



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Dec 2, 2019 – 11:13 AM EST

PDB ID : 6Q1F
EMDB ID: : EMD-20557
Title : Atomic structure of the Human Herpesvirus 6B Capsid and Capsid-Associated Tegument Complexes
Authors : Zhang, Y.B.; Liu, W.; Li, Z.H.; Kumar, V.; Alvarez-Cabrera, A.L.; Leibovitch, E.; Cui, Y.X.; Mei, Y.; Bi, G.Q.; Jacobson, S.; Zhou, Z.H.
Deposited on : 2019-08-03
Resolution : 9.00 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

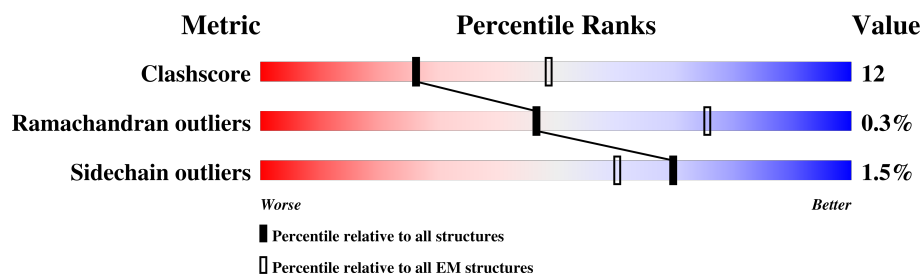
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 Å.

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



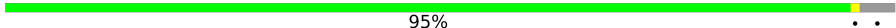
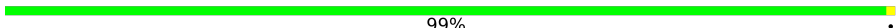
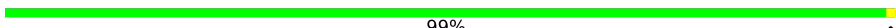
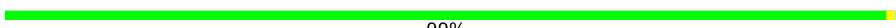
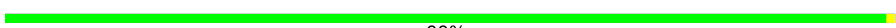








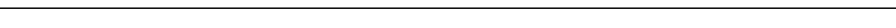











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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 ≥ 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	1345	79% 20%
1	B	1345	78% 21%
1	C	1345	80% 18% ..
1	D	1345	79% 20% .
1	E	1345	77% 22% .
1	F	1345	78% 21% .
1	G	1345	76% 23% .
1	H	1345	80% 19% .
1	I	1345	83% 17% .


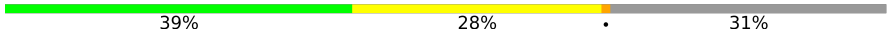

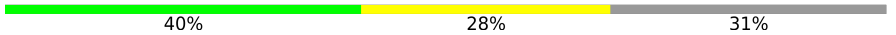
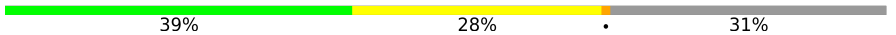
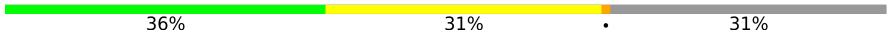
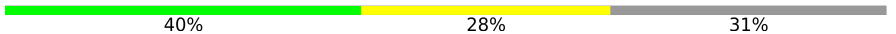














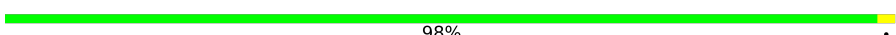
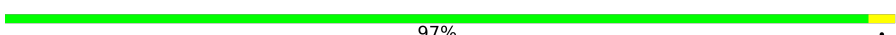
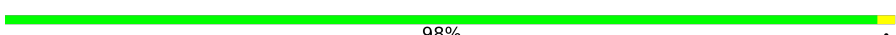
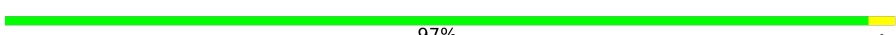
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Mol	Chain	Length	Quality of chain
1	q	1345	 95%
1	r	1345	 99%
1	s	1345	 99%
1	t	1345	 99%
1	u	1345	 99%
1	v	1345	 96%
1	w	1345	 92% 7%
2	e	858	 31% 69%
2	f	858	 31% 69%
2	g	858	 30% 69%
2	h	858	 31% 69%
2	i	858	 30% 69%
2	j	858	 30% 69%
2	k	858	 30% 69%
2	l	858	 30% 69%
2	m	858	 31% 69%
2	n	858	 30% 69%
2	o	858	 30% 69%
2	p	858	 31% 69%
3	1	89	 46% 22% 31%
3	2	89	 45% 24% 31%
3	3	89	 47% 21% 31%
3	4	89	 44% 20% 35%
3	J	89	 42% 24% 31%
3	K	89	 42% 27% 31%

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Mol	Chain	Length	Quality of chain
3	L	89	
3	M	89	
3	N	89	
3	O	89	
3	P	89	
3	Q	89	
3	R	89	
3	x	89	
3	y	89	
3	z	89	
4	5	299	
4	S	299	
4	T	299	
4	U	299	
4	V	299	
5	6	296	
5	7	296	
5	W	296	
5	X	296	
5	Y	296	
5	Z	296	
5	a	296	
5	b	296	
5	c	296	
5	d	296	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 238552 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	B	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	C	1325	Total	C	N	O	S	0	0
			10552	6709	1792	1991	60		
1	D	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	E	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	F	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	G	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	H	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	I	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	q	1296	Total	C	N	O	S	0	0
			10313	6561	1751	1942	59		
1	r	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	s	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	t	1343	Total	C	N	O	S	0	0
			10682	6792	1813	2017	60		
1	u	1344	Total	C	N	O	S	0	0
			10690	6797	1814	2018	61		
1	v	1301	Total	C	N	O	S	0	0
			10331	6564	1759	1948	60		
1	w	1248	Total	C	N	O	S	0	0
			9933	6324	1691	1860	58		

- Molecule 2 is a protein called Large structural phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	f	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	g	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	h	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	i	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	j	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	k	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	l	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	m	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	n	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	o	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		
2	p	269	Total	C	N	O	S	0	0
			2224	1417	376	426	5		

- Molecule 3 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	K	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	L	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	M	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	N	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	O	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	P	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	Q	61	Total	C	N	O	S	0	0
			483	308	89	83	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	x	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	y	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	z	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	1	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	2	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	3	61	Total	C	N	O	S	0	0
			483	308	89	83	3		
3	4	58	Total	C	N	O	S	0	0
			456	292	85	76	3		

- Molecule 4 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	251	Total	C	N	O	S	0	0
			2023	1306	327	376	14		
4	S	299	Total	C	N	O	S	0	0
			2398	1542	395	446	15		
4	T	299	Total	C	N	O	S	0	0
			2398	1542	395	446	15		
4	U	299	Total	C	N	O	S	0	0
			2398	1542	395	446	15		
4	V	299	Total	C	N	O	S	0	0
			2398	1542	395	446	15		

- Molecule 5 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	282	Total	C	N	O	S	0	0
			2226	1422	370	415	19		
5	W	296	Total	C	N	O	S	0	0
			2337	1486	393	437	21		
5	X	296	Total	C	N	O	S	0	0
			2337	1486	393	437	21		
5	Y	296	Total	C	N	O	S	0	0
			2337	1486	393	437	21		

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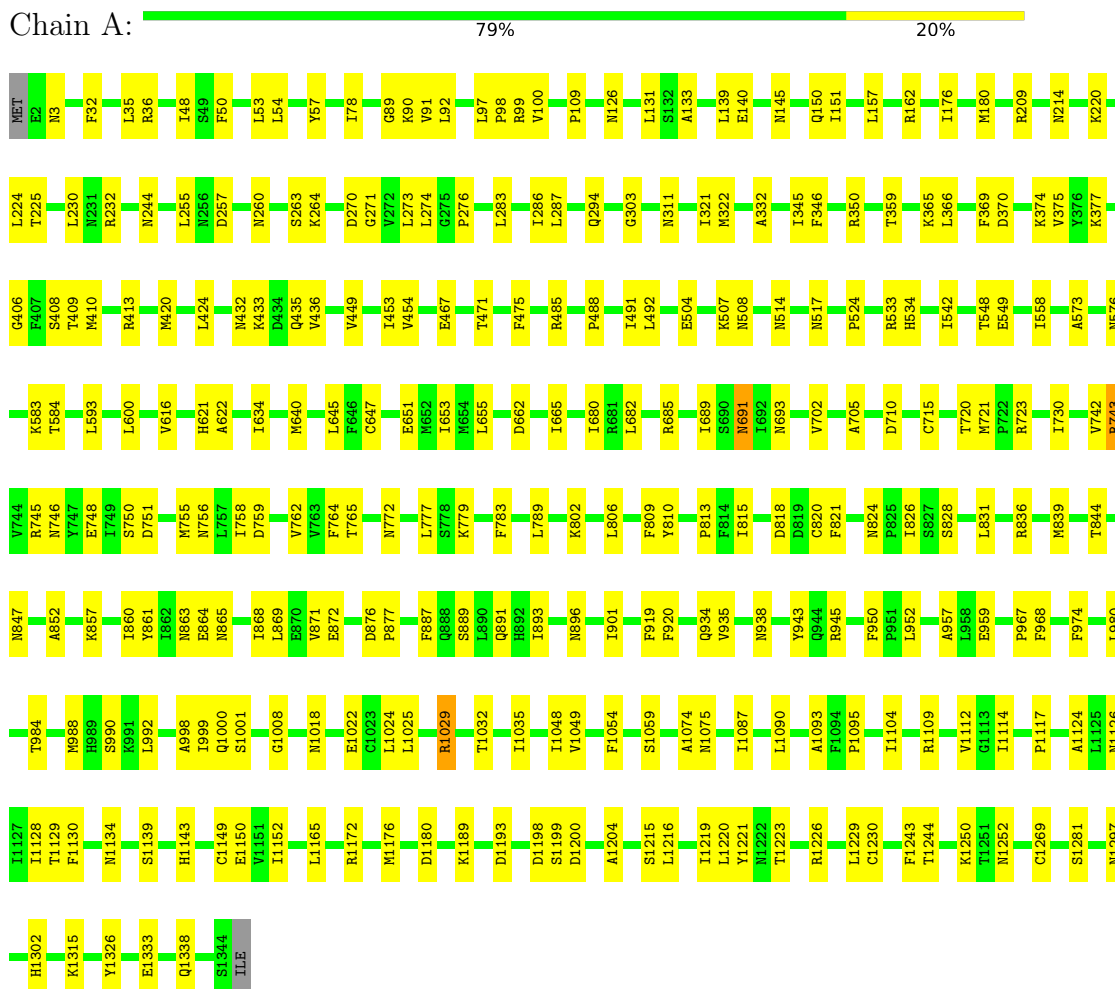
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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Z	296	Total	C	N	O	S	0	0
			2337	1486	393	437	21		
5	7	296	Total	C	N	O	S	0	0
			2337	1486	393	437	21		
5	a	295	Total	C	N	O	S	0	0
			2329	1481	392	436	20		
5	b	295	Total	C	N	O	S	0	0
			2329	1481	392	436	20		
5	c	295	Total	C	N	O	S	0	0
			2329	1481	392	436	20		
5	d	295	Total	C	N	O	S	0	0
			2329	1481	392	436	20		

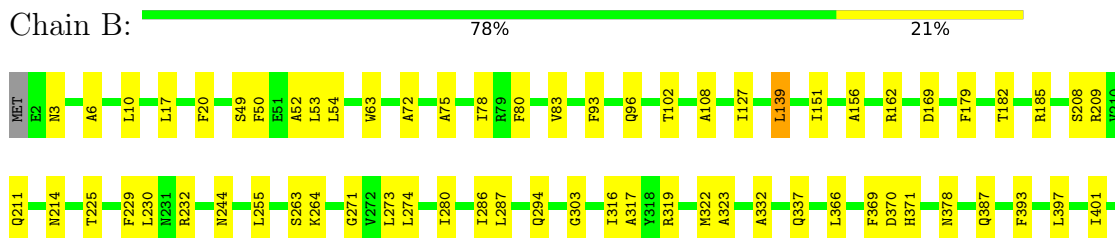
3 Residue-property plots

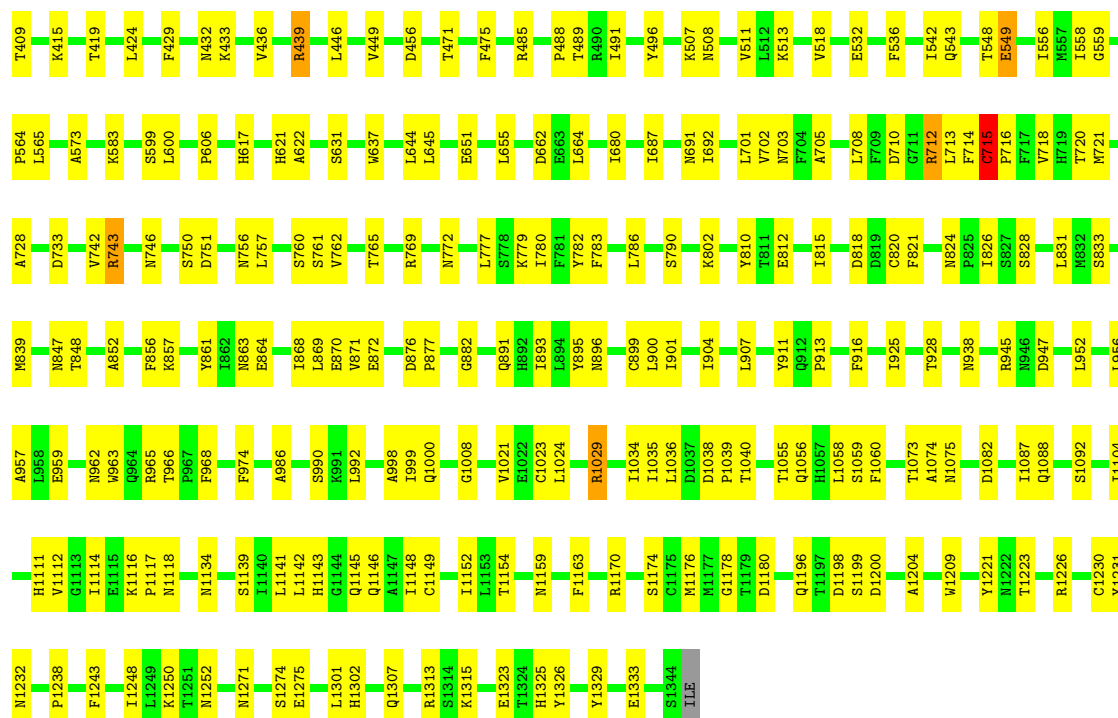
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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: Major capsid protein



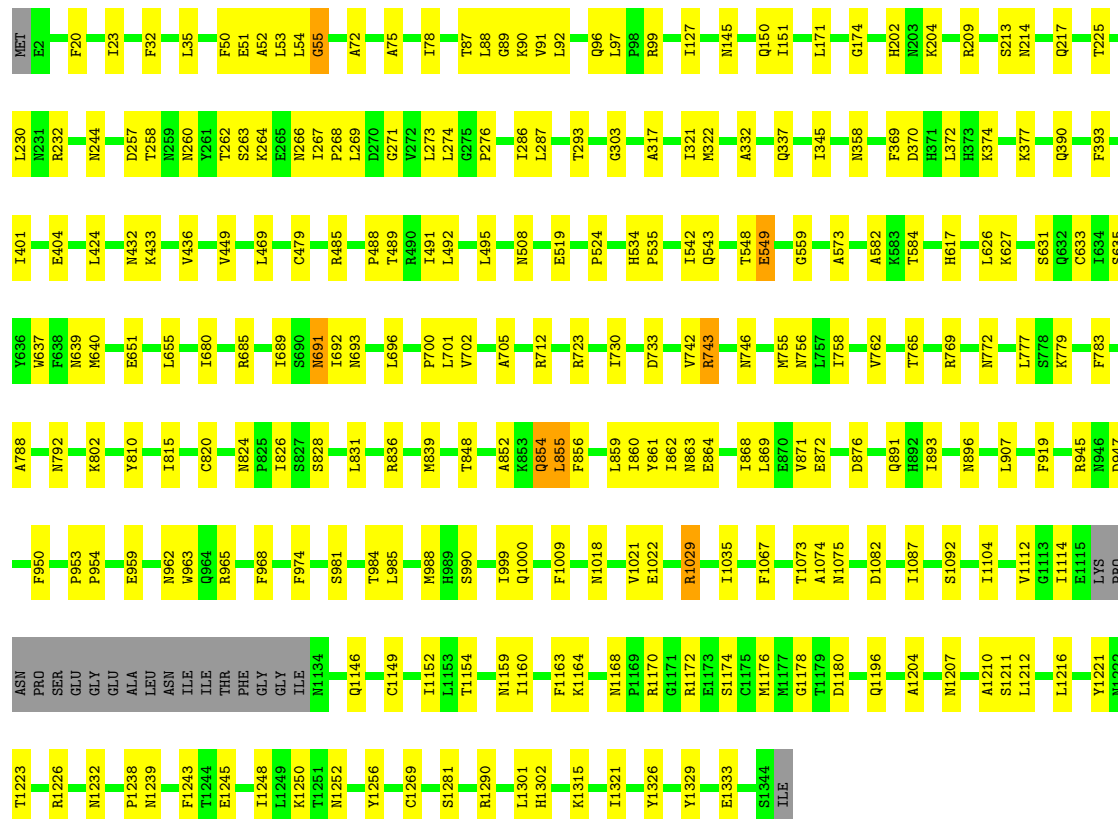
- Molecule 1: Major capsid protein






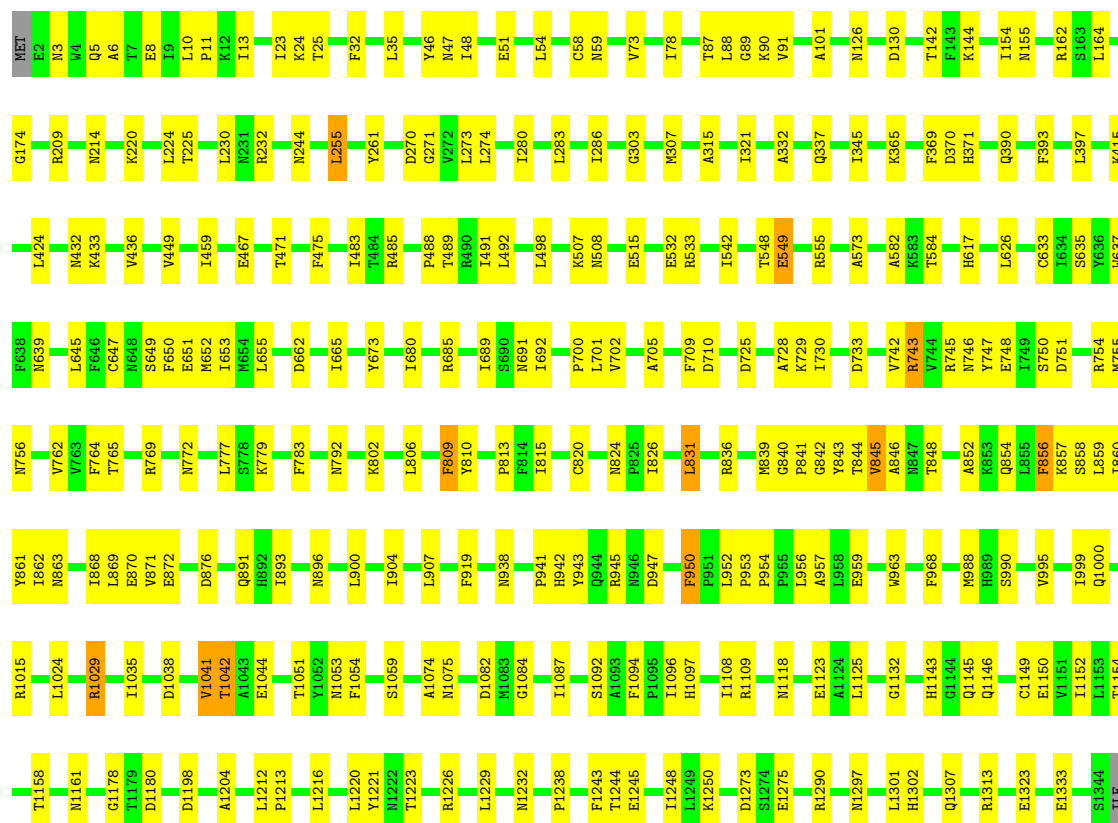
• Molecule 1: Major capsid protein

Chain C: 80% 18% **




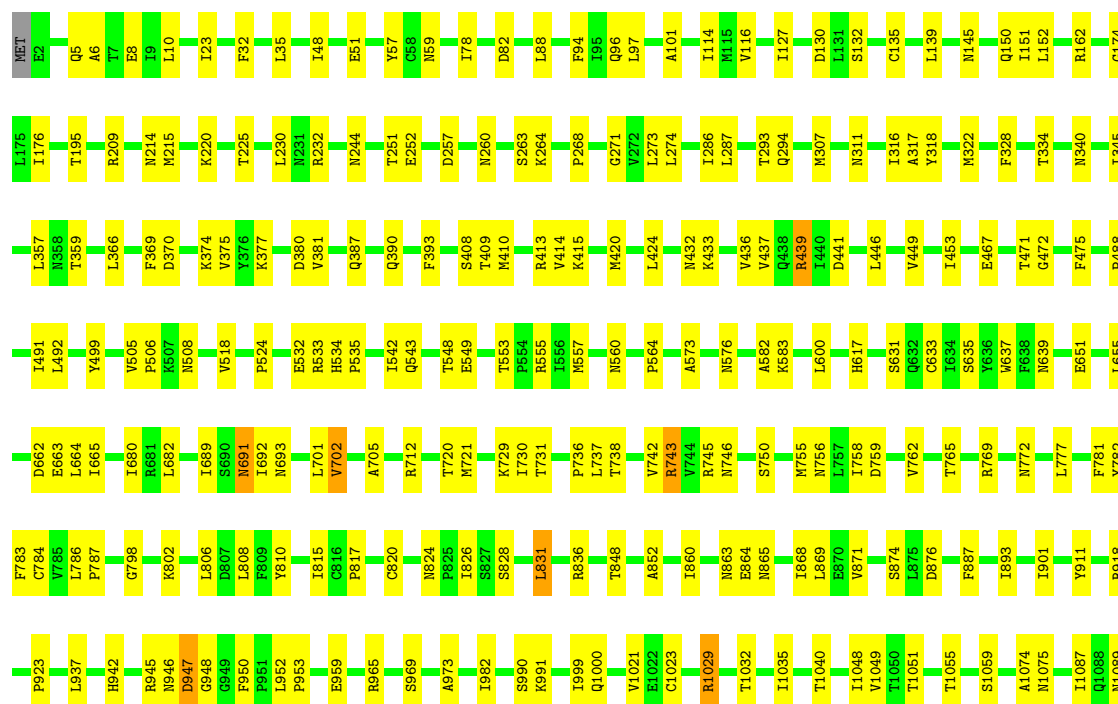
• Molecule 1: Major capsid protein

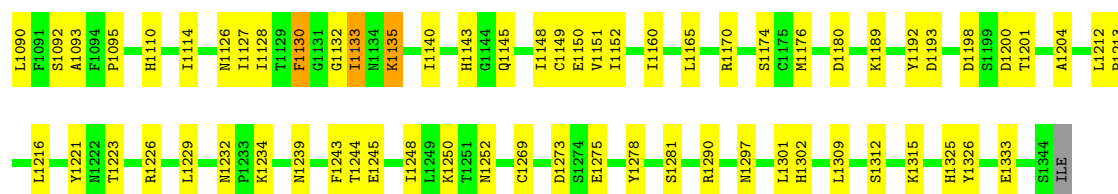
Chain D:  79% 20%



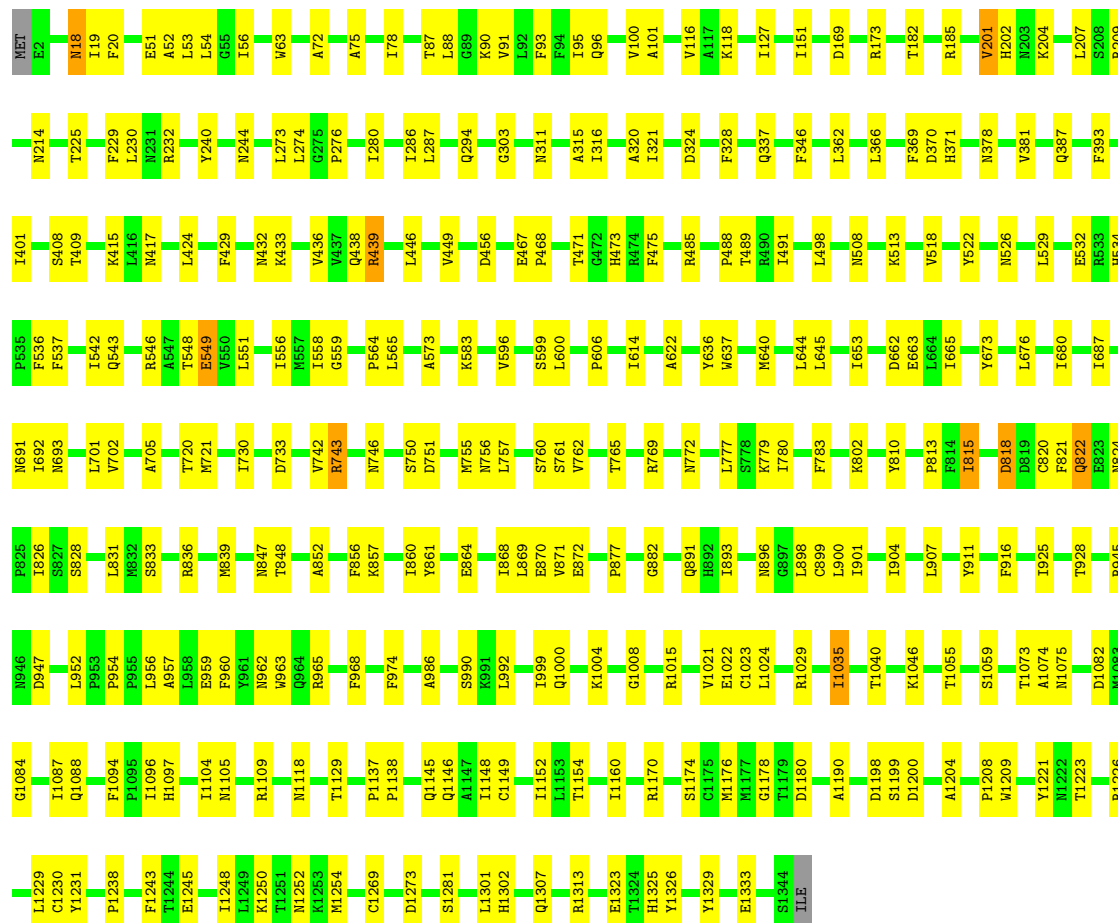
• Molecule 1: Major capsid protein

Chain E:  77% 22%

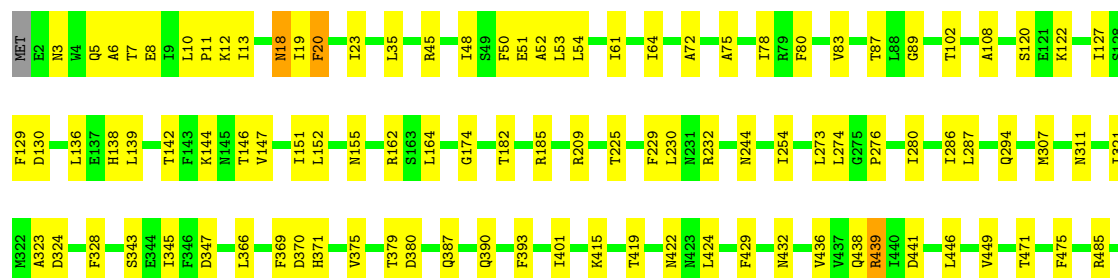


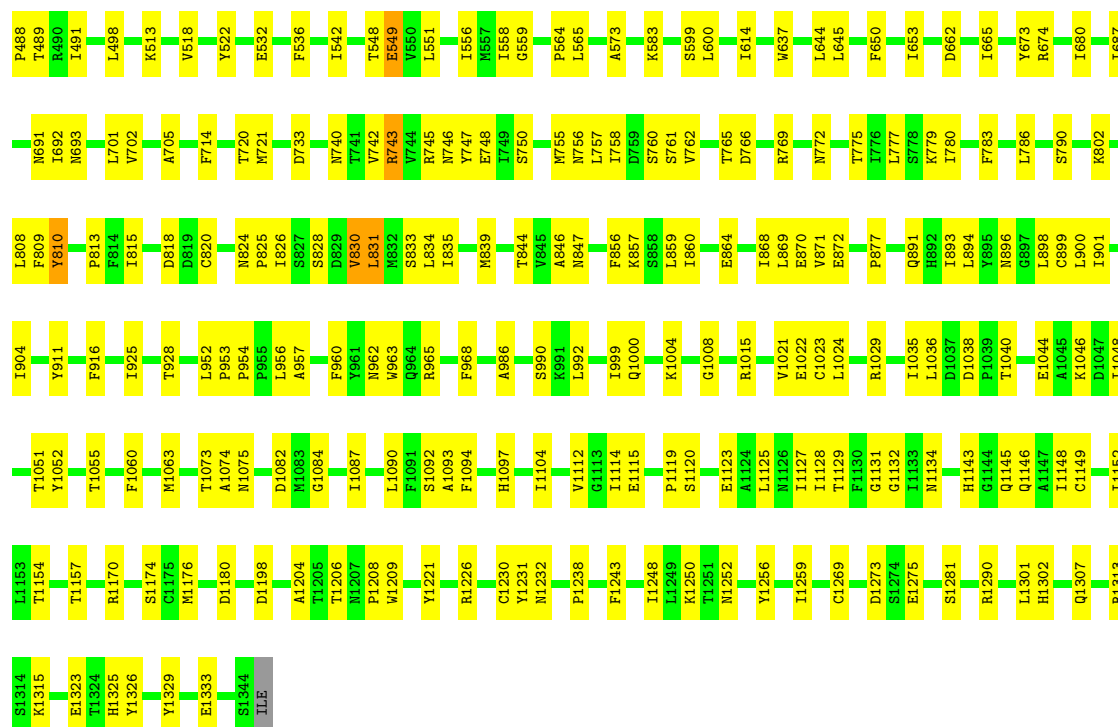


- Molecule 1: Major capsid protein



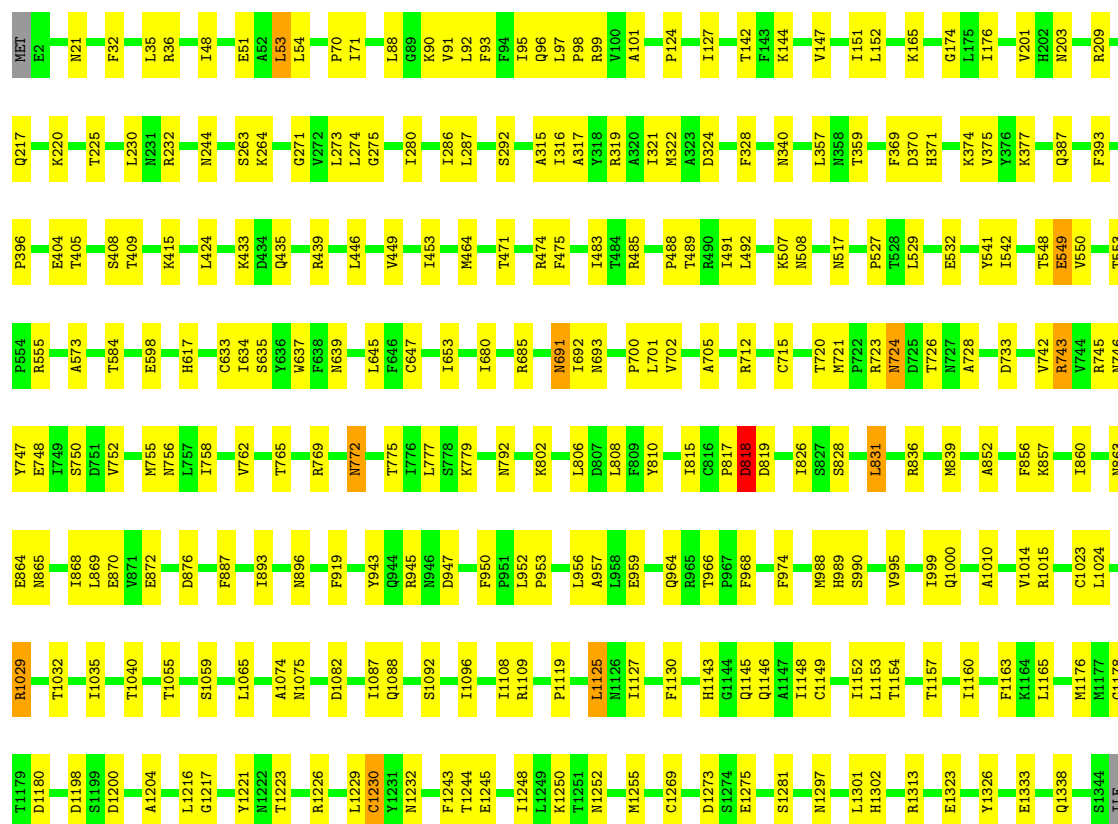
- Molecule 1: Major capsid protein





• Molecule 1: Major capsid protein

Chain H: 80% 19%



• Molecule 1: Major capsid protein

- Molecule 1: Major capsid protein

Chain t:  99%



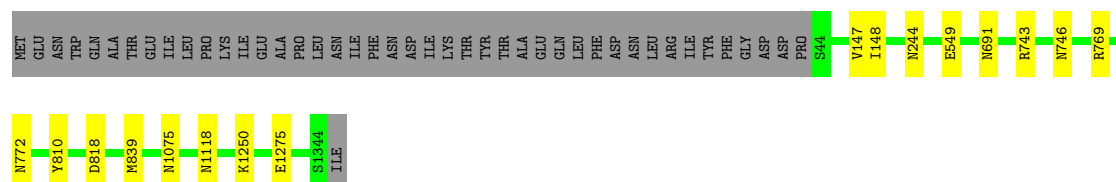
- Molecule 1: Major capsid protein

Chain u:  99%



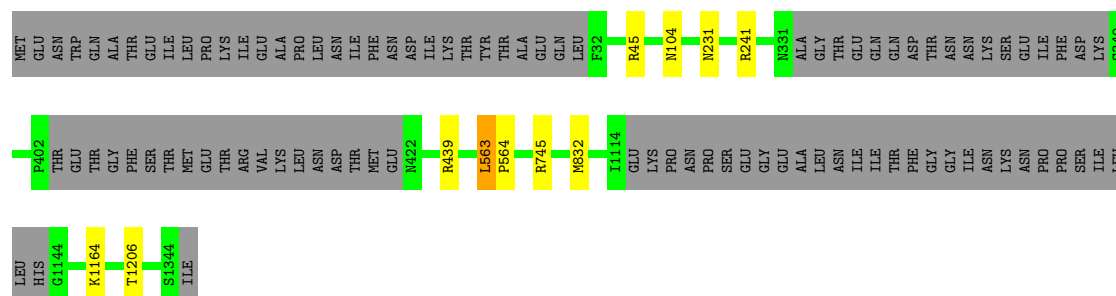
- Molecule 1: Major capsid protein

Chain v:  96%



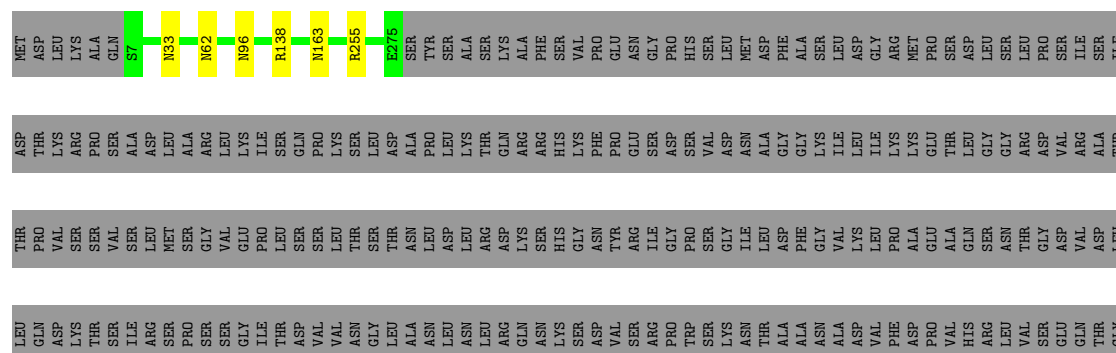
- Molecule 1: Major capsid protein

Chain w: 92% • 7%



- Molecule 2: Large structural phosphoprotein

Chain e: 31% . 69%



[illegible]

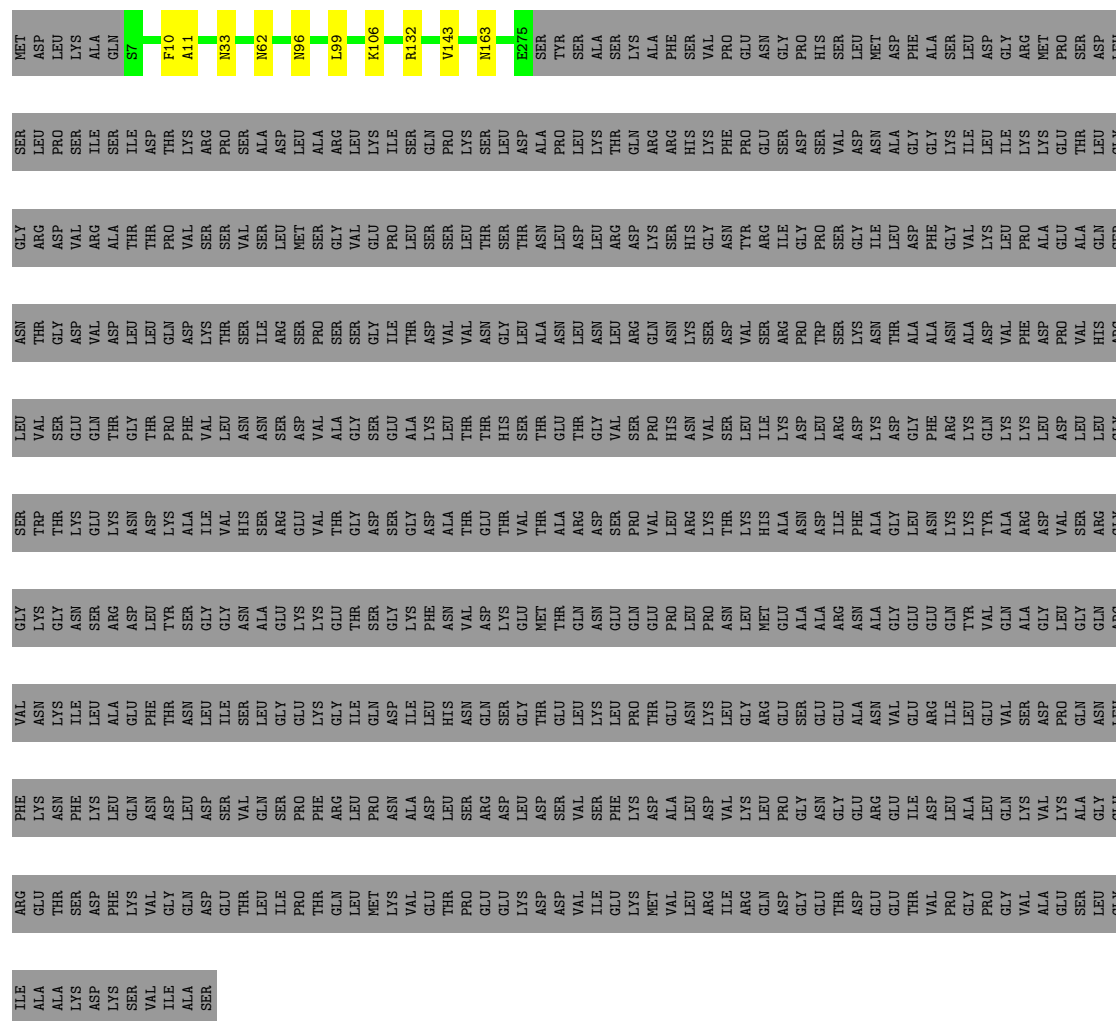
- Molecule 2: Large structural phosphoprotein

Chain f:  31% 69%

[illegible]

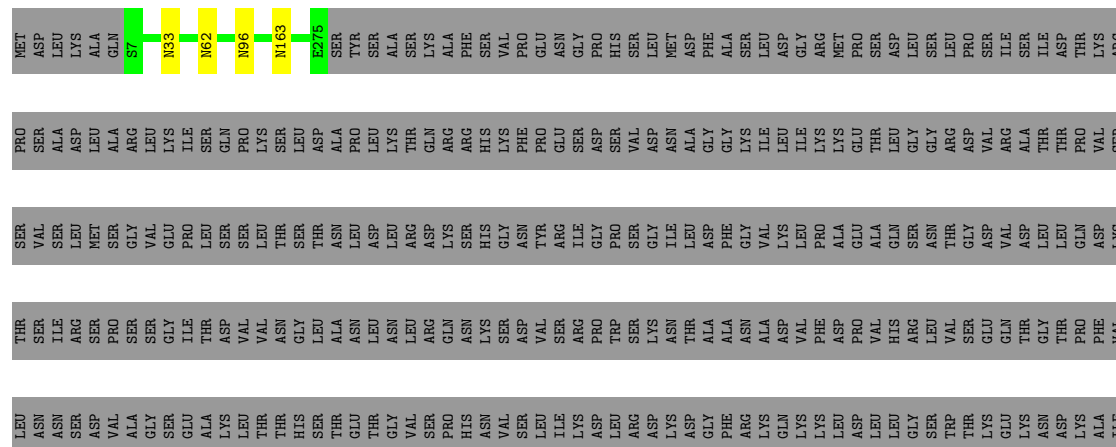
- Molecule 2: Large structural phosphoprotein

Chain g: 30% 69%



- Molecule 2: Large structural phosphoprotein

Chain h:  31% 69%



[illegible]

- Molecule 2: Large structural phosphoprotein

Chain i: 

[illegible]

- Molecule 2: Large structural phosphoprotein

Chain j:  30% . 69%

[illegible]

- Molecule 2: Large structural phosphoprotein

Chain k:  30% 69%

[illegible]

[illegible]

- Molecule 2: Large structural phosphoprotein

Chain 1: 30% 69%

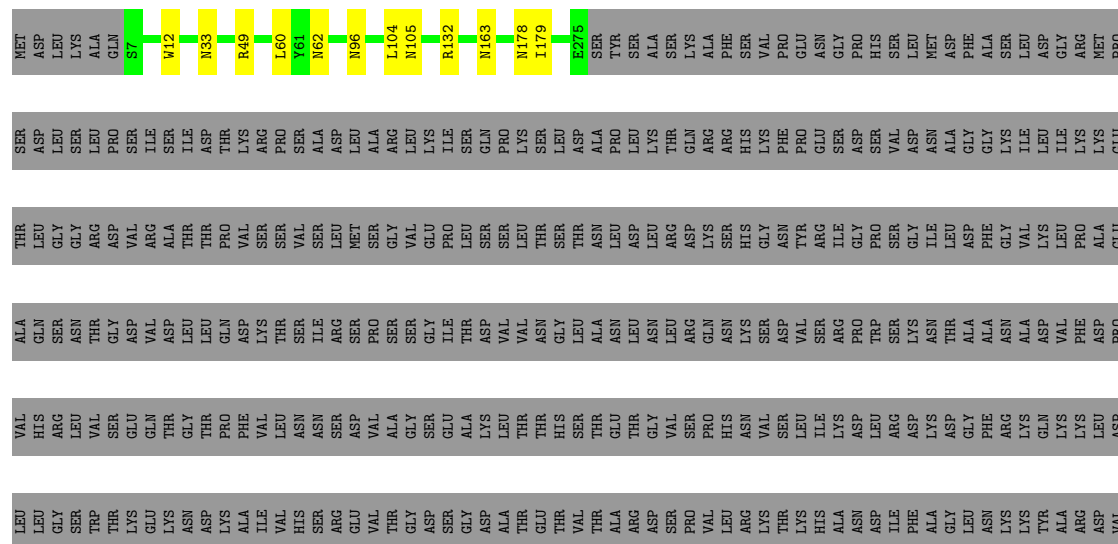
[illegible]

- Molecule 2: Large structural phosphoprotein

Chain m:  31% . 69%



- Molecule 2: Large structural phosphoprotein



[illegible]

- Molecule 2: Large structural phosphoprotein

Chain o: 30% 69%

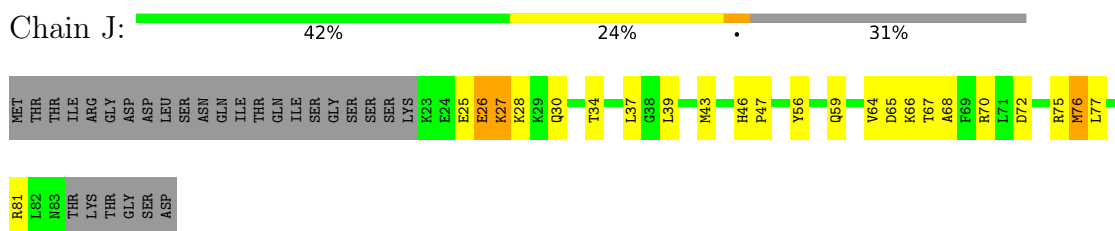
[illegible]

- Molecule 2: Large structural phosphoprotein

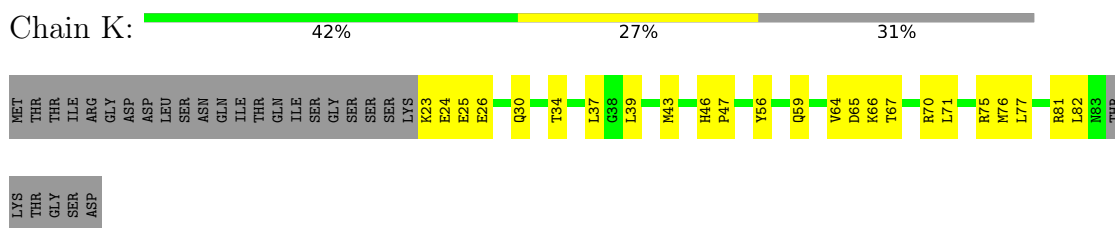
Chain p:  31% . 69%



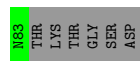
- Molecule 3: Small capsomere-interacting protein




- Molecule 3: Small capsomere-interacting protein




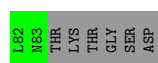
- Molecule 3: Small capsomere-interacting protein



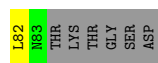
- Chain M: 




- Chain N: 




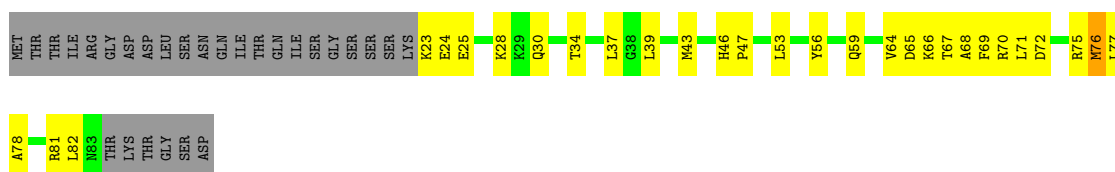
- Chain O:



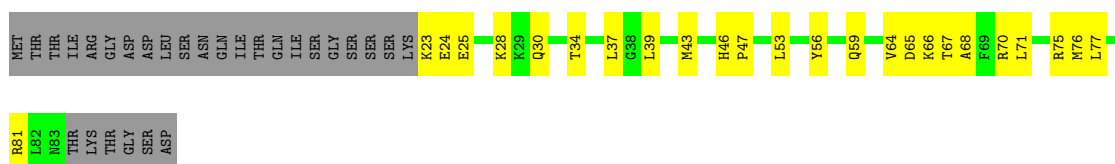
- Chain P: 
- | Category | Percentage |
|----------|------------|
| Green | 39% |
| Yellow | 28% |
| Grey | 31% |



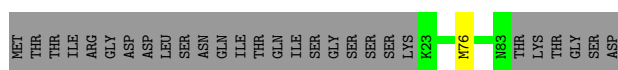
- Chain Q:  36% 31% 0% 31%



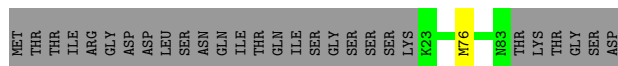
- Molecule 3: Small capsomere-interacting protein



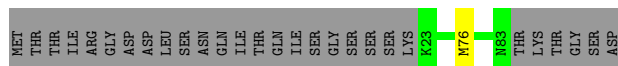
- Molecule 3: Small capsomere-interacting protein



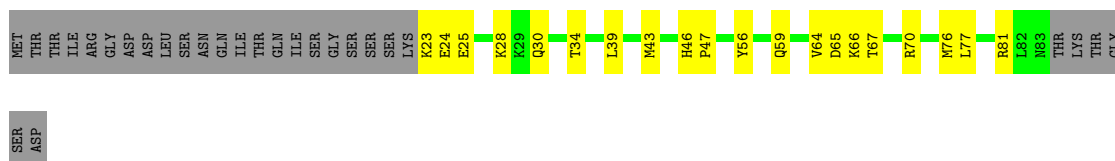
- Molecule 3: Small capsomere-interacting protein



- Molecule 3: Small capsomere-interacting protein

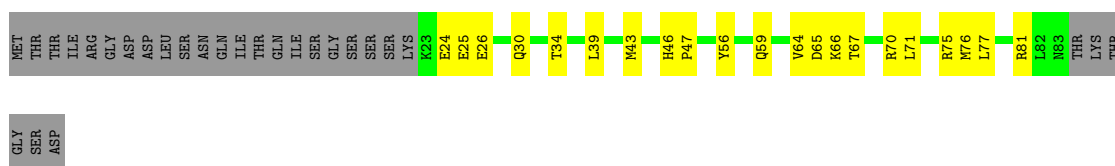


- Molecule 3: Small capsomere-interacting protein

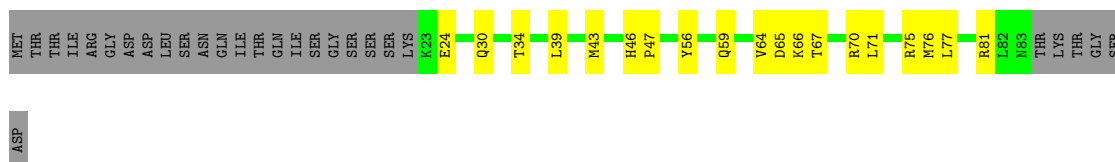


- Molecule 3: Small capsomere-interacting protein

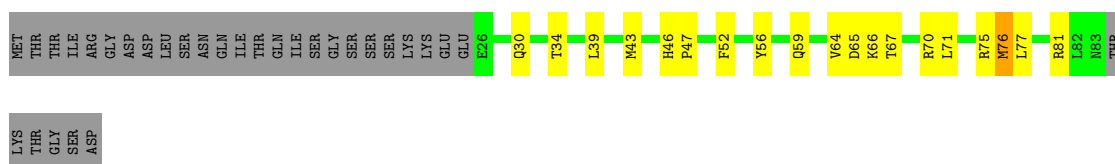




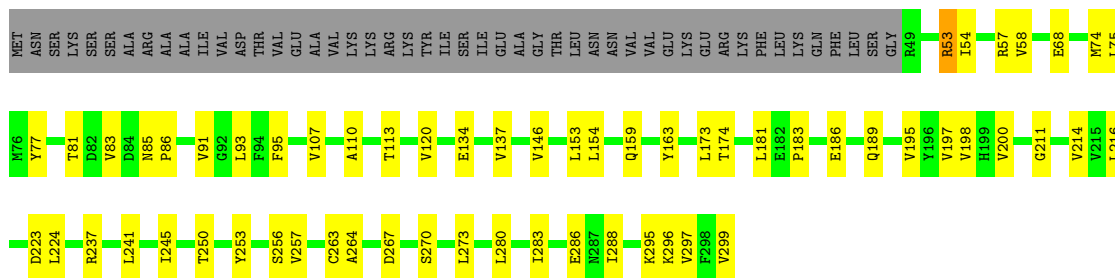
- Molecule 3: Small capsomere-interacting protein



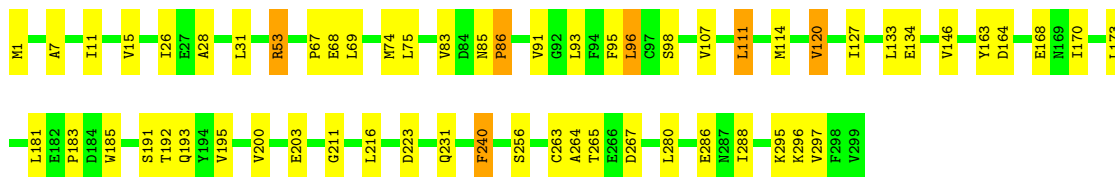
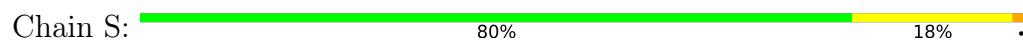
- Molecule 3: Small capsomere-interacting protein



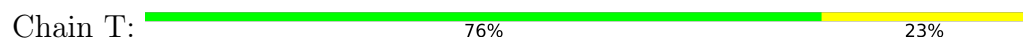
- Molecule 4: Triplex capsid protein 1

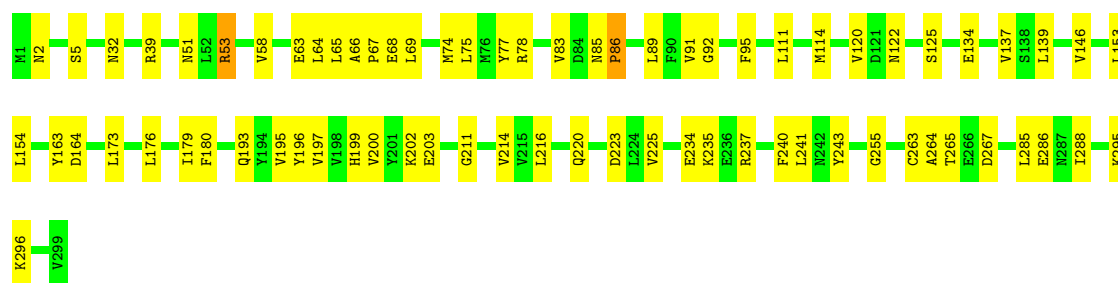


- Molecule 4: Triplex capsid protein 1



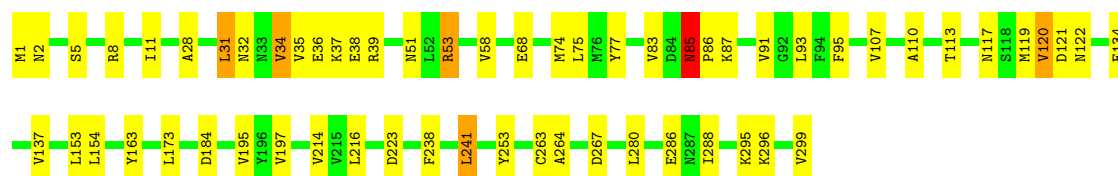
- Molecule 4: Triplex capsid protein 1





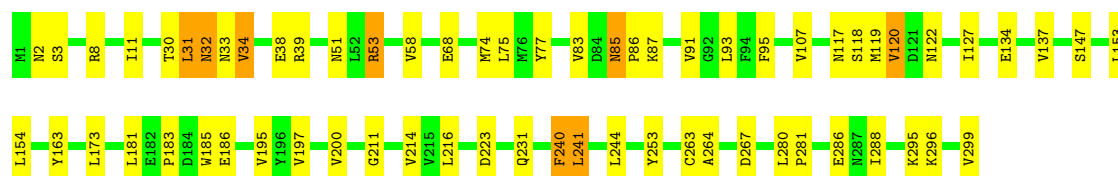
- Molecule 4: Triplex capsid protein 1

Chain U: 80% 18% .



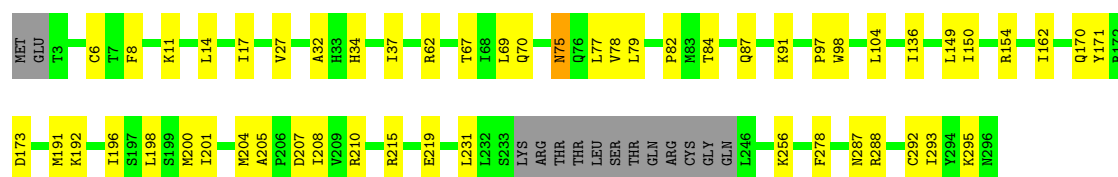
- Molecule 4: Triplex capsid protein 1

Chain V: 78% 19% .



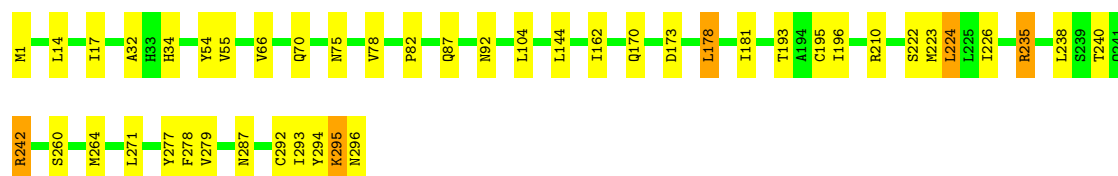
- Molecule 5: Triplex capsid protein 2

Chain 6: 77% 18% 5%

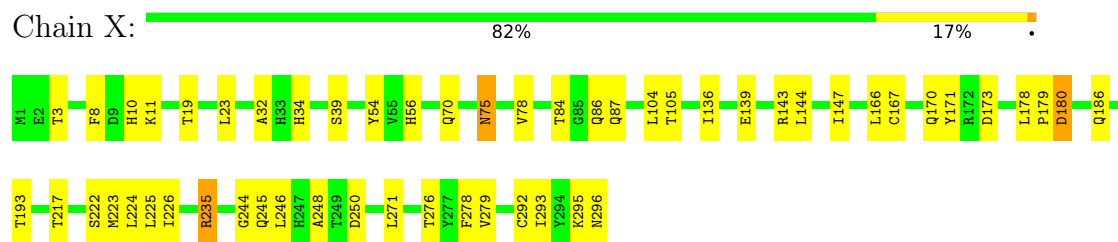


- Molecule 5: Triplex capsid protein 2

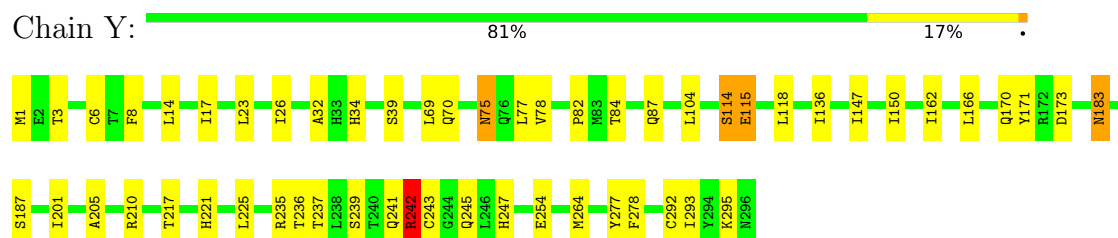
Chain W: 85% 14% .



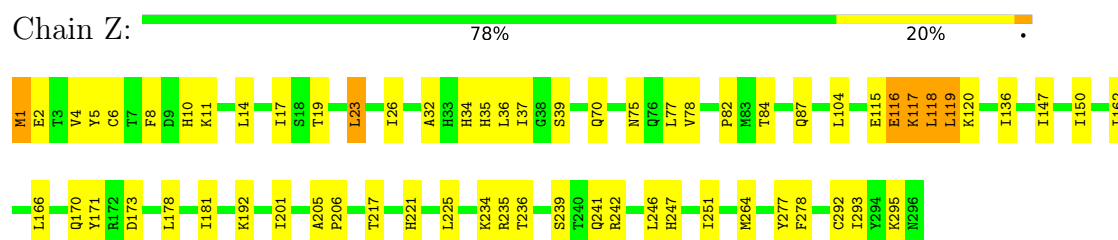
- Molecule 5: Triplex capsid protein 2



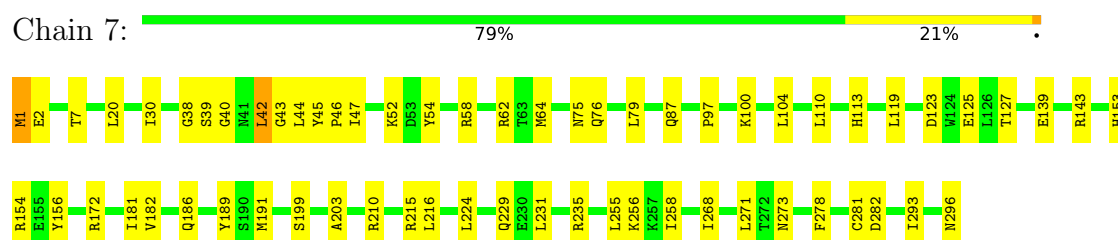
- Molecule 5: Triplex capsid protein 2



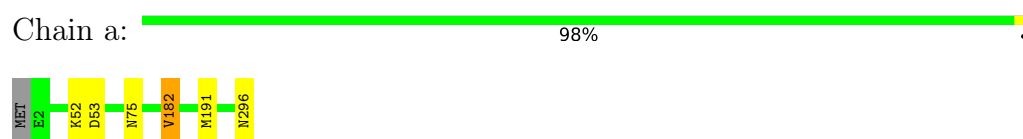
- Molecule 5: Triplex capsid protein 2



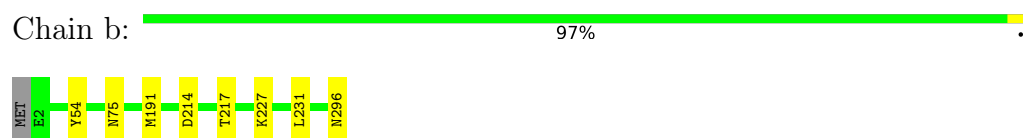
- Molecule 5: Triplex capsid protein 2



- Molecule 5: Triplex capsid protein 2



- Molecule 5: Triplex capsid protein 2



- Molecule 5: Triplex capsid protein 2

Chain c:  98% .



- Molecule 5: Triplex capsid protein 2

Chain d:  97% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	6443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (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	0.51	0/10927	0.68	0/14860
1	B	0.46	0/10927	0.66	0/14860
1	C	0.46	0/10793	0.63	0/14676
1	D	0.46	0/10927	0.64	1/14860 (0.0%)
1	E	0.50	0/10927	0.66	0/14860
1	F	0.42	0/10927	0.65	0/14860
1	G	0.42	1/10927 (0.0%)	0.66	0/14860
1	H	0.50	0/10927	0.66	0/14860
1	I	0.47	0/10927	0.64	0/14860
1	q	0.42	0/10550	0.64	0/14349
1	r	0.38	0/10927	0.62	0/14860
1	s	0.39	0/10927	0.64	0/14860
1	t	0.40	0/10927	0.63	0/14860
1	u	0.38	0/10935	0.62	0/14870
1	v	0.38	0/10566	0.62	0/14366
1	w	0.38	0/10161	0.66	1/13814 (0.0%)
2	e	0.32	0/2272	0.54	0/3084
2	f	0.34	0/2272	0.62	0/3084
2	g	0.35	0/2272	0.62	0/3084
2	h	0.31	0/2272	0.56	0/3084
2	i	0.32	0/2272	0.63	0/3084
2	j	0.32	0/2272	0.59	0/3084
2	k	0.33	0/2272	0.58	0/3084
2	l	0.32	0/2272	0.57	1/3084 (0.0%)
2	m	0.36	0/2272	0.60	1/3084 (0.0%)
2	n	0.34	0/2272	0.63	1/3084 (0.0%)
2	o	0.40	0/2272	0.66	0/3084
2	p	0.34	0/2272	0.60	0/3084
3	1	0.29	0/490	0.44	0/656
3	2	0.29	0/490	0.44	0/656
3	3	0.28	0/490	0.44	0/656
3	4	0.29	0/463	0.44	0/621
3	J	0.28	0/490	0.44	0/656
3	K	0.28	0/490	0.44	0/656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
3	L	0.29	0/490	0.44	0/656
3	M	0.29	0/490	0.44	0/656
3	N	0.29	0/490	0.44	0/656
3	O	0.29	0/490	0.44	0/656
3	P	0.29	0/490	0.44	0/656
3	Q	0.28	0/490	0.44	0/656
3	R	0.29	0/490	0.44	0/656
3	x	0.29	0/490	0.44	0/656
3	y	0.29	0/490	0.44	0/656
3	z	0.29	0/490	0.44	0/656
4	5	0.39	0/2062	0.67	0/2793
4	S	0.49	0/2440	0.67	0/3297
4	T	0.48	0/2440	0.70	0/3297
4	U	0.41	0/2440	0.67	0/3297
4	V	0.41	0/2440	0.66	0/3297
5	6	0.39	0/2262	0.67	0/3069
5	7	0.33	0/2374	0.66	0/3219
5	W	0.42	0/2374	0.68	0/3219
5	X	0.38	0/2374	0.62	0/3219
5	Y	0.39	0/2374	0.68	0/3219
5	Z	0.41	0/2374	0.72	0/3219
5	a	0.44	0/2366	0.73	0/3209
5	b	0.44	0/2366	0.73	0/3209
5	c	0.52	0/2366	0.77	0/3209
5	d	0.41	0/2366	0.75	0/3209
All	All	0.42	1/243697 (0.0%)	0.64	5/330985 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	o	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	1115	GLU	C-N	-5.30	1.21	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	w	563	LEU	C-N-CD	-8.35	102.23	120.60
2	l	181	ASP	N-CA-C	5.66	126.28	111.00
2	m	154	ALA	N-CA-C	5.37	125.51	111.00
2	n	179	ILE	N-CA-C	-5.11	97.21	111.00
1	D	255	LEU	CA-CB-CG	5.01	126.82	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	o	7	SER	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10682	0	10575	240	0
1	B	10682	0	10575	257	0
1	C	10552	0	10444	226	0
1	D	10682	0	10575	249	0
1	E	10682	0	10574	297	0
1	F	10682	0	10574	288	0
1	G	10682	0	10575	334	0
1	H	10682	0	10574	260	0
1	I	10682	0	10575	192	0
1	q	10313	0	10230	0	0
1	r	10682	0	10575	0	0
1	s	10682	0	10574	0	0
1	t	10682	0	10575	0	0
1	u	10690	0	10587	0	0
1	v	10331	0	10242	0	0
1	w	9933	0	9844	0	0
2	e	2224	0	2186	0	0
2	f	2224	0	2186	0	0
2	g	2224	0	2186	0	0
2	h	2224	0	2186	0	0
2	i	2224	0	2186	0	0
2	j	2224	0	2186	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	k	2224	0	2186	0	0
2	l	2224	0	2186	0	0
2	m	2224	0	2186	0	0
2	n	2224	0	2186	0	0
2	o	2224	0	2186	0	0
2	p	2224	0	2186	0	0
3	1	483	0	513	16	0
3	2	483	0	513	13	0
3	3	483	0	513	12	0
3	4	456	0	488	11	0
3	J	483	0	513	57	0
3	K	483	0	513	34	0
3	L	483	0	513	34	0
3	M	483	0	513	50	0
3	N	483	0	513	54	0
3	O	483	0	513	43	0
3	P	483	0	513	45	0
3	Q	483	0	513	64	0
3	R	483	0	513	52	0
3	x	483	0	513	0	0
3	y	483	0	513	0	0
3	z	483	0	513	0	0
4	5	2023	0	2034	39	0
4	S	2398	0	2438	82	0
4	T	2398	0	2438	63	0
4	U	2398	0	2438	59	0
4	V	2398	0	2438	91	0
5	6	2226	0	2318	39	0
5	7	2337	0	2437	61	0
5	W	2337	0	2436	84	0
5	X	2337	0	2437	82	0
5	Y	2337	0	2437	37	0
5	Z	2337	0	2437	46	0
5	a	2329	0	2425	0	0
5	b	2329	0	2419	0	0
5	c	2329	0	2425	0	0
5	d	2329	0	2425	0	0
All	All	238552	0	238065	2801	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 12.

All (2801) 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:I:810:TYR:CE2	3:R:37:LEU:HD12	1.33	1.59
1:F:1109:ARG:NH1	5:X:223:MET:CE	1.70	1.51
1:H:810:TYR:CZ	3:Q:37:LEU:HD12	1.47	1.49
1:I:335:GLU:CD	4:V:31:LEU:HG	1.20	1.48
1:D:862:ILE:HD11	3:M:75:ARG:NH1	1.24	1.46
1:H:817:PRO:HG3	3:Q:43:MET:SD	1.57	1.44
1:D:810:TYR:CE2	3:M:37:LEU:HD12	1.53	1.40
1:F:810:TYR:CE2	3:O:37:LEU:HD12	1.57	1.38
1:F:1096:ILE:CD1	5:X:224:LEU:HD21	1.56	1.34
1:H:756:ASN:OD1	3:Q:65:ASP:HB2	1.22	1.34
1:I:335:GLU:OE2	4:V:31:LEU:CG	1.76	1.33
5:7:45:TYR:CE2	5:7:125:GLU:HG2	1.64	1.33
1:F:1109:ARG:CZ	5:X:223:MET:CE	2.08	1.32
1:A:534:HIS:CE1	1:A:1216:LEU:HD13	1.64	1.31
1:G:1044:GLU:OE1	5:W:1:MET:CE	1.78	1.31
4:V:85:ASN:HB3	4:V:86:PRO:CD	1.59	1.31
1:F:1096:ILE:HD11	5:X:224:LEU:CD2	1.58	1.29
1:F:1096:ILE:CD1	5:X:224:LEU:CD2	2.10	1.29
5:W:82:PRO:HG2	5:W:295:LYS:CG	1.62	1.27
1:D:1132:GLY:HA2	4:V:185:TRP:CZ2	1.69	1.27
1:D:810:TYR:OH	3:M:37:LEU:HB2	1.08	1.26
1:I:335:GLU:OE1	4:V:31:LEU:HG	1.31	1.25
1:F:810:TYR:CZ	3:O:37:LEU:HD12	1.71	1.24
1:E:810:TYR:CE1	3:N:37:LEU:HD12	1.73	1.24
4:U:85:ASN:HB3	4:U:86:PRO:CD	1.60	1.24
1:G:810:TYR:CE2	3:P:37:LEU:HD12	1.73	1.23
4:U:85:ASN:CB	4:U:86:PRO:HD3	1.67	1.23
4:V:85:ASN:CB	4:V:86:PRO:HD3	1.66	1.22
1:I:810:TYR:CZ	3:R:37:LEU:HD12	1.74	1.22
1:E:415:LYS:NZ	1:F:1326:TYR:OH	1.71	1.22
1:G:756:ASN:OD1	3:P:65:ASP:HB2	1.40	1.21
1:H:810:TYR:CE2	3:Q:37:LEU:HD12	1.75	1.21
1:D:1038:ASP:OD2	4:V:2:ASN:O	1.58	1.21
1:F:1109:ARG:NH1	5:X:223:MET:HE2	1.35	1.20
1:E:810:TYR:CZ	3:N:37:LEU:HD12	1.76	1.19
1:G:810:TYR:CZ	3:P:37:LEU:HD12	1.79	1.18
1:A:1220:LEU:O	1:A:1221:TYR:CD1	1.96	1.17
1:G:830:VAL:O	1:G:834:LEU:HB2	1.43	1.17
1:C:815:ILE:CD1	3:L:37:LEU:HD11	1.73	1.17
1:F:810:TYR:OH	3:O:37:LEU:HB2	1.42	1.17
1:A:810:TYR:OH	3:J:37:LEU:HB2	1.44	1.17
1:I:335:GLU:CD	4:V:31:LEU:CG	2.12	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:810:TYR:CZ	3:M:37:LEU:HD12	1.79	1.16
1:F:1109:ARG:CZ	5:X:223:MET:HE2	1.71	1.16
1:D:845:VAL:HG12	1:D:846:ALA:H	1.01	1.15
1:B:1038:ASP:OD1	1:B:1039:PRO:HD2	1.45	1.15
1:E:51:GLU:OE2	1:F:90:LYS:NZ	1.80	1.15
1:F:1096:ILE:HD11	5:X:224:LEU:HD23	1.20	1.15
1:G:53:LEU:HD11	1:H:92:LEU:CD1	1.75	1.15
5:W:82:PRO:CG	5:W:295:LYS:CD	2.23	1.15
5:W:82:PRO:CG	5:W:295:LYS:HG2	1.76	1.15
5:W:82:PRO:HG2	5:W:295:LYS:HG2	1.26	1.14
1:I:810:TYR:CE2	3:R:37:LEU:CD1	2.29	1.14
1:B:52:ALA:HA	1:C:321:ILE:CG2	1.78	1.13
1:B:53:LEU:HD23	1:C:322:MET:CE	1.78	1.13
1:E:810:TYR:OH	3:N:37:LEU:CB	1.94	1.13
1:A:810:TYR:CZ	3:J:37:LEU:HD12	1.84	1.12
5:W:82:PRO:CB	5:W:295:LYS:HG2	1.78	1.12
1:I:802:LYS:HD3	3:R:67:THR:HG21	1.29	1.12
5:W:82:PRO:CG	5:W:295:LYS:HD3	1.77	1.12
1:D:862:ILE:CD1	3:M:75:ARG:NH1	2.13	1.12
1:A:802:LYS:HD3	3:J:67:THR:HG21	1.17	1.12
1:B:1275:GLU:OE2	1:C:209:ARG:NE	1.84	1.11
1:D:857:LYS:O	1:D:860:ILE:HG22	1.50	1.11
4:V:31:LEU:HD21	4:V:33:ASN:HB3	1.29	1.11
1:B:802:LYS:HD3	3:K:67:THR:HG21	1.15	1.11
1:I:818:ASP:OD2	3:R:46:HIS:HE1	1.31	1.11
1:G:1038:ASP:HB3	4:S:1:MET:HB2	1.24	1.11
1:G:1038:ASP:CB	4:S:1:MET:HB2	1.81	1.10
1:I:335:GLU:OE2	4:V:31:LEU:CD1	1.97	1.10
1:I:756:ASN:OD1	3:R:65:ASP:HB2	1.49	1.10
1:F:1109:ARG:CZ	5:X:223:MET:HE1	1.73	1.10
1:E:802:LYS:HD3	3:N:67:THR:HG21	1.28	1.10
1:H:817:PRO:CG	3:Q:43:MET:SD	2.39	1.10
3:J:27:LYS:HZ2	3:J:28:LYS:HD3	1.12	1.10
1:H:810:TYR:CZ	3:Q:37:LEU:CD1	2.29	1.10
3:J:27:LYS:NZ	3:J:28:LYS:HD3	1.63	1.10
1:G:802:LYS:HD3	3:P:67:THR:HG21	1.15	1.10
1:G:1044:GLU:OE1	5:W:1:MET:HE3	1.51	1.09
1:B:415:LYS:NZ	1:C:1326:TYR:OH	1.83	1.09
1:G:810:TYR:OH	3:P:37:LEU:HB2	1.52	1.08
1:H:755:MET:HB2	3:Q:68:ALA:HB1	1.24	1.08
1:B:810:TYR:CZ	3:K:37:LEU:HD12	1.87	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1132:GLY:HA3	1:E:1234:LYS:HD3	1.33	1.07
1:I:449:VAL:HG23	1:I:1152:ILE:HD11	1.25	1.07
1:E:947:ASP:HA	1:E:973:ALA:HB2	1.34	1.07
5:X:84:THR:HA	5:X:295:LYS:HB3	1.35	1.07
5:X:279:VAL:N	5:X:292:CYS:SG	2.27	1.07
1:F:201:VAL:HG23	1:F:207:LEU:CD1	1.83	1.07
5:W:82:PRO:HG2	5:W:295:LYS:CD	1.83	1.06
1:F:201:VAL:HG23	1:F:207:LEU:HD12	1.06	1.06
1:B:52:ALA:HA	1:C:321:ILE:HG22	1.28	1.06
1:F:201:VAL:HG21	1:F:207:LEU:HA	1.34	1.05
1:D:845:VAL:HG12	1:D:846:ALA:N	1.65	1.05
1:G:830:VAL:HG12	1:G:834:LEU:HD22	1.14	1.05
1:E:114:ILE:HD12	1:G:23:ILE:HD12	1.37	1.05
1:D:810:TYR:OH	3:M:37:LEU:CB	2.03	1.05
1:C:449:VAL:HG23	1:C:1152:ILE:HD11	1.37	1.05
1:C:815:ILE:HD13	3:L:37:LEU:HD11	1.33	1.05
1:G:830:VAL:HA	1:G:834:LEU:HD13	1.39	1.04
1:A:1143:HIS:NE2	1:B:1200:ASP:OD1	1.90	1.04
4:V:240:PHE:CD2	4:V:244:LEU:CD1	2.41	1.04
4:V:240:PHE:CD2	4:V:244:LEU:HD11	1.93	1.04
1:F:802:LYS:HD3	3:O:67:THR:HG21	1.04	1.03
5:W:82:PRO:HG3	5:W:295:LYS:HD3	1.36	1.03
1:G:415:LYS:NZ	1:H:1326:TYR:OH	1.89	1.03
1:E:810:TYR:OH	3:N:37:LEU:CA	2.05	1.03
1:G:1052:TYR:CE2	4:S:11:ILE:HG12	1.94	1.03
1:D:1132:GLY:CA	4:V:185:TRP:HZ2	1.66	1.02
4:T:65:LEU:HD12	4:T:68:GLU:OE1	1.59	1.02
1:I:335:GLU:OE2	4:V:31:LEU:HG	1.36	1.02
1:D:810:TYR:CZ	3:M:37:LEU:HB2	1.93	1.02
5:W:295:LYS:HA	5:W:295:LYS:HE2	1.41	1.02
1:G:1044:GLU:OE1	5:W:1:MET:CG	2.07	1.02
1:B:53:LEU:HD23	1:C:322:MET:HE3	1.41	1.02
1:F:93:PHE:HB2	1:F:116:VAL:CG2	1.89	1.02
1:H:756:ASN:OD1	3:Q:65:ASP:CB	2.05	1.02
1:D:1042:THR:HG23	1:D:1053:ASN:HB3	1.39	1.01
1:H:756:ASN:HD21	3:Q:64:VAL:HB	1.20	1.01
1:D:844:THR:HA	1:D:848:THR:CG2	1.90	1.01
1:E:810:TYR:OH	3:N:37:LEU:HB2	1.54	1.01
1:F:810:TYR:CZ	3:O:37:LEU:CD1	2.44	1.01
1:E:1133:ILE:HG22	1:E:1232:ASN:OD1	1.59	1.01
4:V:31:LEU:HD22	4:V:33:ASN:H	1.23	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:VAL:HG12	1:F:54:LEU:HB2	1.43	1.00
1:G:53:LEU:HD11	1:H:92:LEU:HD11	1.42	1.00
4:U:95:PHE:HE1	4:U:120:VAL:HG22	1.22	1.00
5:W:222:SER:O	5:W:226:ILE:HG13	1.61	1.00
1:F:802:LYS:CD	3:O:67:THR:HG21	1.91	1.00
1:F:1109:ARG:NH2	5:X:223:MET:CE	2.24	1.00
1:F:802:LYS:HD3	3:O:67:THR:CG2	1.92	1.00
1:F:201:VAL:CG2	1:F:207:LEU:HA	1.90	1.00
1:F:1109:ARG:NH1	5:X:223:MET:HE1	1.59	1.00
1:F:820:CYS:O	1:F:824:ASN:HB2	1.62	1.00
1:I:818:ASP:OD2	3:R:46:HIS:CE1	2.15	1.00
1:A:802:LYS:CD	3:J:67:THR:HG21	1.92	0.99
1:D:1042:THR:CG2	1:D:1053:ASN:HB3	1.92	0.99
1:D:810:TYR:CE2	3:M:37:LEU:CD1	2.45	0.99
1:F:93:PHE:HB2	1:F:116:VAL:HG22	1.44	0.99
1:B:1034:ILE:HG13	1:B:1060:PHE:CD1	1.97	0.99
1:F:1109:ARG:NH2	5:X:223:MET:HE2	1.77	0.99
1:E:810:TYR:OH	3:N:37:LEU:HA	1.60	0.98
1:G:820:CYS:O	1:G:824:ASN:HB2	1.63	0.98
1:A:517:ASN:ND2	1:F:1004:LYS:HE3	1.79	0.98
1:H:54:LEU:HB2	1:I:91:VAL:HG12	1.46	0.97
1:E:408:SER:HB3	1:E:1326:TYR:CE1	1.99	0.97
1:I:810:TYR:CZ	3:R:37:LEU:CD1	2.47	0.97
1:F:756:ASN:OD1	3:O:65:ASP:HB2	1.62	0.97
4:U:95:PHE:CE1	4:U:120:VAL:HG22	1.97	0.97
1:A:534:HIS:CE1	1:A:1216:LEU:CD1	2.46	0.97
1:I:335:GLU:OE2	4:V:31:LEU:HD11	1.64	0.97
3:J:27:LYS:NZ	3:J:28:LYS:CD	2.27	0.97
1:F:856:PHE:HE2	3:O:81:ARG:HD2	1.30	0.97
1:H:810:TYR:CE1	3:Q:37:LEU:HD12	1.98	0.96
1:G:802:LYS:CD	3:P:67:THR:HG21	1.94	0.96
1:I:802:LYS:CD	3:R:67:THR:HG21	1.95	0.96
5:W:82:PRO:HB2	5:W:295:LYS:HG2	1.45	0.96
1:I:810:TYR:OH	3:R:37:LEU:HB2	1.64	0.95
1:G:1038:ASP:CG	4:S:1:MET:H1	1.70	0.95
5:W:82:PRO:CG	5:W:295:LYS:CG	2.32	0.95
1:H:324:ASP:O	1:H:328:PHE:HB2	1.67	0.95
5:W:224:LEU:HD22	5:W:224:LEU:H	1.30	0.95
1:B:820:CYS:O	1:B:824:ASN:HB2	1.66	0.94
1:G:51:GLU:OE2	1:H:90:LYS:NZ	2.00	0.94
1:D:845:VAL:CG1	1:D:846:ALA:H	1.79	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:810:TYR:CE2	3:L:37:LEU:HD12	2.01	0.94
5:7:45:TYR:CD2	5:7:125:GLU:HG2	2.02	0.94
1:E:663:GLU:OE2	1:F:636:TYR:HE1	1.48	0.94
1:D:802:LYS:HD3	3:M:67:THR:HG21	1.49	0.94
1:E:1315:LYS:HE2	1:F:1323:GLU:OE2	1.66	0.94
1:G:830:VAL:CG1	1:G:834:LEU:HD22	1.98	0.94
4:T:64:LEU:CD2	4:T:89:LEU:HD11	1.98	0.94
1:C:854:GLN:HE21	1:C:854:GLN:HA	1.30	0.93
1:D:1132:GLY:HA2	4:V:185:TRP:HZ2	1.05	0.93
1:D:59:ASN:ND2	1:G:20:PHE:HZ	1.66	0.93
1:G:1044:GLU:OE1	5:W:1:MET:HE2	1.69	0.93
5:7:45:TYR:HE2	5:7:125:GLU:HG2	1.16	0.93
1:A:90:LYS:NZ	1:F:51:GLU:OE2	2.01	0.93
1:G:1052:TYR:CZ	4:S:11:ILE:HG12	2.03	0.93
1:E:97:LEU:HD11	1:G:23:ILE:HD11	1.48	0.93
1:C:859:LEU:HG	1:C:862:ILE:HG23	1.50	0.92
1:D:1044:GLU:OE1	5:Z:1:MET:N	2.01	0.92
5:W:82:PRO:HG3	5:W:295:LYS:CD	1.95	0.92
1:F:201:VAL:HG21	1:F:207:LEU:CA	1.99	0.92
1:F:201:VAL:CG2	1:F:207:LEU:HD12	1.98	0.92
1:F:779:LYS:O	1:F:783:PHE:HB3	1.70	0.92
1:B:810:TYR:OH	3:K:37:LEU:HB2	1.70	0.92
1:E:738:THR:HG21	1:H:152:LEU:HD21	123.90	0.92
1:G:779:LYS:O	1:G:783:PHE:HB3	1.70	0.91
1:G:1038:ASP:CG	4:S:1:MET:N	2.24	0.91
1:G:810:TYR:CZ	3:P:37:LEU:CD1	2.53	0.91
1:E:802:LYS:CD	3:N:67:THR:HG21	2.00	0.91
5:W:222:SER:HB2	5:W:224:LEU:CD2	2.00	0.91
5:X:295:LYS:HD3	5:X:296:ASN:N	1.86	0.91
1:I:335:GLU:OE1	4:V:31:LEU:CG	2.17	0.91
1:C:802:LYS:HD3	3:L:67:THR:HG21	1.52	0.90
1:D:810:TYR:CZ	3:M:37:LEU:CD1	2.53	0.90
1:F:1254:MET:SD	3:R:30:GLN:HB2	182.69	0.90
1:A:534:HIS:HE1	1:A:1216:LEU:CD1	1.83	0.90
1:D:810:TYR:HH	3:M:37:LEU:HB2	1.35	0.90
1:B:1038:ASP:OD1	1:B:1039:PRO:CD	2.20	0.90
1:I:820:CYS:O	1:I:824:ASN:HB2	1.72	0.90
1:D:59:ASN:HD21	1:G:20:PHE:HZ	1.17	0.89
1:G:830:VAL:HG12	1:G:834:LEU:CD2	2.01	0.89
1:D:862:ILE:CD1	3:M:75:ARG:HH11	1.81	0.89
1:G:756:ASN:OD1	3:P:65:ASP:CB	2.20	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:802:LYS:HD3	3:J:67:THR:CG2	2.01	0.89
1:H:755:MET:CB	3:Q:68:ALA:HB1	2.01	0.89
1:A:1139:SER:OG	1:B:1196:GLN:OE1	1.88	0.89
4:T:64:LEU:HD22	4:T:89:LEU:HD11	1.55	0.89
4:V:85:ASN:HB3	4:V:86:PRO:HD3	0.89	0.89
3:J:27:LYS:HZ2	3:J:28:LYS:CD	1.84	0.88
1:A:534:HIS:HE1	1:A:1216:LEU:HD13	1.32	0.88
3:K:23:LYS:HE2	3:K:26:GLU:OE2	1.73	0.88
4:U:1:MET:N	4:U:1:MET:HE2	5.27	0.88
4:V:31:LEU:HD21	4:V:33:ASN:CB	2.04	0.88
1:A:810:TYR:CE1	3:J:37:LEU:HD12	2.07	0.88
1:C:815:ILE:HD11	3:L:37:LEU:HD11	1.55	0.88
1:B:802:LYS:HD3	3:K:67:THR:CG2	2.02	0.88
1:E:923:PRO:HG3	1:E:950:PHE:CD1	2.09	0.88
1:A:449:VAL:HG23	1:A:1152:ILE:HD11	1.54	0.88
1:E:693:ASN:CG	1:F:945:ARG:HH22	1.77	0.88
1:H:755:MET:HB2	3:Q:68:ALA:CB	2.04	0.87
1:D:844:THR:HA	1:D:848:THR:HG23	1.57	0.87
1:H:755:MET:HB3	3:Q:68:ALA:HA	1.53	0.87
1:B:756:ASN:OD1	3:K:65:ASP:HB2	1.74	0.87
4:T:63:GLU:OE1	4:T:63:GLU:N	2.08	0.87
3:J:27:LYS:CE	3:J:28:LYS:HD3	2.05	0.87
1:B:810:TYR:CE2	3:K:37:LEU:HD12	2.08	0.86
1:F:1096:ILE:HD12	5:X:224:LEU:CD2	2.02	0.86
1:D:779:LYS:O	1:D:783:PHE:HB3	1.75	0.86
1:E:114:ILE:CD1	1:G:23:ILE:HD12	2.05	0.86
1:E:817:PRO:HD3	3:N:43:MET:SD	2.15	0.86
5:X:224:LEU:HD22	5:X:224:LEU:H	1.39	0.86
1:C:859:LEU:HG	1:C:862:ILE:CG2	2.04	0.86
1:D:810:TYR:CD2	3:M:37:LEU:HD12	2.10	0.86
1:C:810:TYR:OH	3:L:37:LEU:HB2	1.75	0.86
1:E:1143:HIS:NE2	1:F:1200:ASP:OD1	2.08	0.86
1:A:3:ASN:ND2	1:B:317:ALA:O	2.08	0.86
1:B:53:LEU:HD23	1:C:322:MET:HE1	1.58	0.86
1:E:415:LYS:NZ	1:F:1326:TYR:CZ	2.44	0.85
1:G:1044:GLU:OE1	5:W:1:MET:HB3	1.75	0.85
1:A:600:LEU:CD2	1:A:901:ILE:HD11	2.06	0.85
5:W:82:PRO:HB2	5:W:295:LYS:CG	2.06	0.85
1:G:1038:ASP:OD1	4:S:1:MET:N	2.10	0.84
1:C:820:CYS:O	1:C:824:ASN:HB2	1.76	0.84
1:D:844:THR:HA	1:D:848:THR:HG21	1.55	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:1216:LEU:HD12	1:I:1217:GLY:N	1.91	0.84
5:Z:118:LEU:H	5:Z:118:LEU:HD23	1.42	0.84
1:I:756:ASN:OD1	3:R:65:ASP:CB	2.25	0.84
4:V:240:PHE:CE2	4:V:244:LEU:HD11	2.12	0.84
1:G:802:LYS:HD3	3:P:67:THR:CG2	2.05	0.84
1:E:810:TYR:CE1	3:N:37:LEU:CD1	2.58	0.84
1:D:59:ASN:ND2	1:G:20:PHE:CZ	2.45	0.84
1:F:856:PHE:CE2	3:O:81:ARG:HD2	2.14	0.83
1:A:1326:TYR:OH	1:F:415:LYS:NZ	2.11	0.83
1:A:810:TYR:CE1	3:J:37:LEU:CD1	2.61	0.83
1:D:802:LYS:CD	3:M:67:THR:HG21	2.08	0.83
1:I:105:ASP:OD2	4:V:147:SER:OG	1.96	0.83
1:E:408:SER:HB3	1:E:1326:TYR:CD1	2.13	0.83
1:B:802:LYS:CD	3:K:67:THR:HG21	2.05	0.83
5:W:70:GLN:O	5:W:78:VAL:HB	1.78	0.83
1:C:779:LYS:O	1:C:783:PHE:HB3	1.77	0.82
5:W:82:PRO:HG2	5:W:295:LYS:HD3	1.49	0.82
1:G:1044:GLU:OE1	5:W:1:MET:CB	2.27	0.82
4:T:58:VAL:HB	4:T:154:LEU:O	1.79	0.82
1:A:600:LEU:HD22	1:A:901:ILE:HD11	1.61	0.82
1:B:52:ALA:CA	1:C:321:ILE:CG2	2.57	0.82
1:D:1132:GLY:CA	4:V:185:TRP:CZ2	2.51	0.82
1:F:810:TYR:HH	3:O:37:LEU:HB2	1.44	0.82
1:D:449:VAL:HG23	1:D:1152:ILE:HD11	1.62	0.82
1:H:802:LYS:HD3	3:Q:67:THR:HG21	1.60	0.82
1:F:201:VAL:CG2	1:F:207:LEU:CD1	2.58	0.81
1:A:756:ASN:HD21	3:J:64:VAL:HB	1.45	0.81
1:B:712:ARG:NH2	1:B:876:ASP:HA	1.95	0.81
1:B:52:ALA:CA	1:C:321:ILE:HG22	2.10	0.81
1:E:810:TYR:CZ	3:N:37:LEU:CD1	2.59	0.81
1:G:1044:GLU:OE1	5:W:1:MET:HG3	1.79	0.81
1:E:252:GLU:HB3	1:G:19:ILE:HG12	1.60	0.81
3:R:53:LEU:O	3:R:53:LEU:HD12	5.90	0.81
1:E:340:ASN:HB3	1:G:13:ILE:HG13	1.61	0.80
5:7:44:LEU:HG	5:7:47:ILE:HB	1.63	0.80
1:H:802:LYS:CD	3:Q:67:THR:HG21	2.12	0.80
1:I:335:GLU:OE2	4:V:31:LEU:CD2	2.28	0.80
4:T:69:LEU:HA	4:T:146:VAL:HG21	1.63	0.80
1:G:1038:ASP:CG	4:S:1:MET:HB2	2.02	0.80
1:F:1096:ILE:HD12	5:X:224:LEU:HD21	1.60	0.80
4:V:34:VAL:HG23	4:V:39:ARG:NH1	1.97	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:LEU:O	1:C:53:LEU:HD12	1.80	0.80
1:C:810:TYR:CZ	3:L:37:LEU:HD12	2.17	0.80
1:I:815:ILE:HG21	3:R:39:LEU:HD21	1.62	0.80
1:G:756:ASN:HD21	3:P:64:VAL:HB	1.46	0.80
4:S:85:ASN:HB3	4:S:86:PRO:HD3	1.64	0.79
1:B:713:LEU:HD11	1:B:783:PHE:CE2	2.16	0.79
1:D:862:ILE:HD11	3:M:75:ARG:HH12	1.47	0.79
1:H:471:THR:O	1:H:475:PHE:HB2	1.81	0.79
5:X:217:THR:HA	5:X:225:LEU:HD21	1.62	0.79
1:I:756:ASN:HD21	3:R:64:VAL:HB	1.46	0.79
5:Y:23:LEU:HG	5:Y:26:ILE:HD12	1.64	0.79
1:E:1152:ILE:HD12	1:E:1216:LEU:HD21	1.64	0.79
1:E:410:MET:HB2	1:E:413:ARG:HD2	1.63	0.79
4:U:95:PHE:CE1	4:U:120:VAL:CG2	2.65	0.79
1:G:1038:ASP:HB3	4:S:1:MET:CB	2.08	0.79
1:F:1096:ILE:HD13	5:X:224:LEU:HD21	1.62	0.79
1:F:1109:ARG:HH22	5:X:223:MET:HE2	1.47	0.78
1:C:1152:ILE:HD12	1:C:1216:LEU:HD21	1.65	0.78
1:E:1132:GLY:HA3	1:E:1234:LYS:CD	2.11	0.78
1:H:810:TYR:CE2	3:Q:37:LEU:CD1	2.60	0.78
1:H:756:ASN:ND2	3:Q:64:VAL:HB	1.98	0.78
3:Q:53:LEU:HD12	3:Q:53:LEU:O	5.90	0.78
1:B:712:ARG:HH21	1:B:876:ASP:HA	1.48	0.78
1:B:1036:LEU:HB3	1:B:1058:LEU:HD23	1.66	0.78
1:H:755:MET:CB	3:Q:68:ALA:CB	2.60	0.77
1:E:810:TYR:CZ	3:N:37:LEU:HB2	2.19	0.77
1:B:779:LYS:O	1:B:783:PHE:HB2	1.84	0.77
1:I:255:LEU:HD21	1:I:1063:MET:CE	2.15	0.77
5:X:87:GLN:HB2	5:X:293:ILE:HG22	1.65	0.77
1:D:255:LEU:HD22	5:Z:162:ILE:HG23	69.39	0.77
1:E:97:LEU:HD11	1:G:23:ILE:CD1	2.13	0.77
1:B:714:PHE:CE2	1:B:871:VAL:HG11	2.20	0.77
1:I:810:TYR:HE2	3:R:37:LEU:HD12	1.38	0.77
1:E:806:LEU:CD1	3:N:67:THR:HG23	2.14	0.77
5:7:38:GLY:O	5:7:42:LEU:HD11	1.85	0.77
1:A:755:MET:HB2	3:J:68:ALA:HB1	1.67	0.76
1:B:1036:LEU:O	1:B:1036:LEU:HD12	1.84	0.76
1:F:822:GLN:C	1:F:822:GLN:HE21	1.88	0.76
1:H:817:PRO:CD	3:Q:43:MET:SD	2.73	0.76
4:S:83:VAL:HG12	4:S:86:PRO:HD2	1.66	0.76
1:B:471:THR:O	1:B:475:PHE:HB2	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1307:GLN:CD	1:H:1160:ILE:HD12	2.06	0.76
1:A:600:LEU:HD22	1:A:901:ILE:CD1	2.16	0.76
1:A:600:LEU:CD2	1:A:901:ILE:CD1	2.64	0.76
1:A:756:ASN:OD1	3:J:65:ASP:HB2	1.86	0.76
1:A:517:ASN:HD21	1:F:1004:LYS:HE3	1.51	0.76
1:G:53:LEU:HD12	1:H:90:LYS:HG3	1.66	0.76
1:H:806:LEU:HD11	3:Q:67:THR:HG23	1.66	0.76
1:C:54:LEU:O	1:C:55:GLY:O	2.03	0.75
1:H:750:SER:OG	3:Q:75:ARG:NE	2.19	0.75
4:S:83:VAL:HG12	4:S:86:PRO:CD	2.15	0.75
1:B:715:CYS:HB2	1:B:716:PRO:HD2	1.67	0.75
1:D:756:ASN:HD21	3:M:64:VAL:HB	1.51	0.75
1:B:815:ILE:HG23	3:K:39:LEU:HD21	1.68	0.75
1:C:51:GLU:OE2	1:D:90:LYS:NZ	2.18	0.75
1:D:845:VAL:CG1	1:D:846:ALA:N	2.40	0.75
1:E:415:LYS:NZ	1:F:1326:TYR:CE1	2.53	0.75
1:G:857:LYS:HE3	3:P:82:LEU:HA	1.68	0.75
1:E:252:GLU:H	1:G:19:ILE:HB	1.49	0.75
1:B:712:ARG:HB3	1:B:963:TRP:CZ2	2.21	0.75
1:E:947:ASP:HA	1:E:973:ALA:CB	2.12	0.75
1:I:755:MET:HB2	3:R:68:ALA:HB1	1.67	0.75
1:G:1038:ASP:OD2	4:S:1:MET:HG3	1.86	0.75
1:H:1216:LEU:HD12	1:H:1217:GLY:N	2.00	0.75
1:G:19:ILE:N	1:G:19:ILE:HD13	2.02	0.74
1:I:449:VAL:HG23	1:I:1152:ILE:CD1	2.11	0.74
1:H:53:LEU:HD12	1:I:92:LEU:HD13	1.67	0.74
1:A:750:SER:OG	3:J:75:ARG:NE	2.20	0.74
1:G:1038:ASP:CG	4:S:1:MET:CA	2.55	0.74
1:B:52:ALA:HA	1:C:321:ILE:HG23	1.70	0.74
1:E:802:LYS:HD3	3:N:67:THR:CG2	2.14	0.74
1:I:255:LEU:HD21	1:I:1063:MET:SD	2.27	0.74
1:F:202:HIS:NE2	1:F:204:LYS:HG2	2.02	0.74
1:F:826:ILE:HG23	1:F:828:SER:H	1.53	0.74
1:A:1130:PHE:CZ	4:U:86:PRO:HG2	2.22	0.74
1:F:1109:ARG:NH1	5:X:223:MET:SD	2.60	0.74
1:A:810:TYR:CZ	3:J:37:LEU:CD1	2.65	0.74
4:V:240:PHE:HD2	4:V:244:LEU:CD1	1.99	0.74
4:U:1:MET:H3	4:U:1:MET:HE2	5.57	0.74
1:E:114:ILE:HD12	1:G:23:ILE:CD1	2.15	0.73
4:V:31:LEU:HD22	4:V:33:ASN:N	1.99	0.73
1:F:822:GLN:HE21	1:F:822:GLN:CA	2.01	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:755:MET:HB2	3:P:68:ALA:HB1	1.70	0.73
1:D:471:THR:O	1:D:475:PHE:HB2	1.89	0.73
1:E:663:GLU:OE2	1:F:636:TYR:CE1	2.36	0.73
4:V:31:LEU:CD2	4:V:33:ASN:H	2.01	0.73
5:W:222:SER:CB	5:W:224:LEU:CD2	2.66	0.73
1:G:471:THR:O	1:G:475:PHE:HB2	1.87	0.73
3:N:48:VAL:HG21	3:N:58:LYS:HB3	19.78	0.73
1:H:806:LEU:CD1	3:Q:67:THR:HG23	2.18	0.73
1:D:750:SER:OG	3:M:75:ARG:NE	2.22	0.73
5:Z:82:PRO:HG2	5:Z:295:LYS:HE3	1.70	0.73
1:G:1044:GLU:OE1	5:W:1:MET:SD	2.46	0.73
1:B:714:PHE:HE2	1:B:871:VAL:HG11	1.53	0.72
5:Y:242:ARG:HB2	5:Y:245:GLN:HB2	1.71	0.72
1:E:409:THR:O	1:E:410:MET:HG2	1.89	0.72
1:G:1038:ASP:CG	4:S:1:MET:CB	2.57	0.72
1:C:859:LEU:HD23	1:C:859:LEU:O	1.89	0.72
5:Z:70:GLN:O	5:Z:78:VAL:HB	1.89	0.72
1:A:1130:PHE:CE2	4:U:86:PRO:HG2	2.24	0.72
5:X:295:LYS:CD	5:X:296:ASN:O	2.37	0.72
1:G:1038:ASP:CB	4:S:1:MET:N	2.53	0.72
1:G:1256:TYR:HB3	4:S:31:LEU:HA	81.12	0.72
1:H:755:MET:HB3	3:Q:68:ALA:CA	2.19	0.72
1:A:488:PRO:HA	1:A:491:ILE:HG12	1.72	0.72
1:C:863:ASN:HB3	1:C:896:ASN:HD21	1.54	0.72
5:W:295:LYS:CA	5:W:295:LYS:HE2	2.17	0.72
1:C:815:ILE:CD1	3:L:37:LEU:CD1	2.62	0.72
1:H:724:ASN:ND2	1:H:726:THR:O	2.23	0.71
1:I:857:LYS:HG2	3:R:81:ARG:O	1.90	0.71
3:R:24:GLU:OE2	3:R:24:GLU:N	2.20	0.71
1:B:53:LEU:CD2	1:C:322:MET:CE	2.63	0.71
1:H:54:LEU:N	1:H:54:LEU:HD23	2.04	0.71
5:X:86:GLN:O	5:X:293:ILE:HA	1.89	0.71
1:D:1041:VAL:HG22	1:D:1054:PHE:CD1	2.26	0.71
1:H:756:ASN:HD21	3:Q:64:VAL:CB	2.02	0.71
4:V:32:ASN:ND2	4:V:32:ASN:O	2.23	0.71
1:D:756:ASN:ND2	3:M:64:VAL:HB	2.06	0.71
1:E:252:GLU:CB	1:G:19:ILE:HG12	2.20	0.71
1:A:224:LEU:O	1:A:224:LEU:HD12	5.53	0.71
1:G:1256:TYR:CB	4:S:31:LEU:HA	82.06	0.71
3:J:27:LYS:O	3:J:27:LYS:HD2	1.90	0.71
1:A:97:LEU:HD22	1:F:378:ASN:HD21	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:855:LEU:HD12	1:C:855:LEU:C	2.12	0.70
1:C:756:ASN:HD21	3:L:64:VAL:HB	1.56	0.70
1:E:806:LEU:HD11	3:N:67:THR:HG23	1.72	0.70
5:Y:23:LEU:O	5:Y:23:LEU:HD23	1.91	0.70
3:2:25:GLU:N	3:2:25:GLU:OE2	2.19	0.70
1:I:743:ARG:HH21	1:I:762:VAL:HG11	1.56	0.70
3:1:24:GLU:N	3:1:24:GLU:OE2	2.20	0.70
1:F:945:ARG:HG2	1:F:947:ASP:H	1.56	0.70
1:G:826:ILE:HG23	1:G:828:SER:H	1.56	0.70
1:H:53:LEU:O	1:H:53:LEU:HD23	1.91	0.70
4:U:85:ASN:HB3	4:U:86:PRO:HD3	0.79	0.70
1:A:53:LEU:HD22	1:B:322:MET:SD	2.31	0.70
1:G:1052:TYR:CE2	4:S:11:ILE:CG1	2.74	0.70
1:G:424:LEU:HD11	1:G:573:ALA:HB1	1.73	0.70
1:G:856:PHE:HE2	3:P:81:ARG:HD2	1.57	0.70
1:I:255:LEU:HD11	1:I:1030:ALA:HB1	1.71	0.70
5:7:42:LEU:N	5:7:42:LEU:HD23	2.06	0.70
1:B:712:ARG:HD3	1:B:712:ARG:H	1.57	0.70
3:K:23:LYS:CE	3:K:26:GLU:OE2	2.39	0.70
1:A:820:CYS:O	1:A:824:ASN:HB2	1.91	0.70
1:F:471:THR:O	1:F:475:PHE:HB2	1.91	0.70
3:P:24:GLU:OE2	3:P:24:GLU:N	2.19	0.70
5:W:224:LEU:HD13	5:W:224:LEU:N	2.05	0.70
1:F:857:LYS:HG2	3:O:81:ARG:O	1.92	0.70
5:Y:70:GLN:O	5:Y:78:VAL:HB	1.91	0.70
5:Z:6:CYS:HB3	5:Z:77:LEU:HB3	1.74	0.70
3:L:23:LYS:HD2	3:L:23:LYS:N	2.07	0.70
1:A:1315:LYS:NZ	1:B:409:THR:OG1	2.16	0.70
4:T:85:ASN:HB3	4:T:86:PRO:HD3	1.73	0.70
1:F:822:GLN:O	1:F:822:GLN:NE2	2.25	0.69
1:G:380:ASP:HA	1:H:203:ASN:HB2	1.74	0.69
4:S:98:SER:HB3	4:S:111:LEU:HD11	1.72	0.69
1:B:424:LEU:HD11	1:B:573:ALA:HB1	1.73	0.69
1:E:453:ILE:HD11	1:E:1229:LEU:HD13	1.73	0.69
1:A:517:ASN:HD21	1:F:1004:LYS:CE	2.05	0.69
3:O:24:GLU:OE2	3:O:24:GLU:N	2.21	0.69
5:X:87:GLN:HB2	5:X:293:ILE:CG2	2.21	0.69
1:C:52:ALA:O	1:D:89:GLY:HA2	1.92	0.69
1:G:743:ARG:HH21	1:G:762:VAL:HG11	1.58	0.69
1:H:449:VAL:HG23	1:H:1152:ILE:HD11	1.75	0.69
1:H:863:ASN:HB3	1:H:896:ASN:HD21	1.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:756:ASN:OD1	3:L:65:ASP:HB2	1.92	0.69
4:U:58:VAL:HB	4:U:154:LEU:O	1.93	0.69
1:E:782:TYR:O	1:E:787:PRO:HD3	1.91	0.69
1:G:53:LEU:HD11	1:H:92:LEU:HD13	1.69	0.69
1:H:743:ARG:HH21	1:H:762:VAL:HG11	1.56	0.69
5:X:178:LEU:HD23	5:X:178:LEU:H	1.55	0.69
4:5:58:VAL:HB	4:5:154:LEU:O	1.92	0.69
5:7:45:TYR:CE2	5:7:125:GLU:CG	2.60	0.69
4:V:117:ASN:O	4:V:120:VAL:HG13	1.92	0.69
4:V:58:VAL:HB	4:V:154:LEU:O	1.93	0.69
1:B:151:ILE:HA	1:C:337:GLN:HE22	1.58	0.69
1:F:857:LYS:HE3	3:O:82:LEU:HA	1.75	0.69
1:B:1034:ILE:HG13	1:B:1060:PHE:CE1	2.27	0.69
5:7:40:GLY:O	5:7:42:LEU:HD22	1.92	0.69
1:B:50:PHE:CE2	1:C:321:ILE:HG21	2.28	0.68
1:F:449:VAL:HG23	1:F:1152:ILE:HD11	1.75	0.68
4:V:31:LEU:H	4:V:31:LEU:CD1	2.06	0.68
1:B:818:ASP:HA	1:B:821:PHE:HB3	1.74	0.68
1:F:424:LEU:HD11	1:F:573:ALA:HB1	1.74	0.68
1:D:10:LEU:HB3	1:H:328:PHE:HZ	1.58	0.68
4:S:83:VAL:CG1	4:S:86:PRO:HD2	2.22	0.68
4:V:31:LEU:CD2	4:V:33:ASN:CB	2.72	0.68
5:7:45:TYR:HE2	5:7:125:GLU:CG	2.00	0.68
1:B:151:ILE:HD11	1:C:332:ALA:HB1	1.74	0.68
1:H:1096:ILE:HB	1:H:1125:LEU:HD11	1.76	0.68
3:3:24:GLU:N	3:3:24:GLU:OE2	2.22	0.68
1:E:471:THR:O	1:E:475:PHE:HB2	1.93	0.68
3:Q:24:GLU:OE2	3:Q:24:GLU:N	2.18	0.68
1:E:742:VAL:HG11	1:E:765:THR:HG23	1.74	0.68
4:T:64:LEU:HD21	4:T:89:LEU:HD11	1.72	0.68
5:Y:82:PRO:HG2	5:Y:295:LYS:HE3	1.73	0.68
1:I:818:ASP:CG	3:R:46:HIS:HE1	1.96	0.68
1:H:1127:ILE:HG23	4:V:83:VAL:HG22	1.75	0.68
1:C:854:GLN:NE2	1:C:854:GLN:HA	2.06	0.68
1:G:758:ILE:HG22	1:G:864:GLU:HG3	1.75	0.68
1:A:779:LYS:O	1:A:783:PHE:HB3	1.94	0.68
1:E:1130:PHE:CE1	4:S:83:VAL:HG21	2.28	0.68
1:I:863:ASN:HB3	1:I:896:ASN:HD21	1.59	0.68
1:E:755:MET:HB2	3:N:68:ALA:HB1	1.74	0.68
4:T:65:LEU:CD1	4:T:68:GLU:OE1	2.38	0.68
1:A:100:VAL:HG11	1:F:381:VAL:HG22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:756:ASN:OD1	3:O:65:ASP:CB	2.41	0.68
3:J:27:LYS:HZ1	3:J:28:LYS:HE3	1.59	0.68
3:L:24:GLU:N	3:L:24:GLU:OE2	2.21	0.68
1:G:1038:ASP:CB	4:S:1:MET:H3	2.07	0.68
4:V:31:LEU:CD2	4:V:33:ASN:HB3	2.16	0.68
5:W:224:LEU:N	5:W:224:LEU:HD22	2.05	0.68
5:7:45:TYR:HB3	5:7:46:PRO:HD3	1.76	0.67
4:T:68:GLU:OE2	4:T:92:GLY:HA2	1.94	0.67
1:E:488:PRO:HA	1:E:491:ILE:HG12	1.76	0.67
4:S:83:VAL:CG1	4:S:86:PRO:CD	2.72	0.67
1:E:1130:PHE:HZ	4:S:86:PRO:CG	2.07	0.67
1:B:713:LEU:O	1:B:779:LYS:HD3	1.95	0.67
1:I:471:THR:O	1:I:475:PHE:HB2	1.95	0.67
3:J:27:LYS:HE3	3:J:28:LYS:HD3	1.73	0.67
3:K:24:GLU:OE2	3:K:24:GLU:N	2.19	0.67
4:T:64:LEU:HD12	4:T:64:LEU:N	2.09	0.67
1:E:810:TYR:CD1	3:N:37:LEU:HD12	2.29	0.67
1:I:755:MET:HB3	3:R:68:ALA:HA	1.75	0.67
5:6:207:ASP:OD1	5:7:235:ARG:NH2	2.25	0.67
1:D:1082:ASP:HB3	1:D:1146:GLN:HB3	1.77	0.67
1:E:437:VAL:HG21	1:F:1160:ILE:HG22	1.76	0.67
1:A:534:HIS:ND1	1:A:1216:LEU:HD13	2.05	0.67
1:C:859:LEU:C	1:C:859:LEU:HD23	2.15	0.67
1:D:862:ILE:HD11	3:M:75:ARG:HH11	0.85	0.67
1:G:750:SER:OG	3:P:75:ARG:NE	2.28	0.67
4:U:34:VAL:HG22	4:U:38:GLU:HB2	1.77	0.67
5:Z:119:LEU:HD22	5:Z:120:LYS:H	1.59	0.67
1:B:53:LEU:CD2	1:C:322:MET:HE1	2.25	0.67
1:E:409:THR:O	1:E:410:MET:CG	2.43	0.67
4:V:95:PHE:HE1	4:V:120:VAL:HG23	1.59	0.67
1:B:449:VAL:HG23	1:B:1152:ILE:HD11	1.75	0.67
1:B:856:PHE:HE2	3:K:81:ARG:HD2	1.60	0.67
5:X:245:GLN:C	5:X:246:LEU:HD22	2.15	0.67
1:E:307:MET:N	1:E:307:MET:SD	2.68	0.66
1:E:532:GLU:OE2	1:E:555:ARG:NH1	2.28	0.66
4:T:66:ALA:HB3	4:T:67:PRO:HD3	1.77	0.66
3:3:24:GLU:H	3:3:24:GLU:CD	1.98	0.66
5:X:224:LEU:HD22	5:X:224:LEU:N	2.09	0.66
1:A:1165:LEU:CD1	1:F:436:VAL:HG22	2.26	0.66
1:A:294:GLN:HE22	1:A:366:LEU:HD13	1.59	0.66
1:E:693:ASN:CG	1:F:945:ARG:NH2	2.49	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:826:ILE:HG23	1:B:828:SER:H	1.59	0.66
1:C:836:ARG:NH1	1:C:848:THR:O	2.29	0.66
1:F:743:ARG:HH21	1:F:762:VAL:HG11	1.59	0.66
1:G:61:ILE:HD11	1:H:96:GLN:HB2	1.77	0.66
3:K:24:GLU:CD	3:K:24:GLU:H	1.99	0.66
4:U:95:PHE:HE1	4:U:120:VAL:CG2	2.02	0.66
1:B:848:THR:HB	1:B:852:ALA:HB2	1.78	0.66
1:E:152:LEU:HG	1:G:740:ASN:HD22	109.09	0.66
1:I:810:TYR:HH	3:R:37:LEU:HB2	1.61	0.66
1:G:1044:GLU:CD	5:W:1:MET:CE	2.63	0.66
3:2:24:GLU:CD	3:2:24:GLU:H	1.98	0.66
4:U:34:VAL:HG12	4:U:39:ARG:NH1	2.10	0.66
5:Y:292:CYS:SG	5:Y:293:ILE:N	2.69	0.66
1:A:424:LEU:HD11	1:A:573:ALA:HB1	1.78	0.66
1:E:947:ASP:N	1:E:947:ASP:OD1	2.29	0.66
1:G:809:PHE:HZ	1:G:859:LEU:HD13	1.61	0.66
4:T:65:LEU:HD12	4:T:68:GLU:CD	2.15	0.66
5:X:246:LEU:N	5:X:246:LEU:HD22	2.11	0.66
1:C:743:ARG:HH21	1:C:762:VAL:HG11	1.61	0.66
1:E:810:TYR:CZ	3:N:37:LEU:CB	2.79	0.66
1:I:802:LYS:CE	3:R:67:THR:HG21	2.26	0.66
1:D:488:PRO:HA	1:D:491:ILE:HG12	1.78	0.65
4:V:91:VAL:HG13	4:V:95:PHE:HD2	1.61	0.65
1:H:818:ASP:OD1	3:Q:46:HIS:HE1	1.79	0.65
4:T:68:GLU:OE2	4:T:92:GLY:CA	2.44	0.65
5:Z:217:THR:HA	5:Z:225:LEU:HD21	1.78	0.65
1:B:1275:GLU:OE2	1:C:209:ARG:CD	2.44	0.65
1:C:836:ARG:HH12	1:C:852:ALA:HB2	1.61	0.65
1:H:817:PRO:O	1:H:819:ASP:N	2.25	0.65
1:I:449:VAL:CG2	1:I:1152:ILE:HD11	2.15	0.65
1:C:802:LYS:CD	3:L:67:THR:HG21	2.25	0.65
4:V:31:LEU:H	4:V:31:LEU:HD13	1.60	0.65
4:V:85:ASN:CG	4:V:86:PRO:HD3	2.16	0.65
1:E:1135:LYS:HD2	1:E:1135:LYS:N	2.11	0.65
1:C:810:TYR:HB2	3:L:74:ILE:HD11	1.77	0.65
1:C:54:LEU:HB2	1:D:91:VAL:HG12	1.78	0.65
3:N:24:GLU:N	3:N:24:GLU:OE2	2.30	0.65
1:G:1044:GLU:HB2	5:W:1:MET:HG3	1.79	0.65
1:D:843:TYR:O	1:D:848:THR:HG23	1.97	0.65
1:I:1302:HIS:HB2	1:I:1333:GLU:HB2	1.79	0.65
4:T:65:LEU:N	4:T:65:LEU:HD22	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:1:MET:HE3	4:U:1:MET:O	3.95	0.65
1:A:810:TYR:CE2	3:J:37:LEU:HD12	2.32	0.65
5:6:82:PRO:HG2	5:6:295:LYS:HE3	1.78	0.65
1:F:756:ASN:HD21	3:O:64:VAL:HB	1.61	0.65
1:G:162:ARG:NH2	1:H:96:GLN:OE1	2.30	0.64
4:V:240:PHE:CD2	4:V:244:LEU:HD13	2.32	0.64
5:Y:87:GLN:HA	5:Y:292:CYS:O	1.97	0.64
1:D:1109:ARG:NH1	1:D:1118:ASN:OD1	2.29	0.64
1:D:813:PRO:HG2	1:D:826:ILE:HD12	1.79	0.64
1:E:294:GLN:HE22	1:E:366:LEU:HD13	1.61	0.64
1:G:53:LEU:CD1	1:H:90:LYS:HG3	2.26	0.64
4:U:35:VAL:HG12	4:U:37:LYS:H	1.61	0.64
4:U:91:VAL:HG13	4:U:95:PHE:HD2	1.61	0.64
1:C:488:PRO:HA	1:C:491:ILE:HG12	1.80	0.64
3:M:24:GLU:OE2	3:M:24:GLU:N	2.20	0.64
3:O:24:GLU:H	3:O:24:GLU:CD	2.00	0.64
1:G:1123:GLU:HB3	4:S:231:GLN:OE1	1.97	0.64
1:G:830:VAL:CA	1:G:834:LEU:HD13	2.22	0.64
1:H:817:PRO:HD3	3:Q:43:MET:SD	2.36	0.64
1:B:877:PRO:HB2	1:B:1104:ILE:HD11	1.78	0.64
1:B:712:ARG:HB3	1:B:963:TRP:HZ2	1.62	0.64
1:G:831:LEU:O	1:G:835:ILE:HG12	1.97	0.64
1:I:255:LEU:CD2	1:I:1063:MET:SD	2.86	0.64
4:V:240:PHE:HD2	4:V:244:LEU:HD11	1.54	0.64
1:B:488:PRO:HA	1:B:491:ILE:HG12	1.80	0.64
1:B:743:ARG:HH21	1:B:762:VAL:HG11	1.61	0.64
1:C:1149:CYS:SG	1:C:1239:ASN:ND2	2.70	0.64
1:F:877:PRO:HB2	1:F:1104:ILE:HD11	1.79	0.64
5:Y:217:THR:HA	5:Y:225:LEU:HD21	1.80	0.64
1:G:743:ARG:HH22	1:G:757:LEU:HD13	1.63	0.64
1:G:53:LEU:CD1	1:H:92:LEU:HD11	2.23	0.64
4:T:69:LEU:HB2	4:T:146:VAL:HG11	1.79	0.64
1:A:471:THR:O	1:A:475:PHE:HB2	1.98	0.64
1:I:818:ASP:OD1	3:R:81:ARG:NH2	2.27	0.64
4:T:32:ASN:HA	4:T:39:ARG:HH12	1.63	0.64
1:B:810:TYR:CZ	3:K:37:LEU:CD1	2.74	0.63
1:E:600:LEU:HA	1:E:901:ILE:HD11	1.80	0.63
3:J:27:LYS:C	3:J:27:LYS:HD2	2.19	0.63
4:T:91:VAL:HG13	4:T:95:PHE:HD2	1.63	0.63
5:Z:292:CYS:SG	5:Z:293:ILE:N	2.71	0.63
4:5:181:LEU:HD12	4:5:183:PRO:HD3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1149:CYS:HB2	1:D:1238:PRO:HD2	1.79	0.63
1:G:449:VAL:HG23	1:G:1152:ILE:HD11	1.80	0.63
4:U:85:ASN:CB	4:U:86:PRO:CD	2.42	0.63
3:2:24:GLU:OE2	3:2:24:GLU:N	2.22	0.63
1:H:54:LEU:CB	1:I:91:VAL:HG12	2.26	0.63
5:6:170:GLN:HE21	5:6:173:ASP:HA	1.63	0.63
1:H:826:ILE:HG23	1:H:828:SER:H	1.63	0.63
1:C:424:LEU:HD11	1:C:573:ALA:HB1	1.79	0.63
1:E:810:TYR:HH	3:N:37:LEU:HA	1.64	0.63
5:X:224:LEU:CD2	5:X:224:LEU:H	2.12	0.63
3:1:56:TYR:HA	3:1:59:GLN:HE21	1.64	0.63
1:C:742:VAL:HG11	1:C:765:THR:HG23	1.80	0.63
1:E:705:ALA:HB2	1:E:999:ILE:HD11	1.79	0.63
1:E:97:LEU:CD1	1:G:23:ILE:HD11	2.24	0.63
5:7:54:TYR:HB2	5:7:189:TYR:HB3	1.81	0.63
1:D:743:ARG:HH21	1:D:762:VAL:HG11	1.62	0.63
1:H:712:ARG:HH21	1:H:876:ASP:HA	1.64	0.63
1:I:964:GLN:HE21	1:I:989:HIS:HE1	1.46	0.63
5:W:223:MET:HA	5:W:226:ILE:HD12	1.80	0.63
4:5:237:ARG:HH12	5:6:196:ILE:HD13	1.62	0.63
1:A:705:ALA:HB2	1:A:999:ILE:HD11	1.79	0.63
1:D:492:LEU:HD12	1:D:868:ILE:HG12	1.80	0.63
1:E:174:GLY:HA3	1:F:101:ALA:HB3	1.80	0.63
3:R:56:TYR:HA	3:R:59:GLN:HE21	1.64	0.63
3:3:56:TYR:HA	3:3:59:GLN:HE21	1.64	0.63
1:B:945:ARG:HG2	1:B:947:ASP:H	1.64	0.63
1:C:1172:ARG:HB3	1:C:1211:SER:OG	1.98	0.63
1:F:202:HIS:CD2	1:F:204:LYS:H	2.17	0.63
1:A:491:ILE:HD11	1:A:868:ILE:HG21	1.81	0.62
1:E:524:PRO:HG3	1:E:1204:ALA:HB2	1.81	0.62
1:F:810:TYR:CE2	3:O:37:LEU:CD1	2.54	0.62
1:G:877:PRO:HB2	1:G:1104:ILE:HD11	1.81	0.62
3:M:24:GLU:CD	3:M:24:GLU:H	2.00	0.62
3:Q:56:TYR:HA	3:Q:59:GLN:HE21	1.64	0.62
3:1:24:GLU:CD	3:1:24:GLU:H	2.03	0.62
1:A:1302:HIS:HB2	1:A:1333:GLU:HB2	1.81	0.62
1:C:52:ALA:HB2	1:D:321:ILE:HB	1.81	0.62
1:G:542:ILE:O	1:G:549:GLU:HB3	1.99	0.62
1:H:747:TYR:O	3:Q:75:ARG:NH2	2.32	0.62
3:M:56:TYR:HA	3:M:59:GLN:HE21	1.64	0.62
1:D:1038:ASP:CG	4:V:2:ASN:O	2.37	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:178:LEU:HD23	5:X:178:LEU:N	2.13	0.62
1:B:52:ALA:CB	1:C:321:ILE:CG2	2.77	0.62
1:C:815:ILE:HD13	3:L:37:LEU:CD1	2.19	0.62
1:E:1302:HIS:HB2	1:E:1333:GLU:HB2	1.81	0.62
3:K:56:TYR:HA	3:K:59:GLN:HE21	1.64	0.62
1:A:877:PRO:HB2	1:A:1104:ILE:HD11	1.80	0.62
1:H:488:PRO:HA	1:H:491:ILE:HG12	1.80	0.62
3:R:24:GLU:CD	3:R:24:GLU:H	2.01	0.62
1:G:1038:ASP:OD2	4:S:1:MET:CG	2.48	0.62
1:C:1302:HIS:HB2	1:C:1333:GLU:HB2	1.80	0.62
1:F:542:ILE:O	1:F:549:GLU:HB3	2.00	0.62
3:O:56:TYR:HA	3:O:59:GLN:HE21	1.64	0.62
3:R:64:VAL:HG23	3:R:65:ASP:H	1.65	0.62
5:W:82:PRO:CB	5:W:295:LYS:CG	2.57	0.62
1:A:1129:THR:OG1	1:A:1230:CYS:SG	2.58	0.62
1:D:1223:THR:HA	1:D:1226:ARG:HB3	1.81	0.62
1:E:923:PRO:CG	1:E:950:PHE:CD1	2.82	0.62
1:F:201:VAL:HB	1:F:207:LEU:HD13	1.80	0.62
1:G:742:VAL:HG11	1:G:765:THR:HG23	1.82	0.62
1:G:809:PHE:HE2	3:P:74:ILE:HG23	1.64	0.62
3:K:64:VAL:HG23	3:K:65:ASP:H	1.65	0.62
5:X:87:GLN:CB	5:X:293:ILE:HG22	2.29	0.62
1:D:174:GLY:HA3	1:E:101:ALA:HB3	1.81	0.62
1:E:1130:PHE:CZ	4:S:86:PRO:HG3	2.34	0.62
3:M:64:VAL:HG23	3:M:65:ASP:H	1.65	0.62
3:N:56:TYR:HA	3:N:59:GLN:HE21	1.64	0.62
3:N:64:VAL:HG23	3:N:65:ASP:H	1.65	0.62
3:2:56:TYR:HA	3:2:59:GLN:HE21	1.64	0.62
1:D:10:LEU:HB3	1:H:328:PHE:CZ	2.35	0.62
3:L:64:VAL:HG23	3:L:65:ASP:H	1.65	0.62
1:I:335:GLU:OE2	4:V:31:LEU:HD21	2.00	0.62
5:X:279:VAL:H	5:X:292:CYS:HG	1.40	0.62
3:4:56:TYR:HA	3:4:59:GLN:HE21	1.64	0.62
1:C:432:ASN:HD22	1:C:436:VAL:HB	1.64	0.62
1:E:449:VAL:HG23	1:E:1152:ILE:HD11	1.80	0.62
1:G:20:PHE:HD1	1:G:20:PHE:O	1.83	0.62
1:G:393:PHE:HB3	1:G:1301:LEU:HD22	1.82	0.62
1:G:64:ILE:HG12	1:G:375:VAL:HG12	1.81	0.62
1:H:424:LEU:HD11	1:H:573:ALA:HB1	1.81	0.62
3:P:56:TYR:HA	3:P:59:GLN:HE21	1.64	0.62
5:X:295:LYS:HD3	5:X:295:LYS:C	2.20	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:7:210:ARG:HH22	5:7:229:GLN:HE22	1.47	0.62
1:A:1223:THR:HA	1:A:1226:ARG:HB3	1.80	0.62
1:C:1176:MET:SD	1:C:1252:ASN:ND2	2.73	0.62
1:C:225:THR:O	1:C:232:ARG:NH1	2.31	0.62
1:D:862:ILE:CD1	3:M:75:ARG:HH12	2.08	0.62
3:J:56:TYR:HA	3:J:59:GLN:HE21	1.64	0.62
3:O:64:VAL:HG23	3:O:65:ASP:H	1.65	0.62
1:B:715:CYS:CB	1:B:716:PRO:HD2	2.30	0.61
3:Q:64:VAL:HG23	3:Q:65:ASP:H	1.65	0.61
3:2:64:VAL:HG23	3:2:65:ASP:H	1.65	0.61
5:6:97:PRO:O	5:6:287:ASN:ND2	2.32	0.61
1:E:783:PHE:O	1:E:787:PRO:HG3	2.00	0.61
1:G:1038:ASP:OD2	4:S:1:MET:CB	2.48	0.61
4:U:1:MET:H2	4:U:1:MET:HE2	5.98	0.61
1:B:393:PHE:HB3	1:B:1301:LEU:HD22	1.82	0.61
1:D:792:ASN:HD21	1:D:919:PHE:HD1	1.47	0.61
1:E:693:ASN:ND2	1:F:945:ARG:HH22	1.98	0.61
1:H:818:ASP:OD1	3:Q:46:HIS:CE1	2.53	0.61
5:Z:119:LEU:HD13	5:Z:120:LYS:N	2.15	0.61
1:E:635:SER:O	1:E:639:ASN:HB2	1.99	0.61
1:E:808:LEU:HD21	1:E:831:LEU:HD12	1.81	0.61
1:F:202:HIS:NE2	1:F:204:LYS:CG	2.64	0.61
1:I:856:PHE:HE2	3:R:81:ARG:HD2	1.65	0.61
3:P:24:GLU:H	3:P:24:GLU:CD	2.02	0.61
1:E:1130:PHE:HE1	4:S:83:VAL:HG11	1.65	0.61
1:A:748:GLU:O	3:J:76:MET:HE1	2.01	0.61
5:X:295:LYS:HD2	5:X:296:ASN:O	2.00	0.61
1:B:708:LEU:HA	1:B:713:LEU:HD23	1.80	0.61
1:C:492:LEU:HD12	1:C:868:ILE:HG12	1.83	0.61
1:B:583:LYS:NZ	1:C:974:PHE:O	2.33	0.61
1:D:273:LEU:O	1:D:369:PHE:HA	2.01	0.61
1:I:869:LEU:HB2	1:I:893:ILE:HG23	1.81	0.61
3:J:27:LYS:HE3	3:J:28:LYS:NZ	2.16	0.61
3:J:64:VAL:HG23	3:J:65:ASP:H	1.65	0.61
1:A:802:LYS:CD	3:J:67:THR:CG2	2.72	0.61
3:L:56:TYR:HA	3:L:59:GLN:HE21	1.64	0.61
1:H:810:TYR:CE1	3:Q:37:LEU:CD1	2.73	0.61
4:5:245:ILE:HA	5:6:204:MET:SD	2.41	0.61
1:A:32:PHE:HB2	1:A:35:LEU:HD23	1.81	0.61
1:E:1130:PHE:CD1	4:S:83:VAL:HG21	2.36	0.61
1:E:923:PRO:HB3	1:E:950:PHE:CE1	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:87:THR:O	1:G:122:LYS:NZ	2.34	0.61
1:I:488:PRO:HA	1:I:491:ILE:HG12	1.82	0.61
3:P:64:VAL:HG23	3:P:65:ASP:H	1.65	0.61
3:4:64:VAL:HG23	3:4:65:ASP:H	1.65	0.61
5:7:45:TYR:CD2	5:7:125:GLU:CG	2.80	0.61
1:A:600:LEU:HD23	1:A:901:ILE:CD1	2.30	0.61
1:E:1130:PHE:CZ	4:S:86:PRO:CG	2.84	0.61
1:E:663:GLU:OE2	1:F:640:MET:HG3	2.00	0.61
1:G:488:PRO:HA	1:G:491:ILE:HG12	1.82	0.61
1:I:635:SER:O	1:I:639:ASN:HB2	2.01	0.61
4:S:91:VAL:HG13	4:S:95:PHE:HD2	1.66	0.61
1:A:869:LEU:HB2	1:A:893:ILE:HG23	1.83	0.61
1:F:488:PRO:HA	1:F:491:ILE:HG12	1.82	0.61
1:F:743:ARG:HH22	1:F:757:LEU:HD13	1.66	0.61
3:L:24:GLU:CD	3:L:24:GLU:H	2.03	0.61
5:Z:87:GLN:HA	5:Z:292:CYS:O	2.01	0.61
3:3:64:VAL:HG23	3:3:65:ASP:H	1.65	0.61
1:E:1133:ILE:HG22	1:E:1232:ASN:CG	2.20	0.61
3:1:64:VAL:HG23	3:1:65:ASP:H	1.65	0.60
1:A:802:LYS:CG	3:J:67:THR:HG21	2.31	0.60
1:B:50:PHE:CD2	1:C:321:ILE:CG2	2.84	0.60
1:E:1176:MET:SD	1:E:1252:ASN:ND2	2.73	0.60
4:5:267:ASP:HB3	4:5:286:GLU:HB3	1.83	0.60
5:7:38:GLY:C	5:7:42:LEU:HD11	2.20	0.60
1:A:89:GLY:HA2	1:F:52:ALA:O	2.01	0.60
1:C:869:LEU:HB2	1:C:893:ILE:HG23	1.83	0.60
1:G:209:ARG:HH22	1:G:1180:ASP:HB2	1.66	0.60
1:I:424:LEU:HD11	1:I:573:ALA:HB1	1.83	0.60
1:G:809:PHE:O	1:G:810:TYR:CB	2.50	0.60
1:A:810:TYR:CE1	3:J:37:LEU:HD13	2.34	0.60
4:S:95:PHE:HE1	4:S:120:VAL:HG23	1.66	0.60
4:U:31:LEU:HD23	4:U:31:LEU:O	2.01	0.60
5:W:170:GLN:HE21	5:W:173:ASP:HA	1.65	0.60
5:7:44:LEU:HD12	5:7:64:MET:SD	2.41	0.60
1:D:990:SER:OG	1:D:1000:GLN:NE2	2.35	0.60
1:E:508:ASN:ND2	1:E:959:GLU:OE1	2.34	0.60
3:M:23:LYS:N	3:M:25:GLU:OE1	2.35	0.60
1:C:859:LEU:O	1:C:861:TYR:N	2.35	0.60
1:D:626:LEU:HG	1:D:858:SER:HB3	1.82	0.60
1:F:393:PHE:HB3	1:F:1301:LEU:HD22	1.83	0.60
4:T:83:VAL:HG12	4:T:86:PRO:HD2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:507:LYS:NZ	1:F:693:ASN:HB2	2.16	0.60
1:A:826:ILE:HG23	1:A:828:SER:H	1.67	0.60
1:E:59:ASN:HB2	1:F:95:ILE:HA	1.84	0.60
1:G:19:ILE:HG22	1:G:19:ILE:O	2.01	0.60
1:G:286:ILE:HG13	1:G:287:LEU:HG	1.83	0.60
1:G:809:PHE:CZ	1:G:859:LEU:CD1	2.84	0.60
1:G:830:VAL:O	1:G:834:LEU:CB	2.36	0.60
4:V:31:LEU:N	4:V:31:LEU:HD13	2.15	0.60
1:F:1046:LYS:NZ	5:X:87:GLN:OE1	2.18	0.60
5:7:44:LEU:O	5:7:44:LEU:HD23	2.01	0.60
1:B:50:PHE:HE2	1:C:321:ILE:HG21	1.65	0.60
1:E:491:ILE:HD11	1:E:868:ILE:HG21	1.83	0.60
1:F:622:ALA:HB2	1:F:861:TYR:HD2	1.67	0.60
1:I:815:ILE:CG2	3:R:39:LEU:HD21	2.30	0.60
5:X:170:GLN:HE21	5:X:173:ASP:HA	1.66	0.60
5:6:215:ARG:HG2	5:7:153:HIS:HA	1.82	0.60
1:G:1302:HIS:HB2	1:G:1333:GLU:HB2	1.83	0.60
1:H:1109:ARG:HH12	1:H:1119:PRO:HG3	1.65	0.60
1:H:1176:MET:SD	1:H:1252:ASN:ND2	2.75	0.60
1:H:755:MET:HB3	3:Q:68:ALA:CB	2.32	0.60
1:A:276:PRO:HG3	1:A:1022:GLU:HB2	1.84	0.60
1:A:507:LYS:HZ3	1:F:693:ASN:HB2	1.66	0.60
1:E:424:LEU:HD11	1:E:573:ALA:HB1	1.82	0.60
1:F:1109:ARG:HH22	5:X:223:MET:CE	2.05	0.60
1:F:1313:ARG:HH11	1:F:1323:GLU:HB2	1.67	0.60
1:F:810:TYR:CZ	3:O:37:LEU:HB2	2.37	0.60
5:W:292:CYS:SG	5:W:293:ILE:N	2.75	0.60
1:B:713:LEU:HD11	1:B:783:PHE:CZ	2.36	0.59
1:H:1223:THR:HG22	1:H:1226:ARG:HD2	1.84	0.59
4:U:267:ASP:HB3	4:U:286:GLU:HB3	1.84	0.59
1:A:1176:MET:SD	1:A:1252:ASN:ND2	2.75	0.59
1:E:433:LYS:NZ	1:F:214:ASN:OD1	2.34	0.59
1:A:406:GLY:O	1:F:417:ASN:CB	2.50	0.59
1:I:680:ILE:HG22	1:I:777:LEU:HD22	1.82	0.59
4:T:66:ALA:HB3	4:T:67:PRO:CD	2.32	0.59
4:V:267:ASP:HB3	4:V:286:GLU:HB3	1.84	0.59
5:Y:183:ASN:ND2	5:Y:187:SER:OG	2.35	0.59
5:7:39:SER:C	5:7:42:LEU:HD21	2.23	0.59
1:A:48:ILE:HD13	1:B:316:ILE:HG12	1.84	0.59
1:D:836:ARG:HH12	1:D:852:ALA:HB2	1.68	0.59
1:G:583:LYS:NZ	1:H:974:PHE:O	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:492:LEU:HD12	1:I:868:ILE:HG12	1.83	0.59
3:J:27:LYS:HE3	3:J:28:LYS:HZ2	1.66	0.59
5:X:87:GLN:HG3	5:X:293:ILE:HG23	1.85	0.59
1:A:1223:THR:HG22	1:A:1226:ARG:HD2	1.85	0.59
1:A:346:PHE:CZ	1:F:54:LEU:HD13	2.38	0.59
1:E:1089:ASN:HD21	1:E:1114:ILE:HD11	1.68	0.59
1:F:742:VAL:HG11	1:F:765:THR:HG23	1.84	0.59
1:F:818:ASP:HA	1:F:821:PHE:HB3	1.84	0.59
1:F:833:SER:OG	1:F:847:ASN:ND2	2.36	0.59
1:G:324:ASP:O	1:G:328:PHE:HB2	2.01	0.59
1:H:225:THR:O	1:H:232:ARG:NH1	2.34	0.59
1:H:869:LEU:HB2	1:H:893:ILE:HG23	1.83	0.59
1:A:151:ILE:HD13	1:B:337:GLN:NE2	2.18	0.59
1:C:266:ASN:HB3	1:C:267:ILE:HG13	1.83	0.59
1:H:433:LYS:NZ	1:I:214:ASN:OD1	2.34	0.59
3:J:27:LYS:CE	3:J:28:LYS:CD	2.77	0.59
3:J:27:LYS:CE	3:J:28:LYS:CE	2.80	0.59
1:A:810:TYR:CZ	3:J:37:LEU:HB2	2.36	0.59
1:A:600:LEU:HD23	1:A:901:ILE:HD11	1.83	0.59
1:B:415:LYS:NZ	1:C:1326:TYR:HH	1.96	0.59
1:B:742:VAL:HG11	1:B:765:THR:HG23	1.83	0.59
1:D:869:LEU:HB2	1:D:893:ILE:HG23	1.83	0.59
1:G:51:GLU:HG2	1:H:88:LEU:HB2	1.84	0.59
1:I:750:SER:OG	3:R:75:ARG:NE	2.35	0.59
1:D:844:THR:CA	1:D:848:THR:HG23	2.31	0.59
1:E:693:ASN:ND2	1:F:945:ARG:NH2	2.51	0.59
1:G:491:ILE:HD11	1:G:868:ILE:HG21	1.84	0.59
1:E:810:TYR:CZ	3:N:37:LEU:CG	2.86	0.59
4:5:91:VAL:HG13	4:5:95:PHE:HD2	1.67	0.59
1:I:802:LYS:CE	3:R:67:THR:CG2	2.80	0.59
4:S:53:ARG:NH1	4:S:164:ASP:O	2.30	0.59
5:Z:32:ALA:HB1	5:Z:34:HIS:HD2	1.68	0.59
1:C:78:ILE:O	1:C:1035:ILE:HA	2.03	0.59
1:B:1139:SER:H	1:C:1196:GLN:HE22	1.51	0.59
1:E:662:ASP:HA	1:E:665:ILE:HG22	1.83	0.59
1:G:1127:ILE:HG12	4:S:185:TRP:HB2	1.84	0.59
4:T:200:VAL:O	4:T:211:GLY:N	2.36	0.59
4:T:66:ALA:H	4:T:67:PRO:HD2	1.68	0.59
4:T:64:LEU:HD21	4:T:89:LEU:HD21	1.84	0.59
1:F:990:SER:OG	1:F:1000:GLN:NE2	2.36	0.58
1:I:432:ASN:HD22	1:I:436:VAL:HB	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:W:295:LYS:C	5:W:295:LYS:HZ3	2.07	0.58
5:7:52:LYS:HD3	5:7:189:TYR:HA	1.84	0.58
1:A:492:LEU:HD12	1:A:868:ILE:HG12	1.84	0.58
1:C:1092:SER:O	1:C:1232:ASN:ND2	2.36	0.58
1:C:54:LEU:HB3	1:D:345:ILE:HD13	1.84	0.58
1:A:345:ILE:HD13	1:F:54:LEU:HB3	1.85	0.58
1:G:1313:ARG:HH11	1:G:1323:GLU:HB2	1.67	0.58
1:I:1126:ASN:O	1:I:1130:PHE:HB2	2.03	0.58
4:T:64:LEU:HD12	4:T:64:LEU:H	1.68	0.58
5:X:179:PRO:O	5:X:180:ASP:CB	2.51	0.58
1:B:491:ILE:HD11	1:B:868:ILE:HG21	1.85	0.58
4:V:181:LEU:HD12	4:V:183:PRO:HD3	1.83	0.58
1:G:1044:GLU:CD	5:W:1:MET:HE2	2.21	0.58
5:Y:1:MET:SD	5:Y:3:THR:O	2.61	0.58
4:5:250:THR:HA	5:6:256:LYS:HG3	1.85	0.58
1:B:990:SER:OG	1:B:1000:GLN:NE2	2.37	0.58
1:E:1269:CYS:HB3	1:E:1281:SER:HA	1.86	0.58
1:F:18:ASN:O	1:F:20:PHE:N	2.30	0.58
1:A:92:LEU:O	1:F:56:ILE:HA	2.03	0.58
1:B:712:ARG:CD	1:B:712:ARG:H	2.16	0.58
1:C:831:LEU:HD11	1:C:907:LEU:HD21	1.86	0.58
1:F:826:ILE:HB	1:F:848:THR:HG21	1.85	0.58
1:G:1046:LYS:HE3	5:W:1:MET:HE2	1.84	0.58
1:I:1176:MET:SD	1:I:1252:ASN:ND2	2.75	0.58
1:H:750:SER:O	3:Q:72:ASP:OD2	2.22	0.58
1:G:164:LEU:HD22	4:S:7:ALA:HB1	1.85	0.58
1:D:508:ASN:ND2	1:D:959:GLU:OE1	2.36	0.58
1:E:82:ASP:OD1	1:G:146:THR:HG21	2.04	0.58
3:J:27:LYS:NZ	3:J:28:LYS:CE	2.66	0.58
4:5:263:CYS:SG	4:5:264:ALA:N	2.77	0.58
1:B:332:ALA:O	1:B:337:GLN:NE2	2.33	0.58
1:F:491:ILE:HD11	1:F:868:ILE:HG21	1.86	0.58
5:Y:241:GLN:O	5:Y:243:CYS:N	2.36	0.58
1:B:1302:HIS:HB2	1:B:1333:GLU:HB2	1.84	0.58
1:B:225:THR:O	1:B:232:ARG:NH1	2.36	0.58
1:I:209:ARG:HH22	1:I:1180:ASP:HB2	1.67	0.58
5:Z:84:THR:HA	5:Z:295:LYS:HB3	1.86	0.58
1:A:693:ASN:HB2	1:B:507:LYS:HZ1	1.68	0.58
1:C:449:VAL:HG23	1:C:1152:ILE:CD1	2.23	0.58
1:F:1176:MET:SD	1:F:1252:ASN:ND2	2.77	0.58
1:H:1216:LEU:C	1:H:1216:LEU:HD12	2.24	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:174:GLY:HA3	1:I:101:ALA:HB3	1.85	0.58
1:H:818:ASP:N	1:H:818:ASP:OD1	2.35	0.58
1:D:815:ILE:CG2	3:M:39:LEU:HD21	2.34	0.58
4:S:173:LEU:H	4:S:288:ILE:HD13	1.69	0.58
1:B:1034:ILE:CG1	1:B:1060:PHE:CE1	2.87	0.58
1:F:1302:HIS:HB2	1:F:1333:GLU:HB2	1.86	0.58
1:H:209:ARG:NH1	1:H:1178:GLY:O	2.37	0.58
1:H:492:LEU:HD12	1:H:868:ILE:HG12	1.85	0.58
4:S:267:ASP:HB3	4:S:286:GLU:HB3	1.85	0.58
4:T:263:CYS:SG	4:T:264:ALA:N	2.77	0.58
5:Y:23:LEU:CD1	5:Y:118:LEU:HD22	2.34	0.58
1:C:145:ASN:OD1	1:C:150:GLN:NE2	2.37	0.57
1:C:273:LEU:O	1:C:369:PHE:HA	2.04	0.57
1:C:485:ARG:NH2	1:C:872:GLU:OE2	2.36	0.57
1:E:437:VAL:HG21	1:F:1160:ILE:CG2	2.33	0.57
1:E:806:LEU:HD11	3:N:67:THR:CG2	2.33	0.57
1:F:755:MET:HB2	3:O:68:ALA:HB1	1.85	0.57
5:6:208:ILE:HG23	5:7:153:HIS:CE1	2.39	0.57
1:A:1149:CYS:SG	1:A:1150:GLU:N	2.75	0.57
5:Y:1:MET:SD	5:Y:3:THR:N	2.75	0.57
5:Z:115:GLU:O	5:Z:117:LYS:N	2.36	0.57
4:5:134:GLU:O	4:5:295:LYS:NZ	2.36	0.57
1:A:453:ILE:HD11	1:A:1229:LEU:HD13	1.87	0.57
1:G:687:ILE:HG12	1:G:986:ALA:HB1	1.86	0.57
4:V:85:ASN:CB	4:V:86:PRO:CD	2.39	0.57
5:Y:242:ARG:NH1	5:Y:245:GLN:OE1	2.35	0.57
1:G:225:THR:O	1:G:232:ARG:NH1	2.36	0.57
1:G:809:PHE:CE1	1:G:859:LEU:HD22	2.39	0.57
3:R:23:LYS:N	3:R:25:GLU:OE1	2.37	0.57
4:S:83:VAL:HG12	4:S:86:PRO:HD3	1.86	0.57
1:B:1116:LYS:HD3	1:B:1117:PRO:HD2	1.87	0.57
1:C:258:THR:O	1:C:262:THR:OG1	2.22	0.57
1:E:662:ASP:OD1	1:F:640:MET:HB3	2.05	0.57
1:G:19:ILE:H	1:G:19:ILE:HD13	1.69	0.57
1:G:809:PHE:CZ	1:G:859:LEU:HD13	2.40	0.57
1:G:871:VAL:HB	1:G:891:GLN:HB2	1.86	0.57
1:I:225:THR:O	1:I:232:ARG:NH1	2.38	0.57
1:I:710:ASP:O	1:I:779:LYS:NZ	2.37	0.57
1:E:1130:PHE:HZ	4:S:86:PRO:HG2	1.69	0.57
4:U:134:GLU:O	4:U:295:LYS:NZ	2.37	0.57
5:X:87:GLN:CB	5:X:293:ILE:CG2	2.82	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1143:HIS:NE2	1:E:1200:ASP:OD1	2.37	0.57
1:D:209:ARG:NH1	1:D:1178:GLY:O	2.36	0.57
1:E:5:GLN:HA	1:E:8:GLU:HB2	1.87	0.57
1:E:755:MET:CB	3:N:68:ALA:HB1	2.35	0.57
1:I:1223:THR:HA	1:I:1226:ARG:HB3	1.86	0.57
1:H:802:LYS:HZ3	3:Q:67:THR:HB	1.69	0.57
4:T:223:ASP:OD1	4:T:296:LYS:NZ	2.37	0.57
4:V:30:THR:HG22	4:V:30:THR:O	2.03	0.57
5:6:87:GLN:HA	5:6:292:CYS:O	2.05	0.57
5:6:6:CYS:HB3	5:6:77:LEU:HB3	1.87	0.57
1:B:179:PHE:CD1	1:B:1034:ILE:HD11	2.40	0.57
1:E:257:ASP:OD2	1:E:260:ASN:ND2	2.38	0.57
1:G:813:PRO:HG2	1:G:826:ILE:HD12	1.87	0.57
1:G:830:VAL:CG1	1:G:834:LEU:CD2	2.70	0.57
1:H:1223:THR:HA	1:H:1226:ARG:HB3	1.86	0.57
5:Z:104:LEU:HB2	5:Z:278:PHE:HB2	1.87	0.57
5:7:113:HIS:HD2	5:7:186:GLN:HB3	1.69	0.57
1:C:52:ALA:CB	1:D:321:ILE:HB	2.35	0.57
1:F:818:ASP:N	1:F:818:ASP:OD1	2.35	0.57
1:G:990:SER:OG	1:G:1000:GLN:NE2	2.37	0.57
1:G:693:ASN:HB2	1:H:507:LYS:NZ	2.20	0.57
1:H:532:GLU:OE2	1:H:555:ARG:NH1	2.37	0.57
4:V:134:GLU:O	4:V:295:LYS:NZ	2.38	0.57
1:A:270:ASP:OD2	1:A:365:LYS:NZ	2.37	0.57
1:B:433:LYS:NZ	1:C:214:ASN:OD1	2.36	0.57
1:E:1223:THR:H	1:E:1244:THR:HG22	1.69	0.57
1:E:651:GLU:O	1:E:655:LEU:HB2	2.04	0.57
4:V:263:CYS:SG	4:V:264:ALA:N	2.78	0.57
1:B:542:ILE:O	1:B:549:GLU:HB3	2.05	0.57
1:C:78:ILE:HA	1:C:303:GLY:O	2.04	0.57
1:C:990:SER:OG	1:C:1000:GLN:NE2	2.37	0.57
1:E:225:THR:O	1:E:232:ARG:NH1	2.38	0.57
1:E:869:LEU:HB2	1:E:893:ILE:HG23	1.87	0.57
1:G:1143:HIS:CE1	1:H:217:GLN:OE1	2.57	0.57
1:G:833:SER:OG	1:G:847:ASN:ND2	2.37	0.57
5:6:208:ILE:HG23	5:7:153:HIS:HE1	1.69	0.56
5:7:42:LEU:H	5:7:42:LEU:HD23	1.69	0.56
1:B:703:ASN:OD1	1:B:710:ASP:HB2	2.04	0.56
1:B:871:VAL:HB	1:B:891:GLN:HB2	1.87	0.56
1:C:945:ARG:HE	1:C:947:ASP:HB2	1.68	0.56
1:D:6:ALA:O	1:D:10:LEU:HB2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:810:TYR:CZ	3:M:37:LEU:CB	2.81	0.56
1:E:952:LEU:O	1:E:953:PRO:C	2.40	0.56
1:F:1094:PHE:HB3	1:F:1097:HIS:HD2	1.70	0.56
1:G:1038:ASP:CB	4:S:1:MET:CB	2.70	0.56
4:T:64:LEU:H	4:T:64:LEU:CD1	2.18	0.56
5:X:70:GLN:O	5:X:78:VAL:HB	2.04	0.56
1:A:1035:ILE:HG13	1:A:1059:SER:HB3	1.87	0.56
1:C:962:ASN:O	1:C:965:ARG:NH1	2.38	0.56
1:G:485:ARG:NH2	1:G:872:GLU:OE2	2.38	0.56
3:J:27:LYS:HZ1	3:J:28:LYS:CD	2.16	0.56
5:Z:23:LEU:HG	5:Z:26:ILE:HD12	1.87	0.56
1:A:693:ASN:HB2	1:B:507:LYS:NZ	2.20	0.56
1:B:209:ARG:NH1	1:B:1178:GLY:O	2.38	0.56
1:D:700:PRO:HB3	1:E:942:HIS:HB3	1.86	0.56
1:E:730:ILE:HG12	1:E:871:VAL:HG22	1.86	0.56
1:H:165:LYS:HG3	4:V:38:GLU:OE2	2.04	0.56
1:G:3:ASN:ND2	1:H:317:ALA:O	2.38	0.56
1:H:491:ILE:HD11	1:H:868:ILE:HG21	1.87	0.56
1:D:856:PHE:CD2	3:M:78:ALA:HB2	2.41	0.56
4:U:263:CYS:SG	4:U:264:ALA:N	2.78	0.56
5:Y:150:ILE:HG21	5:Y:162:ILE:HG21	1.86	0.56
1:A:622:ALA:HB2	1:A:861:TYR:HD2	1.69	0.56
1:C:274:LEU:HA	1:C:370:ASP:O	2.05	0.56
1:D:315:ALA:HB2	1:D:321:ILE:HD11	1.87	0.56
1:G:1307:GLN:OE1	1:H:1160:ILE:HD12	2.06	0.56
1:H:53:LEU:HD12	1:I:92:LEU:CD1	2.35	0.56
1:H:723:ARG:HH22	1:H:772:ASN:HA	1.70	0.56
5:Z:104:LEU:O	5:Z:277:TYR:N	2.36	0.56
5:6:292:CYS:SG	5:6:293:ILE:N	2.79	0.56
1:A:524:PRO:HG3	1:A:1204:ALA:HB2	1.86	0.56
1:A:508:ASN:ND2	1:A:959:GLU:OE1	2.38	0.56
1:H:1092:SER:O	1:H:1232:ASN:ND2	2.38	0.56
3:J:27:LYS:HZ1	3:J:28:LYS:CE	2.18	0.56
1:F:750:SER:OG	3:O:75:ARG:NE	2.38	0.56
5:X:139:GLU:OE2	5:X:143:ARG:NH1	2.39	0.56
1:B:255:LEU:HD11	5:X:166:LEU:HD12	99.25	0.56
1:C:390:GLN:HB2	1:C:1290:ARG:HG2	1.88	0.56
1:G:436:VAL:HG22	1:H:1165:LEU:HD13	1.87	0.56
1:G:810:TYR:HH	3:P:37:LEU:HB2	1.70	0.56
1:A:1152:ILE:HD12	1:A:1216:LEU:HD21	1.87	0.56
1:I:1216:LEU:C	1:I:1216:LEU:HD12	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:755:MET:HB2	3:L:68:ALA:HB1	1.88	0.56
1:H:806:LEU:HD11	3:Q:67:THR:CG2	2.35	0.56
1:B:294:GLN:HE22	1:B:366:LEU:HD13	1.71	0.56
1:F:225:THR:O	1:F:232:ARG:NH1	2.38	0.56
1:F:324:ASP:O	1:F:328:PHE:HB2	2.04	0.56
1:I:1092:SER:O	1:I:1232:ASN:ND2	2.38	0.56
5:W:295:LYS:HA	5:W:295:LYS:CE	2.28	0.56
1:A:294:GLN:HE21	1:A:359:THR:HG21	1.70	0.56
1:A:742:VAL:HG11	1:A:765:THR:HG23	1.87	0.56
1:B:1313:ARG:HH11	1:B:1323:GLU:HB2	1.70	0.56
1:E:273:LEU:O	1:E:369:PHE:HA	2.06	0.56
1:F:286:ILE:HG13	1:F:287:LEU:HG	1.88	0.56
1:F:273:LEU:O	1:F:369:PHE:HA	2.05	0.56
1:F:813:PRO:HG2	1:F:826:ILE:HD12	1.86	0.56
3:Q:24:GLU:O	3:Q:28:LYS:HG2	2.06	0.56
1:C:1212:LEU:N	1:C:1212:LEU:HD12	2.21	0.56
1:C:945:ARG:HG2	1:C:947:ASP:H	1.71	0.56
1:D:802:LYS:CG	3:M:67:THR:HG21	2.36	0.56
1:E:380:ASP:OD2	1:F:204:LYS:HD3	2.06	0.56
1:G:273:LEU:O	1:G:369:PHE:HA	2.05	0.56
5:Y:84:THR:HA	5:Y:295:LYS:HB3	1.86	0.56
1:A:743:ARG:HH21	1:A:762:VAL:HG11	1.71	0.56
1:B:1271:ASN:ND2	1:B:1274:SER:OG	2.39	0.56
1:B:687:ILE:HG12	1:B:986:ALA:HB1	1.87	0.56
1:C:859:LEU:O	1:C:860:ILE:C	2.42	0.56
1:D:1035:ILE:HG13	1:D:1059:SER:HB3	1.88	0.56
1:E:1092:SER:O	1:E:1232:ASN:ND2	2.39	0.56
1:H:230:LEU:HD23	1:H:1074:ALA:HB1	1.88	0.56
1:I:453:ILE:HD11	1:I:1229:LEU:HD13	1.87	0.56
5:Y:104:LEU:HB2	5:Y:278:PHE:HB2	1.88	0.56
1:D:432:ASN:HD22	1:D:436:VAL:HB	1.71	0.55
1:F:1105:ASN:HD22	5:X:226:ILE:CD1	2.19	0.55
1:D:24:LYS:NZ	1:H:203:ASN:HB3	2.21	0.55
1:C:815:ILE:HG23	3:L:39:LEU:HD21	1.89	0.55
5:X:295:LYS:NZ	5:X:296:ASN:O	2.38	0.55
1:D:862:ILE:HD12	1:D:862:ILE:O	2.06	0.55
1:D:863:ASN:HB3	1:D:896:ASN:HD21	1.71	0.55
4:T:75:LEU:HG	4:T:173:LEU:HD11	1.88	0.55
3:1:23:LYS:N	3:1:25:GLU:OE1	2.39	0.55
1:A:1220:LEU:O	1:A:1221:TYR:HD1	1.79	0.55
1:A:730:ILE:HG12	1:A:871:VAL:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:5:GLN:HA	1:G:8:GLU:HB2	1.88	0.55
1:H:374:LYS:HA	1:H:377:LYS:HG3	1.88	0.55
1:H:724:ASN:HD21	1:H:728:ALA:H	1.54	0.55
1:I:945:ARG:HG2	1:I:947:ASP:H	1.71	0.55
4:V:34:VAL:HG23	4:V:39:ARG:CZ	2.35	0.55
5:X:193:THR:HG23	5:X:271:LEU:HD21	1.89	0.55
1:A:990:SER:OG	1:A:1000:GLN:NE2	2.39	0.55
1:B:286:ILE:HG13	1:B:287:LEU:HG	1.88	0.55
1:C:826:ILE:HG23	1:C:828:SER:H	1.71	0.55
1:E:1149:CYS:SG	1:E:1150:GLU:N	2.79	0.55
1:E:758:ILE:O	1:E:865:ASN:ND2	2.40	0.55
1:F:705:ALA:HB2	1:F:999:ILE:HD11	1.88	0.55
3:J:27:LYS:HE3	3:J:28:LYS:CD	2.36	0.55
4:U:34:VAL:HG12	4:U:39:ARG:CZ	2.35	0.55
1:A:273:LEU:O	1:A:369:PHE:HA	2.06	0.55
1:C:1269:CYS:HB3	1:C:1281:SER:HA	1.88	0.55
1:C:230:LEU:HD23	1:C:1074:ALA:HB1	1.89	0.55
1:E:680:ILE:HG22	1:E:777:LEU:HD22	1.88	0.55
1:G:1143:HIS:HE1	1:H:217:GLN:OE1	1.90	0.55
1:C:810:TYR:HH	3:L:37:LEU:HB2	1.69	0.55
4:V:85:ASN:ND2	4:V:86:PRO:HD3	2.21	0.55
4:5:223:ASP:OD1	4:5:296:LYS:NZ	2.38	0.55
5:7:45:TYR:N	5:7:46:PRO:CD	2.69	0.55
1:A:844:THR:HB	1:A:847:ASN:HA	1.89	0.55
1:B:1139:SER:H	1:C:1196:GLN:NE2	2.04	0.55
1:D:270:ASP:OD2	1:D:365:LYS:NZ	2.39	0.55
1:F:662:ASP:HA	1:F:665:ILE:HG22	1.88	0.55
1:E:583:LYS:NZ	1:F:974:PHE:O	2.39	0.55
1:G:61:ILE:HG23	1:H:98:PRO:HB3	1.89	0.55
1:E:1315:LYS:HE2	1:F:1323:GLU:CD	2.25	0.55
1:F:779:LYS:O	1:F:783:PHE:CB	2.52	0.55
1:G:130:ASP:HB3	1:G:1051:THR:HG22	1.89	0.55
1:I:742:VAL:HG11	1:I:765:THR:HG23	1.88	0.55
4:S:98:SER:CB	4:S:111:LEU:HD11	2.35	0.55
1:C:54:LEU:O	1:D:91:VAL:HG12	2.06	0.55
1:D:730:ILE:HG12	1:D:871:VAL:HG22	1.89	0.55
1:F:294:GLN:HE22	1:F:366:LEU:HD13	1.72	0.55
1:G:151:ILE:O	1:G:155:ASN:ND2	2.40	0.55
1:H:720:THR:OG1	1:H:721:MET:N	2.40	0.55
1:I:286:ILE:HG13	1:I:287:LEU:HG	1.87	0.55
1:I:830:VAL:HA	1:I:834:LEU:HD13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:836:ARG:HH12	1:A:852:ALA:HB2	1.72	0.55
1:D:130:ASP:HB3	1:D:1051:THR:HG22	1.89	0.55
1:E:409:THR:C	1:E:410:MET:HG2	2.27	0.55
1:G:1128:ILE:HD11	1:G:1134:ASN:HD21	1.71	0.55
1:H:1223:THR:H	1:H:1244:THR:HG22	1.71	0.55
5:W:193:THR:HA	5:W:196:ILE:HD12	1.89	0.55
5:6:210:ARG:HH22	5:7:235:ARG:HE	1.55	0.55
1:C:209:ARG:NH1	1:C:1178:GLY:O	2.40	0.55
1:D:952:LEU:HB2	1:D:957:ALA:HB2	1.88	0.55
3:Q:24:GLU:CD	3:Q:24:GLU:H	2.08	0.55
1:C:433:LYS:NZ	1:D:214:ASN:OD1	2.40	0.54
1:D:1223:THR:H	1:D:1244:THR:HG22	1.72	0.54
1:D:485:ARG:NH2	1:D:872:GLU:OE2	2.40	0.54
1:E:492:LEU:HD12	1:E:868:ILE:HG12	1.89	0.54
1:E:617:HIS:CG	1:E:863:ASN:HD21	2.25	0.54
1:A:98:PRO:CG	1:F:173:ARG:HH22	2.20	0.54
1:F:687:ILE:HG12	1:F:986:ALA:HB1	1.88	0.54
5:W:295:LYS:CA	5:W:295:LYS:CE	2.86	0.54
5:6:162:ILE:HD12	5:7:255:LEU:HD22	1.89	0.54
1:D:1053:ASN:HD21	5:Z:35:HIS:CD2	2.25	0.54
1:E:663:GLU:CD	1:F:636:TYR:HE1	2.09	0.54
1:G:294:GLN:HE22	1:G:366:LEU:HD13	1.72	0.54
1:G:422:ASN:ND2	1:H:405:THR:HA	2.22	0.54
1:I:802:LYS:HE2	3:R:67:THR:HG22	1.89	0.54
1:D:224:LEU:HD13	5:Z:192:LYS:HG3	58.54	0.54
1:D:532:GLU:OE2	1:D:555:ARG:NH1	2.40	0.54
1:E:836:ARG:HH12	1:E:852:ALA:HB2	1.71	0.54
1:G:52:ALA:N	1:H:88:LEU:O	2.41	0.54
1:H:860:ILE:CG2	3:Q:78:ALA:HB3	2.37	0.54
1:A:97:LEU:HD22	1:F:378:ASN:ND2	2.22	0.54
1:B:273:LEU:O	1:B:369:PHE:HA	2.08	0.54
1:D:680:ILE:HG22	1:D:777:LEU:HD22	1.90	0.54
1:D:747:TYR:CG	1:D:861:TYR:HD1	2.26	0.54
1:G:1154:THR:HG22	1:G:1209:TRP:HZ3	1.72	0.54
1:H:273:LEU:O	1:H:369:PHE:HA	2.08	0.54
4:S:83:VAL:CG1	4:S:86:PRO:HD3	2.38	0.54
5:6:84:THR:HA	5:6:295:LYS:HB3	1.89	0.54
1:E:271:GLY:H	1:E:1029:ARG:HB3	1.73	0.54
1:E:729:LYS:O	1:E:871:VAL:HA	2.07	0.54
1:F:230:LEU:HD23	1:F:1074:ALA:HB1	1.89	0.54
1:G:1044:GLU:CB	5:W:1:MET:HG3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:429:PHE:CE1	1:G:439:ARG:HG3	2.42	0.54
5:X:87:GLN:CG	5:X:293:ILE:HG23	2.38	0.54
4:5:173:LEU:H	4:5:288:ILE:HD13	1.73	0.54
1:B:714:PHE:HE2	1:B:871:VAL:CG1	2.19	0.54
1:C:1223:THR:HG22	1:C:1226:ARG:HD2	1.89	0.54
1:E:518:VAL:HG12	1:E:564:PRO:HA	1.89	0.54
1:F:485:ARG:NH2	1:F:872:GLU:OE2	2.41	0.54
1:G:1315:LYS:HE2	1:H:1323:GLU:HG2	1.90	0.54
1:H:273:LEU:HD11	1:H:1024:LEU:HD13	1.90	0.54
4:U:117:ASN:O	4:U:120:VAL:HG12	2.07	0.54
5:W:222:SER:OG	5:W:224:LEU:HD23	2.08	0.54
1:B:750:SER:OG	3:K:75:ARG:NE	2.41	0.54
1:C:859:LEU:CG	1:C:862:ILE:HG23	2.32	0.54
1:F:821:PHE:HE2	3:O:81:ARG:HD3	1.72	0.54
1:G:419:THR:HG21	1:H:404:GLU:HG3	1.90	0.54
1:G:432:ASN:HD22	1:G:436:VAL:HB	1.71	0.54
1:G:705:ALA:HB2	1:G:999:ILE:HD11	1.90	0.54
1:H:723:ARG:NH2	1:H:775:THR:OG1	2.40	0.54
5:6:6:CYS:HA	5:6:37:ILE:O	2.07	0.54
1:B:705:ALA:HB2	1:B:999:ILE:HD11	1.90	0.54
1:C:54:LEU:HB2	1:D:91:VAL:CG1	2.37	0.54
1:E:414:VAL:CG1	1:E:1312:SER:OG	2.56	0.54
1:G:1131:GLY:O	4:S:185:TRP:CH2	2.61	0.54
4:V:31:LEU:C	4:V:31:LEU:HD22	2.28	0.54
5:X:19:THR:O	5:X:23:LEU:HB2	2.08	0.54
1:C:779:LYS:O	1:C:783:PHE:CB	2.52	0.54
1:D:393:PHE:HB3	1:D:1301:LEU:HD22	1.89	0.54
1:H:508:ASN:ND2	1:H:959:GLU:OE1	2.41	0.54
1:I:945:ARG:HE	1:I:947:ASP:HB2	1.73	0.54
1:H:815:ILE:CG2	3:Q:39:LEU:HD21	2.38	0.54
1:B:833:SER:OG	1:B:847:ASN:ND2	2.41	0.54
1:E:1212:LEU:HD23	1:E:1213:PRO:HD2	1.89	0.54
1:G:422:ASN:HD21	1:H:405:THR:HA	1.73	0.54
1:H:742:VAL:HG11	1:H:765:THR:HG23	1.89	0.54
1:I:508:ASN:ND2	1:I:959:GLU:OE1	2.41	0.54
1:A:449:VAL:HG23	1:A:1152:ILE:CD1	2.31	0.53
1:A:651:GLU:O	1:A:655:LEU:HB2	2.08	0.53
1:A:980:LEU:O	1:A:984:THR:HB	2.07	0.53
1:B:1112:VAL:HG23	1:B:1114:ILE:HG12	1.90	0.53
1:B:1315:LYS:HG2	1:C:1321:ILE:HG21	1.90	0.53
1:D:459:ILE:HG13	1:D:1229:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:6:ALA:O	1:E:10:LEU:HB2	2.07	0.53
1:E:810:TYR:CE1	3:N:37:LEU:HB2	2.43	0.53
1:G:401:ILE:HD11	1:G:1329:TYR:HB3	1.91	0.53
1:I:524:PRO:HG3	1:I:1204:ALA:HB2	1.90	0.53
1:E:145:ASN:OD1	1:E:150:GLN:NE2	2.39	0.53
1:F:387:GLN:NE2	1:F:1023:CYS:SG	2.82	0.53
5:W:224:LEU:HD13	5:W:224:LEU:H	1.73	0.53
1:B:513:LYS:NZ	1:B:532:GLU:OE2	2.33	0.53
1:D:32:PHE:HB2	1:D:35:LEU:HD23	1.90	0.53
1:D:747:TYR:CD1	1:D:861:TYR:HD1	2.25	0.53
1:E:806:LEU:CD1	3:N:67:THR:CG2	2.87	0.53
1:G:415:LYS:NZ	1:H:1326:TYR:HH	2.01	0.53
1:H:449:VAL:HG23	1:H:1152:ILE:CD1	2.38	0.53
1:E:810:TYR:CE2	3:N:37:LEU:HD12	2.36	0.53
5:W:222:SER:CB	5:W:224:LEU:HD22	2.37	0.53
1:F:209:ARG:HH22	1:F:1180:ASP:HB2	1.73	0.53
1:A:1165:LEU:HD13	1:F:436:VAL:HG22	1.89	0.53
1:H:990:SER:OG	1:H:1000:GLN:NE2	2.42	0.53
4:S:263:CYS:SG	4:S:264:ALA:N	2.81	0.53
5:W:87:GLN:HA	5:W:292:CYS:O	2.09	0.53
5:6:104:LEU:HB2	5:6:278:PHE:HB2	1.90	0.53
5:6:98:TRP:HB2	5:6:287:ASN:HD21	1.73	0.53
1:C:810:TYR:CZ	3:L:37:LEU:CD1	2.89	0.53
1:E:1145:GLN:NE2	1:E:1273:ASP:O	2.41	0.53
1:E:286:ILE:HG13	1:E:287:LEU:HG	1.89	0.53
1:E:783:PHE:O	1:E:787:PRO:CG	2.57	0.53
1:G:127:ILE:HD11	1:H:101:ALA:HA	1.91	0.53
1:I:507:LYS:NZ	1:I:515:GLU:OE2	2.39	0.53
5:X:244:GLY:O	5:X:245:GLN:HG2	2.09	0.53
1:C:449:VAL:CG2	1:C:1152:ILE:HD11	2.25	0.53
1:E:410:MET:CB	1:E:413:ARG:HD2	2.36	0.53
1:G:174:GLY:HA3	1:H:101:ALA:HB3	1.90	0.53
1:H:1035:ILE:HG13	1:H:1059:SER:HB3	1.89	0.53
1:I:294:GLN:HE22	1:I:366:LEU:HD13	1.74	0.53
1:I:692:ILE:HB	1:I:701:LEU:HD23	1.91	0.53
1:H:810:TYR:CD2	3:Q:37:LEU:HD12	2.37	0.53
4:S:69:LEU:HA	4:S:146:VAL:HG11	1.90	0.53
5:Y:32:ALA:HB1	5:Y:34:HIS:HD2	1.74	0.53
1:A:1130:PHE:CE1	4:U:119:MET:CE	2.92	0.53
1:A:98:PRO:HB2	1:F:173:ARG:NH2	2.24	0.53
1:A:50:PHE:HA	1:B:319:ARG:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:THR:HG21	1:C:404:GLU:HG3	1.91	0.53
1:H:952:LEU:HB2	1:H:957:ALA:HB2	1.91	0.53
1:H:964:GLN:HE21	1:H:989:HIS:HE1	1.56	0.53
1:A:755:MET:CB	3:J:68:ALA:HB1	2.36	0.53
3:N:24:GLU:H	3:N:24:GLU:CD	2.11	0.53
4:T:267:ASP:HB3	4:T:286:GLU:HB3	1.91	0.53
1:A:1109:ARG:HH22	1:A:1117:PRO:HA	1.73	0.53
1:A:779:LYS:O	1:A:783:PHE:CB	2.56	0.53
1:B:179:PHE:CE1	1:B:1034:ILE:HD11	2.42	0.53
1:C:700:PRO:HG3	1:D:941:PRO:HB2	1.90	0.53
1:E:1189:LYS:NZ	1:E:1193:ASP:OD2	2.36	0.53
1:E:756:ASN:OD1	3:N:65:ASP:HB2	2.09	0.53
5:X:278:PHE:HB3	5:X:292:CYS:SG	2.49	0.53
1:B:743:ARG:HH22	1:B:757:LEU:HD13	1.73	0.53
1:C:87:THR:HG22	1:C:88:LEU:HG	1.90	0.53
1:D:467:GLU:OE1	1:D:533:ARG:NH1	2.41	0.53
1:D:857:LYS:O	1:D:860:ILE:CG2	2.41	0.53
1:H:1145:GLN:NE2	1:H:1273:ASP:O	2.41	0.53
1:H:1302:HIS:HB2	1:H:1333:GLU:HB2	1.89	0.53
3:O:24:GLU:O	3:O:28:LYS:HG2	2.08	0.53
4:T:196:TYR:HE2	4:T:225:VAL:HG21	1.73	0.53
5:W:222:SER:OG	5:W:224:LEU:CD2	2.56	0.53
5:W:222:SER:CB	5:W:224:LEU:HD23	2.39	0.53
5:W:238:LEU:HD13	5:W:240:THR:H	1.73	0.53
1:A:406:GLY:O	1:F:417:ASN:HB3	2.09	0.53
1:B:703:ASN:OD1	1:B:710:ASP:CB	2.57	0.53
1:D:1149:CYS:SG	1:D:1150:GLU:N	2.80	0.53
1:E:57:TYR:HH	1:F:346:PHE:HD2	1.57	0.53
1:I:802:LYS:HE2	3:R:67:THR:CG2	2.39	0.53
3:P:24:GLU:O	3:P:28:LYS:HG2	2.09	0.53
1:H:857:LYS:HE3	3:Q:82:LEU:HA	1.90	0.53
1:G:1038:ASP:HB3	4:S:1:MET:H3	1.72	0.53
4:S:68:GLU:HG2	4:S:74:MET:HG3	1.91	0.53
1:A:224:LEU:HD11	5:W:195:CYS:SG	119.71	0.53
1:H:802:LYS:CG	3:Q:67:THR:HG21	2.39	0.52
1:I:1149:CYS:SG	1:I:1150:GLU:N	2.77	0.52
5:X:105:THR:HG22	5:X:276:THR:HA	1.91	0.52
5:X:87:GLN:HA	5:X:292:CYS:O	2.09	0.52
1:A:1095:PRO:HG2	1:A:1128:ILE:HD13	1.91	0.52
1:E:802:LYS:CG	3:N:67:THR:HG21	2.38	0.52
1:F:1154:THR:HG22	1:F:1209:TRP:HZ3	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:209:ARG:HH22	1:H:1180:ASP:HB2	1.74	0.52
1:H:387:GLN:NE2	1:H:1023:CYS:SG	2.82	0.52
1:F:209:ARG:NH1	1:F:1178:GLY:O	2.43	0.52
1:G:844:THR:HB	1:G:847:ASN:HA	1.89	0.52
1:B:83:VAL:HG21	1:B:1035:ILE:HG13	1.91	0.52
1:B:714:PHE:CD2	1:B:871:VAL:HG21	2.44	0.52
1:B:945:ARG:HE	1:B:947:ASP:HB2	1.73	0.52
1:G:324:ASP:O	1:G:328:PHE:CB	2.57	0.52
3:M:24:GLU:O	3:M:28:LYS:HG2	2.09	0.52
4:T:173:LEU:H	4:T:288:ILE:HD13	1.73	0.52
5:W:92:ASN:ND2	5:W:287:ASN:O	2.38	0.52
1:A:374:LYS:HA	1:A:377:LYS:HG3	1.90	0.52
1:C:174:GLY:HA3	1:D:101:ALA:HB3	1.91	0.52
1:D:755:MET:HB3	3:M:68:ALA:HB1	1.92	0.52
1:H:71:ILE:HD13	1:H:274:LEU:HD21	1.92	0.52
1:H:32:PHE:HB2	1:H:35:LEU:HD23	1.91	0.52
1:H:1143:HIS:NE2	1:I:1200:ASP:OD1	2.42	0.52
5:7:40:GLY:C	5:7:42:LEU:CD2	2.78	0.52
1:B:230:LEU:HD23	1:B:1074:ALA:HB1	1.90	0.52
1:B:485:ARG:NH2	1:B:872:GLU:OE2	2.42	0.52
1:E:1198:ASP:H	1:E:1204:ALA:HA	1.75	0.52
1:F:1035:ILE:HG13	1:F:1059:SER:HB3	1.90	0.52
1:G:809:PHE:HE2	3:P:74:ILE:CG2	2.23	0.52
1:H:393:PHE:HB3	1:H:1301:LEU:HD22	1.92	0.52
1:I:491:ILE:HD11	1:I:868:ILE:HG21	1.91	0.52
1:A:286:ILE:HG13	1:A:287:LEU:HG	1.92	0.52
1:B:712:ARG:N	1:B:712:ARG:CD	2.73	0.52
1:B:869:LEU:HB2	1:B:893:ILE:HG23	1.91	0.52
1:E:1133:ILE:CG2	1:E:1232:ASN:OD1	2.47	0.52
1:E:132:SER:HA	1:E:1049:VAL:HG12	1.92	0.52
1:E:750:SER:OG	3:N:75:ARG:NE	2.42	0.52
1:E:946:ASN:HD22	1:E:946:ASN:N	2.06	0.52
1:H:647:CYS:HA	1:H:653:ILE:HD12	1.91	0.52
5:W:235:ARG:O	5:W:235:ARG:NH2	2.42	0.52
3:1:24:GLU:O	3:1:28:LYS:HG2	2.10	0.52
1:E:274:LEU:HA	1:E:370:ASP:O	2.10	0.52
1:F:1170:ARG:HE	1:F:1174:SER:HB3	1.74	0.52
1:F:78:ILE:HG12	1:F:303:GLY:HA3	1.91	0.52
1:I:723:ARG:HH21	1:I:771:SER:HA	1.75	0.52
1:G:755:MET:CB	3:P:68:ALA:HB1	2.39	0.52
1:I:105:ASP:CG	4:V:147:SER:HG	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:77:LEU:O	3:2:81:ARG:HG2	2.10	0.51
3:4:77:LEU:O	3:4:81:ARG:HG2	2.10	0.51
1:A:1124:ALA:O	1:A:1128:ILE:HB	2.10	0.51
1:B:1198:ASP:H	1:B:1204:ALA:HA	1.76	0.51
1:F:201:VAL:CB	1:F:207:LEU:HD13	2.40	0.51
1:G:489:THR:OG1	1:G:733:ASP:OD1	2.26	0.51
1:I:230:LEU:HD23	1:I:1074:ALA:HB1	1.90	0.51
1:I:836:ARG:HH12	1:I:852:ALA:HB2	1.74	0.51
4:T:237:ARG:O	4:T:241:LEU:HG	2.10	0.51
5:Z:8:PHE:HA	5:Z:39:SER:HB3	1.90	0.51
3:1:77:LEU:O	3:1:81:ARG:HG2	2.10	0.51
5:6:149:LEU:HB3	5:7:258:ILE:HD13	1.91	0.51
5:7:42:LEU:N	5:7:42:LEU:CD2	2.73	0.51
1:B:1092:SER:O	1:B:1232:ASN:ND2	2.43	0.51
1:F:1149:CYS:HB2	1:F:1238:PRO:HD2	1.91	0.51
1:F:810:TYR:CZ	3:O:37:LEU:HD13	2.43	0.51
1:G:230:LEU:HD23	1:G:1074:ALA:HB1	1.91	0.51
1:I:393:PHE:HB3	1:I:1301:LEU:HD22	1.92	0.51
5:W:193:THR:HG23	5:W:271:LEU:HD21	1.93	0.51
5:W:104:LEU:HB2	5:W:278:PHE:HB2	1.92	0.51
4:5:57:ARG:O	5:7:100:LYS:NZ	2.38	0.51
1:D:209:ARG:HH22	1:D:1180:ASP:HB2	1.75	0.51
1:G:429:PHE:HE1	1:G:439:ARG:HG3	1.75	0.51
1:H:485:ARG:NH2	1:H:872:GLU:OE2	2.35	0.51
1:E:755:MET:HB3	3:N:68:ALA:HA	1.92	0.51
4:T:58:VAL:O	4:T:153:LEU:HA	2.10	0.51
4:U:299:VAL:HG11	5:Y:264:MET:HE1	1.90	0.51
3:3:77:LEU:O	3:3:81:ARG:HG2	2.10	0.51
1:B:1117:PRO:HG3	1:B:1134:ASN:HB3	1.92	0.51
1:B:274:LEU:HA	1:B:370:ASP:O	2.11	0.51
1:E:374:LYS:HA	1:E:377:LYS:HG3	1.91	0.51
1:E:781:PHE:CE1	1:E:786:LEU:HG	2.45	0.51
1:G:1131:GLY:O	4:S:185:TRP:CZ2	2.62	0.51
1:G:1176:MET:SD	1:G:1252:ASN:ND2	2.84	0.51
1:G:162:ARG:CZ	1:H:96:GLN:HE22	2.23	0.51
1:I:730:ILE:HG12	1:I:871:VAL:HG22	1.92	0.51
3:M:77:LEU:O	3:M:81:ARG:HG2	2.10	0.51
3:N:65:ASP:OD1	3:N:66:LYS:N	2.44	0.51
1:B:401:ILE:HD11	1:B:1329:TYR:HB3	1.93	0.51
1:D:647:CYS:HA	1:D:653:ILE:HD12	1.93	0.51
1:F:1198:ASP:H	1:F:1204:ALA:HA	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:820:CYS:O	1:I:824:ASN:CB	2.53	0.51
3:J:77:LEU:O	3:J:81:ARG:HG2	2.11	0.51
3:K:77:LEU:O	3:K:81:ARG:HG2	2.10	0.51
3:N:77:LEU:O	3:N:81:ARG:HG2	2.10	0.51
4:V:240:PHE:CE2	4:V:244:LEU:CD1	2.85	0.51
5:Z:10:HIS:ND1	5:Z:11:LYS:O	2.43	0.51
1:A:145:ASN:OD1	1:A:150:GLN:NE2	2.43	0.51
1:A:756:ASN:OD1	3:J:65:ASP:CB	2.57	0.51
1:C:1223:THR:HA	1:C:1226:ARG:HB3	1.92	0.51
1:F:274:LEU:HA	1:F:370:ASP:O	2.10	0.51
1:F:871:VAL:HB	1:F:891:GLN:HB2	1.92	0.51
1:I:759:ASP:OD2	1:I:802:LYS:NZ	2.40	0.51
3:L:67:THR:HA	3:L:70:ARG:HG3	1.93	0.51
3:Q:65:ASP:OD1	3:Q:66:LYS:N	2.44	0.51
4:S:193:GLN:NE2	4:S:265:THR:OG1	2.43	0.51
4:V:107:VAL:HG13	4:V:280:LEU:HD11	1.93	0.51
5:W:295:LYS:NZ	5:W:296:ASN:HB2	2.26	0.51
5:6:8:PHE:HB2	5:6:75:ASN:HD21	1.76	0.51
1:B:127:ILE:HG23	1:C:99:ARG:HH21	1.75	0.51
1:C:705:ALA:HB2	1:C:999:ILE:HD11	1.93	0.51
1:D:742:VAL:HG11	1:D:765:THR:HG23	1.92	0.51
1:G:747:TYR:O	3:P:75:ARG:NH2	2.43	0.51
1:I:273:LEU:O	1:I:369:PHE:HA	2.10	0.51
1:A:755:MET:HB3	3:J:68:ALA:HA	1.93	0.51
3:P:77:LEU:O	3:P:81:ARG:HG2	2.10	0.51
4:T:83:VAL:HG12	4:T:86:PRO:CD	2.41	0.51
1:A:542:ILE:O	1:A:548:THR:O	2.29	0.51
1:A:691:ASN:CG	1:B:945:ARG:HD3	2.31	0.51
1:B:1149:CYS:HB2	1:B:1238:PRO:HD2	1.91	0.51
1:B:78:ILE:HG12	1:B:303:GLY:HA3	1.92	0.51
1:B:439:ARG:HD2	1:C:519:GLU:OE2	2.10	0.51
1:D:489:THR:OG1	1:D:733:ASP:OD1	2.27	0.51
1:G:1170:ARG:HE	1:G:1174:SER:HB3	1.74	0.51
1:G:802:LYS:CG	3:P:67:THR:HG21	2.41	0.51
1:G:952:LEU:HB2	1:G:957:ALA:HB2	1.93	0.51
1:G:1307:GLN:CD	1:H:1160:ILE:CD1	2.79	0.51
1:I:622:ALA:HB2	1:I:861:TYR:HD2	1.76	0.51
1:I:485:ARG:NH2	1:I:872:GLU:OE2	2.44	0.51
1:B:815:ILE:O	3:K:43:MET:SD	2.68	0.51
3:M:65:ASP:OD1	3:M:66:LYS:N	2.44	0.51
3:N:67:THR:HA	3:N:70:ARG:HG3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:67:THR:HA	3:P:70:ARG:HG3	1.93	0.51
4:U:223:ASP:OD1	4:U:296:LYS:NZ	2.39	0.51
5:X:32:ALA:HB1	5:X:34:HIS:HD2	1.75	0.51
5:Y:23:LEU:HD12	5:Y:118:LEU:HD22	1.93	0.51
5:Y:247:HIS:CD2	5:Y:254:GLU:HG3	2.46	0.51
3:1:65:ASP:OD1	3:1:66:LYS:N	2.44	0.51
1:A:1172:ARG:NH1	1:A:1204:ALA:O	2.44	0.51
1:B:50:PHE:HD2	1:C:321:ILE:HG22	1.75	0.51
1:D:1092:SER:O	1:D:1232:ASN:ND2	2.43	0.51
1:D:273:LEU:HD11	1:D:1024:LEU:HD13	1.92	0.51
1:E:535:PRO:O	1:E:555:ARG:NH2	2.44	0.51
1:G:518:VAL:HG12	1:G:564:PRO:HA	1.92	0.51
1:G:513:LYS:NZ	1:G:532:GLU:OE2	2.32	0.51
1:I:959:GLU:OE2	1:I:966:THR:OG1	2.25	0.51
3:Q:77:LEU:O	3:Q:81:ARG:HG2	2.10	0.51
5:X:246:LEU:N	5:X:246:LEU:CD2	2.74	0.51
1:A:432:ASN:HD22	1:A:436:VAL:HB	1.76	0.51
1:A:710:ASP:O	1:A:779:LYS:NZ	2.44	0.51
1:A:863:ASN:HB3	1:A:896:ASN:HD21	1.75	0.51
1:G:1230:CYS:SG	1:G:1231:TYR:N	2.84	0.51
1:H:635:SER:O	1:H:639:ASN:HB2	2.11	0.51
3:J:67:THR:HA	3:J:70:ARG:HG3	1.93	0.51
1:F:810:TYR:CD2	3:O:37:LEU:HD12	2.33	0.51
1:G:815:ILE:O	3:P:43:MET:SD	2.68	0.51
3:R:24:GLU:O	3:R:28:LYS:HG2	2.11	0.51
4:S:195:VAL:HG22	4:S:216:LEU:HG	1.93	0.51
5:Y:235:ARG:HG3	5:Y:237:THR:H	1.76	0.51
1:A:220:LYS:HE2	1:A:1297:ASN:HD21	1.75	0.50
1:B:815:ILE:HG23	3:K:39:LEU:CD2	2.40	0.50
1:C:1221:TYR:HB2	1:C:1243:PHE:HD2	1.75	0.50
1:C:542:ILE:O	1:C:548:THR:O	2.29	0.50
1:F:1145:GLN:NE2	1:F:1273:ASP:O	2.44	0.50
1:G:387:GLN:NE2	1:G:1023:CYS:SG	2.84	0.50
3:Q:67:THR:HA	3:Q:70:ARG:HG3	1.93	0.50
3:R:67:THR:HA	3:R:70:ARG:HG3	1.93	0.50
4:S:134:GLU:O	4:S:295:LYS:NZ	2.45	0.50
3:3:67:THR:HA	3:3:70:ARG:HG3	1.93	0.50
1:A:558:ILE:HD11	1:A:1008:GLY:HA3	1.93	0.50
1:C:1168:ASN:ND2	1:C:1174:SER:OG	2.44	0.50
1:D:5:GLN:HA	1:D:8:GLU:HB2	1.91	0.50
1:F:565:LEU:HD13	1:F:1209:TRP:HH2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:274:LEU:HA	1:G:370:ASP:O	2.11	0.50
1:I:1149:CYS:HB2	1:I:1238:PRO:HD2	1.93	0.50
3:K:67:THR:HA	3:K:70:ARG:HG3	1.93	0.50
3:L:65:ASP:OD1	3:L:66:LYS:N	2.44	0.50
3:4:67:THR:HA	3:4:70:ARG:HG3	1.93	0.50
1:A:54:LEU:HA	1:B:323:ALA:HB3	1.93	0.50
1:B:1035:ILE:O	1:B:1035:ILE:HG13	2.12	0.50
1:B:1221:TYR:HB2	1:B:1243:PHE:HD2	1.76	0.50
1:B:714:PHE:HZ	1:B:728:ALA:CB	2.24	0.50
1:B:864:GLU:HB2	1:B:896:ASN:HD22	1.77	0.50
1:C:276:PRO:HG3	1:C:1022:GLU:HB2	1.92	0.50
1:C:286:ILE:HG13	1:C:287:LEU:HG	1.92	0.50
1:D:507:LYS:NZ	1:D:515:GLU:OE2	2.43	0.50
1:E:836:ARG:NH1	1:E:848:THR:O	2.44	0.50
1:E:48:ILE:HD13	1:F:316:ILE:HG12	1.93	0.50
1:F:822:GLN:NE2	1:F:822:GLN:CA	2.73	0.50
1:F:860:ILE:HG22	3:O:75:ARG:O	2.11	0.50
1:G:1198:ASP:H	1:G:1204:ALA:HA	1.75	0.50
3:O:77:LEU:O	3:O:81:ARG:HG2	2.10	0.50
4:U:107:VAL:HG13	4:U:280:LEU:HD11	1.93	0.50
4:V:173:LEU:H	4:V:288:ILE:HD13	1.77	0.50
1:A:621:HIS:HB2	1:A:861:TYR:HE2	1.76	0.50
1:B:209:ARG:HH22	1:B:1180:ASP:HB2	1.76	0.50
1:C:479:CYS:SG	1:C:543:GLN:NE2	2.84	0.50
1:D:225:THR:O	1:D:232:ARG:NH1	2.44	0.50
1:E:32:PHE:HB2	1:E:35:LEU:HD23	1.93	0.50
1:E:543:GLN:HE22	1:E:548:THR:HG22	1.77	0.50
1:G:1149:CYS:HB2	1:G:1238:PRO:HD2	1.93	0.50
1:G:380:ASP:HA	1:H:203:ASN:CB	2.41	0.50
1:G:662:ASP:HA	1:G:665:ILE:HG22	1.93	0.50
1:H:165:LYS:NZ	4:V:38:GLU:OE2	2.43	0.50
3:R:77:LEU:O	3:R:81:ARG:HG2	2.10	0.50
4:T:64:LEU:N	4:T:64:LEU:CD1	2.73	0.50
5:W:222:SER:HB2	5:W:224:LEU:HD22	1.88	0.50
5:Z:178:LEU:HD12	5:Z:181:ILE:HD11	1.93	0.50
1:A:1018:ASN:OD1	1:A:1018:ASN:N	2.42	0.50
1:B:1170:ARG:HE	1:B:1174:SER:HB3	1.76	0.50
1:C:1170:ARG:O	1:C:1211:SER:HB2	2.12	0.50
1:E:415:LYS:NZ	1:F:1326:TYR:HE1	2.06	0.50
1:E:471:THR:O	1:E:475:PHE:CB	2.59	0.50
1:F:869:LEU:HB2	1:F:893:ILE:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:536:PHE:HD1	1:G:992:LEU:HB3	1.77	0.50
1:H:945:ARG:HG2	1:H:947:ASP:H	1.76	0.50
3:K:23:LYS:HE3	3:K:25:GLU:HB3	1.94	0.50
3:R:65:ASP:OD1	3:R:66:LYS:N	2.44	0.50
4:T:95:PHE:CE1	4:T:120:VAL:HG23	2.46	0.50
1:D:705:ALA:HB2	1:D:999:ILE:HD11	1.94	0.50
1:D:779:LYS:O	1:D:783:PHE:CB	2.53	0.50
1:E:311:ASN:ND2	1:E:322:MET:O	2.44	0.50
1:E:693:ASN:OD1	1:F:945:ARG:NH2	2.44	0.50
1:G:565:LEU:HD13	1:G:1209:TRP:HH2	1.76	0.50
1:G:674:ARG:NH1	1:H:598:GLU:OE1	2.44	0.50
1:H:435:GLN:HE21	1:H:1338:GLN:HE21	1.59	0.50
1:I:1209:TRP:O	1:I:1216:LEU:CD1	2.59	0.50
3:L:23:LYS:CD	3:L:23:LYS:N	2.73	0.50
3:M:67:THR:HA	3:M:70:ARG:HG3	1.93	0.50
4:S:111:LEU:HD12	4:S:111:LEU:C	2.31	0.50
4:T:53:ARG:NH1	4:T:164:ASP:O	2.39	0.50
1:C:469:LEU:HD21	1:C:548:THR:HG21	1.93	0.50
1:C:680:ILE:HG22	1:C:777:LEU:HD22	1.93	0.50
1:H:542:ILE:O	1:H:548:THR:O	2.29	0.50
3:L:77:LEU:O	3:L:81:ARG:HG2	2.10	0.50
1:F:802:LYS:CD	3:O:67:THR:CG2	2.70	0.50
4:U:173:LEU:H	4:U:288:ILE:HD13	1.77	0.50
1:G:1046:LYS:HE3	5:W:1:MET:CE	2.42	0.50
5:X:104:LEU:HB2	5:X:278:PHE:HB2	1.93	0.50
1:D:24:LYS:HZ3	1:H:203:ASN:HB3	1.77	0.50
1:D:424:LEU:HD11	1:D:573:ALA:HB1	1.94	0.50
1:D:831:LEU:HD11	1:D:907:LEU:HD21	1.93	0.50
1:E:230:LEU:HD23	1:E:1074:ALA:HB1	1.94	0.50
1:F:432:ASN:HD22	1:F:436:VAL:HB	1.76	0.50
1:H:286:ILE:HG13	1:H:287:LEU:HG	1.93	0.50
1:H:541:TYR:HE1	1:H:550:VAL:HG12	1.77	0.50
1:I:1209:TRP:O	1:I:1216:LEU:HG	2.12	0.50
1:I:542:ILE:O	1:I:548:THR:O	2.30	0.50
3:1:67:THR:HA	3:1:70:ARG:HG3	1.93	0.50
3:2:67:THR:HA	3:2:70:ARG:HG3	1.93	0.50
1:C:535:PRO:HB2	1:C:1009:PHE:HE1	1.77	0.50
1:I:389:LEU:O	1:I:1018:ASN:HA	2.12	0.50
3:P:65:ASP:OD1	3:P:66:LYS:N	2.44	0.50
4:T:51:ASN:O	4:T:163:TYR:OH	2.30	0.50
5:X:136:ILE:HD12	5:X:171:TYR:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:54:ILE:HD13	5:7:293:ILE:HG21	1.94	0.49
1:A:1112:VAL:HG23	1:A:1114:ILE:HG12	1.94	0.49
1:A:720:THR:OG1	1:A:721:MET:N	2.45	0.49
1:B:471:THR:O	1:B:475:PHE:CB	2.57	0.49
1:D:843:TYR:O	1:D:848:THR:CG2	2.59	0.49
1:D:945:ARG:HG2	1:D:947:ASP:H	1.76	0.49
1:E:820:CYS:O	1:E:824:ASN:HB3	2.12	0.49
1:E:758:ILE:HG22	1:E:864:GLU:HA	1.94	0.49
1:F:962:ASN:O	1:F:965:ARG:NH1	2.45	0.49
1:H:808:LEU:HD21	1:H:831:LEU:HD12	1.94	0.49
1:I:1010:ALA:N	1:I:1153:LEU:O	2.45	0.49
1:I:1152:ILE:HB	1:I:1216:LEU:CD2	2.42	0.49
1:G:1123:GLU:HB3	4:S:231:GLN:CD	2.32	0.49
5:Y:201:ILE:O	5:Y:205:ALA:HB2	2.12	0.49
5:Z:19:THR:HG21	5:Z:118:LEU:O	2.12	0.49
5:Z:1:MET:SD	5:Z:2:GLU:N	2.85	0.49
5:6:32:ALA:HB1	5:6:34:HIS:HD2	1.76	0.49
1:A:751:ASP:N	1:A:751:ASP:OD1	2.45	0.49
1:D:710:ASP:O	1:D:779:LYS:NZ	2.45	0.49
1:E:1151:VAL:HG22	1:E:1239:ASN:HD21	1.76	0.49
1:E:802:LYS:CD	3:N:67:THR:CG2	2.80	0.49
1:F:536:PHE:HD1	1:F:992:LEU:HB3	1.76	0.49
1:G:802:LYS:CD	3:P:67:THR:CG2	2.75	0.49
3:O:67:THR:HA	3:O:70:ARG:HG3	1.93	0.49
4:T:195:VAL:HG22	4:T:216:LEU:HG	1.94	0.49
4:T:68:GLU:OE2	4:T:92:GLY:HA3	2.12	0.49
5:W:82:PRO:CB	5:W:295:LYS:CD	2.88	0.49
3:2:65:ASP:OD1	3:2:66:LYS:N	2.44	0.49
5:7:1:MET:SD	5:7:2:GLU:N	2.85	0.49
1:A:408:SER:OG	1:A:409:THR:O	2.29	0.49
1:B:50:PHE:CE2	1:C:321:ILE:CG2	2.94	0.49
1:C:584:THR:HG21	1:C:685:ARG:HD2	1.93	0.49
1:G:779:LYS:O	1:G:783:PHE:CB	2.52	0.49
1:G:756:ASN:ND2	3:P:64:VAL:HB	2.22	0.49
1:B:162:ARG:CZ	1:C:96:GLN:HE22	2.25	0.49
1:B:54:LEU:HD22	1:C:345:ILE:HD13	1.94	0.49
1:B:622:ALA:HB2	1:B:861:TYR:HD2	1.77	0.49
1:F:556:ILE:HG21	1:F:963:TRP:HZ3	1.78	0.49
1:G:307:MET:SD	1:G:307:MET:N	2.84	0.49
1:H:51:GLU:OE2	1:I:90:LYS:NZ	2.34	0.49
3:J:65:ASP:OD1	3:J:66:LYS:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:104:LEU:O	5:Y:277:TYR:N	2.38	0.49
5:Z:170:GLN:HE21	5:Z:173:ASP:HA	1.76	0.49
1:A:647:CYS:HA	1:A:653:ILE:HD12	1.95	0.49
1:B:714:PHE:HZ	1:B:728:ALA:HB3	1.77	0.49
1:F:401:ILE:HD11	1:F:1329:TYR:HB3	1.94	0.49
1:H:1221:TYR:HB2	1:H:1243:PHE:HD2	1.77	0.49
1:I:374:LYS:HA	1:I:377:LYS:HG3	1.95	0.49
1:I:990:SER:OG	1:I:1000:GLN:NE2	2.46	0.49
4:S:96:LEU:HD21	4:S:133:LEU:HD21	1.95	0.49
3:3:65:ASP:OD1	3:3:66:LYS:N	2.44	0.49
1:B:52:ALA:CB	1:C:321:ILE:HG21	2.42	0.49
1:A:57:TYR:HB2	1:B:93:PHE:CD1	2.47	0.49
1:D:1302:HIS:HB2	1:D:1333:GLU:HB2	1.93	0.49
1:G:89:GLY:O	1:G:120:SER:HB3	2.13	0.49
1:I:952:LEU:HB2	1:I:957:ALA:HB2	1.94	0.49
1:A:1221:TYR:HB2	1:A:1243:PHE:HD2	1.77	0.49
1:A:274:LEU:HA	1:A:370:ASP:O	2.13	0.49
1:B:182:THR:HA	1:B:185:ARG:HE	1.78	0.49
1:D:542:ILE:O	1:D:549:GLU:HB3	2.12	0.49
1:F:201:VAL:CG2	1:F:207:LEU:HD13	2.42	0.49
1:H:692:ILE:HB	1:H:701:LEU:HD23	1.95	0.49
3:K:65:ASP:OD1	3:K:66:LYS:N	2.44	0.49
5:X:167:CYS:SG	5:X:178:LEU:HD23	2.53	0.49
4:5:81:THR:HG22	4:5:83:VAL:H	1.77	0.49
1:B:182:THR:OG1	1:B:185:ARG:NH2	2.38	0.49
1:D:1042:THR:HG22	1:D:1053:ASN:O	2.13	0.49
1:I:856:PHE:CE2	3:R:81:ARG:HD2	2.45	0.49
1:G:1052:TYR:OH	4:S:11:ILE:HG12	2.13	0.49
3:4:65:ASP:OD1	3:4:66:LYS:N	2.44	0.49
5:6:14:LEU:HA	5:6:17:ILE:HG22	1.95	0.49
5:7:153:HIS:HB3	5:7:156:TYR:HE2	1.77	0.49
1:A:820:CYS:O	1:A:824:ASN:CB	2.59	0.49
1:C:693:ASN:HD21	1:D:945:ARG:HH22	1.61	0.49
1:B:378:ASN:OD1	1:C:97:LEU:HD22	2.13	0.49
1:D:995:VAL:HG12	1:D:1108:ILE:HD11	1.94	0.49
1:D:820:CYS:SG	1:D:824:ASN:ND2	2.86	0.49
1:E:1130:PHE:C	1:E:1130:PHE:CD1	2.85	0.49
1:F:182:THR:HA	1:F:185:ARG:HE	1.78	0.49
1:G:680:ILE:HG22	1:G:777:LEU:HD22	1.95	0.49
1:I:513:LYS:NZ	1:I:532:GLU:OE2	2.38	0.49
4:S:75:LEU:HG	4:S:173:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1130:PHE:HZ	4:S:86:PRO:HG3	1.71	0.49
1:B:714:PHE:CZ	1:B:728:ALA:CB	2.96	0.49
1:C:1212:LEU:N	1:C:1212:LEU:CD1	2.76	0.49
1:D:274:LEU:HA	1:D:370:ASP:O	2.12	0.49
1:D:953:PRO:O	1:D:956:LEU:N	2.46	0.49
1:E:393:PHE:HB3	1:E:1301:LEU:HD22	1.95	0.49
1:F:864:GLU:HB2	1:F:896:ASN:HD22	1.78	0.49
1:F:488:PRO:HG3	1:F:870:GLU:HG3	1.95	0.49
1:H:280:ILE:HD12	1:H:371:HIS:HB3	1.95	0.49
4:T:66:ALA:N	4:T:67:PRO:HD2	2.25	0.49
1:A:1130:PHE:HZ	4:U:86:PRO:HG2	1.73	0.49
5:7:62:ARG:NH2	5:7:273:ASN:O	2.46	0.48
1:A:176:ILE:HG21	1:A:375:VAL:HG21	1.96	0.48
1:A:260:ASN:HD21	1:A:350:ARG:HH22	1.60	0.48
1:A:471:THR:O	1:A:475:PHE:CB	2.61	0.48
1:A:813:PRO:HG2	1:A:826:ILE:HD12	1.94	0.48
1:E:810:TYR:OH	3:N:37:LEU:CG	2.60	0.48
1:A:91:VAL:CG1	1:F:54:LEU:HB2	2.28	0.48
1:F:777:LEU:HD23	1:F:780:ILE:HD12	1.95	0.48
1:I:1082:ASP:HB3	1:I:1146:GLN:HB3	1.95	0.48
1:I:471:THR:O	1:I:475:PHE:CB	2.61	0.48
3:4:52:PHE:CZ	3:4:76:MET:HE3	2.47	0.48
1:A:53:LEU:HD22	1:B:322:MET:CE	2.43	0.48
1:B:692:ILE:HB	1:B:701:LEU:HD23	1.95	0.48
1:D:1041:VAL:HG22	1:D:1054:PHE:CE1	2.48	0.48
1:F:1040:THR:OG1	1:F:1055:THR:OG1	2.31	0.48
1:F:471:THR:O	1:F:475:PHE:CB	2.60	0.48
1:F:680:ILE:HG22	1:F:777:LEU:HD22	1.94	0.48
1:H:54:LEU:N	1:H:54:LEU:CD2	2.76	0.48
4:T:75:LEU:HD22	4:T:139:LEU:HD11	1.95	0.48
1:A:273:LEU:HD11	1:A:1024:LEU:HD13	1.95	0.48
1:B:542:ILE:O	1:B:548:THR:O	2.30	0.48
1:D:1245:GLU:HA	1:D:1248:ILE:HG22	1.94	0.48
1:G:80:PHE:HD2	1:G:83:VAL:HB	1.78	0.48
1:H:453:ILE:HD11	1:H:1229:LEU:HD13	1.94	0.48
1:I:209:ARG:NH1	1:I:1178:GLY:O	2.44	0.48
1:I:758:ILE:O	1:I:865:ASN:ND2	2.46	0.48
5:X:222:SER:O	5:X:226:ILE:HG13	2.13	0.48
4:5:107:VAL:HG13	4:5:280:LEU:HD11	1.94	0.48
1:B:1176:MET:SD	1:B:1252:ASN:ND2	2.86	0.48
1:D:13:ILE:HG13	1:H:340:ASN:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1130:PHE:CZ	4:S:86:PRO:HG2	2.45	0.48
1:E:945:ARG:C	1:E:946:ASN:HD22	2.17	0.48
1:G:1145:GLN:NE2	1:G:1273:ASP:O	2.47	0.48
1:G:869:LEU:HB2	1:G:893:ILE:HG23	1.95	0.48
1:H:220:LYS:HE2	1:H:1297:ASN:HD21	1.78	0.48
3:O:65:ASP:OD1	3:O:66:LYS:N	2.44	0.48
3:Q:23:LYS:N	3:Q:25:GLU:OE1	2.47	0.48
1:H:815:ILE:HG23	3:Q:39:LEU:HD21	1.95	0.48
5:W:295:LYS:NZ	5:W:296:ASN:CB	2.77	0.48
1:A:1215:SER:O	1:A:1219:ILE:HG12	2.14	0.48
1:B:1230:CYS:SG	1:B:1231:TYR:N	2.86	0.48
1:B:952:LEU:HB2	1:B:957:ALA:HB2	1.95	0.48
1:C:1170:ARG:HG2	1:C:1211:SER:HA	1.95	0.48
1:D:220:LYS:HE2	1:D:1297:ASN:HD21	1.78	0.48
1:D:47:ASN:N	4:S:168:GLU:OE2	2.46	0.48
1:E:542:ILE:O	1:E:548:THR:O	2.32	0.48
1:F:692:ILE:HB	1:F:701:LEU:HD23	1.95	0.48
1:I:1160:ILE:HG23	1:I:1164:LYS:HD2	1.96	0.48
1:I:274:LEU:HA	1:I:370:ASP:O	2.13	0.48
1:I:968:PHE:HE1	1:I:988:MET:HB3	1.79	0.48
1:F:802:LYS:HG3	3:O:71:LEU:HD11	1.95	0.48
1:D:1123:GLU:OE1	4:V:231:GLN:OE1	2.31	0.48
5:6:136:ILE:HD12	5:6:171:TYR:HB3	1.96	0.48
1:A:435:GLN:HE21	1:A:1338:GLN:NE2	2.11	0.48
1:B:1142:LEU:C	1:C:213:SER:HB2	2.34	0.48
1:B:925:ILE:O	1:B:928:THR:OG1	2.31	0.48
1:B:1143:HIS:HE1	1:C:217:GLN:OE1	1.96	0.48
1:D:51:GLU:HG3	1:E:88:LEU:HB2	1.94	0.48
1:E:712:ARG:NH1	1:E:874:SER:O	2.46	0.48
1:F:72:ALA:HA	1:F:75:ALA:HB3	1.95	0.48
1:G:488:PRO:HG3	1:G:870:GLU:HG3	1.94	0.48
1:I:498:LEU:HG	1:I:954:PRO:HG2	1.94	0.48
5:W:295:LYS:HZ3	5:W:296:ASN:N	2.12	0.48
4:5:253:TYR:HA	4:5:299:VAL:HG22	1.94	0.48
5:7:199:SER:O	5:7:203:ALA:HB2	2.14	0.48
1:A:593:LEU:HD22	1:A:789:LEU:HD21	1.96	0.48
1:B:508:ASN:ND2	1:B:959:GLU:OE1	2.47	0.48
1:C:489:THR:OG1	1:C:733:ASP:OD1	2.28	0.48
1:D:164:LEU:HD11	4:V:11:ILE:HD11	1.96	0.48
1:F:836:ARG:HH12	1:F:852:ALA:HB2	1.78	0.48
1:G:78:ILE:O	1:G:1035:ILE:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:777:LEU:HD23	1:G:780:ILE:HD12	1.94	0.48
1:G:54:LEU:HB2	1:H:91:VAL:HG12	1.96	0.48
1:I:1035:ILE:HG13	1:I:1059:SER:HB3	1.95	0.48
1:G:1038:ASP:OD2	4:S:1:MET:HB2	2.12	0.48
4:V:86:PRO:O	4:V:87:LYS:C	2.52	0.48
5:Z:19:THR:HG21	5:Z:118:LEU:HA	1.94	0.48
1:A:584:THR:HG21	1:A:685:ARG:HD2	1.96	0.48
1:B:518:VAL:HG12	1:B:564:PRO:HA	1.96	0.48
1:C:271:GLY:H	1:C:1029:ARG:HB3	1.77	0.48
1:E:51:GLU:H	1:F:320:ALA:HA	1.79	0.48
1:G:102:THR:HG21	1:G:108:ALA:HA	1.95	0.48
4:V:186:GLU:OE2	4:V:186:GLU:HA	2.14	0.48
5:Y:205:ALA:HB3	5:Y:210:ARG:HH12	1.78	0.48
1:B:708:LEU:HA	1:B:713:LEU:CD2	2.43	0.48
1:C:792:ASN:HD21	1:C:919:PHE:HD1	1.61	0.48
1:C:876:ASP:OD1	1:C:876:ASP:N	2.47	0.48
1:C:151:ILE:HA	1:D:337:GLN:HE22	1.79	0.48
1:D:751:ASP:OD1	1:D:751:ASP:N	2.47	0.48
1:E:691:ASN:HA	1:E:702:VAL:HG22	1.96	0.48
1:I:810:TYR:CZ	3:R:37:LEU:HD13	2.43	0.48
5:Z:201:ILE:O	5:Z:205:ALA:HB2	2.13	0.48
1:A:78:ILE:HG12	1:A:303:GLY:HA3	1.96	0.48
1:E:220:LYS:HE2	1:E:1297:ASN:HD21	1.79	0.48
1:G:280:ILE:HD12	1:G:371:HIS:HB3	1.96	0.48
1:G:864:GLU:O	1:G:896:ASN:ND2	2.46	0.48
1:G:556:ILE:HG21	1:G:963:TRP:HZ3	1.78	0.48
1:I:714:PHE:HB3	1:I:893:ILE:HD12	1.95	0.48
3:N:24:GLU:HB2	3:N:28:LYS:HZ3	1.79	0.48
1:G:856:PHE:CE2	3:P:81:ARG:HD2	2.43	0.48
5:7:45:TYR:OH	5:7:123:ASP:O	2.22	0.47
1:A:758:ILE:O	1:A:865:ASN:ND2	2.47	0.47
1:A:876:ASP:N	1:A:876:ASP:OD1	2.46	0.47
1:A:934:GLN:O	1:A:938:ASN:N	2.45	0.47
1:C:508:ASN:ND2	1:C:959:GLU:OE1	2.47	0.47
1:B:662:ASP:HB2	1:C:640:MET:O	2.13	0.47
1:D:859:LEU:CD1	1:D:862:ILE:CG2	2.92	0.47
1:E:130:ASP:HB3	1:E:1051:THR:HG22	1.96	0.47
1:G:809:PHE:CE1	1:G:859:LEU:CD2	2.96	0.47
1:H:263:SER:OG	1:H:264:LYS:N	2.46	0.47
1:H:680:ILE:HG22	1:H:777:LEU:HD22	1.96	0.47
5:W:277:TYR:O	5:W:294:TYR:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:10:HIS:ND1	5:X:11:LYS:O	2.41	0.47
3:1:24:GLU:HB2	3:1:28:LYS:HZ3	1.80	0.47
1:A:133:ALA:N	1:A:1048:ILE:O	2.47	0.47
1:A:1200:ASP:C	1:F:438:GLN:HE22	2.18	0.47
1:A:420:MET:HG3	1:A:576:ASN:HB3	1.95	0.47
1:B:432:ASN:HD22	1:B:436:VAL:HB	1.79	0.47
1:C:891:GLN:HE21	1:C:963:TRP:HD1	1.61	0.47
1:D:651:GLU:O	1:D:655:LEU:HB2	2.13	0.47
1:E:756:ASN:HD21	3:N:64:VAL:HB	1.79	0.47
1:E:759:ASP:OD2	1:E:802:LYS:NZ	2.47	0.47
1:F:1221:TYR:HB2	1:F:1243:PHE:HD2	1.78	0.47
1:F:202:HIS:CD2	1:F:204:LYS:HB2	2.49	0.47
1:E:251:THR:HA	1:G:19:ILE:CG2	2.44	0.47
1:G:692:ILE:HB	1:G:701:LEU:HD23	1.96	0.47
1:G:960:PHE:O	1:G:965:ARG:NH2	2.47	0.47
1:H:408:SER:OG	1:H:409:THR:O	2.32	0.47
1:H:836:ARG:HH12	1:H:852:ALA:HB2	1.78	0.47
3:N:24:GLU:O	3:N:28:LYS:HG2	2.14	0.47
1:G:164:LEU:HD21	4:S:11:ILE:HD11	1.96	0.47
1:A:157:LEU:HD22	4:U:28:ALA:HB1	1.96	0.47
4:T:220:GLN:HE22	5:X:295:LYS:NZ	2.11	0.47
1:D:755:MET:CB	3:M:68:ALA:HB1	2.44	0.47
1:E:946:ASN:ND2	1:E:946:ASN:N	2.60	0.47
1:F:508:ASN:ND2	1:F:959:GLU:OE1	2.47	0.47
1:F:599:SER:HB3	1:F:644:LEU:H	1.78	0.47
1:F:489:THR:OG1	1:F:733:ASP:OD1	2.29	0.47
4:S:256:SER:HB2	4:S:297:VAL:HG12	1.96	0.47
4:T:68:GLU:HG2	4:T:74:MET:HG3	1.96	0.47
1:A:410:MET:HB2	1:A:413:ARG:HB2	1.97	0.47
1:G:1004:LYS:HE3	1:H:517:ASN:ND2	2.29	0.47
1:G:720:THR:OG1	1:G:721:MET:N	2.47	0.47
3:L:24:GLU:HB2	3:L:28:LYS:HZ3	1.79	0.47
4:T:65:LEU:CD2	4:T:65:LEU:N	2.76	0.47
1:A:1129:THR:HG22	4:U:122:ASN:HD21	1.78	0.47
1:A:255:LEU:HD22	5:W:162:ILE:HD12	143.70	0.47
5:W:82:PRO:HB2	5:W:295:LYS:CB	2.44	0.47
5:7:268:ILE:HD11	5:7:271:LEU:HD12	1.96	0.47
1:C:1112:VAL:HG23	1:C:1114:ILE:HG12	1.95	0.47
1:C:859:LEU:C	1:C:861:TYR:N	2.66	0.47
1:E:937:LEU:HD21	1:E:950:PHE:HE1	1.79	0.47
1:F:315:ALA:HB2	1:F:321:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1087:ILE:HA	1:G:1148:ILE:HB	1.95	0.47
1:G:323:ALA:HB1	1:G:345:ILE:HG12	1.96	0.47
1:G:61:ILE:CG2	1:H:98:PRO:HB3	2.44	0.47
4:U:75:LEU:HG	4:U:173:LEU:HD11	1.95	0.47
4:V:299:VAL:HG11	5:Z:264:MET:HE1	1.95	0.47
4:5:54:ILE:HD12	4:5:159:GLN:HB3	1.96	0.47
1:C:321:ILE:O	1:C:321:ILE:HG23	2.13	0.47
1:D:820:CYS:O	1:D:824:ASN:HB2	2.15	0.47
1:E:1035:ILE:HG13	1:E:1059:SER:HB3	1.95	0.47
1:E:410:MET:CE	1:E:1309:LEU:HD22	2.45	0.47
1:F:1082:ASP:HB3	1:F:1146:GLN:HB3	1.96	0.47
1:G:693:ASN:HB2	1:H:507:LYS:HZ1	1.80	0.47
1:G:48:ILE:HD13	1:H:316:ILE:HG12	1.97	0.47
5:W:295:LYS:HZ3	5:W:296:ASN:CB	2.27	0.47
1:B:536:PHE:HD1	1:B:992:LEU:HB3	1.79	0.47
1:B:715:CYS:HA	1:B:783:PHE:CE2	2.50	0.47
1:B:831:LEU:HD11	1:B:907:LEU:HD21	1.97	0.47
1:A:583:LYS:NZ	1:B:974:PHE:O	2.48	0.47
1:D:78:ILE:HG12	1:D:303:GLY:HA3	1.96	0.47
1:D:542:ILE:O	1:D:548:THR:O	2.31	0.47
1:D:860:ILE:HG23	1:D:861:TYR:CD2	2.48	0.47
1:E:990:SER:OG	1:E:1000:GLN:NE2	2.48	0.47
1:E:557:MET:HA	1:E:991:LYS:HA	1.97	0.47
1:F:201:VAL:HG21	1:F:207:LEU:CB	2.45	0.47
1:G:809:PHE:O	1:G:810:TYR:HB3	2.15	0.47
4:S:75:LEU:HD12	4:S:93:LEU:HD22	1.96	0.47
4:U:120:VAL:CG1	4:U:121:ASP:N	2.77	0.47
4:U:51:ASN:O	4:U:163:TYR:OH	2.32	0.47
5:X:179:PRO:O	5:X:180:ASP:HB3	2.13	0.47
5:6:27:VAL:HA	5:6:67:THR:O	2.13	0.47
1:B:565:LEU:HD13	1:B:1209:TRP:HH2	1.80	0.47
1:E:152:LEU:HG	1:G:740:ASN:ND2	109.77	0.47
1:F:229:PHE:HB3	1:F:1074:ALA:HA	1.96	0.47
1:G:72:ALA:HA	1:G:75:ALA:HB3	1.96	0.47
1:G:860:ILE:CG2	3:P:78:ALA:HB3	2.44	0.47
1:G:925:ILE:O	1:G:928:THR:OG1	2.29	0.47
1:H:693:ASN:OD1	1:I:945:ARG:NH1	2.47	0.47
1:I:345:ILE:HG13	1:I:345:ILE:H	1.53	0.47
1:E:815:ILE:HG23	3:N:39:LEU:HD21	1.97	0.47
1:G:755:MET:HB3	3:P:68:ALA:HA	1.96	0.47
3:R:24:GLU:HB2	3:R:28:LYS:HZ3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:35:VAL:HG12	4:U:37:LYS:N	2.30	0.47
5:Y:8:PHE:HA	5:Y:39:SER:HB3	1.96	0.47
1:B:72:ALA:HA	1:B:75:ALA:HB3	1.97	0.47
1:B:488:PRO:HG3	1:B:870:GLU:HG3	1.96	0.47
1:C:209:ARG:HH22	1:C:1180:ASP:HB2	1.80	0.47
1:F:1015:ARG:NH1	1:F:1084:GLY:O	2.48	0.47
1:F:513:LYS:NZ	1:F:532:GLU:OE2	2.32	0.47
1:A:974:PHE:O	1:F:583:LYS:NZ	2.47	0.47
3:J:27:LYS:HE3	3:J:28:LYS:CE	2.45	0.47
3:J:66:LYS:HD3	3:J:66:LYS:HA	1.73	0.47
4:T:78:ARG:O	4:T:137:VAL:HA	2.14	0.47
4:T:77:TYR:HB3	4:T:137:VAL:HG22	1.96	0.47
4:V:118:SER:O	4:V:122:ASN:ND2	2.48	0.47
4:V:51:ASN:O	4:V:163:TYR:OH	2.32	0.47
5:W:178:LEU:HD12	5:W:181:ILE:HD11	1.97	0.47
1:A:1220:LEU:O	1:A:1221:TYR:CE1	2.63	0.47
1:A:815:ILE:HG22	3:J:39:LEU:HD21	1.97	0.47
1:C:635:SER:O	1:C:639:ASN:HB2	2.15	0.47
1:C:730:ILE:HG12	1:C:871:VAL:HG22	1.97	0.47
1:D:271:GLY:H	1:D:1029:ARG:HB3	1.80	0.47
1:D:662:ASP:HA	1:D:665:ILE:HG22	1.96	0.47
1:E:1223:THR:HA	1:E:1226:ARG:HB3	1.97	0.47
1:E:176:ILE:HG21	1:E:375:VAL:HG21	1.97	0.47
1:E:471:THR:OG1	1:E:472:GLY:N	2.47	0.47
1:A:945:ARG:HH22	1:F:693:ASN:HD21	1.62	0.47
1:F:904:ILE:HG21	1:F:911:TYR:HD2	1.80	0.47
1:F:952:LEU:HB2	1:F:957:ALA:HB2	1.96	0.47
1:G:599:SER:HB3	1:G:644:LEU:H	1.80	0.47
1:I:691:ASN:HA	1:I:702:VAL:HG22	1.97	0.47
1:B:815:ILE:CG2	3:K:39:LEU:HD21	2.41	0.47
4:V:75:LEU:HG	4:V:173:LEU:HD11	1.95	0.47
4:V:31:LEU:N	4:V:31:LEU:CD1	2.73	0.47
1:G:1044:GLU:CD	5:W:1:MET:HE3	2.27	0.47
4:5:75:LEU:HG	4:5:173:LEU:HD11	1.96	0.47
1:B:229:PHE:HB3	1:B:1074:ALA:HA	1.96	0.47
1:D:1094:PHE:HB3	1:D:1097:HIS:HD2	1.79	0.47
1:E:251:THR:HA	1:G:19:ILE:HG21	1.96	0.47
1:E:97:LEU:HD11	1:G:23:ILE:CG1	2.45	0.47
1:G:1092:SER:O	1:G:1232:ASN:ND2	2.48	0.47
1:H:634:ILE:HG12	1:H:645:LEU:HB3	1.96	0.47
1:I:1221:TYR:HB2	1:I:1243:PHE:HD2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:647:CYS:HA	1:I:653:ILE:HD12	1.96	0.47
4:U:1:MET:O	4:U:1:MET:HG2	5.02	0.47
5:Z:147:ILE:HD11	5:Z:166:LEU:HD22	1.97	0.47
1:A:715:CYS:SG	1:A:779:LYS:HG3	2.55	0.46
1:B:680:ILE:HG22	1:B:777:LEU:HD22	1.98	0.46
1:C:1082:ASP:HB3	1:C:1146:GLN:HB3	1.97	0.46
1:D:1044:GLU:HB2	5:Z:1:MET:N	2.30	0.46
1:D:842:GLY:O	1:D:843:TYR:CD1	2.68	0.46
1:D:900:LEU:HD11	1:D:904:ILE:HD12	1.95	0.46
1:A:517:ASN:HD22	1:F:1004:LYS:HE3	1.73	0.46
1:F:810:TYR:CD1	1:F:815:ILE:HD11	2.51	0.46
1:G:1040:THR:OG1	1:G:1055:THR:OG1	2.33	0.46
1:G:439:ARG:NE	1:G:441:ASP:OD1	2.42	0.46
1:A:433:LYS:NZ	1:B:214:ASN:OD1	2.48	0.46
1:B:429:PHE:CD2	1:B:1307:GLN:HG3	2.50	0.46
1:C:626:LEU:HD21	1:C:855:LEU:HA	1.96	0.46
1:D:142:THR:OG1	1:D:144:LYS:O	2.33	0.46
1:E:534:HIS:HE1	1:E:1216:LEU:HD13	1.80	0.46
1:H:756:ASN:OD1	3:Q:64:VAL:O	2.34	0.46
4:U:241:LEU:HA	4:U:241:LEU:HD22	1.73	0.46
4:U:253:TYR:HA	4:U:299:VAL:HG22	1.98	0.46
5:W:224:LEU:H	5:W:224:LEU:CD2	1.97	0.46
5:Y:1:MET:C	5:Y:1:MET:SD	2.94	0.46
1:A:99:ARG:HD2	1:A:109:PRO:HB2	1.97	0.46
1:B:280:ILE:HD12	1:B:371:HIS:HB3	1.98	0.46
1:B:756:ASN:OD1	3:K:65:ASP:CB	2.57	0.46
1:C:651:GLU:O	1:C:655:LEU:HB2	2.16	0.46
1:C:723:ARG:NH2	1:D:938:ASN:OD1	2.48	0.46
1:E:446:LEU:HA	1:E:449:VAL:HG12	1.96	0.46
1:E:743:ARG:HH21	1:E:762:VAL:HG11	1.80	0.46
1:H:54:LEU:HB2	1:I:91:VAL:CG1	2.32	0.46
1:I:1223:THR:H	1:I:1244:THR:HG22	1.80	0.46
1:E:860:ILE:HD12	3:N:75:ARG:HB2	1.97	0.46
4:S:203:GLU:HB2	4:S:240:PHE:HE1	1.80	0.46
5:X:54:TYR:HD2	5:X:144:LEU:HD21	1.81	0.46
1:A:691:ASN:HA	1:A:702:VAL:HG22	1.98	0.46
1:B:1154:THR:HG22	1:B:1209:TRP:HZ3	1.79	0.46
1:B:50:PHE:CD2	1:C:321:ILE:HB	2.50	0.46
1:B:54:LEU:HB2	1:C:91:VAL:HG12	1.96	0.46
1:E:151:ILE:HA	1:F:337:GLN:HE22	1.80	0.46
1:G:182:THR:HA	1:G:185:ARG:HE	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:471:THR:O	1:G:475:PHE:CB	2.58	0.46
1:H:271:GLY:H	1:H:1029:ARG:HB3	1.79	0.46
1:H:700:PRO:HG3	1:I:941:PRO:HB2	1.98	0.46
3:L:24:GLU:O	3:L:28:LYS:HG2	2.16	0.46
4:U:77:TYR:HB3	4:U:137:VAL:HG22	1.97	0.46
1:H:1130:PHE:CD1	4:V:119:MET:SD	3.09	0.46
5:W:32:ALA:HB1	5:W:34:HIS:CD2	2.51	0.46
5:Y:6:CYS:HB3	5:Y:77:LEU:HB3	1.98	0.46
1:A:209:ARG:HH22	1:A:1180:ASP:HB2	1.81	0.46
1:B:1087:ILE:HA	1:B:1148:ILE:HB	1.96	0.46
1:D:280:ILE:HD12	1:D:371:HIS:HB3	1.97	0.46
1:D:3:ASN:ND2	1:E:317:ALA:O	2.48	0.46
1:D:87:THR:HG22	1:D:88:LEU:HG	1.98	0.46
1:D:945:ARG:HE	1:D:947:ASP:HB2	1.78	0.46
1:E:1135:LYS:HD2	1:E:1278:TYR:OH	2.15	0.46
1:G:1036:LEU:HD12	1:G:1036:LEU:O	2.16	0.46
1:H:959:GLU:OE2	1:H:966:THR:OG1	2.29	0.46
1:I:727:ASN:OD1	1:I:727:ASN:N	2.47	0.46
1:I:489:THR:OG1	1:I:733:ASP:OD1	2.26	0.46
3:M:24:GLU:HB2	3:M:28:LYS:HZ3	1.81	0.46
1:G:1132:GLY:HA2	4:S:185:TRP:CZ2	2.51	0.46
4:V:117:ASN:H	4:V:120:VAL:CG1	2.27	0.46
5:Z:136:ILE:HD12	5:Z:171:TYR:HB3	1.97	0.46
1:C:696:LEU:HD23	1:C:1104:ILE:HG12	1.98	0.46
1:D:54:LEU:HD22	1:E:345:ILE:HG12	1.97	0.46
1:E:633:CYS:O	1:E:637:TRP:HB2	2.15	0.46
1:E:162:ARG:HD2	1:F:96:GLN:OE1	2.16	0.46
1:G:1112:VAL:HG23	1:G:1114:ILE:HG12	1.98	0.46
1:H:1014:VAL:HG23	1:H:1149:CYS:HB3	1.97	0.46
1:H:1010:ALA:N	1:H:1153:LEU:O	2.45	0.46
1:I:271:GLY:H	1:I:1029:ARG:HB3	1.81	0.46
1:I:295:VAL:HG22	1:I:356:LYS:HG2	1.98	0.46
1:H:53:LEU:HD22	1:I:322:MET:SD	2.55	0.46
4:U:86:PRO:O	4:U:87:LYS:C	2.54	0.46
4:5:77:TYR:HB3	4:5:137:VAL:HG22	1.97	0.46
5:7:215:ARG:HG2	5:7:216:LEU:HG	1.97	0.46
1:A:283:LEU:HD23	1:A:286:ILE:HD11	1.98	0.46
1:F:518:VAL:HG12	1:F:564:PRO:HA	1.95	0.46
1:E:663:GLU:CD	1:F:640:MET:HG3	2.36	0.46
1:G:1082:ASP:HB3	1:G:1146:GLN:HB3	1.96	0.46
1:G:745:ARG:HH11	1:G:766:ASP:H	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:904:ILE:HG21	1:G:911:TYR:HD2	1.79	0.46
4:V:223:ASP:OD1	4:V:296:LYS:NZ	2.39	0.46
5:W:223:MET:O	5:W:226:ILE:HB	2.16	0.46
5:Z:4:VAL:HG12	5:Z:37:ILE:HG12	1.97	0.46
5:7:1:MET:C	5:7:1:MET:SD	2.94	0.46
1:C:617:HIS:CG	1:C:863:ASN:HD21	2.34	0.46
1:D:46:TYR:CD2	1:G:138:HIS:HD2	2.33	0.46
1:E:820:CYS:O	1:E:824:ASN:CB	2.64	0.46
3:Q:24:GLU:HB2	3:Q:28:LYS:HZ3	1.81	0.46
3:Q:66:LYS:HA	3:Q:66:LYS:HD3	1.73	0.46
3:R:46:HIS:CG	3:R:47:PRO:HD2	2.51	0.46
1:E:1127:ILE:HG23	4:S:83:VAL:HG22	1.95	0.46
5:X:248:ALA:O	5:X:250:ASP:N	2.48	0.46
5:X:87:GLN:HA	5:X:293:ILE:HA	1.98	0.46
5:X:8:PHE:HB2	5:X:75:ASN:HD21	1.80	0.46
4:5:197:VAL:HG22	4:5:214:VAL:HG22	1.98	0.46
1:C:542:ILE:O	1:C:549:GLU:HB3	2.15	0.46
1:C:151:ILE:HD11	1:D:332:ALA:HB1	1.97	0.46
1:E:745:ARG:NH2	1:E:863:ASN:OD1	2.49	0.46
1:A:332:ALA:HB1	1:F:151:ILE:HD11	1.98	0.46
1:F:542:ILE:O	1:F:548:THR:O	2.33	0.46
1:G:1004:LYS:HD2	1:H:517:ASN:HD21	1.80	0.46
1:G:1036:LEU:C	1:G:1036:LEU:HD12	2.37	0.46
1:I:891:GLN:HE21	1:I:963:TRP:HD1	1.64	0.46
1:D:806:LEU:HD11	3:M:67:THR:HG23	1.97	0.46
4:V:77:TYR:HB3	4:V:137:VAL:HG22	1.97	0.46
5:X:295:LYS:HD3	5:X:296:ASN:O	2.13	0.46
3:1:46:HIS:CG	3:1:47:PRO:HD2	2.51	0.46
5:6:150:ILE:HG21	5:6:162:ILE:HG21	1.98	0.46
1:A:485:ARG:NH2	1:A:872:GLU:OE2	2.48	0.46
1:C:393:PHE:HB3	1:C:1301:LEU:HD22	1.97	0.46
1:F:831:LEU:HD11	1:F:907:LEU:HD21	1.98	0.46
1:G:254:ILE:HG12	1:G:1063:MET:HB3	1.98	0.46
1:G:962:ASN:O	1:G:965:ARG:NH1	2.48	0.46
1:H:1154:THR:OG1	1:H:1157:THR:OG1	2.31	0.46
1:I:617:HIS:CG	1:I:863:ASN:HD21	2.34	0.46
3:M:46:HIS:CG	3:M:47:PRO:HD2	2.51	0.46
3:N:46:HIS:CG	3:N:47:PRO:HD2	2.51	0.46
1:F:821:PHE:CE2	3:O:81:ARG:HD3	2.49	0.46
3:P:46:HIS:CG	3:P:47:PRO:HD2	2.51	0.46
1:A:1130:PHE:HE2	4:U:86:PRO:HG2	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:46:HIS:CG	3:2:47:PRO:HD2	2.51	0.45
1:A:1220:LEU:O	1:A:1221:TYR:CG	2.61	0.45
1:B:720:THR:OG1	1:B:721:MET:N	2.48	0.45
1:B:713:LEU:CD1	1:B:783:PHE:CE2	2.96	0.45
1:C:1315:LYS:HE2	1:D:1323:GLU:HG2	1.97	0.45
1:F:202:HIS:HD2	1:F:204:LYS:HB2	1.81	0.45
1:G:1221:TYR:HB2	1:G:1243:PHE:HD2	1.81	0.45
1:H:1096:ILE:HG21	1:H:1230:CYS:HB3	1.98	0.45
3:J:25:GLU:OE1	3:J:25:GLU:HA	2.16	0.45
1:D:810:TYR:HH	3:M:36:VAL:HG12	1.81	0.45
4:V:185:TRP:CE3	4:V:186:GLU:HB2	2.51	0.45
5:Z:5:TYR:O	5:Z:37:ILE:N	2.44	0.45
1:C:1160:ILE:HG23	1:C:1164:LYS:HD2	1.97	0.45
1:C:859:LEU:HD21	1:C:862:ILE:HG12	1.98	0.45
1:D:1223:THR:HG22	1:D:1226:ARG:HD2	1.97	0.45
1:D:820:CYS:O	1:D:824:ASN:CB	2.64	0.45
1:D:891:GLN:HE21	1:D:963:TRP:HD1	1.64	0.45
1:E:209:ARG:HH22	1:E:1180:ASP:HB2	1.82	0.45
1:E:631:SER:HB3	1:E:664:LEU:HB3	1.97	0.45
1:E:1315:LYS:CE	1:F:1323:GLU:HG2	2.46	0.45
1:G:809:PHE:CZ	1:G:859:LEU:HD11	2.51	0.45
1:H:1040:THR:OG1	1:H:1055:THR:OG1	2.34	0.45
1:H:752:VAL:HG11	3:Q:69:PHE:CZ	2.52	0.45
3:L:66:LYS:HA	3:L:66:LYS:HD3	1.73	0.45
3:Q:46:HIS:CG	3:Q:47:PRO:HD2	2.51	0.45
1:A:345:ILE:CD1	1:F:54:LEU:HB3	2.45	0.45
1:A:345:ILE:HG13	1:A:345:ILE:H	1.58	0.45
1:B:1082:ASP:HB3	1:B:1146:GLN:HB3	1.98	0.45
1:C:491:ILE:HD11	1:C:868:ILE:HG21	1.99	0.45
1:E:467:GLU:OE1	1:E:533:ARG:NH1	2.48	0.45
1:E:680:ILE:HD11	1:E:781:PHE:HD2	1.80	0.45
1:G:1015:ARG:NH1	1:G:1084:GLY:O	2.49	0.45
1:G:229:PHE:HB3	1:G:1074:ALA:HA	1.97	0.45
1:H:1245:GLU:HA	1:H:1248:ILE:HG22	1.98	0.45
3:O:30:GLN:O	3:O:34:THR:HG23	2.17	0.45
4:S:53:ARG:HG2	4:S:163:TYR:CZ	2.51	0.45
4:V:253:TYR:HA	4:V:299:VAL:HG22	1.98	0.45
5:W:210:ARG:HE	5:W:242:ARG:HH21	1.62	0.45
5:Z:234:LYS:HB3	5:Z:234:LYS:HE3	1.83	0.45
4:5:256:SER:HB2	4:5:297:VAL:HG12	1.98	0.45
5:7:7:THR:HG22	5:7:76:GLN:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:415:LYS:HZ1	1:E:1326:TYR:HH	1.61	0.45
1:E:1135:LYS:CD	1:E:1278:TYR:OH	2.65	0.45
1:E:876:ASP:OD1	1:E:876:ASP:N	2.48	0.45
1:D:162:ARG:NH2	1:E:96:GLN:OE1	2.50	0.45
1:F:1087:ILE:HA	1:F:1148:ILE:HB	1.97	0.45
1:F:1230:CYS:SG	1:F:1231:TYR:N	2.88	0.45
1:F:543:GLN:HE22	1:F:548:THR:HG22	1.81	0.45
1:G:136:LEU:HD11	4:S:15:VAL:HG22	1.99	0.45
1:H:1082:ASP:HB3	1:H:1146:GLN:HB3	1.98	0.45
1:H:1269:CYS:HB3	1:H:1281:SER:HA	1.98	0.45
1:I:78:ILE:O	1:I:1035:ILE:HA	2.16	0.45
3:L:46:HIS:CG	3:L:47:PRO:HD2	2.51	0.45
3:P:30:GLN:O	3:P:34:THR:HG23	2.17	0.45
3:Q:24:GLU:O	3:Q:28:LYS:NZ	2.49	0.45
4:S:26:ILE:HG22	4:S:28:ALA:H	1.79	0.45
3:4:30:GLN:O	3:4:34:THR:HG23	2.17	0.45
1:D:498:LEU:HG	1:D:954:PRO:HG2	1.97	0.45
1:D:859:LEU:HD11	1:D:862:ILE:CG2	2.47	0.45
1:F:63:TRP:CZ3	1:F:169:ASP:HB2	2.51	0.45
1:D:46:TYR:CD2	1:G:138:HIS:CD2	3.04	0.45
1:G:809:PHE:CE2	3:P:74:ILE:CG2	2.99	0.45
1:H:393:PHE:HD2	1:H:1015:ARG:HH21	1.64	0.45
3:J:27:LYS:CE	3:J:28:LYS:NZ	2.78	0.45
3:Q:30:GLN:O	3:Q:34:THR:HG23	2.17	0.45
1:I:756:ASN:ND2	3:R:64:VAL:HB	2.23	0.45
5:X:178:LEU:CD2	5:X:178:LEU:N	2.77	0.45
3:4:66:LYS:HD3	3:4:66:LYS:HA	1.73	0.45
1:A:968:PHE:HE1	1:A:988:MET:HB3	1.82	0.45
1:B:962:ASN:O	1:B:965:ARG:NH1	2.45	0.45
1:E:294:GLN:HE21	1:E:359:THR:HG21	1.82	0.45
1:E:328:PHE:HD1	1:G:11:PRO:HD2	1.81	0.45
1:G:542:ILE:HD13	1:G:551:LEU:HD22	1.98	0.45
1:G:757:LEU:HD23	1:G:760:SER:HB3	1.98	0.45
1:G:127:ILE:HG12	1:H:101:ALA:HB2	1.99	0.45
3:K:30:GLN:O	3:K:34:THR:HG23	2.17	0.45
5:X:8:PHE:HA	5:X:39:SER:HB3	1.99	0.45
5:6:11:LYS:HD3	5:6:11:LYS:HA	1.80	0.45
1:A:225:THR:O	1:A:232:ARG:NH1	2.50	0.45
1:A:230:LEU:HD23	1:A:1074:ALA:HB1	1.99	0.45
1:B:599:SER:HB3	1:B:644:LEU:H	1.81	0.45
1:C:1245:GLU:HA	1:C:1248:ILE:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:968:PHE:HE1	1:C:988:MET:HB3	1.80	0.45
1:D:584:THR:HG21	1:D:685:ARG:HD2	1.99	0.45
1:H:617:HIS:CG	1:H:863:ASN:HD21	2.35	0.45
3:N:66:LYS:HD3	3:N:66:LYS:HA	1.73	0.45
4:T:53:ARG:HG2	4:T:163:TYR:CZ	2.52	0.45
4:T:66:ALA:CB	4:T:67:PRO:CD	2.93	0.45
1:F:1129:THR:HG21	5:X:224:LEU:HD11	1.98	0.45
5:Z:14:LEU:HA	5:Z:17:ILE:HG22	1.97	0.45
1:D:255:LEU:HD22	5:Z:162:ILE:HD12	71.59	0.45
5:6:192:LYS:HG3	5:7:224:LEU:HD22	1.99	0.45
5:7:104:LEU:HB2	5:7:278:PHE:HB2	1.98	0.45
1:A:54:LEU:HA	1:B:323:ALA:CB	2.46	0.45
1:B:1040:THR:OG1	1:B:1055:THR:OG1	2.35	0.45
1:B:714:PHE:CD2	1:B:871:VAL:HG11	2.51	0.45
1:B:857:LYS:HE3	3:K:82:LEU:HA	1.97	0.45
1:E:1143:HIS:HD2	1:F:1199:SER:OG	1.99	0.45
1:G:162:ARG:NH1	1:H:96:GLN:HE22	2.14	0.45
1:G:311:ASN:HB3	1:G:321:ILE:HD12	1.99	0.45
1:G:542:ILE:O	1:G:548:THR:O	2.35	0.45
1:H:745:ARG:NH2	1:H:863:ASN:OD1	2.49	0.45
1:H:93:PHE:HD2	1:H:1065:LEU:HD21	1.82	0.45
1:I:255:LEU:CD1	1:I:1030:ALA:HB1	2.45	0.45
3:J:30:GLN:O	3:J:34:THR:HG23	2.17	0.45
3:J:46:HIS:CG	3:J:47:PRO:HD2	2.52	0.45
3:L:30:GLN:O	3:L:34:THR:HG23	2.17	0.45
3:N:23:LYS:N	3:N:25:GLU:OE1	2.50	0.45
5:W:278:PHE:CZ	5:W:295:LYS:HE3	2.51	0.45
4:5:195:VAL:HG22	4:5:216:LEU:HG	1.99	0.45
1:A:1189:LYS:NZ	1:A:1193:ASP:OD2	2.42	0.45
1:B:631:SER:HB3	1:B:664:LEU:HB3	1.99	0.45
1:C:691:ASN:HA	1:C:702:VAL:HG22	1.99	0.45
1:D:126:ASN:HA	1:D:1054:PHE:O	2.16	0.45
1:C:700:PRO:HB3	1:D:942:HIS:HB3	1.99	0.45
1:F:720:THR:OG1	1:F:721:MET:N	2.50	0.45
1:F:821:PHE:O	1:F:821:PHE:CD1	2.70	0.45
1:H:483:ILE:HG13	1:H:483:ILE:H	1.70	0.45
1:H:529:LEU:HD23	1:H:529:LEU:HA	1.82	0.45
1:G:129:PHE:HB3	1:H:99:ARG:HH22	1.81	0.45
1:I:542:ILE:O	1:I:549:GLU:HB3	2.17	0.45
3:3:30:GLN:O	3:3:34:THR:HG23	2.17	0.45
1:A:758:ILE:HG22	1:A:864:GLU:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:ALA:HB3	1:C:89:GLY:HA2	1.98	0.45
1:C:90:LYS:HE2	1:C:92:LEU:HD11	1.98	0.45
1:D:23:ILE:HD13	1:H:95:ILE:HG21	1.98	0.45
1:D:810:TYR:CE2	3:M:37:LEU:CG	2.99	0.45
1:E:1110:HIS:CE1	1:F:473:HIS:CE1	3.04	0.45
1:F:637:TRP:CD1	1:F:645:LEU:HB2	2.52	0.45
1:G:1129:THR:HG22	1:G:1230:CYS:SG	2.57	0.45
1:I:1096:ILE:HD13	1:I:1125:LEU:HD21	1.98	0.45
1:I:755:MET:SD	3:R:71:LEU:HB3	2.57	0.45
1:I:745:ARG:NH2	1:I:863:ASN:OD1	2.50	0.45
4:S:191:SER:OG	4:S:192:THR:N	2.48	0.45
4:T:202:LYS:HA	4:T:240:PHE:CZ	2.52	0.45
5:W:66:VAL:CG2	5:W:295:LYS:HZ2	2.30	0.45
5:X:279:VAL:O	5:X:292:CYS:SG	2.74	0.45
3:1:30:GLN:O	3:1:34:THR:HG23	2.17	0.44
3:2:30:GLN:O	3:2:34:THR:HG23	2.17	0.44
3:3:46:HIS:CG	3:3:47:PRO:HD2	2.51	0.44
1:A:435:GLN:HE21	1:A:1338:GLN:HE21	1.63	0.44
1:B:387:GLN:NE2	1:B:1023:CYS:SG	2.91	0.44
1:C:1170:ARG:NH1	1:C:1211:SER:OG	2.50	0.44
1:D:617:HIS:CG	1:D:863:ASN:HD21	2.35	0.44
1:D:843:TYR:CD2	1:D:843:TYR:O	2.70	0.44
1:E:263:SER:OG	1:E:264:LYS:N	2.48	0.44
1:E:781:PHE:C	1:E:781:PHE:CD1	2.90	0.44
1:F:429:PHE:CD2	1:F:1307:GLN:HG3	2.52	0.44
1:F:280:ILE:HD12	1:F:371:HIS:HB3	1.99	0.44
1:G:522:TYR:HE1	1:G:1208:PRO:HD3	1.81	0.44
1:I:816:CYS:HB3	1:I:820:CYS:HB3	1.97	0.44
4:T:83:VAL:CG1	4:T:86:PRO:HD2	2.47	0.44
4:V:195:VAL:HG22	4:V:216:LEU:HG	1.98	0.44
5:W:295:LYS:HZ1	5:W:296:ASN:HB2	1.83	0.44
1:B:1145:GLN:NE2	1:B:1274:SER:O	2.35	0.44
1:D:859:LEU:CD1	1:D:862:ILE:HG23	2.47	0.44
1:D:155:ASN:HB3	1:G:45:ARG:HH12	1.82	0.44
1:H:176:ILE:HG21	1:H:375:VAL:HG21	1.99	0.44
1:H:553:THR:HG23	1:H:887:PHE:CE1	2.53	0.44
1:H:584:THR:HG21	1:H:685:ARG:HD2	2.00	0.44
1:I:543:GLN:HE22	1:I:548:THR:HG22	1.82	0.44
3:K:46:HIS:CG	3:K:47:PRO:HD2	2.51	0.44
1:H:860:ILE:HG22	3:Q:78:ALA:HB3	1.98	0.44
4:T:234:GLU:HG3	4:T:235:LYS:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:U:35:VAL:CG1	4:U:36:GLU:N	2.80	0.44
4:V:31:LEU:CD2	4:V:33:ASN:N	2.72	0.44
5:W:224:LEU:N	5:W:224:LEU:CD1	2.73	0.44
5:X:244:GLY:O	5:X:245:GLN:CG	2.65	0.44
5:Z:5:TYR:HB2	5:Z:36:LEU:HD13	2.00	0.44
5:7:43:GLY:O	5:7:127:THR:O	2.35	0.44
1:B:543:GLN:HE22	1:B:548:THR:HG22	1.82	0.44
1:E:918:ARG:HG3	1:E:969:SER:HB3	2.00	0.44
1:F:815:ILE:HA	1:F:815:ILE:HD12	1.78	0.44
1:G:129:PHE:HZ	1:G:164:LEU:HD23	1.83	0.44
1:H:315:ALA:HB2	1:H:321:ILE:HD11	2.00	0.44
1:H:758:ILE:O	1:H:865:ASN:ND2	2.50	0.44
1:I:802:LYS:NZ	3:R:67:THR:HB	2.32	0.44
1:B:810:TYR:HH	3:K:37:LEU:HB2	1.76	0.44
3:M:30:GLN:O	3:M:34:THR:HG23	2.17	0.44
3:O:46:HIS:CG	3:O:47:PRO:HD2	2.51	0.44
4:U:195:VAL:HG22	4:U:216:LEU:HG	1.98	0.44
1:A:1126:ASN:OD1	4:U:83:VAL:CG2	2.65	0.44
4:V:241:LEU:N	4:V:241:LEU:HD23	2.32	0.44
5:W:14:LEU:HA	5:W:17:ILE:HG22	2.00	0.44
5:Y:14:LEU:HA	5:Y:17:ILE:HG22	1.98	0.44
5:6:201:ILE:O	5:6:205:ALA:HB2	2.17	0.44
1:A:263:SER:OG	1:A:264:LYS:N	2.49	0.44
1:C:20:PHE:HB3	1:C:23:ILE:HD11	1.98	0.44
1:D:859:LEU:O	1:D:860:ILE:C	2.55	0.44
1:F:526:ASN:HB3	1:F:529:LEU:HG	2.00	0.44
1:G:53:LEU:HD12	1:G:53:LEU:HA	1.78	0.44
1:H:274:LEU:HA	1:H:370:ASP:O	2.17	0.44
5:Y:221:HIS:HA	5:Y:225:LEU:HD23	1.99	0.44
3:4:46:HIS:CG	3:4:47:PRO:HD2	2.51	0.44
5:7:20:LEU:HD11	5:7:119:LEU:HD11	1.99	0.44
1:A:860:ILE:HG22	3:J:75:ARG:O	2.18	0.44
1:F:1097:HIS:HE1	1:F:1229:LEU:HD22	1.83	0.44
1:F:558:ILE:HD11	1:F:1008:GLY:HA3	2.00	0.44
1:G:1269:CYS:HB3	1:G:1281:SER:HA	2.00	0.44
1:G:558:ILE:HD11	1:G:1008:GLY:HA3	1.98	0.44
1:H:142:THR:OG1	1:H:144:LYS:O	2.36	0.44
1:H:446:LEU:HA	1:H:449:VAL:HG12	1.99	0.44
1:H:860:ILE:HG22	3:Q:75:ARG:O	2.16	0.44
1:H:758:ILE:HG22	1:H:864:GLU:HA	1.99	0.44
3:R:30:GLN:O	3:R:34:THR:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Y:170:GLN:HE21	5:Y:173:ASP:HA	1.82	0.44
1:B:63:TRP:CZ3	1:B:169:ASP:HB2	2.53	0.44
1:C:1212:LEU:CD1	1:C:1212:LEU:H	2.31	0.44
1:B:1275:GLU:OE2	1:C:209:ARG:HD2	2.16	0.44
1:D:1053:ASN:HD21	5:Z:35:HIS:CG	2.36	0.44
1:D:436:VAL:HG22	1:E:1165:LEU:HD13	1.99	0.44
1:E:534:HIS:CE1	1:E:1216:LEU:HD13	2.53	0.44
1:I:540:THR:OG1	1:I:541:TYR:N	2.50	0.44
1:I:779:LYS:O	1:I:783:PHE:HB2	2.18	0.44
5:W:242:ARG:H	5:W:242:ARG:HD2	1.83	0.44
4:5:58:VAL:O	4:5:153:LEU:HA	2.18	0.44
4:5:245:ILE:HD11	5:7:231:LEU:HD13	2.00	0.44
5:7:281:CYS:SG	5:7:282:ASP:N	2.91	0.44
1:A:1223:THR:H	1:A:1244:THR:HG22	1.83	0.44
1:C:171:LEU:HA	1:C:171:LEU:HD23	1.87	0.44
1:C:559:GLY:HA3	1:C:968:PHE:CE1	2.53	0.44
1:D:635:SER:O	1:D:639:ASN:HB2	2.18	0.44
1:F:899:CYS:SG	1:F:900:LEU:N	2.91	0.44
1:G:429:PHE:CD2	1:G:1307:GLN:HG3	2.53	0.44
1:I:1216:LEU:C	1:I:1216:LEU:CD1	2.86	0.44
1:I:532:GLU:OE2	1:I:555:ARG:NH1	2.49	0.44
3:J:27:LYS:C	3:J:27:LYS:CD	2.85	0.44
3:O:24:GLU:O	3:O:28:LYS:NZ	2.51	0.44
4:S:67:PRO:HG2	4:S:68:GLU:HG3	2.00	0.44
5:X:87:GLN:CA	5:X:293:ILE:HG22	2.47	0.44
5:Z:221:HIS:HA	5:Z:225:LEU:HD23	2.00	0.44
1:A:662:ASP:HA	1:A:665:ILE:HG22	2.00	0.44
1:A:723:ARG:HH22	1:B:938:ASN:CG	2.21	0.44
1:C:1207:ASN:HB2	1:C:1210:ALA:HB3	1.99	0.44
1:C:1149:CYS:HB2	1:C:1238:PRO:HD2	2.00	0.44
1:C:209:ARG:NH2	1:C:1180:ASP:HB2	2.33	0.44
1:D:843:TYR:O	1:D:843:TYR:CG	2.70	0.44
1:D:854:GLN:HA	1:D:857:LYS:HE3	2.00	0.44
1:E:414:VAL:O	1:E:414:VAL:HG23	2.16	0.44
1:E:439:ARG:NE	1:E:441:ASP:OD1	2.40	0.44
1:F:273:LEU:HD11	1:F:1024:LEU:HD13	1.99	0.44
1:G:1307:GLN:NE2	1:H:1160:ILE:HD12	2.32	0.44
1:G:436:VAL:HG22	1:H:1165:LEU:CD1	2.48	0.44
4:T:2:ASN:O	4:T:5:SER:HB3	2.18	0.44
5:Z:247:HIS:O	5:Z:247:HIS:ND1	2.51	0.44
1:A:1269:CYS:HB3	1:A:1281:SER:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ILE:HA	1:C:337:GLN:NE2	2.31	0.44
1:B:621:HIS:HB2	1:B:861:TYR:HE2	1.82	0.44
1:C:633:CYS:O	1:C:637:TRP:HB2	2.17	0.44
1:D:1158:THR:HG22	1:D:1161:ASN:H	1.83	0.44
1:D:471:THR:O	1:D:475:PHE:CB	2.63	0.44
1:D:745:ARG:HG3	1:D:764:PHE:HB3	1.99	0.44
1:E:738:THR:CG2	1:H:152:LEU:HD21	124.05	0.44
3:N:30:GLN:O	3:N:34:THR:HG23	2.17	0.44
4:V:240:PHE:HD2	4:V:244:LEU:HD13	1.76	0.44
5:X:147:ILE:HD11	5:X:166:LEU:HD22	1.99	0.44
3:2:39:LEU:HD22	3:2:43:MET:HG2	2.00	0.43
4:5:53:ARG:HG2	4:5:163:TYR:CZ	2.52	0.43
1:A:998:ALA:O	1:A:1001:SER:OG	2.31	0.43
1:B:1034:ILE:HG13	1:B:1060:PHE:HD1	1.72	0.43
1:D:491:ILE:HD11	1:D:868:ILE:HG21	1.99	0.43
1:D:154:ILE:HD13	1:E:334:THR:O	2.17	0.43
1:E:663:GLU:CD	1:F:636:TYR:CE1	2.90	0.43
1:F:429:PHE:CE1	1:F:439:ARG:HG3	2.53	0.43
4:S:223:ASP:OD1	4:S:296:LYS:NZ	2.37	0.43
3:1:66:LYS:HD3	3:1:66:LYS:HA	1.73	0.43
5:6:70:GLN:O	5:6:78:VAL:HB	2.18	0.43
5:7:100:LYS:HE3	5:7:282:ASP:HA	2.00	0.43
1:B:208:SER:HB2	1:B:211:GLN:HG2	2.00	0.43
1:B:3:ASN:ND2	1:C:317:ALA:O	2.51	0.43
1:C:1087:ILE:HG13	1:C:1087:ILE:H	1.59	0.43
1:C:524:PRO:HG3	1:C:1204:ALA:HB2	1.99	0.43
1:C:51:GLU:CD	1:D:90:LYS:HZ1	2.15	0.43
1:E:6:ALA:HA	1:E:10:LEU:HD12	2.00	0.43
1:F:522:TYR:HE1	1:F:1208:PRO:HD3	1.82	0.43
1:F:1269:CYS:HB3	1:F:1281:SER:HA	2.00	0.43
1:F:751:ASP:N	1:F:751:ASP:OD1	2.51	0.43
1:F:925:ILE:O	1:F:928:THR:OG1	2.33	0.43
1:H:70:PRO:HB3	1:H:357:LEU:HD22	2.00	0.43
1:H:945:ARG:HE	1:H:947:ASP:HB2	1.82	0.43
1:I:408:SER:OG	1:I:409:THR:O	2.32	0.43
1:I:645:LEU:O	1:I:673:TYR:OH	2.27	0.43
3:K:39:LEU:HD22	3:K:43:MET:HG2	2.00	0.43
1:C:755:MET:CB	3:L:68:ALA:HB1	2.48	0.43
4:T:134:GLU:O	4:T:295:LYS:NZ	2.51	0.43
5:W:54:TYR:HD2	5:W:144:LEU:HD21	1.82	0.43
5:X:3:THR:HG23	5:X:78:VAL:HG13	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:270:SER:HA	4:5:283:ILE:HD13	2.00	0.43
1:A:600:LEU:HD22	1:A:901:ILE:HD12	1.98	0.43
1:B:556:ILE:HG21	1:B:963:TRP:HZ3	1.81	0.43
1:E:116:VAL:HG12	1:G:35:LEU:HB3	2.00	0.43
1:E:1192:TYR:OH	1:E:1245:GLU:OE1	2.29	0.43
1:F:78:ILE:O	1:F:1035:ILE:HA	2.18	0.43
1:I:47:ASN:OD1	1:I:47:ASN:N	2.51	0.43
3:L:39:LEU:HD22	3:L:43:MET:HG2	2.00	0.43
1:A:1198:ASP:H	1:A:1204:ALA:HA	1.83	0.43
1:A:180:MET:HE1	1:A:1025:LEU:HD22	2.00	0.43
1:B:1159:ASN:HA	1:B:1163:PHE:HD2	1.83	0.43
1:C:1067:PHE:HE2	1:C:1256:TYR:HE1	1.65	0.43
1:C:293:THR:HA	1:C:358:ASN:HA	2.00	0.43
1:E:1126:ASN:O	1:E:1130:PHE:HB3	2.18	0.43
1:E:499:TYR:OH	1:E:953:PRO:HD3	2.18	0.43
1:F:127:ILE:HD13	1:F:127:ILE:HA	1.88	0.43
1:F:202:HIS:CD2	1:F:204:LYS:HG2	2.53	0.43
1:E:94:PHE:HB2	1:G:7:THR:CG2	2.48	0.43
1:H:165:LYS:CG	4:V:38:GLU:OE2	2.66	0.43
1:I:1209:TRP:HB3	1:I:1216:LEU:HG	1.99	0.43
1:I:429:PHE:CD2	1:I:1307:GLN:HG3	2.53	0.43
1:I:220:LYS:HE2	1:I:1297:ASN:HD21	1.82	0.43
1:I:826:ILE:HG12	1:I:848:THR:HG21	2.00	0.43
3:P:24:GLU:HB2	3:P:28:LYS:HZ3	1.83	0.43
1:A:1129:THR:HG22	4:U:122:ASN:ND2	2.33	0.43
4:V:31:LEU:O	4:V:32:ASN:CB	2.67	0.43
5:X:279:VAL:O	5:X:292:CYS:HA	2.18	0.43
3:1:39:LEU:HD22	3:1:43:MET:HG2	2.00	0.43
5:7:97:PRO:O	5:7:172:ARG:NH2	2.52	0.43
1:A:857:LYS:HG2	3:J:81:ARG:O	2.19	0.43
1:B:786:LEU:O	1:B:790:SER:OG	2.30	0.43
1:C:50:PHE:O	1:D:87:THR:N	2.47	0.43
1:E:420:MET:HG3	1:E:576:ASN:HB3	2.01	0.43
1:E:432:ASN:HD22	1:E:436:VAL:HB	1.83	0.43
1:E:1315:LYS:HE3	1:F:1323:GLU:HG2	2.00	0.43
1:G:1325:HIS:CG	1:G:1326:TYR:H	2.36	0.43
1:G:345:ILE:HG13	1:G:345:ILE:H	1.64	0.43
1:G:748:GLU:O	3:P:76:MET:HE1	2.18	0.43
1:H:124:PRO:HG2	1:I:104:ASN:HB2	2.00	0.43
1:H:715:CYS:SG	1:H:779:LYS:HG3	2.59	0.43
1:I:1212:LEU:HD23	1:I:1213:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:488:PRO:HB3	1:I:868:ILE:HB	2.00	0.43
3:J:27:LYS:NZ	3:J:28:LYS:HE3	2.28	0.43
4:S:181:LEU:HD12	4:S:183:PRO:HD3	2.00	0.43
4:V:95:PHE:CE1	4:V:120:VAL:HG23	2.45	0.43
5:7:58:ARG:NH2	5:7:273:ASN:O	2.51	0.43
1:B:49:SER:HB2	1:C:87:THR:OG1	2.19	0.43
1:B:904:ILE:HG21	1:B:911:TYR:HD2	1.83	0.43
1:B:712:ARG:CB	1:B:963:TRP:CZ2	2.98	0.43
1:C:374:LYS:HA	1:C:377:LYS:HG3	1.99	0.43
1:D:1212:LEU:HD23	1:D:1213:PRO:HD2	2.00	0.43
1:D:1313:ARG:HH11	1:D:1323:GLU:HB2	1.83	0.43
1:D:810:TYR:OH	3:M:36:VAL:HG12	2.19	0.43
1:D:48:ILE:HD13	1:E:316:ILE:HG12	2.01	0.43
1:E:662:ASP:OD1	1:F:640:MET:CB	2.67	0.43
1:E:682:LEU:HD23	1:E:682:LEU:HA	1.85	0.43
1:E:97:LEU:CG	1:G:23:ILE:HD11	2.49	0.43
1:G:50:PHE:HA	1:H:319:ARG:O	2.19	0.43
1:G:6:ALA:O	1:G:10:LEU:HB2	2.18	0.43
1:H:1087:ILE:H	1:H:1087:ILE:HG13	1.69	0.43
1:H:54:LEU:HD12	1:I:346:PHE:CZ	2.54	0.43
1:I:696:LEU:HD23	1:I:1104:ILE:HG12	2.01	0.43
1:I:758:ILE:HG22	1:I:864:GLU:HA	2.00	0.43
3:J:39:LEU:HD22	3:J:43:MET:HG2	2.00	0.43
1:H:755:MET:CB	3:Q:68:ALA:CA	2.91	0.43
4:U:197:VAL:HG22	4:U:214:VAL:HG22	2.01	0.43
4:U:2:ASN:HB2	4:U:5:SER:HB3	2.01	0.43
1:A:1198:ASP:OD1	1:A:1199:SER:N	2.52	0.43
1:C:345:ILE:H	1:C:345:ILE:HG13	1.58	0.43
1:D:488:PRO:HG3	1:D:870:GLU:HG3	2.01	0.43
1:F:1245:GLU:HA	1:F:1248:ILE:HG22	2.01	0.43
1:F:916:PHE:HA	1:F:956:LEU:HD13	2.01	0.43
1:G:536:PHE:CD1	1:G:992:LEU:HB3	2.54	0.43
1:H:968:PHE:HE1	1:H:988:MET:HB3	1.84	0.43
3:M:66:LYS:HA	3:M:66:LYS:HD3	1.73	0.43
3:P:24:GLU:O	3:P:28:LYS:NZ	2.51	0.43
4:U:68:GLU:HG2	4:U:74:MET:HG3	2.00	0.43
1:A:467:GLU:OE1	1:A:533:ARG:NH1	2.42	0.43
1:A:935:VAL:HA	1:A:938:ASN:HB2	2.01	0.43
1:B:558:ILE:HD11	1:B:1008:GLY:HA3	2.01	0.43
1:B:916:PHE:HA	1:B:956:LEU:HD13	2.00	0.43
1:F:1223:THR:HA	1:F:1226:ARG:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:755:MET:HB2	3:R:68:ALA:CB	2.44	0.43
3:N:39:LEU:HD22	3:N:43:MET:HG2	2.00	0.43
5:W:279:VAL:O	5:W:292:CYS:HA	2.18	0.43
1:A:257:ASP:OD2	1:A:260:ASN:ND2	2.52	0.43
1:D:968:PHE:HE1	1:D:988:MET:HB3	1.83	0.43
1:E:387:GLN:NE2	1:E:1023:CYS:SG	2.91	0.43
1:E:78:ILE:HB	1:E:1035:ILE:HG22	2.01	0.43
1:E:1135:LYS:CD	1:E:1135:LYS:N	2.81	0.43
1:E:130:ASP:N	1:E:130:ASP:OD1	2.48	0.43
1:F:559:GLY:HA3	1:F:968:PHE:HE1	1.83	0.43
1:H:474:ARG:NH1	1:H:527:PRO:HA	2.33	0.43
1:I:1133:ILE:HG13	1:I:1135:LYS:H	1.83	0.43
1:I:876:ASP:OD1	1:I:876:ASP:N	2.50	0.43
3:M:39:LEU:HD22	3:M:43:MET:HG2	2.00	0.43
3:P:66:LYS:HA	3:P:66:LYS:HD3	1.73	0.43
3:Q:39:LEU:HD22	3:Q:43:MET:HG2	2.00	0.43
4:U:75:LEU:HB2	4:U:93:LEU:HB2	2.01	0.43
4:V:197:VAL:HG22	4:V:214:VAL:HG22	2.01	0.43
4:V:68:GLU:HG2	4:V:74:MET:HG3	2.00	0.43
5:X:295:LYS:CD	5:X:295:LYS:C	2.86	0.43
5:Y:23:LEU:O	5:Y:69:LEU:HD23	2.18	0.43
3:4:39:LEU:HD22	3:4:43:MET:HG2	2.00	0.43
1:A:126:ASN:HA	1:A:1054:PHE:O	2.19	0.43
1:C:274:LEU:HD13	1:C:372:LEU:HD23	2.00	0.43
1:D:748:GLU:O	3:M:76:MET:HE1	2.19	0.43
1:G:498:LEU:HG	1:G:954:PRO:HG2	2.00	0.43
1:H:324:ASP:O	1:H:328:PHE:CB	2.54	0.43
1:H:633:CYS:O	1:H:637:TRP:HB2	2.18	0.43
1:H:415:LYS:NZ	1:I:1326:TYR:OH	2.35	0.43
1:I:73:VAL:HG21	1:I:269:LEU:HD22	2.01	0.43
4:S:200:VAL:O	4:S:211:GLY:N	2.51	0.43
1:A:1130:PHE:HE1	4:U:119:MET:CE	2.30	0.43
5:X:235:ARG:NH2	5:X:235:ARG:O	2.52	0.43
4:5:186:GLU:OE1	4:5:189:GLN:NE2	2.52	0.42
1:A:680:ILE:HG22	1:A:777:LEU:HD22	2.01	0.42
1:B:715:CYS:CB	1:B:716:PRO:CD	2.97	0.42
1:D:645:LEU:O	1:D:673:TYR:OH	2.29	0.42
1:F:960:PHE:O	1:F:965:ARG:NH2	2.51	0.42
1:G:916:PHE:HA	1:G:956:LEU:HD13	2.00	0.42
1:D:25:THR:HG22	1:H:201:VAL:H	1.84	0.42
1:I:1269:CYS:HB3	1:I:1281:SER:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:712:ARG:HH21	1:I:876:ASP:HA	1.83	0.42
1:D:756:ASN:CG	3:M:64:VAL:HB	2.40	0.42
3:R:39:LEU:HD22	3:R:43:MET:HG2	2.00	0.42
5:Z:239:SER:O	5:Z:241:GLN:N	2.52	0.42
5:7:87:GLN:HG2	5:7:293:ILE:HG22	2.00	0.42
1:A:818:ASP:HA	1:A:821:PHE:HB3	2.02	0.42
1:A:820:CYS:SG	1:A:824:ASN:ND2	2.88	0.42
1:E:692:ILE:HB	1:E:701:LEU:HD23	2.00	0.42
1:F:701:LEU:HD21	1:F:999:ILE:HG21	2.01	0.42
1:G:1094:PHE:HB3	1:G:1097:HIS:HD2	1.84	0.42
1:G:637:TRP:CD1	1:G:645:LEU:HB2	2.53	0.42
1:G:714:PHE:CE2	1:G:871:VAL:HG11	2.54	0.42
1:H:127:ILE:HD13	1:H:127:ILE:HA	1.87	0.42
3:O:39:LEU:HD22	3:O:43:MET:HG2	2.00	0.42
4:V:117:ASN:H	4:V:120:VAL:HG13	1.83	0.42
5:W:224:LEU:H	5:W:224:LEU:CD1	2.27	0.42
3:3:39:LEU:HD22	3:3:43:MET:HG2	2.00	0.42
1:B:271:GLY:H	1:B:1029:ARG:HB3	1.83	0.42
1:B:511:VAL:HA	1:B:966:THR:HG21	2.01	0.42
1:C:820:CYS:O	1:C:824:ASN:CB	2.57	0.42
1:D:1145:GLN:NE2	1:D:1273:ASP:O	2.52	0.42
1:C:54:LEU:N	1:D:90:LYS:O	2.29	0.42
1:E:410:MET:HE1	1:E:1309:LEU:HD22	2.00	0.42
1:E:560:ASN:ND2	1:E:965:ARG:H	2.16	0.42
1:E:755:MET:HB3	3:N:68:ALA:CB	2.50	0.42
1:E:923:PRO:HG3	1:E:950:PHE:CG	2.53	0.42
1:F:498:LEU:HG	1:F:954:PRO:HG2	2.00	0.42
1:G:1044:GLU:CD	1:G:1046:LYS:HE3	2.40	0.42
1:G:380:ASP:OD1	1:H:203:ASN:HB2	2.18	0.42
1:H:471:THR:O	1:H:475:PHE:CB	2.60	0.42
1:H:724:ASN:ND2	1:H:728:ALA:H	2.15	0.42
1:H:943:TYR:HB3	1:H:950:PHE:HB2	2.00	0.42
1:I:916:PHE:HA	1:I:956:LEU:HD13	2.01	0.42
3:K:66:LYS:HA	3:K:66:LYS:HD3	1.73	0.42
3:O:24:GLU:HB2	3:O:28:LYS:HZ3	1.84	0.42
4:U:238:PHE:O	4:U:241:LEU:HB2	2.19	0.42
4:V:127:ILE:HA	4:V:127:ILE:HD13	4.35	0.42
5:X:178:LEU:HG	5:X:178:LEU:O	2.19	0.42
4:5:224:LEU:HD11	5:6:62:ARG:HB3	2.00	0.42
1:A:634:ILE:HG12	1:A:645:LEU:HB3	2.02	0.42
1:B:273:LEU:HD11	1:B:1024:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:449:VAL:HG23	1:B:1152:ILE:CD1	2.48	0.42
1:C:534:HIS:CE1	1:C:1216:LEU:HD13	2.55	0.42
1:D:1042:THR:HG23	1:D:1053:ASN:CB	2.27	0.42
1:D:1154:THR:H	1:D:1154:THR:HG23	1.62	0.42
1:D:483:ILE:H	1:D:483:ILE:HG13	1.65	0.42
1:E:1048:ILE:HG23	1:E:1049:VAL:HG22	2.01	0.42
1:E:1221:TYR:HB2	1:E:1243:PHE:HD2	1.83	0.42
1:F:91:VAL:HG22	1:F:118:LYS:HB2	2.02	0.42
1:F:182:THR:OG1	1:F:185:ARG:NH2	2.38	0.42
1:F:653:ILE:HG13	1:F:673:TYR:HD1	1.83	0.42
1:G:18:ASN:HD22	1:G:18:ASN:C	2.23	0.42
1:H:488:PRO:HG3	1:H:870:GLU:HG3	2.02	0.42
3:M:24:GLU:O	3:M:28:LYS:NZ	2.51	0.42
1:H:748:GLU:O	3:Q:76:MET:HE1	2.20	0.42
1:A:214:ASN:OD1	1:F:433:LYS:NZ	2.52	0.42
1:A:809:PHE:HB2	1:A:810:TYR:H	1.69	0.42
1:B:1035:ILE:CG1	1:B:1059:SER:HB3	2.49	0.42
1:B:1223:THR:HA	1:B:1226:ARG:HB3	2.00	0.42
1:B:17:LEU:HD11	1:B:20:PHE:HD1	1.85	0.42
1:B:637:TRP:CD1	1:B:645:LEU:HB2	2.55	0.42
1:B:6:ALA:O	1:B:10:LEU:HB2	2.19	0.42
1:C:1207:ASN:CB	1:C:1210:ALA:HB3	2.50	0.42
1:C:127:ILE:HD13	1:C:127:ILE:HA	1.89	0.42
1:C:72:ALA:HA	1:C:75:ALA:HB3	2.01	0.42
1:D:58:CYS:HB3	1:G:12:LYS:HD2	2.00	0.42
1:D:582:ALA:HA	1:D:689:ILE:HD11	2.01	0.42
1:D:692:ILE:HD13	1:D:701:LEU:HD23	2.01	0.42
1:F:449:VAL:HG23	1:F:1152:ILE:CD1	2.48	0.42
1:G:436:VAL:HA	1:H:1165:LEU:HD11	2.00	0.42
1:H:1152:ILE:HB	1:H:1216:LEU:HD21	2.01	0.42
1:I:1198:ASP:OD1	1:I:1199:SER:N	2.51	0.42
3:R:66:LYS:HA	3:R:66:LYS:HD3	1.73	0.42
5:Y:8:PHE:HB2	5:Y:75:ASN:HD21	1.84	0.42
5:6:231:LEU:HD11	5:7:256:LYS:HZ3	1.84	0.42
1:A:806:LEU:HD23	1:A:806:LEU:HA	1.87	0.42
1:D:840:GLY:HA2	1:D:841:PRO:HD3	1.85	0.42
1:E:1090:LEU:HA	1:E:1093:ALA:HB3	2.01	0.42
1:F:536:PHE:CD1	1:F:992:LEU:HB3	2.54	0.42
1:D:23:ILE:HD11	1:H:97:LEU:HD21	2.00	0.42
5:W:55:VAL:HG22	5:W:144:LEU:HD23	2.01	0.42
1:B:900:LEU:HD11	1:B:904:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:LEU:O	1:C:1029:ARG:NH2	2.53	0.42
1:E:1245:GLU:HA	1:E:1248:ILE:HG22	2.01	0.42
1:E:755:MET:CB	3:N:68:ALA:CB	2.98	0.42
1:G:1048:ILE:HD11	4:S:170:ILE:HD11	2.00	0.42
1:G:127:ILE:HD13	1:G:127:ILE:HA	1.77	0.42
1:H:541:TYR:CE1	1:H:550:VAL:HG12	2.54	0.42
1:H:693:ASN:ND2	1:I:945:ARG:HH22	2.17	0.42
1:H:953:PRO:O	1:H:956:LEU:N	2.49	0.42
1:I:1325:HIS:CD2	1:I:1326:TYR:H	2.37	0.42
3:P:39:LEU:HD22	3:P:43:MET:HG2	2.00	0.42
4:U:1:MET:N	4:U:1:MET:CE	4.98	0.42
4:V:75:LEU:HB2	4:V:93:LEU:HB2	2.01	0.42
5:W:222:SER:HB2	5:W:224:LEU:HD21	1.91	0.42
1:A:271:GLY:H	1:A:1029:ARG:HB3	1.85	0.42
1:A:1087:ILE:HG13	1:A:1087:ILE:H	1.54	0.42
1:A:1220:LEU:C	1:A:1221:TYR:CD1	2.86	0.42
1:A:322:MET:SD	1:F:53:LEU:HD21	2.60	0.42
1:A:682:LEU:HA	1:A:682:LEU:HD23	1.88	0.42
1:A:693:ASN:O	1:B:507:LYS:NZ	2.47	0.42
1:B:1021:VAL:HG11	1:B:1073:THR:HG23	2.02	0.42
1:B:1088:GLN:N	1:B:1148:ILE:O	2.50	0.42
1:B:777:LEU:HD23	1:B:780:ILE:HD12	2.00	0.42
1:B:782:TYR:HD1	1:B:786:LEU:HD12	1.85	0.42
1:C:1159:ASN:O	1:C:1163:PHE:N	2.48	0.42
1:E:1021:VAL:HG12	1:E:1023:CYS:HB2	2.01	0.42
1:E:1087:ILE:HA	1:E:1148:ILE:HB	2.02	0.42
1:G:1157:THR:HG23	1:G:1206:THR:HB	2.02	0.42
1:G:182:THR:HG21	1:G:1060:PHE:HD2	1.85	0.42
1:E:252:GLU:HB2	1:G:19:ILE:HG12	2.01	0.42
1:H:705:ALA:HB2	1:H:999:ILE:HD11	2.01	0.42
3:N:48:VAL:HG21	3:N:58:LYS:CB	18.90	0.42
4:T:111:LEU:HD23	4:T:114:MET:CE	2.49	0.42
4:U:34:VAL:CG2	4:U:38:GLU:HB2	2.47	0.42
5:X:295:LYS:NZ	5:X:296:ASN:OD1	2.45	0.42
4:5:68:GLU:HG2	4:5:74:MET:HG3	2.01	0.42
1:A:759:ASP:OD2	1:A:802:LYS:NZ	2.48	0.42
1:A:992:LEU:HA	1:A:992:LEU:HD23	1.83	0.42
1:C:202:HIS:NE2	1:C:204:LYS:HG2	2.35	0.42
1:C:712:ARG:HH21	1:C:876:ASP:HA	1.85	0.42
1:D:10:LEU:HD23	1:D:10:LEU:HA	1.82	0.42
1:D:1198:ASP:H	1:D:1204:ALA:HA	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1170:ARG:HE	1:E:1174:SER:HB3	1.85	0.42
1:F:606:PRO:HD3	1:F:637:TRP:CZ2	2.55	0.42
1:F:87:THR:HG22	1:F:88:LEU:HG	2.01	0.42
1:G:653:ILE:HG13	1:G:673:TYR:HD1	1.85	0.42
1:H:1198:ASP:H	1:H:1204:ALA:HA	1.85	0.42
5:6:69:LEU:HA	5:6:79:LEU:HD23	2.02	0.42
5:7:139:GLU:OE2	5:7:143:ARG:NE	2.51	0.42
1:A:919:PHE:HB2	1:A:920:PHE:CD2	2.55	0.42
1:C:981:SER:HA	1:C:984:THR:HG22	2.02	0.42
1:E:251:THR:HB	1:G:19:ILE:O	2.19	0.42
1:E:553:THR:HG23	1:E:887:PHE:CE1	2.54	0.42
1:E:720:THR:OG1	1:E:721:MET:N	2.53	0.42
1:E:826:ILE:HG23	1:E:828:SER:H	1.85	0.42
1:F:1088:GLN:N	1:F:1148:ILE:O	2.51	0.42
1:F:1325:HIS:CG	1:F:1326:TYR:H	2.37	0.42
1:G:1038:ASP:HA	4:S:1:MET:N	2.34	0.42
5:Y:136:ILE:HD12	5:Y:171:TYR:HB3	2.02	0.42
1:C:627:LYS:O	1:C:631:SER:OG	2.24	0.41
1:D:1307:GLN:OE1	1:E:1160:ILE:HD12	2.20	0.41
1:E:116:VAL:HG12	1:G:35:LEU:CB	2.51	0.41
1:E:542:ILE:O	1:E:548:THR:C	2.58	0.41
1:H:792:ASN:HD21	1:H:919:PHE:HD1	1.68	0.41
1:B:815:ILE:CG2	3:K:39:LEU:CD2	2.97	0.41
5:6:198:LEU:HD23	5:6:201:ILE:HD12	2.02	0.41
1:A:454:VAL:O	1:A:534:HIS:NE2	2.52	0.41
1:B:496:TYR:OH	1:B:913:PRO:O	2.30	0.41
1:C:1018:ASN:OD1	1:C:1018:ASN:N	2.54	0.41
1:E:1140:ILE:HB	1:F:1190:ALA:HB1	2.03	0.41
1:F:446:LEU:HA	1:F:449:VAL:HG12	2.02	0.41
1:F:600:LEU:HA	1:F:901:ILE:HD11	2.02	0.41
1:F:900:LEU:HD11	1:F:904:ILE:HD12	2.03	0.41
1:G:559:GLY:HA3	1:G:968:PHE:HE1	1.85	0.41
1:H:1313:ARG:HH11	1:H:1323:GLU:HB2	1.85	0.41
1:I:1086:LYS:HE2	1:I:1146:GLN:HG2	2.03	0.41
1:I:176:ILE:HG21	1:I:375:VAL:HG21	2.02	0.41
1:I:900:LEU:HD11	1:I:904:ILE:HD12	2.02	0.41
1:E:802:LYS:HZ3	3:N:67:THR:HB	1.85	0.41
4:S:111:LEU:O	4:S:114:MET:HB2	2.20	0.41
1:G:1038:ASP:CA	4:S:1:MET:H3	2.33	0.41
5:Y:114:SER:O	5:Y:115:GLU:C	2.58	0.41
1:A:1199:SER:OG	1:A:1200:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:899:CYS:SG	1:B:900:LEU:N	2.93	0.41
1:C:758:ILE:HG22	1:C:864:GLU:HA	2.02	0.41
1:D:649:SER:HB3	1:D:652:MET:HB2	2.03	0.41
1:E:268:PRO:HB2	1:E:1029:ARG:HH22	1.86	0.41
1:G:1090:LEU:HA	1:G:1093:ALA:HB3	2.01	0.41
1:G:273:LEU:HD11	1:G:1024:LEU:HD13	2.01	0.41
1:H:553:THR:HG23	1:H:887:PHE:HE1	1.85	0.41
1:I:737:LEU:HD12	1:I:742:VAL:HG22	2.02	0.41
4:U:53:ARG:HG2	4:U:163:TYR:CZ	2.55	0.41
4:V:280:LEU:HA	4:V:281:PRO:HD3	1.93	0.41
5:W:277:TYR:O	5:W:294:TYR:CD2	2.73	0.41
5:6:91:LYS:HA	5:6:288:ARG:O	2.20	0.41
5:7:52:LYS:HE2	5:7:52:LYS:HB3	1.95	0.41
1:A:162:ARG:HH22	1:B:96:GLN:CD	2.23	0.41
1:B:1248:ILE:HA	1:B:1248:ILE:HD12	1.84	0.41
1:B:559:GLY:HA3	1:B:968:PHE:HE1	1.86	0.41
1:B:53:LEU:HD11	1:C:92:LEU:HD13	2.01	0.41
1:D:1216:LEU:O	1:D:1220:LEU:HB2	2.20	0.41
1:D:46:TYR:CD1	1:G:152:LEU:HG	2.55	0.41
1:E:784:CYS:O	1:E:982:ILE:HG23	2.19	0.41
1:F:456:ASP:HA	1:F:882:GLY:HA3	2.02	0.41
1:G:142:THR:OG1	1:G:144:LYS:O	2.38	0.41
1:G:182:THR:OG1	1:G:185:ARG:NH2	2.46	0.41
1:H:542:ILE:O	1:H:548:THR:C	2.59	0.41
1:D:815:ILE:HG21	3:M:37:LEU:HD13	2.02	0.41
1:I:755:MET:CB	3:R:68:ALA:HB1	2.45	0.41
4:S:107:VAL:HG13	4:S:280:LEU:HD11	2.03	0.41
4:T:197:VAL:HG22	4:T:214:VAL:HG22	2.01	0.41
4:U:8:ARG:HA	4:U:11:ILE:HD12	2.02	0.41
5:Z:116:GLU:HB3	5:Z:119:LEU:O	2.20	0.41
5:7:110:LEU:HA	5:7:110:LEU:HD13	1.92	0.41
5:7:210:ARG:HH22	5:7:229:GLN:NE2	2.17	0.41
1:A:131:LEU:O	1:A:1049:VAL:HA	2.20	0.41
1:A:558:ILE:HD13	1:A:992:LEU:HD21	2.01	0.41
1:C:32:PHE:HB2	1:C:35:LEU:HD23	2.02	0.41
1:C:788:ALA:HB2	1:C:985:LEU:HD12	2.02	0.41
1:D:11:PRO:HD2	1:H:328:PHE:CZ	2.55	0.41
1:D:283:LEU:HD23	1:D:286:ILE:HD11	2.03	0.41
1:E:662:ASP:OD1	1:F:640:MET:CA	2.68	0.41
1:E:798:GLY:O	1:E:911:TYR:HA	2.21	0.41
1:F:534:HIS:HB3	1:F:537:PHE:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:640:MET:CE	1:F:663:GLU:OE2	2.68	0.41
1:G:1021:VAL:HG11	1:G:1073:THR:HG23	2.02	0.41
1:H:489:THR:OG1	1:H:733:ASP:OD1	2.32	0.41
1:I:553:THR:HG23	1:I:887:PHE:CE1	2.56	0.41
1:I:627:LYS:O	1:I:631:SER:OG	2.25	0.41
3:1:24:GLU:O	3:1:28:LYS:NZ	2.53	0.41
4:5:200:VAL:O	4:5:211:GLY:N	2.54	0.41
5:6:154:ARG:HH22	5:7:216:LEU:HD21	1.85	0.41
5:7:30:ILE:HD11	5:7:79:LEU:HD13	2.03	0.41
1:A:517:ASN:HD21	1:F:1004:LYS:CD	2.33	0.41
1:B:80:PHE:HD2	1:B:83:VAL:HB	1.85	0.41
1:C:263:SER:OG	1:C:264:LYS:N	2.54	0.41
1:C:859:LEU:CG	1:C:862:ILE:CG2	2.87	0.41
1:D:1015:ARG:NH1	1:D:1084:GLY:O	2.53	0.41
1:D:73:VAL:HG23	1:D:261:TYR:CG	2.55	0.41
1:D:725:ASP:O	1:D:728:ALA:N	2.54	0.41
1:F:1198:ASP:OD1	1:F:1199:SER:N	2.54	0.41
1:G:1256:TYR:HA	1:G:1259:ILE:HG13	2.03	0.41
1:H:542:ILE:HG13	1:H:549:GLU:HB3	2.02	0.41
4:T:199:HIS:O	4:T:255:GLY:CA	2.68	0.41
5:Y:147:ILE:HD11	5:Y:166:LEU:HD22	2.02	0.41
3:2:25:GLU:HG2	3:2:26:GLU:OE2	2.20	0.41
4:5:241:LEU:HD22	5:6:200:MET:SD	2.61	0.41
4:5:75:LEU:HB2	4:5:93:LEU:HB2	2.02	0.41
1:B:53:LEU:HA	1:B:53:LEU:HD12	1.89	0.41
1:D:230:LEU:HD23	1:D:1074:ALA:HB1	2.03	0.41
1:E:1095:PRO:HG3	1:E:1128:ILE:HG21	2.02	0.41
1:E:381:VAL:HG22	1:F:100:VAL:HG11	2.02	0.41
1:G:1256:TYR:HD1	1:G:1259:ILE:HD11	1.86	0.41
1:G:860:ILE:HG22	3:P:78:ALA:HB3	2.02	0.41
1:G:701:LEU:HD21	1:G:999:ILE:HG21	2.03	0.41
1:E:318:TYR:OH	1:H:322:MET:HG2	2.20	0.41
1:I:1020:ASP:HB3	1:I:1077:LYS:HB2	2.03	0.41
1:I:715:CYS:O	1:I:717:PHE:N	2.53	0.41
3:P:25:GLU:CD	3:P:25:GLU:H	2.24	0.41
5:Y:201:ILE:O	5:Y:205:ALA:CB	2.68	0.41
3:2:71:LEU:O	3:2:75:ARG:HG2	2.21	0.41
4:5:85:ASN:HB3	4:5:86:PRO:HD3	2.03	0.41
4:5:245:ILE:HD11	5:7:231:LEU:CD1	2.49	0.41
1:A:1090:LEU:HA	1:A:1093:ALA:HB3	2.02	0.41
1:A:616:VAL:HG12	1:A:622:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:871:VAL:HB	1:A:891:GLN:HB2	2.03	0.41
1:A:887:PHE:HE2	1:A:889:SER:HG	1.69	0.41
1:B:446:LEU:HA	1:B:449:VAL:HG12	2.03	0.41
1:C:855:LEU:HD12	1:C:855:LEU:O	2.21	0.41
1:D:1096:ILE:HD13	1:D:1125:LEU:HD13	2.02	0.41
1:D:1152:ILE:HB	1:D:1216:LEU:HD21	2.02	0.41
1:E:1040:THR:OG1	1:E:1055:THR:OG1	2.38	0.41
1:E:135:CYS:O	1:E:139:LEU:HB2	2.21	0.41
1:E:195:THR:HG22	1:E:215:MET:HG3	2.02	0.41
1:E:449:VAL:HG23	1:E:1152:ILE:CD1	2.46	0.41
1:E:662:ASP:OD1	1:F:640:MET:HA	2.21	0.41
1:F:240:TYR:CE1	1:F:362:LEU:HG	2.56	0.41
1:G:760:SER:OG	1:G:761:SER:N	2.54	0.41
1:G:786:LEU:O	1:G:790:SER:OG	2.33	0.41
1:I:726:THR:OG1	1:I:727:ASN:N	2.54	0.41
4:T:69:LEU:CB	4:T:146:VAL:HG11	2.47	0.41
4:T:176:LEU:HB3	4:T:179:ILE:HG12	2.02	0.41
4:T:216:LEU:HD21	4:T:285:LEU:HD21	2.03	0.41
3:1:25:GLU:CD	3:1:25:GLU:H	2.24	0.41
5:7:40:GLY:N	5:7:42:LEU:HD21	2.35	0.41
1:B:718:VAL:HG23	1:B:895:TYR:HD1	1.86	0.41
1:F:1021:VAL:HG11	1:F:1073:THR:HG23	2.02	0.41
1:G:1125:LEU:O	1:G:1129:THR:HG23	2.21	0.41
1:G:775:THR:HG22	1:G:779:LYS:HE2	2.03	0.41
1:H:292:SER:O	1:H:359:THR:OG1	2.29	0.41
1:D:806:LEU:CD1	3:M:67:THR:HG23	2.50	0.41
3:M:71:LEU:O	3:M:75:ARG:HG2	2.21	0.41
3:Q:71:LEU:O	3:Q:75:ARG:HG2	2.21	0.41
3:R:71:LEU:O	3:R:75:ARG:HG2	2.21	0.41
4:V:58:VAL:O	4:V:153:LEU:HA	2.21	0.41
5:W:260:SER:O	5:W:264:MET:HG2	2.20	0.41
1:B:1325:HIS:CG	1:B:1326:TYR:H	2.39	0.41
1:B:760:SER:OG	1:B:761:SER:N	2.52	0.41
1:C:262:THR:HA	1:C:268:PRO:HA	2.03	0.41
1:C:488:PRO:HB3	1:C:868:ILE:HB	2.02	0.41
1:C:495:LEU:HG	1:C:953:PRO:HG2	2.03	0.41
1:C:953:PRO:HA	1:C:954:PRO:HD3	1.93	0.41
1:D:390:GLN:HB2	1:D:1290:ARG:HG2	2.03	0.41
1:E:505:VAL:HA	1:E:506:PRO:HD3	1.95	0.41
1:E:737:LEU:HD12	1:E:742:VAL:HG22	2.02	0.41
1:F:408:SER:OG	1:F:409:THR:O	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:757:LEU:HD23	1:F:760:SER:HB3	2.03	0.41
1:F:810:TYR:O	1:F:815:ILE:HG12	2.21	0.41
1:H:691:ASN:HA	1:H:702:VAL:HG22	2.03	0.41
1:A:750:SER:O	3:J:72:ASP:OD2	2.38	0.41
4:T:203:GLU:HG3	4:T:243:TYR:CZ	2.56	0.41
4:U:58:VAL:O	4:U:153:LEU:HA	2.20	0.41
5:X:56:HIS:HB2	5:X:186:GLN:HE22	1.86	0.41
5:6:219:GLU:OE2	5:7:154:ARG:NH2	2.54	0.41
1:A:514:ASN:HD21	1:A:967:PRO:HD3	1.86	0.41
1:B:1036:LEU:HD22	1:B:1056:GLN:NE2	2.36	0.41
1:B:127:ILE:HA	1:B:127:ILE:HD13	1.86	0.41
1:B:429:PHE:CE2	1:B:1307:GLN:HG3	2.56	0.41
1:C:1021:VAL:HG11	1:C:1073:THR:HG23	2.03	0.41
1:E:293:THR:HA	1:E:357:LEU:O	2.20	0.41
1:E:390:GLN:HB2	1:E:1290:ARG:HG2	2.03	0.41
1:F:542:ILE:HD13	1:F:551:LEU:HD22	2.03	0.41
1:F:730:ILE:HG12	1:F:871:VAL:HG22	2.03	0.41
1:G:129:PHE:HB3	1:H:99:ARG:NH2	2.36	0.41
1:G:953:PRO:HA	1:G:954:PRO:HD3	1.88	0.41
1:H:995:VAL:HG12	1:H:1108:ILE:HD11	2.03	0.41
1:H:275:GLY:H	1:H:280:ILE:HD11	1.85	0.41
1:H:752:VAL:HG11	3:Q:69:PHE:CE1	2.56	0.41
1:I:439:ARG:NE	1:I:441:ASP:OD1	2.53	0.41
3:L:71:LEU:O	3:L:75:ARG:HG2	2.21	0.41
5:Z:251:ILE:HD12	5:Z:251:ILE:HA	1.87	0.41
3:4:71:LEU:O	3:4:75:ARG:HG2	2.21	0.40
4:5:237:ARG:O	4:5:241:LEU:HG	2.20	0.40
1:B:1141:LEU:HD22	1:B:1275:GLU:HB3	2.03	0.40
1:B:651:GLU:O	1:B:655:LEU:HB2	2.20	0.40
1:B:489:THR:OG1	1:B:733:ASP:OD1	2.29	0.40
1:C:257:ASP:HB3	1:C:260:ASN:HB2	2.03	0.40
1:C:401:ILE:HD11	1:C:1329:TYR:HB3	2.03	0.40
1:D:23:ILE:HD11	1:H:97:LEU:HD11	2.03	0.40
1:D:633:CYS:O	1:D:637:TRP:HB2	2.21	0.40
1:E:1130:PHE:O	1:E:1130:PHE:CG	2.73	0.40
1:E:252:GLU:H	1:G:19:ILE:CB	2.26	0.40
1:F:596:VAL:HG21	1:F:676:LEU:HD11	2.03	0.40
1:G:276:PRO:HG3	1:G:1022:GLU:HB2	2.03	0.40
1:G:53:LEU:CD1	1:H:92:LEU:CD1	2.69	0.40
1:I:802:LYS:CD	3:R:67:THR:CG2	2.82	0.40
1:B:856:PHE:CE2	3:K:81:ARG:HD2	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:25:GLU:CD	3:N:25:GLU:H	2.25	0.40
1:F:860:ILE:HG23	3:O:78:ALA:HB3	2.01	0.40
3:P:71:LEU:O	3:P:75:ARG:HG2	2.21	0.40
3:3:66:LYS:HD3	3:3:66:LYS:HA	1.73	0.40
4:5:198:VAL:HG22	4:5:257:VAL:HG23	2.04	0.40
1:A:689:ILE:HA	1:A:689:ILE:HD13	1.94	0.40
1:C:582:ALA:HA	1:C:689:ILE:HD11	2.03	0.40
1:D:1221:TYR:HB2	1:D:1243:PHE:HD2	1.86	0.40
1:E:127:ILE:HD13	1:E:127:ILE:HA	1.91	0.40
1:E:1325:HIS:CD2	1:E:1326:TYR:H	2.39	0.40
1:F:1035:ILE:HG12	1:F:1035:ILE:H	1.51	0.40
1:F:467:GLU:HA	1:F:468:PRO:HD3	1.93	0.40
1:F:760:SER:OG	1:F:761:SER:N	2.53	0.40
1:G:343:SER:O	1:G:347:ASP:N	2.48	0.40
1:G:600:LEU:HA	1:G:901:ILE:HD11	2.03	0.40
1:G:826:ILE:HG21	1:G:833:SER:HB2	2.03	0.40
1:G:894:LEU:HA	1:G:894:LEU:HD12	1.87	0.40
1:I:1036:LEU:HD13	1:I:1056:GLN:HE21	1.86	0.40
1:I:1168:ASN:ND2	1:I:1174:SER:OG	2.54	0.40
3:O:71:LEU:O	3:O:75:ARG:HG2	2.21	0.40
1:H:856:PHE:HE2	3:Q:81:ARG:HD2	1.86	0.40
4:V:8:ARG:HD2	4:V:11:ILE:HD12	2.03	0.40
4:V:53:ARG:HG2	4:V:163:TYR:CZ	2.55	0.40
1:D:255:LEU:HD13	5:Z:150:ILE:HG13	71.56	0.40
5:6:149:LEU:HG	5:6:191:MET:HG3	2.03	0.40
1:A:311:ASN:HB3	1:A:321:ILE:HD12	2.03	0.40
1:A:952:LEU:HB2	1:A:957:ALA:HB2	2.04	0.40
1:B:998:ALA:HB1	1:B:1111:HIS:CD2	2.56	0.40
1:B:263:SER:OG	1:B:264:LYS:N	2.54	0.40
1:C:692:ILE:HD13	1:C:701:LEU:HD23	2.03	0.40
1:B:127:ILE:CG2	1:C:99:ARG:HH21	2.35	0.40
1:D:650:PHE:HA	1:D:653:ILE:HG22	2.02	0.40
1:D:859:LEU:HD12	1:D:862:ILE:HG23	2.03	0.40
1:D:876:ASP:OD1	1:D:876:ASP:N	2.54	0.40
1:E:582:ALA:HA	1:E:689:ILE:HD11	2.02	0.40
1:F:614:ILE:HG23	1:F:898:LEU:HD13	2.03	0.40
1:G:1226:ARG:HG2	1:G:1231:TYR:CE1	2.57	0.40
1:G:1248:ILE:HD12	1:G:1248:ILE:HA	1.87	0.40
1:G:446:LEU:HA	1:G:449:VAL:HG12	2.03	0.40
1:G:614:ILE:HG23	1:G:898:LEU:HD13	2.03	0.40
1:H:396:PRO:HB3	1:H:1163:PHE:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:815:ILE:HG21	3:J:37:LEU:HD13	2.04	0.40
3:O:25:GLU:H	3:O:25:GLU:CD	2.24	0.40
3:O:66:LYS:HA	3:O:66:LYS:HD3	1.73	0.40
4:U:110:ALA:O	4:U:113:THR:OG1	2.34	0.40
4:V:200:VAL:O	4:V:211:GLY:N	2.54	0.40
5:Z:205:ALA:HA	5:Z:206:PRO:HD3	1.89	0.40
4:5:110:ALA:O	4:5:113:THR:OG1	2.33	0.40
4:5:146:VAL:HA	4:5:154:LEU:HD23	2.02	0.40
1:A:224:LEU:C	1:A:224:LEU:HD12	5.04	0.40
1:A:504:GLU:OE1	1:A:943:TYR:OH	2.28	0.40
1:A:542:ILE:O	1:A:548:THR:C	2.60	0.40
1:B:102:THR:HG21	1:B:108:ALA:HA	2.02	0.40
1:B:1198:ASP:OD1	1:B:1199:SER:N	2.54	0.40
1:B:139:LEU:HD22	1:B:156:ALA:HB1	2.04	0.40
1:B:617:HIS:CG	1:B:863:ASN:HD21	2.39	0.40
1:D:1087:ILE:HG13	1:D:1087:ILE:H	1.55	0.40
1:D:433:LYS:NZ	1:E:214:ASN:OD1	2.54	0.40
1:D:701:LEU:HD21	1:D:999:ILE:HG21	2.03	0.40
1:D:809:PHE:HB2	1:D:810:TYR:H	1.77	0.40
1:E:10:LEU:HD23	1:E:10:LEU:HA	1.83	0.40
1:F:276:PRO:HG3	1:F:1022:GLU:HB2	2.03	0.40
1:F:311:ASN:HB3	1:F:321:ILE:HD12	2.03	0.40
1:G:147:VAL:O	1:G:151:ILE:HG12	2.21	0.40
1:G:379:THR:O	1:H:203:ASN:OD1	2.39	0.40
1:G:650:PHE:HA	1:G:653:ILE:HG22	2.04	0.40
1:G:900:LEU:HD11	1:G:904:ILE:HD12	2.04	0.40
1:H:48:ILE:HD13	1:I:316:ILE:HG12	2.03	0.40
1:I:474:ARG:NH1	1:I:527:PRO:HA	2.37	0.40
4:T:122:ASN:O	4:T:125:SER:OG	2.28	0.40
4:T:193:GLN:NE2	4:T:265:THR:OG1	2.53	0.40
3:3:71:LEU:O	3:3:75:ARG:HG2	2.21	0.40
4:5:174:THR:HG21	4:5:273:LEU:HD11	2.04	0.40
1:A:745:ARG:HG2	1:A:764:PHE:HB3	2.04	0.40
1:B:600:LEU:HA	1:B:901:ILE:HD11	2.04	0.40
1:B:606:PRO:HD3	1:B:637:TRP:CZ2	2.56	0.40
1:B:751:ASP:OD1	1:B:751:ASP:N	2.55	0.40
1:B:456:ASP:HA	1:B:882:GLY:HA3	2.03	0.40
1:C:1154:THR:H	1:C:1154:THR:HG23	1.56	0.40
1:C:856:PHE:C	1:C:856:PHE:CD1	2.95	0.40
1:D:943:TYR:HB3	1:D:950:PHE:HB2	2.04	0.40
1:E:162:ARG:CZ	1:F:96:GLN:HE22	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:731:THR:HG22	1:E:736:PRO:HA	2.04	0.40
1:F:1137:PRO:HA	1:F:1138:PRO:HD3	1.90	0.40
1:F:201:VAL:CG2	1:F:207:LEU:CA	2.74	0.40
1:G:390:GLN:HB2	1:G:1290:ARG:HG2	2.04	0.40
1:G:825:PRO:HB3	1:G:846:ALA:HB1	2.03	0.40
1:G:899:CYS:SG	1:G:900:LEU:N	2.94	0.40
1:H:1088:GLN:N	1:H:1148:ILE:O	2.53	0.40
1:G:438:GLN:HE22	1:H:1200:ASP:C	2.24	0.40
1:H:147:VAL:O	1:H:151:ILE:HG12	2.21	0.40
3:K:71:LEU:O	3:K:75:ARG:HG2	2.21	0.40
4:S:127:ILE:HD13	4:S:127:ILE:HA	4.34	0.40
5:Z:150:ILE:HG21	5:Z:162:ILE:HG21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1341/1345 (100%)	1238 (92%)	102 (8%)	1 (0%)	53	88
1	B	1341/1345 (100%)	1251 (93%)	87 (6%)	3 (0%)	49	85
1	C	1321/1345 (98%)	1239 (94%)	80 (6%)	2 (0%)	49	85
1	D	1341/1345 (100%)	1248 (93%)	89 (7%)	4 (0%)	43	81
1	E	1341/1345 (100%)	1243 (93%)	94 (7%)	4 (0%)	43	81
1	F	1341/1345 (100%)	1243 (93%)	96 (7%)	2 (0%)	53	88
1	G	1341/1345 (100%)	1253 (93%)	83 (6%)	5 (0%)	36	77
1	H	1341/1345 (100%)	1253 (93%)	84 (6%)	4 (0%)	43	81
1	I	1341/1345 (100%)	1242 (93%)	98 (7%)	1 (0%)	53	88
1	q	1292/1345 (96%)	1190 (92%)	99 (8%)	3 (0%)	49	85

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	r	1341/1345 (100%)	1235 (92%)	103 (8%)	3 (0%)	49	85
1	s	1341/1345 (100%)	1246 (93%)	93 (7%)	2 (0%)	53	88
1	t	1341/1345 (100%)	1240 (92%)	98 (7%)	3 (0%)	49	85
1	u	1342/1345 (100%)	1234 (92%)	106 (8%)	2 (0%)	53	88
1	v	1299/1345 (97%)	1204 (93%)	89 (7%)	6 (0%)	31	74
1	w	1240/1345 (92%)	1141 (92%)	98 (8%)	1 (0%)	53	88
2	e	267/858 (31%)	254 (95%)	13 (5%)	0	100	100
2	f	267/858 (31%)	248 (93%)	16 (6%)	3 (1%)	16	58
2	g	267/858 (31%)	255 (96%)	9 (3%)	3 (1%)	16	58
2	h	267/858 (31%)	248 (93%)	19 (7%)	0	100	100
2	i	267/858 (31%)	245 (92%)	17 (6%)	5 (2%)	9	45
2	j	267/858 (31%)	249 (93%)	16 (6%)	2 (1%)	24	67
2	k	267/858 (31%)	249 (93%)	17 (6%)	1 (0%)	36	77
2	l	267/858 (31%)	247 (92%)	19 (7%)	1 (0%)	36	77
2	m	267/858 (31%)	248 (93%)	18 (7%)	1 (0%)	36	77
2	n	267/858 (31%)	244 (91%)	18 (7%)	5 (2%)	9	45
2	o	267/858 (31%)	247 (92%)	16 (6%)	4 (2%)	11	51
2	p	267/858 (31%)	249 (93%)	18 (7%)	0	100	100
3	1	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	2	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	3	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	4	56/89 (63%)	49 (88%)	7 (12%)	0	100	100
3	J	59/89 (66%)	51 (86%)	7 (12%)	1 (2%)	10	49
3	K	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	L	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	M	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	N	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	O	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	P	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	Q	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	R	59/89 (66%)	52 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	x	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	y	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
3	z	59/89 (66%)	52 (88%)	7 (12%)	0	100	100
4	5	249/299 (83%)	226 (91%)	23 (9%)	0	100	100
4	S	297/299 (99%)	269 (91%)	27 (9%)	1 (0%)	43	81
4	T	297/299 (99%)	275 (93%)	21 (7%)	1 (0%)	43	81
4	U	297/299 (99%)	267 (90%)	29 (10%)	1 (0%)	43	81
4	V	297/299 (99%)	268 (90%)	27 (9%)	2 (1%)	24	67
5	6	278/296 (94%)	260 (94%)	18 (6%)	0	100	100
5	7	294/296 (99%)	259 (88%)	32 (11%)	3 (1%)	17	60
5	W	294/296 (99%)	277 (94%)	17 (6%)	0	100	100
5	X	294/296 (99%)	273 (93%)	20 (7%)	1 (0%)	43	81
5	Y	294/296 (99%)	269 (92%)	22 (8%)	3 (1%)	17	60
5	Z	294/296 (99%)	274 (93%)	19 (6%)	1 (0%)	43	81
5	a	293/296 (99%)	262 (89%)	28 (10%)	3 (1%)	17	60
5	b	293/296 (99%)	268 (92%)	24 (8%)	1 (0%)	43	81
5	c	293/296 (99%)	259 (88%)	33 (11%)	1 (0%)	43	81
5	d	293/296 (99%)	258 (88%)	30 (10%)	5 (2%)	10	49
All	All	29747/37695 (79%)	27475 (92%)	2177 (7%)	95 (0%)	47	81

All (95) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	55	GLY
1	F	19	ILE
1	G	810	TYR
1	H	21	ASN
1	H	818	ASP
1	v	148	ILE
1	v	810	TYR
1	v	818	ASP
1	w	564	PRO
2	f	178	ASN
2	g	10	PHE
2	i	108	ASN
2	j	149	TYR

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Mol	Chain	Res	Type
2	n	178	ASN
2	o	10	PHE
4	U	85	ASN
4	V	85	ASN
5	X	180	ASP
5	Y	242	ARG
5	Z	116	GLU
5	7	182	VAL
5	a	182	VAL
5	d	182	VAL
1	r	55	GLY
2	i	105	ASN
2	i	150	VAL
4	S	86	PRO
4	T	86	PRO
5	7	191	MET
5	a	52	LYS
5	b	191	MET
5	c	191	MET
5	d	191	MET
1	E	549	GLU
1	G	1120	SER
1	H	549	GLU
1	I	549	GLU
2	f	105	ASN
2	g	11	ALA
2	n	104	LEU
2	n	105	ASN
2	o	149	TYR
3	J	26	GLU
5	a	191	MET
5	d	251	ILE
1	A	549	GLU
1	B	549	GLU
1	C	549	GLU
1	D	549	GLU
1	D	845	VAL
1	E	23	ILE
1	E	948	GLY
1	E	1275	GLU
1	F	549	GLU
1	G	549	GLU

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Mol	Chain	Res	Type
1	G	1119	PRO
1	G	1275	GLU
1	H	1275	GLU
1	q	549	GLU
1	r	1275	GLU
1	t	549	GLU
1	u	549	GLU
1	v	549	GLU
1	v	1275	GLU
2	i	178	ASN
2	n	49	ARG
2	o	144	PRO
5	Y	114	SER
5	Y	115	GLU
1	D	1041	VAL
1	D	1275	GLU
1	r	549	GLU
1	s	549	GLU
1	s	1275	GLU
1	u	1275	GLU
2	i	148	PRO
2	j	148	PRO
2	l	110	GLU
2	m	146	ASP
2	n	12	TRP
5	d	183	ASN
1	q	1275	GLU
1	t	716	PRO
1	t	1275	GLU
2	f	104	LEU
4	V	3	SER
1	B	715	CYS
1	v	147	VAL
1	B	812	GLU
5	7	181	ILE
5	d	181	ILE
2	g	143	VAL
2	o	145	ILE
1	q	716	PRO
2	k	143	VAL

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	1218/1220 (100%)	1202 (99%)	16 (1%)	71	86
1	B	1218/1220 (100%)	1201 (99%)	17 (1%)	69	85
1	C	1204/1220 (99%)	1191 (99%)	13 (1%)	76	88
1	D	1218/1220 (100%)	1197 (98%)	21 (2%)	63	83
1	E	1218/1220 (100%)	1200 (98%)	18 (2%)	67	85
1	F	1218/1220 (100%)	1198 (98%)	20 (2%)	65	84
1	G	1218/1220 (100%)	1199 (98%)	19 (2%)	65	84
1	H	1218/1220 (100%)	1197 (98%)	21 (2%)	63	83
1	I	1218/1220 (100%)	1204 (99%)	14 (1%)	76	88
1	q	1180/1220 (97%)	1168 (99%)	12 (1%)	78	89
1	r	1218/1220 (100%)	1204 (99%)	14 (1%)	76	88
1	s	1218/1220 (100%)	1202 (99%)	16 (1%)	71	86
1	t	1218/1220 (100%)	1207 (99%)	11 (1%)	81	90
1	u	1219/1220 (100%)	1205 (99%)	14 (1%)	76	88
1	v	1180/1220 (97%)	1170 (99%)	10 (1%)	83	92
1	w	1133/1220 (93%)	1123 (99%)	10 (1%)	81	90
2	e	253/761 (33%)	247 (98%)	6 (2%)	52	75
2	f	253/761 (33%)	253 (100%)	0	100	100
2	g	253/761 (33%)	246 (97%)	7 (3%)	47	71
2	h	253/761 (33%)	249 (98%)	4 (2%)	65	84
2	i	253/761 (33%)	245 (97%)	8 (3%)	42	68
2	j	253/761 (33%)	246 (97%)	7 (3%)	47	71
2	k	253/761 (33%)	246 (97%)	7 (3%)	47	71
2	l	253/761 (33%)	246 (97%)	7 (3%)	47	71
2	m	253/761 (33%)	249 (98%)	4 (2%)	65	84
2	n	253/761 (33%)	247 (98%)	6 (2%)	52	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	o	253/761 (33%)	247 (98%)	6 (2%)	52	75
2	p	253/761 (33%)	248 (98%)	5 (2%)	58	79
3	1	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	2	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	3	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	4	49/77 (64%)	48 (98%)	1 (2%)	58	79
3	J	52/77 (68%)	49 (94%)	3 (6%)	22	52
3	K	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	L	52/77 (68%)	50 (96%)	2 (4%)	36	64
3	M	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	N	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	O	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	P	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	Q	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	R	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	x	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	y	52/77 (68%)	51 (98%)	1 (2%)	60	80
3	z	52/77 (68%)	51 (98%)	1 (2%)	60	80
4	5	232/273 (85%)	230 (99%)	2 (1%)	81	90
4	S	273/273 (100%)	268 (98%)	5 (2%)	62	82
4	T	273/273 (100%)	271 (99%)	2 (1%)	85	93
4	U	273/273 (100%)	265 (97%)	8 (3%)	45	70
4	V	273/273 (100%)	266 (97%)	7 (3%)	49	73
5	6	261/274 (95%)	260 (100%)	1 (0%)	92	95
5	7	274/274 (100%)	270 (98%)	4 (2%)	67	85
5	W	274/274 (100%)	268 (98%)	6 (2%)	55	77
5	X	274/274 (100%)	272 (99%)	2 (1%)	85	93
5	Y	274/274 (100%)	269 (98%)	5 (2%)	62	82
5	Z	274/274 (100%)	264 (96%)	10 (4%)	38	65
5	a	273/274 (100%)	269 (98%)	4 (2%)	67	85
5	b	273/274 (100%)	266 (97%)	7 (3%)	49	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	c	273/274 (100%)	268 (98%)	5 (2%)	62	82
5	d	273/274 (100%)	269 (98%)	4 (2%)	67	85
All	All	27226/33989 (80%)	26822 (98%)	404 (2%)	70	85

All (404) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	139	LEU
1	A	140	GLU
1	A	244	ASN
1	A	691	ASN
1	A	743	ARG
1	A	746	ASN
1	A	772	ASN
1	A	831	LEU
1	A	839	MET
1	A	950	PHE
1	A	1029	ARG
1	A	1032	THR
1	A	1075	ASN
1	A	1134	ASN
1	A	1250	LYS
1	B	139	LEU
1	B	244	ASN
1	B	397	LEU
1	B	439	ARG
1	B	691	ASN
1	B	702	VAL
1	B	712	ARG
1	B	715	CYS
1	B	743	ARG
1	B	746	ASN
1	B	769	ARG
1	B	772	ASN
1	B	839	MET
1	B	1029	ARG
1	B	1075	ASN
1	B	1118	ASN
1	B	1250	LYS
1	C	244	ASN

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Mol	Chain	Res	Type
1	C	691	ASN
1	C	743	ARG
1	C	746	ASN
1	C	769	ARG
1	C	772	ASN
1	C	839	MET
1	C	854	GLN
1	C	855	LEU
1	C	950	PHE
1	C	1029	ARG
1	C	1075	ASN
1	C	1250	LYS
1	D	244	ASN
1	D	307	MET
1	D	397	LEU
1	D	691	ASN
1	D	702	VAL
1	D	709	PHE
1	D	729	LYS
1	D	743	ARG
1	D	746	ASN
1	D	754	ARG
1	D	769	ARG
1	D	772	ASN
1	D	809	PHE
1	D	831	LEU
1	D	839	MET
1	D	856	PHE
1	D	950	PHE
1	D	1029	ARG
1	D	1042	THR
1	D	1075	ASN
1	D	1250	LYS
1	E	244	ASN
1	E	439	ARG
1	E	691	ASN
1	E	702	VAL
1	E	743	ARG
1	E	746	ASN
1	E	769	ARG
1	E	772	ASN
1	E	831	LEU

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Mol	Chain	Res	Type
1	E	947	ASP
1	E	1029	ARG
1	E	1032	THR
1	E	1075	ASN
1	E	1130	PHE
1	E	1133	ILE
1	E	1135	LYS
1	E	1201	THR
1	E	1250	LYS
1	F	18	ASN
1	F	201	VAL
1	F	244	ASN
1	F	439	ARG
1	F	546	ARG
1	F	691	ASN
1	F	702	VAL
1	F	743	ARG
1	F	746	ASN
1	F	769	ARG
1	F	772	ASN
1	F	815	ILE
1	F	818	ASP
1	F	822	GLN
1	F	839	MET
1	F	1029	ARG
1	F	1035	ILE
1	F	1075	ASN
1	F	1118	ASN
1	F	1250	LYS
1	G	18	ASN
1	G	20	PHE
1	G	139	LEU
1	G	244	ASN
1	G	439	ARG
1	G	691	ASN
1	G	702	VAL
1	G	743	ARG
1	G	746	ASN
1	G	769	ARG
1	G	772	ASN
1	G	808	LEU
1	G	818	ASP

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Mol	Chain	Res	Type
1	G	830	VAL
1	G	831	LEU
1	G	839	MET
1	G	1029	ARG
1	G	1075	ASN
1	G	1250	LYS
1	H	36	ARG
1	H	53	LEU
1	H	244	ASN
1	H	439	ARG
1	H	464	MET
1	H	691	ASN
1	H	724	ASN
1	H	743	ARG
1	H	746	ASN
1	H	769	ARG
1	H	772	ASN
1	H	818	ASP
1	H	831	LEU
1	H	839	MET
1	H	1029	ARG
1	H	1032	THR
1	H	1075	ASN
1	H	1125	LEU
1	H	1230	CYS
1	H	1250	LYS
1	H	1255	MET
1	I	244	ASN
1	I	255	LEU
1	I	439	ARG
1	I	691	ASN
1	I	743	ARG
1	I	746	ASN
1	I	769	ARG
1	I	772	ASN
1	I	1029	ARG
1	I	1075	ASN
1	I	1126	ASN
1	I	1201	THR
1	I	1216	LEU
1	I	1250	LYS
1	q	90	LYS

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Mol	Chain	Res	Type
1	q	139	LEU
1	q	244	ASN
1	q	691	ASN
1	q	746	ASN
1	q	769	ARG
1	q	772	ASN
1	q	831	LEU
1	q	832	MET
1	q	1029	ARG
1	q	1075	ASN
1	q	1250	LYS
1	r	3	ASN
1	r	18	ASN
1	r	36	ARG
1	r	244	ASN
1	r	439	ARG
1	r	691	ASN
1	r	743	ARG
1	r	746	ASN
1	r	769	ARG
1	r	772	ASN
1	r	839	MET
1	r	1029	ARG
1	r	1075	ASN
1	r	1250	LYS
1	s	18	ASN
1	s	36	ARG
1	s	204	LYS
1	s	244	ASN
1	s	439	ARG
1	s	691	ASN
1	s	743	ARG
1	s	746	ASN
1	s	769	ARG
1	s	772	ASN
1	s	839	MET
1	s	860	ILE
1	s	1029	ARG
1	s	1075	ASN
1	s	1129	THR
1	s	1250	LYS
1	t	36	ARG

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Mol	Chain	Res	Type
1	t	244	ASN
1	t	439	ARG
1	t	691	ASN
1	t	743	ARG
1	t	746	ASN
1	t	772	ASN
1	t	839	MET
1	t	1029	ARG
1	t	1075	ASN
1	t	1250	LYS
1	u	1	MET
1	u	36	ARG
1	u	200	LYS
1	u	244	ASN
1	u	691	ASN
1	u	743	ARG
1	u	746	ASN
1	u	769	ARG
1	u	772	ASN
1	u	839	MET
1	u	1029	ARG
1	u	1036	LEU
1	u	1075	ASN
1	u	1250	LYS
1	v	244	ASN
1	v	691	ASN
1	v	743	ARG
1	v	746	ASN
1	v	769	ARG
1	v	772	ASN
1	v	839	MET
1	v	1075	ASN
1	v	1118	ASN
1	v	1250	LYS
1	w	45	ARG
1	w	104	ASN
1	w	231	ASN
1	w	241	ARG
1	w	439	ARG
1	w	563	LEU
1	w	745	ARG
1	w	832	MET

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Mol	Chain	Res	Type
1	w	1164	LYS
1	w	1206	THR
2	e	33	ASN
2	e	62	ASN
2	e	96	ASN
2	e	138	ARG
2	e	163	ASN
2	e	255	ARG
2	g	33	ASN
2	g	62	ASN
2	g	96	ASN
2	g	99	LEU
2	g	106	LYS
2	g	132	ARG
2	g	163	ASN
2	h	33	ASN
2	h	62	ASN
2	h	96	ASN
2	h	163	ASN
2	i	33	ASN
2	i	44	ASN
2	i	49	ARG
2	i	96	ASN
2	i	112	MET
2	i	138	ARG
2	i	163	ASN
2	i	171	MET
2	j	33	ASN
2	j	60	LEU
2	j	62	ASN
2	j	96	ASN
2	j	105	ASN
2	j	163	ASN
2	j	255	ARG
2	k	33	ASN
2	k	62	ASN
2	k	96	ASN
2	k	99	LEU
2	k	106	LYS
2	k	132	ARG
2	k	163	ASN
2	l	31	LEU

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Mol	Chain	Res	Type
2	l	33	ASN
2	l	62	ASN
2	l	96	ASN
2	l	108	ASN
2	l	163	ASN
2	l	180	ASN
2	m	33	ASN
2	m	62	ASN
2	m	96	ASN
2	m	163	ASN
2	n	33	ASN
2	n	60	LEU
2	n	62	ASN
2	n	96	ASN
2	n	132	ARG
2	n	163	ASN
2	o	10	PHE
2	o	31	LEU
2	o	33	ASN
2	o	96	ASN
2	o	132	ARG
2	o	163	ASN
2	p	33	ASN
2	p	62	ASN
2	p	96	ASN
2	p	108	ASN
2	p	163	ASN
3	J	26	GLU
3	J	27	LYS
3	J	76	MET
3	K	76	MET
3	L	23	LYS
3	L	76	MET
3	M	76	MET
3	N	76	MET
3	O	76	MET
3	P	76	MET
3	Q	76	MET
3	R	76	MET
3	x	76	MET
3	y	76	MET
3	z	76	MET

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Mol	Chain	Res	Type
3	1	76	MET
3	2	76	MET
3	3	76	MET
3	4	76	MET
4	5	53	ARG
4	5	120	VAL
4	S	53	ARG
4	S	96	LEU
4	S	111	LEU
4	S	120	VAL
4	S	240	PHE
4	T	53	ARG
4	T	180	PHE
4	U	31	LEU
4	U	32	ASN
4	U	34	VAL
4	U	53	ARG
4	U	85	ASN
4	U	120	VAL
4	U	184	ASP
4	U	241	LEU
4	V	31	LEU
4	V	32	ASN
4	V	34	VAL
4	V	53	ARG
4	V	120	VAL
4	V	240	PHE
4	V	241	LEU
5	6	75	ASN
5	W	75	ASN
5	W	178	LEU
5	W	224	LEU
5	W	235	ARG
5	W	242	ARG
5	W	295	LYS
5	X	75	ASN
5	X	235	ARG
5	Y	75	ASN
5	Y	183	ASN
5	Y	236	THR
5	Y	239	SER
5	Y	242	ARG

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Mol	Chain	Res	Type
5	Z	1	MET
5	Z	23	LEU
5	Z	75	ASN
5	Z	117	LYS
5	Z	118	LEU
5	Z	119	LEU
5	Z	235	ARG
5	Z	236	THR
5	Z	242	ARG
5	Z	246	LEU
5	7	1	MET
5	7	42	LEU
5	7	75	ASN
5	7	296	ASN
5	a	53	ASP
5	a	75	ASN
5	a	182	VAL
5	a	296	ASN
5	b	54	TYR
5	b	75	ASN
5	b	214	ASP
5	b	217	THR
5	b	227	LYS
5	b	231	LEU
5	b	296	ASN
5	c	52	LYS
5	c	75	ASN
5	c	181	ILE
5	c	185	LYS
5	c	296	ASN
5	d	75	ASN
5	d	216	LEU
5	d	231	LEU
5	d	296	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (534) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	244	ASN
1	A	260	ASN
1	A	294	GLN
1	A	432	ASN

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Mol	Chain	Res	Type
1	A	435	GLN
1	A	438	GLN
1	A	477	GLN
1	A	691	ASN
1	A	727	ASN
1	A	772	ASN
1	A	791	ASN
1	A	863	ASN
1	A	888	GLN
1	A	892	HIS
1	A	896	ASN
1	A	977	ASN
1	A	1000	GLN
1	A	1006	HIS
1	A	1111	HIS
1	B	155	ASN
1	B	211	GLN
1	B	244	ASN
1	B	294	GLN
1	B	387	GLN
1	B	432	ASN
1	B	543	GLN
1	B	581	HIS
1	B	691	ASN
1	B	746	ASN
1	B	772	ASN
1	B	847	ASN
1	B	891	GLN
1	B	896	ASN
1	B	1000	GLN
1	B	1110	HIS
1	B	1111	HIS
1	B	1118	ASN
1	B	1143	HIS
1	B	1159	ASN
1	B	1271	ASN
1	C	244	ASN
1	C	311	ASN
1	C	337	GLN
1	C	432	ASN
1	C	438	GLN
1	C	477	GLN

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Mol	Chain	Res	Type
1	C	543	GLN
1	C	691	ASN
1	C	746	ASN
1	C	772	ASN
1	C	854	GLN
1	C	896	ASN
1	C	1000	GLN
1	C	1168	ASN
1	C	1239	ASN
1	C	1320	GLN
1	C	1325	HIS
1	D	244	ASN
1	D	331	ASN
1	D	435	GLN
1	D	581	HIS
1	D	691	ASN
1	D	739	GLN
1	D	746	ASN
1	D	772	ASN
1	D	891	GLN
1	D	896	ASN
1	D	1000	GLN
1	D	1053	ASN
1	D	1105	ASN
1	D	1111	HIS
1	D	1159	ASN
1	D	1194	HIS
1	D	1325	HIS
1	E	18	ASN
1	E	202	HIS
1	E	244	ASN
1	E	260	ASN
1	E	294	GLN
1	E	378	ASN
1	E	387	GLN
1	E	432	ASN
1	E	435	GLN
1	E	438	GLN
1	E	534	HIS
1	E	543	GLN
1	E	691	ASN
1	E	772	ASN

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Mol	Chain	Res	Type
1	E	791	ASN
1	E	946	ASN
1	E	1000	GLN
1	E	1089	ASN
1	E	1101	ASN
1	E	1111	HIS
1	E	1134	ASN
1	E	1159	ASN
1	E	1239	ASN
1	E	1325	HIS
1	F	18	ASN
1	F	203	ASN
1	F	244	ASN
1	F	294	GLN
1	F	378	ASN
1	F	387	GLN
1	F	432	ASN
1	F	438	GLN
1	F	473	HIS
1	F	543	GLN
1	F	581	HIS
1	F	691	ASN
1	F	746	ASN
1	F	772	ASN
1	F	822	GLN
1	F	847	ASN
1	F	891	GLN
1	F	896	ASN
1	F	938	ASN
1	F	1000	GLN
1	F	1057	HIS
1	F	1097	HIS
1	F	1101	ASN
1	F	1105	ASN
1	F	1111	HIS
1	F	1118	ASN
1	F	1143	HIS
1	G	5	GLN
1	G	18	ASN
1	G	123	HIS
1	G	138	HIS
1	G	155	ASN

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Mol	Chain	Res	Type
1	G	203	ASN
1	G	244	ASN
1	G	294	GLN
1	G	387	GLN
1	G	432	ASN
1	G	438	GLN
1	G	543	GLN
1	G	581	HIS
1	G	691	ASN
1	G	740	ASN
1	G	746	ASN
1	G	772	ASN
1	G	847	ASN
1	G	863	ASN
1	G	888	GLN
1	G	891	GLN
1	G	896	ASN
1	G	938	ASN
1	G	964	GLN
1	G	1000	GLN
1	G	1097	HIS
1	G	1111	HIS
1	G	1134	ASN
1	G	1143	HIS
1	H	244	ASN
1	H	331	ASN
1	H	387	GLN
1	H	435	GLN
1	H	581	HIS
1	H	691	ASN
1	H	724	ASN
1	H	739	GLN
1	H	740	ASN
1	H	746	ASN
1	H	772	ASN
1	H	888	GLN
1	H	896	ASN
1	H	964	GLN
1	H	1000	GLN
1	H	1101	ASN
1	H	1111	HIS
1	H	1159	ASN

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Mol	Chain	Res	Type
1	I	244	ASN
1	I	294	GLN
1	I	432	ASN
1	I	438	GLN
1	I	543	GLN
1	I	581	HIS
1	I	691	ASN
1	I	746	ASN
1	I	772	ASN
1	I	896	ASN
1	I	964	GLN
1	I	1000	GLN
1	I	1101	ASN
1	I	1111	HIS
1	I	1126	ASN
1	I	1159	ASN
1	I	1325	HIS
1	q	203	ASN
1	q	211	GLN
1	q	244	ASN
1	q	294	GLN
1	q	432	ASN
1	q	438	GLN
1	q	543	GLN
1	q	581	HIS
1	q	691	ASN
1	q	746	ASN
1	q	772	ASN
1	q	791	ASN
1	q	891	GLN
1	q	942	HIS
1	q	1000	GLN
1	q	1111	HIS
1	q	1168	ASN
1	q	1182	HIS
1	r	3	ASN
1	r	5	GLN
1	r	21	ASN
1	r	138	HIS
1	r	155	ASN
1	r	244	ASN
1	r	294	GLN

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Mol	Chain	Res	Type
1	r	387	GLN
1	r	432	ASN
1	r	435	GLN
1	r	438	GLN
1	r	543	GLN
1	r	581	HIS
1	r	658	ASN
1	r	691	ASN
1	r	746	ASN
1	r	772	ASN
1	r	847	ASN
1	r	888	GLN
1	r	891	GLN
1	r	1000	GLN
1	r	1111	HIS
1	r	1168	ASN
1	r	1241	GLN
1	r	1325	HIS
1	s	18	ASN
1	s	119	HIS
1	s	138	HIS
1	s	244	ASN
1	s	294	GLN
1	s	378	ASN
1	s	382	ASN
1	s	387	GLN
1	s	432	ASN
1	s	435	GLN
1	s	438	GLN
1	s	543	GLN
1	s	560	ASN
1	s	672	HIS
1	s	691	ASN
1	s	746	ASN
1	s	772	ASN
1	s	847	ASN
1	s	891	GLN
1	s	1000	GLN
1	s	1105	ASN
1	s	1111	HIS
1	s	1168	ASN
1	s	1252	ASN

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Mol	Chain	Res	Type
1	t	145	ASN
1	t	150	GLN
1	t	244	ASN
1	t	294	GLN
1	t	387	GLN
1	t	432	ASN
1	t	438	GLN
1	t	543	GLN
1	t	581	HIS
1	t	691	ASN
1	t	746	ASN
1	t	772	ASN
1	t	847	ASN
1	t	891	GLN
1	t	892	HIS
1	t	1000	GLN
1	t	1111	HIS
1	t	1168	ASN
1	t	1338	GLN
1	u	244	ASN
1	u	294	GLN
1	u	304	HIS
1	u	387	GLN
1	u	432	ASN
1	u	435	GLN
1	u	438	GLN
1	u	543	GLN
1	u	560	ASN
1	u	581	HIS
1	u	672	HIS
1	u	691	ASN
1	u	746	ASN
1	u	772	ASN
1	u	891	GLN
1	u	892	HIS
1	u	896	ASN
1	u	1000	GLN
1	u	1097	HIS
1	u	1101	ASN
1	u	1111	HIS
1	u	1168	ASN
1	v	155	ASN

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Mol	Chain	Res	Type
1	v	211	GLN
1	v	244	ASN
1	v	294	GLN
1	v	331	ASN
1	v	432	ASN
1	v	435	GLN
1	v	438	GLN
1	v	543	GLN
1	v	659	HIS
1	v	691	ASN
1	v	746	ASN
1	v	772	ASN
1	v	888	GLN
1	v	891	GLN
1	v	892	HIS
1	v	1000	GLN
1	v	1111	HIS
1	v	1118	ASN
1	v	1241	GLN
1	v	1325	HIS
1	w	104	ASN
1	w	119	HIS
1	w	141	ASN
1	w	202	HIS
1	w	387	GLN
1	w	432	ASN
1	w	466	ASN
1	w	477	GLN
1	w	514	ASN
1	w	617	HIS
1	w	746	ASN
1	w	847	ASN
1	w	854	GLN
1	w	863	ASN
1	w	879	GLN
1	w	881	HIS
1	w	934	GLN
1	w	964	GLN
1	w	1088	GLN
1	w	1097	HIS
1	w	1182	HIS
1	w	1297	ASN

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Mol	Chain	Res	Type
1	w	1318	ASN
2	e	33	ASN
2	e	71	HIS
2	e	96	ASN
2	f	33	ASN
2	f	71	HIS
2	f	82	ASN
2	f	105	ASN
2	f	163	ASN
2	f	194	ASN
2	f	248	GLN
2	g	33	ASN
2	g	44	ASN
2	g	71	HIS
2	g	92	GLN
2	g	115	ASN
2	g	122	GLN
2	g	163	ASN
2	g	194	ASN
2	h	27	ASN
2	h	30	ASN
2	h	33	ASN
2	h	71	HIS
2	h	92	GLN
2	h	122	GLN
2	h	194	ASN
2	h	237	ASN
2	i	27	ASN
2	i	33	ASN
2	i	39	HIS
2	i	44	ASN
2	i	71	HIS
2	i	96	ASN
2	i	194	ASN
2	j	33	ASN
2	j	71	HIS
2	j	96	ASN
2	j	105	ASN
2	j	163	ASN
2	j	248	GLN
2	k	30	ASN
2	k	33	ASN

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Mol	Chain	Res	Type
2	k	44	ASN
2	k	71	HIS
2	k	92	GLN
2	k	108	ASN
2	k	163	ASN
2	k	239	ASN
2	l	33	ASN
2	l	71	HIS
2	l	92	GLN
2	l	108	ASN
2	l	142	ASN
2	l	163	ASN
2	l	180	ASN
2	l	237	ASN
2	m	33	ASN
2	m	62	ASN
2	m	71	HIS
2	m	92	GLN
2	n	62	ASN
2	n	71	HIS
2	n	92	GLN
2	n	96	ASN
2	n	248	GLN
2	n	254	GLN
2	o	27	ASN
2	o	33	ASN
2	o	44	ASN
2	o	62	ASN
2	o	71	HIS
2	o	92	GLN
2	o	111	ASN
2	p	27	ASN
2	p	30	ASN
2	p	33	ASN
2	p	71	HIS
2	p	108	ASN
2	p	115	ASN
2	p	142	ASN
2	p	186	ASN
3	J	46	HIS
3	J	59	GLN
3	J	60	ASN

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Mol	Chain	Res	Type
3	K	46	HIS
3	K	59	GLN
3	K	60	ASN
3	L	46	HIS
3	L	59	GLN
3	L	60	ASN
3	M	46	HIS
3	M	59	GLN
3	M	60	ASN
3	N	46	HIS
3	N	59	GLN
3	N	60	ASN
3	O	46	HIS
3	O	59	GLN
3	O	60	ASN
3	P	46	HIS
3	P	59	GLN
3	P	60	ASN
3	Q	46	HIS
3	Q	59	GLN
3	Q	60	ASN
3	R	46	HIS
3	R	59	GLN
3	R	60	ASN
3	x	46	HIS
3	x	59	GLN
3	x	60	ASN
3	y	46	HIS
3	y	59	GLN
3	y	60	ASN
3	z	46	HIS
3	z	59	GLN
3	z	60	ASN
3	1	46	HIS
3	1	59	GLN
3	1	60	ASN
3	2	46	HIS
3	2	59	GLN
3	2	60	ASN
3	3	59	GLN
3	3	60	ASN
3	4	46	HIS

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Mol	Chain	Res	Type
3	4	59	GLN
3	4	60	ASN
4	S	193	GLN
4	T	220	GLN
4	T	242	ASN
4	U	122	ASN
4	V	122	ASN
4	V	161	ASN
5	6	34	HIS
5	6	75	ASN
5	6	170	GLN
5	W	34	HIS
5	W	75	ASN
5	W	170	GLN
5	W	221	HIS
5	X	34	HIS
5	X	75	ASN
5	X	170	GLN
5	X	186	GLN
5	X	247	HIS
5	Y	34	HIS
5	Y	75	ASN
5	Y	153	HIS
5	Y	170	GLN
5	Y	183	ASN
5	Y	221	HIS
5	Y	269	ASN
5	Z	34	HIS
5	Z	75	ASN
5	Z	76	GLN
5	Z	153	HIS
5	Z	170	GLN
5	Z	221	HIS
5	Z	269	ASN
5	7	75	ASN
5	7	76	GLN
5	7	113	HIS
5	7	229	GLN
5	7	296	ASN
5	a	51	ASN
5	a	75	ASN
5	a	76	GLN

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Mol	Chain	Res	Type
5	a	87	GLN
5	a	92	ASN
5	a	229	GLN
5	a	296	ASN
5	b	56	HIS
5	b	75	ASN
5	b	87	GLN
5	b	92	ASN
5	b	229	GLN
5	b	267	GLN
5	b	296	ASN
5	c	75	ASN
5	c	113	HIS
5	c	153	HIS
5	c	229	GLN
5	c	247	HIS
5	c	296	ASN
5	d	75	ASN
5	d	87	GLN
5	d	92	ASN
5	d	113	HIS
5	d	157	ASN
5	d	221	HIS
5	d	245	GLN
5	d	247	HIS
5	d	296	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.