.02	1.53	1.46
1	F	240	LEU	C-O	-6.02	1.17	1.24
1	H	740	ALA	C-O	6.02	1.31	1.24
1	G	566	HIS	N-CA	-6.02	1.39	1.46
1	G	738	MET	SD-CE	6.01	1.94	1.79
1	B	530	ARG	C-O	6.01	1.31	1.24
1	J	859	ALA	CA-C	6.01	1.60	1.52
1	C	807	ALA	C-N	6.00	1.42	1.33
1	A	793	LEU	N-CA	-6.00	1.39	1.46
1	B	862	HIS	CG-ND1	6.00	1.44	1.38
1	H	865	MET	CG-SD	6.00	1.95	1.80
1	H	906	ARG	N-CA	6.00	1.54	1.46
1	C	503	MET	SD-CE	5.99	1.94	1.79
1	F	477	ILE	N-CA	5.98	1.54	1.46
1	J	768	VAL	N-CA	-5.98	1.40	1.46
1	B	247	GLY	CA-C	-5.98	1.43	1.51
1	E	429	MET	CG-SD	5.97	1.95	1.80
1	C	433	GLU	N-CA	5.97	1.53	1.45
1	J	867	ALA	C-O	-5.97	1.17	1.24
1	G	390	PRO	N-CA	5.97	1.54	1.47
1	H	894	LEU	C-O	5.97	1.30	1.24
1	A	397	SER	N-CA	-5.96	1.39	1.46
1	A	592	GLN	C-O	-5.96	1.17	1.24
1	D	308	PRO	N-CD	5.96	1.56	1.47
1	H	565	PHE	CA-C	5.96	1.60	1.52
1	A	252	LEU	C-N	5.96	1.41	1.33
1	E	714	ASN	N-CA	5.96	1.53	1.46
1	G	228	MET	CG-SD	5.96	1.95	1.80
1	F	876	ARG	C-O	-5.95	1.16	1.24
1	B	268	VAL	C-N	5.95	1.42	1.34
1	H	738	MET	C-N	5.95	1.41	1.33
1	B	331	SER	C-O	-5.95	1.16	1.24
1	B	548	MET	CG-SD	5.95	1.95	1.80
1	B	605	LEU	CA-C	5.95	1.60	1.52
1	J	487	SER	C-N	5.95	1.41	1.33
1	A	795	ASP	CA-C	5.94	1.60	1.52
1	A	527	ALA	N-CA	5.94	1.53	1.46
1	H	839	LEU	CA-C	5.93	1.60	1.52
1	A	696	ASP	C-N	5.93	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	560	ASP	N-CA	5.93	1.53	1.46
1	F	580	LEU	C-O	5.93	1.31	1.24
1	B	307	PHE	C-N	5.93	1.41	1.34
1	C	402	ASP	N-CA	5.93	1.53	1.45
1	B	234	MET	SD-CE	5.93	1.94	1.79
1	B	503	MET	CG-SD	5.93	1.95	1.80
1	G	784	LEU	CA-C	5.93	1.60	1.52
1	J	444	ARG	CA-CB	-5.93	1.45	1.54
1	I	394	LEU	C-O	5.92	1.30	1.24
1	G	275	HIS	CE1-NE2	-5.92	1.26	1.32
1	D	670	ALA	C-O	5.92	1.30	1.24
1	G	230	ILE	N-CA	-5.92	1.39	1.46
1	A	755	MET	SD-CE	5.92	1.94	1.79
1	B	895	GLU	N-CA	5.92	1.53	1.46
1	A	232	LYS	C-O	5.91	1.31	1.24
1	D	708	ASP	C-O	5.91	1.30	1.24
1	D	429	MET	SD-CE	5.91	1.94	1.79
1	F	265	LYS	C-O	5.91	1.30	1.24
1	D	781	ALA	N-CA	-5.91	1.39	1.46
1	F	755	MET	SD-CE	5.91	1.94	1.79
1	I	769	GLU	C-O	-5.90	1.16	1.23
1	A	571	SER	N-CA	5.90	1.53	1.46
1	B	733	GLN	N-CA	-5.90	1.39	1.46
1	J	383	CYS	N-CA	-5.90	1.39	1.46
1	C	502	VAL	CA-CB	-5.90	1.46	1.54
1	J	403	LEU	N-CA	-5.90	1.39	1.46
1	J	816	THR	CA-C	-5.89	1.44	1.52
1	D	514	GLU	N-CA	-5.88	1.39	1.46
1	J	769	GLU	CD-OE2	5.88	1.36	1.25
1	F	410	GLN	CA-C	-5.88	1.45	1.52
1	J	358	ILE	CA-CB	-5.88	1.46	1.54
1	H	492	PHE	CA-C	-5.88	1.45	1.53
1	B	706	LYS	C-N	5.87	1.41	1.33
1	F	606	SER	CA-C	5.87	1.59	1.53
1	C	651	VAL	C-O	-5.87	1.17	1.24
1	F	835	GLN	C-O	5.87	1.31	1.24
1	G	243	LYS	C-N	5.87	1.40	1.33
1	G	544	ASN	C-N	-5.87	1.25	1.33
1	A	327	GLU	C-O	5.86	1.31	1.24
1	E	664	LEU	C-N	-5.86	1.26	1.33
1	H	763	LYS	N-CA	5.86	1.52	1.46
1	J	250	VAL	CA-CB	5.86	1.60	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	738	MET	SD-CE	5.86	1.94	1.79
1	E	313	ALA	C-O	-5.86	1.17	1.24
1	C	486	GLY	C-O	-5.85	1.16	1.23
1	H	586	ASP	C-O	5.85	1.30	1.24
1	J	329	ASN	N-CA	5.85	1.53	1.46
1	A	673	PRO	C-O	-5.84	1.17	1.24
1	F	543	TYR	N-CA	-5.84	1.40	1.46
1	F	638	GLY	CA-C	5.84	1.58	1.52
1	F	520	LYS	CA-C	-5.84	1.44	1.52
1	J	353	PRO	CA-C	5.84	1.58	1.52
1	J	429	MET	CG-SD	5.84	1.95	1.80
1	C	303	ASP	N-CA	5.84	1.53	1.46
1	I	700	ILE	N-CA	5.84	1.53	1.46
1	A	228	MET	CG-SD	5.83	1.95	1.80
1	F	681	ASP	N-CA	5.83	1.53	1.46
1	B	517	MET	SD-CE	5.83	1.94	1.79
1	C	419	GLY	CA-C	5.83	1.59	1.51
1	H	662	LYS	N-CA	5.83	1.53	1.46
1	I	294	LEU	CA-C	5.83	1.59	1.52
1	B	486	GLY	C-N	5.83	1.42	1.34
1	F	865	MET	CG-SD	5.83	1.95	1.80
1	H	517	MET	SD-CE	5.83	1.94	1.79
1	B	288	ARG	C-N	5.83	1.40	1.33
1	B	413	ARG	CZ-NH2	-5.82	1.25	1.33
1	I	527	ALA	N-CA	5.82	1.53	1.46
1	F	254	SER	N-CA	-5.82	1.39	1.46
1	J	706	LYS	C-N	-5.81	1.26	1.33
1	C	664	LEU	C-O	-5.81	1.17	1.24
1	D	794	ARG	CZ-NH1	5.81	1.40	1.32
1	H	228	MET	CG-SD	5.81	1.95	1.80
1	B	300	ALA	N-CA	5.80	1.53	1.46
1	I	452	TYR	C-O	-5.80	1.16	1.23
1	H	475	ALA	CA-C	-5.80	1.45	1.52
1	C	488	HIS	CG-CD2	-5.80	1.29	1.35
1	A	902	GLU	CA-C	5.80	1.60	1.52
1	J	631	GLN	C-O	5.80	1.31	1.24
1	D	250	VAL	C-O	-5.80	1.18	1.24
1	D	310	LEU	N-CA	-5.80	1.39	1.46
1	D	845	MET	CG-SD	5.80	1.95	1.80
1	F	730	GLU	C-N	5.80	1.42	1.34
1	H	732	GLU	N-CA	5.80	1.53	1.46
1	A	394	LEU	CA-C	-5.79	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	509	LEU	N-CA	5.79	1.53	1.46
1	E	228	MET	SD-CE	5.79	1.94	1.79
1	J	723	VAL	C-O	-5.79	1.17	1.24
1	H	302	VAL	CA-C	5.79	1.59	1.52
1	F	845	MET	N-CA	5.78	1.53	1.46
1	J	755	MET	SD-CE	5.78	1.94	1.79
1	D	755	MET	SD-CE	5.78	1.94	1.79
1	F	904	LEU	N-CA	-5.78	1.39	1.46
1	D	701	SER	CA-C	5.77	1.60	1.52
1	F	582	LYS	C-O	5.77	1.30	1.24
1	A	845	MET	CG-SD	5.77	1.95	1.80
1	C	517	MET	CG-SD	5.76	1.95	1.80
1	E	794	ARG	N-CA	5.76	1.53	1.46
1	J	296	ASN	C-O	-5.76	1.17	1.23
1	C	324	THR	C-O	-5.76	1.17	1.24
1	I	650	THR	CA-C	5.76	1.60	1.52
1	F	265	LYS	CA-C	-5.76	1.45	1.52
1	A	730	GLU	CA-C	5.75	1.60	1.52
1	D	548	MET	N-CA	5.75	1.52	1.46
1	F	649	ALA	N-CA	-5.75	1.39	1.46
1	J	429	MET	SD-CE	5.75	1.94	1.79
1	G	538	GLN	C-N	5.75	1.41	1.34
1	H	753	GLU	N-CA	5.75	1.53	1.46
1	D	252	LEU	CA-C	5.75	1.60	1.52
1	D	867	ALA	C-O	-5.74	1.17	1.24
1	B	735	GLN	C-O	-5.74	1.16	1.24
1	E	563	HIS	C-O	-5.73	1.17	1.24
1	I	554	LEU	C-N	-5.73	1.26	1.33
1	D	566	HIS	ND1-CE1	5.73	1.38	1.32
1	H	675	ALA	C-O	5.73	1.30	1.24
1	C	729	ALA	C-O	5.73	1.30	1.24
1	I	354	ASP	C-N	5.73	1.38	1.33
1	E	449	LYS	N-CA	-5.73	1.37	1.45
1	B	658	GLN	C-O	-5.73	1.17	1.24
1	D	606	SER	C-N	-5.72	1.26	1.33
1	D	834	ALA	CA-C	5.72	1.60	1.52
1	A	224	ASP	C-N	-5.72	1.26	1.33
1	D	633	ASP	N-CA	-5.72	1.39	1.46
1	G	659	HIS	CB-CG	5.71	1.58	1.50
1	D	734	CYS	C-O	5.71	1.30	1.24
1	F	842	ASN	N-CA	5.71	1.53	1.46
1	G	574	ARG	CZ-NH2	5.71	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	609	PRO	N-CA	5.71	1.54	1.47
1	I	740	ALA	N-CA	5.71	1.53	1.46
1	B	748	ARG	C-O	5.71	1.30	1.24
1	D	342	PRO	N-CD	5.71	1.55	1.47
1	J	410	GLN	N-CA	-5.70	1.39	1.46
1	C	889	ARG	CA-C	5.70	1.60	1.52
1	H	284	MET	C-N	-5.70	1.26	1.33
1	E	629	HIS	CA-CB	5.70	1.62	1.53
1	D	228	MET	CA-C	-5.70	1.45	1.52
1	E	884	HIS	ND1-CE1	-5.70	1.26	1.32
1	F	884	HIS	CG-CD2	5.70	1.42	1.35
1	H	234	MET	CG-SD	5.70	1.95	1.80
1	J	600	ARG	CZ-NH2	-5.70	1.26	1.33
1	D	865	MET	SD-CE	5.69	1.93	1.79
1	A	591	ASP	CA-C	-5.69	1.45	1.52
1	D	755	MET	CG-SD	5.69	1.95	1.80
1	G	312	LEU	CA-CB	5.69	1.61	1.54
1	C	350	PRO	N-CD	5.69	1.55	1.47
1	I	600	ARG	CZ-NH1	5.69	1.40	1.32
1	D	226	ASN	C-N	-5.69	1.26	1.33
1	E	845	MET	CG-SD	5.69	1.95	1.80
1	F	342	PRO	CA-C	5.69	1.58	1.52
1	B	659	HIS	C-O	-5.68	1.17	1.24
1	I	718	GLN	CA-C	5.68	1.60	1.52
1	J	850	TYR	C-O	5.68	1.31	1.24
1	B	556	ALA	C-O	5.68	1.30	1.24
1	J	752	LYS	CA-C	-5.68	1.45	1.52
1	H	550	ALA	C-N	-5.68	1.26	1.34
1	H	698	ILE	C-N	5.68	1.41	1.33
1	B	293	THR	C-O	-5.67	1.17	1.24
1	G	636	CYS	CA-C	5.67	1.60	1.52
1	B	427	THR	N-CA	5.67	1.53	1.45
1	J	705	TYR	C-N	-5.67	1.26	1.34
1	H	710	ASP	CA-CB	-5.67	1.43	1.53
1	J	678	VAL	C-O	5.67	1.30	1.24
1	D	412	SER	N-CA	-5.67	1.39	1.46
1	J	701	SER	C-O	-5.66	1.17	1.24
1	D	890	ARG	CZ-NH1	-5.66	1.24	1.32
1	F	429	MET	CG-SD	5.66	1.94	1.80
1	H	362	GLY	C-O	5.66	1.31	1.23
1	E	556	ALA	C-O	5.66	1.30	1.24
1	G	802	LEU	C-O	-5.66	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	386	TYR	C-O	-5.66	1.17	1.24
1	D	313	ALA	C-O	-5.65	1.17	1.24
1	H	568	PHE	C-N	-5.65	1.26	1.33
1	E	316	THR	CA-C	5.65	1.60	1.52
1	H	743	ASN	CA-C	5.65	1.60	1.52
1	I	517	MET	CG-SD	5.65	1.94	1.80
1	H	226	ASN	C-O	-5.64	1.16	1.24
1	B	771	ASP	CA-CB	5.64	1.62	1.53
1	C	492	PHE	C-O	5.64	1.32	1.23
1	A	852	ARG	C-O	5.64	1.31	1.24
1	D	360	LEU	C-N	5.63	1.40	1.33
1	D	850	TYR	C-O	-5.63	1.17	1.24
1	E	500	THR	C-O	-5.63	1.17	1.23
1	F	585	LEU	C-O	5.63	1.31	1.24
1	A	579	THR	CA-C	5.63	1.60	1.52
1	G	640	THR	C-O	-5.63	1.17	1.24
1	J	897	VAL	N-CA	-5.62	1.39	1.46
1	B	633	ASP	C-O	-5.62	1.17	1.24
1	D	593	LEU	CA-C	5.62	1.59	1.52
1	D	905	HIS	CG-CD2	-5.62	1.29	1.35
1	H	275	HIS	C-O	-5.62	1.17	1.24
1	H	739	LYS	N-CA	5.62	1.53	1.46
1	D	905	HIS	C-N	5.62	1.42	1.33
1	C	381	GLU	CA-C	-5.61	1.45	1.52
1	C	389	GLY	C-O	-5.61	1.16	1.24
1	H	353	PRO	C-O	5.61	1.29	1.23
1	C	302	VAL	CA-C	5.61	1.59	1.52
1	D	397	SER	C-N	5.61	1.40	1.33
1	E	665	ASP	C-O	-5.61	1.17	1.24
1	I	275	HIS	CG-CD2	-5.61	1.29	1.35
1	B	644	VAL	N-CA	-5.61	1.39	1.46
1	F	530	ARG	NE-CZ	-5.60	1.26	1.33
1	C	227	MET	N-CA	-5.60	1.39	1.46
1	F	875	ALA	C-N	5.60	1.41	1.34
1	H	873	LYS	C-O	-5.60	1.17	1.24
1	D	686	VAL	CA-CB	5.60	1.61	1.54
1	F	549	SER	C-N	-5.60	1.26	1.33
1	G	457	SER	CA-C	5.60	1.59	1.52
1	A	517	MET	SD-CE	5.60	1.93	1.79
1	C	487	SER	C-O	-5.59	1.17	1.24
1	F	574	ARG	CZ-NH1	5.59	1.40	1.32
1	C	739	LYS	C-O	5.59	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	845	MET	CG-SD	5.59	1.94	1.80
1	H	363	TYR	C-O	5.59	1.30	1.23
1	E	903	GLU	N-CA	5.59	1.53	1.46
1	H	447	PRO	CA-C	-5.59	1.45	1.52
1	J	489	PRO	C-N	-5.59	1.26	1.33
1	H	907	ILE	CA-C	5.58	1.60	1.52
1	C	825	PHE	N-CA	5.58	1.52	1.46
1	E	278	LEU	C-O	-5.58	1.19	1.24
1	I	302	VAL	C-O	-5.58	1.18	1.24
1	C	607	PRO	N-CD	-5.58	1.40	1.47
1	E	738	MET	CG-SD	5.58	1.94	1.80
1	J	577	LEU	CA-CB	-5.58	1.44	1.53
1	A	624	ASP	CA-C	5.57	1.60	1.52
1	A	865	MET	SD-CE	5.57	1.93	1.79
1	A	884	HIS	CD2-NE2	5.57	1.44	1.37
1	J	428	LYS	C-O	5.57	1.30	1.23
1	H	229	PHE	CA-CB	5.57	1.61	1.53
1	A	656	ILE	CA-C	5.56	1.59	1.52
1	G	683	ALA	N-CA	5.56	1.53	1.46
1	H	845	MET	CG-SD	5.56	1.94	1.80
1	J	698	ILE	N-CA	-5.56	1.39	1.46
1	J	876	ARG	NE-CZ	5.56	1.39	1.33
1	E	897	VAL	CA-C	-5.56	1.46	1.52
1	H	262	SER	C-O	5.56	1.30	1.24
1	B	421	ARG	N-CA	5.56	1.52	1.46
1	F	630	ARG	NE-CZ	5.56	1.39	1.33
1	A	246	GLN	C-O	-5.55	1.17	1.24
1	A	855	ARG	C-O	5.55	1.30	1.24
1	H	691	SER	N-CA	5.55	1.52	1.46
1	D	388	ARG	C-O	-5.55	1.17	1.24
1	H	862	HIS	N-CA	5.55	1.53	1.46
1	I	260	SER	C-O	-5.55	1.17	1.24
1	C	395	ALA	C-O	-5.55	1.17	1.23
1	F	766	ILE	C-O	-5.55	1.18	1.24
1	J	767	ILE	CA-C	5.55	1.59	1.52
1	C	708	ASP	N-CA	-5.54	1.40	1.46
1	F	535	THR	C-N	-5.54	1.26	1.33
1	I	782	ALA	CA-C	-5.54	1.45	1.52
1	G	808	LYS	C-N	5.54	1.40	1.33
1	I	445	GLN	N-CA	5.54	1.53	1.46
1	J	593	LEU	CA-C	5.54	1.59	1.52
1	B	505	LEU	C-O	-5.53	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	768	VAL	C-O	5.53	1.31	1.24
1	E	905	HIS	ND1-CE1	5.53	1.38	1.32
1	G	384	ASP	C-O	5.52	1.30	1.24
1	B	267	SER	N-CA	-5.52	1.39	1.46
1	G	227	MET	CG-SD	5.52	1.94	1.80
1	F	824	VAL	C-O	5.52	1.30	1.24
1	I	444	ARG	CD-NE	5.52	1.53	1.46
1	H	350	PRO	N-CD	5.52	1.55	1.47
1	H	654	SER	CA-C	5.52	1.60	1.52
1	E	492	PHE	C-O	-5.51	1.15	1.23
1	C	355	LEU	N-CA	5.51	1.54	1.46
1	D	672	HIS	CA-C	5.51	1.57	1.53
1	D	692	TYR	N-CA	5.50	1.52	1.46
1	G	524	THR	C-N	5.50	1.40	1.33
1	A	377	ARG	CZ-NH1	-5.50	1.25	1.32
1	F	314	ARG	CD-NE	5.50	1.53	1.46
1	D	306	GLU	C-O	-5.50	1.17	1.23
1	G	478	ASN	N-CA	5.50	1.53	1.46
1	I	446	TYR	CA-CB	5.49	1.59	1.53
1	C	853	PHE	N-CA	5.49	1.51	1.46
1	I	730	GLU	N-CA	5.49	1.52	1.46
1	H	276	GLU	N-CA	5.49	1.52	1.46
1	D	403	LEU	CA-C	5.49	1.60	1.52
1	G	897	VAL	CA-C	5.48	1.59	1.52
1	H	773	PRO	CA-C	5.48	1.58	1.52
1	A	559	ASP	N-CA	-5.48	1.39	1.46
1	D	713	PRO	C-O	5.48	1.30	1.24
1	E	738	MET	SD-CE	5.47	1.93	1.79
1	G	723	VAL	C-O	5.47	1.30	1.24
1	J	566	HIS	CB-CG	5.47	1.57	1.50
1	F	520	LYS	CA-CB	-5.47	1.43	1.53
1	D	363	TYR	C-O	-5.47	1.17	1.23
1	E	718	GLN	CA-CB	-5.47	1.44	1.53
1	G	829	VAL	C-N	5.46	1.41	1.33
1	F	692	TYR	C-N	5.46	1.41	1.33
1	E	631	GLN	CA-C	-5.46	1.45	1.52
1	G	880	LYS	C-O	5.46	1.30	1.24
1	G	761	ALA	CA-C	5.46	1.60	1.52
1	H	828	ALA	N-CA	-5.46	1.40	1.46
1	F	454	GLY	C-O	-5.46	1.18	1.24
1	I	570	SER	N-CA	5.46	1.53	1.46
1	G	641	ARG	NE-CZ	5.46	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	438	ALA	C-O	-5.45	1.17	1.24
1	A	766	ILE	N-CA	5.45	1.52	1.46
1	H	888	ILE	C-O	-5.45	1.17	1.24
1	B	416	ASP	CA-C	-5.45	1.47	1.52
1	J	417	PRO	C-N	-5.45	1.25	1.33
1	G	723	VAL	N-CA	-5.44	1.40	1.46
1	J	603	GLU	C-O	5.44	1.31	1.23
1	A	450	LEU	CA-CB	5.44	1.61	1.53
1	A	476	SER	CA-CB	-5.44	1.44	1.53
1	E	753	GLU	C-O	-5.44	1.17	1.24
1	H	392	ILE	CA-CB	5.44	1.59	1.53
1	B	430	ASP	C-N	5.44	1.40	1.33
1	C	560	ASP	N-CA	5.44	1.52	1.46
1	F	882	ARG	C-O	5.44	1.30	1.24
1	B	284	MET	C-O	-5.43	1.17	1.24
1	D	478	ASN	N-CA	5.43	1.53	1.46
1	E	739	LYS	N-CA	-5.43	1.39	1.46
1	F	362	GLY	N-CA	-5.43	1.36	1.45
1	G	798	ASP	C-N	5.43	1.40	1.33
1	J	271	ALA	N-CA	-5.43	1.39	1.46
1	B	746	GLY	C-O	5.43	1.31	1.23
1	F	293	THR	C-O	-5.43	1.17	1.24
1	J	907	ILE	CA-CB	5.43	1.61	1.54
1	D	831	THR	CA-C	5.43	1.60	1.52
1	B	293	THR	CA-CB	5.42	1.60	1.53
1	J	628	TRP	NE1-CE2	-5.42	1.31	1.37
1	B	278	LEU	CA-CB	5.42	1.60	1.54
1	I	767	ILE	CA-C	5.42	1.59	1.52
1	G	322	GLN	CA-C	-5.42	1.46	1.52
1	D	457	SER	N-CA	-5.42	1.39	1.46
1	A	748	ARG	NE-CZ	-5.42	1.27	1.33
1	F	738	MET	CA-C	-5.42	1.46	1.52
1	D	347	ILE	CA-C	-5.42	1.46	1.52
1	E	900	LYS	CA-C	5.41	1.59	1.52
1	G	453	VAL	C-N	5.41	1.38	1.33
1	H	563	HIS	CE1-NE2	-5.41	1.27	1.32
1	H	810	ARG	CZ-NH1	5.41	1.40	1.32
1	A	233	LYS	CA-CB	-5.41	1.44	1.53
1	D	452	TYR	N-CA	5.41	1.52	1.45
1	H	308	PRO	N-CA	5.40	1.54	1.47
1	E	865	MET	SD-CE	5.40	1.93	1.79
1	H	886	ASP	C-N	-5.40	1.27	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	434	PRO	CA-CB	-5.40	1.46	1.53
1	E	586	ASP	CA-C	-5.40	1.46	1.52
1	F	228	MET	CG-SD	5.40	1.94	1.80
1	G	706	LYS	C-O	5.40	1.30	1.24
1	B	867	ALA	N-CA	-5.40	1.39	1.46
1	E	790	ALA	N-CA	-5.40	1.39	1.46
1	B	491	GLU	N-CA	5.39	1.53	1.46
1	H	275	HIS	CA-C	5.39	1.57	1.52
1	J	853	PHE	C-N	5.39	1.40	1.34
1	G	456	ILE	C-O	5.39	1.30	1.24
1	E	706	LYS	C-O	5.39	1.30	1.24
1	G	255	ILE	CA-CB	-5.39	1.47	1.54
1	B	272	ILE	N-CA	-5.39	1.40	1.46
1	E	818	LYS	CA-C	5.39	1.59	1.52
1	F	445	GLN	N-CA	-5.39	1.40	1.46
1	F	297	ASP	CA-C	5.38	1.59	1.53
1	D	532	LEU	CB-CG	5.38	1.64	1.53
1	F	325	LEU	N-CA	-5.38	1.39	1.46
1	G	898	LEU	C-O	5.38	1.30	1.24
1	E	503	MET	SD-CE	5.38	1.93	1.79
1	F	586	ASP	N-CA	-5.38	1.40	1.46
1	D	444	ARG	CA-CB	-5.37	1.46	1.54
1	E	486	GLY	C-N	-5.37	1.26	1.33
1	F	872	GLU	C-O	-5.37	1.17	1.24
1	J	865	MET	SD-CE	5.37	1.93	1.79
1	C	234	MET	CG-SD	5.37	1.94	1.80
1	G	293	THR	C-O	5.37	1.30	1.24
1	D	265	LYS	C-O	5.37	1.30	1.24
1	D	651	VAL	CA-C	-5.37	1.46	1.52
1	B	245	GLY	C-N	5.37	1.40	1.33
1	A	386	TYR	C-O	-5.36	1.17	1.24
1	B	292	LEU	CA-CB	5.36	1.60	1.53
1	E	541	VAL	N-CA	5.36	1.52	1.46
1	J	879	PRO	CA-C	5.36	1.59	1.52
1	C	436	LYS	CA-C	-5.36	1.45	1.52
1	B	434	PRO	N-CD	-5.36	1.40	1.47
1	H	667	SER	C-O	5.36	1.29	1.23
1	E	293	THR	C-O	-5.35	1.18	1.24
1	D	566	HIS	CD2-NE2	5.35	1.43	1.37
1	E	396	ILE	C-N	5.35	1.40	1.33
1	E	865	MET	CG-SD	5.35	1.94	1.80
1	H	890	ARG	NE-CZ	5.35	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	726	VAL	N-CA	5.35	1.52	1.46
1	D	554	LEU	CA-C	5.35	1.59	1.52
1	B	438	ALA	N-CA	-5.35	1.39	1.46
1	F	291	GLU	CA-C	5.34	1.59	1.52
1	B	351	ASN	CA-C	-5.34	1.45	1.52
1	C	610	ARG	CZ-NH2	-5.34	1.26	1.33
1	F	549	SER	CA-C	-5.34	1.46	1.52
1	B	551	GLU	N-CA	5.34	1.52	1.46
1	D	384	ASP	CG-OD2	-5.34	1.15	1.25
1	E	324	THR	C-O	-5.34	1.17	1.24
1	E	619	PRO	N-CD	5.34	1.55	1.47
1	H	505	LEU	CA-CB	5.33	1.61	1.53
1	J	532	LEU	C-N	5.33	1.40	1.33
1	J	703	LYS	CA-CB	5.33	1.58	1.54
1	G	584	ALA	C-N	5.33	1.41	1.34
1	E	862	HIS	N-CA	-5.33	1.40	1.46
1	J	315	VAL	N-CA	5.33	1.52	1.46
1	E	829	VAL	CA-C	5.32	1.59	1.52
1	I	526	GLU	CG-CD	-5.32	1.38	1.52
1	D	674	SER	CA-C	5.32	1.59	1.52
1	H	423	ILE	CA-C	-5.32	1.46	1.52
1	H	646	ARG	N-CA	5.32	1.52	1.46
1	J	517	MET	C-O	5.32	1.30	1.24
1	H	250	VAL	CA-C	-5.32	1.45	1.52
1	B	797	ALA	CA-C	-5.31	1.46	1.52
1	D	270	GLU	N-CA	-5.31	1.40	1.46
1	D	442	SER	C-O	-5.31	1.18	1.24
1	C	294	LEU	N-CA	-5.31	1.39	1.45
1	E	890	ARG	CZ-NH2	5.31	1.40	1.33
1	G	894	LEU	C-N	5.31	1.40	1.33
1	H	850	TYR	C-N	-5.31	1.26	1.33
1	I	829	VAL	N-CA	-5.31	1.40	1.46
1	C	304	TYR	CA-C	-5.31	1.46	1.52
1	D	253	PRO	N-CD	5.30	1.55	1.47
1	E	356	SER	C-N	5.30	1.41	1.33
1	H	303	ASP	CA-CB	5.30	1.59	1.53
1	H	864	HIS	N-CA	5.30	1.52	1.46
1	A	388	ARG	C-N	-5.30	1.25	1.33
1	A	677	LYS	C-N	5.30	1.40	1.33
1	D	245	GLY	CA-C	-5.30	1.46	1.52
1	B	715	GLU	C-O	-5.30	1.18	1.24
1	H	327	GLU	CA-C	5.29	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	723	VAL	C-N	-5.29	1.27	1.33
1	G	481	GLU	CA-C	5.29	1.59	1.52
1	I	498	VAL	N-CA	5.29	1.52	1.46
1	H	282	SER	C-O	-5.29	1.19	1.24
1	H	528	ILE	N-CA	-5.29	1.40	1.46
1	I	898	LEU	CA-C	5.29	1.59	1.52
1	B	279	PRO	CA-C	5.29	1.58	1.52
1	F	272	ILE	C-N	-5.28	1.28	1.34
1	G	621	ALA	C-O	5.28	1.30	1.23
1	H	801	SER	C-O	-5.28	1.18	1.24
1	A	437	GLY	C-O	-5.28	1.17	1.23
1	F	282	SER	N-CA	-5.28	1.40	1.47
1	J	510	LEU	N-CA	-5.28	1.40	1.46
1	B	282	SER	C-O	5.28	1.29	1.24
1	J	519	SER	N-CA	5.28	1.52	1.46
1	F	437	GLY	N-CA	5.28	1.52	1.45
1	G	903	GLU	C-O	5.28	1.30	1.24
1	I	535	THR	CA-CB	-5.28	1.45	1.53
1	A	392	ILE	CA-CB	-5.27	1.48	1.53
1	C	875	ALA	N-CA	5.27	1.52	1.46
1	J	229	PHE	C-O	-5.27	1.18	1.24
1	C	802	LEU	C-O	-5.27	1.18	1.24
1	G	297	ASP	C-O	-5.27	1.17	1.23
1	E	656	ILE	C-O	5.27	1.30	1.24
1	A	618	LEU	N-CA	5.27	1.53	1.46
1	E	498	VAL	C-O	-5.27	1.17	1.24
1	A	492	PHE	C-O	-5.27	1.17	1.23
1	E	308	PRO	N-CD	5.26	1.55	1.47
1	H	328	LEU	CA-C	5.26	1.59	1.52
1	B	865	MET	CG-SD	5.26	1.93	1.80
1	A	448	LEU	C-O	5.26	1.30	1.23
1	H	629	HIS	CG-ND1	-5.26	1.32	1.38
1	B	331	SER	C-N	5.25	1.40	1.33
1	H	286	THR	C-N	-5.25	1.27	1.33
1	I	642	LEU	C-O	5.25	1.30	1.23
1	B	472	ASN	C-O	-5.25	1.17	1.23
1	E	431	LEU	C-N	-5.25	1.27	1.33
1	E	711	ILE	CA-CB	5.25	1.60	1.54
1	E	385	LYS	CA-C	-5.25	1.46	1.52
1	E	477	ILE	CA-C	-5.25	1.45	1.52
1	C	411	ALA	C-N	5.24	1.40	1.33
1	G	676	ARG	CA-C	-5.24	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	347	ILE	C-N	5.24	1.40	1.33
1	A	630	ARG	CD-NE	5.24	1.53	1.46
1	A	716	TRP	N-CA	-5.24	1.40	1.46
1	D	808	LYS	C-N	5.24	1.40	1.33
1	F	733	GLN	C-O	-5.24	1.18	1.24
1	I	422	THR	C-O	-5.24	1.18	1.23
1	A	447	PRO	CA-CB	-5.24	1.47	1.53
1	C	865	MET	CG-SD	5.24	1.93	1.80
1	C	355	LEU	C-O	5.24	1.29	1.24
1	J	690	ARG	C-O	-5.24	1.17	1.24
1	E	520	LYS	C-N	5.23	1.40	1.33
1	G	581	LEU	C-O	-5.23	1.18	1.24
1	G	258	ILE	CA-C	5.23	1.59	1.52
1	J	615	ILE	CA-C	5.23	1.60	1.52
1	A	800	LEU	N-CA	5.23	1.52	1.46
1	F	340	ASP	CA-CB	5.23	1.61	1.53
1	B	432	VAL	N-CA	5.23	1.52	1.46
1	H	488	HIS	CB-CG	5.23	1.57	1.50
1	I	351	ASN	C-N	5.22	1.39	1.33
1	C	857	VAL	N-CA	5.22	1.52	1.46
1	I	408	ALA	N-CA	-5.22	1.40	1.46
1	A	810	ARG	NE-CZ	-5.22	1.27	1.33
1	E	350	PRO	C-O	-5.22	1.18	1.24
1	B	722	HIS	CA-C	-5.21	1.46	1.52
1	I	590	LEU	N-CA	5.21	1.52	1.46
1	H	863	GLU	CA-C	5.21	1.59	1.52
1	C	396	ILE	CA-C	5.21	1.58	1.52
1	J	303	ASP	C-N	-5.21	1.26	1.33
1	B	524	THR	N-CA	-5.21	1.40	1.46
1	B	563	HIS	CG-ND1	5.21	1.44	1.38
1	I	436	LYS	C-O	5.21	1.30	1.24
1	J	548	MET	SD-CE	5.21	1.92	1.79
1	A	806	ALA	C-O	-5.21	1.18	1.24
1	G	706	LYS	C-N	5.21	1.40	1.33
1	J	627	TYR	C-O	-5.21	1.18	1.24
1	B	400	ASP	CA-C	5.20	1.59	1.52
1	C	245	GLY	N-CA	5.20	1.52	1.45
1	E	326	THR	C-N	5.20	1.40	1.33
1	A	598	TRP	C-N	5.20	1.40	1.33
1	B	835	GLN	C-O	5.20	1.30	1.24
1	I	309	ASP	C-O	-5.20	1.18	1.24
1	G	547	PRO	N-CA	-5.20	1.40	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	638	GLY	N-CA	-5.19	1.39	1.45
1	I	522	ASN	N-CA	5.19	1.52	1.46
1	B	507	LYS	CA-C	5.19	1.59	1.52
1	I	529	GLN	CA-CB	-5.19	1.45	1.53
1	J	774	SER	C-O	-5.19	1.18	1.24
1	G	603	GLU	CA-C	5.19	1.59	1.52
1	B	319	SER	N-CA	5.18	1.52	1.46
1	G	517	MET	CG-SD	5.18	1.93	1.80
1	H	445	GLN	CA-C	-5.18	1.45	1.52
1	D	417	PRO	C-O	5.18	1.30	1.24
1	D	646	ARG	CZ-NH2	5.18	1.40	1.33
1	D	772	HIS	CA-CB	-5.18	1.46	1.53
1	F	627	TYR	N-CA	5.18	1.52	1.46
1	H	717	ALA	C-O	5.18	1.30	1.24
1	B	395	ALA	C-O	-5.18	1.17	1.24
1	B	482	LYS	N-CA	5.18	1.52	1.46
1	C	379	ILE	C-N	5.18	1.41	1.34
1	A	234	MET	CA-CB	-5.18	1.45	1.53
1	H	893	LEU	C-O	5.18	1.30	1.24
1	D	784	LEU	C-N	5.17	1.40	1.33
1	F	866	HIS	ND1-CE1	-5.17	1.27	1.32
1	G	875	ALA	CA-C	-5.17	1.46	1.52
1	I	228	MET	SD-CE	5.17	1.92	1.79
1	I	626	PRO	CB-CG	5.17	1.75	1.49
1	I	227	MET	CG-SD	5.17	1.93	1.80
1	J	228	MET	CG-SD	5.17	1.93	1.80
1	E	557	SER	C-O	5.17	1.30	1.24
1	F	331	SER	N-CA	5.17	1.52	1.46
1	H	405	ASN	C-O	-5.17	1.17	1.24
1	H	704	PRO	C-N	-5.17	1.26	1.33
1	G	429	MET	CG-SD	5.16	1.93	1.80
1	I	686	VAL	C-N	-5.16	1.27	1.33
1	G	560	ASP	CG-OD2	5.16	1.35	1.25
1	E	383	CYS	C-O	-5.16	1.18	1.24
1	G	901	ILE	N-CA	5.16	1.52	1.46
1	D	771	ASP	C-N	5.16	1.41	1.34
1	G	750	LYS	N-CA	-5.16	1.40	1.46
1	J	293	THR	C-O	-5.16	1.18	1.24
1	F	700	ILE	C-O	5.15	1.30	1.24
1	G	639	LEU	C-O	-5.15	1.18	1.24
1	G	482	LYS	N-CA	5.15	1.52	1.46
1	A	521	LEU	N-CA	5.15	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	503	MET	C-N	5.15	1.41	1.33
1	D	885	LEU	CA-C	-5.15	1.46	1.52
1	D	234	MET	CG-SD	5.15	1.93	1.80
1	F	302	VAL	C-N	-5.15	1.26	1.33
1	F	418	ARG	N-CA	5.15	1.52	1.46
1	G	640	THR	CA-C	-5.15	1.46	1.52
1	H	457	SER	C-O	-5.15	1.17	1.24
1	J	486	GLY	C-O	-5.15	1.17	1.23
1	A	725	GLY	N-CA	5.14	1.52	1.45
1	C	641	ARG	C-N	-5.14	1.26	1.33
1	D	246	GLN	N-CA	5.14	1.52	1.46
1	E	376	LYS	CA-C	-5.14	1.46	1.52
1	A	773	PRO	C-N	-5.14	1.26	1.33
1	G	694	THR	CB-OG1	-5.14	1.35	1.43
1	D	705	TYR	N-CA	5.14	1.52	1.46
1	I	267	SER	C-O	-5.14	1.18	1.24
1	B	249	THR	C-O	-5.13	1.18	1.23
1	E	656	ILE	CA-C	-5.13	1.46	1.52
1	H	680	SER	N-CA	5.13	1.52	1.46
1	I	227	MET	SD-CE	5.13	1.92	1.79
1	A	439	ALA	C-N	-5.13	1.27	1.33
1	C	386	TYR	C-O	5.13	1.30	1.24
1	E	829	VAL	CA-CB	5.13	1.60	1.54
1	F	725	GLY	C-N	5.13	1.40	1.33
1	E	290	ILE	CA-CB	-5.13	1.47	1.53
1	A	875	ALA	C-O	-5.13	1.17	1.24
1	A	892	GLU	CA-CB	-5.13	1.45	1.53
1	B	341	ASP	CA-C	5.13	1.58	1.53
1	B	693	ALA	C-O	5.13	1.30	1.24
1	G	628	TRP	C-O	5.13	1.30	1.24
1	A	231	THR	N-CA	-5.12	1.40	1.46
1	A	869	GLY	N-CA	5.12	1.52	1.45
1	B	492	PHE	C-N	-5.12	1.25	1.33
1	D	896	THR	N-CA	5.12	1.52	1.46
1	B	484	TYR	N-CA	5.12	1.52	1.46
1	C	440	ILE	C-N	5.12	1.40	1.33
1	B	441	LEU	C-O	-5.12	1.18	1.24
1	B	319	SER	C-N	5.12	1.40	1.33
1	J	711	ILE	CA-C	5.12	1.58	1.52
1	A	235	ILE	C-O	-5.11	1.18	1.24
1	G	522	ASN	C-O	5.11	1.30	1.24
1	H	270	GLU	CA-C	5.11	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	503	MET	CG-SD	5.11	1.93	1.80
1	E	622	ASP	C-N	-5.11	1.26	1.33
1	J	505	LEU	C-O	5.11	1.29	1.24
1	B	629	HIS	CD2-NE2	5.11	1.43	1.37
1	C	800	LEU	C-N	5.11	1.40	1.33
1	H	629	HIS	CG-CD2	5.11	1.41	1.35
1	F	694	THR	C-N	-5.11	1.27	1.33
1	G	503	MET	CG-SD	5.11	1.93	1.80
1	J	441	LEU	C-O	-5.11	1.18	1.24
1	C	789	GLU	C-O	-5.10	1.17	1.24
1	A	757	PHE	CA-C	5.10	1.59	1.52
1	B	583	ASP	CA-C	-5.10	1.46	1.52
1	B	659	HIS	C-N	5.10	1.40	1.33
1	J	534	GLU	CA-C	5.10	1.59	1.52
1	F	287	ARG	C-N	5.10	1.40	1.33
1	B	606	SER	CA-C	5.09	1.59	1.53
1	H	273	VAL	C-N	5.09	1.40	1.33
1	J	554	LEU	C-N	5.09	1.40	1.33
1	G	521	LEU	N-CA	5.09	1.52	1.46
1	H	427	THR	CB-OG1	-5.09	1.35	1.43
1	H	767	ILE	C-O	5.09	1.29	1.24
1	G	404	ALA	N-CA	5.09	1.53	1.46
1	I	817	ASN	N-CA	5.09	1.53	1.46
1	F	381	GLU	C-O	5.09	1.30	1.24
1	E	517	MET	SD-CE	5.09	1.92	1.79
1	B	851	VAL	CA-C	5.09	1.59	1.52
1	E	548	MET	CA-CB	-5.08	1.44	1.53
1	J	300	ALA	C-O	5.08	1.30	1.24
1	J	725	GLY	C-N	5.08	1.40	1.33
1	E	846	LEU	C-N	-5.08	1.27	1.34
1	J	353	PRO	CA-CB	-5.08	1.48	1.54
1	A	269	LEU	C-N	-5.08	1.27	1.33
1	F	517	MET	CG-SD	5.08	1.93	1.80
1	G	308	PRO	C-O	5.08	1.30	1.24
1	H	658	GLN	CA-C	5.08	1.59	1.52
1	I	436	LYS	CA-C	-5.08	1.46	1.52
1	I	708	ASP	CA-CB	-5.08	1.47	1.53
1	B	682	ALA	C-N	-5.08	1.27	1.33
1	F	498	VAL	C-O	5.08	1.30	1.24
1	A	350	PRO	C-O	-5.08	1.18	1.24
1	A	794	ARG	N-CA	-5.08	1.40	1.46
1	D	642	LEU	C-O	-5.08	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	316	THR	C-O	5.08	1.30	1.24
1	J	386	TYR	CG-CD1	-5.08	1.28	1.39
1	A	676	ARG	NE-CZ	-5.07	1.27	1.33
1	B	239	ASN	N-CA	-5.07	1.40	1.46
1	C	659	HIS	CG-CD2	-5.07	1.30	1.35
1	D	403	LEU	C-N	-5.07	1.27	1.33
1	E	818	LYS	C-O	5.07	1.30	1.24
1	H	241	LEU	CA-CB	-5.07	1.45	1.53
1	I	780	SER	N-CA	-5.07	1.39	1.45
1	E	419	GLY	N-CA	-5.07	1.38	1.45
1	G	379	ILE	CA-CB	-5.07	1.48	1.54
1	D	424	GLY	CA-C	5.07	1.55	1.52
1	D	548	MET	CG-SD	5.07	1.93	1.80
1	E	869	GLY	C-O	-5.06	1.17	1.23
1	H	854	PRO	CA-C	5.06	1.59	1.52
1	I	566	HIS	CD2-NE2	-5.06	1.32	1.37
1	J	859	ALA	N-CA	-5.06	1.40	1.46
1	D	823	GLU	N-CA	5.06	1.52	1.46
1	F	255	ILE	CA-C	-5.06	1.47	1.52
1	F	296	ASN	C-N	5.06	1.40	1.33
1	I	299	GLU	CA-C	5.06	1.59	1.52
1	F	900	LYS	C-N	-5.06	1.27	1.33
1	C	893	LEU	N-CA	5.06	1.52	1.46
1	B	754	VAL	C-O	-5.05	1.17	1.24
1	F	871	LEU	N-CA	5.05	1.52	1.46
1	D	761	ALA	C-O	-5.05	1.17	1.24
1	A	589	VAL	C-O	5.05	1.29	1.24
1	G	667	SER	C-O	-5.05	1.17	1.23
1	H	227	MET	SD-CE	5.05	1.92	1.79
1	H	345	LEU	C-O	-5.05	1.17	1.23
1	A	239	ASN	C-O	5.05	1.29	1.24
1	D	227	MET	C-N	-5.05	1.26	1.33
1	F	453	VAL	CA-CB	5.05	1.60	1.54
1	I	786	ARG	CA-CB	5.05	1.61	1.53
1	A	661	GLU	CA-C	5.04	1.59	1.52
1	C	234	MET	SD-CE	5.04	1.92	1.79
1	H	418	ARG	C-N	-5.04	1.27	1.33
1	D	409	LEU	C-O	-5.04	1.18	1.24
1	E	797	ALA	C-N	5.04	1.40	1.33
1	F	476	SER	CA-CB	5.04	1.61	1.53
1	D	651	VAL	C-O	5.04	1.29	1.24
1	G	756	SER	CA-C	5.04	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	714	ASN	N-CA	-5.04	1.40	1.46
1	C	659	HIS	C-N	5.03	1.40	1.33
1	B	794	ARG	CZ-NH2	-5.03	1.26	1.33
1	F	609	PRO	C-O	5.03	1.31	1.24
1	B	661	GLU	N-CA	5.03	1.52	1.46
1	B	689	ASP	C-O	5.03	1.29	1.24
1	H	743	ASN	N-CA	5.03	1.52	1.46
1	I	456	ILE	N-CA	5.03	1.52	1.46
1	G	600	ARG	CA-C	5.02	1.59	1.52
1	G	677	LYS	C-O	-5.02	1.18	1.24
1	A	282	SER	C-O	-5.02	1.17	1.24
1	B	245	GLY	C-O	5.02	1.30	1.23
1	G	278	LEU	C-N	5.02	1.38	1.33
1	I	473	LEU	N-CA	-5.02	1.39	1.46
1	A	494	PRO	N-CD	5.02	1.54	1.47
1	F	314	ARG	CA-CB	-5.02	1.45	1.53
1	I	871	LEU	C-O	5.02	1.29	1.24
1	A	402	ASP	C-O	5.02	1.30	1.23
1	F	672	HIS	CG-CD2	-5.02	1.30	1.35
1	I	350	PRO	CA-C	5.02	1.60	1.52
1	C	515	GLN	C-O	-5.01	1.18	1.24
1	H	524	THR	C-O	-5.01	1.18	1.24
1	C	391	ASN	C-N	5.01	1.38	1.33
1	F	870	GLY	C-O	-5.01	1.18	1.24
1	A	864	HIS	C-O	5.01	1.29	1.24
1	A	530	ARG	N-CA	5.01	1.52	1.46
1	D	530	ARG	CZ-NH1	-5.01	1.25	1.32
1	J	735	GLN	CA-C	5.01	1.59	1.52
1	A	642	LEU	CA-C	-5.00	1.46	1.52
1	A	851	VAL	CA-C	-5.00	1.46	1.52
1	B	735	GLN	C-N	-5.00	1.27	1.34
1	C	267	SER	CA-C	-5.00	1.46	1.52
1	E	250	VAL	CA-C	5.00	1.59	1.52
1	G	520	LYS	CA-C	-5.00	1.45	1.52
1	J	720	ARG	N-CA	5.00	1.52	1.46

All (243) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	483	ASN	N-CA-C	12.59	124.54	111.07
1	H	445	GLN	CA-C-N	-12.37	110.87	122.37
1	H	445	GLN	C-N-CA	-12.37	110.87	122.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	440	ILE	N-CA-C	12.28	122.07	110.53
1	D	445	GLN	CA-C-N	-11.20	111.95	122.37
1	D	445	GLN	C-N-CA	-11.20	111.95	122.37
1	D	227	MET	N-CA-C	11.10	123.45	111.36
1	E	244	VAL	N-CA-C	10.98	121.81	110.72
1	D	483	ASN	N-CA-C	10.59	122.90	111.36
1	E	440	ILE	N-CA-C	10.50	122.44	111.00
1	A	445	GLN	CA-C-N	-10.47	112.63	122.37
1	A	445	GLN	C-N-CA	-10.47	112.63	122.37
1	D	440	ILE	N-CA-C	10.24	120.75	110.82
1	D	500	THR	N-CA-C	10.21	124.60	109.07
1	D	496	SER	N-CA-C	-10.10	96.91	110.55
1	A	244	VAL	N-CA-C	10.04	120.90	110.36
1	A	483	ASN	N-CA-C	9.92	121.85	111.14
1	H	496	SER	N-CA-C	-9.91	96.53	110.50
1	J	483	ASN	N-CA-C	9.86	123.81	111.69
1	D	244	VAL	CB-CA-C	-9.62	99.15	112.14
1	E	244	VAL	CB-CA-C	-9.50	99.11	112.22
1	H	440	ILE	N-CA-C	9.47	120.00	110.82
1	A	435	GLU	N-CA-C	-9.33	101.11	111.28
1	H	500	THR	N-CA-C	9.30	122.82	108.96
1	A	262	SER	N-CA-C	-8.98	101.57	111.36
1	A	244	VAL	CB-CA-C	-8.88	100.52	111.88
1	J	484	TYR	N-CA-C	8.86	120.94	111.28
1	D	250	VAL	N-CA-C	8.85	122.17	109.51
1	E	500	THR	N-CA-C	8.80	122.25	108.79
1	J	440	ILE	N-CA-C	8.78	119.34	110.82
1	J	229	PHE	N-CA-C	8.65	120.71	111.28
1	J	262	SER	N-CA-C	-8.49	101.98	111.07
1	A	496	SER	N-CA-C	-8.44	99.15	110.55
1	J	500	THR	N-CA-C	8.38	121.62	108.79
1	E	445	GLN	CA-C-N	-8.37	113.65	122.85
1	E	445	GLN	C-N-CA	-8.37	113.65	122.85
1	J	252	LEU	CA-C-N	-8.23	112.37	120.52
1	J	252	LEU	C-N-CA	-8.23	112.37	120.52
1	A	500	THR	N-CA-C	8.13	120.47	108.60
1	J	496	SER	N-CA-C	-8.08	98.52	110.48
1	E	262	SER	N-CA-C	-8.03	102.47	111.14
1	H	227	MET	N-CA-C	8.02	119.80	111.14
1	H	483	ASN	N-CA-C	7.91	119.98	111.36
1	A	491	GLU	O-C-N	-7.80	113.25	122.15
1	H	244	VAL	CB-CA-C	-7.78	102.01	111.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	THR	N-CA-C	-7.76	102.82	111.28
1	A	224	ASP	CA-C-N	7.76	131.31	120.29
1	A	224	ASP	C-N-CA	7.76	131.31	120.29
1	D	249	THR	N-CA-C	-7.61	103.06	111.36
1	A	445	GLN	N-CA-C	-7.59	103.01	111.82
1	A	250	VAL	N-CA-C	7.47	120.19	109.51
1	H	244	VAL	N-CA-C	7.46	117.58	110.42
1	H	249	THR	N-CA-C	-7.44	103.25	111.36
1	J	224	ASP	CA-C-N	7.33	130.70	120.29
1	J	224	ASP	C-N-CA	7.33	130.70	120.29
1	E	249	THR	N-CA-C	-7.29	103.33	111.28
1	A	251	THR	N-CA-C	7.28	119.22	108.60
1	A	493	GLY	CA-C-N	-7.27	112.48	119.90
1	A	493	GLY	C-N-CA	-7.27	112.48	119.90
1	D	484	TYR	N-CA-C	7.26	119.27	111.36
1	D	241	LEU	N-CA-C	-7.18	103.49	111.82
1	D	244	VAL	N-CA-C	7.14	117.90	110.62
1	D	240	LEU	N-CA-C	7.13	119.06	111.28
1	J	251	THR	N-CA-C	7.10	117.89	107.88
1	E	251	THR	N-CA-C	7.06	118.91	108.60
1	J	250	VAL	N-CA-C	7.06	118.69	109.58
1	E	250	VAL	N-CA-C	7.06	119.79	109.63
1	E	493	GLY	CA-C-N	-7.04	112.72	119.90
1	E	493	GLY	C-N-CA	-7.04	112.72	119.90
1	A	227	MET	N-CA-C	7.00	118.70	111.14
1	D	435	GLU	N-CA-C	-6.97	103.76	111.36
1	J	244	VAL	CB-CA-C	-6.95	102.98	111.88
1	E	496	SER	N-CA-C	-6.94	100.72	110.50
1	D	251	THR	N-CA-C	6.86	118.62	108.60
1	J	435	GLU	N-CA-C	-6.86	103.73	111.07
1	H	566	HIS	CA-CB-CG	6.85	120.65	113.80
1	J	493	GLY	CA-C-N	-6.77	112.69	119.93
1	J	493	GLY	C-N-CA	-6.77	112.69	119.93
1	D	234	MET	CB-CG-SD	-6.73	92.52	112.70
1	A	310	LEU	N-CA-C	-6.71	100.24	109.71
1	E	224	ASP	CA-C-N	6.63	129.06	120.44
1	E	224	ASP	C-N-CA	6.63	129.06	120.44
1	E	236	GLU	N-CA-C	-6.61	104.16	111.82
1	C	317	ASP	CA-CB-CG	6.56	119.16	112.60
1	H	435	GLU	N-CA-C	-6.47	104.30	111.36
1	A	273	VAL	N-CA-C	6.44	119.10	111.05
1	A	226	ASN	N-CA-C	-6.43	104.32	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	224	ASP	CA-C-N	6.40	129.49	120.28
1	D	224	ASP	C-N-CA	6.40	129.49	120.28
1	J	244	VAL	N-CA-C	6.39	117.07	110.36
1	H	433	GLU	CA-C-N	6.34	126.26	119.28
1	H	433	GLU	C-N-CA	6.34	126.26	119.28
1	H	252	LEU	CA-C-N	-6.34	114.13	120.21
1	H	252	LEU	C-N-CA	-6.34	114.13	120.21
1	F	226	ASN	N-CA-C	-6.28	104.54	111.82
1	J	341	ASP	CA-C-N	-6.27	112.01	119.84
1	J	341	ASP	C-N-CA	-6.27	112.01	119.84
1	A	252	LEU	CA-C-N	-6.21	114.33	120.98
1	A	252	LEU	C-N-CA	-6.21	114.33	120.98
1	H	262	SER	N-CA-C	-6.20	104.15	111.03
1	J	227	MET	N-CA-C	6.16	118.07	111.36
1	A	433	GLU	CA-C-N	6.13	125.69	119.19
1	A	433	GLU	C-N-CA	6.13	125.69	119.19
1	H	250	VAL	N-CA-C	6.13	118.46	109.63
1	C	630	ARG	NE-CZ-NH1	-6.07	115.43	121.50
1	H	238	ARG	N-CA-C	-6.06	104.67	111.28
1	A	298	PRO	N-CA-C	-6.04	100.98	111.32
1	C	559	ASP	N-CA-C	-6.04	104.76	111.71
1	A	311	GLY	N-CA-C	6.04	118.88	111.93
1	H	251	THR	N-CA-C	6.03	117.41	108.60
1	H	234	MET	CB-CG-SD	-6.02	94.64	112.70
1	J	249	THR	N-CA-C	-6.00	104.86	111.82
1	E	252	LEU	CA-C-N	-6.00	114.58	120.52
1	E	252	LEU	C-N-CA	-6.00	114.58	120.52
1	D	488	HIS	CA-C-N	-5.99	112.84	119.19
1	D	488	HIS	C-N-CA	-5.99	112.84	119.19
1	E	241	LEU	N-CA-C	-5.99	104.67	111.07
1	J	438	ALA	N-CA-C	-5.98	104.84	111.36
1	F	609	PRO	CA-C-N	5.94	132.39	121.70
1	F	609	PRO	C-N-CA	5.94	132.39	121.70
1	J	304	TYR	CA-C-N	5.91	126.64	122.33
1	J	304	TYR	C-N-CA	5.91	126.64	122.33
1	C	660	VAL	CA-C-O	5.89	126.61	120.25
1	F	225	ASP	N-CA-C	5.88	117.36	111.07
1	E	441	LEU	N-CA-C	-5.85	104.98	111.36
1	A	228	MET	N-CA-C	-5.84	104.92	111.28
1	F	238	ARG	NE-CZ-NH1	-5.81	115.69	121.50
1	A	246	GLN	N-CA-C	5.81	117.41	111.14
1	E	298	PRO	N-CA-C	-5.80	101.40	111.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	234	MET	CB-CG-SD	-5.78	95.36	112.70
1	H	282	SER	CB-CA-C	-5.78	109.90	116.54
1	A	253	PRO	N-CA-C	5.77	119.70	110.40
1	G	788	ARG	NE-CZ-NH2	5.77	124.39	119.20
1	J	787	GLY	N-CA-C	-5.75	105.42	112.77
1	D	262	SER	N-CA-C	-5.73	104.96	111.14
1	A	441	LEU	N-CA-C	-5.70	105.07	111.28
1	E	441	LEU	CA-C-N	-5.68	114.99	123.00
1	E	441	LEU	C-N-CA	-5.68	114.99	123.00
1	J	600	ARG	N-CA-C	-5.68	102.95	110.40
1	J	492	PHE	CA-CB-CG	5.68	119.48	113.80
1	E	494	PRO	N-CA-C	5.67	120.11	111.15
1	H	494	PRO	N-CA-C	5.66	119.75	111.03
1	J	246	GLN	N-CA-C	5.64	117.11	111.07
1	J	266	SER	N-CA-C	-5.63	105.06	111.14
1	A	437	GLY	N-CA-C	-5.61	105.59	112.77
1	A	438	ALA	CA-C-N	-5.59	111.02	120.58
1	A	438	ALA	C-N-CA	-5.59	111.02	120.58
1	E	405	ASN	N-CA-C	5.58	117.37	111.28
1	J	792	PHE	CA-C-O	5.58	126.68	120.82
1	H	268	VAL	N-CA-C	-5.57	104.94	110.62
1	H	487	SER	N-CA-C	-5.56	105.30	111.36
1	H	341	ASP	CA-C-N	-5.55	112.90	119.84
1	H	341	ASP	C-N-CA	-5.55	112.90	119.84
1	E	261	GLN	N-CA-C	5.54	117.76	111.11
1	H	224	ASP	CA-C-N	5.52	128.13	120.29
1	H	224	ASP	C-N-CA	5.52	128.13	120.29
1	J	433	GLU	CA-C-N	5.52	125.19	119.56
1	J	433	GLU	C-N-CA	5.52	125.19	119.56
1	J	310	LEU	N-CA-C	-5.50	101.38	109.62
1	E	281	GLY	N-CA-C	5.49	121.37	110.77
1	I	627	TYR	CA-C-O	5.49	126.02	119.10
1	E	311	GLY	N-CA-C	5.49	119.22	112.14
1	H	228	MET	N-CA-C	-5.49	105.38	111.36
1	J	708	ASP	O-C-N	5.48	125.07	121.23
1	E	230	ILE	N-CA-C	-5.47	105.19	110.72
1	H	444	ARG	N-CA-C	-5.45	106.55	114.12
1	H	387	ILE	CB-CA-C	-5.44	104.94	112.24
1	J	232	LYS	N-CA-C	5.44	116.89	111.07
1	F	709	PRO	N-CA-CB	-5.43	98.49	102.35
1	E	240	LEU	N-CA-C	5.43	117.20	111.28
1	E	278	LEU	O-C-N	5.43	125.19	121.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	228	MET	CA-C-N	5.43	127.55	120.28
1	J	228	MET	C-N-CA	5.43	127.55	120.28
1	H	491	GLU	O-C-N	-5.40	115.99	122.15
1	D	434	PRO	N-CA-C	-5.39	106.83	113.84
1	D	405	ASN	N-CA-C	5.38	117.90	111.71
1	E	234	MET	CB-CG-SD	-5.38	96.57	112.70
1	H	226	ASN	N-CA-C	-5.37	105.83	112.38
1	F	751	LEU	N-CA-C	5.37	117.89	111.71
1	A	484	TYR	N-CA-C	5.37	117.13	111.28
1	E	500	THR	N-CA-CB	5.37	119.88	111.56
1	A	341	ASP	CA-C-N	-5.37	113.13	119.84
1	A	341	ASP	C-N-CA	-5.37	113.13	119.84
1	J	271	ALA	N-CA-C	-5.36	105.44	111.28
1	D	410	GLN	OE1-CD-NE2	-5.35	117.25	122.60
1	E	438	ALA	CA-C-N	-5.35	113.16	120.44
1	E	438	ALA	C-N-CA	-5.35	113.16	120.44
1	E	434	PRO	N-CA-C	-5.33	106.46	113.65
1	G	327	GLU	CA-C-O	-5.32	114.78	120.42
1	H	494	PRO	CB-CA-C	-5.31	104.95	111.64
1	J	248	SER	N-CA-C	-5.31	101.66	109.62
1	A	406	SER	N-CA-C	5.30	117.38	109.59
1	D	696	ASP	CA-CB-CG	-5.29	107.31	112.60
1	B	421	ARG	NE-CZ-NH1	-5.29	116.21	121.50
1	A	234	MET	CB-CG-SD	-5.29	96.82	112.70
1	G	795	ASP	CA-CB-CG	5.29	117.89	112.60
1	D	228	MET	N-CA-C	-5.26	105.22	111.69
1	J	238	ARG	N-CA-C	-5.26	105.63	111.36
1	A	236	GLU	N-CA-C	-5.24	105.56	111.28
1	J	676	ARG	NE-CZ-NH1	-5.24	116.27	121.50
1	A	882	ARG	NE-CZ-NH1	-5.22	116.28	121.50
1	A	568	PHE	CA-CB-CG	-5.22	108.58	113.80
1	H	229	PHE	N-CA-C	5.22	116.97	111.28
1	H	229	PHE	CA-CB-CG	5.21	119.01	113.80
1	H	355	LEU	CA-C-O	-5.20	115.78	121.14
1	E	238	ARG	NE-CZ-NH1	-5.20	116.30	121.50
1	E	586	ASP	CA-CB-CG	5.19	117.79	112.60
1	J	678	VAL	O-C-N	-5.19	116.48	121.83
1	H	240	LEU	N-CA-C	5.18	117.01	111.36
1	D	228	MET	CA-C-O	-5.17	114.50	120.24
1	A	528	ILE	O-C-N	-5.16	116.86	121.87
1	C	803	ARG	NE-CZ-NH2	5.16	123.85	119.20
1	H	406	SER	N-CA-C	5.15	117.90	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	310	LEU	N-CA-C	-5.15	101.90	109.62
1	H	239	ASN	CB-CA-C	-5.13	102.27	110.79
1	I	877	GLU	N-CA-C	5.13	116.68	111.14
1	D	433	GLU	CA-C-N	5.12	124.79	119.56
1	D	433	GLU	C-N-CA	5.12	124.79	119.56
1	G	852	ARG	NE-CZ-NH1	-5.12	116.38	121.50
1	C	907	ILE	O-C-N	-5.11	116.23	122.06
1	H	493	GLY	CA-C-N	-5.11	114.31	119.83
1	H	493	GLY	C-N-CA	-5.11	114.31	119.83
1	J	499	SER	CA-C-O	-5.10	115.19	120.70
1	E	488	HIS	CA-C-N	-5.10	113.29	118.85
1	E	488	HIS	C-N-CA	-5.10	113.29	118.85
1	E	484	TYR	N-CA-C	5.09	117.49	111.33
1	E	287	ARG	N-CA-C	5.09	116.83	111.28
1	H	866	HIS	N-CA-C	-5.08	105.83	112.23
1	H	324	THR	CA-C-O	5.07	126.33	121.00
1	D	478	ASN	N-CA-C	-5.07	105.84	112.23
1	E	238	ARG	NE-CZ-NH2	5.06	123.75	119.20
1	C	799	ILE	O-C-N	-5.05	116.94	121.89
1	H	498	VAL	CB-CA-C	-5.05	105.79	111.45
1	A	522	ASN	N-CA-C	5.05	116.47	110.97
1	A	444	ARG	CA-C-O	5.04	124.73	119.03
1	A	304	TYR	CA-C-N	5.04	125.08	121.65
1	A	304	TYR	C-N-CA	5.04	125.08	121.65
1	D	297	ASP	O-C-N	5.03	127.11	121.32
1	H	253	PRO	N-CA-C	5.03	118.26	111.22
1	G	255	ILE	N-CA-CB	5.01	116.72	111.00
1	C	899	GLY	N-CA-C	5.01	118.31	112.50
1	A	405	ASN	N-CA-C	5.01	117.47	111.71
1	D	820	TYR	CA-C-O	-5.00	113.11	119.31

There are no chirality outliers.

All (151) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	314	ARG	Sidechain
1	A	388	ARG	Sidechain
1	A	393	ILE	Peptide
1	A	394	LEU	Peptide
1	A	444	ARG	Sidechain
1	A	538	GLN	Sidechain
1	A	596	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	624	ASP	Sidechain
1	A	630	ARG	Sidechain
1	A	676	ARG	Sidechain
1	A	720	ARG	Sidechain
1	A	803	ARG	Sidechain
1	A	852	ARG	Sidechain
1	A	876	ARG	Sidechain
1	A	889	ARG	Sidechain
1	B	314	ARG	Sidechain
1	B	421	ARG	Sidechain
1	B	542	GLN	Sidechain
1	B	574	ARG	Sidechain
1	B	596	ARG	Sidechain
1	B	610	ARG	Sidechain
1	B	796	ARG	Sidechain
1	B	805	GLN	Sidechain
1	B	852	ARG	Sidechain
1	B	856	GLU	Sidechain
1	C	238	ARG	Sidechain
1	C	303	ASP	Sidechain
1	C	388	ARG	Sidechain
1	C	445	GLN	Sidechain
1	C	514	GLU	Sidechain
1	C	544	ASN	Sidechain
1	C	574	ARG	Sidechain
1	C	630	ARG	Sidechain
1	C	657	GLN	Sidechain
1	C	786	ARG	Sidechain
1	C	788	ARG	Sidechain
1	C	796	ARG	Sidechain
1	C	810	ARG	Sidechain
1	C	852	ARG	Sidechain
1	C	883	ARG	Sidechain
1	C	889	ARG	Sidechain
1	C	890	ARG	Sidechain
1	D	253	PRO	Mainchain
1	D	388	ARG	Sidechain
1	D	410	GLN	Sidechain
1	D	444	ARG	Sidechain
1	D	600	ARG	Sidechain
1	D	676	ARG	Sidechain
1	D	876	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	E	253	PRO	Mainchain
1	E	287	ARG	Sidechain
1	E	314	ARG	Sidechain
1	E	377	ARG	Sidechain
1	E	479	ARG	Sidechain
1	E	526	GLU	Sidechain
1	E	538	GLN	Sidechain
1	E	559	ASP	Sidechain
1	E	596	ARG	Sidechain
1	E	600	ARG	Sidechain
1	E	610	ARG	Sidechain
1	E	611	GLU	Sidechain
1	E	676	ARG	Sidechain
1	E	712	GLN	Sidechain
1	E	753	GLU	Sidechain
1	E	855	ARG	Sidechain
1	E	882	ARG	Sidechain
1	F	421	ARG	Sidechain
1	F	516	GLN	Sidechain
1	F	542	GLN	Sidechain
1	F	574	ARG	Sidechain
1	F	578	GLN	Sidechain
1	F	583	ASP	Sidechain
1	F	596	ARG	Sidechain
1	F	607	PRO	Peptide
1	F	610	ARG	Sidechain
1	F	613	ASP	Sidechain
1	F	630	ARG	Sidechain
1	F	646	ARG	Sidechain
1	F	658	GLN	Sidechain
1	F	748	ARG	Sidechain
1	F	759	ASP	Sidechain
1	F	762	ARG	Sidechain
1	F	771	ASP	Sidechain
1	F	803	ARG	Sidechain
1	F	811	GLN	Sidechain
1	F	872	GLU	Sidechain
1	F	883	ARG	Sidechain
1	G	226	ASN	Sidechain
1	G	238	ARG	Sidechain
1	G	478	ASN	Sidechain
1	G	574	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	G	586	ASP	Sidechain
1	G	610	ARG	Sidechain
1	G	657	GLN	Sidechain
1	G	718	GLN	Sidechain
1	G	795	ASP	Sidechain
1	G	811	GLN	Sidechain
1	G	823	GLU	Sidechain
1	G	906	ARG	Sidechain
1	H	225	ASP	Sidechain
1	H	253	PRO	Mainchain
1	H	283	ASN	Sidechain
1	H	291	GLU	Sidechain
1	H	314	ARG	Sidechain
1	H	344	ARG	Sidechain
1	H	388	ARG	Sidechain
1	H	397	SER	Peptide
1	H	611	GLU	Sidechain
1	H	646	ARG	Sidechain
1	H	714	ASN	Sidechain
1	H	730	GLU	Sidechain
1	H	753	GLU	Sidechain
1	H	803	ARG	Sidechain
1	I	283	ASN	Sidechain
1	I	344	ARG	Sidechain
1	I	388	ARG	Sidechain
1	I	421	ARG	Sidechain
1	I	443	ASP	Sidechain
1	I	444	ARG	Sidechain
1	I	479	ARG	Sidechain
1	I	506	ARG	Sidechain
1	I	530	ARG	Sidechain
1	I	551	GLU	Sidechain
1	I	564	GLN	Sidechain
1	I	574	ARG	Sidechain
1	I	611	GLU	Sidechain
1	I	630	ARG	Sidechain
1	I	681	ASP	Sidechain
1	I	690	ARG	Sidechain
1	I	794	ARG	Sidechain
1	I	798	ASP	Sidechain
1	I	883	ARG	Sidechain
1	I	906	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	J	253	PRO	Mainchain
1	J	276	GLU	Sidechain
1	J	287	ARG	Sidechain
1	J	322	GLN	Sidechain
1	J	388	ARG	Sidechain
1	J	433	GLU	Sidechain
1	J	480	ASN	Sidechain
1	J	614	ASN	Sidechain
1	J	630	ARG	Sidechain
1	J	646	ARG	Sidechain
1	J	712	GLN	Sidechain
1	J	728	GLN	Sidechain
1	J	743	ASN	Sidechain
1	J	765	GLU	Sidechain
1	J	769	GLU	Sidechain
1	J	810	ARG	Sidechain
1	J	876	ARG	Sidechain
1	J	889	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5152	0	5223	593	0
1	B	5152	0	5223	244	0
1	C	5152	0	5223	186	0
1	D	5152	0	5222	429	0
1	E	5152	0	5221	491	0
1	F	5152	0	5223	200	0
1	G	5152	0	5223	240	0
1	H	5152	0	5222	476	0
1	I	5152	0	5223	319	0
1	J	5152	0	5222	514	0
All	All	51520	0	52225	3481	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 34.

All (3481) 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:J:441:LEU:HD23	1:J:498:VAL:CB	1.14	1.60
1:A:426:ILE:CD1	1:A:440:ILE:HG22	1.21	1.60
1:H:441:LEU:HD23	1:H:498:VAL:CB	1.12	1.59
1:E:441:LEU:HD23	1:E:498:VAL:CB	1.19	1.59
1:I:626:PRO:CB	1:I:626:PRO:CG	1.75	1.59
1:A:441:LEU:CD2	1:A:498:VAL:HB	1.17	1.59
1:A:540:LYS:CD	1:I:626:PRO:CB	1.79	1.58
1:A:540:LYS:CE	1:I:626:PRO:CG	1.79	1.58
1:A:540:LYS:CE	1:I:626:PRO:CA	1.82	1.58
1:A:426:ILE:HD13	1:A:440:ILE:CG2	1.35	1.57
1:I:626:PRO:CG	1:I:626:PRO:CD	1.80	1.57
1:D:441:LEU:HD23	1:D:498:VAL:CB	1.24	1.56
1:J:426:ILE:CD1	1:J:440:ILE:HG22	1.26	1.56
1:E:426:ILE:CD1	1:E:440:ILE:HG22	1.19	1.56
1:A:441:LEU:HD23	1:A:498:VAL:CB	1.12	1.55
1:A:540:LYS:CD	1:I:626:PRO:CD	1.81	1.55
1:D:426:ILE:CD1	1:D:440:ILE:HG22	1.31	1.55
1:A:540:LYS:HE2	1:I:626:PRO:C	1.31	1.54
1:J:441:LEU:CD2	1:J:498:VAL:HB	1.31	1.54
1:I:626:PRO:CB	1:I:626:PRO:CA	1.86	1.52
1:H:441:LEU:CD2	1:H:498:VAL:HB	1.35	1.50
1:E:441:LEU:CD2	1:E:498:VAL:HB	1.40	1.49
1:A:540:LYS:CD	1:I:626:PRO:CA	1.87	1.49
1:D:441:LEU:CD2	1:D:498:VAL:HB	1.40	1.48
1:H:426:ILE:CD1	1:H:440:ILE:HG22	1.43	1.48
1:G:503:MET:CE	1:G:503:MET:SD	2.01	1.47
1:H:228:MET:CE	1:H:228:MET:SD	2.02	1.47
1:A:272:ILE:HG23	1:A:278:LEU:CD1	1.44	1.47
1:I:429:MET:SD	1:I:429:MET:CG	2.01	1.47
1:E:426:ILE:HD13	1:E:440:ILE:CG2	1.40	1.47
1:A:738:MET:CG	1:A:738:MET:SD	2.02	1.46
1:J:738:MET:SD	1:J:738:MET:CG	2.02	1.45
1:A:540:LYS:HE2	1:I:627:TYR:N	1.28	1.44
1:E:285:ILE:HD12	1:E:287:ARG:N	1.31	1.44
1:I:626:PRO:CD	1:I:626:PRO:N	1.76	1.44
1:J:426:ILE:CD1	1:J:440:ILE:CG2	1.92	1.44
1:I:626:PRO:CA	1:I:626:PRO:N	1.80	1.44
1:A:540:LYS:CD	1:I:626:PRO:N	1.81	1.43
1:H:401:THR:CG2	1:H:410:GLN:HG2	1.49	1.42
1:A:540:LYS:CE	1:I:626:PRO:CB	1.97	1.41
1:A:540:LYS:CE	1:I:626:PRO:CD	1.96	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:LYS:CE	1:I:626:PRO:N	1.85	1.39
1:A:285:ILE:CD1	1:A:287:ARG:HB2	1.50	1.38
1:A:540:LYS:CD	1:I:626:PRO:CG	2.02	1.38
1:E:260:SER:O	1:E:264:GLY:N	1.57	1.38
1:J:426:ILE:HD13	1:J:440:ILE:CG2	1.50	1.38
1:A:269:LEU:HD21	1:A:457:SER:CB	1.53	1.37
1:E:285:ILE:CD1	1:E:287:ARG:HB2	1.53	1.37
1:H:426:ILE:CD1	1:H:440:ILE:CG2	2.02	1.36
1:J:285:ILE:CD1	1:J:287:ARG:HB2	1.54	1.36
1:E:478:ASN:ND2	1:E:482:LYS:HZ1	1.22	1.35
1:H:426:ILE:HD13	1:H:440:ILE:CG2	1.56	1.35
1:A:536:THR:CG2	1:I:630:ARG:HD2	1.54	1.34
1:J:285:ILE:HD12	1:J:287:ARG:N	1.41	1.34
1:D:426:ILE:CD1	1:D:440:ILE:CG2	2.05	1.33
1:E:426:ILE:CD1	1:E:440:ILE:CG2	1.98	1.32
1:D:426:ILE:HD13	1:D:440:ILE:CG2	1.60	1.31
1:D:260:SER:O	1:D:264:GLY:N	1.61	1.31
1:A:536:THR:HG22	1:I:630:ARG:CD	1.59	1.31
1:J:478:ASN:ND2	1:J:482:LYS:HZ1	1.26	1.31
1:A:540:LYS:CG	1:I:626:PRO:CG	2.08	1.31
1:A:540:LYS:HE3	1:I:626:PRO:CG	1.42	1.31
1:A:260:SER:O	1:A:264:GLY:N	1.63	1.31
1:J:285:ILE:CD1	1:J:287:ARG:H	1.43	1.31
1:H:478:ASN:ND2	1:H:482:LYS:HZ1	1.28	1.30
1:J:229:PHE:CD1	1:J:232:LYS:HD2	1.67	1.29
1:H:441:LEU:HD23	1:H:498:VAL:CG1	1.62	1.28
1:A:540:LYS:CB	1:I:626:PRO:HG3	1.63	1.28
1:D:285:ILE:CD1	1:D:287:ARG:HB2	1.64	1.27
1:J:276:GLU:OE2	1:J:318:PHE:CE2	1.87	1.26
1:B:630:ARG:CB	1:J:540:LYS:HG3	1.66	1.26
1:A:540:LYS:HB3	1:I:626:PRO:CG	1.65	1.25
1:J:441:LEU:HD23	1:J:498:VAL:CG1	1.66	1.25
1:J:272:ILE:HG23	1:J:278:LEU:CD1	1.67	1.25
1:E:269:LEU:HD11	1:E:457:SER:O	1.09	1.24
1:A:540:LYS:HE2	1:I:626:PRO:CA	1.47	1.24
1:A:272:ILE:CG2	1:A:278:LEU:HD12	1.66	1.24
1:E:441:LEU:HD23	1:E:498:VAL:CG1	1.66	1.23
1:J:478:ASN:ND2	1:J:482:LYS:NZ	1.87	1.22
1:J:540:LYS:C	1:J:540:LYS:HE2	1.64	1.22
1:A:269:LEU:HD11	1:A:457:SER:O	1.05	1.22
1:H:269:LEU:HD21	1:H:457:SER:OG	1.33	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:LYS:CD	1:A:540:LYS:CE	2.18	1.21
1:H:269:LEU:HD21	1:H:457:SER:CB	1.68	1.21
1:H:269:LEU:CD1	1:H:457:SER:O	1.88	1.21
1:D:478:ASN:ND2	1:D:482:LYS:NZ	1.90	1.20
1:H:272:ILE:HG23	1:H:278:LEU:CD1	1.72	1.20
1:H:260:SER:O	1:H:264:GLY:N	1.74	1.20
1:J:260:SER:O	1:J:264:GLY:N	1.71	1.20
1:A:540:LYS:CB	1:I:626:PRO:CG	2.19	1.20
1:H:478:ASN:ND2	1:H:482:LYS:NZ	1.89	1.20
1:A:394:LEU:HD22	1:A:395:ALA:HB2	1.21	1.19
1:D:285:ILE:CD1	1:D:287:ARG:H	1.54	1.19
1:D:478:ASN:ND2	1:D:482:LYS:HZ1	1.40	1.19
1:A:276:GLU:OE2	1:A:318:PHE:HE2	1.25	1.19
1:H:401:THR:HB	1:H:410:GLN:CA	1.73	1.19
1:E:269:LEU:HD21	1:E:457:SER:CB	1.72	1.19
1:G:642:LEU:HD22	1:G:643:GLY:N	1.57	1.18
1:A:276:GLU:OE2	1:A:318:PHE:CE2	1.97	1.18
1:E:272:ILE:HG23	1:E:278:LEU:CD1	1.74	1.17
1:A:540:LYS:NZ	1:I:626:PRO:CD	2.05	1.17
1:E:285:ILE:HD13	1:E:287:ARG:CB	1.73	1.17
1:A:441:LEU:HD23	1:A:498:VAL:CG1	1.73	1.17
1:H:401:THR:CB	1:H:410:GLN:HA	1.75	1.16
1:D:269:LEU:HD11	1:D:457:SER:O	1.04	1.16
1:E:441:LEU:CD2	1:E:498:VAL:CB	2.09	1.16
1:H:407:THR:HB	1:H:414:ARG:HD3	1.24	1.16
1:J:269:LEU:HD11	1:J:457:SER:O	1.00	1.16
1:A:540:LYS:CG	1:I:626:PRO:CD	2.23	1.16
1:A:540:LYS:HD2	1:I:626:PRO:N	1.46	1.16
1:J:269:LEU:CD1	1:J:457:SER:O	1.93	1.16
1:A:285:ILE:CD1	1:A:287:ARG:H	1.58	1.16
1:A:394:LEU:HG	1:A:422:THR:OG1	1.42	1.16
1:D:269:LEU:HD21	1:D:457:SER:OG	1.44	1.15
1:B:630:ARG:HD3	1:J:540:LYS:HB2	1.23	1.15
1:C:630:ARG:HD3	1:C:630:ARG:C	1.67	1.15
1:D:272:ILE:HG23	1:D:278:LEU:CD1	1.76	1.15
1:J:276:GLU:OE2	1:J:318:PHE:HE2	1.19	1.15
1:D:269:LEU:HD21	1:D:457:SER:CB	1.75	1.15
1:E:285:ILE:CD1	1:E:287:ARG:H	1.59	1.15
1:A:394:LEU:CD2	1:A:395:ALA:HB2	1.76	1.14
1:I:625:SER:HB3	1:I:628:TRP:CD1	1.82	1.14
1:A:540:LYS:CB	1:I:626:PRO:HB3	1.77	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LEU:CD2	1:A:457:SER:CB	2.25	1.14
1:A:269:LEU:CD1	1:A:457:SER:O	1.95	1.14
1:A:285:ILE:HD12	1:A:287:ARG:N	1.62	1.14
1:A:478:ASN:ND2	1:A:482:LYS:HZ1	1.45	1.14
1:H:269:LEU:CD2	1:H:457:SER:OG	1.95	1.14
1:A:537:TYR:HE2	1:I:612:PRO:CG	1.60	1.13
1:D:273:VAL:HG21	1:D:457:SER:HB3	1.29	1.13
1:A:537:TYR:CE2	1:I:612:PRO:HG2	1.81	1.13
1:H:285:ILE:HD13	1:H:287:ARG:HB2	1.21	1.13
1:D:272:ILE:HG23	1:D:278:LEU:HD12	1.13	1.12
1:H:441:LEU:CD2	1:H:498:VAL:CB	2.04	1.12
1:A:540:LYS:CE	1:I:627:TYR:N	2.11	1.12
1:D:426:ILE:HD11	1:D:440:ILE:HG22	1.30	1.12
1:E:478:ASN:ND2	1:E:482:LYS:NZ	1.97	1.12
1:A:269:LEU:CD2	1:A:457:SER:OG	1.97	1.12
1:E:269:LEU:CD1	1:E:457:SER:O	1.98	1.12
1:J:426:ILE:HD13	1:J:440:ILE:HG21	1.16	1.12
1:A:540:LYS:CB	1:I:626:PRO:CB	2.27	1.12
1:D:269:LEU:CD1	1:D:457:SER:O	1.97	1.12
1:A:286:THR:HB	1:A:361:PRO:HB3	1.32	1.11
1:E:441:LEU:HG	1:E:498:VAL:HG12	1.28	1.11
1:H:269:LEU:HD11	1:H:457:SER:O	0.94	1.11
1:D:285:ILE:HD13	1:D:287:ARG:HB2	1.31	1.11
1:H:412:SER:O	1:H:413:ARG:HG3	1.50	1.11
1:A:478:ASN:ND2	1:A:482:LYS:NZ	1.98	1.11
1:E:472:ASN:HD21	1:E:475:ALA:HB3	1.04	1.11
1:H:278:LEU:HD21	1:H:280:LYS:HD3	1.31	1.11
1:H:285:ILE:HD12	1:H:287:ARG:H	0.95	1.10
1:J:426:ILE:HD11	1:J:440:ILE:CG2	1.69	1.10
1:A:394:LEU:HD22	1:A:395:ALA:CB	1.80	1.10
1:E:472:ASN:ND2	1:E:475:ALA:HB3	1.65	1.10
1:H:273:VAL:HG21	1:H:457:SER:HB3	1.30	1.10
1:J:307:PHE:CE1	1:J:345:LEU:HD21	1.85	1.10
1:A:426:ILE:HD13	1:A:440:ILE:HG21	1.30	1.10
1:A:478:ASN:HD21	1:A:482:LYS:NZ	1.48	1.10
1:A:537:TYR:HD1	1:I:630:ARG:NH2	1.50	1.10
1:J:278:LEU:HD21	1:J:280:LYS:HD3	1.10	1.10
1:A:426:ILE:HD11	1:A:440:ILE:HG22	1.34	1.09
1:A:441:LEU:HG	1:A:498:VAL:HG12	1.29	1.09
1:A:540:LYS:HD3	1:I:626:PRO:CA	1.65	1.09
1:A:540:LYS:HB2	1:I:626:PRO:HB3	1.32	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:ILE:HD12	1:D:287:ARG:N	1.65	1.09
1:H:285:ILE:HD12	1:H:287:ARG:N	1.66	1.09
1:G:261:GLN:NE2	1:J:401:THR:HG23	1.68	1.09
1:A:278:LEU:HD21	1:A:280:LYS:HD3	1.35	1.09
1:A:540:LYS:HD3	1:I:626:PRO:CB	1.64	1.09
1:B:781:ALA:HB2	1:E:778:GLY:N	1.68	1.09
1:B:781:ALA:HB2	1:E:778:GLY:CA	1.82	1.08
1:G:642:LEU:HD22	1:G:643:GLY:H	0.94	1.08
1:E:426:ILE:HD13	1:E:440:ILE:HG21	1.32	1.08
1:J:269:LEU:HA	1:J:272:ILE:HD12	1.28	1.08
1:A:540:LYS:HB3	1:I:626:PRO:HG3	1.11	1.08
1:H:377:ARG:HG2	1:H:377:ARG:HH21	1.11	1.08
1:H:407:THR:HG21	1:H:414:ARG:NH1	1.68	1.08
1:A:279:PRO:HG2	1:A:325:LEU:HD21	1.31	1.07
1:A:537:TYR:HE2	1:I:612:PRO:HG2	1.00	1.07
1:D:276:GLU:CD	1:D:318:PHE:HE2	1.62	1.07
1:H:434:PRO:HB3	1:H:491:GLU:HG3	1.34	1.07
1:D:488:HIS:HB3	1:D:491:GLU:HG2	1.34	1.07
1:D:279:PRO:HG2	1:D:325:LEU:HD21	1.18	1.07
1:E:273:VAL:HG21	1:E:457:SER:HB3	1.31	1.07
1:F:357:LEU:HD23	1:F:357:LEU:C	1.79	1.07
1:A:540:LYS:CE	1:I:627:TYR:H	1.68	1.06
1:D:426:ILE:HD12	1:D:440:ILE:HG22	1.37	1.06
1:D:441:LEU:HD23	1:D:498:VAL:CG1	1.84	1.06
1:H:401:THR:CG2	1:H:410:GLN:CG	2.32	1.06
1:D:269:LEU:CD2	1:D:457:SER:OG	2.03	1.06
1:E:279:PRO:HG2	1:E:325:LEU:HD21	1.38	1.06
1:B:630:ARG:HB2	1:J:540:LYS:CG	1.85	1.06
1:B:630:ARG:HE	1:J:540:LYS:HB3	1.14	1.06
1:H:403:LEU:HD23	1:H:403:LEU:H	1.14	1.06
1:A:540:LYS:HE3	1:I:626:PRO:HG2	1.06	1.06
1:H:426:ILE:HD13	1:H:440:ILE:HG21	1.34	1.06
1:H:441:LEU:HD21	1:H:499:SER:H	1.21	1.06
1:J:308:PRO:HG3	1:J:344:ARG:HB2	1.38	1.05
1:D:278:LEU:HD21	1:D:280:LYS:HD3	1.31	1.05
1:D:426:ILE:HD13	1:D:440:ILE:HG21	1.27	1.05
1:H:441:LEU:CG	1:H:498:VAL:HG12	1.86	1.05
1:J:285:ILE:HD13	1:J:287:ARG:CB	1.86	1.05
1:A:269:LEU:CD2	1:A:457:SER:HB2	1.86	1.05
1:A:426:ILE:CD1	1:A:440:ILE:CG2	2.07	1.05
1:A:540:LYS:NZ	1:I:626:PRO:N	2.04	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:272:ILE:HG23	1:H:278:LEU:HD12	1.35	1.05
1:J:285:ILE:CD1	1:J:287:ARG:CB	2.35	1.05
1:D:234:MET:O	1:D:237:ILE:HG22	1.56	1.05
1:I:613:ASP:HB3	1:I:627:TYR:CE1	1.92	1.04
1:A:269:LEU:HD21	1:A:457:SER:HB2	1.35	1.04
1:A:285:ILE:CD1	1:A:287:ARG:CB	2.35	1.04
1:A:540:LYS:HD2	1:I:626:PRO:CD	1.86	1.04
1:A:307:PHE:CE1	1:A:345:LEU:HD21	1.93	1.04
1:E:285:ILE:CD1	1:E:287:ARG:CB	2.30	1.04
1:H:441:LEU:HD21	1:H:499:SER:N	1.73	1.04
1:D:272:ILE:HG22	1:D:277:PHE:HA	1.40	1.03
1:E:233:LYS:N	1:E:233:LYS:HE3	1.72	1.03
1:J:272:ILE:HG23	1:J:278:LEU:HD12	1.34	1.03
1:E:269:LEU:HA	1:E:272:ILE:HD12	1.35	1.03
1:E:441:LEU:CG	1:E:498:VAL:HG12	1.88	1.03
1:H:401:THR:HG22	1:H:410:GLN:CG	1.88	1.03
1:H:478:ASN:HD21	1:H:482:LYS:NZ	1.52	1.03
1:A:540:LYS:HZ2	1:I:626:PRO:CD	1.65	1.03
1:A:537:TYR:CE1	1:I:627:TYR:HB2	1.93	1.03
1:B:878:ASP:HB3	1:B:881:VAL:HG12	1.39	1.03
1:A:540:LYS:HG2	1:I:626:PRO:HD3	1.35	1.02
1:H:426:ILE:HD12	1:H:440:ILE:HG22	1.04	1.02
1:H:441:LEU:HG	1:H:498:VAL:HG12	1.39	1.02
1:A:285:ILE:HD13	1:A:287:ARG:HB2	1.07	1.02
1:B:630:ARG:HE	1:J:540:LYS:CB	1.73	1.02
1:D:276:GLU:OE2	1:D:318:PHE:CE2	2.11	1.02
1:E:272:ILE:HG23	1:E:278:LEU:HD12	1.05	1.02
1:E:486:GLY:O	1:E:489:PRO:HD3	1.59	1.02
1:J:269:LEU:HD21	1:J:457:SER:OG	1.58	1.02
1:A:540:LYS:CD	1:I:626:PRO:HB3	1.89	1.01
1:G:261:GLN:CG	1:J:402:ASP:HB2	1.89	1.01
1:J:284:MET:HG2	1:J:286:THR:CG2	1.89	1.01
1:H:241:LEU:O	1:H:244:VAL:HG23	1.59	1.01
1:A:453:VAL:HG11	1:A:505:LEU:HB2	1.39	1.00
1:A:540:LYS:CG	1:I:626:PRO:HD3	1.87	1.00
1:H:434:PRO:CB	1:H:491:GLU:HG3	1.89	1.00
1:E:278:LEU:HD21	1:E:280:LYS:HD3	1.41	1.00
1:J:251:THR:HG22	1:J:252:LEU:H	1.24	1.00
1:B:488:HIS:HB3	1:B:491:GLU:HG3	1.44	1.00
1:E:472:ASN:HD21	1:E:475:ALA:CB	1.73	1.00
1:D:486:GLY:O	1:D:489:PRO:HD3	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:ILE:HD12	1:D:287:ARG:H	0.85	0.99
1:J:273:VAL:HG11	1:J:457:SER:HB2	1.43	0.99
1:A:393:ILE:HG12	1:A:394:LEU:CA	1.91	0.99
1:A:278:LEU:O	1:A:278:LEU:HD13	1.63	0.98
1:J:278:LEU:HD21	1:J:280:LYS:CD	1.93	0.98
1:E:233:LYS:HE2	1:E:233:LYS:HA	1.46	0.98
1:J:272:ILE:HG23	1:J:278:LEU:HD13	1.43	0.98
1:A:455:VAL:HG12	1:A:501:GLY:H	1.24	0.98
1:A:540:LYS:HZ2	1:I:626:PRO:HD2	1.27	0.98
1:H:279:PRO:HG2	1:H:325:LEU:HD21	1.45	0.98
1:H:486:GLY:O	1:H:489:PRO:HD3	1.63	0.98
1:D:488:HIS:HB3	1:D:491:GLU:CG	1.93	0.98
1:G:261:GLN:HG3	1:J:402:ASP:HB2	1.00	0.98
1:A:235:ILE:O	1:A:235:ILE:HD12	1.63	0.98
1:A:429:MET:HE2	1:A:437:GLY:HA2	1.42	0.98
1:A:285:ILE:HD12	1:A:287:ARG:H	0.83	0.97
1:A:540:LYS:HE3	1:I:626:PRO:CB	1.92	0.97
1:D:286:THR:CB	1:D:361:PRO:HB3	1.94	0.97
1:D:284:MET:HG2	1:D:286:THR:CG2	1.94	0.97
1:E:269:LEU:HD21	1:E:457:SER:OG	1.64	0.97
1:E:426:ILE:HD11	1:E:440:ILE:HG22	0.98	0.97
1:J:284:MET:HG2	1:J:286:THR:HG22	1.44	0.97
1:A:472:ASN:HD21	1:A:475:ALA:HB3	1.29	0.97
1:A:540:LYS:CD	1:I:626:PRO:HD3	1.95	0.97
1:A:540:LYS:HG2	1:I:626:PRO:CD	1.87	0.97
1:E:284:MET:HG2	1:E:286:THR:HG22	1.47	0.97
1:H:285:ILE:CD1	1:H:287:ARG:H	1.78	0.97
1:D:383:CYS:O	1:D:387:ILE:HG13	1.62	0.97
1:I:854:PRO:HB2	1:I:855:ARG:NH2	1.79	0.96
1:J:278:LEU:CD2	1:J:280:LYS:HD3	1.94	0.96
1:A:537:TYR:HD1	1:I:630:ARG:HH21	1.05	0.96
1:H:375:LEU:HD23	1:H:375:LEU:N	1.78	0.96
1:J:363:TYR:HE1	1:J:383:CYS:SG	1.87	0.96
1:D:235:ILE:HD12	1:D:235:ILE:O	1.65	0.96
1:J:229:PHE:CE1	1:J:232:LYS:HD2	1.99	0.96
1:A:276:GLU:CD	1:A:318:PHE:HE2	1.73	0.96
1:A:433:GLU:O	1:A:436:LYS:HB2	1.62	0.96
1:E:278:LEU:CD2	1:E:280:LYS:HD3	1.95	0.96
1:E:284:MET:HG2	1:E:286:THR:CG2	1.94	0.96
1:A:246:GLN:HG2	1:A:247:GLY:N	1.78	0.96
1:D:441:LEU:HG	1:D:498:VAL:HG12	1.48	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:279:PRO:HB3	1:J:322:GLN:CB	1.95	0.96
1:D:363:TYR:HE1	1:D:383:CYS:SG	1.88	0.96
1:E:307:PHE:CE1	1:E:345:LEU:HD21	2.00	0.96
1:I:625:SER:HB3	1:I:628:TRP:HD1	1.25	0.95
1:E:441:LEU:CD2	1:E:498:VAL:CG1	2.40	0.95
1:A:273:VAL:HG21	1:A:457:SER:HB3	1.46	0.95
1:B:261:GLN:H	1:B:261:GLN:CD	1.75	0.95
1:E:285:ILE:CD1	1:E:287:ARG:N	2.21	0.95
1:A:278:LEU:CD2	1:A:280:LYS:HD3	1.97	0.95
1:B:626:PRO:O	1:J:540:LYS:HD2	1.67	0.95
1:E:240:LEU:N	1:E:240:LEU:HD23	1.82	0.95
1:E:376:LYS:NZ	1:E:379:ILE:HD12	1.80	0.95
1:J:488:HIS:HB3	1:J:491:GLU:HG2	1.48	0.95
1:A:540:LYS:CG	1:I:626:PRO:HG3	1.86	0.95
1:E:297:ASP:CG	1:E:300:ALA:HB3	1.92	0.95
1:G:405:ASN:CG	1:J:261:GLN:HB3	1.91	0.94
1:E:269:LEU:CD2	1:E:457:SER:OG	2.15	0.94
1:J:441:LEU:CD2	1:J:498:VAL:CB	2.08	0.94
1:A:540:LYS:HE2	1:I:627:TYR:H	1.23	0.94
1:B:630:ARG:NE	1:J:540:LYS:HB3	1.83	0.94
1:D:251:THR:HG22	1:D:252:LEU:H	1.32	0.94
1:A:540:LYS:CG	1:I:626:PRO:CB	2.45	0.94
1:E:383:CYS:O	1:E:387:ILE:HG13	1.65	0.94
1:A:441:LEU:CG	1:A:498:VAL:HG12	1.97	0.94
1:H:488:HIS:HB3	1:H:491:GLU:HG2	1.50	0.94
1:A:540:LYS:HD3	1:I:626:PRO:HB3	1.45	0.94
1:B:781:ALA:HB2	1:E:778:GLY:HA2	1.47	0.94
1:E:453:VAL:HG11	1:E:505:LEU:HB2	1.50	0.94
1:J:244:VAL:HB	1:J:248:SER:OG	1.67	0.94
1:B:630:ARG:HB2	1:J:540:LYS:HG3	0.95	0.93
1:D:269:LEU:CD2	1:D:457:SER:CB	2.46	0.93
1:E:429:MET:HE2	1:E:437:GLY:HA2	1.49	0.93
1:G:364:ILE:HA	1:J:405:ASN:OD1	1.66	0.93
1:A:393:ILE:HG12	1:A:394:LEU:HA	1.51	0.93
1:G:611:GLU:H	1:G:612:PRO:HD2	1.32	0.93
1:H:269:LEU:HD11	1:H:457:SER:C	1.93	0.93
1:H:273:VAL:HG11	1:H:457:SER:HB2	1.50	0.93
1:H:403:LEU:H	1:H:403:LEU:CD2	1.80	0.93
1:A:441:LEU:CD2	1:A:498:VAL:CB	1.99	0.93
1:D:478:ASN:HD21	1:D:482:LYS:NZ	1.60	0.93
1:H:441:LEU:CD2	1:H:498:VAL:CG1	2.38	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:273:VAL:HG21	1:J:457:SER:HB3	1.51	0.93
1:E:272:ILE:CG2	1:E:278:LEU:HD12	1.98	0.93
1:G:878:ASP:HB3	1:G:881:VAL:HG12	1.51	0.93
1:H:235:ILE:HD12	1:H:235:ILE:O	1.69	0.93
1:D:297:ASP:OD2	1:D:300:ALA:HB3	1.69	0.93
1:J:269:LEU:HD21	1:J:457:SER:CB	1.99	0.93
1:D:244:VAL:HB	1:D:248:SER:OG	1.70	0.92
1:D:441:LEU:CD2	1:D:498:VAL:CB	2.16	0.92
1:H:285:ILE:HD13	1:H:287:ARG:CB	1.99	0.92
1:H:272:ILE:HG22	1:H:277:PHE:HA	1.49	0.92
1:I:903:GLU:HG3	1:I:906:ARG:NH2	1.84	0.92
1:A:537:TYR:CD1	1:I:630:ARG:NH2	2.38	0.92
1:J:285:ILE:HD13	1:J:287:ARG:HB2	0.95	0.92
1:A:540:LYS:NZ	1:I:626:PRO:HD2	1.77	0.92
1:J:363:TYR:HD2	1:J:407:THR:HB	1.31	0.92
1:H:401:THR:HG22	1:H:410:GLN:HG2	0.93	0.92
1:A:472:ASN:ND2	1:A:475:ALA:HB3	1.84	0.91
1:H:272:ILE:HG23	1:H:278:LEU:HD13	1.51	0.91
1:A:485:PHE:CD2	1:A:492:PHE:CD1	2.57	0.91
1:J:878:ASP:HB3	1:J:881:VAL:HG22	1.50	0.91
1:D:269:LEU:O	1:D:273:VAL:HG13	1.69	0.91
1:D:286:THR:HB	1:D:361:PRO:HB3	1.50	0.91
1:H:407:THR:CB	1:H:414:ARG:HD3	1.99	0.91
1:A:375:LEU:N	1:A:375:LEU:HD23	1.81	0.91
1:G:405:ASN:HD21	1:J:260:SER:HB3	1.34	0.91
1:A:540:LYS:HB3	1:I:626:PRO:CB	1.99	0.91
1:J:493:GLY:O	1:J:496:SER:HB3	1.71	0.91
1:B:630:ARG:NE	1:J:540:LYS:CB	2.33	0.91
1:E:269:LEU:CD2	1:E:457:SER:CB	2.49	0.91
1:B:630:ARG:CD	1:J:540:LYS:HB2	1.99	0.90
1:C:260:SER:O	1:C:264:GLY:N	2.04	0.90
1:D:265:LYS:O	1:D:268:VAL:HG23	1.71	0.90
1:A:272:ILE:HG12	1:A:278:LEU:HD11	1.53	0.90
1:G:405:ASN:HB2	1:J:261:GLN:HB3	1.52	0.90
1:C:285:ILE:HD12	1:C:287:ARG:H	1.36	0.90
1:D:276:GLU:OE2	1:D:318:PHE:HE2	1.46	0.90
1:E:229:PHE:CE1	1:E:232:LYS:HD2	2.06	0.90
1:E:485:PHE:CD2	1:E:492:PHE:CD1	2.59	0.90
1:J:434:PRO:CB	1:J:491:GLU:HG3	2.01	0.90
1:A:269:LEU:HD21	1:A:457:SER:OG	1.61	0.90
1:A:394:LEU:HD22	1:A:395:ALA:N	1.87	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:ARG:HD2	1:I:600:ARG:HH12	1.34	0.90
1:A:279:PRO:HB3	1:A:322:GLN:HA	1.52	0.90
1:A:441:LEU:HD21	1:A:499:SER:N	1.87	0.90
1:A:273:VAL:HG11	1:A:457:SER:HB2	1.52	0.90
1:J:376:LYS:HA	1:J:376:LYS:NZ	1.87	0.90
1:E:257:VAL:CG2	1:E:359:ASP:HA	2.01	0.90
1:G:405:ASN:CB	1:J:261:GLN:HB3	2.02	0.90
1:G:642:LEU:CD2	1:G:643:GLY:H	1.81	0.90
1:J:273:VAL:HG11	1:J:457:SER:CB	2.00	0.90
1:E:229:PHE:CD1	1:E:232:LYS:HD2	2.06	0.89
1:A:279:PRO:CB	1:A:322:GLN:HA	2.03	0.89
1:A:394:LEU:CG	1:A:422:THR:OG1	2.21	0.89
1:H:377:ARG:HH21	1:H:377:ARG:CG	1.84	0.89
1:H:407:THR:HB	1:H:414:ARG:CD	2.03	0.89
1:A:272:ILE:CG2	1:A:278:LEU:CD1	2.36	0.89
1:J:276:GLU:CD	1:J:318:PHE:HE2	1.78	0.89
1:B:284:MET:HG2	1:B:286:THR:CG2	2.02	0.89
1:H:474:LEU:HG	1:H:475:ALA:H	1.36	0.88
1:J:286:THR:HB	1:J:361:PRO:HB3	1.55	0.88
1:J:429:MET:HE2	1:J:437:GLY:HA2	1.53	0.88
1:G:878:ASP:HB3	1:G:881:VAL:CG1	2.03	0.88
1:H:407:THR:HG21	1:H:414:ARG:HH11	1.36	0.88
1:D:382:LEU:C	1:D:382:LEU:HD12	1.97	0.88
1:D:434:PRO:CB	1:D:491:GLU:HG3	2.04	0.88
1:E:286:THR:HB	1:E:361:PRO:HB3	1.51	0.88
1:J:279:PRO:CB	1:J:322:GLN:HA	2.04	0.88
1:E:312:LEU:N	1:E:312:LEU:HD23	1.88	0.88
1:A:393:ILE:O	1:A:394:LEU:HB2	1.71	0.88
1:H:285:ILE:CD1	1:H:287:ARG:HB2	2.04	0.88
1:H:434:PRO:HB3	1:H:491:GLU:CG	2.03	0.88
1:J:540:LYS:C	1:J:540:LYS:CE	2.47	0.88
1:H:412:SER:OG	1:H:413:ARG:HD3	1.72	0.88
1:J:229:PHE:HA	1:J:232:LYS:CG	2.04	0.88
1:A:540:LYS:HG2	1:I:626:PRO:CG	2.03	0.88
1:J:229:PHE:CE2	1:J:233:LYS:HD2	2.09	0.87
1:D:277:PHE:HD1	1:D:278:LEU:N	1.73	0.87
1:D:441:LEU:CG	1:D:498:VAL:HG12	2.04	0.87
1:J:279:PRO:HB3	1:J:322:GLN:CA	2.04	0.87
1:A:485:PHE:HD2	1:A:492:PHE:O	1.55	0.87
1:A:610:ARG:HA	1:A:610:ARG:HE	1.38	0.87
1:H:269:LEU:HD23	1:H:270:GLU:N	1.89	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:269:LEU:HD23	1:J:270:GLU:N	1.90	0.87
1:B:261:GLN:H	1:B:261:GLN:NE2	1.73	0.87
1:E:229:PHE:HA	1:E:232:LYS:HG2	1.57	0.87
1:E:376:LYS:HZ1	1:E:379:ILE:HD12	1.36	0.87
1:E:441:LEU:HD21	1:E:499:SER:N	1.90	0.87
1:C:630:ARG:C	1:C:630:ARG:CD	2.48	0.87
1:F:357:LEU:C	1:F:357:LEU:CD2	2.47	0.87
1:F:260:SER:O	1:F:264:GLY:N	2.08	0.86
1:H:307:PHE:CE1	1:H:345:LEU:HD21	2.10	0.86
1:J:441:LEU:HD21	1:J:499:SER:H	1.40	0.86
1:H:269:LEU:CD2	1:H:457:SER:CB	2.47	0.86
1:H:401:THR:HG21	1:H:410:GLN:CG	2.02	0.86
1:J:478:ASN:HD21	1:J:482:LYS:HZ1	0.89	0.86
1:A:267:SER:HB3	1:A:396:ILE:HG13	1.56	0.86
1:J:286:THR:CB	1:J:361:PRO:HB3	2.04	0.86
1:A:394:LEU:HD22	1:A:395:ALA:CA	2.05	0.86
1:G:261:GLN:HG3	1:J:402:ASP:CB	1.97	0.86
1:J:269:LEU:CD2	1:J:457:SER:OG	2.23	0.86
1:E:272:ILE:HG21	1:E:277:PHE:HD1	1.40	0.86
1:E:441:LEU:HD21	1:E:499:SER:H	1.36	0.86
1:J:383:CYS:O	1:J:387:ILE:HG13	1.75	0.86
1:E:241:LEU:O	1:E:244:VAL:HG23	1.75	0.85
1:E:455:VAL:HG12	1:E:501:GLY:H	1.41	0.85
1:H:287:ARG:HH11	1:H:287:ARG:HG3	1.40	0.85
1:A:269:LEU:O	1:A:273:VAL:HG13	1.76	0.85
1:E:426:ILE:HD11	1:E:440:ILE:CG2	1.86	0.85
1:H:363:TYR:HE1	1:H:383:CYS:SG	1.98	0.85
1:E:269:LEU:HD21	1:E:457:SER:HB2	1.57	0.85
1:H:377:ARG:HG2	1:H:377:ARG:NH2	1.92	0.85
1:D:251:THR:HG22	1:D:252:LEU:N	1.91	0.85
1:E:363:TYR:HE1	1:E:383:CYS:SG	2.00	0.85
1:I:903:GLU:HG3	1:I:906:ARG:HH22	1.41	0.85
1:A:326:THR:HA	1:A:329:ASN:ND2	1.90	0.85
1:A:441:LEU:HD21	1:A:498:VAL:HB	1.55	0.85
1:B:286:THR:HB	1:B:361:PRO:HB3	1.58	0.85
1:F:376:LYS:NZ	1:F:379:ILE:HD12	1.91	0.85
1:G:402:ASP:HB2	1:J:261:GLN:CG	2.07	0.85
1:J:453:VAL:HG11	1:J:505:LEU:HB2	1.56	0.85
1:A:286:THR:HB	1:A:361:PRO:CB	2.07	0.85
1:D:441:LEU:HD21	1:D:499:SER:N	1.91	0.85
1:A:455:VAL:HG12	1:A:501:GLY:N	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:434:PRO:HG2	1:J:488:HIS:CG	2.11	0.85
1:G:615:ILE:HD11	1:G:803:ARG:HE	1.41	0.84
1:A:251:THR:HG22	1:A:252:LEU:H	1.40	0.84
1:A:297:ASP:CG	1:A:300:ALA:HB3	2.03	0.84
1:H:401:THR:HG21	1:H:410:GLN:HG2	1.52	0.84
1:J:441:LEU:HD21	1:J:499:SER:N	1.92	0.84
1:A:278:LEU:HD21	1:A:280:LYS:CD	2.07	0.84
1:J:279:PRO:HB3	1:J:322:GLN:HA	1.58	0.84
1:A:279:PRO:HB3	1:A:322:GLN:CA	2.07	0.84
1:A:286:THR:CB	1:A:361:PRO:HB3	2.07	0.84
1:B:284:MET:O	1:B:286:THR:HG23	1.75	0.84
1:D:273:VAL:HG11	1:D:457:SER:HB2	1.59	0.84
1:F:879:PRO:HG3	1:H:630:ARG:HD2	1.60	0.84
1:B:630:ARG:HD3	1:J:540:LYS:CB	2.05	0.84
1:D:375:LEU:N	1:D:375:LEU:HD23	1.92	0.84
1:B:488:HIS:HB3	1:B:491:GLU:CG	2.08	0.84
1:D:278:LEU:HD21	1:D:280:LYS:CD	2.06	0.84
1:H:308:PRO:HG3	1:H:344:ARG:HB2	1.59	0.84
1:B:630:ARG:CD	1:J:540:LYS:CB	2.56	0.84
1:J:279:PRO:HB3	1:J:322:GLN:HB2	1.60	0.84
1:H:610:ARG:HA	1:H:610:ARG:HE	1.43	0.84
1:A:537:TYR:CE2	1:I:612:PRO:CG	2.52	0.84
1:E:269:LEU:O	1:E:273:VAL:HG13	1.77	0.84
1:D:279:PRO:HB3	1:D:322:GLN:CB	2.07	0.83
1:D:478:ASN:CG	1:D:482:LYS:NZ	2.36	0.83
1:E:235:ILE:HD12	1:E:235:ILE:O	1.77	0.83
1:A:394:LEU:HB3	1:A:423:ILE:O	1.77	0.83
1:D:284:MET:HG2	1:D:286:THR:HG22	1.59	0.83
1:G:687:LEU:HD22	1:G:845:MET:HE2	1.57	0.83
1:H:286:THR:O	1:H:361:PRO:HB3	1.77	0.83
1:H:441:LEU:HB3	1:H:498:VAL:HG11	1.59	0.83
1:J:434:PRO:HB2	1:J:491:GLU:HG3	1.60	0.83
1:H:363:TYR:HE1	1:H:383:CYS:HG	0.86	0.83
1:E:251:THR:HG22	1:E:252:LEU:H	1.40	0.83
1:A:363:TYR:HE1	1:A:383:CYS:SG	2.02	0.83
1:A:537:TYR:HA	1:I:630:ARG:CZ	2.08	0.83
1:D:269:LEU:CD2	1:D:457:SER:HB2	2.08	0.83
1:A:426:ILE:HD12	1:A:440:ILE:HG22	1.55	0.82
1:J:272:ILE:HG22	1:J:277:PHE:HA	1.60	0.82
1:D:278:LEU:CD2	1:D:280:LYS:HD3	2.09	0.82
1:E:233:LYS:HE2	1:E:233:LYS:CA	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:284:MET:N	1:H:284:MET:SD	2.48	0.82
1:B:843:VAL:O	1:B:847:ASN:HB2	1.80	0.82
1:G:402:ASP:HB2	1:J:261:GLN:HG3	1.59	0.82
1:E:339:THR:HG23	1:E:340:ASP:N	1.94	0.82
1:H:434:PRO:HG2	1:H:488:HIS:ND1	1.93	0.82
1:E:233:LYS:CA	1:E:233:LYS:CE	2.57	0.82
1:G:611:GLU:N	1:G:612:PRO:HD2	1.93	0.82
1:B:878:ASP:HB3	1:B:881:VAL:CG1	2.10	0.82
1:D:285:ILE:CD1	1:D:287:ARG:CB	2.54	0.82
1:E:272:ILE:HG22	1:E:277:PHE:HA	1.61	0.81
1:F:480:ASN:HA	1:F:483:ASN:OD1	1.80	0.81
1:H:403:LEU:HD23	1:H:403:LEU:N	1.94	0.81
1:J:229:PHE:HA	1:J:232:LYS:HG2	1.62	0.81
1:A:240:LEU:N	1:A:240:LEU:HD23	1.93	0.81
1:B:574:ARG:NH2	1:B:842:ASN:ND2	2.28	0.81
1:C:578:GLN:HA	1:C:838:VAL:HG21	1.60	0.81
1:D:267:SER:HB3	1:D:396:ILE:HG13	1.61	0.81
1:E:233:LYS:N	1:E:233:LYS:CE	2.42	0.81
1:H:434:PRO:HG2	1:H:488:HIS:CG	2.15	0.81
1:E:285:ILE:HD12	1:E:287:ARG:CA	2.09	0.81
1:H:455:VAL:HG12	1:H:501:GLY:H	1.44	0.81
1:A:269:LEU:HD21	1:A:457:SER:CA	2.11	0.81
1:D:229:PHE:HA	1:D:232:LYS:HG2	1.60	0.81
1:D:287:ARG:HH11	1:D:287:ARG:HG3	1.44	0.81
1:H:257:VAL:CG2	1:H:359:ASP:HA	2.10	0.81
1:H:572:PHE:O	1:H:576:GLN:NE2	2.13	0.81
1:J:272:ILE:CG2	1:J:278:LEU:CD1	2.56	0.81
1:J:363:TYR:CD2	1:J:407:THR:HB	2.15	0.81
1:J:426:ILE:HD11	1:J:440:ILE:HG22	0.82	0.81
1:E:749:LYS:H	1:E:749:LYS:HD2	1.45	0.81
1:A:232:LYS:HG3	1:A:233:LYS:HE3	1.61	0.81
1:G:605:LEU:HD22	1:G:606:SER:O	1.79	0.81
1:A:540:LYS:HZ2	1:I:626:PRO:N	1.75	0.81
1:E:441:LEU:CG	1:E:498:VAL:CG1	2.58	0.81
1:J:441:LEU:CD2	1:J:498:VAL:CG1	2.48	0.81
1:H:278:LEU:HD22	1:H:279:PRO:O	1.81	0.81
1:H:388:ARG:O	1:H:421:ARG:NH2	2.13	0.81
1:H:441:LEU:CG	1:H:498:VAL:CG1	2.59	0.81
1:I:235:ILE:HD13	1:I:356:SER:HB2	1.61	0.81
1:E:269:LEU:CD2	1:E:457:SER:HB2	2.11	0.80
1:J:485:PHE:CD2	1:J:492:PHE:CD1	2.69	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:611:GLU:N	1:C:612:PRO:HD2	1.95	0.80
1:D:278:LEU:HD22	1:D:279:PRO:O	1.81	0.80
1:J:441:LEU:CG	1:J:498:VAL:HG12	2.11	0.80
1:C:616:ILE:HG23	1:C:617:ASP:OD1	1.81	0.80
1:G:322:GLN:O	1:G:326:THR:OG1	1.99	0.80
1:J:279:PRO:HG2	1:J:325:LEU:HD21	1.62	0.80
1:J:279:PRO:O	1:J:280:LYS:HD2	1.82	0.80
1:B:863:GLU:O	1:B:867:ALA:HB3	1.81	0.80
1:D:376:LYS:HA	1:D:376:LYS:NZ	1.96	0.80
1:D:269:LEU:HA	1:D:272:ILE:HD12	1.60	0.80
1:J:441:LEU:HD22	1:J:498:VAL:HB	1.60	0.80
1:G:405:ASN:CG	1:J:261:GLN:CB	2.53	0.80
1:E:244:VAL:HB	1:E:248:SER:OG	1.82	0.80
1:A:383:CYS:O	1:A:387:ILE:HG13	1.80	0.80
1:A:537:TYR:HE1	1:I:627:TYR:N	1.79	0.80
1:J:269:LEU:HA	1:J:272:ILE:CD1	2.11	0.80
1:A:279:PRO:HG2	1:A:325:LEU:CD2	2.12	0.80
1:J:232:LYS:HA	1:J:235:ILE:CG2	2.11	0.80
1:J:269:LEU:HD23	1:J:269:LEU:C	2.07	0.80
1:D:480:ASN:HA	1:D:483:ASN:OD1	1.82	0.80
1:H:233:LYS:HE2	1:H:233:LYS:HA	1.62	0.80
1:H:363:TYR:HD2	1:H:408:ALA:HB2	1.47	0.80
1:A:454:GLY:O	1:A:500:THR:HB	1.81	0.79
1:A:537:TYR:CE1	1:A:540:LYS:HE3	2.17	0.79
1:A:540:LYS:HD3	1:I:626:PRO:HA	1.64	0.79
1:A:441:LEU:HD21	1:A:499:SER:H	1.46	0.79
1:D:272:ILE:CG2	1:D:277:PHE:HA	2.12	0.79
1:A:231:THR:O	1:A:235:ILE:HG22	1.82	0.79
1:D:478:ASN:HD21	1:D:482:LYS:HZ1	0.80	0.79
1:E:229:PHE:CG	1:E:232:LYS:HD2	2.16	0.79
1:E:434:PRO:HG2	1:E:488:HIS:ND1	1.97	0.79
1:D:277:PHE:HD1	1:D:278:LEU:H	1.27	0.79
1:D:279:PRO:CG	1:D:325:LEU:HD21	2.07	0.79
1:E:441:LEU:HB3	1:E:498:VAL:HG11	1.63	0.79
1:H:272:ILE:HG21	1:H:277:PHE:HD1	1.47	0.79
1:E:278:LEU:HB2	1:E:279:PRO:HD2	1.65	0.79
1:E:478:ASN:CG	1:E:482:LYS:NZ	2.40	0.79
1:E:269:LEU:HD11	1:E:457:SER:C	2.05	0.79
1:H:273:VAL:HG11	1:H:457:SER:CB	2.12	0.79
1:J:441:LEU:HD23	1:J:498:VAL:CA	2.10	0.79
1:A:286:THR:O	1:A:361:PRO:HB3	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:LEU:HG	1:A:422:THR:HG1	1.48	0.79
1:D:286:THR:OG1	1:D:361:PRO:HB3	1.83	0.79
1:A:485:PHE:CD2	1:A:492:PHE:HD1	1.99	0.79
1:E:434:PRO:CB	1:E:491:GLU:HG3	2.13	0.78
1:H:276:GLU:OE2	1:H:318:PHE:HE2	1.65	0.78
1:A:572:PHE:O	1:A:576:GLN:NE2	2.16	0.78
1:D:286:THR:O	1:D:361:PRO:CG	2.32	0.78
1:E:279:PRO:HB3	1:E:322:GLN:CB	2.14	0.78
1:H:485:PHE:HD2	1:H:492:PHE:O	1.65	0.78
1:J:434:PRO:HG2	1:J:488:HIS:ND1	1.98	0.78
1:D:429:MET:HE2	1:D:437:GLY:HA2	1.65	0.78
1:A:445:GLN:O	1:A:446:TYR:CD1	2.37	0.78
1:A:694:THR:HG21	1:A:845:MET:HB2	1.64	0.78
1:E:272:ILE:HG21	1:E:277:PHE:CD1	2.18	0.78
1:H:244:VAL:HB	1:H:248:SER:OG	1.83	0.78
1:H:279:PRO:HB3	1:H:322:GLN:CB	2.14	0.78
1:I:284:MET:HG2	1:I:286:THR:CG2	2.13	0.78
1:J:478:ASN:CG	1:J:482:LYS:HZ2	1.91	0.78
1:E:376:LYS:HA	1:E:376:LYS:HZ3	1.48	0.78
1:A:279:PRO:HB3	1:A:322:GLN:CB	2.13	0.78
1:C:322:GLN:O	1:C:326:THR:OG1	1.99	0.78
1:C:609:PRO:HB2	1:C:610:ARG:C	2.09	0.78
1:E:285:ILE:HD13	1:E:287:ARG:HB2	0.82	0.78
1:A:434:PRO:HB3	1:A:491:GLU:HG3	1.66	0.78
1:E:286:THR:CB	1:E:361:PRO:HB3	2.13	0.78
1:G:578:GLN:HA	1:G:838:VAL:HG21	1.65	0.78
1:J:241:LEU:O	1:J:244:VAL:HG23	1.84	0.78
1:A:537:TYR:HE1	1:I:627:TYR:H	1.32	0.78
1:D:434:PRO:HB3	1:D:491:GLU:CB	2.13	0.78
1:E:279:PRO:CB	1:E:322:GLN:HA	2.13	0.78
1:H:278:LEU:CD2	1:H:280:LYS:HD3	2.10	0.78
1:J:285:ILE:CD1	1:J:287:ARG:N	2.19	0.78
1:B:258:ILE:HG22	1:B:360:LEU:HD11	1.64	0.77
1:D:272:ILE:CG2	1:D:278:LEU:HD12	2.05	0.77
1:D:276:GLU:CD	1:D:318:PHE:CE2	2.53	0.77
1:E:234:MET:O	1:E:237:ILE:HG22	1.83	0.77
1:H:276:GLU:OE2	1:H:318:PHE:CE2	2.37	0.77
1:A:268:VAL:O	1:A:272:ILE:HG13	1.85	0.77
1:E:279:PRO:HB3	1:E:322:GLN:HA	1.64	0.77
1:I:618:LEU:HD22	1:I:628:TRP:CE3	2.19	0.77
1:C:611:GLU:H	1:C:612:PRO:HD2	1.50	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:269:LEU:HA	1:H:272:ILE:HD12	1.65	0.77
1:A:574:ARG:H	1:A:575:PRO:HD2	1.49	0.77
1:D:269:LEU:HD21	1:D:457:SER:HB2	1.65	0.77
1:G:402:ASP:CB	1:J:261:GLN:CG	2.63	0.77
1:I:285:ILE:HD13	1:I:332:VAL:HG22	1.66	0.77
1:B:284:MET:N	1:B:284:MET:SD	2.57	0.77
1:I:618:LEU:CD2	1:I:628:TRP:CE3	2.68	0.77
1:A:657:GLN:HE22	1:A:684:ALA:HA	1.48	0.76
1:B:260:SER:O	1:B:264:GLY:N	2.17	0.76
1:D:285:ILE:CD1	1:D:287:ARG:N	2.37	0.76
1:E:272:ILE:HG12	1:E:278:LEU:CD1	2.15	0.76
1:F:843:VAL:O	1:F:847:ASN:HB2	1.85	0.76
1:G:402:ASP:CB	1:J:261:GLN:HG2	2.15	0.76
1:H:682:ALA:O	1:H:685:THR:HG22	1.84	0.76
1:J:286:THR:O	1:J:361:PRO:HB3	1.84	0.76
1:D:286:THR:O	1:D:361:PRO:HG3	1.86	0.76
1:D:441:LEU:HB3	1:D:498:VAL:HG11	1.66	0.76
1:G:609:PRO:HB2	1:G:610:ARG:C	2.11	0.76
1:H:246:GLN:HG2	1:H:247:GLY:N	2.00	0.76
1:H:258:ILE:HG22	1:H:360:LEU:HD11	1.67	0.76
1:D:453:VAL:HG11	1:D:505:LEU:HB2	1.65	0.76
1:E:269:LEU:CA	1:E:272:ILE:HD12	2.14	0.76
1:E:376:LYS:HE2	1:E:376:LYS:N	2.01	0.76
1:H:441:LEU:HB3	1:H:498:VAL:CG1	2.15	0.76
1:A:441:LEU:CD2	1:A:498:VAL:CG1	2.48	0.76
1:A:537:TYR:HE1	1:I:627:TYR:HB2	1.50	0.76
1:E:251:THR:HG22	1:E:252:LEU:N	2.01	0.76
1:F:434:PRO:HG2	1:F:488:HIS:CG	2.20	0.76
1:I:285:ILE:HD12	1:I:287:ARG:H	1.49	0.76
1:D:264:GLY:O	1:D:268:VAL:HG22	1.85	0.76
1:E:275:HIS:CG	1:E:276:GLU:H	2.03	0.76
1:J:251:THR:HG22	1:J:252:LEU:N	1.92	0.76
1:D:285:ILE:HG13	1:D:286:THR:H	1.51	0.76
1:H:240:LEU:HD23	1:H:240:LEU:N	2.00	0.76
1:D:277:PHE:CD1	1:D:278:LEU:N	2.53	0.76
1:H:278:LEU:HD21	1:H:280:LYS:CD	2.15	0.76
1:I:642:LEU:HD22	1:I:643:GLY:H	1.50	0.76
1:D:436:LYS:O	1:D:440:ILE:HG13	1.85	0.76
1:E:455:VAL:HG12	1:E:501:GLY:N	2.01	0.76
1:F:357:LEU:HD23	1:F:358:ILE:N	2.00	0.76
1:I:260:SER:O	1:I:264:GLY:N	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:627:TYR:HD2	1:I:628:TRP:CZ3	2.04	0.76
1:J:478:ASN:ND2	1:J:482:LYS:HZ2	1.83	0.76
1:H:237:ILE:O	1:H:237:ILE:HD13	1.86	0.75
1:J:235:ILE:HD12	1:J:235:ILE:O	1.86	0.75
1:E:284:MET:O	1:E:284:MET:SD	2.43	0.75
1:G:261:GLN:NE2	1:J:405:ASN:CB	2.50	0.75
1:J:376:LYS:HA	1:J:376:LYS:HZ3	1.51	0.75
1:E:485:PHE:CE2	1:E:500:THR:OG1	2.39	0.75
1:I:627:TYR:C	1:I:628:TRP:CE3	2.64	0.75
1:D:441:LEU:HB3	1:D:498:VAL:CG1	2.16	0.75
1:E:273:VAL:HG11	1:E:457:SER:HB2	1.67	0.75
1:E:285:ILE:CD1	1:E:287:ARG:CA	2.64	0.75
1:G:261:GLN:HB3	1:J:405:ASN:ND2	2.01	0.75
1:G:364:ILE:CA	1:J:405:ASN:OD1	2.33	0.75
1:G:585:LEU:HD12	1:G:834:ALA:HB2	1.67	0.75
1:I:664:LEU:HD23	1:I:676:ARG:HG3	1.69	0.75
1:J:478:ASN:HD21	1:J:482:LYS:NZ	1.67	0.75
1:C:235:ILE:HD13	1:C:356:SER:HB2	1.69	0.75
1:D:434:PRO:HB3	1:D:491:GLU:HG3	1.68	0.75
1:E:229:PHE:CZ	1:E:232:LYS:HD2	2.20	0.75
1:A:394:LEU:HD21	1:A:395:ALA:HB2	1.67	0.75
1:B:781:ALA:N	1:E:778:GLY:HA3	2.02	0.75
1:D:279:PRO:HG2	1:D:325:LEU:CD2	2.10	0.75
1:D:445:GLN:O	1:D:446:TYR:CD1	2.40	0.75
1:D:441:LEU:CD2	1:D:498:VAL:CG1	2.60	0.75
1:D:572:PHE:O	1:D:576:GLN:NE2	2.19	0.75
1:H:453:VAL:HG11	1:H:505:LEU:HB2	1.69	0.75
1:A:363:TYR:CE1	1:A:383:CYS:SG	2.79	0.74
1:A:441:LEU:CG	1:A:498:VAL:CG1	2.64	0.74
1:B:781:ALA:CB	1:E:778:GLY:CA	2.64	0.74
1:E:308:PRO:HG3	1:E:344:ARG:HB2	1.69	0.74
1:H:272:ILE:CG2	1:H:278:LEU:CD1	2.62	0.74
1:A:485:PHE:CE2	1:A:500:THR:OG1	2.38	0.74
1:C:611:GLU:H	1:C:612:PRO:CD	2.00	0.74
1:I:284:MET:SD	1:I:284:MET:N	2.59	0.74
1:J:441:LEU:HG	1:J:498:VAL:HG12	1.66	0.74
1:J:540:LYS:CE	1:J:540:LYS:O	2.35	0.74
1:G:261:GLN:HB3	1:J:405:ASN:CG	2.12	0.74
1:I:843:VAL:O	1:I:847:ASN:HB2	1.87	0.74
1:E:267:SER:HB3	1:E:396:ILE:HG13	1.68	0.74
1:J:231:THR:O	1:J:235:ILE:HG22	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:237:ILE:HD13	1:J:237:ILE:O	1.87	0.74
1:C:854:PRO:HB2	1:C:855:ARG:NH2	2.03	0.74
1:D:285:ILE:HG13	1:D:286:THR:N	2.02	0.74
1:F:739:LYS:HD2	1:F:742:GLU:OE1	1.86	0.74
1:H:269:LEU:HD21	1:H:457:SER:HB2	1.65	0.74
1:H:377:ARG:CG	1:H:377:ARG:NH2	2.47	0.74
1:J:485:PHE:HD2	1:J:492:PHE:O	1.71	0.74
1:G:260:SER:O	1:G:264:GLY:N	2.21	0.74
1:G:261:GLN:NE2	1:J:401:THR:CG2	2.49	0.74
1:J:434:PRO:HB3	1:J:491:GLU:HG3	1.70	0.74
1:A:272:ILE:HG23	1:A:278:LEU:HD12	0.76	0.74
1:D:278:LEU:HB2	1:D:279:PRO:HD2	1.70	0.74
1:J:273:VAL:CG1	1:J:457:SER:HB2	2.17	0.74
1:J:284:MET:N	1:J:284:MET:SD	2.54	0.74
1:E:339:THR:HG23	1:E:340:ASP:H	1.52	0.74
1:J:270:GLU:O	1:J:273:VAL:HG22	1.87	0.74
1:A:394:LEU:CD2	1:A:395:ALA:CB	2.53	0.74
1:B:781:ALA:HB2	1:E:778:GLY:H	1.51	0.74
1:G:453:VAL:HG11	1:G:505:LEU:HB2	1.70	0.74
1:J:485:PHE:CE2	1:J:500:THR:OG1	2.39	0.74
1:G:605:LEU:CD2	1:G:606:SER:O	2.36	0.74
1:J:246:GLN:HG2	1:J:247:GLY:N	2.02	0.74
1:J:486:GLY:O	1:J:489:PRO:HD3	1.88	0.74
1:D:230:ILE:O	1:D:234:MET:HG3	1.87	0.73
1:D:279:PRO:HB3	1:D:322:GLN:HB2	1.70	0.73
1:E:434:PRO:HG2	1:E:488:HIS:CG	2.22	0.73
1:G:611:GLU:H	1:G:612:PRO:CD	2.00	0.73
1:E:434:PRO:HB3	1:E:491:GLU:CB	2.19	0.73
1:A:238:ARG:NH2	1:A:356:SER:OG	2.21	0.73
1:A:244:VAL:HB	1:A:248:SER:OG	1.88	0.73
1:E:232:LYS:C	1:E:233:LYS:HE3	2.13	0.73
1:H:269:LEU:CD2	1:H:457:SER:HB2	2.17	0.73
1:H:285:ILE:CD1	1:H:287:ARG:N	2.45	0.73
1:A:393:ILE:HG12	1:A:394:LEU:N	1.95	0.73
1:H:269:LEU:O	1:H:273:VAL:HG13	1.87	0.73
1:H:610:ARG:HA	1:H:610:ARG:NE	2.02	0.73
1:J:480:ASN:HA	1:J:483:ASN:OD1	1.89	0.73
1:A:255:ILE:HD11	1:A:355:LEU:HG	1.70	0.73
1:A:488:HIS:HB3	1:A:491:GLU:HG2	1.69	0.73
1:B:630:ARG:NH1	1:J:537:TYR:HD1	1.86	0.73
1:A:285:ILE:CD1	1:A:287:ARG:N	2.35	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ILE:CG1	1:A:394:LEU:HA	2.19	0.73
1:C:258:ILE:HG22	1:C:360:LEU:HD11	1.69	0.73
1:G:642:LEU:CD2	1:G:643:GLY:N	2.47	0.73
1:J:339:THR:HG23	1:J:340:ASP:N	2.02	0.73
1:F:610:ARG:HD2	1:F:613:ASP:OD1	1.89	0.73
1:G:285:ILE:HD12	1:G:287:ARG:H	1.54	0.73
1:J:478:ASN:CG	1:J:482:LYS:NZ	2.45	0.73
1:J:285:ILE:HD11	1:J:287:ARG:HB2	1.68	0.73
1:J:363:TYR:HE1	1:J:383:CYS:HG	0.79	0.73
1:A:269:LEU:HA	1:A:272:ILE:HD12	1.69	0.73
1:J:352:ILE:HD12	1:J:352:ILE:O	1.89	0.73
1:A:307:PHE:CE1	1:A:345:LEU:CD2	2.72	0.72
1:A:540:LYS:NZ	1:I:627:TYR:H	1.85	0.72
1:H:376:LYS:HA	1:H:376:LYS:HZ2	1.54	0.72
1:A:251:THR:HG22	1:A:252:LEU:N	2.02	0.72
1:A:376:LYS:N	1:A:376:LYS:HE2	2.04	0.72
1:A:610:ARG:HA	1:A:610:ARG:NE	2.05	0.72
1:H:238:ARG:HA	1:H:241:LEU:HD12	1.72	0.72
1:H:488:HIS:HB3	1:H:491:GLU:CG	2.18	0.72
1:A:284:MET:SD	1:A:284:MET:N	2.60	0.72
1:A:707:PHE:CZ	1:B:847:ASN:ND2	2.58	0.72
1:C:630:ARG:HD3	1:C:631:GLN:N	2.04	0.72
1:D:485:PHE:HD2	1:D:492:PHE:O	1.73	0.72
1:C:627:TYR:HE2	1:C:628:TRP:CZ3	2.08	0.72
1:E:279:PRO:HB3	1:E:322:GLN:CA	2.19	0.72
1:J:285:ILE:CD1	1:J:287:ARG:CA	2.67	0.72
1:E:229:PHE:CE1	1:E:232:LYS:CE	2.73	0.72
1:H:238:ARG:NH2	1:H:356:SER:OG	2.23	0.72
1:I:626:PRO:HB2	1:I:630:ARG:HE	1.53	0.72
1:J:286:THR:O	1:J:361:PRO:CG	2.37	0.72
1:A:272:ILE:HG22	1:A:277:PHE:HA	1.70	0.72
1:E:230:ILE:O	1:E:234:MET:HG3	1.89	0.72
1:G:405:ASN:ND2	1:J:261:GLN:H	1.87	0.72
1:I:615:ILE:HD11	1:I:803:ARG:HE	1.54	0.72
1:A:540:LYS:HE2	1:I:626:PRO:CB	2.14	0.72
1:G:364:ILE:HG23	1:J:405:ASN:OD1	1.90	0.72
1:H:233:LYS:N	1:H:233:LYS:HE3	2.04	0.72
1:A:257:VAL:CG2	1:A:359:ASP:HA	2.19	0.72
1:A:297:ASP:OD2	1:A:300:ALA:HB3	1.90	0.72
1:A:396:ILE:HG22	1:A:425:VAL:HB	1.72	0.72
1:G:261:GLN:NE2	1:J:405:ASN:HB3	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:LYS:CG	1:I:626:PRO:HB3	2.17	0.71
1:B:863:GLU:O	1:B:867:ALA:CB	2.38	0.71
1:E:229:PHE:CD1	1:E:232:LYS:HE3	2.25	0.71
1:A:273:VAL:HG21	1:A:457:SER:CB	2.19	0.71
1:A:278:LEU:HB2	1:A:279:PRO:HD2	1.70	0.71
1:B:781:ALA:CB	1:E:778:GLY:N	2.48	0.71
1:F:610:ARG:HB2	1:F:611:GLU:HA	1.72	0.71
1:A:273:VAL:HG11	1:A:457:SER:CB	2.20	0.71
1:A:778:GLY:C	1:A:779:PHE:HD2	1.98	0.71
1:B:609:PRO:HB2	1:B:610:ARG:C	2.15	0.71
1:H:485:PHE:CD2	1:H:492:PHE:CD1	2.78	0.71
1:D:287:ARG:HH11	1:D:287:ARG:CG	2.03	0.71
1:E:297:ASP:OD2	1:E:300:ALA:HB3	1.90	0.71
1:G:530:ARG:HG2	1:G:530:ARG:HH11	1.55	0.71
1:B:239:ASN:HD21	1:B:293:THR:HG21	1.56	0.71
1:E:376:LYS:NZ	1:E:376:LYS:HA	2.05	0.71
1:H:376:LYS:HA	1:H:376:LYS:NZ	2.06	0.71
1:J:308:PRO:CG	1:J:344:ARG:HB2	2.17	0.71
1:D:272:ILE:CG2	1:D:278:LEU:CD1	2.65	0.71
1:D:853:PHE:HB3	1:D:854:PRO:HD3	1.71	0.71
1:H:294:LEU:HB3	1:H:352:ILE:HD13	1.70	0.71
1:H:413:ARG:NH1	1:H:446:TYR:CE1	2.58	0.71
1:A:434:PRO:CB	1:A:491:GLU:HG3	2.21	0.71
1:B:626:PRO:C	1:J:540:LYS:HD2	2.16	0.71
1:E:229:PHE:CE1	1:E:232:LYS:CD	2.74	0.71
1:H:275:HIS:CG	1:H:276:GLU:H	2.08	0.71
1:H:397:SER:HB3	1:H:411:ALA:HB1	1.71	0.71
1:A:434:PRO:HG2	1:A:488:HIS:CG	2.26	0.71
1:A:454:GLY:H	1:A:500:THR:HG22	1.56	0.71
1:D:272:ILE:HG23	1:D:278:LEU:H	1.55	0.71
1:D:363:TYR:CE1	1:D:383:CYS:SG	2.73	0.71
1:E:889:ARG:HG3	1:E:890:ARG:N	2.04	0.71
1:A:376:LYS:NZ	1:A:379:ILE:HD12	2.05	0.71
1:C:672:HIS:HD2	1:C:877:GLU:HB2	1.56	0.71
1:H:236:GLU:O	1:H:239:ASN:HB2	1.91	0.71
1:I:259:GLY:HA2	1:I:408:ALA:HB2	1.73	0.71
1:I:628:TRP:CD2	1:I:628:TRP:N	2.53	0.71
1:F:453:VAL:HG11	1:F:505:LEU:HB2	1.73	0.70
1:H:268:VAL:O	1:H:272:ILE:HG13	1.89	0.70
1:J:441:LEU:HB3	1:J:498:VAL:CG1	2.20	0.70
1:B:285:ILE:HD12	1:B:287:ARG:H	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:279:PRO:CB	1:D:322:GLN:HA	2.20	0.70
1:E:485:PHE:HD2	1:E:492:PHE:O	1.73	0.70
1:H:429:MET:HE2	1:H:437:GLY:HA2	1.72	0.70
1:H:441:LEU:HD23	1:H:498:VAL:HB	0.71	0.70
1:J:441:LEU:HB3	1:J:498:VAL:HG11	1.70	0.70
1:G:605:LEU:HD22	1:G:606:SER:N	2.05	0.70
1:H:474:LEU:HG	1:H:475:ALA:N	2.07	0.70
1:C:665:ASP:OD1	1:C:676:ARG:NH1	2.24	0.70
1:D:775:GLY:HA2	1:D:779:PHE:O	1.91	0.70
1:E:363:TYR:CE1	1:E:383:CYS:SG	2.80	0.70
1:H:284:MET:HG2	1:H:286:THR:HG22	1.74	0.70
1:D:377:ARG:HG2	1:D:377:ARG:HH21	1.56	0.70
1:D:492:PHE:O	1:D:492:PHE:HD1	1.74	0.70
1:A:286:THR:O	1:A:361:PRO:CG	2.40	0.70
1:H:485:PHE:CE2	1:H:500:THR:OG1	2.44	0.70
1:C:224:ASP:HB3	1:C:227:MET:HB2	1.72	0.70
1:J:352:ILE:HD12	1:J:352:ILE:C	2.17	0.70
1:A:234:MET:O	1:A:237:ILE:HG22	1.91	0.70
1:A:284:MET:HG2	1:A:286:THR:CG2	2.22	0.70
1:E:272:ILE:CG2	1:E:278:LEU:CD1	2.61	0.70
1:I:434:PRO:HG2	1:I:488:HIS:CG	2.27	0.70
1:D:273:VAL:HG11	1:D:457:SER:CB	2.21	0.70
1:D:878:ASP:HB3	1:D:881:VAL:HG22	1.73	0.70
1:E:257:VAL:HG22	1:E:359:ASP:HA	1.73	0.70
1:G:284:MET:N	1:G:284:MET:SD	2.65	0.70
1:A:537:TYR:CE1	1:I:627:TYR:CB	2.73	0.70
1:E:339:THR:CG2	1:E:340:ASP:H	2.04	0.70
1:A:272:ILE:HG12	1:A:278:LEU:CD1	2.22	0.69
1:A:349:SER:O	1:A:352:ILE:HG13	1.92	0.69
1:D:434:PRO:HG2	1:D:488:HIS:ND1	2.06	0.69
1:E:272:ILE:CG2	1:E:277:PHE:HA	2.22	0.69
1:H:272:ILE:HG21	1:H:277:PHE:CD1	2.25	0.69
1:H:405:ASN:C	1:H:410:GLN:NE2	2.50	0.69
1:J:540:LYS:HE2	1:J:541:VAL:N	2.07	0.69
1:A:276:GLU:OE2	1:A:318:PHE:CD2	2.45	0.69
1:B:574:ARG:NH2	1:B:842:ASN:HD21	1.88	0.69
1:E:429:MET:HE2	1:E:437:GLY:CA	2.22	0.69
1:E:434:PRO:HB3	1:E:491:GLU:HG3	1.73	0.69
1:E:441:LEU:HD23	1:E:498:VAL:HB	0.71	0.69
1:E:445:GLN:O	1:E:446:TYR:CD1	2.45	0.69
1:F:255:ILE:HD11	1:F:355:LEU:HG	1.71	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:485:PHE:CE2	1:D:500:THR:OG1	2.46	0.69
1:E:388:ARG:O	1:E:421:ARG:NH2	2.25	0.69
1:G:261:GLN:HE21	1:J:405:ASN:HB2	1.57	0.69
1:H:279:PRO:CB	1:H:322:GLN:HA	2.22	0.69
1:J:275:HIS:CG	1:J:276:GLU:H	2.11	0.69
1:E:454:GLY:O	1:E:500:THR:HG22	1.92	0.69
1:H:441:LEU:CD2	1:H:498:VAL:HG12	2.11	0.69
1:D:269:LEU:HD23	1:D:270:GLU:N	2.07	0.69
1:H:339:THR:HG23	1:H:340:ASP:N	2.08	0.69
1:J:308:PRO:HG3	1:J:344:ARG:CB	2.18	0.69
1:E:396:ILE:HG22	1:E:425:VAL:HB	1.74	0.69
1:F:258:ILE:HG22	1:F:360:LEU:HD11	1.74	0.69
1:G:402:ASP:HB3	1:J:261:GLN:HG2	1.74	0.69
1:E:225:ASP:N	1:E:225:ASP:OD1	2.20	0.69
1:E:278:LEU:HD21	1:E:280:LYS:CD	2.20	0.69
1:E:278:LEU:HD22	1:E:279:PRO:O	1.93	0.69
1:G:261:GLN:CD	1:J:405:ASN:HD22	2.00	0.69
1:G:284:MET:O	1:G:286:THR:HG23	1.92	0.69
1:J:236:GLU:O	1:J:239:ASN:HB2	1.91	0.69
1:J:493:GLY:O	1:J:496:SER:CB	2.41	0.69
1:A:285:ILE:HD11	1:A:287:ARG:HB2	1.67	0.69
1:A:393:ILE:CG1	1:A:394:LEU:N	2.55	0.69
1:C:387:ILE:O	1:C:421:ARG:NH2	2.25	0.69
1:D:297:ASP:CG	1:D:300:ALA:HB3	2.18	0.69
1:H:265:LYS:O	1:H:268:VAL:HG23	1.92	0.69
1:I:613:ASP:HB3	1:I:627:TYR:CD1	2.28	0.69
1:B:261:GLN:NE2	1:B:261:GLN:N	2.41	0.69
1:B:285:ILE:HG12	1:B:329:ASN:O	1.92	0.69
1:D:441:LEU:HD21	1:D:499:SER:H	1.56	0.69
1:E:279:PRO:HG2	1:E:325:LEU:CD2	2.20	0.69
1:E:694:THR:HG21	1:E:845:MET:HB2	1.75	0.69
1:I:284:MET:HG2	1:I:286:THR:HG22	1.74	0.69
1:A:285:ILE:HD12	1:A:285:ILE:C	2.18	0.68
1:C:285:ILE:HG12	1:C:329:ASN:O	1.93	0.68
1:E:478:ASN:O	1:E:482:LYS:HG2	1.93	0.68
1:G:364:ILE:O	1:J:405:ASN:HA	1.93	0.68
1:A:533:GLU:HB2	1:I:596:ARG:NH1	2.09	0.68
1:D:257:VAL:HG22	1:D:359:ASP:HA	1.75	0.68
1:E:276:GLU:CD	1:E:318:PHE:HE2	2.01	0.68
1:H:382:LEU:C	1:H:382:LEU:HD12	2.19	0.68
1:I:624:ASP:HA	1:I:629:HIS:HD2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:PHE:CD2	1:A:492:PHE:O	2.42	0.68
1:J:310:LEU:N	1:J:310:LEU:HD23	2.09	0.68
1:J:434:PRO:HB3	1:J:491:GLU:CG	2.23	0.68
1:B:596:ARG:HH22	1:J:533:GLU:HG2	1.59	0.68
1:G:261:GLN:HE21	1:J:405:ASN:CB	2.06	0.68
1:I:854:PRO:CB	1:I:855:ARG:NH2	2.57	0.68
1:C:630:ARG:HD3	1:C:630:ARG:O	1.94	0.68
1:D:455:VAL:HG12	1:D:501:GLY:H	1.58	0.68
1:F:376:LYS:HZ1	1:F:379:ILE:HD12	1.58	0.68
1:E:441:LEU:CD2	1:E:498:VAL:HG12	2.15	0.68
1:H:456:ILE:HD12	1:H:457:SER:N	2.08	0.68
1:J:257:VAL:CG2	1:J:359:ASP:HA	2.23	0.68
1:J:276:GLU:OE2	1:J:318:PHE:CD2	2.44	0.68
1:J:664:LEU:HB3	1:J:676:ARG:NH2	2.08	0.68
1:J:818:LYS:HE3	1:J:819:TYR:CZ	2.29	0.68
1:B:261:GLN:CD	1:B:261:GLN:N	2.50	0.68
1:J:572:PHE:O	1:J:576:GLN:NE2	2.26	0.68
1:D:242:GLN:HE22	1:D:344:ARG:HD2	1.59	0.68
1:E:246:GLN:HG2	1:E:247:GLY:N	2.08	0.68
1:G:349:SER:HB3	1:G:352:ILE:HG23	1.74	0.68
1:H:375:LEU:N	1:H:375:LEU:CD2	2.53	0.68
1:I:687:LEU:HD22	1:I:845:MET:HE2	1.75	0.68
1:A:326:THR:HA	1:A:329:ASN:HD22	1.57	0.68
1:A:540:LYS:HG2	1:I:626:PRO:HG3	1.70	0.68
1:B:630:ARG:HE	1:J:540:LYS:CG	2.07	0.68
1:D:273:VAL:HG21	1:D:457:SER:CB	2.18	0.68
1:J:237:ILE:HD11	1:J:897:VAL:HG13	1.75	0.68
1:A:537:TYR:CE1	1:A:540:LYS:CE	2.77	0.67
1:A:545:GLU:OE1	1:I:630:ARG:HB2	1.94	0.67
1:A:640:THR:HG21	1:A:706:LYS:HA	1.74	0.67
1:E:229:PHE:CE2	1:E:232:LYS:HD2	2.29	0.67
1:F:279:PRO:HB3	1:F:322:GLN:HA	1.75	0.67
1:B:615:ILE:HD11	1:B:803:ARG:HE	1.59	0.67
1:B:627:TYR:CD1	1:B:630:ARG:NH2	2.62	0.67
1:B:687:LEU:HD22	1:B:845:MET:HE2	1.76	0.67
1:D:423:ILE:HG22	1:D:450:LEU:HD13	1.76	0.67
1:D:485:PHE:CD2	1:D:492:PHE:CD1	2.82	0.67
1:H:441:LEU:HD23	1:H:498:VAL:CA	2.17	0.67
1:J:286:THR:O	1:J:361:PRO:HG3	1.94	0.67
1:J:382:LEU:C	1:J:382:LEU:HD12	2.19	0.67
1:A:376:LYS:HZ3	1:A:376:LYS:HA	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:MET:HG2	1:B:286:THR:HG22	1.75	0.67
1:E:526:GLU:OE1	1:E:530:ARG:NH1	2.28	0.67
1:H:272:ILE:CG2	1:H:277:PHE:HA	2.24	0.67
1:H:339:THR:HG23	1:H:340:ASP:H	1.60	0.67
1:E:242:GLN:HE22	1:E:344:ARG:CD	2.07	0.67
1:G:434:PRO:HG2	1:G:488:HIS:CG	2.29	0.67
1:H:705:TYR:CE1	1:H:832:LYS:HD3	2.30	0.67
1:J:441:LEU:HD23	1:J:498:VAL:HB	0.68	0.67
1:B:781:ALA:CB	1:E:778:GLY:HA2	2.23	0.67
1:E:339:THR:CG2	1:E:340:ASP:N	2.58	0.67
1:F:259:GLY:HA2	1:F:408:ALA:HB2	1.76	0.67
1:F:611:GLU:N	1:F:612:PRO:HD2	2.10	0.67
1:H:276:GLU:CD	1:H:318:PHE:HE2	2.02	0.67
1:H:412:SER:C	1:H:413:ARG:HG3	2.19	0.67
1:J:472:ASN:HD21	1:J:475:ALA:HB3	1.58	0.67
1:D:278:LEU:O	1:D:278:LEU:HD13	1.95	0.67
1:E:363:TYR:HE1	1:E:383:CYS:HG	0.81	0.67
1:J:639:LEU:O	1:J:642:LEU:HD23	1.94	0.67
1:D:239:ASN:O	1:D:242:GLN:HB3	1.95	0.67
1:J:540:LYS:HE2	1:J:540:LYS:O	1.95	0.67
1:B:607:PRO:HG3	1:B:762:ARG:HG3	1.76	0.67
1:D:272:ILE:CG2	1:D:278:LEU:H	2.07	0.67
1:E:229:PHE:CD2	1:E:232:LYS:HD2	2.30	0.67
1:E:237:ILE:HD11	1:E:897:VAL:HG13	1.76	0.67
1:E:576:GLN:NE2	1:E:576:GLN:H	1.92	0.67
1:G:258:ILE:HG22	1:G:360:LEU:HD11	1.77	0.67
1:G:524:THR:O	1:G:528:ILE:HG13	1.94	0.67
1:G:598:TRP:HE3	1:G:796:ARG:NH1	1.92	0.67
1:H:225:ASP:O	1:H:229:PHE:HD1	1.77	0.67
1:H:286:THR:O	1:H:361:PRO:CB	2.42	0.67
1:I:878:ASP:HB3	1:I:881:VAL:HG12	1.77	0.67
1:A:276:GLU:CD	1:A:318:PHE:CE2	2.61	0.67
1:E:231:THR:O	1:E:235:ILE:HG22	1.94	0.67
1:F:627:TYR:HE2	1:F:628:TRP:CZ3	2.13	0.67
1:H:426:ILE:HD12	1:H:440:ILE:CG2	1.92	0.67
1:H:478:ASN:CG	1:H:482:LYS:NZ	2.53	0.67
1:J:267:SER:HB2	1:J:396:ILE:CD1	2.25	0.67
1:C:627:TYR:OH	1:C:631:GLN:NE2	2.28	0.66
1:D:270:GLU:O	1:D:273:VAL:HG22	1.95	0.66
1:H:263:SER:OG	1:H:397:SER:HA	1.94	0.66
1:A:478:ASN:HD21	1:A:482:LYS:HZ1	0.72	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:611:GLU:N	1:C:612:PRO:CD	2.57	0.66
1:D:434:PRO:HB3	1:D:491:GLU:CG	2.25	0.66
1:F:578:GLN:HA	1:F:838:VAL:HG21	1.77	0.66
1:H:454:GLY:O	1:H:500:THR:HB	1.96	0.66
1:D:434:PRO:HG2	1:D:488:HIS:CG	2.30	0.66
1:E:434:PRO:HB3	1:E:491:GLU:HB2	1.76	0.66
1:B:642:LEU:HD22	1:B:643:GLY:H	1.59	0.66
1:E:229:PHE:CE1	1:E:232:LYS:HE3	2.30	0.66
1:H:233:LYS:HE2	1:H:233:LYS:CA	2.26	0.66
1:H:574:ARG:H	1:H:575:PRO:HD2	1.60	0.66
1:A:307:PHE:CD1	1:A:345:LEU:HD21	2.30	0.66
1:D:478:ASN:ND2	1:D:482:LYS:HZ3	1.92	0.66
1:J:229:PHE:CD1	1:J:232:LYS:CD	2.62	0.66
1:C:269:LEU:HA	1:C:272:ILE:HD12	1.76	0.66
1:E:307:PHE:CD1	1:E:345:LEU:HD21	2.29	0.66
1:E:574:ARG:H	1:E:575:PRO:HD2	1.61	0.66
1:H:273:VAL:HG21	1:H:457:SER:CB	2.17	0.66
1:J:307:PHE:CD1	1:J:345:LEU:HD21	2.31	0.66
1:J:485:PHE:CD2	1:J:492:PHE:HD1	2.11	0.66
1:A:472:ASN:HD21	1:A:475:ALA:CB	2.06	0.66
1:A:488:HIS:HB3	1:A:491:GLU:CG	2.26	0.66
1:D:276:GLU:OE2	1:D:318:PHE:CD2	2.48	0.66
1:D:388:ARG:O	1:D:421:ARG:NH2	2.27	0.66
1:E:269:LEU:HD21	1:E:457:SER:CA	2.26	0.66
1:H:434:PRO:HB3	1:H:491:GLU:CB	2.25	0.66
1:J:286:THR:O	1:J:361:PRO:CB	2.44	0.66
1:J:396:ILE:HG22	1:J:425:VAL:HB	1.78	0.66
1:A:286:THR:O	1:A:361:PRO:CB	2.43	0.66
1:B:630:ARG:CB	1:J:540:LYS:CG	2.59	0.66
1:D:246:GLN:HG2	1:D:247:GLY:N	2.09	0.66
1:D:441:LEU:CG	1:D:498:VAL:CG1	2.73	0.66
1:I:622:ASP:OD1	1:I:623:PRO:HD2	1.96	0.66
1:J:278:LEU:HD22	1:J:280:LYS:HG2	1.78	0.66
1:E:339:THR:O	1:E:340:ASP:HB3	1.96	0.66
1:A:237:ILE:O	1:A:237:ILE:HD13	1.96	0.65
1:A:246:GLN:CG	1:A:247:GLY:N	2.55	0.65
1:D:272:ILE:HG21	1:D:277:PHE:CD1	2.31	0.65
1:G:249:THR:OG1	1:G:531:GLU:OE1	2.11	0.65
1:H:485:PHE:CD2	1:H:492:PHE:O	2.48	0.65
1:J:278:LEU:CD2	1:J:280:LYS:CD	2.64	0.65
1:J:285:ILE:HD12	1:J:287:ARG:H	0.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:LEU:HD13	1:A:278:LEU:C	2.19	0.65
1:E:312:LEU:N	1:E:312:LEU:CD2	2.58	0.65
1:J:232:LYS:HA	1:J:235:ILE:HG22	1.77	0.65
1:J:540:LYS:O	1:J:540:LYS:HE3	1.94	0.65
1:A:275:HIS:CG	1:A:276:GLU:H	2.15	0.65
1:A:394:LEU:HD21	1:A:412:SER:CB	2.27	0.65
1:A:707:PHE:CE2	1:B:847:ASN:ND2	2.65	0.65
1:B:257:VAL:HG12	1:B:394:LEU:HB3	1.78	0.65
1:E:229:PHE:CD1	1:E:232:LYS:CD	2.79	0.65
1:E:376:LYS:HE2	1:E:376:LYS:CA	2.26	0.65
1:F:360:LEU:HB2	1:F:361:PRO:HD2	1.78	0.65
1:H:232:LYS:HA	1:H:235:ILE:HG22	1.76	0.65
1:J:234:MET:O	1:J:237:ILE:HG22	1.95	0.65
1:J:817:ASN:HB3	1:J:820:TYR:HB2	1.78	0.65
1:A:441:LEU:CD2	1:A:498:VAL:CA	2.74	0.65
1:F:430:ASP:HB3	1:F:456:ILE:HG12	1.78	0.65
1:G:402:ASP:CB	1:J:261:GLN:HG3	2.27	0.65
1:H:441:LEU:CD2	1:H:498:VAL:CA	2.74	0.65
1:A:269:LEU:HD23	1:A:457:SER:HB2	1.74	0.65
1:A:326:THR:O	1:A:329:ASN:HB2	1.97	0.65
1:A:485:PHE:HA	1:A:492:PHE:HE1	1.62	0.65
1:H:478:ASN:O	1:H:482:LYS:HG2	1.96	0.65
1:J:475:ALA:O	1:J:479:ARG:HG2	1.97	0.65
1:B:376:LYS:NZ	1:B:379:ILE:HD12	2.11	0.65
1:D:279:PRO:HB3	1:D:322:GLN:HA	1.78	0.65
1:D:284:MET:HG2	1:D:286:THR:HG23	1.77	0.65
1:I:444:ARG:O	1:I:447:PRO:HD3	1.96	0.65
1:J:269:LEU:CD2	1:J:457:SER:CB	2.74	0.65
1:E:478:ASN:CG	1:E:482:LYS:HZ2	2.02	0.65
1:J:488:HIS:HB3	1:J:491:GLU:CG	2.27	0.65
1:H:229:PHE:O	1:H:233:LYS:HG2	1.97	0.65
1:A:483:ASN:C	1:A:483:ASN:ND2	2.55	0.65
1:C:524:THR:O	1:C:528:ILE:HG13	1.97	0.65
1:C:690:ARG:NH1	1:C:844:GLU:OE2	2.30	0.65
1:D:297:ASP:HB3	1:D:349:SER:C	2.22	0.65
1:A:768:VAL:HG23	1:A:770:GLY:H	1.63	0.64
1:E:441:LEU:HB3	1:E:498:VAL:CG1	2.26	0.64
1:B:755:MET:HE3	1:B:790:ALA:HB1	1.79	0.64
1:E:477:ILE:O	1:E:477:ILE:HG22	1.97	0.64
1:F:627:TYR:HE2	1:F:628:TRP:CH2	2.15	0.64
1:H:241:LEU:HD21	1:H:528:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:PHE:CD1	1:A:345:LEU:CD2	2.81	0.64
1:B:255:ILE:HD11	1:B:355:LEU:HG	1.78	0.64
1:B:596:ARG:HH22	1:J:533:GLU:CG	2.10	0.64
1:B:757:PHE:HA	1:B:760:LYS:HD2	1.79	0.64
1:F:387:ILE:O	1:F:421:ARG:NH2	2.30	0.64
1:F:863:GLU:O	1:F:867:ALA:CB	2.46	0.64
1:H:441:LEU:CB	1:H:498:VAL:CG1	2.75	0.64
1:J:272:ILE:CG2	1:J:278:LEU:HD13	2.23	0.64
1:J:574:ARG:H	1:J:575:PRO:HD2	1.62	0.64
1:A:272:ILE:CG2	1:A:278:LEU:H	2.10	0.64
1:A:339:THR:HG23	1:A:340:ASP:H	1.63	0.64
1:D:297:ASP:N	1:D:298:PRO:HD3	2.12	0.64
1:E:252:LEU:HD23	1:E:524:THR:HG21	1.79	0.64
1:F:429:MET:HE1	1:F:441:LEU:HB2	1.79	0.64
1:H:286:THR:O	1:H:361:PRO:CG	2.45	0.64
1:H:454:GLY:O	1:H:500:THR:CG2	2.45	0.64
1:A:308:PRO:HG3	1:A:344:ARG:HB2	1.78	0.64
1:F:879:PRO:HG3	1:H:630:ARG:CD	2.27	0.64
1:J:258:ILE:HG22	1:J:360:LEU:HD11	1.79	0.64
1:D:525:THR:HA	1:D:528:ILE:HD12	1.79	0.64
1:E:269:LEU:HD23	1:E:270:GLU:N	2.13	0.64
1:J:665:ASP:OD1	1:J:676:ARG:NH2	2.31	0.64
1:A:270:GLU:HA	1:A:273:VAL:HG22	1.79	0.64
1:A:376:LYS:HE2	1:A:376:LYS:CA	2.28	0.64
1:D:238:ARG:HA	1:D:241:LEU:HD12	1.79	0.64
1:D:311:GLY:O	1:D:312:LEU:HB2	1.96	0.64
1:G:598:TRP:CE3	1:G:796:ARG:NH1	2.65	0.64
1:H:232:LYS:O	1:H:235:ILE:HG23	1.96	0.64
1:C:863:GLU:O	1:C:867:ALA:CB	2.46	0.64
1:D:279:PRO:HB3	1:D:322:GLN:CA	2.28	0.64
1:D:433:GLU:O	1:D:436:LYS:HB2	1.96	0.64
1:E:310:LEU:N	1:E:310:LEU:HD23	2.12	0.64
1:H:441:LEU:CB	1:H:498:VAL:HG12	2.26	0.64
1:A:278:LEU:CD2	1:A:280:LYS:CD	2.73	0.64
1:D:296:ASN:C	1:D:298:PRO:HD3	2.23	0.64
1:D:396:ILE:HG22	1:D:425:VAL:HB	1.78	0.64
1:E:485:PHE:CZ	1:E:500:THR:OG1	2.50	0.64
1:H:279:PRO:HG2	1:H:325:LEU:CD2	2.25	0.64
1:C:818:LYS:HE3	1:C:819:TYR:CE2	2.33	0.64
1:E:307:PHE:CE1	1:E:345:LEU:CD2	2.80	0.64
1:J:272:ILE:CG2	1:J:277:PHE:HA	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:430:ASP:C	1:E:430:ASP:OD1	2.41	0.63
1:F:328:LEU:HD13	1:F:343:ILE:HD13	1.79	0.63
1:J:871:LEU:O	1:J:874:PHE:HB3	1.98	0.63
1:A:363:TYR:HE1	1:A:383:CYS:HG	0.82	0.63
1:E:286:THR:O	1:E:361:PRO:HB3	1.97	0.63
1:E:376:LYS:HZ1	1:E:379:ILE:CD1	2.07	0.63
1:H:297:ASP:HB3	1:H:349:SER:C	2.24	0.63
1:H:310:LEU:N	1:H:310:LEU:HD23	2.13	0.63
1:I:903:GLU:HA	1:I:906:ARG:HH21	1.63	0.63
1:A:297:ASP:HB3	1:A:349:SER:C	2.24	0.63
1:C:705:TYR:CE1	1:C:832:LYS:HD3	2.33	0.63
1:D:328:LEU:HD13	1:D:343:ILE:HD13	1.81	0.63
1:D:456:ILE:O	1:D:481:GLU:OE2	2.16	0.63
1:E:238:ARG:NH2	1:E:356:SER:OG	2.31	0.63
1:E:596:ARG:HG3	1:E:635:ALA:HB2	1.79	0.63
1:E:690:ARG:NH1	1:E:844:GLU:OE2	2.31	0.63
1:F:273:VAL:HG11	1:F:457:SER:HB3	1.80	0.63
1:A:318:PHE:HD1	1:A:321:ILE:HD12	1.62	0.63
1:A:537:TYR:OH	1:I:612:PRO:HB2	1.99	0.63
1:E:572:PHE:O	1:E:576:GLN:NE2	2.32	0.63
1:G:261:GLN:HG2	1:G:262:SER:N	2.13	0.63
1:H:286:THR:HB	1:H:361:PRO:HB3	1.80	0.63
1:I:429:MET:HE1	1:I:441:LEU:HB2	1.80	0.63
1:J:286:THR:HB	1:J:361:PRO:CB	2.28	0.63
1:A:454:GLY:O	1:A:500:THR:CB	2.47	0.63
1:D:229:PHE:HA	1:D:232:LYS:CG	2.28	0.63
1:D:376:LYS:HA	1:D:376:LYS:HZ3	1.64	0.63
1:D:485:PHE:CD2	1:D:492:PHE:O	2.51	0.63
1:E:376:LYS:HA	1:E:376:LYS:CE	2.28	0.63
1:E:528:ILE:HG23	1:E:894:LEU:HD22	1.81	0.63
1:F:357:LEU:HD23	1:F:357:LEU:O	1.97	0.63
1:I:623:PRO:O	1:I:629:HIS:CD2	2.51	0.63
1:J:268:VAL:O	1:J:272:ILE:HG13	1.98	0.63
1:A:267:SER:HB3	1:A:396:ILE:CG1	2.28	0.63
1:A:339:THR:HG23	1:A:340:ASP:N	2.13	0.63
1:E:478:ASN:HD21	1:E:482:LYS:HZ1	1.37	0.63
1:H:233:LYS:CA	1:H:233:LYS:CE	2.76	0.63
1:I:402:ASP:HB3	1:I:405:ASN:HB2	1.81	0.63
1:C:607:PRO:HG3	1:C:762:ARG:HG3	1.80	0.63
1:D:252:LEU:HD23	1:D:524:THR:HG21	1.81	0.63
1:E:434:PRO:HB3	1:E:491:GLU:CG	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:493:GLY:O	1:E:496:SER:HB3	1.98	0.63
1:G:285:ILE:HG12	1:G:329:ASN:O	1.98	0.63
1:G:405:ASN:CG	1:J:261:GLN:H	2.06	0.63
1:A:376:LYS:HA	1:A:376:LYS:CE	2.28	0.63
1:D:286:THR:HB	1:D:361:PRO:CB	2.25	0.63
1:E:272:ILE:HG12	1:E:278:LEU:HD13	1.81	0.63
1:F:627:TYR:CE2	1:F:628:TRP:CZ3	2.86	0.63
1:H:529:GLN:HG2	1:H:898:LEU:HD21	1.81	0.63
1:C:318:PHE:CD1	1:C:321:ILE:HD12	2.34	0.62
1:H:441:LEU:HD22	1:H:498:VAL:HB	1.68	0.62
1:I:278:LEU:HD21	1:I:280:LYS:HD3	1.81	0.62
1:J:259:GLY:HA2	1:J:408:ALA:HB2	1.81	0.62
1:J:878:ASP:HB3	1:J:881:VAL:CG2	2.27	0.62
1:A:285:ILE:HD11	1:A:287:ARG:CB	2.24	0.62
1:B:574:ARG:CZ	1:B:842:ASN:ND2	2.62	0.62
1:F:524:THR:O	1:F:528:ILE:HG13	2.00	0.62
1:G:843:VAL:HG21	1:H:704:PRO:HA	1.80	0.62
1:J:388:ARG:O	1:J:421:ARG:NH2	2.30	0.62
1:J:423:ILE:HG22	1:J:450:LEU:HD13	1.80	0.62
1:C:285:ILE:HD12	1:C:287:ARG:N	2.11	0.62
1:E:284:MET:HG2	1:E:286:THR:HG23	1.79	0.62
1:E:287:ARG:HH11	1:E:287:ARG:HG3	1.64	0.62
1:E:475:ALA:O	1:E:479:ARG:HG2	2.00	0.62
1:G:754:VAL:HG22	1:G:779:PHE:CD2	2.34	0.62
1:H:279:PRO:HB3	1:H:322:GLN:HB2	1.81	0.62
1:H:363:TYR:HD2	1:H:408:ALA:CB	2.13	0.62
1:I:275:HIS:CG	1:I:276:GLU:H	2.17	0.62
1:I:401:THR:HG22	1:I:405:ASN:HB3	1.80	0.62
1:J:267:SER:HB3	1:J:396:ILE:HG13	1.81	0.62
1:A:263:SER:OG	1:A:397:SER:HA	1.99	0.62
1:D:257:VAL:CG2	1:D:359:ASP:HA	2.30	0.62
1:D:694:THR:HG21	1:D:845:MET:HB2	1.82	0.62
1:F:292:LEU:HD12	1:F:357:LEU:HD22	1.82	0.62
1:H:279:PRO:HG3	1:H:322:GLN:HA	1.80	0.62
1:A:238:ARG:HA	1:A:241:LEU:HD12	1.82	0.62
1:D:278:LEU:CD2	1:D:280:LYS:CD	2.75	0.62
1:H:257:VAL:HG22	1:H:358:ILE:O	1.99	0.62
1:H:407:THR:CG2	1:H:414:ARG:HD3	2.29	0.62
1:A:478:ASN:ND2	1:A:482:LYS:HZ2	1.94	0.62
1:A:537:TYR:CA	1:I:630:ARG:CZ	2.77	0.62
1:C:854:PRO:O	1:C:858:GLU:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:401:THR:HB	1:H:410:GLN:HA	0.80	0.62
1:H:455:VAL:HG12	1:H:501:GLY:N	2.14	0.62
1:H:456:ILE:O	1:H:481:GLU:OE2	2.17	0.62
1:H:754:VAL:HA	1:H:779:PHE:HE1	1.63	0.62
1:E:307:PHE:CD1	1:E:345:LEU:CD2	2.82	0.62
1:F:322:GLN:O	1:F:326:THR:OG1	2.06	0.62
1:H:453:VAL:HG21	1:H:505:LEU:HD23	1.80	0.62
1:J:375:LEU:N	1:J:375:LEU:HD23	2.15	0.62
1:A:229:PHE:O	1:A:233:LYS:HG2	2.00	0.62
1:A:387:ILE:CG2	1:A:393:ILE:HD12	2.29	0.62
1:C:434:PRO:HG2	1:C:488:HIS:CG	2.34	0.62
1:D:238:ARG:NH2	1:D:356:SER:OG	2.33	0.62
1:D:279:PRO:O	1:D:280:LYS:HD2	2.00	0.62
1:D:308:PRO:HG3	1:D:344:ARG:HG3	1.82	0.62
1:D:454:GLY:O	1:D:455:VAL:CG1	2.48	0.62
1:E:878:ASP:HB3	1:E:881:VAL:HG22	1.82	0.62
1:I:578:GLN:HA	1:I:838:VAL:HG21	1.81	0.62
1:A:241:LEU:O	1:A:244:VAL:HG23	1.99	0.62
1:A:294:LEU:HB3	1:A:352:ILE:HD13	1.81	0.62
1:A:458:LYS:C	1:A:458:LYS:HZ3	2.06	0.62
1:A:537:TYR:HA	1:I:630:ARG:NE	2.14	0.62
1:D:478:ASN:CG	1:D:482:LYS:HZ2	2.08	0.62
1:H:878:ASP:HB3	1:H:881:VAL:HG22	1.82	0.62
1:J:272:ILE:CG2	1:J:278:LEU:HD12	2.20	0.62
1:J:279:PRO:O	1:J:280:LYS:CD	2.47	0.62
1:A:394:LEU:CD2	1:A:412:SER:HB2	2.30	0.62
1:B:376:LYS:CA	1:B:376:LYS:HE2	2.30	0.62
1:B:434:PRO:HG2	1:B:488:HIS:CG	2.35	0.62
1:E:273:VAL:HG11	1:E:457:SER:CB	2.29	0.62
1:E:454:GLY:O	1:E:500:THR:CG2	2.48	0.62
1:F:664:LEU:HD23	1:F:676:ARG:HG3	1.80	0.62
1:G:405:ASN:ND2	1:J:260:SER:HB3	2.12	0.62
1:B:227:MET:HA	1:B:230:ILE:HG22	1.81	0.61
1:E:240:LEU:N	1:E:240:LEU:CD2	2.51	0.61
1:E:259:GLY:HA2	1:E:408:ALA:HB2	1.82	0.61
1:E:267:SER:HB2	1:E:396:ILE:CD1	2.30	0.61
1:E:360:LEU:HB2	1:E:361:PRO:HD2	1.82	0.61
1:E:690:ARG:CZ	1:E:848:ASP:OD2	2.48	0.61
1:F:616:ILE:HD12	1:F:616:ILE:O	2.00	0.61
1:J:260:SER:N	1:J:263:SER:HB3	2.15	0.61
1:F:484:TYR:O	1:F:487:SER:HB3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:854:PRO:HB2	1:I:855:ARG:CZ	2.29	0.61
1:J:441:LEU:CD2	1:J:498:VAL:HG12	2.25	0.61
1:A:286:THR:O	1:A:361:PRO:HG3	2.01	0.61
1:A:394:LEU:CD1	1:A:423:ILE:O	2.48	0.61
1:E:492:PHE:O	1:E:492:PHE:HD1	1.82	0.61
1:J:472:ASN:ND2	1:J:475:ALA:HB3	2.15	0.61
1:A:229:PHE:HA	1:A:232:LYS:HG2	1.82	0.61
1:D:488:HIS:HB3	1:D:491:GLU:HG3	1.80	0.61
1:H:434:PRO:CG	1:H:488:HIS:CG	2.83	0.61
1:J:657:GLN:HE22	1:J:684:ALA:HA	1.65	0.61
1:A:269:LEU:HD23	1:A:269:LEU:C	2.25	0.61
1:D:229:PHE:O	1:D:232:LYS:HG3	2.01	0.61
1:E:474:LEU:HG	1:E:475:ALA:H	1.66	0.61
1:E:574:ARG:N	1:E:575:PRO:HD2	2.15	0.61
1:F:257:VAL:HG12	1:F:394:LEU:HB3	1.82	0.61
1:J:444:ARG:O	1:J:447:PRO:HD3	2.00	0.61
1:C:284:MET:O	1:C:286:THR:HG23	2.01	0.61
1:F:357:LEU:CD2	1:F:357:LEU:O	2.48	0.61
1:H:405:ASN:C	1:H:410:GLN:HE21	2.08	0.61
1:C:258:ILE:HG21	1:C:387:ILE:HD11	1.81	0.61
1:D:246:GLN:CG	1:D:247:GLY:N	2.63	0.61
1:E:278:LEU:CD2	1:E:280:LYS:CD	2.73	0.61
1:G:605:LEU:HD22	1:G:605:LEU:C	2.26	0.61
1:H:272:ILE:CG2	1:H:278:LEU:HD12	2.23	0.61
1:A:267:SER:HB2	1:A:396:ILE:CD1	2.30	0.61
1:A:296:ASN:C	1:A:298:PRO:HD3	2.26	0.61
1:C:585:LEU:HD12	1:C:834:ALA:HB2	1.83	0.61
1:I:224:ASP:HB3	1:I:227:MET:HB2	1.81	0.61
1:I:762:ARG:HG2	1:I:762:ARG:NH1	2.15	0.61
1:J:229:PHE:O	1:J:232:LYS:HG3	2.01	0.61
1:J:525:THR:HA	1:J:528:ILE:HD12	1.82	0.61
1:A:388:ARG:O	1:A:421:ARG:NH2	2.32	0.61
1:E:488:HIS:HB3	1:E:491:GLU:HG2	1.83	0.61
1:H:307:PHE:CE1	1:H:345:LEU:CD2	2.84	0.61
1:J:238:ARG:HA	1:J:241:LEU:HD12	1.81	0.61
1:G:297:ASP:HB3	1:G:349:SER:C	2.26	0.61
1:G:610:ARG:HB3	1:G:613:ASP:OD1	2.00	0.61
1:I:628:TRP:CE3	1:I:628:TRP:N	2.68	0.61
1:J:307:PHE:CE1	1:J:345:LEU:CD2	2.74	0.61
1:A:434:PRO:HG2	1:A:488:HIS:ND1	2.16	0.60
1:A:441:LEU:HB3	1:A:498:VAL:HG11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:627:TYR:CE2	1:C:628:TRP:CZ3	2.89	0.60
1:G:387:ILE:O	1:G:421:ARG:NH2	2.33	0.60
1:H:287:ARG:HH11	1:H:287:ARG:CG	2.12	0.60
1:H:307:PHE:CZ	1:H:345:LEU:HD21	2.36	0.60
1:H:614:ASN:OD1	1:H:616:ILE:HG22	2.01	0.60
1:A:257:VAL:HG22	1:A:358:ILE:O	2.01	0.60
1:B:627:TYR:OH	1:B:631:GLN:NE2	2.34	0.60
1:C:272:ILE:HG23	1:C:277:PHE:HA	1.83	0.60
1:C:510:LEU:HD23	1:C:510:LEU:C	2.26	0.60
1:E:488:HIS:HB3	1:E:491:GLU:CG	2.31	0.60
1:E:853:PHE:HB3	1:E:854:PRO:HD3	1.83	0.60
1:F:285:ILE:HD13	1:F:332:VAL:HG22	1.82	0.60
1:H:252:LEU:HD23	1:H:524:THR:HG21	1.82	0.60
1:A:705:TYR:CE1	1:A:832:LYS:HD3	2.36	0.60
1:B:387:ILE:O	1:B:421:ARG:NH2	2.35	0.60
1:F:883:ARG:HH22	1:H:634:THR:HG21	1.65	0.60
1:J:339:THR:CG2	1:J:340:ASP:N	2.64	0.60
1:A:423:ILE:HG22	1:A:450:LEU:HD13	1.82	0.60
1:D:441:LEU:CB	1:D:498:VAL:HG12	2.32	0.60
1:D:778:GLY:O	1:D:779:PHE:HD2	1.84	0.60
1:H:454:GLY:O	1:H:500:THR:HG22	2.00	0.60
1:J:252:LEU:HD23	1:J:524:THR:HG21	1.82	0.60
1:J:690:ARG:NH1	1:J:844:GLU:OE2	2.34	0.60
1:A:270:GLU:O	1:A:273:VAL:HG22	2.01	0.60
1:A:485:PHE:CE2	1:A:492:PHE:CD1	2.90	0.60
1:B:840:PHE:CZ	1:B:844:GLU:HG3	2.36	0.60
1:D:269:LEU:HD23	1:D:269:LEU:C	2.26	0.60
1:D:508:LYS:O	1:D:512:VAL:HG23	2.01	0.60
1:E:665:ASP:OD1	1:E:676:ARG:NH2	2.34	0.60
1:G:400:ASP:HB3	1:J:400:ASP:OD2	2.01	0.60
1:J:278:LEU:HD22	1:J:279:PRO:O	2.02	0.60
1:J:434:PRO:CG	1:J:488:HIS:CG	2.83	0.60
1:D:322:GLN:O	1:D:326:THR:OG1	2.12	0.60
1:H:270:GLU:O	1:H:273:VAL:HG22	2.00	0.60
1:A:269:LEU:HD21	1:A:457:SER:C	2.26	0.60
1:A:279:PRO:HG3	1:A:321:ILE:HG22	1.84	0.60
1:A:484:TYR:CD1	1:A:484:TYR:C	2.79	0.60
1:E:615:ILE:H	1:E:615:ILE:HD12	1.65	0.60
1:I:625:SER:CB	1:I:628:TRP:CD1	2.73	0.60
1:J:441:LEU:CG	1:J:498:VAL:CG1	2.78	0.60
1:A:267:SER:CB	1:A:396:ILE:CD1	2.80	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:817:ASN:HB3	1:A:820:TYR:HB2	1.84	0.60
1:B:630:ARG:CG	1:J:540:LYS:HG3	2.28	0.60
1:C:434:PRO:HG2	1:C:488:HIS:ND1	2.17	0.60
1:D:787:GLY:O	1:D:791:VAL:HG23	2.02	0.60
1:E:376:LYS:CA	1:E:376:LYS:CE	2.79	0.60
1:H:229:PHE:HA	1:H:232:LYS:HG2	1.82	0.60
1:H:278:LEU:HD22	1:H:280:LYS:HG2	1.83	0.60
1:A:537:TYR:CE1	1:I:627:TYR:N	2.66	0.60
1:C:625:SER:HG	1:C:628:TRP:CD1	2.20	0.60
1:C:640:THR:HG21	1:C:706:LYS:HA	1.83	0.60
1:G:257:VAL:HG12	1:G:394:LEU:HB3	1.84	0.60
1:J:257:VAL:HG22	1:J:359:ASP:HA	1.82	0.60
1:C:484:TYR:HD1	1:C:485:PHE:CD1	2.20	0.60
1:D:273:VAL:CG2	1:D:457:SER:HB3	2.20	0.60
1:D:225:ASP:OD1	1:D:225:ASP:N	2.33	0.59
1:D:308:PRO:HG3	1:D:344:ARG:HB2	1.85	0.59
1:E:339:THR:HG23	1:E:341:ASP:H	1.66	0.59
1:E:363:TYR:N	1:E:363:TYR:CD1	2.69	0.59
1:E:499:SER:O	1:E:500:THR:HG23	2.01	0.59
1:G:661:GLU:OE2	1:G:676:ARG:NH2	2.35	0.59
1:H:397:SER:CB	1:H:411:ALA:HB1	2.32	0.59
1:A:441:LEU:HB3	1:A:498:VAL:CG1	2.32	0.59
1:A:778:GLY:C	1:A:779:PHE:CD2	2.80	0.59
1:D:387:ILE:CG2	1:D:415:VAL:HG21	2.32	0.59
1:F:255:ILE:HG13	1:F:357:LEU:HA	1.84	0.59
1:H:286:THR:CB	1:H:361:PRO:HB3	2.32	0.59
1:H:363:TYR:CD2	1:H:408:ALA:HB2	2.33	0.59
1:I:284:MET:O	1:I:286:THR:HG23	2.02	0.59
1:J:260:SER:HB2	1:J:263:SER:HB2	1.83	0.59
1:J:263:SER:OG	1:J:397:SER:HA	2.02	0.59
1:J:284:MET:HG2	1:J:286:THR:HG23	1.79	0.59
1:A:235:ILE:HD12	1:A:235:ILE:C	2.24	0.59
1:A:275:HIS:CD2	1:A:275:HIS:H	2.20	0.59
1:C:863:GLU:O	1:C:867:ALA:HB3	2.02	0.59
1:D:268:VAL:O	1:D:272:ILE:HG13	2.01	0.59
1:D:574:ARG:H	1:D:575:PRO:HD2	1.67	0.59
1:E:286:THR:HB	1:E:361:PRO:CB	2.27	0.59
1:F:426:ILE:HG21	1:F:429:MET:HE3	1.83	0.59
1:H:232:LYS:HA	1:H:235:ILE:CG2	2.31	0.59
1:H:741:LEU:HG	1:H:751:LEU:HD11	1.84	0.59
1:H:800:LEU:O	1:H:804:ILE:HG13	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:242:GLN:OE1	1:J:291:GLU:OE1	2.21	0.59
1:A:878:ASP:HB3	1:A:881:VAL:HG22	1.84	0.59
1:D:326:THR:HA	1:D:329:ASN:ND2	2.18	0.59
1:E:230:ILE:HG13	1:E:904:LEU:HD11	1.84	0.59
1:A:278:LEU:HD11	1:A:280:LYS:HG3	1.85	0.59
1:A:394:LEU:CD2	1:A:395:ALA:N	2.63	0.59
1:A:434:PRO:HB3	1:A:491:GLU:CG	2.32	0.59
1:B:383:CYS:O	1:B:387:ILE:HG13	2.03	0.59
1:H:273:VAL:CG1	1:H:457:SER:HB2	2.29	0.59
1:H:279:PRO:HB3	1:H:322:GLN:HA	1.84	0.59
1:H:456:ILE:O	1:H:456:ILE:HG23	2.03	0.59
1:J:278:LEU:HD22	1:J:278:LEU:C	2.26	0.59
1:D:429:MET:CE	1:D:437:GLY:HA2	2.31	0.59
1:D:441:LEU:HD23	1:D:498:VAL:HB	0.62	0.59
1:F:269:LEU:O	1:F:272:ILE:HB	2.02	0.59
1:F:863:GLU:O	1:F:867:ALA:HB3	2.02	0.59
1:G:261:GLN:HE22	1:J:401:THR:HG23	1.62	0.59
1:H:363:TYR:N	1:H:363:TYR:CD1	2.68	0.59
1:H:477:ILE:O	1:H:477:ILE:HG22	2.01	0.59
1:H:508:LYS:O	1:H:512:VAL:HG23	2.02	0.59
1:H:540:LYS:HE2	1:H:545:GLU:OE1	2.02	0.59
1:D:298:PRO:O	1:D:299:GLU:HB3	2.02	0.59
1:D:488:HIS:CB	1:D:491:GLU:HG2	2.22	0.59
1:D:657:GLN:HE22	1:D:684:ALA:HA	1.67	0.59
1:D:665:ASP:OD1	1:D:676:ARG:NH2	2.36	0.59
1:G:261:GLN:CD	1:J:405:ASN:ND2	2.60	0.59
1:G:308:PRO:HG3	1:G:344:ARG:HB2	1.85	0.59
1:I:255:ILE:HA	1:I:392:ILE:O	2.03	0.59
1:J:273:VAL:HG21	1:J:457:SER:CB	2.29	0.59
1:J:441:LEU:CD2	1:J:498:VAL:CA	2.78	0.59
1:J:778:GLY:C	1:J:779:PHE:HD2	2.11	0.59
1:A:537:TYR:HE1	1:I:627:TYR:CB	2.15	0.59
1:B:376:LYS:HZ3	1:B:379:ILE:HD12	1.68	0.59
1:B:627:TYR:HE2	1:B:628:TRP:CZ3	2.21	0.59
1:C:254:SER:HB2	1:C:356:SER:O	2.03	0.59
1:D:235:ILE:HD12	1:D:235:ILE:C	2.27	0.59
1:D:272:ILE:HG12	1:D:278:LEU:CD1	2.33	0.59
1:H:270:GLU:HA	1:H:273:VAL:HG22	1.83	0.59
1:J:485:PHE:CD2	1:J:492:PHE:O	2.55	0.59
1:C:704:PRO:HA	1:D:843:VAL:HG21	1.85	0.59
1:G:261:GLN:HE21	1:J:401:THR:HG23	1.62	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:405:ASN:ND2	1:J:261:GLN:N	2.51	0.59
1:H:275:HIS:CG	1:H:276:GLU:N	2.71	0.59
1:H:401:THR:HG21	1:H:410:GLN:HG3	1.81	0.59
1:H:478:ASN:HD21	1:H:482:LYS:HZ1	0.67	0.59
1:A:454:GLY:O	1:A:500:THR:CG2	2.51	0.59
1:D:276:GLU:HG2	1:D:277:PHE:N	2.16	0.59
1:D:576:GLN:NE2	1:D:576:GLN:H	2.01	0.59
1:D:671:LYS:HD2	1:D:671:LYS:N	2.18	0.59
1:E:387:ILE:CG2	1:E:415:VAL:HG21	2.33	0.59
1:E:400:ASP:N	1:E:400:ASP:OD1	2.35	0.59
1:F:883:ARG:HH22	1:H:634:THR:CG2	2.15	0.59
1:A:272:ILE:HG23	1:A:278:LEU:HD13	1.68	0.58
1:A:278:LEU:CD2	1:A:280:LYS:HG2	2.32	0.58
1:B:429:MET:HE2	1:B:437:GLY:HA2	1.84	0.58
1:E:269:LEU:HA	1:E:272:ILE:CD1	2.23	0.58
1:E:272:ILE:CG2	1:E:277:PHE:HD1	2.14	0.58
1:E:308:PRO:HG3	1:E:344:ARG:HG3	1.85	0.58
1:H:273:VAL:CG2	1:H:457:SER:HB3	2.19	0.58
1:B:630:ARG:NE	1:J:540:LYS:CG	2.65	0.58
1:D:278:LEU:CD2	1:D:280:LYS:HG2	2.33	0.58
1:E:229:PHE:HA	1:E:232:LYS:CG	2.32	0.58
1:E:581:LEU:HD12	1:E:838:VAL:HG23	1.84	0.58
1:F:785:ALA:HA	1:F:788:ARG:NH1	2.18	0.58
1:G:878:ASP:CB	1:G:881:VAL:HG12	2.29	0.58
1:H:817:ASN:HB3	1:H:820:TYR:HB2	1.83	0.58
1:J:294:LEU:HB2	1:J:355:LEU:H	1.69	0.58
1:A:394:LEU:HD13	1:A:395:ALA:H	1.67	0.58
1:A:508:LYS:O	1:A:512:VAL:HG23	2.03	0.58
1:B:456:ILE:HG23	1:B:456:ILE:O	2.02	0.58
1:B:510:LEU:C	1:B:510:LEU:HD23	2.28	0.58
1:C:615:ILE:HD11	1:C:803:ARG:HE	1.68	0.58
1:E:246:GLN:N	1:E:246:GLN:OE1	2.34	0.58
1:E:363:TYR:N	1:E:363:TYR:HD1	2.01	0.58
1:J:499:SER:O	1:J:500:THR:CG2	2.51	0.58
1:A:269:LEU:HD23	1:A:457:SER:CB	2.26	0.58
1:A:276:GLU:OE1	1:A:303:ASP:OD1	2.20	0.58
1:A:376:LYS:NZ	1:A:376:LYS:HA	2.18	0.58
1:A:394:LEU:HD21	1:A:412:SER:HB2	1.86	0.58
1:F:396:ILE:HG22	1:F:425:VAL:HB	1.84	0.58
1:F:667:SER:OG	1:F:668:SER:N	2.37	0.58
1:H:272:ILE:CG2	1:H:277:PHE:HD1	2.14	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:613:ASP:HB3	1:I:627:TYR:CZ	2.38	0.58
1:I:615:ILE:O	1:I:618:LEU:HB2	2.04	0.58
1:J:510:LEU:O	1:J:510:LEU:HD22	2.03	0.58
1:A:278:LEU:HD21	1:A:280:LYS:CG	2.33	0.58
1:A:355:LEU:HD23	1:A:357:LEU:CD2	2.32	0.58
1:H:251:THR:HG22	1:H:252:LEU:H	1.68	0.58
1:H:478:ASN:ND2	1:H:482:LYS:HZ2	1.92	0.58
1:A:434:PRO:CG	1:A:488:HIS:CG	2.87	0.58
1:H:617:ASP:OD1	1:H:617:ASP:N	2.37	0.58
1:A:279:PRO:CG	1:A:325:LEU:HD21	2.22	0.58
1:A:526:GLU:OE1	1:A:530:ARG:NH1	2.37	0.58
1:A:865:MET:HB3	1:A:871:LEU:HB2	1.86	0.58
1:B:534:GLU:OE2	1:D:646:ARG:NH2	2.26	0.58
1:D:260:SER:N	1:D:263:SER:HB3	2.19	0.58
1:F:855:ARG:NH2	1:G:559:ASP:OD2	2.36	0.58
1:G:402:ASP:HB2	1:J:261:GLN:HG2	1.78	0.58
1:D:296:ASN:HB2	1:D:354:ASP:OD2	2.04	0.58
1:E:296:ASN:C	1:E:298:PRO:HD3	2.29	0.58
1:A:232:LYS:HA	1:A:235:ILE:CG2	2.34	0.58
1:A:285:ILE:CD1	1:A:287:ARG:CA	2.82	0.58
1:D:286:THR:O	1:D:361:PRO:HD3	2.04	0.58
1:E:298:PRO:O	1:E:299:GLU:HB3	2.03	0.58
1:I:484:TYR:HD1	1:I:485:PHE:CD1	2.21	0.58
1:B:528:ILE:O	1:B:531:GLU:HG2	2.04	0.58
1:C:318:PHE:HD1	1:C:321:ILE:HD12	1.68	0.58
1:D:376:LYS:HA	1:D:376:LYS:CE	2.33	0.58
1:E:484:TYR:HE1	1:E:492:PHE:CZ	2.21	0.58
1:G:400:ASP:N	1:G:400:ASP:OD1	2.37	0.58
1:H:278:LEU:HB2	1:H:279:PRO:HD2	1.85	0.58
1:I:258:ILE:HG22	1:I:360:LEU:HD11	1.85	0.58
1:I:597:TYR:HA	1:I:627:TYR:OH	2.04	0.58
1:J:300:ALA:C	1:J:301:LYS:HD3	2.29	0.58
1:J:578:GLN:HA	1:J:838:VAL:HG21	1.85	0.58
1:A:492:PHE:O	1:A:492:PHE:HD1	1.87	0.57
1:D:297:ASP:N	1:D:298:PRO:CD	2.67	0.57
1:E:576:GLN:H	1:E:576:GLN:HE21	1.52	0.57
1:E:640:THR:HG21	1:E:706:LYS:HA	1.86	0.57
1:G:405:ASN:HB2	1:J:261:GLN:CB	2.27	0.57
1:I:661:GLU:OE2	1:I:676:ARG:NH2	2.36	0.57
1:A:429:MET:HE2	1:A:437:GLY:CA	2.27	0.57
1:E:485:PHE:HA	1:E:492:PHE:HE1	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:297:ASP:HB3	1:F:349:SER:C	2.29	0.57
1:J:499:SER:O	1:J:500:THR:HG23	2.03	0.57
1:A:384:ASP:C	1:A:384:ASP:OD1	2.45	0.57
1:A:593:LEU:HD21	1:A:823:GLU:HG3	1.86	0.57
1:B:376:LYS:HE2	1:B:376:LYS:N	2.18	0.57
1:G:249:THR:HG23	1:G:250:VAL:O	2.04	0.57
1:H:308:PRO:HG3	1:H:344:ARG:CB	2.33	0.57
1:I:625:SER:O	1:I:628:TRP:CD1	2.56	0.57
1:I:626:PRO:C	1:I:628:TRP:N	2.57	0.57
1:I:627:TYR:CD2	1:I:628:TRP:CZ3	2.91	0.57
1:A:536:THR:HB	1:I:630:ARG:HH11	1.69	0.57
1:B:640:THR:HG22	1:B:706:LYS:HG2	1.86	0.57
1:C:429:MET:HE1	1:C:441:LEU:HB2	1.87	0.57
1:D:377:ARG:HH21	1:D:377:ARG:CG	2.17	0.57
1:E:246:GLN:CG	1:E:247:GLY:N	2.67	0.57
1:H:456:ILE:HD12	1:H:456:ILE:C	2.29	0.57
1:A:716:TRP:CE3	1:A:815:LEU:HD23	2.40	0.57
1:D:284:MET:N	1:D:284:MET:SD	2.76	0.57
1:E:237:ILE:O	1:E:237:ILE:HD13	2.05	0.57
1:E:441:LEU:CB	1:E:498:VAL:CG1	2.82	0.57
1:J:433:GLU:O	1:J:436:LYS:HB2	2.03	0.57
1:A:240:LEU:N	1:A:240:LEU:CD2	2.64	0.57
1:D:727:LEU:HD21	1:D:823:GLU:HG2	1.86	0.57
1:E:257:VAL:HG22	1:E:358:ILE:O	2.04	0.57
1:F:264:GLY:HA2	1:F:267:SER:HB3	1.85	0.57
1:H:768:VAL:HG23	1:H:770:GLY:H	1.70	0.57
1:I:431:LEU:H	1:I:431:LEU:HD23	1.70	0.57
1:I:449:LYS:C	1:I:451:GLY:H	2.11	0.57
1:A:480:ASN:HA	1:A:483:ASN:OD1	2.05	0.57
1:D:243:LYS:O	1:D:243:LYS:HG2	2.03	0.57
1:D:387:ILE:O	1:D:421:ARG:NH2	2.37	0.57
1:F:855:ARG:HA	1:F:855:ARG:HE	1.70	0.57
1:A:230:ILE:O	1:A:234:MET:HG3	2.04	0.57
1:A:749:LYS:H	1:A:749:LYS:HD2	1.70	0.57
1:D:265:LYS:HA	1:D:268:VAL:CG2	2.35	0.57
1:G:429:MET:HE1	1:G:441:LEU:HB2	1.87	0.57
1:H:272:ILE:HG12	1:H:280:LYS:HG3	1.85	0.57
1:J:233:LYS:HA	1:J:233:LYS:HE2	1.85	0.57
1:J:705:TYR:CE1	1:J:832:LYS:HD3	2.40	0.57
1:A:326:THR:HA	1:A:329:ASN:CG	2.30	0.57
1:A:376:LYS:CA	1:A:376:LYS:CE	2.82	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:LEU:HD21	1:A:498:VAL:CB	2.23	0.57
1:D:285:ILE:CG1	1:D:286:THR:N	2.67	0.57
1:D:889:ARG:HG3	1:D:890:ARG:N	2.19	0.57
1:E:272:ILE:CG2	1:E:278:LEU:H	2.17	0.57
1:E:433:GLU:O	1:E:436:LYS:HB2	2.05	0.57
1:F:610:ARG:HE	1:F:613:ASP:HB2	1.70	0.57
1:F:661:GLU:OE2	1:F:676:ARG:NH2	2.38	0.57
1:G:843:VAL:O	1:G:847:ASN:HB2	2.05	0.57
1:A:269:LEU:HD22	1:A:457:SER:OG	1.98	0.57
1:A:278:LEU:CD1	1:A:280:LYS:HG2	2.34	0.57
1:C:259:GLY:HA2	1:C:408:ALA:HB2	1.87	0.57
1:D:260:SER:H	1:D:263:SER:HB3	1.70	0.57
1:H:284:MET:HG2	1:H:286:THR:CG2	2.34	0.57
1:I:429:MET:HE2	1:I:437:GLY:HA2	1.85	0.57
1:J:749:LYS:O	1:J:753:GLU:HG3	2.05	0.57
1:J:791:VAL:HG13	1:J:794:ARG:NH2	2.20	0.57
1:A:278:LEU:CD2	1:A:280:LYS:CG	2.83	0.56
1:D:255:ILE:HA	1:D:392:ILE:O	2.05	0.56
1:G:377:ARG:HG3	1:G:377:ARG:O	2.05	0.56
1:H:279:PRO:HB3	1:H:322:GLN:CA	2.34	0.56
1:I:257:VAL:HG12	1:I:394:LEU:HB3	1.86	0.56
1:I:275:HIS:CE1	1:I:278:LEU:HD12	2.40	0.56
1:I:803:ARG:NH1	1:I:806:ALA:HB1	2.19	0.56
1:A:542:GLN:C	1:A:543:TYR:CD2	2.83	0.56
1:B:433:GLU:O	1:B:436:LYS:HB2	2.04	0.56
1:D:275:HIS:CG	1:D:276:GLU:H	2.23	0.56
1:E:349:SER:O	1:E:352:ILE:HG13	2.05	0.56
1:E:436:LYS:O	1:E:440:ILE:HG13	2.04	0.56
1:E:455:VAL:HG12	1:E:501:GLY:CA	2.35	0.56
1:H:361:PRO:CG	1:H:382:LEU:HD21	2.35	0.56
1:A:272:ILE:HG23	1:A:278:LEU:H	1.69	0.56
1:A:272:ILE:CG1	1:A:278:LEU:HD11	2.31	0.56
1:A:454:GLY:O	1:A:455:VAL:HG13	2.05	0.56
1:B:772:HIS:HB3	1:E:774:SER:OG	2.04	0.56
1:B:774:SER:O	1:B:781:ALA:HA	2.06	0.56
1:D:285:ILE:HD11	1:D:287:ARG:HB2	1.77	0.56
1:D:477:ILE:HG22	1:D:477:ILE:O	2.05	0.56
1:D:526:GLU:OE1	1:D:530:ARG:NH1	2.38	0.56
1:E:279:PRO:HB3	1:E:322:GLN:CG	2.35	0.56
1:E:387:ILE:HG22	1:E:415:VAL:HG21	1.86	0.56
1:F:855:ARG:HA	1:F:855:ARG:NE	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:508:LYS:O	1:G:512:VAL:HG23	2.04	0.56
1:H:279:PRO:CG	1:H:322:GLN:HA	2.35	0.56
1:H:441:LEU:CD2	1:H:499:SER:N	2.60	0.56
1:H:454:GLY:O	1:H:455:VAL:CG1	2.54	0.56
1:H:749:LYS:H	1:H:749:LYS:HD2	1.70	0.56
1:J:229:PHE:CE1	1:J:232:LYS:CD	2.81	0.56
1:J:230:ILE:O	1:J:234:MET:HG3	2.05	0.56
1:J:376:LYS:NZ	1:J:379:ILE:HD12	2.20	0.56
1:J:524:THR:O	1:J:528:ILE:HG13	2.05	0.56
1:A:277:PHE:HD1	1:A:278:LEU:H	1.52	0.56
1:A:326:THR:HG22	1:A:329:ASN:HD22	1.69	0.56
1:D:441:LEU:CB	1:D:498:VAL:CG1	2.83	0.56
1:E:229:PHE:O	1:E:232:LYS:HG3	2.06	0.56
1:F:294:LEU:HB3	1:F:352:ILE:HD13	1.85	0.56
1:F:664:LEU:HB3	1:F:676:ARG:NH1	2.20	0.56
1:G:261:GLN:H	1:J:405:ASN:ND2	2.02	0.56
1:G:701:SER:O	1:G:704:PRO:HD2	2.06	0.56
1:A:285:ILE:O	1:A:286:THR:OG1	2.23	0.56
1:B:227:MET:O	1:B:230:ILE:HG22	2.05	0.56
1:B:254:SER:HB2	1:B:356:SER:O	2.06	0.56
1:E:297:ASP:HB3	1:E:349:SER:C	2.31	0.56
1:F:268:VAL:O	1:F:272:ILE:HG13	2.05	0.56
1:H:238:ARG:NH2	1:H:356:SER:HG	2.02	0.56
1:H:485:PHE:CD2	1:H:492:PHE:HD1	2.23	0.56
1:A:355:LEU:HD23	1:A:357:LEU:HD22	1.87	0.56
1:H:387:ILE:CG2	1:H:415:VAL:HG21	2.36	0.56
1:J:682:ALA:O	1:J:685:THR:HG22	2.05	0.56
1:A:225:ASP:OD1	1:A:225:ASP:N	2.37	0.56
1:A:272:ILE:HG21	1:A:277:PHE:CD1	2.40	0.56
1:B:308:PRO:HG3	1:B:344:ARG:HB2	1.87	0.56
1:E:265:LYS:O	1:E:268:VAL:HG23	2.06	0.56
1:H:279:PRO:CG	1:H:325:LEU:HD21	2.28	0.56
1:H:296:ASN:C	1:H:298:PRO:HD3	2.31	0.56
1:H:493:GLY:O	1:H:496:SER:HB3	2.05	0.56
1:H:673:PRO:HD2	1:H:877:GLU:OE1	2.05	0.56
1:J:272:ILE:HG12	1:J:278:LEU:CD1	2.35	0.56
1:J:272:ILE:HG21	1:J:277:PHE:HD1	1.71	0.56
1:J:456:ILE:HG23	1:J:456:ILE:O	2.06	0.56
1:J:749:LYS:HD2	1:J:749:LYS:H	1.70	0.56
1:A:454:GLY:N	1:A:500:THR:HG22	2.19	0.56
1:D:363:TYR:N	1:D:363:TYR:CD1	2.74	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:648:ALA:HB1	1:D:841:LEU:HD12	1.86	0.56
1:E:279:PRO:O	1:E:280:LYS:CD	2.54	0.56
1:E:642:LEU:HD12	1:E:643:GLY:N	2.21	0.56
1:H:257:VAL:HG22	1:H:359:ASP:HA	1.86	0.56
1:H:266:SER:HB2	1:H:427:THR:OG1	2.06	0.56
1:H:272:ILE:CG2	1:H:278:LEU:HD13	2.32	0.56
1:I:249:THR:OG1	1:I:531:GLU:OE1	2.19	0.56
1:A:540:LYS:HD2	1:I:626:PRO:CA	2.19	0.56
1:B:475:ALA:O	1:B:479:ARG:HG2	2.05	0.56
1:C:239:ASN:HD21	1:C:293:THR:HG21	1.71	0.56
1:C:284:MET:N	1:C:284:MET:SD	2.75	0.56
1:D:778:GLY:C	1:D:779:PHE:HD2	2.14	0.56
1:F:627:TYR:OH	1:F:631:GLN:NE2	2.38	0.56
1:H:485:PHE:HA	1:H:492:PHE:HE1	1.71	0.56
1:I:268:VAL:O	1:I:272:ILE:HG13	2.05	0.56
1:I:803:ARG:NH1	1:I:806:ALA:CB	2.69	0.56
1:J:296:ASN:HB2	1:J:354:ASP:OD2	2.06	0.56
1:A:255:ILE:HA	1:A:392:ILE:O	2.06	0.56
1:A:434:PRO:HB3	1:A:491:GLU:CB	2.36	0.56
1:E:275:HIS:CG	1:E:276:GLU:N	2.73	0.56
1:G:627:TYR:OH	1:G:631:GLN:NE2	2.39	0.56
1:H:426:ILE:CD1	1:H:440:ILE:HG23	2.28	0.56
1:H:426:ILE:HD13	1:H:440:ILE:HG23	1.78	0.56
1:H:450:LEU:HD22	1:H:512:VAL:HG22	1.88	0.56
1:J:445:GLN:O	1:J:446:TYR:CD1	2.58	0.56
1:J:575:PRO:O	1:J:578:GLN:HB3	2.06	0.56
1:B:563:HIS:CD2	1:C:566:HIS:CE1	2.94	0.55
1:C:672:HIS:CD2	1:C:877:GLU:HB2	2.38	0.55
1:C:843:VAL:HG21	1:D:704:PRO:HA	1.89	0.55
1:D:232:LYS:HG3	1:D:233:LYS:HE3	1.88	0.55
1:E:444:ARG:O	1:E:447:PRO:HD3	2.06	0.55
1:E:456:ILE:O	1:E:481:GLU:OE2	2.23	0.55
1:G:720:ARG:NH1	1:G:813:LYS:HA	2.21	0.55
1:G:878:ASP:HB3	1:G:881:VAL:HG11	1.83	0.55
1:I:411:ALA:O	1:I:414:ARG:HB3	2.06	0.55
1:I:855:ARG:NE	1:I:855:ARG:HA	2.21	0.55
1:J:279:PRO:HG2	1:J:325:LEU:CD2	2.34	0.55
1:J:640:THR:HG21	1:J:706:LYS:HA	1.87	0.55
1:A:297:ASP:OD1	1:A:300:ALA:HB3	2.04	0.55
1:B:528:ILE:HA	1:B:531:GLU:CD	2.32	0.55
1:C:755:MET:HE3	1:C:790:ALA:HB1	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:LEU:HD21	1:D:280:LYS:CG	2.35	0.55
1:D:279:PRO:HG3	1:D:321:ILE:HG22	1.88	0.55
1:E:266:SER:HB2	1:E:427:THR:OG1	2.07	0.55
1:E:309:ASP:C	1:E:310:LEU:HD23	2.31	0.55
1:E:642:LEU:HD12	1:E:643:GLY:C	2.31	0.55
1:H:285:ILE:CD1	1:H:287:ARG:CB	2.75	0.55
1:I:642:LEU:HD22	1:I:643:GLY:N	2.21	0.55
1:J:485:PHE:O	1:J:489:PRO:HA	2.06	0.55
1:B:249:THR:OG1	1:B:531:GLU:OE1	2.19	0.55
1:B:326:THR:O	1:B:329:ASN:HB2	2.06	0.55
1:B:357:LEU:HD23	1:B:357:LEU:H	1.71	0.55
1:B:611:GLU:N	1:B:612:PRO:HD2	2.22	0.55
1:C:235:ILE:HD13	1:C:356:SER:CB	2.35	0.55
1:D:275:HIS:HB2	1:D:352:ILE:HG21	1.87	0.55
1:E:564:GLN:HG2	1:E:663:LEU:HD11	1.89	0.55
1:E:817:ASN:HB3	1:E:820:TYR:HB2	1.89	0.55
1:G:611:GLU:N	1:G:612:PRO:CD	2.61	0.55
1:H:239:ASN:HB3	1:H:240:LEU:HD23	1.88	0.55
1:H:285:ILE:HD12	1:H:286:THR:N	2.20	0.55
1:J:339:THR:HG23	1:J:340:ASP:H	1.69	0.55
1:J:401:THR:HG22	1:J:402:ASP:O	2.06	0.55
1:J:521:LEU:HD13	1:J:521:LEU:C	2.31	0.55
1:A:441:LEU:HG	1:A:498:VAL:CG1	2.16	0.55
1:A:478:ASN:CG	1:A:482:LYS:NZ	2.62	0.55
1:G:252:LEU:HD23	1:G:524:THR:HG21	1.89	0.55
1:H:363:TYR:CE1	1:H:383:CYS:SG	2.84	0.55
1:H:399:ALA:HA	1:H:411:ALA:HB3	1.88	0.55
1:H:710:ASP:O	1:H:832:LYS:NZ	2.39	0.55
1:J:278:LEU:CD2	1:J:280:LYS:HG2	2.36	0.55
1:C:837:ALA:O	1:C:841:LEU:HB2	2.05	0.55
1:D:272:ILE:HG23	1:D:278:LEU:N	2.22	0.55
1:D:278:LEU:CD2	1:D:280:LYS:CG	2.84	0.55
1:D:278:LEU:HD22	1:D:280:LYS:HG2	1.88	0.55
1:E:278:LEU:HD22	1:E:280:LYS:HG2	1.89	0.55
1:G:364:ILE:CG2	1:J:405:ASN:OD1	2.53	0.55
1:A:308:PRO:HG3	1:A:344:ARG:HG3	1.87	0.55
1:A:387:ILE:CG2	1:A:415:VAL:HG21	2.36	0.55
1:E:485:PHE:CD2	1:E:492:PHE:HD1	2.18	0.55
1:F:272:ILE:HD11	1:F:280:LYS:HB2	1.89	0.55
1:F:442:SER:HB2	1:F:498:VAL:HG12	1.88	0.55
1:H:275:HIS:H	1:H:275:HIS:CD2	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:627:TYR:HD2	1:I:628:TRP:HZ3	1.54	0.55
1:I:832:LYS:O	1:I:836:THR:HG22	2.06	0.55
1:J:255:ILE:HA	1:J:392:ILE:O	2.06	0.55
1:J:297:ASP:HB3	1:J:349:SER:C	2.31	0.55
1:J:672:HIS:HA	1:J:877:GLU:OE2	2.06	0.55
1:A:269:LEU:CG	1:A:457:SER:O	2.53	0.55
1:A:297:ASP:OD1	1:A:300:ALA:CB	2.55	0.55
1:A:339:THR:CG2	1:A:340:ASP:H	2.20	0.55
1:E:524:THR:O	1:E:528:ILE:HG13	2.06	0.55
1:I:705:TYR:CE1	1:I:832:LYS:HD3	2.42	0.55
1:J:278:LEU:CD2	1:J:280:LYS:CG	2.85	0.55
1:J:455:VAL:HG12	1:J:501:GLY:H	1.72	0.55
1:D:349:SER:O	1:D:352:ILE:HG13	2.07	0.55
1:E:255:ILE:HD11	1:E:355:LEU:HG	1.89	0.55
1:E:255:ILE:HA	1:E:392:ILE:O	2.07	0.55
1:E:298:PRO:O	1:E:299:GLU:CB	2.55	0.55
1:E:657:GLN:HE22	1:E:684:ALA:HA	1.70	0.55
1:F:269:LEU:HD11	1:F:457:SER:O	2.07	0.55
1:G:267:SER:CB	1:G:396:ILE:HG13	2.36	0.55
1:G:607:PRO:HD3	1:G:762:ARG:HG3	1.89	0.55
1:H:251:THR:HG22	1:H:252:LEU:N	2.22	0.55
1:J:286:THR:OG1	1:J:361:PRO:HB3	2.07	0.55
1:J:311:GLY:O	1:J:312:LEU:HB2	2.06	0.55
1:D:275:HIS:HB2	1:D:352:ILE:CG2	2.37	0.55
1:D:279:PRO:O	1:D:280:LYS:CD	2.55	0.55
1:D:750:LYS:HE2	1:G:772:HIS:ND1	2.22	0.55
1:G:518:SER:O	1:G:521:LEU:HB3	2.07	0.55
1:J:285:ILE:HD12	1:J:287:ARG:CA	2.27	0.55
1:A:242:GLN:HE22	1:A:344:ARG:CD	2.20	0.55
1:B:376:LYS:HE2	1:B:376:LYS:HA	1.88	0.55
1:D:263:SER:HA	1:D:266:SER:OG	2.07	0.55
1:D:272:ILE:HG12	1:D:278:LEU:HD11	1.89	0.55
1:D:286:THR:O	1:D:361:PRO:CD	2.55	0.55
1:D:454:GLY:O	1:D:455:VAL:HG13	2.07	0.55
1:D:817:ASN:HB3	1:D:820:TYR:HB2	1.89	0.55
1:E:272:ILE:CG1	1:E:278:LEU:CD1	2.83	0.55
1:J:240:LEU:N	1:J:240:LEU:HD23	2.22	0.55
1:J:307:PHE:CD1	1:J:345:LEU:CD2	2.90	0.55
1:B:578:GLN:HA	1:B:838:VAL:HG21	1.89	0.54
1:C:284:MET:HG2	1:C:286:THR:HG22	1.88	0.54
1:G:401:THR:HA	1:J:262:SER:OG	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:472:ASN:OD1	1:G:475:ALA:HB3	2.07	0.54
1:G:708:ASP:OD1	1:G:710:ASP:HB3	2.07	0.54
1:H:694:THR:HG21	1:H:845:MET:HB2	1.88	0.54
1:H:832:LYS:O	1:H:835:GLN:HG2	2.07	0.54
1:A:275:HIS:CG	1:A:276:GLU:N	2.75	0.54
1:D:246:GLN:CD	1:D:247:GLY:H	2.15	0.54
1:E:276:GLU:OE1	1:E:318:PHE:HE2	1.89	0.54
1:E:456:ILE:HD12	1:E:457:SER:N	2.22	0.54
1:J:229:PHE:HA	1:J:232:LYS:HG3	1.83	0.54
1:J:242:GLN:HE22	1:J:344:ARG:CD	2.20	0.54
1:J:255:ILE:HG13	1:J:357:LEU:HA	1.89	0.54
1:A:273:VAL:CG1	1:A:457:SER:HB2	2.31	0.54
1:A:540:LYS:NZ	1:I:625:SER:C	2.64	0.54
1:G:405:ASN:CB	1:J:261:GLN:CB	2.83	0.54
1:H:387:ILE:HG22	1:H:415:VAL:HG21	1.90	0.54
1:I:275:HIS:CG	1:I:276:GLU:N	2.75	0.54
1:I:375:LEU:HB2	1:I:376:LYS:HE2	1.90	0.54
1:J:279:PRO:HG3	1:J:321:ILE:HG22	1.88	0.54
1:A:287:ARG:HH11	1:A:287:ARG:HG3	1.72	0.54
1:A:393:ILE:O	1:A:394:LEU:CB	2.47	0.54
1:B:268:VAL:HB	1:B:280:LYS:HB3	1.90	0.54
1:C:780:SER:OG	1:C:783:LEU:HB2	2.08	0.54
1:D:240:LEU:N	1:D:240:LEU:HD23	2.22	0.54
1:D:492:PHE:O	1:D:492:PHE:CD1	2.56	0.54
1:D:499:SER:O	1:D:500:THR:CG2	2.56	0.54
1:E:454:GLY:O	1:E:455:VAL:HG13	2.07	0.54
1:F:269:LEU:CD2	1:F:457:SER:HB2	2.37	0.54
1:F:854:PRO:HB2	1:F:855:ARG:CZ	2.38	0.54
1:G:618:LEU:HG	1:G:803:ARG:NH2	2.23	0.54
1:H:425:VAL:HA	1:H:453:VAL:O	2.08	0.54
1:I:328:LEU:HD13	1:I:343:ILE:HD13	1.90	0.54
1:I:585:LEU:HD12	1:I:834:ALA:HB2	1.88	0.54
1:A:484:TYR:HE1	1:A:492:PHE:CZ	2.26	0.54
1:D:382:LEU:HD12	1:D:382:LEU:O	2.07	0.54
1:E:229:PHE:CD1	1:E:232:LYS:CE	2.90	0.54
1:E:269:LEU:HD21	1:E:457:SER:C	2.33	0.54
1:F:273:VAL:HG12	1:F:477:ILE:HD13	1.88	0.54
1:I:402:ASP:CB	1:I:405:ASN:HB2	2.37	0.54
1:I:616:ILE:HD12	1:I:616:ILE:O	2.07	0.54
1:A:318:PHE:CD1	1:A:321:ILE:HD12	2.43	0.54
1:A:832:LYS:O	1:A:836:THR:HG22	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:426:ILE:HG21	1:C:429:MET:HE3	1.90	0.54
1:D:640:THR:HG21	1:D:706:LYS:HA	1.90	0.54
1:E:441:LEU:CB	1:E:498:VAL:HG12	2.38	0.54
1:E:492:PHE:CD1	1:E:492:PHE:O	2.61	0.54
1:F:376:LYS:HZ3	1:F:379:ILE:HD12	1.69	0.54
1:H:269:LEU:HD23	1:H:270:GLU:CA	2.38	0.54
1:J:339:THR:CG2	1:J:340:ASP:H	2.19	0.54
1:A:483:ASN:C	1:A:483:ASN:HD22	2.16	0.54
1:A:529:GLN:HG2	1:A:898:LEU:HD21	1.89	0.54
1:D:387:ILE:HG22	1:D:415:VAL:HG21	1.90	0.54
1:D:723:VAL:O	1:D:727:LEU:HB2	2.07	0.54
1:E:238:ARG:NH2	1:E:356:SER:HG	2.05	0.54
1:E:392:ILE:HD12	1:E:421:ARG:O	2.06	0.54
1:F:642:LEU:HD22	1:F:643:GLY:H	1.70	0.54
1:G:832:LYS:O	1:G:835:GLN:HG2	2.07	0.54
1:H:232:LYS:O	1:H:235:ILE:CG2	2.55	0.54
1:J:272:ILE:CG2	1:J:278:LEU:H	2.20	0.54
1:J:441:LEU:HD23	1:J:498:VAL:HG12	1.72	0.54
1:A:393:ILE:HG12	1:A:394:LEU:CB	2.36	0.54
1:E:376:LYS:NZ	1:E:379:ILE:CD1	2.64	0.54
1:F:637:SER:O	1:F:641:ARG:HB2	2.08	0.54
1:H:349:SER:HB3	1:H:352:ILE:HG23	1.88	0.54
1:H:578:GLN:HA	1:H:838:VAL:HG21	1.90	0.54
1:I:699:GLU:OE1	1:I:699:GLU:HA	2.06	0.54
1:A:259:GLY:HA2	1:A:408:ALA:HB2	1.89	0.54
1:A:310:LEU:HD23	1:A:310:LEU:N	2.23	0.54
1:A:363:TYR:N	1:A:363:TYR:CD1	2.74	0.54
1:A:363:TYR:N	1:A:363:TYR:HD1	2.06	0.54
1:B:235:ILE:HD11	1:B:293:THR:HG22	1.90	0.54
1:B:627:TYR:HD1	1:B:630:ARG:NH2	2.05	0.54
1:J:264:GLY:O	1:J:268:VAL:HG22	2.07	0.54
1:J:269:LEU:O	1:J:273:VAL:HG13	2.08	0.54
1:A:246:GLN:HG2	1:A:247:GLY:H	1.70	0.54
1:A:436:LYS:O	1:A:440:ILE:HG13	2.08	0.54
1:E:483:ASN:C	1:E:483:ASN:HD22	2.15	0.54
1:E:672:HIS:HA	1:E:877:GLU:OE2	2.08	0.54
1:G:269:LEU:HA	1:G:272:ILE:HD12	1.89	0.54
1:H:387:ILE:O	1:H:421:ARG:NH2	2.41	0.54
1:I:626:PRO:CB	1:I:626:PRO:C	2.76	0.54
1:I:843:VAL:HG21	1:J:704:PRO:HA	1.90	0.54
1:J:272:ILE:HG23	1:J:278:LEU:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:474:LEU:HG	1:J:475:ALA:H	1.73	0.54
1:J:508:LYS:O	1:J:512:VAL:HG23	2.08	0.54
1:A:375:LEU:N	1:A:375:LEU:CD2	2.56	0.53
1:A:376:LYS:HZ1	1:A:379:ILE:HD12	1.72	0.53
1:A:454:GLY:O	1:A:455:VAL:CG1	2.56	0.53
1:E:238:ARG:HA	1:E:241:LEU:HD12	1.89	0.53
1:E:749:LYS:H	1:E:749:LYS:CD	2.16	0.53
1:G:261:GLN:HE21	1:J:401:THR:CG2	2.19	0.53
1:J:225:ASP:N	1:J:225:ASP:OD1	2.39	0.53
1:J:441:LEU:CB	1:J:498:VAL:HG12	2.38	0.53
1:A:275:HIS:HB2	1:A:352:ILE:CG2	2.38	0.53
1:D:254:SER:HB2	1:D:356:SER:O	2.08	0.53
1:E:269:LEU:HD23	1:E:457:SER:OG	2.06	0.53
1:E:287:ARG:HH11	1:E:287:ARG:CG	2.20	0.53
1:E:308:PRO:CG	1:E:344:ARG:HG3	2.38	0.53
1:E:610:ARG:HE	1:E:611:GLU:N	2.07	0.53
1:F:325:LEU:C	1:F:325:LEU:HD12	2.33	0.53
1:G:387:ILE:HG22	1:G:415:VAL:HG21	1.90	0.53
1:J:263:SER:HA	1:J:266:SER:OG	2.08	0.53
1:J:673:PRO:HD2	1:J:877:GLU:OE1	2.07	0.53
1:F:244:VAL:HA	1:F:893:LEU:HD13	1.89	0.53
1:G:360:LEU:HB2	1:G:361:PRO:HD2	1.89	0.53
1:H:241:LEU:CD2	1:H:528:ILE:HD11	2.38	0.53
1:H:296:ASN:O	1:H:298:PRO:HD3	2.08	0.53
1:H:412:SER:C	1:H:413:ARG:CG	2.82	0.53
1:H:754:VAL:HA	1:H:779:PHE:CE1	2.43	0.53
1:I:269:LEU:O	1:I:272:ILE:HB	2.09	0.53
1:J:484:TYR:C	1:J:486:GLY:H	2.16	0.53
1:A:528:ILE:HG23	1:A:894:LEU:HD22	1.90	0.53
1:B:627:TYR:HA	1:J:540:LYS:HD3	1.89	0.53
1:D:263:SER:OG	1:D:397:SER:HA	2.09	0.53
1:G:255:ILE:HD11	1:G:355:LEU:HG	1.89	0.53
1:H:434:PRO:HG2	1:H:488:HIS:CE1	2.44	0.53
1:H:454:GLY:O	1:H:455:VAL:HG13	2.08	0.53
1:I:873:LYS:O	1:I:877:GLU:HG3	2.09	0.53
1:A:456:ILE:O	1:A:481:GLU:OE2	2.25	0.53
1:B:630:ARG:CZ	1:J:537:TYR:HD1	2.21	0.53
1:C:572:PHE:HB3	1:C:850:TYR:OH	2.07	0.53
1:C:609:PRO:HB2	1:C:610:ARG:CA	2.38	0.53
1:D:229:PHE:O	1:D:233:LYS:HG2	2.09	0.53
1:D:231:THR:O	1:D:235:ILE:HG22	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:237:ILE:O	1:D:237:ILE:HD13	2.09	0.53
1:E:272:ILE:HG12	1:E:278:LEU:HD11	1.91	0.53
1:E:529:GLN:HG2	1:E:898:LEU:HD21	1.91	0.53
1:F:235:ILE:HD12	1:F:235:ILE:O	2.09	0.53
1:F:434:PRO:HG2	1:F:488:HIS:ND1	2.23	0.53
1:F:690:ARG:NH1	1:F:844:GLU:OE2	2.41	0.53
1:G:259:GLY:HA2	1:G:408:ALA:HB2	1.89	0.53
1:H:454:GLY:O	1:H:500:THR:CB	2.57	0.53
1:H:528:ILE:HG23	1:H:894:LEU:HD22	1.90	0.53
1:H:640:THR:HG21	1:H:706:LYS:HA	1.91	0.53
1:J:238:ARG:NH2	1:J:356:SER:OG	2.40	0.53
1:J:454:GLY:O	1:J:455:VAL:HG13	2.08	0.53
1:A:278:LEU:HD22	1:A:279:PRO:O	2.08	0.53
1:E:297:ASP:CG	1:E:300:ALA:CB	2.76	0.53
1:E:762:ARG:NH1	1:E:762:ARG:HG2	2.22	0.53
1:H:239:ASN:C	1:H:240:LEU:HD23	2.34	0.53
1:I:762:ARG:HG2	1:I:762:ARG:HH11	1.73	0.53
1:J:275:HIS:CG	1:J:276:GLU:N	2.75	0.53
1:B:285:ILE:HD13	1:B:332:VAL:HG22	1.91	0.53
1:C:249:THR:OG1	1:C:531:GLU:OE1	2.17	0.53
1:E:272:ILE:HG23	1:E:278:LEU:H	1.73	0.53
1:H:363:TYR:HE2	1:H:407:THR:OG1	1.91	0.53
1:H:565:PHE:HA	1:H:663:LEU:HD21	1.91	0.53
1:I:269:LEU:HA	1:I:272:ILE:HD12	1.89	0.53
1:J:387:ILE:CG2	1:J:415:VAL:HG21	2.38	0.53
1:J:775:GLY:HA2	1:J:779:PHE:O	2.09	0.53
1:A:233:LYS:HE2	1:A:233:LYS:HA	1.91	0.53
1:B:575:PRO:O	1:B:578:GLN:HB3	2.09	0.53
1:C:272:ILE:HD11	1:C:280:LYS:HB2	1.90	0.53
1:D:267:SER:CB	1:D:396:ILE:HG13	2.37	0.53
1:D:694:THR:HG21	1:D:845:MET:HE3	1.91	0.53
1:E:704:PRO:HA	1:F:843:VAL:HG21	1.89	0.53
1:F:308:PRO:HG3	1:F:344:ARG:HB2	1.89	0.53
1:G:678:VAL:HG11	1:G:861:LEU:HD23	1.91	0.53
1:J:388:ARG:O	1:J:389:GLY:C	2.52	0.53
1:J:657:GLN:HE22	1:J:684:ALA:CA	2.21	0.53
1:A:665:ASP:OD1	1:A:676:ARG:NH2	2.42	0.53
1:A:738:MET:SD	1:A:738:MET:CB	2.94	0.53
1:B:233:LYS:HE3	1:B:900:LYS:HD2	1.91	0.53
1:B:564:GLN:HG2	1:B:663:LEU:HG	1.90	0.53
1:C:308:PRO:HG3	1:C:344:ARG:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:LYS:O	1:D:235:ILE:HG23	2.09	0.53
1:D:269:LEU:HD23	1:D:457:SER:OG	2.03	0.53
1:D:499:SER:O	1:D:500:THR:HG23	2.09	0.53
1:E:257:VAL:HG23	1:E:359:ASP:HA	1.88	0.53
1:E:673:PRO:HD2	1:E:877:GLU:OE1	2.08	0.53
1:H:269:LEU:HD23	1:H:457:SER:OG	1.99	0.53
1:H:433:GLU:O	1:H:436:LYS:HB2	2.08	0.53
1:B:611:GLU:H	1:B:612:PRO:HD2	1.74	0.53
1:D:484:TYR:HD1	1:D:485:PHE:CD1	2.27	0.53
1:G:363:TYR:CD2	1:G:407:THR:HB	2.44	0.53
1:H:272:ILE:CG2	1:H:278:LEU:H	2.22	0.53
1:J:284:MET:O	1:J:286:THR:HG23	2.09	0.53
1:J:387:ILE:HG22	1:J:415:VAL:HG21	1.91	0.53
1:A:254:SER:O	1:A:391:ASN:HB3	2.09	0.52
1:A:269:LEU:HD21	1:A:457:SER:O	2.10	0.52
1:A:576:GLN:NE2	1:A:576:GLN:H	2.07	0.52
1:A:705:TYR:CD1	1:A:832:LYS:HD3	2.43	0.52
1:B:425:VAL:HA	1:B:453:VAL:O	2.09	0.52
1:B:705:TYR:CE1	1:B:832:LYS:HD3	2.45	0.52
1:E:434:PRO:CG	1:E:488:HIS:CG	2.92	0.52
1:E:834:ALA:O	1:E:838:VAL:HB	2.08	0.52
1:H:233:LYS:N	1:H:233:LYS:CE	2.72	0.52
1:H:708:ASP:OD1	1:H:710:ASP:HB3	2.09	0.52
1:G:382:LEU:C	1:G:382:LEU:HD12	2.34	0.52
1:J:269:LEU:CA	1:J:272:ILE:HD12	2.20	0.52
1:J:574:ARG:N	1:J:575:PRO:HD2	2.24	0.52
1:A:232:LYS:HA	1:A:235:ILE:HG22	1.91	0.52
1:A:542:GLN:O	1:A:543:TYR:CD2	2.63	0.52
1:A:704:PRO:HA	1:B:843:VAL:HG21	1.90	0.52
1:B:255:ILE:HA	1:B:392:ILE:O	2.09	0.52
1:C:227:MET:HA	1:C:230:ILE:HG22	1.91	0.52
1:E:258:ILE:HG22	1:E:360:LEU:HD11	1.91	0.52
1:E:286:THR:O	1:E:361:PRO:CG	2.58	0.52
1:E:610:ARG:NE	1:E:610:ARG:HA	2.23	0.52
1:E:639:LEU:O	1:E:642:LEU:HD23	2.10	0.52
1:F:249:THR:OG1	1:F:531:GLU:OE1	2.23	0.52
1:G:405:ASN:HA	1:J:364:ILE:O	2.10	0.52
1:J:529:GLN:HG2	1:J:898:LEU:HD21	1.90	0.52
1:J:865:MET:HB3	1:J:871:LEU:HB2	1.91	0.52
1:H:657:GLN:HE22	1:H:684:ALA:HA	1.74	0.52
1:I:251:THR:HG22	1:I:252:LEU:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:SER:O	1:A:332:VAL:HB	2.08	0.52
1:D:275:HIS:H	1:D:275:HIS:CD2	2.26	0.52
1:D:286:THR:O	1:D:361:PRO:HB3	2.09	0.52
1:D:287:ARG:CG	1:D:287:ARG:NH1	2.66	0.52
1:H:231:THR:O	1:H:235:ILE:HG22	2.08	0.52
1:H:405:ASN:O	1:H:410:GLN:NE2	2.43	0.52
1:A:540:LYS:HZ3	1:I:627:TYR:H	1.57	0.52
1:B:277:PHE:HB2	1:B:473:LEU:HD23	1.92	0.52
1:C:631:GLN:OE1	1:C:631:GLN:HA	2.09	0.52
1:F:444:ARG:O	1:F:447:PRO:HD3	2.09	0.52
1:F:754:VAL:HG21	1:F:783:LEU:HD22	1.92	0.52
1:G:429:MET:HE2	1:G:437:GLY:HA2	1.92	0.52
1:H:818:LYS:HD2	1:H:825:PHE:CE1	2.45	0.52
1:J:560:ASP:OD2	1:J:668:SER:OG	2.26	0.52
1:A:537:TYR:N	1:I:630:ARG:NH1	2.56	0.52
1:C:617:ASP:OD1	1:C:617:ASP:N	2.42	0.52
1:C:744:SER:OG	1:C:786:ARG:NH2	2.42	0.52
1:D:259:GLY:HA2	1:D:408:ALA:HB2	1.92	0.52
1:D:266:SER:HB2	1:D:427:THR:OG1	2.10	0.52
1:F:279:PRO:HG2	1:F:325:LEU:HD21	1.91	0.52
1:F:285:ILE:HG12	1:F:329:ASN:O	2.10	0.52
1:G:648:ALA:HB1	1:G:841:LEU:HD12	1.91	0.52
1:A:376:LYS:HE2	1:A:376:LYS:HA	1.91	0.52
1:A:441:LEU:CB	1:A:498:VAL:HG12	2.39	0.52
1:H:775:GLY:HA2	1:H:779:PHE:O	2.10	0.52
1:I:241:LEU:HD21	1:I:528:ILE:HD13	1.91	0.52
1:J:278:LEU:HB2	1:J:279:PRO:HD2	1.92	0.52
1:A:363:TYR:CD2	1:A:407:THR:HB	2.45	0.52
1:A:499:SER:O	1:A:500:THR:CG2	2.58	0.52
1:A:537:TYR:HE1	1:I:627:TYR:CA	2.22	0.52
1:B:272:ILE:HD11	1:B:280:LYS:HB2	1.92	0.52
1:B:393:ILE:HD11	1:B:412:SER:HB2	1.91	0.52
1:B:780:SER:OG	1:B:783:LEU:HB2	2.10	0.52
1:B:803:ARG:HD2	1:B:823:GLU:OE2	2.10	0.52
1:E:308:PRO:HD2	1:E:344:ARG:O	2.09	0.52
1:F:640:THR:HG21	1:F:706:LYS:HA	1.92	0.52
1:I:279:PRO:HG3	1:I:322:GLN:HA	1.91	0.52
1:I:855:ARG:HA	1:I:855:ARG:HE	1.75	0.52
1:J:426:ILE:HG21	1:J:429:MET:HE3	1.91	0.52
1:B:286:THR:CB	1:B:361:PRO:HB3	2.37	0.52
1:D:278:LEU:CD1	1:D:278:LEU:N	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:355:LEU:HD23	1:D:357:LEU:HD22	1.92	0.52
1:E:484:TYR:HE1	1:E:492:PHE:HZ	1.57	0.52
1:E:499:SER:O	1:E:500:THR:CG2	2.57	0.52
1:F:279:PRO:CB	1:F:322:GLN:HA	2.38	0.52
1:G:530:ARG:HG2	1:G:530:ARG:NH1	2.24	0.52
1:G:617:ASP:OD1	1:G:617:ASP:N	2.43	0.52
1:G:663:LEU:O	1:G:667:SER:HB2	2.10	0.52
1:H:297:ASP:HB3	1:H:350:PRO:N	2.25	0.52
1:B:642:LEU:HD22	1:B:643:GLY:N	2.25	0.51
1:E:476:SER:OG	1:E:477:ILE:N	2.40	0.51
1:E:485:PHE:HD2	1:E:492:PHE:HD1	1.57	0.51
1:H:363:TYR:N	1:H:363:TYR:HD1	2.08	0.51
1:H:653:ALA:HA	1:H:687:LEU:HD13	1.93	0.51
1:I:268:VAL:HB	1:I:280:LYS:HB3	1.92	0.51
1:A:284:MET:HG2	1:A:286:THR:HG23	1.92	0.51
1:A:322:GLN:O	1:A:326:THR:OG1	2.18	0.51
1:B:276:GLU:HG2	1:B:277:PHE:N	2.25	0.51
1:B:616:ILE:O	1:B:619:PRO:HD2	2.10	0.51
1:D:298:PRO:O	1:D:299:GLU:CB	2.59	0.51
1:D:393:ILE:HG23	1:D:422:THR:HB	1.93	0.51
1:E:276:GLU:OE1	1:E:303:ASP:OD1	2.28	0.51
1:E:723:VAL:O	1:E:727:LEU:HB2	2.10	0.51
1:H:286:THR:O	1:H:361:PRO:HG3	2.09	0.51
1:H:474:LEU:CG	1:H:475:ALA:N	2.71	0.51
1:I:817:ASN:HB2	1:I:820:TYR:HB2	1.92	0.51
1:J:278:LEU:HD21	1:J:280:LYS:CG	2.40	0.51
1:C:480:ASN:HA	1:C:483:ASN:OD1	2.11	0.51
1:D:230:ILE:HG13	1:D:904:LEU:HD11	1.91	0.51
1:D:232:LYS:HA	1:D:235:ILE:CG2	2.40	0.51
1:H:276:GLU:OE1	1:H:303:ASP:CG	2.52	0.51
1:J:441:LEU:CB	1:J:498:VAL:CG1	2.87	0.51
1:A:387:ILE:HG22	1:A:415:VAL:HG21	1.91	0.51
1:A:720:ARG:HG2	1:A:720:ARG:HH11	1.76	0.51
1:D:375:LEU:N	1:D:375:LEU:CD2	2.67	0.51
1:E:273:VAL:CG2	1:E:457:SER:HB3	2.21	0.51
1:H:277:PHE:HD1	1:H:278:LEU:H	1.56	0.51
1:H:480:ASN:HA	1:H:483:ASN:OD1	2.11	0.51
1:I:616:ILE:O	1:I:619:PRO:HD2	2.10	0.51
1:J:376:LYS:HA	1:J:376:LYS:CE	2.39	0.51
1:J:429:MET:HE2	1:J:437:GLY:CA	2.35	0.51
1:A:278:LEU:HD22	1:A:280:LYS:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:VAL:HG12	1:A:501:GLY:CA	2.40	0.51
1:C:267:SER:HB3	1:C:396:ILE:HG13	1.93	0.51
1:E:454:GLY:O	1:E:455:VAL:CG1	2.59	0.51
1:G:264:GLY:HA2	1:G:267:SER:HB3	1.93	0.51
1:I:616:ILE:HD13	1:I:802:LEU:HD13	1.92	0.51
1:J:269:LEU:HD23	1:J:270:GLU:CA	2.40	0.51
1:A:263:SER:HA	1:A:266:SER:OG	2.11	0.51
1:E:267:SER:CB	1:E:396:ILE:HG13	2.37	0.51
1:G:261:GLN:CG	1:G:262:SER:N	2.73	0.51
1:H:269:LEU:HD23	1:H:269:LEU:C	2.35	0.51
1:H:682:ALA:HA	1:H:685:THR:HG22	1.92	0.51
1:C:596:ARG:HH21	1:C:634:THR:HB	1.76	0.51
1:D:307:PHE:N	1:D:307:PHE:HD1	2.09	0.51
1:E:272:ILE:CG1	1:E:278:LEU:HD11	2.41	0.51
1:F:600:ARG:CZ	1:F:600:ARG:HB3	2.40	0.51
1:H:667:SER:OG	1:H:668:SER:N	2.44	0.51
1:I:360:LEU:HB2	1:I:361:PRO:HD2	1.93	0.51
1:I:611:GLU:N	1:I:612:PRO:HD2	2.26	0.51
1:A:841:LEU:HD23	1:A:845:MET:HB3	1.92	0.51
1:E:429:MET:CE	1:E:437:GLY:HA2	2.31	0.51
1:F:269:LEU:HD21	1:F:457:SER:HB2	1.93	0.51
1:F:279:PRO:O	1:F:280:LYS:HD2	2.11	0.51
1:H:276:GLU:HG2	1:H:277:PHE:N	2.26	0.51
1:H:308:PRO:HG3	1:H:344:ARG:HG3	1.92	0.51
1:J:244:VAL:HG11	1:J:894:LEU:HD21	1.92	0.51
1:J:456:ILE:O	1:J:481:GLU:OE2	2.29	0.51
1:E:478:ASN:HD22	1:E:482:LYS:HZ1	1.40	0.51
1:G:272:ILE:HD11	1:G:280:LYS:HB2	1.90	0.51
1:G:430:ASP:HB3	1:G:456:ILE:HG12	1.93	0.51
1:H:278:LEU:CD2	1:H:280:LYS:HG2	2.41	0.51
1:H:454:GLY:C	1:H:455:VAL:HG13	2.36	0.51
1:H:682:ALA:O	1:H:685:THR:CG2	2.58	0.51
1:I:234:MET:HA	1:I:237:ILE:HG22	1.91	0.51
1:I:322:GLN:O	1:I:326:THR:OG1	2.13	0.51
1:A:499:SER:O	1:A:500:THR:HG23	2.11	0.51
1:A:694:THR:HG21	1:A:845:MET:HE3	1.93	0.51
1:B:294:LEU:HB2	1:B:355:LEU:H	1.76	0.51
1:B:840:PHE:CE1	1:B:844:GLU:HG3	2.45	0.51
1:C:453:VAL:HG11	1:C:505:LEU:HB2	1.93	0.51
1:D:454:GLY:C	1:D:455:VAL:HG13	2.36	0.51
1:E:278:LEU:HD22	1:E:280:LYS:HD3	1.86	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:279:PRO:O	1:E:280:LYS:HD2	2.10	0.51
1:F:321:ILE:HA	1:F:324:THR:OG1	2.11	0.51
1:F:621:ALA:O	1:F:820:TYR:OH	2.27	0.51
1:I:274:GLY:O	1:I:506:ARG:HD2	2.11	0.51
1:J:275:HIS:H	1:J:275:HIS:CD2	2.28	0.51
1:J:484:TYR:C	1:J:486:GLY:N	2.68	0.51
1:J:503:MET:HG2	1:J:506:ARG:NH2	2.26	0.51
1:J:670:ALA:HB1	1:J:671:LYS:HZ2	1.75	0.51
1:B:661:GLU:OE2	1:B:676:ARG:NH2	2.44	0.50
1:C:255:ILE:HA	1:C:392:ILE:O	2.10	0.50
1:C:279:PRO:HG3	1:C:322:GLN:HA	1.93	0.50
1:C:667:SER:OG	1:C:668:SER:N	2.44	0.50
1:D:376:LYS:NZ	1:D:379:ILE:HD12	2.26	0.50
1:D:903:GLU:HG3	1:D:906:ARG:HH21	1.76	0.50
1:E:284:MET:SD	1:E:284:MET:N	2.77	0.50
1:J:235:ILE:HD12	1:J:235:ILE:C	2.36	0.50
1:J:478:ASN:O	1:J:482:LYS:HG2	2.11	0.50
1:B:842:ASN:O	1:B:846:LEU:HB3	2.11	0.50
1:C:279:PRO:O	1:C:280:LYS:HD2	2.11	0.50
1:H:484:TYR:C	1:H:484:TYR:CD1	2.89	0.50
1:I:231:THR:O	1:I:235:ILE:HG22	2.11	0.50
1:I:837:ALA:O	1:I:841:LEU:HB2	2.11	0.50
1:J:272:ILE:HG21	1:J:277:PHE:CD1	2.46	0.50
1:A:277:PHE:HD1	1:A:278:LEU:N	2.08	0.50
1:B:224:ASP:HB3	1:B:227:MET:HB2	1.92	0.50
1:C:588:LYS:O	1:C:591:ASP:HB2	2.11	0.50
1:D:270:GLU:HA	1:D:273:VAL:HG22	1.93	0.50
1:E:682:ALA:O	1:E:686:VAL:HG23	2.11	0.50
1:E:775:GLY:HA2	1:E:779:PHE:O	2.12	0.50
1:J:269:LEU:CD2	1:J:457:SER:HB2	2.41	0.50
1:A:264:GLY:O	1:A:268:VAL:HG22	2.11	0.50
1:A:458:LYS:HG3	1:A:458:LYS:O	2.11	0.50
1:D:286:THR:O	1:D:361:PRO:CB	2.59	0.50
1:E:308:PRO:HG3	1:E:344:ARG:CB	2.40	0.50
1:H:423:ILE:HG22	1:H:450:LEU:HD13	1.92	0.50
1:H:434:PRO:HB2	1:H:491:GLU:HG3	1.87	0.50
1:H:863:GLU:O	1:H:867:ALA:HB3	2.11	0.50
1:I:269:LEU:O	1:I:273:VAL:HG13	2.12	0.50
1:I:524:THR:O	1:I:528:ILE:HG13	2.11	0.50
1:I:787:GLY:O	1:I:791:VAL:HG23	2.11	0.50
1:J:485:PHE:HA	1:J:492:PHE:HE1	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:THR:HG22	1:A:329:ASN:ND2	2.26	0.50
1:A:455:VAL:CG1	1:A:501:GLY:H	2.11	0.50
1:D:355:LEU:HG	1:D:356:SER:H	1.76	0.50
1:E:273:VAL:HG21	1:E:457:SER:CB	2.21	0.50
1:E:297:ASP:OD1	1:E:300:ALA:HB3	2.11	0.50
1:E:485:PHE:HD2	1:E:492:PHE:CD1	2.24	0.50
1:E:710:ASP:O	1:E:832:LYS:NZ	2.38	0.50
1:F:227:MET:O	1:F:230:ILE:HG22	2.12	0.50
1:F:426:ILE:HG22	1:F:429:MET:HG3	1.94	0.50
1:H:499:SER:O	1:H:500:THR:HG23	2.12	0.50
1:I:602:ILE:CG1	1:I:792:PHE:HB2	2.41	0.50
1:J:297:ASP:CG	1:J:300:ALA:HB3	2.36	0.50
1:J:593:LEU:HD21	1:J:823:GLU:HG3	1.92	0.50
1:J:670:ALA:HB1	1:J:671:LYS:NZ	2.27	0.50
1:B:429:MET:HE1	1:B:441:LEU:HB2	1.93	0.50
1:D:363:TYR:HD2	1:D:407:THR:HB	1.77	0.50
1:E:296:ASN:HB2	1:E:354:ASP:OD2	2.12	0.50
1:E:627:TYR:CZ	1:E:631:GLN:NE2	2.79	0.50
1:F:400:ASP:OD1	1:F:400:ASP:N	2.43	0.50
1:I:357:LEU:HD23	1:I:357:LEU:H	1.76	0.50
1:I:543:TYR:O	1:I:546:GLN:HB3	2.10	0.50
1:J:377:ARG:HH21	1:J:377:ARG:HG3	1.77	0.50
1:J:436:LYS:O	1:J:440:ILE:HG13	2.11	0.50
1:A:537:TYR:CE2	1:I:613:ASP:OD2	2.65	0.50
1:A:543:TYR:HB3	1:A:884:HIS:CE1	2.47	0.50
1:C:321:ILE:O	1:C:325:LEU:HG	2.12	0.50
1:D:307:PHE:N	1:D:307:PHE:CD1	2.80	0.50
1:E:646:ARG:NH2	1:G:534:GLU:OE2	2.37	0.50
1:I:607:PRO:HG3	1:I:762:ARG:HG3	1.93	0.50
1:D:284:MET:SD	1:D:284:MET:O	2.69	0.50
1:D:441:LEU:HB3	1:D:498:VAL:HG12	1.92	0.50
1:E:454:GLY:O	1:E:500:THR:HB	2.12	0.50
1:E:481:GLU:OE1	1:E:481:GLU:N	2.45	0.50
1:F:611:GLU:N	1:F:612:PRO:CD	2.75	0.50
1:G:704:PRO:HA	1:H:843:VAL:HG21	1.94	0.50
1:H:818:LYS:HG2	1:H:819:TYR:N	2.26	0.50
1:I:387:ILE:O	1:I:421:ARG:NH2	2.45	0.50
1:B:426:ILE:HG21	1:B:429:MET:HE3	1.94	0.50
1:E:224:ASP:N	1:E:225:ASP:OD1	2.44	0.50
1:F:269:LEU:HA	1:F:272:ILE:HD12	1.94	0.50
1:F:285:ILE:HD12	1:F:287:ARG:H	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:361:PRO:HG2	1:H:382:LEU:HD21	1.93	0.50
1:A:493:GLY:O	1:A:496:SER:HB3	2.12	0.49
1:A:723:VAL:HG21	1:A:824:VAL:HA	1.93	0.49
1:D:376:LYS:CE	1:D:376:LYS:CA	2.90	0.49
1:D:472:ASN:O	1:D:472:ASN:ND2	2.45	0.49
1:E:235:ILE:HD12	1:E:235:ILE:C	2.37	0.49
1:E:667:SER:OG	1:E:668:SER:N	2.45	0.49
1:F:234:MET:HA	1:F:237:ILE:HG22	1.94	0.49
1:F:488:HIS:HB3	1:F:491:GLU:HG3	1.94	0.49
1:G:275:HIS:CG	1:G:276:GLU:H	2.29	0.49
1:G:744:SER:OG	1:G:786:ARG:NH2	2.40	0.49
1:I:618:LEU:CD2	1:I:628:TRP:CZ3	2.95	0.49
1:I:627:TYR:CE1	1:I:631:GLN:NE2	2.80	0.49
1:I:665:ASP:OD1	1:I:676:ARG:NH1	2.46	0.49
1:A:297:ASP:N	1:A:298:PRO:HD3	2.27	0.49
1:A:394:LEU:HD13	1:A:423:ILE:O	2.12	0.49
1:A:441:LEU:CB	1:A:498:VAL:CG1	2.91	0.49
1:D:311:GLY:O	1:D:312:LEU:CB	2.59	0.49
1:D:441:LEU:CD2	1:D:498:VAL:CA	2.89	0.49
1:D:485:PHE:HE2	1:D:500:THR:OG1	1.92	0.49
1:E:229:PHE:O	1:E:233:LYS:HG2	2.13	0.49
1:E:307:PHE:CD1	1:E:307:PHE:N	2.79	0.49
1:F:428:LYS:HB3	1:F:431:LEU:HD21	1.93	0.49
1:F:873:LYS:O	1:F:877:GLU:HG3	2.11	0.49
1:H:297:ASP:OD2	1:H:300:ALA:HB3	2.11	0.49
1:H:376:LYS:HZ1	1:H:379:ILE:HD12	1.77	0.49
1:H:426:ILE:HG21	1:H:440:ILE:HG21	1.93	0.49
1:I:269:LEU:HD21	1:I:457:SER:HB2	1.93	0.49
1:I:276:GLU:HG2	1:I:277:PHE:N	2.27	0.49
1:J:381:GLU:OE1	1:J:381:GLU:HA	2.12	0.49
1:J:479:ARG:HH21	1:J:482:LYS:HZ3	1.59	0.49
1:A:565:PHE:CZ	1:A:853:PHE:HD2	2.30	0.49
1:C:400:ASP:OD1	1:C:400:ASP:N	2.46	0.49
1:E:238:ARG:NE	1:E:356:SER:OG	2.44	0.49
1:E:664:LEU:HB3	1:E:676:ARG:NH2	2.27	0.49
1:H:239:ASN:O	1:H:242:GLN:HB3	2.12	0.49
1:H:246:GLN:CG	1:H:247:GLY:N	2.72	0.49
1:A:411:ALA:HA	1:A:414:ARG:HB3	1.93	0.49
1:D:229:PHE:CG	1:D:232:LYS:HD2	2.47	0.49
1:D:232:LYS:HA	1:D:235:ILE:HG22	1.94	0.49
1:E:232:LYS:HA	1:E:235:ILE:CG2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:238:ARG:CZ	1:E:356:SER:OG	2.60	0.49
1:H:355:LEU:HD23	1:H:357:LEU:HD22	1.94	0.49
1:I:626:PRO:HA	1:I:630:ARG:H	1.77	0.49
1:B:227:MET:C	1:B:230:ILE:HG22	2.38	0.49
1:B:559:ASP:OD2	1:C:855:ARG:NH2	2.45	0.49
1:D:605:LEU:HD21	1:D:784:LEU:HD12	1.92	0.49
1:E:296:ASN:O	1:E:298:PRO:HD3	2.13	0.49
1:E:297:ASP:OD1	1:E:300:ALA:CB	2.60	0.49
1:E:401:THR:HG22	1:E:402:ASP:O	2.12	0.49
1:F:837:ALA:O	1:F:841:LEU:HB2	2.13	0.49
1:H:241:LEU:C	1:H:244:VAL:HG23	2.34	0.49
1:H:279:PRO:HB3	1:H:322:GLN:CG	2.43	0.49
1:H:499:SER:O	1:H:500:THR:CG2	2.60	0.49
1:H:682:ALA:C	1:H:685:THR:HG22	2.38	0.49
1:I:325:LEU:HA	1:I:328:LEU:HD12	1.94	0.49
1:I:755:MET:HE3	1:I:790:ALA:HB1	1.94	0.49
1:A:285:ILE:HD12	1:A:287:ARG:HB2	1.74	0.49
1:A:394:LEU:HD21	1:A:412:SER:HB3	1.93	0.49
1:A:478:ASN:CG	1:A:482:LYS:HZ2	2.20	0.49
1:A:536:THR:CB	1:I:630:ARG:HH11	2.25	0.49
1:B:904:LEU:HD12	1:B:904:LEU:O	2.13	0.49
1:C:642:LEU:HD22	1:C:643:GLY:H	1.77	0.49
1:D:457:SER:O	1:D:458:LYS:HB2	2.11	0.49
1:E:267:SER:HB2	1:E:396:ILE:HD12	1.95	0.49
1:F:587:GLN:OE1	1:F:587:GLN:HA	2.12	0.49
1:H:255:ILE:HA	1:H:392:ILE:O	2.13	0.49
1:H:279:PRO:O	1:H:280:LYS:CD	2.61	0.49
1:H:694:THR:HG22	1:H:844:GLU:CG	2.43	0.49
1:I:349:SER:O	1:I:352:ILE:HG13	2.12	0.49
1:J:475:ALA:O	1:J:478:ASN:HB3	2.12	0.49
1:J:779:PHE:CD2	1:J:779:PHE:N	2.80	0.49
1:C:640:THR:HG22	1:C:706:LYS:HG2	1.94	0.49
1:D:229:PHE:CD1	1:D:232:LYS:HE3	2.47	0.49
1:E:483:ASN:C	1:E:483:ASN:ND2	2.71	0.49
1:F:800:LEU:O	1:F:804:ILE:HG13	2.12	0.49
1:H:232:LYS:CA	1:H:235:ILE:HG22	2.41	0.49
1:H:491:GLU:H	1:H:491:GLU:CD	2.19	0.49
1:I:303:ASP:OD1	1:I:349:SER:HB2	2.13	0.49
1:I:627:TYR:HB3	1:I:628:TRP:CZ3	2.48	0.49
1:J:409:LEU:O	1:J:413:ARG:HG3	2.13	0.49
1:J:455:VAL:CG1	1:J:501:GLY:H	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:558:LEU:HD12	1:F:861:LEU:HD12	1.94	0.49
1:G:632:LEU:O	1:G:635:ALA:HB3	2.13	0.49
1:J:441:LEU:HB3	1:J:498:VAL:HG12	1.94	0.49
1:A:441:LEU:HD21	1:A:498:VAL:C	2.38	0.49
1:A:450:LEU:HD22	1:A:512:VAL:HG22	1.94	0.49
1:E:294:LEU:HB3	1:E:352:ILE:HD13	1.93	0.49
1:E:832:LYS:O	1:E:836:THR:HG22	2.13	0.49
1:G:653:ALA:HB2	1:G:845:MET:HE1	1.95	0.49
1:I:227:MET:HA	1:I:230:ILE:HG22	1.94	0.49
1:I:364:ILE:HD12	1:I:376:LYS:HZ2	1.78	0.49
1:I:485:PHE:HE2	1:I:500:THR:HG1	1.60	0.49
1:J:376:LYS:HZ2	1:J:379:ILE:HD12	1.77	0.49
1:J:477:ILE:O	1:J:477:ILE:HG22	2.13	0.49
1:J:499:SER:C	1:J:500:THR:HG23	2.38	0.49
1:A:307:PHE:CD1	1:A:307:PHE:N	2.81	0.49
1:A:339:THR:CG2	1:A:340:ASP:N	2.75	0.49
1:A:701:SER:O	1:A:704:PRO:HD2	2.13	0.49
1:A:800:LEU:O	1:A:804:ILE:HG13	2.13	0.49
1:B:284:MET:HG2	1:B:286:THR:HG23	1.89	0.49
1:C:257:VAL:HG12	1:C:394:LEU:HB3	1.95	0.49
1:C:377:ARG:HH21	1:C:377:ARG:CG	2.26	0.49
1:D:307:PHE:CE1	1:D:345:LEU:HD21	2.47	0.49
1:E:454:GLY:H	1:E:500:THR:HG22	1.78	0.49
1:F:616:ILE:HD12	1:F:616:ILE:C	2.38	0.49
1:H:254:SER:HB2	1:H:356:SER:O	2.13	0.49
1:H:406:SER:O	1:H:410:GLN:HG3	2.12	0.49
1:I:272:ILE:HG23	1:I:277:PHE:HA	1.95	0.49
1:I:624:ASP:HA	1:I:629:HIS:CD2	2.44	0.49
1:J:614:ASN:OD1	1:J:615:ILE:HD12	2.13	0.49
1:A:533:GLU:HB2	1:I:596:ARG:HH12	1.75	0.48
1:B:722:HIS:O	1:B:726:VAL:HG23	2.13	0.48
1:F:449:LYS:C	1:F:451:GLY:H	2.20	0.48
1:G:605:LEU:HD22	1:G:606:SER:C	2.37	0.48
1:H:278:LEU:CD2	1:H:280:LYS:CD	2.84	0.48
1:H:491:GLU:CD	1:H:491:GLU:N	2.70	0.48
1:I:275:HIS:CD2	1:I:276:GLU:H	2.31	0.48
1:I:413:ARG:NH2	1:I:446:TYR:CD1	2.81	0.48
1:J:254:SER:HB2	1:J:356:SER:O	2.13	0.48
1:J:272:ILE:HG12	1:J:280:LYS:HG3	1.95	0.48
1:J:742:GLU:CD	1:J:748:ARG:HE	2.20	0.48
1:A:441:LEU:HD21	1:A:498:VAL:CA	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:LEU:HG	1:A:475:ALA:H	1.77	0.48
1:A:540:LYS:HZ2	1:I:625:SER:C	2.19	0.48
1:A:657:GLN:HE22	1:A:684:ALA:CA	2.23	0.48
1:A:664:LEU:HB3	1:A:676:ARG:NH2	2.27	0.48
1:B:294:LEU:HB3	1:B:352:ILE:HD13	1.94	0.48
1:B:389:GLY:O	1:B:391:ASN:N	2.43	0.48
1:B:640:THR:HG21	1:B:706:LYS:HA	1.95	0.48
1:C:262:SER:O	1:C:266:SER:OG	2.27	0.48
1:C:530:ARG:HD3	1:C:530:ARG:HA	1.61	0.48
1:D:229:PHE:CD2	1:D:232:LYS:HD2	2.48	0.48
1:F:687:LEU:HD22	1:F:845:MET:HE2	1.95	0.48
1:G:227:MET:O	1:G:230:ILE:HG22	2.13	0.48
1:G:772:HIS:HD2	1:G:775:GLY:O	1.96	0.48
1:H:690:ARG:NH1	1:H:844:GLU:OE2	2.46	0.48
1:I:586:ASP:O	1:I:589:VAL:HB	2.13	0.48
1:I:602:ILE:HG12	1:I:792:PHE:HB2	1.93	0.48
1:J:694:THR:HG21	1:J:845:MET:HB2	1.93	0.48
1:A:257:VAL:HG22	1:A:359:ASP:HA	1.93	0.48
1:A:276:GLU:HG2	1:A:277:PHE:N	2.28	0.48
1:A:278:LEU:HD11	1:A:280:LYS:CG	2.43	0.48
1:A:382:LEU:C	1:A:382:LEU:HD12	2.38	0.48
1:A:456:ILE:HD12	1:A:457:SER:N	2.28	0.48
1:A:533:GLU:CD	1:A:533:GLU:C	2.80	0.48
1:H:360:LEU:HD13	1:H:383:CYS:SG	2.53	0.48
1:H:723:VAL:HG21	1:H:824:VAL:HA	1.95	0.48
1:I:255:ILE:HD11	1:I:355:LEU:HG	1.95	0.48
1:I:873:LYS:HB2	1:I:873:LYS:HE3	1.53	0.48
1:J:285:ILE:HD12	1:J:285:ILE:C	2.38	0.48
1:J:710:ASP:O	1:J:832:LYS:NZ	2.42	0.48
1:A:387:ILE:HG21	1:A:393:ILE:HD12	1.95	0.48
1:A:457:SER:O	1:A:458:LYS:HB2	2.13	0.48
1:A:614:ASN:OD1	1:A:615:ILE:HD12	2.12	0.48
1:C:723:VAL:O	1:C:727:LEU:HB2	2.14	0.48
1:D:270:GLU:C	1:D:270:GLU:CD	2.82	0.48
1:D:434:PRO:HB3	1:D:491:GLU:HB2	1.92	0.48
1:E:484:TYR:CE1	1:E:492:PHE:HZ	2.31	0.48
1:F:376:LYS:HZ1	1:F:379:ILE:CD1	2.26	0.48
1:G:235:ILE:HD13	1:G:356:SER:HB2	1.95	0.48
1:G:294:LEU:HB2	1:G:355:LEU:H	1.78	0.48
1:J:444:ARG:CZ	1:J:447:PRO:HB3	2.44	0.48
1:J:485:PHE:HE2	1:J:500:THR:OG1	1.89	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:ASP:OD1	1:A:349:SER:HB2	2.13	0.48
1:B:262:SER:O	1:B:266:SER:OG	2.32	0.48
1:B:270:GLU:O	1:B:273:VAL:HG22	2.14	0.48
1:B:653:ALA:HB2	1:B:845:MET:HE1	1.95	0.48
1:B:690:ARG:NH1	1:B:844:GLU:OE2	2.47	0.48
1:B:697:GLY:HA3	1:B:840:PHE:CE1	2.49	0.48
1:D:229:PHE:CD1	1:D:232:LYS:HD2	2.48	0.48
1:E:276:GLU:HG2	1:E:277:PHE:N	2.28	0.48
1:F:752:LYS:HA	1:F:755:MET:HB2	1.96	0.48
1:G:276:GLU:HG2	1:G:277:PHE:N	2.29	0.48
1:G:891:LYS:O	1:G:895:GLU:HG3	2.12	0.48
1:H:485:PHE:CZ	1:H:500:THR:OG1	2.57	0.48
1:I:420:GLU:HG3	1:I:449:LYS:HE3	1.96	0.48
1:J:694:THR:O	1:J:698:ILE:HG13	2.13	0.48
1:J:780:SER:OG	1:J:783:LEU:HB2	2.14	0.48
1:A:278:LEU:CD1	1:A:280:LYS:CG	2.91	0.48
1:A:279:PRO:HB3	1:A:322:GLN:CG	2.43	0.48
1:A:441:LEU:CD2	1:A:498:VAL:HG12	2.31	0.48
1:B:273:VAL:HG11	1:B:457:SER:HB3	1.95	0.48
1:B:276:GLU:HG2	1:B:277:PHE:H	1.78	0.48
1:B:677:LYS:NZ	1:B:681:ASP:OD2	2.47	0.48
1:C:673:PRO:HD2	1:C:877:GLU:OE1	2.14	0.48
1:D:456:ILE:HD12	1:D:457:SER:N	2.29	0.48
1:E:610:ARG:HE	1:E:611:GLU:H	1.60	0.48
1:I:625:SER:HB3	1:I:628:TRP:NE1	2.25	0.48
1:J:889:ARG:HG3	1:J:890:ARG:N	2.28	0.48
1:A:540:LYS:CE	1:I:626:PRO:HG2	1.84	0.48
1:B:326:THR:HA	1:B:329:ASN:ND2	2.28	0.48
1:C:296:ASN:HB2	1:C:354:ASP:OD2	2.13	0.48
1:E:278:LEU:CD2	1:E:280:LYS:CG	2.91	0.48
1:E:286:THR:O	1:E:361:PRO:CB	2.61	0.48
1:F:574:ARG:O	1:F:577:LEU:HB2	2.13	0.48
1:G:664:LEU:HD23	1:G:676:ARG:HG3	1.95	0.48
1:I:269:LEU:CD2	1:I:457:SER:HB2	2.44	0.48
1:I:297:ASP:HB3	1:I:349:SER:C	2.39	0.48
1:I:640:THR:HG22	1:I:706:LYS:HG2	1.95	0.48
1:A:393:ILE:HD11	1:A:394:LEU:HD23	1.94	0.48
1:A:621:ALA:O	1:A:820:TYR:OH	2.23	0.48
1:B:521:LEU:HD13	1:B:521:LEU:C	2.39	0.48
1:B:558:LEU:HD12	1:B:861:LEU:HD12	1.96	0.48
1:C:289:PRO:HB2	1:C:342:PRO:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:PRO:CG	1:D:488:HIS:CG	2.97	0.48
1:E:275:HIS:H	1:E:275:HIS:CD2	2.31	0.48
1:E:393:ILE:HG23	1:E:422:THR:HB	1.95	0.48
1:E:615:ILE:H	1:E:615:ILE:CD1	2.24	0.48
1:H:261:GLN:CD	1:H:261:GLN:N	2.72	0.48
1:H:478:ASN:CG	1:H:482:LYS:HZ2	2.20	0.48
1:H:875:ALA:HB1	1:H:885:LEU:CD1	2.44	0.48
1:J:224:ASP:N	1:J:225:ASP:OD1	2.47	0.48
1:A:703:LYS:HE3	1:C:544:ASN:HB3	1.96	0.48
1:B:241:LEU:HD13	1:B:250:VAL:O	2.13	0.48
1:B:769:GLU:H	1:B:769:GLU:CD	2.21	0.48
1:B:810:ARG:HG3	1:B:810:ARG:O	2.13	0.48
1:E:345:LEU:HA	1:E:345:LEU:HD23	1.64	0.48
1:E:363:TYR:CD2	1:E:407:THR:HB	2.49	0.48
1:E:458:LYS:HD2	1:E:458:LYS:C	2.39	0.48
1:F:542:GLN:C	1:F:543:TYR:CG	2.92	0.48
1:G:430:ASP:OD1	1:G:430:ASP:C	2.57	0.48
1:H:272:ILE:HG12	1:H:278:LEU:CD1	2.43	0.48
1:H:297:ASP:CG	1:H:300:ALA:HB3	2.39	0.48
1:J:272:ILE:HG12	1:J:278:LEU:HD11	1.95	0.48
1:A:272:ILE:HG12	1:A:280:LYS:HG3	1.95	0.48
1:A:810:ARG:O	1:A:813:LYS:HB2	2.14	0.48
1:B:387:ILE:HG22	1:B:415:VAL:HG21	1.95	0.48
1:B:605:LEU:HD13	1:B:606:SER:O	2.14	0.48
1:E:560:ASP:OD2	1:E:668:SER:OG	2.30	0.48
1:E:762:ARG:HG2	1:E:762:ARG:HH11	1.78	0.48
1:F:855:ARG:NE	1:F:855:ARG:CA	2.77	0.48
1:G:261:GLN:OE1	1:G:261:GLN:N	2.46	0.48
1:H:339:THR:CG2	1:H:340:ASP:H	2.26	0.48
1:I:625:SER:O	1:I:628:TRP:CG	2.67	0.48
1:I:626:PRO:O	1:I:628:TRP:N	2.46	0.48
1:J:267:SER:CB	1:J:396:ILE:HG13	2.43	0.48
1:J:738:MET:O	1:J:741:LEU:HB3	2.14	0.48
1:A:267:SER:HB3	1:A:396:ILE:CD1	2.44	0.47
1:A:454:GLY:C	1:A:455:VAL:HG13	2.39	0.47
1:B:385:LYS:HE2	1:B:385:LYS:HB3	1.66	0.47
1:B:906:ARG:HG2	1:B:906:ARG:HH11	1.78	0.47
1:C:325:LEU:HD12	1:C:326:THR:N	2.29	0.47
1:D:243:LYS:O	1:D:243:LYS:CG	2.61	0.47
1:D:303:ASP:OD1	1:D:349:SER:HB2	2.14	0.47
1:E:286:THR:O	1:E:361:PRO:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:472:ASN:ND2	1:E:472:ASN:O	2.46	0.47
1:E:752:LYS:HA	1:E:755:MET:CE	2.44	0.47
1:G:241:LEU:HA	1:G:244:VAL:HG13	1.96	0.47
1:G:279:PRO:HG3	1:G:321:ILE:HG22	1.96	0.47
1:G:572:PHE:HB3	1:G:850:TYR:OH	2.14	0.47
1:H:448:LEU:H	1:H:448:LEU:HD12	1.80	0.47
1:I:279:PRO:HB3	1:I:322:GLN:CD	2.38	0.47
1:J:257:VAL:HG23	1:J:257:VAL:O	2.14	0.47
1:J:450:LEU:HD22	1:J:512:VAL:HG22	1.94	0.47
1:A:270:GLU:C	1:A:270:GLU:CD	2.82	0.47
1:A:275:HIS:HB2	1:A:352:ILE:HG21	1.96	0.47
1:B:283:ASN:ND2	1:B:283:ASN:C	2.72	0.47
1:B:297:ASP:HB3	1:B:349:SER:C	2.39	0.47
1:B:401:THR:HG22	1:B:402:ASP:N	2.30	0.47
1:B:615:ILE:HG21	1:B:799:ILE:HG23	1.96	0.47
1:B:904:LEU:HD12	1:B:904:LEU:C	2.39	0.47
1:D:244:VAL:HB	1:D:248:SER:HG	1.77	0.47
1:E:255:ILE:HD12	1:E:357:LEU:HB3	1.96	0.47
1:E:726:VAL:O	1:E:729:ALA:HB3	2.14	0.47
1:H:238:ARG:HH21	1:H:356:SER:HG	1.54	0.47
1:H:260:SER:O	1:H:264:GLY:CA	2.58	0.47
1:H:637:SER:O	1:H:641:ARG:HB2	2.14	0.47
1:H:815:LEU:O	1:H:815:LEU:HD22	2.14	0.47
1:I:387:ILE:HG22	1:I:415:VAL:HG21	1.96	0.47
1:I:744:SER:OG	1:I:786:ARG:NH2	2.47	0.47
1:J:296:ASN:O	1:J:298:PRO:HD3	2.14	0.47
1:A:455:VAL:CG1	1:A:501:GLY:N	2.73	0.47
1:C:553:TYR:O	1:C:553:TYR:CD1	2.67	0.47
1:F:617:ASP:OD1	1:F:617:ASP:N	2.37	0.47
1:H:257:VAL:HG23	1:H:257:VAL:O	2.14	0.47
1:I:403:LEU:HD21	1:I:440:ILE:HG23	1.96	0.47
1:J:284:MET:SD	1:J:284:MET:O	2.73	0.47
1:J:614:ASN:HB3	1:J:616:ILE:HG22	1.95	0.47
1:C:297:ASP:HB3	1:C:349:SER:C	2.39	0.47
1:C:906:ARG:HG2	1:C:906:ARG:HH11	1.78	0.47
1:D:441:LEU:CD2	1:D:498:VAL:HG12	2.35	0.47
1:G:244:VAL:HA	1:G:893:LEU:HD13	1.97	0.47
1:G:784:LEU:HD23	1:G:784:LEU:HA	1.79	0.47
1:H:232:LYS:HG3	1:H:233:LYS:HE3	1.97	0.47
1:H:474:LEU:O	1:H:475:ALA:C	2.57	0.47
1:H:751:LEU:HA	1:H:754:VAL:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:257:VAL:HG22	1:J:358:ILE:O	2.15	0.47
1:J:297:ASP:OD2	1:J:300:ALA:HB3	2.14	0.47
1:A:255:ILE:HG13	1:A:357:LEU:HA	1.95	0.47
1:A:298:PRO:O	1:A:299:GLU:HB3	2.15	0.47
1:A:754:VAL:HA	1:A:779:PHE:HE1	1.80	0.47
1:B:627:TYR:CE2	1:B:628:TRP:CZ3	3.01	0.47
1:B:630:ARG:CZ	1:J:537:TYR:CD1	2.97	0.47
1:D:278:LEU:HD13	1:D:278:LEU:C	2.39	0.47
1:F:284:MET:SD	1:F:284:MET:N	2.87	0.47
1:G:268:VAL:HG23	1:G:269:LEU:N	2.30	0.47
1:H:685:THR:HG23	1:H:686:VAL:N	2.30	0.47
1:I:393:ILE:HG23	1:I:422:THR:HB	1.96	0.47
1:J:454:GLY:O	1:J:500:THR:HB	2.15	0.47
1:J:617:ASP:OD1	1:J:617:ASP:N	2.47	0.47
1:D:277:PHE:CD1	1:D:277:PHE:C	2.89	0.47
1:D:363:TYR:N	1:D:363:TYR:HD1	2.11	0.47
1:E:432:VAL:HB	1:E:436:LYS:HB3	1.96	0.47
1:F:829:VAL:O	1:F:833:LEU:HG	2.14	0.47
1:G:449:LYS:C	1:G:451:GLY:H	2.22	0.47
1:J:270:GLU:CD	1:J:270:GLU:C	2.83	0.47
1:A:265:LYS:O	1:A:268:VAL:HG23	2.15	0.47
1:A:392:ILE:HD12	1:A:421:ARG:O	2.15	0.47
1:B:375:LEU:C	1:B:376:LYS:HE2	2.40	0.47
1:B:538:GLN:HA	1:B:541:VAL:HG12	1.97	0.47
1:B:891:LYS:HG2	1:B:895:GLU:OE2	2.14	0.47
1:C:891:LYS:O	1:C:895:GLU:HG3	2.15	0.47
1:D:267:SER:HB2	1:D:396:ILE:CD1	2.45	0.47
1:D:296:ASN:C	1:D:298:PRO:CD	2.87	0.47
1:D:455:VAL:HG12	1:D:501:GLY:N	2.26	0.47
1:D:778:GLY:C	1:D:779:PHE:CD2	2.92	0.47
1:D:865:MET:HB3	1:D:871:LEU:HB2	1.97	0.47
1:E:263:SER:OG	1:E:397:SER:HA	2.13	0.47
1:E:441:LEU:CD2	1:E:498:VAL:CA	2.88	0.47
1:E:621:ALA:O	1:E:820:TYR:OH	2.27	0.47
1:F:863:GLU:O	1:F:867:ALA:HB2	2.15	0.47
1:F:880:LYS:NZ	1:H:633:ASP:HB3	2.29	0.47
1:G:364:ILE:HD12	1:G:376:LYS:NZ	2.30	0.47
1:G:713:PRO:O	1:G:716:TRP:HB3	2.14	0.47
1:H:239:ASN:CB	1:H:240:LEU:HD23	2.44	0.47
1:H:454:GLY:H	1:H:500:THR:HG22	1.79	0.47
1:I:426:ILE:HG21	1:I:429:MET:HE3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:664:LEU:CD2	1:I:676:ARG:HG3	2.42	0.47
1:I:690:ARG:NH1	1:I:844:GLU:OE2	2.48	0.47
1:I:855:ARG:NE	1:I:855:ARG:CA	2.77	0.47
1:J:269:LEU:CG	1:J:457:SER:O	2.61	0.47
1:J:303:ASP:OD1	1:J:349:SER:HB2	2.15	0.47
1:J:615:ILE:HD12	1:J:615:ILE:H	1.79	0.47
1:A:454:GLY:O	1:A:500:THR:HG22	2.13	0.47
1:D:481:GLU:OE1	1:D:481:GLU:N	2.48	0.47
1:D:738:MET:O	1:D:742:GLU:HG3	2.14	0.47
1:E:239:ASN:C	1:E:240:LEU:HD23	2.38	0.47
1:F:441:LEU:HD23	1:F:498:VAL:HB	1.97	0.47
1:G:239:ASN:HD21	1:G:293:THR:HG21	1.80	0.47
1:I:307:PHE:CE1	1:I:345:LEU:HD21	2.50	0.47
1:I:626:PRO:O	1:I:627:TYR:C	2.51	0.47
1:A:269:LEU:HD23	1:A:270:GLU:N	2.29	0.47
1:A:484:TYR:HE1	1:A:492:PHE:HZ	1.62	0.47
1:B:568:PHE:O	1:B:571:SER:N	2.48	0.47
1:C:269:LEU:O	1:C:272:ILE:HB	2.15	0.47
1:C:843:VAL:O	1:C:847:ASN:HB2	2.14	0.47
1:C:861:LEU:HD23	1:C:861:LEU:HA	1.71	0.47
1:D:279:PRO:HB3	1:D:322:GLN:CG	2.43	0.47
1:D:694:THR:HG22	1:D:844:GLU:HG3	1.97	0.47
1:F:456:ILE:O	1:F:456:ILE:HG23	2.14	0.47
1:G:364:ILE:C	1:J:405:ASN:OD1	2.57	0.47
1:J:272:ILE:HA	1:J:278:LEU:HD12	1.96	0.47
1:J:444:ARG:NE	1:J:444:ARG:HA	2.29	0.47
1:A:296:ASN:CG	1:A:298:PRO:HD3	2.40	0.47
1:A:360:LEU:HB2	1:A:361:PRO:HD2	1.97	0.47
1:A:709:PRO:O	1:A:711:ILE:HG12	2.15	0.47
1:A:878:ASP:OD1	1:A:880:LYS:HB2	2.15	0.47
1:B:416:ASP:OD2	1:B:422:THR:HG22	2.15	0.47
1:B:781:ALA:N	1:E:778:GLY:CA	2.76	0.47
1:D:345:LEU:HD23	1:D:345:LEU:HA	1.66	0.47
1:E:453:VAL:HG21	1:E:505:LEU:HD23	1.97	0.47
1:E:711:ILE:HD12	1:E:828:ALA:HB1	1.95	0.47
1:F:232:LYS:HG3	1:F:354:ASP:CG	2.40	0.47
1:F:319:SER:O	1:F:322:GLN:HB3	2.15	0.47
1:G:261:GLN:CB	1:J:405:ASN:ND2	2.76	0.47
1:I:625:SER:O	1:I:628:TRP:HB2	2.14	0.47
1:A:453:VAL:HG11	1:A:505:LEU:CB	2.28	0.46
1:D:272:ILE:HG23	1:D:278:LEU:HD13	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:581:LEU:HD12	1:D:838:VAL:HG23	1.97	0.46
1:D:842:ASN:O	1:D:846:LEU:HB3	2.15	0.46
1:E:237:ILE:HD12	1:E:241:LEU:HD11	1.96	0.46
1:E:273:VAL:CG1	1:E:457:SER:HB2	2.41	0.46
1:E:480:ASN:HA	1:E:483:ASN:OD1	2.15	0.46
1:F:268:VAL:HB	1:F:280:LYS:HB3	1.97	0.46
1:G:364:ILE:HA	1:J:405:ASN:CG	2.36	0.46
1:G:722:HIS:O	1:G:726:VAL:HG23	2.15	0.46
1:G:753:GLU:O	1:G:756:SER:HB2	2.15	0.46
1:H:235:ILE:HD12	1:H:235:ILE:C	2.34	0.46
1:H:401:THR:CB	1:H:410:GLN:CA	2.59	0.46
1:H:742:GLU:CD	1:H:748:ARG:HE	2.23	0.46
1:A:255:ILE:HD12	1:A:357:LEU:HB3	1.98	0.46
1:B:630:ARG:HE	1:J:540:LYS:CD	2.27	0.46
1:D:424:GLY:O	1:D:452:TYR:HA	2.16	0.46
1:D:528:ILE:HG23	1:D:894:LEU:HD22	1.97	0.46
1:E:242:GLN:NE2	1:E:344:ARG:CD	2.78	0.46
1:E:278:LEU:HD22	1:E:280:LYS:CD	2.44	0.46
1:F:488:HIS:HB3	1:F:491:GLU:CG	2.45	0.46
1:I:349:SER:HB3	1:I:352:ILE:HG12	1.96	0.46
1:J:276:GLU:OE1	1:J:303:ASP:OD1	2.33	0.46
1:A:230:ILE:HG13	1:A:904:LEU:HD11	1.97	0.46
1:A:307:PHE:N	1:A:307:PHE:HD1	2.14	0.46
1:B:227:MET:HA	1:B:230:ILE:CG2	2.45	0.46
1:B:253:PRO:HG2	1:B:517:MET:HG2	1.96	0.46
1:C:255:ILE:HG13	1:C:357:LEU:HA	1.97	0.46
1:E:232:LYS:O	1:E:235:ILE:HG23	2.14	0.46
1:E:485:PHE:CD2	1:E:492:PHE:CE1	3.03	0.46
1:G:364:ILE:HD12	1:G:376:LYS:HZ2	1.80	0.46
1:G:387:ILE:CG2	1:G:393:ILE:HD12	2.46	0.46
1:H:264:GLY:O	1:H:268:VAL:HG22	2.16	0.46
1:J:242:GLN:HE22	1:J:344:ARG:HD3	1.80	0.46
1:J:243:LYS:O	1:J:243:LYS:HG2	2.14	0.46
1:J:363:TYR:CE1	1:J:383:CYS:SG	2.79	0.46
1:A:456:ILE:O	1:A:456:ILE:HG23	2.16	0.46
1:B:510:LEU:HD23	1:B:511:GLN:N	2.29	0.46
1:C:360:LEU:HB2	1:C:361:PRO:HD2	1.97	0.46
1:C:430:ASP:HB3	1:C:456:ILE:HG12	1.97	0.46
1:D:285:ILE:HD12	1:D:287:ARG:HB2	1.73	0.46
1:D:308:PRO:HG3	1:D:344:ARG:CG	2.45	0.46
1:D:429:MET:HE2	1:D:437:GLY:CA	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:279:PRO:CG	1:E:322:GLN:HA	2.45	0.46
1:F:572:PHE:HB3	1:F:850:TYR:OH	2.16	0.46
1:H:600:ARG:HB3	1:H:601:PRO:HD2	1.97	0.46
1:I:407:THR:HG22	1:I:410:GLN:OE1	2.15	0.46
1:I:653:ALA:HB2	1:I:845:MET:HE1	1.96	0.46
1:J:520:LYS:HA	1:J:520:LYS:HD3	1.75	0.46
1:A:542:GLN:HB3	1:A:543:TYR:CE2	2.51	0.46
1:B:400:ASP:N	1:B:400:ASP:OD1	2.48	0.46
1:D:276:GLU:HG2	1:D:277:PHE:H	1.79	0.46
1:F:264:GLY:O	1:F:268:VAL:HG22	2.15	0.46
1:F:607:PRO:HD2	1:F:762:ARG:O	2.16	0.46
1:F:854:PRO:HB2	1:F:855:ARG:NH2	2.31	0.46
1:G:297:ASP:CG	1:G:300:ALA:HB3	2.40	0.46
1:H:268:VAL:HG12	1:H:280:LYS:HE3	1.96	0.46
1:H:376:LYS:NZ	1:H:379:ILE:HD12	2.30	0.46
1:J:363:TYR:HD2	1:J:407:THR:CB	2.15	0.46
1:J:434:PRO:HG2	1:J:488:HIS:CE1	2.50	0.46
1:J:457:SER:O	1:J:458:LYS:HB2	2.15	0.46
1:J:751:LEU:HA	1:J:754:VAL:HG12	1.97	0.46
1:B:294:LEU:HB3	1:B:352:ILE:CD1	2.46	0.46
1:B:554:LEU:HD21	1:B:865:MET:HG3	1.97	0.46
1:C:863:GLU:O	1:C:867:ALA:HB2	2.15	0.46
1:E:444:ARG:HD2	1:E:444:ARG:HA	1.52	0.46
1:F:611:GLU:H	1:F:612:PRO:HD2	1.76	0.46
1:G:237:ILE:HD11	1:G:897:VAL:HG13	1.96	0.46
1:H:499:SER:C	1:H:500:THR:HG23	2.41	0.46
1:J:267:SER:HB2	1:J:396:ILE:HD12	1.97	0.46
1:A:444:ARG:CZ	1:A:447:PRO:HB3	2.45	0.46
1:D:565:PHE:HA	1:D:663:LEU:HD21	1.97	0.46
1:D:642:LEU:HD12	1:D:643:GLY:N	2.30	0.46
1:E:251:THR:CG2	1:E:252:LEU:H	2.22	0.46
1:E:276:GLU:OE1	1:E:318:PHE:CE2	2.68	0.46
1:E:311:GLY:C	1:E:312:LEU:HD23	2.40	0.46
1:F:270:GLU:O	1:F:273:VAL:HG22	2.16	0.46
1:H:263:SER:HA	1:H:266:SER:OG	2.16	0.46
1:H:484:TYR:HD1	1:H:485:PHE:CD1	2.33	0.46
1:H:520:LYS:HD3	1:H:520:LYS:HA	1.59	0.46
1:H:683:ALA:HB2	1:H:853:PHE:CE1	2.51	0.46
1:J:258:ILE:HG21	1:J:387:ILE:HD11	1.98	0.46
1:J:275:HIS:CD2	1:J:275:HIS:N	2.84	0.46
1:J:426:ILE:CD1	1:J:440:ILE:HG21	1.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:818:LYS:HE3	1:J:819:TYR:CE2	2.50	0.46
1:A:450:LEU:HD22	1:A:512:VAL:CG2	2.45	0.46
1:B:396:ILE:HG22	1:B:425:VAL:HB	1.98	0.46
1:C:627:TYR:CZ	1:C:631:GLN:NE2	2.83	0.46
1:D:485:PHE:CD2	1:D:492:PHE:HD1	2.29	0.46
1:D:499:SER:C	1:D:500:THR:HG23	2.41	0.46
1:D:576:GLN:H	1:D:576:GLN:HE21	1.63	0.46
1:E:272:ILE:HG23	1:E:278:LEU:HD13	1.85	0.46
1:E:377:ARG:HH21	1:E:377:ARG:CG	2.29	0.46
1:G:261:GLN:CD	1:G:262:SER:H	2.22	0.46
1:G:564:GLN:HG2	1:G:663:LEU:HD11	1.98	0.46
1:H:277:PHE:CD1	1:H:278:LEU:N	2.84	0.46
1:I:296:ASN:H	1:I:354:ASP:HB3	1.81	0.46
1:B:450:LEU:HD22	1:B:512:VAL:CG2	2.46	0.46
1:B:762:ARG:NH1	1:B:762:ARG:HG2	2.31	0.46
1:C:596:ARG:NH2	1:C:630:ARG:HH21	2.13	0.46
1:D:232:LYS:O	1:D:235:ILE:CG2	2.63	0.46
1:D:485:PHE:CE2	1:D:492:PHE:CD1	3.04	0.46
1:E:307:PHE:N	1:E:307:PHE:HD1	2.13	0.46
1:H:478:ASN:O	1:H:482:LYS:CG	2.62	0.46
1:H:593:LEU:HD21	1:H:823:GLU:HG3	1.97	0.46
1:J:288:ARG:HA	1:J:289:PRO:HD3	1.77	0.46
1:J:657:GLN:HE21	1:J:657:GLN:HB2	1.59	0.46
1:A:234:MET:HE1	1:A:518:SER:OG	2.16	0.46
1:C:873:LYS:HB2	1:C:873:LYS:HE3	1.65	0.46
1:D:241:LEU:O	1:D:244:VAL:HG23	2.16	0.46
1:D:757:PHE:CD2	1:D:757:PHE:C	2.94	0.46
1:E:242:GLN:HE22	1:E:344:ARG:HD2	1.81	0.46
1:E:377:ARG:HH21	1:E:377:ARG:HG2	1.80	0.46
1:E:520:LYS:HA	1:E:520:LYS:HD3	1.82	0.46
1:F:818:LYS:HE3	1:F:819:TYR:CE2	2.51	0.46
1:G:404:ALA:HB1	1:J:364:ILE:CG2	2.46	0.46
1:G:404:ALA:O	1:J:364:ILE:HG22	2.16	0.46
1:I:264:GLY:HA2	1:I:267:SER:HB3	1.98	0.46
1:I:615:ILE:O	1:I:615:ILE:HD13	2.16	0.46
1:I:625:SER:O	1:I:628:TRP:CB	2.64	0.46
1:J:360:LEU:HD13	1:J:383:CYS:SG	2.56	0.46
1:J:376:LYS:HA	1:J:376:LYS:HZ1	1.77	0.46
1:J:832:LYS:O	1:J:836:THR:HG22	2.16	0.46
1:B:488:HIS:O	1:B:491:GLU:HG2	2.16	0.45
1:C:697:GLY:HA3	1:C:840:PHE:CZ	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269:LEU:HD11	1:D:458:LYS:HB2	1.97	0.45
1:D:703:LYS:N	1:D:704:PRO:HD2	2.31	0.45
1:F:640:THR:HG22	1:F:706:LYS:HG2	1.98	0.45
1:G:396:ILE:HG22	1:G:425:VAL:HB	1.98	0.45
1:H:279:PRO:O	1:H:280:LYS:CG	2.65	0.45
1:H:339:THR:CG2	1:H:340:ASP:N	2.77	0.45
1:H:657:GLN:HE22	1:H:684:ALA:CA	2.29	0.45
1:H:701:SER:O	1:H:704:PRO:HD2	2.15	0.45
1:I:254:SER:HB2	1:I:356:SER:O	2.16	0.45
1:J:325:LEU:HA	1:J:328:LEU:HD12	1.97	0.45
1:J:360:LEU:HB2	1:J:361:PRO:HD2	1.98	0.45
1:B:272:ILE:HA	1:B:278:LEU:HD12	1.99	0.45
1:B:554:LEU:CD2	1:B:865:MET:HG3	2.46	0.45
1:F:279:PRO:HG3	1:F:321:ILE:HG22	1.98	0.45
1:H:279:PRO:O	1:H:280:LYS:HG2	2.16	0.45
1:I:434:PRO:HG2	1:I:488:HIS:ND1	2.30	0.45
1:I:507:LYS:HB2	1:I:507:LYS:HE3	1.77	0.45
1:I:664:LEU:HB3	1:I:676:ARG:NH1	2.31	0.45
1:J:843:VAL:HG12	1:J:844:GLU:N	2.31	0.45
1:A:267:SER:HB2	1:A:396:ILE:HD12	1.96	0.45
1:C:279:PRO:HG2	1:C:325:LEU:HD21	1.98	0.45
1:C:510:LEU:HD23	1:C:511:GLN:N	2.32	0.45
1:D:269:LEU:HD23	1:D:457:SER:CB	2.44	0.45
1:D:275:HIS:CG	1:D:276:GLU:N	2.85	0.45
1:D:297:ASP:OD1	1:D:348:HIS:HB3	2.16	0.45
1:D:389:GLY:O	1:D:391:ASN:N	2.44	0.45
1:D:900:LYS:HD3	1:D:900:LYS:HA	1.73	0.45
1:E:285:ILE:O	1:E:286:THR:OG1	2.24	0.45
1:E:565:PHE:HA	1:E:663:LEU:HD21	1.99	0.45
1:G:692:TYR:C	1:G:692:TYR:CD2	2.94	0.45
1:H:383:CYS:O	1:H:387:ILE:HG13	2.16	0.45
1:A:233:LYS:HE3	1:A:233:LYS:N	2.32	0.45
1:A:270:GLU:CA	1:A:273:VAL:HG22	2.46	0.45
1:A:279:PRO:HG3	1:A:321:ILE:C	2.40	0.45
1:A:537:TYR:CD2	1:I:613:ASP:OD2	2.69	0.45
1:A:593:LEU:CD2	1:A:823:GLU:HG3	2.47	0.45
1:A:853:PHE:HB3	1:A:854:PRO:HD3	1.98	0.45
1:B:231:THR:O	1:B:235:ILE:HG22	2.17	0.45
1:B:453:VAL:HG11	1:B:505:LEU:HB2	1.98	0.45
1:D:363:TYR:CD2	1:D:407:THR:HB	2.51	0.45
1:D:524:THR:O	1:D:528:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:242:GLN:HE22	1:E:344:ARG:HD3	1.82	0.45
1:F:254:SER:O	1:F:391:ASN:HB2	2.17	0.45
1:F:842:ASN:O	1:F:846:LEU:HB3	2.15	0.45
1:G:545:GLU:O	1:G:547:PRO:HD3	2.16	0.45
1:G:755:MET:HE3	1:G:790:ALA:HB1	1.99	0.45
1:H:272:ILE:HG13	1:H:272:ILE:H	1.62	0.45
1:H:533:GLU:OE1	1:H:534:GLU:N	2.49	0.45
1:I:738:MET:HE1	1:I:755:MET:HE1	1.98	0.45
1:J:267:SER:HB2	1:J:396:ILE:HD11	1.97	0.45
1:J:276:GLU:HG2	1:J:277:PHE:N	2.31	0.45
1:B:882:ARG:HG2	1:B:882:ARG:HH11	1.80	0.45
1:C:300:ALA:C	1:C:301:LYS:HD3	2.42	0.45
1:C:377:ARG:CG	1:C:377:ARG:NH2	2.78	0.45
1:D:617:ASP:OD1	1:D:617:ASP:N	2.48	0.45
1:D:690:ARG:NH1	1:D:844:GLU:OE2	2.49	0.45
1:E:425:VAL:HA	1:E:453:VAL:O	2.16	0.45
1:E:843:VAL:HG21	1:F:704:PRO:HA	1.97	0.45
1:H:358:ILE:O	1:H:358:ILE:HG12	2.16	0.45
1:H:597:TYR:CE2	1:H:822:PRO:HG3	2.50	0.45
1:I:233:LYS:HE3	1:I:900:LYS:HD2	1.98	0.45
1:I:352:ILE:C	1:I:352:ILE:HD12	2.42	0.45
1:A:267:SER:HB2	1:A:396:ILE:HD11	1.97	0.45
1:A:443:ASP:O	1:A:444:ARG:HD2	2.15	0.45
1:A:485:PHE:HE2	1:A:500:THR:OG1	1.94	0.45
1:A:736:ALA:O	1:A:737:ALA:C	2.58	0.45
1:B:227:MET:CA	1:B:230:ILE:HG22	2.44	0.45
1:C:596:ARG:CZ	1:C:630:ARG:HH21	2.29	0.45
1:C:597:TYR:CE2	1:C:822:PRO:HG3	2.51	0.45
1:C:823:GLU:OE1	1:C:823:GLU:N	2.45	0.45
1:D:255:ILE:HG12	1:D:513:LEU:HD21	1.99	0.45
1:D:288:ARG:HA	1:D:289:PRO:HD3	1.78	0.45
1:F:387:ILE:HG22	1:F:415:VAL:HG21	1.97	0.45
1:G:387:ILE:HG21	1:G:393:ILE:HD12	1.97	0.45
1:G:590:LEU:HA	1:G:590:LEU:HD22	1.73	0.45
1:H:299:GLU:O	1:H:299:GLU:HG2	2.17	0.45
1:I:279:PRO:HG2	1:I:325:LEU:HD21	1.99	0.45
1:J:485:PHE:CE2	1:J:492:PHE:CD1	3.04	0.45
1:D:327:GLU:HA	1:D:327:GLU:OE1	2.17	0.45
1:D:815:LEU:O	1:D:815:LEU:HD22	2.17	0.45
1:E:229:PHE:CZ	1:E:232:LYS:CD	2.95	0.45
1:E:278:LEU:CD2	1:E:280:LYS:HG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:285:ILE:C	1:E:287:ARG:H	2.25	0.45
1:E:454:GLY:O	1:E:500:THR:CB	2.64	0.45
1:F:389:GLY:O	1:F:391:ASN:N	2.44	0.45
1:G:525:THR:O	1:G:529:GLN:HG3	2.16	0.45
1:H:285:ILE:HG12	1:H:332:VAL:HG22	1.99	0.45
1:H:413:ARG:NE	1:H:422:THR:HG21	2.32	0.45
1:I:486:GLY:O	1:I:489:PRO:HD3	2.16	0.45
1:A:394:LEU:HD13	1:A:395:ALA:HB3	1.98	0.45
1:A:742:GLU:CD	1:A:748:ARG:HE	2.25	0.45
1:B:242:GLN:OE1	1:B:251:THR:HG21	2.16	0.45
1:C:266:SER:HB2	1:C:427:THR:OG1	2.17	0.45
1:C:441:LEU:HD23	1:C:498:VAL:HB	1.99	0.45
1:E:326:THR:HA	1:E:329:ASN:ND2	2.32	0.45
1:F:429:MET:HE2	1:F:437:GLY:HA2	1.97	0.45
1:F:653:ALA:HB2	1:F:845:MET:HE1	1.99	0.45
1:F:727:LEU:HD12	1:F:727:LEU:HA	1.82	0.45
1:F:738:MET:O	1:F:742:GLU:HG3	2.17	0.45
1:H:232:LYS:C	1:H:235:ILE:HG22	2.41	0.45
1:H:275:HIS:CD2	1:H:275:HIS:N	2.84	0.45
1:H:705:TYR:CD1	1:H:832:LYS:HD3	2.52	0.45
1:J:476:SER:C	1:J:478:ASN:N	2.69	0.45
1:A:257:VAL:O	1:A:257:VAL:HG23	2.17	0.45
1:B:278:LEU:HD13	1:B:280:LYS:HG2	1.99	0.45
1:B:480:ASN:HA	1:B:483:ASN:OD1	2.17	0.45
1:C:224:ASP:CB	1:C:227:MET:HB2	2.45	0.45
1:C:224:ASP:O	1:C:227:MET:N	2.49	0.45
1:C:572:PHE:CD2	1:C:846:LEU:HD11	2.51	0.45
1:C:653:ALA:HB2	1:C:845:MET:HE1	1.98	0.45
1:E:238:ARG:CZ	1:E:356:SER:HG	2.29	0.45
1:E:426:ILE:HD13	1:E:440:ILE:CB	2.35	0.45
1:F:627:TYR:CE2	1:F:628:TRP:CH2	3.02	0.45
1:H:287:ARG:CG	1:H:287:ARG:NH1	2.76	0.45
1:H:413:ARG:NH1	1:H:446:TYR:CD1	2.70	0.45
1:I:627:TYR:O	1:I:628:TRP:CE3	2.70	0.45
1:J:293:THR:OG1	1:J:346:THR:HG23	2.16	0.45
1:J:672:HIS:HA	1:J:877:GLU:CD	2.40	0.45
1:A:275:HIS:CD2	1:A:275:HIS:N	2.84	0.45
1:B:732:GLU:O	1:B:733:GLN:C	2.57	0.45
1:E:703:LYS:HE3	1:G:544:ASN:HB3	1.98	0.45
1:F:278:LEU:HD13	1:F:280:LYS:HG2	1.99	0.45
1:F:563:HIS:CD2	1:G:566:HIS:NE2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:878:ASP:OD2	1:F:879:PRO:HD2	2.17	0.45
1:G:690:ARG:HA	1:G:690:ARG:HD3	1.66	0.45
1:H:257:VAL:HG21	1:H:359:ASP:HB2	1.99	0.45
1:H:307:PHE:CD1	1:H:345:LEU:CD2	3.00	0.45
1:H:407:THR:CG2	1:H:414:ARG:HH11	2.15	0.45
1:A:267:SER:CB	1:A:396:ILE:HG13	2.36	0.44
1:A:754:VAL:HA	1:A:779:PHE:CE1	2.51	0.44
1:A:832:LYS:O	1:A:835:GLN:HG2	2.17	0.44
1:B:279:PRO:CB	1:B:322:GLN:HA	2.47	0.44
1:B:290:ILE:HG22	1:B:292:LEU:CD2	2.46	0.44
1:E:377:ARG:O	1:E:380:THR:OG1	2.30	0.44
1:E:476:SER:C	1:E:478:ASN:N	2.75	0.44
1:F:529:GLN:O	1:F:533:GLU:HG3	2.17	0.44
1:G:605:LEU:CD2	1:G:606:SER:N	2.77	0.44
1:G:656:ILE:HD11	1:G:846:LEU:HD12	1.99	0.44
1:G:873:LYS:HB2	1:G:873:LYS:HE3	1.71	0.44
1:H:272:ILE:HG23	1:H:278:LEU:H	1.82	0.44
1:I:375:LEU:N	1:I:375:LEU:HD23	2.32	0.44
1:I:472:ASN:O	1:I:476:SER:HB3	2.18	0.44
1:I:613:ASP:CB	1:I:627:TYR:CE1	2.83	0.44
1:J:260:SER:OG	1:J:407:THR:OG1	2.34	0.44
1:J:262:SER:O	1:J:266:SER:OG	2.34	0.44
1:B:227:MET:HE3	1:B:227:MET:HB3	1.71	0.44
1:B:873:LYS:HB2	1:B:873:LYS:HE3	1.79	0.44
1:C:599:ASN:C	1:C:600:ARG:HD2	2.42	0.44
1:C:663:LEU:HD12	1:C:663:LEU:HA	1.84	0.44
1:D:255:ILE:HG13	1:D:357:LEU:HA	1.99	0.44
1:D:258:ILE:HG22	1:D:360:LEU:HD11	2.00	0.44
1:D:269:LEU:CG	1:D:457:SER:O	2.63	0.44
1:E:279:PRO:HG3	1:E:322:GLN:HA	1.99	0.44
1:E:303:ASP:OD1	1:E:349:SER:HB2	2.16	0.44
1:E:381:GLU:OE1	1:E:381:GLU:HA	2.17	0.44
1:E:585:LEU:HD23	1:E:585:LEU:HA	1.77	0.44
1:F:664:LEU:CD2	1:F:676:ARG:HG3	2.45	0.44
1:G:289:PRO:HB2	1:G:342:PRO:HB3	1.99	0.44
1:G:444:ARG:O	1:G:447:PRO:HD3	2.17	0.44
1:G:642:LEU:O	1:G:644:VAL:N	2.50	0.44
1:H:272:ILE:HG12	1:H:278:LEU:HD11	2.00	0.44
1:H:615:ILE:H	1:H:615:ILE:HD12	1.81	0.44
1:I:294:LEU:HB2	1:I:355:LEU:H	1.81	0.44
1:I:296:ASN:HB2	1:I:354:ASP:OD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:530:ARG:HA	1:I:530:ARG:HD3	1.70	0.44
1:J:296:ASN:C	1:J:298:PRO:HD3	2.42	0.44
1:J:690:ARG:O	1:J:694:THR:HG23	2.17	0.44
1:B:572:PHE:CD2	1:B:846:LEU:HD11	2.53	0.44
1:C:258:ILE:HD13	1:C:387:ILE:HD13	1.98	0.44
1:C:618:LEU:N	1:C:619:PRO:HD2	2.32	0.44
1:C:738:MET:HE1	1:C:755:MET:HE1	1.98	0.44
1:C:784:LEU:HA	1:C:784:LEU:HD23	1.79	0.44
1:D:257:VAL:O	1:D:257:VAL:HG23	2.16	0.44
1:E:285:ILE:HG13	1:E:286:THR:N	2.31	0.44
1:E:392:ILE:HG21	1:E:513:LEU:HD22	1.98	0.44
1:E:652:ALA:O	1:E:656:ILE:HG13	2.17	0.44
1:F:276:GLU:HG2	1:F:277:PHE:N	2.31	0.44
1:H:344:ARG:H	1:H:344:ARG:HG2	1.54	0.44
1:H:534:GLU:O	1:H:537:TYR:HB3	2.17	0.44
1:I:407:THR:HA	1:I:410:GLN:OE1	2.18	0.44
1:J:285:ILE:HD12	1:J:286:THR:N	2.33	0.44
1:J:426:ILE:HD13	1:J:440:ILE:CB	2.37	0.44
1:A:243:LYS:O	1:A:243:LYS:HG2	2.17	0.44
1:A:394:LEU:CG	1:A:395:ALA:N	2.79	0.44
1:A:394:LEU:HD12	1:A:423:ILE:O	2.17	0.44
1:A:536:THR:CG2	1:I:630:ARG:CD	2.49	0.44
1:A:610:ARG:NE	1:A:610:ARG:CA	2.77	0.44
1:D:279:PRO:O	1:D:280:LYS:CG	2.65	0.44
1:D:279:PRO:O	1:D:280:LYS:HG2	2.17	0.44
1:D:667:SER:OG	1:D:668:SER:N	2.49	0.44
1:D:711:ILE:HD12	1:D:828:ALA:HB1	2.00	0.44
1:E:454:GLY:N	1:E:500:THR:HG22	2.33	0.44
1:F:303:ASP:OD1	1:F:349:SER:HB2	2.18	0.44
1:F:777:GLY:C	1:F:779:PHE:H	2.26	0.44
1:G:297:ASP:OD2	1:G:300:ALA:HB3	2.18	0.44
1:H:450:LEU:HD22	1:H:512:VAL:CG2	2.48	0.44
1:I:450:LEU:O	1:I:508:LYS:NZ	2.50	0.44
1:A:307:PHE:HB2	1:A:310:LEU:HB2	2.00	0.44
1:C:227:MET:O	1:C:231:THR:OG1	2.35	0.44
1:C:357:LEU:HD23	1:C:357:LEU:H	1.82	0.44
1:E:243:LYS:HG2	1:E:243:LYS:O	2.17	0.44
1:E:246:GLN:HE22	1:E:890:ARG:NH1	2.16	0.44
1:E:269:LEU:HD21	1:E:457:SER:O	2.17	0.44
1:E:281:GLY:O	1:E:282:SER:C	2.61	0.44
1:F:425:VAL:HG12	1:F:427:THR:HG23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:269:LEU:HD11	1:G:457:SER:O	2.18	0.44
1:G:383:CYS:O	1:G:387:ILE:HG13	2.18	0.44
1:G:615:ILE:HD13	1:G:615:ILE:O	2.17	0.44
1:G:648:ALA:HB1	1:G:841:LEU:CD1	2.46	0.44
1:G:873:LYS:O	1:G:877:GLU:HG3	2.17	0.44
1:H:255:ILE:HD11	1:H:355:LEU:HG	2.00	0.44
1:H:610:ARG:HE	1:H:611:GLU:H	1.64	0.44
1:J:285:ILE:HG12	1:J:332:VAL:HG22	1.99	0.44
1:J:361:PRO:HD2	1:J:382:LEU:HD21	1.99	0.44
1:A:285:ILE:HD12	1:A:287:ARG:CA	2.41	0.44
1:A:537:TYR:CE1	1:I:627:TYR:CA	3.00	0.44
1:A:894:LEU:HD23	1:A:894:LEU:HA	1.80	0.44
1:B:450:LEU:O	1:B:508:LYS:NZ	2.44	0.44
1:C:279:PRO:HB3	1:C:322:GLN:CD	2.43	0.44
1:C:701:SER:O	1:C:704:PRO:HD2	2.18	0.44
1:D:382:LEU:C	1:D:382:LEU:CD1	2.71	0.44
1:D:791:VAL:O	1:D:792:PHE:C	2.60	0.44
1:E:308:PRO:HG3	1:E:344:ARG:CG	2.47	0.44
1:E:458:LYS:C	1:E:458:LYS:CD	2.89	0.44
1:E:574:ARG:N	1:E:575:PRO:CD	2.80	0.44
1:E:617:ASP:OD1	1:E:617:ASP:N	2.50	0.44
1:E:723:VAL:HG11	1:E:823:GLU:HB3	2.00	0.44
1:G:754:VAL:HG22	1:G:779:PHE:CE2	2.52	0.44
1:G:754:VAL:HG21	1:G:783:LEU:HD22	1.99	0.44
1:H:279:PRO:O	1:H:280:LYS:HD2	2.17	0.44
1:J:434:PRO:HB3	1:J:491:GLU:CB	2.47	0.44
1:A:278:LEU:HD13	1:A:280:LYS:HG2	1.98	0.44
1:A:524:THR:O	1:A:527:ALA:HB3	2.17	0.44
1:B:450:LEU:HD22	1:B:512:VAL:HG22	2.00	0.44
1:C:444:ARG:NH1	1:C:447:PRO:HB3	2.32	0.44
1:E:778:GLY:C	1:E:779:PHE:HD2	2.25	0.44
1:F:289:PRO:HB2	1:F:342:PRO:HB3	2.00	0.44
1:F:445:GLN:C	1:F:447:PRO:HD3	2.43	0.44
1:G:275:HIS:CG	1:G:276:GLU:N	2.86	0.44
1:H:255:ILE:HG13	1:H:357:LEU:HA	2.00	0.44
1:I:553:TYR:O	1:I:557:SER:OG	2.35	0.44
1:I:627:TYR:HB3	1:I:628:TRP:CH2	2.53	0.44
1:J:237:ILE:HD11	1:J:897:VAL:CG1	2.44	0.44
1:A:279:PRO:HB3	1:A:322:GLN:HB2	1.94	0.44
1:A:416:ASP:OD2	1:A:421:ARG:HG2	2.18	0.44
1:A:441:LEU:HD23	1:A:498:VAL:HB	0.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:784:LEU:HD23	1:B:784:LEU:HA	1.87	0.44
1:C:252:LEU:HD23	1:C:524:THR:HG21	2.00	0.44
1:C:526:GLU:C	1:C:526:GLU:OE1	2.61	0.44
1:D:294:LEU:HB3	1:D:352:ILE:HD13	2.00	0.44
1:D:400:ASP:N	1:D:400:ASP:OD1	2.51	0.44
1:D:560:ASP:OD2	1:D:668:SER:OG	2.30	0.44
1:E:485:PHE:HE2	1:E:500:THR:OG1	1.94	0.44
1:E:749:LYS:O	1:E:753:GLU:HG3	2.17	0.44
1:F:296:ASN:N	1:F:354:ASP:HB3	2.33	0.44
1:F:611:GLU:H	1:F:612:PRO:CD	2.31	0.44
1:F:754:VAL:HG22	1:F:779:PHE:CD2	2.52	0.44
1:H:282:SER:HB2	1:H:283:ASN:H	1.60	0.44
1:A:775:GLY:HA2	1:A:779:PHE:O	2.17	0.44
1:B:259:GLY:HA2	1:B:408:ALA:HB2	1.99	0.44
1:D:246:GLN:CD	1:D:247:GLY:N	2.76	0.44
1:D:275:HIS:CD2	1:D:275:HIS:N	2.86	0.44
1:D:396:ILE:HA	1:D:425:VAL:O	2.18	0.44
1:D:450:LEU:O	1:D:508:LYS:NZ	2.49	0.44
1:E:233:LYS:HA	1:E:233:LYS:CE	2.22	0.44
1:E:270:GLU:HA	1:E:273:VAL:HG22	1.98	0.44
1:E:543:TYR:CE1	1:E:884:HIS:HB2	2.53	0.44
1:E:762:ARG:HH11	1:E:762:ARG:CG	2.31	0.44
1:F:266:SER:HA	1:F:269:LEU:HD22	1.99	0.44
1:G:450:LEU:O	1:G:508:LYS:NZ	2.50	0.44
1:H:477:ILE:O	1:H:477:ILE:CG2	2.64	0.44
1:H:694:THR:HG22	1:H:844:GLU:HG3	1.99	0.44
1:I:260:SER:N	1:I:263:SER:HB3	2.33	0.44
1:I:485:PHE:CD1	1:I:485:PHE:N	2.86	0.44
1:A:272:ILE:CB	1:A:278:LEU:CD1	2.96	0.43
1:A:384:ASP:OD1	1:A:384:ASP:O	2.36	0.43
1:A:520:LYS:HD3	1:A:520:LYS:HA	1.57	0.43
1:D:782:ALA:O	1:D:786:ARG:HD3	2.18	0.43
1:E:285:ILE:HG13	1:E:286:THR:H	1.83	0.43
1:E:640:THR:HG22	1:E:706:LYS:HG2	2.00	0.43
1:F:611:GLU:HG3	1:F:611:GLU:O	2.17	0.43
1:G:272:ILE:HA	1:G:278:LEU:HD12	1.99	0.43
1:G:363:TYR:HD2	1:G:407:THR:HB	1.82	0.43
1:G:575:PRO:O	1:G:578:GLN:HB3	2.17	0.43
1:I:716:TRP:CE2	1:I:815:LEU:HA	2.53	0.43
1:J:237:ILE:HD13	1:J:241:LEU:HG	1.99	0.43
1:J:252:LEU:HD23	1:J:252:LEU:HA	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:683:ALA:HB2	1:J:853:PHE:CE1	2.53	0.43
1:A:238:ARG:NH2	1:A:356:SER:HG	2.15	0.43
1:A:308:PRO:HD2	1:A:344:ARG:O	2.18	0.43
1:B:321:ILE:HA	1:B:324:THR:OG1	2.17	0.43
1:B:344:ARG:H	1:B:344:ARG:HG2	1.56	0.43
1:B:565:PHE:CZ	1:B:853:PHE:HD2	2.36	0.43
1:B:627:TYR:HA	1:J:540:LYS:CD	2.48	0.43
1:B:781:ALA:CA	1:E:778:GLY:CA	2.96	0.43
1:C:449:LYS:C	1:C:450:LEU:HG	2.42	0.43
1:C:475:ALA:O	1:C:479:ARG:HG2	2.17	0.43
1:D:454:GLY:O	1:D:500:THR:HG22	2.17	0.43
1:E:260:SER:N	1:E:263:SER:HB3	2.34	0.43
1:E:488:HIS:HB3	1:E:491:GLU:HG3	1.98	0.43
1:G:251:THR:HG22	1:G:252:LEU:H	1.83	0.43
1:H:261:GLN:N	1:H:261:GLN:OE1	2.51	0.43
1:H:286:THR:HB	1:H:361:PRO:CB	2.48	0.43
1:H:381:GLU:OE1	1:H:381:GLU:HA	2.18	0.43
1:H:832:LYS:O	1:H:836:THR:HG22	2.18	0.43
1:A:307:PHE:CZ	1:A:345:LEU:HD21	2.48	0.43
1:B:667:SER:OG	1:B:668:SER:N	2.51	0.43
1:C:529:GLN:O	1:C:533:GLU:HG3	2.18	0.43
1:C:673:PRO:HA	1:C:676:ARG:HB3	2.00	0.43
1:E:375:LEU:N	1:E:375:LEU:HD23	2.33	0.43
1:G:605:LEU:CD2	1:G:605:LEU:C	2.90	0.43
1:G:618:LEU:HG	1:G:803:ARG:HH21	1.83	0.43
1:I:677:LYS:NZ	1:I:681:ASP:OD2	2.45	0.43
1:A:282:SER:HB2	1:A:283:ASN:H	1.64	0.43
1:A:618:LEU:HB3	1:A:619:PRO:HD3	1.98	0.43
1:A:690:ARG:O	1:A:694:THR:HG23	2.19	0.43
1:B:492:PHE:HB3	1:B:498:VAL:HG21	1.99	0.43
1:C:876:ARG:NH1	1:C:886:ASP:OD1	2.51	0.43
1:D:253:PRO:HG3	1:D:516:GLN:OE1	2.17	0.43
1:E:279:PRO:CG	1:E:325:LEU:HD21	2.27	0.43
1:E:519:SER:OG	1:E:520:LYS:N	2.51	0.43
1:F:878:ASP:OD2	1:F:878:ASP:C	2.62	0.43
1:G:268:VAL:HB	1:G:280:LYS:HB3	2.00	0.43
1:G:705:TYR:CE1	1:G:832:LYS:HD3	2.53	0.43
1:H:312:LEU:N	1:H:312:LEU:HD23	2.34	0.43
1:H:540:LYS:HA	1:H:545:GLU:HG3	2.00	0.43
1:H:540:LYS:HB2	1:H:540:LYS:HE3	1.71	0.43
1:J:294:LEU:HB3	1:J:352:ILE:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:723:VAL:HG11	1:J:823:GLU:HB3	1.99	0.43
1:A:258:ILE:HG22	1:A:360:LEU:HD11	1.99	0.43
1:A:425:VAL:HA	1:A:453:VAL:O	2.18	0.43
1:D:255:ILE:HA	1:D:392:ILE:HG23	2.01	0.43
1:D:306:GLU:C	1:D:307:PHE:HD1	2.26	0.43
1:E:875:ALA:O	1:E:881:VAL:HG23	2.18	0.43
1:F:510:LEU:HD23	1:F:510:LEU:C	2.44	0.43
1:F:646:ARG:HA	1:F:646:ARG:HD2	1.86	0.43
1:F:755:MET:HE3	1:F:790:ALA:HB1	1.99	0.43
1:G:257:VAL:HA	1:G:394:LEU:O	2.18	0.43
1:G:294:LEU:HB3	1:G:352:ILE:CD1	2.48	0.43
1:G:364:ILE:O	1:J:405:ASN:CG	2.62	0.43
1:G:405:ASN:CG	1:J:261:GLN:HB2	2.41	0.43
1:G:840:PHE:CZ	1:G:844:GLU:HG3	2.54	0.43
1:H:298:PRO:O	1:H:299:GLU:HB3	2.18	0.43
1:J:232:LYS:O	1:J:235:ILE:HG23	2.19	0.43
1:J:263:SER:CA	1:J:266:SER:OG	2.67	0.43
1:A:297:ASP:N	1:A:298:PRO:CD	2.80	0.43
1:A:537:TYR:CZ	1:I:627:TYR:HB2	2.46	0.43
1:A:778:GLY:O	1:A:779:PHE:HD2	2.00	0.43
1:B:430:ASP:HB3	1:B:456:ILE:HG12	2.01	0.43
1:B:678:VAL:HG11	1:B:861:LEU:HD23	2.00	0.43
1:C:227:MET:HE3	1:C:227:MET:HB3	1.95	0.43
1:C:303:ASP:OD1	1:C:349:SER:HB2	2.18	0.43
1:E:279:PRO:HG3	1:E:321:ILE:HG22	2.01	0.43
1:E:381:GLU:OE1	1:E:381:GLU:CA	2.66	0.43
1:F:360:LEU:HD13	1:F:383:CYS:SG	2.59	0.43
1:F:544:ASN:ND2	1:H:703:LYS:HE3	2.34	0.43
1:G:240:LEU:HD23	1:G:240:LEU:HA	1.81	0.43
1:G:671:LYS:C	1:G:672:HIS:CG	2.96	0.43
1:G:854:PRO:HB2	1:G:855:ARG:NH2	2.33	0.43
1:H:436:LYS:O	1:H:440:ILE:HG13	2.19	0.43
1:I:585:LEU:HB3	1:I:830:ALA:HB1	2.01	0.43
1:I:640:THR:HG21	1:I:706:LYS:HA	2.00	0.43
1:A:309:ASP:C	1:A:310:LEU:HD23	2.42	0.43
1:A:394:LEU:HA	1:A:394:LEU:HD23	1.84	0.43
1:A:499:SER:C	1:A:500:THR:HG23	2.43	0.43
1:A:682:ALA:O	1:A:686:VAL:HG23	2.18	0.43
1:A:883:ARG:O	1:A:887:LEU:HB2	2.18	0.43
1:B:474:LEU:HG	1:B:475:ALA:H	1.84	0.43
1:D:308:PRO:HD2	1:D:344:ARG:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:376:LYS:CA	1:D:376:LYS:HE2	2.49	0.43
1:D:480:ASN:O	1:D:480:ASN:OD1	2.37	0.43
1:D:712:GLN:HB2	1:D:714:ASN:ND2	2.34	0.43
1:D:784:LEU:HD13	1:D:784:LEU:HA	1.95	0.43
1:D:907:ILE:HD12	1:D:907:ILE:HA	1.85	0.43
1:G:294:LEU:HB3	1:G:352:ILE:HD13	2.00	0.43
1:H:307:PHE:CD1	1:H:345:LEU:HD21	2.53	0.43
1:H:443:ASP:OD1	1:H:445:GLN:HB2	2.19	0.43
1:I:263:SER:OG	1:I:396:ILE:O	2.36	0.43
1:I:558:LEU:HD12	1:I:861:LEU:HD12	1.99	0.43
1:J:255:ILE:HG23	1:J:392:ILE:HG23	2.00	0.43
1:J:297:ASP:OD1	1:J:348:HIS:HB3	2.18	0.43
1:J:876:ARG:HB3	1:J:882:ARG:HH21	1.84	0.43
1:A:605:LEU:HD21	1:A:784:LEU:HD12	2.01	0.43
1:A:615:ILE:HD12	1:A:615:ILE:H	1.83	0.43
1:A:779:PHE:CD2	1:A:779:PHE:N	2.86	0.43
1:B:241:LEU:O	1:B:244:VAL:HG13	2.18	0.43
1:B:423:ILE:HG22	1:B:450:LEU:HD13	2.01	0.43
1:C:269:LEU:HD11	1:C:457:SER:O	2.19	0.43
1:D:237:ILE:HD11	1:D:897:VAL:HG13	2.00	0.43
1:D:540:LYS:HA	1:D:545:GLU:HG3	1.99	0.43
1:E:297:ASP:OD1	1:E:348:HIS:HB3	2.18	0.43
1:G:230:ILE:HG13	1:G:904:LEU:HD11	2.00	0.43
1:G:279:PRO:CB	1:G:322:GLN:HA	2.49	0.43
1:G:456:ILE:HG23	1:G:456:ILE:O	2.19	0.43
1:G:475:ALA:O	1:G:479:ARG:HG2	2.19	0.43
1:H:224:ASP:OD2	1:H:227:MET:HB2	2.19	0.43
1:H:230:ILE:O	1:H:234:MET:HG3	2.18	0.43
1:H:402:ASP:O	1:H:410:GLN:CD	2.62	0.43
1:I:625:SER:C	1:I:626:PRO:CA	2.79	0.43
1:I:702:LEU:HD23	1:I:702:LEU:HA	1.80	0.43
1:J:604:ASP:C	1:J:605:LEU:HD12	2.43	0.43
1:A:267:SER:CB	1:A:396:ILE:HD11	2.49	0.43
1:A:270:GLU:C	1:A:273:VAL:HG22	2.44	0.43
1:A:296:ASN:C	1:A:298:PRO:CD	2.92	0.43
1:A:673:PRO:HD2	1:A:877:GLU:OE1	2.19	0.43
1:B:630:ARG:CD	1:J:540:LYS:CG	2.96	0.43
1:B:861:LEU:HD23	1:B:861:LEU:HA	1.85	0.43
1:C:263:SER:HA	1:C:266:SER:OG	2.18	0.43
1:E:396:ILE:HA	1:E:425:VAL:O	2.18	0.43
1:E:783:LEU:HD23	1:E:783:LEU:HA	1.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:627:TYR:CZ	1:F:631:GLN:NE2	2.87	0.43
1:G:268:VAL:HG12	1:G:280:LYS:HE3	2.01	0.43
1:G:273:VAL:HG21	1:G:457:SER:HB3	2.01	0.43
1:G:508:LYS:HE2	1:G:508:LYS:HB3	1.82	0.43
1:H:276:GLU:HG2	1:H:277:PHE:H	1.83	0.43
1:H:657:GLN:HE21	1:H:657:GLN:HB2	1.44	0.43
1:H:679:ILE:O	1:H:682:ALA:HB3	2.18	0.43
1:I:409:LEU:O	1:I:413:ARG:HG3	2.19	0.43
1:J:345:LEU:HD23	1:J:345:LEU:HA	1.82	0.43
1:J:349:SER:O	1:J:352:ILE:HG13	2.19	0.43
1:J:832:LYS:O	1:J:835:GLN:HG2	2.19	0.43
1:A:543:TYR:CE1	1:A:884:HIS:HB2	2.54	0.43
1:A:878:ASP:HA	1:A:879:PRO:HD3	1.91	0.43
1:B:227:MET:O	1:B:231:THR:OG1	2.37	0.43
1:C:224:ASP:O	1:C:225:ASP:C	2.61	0.43
1:D:694:THR:HG22	1:D:844:GLU:CG	2.49	0.43
1:D:720:ARG:CZ	1:D:813:LYS:HG3	2.49	0.43
1:F:723:VAL:HG21	1:F:824:VAL:HA	2.00	0.43
1:G:232:LYS:HB3	1:G:232:LYS:HE2	1.76	0.43
1:G:400:ASP:CB	1:J:400:ASP:OD2	2.65	0.43
1:H:286:THR:C	1:H:361:PRO:HB3	2.44	0.43
1:I:257:VAL:HA	1:I:394:LEU:O	2.19	0.43
1:A:237:ILE:HD12	1:A:241:LEU:HD11	2.01	0.42
1:A:260:SER:O	1:A:264:GLY:CA	2.60	0.42
1:A:670:ALA:C	1:A:671:LYS:HE3	2.44	0.42
1:B:803:ARG:HD2	1:B:823:GLU:CD	2.43	0.42
1:C:429:MET:HE2	1:C:437:GLY:HA2	2.00	0.42
1:D:308:PRO:CG	1:D:344:ARG:HG3	2.48	0.42
1:D:388:ARG:HE	1:D:388:ARG:HB2	1.54	0.42
1:D:799:ILE:O	1:D:803:ARG:HG2	2.19	0.42
1:E:268:VAL:O	1:E:272:ILE:HG13	2.19	0.42
1:E:420:GLU:HG3	1:E:449:LYS:CE	2.48	0.42
1:H:340:ASP:O	1:H:340:ASP:CG	2.62	0.42
1:I:585:LEU:HD23	1:I:585:LEU:HA	1.81	0.42
1:J:627:TYR:HE2	1:J:628:TRP:CZ3	2.37	0.42
1:A:430:ASP:O	1:A:430:ASP:OD1	2.37	0.42
1:A:485:PHE:CZ	1:A:500:THR:OG1	2.54	0.42
1:B:261:GLN:HG3	1:B:364:ILE:HA	2.01	0.42
1:B:630:ARG:CD	1:J:540:LYS:HG3	2.48	0.42
1:D:416:ASP:OD2	1:D:422:THR:HG22	2.20	0.42
1:E:252:LEU:HD23	1:E:252:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:751:LEU:HD23	1:E:755:MET:HE2	2.01	0.42
1:F:234:MET:HE1	1:F:517:MET:C	2.44	0.42
1:F:234:MET:HE1	1:F:517:MET:O	2.19	0.42
1:F:542:GLN:O	1:F:543:TYR:CD1	2.72	0.42
1:H:398:ALA:O	1:H:399:ALA:HB2	2.18	0.42
1:H:723:VAL:O	1:H:727:LEU:HB2	2.18	0.42
1:A:272:ILE:HG13	1:A:272:ILE:H	1.69	0.42
1:A:708:ASP:OD1	1:A:710:ASP:HB3	2.19	0.42
1:C:588:LYS:HD3	1:C:588:LYS:HA	1.77	0.42
1:C:723:VAL:HG21	1:C:824:VAL:HA	1.99	0.42
1:C:757:PHE:O	1:C:760:LYS:HB2	2.20	0.42
1:C:847:ASN:ND2	1:D:707:PHE:CZ	2.87	0.42
1:E:349:SER:HB3	1:E:352:ILE:CG2	2.50	0.42
1:G:357:LEU:H	1:G:357:LEU:HD23	1.84	0.42
1:H:267:SER:HB3	1:H:396:ILE:HG13	2.01	0.42
1:H:278:LEU:HD13	1:H:278:LEU:O	2.19	0.42
1:I:750:LYS:O	1:I:754:VAL:HG23	2.19	0.42
1:J:870:GLY:O	1:J:874:PHE:HB2	2.19	0.42
1:A:289:PRO:HB2	1:A:342:PRO:HB3	2.02	0.42
1:B:230:ILE:O	1:B:234:MET:HG3	2.19	0.42
1:B:781:ALA:CA	1:E:778:GLY:HA2	2.50	0.42
1:C:553:TYR:O	1:C:557:SER:OG	2.36	0.42
1:C:558:LEU:HD12	1:C:861:LEU:HD12	2.01	0.42
1:C:803:ARG:HD3	1:C:803:ARG:HA	1.51	0.42
1:D:242:GLN:HE22	1:D:344:ARG:CD	2.28	0.42
1:D:574:ARG:N	1:D:575:PRO:HD2	2.32	0.42
1:D:642:LEU:O	1:D:644:VAL:N	2.50	0.42
1:E:278:LEU:HD22	1:E:280:LYS:CG	2.49	0.42
1:G:404:ALA:O	1:J:364:ILE:CG2	2.67	0.42
1:H:308:PRO:HG3	1:H:344:ARG:CG	2.48	0.42
1:I:262:SER:O	1:I:266:SER:OG	2.37	0.42
1:I:723:VAL:HG11	1:I:823:GLU:HB3	2.01	0.42
1:I:861:LEU:HA	1:I:861:LEU:HD23	1.75	0.42
1:J:363:TYR:CD1	1:J:363:TYR:N	2.88	0.42
1:C:553:TYR:CD1	1:C:553:TYR:C	2.97	0.42
1:D:285:ILE:HD11	1:D:287:ARG:H	1.66	0.42
1:D:484:TYR:HE1	1:D:492:PHE:CZ	2.38	0.42
1:E:272:ILE:HG23	1:E:278:LEU:N	2.35	0.42
1:E:278:LEU:HD13	1:E:280:LYS:HG2	2.01	0.42
1:F:304:TYR:CD2	1:F:314:ARG:HD3	2.55	0.42
1:F:639:LEU:O	1:F:642:LEU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:744:SER:OG	1:F:786:ARG:NH2	2.53	0.42
1:G:663:LEU:HD12	1:G:663:LEU:HA	1.90	0.42
1:H:276:GLU:OE2	1:H:318:PHE:CD2	2.73	0.42
1:H:321:ILE:HA	1:H:324:THR:OG1	2.19	0.42
1:H:322:GLN:O	1:H:326:THR:OG1	2.24	0.42
1:I:449:LYS:C	1:I:451:GLY:N	2.78	0.42
1:J:491:GLU:H	1:J:491:GLU:CD	2.27	0.42
1:J:496:SER:OG	1:J:498:VAL:HG22	2.19	0.42
1:A:272:ILE:CG1	1:A:278:LEU:CD1	2.95	0.42
1:A:281:GLY:O	1:A:282:SER:C	2.62	0.42
1:A:657:GLN:HE21	1:A:657:GLN:HB2	1.60	0.42
1:B:241:LEU:HA	1:B:244:VAL:HG13	2.01	0.42
1:B:269:LEU:HD11	1:B:457:SER:O	2.19	0.42
1:D:233:LYS:HE2	1:D:233:LYS:HA	2.00	0.42
1:F:258:ILE:HG21	1:F:387:ILE:HD11	2.02	0.42
1:G:863:GLU:O	1:G:867:ALA:CB	2.67	0.42
1:H:409:LEU:HD23	1:H:409:LEU:HA	1.90	0.42
1:H:574:ARG:N	1:H:575:PRO:HD2	2.30	0.42
1:H:834:ALA:O	1:H:838:VAL:HB	2.19	0.42
1:I:607:PRO:HD3	1:I:762:ARG:HG3	2.02	0.42
1:J:272:ILE:HG12	1:J:278:LEU:HD13	2.02	0.42
1:J:298:PRO:O	1:J:299:GLU:HB3	2.19	0.42
1:J:687:LEU:HA	1:J:687:LEU:HD23	1.81	0.42
1:A:723:VAL:O	1:A:727:LEU:HB2	2.20	0.42
1:B:757:PHE:HA	1:B:760:LYS:CD	2.47	0.42
1:C:296:ASN:H	1:C:354:ASP:HB3	1.84	0.42
1:D:574:ARG:CZ	1:D:839:LEU:HD12	2.49	0.42
1:E:263:SER:HA	1:E:266:SER:OG	2.20	0.42
1:E:298:PRO:O	1:E:298:PRO:CD	2.67	0.42
1:E:423:ILE:HG22	1:E:450:LEU:HD13	2.01	0.42
1:E:578:GLN:HA	1:E:838:VAL:HG21	2.02	0.42
1:F:276:GLU:HG3	1:F:474:LEU:HD23	2.01	0.42
1:F:363:TYR:N	1:F:363:TYR:CD1	2.88	0.42
1:F:454:GLY:O	1:F:500:THR:HG22	2.19	0.42
1:F:610:ARG:NE	1:F:613:ASP:HB2	2.35	0.42
1:G:286:THR:HB	1:G:361:PRO:HB3	2.01	0.42
1:H:473:LEU:HD12	1:H:473:LEU:HA	1.81	0.42
1:H:709:PRO:O	1:H:711:ILE:HG12	2.19	0.42
1:A:536:THR:HG22	1:I:630:ARG:HD2	0.62	0.42
1:B:345:LEU:HD23	1:B:345:LEU:HA	1.94	0.42
1:B:837:ALA:O	1:B:841:LEU:HB2	2.20	0.42

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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	0.42
1:C:308:PRO:O	1:C:309:ASP:C	2.62	0.42
1:D:269:LEU:HD23	1:D:270:GLU:CA	2.50	0.42
1:D:387:ILE:O	1:D:388:ARG:C	2.61	0.42
1:D:639:LEU:O	1:D:642:LEU:HD23	2.20	0.42
1:H:270:GLU:CA	1:H:273:VAL:HG22	2.50	0.42
1:H:429:MET:HE2	1:H:437:GLY:CA	2.45	0.42
1:J:228:MET:O	1:J:231:THR:HB	2.20	0.42
1:J:425:VAL:HA	1:J:453:VAL:O	2.20	0.42
1:J:453:VAL:HG21	1:J:505:LEU:HD23	2.01	0.42
1:J:454:GLY:H	1:J:500:THR:HG22	1.83	0.42
1:J:727:LEU:HA	1:J:727:LEU:HD12	1.83	0.42
1:A:308:PRO:HG2	1:A:309:ASP:H	1.85	0.42
1:B:513:LEU:CD2	1:B:517:MET:HE2	2.50	0.42
1:B:781:ALA:H	1:E:778:GLY:HA3	1.82	0.42
1:C:267:SER:CB	1:C:396:ILE:HG13	2.49	0.42
1:C:268:VAL:HB	1:C:280:LYS:HB3	2.02	0.42
1:C:409:LEU:O	1:C:413:ARG:HG3	2.19	0.42
1:C:757:PHE:CE1	1:C:777:GLY:HA3	2.55	0.42
1:D:272:ILE:CG2	1:D:277:PHE:CD1	3.02	0.42
1:D:430:ASP:O	1:D:430:ASP:OD1	2.38	0.42
1:D:434:PRO:HB3	1:D:491:GLU:HB3	1.97	0.42
1:F:873:LYS:O	1:F:876:ARG:HB2	2.20	0.42
1:G:842:ASN:O	1:G:846:LEU:HB3	2.19	0.42
1:J:233:LYS:HA	1:J:233:LYS:CE	2.47	0.42
1:J:233:LYS:CA	1:J:233:LYS:CE	2.98	0.42
1:J:697:GLY:HA3	1:J:840:PHE:CZ	2.55	0.42
1:A:492:PHE:CD1	1:A:492:PHE:O	2.69	0.42
1:A:578:GLN:HA	1:A:838:VAL:HG21	2.00	0.42
1:B:273:VAL:HG12	1:B:477:ILE:HD13	2.02	0.42
1:C:541:VAL:HG13	1:C:542:GLN:CG	2.50	0.42
1:C:582:LYS:HE2	1:C:831:THR:HG23	2.01	0.42
1:D:279:PRO:CG	1:D:322:GLN:HA	2.49	0.42
1:D:279:PRO:C	1:D:280:LYS:HG2	2.45	0.42
1:D:485:PHE:CD1	1:D:485:PHE:N	2.88	0.42
1:D:818:LYS:HG2	1:D:819:TYR:N	2.34	0.42
1:E:377:ARG:CG	1:E:377:ARG:NH2	2.82	0.42
1:E:432:VAL:HB	1:E:436:LYS:CB	2.50	0.42
1:E:477:ILE:O	1:E:477:ILE:CG2	2.67	0.42
1:E:505:LEU:HD13	1:E:505:LEU:C	2.45	0.42
1:E:508:LYS:O	1:E:512:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:582:LYS:O	1:E:586:ASP:HB2	2.20	0.42
1:F:450:LEU:O	1:F:508:LYS:NZ	2.52	0.42
1:F:506:ARG:O	1:F:507:LYS:C	2.63	0.42
1:G:639:LEU:HD12	1:G:639:LEU:HA	1.90	0.42
1:H:285:ILE:CD1	1:H:287:ARG:CA	2.98	0.42
1:H:524:THR:O	1:H:528:ILE:HG13	2.20	0.42
1:I:610:ARG:HE	1:I:613:ASP:HB2	1.85	0.42
1:A:574:ARG:N	1:A:575:PRO:HD2	2.27	0.41
1:C:392:ILE:HD12	1:C:421:ARG:O	2.19	0.41
1:D:474:LEU:HG	1:D:475:ALA:H	1.85	0.41
1:D:569:ALA:HB1	1:D:850:TYR:CE1	2.54	0.41
1:E:229:PHE:CD2	1:E:233:LYS:HD2	2.55	0.41
1:E:430:ASP:OD1	1:E:431:LEU:N	2.52	0.41
1:E:610:ARG:HE	1:E:610:ARG:HA	1.82	0.41
1:F:771:ASP:OD1	1:F:771:ASP:N	2.51	0.41
1:G:387:ILE:CG2	1:G:415:VAL:HG21	2.49	0.41
1:H:278:LEU:O	1:H:279:PRO:C	2.59	0.41
1:H:407:THR:CG2	1:H:414:ARG:NH1	2.60	0.41
1:H:413:ARG:HG2	1:H:422:THR:HG21	2.02	0.41
1:H:444:ARG:HA	1:H:444:ARG:HD2	1.81	0.41
1:H:576:GLN:NE2	1:H:576:GLN:H	2.18	0.41
1:H:610:ARG:NE	1:H:610:ARG:CA	2.80	0.41
1:I:310:LEU:O	1:I:313:ALA:HB3	2.20	0.41
1:J:269:LEU:HD11	1:J:458:LYS:HB2	2.02	0.41
1:J:278:LEU:HD13	1:J:278:LEU:H	1.85	0.41
1:B:428:LYS:HB3	1:B:431:LEU:HD21	2.01	0.41
1:B:808:LYS:HB3	1:B:808:LYS:HE2	1.83	0.41
1:C:528:ILE:HA	1:C:531:GLU:HG2	2.01	0.41
1:D:257:VAL:HG22	1:D:358:ILE:O	2.21	0.41
1:D:426:ILE:HD12	1:D:440:ILE:CG2	2.16	0.41
1:E:254:SER:O	1:E:391:ASN:HB3	2.20	0.41
1:E:349:SER:HB3	1:E:352:ILE:HG23	2.01	0.41
1:E:424:GLY:HA3	1:E:452:TYR:CD2	2.54	0.41
1:E:431:LEU:O	1:E:432:VAL:HG13	2.20	0.41
1:F:284:MET:HG2	1:F:286:THR:CG2	2.50	0.41
1:G:441:LEU:HD12	1:G:441:LEU:HA	1.81	0.41
1:G:582:LYS:HE2	1:G:831:THR:HG23	2.01	0.41
1:H:349:SER:HB3	1:H:352:ILE:CG2	2.50	0.41
1:H:403:LEU:CD2	1:H:403:LEU:N	2.59	0.41
1:A:224:ASP:CG	1:A:224:ASP:O	2.62	0.41
1:A:308:PRO:HG3	1:A:344:ARG:CB	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:LYS:O	1:A:458:LYS:CG	2.68	0.41
1:A:488:HIS:HB3	1:A:491:GLU:HG3	2.02	0.41
1:A:610:ARG:HE	1:A:610:ARG:CA	2.20	0.41
1:A:905:HIS:O	1:A:908:SER:O	2.38	0.41
1:B:271:ALA:O	1:B:275:HIS:CE1	2.73	0.41
1:B:757:PHE:O	1:B:760:LYS:HB2	2.20	0.41
1:D:229:PHE:CE1	1:D:232:LYS:HE3	2.55	0.41
1:D:285:ILE:HD12	1:D:287:ARG:CB	2.38	0.41
1:D:485:PHE:HA	1:D:492:PHE:HE1	1.85	0.41
1:E:276:GLU:OE1	1:E:303:ASP:CG	2.63	0.41
1:E:376:LYS:HZ3	1:E:379:ILE:HD12	1.77	0.41
1:G:233:LYS:HD2	1:G:236:GLU:OE1	2.20	0.41
1:G:433:GLU:O	1:G:436:LYS:HB2	2.20	0.41
1:H:242:GLN:HE22	1:H:344:ARG:CD	2.33	0.41
1:H:396:ILE:HA	1:H:425:VAL:O	2.20	0.41
1:H:399:ALA:HA	1:H:411:ALA:CB	2.50	0.41
1:I:582:LYS:HB2	1:I:582:LYS:HE3	1.86	0.41
1:J:255:ILE:HD11	1:J:355:LEU:HG	2.01	0.41
1:J:671:LYS:HD2	1:J:671:LYS:N	2.36	0.41
1:J:711:ILE:HD12	1:J:828:ALA:HB1	2.02	0.41
1:A:400:ASP:OD1	1:A:400:ASP:N	2.54	0.41
1:A:433:GLU:HA	1:A:434:PRO:HD2	1.75	0.41
1:B:530:ARG:HD3	1:B:530:ARG:HA	1.86	0.41
1:C:235:ILE:HD11	1:C:293:THR:HG22	2.01	0.41
1:E:279:PRO:HB3	1:E:322:GLN:HB2	1.97	0.41
1:E:575:PRO:O	1:E:578:GLN:HB3	2.20	0.41
1:F:294:LEU:HB3	1:F:352:ILE:CD1	2.49	0.41
1:G:255:ILE:HA	1:G:392:ILE:O	2.21	0.41
1:H:307:PHE:CD1	1:H:307:PHE:N	2.88	0.41
1:H:441:LEU:HD21	1:H:498:VAL:CA	2.49	0.41
1:I:572:PHE:HB3	1:I:850:TYR:OH	2.20	0.41
1:J:351:ASN:CG	1:J:474:LEU:HD13	2.45	0.41
1:J:432:VAL:HB	1:J:436:LYS:HB2	2.03	0.41
1:J:694:THR:HG22	1:J:844:GLU:CG	2.50	0.41
1:A:505:LEU:O	1:A:505:LEU:HD22	2.20	0.41
1:A:537:TYR:HE1	1:A:540:LYS:CE	2.30	0.41
1:A:540:LYS:HD2	1:I:626:PRO:HD3	1.80	0.41
1:B:491:GLU:HG2	1:B:491:GLU:H	1.57	0.41
1:D:285:ILE:HD13	1:D:332:VAL:HG22	2.01	0.41
1:D:728:GLN:HA	1:D:804:ILE:HD11	2.02	0.41
1:E:240:LEU:HD23	1:E:240:LEU:H	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:478:ASN:O	1:E:482:LYS:CG	2.65	0.41
1:G:493:GLY:O	1:G:496:SER:HB3	2.21	0.41
1:I:267:SER:HB2	1:I:396:ILE:CD1	2.50	0.41
1:J:285:ILE:HD11	1:J:287:ARG:CB	2.37	0.41
1:J:289:PRO:HB2	1:J:342:PRO:HB3	2.01	0.41
1:A:233:LYS:CA	1:A:233:LYS:CE	2.98	0.41
1:A:237:ILE:HD11	1:A:897:VAL:HG13	2.01	0.41
1:A:339:THR:O	1:A:340:ASP:HB3	2.21	0.41
1:A:581:LEU:HD12	1:A:838:VAL:HG23	2.01	0.41
1:A:598:TRP:CD1	1:A:598:TRP:N	2.88	0.41
1:C:878:ASP:HB3	1:C:881:VAL:HG12	2.01	0.41
1:D:278:LEU:CB	1:D:279:PRO:HD2	2.45	0.41
1:D:348:HIS:ND1	1:D:348:HIS:N	2.69	0.41
1:D:434:PRO:CG	1:D:491:GLU:HG3	2.49	0.41
1:D:548:MET:HG3	1:D:549:SER:N	2.36	0.41
1:E:287:ARG:CG	1:E:287:ARG:NH1	2.82	0.41
1:G:258:ILE:HG21	1:G:387:ILE:HD11	2.02	0.41
1:H:284:MET:SD	1:H:284:MET:O	2.79	0.41
1:I:642:LEU:O	1:I:644:VAL:N	2.51	0.41
1:J:861:LEU:HD23	1:J:861:LEU:HA	1.89	0.41
1:A:475:ALA:O	1:A:478:ASN:HB3	2.21	0.41
1:B:349:SER:HB3	1:B:352:ILE:HG12	2.02	0.41
1:B:776:ALA:HB3	1:B:784:LEU:HD11	2.03	0.41
1:C:294:LEU:HB3	1:C:352:ILE:HD13	2.02	0.41
1:C:454:GLY:O	1:C:500:THR:HG22	2.21	0.41
1:D:250:VAL:C	1:D:251:THR:HG1	2.29	0.41
1:D:295:VAL:HG12	1:D:296:ASN:O	2.20	0.41
1:D:376:LYS:HZ1	1:D:379:ILE:HD12	1.84	0.41
1:E:304:TYR:CZ	1:E:314:ARG:NH1	2.88	0.41
1:F:450:LEU:HD22	1:F:512:VAL:HG22	2.03	0.41
1:G:276:GLU:HG2	1:G:277:PHE:H	1.84	0.41
1:I:285:ILE:HD12	1:I:287:ARG:HB2	2.03	0.41
1:I:383:CYS:O	1:I:384:ASP:C	2.62	0.41
1:J:229:PHE:CG	1:J:232:LYS:HD2	2.39	0.41
1:J:295:VAL:O	1:J:352:ILE:HD11	2.21	0.41
1:A:269:LEU:CD2	1:A:457:SER:O	2.68	0.41
1:A:297:ASP:HB3	1:A:350:PRO:N	2.35	0.41
1:B:572:PHE:HD2	1:B:846:LEU:HD11	1.84	0.41
1:B:755:MET:HG2	1:B:791:VAL:HG22	2.03	0.41
1:C:401:THR:HG22	1:C:402:ASP:N	2.35	0.41
1:D:276:GLU:OE1	1:D:303:ASP:OD1	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:ILE:CD1	1:D:287:ARG:CA	2.99	0.41
1:D:377:ARG:CG	1:D:377:ARG:NH2	2.78	0.41
1:D:441:LEU:HD21	1:D:498:VAL:C	2.43	0.41
1:D:903:GLU:CG	1:D:906:ARG:NH2	2.83	0.41
1:E:285:ILE:CG1	1:E:286:THR:N	2.84	0.41
1:E:656:ILE:O	1:E:660:VAL:HG23	2.21	0.41
1:E:727:LEU:HD21	1:E:823:GLU:HG2	2.02	0.41
1:F:602:ILE:CG1	1:F:792:PHE:HB2	2.51	0.41
1:F:602:ILE:HG12	1:F:792:PHE:HB2	2.03	0.41
1:F:750:LYS:HE3	1:F:750:LYS:HB3	1.92	0.41
1:G:431:LEU:O	1:G:432:VAL:HG13	2.21	0.41
1:H:355:LEU:HD23	1:H:357:LEU:CD2	2.51	0.41
1:H:861:LEU:HD23	1:H:861:LEU:HA	1.94	0.41
1:I:307:PHE:CD1	1:I:307:PHE:N	2.89	0.41
1:I:529:GLN:O	1:I:533:GLU:HG3	2.20	0.41
1:I:611:GLU:H	1:I:612:PRO:HD2	1.84	0.41
1:J:344:ARG:H	1:J:344:ARG:HG2	1.74	0.41
1:J:387:ILE:HG21	1:J:393:ILE:HD12	2.03	0.41
1:J:521:LEU:HD13	1:J:521:LEU:O	2.21	0.41
1:J:784:LEU:O	1:J:788:ARG:HG3	2.21	0.41
1:A:262:SER:O	1:A:266:SER:OG	2.38	0.41
1:A:565:PHE:HA	1:A:663:LEU:HD21	2.02	0.41
1:A:617:ASP:OD1	1:A:617:ASP:N	2.54	0.41
1:A:637:SER:O	1:A:641:ARG:HB2	2.21	0.41
1:B:258:ILE:HG21	1:B:387:ILE:HD11	2.01	0.41
1:B:513:LEU:HD23	1:B:517:MET:HE2	2.03	0.41
1:C:764:GLY:O	1:C:765:GLU:C	2.64	0.41
1:D:483:ASN:C	1:D:483:ASN:ND2	2.79	0.41
1:D:903:GLU:CG	1:D:906:ARG:HH21	2.34	0.41
1:E:238:ARG:HD2	1:E:252:LEU:O	2.21	0.41
1:E:253:PRO:HG3	1:E:516:GLN:OE1	2.21	0.41
1:E:325:LEU:HD12	1:E:326:THR:N	2.36	0.41
1:E:420:GLU:HG3	1:E:449:LYS:HE3	2.01	0.41
1:E:554:LEU:HD13	1:E:865:MET:HE3	2.03	0.41
1:E:575:PRO:HG2	1:E:576:GLN:NE2	2.36	0.41
1:F:270:GLU:O	1:F:271:ALA:C	2.63	0.41
1:F:387:ILE:HG21	1:F:393:ILE:HD12	2.03	0.41
1:F:484:TYR:CD1	1:F:484:TYR:C	2.99	0.41
1:F:485:PHE:CD1	1:F:485:PHE:N	2.88	0.41
1:F:507:LYS:HB2	1:F:507:LYS:HE3	1.84	0.41
1:G:285:ILE:HD12	1:G:287:ARG:N	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:488:HIS:HB3	1:G:491:GLU:HG3	2.03	0.41
1:G:510:LEU:C	1:G:510:LEU:HD23	2.45	0.41
1:G:766:ILE:HG13	1:G:767:ILE:N	2.35	0.41
1:H:441:LEU:HD21	1:H:498:VAL:C	2.39	0.41
1:H:846:LEU:HD12	1:H:846:LEU:HA	1.84	0.41
1:I:241:LEU:HA	1:I:244:VAL:HG13	2.03	0.41
1:I:278:LEU:HD22	1:I:279:PRO:N	2.35	0.41
1:I:293:THR:OG1	1:I:346:THR:HG23	2.20	0.41
1:I:376:LYS:HZ3	1:I:379:ILE:HD12	1.86	0.41
1:I:441:LEU:HD23	1:I:498:VAL:HB	2.02	0.41
1:I:493:GLY:H	1:I:496:SER:HB3	1.85	0.41
1:I:537:TYR:O	1:I:541:VAL:HG12	2.21	0.41
1:I:575:PRO:O	1:I:578:GLN:HB3	2.21	0.41
1:I:580:LEU:HD23	1:I:580:LEU:HA	1.94	0.41
1:J:229:PHE:O	1:J:230:ILE:C	2.61	0.41
1:J:279:PRO:CG	1:J:322:GLN:HA	2.51	0.41
1:J:421:ARG:HH11	1:J:421:ARG:HD3	1.70	0.41
1:J:443:ASP:O	1:J:444:ARG:HD2	2.21	0.41
1:J:478:ASN:O	1:J:482:LYS:CG	2.68	0.41
1:J:510:LEU:HD13	1:J:510:LEU:C	2.46	0.41
1:J:835:GLN:CG	1:J:836:THR:N	2.84	0.41
1:A:294:LEU:HB2	1:A:354:ASP:HA	2.03	0.41
1:B:310:LEU:O	1:B:311:GLY:C	2.64	0.41
1:B:436:LYS:O	1:B:437:GLY:C	2.63	0.41
1:C:293:THR:O	1:C:346:THR:HA	2.20	0.41
1:C:364:ILE:HD12	1:C:376:LYS:NZ	2.36	0.41
1:C:832:LYS:O	1:C:836:THR:HG22	2.20	0.41
1:D:260:SER:O	1:D:263:SER:C	2.51	0.41
1:D:454:GLY:O	1:D:455:VAL:HG12	2.20	0.41
1:D:569:ALA:CB	1:D:850:TYR:CE1	3.03	0.41
1:D:825:PHE:CD2	1:D:825:PHE:C	2.99	0.41
1:E:483:ASN:ND2	1:E:484:TYR:N	2.68	0.41
1:E:605:LEU:HD21	1:E:784:LEU:HD12	2.02	0.41
1:F:519:SER:OG	1:F:520:LYS:HE2	2.21	0.41
1:H:491:GLU:N	1:H:491:GLU:OE2	2.53	0.41
1:H:610:ARG:HE	1:H:611:GLU:N	2.19	0.41
1:H:626:PRO:O	1:H:630:ARG:HB3	2.20	0.41
1:I:618:LEU:HG	1:I:803:ARG:NH2	2.36	0.41
1:I:903:GLU:CG	1:I:906:ARG:NH2	2.71	0.41
1:J:727:LEU:HD21	1:J:823:GLU:HG2	2.02	0.41
1:J:908:SER:O	1:J:909:SER:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ILE:O	1:A:421:ARG:NH2	2.55	0.40
1:A:627:TYR:O	1:A:631:GLN:HB2	2.21	0.40
1:B:485:PHE:CD2	1:B:492:PHE:CD1	3.09	0.40
1:C:425:VAL:HA	1:C:453:VAL:O	2.21	0.40
1:C:593:LEU:HD13	1:C:823:GLU:HG3	2.02	0.40
1:D:279:PRO:CG	1:D:321:ILE:HG22	2.51	0.40
1:D:454:GLY:C	1:D:455:VAL:CG1	2.93	0.40
1:D:457:SER:O	1:D:458:LYS:CB	2.68	0.40
1:D:640:THR:HG22	1:D:706:LYS:HG2	2.02	0.40
1:E:268:VAL:O	1:E:272:ILE:CD1	2.70	0.40
1:F:430:ASP:HB3	1:F:456:ILE:CG1	2.48	0.40
1:F:610:ARG:HB3	1:F:613:ASP:OD1	2.22	0.40
1:G:278:LEU:HD13	1:G:278:LEU:O	2.20	0.40
1:H:278:LEU:CD2	1:H:280:LYS:CG	2.98	0.40
1:H:454:GLY:N	1:H:500:THR:HG22	2.36	0.40
1:H:602:ILE:HG12	1:H:762:ARG:CZ	2.51	0.40
1:H:631:GLN:OE1	1:H:631:GLN:HA	2.20	0.40
1:J:270:GLU:HA	1:J:273:VAL:HG22	2.03	0.40
1:J:308:PRO:CG	1:J:344:ARG:HG3	2.51	0.40
1:J:750:LYS:O	1:J:753:GLU:HB2	2.21	0.40
1:A:787:GLY:O	1:A:791:VAL:HG23	2.21	0.40
1:B:376:LYS:CA	1:B:376:LYS:CE	2.97	0.40
1:B:521:LEU:HD13	1:B:521:LEU:O	2.21	0.40
1:C:355:LEU:HD23	1:C:357:LEU:HD22	2.03	0.40
1:E:269:LEU:HD23	1:E:269:LEU:C	2.45	0.40
1:E:289:PRO:HB2	1:E:342:PRO:HB3	2.03	0.40
1:E:754:VAL:HA	1:E:779:PHE:CE1	2.56	0.40
1:F:344:ARG:H	1:F:344:ARG:HG2	1.68	0.40
1:F:441:LEU:CD2	1:F:498:VAL:HB	2.52	0.40
1:F:702:LEU:O	1:F:706:LYS:HG3	2.21	0.40
1:H:263:SER:OG	1:H:397:SER:CA	2.66	0.40
1:H:348:HIS:N	1:H:348:HIS:ND1	2.69	0.40
1:J:270:GLU:O	1:J:273:VAL:CG2	2.65	0.40
1:J:581:LEU:HD23	1:J:581:LEU:HA	1.88	0.40
1:A:242:GLN:HE22	1:A:344:ARG:HD2	1.85	0.40
1:A:394:LEU:HD12	1:A:423:ILE:C	2.46	0.40
1:A:576:GLN:H	1:A:576:GLN:HE21	1.68	0.40
1:B:472:ASN:OD1	1:B:475:ALA:HB3	2.21	0.40
1:B:852:ARG:HH21	1:B:852:ARG:HD2	1.65	0.40
1:C:275:HIS:CG	1:C:276:GLU:N	2.89	0.40
1:D:308:PRO:HG3	1:D:344:ARG:CB	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:285:ILE:HG12	1:E:329:ASN:O	2.21	0.40
1:E:676:ARG:HG2	1:E:677:LYS:N	2.37	0.40
1:E:861:LEU:HD23	1:E:861:LEU:HA	1.69	0.40
1:F:653:ALA:O	1:F:654:SER:C	2.62	0.40
1:H:241:LEU:O	1:H:244:VAL:CG2	2.49	0.40
1:H:509:LEU:HD23	1:H:509:LEU:HA	1.92	0.40
1:A:246:GLN:NE2	1:A:890:ARG:HH12	2.20	0.40
1:A:476:SER:OG	1:A:477:ILE:N	2.54	0.40
1:A:528:ILE:HD13	1:A:528:ILE:HG21	1.89	0.40
1:A:754:VAL:O	1:A:758:VAL:HG23	2.22	0.40
1:B:720:ARG:O	1:B:724:VAL:HG23	2.21	0.40
1:C:853:PHE:HB3	1:C:854:PRO:HD3	2.04	0.40
1:E:376:LYS:HA	1:E:376:LYS:HE2	1.95	0.40
1:G:632:LEU:O	1:G:632:LEU:HD22	2.21	0.40
1:G:861:LEU:HD23	1:G:861:LEU:HA	1.93	0.40
1:H:396:ILE:HG22	1:H:425:VAL:HB	2.03	0.40
1:I:232:LYS:HB3	1:I:232:LYS:HE2	1.85	0.40
1:I:626:PRO:CB	1:I:630:ARG:HE	2.30	0.40
1:J:448:LEU:HD11	1:J:452:TYR:CE1	2.57	0.40
1:A:727:LEU:HD12	1:A:727:LEU:HA	1.98	0.40
1:B:319:SER:O	1:B:322:GLN:HB3	2.20	0.40
1:C:255:ILE:HG13	1:C:357:LEU:CA	2.52	0.40
1:C:275:HIS:CG	1:C:276:GLU:H	2.40	0.40
1:C:319:SER:O	1:C:322:GLN:HB3	2.22	0.40
1:C:507:LYS:HB2	1:C:507:LYS:HE3	1.84	0.40
1:C:628:TRP:CE3	1:C:628:TRP:HA	2.56	0.40
1:D:269:LEU:CD2	1:D:269:LEU:C	2.92	0.40
1:D:611:GLU:H	1:D:611:GLU:HG2	1.69	0.40
1:F:840:PHE:CE1	1:F:844:GLU:HG3	2.57	0.40
1:F:873:LYS:HA	1:F:876:ARG:HB2	2.04	0.40
1:H:279:PRO:C	1:H:280:LYS:HG2	2.46	0.40
1:H:433:GLU:HA	1:H:434:PRO:HD2	1.80	0.40
1:H:449:LYS:C	1:H:450:LEU:HG	2.46	0.40
1:I:615:ILE:HD11	1:I:803:ARG:HG2	2.02	0.40
1:I:702:LEU:HD13	1:I:833:LEU:HD22	2.04	0.40
1:J:270:GLU:C	1:J:273:VAL:HG22	2.47	0.40
1:J:653:ALA:HA	1:J:687:LEU:HD13	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	651/695 (94%)	614 (94%)	34 (5%)	3 (0%)	24	63
1	B	651/695 (94%)	616 (95%)	34 (5%)	1 (0%)	43	78
1	C	651/695 (94%)	616 (95%)	32 (5%)	3 (0%)	24	63
1	D	651/695 (94%)	622 (96%)	27 (4%)	2 (0%)	36	72
1	E	651/695 (94%)	620 (95%)	31 (5%)	0	100	100
1	F	651/695 (94%)	617 (95%)	32 (5%)	2 (0%)	36	72
1	G	651/695 (94%)	618 (95%)	30 (5%)	3 (0%)	24	63
1	H	651/695 (94%)	618 (95%)	27 (4%)	6 (1%)	14	51
1	I	651/695 (94%)	614 (94%)	36 (6%)	1 (0%)	43	78
1	J	651/695 (94%)	624 (96%)	25 (4%)	2 (0%)	36	72
All	All	6510/6950 (94%)	6179 (95%)	308 (5%)	23 (0%)	31	67

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	LEU
1	H	405	ASN
1	H	410	GLN
1	D	643	GLY
1	H	399	ALA
1	H	414	ARG
1	C	356	SER
1	H	412	SER
1	A	574	ARG
1	G	611	GLU
1	C	574	ARG
1	C	611	GLU
1	F	574	ARG
1	F	611	GLU

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Mol	Chain	Res	Type
1	I	611	GLU
1	J	389	GLY
1	J	843	VAL
1	B	611	GLU
1	G	844	GLU
1	G	574	ARG
1	H	574	ARG
1	D	574	ARG
1	A	342	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	563/594 (95%)	457 (81%)	106 (19%)	1	8
1	B	563/594 (95%)	477 (85%)	86 (15%)	3	12
1	C	563/594 (95%)	471 (84%)	92 (16%)	2	10
1	D	563/594 (95%)	456 (81%)	107 (19%)	1	8
1	E	563/594 (95%)	449 (80%)	114 (20%)	1	7
1	F	563/594 (95%)	481 (85%)	82 (15%)	3	13
1	G	563/594 (95%)	479 (85%)	84 (15%)	3	12
1	H	563/594 (95%)	448 (80%)	115 (20%)	1	7
1	I	563/594 (95%)	486 (86%)	77 (14%)	3	14
1	J	563/594 (95%)	453 (80%)	110 (20%)	1	7
All	All	5630/5940 (95%)	4657 (83%)	973 (17%)	4	9

All (973) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	ASP
1	A	227	MET
1	A	228	MET
1	A	229	PHE

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Mol	Chain	Res	Type
1	A	230	ILE
1	A	233	LYS
1	A	235	ILE
1	A	237	ILE
1	A	240	LEU
1	A	241	LEU
1	A	243	LYS
1	A	244	VAL
1	A	251	THR
1	A	255	ILE
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	287	ARG
1	A	303	ASP
1	A	320	LEU
1	A	344	ARG
1	A	346	THR
1	A	351	ASN
1	A	354	ASP
1	A	357	LEU
1	A	358	ILE
1	A	360	LEU
1	A	363	TYR
1	A	375	LEU
1	A	376	LYS
1	A	377	ARG
1	A	378	LYS
1	A	382	LEU
1	A	383	CYS
1	A	385	LYS
1	A	387	ILE
1	A	388	ARG
1	A	392	ILE
1	A	393	ILE
1	A	394	LEU
1	A	396	ILE
1	A	400	ASP

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Mol	Chain	Res	Type
1	A	402	ASP
1	A	405	ASN
1	A	407	THR
1	A	412	SER
1	A	423	ILE
1	A	427	THR
1	A	432	VAL
1	A	433	GLU
1	A	434	PRO
1	A	448	LEU
1	A	450	LEU
1	A	456	ILE
1	A	457	SER
1	A	458	LYS
1	A	474	LEU
1	A	479	ARG
1	A	483	ASN
1	A	499	SER
1	A	505	LEU
1	A	507	LYS
1	A	510	LEU
1	A	513	LEU
1	A	515	GLN
1	A	516	GLN
1	A	546	GLN
1	A	560	ASP
1	A	576	GLN
1	A	590	LEU
1	A	596	ARG
1	A	610	ARG
1	A	615	ILE
1	A	616	ILE
1	A	617	ASP
1	A	632	LEU
1	A	640	THR
1	A	642	LEU
1	A	647	LEU
1	A	657	GLN
1	A	671	LYS
1	A	714	ASN
1	A	727	LEU
1	A	739	LYS

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Mol	Chain	Res	Type
1	A	749	LYS
1	A	762	ARG
1	A	768	VAL
1	A	769	GLU
1	A	783	LEU
1	A	784	LEU
1	A	802	LEU
1	A	836	THR
1	A	838	VAL
1	A	839	LEU
1	A	841	LEU
1	A	871	LEU
1	A	892	GLU
1	A	893	LEU
1	A	898	LEU
1	A	903	GLU
1	A	904	LEU
1	A	905	HIS
1	B	227	MET
1	B	231	THR
1	B	235	ILE
1	B	237	ILE
1	B	244	VAL
1	B	251	THR
1	B	255	ILE
1	B	261	GLN
1	B	266	SER
1	B	269	LEU
1	B	278	LEU
1	B	282	SER
1	B	284	MET
1	B	287	ARG
1	B	303	ASP
1	B	310	LEU
1	B	317	ASP
1	B	320	LEU
1	B	321	ILE
1	B	325	LEU
1	B	339	THR
1	B	344	ARG
1	B	346	THR
1	B	358	ILE

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Mol	Chain	Res	Type
1	B	376	LYS
1	B	377	ARG
1	B	378	LYS
1	B	382	LEU
1	B	385	LYS
1	B	388	ARG
1	B	392	ILE
1	B	393	ILE
1	B	394	LEU
1	B	396	ILE
1	B	400	ASP
1	B	405	ASN
1	B	422	THR
1	B	423	ILE
1	B	430	ASP
1	B	433	GLU
1	B	435	GLU
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	500	THR
1	B	503	MET
1	B	505	LEU
1	B	571	SER
1	B	574	ARG
1	B	590	LEU
1	B	600	ARG
1	B	603	GLU
1	B	605	LEU
1	B	611	GLU
1	B	613	ASP
1	B	615	ILE
1	B	618	LEU
1	B	632	LEU
1	B	642	LEU
1	B	666	LYS

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Mol	Chain	Res	Type
1	B	676	ARG
1	B	690	ARG
1	B	723	VAL
1	B	727	LEU
1	B	741	LEU
1	B	748	ARG
1	B	762	ARG
1	B	767	ILE
1	B	768	VAL
1	B	803	ARG
1	B	810	ARG
1	B	811	GLN
1	B	815	LEU
1	B	817	ASN
1	B	824	VAL
1	B	838	VAL
1	B	841	LEU
1	B	860	LYS
1	B	880	LYS
1	B	904	LEU
1	C	227	MET
1	C	231	THR
1	C	237	ILE
1	C	244	VAL
1	C	251	THR
1	C	255	ILE
1	C	266	SER
1	C	269	LEU
1	C	278	LEU
1	C	282	SER
1	C	283	ASN
1	C	284	MET
1	C	285	ILE
1	C	303	ASP
1	C	325	LEU
1	C	339	THR
1	C	344	ARG
1	C	346	THR
1	C	352	ILE
1	C	354	ASP
1	C	358	ILE
1	C	375	LEU

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Mol	Chain	Res	Type
1	C	376	LYS
1	C	377	ARG
1	C	378	LYS
1	C	382	LEU
1	C	385	LYS
1	C	386	TYR
1	C	388	ARG
1	C	392	ILE
1	C	393	ILE
1	C	394	LEU
1	C	396	ILE
1	C	400	ASP
1	C	402	ASP
1	C	405	ASN
1	C	412	SER
1	C	423	ILE
1	C	430	ASP
1	C	431	LEU
1	C	433	GLU
1	C	448	LEU
1	C	458	LYS
1	C	474	LEU
1	C	479	ARG
1	C	481	GLU
1	C	482	LYS
1	C	483	ASN
1	C	490	THR
1	C	491	GLU
1	C	492	PHE
1	C	495	ASP
1	C	500	THR
1	C	503	MET
1	C	512	VAL
1	C	544	ASN
1	C	557	SER
1	C	590	LEU
1	C	600	ARG
1	C	605	LEU
1	C	611	GLU
1	C	613	ASP
1	C	615	ILE
1	C	616	ILE

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Mol	Chain	Res	Type
1	C	617	ASP
1	C	618	LEU
1	C	622	ASP
1	C	630	ARG
1	C	631	GLN
1	C	632	LEU
1	C	640	THR
1	C	644	VAL
1	C	651	VAL
1	C	654	SER
1	C	666	LYS
1	C	690	ARG
1	C	721	GLU
1	C	723	VAL
1	C	727	LEU
1	C	741	LEU
1	C	762	ARG
1	C	767	ILE
1	C	803	ARG
1	C	815	LEU
1	C	817	ASN
1	C	824	VAL
1	C	836	THR
1	C	838	VAL
1	C	841	LEU
1	C	860	LYS
1	C	873	LYS
1	C	904	LEU
1	D	225	ASP
1	D	228	MET
1	D	229	PHE
1	D	230	ILE
1	D	235	ILE
1	D	237	ILE
1	D	240	LEU
1	D	241	LEU
1	D	243	LYS
1	D	244	VAL
1	D	249	THR
1	D	251	THR
1	D	255	ILE
1	D	266	SER

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Mol	Chain	Res	Type
1	D	268	VAL
1	D	269	LEU
1	D	272	ILE
1	D	278	LEU
1	D	282	SER
1	D	284	MET
1	D	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	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	385	LYS
1	D	388	ARG
1	D	392	ILE
1	D	393	ILE
1	D	394	LEU
1	D	396	ILE
1	D	400	ASP
1	D	402	ASP
1	D	422	THR
1	D	423	ILE
1	D	433	GLU
1	D	434	PRO
1	D	448	LEU
1	D	449	LYS
1	D	450	LEU
1	D	456	ILE
1	D	457	SER
1	D	458	LYS
1	D	474	LEU
1	D	479	ARG

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Mol	Chain	Res	Type
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	505	LEU
1	D	507	LYS
1	D	513	LEU
1	D	516	GLN
1	D	521	LEU
1	D	546	GLN
1	D	548	MET
1	D	557	SER
1	D	560	ASP
1	D	576	GLN
1	D	581	LEU
1	D	586	ASP
1	D	590	LEU
1	D	610	ARG
1	D	615	ILE
1	D	616	ILE
1	D	617	ASP
1	D	632	LEU
1	D	640	THR
1	D	642	LEU
1	D	647	LEU
1	D	654	SER
1	D	657	GLN
1	D	668	SER
1	D	671	LYS
1	D	690	ARG
1	D	714	ASN
1	D	727	LEU
1	D	739	LYS
1	D	749	LYS
1	D	768	VAL
1	D	769	GLU
1	D	783	LEU
1	D	802	LEU
1	D	811	GLN
1	D	815	LEU

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Mol	Chain	Res	Type
1	D	836	THR
1	D	838	VAL
1	D	839	LEU
1	D	842	ASN
1	D	892	GLU
1	D	893	LEU
1	D	898	LEU
1	D	903	GLU
1	D	907	ILE
1	E	225	ASP
1	E	228	MET
1	E	229	PHE
1	E	233	LYS
1	E	235	ILE
1	E	237	ILE
1	E	240	LEU
1	E	243	LYS
1	E	244	VAL
1	E	252	LEU
1	E	255	ILE
1	E	266	SER
1	E	268	VAL
1	E	269	LEU
1	E	272	ILE
1	E	273	VAL
1	E	275	HIS
1	E	278	LEU
1	E	282	SER
1	E	283	ASN
1	E	284	MET
1	E	287	ARG
1	E	303	ASP
1	E	310	LEU
1	E	312	LEU
1	E	320	LEU
1	E	323	LYS
1	E	325	LEU
1	E	344	ARG
1	E	346	THR
1	E	354	ASP
1	E	358	ILE
1	E	360	LEU

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Mol	Chain	Res	Type
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	407	THR
1	E	412	SER
1	E	422	THR
1	E	423	ILE
1	E	430	ASP
1	E	433	GLU
1	E	434	PRO
1	E	448	LEU
1	E	450	LEU
1	E	456	ILE
1	E	457	SER
1	E	458	LYS
1	E	474	LEU
1	E	476	SER
1	E	479	ARG
1	E	481	GLU
1	E	483	ASN
1	E	490	THR
1	E	491	GLU
1	E	495	ASP
1	E	498	VAL
1	E	499	SER
1	E	507	LYS
1	E	510	LEU
1	E	515	GLN
1	E	516	GLN

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Mol	Chain	Res	Type
1	E	546	GLN
1	E	557	SER
1	E	560	ASP
1	E	571	SER
1	E	572	PHE
1	E	576	GLN
1	E	590	LEU
1	E	610	ARG
1	E	615	ILE
1	E	617	ASP
1	E	640	THR
1	E	642	LEU
1	E	646	ARG
1	E	647	LEU
1	E	651	VAL
1	E	654	SER
1	E	657	GLN
1	E	668	SER
1	E	671	LYS
1	E	676	ARG
1	E	714	ASN
1	E	727	LEU
1	E	739	LYS
1	E	749	LYS
1	E	762	ARG
1	E	768	VAL
1	E	769	GLU
1	E	802	LEU
1	E	811	GLN
1	E	815	LEU
1	E	836	THR
1	E	838	VAL
1	E	839	LEU
1	E	841	LEU
1	E	872	GLU
1	E	892	GLU
1	E	893	LEU
1	E	903	GLU
1	E	904	LEU
1	F	231	THR
1	F	235	ILE
1	F	237	ILE

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Mol	Chain	Res	Type
1	F	244	VAL
1	F	251	THR
1	F	255	ILE
1	F	266	SER
1	F	269	LEU
1	F	277	PHE
1	F	278	LEU
1	F	282	SER
1	F	283	ASN
1	F	284	MET
1	F	302	VAL
1	F	303	ASP
1	F	320	LEU
1	F	325	LEU
1	F	339	THR
1	F	344	ARG
1	F	346	THR
1	F	357	LEU
1	F	358	ILE
1	F	376	LYS
1	F	377	ARG
1	F	378	LYS
1	F	382	LEU
1	F	385	LYS
1	F	388	ARG
1	F	392	ILE
1	F	393	ILE
1	F	394	LEU
1	F	396	ILE
1	F	423	ILE
1	F	429	MET
1	F	430	ASP
1	F	431	LEU
1	F	432	VAL
1	F	435	GLU
1	F	436	LYS
1	F	448	LEU
1	F	456	ILE
1	F	457	SER
1	F	458	LYS
1	F	474	LEU
1	F	481	GLU

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Mol	Chain	Res	Type
1	F	490	THR
1	F	491	GLU
1	F	495	ASP
1	F	500	THR
1	F	503	MET
1	F	505	LEU
1	F	552	SER
1	F	557	SER
1	F	600	ARG
1	F	605	LEU
1	F	611	GLU
1	F	613	ASP
1	F	615	ILE
1	F	616	ILE
1	F	617	ASP
1	F	618	LEU
1	F	640	THR
1	F	642	LEU
1	F	644	VAL
1	F	654	SER
1	F	666	LYS
1	F	676	ARG
1	F	690	ARG
1	F	714	ASN
1	F	721	GLU
1	F	727	LEU
1	F	741	LEU
1	F	748	ARG
1	F	762	ARG
1	F	786	ARG
1	F	803	ARG
1	F	815	LEU
1	F	817	ASN
1	F	824	VAL
1	F	838	VAL
1	F	841	LEU
1	F	880	LYS
1	G	231	THR
1	G	237	ILE
1	G	244	VAL
1	G	251	THR
1	G	255	ILE

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Mol	Chain	Res	Type
1	G	266	SER
1	G	269	LEU
1	G	278	LEU
1	G	282	SER
1	G	284	MET
1	G	285	ILE
1	G	302	VAL
1	G	303	ASP
1	G	320	LEU
1	G	321	ILE
1	G	325	LEU
1	G	339	THR
1	G	344	ARG
1	G	346	THR
1	G	351	ASN
1	G	352	ILE
1	G	354	ASP
1	G	358	ILE
1	G	376	LYS
1	G	377	ARG
1	G	378	LYS
1	G	382	LEU
1	G	386	TYR
1	G	388	ARG
1	G	392	ILE
1	G	393	ILE
1	G	394	LEU
1	G	396	ILE
1	G	400	ASP
1	G	412	SER
1	G	423	ILE
1	G	427	THR
1	G	430	ASP
1	G	448	LEU
1	G	457	SER
1	G	458	LYS
1	G	474	LEU
1	G	479	ARG
1	G	481	GLU
1	G	483	ASN
1	G	490	THR
1	G	491	GLU

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Mol	Chain	Res	Type
1	G	495	ASP
1	G	500	THR
1	G	503	MET
1	G	505	LEU
1	G	557	SER
1	G	590	LEU
1	G	600	ARG
1	G	605	LEU
1	G	611	GLU
1	G	613	ASP
1	G	615	ILE
1	G	616	ILE
1	G	617	ASP
1	G	618	LEU
1	G	640	THR
1	G	642	LEU
1	G	654	SER
1	G	666	LYS
1	G	690	ARG
1	G	695	SER
1	G	714	ASN
1	G	727	LEU
1	G	741	LEU
1	G	752	LYS
1	G	762	ARG
1	G	783	LEU
1	G	803	ARG
1	G	811	GLN
1	G	815	LEU
1	G	817	ASN
1	G	824	VAL
1	G	838	VAL
1	G	841	LEU
1	G	860	LYS
1	G	880	LYS
1	G	904	LEU
1	G	906	ARG
1	H	225	ASP
1	H	228	MET
1	H	233	LYS
1	H	235	ILE
1	H	237	ILE

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Mol	Chain	Res	Type
1	H	240	LEU
1	H	241	LEU
1	H	243	LYS
1	H	244	VAL
1	H	251	THR
1	H	252	LEU
1	H	255	ILE
1	H	261	GLN
1	H	262	SER
1	H	263	SER
1	H	266	SER
1	H	268	VAL
1	H	269	LEU
1	H	272	ILE
1	H	278	LEU
1	H	282	SER
1	H	284	MET
1	H	287	ARG
1	H	310	LEU
1	H	312	LEU
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	375	LEU
1	H	376	LYS
1	H	377	ARG
1	H	378	LYS
1	H	382	LEU
1	H	385	LYS
1	H	386	TYR
1	H	387	ILE
1	H	388	ARG
1	H	392	ILE
1	H	393	ILE
1	H	394	LEU
1	H	396	ILE

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Mol	Chain	Res	Type
1	H	400	ASP
1	H	402	ASP
1	H	403	LEU
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	436	LYS
1	H	445	GLN
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	481	GLU
1	H	483	ASN
1	H	491	GLU
1	H	498	VAL
1	H	499	SER
1	H	507	LYS
1	H	510	LEU
1	H	513	LEU
1	H	515	GLN
1	H	516	GLN
1	H	546	GLN
1	H	560	ASP
1	H	581	LEU
1	H	590	LEU
1	H	610	ARG
1	H	615	ILE
1	H	616	ILE
1	H	617	ASP
1	H	632	LEU
1	H	640	THR
1	H	642	LEU
1	H	647	LEU
1	H	657	GLN

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Mol	Chain	Res	Type
1	H	668	SER
1	H	671	LYS
1	H	676	ARG
1	H	690	ARG
1	H	714	ASN
1	H	727	LEU
1	H	739	LYS
1	H	749	LYS
1	H	752	LYS
1	H	768	VAL
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	839	LEU
1	H	841	LEU
1	H	863	GLU
1	H	871	LEU
1	H	872	GLU
1	H	889	ARG
1	H	892	GLU
1	H	893	LEU
1	H	903	GLU
1	H	907	ILE
1	I	231	THR
1	I	235	ILE
1	I	237	ILE
1	I	244	VAL
1	I	251	THR
1	I	255	ILE
1	I	266	SER
1	I	269	LEU
1	I	273	VAL
1	I	278	LEU
1	I	282	SER
1	I	284	MET
1	I	285	ILE
1	I	287	ARG
1	I	303	ASP
1	I	310	LEU

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Mol	Chain	Res	Type
1	I	320	LEU
1	I	344	ARG
1	I	346	THR
1	I	358	ILE
1	I	375	LEU
1	I	376	LYS
1	I	377	ARG
1	I	378	LYS
1	I	382	LEU
1	I	385	LYS
1	I	388	ARG
1	I	393	ILE
1	I	394	LEU
1	I	396	ILE
1	I	402	ASP
1	I	412	SER
1	I	423	ILE
1	I	430	ASP
1	I	448	LEU
1	I	456	ILE
1	I	458	LYS
1	I	472	ASN
1	I	474	LEU
1	I	479	ARG
1	I	481	GLU
1	I	483	ASN
1	I	490	THR
1	I	492	PHE
1	I	495	ASP
1	I	500	THR
1	I	503	MET
1	I	505	LEU
1	I	557	SER
1	I	581	LEU
1	I	600	ARG
1	I	605	LEU
1	I	611	GLU
1	I	613	ASP
1	I	615	ILE
1	I	617	ASP
1	I	618	LEU
1	I	624	ASP

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Mol	Chain	Res	Type
1	I	631	GLN
1	I	632	LEU
1	I	642	LEU
1	I	666	LYS
1	I	695	SER
1	I	721	GLU
1	I	722	HIS
1	I	741	LEU
1	I	762	ARG
1	I	767	ILE
1	I	803	ARG
1	I	815	LEU
1	I	817	ASN
1	I	824	VAL
1	I	838	VAL
1	I	841	LEU
1	I	860	LYS
1	I	873	LYS
1	I	880	LYS
1	J	225	ASP
1	J	228	MET
1	J	230	ILE
1	J	232	LYS
1	J	233	LYS
1	J	235	ILE
1	J	237	ILE
1	J	241	LEU
1	J	243	LYS
1	J	244	VAL
1	J	252	LEU
1	J	255	ILE
1	J	262	SER
1	J	263	SER
1	J	266	SER
1	J	268	VAL
1	J	269	LEU
1	J	272	ILE
1	J	278	LEU
1	J	282	SER
1	J	284	MET
1	J	287	ARG
1	J	303	ASP

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Mol	Chain	Res	Type
1	J	310	LEU
1	J	320	LEU
1	J	321	ILE
1	J	325	LEU
1	J	344	ARG
1	J	346	THR
1	J	352	ILE
1	J	354	ASP
1	J	358	ILE
1	J	360	LEU
1	J	363	TYR
1	J	375	LEU
1	J	376	LYS
1	J	377	ARG
1	J	378	LYS
1	J	380	THR
1	J	382	LEU
1	J	383	CYS
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	412	SER
1	J	422	THR
1	J	423	ILE
1	J	430	ASP
1	J	432	VAL
1	J	433	GLU
1	J	434	PRO
1	J	448	LEU
1	J	449	LYS
1	J	450	LEU
1	J	456	ILE
1	J	457	SER
1	J	458	LYS
1	J	474	LEU
1	J	479	ARG
1	J	481	GLU

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Mol	Chain	Res	Type
1	J	483	ASN
1	J	490	THR
1	J	491	GLU
1	J	498	VAL
1	J	499	SER
1	J	502	VAL
1	J	505	LEU
1	J	507	LYS
1	J	510	LEU
1	J	515	GLN
1	J	516	GLN
1	J	534	GLU
1	J	540	LYS
1	J	546	GLN
1	J	548	MET
1	J	557	SER
1	J	571	SER
1	J	576	GLN
1	J	590	LEU
1	J	591	ASP
1	J	610	ARG
1	J	615	ILE
1	J	617	ASP
1	J	640	THR
1	J	642	LEU
1	J	657	GLN
1	J	664	LEU
1	J	668	SER
1	J	671	LYS
1	J	714	ASN
1	J	727	LEU
1	J	739	LYS
1	J	749	LYS
1	J	762	ARG
1	J	768	VAL
1	J	769	GLU
1	J	802	LEU
1	J	815	LEU
1	J	818	LYS
1	J	836	THR
1	J	838	VAL
1	J	841	LEU

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Mol	Chain	Res	Type
1	J	873	LYS
1	J	893	LEU
1	J	903	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (117) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	A	275	HIS
1	A	296	ASN
1	A	329	ASN
1	A	351	ASN
1	A	472	ASN
1	A	478	ASN
1	A	488	HIS
1	A	516	GLN
1	A	576	GLN
1	A	592	GLN
1	A	657	GLN
1	A	659	HIS
1	A	722	HIS
1	A	842	ASN
1	A	847	ASN
1	A	866	HIS
1	A	884	HIS
1	B	239	ASN
1	B	283	ASN
1	B	329	ASN
1	B	478	ASN
1	B	480	ASN
1	B	488	HIS
1	B	529	GLN
1	B	538	GLN
1	B	542	GLN
1	B	563	HIS
1	B	659	HIS
1	B	712	GLN
1	B	842	ASN
1	C	239	ASN
1	C	261	GLN
1	C	511	GLN
1	C	566	HIS

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Mol	Chain	Res	Type
1	C	657	GLN
1	C	672	HIS
1	C	772	HIS
1	D	242	GLN
1	D	261	GLN
1	D	275	HIS
1	D	472	ASN
1	D	478	ASN
1	D	480	ASN
1	D	529	GLN
1	D	576	GLN
1	D	657	GLN
1	D	659	HIS
1	D	714	ASN
1	D	811	GLN
1	D	866	HIS
1	E	242	GLN
1	E	261	GLN
1	E	275	HIS
1	E	351	ASN
1	E	472	ASN
1	E	478	ASN
1	E	483	ASN
1	E	515	GLN
1	E	546	GLN
1	E	576	GLN
1	E	657	GLN
1	E	672	HIS
1	E	714	ASN
1	E	842	ASN
1	E	866	HIS
1	F	391	ASN
1	F	488	HIS
1	F	511	GLN
1	F	538	GLN
1	F	563	HIS
1	F	592	GLN
1	F	631	GLN
1	F	672	HIS
1	F	712	GLN
1	G	405	ASN
1	G	480	ASN

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Mol	Chain	Res	Type
1	G	483	ASN
1	G	488	HIS
1	G	592	GLN
1	G	631	GLN
1	G	772	HIS
1	G	864	HIS
1	H	242	GLN
1	H	275	HIS
1	H	410	GLN
1	H	472	ASN
1	H	478	ASN
1	H	483	ASN
1	H	488	HIS
1	H	576	GLN
1	H	592	GLN
1	H	657	GLN
1	H	659	HIS
1	H	847	ASN
1	H	864	HIS
1	H	884	HIS
1	I	483	ASN
1	I	488	HIS
1	I	529	GLN
1	I	629	HIS
1	I	722	HIS
1	I	866	HIS
1	J	242	GLN
1	J	275	HIS
1	J	472	ASN
1	J	478	ASN
1	J	515	GLN
1	J	546	GLN
1	J	563	HIS
1	J	576	GLN
1	J	592	GLN
1	J	657	GLN
1	J	772	HIS
1	J	811	GLN
1	J	866	HIS
1	J	884	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	J	1
1	D	1
1	H	1
1	E	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	1.15
1	J	253:PRO	C	254:SER	N	1.12
1	D	253:PRO	C	254:SER	N	1.11
1	H	253:PRO	C	254:SER	N	1.11
1	E	253:PRO	C	254:SER	N	1.08

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10065. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

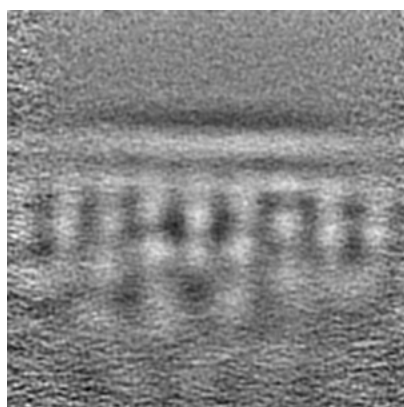


Y

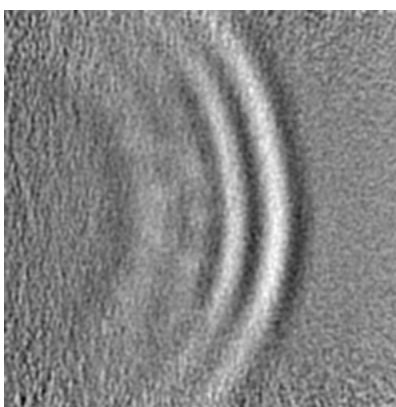


Z

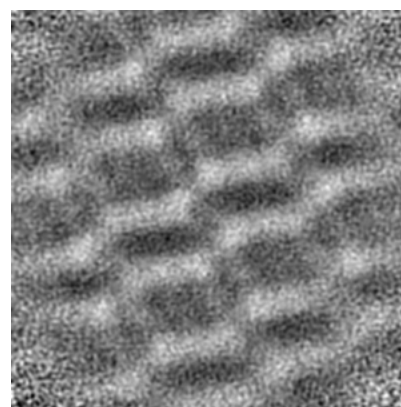
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

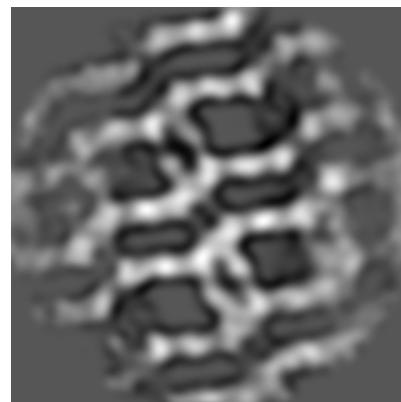
6.2.1 Primary map



X Index: 80



Y Index: 80



Z Index: 80

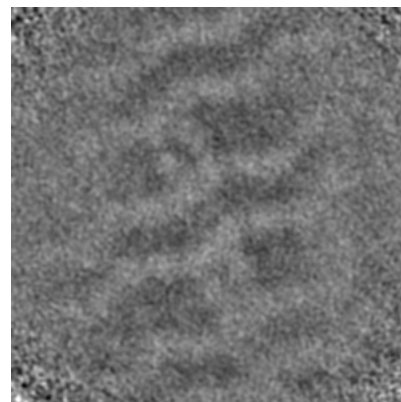
6.2.2 Raw map



X Index: 80



Y Index: 80



Z Index: 80

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

6.3 Largest variance slices [i](#)

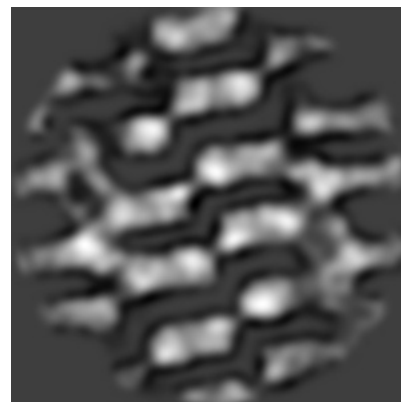
6.3.1 Primary map



X Index: 59

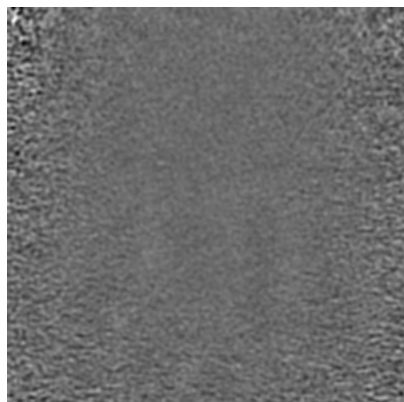


Y Index: 93

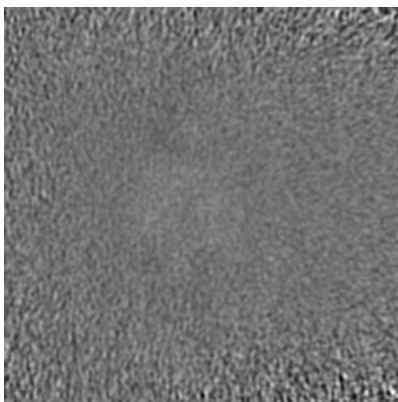


Z Index: 63

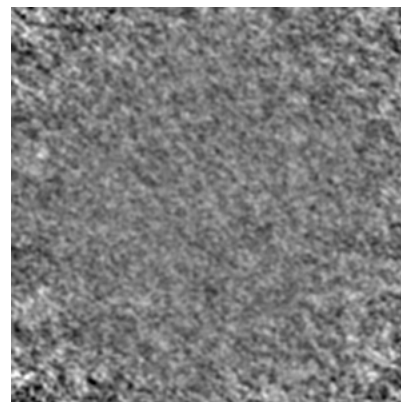
6.3.2 Raw map



X Index: 1



Y Index: 1

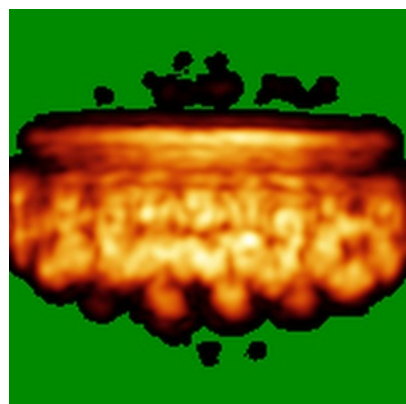


Z Index: 0

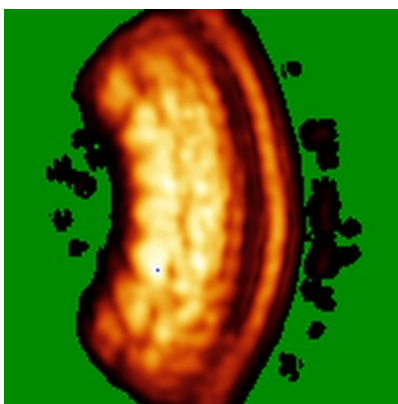
The images above show the largest variance slices of the map in three orthogonal directions.

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

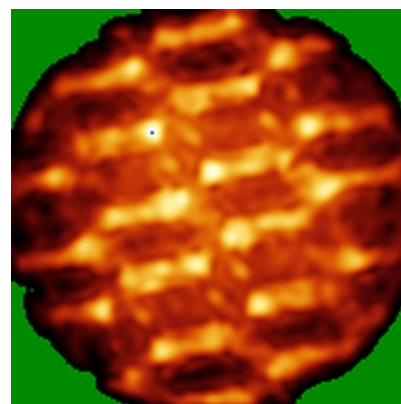
6.4.1 Primary map



X

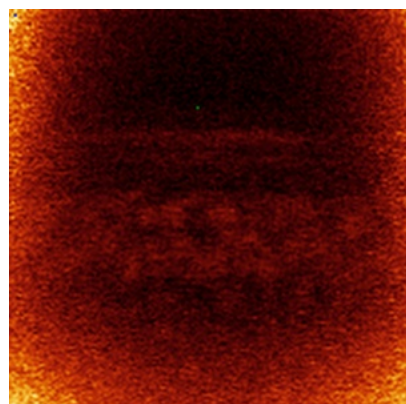


Y

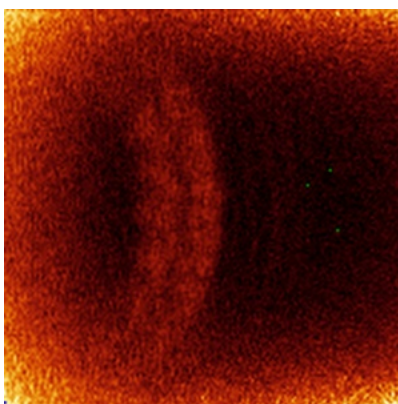


Z

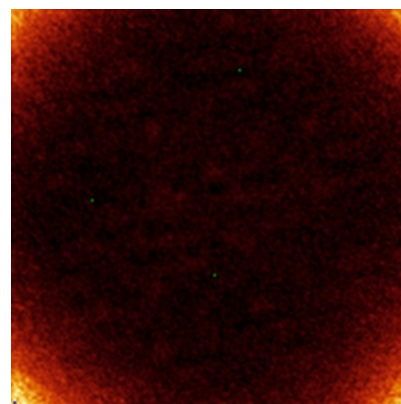
6.4.2 Raw map



X



Y



Z

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

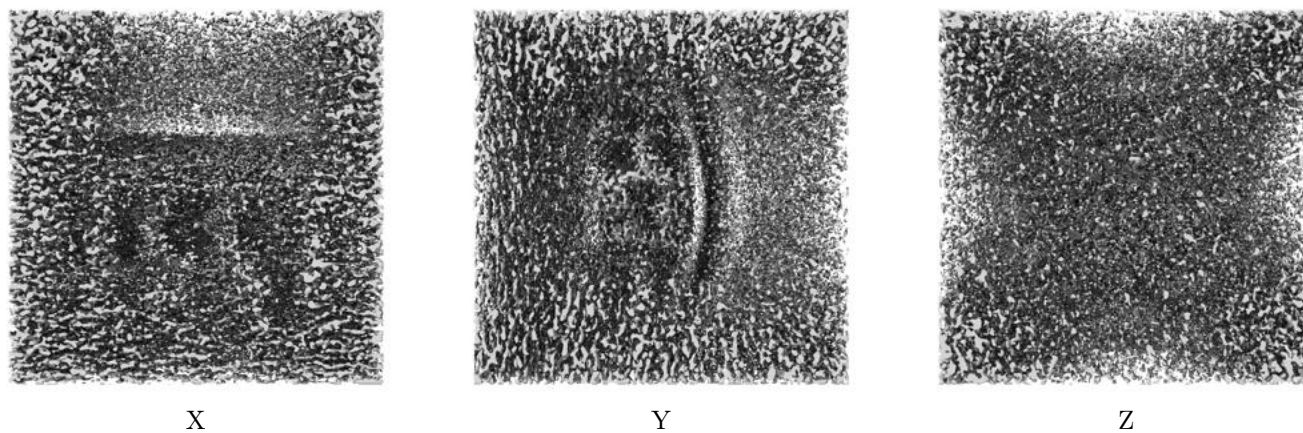
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.67. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

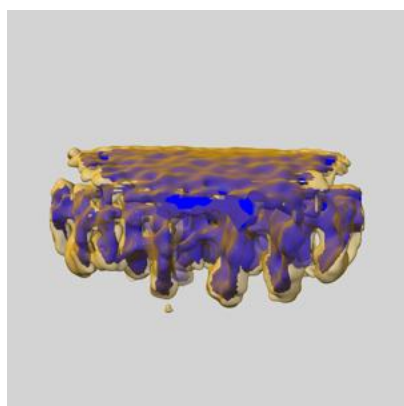
6.6 Mask visualisation [i](#)

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

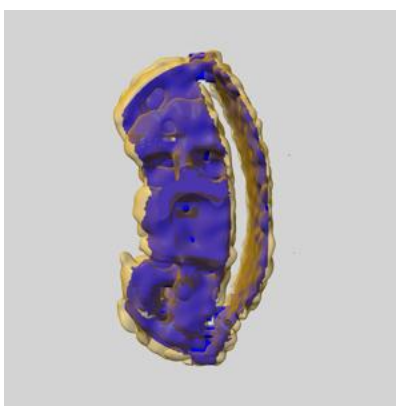
A mask typically either:

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

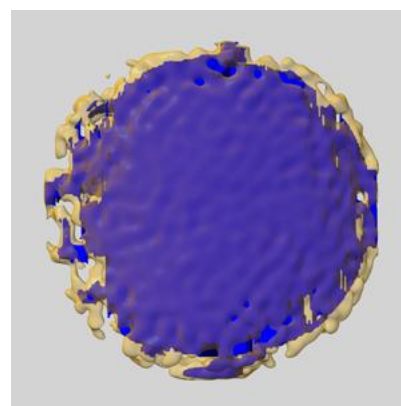
6.6.1 emd_10065_msk_1.map [i](#)



X



Y

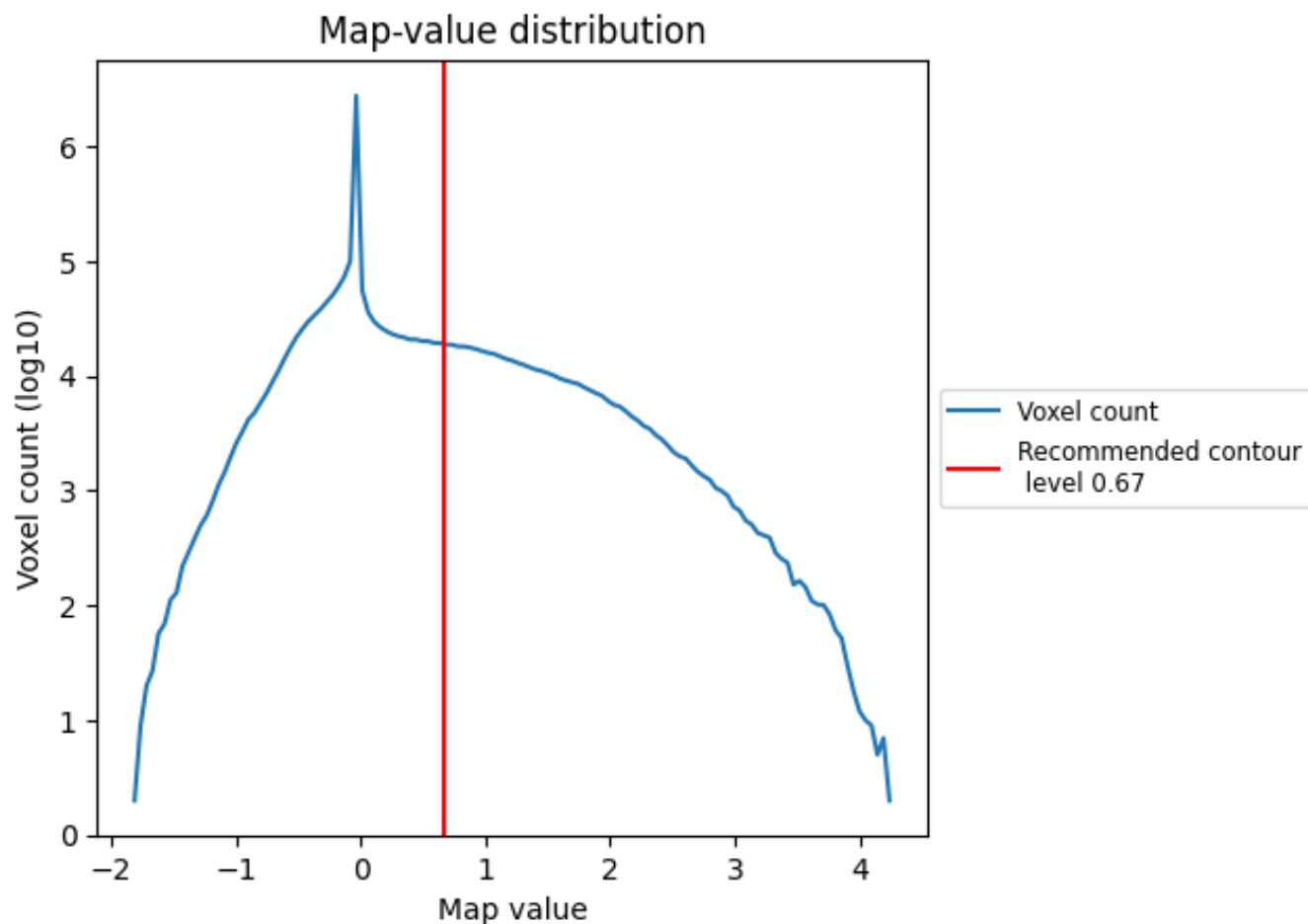


Z

7 Map analysis [i](#)

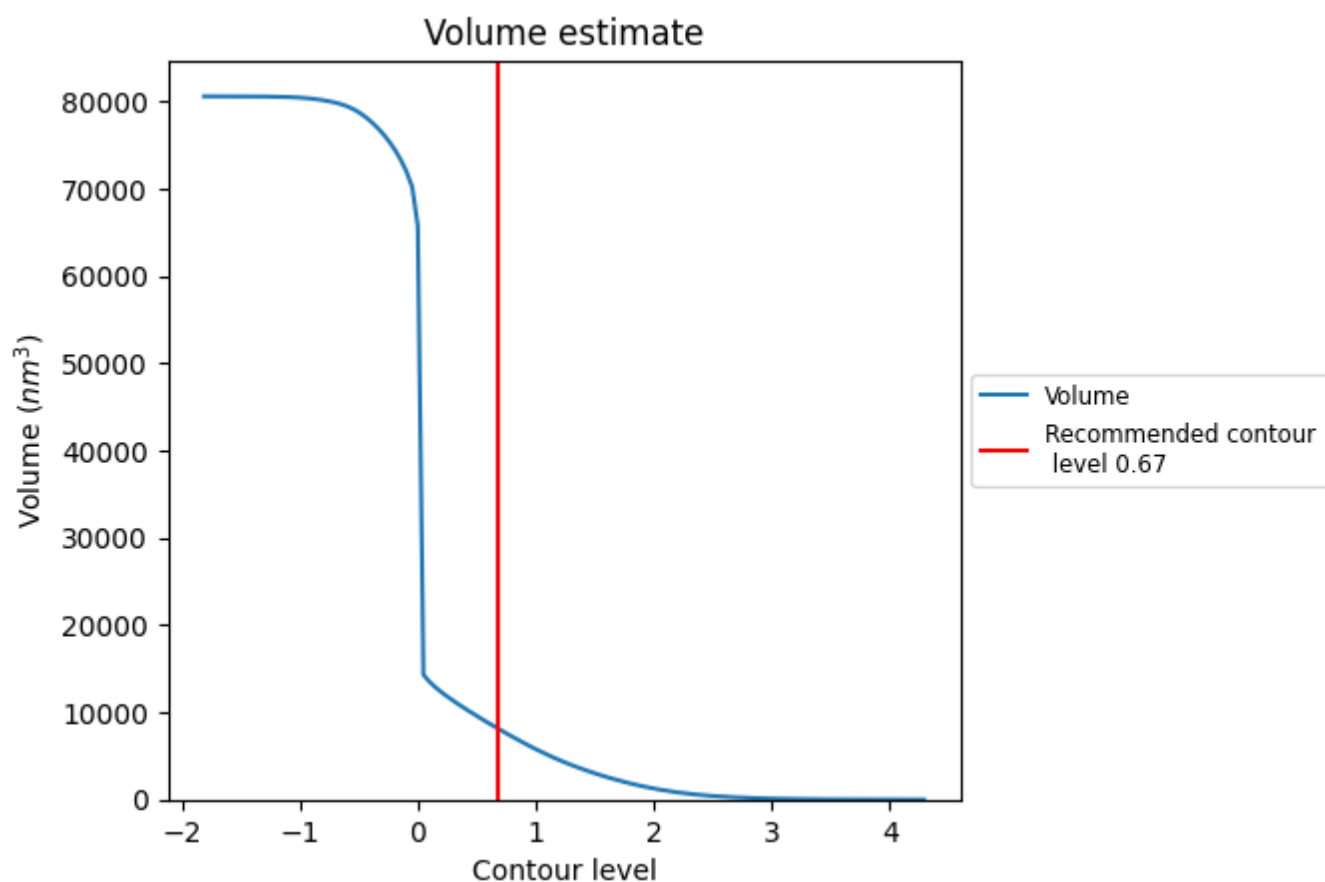
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

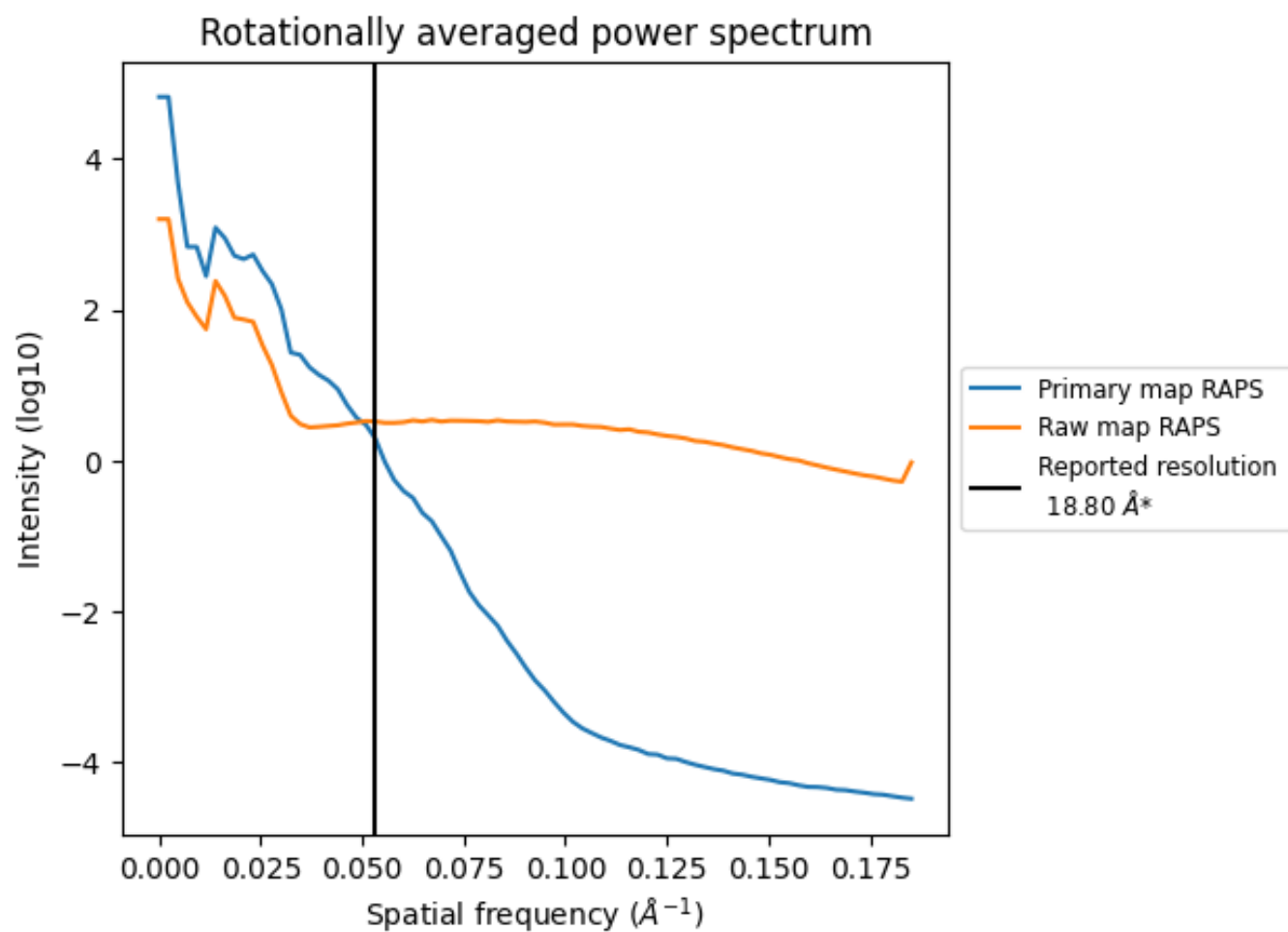
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 8207 nm³; this corresponds to an approximate mass of 7413 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

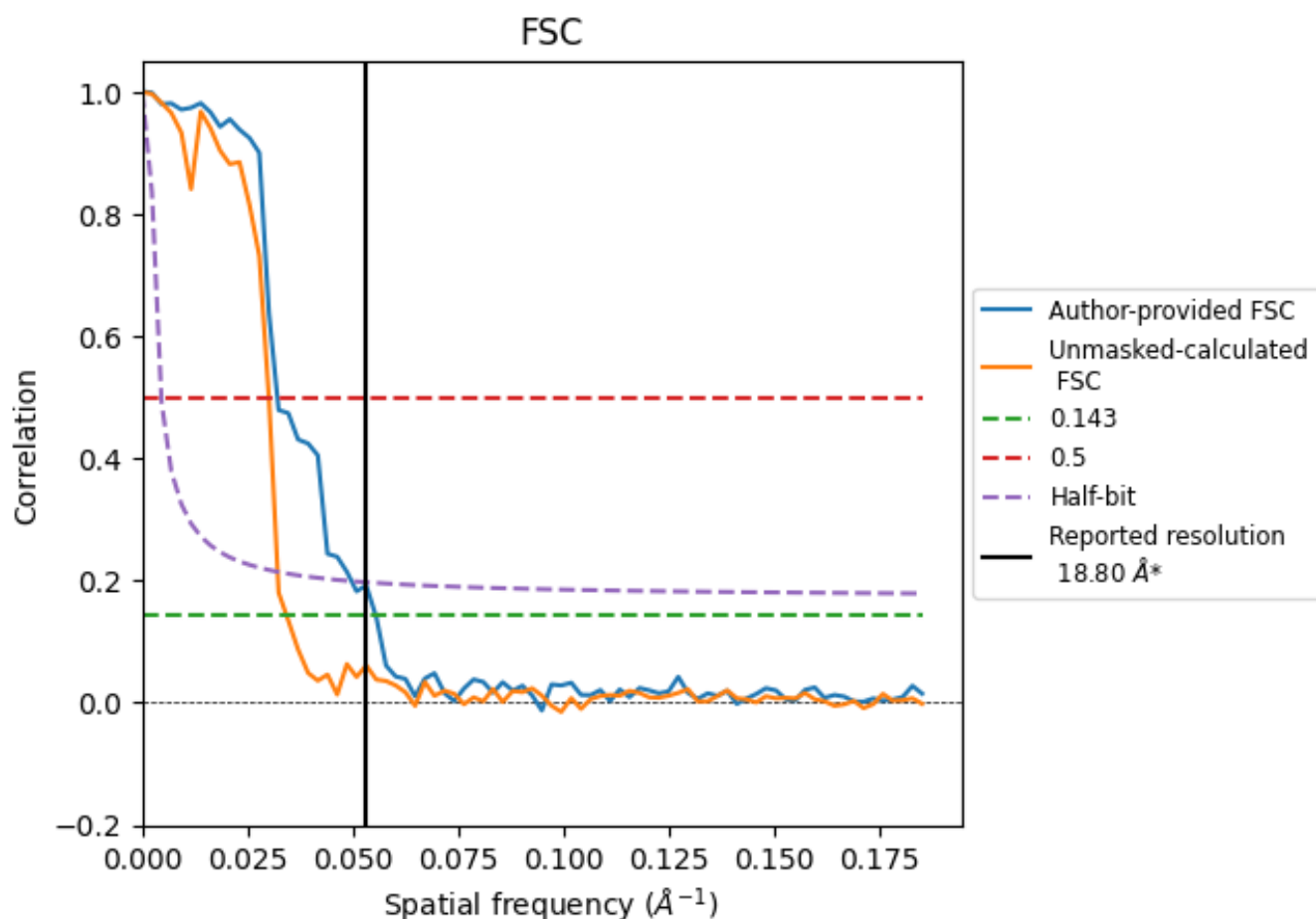


*Reported resolution corresponds to spatial frequency of 0.053 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.053 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

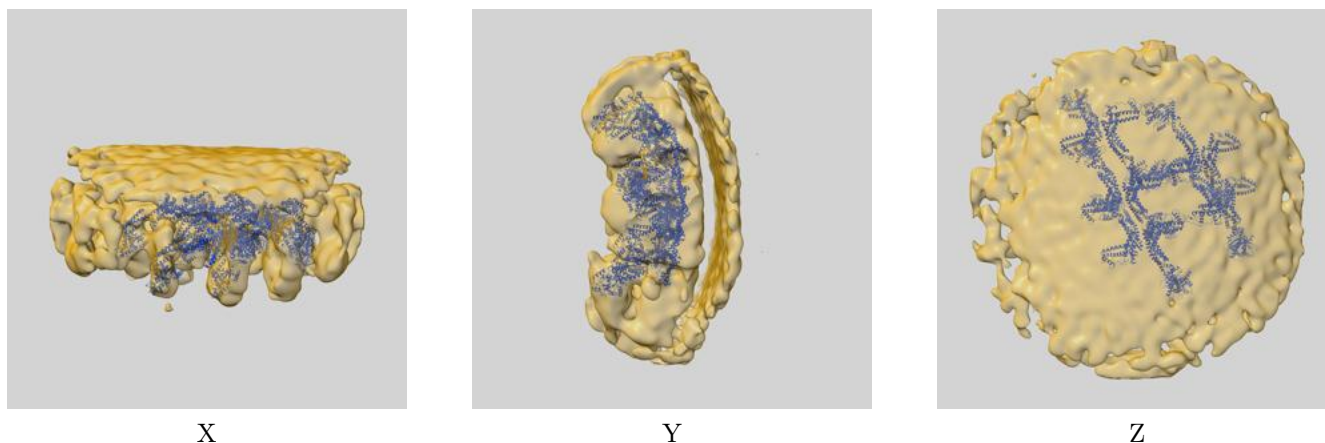
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	18.80	-	-
Author-provided FSC curve	18.05	31.15	20.08
Unmasked-calculated*	29.15	33.22	31.06

*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 29.15 differs from the reported value 18.8 by more than 10 %

9 Map-model fit [i](#)

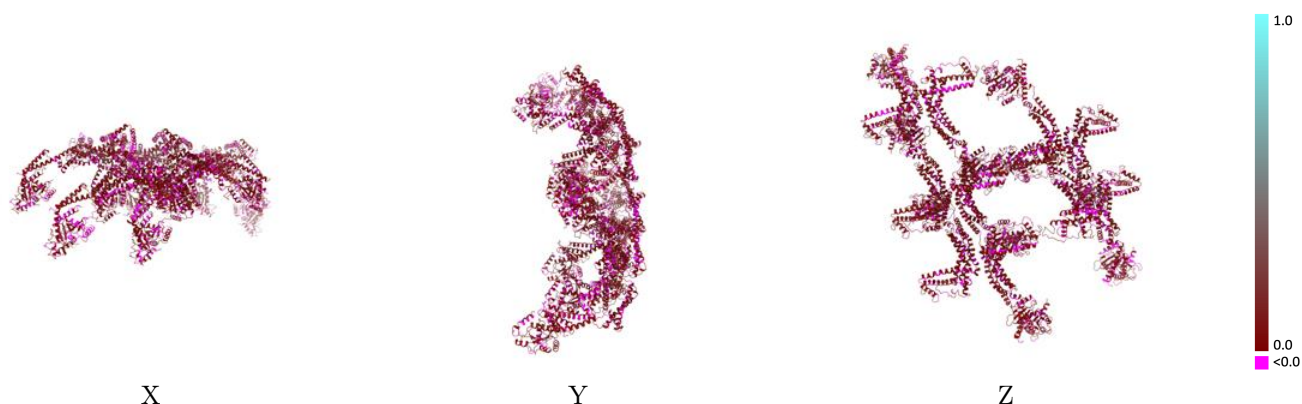
This section contains information regarding the fit between EMDB map EMD-10065 and PDB model 6RZW. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



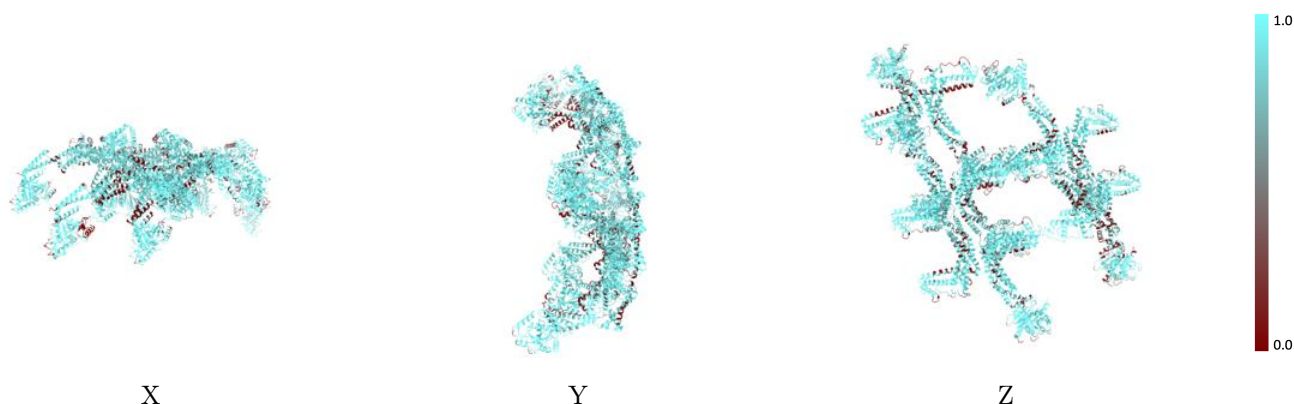
The images above show the 3D surface view of the map at the recommended contour level 0.67 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



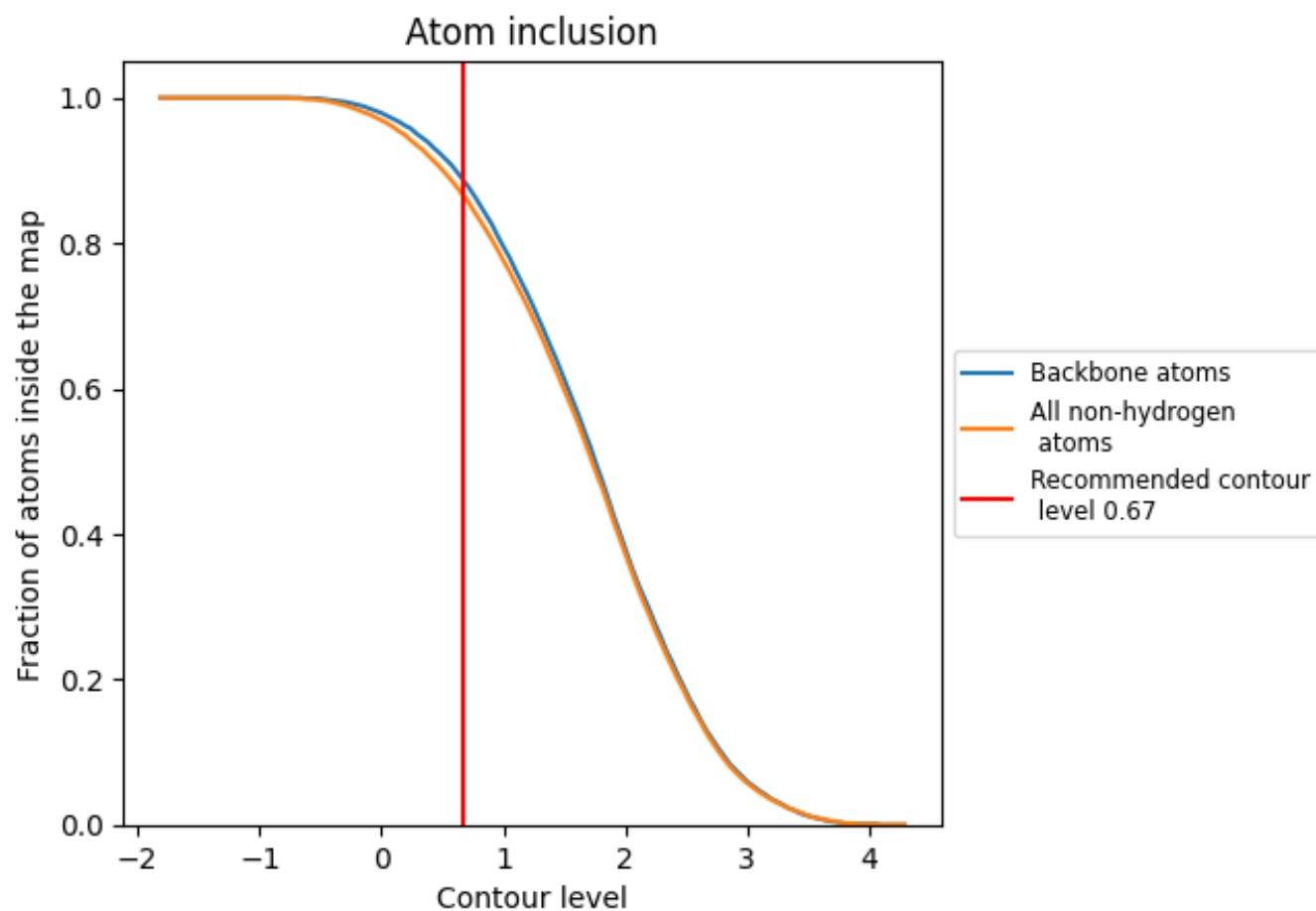
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.67).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.67) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8660	0.0580
A	0.8920	0.0610
B	0.9060	0.0590
C	0.8980	0.0590
D	0.8890	0.0620
E	0.8660	0.0620
F	0.8500	0.0550
G	0.8850	0.0580
H	0.7690	0.0490
I	0.8560	0.0570
J	0.8510	0.0560

1.0

0.0

<0.0