Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 08:08 pm GMT

PDB ID	:	6EMK
EMDB ID	:	EMD-3896
Title	:	Cryo-EM Structure of Saccharomyces cerevisiae Target of Rapamycin Complex 2
Authors	:	Karuppasamy, M.; Kusmider, B.; Oliveira, T.M.; Gaubitz, C.; Prouteau, M.; Loewith, R.; Schaffitzel, C.
Deposited on	:	2017-10-02
Resolution	:	8.00 Å(reported)
Based on initial model	:	5FVM

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

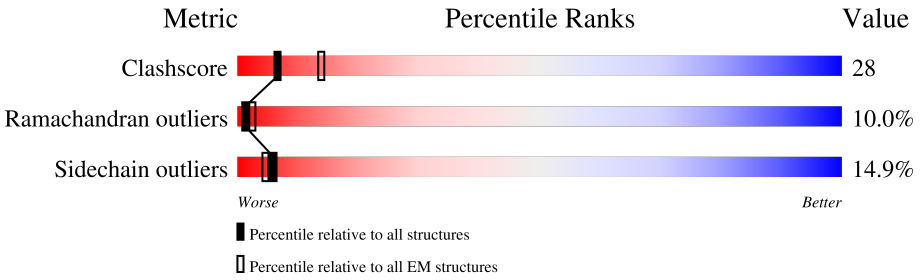
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 8.00 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2474	38% 42% 10% • 9%
1	C	2474	38% 43% 9% • 9%
2	B	303	41% 47% 10% ••
2	D	303	44% 44% 9% ••
3	E	303	91% 9%
3	F	303	88% 12%
4	G	426	33% • 64%
4	H	426	30% 5% • 64%

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Mol	Chain	Length	Quality of chain
5	I	1176	
5	J	1176	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 48012 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 Serine/threonine-protein kinase TOR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2262	Total 18186	C 11650	N 3110	O 3345	S 81	0	0
1	C	2262	Total 18186	C 11650	N 3110	O 3345	S 81	0	0

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	300	Total 2372	C 1468	N 433	O 460	S 11	0	0
2	D	300	Total 2372	C 1468	N 433	O 460	S 11	0	0

- Molecule 3 is a protein called Target of rapamycin complex 2 subunit TSC11.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	303	Total 1515	C 909	N 303	O 303	0	0
3	F	303	Total 1515	C 909	N 303	O 303	0	0

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit AVO2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	155	Total 762	C 452	N 155	O 155	0	0
4	H	155	Total 762	C 452	N 155	O 155	0	0

- Molecule 5 is a protein called Target of rapamycin complex 2 subunit AVO1.

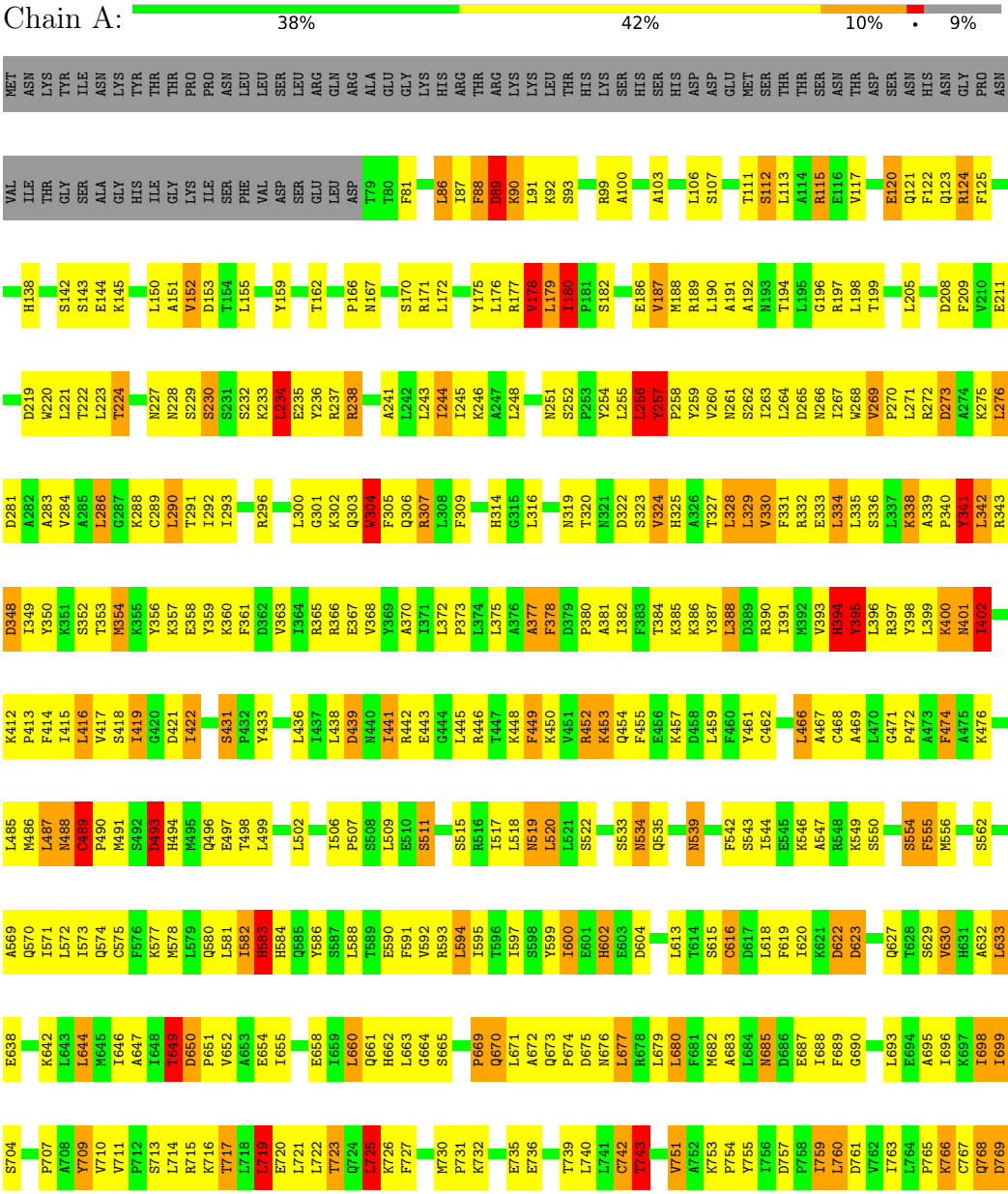
Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	S	0	0
			1171	739	187	242	3		
5	J	146	Total	C	N	O	S	0	0
			1171	739	187	242	3		

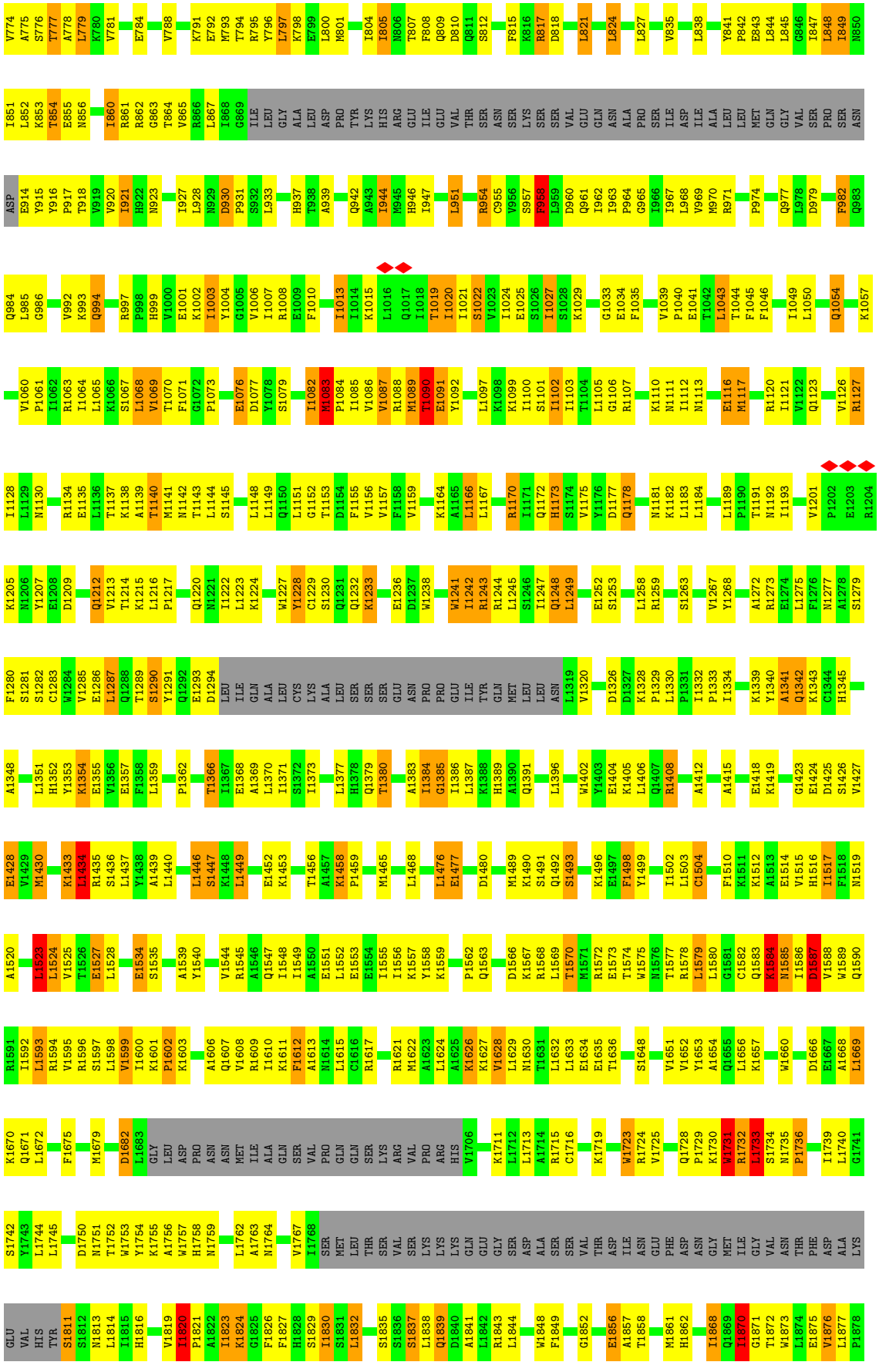
3 Residue-property plots (i)

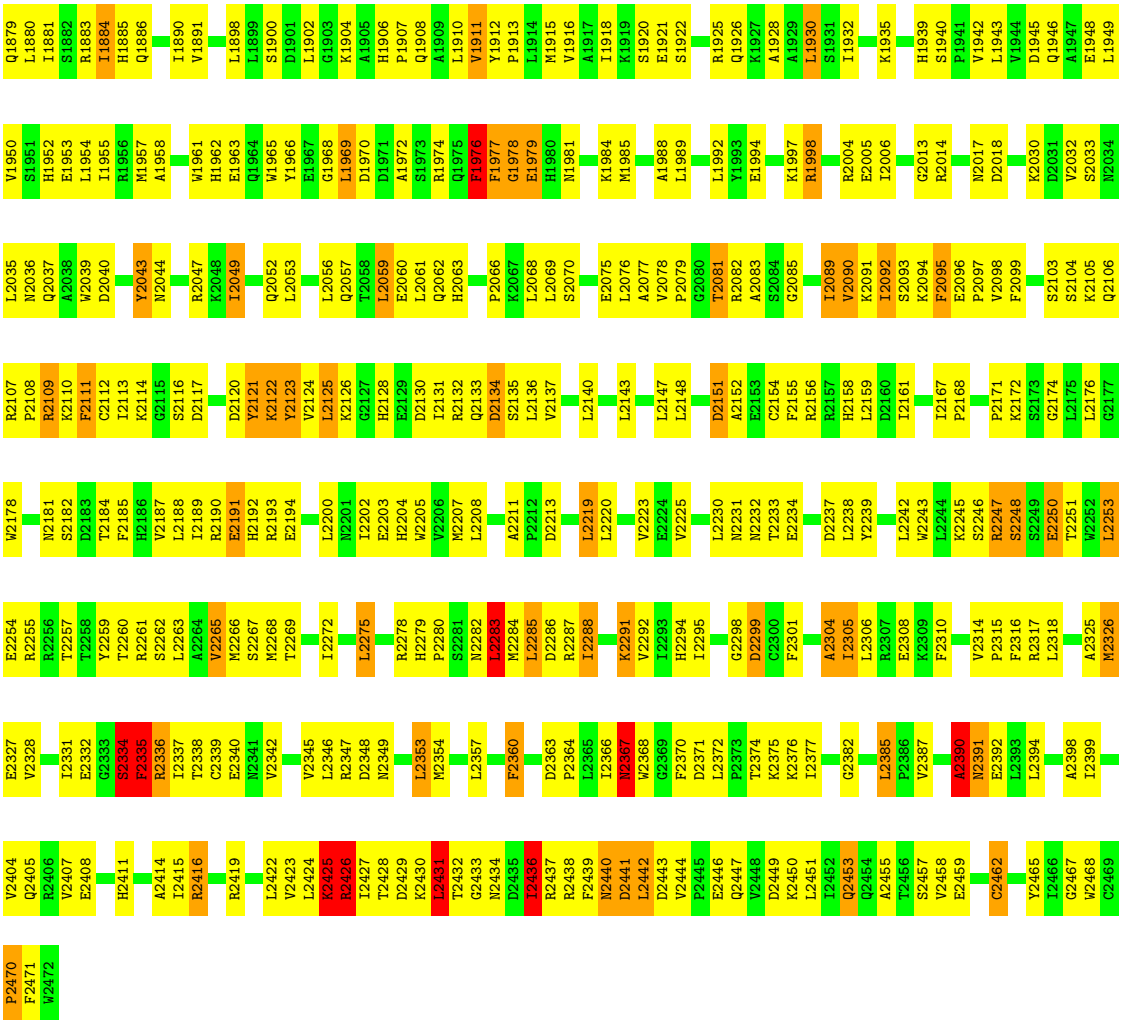
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Serine/threonine-protein kinase TOR2

Chain A:

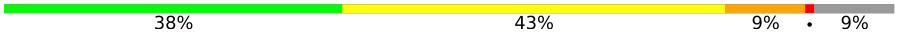


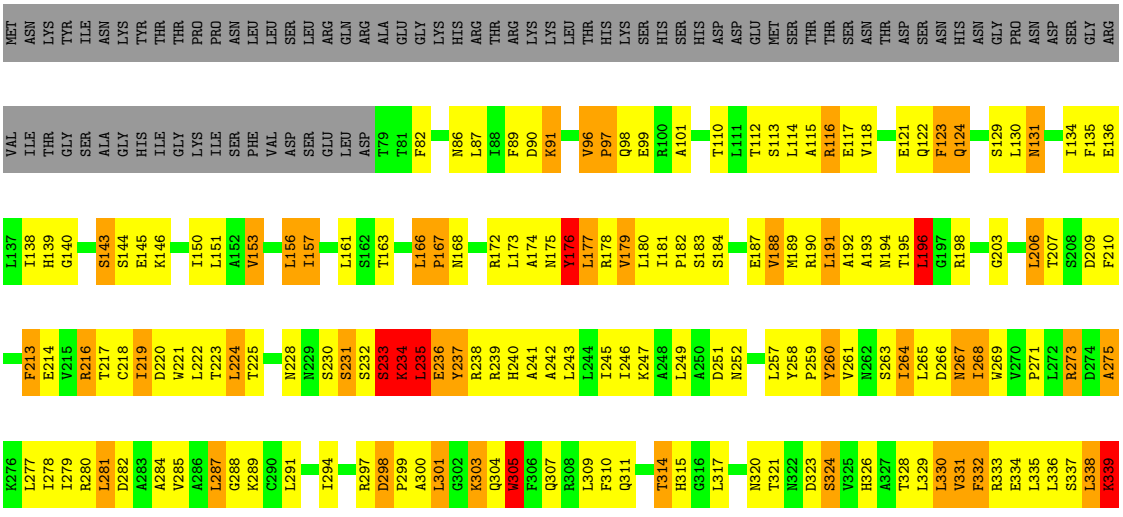


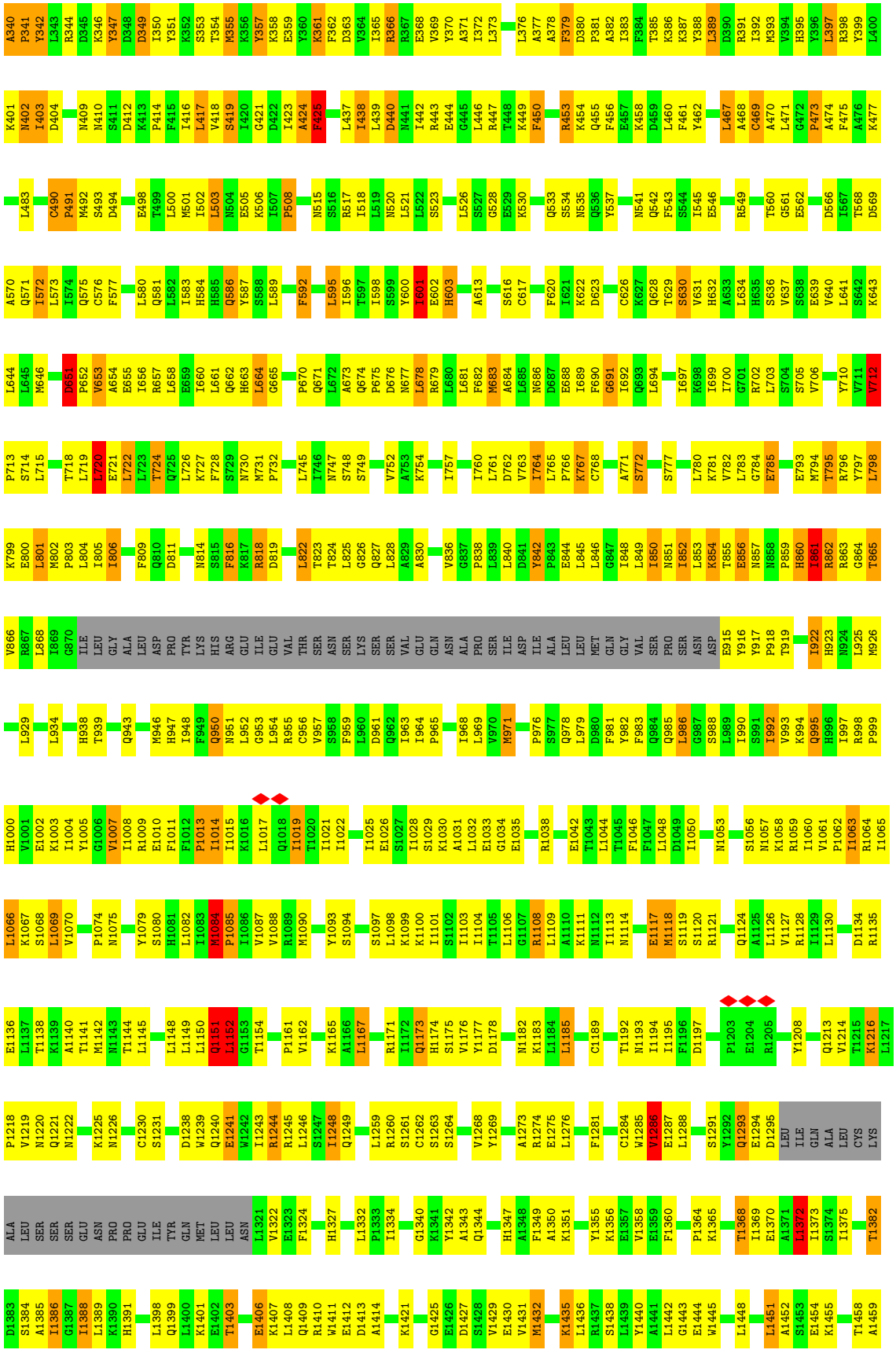


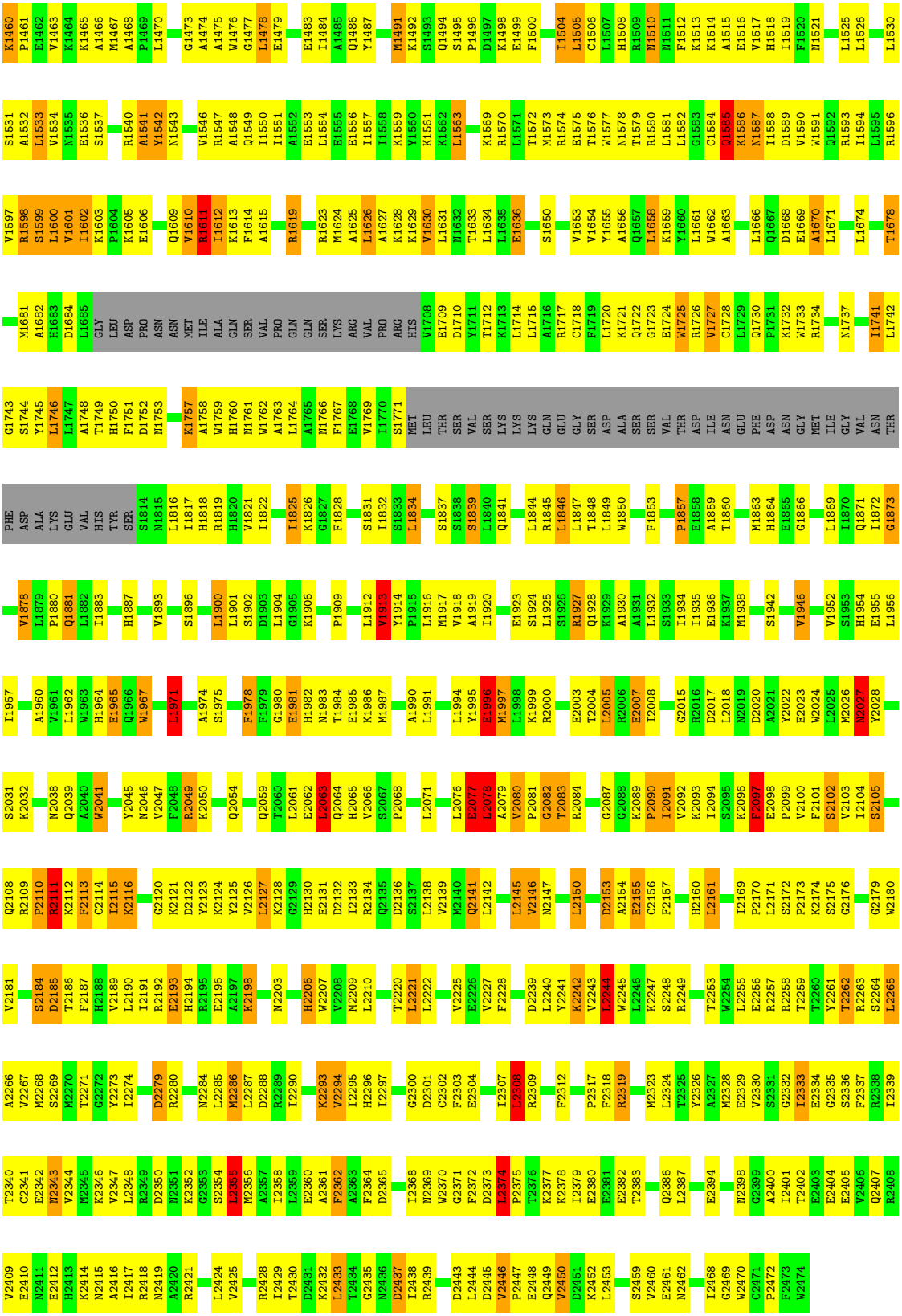
• Molecule 1: Serine/threonine-protein kinase TOR2

Chain C:



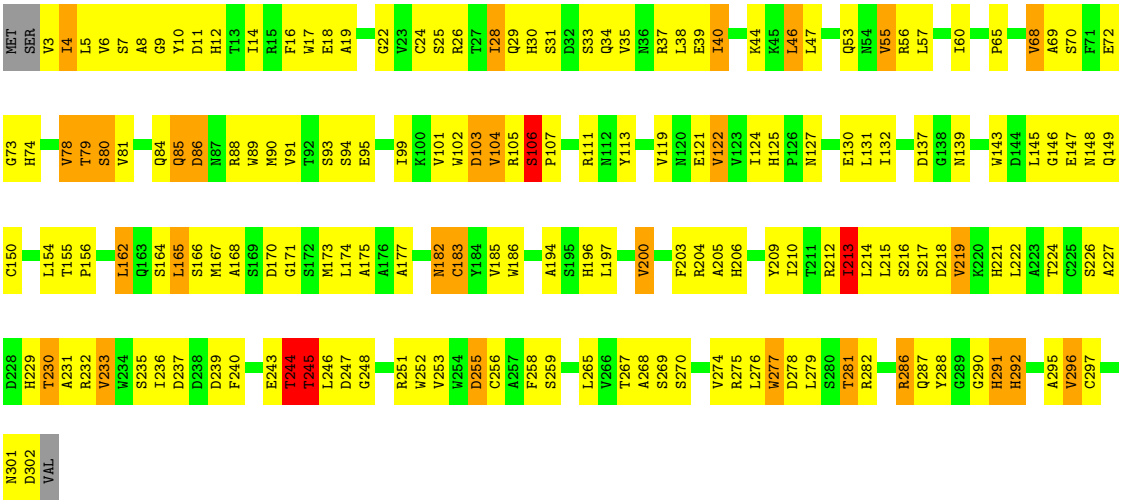






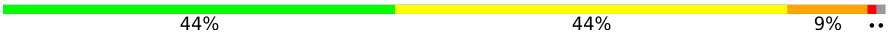
• Molecule 2: Target of rapamycin complex subunit LST8

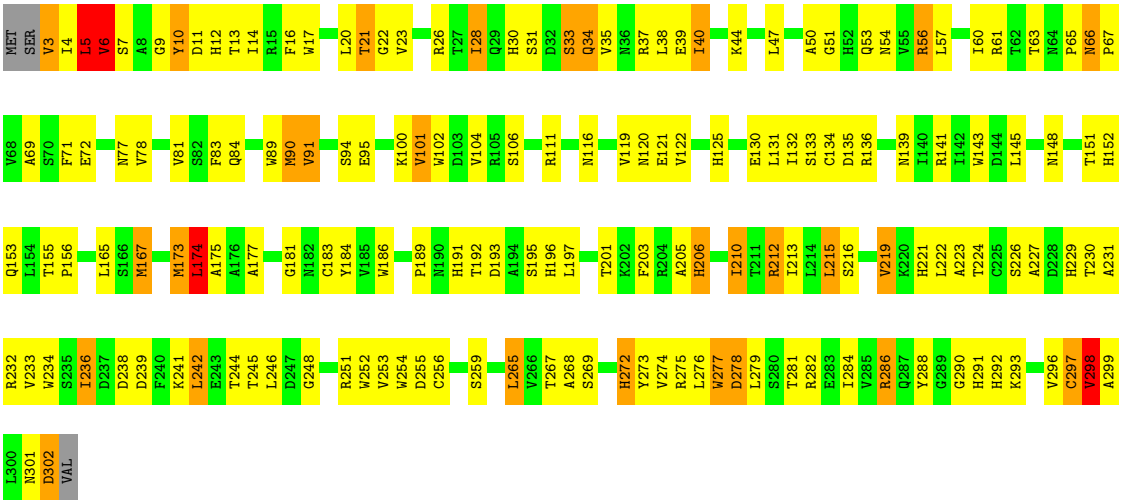
Chain B: 41% 47% 10%



• Molecule 2: Target of rapamycin complex subunit LST8

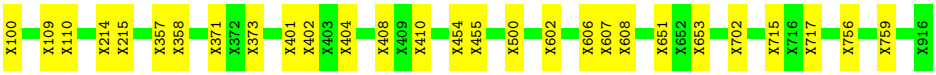
Chain D:





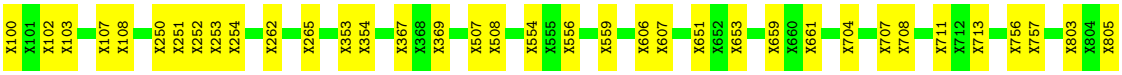
• Molecule 3: Target of rapamycin complex 2 subunit TSC11

Chain E:



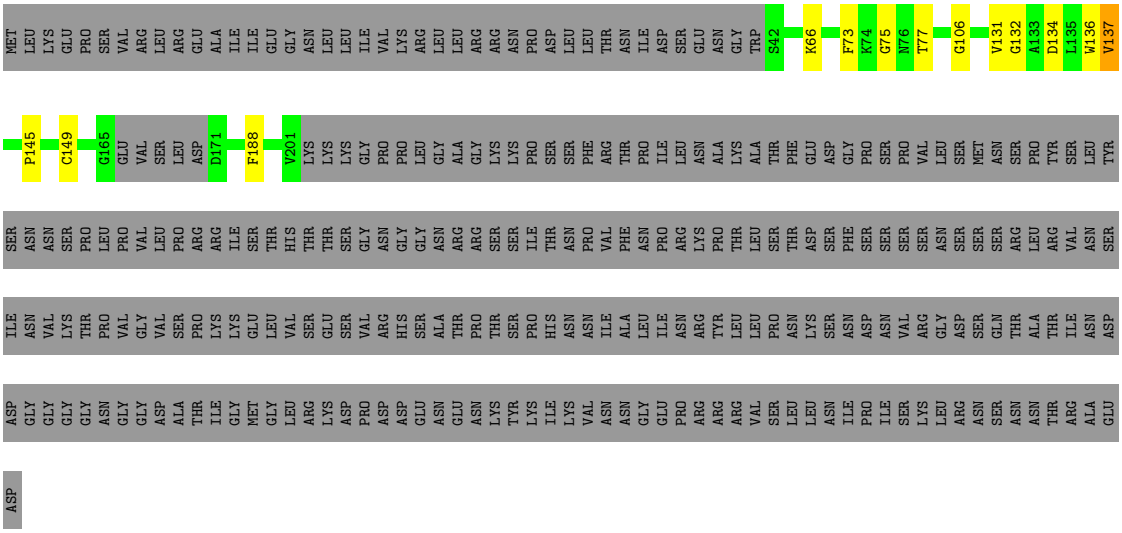
• Molecule 3: Target of rapamycin complex 2 subunit TSC11

Chain F:



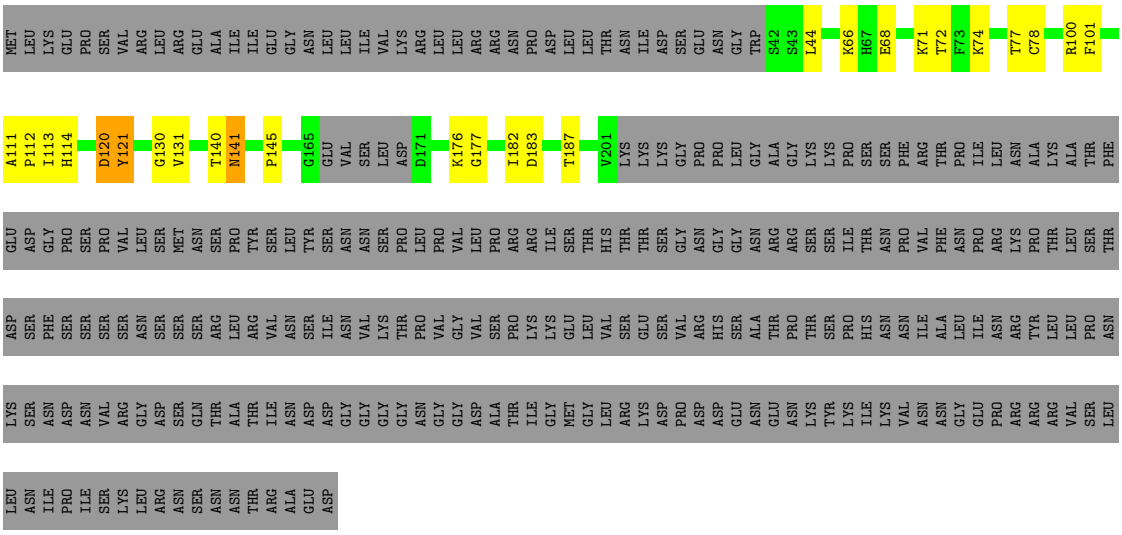
• Molecule 4: Target of rapamycin complex 2 subunit AVO2

Chain G:



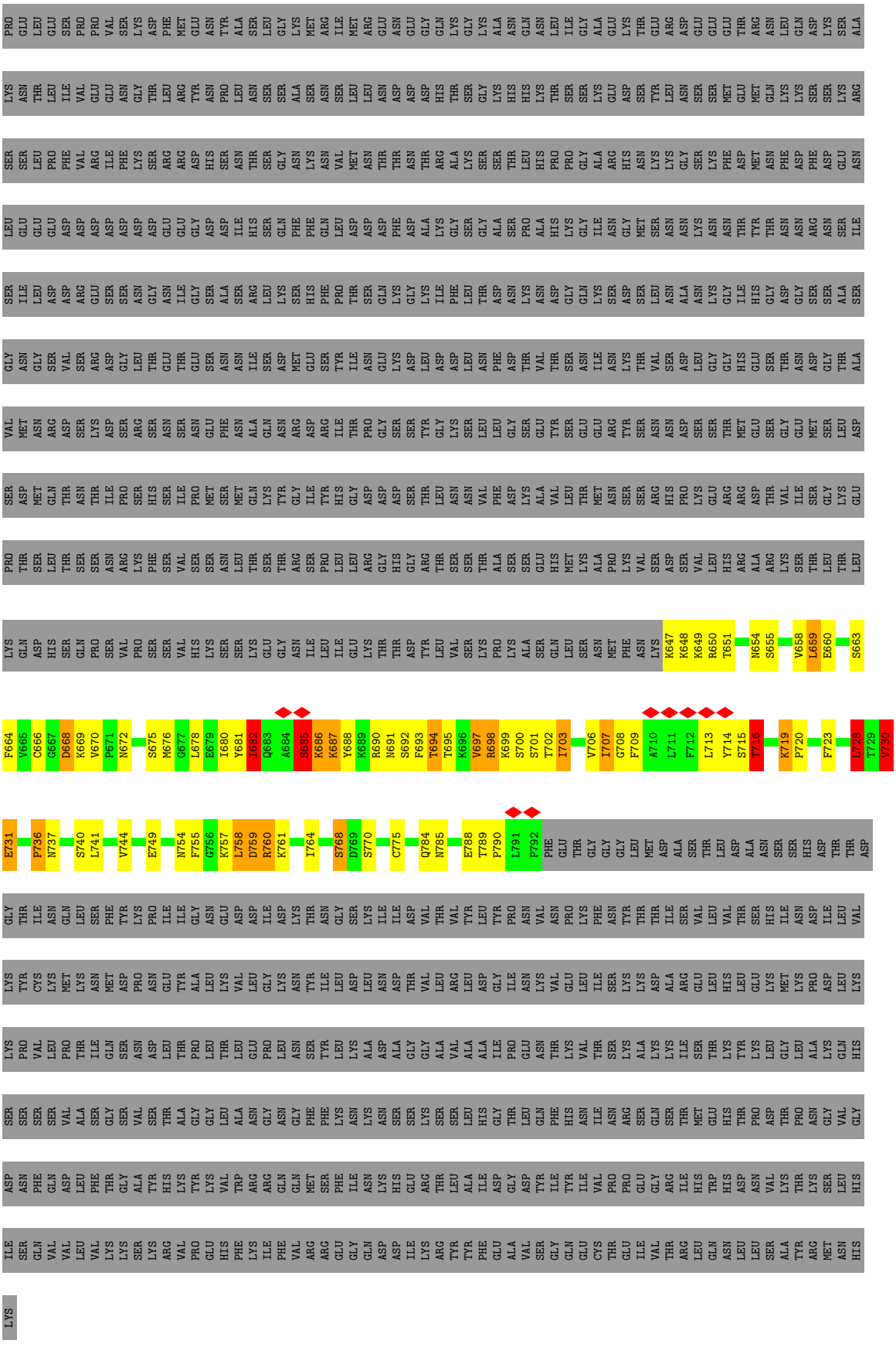
• Molecule 4: Target of rapamycin complex 2 subunit AVO2

Chain H:

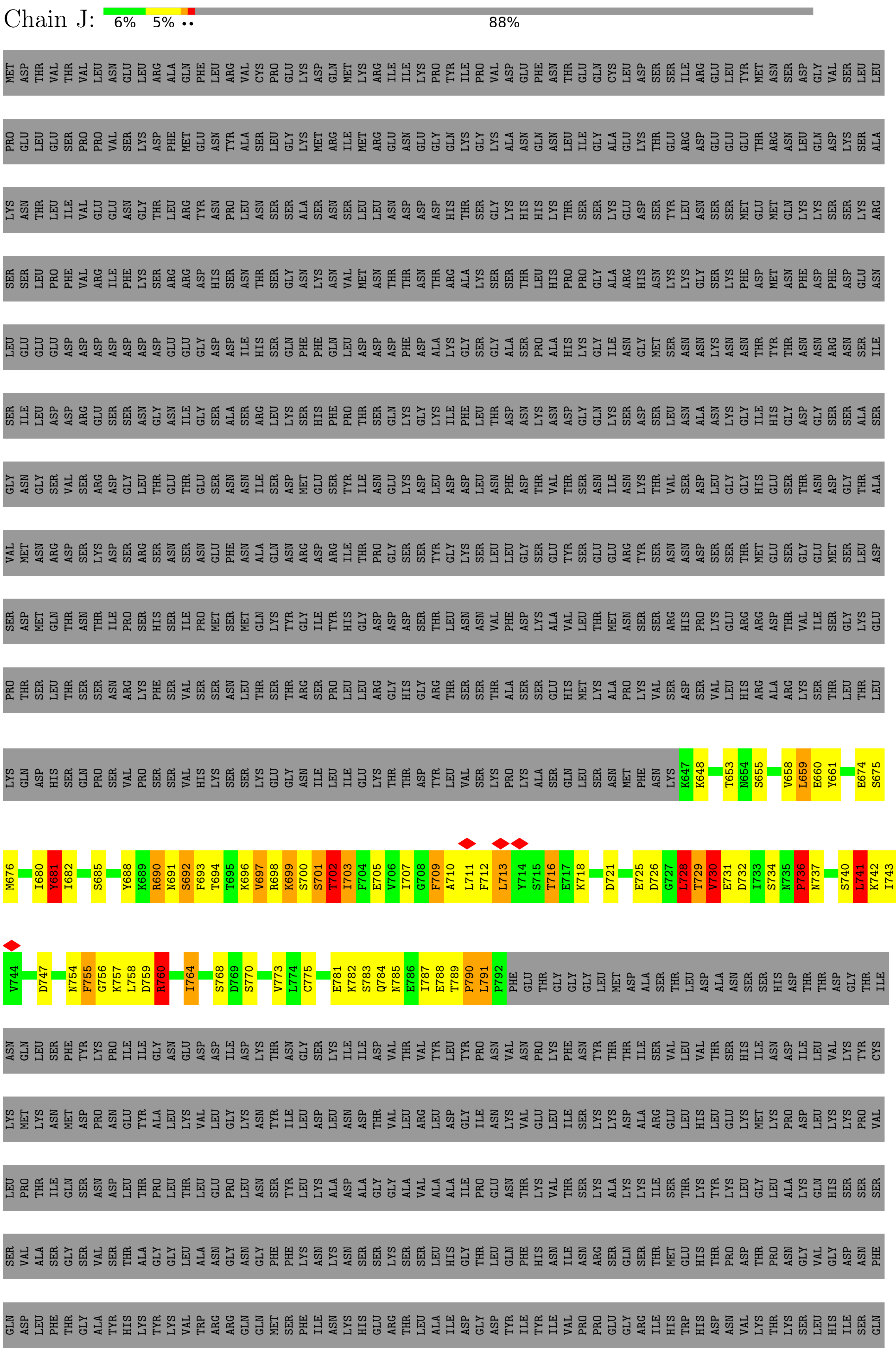


• Molecule 5: Target of rapamycin complex 2 subunit AVO1

Chain I:



• Molecule 5: Target of rapamycin complex 2 subunit AVO1


Chain J:
6%
5%
88%
MET ASP THR VAL THR VAL LEU ASN GLU LEU ARG ALA GLN PHE LEU ARG VAL CYS PRO GLU LYS ASP GLN MET LYS ARG ILE ILE LYS PRO TYR ILE PRO VAL ASP GLU PHE ASN THR GLU GLN CYS LEU ASP SER SER ILE ARG GLU LEU TYR MET ASN SER ASP GLY VAL SER LEU LEU
PRO GLU LEU GLU SER PRO PRO VAL SER LYS ASP PHE MET GLU ASN TYR ALA SER LEU GLY LYS MET ARG ILE MET ARG GLU ASN GLU GLY GLN LYS GLY LYS ALA ASN GLN ASN LEU ILE GLY ALA GLU LYS THR GLU ARG ASP GLU GLU GLU THR ARG ASN LEU GLN ASP LYS SER ALA
LYS ASN THR LEU ILE VAL GLU GLU ASN GLY THR LEU ARG TYR ASN PRO LEU ASN SER SER ALA SER ASN SER LEU LEU ASN ASP ASP ASP HIS THR SER GLY LYS HIS HIS LYS THR SER SER LYS GLU ASP SER TYR LEU ASN SER SER MET GLU MET GLN LYS LYS SER SER LYS ARG
SER SER LEU PRO PHE VAL ARG ILE PHE LYS SER ARG ARG ASP HIS SER ASN THR SER GLY ASN LYS ASN VAL MET ASN THR THR ASN THR ARG ALA LYS SER SER THR LEU HIS PRO PRO GLY ALA ARG HIS ASN LYS LYS GLY SER LYS PHE ASP MET ASN PHE ASP PHE ASP GLU ASN
LEU GLU GLU GLU ASP ASP ASP ASP ASP ASP GLU GLU GLY ASP ASP ILE HIS SER GLN PHE PHE GLN LEU ASP ASP ASP PHE ASP ALA LYS GLY SER GLY ALA SER PRO ALA HIS LYS GLY ILE ASN GLY MET SER ASN ASN LYS ASN ASN THR TYR THR ASN ASN ARG ASN SER ILE
SER ILE LEU ASP ASP ARG GLU SER SER ASN GLY ASN ILE GLY SER ALA SER ARG LEU LYS SER HIS PHE PRO THR SER GLN LYS GLY LYS ILE PHE LEU THR ASP ASN LYS ASN ASP GLY GLN LYS SER ASP SER LEU ASN ALA ASN LYS GLY ILE HIS GLY ASP GLY SER SER ALA SER
GLY ASN GLY SER VAL SER ARG ASP GLY LEU THR GLU THR GLU SER ASN ASN ILE SER ASP MET GLU SER TYR ILE ASN GLU LYS ASP LEU ASP ASP LEU ASN PHE ASP THR VAL THR SER ASN ILE ASN LYS THR VAL SER ASP LEU GLY GLY HIS GLU SER THR ASN ASP GLY THR ALA
VAL MET ASN ARG ASP SER LYS ASP SER ARG SER ASN SER ASN GLU PHE ASN ALA GLN ASN ARG ASP ARG ILE THR PRO GLY SER SER TYR GLY LYS SER LEU LEU GLY SER GLU TYR SER GLU GLU ARG TYR SER ASN ASN ASP SER SER THR MET GLU SER GLY GLU MET SER LEU ASP
SER ASP MET GLN THR ASN THR ILE PRO SER HIS SER ILE PRO MET SER MET GLN LYS TYR GLY ILE TYR HIS GLY ASP ASP SER THR LEU ASN ASN VAL PHE ASP LYS ALA VAL LEU THR MET ASN SER SER ARG HIS PRO LYS GLU ARG ARG ASP THR VAL ILE SER GLY LYS GLU
PRO THR SER LEU THR SER SER ASN ARG LYS PHE SER VAL SER SER ASN LEU THR SER THR ARG SER PRO LEU LEU ARG GLY HIS GLY ARG THR SER SER THR ALA SER SER GLU HIS MET LYS ALA PRO LYS VAL SER ASP SER VAL LEU HIS ARG ALA ARG LYS SER THR LEU THR LEU
LYS GLN ASP HIS SER GLN PRO SER VAL PRO SER SER VAL HIS LYS SER SER LYS GLU GLY ASN ILE LEU ILE GLU LYS THR THR ASP TYR LEU VAL SER LYS PRO LYS ALA SER GLN LEU SER ASN MET PHE ASN LYS K647 K648 T653 N654 S655 V658 L659 E660 Y661 E674 S675
M676 I680 Y681 I682 S685 Y688 K689 R690 N691 S692 F693 T694 T695 K696 V697 R698 K699 S700 S701 T702 I703 F704 E705 V706 I707 G708 F709 A710 L711 F712 L713 Y714 S715 T716 E717 K718 D721 E725 D726 G727 L728 T729 V730 E731 D732 I733 S734 N735 P736 N737 S740 L741 K742 I743
V744 D747 N754 F755 G756 K757 L758 D759 R760 I764 S768 D769 S770 V773 L774 C775 E781 K782 S783 Q784 N785 E786 I787 E788 T789 P790 L791 P792 PHE GLU THR GLY GLY LEU MET ASP ALA SER THR LEU ASP ALA ASN SER SER HIS ASP THR THR ASP GLY THR ILE
ASN GLN LEU SER PHE TYR LYS PRO ILE ILE GLY ASN GLU ASP ASP ILE ASP LYS THR ASN GLY SER LYS ILE ILE ASP VAL THR VAL TYR LEU TYR PRO ASN VAL ASN PRO LYS PHE ASN TYR THR THR ILE SER VAL LEU VAL THR SER HIS ILE ASN ASP ILE LEU VAL LYS TYR CYS
LYS MET LYS ASN MET ASP PRO ASN GLU TYR ALA LEU LYS VAL LEU GLY LYS ASN TYR ILE LEU ASP LEU ASN ASP THR VAL LEU ARG LEU ASP GLY ILE ASN LYS VAL GLU LEU ILE SER LYS LYS ASP ALA ARG GLU LEU HIS LEU GLU LYS MET LYS PRO ASP LEU LYS LYS PRO VAL
LEU PRO THR ILE GLN SER ASN ASP LEU THR PRO LEU THR LEU GLU PRO LEU ASN SER TYR LEU LYS ALA ASP ALA GLY ALA VAL ALA ALA ILE PRO GLU ASN THR LYS VAL THR SER LYS ALA LYS LYS ILE SER THR LYS TYR LYS LEU GLY LEU ALA LYS GLN HIS SER SER SER
SER VAL ALA SER GLY SER VAL SER THR ALA GLY GLY LEU ALA ASN GLY ASN GLY PHE PHE LYS ASN LYS ASN SER SER LYS SER SER LEU HIS GLY THR LEU GLN PHE HIS ASN ILE ASN ARG SER GLN SER THR MET GLU HIS THR PRO ASP THR PRO ASN GLY VAL GLY ASP ASN PHE
GLN ASP LEU PHE THR GLY ALA TYR HIS LYS TYR LYS VAL TRP ARG ARG GLN GLN MET SER PHE ILE ASN LYS HIS GLU ARG THR LEU ALA ILE ASP GLY ASP TYR ILE TYR ILE VAL PRO PRO GLU GLY ARG ILE HIS TRP HIS ASP ASN VAL LYS THR LYS SER LEU HIS ILE SER GLN

VAL VAL LEU VAL LYS LYS SER LYS ARG VAL PRO GLU HIS PHE LYS ILE PHE VAL ARG ARG GLU GLY GLN ASP ASP ILE LYS ARG TYR TYR PHE GLU ALA VAL SER GLY GLN GLU CYS THR GLU ILE VAL THR ARG LEU GLN ASN LEU LEU SER ALA TYR ARG MET ASN HIS LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	16190, 10663	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50, 47	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON II (4k x 4k), GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0147	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.60	0/18019	0.94	52/23495 (0.2%)
1	C	0.60	0/17986	0.93	40/23389 (0.2%)
2	B	0.60	0/2362	0.89	7/3108 (0.2%)
2	D	0.60	0/2353	0.93	4/3080 (0.1%)
4	G	0.48	0/715	0.68	0/918
4	H	0.49	0/718	0.87	2/927 (0.2%)
5	I	1.03	2/1165 (0.2%)	1.09	7/1526 (0.5%)
5	J	0.88	0/1160	1.01	8/1509 (0.5%)
All	All	0.62	2/44478 (0.0%)	0.93	120/57952 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	28
1	C	0	25
2	B	0	4
2	D	0	2
5	I	0	2
5	J	0	2
All	All	1	63

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	713	LEU	N-CA	5.35	1.57	1.46
5	I	714	TYR	N-CA	5.27	1.56	1.46

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	1084	MET	C-N-CD	-9.18	100.41	120.60
2	D	174	LEU	CA-CB-CG	8.54	134.94	115.30
1	A	2426	ARG	N-CA-C	7.87	132.25	111.00
2	B	106	SER	C-N-CD	-7.69	103.69	120.60
5	I	713	LEU	CA-CB-CG	7.55	132.67	115.30
1	C	467	LEU	CA-CB-CG	7.49	132.52	115.30
1	A	234	LEU	CA-CB-CG	7.28	132.05	115.30
1	C	822	LEU	CA-CB-CG	7.16	131.77	115.30
1	C	2355	LEU	N-CA-C	7.16	130.33	111.00
1	A	2431	LEU	CA-CB-CG	7.04	131.50	115.30
1	C	233	SER	N-CA-C	7.03	129.97	111.00
1	C	281	LEU	CA-CB-CG	6.98	131.34	115.30
1	C	235	LEU	CA-CB-CG	6.96	131.31	115.30
1	C	2190	LEU	CA-CB-CG	6.95	131.29	115.30
2	B	245	THR	N-CA-C	6.87	129.54	111.00
1	C	175	ASN	C-N-CA	6.81	138.72	121.70
1	C	1185	LEU	CA-CB-CG	6.78	130.90	115.30
1	A	286	LEU	CB-CG-CD1	-6.78	99.48	111.00
1	A	178	VAL	CB-CA-C	6.77	124.26	111.40
1	C	1834	LEU	CA-CB-CG	6.74	130.80	115.30
5	I	728	LEU	CA-CB-CG	6.69	130.69	115.30
5	J	728	LEU	CA-CB-CG	6.67	130.63	115.30
5	I	685	SER	C-N-CA	6.60	138.21	121.70
5	I	659	LEU	CA-CB-CG	6.49	130.24	115.30
1	C	1996	GLU	N-CA-C	6.46	128.43	111.00
5	J	659	LEU	CA-CB-CG	6.37	129.96	115.30
1	A	1731	TRP	C-N-CA	6.35	137.58	121.70
2	D	215	LEU	CA-CB-CG	6.33	129.86	115.30
2	B	104	VAL	N-CA-C	-6.31	93.95	111.00
5	J	701	SER	C-N-CA	6.30	137.45	121.70
1	C	2078	LEU	CA-CB-CG	-6.25	100.91	115.30
1	C	305	TRP	CA-CB-CG	6.20	125.48	113.70
1	A	1083	MET	N-CA-C	6.18	127.70	111.00
2	D	5	LEU	CA-CB-CG	6.18	129.52	115.30
1	A	344	ASP	C-N-CA	6.16	137.09	121.70
1	C	424	ALA	C-N-CA	6.10	136.96	121.70
1	C	2308	LEU	CA-CB-CG	6.10	129.32	115.30
1	C	1286	VAL	C-N-CA	6.08	136.91	121.70
1	C	2155	GLU	N-CA-C	6.08	127.42	111.00
1	A	594	LEU	CA-CB-CG	6.06	129.25	115.30
2	D	265	LEU	CA-CB-CG	6.02	129.14	115.30
5	J	701	SER	N-CA-C	5.97	127.11	111.00
1	A	974	PRO	C-N-CD	-5.96	107.49	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	2161	LEU	CA-CB-CG	5.93	128.94	115.30
1	A	347	ASP	C-N-CA	5.93	136.52	121.70
5	J	741	LEU	CA-CB-CG	5.91	128.90	115.30
1	A	742	CYS	C-N-CA	5.90	136.44	121.70
1	C	1981	GLU	N-CA-C	5.89	126.90	111.00
1	C	417	LEU	CA-CB-CG	5.88	128.83	115.30
1	A	1449	LEU	CA-CB-CG	5.87	128.81	115.30
1	C	1971	LEU	CA-CB-CG	5.87	128.80	115.30
1	C	1585	GLN	N-CA-C	5.87	126.85	111.00
1	A	2440	ASN	C-N-CA	5.85	136.31	121.70
1	C	1293	GLN	N-CA-C	5.85	126.78	111.00
1	A	2018	ASP	N-CA-C	5.84	126.77	111.00
1	C	2221	LEU	CA-CB-CG	5.83	128.72	115.30
2	B	165	LEU	CA-CB-CG	5.82	128.69	115.30
1	A	588	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	1090	THR	C-N-CA	5.75	136.07	121.70
1	A	482	LEU	CA-CB-CG	5.74	128.50	115.30
1	C	1372	LEU	CA-CB-CG	5.72	128.46	115.30
1	A	797	LEU	CA-CB-CG	5.71	128.42	115.30
1	C	2244	LEU	CA-CB-CG	5.67	128.34	115.30
2	B	162	LEU	CA-CB-CG	5.66	128.32	115.30
1	A	768	GLN	C-N-CA	5.66	135.84	121.70
1	A	2335	PHE	N-CA-C	-5.63	95.79	111.00
1	A	1584	LYS	N-CA-C	5.59	126.10	111.00
1	A	1396	LEU	CA-CB-CG	5.56	128.10	115.30
1	A	2425	LYS	C-N-CA	5.55	135.57	121.70
1	C	595	LEU	CA-CB-CG	5.51	127.97	115.30
1	A	2018	ASP	C-N-CA	5.49	135.43	121.70
1	A	394	HIS	C-N-CA	5.49	135.42	121.70
1	A	1446	LEU	C-N-CA	5.49	135.41	121.70
5	I	719	LYS	C-N-CD	-5.48	108.55	120.60
1	A	1434	LEU	CA-CB-CG	5.47	127.88	115.30
1	C	2077	GLU	N-CA-C	5.46	125.75	111.00
5	I	758	LEU	CA-CB-CG	5.46	127.85	115.30
5	J	681	TYR	CA-CB-CG	5.46	123.77	113.40
1	C	1996	GLU	C-N-CA	5.45	135.34	121.70
4	H	66	LYS	N-CA-C	5.45	125.72	111.00
1	A	2441	ASP	N-CA-C	5.40	125.59	111.00
1	A	2390	ALA	C-N-CA	5.38	135.14	121.70
1	C	691	GLY	N-CA-C	5.34	126.46	113.10
2	B	46	LEU	CA-CB-CG	5.33	127.57	115.30
1	C	196	LEU	CA-CB-CG	5.33	127.55	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1166	LEU	CA-CB-CG	5.31	127.52	115.30
1	C	503	LEU	CA-CB-CG	5.31	127.51	115.30
1	A	719	LEU	CA-CB-CG	5.30	127.50	115.30
1	A	221	LEU	CA-CB-CG	5.27	127.41	115.30
1	A	644	LEU	CA-CB-CG	5.26	127.41	115.30
1	A	1082	ILE	C-N-CA	5.26	134.84	121.70
4	H	182	ILE	C-N-CA	5.24	134.81	121.70
5	I	741	LEU	CA-CB-CG	5.23	127.33	115.30
5	J	713	LEU	CA-CB-CG	5.21	127.29	115.30
1	C	130	LEU	CA-CB-CG	5.21	127.28	115.30
1	C	1167	LEU	CA-CB-CG	5.20	127.26	115.30
1	A	821	LEU	CA-CB-CG	5.18	127.22	115.30
1	A	725	LEU	CA-CB-CG	5.18	127.21	115.30
2	B	213	ILE	CB-CA-C	5.17	121.93	111.60
1	A	416	LEU	CA-CB-CG	5.17	127.18	115.30
5	J	791	LEU	CA-CB-CG	5.11	127.06	115.30
1	A	1731	TRP	N-CA-C	5.11	124.80	111.00
1	A	1498	PHE	C-N-CA	5.11	134.47	121.70
1	A	649	THR	C-N-CA	5.10	134.46	121.70
1	A	1579	LEU	CA-CB-CG	5.10	127.03	115.30
1	C	347	TYR	C-N-CA	5.10	134.45	121.70
1	C	1293	GLN	C-N-CA	5.09	134.43	121.70
1	A	1341	ALA	C-N-CA	5.08	134.40	121.70
1	A	2436	ILE	N-CA-C	5.08	124.71	111.00
1	C	798	LEU	CA-CB-CG	5.07	126.96	115.30
1	A	1587	ASP	C-N-CA	5.06	134.35	121.70
1	C	232	SER	C-N-CA	5.06	134.35	121.70
1	A	1733	LEU	C-N-CA	5.05	134.33	121.70
1	A	328	LEU	CA-CB-CG	5.04	126.90	115.30
1	A	1476	LEU	CA-CB-CG	5.04	126.90	115.30
1	A	2136	LEU	CA-CB-CG	5.03	126.86	115.30
1	C	720	LEU	CA-CB-CG	5.02	126.84	115.30
1	A	2283	LEU	CA-CB-CG	5.01	126.82	115.30
1	A	740	LEU	CA-CB-CG	5.00	126.81	115.30
1	A	768	GLN	N-CA-C	-5.00	97.50	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	257	TYR	CA

All (63) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1089	MET	Peptide
1	A	1241	TRP	Peptide
1	A	1385	GLY	Peptide
1	A	1523	LEU	Peptide
1	A	1587	ASP	Peptide
1	A	1731	TRP	Peptide
1	A	178	VAL	Peptide
1	A	180	ILE	Peptide
1	A	1976	PHE	Peptide
1	A	2121	TYR	Peptide
1	A	2123	TYR	Peptide
1	A	2334	SER	Peptide
1	A	2367	ASN	Peptide
1	A	2385	LEU	Peptide
1	A	2431	LEU	Peptide
1	A	2436	ILE	Peptide
1	A	256	LEU	Peptide
1	A	257	TYR	Peptide
1	A	347	ASP	Peptide
1	A	394	HIS	Peptide
1	A	400	LYS	Peptide
1	A	401	ASN	Peptide
1	A	402	ILE	Peptide
1	A	488	ASN	Peptide
1	A	489	CYS	Peptide
1	A	604	ASP	Peptide
1	A	649	THR	Peptide
1	A	958	PHE	Peptide
2	B	103	ASP	Peptide
2	B	244	THR	Peptide
2	B	291	HIS	Peptide
2	B	31	SER	Peptide
1	C	1084	MET	Peptide
1	C	1151	GLN	Peptide
1	C	1152	LEU	Peptide
1	C	1286	VAL	Peptide
1	C	131	ASN	Peptide
1	C	1610	VAL	Peptide
1	C	1611	ARG	Peptide
1	C	1636	GLU	Peptide
1	C	1670	ALA	Peptide
1	C	1995	TYR	Peptide
1	C	2027	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	C	2076	LEU	Peptide
1	C	2077	GLU	Peptide
1	C	2078	LEU	Peptide
1	C	2145	LEU	Peptide
1	C	2155	GLU	Peptide
1	C	2308	LEU	Peptide
1	C	235	LEU	Peptide
1	C	2416	ALA	Peptide
1	C	403	ILE	Peptide
1	C	646	MET	Peptide
1	C	651	ASP	Peptide
1	C	665	GLY	Peptide
1	C	712	VAL	Peptide
1	C	916	TYR	Peptide
2	D	173	MET	Peptide
2	D	34	GLN	Peptide
5	I	682	ILE	Peptide
5	I	697	VAL	Peptide
5	J	736	PRO	Peptide
5	J	760	ARG	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18186	0	18002	1077	0
1	C	18186	0	17976	1069	0
2	B	2372	0	2199	140	0
2	D	2372	0	2191	145	0
3	E	1515	0	491	15	0
3	F	1515	0	490	23	0
4	G	762	0	290	6	0
4	H	762	0	293	9	0
5	I	1171	0	1119	61	0
5	J	1171	0	1116	54	0
All	All	48012	0	44167	2571	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 28.

All (2571) 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:A:2060:GLU:HB3	1:A:2062:GLN:HG2	1.25	1.18
1:A:841:TYR:HB2	1:A:843:GLU:HG2	1.16	1.13
1:C:983:PHE:HB3	1:C:1022:ILE:HG12	1.31	1.10
1:A:179:LEU:HD22	1:A:233:LYS:HG3	1.31	1.10
2:D:297:CYS:HA	2:D:298:VAL:HB	1.25	1.09
1:A:1083:MET:HB3	1:A:1084:PRO:HD3	1.34	1.08
1:C:265:LEU:HA	1:C:307:GLN:HB3	1.29	1.07
1:C:2337:PHE:HZ	1:C:2450:VAL:HG13	1.16	1.07
1:C:230:SER:HB3	1:C:233:SER:HB2	1.34	1.07
2:D:4:ILE:HG12	2:D:60:ILE:HG12	1.36	1.05
2:B:4:ILE:HG12	2:B:60:ILE:HG12	1.38	1.05
1:C:1442:LEU:HB3	1:C:1624:MET:HG2	1.36	1.05
1:A:650:ASP:H	1:A:651:PRO:HD3	1.20	1.04
5:J:655:SER:HA	5:J:659:LEU:HB2	1.40	1.02
1:C:2374:LEU:HD11	1:C:2417:ILE:HB	1.39	1.02
1:A:652:VAL:HB	3:F:100:UNK:H2	1.22	1.01
1:A:1151:LEU:CB	1:A:1152:GLY:HA2	1.90	1.01
1:C:1612:ILE:HG23	1:C:1615:ALA:HB3	1.39	1.00
1:C:842:TYR:HB3	1:C:844:GLU:HG2	1.41	1.00
5:J:699:LYS:HE2	5:J:737:ASN:HB2	1.44	0.99
2:D:84:GLN:HB3	2:D:89:TRP:HB2	1.45	0.99
1:A:2121:TYR:HA	1:A:2122:LYS:HB2	1.45	0.96
1:A:1263:SER:HB3	1:A:1268:TYR:HE2	1.30	0.96
1:C:297:ARG:HD2	1:C:339:LYS:HG3	1.48	0.96
1:C:1763:ALA:HB1	1:C:1825:ILE:HA	1.45	0.96
1:C:857:ASN:HB3	1:C:1586:LYS:HA	1.47	0.96
5:I:693:PHE:CE2	5:I:760:ARG:HB3	2.01	0.95
1:A:2126:LYS:HD3	1:A:2131:ILE:HD11	1.48	0.95
1:C:2062:GLU:HA	1:C:2063:LEU:HB2	1.48	0.94
1:A:581:LEU:HA	1:A:583:HIS:N	1.81	0.94
1:C:401:LYS:HA	1:C:403:ILE:HG23	1.49	0.94
2:B:265:LEU:HB2	2:B:279:LEU:HD12	1.46	0.94
1:C:1011:PHE:HD1	1:C:1022:ILE:HG23	1.29	0.94
1:A:801:MET:HA	1:A:804:ILE:HB	1.47	0.94
1:A:280:LEU:HA	1:A:330:VAL:HG22	1.48	0.94
1:A:771:SER:HB2	1:A:774:VAL:HB	1.50	0.94
2:B:4:ILE:HG21	2:B:40:ILE:HD11	1.47	0.93
1:C:1630:VAL:HB	1:C:1634:LEU:HG	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:346:LYS:HD3	1:C:350:ILE:HG12	1.51	0.93
1:A:1043:LEU:HD11	1:C:702:ARG:HD3	1.52	0.92
1:A:650:ASP:H	1:A:651:PRO:CD	1.80	0.92
1:C:2045:TYR:HB3	1:C:2049:ARG:HH12	1.33	0.91
1:C:1850:TRP:HZ2	1:C:1859:ALA:HB1	1.36	0.91
1:C:2337:PHE:CZ	1:C:2450:VAL:HG13	2.05	0.91
1:A:281:ASP:HA	1:A:284:VAL:HB	1.52	0.90
1:A:2112:CYS:HB2	1:A:2120:ASP:HB3	1.51	0.90
2:D:229:HIS:HB3	2:D:251:ARG:HB2	1.53	0.90
1:A:636:VAL:HG13	1:A:675:ASP:HB3	1.52	0.89
1:C:2004:THR:HG1	1:C:2008:ILE:N	1.68	0.89
1:A:1371:ILE:HD13	1:A:1387:LEU:HG	1.53	0.89
1:A:2078:VAL:HG13	1:A:2089:ILE:HA	1.53	0.89
1:A:856:ASN:HB2	1:A:1580:LEU:HA	1.54	0.89
1:C:188:VAL:HG21	1:C:233:SER:HB3	1.52	0.89
1:A:704:SER:HB2	1:A:709:TYR:HB2	1.55	0.88
1:A:824:LEU:HD21	1:A:1534:GLU:HB2	1.55	0.88
1:A:1212:GLN:HB2	1:A:1252:GLU:HG3	1.55	0.88
1:A:2337:ILE:HA	1:A:2340:GLU:HG2	1.55	0.87
2:B:9:GLY:HA2	2:B:296:VAL:HG23	1.54	0.87
1:A:1617:ARG:HE	1:A:1657:LYS:HB3	1.39	0.87
1:A:117:VAL:HB	1:A:120:GLU:HA	1.57	0.86
1:A:768:GLN:HB2	1:A:770:ALA:H	1.40	0.86
1:A:849:ILE:HG12	1:A:1548:ILE:HA	1.57	0.86
1:A:1045:PHE:HZ	1:A:1064:ILE:HA	1.40	0.86
1:C:1547:ARG:HA	1:C:1550:ILE:HD12	1.57	0.86
1:C:1850:TRP:CZ2	1:C:1859:ALA:HB1	2.10	0.86
1:A:835:VAL:HG11	1:A:844:LEU:HB2	1.58	0.86
1:A:1820:ILE:H	1:A:1821:PRO:HD3	1.40	0.86
1:C:333:ARG:HB3	1:C:373:LEU:HB2	1.55	0.86
1:A:177:ARG:H	1:A:178:VAL:CG2	1.88	0.86
1:A:581:LEU:HA	1:A:583:HIS:H	1.36	0.85
2:B:210:ILE:HD13	2:B:224:THR:CG2	2.06	0.85
1:C:1011:PHE:CD1	1:C:1022:ILE:HG23	2.11	0.85
1:C:1619:ARG:HA	1:C:1626:LEU:HG	1.58	0.85
2:B:210:ILE:HD13	2:B:224:THR:HG23	1.58	0.85
1:C:2145:LEU:HB3	1:C:2146:VAL:HG13	1.59	0.85
1:A:1151:LEU:HB3	1:A:1152:GLY:HA2	1.58	0.85
2:D:26:ARG:HE	2:D:60:ILE:HD12	1.38	0.84
1:A:1151:LEU:HB2	1:A:1152:GLY:HA2	1.57	0.84
1:A:1589:TRP:HE3	1:A:1612:PHE:HE1	1.23	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2064:GLN:HG3	1:C:2065:HIS:CD2	2.13	0.84
1:A:1216:LEU:HA	1:A:1217:PRO:HA	1.59	0.84
1:C:2247:LYS:HA	1:C:2249:ARG:H	1.41	0.84
2:B:127:ASN:HD21	2:B:130:GLU:HB2	1.41	0.84
1:C:634:LEU:HD22	1:C:675:PRO:HG2	1.58	0.84
1:A:1545:ARG:HA	1:A:1548:ILE:HD12	1.60	0.83
1:A:2259:TYR:HA	1:A:2262:SER:HB2	1.58	0.83
1:A:860:ILE:HG22	1:A:863:GLY:HA3	1.59	0.83
1:C:1615:ALA:HB2	1:C:1629:LYS:HE2	1.60	0.83
2:D:14:ILE:HG22	2:D:38:LEU:HD23	1.60	0.83
4:H:120:ASP:HA	4:H:121:TYR:CB	2.08	0.83
1:A:1116:GLU:O	1:C:664:LEU:HB2	1.77	0.83
1:A:177:ARG:H	1:A:178:VAL:HG23	1.41	0.83
2:B:14:ILE:HG22	2:B:38:LEU:HD23	1.60	0.83
1:A:1587:ASP:N	1:A:1588:VAL:HB	1.94	0.83
5:I:647:LYS:HD3	5:I:649:LYS:HE3	1.61	0.83
1:C:1246:LEU:HA	1:C:1276:LEU:HD23	1.59	0.83
2:D:286:ARG:HB3	2:D:288:TYR:OH	1.79	0.83
1:A:1341:ALA:HB3	1:A:1342:GLN:HB2	1.61	0.82
1:C:113:SER:C	1:C:114:LEU:HA	2.00	0.82
1:A:345:LYS:HE3	1:A:349:ILE:HG12	1.61	0.82
1:C:1491:MET:HG3	1:C:1492:LYS:N	1.93	0.82
1:A:124:ARG:HG3	1:A:155:LEU:HD11	1.59	0.82
1:A:331:PHE:HE2	1:A:349:ILE:HG21	1.44	0.82
1:A:2200:LEU:HG	1:A:2471:PHE:HZ	1.45	0.82
1:A:124:ARG:HH21	1:A:170:SER:HB3	1.44	0.82
3:F:507:UNK:C	3:F:508:UNK:HA	2.10	0.81
1:C:721:GLU:HB3	1:C:722:LEU:HB2	1.62	0.81
1:C:1722:GLN:HG2	1:C:1748:ALA:HB1	1.60	0.81
1:A:722:LEU:HA	1:A:760:LEU:HD13	1.63	0.81
1:A:652:VAL:HB	3:F:100:UNK:N	1.95	0.81
2:B:90:MET:N	2:B:104:VAL:HG22	1.95	0.81
1:C:335:LEU:HD23	1:C:338:LEU:HD22	1.63	0.81
1:C:189:MET:HA	1:C:193:ALA:HB3	1.63	0.81
1:A:138:HIS:NE2	1:A:178:VAL:HG12	1.97	0.80
1:C:1414:ALA:HB1	1:C:1442:LEU:HD11	1.64	0.80
1:A:2075:GLU:HA	1:A:2091:LYS:HG2	1.62	0.80
1:C:346:LYS:HA	1:C:349:ASP:HB2	1.62	0.80
1:A:1446:LEU:H	1:A:1447:SER:HB2	1.47	0.80
1:A:1263:SER:HB3	1:A:1268:TYR:CE2	2.17	0.80
1:C:346:LYS:HD3	1:C:350:ILE:CG1	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:726:LEU:HB2	1:C:761:LEU:HB3	1.64	0.80
1:A:366:ARG:HD3	1:A:413:PRO:HB2	1.64	0.80
5:I:757:LYS:HG3	5:I:784:GLN:HG2	1.63	0.80
1:A:1097:LEU:HA	1:A:1100:ILE:HB	1.65	0.79
1:C:2288:ASP:HB3	1:C:2290:ILE:HG13	1.65	0.79
1:A:188:MET:HG3	1:A:236:TYR:HB3	1.63	0.79
2:B:46:LEU:HD22	2:B:68:VAL:HG11	1.64	0.79
1:A:356:TYR:HB3	1:A:365:ARG:HE	1.48	0.79
1:C:569:ASP:HA	1:C:573:LEU:HD12	1.63	0.79
1:A:91:LEU:HD11	1:A:143:SER:HB3	1.64	0.79
1:A:257:TYR:HB3	1:A:258:PRO:C	2.03	0.79
1:C:332:PHE:HZ	1:C:350:ILE:HG12	1.48	0.79
1:A:2426:ARG:O	1:A:2433:GLY:HA2	1.82	0.79
1:C:2061:LEU:O	1:C:2100:VAL:HA	1.82	0.79
1:C:918:PRO:HB3	1:C:1214:VAL:HG21	1.63	0.79
1:A:113:LEU:HB2	1:A:117:VAL:HG22	1.65	0.79
1:A:1814:LEU:HD23	1:A:1819:VAL:HG21	1.65	0.78
1:A:1820:ILE:N	1:A:1821:PRO:HD3	1.97	0.78
1:C:1590:VAL:O	1:C:1594:ILE:HG13	1.83	0.78
1:C:188:VAL:CG1	1:C:234:LYS:HA	2.13	0.78
1:A:2091:LYS:C	1:A:2092:ILE:HA	2.03	0.78
1:C:1454:GLU:O	1:C:1458:THR:HG23	1.84	0.78
1:C:1612:ILE:CG2	1:C:1615:ALA:HB3	2.13	0.78
5:I:785:ASN:HB3	5:I:788:GLU:N	1.98	0.78
1:A:178:VAL:HG11	1:A:190:LEU:HD12	1.65	0.78
1:C:266:ASP:N	1:C:267:ASN:HB2	1.98	0.78
1:C:1496:PRO:HB3	1:C:1525:LEU:HB3	1.64	0.78
1:A:1730:LYS:HB3	1:A:1735:ASN:HB3	1.65	0.78
1:C:337:SER:HB2	1:C:376:LEU:HB2	1.64	0.78
1:A:1588:VAL:O	1:A:1592:ILE:HG12	1.84	0.78
1:A:436:LEU:HA	1:A:439:ASP:HB2	1.65	0.77
1:C:437:LEU:HA	1:C:440:ASP:HB2	1.65	0.77
5:J:699:LYS:HB2	5:J:760:ARG:HB2	1.66	0.77
1:A:1492:GLN:HA	1:A:1493:SER:N	1.99	0.77
1:C:700:ILE:HD12	1:C:718:THR:HG22	1.66	0.77
1:C:983:PHE:HB3	1:C:1022:ILE:CG1	2.12	0.77
1:C:2339:ILE:HA	1:C:2342:GLU:HG2	1.66	0.77
1:A:1083:MET:HB3	1:A:1084:PRO:CD	2.13	0.77
5:I:730:VAL:HG11	5:I:790:PRO:HD2	1.67	0.77
1:C:2007:GLU:HB3	1:C:2065:HIS:HB3	1.65	0.77
1:A:1900:SER:HB3	1:A:1932:ILE:HD12	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1011:PHE:HD1	1:C:1022:ILE:CG2	1.98	0.77
1:A:270:PRO:HB2	1:A:279:ARG:HB2	1.64	0.77
1:A:2425:LYS:HA	1:A:2434:ASN:HD22	1.49	0.77
1:C:1108:ARG:HA	1:C:1150:LEU:HD11	1.66	0.77
1:A:399:LEU:O	1:A:402:ILE:HG23	1.85	0.76
5:J:710:ALA:HB1	5:J:718:LYS:HG2	1.65	0.76
5:I:700:SER:HA	5:I:731:GLU:HB3	1.67	0.76
1:A:2283:LEU:HD21	1:A:2317:ARG:HD3	1.67	0.76
2:B:8:ALA:HB1	2:B:12:HIS:HA	1.66	0.76
1:C:1952:VAL:HA	1:C:1955:GLU:HB2	1.68	0.76
1:A:234:LEU:HD11	1:A:270:PRO:HG3	1.68	0.76
1:A:1110:LYS:HD3	1:A:1148:LEU:HD21	1.67	0.76
1:C:956:CYS:HG	1:C:957:VAL:N	1.83	0.76
1:C:468:ALA:HA	1:C:469:CYS:HA	1.67	0.76
1:C:992:ILE:N	1:C:993:VAL:HA	2.00	0.76
1:C:98:GLN:HA	1:C:101:ALA:HB3	1.66	0.76
5:J:693:PHE:CZ	5:J:760:ARG:HB3	2.21	0.76
1:A:1601:LYS:HB2	1:A:1602:PRO:HD2	1.68	0.75
1:C:261:VAL:HG11	1:C:303:LYS:HD2	1.68	0.75
1:C:1140:ALA:HB1	1:C:1173:GLN:CB	2.15	0.75
1:C:1557:ILE:HD13	1:C:1577:TRP:CZ2	2.22	0.75
5:J:698:ARG:HG3	5:J:788:GLU:HG2	1.65	0.75
1:A:1969:LEU:HB3	1:A:1970:ASP:HA	1.66	0.75
1:A:1848:TRP:HZ2	1:A:1857:ALA:HB1	1.50	0.75
2:B:122:VAL:HG13	2:B:131:LEU:HD11	1.69	0.75
1:A:1215:LYS:HD2	1:A:1249:LEU:HA	1.68	0.75
1:A:367:GLU:HA	1:A:370:ALA:HB3	1.69	0.75
1:C:2222:LEU:HD21	2:D:227:ALA:HB2	1.69	0.75
1:A:391:ILE:HA	1:A:395:TYR:HD2	1.51	0.75
1:C:240:HIS:HA	1:C:241:ALA:C	2.08	0.75
2:B:79:THR:HG1	2:B:95:GLU:N	1.84	0.75
1:A:2161:ILE:HG12	1:A:2266:MET:HB2	1.67	0.74
1:C:395:HIS:HE1	1:C:438:ILE:HG21	1.52	0.74
1:C:1013:PRO:HA	1:C:1022:ILE:O	1.85	0.74
1:C:1111:LYS:HD2	1:C:1149:LEU:HD21	1.68	0.74
1:C:2104:ILE:HA	1:C:2105:SER:HB2	1.68	0.74
1:C:332:PHE:CZ	1:C:350:ILE:HG12	2.21	0.74
1:A:2266:MET:HB2	1:A:2292:VAL:HG21	1.68	0.74
1:C:1100:LYS:HA	1:C:1103:ILE:HB	1.67	0.74
1:C:2131:GLU:HB3	1:C:2132:ASP:N	2.03	0.74
1:C:2263:ARG:HG2	1:C:2339:ILE:HD13	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1971:LEU:HD13	1:C:1991:LEU:HD21	1.70	0.74
2:B:40:ILE:HG23	2:B:47:LEU:HB3	1.70	0.73
1:C:1430:GLU:HB2	1:C:1431:VAL:N	2.02	0.73
1:A:1734:SER:HB3	1:A:1735:ASN:HB2	1.69	0.73
2:B:33:SER:HG	2:B:34:GLN:N	1.87	0.73
4:H:68:GLU:O	4:H:71:LYS:N	2.21	0.73
2:B:12:HIS:CE1	2:B:35:VAL:H	2.07	0.73
1:C:1058:LYS:HD2	1:C:1060:ILE:HD12	1.69	0.73
1:A:2185:PHE:HA	1:A:2188:LEU:HG	1.70	0.73
1:C:1978:PHE:HA	1:C:1983:ASN:HB2	1.71	0.73
1:A:188:MET:HA	1:A:192:ALA:HB3	1.71	0.73
1:A:677:LEU:HG	1:A:726:LYS:HB3	1.71	0.73
1:A:698:ILE:HG23	1:C:1079:TYR:CE2	2.24	0.73
1:A:1060:VAL:HA	1:A:1063:ARG:HD2	1.71	0.73
1:A:1723:TRP:HE1	1:A:1739:ILE:HG23	1.54	0.73
1:A:2061:LEU:HD12	1:A:2097:PRO:HA	1.69	0.73
1:A:2423:VAL:O	1:A:2426:ARG:HB3	1.89	0.72
1:C:2126:VAL:HG12	1:C:2180:TRP:HE3	1.53	0.72
1:C:674:GLN:OE1	1:C:720:LEU:HD22	1.89	0.72
1:C:315:HIS:CD2	1:C:320:ASN:HD21	2.08	0.72
1:C:1140:ALA:HB1	1:C:1173:GLN:HB2	1.69	0.72
1:C:1026:GLU:HG3	1:C:1030:LYS:HE2	1.69	0.72
1:A:1223:LEU:HD13	1:A:1244:ARG:HH22	1.54	0.72
4:H:100:ARG:C	4:H:101:PHE:HA	2.09	0.72
1:A:303:GLN:HB3	1:A:307:ARG:HB2	1.72	0.72
1:A:1440:LEU:HD22	1:A:1622:MET:HG2	1.71	0.72
1:C:842:TYR:HB3	1:C:844:GLU:CG	2.20	0.72
1:C:518:ILE:HG22	1:C:520:ASN:H	1.54	0.72
1:A:673:GLN:HA	1:A:676:ASN:ND2	2.04	0.72
1:A:2223:VAL:HG22	1:A:2459:GLU:HB3	1.71	0.72
1:C:401:LYS:HG3	1:C:403:ILE:HG12	1.72	0.72
1:C:797:TYR:CE2	1:C:844:GLU:HB3	2.25	0.72
1:C:2096:LYS:HA	1:C:2097:PHE:CG	2.25	0.72
2:B:53:GLN:HE21	2:B:94:SER:HB3	1.55	0.71
5:I:703:ILE:HG13	5:I:703:ILE:O	1.89	0.71
1:A:1027:ILE:HG21	1:A:1071:PHE:HA	1.72	0.71
5:J:690:ARG:HG2	5:J:691:ASN:HB2	1.72	0.71
1:A:2325:ALA:HA	1:A:2326:MET:C	2.11	0.71
1:C:235:LEU:HG	1:C:236:GLU:HA	1.71	0.71
1:A:1849:PHE:HB3	1:A:1886:GLN:HG3	1.72	0.71
1:A:704:SER:OG	1:A:714:LEU:HA	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:836:VAL:HG21	1:C:845:LEU:HB2	1.73	0.71
1:C:1505:LEU:HB3	1:C:1514:LYS:HG2	1.73	0.71
1:A:284:VAL:HG22	1:A:334:LEU:HD11	1.72	0.71
1:C:947:HIS:HA	1:C:950:GLN:HB2	1.72	0.71
1:A:1630:ASN:HA	1:A:1633:LEU:HD13	1.72	0.70
1:C:674:GLN:HB3	1:C:720:LEU:HB3	1.72	0.70
1:A:856:ASN:HB3	1:A:1584:LYS:HG2	1.73	0.70
1:A:1151:LEU:HB2	1:A:1152:GLY:CA	2.21	0.70
1:C:242:ALA:HA	1:C:245:ILE:HB	1.73	0.70
1:A:845:LEU:HG	1:A:1525:VAL:HG23	1.73	0.70
1:C:2145:LEU:CB	1:C:2146:VAL:HG13	2.22	0.70
1:C:797:TYR:HE2	1:C:844:GLU:HB3	1.55	0.70
1:C:1451:LEU:O	1:C:1455:LYS:N	2.16	0.70
1:C:2077:GLU:HA	1:C:2093:LYS:HG2	1.74	0.70
2:D:201:THR:HB	2:D:203:PHE:HE1	1.54	0.70
1:A:797:LEU:O	1:A:800:LEU:HB2	1.90	0.70
1:C:89:PHE:HA	1:C:101:ALA:HB2	1.71	0.70
1:C:260:TYR:HE1	1:C:300:ALA:HB1	1.56	0.70
1:C:490:CYS:HB3	1:C:491:PRO:HD3	1.74	0.70
1:C:777:SER:HA	1:C:780:LEU:HB3	1.71	0.70
1:A:142:SER:HA	1:A:145:LYS:HE3	1.74	0.70
1:A:2035:LEU:HD21	5:I:648:LYS:HE2	1.72	0.70
1:A:2053:LEU:HG	1:A:2056:LEU:HD22	1.73	0.70
1:C:157:ILE:HG12	1:C:172:ARG:HH22	1.55	0.70
1:C:336:LEU:HD22	1:C:342:TYR:HB3	1.74	0.70
5:J:730:VAL:HG21	5:J:789:THR:HA	1.72	0.70
1:C:1832:ILE:HD13	1:C:1837:SER:HB3	1.72	0.70
1:C:1920:ILE:HD13	1:C:1935:ILE:HD11	1.74	0.70
1:A:702:LEU:HD23	1:A:713:SER:HB3	1.74	0.70
1:C:1409:GLN:H	1:C:1410:ARG:HB3	1.56	0.69
1:A:91:LEU:HD11	1:A:143:SER:CB	2.21	0.69
1:A:841:TYR:CB	1:A:843:GLU:HG2	2.09	0.69
1:C:1983:ASN:HB3	1:C:1986:LYS:HB3	1.73	0.69
2:B:253:VAL:HB	2:B:267:THR:HG23	1.73	0.69
1:C:1097:SER:HG	1:C:1098:LEU:N	1.91	0.69
1:C:1718:CYS:HB2	1:C:1759:TRP:CH2	2.26	0.69
1:A:1503:LEU:HB3	1:A:1512:LYS:HG2	1.73	0.69
1:A:394:HIS:HB2	1:A:395:TYR:CG	2.27	0.69
1:A:1380:THR:HA	1:A:1383:ALA:HB3	1.75	0.69
1:A:1555:ILE:HG13	1:A:1556:ILE:H	1.57	0.69
1:C:329:LEU:HD21	1:C:357:TYR:CD2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1088:VAL:HA	1:C:1100:LYS:HD2	1.73	0.69
1:C:1818:HIS:HA	1:C:1821:VAL:H	1.58	0.69
1:C:2031:SER:HG	1:C:2032:LYS:N	1.90	0.69
1:A:180:ILE:HG22	1:A:223:LEU:CD1	2.22	0.69
2:D:278:ASP:HB3	2:D:281:THR:HB	1.75	0.69
1:A:187:VAL:HG11	1:A:233:LYS:HA	1.73	0.69
1:C:179:VAL:HG11	1:C:191:LEU:HD13	1.74	0.69
1:C:1070:VAL:HG11	1:C:1109:LEU:HD23	1.74	0.69
2:D:83:PHE:CE1	2:D:104:VAL:HG21	2.27	0.69
1:A:296:ARG:HH11	1:A:338:LYS:HG2	1.58	0.69
1:A:361:PHE:HE1	1:A:414:PHE:CZ	2.10	0.69
1:A:1082:ILE:HG23	1:A:1085:ILE:HG12	1.74	0.69
1:A:1415:ALA:HA	1:A:1418:GLU:HB2	1.74	0.69
1:C:280:ARG:HH12	1:C:328:THR:HB	1.58	0.69
1:C:688:GLU:C	1:C:691:GLY:H	1.97	0.69
5:I:730:VAL:HB	5:I:788:GLU:O	1.92	0.69
1:C:681:LEU:HD11	1:C:724:THR:HG22	1.75	0.69
1:A:1668:ALA:HA	1:A:1671:GLN:HB2	1.74	0.69
1:A:2184:THR:HB	1:A:2284:MET:HB2	1.75	0.69
1:C:1612:ILE:HG23	1:C:1615:ALA:CB	2.22	0.69
1:C:260:TYR:CE1	1:C:300:ALA:HB1	2.28	0.68
1:C:628:GLN:O	1:C:631:VAL:HG22	1.92	0.68
1:C:818:ARG:HD2	1:C:868:LEU:HD13	1.76	0.68
1:C:2193:GLU:HA	1:C:2196:GLU:HB2	1.76	0.68
1:C:2319:ARG:HG2	1:C:2470:TRP:HZ3	1.58	0.68
1:C:378:ALA:HA	1:C:379:PHE:N	2.08	0.68
1:C:334:GLU:HG3	1:C:372:ILE:HD12	1.75	0.68
2:D:120:ASN:HD21	2:D:136:ARG:HA	1.59	0.68
1:A:453:LYS:N	1:A:454:GLN:HA	2.08	0.68
1:A:533:SER:HA	1:A:534:ASN:C	2.14	0.68
2:B:217:SER:HG	2:B:218:ASP:N	1.92	0.68
1:C:1421:LYS:HE2	1:C:1435:LYS:HD2	1.76	0.68
1:C:2186:THR:HA	1:C:2286:MET:HA	1.75	0.68
2:B:53:GLN:HG3	2:B:78:VAL:HG13	1.75	0.68
1:C:783:LEU:H	1:C:784:GLY:HA3	1.57	0.68
1:C:1474:ALA:HA	1:C:1478:LEU:H	1.57	0.68
2:B:12:HIS:HB3	2:B:30:HIS:O	1.93	0.68
1:A:300:LEU:HA	1:A:303:GLN:HB2	1.75	0.68
1:A:841:TYR:HB2	1:A:843:GLU:CG	2.10	0.68
1:A:2411:HIS:HA	1:A:2414:ALA:HB3	1.76	0.68
5:J:694:THR:C	5:J:696:LYS:H	1.97	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:ARG:HD3	1:A:453:LYS:HB2	1.76	0.68
1:C:115:ALA:HB1	1:C:161:LEU:HB2	1.76	0.68
1:A:2211:ALA:HB2	1:A:2225:VAL:HG21	1.76	0.68
1:C:1533:LEU:C	1:C:1534:VAL:HA	2.14	0.68
2:D:232:ARG:HG2	2:D:245:THR:HA	1.76	0.68
1:A:1087:VAL:HB	1:A:1102:ILE:HG21	1.76	0.67
1:A:2315:PRO:HB3	1:A:2451:LEU:HB3	1.77	0.67
1:C:1611:ARG:C	1:C:1613:LYS:H	1.96	0.67
1:C:2409:VAL:N	1:C:2410:GLU:HG2	2.09	0.67
1:A:627:GLN:O	1:A:630:VAL:HG12	1.94	0.67
1:A:1516:HIS:HA	1:A:1519:ASN:HB2	1.75	0.67
1:A:1159:VAL:HG21	1:C:622:LYS:HD3	1.75	0.67
1:C:2142:LEU:HD11	1:C:2362:PHE:CE2	2.28	0.67
1:C:2370:TRP:N	1:C:2371:GLY:HA3	2.10	0.67
1:A:314:HIS:HD2	1:A:328:LEU:HD11	1.60	0.67
1:A:1906:HIS:HA	1:A:1908:GLN:HB3	1.76	0.67
5:I:685:SER:HB3	5:I:686:LYS:HB2	1.77	0.67
1:A:1573:GLU:O	1:A:1577:THR:N	2.27	0.67
1:C:1920:ILE:HG12	1:C:1932:LEU:HG	1.74	0.67
2:D:10:TYR:HE2	2:D:293:LYS:HG3	1.60	0.67
1:A:835:VAL:HG13	1:A:1525:VAL:HG11	1.76	0.67
1:C:1542:TYR:H	1:C:1543:ASN:HA	1.58	0.67
2:B:5:LEU:HA	2:B:6:VAL:N	2.10	0.67
1:C:268:ILE:HG23	1:C:311:GLN:HG3	1.77	0.67
1:C:1844:LEU:HB2	1:C:2358:ILE:HG21	1.77	0.67
1:A:396:LEU:HD23	1:A:400:LYS:HG2	1.76	0.67
1:A:1558:TYR:HA	1:A:1562:PRO:HD2	1.77	0.67
1:C:1382:THR:HA	1:C:1385:ALA:HB3	1.77	0.66
1:C:961:ASP:HB3	1:C:965:PRO:HG2	1.77	0.66
1:C:2354:SER:HA	1:C:2356:MET:H	1.60	0.66
1:A:650:ASP:N	1:A:651:PRO:HD3	2.04	0.66
1:A:2363:ASP:HB2	1:A:2367:ASN:O	1.96	0.66
1:A:257:TYR:CG	1:A:286:LEU:HD11	2.31	0.66
2:B:22:GLY:HA3	2:B:286:ARG:HD3	1.76	0.66
2:B:255:ASP:OD1	2:B:297:CYS:HA	1.95	0.66
1:C:188:VAL:HA	1:C:192:ALA:HB3	1.76	0.66
1:A:704:SER:HG	1:A:714:LEU:HA	1.60	0.66
1:A:855:GLU:O	1:A:1588:VAL:HG22	1.94	0.66
1:A:1228:TYR:HE1	1:A:1293:GLU:HB2	1.61	0.66
1:C:271:PRO:HG2	1:C:280:ARG:HB2	1.78	0.66
1:C:418:VAL:HB	1:C:419:SER:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:ALA:HA	1:A:698:ILE:HB	1.76	0.66
1:A:2283:LEU:HD21	1:A:2317:ARG:CD	2.25	0.66
1:C:2374:LEU:HD21	1:C:2417:ILE:HD12	1.78	0.66
1:A:178:VAL:HB	1:A:179:LEU:HG	1.78	0.66
1:A:179:LEU:HD13	1:A:233:LYS:HE3	1.76	0.66
1:A:1020:ILE:HG21	1:A:1024:ILE:HB	1.78	0.66
1:A:1918:ILE:HG12	1:A:1930:LEU:HG	1.78	0.66
2:D:205:ALA:HB3	2:D:206:HIS:HB2	1.78	0.66
2:D:229:HIS:CB	2:D:251:ARG:HB2	2.25	0.66
1:A:664:GLY:HA2	1:A:671:LEU:HG	1.77	0.66
1:A:2251:THR:HA	1:A:2254:GLU:HB3	1.75	0.66
1:C:181:ILE:HG22	1:C:228:ASN:HD21	1.60	0.66
1:C:188:VAL:HG11	1:C:234:LYS:HA	1.76	0.66
1:C:1056:SER:HG	1:C:1057:ASN:N	1.94	0.66
1:C:1440:TYR:HE1	1:C:1473:GLY:HA3	1.61	0.66
1:A:197:ARG:C	1:A:199:THR:HG23	2.16	0.66
1:A:687:GLU:C	1:A:690:GLY:H	1.99	0.66
1:C:268:ILE:CG2	1:C:311:GLN:HG3	2.26	0.66
1:A:835:VAL:HG21	1:A:844:LEU:H	1.61	0.66
1:C:90:ASP:HB3	1:C:91:LYS:HG2	1.77	0.66
1:C:2114:CYS:HB3	1:C:2123:TYR:C	2.17	0.66
1:A:391:ILE:HA	1:A:395:TYR:CD2	2.31	0.65
1:A:1848:TRP:CZ2	1:A:1857:ALA:HB1	2.30	0.65
1:A:1858:THR:HA	1:A:1862:HIS:HB3	1.78	0.65
1:A:2078:VAL:HG22	1:A:2089:ILE:HG23	1.78	0.65
2:D:297:CYS:CA	2:D:298:VAL:HB	2.15	0.65
1:A:2407:VAL:HG13	1:A:2408:GLU:OE1	1.97	0.65
2:B:216:SER:HG	2:B:221:HIS:N	1.95	0.65
1:C:1505:LEU:HB3	1:C:1514:LYS:CG	2.26	0.65
2:B:3:VAL:HG11	2:B:19:ALA:HB3	1.79	0.65
1:C:1284:CYS:SG	1:C:1288:LEU:HB3	2.36	0.65
1:C:2114:CYS:HB2	1:C:2122:ASP:HB3	1.78	0.65
2:D:272:HIS:HA	2:D:293:LYS:O	1.95	0.65
1:A:280:LEU:O	1:A:283:ALA:N	2.30	0.65
1:A:2261:ARG:HG2	1:A:2337:ILE:HD13	1.78	0.65
1:C:572:ILE:HG22	1:C:573:LEU:HG	1.78	0.65
2:D:33:SER:CB	2:D:51:GLY:HA2	2.27	0.65
1:A:259:TYR:CD1	1:A:260:VAL:HG23	2.32	0.65
1:A:632:ALA:HA	1:A:635:SER:HB2	1.77	0.65
1:A:2286:ASP:HB3	1:A:2288:ILE:HG13	1.79	0.65
1:C:1248:ILE:HG12	1:C:1260:ARG:HH12	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:TYR:N	1:A:293:ILE:HA	2.12	0.65
1:A:1723:TRP:NE1	1:A:1739:ILE:HG23	2.11	0.65
1:C:2015:GLY:HA2	1:C:2018:LEU:HG	1.79	0.65
1:A:345:LYS:O	1:A:372:LEU:HD21	1.96	0.65
2:D:101:VAL:HG11	2:D:143:TRP:CH2	2.31	0.65
1:A:682:MET:O	1:A:685:ASN:HB2	1.97	0.64
1:A:2432:THR:H	1:A:2447:GLN:NE2	1.95	0.64
1:C:402:ASN:HA	1:C:414:PRO:HG3	1.80	0.64
1:C:662:GLN:HE22	1:C:677:ASN:HA	1.60	0.64
1:C:1007:VAL:HG13	1:C:1009:ARG:CZ	2.27	0.64
1:C:1575:GLU:O	1:C:1579:THR:N	2.30	0.64
2:D:216:SER:HG	2:D:221:HIS:N	1.94	0.64
1:C:1495:SER:HG	1:C:1498:LYS:N	1.94	0.64
1:C:1954:HIS:HA	1:C:1957:ILE:HG22	1.78	0.64
5:J:694:THR:HG22	5:J:696:LYS:HB2	1.78	0.64
1:A:854:THR:HB	1:A:1579:LEU:HB2	1.80	0.64
1:A:2095:PHE:HB2	1:A:2096:GLU:N	2.11	0.64
1:C:533:GLN:C	1:C:535:ASN:H	2.00	0.64
1:C:1725:TRP:HE1	1:C:1741:ILE:HG22	1.63	0.64
1:A:360:LYS:HE2	1:A:365:ARG:HH22	1.62	0.64
1:A:1627:LYS:O	1:A:1630:ASN:N	2.31	0.64
1:C:601:ILE:HG12	1:C:603:HIS:HB2	1.79	0.64
1:C:1510:ASN:ND2	4:G:73:PHE:HA	2.12	0.64
1:A:1517:ILE:HG12	1:A:1553:GLU:HB3	1.78	0.64
1:A:1559:LYS:N	1:A:1572:ARG:HH22	1.95	0.64
1:A:1041:GLU:HA	1:A:1044:THR:HG22	1.80	0.64
1:A:1453:LYS:HE3	1:A:1465:MET:CE	2.28	0.64
5:I:740:SER:HB2	5:I:768:SER:HA	1.80	0.64
1:A:633:LEU:HA	1:A:636:VAL:HB	1.79	0.64
1:A:742:CYS:HB2	1:A:743:THR:OG1	1.97	0.64
1:C:2374:LEU:HB3	1:C:2375:PRO:HD3	1.79	0.64
2:D:201:THR:HB	2:D:203:PHE:CE1	2.32	0.64
1:A:1963:GLU:HG2	1:A:2056:LEU:HD21	1.80	0.64
1:C:2244:LEU:HD11	1:C:2328:MET:HA	1.79	0.64
1:A:331:PHE:HZ	1:A:345:LYS:HE2	1.63	0.63
1:A:1829:SER:HG	1:A:1830:ILE:N	1.96	0.63
1:C:1725:TRP:NE1	1:C:1741:ILE:HG22	2.13	0.63
1:A:613:LEU:HA	1:A:616:CYS:HB3	1.80	0.63
1:A:856:ASN:HA	1:A:1584:LYS:HA	1.80	0.63
1:A:124:ARG:NH2	1:A:170:SER:HB3	2.12	0.63
1:A:1291:TYR:HE1	1:A:1340:TYR:HE2	1.45	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1837:SER:HG	1:A:1839:GLN:N	1.96	0.63
1:C:188:VAL:HG13	1:C:234:LYS:HA	1.79	0.63
1:C:948:ILE:HG13	1:C:952:LEU:HD13	1.81	0.63
5:J:730:VAL:HG11	5:J:790:PRO:HD2	1.81	0.63
1:A:2259:TYR:HA	1:A:2262:SER:CB	2.26	0.63
1:A:1617:ARG:HA	1:A:1624:LEU:HD22	1.81	0.63
1:C:1758:ALA:HA	1:C:1761:ASN:HD22	1.62	0.63
1:A:1969:LEU:HD13	1:A:1989:LEU:HD21	1.80	0.63
1:A:2266:MET:HA	1:A:2269:THR:HB	1.79	0.63
1:C:115:ALA:C	1:C:117:GLU:H	2.02	0.63
1:C:1965:GLU:OE1	1:C:2054:GLN:HG3	1.99	0.63
2:B:55:VAL:HA	2:B:81:VAL:HG21	1.80	0.63
1:C:453:ARG:HD3	1:C:454:LYS:HB2	1.81	0.63
5:I:678:LEU:HD21	5:I:688:TYR:CE2	2.34	0.63
1:C:309:LEU:HA	1:C:346:LYS:HZ1	1.63	0.63
1:C:1978:PHE:HB2	1:C:1987:MET:HB2	1.79	0.62
1:C:1983:ASN:HD22	1:C:1987:MET:HG3	1.64	0.62
1:C:2141:GLN:C	1:C:2142:LEU:HA	2.19	0.62
1:C:2433:LEU:HD22	1:C:2449:GLN:HA	1.81	0.62
3:E:404:UNK:O	3:E:408:UNK:N	2.27	0.62
1:C:825:LEU:HA	1:C:828:LEU:HB2	1.81	0.62
1:C:1119:SER:HG	1:C:1120:SER:N	1.97	0.62
1:C:1440:TYR:HD1	1:C:1445:TRP:HE1	1.45	0.62
3:E:401:UNK:C	3:E:402:UNK:HA	2.29	0.62
5:I:655:SER:HA	5:I:659:LEU:CB	2.29	0.62
5:I:707:ILE:HD13	5:I:728:LEU:HG	1.80	0.62
1:C:379:PHE:HB2	1:C:381:PRO:HD2	1.80	0.62
1:C:849:LEU:HD22	1:C:1549:GLN:HB3	1.82	0.62
1:A:341:TYR:CE2	1:A:345:LYS:HE2	2.35	0.62
1:C:865:THR:HA	1:C:868:LEU:HD12	1.81	0.62
1:A:1555:ILE:HD13	1:A:1575:TRP:CZ2	2.34	0.62
1:A:1566:ASP:HB3	1:A:1568:ARG:HG3	1.81	0.62
2:B:232:ARG:HG2	2:B:245:THR:HA	1.79	0.62
1:C:1429:VAL:HB	1:C:1435:LYS:HZ2	1.64	0.62
5:I:655:SER:HA	5:I:659:LEU:HB2	1.81	0.62
1:A:2059:LEU:HD21	1:A:2099:PHE:HB2	1.81	0.62
1:C:181:ILE:H	1:C:182:PRO:N	1.96	0.62
1:C:305:TRP:HE1	1:C:341:PRO:HG2	1.64	0.62
1:C:670:PRO:HD2	1:C:671:GLN:N	2.14	0.62
1:C:760:ILE:HG13	1:C:761:LEU:HA	1.82	0.62
1:C:1956:LEU:HD21	1:C:2127:LEU:HD22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:VAL:HG11	1:A:232:SER:O	1.99	0.62
1:A:600:ILE:H	1:A:602:HIS:HB2	1.64	0.62
1:A:2043:TYR:HB3	1:A:2047:ARG:HH12	1.63	0.62
1:A:593:ARG:O	1:A:597:ILE:N	2.33	0.62
1:A:849:ILE:HB	1:A:1551:GLU:N	2.15	0.62
1:A:993:LYS:HA	1:A:994:GLN:HB2	1.80	0.62
1:A:1555:ILE:HG13	1:A:1556:ILE:N	2.15	0.62
1:A:2457:SER:HA	1:A:2458:VAL:HA	1.82	0.62
5:J:701:SER:H	5:J:702:THR:HB	1.65	0.62
1:A:300:LEU:HD13	1:A:303:GLN:HB2	1.81	0.62
1:A:499:LEU:HA	1:A:502:LEU:HB2	1.81	0.62
1:A:845:LEU:HD22	1:A:1547:GLN:HG3	1.80	0.62
1:C:764:ILE:HA	1:C:806:ILE:HG21	1.80	0.62
1:C:1274:ARG:HB2	1:C:1327:HIS:HE1	1.64	0.62
2:D:254:TRP:CD1	2:D:296:VAL:HA	2.35	0.62
1:A:1291:TYR:HE1	1:A:1340:TYR:CE2	2.17	0.62
1:A:1371:ILE:CD1	1:A:1387:LEU:HG	2.28	0.62
1:A:1634:GLU:HG3	1:A:1651:VAL:HG11	1.82	0.62
1:A:1820:ILE:N	1:A:1821:PRO:CD	2.63	0.62
1:A:2078:VAL:N	1:A:2090:VAL:O	2.32	0.62
1:C:221:TRP:HA	1:C:235:LEU:HD13	1.82	0.62
1:C:355:MET:SD	1:C:389:LEU:HD13	2.40	0.62
1:A:1592:ILE:HD12	1:A:1596:ARG:HD3	1.82	0.61
1:A:2301:PHE:N	1:A:2374:THR:HG1	1.98	0.61
1:C:1218:PRO:HB2	1:C:1221:GLN:HB2	1.81	0.61
1:A:517:ILE:HG22	1:A:519:ASN:H	1.65	0.61
1:C:793:GLU:HG3	1:C:795:THR:OG1	2.00	0.61
1:C:1964:HIS:NE2	1:C:2008:ILE:HA	2.15	0.61
1:C:2062:GLU:HG2	1:C:2064:GLN:H	1.64	0.61
1:A:443:GLU:HB3	1:A:446:ARG:HH11	1.64	0.61
1:A:280:LEU:HA	1:A:330:VAL:CG2	2.26	0.61
1:A:776:SER:HA	1:A:779:LEU:HB3	1.81	0.61
1:A:1224:LYS:HB2	1:A:1241:TRP:CE2	2.36	0.61
1:C:203:GLY:HA2	1:C:206:LEU:HB3	1.82	0.61
1:C:351:TYR:HH	1:C:386:LYS:N	1.98	0.61
2:B:210:ILE:HD13	2:B:224:THR:HG22	1.82	0.61
1:C:1557:ILE:CG2	1:C:1577:TRP:HE1	2.13	0.61
1:C:2096:LYS:HA	1:C:2097:PHE:CB	2.30	0.61
2:B:233:VAL:O	2:B:243:GLU:HB3	1.99	0.61
1:C:264:ILE:O	1:C:268:ILE:HB	2.00	0.61
1:C:938:HIS:HE1	1:C:978:GLN:HA	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1295:ASP:CG	1:C:1342:TYR:OH	2.38	0.61
5:J:730:VAL:HG21	5:J:790:PRO:HD2	1.81	0.61
1:A:1592:ILE:HB	1:A:1596:ARG:HB3	1.82	0.61
1:C:2185:ASP:O	1:C:2287:LEU:HG	2.01	0.61
1:C:2354:SER:HA	1:C:2356:MET:N	2.15	0.61
1:A:331:PHE:HZ	1:A:345:LYS:CE	2.13	0.61
1:A:1084:PRO:HG2	1:A:1117:MET:SD	2.41	0.61
2:B:127:ASN:ND2	2:B:130:GLU:HB2	2.14	0.61
1:C:1074:PRO:HA	1:C:1075:ASN:HB2	1.81	0.61
1:C:1151:GLN:HA	1:C:1151:GLN:NE2	2.15	0.61
1:C:1391:HIS:HB2	1:C:2334:GLU:HG2	1.81	0.61
1:A:345:LYS:HG3	1:A:349:ILE:CG1	2.31	0.61
1:C:213:PHE:O	1:C:217:THR:N	2.33	0.61
1:C:265:LEU:CA	1:C:307:GLN:HB3	2.20	0.61
1:C:630:SER:O	1:C:634:LEU:HG	2.01	0.61
1:A:346:TYR:OH	1:A:382:ILE:HG13	2.00	0.61
1:A:360:LYS:HE2	1:A:365:ARG:NH2	2.16	0.61
1:C:1591:TRP:HE3	1:C:1614:PHE:HE1	1.49	0.61
1:C:1906:LYS:C	1:C:1909:PRO:HD3	2.21	0.61
1:C:2268:MET:HA	1:C:2271:THR:HB	1.81	0.61
2:D:183:CYS:SG	2:D:213:ILE:HG21	2.41	0.61
1:A:835:VAL:HB	1:A:844:LEU:HD23	1.83	0.60
2:D:9:GLY:O	2:D:12:HIS:CE1	2.54	0.60
3:E:408:UNK:C	3:E:410:UNK:H	2.13	0.60
1:C:766:PRO:HG3	1:C:809:PHE:HB3	1.83	0.60
1:C:1140:ALA:HB1	1:C:1173:GLN:HB3	1.83	0.60
1:C:1938:MET:HB3	1:C:1946:VAL:HG11	1.82	0.60
1:A:182:SER:HB3	1:A:187:VAL:HG23	1.81	0.60
1:A:324:VAL:HG22	1:A:327:THR:CG2	2.31	0.60
2:B:182:ASN:HA	2:B:183:CYS:HB2	1.82	0.60
1:C:681:LEU:HD22	1:C:728:PHE:HD1	1.66	0.60
1:C:1661:LEU:HG	1:C:1666:LEU:HB2	1.83	0.60
5:I:759:ASP:HB2	5:I:761:LYS:H	1.66	0.60
1:A:1679:MET:HA	1:A:1682:ASP:HB2	1.84	0.60
1:C:173:LEU:HD21	1:C:209:ASP:HA	1.81	0.60
3:E:214:UNK:C	3:E:215:UNK:H2	2.13	0.60
5:J:699:LYS:HD3	5:J:760:ARG:HD2	1.84	0.60
1:A:699:ILE:HG23	1:A:717:THR:HG22	1.82	0.60
1:A:1716:CYS:HB2	1:A:1757:TRP:CH2	2.37	0.60
1:C:235:LEU:CG	1:C:236:GLU:HA	2.31	0.60
1:C:1389:LEU:HD11	1:C:1403:THR:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1625:ALA:O	1:C:1626:LEU:N	2.34	0.60
1:C:2026:MET:HG3	1:C:2027:ASN:H	1.66	0.60
2:D:206:HIS:CD2	2:D:224:THR:HG22	2.36	0.60
1:A:381:ALA:HB1	1:A:385:LYS:HD3	1.84	0.60
1:A:2132:ARG:HA	1:A:2135:SER:HB2	1.83	0.60
2:B:99:ILE:HD13	2:B:122:VAL:HG21	1.82	0.60
1:C:285:VAL:HG22	1:C:335:LEU:CD1	2.31	0.60
1:C:1025:ILE:HA	1:C:1028:ILE:HG12	1.82	0.60
1:A:1885:HIS:HA	1:A:1886:GLN:N	2.17	0.60
1:A:2336:ARG:HA	1:A:2339:CYS:HB2	1.83	0.60
2:B:246:LEU:HD11	2:B:282:ARG:O	2.02	0.60
1:C:181:ILE:HG22	1:C:224:LEU:HD13	1.82	0.60
1:C:767:LYS:HB3	1:C:772:SER:HA	1.83	0.60
2:D:100:LYS:HA	2:D:101:VAL:HG12	1.83	0.60
1:C:1881:GLN:HG2	1:C:2134:ARG:HH21	1.65	0.60
2:D:37:ARG:HH22	2:D:212:ARG:HH22	1.48	0.60
1:A:1139:ALA:HB1	1:A:1172:GLN:OE1	2.02	0.60
2:B:206:HIS:CE1	2:B:226:SER:HB2	2.37	0.60
1:C:2063:LEU:H	1:C:2066:VAL:H	1.50	0.60
1:C:2407:GLN:O	1:C:2409:VAL:N	2.34	0.60
5:J:730:VAL:CG2	5:J:789:THR:HA	2.32	0.60
1:A:2238:LEU:HB3	1:A:2326:MET:H	1.67	0.60
1:C:997:ILE:HA	1:C:1000:HIS:HD2	1.67	0.60
1:A:683:ALA:HA	1:A:688:ILE:HD13	1.84	0.59
1:A:1283:CYS:HA	1:A:1287:LEU:N	2.17	0.59
1:A:2187:VAL:HA	1:A:2190:ARG:HG2	1.84	0.59
1:A:2266:MET:CB	1:A:2292:VAL:HG21	2.32	0.59
1:C:1541:ALA:CB	1:C:1542:TYR:HA	2.32	0.59
1:C:2062:GLU:CA	1:C:2063:LEU:HB2	2.28	0.59
3:E:607:UNK:HA	3:E:608:UNK:C	2.32	0.59
1:A:233:LYS:HE2	1:A:237:ARG:HG2	1.83	0.59
1:A:314:HIS:HB2	1:A:328:LEU:HD21	1.85	0.59
1:A:347:ASP:N	1:A:348:ASP:HB2	2.17	0.59
1:A:1600:ILE:HG13	1:A:1601:LYS:H	1.65	0.59
1:C:1578:ASN:C	1:C:1579:THR:N	2.55	0.59
1:C:1612:ILE:HG21	1:C:1656:ALA:HB1	1.83	0.59
1:C:176:TYR:CE1	1:C:191:LEU:HD22	2.37	0.59
1:A:569:ALA:O	1:A:573:ILE:HG13	2.03	0.59
1:A:1945:ASP:HA	1:A:1948:GLU:HB2	1.85	0.59
1:C:280:ARG:HH22	1:C:328:THR:HB	1.68	0.59
1:C:801:LEU:HD23	1:C:805:ILE:HD11	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1474:ALA:HB1	1:C:1478:LEU:HD23	1.84	0.59
1:C:1661:LEU:O	1:C:1666:LEU:N	2.35	0.59
1:A:824:LEU:CD2	1:A:1534:GLU:HB2	2.31	0.59
2:B:276:LEU:O	2:B:286:ARG:N	2.35	0.59
1:C:2064:GLN:HG3	1:C:2065:HIS:HD2	1.64	0.59
1:C:2247:LYS:HA	1:C:2249:ARG:N	2.16	0.59
5:J:674:GLU:HB2	5:J:693:PHE:CE2	2.37	0.59
1:A:818:ASP:HA	1:A:821:LEU:HB3	1.83	0.59
1:A:864:THR:HG23	1:A:867:LEU:HD12	1.84	0.59
1:A:1320:VAL:HG22	1:A:1345:HIS:CE1	2.38	0.59
1:A:1423:GLY:HA3	1:A:1424:GLU:HG3	1.84	0.59
1:C:1674:LEU:O	1:C:1678:THR:N	2.36	0.59
1:C:1844:LEU:HD11	1:C:1878:VAL:HG11	1.84	0.59
1:C:2024:TRP:HB2	1:C:2039:GLN:HG2	1.85	0.59
2:D:17:TRP:HZ2	2:D:290:GLY:HA3	1.67	0.59
1:A:211:GLU:HG3	1:A:211:GLU:O	2.01	0.59
1:A:300:LEU:HD12	1:A:339:ALA:HB2	1.85	0.59
1:A:419:ILE:HG21	1:A:462:CYS:HB3	1.85	0.59
1:A:732:LYS:HB3	1:A:735:GLU:HB2	1.84	0.59
1:A:2079:PRO:HD3	1:A:2090:VAL:HG13	1.83	0.59
1:A:2394:LEU:HD21	1:A:2404:VAL:HG13	1.83	0.59
1:C:1757:LYS:HA	1:C:1832:ILE:HG21	1.85	0.59
1:C:2080:VAL:HA	1:C:2092:VAL:HG12	1.84	0.59
1:A:2204:HIS:CE1	1:A:2470:PRO:HD2	2.37	0.59
1:A:2242:LEU:HD11	1:A:2326:MET:HA	1.83	0.59
2:B:229:HIS:HD2	2:B:252:TRP:H	1.50	0.59
1:A:594:LEU:HD23	1:A:597:ILE:HD12	1.84	0.59
1:A:1049:ILE:HD12	1:A:1064:ILE:HG12	1.85	0.59
1:C:188:VAL:CG2	1:C:233:SER:HB3	2.31	0.59
1:C:2062:GLU:O	1:C:2065:HIS:HB2	2.03	0.59
1:A:194:THR:HG22	1:A:197:ARG:HH21	1.68	0.58
1:A:260:VAL:HG22	1:A:303:GLN:HE21	1.68	0.58
1:A:336:SER:HB2	1:A:375:LEU:HB2	1.85	0.58
1:A:688:ILE:HG13	1:A:689:PHE:N	2.18	0.58
1:A:1054:GLN:HE21	1:A:1057:LYS:HG2	1.68	0.58
1:A:1178:GLN:HA	1:A:1181:ASN:HB2	1.83	0.58
1:A:1232:GLN:O	1:A:1233:LYS:HB2	2.03	0.58
1:C:353:SER:HB3	1:C:357:TYR:CE2	2.38	0.58
1:C:2258:ARG:O	1:C:2262:THR:N	2.36	0.58
1:A:515:SER:O	1:A:518:LEU:HG	2.03	0.58
1:C:1294:GLU:HA	1:C:1295:ASP:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1494:GLN:HA	1:C:1495:SER:N	2.19	0.58
1:A:241:ALA:HA	1:A:244:ILE:HB	1.83	0.58
1:A:554:SER:H	1:A:555:PHE:HB2	1.66	0.58
1:A:2060:GLU:HG2	1:A:2097:PRO:C	2.23	0.58
1:C:116:ARG:NH2	1:C:156:LEU:HD23	2.18	0.58
1:C:260:TYR:H	1:C:260:TYR:HD2	1.50	0.58
1:C:651:ASP:HB3	1:C:652:PRO:HA	1.85	0.58
1:C:1430:GLU:HA	1:C:1458:THR:HG22	1.85	0.58
1:A:353:THR:OG1	1:A:368:VAL:HG12	2.03	0.58
1:A:1273:ARG:HE	1:A:1277:ASN:HD22	1.49	0.58
1:C:857:ASN:HB3	1:C:1586:LYS:CA	2.27	0.58
1:C:2080:VAL:HG12	1:C:2083:THR:HB	1.84	0.58
1:A:445:LEU:HG	1:A:449:PHE:CE2	2.39	0.58
1:A:1574:THR:HG22	1:A:1578:ARG:HB2	1.86	0.58
1:A:2425:LYS:HA	1:A:2434:ASN:ND2	2.16	0.58
1:C:471:LEU:HD13	1:C:475:PHE:HB2	1.84	0.58
1:C:710:TYR:N	1:C:714:SER:HG	2.01	0.58
1:C:1373:ILE:HD13	1:C:1389:LEU:HD23	1.84	0.58
1:C:1384:SER:HB3	1:C:2335:GLY:HA3	1.84	0.58
1:C:1451:LEU:O	1:C:1454:GLU:N	2.37	0.58
1:C:1914:TYR:O	1:C:1918:VAL:HG23	2.03	0.58
1:A:276:LEU:HB3	1:A:279:ARG:HH21	1.68	0.58
1:C:2446:VAL:O	1:C:2450:VAL:HB	2.03	0.58
1:A:187:VAL:HA	1:A:191:ALA:HB3	1.85	0.58
1:A:1870:ILE:HG22	1:A:1873:TRP:N	2.17	0.58
2:B:105:ARG:O	2:B:106:SER:HB2	2.04	0.58
1:C:681:LEU:HD13	1:C:728:PHE:HA	1.85	0.58
1:A:246:LYS:N	1:A:289:CYS:HG	2.01	0.58
1:A:1113:ASN:HB3	1:A:1149:LEU:HB3	1.86	0.58
1:A:1602:PRO:HG2	1:A:1635:GLU:HG2	1.86	0.58
1:C:378:ALA:HB2	1:C:386:LYS:HD2	1.85	0.58
1:C:2268:MET:SD	1:C:2296:HIS:N	2.77	0.58
2:D:16:PHE:HB2	2:D:26:ARG:HB3	1.84	0.58
2:D:233:VAL:HG21	2:D:279:LEU:HD11	1.86	0.58
1:C:213:PHE:CE1	1:C:239:ARG:HA	2.38	0.58
1:C:214:GLU:HA	1:C:217:THR:HG22	1.86	0.58
1:C:1629:LYS:HE3	1:C:1633:THR:HG21	1.86	0.58
1:C:1743:GLY:HA3	1:C:1746:LEU:HB2	1.85	0.58
1:C:1832:ILE:HD13	1:C:1837:SER:CB	2.32	0.58
1:C:2115:ILE:HG13	1:C:2125:TYR:CE2	2.39	0.58
1:A:1049:ILE:HG23	1:A:1064:ILE:HD13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1446:LEU:N	1:A:1447:SER:HB2	2.17	0.58
1:A:331:PHE:CE2	1:A:349:ILE:HG21	2.34	0.57
1:A:519:ASN:HB3	1:A:520:LEU:HD13	1.85	0.57
1:A:680:LEU:HD13	1:A:727:PHE:HA	1.84	0.57
1:A:1139:ALA:HA	1:A:1172:GLN:HB3	1.84	0.57
1:C:89:PHE:HE2	1:C:131:ASN:ND2	2.01	0.57
1:C:1819:ARG:HE	1:C:1853:PHE:HZ	1.51	0.57
1:A:1061:PRO:HA	1:A:1064:ILE:HD12	1.86	0.57
1:C:213:PHE:HE1	1:C:239:ARG:HA	1.68	0.57
1:C:1009:ARG:HB2	1:C:1011:PHE:CD2	2.40	0.57
1:C:2112:LYS:HD2	1:C:2180:TRP:HZ3	1.69	0.57
1:A:344:ASP:HB2	1:A:345:LYS:HB2	1.86	0.57
1:A:345:LYS:HG3	1:A:349:ILE:HG12	1.86	0.57
1:A:669:PRO:HG2	1:A:719:LEU:HD21	1.86	0.57
1:A:693:LEU:HA	1:A:696:ILE:HD12	1.85	0.57
1:A:1821:PRO:HA	1:A:1824:LYS:HG3	1.86	0.57
2:B:29:GLN:HB3	5:I:682:ILE:HG21	1.84	0.57
1:C:2180:TRP:HA	1:C:2181:VAL:HB	1.84	0.57
2:D:186:TRP:HB3	2:D:197:LEU:HB3	1.86	0.57
1:A:232:SER:HB2	1:A:236:TYR:HE2	1.69	0.57
1:A:848:LEU:H	1:A:1547:GLN:HE22	1.52	0.57
1:A:947:ILE:HG13	1:A:951:LEU:HD13	1.85	0.57
1:A:1010:PHE:HD1	1:A:1021:ILE:HG23	1.70	0.57
1:A:1034:GLU:HA	1:A:1035:PHE:N	2.19	0.57
1:A:1099:LYS:HA	1:A:1102:ILE:HB	1.85	0.57
1:A:1453:LYS:HE3	1:A:1465:MET:HE3	1.87	0.57
1:A:1502:ILE:HB	1:A:1594:ARG:HH22	1.69	0.57
1:A:1596:ARG:C	1:A:1598:LEU:H	2.06	0.57
1:C:135:PHE:HA	1:C:145:GLU:O	2.04	0.57
1:C:694:LEU:HD12	1:C:697:ILE:HD12	1.86	0.57
1:C:2138:LEU:O	1:C:2142:LEU:N	2.37	0.57
1:A:1384:ILE:HD13	1:A:1408:ARG:NH2	2.20	0.57
1:C:359:GLU:HG3	1:C:389:LEU:HD21	1.85	0.57
1:A:1856:GLU:O	1:A:1861:MET:N	2.37	0.57
1:A:1935:LYS:O	1:A:1939:HIS:N	2.37	0.57
1:C:193:ALA:HA	1:C:196:LEU:HB3	1.86	0.57
1:C:689:ILE:HG13	1:C:690:PHE:N	2.20	0.57
1:C:1448:LEU:HD13	1:C:1470:LEU:HA	1.85	0.57
5:I:693:PHE:CZ	5:I:760:ARG:HB3	2.39	0.57
2:B:231:ALA:HB1	2:B:265:LEU:HD21	1.86	0.57
1:C:1443:GLY:HA3	1:C:1628:LYS:HD2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1771:SER:HB2	1:C:1845:ARG:HH22	1.70	0.57
1:C:2344:VAL:O	1:C:2348:LEU:HG	2.03	0.57
1:A:1039:VAL:HG23	1:A:1040:PRO:HD3	1.85	0.57
2:D:267:THR:HG1	2:D:277:TRP:HE1	1.51	0.57
1:A:768:GLN:HB2	1:A:770:ALA:N	2.16	0.57
1:A:1969:LEU:CB	1:A:1970:ASP:HA	2.35	0.57
2:B:278:ASP:HB3	2:B:281:THR:HB	1.87	0.57
1:C:280:ARG:HH12	1:C:328:THR:CB	2.18	0.57
1:C:347:TYR:OH	1:C:383:ILE:O	2.22	0.57
1:C:700:ILE:HD12	1:C:718:THR:CG2	2.35	0.57
1:C:860:HIS:O	1:C:862:ARG:N	2.34	0.57
1:C:2288:ASP:HB3	1:C:2290:ILE:CG1	2.35	0.57
2:D:231:ALA:HB2	2:D:253:VAL:HG11	1.86	0.57
1:A:259:TYR:HD1	1:A:260:VAL:HG23	1.68	0.57
1:A:471:GLY:C	4:H:187:THR:HA	2.25	0.57
1:A:569:ALA:HA	1:A:591:PHE:HE1	1.69	0.57
1:A:766:LYS:O	1:A:768:GLN:N	2.31	0.57
1:A:1001:GLU:HG2	1:A:1044:THR:HG21	1.86	0.57
1:A:1020:ILE:CG2	1:A:1024:ILE:HB	2.35	0.57
1:A:1103:ILE:HB	1:A:1141:MET:HE2	1.86	0.57
1:A:1406:LEU:HD13	1:A:1412:ALA:HA	1.85	0.57
1:C:450:PHE:HB3	1:C:453:ARG:HD2	1.87	0.57
1:C:2352:LYS:O	1:C:2356:MET:HG2	2.04	0.57
5:J:755:PHE:CE2	5:J:781:GLU:HB3	2.39	0.57
1:A:177:ARG:H	1:A:178:VAL:HG22	1.69	0.56
1:A:1010:PHE:HE1	1:A:1022:SER:HB2	1.69	0.56
1:A:2112:CYS:HB3	1:A:2122:LYS:N	2.20	0.56
1:C:216:ARG:HD2	1:C:234:LYS:NZ	2.20	0.56
1:C:346:LYS:HB3	1:C:350:ILE:HG13	1.87	0.56
1:C:828:LEU:HD11	1:C:848:ILE:HG21	1.87	0.56
1:C:1407:LYS:HD2	1:C:1413:ASP:N	2.20	0.56
2:D:276:LEU:HB3	2:D:286:ARG:HB2	1.87	0.56
1:A:457:LYS:HB3	1:A:485:LEU:HD11	1.87	0.56
1:A:1076:GLU:HB3	1:A:1079:SER:OG	2.05	0.56
1:A:1090:THR:HG23	1:A:1091:GLU:HB2	1.86	0.56
1:A:2453:GLN:O	1:A:2457:SER:N	2.34	0.56
2:B:17:TRP:HZ2	2:B:290:GLY:HA2	1.69	0.56
1:C:234:LYS:HE3	1:C:238:ARG:HG2	1.86	0.56
1:C:804:LEU:HD23	1:C:851:ASN:HB2	1.87	0.56
1:C:862:ARG:HG3	1:C:863:ARG:H	1.70	0.56
1:C:2097:PHE:HD1	1:C:2097:PHE:C	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2125:TYR:HA	1:C:2179:GLY:HA2	1.86	0.56
1:C:2432:LYS:HE2	1:C:2433:LEU:N	2.20	0.56
1:A:198:LEU:HA	1:A:248:LEU:HG	1.88	0.56
1:A:856:ASN:CB	1:A:1580:LEU:HA	2.31	0.56
1:A:861:ARG:HB3	1:A:1540:TYR:CD2	2.41	0.56
1:A:1510:PHE:CZ	1:A:1514:GLU:HA	2.40	0.56
1:A:2301:PHE:HZ	1:A:2423:VAL:HG22	1.70	0.56
1:C:112:THR:HG22	1:C:114:LEU:HD12	1.85	0.56
1:C:853:LEU:HD12	1:C:1580:ARG:HD3	1.87	0.56
1:C:1349:PHE:HD2	1:C:1351:LYS:N	2.03	0.56
1:C:1594:ILE:HB	1:C:1598:ARG:HB3	1.87	0.56
1:C:1831:SER:HG	1:C:1832:ILE:N	2.01	0.56
1:C:2437:ASP:HB3	1:C:2438:ILE:HG12	1.86	0.56
2:D:10:TYR:CE2	2:D:293:LYS:HG3	2.38	0.56
1:A:1427:VAL:HG23	1:A:1428:GLU:H	1.70	0.56
1:A:1584:LYS:O	1:A:1585:ASN:HB3	2.05	0.56
1:A:1666:ASP:O	1:A:1670:LYS:N	2.38	0.56
1:C:2157:PHE:O	1:C:2160:HIS:HB2	2.05	0.56
1:C:2448:GLU:C	1:C:2449:GLN:N	2.59	0.56
1:A:387:TYR:O	1:A:391:ILE:N	2.38	0.56
1:A:655:ILE:HA	1:A:658:GLU:HB2	1.88	0.56
1:A:2060:GLU:HG3	1:A:2098:VAL:HG23	1.85	0.56
1:C:444:GLU:HA	1:C:447:ARG:HB2	1.88	0.56
1:C:1370:GLU:HA	1:C:1373:ILE:HD12	1.88	0.56
1:C:1584:CYS:O	1:C:1585:GLN:HB2	2.05	0.56
1:A:827:LEU:HD11	1:A:847:ILE:HG21	1.86	0.56
1:A:1243:ARG:HH21	1:A:1259:ARG:HG2	1.71	0.56
1:C:2126:VAL:HG12	1:C:2180:TRP:CE3	2.38	0.56
1:A:1458:LYS:HB3	1:A:1459:PRO:HD3	1.87	0.56
1:C:285:VAL:HG22	1:C:335:LEU:HD11	1.86	0.56
1:C:1421:LYS:HG3	1:C:1435:LYS:HD2	1.87	0.56
1:A:233:LYS:HE2	1:A:237:ARG:CG	2.35	0.56
1:A:1100:ILE:HG23	1:A:1141:MET:SD	2.46	0.56
1:A:1140:THR:HG22	1:A:1172:GLN:NE2	2.21	0.56
1:A:2318:LEU:HD11	1:A:2455:ALA:HB1	1.86	0.56
5:I:693:PHE:HE2	5:I:760:ARG:HH21	1.54	0.56
1:A:1164:LYS:C	1:A:1166:LEU:H	2.09	0.56
1:A:1428:GLU:HA	1:A:1456:THR:HG22	1.87	0.56
1:C:221:TRP:HA	1:C:235:LEU:CD1	2.36	0.56
1:C:1410:ARG:HG3	1:C:1411:TRP:N	2.20	0.56
1:C:2171:LEU:H	1:C:2176:GLY:HA2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:40:ILE:HG23	2:D:47:LEU:HD23	1.87	0.56
5:J:655:SER:HA	5:J:659:LEU:CB	2.27	0.56
1:C:297:ARG:HD2	1:C:339:LYS:CG	2.31	0.56
1:C:1061:VAL:N	1:C:1062:PRO:CD	2.70	0.56
1:C:1085:PRO:HG3	1:C:1118:MET:SD	2.46	0.56
1:C:1406:GLU:HG3	1:C:1409:GLN:HG3	1.88	0.56
1:C:1761:ASN:HA	1:C:1764:LEU:HD12	1.88	0.56
1:C:281:LEU:CD1	1:C:330:LEU:HB3	2.36	0.55
1:C:515:ASN:HA	1:C:518:ILE:HD12	1.87	0.55
1:C:2323:MET:HA	1:C:2326:TYR:HB3	1.87	0.55
5:I:720:PRO:HD3	5:I:723:PHE:HB2	1.87	0.55
1:A:1252:GLU:HG2	1:A:1253:SER:H	1.70	0.55
1:A:1961:TRP:HB2	1:A:2006:ILE:HG12	1.87	0.55
1:C:146:LYS:HG2	1:C:191:LEU:HD11	1.87	0.55
1:C:195:THR:HG22	1:C:198:ARG:HH21	1.71	0.55
1:C:1594:ILE:HA	1:C:1597:VAL:HB	1.88	0.55
1:C:2374:LEU:HD12	1:C:2421:ARG:HH22	1.70	0.55
1:A:821:LEU:HA	1:A:824:LEU:HB2	1.87	0.55
1:A:1143:THR:HB	1:A:1177:ASP:HB2	1.88	0.55
1:A:1830:ILE:HG22	1:A:1832:LEU:HD22	1.89	0.55
1:A:1952:HIS:HA	1:A:1955:ILE:HG22	1.88	0.55
2:B:236:ILE:HG23	2:B:237:ASP:HB3	1.88	0.55
1:C:2079:ALA:HB2	1:C:2094:ILE:HG12	1.88	0.55
2:D:223:ALA:HB2	2:D:233:VAL:HG23	1.88	0.55
1:A:89:ASP:HB3	1:A:90:LYS:HG2	1.87	0.55
1:A:487:LEU:HD23	1:A:488:ASN:H	1.71	0.55
1:C:329:LEU:HD23	1:C:366:ARG:HD3	1.89	0.55
1:C:1222:ASN:HA	1:C:1225:LYS:HD2	1.89	0.55
1:C:2103:VAL:HA	1:C:2111:ARG:HA	1.88	0.55
1:A:352:SER:HB3	1:A:356:TYR:CE2	2.42	0.55
1:A:1452:GLU:O	1:A:1456:THR:HG23	2.07	0.55
1:A:1821:PRO:HA	1:A:1824:LYS:CG	2.36	0.55
1:A:2436:ILE:HG13	1:A:2438:ARG:H	1.72	0.55
1:A:2442:LEU:O	1:A:2446:GLU:HB2	2.06	0.55
2:D:12:HIS:O	2:D:13:THR:N	2.39	0.55
2:D:14:ILE:HD11	2:D:28:ILE:HD12	1.89	0.55
1:A:1563:GLN:C	1:A:1568:ARG:HD2	2.27	0.55
1:A:2035:LEU:HD21	5:I:648:LYS:HG3	1.89	0.55
1:C:2008:ILE:HD11	1:C:2066:VAL:HG23	1.87	0.55
1:A:187:VAL:CG1	1:A:233:LYS:HA	2.37	0.55
1:A:1183:LEU:HD13	1:A:1189:LEU:HD22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1502:ILE:HB	1:A:1594:ARG:NH2	2.22	0.55
1:C:2124:LYS:HB3	1:C:2180:TRP:C	2.27	0.55
1:C:2207:TRP:HA	1:C:2210:LEU:HD12	1.88	0.55
5:I:690:ARG:HG2	5:I:691:ASN:HB2	1.88	0.55
5:J:781:GLU:C	5:J:784:GLN:HB3	2.27	0.55
1:A:1020:ILE:C	1:A:1025:GLU:HB2	2.27	0.55
1:A:1215:LYS:HB2	1:A:1249:LEU:HB3	1.89	0.55
1:A:1621:ARG:HG2	1:A:1624:LEU:HD23	1.88	0.55
1:A:1962:HIS:NE2	1:A:2006:ILE:HA	2.22	0.55
2:B:46:LEU:HD13	2:B:57:LEU:HD13	1.89	0.55
5:I:659:LEU:HD21	5:I:690:ARG:HH12	1.72	0.55
1:C:866:VAL:N	1:C:1537:SER:HG	2.03	0.55
1:C:1014:ILE:HG23	1:C:1064:ARG:HE	1.72	0.55
1:C:2222:LEU:HB3	2:D:254:TRP:HZ3	1.72	0.55
1:A:1238:TRP:O	1:A:1241:TRP:N	2.40	0.55
1:A:1291:TYR:CE1	1:A:1340:TYR:HE2	2.24	0.55
1:A:2429:ASP:HB2	1:A:2439:PHE:HB3	1.88	0.55
1:C:282:ASP:HA	1:C:285:VAL:HB	1.89	0.55
1:C:780:LEU:HD11	1:C:816:PHE:HB2	1.89	0.55
3:E:715:UNK:C	3:E:717:UNK:H	2.20	0.55
2:B:7:SER:HB3	2:B:295:ALA:CB	2.36	0.54
1:C:1009:ARG:HB2	1:C:1011:PHE:CE2	2.41	0.54
1:A:954:ARG:NH1	1:A:992:VAL:H	2.06	0.54
1:A:1419:LYS:HG3	1:A:1433:LYS:HD2	1.89	0.54
1:C:1114:ASN:HB3	1:C:1150:LEU:HA	1.88	0.54
1:C:1165:LYS:HE3	1:C:1171:ARG:HG3	1.89	0.54
1:C:2191:ILE:HD12	1:C:2194:HIS:HD2	1.72	0.54
1:A:455:PHE:HB2	1:A:491:MET:HG3	1.89	0.54
1:A:849:ILE:HG23	1:A:853:LYS:N	2.22	0.54
1:A:993:LYS:HA	1:A:994:GLN:CB	2.38	0.54
1:A:1217:PRO:HB2	1:A:1220:GLN:HB2	1.88	0.54
1:A:1291:TYR:CE1	1:A:1340:TYR:CE2	2.95	0.54
1:C:347:TYR:HE2	1:C:383:ILE:HG12	1.72	0.54
1:C:1031:ALA:HB1	1:C:1034:GLY:O	2.07	0.54
1:C:2360:GLU:C	1:C:2361:ALA:HA	2.28	0.54
5:I:699:LYS:HZ1	5:I:702:THR:HG21	1.71	0.54
5:J:698:ARG:C	5:J:700:SER:H	2.09	0.54
5:J:754:ASN:HB3	5:J:760:ARG:HG3	1.89	0.54
2:D:35:VAL:HG22	2:D:38:LEU:HD21	1.89	0.54
3:F:102:UNK:C	3:F:103:UNK:HA	2.36	0.54
1:A:177:ARG:N	1:A:178:VAL:HG23	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:97:PRO:HB2	1:C:144:SER:HB3	1.90	0.54
1:C:1504:ILE:HG21	1:C:1596:ARG:HH12	1.72	0.54
1:C:1611:ARG:C	1:C:1613:LYS:N	2.61	0.54
2:D:165:LEU:HD11	2:D:174:LEU:HD23	1.88	0.54
5:J:658:VAL:HG23	5:J:659:LEU:HD12	1.89	0.54
1:A:1010:PHE:HD1	1:A:1021:ILE:CG2	2.21	0.54
2:B:113:TYR:OH	2:B:150:CYS:HA	2.07	0.54
1:C:2147:ASN:HA	1:C:2150:LEU:HB2	1.88	0.54
2:D:259:SER:HB2	2:D:302:ASP:OD2	2.07	0.54
5:I:700:SER:HA	5:I:731:GLU:CB	2.35	0.54
1:A:152:VAL:HA	1:A:155:LEU:HB3	1.89	0.54
1:A:378:PHE:HB2	1:A:380:PRO:HD2	1.89	0.54
1:A:1499:TYR:H	1:A:1594:ARG:NH2	2.05	0.54
1:A:1713:LEU:HA	1:A:1752:THR:HG21	1.89	0.54
1:A:2044:ASN:HA	1:A:2047:ARG:NH1	2.21	0.54
1:C:2038:ASN:HA	1:C:2041:TRP:HB2	1.88	0.54
2:D:54:ASN:HA	2:D:72:GLU:HG2	1.90	0.54
1:A:358:GLU:HG3	1:A:388:LEU:HD21	1.90	0.54
1:A:542:PHE:HB2	1:A:544:ILE:HG23	1.90	0.54
1:A:635:SER:HA	1:A:638:GLU:HB3	1.89	0.54
1:A:699:ILE:HD12	1:A:717:THR:CG2	2.37	0.54
1:C:2308:LEU:HB3	1:C:2309:ARG:HB2	1.90	0.54
1:C:2412:GLU:HA	1:C:2415:ASN:HB2	1.90	0.54
1:A:650:ASP:N	1:A:651:PRO:CD	2.61	0.54
1:A:1876:VAL:O	1:A:1880:LEU:HG	2.08	0.54
1:A:2043:TYR:CE1	5:I:660:GLU:HG3	2.42	0.54
1:C:168:ASN:HD21	1:C:172:ARG:HH21	1.56	0.54
1:C:358:LYS:HD3	1:C:393:MET:HG3	1.90	0.54
1:C:1585:GLN:O	1:C:1586:LYS:HB2	2.08	0.54
1:C:1662:TRP:HZ3	1:C:1726:ARG:CZ	2.20	0.54
1:C:2102:SER:H	1:C:2113:PHE:HE2	1.56	0.54
2:D:215:LEU:HD22	2:D:236:ILE:HD12	1.90	0.54
5:I:730:VAL:HG21	5:I:789:THR:HA	1.89	0.54
1:A:322:ASP:O	1:A:324:VAL:HG23	2.08	0.54
1:A:445:LEU:HA	1:A:448:LYS:HB2	1.89	0.54
1:A:673:GLN:HG2	1:A:719:LEU:HD13	1.88	0.54
1:A:960:ASP:C	1:A:961:GLN:N	2.61	0.54
1:A:1040:PRO:HA	1:A:1043:LEU:HG	1.90	0.54
1:A:1232:GLN:HG3	1:A:1294:ASP:O	2.08	0.54
1:A:1437:LEU:HB3	1:A:1446:LEU:HD21	1.88	0.54
2:B:84:GLN:HB3	2:B:89:TRP:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:VAL:HG22	2:B:99:ILE:HD11	1.90	0.54
2:B:275:ARG:HG3	2:B:287:GLN:HG3	1.90	0.54
1:C:421:GLY:HA2	1:C:424:ALA:HB2	1.90	0.54
1:C:745:LEU:HD22	1:C:782:VAL:HG21	1.90	0.54
1:C:1459:ALA:HA	1:C:1460:LYS:C	2.27	0.54
1:C:2062:GLU:HA	1:C:2063:LEU:CB	2.31	0.54
1:C:2255:LEU:O	1:C:2259:THR:N	2.37	0.54
1:C:2273:TYR:CD1	1:C:2317:PRO:HA	2.43	0.54
1:C:2373:ASP:HB3	1:C:2418:ARG:HH21	1.73	0.54
1:A:235:GLU:HB3	1:A:278:ILE:HB	1.90	0.53
1:A:1588:VAL:HG12	1:A:1612:PHE:CD1	2.43	0.53
1:A:1589:TRP:HE3	1:A:1612:PHE:CE1	2.15	0.53
1:A:1950:VAL:HA	1:A:1953:GLU:HB2	1.89	0.53
1:C:473:PRO:O	1:C:477:LYS:HG2	2.08	0.53
1:C:951:ASN:HB3	1:C:954:LEU:H	1.72	0.53
3:E:109:UNK:C	3:E:110:UNK:HA	2.39	0.53
1:C:763:VAL:HG12	1:C:806:ILE:HB	1.90	0.53
1:C:818:ARG:HD2	1:C:868:LEU:CD1	2.38	0.53
1:C:1982:HIS:HB3	1:C:1984:THR:N	2.22	0.53
1:C:2080:VAL:HB	1:C:2084:ARG:HG3	1.90	0.53
1:C:2109:ARG:N	1:C:2110:PRO:HD3	2.22	0.53
3:F:659:UNK:O	3:F:661:UNK:N	2.41	0.53
1:A:397:ARG:HB3	1:A:399:LEU:HB2	1.91	0.53
1:A:725:LEU:HG	1:A:726:LYS:N	2.23	0.53
1:A:1652:VAL:HG12	1:A:1656:LEU:HB2	1.91	0.53
1:A:1916:VAL:HG11	1:A:2168:PRO:HB2	1.89	0.53
1:A:2032:VAL:HA	1:A:2035:LEU:HD22	1.90	0.53
1:A:2253:LEU:O	1:A:2257:THR:N	2.42	0.53
1:A:2306:LEU:HD12	1:A:2376:LYS:H	1.73	0.53
1:C:542:GLN:C	1:C:543:PHE:N	2.61	0.53
1:C:573:LEU:HD23	1:C:576:CYS:HB2	1.91	0.53
1:C:1340:GLY:HA2	1:C:1343:ALA:H	1.73	0.53
1:C:1655:TYR:HE1	1:C:1720:LEU:HD21	1.73	0.53
1:C:2172:SER:HB3	1:C:2173:PRO:HD2	1.88	0.53
1:C:2445:ASP:O	1:C:2449:GLN:HB2	2.07	0.53
1:A:689:PHE:HZ	1:A:732:LYS:HD3	1.73	0.53
1:A:1046:PHE:HA	1:A:1049:ILE:HG12	1.90	0.53
1:A:1498:PHE:HD2	1:A:1499:TYR:CD2	2.26	0.53
1:A:1928:ALA:O	1:A:1932:ILE:HG12	2.09	0.53
2:B:231:ALA:HB3	2:B:246:LEU:HB3	1.89	0.53
1:C:862:ARG:HB2	1:C:1537:SER:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1581:LEU:HD12	1:C:1582:LEU:HD23	1.91	0.53
2:D:246:LEU:HD11	2:D:282:ARG:HA	1.89	0.53
1:A:770:ALA:HA	1:A:810:ASP:HB2	1.91	0.53
1:A:1089:MET:HB3	1:A:1092:TYR:CD2	2.44	0.53
1:A:2111:PHE:HD1	1:A:2112:CYS:HA	1.74	0.53
2:B:235:SER:HB3	2:B:239:ASP:HB3	1.89	0.53
1:C:395:HIS:CE1	1:C:438:ILE:HG21	2.38	0.53
1:C:852:ILE:HG21	1:C:1584:CYS:HB2	1.90	0.53
2:D:84:GLN:HB2	2:D:145:LEU:HD22	1.90	0.53
1:A:212:PHE:HE1	1:A:238:ARG:HA	1.72	0.53
1:A:1406:LEU:HD21	1:A:1436:SER:HB3	1.90	0.53
1:A:2057:GLN:HE22	1:A:2103:SER:HB2	1.74	0.53
2:B:16:PHE:HB3	2:B:60:ILE:HD13	1.91	0.53
2:B:79:THR:HG23	2:B:95:GLU:HG3	1.91	0.53
2:B:131:LEU:HB3	2:B:143:TRP:O	2.08	0.53
1:C:214:GLU:HG2	1:C:218:CYS:SG	2.48	0.53
1:C:366:ARG:HA	1:C:369:VAL:HB	1.90	0.53
1:C:1962:LEU:HB2	1:C:1965:GLU:N	2.23	0.53
2:D:156:PRO:HB3	2:D:184:TYR:HB2	1.91	0.53
1:A:520:LEU:O	1:A:522:SER:HA	2.08	0.53
1:C:636:SER:HA	1:C:639:GLU:HB3	1.90	0.53
1:C:2097:PHE:C	1:C:2097:PHE:CD1	2.81	0.53
1:A:354:MET:SD	1:A:388:LEU:HD13	2.48	0.53
1:A:1213:VAL:HG22	1:A:1248:GLN:HE21	1.72	0.53
1:A:1352:HIS:NE2	1:A:2250:GLU:HG3	2.24	0.53
1:A:2262:SER:HB3	1:A:2292:VAL:N	2.24	0.53
2:B:143:TRP:HE1	2:B:148:ASN:HA	1.74	0.53
2:B:258:PHE:CE1	2:B:279:LEU:HD13	2.43	0.53
1:C:173:LEU:HD21	1:C:209:ASP:OD1	2.09	0.53
1:C:284:ALA:HB3	1:C:331:VAL:HG11	1.91	0.53
1:C:333:ARG:NH1	1:C:354:THR:HB	2.24	0.53
1:C:1082:LEU:HA	1:C:1085:PRO:HG2	1.90	0.53
1:C:2304:GLU:O	1:C:2308:LEU:HD13	2.09	0.53
2:D:268:ALA:HB2	2:D:298:VAL:HG21	1.90	0.53
1:A:304:TRP:HB2	1:A:341:TYR:CE2	2.44	0.53
1:A:920:VAL:HG12	1:A:923:ASN:HB2	1.91	0.53
1:A:1328:LYS:HB2	1:A:1329:PRO:HD3	1.91	0.53
1:A:1559:LYS:N	1:A:1572:ARG:NH2	2.57	0.53
1:A:1972:ALA:C	1:A:1974:ARG:H	2.12	0.53
1:A:2059:LEU:C	1:A:2098:VAL:HA	2.29	0.53
1:A:2132:ARG:HB3	1:A:2366:ILE:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:GLU:C	1:C:123:PHE:H	2.12	0.53
1:C:236:GLU:HG2	1:C:279:ILE:HB	1.90	0.53
1:C:332:PHE:CE1	1:C:336:LEU:HD11	2.44	0.53
1:C:862:ARG:HG3	1:C:863:ARG:N	2.24	0.53
1:C:1510:ASN:HD21	4:G:73:PHE:HA	1.72	0.53
1:C:2081:PRO:HB2	1:C:2123:TYR:CE2	2.44	0.53
2:D:12:HIS:HB3	2:D:30:HIS:O	2.09	0.53
2:B:7:SER:HB2	2:B:274:VAL:HB	1.91	0.53
1:C:938:HIS:CE1	1:C:978:GLN:HA	2.44	0.53
1:C:1149:LEU:HD12	1:C:1194:ILE:HG21	1.91	0.53
1:C:1504:ILE:HG12	1:C:1508:HIS:NE2	2.24	0.53
5:I:737:ASN:HB3	5:I:754:ASN:O	2.08	0.53
1:A:273:ASP:HA	1:A:276:LEU:HD11	1.89	0.52
1:A:853:LYS:HG3	1:A:1582:CYS:HB3	1.89	0.52
1:A:2121:TYR:HA	1:A:2122:LYS:CB	2.30	0.52
1:A:2347:ARG:HH22	1:A:2444:VAL:H	1.56	0.52
1:C:705:SER:HB2	1:C:710:TYR:HB3	1.91	0.52
1:C:857:ASN:CB	1:C:1586:LYS:HA	2.29	0.52
1:C:1021:ILE:HG21	1:C:1025:ILE:HB	1.89	0.52
4:G:75:GLY:HA3	4:G:106:GLY:HA2	1.91	0.52
1:A:2345:VAL:HA	1:A:2348:ASP:OD1	2.09	0.52
1:C:443:ARG:O	1:C:447:ARG:N	2.43	0.52
1:A:267:ILE:O	1:A:279:ARG:HD2	2.08	0.52
1:A:283:ALA:O	1:A:307:ARG:NH2	2.41	0.52
1:A:1191:THR:C	1:A:1193:ILE:H	2.13	0.52
1:A:2155:PHE:HA	1:A:2158:HIS:HB2	1.91	0.52
2:B:154:LEU:HD23	2:B:197:LEU:HD12	1.91	0.52
1:C:265:LEU:HA	1:C:307:GLN:CB	2.19	0.52
1:C:1403:THR:HG23	1:C:1407:LYS:HE2	1.91	0.52
1:C:1505:LEU:HD22	1:C:1514:LYS:HE2	1.90	0.52
1:C:1816:LEU:N	1:C:1817:ILE:HA	2.23	0.52
1:C:2097:PHE:HB3	1:C:2115:ILE:HA	1.92	0.52
2:D:56:ARG:HD3	2:D:67:PRO:HD3	1.90	0.52
1:A:176:LEU:HA	1:A:179:LEU:HB2	1.90	0.52
1:A:565:ASP:O	1:A:570:GLN:N	2.42	0.52
1:A:1852:GLY:HA2	1:A:1891:VAL:HG21	1.91	0.52
1:C:842:TYR:O	1:C:844:GLU:N	2.42	0.52
1:C:2369:ASN:O	1:C:2418:ARG:NH2	2.43	0.52
2:D:44:LYS:HE2	2:D:61:ARG:NH2	2.24	0.52
3:F:353:UNK:C	3:F:354:UNK:H	2.22	0.52
4:H:141:ASN:O	4:H:176:LYS:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:572:LEU:HA	1:A:575:CYS:HB2	1.92	0.52
1:A:963:ILE:HG23	1:A:964:PRO:HD3	1.90	0.52
2:B:8:ALA:HB3	2:B:38:LEU:HD21	1.92	0.52
2:B:156:PRO:HA	2:B:186:TRP:HZ2	1.73	0.52
1:C:1050:ILE:HD12	1:C:1065:ILE:HG12	1.91	0.52
1:C:1144:THR:HG22	1:C:1178:ASP:HB2	1.92	0.52
1:A:436:LEU:HD22	1:A:474:PHE:HZ	1.74	0.52
2:B:55:VAL:HG22	2:B:57:LEU:HD21	1.90	0.52
1:C:573:LEU:HB3	1:C:577:PHE:HD2	1.74	0.52
1:C:1388:ILE:HA	1:C:1391:HIS:HB3	1.91	0.52
1:C:2047:VAL:HA	1:C:2050:LYS:HD2	1.90	0.52
1:C:2084:ARG:HH22	1:C:2169:ILE:HG12	1.75	0.52
1:C:2280:ARG:HB3	1:C:2319:ARG:HH11	1.74	0.52
2:D:101:VAL:HG13	2:D:111:ARG:HB2	1.92	0.52
3:E:357:UNK:C	3:E:358:UNK:H	2.22	0.52
1:A:669:PRO:CG	1:A:719:LEU:HD21	2.39	0.52
1:A:1351:LEU:O	1:A:1355:GLU:HB2	2.10	0.52
1:A:1908:GLN:HB2	1:A:1939:HIS:NE2	2.25	0.52
1:A:1962:HIS:NE2	1:A:2005:GLU:O	2.37	0.52
1:C:231:SER:HA	1:C:234:LYS:HB3	1.90	0.52
1:C:490:CYS:HB3	1:C:491:PRO:CD	2.40	0.52
1:C:998:ARG:NE	1:C:1035:GLU:H	2.08	0.52
1:C:2194:HIS:CE1	1:C:2243:VAL:HB	2.45	0.52
1:A:2049:ILE:O	1:A:2052:GLN:HB3	2.10	0.52
1:C:310:PHE:HA	1:C:317:LEU:HD11	1.92	0.52
1:C:855:THR:HA	1:C:1550:ILE:HG21	1.91	0.52
2:B:227:ALA:HA	2:B:252:TRP:HA	1.92	0.52
1:C:446:LEU:HA	1:C:449:LYS:HB2	1.91	0.52
1:C:450:PHE:CD1	1:C:456:PHE:HA	2.45	0.52
1:C:462:TYR:CD2	1:C:498:GLU:HB3	2.45	0.52
1:C:573:LEU:HB3	1:C:577:PHE:CD2	2.45	0.52
2:D:77:ASN:H	2:D:95:GLU:HB2	1.75	0.52
2:D:212:ARG:NH2	2:D:297:CYS:SG	2.83	0.52
2:D:233:VAL:HG12	2:D:244:THR:HB	1.91	0.52
1:A:290:LEU:HA	1:A:293:ILE:HB	1.92	0.52
1:A:1920:SER:HB3	1:A:2171:PRO:HD3	1.91	0.52
1:C:90:ASP:HA	1:C:131:ASN:O	2.10	0.52
1:C:2063:LEU:HB3	1:C:2099:PRO:HA	1.90	0.52
1:C:2261:TYR:HA	1:C:2264:SER:HB2	1.91	0.52
1:A:409:ASN:HB2	1:A:452:ARG:HD2	1.90	0.51
1:A:581:LEU:HA	1:A:582:ILE:C	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1968:GLY:HA3	1:A:1992:LEU:HD21	1.92	0.51
1:A:2066:PRO:HA	1:A:2069:LEU:HB3	1.92	0.51
1:A:2078:VAL:HG12	1:A:2081:THR:HG22	1.92	0.51
2:B:229:HIS:HA	2:B:251:ARG:HB2	1.91	0.51
2:B:278:ASP:O	2:B:282:ARG:N	2.42	0.51
1:C:264:ILE:HG23	1:C:268:ILE:HD12	1.91	0.51
1:C:1743:GLY:HA2	1:C:1744:SER:C	2.30	0.51
2:D:71:PHE:HB3	2:D:90:MET:HE1	1.92	0.51
1:A:436:LEU:HD12	1:A:439:ASP:HB3	1.91	0.51
1:A:436:LEU:HD13	1:A:474:PHE:CE1	2.45	0.51
1:A:1134:ARG:HG3	1:A:1138:LYS:HB2	1.91	0.51
1:A:1592:ILE:HA	1:A:1595:VAL:HB	1.93	0.51
2:B:229:HIS:CD2	2:B:252:TRP:H	2.29	0.51
2:B:253:VAL:HA	2:B:268:ALA:O	2.10	0.51
1:C:180:LEU:HG	1:C:234:LYS:HD2	1.92	0.51
1:C:424:ALA:HB3	1:C:425:PHE:HB2	1.93	0.51
1:C:919:THR:HA	1:C:922:ILE:HB	1.91	0.51
1:C:1512:PHE:CZ	1:C:1516:GLU:HA	2.46	0.51
1:C:2100:VAL:O	1:C:2101:PHE:N	2.44	0.51
1:C:2187:PHE:N	1:C:2285:LEU:O	2.43	0.51
2:D:12:HIS:HE1	2:D:35:VAL:HB	1.75	0.51
1:A:220:TRP:HA	1:A:270:PRO:HG3	1.92	0.51
1:A:280:LEU:C	1:A:284:VAL:HG23	2.31	0.51
1:A:1045:PHE:CZ	1:A:1064:ILE:HA	2.33	0.51
1:A:1883:ARG:HG2	1:A:2364:PRO:HG2	1.91	0.51
1:A:2282:ASN:HA	1:A:2295:ILE:O	2.09	0.51
2:B:111:ARG:HH12	2:B:146:GLY:HA3	1.75	0.51
1:C:307:GLN:HA	1:C:310:PHE:HB3	1.91	0.51
1:C:983:PHE:HA	1:C:986:LEU:HD22	1.93	0.51
1:C:1570:ARG:HA	1:C:1573:MET:HG2	1.92	0.51
1:C:2139:VAL:O	1:C:2142:LEU:N	2.43	0.51
1:C:2266:ALA:HB1	1:C:2343:ASN:HD21	1.76	0.51
4:H:120:ASP:CA	4:H:121:TYR:CB	2.85	0.51
1:A:324:VAL:HG22	1:A:327:THR:HG22	1.92	0.51
1:A:1368:GLU:HA	1:A:1371:ILE:HD12	1.92	0.51
1:A:1449:LEU:HB3	1:A:1452:GLU:HB2	1.93	0.51
1:A:2239:TYR:HA	1:A:2242:LEU:HD12	1.92	0.51
1:C:260:TYR:HA	1:C:287:LEU:HD11	1.92	0.51
1:C:569:ASP:HB3	1:C:570:ALA:N	2.25	0.51
1:C:992:ILE:HD12	1:C:994:LYS:HB3	1.91	0.51
1:C:1261:SER:HG	1:C:1263:SER:N	2.07	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1500:PHE:CD1	1:C:1551:ILE:HG23	2.46	0.51
1:C:1670:ALA:O	1:C:1674:LEU:N	2.43	0.51
1:C:1901:LEU:HA	1:C:1904:LEU:HB2	1.91	0.51
2:D:212:ARG:HE	2:D:255:ASP:HB3	1.75	0.51
1:A:138:HIS:NE2	1:A:178:VAL:CG1	2.73	0.51
1:A:1978:GLY:O	1:A:1979:GLU:HB2	2.10	0.51
1:A:2124:VAL:HG12	1:A:2178:TRP:HE3	1.75	0.51
1:C:446:LEU:HD12	1:C:449:LYS:HD2	1.92	0.51
1:C:1100:LYS:O	1:C:1104:ILE:HG12	2.11	0.51
1:C:1429:VAL:HG23	1:C:1430:GLU:H	1.76	0.51
1:C:2128:LYS:HD3	1:C:2131:GLU:HG3	1.92	0.51
1:C:2365:ASP:HB3	1:C:2369:ASN:O	2.10	0.51
1:C:2429:ILE:HD13	1:C:2435:GLY:N	2.25	0.51
5:J:736:PRO:HA	5:J:755:PHE:CD1	2.46	0.51
1:A:288:LYS:O	1:A:292:ILE:HG23	2.11	0.51
1:A:304:TRP:HE1	1:A:340:PRO:HG2	1.76	0.51
1:A:1010:PHE:CD1	1:A:1021:ILE:HG23	2.45	0.51
1:A:2411:HIS:O	1:A:2415:ILE:N	2.43	0.51
1:A:2430:LYS:HA	1:A:2450:LYS:HG3	1.93	0.51
2:B:37:ARG:HH21	2:B:80:SER:HA	1.76	0.51
1:C:1002:GLU:HG2	1:C:1042:GLU:HG3	1.93	0.51
1:C:1570:ARG:O	1:C:1574:ARG:HB2	2.10	0.51
3:E:454:UNK:HA	3:E:455:UNK:C	2.41	0.51
1:A:1065:LEU:HD13	1:A:1101:SER:HB3	1.93	0.51
1:C:314:THR:HA	1:C:317:LEU:HB2	1.93	0.51
1:C:1443:GLY:N	1:C:1628:LYS:HZ2	2.09	0.51
1:C:1475:ALA:HB1	1:C:1484:ILE:HG13	1.93	0.51
1:C:1598:ARG:HA	1:C:1600:LEU:HG	1.92	0.51
1:C:2098:GLU:HB3	1:C:2100:VAL:C	2.31	0.51
1:C:2346:LYS:HG3	1:C:2350:ASP:OD2	2.10	0.51
1:A:722:LEU:CA	1:A:760:LEU:HD13	2.38	0.51
1:A:2044:ASN:HA	1:A:2047:ARG:HH11	1.76	0.51
1:A:2191:GLU:HA	1:A:2194:GLU:HB2	1.93	0.51
2:B:14:ILE:HD11	2:B:28:ILE:HD12	1.93	0.51
2:B:121:GLU:OE1	2:B:165:LEU:HB3	2.11	0.51
2:B:186:TRP:HB3	2:B:197:LEU:HB3	1.92	0.51
1:C:183:SER:HB3	1:C:230:SER:O	2.10	0.51
1:C:1547:ARG:HB3	1:C:1593:ARG:HH21	1.75	0.51
3:F:250:UNK:O	3:F:254:UNK:N	2.44	0.51
5:I:699:LYS:HB2	5:I:760:ARG:HB2	1.91	0.51
1:A:590:GLU:HB3	1:A:594:LEU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:721:LEU:HD22	1:A:757:ASP:HB3	1.93	0.51
1:A:1524:LEU:HD11	1:A:1549:ILE:HB	1.91	0.51
1:A:2200:LEU:HG	1:A:2471:PHE:CZ	2.35	0.51
1:A:2239:TYR:O	1:A:2243:TRP:N	2.44	0.51
1:C:138:ILE:C	1:C:140:GLY:H	2.14	0.51
1:C:1518:HIS:HA	1:C:1521:ASN:HB2	1.93	0.51
1:C:1554:LEU:HA	1:C:1557:ILE:HG23	1.92	0.51
1:C:1909:PRO:HB2	1:C:1913:VAL:HB	1.92	0.51
1:C:2026:MET:HG3	1:C:2027:ASN:N	2.25	0.51
2:D:83:PHE:HE1	2:D:104:VAL:HG21	1.74	0.51
5:I:699:LYS:HD3	5:I:737:ASN:HD22	1.74	0.51
5:I:709:PHE:CE2	5:I:716:THR:HB	2.46	0.51
1:A:347:ASP:N	1:A:348:ASP:CB	2.74	0.51
1:A:361:PHE:HE1	1:A:414:PHE:CE1	2.29	0.51
1:A:412:LYS:HZ1	1:A:445:LEU:HD22	1.76	0.51
1:A:774:VAL:O	1:A:777:THR:OG1	2.22	0.51
1:A:1069:VAL:CG1	1:A:1105:LEU:HG	2.41	0.51
1:A:1453:LYS:HG2	1:A:1465:MET:HG2	1.93	0.51
1:A:1879:GLN:HG2	1:A:2132:ARG:HH21	1.76	0.51
1:C:1661:LEU:HD21	1:C:1669:GLU:HB3	1.91	0.51
1:C:1822:ILE:HG23	1:C:1826:LYS:HD2	1.92	0.51
2:D:90:MET:HB3	2:D:102:TRP:HB2	1.92	0.51
2:D:265:LEU:HA	2:D:279:LEU:HD12	1.92	0.51
5:I:664:PHE:HE1	5:I:691:ASN:HD22	1.57	0.51
1:A:120:GLU:HG2	1:A:123:GLN:HB3	1.93	0.50
1:A:341:TYR:CG	1:A:345:LYS:HG2	2.46	0.50
1:A:1008:ARG:HB2	1:A:1010:PHE:CE2	2.46	0.50
1:A:1127:ARG:HG2	1:A:1128:ILE:N	2.26	0.50
1:C:674:GLN:HG2	1:C:720:LEU:HD13	1.92	0.50
1:C:1386:ILE:HG12	1:C:1406:GLU:HB3	1.92	0.50
1:C:2346:LYS:O	1:C:2350:ASP:N	2.44	0.50
1:C:2446:VAL:HB	1:C:2447:PRO:HD3	1.92	0.50
1:A:1544:VAL:O	1:A:1548:ILE:HG13	2.11	0.50
2:B:132:ILE:HG21	2:B:174:LEU:HD11	1.93	0.50
1:C:1015:ILE:HD11	1:C:1067:LYS:HE2	1.93	0.50
1:C:1084:MET:SD	1:C:1084:MET:O	2.69	0.50
1:C:2112:LYS:HA	1:C:2126:VAL:HA	1.93	0.50
2:D:13:THR:HG21	2:D:292:HIS:H	1.75	0.50
2:D:44:LYS:HE2	2:D:61:ARG:HH22	1.75	0.50
5:J:661:TYR:CD2	5:J:697:VAL:HG11	2.47	0.50
5:J:730:VAL:HG21	5:J:790:PRO:CD	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:730:VAL:HB	5:J:788:GLU:O	2.12	0.50
1:A:256:LEU:HD22	1:A:259:TYR:CE2	2.47	0.50
1:A:272:ARG:N	1:A:322:ASP:OD1	2.45	0.50
1:A:673:GLN:OE1	1:A:719:LEU:HD22	2.12	0.50
1:A:1609:ARG:C	1:A:1610:ILE:N	2.65	0.50
1:A:1862:HIS:CD2	1:A:1898:LEU:HD23	2.46	0.50
1:A:2192:HIS:CG	1:A:2237:ASP:HB3	2.46	0.50
1:A:1013:ILE:HG23	1:A:1063:ARG:HE	1.76	0.50
1:A:2334:SER:HA	1:A:2337:ILE:HD12	1.92	0.50
2:B:121:GLU:HG3	2:B:165:LEU:N	2.26	0.50
1:C:502:ILE:HA	1:C:505:GLU:HG2	1.94	0.50
1:C:1135:ARG:HB2	1:C:1136:GLU:HA	1.94	0.50
1:C:1900:LEU:O	1:C:1904:LEU:HG	2.11	0.50
1:A:86:LEU:HA	1:A:89:ASP:HB2	1.92	0.50
1:A:215:ARG:HG3	1:A:233:LYS:HZ3	1.76	0.50
1:A:595:ILE:HG13	1:A:599:TYR:HD2	1.76	0.50
1:A:835:VAL:HG13	1:A:1525:VAL:CG1	2.42	0.50
1:A:1419:LYS:HG3	1:A:1433:LYS:HZ3	1.77	0.50
1:A:2092:ILE:HG22	1:A:2114:LYS:O	2.11	0.50
1:A:2121:TYR:CA	1:A:2122:LYS:HB2	2.30	0.50
1:A:2268:MET:HG2	1:A:2342:VAL:HA	1.94	0.50
2:B:99:ILE:CD1	2:B:122:VAL:HG21	2.41	0.50
1:C:1059:ARG:HD2	1:C:1099:LYS:HB3	1.94	0.50
1:C:1483:GLU:HA	1:C:1486:GLN:HE22	1.77	0.50
1:C:1960:ALA:O	1:C:2111:ARG:NH1	2.45	0.50
2:D:3:VAL:C	2:D:4:ILE:HG13	2.31	0.50
1:A:81:PHE:HB3	1:A:107:SER:HA	1.92	0.50
1:A:256:LEU:HD22	1:A:259:TYR:HE2	1.77	0.50
1:A:1527:GLU:O	1:A:1528:LEU:N	2.44	0.50
1:A:1759:ASN:HA	1:A:1762:LEU:HD12	1.93	0.50
1:C:143:SER:CB	1:C:190:ARG:HE	2.25	0.50
1:C:1445:TRP:O	1:C:1448:LEU:N	2.44	0.50
1:C:1598:ARG:C	1:C:1600:LEU:H	2.14	0.50
1:C:2026:MET:CG	1:C:2027:ASN:H	2.24	0.50
1:C:2061:LEU:HG	1:C:2101:PHE:N	2.27	0.50
2:D:242:LEU:HD11	2:D:245:THR:HG23	1.94	0.50
5:I:709:PHE:HE2	5:I:716:THR:HB	1.77	0.50
5:J:698:ARG:C	5:J:700:SER:N	2.65	0.50
1:A:263:ILE:HA	1:A:266:ASN:HB2	1.93	0.50
1:A:781:VAL:O	1:A:784:GLU:HB3	2.12	0.50
1:A:848:LEU:HD22	1:A:1547:GLN:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:TYR:O	1:A:1007:ILE:N	2.44	0.50
1:C:166:LEU:HB3	1:C:167:PRO:HD3	1.94	0.50
1:C:757:ILE:O	1:C:761:LEU:HG	2.10	0.50
1:C:1285:TRP:O	1:C:1286:VAL:HB	2.11	0.50
1:C:1844:LEU:HD21	1:C:1878:VAL:HG21	1.94	0.50
1:C:2153:ASP:HB2	1:C:2346:LYS:HG2	1.93	0.50
2:D:83:PHE:CD1	2:D:104:VAL:HG11	2.47	0.50
5:I:698:ARG:HB2	5:I:700:SER:H	1.77	0.50
5:I:730:VAL:CG2	5:I:789:THR:HA	2.41	0.50
1:A:2367:ASN:HB3	1:A:2371:ASP:HB2	1.93	0.50
2:B:274:VAL:HG12	2:B:291:HIS:HE1	1.75	0.50
1:C:458:LYS:HE3	1:C:461:PHE:HD2	1.77	0.50
1:C:982:TYR:HA	1:C:985:GLN:HB2	1.94	0.50
1:C:1127:VAL:HG23	1:C:1167:LEU:HD11	1.94	0.50
1:C:1487:TYR:HE2	1:C:1498:LYS:HE3	1.77	0.50
1:C:2284:ASN:HB3	1:C:2296:HIS:NE2	2.27	0.50
1:A:260:VAL:O	1:A:263:ILE:N	2.45	0.50
1:A:569:ALA:HA	1:A:591:PHE:CE1	2.47	0.50
2:B:26:ARG:HE	2:B:60:ILE:HD12	1.76	0.50
1:C:571:GLN:O	1:C:575:GLN:N	2.44	0.50
1:C:1165:LYS:C	1:C:1167:LEU:H	2.15	0.50
1:A:1245:LEU:HA	1:A:1275:LEU:HD23	1.94	0.49
1:A:2104:SER:HG	1:A:2106:GLN:N	2.10	0.49
2:B:7:SER:CB	2:B:274:VAL:HB	2.42	0.49
1:C:595:LEU:HA	1:C:598:ILE:HB	1.94	0.49
1:C:998:ARG:HE	1:C:1035:GLU:H	1.60	0.49
1:C:1712:THR:HA	1:C:1715:LEU:HG	1.94	0.49
1:C:2288:ASP:OD2	1:C:2293:LYS:HG3	2.12	0.49
2:D:229:HIS:HD2	2:D:252:TRP:H	1.60	0.49
1:A:971:ARG:HD3	1:A:977:GLN:HE21	1.77	0.49
1:A:1606:ALA:O	1:A:1610:ILE:N	2.44	0.49
1:C:822:LEU:HA	1:C:825:LEU:HB2	1.94	0.49
2:D:121:GLU:HG3	2:D:165:LEU:H	1.77	0.49
2:D:125:HIS:HB3	2:D:130:GLU:HB2	1.94	0.49
3:F:704:UNK:O	3:F:708:UNK:N	2.45	0.49
5:I:650:ARG:HG3	5:I:651:THR:HG23	1.93	0.49
1:A:633:LEU:HB3	1:A:674:PRO:HG2	1.94	0.49
1:A:1976:PHE:HB2	1:A:1985:MET:HB2	1.93	0.49
2:B:57:LEU:HD12	2:B:69:ALA:HB3	1.94	0.49
1:C:157:ILE:HG12	1:C:172:ARG:NH2	2.25	0.49
1:C:1839:SER:OG	1:C:1841:GLN:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:VAL:HA	1:A:366:ARG:HG3	1.94	0.49
1:A:438:LEU:O	1:A:442:ARG:N	2.45	0.49
1:A:633:LEU:HD21	1:A:665:SER:HA	1.94	0.49
1:A:849:ILE:HG21	1:A:1548:ILE:HG23	1.95	0.49
1:A:1660:TRP:HZ3	1:A:1724:ARG:CZ	2.25	0.49
1:A:1811:SER:HB2	1:A:1843:ARG:HH22	1.78	0.49
2:B:16:PHE:HB2	2:B:26:ARG:HB3	1.95	0.49
1:C:1425:GLY:HA2	1:C:1429:VAL:HG13	1.94	0.49
1:C:2339:ILE:HA	1:C:2342:GLU:CG	2.41	0.49
2:D:37:ARG:NH2	2:D:212:ARG:HH22	2.10	0.49
2:D:183:CYS:SG	2:D:222:LEU:HD21	2.52	0.49
5:J:789:THR:O	5:J:791:LEU:N	2.45	0.49
1:A:180:ILE:O	1:A:230:SER:OG	2.30	0.49
1:A:954:ARG:H	1:A:955:CYS:N	2.11	0.49
1:A:2390:ALA:HB3	1:A:2391:ASN:HB2	1.94	0.49
2:B:12:HIS:CB	2:B:30:HIS:O	2.61	0.49
1:C:173:LEU:CD2	1:C:209:ASP:HA	2.42	0.49
1:C:366:ARG:HA	1:C:369:VAL:CG2	2.43	0.49
1:C:1118:MET:HG3	1:C:1121:ARG:CG	2.42	0.49
1:A:636:VAL:CG1	1:A:675:ASP:HB3	2.34	0.49
1:C:281:LEU:HD11	1:C:330:LEU:HB3	1.95	0.49
1:C:690:PHE:HD1	1:C:728:PHE:HZ	1.60	0.49
1:C:1444:GLU:C	1:C:1445:TRP:HA	2.33	0.49
1:C:1732:LYS:HA	1:C:1737:ASN:HB2	1.94	0.49
2:D:101:VAL:HG11	2:D:143:TRP:HH2	1.74	0.49
1:A:649:THR:HB	1:A:650:ASP:HB2	1.95	0.49
1:A:1608:VAL:HA	1:A:1611:LYS:HB2	1.94	0.49
1:A:2286:ASP:HB2	1:A:2291:LYS:H	1.77	0.49
1:C:537:TYR:HB2	1:C:543:PHE:CE2	2.48	0.49
1:C:626:CYS:HB2	1:C:629:THR:HG22	1.93	0.49
1:C:826:GLY:HA3	1:C:827:GLN:HG2	1.93	0.49
1:C:939:THR:HG21	1:C:1262:CYS:SG	2.53	0.49
1:C:1429:VAL:HB	1:C:1435:LYS:NZ	2.27	0.49
1:C:2046:ASN:HA	1:C:2049:ARG:HH11	1.78	0.49
1:A:704:SER:HB2	1:A:709:TYR:CB	2.33	0.49
1:A:933:LEU:HD13	1:A:939:ALA:HB2	1.93	0.49
1:A:993:LYS:HZ2	1:A:1029:LYS:HE3	1.77	0.49
1:A:1120:ARG:HA	1:A:1123:GLN:HG2	1.95	0.49
1:A:1155:PHE:CE2	1:C:622:LYS:HB3	2.47	0.49
1:A:1383:ALA:HA	1:A:1386:ILE:HG22	1.95	0.49
1:A:2126:LYS:HD2	1:A:2176:LEU:HG	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2354:MET:SD	1:A:2427:ILE:HG21	2.53	0.49
2:B:244:THR:HG22	2:B:245:THR:O	2.13	0.49
1:C:543:PHE:CD1	1:C:545:ILE:HG23	2.47	0.49
1:C:573:LEU:HD13	1:C:577:PHE:HE2	1.76	0.49
1:C:1887:HIS:HB2	1:C:1927:ARG:HG2	1.95	0.49
2:D:205:ALA:O	2:D:224:THR:HG21	2.12	0.49
1:A:1341:ALA:H	1:A:1342:GLN:HB3	1.77	0.49
1:A:2043:TYR:HE1	5:I:660:GLU:HG3	1.78	0.49
2:B:26:ARG:NH2	2:B:47:LEU:HD21	2.28	0.49
1:C:682:PHE:C	1:C:684:ALA:H	2.15	0.49
1:C:1061:VAL:N	1:C:1062:PRO:HD3	2.27	0.49
1:A:232:SER:HB2	1:A:236:TYR:CE2	2.48	0.49
1:A:264:LEU:HB2	1:A:306:GLN:CD	2.33	0.49
1:A:1177:ASP:O	1:A:1181:ASN:N	2.46	0.49
1:A:1729:PRO:HD2	1:A:1730:LYS:HD2	1.95	0.49
1:A:2111:PHE:HD1	1:A:2112:CYS:CA	2.25	0.49
1:C:424:ALA:N	1:C:425:PHE:HB2	2.28	0.49
1:C:1760:HIS:CD2	1:C:1832:ILE:HG13	2.48	0.49
2:D:231:ALA:H	2:D:246:LEU:C	2.16	0.49
2:D:253:VAL:N	2:D:269:SER:HG	2.10	0.49
1:A:642:LYS:HE2	1:A:646:ILE:HG12	1.94	0.48
1:A:690:GLY:HA2	1:A:693:LEU:H	1.77	0.48
1:A:792:GLU:HB3	1:A:795:ARG:H	1.78	0.48
1:A:964:PRO:HB3	1:A:967:ILE:HB	1.95	0.48
1:A:1440:LEU:HD13	1:A:1622:MET:CE	2.44	0.48
1:A:1458:LYS:HB3	1:A:1459:PRO:CD	2.42	0.48
2:B:40:ILE:HG21	2:B:44:LYS:HA	1.94	0.48
2:B:78:VAL:HA	2:B:94:SER:HA	1.94	0.48
1:C:439:LEU:HA	1:C:442:ILE:HG12	1.95	0.48
1:C:469:CYS:HG	1:C:470:ALA:N	2.10	0.48
1:C:678:LEU:HD23	1:C:727:LYS:HB3	1.94	0.48
1:C:1763:ALA:HB2	1:C:1828:PHE:HB3	1.94	0.48
1:C:1826:LYS:HB2	1:C:1863:MET:SD	2.53	0.48
2:D:12:HIS:NE2	2:D:34:GLN:HG3	2.28	0.48
5:I:698:ARG:HA	5:I:759:ASP:HA	1.93	0.48
5:J:730:VAL:HG21	5:J:789:THR:CA	2.41	0.48
1:A:817:ARG:HD2	1:A:867:LEU:CD1	2.43	0.48
1:A:1440:LEU:HB3	1:A:1622:MET:SD	2.53	0.48
1:C:91:LYS:HD3	1:C:134:ILE:HG21	1.95	0.48
1:C:285:VAL:HA	1:C:335:LEU:HD13	1.95	0.48
1:C:1515:ALA:O	1:C:1518:HIS:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2157:PHE:HD1	1:C:2160:HIS:CD2	2.30	0.48
2:D:131:LEU:O	2:D:143:TRP:N	2.46	0.48
2:D:297:CYS:HA	2:D:298:VAL:CB	2.18	0.48
4:G:132:GLY:O	4:G:134:ASP:N	2.46	0.48
1:A:90:LYS:HB3	1:A:133:ILE:HG21	1.95	0.48
1:A:1245:LEU:HD12	1:A:1275:LEU:HD23	1.94	0.48
1:A:1724:ARG:HG3	1:A:1725:VAL:HG13	1.96	0.48
1:C:842:TYR:CB	1:C:844:GLU:HG2	2.30	0.48
1:C:969:LEU:HD13	1:C:985:GLN:HB3	1.95	0.48
1:C:1088:VAL:HG22	1:C:1103:ILE:HG21	1.94	0.48
1:C:1356:LYS:HD2	1:C:1375:ILE:HD13	1.96	0.48
1:C:1857:PRO:C	1:C:1859:ALA:N	2.65	0.48
1:C:2444:LEU:HD13	1:C:2452:LYS:HE3	1.96	0.48
1:A:215:ARG:O	1:A:219:ASP:HB2	2.14	0.48
1:A:335:LEU:HD13	1:A:341:TYR:HB3	1.94	0.48
1:A:546:LYS:O	1:A:550:SER:N	2.45	0.48
1:A:1069:VAL:HG13	1:A:1105:LEU:HG	1.95	0.48
1:A:1130:ASN:HB3	1:A:1166:LEU:HB3	1.96	0.48
1:A:2305:ILE:HB	1:A:2375:LYS:HD3	1.94	0.48
2:B:18:GLU:HG2	2:B:25:SER:HB2	1.95	0.48
1:C:818:ARG:HB2	1:C:818:ARG:HH11	1.77	0.48
1:C:1069:LEU:HD22	1:C:1106:LEU:O	2.13	0.48
1:C:1192:THR:C	1:C:1194:ILE:H	2.17	0.48
1:C:1273:ALA:HB3	1:C:1324:PHE:CE1	2.48	0.48
3:F:507:UNK:C	3:F:508:UNK:CA	2.88	0.48
1:A:357:LYS:HZ3	1:A:366:ARG:HA	1.79	0.48
1:A:1164:LYS:HB3	1:A:1170:ARG:HG3	1.95	0.48
1:A:1586:ILE:C	1:A:1587:ASP:HB2	2.34	0.48
1:A:2147:LEU:HD22	1:A:2353:LEU:HD13	1.96	0.48
1:C:581:GLN:HG3	1:C:589:LEU:HD22	1.95	0.48
1:C:1668:ASP:HA	1:C:1671:LEU:HD12	1.94	0.48
1:C:1902:SER:HB3	1:C:1934:ILE:HD12	1.96	0.48
2:D:39:GLU:HA	2:D:299:ALA:HB2	1.96	0.48
2:D:210:ILE:HD11	2:D:224:THR:HA	1.95	0.48
1:A:698:ILE:HG23	1:C:1079:TYR:HE2	1.73	0.48
1:A:1548:ILE:HG22	1:A:1552:LEU:HD22	1.96	0.48
1:A:1994:GLU:O	1:A:1997:LYS:HB2	2.12	0.48
1:A:2133:GLN:HG3	1:A:2370:PHE:CZ	2.49	0.48
1:C:377:ALA:HB1	1:C:382:ALA:HB1	1.95	0.48
1:C:1460:LYS:HB2	1:C:1461:PRO:HD2	1.95	0.48
1:C:1557:ILE:HG22	1:C:1577:TRP:HE1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1578:ASN:HA	1:C:1581:LEU:HG	1.95	0.48
1:C:2279:ASP:HA	1:C:2309:ARG:HH22	1.79	0.48
2:D:37:ARG:HG3	2:D:81:VAL:N	2.29	0.48
5:J:693:PHE:CZ	5:J:760:ARG:HD3	2.48	0.48
1:A:594:LEU:O	1:A:595:ILE:HD12	2.14	0.48
1:A:765:PRO:O	1:A:766:LYS:C	2.51	0.48
1:A:1966:TYR:HB2	1:A:2049:ILE:HD12	1.95	0.48
1:A:2459:GLU:HA	1:A:2462:CYS:HB3	1.94	0.48
1:C:601:ILE:HA	1:C:602:GLU:HA	1.72	0.48
1:C:915:GLU:HB3	1:C:917:TYR:HB2	1.94	0.48
1:C:1244:ARG:HG3	1:C:1269:TYR:OH	2.14	0.48
1:C:2062:GLU:CG	1:C:2099:PRO:HB2	2.44	0.48
5:J:698:ARG:HB2	5:J:700:SER:H	1.78	0.48
1:A:280:LEU:HD11	1:A:333:GLU:OE1	2.14	0.48
1:A:731:PRO:HB3	1:A:736:GLU:HB2	1.95	0.48
1:A:1814:LEU:HB2	1:A:1816:HIS:CD2	2.48	0.48
2:B:6:VAL:HG22	2:B:38:LEU:HD22	1.94	0.48
1:C:280:ARG:NH1	1:C:328:THR:HB	2.27	0.48
1:C:640:VAL:HG13	1:C:643:LYS:HB3	1.96	0.48
1:C:1030:LYS:C	1:C:1032:LEU:H	2.17	0.48
1:C:1121:ARG:HA	1:C:1124:GLN:HG2	1.95	0.48
1:C:1344:GLN:CD	1:C:1350:ALA:H	2.17	0.48
1:C:1623:ARG:CZ	1:C:1663:ALA:HB1	2.44	0.48
1:C:1826:LYS:HE3	1:C:1863:MET:HB2	1.95	0.48
2:D:275:ARG:HD3	2:D:284:ILE:HG12	1.95	0.48
3:F:556:UNK:O	3:F:559:UNK:N	2.47	0.48
1:A:468:CYS:SG	1:A:469:ALA:N	2.87	0.48
1:A:590:GLU:C	1:A:594:LEU:H	2.16	0.48
1:A:619:PHE:HA	1:A:622:ASP:HB3	1.94	0.48
1:A:1060:VAL:N	1:A:1061:PRO:HD2	2.29	0.48
1:A:1434:LEU:HD13	1:A:1468:LEU:HD21	1.95	0.48
1:C:508:PRO:HG3	4:G:188:PHE:HA	1.94	0.48
1:C:631:VAL:HA	1:C:634:LEU:HB2	1.95	0.48
1:C:849:LEU:HD21	1:C:1546:VAL:HB	1.96	0.48
1:C:1014:ILE:HD11	1:C:1022:ILE:HD12	1.96	0.48
1:C:1195:ILE:O	1:C:1195:ILE:HG22	2.14	0.48
1:C:2138:LEU:HD11	1:C:2362:PHE:CZ	2.49	0.48
5:J:707:ILE:HD13	5:J:728:LEU:HD22	1.95	0.48
1:A:323:SER:HB2	1:A:325:HIS:CD2	2.49	0.48
1:A:1489:MET:SD	1:A:1490:LYS:HG2	2.54	0.48
1:A:1556:ILE:O	1:A:1559:LYS:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1823:ILE:HG23	1:A:1824:LYS:H	1.79	0.48
1:C:1050:ILE:CD1	1:C:1065:ILE:HG12	2.43	0.48
1:C:1496:PRO:HA	1:C:1525:LEU:HD22	1.95	0.48
1:C:1591:TRP:HB3	1:C:1614:PHE:HZ	1.79	0.48
1:C:1612:ILE:HG21	1:C:1656:ALA:CB	2.43	0.48
1:C:1745:TYR:O	1:C:1762:TRP:NE1	2.47	0.48
1:C:1866:GLY:HA2	1:C:1869:LEU:HG	1.95	0.48
1:C:1918:VAL:HG22	1:C:2170:PRO:O	2.14	0.48
3:F:554:UNK:C	3:F:556:UNK:N	2.73	0.48
1:A:284:VAL:HG13	1:A:334:LEU:HD21	1.96	0.47
1:A:367:GLU:HA	1:A:370:ALA:CB	2.43	0.47
1:A:1922:SER:HB2	1:A:1926:GLN:HB3	1.96	0.47
1:C:2255:LEU:HG	1:C:2259:THR:HB	1.96	0.47
5:I:699:LYS:NZ	5:I:702:THR:HG21	2.29	0.47
1:A:461:TYR:CD2	1:A:497:GLU:HB3	2.48	0.47
1:A:1736:PRO:HA	1:A:1739:ILE:HB	1.95	0.47
1:A:1972:ALA:HB1	1:A:1988:ALA:CB	2.44	0.47
1:A:2265:VAL:HG23	1:A:2266:MET:H	1.78	0.47
2:B:9:GLY:O	2:B:12:HIS:CE1	2.67	0.47
1:C:401:LYS:O	1:C:414:PRO:HG3	2.14	0.47
1:C:948:ILE:HA	1:C:952:LEU:HB2	1.95	0.47
1:C:1244:ARG:NH2	1:C:1260:ARG:HD3	2.29	0.47
1:C:1601:VAL:O	1:C:1602:ILE:HB	2.14	0.47
1:C:1626:LEU:O	1:C:1630:VAL:HG22	2.13	0.47
1:C:2279:ASP:HB3	1:C:2284:ASN:ND2	2.29	0.47
1:C:2421:ARG:HA	1:C:2424:LEU:HB3	1.94	0.47
3:E:602:UNK:O	3:E:606:UNK:N	2.47	0.47
1:A:453:LYS:H	1:A:454:GLN:HA	1.76	0.47
1:A:1558:TYR:HB2	1:A:1572:ARG:HE	1.80	0.47
1:A:1601:LYS:O	1:A:1603:LYS:N	2.46	0.47
2:B:68:VAL:HG12	2:B:69:ALA:N	2.29	0.47
1:C:347:TYR:O	1:C:351:TYR:HB3	2.15	0.47
1:C:1448:LEU:HD23	1:C:1451:LEU:HD13	1.95	0.47
1:C:2194:HIS:O	1:C:2198:LYS:HD3	2.14	0.47
1:C:2432:LYS:O	1:C:2449:GLN:HG2	2.14	0.47
2:D:10:TYR:O	2:D:12:HIS:CD2	2.67	0.47
1:A:89:ASP:HB3	1:A:90:LYS:H	1.29	0.47
1:A:759:ILE:O	1:A:763:ILE:N	2.47	0.47
1:A:862:ARG:HB3	1:A:2156:ARG:HA	1.96	0.47
1:A:1449:LEU:O	1:A:1453:LYS:N	2.32	0.47
1:A:2061:LEU:H	1:A:2097:PRO:C	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2107:ARG:N	1:A:2108:PRO:CD	2.77	0.47
1:C:368:GLU:HA	1:C:371:ALA:HB2	1.96	0.47
1:C:2337:PHE:O	1:C:2341:CYS:N	2.47	0.47
2:D:40:ILE:HD13	2:D:301:ASN:HB2	1.95	0.47
2:D:84:GLN:CB	2:D:89:TRP:HB2	2.33	0.47
2:D:246:LEU:HD22	2:D:277:TRP:CZ3	2.49	0.47
3:E:756:UNK:HA	3:E:759:UNK:H2	1.79	0.47
1:A:272:ARG:HG2	1:A:273:ASP:H	1.79	0.47
1:A:400:LYS:HG3	1:A:402:ILE:HG12	1.95	0.47
1:A:673:GLN:HA	1:A:676:ASN:HD21	1.76	0.47
1:A:710:VAL:HG12	1:A:711:VAL:HA	1.96	0.47
1:A:1027:ILE:HB	1:A:1070:THR:HB	1.96	0.47
1:A:2075:GLU:O	1:A:2091:LYS:HA	2.15	0.47
1:C:235:LEU:CB	1:C:236:GLU:HA	2.44	0.47
1:C:260:TYR:HD2	1:C:260:TYR:N	2.12	0.47
1:C:301:LEU:HG	1:C:340:ALA:HA	1.96	0.47
1:C:506:LYS:HD3	1:C:508:PRO:O	2.14	0.47
1:C:690:PHE:CE1	1:C:731:MET:HB3	2.50	0.47
1:C:793:GLU:HG2	1:C:796:ARG:HG3	1.97	0.47
5:I:698:ARG:HG3	5:I:788:GLU:HG2	1.95	0.47
1:A:180:ILE:HG22	1:A:223:LEU:HD13	1.93	0.47
1:A:937:HIS:HE1	1:A:977:GLN:HA	1.79	0.47
1:A:1073:PRO:HB3	1:A:1110:LYS:H	1.79	0.47
1:A:1427:VAL:O	1:A:1433:LYS:HE2	2.13	0.47
1:A:2082:ARG:HH12	1:A:2167:ILE:HD13	1.79	0.47
1:A:2189:ILE:O	1:A:2193:ARG:HG3	2.15	0.47
1:C:634:LEU:HA	1:C:637:VAL:HB	1.96	0.47
1:C:651:ASP:CB	1:C:652:PRO:HA	2.44	0.47
1:C:1655:TYR:HA	1:C:1658:LEU:HB2	1.96	0.47
2:D:11:ASP:HB3	2:D:293:LYS:H	1.80	0.47
2:D:213:ILE:HG22	2:D:224:THR:HG23	1.97	0.47
5:I:693:PHE:O	5:I:694:THR:N	2.48	0.47
1:A:115:ARG:HB2	1:A:159:TYR:HB3	1.97	0.47
1:A:125:PHE:O	1:A:129:LEU:HB3	2.14	0.47
1:A:259:TYR:HB3	1:A:293:ILE:HD13	1.95	0.47
1:A:300:LEU:HD22	1:A:303:GLN:HG3	1.95	0.47
1:A:796:TYR:HE2	1:A:843:GLU:HB3	1.79	0.47
1:A:841:TYR:O	1:A:843:GLU:N	2.47	0.47
1:A:848:LEU:H	1:A:1547:GLN:NE2	2.13	0.47
1:A:1516:HIS:O	1:A:1520:ALA:N	2.47	0.47
1:A:1613:ALA:O	1:A:1617:ARG:HG2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1870:ILE:HG12	1:A:1902:LEU:HA	1.96	0.47
1:A:2245:LYS:HE3	1:A:2287:ARG:HH11	1.78	0.47
1:A:2275:LEU:HG	1:A:2299:ASP:C	2.35	0.47
1:A:2449:ASP:O	1:A:2453:GLN:HB2	2.15	0.47
2:B:91:VAL:HB	2:B:145:LEU:HD21	1.97	0.47
1:C:112:THR:O	1:C:114:LEU:HG	2.15	0.47
1:C:157:ILE:O	1:C:163:THR:HG21	2.15	0.47
1:C:260:TYR:N	1:C:260:TYR:CD2	2.80	0.47
1:C:500:LEU:HD12	1:C:503:LEU:HD12	1.96	0.47
1:C:573:LEU:O	1:C:577:PHE:HB2	2.14	0.47
1:C:620:PHE:HD1	1:C:623:ASP:HB3	1.78	0.47
1:C:712:VAL:HB	1:C:713:PRO:CD	2.45	0.47
1:C:926:MET:HA	1:C:929:LEU:HD23	1.95	0.47
1:C:1541:ALA:HB1	1:C:1542:TYR:HA	1.97	0.47
1:C:1561:LYS:HA	1:C:1570:ARG:HH21	1.78	0.47
1:C:1893:VAL:O	1:C:1896:SER:HB2	2.15	0.47
1:C:1916:LEU:HA	1:C:1919:ALA:HB2	1.96	0.47
2:D:83:PHE:HD1	2:D:104:VAL:HG11	1.78	0.47
2:D:173:MET:HB3	2:D:174:LEU:CA	2.44	0.47
5:J:703:ILE:HG21	5:J:732:ASP:CG	2.34	0.47
1:A:324:VAL:HA	1:A:325:HIS:N	2.30	0.47
1:A:2220:LEU:HD13	2:B:209:TYR:HD2	1.79	0.47
2:B:7:SER:OG	2:B:274:VAL:HB	2.14	0.47
2:B:233:VAL:HG11	2:B:279:LEU:HD21	1.97	0.47
1:C:818:ARG:O	1:C:822:LEU:HB3	2.15	0.47
1:C:1239:TRP:O	1:C:1243:ILE:HG12	2.15	0.47
2:D:4:ILE:O	2:D:5:LEU:HB3	2.14	0.47
5:J:681:TYR:O	5:J:681:TYR:CD1	2.68	0.47
1:A:259:TYR:HB2	1:A:290:LEU:CD1	2.45	0.47
1:A:1126:VAL:HG23	1:A:1166:LEU:HD11	1.97	0.47
1:A:2113:ILE:HG13	1:A:2123:TYR:CE2	2.49	0.47
1:C:260:TYR:HE1	1:C:300:ALA:CB	2.27	0.47
1:C:410:ASN:O	1:C:450:PHE:HD2	1.97	0.47
1:C:417:LEU:HD13	1:C:460:LEU:HD11	1.97	0.47
1:C:1513:LYS:HA	1:C:1516:GLU:HB3	1.97	0.47
1:C:1587:ASN:O	1:C:1590:VAL:HG23	2.14	0.47
1:C:2432:LYS:HD3	1:C:2437:ASP:HB2	1.97	0.47
2:D:221:HIS:HB3	2:D:233:VAL:HG22	1.97	0.47
4:G:136:TRP:HA	4:G:137:VAL:O	2.15	0.47
5:I:737:ASN:OD1	5:I:768:SER:HB2	2.15	0.47
1:A:328:LEU:O	1:A:368:VAL:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:TYR:CG	1:A:441:ILE:HB	2.50	0.47
1:A:620:ILE:HA	1:A:660:LEU:HD21	1.97	0.47
1:A:947:ILE:HA	1:A:951:LEU:HD13	1.96	0.47
1:A:1087:VAL:HA	1:A:1099:LYS:HD2	1.97	0.47
1:A:1227:TRP:CH2	1:A:1238:TRP:HE3	2.33	0.47
1:C:382:ALA:C	1:C:386:LYS:HD3	2.35	0.47
1:C:721:GLU:CB	1:C:722:LEU:HB2	2.40	0.47
1:C:836:VAL:CG2	1:C:845:LEU:HD12	2.45	0.47
1:C:1070:VAL:CG2	1:C:1106:LEU:HG	2.45	0.47
1:C:1521:ASN:HB3	1:C:1525:LEU:HD21	1.95	0.47
1:C:1636:GLU:HG2	1:C:1653:VAL:HG21	1.96	0.47
1:A:145:LYS:HD3	1:A:186:GLU:HG3	1.97	0.46
1:A:399:LEU:HB3	1:A:405:ASN:O	2.15	0.46
1:A:1555:ILE:HG21	1:A:1575:TRP:NE1	2.30	0.46
2:B:125:HIS:HA	2:B:167:MET:HE1	1.96	0.46
2:B:221:HIS:CE1	2:B:279:LEU:HD22	2.49	0.46
1:C:1757:LYS:HD2	1:C:1832:ILE:HG21	1.97	0.46
1:A:676:ASN:HB3	1:A:723:THR:HA	1.96	0.46
1:A:788:VAL:HB	1:A:795:ARG:HH11	1.80	0.46
1:A:1820:ILE:HG23	1:A:1824:LYS:HG2	1.97	0.46
1:A:1877:LEU:HD23	1:A:1913:PRO:HD2	1.96	0.46
2:B:40:ILE:HG23	2:B:47:LEU:HD23	1.96	0.46
2:B:105:ARG:O	2:B:106:SER:CB	2.62	0.46
2:B:168:ALA:HB3	2:B:171:GLY:H	1.80	0.46
1:C:1044:LEU:O	1:C:1048:LEU:HB2	2.15	0.46
1:C:2192:ARG:O	1:C:2196:GLU:N	2.46	0.46
1:A:91:LEU:HD13	1:A:144:GLU:HG3	1.97	0.46
1:A:698:ILE:O	1:C:1079:TYR:HE2	1.98	0.46
1:A:1504:CYS:SG	1:A:1510:PHE:HA	2.55	0.46
1:A:2182:SER:HA	1:A:2287:ARG:H	1.81	0.46
2:B:91:VAL:HG11	2:B:131:LEU:HD13	1.97	0.46
2:B:233:VAL:HG21	2:B:279:LEU:HG	1.96	0.46
1:C:269:TRP:HB2	1:C:310:PHE:HE2	1.80	0.46
1:C:601:ILE:HA	1:C:603:HIS:HB2	1.98	0.46
1:C:703:LEU:HD13	1:C:714:SER:HB3	1.96	0.46
1:C:1295:ASP:CG	1:C:1342:TYR:HH	2.18	0.46
1:C:1369:ILE:HA	1:C:1372:LEU:HD23	1.97	0.46
1:C:1432:MET:O	1:C:1435:LYS:HG3	2.14	0.46
1:C:1627:ALA:O	1:C:1631:LEU:HG	2.16	0.46
1:C:2133:ILE:CD1	1:C:2176:GLY:HA3	2.45	0.46
1:C:2194:HIS:CE1	1:C:2239:ASP:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:GLY:HA2	1:A:304:TRP:NE1	2.31	0.46
1:A:644:LEU:HA	1:A:647:ALA:HB3	1.98	0.46
1:A:689:PHE:CZ	1:A:732:LYS:HD3	2.51	0.46
1:A:1555:ILE:HG13	1:A:1556:ILE:HG13	1.98	0.46
1:A:1730:LYS:HB3	1:A:1735:ASN:CB	2.41	0.46
1:C:2253:THR:HG22	1:C:2257:ARG:HD2	1.97	0.46
2:D:6:VAL:HG13	2:D:7:SER:HB3	1.97	0.46
1:A:328:LEU:HB3	1:A:368:VAL:HG13	1.98	0.46
1:A:1351:LEU:HD22	1:A:1377:LEU:HD22	1.97	0.46
2:B:60:ILE:O	2:B:60:ILE:HG13	2.15	0.46
2:B:175:ALA:C	2:B:222:LEU:HD21	2.36	0.46
1:C:1445:TRP:HB2	1:C:1478:LEU:HB3	1.97	0.46
1:C:1760:HIS:CG	1:C:1832:ILE:HG13	2.50	0.46
2:D:16:PHE:O	2:D:26:ARG:N	2.48	0.46
2:D:181:GLY:HA2	2:D:210:ILE:HB	1.96	0.46
1:A:763:ILE:HG23	1:A:805:ILE:HD12	1.98	0.46
1:A:1084:PRO:HA	1:A:1087:VAL:HG13	1.98	0.46
1:A:1628:VAL:HB	1:A:1632:LEU:HD12	1.98	0.46
1:A:1884:ILE:HB	1:A:1925:ARG:HD2	1.97	0.46
1:A:2134:ASP:HA	1:A:2137:VAL:HB	1.97	0.46
1:A:2211:ALA:HB1	1:A:2213:ASP:C	2.36	0.46
1:A:2246:SER:O	1:A:2248:SER:N	2.49	0.46
1:C:640:VAL:HB	1:C:679:ARG:HH22	1.79	0.46
1:C:715:LEU:O	1:C:719:LEU:HB3	2.15	0.46
1:C:850:ILE:HG12	1:C:1550:ILE:HA	1.96	0.46
1:C:998:ARG:C	1:C:999:PRO:N	2.68	0.46
1:C:1655:TYR:CE1	1:C:1720:LEU:HD21	2.51	0.46
1:C:2128:LYS:HD2	1:C:2133:ILE:HD11	1.98	0.46
1:C:2222:LEU:HG	2:D:252:TRP:CZ3	2.50	0.46
5:J:701:SER:N	5:J:702:THR:HB	2.29	0.46
1:A:774:VAL:N	1:A:775:ALA:HB2	2.31	0.46
1:A:1610:ILE:HG23	1:A:1654:ALA:HB2	1.98	0.46
1:A:2185:PHE:HB3	1:A:2280:PRO:HA	1.96	0.46
1:A:2368:TRP:HA	1:A:2416:ARG:HH22	1.79	0.46
1:C:89:PHE:HD1	1:C:101:ALA:HB1	1.81	0.46
1:C:533:GLN:C	1:C:535:ASN:N	2.68	0.46
1:C:1090:MET:HB3	1:C:1093:TYR:CD2	2.50	0.46
1:C:1871:GLN:HE21	1:C:1873:GLY:HA3	1.81	0.46
4:H:111:ALA:O	4:H:114:HIS:N	2.49	0.46
5:J:725:GLU:HG3	5:J:726:ASP:H	1.80	0.46
1:A:227:ASN:O	1:A:230:SER:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:ARG:HD2	1:A:368:VAL:HG21	1.98	0.46
1:A:449:PHE:HB3	1:A:452:ARG:HD2	1.97	0.46
1:A:636:VAL:HG13	1:A:675:ASP:CB	2.37	0.46
1:A:773:ALA:N	1:A:775:ALA:HB2	2.30	0.46
1:A:1280:PHE:HA	1:A:1281:SER:HA	1.76	0.46
1:A:1587:ASP:N	1:A:1588:VAL:CB	2.75	0.46
1:A:1588:VAL:HG11	1:A:1615:LEU:CD2	2.46	0.46
1:A:1601:LYS:HD2	1:A:1635:GLU:HG3	1.98	0.46
1:A:2099:PHE:HA	1:A:2111:PHE:HE2	1.79	0.46
2:B:230:THR:HG22	2:B:246:LEU:H	1.81	0.46
1:C:346:LYS:HD3	1:C:350:ILE:HG13	1.97	0.46
1:C:1734:ARG:HH12	1:C:1771:SER:HB3	1.80	0.46
1:C:2082:GLY:HA3	1:C:2123:TYR:CE1	2.50	0.46
2:D:53:GLN:HE21	2:D:94:SER:HB3	1.80	0.46
5:I:730:VAL:HG21	5:I:790:PRO:N	2.31	0.46
1:A:361:PHE:CE1	1:A:414:PHE:CZ	2.99	0.46
1:A:1599:VAL:HA	1:A:1600:ILE:HA	1.70	0.46
1:A:1622:MET:O	1:A:1626:LYS:HD3	2.15	0.46
1:A:1911:VAL:O	1:A:1915:MET:N	2.49	0.46
1:A:2109:ARG:HG3	1:A:2125:LEU:HD13	1.98	0.46
1:A:2112:CYS:HB3	1:A:2122:LYS:H	1.79	0.46
1:A:2190:ARG:O	1:A:2194:GLU:N	2.43	0.46
2:B:74:HIS:HE1	2:B:102:TRP:HE1	1.64	0.46
1:C:1526:LEU:HD22	1:C:1548:ALA:HB1	1.98	0.46
1:C:2061:LEU:HD21	1:C:2101:PHE:HB2	1.97	0.46
1:C:2080:VAL:HA	1:C:2092:VAL:CG1	2.46	0.46
1:C:2404:GLU:HB3	1:C:2405:GLU:N	2.30	0.46
1:A:145:LYS:HB3	1:A:189:ARG:HB3	1.98	0.46
1:A:1384:ILE:HD13	1:A:1408:ARG:HH21	1.80	0.46
1:A:1740:LEU:O	1:A:1744:LEU:HG	2.16	0.46
1:A:2030:LYS:HD2	1:A:2033:SER:HB2	1.98	0.46
1:A:2368:TRP:HA	1:A:2416:ARG:NH2	2.31	0.46
1:A:2423:VAL:C	1:A:2426:ARG:HB3	2.36	0.46
2:B:147:GLU:HG2	2:B:149:GLN:HB3	1.98	0.46
2:B:156:PRO:HB3	2:B:186:TRP:HE1	1.81	0.46
1:C:289:LYS:HG3	1:C:338:LEU:HD21	1.98	0.46
1:C:462:TYR:OH	1:C:501:MET:HB2	2.15	0.46
2:D:4:ILE:O	2:D:5:LEU:CB	2.64	0.46
4:H:111:ALA:C	4:H:113:ILE:H	2.18	0.46
5:I:675:SER:HB3	5:I:687:LYS:HD3	1.97	0.46
5:I:698:ARG:HA	5:I:759:ASP:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LYS:HE2	1:A:237:ARG:CD	2.46	0.45
1:A:305:PHE:HD2	1:A:306:GLN:HE21	1.64	0.45
1:A:412:LYS:HZ1	1:A:442:ARG:HD3	1.81	0.45
1:A:725:LEU:HB3	1:A:760:LEU:HB3	1.97	0.45
1:A:1216:LEU:HA	1:A:1217:PRO:CA	2.39	0.45
1:A:2004:ARG:HB3	1:A:2063:HIS:CD2	2.52	0.45
1:A:2377:ILE:HD11	1:A:2415:ILE:HD13	1.98	0.45
1:C:163:THR:O	1:C:168:ASN:HB3	2.16	0.45
1:C:245:ILE:HG12	1:C:249:LEU:HD12	1.97	0.45
1:C:265:LEU:HD13	1:C:307:GLN:HE21	1.82	0.45
1:C:682:PHE:O	1:C:684:ALA:N	2.46	0.45
1:C:747:ASN:C	1:C:749:SER:H	2.20	0.45
1:C:1559:LYS:HG2	1:C:1563:LEU:HD13	1.98	0.45
2:D:4:ILE:HG23	2:D:60:ILE:HD13	1.97	0.45
2:D:6:VAL:O	2:D:274:VAL:HG21	2.16	0.45
3:E:651:UNK:O	3:E:653:UNK:N	2.49	0.45
1:A:357:LYS:HZ2	1:A:414:PHE:HD1	1.62	0.45
1:A:1286:GLU:HA	1:A:1289:THR:HG22	1.97	0.45
1:A:1838:LEU:HA	1:A:1841:ALA:HB3	1.98	0.45
2:B:11:ASP:HB2	2:B:292:HIS:HB2	1.98	0.45
2:B:185:VAL:HG11	2:B:240:PHE:CZ	2.52	0.45
1:C:596:ILE:CD1	1:C:600:TYR:HD2	2.29	0.45
2:D:156:PRO:HA	2:D:186:TRP:HZ2	1.81	0.45
3:F:756:UNK:C	3:F:757:UNK:HA	2.45	0.45
1:A:220:TRP:N	1:A:234:LEU:HD13	2.32	0.45
1:A:354:MET:HG3	1:A:388:LEU:HD22	1.98	0.45
1:A:574:GLN:O	1:A:578:MET:HG2	2.16	0.45
1:A:1555:ILE:O	1:A:1572:ARG:NH2	2.50	0.45
1:A:1758:HIS:CG	1:A:1830:ILE:HD11	2.51	0.45
1:A:2278:ARG:O	1:A:2317:ARG:HD2	2.17	0.45
1:A:2446:GLU:O	1:A:2450:LYS:N	2.43	0.45
2:B:8:ALA:HB3	2:B:35:VAL:HG21	1.97	0.45
2:B:164:SER:CB	2:B:212:ARG:HA	2.46	0.45
2:B:248:GLY:HA3	2:B:251:ARG:NE	2.31	0.45
1:C:329:LEU:O	1:C:369:VAL:HG13	2.16	0.45
1:C:361:LYS:HE3	1:C:366:ARG:NH2	2.31	0.45
1:C:397:LEU:HD23	1:C:401:LYS:HG2	1.99	0.45
1:C:1430:GLU:HA	1:C:1458:THR:CG2	2.45	0.45
1:C:1556:GLU:HA	1:C:1559:LYS:HE3	1.98	0.45
1:C:2258:ARG:O	1:C:2261:TYR:N	2.50	0.45
1:A:115:ARG:HE	1:A:166:PRO:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:815:PHE:HB3	1:A:818:ASP:C	2.36	0.45
1:A:1142:ASN:HA	1:A:1145:SER:HB3	1.98	0.45
1:A:1181:ASN:HA	1:A:1184:LEU:HB3	1.97	0.45
1:A:2203:GLU:O	1:A:2207:MET:N	2.49	0.45
1:C:176:TYR:HA	1:C:179:VAL:HG22	1.98	0.45
1:C:715:LEU:HD21	1:C:754:LYS:HG3	1.99	0.45
1:C:799:LYS:C	1:C:800:GLU:N	2.70	0.45
1:C:923:HIS:O	1:C:923:HIS:CG	2.69	0.45
1:C:1860:THR:HA	1:C:1864:HIS:HB3	1.97	0.45
1:C:1880:PRO:HA	1:C:1883:ILE:HG12	1.97	0.45
1:C:2157:PHE:HD1	1:C:2160:HIS:CG	2.34	0.45
1:C:2189:VAL:HA	1:C:2192:ARG:HG2	1.98	0.45
1:A:482:LEU:HD11	1:A:498:THR:HG21	1.98	0.45
1:A:768:GLN:HG3	1:A:770:ALA:O	2.16	0.45
1:A:918:THR:HA	1:A:921:ILE:HB	1.99	0.45
1:A:1453:LYS:HG2	1:A:1465:MET:HE3	1.99	0.45
1:A:1634:GLU:HB3	1:A:1636:THR:H	1.81	0.45
1:A:1675:PHE:HB3	1:A:1715:ARG:CZ	2.46	0.45
1:A:2128:HIS:HA	1:A:2172:LYS:HG3	1.97	0.45
1:A:2130:ASP:HB2	1:A:2366:ILE:HG23	1.97	0.45
1:A:2282:ASN:HB3	1:A:2294:HIS:CD2	2.51	0.45
1:A:2377:ILE:HD12	1:A:2415:ILE:HG21	1.99	0.45
2:B:137:ASP:HB3	2:B:139:ASN:N	2.30	0.45
1:C:271:PRO:CG	1:C:280:ARG:HB2	2.47	0.45
1:C:801:LEU:HB3	1:C:805:ILE:HG13	1.98	0.45
1:C:1007:VAL:H	1:C:1008:ILE:HG12	1.82	0.45
1:C:1924:SER:HB3	1:C:1927:ARG:HD2	1.97	0.45
5:J:707:ILE:HD13	5:J:728:LEU:CD2	2.47	0.45
1:A:1155:PHE:HE2	1:C:622:LYS:HB3	1.82	0.45
1:A:1953:GLU:O	1:A:1957:MET:N	2.50	0.45
2:B:85:GLN:H	2:B:124:ILE:HD13	1.82	0.45
2:B:230:THR:HA	2:B:247:ASP:HA	1.99	0.45
1:C:275:ALA:O	1:C:277:LEU:N	2.50	0.45
1:C:856:GLU:HG3	1:C:1590:VAL:HG13	1.98	0.45
1:C:952:LEU:HD21	1:C:988:SER:O	2.16	0.45
1:C:1734:ARG:NH2	1:C:1771:SER:O	2.49	0.45
1:C:2109:ARG:N	1:C:2110:PRO:CD	2.80	0.45
1:C:2269:SER:HB3	1:C:2318:PHE:CE2	2.51	0.45
2:D:65:PRO:HB2	2:D:66:ASN:C	2.37	0.45
2:D:275:ARG:HB3	2:D:284:ILE:HG23	1.99	0.45
5:J:676:MET:CE	5:J:699:LYS:HE3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ALA:HA	1:A:106:LEU:HB2	1.98	0.45
1:A:179:LEU:CD2	1:A:233:LYS:HG3	2.23	0.45
1:A:366:ARG:HD3	1:A:413:PRO:CB	2.41	0.45
1:A:623:ASP:N	1:A:629:SER:HG	2.15	0.45
1:A:663:LEU:N	1:C:1117:GLU:HB2	2.31	0.45
1:A:999:HIS:HA	1:A:1002:LYS:HB2	1.98	0.45
1:A:1419:LYS:HE2	1:A:1433:LYS:NZ	2.32	0.45
1:A:1672:LEU:HD11	1:A:1719:LYS:HG3	1.99	0.45
1:A:2082:ARG:NH1	1:A:2167:ILE:HG21	2.31	0.45
1:A:2155:PHE:HD1	1:A:2158:HIS:CG	2.35	0.45
2:B:93:SER:HB2	2:B:119:VAL:HG22	1.99	0.45
2:B:182:ASN:CG	2:B:204:ARG:HE	2.20	0.45
1:C:138:ILE:HG22	1:C:140:GLY:H	1.82	0.45
1:C:763:VAL:HG11	1:C:803:PRO:HA	1.97	0.45
1:C:857:ASN:O	1:C:1585:GLN:N	2.49	0.45
1:C:1173:GLN:O	1:C:1177:TYR:HB2	2.17	0.45
1:C:1504:ILE:HB	1:C:1596:ARG:HH22	1.82	0.45
5:I:703:ILE:HD12	5:I:706:VAL:HG21	1.98	0.45
5:J:709:PHE:HE2	5:J:716:THR:HG1	1.61	0.45
1:A:162:THR:HG1	1:A:167:ASN:N	2.15	0.45
1:A:234:LEU:HD11	1:A:270:PRO:CG	2.41	0.45
1:A:765:PRO:HG3	1:A:805:ILE:HG22	1.99	0.45
1:A:1279:SER:O	1:A:1282:SER:N	2.50	0.45
1:A:2279:HIS:HA	1:A:2467:GLY:O	2.17	0.45
2:B:44:LYS:HD2	2:B:301:ASN:HB3	1.98	0.45
1:C:174:ALA:HB1	1:C:178:ARG:CZ	2.47	0.45
1:C:269:TRP:HB2	1:C:310:PHE:CE2	2.52	0.45
1:C:281:LEU:O	1:C:285:VAL:N	2.50	0.45
1:C:291:LEU:HA	1:C:294:ILE:HD12	1.97	0.45
1:C:690:PHE:CD1	1:C:728:PHE:HZ	2.34	0.45
1:C:2063:LEU:HD12	1:C:2099:PRO:HA	1.99	0.45
1:C:2133:ILE:HD13	1:C:2176:GLY:HA3	1.99	0.45
1:C:2264:SER:O	1:C:2267:VAL:HG12	2.16	0.45
1:C:2280:ARG:HB3	1:C:2319:ARG:HD2	1.98	0.45
1:C:2407:GLN:O	1:C:2409:VAL:CA	2.65	0.45
2:D:13:THR:OG1	2:D:291:HIS:HA	2.16	0.45
3:F:651:UNK:O	3:F:653:UNK:N	2.50	0.45
1:A:1065:LEU:HA	1:A:1068:LEU:HB2	1.98	0.45
1:A:1077:ASP:HB2	1:C:699:ILE:HG12	1.97	0.45
2:B:44:LYS:HB3	2:B:301:ASN:HB3	1.98	0.45
1:C:731:MET:HA	1:C:732:PRO:HD2	1.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:969:LEU:HD22	1:C:985:GLN:HG3	1.98	0.45
1:C:1104:ILE:HB	1:C:1142:MET:HB3	1.99	0.45
1:C:1619:ARG:CA	1:C:1626:LEU:HG	2.37	0.45
1:C:1974:ALA:HB1	1:C:1990:ALA:HB3	1.98	0.45
1:C:2017:ASP:O	1:C:2020:ASP:N	2.50	0.45
3:F:606:UNK:HA	3:F:607:UNK:C	2.47	0.45
5:I:736:PRO:HA	5:I:755:PHE:HE1	1.81	0.45
5:J:736:PRO:HA	5:J:755:PHE:HD1	1.80	0.45
1:A:303:GLN:HB3	1:A:307:ARG:CB	2.46	0.45
1:A:449:PHE:CD1	1:A:455:PHE:HA	2.52	0.45
1:A:721:LEU:O	1:A:760:LEU:HB2	2.16	0.45
1:A:964:PRO:HA	1:A:965:GLY:HA3	1.72	0.45
1:A:2043:TYR:HB3	1:A:2047:ARG:HH22	1.81	0.45
1:A:2060:GLU:CB	1:A:2062:GLN:HG2	2.18	0.45
1:A:2205:TRP:HA	1:A:2208:LEU:HB2	1.98	0.45
2:B:229:HIS:CB	2:B:251:ARG:HB2	2.47	0.45
1:C:1531:SER:C	1:C:1532:ALA:HA	2.37	0.45
5:I:647:LYS:HZ2	5:I:649:LYS:HZ1	1.65	0.45
1:A:244:ILE:HA	1:A:248:LEU:HB2	2.00	0.44
1:A:381:ALA:CB	1:A:385:LYS:HD3	2.46	0.44
1:A:1258:LEU:HD23	1:A:1258:LEU:HA	1.92	0.44
1:A:1586:ILE:N	1:A:1615:LEU:HD21	2.32	0.44
1:C:917:TYR:N	1:C:918:PRO:CD	2.79	0.44
1:C:1214:VAL:HG22	1:C:1249:GLN:HE21	1.81	0.44
1:C:1465:LYS:HG3	1:C:1492:LYS:HZ1	1.83	0.44
1:C:1732:LYS:CA	1:C:1737:ASN:HB2	2.47	0.44
1:C:2409:VAL:HA	1:C:2410:GLU:C	2.37	0.44
2:D:205:ALA:N	2:D:206:HIS:O	2.50	0.44
2:D:274:VAL:N	2:D:288:TYR:O	2.50	0.44
1:A:87:ILE:HG12	1:A:99:ARG:HH21	1.83	0.44
1:A:914:GLU:O	1:A:915:TYR:N	2.50	0.44
1:A:1117:MET:HG3	1:A:1120:ARG:HG3	1.99	0.44
2:B:70:SER:HB3	2:B:72:GLU:HG3	1.98	0.44
1:C:632:HIS:O	1:C:636:SER:N	2.51	0.44
1:C:805:ILE:HG12	1:C:851:ASN:CG	2.36	0.44
1:C:1578:ASN:C	1:C:1581:LEU:HG	2.36	0.44
2:D:143:TRP:HE1	2:D:148:ASN:HA	1.81	0.44
1:A:1354:LYS:HE3	1:A:1373:ILE:HD13	1.98	0.44
1:C:177:LEU:HD12	1:C:238:ARG:NH2	2.33	0.44
1:C:288:GLY:O	1:C:338:LEU:HD23	2.17	0.44
1:C:444:GLU:HB3	1:C:447:ARG:HH11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1000:HIS:HA	1:C:1003:LYS:HB2	1.98	0.44
1:C:1216:LYS:HB3	1:C:1249:GLN:O	2.18	0.44
1:C:1602:ILE:HG22	1:C:1606:GLU:HB2	2.00	0.44
1:C:1749:THR:HB	1:C:1762:TRP:CE3	2.53	0.44
1:A:314:HIS:NE2	1:A:319:ASN:OD1	2.51	0.44
1:A:534:ASN:C	1:A:535:GLN:N	2.71	0.44
1:A:600:ILE:N	1:A:602:HIS:HB2	2.32	0.44
1:C:143:SER:HB3	1:C:190:ARG:HE	1.83	0.44
1:C:220:ASP:O	1:C:235:LEU:HD22	2.18	0.44
1:C:560:THR:O	1:C:562:GLU:N	2.51	0.44
1:C:850:ILE:CD1	1:C:1553:GLU:HB2	2.46	0.44
1:C:1185:LEU:HD13	1:C:1189:CYS:HA	2.00	0.44
2:D:254:TRP:HD1	2:D:296:VAL:HA	1.80	0.44
3:F:252:UNK:O	3:F:253:UNK:N	2.47	0.44
5:J:680:ILE:C	5:J:682:ILE:H	2.21	0.44
5:J:737:ASN:HB3	5:J:754:ASN:HB2	1.98	0.44
1:A:370:ALA:CB	1:A:417:VAL:HA	2.48	0.44
1:A:1567:LYS:O	1:A:1568:ARG:N	2.50	0.44
1:A:2111:PHE:CD1	1:A:2123:TYR:HE2	2.36	0.44
1:A:2116:SER:C	1:A:2117:ASP:HA	2.37	0.44
1:A:2148:LEU:O	1:A:2158:HIS:NE2	2.50	0.44
1:A:2260:THR:HA	1:A:2327:GLU:OE1	2.18	0.44
1:A:2430:LYS:N	1:A:2442:LEU:HD12	2.33	0.44
1:C:297:ARG:HH21	1:C:341:PRO:HA	1.81	0.44
1:C:359:GLU:HG2	1:C:393:MET:HG2	2.00	0.44
1:C:660:ILE:HA	1:C:663:HIS:HB3	1.98	0.44
1:C:1749:THR:HG23	1:C:1759:TRP:HE3	1.82	0.44
1:C:1752:ASP:HA	1:C:1759:TRP:CZ3	2.52	0.44
1:C:2309:ARG:C	1:C:2380:GLU:OE2	2.55	0.44
2:D:4:ILE:HG23	2:D:16:PHE:CD1	2.52	0.44
2:D:12:HIS:CE1	2:D:35:VAL:HB	2.52	0.44
1:A:172:LEU:HD23	1:A:176:LEU:HD13	1.99	0.44
1:A:554:SER:N	1:A:555:PHE:HB2	2.31	0.44
1:A:1589:TRP:O	1:A:1593:LEU:N	2.49	0.44
1:A:1621:ARG:HA	1:A:1624:LEU:HB3	1.99	0.44
1:A:1732:ARG:NH2	1:A:1733:LEU:HG	2.32	0.44
1:A:2181:ASN:HA	1:A:2182:SER:N	2.32	0.44
2:B:86:ASP:HB3	2:B:88:ARG:H	1.81	0.44
1:C:176:TYR:H	1:C:179:VAL:HG22	1.82	0.44
1:C:827:GLN:H	1:C:830:ALA:HB1	1.83	0.44
1:C:1561:LYS:HE3	1:C:1601:VAL:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:TYR:CE1	1:A:498:THR:HA	2.52	0.44
1:A:466:LEU:O	1:A:467:ALA:HB3	2.17	0.44
1:A:507:PRO:HB2	1:A:509:LEU:HD23	1.99	0.44
1:A:675:ASP:N	1:A:675:ASP:OD1	2.50	0.44
1:A:699:ILE:HD13	1:A:699:ILE:HA	1.89	0.44
1:A:796:TYR:OH	1:A:844:LEU:HD22	2.18	0.44
1:A:1025:GLU:HG3	1:A:1029:LYS:HE2	1.98	0.44
1:A:1088:ARG:NH2	1:A:1120:ARG:HB2	2.32	0.44
1:A:1389:HIS:HB2	1:A:2332:GLU:HG2	1.98	0.44
1:A:1725:VAL:HA	1:A:1728:GLN:HB3	1.99	0.44
1:C:216:ARG:HD2	1:C:234:LYS:HZ1	1.82	0.44
1:C:249:LEU:HA	1:C:252:ASN:HB3	2.00	0.44
1:C:355:MET:HB2	1:C:389:LEU:HD22	1.99	0.44
1:C:688:GLU:HB3	1:C:692:ILE:HG13	2.00	0.44
1:C:700:ILE:HG13	1:C:721:GLU:CD	2.38	0.44
1:C:771:ALA:HA	1:C:811:ASP:HB2	1.99	0.44
1:C:1238:ASP:HA	1:C:1241:GLU:HB2	1.98	0.44
1:C:1554:LEU:HA	1:C:1557:ILE:CG2	2.47	0.44
1:C:2116:LYS:HA	1:C:2122:ASP:HA	1.99	0.44
2:D:131:LEU:HB3	2:D:143:TRP:O	2.18	0.44
1:A:328:LEU:HD12	1:A:365:ARG:HD2	1.99	0.44
1:A:676:ASN:HB3	1:A:726:LYS:HE2	2.00	0.44
1:A:861:ARG:NH1	1:A:1540:TYR:HB3	2.33	0.44
1:A:1112:ILE:HG22	1:A:1112:ILE:O	2.18	0.44
1:A:1755:LYS:C	1:A:1758:HIS:HB3	2.38	0.44
1:A:2110:LYS:HD2	1:A:2178:TRP:HZ3	1.83	0.44
1:A:2465:TYR:HA	1:A:2468:TRP:HB3	2.00	0.44
1:C:181:ILE:CG2	1:C:224:LEU:HD13	2.47	0.44
1:C:655:GLU:CG	1:C:658:LEU:HB3	2.48	0.44
1:C:856:GLU:O	1:C:1590:VAL:HA	2.18	0.44
1:C:1344:GLN:HE22	1:C:1351:LYS:N	2.16	0.44
1:C:1504:ILE:HB	1:C:1596:ARG:NH2	2.33	0.44
1:C:2227:VAL:C	1:C:2228:PHE:N	2.71	0.44
1:C:2264:SER:HB3	1:C:2294:VAL:H	1.82	0.44
1:C:2265:LEU:CD1	1:C:2333:ILE:HG22	2.48	0.44
1:C:2317:PRO:HB3	1:C:2453:LEU:HD13	2.00	0.44
1:A:142:SER:HB3	1:A:189:ARG:NE	2.33	0.44
1:A:220:TRP:HH2	1:A:262:SER:HG	1.65	0.44
1:A:256:LEU:HB3	1:A:258:PRO:HA	1.99	0.44
1:A:1060:VAL:N	1:A:1061:PRO:CD	2.81	0.44
1:A:2335:PHE:O	1:A:2339:CYS:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2446:GLU:O	1:A:2450:LYS:HG2	2.18	0.44
1:C:332:PHE:C	1:C:333:ARG:HA	2.38	0.44
1:C:399:TYR:CZ	1:C:442:ILE:HG21	2.53	0.44
1:C:819:ASP:O	1:C:823:THR:N	2.51	0.44
1:C:1007:VAL:N	1:C:1008:ILE:HG12	2.32	0.44
1:C:1996:GLU:O	1:C:1999:LYS:HB3	2.18	0.44
1:C:2346:LYS:HD2	1:C:2346:LYS:HA	1.87	0.44
2:D:57:LEU:HD12	2:D:69:ALA:HB3	1.98	0.44
1:A:113:LEU:HD13	1:A:117:VAL:HG13	1.98	0.43
1:A:807:THR:HA	1:A:1578:ARG:CZ	2.47	0.43
1:A:1134:ARG:HG2	1:A:1138:LYS:HE2	1.99	0.43
1:C:239:ARG:NH1	1:C:271:PRO:HG2	2.33	0.43
1:C:583:ILE:HA	1:C:584:HIS:HA	1.76	0.43
1:C:586:GLN:HB3	1:C:629:THR:OG1	2.18	0.43
1:C:950:GLN:O	1:C:953:GLY:N	2.51	0.43
1:C:963:ILE:HG13	1:C:964:ILE:N	2.33	0.43
1:C:965:PRO:O	1:C:969:LEU:HG	2.18	0.43
1:C:1322:VAL:HG22	1:C:1347:HIS:CE1	2.53	0.43
1:C:1421:LYS:NZ	1:C:1451:LEU:HD11	2.33	0.43
1:C:1923:GLU:HB2	1:C:1925:LEU:HG	1.98	0.43
1:C:1975:SER:HA	1:C:1978:PHE:HB3	1.99	0.43
2:D:125:HIS:HB2	2:D:167:MET:SD	2.58	0.43
3:F:367:UNK:C	3:F:369:UNK:N	2.80	0.43
5:J:676:MET:HB3	5:J:688:TYR:HD2	1.82	0.43
1:A:568:ASP:HA	1:A:572:LEU:HD22	2.00	0.43
1:A:1138:LYS:HA	1:A:1141:MET:HB2	2.00	0.43
1:A:1653:TYR:HA	1:A:1656:LEU:HB3	2.00	0.43
1:A:1904:LYS:HA	1:A:1907:PRO:HG3	2.00	0.43
1:A:1946:GLN:C	1:A:1949:LEU:HB2	2.38	0.43
2:B:253:VAL:N	2:B:269:SER:HG	2.16	0.43
1:C:346:LYS:HB3	1:C:350:ILE:CG1	2.48	0.43
1:C:783:LEU:HG	1:C:800:GLU:HG2	1.99	0.43
1:C:846:LEU:HD22	1:C:1549:GLN:HG3	1.99	0.43
1:C:1046:PHE:O	1:C:1050:ILE:HG12	2.18	0.43
2:D:37:ARG:O	2:D:50:ALA:N	2.51	0.43
2:D:151:THR:HA	2:D:152:HIS:HA	2.00	0.43
3:F:659:UNK:C	3:F:661:UNK:N	2.82	0.43
1:A:329:LEU:HD11	1:A:367:GLU:HB2	2.01	0.43
1:A:754:PRO:C	1:A:755:TYR:HA	2.39	0.43
1:A:1391:GLN:NE2	1:A:1405:LYS:HE2	2.34	0.43
1:A:1830:ILE:HD13	1:A:1835:SER:CB	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2154:CYS:SG	1:A:2340:GLU:HB3	2.58	0.43
1:C:291:LEU:HD22	1:C:301:LEU:HD22	2.00	0.43
1:C:362:PHE:CE1	1:C:393:MET:HE3	2.53	0.43
1:C:456:PHE:N	1:C:492:MET:HG3	2.32	0.43
1:C:1070:VAL:HG13	1:C:1106:LEU:HA	2.00	0.43
1:C:1492:LYS:O	1:C:1498:LYS:HB2	2.19	0.43
1:C:2400:ALA:O	1:C:2401:ILE:HG13	2.19	0.43
2:D:12:HIS:CE1	2:D:34:GLN:HG3	2.54	0.43
2:D:134:CYS:SG	2:D:165:LEU:HD13	2.58	0.43
2:D:206:HIS:CD2	2:D:226:SER:HB2	2.53	0.43
1:A:151:ALA:O	1:A:155:LEU:HB2	2.18	0.43
1:A:373:PRO:O	1:A:377:ALA:HB2	2.17	0.43
1:A:502:LEU:HB3	1:A:511:SER:OG	2.18	0.43
1:A:796:TYR:CE2	1:A:843:GLU:HB3	2.53	0.43
1:A:805:ILE:O	1:A:808:PHE:HB3	2.19	0.43
1:A:2140:LEU:HD21	1:A:2360:PHE:HE2	1.83	0.43
1:C:461:PHE:HE2	1:C:483:LEU:HD13	1.82	0.43
1:C:994:LYS:HA	1:C:995:GLN:HB2	1.99	0.43
1:C:1476:TRP:HE1	1:C:1599:SER:HG	1.63	0.43
1:C:2064:GLN:CG	1:C:2065:HIS:CD2	2.93	0.43
1:C:2104:ILE:HD12	1:C:2110:PRO:HD2	2.01	0.43
1:C:2104:ILE:HG12	1:C:2112:LYS:HD3	2.00	0.43
1:A:235:GLU:OE1	1:A:275:LYS:HB2	2.19	0.43
1:A:280:LEU:CD1	1:A:329:LEU:HB3	2.48	0.43
1:A:370:ALA:HB1	1:A:417:VAL:HA	2.01	0.43
1:A:634:HIS:HA	1:A:637:SER:HB2	2.00	0.43
1:A:1156:VAL:HG13	1:A:1157:VAL:HG13	2.01	0.43
1:A:1167:LEU:HG	1:A:1167:LEU:O	2.18	0.43
1:A:1258:LEU:HD22	1:A:1268:TYR:CE2	2.53	0.43
1:A:1436:SER:HB2	1:A:1440:LEU:CD1	2.49	0.43
1:A:2205:TRP:CA	1:A:2208:LEU:HB2	2.48	0.43
1:A:2430:LYS:O	1:A:2447:GLN:HG2	2.19	0.43
2:B:185:VAL:C	2:B:200:VAL:H	2.21	0.43
1:C:257:LEU:HD22	1:C:260:TYR:CG	2.53	0.43
1:C:389:LEU:HA	1:C:392:ILE:HB	1.99	0.43
1:C:857:ASN:CG	1:C:1586:LYS:HG2	2.39	0.43
1:C:1178:ASP:C	1:C:1182:ASN:H	2.22	0.43
1:C:1930:ALA:O	1:C:1934:ILE:HG12	2.18	0.43
1:C:2286:MET:HB3	1:C:2295:ILE:HB	2.00	0.43
1:C:2333:ILE:O	1:C:2333:ILE:HG13	2.18	0.43
2:D:4:ILE:HG23	2:D:16:PHE:HD1	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:720:PRO:CD	5:I:723:PHE:HB2	2.49	0.43
1:A:345:LYS:HD2	1:A:348:ASP:OD2	2.18	0.43
1:A:852:LEU:HD13	1:A:1575:TRP:HA	1.99	0.43
1:A:1898:LEU:O	1:A:1902:LEU:HG	2.19	0.43
1:A:2037:GLN:NE2	1:A:2040:ASP:HB3	2.34	0.43
2:B:269:SER:N	2:B:295:ALA:HB3	2.34	0.43
1:C:1063:ILE:HG22	1:C:1064:ARG:N	2.32	0.43
1:C:1654:VAL:O	1:C:1658:LEU:N	2.50	0.43
1:C:1767:PHE:HD1	1:C:1825:ILE:HG21	1.84	0.43
1:C:2062:GLU:HG2	1:C:2064:GLN:N	2.32	0.43
2:D:6:VAL:HG22	2:D:7:SER:HA	2.00	0.43
2:D:291:HIS:HB3	2:D:293:LYS:O	2.19	0.43
1:A:88:PHE:HD1	1:A:100:ALA:HB1	1.83	0.43
1:A:257:TYR:CD1	1:A:286:LEU:HD11	2.53	0.43
1:A:715:ARG:O	1:A:719:LEU:N	2.52	0.43
1:A:1088:ARG:HH22	1:A:1120:ARG:HB2	1.84	0.43
1:A:1097:LEU:HD23	1:A:1100:ILE:HG21	2.00	0.43
1:A:2268:MET:SD	1:A:2342:VAL:HG23	2.59	0.43
2:B:274:VAL:HG13	2:B:288:TYR:HB2	2.01	0.43
1:C:188:VAL:HB	1:C:237:TYR:CD2	2.54	0.43
1:C:763:VAL:HG12	1:C:763:VAL:O	2.19	0.43
1:C:1841:GLN:O	1:C:1844:LEU:N	2.51	0.43
2:D:26:ARG:HH22	2:D:47:LEU:HD11	1.83	0.43
2:D:248:GLY:HA3	2:D:251:ARG:CZ	2.48	0.43
5:J:676:MET:O	5:J:688:TYR:N	2.51	0.43
1:A:234:LEU:HD21	1:A:270:PRO:HB3	2.01	0.43
1:A:699:ILE:HD12	1:A:717:THR:HG23	1.99	0.43
1:A:701:ARG:O	1:C:1044:LEU:HD11	2.18	0.43
1:A:1073:PRO:HB3	1:A:1110:LYS:N	2.34	0.43
1:A:1241:TRP:N	1:A:1243:ARG:H	2.16	0.43
1:A:2053:LEU:HA	1:A:2056:LEU:HD13	2.00	0.43
1:A:2306:LEU:HG	1:A:2376:LYS:HB2	2.00	0.43
1:C:1407:LYS:HB3	1:C:1412:GLU:HB3	2.00	0.43
1:C:1421:LYS:HZ2	1:C:1451:LEU:HD11	1.84	0.43
1:C:1435:LYS:HE3	1:C:1436:LEU:HG	2.01	0.43
1:C:1749:THR:HB	1:C:1762:TRP:CD2	2.54	0.43
1:A:268:TRP:CZ3	1:A:316:LEU:HD23	2.54	0.43
1:A:331:PHE:HZ	1:A:345:LYS:HE3	1.84	0.43
1:A:409:ASN:O	1:A:449:PHE:HD2	2.01	0.43
1:A:954:ARG:NH1	1:A:958:PHE:HE2	2.16	0.43
1:A:1953:GLU:HB3	1:A:2068:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2036:ASN:HA	1:A:2039:TRP:CB	2.49	0.43
1:A:2314:VAL:HB	1:A:2315:PRO:HD2	2.01	0.43
1:C:326:HIS:HB3	1:C:365:ILE:HB	2.01	0.43
1:C:388:TYR:O	1:C:392:ILE:N	2.52	0.43
1:C:389:LEU:O	1:C:393:MET:N	2.52	0.43
1:C:414:PRO:C	1:C:417:LEU:HB3	2.39	0.43
1:C:537:TYR:OH	1:C:545:ILE:HD13	2.19	0.43
1:C:700:ILE:HD13	1:C:703:LEU:HD12	2.01	0.43
1:C:840:LEU:O	1:C:842:TYR:N	2.51	0.43
1:C:1615:ALA:HB2	1:C:1629:LYS:HG2	2.00	0.43
1:C:2007:GLU:HG2	1:C:2066:VAL:HB	2.00	0.43
1:C:2063:LEU:O	1:C:2068:PRO:HA	2.19	0.43
1:A:442:ARG:O	1:A:446:ARG:N	2.49	0.43
1:A:714:LEU:HD13	1:A:753:LYS:HE2	2.01	0.43
1:A:771:SER:O	1:A:773:ALA:N	2.52	0.43
1:A:1339:LYS:C	1:A:1343:LYS:HG2	2.38	0.43
1:A:1617:ARG:HD2	1:A:1624:LEU:CD2	2.48	0.43
1:A:2109:ARG:H	1:A:2109:ARG:HG2	1.58	0.43
2:B:30:HIS:CE1	2:B:35:VAL:HG23	2.53	0.43
1:C:121:GLU:OE2	1:C:124:GLN:N	2.52	0.43
1:C:246:ILE:CD1	1:C:258:TYR:N	2.81	0.43
1:C:333:ARG:HG2	1:C:350:ILE:HD13	2.01	0.43
1:C:378:ALA:O	1:C:379:PHE:N	2.52	0.43
1:C:454:LYS:C	1:C:455:GLN:HA	2.38	0.43
1:C:705:SER:HA	1:C:706:VAL:C	2.38	0.43
1:C:1878:VAL:O	1:C:1878:VAL:HG12	2.18	0.43
1:C:1974:ALA:HB1	1:C:1990:ALA:CB	2.49	0.43
1:C:2340:THR:O	1:C:2344:VAL:HG12	2.19	0.43
2:D:21:THR:O	2:D:286:ARG:CZ	2.67	0.43
2:D:177:ALA:HB2	2:D:183:CYS:HA	2.01	0.43
2:D:232:ARG:HA	2:D:244:THR:HG22	2.01	0.43
5:J:729:THR:HB	5:J:730:VAL:HG22	2.00	0.43
5:J:734:SER:HB3	5:J:773:VAL:HB	2.01	0.43
1:A:115:ARG:HH12	1:A:124:ARG:HG3	1.84	0.42
1:A:422:ILE:HG23	1:A:466:LEU:HB2	2.01	0.42
1:A:1904:LYS:HG3	1:A:1939:HIS:HB2	2.00	0.42
1:A:2062:GLN:HG3	1:A:2063:HIS:N	2.34	0.42
1:C:570:ALA:HA	1:C:596:ILE:CD1	2.49	0.42
1:C:814:ASN:C	1:C:818:ARG:HG3	2.39	0.42
1:C:1108:ARG:HD2	1:C:1145:LEU:HB3	1.99	0.42
1:C:1138:THR:HG22	1:C:1142:MET:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1148:LEU:O	1:C:1151:GLN:HB2	2.18	0.42
1:C:1574:ARG:C	1:C:1575:GLU:N	2.73	0.42
2:D:78:VAL:HG21	2:D:81:VAL:HG13	2.01	0.42
2:D:248:GLY:HA3	2:D:251:ARG:NE	2.34	0.42
1:A:171:ARG:O	1:A:171:ARG:HG2	2.19	0.42
1:A:280:LEU:HD13	1:A:329:LEU:HB3	2.02	0.42
1:A:388:LEU:HA	1:A:391:ILE:HB	2.01	0.42
1:A:390:ARG:HA	1:A:393:VAL:HB	2.00	0.42
1:A:413:PRO:HA	1:A:416:LEU:HB3	2.02	0.42
1:A:676:ASN:CB	1:A:726:LYS:HE2	2.49	0.42
1:A:861:ARG:O	1:A:865:VAL:HG23	2.19	0.42
1:A:862:ARG:NH1	1:A:2152:ALA:O	2.51	0.42
1:A:1126:VAL:HG23	1:A:1166:LEU:HD21	2.01	0.42
1:A:1371:ILE:HG21	1:A:1387:LEU:CD1	2.49	0.42
1:A:1430:MET:O	1:A:1433:LYS:HE3	2.17	0.42
1:A:1950:VAL:HG13	1:A:2068:LEU:HD21	2.01	0.42
1:A:2342:VAL:O	1:A:2346:LEU:HG	2.19	0.42
1:C:724:THR:O	1:C:728:PHE:N	2.53	0.42
1:C:1005:TYR:C	1:C:1007:VAL:N	2.72	0.42
1:C:1355:TYR:HA	1:C:1358:VAL:HG12	1.99	0.42
1:C:2104:ILE:O	1:C:2109:ARG:HA	2.20	0.42
5:I:647:LYS:NZ	5:I:649:LYS:NZ	2.67	0.42
5:I:676:MET:HB2	5:I:702:THR:CG2	2.49	0.42
1:A:443:GLU:HA	1:A:446:ARG:HB2	2.01	0.42
1:A:461:TYR:C	1:A:462:CYS:N	2.72	0.42
1:A:482:LEU:HA	1:A:485:LEU:HB2	1.99	0.42
1:A:489:CYS:HA	1:A:539:ASN:HD22	1.84	0.42
1:A:916:TYR:N	1:A:917:PRO:CD	2.82	0.42
1:A:1013:ILE:HD11	1:A:1021:ILE:HD12	2.01	0.42
1:A:1244:ARG:HA	1:A:1247:ILE:HD12	2.01	0.42
1:A:1607:GLN:HA	1:A:1610:ILE:HD12	2.01	0.42
1:A:1943:LEU:HB3	1:A:2076:LEU:HD22	2.01	0.42
1:A:2349:ASN:O	1:A:2353:LEU:N	2.52	0.42
1:C:124:GLN:OE1	1:C:124:GLN:HA	2.17	0.42
1:C:521:LEU:HD23	1:C:537:TYR:HD1	1.84	0.42
1:C:990:ILE:HD11	1:C:1208:TYR:HE2	1.84	0.42
5:I:676:MET:HB3	5:I:688:TYR:HB2	2.00	0.42
1:A:212:PHE:O	1:A:216:THR:HG22	2.19	0.42
1:A:673:GLN:HB3	1:A:719:LEU:HB3	2.01	0.42
1:A:730:MET:HA	1:A:731:PRO:HD2	1.75	0.42
1:A:824:LEU:HA	1:A:827:LEU:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:944:ILE:O	1:A:947:ILE:HB	2.19	0.42
1:A:1117:MET:HG2	1:A:1121:ILE:HG13	2.01	0.42
1:A:1525:VAL:O	1:A:1528:LEU:HD23	2.19	0.42
1:A:1567:LYS:O	1:A:1570:THR:N	2.52	0.42
2:B:40:ILE:CG2	2:B:44:LYS:HA	2.49	0.42
1:C:333:ARG:HH11	1:C:354:THR:HB	1.84	0.42
1:C:377:ALA:O	1:C:382:ALA:HB3	2.20	0.42
1:C:458:LYS:HE3	1:C:461:PHE:CD2	2.54	0.42
1:C:688:GLU:C	1:C:690:PHE:N	2.72	0.42
1:C:1430:GLU:O	1:C:1436:LEU:HD11	2.20	0.42
1:C:1681:MET:HA	1:C:1684:ASP:HB3	2.00	0.42
1:C:1766:ASN:O	1:C:1769:VAL:HB	2.19	0.42
1:C:2116:LYS:HZ3	1:C:2120:GLY:N	2.17	0.42
5:I:736:PRO:HA	5:I:755:PHE:CE1	2.54	0.42
1:A:583:HIS:HB3	1:A:584:HIS:H	1.61	0.42
1:A:865:VAL:HG22	1:A:1535:SER:HB3	2.01	0.42
1:A:1242:ILE:HD12	1:A:1272:ALA:HB1	2.02	0.42
1:A:1586:ILE:HA	1:A:1587:ASP:N	2.34	0.42
1:A:1981:ASN:HB3	1:A:1984:LYS:HB3	2.01	0.42
1:C:1452:ALA:HA	1:C:1455:LYS:HE2	2.00	0.42
1:C:2225:VAL:HG22	1:C:2461:GLU:HB2	2.02	0.42
2:D:222:LEU:HB3	2:D:234:TRP:HB2	2.01	0.42
5:I:668:ASP:HA	5:I:669:LYS:HA	1.93	0.42
1:A:928:LEU:HD21	1:A:942:GLN:CB	2.48	0.42
1:A:1287:LEU:HA	1:A:1290:SER:OG	2.20	0.42
1:A:1435:ARG:O	1:A:1439:ALA:N	2.52	0.42
1:A:2299:ASP:O	1:A:2301:PHE:N	2.53	0.42
1:A:2331:ILE:HA	1:A:2334:SER:HB2	2.02	0.42
2:B:246:LEU:HG	2:B:277:TRP:CZ3	2.55	0.42
1:C:247:LYS:O	1:C:251:ASP:N	2.53	0.42
1:C:654:ALA:HA	1:C:657:ARG:HB2	2.02	0.42
1:C:827:GLN:H	1:C:830:ALA:CB	2.32	0.42
1:C:1161:PRO:HB2	1:C:1162:VAL:N	2.34	0.42
1:C:1610:VAL:C	1:C:1611:ARG:O	2.58	0.42
1:C:1674:LEU:HD11	1:C:1721:LYS:HG3	2.02	0.42
1:C:1980:GLY:HA2	5:J:648:LYS:NZ	2.34	0.42
1:C:2062:GLU:CD	1:C:2064:GLN:HG2	2.39	0.42
2:D:213:ILE:HD12	2:D:222:LEU:HD11	2.02	0.42
4:H:100:ARG:O	4:H:101:PHE:HA	2.19	0.42
5:J:782:LYS:HA	5:J:785:ASN:O	2.20	0.42
1:A:235:GLU:CD	1:A:275:LYS:HB2	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:PHE:CZ	1:A:345:LYS:HE3	2.54	0.42
1:A:556:MET:HA	1:A:590:GLU:CD	2.40	0.42
1:A:577:LYS:HE3	1:A:618:LEU:HD13	2.02	0.42
1:A:1490:LYS:O	1:A:1496:LYS:HB3	2.20	0.42
1:A:1617:ARG:HD2	1:A:1624:LEU:HD21	2.02	0.42
1:A:1666:ASP:HA	1:A:1669:LEU:HB2	2.01	0.42
1:A:2114:LYS:HA	1:A:2120:ASP:HA	2.01	0.42
1:A:2151:ASP:C	1:A:2155:PHE:HB2	2.40	0.42
1:C:146:LYS:HD2	1:C:190:ARG:HG3	2.01	0.42
1:C:189:MET:HG3	1:C:237:TYR:HB3	2.02	0.42
1:C:213:PHE:CE1	1:C:217:THR:HB	2.55	0.42
1:C:268:ILE:HG21	1:C:311:GLN:HG3	2.00	0.42
1:C:801:LEU:O	1:C:805:ILE:N	2.52	0.42
1:C:917:TYR:N	1:C:918:PRO:HD2	2.35	0.42
5:I:655:SER:HA	5:I:659:LEU:HB3	1.99	0.42
5:I:699:LYS:HG2	5:I:755:PHE:HA	2.01	0.42
5:J:710:ALA:HB1	5:J:718:LYS:CG	2.43	0.42
1:A:259:TYR:HB2	1:A:290:LEU:HD11	2.01	0.42
1:A:300:LEU:HD13	1:A:303:GLN:CB	2.49	0.42
1:A:807:THR:HA	1:A:1578:ARG:NE	2.35	0.42
1:A:969:VAL:HG22	1:A:1003:ILE:HD11	2.00	0.42
1:A:2094:LYS:HD2	1:A:2095:PHE:CZ	2.55	0.42
1:C:398:ARG:O	1:C:401:LYS:HB2	2.19	0.42
1:C:500:LEU:O	1:C:503:LEU:HB2	2.20	0.42
1:C:955:ARG:HH11	1:C:959:PHE:HE2	1.67	0.42
1:C:1098:LEU:N	1:C:1101:ILE:HD12	2.35	0.42
1:C:1952:VAL:O	1:C:1956:LEU:N	2.53	0.42
1:C:2045:TYR:HB3	1:C:2049:ARG:NH1	2.16	0.42
1:C:2362:PHE:N	1:C:2362:PHE:CD1	2.86	0.42
1:A:759:ILE:HG21	1:A:798:LYS:C	2.40	0.42
1:A:930:ASP:HA	1:A:931:PRO:HD3	1.92	0.42
1:A:946:HIS:C	1:A:947:ILE:N	2.73	0.42
1:A:1006:VAL:O	1:A:1007:ILE:N	2.53	0.42
1:A:1580:LEU:HB3	1:A:1584:LYS:HZ1	1.85	0.42
1:A:2304:ALA:C	1:A:2306:LEU:H	2.22	0.42
2:B:84:GLN:OE1	2:B:89:TRP:HB2	2.20	0.42
1:C:146:LYS:HD3	1:C:187:GLU:HG2	2.01	0.42
1:C:781:LYS:O	1:C:785:GLU:N	2.50	0.42
1:C:1504:ILE:HD13	1:C:1596:ARG:CZ	2.50	0.42
1:C:1925:LEU:N	1:C:1928:GLN:HG2	2.34	0.42
1:C:2303:PHE:HB3	1:C:2377:LYS:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2317:PRO:HB2	1:C:2318:PHE:CD2	2.55	0.42
2:D:239:ASP:C	2:D:241:LYS:N	2.73	0.42
1:A:248:LEU:O	1:A:251:ASN:HB3	2.20	0.42
1:A:415:ILE:HG12	1:A:438:LEU:HD13	2.02	0.42
1:A:486:MET:HG3	1:A:494:HIS:HB2	2.02	0.42
1:A:661:GLN:HE21	1:A:672:ALA:HB1	1.84	0.42
1:A:1600:ILE:HG13	1:A:1601:LYS:N	2.33	0.42
1:A:1732:ARG:O	1:A:1734:SER:HB2	2.20	0.42
1:A:1754:TYR:HD1	1:A:1826:PHE:CZ	2.38	0.42
1:A:2334:SER:HB3	1:A:2335:PHE:HA	2.02	0.42
1:A:2398:ALA:HB1	1:A:2399:ILE:HG13	2.02	0.42
1:A:2405:GLN:C	1:A:2407:VAL:H	2.22	0.42
1:A:2436:ILE:HG13	1:A:2438:ARG:N	2.35	0.42
2:B:91:VAL:HA	2:B:101:VAL:HA	2.01	0.42
1:C:136:GLU:HA	1:C:179:VAL:HA	2.01	0.42
1:C:661:LEU:C	1:C:664:LEU:HB3	2.39	0.42
1:C:2203:ASN:O	1:C:2207:TRP:N	2.48	0.42
2:D:7:SER:HB2	2:D:38:LEU:HB2	2.02	0.42
2:D:14:ILE:HD12	2:D:16:PHE:HE2	1.85	0.42
2:D:173:MET:HB3	2:D:174:LEU:HA	2.02	0.42
5:I:698:ARG:HA	5:I:759:ASP:CA	2.50	0.42
5:I:698:ARG:O	5:I:701:SER:N	2.53	0.42
5:J:725:GLU:HG3	5:J:726:ASP:N	2.35	0.42
1:A:212:PHE:CE1	1:A:238:ARG:HA	2.53	0.41
1:A:577:LYS:HZ3	1:A:615:SER:HA	1.85	0.41
1:A:660:LEU:HA	1:A:663:LEU:HB3	2.01	0.41
1:A:843:GLU:C	1:A:845:LEU:H	2.23	0.41
1:A:1954:LEU:O	1:A:1958:ALA:N	2.53	0.41
1:A:1962:HIS:HE2	1:A:2006:ILE:HA	1.85	0.41
1:A:2140:LEU:HD21	1:A:2360:PHE:CE2	2.55	0.41
1:A:2232:ASN:OD1	1:A:2233:THR:N	2.53	0.41
1:A:2436:ILE:HD11	1:A:2438:ARG:HB2	2.02	0.41
2:B:267:THR:HB	2:B:277:TRP:HE1	1.84	0.41
1:C:236:GLU:OE2	1:C:271:PRO:HB3	2.19	0.41
1:C:315:HIS:CD2	1:C:320:ASN:ND2	2.83	0.41
1:C:315:HIS:NE2	1:C:320:ASN:OD1	2.53	0.41
1:C:333:ARG:HG2	1:C:373:LEU:HD13	2.02	0.41
1:C:474:ALA:HA	1:C:477:LYS:NZ	2.35	0.41
1:C:836:VAL:HG22	1:C:845:LEU:HD12	2.02	0.41
1:C:1365:LYS:H	1:C:1368:THR:HG22	1.84	0.41
1:C:1435:LYS:HZ1	1:C:1436:LEU:HG	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1478:LEU:C	1:C:1479:GLU:N	2.73	0.41
1:C:1609:GLN:C	1:C:1611:ARG:O	2.59	0.41
1:C:2112:LYS:C	1:C:2113:PHE:N	2.73	0.41
1:C:2340:THR:HA	1:C:2343:ASN:ND2	2.35	0.41
2:D:26:ARG:HD2	2:D:63:THR:HA	2.02	0.41
2:D:191:HIS:CG	2:D:192:THR:H	2.38	0.41
1:A:335:LEU:HD22	1:A:341:TYR:HB2	2.02	0.41
1:A:350:TYR:OH	1:A:385:LYS:HA	2.19	0.41
1:A:493:ASP:HA	1:A:496:GLN:HG2	2.02	0.41
1:A:675:ASP:O	1:A:679:LEU:N	2.53	0.41
1:A:709:TYR:HA	1:A:713:SER:HB2	2.02	0.41
1:A:742:CYS:HB2	1:A:743:THR:HG1	1.85	0.41
1:A:1060:VAL:O	1:A:1063:ARG:HB2	2.21	0.41
1:A:1351:LEU:HD23	1:A:1373:ILE:HD12	2.02	0.41
1:A:1408:ARG:CZ	1:A:1408:ARG:HB2	2.50	0.41
1:A:1763:ALA:O	1:A:1767:VAL:HG13	2.19	0.41
1:A:2107:ARG:N	1:A:2108:PRO:HD3	2.35	0.41
2:B:183:CYS:SG	2:B:205:ALA:HB2	2.60	0.41
1:C:1061:VAL:HA	1:C:1064:ARG:HB2	2.02	0.41
1:C:1274:ARG:HB2	1:C:1327:HIS:CE1	2.50	0.41
1:C:1281:PHE:CD2	1:C:1332:LEU:HD22	2.56	0.41
1:C:1408:LEU:HD21	1:C:1438:SER:HB3	2.01	0.41
1:C:2307:ILE:HB	1:C:2377:LYS:HD3	2.01	0.41
1:C:2317:PRO:HB3	1:C:2453:LEU:HD22	2.01	0.41
2:D:91:VAL:HG23	2:D:101:VAL:HB	2.01	0.41
2:D:174:LEU:HB3	2:D:175:ALA:H	1.75	0.41
5:J:741:LEU:HB3	5:J:742:LYS:H	1.66	0.41
1:A:281:ASP:CA	1:A:284:VAL:HB	2.35	0.41
1:A:506:ILE:N	1:A:507:PRO:HD2	2.35	0.41
1:A:547:ALA:HA	1:A:550:SER:OG	2.19	0.41
1:A:567:THR:HA	1:A:571:ILE:HG13	2.02	0.41
1:A:769:ASP:HA	1:A:809:GLN:HB2	2.02	0.41
1:A:804:ILE:HG22	1:A:805:ILE:HD13	2.01	0.41
1:A:923:ASN:HD22	1:A:923:ASN:N	2.18	0.41
1:A:1384:ILE:HA	1:A:1385:GLY:HA2	1.74	0.41
1:A:1824:LYS:O	1:A:1827:PHE:HB3	2.20	0.41
1:A:1881:ILE:HG21	1:A:1913:PRO:O	2.20	0.41
1:A:2247:ARG:O	1:A:2248:SER:HB3	2.20	0.41
1:A:2407:VAL:HA	1:A:2411:HIS:HB2	2.01	0.41
1:C:136:GLU:HA	1:C:179:VAL:HG12	2.01	0.41
1:C:153:VAL:HB	1:C:176:TYR:HE2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:VAL:HG22	1:C:335:LEU:HD13	2.02	0.41
1:C:929:LEU:HD21	1:C:943:GLN:HB2	2.02	0.41
1:C:998:ARG:HG2	1:C:1038:ARG:HG2	2.02	0.41
1:C:1589:ASP:HA	1:C:1591:TRP:CE2	2.55	0.41
1:C:1846:LEU:O	1:C:1847:LEU:HA	2.21	0.41
1:C:1984:THR:O	1:C:1986:LYS:N	2.53	0.41
1:C:2206:HIS:NE2	1:C:2472:PRO:HD2	2.35	0.41
1:C:2274:ILE:HD13	1:C:2274:ILE:HA	1.98	0.41
1:C:2459:SER:HA	1:C:2460:VAL:HA	1.47	0.41
2:D:132:ILE:HG21	2:D:174:LEU:HD11	2.00	0.41
1:A:175:TYR:HD1	1:A:190:LEU:HD13	1.85	0.41
1:A:196:GLY:HA2	1:A:198:LEU:HD12	2.01	0.41
1:A:800:LEU:HB3	1:A:804:ILE:HD12	2.02	0.41
1:A:1593:LEU:HD23	1:A:1596:ARG:HH21	1.85	0.41
1:A:2267:SER:HB3	1:A:2316:PHE:CE2	2.54	0.41
1:C:180:LEU:HD21	1:C:192:ALA:HB2	2.01	0.41
1:C:219:ILE:O	1:C:219:ILE:CG2	2.68	0.41
1:C:257:LEU:HD21	1:C:294:ILE:HG21	2.03	0.41
1:C:798:LEU:O	1:C:801:LEU:HB2	2.21	0.41
1:C:849:LEU:HD21	1:C:1546:VAL:CG2	2.51	0.41
1:C:1033:GLU:OE1	1:C:1075:ASN:ND2	2.53	0.41
1:C:1455:LYS:HE3	1:C:1467:MET:CE	2.49	0.41
1:C:1569:LYS:O	1:C:1573:MET:N	2.44	0.41
1:C:1766:ASN:O	1:C:1767:PHE:N	2.53	0.41
1:C:2174:LYS:O	1:C:2175:SER:HB2	2.20	0.41
1:A:271:LEU:O	1:A:272:ARG:HB2	2.21	0.41
1:A:332:ARG:HA	1:A:372:LEU:HD13	2.02	0.41
1:A:928:LEU:HD21	1:A:942:GLN:HB3	2.02	0.41
1:A:1629:LEU:O	1:A:1630:ASN:N	2.53	0.41
1:C:631:VAL:HA	1:C:634:LEU:HD12	2.01	0.41
1:C:854:LYS:HG3	1:C:1584:CYS:HB2	2.02	0.41
1:C:1113:ILE:N	1:C:1150:LEU:HD22	2.36	0.41
1:C:1817:ILE:O	1:C:1821:VAL:HG23	2.21	0.41
1:C:2157:PHE:CD1	1:C:2160:HIS:CG	3.09	0.41
2:D:84:GLN:HB3	2:D:89:TRP:CB	2.32	0.41
3:F:107:UNK:C	3:F:108:UNK:HA	2.50	0.41
1:A:87:ILE:HG23	1:A:99:ARG:HE	1.86	0.41
1:A:971:ARG:HH22	1:A:984:GLN:HG3	1.84	0.41
1:A:1626:LYS:HB2	1:A:1629:LEU:HG	2.01	0.41
1:A:2419:ARG:HA	1:A:2422:LEU:HB3	2.02	0.41
2:B:166:SER:HG	2:B:215:LEU:N	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:173:MET:HB2	2:B:215:LEU:HD11	2.01	0.41
1:C:1249:GLN:NE2	1:C:1275:GLU:HG2	2.36	0.41
1:C:1430:GLU:CB	1:C:1431:VAL:N	2.81	0.41
1:C:1857:PRO:C	1:C:1859:ALA:H	2.24	0.41
1:C:1909:PRO:HA	1:C:1912:LEU:N	2.35	0.41
1:C:2113:PHE:N	1:C:2125:TYR:O	2.53	0.41
2:D:189:PRO:HG2	2:D:196:HIS:H	1.86	0.41
3:F:711:UNK:O	3:F:713:UNK:N	2.53	0.41
5:I:703:ILE:HA	5:I:706:VAL:HG23	2.01	0.41
5:I:719:LYS:HA	5:I:720:PRO:HA	1.91	0.41
5:J:705:GLU:O	5:J:709:PHE:N	2.53	0.41
1:A:88:PHE:HZ	1:A:151:ALA:HB2	1.85	0.41
1:A:305:PHE:O	1:A:309:PHE:HB2	2.20	0.41
1:A:854:THR:HG22	1:A:855:GLU:N	2.35	0.41
1:A:1280:PHE:CZ	1:A:1330:LEU:HD13	2.55	0.41
1:A:1386:ILE:HA	1:A:1389:HIS:HB3	2.02	0.41
1:A:2219:LEU:O	1:A:2223:VAL:HG23	2.20	0.41
2:B:17:TRP:CE2	2:B:288:TYR:HB3	2.56	0.41
1:C:131:ASN:HB3	1:C:135:PHE:CE2	2.55	0.41
1:C:153:VAL:HG11	1:C:172:ARG:HG3	2.03	0.41
1:C:653:VAL:CG2	3:E:100:UNK:HA	2.51	0.41
1:C:766:PRO:HD3	1:C:806:ILE:HG22	2.03	0.41
1:C:1720:LEU:O	1:C:1724:GLU:HB3	2.21	0.41
1:C:2080:VAL:HG13	1:C:2091:ILE:HA	2.01	0.41
1:A:291:THR:HG22	1:A:296:ARG:HB3	2.03	0.41
1:A:472:PRO:HG2	1:A:476:LYS:HB3	2.03	0.41
1:A:687:GLU:O	1:A:689:PHE:N	2.53	0.41
1:A:784:GLU:O	1:A:788:VAL:HG22	2.21	0.41
1:A:792:GLU:HG3	1:A:794:THR:OG1	2.21	0.41
1:A:812:SER:HB2	1:A:851:ILE:HG13	2.02	0.41
1:A:1222:ILE:HG12	1:A:1285:VAL:HG11	2.03	0.41
1:A:1824:LYS:HD2	1:A:1861:MET:HB2	2.01	0.41
1:A:1870:ILE:O	1:A:1872:THR:N	2.54	0.41
1:C:437:LEU:HA	1:C:440:ASP:CB	2.44	0.41
1:C:783:LEU:N	1:C:784:GLY:HA3	2.28	0.41
1:C:862:ARG:HH22	1:C:1542:TYR:HB3	1.85	0.41
1:C:1360:PHE:HB3	1:C:1372:LEU:HD22	2.03	0.41
1:C:1431:VAL:HG22	1:C:1463:VAL:HG13	2.03	0.41
1:C:1512:PHE:O	1:C:1515:ALA:N	2.53	0.41
1:C:1541:ALA:CB	1:C:1542:TYR:CA	2.97	0.41
1:C:1576:THR:O	1:C:1580:ARG:N	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1615:ALA:O	1:C:1619:ARG:N	2.53	0.41
1:C:1714:LEU:HD21	1:C:1751:PHE:O	2.20	0.41
1:C:2187:PHE:HE1	1:C:2324:LEU:HD13	1.85	0.41
1:C:2242:LYS:O	1:C:2243:VAL:N	2.53	0.41
1:C:2414:LYS:HA	1:C:2417:ILE:HG13	2.03	0.41
3:F:704:UNK:O	3:F:707:UNK:N	2.54	0.41
1:A:205:LEU:HA	1:A:209:PHE:HB3	2.03	0.41
1:A:260:VAL:HG22	1:A:303:GLN:HG2	2.03	0.41
1:A:417:VAL:HB	1:A:418:SER:N	2.36	0.41
1:A:422:ILE:HG12	1:A:466:LEU:HD13	2.03	0.41
1:A:422:ILE:CG1	1:A:466:LEU:HD13	2.50	0.41
1:A:817:ARG:HD2	1:A:867:LEU:HD13	2.02	0.41
1:A:979:ASP:HA	1:A:982:PHE:CD2	2.56	0.41
1:A:1366:THR:HA	1:A:1369:ALA:HB3	2.02	0.41
1:A:1499:TYR:H	1:A:1594:ARG:HH21	1.68	0.41
1:A:1630:ASN:O	1:A:1633:LEU:HB2	2.21	0.41
1:A:1669:LEU:O	1:A:1672:LEU:HB3	2.20	0.41
1:A:1715:ARG:HH21	1:A:1719:LYS:HE3	1.85	0.41
1:A:1910:LEU:HB3	1:A:1912:TYR:H	1.85	0.41
1:A:1997:LYS:H	1:A:1998:ARG:N	2.19	0.41
1:A:2124:VAL:HG12	1:A:2178:TRP:CE3	2.54	0.41
1:A:2285:LEU:HB2	1:A:2286:ASP:H	1.78	0.41
1:A:2404:VAL:HB	1:A:2408:GLU:HB2	2.03	0.41
1:A:2424:LEU:C	1:A:2427:ILE:H	2.23	0.41
1:A:2431:LEU:HA	1:A:2447:GLN:CG	2.51	0.41
2:B:55:VAL:HG13	2:B:57:LEU:HG	2.03	0.41
2:B:232:ARG:HA	2:B:244:THR:HB	2.02	0.41
1:C:114:LEU:N	1:C:118:VAL:HG22	2.35	0.41
1:C:143:SER:HA	1:C:146:LYS:HE3	2.02	0.41
1:C:217:THR:O	1:C:221:TRP:CG	2.74	0.41
1:C:234:LYS:NZ	1:C:238:ARG:HE	2.18	0.41
1:C:330:LEU:O	1:C:334:GLU:HB2	2.20	0.41
1:C:362:PHE:CD2	1:C:362:PHE:C	2.94	0.41
1:C:378:ALA:CA	1:C:379:PHE:N	2.80	0.41
1:C:613:ALA:HB1	1:C:643:LYS:NZ	2.36	0.41
1:C:683:MET:O	1:C:686:ASN:HB2	2.21	0.41
1:C:721:GLU:HG3	1:C:722:LEU:HD12	2.03	0.41
1:C:801:LEU:O	1:C:802:MET:N	2.53	0.41
1:C:824:THR:C	1:C:826:GLY:H	2.24	0.41
1:C:1053:ASN:HD21	1:C:1061:VAL:HG21	1.85	0.41
1:C:1066:LEU:HD11	1:C:1103:ILE:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1088:VAL:HG22	1:C:1103:ILE:CG2	2.50	0.41
1:C:1281:PHE:CE1	1:C:1332:LEU:HD13	2.56	0.41
1:C:1421:LYS:HB2	1:C:1435:LYS:HB2	2.01	0.41
1:C:1655:TYR:O	1:C:1659:LYS:N	2.53	0.41
1:C:1726:ARG:HG3	1:C:1727:VAL:H	1.84	0.41
1:C:2134:ARG:HB3	1:C:2368:ILE:HB	2.02	0.41
1:C:2185:ASP:O	1:C:2286:MET:HG3	2.21	0.41
1:C:2258:ARG:HD2	1:C:2329:GLU:HB2	2.03	0.41
2:D:9:GLY:HA2	2:D:296:VAL:HG23	2.03	0.41
2:D:141:ARG:HG2	2:D:153:GLN:HB3	2.02	0.41
1:A:543:SER:O	1:A:544:ILE:HG13	2.21	0.41
1:A:759:ILE:HG13	1:A:760:LEU:N	2.36	0.41
1:A:1049:ILE:HD13	1:A:1049:ILE:N	2.36	0.41
1:A:1756:ALA:O	1:A:1759:ASN:HB2	2.21	0.41
1:C:280:ARG:NH2	1:C:328:THR:HB	2.34	0.41
1:C:500:LEU:HA	1:C:503:LEU:HD12	2.04	0.41
1:C:576:CYS:HB3	1:C:580:LEU:HD22	2.03	0.41
1:C:678:LEU:HB2	1:C:727:LYS:HD2	2.03	0.41
1:C:859:PRO:HG3	1:C:1543:ASN:CG	2.42	0.41
1:C:963:ILE:HG13	1:C:964:ILE:H	1.85	0.41
1:C:968:ILE:HA	1:C:971:MET:HB3	2.01	0.41
1:C:994:LYS:HA	1:C:995:GLN:CB	2.51	0.41
1:C:1093:TYR:O	1:C:1100:LYS:HD3	2.21	0.41
1:C:1967:TRP:CD1	1:C:1994:LEU:O	2.74	0.41
1:C:2068:PRO:HB3	1:C:2071:LEU:HD13	2.02	0.41
1:C:2089:LYS:N	1:C:2090:PRO:CD	2.84	0.41
5:J:757:LYS:HB2	5:J:784:GLN:HG2	2.02	0.41
1:A:180:ILE:H	1:A:180:ILE:HG12	1.78	0.40
1:A:1173:HIS:CD2	1:A:1178:GLN:HB2	2.56	0.40
1:A:1523:LEU:HD12	1:A:1524:LEU:HG	2.03	0.40
1:A:1985:MET:HA	1:A:1988:ALA:HB2	2.02	0.40
1:A:2251:THR:CG2	1:A:2255:ARG:HD2	2.51	0.40
2:B:213:ILE:HB	2:B:214:LEU:CA	2.51	0.40
1:C:1991:LEU:HA	1:C:1994:LEU:HG	2.03	0.40
1:C:2470:TRP:CD1	1:C:2472:PRO:HD3	2.56	0.40
1:A:661:GLN:HG2	1:A:672:ALA:HB1	2.03	0.40
1:A:986:GLY:N	1:A:1019:THR:HG1	2.19	0.40
1:A:1580:LEU:HB3	1:A:1584:LYS:NZ	2.36	0.40
1:A:1764:ASN:C	1:A:1767:VAL:HG22	2.41	0.40
1:A:2431:LEU:HA	1:A:2447:GLN:HG2	2.03	0.40
2:B:25:SER:OG	2:B:60:ILE:HD11	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:ILE:HD12	2:B:301:ASN:HB2	2.03	0.40
2:B:194:ALA:HB1	2:B:196:HIS:NE2	2.36	0.40
1:C:97:PRO:C	1:C:99:GLU:H	2.24	0.40
1:C:857:ASN:HB3	1:C:1586:LYS:N	2.37	0.40
1:C:861:ILE:HG22	1:C:864:GLY:N	2.36	0.40
1:C:976:PRO:HA	1:C:979:LEU:HB2	2.03	0.40
1:C:981:PHE:C	1:C:985:GLN:HG2	2.42	0.40
1:C:2000:ARG:HG3	1:C:2003:GLU:OE1	2.21	0.40
1:C:2108:GLN:HE22	1:C:2130:HIS:HB2	1.86	0.40
1:A:120:GLU:HG3	1:A:159:TYR:CZ	2.56	0.40
1:A:172:LEU:HD21	1:A:208:ASP:OD1	2.21	0.40
1:A:1151:LEU:HD11	1:A:1184:LEU:HD21	2.03	0.40
1:A:2077:ALA:HB2	1:A:2091:LYS:C	2.42	0.40
1:A:2095:PHE:CD2	1:A:2113:ILE:HG12	2.56	0.40
1:A:2140:LEU:HA	1:A:2143:LEU:HB2	2.04	0.40
1:A:2202:ILE:HA	1:A:2205:TRP:HB3	2.03	0.40
1:A:2398:ALA:HA	1:A:2399:ILE:HA	1.82	0.40
1:C:194:ASN:H	1:C:195:THR:N	2.19	0.40
1:C:277:LEU:HD11	1:C:324:SER:HB2	2.02	0.40
1:C:389:LEU:C	1:C:391:ARG:H	2.24	0.40
1:C:439:LEU:O	1:C:443:ARG:HG2	2.20	0.40
1:C:446:LEU:HG	1:C:450:PHE:CE2	2.56	0.40
1:C:546:GLU:HA	1:C:549:ARG:CB	2.52	0.40
1:C:763:VAL:HG21	1:C:803:PRO:HB3	2.02	0.40
1:C:983:PHE:CB	1:C:1022:ILE:HG12	2.23	0.40
1:C:1452:ALA:HA	1:C:1455:LYS:HB3	2.03	0.40
1:C:1723:GLY:HA2	1:C:1726:ARG:HD3	2.03	0.40
3:F:251:UNK:HA	3:F:254:UNK:CB	2.51	0.40
3:F:262:UNK:O	3:F:265:UNK:N	2.53	0.40
5:I:654:ASN:O	5:I:659:LEU:HB2	2.20	0.40
1:A:277:ILE:H	1:A:277:ILE:HG13	1.78	0.40
1:A:416:LEU:HD12	1:A:459:LEU:HD21	2.03	0.40
1:A:654:GLU:O	1:A:658:GLU:N	2.54	0.40
1:A:670:GLN:HE22	1:A:716:LYS:HB2	1.86	0.40
1:A:1024:ILE:O	1:A:1024:ILE:HG22	2.22	0.40
1:A:1033:GLY:HA2	1:A:1034:GLU:HA	1.77	0.40
1:A:1440:LEU:CD2	1:A:1622:MET:HG2	2.47	0.40
1:A:1558:TYR:C	1:A:1572:ARG:HH21	2.25	0.40
1:A:2131:ILE:HD13	1:A:2174:GLY:HA3	2.03	0.40
1:A:2450:LYS:HD3	1:A:2450:LYS:HA	1.89	0.40
1:C:86:ASN:HD21	1:C:124:GLN:HB3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:ARG:HA	1:C:369:VAL:CB	2.51	0.40
1:C:602:GLU:HA	1:C:603:HIS:O	2.22	0.40
1:C:726:LEU:HD13	1:C:761:LEU:HD23	2.03	0.40
1:C:1151:GLN:HB3	1:C:1152:LEU:H	1.61	0.40
1:C:1226:ASN:HD22	1:C:1286:VAL:HG13	1.86	0.40
1:C:1259:LEU:HD23	1:C:1259:LEU:HA	1.93	0.40
1:C:1541:ALA:HB3	1:C:1542:TYR:HA	2.04	0.40
1:C:2005:LEU:O	1:C:2065:HIS:HA	2.22	0.40
1:C:2432:LYS:HA	1:C:2444:LEU:HD12	2.02	0.40
3:E:500:UNK:CB	3:E:702:UNK:HA	2.51	0.40
3:F:803:UNK:C	3:F:805:UNK:N	2.85	0.40
5:J:730:VAL:HG21	5:J:790:PRO:N	2.36	0.40
1:A:138:HIS:HB3	1:A:145:LYS:HE2	2.03	0.40
1:A:431:SER:C	1:A:433:TYR:H	2.25	0.40
1:A:600:ILE:HA	1:A:602:HIS:HB2	2.03	0.40
1:A:699:ILE:HD12	1:A:717:THR:HG22	2.03	0.40
1:A:1164:LYS:CB	1:A:1170:ARG:HG3	2.52	0.40
1:A:1359:LEU:HA	1:A:1362:PRO:HD3	2.03	0.40
1:A:1910:LEU:C	1:A:1911:VAL:HG12	2.42	0.40
1:A:2458:VAL:HG13	1:A:2459:GLU:H	1.87	0.40
1:C:157:ILE:CG1	1:C:172:ARG:HH22	2.31	0.40
1:C:216:ARG:HD2	1:C:234:LYS:HZ3	1.86	0.40
1:C:309:LEU:HA	1:C:346:LYS:NZ	2.35	0.40
1:C:577:PHE:CG	1:C:592:PHE:HB2	2.57	0.40
1:C:818:ARG:HB2	1:C:818:ARG:NH1	2.37	0.40
1:C:1431:VAL:HG13	1:C:1466:ALA:CB	2.52	0.40
1:C:1682:ALA:HB2	1:C:1717:ARG:HH22	1.87	0.40
1:C:1742:LEU:O	1:C:1746:LEU:HD13	2.21	0.40
1:C:1762:TRP:CE3	1:C:1763:ALA:HA	2.56	0.40
1:C:1913:VAL:O	1:C:1917:MET:N	2.52	0.40
1:C:2023:GLU:HA	1:C:2026:MET:HG2	2.02	0.40
3:E:371:UNK:C	3:E:373:UNK:N	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1309/2474 (53%)	872 (67%)	313 (24%)	124 (10%)	0 10
1	C	1267/2474 (51%)	849 (67%)	290 (23%)	128 (10%)	0 9
2	B	178/303 (59%)	122 (68%)	45 (25%)	11 (6%)	1 17
2	D	173/303 (57%)	113 (65%)	44 (25%)	16 (9%)	1 11
4	G	75/426 (18%)	57 (76%)	12 (16%)	6 (8%)	1 12
4	H	80/426 (19%)	43 (54%)	22 (28%)	15 (19%)	0 2
5	I	95/1176 (8%)	52 (55%)	29 (30%)	14 (15%)	0 4
5	J	88/1176 (8%)	52 (59%)	23 (26%)	13 (15%)	0 3
All	All	3265/8758 (37%)	2160 (66%)	778 (24%)	327 (10%)	1 9

All (327) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	ASP
1	A	112	SER
1	A	224	THR
1	A	257	TYR
1	A	342	LEU
1	A	348	ASP
1	A	402	ILE
1	A	490	PRO
1	A	582	ILE
1	A	583	HIS
1	A	586	TYR
1	A	650	ASP
1	A	767	CYS
1	A	769	ASP
1	A	771	SER
1	A	791	LYS
1	A	854	THR
1	A	1083	MET
1	A	1135	GLU
1	A	1192	ASN
1	A	1342	GLN
1	A	1428	GLU
1	A	1447	SER

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Mol	Chain	Res	Type
1	A	1477	GLU
1	A	1583	GLN
1	A	1732	ARG
1	A	1750	ASP
1	A	1753	TRP
1	A	1871	GLY
1	A	1977	PHE
1	A	1978	GLY
1	A	2089	ILE
1	A	2247	ARG
1	A	2248	SER
1	A	2288	ILE
1	A	2328	VAL
1	A	2334	SER
1	A	2391	ASN
1	A	2392	GLU
1	A	2426	ARG
1	A	2436	ILE
1	A	2440	ASN
1	A	2441	ASP
1	A	2442	LEU
1	A	2453	GLN
2	B	106	SER
2	B	107	PRO
2	B	213	ILE
1	C	167	PRO
1	C	233	SER
1	C	273	ARG
1	C	409	ASN
1	C	425	PHE
1	C	473	PRO
1	C	490	CYS
1	C	491	PRO
1	C	530	LYS
1	C	534	SER
1	C	673	ALA
1	C	838	PRO
1	C	861	ILE
1	C	1085	PRO
1	C	1152	LEU
1	C	1193	ASN
1	C	1286	VAL

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Mol	Chain	Res	Type
1	C	1287	GLU
1	C	1293	GLN
1	C	1585	GLN
1	C	1586	LYS
1	C	1588	ILE
1	C	1750	HIS
1	C	1857	PRO
1	C	1878	VAL
1	C	1985	GLU
1	C	1997	MET
1	C	2090	PRO
1	C	2241	TYR
1	C	2330	VAL
1	C	2355	LEU
1	C	2378	LYS
1	C	2394	GLU
2	D	5	LEU
2	D	33	SER
2	D	56	ARG
2	D	298	VAL
4	H	121	TYR
4	H	140	THR
4	H	141	ASN
5	I	687	LYS
5	I	764	ILE
5	J	692	SER
5	J	741	LEU
5	J	764	ILE
1	A	178	VAL
1	A	261	ASN
1	A	341	TYR
1	A	359	TYR
1	A	395	TYR
1	A	493	ASP
1	A	539	ASN
1	A	600	ILE
1	A	669	PRO
1	A	743	THR
1	A	751	VAL
1	A	838	LEU
1	A	1022	SER
1	A	1091	GLU

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Mol	Chain	Res	Type
1	A	1590	GLN
1	A	1628	VAL
1	A	1731	TRP
1	A	1733	LEU
1	A	1868	ILE
1	A	1942	VAL
1	A	1979	GLU
1	A	2298	GLY
1	A	2390	ALA
2	B	245	THR
2	B	296	VAL
1	C	97	PRO
1	C	177	LEU
1	C	184	SER
1	C	234	LYS
1	C	235	LEU
1	C	324	SER
1	C	338	LEU
1	C	416	ILE
1	C	601	ILE
1	C	603	HIS
1	C	656	ILE
1	C	748	SER
1	C	925	LEU
1	C	1176	VAL
1	C	1477	GLY
1	C	1519	ILE
1	C	1541	ALA
1	C	1602	ILE
1	C	1612	ILE
1	C	1873	GLY
1	C	1913	VAL
1	C	2087	GLY
1	C	2091	ILE
1	C	2146	VAL
1	C	2184	SER
1	C	2185	ASP
1	C	2279	ASP
1	C	2308	LEU
1	C	2332	GLY
2	D	6	VAL
4	G	66	LYS

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Mol	Chain	Res	Type
4	G	77	THR
4	H	72	THR
4	H	77	THR
4	H	78	CYS
4	H	131	VAL
5	I	686	LYS
5	I	716	THR
5	J	653	THR
5	J	702	THR
5	J	730	VAL
5	J	747	ASP
5	J	755	PHE
5	J	790	PRO
1	A	304	TRP
1	A	377	ALA
1	A	450	LYS
1	A	555	PHE
1	A	568	ASP
1	A	602	HIS
1	A	766	LYS
1	A	778	ALA
1	A	1233	LYS
1	A	1523	LEU
1	A	1593	LEU
1	A	1736	PRO
1	A	1813	ASN
1	A	2083	ALA
1	A	2122	LYS
1	A	2326	MET
1	A	2382	GLY
1	A	2443	ASP
2	B	177	ALA
1	C	122	GLN
1	C	176	TYR
1	C	224	LEU
1	C	259	PRO
1	C	267	ASN
1	C	275	ALA
1	C	341	PRO
1	C	683	MET
1	C	712	VAL
1	C	772	SER

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Mol	Chain	Res	Type
1	C	1013	PRO
1	C	1197	ASP
1	C	1839	SER
1	C	2063	LEU
1	C	2097	PHE
1	C	2116	LYS
1	C	2154	ALA
1	C	2302	CYS
1	C	2374	LEU
2	D	193	ASP
2	D	195	SER
2	D	238	ASP
4	G	131	VAL
4	H	112	PRO
4	H	120	ASP
4	H	177	GLY
4	H	183	ASP
5	I	663	SER
5	I	668	ASP
1	A	519	ASN
1	A	717	THR
1	A	720	GLU
1	A	1076	GLU
1	A	1248	GLN
1	A	1333	PRO
1	A	1539	ALA
1	A	1597	SER
1	A	1602	PRO
1	A	1711	LYS
1	A	1751	ASN
1	A	1870	ILE
1	A	2304	ALA
2	B	73	GLY
2	B	277	TRP
1	C	116	ARG
1	C	139	HIS
1	C	339	LYS
1	C	340	ALA
1	C	370	TYR
1	C	493	SER
1	C	592	PHE
1	C	1084	MET

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Mol	Chain	Res	Type
1	C	1216	LYS
1	C	1733	TRP
1	C	2111	ARG
2	D	206	HIS
2	D	242	LEU
4	G	145	PRO
4	H	44	LEU
4	H	74	LYS
5	I	698	ARG
5	I	708	GLY
5	I	730	VAL
1	A	269	VAL
1	A	580	GLN
1	A	1584	LYS
1	A	1599	VAL
1	A	1820	ILE
1	A	2085	GLY
2	B	219	VAL
1	C	96	VAL
1	C	995	GLN
1	C	1510	ASN
1	C	1599	SER
1	C	1611	ARG
1	C	1848	THR
1	C	2083	THR
1	C	2110	PRO
1	C	2419	ASN
2	D	272	HIS
4	G	137	VAL
4	G	149	CYS
5	I	670	VAL
5	I	715	SER
5	I	736	PRO
5	J	736	PRO
1	A	122	PHE
1	A	842	PRO
1	A	994	GLN
1	A	1106	GLY
1	A	1205	LYS
1	A	1348	ALA
1	A	2470	PRO
2	B	183	CYS

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Mol	Chain	Res	Type
1	C	143	SER
1	C	298	ASP
1	C	1248	ILE
1	C	1388	ILE
1	C	2379	ILE
2	D	22	GLY
2	D	91	VAL
2	D	277	TRP
4	H	145	PRO
5	J	699	LYS
1	A	1242	ILE
1	A	1890	ILE
1	A	1940	SER
1	A	2305	ILE
1	C	299	PRO
1	C	528	GLY
1	C	561	GLY
1	C	1019	ILE
1	C	1563	LEU
1	C	1601	VAL
1	C	2300	GLY
1	C	2312	PHE
1	C	2347	VAL
1	C	2469	GLY
2	D	219	VAL
4	H	130	GLY
5	I	749	GLU
1	A	707	PRO
1	A	1334	ILE
1	A	1458	LYS
1	A	2013	GLY
1	C	166	LEU
1	C	508	PRO
1	C	752	VAL
1	C	1630	VAL
1	C	2446	VAL
5	I	682	ILE
1	A	930	ASP
1	C	1364	PRO
1	C	1727	VAL
1	C	1942	SER
1	C	2115	ILE

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Mol	Chain	Res	Type
2	D	23	VAL
1	A	1517	ILE
1	A	2265	VAL
2	B	65	PRO
1	C	1468	ALA
1	C	2082	GLY
1	C	2333	ILE
5	J	703	ILE
5	J	756	GLY
1	A	2310	PHE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	2029/2219 (91%)	1734 (86%)	295 (14%)	3 15
1	C	2029/2219 (91%)	1722 (85%)	307 (15%)	3 14
2	B	264/267 (99%)	229 (87%)	35 (13%)	4 18
2	D	264/267 (99%)	230 (87%)	34 (13%)	4 18
5	I	137/1066 (13%)	113 (82%)	24 (18%)	2 11
5	J	137/1066 (13%)	108 (79%)	29 (21%)	1 6
All	All	4860/7104 (68%)	4136 (85%)	724 (15%)	6 15

All (724) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	LEU
1	A	88	PHE
1	A	89	ASP
1	A	90	LYS
1	A	92	LYS
1	A	93	SER
1	A	111	THR
1	A	112	SER

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Mol	Chain	Res	Type
1	A	115	ARG
1	A	120	GLU
1	A	121	GLN
1	A	124	ARG
1	A	128	SER
1	A	133	ILE
1	A	150	LEU
1	A	152	VAL
1	A	153	ASP
1	A	179	LEU
1	A	180	ILE
1	A	187	VAL
1	A	212	PHE
1	A	216	THR
1	A	222	THR
1	A	224	THR
1	A	228	ASN
1	A	229	SER
1	A	230	SER
1	A	234	LEU
1	A	238	ARG
1	A	243	LEU
1	A	244	ILE
1	A	245	ILE
1	A	252	SER
1	A	255	LEU
1	A	256	LEU
1	A	257	TYR
1	A	265	ASP
1	A	269	VAL
1	A	273	ASP
1	A	276	LEU
1	A	290	LEU
1	A	302	LYS
1	A	304	TRP
1	A	307	ARG
1	A	320	THR
1	A	324	VAL
1	A	329	LEU
1	A	330	VAL
1	A	334	LEU
1	A	338	LYS

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Mol	Chain	Res	Type
1	A	341	TYR
1	A	342	LEU
1	A	343	ARG
1	A	354	MET
1	A	378	PHE
1	A	384	THR
1	A	386	LYS
1	A	388	LEU
1	A	395	TYR
1	A	401	ASN
1	A	402	ILE
1	A	409	ASN
1	A	419	ILE
1	A	421	ASP
1	A	422	ILE
1	A	431	SER
1	A	439	ASP
1	A	441	ILE
1	A	449	PHE
1	A	452	ARG
1	A	453	LYS
1	A	466	LEU
1	A	474	PHE
1	A	480	LYS
1	A	487	LEU
1	A	489	CYS
1	A	493	ASP
1	A	511	SER
1	A	520	LEU
1	A	534	ASN
1	A	549	LYS
1	A	554	SER
1	A	562	SER
1	A	583	HIS
1	A	592	VAL
1	A	616	CYS
1	A	622	ASP
1	A	623	ASP
1	A	630	VAL
1	A	633	LEU
1	A	636	VAL
1	A	660	LEU

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Mol	Chain	Res	Type
1	A	662	HIS
1	A	670	GLN
1	A	677	LEU
1	A	680	LEU
1	A	685	ASN
1	A	698	ILE
1	A	699	ILE
1	A	701	ARG
1	A	703	SER
1	A	709	TYR
1	A	719	LEU
1	A	723	THR
1	A	725	LEU
1	A	739	THR
1	A	743	THR
1	A	751	VAL
1	A	759	ILE
1	A	760	LEU
1	A	761	ASP
1	A	772	SER
1	A	777	THR
1	A	779	LEU
1	A	793	MET
1	A	805	ILE
1	A	817	ARG
1	A	824	LEU
1	A	848	LEU
1	A	849	ILE
1	A	860	ILE
1	A	921	ILE
1	A	927	ILE
1	A	944	ILE
1	A	951	LEU
1	A	954	ARG
1	A	957	SER
1	A	958	PHE
1	A	962	ILE
1	A	968	LEU
1	A	970	MET
1	A	982	PHE
1	A	985	LEU
1	A	997	ARG

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Mol	Chain	Res	Type
1	A	1003	ILE
1	A	1013	ILE
1	A	1015	LYS
1	A	1019	THR
1	A	1020	ILE
1	A	1027	ILE
1	A	1043	LEU
1	A	1050	LEU
1	A	1054	GLN
1	A	1067	SER
1	A	1068	LEU
1	A	1069	VAL
1	A	1083	MET
1	A	1086	VAL
1	A	1087	VAL
1	A	1090	THR
1	A	1102	ILE
1	A	1107	ARG
1	A	1111	ASN
1	A	1116	GLU
1	A	1117	MET
1	A	1127	ARG
1	A	1137	THR
1	A	1140	THR
1	A	1144	LEU
1	A	1153	THR
1	A	1170	ARG
1	A	1173	HIS
1	A	1175	VAL
1	A	1178	GLN
1	A	1182	LYS
1	A	1201	VAL
1	A	1207	TYR
1	A	1209	ASP
1	A	1212	GLN
1	A	1214	THR
1	A	1228	TYR
1	A	1229	CYS
1	A	1230	SER
1	A	1236	GLU
1	A	1243	ARG
1	A	1249	LEU

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Mol	Chain	Res	Type
1	A	1267	VAL
1	A	1287	LEU
1	A	1290	SER
1	A	1326	ASP
1	A	1332	ILE
1	A	1353	TYR
1	A	1354	LYS
1	A	1357	GLU
1	A	1366	THR
1	A	1370	LEU
1	A	1379	GLN
1	A	1380	THR
1	A	1384	ILE
1	A	1402	TRP
1	A	1404	GLU
1	A	1408	ARG
1	A	1425	ASP
1	A	1426	SER
1	A	1430	MET
1	A	1433	LYS
1	A	1434	LEU
1	A	1476	LEU
1	A	1477	GLU
1	A	1480	ASP
1	A	1491	SER
1	A	1493	SER
1	A	1504	CYS
1	A	1515	VAL
1	A	1523	LEU
1	A	1524	LEU
1	A	1527	GLU
1	A	1534	GLU
1	A	1557	LYS
1	A	1569	LEU
1	A	1570	THR
1	A	1585	ASN
1	A	1587	ASP
1	A	1612	PHE
1	A	1626	LYS
1	A	1648	SER
1	A	1669	LEU
1	A	1682	ASP

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Mol	Chain	Res	Type
1	A	1723	TRP
1	A	1731	TRP
1	A	1742	SER
1	A	1745	LEU
1	A	1811	SER
1	A	1820	ILE
1	A	1823	ILE
1	A	1824	LYS
1	A	1830	ILE
1	A	1832	LEU
1	A	1837	SER
1	A	1839	GLN
1	A	1844	LEU
1	A	1856	GLU
1	A	1868	ILE
1	A	1870	ILE
1	A	1875	GLU
1	A	1876	VAL
1	A	1884	ILE
1	A	1911	VAL
1	A	1921	GLU
1	A	1930	LEU
1	A	1965	TRP
1	A	1969	LEU
1	A	1976	PHE
1	A	1977	PHE
1	A	1998	ARG
1	A	2014	ARG
1	A	2017	ASN
1	A	2043	TYR
1	A	2049	ILE
1	A	2059	LEU
1	A	2070	SER
1	A	2081	THR
1	A	2090	VAL
1	A	2092	ILE
1	A	2093	SER
1	A	2095	PHE
1	A	2105	LYS
1	A	2109	ARG
1	A	2111	PHE
1	A	2125	LEU

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Mol	Chain	Res	Type
1	A	2134	ASP
1	A	2151	ASP
1	A	2159	LEU
1	A	2191	GLU
1	A	2219	LEU
1	A	2230	LEU
1	A	2231	ASN
1	A	2234	GLU
1	A	2250	GLU
1	A	2253	LEU
1	A	2263	LEU
1	A	2272	ILE
1	A	2275	LEU
1	A	2283	LEU
1	A	2285	LEU
1	A	2291	LYS
1	A	2299	ASP
1	A	2308	GLU
1	A	2335	PHE
1	A	2336	ARG
1	A	2338	THR
1	A	2353	LEU
1	A	2357	LEU
1	A	2360	PHE
1	A	2367	ASN
1	A	2372	LEU
1	A	2385	LEU
1	A	2387	VAL
1	A	2416	ARG
1	A	2425	LYS
1	A	2426	ARG
1	A	2428	THR
1	A	2431	LEU
1	A	2437	ARG
1	A	2462	CYS
2	B	4	ILE
2	B	10	TYR
2	B	24	CYS
2	B	28	ILE
2	B	39	GLU
2	B	40	ILE
2	B	55	VAL

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Mol	Chain	Res	Type
2	B	56	ARG
2	B	68	VAL
2	B	78	VAL
2	B	79	THR
2	B	80	SER
2	B	85	GLN
2	B	86	ASP
2	B	103	ASP
2	B	122	VAL
2	B	155	THR
2	B	162	LEU
2	B	170	ASP
2	B	182	ASN
2	B	200	VAL
2	B	203	PHE
2	B	213	ILE
2	B	219	VAL
2	B	230	THR
2	B	233	VAL
2	B	244	THR
2	B	255	ASP
2	B	256	CYS
2	B	259	SER
2	B	270	SER
2	B	281	THR
2	B	286	ARG
2	B	292	HIS
2	B	302	ASP
1	C	82	PHE
1	C	87	LEU
1	C	91	LYS
1	C	96	VAL
1	C	110	THR
1	C	123	PHE
1	C	124	GLN
1	C	129	SER
1	C	150	ILE
1	C	151	LEU
1	C	153	VAL
1	C	156	LEU
1	C	157	ILE
1	C	176	TYR

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Mol	Chain	Res	Type
1	C	179	VAL
1	C	188	VAL
1	C	191	LEU
1	C	196	LEU
1	C	206	LEU
1	C	207	THR
1	C	210	PHE
1	C	213	PHE
1	C	216	ARG
1	C	219	ILE
1	C	222	LEU
1	C	223	THR
1	C	225	THR
1	C	231	SER
1	C	234	LYS
1	C	235	LEU
1	C	236	GLU
1	C	237	TYR
1	C	243	LEU
1	C	260	TYR
1	C	263	SER
1	C	264	ILE
1	C	268	ILE
1	C	273	ARG
1	C	278	ILE
1	C	287	LEU
1	C	298	ASP
1	C	301	LEU
1	C	303	LYS
1	C	304	GLN
1	C	305	TRP
1	C	314	THR
1	C	321	THR
1	C	323	ASP
1	C	330	LEU
1	C	331	VAL
1	C	332	PHE
1	C	339	LYS
1	C	342	TYR
1	C	344	ARG
1	C	349	ASP
1	C	355	MET

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Mol	Chain	Res	Type
1	C	357	TYR
1	C	361	LYS
1	C	363	ASP
1	C	366	ARG
1	C	379	PHE
1	C	380	ASP
1	C	385	THR
1	C	387	LYS
1	C	389	LEU
1	C	397	LEU
1	C	402	ASN
1	C	404	ASP
1	C	412	ASP
1	C	419	SER
1	C	423	ILE
1	C	425	PHE
1	C	438	ILE
1	C	440	ASP
1	C	450	PHE
1	C	453	ARG
1	C	467	LEU
1	C	469	CYS
1	C	494	ASP
1	C	517	ARG
1	C	523	SER
1	C	526	LEU
1	C	541	ASN
1	C	566	ASP
1	C	568	THR
1	C	572	ILE
1	C	586	GLN
1	C	587	TYR
1	C	601	ILE
1	C	616	SER
1	C	617	CYS
1	C	630	SER
1	C	641	LEU
1	C	644	LEU
1	C	651	ASP
1	C	653	VAL
1	C	664	LEU
1	C	676	ASP

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Mol	Chain	Res	Type
1	C	678	LEU
1	C	712	VAL
1	C	720	LEU
1	C	722	LEU
1	C	724	THR
1	C	730	ASN
1	C	762	ASP
1	C	764	ILE
1	C	765	LEU
1	C	767	LYS
1	C	768	CYS
1	C	785	GLU
1	C	794	MET
1	C	795	THR
1	C	801	LEU
1	C	806	ILE
1	C	816	PHE
1	C	818	ARG
1	C	842	TYR
1	C	850	ILE
1	C	852	ILE
1	C	854	LYS
1	C	856	GLU
1	C	860	HIS
1	C	861	ILE
1	C	862	ARG
1	C	865	THR
1	C	922	ILE
1	C	934	LEU
1	C	946	MET
1	C	950	GLN
1	C	971	MET
1	C	986	LEU
1	C	992	ILE
1	C	1004	ILE
1	C	1007	VAL
1	C	1010	GLU
1	C	1014	ILE
1	C	1017	LEU
1	C	1019	ILE
1	C	1029	SER
1	C	1063	ILE

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Mol	Chain	Res	Type
1	C	1066	LEU
1	C	1068	SER
1	C	1069	LEU
1	C	1080	SER
1	C	1087	VAL
1	C	1094	SER
1	C	1108	ARG
1	C	1117	GLU
1	C	1118	MET
1	C	1126	LEU
1	C	1128	ARG
1	C	1130	LEU
1	C	1134	ASP
1	C	1141	THR
1	C	1151	GLN
1	C	1154	THR
1	C	1173	GLN
1	C	1174	HIS
1	C	1175	SER
1	C	1183	LYS
1	C	1213	GLN
1	C	1219	VAL
1	C	1220	ASN
1	C	1230	CYS
1	C	1231	SER
1	C	1240	GLN
1	C	1241	GLU
1	C	1244	ARG
1	C	1245	ARG
1	C	1264	SER
1	C	1268	VAL
1	C	1291	SER
1	C	1334	ILE
1	C	1368	THR
1	C	1372	LEU
1	C	1382	THR
1	C	1386	ILE
1	C	1398	LEU
1	C	1399	GLN
1	C	1401	LYS
1	C	1403	THR
1	C	1406	GLU

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Mol	Chain	Res	Type
1	C	1427	ASP
1	C	1432	MET
1	C	1435	LYS
1	C	1451	LEU
1	C	1460	LYS
1	C	1478	LEU
1	C	1491	MET
1	C	1499	GLU
1	C	1504	ILE
1	C	1505	LEU
1	C	1506	CYS
1	C	1517	VAL
1	C	1530	LEU
1	C	1533	LEU
1	C	1536	GLU
1	C	1540	ARG
1	C	1542	TYR
1	C	1572	THR
1	C	1587	ASN
1	C	1598	ARG
1	C	1600	LEU
1	C	1603	LYS
1	C	1605	LYS
1	C	1611	ARG
1	C	1619	ARG
1	C	1626	LEU
1	C	1650	SER
1	C	1658	LEU
1	C	1678	THR
1	C	1709	GLU
1	C	1710	ASP
1	C	1725	TRP
1	C	1728	CYS
1	C	1730	GLN
1	C	1741	ILE
1	C	1746	LEU
1	C	1753	ASN
1	C	1757	LYS
1	C	1825	ILE
1	C	1834	LEU
1	C	1846	LEU
1	C	1849	LEU

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Mol	Chain	Res	Type
1	C	1872	ILE
1	C	1881	GLN
1	C	1900	LEU
1	C	1913	VAL
1	C	1927	ARG
1	C	1936	GLU
1	C	1946	VAL
1	C	1965	GLU
1	C	1967	TRP
1	C	1971	LEU
1	C	1978	PHE
1	C	1981	GLU
1	C	1996	GLU
1	C	1997	MET
1	C	2005	LEU
1	C	2007	GLU
1	C	2022	TYR
1	C	2027	ASN
1	C	2028	TYR
1	C	2041	TRP
1	C	2049	ARG
1	C	2059	GLN
1	C	2063	LEU
1	C	2078	LEU
1	C	2080	VAL
1	C	2097	PHE
1	C	2102	SER
1	C	2105	SER
1	C	2111	ARG
1	C	2113	PHE
1	C	2121	LYS
1	C	2127	LEU
1	C	2136	ASP
1	C	2141	GLN
1	C	2150	LEU
1	C	2153	ASP
1	C	2156	CYS
1	C	2161	LEU
1	C	2184	SER
1	C	2193	GLU
1	C	2198	LYS
1	C	2206	HIS

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Mol	Chain	Res	Type
1	C	2209	MET
1	C	2220	THR
1	C	2221	LEU
1	C	2240	LEU
1	C	2242	LYS
1	C	2244	LEU
1	C	2245	TRP
1	C	2248	SER
1	C	2256	GLU
1	C	2262	THR
1	C	2265	LEU
1	C	2286	MET
1	C	2293	LYS
1	C	2294	VAL
1	C	2297	ILE
1	C	2301	ASP
1	C	2308	LEU
1	C	2319	ARG
1	C	2336	SER
1	C	2343	ASN
1	C	2355	LEU
1	C	2362	PHE
1	C	2364	PHE
1	C	2372	PHE
1	C	2374	LEU
1	C	2382	GLU
1	C	2383	THR
1	C	2386	GLN
1	C	2387	LEU
1	C	2398	ASN
1	C	2402	THR
1	C	2425	VAL
1	C	2428	ARG
1	C	2430	THR
1	C	2433	LEU
1	C	2437	ASP
1	C	2439	ARG
1	C	2443	ASP
1	C	2450	VAL
1	C	2462	ASN
1	C	2468	ILE
2	D	3	VAL

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Mol	Chain	Res	Type
2	D	5	LEU
2	D	6	VAL
2	D	10	TYR
2	D	20	LEU
2	D	21	THR
2	D	28	ILE
2	D	31	SER
2	D	40	ILE
2	D	66	ASN
2	D	90	MET
2	D	101	VAL
2	D	106	SER
2	D	116	ASN
2	D	119	VAL
2	D	122	VAL
2	D	133	SER
2	D	135	ASP
2	D	139	ASN
2	D	155	THR
2	D	167	MET
2	D	174	LEU
2	D	210	ILE
2	D	212	ARG
2	D	219	VAL
2	D	230	THR
2	D	236	ILE
2	D	256	CYS
2	D	273	TYR
2	D	278	ASP
2	D	286	ARG
2	D	297	CYS
2	D	298	VAL
2	D	302	ASP
5	I	658	VAL
5	I	666	CYS
5	I	672	ASN
5	I	680	ILE
5	I	681	TYR
5	I	682	ILE
5	I	685	SER
5	I	692	SER
5	I	694	THR

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Mol	Chain	Res	Type
5	I	695	THR
5	I	697	VAL
5	I	703	ILE
5	I	707	ILE
5	I	716	THR
5	I	728	LEU
5	I	730	VAL
5	I	731	GLU
5	I	744	VAL
5	I	758	LEU
5	I	759	ASP
5	I	760	ARG
5	I	768	SER
5	I	770	SER
5	I	775	CYS
5	J	660	GLU
5	J	675	SER
5	J	681	TYR
5	J	685	SER
5	J	690	ARG
5	J	692	SER
5	J	697	VAL
5	J	702	THR
5	J	709	PHE
5	J	711	LEU
5	J	712	PHE
5	J	713	LEU
5	J	716	THR
5	J	721	ASP
5	J	728	LEU
5	J	729	THR
5	J	730	VAL
5	J	731	GLU
5	J	740	SER
5	J	743	ILE
5	J	758	LEU
5	J	759	ASP
5	J	760	ARG
5	J	764	ILE
5	J	768	SER
5	J	770	SER
5	J	775	CYS

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Mol	Chain	Res	Type
5	J	783	SER
5	J	787	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	ASN
1	A	303	GLN
1	A	310	GLN
1	A	319	ASN
1	A	454	GLN
1	A	484	ASN
1	A	539	ASN
1	A	540	ASN
1	A	553	GLN
1	A	574	GLN
1	A	583	HIS
1	A	661	GLN
1	A	706	ASN
1	A	813	ASN
1	A	923	ASN
1	A	937	HIS
1	A	950	ASN
1	A	977	GLN
1	A	1054	GLN
1	A	1113	ASN
1	A	1173	HIS
1	A	1185	ASN
1	A	1231	GLN
1	A	1277	ASN
1	A	1379	GLN
1	A	1547	GLN
1	A	1728	GLN
1	A	1759	ASN
1	A	1981	ASN
1	A	2010	ASN
1	A	2036	ASN
1	A	2057	GLN
1	A	2145	ASN
1	A	2204	HIS
1	A	2209	GLN
1	A	2231	ASN

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Mol	Chain	Res	Type
1	A	2279	HIS
1	A	2282	ASN
1	A	2341	ASN
1	A	2447	GLN
1	A	2454	GLN
2	B	12	HIS
2	B	29	GLN
2	B	53	GLN
2	B	127	ASN
2	B	152	HIS
2	B	229	HIS
1	C	86	ASN
1	C	124	GLN
1	C	128	ASN
1	C	131	ASN
1	C	132	ASN
1	C	168	ASN
1	C	228	ASN
1	C	252	ASN
1	C	307	GLN
1	C	311	GLN
1	C	320	ASN
1	C	395	HIS
1	C	402	ASN
1	C	485	ASN
1	C	540	ASN
1	C	553	ASN
1	C	585	HIS
1	C	662	GLN
1	C	667	ASN
1	C	671	GLN
1	C	693	GLN
1	C	725	GLN
1	C	814	ASN
1	C	827	GLN
1	C	858	ASN
1	C	924	ASN
1	C	938	HIS
1	C	943	GLN
1	C	1000	HIS
1	C	1226	ASN
1	C	1232	GLN

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Mol	Chain	Res	Type
1	C	1233	GLN
1	C	1249	GLN
1	C	1289	GLN
1	C	1293	GLN
1	C	1510	ASN
1	C	1521	ASN
1	C	1543	ASN
1	C	1722	GLN
1	C	1761	ASN
1	C	1871	GLN
1	C	1977	GLN
1	C	1983	ASN
1	C	2011	GLN
1	C	2012	ASN
1	C	2038	ASN
1	C	2064	GLN
1	C	2065	HIS
1	C	2108	GLN
1	C	2135	GLN
1	C	2194	HIS
1	C	2281	HIS
1	C	2284	ASN
1	C	2343	ASN
1	C	2407	GLN
1	C	2436	ASN
1	C	2449	GLN
1	C	2456	GLN
2	D	12	HIS
2	D	77	ASN
2	D	120	ASN
2	D	149	GLN
2	D	152	HIS
2	D	229	HIS
2	D	301	ASN
5	I	691	ASN
5	I	735	ASN
5	I	754	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	567
1	A	534
3	E	90
3	F	87
2	D	75
2	B	66
4	G	45
4	H	42
5	J	31
5	I	26

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	416:UNK	C	450:UNK	N	40.12
1	F	416:UNK	C	450:UNK	N	39.07
1	E	512:UNK	C	550:UNK	N	33.98
1	F	717:UNK	C	750:UNK	N	33.97
1	E	717:UNK	C	750:UNK	N	33.43
1	F	512:UNK	C	550:UNK	N	33.24
1	F	118:UNK	C	150:UNK	N	32.46

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	118:UNK	C	150:UNK	N	32.20
1	F	867:UNK	C	900:UNK	N	31.99
1	E	867:UNK	C	900:UNK	N	30.60
1	F	318:UNK	C	350:UNK	N	27.65
1	E	318:UNK	C	350:UNK	N	27.26
1	E	381:UNK	C	400:UNK	N	25.02
1	F	381:UNK	C	400:UNK	N	24.83
1	E	468:UNK	C	500:UNK	N	24.07
1	F	468:UNK	C	500:UNK	N	23.91
1	F	567:UNK	C	600:UNK	N	23.32
1	E	567:UNK	C	600:UNK	N	22.55
1	F	169:UNK	C	200:UNK	N	22.46
1	E	169:UNK	C	200:UNK	N	22.15
1	F	665:UNK	C	700:UNK	N	17.20
1	E	665:UNK	C	700:UNK	N	16.83
1	E	813:UNK	C	850:UNK	N	13.94
1	F	218:UNK	C	250:UNK	N	13.04
1	F	813:UNK	C	850:UNK	N	13.02
1	E	218:UNK	C	250:UNK	N	12.00
1	A	1811:SER	C	1812:SER	N	10.40
1	E	761:UNK	C	800:UNK	N	10.32
1	A	1637:ASP	C	1638:ASP	N	9.38
1	F	761:UNK	C	800:UNK	N	9.33
1	C	1639:ASP	C	1640:ASP	N	9.18
1	F	612:UNK	C	650:UNK	N	8.93
1	C	668:PHE	C	669:ASP	N	8.41
1	E	612:UNK	C	650:UNK	N	8.32
1	A	667:PHE	C	668:ASP	N	8.25
1	A	225:ALA	C	226:ASP	N	7.67
1	A	1422:ALA	C	1423:GLY	N	7.39
1	C	226:ALA	C	227:ASP	N	7.36
1	J	721:ASP	C	722:ASN	N	7.31
1	I	779:ASP	C	780:ALA	N	6.42
1	C	123:PHE	C	124:GLN	N	6.40
1	C	1202:VAL	C	1203:PRO	N	6.36
1	A	1018:ILE	C	1019:THR	N	6.23
1	A	1202:PRO	C	1203:GLU	N	6.23
1	J	791:LEU	C	792:PRO	N	6.20
1	C	814:ASN	C	815:SER	N	6.18
1	A	2400:THR	C	2401:GLU	N	6.14
1	I	720:PRO	C	721:ASP	N	6.09
1	A	710:VAL	C	711:VAL	N	6.07

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	653:THR	C	654:ASN	N	6.02
1	C	242:ALA	C	243:LEU	N	5.89
1	C	1472:ALA	C	1473:GLY	N	5.86
1	C	2386:GLN	C	2387:LEU	N	5.84
1	A	2376:LYS	C	2377:ILE	N	5.81
1	C	118:VAL	C	119:SER	N	5.81
1	A	813:ASN	C	814:SER	N	5.77
1	C	209:ASP	C	210:PHE	N	5.76
1	A	1633:LEU	C	1634:GLU	N	5.74
1	J	733:ILE	C	734:SER	N	5.73
1	A	84:LEU	C	85:ASN	N	5.67
1	C	2375:PRO	C	2376:THR	N	5.65
1	B	3:VAL	C	4:ILE	N	5.55
1	C	1017:LEU	C	1018:GLN	N	5.55
1	A	1014:ILE	C	1015:LYS	N	5.49
1	A	116:GLU	C	117:VAL	N	5.48
1	E	808:UNK	C	809:UNK	N	5.48
1	D	165:LEU	C	166:SER	N	5.44
1	C	2243:VAL	C	2244:LEU	N	5.43
1	A	2377:ILE	C	2378:GLU	N	5.42
1	C	265:LEU	C	266:ASP	N	5.40
1	A	1169:ASN	C	1170:ARG	N	5.39
1	C	104:ALA	C	105:ASN	N	5.34
1	A	1133:ASP	C	1134:ARG	N	5.32
1	C	294:ILE	C	295:GLN	N	5.31
1	C	468:ALA	C	469:CYS	N	5.31
1	A	315:GLY	C	316:LEU	N	5.29
1	A	106:LEU	C	107:SER	N	5.28
1	I	787:ILE	C	788:GLU	N	5.27
1	A	219:ASP	C	220:TRP	N	5.26
1	I	747:ASP	C	748:GLY	N	5.26
1	C	2388:PRO	C	2389:VAL	N	5.24
1	A	1144:LEU	C	1145:SER	N	5.22
1	C	2395:LEU	C	2396:LEU	N	5.22
1	A	408:ASN	C	409:ASN	N	5.21
1	A	2387:VAL	C	2388:MET	N	5.18
1	C	287:LEU	C	288:GLY	N	5.18
1	J	708:GLY	C	709:PHE	N	5.17
1	A	307:ARG	C	308:LEU	N	5.15
1	A	318:LEU	C	319:ASN	N	5.15
1	C	1911:ALA	C	1912:LEU	N	5.12
1	A	1201:VAL	C	1202:PRO	N	5.11

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	508:SER	C	509:LEU	N	5.08
1	A	117:VAL	C	118:SER	N	5.07
1	C	1764:LEU	C	1765:ALA	N	5.05
1	A	1531:LEU	C	1532:VAL	N	5.02
1	C	1132:ASN	C	1133:GLY	N	5.02
1	J	668:ASP	C	669:LYS	N	5.02
1	J	775:CYS	C	776:LYS	N	5.02
1	A	120:GLU	C	121:GLN	N	5.00
1	A	2396:ASN	C	2397:GLY	N	5.00
1	A	286:LEU	C	287:GLY	N	4.99
1	D	59:ASP	C	60:ILE	N	4.97
1	C	430:SER	C	431:ILE	N	4.95
1	J	766:SER	C	767:ILE	N	4.91
1	A	521:LEU	C	522:SER	N	4.90
1	A	2095:PHE	C	2096:GLU	N	4.90
1	G	155:ILE	C	156:SER	N	4.89
1	A	590:GLU	C	591:PHE	N	4.87
1	G	197:VAL	C	198:LEU	N	4.87
1	A	1016:LEU	C	1017:GLN	N	4.86
1	J	648:LYS	C	649:LYS	N	4.85
1	C	130:LEU	C	131:ASN	N	4.84
1	C	703:LEU	C	704:SER	N	4.83
1	D	58:TYR	C	59:ASP	N	4.82
1	A	2205:TRP	C	2206:VAL	N	4.81
1	A	2450:LYS	C	2451:LEU	N	4.81
1	C	1497:ASP	C	1498:LYS	N	4.80
1	C	241:ALA	C	242:ALA	N	4.79
1	C	309:LEU	C	310:PHE	N	4.78
1	J	723:PHE	C	724:GLU	N	4.77
1	C	222:LEU	C	223:THR	N	4.75
1	A	2434:ASN	C	2435:ASP	N	4.74
1	C	1819:ARG	C	1820:HIS	N	4.72
1	B	38:LEU	C	39:GLU	N	4.71
1	C	1206:LYS	C	1207:ASN	N	4.71
1	C	1671:LEU	C	1672:LYS	N	4.69
1	A	95:VAL	C	96:PRO	N	4.68
1	A	1216:LEU	C	1217:PRO	N	4.68
1	B	69:ALA	C	70:SER	N	4.68
1	C	229:ASN	C	230:SER	N	4.68
1	C	869:ILE	C	870:GLY	N	4.68
1	A	772:SER	C	773:ALA	N	4.67
1	C	89:PHE	C	90:ASP	N	4.65

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	126:SER	C	127:ASN	N	4.64
1	C	216:ARG	C	217:THR	N	4.64
1	A	429:SER	C	430:ILE	N	4.62
1	C	817:LYS	C	818:ARG	N	4.62
1	D	38:LEU	C	39:GLU	N	4.62
1	I	743:ILE	C	744:VAL	N	4.62
1	C	467:LEU	C	468:ALA	N	4.60
1	C	1115:LEU	C	1116:SER	N	4.60
1	C	2309:ARG	C	2310:GLU	N	4.60
1	C	2408:ARG	C	2409:VAL	N	4.60
1	A	949:GLN	C	950:ASN	N	4.59
1	A	1970:ASP	C	1971:ASP	N	4.59
1	C	127:SER	C	128:ASN	N	4.59
1	E	465:UNK	C	466:UNK	N	4.57
1	I	775:CYS	C	776:LYS	N	4.57
1	G	51:GLY	C	52:ARG	N	4.56
1	F	913:UNK	C	914:UNK	N	4.55
1	A	230:SER	C	231:SER	N	4.54
1	A	1212:GLN	C	1213:VAL	N	4.54
1	C	194:ASN	C	195:THR	N	4.54
1	C	385:THR	C	386:LYS	N	4.54
1	C	1542:TYR	C	1543:ASN	N	4.54
1	A	2036:ASN	C	2037:GLN	N	4.53
1	H	63:GLY	C	64:HIS	N	4.53
1	A	193:ASN	C	194:THR	N	4.52
1	A	480:LYS	C	481:ASP	N	4.51
1	C	334:GLU	C	335:LEU	N	4.51
1	H	91:LEU	C	92:HIS	N	4.51
1	C	2249:ARG	C	2250:SER	N	4.50
1	A	168:GLN	C	169:THR	N	4.49
1	C	1516:GLU	C	1517:VAL	N	4.48
1	D	48:ALA	C	49:THR	N	4.48
1	A	417:VAL	C	418:SER	N	4.47
1	C	1534:VAL	C	1535:ASN	N	4.47
1	C	1961:VAL	C	1962:LEU	N	4.47
1	I	672:ASN	C	673:TYR	N	4.47
1	A	292:ILE	C	293:ILE	N	4.46
1	F	371:UNK	C	372:UNK	N	4.45
1	A	427:GLY	C	428:SER	N	4.44
1	A	1743:TYR	C	1744:LEU	N	4.44
1	C	307:GLN	C	308:ARG	N	4.43
1	C	150:ILE	C	151:LEU	N	4.41

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1455:GLY	C	1456:THR	N	4.40
1	A	1514:GLU	C	1515:VAL	N	4.40
1	A	142:SER	C	143:SER	N	4.39
1	A	335:LEU	C	336:SER	N	4.39
1	A	526:SER	C	527:GLY	N	4.39
1	C	1200:ASN	C	1201:GLU	N	4.39
1	E	711:UNK	C	712:UNK	N	4.39
1	I	651:THR	C	652:ASN	N	4.39
1	A	91:LEU	C	92:LYS	N	4.38
1	C	823:THR	C	824:THR	N	4.37
1	C	1919:ALA	C	1920:ILE	N	4.37
1	A	1524:LEU	C	1525:VAL	N	4.36
1	A	1581:GLY	C	1582:CYS	N	4.36
1	A	2126:LYS	C	2127:GLY	N	4.36
1	C	957:VAL	C	958:SER	N	4.36
1	A	1206:ASN	C	1207:TYR	N	4.35
1	C	2207:TRP	C	2208:VAL	N	4.35
1	A	404:MET	C	405:ASN	N	4.34
1	A	819:ALA	C	820:ALA	N	4.34
1	A	1114:LEU	C	1115:SER	N	4.34
1	D	199:PRO	C	200:VAL	N	4.34
1	A	1397:GLN	C	1398:LEU	N	4.33
1	C	2460:VAL	C	2461:GLU	N	4.33
1	I	680:ILE	C	681:TYR	N	4.33
1	A	502:LEU	C	503:ASN	N	4.32
1	C	1172:ILE	C	1173:GLN	N	4.32
1	C	1213:GLN	C	1214:VAL	N	4.31
1	A	1726:CYS	C	1727:LEU	N	4.30
1	A	2111:PHE	C	2112:CYS	N	4.30
1	B	290:GLY	C	291:HIS	N	4.30
1	C	1294:GLU	C	1295:ASP	N	4.30
1	C	2434:THR	C	2435:GLY	N	4.30
1	A	816:LYS	C	817:ARG	N	4.29
1	C	250:ALA	C	251:ASP	N	4.29
1	C	990:ILE	C	991:SER	N	4.29
1	F	710:UNK	C	711:UNK	N	4.29
1	I	732:ASP	C	733:ILE	N	4.29
1	B	88:ARG	C	89:TRP	N	4.28
1	C	767:LYS	C	768:CYS	N	4.28
1	C	950:GLN	C	951:ASN	N	4.28
1	D	83:PHE	C	84:GLN	N	4.28
1	G	133:ALA	C	134:ASP	N	4.28

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	700:SER	C	701:SER	N	4.28
1	A	203:GLY	C	204:THR	N	4.27
1	A	277:ILE	C	278:ILE	N	4.27
1	A	1851:PHE	C	1852:GLY	N	4.26
1	B	55:VAL	C	56:ARG	N	4.26
1	C	181:ILE	C	182:PRO	N	4.26
1	C	706:VAL	C	707:ASN	N	4.26
1	C	1607:ASP	C	1608:ALA	N	4.25
1	A	2116:SER	C	2117:ASP	N	4.24
1	A	1957:MET	C	1958:ALA	N	4.23
1	A	2401:GLU	C	2402:GLU	N	4.22
1	A	1960:LEU	C	1961:TRP	N	4.21
1	A	1343:LYS	C	1344:CYS	N	4.20
1	B	54:ASN	C	55:VAL	N	4.20
1	C	151:LEU	C	152:ALA	N	4.20
1	C	205:THR	C	206:LEU	N	4.20
1	E	458:UNK	C	459:UNK	N	4.20
1	C	1221:GLN	C	1222:ASN	N	4.19
1	C	845:LEU	C	846:LEU	N	4.18
1	G	113:ILE	C	114:HIS	N	4.18
1	A	467:ALA	C	468:CYS	N	4.17
1	A	2008:PHE	C	2009:GLN	N	4.17
1	B	59:ASP	C	60:ILE	N	4.17
1	C	1405:TYR	C	1406:GLU	N	4.17
1	A	200:VAL	C	201:PRO	N	4.16
1	D	256:CYS	C	257:ALA	N	4.16
1	B	293:LYS	C	294:GLY	N	4.15
1	D	80:SER	C	81:VAL	N	4.15
1	G	70:ILE	C	71:LYS	N	4.15
1	C	293:ILE	C	294:ILE	N	4.14
1	C	1350:ALA	C	1351:LYS	N	4.14
1	E	552:UNK	C	553:UNK	N	4.13
1	A	1575:TRP	C	1576:ASN	N	4.12
1	C	454:LYS	C	455:GLN	N	4.12
1	C	1713:LYS	C	1714:LEU	N	4.12
1	C	2404:GLU	C	2405:GLU	N	4.12
1	F	309:UNK	C	310:UNK	N	4.12
1	J	649:LYS	C	650:ARG	N	4.12
1	A	810:ASP	C	811:GLN	N	4.11
1	A	2151:ASP	C	2152:ALA	N	4.11
1	A	2330:GLY	C	2331:ILE	N	4.11
1	C	709:ALA	C	710:TYR	N	4.11

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1051:LEU	C	1052:GLU	N	4.11
1	G	91:LEU	C	92:HIS	N	4.11
1	A	2332:GLU	C	2333:GLY	N	4.10
1	C	295:GLN	C	296:ASP	N	4.10
1	C	317:LEU	C	318:SER	N	4.10
1	J	718:LYS	C	719:LYS	N	4.10
1	A	1030:ALA	C	1031:LEU	N	4.09
1	C	811:ASP	C	812:GLN	N	4.09
1	C	2181:VAL	C	2182:PRO	N	4.09
1	D	81:VAL	C	82:SER	N	4.08
1	D	269:SER	C	270:SER	N	4.08
1	H	93:LEU	C	94:LEU	N	4.08
1	B	256:CYS	C	257:ALA	N	4.07
1	C	382:ALA	C	383:ILE	N	4.07
1	A	1553:GLU	C	1554:GLU	N	4.06
1	C	1282:SER	C	1283:SER	N	4.06
1	D	87:ASN	C	88:ARG	N	4.06
1	E	268:UNK	C	300:UNK	N	4.06
1	H	79:VAL	C	80:HIS	N	4.06
1	C	1846:LEU	C	1847:LEU	N	4.05
1	F	557:UNK	C	558:UNK	N	4.05
1	H	97:GLN	C	98:PHE	N	4.05
1	A	171:ARG	C	172:LEU	N	4.04
1	C	84:THR	C	85:LEU	N	4.04
1	C	332:PHE	C	333:ARG	N	4.04
1	A	301:GLY	C	302:LYS	N	4.03
1	A	2054:PRO	C	2055:GLN	N	4.03
1	C	243:LEU	C	244:LEU	N	4.03
1	C	617:CYS	C	618:ASP	N	4.03
1	I	758:LEU	C	759:ASP	N	4.03
1	J	655:SER	C	656:VAL	N	4.03
1	A	1966:TYR	C	1967:GLU	N	4.02
1	D	121:GLU	C	122:VAL	N	4.02
1	D	183:CYS	C	184:TYR	N	4.01
1	A	1997:LYS	C	1998:ARG	N	4.00
1	C	568:THR	C	569:ASP	N	4.00
1	C	2135:GLN	C	2136:ASP	N	4.00
1	A	2004:ARG	C	2005:GLU	N	3.99
1	B	145:LEU	C	146:GLY	N	3.99
1	F	466:UNK	C	467:UNK	N	3.99
1	A	664:GLY	C	665:SER	N	3.98
1	C	414:PRO	C	415:PHE	N	3.98

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	991:SER	C	992:ILE	N	3.98
1	A	703:SER	C	704:SER	N	3.97
1	A	954:ARG	C	955:CYS	N	3.97
1	C	1755:TRP	C	1756:TYR	N	3.97
1	J	682:ILE	C	683:GLN	N	3.97
1	A	262:SER	C	263:ILE	N	3.96
1	A	1339:LYS	C	1340:TYR	N	3.96
1	E	262:UNK	C	263:UNK	N	3.96
1	A	505:LYS	C	506:ILE	N	3.95
1	A	2460:ASN	C	2461:LEU	N	3.95
1	F	611:UNK	C	612:UNK	N	3.95
1	H	134:ASP	C	135:LEU	N	3.95
1	J	732:ASP	C	733:ILE	N	3.95
1	A	166:PRO	C	167:ASN	N	3.94
1	A	594:LEU	C	595:ILE	N	3.94
1	A	645:MET	C	646:ILE	N	3.94
1	B	257:ALA	C	258:PHE	N	3.94
1	C	2049:ARG	C	2050:LYS	N	3.94
1	C	2433:LEU	C	2434:THR	N	3.94
1	D	66:ASN	C	67:PRO	N	3.94
1	E	466:UNK	C	467:UNK	N	3.94
1	C	667:ASN	C	668:PHE	N	3.93
1	A	687:GLU	C	688:ILE	N	3.92
1	C	2088:GLY	C	2089:LYS	N	3.92
1	H	157:CYS	C	158:MET	N	3.92
1	H	178:ASN	C	179:TRP	N	3.92
1	J	715:SER	C	716:THR	N	3.92
1	A	857:ASN	C	858:PRO	N	3.91
1	A	2105:LYS	C	2106:GLN	N	3.91
1	A	2466:ILE	C	2467:GLY	N	3.91
1	C	1427:ASP	C	1428:SER	N	3.91
1	D	65:PRO	C	66:ASN	N	3.91
1	A	1551:GLU	C	1552:LEU	N	3.90
1	C	1444:GLU	C	1445:TRP	N	3.90
1	C	1545:VAL	C	1546:VAL	N	3.90
1	C	1623:ARG	C	1624:MET	N	3.90
1	E	156:UNK	C	157:UNK	N	3.90
1	A	2324:TYR	C	2325:ALA	N	3.89
1	C	2428:ARG	C	2429:ILE	N	3.89
1	G	67:HIS	C	68:GLU	N	3.89
1	A	2130:ASP	C	2131:ILE	N	3.88
1	B	221:HIS	C	222:LEU	N	3.88

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2410:GLU	C	2411:ASN	N	3.88
1	C	984:GLN	C	985:GLN	N	3.87
1	C	1583:GLY	C	1584:CYS	N	3.87
1	J	739:PHE	C	740:SER	N	3.87
1	C	989:LEU	C	990:ILE	N	3.86
1	A	811:GLN	C	812:SER	N	3.85
1	A	1566:ASP	C	1567:LYS	N	3.85
1	C	81:THR	C	82:PHE	N	3.85
1	C	371:ALA	C	372:ILE	N	3.85
1	C	952:LEU	C	953:GLY	N	3.85
1	C	1341:LYS	C	1342:TYR	N	3.85
1	C	1442:LEU	C	1443:GLY	N	3.85
1	E	709:UNK	C	710:UNK	N	3.85
1	E	753:UNK	C	754:UNK	N	3.85
1	G	99:PRO	C	100:ARG	N	3.85
1	I	765:GLN	C	766:SER	N	3.85
1	C	1889:PRO	C	1890:ASN	N	3.84
1	C	1959:MET	C	1960:ALA	N	3.84
1	C	2422:ALA	C	2423:MET	N	3.84
1	E	603:UNK	C	604:UNK	N	3.84
1	G	110:ARG	C	111:ALA	N	3.84
1	A	622:ASP	C	623:ASP	N	3.83
1	A	1965:TRP	C	1966:TYR	N	3.83
1	A	2444:VAL	C	2445:PRO	N	3.83
1	C	840:LEU	C	841:ASP	N	3.83
1	F	563:UNK	C	564:UNK	N	3.83
1	C	1114:ASN	C	1115:LEU	N	3.82
1	C	1119:SER	C	1120:SER	N	3.82
1	C	1833:SER	C	1834:LEU	N	3.82
1	F	313:UNK	C	314:UNK	N	3.82
1	F	910:UNK	C	911:UNK	N	3.82
1	J	706:VAL	C	707:ILE	N	3.82
1	A	302:LYS	C	303:GLN	N	3.81
1	A	589:THR	C	590:GLU	N	3.81
1	C	1073:GLY	C	1074:PRO	N	3.81
1	A	1504:CYS	C	1505:LEU	N	3.80
1	C	1182:ASN	C	1183:LYS	N	3.80
1	E	150:UNK	C	151:UNK	N	3.80
1	F	250:UNK	C	251:UNK	N	3.80
1	G	87:HIS	C	88:GLU	N	3.80
1	J	781:GLU	C	782:LYS	N	3.80
1	C	366:ARG	C	367:ARG	N	3.79

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	402:ASN	C	403:ILE	N	3.79
1	C	1178:ASP	C	1179:GLN	N	3.79
1	C	1684:ASP	C	1685:LEU	N	3.79
1	D	132:ILE	C	133:SER	N	3.79
1	A	143:SER	C	144:GLU	N	3.78
1	A	852:LEU	C	853:LYS	N	3.78
1	C	729:SER	C	730:ASN	N	3.78
1	C	851:ASN	C	852:ILE	N	3.78
1	C	1075:ASN	C	1076:LEU	N	3.78
1	G	63:GLY	C	64:HIS	N	3.78
1	H	115:ILE	C	116:ALA	N	3.78
1	A	1625:ALA	C	1626:LYS	N	3.77
1	B	89:TRP	C	90:MET	N	3.77
1	C	276:LYS	C	277:LEU	N	3.77
1	C	364:VAL	C	365:ILE	N	3.77
1	E	554:UNK	C	555:UNK	N	3.77
1	A	279:ARG	C	280:LEU	N	3.76
1	A	1032:GLU	C	1033:GLY	N	3.76
1	A	1638:ASP	C	1639:PRO	N	3.76
1	A	2421:MET	C	2422:LEU	N	3.76
1	A	324:VAL	C	325:HIS	N	3.75
1	A	973:CYS	C	974:PRO	N	3.75
1	C	1531:SER	C	1532:ALA	N	3.75
1	C	2113:PHE	C	2114:CYS	N	3.75
1	C	2380:GLU	C	2381:GLU	N	3.75
1	F	310:UNK	C	311:UNK	N	3.75
1	C	1822:ILE	C	1823:PRO	N	3.74
1	C	2383:THR	C	2384:GLY	N	3.74
1	H	149:CYS	C	150:LEU	N	3.74
1	J	670:VAL	C	671:PRO	N	3.74
1	A	1045:PHE	C	1046:PHE	N	3.73
1	A	2081:THR	C	2082:ARG	N	3.73
1	C	256:LEU	C	257:LEU	N	3.73
1	C	1647:ALA	C	1648:LYS	N	3.73
1	C	2208:VAL	C	2209:MET	N	3.73
1	D	166:SER	C	167:MET	N	3.73
1	A	856:ASN	C	857:ASN	N	3.72
1	A	1903:GLY	C	1904:LYS	N	3.72
1	C	113:SER	C	114:LEU	N	3.72
1	C	135:PHE	C	136:GLU	N	3.72
1	C	710:TYR	C	711:VAL	N	3.72
1	C	1171:ARG	C	1172:ILE	N	3.72

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1460:LYS	C	1461:PRO	N	3.72
1	D	101:VAL	C	102:TRP	N	3.72
1	A	757:ASP	C	758:PRO	N	3.71
1	A	2341:ASN	C	2342:VAL	N	3.71
1	C	134:ILE	C	135:PHE	N	3.71
1	C	2360:GLU	C	2361:ALA	N	3.71
1	E	809:UNK	C	810:UNK	N	3.71
1	A	2077:ALA	C	2078:VAL	N	3.70
1	C	1256:SER	C	1257:ALA	N	3.70
1	E	464:UNK	C	465:UNK	N	3.70
1	E	502:UNK	C	503:UNK	N	3.70
1	F	859:UNK	C	860:UNK	N	3.70
1	A	1430:MET	C	1431:MET	N	3.69
1	A	2010:ASN	C	2011:SER	N	3.69
1	A	2312:GLU	C	2313:LYS	N	3.69
1	C	103:GLY	C	104:ALA	N	3.69
1	C	632:HIS	C	633:ALA	N	3.69
1	C	2072:SER	C	2073:ALA	N	3.69
1	C	2224:LYS	C	2225:VAL	N	3.69
1	D	273:TYR	C	274:VAL	N	3.69
1	H	80:HIS	C	81:LEU	N	3.69
1	I	780:ALA	C	781:GLU	N	3.69
1	J	711:LEU	C	712:PHE	N	3.69
1	A	1902:LEU	C	1903:GLY	N	3.68
1	A	2217:LEU	C	2218:THR	N	3.68
1	A	1077:ASP	C	1078:TYR	N	3.67
1	A	1488:VAL	C	1489:MET	N	3.67
1	A	1619:SER	C	1620:GLY	N	3.67
1	A	2339:CYS	C	2340:GLU	N	3.67
1	D	128:GLN	C	129:GLY	N	3.67
1	H	90:THR	C	91:LEU	N	3.67
1	A	280:LEU	C	281:ASP	N	3.66
1	A	1892:SER	C	1893:ARG	N	3.66
1	B	181:GLY	C	182:ASN	N	3.66
1	C	1235:THR	C	1236:LYS	N	3.66
1	C	1392:ALA	C	1393:GLN	N	3.66
1	A	297:ASP	C	298:PRO	N	3.65
1	A	944:ILE	C	945:MET	N	3.65
1	C	547:LYS	C	548:ALA	N	3.65
1	C	642:SER	C	643:LYS	N	3.65
1	C	2314:GLU	C	2315:LYS	N	3.65
1	D	127:ASN	C	128:GLN	N	3.65

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	151:UNK	C	152:UNK	N	3.65
1	E	905:UNK	C	906:UNK	N	3.65
1	A	560:GLY	C	561:GLU	N	3.64
1	A	1050:LEU	C	1051:GLU	N	3.64
1	A	1891:VAL	C	1892:SER	N	3.64
1	C	659:GLU	C	660:ILE	N	3.64
1	C	698:LYS	C	699:ILE	N	3.64
1	D	45:LYS	C	46:LEU	N	3.64
1	F	900:UNK	C	901:UNK	N	3.64
1	H	100:ARG	C	101:PHE	N	3.64
1	A	167:ASN	C	168:GLN	N	3.63
1	A	963:ILE	C	964:PRO	N	3.63
1	A	1915:MET	C	1916:VAL	N	3.63
1	A	2313:LYS	C	2314:VAL	N	3.63
1	C	1447:GLU	C	1448:LEU	N	3.63
1	C	2119:ASP	C	2120:GLY	N	3.63
1	E	754:UNK	C	755:UNK	N	3.63
1	F	107:UNK	C	108:UNK	N	3.63
1	G	43:SER	C	44:LEU	N	3.63
1	G	157:CYS	C	158:MET	N	3.63
1	A	231:SER	C	232:SER	N	3.62
1	A	293:ILE	C	294:GLN	N	3.62
1	B	130:GLU	C	131:LEU	N	3.62
1	C	236:GLU	C	237:TYR	N	3.62
1	C	570:ALA	C	571:GLN	N	3.62
1	C	939:THR	C	940:ALA	N	3.62
1	C	2131:GLU	C	2132:ASP	N	3.62
1	D	253:VAL	C	254:TRP	N	3.62
1	A	1285:VAL	C	1286:GLU	N	3.61
1	A	1860:ALA	C	1861:MET	N	3.61
1	A	1907:PRO	C	1908:GLN	N	3.61
1	C	423:ILE	C	424:ALA	N	3.61
1	C	736:GLU	C	737:GLU	N	3.61
1	C	1348:ALA	C	1349:PHE	N	3.60
1	C	2084:ARG	C	2085:ALA	N	3.60
1	E	909:UNK	C	910:UNK	N	3.60
1	A	623:ASP	C	624:ILE	N	3.59
1	A	2242:LEU	C	2243:TRP	N	3.59
1	C	442:ILE	C	443:ARG	N	3.59
1	C	1222:ASN	C	1223:ILE	N	3.59
1	C	1330:LYS	C	1331:PRO	N	3.59
1	C	1432:MET	C	1433:MET	N	3.59

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	69:ALA	C	70:SER	N	3.59
1	E	716:UNK	C	717:UNK	N	3.59
1	A	2256:ARG	C	2257:THR	N	3.58
1	A	2368:TRP	C	2369:GLY	N	3.58
1	B	175:ALA	C	176:ALA	N	3.58
1	C	1473:GLY	C	1474:ALA	N	3.58
1	E	451:UNK	C	452:UNK	N	3.58
1	F	511:UNK	C	512:UNK	N	3.58
1	F	564:UNK	C	565:UNK	N	3.58
1	A	271:LEU	C	272:ARG	N	3.57
1	A	435:THR	C	436:LEU	N	3.57
1	A	1094:ALA	C	1095:GLY	N	3.57
1	A	1132:GLY	C	1133:ASP	N	3.57
1	A	1486:THR	C	1487:SER	N	3.57
1	C	618:ASP	C	619:LEU	N	3.57
1	C	1254:SER	C	1255:PRO	N	3.57
1	C	1625:ALA	C	1626:LEU	N	3.57
1	C	1905:GLY	C	1906:LYS	N	3.57
1	A	1434:LEU	C	1435:ARG	N	3.56
1	A	1565:SER	C	1566:ASP	N	3.56
1	D	118:PRO	C	119:VAL	N	3.56
1	E	112:UNK	C	113:UNK	N	3.56
1	G	196:LYS	C	197:VAL	N	3.56
1	A	779:LEU	C	780:LYS	N	3.55
1	A	2372:LEU	C	2373:PRO	N	3.55
1	C	499:THR	C	500:LEU	N	3.55
1	C	1924:SER	C	1925:LEU	N	3.55
1	C	2213:ALA	C	2214:PRO	N	3.55
1	D	125:HIS	C	126:PRO	N	3.55
1	D	188:MET	C	189:PRO	N	3.55
1	F	102:UNK	C	103:UNK	N	3.55
1	H	70:ILE	C	71:LYS	N	3.55
1	A	234:LEU	C	235:GLU	N	3.54
1	A	345:LYS	C	346:TYR	N	3.54
1	A	1765:PHE	C	1766:GLU	N	3.54
1	A	1917:ALA	C	1918:ILE	N	3.54
1	B	80:SER	C	81:VAL	N	3.54
1	B	189:PRO	C	190:ASN	N	3.54
1	C	161:LEU	C	162:SER	N	3.54
1	C	604:GLU	C	605:ASP	N	3.54
1	C	1344:GLN	C	1345:LYS	N	3.54
1	C	1413:ASP	C	1414:ALA	N	3.54

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1978:PHE	C	1979:PHE	N	3.54
1	D	196:HIS	C	197:LEU	N	3.54
1	E	702:UNK	C	703:UNK	N	3.54
1	J	704:PHE	C	705:GLU	N	3.54
1	A	1034:GLU	C	1035:PHE	N	3.53
1	A	1508:ASN	C	1509:ASN	N	3.53
1	C	178:ARG	C	179:VAL	N	3.53
1	C	206:LEU	C	207:THR	N	3.53
1	C	2262:THR	C	2263:ARG	N	3.53
1	E	812:UNK	C	813:UNK	N	3.53
1	I	659:LEU	C	660:GLU	N	3.53
1	A	598:SER	C	599:TYR	N	3.52
1	A	1728:GLN	C	1729:PRO	N	3.52
1	A	1967:GLU	C	1968:GLY	N	3.52
1	C	418:VAL	C	419:SER	N	3.52
1	C	1963:TRP	C	1964:HIS	N	3.52
1	C	2318:PHE	C	2319:ARG	N	3.52
1	D	114:LYS	C	115:HIS	N	3.52
1	F	862:UNK	C	863:UNK	N	3.52
1	A	1532:VAL	C	1533:ASN	N	3.51
1	A	2302:GLU	C	2303:ALA	N	3.51
1	A	2438:ARG	C	2439:PHE	N	3.51
1	C	536:GLN	C	537:TYR	N	3.51
1	C	688:GLU	C	689:ILE	N	3.51
1	C	956:CYS	C	957:VAL	N	3.51
1	C	1217:LEU	C	1218:PRO	N	3.51
1	E	165:UNK	C	166:UNK	N	3.51
1	A	1006:VAL	C	1007:ILE	N	3.50
1	A	1956:ARG	C	1957:MET	N	3.50
1	C	707:ASN	C	708:PRO	N	3.50
1	C	2150:LEU	C	2151:GLN	N	3.50
1	C	2411:ASN	C	2412:GLU	N	3.50
1	F	610:UNK	C	611:UNK	N	3.50
1	G	183:ASP	C	184:VAL	N	3.50
1	I	648:LYS	C	649:LYS	N	3.50
1	A	104:ASN	C	105:GLU	N	3.49
1	A	609:LYS	C	610:LEU	N	3.49
1	A	1000:VAL	C	1001:GLU	N	3.49
1	A	1194:ILE	C	1195:PHE	N	3.49
1	A	1755:LYS	C	1756:ALA	N	3.49
1	A	2364:PRO	C	2365:LEU	N	3.49
1	C	1836:GLU	C	1837:SER	N	3.49

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2033:ASP	C	2034:VAL	N	3.49
1	F	350:UNK	C	351:UNK	N	3.49
1	F	414:UNK	C	415:UNK	N	3.49
1	A	249:ALA	C	250:ASP	N	3.48
1	A	346:TYR	C	347:ASP	N	3.48
1	A	441:ILE	C	442:ARG	N	3.48
1	A	485:LEU	C	486:MET	N	3.48
1	C	1212:MET	C	1213:GLN	N	3.48
1	C	1524:ASP	C	1525:LEU	N	3.48
1	C	2437:ASP	C	2438:ILE	N	3.48
1	E	202:UNK	C	203:UNK	N	3.48
1	E	258:UNK	C	259:UNK	N	3.48
1	H	135:LEU	C	136:TRP	N	3.48
1	A	1326:ASP	C	1327:ASP	N	3.47
1	A	1496:LYS	C	1497:GLU	N	3.47
1	A	1629:LEU	C	1630:ASN	N	3.47
1	C	1737:ASN	C	1738:PRO	N	3.47
1	D	102:TRP	C	103:ASP	N	3.47
1	F	658:UNK	C	659:UNK	N	3.47
1	G	94:LEU	C	95:LEU	N	3.47
1	H	196:LYS	C	197:VAL	N	3.47
1	I	756:GLY	C	757:LYS	N	3.47
1	A	499:LEU	C	500:MET	N	3.46
1	A	1762:LEU	C	1763:ALA	N	3.46
1	A	1182:LYS	C	1183:LEU	N	3.45
1	A	1591:ARG	C	1592:ILE	N	3.45
1	C	2457:ALA	C	2458:THR	N	3.45
1	E	306:UNK	C	307:UNK	N	3.45
1	E	309:UNK	C	310:UNK	N	3.45
1	G	186:GLN	C	187:THR	N	3.45
1	H	175:ASP	C	176:LYS	N	3.45
1	A	185:ILE	C	186:GLU	N	3.44
1	A	282:ALA	C	283:ALA	N	3.44
1	A	1586:ILE	C	1587:ASP	N	3.44
1	C	329:LEU	C	330:LEU	N	3.44
1	C	692:ILE	C	693:GLN	N	3.44
1	C	2001:GLY	C	2002:PRO	N	3.44
1	C	2321:THR	C	2322:ARG	N	3.44
1	E	560:UNK	C	561:UNK	N	3.44
1	F	914:UNK	C	915:UNK	N	3.44
1	A	975:PRO	C	976:SER	N	3.43
1	A	2041:ILE	C	2042:TYR	N	3.43

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	365:ILE	C	366:ARG	N	3.43
1	C	569:ASP	C	570:ALA	N	3.43
1	C	608:VAL	C	609:ARG	N	3.43
1	C	850:ILE	C	851:ASN	N	3.43
1	C	1081:HIS	C	1082:LEU	N	3.43
1	C	1338:THR	C	1339:LEU	N	3.43
1	C	1491:MET	C	1492:LYS	N	3.43
1	D	151:THR	C	152:HIS	N	3.43
1	A	1157:VAL	C	1158:PHE	N	3.42
1	A	1363:LYS	C	1364:ASN	N	3.42
1	A	1622:MET	C	1623:ALA	N	3.42
1	C	697:ILE	C	698:LYS	N	3.42
1	E	406:UNK	C	407:UNK	N	3.42
1	E	904:UNK	C	905:UNK	N	3.42
1	F	214:UNK	C	215:UNK	N	3.42
1	A	1546:ALA	C	1547:GLN	N	3.41
1	B	155:THR	C	156:PRO	N	3.41
1	C	88:ILE	C	89:PHE	N	3.41
1	C	335:LEU	C	336:LEU	N	3.41
1	C	1057:ASN	C	1058:LYS	N	3.41
1	A	1130:ASN	C	1131:ASN	N	3.40
1	A	1152:GLY	C	1153:THR	N	3.40
1	B	200:VAL	C	201:THR	N	3.40
1	C	2223:GLN	C	2224:LYS	N	3.40
1	C	2473:PHE	C	2474:TRP	N	3.40
1	E	203:UNK	C	204:UNK	N	3.40
1	F	909:UNK	C	910:UNK	N	3.40
1	A	666:ASN	C	667:PHE	N	3.39
1	C	2365:ASP	C	2366:PRO	N	3.39
1	D	19:ALA	C	20:LEU	N	3.39
1	A	500:MET	C	501:ILE	N	3.38
1	A	2144:VAL	C	2145:ASN	N	3.38
1	A	2260:THR	C	2261:ARG	N	3.38
1	C	1054:ASP	C	1055:GLN	N	3.38
1	A	1848:TRP	C	1849:PHE	N	3.37
1	A	2048:LYS	C	2049:ILE	N	3.37
1	C	270:VAL	C	271:PRO	N	3.37
1	C	1104:ILE	C	1105:THR	N	3.37
1	C	1849:LEU	C	1850:TRP	N	3.37
1	C	2219:LEU	C	2220:THR	N	3.37
1	D	12:HIS	C	13:THR	N	3.37
1	H	127:LEU	C	128:LEU	N	3.37

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	164:GLU	C	165:LEU	N	3.36
1	A	691:ILE	C	692:GLN	N	3.36
1	A	731:PRO	C	732:LYS	N	3.36
1	A	1950:VAL	C	1951:SER	N	3.36
1	A	2047:ARG	C	2048:LYS	N	3.36
1	A	2379:GLU	C	2380:GLU	N	3.36
1	C	815:SER	C	816:PHE	N	3.36
1	C	853:LEU	C	854:LYS	N	3.36
1	C	936:ILE	C	937:HIS	N	3.36
1	C	1489:SER	C	1490:VAL	N	3.36
1	C	1525:LEU	C	1526:LEU	N	3.36
1	C	2231:ALA	C	2232:LEU	N	3.36
1	D	42:ASN	C	43:ASP	N	3.36
1	D	189:PRO	C	190:ASN	N	3.36
1	D	288:TYR	C	289:GLY	N	3.36
1	D	300:LEU	C	301:ASN	N	3.36
1	F	655:UNK	C	656:UNK	N	3.36
1	A	80:THR	C	81:PHE	N	3.35
1	A	337:LEU	C	338:LYS	N	3.35
1	A	507:PRO	C	508:SER	N	3.35
1	A	517:ILE	C	518:LEU	N	3.35
1	A	569:ALA	C	570:GLN	N	3.35
1	A	629:SER	C	630:VAL	N	3.35
1	A	679:LEU	C	680:LEU	N	3.35
1	A	1344:CYS	C	1345:HIS	N	3.35
1	A	1723:TRP	C	1724:ARG	N	3.35
1	A	1885:HIS	C	1886:GLN	N	3.35
1	A	1923:LEU	C	1924:SER	N	3.35
1	A	1999:GLY	C	2000:PRO	N	3.35
1	A	2080:GLY	C	2081:THR	N	3.35
1	A	2192:HIS	C	2193:ARG	N	3.35
1	B	300:LEU	C	301:ASN	N	3.35
1	C	1091:THR	C	1092:GLU	N	3.35
1	C	1130:LEU	C	1131:ASN	N	3.35
1	C	1533:LEU	C	1534:VAL	N	3.35
1	C	1606:GLU	C	1607:ASP	N	3.35
1	C	1753:ASN	C	1754:THR	N	3.35
1	C	2412:GLU	C	2413:HIS	N	3.35
1	E	503:UNK	C	504:UNK	N	3.35
1	H	101:PHE	C	102:ILE	N	3.35
1	H	113:ILE	C	114:HIS	N	3.35
1	H	133:ALA	C	134:ASP	N	3.35

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	162:LEU	C	163:ASN	N	3.35
1	A	715:ARG	C	716:LYS	N	3.34
1	A	935:ILE	C	936:HIS	N	3.34
1	A	1763:ALA	C	1764:ASN	N	3.34
1	A	1859:GLN	C	1860:ALA	N	3.34
1	A	1872:THR	C	1873:TRP	N	3.34
1	A	2212:PRO	C	2213:ASP	N	3.34
1	A	2416:ARG	C	2417:ASN	N	3.34
1	B	167:MET	C	168:ALA	N	3.34
1	C	1380:HIS	C	1381:GLN	N	3.34
1	C	1414:ALA	C	1415:LEU	N	3.34
1	C	1430:GLU	C	1431:VAL	N	3.34
1	C	1530:LEU	C	1531:SER	N	3.34
1	C	1709:GLU	C	1710:ASP	N	3.34
1	C	2242:LYS	C	2243:VAL	N	3.34
1	C	2452:LYS	C	2453:LEU	N	3.34
1	E	380:UNK	C	381:UNK	N	3.34
1	E	450:UNK	C	451:UNK	N	3.34
1	E	601:UNK	C	602:UNK	N	3.34
1	E	864:UNK	C	865:UNK	N	3.34
1	F	268:UNK	C	300:UNK	N	3.34
1	F	453:UNK	C	454:UNK	N	3.34
1	F	903:UNK	C	904:UNK	N	3.34
1	G	53:TYR	C	54:LEU	N	3.34
1	H	124:CYS	C	125:LEU	N	3.34
1	H	161:LEU	C	162:LEU	N	3.34
1	A	834:VAL	C	835:VAL	N	3.33
1	A	1084:PRO	C	1085:ILE	N	3.33
1	A	1117:MET	C	1118:SER	N	3.33
1	A	1350:ALA	C	1351:LEU	N	3.33
1	A	1734:SER	C	1735:ASN	N	3.33
1	A	2067:LYS	C	2068:LEU	N	3.33
1	A	2091:LYS	C	2092:ILE	N	3.33
1	A	2181:ASN	C	2182:SER	N	3.33
1	A	2237:ASP	C	2238:LEU	N	3.33
1	A	2412:LYS	C	2413:ASN	N	3.33
1	B	195:SER	C	196:HIS	N	3.33
1	C	495:HIS	C	496:MET	N	3.33
1	C	541:ASN	C	542:GLN	N	3.33
1	C	639:GLU	C	640:VAL	N	3.33
1	C	760:ILE	C	761:LEU	N	3.33
1	C	1393:GLN	C	1394:GLN	N	3.33

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1526:LEU	C	1527:VAL	N	3.33
1	C	1708:VAL	C	1709:GLU	N	3.33
1	C	2148:THR	C	2149:LEU	N	3.33
1	D	163:GLN	C	164:SER	N	3.33
1	F	560:UNK	C	561:UNK	N	3.33
1	F	908:UNK	C	909:UNK	N	3.33
1	G	81:LEU	C	82:ALA	N	3.33
1	G	151:GLU	C	152:TYR	N	3.33
1	G	198:LEU	C	199:LYS	N	3.33
1	H	57:VAL	C	58:TYR	N	3.33
1	H	191:GLY	C	192:ASN	N	3.33
1	A	343:ARG	C	344:ASP	N	3.32
1	A	472:PRO	C	473:ALA	N	3.32
1	A	850:ASN	C	851:ILE	N	3.32
1	A	1277:ASN	C	1278:ALA	N	3.32
1	A	1910:LEU	C	1911:VAL	N	3.32
1	A	2058:THR	C	2059:LEU	N	3.32
1	A	2399:ILE	C	2400:THR	N	3.32
1	A	2423:VAL	C	2424:LEU	N	3.32
1	C	318:SER	C	319:LEU	N	3.32
1	C	496:MET	C	497:GLN	N	3.32
1	C	865:THR	C	866:VAL	N	3.32
1	C	1232:GLN	C	1233:GLN	N	3.32
1	C	1557:ILE	C	1558:ILE	N	3.32
1	C	1664:THR	C	1665:GLY	N	3.32
1	C	1680:ARG	C	1681:MET	N	3.32
1	C	1748:ALA	C	1749:THR	N	3.32
1	C	1766:ASN	C	1767:PHE	N	3.32
1	C	1888:GLN	C	1889:PRO	N	3.32
1	E	462:UNK	C	463:UNK	N	3.32
1	E	756:UNK	C	757:UNK	N	3.32
1	F	902:UNK	C	903:UNK	N	3.32
1	G	88:GLU	C	89:GLN	N	3.32
1	G	184:VAL	C	185:ALA	N	3.32
1	H	106:GLY	C	107:GLU	N	3.32
1	J	687:LYS	C	688:TYR	N	3.32
1	A	471:GLY	C	472:PRO	N	3.31
1	A	725:LEU	C	726:LYS	N	3.31
1	A	860:ILE	C	861:ARG	N	3.31
1	A	1215:LYS	C	1216:LEU	N	3.31
1	A	1558:TYR	C	1559:LYS	N	3.31
1	A	1574:THR	C	1575:TRP	N	3.31

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1655:GLN	C	1656:LEU	N	3.31
1	A	1721:GLY	C	1722:GLU	N	3.31
1	A	1930:LEU	C	1931:SER	N	3.31
1	A	1962:HIS	C	1963:GLU	N	3.31
1	A	1990:GLU	C	1991:PRO	N	3.31
1	A	2187:VAL	C	2188:LEU	N	3.31
1	A	2457:SER	C	2458:VAL	N	3.31
1	B	216:SER	C	217:SER	N	3.31
1	C	326:HIS	C	327:ALA	N	3.31
1	C	406:ASN	C	407:ALA	N	3.31
1	C	695:GLU	C	696:ALA	N	3.31
1	C	940:ALA	C	941:ALA	N	3.31
1	C	1056:SER	C	1057:ASN	N	3.31
1	C	1281:PHE	C	1282:SER	N	3.31
1	C	1440:TYR	C	1441:ALA	N	3.31
1	C	1944:VAL	C	1945:LEU	N	3.31
1	C	2239:ASP	C	2240:LEU	N	3.31
1	D	96:ASP	C	97:GLY	N	3.31
1	E	163:UNK	C	164:UNK	N	3.31
1	F	114:UNK	C	115:UNK	N	3.31
1	F	166:UNK	C	167:UNK	N	3.31
1	F	701:UNK	C	702:UNK	N	3.31
1	G	59:LEU	C	60:ILE	N	3.31
1	G	72:THR	C	73:PHE	N	3.31
1	G	97:GLN	C	98:PHE	N	3.31
1	G	173:VAL	C	174:ARG	N	3.31
1	A	351:LYS	C	352:SER	N	3.30
1	A	1540:TYR	C	1541:ASN	N	3.30
1	A	1669:LEU	C	1670:LYS	N	3.30
1	A	1764:ASN	C	1765:PHE	N	3.30
1	A	2179:VAL	C	2180:PRO	N	3.30
1	A	2210:MET	C	2211:ALA	N	3.30
1	C	91:LYS	C	92:LEU	N	3.30
1	C	147:ILE	C	148:GLY	N	3.30
1	C	498:GLU	C	499:THR	N	3.30
1	C	574:ILE	C	575:GLN	N	3.30
1	C	663:HIS	C	664:LEU	N	3.30
1	C	1080:SER	C	1081:HIS	N	3.30
1	C	1146:SER	C	1147:LEU	N	3.30
1	C	1667:GLN	C	1668:ASP	N	3.30
1	C	1716:ALA	C	1717:ARG	N	3.30
1	C	2182:PRO	C	2183:ASN	N	3.30

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2432:LYS	C	2433:LEU	N	3.30
1	D	88:ARG	C	89:TRP	N	3.30
1	D	117:ALA	C	118:PRO	N	3.30
1	E	256:UNK	C	257:UNK	N	3.30
1	E	308:UNK	C	309:UNK	N	3.30
1	E	559:UNK	C	560:UNK	N	3.30
1	F	304:UNK	C	305:UNK	N	3.30
1	F	375:UNK	C	376:UNK	N	3.30
1	F	410:UNK	C	411:UNK	N	3.30
1	G	90:THR	C	91:LEU	N	3.30
1	G	172:ASN	C	173:VAL	N	3.30
1	H	85:LYS	C	86:GLY	N	3.30
1	J	694:THR	C	695:THR	N	3.30
1	J	750:PRO	C	751:PHE	N	3.30
1	J	767:ILE	C	768:SER	N	3.30
1	A	762:VAL	C	763:ILE	N	3.29
1	A	1438:TYR	C	1439:ALA	N	3.29
1	A	1460:GLU	C	1461:VAL	N	3.29
1	A	1816:HIS	C	1817:ARG	N	3.29
1	A	2006:ILE	C	2007:SER	N	3.29
1	A	2043:TYR	C	2044:ASN	N	3.29
1	B	217:SER	C	218:ASP	N	3.29
1	C	159:PHE	C	160:TYR	N	3.29
1	C	204:GLY	C	205:THR	N	3.29
1	C	554:GLN	C	555:SER	N	3.29
1	C	614:LEU	C	615:THR	N	3.29
1	C	774:ALA	C	775:VAL	N	3.29
1	C	780:LEU	C	781:LYS	N	3.29
1	C	856:GLU	C	857:ASN	N	3.29
1	C	1869:LEU	C	1870:ILE	N	3.29
1	C	1967:TRP	C	1968:TYR	N	3.29
1	C	2187:PHE	C	2188:HIS	N	3.29
1	C	2369:ASN	C	2370:TRP	N	3.29
1	C	2385:ILE	C	2386:GLN	N	3.29
1	D	73:GLY	C	74:HIS	N	3.29
1	F	707:UNK	C	708:UNK	N	3.29
1	F	864:UNK	C	865:UNK	N	3.29
1	G	71:LYS	C	72:THR	N	3.29
1	H	92:HIS	C	93:LEU	N	3.29
1	I	701:SER	C	702:THR	N	3.29
1	A	155:LEU	C	156:ILE	N	3.28
1	A	528:GLU	C	529:LYS	N	3.28

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	749:ASP	C	750:GLU	N	3.28
1	A	943:ALA	C	944:ILE	N	3.28
1	A	1253:SER	C	1254:PRO	N	3.28
1	A	1360:GLU	C	1361:GLU	N	3.28
1	A	1972:ALA	C	1973:SER	N	3.28
1	A	2128:HIS	C	2129:GLU	N	3.28
1	A	2459:GLU	C	2460:ASN	N	3.28
1	B	234:TRP	C	235:SER	N	3.28
1	C	93:LYS	C	94:SER	N	3.28
1	C	735:LYS	C	736:GLU	N	3.28
1	C	980:ASP	C	981:PHE	N	3.28
1	C	1211:GLU	C	1212:MET	N	3.28
1	C	2067:SER	C	2068:PRO	N	3.28
1	C	2216:TYR	C	2217:ASP	N	3.28
1	C	2264:SER	C	2265:LEU	N	3.28
1	C	2282:PRO	C	2283:SER	N	3.28
1	C	2363:ALA	C	2364:PHE	N	3.28
1	C	2424:LEU	C	2425:VAL	N	3.28
1	D	13:THR	C	14:ILE	N	3.28
1	E	369:UNK	C	370:UNK	N	3.28
1	E	911:UNK	C	912:UNK	N	3.28
1	F	756:UNK	C	757:UNK	N	3.28
1	H	54:LEU	C	55:ILE	N	3.28
1	H	143:ASP	C	144:THR	N	3.28
1	A	156:ILE	C	157:SER	N	3.27
1	A	197:ARG	C	198:LEU	N	3.27
1	A	291:THR	C	292:ILE	N	3.27
1	A	818:ASP	C	819:ALA	N	3.27
1	A	1373:ILE	C	1374:ASN	N	3.27
1	A	1876:VAL	C	1877:LEU	N	3.27
1	A	2160:ASP	C	2161:ILE	N	3.27
1	A	2395:SER	C	2396:ASN	N	3.27
1	B	237:ASP	C	238:ASP	N	3.27
1	C	531:PHE	C	532:ILE	N	3.27
1	C	803:PRO	C	804:LEU	N	3.27
1	C	1065:ILE	C	1066:LEU	N	3.27
1	C	1125:ALA	C	1126:LEU	N	3.27
1	C	1335:PRO	C	1336:ILE	N	3.27
1	C	1412:GLU	C	1413:ASP	N	3.27
1	C	1744:SER	C	1745:TYR	N	3.27
1	C	2095:SER	C	2096:LYS	N	3.27
1	C	2141:GLN	C	2142:LEU	N	3.27

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2366:PRO	C	2367:LEU	N	3.27
1	D	84:GLN	C	85:GLN	N	3.27
1	E	155:UNK	C	156:UNK	N	3.27
1	E	206:UNK	C	207:UNK	N	3.27
1	E	317:UNK	C	318:UNK	N	3.27
1	F	558:UNK	C	559:UNK	N	3.27
1	F	850:UNK	C	851:UNK	N	3.27
1	G	103:ASN	C	104:HIS	N	3.27
1	I	654:ASN	C	655:SER	N	3.27
1	A	332:ARG	C	333:GLU	N	3.26
1	A	985:LEU	C	986:GLY	N	3.26
1	A	1007:ILE	C	1008:ARG	N	3.26
1	A	1178:GLN	C	1179:LEU	N	3.26
1	A	1328:LYS	C	1329:PRO	N	3.26
1	A	1844:LEU	C	1845:LEU	N	3.26
1	A	2079:PRO	C	2080:GLY	N	3.26
1	A	2224:GLU	C	2225:VAL	N	3.26
1	A	2295:ILE	C	2296:ASP	N	3.26
1	A	2420:ALA	C	2421:MET	N	3.26
1	C	581:GLN	C	582:LEU	N	3.26
1	C	586:GLN	C	587:TYR	N	3.26
1	C	689:ILE	C	690:PHE	N	3.26
1	C	733:LYS	C	734:LYS	N	3.26
1	C	744:THR	C	745:LEU	N	3.26
1	C	812:GLN	C	813:SER	N	3.26
1	C	816:PHE	C	817:LYS	N	3.26
1	C	852:ILE	C	853:LEU	N	3.26
1	C	1376:ASN	C	1377:ASN	N	3.26
1	C	1830:HIS	C	1831:SER	N	3.26
1	C	1892:ILE	C	1893:VAL	N	3.26
1	C	2007:GLU	C	2008:ILE	N	3.26
1	C	2290:ILE	C	2291:THR	N	3.26
1	F	255:UNK	C	256:UNK	N	3.26
1	F	316:UNK	C	317:UNK	N	3.26
1	G	62:LEU	C	63:GLY	N	3.26
1	G	106:GLY	C	107:GLU	N	3.26
1	H	45:HIS	C	46:TYR	N	3.26
1	I	693:PHE	C	694:THR	N	3.26
1	I	741:LEU	C	742:LYS	N	3.26
1	J	765:GLN	C	766:SER	N	3.26
1	A	822:THR	C	823:THR	N	3.25
1	A	825:GLY	C	826:GLN	N	3.25

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	914:GLU	C	915:TYR	N	3.25
1	A	924:LEU	C	925:MET	N	3.25
1	A	1028:SER	C	1029:LYS	N	3.25
1	A	1053:ASP	C	1054:GLN	N	3.25
1	A	1207:TYR	C	1208:GLU	N	3.25
1	A	1542:VAL	C	1543:VAL	N	3.25
1	A	1719:LYS	C	1720:GLN	N	3.25
1	A	1742:SER	C	1743:TYR	N	3.25
1	A	1964:GLN	C	1965:TRP	N	3.25
1	A	2314:VAL	C	2315:PRO	N	3.25
1	B	193:ASP	C	194:ALA	N	3.25
1	C	654:ALA	C	655:GLU	N	3.25
1	C	970:VAL	C	971:MET	N	3.25
1	C	972:ARG	C	973:SER	N	3.25
1	C	1262:CYS	C	1263:SER	N	3.25
1	C	1366:ASN	C	1367:SER	N	3.25
1	C	1950:GLU	C	1951:LEU	N	3.25
1	C	2030:LYS	C	2031:SER	N	3.25
1	C	2055:LEU	C	2056:PRO	N	3.25
1	C	2277:LEU	C	2278:GLY	N	3.25
1	D	41:THR	C	42:ASN	N	3.25
1	D	49:THR	C	50:ALA	N	3.25
1	D	82:SER	C	83:PHE	N	3.25
1	E	310:UNK	C	311:UNK	N	3.25
1	E	566:UNK	C	567:UNK	N	3.25
1	E	858:UNK	C	859:UNK	N	3.25
1	F	262:UNK	C	263:UNK	N	3.25
1	F	303:UNK	C	304:UNK	N	3.25
1	F	463:UNK	C	464:UNK	N	3.25
1	F	805:UNK	C	806:UNK	N	3.25
1	H	171:ASP	C	172:ASN	N	3.25
1	A	162:THR	C	163:GLU	N	3.24
1	A	744:LEU	C	745:ILE	N	3.24
1	A	754:PRO	C	755:TYR	N	3.24
1	A	824:LEU	C	825:GLY	N	3.24
1	A	849:ILE	C	850:ASN	N	3.24
1	A	940:ALA	C	941:ILE	N	3.24
1	A	1138:LYS	C	1139:ALA	N	3.24
1	A	1527:GLU	C	1528:LEU	N	3.24
1	A	1580:LEU	C	1581:GLY	N	3.24
1	A	1959:VAL	C	1960:LEU	N	3.24
1	A	2204:HIS	C	2205:TRP	N	3.24

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2383:ILE	C	2384:GLN	N	3.24
1	B	22:GLY	C	23:VAL	N	3.24
1	C	846:LEU	C	847:GLY	N	3.24
1	C	981:PHE	C	982:TYR	N	3.24
1	C	1106:LEU	C	1107:GLY	N	3.24
1	C	1112:ASN	C	1113:ILE	N	3.24
1	C	1156:PHE	C	1157:VAL	N	3.24
1	C	1236:LYS	C	1237:GLU	N	3.24
1	C	1661:LEU	C	1662:TRP	N	3.24
1	C	1665:GLY	C	1666:LEU	N	3.24
1	C	1908:HIS	C	1909:PRO	N	3.24
1	D	37:ARG	C	38:LEU	N	3.24
1	F	159:UNK	C	160:UNK	N	3.24
1	A	383:PHE	C	384:THR	N	3.23
1	A	532:GLN	C	533:SER	N	3.23
1	A	1042:THR	C	1043:LEU	N	3.23
1	A	1056:ASN	C	1057:LYS	N	3.23
1	A	1131:ASN	C	1132:GLY	N	3.23
1	A	1352:HIS	C	1353:TYR	N	3.23
1	A	1612:PHE	C	1613:ALA	N	3.23
1	A	2203:GLU	C	2204:HIS	N	3.23
1	A	2234:GLU	C	2235:GLY	N	3.23
1	C	422:ASP	C	423:ILE	N	3.23
1	C	643:LYS	C	644:LEU	N	3.23
1	C	1043:THR	C	1044:LEU	N	3.23
1	C	1214:VAL	C	1215:THR	N	3.23
1	C	1492:LYS	C	1493:SER	N	3.23
1	C	1852:THR	C	1853:PHE	N	3.23
1	C	1894:SER	C	1895:ARG	N	3.23
1	C	1952:VAL	C	1953:SER	N	3.23
1	C	1970:GLY	C	1971:LEU	N	3.23
1	C	2031:SER	C	2032:LYS	N	3.23
1	C	2149:LEU	C	2150:LEU	N	3.23
1	D	149:GLN	C	150:CYS	N	3.23
1	G	49:TYR	C	50:HIS	N	3.23
1	G	82:ALA	C	83:LEU	N	3.23
1	G	182:ILE	C	183:ASP	N	3.23
1	H	88:GLU	C	89:GLN	N	3.23
1	H	159:LYS	C	160:MET	N	3.23
1	A	181:PRO	C	182:SER	N	3.22
1	A	245:ILE	C	246:LYS	N	3.22
1	A	728:SER	C	729:ASN	N	3.22

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	729:ASN	C	730:MET	N	3.22
1	A	836:GLY	C	837:PRO	N	3.22
1	A	1070:THR	C	1071:PHE	N	3.22
1	A	1530:ALA	C	1531:LEU	N	3.22
1	A	1550:ALA	C	1551:GLU	N	3.22
1	A	1838:LEU	C	1839:GLN	N	3.22
1	A	2206:VAL	C	2207:MET	N	3.22
1	A	2259:TYR	C	2260:THR	N	3.22
1	A	2300:CYS	C	2301:PHE	N	3.22
1	B	5:LEU	C	6:VAL	N	3.22
1	B	82:SER	C	83:PHE	N	3.22
1	C	153:VAL	C	154:ASP	N	3.22
1	C	1025:ILE	C	1026:GLU	N	3.22
1	C	1186:ASN	C	1187:ASN	N	3.22
1	C	1715:LEU	C	1716:ALA	N	3.22
1	C	1767:PHE	C	1768:GLU	N	3.22
1	C	2075:ASP	C	2076:LEU	N	3.22
1	C	2454:ILE	C	2455:GLN	N	3.22
1	D	86:ASP	C	87:ASN	N	3.22
1	D	281:THR	C	282:ARG	N	3.22
1	E	859:UNK	C	860:UNK	N	3.22
1	F	264:UNK	C	265:UNK	N	3.22
1	F	806:UNK	C	807:UNK	N	3.22
1	G	195:SER	C	196:LYS	N	3.22
1	H	102:ILE	C	103:ASN	N	3.22
1	I	726:ASP	C	727:GLY	N	3.22
1	A	1003:ILE	C	1004:TYR	N	3.21
1	A	1026:SER	C	1027:ILE	N	3.21
1	A	1494:PRO	C	1495:ASP	N	3.21
1	A	2149:GLN	C	2150:ASN	N	3.21
1	A	2350:LYS	C	2351:GLY	N	3.21
1	A	2397:GLY	C	2398:ALA	N	3.21
1	B	41:THR	C	42:ASN	N	3.21
1	B	90:MET	C	91:VAL	N	3.21
1	B	172:SER	C	173:MET	N	3.21
1	B	273:TYR	C	274:VAL	N	3.21
1	C	635:HIS	C	636:SER	N	3.21
1	C	699:ILE	C	700:ILE	N	3.21
1	C	1038:ARG	C	1039:PHE	N	3.21
1	C	1155:ASP	C	1156:PHE	N	3.21
1	C	1160:VAL	C	1161:PRO	N	3.21
1	C	1843:ALA	C	1844:LEU	N	3.21

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2164:GLN	C	2165:GLN	N	3.21
1	C	2295:ILE	C	2296:HIS	N	3.21
1	C	2342:GLU	C	2343:ASN	N	3.21
1	C	2467:TYR	C	2468:ILE	N	3.21
1	D	74:HIS	C	75:ARG	N	3.21
1	D	135:ASP	C	136:ARG	N	3.21
1	F	153:UNK	C	154:UNK	N	3.21
1	F	307:UNK	C	308:UNK	N	3.21
1	A	148:GLY	C	149:ILE	N	3.20
1	A	1604:GLU	C	1605:ASP	N	3.20
1	A	1829:SER	C	1830:ILE	N	3.20
1	A	2227:THR	C	2228:TYR	N	3.20
1	B	39:GLU	C	40:ILE	N	3.20
1	B	169:SER	C	170:ASP	N	3.20
1	C	257:LEU	C	258:TYR	N	3.20
1	C	1064:ARG	C	1065:ILE	N	3.20
1	C	1245:ARG	C	1246:LEU	N	3.20
1	C	1508:HIS	C	1509:ARG	N	3.20
1	C	1826:LYS	C	1827:GLY	N	3.20
1	C	1831:SER	C	1832:ILE	N	3.20
1	E	215:UNK	C	216:UNK	N	3.20
1	E	217:UNK	C	218:UNK	N	3.20
1	H	151:GLU	C	152:TYR	N	3.20
1	A	683:ALA	C	684:LEU	N	3.19
1	A	782:LEU	C	783:GLY	N	3.19
1	A	1107:ARG	C	1108:LEU	N	3.19
1	A	2343:MET	C	2344:LYS	N	3.19
1	B	68:VAL	C	69:ALA	N	3.19
1	B	94:SER	C	95:GLU	N	3.19
1	C	1110:ALA	C	1111:LYS	N	3.19
1	C	1251:LEU	C	1252:LYS	N	3.19
1	C	1645:ASN	C	1646:THR	N	3.19
1	C	1762:TRP	C	1763:ALA	N	3.19
1	C	2204:ILE	C	2205:GLU	N	3.19
1	D	234:TRP	C	235:SER	N	3.19
1	D	260:ALA	C	261:ASP	N	3.19
1	D	287:GLN	C	288:TYR	N	3.19
1	E	856:UNK	C	857:UNK	N	3.19
1	E	866:UNK	C	867:UNK	N	3.19
1	F	377:UNK	C	378:UNK	N	3.19
1	F	412:UNK	C	413:UNK	N	3.19
1	F	608:UNK	C	609:UNK	N	3.19

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	675:SER	C	676:MET	N	3.19
1	J	714:TYR	C	715:SER	N	3.19
1	A	497:GLU	C	498:THR	N	3.18
1	A	611:ALA	C	612:ALA	N	3.18
1	A	948:PHE	C	949:GLN	N	3.18
1	A	1059:ILE	C	1060:VAL	N	3.18
1	A	1284:TRP	C	1285:VAL	N	3.18
1	A	1981:ASN	C	1982:THR	N	3.18
1	A	2101:VAL	C	2102:ILE	N	3.18
1	A	2369:GLY	C	2370:PHE	N	3.18
1	A	2429:ASP	C	2430:LYS	N	3.18
1	B	188:MET	C	189:PRO	N	3.18
1	B	211:THR	C	212:ARG	N	3.18
1	C	268:ILE	C	269:TRP	N	3.18
1	C	717:LYS	C	718:THR	N	3.18
1	C	1163:ILE	C	1164:ASN	N	3.18
1	C	1180:LEU	C	1181:VAL	N	3.18
1	C	1231:SER	C	1232:GLN	N	3.18
1	C	1765:ALA	C	1766:ASN	N	3.18
1	C	1885:ARG	C	1886:ILE	N	3.18
1	C	1886:ILE	C	1887:HIS	N	3.18
1	C	1955:GLU	C	1956:LEU	N	3.18
1	E	608:UNK	C	609:UNK	N	3.18
1	F	252:UNK	C	253:UNK	N	3.18
1	F	364:UNK	C	365:UNK	N	3.18
1	F	510:UNK	C	511:UNK	N	3.18
1	F	758:UNK	C	759:UNK	N	3.18
1	H	49:TYR	C	50:HIS	N	3.18
1	H	107:GLU	C	108:ASN	N	3.18
1	A	566:ILE	C	567:THR	N	3.17
1	A	662:HIS	C	663:LEU	N	3.17
1	A	738:ALA	C	739:THR	N	3.17
1	A	798:LYS	C	799:GLU	N	3.17
1	A	814:SER	C	815:PHE	N	3.17
1	A	971:ARG	C	972:SER	N	3.17
1	A	1020:ILE	C	1021:ILE	N	3.17
1	A	1642:PRO	C	1643:ASN	N	3.17
1	A	2195:ALA	C	2196:LYS	N	3.17
1	A	2340:GLU	C	2341:ASN	N	3.17
1	C	480:ASN	C	481:LYS	N	3.17
1	C	670:PRO	C	671:GLN	N	3.17
1	C	719:LEU	C	720:LEU	N	3.17

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	834:TYR	C	835:VAL	N	3.17
1	C	1124:GLN	C	1125:ALA	N	3.17
1	C	1475:ALA	C	1476:TRP	N	3.17
1	C	2179:GLY	C	2180:TRP	N	3.17
1	C	2349:ARG	C	2350:ASP	N	3.17
1	E	109:UNK	C	110:UNK	N	3.17
1	E	204:UNK	C	205:UNK	N	3.17
1	E	401:UNK	C	402:UNK	N	3.17
1	E	706:UNK	C	707:UNK	N	3.17
1	G	96:GLN	C	97:GLN	N	3.17
1	I	674:GLU	C	675:SER	N	3.17
1	J	727:GLY	C	728:LEU	N	3.17
1	A	457:LYS	C	458:ASP	N	3.16
1	A	545:GLU	C	546:LYS	N	3.16
1	A	596:THR	C	597:ILE	N	3.16
1	A	639:VAL	C	640:LEU	N	3.16
1	A	711:VAL	C	712:PRO	N	3.16
1	A	1569:LEU	C	1570:THR	N	3.16
1	A	2039:TRP	C	2040:ASP	N	3.16
1	A	2145:ASN	C	2146:THR	N	3.16
1	A	2156:ARG	C	2157:ARG	N	3.16
1	C	179:VAL	C	180:LEU	N	3.16
1	C	239:ARG	C	240:HIS	N	3.16
1	C	513:THR	C	514:VAL	N	3.16
1	C	716:ARG	C	717:LYS	N	3.16
1	C	758:ASP	C	759:PRO	N	3.16
1	C	765:LEU	C	766:PRO	N	3.16
1	C	769:GLN	C	770:ASP	N	3.16
1	C	1161:PRO	C	1162:VAL	N	3.16
1	C	1331:PRO	C	1332:LEU	N	3.16
1	C	1428:SER	C	1429:VAL	N	3.16
1	C	1494:GLN	C	1495:SER	N	3.16
1	C	1622:GLY	C	1623:ARG	N	3.16
1	C	2168:ALA	C	2169:ILE	N	3.16
1	C	2180:TRP	C	2181:VAL	N	3.16
1	C	2429:ILE	C	2430:THR	N	3.16
1	C	2439:ARG	C	2440:ARG	N	3.16
1	C	2456:GLN	C	2457:ALA	N	3.16
1	D	78:VAL	C	79:THR	N	3.16
1	F	551:UNK	C	552:UNK	N	3.16
1	I	690:ARG	C	691:ASN	N	3.16
1	A	397:ARG	C	398:TYR	N	3.15

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1469:ALA	C	1470:ALA	N	3.15
1	A	1492:GLN	C	1493:SER	N	3.15
1	A	1552:LEU	C	1553:GLU	N	3.15
1	A	1656:LEU	C	1657:LYS	N	3.15
1	A	1831:SER	C	1832:LEU	N	3.15
1	A	1858:THR	C	1859:GLN	N	3.15
1	A	2215:ASP	C	2216:ASN	N	3.15
1	A	2220:LEU	C	2221:GLN	N	3.15
1	A	2352:SER	C	2353:LEU	N	3.15
1	A	2465:TYR	C	2466:ILE	N	3.15
1	B	228:ASP	C	229:HIS	N	3.15
1	B	236:ILE	C	237:ASP	N	3.15
1	C	200:THR	C	201:VAL	N	3.15
1	C	360:TYR	C	361:LYS	N	3.15
1	C	713:PRO	C	714:SER	N	3.15
1	C	915:GLU	C	916:TYR	N	3.15
1	C	1567:SER	C	1568:ASP	N	3.15
1	C	2465:GLN	C	2466:HIS	N	3.15
1	D	142:ILE	C	143:TRP	N	3.15
1	E	208:UNK	C	209:UNK	N	3.15
1	F	507:UNK	C	508:UNK	N	3.15
1	H	186:GLN	C	187:THR	N	3.15
1	A	1727:LEU	C	1728:GLN	N	3.14
1	A	2106:GLN	C	2107:ARG	N	3.14
1	A	2447:GLN	C	2448:VAL	N	3.14
1	B	140:ILE	C	141:ARG	N	3.14
1	B	192:THR	C	193:ASP	N	3.14
1	C	510:LEU	C	511:GLU	N	3.14
1	C	1226:ASN	C	1227:ALA	N	3.14
1	C	1410:ARG	C	1411:TRP	N	3.14
1	C	1832:ILE	C	1833:SER	N	3.14
1	C	2019:ASN	C	2020:ASP	N	3.14
1	C	2259:THR	C	2260:THR	N	3.14
1	D	246:LEU	C	247:ASP	N	3.14
1	A	459:LEU	C	460:PHE	N	3.13
1	A	678:ARG	C	679:LEU	N	3.13
1	A	1266:SER	C	1267:VAL	N	3.13
1	A	1709:TYR	C	1710:THR	N	3.13
1	A	1747:THR	C	1748:HIS	N	3.13
1	A	2049:ILE	C	2050:GLY	N	3.13
1	B	220:LYS	C	221:HIS	N	3.13
1	C	458:LYS	C	459:ASP	N	3.13

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	476:ALA	C	477:LYS	N	3.13
1	C	775:VAL	C	776:ALA	N	3.13
1	C	790:GLY	C	791:GLY	N	3.13
1	C	1060:ILE	C	1061:VAL	N	3.13
1	C	1188:GLU	C	1189:CYS	N	3.13
1	C	1228:TRP	C	1229:TYR	N	3.13
1	C	1964:HIS	C	1965:GLU	N	3.13
1	D	129:GLY	C	130:GLU	N	3.13
1	D	201:THR	C	202:LYS	N	3.13
1	E	565:UNK	C	566:UNK	N	3.13
1	G	101:PHE	C	102:ILE	N	3.13
1	A	709:TYR	C	710:VAL	N	3.12
1	A	806:ASN	C	807:THR	N	3.12
1	A	1568:ARG	C	1569:LEU	N	3.12
1	A	1946:GLN	C	1947:ALA	N	3.12
1	A	2059:LEU	C	2060:GLU	N	3.12
1	A	2097:PRO	C	2098:VAL	N	3.12
1	A	2226:PHE	C	2227:THR	N	3.12
1	A	2331:ILE	C	2332:GLU	N	3.12
1	C	352:LYS	C	353:SER	N	3.12
1	C	802:MET	C	803:PRO	N	3.12
1	C	926:MET	C	927:LYS	N	3.12
1	C	932:PRO	C	933:SER	N	3.12
1	C	1027:SER	C	1028:ILE	N	3.12
1	C	1321:LEU	C	1322:VAL	N	3.12
1	C	1983:ASN	C	1984:THR	N	3.12
1	C	2173:PRO	C	2174:LYS	N	3.12
1	C	2350:ASP	C	2351:ASN	N	3.12
1	D	220:LYS	C	221:HIS	N	3.12
1	E	758:UNK	C	759:UNK	N	3.12
1	F	704:UNK	C	705:UNK	N	3.12
1	H	150:LEU	C	151:GLU	N	3.12
1	A	398:TYR	C	399:LEU	N	3.11
1	A	477:HIS	C	478:LEU	N	3.11
1	A	688:ILE	C	689:PHE	N	3.11
1	A	1980:HIS	C	1981:ASN	N	3.11
1	A	2197:LYS	C	2198:ILE	N	3.11
1	B	246:LEU	C	247:ASP	N	3.11
1	C	245:ILE	C	246:ILE	N	3.11
1	C	700:ILE	C	701:GLY	N	3.11
1	C	1347:HIS	C	1348:ALA	N	3.11
1	C	1966:GLN	C	1967:TRP	N	3.11

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2002:PRO	C	2003:GLU	N	3.11
1	D	223:ALA	C	224:THR	N	3.11
1	A	760:LEU	C	761:ASP	N	3.10
1	A	785:LEU	C	786:SER	N	3.10
1	A	1754:TYR	C	1755:LYS	N	3.10
1	A	2344:LYS	C	2345:VAL	N	3.10
1	B	127:ASN	C	128:GLN	N	3.10
1	C	946:MET	C	947:HIS	N	3.10
1	C	1093:TYR	C	1094:SER	N	3.10
1	C	1646:THR	C	1647:ALA	N	3.10
1	D	252:TRP	C	253:VAL	N	3.10
1	G	181:PRO	C	182:ILE	N	3.10
1	A	440:ASN	C	441:ILE	N	3.09
1	A	549:LYS	C	550:SER	N	3.09
1	A	807:THR	C	808:PHE	N	3.09
1	A	1184:LEU	C	1185:ASN	N	3.09
1	A	2271:TYR	C	2272:ILE	N	3.09
1	A	2419:ARG	C	2420:ALA	N	3.09
1	B	185:VAL	C	186:TRP	N	3.09
1	B	284:ILE	C	285:VAL	N	3.09
1	C	315:HIS	C	316:GLY	N	3.09
1	C	1723:GLY	C	1724:GLU	N	3.09
1	C	2008:ILE	C	2009:SER	N	3.09
1	C	2036:ASN	C	2037:LEU	N	3.09
1	C	2316:VAL	C	2317:PRO	N	3.09
1	D	274:VAL	C	275:ARG	N	3.09
1	F	105:UNK	C	106:UNK	N	3.09
1	F	211:UNK	C	212:UNK	N	3.09
1	G	159:LYS	C	160:MET	N	3.09
1	J	672:ASN	C	673:TYR	N	3.09
1	A	559:THR	C	560:GLY	N	3.08
1	A	722:LEU	C	723:THR	N	3.08
1	B	33:SER	C	34:GLN	N	3.08
1	C	384:PHE	C	385:THR	N	3.08
1	C	1042:GLU	C	1043:THR	N	3.08
1	C	1225:LYS	C	1226:ASN	N	3.08
1	C	1603:LYS	C	1604:PRO	N	3.08
1	C	1658:LEU	C	1659:LYS	N	3.08
1	C	2048:PHE	C	2049:ARG	N	3.08
1	C	2186:THR	C	2187:PHE	N	3.08
1	D	286:ARG	C	287:GLN	N	3.08
1	E	357:UNK	C	358:UNK	N	3.08

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	407:UNK	C	408:UNK	N	3.08
1	F	216:UNK	C	217:UNK	N	3.08
1	A	980:PHE	C	981:TYR	N	3.07
1	A	1213:VAL	C	1214:THR	N	3.07
1	A	1706:VAL	C	1707:GLU	N	3.07
1	A	2273:LEU	C	2274:GLY	N	3.07
1	C	1063:ILE	C	1064:ARG	N	3.07
1	C	1107:GLY	C	1108:ARG	N	3.07
1	C	2054:GLN	C	2055:LEU	N	3.07
1	C	2117:GLY	C	2118:SER	N	3.07
1	E	505:UNK	C	506:UNK	N	3.07
1	G	147:HIS	C	148:VAL	N	3.07
1	A	1064:ILE	C	1065:LEU	N	3.06
1	A	1240:GLU	C	1241:TRP	N	3.06
1	A	1286:GLU	C	1287:LEU	N	3.06
1	A	1464:ALA	C	1465:MET	N	3.06
1	A	1614:ASN	C	1615:LEU	N	3.06
1	A	1938:ILE	C	1939:HIS	N	3.06
1	A	2462:CYS	C	2463:GLN	N	3.06
1	B	13:THR	C	14:ILE	N	3.06
1	B	118:PRO	C	119:VAL	N	3.06
1	B	214:LEU	C	215:LEU	N	3.06
1	C	732:PRO	C	733:LYS	N	3.06
1	C	1039:PHE	C	1040:VAL	N	3.06
1	C	2221:LEU	C	2222:LEU	N	3.06
1	D	77:ASN	C	78:VAL	N	3.06
1	J	660:GLU	C	661:TYR	N	3.06
1	A	1576:ASN	C	1577:THR	N	3.05
1	A	2094:LYS	C	2095:PHE	N	3.05
1	A	2154:CYS	C	2155:PHE	N	3.05
1	B	252:TRP	C	253:VAL	N	3.05
1	C	469:CYS	C	470:ALA	N	3.05
1	C	801:LEU	C	802:MET	N	3.05
1	C	923:HIS	C	924:ASN	N	3.05
1	C	1482:ASP	C	1483:GLU	N	3.05
1	C	1736:SER	C	1737:ASN	N	3.05
1	E	403:UNK	C	404:UNK	N	3.05
1	F	116:UNK	C	117:UNK	N	3.05
1	A	543:SER	C	544:ILE	N	3.04
1	A	642:LYS	C	643:LEU	N	3.04
1	A	1567:LYS	C	1568:ARG	N	3.04
1	A	1651:VAL	C	1652:VAL	N	3.04

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1818:HIS	C	1819:VAL	N	3.04
1	A	1899:LEU	C	1900:SER	N	3.04
1	A	2042:TYR	C	2043:TYR	N	3.04
1	B	85:GLN	C	86:ASP	N	3.04
1	C	1267:SER	C	1268:VAL	N	3.04
1	C	1383:ASP	C	1384:SER	N	3.04
1	C	1815:ASN	C	1816:LEU	N	3.04
1	C	2053:LYS	C	2054:GLN	N	3.04
1	C	2291:THR	C	2292:GLY	N	3.04
1	E	113:UNK	C	114:UNK	N	3.04
1	F	208:UNK	C	209:UNK	N	3.04
1	G	56:CYS	C	57:VAL	N	3.04
1	A	922:HIS	C	923:ASN	N	3.03
1	A	1281:SER	C	1282:SER	N	3.03
1	A	1519:ASN	C	1520:ALA	N	3.03
1	A	1988:ALA	C	1989:LEU	N	3.03
1	C	1580:ARG	C	1581:LEU	N	3.03
1	C	2043:ILE	C	2044:TYR	N	3.03
1	H	181:PRO	C	182:ILE	N	3.03
1	I	767:ILE	C	768:SER	N	3.03
1	C	1517:VAL	C	1518:HIS	N	3.02
1	C	1881:GLN	C	1882:LEU	N	3.02
1	D	213:ILE	C	214:LEU	N	3.02
1	A	221:LEU	C	222:THR	N	3.01
1	A	756:ILE	C	757:ASP	N	3.01
1	A	967:ILE	C	968:LEU	N	3.01
1	A	1380:THR	C	1381:ASP	N	3.01
1	C	938:HIS	C	939:THR	N	3.01
1	C	1486:GLN	C	1487:TYR	N	3.01
1	E	604:UNK	C	605:UNK	N	3.01
1	B	148:ASN	C	149:GLN	N	3.00
1	C	1224:LEU	C	1225:LYS	N	3.00
1	C	1561:LYS	C	1562:LYS	N	3.00
1	D	216:SER	C	217:SER	N	3.00
1	D	265:LEU	C	266:VAL	N	3.00
1	A	364:ILE	C	365:ARG	N	2.99
1	A	968:LEU	C	969:VAL	N	2.99
1	A	1526:THR	C	1527:GLU	N	2.99
1	A	2315:PRO	C	2316:PHE	N	2.99
1	C	462:TYR	C	463:CYS	N	2.99
1	C	494:ASP	C	495:HIS	N	2.99
1	C	1014:ILE	C	1015:ILE	N	2.99

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1677:PHE	C	1678:THR	N	2.99
1	C	2126:VAL	C	2127:LEU	N	2.99
1	C	2229:THR	C	2230:TYR	N	2.99
1	C	2413:HIS	C	2414:LYS	N	2.99
1	F	407:UNK	C	408:UNK	N	2.99
1	G	142:GLY	C	143:ASP	N	2.99
1	A	253:PRO	C	254:TYR	N	2.98
1	A	718:LEU	C	719:LEU	N	2.98
1	A	2014:ARG	C	2015:ASP	N	2.98
1	A	2045:VAL	C	2046:PHE	N	2.98
1	A	2184:THR	C	2185:PHE	N	2.98
1	B	16:PHE	C	17:TRP	N	2.98
1	C	1158:VAL	C	1159:PHE	N	2.98
1	C	2233:ASN	C	2234:ASN	N	2.98
1	D	28:ILE	C	29:GLN	N	2.98
1	D	89:TRP	C	90:MET	N	2.98
1	A	797:LEU	C	798:LYS	N	2.97
1	A	1219:ASN	C	1220:GLN	N	2.97
1	C	516:SER	C	517:ARG	N	2.97
1	C	974:CYS	C	975:PRO	N	2.97
1	C	1514:LYS	C	1515:ALA	N	2.97
1	C	1641:PRO	C	1642:ASP	N	2.97
1	C	1747:LEU	C	1748:ALA	N	2.97
1	C	1871:GLN	C	1872:ILE	N	2.97
1	C	2069:LYS	C	2070:LEU	N	2.97
1	D	25:SER	C	26:ARG	N	2.97
1	E	361:UNK	C	362:UNK	N	2.97
1	A	928:LEU	C	929:ASN	N	2.96
1	A	1061:PRO	C	1062:ILE	N	2.96
1	A	1265:VAL	C	1266:SER	N	2.96
1	A	1537:ASN	C	1538:ARG	N	2.96
1	A	1933:ILE	C	1934:GLU	N	2.96
1	C	778:THR	C	779:ALA	N	2.96
1	C	969:LEU	C	970:VAL	N	2.96
1	C	2108:GLN	C	2109:ARG	N	2.96
1	C	2471:CYS	C	2472:PRO	N	2.96
1	B	43:ASP	C	44:LYS	N	2.95
1	B	164:SER	C	165:LEU	N	2.95
1	C	550:LYS	C	551:SER	N	2.95
1	C	661:LEU	C	662:GLN	N	2.95
1	F	353:UNK	C	354:UNK	N	2.95
1	A	1069:VAL	C	1070:THR	N	2.94

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2284:MET	C	2285:LEU	N	2.94
1	A	326:ALA	C	327:THR	N	2.93
1	A	371:ILE	C	372:LEU	N	2.93
1	A	414:PHE	C	415:ILE	N	2.93
1	A	1228:TYR	C	1229:CYS	N	2.93
1	B	260:ALA	C	261:ASP	N	2.93
1	B	275:ARG	C	276:LEU	N	2.93
1	C	1993:PRO	C	1994:LEU	N	2.93
1	A	1346:ALA	C	1347:PHE	N	2.92
1	A	1947:ALA	C	1948:GLU	N	2.92
1	C	455:GLN	C	456:PHE	N	2.92
1	C	847:GLY	C	848:ILE	N	2.92
1	C	2251:SER	C	2252:GLU	N	2.92
1	A	1119:SER	C	1120:ARG	N	2.91
1	C	1277:PHE	C	1278:ASN	N	2.91
1	C	1591:TRP	C	1592:GLN	N	2.91
1	A	780:LYS	C	781:VAL	N	2.90
1	A	1062:ILE	C	1063:ARG	N	2.90
1	A	1680:ALA	C	1681:HIS	N	2.90
1	C	378:ALA	C	379:PHE	N	2.90
1	C	793:GLU	C	794:MET	N	2.90
1	C	948:ILE	C	949:PHE	N	2.90
1	C	1483:GLU	C	1484:ILE	N	2.90
1	A	218:ILE	C	219:ASP	N	2.89
1	A	1855:PRO	C	1856:GLU	N	2.89
1	B	66:ASN	C	67:PRO	N	2.89
1	C	1618:CYS	C	1619:ARG	N	2.89
1	C	1840:LEU	C	1841:GLN	N	2.89
1	C	2123:TYR	C	2124:LYS	N	2.89
1	C	2133:ILE	C	2134:ARG	N	2.89
1	A	270:PRO	C	271:LEU	N	2.88
1	A	1079:SER	C	1080:HIS	N	2.88
1	B	241:LYS	C	242:LEU	N	2.88
1	C	1469:PRO	C	1470:LEU	N	2.88
1	C	1943:PRO	C	1944:VAL	N	2.88
1	A	424:PHE	C	425:GLU	N	2.86
1	A	1001:GLU	C	1002:LYS	N	2.86
1	C	1122:ILE	C	1123:VAL	N	2.86
1	C	1520:PHE	C	1521:ASN	N	2.86
1	C	2100:VAL	C	2101:PHE	N	2.86
1	A	1291:TYR	C	1292:GLN	N	2.85
1	A	2291:LYS	C	2292:VAL	N	2.85

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	753:ALA	C	754:LYS	N	2.85
1	C	1446:GLU	C	1447:GLU	N	2.85
1	C	556:PHE	C	557:MET	N	2.84
1	C	966:GLY	C	967:ILE	N	2.84
1	C	1898:LEU	C	1899:SER	N	2.84
1	C	2156:CYS	C	2157:PHE	N	2.84
1	C	2337:PHE	C	2338:ARG	N	2.84
1	E	214:UNK	C	215:UNK	N	2.84
1	A	723:THR	C	724:GLN	N	2.83
1	A	957:SER	C	958:PHE	N	2.83
1	A	1824:LYS	C	1825:GLY	N	2.83
1	C	566:ASP	C	567:ILE	N	2.83
1	C	1240:GLN	C	1241:GLU	N	2.83
1	C	2098:GLU	C	2099:PRO	N	2.83
1	A	2137:VAL	C	2138:MET	N	2.82
1	A	2320:ARG	C	2321:MET	N	2.82
1	A	2322:LEU	C	2323:THR	N	2.82
1	C	2139:VAL	C	2140:MET	N	2.82
1	C	804:LEU	C	805:ILE	N	2.81
1	C	2287:LEU	C	2288:ASP	N	2.81
1	C	392:ILE	C	393:MET	N	2.80
1	D	249:HIS	C	250:GLN	N	2.80
1	C	1097:SER	C	1098:LEU	N	2.79
1	C	1652:PRO	C	1653:VAL	N	2.79
1	A	671:LEU	C	672:ALA	N	2.78
1	C	2021:ALA	C	2022:TYR	N	2.78
1	B	136:ARG	C	137:ASP	N	2.77
1	C	964:ILE	C	965:PRO	N	2.77
1	A	2019:ALA	C	2020:TYR	N	2.76
1	A	673:GLN	C	674:PRO	N	2.75
1	A	946:HIS	C	947:ILE	N	2.73
1	C	1478:LEU	C	1479:GLU	N	2.73
1	C	1574:ARG	C	1575:GLU	N	2.73
1	C	2112:LYS	C	2113:PHE	N	2.73
1	A	461:TYR	C	462:CYS	N	2.72
1	A	534:ASN	C	535:GLN	N	2.71
1	C	2227:VAL	C	2228:PHE	N	2.71
1	C	799:LYS	C	800:GLU	N	2.70
1	C	998:ARG	C	999:PRO	N	2.68
1	A	1609:ARG	C	1610:ILE	N	2.65
1	A	960:ASP	C	961:GLN	N	2.61
1	C	542:GLN	C	543:PHE	N	2.61

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2448:GLU	C	2449:GLN	N	2.59
1	C	1578:ASN	C	1579:THR	N	2.55

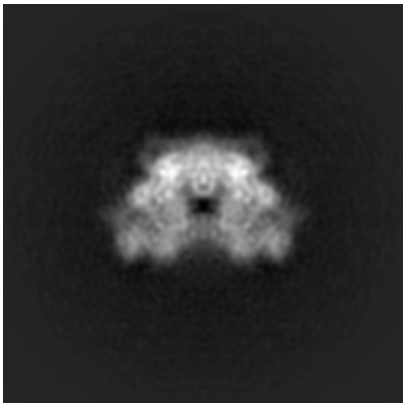
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3896. These allow visual inspection of the internal detail of the map and identification of artifacts.

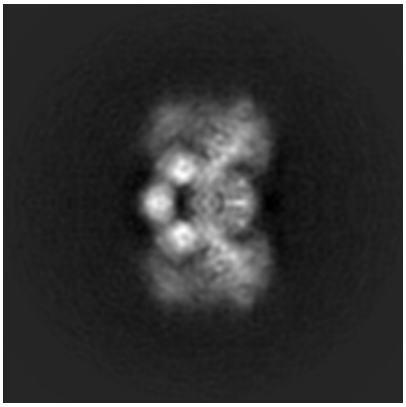
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

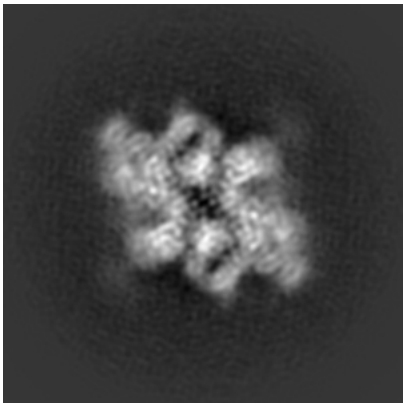
6.1.1 Primary map



X



Y

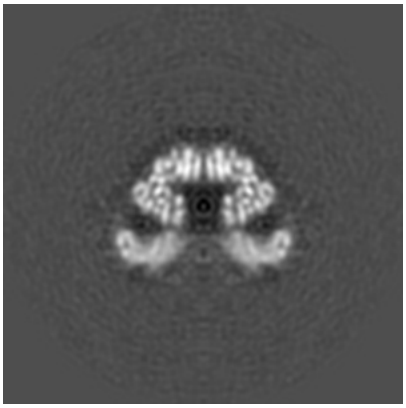


Z

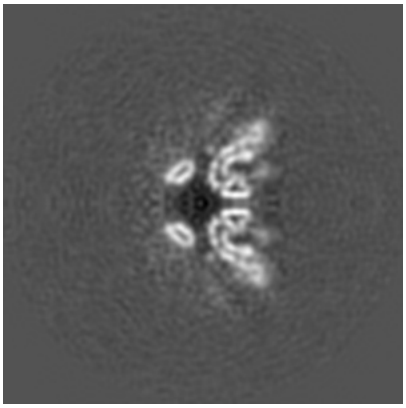
The images above show the map projected in three orthogonal directions.

6.2 Central slices

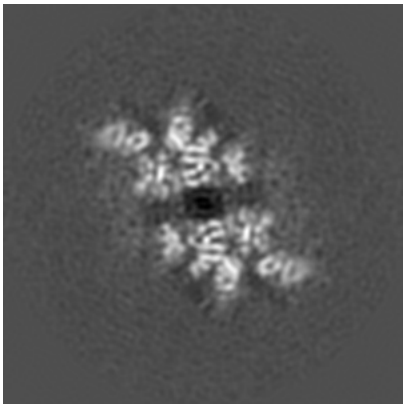
6.2.1 Primary map



X Index: 160



Y Index: 160

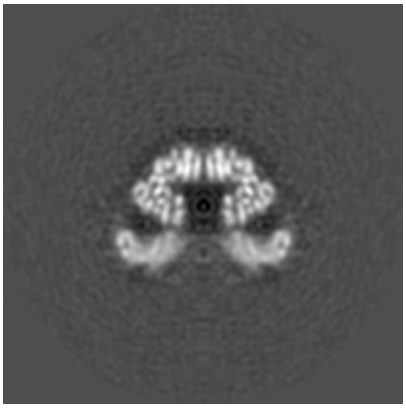


Z Index: 160

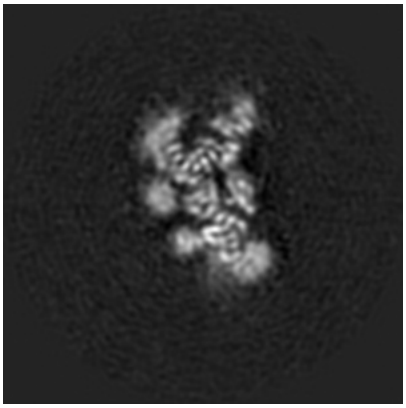
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

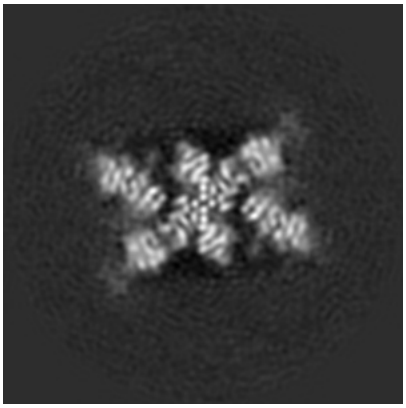
6.3.1 Primary map



X Index: 160



Y Index: 133

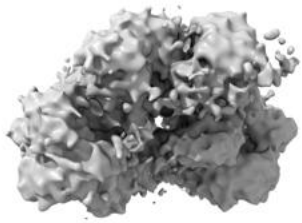


Z Index: 190

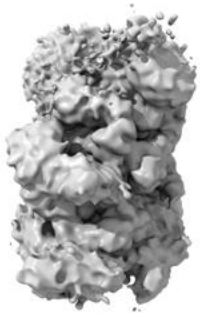
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

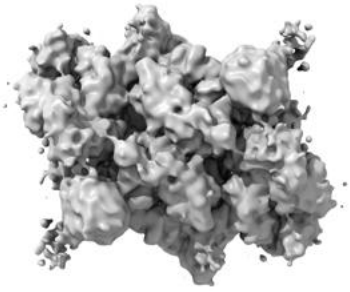
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

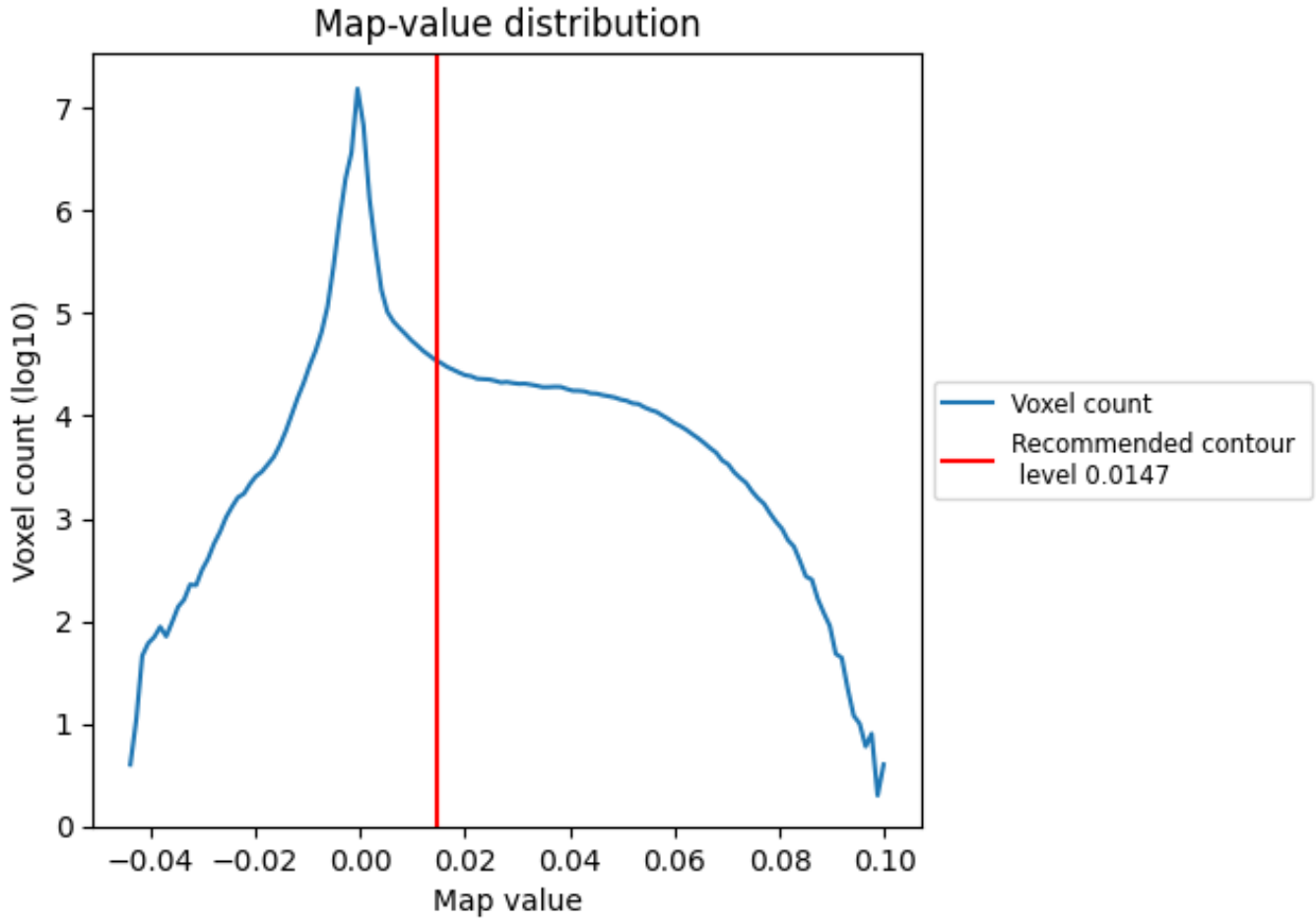
6.5 Mask visualisation (i)

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

7 Map analysis

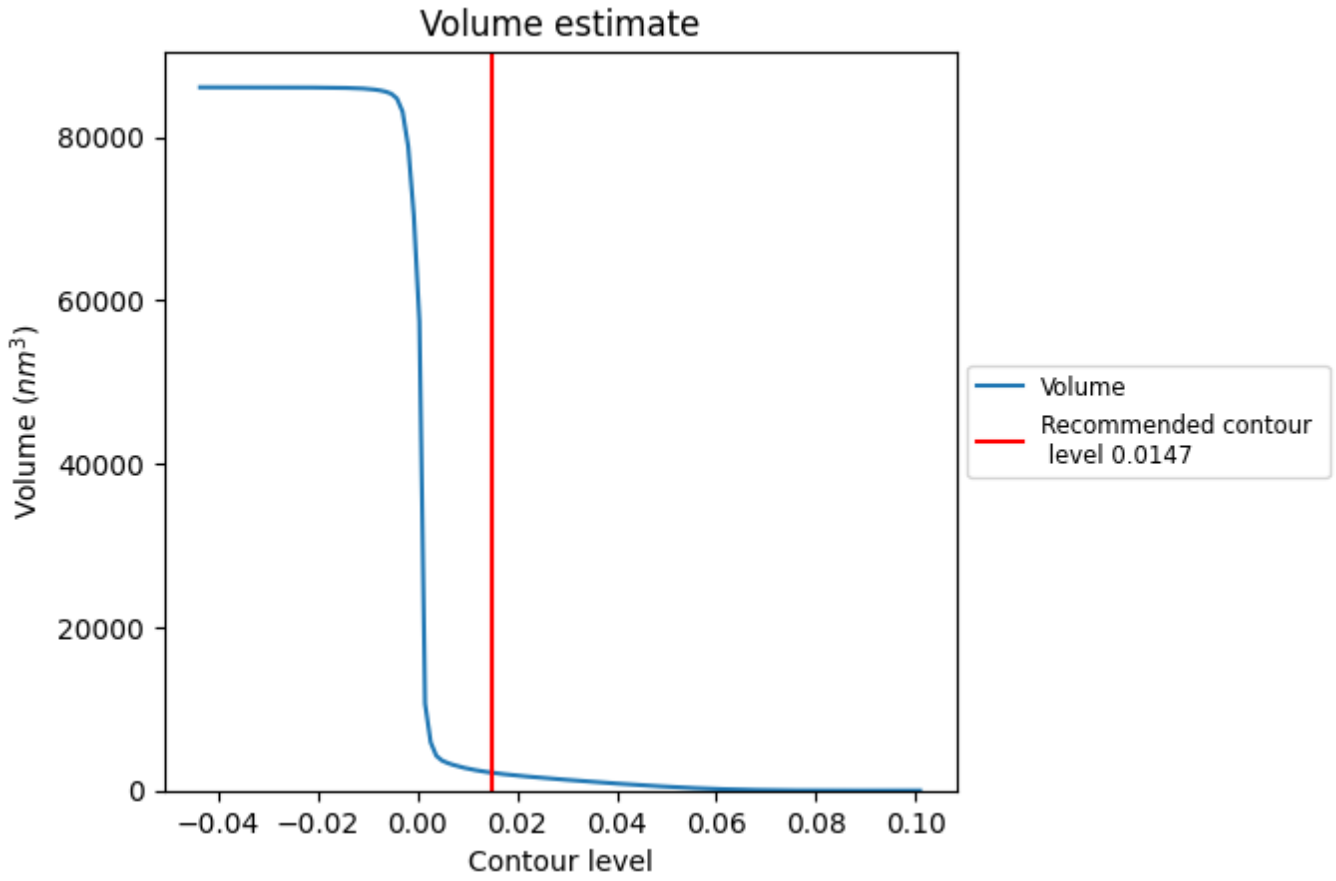
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

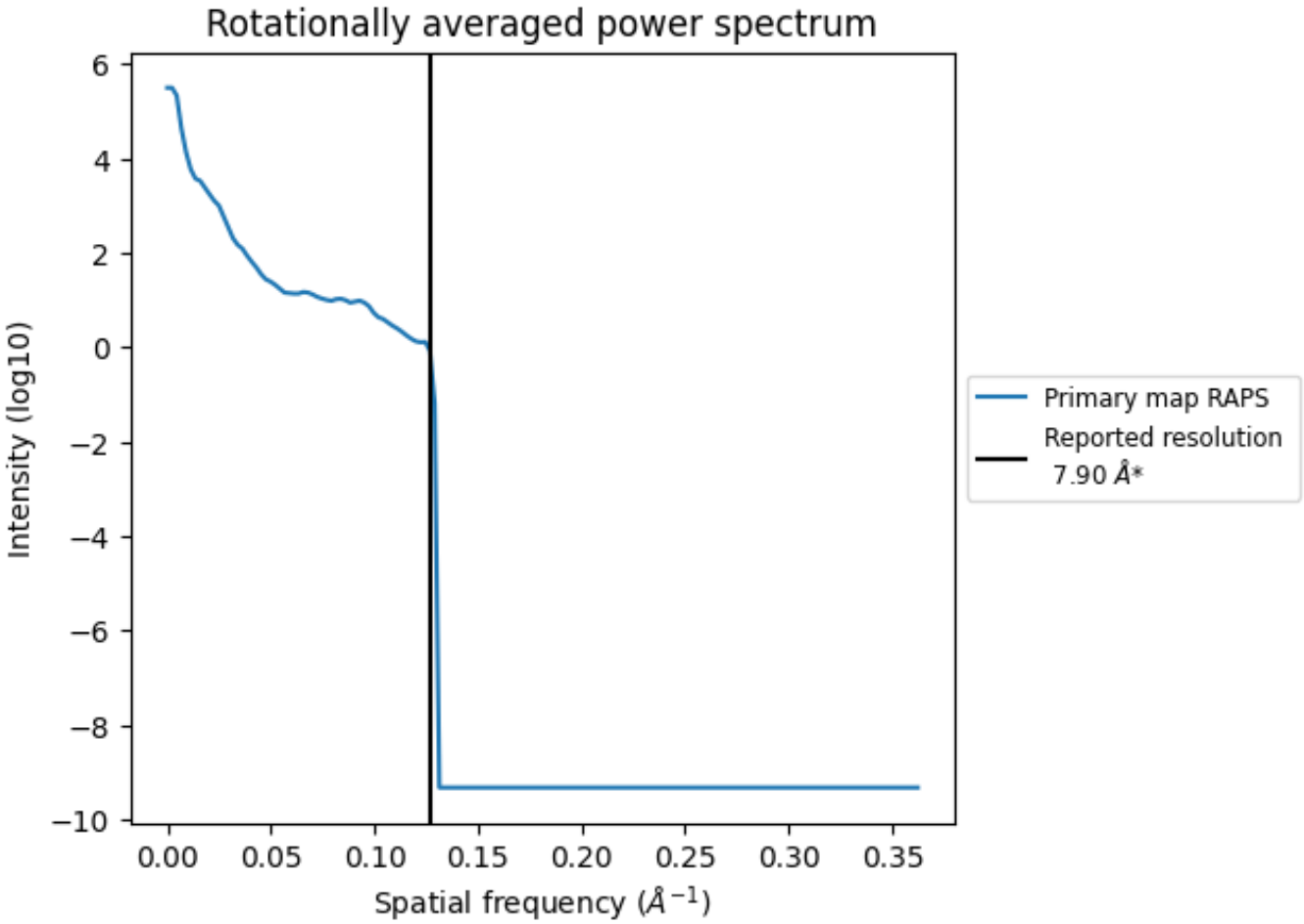
7.2 Volume estimate



The volume at the recommended contour level is 2205 nm^3; this corresponds to an approximate mass of 1992 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.127 Å^{-1}

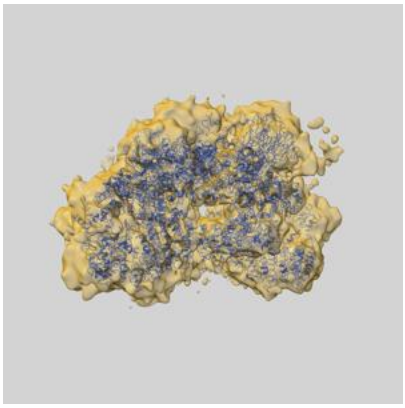
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

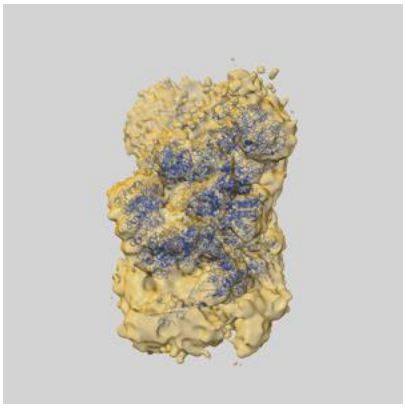
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3896 and PDB model 6EMK. Per-residue inclusion information can be found in section 3 on page 6.

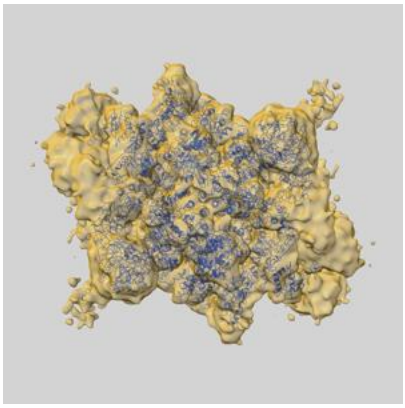
9.1 Map-model overlay



X



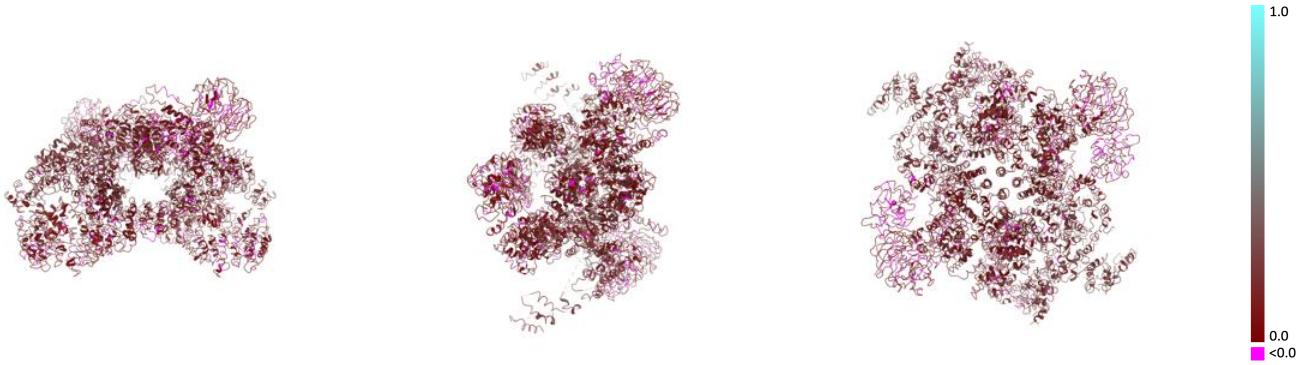
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0147 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.

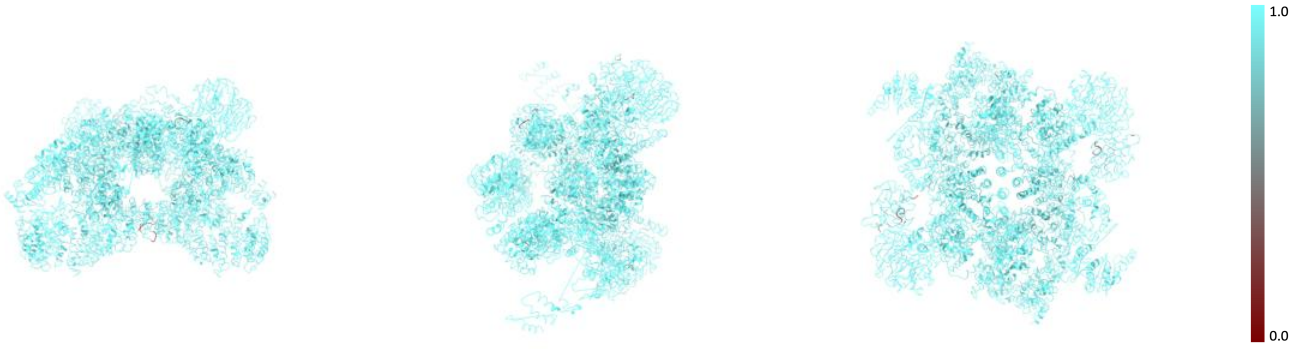
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

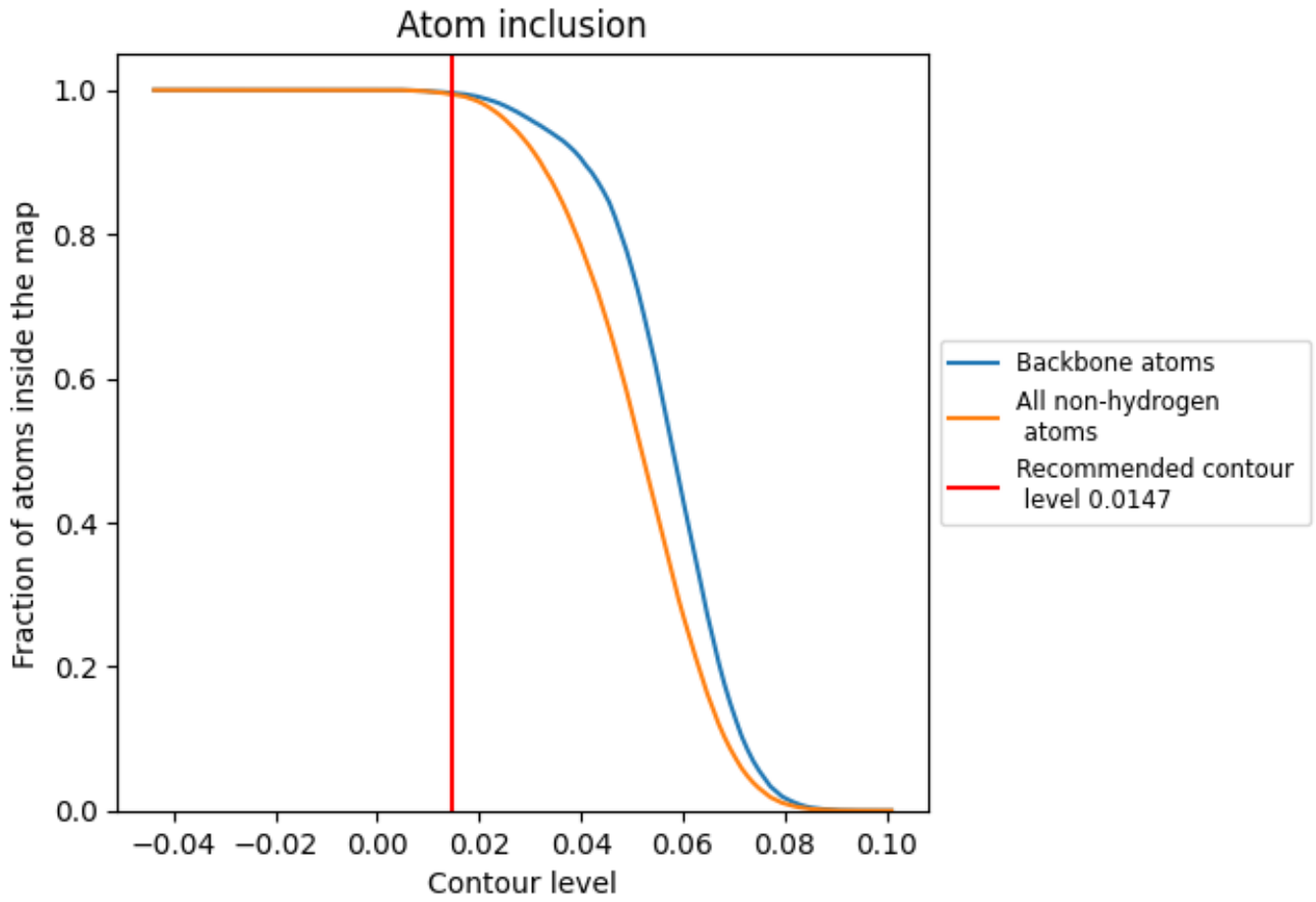
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0147).

9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9939	0.1450
A	0.9954	0.1430
B	1.0000	0.1080
C	0.9955	0.1410
D	1.0000	0.1070
E	1.0000	0.2680
F	1.0000	0.2690
G	1.0000	0.2330
H	1.0000	0.2340
I	0.9344	0.0480
J	0.9568	0.0550