



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:55 PM BST

PDB ID : 3J96  
EMDB ID: : EMD-6206  
Title : Structure of 20S supercomplex determined by single particle cryoelectron microscopy (State I)  
Authors : Zhao, M.; Wu, S.; Cheng, Y.; Brunger, A.T.  
Deposited on : 2014-12-05  
Resolution : 7.60 Å(reported)  
Based on PDB ID : 1QCS, 1NSF, 1N7S

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

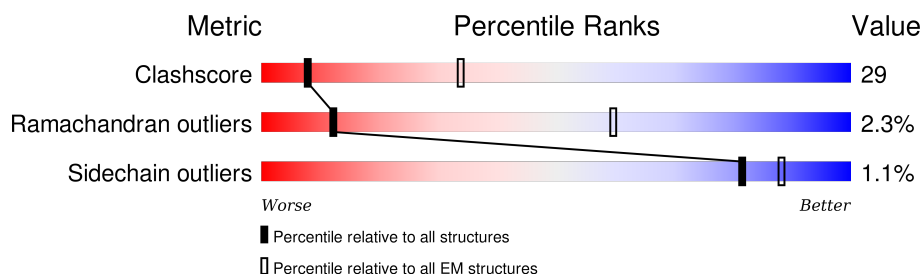
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.60 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	747	45% 42% . . 9%
1	B	747	46% 41% . 10%
1	C	747	47% 41% . 10%
1	D	747	45% 43% . 10%
1	E	747	45% 42% . 10%
1	F	747	44% 41% . 12%
2	G	297	49% 44% . .
2	H	297	54% 41% . .
2	I	297	57% 38% . .

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Mol	Chain	Length	Quality of chain
2	J	297	<div><div></div><div>52%</div><div>42%</div><div></div><div></div></div>
3	K	63	<div><div></div><div>38%</div><div>57%</div><div></div><div></div></div>
4	L	67	<div><div></div><div>51%</div><div>43%</div><div></div><div></div></div>
5	M	188	<div><div></div><div>29%</div><div>40%</div><div>30%</div><div></div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 41139 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 Vesicle-fusing ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	678	Total	C	N	O	S	0	0
			5048	3203	876	946	23		
1	B	672	Total	C	N	O	S	0	0
			5037	3197	872	944	24		
1	C	676	Total	C	N	O	S	0	0
			5039	3196	872	948	23		
1	D	673	Total	C	N	O	S	0	0
			4994	3174	857	939	24		
1	E	670	Total	C	N	O	S	0	0
			5012	3183	866	939	24		
1	F	654	Total	C	N	O	S	0	0
			4926	3130	849	923	24		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P18708
A	-1	ALA	-	EXPRESSION TAG	UNP P18708
A	0	HIS	-	EXPRESSION TAG	UNP P18708
B	-2	GLY	-	EXPRESSION TAG	UNP P18708
B	-1	ALA	-	EXPRESSION TAG	UNP P18708
B	0	HIS	-	EXPRESSION TAG	UNP P18708
C	-2	GLY	-	EXPRESSION TAG	UNP P18708
C	-1	ALA	-	EXPRESSION TAG	UNP P18708
C	0	HIS	-	EXPRESSION TAG	UNP P18708
D	-2	GLY	-	EXPRESSION TAG	UNP P18708
D	-1	ALA	-	EXPRESSION TAG	UNP P18708
D	0	HIS	-	EXPRESSION TAG	UNP P18708
E	-2	GLY	-	EXPRESSION TAG	UNP P18708
E	-1	ALA	-	EXPRESSION TAG	UNP P18708
E	0	HIS	-	EXPRESSION TAG	UNP P18708
F	-2	GLY	-	EXPRESSION TAG	UNP P18708
F	-1	ALA	-	EXPRESSION TAG	UNP P18708
F	0	HIS	-	EXPRESSION TAG	UNP P18708

- Molecule 2 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	H	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	I	286	Total	C	N	O	S	0	0
			2251	1421	372	441	17		
2	J	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	GLY	-	EXPRESSION TAG	UNP P54921
G	0	SER	-	EXPRESSION TAG	UNP P54921
H	-1	GLY	-	EXPRESSION TAG	UNP P54921
H	0	SER	-	EXPRESSION TAG	UNP P54921
I	-1	GLY	-	EXPRESSION TAG	UNP P54921
I	0	SER	-	EXPRESSION TAG	UNP P54921
J	-1	GLY	-	EXPRESSION TAG	UNP P54921
J	0	SER	-	EXPRESSION TAG	UNP P54921

- Molecule 3 is a protein called Vesicle-associated membrane protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	61	Total	C	N	O	S	0	0
			493	301	93	98	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	27	GLY	-	EXPRESSION TAG	UNP P63045

- Molecule 4 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	66	Total	C	N	O	S	0	0
			536	331	91	109	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	MET	-	EXPRESSION TAG	UNP P32851

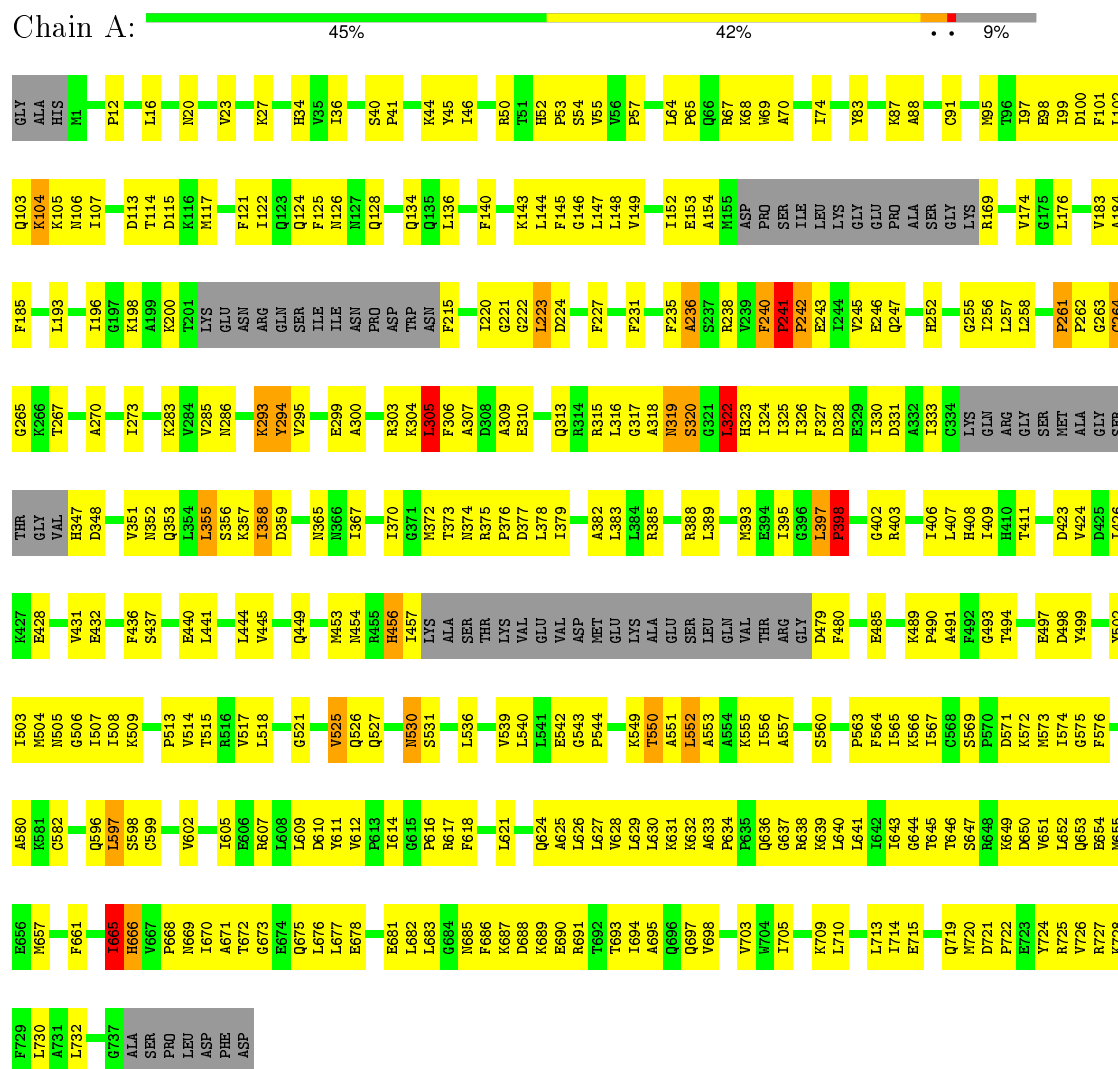
- Molecule 5 is a protein called Synaptosomal-associated protein 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	131	Total	C	N	O	S	0	0
			1038	614	194	221	9		

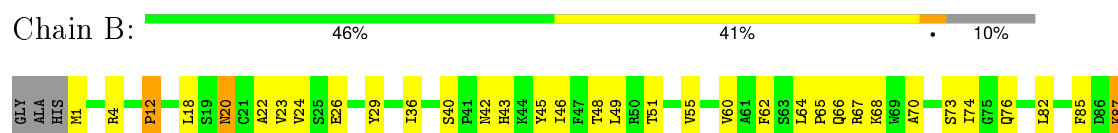
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Vesicle-fusing ATPase



#### • Molecule 1: Vesicle-fusing ATPase



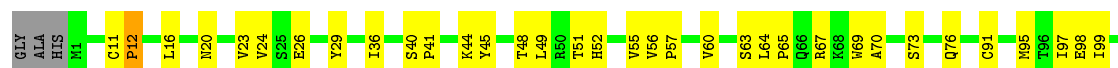
I707	K708	K709	L710	L711	M712	L713	L714	E715	M716	Q719	M720	D721	Y724	L728	F729	L732	ALA	SER	PRO	LEU	ASP	PHE	ASP	F661	S662	T663	I664	I665	H666	V667	P668	N669	I670	Q675	L676	L677	E681	L682	L683	F686	E690	P694	A695	K699	G706														
K555	I556	E559	S560	M561	E562	P563	K566	I567	C568	S569	P570	D571	I574	G575	F576	S577	A578	T579	A580	K581	C582	Q583	A584	E585	T588	P589	Y593	Q596	L597	V600	D603	D604	I605	E606	R607	L608	L609	D610	Y611	V612	P613	I614	G615	P616	R617	F618	S619	N620	L621	V622	L623	Q624							
ARG	GLY	D479	E485	I488	K489	P490	A491	Y499	Y502	I503	G506	I507	F508	K509	M510	D512	P513	R516	V517	L518	D519	L523	L524	V525	Q526	T527	T528	S531	D532	R533	T534	P535	L536	V537	S538	V539	L540	L541	E542	G543	P544	P545	H546	S547	ALA	GLU	SER	LEU	L552	G553	VAL	THR	A554						
D399	D402	R403	L404	Q405	L406	L407	H408	L409	R413	M414	D423	I426	K427	E428	V431	E432	F436	S437	G438	A439	L440	L441	Q444	Q449	S450	T451	A452	M453	M454	R455	R456	L457	LYS	ALA	SER	THR	LYS	VAL	GLU	VAL	ASP	MET	GLU	LYS	ALA	GLU	SER	LEU	L396	L397	F398								
I325	I326	F327	I330	ASP	ALA	ILE	CYS	GLN	ARG	GLY	ALA	GLY	SER	THR	VAL	H347	N352	Q353	L354	L355	S356	L290	L291	K292	K293	V294	V295	I367	L368	V369	I370	G371	M372	D377	L378	F306	A307	D308	A309	E310	E311	L383	L384	R385	Q313	R314	R315	L316	G317	E390	V391	I395	G396	L397	F398				
G255	I256	Y259	G260	G263	C264	G265	K266	T267	L268	L269	A270	MET	R271	Q272	I273	E281	P282	K283	GLN	V284	V285	N286	G287	Q288	E289	S290	L291	K292	K293	V294	V295	I367	L368	V369	I370	G371	M372	D377	L378	F306	A307	D308	A309	E310	E311	L383	L384	R385	Q313	R314	R315	L316	G317	E390	V391	I395	G396	L397	F398
LYS	R169	Q170	K171	I172	E173	V174	G175	L176	M180	V183	L193	T201	LYS	ASN	PHE	GLU	K217	M218	G219	TRP	ASN	PHE	GLU	K217	M218	G219	D224	R224	S228	D229	I230	F231	R232	A236	V239	F240	P241	P242	E243	I244	V245	E246	LYS	Q247	M248	G249	C250	ALA	SER	GLY	GLY	ALA	SER	GLY					

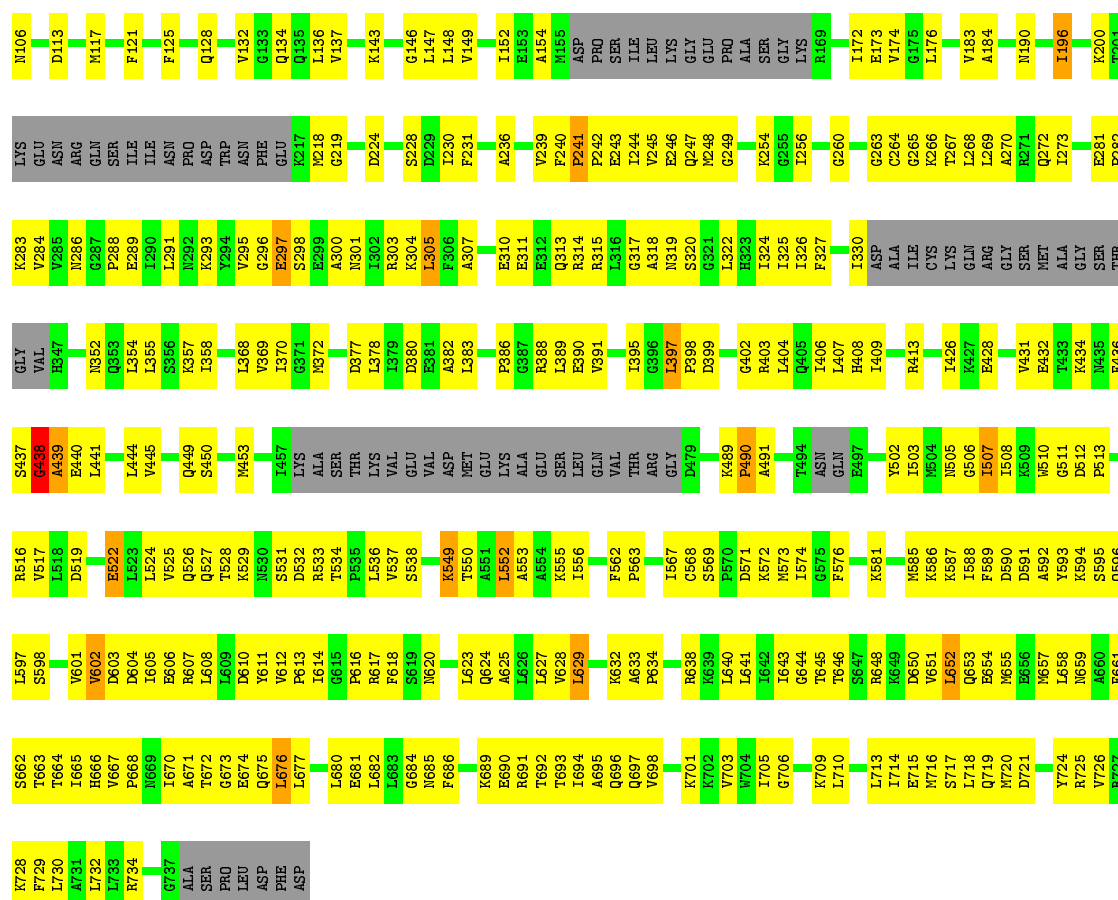
• Molecule 1: Vesicle-fusing ATPase

Chain C:

GLY	ALA	HIS	M1	PI2	TI3	D14	L18	S19	R20	V23	V24	K44	Y45	I46	T48	L49	R50	T51	H52	P53	S54	L64	P65	Q66	R67	K68	H69	A70	I74	Y83	D86	A88	C91	N95	E98	F101	I107	T114	L122	F125	N126	Q127	V132	G133	Q134	Q135	L136	V137	F138	S139	K143	L144	V145	G146	I152	E153	A154	M155	ASP	PRO	SER	ILE	LEU	L169	E173	V174	G175	L176	N180	V183	A184	N190	E198	L193	N194	L195	A199	K200
T201	LYS	GLU	ASN	ARG	GLN	SER	ILE	ILE	ASN	PRO	ASP	TRP	ASN	PHE	GLU	K217	R218	G219	F227	F231	R232	R233	A234	F235	R313	R314	R315	S237	L316	G317	A318	N319	S320	G321	C334	L326	F327	I330	D331	A332	C334	L326	GLN	ARG	GLY	SER	MET	ALA	GLY	L268	A270	R271	I273																									
E281	V284	V285	P288	E289	L291	K293	Y294	V295	G296	S298	E299	L305	D308	A309	E311	E312	Q313	R314	R315	L316	G317	A318	N319	S320	G321	C334	L326	F327	I330	D331	A332	C334	L326	GLN	ARG	GLY	SER	MET	ALA	GLY	L268	A270	R271	I273																																		
D348	T349	V350	V351	N352	Q353	L354	L355	L358	N365	N366	L367	L368	V369	I370	G371	R375	P376	D377	L378	I379	L383	P386	G387	R388	L389	E390	V391	D399	K401	G402	R403	L404	L407	H408	T411	A412	N414	K426	K427	D428	V431	E432	F436	S437	G438	A439																																
E440	L441	V445	R446	Q449	A452	M453	H456	L457	LYS	ALA	THR	LYS	VAL	GLU	VAL	VAL	ASP	NET	GLU	LYS	ALA	LYS	GLU	LEU	GLN	VAL	THR	ARG	GLY	D479	P490	A491	F492	Q496	E497	D498	Y499	M505	G506	I507	I508	K509	M510	D512	P513	R516	V517	L518	G519	D520																												
G521	E522	L523	L524	V525	Q526	G527	K529	N530	R533	L536	V537	S538	V539	L540	L541	E542	G543	P544	H545	G546	S547	G548	K549	T550	A551	L552	K555	L556	A557	E558	E559	S560	M561	F562	P563	F564	I565	K566	L567	S569	K572	M573	I574	Q575	F576	S577	E578	T579	A580	K581	Q582	Q583	A584																									

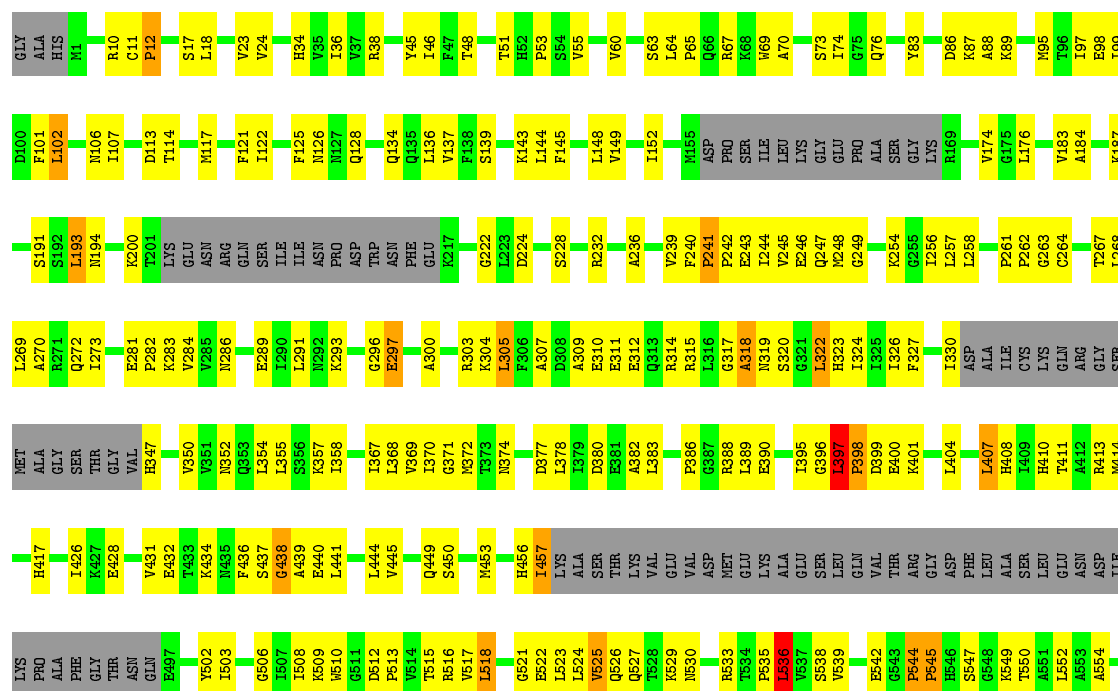




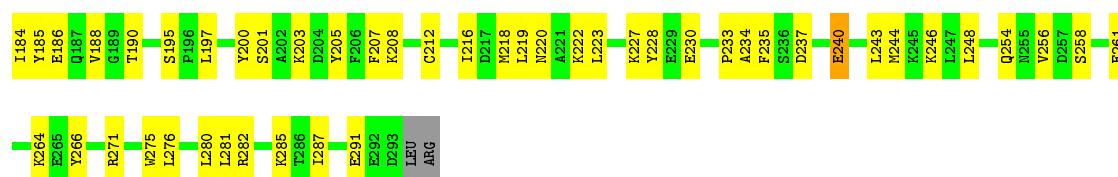


• Molecule 1: Vesicle-fusing ATPase

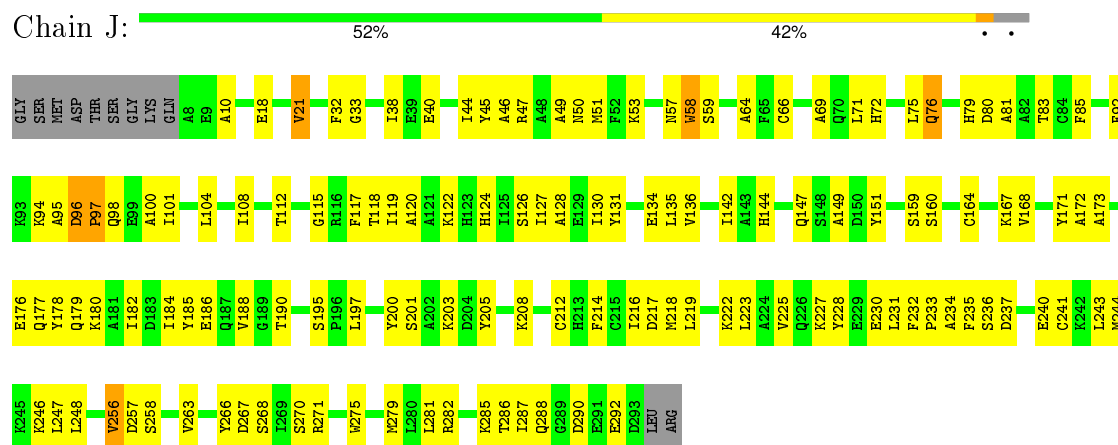
Chain F: 44% 41% 12%



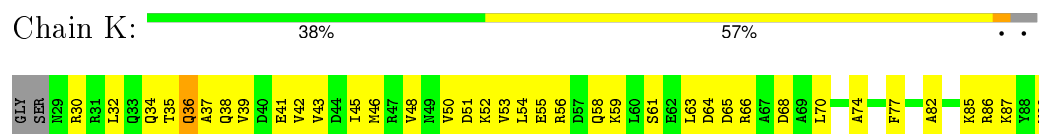




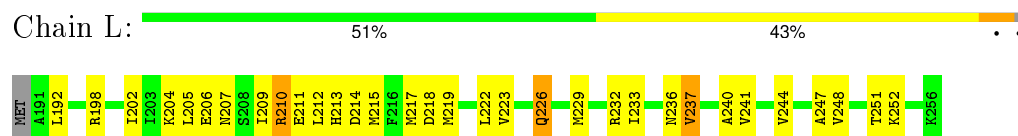
- Molecule 2: Alpha-soluble NSF attachment protein



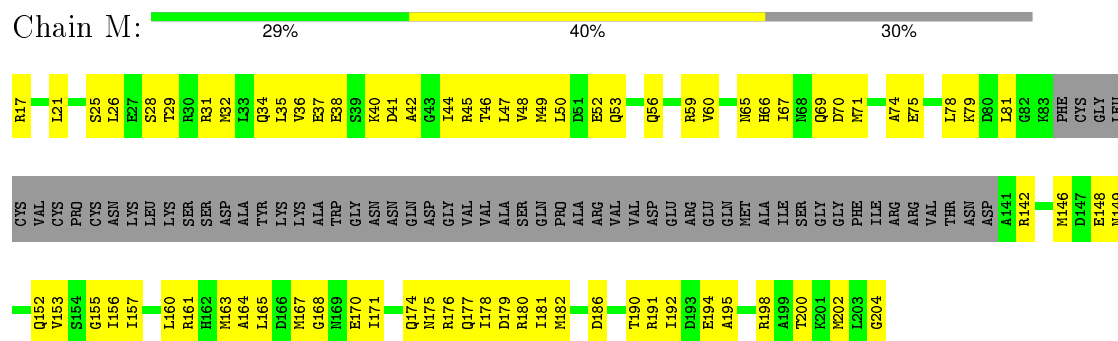
- Molecule 3: Vesicle-associated membrane protein 2



- Molecule 4: Syntaxin-1A



- Molecule 5: Synaptosomal-associated protein 25



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	29717	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	44	Depositor
Minimum defocus (nm)	-1800	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 (4k x 4k)	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  >2	RMSZ	# Z  >2
1	A	0.46	1/5124 (0.0%)	0.85	13/6935 (0.2%)
1	B	0.41	1/5113 (0.0%)	0.77	7/6915 (0.1%)
1	C	0.39	0/5115	0.75	6/6922 (0.1%)
1	D	0.43	0/5069	0.77	8/6864 (0.1%)
1	E	0.44	0/5088	0.83	14/6881 (0.2%)
1	F	0.44	1/5001 (0.0%)	0.81	14/6760 (0.2%)
2	G	0.36	0/2295	0.65	0/3086
2	H	0.36	0/2295	0.62	2/3086 (0.1%)
2	I	0.35	0/2291	0.61	0/3082
2	J	0.35	0/2295	0.62	1/3086 (0.0%)
3	K	0.24	0/496	0.41	0/664
4	L	0.24	0/541	0.43	0/723
5	M	0.22	0/1038	0.41	0/1381
All	All	0.41	3/41761 (0.0%)	0.75	65/56385 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	E	0	1
1	F	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	SER	CB-OG	-6.72	1.33	1.42
1	B	708	LYS	CE-NZ	5.60	1.63	1.49
1	F	545	PRO	N-CD	5.21	1.55	1.47

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	708	LYS	CD-CE-NZ	14.61	145.29	111.70
1	F	518	LEU	CB-CG-CD1	-10.49	93.17	111.00
1	A	597	LEU	CB-CG-CD2	-10.05	93.91	111.00
1	F	397	LEU	CA-CB-CG	9.14	136.32	115.30
1	C	322	LEU	CA-CB-CG	8.22	134.21	115.30
1	D	713	LEU	CB-CG-CD2	-8.18	97.09	111.00
1	D	504	MET	C-N-CA	-7.93	101.87	121.70
1	F	305	LEU	CA-CB-CG	7.29	132.07	115.30
1	E	629	LEU	CB-CG-CD1	-7.20	98.77	111.00
1	A	552	LEU	CA-CB-CG	7.06	131.54	115.30
1	E	549	LYS	CB-CG-CD	7.04	129.90	111.60
2	J	96	ASP	CB-CG-OD1	6.96	124.56	118.30
1	E	305	LEU	CA-CB-CG	6.83	131.01	115.30
1	B	305	LEU	CA-CB-CG	6.83	131.00	115.30
1	A	261	PRO	C-N-CD	-6.54	106.22	120.60
1	E	652	LEU	CB-CG-CD2	-6.50	99.94	111.00
1	A	322	LEU	CA-CB-CG	6.35	129.91	115.30
1	C	677	LEU	CA-CB-CG	6.34	129.87	115.30
1	F	609	LEU	CB-CG-CD2	-6.30	100.29	111.00
1	D	627	LEU	CB-CG-CD2	-6.18	100.48	111.00
1	B	395	ILE	CG1-CB-CG2	-6.15	97.88	111.40
1	D	609	LEU	CA-CB-CG	6.10	129.33	115.30
1	E	552	LEU	CA-CB-CG	6.04	129.18	115.30
1	F	536	LEU	CA-CB-CG	5.99	129.08	115.30
1	A	305	LEU	CA-CB-CG	5.94	128.97	115.30
1	C	387	GLY	N-CA-C	-5.92	98.31	113.10
1	E	549	LYS	CG-CD-CE	-5.83	94.41	111.90
1	B	658	LEU	CB-CG-CD1	-5.82	101.10	111.00
1	D	643	ILE	CB-CA-C	-5.81	99.97	111.60
1	E	438	GLY	N-CA-C	5.81	127.62	113.10
1	A	665	ILE	CG1-CB-CG2	-5.80	98.65	111.40
1	F	640	LEU	CA-CB-CG	5.76	128.55	115.30
1	F	457	ILE	CG1-CB-CG2	-5.75	98.76	111.40
1	F	544	PRO	C-N-CD	5.75	140.47	128.40
1	D	416	GLY	N-CA-C	-5.74	98.76	113.10
1	D	643	ILE	CG1-CB-CG2	-5.73	98.79	111.40
1	D	404	LEU	CA-CB-CG	5.72	128.46	115.30
1	F	656	GLU	CA-CB-CG	5.67	125.87	113.40
1	C	677	LEU	CB-CG-CD2	-5.59	101.50	111.00
2	H	219	LEU	CA-CB-CG	5.59	128.15	115.30
1	A	641	LEU	CA-CB-CG	5.54	128.04	115.30
1	A	236	ALA	N-CA-C	-5.51	96.11	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	541	LEU	CA-CB-CG	5.51	127.97	115.30
1	F	407	LEU	CA-CB-CG	5.48	127.91	115.30
1	A	525	VAL	CG1-CB-CG2	5.45	119.62	110.90
1	F	574	ILE	CG1-CB-CG2	-5.41	99.51	111.40
1	A	355	LEU	CA-CB-CG	5.38	127.67	115.30
1	E	655	MET	CA-CB-CG	5.38	122.44	113.30
1	F	597	LEU	CA-CB-CG	5.35	127.61	115.30
1	A	441	LEU	CB-CG-CD2	-5.35	101.91	111.00
1	C	316	LEU	CB-CG-CD1	5.35	120.09	111.00
1	E	549	LYS	CA-CB-CG	-5.31	101.71	113.40
1	E	397	LEU	CA-CB-CG	5.26	127.41	115.30
1	E	231	PHE	N-CA-C	-5.22	96.91	111.00
1	E	652	LEU	CA-CB-CG	5.21	127.27	115.30
1	C	640	LEU	CA-CB-CG	5.19	127.23	115.30
1	A	319	ASN	N-CA-C	-5.17	97.05	111.00
1	F	525	VAL	CG1-CB-CG2	5.17	119.17	110.90
2	H	292	GLU	C-N-CA	-5.15	108.81	121.70
1	E	676	LEU	CA-CB-CG	5.15	127.15	115.30
1	A	398	PRO	CA-N-CD	-5.13	104.32	111.50
1	B	658	LEU	CA-CB-CG	5.09	127.00	115.30
1	B	543	GLY	N-CA-C	-5.07	100.43	113.10
1	E	522	GLU	CA-CB-CG	5.07	124.55	113.40
1	F	397	LEU	C-N-CD	5.05	139.00	128.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	438	GLY	Peptide
1	E	438	GLY	Peptide
1	F	438	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5048	0	4974	346	0
1	B	5037	0	4996	313	0
1	C	5039	0	4965	309	0
1	D	4994	0	4923	331	0
1	E	5012	0	4954	336	0
1	F	4926	0	4896	311	0
2	G	2255	0	2199	142	0
2	H	2255	0	2199	113	0
2	I	2251	0	2188	117	0
2	J	2255	0	2199	125	0
3	K	493	0	491	61	0
4	L	536	0	527	58	0
5	M	1038	0	1011	117	0
All	All	41139	0	40522	2385	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 29.

All (2385) 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:F:263:GLY:HA3	1:F:437:SER:HB2	1.29	1.14
1:A:549:LYS:NZ	1:A:647:SER:OG	1.93	1.01
2:H:271:ARG:HH11	2:I:234:ALA:HB2	1.28	0.98
2:I:200:TYR:HB3	5:M:161:ARG:HD2	1.43	0.97
2:H:219:LEU:HB2	2:H:222:LYS:HB3	1.46	0.97
2:J:219:LEU:HB2	2:J:222:LYS:HB3	1.48	0.96
1:E:528:THR:HG22	1:E:537:VAL:HG21	1.49	0.94
1:C:327:PHE:HB3	1:C:330:ILE:HD11	1.44	0.94
1:D:509:LYS:HG2	1:D:515:THR:HG23	1.49	0.94
1:E:720:MET:HG3	1:E:728:LYS:HE3	1.49	0.94
1:D:406:ILE:HG22	1:D:441:LEU:HD22	1.50	0.93
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.49	0.93
3:K:39:VAL:HG22	5:M:157:ILE:HG12	1.50	0.92
2:J:228:TYR:OH	2:J:237:ASP:OD1	1.88	0.92
1:C:386:PRO:HA	1:C:390:GLU:HA	1.52	0.91
1:C:407:LEU:HD11	1:C:426:ILE:HG23	1.50	0.91
1:B:649:LYS:HE3	1:B:658:LEU:HD11	1.53	0.91
1:C:724:TYR:HD2	1:C:727:ARG:HH21	1.19	0.91
1:B:256:ILE:HG13	1:B:370:ILE:HG22	1.53	0.90
1:A:331:ASP:HA	1:A:379:ILE:HD11	1.53	0.89
1:C:618:PHE:HE2	1:D:614:ILE:HD11	1.38	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:585:MET:HG3	1:E:589:PHE:CZ	2.08	0.89
1:C:497:GLU:O	1:C:499:TYR:N	2.06	0.89
1:E:596:GLN:HA	1:E:638:ARG:HG2	1.52	0.89
1:F:386:PRO:HA	1:F:390:GLU:HA	1.54	0.89
1:A:569:SER:OG	1:A:571:ASP:OD1	1.89	0.89
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.55	0.89
1:E:240:PHE:HZ	1:F:456:HIS:HB2	1.35	0.88
1:F:256:ILE:HG13	1:F:370:ILE:HG22	1.53	0.88
1:B:240:PHE:HD2	1:B:244:ILE:HG21	1.34	0.88
1:A:264:CYS:SG	1:A:265:GLY:N	2.46	0.88
2:G:219:LEU:HB2	2:G:222:LYS:HB3	1.56	0.87
1:A:685:ASN:OD1	1:F:533:ARG:NH1	2.07	0.87
1:A:449:GLN:NE2	1:F:248:MET:O	2.08	0.87
3:K:52:LYS:HB3	5:M:171:ILE:HG21	1.53	0.87
1:E:256:ILE:HG13	1:E:370:ILE:HG22	1.56	0.87
1:A:295:VAL:HB	1:B:294:TYR:HB2	1.55	0.87
1:C:313:GLN:O	1:C:317:GLY:N	2.07	0.87
2:G:231:LEU:HB3	2:J:271:ARG:HG3	1.56	0.87
2:H:213:HIS:HE1	2:H:221:ALA:HB2	1.38	0.86
1:A:503:ILE:HG23	1:A:506:GLY:HA2	1.57	0.86
2:G:271:ARG:HH22	2:H:234:ALA:HB2	1.40	0.86
1:E:686:PHE:HE1	1:E:714:ILE:HG23	1.41	0.86
2:G:38:ILE:HD11	2:G:71:LEU:HB3	1.57	0.86
1:F:263:GLY:HA3	1:F:437:SER:CB	2.07	0.85
1:A:353:GLN:HA	1:B:288:PRO:HG3	1.58	0.85
1:F:521:GLY:HA2	1:F:524:LEU:HD12	1.55	0.85
1:B:407:LEU:HD11	1:B:426:ILE:HG23	1.58	0.85
1:B:526:GLN:HE21	1:C:719:GLN:HB3	1.40	0.84
1:F:240:PHE:HD2	1:F:244:ILE:HG21	1.43	0.84
1:C:240:PHE:HD2	1:C:244:ILE:HG21	1.42	0.84
1:B:541:LEU:HD11	1:B:549:LYS:HA	1.57	0.84
1:D:256:ILE:HG13	1:D:370:ILE:HG22	1.59	0.84
2:H:119:ILE:HD12	2:H:122:LYS:HB2	1.59	0.84
1:B:566:LYS:HD2	1:B:588:ILE:HG23	1.59	0.83
5:M:49:MET:HB3	5:M:53:GLN:HE21	1.43	0.83
1:F:10:ARG:HG3	1:F:67:ARG:HH22	1.44	0.83
1:D:606:GLU:HA	1:D:609:LEU:HG	1.59	0.83
1:E:624:GLN:NE2	1:F:610:ASP:OD1	2.11	0.83
1:C:627:LEU:HD12	1:D:607:ARG:HH12	1.41	0.83
1:A:686:PHE:HE2	1:A:714:ILE:HG12	1.44	0.82
2:G:268:SER:HA	2:H:233:PRO:HG3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:545:PRO:HA	1:F:547:SER:H	1.44	0.82
1:E:589:PHE:CZ	1:E:629:LEU:HD11	2.15	0.82
1:E:603:ASP:OD2	1:E:645:THR:OG1	1.97	0.82
1:E:240:PHE:HD2	1:E:244:ILE:HG21	1.45	0.82
1:E:386:PRO:HA	1:E:390:GLU:HA	1.61	0.82
5:M:50:LEU:HB3	5:M:170:GLU:HG2	1.63	0.81
2:I:235:PHE:CE1	3:K:34:GLN:HA	2.15	0.81
1:B:386:PRO:HA	1:B:390:GLU:HA	1.60	0.81
1:E:527:GLN:O	1:E:531:SER:OG	1.99	0.81
1:E:593:TYR:O	1:E:638:ARG:NH1	2.13	0.81
1:F:536:LEU:HD11	1:F:634:PRO:HD3	1.61	0.81
1:A:502:TYR:HE2	1:A:567:ILE:HG21	1.46	0.81
1:F:570:PRO:HG2	1:F:604:ASP:HB2	1.61	0.81
1:A:497:GLU:O	1:A:499:TYR:N	2.14	0.81
1:F:327:PHE:HB2	1:F:330:ILE:HG22	1.60	0.81
1:A:705:ILE:HD13	1:A:710:LEU:HD12	1.62	0.80
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.60	0.80
1:A:542:GLU:HG2	1:A:649:LYS:HD2	1.63	0.80
1:D:386:PRO:HA	1:D:390:GLU:HA	1.64	0.80
1:A:624:GLN:HG3	1:B:610:ASP:HB2	1.62	0.80
1:A:305:LEU:HD23	1:A:325:ILE:HG21	1.64	0.80
1:E:587:LYS:NZ	1:E:587:LYS:O	2.13	0.80
1:F:240:PHE:CD2	1:F:244:ILE:HG21	2.16	0.79
2:G:235:PHE:CG	5:M:31:ARG:HG2	2.17	0.79
1:D:510:TRP:HE3	1:D:675:GLN:HG2	1.45	0.79
1:E:653:GLN:HA	1:E:658:LEU:HB2	1.63	0.79
2:H:38:ILE:HD11	2:H:71:LEU:HB3	1.63	0.79
1:E:528:THR:HG21	1:E:641:LEU:HD23	1.64	0.79
1:E:625:ALA:HA	1:F:574:ILE:HD11	1.64	0.79
1:A:309:ALA:HB1	1:A:367:ILE:HG21	1.64	0.79
1:D:312:GLU:OE1	1:D:323:HIS:ND1	2.15	0.79
1:B:656:GLU:OE1	1:C:648:ARG:NH2	2.16	0.79
3:K:43:VAL:HA	4:L:212:LEU:HD13	1.65	0.79
1:C:618:PHE:CE2	1:D:614:ILE:HD11	2.18	0.79
1:E:490:PRO:HA	1:E:491:ALA:HB3	1.62	0.79
1:C:540:LEU:HB3	1:C:664:THR:HG22	1.63	0.79
1:F:564:PHE:O	1:F:598:SER:OG	2.00	0.79
1:E:407:LEU:HD11	1:E:426:ILE:HG23	1.64	0.78
1:E:606:GLU:OE2	1:E:646:THR:OG1	1.99	0.78
1:F:569:SER:OG	1:F:571:ASP:OD2	2.01	0.78
1:D:518:LEU:HD21	1:D:552:LEU:HD22	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:581:LYS:NZ	1:B:608:LEU:O	2.16	0.78
1:E:73:SER:HA	2:G:218:MET:SD	2.24	0.77
2:G:216:ILE:HD13	2:G:220:ASN:HB3	1.65	0.77
1:D:240:PHE:HD2	1:D:244:ILE:HG21	1.47	0.77
1:E:686:PHE:HB3	1:E:690:GLU:HB2	1.65	0.77
1:A:398:PRO:HG3	1:A:436:PHE:O	1.83	0.77
1:B:648:ARG:NH1	1:B:651:VAL:HG22	1.99	0.77
2:I:203:LYS:HE2	5:M:161:ARG:HH12	1.48	0.77
1:F:539:VAL:HB	1:F:643:ILE:HG12	1.65	0.77
2:G:158:ASN:O	2:G:162:ASN:ND2	2.17	0.77
1:D:399:ASP:O	1:D:403:ARG:N	2.17	0.76
1:B:300:ALA:O	1:B:304:LYS:HG2	1.85	0.76
1:C:496:GLN:O	1:C:498:ASP:N	2.19	0.76
1:C:236:ALA:HB1	1:D:453:MET:HB3	1.67	0.76
1:C:544:PRO:O	1:C:547:SER:OG	2.03	0.76
1:E:618:PHE:HZ	1:F:612:VAL:HG11	1.49	0.76
1:B:311:GLU:OE1	1:B:314:ARG:NE	2.15	0.76
1:E:300:ALA:O	1:E:304:LYS:HG2	1.86	0.76
1:E:196:ILE:HD13	1:E:196:ILE:H	1.51	0.76
1:E:652:LEU:HD23	1:E:657:MET:HB3	1.68	0.75
1:C:718:LEU:O	1:C:725:ARG:NH1	2.19	0.75
1:A:196:ILE:HG22	1:A:319:ASN:ND2	2.01	0.75
1:D:711:LEU:HA	1:D:714:ILE:HD12	1.68	0.75
1:A:557:ALA:O	1:A:560:SER:OG	2.03	0.75
1:C:256:ILE:HG13	1:C:370:ILE:HG22	1.67	0.75
1:F:300:ALA:O	1:F:304:LYS:HG2	1.87	0.75
1:D:527:GLN:HE21	1:E:715:GLU:HG3	1.52	0.74
1:D:510:TRP:CD2	1:D:670:ILE:HG22	2.21	0.74
1:D:240:PHE:HB3	1:D:244:ILE:HD13	1.68	0.74
1:B:624:GLN:NE2	1:C:610:ASP:O	2.20	0.74
1:F:437:SER:OG	1:F:440:GLU:HG2	1.87	0.74
1:C:18:LEU:HD13	1:C:139:SER:HB2	1.68	0.74
1:B:540:LEU:HD23	1:B:661:PHE:CD1	2.23	0.74
1:C:687:LYS:N	1:C:690:GLU:OE2	2.20	0.74
1:D:543:GLY:H	1:D:549:LYS:HD3	1.52	0.74
1:A:672:THR:OG1	1:A:675:GLN:OE1	2.05	0.74
1:E:624:GLN:HG3	1:F:610:ASP:OD2	1.86	0.74
2:G:268:SER:HA	2:H:233:PRO:CG	2.18	0.74
1:E:246:GLU:O	1:F:413:ARG:NH1	2.19	0.74
1:D:573:MET:SD	1:D:581:LYS:HD3	2.28	0.74
1:F:613:PRO:HD3	1:F:648:ARG:HH12	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:PHE:CE1	1:A:566:LYS:HB2	2.22	0.74
2:G:128:ALA:HB2	2:G:144:HIS:HB2	1.69	0.73
1:A:262:PRO:HG2	1:A:374:ASN:OD1	1.87	0.73
1:B:627:LEU:HD21	1:B:657:MET:HG3	1.70	0.73
1:B:713:LEU:HD22	1:B:732:LEU:HB3	1.70	0.73
1:D:301:ASN:HA	1:D:304:LYS:HD3	1.69	0.73
1:E:585:MET:HA	1:E:588:ILE:HD12	1.68	0.73
1:C:596:GLN:HA	1:C:638:ARG:HD3	1.69	0.73
1:D:545:PRO:HD3	1:D:647:SER:OG	1.88	0.73
1:D:358:ILE:HD12	1:D:388:ARG:HB3	1.71	0.73
1:B:67:ARG:HH11	2:I:218:MET:HG2	1.54	0.73
1:A:285:VAL:HG13	1:A:326:ILE:HD11	1.70	0.73
1:E:240:PHE:CZ	1:F:456:HIS:HB2	2.23	0.72
1:E:240:PHE:HZ	1:F:456:HIS:CB	2.01	0.72
1:E:624:GLN:OE1	1:E:624:GLN:HA	1.89	0.72
5:M:177:GLN:HA	5:M:180:ARG:NH1	2.04	0.72
1:C:691:ARG:HA	1:C:694:ILE:HD12	1.71	0.72
1:F:565:ILE:HG23	1:F:599:CYS:HB3	1.71	0.72
1:A:423:ASP:HB2	1:A:480:PHE:CB	2.19	0.72
1:F:194:ASN:ND2	1:F:312:GLU:HG2	2.05	0.72
1:B:12:PRO:HG2	1:B:23:VAL:HG11	1.72	0.72
1:A:713:LEU:HD21	1:A:732:LEU:HB3	1.69	0.72
1:E:549:LYS:HA	1:E:552:LEU:HD12	1.71	0.72
1:F:264:CYS:SG	1:F:395:ILE:HG22	2.29	0.72
1:F:311:GLU:OE1	1:F:314:ARG:NE	2.21	0.72
2:G:228:TYR:OH	2:G:237:ASP:OD1	2.07	0.72
1:F:517:VAL:HG13	1:F:665:ILE:HG21	1.69	0.72
1:E:706:GLY:O	1:E:710:LEU:N	2.19	0.72
1:E:586:LYS:NZ	1:F:574:ILE:O	2.21	0.72
1:B:240:PHE:CD2	1:B:244:ILE:HG21	2.23	0.72
1:A:326:ILE:HG22	1:A:370:ILE:HG12	1.71	0.71
1:A:456:HIS:HB2	1:F:240:PHE:CZ	2.26	0.71
2:J:246:LYS:NZ	2:J:258:SER:OG	2.22	0.71
1:F:721:ASP:HB2	1:F:724:TYR:HD1	1.54	0.71
1:C:513:PRO:O	1:C:516:ARG:HG2	1.90	0.71
1:E:307:ALA:O	1:E:311:GLU:HG2	1.90	0.71
1:C:564:PHE:O	1:C:598:SER:OG	2.08	0.71
3:K:59:LYS:HB3	5:M:178:ILE:HG21	1.71	0.71
1:E:620:ASN:O	1:E:624:GLN:HG2	1.89	0.71
1:D:73:SER:OG	2:J:217:ASP:OD1	2.08	0.71
1:C:676:LEU:HD12	1:C:705:ILE:HG21	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:10:ARG:HG3	1:F:67:ARG:NH2	2.04	0.71
1:D:627:LEU:HD21	1:D:657:MET:HG3	1.71	0.71
1:C:331:ASP:HA	1:C:379:ILE:HD11	1.72	0.71
1:E:628:VAL:HB	1:F:574:ILE:HD12	1.72	0.71
1:F:525:VAL:HG13	1:F:562:PHE:CE1	2.25	0.71
3:K:50:VAL:O	3:K:54:LEU:HD23	1.90	0.71
1:C:576:PHE:HB2	1:C:581:LYS:HE3	1.72	0.71
2:G:207:PHE:HB2	2:G:240:GLU:HG2	1.71	0.71
1:D:513:PRO:HA	1:D:516:ARG:HG2	1.71	0.71
1:E:327:PHE:HB2	1:E:330:ILE:HG22	1.73	0.71
1:F:125:PHE:HA	1:F:128:GLN:NE2	2.05	0.70
1:B:74:ILE:H	2:I:218:MET:HE3	1.56	0.70
1:E:437:SER:O	1:E:440:GLU:HB2	1.91	0.70
1:E:526:GLN:NE2	1:F:719:GLN:O	2.23	0.70
1:F:549:LYS:HE2	1:F:645:THR:HB	1.72	0.70
1:D:125:PHE:HA	1:D:128:GLN:NE2	2.06	0.70
1:F:317:GLY:O	1:F:318:ALA:CB	2.39	0.70
1:B:533:ARG:HG3	1:B:534:THR:H	1.57	0.70
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.74	0.70
1:E:240:PHE:CD2	1:E:244:ILE:HG21	2.25	0.70
1:F:263:GLY:CA	1:F:437:SER:HB2	2.18	0.70
1:A:549:LYS:HE3	1:A:646:THR:C	2.12	0.70
1:C:695:ALA:HB1	1:C:699:LYS:HE3	1.74	0.70
1:A:236:ALA:HB1	1:B:453:MET:HB3	1.74	0.70
1:F:606:GLU:N	1:F:606:GLU:OE1	2.22	0.70
2:G:235:PHE:CD1	5:M:31:ARG:HG2	2.27	0.69
1:D:240:PHE:CD2	1:D:244:ILE:HG21	2.26	0.69
5:M:179:ASP:HA	5:M:182:MET:HE3	1.74	0.69
2:I:201:SER:HB3	5:M:165:LEU:HD13	1.72	0.69
1:A:113:ASP:OD2	1:A:316:LEU:HD21	1.92	0.69
1:F:695:ALA:HB1	1:F:699:LYS:HE3	1.75	0.69
1:C:318:ALA:O	1:C:319:ASN:ND2	2.26	0.69
1:B:526:GLN:NE2	1:C:719:GLN:HB3	2.07	0.69
1:A:316:LEU:O	1:A:320:SER:OG	2.10	0.69
1:C:125:PHE:HA	1:C:128:GLN:NE2	2.07	0.69
1:D:632:LYS:HZ1	1:E:571:ASP:HB3	1.57	0.69
1:B:18:LEU:HD13	1:B:139:SER:HB3	1.74	0.69
2:G:72:HIS:HE1	2:G:80:ASP:HB2	1.58	0.69
1:A:353:GLN:HA	1:B:288:PRO:CG	2.21	0.69
1:D:510:TRP:CE3	1:D:670:ILE:HG22	2.27	0.69
1:F:187:LYS:HB2	1:F:191:SER:HB3	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:VAL:O	1:A:355:LEU:HG	1.92	0.69
1:E:625:ALA:O	1:E:629:LEU:HG	1.92	0.69
1:E:326:ILE:HG22	1:E:370:ILE:HG13	1.75	0.69
1:F:303:ARG:HG3	1:F:357:LYS:HE2	1.74	0.69
2:G:108:ILE:HD11	2:G:127:ILE:HG13	1.73	0.69
1:B:538:SER:HB3	1:B:661:PHE:CD2	2.27	0.68
1:A:677:LEU:HD21	1:A:695:ALA:HA	1.73	0.68
2:I:101:ILE:HG21	2:I:135:LEU:HD11	1.74	0.68
1:E:563:PRO:HG2	1:E:595:SER:OG	1.94	0.68
1:E:510:TRP:CZ3	1:E:670:ILE:HG13	2.28	0.68
1:F:397:LEU:HB3	1:F:398:PRO:CD	2.22	0.68
1:A:50:ARG:NH1	2:H:293:ASP:O	2.26	0.68
1:C:64:LEU:HA	1:C:67:ARG:HE	1.58	0.68
2:H:235:PHE:HD1	4:L:204:LYS:HG3	1.58	0.68
1:D:528:THR:OG1	1:D:537:VAL:HG21	1.94	0.68
1:C:624:GLN:NE2	1:D:610:ASP:HB2	2.09	0.68
1:A:125:PHE:HA	1:A:128:GLN:NE2	2.08	0.68
1:D:686:PHE:HE1	1:D:714:ILE:HG23	1.59	0.68
1:A:610:ASP:OD1	1:F:620:ASN:ND2	2.26	0.68
1:E:586:LYS:HA	1:E:589:PHE:CD2	2.28	0.68
1:B:303:ARG:HG3	1:B:357:LYS:HE2	1.74	0.68
1:F:538:SER:HB3	1:F:662:SER:H	1.57	0.68
3:K:39:VAL:HG11	4:L:209:ILE:HG12	1.74	0.67
1:A:50:ARG:CZ	2:H:293:ASP:OD1	2.42	0.67
1:A:683:LEU:HB3	1:A:685:ASN:ND2	2.08	0.67
1:D:326:ILE:HG22	1:D:370:ILE:HG13	1.75	0.67
1:A:627:LEU:HD13	1:B:607:ARG:HH12	1.58	0.67
1:B:528:THR:O	1:B:639:LYS:HD2	1.93	0.67
1:D:620:ASN:O	1:D:624:GLN:HG2	1.93	0.67
1:A:553:ALA:HA	1:A:556:ILE:HD12	1.77	0.67
1:C:386:PRO:HD2	1:D:440:GLU:OE1	1.94	0.67
2:G:243:LEU:HD13	2:G:266:TYR:HB2	1.75	0.67
2:H:72:HIS:HE1	2:H:80:ASP:HB2	1.59	0.67
1:A:602:VAL:HG12	1:A:605:ILE:HG12	1.76	0.67
1:E:106:ASN:HB3	1:E:143:LYS:NZ	2.09	0.67
2:J:149:ALA:HB2	2:J:164:CYS:HB2	1.77	0.67
1:C:611:TYR:CE1	1:C:616:PRO:HB2	2.29	0.67
3:K:50:VAL:O	3:K:53:VAL:HG12	1.94	0.67
1:A:607:ARG:HD3	1:F:624:GLN:HE22	1.60	0.67
1:B:245:VAL:O	1:B:249:GLY:N	2.27	0.67
1:D:12:PRO:HG2	1:D:23:VAL:HG11	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:630:LEU:HD11	1:C:661:PHE:CE1	2.30	0.67
1:C:690:GLU:HB2	1:C:726:VAL:HG21	1.76	0.67
1:E:508:ILE:HB	1:E:682:LEU:HD13	1.76	0.67
2:G:231:LEU:HB2	2:G:234:ALA:HB3	1.76	0.67
1:F:634:PRO:HB2	1:F:638:ARG:HG3	1.77	0.67
1:B:546:HIS:O	1:B:547:SER:OG	2.13	0.67
1:F:258:LEU:HB3	1:F:395:ILE:HD11	1.75	0.67
1:D:632:LYS:NZ	1:E:571:ASP:HB3	2.10	0.67
1:E:553:ALA:HA	1:E:556:ILE:HD12	1.76	0.67
1:A:12:PRO:HG2	1:A:23:VAL:HG11	1.77	0.67
1:D:527:GLN:HE22	1:E:715:GLU:C	1.98	0.67
1:E:64:LEU:N	1:E:67:ARG:HH21	1.93	0.67
1:E:686:PHE:CE1	1:E:714:ILE:HG23	2.28	0.67
1:A:313:GLN:NE2	1:A:365:ASN:O	2.28	0.67
2:I:124:HIS:HE1	2:I:147:GLN:HB3	1.60	0.67
1:C:358:ILE:CB	1:C:388:ARG:HG3	2.25	0.67
1:D:544:PRO:O	1:D:547:SER:HB3	1.95	0.66
1:A:508:ILE:HB	1:A:682:LEU:HD22	1.76	0.66
1:C:285:VAL:HG13	1:C:326:ILE:HD11	1.76	0.66
1:E:604:ASP:HB3	1:E:607:ARG:HB3	1.78	0.66
1:F:245:VAL:O	1:F:249:GLY:N	2.29	0.66
1:D:319:ASN:HB3	1:D:320:SER:HB2	1.77	0.66
2:G:233:PRO:HB3	2:J:268:SER:O	1.94	0.66
4:L:237:VAL:HG21	5:M:60:VAL:HG13	1.76	0.66
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.77	0.66
1:D:533:ARG:HD2	1:E:505:ASN:ND2	2.10	0.66
1:D:513:PRO:HB3	1:D:516:ARG:HE	1.59	0.66
2:H:38:ILE:HG23	2:H:75:LEU:HD12	1.76	0.66
1:D:695:ALA:HB1	1:D:699:LYS:HE3	1.78	0.66
1:B:307:ALA:O	1:B:311:GLU:HG2	1.94	0.66
1:B:449:GLN:O	1:B:453:MET:HG2	1.95	0.66
1:D:605:ILE:HD11	1:D:644:GLY:HA3	1.78	0.66
1:E:64:LEU:HB3	1:E:65:PRO:HD3	1.78	0.66
1:B:73:SER:O	1:B:76:GLN:HG2	1.96	0.66
1:F:224:ASP:O	1:F:228:SER:HB2	1.95	0.66
1:C:616:PRO:HG2	1:D:614:ILE:HD13	1.77	0.66
1:A:653:GLN:NE2	1:A:653:GLN:O	2.29	0.66
2:J:201:SER:HB2	5:M:44:ILE:HD13	1.78	0.66
1:B:326:ILE:HG22	1:B:370:ILE:HG13	1.77	0.66
1:C:618:PHE:HZ	1:D:612:VAL:HG11	1.61	0.66
1:C:48:THR:HG21	1:C:128:GLN:HG2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:PHE:HA	1:B:128:GLN:NE2	2.10	0.66
1:D:245:VAL:O	1:D:249:GLY:N	2.29	0.66
1:A:628:VAL:HG11	1:B:571:ASP:HA	1.78	0.66
1:F:518:LEU:H	1:F:518:LEU:HD12	1.61	0.66
4:L:202:ILE:HD12	5:M:25:SER:HB3	1.78	0.65
1:E:681:GLU:HA	1:E:691:ARG:HE	1.59	0.65
1:D:230:ILE:HD11	1:D:256:ILE:HD13	1.78	0.65
1:E:670:ILE:HG22	1:E:672:THR:H	1.60	0.65
1:F:12:PRO:HG2	1:F:23:VAL:HG11	1.78	0.65
1:F:535:PRO:HA	1:F:639:LYS:HG2	1.78	0.65
2:I:216:ILE:HG12	2:I:220:ASN:HB2	1.77	0.65
1:F:317:GLY:O	1:F:318:ALA:HB2	1.96	0.65
2:G:188:VAL:HG13	2:G:205:TYR:HD2	1.61	0.65
1:A:710:LEU:O	1:A:714:ILE:HG13	1.96	0.65
1:E:680:LEU:HD13	1:E:694:ILE:HD13	1.77	0.65
1:C:436:PHE:HB3	1:C:440:GLU:OE1	1.96	0.65
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.78	0.65
1:A:549:LYS:HE3	1:A:646:THR:O	1.97	0.65
2:G:235:PHE:CD2	5:M:31:ARG:HA	2.31	0.65
5:M:56:GLN:O	5:M:60:VAL:HG23	1.97	0.65
1:D:686:PHE:CE1	1:D:714:ILE:HG23	2.32	0.65
1:C:711:LEU:O	1:C:715:GLU:HG2	1.97	0.65
5:M:26:LEU:HB2	5:M:146:MET:HE2	1.79	0.65
2:J:72:HIS:HE1	2:J:80:ASP:HB2	1.61	0.65
1:A:327:PHE:CD1	1:A:330:ILE:HG22	2.32	0.65
1:E:527:GLN:HE22	1:F:716:MET:HG2	1.60	0.65
1:B:67:ARG:NH1	2:I:218:MET:HG2	2.12	0.65
1:D:299:GLU:OE1	1:D:350:VAL:HG13	1.97	0.65
1:A:720:MET:O	1:A:725:ARG:NE	2.22	0.65
1:E:513:PRO:HA	1:E:516:ARG:HG2	1.77	0.65
1:C:649:LYS:HE2	1:C:658:LEU:HD13	1.78	0.65
1:B:589:PHE:HD2	1:B:629:LEU:HD22	1.62	0.65
1:E:12:PRO:HG2	1:E:23:VAL:HG11	1.79	0.65
1:B:224:ASP:O	1:B:228:SER:HB2	1.97	0.65
1:E:697:GLN:HG3	1:E:730:LEU:HD11	1.79	0.65
1:A:521:GLY:O	1:A:525:VAL:HG23	1.97	0.65
1:E:648:ARG:NE	1:E:650:ASP:OD1	2.26	0.65
1:A:550:THR:HA	1:A:645:THR:HG21	1.79	0.65
1:A:503:ILE:CG2	1:A:506:GLY:HA2	2.27	0.64
1:F:635:PRO:O	1:F:638:ARG:HG2	1.96	0.64
1:F:410:HIS:O	1:F:414:MET:HG2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:VAL:HG13	1:A:643:ILE:HA	1.78	0.64
1:A:124:GLN:HE21	1:A:125:PHE:HE1	1.43	0.64
2:H:101:ILE:HG21	2:H:135:LEU:HD11	1.79	0.64
1:B:358:ILE:HD12	1:B:388:ARG:HB3	1.79	0.64
1:B:563:PRO:HD2	1:B:597:LEU:HB2	1.79	0.64
1:C:728:LYS:O	1:C:732:LEU:HG	1.97	0.64
1:B:540:LEU:HD11	1:B:649:LYS:NZ	2.12	0.64
3:K:70:LEU:HD11	5:M:192:ILE:HD12	1.77	0.64
1:F:538:SER:HG	1:F:661:PHE:HD1	1.46	0.64
1:A:678:GLU:O	1:A:682:LEU:HD12	1.98	0.64
1:A:502:TYR:CE2	1:A:567:ILE:HG21	2.31	0.64
1:D:713:LEU:HD21	1:D:732:LEU:HB2	1.79	0.64
1:C:590:ASP:HA	1:C:593:TYR:CD2	2.33	0.64
1:F:326:ILE:HG22	1:F:370:ILE:HG13	1.80	0.64
1:B:240:PHE:CE1	1:C:457:ILE:HD11	2.33	0.64
1:B:361:VAL:O	1:C:271:ARG:HD2	1.98	0.64
1:E:602:VAL:O	1:E:644:GLY:HA2	1.98	0.64
1:F:554:ALA:O	1:F:558:GLU:HG3	1.98	0.64
1:D:256:ILE:CG1	1:D:370:ILE:HG22	2.28	0.64
1:F:612:VAL:HG12	1:F:617:ARG:HB2	1.80	0.64
1:A:196:ILE:HB	1:A:319:ASN:O	1.98	0.64
2:H:267:ASP:O	2:I:233:PRO:HB3	1.98	0.64
1:C:240:PHE:CD2	1:C:244:ILE:HG21	2.30	0.63
1:C:18:LEU:HA	1:C:137:VAL:HG23	1.79	0.63
2:J:235:PHE:CD1	5:M:152:GLN:HG2	2.33	0.63
2:I:155:GLU:O	5:M:176:ARG:NH2	2.31	0.63
1:F:589:PHE:HD2	1:F:629:LEU:HD13	1.63	0.63
1:D:105:LYS:O	1:D:105:LYS:HD2	1.98	0.63
1:A:353:GLN:HE21	1:A:357:LYS:HG2	1.63	0.63
1:A:196:ILE:HG22	1:A:319:ASN:HD22	1.63	0.63
1:A:617:ARG:HH11	1:A:617:ARG:HG3	1.63	0.63
1:D:680:LEU:HB2	1:D:691:ARG:HH21	1.63	0.63
1:C:375:ARG:HH12	1:C:378:LEU:HG	1.64	0.63
1:E:284:VAL:HG23	1:E:324:ILE:O	1.98	0.63
1:B:289:GLU:O	1:B:291:LEU:N	2.26	0.63
1:D:713:LEU:HD21	1:D:732:LEU:CB	2.27	0.63
1:B:589:PHE:HE1	1:B:600:VAL:HG11	1.63	0.63
1:F:407:LEU:HD11	1:F:426:ILE:HG23	1.81	0.63
1:A:457:ILE:HD12	1:F:232:ARG:HH21	1.64	0.63
3:K:46:MET:O	3:K:50:VAL:HG23	1.97	0.63
1:B:67:ARG:HD2	2:I:218:MET:HE2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:175:LEU:HD23	2:G:177:GLN:HE21	1.63	0.63
1:C:245:VAL:O	1:C:249:GLY:N	2.30	0.63
1:E:125:PHE:HA	1:E:128:GLN:NE2	2.14	0.63
2:I:175:LEU:HD23	2:I:177:GLN:HE21	1.63	0.63
1:A:330:ILE:HG13	1:A:373:THR:HB	1.78	0.63
1:D:651:VAL:O	1:D:655:MET:HG2	1.99	0.63
1:A:258:LEU:HA	1:A:393:MET:O	1.99	0.63
2:G:271:ARG:NH2	2:H:234:ALA:HB2	2.13	0.63
1:E:685:ASN:HB3	1:E:718:LEU:HD11	1.78	0.63
1:E:654:GLU:HG2	1:F:614:ILE:HD11	1.81	0.63
1:D:547:SER:OG	1:D:549:LYS:HG3	1.99	0.63
1:E:311:GLU:OE1	1:E:314:ARG:NE	2.29	0.63
1:A:355:LEU:HA	1:A:358:ILE:HD11	1.80	0.63
1:E:536:LEU:HD12	1:E:640:LEU:O	1.99	0.63
1:F:525:VAL:HG13	1:F:562:PHE:HE1	1.63	0.63
1:D:40:SER:HB2	1:D:41:PRO:HD2	1.81	0.63
2:H:236:SER:OG	4:L:211:GLU:HG2	1.99	0.63
1:F:106:ASN:HB3	1:F:143:LYS:NZ	2.13	0.63
1:E:264:CYS:SG	1:E:395:ILE:HG21	2.39	0.63
1:D:593:TYR:O	1:D:638:ARG:HG2	1.98	0.63
1:D:67:ARG:HH12	1:D:74:ILE:HD11	1.63	0.63
1:F:545:PRO:HA	1:F:547:SER:N	2.14	0.62
1:F:542:GLU:HB2	1:F:666:HIS:HA	1.80	0.62
1:F:550:THR:HA	1:F:645:THR:HG21	1.80	0.62
1:C:377:ASP:OD2	1:C:377:ASP:N	2.32	0.62
1:F:327:PHE:HB2	1:F:330:ILE:CG2	2.29	0.62
2:G:213:HIS:ND1	2:G:216:ILE:HD12	2.13	0.62
1:D:527:GLN:NE2	1:E:715:GLU:O	2.28	0.62
1:C:546:HIS:HA	1:C:708:LYS:HD3	1.81	0.62
1:A:242:PRO:HD2	1:A:243:GLU:CD	2.19	0.62
1:C:521:GLY:HA3	1:C:556:ILE:HD13	1.80	0.62
1:A:267:THR:OG1	1:A:328:ASP:OD2	2.16	0.62
1:D:677:LEU:O	1:D:691:ARG:NH2	2.32	0.62
1:D:657:MET:HG2	1:D:661:PHE:CE2	2.34	0.62
1:A:382:ALA:O	1:A:385:ARG:HG2	1.99	0.62
1:E:240:PHE:HE1	1:F:457:ILE:HD12	1.64	0.62
1:E:398:PRO:HG3	1:E:436:PHE:O	2.00	0.62
1:B:327:PHE:HB2	1:B:330:ILE:HG22	1.81	0.62
1:D:436:PHE:HE2	1:D:444:LEU:HD12	1.64	0.62
1:F:404:LEU:O	1:F:408:HIS:HB2	1.99	0.62
1:A:503:ILE:HG23	1:A:506:GLY:CA	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:538:SER:OG	1:E:661:PHE:HA	1.99	0.62
1:B:670:ILE:HG23	1:B:675:GLN:HB2	1.80	0.62
1:A:540:LEU:HD11	1:A:646:THR:HG22	1.82	0.62
1:D:657:MET:HG2	1:D:661:PHE:HE2	1.65	0.62
1:F:354:LEU:O	1:F:358:ILE:HG12	2.00	0.62
1:E:224:ASP:O	1:E:228:SER:HB2	2.00	0.62
1:A:104:LYS:HA	1:A:107:ILE:CD1	2.29	0.62
1:B:407:LEU:CD1	1:B:426:ILE:HG23	2.30	0.62
1:E:303:ARG:HG3	1:E:357:LYS:HE2	1.80	0.62
2:G:104:LEU:HB3	2:G:127:ILE:HD12	1.80	0.62
2:G:231:LEU:HD22	2:J:271:ARG:HH11	1.63	0.62
1:F:64:LEU:HB3	1:F:65:PRO:HD3	1.81	0.62
1:E:404:LEU:O	1:E:408:HIS:HB2	2.00	0.62
1:F:513:PRO:O	1:F:517:VAL:HG23	1.99	0.62
2:I:128:ALA:HB2	2:I:144:HIS:HB2	1.81	0.62
2:G:267:ASP:O	2:H:233:PRO:HG2	1.99	0.62
1:E:674:GLU:HA	1:E:677:LEU:HD12	1.82	0.62
1:E:358:ILE:HD12	1:E:388:ARG:HB3	1.81	0.61
1:C:289:GLU:O	1:C:291:LEU:N	2.27	0.61
2:I:47:ARG:O	2:I:50:ASN:HB3	2.00	0.61
1:E:652:LEU:CD2	1:E:657:MET:HB3	2.30	0.61
1:F:535:PRO:HB2	1:F:536:LEU:HD13	1.83	0.61
1:E:693:THR:O	1:E:697:GLN:NE2	2.18	0.61
2:J:112:THR:HG23	2:J:117:PHE:HE1	1.64	0.61
1:D:521:GLY:O	1:D:525:VAL:HG23	2.00	0.61
1:A:490:PRO:HA	1:A:491:ALA:CB	2.19	0.61
1:B:542:GLU:HB3	1:B:649:LYS:HG3	1.82	0.61
1:A:624:GLN:HG3	1:B:610:ASP:CB	2.29	0.61
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.82	0.61
1:F:529:LYS:HG3	1:F:597:LEU:HD11	1.81	0.61
1:D:604:ASP:HB3	1:D:607:ARG:CB	2.31	0.61
1:A:527:GLN:HB2	1:B:719:GLN:HG3	1.82	0.61
1:B:437:SER:O	1:B:440:GLU:HB2	1.99	0.61
1:E:710:LEU:O	1:E:714:ILE:HG13	2.01	0.61
1:E:623:LEU:HD23	1:E:624:GLN:NE2	2.16	0.61
1:D:527:GLN:NE2	1:E:716:MET:HA	2.15	0.61
1:C:295:VAL:O	1:D:294:TYR:HB2	2.00	0.61
1:B:728:LYS:HE3	1:B:732:LEU:HD21	1.83	0.61
1:C:540:LEU:HD23	1:C:649:LYS:HE3	1.83	0.61
1:C:511:GLY:HA3	1:C:513:PRO:HD2	1.82	0.61
1:B:499:TYR:HA	1:B:502:TYR:CD2	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:142:ILE:HG23	2:J:168:VAL:HG13	1.83	0.61
1:E:245:VAL:O	1:E:249:GLY:N	2.33	0.61
2:J:200:TYR:HB3	5:M:40:LYS:NZ	2.15	0.61
1:F:562:PHE:HE2	1:F:597:LEU:HD12	1.65	0.61
1:A:299:GLU:HG2	1:A:353:GLN:HG2	1.82	0.61
1:D:728:LYS:HE3	1:D:732:LEU:HD11	1.82	0.61
3:K:63:LEU:HD13	5:M:182:MET:HA	1.81	0.61
1:C:536:LEU:HD12	1:C:640:LEU:HB3	1.83	0.61
1:D:46:ILE:HD12	1:D:174:VAL:HG11	1.82	0.61
3:K:87:LYS:HE3	5:M:204:GLY:HA2	1.82	0.61
2:H:120:ALA:O	2:H:124:HIS:HB2	2.01	0.60
1:D:234:ALA:HA	1:D:253:VAL:HG11	1.83	0.60
1:D:513:PRO:O	1:D:516:ARG:HG2	2.01	0.60
1:D:534:THR:OG1	1:E:715:GLU:HG2	2.01	0.60
1:D:300:ALA:O	1:D:303:ARG:HB3	2.01	0.60
1:A:247:GLN:O	1:B:414:MET:HE3	2.01	0.60
2:J:96:ASP:OD1	2:J:97:PRO:HD3	2.01	0.60
1:A:238:ARG:HA	1:A:252:HIS:CE1	2.36	0.60
1:A:625:ALA:O	1:A:629:LEU:HG	2.00	0.60
1:A:671:ALA:HA	1:A:703:VAL:O	2.01	0.60
1:B:538:SER:HB3	1:B:661:PHE:HD2	1.66	0.60
1:D:64:LEU:HD21	2:J:290:ASP:OD1	2.00	0.60
1:F:538:SER:O	1:F:663:THR:HG22	2.01	0.60
1:D:383:LEU:O	1:D:389:LEU:HB2	2.00	0.60
1:B:589:PHE:HE2	1:B:629:LEU:HB3	1.65	0.60
1:F:411:THR:O	1:F:414:MET:HB2	2.02	0.60
1:A:104:LYS:NZ	1:A:104:LYS:HB3	2.16	0.60
1:A:715:GLU:HG3	1:F:527:GLN:HE21	1.66	0.60
1:F:18:LEU:HD13	1:F:139:SER:OG	2.00	0.60
1:F:95:MET:HG3	1:F:152:ILE:HG12	1.82	0.60
2:J:160:SER:OG	5:M:52:GLU:OE2	2.18	0.60
1:D:116:LYS:HB3	1:D:116:LYS:NZ	2.16	0.60
1:C:399:ASP:O	1:C:403:ARG:N	2.30	0.60
2:H:207:PHE:HB2	2:H:240:GLU:HG2	1.82	0.60
1:E:640:LEU:HD12	1:E:641:LEU:N	2.17	0.60
1:F:521:GLY:O	1:F:525:VAL:HG23	2.02	0.60
1:B:404:LEU:O	1:B:408:HIS:HB2	2.01	0.60
1:D:256:ILE:HG22	1:D:391:VAL:HG12	1.83	0.60
1:E:397:LEU:HD13	1:E:398:PRO:HD2	1.83	0.60
1:F:650:ASP:O	1:F:653:GLN:HG3	2.02	0.60
1:B:385:ARG:HH21	1:B:388:ARG:CZ	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:621:LEU:HD11	1:C:575:GLY:HA2	1.82	0.60
1:B:548:GLY:O	1:B:552:LEU:HB2	2.01	0.60
5:M:40:LYS:HG3	5:M:163:MET:CE	2.32	0.60
1:E:627:LEU:HG	1:E:657:MET:HE1	1.82	0.60
1:D:546:HIS:ND1	1:D:709:LYS:HD3	2.17	0.60
1:C:579:THR:O	1:C:583:GLN:HG2	2.02	0.60
1:A:355:LEU:HB3	1:A:388:ARG:NH1	2.17	0.60
1:D:436:PHE:CE2	1:D:444:LEU:HD12	2.37	0.60
1:C:589:PHE:CD2	1:C:629:LEU:HD13	2.37	0.60
1:E:399:ASP:O	1:E:403:ARG:N	2.32	0.60
2:H:149:ALA:HB2	2:H:164:CYS:HB2	1.82	0.60
1:B:284:VAL:HG23	1:B:324:ILE:O	2.02	0.60
1:B:576:PHE:HB3	1:B:580:ALA:HB3	1.83	0.60
1:F:307:ALA:O	1:F:311:GLU:HG2	2.01	0.60
1:D:236:ALA:HB1	1:E:453:MET:HG3	1.83	0.60
1:E:95:MET:HG3	1:E:152:ILE:HG12	1.83	0.60
1:A:687:LYS:N	1:A:690:GLU:OE1	2.33	0.60
4:L:207:ASN:HA	4:L:210:ARG:HB2	1.83	0.60
1:D:528:THR:OG1	1:D:641:LEU:HD12	2.02	0.60
2:I:53:LYS:HE3	2:J:117:PHE:CE2	2.36	0.60
1:E:399:ASP:HB2	1:E:402:GLY:H	1.67	0.60
1:A:270:ALA:O	1:A:273:ILE:HG22	2.02	0.60
2:J:256:VAL:HG11	2:J:288:GLN:HG2	1.84	0.60
1:C:613:PRO:HD3	1:C:648:ARG:HH22	1.66	0.59
1:D:239:VAL:HG13	1:D:240:PHE:CD1	2.37	0.59
1:D:648:ARG:HG3	1:D:651:VAL:HG23	1.84	0.59
1:A:102:LEU:HD23	1:A:144:LEU:HB3	1.84	0.59
5:M:81:LEU:HD23	5:M:202:MET:SD	2.42	0.59
1:A:670:ILE:HG23	1:A:675:GLN:HB2	1.84	0.59
1:F:194:ASN:HD21	1:F:312:GLU:HG2	1.65	0.59
1:D:249:GLY:HA3	1:E:413:ARG:NH1	2.17	0.59
1:E:532:ASP:OD2	1:E:533:ARG:N	2.34	0.59
1:A:630:LEU:HD11	1:A:657:MET:HE3	1.84	0.59
2:G:200:TYR:CE2	5:M:38:GLU:HG2	2.38	0.59
1:B:65:PRO:HG2	1:B:137:VAL:HG13	1.84	0.59
1:D:12:PRO:HB3	1:D:54:SER:OG	2.03	0.59
1:D:625:ALA:O	1:D:629:LEU:HG	2.02	0.59
1:A:720:MET:HG3	1:A:728:LYS:HD2	1.85	0.59
1:F:428:GLU:O	1:F:432:GLU:HG2	2.02	0.59
2:J:232:PHE:C	2:J:234:ALA:H	2.05	0.59
1:E:623:LEU:HD23	1:E:624:GLN:HE22	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:196:ILE:N	1:E:196:ILE:HD13	2.16	0.59
1:E:67:ARG:NH1	2:G:217:ASP:OD2	2.36	0.59
1:E:507:ILE:CD1	1:E:555:LYS:HB2	2.32	0.59
1:D:404:LEU:HD11	1:D:427:LYS:HE3	1.84	0.59
1:D:407:LEU:HG	1:D:441:LEU:HD11	1.85	0.59
2:J:230:GLU:HG2	2:J:231:LEU:N	2.18	0.59
1:E:589:PHE:CD2	1:E:629:LEU:HD21	2.37	0.59
2:G:271:ARG:NH2	2:H:231:LEU:HB2	2.18	0.59
1:E:705:ILE:HD12	1:E:713:LEU:HD12	1.84	0.59
3:K:43:VAL:HG22	4:L:212:LEU:HB2	1.84	0.59
1:B:570:PRO:HD3	1:B:603:ASP:HB3	1.83	0.59
1:D:628:VAL:HG11	1:E:574:ILE:HG21	1.84	0.59
1:B:171:LYS:HB2	1:B:171:LYS:NZ	2.17	0.59
1:D:268:LEU:HA	1:D:271:ARG:HD2	1.85	0.59
1:F:114:THR:HG21	1:F:200:LYS:HG2	1.85	0.59
2:I:188:VAL:HG13	2:I:205:TYR:HD2	1.68	0.59
4:L:237:VAL:HG11	5:M:60:VAL:HA	1.84	0.59
1:C:711:LEU:HA	1:C:714:ILE:HD12	1.85	0.59
2:J:69:ALA:HB1	2:J:85:PHE:CE1	2.38	0.59
1:C:334:CYS:HA	1:C:351:VAL:HG22	1.85	0.59
1:A:598:SER:OG	1:A:640:LEU:HD12	2.02	0.59
1:C:407:LEU:CD1	1:C:426:ILE:HG23	2.27	0.59
1:B:289:GLU:C	1:B:291:LEU:H	2.05	0.59
5:M:170:GLU:HG3	5:M:174:GLN:HE21	1.67	0.59
5:M:42:ALA:HA	5:M:45:ARG:HD3	1.84	0.59
2:G:268:SER:O	2:H:233:PRO:HB3	2.02	0.59
1:F:380:ASP:OD1	1:F:382:ALA:N	2.36	0.59
2:H:271:ARG:NH1	2:I:234:ALA:HB2	2.11	0.59
1:C:624:GLN:O	1:C:628:VAL:HG23	2.03	0.59
2:G:115:GLY:HA3	2:J:50:ASN:HD21	1.66	0.59
1:A:536:LEU:HD23	1:A:634:PRO:HD3	1.85	0.59
1:A:40:SER:HB2	1:A:41:PRO:HD2	1.85	0.59
1:E:536:LEU:HD22	1:E:634:PRO:HD3	1.85	0.58
1:C:542:GLU:CB	1:C:649:LYS:HD3	2.33	0.58
1:B:570:PRO:HG3	1:B:608:LEU:HD23	1.84	0.58
2:H:235:PHE:CE1	4:L:204:LYS:HA	2.37	0.58
2:I:80:ASP:OD1	5:M:66:HIS:CD2	2.56	0.58
2:H:116:ARG:NH1	5:M:186:ASP:OD2	2.36	0.58
5:M:153:VAL:O	5:M:157:ILE:HD13	2.02	0.58
1:C:614:ILE:C	1:C:616:PRO:HA	2.22	0.58
2:H:230:GLU:HG2	2:H:231:LEU:N	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:686:PHE:CE2	1:A:714:ILE:HG12	2.32	0.58
1:E:659:ASN:HD21	1:F:545:PRO:HB2	1.68	0.58
1:B:540:LEU:HA	1:B:644:GLY:O	2.03	0.58
1:A:257:LEU:HG	1:A:389:LEU:HD12	1.84	0.58
1:F:358:ILE:HD12	1:F:388:ARG:HB3	1.84	0.58
1:A:322:LEU:HD12	1:A:323:HIS:H	1.68	0.58
1:C:578:GLU:HB3	1:C:621:LEU:HB3	1.83	0.58
2:I:203:LYS:HB3	2:I:240:GLU:HG3	1.84	0.58
4:L:206:GLU:HA	5:M:32:MET:HG2	1.84	0.58
5:M:31:ARG:O	5:M:35:LEU:HG	2.04	0.58
1:F:284:VAL:HG23	1:F:324:ILE:O	2.02	0.58
1:B:404:LEU:HG	1:B:426:ILE:HG22	1.85	0.58
4:L:207:ASN:HA	4:L:210:ARG:HD3	1.84	0.58
1:E:36:ILE:HD11	1:E:44:LYS:HB3	1.85	0.58
1:B:313:GLN:O	1:B:317:GLY:N	2.37	0.58
1:F:121:PHE:CD2	1:F:183:VAL:HG21	2.38	0.58
1:C:540:LEU:HD12	1:C:644:GLY:O	2.04	0.58
1:D:686:PHE:HB3	1:D:690:GLU:HG3	1.83	0.58
2:G:124:HIS:HE1	2:G:147:GLN:HB3	1.68	0.58
1:D:654:GLU:HB3	1:E:614:ILE:HD11	1.83	0.58
3:K:45:ILE:CD1	5:M:161:ARG:HG3	2.34	0.58
2:H:17:ALA:O	2:H:21:VAL:HG12	2.03	0.58
1:A:563:PRO:HD2	1:A:597:LEU:CD2	2.33	0.58
1:C:606:GLU:HG2	1:C:607:ARG:N	2.18	0.58
1:E:604:ASP:O	1:E:608:LEU:N	2.37	0.58
1:C:404:LEU:O	1:C:408:HIS:HB2	2.04	0.58
2:H:21:VAL:HG21	2:H:71:LEU:HD22	1.85	0.58
1:C:653:GLN:HG3	1:C:658:LEU:HD23	1.84	0.58
1:E:513:PRO:O	1:E:517:VAL:HG23	2.03	0.58
1:E:270:ALA:O	1:E:273:ILE:HG22	2.04	0.58
1:C:555:LYS:HA	1:C:558:GLU:OE1	2.03	0.58
1:E:596:GLN:CA	1:E:638:ARG:HG2	2.31	0.58
4:L:229:MET:O	4:L:233:ILE:HG13	2.04	0.58
1:C:281:GLU:CB	1:C:324:ILE:HD13	2.34	0.58
1:F:436:PHE:HB3	1:F:440:GLU:CB	2.34	0.58
1:F:256:ILE:O	1:F:370:ILE:HA	2.03	0.58
1:D:256:ILE:O	1:D:370:ILE:HA	2.04	0.58
1:A:315:ARG:HG2	1:A:316:LEU:CD1	2.33	0.58
1:D:284:VAL:HG23	1:D:324:ILE:O	2.04	0.58
1:C:233:ARG:HA	1:D:450:SER:HB2	1.86	0.58
2:I:235:PHE:CD2	3:K:37:ALA:HB3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:686:PHE:HB3	1:B:690:GLU:HB2	1.85	0.57
1:A:503:ILE:O	1:A:505:ASN:N	2.36	0.57
2:J:75:LEU:HD23	2:J:76:GLN:HG2	1.85	0.57
1:E:671:ALA:HA	1:E:703:VAL:O	2.04	0.57
1:A:542:GLU:OE2	1:A:666:HIS:NE2	2.37	0.57
2:I:149:ALA:HB2	2:I:164:CYS:HB2	1.86	0.57
1:F:670:ILE:HG23	1:F:675:GLN:HB2	1.85	0.57
2:H:119:ILE:HD11	2:H:123:HIS:ND1	2.19	0.57
1:F:570:PRO:HG2	1:F:604:ASP:CB	2.32	0.57
1:B:296:GLY:H	1:B:297:GLU:CB	2.18	0.57
1:B:236:ALA:HA	1:B:239:VAL:HG12	1.87	0.57
2:I:244:MET:O	2:I:248:LEU:HG	2.05	0.57
5:M:46:THR:HA	5:M:49:MET:HE3	1.86	0.57
1:A:726:VAL:O	1:A:730:LEU:HG	2.04	0.57
1:D:286:ASN:HB2	1:D:327:PHE:HD1	1.68	0.57
1:D:404:LEU:HA	1:D:407:LEU:HD12	1.86	0.57
1:A:457:ILE:HG13	1:F:240:PHE:CE1	2.40	0.57
1:C:688:ASP:O	1:C:692:THR:HG23	2.04	0.57
1:F:310:GLU:OE2	1:F:357:LYS:NZ	2.38	0.57
2:H:235:PHE:CD1	4:L:204:LYS:HG3	2.39	0.57
1:E:26:GLU:HG2	1:E:51:THR:HB	1.86	0.57
1:F:236:ALA:HA	1:F:239:VAL:HG12	1.87	0.57
2:J:101:ILE:HG21	2:J:135:LEU:HD11	1.87	0.57
1:C:132:VAL:HG23	1:C:173:GLU:O	2.04	0.57
2:G:69:ALA:HB1	2:G:85:PHE:CE1	2.39	0.57
1:C:330:ILE:HG22	1:C:379:ILE:CD1	2.34	0.57
1:E:618:PHE:CZ	1:F:612:VAL:HG11	2.37	0.57
1:C:14:ASP:O	1:C:18:LEU:HG	2.04	0.57
1:B:428:GLU:O	1:B:432:GLU:HG2	2.05	0.57
1:C:194:ASN:ND2	1:C:316:LEU:HG	2.20	0.57
1:E:113:ASP:O	1:E:117:MET:HG3	2.05	0.57
5:M:44:ILE:O	5:M:48:VAL:HG23	2.04	0.57
1:A:397:LEU:CB	1:A:398:PRO:HD3	2.34	0.57
1:F:721:ASP:HB2	1:F:724:TYR:CD1	2.38	0.57
1:F:515:THR:HA	1:F:518:LEU:CD1	2.35	0.57
1:B:625:ALA:O	1:B:629:LEU:HG	2.05	0.57
5:M:190:THR:O	5:M:194:GLU:HG3	2.04	0.57
3:K:56:ARG:HH12	4:L:226:GLN:HE21	1.53	0.57
1:E:296:GLY:H	1:E:297:GLU:CB	2.17	0.57
1:A:724:TYR:HD1	1:A:727:ARG:HH12	1.51	0.57
1:D:585:MET:O	1:D:589:PHE:HD2	1.88	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:ARG:NH1	1:C:74:ILE:HD11	2.20	0.57
1:F:11:CYS:SG	1:F:17:SER:HB2	2.45	0.57
1:E:289:GLU:O	1:E:291:LEU:N	2.28	0.57
1:F:566:LYS:HD2	1:F:567:ILE:N	2.20	0.57
1:B:20:ASN:HD22	1:B:66:GLN:NE2	2.03	0.57
1:B:113:ASP:O	1:B:117:MET:HG3	2.04	0.57
1:E:640:LEU:HD12	1:E:641:LEU:H	1.70	0.56
2:J:159:SER:OG	5:M:48:VAL:O	2.15	0.56
5:M:49:MET:HB3	5:M:53:GLN:NE2	2.19	0.56
1:D:510:TRP:HB3	1:D:679:ALA:HB2	1.87	0.56
1:C:353:GLN:HA	1:D:288:PRO:HG3	1.87	0.56
3:K:45:ILE:HG21	5:M:164:ALA:HB1	1.87	0.56
1:E:525:VAL:O	1:E:528:THR:OG1	2.14	0.56
2:G:195:SER:C	2:G:197:LEU:H	2.08	0.56
1:A:64:LEU:HA	1:A:67:ARG:HE	1.70	0.56
1:A:67:ARG:NH1	1:A:74:ILE:HD11	2.20	0.56
2:I:38:ILE:HD11	2:I:71:LEU:HB3	1.87	0.56
2:J:18:GLU:HA	2:J:21:VAL:HG12	1.87	0.56
1:F:536:LEU:HD21	1:F:632:LYS:O	2.05	0.56
3:K:46:MET:HB3	4:L:215:MET:SD	2.46	0.56
1:B:67:ARG:HB2	1:B:67:ARG:NH1	2.20	0.56
5:M:177:GLN:HG3	5:M:180:ARG:NH2	2.20	0.56
2:G:119:ILE:HD12	2:G:122:LYS:HB2	1.85	0.56
1:B:571:ASP:OD2	1:B:571:ASP:N	2.35	0.56
1:A:550:THR:HG23	1:A:645:THR:OG1	2.04	0.56
2:H:142:ILE:HG23	2:H:168:VAL:HG13	1.86	0.56
1:D:618:PHE:HE1	1:E:612:VAL:HG21	1.69	0.56
1:A:544:PRO:HB2	1:A:669:ASN:ND2	2.20	0.56
1:E:383:LEU:O	1:E:389:LEU:HB2	2.06	0.56
1:C:231:PHE:O	1:C:235:PHE:HB2	2.05	0.56
1:C:98:GLU:HB3	1:C:148:LEU:HB3	1.85	0.56
2:I:254:GLN:HB2	2:I:291:GLU:HG2	1.87	0.56
4:L:232:ARG:O	4:L:236:ASN:ND2	2.36	0.56
1:B:589:PHE:CE2	1:B:629:LEU:HB3	2.40	0.56
1:F:270:ALA:O	1:F:273:ILE:HG22	2.05	0.56
1:B:559:GLU:O	1:B:561:ASN:ND2	2.37	0.56
1:F:686:PHE:HE1	1:F:714:ILE:HG23	1.71	0.56
3:K:48:VAL:HG12	3:K:52:LYS:NZ	2.20	0.56
1:C:490:PRO:HB2	1:C:492:PHE:N	2.19	0.56
1:D:652:LEU:HB3	1:D:658:LEU:HB2	1.87	0.56
1:A:563:PRO:HD2	1:A:597:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:502:TYR:CZ	1:E:567:ILE:HG21	2.41	0.56
2:G:21:VAL:HG21	2:G:71:LEU:HD22	1.86	0.56
5:M:177:GLN:HA	5:M:180:ARG:HH12	1.69	0.56
1:C:577:SER:O	1:C:580:ALA:N	2.33	0.56
1:A:694:ILE:O	1:A:698:VAL:HG13	2.04	0.56
1:A:231:PHE:CD1	1:A:235:PHE:HE2	2.22	0.56
1:E:428:GLU:O	1:E:432:GLU:HG2	2.05	0.56
1:B:654:GLU:O	1:C:613:PRO:HG3	2.06	0.56
1:E:585:MET:HG3	1:E:589:PHE:HZ	1.65	0.56
1:E:721:ASP:O	1:E:725:ARG:HG3	2.06	0.56
2:J:127:ILE:HG23	2:J:131:TYR:CE1	2.41	0.56
1:C:613:PRO:HD3	1:C:648:ARG:NH2	2.20	0.56
1:B:549:LYS:HZ2	1:B:647:SER:HA	1.69	0.56
1:D:604:ASP:HB3	1:D:607:ARG:HB3	1.87	0.56
1:D:524:LEU:O	1:D:527:GLN:HB3	2.06	0.56
1:D:353:GLN:HE22	1:E:288:PRO:CG	2.19	0.56
2:G:112:THR:HG23	2:G:117:PHE:HE1	1.70	0.56
1:B:383:LEU:O	1:B:389:LEU:HB2	2.06	0.56
1:C:312:GLU:O	1:C:316:LEU:HD13	2.06	0.56
1:C:584:ALA:O	1:C:588:ILE:HG13	2.06	0.56
1:D:45:TYR:CE2	1:D:70:ALA:HA	2.41	0.56
1:E:132:VAL:HG23	1:E:173:GLU:O	2.06	0.56
4:L:218:ASP:O	4:L:222:LEU:HG	2.06	0.56
3:K:56:ARG:NH1	4:L:226:GLN:NE2	2.54	0.56
1:D:527:GLN:HE22	1:E:716:MET:HA	1.71	0.56
1:E:670:ILE:HD12	1:E:670:ILE:H	1.71	0.56
1:E:672:THR:OG1	1:E:675:GLN:HB2	2.05	0.56
1:F:713:LEU:HD22	1:F:732:LEU:HB3	1.87	0.56
2:J:188:VAL:HG13	2:J:205:TYR:HD2	1.71	0.56
3:K:56:ARG:NH1	4:L:226:GLN:HE21	2.03	0.56
1:C:67:ARG:HH12	1:C:74:ILE:HD11	1.70	0.56
1:B:240:PHE:HB3	1:B:244:ILE:HB	1.88	0.55
1:D:353:GLN:HE22	1:E:288:PRO:HG2	1.71	0.55
1:D:284:VAL:HG21	1:D:325:ILE:HG22	1.88	0.55
1:A:46:ILE:HD12	1:A:174:VAL:HG11	1.87	0.55
1:D:512:ASP:O	1:D:515:THR:OG1	2.20	0.55
1:E:311:GLU:O	1:E:314:ARG:HG2	2.07	0.55
1:D:104:LYS:HD3	2:J:257:ASP:OD2	2.06	0.55
1:F:715:GLU:O	1:F:719:GLN:HG2	2.07	0.55
1:A:457:ILE:HG13	1:F:240:PHE:HE1	1.72	0.55
1:C:596:GLN:HA	1:C:638:ARG:CD	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:538:SER:H	1:F:662:SER:HB3	1.70	0.55
1:C:239:VAL:HG11	1:D:457:ILE:HD11	1.87	0.55
1:C:428:GLU:O	1:C:432:GLU:HG2	2.07	0.55
1:F:63:SER:O	1:F:67:ARG:HG3	2.06	0.55
2:J:235:PHE:HE2	5:M:155:GLY:HA3	1.72	0.55
1:E:689:LYS:O	1:E:692:THR:OG1	2.21	0.55
1:E:528:THR:HG21	1:E:641:LEU:CD2	2.34	0.55
1:D:543:GLY:O	1:D:647:SER:HA	2.06	0.55
1:F:314:ARG:HG3	1:F:315:ARG:N	2.22	0.55
1:F:242:PRO:HD2	1:F:243:GLU:H	1.72	0.55
1:D:554:ALA:O	1:D:558:GLU:HG2	2.07	0.55
1:E:380:ASP:OD1	1:E:382:ALA:N	2.36	0.55
1:B:536:LEU:HD22	1:B:632:LYS:O	2.06	0.55
1:D:135:GLN:HG2	1:D:148:LEU:HD13	1.89	0.55
5:M:40:LYS:HG3	5:M:163:MET:HE1	1.89	0.55
1:A:449:GLN:O	1:A:453:MET:HG2	2.06	0.55
1:F:617:ARG:HG3	1:F:617:ARG:HH11	1.72	0.55
4:L:229:MET:HG3	4:L:232:ARG:NH2	2.21	0.55
4:L:236:ASN:HD22	4:L:236:ASN:H	1.53	0.55
2:G:119:ILE:HD11	2:G:123:HIS:CE1	2.42	0.55
1:A:286:ASN:HB2	1:A:327:PHE:HB3	1.88	0.55
1:E:91:CYS:O	1:E:154:ALA:HA	2.07	0.55
2:H:219:LEU:HD12	2:H:223:LEU:HB2	1.88	0.55
1:E:705:ILE:CD1	1:E:713:LEU:HD12	2.37	0.55
1:B:569:SER:HA	1:B:603:ASP:HB3	1.88	0.55
1:C:91:CYS:O	1:C:154:ALA:HA	2.06	0.55
1:B:132:VAL:HG23	1:B:173:GLU:O	2.07	0.55
2:H:188:VAL:HG13	2:H:205:TYR:HD2	1.71	0.55
1:A:485:GLU:O	1:A:489:LYS:CB	2.54	0.55
1:F:67:ARG:NH1	1:F:74:ILE:HD11	2.22	0.55
1:B:385:ARG:NH1	1:C:263:GLY:HA2	2.22	0.55
1:D:592:ALA:HB1	1:D:640:LEU:HD13	1.88	0.55
1:A:122:ILE:O	1:A:126:ASN:HB3	2.07	0.55
1:C:12:PRO:HG2	1:C:23:VAL:HG11	1.89	0.55
5:M:45:ARG:O	5:M:49:MET:HG3	2.07	0.55
1:C:577:SER:O	1:C:579:THR:N	2.40	0.55
1:B:124:GLN:HE21	1:B:125:PHE:HE1	1.53	0.55
2:G:200:TYR:HB3	4:L:217:MET:HE1	1.89	0.55
1:F:102:LEU:H	1:F:145:PHE:HA	1.72	0.55
1:E:121:PHE:CD2	1:E:183:VAL:HG21	2.42	0.55
1:C:721:ASP:O	1:C:725:ARG:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:212:LEU:HA	4:L:215:MET:HE2	1.89	0.55
1:D:731:ALA:HA	1:D:734:ARG:NH1	2.21	0.55
1:C:308:ASP:OD1	1:C:309:ALA:N	2.40	0.55
1:F:284:VAL:O	1:F:326:ILE:HG12	2.06	0.54
1:A:128:GLN:O	1:A:176:LEU:HD12	2.07	0.54
1:D:380:ASP:OD1	1:D:382:ALA:N	2.40	0.54
1:B:614:ILE:O	1:B:616:PRO:HA	2.08	0.54
1:D:303:ARG:HD3	1:D:353:GLN:CG	2.38	0.54
1:E:40:SER:OG	1:E:41:PRO:HD2	2.07	0.54
1:A:406:ILE:O	1:A:409:ILE:HG22	2.08	0.54
2:I:177:GLN:HB3	2:I:180:LYS:HB2	1.89	0.54
1:F:612:VAL:CG1	1:F:617:ARG:HB2	2.37	0.54
2:G:243:LEU:HD22	2:G:266:TYR:CG	2.42	0.54
1:D:686:PHE:HB2	1:D:691:ARG:HG2	1.89	0.54
1:F:606:GLU:OE2	1:F:647:SER:HB2	2.07	0.54
1:E:106:ASN:HB3	1:E:143:LYS:HZ2	1.71	0.54
2:J:72:HIS:CE1	2:J:80:ASP:HB2	2.40	0.54
1:F:267:THR:HA	1:F:372:MET:SD	2.47	0.54
3:K:64:ASP:O	3:K:68:ASP:HB2	2.07	0.54
1:F:296:GLY:H	1:F:297:GLU:CB	2.20	0.54
2:I:243:LEU:HD22	2:I:266:TYR:CD2	2.42	0.54
1:E:596:GLN:HA	1:E:638:ARG:CG	2.34	0.54
1:A:683:LEU:HB3	1:A:685:ASN:HD22	1.72	0.54
1:A:300:ALA:O	1:A:304:LYS:HG3	2.08	0.54
1:C:686:PHE:HE1	1:C:714:ILE:HG23	1.72	0.54
1:B:436:PHE:HB3	1:B:440:GLU:CB	2.37	0.54
1:B:695:ALA:HB1	1:B:699:LYS:HE3	1.89	0.54
1:C:691:ARG:HH11	1:C:691:ARG:HB2	1.72	0.54
1:A:313:GLN:OE1	1:A:317:GLY:HA2	2.08	0.54
1:A:493:GLY:HA2	1:A:494:THR:CB	2.37	0.54
1:F:437:SER:O	1:F:440:GLU:HB2	2.07	0.54
3:K:48:VAL:HG12	3:K:52:LYS:HZ1	1.72	0.54
1:D:312:GLU:HG2	1:D:313:GLN:H	1.72	0.54
1:A:315:ARG:HG2	1:A:316:LEU:HD13	1.90	0.54
2:G:115:GLY:HA3	2:J:50:ASN:ND2	2.22	0.54
2:I:72:HIS:CE1	2:I:80:ASP:HB2	2.42	0.54
1:A:306:PHE:CD1	1:A:357:LYS:HB3	2.43	0.54
1:C:540:LEU:HB2	1:C:661:PHE:CD2	2.42	0.54
1:A:121:PHE:HD2	1:A:183:VAL:HG21	1.73	0.54
1:B:1:MET:HG2	1:B:82:LEU:HB2	1.90	0.54
1:E:620:ASN:ND2	1:F:617:ARG:HB3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:ILE:HA	1:C:391:VAL:HG13	1.90	0.54
1:F:128:GLN:O	1:F:176:LEU:HD12	2.08	0.54
1:B:354:LEU:O	1:B:358:ILE:HG12	2.08	0.54
1:E:354:LEU:O	1:E:358:ILE:HG12	2.08	0.54
1:A:690:GLU:O	1:A:694:ILE:HG13	2.07	0.54
2:G:200:TYR:HB3	4:L:217:MET:CE	2.38	0.54
2:G:235:PHE:HB3	5:M:31:ARG:HG2	1.90	0.54
1:F:383:LEU:O	1:F:389:LEU:HB2	2.08	0.54
1:A:690:GLU:HB3	1:A:726:VAL:HG22	1.89	0.54
2:G:246:LYS:HZ1	2:G:258:SER:HB3	1.73	0.54
2:H:92:PHE:HD1	2:H:97:PRO:HG2	1.73	0.54
2:G:49:ALA:HB2	2:G:64:ALA:HB3	1.89	0.54
3:K:45:ILE:HD13	5:M:161:ARG:HG3	1.89	0.54
1:E:654:GLU:CG	1:F:614:ILE:HD11	2.37	0.54
1:D:599:CYS:SG	1:D:641:LEU:HD22	2.48	0.54
1:B:327:PHE:HB2	1:B:330:ILE:CG2	2.38	0.54
1:A:536:LEU:HD23	1:A:633:ALA:HA	1.89	0.54
1:B:270:ALA:O	1:B:273:ILE:HG22	2.08	0.54
2:J:167:LYS:HE2	2:J:171:TYR:HE2	1.73	0.54
2:G:101:ILE:HG13	2:G:102:ASN:N	2.23	0.54
1:C:614:ILE:O	1:C:616:PRO:HA	2.07	0.53
1:E:552:LEU:HD11	1:E:667:VAL:HG11	1.90	0.53
1:C:694:ILE:O	1:C:698:VAL:HG22	2.08	0.53
1:D:533:ARG:HD2	1:E:505:ASN:HD22	1.73	0.53
5:M:152:GLN:O	5:M:156:ILE:HG13	2.08	0.53
1:D:568:CYS:N	1:D:601:VAL:O	2.21	0.53
1:A:293:LYS:O	1:A:294:TYR:CG	2.61	0.53
1:F:712:MET:O	1:F:716:MET:HG3	2.07	0.53
1:C:606:GLU:HB2	1:C:648:ARG:HD2	1.90	0.53
1:B:310:GLU:OE2	1:B:357:LYS:NZ	2.41	0.53
1:C:510:TRP:CZ3	1:C:670:ILE:HG12	2.43	0.53
2:J:235:PHE:CE2	5:M:155:GLY:HA3	2.42	0.53
2:I:276:LEU:O	2:I:280:LEU:HG	2.08	0.53
2:J:38:ILE:HD11	2:J:71:LEU:HB3	1.90	0.53
1:B:149:VAL:HG11	1:B:152:ILE:HD11	1.90	0.53
3:K:42:VAL:HA	3:K:45:ILE:HD12	1.89	0.53
2:J:200:TYR:HB3	5:M:40:LYS:HZ2	1.73	0.53
1:E:713:LEU:HD22	1:E:732:LEU:HD13	1.90	0.53
1:B:533:ARG:HH22	1:C:683:LEU:HD22	1.72	0.53
1:E:664:THR:C	1:E:665:ILE:HD13	2.28	0.53
4:L:198:ARG:O	4:L:202:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:649:LYS:HE3	1:B:658:LEU:CD1	2.31	0.53
1:F:560:SER:HB2	1:F:562:PHE:CD1	2.44	0.53
1:B:22:ALA:HB3	1:B:49:LEU:HD23	1.89	0.53
1:C:708:LYS:HA	1:C:711:LEU:HG	1.90	0.53
2:G:119:ILE:HD13	3:K:65:ASP:OD1	2.08	0.53
1:B:46:ILE:HD12	1:B:174:VAL:HG21	1.91	0.53
2:J:179:GLN:O	2:J:182:ILE:HG12	2.09	0.53
1:E:592:ALA:HB1	1:E:640:LEU:HD22	1.90	0.53
1:E:549:LYS:HG3	1:E:550:THR:N	2.24	0.53
2:I:216:ILE:HD11	2:I:218:MET:HB2	1.90	0.53
1:D:43:HIS:HB3	1:D:45:TYR:HE1	1.73	0.53
1:A:509:LYS:HG2	1:A:515:THR:OG1	2.09	0.53
2:G:155:GLU:C	2:G:157:SER:H	2.11	0.53
1:B:40:SER:HB2	1:B:43:HIS:ND1	2.23	0.53
1:A:136:LEU:HD23	1:A:136:LEU:N	2.22	0.53
2:I:185:TYR:HA	2:I:188:VAL:HG12	1.90	0.53
1:D:512:ASP:N	1:D:513:PRO:CD	2.72	0.53
1:E:240:PHE:HD2	1:E:244:ILE:CG2	2.19	0.53
1:E:705:ILE:HG13	1:E:709:LYS:HG3	1.90	0.53
1:C:547:SER:HB2	1:C:549:LYS:HG3	1.89	0.53
1:C:256:ILE:HG22	1:C:391:VAL:HG11	1.88	0.53
1:A:626:LEU:HD21	1:A:657:MET:HE1	1.90	0.53
2:J:182:ILE:O	2:J:186:GLU:HG2	2.08	0.53
2:H:128:ALA:HB2	2:H:144:HIS:HB2	1.90	0.53
1:A:307:ALA:O	1:A:310:GLU:HG3	2.08	0.53
1:C:533:ARG:O	1:D:505:ASN:ND2	2.41	0.53
1:C:542:GLU:HB3	1:C:649:LYS:HD3	1.89	0.53
1:E:407:LEU:CD1	1:E:426:ILE:HG23	2.35	0.53
1:E:247:GLN:HA	1:F:417:HIS:ND1	2.24	0.53
1:D:540:LEU:HD12	1:D:661:PHE:CE1	2.44	0.53
1:B:571:ASP:O	1:B:574:ILE:HG13	2.09	0.53
1:A:687:LYS:HB2	1:A:690:GLU:HG3	1.91	0.53
1:F:526:GLN:O	1:F:530:ASN:HB2	2.08	0.53
1:A:428:GLU:O	1:A:432:GLU:HG2	2.08	0.53
3:K:41:GLU:O	3:K:45:ILE:HG13	2.09	0.53
5:M:29:THR:HA	5:M:32:MET:HE3	1.89	0.53
5:M:167:MET:O	5:M:171:ILE:HG13	2.09	0.53
1:F:570:PRO:HA	1:F:573:MET:HE2	1.90	0.53
1:D:312:GLU:CG	1:D:313:GLN:H	2.22	0.53
1:C:510:TRP:CE3	1:C:670:ILE:HG12	2.43	0.53
1:A:352:ASN:HA	1:A:355:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:101:ILE:HD13	2:G:135:LEU:HD11	1.90	0.53
1:A:513:PRO:O	1:A:517:VAL:HG23	2.08	0.53
2:H:244:MET:O	2:H:248:LEU:HG	2.09	0.53
2:I:92:PHE:HB3	2:I:98:GLN:O	2.08	0.53
2:H:108:ILE:HD12	2:H:127:ILE:HD12	1.90	0.53
1:D:313:GLN:O	1:D:317:GLY:N	2.41	0.53
1:B:406:ILE:HB	1:B:441:LEU:HD13	1.91	0.53
1:C:311:GLU:HA	1:C:314:ARG:HG2	1.89	0.53
1:D:407:LEU:O	1:D:411:THR:HG23	2.09	0.53
1:B:627:LEU:CD2	1:B:657:MET:HG3	2.39	0.53
1:D:326:ILE:HG22	1:D:370:ILE:CG1	2.39	0.53
5:M:174:GLN:O	5:M:178:ILE:HG13	2.09	0.53
1:A:564:PHE:HE1	1:A:566:LYS:HB2	1.72	0.53
1:D:67:ARG:NH1	1:D:74:ILE:HD11	2.23	0.53
1:C:227:PHE:O	1:C:231:PHE:HB2	2.09	0.53
1:E:573:MET:O	1:E:576:PHE:HB2	2.09	0.53
2:G:18:GLU:HA	2:G:21:VAL:HG12	1.90	0.52
1:F:64:LEU:HA	1:F:67:ARG:HD2	1.91	0.52
1:E:696:GLN:HB3	1:E:697:GLN:NE2	2.24	0.52
1:F:407:LEU:CD1	1:F:426:ILE:HG23	2.39	0.52
2:G:57:ASN:O	2:G:59:SER:N	2.42	0.52
1:C:525:VAL:HG13	1:C:562:PHE:CZ	2.44	0.52
1:D:136:LEU:N	1:D:136:LEU:HD23	2.24	0.52
2:G:231:LEU:HD13	2:J:271:ARG:HB3	1.91	0.52
1:A:256:ILE:HG13	1:A:370:ILE:HG22	1.90	0.52
1:F:149:VAL:HG11	1:F:152:ILE:HD11	1.91	0.52
1:A:614:ILE:HD12	1:F:654:GLU:HG2	1.91	0.52
2:J:182:ILE:HG22	2:J:212:CYS:HB2	1.92	0.52
2:I:203:LYS:HE2	5:M:161:ARG:NH1	2.22	0.52
3:K:53:VAL:HG23	4:L:226:GLN:HE22	1.73	0.52
1:D:298:SER:O	1:D:301:ASN:HB3	2.10	0.52
1:F:517:VAL:HG21	1:F:667:VAL:HG22	1.92	0.52
1:A:236:ALA:HB1	1:B:453:MET:CB	2.40	0.52
1:A:106:ASN:HB3	1:A:143:LYS:NZ	2.24	0.52
2:I:18:GLU:HA	2:I:21:VAL:HG12	1.90	0.52
1:A:95:MET:HG3	1:A:152:ILE:HG12	1.90	0.52
2:I:116:ARG:HH11	2:I:116:ARG:HG3	1.72	0.52
2:I:219:LEU:H	2:I:219:LEU:HD23	1.74	0.52
1:F:538:SER:OG	1:F:661:PHE:HD1	1.91	0.52
1:A:678:GLU:O	1:A:681:GLU:HG2	2.09	0.52
1:E:674:GLU:O	1:E:677:LEU:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:92:PHE:HA	2:J:95:ALA:HB3	1.90	0.52
4:L:207:ASN:O	4:L:210:ARG:HB2	2.09	0.52
1:F:707:ILE:O	1:F:710:LEU:HB3	2.10	0.52
1:B:267:THR:HA	1:B:372:MET:SD	2.49	0.52
1:A:454:ASN:HA	1:F:232:ARG:NH2	2.25	0.52
1:D:681:GLU:HG2	1:D:691:ARG:NH1	2.25	0.52
1:D:690:GLU:O	1:D:693:THR:OG1	2.24	0.52
1:D:543:GLY:N	1:D:549:LYS:HD3	2.22	0.52
1:B:533:ARG:HD2	1:C:711:LEU:HD13	1.92	0.52
2:H:80:ASP:OD2	5:M:191:ARG:NH2	2.42	0.52
1:A:184:ALA:HB1	1:A:200:LYS:O	2.09	0.52
1:C:46:ILE:HD12	1:C:174:VAL:HG21	1.92	0.52
5:M:29:THR:HA	5:M:32:MET:CE	2.40	0.52
1:A:300:ALA:HA	1:A:303:ARG:HG2	1.90	0.52
1:A:677:LEU:HG	1:A:695:ALA:HB2	1.90	0.52
1:A:686:PHE:O	1:A:691:ARG:NH2	2.43	0.52
1:E:653:GLN:OE1	1:E:658:LEU:HD23	2.09	0.52
1:C:690:GLU:CB	1:C:726:VAL:HG21	2.40	0.52
1:C:686:PHE:CE1	1:C:714:ILE:HG23	2.44	0.52
2:G:101:ILE:HG21	2:G:135:LEU:HD11	1.92	0.52
2:I:228:TYR:OH	2:I:237:ASP:OD1	2.22	0.52
3:K:82:ALA:HB1	3:K:86:ARG:HH12	1.75	0.52
1:A:611:TYR:CE2	1:A:651:VAL:HG11	2.45	0.52
1:E:136:LEU:N	1:E:136:LEU:HD23	2.25	0.52
1:D:312:GLU:CD	1:D:323:HIS:ND1	2.63	0.52
4:L:233:ILE:O	4:L:237:VAL:HG23	2.10	0.52
1:F:309:ALA:HA	1:F:312:GLU:OE1	2.10	0.52
1:F:503:ILE:HG22	1:F:506:GLY:H	1.73	0.52
1:E:128:GLN:O	1:E:176:LEU:HD12	2.10	0.52
2:H:124:HIS:HE1	2:H:147:GLN:HB3	1.75	0.52
1:C:20:ASN:ND2	1:C:66:GLN:HE21	2.08	0.52
1:A:531:SER:O	1:A:639:LYS:HE2	2.10	0.52
3:K:59:LYS:HD3	5:M:178:ILE:HB	1.91	0.52
1:B:26:GLU:HG2	1:B:51:THR:HB	1.92	0.52
1:E:516:ARG:O	1:E:519:ASP:OD1	2.27	0.52
5:M:149:ASN:O	5:M:153:VAL:HG23	2.09	0.52
2:G:197:LEU:HD22	5:M:45:ARG:CZ	2.40	0.52
1:C:658:LEU:HD11	1:C:664:THR:HG21	1.90	0.52
2:I:216:ILE:HG13	2:I:218:MET:H	1.75	0.52
1:B:128:GLN:O	1:B:176:LEU:HD12	2.10	0.52
2:J:108:ILE:HD12	2:J:127:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:69:ALA:HB1	2:H:85:PHE:CE1	2.45	0.52
1:D:721:ASP:O	1:D:725:ARG:HG3	2.09	0.52
2:J:219:LEU:HD12	2:J:223:LEU:HB2	1.92	0.51
1:C:331:ASP:HA	1:C:379:ILE:CD1	2.41	0.51
1:F:307:ALA:HA	1:F:310:GLU:HG2	1.92	0.51
1:D:593:TYR:OH	1:D:632:LYS:HD2	2.10	0.51
1:F:589:PHE:CD2	1:F:629:LEU:HD22	2.45	0.51
2:I:49:ALA:HB2	2:I:64:ALA:HB3	1.91	0.51
1:F:608:LEU:HD12	1:F:609:LEU:N	2.24	0.51
1:D:18:LEU:HA	1:D:137:VAL:HG23	1.91	0.51
1:C:247:GLN:HA	1:D:417:HIS:CD2	2.45	0.51
1:A:650:ASP:OD1	1:A:650:ASP:N	2.43	0.51
4:L:202:ILE:CD1	5:M:25:SER:HB3	2.40	0.51
2:G:231:LEU:HB2	2:G:234:ALA:CB	2.40	0.51
1:D:626:LEU:HB3	1:D:657:MET:HE3	1.92	0.51
2:H:40:GLU:O	2:H:44:ILE:HG12	2.10	0.51
2:I:182:ILE:O	2:I:186:GLU:HG2	2.11	0.51
2:H:118:THR:O	2:H:122:LYS:HG2	2.09	0.51
2:H:38:ILE:CD1	2:H:71:LEU:HB3	2.38	0.51
2:H:159:SER:OG	3:K:54:LEU:HB3	2.10	0.51
1:E:327:PHE:HB2	1:E:330:ILE:CG2	2.39	0.51
1:C:560:SER:HB2	1:C:562:PHE:CE1	2.45	0.51
1:A:101:PHE:HE1	1:A:193:LEU:HB2	1.75	0.51
1:F:327:PHE:CZ	1:F:369:VAL:HG21	2.46	0.51
1:F:236:ALA:O	1:F:239:VAL:HG12	2.11	0.51
1:D:258:LEU:HB2	1:D:395:ILE:HD11	1.91	0.51
1:E:236:ALA:O	1:E:239:VAL:HG12	2.09	0.51
2:H:167:LYS:HE2	2:H:171:TYR:HE2	1.74	0.51
1:C:24:VAL:O	1:C:51:THR:HA	2.11	0.51
1:D:143:LYS:HB3	1:D:145:PHE:HE1	1.74	0.51
1:D:95:MET:HG3	1:D:152:ILE:HG12	1.93	0.51
1:D:509:LYS:HE2	1:D:515:THR:HG22	1.92	0.51
3:K:36:GLN:HA	4:L:205:LEU:HD13	1.92	0.51
5:M:46:THR:O	5:M:50:LEU:HG	2.09	0.51
1:D:609:LEU:CD1	1:D:611:TYR:HB2	2.41	0.51
1:A:676:LEU:CD1	1:A:710:LEU:HD11	2.40	0.51
2:H:72:HIS:CE1	2:H:80:ASP:HB2	2.42	0.51
1:C:383:LEU:HD22	1:C:388:ARG:HD2	1.93	0.51
1:A:231:PHE:CE1	1:A:235:PHE:HE2	2.28	0.51
2:G:167:LYS:HE2	2:G:171:TYR:HE2	1.75	0.51
2:H:57:ASN:O	2:H:59:SER:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:284:VAL:O	1:E:326:ILE:HG12	2.09	0.51
1:D:527:GLN:NE2	1:E:715:GLU:HG3	2.24	0.51
2:I:219:LEU:HB2	2:I:222:LYS:CB	2.40	0.51
2:I:142:ILE:HG23	2:I:168:VAL:HG13	1.93	0.51
1:F:101:PHE:CB	1:F:107:ILE:HG12	2.40	0.51
5:M:25:SER:O	5:M:29:THR:HG23	2.11	0.51
5:M:28:SER:HA	5:M:31:ARG:CZ	2.41	0.51
1:C:728:LYS:HE3	1:C:732:LEU:HD21	1.93	0.51
1:C:101:PHE:CD2	1:C:107:ILE:HA	2.46	0.51
3:K:77:PHE:CE2	4:L:247:ALA:HB1	2.46	0.51
2:J:244:MET:O	2:J:248:LEU:HG	2.10	0.51
1:B:136:LEU:N	1:B:136:LEU:HD23	2.26	0.51
1:D:407:LEU:HB2	1:D:426:ILE:HG23	1.92	0.51
1:D:604:ASP:HB3	1:D:607:ARG:HB2	1.92	0.51
2:H:67:GLN:O	2:H:71:LEU:HG	2.11	0.51
1:C:544:PRO:HG2	1:C:669:ASN:CG	2.31	0.51
2:H:127:ILE:HG23	2:H:131:TYR:CE1	2.46	0.51
1:B:423:ASP:C	1:B:479:ASP:N	2.64	0.51
2:G:235:PHE:CB	5:M:31:ARG:HG2	2.41	0.51
1:F:524:LEU:HD13	1:F:539:VAL:HG22	1.91	0.51
1:A:246:GLU:O	1:B:413:ARG:NH1	2.41	0.51
2:I:124:HIS:CE1	2:I:147:GLN:HB3	2.42	0.51
2:G:53:LYS:HE3	2:H:117:PHE:CE2	2.46	0.51
1:E:503:ILE:HG12	1:E:507:ILE:HD11	1.93	0.51
1:D:98:GLU:HB3	1:D:148:LEU:HB3	1.93	0.51
1:C:45:TYR:CE2	1:C:70:ALA:HA	2.45	0.51
1:F:222:GLY:HA3	1:F:399:ASP:OD2	2.11	0.51
1:A:222:GLY:O	1:A:224:ASP:N	2.43	0.51
2:J:188:VAL:HG13	2:J:205:TYR:CD2	2.46	0.51
1:C:611:TYR:CZ	1:C:651:VAL:HG11	2.45	0.51
3:K:53:VAL:CG2	4:L:226:GLN:HE22	2.24	0.51
1:E:436:PHE:HB3	1:E:440:GLU:CB	2.41	0.51
1:E:352:ASN:HA	1:E:355:LEU:HD12	1.93	0.51
5:M:17:ARG:O	5:M:21:LEU:HG	2.10	0.51
2:G:78:LYS:HB3	2:G:110:ILE:HG23	1.92	0.51
1:B:578:GLU:HG3	1:B:619:SER:HB2	1.93	0.51
2:G:179:GLN:O	2:G:182:ILE:HG12	2.11	0.51
1:E:263:GLY:O	1:E:439:ALA:HB3	2.11	0.51
1:C:386:PRO:HA	1:C:390:GLU:CA	2.35	0.50
1:A:356:SER:CB	1:B:288:PRO:HD3	2.40	0.50
4:L:226:GLN:HA	4:L:229:MET:CE	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:310:GLU:OE2	1:E:357:LYS:NZ	2.44	0.50
1:A:242:PRO:HD2	1:A:243:GLU:OE1	2.11	0.50
1:A:628:VAL:CG1	1:B:571:ASP:HA	2.41	0.50
1:C:233:ARG:CZ	1:C:233:ARG:HB2	2.41	0.50
1:F:522:GLU:OE2	1:F:526:GLN:HG2	2.10	0.50
1:E:260:GLY:HA3	1:E:266:LYS:HD3	1.93	0.50
1:E:184:ALA:HB1	1:E:200:LYS:O	2.10	0.50
1:A:709:LYS:HA	1:A:709:LYS:HE2	1.93	0.50
5:M:200:THR:O	5:M:200:THR:HG22	2.12	0.50
1:B:540:LEU:HD11	1:B:649:LYS:HZ2	1.75	0.50
1:F:258:LEU:CB	1:F:395:ILE:HD11	2.41	0.50
2:I:230:GLU:HG3	2:I:237:ASP:CB	2.40	0.50
1:C:730:LEU:O	1:C:734:ARG:HG3	2.11	0.50
1:D:190:ASN:HB3	1:D:316:LEU:HG	1.93	0.50
1:E:620:ASN:HD21	1:F:617:ARG:HB3	1.77	0.50
1:A:673:GLY:O	1:A:677:LEU:HD22	2.10	0.50
1:D:312:GLU:CG	1:D:313:GLN:N	2.74	0.50
1:D:687:LYS:O	1:D:691:ARG:HG3	2.11	0.50
2:G:117:PHE:CD2	2:J:53:LYS:HE3	2.46	0.50
2:G:188:VAL:HG13	2:G:205:TYR:CD2	2.44	0.50
1:A:721:ASP:O	1:A:725:ARG:HG3	2.12	0.50
4:L:240:ALA:O	4:L:244:VAL:HG23	2.12	0.50
1:E:242:PRO:HD2	1:E:243:GLU:H	1.76	0.50
1:E:73:SER:O	1:E:76:GLN:HG2	2.11	0.50
1:F:632:LYS:HD2	1:F:633:ALA:H	1.76	0.50
1:D:611:TYR:CE2	1:D:613:PRO:HA	2.47	0.50
2:G:104:LEU:HB3	2:G:127:ILE:CD1	2.41	0.50
1:D:11:CYS:SG	1:D:17:SER:HB2	2.51	0.50
1:B:264:CYS:HA	1:B:437:SER:HB2	1.93	0.50
1:B:686:PHE:HE1	1:B:714:ILE:HG23	1.76	0.50
1:E:581:LYS:NZ	1:E:610:ASP:OD1	2.41	0.50
1:D:233:ARG:HA	1:E:450:SER:HB2	1.94	0.50
3:K:39:VAL:CG1	4:L:209:ILE:HG12	2.41	0.50
1:B:542:GLU:OE1	1:B:649:LYS:HD3	2.12	0.50
1:D:713:LEU:HD21	1:D:732:LEU:HB3	1.93	0.50
1:C:236:ALA:HB1	1:D:453:MET:CB	2.37	0.50
1:A:610:ASP:HA	1:F:624:GLN:NE2	2.27	0.50
1:B:552:LEU:O	1:B:556:ILE:HG13	2.11	0.50
1:D:268:LEU:HA	1:D:271:ARG:CD	2.42	0.50
1:F:605:ILE:HD11	1:F:644:GLY:HA3	1.93	0.50
1:E:281:GLU:N	1:E:282:PRO:HA	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:277:THR:O	2:H:281:LEU:HB2	2.12	0.50
1:C:445:VAL:HG12	1:C:449:GLN:HE22	1.77	0.50
4:L:219:MET:O	4:L:223:VAL:HG23	2.11	0.50
2:I:79:HIS:CD2	5:M:69:GLN:HG3	2.47	0.50
1:F:256:ILE:CG1	1:F:370:ILE:HG22	2.35	0.50
2:H:75:LEU:O	2:H:76:GLN:HB3	2.12	0.50
1:C:688:ASP:OD1	1:C:691:ARG:NH2	2.31	0.50
1:F:512:ASP:OD1	1:F:513:PRO:HD3	2.12	0.50
1:C:511:GLY:C	1:C:513:PRO:HD2	2.32	0.50
1:B:531:SER:CB	1:B:639:LYS:HD3	2.40	0.50
1:B:589:PHE:CE1	1:B:600:VAL:HG11	2.47	0.50
2:J:235:PHE:CG	5:M:152:GLN:HA	2.46	0.50
1:B:20:ASN:ND2	1:B:66:GLN:HE21	2.09	0.50
1:F:609:LEU:HD21	1:F:623:LEU:HD13	1.93	0.50
1:E:666:HIS:CD2	1:E:668:PRO:HD3	2.46	0.50
1:A:688:ASP:OD1	1:A:689:LYS:N	2.44	0.50
2:I:178:TYR:OH	2:I:282:ARG:HG2	2.12	0.50
1:D:589:PHE:CE2	1:D:629:LEU:HD13	2.47	0.50
1:D:567:ILE:HG23	1:D:601:VAL:HB	1.94	0.50
1:A:428:GLU:O	1:A:431:VAL:HG12	2.11	0.50
1:A:611:TYR:HA	1:A:618:PHE:HB3	1.94	0.50
1:E:236:ALA:HA	1:E:239:VAL:HG12	1.94	0.50
1:B:309:ALA:HB1	1:B:367:ILE:HG21	1.94	0.50
1:D:24:VAL:O	1:D:51:THR:HA	2.12	0.50
3:K:32:LEU:HD11	4:L:202:ILE:HG12	1.94	0.50
2:J:184:ILE:O	2:J:188:VAL:HG12	2.12	0.50
2:G:233:PRO:HB2	2:J:271:ARG:HG2	1.94	0.50
1:A:502:TYR:O	1:A:551:ALA:HB1	2.11	0.50
1:A:227:PHE:CE1	1:A:273:ILE:HD13	2.46	0.50
1:B:352:ASN:HA	1:B:355:LEU:HD12	1.93	0.50
1:C:136:LEU:HD23	1:C:136:LEU:N	2.26	0.50
1:F:559:GLU:OE1	1:F:559:GLU:HA	2.11	0.50
1:A:198:LYS:HB2	1:A:198:LYS:NZ	2.26	0.50
1:A:315:ARG:O	1:A:316:LEU:HD12	2.12	0.50
1:C:689:LYS:O	1:C:692:THR:OG1	2.17	0.50
1:D:560:SER:HB2	1:D:562:PHE:CD1	2.46	0.50
1:C:388:ARG:NH1	1:C:388:ARG:HB2	2.27	0.50
1:A:286:ASN:HB2	1:A:327:PHE:CB	2.41	0.50
1:A:103:GLN:O	1:A:107:ILE:HG13	2.11	0.50
1:F:18:LEU:HA	1:F:137:VAL:HG23	1.93	0.50
1:F:710:LEU:O	1:F:714:ILE:HG13	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:LYS:HE3	1:A:514:VAL:HG12	1.94	0.50
1:B:98:GLU:HB3	1:B:148:LEU:HB3	1.93	0.50
5:M:75:GLU:O	5:M:79:LYS:HG2	2.12	0.50
1:F:136:LEU:N	1:F:136:LEU:HD23	2.26	0.50
1:C:569:SER:HB3	1:C:572:LYS:HG2	1.94	0.50
1:E:673:GLY:HA3	1:E:698:VAL:HB	1.93	0.49
1:B:414:MET:N	1:B:414:MET:HE2	2.27	0.49
1:E:506:GLY:O	1:E:508:ILE:N	2.45	0.49
2:G:185:TYR:HA	2:G:188:VAL:HG12	1.94	0.49
1:E:428:GLU:O	1:E:431:VAL:HG12	2.12	0.49
1:A:283:LYS:HA	1:A:324:ILE:O	2.12	0.49
1:A:596:GLN:HA	1:A:638:ARG:HD3	1.94	0.49
1:D:690:GLU:O	1:D:694:ILE:HG13	2.12	0.49
1:C:688:ASP:HA	1:C:691:ARG:NH1	2.27	0.49
1:F:720:MET:HB3	1:F:724:TYR:HB2	1.94	0.49
1:D:149:VAL:HG11	1:D:152:ILE:HD11	1.93	0.49
2:J:216:ILE:HG13	2:J:218:MET:H	1.76	0.49
1:B:265:GLY:O	1:B:268:LEU:HG	2.11	0.49
1:C:349:THR:O	1:C:352:ASN:HB3	2.12	0.49
2:H:256:VAL:HG21	2:H:288:GLN:HG3	1.94	0.49
1:A:575:GLY:HA3	1:F:586:LYS:CE	2.43	0.49
2:H:159:SER:HB3	3:K:58:GLN:OE1	2.11	0.49
1:A:247:GLN:O	1:B:413:ARG:NH1	2.46	0.49
1:D:628:VAL:HG11	1:E:574:ILE:CG2	2.42	0.49
1:A:114:THR:HG21	1:A:200:LYS:HG2	1.95	0.49
1:A:611:TYR:CE1	1:A:616:PRO:HB2	2.46	0.49
1:E:267:THR:HA	1:E:372:MET:SD	2.52	0.49
2:G:149:ALA:HB2	2:G:164:CYS:HB2	1.93	0.49
1:B:315:ARG:HG3	1:B:316:LEU:HD12	1.94	0.49
1:D:564:PHE:HB3	1:D:598:SER:CB	2.42	0.49
1:C:242:PRO:HD2	1:C:243:GLU:H	1.77	0.49
1:A:540:LEU:HD12	1:A:644:GLY:O	2.13	0.49
1:B:549:LYS:NZ	1:B:647:SER:HA	2.26	0.49
2:G:243:LEU:HD22	2:G:266:TYR:CD2	2.48	0.49
1:A:624:GLN:HA	1:A:624:GLN:OE1	2.13	0.49
1:D:527:GLN:HA	1:E:719:GLN:HG3	1.94	0.49
1:D:528:THR:CB	1:D:641:LEU:HD12	2.42	0.49
2:H:260:THR:HG21	2:H:284:LYS:HE3	1.93	0.49
1:F:257:LEU:HB2	1:F:389:LEU:HD13	1.95	0.49
1:F:184:ALA:HB1	1:F:200:LYS:O	2.12	0.49
1:A:153:GLU:OE1	1:A:169:ARG:HD3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:MET:HG3	1:C:152:ILE:HG12	1.94	0.49
2:J:128:ALA:HB2	2:J:144:HIS:HB2	1.93	0.49
1:B:380:ASP:OD1	1:B:382:ALA:N	2.41	0.49
1:A:652:LEU:HA	1:A:655:MET:SD	2.52	0.49
3:K:55:GLU:HB3	3:K:59:LYS:NZ	2.28	0.49
1:A:397:LEU:CB	1:A:398:PRO:CD	2.90	0.49
2:G:123:HIS:O	2:G:127:ILE:HG12	2.12	0.49
1:F:98:GLU:HB3	1:F:148:LEU:HB3	1.94	0.49
1:A:719:GLN:HG2	1:F:523:LEU:HD21	1.92	0.49
1:F:113:ASP:O	1:F:117:MET:HG3	2.13	0.49
1:F:261:PRO:O	1:F:264:CYS:HB2	2.11	0.49
1:E:397:LEU:HD22	1:E:398:PRO:HD2	1.95	0.49
1:B:533:ARG:HG3	1:B:534:THR:N	2.25	0.49
1:A:69:TRP:NE1	1:A:134:GLN:HA	2.27	0.49
1:B:353:GLN:OE1	1:C:288:PRO:HG2	2.13	0.49
1:E:586:LYS:NZ	1:F:575:GLY:HA3	2.28	0.49
1:F:326:ILE:HG22	1:F:370:ILE:CG1	2.41	0.49
2:H:45:TYR:HB2	2:H:68:ALA:HB2	1.94	0.49
2:H:147:GLN:HG2	2:H:151:TYR:CE2	2.47	0.49
2:G:239:ARG:HH11	4:L:210:ARG:HH12	1.59	0.49
1:C:315:ARG:HB2	1:C:316:LEU:HD12	1.95	0.49
2:I:21:VAL:HG21	2:I:71:LEU:HD22	1.94	0.49
1:F:686:PHE:CE1	1:F:714:ILE:HG23	2.48	0.49
1:E:598:SER:O	1:E:640:LEU:HA	2.13	0.49
1:D:257:LEU:HB2	1:D:389:LEU:HD13	1.95	0.49
1:C:128:GLN:O	1:C:176:LEU:HD12	2.11	0.49
2:J:47:ARG:O	2:J:50:ASN:HB3	2.13	0.49
1:B:236:ALA:O	1:B:239:VAL:HG12	2.13	0.49
1:C:533:ARG:HB2	1:D:715:GLU:OE1	2.13	0.49
2:G:182:ILE:CG2	2:G:212:CYS:HB2	2.42	0.49
2:G:244:MET:O	2:G:248:LEU:HG	2.13	0.49
1:D:536:LEU:HD21	1:D:630:LEU:O	2.12	0.49
2:H:195:SER:C	2:H:197:LEU:H	2.15	0.49
1:B:606:GLU:N	1:B:606:GLU:OE1	2.45	0.49
1:F:436:PHE:HB3	1:F:440:GLU:HB2	1.95	0.49
1:F:324:ILE:HG12	1:F:368:LEU:HD11	1.94	0.49
1:D:627:LEU:CD2	1:D:657:MET:HG3	2.42	0.49
1:A:247:GLN:O	1:B:414:MET:CE	2.60	0.49
1:E:569:SER:HB2	1:E:572:LYS:HG2	1.95	0.49
1:A:531:SER:OG	1:B:715:GLU:OE1	2.30	0.49
1:F:615:GLY:HA3	1:F:616:PRO:C	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:688:ASP:O	1:D:692:THR:HG23	2.12	0.49
1:F:38:ARG:HH11	1:F:38:ARG:HG2	1.78	0.49
1:A:503:ILE:HG22	1:A:506:GLY:H	1.78	0.49
5:M:41:ASP:O	5:M:45:ARG:HD3	2.13	0.49
1:D:552:LEU:O	1:D:556:ILE:HG13	2.13	0.49
1:D:547:SER:HG	1:D:549:LYS:HG3	1.77	0.49
1:C:512:ASP:N	1:C:513:PRO:CD	2.76	0.49
1:F:653:GLN:HA	1:F:658:LEU:HB3	1.94	0.49
2:J:112:THR:HG23	2:J:117:PHE:CE1	2.45	0.49
1:C:586:LYS:NZ	1:D:574:ILE:O	2.40	0.49
1:C:86:ASP:C	1:C:88:ALA:H	2.15	0.49
1:D:242:PRO:HD2	1:D:243:GLU:H	1.78	0.49
1:A:457:ILE:HD12	1:F:232:ARG:NH2	2.28	0.48
1:D:686:PHE:HB2	1:D:691:ARG:CG	2.43	0.48
1:E:697:GLN:HG3	1:E:730:LEU:CD1	2.43	0.48
2:I:50:ASN:HD21	2:J:115:GLY:CA	2.25	0.48
2:H:164:CYS:O	2:H:168:VAL:HG23	2.13	0.48
1:A:598:SER:O	1:A:640:LEU:HA	2.13	0.48
1:C:284:VAL:HB	1:C:325:ILE:HA	1.95	0.48
1:C:231:PHE:CE1	1:C:235:PHE:HD2	2.30	0.48
1:A:231:PHE:CD2	1:A:235:PHE:HD2	2.31	0.48
2:I:118:THR:O	2:I:122:LYS:HG2	2.13	0.48
2:H:177:GLN:OE1	2:H:180:LYS:HD3	2.13	0.48
2:I:167:LYS:HE2	2:I:171:TYR:HE2	1.78	0.48
2:G:266:TYR:CZ	2:G:270:SER:HB2	2.48	0.48
1:B:533:ARG:HG3	1:B:534:THR:HG23	1.95	0.48
1:A:383:LEU:O	1:A:389:LEU:HB2	2.13	0.48
1:D:602:VAL:O	1:D:644:GLY:HA2	2.13	0.48
5:M:142:ARG:O	5:M:146:MET:HB2	2.12	0.48
1:B:440:GLU:O	1:B:444:LEU:HG	2.13	0.48
1:F:236:ALA:HA	1:F:239:VAL:CG1	2.43	0.48
1:E:705:ILE:HD13	1:E:710:LEU:HD13	1.95	0.48
1:E:627:LEU:HG	1:E:657:MET:CE	2.43	0.48
1:D:681:GLU:HG2	1:D:691:ARG:CZ	2.43	0.48
1:B:23:VAL:HG12	1:B:55:VAL:CG2	2.43	0.48
1:D:652:LEU:HD13	1:D:657:MET:HB3	1.94	0.48
1:A:612:VAL:HG11	1:F:618:PHE:HZ	1.78	0.48
1:A:322:LEU:HD12	1:A:323:HIS:N	2.28	0.48
1:B:45:TYR:CE2	1:B:70:ALA:HA	2.49	0.48
2:J:195:SER:C	2:J:197:LEU:H	2.17	0.48
1:B:87:LYS:C	1:B:89:LYS:H	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:ILE:O	1:C:126:ASN:HB3	2.12	0.48
1:A:16:LEU:HD11	1:A:52:HIS:HD2	1.78	0.48
3:K:35:THR:O	3:K:39:VAL:HG23	2.13	0.48
5:M:163:MET:O	5:M:167:MET:HG2	2.13	0.48
1:B:284:VAL:O	1:B:326:ILE:HG12	2.13	0.48
1:D:606:GLU:O	1:D:610:ASP:N	2.46	0.48
1:A:196:ILE:HD12	1:A:316:LEU:HD22	1.96	0.48
1:E:307:ALA:HA	1:E:310:GLU:HG2	1.95	0.48
2:G:118:THR:O	2:G:122:LYS:HG2	2.12	0.48
1:E:95:MET:CE	1:E:97:ILE:HD11	2.42	0.48
1:C:322:LEU:HD12	1:C:324:ILE:HD11	1.94	0.48
1:B:43:HIS:HB3	1:B:45:TYR:HE1	1.79	0.48
1:D:564:PHE:HB3	1:D:598:SER:HB3	1.95	0.48
1:A:403:ARG:O	1:A:407:LEU:HG	2.13	0.48
2:I:69:ALA:HB1	2:I:85:PHE:CE1	2.48	0.48
1:F:539:VAL:CB	1:F:643:ILE:HG12	2.39	0.48
4:L:237:VAL:CG2	5:M:60:VAL:HG13	2.43	0.48
1:B:67:ARG:HB2	1:B:67:ARG:HH11	1.79	0.48
1:C:656:GLU:OE2	1:D:648:ARG:NH1	2.46	0.48
1:A:104:LYS:C	1:A:106:ASN:H	2.17	0.48
2:H:256:VAL:HG21	2:H:288:GLN:CG	2.43	0.48
1:B:256:ILE:O	1:B:370:ILE:HA	2.14	0.48
1:C:611:TYR:HE1	1:C:616:PRO:HB2	1.78	0.48
2:H:160:SER:OG	3:K:58:GLN:NE2	2.41	0.48
1:A:436:PHE:HA	1:A:440:GLU:OE2	2.14	0.48
1:B:64:LEU:O	1:B:68:LYS:HG3	2.14	0.48
1:C:64:LEU:HB2	1:C:67:ARG:HH21	1.79	0.48
1:B:528:THR:HG21	1:B:641:LEU:HD13	1.96	0.48
1:E:726:VAL:O	1:E:730:LEU:HG	2.14	0.48
1:D:655:MET:O	1:D:656:GLU:HB2	2.13	0.48
2:G:246:LYS:NZ	2:G:258:SER:HB3	2.29	0.48
1:A:411:THR:HG21	1:A:426:ILE:HD11	1.95	0.48
1:D:402:GLY:HA2	1:D:405:GLN:OE1	2.14	0.48
3:K:85:LYS:HG3	3:K:89:TRP:HE3	1.79	0.48
1:B:36:ILE:O	1:B:36:ILE:HG23	2.13	0.48
1:C:612:VAL:CG2	1:C:613:PRO:HD2	2.44	0.48
2:G:231:LEU:HD22	2:J:271:ARG:NH1	2.29	0.48
1:F:542:GLU:O	1:F:666:HIS:ND1	2.46	0.48
1:D:582:CYS:O	1:D:586:LYS:HG3	2.14	0.48
1:F:658:LEU:HA	1:F:661:PHE:HD2	1.79	0.48
2:I:81:ALA:O	2:I:85:PHE:HD1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:281:GLU:N	1:F:282:PRO:HA	2.29	0.48
2:J:200:TYR:O	2:J:203:LYS:HE2	2.13	0.48
2:G:17:ALA:O	2:G:21:VAL:HG12	2.14	0.48
1:A:315:ARG:C	1:A:316:LEU:HD12	2.34	0.48
1:A:423:ASP:O	1:A:479:ASP:N	2.46	0.48
1:F:653:GLN:HB3	1:F:658:LEU:HD23	1.96	0.48
1:A:715:GLU:HG3	1:F:527:GLN:NE2	2.27	0.48
2:G:239:ARG:HH11	4:L:210:ARG:NH1	2.10	0.48
2:G:101:ILE:HG13	2:G:102:ASN:H	1.79	0.48
1:D:542:GLU:OE2	1:D:649:LYS:HD2	2.14	0.48
1:E:248:MET:HA	1:F:449:GLN:OE1	2.13	0.48
1:D:609:LEU:HD12	1:D:611:TYR:H	1.77	0.48
1:D:530:ASN:ND2	1:E:719:GLN:OE1	2.40	0.48
1:D:358:ILE:CD1	1:D:388:ARG:HB3	2.42	0.48
1:B:67:ARG:HH11	1:B:67:ARG:CB	2.27	0.48
1:B:67:ARG:HB3	2:I:218:MET:SD	2.53	0.48
1:C:576:PHE:HB3	1:C:580:ALA:HB3	1.96	0.48
1:B:545:PRO:O	1:B:546:HIS:HB2	2.13	0.48
2:I:138:VAL:O	2:I:142:ILE:HG13	2.14	0.48
1:E:721:ASP:HB2	1:E:724:TYR:CD2	2.48	0.48
2:H:281:LEU:O	2:H:285:LYS:HG3	2.14	0.48
1:C:122:ILE:HD11	1:C:183:VAL:HG23	1.96	0.48
2:J:232:PHE:O	2:J:234:ALA:N	2.47	0.48
1:B:74:ILE:HG13	2:I:218:MET:CE	2.44	0.48
1:C:436:PHE:CD1	1:C:436:PHE:N	2.82	0.48
1:C:590:ASP:HA	1:C:593:TYR:HD2	1.77	0.48
1:B:232:ARG:O	1:B:236:ALA:HB3	2.14	0.48
2:I:98:GLN:CD	2:I:98:GLN:H	2.17	0.48
1:A:97:ILE:HG21	1:A:147:LEU:HD22	1.94	0.48
1:F:86:ASP:C	1:F:88:ALA:H	2.17	0.48
1:D:184:ALA:HB1	1:D:200:LYS:O	2.14	0.48
1:F:440:GLU:O	1:F:444:LEU:HG	2.14	0.47
2:J:223:LEU:O	2:J:227:LYS:HG3	2.14	0.47
1:A:445:VAL:O	1:A:449:GLN:HG2	2.14	0.47
1:F:635:PRO:HB2	1:F:638:ARG:NH1	2.29	0.47
1:B:541:LEU:HA	1:B:665:ILE:O	2.14	0.47
1:F:286:ASN:OD1	1:F:327:PHE:HD1	1.97	0.47
1:A:113:ASP:OD2	1:A:316:LEU:HD11	2.14	0.47
1:D:635:PRO:O	1:D:638:ARG:HB2	2.14	0.47
1:A:258:LEU:O	1:A:258:LEU:HD12	2.13	0.47
1:A:104:LYS:HA	1:A:107:ILE:HG13	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:287:ILE:O	2:I:291:GLU:HG3	2.13	0.47
1:B:593:TYR:O	1:B:638:ARG:NE	2.46	0.47
1:C:265:GLY:O	1:C:268:LEU:HG	2.14	0.47
1:D:499:TYR:N	1:D:499:TYR:CD1	2.80	0.47
2:J:243:LEU:HD13	2:J:266:TYR:HB2	1.95	0.47
1:E:404:LEU:HG	1:E:426:ILE:HG22	1.96	0.47
1:B:576:PHE:HB2	1:B:581:LYS:HG3	1.96	0.47
1:D:527:GLN:NE2	1:E:715:GLU:C	2.66	0.47
1:C:513:PRO:HA	1:C:516:ARG:HG2	1.95	0.47
1:E:64:LEU:N	1:E:67:ARG:NH2	2.59	0.47
2:I:147:GLN:HG2	2:I:151:TYR:CE2	2.48	0.47
2:J:40:GLU:O	2:J:44:ILE:HG12	2.14	0.47
1:D:578:GLU:OE1	1:D:621:LEU:HD13	2.15	0.47
1:B:516:ARG:O	1:B:519:ASP:OD1	2.32	0.47
1:C:237:SER:OG	1:C:252:HIS:ND1	2.41	0.47
1:F:655:MET:O	1:F:656:GLU:CG	2.62	0.47
2:I:246:LYS:HZ1	2:I:258:SER:HB3	1.79	0.47
1:F:34:HIS:HB2	1:F:83:TYR:O	2.14	0.47
1:C:270:ALA:O	1:C:273:ILE:HG22	2.15	0.47
1:A:489:LYS:N	1:A:490:PRO:HD2	2.29	0.47
2:G:21:VAL:HG23	2:G:38:ILE:HD13	1.95	0.47
2:H:232:PHE:HB2	2:H:233:PRO:HD3	1.96	0.47
1:C:609:LEU:O	1:C:610:ASP:HB2	2.14	0.47
1:D:593:TYR:HB3	1:D:635:PRO:HD3	1.96	0.47
1:F:396:GLY:O	1:F:397:LEU:HG	2.14	0.47
1:C:135:GLN:HG2	1:C:148:LEU:HD13	1.97	0.47
1:A:231:PHE:CE2	1:A:235:PHE:HD2	2.33	0.47
1:A:347:HIS:N	1:A:348:ASP:HA	2.29	0.47
5:M:36:VAL:HG23	5:M:37:GLU:N	2.29	0.47
1:A:34:HIS:HB2	1:A:83:TYR:O	2.14	0.47
1:D:669:ASN:N	1:D:669:ASN:OD1	2.47	0.47
2:J:188:VAL:HG22	2:J:205:TYR:HE2	1.79	0.47
1:D:101:PHE:CD2	1:D:107:ILE:HA	2.48	0.47
1:F:557:ALA:HB2	1:F:601:VAL:HG21	1.96	0.47
1:A:100:ASP:O	1:A:146:GLY:N	2.48	0.47
1:C:618:PHE:HE1	1:C:620:ASN:OD1	1.97	0.47
3:K:59:LYS:HE2	5:M:175:ASN:HB3	1.95	0.47
1:E:549:LYS:HD2	1:E:645:THR:HB	1.96	0.47
3:K:30:ARG:O	3:K:34:GLN:HB2	2.14	0.47
1:A:388:ARG:O	1:A:389:LEU:HD22	2.15	0.47
2:G:117:PHE:HD2	2:J:53:LYS:HE3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:80:ASP:OD2	5:M:191:ARG:NH1	2.48	0.47
1:A:64:LEU:O	1:A:68:LYS:HG3	2.15	0.47
1:D:265:GLY:O	1:D:268:LEU:HG	2.14	0.47
1:B:451:THR:HG22	1:B:455:ARG:HH21	1.79	0.47
1:A:91:CYS:O	1:A:154:ALA:HA	2.14	0.47
1:F:569:SER:O	1:F:572:LYS:HB2	2.14	0.47
1:C:232:ARG:O	1:C:236:ALA:HB3	2.14	0.47
1:D:690:GLU:HB2	1:D:726:VAL:CG2	2.44	0.47
1:A:424:VAL:HG22	1:A:479:ASP:O	2.15	0.47
1:E:303:ARG:CG	1:E:357:LYS:HE2	2.44	0.47
1:D:528:THR:HG22	1:D:597:LEU:HD11	1.95	0.47
1:A:627:LEU:O	1:A:631:LYS:NZ	2.47	0.47
1:D:268:LEU:O	1:D:271:ARG:HG2	2.14	0.47
2:G:276:LEU:O	2:G:280:LEU:HG	2.14	0.47
2:J:124:HIS:HE1	2:J:147:GLN:HB3	1.80	0.47
1:E:633:ALA:HA	1:E:634:PRO:HD3	1.81	0.47
2:G:235:PHE:HB3	5:M:31:ARG:CG	2.45	0.47
2:J:203:LYS:NZ	2:J:236:SER:HB3	2.29	0.47
1:A:571:ASP:HA	1:A:574:ILE:HG23	1.95	0.47
1:B:523:LEU:HA	1:B:526:GLN:HG2	1.95	0.47
1:C:240:PHE:HZ	1:D:456:HIS:HB3	1.80	0.47
1:E:550:THR:HG23	1:E:603:ASP:OD1	2.14	0.47
1:A:326:ILE:HG22	1:A:370:ILE:CG1	2.43	0.47
1:C:510:TRP:O	1:C:675:GLN:HG3	2.14	0.47
3:K:70:LEU:CD1	5:M:192:ILE:HD12	2.43	0.47
1:A:617:ARG:NH1	1:A:617:ARG:HG3	2.29	0.47
1:C:399:ASP:O	1:C:402:GLY:N	2.48	0.47
2:I:72:HIS:HE1	2:I:80:ASP:HB2	1.80	0.47
1:C:284:VAL:HG11	1:C:305:LEU:HD11	1.96	0.47
1:E:289:GLU:C	1:E:291:LEU:H	2.14	0.47
1:B:640:LEU:CD2	1:B:642:ILE:HG13	2.45	0.47
4:L:248:VAL:O	4:L:252:LYS:HG3	2.15	0.47
1:D:231:PHE:CD1	1:D:235:PHE:HD2	2.32	0.47
1:E:406:ILE:HB	1:E:441:LEU:HD13	1.96	0.47
1:E:272:GLN:HA	1:E:272:GLN:OE1	2.15	0.47
2:J:281:LEU:O	2:J:285:LYS:HG3	2.15	0.47
2:H:243:LEU:HD22	2:H:266:TYR:CD2	2.49	0.47
1:F:508:ILE:C	1:F:509:LYS:HD3	2.34	0.47
2:I:203:LYS:CE	5:M:161:ARG:HH12	2.21	0.47
1:D:609:LEU:O	1:D:610:ASP:OD1	2.33	0.47
1:C:285:VAL:HA	1:C:326:ILE:HG13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:546:HIS:HB3	1:D:708:LYS:HB3	1.97	0.47
1:D:608:LEU:O	1:D:622:VAL:HG11	2.15	0.47
1:C:511:GLY:CA	1:C:513:PRO:HD2	2.45	0.47
1:B:499:TYR:HA	1:B:502:TYR:CE2	2.50	0.47
1:F:121:PHE:HD2	1:F:183:VAL:HG21	1.79	0.47
1:C:353:GLN:HA	1:D:288:PRO:CG	2.44	0.47
1:A:215:PHE:N	1:A:231:PHE:CZ	2.83	0.47
1:B:85:PHE:HE2	1:B:174:VAL:HG22	1.79	0.47
1:F:450:SER:O	1:F:453:MET:HB2	2.15	0.47
1:D:330:ILE:HD12	1:D:331:ASP:N	2.30	0.47
2:H:51:MET:O	2:H:54:MET:HB3	2.15	0.47
4:L:237:VAL:HG21	5:M:60:VAL:HG22	1.96	0.47
1:E:563:PRO:HD2	1:E:597:LEU:O	2.15	0.47
1:B:388:ARG:O	1:B:389:LEU:HD23	2.15	0.47
5:M:156:ILE:O	5:M:160:LEU:HG	2.15	0.47
1:F:428:GLU:O	1:F:431:VAL:HG12	2.15	0.47
2:I:116:ARG:NH1	5:M:65:ASN:ND2	2.63	0.47
1:E:172:ILE:HD12	1:E:174:VAL:O	2.15	0.47
1:A:299:GLU:OE1	1:A:303:ARG:NH2	2.44	0.47
1:F:597:LEU:HA	1:F:639:LYS:O	2.15	0.47
2:H:63:ASN:O	2:H:67:GLN:HG3	2.14	0.47
1:D:694:ILE:O	1:D:698:VAL:HG22	2.15	0.47
1:D:581:LYS:O	1:D:585:MET:HG2	2.15	0.47
1:D:586:LYS:HG2	1:E:574:ILE:CD1	2.45	0.47
1:C:582:CYS:SG	1:C:621:LEU:HG	2.55	0.47
1:B:428:GLU:O	1:B:431:VAL:HG12	2.15	0.47
1:D:18:LEU:HA	1:D:137:VAL:CG2	2.44	0.47
1:E:717:SER:OG	1:E:729:PHE:HB2	2.15	0.47
2:I:75:LEU:O	2:I:76:GLN:HB2	2.15	0.47
1:B:605:ILE:HD11	1:B:644:GLY:HA3	1.96	0.46
1:C:555:LYS:O	1:C:559:GLU:HG2	2.15	0.46
1:C:453:MET:O	1:C:457:ILE:HD12	2.14	0.46
1:D:627:LEU:CD1	1:E:607:ARG:HH12	2.28	0.46
1:B:533:ARG:HD2	1:C:711:LEU:CD1	2.45	0.46
2:G:124:HIS:HA	2:G:127:ILE:HG12	1.97	0.46
1:E:106:ASN:HB3	1:E:143:LYS:HZ1	1.77	0.46
1:C:593:TYR:CE2	1:C:632:LYS:NZ	2.83	0.46
2:G:263:VAL:HG23	2:G:280:LEU:HD13	1.96	0.46
1:B:319:ASN:HB3	1:B:320:SER:HB2	1.97	0.46
1:F:46:ILE:HD12	1:F:174:VAL:HG21	1.97	0.46
1:B:104:LYS:HA	1:B:107:ILE:HG13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:49:ALA:HB2	2:J:64:ALA:HB3	1.97	0.46
1:B:503:ILE:HD11	1:B:554:ALA:HB3	1.96	0.46
1:A:299:GLU:HG3	1:B:289:GLU:CB	2.45	0.46
2:H:232:PHE:N	2:H:233:PRO:CD	2.78	0.46
1:E:246:GLU:HG2	1:E:247:GLN:N	2.30	0.46
2:J:182:ILE:CG2	2:J:212:CYS:HB2	2.45	0.46
2:H:81:ALA:O	2:H:85:PHE:HD1	1.97	0.46
1:D:267:THR:HA	1:D:372:MET:SD	2.55	0.46
5:M:74:ALA:O	5:M:78:LEU:HG	2.15	0.46
1:A:169:ARG:HG2	1:A:169:ARG:HH11	1.80	0.46
1:A:407:LEU:O	1:A:411:THR:HG23	2.15	0.46
2:G:96:ASP:N	2:G:97:PRO:HD2	2.31	0.46
2:H:216:ILE:HG12	2:H:220:ASN:HB2	1.97	0.46
1:A:45:TYR:CE2	1:A:70:ALA:HA	2.50	0.46
3:K:39:VAL:HA	5:M:157:ILE:HG21	1.97	0.46
1:E:241:PRO:HA	1:E:242:PRO:HA	1.62	0.46
1:B:242:PRO:HD2	1:B:243:GLU:H	1.79	0.46
2:H:213:HIS:CE1	2:H:221:ALA:HB2	2.30	0.46
1:A:686:PHE:CE2	1:A:714:ILE:HG23	2.50	0.46
2:G:266:TYR:C	2:G:268:SER:H	2.19	0.46
1:A:240:PHE:HD2	1:B:453:MET:SD	2.38	0.46
1:B:327:PHE:CE2	1:B:369:VAL:HG21	2.50	0.46
1:A:101:PHE:CE1	1:A:193:LEU:HD13	2.50	0.46
3:K:77:PHE:CZ	5:M:195:ALA:HB1	2.50	0.46
1:B:677:LEU:O	1:B:681:GLU:HG3	2.15	0.46
1:B:579:THR:O	1:B:583:GLN:HG2	2.15	0.46
2:H:162:ASN:O	2:H:166:LEU:HG	2.15	0.46
2:I:271:ARG:HA	2:I:271:ARG:HD3	1.75	0.46
2:I:166:LEU:HD21	2:I:205:TYR:CE2	2.50	0.46
1:E:240:PHE:HE1	1:F:457:ILE:CD1	2.26	0.46
1:C:681:GLU:HG3	1:C:691:ARG:HD2	1.98	0.46
1:A:607:ARG:HD3	1:F:624:GLN:NE2	2.29	0.46
2:J:95:ALA:HB1	2:J:97:PRO:HD2	1.97	0.46
1:D:116:LYS:HZ3	1:D:116:LYS:HB3	1.79	0.46
1:C:194:ASN:ND2	1:C:316:LEU:CG	2.79	0.46
1:D:223:LEU:HD12	1:D:395:ILE:HG23	1.96	0.46
1:D:153:GLU:OE1	1:D:169:ARG:HD3	2.15	0.46
1:E:398:PRO:HG2	1:E:434:LYS:O	2.15	0.46
2:I:46:ALA:O	2:I:50:ASN:HB2	2.14	0.46
1:A:223:LEU:CD1	1:A:227:PHE:HB2	2.46	0.46
2:I:67:GLN:O	2:I:71:LEU:HG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:LYS:NZ	1:A:518:LEU:HD11	2.31	0.46
1:C:299:GLU:OE2	1:C:349:THR:OG1	2.22	0.46
1:B:320:SER:OG	1:B:320:SER:O	2.32	0.46
2:I:126:SER:O	2:I:130:ILE:HG13	2.16	0.46
1:E:319:ASN:HB3	1:E:320:SER:HB2	1.96	0.46
1:D:264:CYS:HA	1:D:437:SER:HB3	1.96	0.46
1:E:327:PHE:CZ	1:E:369:VAL:HG21	2.50	0.46
1:E:36:ILE:O	1:E:36:ILE:HG23	2.15	0.46
1:F:241:PRO:HA	1:F:242:PRO:HA	1.67	0.46
1:B:596:GLN:HA	1:B:638:ARG:HG2	1.97	0.46
1:B:612:VAL:HG13	1:B:614:ILE:O	2.16	0.46
2:G:260:THR:HA	2:G:263:VAL:HG12	1.97	0.46
1:D:113:ASP:HA	1:D:196:ILE:HG13	1.98	0.46
1:A:99:ILE:HB	1:A:185:PHE:HD2	1.79	0.46
1:A:582:CYS:SG	1:A:621:LEU:HG	2.56	0.46
1:A:261:PRO:HD2	1:A:395:ILE:O	2.15	0.46
1:C:652:LEU:HD22	1:C:657:MET:HG2	1.97	0.46
1:D:121:PHE:CD2	1:D:183:VAL:HG21	2.50	0.46
2:I:101:ILE:HB	2:I:131:TYR:OH	2.16	0.46
1:A:597:LEU:C	1:A:597:LEU:HD23	2.36	0.46
1:A:149:VAL:HG11	1:A:152:ILE:HD11	1.98	0.46
1:F:577:SER:O	1:F:581:LYS:HG3	2.16	0.46
1:C:566:LYS:HD2	1:C:567:ILE:H	1.80	0.46
2:G:232:PHE:HB2	2:G:233:PRO:HD3	1.98	0.46
1:E:714:ILE:O	1:E:718:LEU:HG	2.16	0.46
1:F:542:GLU:N	1:F:665:ILE:O	2.48	0.46
1:E:436:PHE:CD1	1:E:436:PHE:N	2.83	0.46
1:E:519:ASP:O	1:E:522:GLU:HB2	2.16	0.46
1:C:325:ILE:HG13	1:C:369:VAL:HG23	1.97	0.46
1:B:397:LEU:HD11	1:B:638:ARG:NH2	2.30	0.46
2:H:184:ILE:O	2:H:188:VAL:HG12	2.14	0.46
1:D:731:ALA:HA	1:D:734:ARG:HH12	1.81	0.46
1:D:136:LEU:H	1:D:136:LEU:HD23	1.80	0.46
2:I:179:GLN:HA	2:I:182:ILE:HG12	1.98	0.46
4:L:247:ALA:O	4:L:251:THR:HG23	2.16	0.46
2:G:260:THR:HG21	2:G:284:LYS:HE3	1.96	0.46
1:B:631:LYS:NZ	1:C:604:ASP:OD2	2.45	0.46
2:J:118:THR:O	2:J:122:LYS:HG2	2.16	0.46
1:E:56:VAL:HG13	1:E:57:PRO:HD2	1.98	0.46
1:C:143:LYS:HB3	1:C:145:PHE:HE1	1.81	0.46
1:B:121:PHE:CD2	1:B:183:VAL:HG21	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:192:LEU:HD22	4:L:192:LEU:N	2.31	0.46
2:I:200:TYR:HD1	2:I:200:TYR:H	1.62	0.46
1:E:524:LEU:HD11	1:E:663:THR:HG21	1.98	0.46
1:F:254:LYS:O	1:F:368:LEU:HA	2.16	0.46
1:E:549:LYS:O	1:E:552:LEU:HB2	2.15	0.46
1:D:510:TRP:CE3	1:D:675:GLN:HG2	2.37	0.46
2:I:127:ILE:HG23	2:I:131:TYR:CE1	2.51	0.46
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.98	0.46
1:E:648:ARG:NE	1:E:651:VAL:HG13	2.31	0.46
1:B:327:PHE:CZ	1:B:369:VAL:HG21	2.50	0.46
1:B:593:TYR:OH	1:B:632:LYS:HG2	2.16	0.46
2:J:118:THR:HB	5:M:59:ARG:HH12	1.81	0.46
2:I:40:GLU:O	2:I:44:ILE:HG12	2.16	0.46
2:G:208:LYS:HG2	2:G:275:TRP:CZ3	2.51	0.46
1:B:721:ASP:HB2	1:B:724:TYR:CD1	2.51	0.46
2:J:180:LYS:O	2:J:184:ILE:HG13	2.16	0.46
2:G:45:TYR:HE2	2:G:71:LEU:HD11	1.81	0.46
1:E:624:GLN:CD	1:F:610:ASP:OD1	2.53	0.46
2:G:213:HIS:HE1	2:G:221:ALA:HB2	1.81	0.46
1:D:545:PRO:O	1:D:546:HIS:HB2	2.16	0.46
1:C:677:LEU:HD21	1:C:695:ALA:CB	2.46	0.46
1:D:528:THR:HG21	1:D:641:LEU:HD12	1.98	0.46
1:A:609:LEU:O	1:A:610:ASP:HB3	2.16	0.46
1:E:696:GLN:HA	1:E:696:GLN:OE1	2.15	0.46
1:F:502:TYR:CD2	1:F:503:ILE:HG13	2.51	0.46
2:J:186:GLU:O	2:J:190:THR:HG23	2.16	0.46
1:C:560:SER:HB2	1:C:562:PHE:CZ	2.51	0.46
1:D:121:PHE:HD2	1:D:183:VAL:HG21	1.81	0.46
3:K:51:ASP:O	3:K:55:GLU:HG3	2.15	0.45
1:F:323:HIS:HB2	1:F:367:ILE:HG22	1.98	0.45
1:E:325:ILE:O	1:E:369:VAL:HG23	2.15	0.45
1:D:128:GLN:O	1:D:176:LEU:HD12	2.15	0.45
1:E:125:PHE:HA	1:E:128:GLN:HE22	1.81	0.45
2:H:138:VAL:O	2:H:142:ILE:HG13	2.16	0.45
2:I:80:ASP:OD1	5:M:66:HIS:HD2	1.98	0.45
1:D:616:PRO:HG2	1:E:614:ILE:HG21	1.98	0.45
1:C:322:LEU:HD22	1:C:366:ASN:O	2.17	0.45
1:D:577:SER:O	1:D:580:ALA:N	2.49	0.45
1:C:540:LEU:HD22	1:C:661:PHE:CE2	2.51	0.45
1:E:307:ALA:O	1:E:310:GLU:HG2	2.16	0.45
1:F:388:ARG:O	1:F:389:LEU:HD23	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:231:PHE:CE1	1:C:235:PHE:CD2	3.04	0.45
1:C:428:GLU:O	1:C:431:VAL:HG12	2.16	0.45
1:E:121:PHE:CE2	1:E:183:VAL:HG21	2.52	0.45
1:B:122:ILE:O	1:B:126:ASN:HB3	2.15	0.45
1:C:69:TRP:CE2	1:C:134:GLN:HA	2.51	0.45
1:D:508:ILE:HG12	1:D:683:LEU:HD21	1.97	0.45
1:A:36:ILE:O	1:A:36:ILE:HG23	2.17	0.45
2:H:203:LYS:HB2	2:H:203:LYS:HE3	1.74	0.45
1:F:400:GLU:OE2	1:F:434:LYS:HA	2.15	0.45
3:K:48:VAL:O	3:K:52:LYS:HG3	2.16	0.45
1:C:508:ILE:HD13	1:C:683:LEU:HD21	1.98	0.45
1:A:241:PRO:HA	1:A:242:PRO:HA	1.52	0.45
1:A:258:LEU:O	1:A:372:MET:HA	2.16	0.45
2:I:45:TYR:HE2	2:I:71:LEU:HD11	1.81	0.45
2:I:243:LEU:HD22	2:I:266:TYR:CG	2.50	0.45
2:I:223:LEU:O	2:I:227:LYS:HG3	2.17	0.45
1:E:16:LEU:HD11	1:E:52:HIS:HD2	1.82	0.45
1:F:319:ASN:HB3	1:F:320:SER:HB2	1.99	0.45
1:F:377:ASP:OD1	1:F:378:LEU:N	2.49	0.45
1:F:579:THR:O	1:F:583:GLN:HG2	2.17	0.45
2:H:10:ALA:HB1	2:H:52:PHE:CZ	2.50	0.45
2:H:53:LYS:HE3	2:I:117:PHE:CE2	2.51	0.45
2:I:200:TYR:CB	5:M:161:ARG:HD2	2.32	0.45
5:M:161:ARG:HG2	5:M:165:LEU:HG	1.98	0.45
1:D:303:ARG:HD3	1:D:353:GLN:CD	2.37	0.45
1:D:618:PHE:CE2	1:E:614:ILE:HD12	2.52	0.45
1:A:121:PHE:CD2	1:A:183:VAL:HG21	2.51	0.45
1:E:573:MET:SD	1:E:581:LYS:HG2	2.55	0.45
1:A:611:TYR:HD1	1:A:618:PHE:HB3	1.81	0.45
1:B:452:ALA:HA	1:B:455:ARG:NH2	2.32	0.45
1:A:36:ILE:HD11	1:A:44:LYS:HB3	1.97	0.45
1:D:281:GLU:N	1:D:282:PRO:HA	2.31	0.45
1:D:377:ASP:OD1	1:D:378:LEU:N	2.50	0.45
2:G:176:GLU:O	2:G:178:TYR:N	2.49	0.45
1:D:246:GLU:HG2	1:D:247:GLN:N	2.32	0.45
2:I:184:ILE:O	2:I:188:VAL:HG12	2.17	0.45
1:E:531:SER:HB3	1:E:534:THR:O	2.16	0.45
1:E:534:THR:HG23	1:F:715:GLU:HG3	1.97	0.45
3:K:52:LYS:HE2	5:M:168:GLY:CA	2.46	0.45
1:F:327:PHE:CE2	1:F:369:VAL:HG21	2.51	0.45
1:F:309:ALA:HB1	1:F:367:ILE:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:327:PHE:CE2	1:E:369:VAL:HG21	2.52	0.45
1:B:589:PHE:CD2	1:B:629:LEU:HD13	2.51	0.45
1:F:502:TYR:CE2	1:F:554:ALA:HB2	2.50	0.45
1:F:686:PHE:HB3	1:F:690:GLU:HB2	1.99	0.45
1:E:666:HIS:HD2	1:E:668:PRO:HD3	1.81	0.45
2:G:10:ALA:O	2:G:14:LEU:HG	2.17	0.45
1:C:703:VAL:O	1:C:704:TRP:HD1	2.00	0.45
1:B:4:ARG:HD3	1:B:29:TYR:OH	2.17	0.45
2:G:75:LEU:O	2:G:76:GLN:HB3	2.17	0.45
1:E:586:LYS:O	1:E:589:PHE:HB2	2.17	0.45
1:B:241:PRO:HA	1:B:242:PRO:HA	1.61	0.45
2:G:222:LYS:HA	2:G:225:VAL:HG12	1.98	0.45
1:A:502:TYR:N	1:A:502:TYR:CD1	2.84	0.45
1:C:691:ARG:HB2	1:C:691:ARG:NH1	2.32	0.45
1:A:358:ILE:HD12	1:A:359:ASP:H	1.81	0.45
1:D:624:GLN:OE1	1:D:624:GLN:HA	2.16	0.45
1:C:378:LEU:HA	1:C:378:LEU:HD23	1.85	0.45
4:L:214:ASP:O	4:L:217:MET:HB2	2.17	0.45
2:I:119:ILE:HD11	2:I:123:HIS:HE1	1.82	0.45
1:B:540:LEU:HD11	1:B:649:LYS:HZ1	1.81	0.45
1:B:485:GLU:O	1:B:490:PRO:HD3	2.17	0.45
1:E:286:ASN:OD1	1:E:327:PHE:HD1	2.00	0.45
1:A:327:PHE:CE1	1:A:330:ILE:HG22	2.52	0.45
1:C:333:ILE:O	1:C:351:VAL:HG22	2.17	0.45
2:G:114:MET:O	2:J:50:ASN:ND2	2.41	0.45
1:B:612:VAL:HG12	1:B:617:ARG:O	2.16	0.45
1:D:564:PHE:HD2	1:D:598:SER:HB2	1.81	0.45
1:E:24:VAL:HG21	1:E:29:TYR:HB2	1.98	0.45
1:F:36:ILE:O	1:F:36:ILE:HG23	2.17	0.45
2:H:255:ASN:OD1	2:H:258:SER:N	2.46	0.45
1:B:281:GLU:N	1:B:282:PRO:HA	2.31	0.45
1:A:331:ASP:CA	1:A:379:ILE:HD11	2.38	0.45
1:E:587:LYS:HZ1	1:E:591:ASP:CG	2.20	0.45
1:A:566:LYS:HA	1:A:566:LYS:HD3	1.63	0.45
1:F:552:LEU:HD12	1:F:667:VAL:HG21	1.98	0.45
1:A:355:LEU:HD22	1:A:388:ARG:NH1	2.32	0.45
1:F:23:VAL:HG12	1:F:55:VAL:CG2	2.46	0.45
2:H:167:LYS:HE2	2:H:171:TYR:CE2	2.52	0.45
1:B:423:ASP:HB3	1:B:479:ASP:N	2.31	0.45
1:F:136:LEU:H	1:F:136:LEU:HD23	1.82	0.45
1:C:241:PRO:HA	1:C:242:PRO:HA	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:99:ILE:HG23	1:F:193:LEU:HD23	1.99	0.45
1:C:36:ILE:HG23	1:C:36:ILE:O	2.16	0.45
1:E:611:TYR:CE1	1:E:616:PRO:HB2	2.52	0.45
2:G:254:GLN:HB2	2:G:291:GLU:HG2	1.98	0.45
2:I:162:ASN:O	2:I:166:LEU:HG	2.17	0.45
1:C:331:ASP:CA	1:C:379:ILE:HD11	2.45	0.45
2:I:195:SER:C	2:I:197:LEU:H	2.19	0.45
1:C:612:VAL:CG1	1:C:617:ARG:HB3	2.47	0.45
2:J:263:VAL:O	2:J:267:ASP:HB2	2.17	0.45
1:A:215:PHE:N	1:A:231:PHE:CE2	2.85	0.45
2:G:142:ILE:HG23	2:G:168:VAL:HG13	1.99	0.45
1:F:24:VAL:HG12	1:F:60:VAL:HG13	1.98	0.45
1:D:486:ASN:O	1:D:490:PRO:HD3	2.17	0.45
1:F:588:ILE:O	1:F:591:ASP:HB2	2.17	0.45
1:C:528:THR:O	1:C:639:LYS:HD3	2.16	0.45
4:L:205:LEU:O	4:L:209:ILE:HG13	2.17	0.45
2:J:203:LYS:HZ3	2:J:236:SER:HB3	1.82	0.45
1:C:401:LYS:O	1:C:404:LEU:HB3	2.16	0.45
1:A:571:ASP:OD1	1:A:572:LYS:N	2.49	0.45
1:D:388:ARG:O	1:D:389:LEU:HD23	2.17	0.45
1:F:322:LEU:HD12	1:F:323:HIS:N	2.32	0.45
1:C:705:ILE:HD11	1:C:710:LEU:HA	1.98	0.45
1:C:576:PHE:HB2	1:C:581:LYS:HG2	1.98	0.45
1:A:255:GLY:HA3	1:A:389:LEU:HD13	1.99	0.45
2:J:81:ALA:O	2:J:85:PHE:HD1	1.99	0.45
1:B:268:LEU:HD12	1:B:269:LEU:N	2.32	0.45
2:J:147:GLN:HG2	2:J:151:TYR:CE2	2.52	0.45
2:J:57:ASN:O	2:J:59:SER:N	2.48	0.45
2:G:126:SER:O	2:G:130:ILE:HG13	2.17	0.45
2:J:10:ALA:N	2:J:51:MET:SD	2.90	0.45
4:L:206:GLU:O	4:L:209:ILE:HB	2.17	0.44
3:K:52:LYS:HE2	5:M:168:GLY:HA2	1.99	0.44
1:C:611:TYR:HE2	1:C:648:ARG:NH1	2.14	0.44
2:G:67:GLN:O	2:G:71:LEU:HG	2.17	0.44
2:G:120:ALA:O	2:G:124:HIS:HB2	2.17	0.44
2:G:124:HIS:CE1	2:G:147:GLN:HB3	2.50	0.44
1:A:124:GLN:NE2	1:A:125:PHE:CE1	2.82	0.44
1:E:65:PRO:HG2	1:E:137:VAL:HG13	1.99	0.44
1:C:325:ILE:O	1:C:369:VAL:HA	2.17	0.44
1:D:286:ASN:CB	1:D:327:PHE:HD1	2.30	0.44
1:B:20:ASN:ND2	1:B:66:GLN:NE2	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:311:GLU:O	1:C:314:ARG:HG2	2.18	0.44
1:E:236:ALA:HB1	1:F:453:MET:HB3	1.98	0.44
2:G:182:ILE:O	2:G:186:GLU:HG2	2.17	0.44
1:C:604:ASP:N	1:C:645:THR:OG1	2.44	0.44
1:D:132:VAL:HG23	1:D:173:GLU:O	2.17	0.44
1:C:114:THR:CB	1:C:199:ALA:HB3	2.47	0.44
1:B:626:LEU:O	1:B:630:LEU:HG	2.17	0.44
1:F:677:LEU:O	1:F:681:GLU:HG3	2.17	0.44
1:E:628:VAL:O	1:E:632:LYS:N	2.48	0.44
2:H:118:THR:HG21	3:K:66:ARG:NH2	2.32	0.44
1:F:604:ASP:HB3	1:F:607:ARG:HB2	2.00	0.44
1:B:24:VAL:O	1:B:51:THR:HA	2.17	0.44
1:A:240:PHE:CE1	1:B:457:ILE:HD11	2.52	0.44
1:E:23:VAL:HG12	1:E:55:VAL:HG21	1.98	0.44
1:F:95:MET:CE	1:F:97:ILE:HD11	2.47	0.44
1:A:687:LYS:NZ	1:A:722:PRO:HB3	2.32	0.44
1:A:407:LEU:CD1	1:A:426:ILE:HG23	2.47	0.44
1:B:101:PHE:CE1	1:B:193:LEU:HD13	2.52	0.44
1:B:272:GLN:OE1	1:B:272:GLN:HA	2.16	0.44
1:A:646:THR:HG21	1:A:652:LEU:HD22	2.00	0.44
2:J:232:PHE:C	2:J:234:ALA:N	2.70	0.44
1:C:499:TYR:HB3	1:C:558:GLU:OE2	2.17	0.44
1:B:297:GLU:O	1:B:300:ALA:HB3	2.17	0.44
5:M:26:LEU:HB2	5:M:146:MET:CE	2.46	0.44
1:A:612:VAL:HG12	1:A:617:ARG:HB2	1.99	0.44
1:A:270:ALA:HA	1:A:273:ILE:HG22	1.99	0.44
1:A:563:PRO:HG2	1:A:597:LEU:O	2.17	0.44
2:I:149:ALA:HB2	2:I:164:CYS:CB	2.47	0.44
1:D:95:MET:CE	1:D:97:ILE:HD11	2.47	0.44
1:C:526:GLN:OE1	1:C:530:ASN:ND2	2.50	0.44
1:C:499:TYR:OH	1:C:565:ILE:HB	2.17	0.44
2:G:271:ARG:HH21	2:H:231:LEU:HB2	1.82	0.44
1:E:713:LEU:CD2	1:E:732:LEU:HD13	2.47	0.44
1:E:510:TRP:CE3	1:E:511:GLY:HA3	2.52	0.44
1:A:67:ARG:HH12	1:A:74:ILE:HD11	1.81	0.44
2:I:53:LYS:HE3	2:J:117:PHE:CD2	2.51	0.44
2:I:95:ALA:HB1	2:I:97:PRO:HD2	1.99	0.44
1:C:671:ALA:HA	1:C:703:VAL:O	2.17	0.44
1:E:190:ASN:OD1	1:E:315:ARG:HA	2.18	0.44
1:B:609:LEU:HD23	1:B:622:VAL:HB	1.99	0.44
1:D:685:ASN:HB3	1:D:718:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:179:GLN:O	2:H:182:ILE:HG12	2.17	0.44
2:G:40:GLU:O	2:G:44:ILE:HG12	2.17	0.44
1:C:519:ASP:O	1:C:523:LEU:HG	2.16	0.44
1:C:347:HIS:O	1:C:350:VAL:HG22	2.17	0.44
1:B:377:ASP:OD1	1:B:378:LEU:N	2.50	0.44
1:C:624:GLN:CD	1:D:610:ASP:HB2	2.36	0.44
2:I:218:MET:HB3	2:I:219:LEU:H	1.51	0.44
1:C:677:LEU:O	1:C:681:GLU:OE1	2.35	0.44
1:D:656:GLU:OE1	1:E:613:PRO:HB3	2.17	0.44
1:B:686:PHE:CE1	1:B:714:ILE:HG23	2.53	0.44
1:D:715:GLU:O	1:D:719:GLN:HG2	2.18	0.44
1:B:626:LEU:HA	1:B:626:LEU:HD23	1.66	0.44
2:H:134:GLU:O	2:H:136:VAL:HG23	2.18	0.44
1:D:122:ILE:O	1:D:126:ASN:HB3	2.17	0.44
2:J:32:PHE:H	2:J:32:PHE:HD1	1.66	0.44
2:J:173:ALA:HB3	2:J:275:TRP:HE1	1.82	0.44
2:H:122:LYS:HD2	2:H:152:TYR:OH	2.18	0.44
4:L:226:GLN:HE21	4:L:226:GLN:HB2	1.56	0.44
1:E:264:CYS:HA	1:E:437:SER:HB2	1.98	0.44
1:E:684:GLY:HA2	1:E:691:ARG:NH2	2.33	0.44
1:B:236:ALA:HA	1:B:239:VAL:CG1	2.48	0.44
2:H:188:VAL:HG13	2:H:205:TYR:CD2	2.52	0.44
1:F:605:ILE:O	1:F:608:LEU:HG	2.17	0.44
1:D:99:ILE:HD11	1:D:145:PHE:CD2	2.52	0.44
1:F:86:ASP:OD2	1:F:88:ALA:HB3	2.17	0.44
1:F:24:VAL:O	1:F:51:THR:HA	2.18	0.44
1:B:524:LEU:HD21	1:B:663:THR:HG21	1.98	0.44
1:E:218:MET:HA	1:E:219:GLY:HA2	1.81	0.44
1:E:313:GLN:O	1:E:317:GLY:N	2.50	0.44
1:A:576:PHE:HB3	1:A:580:ALA:HB3	1.99	0.44
1:F:272:GLN:OE1	1:F:272:GLN:HA	2.18	0.44
1:B:254:LYS:O	1:B:368:LEU:HA	2.18	0.44
1:B:627:LEU:HB3	1:C:607:ARG:CZ	2.47	0.44
1:B:541:LEU:O	1:B:541:LEU:HD12	2.17	0.44
1:C:638:ARG:HH11	1:C:638:ARG:HG3	1.82	0.44
1:A:240:PHE:CD2	1:B:453:MET:SD	3.11	0.44
1:F:658:LEU:HD12	1:F:658:LEU:O	2.17	0.44
1:F:23:VAL:HG12	1:F:55:VAL:HG21	2.00	0.44
1:B:286:ASN:OD1	1:B:327:PHE:HD1	2.01	0.44
2:J:66:CYS:SG	2:J:92:PHE:HE2	2.41	0.44
1:A:657:MET:HE2	1:A:661:PHE:HE1	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:LEU:HD23	1:D:137:VAL:HG21	2.00	0.44
1:D:223:LEU:O	1:D:223:LEU:HD23	2.18	0.44
1:F:45:TYR:CE2	1:F:70:ALA:HA	2.52	0.44
1:E:265:GLY:O	1:E:268:LEU:HG	2.18	0.44
1:F:352:ASN:HA	1:F:355:LEU:HD12	1.99	0.44
1:C:441:LEU:HA	1:C:441:LEU:HD23	1.83	0.44
1:F:69:TRP:NE1	1:F:134:GLN:HA	2.33	0.44
4:L:205:LEU:HG	5:M:32:MET:SD	2.57	0.44
2:J:185:TYR:HA	2:J:188:VAL:HG12	2.00	0.44
2:J:185:TYR:CZ	2:J:208:LYS:HD3	2.53	0.44
1:C:611:TYR:HE2	1:C:648:ARG:CZ	2.30	0.44
1:C:618:PHE:CZ	1:D:612:VAL:HG11	2.47	0.44
1:E:590:ASP:O	1:E:593:TYR:HB2	2.18	0.44
1:A:242:PRO:HD2	1:A:243:GLU:H	1.81	0.44
1:D:331:ASP:HA	1:D:379:ILE:HD11	2.00	0.44
1:D:331:ASP:O	1:D:332:ALA:HB3	2.18	0.44
1:E:320:SER:O	1:E:320:SER:OG	2.33	0.44
1:D:22:ALA:HB3	1:D:49:LEU:HD23	2.00	0.44
1:A:117:MET:HE3	1:A:140:PHE:CD2	2.53	0.44
1:B:180:ASN:ND2	1:B:180:ASN:O	2.42	0.44
2:H:223:LEU:O	2:H:227:LYS:HG3	2.18	0.44
1:A:685:ASN:OD1	1:F:533:ARG:CZ	2.66	0.44
2:J:243:LEU:O	2:J:247:LEU:HG	2.18	0.44
2:J:266:TYR:C	2:J:268:SER:H	2.21	0.44
2:H:119:ILE:HD11	2:H:123:HIS:CE1	2.53	0.44
1:A:677:LEU:HD13	1:A:677:LEU:HA	1.79	0.44
1:A:113:ASP:OD1	1:A:115:ASP:HB2	2.17	0.44
1:B:24:VAL:HG12	1:B:60:VAL:HG13	2.00	0.44
1:F:48:THR:HG21	1:F:128:GLN:HG2	2.00	0.44
2:I:108:ILE:HD12	2:I:127:ILE:HD12	1.99	0.44
1:A:64:LEU:HA	1:A:67:ARG:HH21	1.82	0.44
1:E:23:VAL:HG12	1:E:55:VAL:CG2	2.48	0.44
2:J:256:VAL:HG21	2:J:288:GLN:HG3	1.99	0.44
2:I:63:ASN:O	2:I:67:GLN:HG3	2.18	0.44
2:I:281:LEU:O	2:I:285:LYS:HG3	2.17	0.44
2:G:218:MET:HG3	2:G:219:LEU:N	2.32	0.43
1:C:18:LEU:HD23	1:C:137:VAL:HG21	2.00	0.43
1:D:257:LEU:HG	1:D:371:GLY:O	2.17	0.43
1:E:507:ILE:HD12	1:E:555:LYS:HB2	1.98	0.43
1:B:536:LEU:HD12	1:B:640:LEU:O	2.18	0.43
1:B:250:CYS:SG	1:C:446:ARG:HA	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:498:ASP:O	1:D:501:SER:HB3	2.18	0.43
1:E:69:TRP:CE2	1:E:134:GLN:HA	2.53	0.43
1:F:436:PHE:HD2	1:F:444:LEU:HD11	1.83	0.43
1:E:596:GLN:O	1:E:638:ARG:HA	2.17	0.43
1:C:240:PHE:HB3	1:C:244:ILE:HB	2.00	0.43
1:D:256:ILE:HG22	1:D:391:VAL:CG1	2.48	0.43
1:F:648:ARG:O	1:F:652:LEU:HD23	2.18	0.43
1:B:64:LEU:HA	1:B:67:ARG:CZ	2.48	0.43
1:D:73:SER:O	1:D:76:GLN:HG2	2.18	0.43
2:G:112:THR:HG23	2:G:117:PHE:CE1	2.50	0.43
1:E:63:SER:C	1:E:67:ARG:HE	2.22	0.43
1:B:48:THR:HG21	1:B:128:GLN:HG2	2.00	0.43
1:B:172:ILE:HD12	1:B:174:VAL:O	2.18	0.43
1:A:614:ILE:HG23	1:A:614:ILE:O	2.18	0.43
1:E:406:ILE:O	1:E:409:ILE:HG22	2.18	0.43
1:B:318:ALA:O	1:B:319:ASN:ND2	2.51	0.43
2:J:119:ILE:O	2:J:122:LYS:HB2	2.18	0.43
1:D:263:GLY:O	1:D:439:ALA:N	2.51	0.43
1:E:673:GLY:O	1:E:676:LEU:HB3	2.18	0.43
1:E:713:LEU:HD23	1:E:713:LEU:HA	1.82	0.43
2:G:35:SER:HA	2:G:38:ILE:HG22	2.01	0.43
1:A:673:GLY:O	1:A:676:LEU:HB3	2.18	0.43
2:H:21:VAL:HG23	2:H:38:ILE:HD13	2.01	0.43
4:L:237:VAL:O	4:L:241:VAL:HG23	2.17	0.43
1:D:694:ILE:HG12	1:D:726:VAL:HG13	2.00	0.43
2:G:122:LYS:HA	2:G:152:TYR:OH	2.18	0.43
2:J:80:ASP:O	2:J:83:THR:OG1	2.31	0.43
1:C:24:VAL:HG11	1:C:49:LEU:HD22	2.00	0.43
2:H:243:LEU:HD13	2:H:266:TYR:HB2	1.99	0.43
1:F:36:ILE:HG13	1:F:45:TYR:O	2.18	0.43
1:E:190:ASN:OD1	1:E:315:ARG:CB	2.66	0.43
2:G:154:GLY:HA2	2:J:94:LYS:HD3	1.99	0.43
1:F:516:ARG:NH1	1:F:516:ARG:HB3	2.34	0.43
1:C:490:PRO:HA	1:C:491:ALA:CB	2.36	0.43
1:A:624:GLN:NE2	1:B:610:ASP:HA	2.33	0.43
1:B:259:TYR:C	1:B:395:ILE:HD13	2.38	0.43
1:F:18:LEU:HA	1:F:137:VAL:CG2	2.48	0.43
1:E:449:GLN:O	1:E:453:MET:HG2	2.18	0.43
1:A:122:ILE:HD11	1:A:183:VAL:HG23	2.01	0.43
2:J:167:LYS:HE2	2:J:171:TYR:CE2	2.51	0.43
1:B:578:GLU:CG	1:B:619:SER:HB2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:573:MET:HA	1:A:576:PHE:CD2	2.53	0.43
1:E:48:THR:HG22	1:E:49:LEU:N	2.32	0.43
1:C:34:HIS:HB2	1:C:83:TYR:O	2.19	0.43
1:C:193:LEU:HD21	1:C:195:LEU:HD21	2.01	0.43
2:H:161:ALA:O	2:H:165:LEU:HG	2.18	0.43
1:C:696:GLN:NE2	1:C:696:GLN:O	2.51	0.43
2:G:134:GLU:O	2:G:136:VAL:HG23	2.18	0.43
1:E:590:ASP:OD2	1:E:594:LYS:NZ	2.50	0.43
1:F:562:PHE:HB2	1:F:565:ILE:HG12	1.99	0.43
1:B:610:ASP:CG	1:B:610:ASP:O	2.56	0.43
2:H:45:TYR:HE2	2:H:71:LEU:HD11	1.83	0.43
1:C:573:MET:HB3	1:C:576:PHE:CD2	2.53	0.43
2:J:287:ILE:O	2:J:290:ASP:HB3	2.19	0.43
1:F:397:LEU:HB3	1:F:398:PRO:HD3	1.99	0.43
1:B:406:ILE:O	1:B:409:ILE:HG22	2.19	0.43
1:D:258:LEU:HD11	1:D:372:MET:HG2	1.99	0.43
1:D:571:ASP:O	1:D:574:ILE:HG13	2.19	0.43
1:A:98:GLU:HB3	1:A:148:LEU:HB3	2.00	0.43
1:B:91:CYS:O	1:B:154:ALA:HA	2.19	0.43
2:J:126:SER:O	2:J:130:ILE:HG13	2.18	0.43
1:C:330:ILE:HD13	1:C:330:ILE:HA	1.71	0.43
1:D:221:GLY:HA3	1:D:406:ILE:HD13	2.00	0.43
1:B:523:LEU:HD22	1:B:526:GLN:NE2	2.33	0.43
3:K:34:GLN:O	3:K:38:GLN:HG3	2.19	0.43
1:C:326:ILE:HB	1:C:370:ILE:HD11	2.00	0.43
1:B:24:VAL:HG11	1:B:49:LEU:HD22	2.00	0.43
1:B:533:ARG:CG	1:B:534:THR:H	2.24	0.43
1:C:355:LEU:HG	1:C:388:ARG:CZ	2.47	0.43
4:L:210:ARG:HH11	4:L:210:ARG:HG3	1.84	0.43
1:E:721:ASP:HB2	1:E:724:TYR:HD2	1.84	0.43
2:J:118:THR:HB	5:M:59:ARG:NH1	2.34	0.43
1:B:246:GLU:HG2	1:B:247:GLN:N	2.34	0.43
1:A:377:ASP:OD2	1:A:378:LEU:HD23	2.17	0.43
2:H:282:ARG:O	2:H:286:THR:HG23	2.19	0.43
1:B:507:ILE:CG1	1:B:555:LYS:HD3	2.48	0.43
1:E:534:THR:HG21	1:F:712:MET:HA	2.01	0.43
1:B:540:LEU:O	1:B:540:LEU:HD12	2.19	0.43
1:C:721:ASP:HB2	1:C:724:TYR:CD1	2.53	0.43
1:D:589:PHE:CD2	1:D:629:LEU:HD13	2.52	0.43
1:A:50:ARG:HH11	1:A:50:ARG:HG2	1.82	0.43
1:D:272:GLN:HA	1:D:272:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:ASP:O	1:B:479:ASP:N	2.52	0.43
2:J:282:ARG:O	2:J:286:THR:HG23	2.19	0.43
1:C:552:LEU:HD23	1:C:552:LEU:HA	1.75	0.43
1:F:436:PHE:CD2	1:F:444:LEU:HD11	2.54	0.43
1:A:453:MET:C	1:F:232:ARG:HH22	2.22	0.43
1:A:503:ILE:CG2	1:A:506:GLY:H	2.31	0.43
2:G:266:TYR:C	2:G:268:SER:N	2.72	0.43
1:D:728:LYS:O	1:D:732:LEU:HG	2.19	0.43
3:K:53:VAL:HG13	3:K:54:LEU:HD22	2.01	0.43
1:C:542:GLU:HG2	1:C:666:HIS:HA	2.00	0.43
1:B:546:HIS:HD2	1:B:708:LYS:HD2	1.83	0.43
2:G:184:ILE:O	2:G:188:VAL:HG12	2.18	0.43
1:F:503:ILE:O	1:F:503:ILE:HG22	2.19	0.43
2:G:203:LYS:HE3	2:G:203:LYS:HB2	1.75	0.43
1:F:510:TRP:HZ3	1:F:675:GLN:NE2	2.17	0.43
2:J:134:GLU:O	2:J:136:VAL:HG23	2.19	0.43
2:H:178:TYR:OH	2:H:282:ARG:HG2	2.19	0.43
2:J:100:ALA:O	2:J:104:LEU:HG	2.19	0.43
1:E:377:ASP:OD1	1:E:378:LEU:N	2.51	0.43
1:D:218:MET:HA	1:D:219:GLY:HA2	1.76	0.43
2:H:208:LYS:HG2	2:H:275:TRP:CZ3	2.54	0.43
1:E:524:LEU:O	1:E:528:THR:HG23	2.18	0.43
1:E:562:PHE:HE2	1:E:641:LEU:CD2	2.31	0.43
1:E:512:ASP:N	1:E:513:PRO:CD	2.82	0.43
1:A:231:PHE:CD2	1:A:235:PHE:CD2	3.07	0.43
3:K:77:PHE:CD2	4:L:247:ALA:HB1	2.54	0.43
1:A:507:ILE:HD12	1:A:555:LYS:HG2	1.99	0.43
2:I:200:TYR:CE2	3:K:41:GLU:HG3	2.54	0.43
2:I:207:PHE:HB2	2:I:240:GLU:HG2	1.99	0.43
2:J:227:LYS:NZ	2:J:227:LYS:HB3	2.34	0.43
1:C:327:PHE:O	1:C:371:GLY:HA2	2.18	0.43
1:C:624:GLN:OE1	1:C:624:GLN:HA	2.18	0.43
1:C:540:LEU:HD22	1:C:661:PHE:CD2	2.54	0.43
1:F:303:ARG:CG	1:F:357:LYS:HE2	2.44	0.43
1:C:715:GLU:HA	1:C:715:GLU:OE1	2.19	0.43
2:H:263:VAL:O	2:H:267:ASP:HB2	2.19	0.43
1:F:106:ASN:HB3	1:F:143:LYS:HZ2	1.83	0.43
2:I:208:LYS:HG2	2:I:275:TRP:CZ3	2.54	0.43
1:C:20:ASN:HD22	1:C:66:GLN:NE2	2.17	0.43
1:A:411:THR:OG1	1:A:426:ILE:HD11	2.18	0.43
1:A:87:LYS:HA	1:A:91:CYS:SG	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:24:VAL:HG12	1:E:60:VAL:HG13	2.00	0.43
1:C:114:THR:HB	1:C:199:ALA:HB3	2.01	0.43
1:B:103:GLN:C	1:B:105:LYS:H	2.22	0.43
1:E:45:TYR:CE2	1:E:70:ALA:HA	2.54	0.43
1:A:636:GLN:HA	1:A:637:GLY:HA2	1.52	0.43
1:A:543:GLY:N	1:A:549:LYS:HD3	2.34	0.42
1:A:456:HIS:HB2	1:F:240:PHE:CE2	2.53	0.42
2:G:195:SER:C	2:G:197:LEU:N	2.72	0.42
1:D:573:MET:SD	1:D:608:LEU:HD22	2.59	0.42
5:M:177:GLN:HG3	5:M:180:ARG:HH22	1.83	0.42
1:F:721:ASP:O	1:F:725:ARG:HG3	2.18	0.42
1:D:538:SER:OG	1:D:661:PHE:HA	2.19	0.42
2:H:235:PHE:CD1	4:L:204:LYS:HA	2.54	0.42
2:H:260:THR:HA	2:H:263:VAL:HG12	2.00	0.42
1:B:502:TYR:CE2	1:B:567:ILE:HD13	2.54	0.42
4:L:213:HIS:O	4:L:217:MET:HG2	2.19	0.42
1:F:102:LEU:HD23	1:F:144:LEU:HB3	1.99	0.42
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.19	0.42
1:F:262:PRO:HB3	1:F:374:ASN:OD1	2.18	0.42
3:K:45:ILE:CG2	5:M:164:ALA:HB1	2.49	0.42
5:M:161:ARG:HA	5:M:164:ALA:HB3	2.00	0.42
2:J:201:SER:OG	2:J:205:TYR:HE1	2.01	0.42
1:C:542:GLU:HB2	1:C:649:LYS:HD3	2.01	0.42
1:E:571:ASP:O	1:E:574:ILE:HG13	2.19	0.42
1:A:607:ARG:CZ	1:F:627:LEU:HD22	2.48	0.42
5:M:176:ARG:HH11	5:M:176:ARG:HG2	1.83	0.42
1:B:325:ILE:HG13	1:B:369:VAL:HB	2.01	0.42
1:A:235:PHE:CD1	1:A:235:PHE:N	2.86	0.42
2:I:92:PHE:HD1	2:I:97:PRO:HG2	1.83	0.42
1:F:602:VAL:O	1:F:644:GLY:HA2	2.19	0.42
2:H:256:VAL:HG22	2:H:256:VAL:O	2.19	0.42
1:F:441:LEU:O	1:F:445:VAL:HG23	2.19	0.42
2:G:287:ILE:O	2:G:291:GLU:HG3	2.19	0.42
2:J:130:ILE:O	2:J:134:GLU:HB2	2.19	0.42
1:D:539:VAL:HG13	1:D:643:ILE:HG13	2.01	0.42
1:E:701:LYS:HE3	1:E:734:ARG:HH22	1.84	0.42
1:C:709:LYS:HD2	1:C:709:LYS:HA	1.83	0.42
2:J:225:VAL:HG23	2:J:241:CYS:HB2	2.00	0.42
2:H:192:ALA:O	2:H:198:LEU:HB2	2.19	0.42
1:E:230:ILE:HD11	1:E:391:VAL:HG11	2.00	0.42
1:C:320:SER:O	1:C:320:SER:OG	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:404:LEU:HG	1:C:426:ILE:HG22	2.01	0.42
1:B:543:GLY:O	1:B:549:LYS:NZ	2.52	0.42
1:F:314:ARG:CG	1:F:315:ARG:N	2.82	0.42
1:C:511:GLY:HA3	1:C:675:GLN:HE21	1.83	0.42
2:I:106:ARG:O	2:I:109:GLU:HB3	2.19	0.42
1:C:452:ALA:O	1:C:456:HIS:ND1	2.52	0.42
1:E:324:ILE:HG12	1:E:368:LEU:HD11	2.02	0.42
1:A:299:GLU:HG2	1:A:353:GLN:CG	2.48	0.42
1:A:357:LYS:HE3	1:A:357:LYS:HA	2.00	0.42
1:D:227:PHE:O	1:D:230:ILE:HG22	2.18	0.42
1:A:502:TYR:N	1:A:502:TYR:HD1	2.15	0.42
1:C:18:LEU:HD23	1:C:137:VAL:CG2	2.48	0.42
1:E:677:LEU:HD11	1:E:695:ALA:HA	2.00	0.42
1:F:18:LEU:HD23	1:F:137:VAL:HG21	2.01	0.42
1:D:268:LEU:HD12	1:D:269:LEU:N	2.33	0.42
1:D:271:ARG:HG2	1:D:272:GLN:N	2.35	0.42
2:J:46:ALA:O	2:J:50:ASN:HB2	2.19	0.42
2:I:95:ALA:CB	2:I:97:PRO:HD2	2.49	0.42
1:B:513:PRO:O	1:B:517:VAL:HG23	2.19	0.42
5:M:25:SER:O	5:M:28:SER:HB3	2.20	0.42
2:J:267:ASP:OD1	2:J:271:ARG:HD3	2.20	0.42
1:B:64:LEU:HA	1:B:67:ARG:NH2	2.35	0.42
1:B:23:VAL:HG12	1:B:55:VAL:HG21	2.02	0.42
2:G:185:TYR:HB2	2:G:209:ALA:HB2	2.02	0.42
1:B:264:CYS:SG	1:B:395:ILE:HG21	2.59	0.42
1:D:618:PHE:CE1	1:E:612:VAL:HG21	2.53	0.42
2:I:10:ALA:O	2:I:14:LEU:HG	2.19	0.42
1:D:36:ILE:HG23	1:D:36:ILE:O	2.20	0.42
5:M:198:ARG:HH11	5:M:198:ARG:HG3	1.85	0.42
5:M:40:LYS:O	5:M:44:ILE:HG13	2.20	0.42
1:C:611:TYR:CE2	1:C:648:ARG:CZ	3.02	0.42
2:G:38:ILE:CD1	2:G:71:LEU:HB3	2.41	0.42
1:D:510:TRP:CB	1:D:679:ALA:HB2	2.49	0.42
1:A:285:VAL:HG13	1:A:326:ILE:CD1	2.46	0.42
1:F:401:LYS:O	1:F:404:LEU:HB3	2.20	0.42
1:F:270:ALA:HA	1:F:273:ILE:HG22	2.02	0.42
1:F:728:LYS:O	1:F:732:LEU:HG	2.20	0.42
1:E:298:SER:O	1:E:301:ASN:HB2	2.20	0.42
1:F:697:GLN:HG3	1:F:730:LEU:HD11	2.02	0.42
1:B:576:PHE:HB2	1:B:581:LYS:CG	2.49	0.42
1:B:307:ALA:HA	1:B:310:GLU:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:311:GLU:O	1:B:314:ARG:HG2	2.19	0.42
1:C:677:LEU:HD11	1:C:698:VAL:CG2	2.50	0.42
1:E:397:LEU:HD13	1:E:398:PRO:CD	2.48	0.42
2:G:119:ILE:HD11	2:G:123:HIS:HE1	1.82	0.42
2:J:58:TRP:HB3	2:J:95:ALA:HB2	2.02	0.42
1:B:690:GLU:O	1:B:694:ILE:HG13	2.20	0.42
1:F:242:PRO:HD2	1:F:243:GLU:N	2.35	0.42
1:E:438:GLY:O	1:E:441:LEU:N	2.42	0.42
2:H:78:LYS:HB3	2:H:110:ILE:HG23	2.01	0.42
1:F:436:PHE:N	1:F:436:PHE:CD1	2.85	0.42
2:J:203:LYS:HE3	2:J:203:LYS:HB2	1.80	0.42
2:J:230:GLU:HG3	2:J:237:ASP:CB	2.49	0.42
2:H:119:ILE:HD11	2:H:123:HIS:HD1	1.84	0.42
1:A:624:GLN:HG3	1:B:610:ASP:OD2	2.19	0.42
1:C:536:LEU:CD1	1:C:640:LEU:HB3	2.49	0.42
2:H:117:PHE:HA	2:H:120:ALA:HB3	2.00	0.42
2:I:182:ILE:CG2	2:I:212:CYS:HB2	2.49	0.42
1:B:309:ALA:HA	1:B:312:GLU:OE1	2.19	0.42
1:D:231:PHE:CD1	1:D:235:PHE:CD2	3.07	0.42
1:F:289:GLU:C	1:F:291:LEU:H	2.21	0.42
2:J:172:ALA:O	2:J:177:GLN:HB2	2.19	0.42
1:A:705:ILE:HD13	1:A:710:LEU:CD1	2.42	0.42
1:A:398:PRO:HG3	1:A:436:PHE:C	2.38	0.42
1:A:242:PRO:O	1:A:245:VAL:HG12	2.19	0.42
1:B:249:GLY:HA3	1:C:414:MET:CE	2.50	0.42
2:G:175:LEU:HD23	2:G:177:GLN:NE2	2.33	0.42
1:A:632:LYS:HE3	1:A:633:ALA:O	2.20	0.42
1:F:709:LYS:O	1:F:713:LEU:HG	2.19	0.42
1:E:268:LEU:HD12	1:E:269:LEU:N	2.35	0.42
2:G:92:PHE:CG	2:G:99:GLU:HB2	2.54	0.42
1:D:308:ASP:O	1:D:311:GLU:HB3	2.20	0.42
1:B:712:MET:O	1:B:716:MET:HG3	2.20	0.42
2:I:261:GLU:O	2:I:264:LYS:HB3	2.20	0.42
1:E:568:CYS:HB3	1:E:601:VAL:O	2.19	0.42
2:J:98:GLN:H	2:J:98:GLN:CD	2.23	0.42
1:E:527:GLN:HA	1:F:719:GLN:CD	2.40	0.42
1:F:596:GLN:O	1:F:638:ARG:HA	2.20	0.42
1:D:705:ILE:CD1	1:D:713:LEU:HD12	2.50	0.42
1:D:569:SER:HA	1:D:570:PRO:HD3	1.89	0.42
1:B:74:ILE:H	2:I:218:MET:CE	2.28	0.42
1:C:676:LEU:HD12	1:C:705:ILE:CG2	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:63:LEU:HB2	5:M:182:MET:HG2	2.01	0.42
1:F:502:TYR:HD2	1:F:503:ILE:HG13	1.85	0.42
1:D:618:PHE:O	1:E:617:ARG:NH2	2.52	0.42
3:K:77:PHE:CZ	5:M:78:LEU:HD11	2.55	0.42
2:H:182:ILE:HG22	2:H:209:ALA:HA	2.02	0.42
1:C:138:PHE:HB2	1:C:147:LEU:HD11	2.01	0.42
1:D:720:MET:HB3	1:D:724:TYR:CE1	2.55	0.42
1:C:539:VAL:HG23	1:C:663:THR:HG23	2.02	0.42
1:A:220:ILE:HG22	1:A:221:GLY:N	2.35	0.42
2:I:200:TYR:CD1	2:I:200:TYR:N	2.88	0.41
1:C:313:GLN:NE2	1:C:365:ASN:O	2.51	0.41
1:A:243:GLU:O	1:A:246:GLU:HG2	2.19	0.41
1:A:720:MET:HG3	1:A:728:LYS:CD	2.50	0.41
1:E:11:CYS:HA	1:E:12:PRO:HD3	1.95	0.41
1:F:106:ASN:HB3	1:F:143:LYS:HZ1	1.84	0.41
1:C:640:LEU:HG	1:C:642:ILE:HG13	2.02	0.41
2:G:95:ALA:HB1	2:G:97:PRO:HD2	2.02	0.41
2:H:200:TYR:O	2:H:203:LYS:HE2	2.19	0.41
1:C:528:THR:OG1	1:C:537:VAL:HG21	2.20	0.41
1:B:707:ILE:O	1:B:711:LEU:HG	2.20	0.41
1:A:27:LYS:HD2	1:A:57:PRO:HG3	2.01	0.41
1:E:525:VAL:O	1:E:529:LYS:HG2	2.21	0.41
2:J:203:LYS:HG2	2:J:228:TYR:OH	2.20	0.41
1:D:510:TRP:NE1	1:D:514:VAL:HG21	2.35	0.41
1:A:713:LEU:CD2	1:A:732:LEU:HB3	2.44	0.41
1:B:436:PHE:N	1:B:436:PHE:CD1	2.86	0.41
1:A:223:LEU:HD12	1:A:227:PHE:HB2	2.02	0.41
2:G:81:ALA:O	2:G:85:PHE:HD1	2.03	0.41
2:I:243:LEU:HD13	2:I:266:TYR:HB2	2.03	0.41
1:F:268:LEU:HD12	1:F:269:LEU:N	2.35	0.41
1:D:103:GLN:OE1	1:D:106:ASN:ND2	2.53	0.41
2:J:208:LYS:HG2	2:J:275:TRP:CZ3	2.56	0.41
2:J:231:LEU:O	2:J:234:ALA:N	2.53	0.41
1:B:326:ILE:HG22	1:B:370:ILE:CG1	2.47	0.41
1:F:64:LEU:HD21	2:G:292:GLU:HB3	2.03	0.41
1:B:648:ARG:HG3	1:B:651:VAL:CG2	2.50	0.41
1:F:549:LYS:HE3	1:F:646:THR:C	2.40	0.41
1:A:240:PHE:HD1	1:A:240:PHE:HA	1.72	0.41
1:C:318:ALA:C	1:C:319:ASN:HD22	2.23	0.41
1:A:255:GLY:C	1:A:389:LEU:HD13	2.40	0.41
1:A:607:ARG:HD3	1:A:607:ARG:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:205:TYR:HD1	2:G:205:TYR:H	1.68	0.41
1:E:513:PRO:O	1:E:516:ARG:HG2	2.20	0.41
1:A:693:THR:O	1:A:697:GLN:OE1	2.37	0.41
1:A:694:ILE:HA	1:A:697:GLN:OE1	2.20	0.41
2:J:75:LEU:O	2:J:76:GLN:HB3	2.20	0.41
1:F:243:GLU:O	1:F:246:GLU:HG2	2.21	0.41
1:A:69:TRP:CE2	1:A:134:GLN:HA	2.55	0.41
1:F:445:VAL:O	1:F:449:GLN:HG2	2.20	0.41
1:C:438:GLY:O	1:C:441:LEU:HB2	2.20	0.41
1:B:669:ASN:CG	1:B:706:GLY:HA2	2.41	0.41
1:A:565:ILE:HA	1:A:599:CYS:O	2.19	0.41
1:E:526:GLN:HA	1:E:529:LYS:HG2	2.02	0.41
2:I:197:LEU:HD22	3:K:48:VAL:HG11	2.01	0.41
1:D:437:SER:O	1:D:440:GLU:HB3	2.19	0.41
1:C:408:HIS:HD1	1:C:412:ALA:HB2	1.86	0.41
1:A:300:ALA:O	1:A:303:ARG:HG2	2.20	0.41
1:B:584:ALA:O	1:B:588:ILE:HG13	2.19	0.41
1:A:676:LEU:HD12	1:A:710:LEU:HD11	2.01	0.41
4:L:226:GLN:HA	4:L:229:MET:HE2	2.03	0.41
1:B:62:PHE:HB2	1:B:67:ARG:CG	2.49	0.41
1:A:552:LEU:HD22	1:A:556:ILE:HD11	2.01	0.41
2:I:116:ARG:CZ	5:M:65:ASN:ND2	2.83	0.41
2:G:163:LYS:O	2:G:167:LYS:HG2	2.21	0.41
1:B:250:CYS:HB2	1:C:449:GLN:CD	2.41	0.41
2:H:182:ILE:CG2	2:H:212:CYS:HB2	2.51	0.41
1:F:705:ILE:HG12	1:F:706:GLY:O	2.19	0.41
1:B:218:MET:HA	1:B:219:GLY:HA2	1.80	0.41
1:B:99:ILE:HD11	1:B:145:PHE:CD2	2.55	0.41
1:B:260:GLY:HA3	1:B:266:LYS:HD3	2.02	0.41
1:E:98:GLU:HB3	1:E:148:LEU:HB3	2.01	0.41
2:G:271:ARG:HG2	2:G:271:ARG:HH11	1.86	0.41
1:E:676:LEU:HD12	1:E:710:LEU:HD21	2.02	0.41
1:F:64:LEU:CD2	2:G:292:GLU:HB3	2.50	0.41
1:D:531:SER:OG	1:D:534:THR:OG1	2.31	0.41
1:E:605:ILE:HA	1:E:608:LEU:HB3	2.03	0.41
1:B:533:ARG:NH1	1:C:711:LEU:HD13	2.35	0.41
2:G:117:PHE:HA	2:G:120:ALA:HB3	2.01	0.41
2:J:149:ALA:HB2	2:J:164:CYS:CB	2.49	0.41
1:D:23:VAL:HG12	1:D:55:VAL:HG21	2.02	0.41
1:A:104:LYS:HA	1:A:107:ILE:CG1	2.50	0.41
1:B:694:ILE:HD13	1:B:729:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:275:TRP:CE3	2:I:276:LEU:HD23	2.54	0.41
1:B:609:LEU:HA	1:B:609:LEU:HD23	1.67	0.41
1:B:508:ILE:HD13	1:B:683:LEU:HD21	2.02	0.41
1:F:347:HIS:O	1:F:350:VAL:HG22	2.21	0.41
1:D:138:PHE:HB2	1:D:147:LEU:HD11	2.03	0.41
1:B:230:ILE:HD11	1:B:391:VAL:HG11	2.01	0.41
1:B:263:GLY:O	1:B:439:ALA:HB3	2.20	0.41
2:J:270:SER:HA	5:M:34:GLN:NE2	2.35	0.41
2:G:45:TYR:CE2	2:G:71:LEU:HD11	2.55	0.41
1:D:670:ILE:HD11	1:D:705:ILE:HG23	2.01	0.41
1:E:652:LEU:HD21	1:E:661:PHE:HE1	1.85	0.41
1:A:262:PRO:CG	1:A:374:ASN:OD1	2.65	0.41
1:D:626:LEU:HD23	1:D:626:LEU:HA	1.81	0.41
1:C:707:ILE:O	1:C:711:LEU:HG	2.21	0.41
1:A:313:GLN:NE2	1:A:365:ASN:OD1	2.54	0.41
2:G:203:LYS:HZ1	2:G:239:ARG:NH2	2.17	0.41
1:D:284:VAL:HB	1:D:325:ILE:HA	2.02	0.41
1:F:609:LEU:HD23	1:F:609:LEU:HA	1.61	0.41
2:H:266:TYR:C	2:H:268:SER:H	2.24	0.41
1:C:36:ILE:HD11	1:C:44:LYS:HB3	2.03	0.41
1:B:138:PHE:HB2	1:B:147:LEU:HD11	2.01	0.41
1:C:218:MET:HA	1:C:219:GLY:HA2	1.83	0.41
2:G:161:ALA:O	2:G:165:LEU:HG	2.20	0.41
1:C:184:ALA:HB1	1:C:200:LYS:O	2.19	0.41
2:I:188:VAL:HG13	2:I:205:TYR:CD2	2.53	0.41
1:E:618:PHE:CD1	1:E:618:PHE:C	2.93	0.41
1:B:648:ARG:HG3	1:B:651:VAL:HG23	2.03	0.41
1:B:24:VAL:CG1	1:B:49:LEU:HD22	2.51	0.41
1:D:92:ILE:HG13	1:D:176:LEU:N	2.35	0.41
1:C:64:LEU:CB	1:C:67:ARG:HH21	2.33	0.41
1:D:562:PHE:CZ	1:D:597:LEU:HD21	2.56	0.41
1:C:375:ARG:NH1	1:C:378:LEU:HG	2.33	0.41
1:B:325:ILE:O	1:B:369:VAL:HG23	2.21	0.41
2:I:164:CYS:O	2:I:168:VAL:HG23	2.20	0.41
2:G:101:ILE:HB	2:G:131:TYR:OH	2.20	0.41
1:A:517:VAL:HG13	1:A:665:ILE:HG21	2.02	0.41
2:H:182:ILE:O	2:H:186:GLU:HG2	2.20	0.41
1:F:578:GLU:OE2	1:F:619:SER:HB3	2.21	0.41
1:C:517:VAL:HG13	1:C:665:ILE:HG21	2.02	0.41
2:G:47:ARG:O	2:G:50:ASN:HB3	2.20	0.41
1:E:240:PHE:HA	1:E:241:PRO:HD3	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:550:THR:CG2	1:E:603:ASP:OD1	2.69	0.41
1:E:95:MET:HE2	1:E:97:ILE:HD11	2.02	0.41
1:C:324:ILE:HD12	1:C:324:ILE:N	2.35	0.41
1:A:235:PHE:HD1	1:A:235:PHE:HA	1.64	0.41
1:E:40:SER:OG	1:E:41:PRO:CD	2.69	0.41
5:M:198:ARG:O	5:M:198:ARG:HG2	2.20	0.41
1:D:103:GLN:NE2	2:J:292:GLU:OE2	2.54	0.41
1:D:513:PRO:CA	1:D:516:ARG:HG2	2.48	0.41
1:B:542:GLU:HG3	1:B:666:HIS:CE1	2.56	0.41
1:B:324:ILE:HG12	1:B:368:LEU:HD11	2.03	0.41
1:B:488:ILE:O	1:B:490:PRO:N	2.54	0.41
1:B:539:VAL:CG2	1:B:665:ILE:HD12	2.51	0.41
1:D:670:ILE:HD11	1:D:705:ILE:CG2	2.51	0.41
1:E:652:LEU:HD22	1:E:658:LEU:HD13	2.01	0.41
1:D:240:PHE:HA	1:D:241:PRO:HD3	1.94	0.41
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.80	0.41
5:M:148:GLU:O	5:M:152:GLN:HG3	2.21	0.41
2:I:155:GLU:HB3	5:M:176:ARG:NH2	2.35	0.41
1:E:399:ASP:N	1:E:399:ASP:OD1	2.54	0.41
1:E:445:VAL:O	1:E:449:GLN:HG2	2.21	0.41
2:J:256:VAL:O	2:J:256:VAL:HG22	2.21	0.41
1:A:102:LEU:HB2	1:A:145:PHE:O	2.20	0.41
2:G:200:TYR:CZ	5:M:38:GLU:HG2	2.55	0.41
1:A:231:PHE:CE2	1:A:235:PHE:CD2	3.09	0.41
1:B:397:LEU:HD13	1:B:596:GLN:HG3	2.02	0.41
1:A:654:GLU:HG2	1:B:614:ILE:HG13	2.03	0.41
2:J:179:GLN:HB3	2:J:214:PHE:HB3	2.03	0.41
1:D:95:MET:HE2	1:D:97:ILE:HD11	2.01	0.41
1:A:407:LEU:HD12	1:A:426:ILE:HG23	2.03	0.41
2:G:95:ALA:CB	2:G:97:PRO:HD2	2.51	0.41
1:E:69:TRP:NE1	1:E:134:GLN:HA	2.36	0.41
1:D:52:HIS:HA	1:D:53:PRO:HD3	1.92	0.41
2:I:161:ALA:O	2:I:165:LEU:HG	2.21	0.41
1:B:142:ASP:OD1	1:B:142:ASP:O	2.38	0.41
2:G:256:VAL:HG22	2:G:256:VAL:O	2.21	0.41
1:F:525:VAL:HG11	1:F:560:SER:HA	2.03	0.41
1:D:670:ILE:HG12	1:D:705:ILE:O	2.20	0.41
1:E:538:SER:OG	1:E:662:SER:N	2.44	0.41
3:K:43:VAL:HG13	4:L:215:MET:HE1	2.02	0.41
4:L:212:LEU:HA	4:L:215:MET:CE	2.51	0.41
1:A:436:PHE:CD2	1:A:444:LEU:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:710:LEU:HG	1:D:714:ILE:HD11	2.03	0.41
2:J:117:PHE:HA	2:J:120:ALA:HB3	2.03	0.41
1:E:502:TYR:OH	1:E:569:SER:OG	2.39	0.41
1:C:525:VAL:HG22	1:C:641:LEU:CD2	2.51	0.41
1:D:330:ILE:CD1	1:D:373:THR:HB	2.52	0.41
1:B:503:ILE:HG22	1:B:506:GLY:H	1.86	0.41
2:H:53:LYS:HE3	2:I:117:PHE:CD2	2.56	0.41
2:G:39:GLU:HB2	2:G:75:LEU:HD11	2.03	0.41
1:C:52:HIS:C	1:C:54:SER:H	2.24	0.41
2:J:176:GLU:O	2:J:178:TYR:N	2.51	0.41
1:D:671:ALA:HA	1:D:703:VAL:O	2.21	0.41
1:D:541:LEU:O	1:D:541:LEU:HD12	2.20	0.41
2:I:201:SER:HB2	2:I:205:TYR:HE1	1.86	0.40
1:D:406:ILE:HG23	1:D:410:HIS:CE1	2.55	0.40
1:F:613:PRO:HD3	1:F:648:ARG:NH1	2.27	0.40
1:D:540:LEU:HB2	1:D:661:PHE:CD1	2.56	0.40
1:D:11:CYS:HA	1:D:12:PRO:HD3	1.94	0.40
1:E:97:ILE:HG21	1:E:147:LEU:HB3	2.03	0.40
1:E:149:VAL:HG11	1:E:152:ILE:HD11	2.02	0.40
1:B:313:GLN:O	1:B:317:GLY:CA	2.70	0.40
1:E:295:VAL:HG23	1:E:296:GLY:N	2.36	0.40
1:B:633:ALA:HA	1:B:634:PRO:HD3	1.89	0.40
2:H:205:TYR:H	2:H:205:TYR:HD1	1.69	0.40
1:A:402:GLY:O	1:A:406:ILE:HD12	2.20	0.40
1:E:236:ALA:HA	1:E:239:VAL:CG1	2.51	0.40
1:C:507:ILE:HD11	1:C:551:ALA:HB1	2.03	0.40
1:B:510:TRP:HH2	1:B:668:PRO:O	2.04	0.40
2:G:82:ALA:O	2:G:86:VAL:HG23	2.21	0.40
1:F:73:SER:O	1:F:76:GLN:HG2	2.20	0.40
1:F:122:ILE:O	1:F:126:ASN:HB3	2.20	0.40
2:I:180:LYS:O	2:I:184:ILE:HG13	2.22	0.40
1:B:649:LYS:NZ	1:B:664:THR:HG21	2.37	0.40
1:B:240:PHE:HA	1:B:241:PRO:HD3	1.87	0.40
1:F:635:PRO:HD2	1:F:638:ARG:HD2	2.02	0.40
5:M:47:LEU:HD23	5:M:50:LEU:HD12	2.02	0.40
1:A:437:SER:O	1:A:440:GLU:HG2	2.22	0.40
1:E:196:ILE:N	1:E:196:ILE:CD1	2.83	0.40
1:E:440:GLU:O	1:E:444:LEU:HG	2.21	0.40
1:E:670:ILE:HG22	1:E:672:THR:N	2.30	0.40
1:D:529:LYS:HD3	1:D:597:LEU:CD2	2.52	0.40
1:E:684:GLY:HA2	1:E:691:ARG:HH21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:45:TYR:HB2	2:I:68:ALA:HB2	2.03	0.40
1:E:721:ASP:O	1:E:724:TYR:HB2	2.22	0.40
1:F:246:GLU:HG2	1:F:247:GLN:N	2.36	0.40
1:A:395:ILE:N	1:A:395:ILE:HD12	2.36	0.40
1:B:512:ASP:N	1:B:513:PRO:CD	2.84	0.40
1:D:397:LEU:HD22	1:D:435:ASN:O	2.22	0.40
1:E:254:LYS:O	1:E:368:LEU:HA	2.21	0.40
1:F:612:VAL:HG13	1:F:614:ILE:O	2.21	0.40
1:C:687:LYS:HB2	1:C:690:GLU:OE1	2.21	0.40
1:D:300:ALA:O	1:D:304:LYS:HG3	2.21	0.40
1:B:24:VAL:C	1:B:55:VAL:HG11	2.41	0.40
1:B:589:PHE:CE2	1:B:629:LEU:HD13	2.57	0.40
3:K:74:ALA:HA	5:M:192:ILE:HG21	2.02	0.40
1:F:257:LEU:HG	1:F:371:GLY:O	2.20	0.40
1:B:710:LEU:O	1:B:714:ILE:HG13	2.21	0.40
1:F:686:PHE:HB2	1:F:691:ARG:HG3	2.03	0.40
1:B:632:LYS:HE3	1:B:633:ALA:O	2.21	0.40
1:D:198:LYS:HG2	1:D:243:GLU:OE2	2.22	0.40
1:C:603:ASP:HA	1:C:645:THR:OG1	2.21	0.40
1:C:709:LYS:HE2	1:C:713:LEU:HD21	2.04	0.40
1:B:544:PRO:HG3	1:B:669:ASN:H	1.86	0.40
2:H:173:ALA:HB1	2:H:279:MET:HE3	2.03	0.40
1:C:153:GLU:OE1	1:C:169:ARG:HD3	2.21	0.40
1:D:186:GLU:O	1:D:186:GLU:HG3	2.22	0.40
1:C:258:LEU:O	1:C:258:LEU:HD12	2.21	0.40
2:J:173:ALA:HB1	2:J:279:MET:HE3	2.03	0.40
1:A:295:VAL:HG12	1:B:293:LYS:N	2.36	0.40
1:D:694:ILE:HD13	1:D:729:PHE:CD2	2.55	0.40
1:D:570:PRO:O	1:D:573:MET:HB3	2.22	0.40
1:D:356:SER:OG	1:E:288:PRO:HB3	2.22	0.40
1:A:256:ILE:CG1	1:A:370:ILE:HG22	2.51	0.40
5:M:177:GLN:O	5:M:181:ILE:HG13	2.22	0.40
1:D:627:LEU:HA	1:D:627:LEU:HD23	1.71	0.40
1:B:533:ARG:HD3	1:C:505:ASN:ND2	2.36	0.40
1:C:64:LEU:O	1:C:68:LYS:HG3	2.21	0.40
1:C:411:THR:O	1:C:414:MET:HB2	2.22	0.40
1:C:629:LEU:HD23	1:C:629:LEU:HA	1.74	0.40
1:E:95:MET:HE3	1:E:97:ILE:HD11	2.03	0.40
2:J:45:TYR:HE2	2:J:71:LEU:HD11	1.86	0.40
1:F:101:PHE:HB2	1:F:107:ILE:HG12	2.03	0.40
2:I:79:HIS:HD2	5:M:69:GLN:HG3	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:HIS:HB2	1:B:367:ILE:HG22	2.03	0.40
1:A:408:HIS:HA	1:A:426:ILE:HD12	2.04	0.40
1:A:426:ILE:HG23	1:A:426:ILE:HD12	1.71	0.40
2:H:243:LEU:O	2:H:247:LEU:HG	2.21	0.40
1:B:720:MET:HB3	1:B:724:TYR:HB2	2.04	0.40
1:A:375:ARG:HA	1:A:376:PRO:HD2	1.97	0.40
1:F:678:GLU:O	1:F:682:LEU:HG	2.21	0.40
1:E:99:ILE:HA	1:E:146:GLY:O	2.21	0.40
1:C:254:LYS:O	1:C:368:LEU:HA	2.22	0.40
1:E:326:ILE:HG22	1:E:370:ILE:CG1	2.49	0.40
1:A:263:GLY:O	1:A:437:SER:HB3	2.21	0.40
1:D:687:LYS:O	1:D:690:GLU:HG2	2.22	0.40
1:D:527:GLN:HE22	1:E:716:MET:CA	2.33	0.40
1:D:527:GLN:O	1:D:527:GLN:HG3	2.20	0.40
1:D:549:LYS:HB3	1:D:645:THR:HB	2.03	0.40
1:A:612:VAL:N	1:A:617:ARG:O	2.46	0.40
1:C:284:VAL:HG23	1:C:324:ILE:O	2.21	0.40
2:I:186:GLU:O	2:I:190:THR:HG23	2.22	0.40
1:D:258:LEU:CD1	1:D:372:MET:HG2	2.51	0.40
1:A:52:HIS:C	1:A:54:SER:H	2.25	0.40
1:B:100:ASP:O	1:B:146:GLY:N	2.55	0.40
1:B:399:ASP:CB	1:B:402:GLY:H	2.34	0.40
1:A:526:GLN:O	1:A:530:ASN:HB2	2.20	0.40
2:G:282:ARG:O	2:G:286:THR:HG23	2.21	0.40
5:M:67:ILE:O	5:M:71:MET:HG2	2.21	0.40
1:E:643:ILE:N	1:E:643:ILE:HD12	2.36	0.40
1:C:626:LEU:HA	1:C:626:LEU:HD23	1.86	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	668/747 (89%)	610 (91%)	43 (6%)	15 (2%)	8	49
1	B	662/747 (89%)	592 (89%)	55 (8%)	15 (2%)	8	48
1	C	666/747 (89%)	616 (92%)	37 (6%)	13 (2%)	9	51
1	D	663/747 (89%)	607 (92%)	44 (7%)	12 (2%)	11	53
1	E	658/747 (88%)	604 (92%)	43 (6%)	11 (2%)	11	55
1	F	644/747 (86%)	583 (90%)	43 (7%)	18 (3%)	6	44
2	G	284/297 (96%)	238 (84%)	34 (12%)	12 (4%)	3	34
2	H	284/297 (96%)	232 (82%)	44 (16%)	8 (3%)	6	44
2	I	284/297 (96%)	233 (82%)	44 (16%)	7 (2%)	7	46
2	J	284/297 (96%)	234 (82%)	41 (14%)	9 (3%)	5	41
3	K	59/63 (94%)	55 (93%)	2 (3%)	2 (3%)	5	40
4	L	64/67 (96%)	60 (94%)	3 (5%)	1 (2%)	12	56
5	M	127/188 (68%)	125 (98%)	2 (2%)	0	100	100
All	All	5347/5988 (89%)	4789 (90%)	435 (8%)	123 (2%)	12	48

All (123) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	293	LYS
1	A	294	TYR
1	A	318	ALA
1	A	333	ILE
1	A	397	LEU
1	A	498	ASP
1	B	283	LYS
1	B	297	GLU
1	B	318	ALA
1	B	439	ALA
1	B	489	LYS
1	C	190	ASN
1	C	297	GLU
1	C	318	ALA
1	C	497	GLU
1	C	498	ASP
1	C	578	GLU
1	D	12	PRO
1	D	283	LYS

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Mol	Chain	Res	Type
1	D	318	ALA
1	D	489	LYS
1	E	12	PRO
1	E	283	LYS
1	E	297	GLU
1	E	318	ALA
1	E	439	ALA
1	E	489	LYS
1	F	283	LYS
1	F	297	GLU
1	F	318	ALA
1	F	397	LEU
1	F	439	ALA
2	G	58	TRP
2	G	76	GLN
2	G	100	ALA
2	H	79	HIS
2	I	58	TRP
2	I	76	GLN
2	J	76	GLN
1	A	88	ALA
1	B	12	PRO
1	B	89	LYS
1	B	502	TYR
1	C	293	LYS
1	C	610	ASP
1	F	12	PRO
1	F	89	LYS
1	F	102	LEU
1	F	193	LEU
2	G	79	HIS
2	G	157	SER
2	G	176	GLU
2	G	177	GLN
2	G	240	GLU
2	H	58	TRP
2	H	76	GLN
2	I	176	GLU
2	J	33	GLY
2	J	58	TRP
2	J	79	HIS
3	K	36	GLN

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Mol	Chain	Res	Type
1	A	105	LYS
1	A	241	PRO
1	A	242	PRO
1	A	264	CYS
1	B	87	LYS
1	B	241	PRO
1	B	293	LYS
1	C	87	LYS
1	C	241	PRO
1	D	293	LYS
1	E	241	PRO
1	E	293	LYS
1	E	507	ILE
1	F	241	PRO
1	F	293	LYS
2	H	254	GLN
2	I	177	GLN
2	J	240	GLU
3	K	61	SER
1	B	88	ALA
1	B	546	HIS
1	C	12	PRO
1	D	13	THR
1	D	87	LYS
1	D	189	GLU
2	G	26	SER
2	G	99	GLU
2	H	196	PRO
2	H	240	GLU
2	H	267	ASP
2	I	79	HIS
2	I	240	GLU
1	A	398	PRO
1	A	668	PRO
1	C	53	PRO
1	D	241	PRO
1	E	438	GLY
2	G	235	PHE
2	I	256	VAL
2	J	21	VAL
2	J	97	PRO
2	J	256	VAL

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Mol	Chain	Res	Type
4	L	237	VAL
1	A	53	PRO
1	B	438	GLY
1	B	490	PRO
1	D	53	PRO
1	E	490	PRO
1	F	87	LYS
1	F	438	GLY
1	F	668	PRO
2	G	256	VAL
1	D	488	ILE
1	D	545	PRO
1	F	684	GLY
1	F	53	PRO
2	J	233	PRO
1	C	490	PRO
1	F	398	PRO
1	F	544	PRO
2	H	233	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	515/638 (81%)	503 (98%)	12 (2%)	58	83
1	B	521/638 (82%)	511 (98%)	10 (2%)	65	86
1	C	516/638 (81%)	511 (99%)	5 (1%)	82	92
1	D	511/638 (80%)	504 (99%)	7 (1%)	74	89
1	E	516/638 (81%)	511 (99%)	5 (1%)	82	92
1	F	512/638 (80%)	509 (99%)	3 (1%)	90	95
2	G	235/244 (96%)	235 (100%)	0	100	100
2	H	235/244 (96%)	234 (100%)	1 (0%)	93	96
2	I	234/244 (96%)	234 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	235/244 (96%)	235 (100%)	0	100	100
3	K	52/54 (96%)	52 (100%)	0	100	100
4	L	60/61 (98%)	58 (97%)	2 (3%)	45	76
5	M	113/161 (70%)	112 (99%)	1 (1%)	84	93
All	All	4255/5080 (84%)	4209 (99%)	46 (1%)	81	91

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	104	LYS
1	A	240	PHE
1	A	305	LEU
1	A	322	LEU
1	A	358	ILE
1	A	456	HIS
1	A	504	MET
1	A	530	ASN
1	A	550	THR
1	A	665	ILE
1	A	666	HIS
1	B	20	ASN
1	B	42	ASN
1	B	180	ASN
1	B	240	PHE
1	B	305	LEU
1	B	313	GLN
1	B	322	LEU
1	B	327	PHE
1	B	610	ASP
1	B	651	VAL
1	C	20	ASN
1	C	180	ASN
1	C	305	LEU
1	C	537	VAL
1	C	676	LEU
1	D	20	ASN
1	D	105	LYS
1	D	189	GLU
1	D	305	LEU
1	D	311	GLU

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Mol	Chain	Res	Type
1	D	663	THR
1	D	713	LEU
1	E	20	ASN
1	E	196	ILE
1	E	305	LEU
1	E	322	LEU
1	E	602	VAL
1	F	305	LEU
1	F	322	LEU
1	F	536	LEU
2	H	183	ASP
4	L	210	ARG
4	L	226	GLN
5	M	70	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	319	ASN
1	A	526	GLN
1	A	530	ASN
1	B	20	ASN
1	B	128	GLN
1	B	319	ASN
1	B	526	GLN
1	B	530	ASN
1	B	546	HIS
1	B	561	ASN
1	C	20	ASN
1	C	194	ASN
1	C	319	ASN
1	C	675	GLN
1	D	103	GLN
1	D	106	ASN
1	D	353	GLN
1	D	527	GLN
1	D	675	GLN
1	E	20	ASN
1	E	43	HIS
1	E	505	ASN
1	E	527	GLN

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Mol	Chain	Res	Type
1	E	620	ASN
1	E	624	GLN
1	E	659	ASN
1	F	194	ASN
1	F	313	GLN
1	F	319	ASN
1	F	454	ASN
1	F	527	GLN
2	G	72	HIS
2	G	124	HIS
2	G	147	GLN
2	H	72	HIS
2	H	213	HIS
2	H	251	HIS
2	I	50	ASN
2	I	72	HIS
2	I	79	HIS
2	I	123	HIS
2	I	124	HIS
2	I	147	GLN
2	I	177	GLN
2	J	72	HIS
2	J	98	GLN
4	L	226	GLN
5	M	34	GLN
5	M	66	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.