



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:01 AM GMT

PDB ID : 3CUE
Title : Crystal structure of a TRAPP subassembly activating the Rab Ypt1p
Authors : Cai, Y.; Reinisch, K.M.
Deposited on : 2008-04-16
Resolution : 3.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

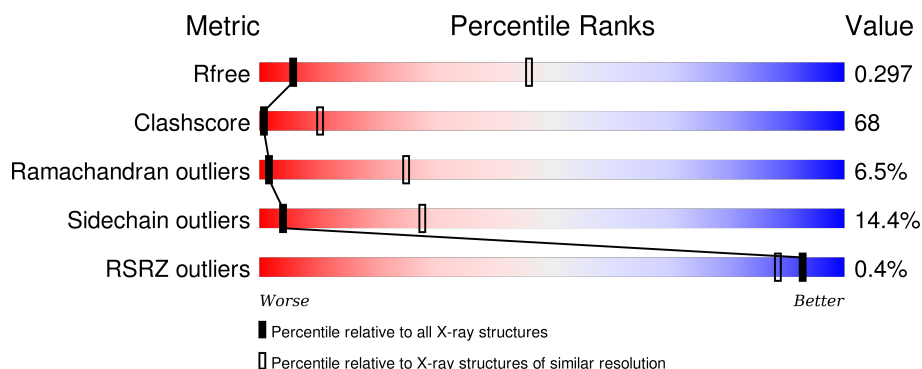
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 Å.

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






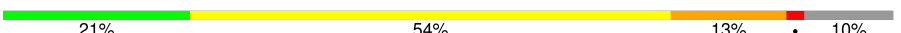
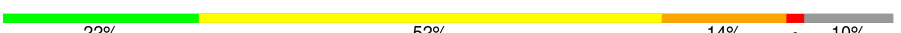
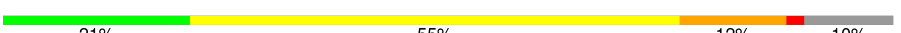
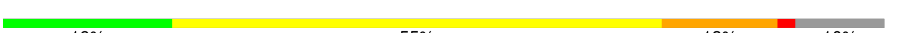




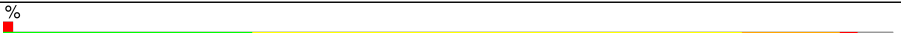

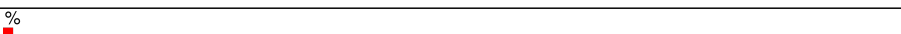

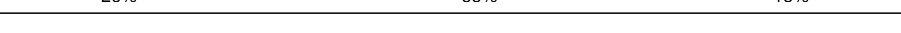
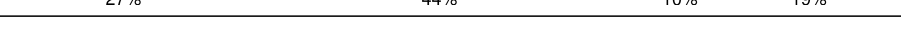
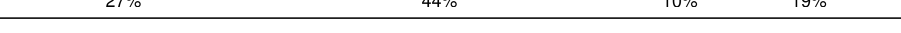
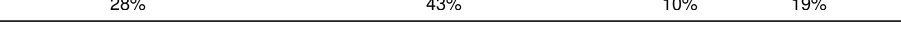
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	219	
1	G	219	
1	M	219	
1	S	219	
2	B	283	

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Mol	Chain	Length	Quality of chain
2	H	283	
2	N	283	
2	T	283	
3	C	159	
3	I	159	
3	O	159	
3	U	159	
4	D	193	
4	E	193	
4	J	193	
4	K	193	
4	P	193	
4	Q	193	
4	V	193	
4	W	193	
5	F	206	
5	L	206	
5	R	206	
5	X	206	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 32776 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Transport protein particle 23 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	27	0	0
			1285	833	204	239	9			
1	G	159	Total	C	N	O	S	27	0	0
			1285	833	204	239	9			
1	M	159	Total	C	N	O	S	27	0	0
			1285	833	204	239	9			
1	S	159	Total	C	N	O	S	27	0	0
			1285	833	204	239	9			

- Molecule 2 is a protein called Transport protein particle 31 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	167	Total	C	N	O	S	47	0	0
			1359	869	235	246	9			
2	H	167	Total	C	N	O	S	47	0	0
			1359	869	235	246	9			
2	N	167	Total	C	N	O	S	47	0	0
			1359	869	235	246	9			
2	T	167	Total	C	N	O	S	47	0	0
			1359	869	235	246	9			

- Molecule 3 is a protein called Transport protein particle 18 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	143	Total	C	N	O	S	12	0	0
			1190	765	201	217	7			
3	I	143	Total	C	N	O	S	16	0	0
			1190	765	201	217	7			
3	O	143	Total	C	N	O	S	12	0	0
			1190	765	201	217	7			
3	U	143	Total	C	N	O	S	16	0	0
			1190	765	201	217	7			

- Molecule 4 is a protein called Transport protein particle 22 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	186	Total	C	N	O	S	28	0	0
			1500	956	246	287	11			
4	E	188	Total	C	N	O	S	1	0	0
			1515	964	249	291	11			
4	J	186	Total	C	N	O	S	28	0	0
			1500	956	246	287	11			
4	K	188	Total	C	N	O	S	1	0	0
			1515	964	249	291	11			
4	P	186	Total	C	N	O	S	28	0	0
			1500	956	246	287	11			
4	Q	188	Total	C	N	O	S	1	0	0
			1515	964	249	291	11			
4	V	186	Total	C	N	O	S	28	0	0
			1500	956	246	287	11			
4	W	188	Total	C	N	O	S	1	0	0
			1515	964	249	291	11			

- Molecule 5 is a protein called GTP-binding protein YPT1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	166	Total	C	N	O	S	33	0	0
			1328	848	215	259	6			
5	L	166	Total	C	N	O	S	33	0	0
			1328	848	215	259	6			
5	R	166	Total	C	N	O	S	33	0	0
			1328	848	215	259	6			
5	X	166	Total	C	N	O	S	33	0	0
			1328	848	215	259	6			

- Molecule 6 is PALMITIC ACID (three-letter code: PLM) (formula: C₁₆H₃₂O₂).

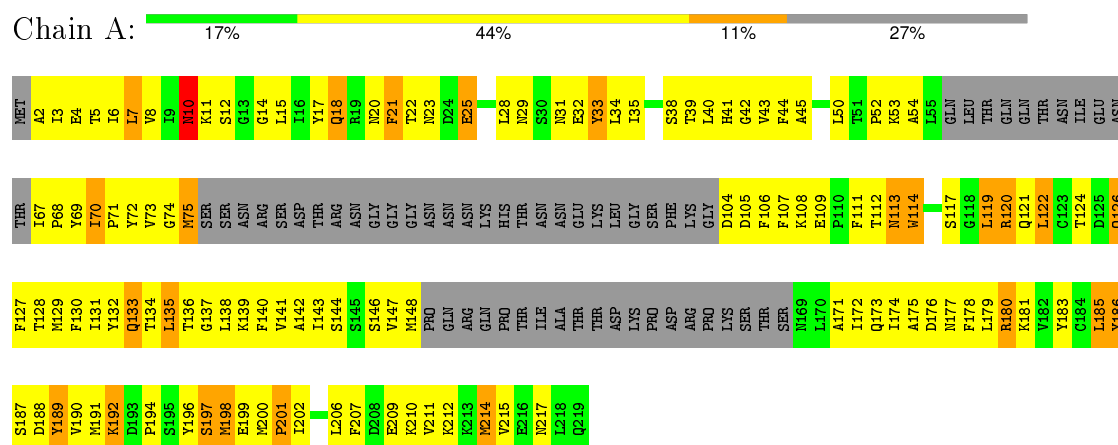


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			17	16	1		
6	K	1	Total	C	O	0	0
			17	16	1		
6	Q	1	Total	C	O	0	0
			17	16	1		
6	W	1	Total	C	O	0	0
			17	16	1		

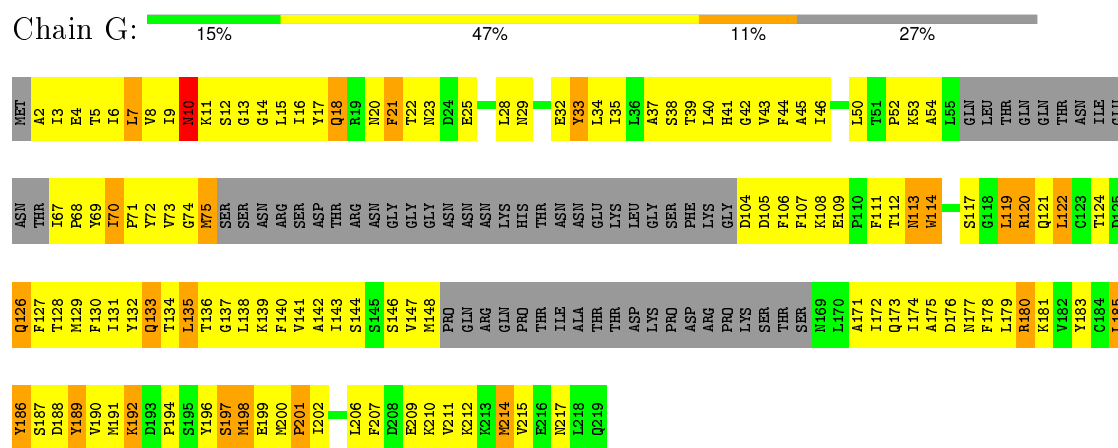
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

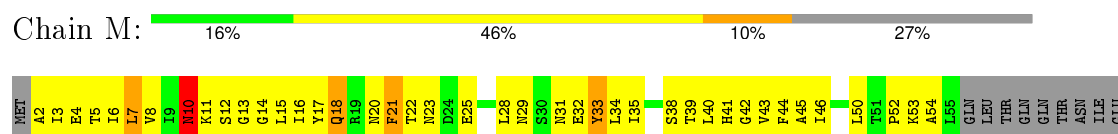
- Molecule 1: Transport protein particle 23 kDa subunit



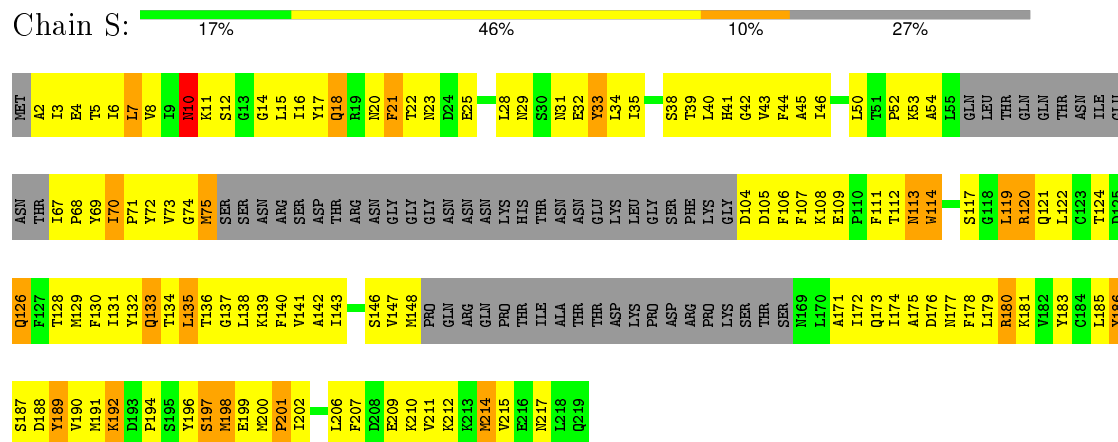
- Molecule 1: Transport protein particle 23 kDa subunit



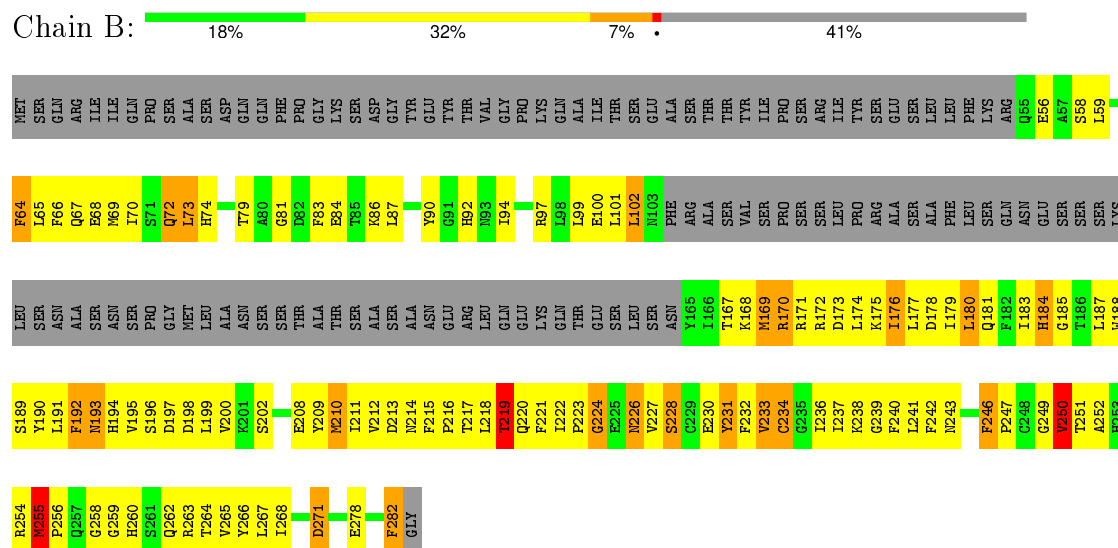
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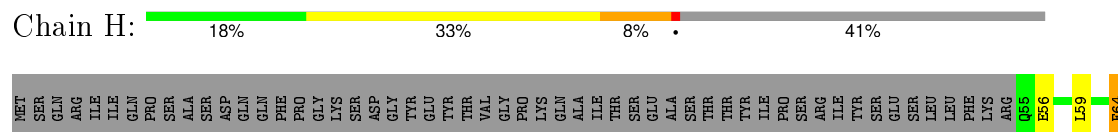
- Molecule 1: Transport protein particle 23 kDa subunit

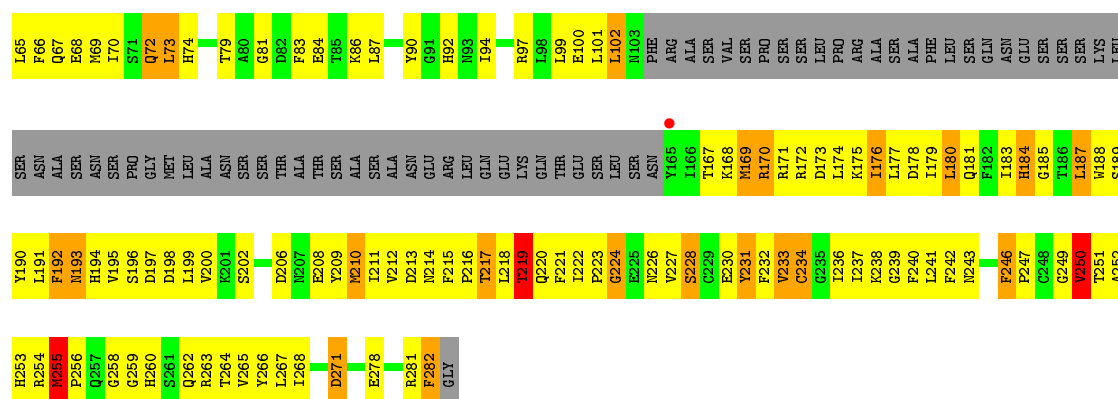


- Molecule 2: Transport protein particle 31 kDa subunit

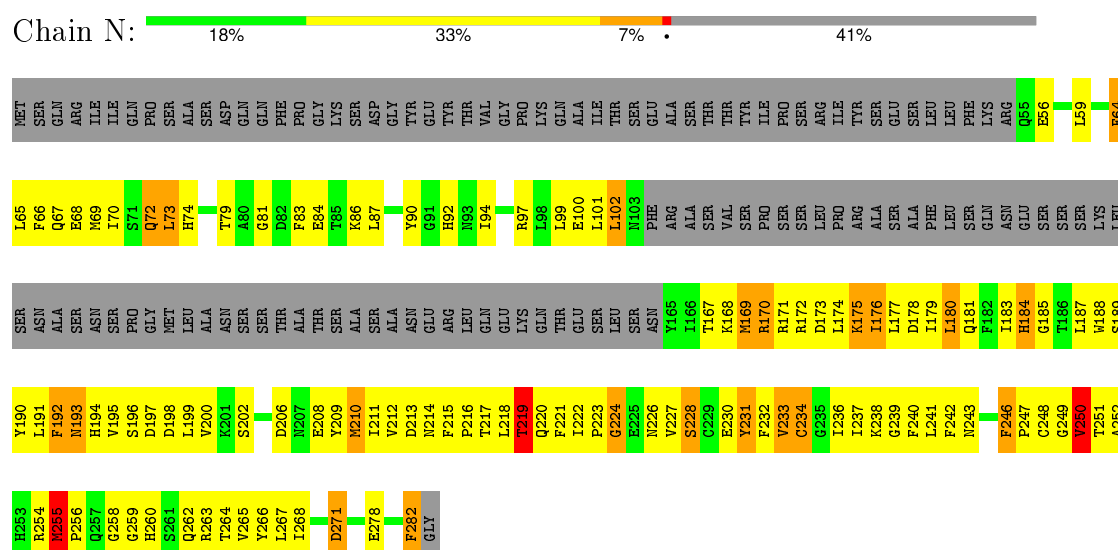


- Molecule 2: Transport protein particle 31 kDa subunit

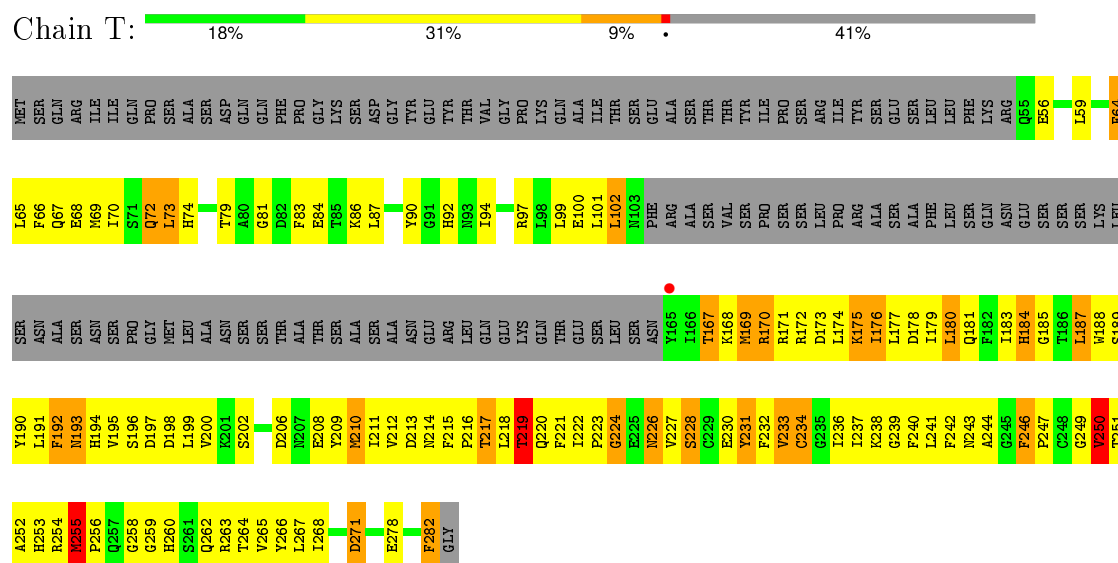




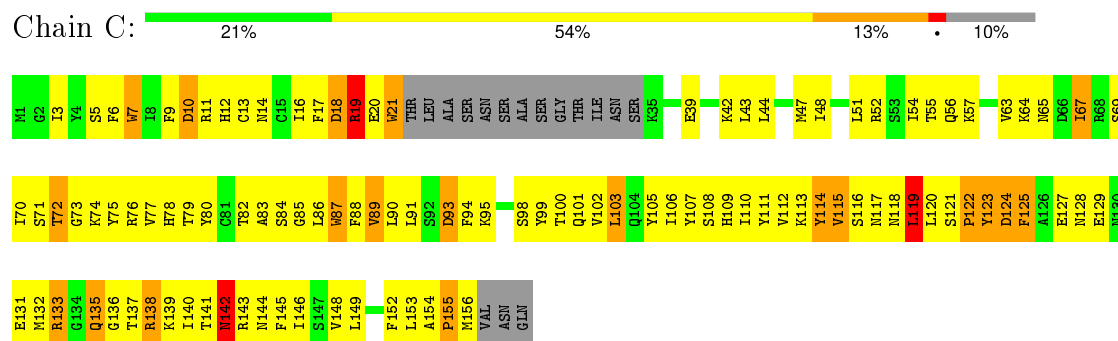
• Molecule 2: Transport protein particle 31 kDa subunit

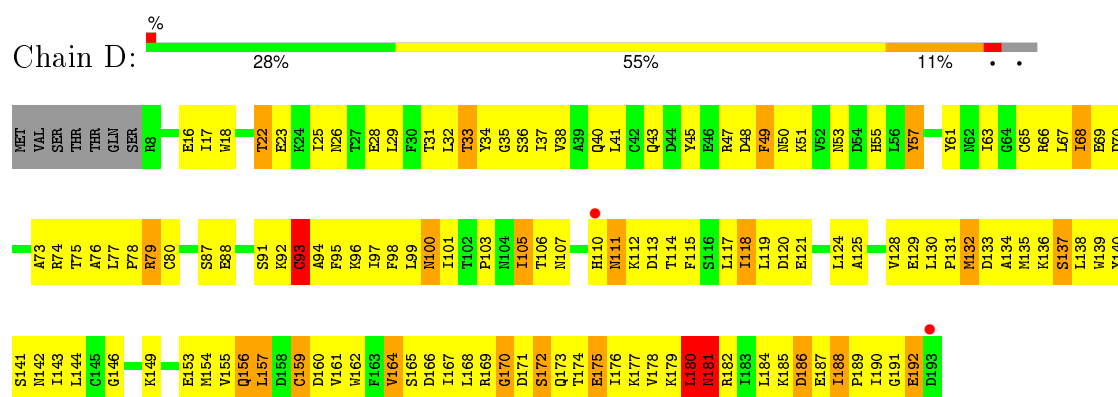


• Molecule 2: Transport protein particle 31 kDa subunit

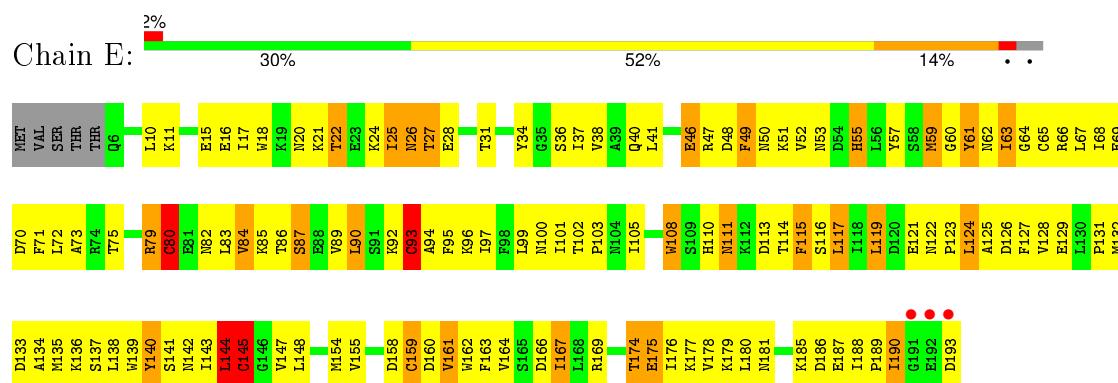


• Molecule 3: Transport protein particle 18 kDa subunit

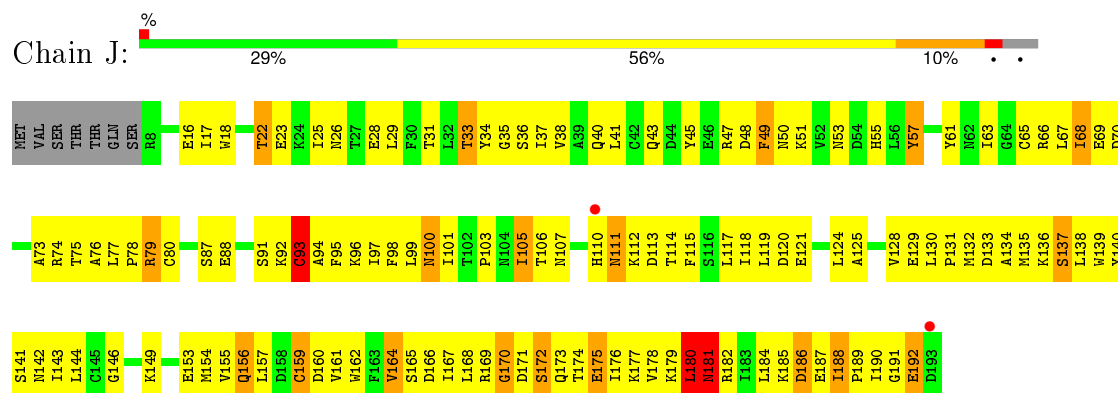




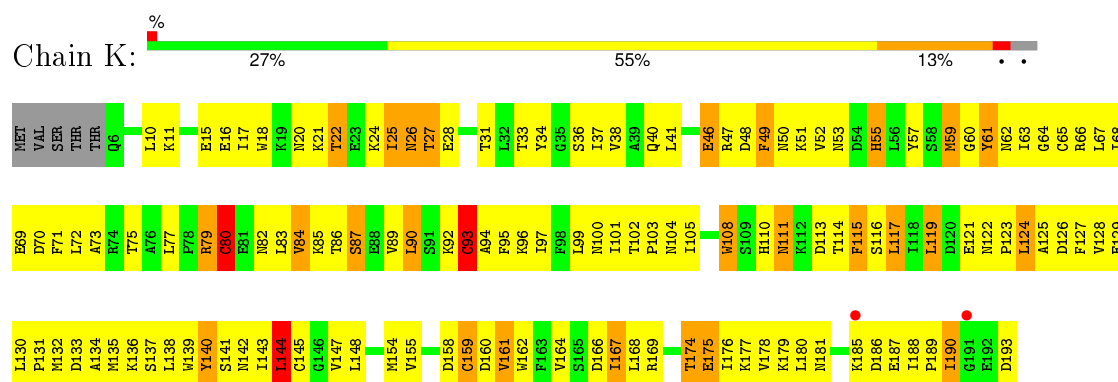
- Molecule 4: Transport protein particle 22 kDa subunit



- Molecule 4: Transport protein particle 22 kDa subunit



- Molecule 4: Transport protein particle 22 kDa subunit



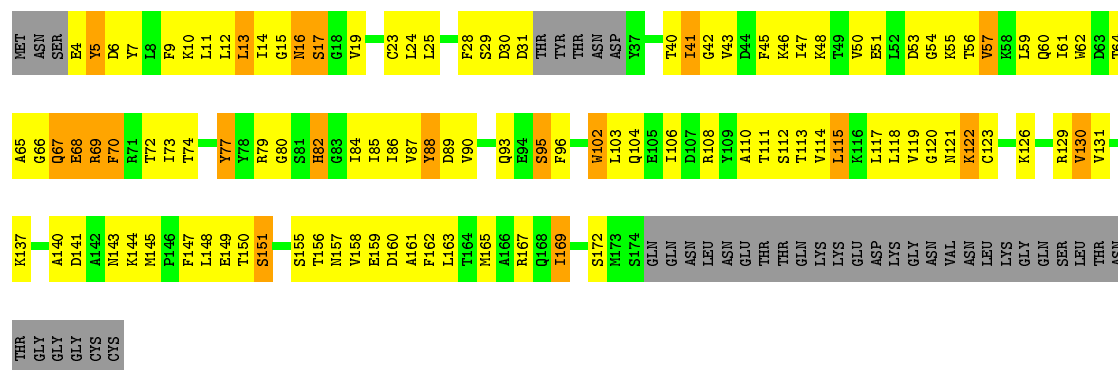
- Chain W: 26% 55% 15%

MET VAL SER THER THR O6
 I68 E89 D70 N82 L83 V84 K85 T86 S87 E88 W89 L90 S91 K92 C93 A94 F95 K96 I97 F98 L99 M100 I101 T102 P103 M104 I105 W108 S109 H110 M111 F112 D113 T114 F115 S116 L117 M118 I119 D120 E121 M122 P123 L124 A125 D126
 L10 K11 E15 E16 I17 W18 I19 M20 K21 T22 E23 K24 L25 M26 T27 E28 L29 F30 F31 T31 L32 T33 Y34 G35 S36 I37 V38 A39 Q40 L41 E46 R47 D48 F49 M50 V51 B52 M53 D54 L55 I56 Y57 S58 M59 G60 Y61 M62 I63



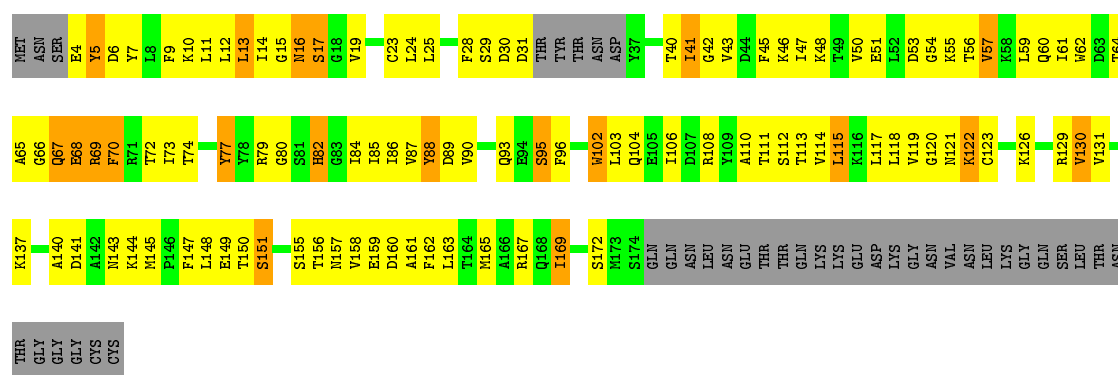
- Molecule 5: GTP-binding protein YPT1

Chain F: 27% 44% 10% 19%



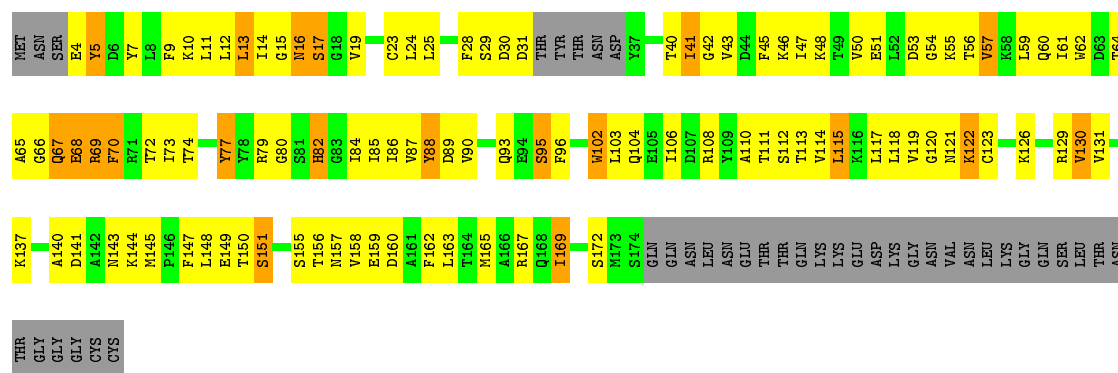
- Molecule 5: GTP-binding protein YPT1

Chain L: 27% 44% 10% 19%

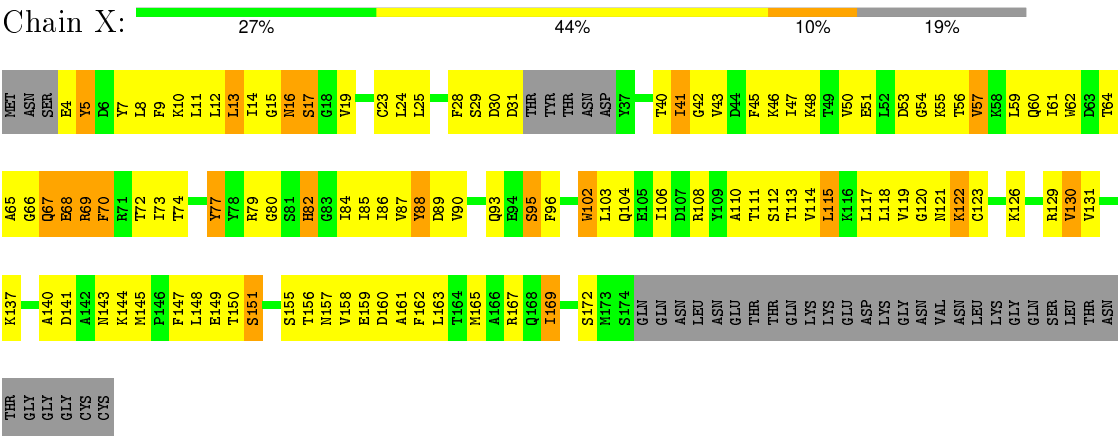


- Molecule 5: GTP-binding protein YPT1

Chain R: 28% 43% 10% 19%



- Molecule 5: GTP-binding protein YPT1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	115.12Å 115.40Å 290.07Å 90.00° 90.28° 90.00°	Depositor
Resolution (Å)	25.00 – 3.70 24.93 – 3.69	Depositor EDS
% Data completeness (in resolution range)	98.5 (25.00-3.70) 96.9 (24.93-3.69)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 3.74Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.265 , 0.299 0.268 , 0.297	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	128.9	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 58.5	EDS
Estimated twinning fraction	0.387 for -k,-h,-l 0.398 for k,h,-l 0.397 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 81195 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	32776	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PLM

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.67	1/1309 (0.1%)	0.82	0/1764
1	G	0.67	1/1309 (0.1%)	0.82	0/1764
1	M	0.66	1/1309 (0.1%)	0.82	0/1764
1	S	0.67	1/1309 (0.1%)	0.83	0/1764
2	B	0.56	0/1388	0.81	1/1869 (0.1%)
2	H	0.56	0/1388	0.81	1/1869 (0.1%)
2	N	0.55	0/1388	0.82	1/1869 (0.1%)
2	T	0.56	0/1388	0.82	1/1869 (0.1%)
3	C	0.68	1/1218 (0.1%)	0.86	1/1640 (0.1%)
3	I	0.68	1/1218 (0.1%)	0.86	1/1640 (0.1%)
3	O	0.67	1/1218 (0.1%)	0.87	0/1640
3	U	0.67	1/1218 (0.1%)	0.87	1/1640 (0.1%)
4	D	0.59	0/1527	0.83	2/2063 (0.1%)
4	E	0.68	1/1542 (0.1%)	0.93	4/2083 (0.2%)
4	J	0.60	0/1527	0.83	2/2063 (0.1%)
4	K	0.68	0/1542	0.93	4/2083 (0.2%)
4	P	0.60	0/1527	0.83	2/2063 (0.1%)
4	Q	0.69	0/1542	0.93	4/2083 (0.2%)
4	V	0.59	0/1527	0.83	2/2063 (0.1%)
4	W	0.68	0/1542	0.93	4/2083 (0.2%)
5	F	0.59	0/1348	0.92	7/1815 (0.4%)
5	L	0.60	0/1348	0.90	5/1815 (0.3%)
5	R	0.57	0/1348	0.89	5/1815 (0.3%)
5	X	0.59	0/1348	0.90	5/1815 (0.3%)
All	All	0.63	9/33328 (0.0%)	0.86	53/44936 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
4	J	0	1
4	P	0	1
4	V	0	1
All	All	0	4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	109	GLU	CD-OE2	7.58	1.33	1.25
1	G	109	GLU	CD-OE2	7.57	1.33	1.25
1	S	109	GLU	CD-OE2	7.45	1.33	1.25
1	A	109	GLU	CD-OE2	7.31	1.33	1.25
3	U	21	TRP	CB-CG	6.09	1.61	1.50
3	C	21	TRP	CB-CG	6.01	1.61	1.50
3	O	21	TRP	CB-CG	5.97	1.60	1.50
3	I	21	TRP	CB-CG	5.79	1.60	1.50
4	E	145	CYS	CB-SG	-5.26	1.73	1.81

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	144	LEU	CA-CB-CG	8.62	135.13	115.30
4	W	144	LEU	CA-CB-CG	8.46	134.75	115.30
4	E	144	LEU	CA-CB-CG	8.43	134.69	115.30
4	Q	144	LEU	CA-CB-CG	8.35	134.50	115.30
5	F	67	GLN	C-N-CA	-7.59	102.72	121.70
4	K	80	CYS	CA-CB-SG	-7.56	100.39	114.00
5	F	68	GLU	CA-C-N	-7.52	100.66	117.20
4	Q	80	CYS	CA-CB-SG	-7.42	100.65	114.00
4	W	80	CYS	CA-CB-SG	-7.40	100.68	114.00
4	V	93	CYS	N-CA-C	7.33	130.80	111.00
4	D	93	CYS	N-CA-C	7.31	130.73	111.00
4	J	93	CYS	N-CA-C	7.27	130.62	111.00
4	E	80	CYS	CA-CB-SG	-7.24	100.96	114.00
4	P	93	CYS	N-CA-C	7.20	130.44	111.00
5	L	68	GLU	CA-C-N	-6.71	102.44	117.20
4	E	190	ILE	CG1-CB-CG2	6.69	126.12	111.40
4	Q	190	ILE	CG1-CB-CG2	6.69	126.12	111.40
4	K	190	ILE	CG1-CB-CG2	6.67	126.08	111.40
4	W	190	ILE	CG1-CB-CG2	6.67	126.08	111.40
4	Q	93	CYS	N-CA-C	6.47	128.46	111.00
5	X	68	GLU	CA-C-N	-6.46	102.99	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	W	93	CYS	N-CA-C	6.42	128.34	111.00
4	E	93	CYS	N-CA-C	6.42	128.32	111.00
4	K	93	CYS	N-CA-C	6.38	128.22	111.00
5	R	68	GLU	CA-C-N	-6.06	103.87	117.20
5	X	67	GLN	C-N-CA	-5.89	106.97	121.70
2	T	224	GLY	N-CA-C	5.88	127.80	113.10
2	N	224	GLY	N-CA-C	5.82	127.66	113.10
2	H	224	GLY	N-CA-C	5.81	127.61	113.10
2	B	224	GLY	N-CA-C	5.79	127.57	113.10
5	R	67	GLN	C-N-CA	-5.78	107.26	121.70
5	L	17	SER	N-CA-C	5.77	126.58	111.00
5	X	17	SER	N-CA-C	5.77	126.58	111.00
5	R	17	SER	N-CA-C	5.72	126.46	111.00
5	F	17	SER	N-CA-C	5.68	126.34	111.00
5	F	74	THR	N-CA-C	5.57	126.05	111.00
5	R	74	THR	N-CA-C	5.55	126.00	111.00
5	X	74	THR	N-CA-C	5.52	125.91	111.00
5	F	67	GLN	N-CA-C	-5.49	96.19	111.00
5	L	67	GLN	C-N-CA	-5.48	107.99	121.70
5	L	74	THR	N-CA-C	5.47	125.78	111.00
4	D	172	SER	N-CA-C	5.29	125.27	111.00
4	P	172	SER	N-CA-C	5.25	125.18	111.00
4	J	172	SER	N-CA-C	5.20	125.05	111.00
5	R	42	GLY	N-CA-C	-5.19	100.12	113.10
5	L	42	GLY	N-CA-C	-5.19	100.12	113.10
4	V	172	SER	N-CA-C	5.16	124.93	111.00
5	X	42	GLY	N-CA-C	-5.15	100.22	113.10
5	F	68	GLU	O-C-N	5.14	130.92	122.70
3	U	115	VAL	N-CA-C	5.10	124.78	111.00
3	C	115	VAL	N-CA-C	5.07	124.69	111.00
5	F	42	GLY	N-CA-C	-5.03	100.53	113.10
3	I	115	VAL	N-CA-C	5.03	124.57	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	57	TYR	Sidechain
4	J	57	TYR	Sidechain
4	P	57	TYR	Sidechain
4	V	57	TYR	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1285	0	1290	216	0
1	G	1285	0	1290	225	0
1	M	1285	0	1290	218	0
1	S	1285	0	1290	218	0
2	B	1359	0	1335	166	0
2	H	1359	0	1335	173	0
2	N	1359	0	1335	169	0
2	T	1359	0	1335	172	0
3	C	1190	0	1166	213	0
3	I	1190	0	1166	220	0
3	O	1190	0	1166	213	0
3	U	1190	0	1166	228	0
4	D	1500	0	1500	211	0
4	E	1515	0	1512	179	0
4	J	1500	0	1500	209	0
4	K	1515	0	1512	187	0
4	P	1500	0	1500	209	0
4	Q	1515	0	1512	200	0
4	V	1500	0	1500	209	0
4	W	1515	0	1512	203	0
5	F	1328	0	1329	178	0
5	L	1328	0	1329	181	0
5	R	1328	0	1329	175	0
5	X	1328	0	1329	182	0
6	E	17	0	31	6	0
6	K	17	0	31	5	0
6	Q	17	0	31	7	0
6	W	17	0	31	6	0
All	All	32776	0	32652	4335	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 68.

All (4335) 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)
4:D:79:ARG:HH21	4:D:190:ILE:HD12	1.04	1.17
4:P:79:ARG:HH21	4:P:190:ILE:HD12	1.01	1.17
3:C:39:GLU:HA	3:C:42:LYS:HE2	1.22	1.16
5:L:68:GLU:HG2	5:L:69:ARG:H	1.09	1.16
4:V:79:ARG:HH21	4:V:190:ILE:HD12	1.02	1.16
3:I:39:GLU:HA	3:I:42:LYS:HE2	1.22	1.16
3:O:119:LEU:H	3:O:119:LEU:HD23	1.06	1.15
3:O:39:GLU:HA	3:O:42:LYS:HE2	1.24	1.15
4:P:49:PHE:HB3	4:P:138:LEU:HD12	1.18	1.15
3:U:39:GLU:HA	3:U:42:LYS:HE2	1.22	1.15
5:F:120:GLY:HA3	5:F:149:GLU:HG3	1.17	1.15
3:C:119:LEU:H	3:C:119:LEU:HD23	1.03	1.14
5:R:68:GLU:CG	5:R:69:ARG:N	2.08	1.14
3:U:119:LEU:HD23	3:U:119:LEU:H	1.05	1.14
4:J:79:ARG:HH21	4:J:190:ILE:HD12	1.02	1.14
4:D:49:PHE:HB3	4:D:138:LEU:HD12	1.18	1.14
5:F:68:GLU:HG2	5:F:69:ARG:H	1.11	1.14
4:Q:37:ILE:HD11	4:W:37:ILE:HD11	1.17	1.13
5:R:120:GLY:HA3	5:R:149:GLU:HG3	1.15	1.13
3:I:119:LEU:H	3:I:119:LEU:HD23	1.07	1.13
4:V:49:PHE:HB3	4:V:138:LEU:HD12	1.20	1.12
5:F:69:ARG:HB2	5:F:72:THR:HG22	1.28	1.10
5:X:120:GLY:HA3	5:X:149:GLU:HG3	1.15	1.10
5:L:120:GLY:HA3	5:L:149:GLU:HG3	1.15	1.10
5:R:68:GLU:HG2	5:R:69:ARG:H	1.08	1.10
4:J:49:PHE:HB3	4:J:138:LEU:HD12	1.17	1.10
5:X:68:GLU:HG2	5:X:69:ARG:H	1.05	1.09
3:C:77:VAL:HG12	3:C:91:LEU:HD22	1.35	1.09
1:A:10:ASN:HD22	1:A:11:LYS:N	1.50	1.09
3:I:77:VAL:HG12	3:I:91:LEU:HD22	1.34	1.09
3:O:77:VAL:HG12	3:O:91:LEU:HD22	1.35	1.08
3:I:82:THR:HG22	3:I:84:SER:H	1.12	1.08
1:M:10:ASN:HD22	1:M:11:LYS:N	1.51	1.08
5:R:69:ARG:HB2	5:R:72:THR:HG22	1.28	1.08
3:C:82:THR:HG22	3:C:84:SER:H	1.14	1.08
5:F:68:GLU:CG	5:F:69:ARG:N	2.10	1.08
3:O:82:THR:HG22	3:O:84:SER:H	1.12	1.08
5:L:68:GLU:CG	5:L:69:ARG:N	2.05	1.07
3:I:7:TRP:HB2	3:I:89:VAL:HG12	1.36	1.07
3:U:77:VAL:HG12	3:U:91:LEU:HD22	1.35	1.07
5:X:69:ARG:HB2	5:X:72:THR:HG22	1.31	1.07
3:U:82:THR:HG22	3:U:84:SER:H	1.14	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:10:ASN:HD22	1:S:11:LYS:N	1.51	1.06
5:F:69:ARG:HB2	5:F:72:THR:CG2	1.85	1.06
3:U:7:TRP:HB2	3:U:89:VAL:HG12	1.38	1.06
4:K:60:GLY:HA2	4:K:63:ILE:HD11	1.37	1.05
1:G:10:ASN:HD22	1:G:11:LYS:N	1.52	1.05
4:W:60:GLY:HA2	4:W:63:ILE:HD11	1.38	1.05
5:F:103:LEU:HD21	5:F:145:MET:HE1	1.31	1.04
2:B:214:ASN:HA	2:B:263:ARG:HG3	1.39	1.04
5:L:69:ARG:HB2	5:L:72:THR:HG22	1.36	1.04
2:H:214:ASN:HA	2:H:263:ARG:HG3	1.39	1.04
5:X:103:LEU:HD21	5:X:145:MET:HE1	1.32	1.04
5:F:150:THR:HB	5:F:155:SER:CB	1.88	1.03
5:R:150:THR:HB	5:R:155:SER:CB	1.88	1.03
3:O:7:TRP:HB2	3:O:89:VAL:HG12	1.38	1.03
1:S:120:ARG:HH11	1:S:120:ARG:HB3	1.23	1.03
2:N:214:ASN:HA	2:N:263:ARG:HG3	1.39	1.03
4:E:60:GLY:HA2	4:E:63:ILE:HD11	1.38	1.03
5:X:150:THR:HB	5:X:155:SER:CB	1.87	1.03
5:L:150:THR:HB	5:L:155:SER:CB	1.87	1.03
5:X:69:ARG:HB2	5:X:72:THR:CG2	1.88	1.03
3:C:7:TRP:HB2	3:C:89:VAL:HG12	1.38	1.03
2:T:214:ASN:HA	2:T:263:ARG:HG3	1.40	1.03
5:X:150:THR:CB	5:X:155:SER:HB2	1.89	1.02
1:M:147:VAL:HG12	1:M:148:MET:H	1.21	1.02
5:R:69:ARG:HB2	5:R:72:THR:CG2	1.88	1.02
5:L:150:THR:CB	5:L:155:SER:HB2	1.89	1.02
5:R:150:THR:CB	5:R:155:SER:HB2	1.90	1.02
1:S:137:GLY:HA2	4:V:188:ILE:HG21	1.42	1.02
5:F:150:THR:CB	5:F:155:SER:HB2	1.90	1.02
2:N:231:TYR:HD2	2:N:234:CYS:HG	1.08	1.02
4:Q:60:GLY:HA2	4:Q:63:ILE:HD11	1.40	1.02
1:M:120:ARG:HH11	1:M:120:ARG:HB3	1.24	1.02
1:A:137:GLY:HA2	4:D:188:ILE:HG21	1.38	1.01
1:G:137:GLY:HA2	4:J:188:ILE:HG21	1.42	1.01
5:X:68:GLU:CG	5:X:69:ARG:H	1.59	1.00
5:X:68:GLU:CG	5:X:69:ARG:N	2.07	1.00
1:G:120:ARG:HH11	1:G:120:ARG:HB3	1.25	1.00
5:X:110:ALA:HB1	5:X:114:VAL:HG21	1.42	1.00
5:R:110:ALA:HB1	5:R:114:VAL:HG21	1.43	1.00
5:F:110:ALA:HB1	5:F:114:VAL:HG21	1.43	1.00
1:M:21:PHE:HD1	1:M:22:THR:H	1.07	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:PHE:HD1	1:A:22:THR:H	1.06	0.99
1:G:147:VAL:HG12	1:G:148:MET:H	1.22	0.98
5:R:103:LEU:HD21	5:R:145:MET:HE1	1.44	0.98
1:A:120:ARG:HB3	1:A:120:ARG:HH11	1.26	0.98
5:L:69:ARG:HB2	5:L:72:THR:CG2	1.93	0.98
2:B:231:TYR:HD2	2:B:234:CYS:HG	1.10	0.98
1:M:137:GLY:HA2	4:P:188:ILE:HG21	1.42	0.98
5:R:68:GLU:CG	5:R:69:ARG:H	1.65	0.97
1:A:147:VAL:HG12	1:A:148:MET:H	1.23	0.97
1:S:126:GLN:HG3	3:U:65:ASN:HB2	1.46	0.97
5:L:68:GLU:HG2	5:L:69:ARG:N	1.71	0.97
1:G:15:LEU:HB3	1:G:34:LEU:HD23	1.46	0.97
5:R:47:ILE:HG12	5:R:60:GLN:HA	1.46	0.97
4:V:180:LEU:H	4:V:180:LEU:HD12	1.30	0.97
4:D:106:THR:HG22	4:D:107:ASN:H	1.30	0.97
1:A:15:LEU:HB3	1:A:34:LEU:HD23	1.47	0.96
4:P:106:THR:HG22	4:P:107:ASN:H	1.30	0.96
5:L:110:ALA:HB1	5:L:114:VAL:HG21	1.44	0.96
3:C:51:LEU:O	3:C:54:ILE:HG22	1.65	0.96
4:D:180:LEU:HD12	4:D:180:LEU:H	1.30	0.96
5:L:103:LEU:HD21	5:L:145:MET:HE1	1.47	0.96
1:A:126:GLN:HG3	3:C:65:ASN:HB2	1.47	0.96
4:P:99:LEU:HD12	4:P:101:ILE:HD11	1.48	0.96
1:S:147:VAL:HG12	1:S:148:MET:H	1.29	0.96
1:S:15:LEU:HB3	1:S:34:LEU:HD23	1.47	0.96
1:M:15:LEU:HB3	1:M:34:LEU:HD23	1.48	0.96
5:F:89:ASP:HA	5:F:121:ASN:HD21	1.31	0.95
4:D:99:LEU:HD12	4:D:101:ILE:HD11	1.48	0.95
1:G:21:PHE:HD1	1:G:22:THR:H	1.08	0.95
2:H:188:TRP:HH2	2:H:266:TYR:HE1	1.09	0.95
4:J:180:LEU:H	4:J:180:LEU:HD12	1.31	0.95
1:S:21:PHE:HD1	1:S:22:THR:H	1.06	0.95
4:P:180:LEU:H	4:P:180:LEU:HD12	1.30	0.95
4:V:99:LEU:HD12	4:V:101:ILE:HD11	1.48	0.95
5:F:47:ILE:HG12	5:F:60:GLN:HA	1.47	0.95
5:R:89:ASP:HA	5:R:121:ASN:HD21	1.31	0.95
1:G:10:ASN:HB3	1:G:14:GLY:H	1.30	0.94
1:G:126:GLN:HG3	3:I:65:ASN:HB2	1.49	0.94
4:V:106:THR:HG22	4:V:107:ASN:H	1.30	0.94
4:W:119:LEU:O	4:W:174:THR:HG21	1.68	0.94
4:J:106:THR:HG22	4:J:107:ASN:H	1.29	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:119:LEU:HD12	4:V:120:ASP:H	1.31	0.94
1:M:126:GLN:HG3	3:O:65:ASN:HB2	1.50	0.94
2:T:188:TRP:HH2	2:T:266:TYR:HE1	1.10	0.94
4:D:119:LEU:HD12	4:D:120:ASP:H	1.31	0.94
5:F:68:GLU:CG	5:F:69:ARG:H	1.66	0.94
4:J:119:LEU:HD12	4:J:120:ASP:H	1.31	0.94
1:S:10:ASN:HB3	1:S:14:GLY:H	1.31	0.93
5:X:68:GLU:HG2	5:X:69:ARG:N	1.75	0.93
2:N:188:TRP:HH2	2:N:266:TYR:HE1	1.09	0.93
1:M:10:ASN:HB3	1:M:14:GLY:H	1.30	0.93
5:X:47:ILE:HG12	5:X:60:GLN:HA	1.47	0.93
4:J:99:LEU:HD12	4:J:101:ILE:HD11	1.50	0.93
2:B:188:TRP:HH2	2:B:266:TYR:HE1	1.09	0.92
5:R:68:GLU:HG2	5:R:69:ARG:N	1.75	0.92
3:O:51:LEU:O	3:O:54:ILE:HG22	1.70	0.92
3:U:51:LEU:O	3:U:54:ILE:HG22	1.69	0.92
5:F:68:GLU:HG2	5:F:69:ARG:N	1.76	0.92
5:L:47:ILE:HG12	5:L:60:GLN:HA	1.49	0.92
2:N:262:GLN:O	2:N:264:THR:HG23	1.70	0.92
4:P:119:LEU:HD12	4:P:120:ASP:H	1.32	0.92
5:L:89:ASP:HA	5:L:121:ASN:HD21	1.32	0.92
1:A:10:ASN:HB3	1:A:14:GLY:H	1.32	0.91
5:L:9:PHE:HB2	5:L:59:LEU:HD23	1.51	0.91
1:A:200:MET:HE3	5:F:7:TYR:HA	1.51	0.91
2:N:232:PHE:O	2:N:236:ILE:HD12	1.69	0.91
2:H:262:GLN:O	2:H:264:THR:HG23	1.69	0.91
4:Q:119:LEU:O	4:Q:174:THR:HG21	1.70	0.91
5:X:89:ASP:HA	5:X:121:ASN:HD21	1.32	0.91
4:K:119:LEU:O	4:K:174:THR:HG21	1.71	0.91
2:B:262:GLN:O	2:B:264:THR:HG23	1.70	0.91
4:P:22:THR:HB	4:P:74:ARG:HH12	1.34	0.91
3:I:51:LEU:O	3:I:54:ILE:HG22	1.69	0.91
4:P:79:ARG:NH2	4:P:190:ILE:HD12	1.86	0.91
3:I:112:VAL:HG12	3:I:117:ASN:ND2	1.84	0.91
4:V:22:THR:HB	4:V:74:ARG:HH12	1.34	0.91
1:M:142:ALA:HB2	1:M:179:LEU:HD21	1.50	0.91
3:U:112:VAL:HG12	3:U:117:ASN:ND2	1.84	0.90
5:X:9:PHE:HB2	5:X:59:LEU:HD23	1.51	0.90
1:A:142:ALA:HB2	1:A:179:LEU:HD21	1.51	0.90
3:C:119:LEU:HD23	3:C:119:LEU:N	1.85	0.90
4:Q:161:VAL:HG13	4:Q:178:VAL:HG22	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:112:VAL:HG12	3:O:117:ASN:ND2	1.85	0.90
4:D:22:THR:HB	4:D:74:ARG:HH12	1.35	0.90
4:V:155:VAL:O	4:V:156:GLN:HG2	1.70	0.90
2:T:232:PHE:O	2:T:236:ILE:HD12	1.70	0.90
2:T:262:GLN:O	2:T:264:THR:HG23	1.70	0.90
1:G:194:PRO:HG3	2:H:67:GLN:HB2	1.51	0.90
4:V:79:ARG:NH2	4:V:190:ILE:HD12	1.87	0.90
4:P:155:VAL:O	4:P:156:GLN:HG2	1.70	0.90
4:E:119:LEU:O	4:E:174:THR:HG21	1.70	0.90
1:G:142:ALA:HB2	1:G:179:LEU:HD21	1.51	0.90
5:F:11:LEU:HD11	5:F:59:LEU:HD22	1.53	0.90
5:F:9:PHE:HB2	5:F:59:LEU:HD23	1.51	0.90
5:F:14:ILE:HG22	5:F:64:THR:HG21	1.54	0.90
1:S:194:PRO:HG3	2:T:67:GLN:HB2	1.52	0.90
3:U:112:VAL:HG12	3:U:117:ASN:HD21	1.36	0.90
4:J:22:THR:HB	4:J:74:ARG:HH12	1.35	0.90
3:C:112:VAL:HG12	3:C:117:ASN:ND2	1.85	0.90
4:E:161:VAL:HG13	4:E:178:VAL:HG22	1.53	0.90
4:J:79:ARG:NH2	4:J:190:ILE:HD12	1.87	0.90
5:F:12:LEU:HD23	5:F:12:LEU:H	1.37	0.90
5:X:11:LEU:HD11	5:X:59:LEU:HD22	1.53	0.89
5:R:9:PHE:HB2	5:R:59:LEU:HD23	1.52	0.89
1:M:200:MET:HE3	5:R:7:TYR:HA	1.52	0.89
1:S:142:ALA:HB2	1:S:179:LEU:HD21	1.54	0.89
1:A:194:PRO:HG3	2:B:67:GLN:HB2	1.54	0.89
4:K:161:VAL:HG13	4:K:178:VAL:HG22	1.52	0.89
4:V:188:ILE:HD11	4:V:190:ILE:HD11	1.54	0.89
5:X:150:THR:HB	5:X:155:SER:HB2	0.93	0.89
3:I:82:THR:HG21	3:I:84:SER:OG	1.72	0.89
2:H:232:PHE:O	2:H:236:ILE:HD12	1.72	0.89
4:J:164:VAL:HB	4:J:175:GLU:OE2	1.72	0.89
4:V:164:VAL:HB	4:V:175:GLU:OE2	1.73	0.89
4:P:188:ILE:HD11	4:P:190:ILE:HD11	1.53	0.89
3:I:112:VAL:HG12	3:I:117:ASN:HD21	1.37	0.89
4:P:188:ILE:CD1	4:P:190:ILE:HD11	2.03	0.88
5:R:14:ILE:HG22	5:R:64:THR:HG21	1.55	0.88
4:J:188:ILE:CD1	4:J:190:ILE:HD11	2.03	0.88
1:M:194:PRO:HG3	2:N:67:GLN:HB2	1.55	0.88
4:D:155:VAL:O	4:D:156:GLN:HG2	1.72	0.88
4:D:79:ARG:NH2	4:D:190:ILE:HD12	1.89	0.88
4:J:155:VAL:O	4:J:156:GLN:HG2	1.72	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:188:TRP:CH2	2:B:266:TYR:HE1	1.91	0.88
2:B:232:PHE:O	2:B:236:ILE:HD12	1.73	0.88
5:X:14:ILE:HG22	5:X:64:THR:HG21	1.55	0.88
3:O:82:THR:HG21	3:O:84:SER:OG	1.74	0.88
4:D:164:VAL:HB	4:D:175:GLU:OE2	1.73	0.88
3:U:119:LEU:HD23	3:U:119:LEU:N	1.87	0.88
4:J:188:ILE:HD11	4:J:190:ILE:HD11	1.54	0.88
5:R:150:THR:HB	5:R:155:SER:HB2	0.94	0.88
5:R:11:LEU:HD11	5:R:59:LEU:HD22	1.55	0.88
5:L:14:ILE:HG22	5:L:64:THR:HG21	1.55	0.88
4:P:164:VAL:HB	4:P:175:GLU:OE2	1.72	0.88
4:D:188:ILE:CD1	4:D:190:ILE:HD11	2.04	0.87
2:N:188:TRP:CH2	2:N:266:TYR:HE1	1.92	0.87
5:R:123:CYS:HB3	5:R:151:SER:HA	1.57	0.87
5:L:150:THR:HB	5:L:155:SER:HB2	0.93	0.87
1:G:200:MET:HE3	5:L:7:TYR:HA	1.55	0.87
3:O:9:PHE:HB2	3:O:87:TRP:HB2	1.56	0.87
3:O:119:LEU:N	3:O:119:LEU:HD23	1.88	0.87
5:F:150:THR:HB	5:F:155:SER:HB2	0.94	0.87
2:H:188:TRP:CH2	2:H:266:TYR:HE1	1.91	0.87
5:L:11:LEU:HD11	5:L:59:LEU:HD22	1.55	0.87
4:P:156:GLN:HA	4:P:184:LEU:HD12	1.55	0.87
4:V:188:ILE:CD1	4:V:190:ILE:HD11	2.05	0.87
2:T:188:TRP:CH2	2:T:266:TYR:HE1	1.92	0.87
5:R:12:LEU:HD23	5:R:12:LEU:H	1.40	0.86
3:I:9:PHE:HB2	3:I:87:TRP:HB2	1.55	0.86
5:X:118:LEU:HB3	5:X:147:PHE:HB2	1.57	0.86
5:X:12:LEU:H	5:X:12:LEU:HD23	1.39	0.86
4:D:188:ILE:HD11	4:D:190:ILE:HD11	1.55	0.86
3:U:9:PHE:HB2	3:U:87:TRP:HB2	1.55	0.86
4:V:156:GLN:HA	4:V:184:LEU:HD12	1.56	0.86
3:I:119:LEU:N	3:I:119:LEU:HD23	1.89	0.86
3:I:43:LEU:HD12	3:I:44:LEU:N	1.90	0.86
3:U:43:LEU:HD12	3:U:44:LEU:N	1.90	0.86
3:C:9:PHE:HB2	3:C:87:TRP:HB2	1.58	0.86
5:L:12:LEU:H	5:L:12:LEU:HD23	1.39	0.85
3:O:3:ILE:HB	3:O:90:LEU:HD11	1.56	0.85
4:W:161:VAL:HG13	4:W:178:VAL:HG22	1.56	0.85
5:F:123:CYS:HB3	5:F:151:SER:HA	1.58	0.85
3:I:71:SER:OG	3:I:76:ARG:HD3	1.76	0.85
3:C:82:THR:HG21	3:C:84:SER:OG	1.77	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:67:LEU:HD11	4:P:98:PHE:CE2	2.12	0.85
4:J:156:GLN:HA	4:J:184:LEU:HD12	1.56	0.85
3:C:43:LEU:HD12	3:C:44:LEU:N	1.89	0.85
1:S:133:GLN:CB	1:S:139:LYS:HG2	2.06	0.85
3:C:119:LEU:H	3:C:119:LEU:CD2	1.83	0.85
3:C:107:TYR:HE2	4:E:73:ALA:HA	1.40	0.85
3:C:112:VAL:HG12	3:C:117:ASN:HD21	1.39	0.85
3:O:43:LEU:HD12	3:O:44:LEU:N	1.89	0.85
3:C:3:ILE:HB	3:C:90:LEU:HD11	1.56	0.85
3:O:112:VAL:HG12	3:O:117:ASN:HD21	1.37	0.85
4:D:156:GLN:HA	4:D:184:LEU:HD12	1.56	0.85
4:K:21:LYS:O	4:K:22:THR:HG23	1.77	0.85
5:L:123:CYS:HB3	5:L:151:SER:HA	1.57	0.85
4:E:143:ILE:O	4:E:147:VAL:HG23	1.76	0.85
5:L:108:ARG:HB2	5:L:108:ARG:NH1	1.92	0.84
3:C:71:SER:OG	3:C:76:ARG:HD3	1.77	0.84
3:U:71:SER:OG	3:U:76:ARG:HD3	1.76	0.84
3:U:3:ILE:HB	3:U:90:LEU:HD11	1.57	0.84
2:H:59:LEU:HD13	4:J:25:ILE:HD11	1.59	0.84
1:M:133:GLN:CB	1:M:139:LYS:HG2	2.07	0.84
4:P:79:ARG:HH21	4:P:190:ILE:CD1	1.87	0.84
5:L:118:LEU:HB3	5:L:147:PHE:HB2	1.59	0.84
4:W:143:ILE:O	4:W:147:VAL:HG23	1.77	0.84
4:D:67:LEU:HD11	4:D:98:PHE:CE2	2.13	0.84
1:S:21:PHE:HD1	1:S:22:THR:N	1.75	0.84
2:B:59:LEU:HD13	4:D:25:ILE:HD11	1.57	0.84
5:F:108:ARG:HB2	5:F:108:ARG:NH1	1.92	0.84
2:T:59:LEU:HD13	4:V:25:ILE:HD11	1.59	0.84
4:Q:143:ILE:O	4:Q:147:VAL:HG23	1.77	0.84
4:V:67:LEU:HD11	4:V:98:PHE:CE2	2.13	0.84
5:X:108:ARG:NH1	5:X:108:ARG:HB2	1.92	0.84
5:X:123:CYS:HB3	5:X:151:SER:HA	1.58	0.84
5:R:108:ARG:HB2	5:R:108:ARG:NH1	1.92	0.84
1:G:133:GLN:CB	1:G:139:LYS:HG2	2.08	0.84
3:I:133:ARG:H	3:I:133:ARG:HD2	1.43	0.84
1:A:21:PHE:HD1	1:A:22:THR:N	1.75	0.83
1:M:200:MET:CE	5:R:7:TYR:HA	2.07	0.83
4:Q:21:LYS:O	4:Q:22:THR:HG23	1.77	0.83
5:R:118:LEU:HB3	5:R:147:PHE:HB2	1.60	0.83
3:O:133:ARG:HD2	3:O:133:ARG:H	1.42	0.83
1:G:75:MET:HE1	1:G:105:ASP:HB3	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:GLN:CB	1:A:139:LYS:HG2	2.08	0.83
5:F:118:LEU:HB3	5:F:147:PHE:HB2	1.60	0.83
4:J:139:TRP:HB2	4:J:142:ASN:HD21	1.44	0.83
4:P:139:TRP:HB2	4:P:142:ASN:HD21	1.43	0.83
1:S:70:ILE:HD12	1:S:108:LYS:HA	1.59	0.83
1:S:75:MET:HE1	1:S:105:ASP:HB3	1.60	0.83
2:N:59:LEU:HD13	4:P:25:ILE:HD11	1.59	0.83
4:K:143:ILE:O	4:K:147:VAL:HG23	1.78	0.83
1:G:21:PHE:HD1	1:G:22:THR:N	1.76	0.83
3:U:39:GLU:HA	3:U:42:LYS:CE	2.07	0.83
3:C:123:TYR:O	3:C:125:PHE:N	2.10	0.83
3:C:72:THR:HG23	3:C:73:GLY:N	1.94	0.83
3:U:133:ARG:H	3:U:133:ARG:HD2	1.43	0.83
4:W:21:LYS:O	4:W:22:THR:HG23	1.79	0.83
3:C:39:GLU:HA	3:C:42:LYS:CE	2.07	0.83
1:S:133:GLN:HE22	4:V:188:ILE:HD12	1.44	0.83
4:P:159:CYS:HB3	4:P:180:LEU:HA	1.60	0.83
3:U:82:THR:HG21	3:U:84:SER:OG	1.78	0.83
1:M:21:PHE:HD1	1:M:22:THR:N	1.76	0.83
3:C:133:ARG:H	3:C:133:ARG:HD2	1.43	0.83
5:F:93:GLN:HE21	5:F:131:VAL:HG12	1.44	0.83
1:G:70:ILE:HD12	1:G:108:LYS:HA	1.60	0.83
4:D:93:CYS:O	4:D:97:ILE:HG13	1.79	0.82
4:D:139:TRP:HB2	4:D:142:ASN:HD21	1.43	0.82
3:O:88:PHE:O	3:O:103:LEU:HD21	1.80	0.82
1:S:50:LEU:HB2	3:U:43:LEU:HD11	1.62	0.82
1:A:133:GLN:HE22	4:D:188:ILE:HD12	1.44	0.82
3:O:119:LEU:CD2	3:O:119:LEU:H	1.86	0.82
4:V:111:ASN:ND2	4:V:113:ASP:HB2	1.95	0.82
4:D:111:ASN:ND2	4:D:113:ASP:HB2	1.93	0.82
4:D:159:CYS:HB3	4:D:180:LEU:HA	1.60	0.82
4:J:93:CYS:O	4:J:97:ILE:HG13	1.78	0.82
3:I:3:ILE:HB	3:I:90:LEU:HD11	1.59	0.82
3:U:123:TYR:O	3:U:125:PHE:N	2.11	0.82
4:V:79:ARG:HH21	4:V:190:ILE:CD1	1.88	0.82
3:I:39:GLU:HA	3:I:42:LYS:CE	2.07	0.82
3:I:88:PHE:O	3:I:103:LEU:HD21	1.80	0.82
3:O:71:SER:OG	3:O:76:ARG:HD3	1.79	0.82
1:G:200:MET:CE	5:L:7:TYR:HA	2.08	0.82
3:I:123:TYR:O	3:I:125:PHE:N	2.11	0.82
3:C:88:PHE:O	3:C:103:LEU:HD21	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:111:ASN:ND2	4:J:113:ASP:HB2	1.95	0.82
4:P:93:CYS:O	4:P:97:ILE:HG13	1.80	0.82
5:R:93:GLN:HE21	5:R:131:VAL:HG12	1.45	0.82
4:J:79:ARG:HH21	4:J:190:ILE:CD1	1.88	0.82
2:H:254:ARG:HA	2:H:264:THR:HG22	1.61	0.82
1:M:70:ILE:HD12	1:M:108:LYS:HA	1.60	0.82
1:A:70:ILE:HD12	1:A:108:LYS:HA	1.60	0.82
4:D:79:ARG:HH21	4:D:190:ILE:CD1	1.89	0.82
3:I:72:THR:HG23	3:I:73:GLY:N	1.95	0.82
3:O:123:TYR:O	3:O:125:PHE:N	2.12	0.82
3:U:119:LEU:CD2	3:U:119:LEU:H	1.85	0.82
2:N:254:ARG:HA	2:N:264:THR:HG22	1.60	0.82
2:N:87:LEU:HD11	2:N:232:PHE:HB2	1.62	0.82
4:E:21:LYS:O	4:E:22:THR:HG23	1.79	0.82
2:T:192:PHE:H	2:T:192:PHE:HD1	1.28	0.82
3:U:72:THR:HG23	3:U:73:GLY:N	1.95	0.81
4:V:139:TRP:HB2	4:V:142:ASN:HD21	1.45	0.81
4:V:93:CYS:O	4:V:97:ILE:HG13	1.79	0.81
2:B:222:ILE:HD12	2:B:222:ILE:H	1.43	0.81
3:O:39:GLU:HA	3:O:42:LYS:CE	2.09	0.81
4:Q:94:ALA:HB1	6:Q:194:PLM:H91	1.62	0.81
5:R:29:SER:N	5:R:48:LYS:HE2	1.95	0.81
1:M:133:GLN:HE22	4:P:188:ILE:HD12	1.45	0.81
5:X:68:GLU:HG3	5:X:69:ARG:N	1.96	0.81
3:U:88:PHE:O	3:U:103:LEU:HD21	1.81	0.81
2:N:188:TRP:HH2	2:N:266:TYR:CE1	1.97	0.81
1:G:107:PHE:HB3	1:G:180:ARG:HH12	1.46	0.81
4:P:111:ASN:ND2	4:P:113:ASP:HB2	1.93	0.81
2:B:188:TRP:HH2	2:B:266:TYR:CE1	1.97	0.81
1:A:200:MET:CE	5:F:7:TYR:HA	2.10	0.81
2:H:192:PHE:HD1	2:H:192:PHE:H	1.29	0.81
5:R:68:GLU:HG3	5:R:69:ARG:N	1.95	0.81
3:C:48:ILE:HG21	3:C:87:TRP:HD1	1.46	0.81
4:E:49:PHE:HZ	4:E:133:ASP:HB3	1.44	0.81
3:O:107:TYR:HE2	4:Q:73:ALA:HA	1.45	0.81
2:H:188:TRP:HH2	2:H:266:TYR:CE1	1.97	0.81
5:F:29:SER:N	5:F:48:LYS:HE2	1.96	0.81
2:B:254:ARG:HA	2:B:264:THR:HG22	1.61	0.81
2:T:254:ARG:HA	2:T:264:THR:HG22	1.62	0.81
4:V:159:CYS:HB3	4:V:180:LEU:HA	1.60	0.81
4:J:159:CYS:HB3	4:J:180:LEU:HA	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:50:LEU:HB2	3:I:43:LEU:HD11	1.63	0.81
4:E:49:PHE:CZ	4:E:133:ASP:HB3	2.16	0.81
5:X:29:SER:N	5:X:48:LYS:HE2	1.95	0.81
1:A:137:GLY:CA	4:D:188:ILE:HG21	2.11	0.81
3:U:107:TYR:HE2	4:W:73:ALA:HA	1.44	0.81
5:L:93:GLN:HE21	5:L:131:VAL:HG12	1.44	0.81
4:E:94:ALA:HB1	6:E:194:PLM:H91	1.63	0.80
1:G:6:ILE:HG22	1:G:142:ALA:HA	1.62	0.80
1:S:107:PHE:HB3	1:S:180:ARG:HH12	1.46	0.80
4:K:49:PHE:HZ	4:K:133:ASP:HB3	1.45	0.80
2:T:222:ILE:HD12	2:T:222:ILE:H	1.43	0.80
2:N:222:ILE:H	2:N:222:ILE:HD12	1.44	0.80
4:Q:49:PHE:HZ	4:Q:133:ASP:HB3	1.45	0.80
1:A:107:PHE:HB3	1:A:180:ARG:HH12	1.45	0.80
2:T:87:LEU:HD11	2:T:232:PHE:HB2	1.63	0.80
3:O:48:ILE:HG21	3:O:87:TRP:HD1	1.47	0.80
3:I:119:LEU:H	3:I:119:LEU:CD2	1.87	0.80
4:J:67:LEU:HD11	4:J:98:PHE:CE2	2.16	0.80
3:U:48:ILE:HG21	3:U:87:TRP:HD1	1.46	0.80
1:S:200:MET:CE	5:X:7:TYR:HA	2.11	0.80
1:S:200:MET:HE3	5:X:7:TYR:HA	1.61	0.80
3:U:155:PRO:HG2	3:U:156:MET:H	1.46	0.80
5:F:28:PHE:CD2	5:F:48:LYS:HD3	2.16	0.80
3:C:122:PRO:HA	4:E:66:ARG:HH22	1.47	0.80
1:A:133:GLN:NE2	4:D:188:ILE:HD12	1.97	0.80
4:W:94:ALA:HB1	6:W:194:PLM:H91	1.63	0.80
2:B:87:LEU:HD11	2:B:232:PHE:HB2	1.64	0.80
3:O:72:THR:HG23	3:O:73:GLY:N	1.97	0.80
2:T:188:TRP:HH2	2:T:266:TYR:CE1	1.98	0.80
3:I:107:TYR:HE2	4:K:73:ALA:HA	1.45	0.80
4:K:94:ALA:HB1	6:K:194:PLM:H91	1.63	0.80
4:Q:49:PHE:CZ	4:Q:133:ASP:HB3	2.17	0.80
4:W:114:THR:HG23	4:W:179:LYS:N	1.97	0.80
1:M:107:PHE:HB3	1:M:180:ARG:HH12	1.45	0.79
1:M:50:LEU:HB2	3:O:43:LEU:HD11	1.63	0.79
4:K:49:PHE:CZ	4:K:133:ASP:HB3	2.17	0.79
2:H:99:LEU:HD22	2:H:243:ASN:HD22	1.47	0.79
4:E:188:ILE:HG23	4:E:188:ILE:O	1.82	0.79
1:S:133:GLN:NE2	4:V:188:ILE:HD12	1.97	0.79
3:I:48:ILE:HG21	3:I:87:TRP:HD1	1.47	0.79
5:X:93:GLN:HE21	5:X:131:VAL:HG12	1.45	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:188:ILE:O	4:Q:188:ILE:HG23	1.82	0.79
2:N:192:PHE:HD1	2:N:192:PHE:H	1.27	0.79
5:L:68:GLU:HG3	5:L:69:ARG:N	1.97	0.79
1:G:133:GLN:HE22	4:J:188:ILE:HD12	1.48	0.79
4:Q:87:SER:HB2	4:Q:115:PHE:CE1	2.18	0.79
2:H:87:LEU:HD11	2:H:232:PHE:HB2	1.64	0.79
4:W:49:PHE:HZ	4:W:133:ASP:HB3	1.46	0.79
1:M:133:GLN:NE2	4:P:188:ILE:HD12	1.98	0.79
5:X:84:ILE:HD11	5:X:114:VAL:HG11	1.64	0.79
4:K:87:SER:HB2	4:K:115:PHE:CE1	2.17	0.79
4:Q:114:THR:HG23	4:Q:179:LYS:N	1.98	0.79
2:T:231:TYR:HD2	2:T:234:CYS:HG	1.30	0.79
3:C:113:LYS:HA	3:C:117:ASN:HD22	1.48	0.79
2:T:99:LEU:HD22	2:T:243:ASN:HD22	1.48	0.79
5:L:29:SER:N	5:L:48:LYS:HE2	1.97	0.79
4:J:49:PHE:CB	4:J:138:LEU:HD12	2.09	0.79
5:R:103:LEU:HD21	5:R:145:MET:CE	2.13	0.79
1:G:40:LEU:HD21	1:G:129:MET:SD	2.23	0.78
1:M:6:ILE:HG22	1:M:142:ALA:HA	1.65	0.78
4:E:87:SER:HB2	4:E:115:PHE:CE1	2.18	0.78
5:R:30:ASP:OD1	5:R:48:LYS:HA	1.83	0.78
4:W:49:PHE:CZ	4:W:133:ASP:HB3	2.18	0.78
2:B:99:LEU:HD22	2:B:243:ASN:HD22	1.47	0.78
1:G:137:GLY:CA	4:J:188:ILE:HG21	2.13	0.78
4:V:138:LEU:H	4:V:169:ARG:NH2	1.81	0.78
4:Q:95:PHE:HB3	4:Q:101:ILE:HG23	1.65	0.78
3:O:113:LYS:HA	3:O:117:ASN:HD22	1.49	0.78
5:R:28:PHE:CD2	5:R:48:LYS:HD3	2.18	0.78
5:L:30:ASP:OD1	5:L:48:LYS:HA	1.83	0.78
2:B:192:PHE:HD1	2:B:192:PHE:H	1.28	0.78
4:W:144:LEU:HD23	6:W:194:PLM:HF2	1.65	0.78
4:W:188:ILE:HG23	4:W:188:ILE:O	1.82	0.78
4:E:144:LEU:HD23	6:E:194:PLM:HF2	1.65	0.78
4:K:114:THR:HG23	4:K:179:LYS:N	1.99	0.78
1:A:75:MET:HE1	1:A:105:ASP:HB3	1.65	0.78
2:N:256:PRO:HG2	2:N:263:ARG:HH21	1.49	0.78
3:U:133:ARG:HE	4:W:189:PRO:HD2	1.49	0.78
3:I:122:PRO:HA	4:K:66:ARG:HH22	1.49	0.78
3:C:107:TYR:CE2	4:E:73:ALA:HA	2.18	0.78
4:W:95:PHE:HB3	4:W:101:ILE:HG23	1.66	0.78
5:L:84:ILE:HD11	5:L:114:VAL:HG11	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:101:ILE:HG21	4:D:121:GLU:O	1.84	0.78
4:K:144:LEU:HD23	6:K:194:PLM:HF2	1.66	0.78
4:W:86:THR:HA	6:W:194:PLM:O1	1.83	0.78
3:I:113:LYS:HA	3:I:117:ASN:HD22	1.48	0.78
5:L:28:PHE:CD2	5:L:48:LYS:HD3	2.18	0.78
4:Q:86:THR:HA	6:Q:194:PLM:O1	1.83	0.77
4:K:188:ILE:HG23	4:K:188:ILE:O	1.82	0.77
4:W:87:SER:HB2	4:W:115:PHE:CE1	2.18	0.77
5:X:28:PHE:CD2	5:X:48:LYS:HD3	2.18	0.77
5:X:30:ASP:OD1	5:X:48:LYS:HA	1.84	0.77
2:B:175:LYS:HG3	2:B:278:GLU:OE2	1.83	0.77
4:K:86:THR:HA	6:K:194:PLM:O1	1.84	0.77
5:R:84:ILE:HD11	5:R:114:VAL:HG11	1.64	0.77
4:J:101:ILE:HG21	4:J:121:GLU:O	1.84	0.77
4:P:38:VAL:HG11	4:P:140:TYR:CE1	2.19	0.77
2:B:256:PRO:HG2	2:B:263:ARG:HH21	1.50	0.77
5:F:84:ILE:HD11	5:F:114:VAL:HG11	1.65	0.77
4:D:119:LEU:HD12	4:D:120:ASP:N	1.99	0.77
1:A:40:LEU:HD21	1:A:129:MET:SD	2.25	0.77
3:O:122:PRO:HA	4:Q:66:ARG:HH22	1.49	0.77
2:N:86:LYS:NZ	2:N:90:TYR:HE1	1.83	0.77
5:F:30:ASP:OD1	5:F:48:LYS:HA	1.84	0.77
3:O:20:GLU:O	3:O:21:TRP:HB2	1.83	0.77
5:F:117:LEU:HD23	5:F:118:LEU:N	1.99	0.77
5:R:117:LEU:HD23	5:R:118:LEU:N	1.99	0.77
4:Q:144:LEU:HD23	6:Q:194:PLM:HF2	1.67	0.77
5:L:103:LEU:HD21	5:L:145:MET:CE	2.15	0.77
1:A:50:LEU:HB2	3:C:43:LEU:HD11	1.67	0.77
4:E:86:THR:HA	6:E:194:PLM:O1	1.84	0.77
3:C:155:PRO:HG2	3:C:156:MET:H	1.50	0.77
2:N:175:LYS:HG3	2:N:278:GLU:OE2	1.84	0.77
1:M:137:GLY:CA	4:P:188:ILE:HG21	2.15	0.77
4:D:138:LEU:H	4:D:169:ARG:NH2	1.82	0.77
4:V:49:PHE:CB	4:V:138:LEU:HD12	2.11	0.77
4:K:95:PHE:HB3	4:K:101:ILE:HG23	1.67	0.77
2:N:87:LEU:CD1	2:N:232:PHE:HB2	2.15	0.77
4:V:38:VAL:HG11	4:V:140:TYR:CE1	2.19	0.77
3:I:155:PRO:HG2	3:I:156:MET:H	1.50	0.77
4:E:95:PHE:HB3	4:E:101:ILE:HG23	1.67	0.76
2:T:86:LYS:NZ	2:T:90:TYR:HE1	1.83	0.76
4:E:114:THR:HG23	4:E:179:LYS:N	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:38:VAL:HG11	4:J:140:TYR:CE1	2.20	0.76
2:H:256:PRO:HG2	2:H:263:ARG:HH21	1.50	0.76
4:P:95:PHE:O	4:P:99:LEU:O	2.03	0.76
2:H:86:LYS:NZ	2:H:90:TYR:HE1	1.83	0.76
2:B:86:LYS:NZ	2:B:90:TYR:HE1	1.83	0.76
3:O:155:PRO:HG2	3:O:156:MET:H	1.50	0.76
3:U:113:LYS:HA	3:U:117:ASN:HD22	1.50	0.76
4:V:119:LEU:HD12	4:V:120:ASP:N	1.99	0.76
3:C:20:GLU:O	3:C:21:TRP:HB2	1.84	0.76
2:T:256:PRO:HG2	2:T:263:ARG:HH21	1.50	0.76
1:G:15:LEU:HD21	1:G:18:GLN:HB2	1.68	0.76
5:L:85:ILE:HG12	5:L:162:PHE:CZ	2.21	0.76
2:N:99:LEU:HD22	2:N:243:ASN:HD22	1.50	0.76
3:U:122:PRO:HA	4:W:66:ARG:HH22	1.51	0.76
4:V:101:ILE:HG21	4:V:121:GLU:O	1.86	0.76
1:M:40:LEU:HD21	1:M:129:MET:SD	2.26	0.76
3:U:20:GLU:O	3:U:21:TRP:HB2	1.84	0.76
2:H:222:ILE:HD12	2:H:222:ILE:H	1.48	0.76
4:Q:141:SER:O	4:Q:144:LEU:HB3	1.86	0.76
4:J:119:LEU:HD12	4:J:120:ASP:N	1.99	0.76
4:D:38:VAL:HG11	4:D:140:TYR:CE1	2.20	0.76
4:Q:159:CYS:HB3	4:Q:179:LYS:O	1.86	0.76
5:R:93:GLN:HB2	5:R:130:VAL:HG11	1.68	0.76
5:L:93:GLN:HB2	5:L:130:VAL:HG11	1.68	0.76
3:I:20:GLU:O	3:I:21:TRP:HB2	1.84	0.76
1:A:174:ILE:HG13	1:A:175:ALA:N	2.01	0.76
5:X:117:LEU:HD23	5:X:118:LEU:N	2.00	0.76
3:U:82:THR:OG1	3:U:86:LEU:HB2	1.86	0.75
4:K:101:ILE:HD12	4:K:121:GLU:O	1.85	0.75
4:D:95:PHE:O	4:D:99:LEU:O	2.05	0.75
4:E:159:CYS:HB3	4:E:179:LYS:O	1.86	0.75
4:K:159:CYS:HB3	4:K:179:LYS:O	1.85	0.75
4:W:159:CYS:HB3	4:W:179:LYS:O	1.85	0.75
4:W:75:THR:HG21	4:W:93:CYS:SG	2.26	0.75
4:Q:110:HIS:O	4:Q:111:ASN:CB	2.34	0.75
2:T:87:LEU:CD1	2:T:232:PHE:HB2	2.16	0.75
5:F:85:ILE:HD12	5:F:85:ILE:H	1.51	0.75
1:M:133:GLN:HB2	1:M:139:LYS:HG2	1.67	0.75
3:U:39:GLU:CA	3:U:42:LYS:HE2	2.12	0.75
4:J:138:LEU:H	4:J:169:ARG:NH2	1.85	0.75
4:P:119:LEU:HD12	4:P:120:ASP:N	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:133:ARG:HE	4:Q:189:PRO:HD2	1.52	0.75
4:D:34:TYR:O	4:D:37:ILE:HG22	1.87	0.75
2:H:175:LYS:HG3	2:H:278:GLU:OE2	1.87	0.75
1:S:137:GLY:CA	4:V:188:ILE:HG21	2.15	0.75
4:P:49:PHE:CB	4:P:138:LEU:HD12	2.10	0.75
4:D:49:PHE:CB	4:D:138:LEU:HD12	2.10	0.75
1:S:29:ASN:HB3	1:S:32:GLU:OE2	1.87	0.75
1:M:174:ILE:HG13	1:M:175:ALA:N	2.01	0.75
4:E:110:HIS:O	4:E:111:ASN:CB	2.35	0.75
5:F:68:GLU:HG3	5:F:69:ARG:N	2.02	0.75
4:W:37:ILE:O	4:W:41:LEU:HG	1.86	0.75
5:L:117:LEU:HD23	5:L:118:LEU:N	2.01	0.75
1:S:15:LEU:HD21	1:S:18:GLN:HB2	1.69	0.75
1:M:29:ASN:HB3	1:M:32:GLU:OE2	1.87	0.75
1:M:189:TYR:N	1:M:189:TYR:CD1	2.54	0.75
1:G:133:GLN:NE2	4:J:188:ILE:HD12	2.02	0.75
4:Q:37:ILE:CD1	4:W:37:ILE:HD11	2.07	0.75
5:F:93:GLN:HB2	5:F:130:VAL:HG11	1.69	0.75
5:X:93:GLN:HB2	5:X:130:VAL:HG11	1.69	0.75
4:P:101:ILE:HG21	4:P:121:GLU:O	1.87	0.74
5:X:85:ILE:HG12	5:X:162:PHE:CZ	2.22	0.74
1:S:133:GLN:HB2	1:S:139:LYS:HG2	1.67	0.74
3:I:107:TYR:CE2	4:K:73:ALA:HA	2.22	0.74
3:C:82:THR:OG1	3:C:86:LEU:HB2	1.87	0.74
4:E:101:ILE:HD12	4:E:121:GLU:O	1.87	0.74
2:B:87:LEU:CD1	2:B:232:PHE:HB2	2.18	0.74
4:W:110:HIS:O	4:W:111:ASN:CB	2.33	0.74
3:C:5:SER:HG	3:C:7:TRP:HZ3	1.34	0.74
4:J:95:PHE:O	4:J:99:LEU:O	2.04	0.74
4:K:37:ILE:O	4:K:41:LEU:HG	1.87	0.74
3:I:39:GLU:CA	3:I:42:LYS:HE2	2.13	0.74
4:E:75:THR:HG21	4:E:93:CYS:SG	2.26	0.74
3:U:107:TYR:CE2	4:W:73:ALA:HA	2.23	0.74
4:P:34:TYR:O	4:P:37:ILE:HG22	1.88	0.74
5:L:120:GLY:CA	5:L:149:GLU:HG3	2.09	0.74
3:I:83:ALA:HB3	4:K:72:LEU:HD11	1.70	0.74
2:H:87:LEU:CD1	2:H:232:PHE:HB2	2.17	0.74
4:K:139:TRP:HB2	4:K:142:ASN:ND2	2.01	0.74
1:S:133:GLN:HB3	1:S:139:LYS:HG2	1.69	0.74
4:E:37:ILE:O	4:E:41:LEU:HG	1.87	0.74
2:T:175:LYS:HG3	2:T:278:GLU:OE2	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:GLN:HB3	1:A:139:LYS:HG2	1.70	0.74
1:S:10:ASN:ND2	1:S:12:SER:H	1.86	0.74
4:W:119:LEU:O	4:W:174:THR:CG2	2.35	0.74
1:G:7:LEU:HD12	1:G:141:VAL:HB	1.69	0.74
1:M:183:TYR:CE2	4:P:73:ALA:HB2	2.23	0.74
3:I:82:THR:OG1	3:I:86:LEU:HB2	1.88	0.74
3:I:7:TRP:HB2	3:I:89:VAL:CG1	2.16	0.74
3:U:83:ALA:HB3	4:W:72:LEU:HD11	1.70	0.74
5:X:103:LEU:HD21	5:X:145:MET:CE	2.15	0.74
4:P:22:THR:HB	4:P:74:ARG:NH1	2.02	0.74
1:A:189:TYR:CD1	1:A:189:TYR:N	2.55	0.74
1:M:4:GLU:HG3	1:M:143:ILE:HG22	1.69	0.73
1:S:174:ILE:HG13	1:S:175:ALA:N	2.00	0.73
1:A:29:ASN:HB3	1:A:32:GLU:OE2	1.88	0.73
1:G:183:TYR:CE2	4:J:73:ALA:HB2	2.23	0.73
4:Q:37:ILE:O	4:Q:41:LEU:HG	1.88	0.73
3:O:107:TYR:CE2	4:Q:73:ALA:HA	2.23	0.73
1:G:133:GLN:HB2	1:G:139:LYS:HG2	1.69	0.73
1:G:194:PRO:HG3	2:H:67:GLN:CB	2.17	0.73
4:K:110:HIS:O	4:K:111:ASN:CB	2.34	0.73
5:R:85:ILE:H	5:R:85:ILE:HD12	1.53	0.73
1:M:133:GLN:HB3	1:M:139:LYS:HG2	1.70	0.73
4:W:36:SER:O	4:W:40:GLN:HB2	1.88	0.73
1:G:133:GLN:HB3	1:G:139:LYS:HG2	1.69	0.73
4:D:22:THR:HB	4:D:74:ARG:NH1	2.03	0.73
3:I:133:ARG:HE	4:K:189:PRO:HD2	1.54	0.73
5:L:93:GLN:HE21	5:L:131:VAL:CG1	2.00	0.73
1:G:174:ILE:HG13	1:G:175:ALA:N	2.00	0.73
5:X:120:GLY:CA	5:X:149:GLU:HG3	2.09	0.73
4:K:141:SER:O	4:K:144:LEU:HB3	1.87	0.73
5:F:103:LEU:HD21	5:F:145:MET:CE	2.15	0.73
1:A:133:GLN:HB2	1:A:139:LYS:HG2	1.69	0.73
4:E:139:TRP:HB2	4:E:142:ASN:ND2	2.03	0.73
4:W:84:VAL:HG23	4:W:108:TRP:CH2	2.23	0.73
2:H:94:ILE:HD11	4:J:33:THR:HA	1.71	0.73
4:W:101:ILE:HD12	4:W:121:GLU:O	1.88	0.73
1:S:40:LEU:HD21	1:S:129:MET:SD	2.29	0.73
1:M:15:LEU:HD21	1:M:18:GLN:HB2	1.69	0.73
4:J:162:TRP:NE1	4:J:177:LYS:HB2	2.04	0.73
5:F:93:GLN:O	5:F:93:GLN:HG2	1.88	0.73
5:F:85:ILE:HG12	5:F:162:PHE:CZ	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:85:ILE:HG12	5:R:162:PHE:CZ	2.24	0.73
4:Q:37:ILE:HD11	4:W:37:ILE:CD1	2.09	0.73
1:A:10:ASN:ND2	1:A:12:SER:H	1.86	0.73
1:G:10:ASN:ND2	1:G:12:SER:H	1.87	0.73
4:P:111:ASN:O	4:P:112:LYS:HG2	1.89	0.73
1:S:194:PRO:HG3	2:T:67:GLN:CB	2.18	0.73
3:C:133:ARG:HE	4:E:189:PRO:HD2	1.54	0.73
5:X:85:ILE:HD12	5:X:85:ILE:H	1.54	0.73
3:I:127:GLU:C	3:I:129:GLU:H	1.93	0.73
3:O:131:GLU:HB3	3:O:135:GLN:OE1	1.89	0.73
1:M:75:MET:HE1	1:M:105:ASP:HB3	1.71	0.73
3:C:83:ALA:HB3	4:E:72:LEU:HD11	1.71	0.72
4:J:22:THR:HB	4:J:74:ARG:NH1	2.03	0.72
3:U:127:GLU:C	3:U:129:GLU:H	1.93	0.72
4:V:34:TYR:O	4:V:37:ILE:HG22	1.89	0.72
5:F:93:GLN:HE21	5:F:131:VAL:CG1	2.01	0.72
2:B:170:ARG:O	2:B:172:ARG:N	2.20	0.72
1:S:189:TYR:CD1	1:S:189:TYR:N	2.54	0.72
4:E:141:SER:O	4:E:144:LEU:HB3	1.89	0.72
1:S:6:ILE:HG22	1:S:142:ALA:HA	1.69	0.72
4:V:95:PHE:O	4:V:99:LEU:O	2.06	0.72
1:A:6:ILE:HG22	1:A:142:ALA:HA	1.69	0.72
5:R:93:GLN:HG2	5:R:93:GLN:O	1.88	0.72
5:X:93:GLN:HG2	5:X:93:GLN:O	1.88	0.72
1:G:189:TYR:N	1:G:189:TYR:CD1	2.54	0.72
4:W:141:SER:O	4:W:144:LEU:HB3	1.88	0.72
2:N:84:GLU:HB3	2:N:231:TYR:CD1	2.24	0.72
4:Q:101:ILE:HD12	4:Q:121:GLU:O	1.89	0.72
5:L:111:THR:O	5:L:114:VAL:HG23	1.89	0.72
2:H:86:LYS:HZ2	2:H:90:TYR:HE1	1.37	0.72
4:E:36:SER:O	4:E:40:GLN:HB2	1.89	0.72
3:C:131:GLU:HB3	3:C:135:GLN:OE1	1.90	0.72
3:C:77:VAL:HG23	3:C:77:VAL:O	1.89	0.72
5:L:165:MET:O	5:L:169:ILE:HG13	1.90	0.72
1:A:15:LEU:HD21	1:A:18:GLN:HB2	1.69	0.72
3:U:131:GLU:HB3	3:U:135:GLN:OE1	1.89	0.72
3:I:82:THR:HG22	3:I:84:SER:N	1.97	0.72
3:O:82:THR:OG1	3:O:86:LEU:HB2	1.90	0.72
5:L:93:GLN:HG2	5:L:93:GLN:O	1.89	0.72
3:I:5:SER:HG	3:I:7:TRP:HZ3	1.37	0.72
1:M:147:VAL:HG12	1:M:148:MET:N	2.01	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:111:ASN:O	4:J:112:LYS:HG2	1.89	0.72
4:V:22:THR:HB	4:V:74:ARG:NH1	2.03	0.72
4:D:138:LEU:H	4:D:169:ARG:CZ	2.02	0.72
3:O:83:ALA:HB3	4:Q:72:LEU:HD11	1.72	0.72
4:W:99:LEU:HB2	4:W:101:ILE:HG22	1.72	0.72
4:E:119:LEU:O	4:E:174:THR:CG2	2.37	0.72
2:T:86:LYS:HZ2	2:T:90:TYR:HE1	1.38	0.72
4:Q:36:SER:O	4:Q:40:GLN:HB2	1.90	0.72
2:H:213:ASP:O	2:H:263:ARG:HG2	1.90	0.72
1:M:189:TYR:N	1:M:189:TYR:HD1	1.88	0.72
2:B:94:ILE:HD11	4:D:33:THR:HA	1.71	0.72
4:P:162:TRP:NE1	4:P:177:LYS:HB2	2.05	0.72
5:X:93:GLN:HE21	5:X:131:VAL:CG1	2.01	0.72
4:J:34:TYR:O	4:J:37:ILE:HG22	1.89	0.72
1:A:10:ASN:ND2	1:A:11:LYS:N	2.34	0.71
3:O:77:VAL:HG23	3:O:77:VAL:O	1.90	0.71
4:K:119:LEU:O	4:K:174:THR:CG2	2.38	0.71
4:Q:139:TRP:HB2	4:Q:142:ASN:ND2	2.04	0.71
4:J:106:THR:HG22	4:J:107:ASN:N	2.03	0.71
1:A:197:SER:O	1:A:200:MET:HB2	1.89	0.71
2:B:213:ASP:O	2:B:263:ARG:HG2	1.90	0.71
2:B:84:GLU:HB3	2:B:231:TYR:CD1	2.25	0.71
4:D:111:ASN:O	4:D:112:LYS:HG2	1.90	0.71
4:W:116:SER:HB3	4:W:175:GLU:HG3	1.72	0.71
5:R:93:GLN:HE21	5:R:131:VAL:CG1	2.01	0.71
2:N:191:LEU:HB2	2:N:192:PHE:HD1	1.55	0.71
1:S:189:TYR:N	1:S:189:TYR:HD1	1.89	0.71
4:Q:75:THR:HG21	4:Q:93:CYS:SG	2.28	0.71
3:I:106:ILE:HD11	3:I:153:LEU:HD21	1.71	0.71
4:P:138:LEU:H	4:P:169:ARG:NH2	1.87	0.71
1:M:10:ASN:ND2	1:M:12:SER:H	1.88	0.71
1:S:28:LEU:HD21	3:U:57:LYS:HD2	1.73	0.71
1:G:189:TYR:N	1:G:189:TYR:HD1	1.89	0.71
4:D:138:LEU:N	4:D:169:ARG:NH2	2.39	0.71
4:K:99:LEU:HB2	4:K:101:ILE:HG22	1.73	0.71
5:F:111:THR:O	5:F:114:VAL:HG23	1.90	0.71
1:G:5:THR:HB	1:G:143:ILE:HB	1.70	0.71
4:V:162:TRP:NE1	4:V:177:LYS:HB2	2.05	0.71
4:D:162:TRP:NE1	4:D:177:LYS:HB2	2.06	0.71
2:T:94:ILE:HD11	4:V:33:THR:HA	1.73	0.71
4:Q:84:VAL:HG23	4:Q:108:TRP:CH2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:213:ASP:O	2:N:263:ARG:HG2	1.90	0.71
4:Q:119:LEU:O	4:Q:174:THR:CG2	2.37	0.71
4:V:111:ASN:O	4:V:112:LYS:HG2	1.90	0.71
4:D:95:PHE:HB3	4:D:101:ILE:HD12	1.72	0.71
4:P:161:VAL:HG12	4:P:176:ILE:CG2	2.20	0.71
4:V:106:THR:HG22	4:V:107:ASN:N	2.03	0.71
2:N:86:LYS:HZ2	2:N:90:TYR:HE1	1.39	0.71
2:B:86:LYS:HZ2	2:B:90:TYR:HE1	1.39	0.71
4:D:139:TRP:HB2	4:D:142:ASN:ND2	2.04	0.71
3:I:131:GLU:HB3	3:I:135:GLN:OE1	1.89	0.71
4:Q:116:SER:HB3	4:Q:175:GLU:HG3	1.72	0.71
4:V:138:LEU:H	4:V:169:ARG:CZ	2.02	0.71
5:X:165:MET:O	5:X:169:ILE:HG13	1.90	0.71
1:M:212:LYS:O	1:M:215:VAL:HG22	1.91	0.71
4:P:99:LEU:HB2	4:P:101:ILE:HG13	1.71	0.71
5:R:87:VAL:HG22	5:R:119:VAL:HB	1.72	0.71
3:U:82:THR:HG22	3:U:84:SER:N	1.99	0.71
5:L:85:ILE:H	5:L:85:ILE:HD12	1.55	0.71
3:O:127:GLU:C	3:O:129:GLU:H	1.93	0.71
1:G:29:ASN:HB3	1:G:32:GLU:OE2	1.91	0.71
1:A:183:TYR:CE2	4:D:73:ALA:HB2	2.26	0.71
5:L:68:GLU:CG	5:L:69:ARG:H	1.66	0.71
3:I:70:ILE:HB	3:I:77:VAL:CG2	2.21	0.71
1:M:10:ASN:HD22	1:M:10:ASN:C	1.88	0.71
4:W:139:TRP:HB2	4:W:142:ASN:ND2	2.04	0.71
2:H:84:GLU:HG2	2:H:228:SER:HB3	1.71	0.71
4:J:139:TRP:HB2	4:J:142:ASN:ND2	2.05	0.71
4:K:36:SER:O	4:K:40:GLN:HB2	1.90	0.71
4:V:138:LEU:N	4:V:169:ARG:NH2	2.39	0.71
3:U:7:TRP:HB2	3:U:89:VAL:CG1	2.18	0.71
1:M:194:PRO:HG3	2:N:67:GLN:CB	2.20	0.71
4:D:99:LEU:HB2	4:D:101:ILE:HG13	1.71	0.71
1:M:197:SER:O	1:M:200:MET:HB2	1.90	0.71
2:T:191:LEU:HB2	2:T:192:PHE:HD1	1.55	0.71
1:S:52:PRO:C	1:S:54:ALA:H	1.94	0.71
4:D:161:VAL:HG12	4:D:176:ILE:CG2	2.21	0.71
1:A:194:PRO:HG3	2:B:67:GLN:CB	2.20	0.71
2:T:84:GLU:HB3	2:T:231:TYR:CD1	2.26	0.71
5:R:29:SER:OG	5:R:46:LYS:HB3	1.90	0.71
1:S:197:SER:O	1:S:200:MET:HB2	1.89	0.71
1:S:183:TYR:CE2	4:V:73:ALA:HB2	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:84:GLU:HG2	2:N:228:SER:HB3	1.71	0.70
4:P:95:PHE:HB3	4:P:101:ILE:HD12	1.72	0.70
3:C:11:ARG:NH1	3:C:125:PHE:HE1	1.89	0.70
2:N:94:ILE:HD11	4:P:33:THR:HA	1.73	0.70
5:L:87:VAL:HG22	5:L:119:VAL:HB	1.73	0.70
1:G:147:VAL:HG12	1:G:148:MET:N	2.01	0.70
5:F:29:SER:OG	5:F:46:LYS:HB3	1.90	0.70
5:X:28:PHE:HB2	5:X:159:GLU:OE2	1.89	0.70
2:T:213:ASP:O	2:T:263:ARG:HG2	1.92	0.70
5:R:111:THR:O	5:R:114:VAL:HG23	1.91	0.70
2:H:84:GLU:HB3	2:H:231:TYR:CD1	2.27	0.70
4:P:139:TRP:HB2	4:P:142:ASN:ND2	2.05	0.70
4:V:139:TRP:HB2	4:V:142:ASN:ND2	2.05	0.70
1:A:189:TYR:HD1	1:A:189:TYR:N	1.90	0.70
1:A:114:TRP:HZ3	4:D:77:LEU:O	1.75	0.70
5:F:69:ARG:CB	5:F:72:THR:HG22	2.16	0.70
1:A:10:ASN:HD22	1:A:10:ASN:C	1.88	0.70
1:S:10:ASN:HD22	1:S:10:ASN:C	1.89	0.70
1:S:126:GLN:HG3	3:U:65:ASN:CB	2.21	0.70
4:J:99:LEU:HB2	4:J:101:ILE:HG13	1.71	0.70
4:P:155:VAL:C	4:P:156:GLN:HG2	2.11	0.70
2:B:191:LEU:HB2	2:B:192:PHE:HD1	1.56	0.70
3:C:127:GLU:C	3:C:129:GLU:H	1.94	0.70
1:M:10:ASN:ND2	1:M:11:LYS:N	2.34	0.70
5:X:111:THR:O	5:X:114:VAL:HG23	1.91	0.70
1:M:5:THR:HB	1:M:143:ILE:HB	1.72	0.70
5:R:149:GLU:O	5:R:150:THR:HG23	1.91	0.70
3:I:82:THR:HB	3:I:86:LEU:H	1.56	0.70
3:U:77:VAL:O	3:U:77:VAL:HG23	1.90	0.70
1:A:21:PHE:CZ	1:A:215:VAL:HG11	2.26	0.70
5:R:165:MET:O	5:R:169:ILE:HG13	1.91	0.70
3:U:82:THR:HB	3:U:86:LEU:H	1.55	0.70
4:W:155:VAL:O	4:W:155:VAL:HG12	1.91	0.70
4:E:84:VAL:HG23	4:E:108:TRP:CH2	2.26	0.70
5:L:108:ARG:HB2	5:L:108:ARG:HH11	1.54	0.70
4:E:116:SER:HB3	4:E:175:GLU:HG3	1.74	0.70
4:V:161:VAL:HG12	4:V:176:ILE:CG2	2.20	0.70
2:H:231:TYR:HD2	2:H:234:CYS:HG	1.38	0.70
4:J:161:VAL:HG12	4:J:176:ILE:CG2	2.20	0.70
5:X:108:ARG:HH11	5:X:108:ARG:HB2	1.55	0.70
4:K:116:SER:HB3	4:K:175:GLU:HG3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:70:ILE:HB	3:U:77:VAL:CG2	2.21	0.70
4:D:161:VAL:HG12	4:D:176:ILE:HG21	1.74	0.70
5:X:29:SER:OG	5:X:46:LYS:HB3	1.90	0.70
4:K:155:VAL:O	4:K:155:VAL:HG12	1.92	0.70
3:U:5:SER:HG	3:U:7:TRP:HZ3	1.38	0.70
2:B:231:TYR:HE2	2:B:251:THR:HA	1.57	0.70
2:B:84:GLU:HG2	2:B:228:SER:HB3	1.72	0.70
4:D:106:THR:HG22	4:D:107:ASN:N	2.04	0.70
2:H:191:LEU:HB2	2:H:192:PHE:HD1	1.56	0.70
2:B:176:ILE:O	2:B:179:ILE:HG22	1.92	0.70
2:T:176:ILE:O	2:T:179:ILE:HG22	1.92	0.70
4:Q:180:LEU:HD23	4:Q:181:ASN:N	2.07	0.70
5:X:87:VAL:HG22	5:X:119:VAL:HB	1.74	0.69
3:I:111:TYR:O	3:I:115:VAL:HB	1.91	0.69
3:I:80:TYR:HB3	3:I:103:LEU:HD23	1.74	0.69
3:O:70:ILE:HB	3:O:77:VAL:CG2	2.22	0.69
4:P:161:VAL:HG12	4:P:176:ILE:HG21	1.74	0.69
4:V:99:LEU:HB2	4:V:101:ILE:HG13	1.71	0.69
4:K:84:VAL:HG23	4:K:108:TRP:CH2	2.26	0.69
1:M:50:LEU:HD13	3:O:43:LEU:HD11	1.73	0.69
3:O:11:ARG:NH1	3:O:125:PHE:HE1	1.90	0.69
1:G:114:TRP:HZ3	4:J:77:LEU:O	1.74	0.69
5:X:149:GLU:O	5:X:150:THR:HG23	1.93	0.69
3:C:80:TYR:HB3	3:C:103:LEU:HD23	1.73	0.69
3:C:111:TYR:O	3:C:115:VAL:HB	1.91	0.69
5:F:165:MET:O	5:F:169:ILE:HG13	1.91	0.69
3:C:7:TRP:HB2	3:C:89:VAL:CG1	2.18	0.69
2:H:238:LYS:HB2	2:H:250:VAL:HG23	1.74	0.69
3:U:133:ARG:HG2	4:W:188:ILE:HA	1.74	0.69
3:O:140:ILE:O	3:O:140:ILE:HG23	1.91	0.69
5:F:28:PHE:HB2	5:F:159:GLU:OE2	1.92	0.69
1:M:171:ALA:O	1:M:174:ILE:HG12	1.92	0.69
5:L:16:ASN:O	5:L:19:VAL:HG23	1.92	0.69
5:F:87:VAL:HG22	5:F:119:VAL:HB	1.73	0.69
3:C:70:ILE:HB	3:C:77:VAL:CG2	2.22	0.69
3:I:70:ILE:HB	3:I:77:VAL:HG22	1.74	0.69
1:A:147:VAL:HG12	1:A:148:MET:N	2.04	0.69
4:P:106:THR:HG22	4:P:107:ASN:N	2.04	0.69
1:A:3:ILE:HG23	1:A:143:ILE:O	1.92	0.69
5:X:41:ILE:H	5:X:41:ILE:HD12	1.58	0.69
3:C:82:THR:HB	3:C:86:LEU:H	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:68:GLU:HG2	4:J:63:ILE:HD11	1.74	0.69
4:W:180:LEU:HD23	4:W:181:ASN:N	2.07	0.69
1:M:114:TRP:HZ3	4:P:77:LEU:O	1.76	0.69
3:O:82:THR:HG22	3:O:84:SER:N	1.97	0.69
2:N:238:LYS:HB2	2:N:250:VAL:HG23	1.74	0.69
1:M:52:PRO:C	1:M:54:ALA:H	1.94	0.69
5:L:29:SER:OG	5:L:46:LYS:HB3	1.91	0.69
1:S:171:ALA:O	1:S:174:ILE:HG12	1.93	0.69
5:X:16:ASN:O	5:X:19:VAL:HG23	1.93	0.69
3:I:77:VAL:HG23	3:I:77:VAL:O	1.91	0.69
4:K:122:ASN:HB3	4:K:126:ASP:CG	2.13	0.69
1:G:21:PHE:CZ	1:G:215:VAL:HG11	2.27	0.69
1:S:21:PHE:CZ	1:S:215:VAL:HG11	2.27	0.69
2:B:238:LYS:HB2	2:B:250:VAL:HG23	1.74	0.69
3:U:11:ARG:NH1	3:U:125:PHE:HE1	1.90	0.69
3:I:11:ARG:NH1	3:I:125:PHE:HE1	1.90	0.69
4:W:110:HIS:O	4:W:111:ASN:HB3	1.92	0.69
2:H:173:ASP:O	2:H:174:LEU:HD23	1.93	0.69
5:L:149:GLU:O	5:L:150:THR:HG23	1.93	0.69
1:S:120:ARG:HH11	1:S:120:ARG:CB	2.04	0.69
4:E:99:LEU:HB2	4:E:101:ILE:HG22	1.73	0.69
4:Q:99:LEU:HB2	4:Q:101:ILE:HG22	1.72	0.69
1:G:212:LYS:O	1:G:215:VAL:HG22	1.92	0.69
2:T:84:GLU:HG2	2:T:228:SER:HB3	1.73	0.69
1:S:114:TRP:HZ3	4:V:77:LEU:O	1.75	0.69
5:L:14:ILE:HG22	5:L:64:THR:CG2	2.23	0.69
4:P:138:LEU:H	4:P:169:ARG:CZ	2.05	0.69
4:J:138:LEU:H	4:J:169:ARG:CZ	2.05	0.69
4:J:49:PHE:CZ	4:J:133:ASP:OD2	2.46	0.69
3:U:111:TYR:O	3:U:115:VAL:HB	1.92	0.69
4:E:122:ASN:OD1	4:E:124:LEU:HB3	1.93	0.69
4:E:122:ASN:HB3	4:E:126:ASP:CG	2.13	0.69
1:A:52:PRO:C	1:A:54:ALA:H	1.94	0.69
1:A:126:GLN:HG3	3:C:65:ASN:CB	2.22	0.69
4:J:161:VAL:HG12	4:J:176:ILE:HG21	1.74	0.69
4:V:95:PHE:HB3	4:V:101:ILE:HD12	1.73	0.69
4:J:95:PHE:HB3	4:J:101:ILE:HD12	1.74	0.69
2:H:87:LEU:CG	2:H:232:PHE:HB2	2.22	0.69
4:D:77:LEU:HD22	4:D:78:PRO:HD2	1.75	0.69
5:R:16:ASN:O	5:R:19:VAL:HG23	1.93	0.69
5:F:53:ASP:O	5:F:55:LYS:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:16:ASN:O	5:F:19:VAL:HG23	1.93	0.69
5:L:53:ASP:O	5:L:55:LYS:N	2.26	0.69
4:Q:110:HIS:O	4:Q:111:ASN:HB3	1.93	0.69
5:X:69:ARG:CB	5:X:72:THR:HG22	2.18	0.69
3:O:7:TRP:HB2	3:O:89:VAL:CG1	2.18	0.69
2:N:231:TYR:HE2	2:N:251:THR:HA	1.58	0.69
1:M:21:PHE:CZ	1:M:215:VAL:HG11	2.27	0.69
3:U:10:ASP:OD2	3:U:12:HIS:HB2	1.93	0.69
4:E:110:HIS:O	4:E:111:ASN:HB3	1.93	0.69
3:O:106:ILE:HD11	3:O:153:LEU:HD21	1.73	0.69
5:F:149:GLU:O	5:F:150:THR:HG23	1.93	0.69
5:F:14:ILE:HG22	5:F:64:THR:CG2	2.23	0.69
5:R:120:GLY:CA	5:R:149:GLU:HG3	2.09	0.69
4:V:161:VAL:HG12	4:V:176:ILE:HG21	1.74	0.69
3:U:140:ILE:O	3:U:140:ILE:HG23	1.94	0.69
2:B:99:LEU:HD12	2:B:99:LEU:H	1.57	0.69
1:A:75:MET:HA	1:A:217:ASN:ND2	2.07	0.69
4:K:180:LEU:HD23	4:K:181:ASN:N	2.07	0.69
2:T:173:ASP:O	2:T:174:LEU:HD23	1.92	0.69
3:C:82:THR:HG22	3:C:84:SER:N	1.99	0.68
1:S:10:ASN:HD22	1:S:11:LYS:H	1.42	0.68
1:G:75:MET:HA	1:G:217:ASN:ND2	2.08	0.68
5:R:28:PHE:HB2	5:R:159:GLU:OE2	1.93	0.68
2:N:176:ILE:O	2:N:179:ILE:HG22	1.93	0.68
4:K:110:HIS:O	4:K:111:ASN:HB3	1.93	0.68
3:C:106:ILE:HD11	3:C:153:LEU:HD21	1.73	0.68
4:K:75:THR:HG21	4:K:93:CYS:SG	2.32	0.68
1:G:10:ASN:HD22	1:G:11:LYS:H	1.41	0.68
4:D:155:VAL:C	4:D:156:GLN:HG2	2.13	0.68
2:H:176:ILE:O	2:H:179:ILE:HG22	1.93	0.68
5:X:53:ASP:O	5:X:55:LYS:N	2.26	0.68
5:R:53:ASP:O	5:R:55:LYS:N	2.26	0.68
3:O:82:THR:HB	3:O:86:LEU:H	1.57	0.68
4:Q:155:VAL:O	4:Q:155:VAL:HG12	1.92	0.68
1:G:197:SER:O	1:G:200:MET:HB2	1.92	0.68
1:S:70:ILE:HG12	1:S:72:TYR:H	1.57	0.68
1:A:171:ALA:O	1:A:174:ILE:HG12	1.94	0.68
1:G:171:ALA:O	1:G:174:ILE:HG12	1.93	0.68
3:U:70:ILE:HB	3:U:77:VAL:HG22	1.74	0.68
1:S:212:LYS:O	1:S:215:VAL:HG22	1.93	0.68
5:F:108:ARG:HH11	5:F:108:ARG:HB2	1.55	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:108:ARG:HH11	5:R:108:ARG:HB2	1.56	0.68
3:I:10:ASP:OD2	3:I:12:HIS:HB2	1.94	0.68
3:C:140:ILE:HG23	3:C:140:ILE:O	1.93	0.68
5:L:28:PHE:HB2	5:L:159:GLU:OE2	1.92	0.68
4:E:180:LEU:HD23	4:E:181:ASN:N	2.08	0.68
2:H:255:MET:O	2:H:255:MET:SD	2.51	0.68
4:Q:122:ASN:HB3	4:Q:126:ASP:CG	2.14	0.68
5:F:85:ILE:HD12	5:F:85:ILE:N	2.07	0.68
2:T:170:ARG:O	2:T:172:ARG:N	2.25	0.68
4:W:122:ASN:HB3	4:W:126:ASP:CG	2.14	0.68
1:G:120:ARG:CB	1:G:120:ARG:HH11	2.05	0.68
2:N:87:LEU:CG	2:N:232:PHE:HB2	2.23	0.68
1:M:75:MET:HA	1:M:217:ASN:ND2	2.08	0.68
5:X:14:ILE:HG22	5:X:64:THR:CG2	2.24	0.68
1:S:28:LEU:HB2	1:S:33:TYR:CE1	2.28	0.68
2:T:231:TYR:HE2	2:T:251:THR:HA	1.57	0.68
3:I:112:VAL:HG11	4:K:70:ASP:HB2	1.74	0.68
1:S:75:MET:HA	1:S:217:ASN:ND2	2.08	0.68
4:P:77:LEU:HD22	4:P:78:PRO:HD2	1.76	0.68
5:L:41:ILE:H	5:L:41:ILE:HD12	1.59	0.68
5:R:14:ILE:HG22	5:R:64:THR:CG2	2.24	0.68
1:G:17:TYR:HB2	1:G:202:ILE:HD12	1.76	0.68
4:V:155:VAL:C	4:V:156:GLN:HG2	2.12	0.68
1:M:28:LEU:HD21	3:O:57:LYS:HD2	1.76	0.68
3:I:140:ILE:HG23	3:I:140:ILE:O	1.94	0.68
3:U:98:SER:HB2	3:U:100:THR:HG23	1.76	0.68
4:D:49:PHE:CZ	4:D:133:ASP:OD2	2.47	0.68
4:J:138:LEU:N	4:J:169:ARG:NH2	2.42	0.68
3:O:111:TYR:O	3:O:115:VAL:HB	1.93	0.68
2:N:184:HIS:HB2	2:N:211:ILE:CD1	2.24	0.68
3:O:133:ARG:HG2	4:Q:188:ILE:HA	1.76	0.68
4:V:77:LEU:HD22	4:V:78:PRO:HD2	1.75	0.68
3:U:106:ILE:HD11	3:U:153:LEU:HD21	1.74	0.68
3:O:5:SER:HG	3:O:7:TRP:HZ3	1.41	0.67
1:M:120:ARG:CB	1:M:120:ARG:HH11	2.05	0.67
1:S:50:LEU:HD13	3:U:43:LEU:HD11	1.74	0.67
1:S:136:THR:HG21	4:V:69:GLU:OE1	1.94	0.67
4:W:122:ASN:OD1	4:W:124:LEU:HB3	1.95	0.67
1:A:17:TYR:HB2	1:A:202:ILE:HD12	1.75	0.67
3:U:112:VAL:HG11	4:W:70:ASP:HB2	1.75	0.67
1:A:28:LEU:HB2	1:A:33:TYR:CE1	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:87:LEU:CG	2:B:232:PHE:HB2	2.24	0.67
3:I:44:LEU:O	3:I:44:LEU:HD23	1.95	0.67
1:A:50:LEU:HD13	3:C:43:LEU:HD11	1.74	0.67
3:O:3:ILE:CB	3:O:90:LEU:HD11	2.24	0.67
1:M:70:ILE:HG12	1:M:72:TYR:H	1.58	0.67
4:Q:49:PHE:CD2	4:Q:134:ALA:HB2	2.30	0.67
5:R:85:ILE:N	5:R:85:ILE:HD12	2.08	0.67
4:J:77:LEU:HD22	4:J:78:PRO:HD2	1.75	0.67
5:F:113:THR:O	5:F:115:LEU:HD23	1.94	0.67
1:S:133:GLN:HA	1:S:138:LEU:O	1.94	0.67
4:V:49:PHE:CZ	4:V:133:ASP:OD2	2.48	0.67
1:G:52:PRO:C	1:G:54:ALA:H	1.96	0.67
3:U:133:ARG:CB	4:W:188:ILE:HG13	2.24	0.67
1:G:70:ILE:HG12	1:G:72:TYR:H	1.59	0.67
2:T:99:LEU:HD12	2:T:99:LEU:H	1.58	0.67
2:N:99:LEU:H	2:N:99:LEU:HD12	1.59	0.67
5:R:41:ILE:H	5:R:41:ILE:HD12	1.58	0.67
4:D:131:PRO:O	4:D:133:ASP:N	2.26	0.67
1:S:17:TYR:HB2	1:S:202:ILE:HD12	1.76	0.67
1:A:192:LYS:HE2	2:B:64:PHE:CZ	2.30	0.67
3:I:114:TYR:N	3:I:114:TYR:CD1	2.62	0.67
3:U:114:TYR:CD1	3:U:114:TYR:N	2.62	0.67
4:K:114:THR:OG1	4:K:179:LYS:HB2	1.94	0.67
1:G:50:LEU:HD13	3:I:43:LEU:HD11	1.75	0.67
5:L:113:THR:O	5:L:115:LEU:HD23	1.94	0.67
3:I:108:SER:HB3	4:K:73:ALA:HB1	1.74	0.67
3:O:70:ILE:HB	3:O:77:VAL:HG22	1.75	0.67
1:M:136:THR:HG21	4:P:69:GLU:OE1	1.93	0.67
4:E:155:VAL:HG12	4:E:155:VAL:O	1.93	0.67
2:B:170:ARG:C	2:B:172:ARG:H	1.97	0.67
2:N:170:ARG:O	2:N:172:ARG:N	2.27	0.67
5:X:113:THR:O	5:X:115:LEU:HD23	1.94	0.67
1:G:28:LEU:HD21	3:I:57:LYS:HD2	1.77	0.67
4:J:114:THR:HG22	4:J:115:PHE:N	2.09	0.67
1:A:130:PHE:CE1	1:A:172:ILE:HA	2.30	0.67
4:V:131:PRO:O	4:V:133:ASP:N	2.27	0.67
3:C:70:ILE:HB	3:C:77:VAL:HG22	1.76	0.67
3:O:112:VAL:HG11	4:Q:70:ASP:HB2	1.76	0.67
4:P:131:PRO:O	4:P:133:ASP:N	2.27	0.67
1:G:129:MET:HG2	1:G:131:ILE:HD12	1.76	0.67
2:H:231:TYR:HE2	2:H:251:THR:HA	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:133:ARG:NE	4:W:189:PRO:HD2	2.08	0.67
3:C:10:ASP:OD2	3:C:12:HIS:HB2	1.94	0.67
1:M:130:PHE:CE1	1:M:172:ILE:HA	2.30	0.67
4:P:138:LEU:N	4:P:169:ARG:NH2	2.43	0.67
3:I:84:SER:OG	3:I:86:LEU:HD13	1.95	0.67
1:S:10:ASN:ND2	1:S:11:LYS:N	2.34	0.67
1:G:10:ASN:C	1:G:10:ASN:HD22	1.91	0.67
1:A:212:LYS:O	1:A:215:VAL:HG22	1.95	0.67
1:G:126:GLN:HG3	3:I:65:ASN:CB	2.25	0.67
4:V:114:THR:HG22	4:V:115:PHE:N	2.10	0.67
3:C:3:ILE:CB	3:C:90:LEU:HD11	2.25	0.67
5:X:85:ILE:HD12	5:X:85:ILE:N	2.09	0.67
3:O:137:THR:O	3:O:139:LYS:N	2.28	0.67
5:L:14:ILE:HB	5:L:102:TRP:HZ3	1.59	0.67
4:P:49:PHE:CZ	4:P:133:ASP:OD2	2.48	0.67
4:K:122:ASN:OD1	4:K:124:LEU:HB3	1.95	0.67
4:Q:34:TYR:CE1	4:Q:143:ILE:HG21	2.30	0.67
1:G:39:THR:O	1:G:43:VAL:HG23	1.95	0.67
2:T:238:LYS:HB2	2:T:250:VAL:HG23	1.77	0.67
1:A:107:PHE:HB3	1:A:180:ARG:NH1	2.10	0.67
2:B:216:PRO:O	2:B:218:LEU:N	2.27	0.67
5:F:41:ILE:H	5:F:41:ILE:HD12	1.58	0.67
1:A:133:GLN:HA	1:A:138:LEU:O	1.95	0.66
4:V:47:ARG:HB3	4:V:49:PHE:CE2	2.30	0.66
4:J:131:PRO:O	4:J:133:ASP:N	2.27	0.66
4:J:47:ARG:HB3	4:J:49:PHE:CE2	2.30	0.66
3:U:80:TYR:HB3	3:U:103:LEU:HD23	1.76	0.66
2:T:87:LEU:CG	2:T:232:PHE:HB2	2.24	0.66
3:I:98:SER:HB2	3:I:100:THR:HG23	1.77	0.66
3:O:98:SER:HB2	3:O:100:THR:HG23	1.77	0.66
5:X:14:ILE:HB	5:X:102:TRP:HZ3	1.59	0.66
1:G:28:LEU:HB2	1:G:33:TYR:CE1	2.30	0.66
1:M:107:PHE:HB3	1:M:180:ARG:NH1	2.10	0.66
1:M:28:LEU:HB2	1:M:33:TYR:CE1	2.30	0.66
2:T:233:VAL:HA	2:T:236:ILE:HD13	1.77	0.66
4:J:155:VAL:C	4:J:156:GLN:HG2	2.13	0.66
3:O:10:ASP:OD2	3:O:12:HIS:HB2	1.94	0.66
3:I:137:THR:O	3:I:139:LYS:N	2.28	0.66
5:F:120:GLY:CA	5:F:149:GLU:HG3	2.10	0.66
4:P:114:THR:HG22	4:P:115:PHE:N	2.10	0.66
3:C:123:TYR:C	3:C:125:PHE:H	1.99	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:49:PHE:CD2	4:K:134:ALA:HB2	2.28	0.66
1:G:130:PHE:CE1	1:G:172:ILE:HA	2.30	0.66
5:R:14:ILE:HB	5:R:102:TRP:HZ3	1.59	0.66
1:G:133:GLN:HA	1:G:138:LEU:O	1.95	0.66
3:O:80:TYR:HB3	3:O:103:LEU:HD23	1.76	0.66
3:C:137:THR:O	3:C:139:LYS:N	2.28	0.66
1:M:133:GLN:HA	1:M:138:LEU:O	1.95	0.66
1:S:107:PHE:HB3	1:S:180:ARG:NH1	2.11	0.66
2:T:184:HIS:HB2	2:T:211:ILE:CD1	2.26	0.66
2:B:216:PRO:C	2:B:218:LEU:H	1.99	0.66
5:X:108:ARG:HH11	5:X:108:ARG:CB	2.09	0.66
3:U:137:THR:O	3:U:139:LYS:N	2.29	0.66
5:R:113:THR:O	5:R:115:LEU:HD23	1.95	0.66
3:C:11:ARG:HH12	4:E:154:MET:CE	2.08	0.66
3:I:123:TYR:C	3:I:125:PHE:H	1.99	0.66
2:H:99:LEU:HD12	2:H:99:LEU:H	1.59	0.66
3:C:98:SER:HB2	3:C:100:THR:HG23	1.77	0.66
4:J:129:GLU:O	4:J:131:PRO:HD3	1.96	0.66
1:G:107:PHE:HB3	1:G:180:ARG:NH1	2.11	0.66
1:A:5:THR:HB	1:A:143:ILE:HB	1.77	0.66
3:C:112:VAL:HG11	4:E:70:ASP:HB2	1.76	0.66
4:E:49:PHE:CD2	4:E:134:ALA:HB2	2.31	0.66
5:F:14:ILE:HB	5:F:102:TRP:HZ3	1.60	0.66
1:S:5:THR:HB	1:S:143:ILE:HB	1.75	0.66
1:G:192:LYS:HE2	2:H:64:PHE:CZ	2.30	0.66
2:B:184:HIS:HB2	2:B:211:ILE:CD1	2.26	0.66
1:A:129:MET:HG2	1:A:131:ILE:HD12	1.77	0.66
5:F:13:LEU:CD2	5:F:25:LEU:HD11	2.26	0.66
3:C:39:GLU:CA	3:C:42:LYS:HE2	2.12	0.66
1:G:7:LEU:CD1	1:G:141:VAL:HB	2.26	0.66
1:M:17:TYR:HB2	1:M:202:ILE:HD12	1.77	0.66
5:L:108:ARG:HH11	5:L:108:ARG:CB	2.09	0.66
5:R:130:VAL:HG12	5:R:131:VAL:N	2.11	0.66
1:A:70:ILE:HG12	1:A:72:TYR:H	1.60	0.66
1:G:114:TRP:CZ3	4:J:77:LEU:O	2.49	0.66
2:N:66:PHE:CZ	2:N:70:ILE:HD11	2.30	0.66
5:X:13:LEU:CD2	5:X:25:LEU:HD11	2.26	0.66
4:P:47:ARG:HB3	4:P:49:PHE:CE2	2.31	0.66
5:F:12:LEU:HD23	5:F:12:LEU:N	2.08	0.66
1:G:136:THR:HG21	4:J:69:GLU:OE1	1.96	0.66
2:B:214:ASN:HA	2:B:263:ARG:CG	2.23	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:114:THR:HG22	4:D:115:PHE:N	2.10	0.66
4:K:87:SER:HB2	4:K:115:PHE:CD1	2.31	0.66
2:H:216:PRO:O	2:H:218:LEU:N	2.29	0.66
3:C:133:ARG:HG2	4:E:188:ILE:HA	1.78	0.66
5:L:85:ILE:HD12	5:L:85:ILE:N	2.10	0.66
1:S:130:PHE:CE1	1:S:172:ILE:HA	2.30	0.66
5:L:68:GLU:HG2	5:L:69:ARG:HB3	1.79	0.65
3:U:84:SER:OG	3:U:86:LEU:HD13	1.96	0.65
3:U:3:ILE:CB	3:U:90:LEU:HD11	2.26	0.65
2:N:218:LEU:HD23	2:N:233:VAL:HG12	1.78	0.65
3:U:123:TYR:C	3:U:125:PHE:H	2.00	0.65
3:O:123:TYR:C	3:O:125:PHE:H	2.00	0.65
1:A:39:THR:O	1:A:43:VAL:HG23	1.96	0.65
3:C:106:ILE:HD13	3:C:149:LEU:HD11	1.78	0.65
5:L:13:LEU:CD2	5:L:25:LEU:HD11	2.26	0.65
4:Q:122:ASN:OD1	4:Q:124:LEU:HB3	1.96	0.65
1:G:52:PRO:HD3	3:I:75:TYR:CE2	2.32	0.65
2:H:87:LEU:HG	2:H:232:PHE:HB2	1.78	0.65
3:O:133:ARG:CB	4:Q:188:ILE:HG13	2.26	0.65
2:N:173:ASP:O	2:N:174:LEU:HD23	1.97	0.65
2:T:255:MET:O	2:T:255:MET:SD	2.54	0.65
3:O:119:LEU:HD11	4:W:36:SER:N	2.11	0.65
2:H:184:HIS:HB2	2:H:211:ILE:CD1	2.27	0.65
3:O:133:ARG:NE	4:Q:189:PRO:HD2	2.10	0.65
4:P:129:GLU:O	4:P:131:PRO:HD3	1.96	0.65
3:I:7:TRP:CB	3:I:89:VAL:HG12	2.20	0.65
1:S:129:MET:HG2	1:S:131:ILE:HD12	1.78	0.65
2:T:68:GLU:HG2	4:V:63:ILE:HD11	1.79	0.65
1:A:7:LEU:HD12	1:A:141:VAL:HB	1.76	0.65
5:R:28:PHE:HB3	5:R:48:LYS:NZ	2.11	0.65
5:F:28:PHE:HB3	5:F:48:LYS:NZ	2.11	0.65
2:N:192:PHE:CD1	2:N:192:PHE:N	2.65	0.65
4:Q:114:THR:OG1	4:Q:179:LYS:HB2	1.95	0.65
5:F:69:ARG:HB2	5:F:72:THR:HG21	1.79	0.65
1:G:10:ASN:ND2	1:G:11:LYS:N	2.35	0.65
1:S:129:MET:HE2	1:S:143:ILE:HD11	1.79	0.65
3:I:133:ARG:HG2	4:K:188:ILE:HA	1.79	0.65
5:X:28:PHE:HB3	5:X:48:LYS:NZ	2.11	0.65
2:N:255:MET:O	2:N:255:MET:SD	2.54	0.65
5:X:68:GLU:HG2	5:X:69:ARG:HB3	1.79	0.65
3:C:72:THR:CG2	3:C:73:GLY:N	2.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:TRP:CZ3	4:D:77:LEU:O	2.49	0.65
4:V:129:GLU:O	4:V:131:PRO:HD3	1.97	0.65
3:I:85:GLY:C	3:I:86:LEU:HD12	2.18	0.65
2:N:216:PRO:O	2:N:218:LEU:N	2.29	0.65
3:O:44:LEU:HD23	3:O:44:LEU:O	1.97	0.65
3:I:106:ILE:HD13	3:I:149:LEU:HD11	1.78	0.65
4:K:34:TYR:CE1	4:K:143:ILE:HG21	2.32	0.65
3:O:7:TRP:CB	3:O:89:VAL:HG12	2.22	0.65
1:A:120:ARG:CB	1:A:120:ARG:HH11	2.07	0.65
2:H:64:PHE:CE1	4:J:67:LEU:HD12	2.32	0.65
2:N:233:VAL:HA	2:N:236:ILE:HD13	1.79	0.65
4:K:115:PHE:CE2	4:K:178:VAL:HB	2.31	0.65
3:U:133:ARG:HB3	4:W:188:ILE:HG13	1.78	0.65
4:D:129:GLU:O	4:D:131:PRO:HD3	1.96	0.65
4:Q:115:PHE:CE2	4:Q:178:VAL:HB	2.31	0.65
4:W:34:TYR:CE1	4:W:143:ILE:HG21	2.32	0.65
2:N:170:ARG:C	2:N:172:ARG:H	2.00	0.65
5:R:86:ILE:HD11	5:R:106:ILE:HD11	1.79	0.65
5:F:90:VAL:HG12	5:F:90:VAL:O	1.97	0.65
3:O:108:SER:HB3	4:Q:73:ALA:HB1	1.77	0.64
2:N:184:HIS:HB2	2:N:211:ILE:HD11	1.79	0.64
1:G:4:GLU:HG3	1:G:143:ILE:HG22	1.77	0.64
4:D:111:ASN:HD22	4:D:113:ASP:CG	2.01	0.64
1:M:129:MET:HG2	1:M:131:ILE:HD12	1.79	0.64
2:T:216:PRO:O	2:T:218:LEU:N	2.30	0.64
1:S:114:TRP:CZ3	4:V:77:LEU:O	2.50	0.64
1:A:28:LEU:HD21	3:C:57:LYS:HD2	1.79	0.64
5:F:108:ARG:CB	5:F:108:ARG:HH11	2.08	0.64
3:O:133:ARG:HB3	4:Q:188:ILE:HG13	1.78	0.64
4:K:95:PHE:CD1	4:K:103:PRO:HG3	2.33	0.64
4:K:101:ILE:CD1	4:K:121:GLU:O	2.46	0.64
2:N:216:PRO:C	2:N:218:LEU:H	2.01	0.64
4:W:87:SER:HB2	4:W:115:PHE:CD1	2.32	0.64
2:B:192:PHE:N	2:B:192:PHE:CD1	2.66	0.64
4:K:129:GLU:O	4:K:129:GLU:HG3	1.96	0.64
5:X:69:ARG:HB2	5:X:72:THR:HG21	1.79	0.64
3:I:85:GLY:O	3:I:86:LEU:HD12	1.98	0.64
4:E:143:ILE:HG23	4:E:144:LEU:N	2.12	0.64
3:O:114:TYR:CD1	3:O:114:TYR:N	2.63	0.64
3:C:114:TYR:CD1	3:C:114:TYR:N	2.63	0.64
3:U:44:LEU:HD23	3:U:44:LEU:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:175:LYS:HG2	2:B:176:ILE:N	2.12	0.64
1:M:114:TRP:CZ3	4:P:77:LEU:O	2.50	0.64
5:L:90:VAL:HG12	5:L:90:VAL:O	1.98	0.64
2:B:255:MET:O	2:B:255:MET:SD	2.55	0.64
5:R:43:VAL:HG23	5:R:43:VAL:O	1.96	0.64
3:I:3:ILE:CB	3:I:90:LEU:HD11	2.28	0.64
1:S:192:LYS:HE2	2:T:64:PHE:CZ	2.32	0.64
2:N:86:LYS:NZ	2:N:90:TYR:CE1	2.66	0.64
3:O:14:ASN:ND2	3:O:132:MET:O	2.30	0.64
5:L:28:PHE:HB3	5:L:48:LYS:NZ	2.12	0.64
2:H:66:PHE:CZ	2:H:70:ILE:HD11	2.32	0.64
3:C:7:TRP:CB	3:C:89:VAL:HG12	2.22	0.64
4:D:118:ILE:HA	4:D:175:GLU:HB3	1.80	0.64
4:P:118:ILE:HA	4:P:175:GLU:HB3	1.80	0.64
3:C:137:THR:O	3:C:139:LYS:HG3	1.98	0.64
4:W:48:ASP:OD1	4:W:51:LYS:HG3	1.98	0.64
5:R:90:VAL:O	5:R:90:VAL:HG12	1.97	0.64
1:M:187:SER:O	1:M:191:MET:HB2	1.98	0.64
4:D:99:LEU:CD1	4:D:101:ILE:HD11	2.27	0.64
4:V:99:LEU:CD1	4:V:101:ILE:HD11	2.27	0.64
4:D:47:ARG:HB3	4:D:49:PHE:CE2	2.32	0.64
4:W:102:THR:HG22	4:W:102:THR:O	1.97	0.64
1:M:43:VAL:HG11	3:O:51:LEU:HG	1.78	0.64
1:G:124:THR:CB	3:I:65:ASN:HD21	2.11	0.64
4:P:99:LEU:CD1	4:P:101:ILE:HD11	2.26	0.64
3:C:44:LEU:O	3:C:44:LEU:HD23	1.98	0.64
4:W:49:PHE:CD2	4:W:134:ALA:HB2	2.31	0.64
2:T:170:ARG:C	2:T:172:ARG:H	2.00	0.64
2:H:170:ARG:O	2:H:172:ARG:N	2.28	0.64
3:O:85:GLY:O	3:O:86:LEU:HD12	1.98	0.64
3:I:133:ARG:CB	4:K:188:ILE:HG13	2.28	0.64
4:Q:129:GLU:O	4:Q:129:GLU:HG3	1.97	0.64
4:V:48:ASP:O	4:V:50:ASN:N	2.31	0.64
4:D:179:LYS:HE2	4:D:181:ASN:HB3	1.80	0.64
4:P:111:ASN:HD22	4:P:113:ASP:CG	2.01	0.64
2:B:86:LYS:NZ	2:B:90:TYR:CE1	2.66	0.64
5:R:108:ARG:CB	5:R:108:ARG:HH11	2.09	0.64
3:I:133:ARG:NE	4:K:189:PRO:HD2	2.12	0.64
3:O:137:THR:O	3:O:139:LYS:HG3	1.98	0.64
5:X:90:VAL:HG12	5:X:90:VAL:O	1.98	0.64
5:R:12:LEU:HD23	5:R:12:LEU:N	2.09	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:48:ASP:O	4:J:50:ASN:N	2.31	0.63
3:U:108:SER:HB3	4:W:73:ALA:HB1	1.78	0.63
1:G:187:SER:O	1:G:191:MET:HB2	1.97	0.63
3:I:129:GLU:HB2	3:I:135:GLN:HE22	1.64	0.63
5:R:13:LEU:CD2	5:R:25:LEU:HD11	2.28	0.63
2:B:66:PHE:CZ	2:B:70:ILE:HD11	2.33	0.63
3:C:108:SER:HB3	4:E:73:ALA:HB1	1.79	0.63
3:U:7:TRP:CB	3:U:89:VAL:HG12	2.22	0.63
4:E:101:ILE:CD1	4:E:121:GLU:O	2.46	0.63
4:V:111:ASN:HD22	4:V:113:ASP:CG	2.02	0.63
4:V:179:LYS:HE2	4:V:181:ASN:HB3	1.80	0.63
3:C:112:VAL:HG11	4:E:70:ASP:CB	2.28	0.63
4:W:17:ILE:HG21	4:W:97:ILE:CD1	2.28	0.63
3:C:133:ARG:CB	4:E:188:ILE:HG13	2.28	0.63
4:E:129:GLU:O	4:E:129:GLU:HG3	1.97	0.63
4:D:61:TYR:HA	4:D:146:GLY:O	1.98	0.63
3:O:39:GLU:CA	3:O:42:LYS:HE2	2.14	0.63
2:H:214:ASN:HA	2:H:263:ARG:CG	2.23	0.63
1:S:124:THR:CB	3:U:65:ASN:HD21	2.12	0.63
1:G:178:PHE:HD2	1:G:179:LEU:HD23	1.63	0.63
4:D:111:ASN:HD22	4:D:113:ASP:HB2	1.63	0.63
2:H:233:VAL:HA	2:H:236:ILE:HD13	1.80	0.63
3:C:14:ASN:ND2	3:C:132:MET:O	2.31	0.63
3:O:106:ILE:HD13	3:O:149:LEU:HD11	1.80	0.63
5:L:86:ILE:HD11	5:L:106:ILE:HD11	1.79	0.63
5:F:86:ILE:HD11	5:F:106:ILE:HD11	1.80	0.63
5:R:12:LEU:HB3	5:R:62:TRP:HB2	1.80	0.63
3:I:82:THR:CG2	3:I:84:SER:H	2.02	0.63
1:S:52:PRO:HD3	3:U:75:TYR:CE2	2.34	0.63
1:M:192:LYS:HE2	2:N:64:PHE:CZ	2.34	0.63
2:N:68:GLU:HG2	4:P:63:ILE:HD11	1.79	0.63
2:B:64:PHE:CE1	4:D:67:LEU:HD12	2.33	0.63
3:C:48:ILE:HG21	3:C:87:TRP:CD1	2.32	0.63
3:O:11:ARG:HH12	4:Q:154:MET:CE	2.11	0.63
4:E:17:ILE:HG21	4:E:97:ILE:CD1	2.28	0.63
3:C:84:SER:OG	3:C:86:LEU:HD13	1.98	0.63
3:O:85:GLY:C	3:O:86:LEU:HD12	2.19	0.63
4:W:99:LEU:HB3	4:W:123:PRO:HG3	1.80	0.63
4:W:115:PHE:CE2	4:W:178:VAL:HB	2.32	0.63
5:F:130:VAL:HG12	5:F:131:VAL:N	2.14	0.63
1:G:72:TYR:CD2	1:G:72:TYR:O	2.51	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:191:LEU:HB2	2:T:192:PHE:CD1	2.34	0.63
1:M:52:PRO:HD3	3:O:75:TYR:CE2	2.34	0.63
3:U:137:THR:O	3:U:139:LYS:HG3	1.98	0.63
4:W:129:GLU:O	4:W:129:GLU:HG3	1.97	0.63
4:Q:87:SER:HB2	4:Q:115:PHE:CD1	2.33	0.63
4:J:134:ALA:HB1	4:J:138:LEU:HD13	1.81	0.63
5:X:12:LEU:N	5:X:12:LEU:HD23	2.09	0.63
3:C:85:GLY:C	3:C:86:LEU:HD12	2.19	0.63
4:W:95:PHE:CD1	4:W:103:PRO:HG3	2.34	0.63
4:E:102:THR:HG22	4:E:102:THR:O	1.98	0.63
4:E:34:TYR:CE1	4:E:143:ILE:HG21	2.33	0.63
1:M:39:THR:O	1:M:43:VAL:HG23	1.99	0.63
3:I:72:THR:CG2	3:I:73:GLY:N	2.61	0.63
4:J:111:ASN:HD22	4:J:113:ASP:CG	2.02	0.63
3:O:112:VAL:HG11	4:Q:70:ASP:CB	2.28	0.63
4:E:87:SER:HB2	4:E:115:PHE:CD1	2.33	0.63
3:O:84:SER:OG	3:O:86:LEU:HD13	1.98	0.63
4:P:111:ASN:HD22	4:P:113:ASP:HB2	1.63	0.63
4:E:115:PHE:CE2	4:E:178:VAL:HB	2.33	0.63
4:V:118:ILE:HA	4:V:175:GLU:HB3	1.81	0.63
4:Q:48:ASP:OD1	4:Q:51:LYS:HG3	1.99	0.63
4:Q:99:LEU:HB3	4:Q:123:PRO:HG3	1.81	0.63
1:G:43:VAL:HG11	3:I:51:LEU:HG	1.80	0.63
4:W:114:THR:OG1	4:W:179:LYS:HB2	1.99	0.63
3:U:106:ILE:HD13	3:U:149:LEU:HD11	1.81	0.63
3:U:72:THR:CG2	3:U:73:GLY:N	2.61	0.63
3:I:14:ASN:ND2	3:I:132:MET:O	2.32	0.63
5:L:93:GLN:HG3	5:L:131:VAL:CG1	2.29	0.63
3:U:127:GLU:O	3:U:129:GLU:N	2.29	0.63
2:H:170:ARG:C	2:H:172:ARG:H	2.02	0.63
1:A:134:THR:HG21	1:A:183:TYR:CD1	2.34	0.62
5:L:43:VAL:HG23	5:L:43:VAL:O	1.98	0.62
1:S:134:THR:HG21	1:S:183:TYR:CD1	2.33	0.62
5:F:12:LEU:HB3	5:F:62:TRP:HB2	1.80	0.62
5:F:43:VAL:O	5:F:43:VAL:HG23	1.98	0.62
4:J:99:LEU:CD1	4:J:101:ILE:HD11	2.27	0.62
3:U:112:VAL:HG11	4:W:70:ASP:CB	2.28	0.62
2:B:99:LEU:HD11	2:B:240:PHE:HA	1.81	0.62
3:I:105:TYR:CD2	3:I:152:PHE:CZ	2.87	0.62
4:P:48:ASP:O	4:P:50:ASN:N	2.32	0.62
1:A:52:PRO:HD3	3:C:75:TYR:CE2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:68:GLU:HG2	4:D:63:ILE:HD11	1.80	0.62
1:A:178:PHE:HD2	1:A:179:LEU:HD23	1.63	0.62
4:E:114:THR:OG1	4:E:179:LYS:HB2	1.97	0.62
2:H:216:PRO:C	2:H:218:LEU:H	2.00	0.62
3:O:48:ILE:HG21	3:O:87:TRP:CD1	2.33	0.62
3:C:133:ARG:NE	4:E:189:PRO:HD2	2.13	0.62
3:I:11:ARG:HH12	4:K:154:MET:CE	2.12	0.62
2:T:175:LYS:HG2	2:T:176:ILE:N	2.14	0.62
1:M:140:PHE:CZ	1:M:183:TYR:HA	2.34	0.62
4:K:60:GLY:HA2	4:K:63:ILE:CD1	2.23	0.62
3:I:112:VAL:HG11	4:K:70:ASP:CB	2.28	0.62
2:T:216:PRO:C	2:T:218:LEU:H	2.01	0.62
2:B:218:LEU:HD23	2:B:233:VAL:HG12	1.81	0.62
3:I:137:THR:O	3:I:139:LYS:HG3	1.99	0.62
1:M:134:THR:HG21	1:M:183:TYR:CD1	2.34	0.62
1:M:183:TYR:CD2	4:P:73:ALA:HB2	2.34	0.62
1:S:140:PHE:CZ	1:S:183:TYR:HA	2.34	0.62
4:V:190:ILE:HG22	4:V:190:ILE:O	2.00	0.62
5:X:43:VAL:O	5:X:43:VAL:HG23	1.98	0.62
4:Q:102:THR:HG22	4:Q:102:THR:O	1.99	0.62
3:I:44:LEU:O	3:I:48:ILE:HG12	1.99	0.62
3:U:14:ASN:ND2	3:U:132:MET:O	2.32	0.62
5:X:93:GLN:HG3	5:X:131:VAL:CG1	2.29	0.62
2:N:99:LEU:HD11	2:N:240:PHE:HA	1.81	0.62
4:D:141:SER:O	4:D:144:LEU:HB2	2.00	0.62
5:L:12:LEU:HB3	5:L:62:TRP:HB2	1.80	0.62
3:U:82:THR:HB	3:U:86:LEU:N	2.14	0.62
1:M:107:PHE:HE1	4:P:17:ILE:HD11	1.64	0.62
4:P:155:VAL:HA	4:P:156:GLN:HE21	1.63	0.62
2:H:86:LYS:NZ	2:H:90:TYR:CE1	2.66	0.62
1:M:72:TYR:O	1:M:72:TYR:CD2	2.52	0.62
1:A:72:TYR:CD2	1:A:72:TYR:O	2.52	0.62
2:H:191:LEU:HB2	2:H:192:PHE:CD1	2.35	0.62
4:J:61:TYR:HA	4:J:146:GLY:O	1.99	0.62
4:J:190:ILE:HG22	4:J:190:ILE:O	2.00	0.62
4:D:48:ASP:O	4:D:50:ASN:N	2.33	0.62
3:I:82:THR:HB	3:I:86:LEU:N	2.14	0.62
4:E:99:LEU:HB3	4:E:123:PRO:HG3	1.82	0.62
2:N:184:HIS:ND1	2:N:199:LEU:HB2	2.15	0.62
4:P:95:PHE:HB3	4:P:101:ILE:CD1	2.30	0.62
1:S:178:PHE:HD2	1:S:179:LEU:HD23	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:155:VAL:CA	4:P:156:GLN:HE21	2.12	0.62
5:F:93:GLN:HG3	5:F:131:VAL:CG1	2.28	0.62
5:L:12:LEU:HD23	5:L:12:LEU:N	2.10	0.62
3:O:119:LEU:HD21	4:W:35:GLY:HA3	1.81	0.62
1:A:187:SER:O	1:A:191:MET:HB2	2.00	0.62
3:O:82:THR:HG22	3:O:83:ALA:N	2.15	0.62
3:U:85:GLY:C	3:U:86:LEU:HD12	2.20	0.62
4:K:102:THR:O	4:K:102:THR:HG22	1.99	0.62
4:E:95:PHE:CD1	4:E:103:PRO:HG3	2.35	0.62
1:A:124:THR:CB	3:C:65:ASN:HD21	2.12	0.62
1:S:39:THR:O	1:S:43:VAL:HG23	1.99	0.62
4:P:179:LYS:HE2	4:P:181:ASN:HB3	1.82	0.62
2:T:184:HIS:HB2	2:T:211:ILE:HD11	1.82	0.62
2:T:86:LYS:NZ	2:T:90:TYR:CE1	2.67	0.62
3:I:133:ARG:HB3	4:K:188:ILE:HG13	1.80	0.62
3:I:127:GLU:O	3:I:129:GLU:N	2.29	0.62
2:T:66:PHE:CZ	2:T:70:ILE:HD11	2.34	0.62
5:F:68:GLU:HG2	5:F:69:ARG:HB3	1.81	0.62
3:U:82:THR:HG22	3:U:83:ALA:N	2.15	0.62
4:Q:124:LEU:HD23	4:Q:124:LEU:C	2.20	0.62
4:Q:143:ILE:HG23	4:Q:144:LEU:N	2.14	0.62
3:C:44:LEU:O	3:C:48:ILE:HG12	2.00	0.62
5:L:130:VAL:HG12	5:L:131:VAL:N	2.12	0.62
2:N:191:LEU:HB2	2:N:192:PHE:CD1	2.34	0.62
2:T:99:LEU:HD11	2:T:240:PHE:HA	1.81	0.62
2:N:70:ILE:HG22	2:N:74:HIS:CD2	2.35	0.62
4:V:141:SER:O	4:V:144:LEU:HB2	2.00	0.62
5:X:86:ILE:HD11	5:X:106:ILE:HD11	1.80	0.62
4:W:26:ASN:HD22	4:W:27:THR:N	1.97	0.62
1:G:140:PHE:CZ	1:G:183:TYR:HA	2.35	0.62
1:S:187:SER:O	1:S:191:MET:HB2	1.99	0.62
4:W:101:ILE:CD1	4:W:121:GLU:O	2.48	0.62
2:T:214:ASN:HA	2:T:263:ARG:CG	2.25	0.62
1:S:21:PHE:CD1	1:S:22:THR:N	2.60	0.62
5:X:89:ASP:HA	5:X:121:ASN:ND2	2.12	0.62
2:T:218:LEU:HD23	2:T:233:VAL:HG12	1.82	0.62
4:K:148:LEU:HD12	4:K:161:VAL:HG11	1.81	0.62
3:U:44:LEU:O	3:U:48:ILE:HG12	2.00	0.62
5:R:93:GLN:HG3	5:R:131:VAL:CG1	2.29	0.62
3:O:72:THR:CG2	3:O:73:GLY:N	2.62	0.62
4:D:141:SER:HB3	4:D:144:LEU:HD12	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:PHE:CZ	1:A:183:TYR:HA	2.35	0.62
1:G:183:TYR:CD2	4:J:73:ALA:HB2	2.35	0.62
4:J:49:PHE:HB3	4:J:138:LEU:CD1	2.11	0.62
5:X:12:LEU:HB3	5:X:62:TRP:HB2	1.80	0.62
4:K:99:LEU:HB3	4:K:123:PRO:HG3	1.82	0.62
2:B:184:HIS:HB2	2:B:211:ILE:HD11	1.82	0.62
4:J:118:ILE:HA	4:J:175:GLU:HB3	1.82	0.62
2:B:191:LEU:HB2	2:B:192:PHE:CD1	2.35	0.62
1:A:10:ASN:HD22	1:A:11:LYS:H	1.42	0.61
1:G:52:PRO:HD3	3:I:75:TYR:CD2	2.36	0.61
2:N:87:LEU:HG	2:N:232:PHE:HB2	1.80	0.61
2:H:99:LEU:HD11	2:H:240:PHE:HA	1.81	0.61
5:X:68:GLU:HG2	5:X:69:ARG:CB	2.30	0.61
3:I:82:THR:HG22	3:I:83:ALA:N	2.16	0.61
4:D:155:VAL:O	4:D:155:VAL:HG12	2.01	0.61
1:S:72:TYR:CD2	1:S:72:TYR:O	2.53	0.61
3:U:129:GLU:HB2	3:U:135:GLN:HE22	1.65	0.61
5:L:68:GLU:HG2	5:L:69:ARG:CB	2.30	0.61
1:S:107:PHE:HE1	4:V:17:ILE:HD11	1.65	0.61
5:F:89:ASP:HA	5:F:121:ASN:ND2	2.11	0.61
5:L:89:ASP:HA	5:L:121:ASN:ND2	2.12	0.61
1:A:107:PHE:HE1	4:D:17:ILE:HD11	1.64	0.61
4:V:155:VAL:HA	4:V:156:GLN:HE21	1.64	0.61
4:P:155:VAL:O	4:P:155:VAL:HG12	2.01	0.61
4:D:155:VAL:CA	4:D:156:GLN:HE21	2.13	0.61
3:U:11:ARG:HH12	4:W:154:MET:CE	2.13	0.61
3:I:6:PHE:H	3:I:19:ARG:HB3	1.64	0.61
5:R:150:THR:CG2	5:R:157:ASN:HB2	2.31	0.61
1:A:136:THR:HG21	4:D:69:GLU:OE1	1.99	0.61
4:Q:95:PHE:CD1	4:Q:103:PRO:HG3	2.35	0.61
1:A:21:PHE:CD1	1:A:22:THR:N	2.60	0.61
2:H:184:HIS:HB2	2:H:211:ILE:HD11	1.83	0.61
2:T:233:VAL:HA	2:T:236:ILE:CD1	2.30	0.61
3:C:133:ARG:HG3	3:C:133:ARG:HH11	1.65	0.61
2:B:70:ILE:HG22	2:B:74:HIS:CD2	2.35	0.61
4:E:26:ASN:HD22	4:E:27:THR:N	1.97	0.61
4:V:61:TYR:HA	4:V:146:GLY:O	2.00	0.61
4:J:141:SER:HB3	4:J:144:LEU:HD12	1.81	0.61
3:O:82:THR:HB	3:O:86:LEU:N	2.15	0.61
4:K:143:ILE:HG23	4:K:144:LEU:N	2.14	0.61
1:M:124:THR:CB	3:O:65:ASN:HD21	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:107:PHE:HE1	4:J:17:ILE:HD11	1.65	0.61
2:T:211:ILE:CG2	2:T:268:ILE:HD11	2.30	0.61
2:B:233:VAL:HA	2:B:236:ILE:HD13	1.82	0.61
3:C:6:PHE:H	3:C:19:ARG:HB3	1.65	0.61
4:Q:36:SER:N	3:U:119:LEU:HD11	2.14	0.61
3:C:69:SER:OG	3:C:76:ARG:HD2	2.00	0.61
1:M:126:GLN:HG3	3:O:65:ASN:CB	2.26	0.61
1:S:129:MET:HG2	1:S:131:ILE:CD1	2.31	0.61
2:B:64:PHE:O	2:B:67:GLN:HG3	1.99	0.61
2:N:233:VAL:HA	2:N:236:ILE:CD1	2.31	0.61
4:D:190:ILE:HG22	4:D:190:ILE:O	1.99	0.61
4:P:190:ILE:O	4:P:190:ILE:HG22	1.99	0.61
1:M:10:ASN:HB3	1:M:14:GLY:N	2.12	0.61
1:S:12:SER:HB3	5:X:10:LYS:HZ1	1.65	0.61
3:C:5:SER:OG	3:C:7:TRP:HZ3	1.84	0.61
4:J:179:LYS:HE2	4:J:181:ASN:HB3	1.82	0.61
1:M:178:PHE:HD2	1:M:179:LEU:HD23	1.65	0.61
4:E:148:LEU:HD12	4:E:161:VAL:HG11	1.82	0.61
3:O:129:GLU:HB2	3:O:135:GLN:HE22	1.65	0.61
4:K:48:ASP:OD1	4:K:51:LYS:HG3	2.01	0.61
4:E:48:ASP:OD1	4:E:51:LYS:HG3	2.01	0.61
3:C:5:SER:HB2	3:C:7:TRP:CZ3	2.36	0.61
1:M:21:PHE:CD1	1:M:22:THR:N	2.60	0.61
5:R:89:ASP:HA	5:R:121:ASN:ND2	2.11	0.61
4:J:95:PHE:HB3	4:J:101:ILE:CD1	2.31	0.61
3:I:142:ASN:C	3:I:142:ASN:HD22	2.04	0.61
4:D:155:VAL:HA	4:D:156:GLN:HE21	1.65	0.61
2:B:87:LEU:HG	2:B:232:PHE:HB2	1.81	0.61
3:C:11:ARG:NH1	4:E:154:MET:CE	2.63	0.61
5:X:130:VAL:HG12	5:X:131:VAL:N	2.13	0.61
4:J:141:SER:O	4:J:144:LEU:HB2	2.01	0.61
3:U:105:TYR:CD2	3:U:152:PHE:CZ	2.89	0.61
3:O:70:ILE:O	3:O:76:ARG:HG3	2.01	0.61
4:D:95:PHE:HB3	4:D:101:ILE:CD1	2.31	0.61
3:C:127:GLU:O	3:C:129:GLU:N	2.30	0.61
4:D:135:MET:HG2	4:D:135:MET:O	2.00	0.61
4:K:26:ASN:HD22	4:K:27:THR:N	1.98	0.61
5:F:150:THR:CG2	5:F:157:ASN:HB2	2.31	0.61
1:G:134:THR:HG21	1:G:183:TYR:CD1	2.35	0.61
1:A:190:VAL:HG12	1:A:191:MET:HE3	1.82	0.61
3:C:82:THR:HB	3:C:86:LEU:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:155:VAL:CA	4:V:156:GLN:HE21	2.13	0.61
2:T:87:LEU:HG	2:T:232:PHE:HB2	1.81	0.61
3:O:44:LEU:O	3:O:48:ILE:HG12	2.01	0.61
1:S:198:MET:O	1:S:200:MET:HG2	2.00	0.61
4:V:134:ALA:HB1	4:V:138:LEU:HD13	1.83	0.60
5:L:150:THR:CG2	5:L:157:ASN:HB2	2.31	0.60
3:I:69:SER:OG	3:I:76:ARG:HD2	2.01	0.60
1:G:12:SER:HB3	5:L:10:LYS:HZ1	1.66	0.60
4:P:99:LEU:HB2	4:P:101:ILE:CG1	2.31	0.60
4:V:95:PHE:HB3	4:V:101:ILE:CD1	2.31	0.60
2:H:218:LEU:HD23	2:H:233:VAL:HG12	1.84	0.60
4:J:155:VAL:HA	4:J:156:GLN:HE21	1.65	0.60
4:D:134:ALA:HB1	4:D:138:LEU:HD13	1.83	0.60
3:U:69:SER:OG	3:U:76:ARG:HD2	2.01	0.60
3:U:85:GLY:O	3:U:86:LEU:HD12	2.02	0.60
1:G:21:PHE:CD1	1:G:22:THR:N	2.60	0.60
4:J:99:LEU:HB2	4:J:101:ILE:CG1	2.31	0.60
2:H:68:GLU:HG2	4:J:63:ILE:CD1	2.31	0.60
4:J:155:VAL:HG12	4:J:155:VAL:O	2.00	0.60
3:I:133:ARG:HH11	3:I:133:ARG:HG3	1.65	0.60
3:C:129:GLU:HB2	3:C:135:GLN:HE22	1.65	0.60
1:A:207:PHE:O	1:A:211:VAL:HG22	2.01	0.60
4:E:53:ASN:OD1	4:E:138:LEU:HD12	2.01	0.60
1:G:207:PHE:O	1:G:211:VAL:HG22	2.00	0.60
4:Q:114:THR:HG23	4:Q:178:VAL:C	2.21	0.60
1:A:10:ASN:ND2	1:A:10:ASN:C	2.55	0.60
3:I:108:SER:CB	4:K:73:ALA:HB1	2.31	0.60
3:I:5:SER:OG	3:I:7:TRP:HZ3	1.83	0.60
5:L:82:HIS:HB2	5:L:169:ILE:HD13	1.83	0.60
3:C:7:TRP:HA	3:C:17:PHE:O	2.01	0.60
2:H:211:ILE:CG2	2:H:268:ILE:HD11	2.31	0.60
2:H:233:VAL:HA	2:H:236:ILE:CD1	2.30	0.60
3:C:133:ARG:HB3	4:E:188:ILE:HG13	1.82	0.60
4:Q:35:GLY:HA3	3:U:119:LEU:HD21	1.83	0.60
1:M:10:ASN:ND2	1:M:10:ASN:C	2.55	0.60
2:N:64:PHE:CE1	4:P:67:LEU:HD12	2.37	0.60
2:N:64:PHE:O	2:N:67:GLN:HG3	2.00	0.60
2:T:64:PHE:CE1	4:V:67:LEU:HD12	2.37	0.60
4:V:99:LEU:HB2	4:V:101:ILE:CG1	2.32	0.60
2:B:184:HIS:ND1	2:B:199:LEU:HB2	2.16	0.60
4:P:141:SER:O	4:P:144:LEU:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:118:ASN:O	3:O:118:ASN:CG	2.40	0.60
4:Q:148:LEU:HD12	4:Q:161:VAL:HG11	1.82	0.60
3:C:82:THR:HG22	3:C:83:ALA:N	2.16	0.60
5:L:10:LYS:H	5:L:82:HIS:CE1	2.19	0.60
4:Q:101:ILE:CD1	4:Q:121:GLU:O	2.49	0.60
1:S:43:VAL:HG11	3:U:51:LEU:HG	1.82	0.60
4:D:99:LEU:HB2	4:D:101:ILE:CG1	2.32	0.60
2:H:184:HIS:ND1	2:H:199:LEU:HB2	2.16	0.60
3:I:7:TRP:HA	3:I:17:PHE:O	2.01	0.60
5:X:82:HIS:HB2	5:X:169:ILE:HD13	1.84	0.60
4:P:99:LEU:HB2	4:P:101:ILE:CD1	2.32	0.60
2:T:184:HIS:ND1	2:T:199:LEU:HB2	2.16	0.60
3:U:114:TYR:HD1	3:U:114:TYR:H	1.49	0.60
3:C:43:LEU:HD12	3:C:43:LEU:C	2.22	0.60
3:U:6:PHE:H	3:U:19:ARG:HB3	1.66	0.60
5:X:150:THR:CG2	5:X:157:ASN:HB2	2.31	0.60
1:M:10:ASN:HD22	1:M:11:LYS:H	1.42	0.60
3:I:114:TYR:HD1	3:I:114:TYR:H	1.49	0.60
3:I:142:ASN:ND2	3:I:144:ASN:H	2.00	0.60
2:B:233:VAL:HA	2:B:236:ILE:CD1	2.31	0.60
5:R:29:SER:HA	5:R:48:LYS:HG2	1.83	0.60
4:W:143:ILE:HG23	4:W:144:LEU:N	2.14	0.60
3:O:7:TRP:HA	3:O:17:PHE:O	2.01	0.60
4:J:155:VAL:CA	4:J:156:GLN:HE21	2.14	0.60
4:P:141:SER:HB3	4:P:144:LEU:HD12	1.84	0.60
4:V:99:LEU:HB2	4:V:101:ILE:CD1	2.32	0.60
1:A:129:MET:HG2	1:A:131:ILE:CD1	2.32	0.60
3:C:142:ASN:HD22	3:C:142:ASN:C	2.04	0.60
3:O:133:ARG:HH11	3:O:133:ARG:HG3	1.67	0.60
3:O:127:GLU:O	3:O:129:GLU:N	2.31	0.60
4:V:141:SER:HB3	4:V:144:LEU:HD12	1.83	0.60
4:Q:26:ASN:HD22	4:Q:27:THR:N	1.99	0.60
4:V:68:ILE:HD13	4:V:154:MET:HB3	1.83	0.60
4:K:16:GLU:OE2	4:K:20:ASN:HB2	2.01	0.60
4:Q:84:VAL:CG1	4:Q:85:LYS:N	2.65	0.60
2:N:256:PRO:HG2	2:N:263:ARG:NH2	2.15	0.60
4:V:155:VAL:O	4:V:155:VAL:HG12	2.01	0.60
4:E:84:VAL:CG1	4:E:85:LYS:N	2.65	0.60
1:M:185:LEU:HB3	1:M:207:PHE:HE1	1.67	0.60
4:V:135:MET:O	4:V:135:MET:HG2	2.00	0.60
3:I:5:SER:HB2	3:I:7:TRP:CZ3	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:124:LEU:C	4:K:124:LEU:HD23	2.23	0.59
2:H:64:PHE:O	2:H:67:GLN:HG3	2.01	0.59
2:H:70:ILE:HG22	2:H:74:HIS:CD2	2.37	0.59
2:T:70:ILE:HG22	2:T:74:HIS:CD2	2.37	0.59
3:C:105:TYR:CD2	3:C:152:PHE:CZ	2.90	0.59
3:O:69:SER:OG	3:O:76:ARG:HD2	2.02	0.59
3:O:82:THR:CG2	3:O:84:SER:H	2.02	0.59
4:E:124:LEU:C	4:E:124:LEU:HD23	2.22	0.59
1:G:129:MET:HG2	1:G:131:ILE:CD1	2.32	0.59
4:D:114:THR:HA	4:D:178:VAL:O	2.02	0.59
4:V:22:THR:CB	4:V:74:ARG:HH12	2.13	0.59
4:E:175:GLU:HG2	4:E:175:GLU:O	2.02	0.59
4:P:134:ALA:HB1	4:P:138:LEU:HD13	1.84	0.59
4:D:111:ASN:HD22	4:D:113:ASP:CB	2.15	0.59
2:B:211:ILE:CG2	2:B:268:ILE:HD11	2.32	0.59
4:W:114:THR:HG23	4:W:178:VAL:C	2.21	0.59
4:Q:17:ILE:HG21	4:Q:97:ILE:CD1	2.32	0.59
2:B:256:PRO:HG2	2:B:263:ARG:NH2	2.15	0.59
2:T:64:PHE:O	2:T:67:GLN:HG3	2.01	0.59
4:J:99:LEU:HB2	4:J:101:ILE:CD1	2.32	0.59
1:A:129:MET:HE2	1:A:143:ILE:HD11	1.85	0.59
3:U:133:ARG:HH11	3:U:133:ARG:HG3	1.67	0.59
4:J:68:ILE:HD13	4:J:154:MET:HB3	1.84	0.59
3:U:7:TRP:HA	3:U:17:PHE:O	2.02	0.59
4:W:124:LEU:C	4:W:124:LEU:HD23	2.23	0.59
4:J:114:THR:HA	4:J:178:VAL:O	2.02	0.59
4:P:87:SER:HB2	4:P:115:PHE:CE1	2.38	0.59
2:B:252:ALA:HA	2:B:266:TYR:HA	1.85	0.59
4:J:22:THR:CB	4:J:74:ARG:HH12	2.13	0.59
3:C:114:TYR:H	3:C:114:TYR:HD1	1.49	0.59
3:O:6:PHE:H	3:O:19:ARG:HB3	1.67	0.59
1:A:183:TYR:CD2	4:D:73:ALA:HB2	2.38	0.59
5:L:69:ARG:HB2	5:L:72:THR:HG21	1.84	0.59
5:F:68:GLU:HG2	5:F:69:ARG:CB	2.32	0.59
3:O:5:SER:OG	3:O:7:TRP:HZ3	1.86	0.59
1:S:52:PRO:HD3	3:U:75:TYR:CD2	2.38	0.59
1:S:147:VAL:HG12	1:S:148:MET:N	2.09	0.59
2:T:231:TYR:HD2	2:T:234:CYS:SG	2.23	0.59
1:M:129:MET:HG2	1:M:131:ILE:CD1	2.33	0.59
4:W:148:LEU:HD12	4:W:161:VAL:HG11	1.83	0.59
5:R:67:GLN:HA	5:R:67:GLN:OE1	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:14:ILE:CB	5:L:102:TRP:HZ3	2.16	0.59
4:E:60:GLY:O	4:E:147:VAL:HA	2.02	0.59
4:P:114:THR:HA	4:P:178:VAL:O	2.03	0.59
4:K:162:TRP:CZ2	4:K:177:LYS:HD3	2.37	0.59
3:O:105:TYR:CD2	3:O:152:PHE:CZ	2.90	0.59
1:S:10:ASN:C	1:S:10:ASN:ND2	2.55	0.59
3:O:5:SER:HB2	3:O:7:TRP:CZ3	2.38	0.59
4:P:22:THR:CB	4:P:74:ARG:HH12	2.12	0.59
4:K:114:THR:HG23	4:K:178:VAL:C	2.21	0.59
4:W:84:VAL:CG1	4:W:85:LYS:N	2.64	0.59
4:W:17:ILE:HG21	4:W:97:ILE:HD13	1.84	0.59
4:P:61:TYR:HA	4:P:146:GLY:O	2.02	0.59
4:P:186:ASP:HB2	5:R:79:ARG:CZ	2.33	0.59
1:S:183:TYR:CD2	4:V:73:ALA:HB2	2.38	0.59
3:C:70:ILE:O	3:C:76:ARG:HG3	2.02	0.59
5:F:82:HIS:HB2	5:F:169:ILE:HD13	1.84	0.59
3:I:70:ILE:O	3:I:76:ARG:HG3	2.02	0.59
3:U:70:ILE:O	3:U:76:ARG:HG3	2.02	0.59
2:H:256:PRO:HG2	2:H:263:ARG:NH2	2.16	0.59
4:P:99:LEU:HD12	4:P:101:ILE:CD1	2.28	0.59
4:D:99:LEU:HD12	4:D:101:ILE:CD1	2.28	0.59
4:J:99:LEU:HD12	4:J:101:ILE:CD1	2.29	0.59
4:D:22:THR:CB	4:D:74:ARG:HH12	2.13	0.59
3:C:142:ASN:ND2	3:C:142:ASN:C	2.56	0.59
1:A:75:MET:HA	1:A:217:ASN:HD22	1.67	0.59
1:A:185:LEU:HB3	1:A:207:PHE:HE1	1.68	0.59
1:S:23:ASN:HB3	1:S:25:GLU:CD	2.23	0.59
4:D:186:ASP:HB2	5:F:79:ARG:CZ	2.33	0.59
5:X:157:ASN:HA	5:X:160:ASP:OD2	2.03	0.59
5:R:82:HIS:HB2	5:R:169:ILE:HD13	1.84	0.59
4:V:111:ASN:HD22	4:V:113:ASP:HB2	1.64	0.59
1:A:198:MET:O	1:A:200:MET:HG2	2.03	0.59
4:K:53:ASN:OD1	4:K:138:LEU:HD12	2.03	0.59
4:P:135:MET:O	4:P:135:MET:HG2	2.02	0.59
5:R:65:ALA:O	5:R:73:ILE:HG13	2.03	0.58
5:X:14:ILE:CB	5:X:102:TRP:HZ3	2.16	0.58
5:X:65:ALA:O	5:X:73:ILE:HG13	2.02	0.58
4:D:99:LEU:HB2	4:D:101:ILE:CD1	2.33	0.58
4:J:111:ASN:HD22	4:J:113:ASP:HB2	1.64	0.58
4:P:111:ASN:HD22	4:P:113:ASP:CB	2.15	0.58
4:P:68:ILE:HD13	4:P:154:MET:HB3	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:142:ASN:ND2	3:C:144:ASN:H	2.01	0.58
4:K:17:ILE:HG21	4:K:97:ILE:CD1	2.33	0.58
1:A:75:MET:CE	1:A:105:ASP:HB3	2.32	0.58
3:O:129:GLU:HB2	3:O:135:GLN:NE2	2.18	0.58
1:G:189:TYR:CD2	1:G:206:LEU:HB3	2.37	0.58
1:G:23:ASN:HB3	1:G:25:GLU:CD	2.23	0.58
4:W:53:ASN:OD1	4:W:138:LEU:HD12	2.03	0.58
1:A:10:ASN:HB3	1:A:14:GLY:N	2.13	0.58
2:N:211:ILE:CG2	2:N:268:ILE:HD11	2.32	0.58
5:L:13:LEU:HD21	5:L:25:LEU:CG	2.32	0.58
4:V:49:PHE:HB3	4:V:138:LEU:CD1	2.13	0.58
3:C:82:THR:CG2	3:C:84:SER:H	2.03	0.58
3:U:5:SER:OG	3:U:7:TRP:HZ3	1.85	0.58
2:H:228:SER:O	2:H:231:TYR:HB2	2.04	0.58
3:O:114:TYR:H	3:O:114:TYR:HD1	1.50	0.58
3:O:142:ASN:C	3:O:142:ASN:HD22	2.06	0.58
3:C:129:GLU:HB2	3:C:135:GLN:NE2	2.18	0.58
5:L:53:ASP:C	5:L:55:LYS:H	2.07	0.58
1:G:185:LEU:HD21	1:G:210:LYS:HB3	1.86	0.58
1:A:23:ASN:HB3	1:A:25:GLU:CD	2.23	0.58
4:W:16:GLU:OE2	4:W:20:ASN:HB2	2.02	0.58
4:J:49:PHE:HZ	4:J:133:ASP:OD2	1.87	0.58
3:C:85:GLY:O	3:C:86:LEU:HD12	2.03	0.58
5:X:10:LYS:H	5:X:82:HIS:CE1	2.21	0.58
5:L:85:ILE:HG12	5:L:162:PHE:CE1	2.39	0.58
1:M:207:PHE:O	1:M:211:VAL:HG22	2.03	0.58
4:E:16:GLU:OE2	4:E:20:ASN:HB2	2.02	0.58
4:D:128:VAL:O	4:D:128:VAL:HG22	2.04	0.58
1:S:133:GLN:HA	1:S:139:LYS:HA	1.84	0.58
4:D:49:PHE:HB3	4:D:138:LEU:CD1	2.12	0.58
5:F:65:ALA:O	5:F:73:ILE:HG13	2.03	0.58
3:U:5:SER:HB2	3:U:7:TRP:CZ3	2.38	0.58
2:T:256:PRO:HG2	2:T:263:ARG:NH2	2.16	0.58
4:Q:60:GLY:HA2	4:Q:63:ILE:CD1	2.25	0.58
1:A:124:THR:O	1:A:147:VAL:HG13	2.03	0.58
1:G:198:MET:O	1:G:200:MET:HG2	2.03	0.58
3:I:154:ALA:HB3	3:I:155:PRO:HD3	1.86	0.58
1:M:75:MET:HA	1:M:217:ASN:HD22	1.68	0.58
4:Q:175:GLU:HG2	4:Q:175:GLU:O	2.03	0.58
5:F:13:LEU:HD21	5:F:25:LEU:CG	2.33	0.58
1:G:185:LEU:HB3	1:G:207:PHE:HE1	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:69:ARG:CB	5:R:72:THR:HG22	2.18	0.58
1:A:189:TYR:CD2	1:A:206:LEU:HB3	2.38	0.58
1:M:75:MET:CE	1:M:105:ASP:HB3	2.33	0.58
1:G:130:PHE:HE1	1:G:172:ILE:HA	1.67	0.58
5:R:51:GLU:OE1	5:R:56:THR:HG23	2.04	0.58
1:S:185:LEU:HD21	1:S:210:LYS:HB3	1.86	0.58
3:U:118:ASN:O	3:U:118:ASN:CG	2.42	0.58
4:V:105:ILE:N	4:V:105:ILE:HD13	2.18	0.58
1:G:3:ILE:HG23	1:G:143:ILE:O	2.03	0.58
1:A:7:LEU:CD1	1:A:141:VAL:HB	2.33	0.58
4:P:155:VAL:C	4:P:156:GLN:HE21	2.07	0.58
5:X:53:ASP:C	5:X:55:LYS:H	2.07	0.58
4:V:186:ASP:HB2	5:X:79:ARG:CZ	2.33	0.58
4:D:68:ILE:HD13	4:D:154:MET:HB3	1.84	0.58
1:S:73:VAL:HG12	1:S:74:GLY:N	2.19	0.58
3:C:118:ASN:CG	3:C:118:ASN:O	2.42	0.58
4:J:135:MET:HG2	4:J:135:MET:O	2.02	0.58
5:R:10:LYS:H	5:R:82:HIS:CE1	2.21	0.58
4:K:60:GLY:O	4:K:147:VAL:HA	2.04	0.58
4:Q:83:LEU:O	4:Q:86:THR:HB	2.03	0.58
2:H:252:ALA:HA	2:H:266:TYR:HA	1.86	0.58
5:F:29:SER:HA	5:F:48:LYS:HG2	1.85	0.58
3:I:106:ILE:HD13	3:I:149:LEU:CD1	2.33	0.58
3:C:106:ILE:HD13	3:C:149:LEU:CD1	2.33	0.58
5:X:13:LEU:HD21	5:X:25:LEU:CG	2.32	0.58
1:A:185:LEU:HD21	1:A:210:LYS:HB3	1.85	0.58
1:M:185:LEU:HD21	1:M:210:LYS:HB3	1.86	0.58
1:M:23:ASN:HB3	1:M:25:GLU:CD	2.24	0.58
3:I:118:ASN:O	3:I:118:ASN:CG	2.42	0.58
5:L:65:ALA:O	5:L:73:ILE:HG13	2.03	0.58
5:L:157:ASN:HA	5:L:160:ASP:OD2	2.04	0.58
3:I:5:SER:OG	3:I:7:TRP:CZ3	2.56	0.58
2:B:228:SER:O	2:B:231:TYR:HB2	2.03	0.58
4:V:114:THR:HA	4:V:178:VAL:O	2.03	0.58
4:V:155:VAL:C	4:V:156:GLN:HE21	2.07	0.58
5:X:29:SER:HA	5:X:48:LYS:HG2	1.84	0.58
4:J:186:ASP:HB2	5:L:79:ARG:CZ	2.33	0.58
4:E:15:GLU:HG2	4:E:96:LYS:HE2	1.86	0.58
5:L:43:VAL:HG22	5:L:77:TYR:HE2	1.68	0.58
5:X:151:SER:N	5:X:155:SER:HB3	2.18	0.58
3:O:108:SER:CB	4:Q:73:ALA:HB1	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:HG11	3:C:51:LEU:HG	1.84	0.58
2:T:252:ALA:HA	2:T:266:TYR:HA	1.86	0.58
3:U:142:ASN:ND2	3:U:144:ASN:H	2.02	0.58
3:O:43:LEU:HD12	3:O:43:LEU:C	2.24	0.58
5:L:51:GLU:OE1	5:L:56:THR:HG23	2.04	0.58
4:P:49:PHE:HB3	4:P:138:LEU:CD1	2.12	0.57
4:Q:60:GLY:O	4:Q:147:VAL:HA	2.03	0.57
1:G:147:VAL:CG1	1:G:148:MET:H	2.06	0.57
4:P:114:THR:CG2	4:P:115:PHE:N	2.67	0.57
3:O:11:ARG:NH1	4:Q:154:MET:CE	2.66	0.57
4:E:17:ILE:HG21	4:E:97:ILE:HD13	1.86	0.57
1:A:189:TYR:HD2	1:A:206:LEU:HB3	1.68	0.57
4:Q:180:LEU:HD23	4:Q:181:ASN:H	1.68	0.57
4:Q:16:GLU:OE2	4:Q:20:ASN:HB2	2.03	0.57
1:S:7:LEU:HD12	1:S:141:VAL:HB	1.85	0.57
1:M:134:THR:O	1:M:137:GLY:N	2.32	0.57
5:R:14:ILE:CB	5:R:102:TRP:HZ3	2.17	0.57
5:F:14:ILE:CB	5:F:102:TRP:HZ3	2.17	0.57
4:K:122:ASN:HB3	4:K:126:ASP:OD2	2.04	0.57
4:K:83:LEU:O	4:K:86:THR:HB	2.03	0.57
1:A:52:PRO:HD3	3:C:75:TYR:CD2	2.38	0.57
4:D:70:ASP:O	4:D:74:ARG:HB2	2.04	0.57
2:B:191:LEU:HB3	4:D:29:LEU:HD12	1.86	0.57
1:S:185:LEU:HB3	1:S:207:PHE:HE1	1.69	0.57
1:S:207:PHE:O	1:S:211:VAL:HG22	2.03	0.57
4:Q:53:ASN:OD1	4:Q:138:LEU:HD12	2.05	0.57
1:M:7:LEU:HD12	1:M:141:VAL:HB	1.86	0.57
2:T:228:SER:O	2:T:231:TYR:HB2	2.05	0.57
4:D:155:VAL:C	4:D:156:GLN:HE21	2.07	0.57
1:G:50:LEU:HG	1:G:50:LEU:O	2.04	0.57
1:G:75:MET:HA	1:G:217:ASN:HD22	1.68	0.57
4:J:105:ILE:N	4:J:105:ILE:HD13	2.19	0.57
4:V:49:PHE:HZ	4:V:133:ASP:OD2	1.87	0.57
1:A:191:MET:SD	4:D:69:GLU:HG3	2.45	0.57
3:C:5:SER:OG	3:C:7:TRP:CZ3	2.57	0.57
1:S:5:THR:OG1	1:S:20:ASN:ND2	2.37	0.57
4:E:114:THR:HG23	4:E:178:VAL:C	2.24	0.57
4:Q:17:ILE:HG21	4:Q:97:ILE:HD13	1.87	0.57
3:I:11:ARG:NH1	4:K:154:MET:CE	2.66	0.57
3:C:154:ALA:HB3	3:C:155:PRO:HD3	1.86	0.57
1:M:189:TYR:CD2	1:M:206:LEU:HB3	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:189:TYR:CD2	1:S:206:LEU:HB3	2.38	0.57
2:B:173:ASP:O	2:B:174:LEU:HD23	2.04	0.57
4:Q:162:TRP:CZ2	4:Q:177:LYS:HD3	2.39	0.57
5:L:151:SER:N	5:L:155:SER:HB3	2.19	0.57
3:U:5:SER:OG	3:U:7:TRP:CZ3	2.57	0.57
1:G:190:VAL:HG12	1:G:191:MET:HE3	1.85	0.57
4:W:122:ASN:HB3	4:W:126:ASP:OD2	2.04	0.57
2:N:252:ALA:HA	2:N:266:TYR:HA	1.87	0.57
4:D:98:PHE:O	4:D:99:LEU:HD23	2.04	0.57
4:Q:32:LEU:HD21	3:U:117:ASN:OD1	2.04	0.57
1:M:198:MET:O	1:M:200:MET:HG2	2.05	0.57
3:C:133:ARG:HG3	3:C:133:ARG:NH1	2.18	0.57
1:M:189:TYR:HD2	1:M:206:LEU:HB3	1.69	0.57
1:G:121:GLN:OE1	1:G:172:ILE:HG12	2.04	0.57
5:R:14:ILE:HB	5:R:102:TRP:CZ3	2.40	0.57
1:G:10:ASN:HB3	1:G:14:GLY:N	2.11	0.57
4:W:60:GLY:O	4:W:147:VAL:HA	2.05	0.57
4:E:60:GLY:HA2	4:E:63:ILE:CD1	2.25	0.57
1:M:147:VAL:CG1	1:M:148:MET:H	2.05	0.57
3:U:11:ARG:NH1	4:W:154:MET:CE	2.66	0.57
1:M:52:PRO:HD3	3:O:75:TYR:CD2	2.38	0.57
5:L:126:LYS:HG2	5:L:129:ARG:HD2	1.86	0.57
5:R:13:LEU:HD21	5:R:25:LEU:CG	2.33	0.57
4:Q:15:GLU:HG2	4:Q:96:LYS:HE2	1.87	0.57
4:P:105:ILE:N	4:P:105:ILE:HD13	2.19	0.57
5:L:69:ARG:CB	5:L:72:THR:HG22	2.24	0.57
3:C:108:SER:CB	4:E:73:ALA:HB1	2.35	0.57
3:I:77:VAL:CG1	3:I:91:LEU:HD22	2.24	0.57
2:N:231:TYR:CE2	2:N:251:THR:HA	2.40	0.57
4:D:114:THR:CG2	4:D:115:PHE:N	2.68	0.57
3:U:48:ILE:HG21	3:U:87:TRP:CD1	2.33	0.57
4:W:48:ASP:CG	4:W:51:LYS:HG3	2.24	0.57
2:H:198:ASP:OD2	2:H:200:VAL:HG23	2.04	0.57
5:F:151:SER:N	5:F:155:SER:HB3	2.19	0.57
4:V:111:ASN:HD22	4:V:113:ASP:CB	2.17	0.57
4:J:111:ASN:HD22	4:J:113:ASP:CB	2.17	0.57
3:U:142:ASN:HD22	3:U:142:ASN:C	2.08	0.57
3:I:129:GLU:HB2	3:I:135:GLN:NE2	2.18	0.57
1:A:121:GLN:OE1	1:A:172:ILE:HG12	2.04	0.57
4:Q:50:ASN:HA	4:Q:53:ASN:HD22	1.69	0.57
1:M:69:TYR:HD1	1:M:173:GLN:NE2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:14:ILE:HB	5:L:102:TRP:CZ3	2.39	0.57
5:F:14:ILE:HB	5:F:102:TRP:CZ3	2.40	0.57
5:R:157:ASN:HA	5:R:160:ASP:OD2	2.04	0.57
5:X:14:ILE:HB	5:X:102:TRP:CZ3	2.39	0.57
5:X:43:VAL:HG22	5:X:77:TYR:HE2	1.69	0.57
1:G:10:ASN:C	1:G:10:ASN:ND2	2.57	0.57
4:Q:59:MET:O	4:Q:63:ILE:HG12	2.04	0.57
3:C:72:THR:HG23	3:C:73:GLY:H	1.69	0.57
3:O:142:ASN:ND2	3:O:144:ASN:H	2.03	0.57
4:E:162:TRP:CZ2	4:E:177:LYS:HD3	2.40	0.57
1:M:50:LEU:O	1:M:50:LEU:HG	2.04	0.57
3:I:43:LEU:HD12	3:I:43:LEU:C	2.24	0.57
4:W:162:TRP:CZ2	4:W:177:LYS:HD3	2.40	0.57
3:U:154:ALA:HB3	3:U:155:PRO:HD3	1.87	0.57
1:M:121:GLN:OE1	1:M:172:ILE:HG12	2.04	0.57
1:S:121:GLN:OE1	1:S:172:ILE:HG12	2.04	0.57
1:M:73:VAL:HG12	1:M:74:GLY:N	2.20	0.57
1:M:133:GLN:HA	1:M:139:LYS:HA	1.86	0.57
1:G:134:THR:O	1:G:137:GLY:N	2.34	0.57
1:S:120:ARG:HB3	1:S:120:ARG:NH1	2.07	0.57
4:V:87:SER:HB2	4:V:115:PHE:CE1	2.39	0.57
4:J:114:THR:CG2	4:J:115:PHE:N	2.67	0.57
4:J:70:ASP:O	4:J:74:ARG:HB2	2.05	0.57
4:J:155:VAL:C	4:J:156:GLN:HE21	2.08	0.57
3:O:133:ARG:NH1	3:O:133:ARG:HG3	2.19	0.57
2:T:192:PHE:CD1	2:T:192:PHE:N	2.66	0.57
5:R:43:VAL:HG22	5:R:77:TYR:HE2	1.69	0.56
5:F:43:VAL:HG22	5:F:77:TYR:HE2	1.69	0.56
1:G:10:ASN:C	1:G:12:SER:N	2.59	0.56
3:U:43:LEU:HD12	3:U:43:LEU:C	2.24	0.56
1:S:75:MET:HA	1:S:217:ASN:HD22	1.69	0.56
1:A:177:ASN:O	1:A:181:LYS:HG3	2.04	0.56
2:H:167:THR:HG22	2:H:169:MET:HB3	1.86	0.56
5:R:53:ASP:C	5:R:55:LYS:H	2.07	0.56
4:V:114:THR:CG2	4:V:115:PHE:N	2.67	0.56
2:T:84:GLU:OE1	2:T:231:TYR:HE1	1.88	0.56
2:H:64:PHE:HE1	4:J:67:LEU:HD12	1.70	0.56
5:L:29:SER:HA	5:L:48:LYS:HG2	1.85	0.56
5:F:53:ASP:C	5:F:55:LYS:H	2.07	0.56
3:O:106:ILE:HD13	3:O:149:LEU:CD1	2.34	0.56
4:K:50:ASN:HA	4:K:53:ASN:HD22	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:10:LYS:H	5:F:82:HIS:CE1	2.22	0.56
3:I:82:THR:CB	3:I:86:LEU:H	2.17	0.56
1:S:10:ASN:C	1:S:12:SER:N	2.59	0.56
4:D:87:SER:HB2	4:D:115:PHE:CE1	2.41	0.56
4:J:87:SER:HB2	4:J:115:PHE:CE1	2.39	0.56
4:J:98:PHE:O	4:J:99:LEU:HD23	2.05	0.56
1:M:3:ILE:HG23	1:M:143:ILE:O	2.04	0.56
3:O:142:ASN:C	3:O:142:ASN:ND2	2.58	0.56
4:K:84:VAL:CG1	4:K:85:LYS:N	2.67	0.56
1:S:50:LEU:HG	1:S:50:LEU:O	2.05	0.56
3:O:154:ALA:HB3	3:O:155:PRO:HD3	1.87	0.56
5:X:85:ILE:HG12	5:X:162:PHE:CE1	2.41	0.56
5:R:85:ILE:HG12	5:R:162:PHE:CE1	2.40	0.56
3:U:129:GLU:HB2	3:U:135:GLN:NE2	2.19	0.56
1:G:189:TYR:HD2	1:G:206:LEU:HB3	1.68	0.56
3:U:106:ILE:HD13	3:U:149:LEU:CD1	2.34	0.56
5:X:51:GLU:OE1	5:X:56:THR:HG23	2.04	0.56
2:B:227:VAL:O	2:B:230:GLU:HB3	2.04	0.56
4:D:105:ILE:N	4:D:105:ILE:HD13	2.20	0.56
5:R:151:SER:N	5:R:155:SER:HB3	2.19	0.56
3:O:120:LEU:HD23	4:W:39:ALA:HB2	1.88	0.56
3:O:5:SER:OG	3:O:7:TRP:CZ3	2.58	0.56
4:P:113:ASP:O	4:P:179:LYS:HA	2.06	0.56
2:T:196:SER:OG	2:T:211:ILE:HD11	2.06	0.56
4:P:70:ASP:O	4:P:74:ARG:HB2	2.05	0.56
2:H:227:VAL:O	2:H:230:GLU:HB3	2.04	0.56
3:I:133:ARG:NH1	3:I:133:ARG:HG3	2.18	0.56
4:Q:188:ILE:O	4:Q:188:ILE:CG2	2.54	0.56
4:E:188:ILE:CG2	4:E:188:ILE:O	2.54	0.56
1:G:71:PRO:HD2	1:G:177:ASN:OD1	2.05	0.56
4:P:128:VAL:O	4:P:128:VAL:HG22	2.06	0.56
1:A:133:GLN:HA	1:A:139:LYS:HA	1.86	0.56
5:F:157:ASN:HA	5:F:160:ASP:OD2	2.05	0.56
2:B:260:HIS:HB2	2:B:263:ARG:HB2	1.87	0.56
3:U:72:THR:CG2	3:U:74:LYS:H	2.19	0.56
4:V:99:LEU:HD12	4:V:101:ILE:CD1	2.29	0.56
1:G:192:LYS:HE2	2:H:64:PHE:CE1	2.40	0.56
3:C:112:VAL:HG11	4:E:70:ASP:OD1	2.06	0.56
3:I:48:ILE:HG21	3:I:87:TRP:CD1	2.34	0.56
1:S:177:ASN:O	1:S:181:LYS:HG3	2.06	0.56
4:K:61:TYR:CE2	4:K:65:CYS:SG	2.99	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:PRO:HD2	1:A:177:ASN:OD1	2.05	0.56
4:W:180:LEU:HD23	4:W:181:ASN:H	1.68	0.56
4:E:180:LEU:HD23	4:E:181:ASN:H	1.70	0.56
5:R:126:LYS:HG2	5:R:129:ARG:HD2	1.87	0.56
1:S:134:THR:O	1:S:137:GLY:N	2.35	0.56
5:R:68:GLU:HG2	5:R:69:ARG:HB3	1.87	0.56
2:N:228:SER:O	2:N:231:TYR:HB2	2.05	0.56
3:C:11:ARG:HH11	3:C:125:PHE:HE1	1.53	0.56
4:W:15:GLU:HG2	4:W:96:LYS:HE2	1.88	0.56
1:G:73:VAL:HG12	1:G:74:GLY:N	2.21	0.56
1:S:10:ASN:HB3	1:S:14:GLY:N	2.12	0.56
1:S:15:LEU:HD11	1:S:17:TYR:O	2.05	0.56
2:H:84:GLU:OE1	2:H:231:TYR:HE1	1.89	0.56
4:J:98:PHE:C	4:J:99:LEU:HD23	2.26	0.56
3:I:133:ARG:HD2	3:I:133:ARG:N	2.18	0.56
2:B:176:ILE:HG23	2:B:177:LEU:N	2.20	0.56
4:K:175:GLU:O	4:K:175:GLU:HG2	2.04	0.56
1:G:177:ASN:O	1:G:181:LYS:HG3	2.06	0.56
5:L:68:GLU:HG2	5:L:69:ARG:CA	2.35	0.56
4:V:50:ASN:HA	4:V:53:ASN:HD22	1.71	0.56
3:U:108:SER:CB	4:W:73:ALA:HB1	2.35	0.56
4:E:122:ASN:HB3	4:E:126:ASP:OD2	2.05	0.56
4:E:59:MET:O	4:E:63:ILE:HG12	2.05	0.56
2:N:84:GLU:OE1	2:N:231:TYR:HE1	1.89	0.56
1:S:124:THR:O	1:S:147:VAL:HG13	2.05	0.56
1:A:192:LYS:HE2	2:B:64:PHE:CE1	2.41	0.56
4:P:180:LEU:CD1	4:P:180:LEU:H	2.12	0.56
2:B:216:PRO:C	2:B:218:LEU:N	2.58	0.56
4:W:175:GLU:HG2	4:W:175:GLU:O	2.03	0.56
4:W:61:TYR:CE2	4:W:65:CYS:SG	2.99	0.56
2:N:176:ILE:HG23	2:N:177:LEU:N	2.20	0.56
2:B:198:ASP:OD2	2:B:200:VAL:HG23	2.06	0.56
2:T:198:ASP:OD2	2:T:200:VAL:HG23	2.05	0.56
4:D:50:ASN:HA	4:D:53:ASN:HD22	1.71	0.56
3:U:82:THR:CB	3:U:86:LEU:H	2.18	0.56
2:B:84:GLU:OE1	2:B:231:TYR:HE1	1.89	0.56
5:L:50:VAL:HG23	5:L:57:VAL:HG12	1.87	0.56
1:G:75:MET:CE	1:G:105:ASP:HB3	2.33	0.56
5:X:126:LYS:HG2	5:X:129:ARG:HD2	1.88	0.56
2:N:198:ASP:OD2	2:N:200:VAL:HG23	2.06	0.56
4:V:128:VAL:O	4:V:128:VAL:HG22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:12:SER:HB3	5:X:10:LYS:NZ	2.21	0.56
4:K:59:MET:O	4:K:63:ILE:HG12	2.05	0.56
4:W:83:LEU:O	4:W:86:THR:HB	2.05	0.56
1:M:15:LEU:HD11	1:M:17:TYR:O	2.05	0.56
3:I:112:VAL:HG21	4:K:70:ASP:HA	1.89	0.56
5:X:11:LEU:O	5:X:61:ILE:HA	2.06	0.56
1:A:50:LEU:O	1:A:50:LEU:HG	2.06	0.56
3:O:3:ILE:HG21	3:O:90:LEU:HD21	1.87	0.56
2:H:192:PHE:N	2:H:192:PHE:CD1	2.66	0.56
4:K:180:LEU:HD23	4:K:181:ASN:H	1.69	0.56
1:A:130:PHE:HE1	1:A:172:ILE:HA	1.68	0.56
1:M:130:PHE:HE1	1:M:172:ILE:HA	1.67	0.56
5:F:126:LYS:HG2	5:F:129:ARG:HD2	1.87	0.56
3:O:93:ASP:OD1	3:O:95:LYS:HB2	2.06	0.56
3:U:77:VAL:CG1	3:U:91:LEU:HD22	2.24	0.55
2:H:260:HIS:HB2	2:H:263:ARG:HB2	1.88	0.55
2:N:254:ARG:CA	2:N:264:THR:HG22	2.35	0.55
4:E:83:LEU:O	4:E:86:THR:HB	2.06	0.55
4:Q:122:ASN:HB3	4:Q:126:ASP:OD2	2.05	0.55
4:D:113:ASP:O	4:D:179:LYS:HA	2.06	0.55
4:V:98:PHE:O	4:V:99:LEU:HD23	2.06	0.55
4:D:37:ILE:O	4:D:41:LEU:HG	2.05	0.55
1:S:69:TYR:HD1	1:S:173:GLN:NE2	2.03	0.55
5:F:51:GLU:OE1	5:F:56:THR:HG23	2.06	0.55
4:J:128:VAL:O	4:J:128:VAL:HG22	2.06	0.55
4:V:137:SER:HA	4:V:169:ARG:HH22	1.71	0.55
4:W:71:PHE:CD1	4:W:71:PHE:C	2.78	0.55
2:N:68:GLU:HG2	4:P:63:ILE:CD1	2.36	0.55
2:T:231:TYR:CE2	2:T:251:THR:HA	2.40	0.55
3:I:142:ASN:C	3:I:142:ASN:ND2	2.56	0.55
3:O:133:ARG:HD2	3:O:133:ARG:N	2.18	0.55
4:Q:61:TYR:CE2	4:Q:65:CYS:SG	3.00	0.55
2:H:176:ILE:HG23	2:H:177:LEU:N	2.20	0.55
3:U:93:ASP:OD1	3:U:95:LYS:HB2	2.06	0.55
1:A:42:GLY:O	1:A:45:ALA:HB3	2.06	0.55
3:I:18:ASP:OD2	3:I:18:ASP:N	2.38	0.55
5:R:68:GLU:HG2	5:R:69:ARG:CB	2.36	0.55
5:X:24:LEU:HD11	5:X:158:VAL:HG21	1.88	0.55
1:M:190:VAL:HG12	1:M:191:MET:HE3	1.86	0.55
1:M:12:SER:CB	5:R:10:LYS:HZ2	2.19	0.55
4:V:160:ASP:HB3	4:V:162:TRP:CZ3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:216:PRO:C	2:H:218:LEU:N	2.59	0.55
5:L:50:VAL:CG2	5:L:57:VAL:HG12	2.36	0.55
3:U:133:ARG:HD2	3:U:133:ARG:N	2.19	0.55
2:N:175:LYS:HG2	2:N:176:ILE:N	2.21	0.55
5:F:24:LEU:HD11	5:F:158:VAL:HG21	1.88	0.55
2:B:64:PHE:HE1	4:D:67:LEU:HD12	1.70	0.55
4:D:98:PHE:C	4:D:99:LEU:HD23	2.26	0.55
2:N:190:TYR:O	4:P:26:ASN:ND2	2.38	0.55
3:U:133:ARG:HG3	3:U:133:ARG:NH1	2.20	0.55
1:S:189:TYR:HD2	1:S:206:LEU:HB3	1.69	0.55
1:A:69:TYR:HD1	1:A:173:GLN:NE2	2.05	0.55
1:A:134:THR:O	1:A:137:GLY:N	2.35	0.55
4:D:137:SER:HA	4:D:169:ARG:HH22	1.72	0.55
1:S:190:VAL:HG12	1:S:191:MET:HE3	1.87	0.55
4:W:34:TYR:CE2	4:W:124:LEU:HD21	2.42	0.55
1:G:15:LEU:HD11	1:G:17:TYR:O	2.06	0.55
4:J:113:ASP:O	4:J:179:LYS:HA	2.06	0.55
4:J:106:THR:CG2	4:J:107:ASN:H	2.10	0.55
2:T:250:VAL:HG13	2:T:268:ILE:HG12	1.88	0.55
4:K:85:LYS:O	4:K:89:VAL:HG23	2.06	0.55
4:K:188:ILE:CG2	4:K:188:ILE:O	2.54	0.55
1:S:75:MET:CE	1:S:105:ASP:HB3	2.33	0.55
5:R:28:PHE:HD2	5:R:48:LYS:HZ3	1.54	0.55
5:F:28:PHE:HB3	5:F:48:LYS:HZ3	1.70	0.55
5:R:13:LEU:H	5:R:13:LEU:HD12	1.70	0.55
2:T:227:VAL:O	2:T:230:GLU:HB3	2.06	0.55
1:S:10:ASN:C	1:S:12:SER:H	2.10	0.55
2:H:231:TYR:CE2	2:H:251:THR:HA	2.40	0.55
1:S:192:LYS:HE2	2:T:64:PHE:CE1	2.41	0.55
5:R:50:VAL:CG2	5:R:57:VAL:HG12	2.36	0.55
2:B:190:TYR:O	4:D:26:ASN:ND2	2.39	0.55
4:W:188:ILE:CG2	4:W:188:ILE:O	2.54	0.55
3:C:102:VAL:HG11	3:C:156:MET:HE3	1.88	0.55
2:T:176:ILE:HG23	2:T:177:LEU:N	2.21	0.55
5:R:77:TYR:N	5:R:77:TYR:CD1	2.73	0.55
4:D:49:PHE:HZ	4:D:133:ASP:OD2	1.87	0.55
5:R:140:ALA:HB1	5:R:145:MET:O	2.06	0.55
1:A:147:VAL:CG1	1:A:148:MET:H	2.07	0.55
2:B:68:GLU:HG2	4:D:63:ILE:CD1	2.36	0.55
4:J:160:ASP:HB3	4:J:162:TRP:CZ3	2.42	0.55
2:T:68:GLU:HG2	4:V:63:ILE:CD1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:85:LYS:O	4:E:89:VAL:HG23	2.07	0.55
5:R:11:LEU:O	5:R:61:ILE:HA	2.06	0.55
5:R:50:VAL:HG23	5:R:57:VAL:HG12	1.88	0.55
2:H:190:TYR:O	4:J:26:ASN:ND2	2.40	0.55
2:T:190:TYR:O	4:V:26:ASN:ND2	2.40	0.55
3:O:116:SER:O	4:Q:66:ARG:HB3	2.07	0.55
3:O:20:GLU:O	3:O:21:TRP:CB	2.54	0.55
1:S:130:PHE:HE1	1:S:172:ILE:HA	1.68	0.55
2:N:227:VAL:O	2:N:230:GLU:HB3	2.06	0.55
1:A:73:VAL:HG12	1:A:74:GLY:N	2.22	0.55
4:P:50:ASN:HA	4:P:53:ASN:HD22	1.72	0.55
1:G:5:THR:OG1	1:G:20:ASN:ND2	2.40	0.55
5:X:50:VAL:CG2	5:X:57:VAL:HG12	2.37	0.55
5:F:85:ILE:HG12	5:F:162:PHE:CE1	2.42	0.55
1:M:71:PRO:HD2	1:M:177:ASN:OD1	2.07	0.55
2:B:72:GLN:HE22	4:D:55:HIS:CE1	2.24	0.55
1:G:133:GLN:HA	1:G:139:LYS:HA	1.88	0.55
4:J:187:GLU:O	4:J:187:GLU:HG3	2.07	0.55
1:A:10:ASN:C	1:A:12:SER:H	2.10	0.55
3:I:5:SER:CB	3:I:7:TRP:CZ3	2.90	0.55
3:U:76:ARG:O	3:U:91:LEU:HA	2.06	0.55
2:B:254:ARG:CA	2:B:264:THR:HG22	2.36	0.55
4:V:113:ASP:O	4:V:179:LYS:HA	2.06	0.55
4:J:162:TRP:HE1	4:J:177:LYS:HB2	1.70	0.55
1:S:194:PRO:HG3	2:T:67:GLN:CA	2.37	0.55
4:V:70:ASP:O	4:V:74:ARG:HB2	2.07	0.55
2:T:191:LEU:HB3	4:V:29:LEU:HD12	1.89	0.55
3:O:131:GLU:O	3:O:135:GLN:HG2	2.07	0.55
4:V:37:ILE:O	4:V:41:LEU:HG	2.07	0.55
4:Q:48:ASP:CG	4:Q:51:LYS:HG3	2.26	0.55
1:S:42:GLY:O	1:S:45:ALA:HB3	2.06	0.55
3:I:72:THR:CG2	3:I:74:LYS:H	2.20	0.55
1:G:107:PHE:CB	1:G:180:ARG:HH12	2.18	0.55
5:R:47:ILE:HD11	5:R:60:GLN:HG3	1.89	0.55
1:S:3:ILE:HG23	1:S:143:ILE:O	2.06	0.55
1:M:5:THR:OG1	1:M:20:ASN:ND2	2.39	0.55
1:A:131:ILE:HG22	1:A:131:ILE:O	2.07	0.55
3:C:3:ILE:HG21	3:C:90:LEU:HD21	1.88	0.55
4:K:49:PHE:HB2	4:K:137:SER:HB3	1.89	0.55
4:P:29:LEU:O	4:P:29:LEU:HD23	2.07	0.55
3:I:116:SER:O	4:K:66:ARG:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:177:ASN:O	1:M:181:LYS:HG3	2.06	0.55
3:I:93:ASP:OD1	3:I:95:LYS:HB2	2.07	0.55
5:F:68:GLU:HG2	5:F:69:ARG:CA	2.36	0.54
5:F:68:GLU:C	5:F:70:PHE:H	2.10	0.54
5:X:82:HIS:HB3	5:X:169:ILE:HG21	1.88	0.54
5:F:140:ALA:HB1	5:F:145:MET:O	2.07	0.54
2:N:256:PRO:CG	2:N:263:ARG:NH2	2.70	0.54
5:F:89:ASP:HB2	5:F:95:SER:HB3	1.89	0.54
2:H:250:VAL:HG13	2:H:268:ILE:HG12	1.89	0.54
5:X:89:ASP:HB2	5:X:95:SER:HB3	1.89	0.54
1:A:107:PHE:CB	1:A:180:ARG:HH12	2.17	0.54
1:A:5:THR:OG1	1:A:20:ASN:ND2	2.39	0.54
1:S:71:PRO:HD2	1:S:177:ASN:OD1	2.07	0.54
4:E:61:TYR:CE2	4:E:65:CYS:SG	3.01	0.54
3:U:127:GLU:C	3:U:129:GLU:N	2.61	0.54
5:X:77:TYR:CD1	5:X:77:TYR:N	2.74	0.54
1:M:120:ARG:HB3	1:M:120:ARG:NH1	2.08	0.54
4:V:162:TRP:HE1	4:V:177:LYS:HB2	1.71	0.54
2:N:216:PRO:C	2:N:218:LEU:N	2.59	0.54
3:O:112:VAL:HG11	4:Q:70:ASP:OD1	2.07	0.54
3:C:20:GLU:O	3:C:21:TRP:CB	2.55	0.54
3:I:127:GLU:C	3:I:129:GLU:N	2.61	0.54
1:G:42:GLY:O	1:G:45:ALA:HB3	2.07	0.54
4:P:49:PHE:HZ	4:P:133:ASP:OD2	1.88	0.54
3:U:67:ILE:HG21	3:U:70:ILE:HD11	1.89	0.54
4:K:99:LEU:O	4:K:100:ASN:C	2.45	0.54
4:Q:71:PHE:C	4:Q:71:PHE:CD1	2.79	0.54
3:I:72:THR:HG23	3:I:73:GLY:H	1.72	0.54
5:L:89:ASP:HB2	5:L:95:SER:HB3	1.90	0.54
5:L:11:LEU:O	5:L:61:ILE:HA	2.07	0.54
2:T:216:PRO:C	2:T:218:LEU:N	2.60	0.54
2:B:90:TYR:CZ	4:D:40:GLN:HG2	2.42	0.54
5:F:93:GLN:HG3	5:F:131:VAL:HG11	1.89	0.54
3:U:155:PRO:HG2	3:U:156:MET:N	2.20	0.54
2:H:179:ILE:HG23	2:H:180:LEU:N	2.23	0.54
3:C:131:GLU:O	3:C:135:GLN:HG2	2.07	0.54
5:F:68:GLU:O	5:F:70:PHE:N	2.28	0.54
1:M:191:MET:SD	4:P:69:GLU:HG3	2.47	0.54
1:G:191:MET:SD	4:J:69:GLU:HG3	2.46	0.54
4:W:60:GLY:HA2	4:W:63:ILE:CD1	2.25	0.54
1:M:192:LYS:HE2	2:N:64:PHE:CE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:106:THR:CG2	4:V:107:ASN:H	2.10	0.54
3:U:11:ARG:HH11	3:U:125:PHE:HE1	1.54	0.54
4:W:50:ASN:HA	4:W:53:ASN:HD22	1.70	0.54
4:V:192:GLU:HG2	4:V:192:GLU:O	2.07	0.54
5:F:77:TYR:CD1	5:F:77:TYR:N	2.74	0.54
5:L:24:LEU:HD11	5:L:158:VAL:HG21	1.89	0.54
3:C:67:ILE:HG21	3:C:70:ILE:HD11	1.90	0.54
3:I:67:ILE:HD13	3:I:79:THR:HG21	1.88	0.54
3:O:67:ILE:HD13	3:O:79:THR:HG21	1.90	0.54
4:K:71:PHE:C	4:K:71:PHE:CD1	2.80	0.54
1:G:12:SER:HB3	5:L:10:LYS:NZ	2.23	0.54
1:A:15:LEU:HD11	1:A:17:TYR:O	2.07	0.54
4:D:160:ASP:HB3	4:D:162:TRP:CZ3	2.43	0.54
2:H:196:SER:OG	2:H:211:ILE:HD11	2.08	0.54
2:B:250:VAL:HG13	2:B:268:ILE:HG12	1.89	0.54
1:M:107:PHE:CB	1:M:180:ARG:HH12	2.18	0.54
3:C:133:ARG:HD2	3:C:133:ARG:N	2.19	0.54
3:I:131:GLU:O	3:I:135:GLN:HG2	2.08	0.54
4:K:48:ASP:CG	4:K:51:LYS:HG3	2.27	0.54
1:G:10:ASN:C	1:G:12:SER:H	2.11	0.54
1:S:107:PHE:CB	1:S:180:ARG:HH12	2.19	0.54
2:H:221:PHE:O	2:H:223:PRO:HD3	2.08	0.54
2:H:227:VAL:O	2:H:230:GLU:CB	2.55	0.54
3:I:11:ARG:HH11	3:I:125:PHE:HE1	1.54	0.54
3:C:116:SER:O	4:E:66:ARG:HB3	2.08	0.54
3:U:116:SER:O	4:W:66:ARG:HB3	2.07	0.54
3:C:129:GLU:CB	3:C:135:GLN:OE1	2.56	0.54
4:E:31:THR:CG2	4:E:127:PHE:CZ	2.91	0.54
2:H:102:LEU:C	2:H:102:LEU:HD23	2.28	0.54
3:I:111:TYR:CZ	3:I:115:VAL:HG11	2.43	0.54
3:O:76:ARG:O	3:O:91:LEU:HA	2.08	0.54
4:W:99:LEU:O	4:W:100:ASN:C	2.45	0.54
4:E:71:PHE:CD1	4:E:71:PHE:C	2.80	0.54
3:C:72:THR:CG2	3:C:74:LYS:H	2.20	0.54
4:D:95:PHE:HB3	4:D:101:ILE:O	2.08	0.54
4:P:160:ASP:HB3	4:P:162:TRP:CZ3	2.43	0.54
4:J:94:ALA:O	4:J:98:PHE:HD1	1.91	0.54
2:H:87:LEU:O	2:H:90:TYR:HB2	2.08	0.54
1:G:50:LEU:HD21	3:I:44:LEU:HG	1.90	0.54
4:E:49:PHE:HB2	4:E:137:SER:HB3	1.90	0.54
4:K:49:PHE:CE2	4:K:134:ALA:HB2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:191:LEU:HB3	4:P:29:LEU:HD12	1.90	0.54
2:T:169:MET:HB3	2:T:174:LEU:HD12	1.90	0.54
4:W:31:THR:CG2	4:W:127:PHE:CZ	2.91	0.54
2:T:102:LEU:HD23	2:T:102:LEU:C	2.28	0.54
5:R:24:LEU:HD11	5:R:158:VAL:HG21	1.89	0.54
3:C:76:ARG:O	3:C:91:LEU:HA	2.08	0.54
1:S:191:MET:SD	4:V:69:GLU:HG3	2.46	0.54
3:C:5:SER:CB	3:C:7:TRP:CZ3	2.90	0.54
4:P:94:ALA:O	4:P:98:PHE:HD1	1.91	0.54
4:P:98:PHE:O	4:P:99:LEU:HD23	2.08	0.54
5:R:89:ASP:HB2	5:R:95:SER:HB3	1.90	0.54
3:O:11:ARG:HH11	3:O:125:PHE:HE1	1.54	0.54
5:X:50:VAL:HG23	5:X:57:VAL:HG12	1.89	0.54
2:B:175:LYS:HG2	2:B:176:ILE:H	1.72	0.54
1:M:42:GLY:O	1:M:45:ALA:HB3	2.08	0.54
2:B:102:LEU:HD23	2:B:102:LEU:C	2.28	0.54
1:A:135:LEU:HD21	4:D:79:ARG:NH1	2.23	0.54
5:X:68:GLU:HG2	5:X:69:ARG:CA	2.37	0.54
3:I:76:ARG:O	3:I:91:LEU:HA	2.07	0.54
5:L:82:HIS:HB3	5:L:169:ILE:HG21	1.89	0.54
2:H:254:ARG:CA	2:H:264:THR:HG22	2.36	0.54
4:E:90:LEU:HD12	6:E:194:PLM:H52	1.90	0.54
4:D:94:ALA:O	4:D:98:PHE:HD1	1.91	0.54
5:F:11:LEU:O	5:F:61:ILE:HA	2.07	0.54
4:K:61:TYR:HD2	4:K:61:TYR:C	2.10	0.54
2:B:175:LYS:HG3	2:B:278:GLU:CD	2.28	0.54
4:E:50:ASN:HA	4:E:53:ASN:HD22	1.72	0.54
3:C:93:ASP:OD1	3:C:95:LYS:HB2	2.08	0.54
4:J:137:SER:HA	4:J:169:ARG:HH22	1.73	0.54
3:C:88:PHE:CE1	3:C:107:TYR:CD1	2.96	0.54
2:B:256:PRO:CG	2:B:263:ARG:NH2	2.71	0.54
2:N:214:ASN:HA	2:N:263:ARG:CG	2.25	0.54
4:E:34:TYR:CE2	4:E:124:LEU:HD21	2.43	0.54
2:N:196:SER:OG	2:N:211:ILE:HD11	2.07	0.54
1:A:52:PRO:C	1:A:54:ALA:N	2.61	0.54
4:K:61:TYR:C	4:K:61:TYR:CD2	2.81	0.54
4:D:29:LEU:O	4:D:29:LEU:HD23	2.08	0.54
2:N:167:THR:HG22	2:N:169:MET:HB3	1.89	0.54
3:U:131:GLU:O	3:U:135:GLN:HG2	2.08	0.54
2:N:72:GLN:HE22	4:P:55:HIS:CE1	2.25	0.54
4:D:192:GLU:O	4:D:192:GLU:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:144:LEU:HD23	6:K:194:PLM:CF	2.37	0.53
4:E:144:LEU:HD23	6:E:194:PLM:CF	2.37	0.53
1:M:194:PRO:HG3	2:N:67:GLN:CA	2.39	0.53
4:V:98:PHE:C	4:V:99:LEU:HD23	2.29	0.53
1:G:194:PRO:HG3	2:H:67:GLN:CA	2.38	0.53
4:J:95:PHE:HB3	4:J:101:ILE:O	2.08	0.53
5:F:50:VAL:HG23	5:F:57:VAL:HG12	1.89	0.53
2:N:221:PHE:O	2:N:223:PRO:HD3	2.08	0.53
2:T:90:TYR:CZ	4:V:40:GLN:HG2	2.43	0.53
5:X:28:PHE:HB3	5:X:48:LYS:HZ3	1.70	0.53
5:L:28:PHE:HD2	5:L:48:LYS:HZ3	1.55	0.53
5:F:13:LEU:HD12	5:F:13:LEU:H	1.72	0.53
3:U:18:ASP:OD2	3:U:18:ASP:N	2.40	0.53
4:J:50:ASN:HA	4:J:53:ASN:HD22	1.73	0.53
5:F:82:HIS:HB3	5:F:169:ILE:HG21	1.89	0.53
1:M:10:ASN:C	1:M:12:SER:H	2.10	0.53
1:M:10:ASN:C	1:M:12:SER:N	2.60	0.53
2:N:260:HIS:HB2	2:N:263:ARG:HB2	1.89	0.53
1:G:131:ILE:HG22	1:G:131:ILE:O	2.06	0.53
5:R:89:ASP:HB2	5:R:95:SER:CB	2.38	0.53
2:T:220:GLN:HG3	2:T:221:PHE:H	1.73	0.53
4:K:17:ILE:HG21	4:K:97:ILE:HD13	1.90	0.53
2:H:191:LEU:HB3	4:J:29:LEU:HD12	1.90	0.53
1:M:52:PRO:C	1:M:54:ALA:N	2.61	0.53
1:G:69:TYR:HD1	1:G:173:GLN:NE2	2.05	0.53
1:A:38:SER:HB3	5:F:45:PHE:CE1	2.43	0.53
4:J:192:GLU:HG2	4:J:192:GLU:O	2.08	0.53
5:L:77:TYR:CD1	5:L:77:TYR:N	2.75	0.53
3:C:107:TYR:CE2	4:E:73:ALA:CA	2.90	0.53
1:M:12:SER:HB3	5:R:10:LYS:NZ	2.23	0.53
4:K:34:TYR:CE2	4:K:124:LEU:HD21	2.43	0.53
2:H:256:PRO:CG	2:H:263:ARG:NH2	2.71	0.53
2:T:260:HIS:HB2	2:T:263:ARG:HB2	1.89	0.53
4:V:95:PHE:HB3	4:V:101:ILE:O	2.08	0.53
5:X:47:ILE:HG12	5:X:60:GLN:CA	2.32	0.53
2:N:87:LEU:O	2:N:90:TYR:HB2	2.08	0.53
3:U:142:ASN:ND2	3:U:142:ASN:C	2.59	0.53
4:V:29:LEU:O	4:V:29:LEU:HD23	2.09	0.53
2:T:179:ILE:HG23	2:T:180:LEU:N	2.24	0.53
2:H:209:TYR:C	2:H:210:MET:HG2	2.29	0.53
4:K:15:GLU:HG2	4:K:96:LYS:HE2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:189:SER:O	2:N:193:ASN:HA	2.08	0.53
4:P:48:ASP:O	4:P:51:LYS:N	2.40	0.53
3:C:67:ILE:HD13	3:C:79:THR:HG21	1.91	0.53
3:C:82:THR:CG2	3:C:84:SER:OG	2.55	0.53
4:K:34:TYR:OH	4:K:140:TYR:O	2.17	0.53
2:H:231:TYR:HD2	2:H:234:CYS:SG	2.30	0.53
2:B:196:SER:OG	2:B:211:ILE:HD11	2.07	0.53
5:X:89:ASP:HB2	5:X:95:SER:CB	2.38	0.53
3:C:112:VAL:HG21	4:E:70:ASP:HA	1.91	0.53
3:I:124:ASP:O	3:I:125:PHE:C	2.46	0.53
4:Q:49:PHE:HB2	4:Q:137:SER:HB3	1.91	0.53
1:S:200:MET:HE1	5:X:7:TYR:HA	1.89	0.53
4:K:111:ASN:OD1	4:K:111:ASN:O	2.26	0.53
5:X:13:LEU:HD12	5:X:13:LEU:H	1.73	0.53
5:L:13:LEU:HD12	5:L:13:LEU:H	1.73	0.53
5:R:86:ILE:HD11	5:R:106:ILE:CD1	2.38	0.53
5:R:13:LEU:HD12	5:R:13:LEU:N	2.23	0.53
4:E:48:ASP:CG	4:E:51:LYS:HG3	2.27	0.53
2:B:189:SER:O	2:B:193:ASN:HA	2.08	0.53
4:P:192:GLU:O	4:P:192:GLU:HG2	2.08	0.53
2:N:102:LEU:C	2:N:102:LEU:HD23	2.29	0.53
3:O:67:ILE:HG21	3:O:70:ILE:HD11	1.91	0.53
3:I:82:THR:CG2	3:I:84:SER:OG	2.52	0.53
3:C:82:THR:CB	3:C:86:LEU:H	2.20	0.53
3:U:5:SER:CB	3:U:7:TRP:CZ3	2.91	0.53
4:W:18:TRP:NE1	4:W:100:ASN:HB2	2.23	0.53
4:W:59:MET:O	4:W:63:ILE:HG12	2.07	0.53
2:T:256:PRO:CG	2:T:263:ARG:NH2	2.71	0.53
4:Q:34:TYR:CE2	4:Q:124:LEU:HD21	2.44	0.53
1:G:119:LEU:C	1:G:119:LEU:HD23	2.29	0.53
5:F:89:ASP:HB2	5:F:95:SER:CB	2.39	0.53
2:T:64:PHE:HE1	4:V:67:LEU:HD12	1.73	0.53
3:O:72:THR:CG2	3:O:74:LYS:H	2.21	0.53
3:O:102:VAL:HG11	3:O:156:MET:HE3	1.90	0.53
4:E:111:ASN:OD1	4:E:111:ASN:O	2.27	0.53
1:A:29:ASN:O	1:A:32:GLU:CG	2.56	0.53
1:M:128:THR:O	1:M:130:PHE:CE2	2.62	0.53
1:S:38:SER:HB3	5:X:45:PHE:CE1	2.43	0.53
1:S:134:THR:HG21	1:S:183:TYR:CE1	2.44	0.53
4:J:188:ILE:HD12	4:J:190:ILE:HD11	1.90	0.53
1:A:10:ASN:C	1:A:12:SER:N	2.60	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:82:THR:CG2	3:U:84:SER:H	2.04	0.53
1:S:52:PRO:C	1:S:54:ALA:N	2.61	0.53
2:N:250:VAL:HG13	2:N:268:ILE:HG12	1.89	0.53
4:Q:139:TRP:HE3	4:Q:142:ASN:HD21	1.57	0.53
4:Q:34:TYR:OH	4:Q:143:ILE:HG22	2.09	0.53
3:U:112:VAL:HG21	4:W:70:ASP:HA	1.91	0.53
4:W:114:THR:HG23	4:W:179:LYS:CA	2.39	0.53
1:G:75:MET:HE1	1:G:105:ASP:CB	2.34	0.53
4:E:61:TYR:C	4:E:61:TYR:CD2	2.82	0.53
4:E:61:TYR:C	4:E:61:TYR:HD2	2.11	0.53
5:R:93:GLN:HG3	5:R:131:VAL:HG11	1.90	0.53
4:W:111:ASN:O	4:W:111:ASN:OD1	2.26	0.53
4:V:187:GLU:HG3	4:V:187:GLU:O	2.09	0.53
4:Q:111:ASN:O	4:Q:111:ASN:OD1	2.27	0.53
5:L:88:TYR:CE2	5:L:119:VAL:O	2.62	0.53
3:C:88:PHE:CE1	3:C:107:TYR:HB2	2.43	0.53
5:R:82:HIS:HB3	5:R:169:ILE:HG21	1.90	0.53
4:W:95:PHE:HE1	4:W:119:LEU:CD2	2.22	0.53
2:T:254:ARG:CA	2:T:264:THR:HG22	2.37	0.53
5:L:89:ASP:HB2	5:L:95:SER:CB	2.38	0.53
5:F:50:VAL:CG2	5:F:57:VAL:HG12	2.38	0.53
3:U:112:VAL:HG11	4:W:70:ASP:OD1	2.08	0.53
2:T:87:LEU:O	2:T:90:TYR:HB2	2.09	0.53
3:O:124:ASP:O	3:O:125:PHE:C	2.47	0.53
2:H:72:GLN:HE22	4:J:55:HIS:CE1	2.26	0.53
4:P:137:SER:HA	4:P:169:ARG:HH22	1.74	0.53
5:X:88:TYR:CE2	5:X:119:VAL:O	2.61	0.53
3:C:80:TYR:CB	3:C:103:LEU:HD23	2.38	0.53
3:O:111:TYR:CZ	3:O:115:VAL:HG11	2.43	0.53
3:O:82:THR:CB	3:O:86:LEU:H	2.20	0.53
1:A:107:PHE:CB	1:A:180:ARG:NH1	2.72	0.53
1:A:132:TYR:HB3	1:A:179:LEU:HD12	1.90	0.53
4:P:155:VAL:C	4:P:156:GLN:CG	2.77	0.53
2:B:87:LEU:O	2:B:90:TYR:HB2	2.09	0.53
3:C:124:ASP:O	3:C:125:PHE:C	2.47	0.53
3:U:124:ASP:O	3:U:125:PHE:C	2.46	0.53
4:W:61:TYR:CD2	4:W:61:TYR:C	2.82	0.53
5:F:28:PHE:HD2	5:F:48:LYS:HZ3	1.56	0.53
4:Q:49:PHE:CE2	4:Q:134:ALA:HB2	2.43	0.53
4:E:128:VAL:HG12	4:E:129:GLU:N	2.24	0.53
3:O:105:TYR:CE1	3:O:109:HIS:ND1	2.67	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:227:VAL:O	2:B:230:GLU:CB	2.57	0.53
5:F:88:TYR:CE2	5:F:119:VAL:O	2.61	0.53
5:X:140:ALA:HB1	5:X:145:MET:O	2.08	0.53
5:L:140:ALA:HB1	5:L:145:MET:O	2.08	0.53
4:P:98:PHE:C	4:P:99:LEU:HD23	2.29	0.53
1:M:131:ILE:O	1:M:131:ILE:HG22	2.09	0.53
5:X:28:PHE:HD2	5:X:48:LYS:HZ3	1.55	0.53
1:S:29:ASN:O	1:S:32:GLU:CG	2.56	0.53
4:P:37:ILE:O	4:P:41:LEU:HG	2.08	0.53
4:J:37:ILE:O	4:J:41:LEU:HG	2.09	0.53
5:L:86:ILE:HD11	5:L:106:ILE:CD1	2.39	0.53
4:Q:31:THR:CG2	4:Q:127:PHE:CZ	2.92	0.53
3:I:80:TYR:CB	3:I:103:LEU:HD23	2.38	0.53
4:E:18:TRP:NE1	4:E:100:ASN:HB2	2.23	0.53
5:R:47:ILE:HG12	5:R:60:GLN:CA	2.30	0.53
4:W:49:PHE:HB2	4:W:137:SER:HB3	1.91	0.53
5:L:28:PHE:HB3	5:L:48:LYS:HZ3	1.71	0.53
2:N:175:LYS:HG3	2:N:278:GLU:CD	2.29	0.53
3:O:127:GLU:C	3:O:129:GLU:N	2.62	0.53
3:O:129:GLU:CB	3:O:135:GLN:OE1	2.57	0.53
5:F:86:ILE:HD11	5:F:106:ILE:CD1	2.39	0.53
3:U:105:TYR:CE1	3:U:109:HIS:ND1	2.68	0.53
5:L:73:ILE:O	5:L:77:TYR:HB2	2.09	0.52
4:D:48:ASP:O	4:D:51:LYS:N	2.41	0.52
1:A:12:SER:HB3	5:F:10:LYS:NZ	2.24	0.52
1:G:186:TYR:O	1:G:190:VAL:HB	2.08	0.52
4:D:114:THR:HG21	4:D:177:LYS:HE2	1.91	0.52
3:O:72:THR:HG23	3:O:73:GLY:H	1.73	0.52
5:R:88:TYR:CE2	5:R:119:VAL:O	2.62	0.52
5:X:86:ILE:HD11	5:X:106:ILE:CD1	2.39	0.52
1:G:38:SER:HB3	5:L:45:PHE:CE1	2.44	0.52
2:T:189:SER:O	2:T:193:ASN:HA	2.09	0.52
1:S:68:PRO:HD2	1:S:111:PHE:O	2.10	0.52
5:R:68:GLU:HG2	5:R:69:ARG:CA	2.39	0.52
4:K:18:TRP:NE1	4:K:100:ASN:HB2	2.24	0.52
3:O:5:SER:CB	3:O:7:TRP:CZ3	2.92	0.52
5:R:84:ILE:CD1	5:R:114:VAL:HG11	2.38	0.52
2:N:90:TYR:CZ	4:P:40:GLN:HG2	2.44	0.52
1:S:50:LEU:HD21	3:U:44:LEU:HG	1.92	0.52
4:W:61:TYR:HD2	4:W:61:TYR:C	2.11	0.52
2:T:175:LYS:HG3	2:T:278:GLU:CD	2.29	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:127:GLU:C	3:C:129:GLU:N	2.62	0.52
2:N:227:VAL:O	2:N:230:GLU:CB	2.57	0.52
1:G:135:LEU:HD21	4:J:79:ARG:NH1	2.24	0.52
4:E:38:VAL:HG11	4:E:140:TYR:CE1	2.44	0.52
4:V:110:HIS:C	4:V:112:LYS:H	2.12	0.52
4:V:114:THR:HG21	4:V:177:LYS:HE2	1.91	0.52
4:P:95:PHE:HB3	4:P:101:ILE:O	2.09	0.52
1:M:107:PHE:CB	1:M:180:ARG:NH1	2.72	0.52
4:Q:61:TYR:CD2	4:Q:61:TYR:C	2.83	0.52
5:L:93:GLN:HG3	5:L:131:VAL:HG11	1.90	0.52
3:C:155:PRO:O	3:C:156:MET:O	2.27	0.52
3:I:105:TYR:CE1	3:I:109:HIS:ND1	2.69	0.52
2:N:72:GLN:HE22	4:P:55:HIS:HE1	1.57	0.52
4:P:187:GLU:O	4:P:187:GLU:HG3	2.09	0.52
5:R:69:ARG:HB2	5:R:72:THR:HG21	1.83	0.52
5:X:68:GLU:C	5:X:70:PHE:H	2.12	0.52
4:Q:144:LEU:HD23	6:Q:194:PLM:CF	2.38	0.52
1:M:21:PHE:CE2	1:M:215:VAL:HG11	2.44	0.52
1:A:21:PHE:CE2	1:A:215:VAL:HG11	2.44	0.52
4:P:114:THR:HG21	4:P:177:LYS:HE2	1.92	0.52
4:V:94:ALA:O	4:V:98:PHE:HD1	1.92	0.52
1:M:104:ASP:HA	1:M:108:LYS:NZ	2.25	0.52
2:H:189:SER:O	2:H:193:ASN:HA	2.10	0.52
2:B:267:LEU:HD23	2:B:267:LEU:O	2.09	0.52
1:M:135:LEU:HD21	4:P:79:ARG:NH1	2.25	0.52
3:I:88:PHE:CE1	3:I:107:TYR:HB2	2.44	0.52
1:M:10:ASN:CB	1:M:14:GLY:O	2.58	0.52
3:I:3:ILE:HD12	3:I:90:LEU:HD11	1.91	0.52
3:I:3:ILE:HG23	3:I:99:TYR:CE2	2.44	0.52
4:E:123:PRO:HG2	4:E:124:LEU:H	1.74	0.52
4:Q:39:ALA:HB2	3:U:120:LEU:HD23	1.91	0.52
4:Q:95:PHE:HE1	4:Q:119:LEU:CD2	2.23	0.52
1:G:129:MET:SD	1:G:131:ILE:HD11	2.50	0.52
2:N:64:PHE:HE1	4:P:67:LEU:HD12	1.73	0.52
1:M:50:LEU:HD21	3:O:44:LEU:HG	1.92	0.52
1:S:75:MET:HE1	1:S:105:ASP:CB	2.36	0.52
3:C:122:PRO:HA	4:E:66:ARG:NH2	2.22	0.52
2:H:175:LYS:HG2	2:H:176:ILE:N	2.25	0.52
3:U:129:GLU:CB	3:U:135:GLN:OE1	2.57	0.52
1:M:38:SER:HB3	5:R:45:PHE:CE1	2.43	0.52
3:O:18:ASP:N	3:O:18:ASP:OD2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:110:HIS:C	4:D:112:LYS:H	2.12	0.52
3:O:112:VAL:HG21	4:Q:70:ASP:HA	1.92	0.52
4:Q:61:TYR:HD2	4:Q:61:TYR:C	2.12	0.52
5:F:28:PHE:CE2	5:F:48:LYS:HD3	2.44	0.52
5:R:13:LEU:H	5:R:13:LEU:CD1	2.22	0.52
3:U:3:ILE:HG23	3:U:99:TYR:CE2	2.44	0.52
4:Q:34:TYR:CE1	4:Q:143:ILE:CG2	2.92	0.52
1:S:28:LEU:CD2	3:U:57:LYS:HD2	2.40	0.52
4:P:162:TRP:HE1	4:P:177:LYS:HB2	1.71	0.52
3:I:155:PRO:O	3:I:156:MET:O	2.26	0.52
1:A:29:ASN:O	1:A:32:GLU:HG2	2.10	0.52
3:I:129:GLU:CB	3:I:135:GLN:OE1	2.57	0.52
2:T:92:HIS:NE2	2:T:239:GLY:HA2	2.24	0.52
1:A:68:PRO:HD2	1:A:111:PHE:O	2.10	0.52
2:T:197:ASP:HB3	2:T:212:VAL:O	2.10	0.52
4:V:48:ASP:O	4:V:51:LYS:N	2.40	0.52
5:X:73:ILE:O	5:X:77:TYR:HB2	2.10	0.52
1:G:52:PRO:C	1:G:54:ALA:N	2.63	0.52
1:A:194:PRO:HG3	2:B:67:GLN:CA	2.40	0.52
4:J:29:LEU:HD23	4:J:29:LEU:O	2.10	0.52
4:E:49:PHE:CE2	4:E:134:ALA:HB2	2.45	0.52
5:X:93:GLN:HG3	5:X:131:VAL:HG11	1.91	0.52
1:S:7:LEU:CD1	1:S:141:VAL:HB	2.40	0.52
4:K:31:THR:CG2	4:K:127:PHE:CZ	2.93	0.52
4:V:88:GLU:O	4:V:92:LYS:HG2	2.09	0.52
4:J:88:GLU:O	4:J:92:LYS:HG2	2.10	0.52
1:G:134:THR:HG21	1:G:183:TYR:CE1	2.45	0.52
1:S:186:TYR:O	1:S:190:VAL:HB	2.09	0.52
5:F:84:ILE:CD1	5:F:114:VAL:HG11	2.39	0.52
1:G:129:MET:HE2	1:G:143:ILE:HD11	1.91	0.52
1:G:132:TYR:HB3	1:G:179:LEU:HD12	1.92	0.52
4:D:162:TRP:HE1	4:D:177:LYS:HB2	1.72	0.52
1:S:132:TYR:HB3	1:S:179:LEU:HD12	1.92	0.52
1:S:4:GLU:HG3	1:S:143:ILE:HG22	1.91	0.52
4:J:110:HIS:C	4:J:112:LYS:H	2.13	0.52
3:O:11:ARG:HH12	4:Q:154:MET:HE1	1.74	0.52
4:P:35:GLY:HA2	4:P:140:TYR:OH	2.10	0.52
1:S:29:ASN:O	1:S:32:GLU:HG2	2.10	0.52
4:Q:128:VAL:HG12	4:Q:129:GLU:N	2.25	0.52
3:C:105:TYR:CE1	3:C:109:HIS:ND1	2.68	0.52
4:D:187:GLU:HG3	4:D:187:GLU:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:68:GLU:CG	5:L:69:ARG:CA	2.85	0.52
4:W:144:LEU:HD23	6:W:194:PLM:CF	2.38	0.52
1:G:107:PHE:CB	1:G:180:ARG:NH1	2.73	0.52
2:B:209:TYR:C	2:B:210:MET:HG2	2.29	0.52
2:T:227:VAL:O	2:T:230:GLU:CB	2.57	0.52
2:B:79:THR:HG22	2:B:81:GLY:H	1.75	0.52
1:M:106:PHE:CD1	1:M:106:PHE:N	2.78	0.52
2:T:72:GLN:HE22	4:V:55:HIS:CE1	2.28	0.52
3:U:67:ILE:HD13	3:U:79:THR:HG21	1.90	0.51
3:U:3:ILE:HG21	3:U:90:LEU:HD21	1.91	0.51
4:E:139:TRP:HE3	4:E:142:ASN:HD21	1.58	0.51
4:E:95:PHE:HE1	4:E:119:LEU:CD2	2.23	0.51
1:S:107:PHE:CB	1:S:180:ARG:NH1	2.73	0.51
4:J:162:TRP:CD1	4:J:177:LYS:HB2	2.45	0.51
4:P:110:HIS:C	4:P:112:LYS:H	2.13	0.51
5:L:28:PHE:CE2	5:L:48:LYS:HD3	2.45	0.51
2:B:179:ILE:HG23	2:B:180:LEU:N	2.23	0.51
2:B:220:GLN:HG3	2:B:221:PHE:H	1.74	0.51
3:O:155:PRO:O	3:O:156:MET:O	2.28	0.51
3:C:155:PRO:HG2	3:C:156:MET:N	2.24	0.51
4:D:35:GLY:HA2	4:D:140:TYR:OH	2.11	0.51
1:A:128:THR:O	1:A:130:PHE:CE2	2.63	0.51
2:N:209:TYR:C	2:N:210:MET:HG2	2.29	0.51
4:Q:46:GLU:O	4:Q:47:ARG:HB2	2.10	0.51
4:E:67:LEU:C	4:E:67:LEU:HD23	2.31	0.51
1:G:106:PHE:CD1	1:G:106:PHE:N	2.78	0.51
4:V:188:ILE:HD12	4:V:190:ILE:HD11	1.92	0.51
4:Q:114:THR:HG23	4:Q:179:LYS:CA	2.40	0.51
3:C:111:TYR:CZ	3:C:115:VAL:HG11	2.45	0.51
3:C:77:VAL:CG1	3:C:91:LEU:HD22	2.24	0.51
3:I:88:PHE:CE1	3:I:107:TYR:CD1	2.98	0.51
4:V:155:VAL:C	4:V:156:GLN:CG	2.78	0.51
4:E:17:ILE:O	4:E:21:LYS:O	2.28	0.51
4:K:139:TRP:HE3	4:K:142:ASN:HD21	1.58	0.51
5:F:13:LEU:HD12	5:F:13:LEU:N	2.25	0.51
5:L:13:LEU:HD21	5:L:25:LEU:HD21	1.92	0.51
2:N:92:HIS:NE2	2:N:239:GLY:HA2	2.25	0.51
2:B:92:HIS:NE2	2:B:239:GLY:HA2	2.25	0.51
1:S:112:THR:HG22	1:S:113:ASN:O	2.10	0.51
4:Q:99:LEU:O	4:Q:100:ASN:C	2.47	0.51
2:B:231:TYR:CE2	2:B:251:THR:HA	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:155:VAL:C	4:D:156:GLN:CG	2.79	0.51
4:W:85:LYS:O	4:W:89:VAL:HG23	2.10	0.51
1:S:104:ASP:HA	1:S:108:LYS:NZ	2.26	0.51
1:A:106:PHE:CD1	1:A:106:PHE:N	2.78	0.51
2:N:79:THR:HG22	2:N:81:GLY:H	1.76	0.51
4:Q:85:LYS:O	4:Q:89:VAL:HG23	2.10	0.51
1:M:12:SER:OG	5:R:80:GLY:HA3	2.11	0.51
1:G:10:ASN:CB	1:G:14:GLY:O	2.58	0.51
4:J:114:THR:HG21	4:J:177:LYS:HE2	1.93	0.51
3:C:11:ARG:HH12	4:E:154:MET:HE1	1.73	0.51
5:F:156:THR:HG22	5:F:156:THR:O	2.11	0.51
2:B:170:ARG:C	2:B:172:ARG:N	2.64	0.51
5:L:13:LEU:HD12	5:L:13:LEU:N	2.25	0.51
1:M:134:THR:HG21	1:M:183:TYR:CE1	2.44	0.51
3:I:67:ILE:HG21	3:I:70:ILE:HD11	1.92	0.51
4:K:95:PHE:HE1	4:K:119:LEU:CD2	2.24	0.51
4:W:38:VAL:HG11	4:W:140:TYR:CE1	2.45	0.51
4:W:90:LEU:HD12	6:W:194:PLM:H52	1.92	0.51
1:G:120:ARG:NH1	1:G:120:ARG:HB3	2.10	0.51
5:F:47:ILE:HG12	5:F:60:GLN:CA	2.31	0.51
1:M:132:TYR:HB3	1:M:179:LEU:HD12	1.91	0.51
4:E:84:VAL:HG13	4:E:85:LYS:N	2.25	0.51
3:O:3:ILE:HD12	3:O:90:LEU:HD11	1.93	0.51
3:O:3:ILE:HG23	3:O:99:TYR:CE2	2.45	0.51
3:C:3:ILE:HG23	3:C:99:TYR:CE2	2.45	0.51
5:X:28:PHE:CE2	5:X:48:LYS:HD3	2.46	0.51
2:T:99:LEU:HD22	2:T:243:ASN:HB3	1.93	0.51
2:T:209:TYR:C	2:T:210:MET:HG2	2.31	0.51
3:C:18:ASP:OD2	3:C:18:ASP:N	2.42	0.51
1:A:10:ASN:CB	1:A:14:GLY:O	2.59	0.51
4:E:99:LEU:O	4:E:100:ASN:C	2.47	0.51
2:N:184:HIS:HB2	2:N:211:ILE:HD13	1.93	0.51
4:Q:18:TRP:NE1	4:Q:100:ASN:HB2	2.25	0.51
6:Q:194:PLM:HG3	4:W:29:LEU:HD21	1.93	0.51
1:S:119:LEU:C	1:S:119:LEU:HD23	2.31	0.51
2:H:68:GLU:CG	4:J:63:ILE:HD11	2.40	0.51
4:K:114:THR:HG23	4:K:179:LYS:CA	2.41	0.51
4:W:84:VAL:HG13	4:W:85:LYS:N	2.24	0.51
5:F:85:ILE:H	5:F:85:ILE:CD1	2.23	0.51
1:M:29:ASN:O	1:M:32:GLU:CG	2.59	0.51
5:F:13:LEU:H	5:F:13:LEU:CD1	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:128:THR:O	1:S:130:PHE:CE2	2.64	0.51
2:H:72:GLN:HE22	4:J:55:HIS:HE1	1.59	0.51
1:M:68:PRO:HD2	1:M:111:PHE:O	2.11	0.51
5:X:68:GLU:O	5:X:70:PHE:N	2.33	0.51
3:O:88:PHE:CE1	3:O:107:TYR:CD1	2.99	0.51
4:D:180:LEU:N	4:D:180:LEU:HD12	2.13	0.51
1:G:21:PHE:CE2	1:G:215:VAL:HG11	2.45	0.51
2:H:188:TRP:CH2	2:H:266:TYR:CE1	2.83	0.51
1:S:21:PHE:CE2	1:S:215:VAL:HG11	2.44	0.51
3:O:117:ASN:OD1	4:W:32:LEU:HD21	2.11	0.51
2:H:218:LEU:O	2:H:220:GLN:N	2.43	0.51
4:W:49:PHE:CE2	4:W:134:ALA:HB2	2.45	0.51
4:K:128:VAL:HG12	4:K:129:GLU:N	2.26	0.51
2:B:72:GLN:HE22	4:D:55:HIS:HE1	1.58	0.51
4:D:136:LYS:C	4:D:169:ARG:HH12	2.14	0.51
4:D:47:ARG:HG3	4:Q:84:VAL:HG21	1.92	0.51
1:A:186:TYR:O	1:A:190:VAL:HB	2.10	0.51
3:O:77:VAL:CG1	3:O:91:LEU:HD22	2.25	0.51
4:K:34:TYR:CE1	4:K:143:ILE:CG2	2.93	0.51
1:M:124:THR:O	1:M:147:VAL:HG13	2.10	0.51
2:T:184:HIS:HB2	2:T:211:ILE:HD13	1.93	0.51
1:A:104:ASP:HA	1:A:108:LYS:NZ	2.26	0.51
5:R:28:PHE:CE2	5:R:48:LYS:HD3	2.46	0.51
3:U:102:VAL:HG11	3:U:156:MET:CE	2.41	0.51
1:A:75:MET:CE	1:A:105:ASP:CB	2.88	0.51
2:H:175:LYS:HG3	2:H:278:GLU:CD	2.30	0.51
1:G:2:ALA:HB3	1:G:146:SER:HB3	1.93	0.51
4:J:91:SER:HB2	4:J:103:PRO:HG2	1.92	0.51
4:D:88:GLU:O	4:D:92:LYS:HG2	2.10	0.51
4:P:88:GLU:O	4:P:92:LYS:HG2	2.10	0.51
1:S:106:PHE:CD1	1:S:106:PHE:N	2.78	0.51
1:M:186:TYR:O	1:M:190:VAL:HB	2.10	0.51
3:U:80:TYR:CB	3:U:103:LEU:HD23	2.41	0.51
3:U:111:TYR:CZ	3:U:115:VAL:HG11	2.46	0.51
3:U:79:THR:HG22	3:U:80:TYR:N	2.26	0.51
3:U:88:PHE:CE1	3:U:107:TYR:CD1	2.99	0.51
1:S:10:ASN:CB	1:S:14:GLY:O	2.59	0.51
4:K:38:VAL:HG11	4:K:140:TYR:CE1	2.45	0.51
4:W:139:TRP:HE3	4:W:142:ASN:HD21	1.59	0.51
1:G:124:THR:HG21	3:I:55:THR:CG2	2.41	0.51
4:E:114:THR:HG23	4:E:179:LYS:CA	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:90:TYR:CZ	4:J:40:GLN:HG2	2.46	0.51
2:T:59:LEU:O	2:T:59:LEU:HD12	2.11	0.51
4:W:128:VAL:HG12	4:W:129:GLU:N	2.26	0.51
2:T:79:THR:HG22	2:T:81:GLY:H	1.76	0.51
4:D:130:LEU:CD2	4:D:168:LEU:HB3	2.41	0.51
2:H:197:ASP:HB3	2:H:212:VAL:O	2.11	0.51
1:G:68:PRO:HD2	1:G:111:PHE:O	2.11	0.51
2:H:79:THR:HG22	2:H:81:GLY:H	1.76	0.51
3:O:82:THR:CG2	3:O:84:SER:OG	2.54	0.50
2:T:188:TRP:CH2	2:T:266:TYR:CE1	2.83	0.50
3:C:142:ASN:HD22	3:C:143:ARG:N	2.09	0.50
2:B:221:PHE:O	2:B:223:PRO:HD3	2.11	0.50
5:R:28:PHE:HB3	5:R:48:LYS:HZ3	1.75	0.50
2:H:99:LEU:HD22	2:H:243:ASN:HB3	1.93	0.50
4:V:38:VAL:HG11	4:V:140:TYR:HE1	1.74	0.50
4:J:35:GLY:HA2	4:J:140:TYR:OH	2.10	0.50
4:W:31:THR:HG21	4:W:127:PHE:CE2	2.46	0.50
1:A:112:THR:HG22	1:A:113:ASN:O	2.10	0.50
4:Q:84:VAL:HG13	4:Q:85:LYS:N	2.26	0.50
1:A:12:SER:CB	5:F:10:LYS:HZ2	2.24	0.50
3:I:79:THR:HG22	3:I:80:TYR:N	2.26	0.50
3:U:99:TYR:CD1	3:U:99:TYR:N	2.79	0.50
1:G:12:SER:CB	5:L:10:LYS:NZ	2.75	0.50
4:W:34:TYR:OH	4:W:143:ILE:HG22	2.11	0.50
2:B:184:HIS:HB2	2:B:211:ILE:HD13	1.93	0.50
2:H:59:LEU:O	2:H:59:LEU:HD12	2.11	0.50
1:G:75:MET:CE	1:G:105:ASP:CB	2.89	0.50
3:C:102:VAL:HG11	3:C:156:MET:CE	2.40	0.50
3:I:102:VAL:HG11	3:I:156:MET:CE	2.42	0.50
1:M:29:ASN:O	1:M:32:GLU:HG2	2.11	0.50
1:G:29:ASN:O	1:G:32:GLU:CG	2.59	0.50
3:O:98:SER:C	3:O:100:THR:H	2.14	0.50
2:B:167:THR:HG22	2:B:167:THR:O	2.11	0.50
1:S:135:LEU:HD21	4:V:79:ARG:NH1	2.27	0.50
4:K:90:LEU:HD12	6:K:194:PLM:H52	1.93	0.50
1:G:190:VAL:HG12	1:G:191:MET:CE	2.42	0.50
2:N:84:GLU:HB3	2:N:231:TYR:CE1	2.46	0.50
2:N:84:GLU:HB3	2:N:231:TYR:HD1	1.74	0.50
1:A:119:LEU:HD23	1:A:119:LEU:C	2.32	0.50
2:N:179:ILE:HG23	2:N:180:LEU:N	2.24	0.50
4:W:75:THR:CG2	4:W:93:CYS:SG	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:29:ASN:O	1:G:32:GLU:HG2	2.11	0.50
5:F:41:ILE:N	5:F:41:ILE:HD12	2.26	0.50
5:L:13:LEU:H	5:L:13:LEU:CD1	2.24	0.50
2:T:92:HIS:CD2	2:T:239:GLY:HA2	2.46	0.50
1:A:134:THR:HG21	1:A:183:TYR:CE1	2.45	0.50
5:F:14:ILE:HA	5:F:64:THR:HG23	1.94	0.50
4:P:106:THR:CG2	4:P:107:ASN:H	2.11	0.50
3:O:99:TYR:CD1	3:O:99:TYR:N	2.79	0.50
3:I:155:PRO:HG2	3:I:156:MET:N	2.24	0.50
3:I:98:SER:C	3:I:100:THR:H	2.14	0.50
5:X:13:LEU:CD1	5:X:13:LEU:H	2.24	0.50
2:H:267:LEU:HD23	2:H:267:LEU:O	2.11	0.50
5:F:67:GLN:HA	5:F:67:GLN:OE1	2.10	0.50
3:U:88:PHE:CE1	3:U:107:TYR:HB2	2.46	0.50
3:U:83:ALA:O	4:W:155:VAL:HG13	2.11	0.50
1:G:12:SER:OG	5:L:80:GLY:HA3	2.11	0.50
4:W:34:TYR:CE1	4:W:143:ILE:CG2	2.93	0.50
4:D:111:ASN:ND2	4:D:113:ASP:OD2	2.37	0.50
2:T:231:TYR:CD2	2:T:234:CYS:SG	3.02	0.50
3:I:142:ASN:HD22	3:I:143:ARG:N	2.09	0.50
1:M:119:LEU:C	1:M:119:LEU:HD23	2.32	0.50
3:O:132:MET:HB2	3:O:133:ARG:NH1	2.27	0.50
4:K:134:ALA:O	4:K:136:LYS:N	2.45	0.50
2:B:99:LEU:HD22	2:B:243:ASN:HB3	1.93	0.50
4:V:35:GLY:HA2	4:V:140:TYR:OH	2.11	0.50
3:C:129:GLU:HB2	3:C:135:GLN:OE1	2.11	0.50
2:T:169:MET:CB	2:T:174:LEU:HD12	2.42	0.50
2:T:168:LYS:C	2:T:170:ARG:H	2.15	0.50
3:U:98:SER:C	3:U:100:THR:H	2.14	0.50
5:R:13:LEU:HD21	5:R:25:LEU:HD21	1.94	0.50
2:B:167:THR:HG22	2:B:169:MET:HB3	1.92	0.50
4:V:91:SER:HB2	4:V:103:PRO:HG2	1.93	0.50
1:M:112:THR:HG22	1:M:113:ASN:O	2.10	0.50
4:W:67:LEU:HD23	4:W:67:LEU:C	2.32	0.50
4:K:67:LEU:C	4:K:67:LEU:HD23	2.32	0.50
5:R:73:ILE:O	5:R:77:TYR:HB2	2.11	0.50
4:V:136:LYS:C	4:V:169:ARG:HH12	2.14	0.50
3:O:80:TYR:CB	3:O:103:LEU:HD23	2.41	0.50
3:O:79:THR:HG22	3:O:80:TYR:N	2.25	0.50
3:O:83:ALA:O	4:Q:155:VAL:HG13	2.12	0.50
3:I:3:ILE:HG21	3:I:90:LEU:HD21	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:99:LEU:O	4:K:101:ILE:N	2.45	0.50
2:B:84:GLU:HB3	2:B:231:TYR:CE1	2.46	0.50
4:J:160:ASP:HB2	4:J:179:LYS:HB3	1.92	0.50
5:X:47:ILE:HD11	5:X:60:GLN:HG3	1.93	0.50
2:H:220:GLN:HG3	2:H:221:PHE:H	1.77	0.50
4:W:17:ILE:O	4:W:21:LYS:O	2.29	0.50
3:U:155:PRO:O	3:U:156:MET:O	2.28	0.50
2:N:176:ILE:HD11	2:N:180:LEU:HD22	1.93	0.50
2:B:92:HIS:CD2	2:B:239:GLY:HA2	2.47	0.50
2:N:197:ASP:HB3	2:N:212:VAL:O	2.11	0.50
4:P:130:LEU:CD2	4:P:168:LEU:HB3	2.42	0.50
5:F:73:ILE:O	5:F:77:TYR:HB2	2.11	0.50
4:J:136:LYS:C	4:J:169:ARG:HH12	2.14	0.50
4:J:48:ASP:O	4:J:51:LYS:N	2.42	0.50
5:X:68:GLU:CG	5:X:69:ARG:CA	2.88	0.50
1:S:12:SER:CB	5:X:10:LYS:NZ	2.75	0.50
2:H:184:HIS:HB2	2:H:211:ILE:HD13	1.94	0.50
4:P:180:LEU:N	4:P:180:LEU:HD12	2.13	0.50
4:J:155:VAL:C	4:J:156:GLN:CG	2.79	0.50
3:C:99:TYR:CD1	3:C:99:TYR:N	2.79	0.50
3:U:12:HIS:O	3:U:13:CYS:HB2	2.12	0.50
4:E:75:THR:CG2	4:E:93:CYS:SG	2.99	0.50
1:M:7:LEU:CD1	1:M:141:VAL:HB	2.41	0.50
2:H:92:HIS:NE2	2:H:239:GLY:HA2	2.26	0.50
3:C:79:THR:HG22	3:C:80:TYR:N	2.25	0.50
3:O:88:PHE:CE1	3:O:107:TYR:HB2	2.46	0.50
4:D:106:THR:CG2	4:D:107:ASN:H	2.11	0.50
4:K:17:ILE:O	4:K:21:LYS:O	2.29	0.50
3:U:132:MET:HB2	3:U:133:ARG:NH1	2.27	0.50
1:A:70:ILE:O	1:A:70:ILE:HG23	2.10	0.50
4:E:131:PRO:O	4:E:133:ASP:N	2.45	0.50
1:M:75:MET:CE	1:M:105:ASP:CB	2.89	0.50
5:F:13:LEU:HD21	5:F:25:LEU:HD21	1.93	0.50
5:L:163:LEU:O	5:L:167:ARG:HG3	2.11	0.50
4:Q:67:LEU:C	4:Q:67:LEU:HD23	2.33	0.50
2:T:267:LEU:HD23	2:T:267:LEU:C	2.32	0.50
3:I:83:ALA:O	4:K:155:VAL:HG13	2.11	0.50
3:I:99:TYR:N	3:I:99:TYR:CD1	2.80	0.50
1:S:124:THR:HG21	3:U:55:THR:CG2	2.42	0.50
1:G:119:LEU:HD23	1:G:119:LEU:O	2.12	0.50
1:S:131:ILE:HG22	1:S:131:ILE:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:129:MET:SD	1:M:131:ILE:HD11	2.52	0.50
1:A:119:LEU:CD2	1:A:131:ILE:HD13	2.42	0.50
1:A:50:LEU:HD21	3:C:44:LEU:HG	1.94	0.50
2:N:59:LEU:HD12	2:N:59:LEU:O	2.12	0.50
5:R:85:ILE:H	5:R:85:ILE:CD1	2.24	0.50
1:G:128:THR:O	1:G:130:PHE:CE2	2.65	0.50
3:C:98:SER:C	3:C:100:THR:H	2.15	0.50
2:N:92:HIS:CD2	2:N:239:GLY:HA2	2.47	0.50
4:Q:30:PHE:HE1	4:W:33:THR:HG1	1.54	0.50
3:O:110:ILE:HD13	3:O:148:VAL:HG13	1.93	0.50
4:V:130:LEU:CD2	4:V:168:LEU:HB3	2.42	0.50
2:B:282:PHE:CD1	2:B:282:PHE:C	2.85	0.50
4:K:166:ASP:O	4:K:167:ILE:C	2.50	0.49
5:F:47:ILE:HD11	5:F:60:GLN:HG3	1.94	0.49
1:A:4:GLU:HG3	1:A:143:ILE:HG22	1.93	0.49
2:T:267:LEU:HD23	2:T:267:LEU:O	2.11	0.49
1:G:112:THR:HG22	1:G:113:ASN:O	2.12	0.49
2:N:267:LEU:HD23	2:N:267:LEU:O	2.12	0.49
5:X:88:TYR:CD1	5:X:96:PHE:CD1	2.99	0.49
1:M:10:ASN:HB2	1:M:14:GLY:O	2.13	0.49
4:W:99:LEU:O	4:W:101:ILE:N	2.46	0.49
1:S:132:TYR:CE2	1:S:180:ARG:HA	2.47	0.49
1:M:28:LEU:CD2	3:O:57:LYS:HD2	2.42	0.49
1:S:75:MET:CE	1:S:105:ASP:CB	2.90	0.49
5:X:156:THR:HG22	5:X:156:THR:O	2.12	0.49
5:X:13:LEU:HD12	5:X:13:LEU:N	2.26	0.49
5:X:13:LEU:CD1	5:X:25:LEU:HD11	2.43	0.49
5:X:13:LEU:HD21	5:X:25:LEU:HG	1.94	0.49
4:D:165:SER:O	4:D:174:THR:HA	2.12	0.49
3:I:110:ILE:HD13	3:I:148:VAL:HG13	1.93	0.49
4:J:187:GLU:O	4:J:188:ILE:O	2.30	0.49
3:U:3:ILE:HD12	3:U:90:LEU:HD11	1.94	0.49
4:E:34:TYR:OH	4:E:143:ILE:HG22	2.13	0.49
4:Q:90:LEU:HD12	6:Q:194:PLM:H52	1.94	0.49
1:A:119:LEU:O	1:A:119:LEU:HD23	2.11	0.49
4:P:68:ILE:CD1	4:P:154:MET:HB3	2.42	0.49
4:J:38:VAL:HG11	4:J:140:TYR:HE1	1.75	0.49
2:B:169:MET:CB	2:B:174:LEU:HD12	2.43	0.49
4:K:46:GLU:O	4:K:47:ARG:HB2	2.11	0.49
4:V:165:SER:O	4:V:174:THR:HA	2.12	0.49
1:A:134:THR:N	1:A:138:LEU:O	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:190:VAL:HG12	1:M:191:MET:CE	2.42	0.49
3:C:83:ALA:O	4:E:155:VAL:HG13	2.12	0.49
1:M:124:THR:HG21	3:O:55:THR:CG2	2.43	0.49
4:D:113:ASP:O	4:D:180:LEU:HD12	2.13	0.49
3:I:114:TYR:HD2	3:I:144:ASN:CB	2.25	0.49
1:A:129:MET:SD	1:A:131:ILE:HD11	2.53	0.49
2:T:221:PHE:O	2:T:223:PRO:HD3	2.12	0.49
4:K:61:TYR:HE2	4:K:65:CYS:SG	2.35	0.49
4:J:34:TYR:CD2	4:J:124:LEU:HG	2.47	0.49
4:J:68:ILE:CD1	4:J:154:MET:HB3	2.43	0.49
2:T:72:GLN:HE22	4:V:55:HIS:HE1	1.60	0.49
2:B:197:ASP:HB3	2:B:212:VAL:O	2.12	0.49
4:J:130:LEU:CD2	4:J:168:LEU:HB3	2.43	0.49
4:P:165:SER:O	4:P:174:THR:HA	2.13	0.49
5:F:120:GLY:O	5:F:150:THR:O	2.31	0.49
5:X:40:THR:HG22	5:X:69:ARG:HH12	1.78	0.49
4:W:166:ASP:O	4:W:167:ILE:C	2.51	0.49
3:U:72:THR:HG23	3:U:73:GLY:H	1.72	0.49
4:E:34:TYR:CE1	4:E:143:ILE:CG2	2.94	0.49
4:D:110:HIS:O	4:D:112:LYS:N	2.46	0.49
5:L:47:ILE:HD11	5:L:60:GLN:HG3	1.93	0.49
3:U:114:TYR:HD2	3:U:144:ASN:CB	2.25	0.49
3:O:114:TYR:HD2	3:O:144:ASN:CB	2.25	0.49
4:K:84:VAL:HG13	4:K:85:LYS:N	2.26	0.49
1:G:104:ASP:HA	1:G:108:LYS:NZ	2.28	0.49
1:G:72:TYR:O	1:G:72:TYR:CG	2.66	0.49
4:E:131:PRO:C	4:E:133:ASP:H	2.16	0.49
4:W:46:GLU:O	4:W:47:ARG:HB2	2.11	0.49
4:P:91:SER:HB2	4:P:103:PRO:HG2	1.94	0.49
2:N:282:PHE:C	2:N:282:PHE:CD1	2.85	0.49
5:X:163:LEU:O	5:X:167:ARG:HG3	2.12	0.49
5:R:68:GLU:CG	5:R:69:ARG:CA	2.88	0.49
4:D:137:SER:N	4:D:169:ARG:NH1	2.61	0.49
5:X:14:ILE:HA	5:X:64:THR:HG23	1.94	0.49
3:I:107:TYR:CE2	4:K:73:ALA:CA	2.94	0.49
4:K:143:ILE:CG2	4:K:144:LEU:N	2.76	0.49
4:J:180:LEU:O	4:J:182:ARG:N	2.45	0.49
3:I:112:VAL:HG11	4:K:70:ASP:OD1	2.11	0.49
1:M:107:PHE:CE1	4:P:17:ILE:HD11	2.45	0.49
4:E:108:TRP:CE2	4:E:115:PHE:HB3	2.48	0.49
2:H:69:MET:HE3	2:H:87:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:108:TRP:CE2	4:W:115:PHE:HB3	2.48	0.49
1:G:106:PHE:HD1	1:G:106:PHE:H	1.61	0.49
2:H:267:LEU:HD23	2:H:267:LEU:C	2.33	0.49
5:R:163:LEU:O	5:R:167:ARG:HG3	2.12	0.49
2:H:183:ILE:CD1	2:H:241:LEU:HD21	2.43	0.49
2:H:282:PHE:C	2:H:282:PHE:CD1	2.86	0.49
3:O:107:TYR:CE2	4:Q:73:ALA:CA	2.95	0.49
1:S:190:VAL:HG12	1:S:191:MET:CE	2.43	0.49
4:E:143:ILE:CG2	4:E:144:LEU:N	2.75	0.49
4:Q:166:ASP:O	4:Q:167:ILE:C	2.50	0.49
3:C:3:ILE:HD12	3:C:90:LEU:HD11	1.94	0.49
2:H:169:MET:CB	2:H:174:LEU:HD12	2.42	0.49
5:L:13:LEU:HD21	5:L:25:LEU:HG	1.94	0.49
4:V:68:ILE:CD1	4:V:154:MET:HB3	2.43	0.49
4:K:34:TYR:OH	4:K:143:ILE:HG22	2.13	0.49
4:E:99:LEU:O	4:E:101:ILE:N	2.45	0.49
1:M:188:ASP:HA	1:M:192:LYS:HD3	1.93	0.49
1:S:119:LEU:O	1:S:119:LEU:HD23	2.12	0.49
4:P:113:ASP:O	4:P:180:LEU:HD12	2.13	0.49
1:G:188:ASP:HA	1:G:192:LYS:HD3	1.94	0.49
1:S:50:LEU:HD11	3:U:44:LEU:HD12	1.95	0.49
5:X:104:GLN:HG3	5:X:108:ARG:NH2	2.28	0.49
3:I:132:MET:HB2	3:I:133:ARG:NH1	2.27	0.49
3:O:12:HIS:O	3:O:13:CYS:HB2	2.13	0.49
2:N:99:LEU:HD22	2:N:243:ASN:HB3	1.94	0.49
3:U:129:GLU:HB2	3:U:135:GLN:OE1	2.13	0.49
2:N:170:ARG:C	2:N:172:ARG:N	2.66	0.49
4:D:91:SER:HB2	4:D:103:PRO:HG2	1.94	0.49
5:L:14:ILE:HA	5:L:64:THR:HG23	1.94	0.49
5:R:62:TRP:O	5:R:64:THR:N	2.44	0.49
4:D:137:SER:HA	4:D:169:ARG:HH12	1.78	0.49
4:Q:161:VAL:HA	4:Q:177:LYS:O	2.13	0.49
1:M:212:LYS:O	1:M:215:VAL:CG2	2.61	0.49
4:V:99:LEU:HB2	4:V:101:ILE:HD11	1.94	0.49
1:M:132:TYR:CE2	1:M:180:ARG:HA	2.48	0.49
4:K:108:TRP:CE2	4:K:115:PHE:HB3	2.48	0.49
2:B:220:GLN:HG3	2:B:221:PHE:N	2.28	0.49
4:W:61:TYR:HE2	4:W:65:CYS:SG	2.35	0.49
5:X:30:ASP:O	5:X:31:ASP:HB2	2.13	0.49
2:T:97:ARG:O	2:T:101:LEU:HG	2.13	0.49
5:R:40:THR:HG22	5:R:69:ARG:HH12	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:108:TRP:CE2	4:Q:115:PHE:HB3	2.48	0.49
5:R:120:GLY:O	5:R:150:THR:O	2.31	0.49
5:X:12:LEU:N	5:X:12:LEU:CD2	2.76	0.49
4:D:162:TRP:CD1	4:D:177:LYS:HB2	2.47	0.49
4:P:110:HIS:O	4:P:112:LYS:N	2.46	0.49
3:C:114:TYR:HD2	3:C:144:ASN:CB	2.26	0.49
5:R:156:THR:HG22	5:R:156:THR:O	2.13	0.49
5:L:156:THR:O	5:L:156:THR:HG22	2.12	0.49
3:O:122:PRO:HA	4:Q:66:ARG:NH2	2.25	0.49
2:T:176:ILE:HD11	2:T:180:LEU:HD22	1.95	0.49
3:I:129:GLU:HB2	3:I:135:GLN:OE1	2.13	0.49
3:O:129:GLU:HB2	3:O:135:GLN:OE1	2.13	0.49
2:H:173:ASP:OD2	2:H:281:ARG:NH1	2.40	0.49
5:R:13:LEU:HD21	5:R:25:LEU:HG	1.95	0.49
2:T:183:ILE:CD1	2:T:241:LEU:HD21	2.43	0.49
3:C:110:ILE:HD13	3:C:148:VAL:HG13	1.95	0.49
2:T:282:PHE:CD1	2:T:282:PHE:C	2.86	0.49
4:P:136:LYS:C	4:P:169:ARG:HH12	2.16	0.48
5:F:43:VAL:CG1	5:F:64:THR:HA	2.44	0.48
5:R:10:LYS:HB2	5:R:80:GLY:O	2.13	0.48
5:X:10:LYS:HB2	5:X:80:GLY:O	2.13	0.48
1:G:10:ASN:HB2	1:G:14:GLY:O	2.13	0.48
2:T:84:GLU:HB3	2:T:231:TYR:CE1	2.47	0.48
1:A:107:PHE:CE1	4:D:17:ILE:HD11	2.46	0.48
2:T:220:GLN:HG3	2:T:221:PHE:N	2.27	0.48
1:A:174:ILE:CG1	1:A:175:ALA:N	2.74	0.48
1:M:75:MET:HE2	1:M:105:ASP:HB2	1.94	0.48
1:M:181:LYS:HB3	1:M:214:MET:HE3	1.94	0.48
4:V:65:CYS:O	4:V:68:ILE:CD1	2.61	0.48
4:D:68:ILE:CD1	4:D:154:MET:HB3	2.43	0.48
1:M:2:ALA:HB3	1:M:146:SER:HB3	1.95	0.48
5:F:163:LEU:O	5:F:167:ARG:HG3	2.13	0.48
5:R:14:ILE:HA	5:R:64:THR:HG23	1.96	0.48
1:G:132:TYR:CE2	1:G:180:ARG:HA	2.48	0.48
1:G:50:LEU:HD11	3:I:44:LEU:HD12	1.95	0.48
1:A:72:TYR:CG	1:A:72:TYR:O	2.66	0.48
5:R:29:SER:CA	5:R:48:LYS:HE2	2.43	0.48
5:X:29:SER:CA	5:X:48:LYS:HE2	2.43	0.48
4:Q:131:PRO:O	4:Q:133:ASP:N	2.47	0.48
2:N:169:MET:CB	2:N:174:LEU:HD12	2.44	0.48
2:T:175:LYS:CG	2:T:176:ILE:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:168:LYS:C	2:B:170:ARG:H	2.15	0.48
5:F:13:LEU:HD21	5:F:25:LEU:HG	1.95	0.48
5:X:13:LEU:HD21	5:X:25:LEU:HD11	1.95	0.48
1:A:23:ASN:HB3	1:A:25:GLU:OE1	2.14	0.48
1:G:181:LYS:HB3	1:G:214:MET:HE3	1.95	0.48
4:E:46:GLU:O	4:E:47:ARG:HB2	2.13	0.48
4:D:187:GLU:O	4:D:188:ILE:O	2.30	0.48
4:P:187:GLU:O	4:P:188:ILE:O	2.30	0.48
5:L:69:ARG:O	5:L:72:THR:HG22	2.12	0.48
1:S:133:GLN:CA	1:S:138:LEU:O	2.61	0.48
1:A:190:VAL:HG12	1:A:191:MET:CE	2.43	0.48
4:E:166:ASP:O	4:E:167:ILE:C	2.51	0.48
4:V:110:HIS:O	4:V:112:LYS:N	2.46	0.48
4:D:160:ASP:HB2	4:D:179:LYS:HB3	1.94	0.48
4:P:99:LEU:HB2	4:P:101:ILE:HD11	1.94	0.48
2:H:84:GLU:HB3	2:H:231:TYR:CE1	2.47	0.48
4:J:113:ASP:O	4:J:180:LEU:HD12	2.13	0.48
3:U:142:ASN:HD22	3:U:143:ARG:N	2.11	0.48
5:R:104:GLN:HG3	5:R:108:ARG:NH2	2.28	0.48
4:J:93:CYS:O	4:J:97:ILE:CG1	2.58	0.48
1:M:72:TYR:O	1:M:72:TYR:CG	2.66	0.48
4:E:24:LYS:O	4:E:25:ILE:HD12	2.13	0.48
2:B:183:ILE:CD1	2:B:241:LEU:HD21	2.43	0.48
5:L:43:VAL:CG1	5:L:64:THR:HA	2.43	0.48
5:F:40:THR:HG22	5:F:69:ARG:HH12	1.78	0.48
1:M:12:SER:CB	5:R:10:LYS:NZ	2.75	0.48
3:U:107:TYR:CE2	4:W:73:ALA:CA	2.94	0.48
1:G:11:LYS:HG3	1:G:136:THR:O	2.14	0.48
2:B:84:GLU:HB3	2:B:231:TYR:HD1	1.76	0.48
4:P:111:ASN:ND2	4:P:113:ASP:OD2	2.39	0.48
2:T:268:ILE:HG22	2:T:268:ILE:O	2.14	0.48
1:M:119:LEU:HD23	1:M:119:LEU:O	2.12	0.48
5:L:104:GLN:HG3	5:L:108:ARG:NH2	2.28	0.48
1:S:72:TYR:CG	1:S:72:TYR:O	2.67	0.48
3:C:12:HIS:O	3:C:13:CYS:HB2	2.14	0.48
1:G:70:ILE:HG23	1:G:70:ILE:O	2.12	0.48
3:U:123:TYR:HD1	3:U:123:TYR:O	1.95	0.48
3:O:11:ARG:NH1	3:O:125:PHE:CE1	2.77	0.48
4:W:134:ALA:O	4:W:136:LYS:N	2.46	0.48
2:B:176:ILE:HD11	2:B:180:LEU:HD22	1.94	0.48
3:O:102:VAL:HG11	3:O:156:MET:CE	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:85:ILE:CD1	5:X:85:ILE:H	2.24	0.48
5:F:13:LEU:HD22	5:F:25:LEU:HD11	1.96	0.48
5:L:13:LEU:CD1	5:L:25:LEU:HD11	2.44	0.48
2:B:267:LEU:HD23	2:B:267:LEU:C	2.32	0.48
4:V:167:ILE:CG2	4:V:168:LEU:N	2.76	0.48
5:L:120:GLY:O	5:L:150:THR:O	2.30	0.48
5:L:10:LYS:HB2	5:L:80:GLY:O	2.14	0.48
4:Q:38:VAL:HG11	4:Q:140:TYR:CE1	2.48	0.48
1:A:124:THR:HG21	3:C:55:THR:CG2	2.44	0.48
4:V:162:TRP:CD1	4:V:177:LYS:HB2	2.49	0.48
1:S:18:GLN:NE2	1:S:18:GLN:O	2.45	0.48
4:W:108:TRP:NE1	4:W:115:PHE:HB3	2.29	0.48
3:I:12:HIS:O	3:I:13:CYS:HB2	2.14	0.48
4:E:134:ALA:O	4:E:136:LYS:N	2.47	0.48
4:K:49:PHE:HB2	4:K:137:SER:CB	2.43	0.48
4:Q:131:PRO:C	4:Q:133:ASP:H	2.17	0.48
1:M:174:ILE:CG1	1:M:175:ALA:N	2.74	0.48
4:P:34:TYR:CD2	4:P:124:LEU:HG	2.48	0.48
5:R:41:ILE:N	5:R:41:ILE:HD12	2.25	0.48
4:K:24:LYS:O	4:K:25:ILE:HD12	2.14	0.48
4:D:167:ILE:CG2	4:D:168:LEU:N	2.76	0.48
2:N:267:LEU:C	2:N:267:LEU:HD23	2.33	0.48
2:B:97:ARG:O	2:B:101:LEU:HG	2.14	0.48
4:J:165:SER:O	4:J:174:THR:HA	2.13	0.48
5:F:88:TYR:CD1	5:F:96:PHE:CD1	3.01	0.48
5:F:68:GLU:CG	5:F:69:ARG:CA	2.87	0.48
5:X:88:TYR:HD2	5:X:88:TYR:H	1.61	0.48
5:F:10:LYS:HB2	5:F:80:GLY:O	2.13	0.48
1:S:12:SER:OG	5:X:80:GLY:HA3	2.13	0.48
4:Q:99:LEU:O	4:Q:101:ILE:N	2.46	0.48
1:G:124:THR:O	1:G:147:VAL:HG13	2.13	0.48
4:V:180:LEU:O	4:V:182:ARG:N	2.47	0.48
1:M:194:PRO:HG3	2:N:67:GLN:HA	1.95	0.48
1:M:119:LEU:CD2	1:M:131:ILE:HD13	2.44	0.48
3:O:142:ASN:HD22	3:O:143:ARG:N	2.11	0.48
4:K:108:TRP:NE1	4:K:115:PHE:HB3	2.29	0.48
3:U:11:ARG:NH1	3:U:125:PHE:CE1	2.77	0.48
5:F:29:SER:CA	5:F:48:LYS:HE2	2.43	0.48
4:K:131:PRO:C	4:K:133:ASP:H	2.17	0.48
3:O:102:VAL:HG21	3:O:156:MET:SD	2.53	0.48
4:V:34:TYR:CD2	4:V:124:LEU:HG	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:92:HIS:CD2	2:H:239:GLY:HA2	2.48	0.48
5:F:12:LEU:CD2	5:F:12:LEU:N	2.76	0.48
5:X:43:VAL:CG1	5:X:64:THR:HA	2.43	0.48
1:G:52:PRO:CD	3:I:75:TYR:CD2	2.96	0.48
4:J:99:LEU:HB2	4:J:101:ILE:HD11	1.95	0.48
2:B:268:ILE:O	2:B:268:ILE:HG22	2.13	0.48
5:L:47:ILE:HG12	5:L:60:GLN:CA	2.34	0.48
1:A:132:TYR:CE2	1:A:180:ARG:HA	2.48	0.48
1:A:178:PHE:CD2	1:A:179:LEU:HD23	2.47	0.48
4:K:114:THR:OG1	4:K:179:LYS:CB	2.61	0.48
5:L:29:SER:CA	5:L:48:LYS:HE2	2.43	0.48
5:X:41:ILE:N	5:X:41:ILE:HD12	2.24	0.48
2:T:170:ARG:C	2:T:172:ARG:N	2.67	0.48
3:I:105:TYR:CE2	3:I:152:PHE:CZ	3.01	0.48
4:Q:24:LYS:O	4:Q:25:ILE:HD12	2.14	0.48
3:O:110:ILE:HG22	3:O:145:PHE:CE1	2.49	0.48
5:X:67:GLN:HA	5:X:67:GLN:OE1	2.13	0.48
5:L:12:LEU:CD2	5:L:12:LEU:N	2.77	0.48
5:L:88:TYR:CD1	5:L:96:PHE:CD1	3.01	0.48
4:W:123:PRO:HG2	4:W:124:LEU:H	1.78	0.48
2:N:220:GLN:HG3	2:N:221:PHE:H	1.77	0.48
4:E:108:TRP:NE1	4:E:115:PHE:HB3	2.29	0.48
2:T:56:GLU:HB3	4:V:25:ILE:O	2.14	0.48
1:S:70:ILE:O	1:S:70:ILE:HG23	2.12	0.48
3:I:11:ARG:NH1	3:I:125:PHE:CE1	2.78	0.48
5:R:88:TYR:HD2	5:R:88:TYR:H	1.60	0.48
2:N:200:VAL:HG12	2:N:210:MET:HG3	1.96	0.48
1:S:35:ILE:O	1:S:38:SER:HB2	2.13	0.48
1:A:12:SER:CB	5:F:10:LYS:NZ	2.77	0.48
1:A:12:SER:HB3	5:F:10:LYS:HZ1	1.77	0.48
4:W:143:ILE:CG2	4:W:144:LEU:N	2.77	0.48
3:U:72:THR:HG22	3:U:75:TYR:H	1.79	0.48
4:Q:101:ILE:HG12	4:Q:102:THR:N	2.28	0.48
5:X:84:ILE:CD1	5:X:114:VAL:HG11	2.38	0.48
1:S:107:PHE:CE1	4:V:17:ILE:HD11	2.47	0.48
1:A:188:ASP:HA	1:A:192:LYS:HD3	1.94	0.48
4:P:162:TRP:CD1	4:P:177:LYS:HB2	2.48	0.48
4:Q:17:ILE:O	4:Q:21:LYS:O	2.31	0.48
3:O:123:TYR:O	3:O:123:TYR:HD1	1.96	0.48
4:J:34:TYR:CE2	4:J:124:LEU:HG	2.49	0.48
1:G:181:LYS:HB3	1:G:214:MET:CE	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:50:ASN:HA	4:D:53:ASN:ND2	2.28	0.48
5:F:62:TRP:O	5:F:64:THR:N	2.45	0.48
4:V:137:SER:N	4:V:169:ARG:NH1	2.61	0.48
3:U:82:THR:CG2	3:U:84:SER:OG	2.58	0.48
1:G:10:ASN:O	1:G:12:SER:N	2.47	0.48
4:Q:143:ILE:CG2	4:Q:144:LEU:N	2.77	0.48
2:N:68:GLU:CG	4:P:63:ILE:HD11	2.44	0.48
4:P:180:LEU:O	4:P:182:ARG:N	2.46	0.48
2:T:218:LEU:O	2:T:220:GLN:N	2.46	0.48
5:R:88:TYR:CD1	5:R:96:PHE:CD1	3.01	0.48
5:L:13:LEU:HD22	5:L:25:LEU:HD11	1.95	0.48
1:M:106:PHE:HD1	1:M:106:PHE:H	1.62	0.48
1:S:106:PHE:HD1	1:S:106:PHE:H	1.62	0.48
4:P:167:ILE:CG2	4:P:168:LEU:N	2.76	0.48
5:L:40:THR:HG22	5:L:69:ARG:HH12	1.79	0.47
4:V:187:GLU:O	4:V:188:ILE:O	2.32	0.47
5:R:120:GLY:N	5:R:147:PHE:HE1	2.12	0.47
4:V:50:ASN:HA	4:V:53:ASN:ND2	2.29	0.47
5:X:120:GLY:O	5:X:150:THR:O	2.31	0.47
4:J:137:SER:HA	4:J:169:ARG:HH12	1.79	0.47
1:A:10:ASN:HB2	1:A:14:GLY:O	2.14	0.47
1:M:18:GLN:NE2	1:M:18:GLN:O	2.47	0.47
2:H:84:GLU:HB3	2:H:231:TYR:HD1	1.77	0.47
4:J:110:HIS:O	4:J:112:LYS:N	2.47	0.47
4:V:117:LEU:O	4:V:118:ILE:C	2.53	0.47
4:K:131:PRO:O	4:K:133:ASP:N	2.47	0.47
4:W:158:ASP:O	4:W:181:ASN:HB2	2.14	0.47
4:W:31:THR:CG2	4:W:127:PHE:CE2	2.97	0.47
4:D:138:LEU:C	4:D:138:LEU:HD23	2.35	0.47
1:G:28:LEU:CD2	3:I:57:LYS:HD2	2.44	0.47
3:C:132:MET:HB2	3:C:133:ARG:NH1	2.30	0.47
4:V:93:CYS:O	4:V:97:ILE:CG1	2.59	0.47
4:W:131:PRO:O	4:W:133:ASP:N	2.47	0.47
3:C:102:VAL:HG21	3:C:156:MET:SD	2.53	0.47
3:I:20:GLU:O	3:I:21:TRP:CB	2.55	0.47
2:H:176:ILE:HD11	2:H:180:LEU:HD22	1.96	0.47
5:F:13:LEU:HD21	5:F:25:LEU:HD11	1.96	0.47
5:X:13:LEU:HD21	5:X:25:LEU:HD21	1.96	0.47
1:S:23:ASN:HB3	1:S:25:GLU:OE1	2.14	0.47
4:J:167:ILE:CG2	4:J:168:LEU:N	2.76	0.47
3:U:110:ILE:HD13	3:U:148:VAL:HG13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:12:LEU:CD2	5:R:12:LEU:N	2.77	0.47
5:R:77:TYR:N	5:R:77:TYR:HD1	2.12	0.47
4:V:138:LEU:HD23	4:V:138:LEU:C	2.35	0.47
1:A:12:SER:OG	5:F:80:GLY:HA3	2.15	0.47
3:I:79:THR:CG2	3:I:80:TYR:N	2.77	0.47
1:G:107:PHE:CE1	4:J:17:ILE:HD11	2.47	0.47
4:V:113:ASP:O	4:V:180:LEU:HD12	2.14	0.47
3:C:123:TYR:O	3:C:123:TYR:HD1	1.96	0.47
3:O:140:ILE:CG2	3:O:140:ILE:O	2.61	0.47
4:Q:61:TYR:HE2	4:Q:65:CYS:SG	2.36	0.47
5:R:30:ASP:O	5:R:31:ASP:HB2	2.14	0.47
3:U:20:GLU:O	3:U:21:TRP:CB	2.56	0.47
3:I:102:VAL:HG11	3:I:156:MET:HE3	1.95	0.47
1:S:174:ILE:CG1	1:S:175:ALA:N	2.73	0.47
4:Q:31:THR:HG21	4:Q:127:PHE:CE2	2.49	0.47
5:L:120:GLY:N	5:L:147:PHE:HE1	2.12	0.47
3:I:82:THR:HB	3:I:85:GLY:H	1.79	0.47
1:M:10:ASN:O	1:M:12:SER:N	2.46	0.47
1:S:10:ASN:O	1:S:12:SER:N	2.47	0.47
1:G:186:TYR:CE1	1:G:190:VAL:HG11	2.49	0.47
3:C:17:PHE:HZ	3:C:146:ILE:HG22	1.79	0.47
3:I:11:ARG:HH12	4:K:154:MET:HE1	1.79	0.47
4:Q:134:ALA:O	4:Q:136:LYS:N	2.48	0.47
4:W:131:PRO:C	4:W:133:ASP:H	2.18	0.47
1:G:174:ILE:CG1	1:G:175:ALA:N	2.73	0.47
5:R:13:LEU:HD22	5:R:25:LEU:HD11	1.97	0.47
4:E:31:THR:HG21	4:E:127:PHE:CE2	2.49	0.47
1:M:134:THR:OG1	1:M:138:LEU:HB2	2.15	0.47
1:S:134:THR:N	1:S:138:LEU:O	2.39	0.47
4:Q:108:TRP:NE1	4:Q:115:PHE:HB3	2.29	0.47
5:X:120:GLY:N	5:X:147:PHE:HE1	2.12	0.47
4:Q:29:LEU:HD21	6:W:194:PLM:HG3	1.97	0.47
2:N:259:GLY:C	2:N:260:HIS:CG	2.88	0.47
2:T:84:GLU:HB3	2:T:231:TYR:HD1	1.77	0.47
3:I:123:TYR:O	3:I:123:TYR:HD1	1.96	0.47
4:V:34:TYR:CE2	4:V:124:LEU:HG	2.49	0.47
1:M:23:ASN:HB3	1:M:25:GLU:OE1	2.15	0.47
1:A:135:LEU:C	1:A:137:GLY:H	2.17	0.47
4:P:137:SER:HA	4:P:169:ARG:HH12	1.79	0.47
4:P:50:ASN:HA	4:P:53:ASN:ND2	2.29	0.47
5:F:88:TYR:HD2	5:F:88:TYR:H	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:137:SER:HA	4:V:169:ARG:HH12	1.79	0.47
4:J:137:SER:N	4:J:169:ARG:NH1	2.62	0.47
4:K:126:ASP:OD2	4:K:167:ILE:HD13	2.15	0.47
1:S:188:ASP:HA	1:S:192:LYS:HD3	1.96	0.47
4:K:161:VAL:HA	4:K:177:LYS:O	2.14	0.47
3:O:124:ASP:OD2	3:O:140:ILE:HB	2.14	0.47
2:H:179:ILE:CG2	2:H:180:LEU:N	2.78	0.47
4:P:34:TYR:CE2	4:P:124:LEU:HG	2.50	0.47
4:Q:75:THR:CG2	4:Q:93:CYS:SG	3.02	0.47
5:F:13:LEU:CD1	5:F:25:LEU:HD11	2.45	0.47
4:J:45:TYR:OH	4:J:55:HIS:CD2	2.67	0.47
5:L:4:GLU:O	5:L:5:TYR:O	2.32	0.47
5:F:120:GLY:N	5:F:147:PHE:HE1	2.12	0.47
5:R:43:VAL:CG1	5:R:64:THR:HA	2.45	0.47
4:D:137:SER:N	4:D:169:ARG:HH12	2.12	0.47
4:V:137:SER:N	4:V:169:ARG:HH12	2.12	0.47
4:J:138:LEU:HD23	4:J:138:LEU:C	2.35	0.47
3:I:82:THR:HB	3:I:85:GLY:N	2.29	0.47
4:E:126:ASP:OD2	4:E:167:ILE:HD13	2.14	0.47
4:D:180:LEU:O	4:D:182:ARG:N	2.47	0.47
4:P:160:ASP:HB2	4:P:179:LYS:HB3	1.96	0.47
2:B:59:LEU:HD12	2:B:59:LEU:O	2.15	0.47
4:E:61:TYR:HE2	4:E:65:CYS:SG	2.37	0.47
2:N:169:MET:HB3	2:N:174:LEU:HD12	1.96	0.47
4:D:34:TYR:CE2	4:D:124:LEU:HG	2.50	0.47
5:R:13:LEU:CD1	5:R:25:LEU:HD11	2.45	0.47
4:Q:25:ILE:HD13	4:W:27:THR:OG1	2.14	0.47
4:J:65:CYS:O	4:J:68:ILE:CD1	2.63	0.47
1:G:23:ASN:HB3	1:G:25:GLU:OE1	2.15	0.47
3:C:110:ILE:HG22	3:C:145:PHE:CE1	2.50	0.47
2:H:97:ARG:O	2:H:101:LEU:HG	2.15	0.47
4:K:117:LEU:HB2	4:K:176:ILE:O	2.15	0.47
5:F:148:LEU:HD12	5:F:148:LEU:N	2.30	0.47
4:K:190:ILE:HA	4:K:190:ILE:HD13	1.67	0.47
4:P:138:LEU:HD23	4:P:138:LEU:C	2.35	0.47
5:F:12:LEU:O	5:F:12:LEU:HG	2.14	0.47
5:L:88:TYR:HD2	5:L:88:TYR:H	1.63	0.47
3:U:72:THR:HG23	3:U:74:LYS:H	1.80	0.47
2:N:237:ILE:HG22	2:N:250:VAL:HG21	1.97	0.47
4:Q:99:LEU:HD21	4:W:29:LEU:CD2	2.45	0.47
1:G:4:GLU:CG	1:G:143:ILE:HG22	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:117:LEU:O	4:P:118:ILE:C	2.53	0.47
4:D:34:TYR:CD2	4:D:124:LEU:HG	2.49	0.47
1:M:181:LYS:HB3	1:M:214:MET:CE	2.45	0.47
3:C:129:GLU:HB3	3:C:135:GLN:OE1	2.14	0.47
2:H:170:ARG:C	2:H:172:ARG:N	2.67	0.47
4:K:16:GLU:HG2	4:K:20:ASN:ND2	2.29	0.47
4:K:31:THR:HG21	4:K:127:PHE:CE2	2.50	0.47
4:V:96:LYS:NZ	4:V:100:ASN:HD21	2.12	0.47
4:V:28:GLU:HA	4:V:31:THR:HG22	1.97	0.47
1:S:133:GLN:HE22	4:V:188:ILE:CD1	2.22	0.47
5:R:68:GLU:C	5:R:70:PHE:H	2.17	0.47
5:F:77:TYR:HD1	5:F:77:TYR:N	2.12	0.47
1:S:11:LYS:HG3	1:S:136:THR:O	2.15	0.47
1:S:194:PRO:HG3	2:T:67:GLN:HA	1.95	0.47
4:E:68:ILE:HG21	4:E:154:MET:CB	2.45	0.47
3:U:102:VAL:HG11	3:U:156:MET:HE3	1.96	0.47
1:M:52:PRO:CD	3:O:75:TYR:CD2	2.98	0.47
3:O:72:THR:HG21	3:O:75:TYR:CE2	2.50	0.47
5:L:13:LEU:HD21	5:L:25:LEU:HD11	1.97	0.47
4:V:68:ILE:HG13	4:V:68:ILE:H	1.35	0.47
3:U:93:ASP:O	3:U:93:ASP:CG	2.53	0.47
1:A:106:PHE:HD1	1:A:106:PHE:H	1.62	0.47
2:N:97:ARG:O	2:N:101:LEU:HG	2.15	0.47
1:S:2:ALA:HB3	1:S:146:SER:HB3	1.96	0.47
1:G:133:GLN:CA	1:G:138:LEU:O	2.63	0.47
4:D:166:ASP:HB3	4:D:169:ARG:CG	2.45	0.47
3:C:107:TYR:O	3:C:111:TYR:HB3	2.14	0.47
3:O:17:PHE:HZ	3:O:146:ILE:HG22	1.80	0.47
5:F:104:GLN:HG3	5:F:108:ARG:NH2	2.30	0.47
5:L:30:ASP:O	5:L:31:ASP:HB2	2.15	0.47
5:L:85:ILE:H	5:L:85:ILE:CD1	2.26	0.47
3:C:67:ILE:HD12	3:C:67:ILE:N	2.30	0.46
4:W:101:ILE:HG12	4:W:102:THR:N	2.30	0.46
4:V:160:ASP:HB2	4:V:179:LYS:HB3	1.96	0.46
1:S:129:MET:HB2	1:S:143:ILE:CD1	2.45	0.46
2:T:211:ILE:HG22	2:T:268:ILE:HD11	1.97	0.46
4:J:117:LEU:O	4:J:118:ILE:C	2.54	0.46
1:G:197:SER:O	1:G:198:MET:O	2.33	0.46
3:I:122:PRO:HA	4:K:66:ARG:NH2	2.24	0.46
1:M:69:TYR:N	1:M:69:TYR:CD1	2.83	0.46
2:N:200:VAL:HG12	2:N:200:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:167:ILE:HG23	4:V:168:LEU:N	2.30	0.46
4:J:28:GLU:HA	4:J:31:THR:HG22	1.97	0.46
5:X:88:TYR:HD1	5:X:96:PHE:HB2	1.79	0.46
5:F:169:ILE:HG13	5:F:169:ILE:H	1.54	0.46
3:I:107:TYR:O	3:I:111:TYR:HB3	2.15	0.46
3:U:79:THR:CG2	3:U:80:TYR:N	2.78	0.46
5:L:84:ILE:CD1	5:L:114:VAL:HG11	2.40	0.46
4:D:99:LEU:HB2	4:D:101:ILE:HD11	1.96	0.46
4:J:159:CYS:CB	4:J:179:LYS:O	2.63	0.46
1:G:194:PRO:HG3	2:H:67:GLN:HA	1.96	0.46
2:N:56:GLU:HB3	4:P:25:ILE:O	2.15	0.46
3:I:121:SER:HA	3:I:122:PRO:HD2	1.79	0.46
2:B:175:LYS:CG	2:B:176:ILE:N	2.77	0.46
3:I:129:GLU:HB3	3:I:135:GLN:OE1	2.15	0.46
5:X:13:LEU:HD22	5:X:25:LEU:HD11	1.97	0.46
3:U:105:TYR:HE1	3:U:109:HIS:HD1	1.54	0.46
4:J:68:ILE:H	4:J:68:ILE:HG13	1.36	0.46
5:X:137:LYS:O	5:X:141:ASP:OD2	2.33	0.46
4:E:190:ILE:HD13	4:E:190:ILE:HA	1.67	0.46
1:M:135:LEU:C	1:M:137:GLY:H	2.18	0.46
1:G:135:LEU:C	1:G:137:GLY:H	2.17	0.46
3:C:79:THR:CG2	3:C:80:TYR:N	2.77	0.46
3:O:79:THR:CG2	3:O:80:TYR:N	2.78	0.46
1:M:12:SER:HB3	5:R:10:LYS:HZ1	1.80	0.46
1:S:10:ASN:HB2	1:S:14:GLY:O	2.15	0.46
2:B:68:GLU:CG	4:D:63:ILE:HD11	2.46	0.46
3:I:114:TYR:CD2	3:I:144:ASN:HB3	2.51	0.46
1:A:50:LEU:HD11	3:C:44:LEU:HD12	1.97	0.46
5:F:30:ASP:O	5:F:31:ASP:HB2	2.15	0.46
3:I:131:GLU:HG3	3:I:135:GLN:HB3	1.97	0.46
1:A:69:TYR:N	1:A:69:TYR:CD1	2.83	0.46
5:L:137:LYS:O	5:L:141:ASP:OD2	2.34	0.46
2:B:246:PHE:CD1	2:B:246:PHE:N	2.83	0.46
1:G:134:THR:N	1:G:138:LEU:O	2.41	0.46
4:J:50:ASN:HA	4:J:53:ASN:ND2	2.30	0.46
5:X:77:TYR:N	5:X:77:TYR:HD1	2.12	0.46
3:U:17:PHE:HZ	3:U:146:ILE:HG22	1.80	0.46
4:K:101:ILE:HG12	4:K:102:THR:N	2.30	0.46
4:Q:29:LEU:CD2	4:W:99:LEU:HD21	2.45	0.46
1:M:129:MET:HB2	1:M:143:ILE:HD11	1.97	0.46
1:M:70:ILE:O	1:M:70:ILE:HG23	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:114:TRP:CH2	4:J:76:ALA:HA	2.51	0.46
5:L:41:ILE:HD12	5:L:41:ILE:N	2.26	0.46
2:T:70:ILE:HG22	2:T:74:HIS:HD2	1.81	0.46
3:O:93:ASP:CG	3:O:93:ASP:O	2.54	0.46
2:N:183:ILE:CD1	2:N:241:LEU:HD21	2.44	0.46
2:N:246:PHE:CD1	2:N:246:PHE:N	2.84	0.46
4:D:28:GLU:HA	4:D:31:THR:HG22	1.98	0.46
5:L:15:GLY:N	5:L:102:TRP:CZ3	2.83	0.46
4:P:137:SER:N	4:P:169:ARG:NH1	2.64	0.46
1:A:10:ASN:O	1:A:12:SER:N	2.47	0.46
3:U:67:ILE:HD12	3:U:67:ILE:N	2.30	0.46
4:Q:123:PRO:HG2	4:Q:124:LEU:H	1.79	0.46
1:S:132:TYR:HE2	1:S:180:ARG:HA	1.80	0.46
2:T:68:GLU:CG	4:V:63:ILE:HD11	2.45	0.46
2:N:220:GLN:HG3	2:N:221:PHE:N	2.31	0.46
1:M:178:PHE:CD2	1:M:179:LEU:HD23	2.49	0.46
4:Q:136:LYS:O	4:Q:169:ARG:NH1	2.48	0.46
3:C:131:GLU:HG3	3:C:135:GLN:HB3	1.98	0.46
2:B:200:VAL:HG12	2:B:210:MET:HG3	1.98	0.46
4:D:45:TYR:OH	4:D:55:HIS:CD2	2.69	0.46
4:E:31:THR:CG2	4:E:127:PHE:CE2	2.98	0.46
4:W:31:THR:HG21	4:W:127:PHE:CZ	2.50	0.46
1:G:69:TYR:N	1:G:69:TYR:CD1	2.83	0.46
1:A:35:ILE:O	1:A:38:SER:HB2	2.14	0.46
4:V:45:TYR:OH	4:V:55:HIS:CD2	2.68	0.46
4:P:28:GLU:HA	4:P:31:THR:HG22	1.98	0.46
4:V:18:TRP:CD1	4:V:18:TRP:O	2.68	0.46
3:I:52:ARG:O	3:I:56:GLN:HG3	2.16	0.46
5:L:77:TYR:HD1	5:L:77:TYR:N	2.13	0.46
5:R:68:GLU:O	5:R:70:PHE:N	2.38	0.46
3:U:119:LEU:CD2	3:U:119:LEU:N	2.60	0.46
4:E:101:ILE:HG12	4:E:102:THR:N	2.30	0.46
2:N:181:GLN:HG3	2:N:199:LEU:HD23	1.97	0.46
1:A:129:MET:CE	1:A:143:ILE:HD11	2.45	0.46
3:O:13:CYS:HB3	4:Q:188:ILE:HD12	1.97	0.46
3:I:105:TYR:HE1	3:I:109:HIS:HD1	1.56	0.46
3:U:105:TYR:CE2	3:U:152:PHE:CZ	3.03	0.46
3:C:93:ASP:O	3:C:93:ASP:CG	2.54	0.46
4:Q:117:LEU:HB2	4:Q:176:ILE:O	2.15	0.46
1:G:117:SER:HB3	4:J:191:GLY:H	1.81	0.46
1:M:133:GLN:HE22	4:P:188:ILE:CD1	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:69:ARG:O	5:F:72:THR:HG22	2.15	0.46
5:X:69:ARG:O	5:X:72:THR:HG22	2.15	0.46
3:O:107:TYR:O	3:O:111:TYR:HB3	2.15	0.46
3:O:67:ILE:HD12	3:O:67:ILE:N	2.31	0.46
1:S:52:PRO:CD	3:U:75:TYR:CD2	2.98	0.46
4:E:124:LEU:HD23	4:E:125:ALA:HB2	1.97	0.46
4:E:71:PHE:HE2	4:E:94:ALA:HA	1.80	0.46
1:A:52:PRO:CD	3:C:75:TYR:CD2	2.99	0.46
1:S:129:MET:CE	1:S:143:ILE:HD11	2.43	0.46
2:B:237:ILE:HG22	2:B:250:VAL:HG21	1.98	0.46
2:T:69:MET:HE3	2:T:87:LEU:HD13	1.96	0.46
4:D:117:LEU:O	4:D:118:ILE:C	2.54	0.46
1:M:50:LEU:HD13	3:O:43:LEU:CD1	2.45	0.46
3:C:140:ILE:O	3:C:140:ILE:CG2	2.62	0.46
4:K:68:ILE:HG21	4:K:154:MET:CB	2.46	0.46
2:N:167:THR:O	2:N:167:THR:HG22	2.15	0.46
3:I:102:VAL:HG21	3:I:156:MET:SD	2.55	0.46
3:U:129:GLU:HB3	3:U:135:GLN:OE1	2.16	0.46
4:D:65:CYS:O	4:D:68:ILE:CD1	2.64	0.46
4:Q:16:GLU:HG2	4:Q:20:ASN:ND2	2.30	0.46
3:U:52:ARG:O	3:U:56:GLN:HG3	2.16	0.46
4:W:11:LYS:HA	4:W:92:LYS:HB3	1.96	0.46
4:W:176:ILE:HD13	4:W:176:ILE:N	2.31	0.46
2:H:265:VAL:O	2:H:265:VAL:HG13	2.15	0.46
1:A:134:THR:OG1	1:A:138:LEU:HB2	2.16	0.46
5:F:15:GLY:N	5:F:102:TRP:CZ3	2.84	0.46
3:I:17:PHE:HZ	3:I:146:ILE:HG22	1.81	0.46
1:G:119:LEU:CD2	1:G:131:ILE:HD13	2.45	0.46
1:G:178:PHE:CD2	1:G:179:LEU:HD23	2.47	0.46
1:G:212:LYS:O	1:G:215:VAL:CG2	2.62	0.46
2:H:64:PHE:CD1	4:J:67:LEU:HD13	2.51	0.46
4:E:36:SER:O	4:E:40:GLN:CB	2.63	0.46
2:T:167:THR:HG22	2:T:167:THR:O	2.15	0.46
1:S:69:TYR:N	1:S:69:TYR:CD1	2.83	0.46
4:P:45:TYR:OH	4:P:55:HIS:CD2	2.69	0.46
4:K:176:ILE:HD13	4:K:176:ILE:N	2.31	0.46
2:H:246:PHE:CD1	2:H:246:PHE:N	2.84	0.46
1:A:133:GLN:CA	1:A:138:LEU:O	2.62	0.46
1:M:134:THR:N	1:M:138:LEU:O	2.40	0.46
4:K:34:TYR:CE2	4:K:140:TYR:CE2	3.04	0.46
1:M:212:LYS:HA	1:M:215:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:54:ILE:CG2	3:C:55:THR:N	2.79	0.46
1:G:20:ASN:ND2	1:G:33:TYR:OH	2.49	0.46
4:D:159:CYS:CB	4:D:179:LYS:O	2.63	0.46
4:J:162:TRP:O	4:J:176:ILE:HG23	2.15	0.46
4:P:159:CYS:CB	4:P:179:LYS:O	2.63	0.46
2:T:181:GLN:HG3	2:T:199:LEU:HD23	1.97	0.46
3:O:114:TYR:CD2	3:O:144:ASN:HB3	2.51	0.46
2:B:179:ILE:CG2	2:B:180:LEU:N	2.79	0.46
3:I:105:TYR:CE2	3:I:152:PHE:CE1	3.04	0.46
1:S:73:VAL:CG1	1:S:74:GLY:N	2.79	0.46
4:W:190:ILE:HA	4:W:190:ILE:HD13	1.67	0.46
4:V:166:ASP:HB3	4:V:169:ARG:CG	2.46	0.46
2:H:259:GLY:C	2:H:260:HIS:CG	2.89	0.46
4:V:159:CYS:CB	4:V:179:LYS:O	2.64	0.46
1:S:129:MET:SD	1:S:131:ILE:HD11	2.57	0.46
1:A:194:PRO:HG3	2:B:67:GLN:HA	1.98	0.46
2:H:268:ILE:HG22	2:H:268:ILE:O	2.16	0.46
1:S:212:LYS:HA	1:S:215:VAL:HG22	1.98	0.46
2:T:237:ILE:HG22	2:T:250:VAL:HG21	1.96	0.46
3:U:114:TYR:CD2	3:U:144:ASN:HB3	2.51	0.46
3:U:124:ASP:OD2	3:U:140:ILE:HB	2.15	0.46
2:N:169:MET:HB3	2:N:174:LEU:CD1	2.46	0.46
2:T:179:ILE:CG2	2:T:180:LEU:N	2.79	0.46
2:H:70:ILE:HG22	2:H:74:HIS:HD2	1.81	0.46
3:U:110:ILE:HG22	3:U:145:PHE:CE1	2.51	0.46
4:P:166:ASP:HB3	4:P:169:ARG:CG	2.46	0.45
2:T:259:GLY:C	2:T:260:HIS:CG	2.89	0.45
4:Q:126:ASP:OD2	4:Q:167:ILE:HD13	2.16	0.45
1:S:20:ASN:ND2	1:S:33:TYR:OH	2.49	0.45
1:G:212:LYS:HA	1:G:215:VAL:HG22	1.98	0.45
1:A:28:LEU:CD2	3:C:57:LYS:HD2	2.46	0.45
2:B:87:LEU:O	2:B:87:LEU:HD12	2.17	0.45
5:L:57:VAL:O	5:L:57:VAL:HG12	2.16	0.45
4:W:161:VAL:HA	4:W:177:LYS:O	2.16	0.45
4:W:68:ILE:HG21	4:W:154:MET:CB	2.46	0.45
4:E:49:PHE:HB2	4:E:137:SER:CB	2.46	0.45
4:K:136:LYS:O	4:K:169:ARG:NH1	2.48	0.45
4:Q:49:PHE:HB2	4:Q:137:SER:CB	2.46	0.45
1:S:200:MET:HE1	5:X:7:TYR:CA	2.45	0.45
4:P:29:LEU:C	4:P:29:LEU:HD23	2.36	0.45
3:O:129:GLU:HB3	3:O:135:GLN:OE1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:83:PHE:CD1	2:H:83:PHE:C	2.88	0.45
4:J:167:ILE:HG23	4:J:168:LEU:N	2.31	0.45
4:V:96:LYS:NZ	4:V:100:ASN:ND2	2.63	0.45
4:V:185:LYS:HD2	4:V:185:LYS:C	2.37	0.45
5:L:67:GLN:HA	5:L:67:GLN:OE1	2.16	0.45
4:J:166:ASP:HB3	4:J:169:ARG:CG	2.46	0.45
3:O:88:PHE:O	3:O:103:LEU:CD2	2.59	0.45
1:M:11:LYS:HG3	1:M:136:THR:O	2.16	0.45
4:W:126:ASP:OD2	4:W:167:ILE:HD13	2.16	0.45
4:Q:71:PHE:HE2	4:Q:94:ALA:HA	1.80	0.45
1:A:212:LYS:O	1:A:215:VAL:CG2	2.64	0.45
1:G:124:THR:HG21	3:I:55:THR:HG21	1.98	0.45
5:F:121:ASN:O	5:F:122:LYS:C	2.54	0.45
3:C:11:ARG:NH1	3:C:125:PHE:CE1	2.77	0.45
5:X:156:THR:HG23	5:X:159:GLU:OE1	2.16	0.45
5:X:57:VAL:O	5:X:57:VAL:HG12	2.16	0.45
3:U:102:VAL:HG21	3:U:156:MET:SD	2.55	0.45
2:N:179:ILE:CG2	2:N:180:LEU:N	2.79	0.45
2:T:175:LYS:HG2	2:T:176:ILE:H	1.80	0.45
5:R:88:TYR:HD1	5:R:96:PHE:HB2	1.80	0.45
1:G:114:TRP:HH2	4:J:76:ALA:HA	1.81	0.45
4:K:158:ASP:O	4:K:181:ASN:HB2	2.16	0.45
4:E:158:ASP:O	4:E:181:ASN:HB2	2.16	0.45
2:H:168:LYS:C	2:H:170:ARG:H	2.20	0.45
2:T:200:VAL:HG12	2:T:210:MET:HG3	1.97	0.45
2:T:200:VAL:O	2:T:200:VAL:HG12	2.16	0.45
4:Q:31:THR:CG2	4:Q:127:PHE:CE2	2.99	0.45
1:G:35:ILE:O	1:G:38:SER:HB2	2.16	0.45
3:O:52:ARG:O	3:O:56:GLN:HG3	2.17	0.45
4:Q:190:ILE:HD13	4:Q:190:ILE:HA	1.67	0.45
4:P:188:ILE:HD12	4:P:190:ILE:HD11	1.91	0.45
5:L:12:LEU:O	5:L:12:LEU:HG	2.16	0.45
3:I:119:LEU:N	3:I:119:LEU:CD2	2.61	0.45
4:W:34:TYR:CE2	4:W:140:TYR:CE2	3.04	0.45
1:M:124:THR:HG21	3:O:55:THR:HG21	1.98	0.45
1:S:119:LEU:CD2	1:S:131:ILE:HD13	2.45	0.45
1:S:212:LYS:O	1:S:215:VAL:CG2	2.63	0.45
5:R:121:ASN:O	5:R:122:LYS:C	2.54	0.45
4:K:65:CYS:O	4:K:68:ILE:HG22	2.17	0.45
1:A:75:MET:HE2	1:A:105:ASP:HB2	1.97	0.45
3:O:155:PRO:CG	3:O:156:MET:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:167:ILE:HG23	4:P:168:LEU:N	2.30	0.45
1:A:117:SER:HB3	4:D:191:GLY:H	1.80	0.45
5:F:4:GLU:O	5:F:5:TYR:O	2.34	0.45
4:J:96:LYS:NZ	4:J:100:ASN:HD21	2.13	0.45
5:L:148:LEU:HD12	5:L:148:LEU:N	2.32	0.45
1:M:133:GLN:CA	1:M:138:LEU:O	2.62	0.45
5:L:72:THR:HG23	5:L:73:ILE:N	2.31	0.45
5:R:15:GLY:N	5:R:102:TRP:CZ3	2.85	0.45
5:L:88:TYR:HD1	5:L:96:PHE:HB2	1.80	0.45
4:E:34:TYR:CE2	4:E:140:TYR:CE2	3.03	0.45
2:N:188:TRP:N	2:N:188:TRP:CD1	2.82	0.45
2:H:181:GLN:HG3	2:H:199:LEU:HD23	1.97	0.45
2:H:231:TYR:CD2	2:H:234:CYS:SG	3.08	0.45
3:U:114:TYR:HD1	3:U:114:TYR:N	2.08	0.45
2:H:220:GLN:HG3	2:H:221:PHE:N	2.30	0.45
3:C:124:ASP:OD2	3:C:140:ILE:HB	2.16	0.45
3:U:122:PRO:HA	4:W:66:ARG:NH2	2.25	0.45
4:W:24:LYS:O	4:W:25:ILE:HD12	2.17	0.45
4:K:25:ILE:HG23	4:K:26:ASN:N	2.31	0.45
1:G:185:LEU:HD11	1:G:210:LYS:HD3	1.98	0.45
2:H:97:ARG:HD3	2:H:100:GLU:OE1	2.17	0.45
4:J:96:LYS:NZ	4:J:100:ASN:ND2	2.64	0.45
5:R:4:GLU:O	5:R:5:TYR:O	2.35	0.45
2:B:247:PRO:HB2	2:B:271:ASP:OD1	2.16	0.45
2:T:246:PHE:CD1	2:T:246:PHE:N	2.84	0.45
3:C:119:LEU:CD2	3:C:119:LEU:N	2.58	0.45
4:Q:36:SER:O	4:Q:40:GLN:CB	2.63	0.45
5:X:88:TYR:HE2	5:X:119:VAL:O	1.99	0.45
1:A:11:LYS:HG3	1:A:136:THR:O	2.16	0.45
1:A:186:TYR:CE1	1:A:190:VAL:HG11	2.52	0.45
1:S:186:TYR:CE1	1:S:190:VAL:HG11	2.51	0.45
2:N:268:ILE:HG22	2:N:268:ILE:O	2.16	0.45
1:A:212:LYS:HA	1:A:215:VAL:HG22	1.98	0.45
4:D:162:TRP:O	4:D:176:ILE:HG23	2.17	0.45
2:H:211:ILE:HG22	2:H:268:ILE:HD11	1.98	0.45
5:X:121:ASN:O	5:X:122:LYS:C	2.54	0.45
2:B:218:LEU:O	2:B:220:GLN:N	2.43	0.45
1:G:200:MET:HE1	5:L:7:TYR:HA	1.92	0.45
4:W:49:PHE:HB2	4:W:137:SER:CB	2.46	0.45
4:P:38:VAL:HG11	4:P:140:TYR:HE1	1.73	0.45
2:B:168:LYS:O	2:B:170:ARG:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:158:ASP:O	4:Q:181:ASN:HB2	2.16	0.45
3:C:105:TYR:CE2	3:C:152:PHE:CZ	3.04	0.45
1:S:38:SER:O	1:S:41:HIS:HB3	2.16	0.45
4:D:167:ILE:HG23	4:D:168:LEU:N	2.30	0.45
4:P:18:TRP:CD1	4:P:18:TRP:O	2.69	0.45
5:F:88:TYR:HD1	5:F:96:PHE:HB2	1.80	0.45
5:L:88:TYR:HE2	5:L:119:VAL:O	2.00	0.45
4:J:169:ARG:O	4:J:170:GLY:O	2.35	0.45
3:U:107:TYR:O	3:U:111:TYR:HB3	2.16	0.45
1:G:3:ILE:HG21	1:G:6:ILE:HG23	1.98	0.45
3:U:114:TYR:HD2	3:U:144:ASN:HB2	1.82	0.45
1:M:50:LEU:HD11	3:O:44:LEU:HD12	1.99	0.45
4:D:25:ILE:HG22	4:D:26:ASN:N	2.32	0.45
4:P:25:ILE:HG22	4:P:26:ASN:N	2.32	0.45
3:U:21:TRP:HH2	3:U:155:PRO:O	2.00	0.45
4:D:29:LEU:HD23	4:D:29:LEU:C	2.37	0.45
2:B:176:ILE:HG23	2:B:177:LEU:H	1.82	0.45
3:C:155:PRO:CG	3:C:156:MET:H	2.24	0.45
2:N:176:ILE:C	2:N:176:ILE:HD13	2.36	0.45
1:M:75:MET:HE3	1:M:181:LYS:HZ2	1.82	0.45
4:K:11:LYS:HA	4:K:92:LYS:HB3	1.98	0.45
4:D:18:TRP:CD1	4:D:18:TRP:O	2.69	0.45
4:D:188:ILE:HD12	4:D:190:ILE:HD11	1.91	0.45
5:F:88:TYR:HE2	5:F:119:VAL:O	1.99	0.45
4:P:65:CYS:O	4:P:68:ILE:CD1	2.65	0.45
4:E:161:VAL:HA	4:E:177:LYS:O	2.17	0.45
3:C:48:ILE:CG2	3:C:87:TRP:CD1	3.00	0.45
3:I:124:ASP:OD2	3:I:140:ILE:HB	2.16	0.45
1:M:104:ASP:HA	1:M:108:LYS:HZ3	1.82	0.45
3:U:121:SER:HA	3:U:122:PRO:HD2	1.80	0.45
4:Q:116:SER:CB	4:Q:175:GLU:HG3	2.45	0.45
1:S:114:TRP:CH2	4:V:76:ALA:HA	2.52	0.45
5:R:90:VAL:HG13	5:R:129:ARG:NH2	2.32	0.45
4:W:16:GLU:HG2	4:W:20:ASN:ND2	2.31	0.45
1:M:117:SER:HB3	4:P:191:GLY:H	1.81	0.45
5:R:77:TYR:HD1	5:R:77:TYR:H	1.63	0.45
4:J:137:SER:N	4:J:169:ARG:HH12	2.14	0.45
3:C:88:PHE:O	3:C:103:LEU:CD2	2.60	0.45
1:G:12:SER:CB	5:L:10:LYS:HZ2	2.30	0.45
2:H:254:ARG:HG3	2:H:264:THR:HG22	1.98	0.45
2:B:188:TRP:CD1	2:B:188:TRP:N	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:129:MET:HE2	1:M:143:ILE:HD11	1.99	0.45
3:I:44:LEU:C	3:I:44:LEU:HD23	2.37	0.45
4:Q:68:ILE:HG21	4:Q:154:MET:CB	2.47	0.45
1:A:181:LYS:HB3	1:A:214:MET:CE	2.47	0.45
2:N:176:ILE:HG23	2:N:177:LEU:H	1.82	0.45
3:U:131:GLU:HG3	3:U:135:GLN:HB3	1.99	0.45
2:T:83:PHE:CD1	2:T:83:PHE:C	2.88	0.45
4:E:25:ILE:HG23	4:E:26:ASN:N	2.31	0.45
4:E:11:LYS:HA	4:E:92:LYS:HB3	1.99	0.45
1:S:135:LEU:C	1:S:137:GLY:H	2.19	0.45
1:G:134:THR:OG1	1:G:138:LEU:HB2	2.17	0.45
4:Q:114:THR:OG1	4:Q:179:LYS:CB	2.62	0.45
5:F:68:GLU:C	5:F:70:PHE:N	2.70	0.45
1:M:186:TYR:CE1	1:M:190:VAL:HG11	2.52	0.45
1:G:132:TYR:HE2	1:G:180:ARG:HA	1.81	0.45
1:A:18:GLN:NE2	1:A:18:GLN:O	2.50	0.45
4:D:161:VAL:HA	4:D:177:LYS:O	2.17	0.45
2:H:188:TRP:N	2:H:188:TRP:CD1	2.83	0.45
3:I:114:TYR:HD1	3:I:114:TYR:N	2.08	0.45
1:M:129:MET:HB2	1:M:143:ILE:CD1	2.46	0.45
3:U:48:ILE:CG2	3:U:87:TRP:CD1	3.00	0.45
5:L:156:THR:HG23	5:L:159:GLU:OE1	2.17	0.45
4:P:38:VAL:HG11	4:P:140:TYR:CD1	2.51	0.45
4:E:41:LEU:HD22	4:E:55:HIS:CD2	2.52	0.45
3:O:105:TYR:CE2	3:O:152:PHE:CZ	3.04	0.45
2:B:189:SER:HA	2:B:194:HIS:N	2.32	0.45
4:E:176:ILE:N	4:E:176:ILE:HD13	2.31	0.45
5:F:137:LYS:O	5:F:141:ASP:OD2	2.35	0.45
3:O:82:THR:HB	3:O:85:GLY:N	2.32	0.45
4:W:124:LEU:HD23	4:W:125:ALA:HB2	1.98	0.45
2:B:259:GLY:C	2:B:260:HIS:CG	2.91	0.45
2:N:184:HIS:CB	2:N:211:ILE:HD13	2.47	0.45
4:Q:124:LEU:HD23	4:Q:125:ALA:HB2	1.98	0.45
1:S:178:PHE:CD2	1:S:179:LEU:HD23	2.48	0.45
4:J:161:VAL:HA	4:J:177:LYS:O	2.17	0.45
2:N:218:LEU:HB3	2:N:219:THR:H	1.66	0.45
2:B:69:MET:HE3	2:B:87:LEU:HD13	1.98	0.45
4:E:66:ARG:O	4:E:69:GLU:HB2	2.17	0.45
3:I:21:TRP:HH2	3:I:155:PRO:O	2.00	0.45
4:K:41:LEU:HD22	4:K:55:HIS:CD2	2.52	0.45
2:T:169:MET:HB3	2:T:174:LEU:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:13:LEU:HD21	5:R:25:LEU:HD11	1.99	0.45
2:H:200:VAL:HG12	2:H:210:MET:HG3	1.98	0.45
1:A:38:SER:CB	5:F:45:PHE:CE1	3.00	0.45
4:K:31:THR:HG21	4:K:127:PHE:CZ	2.52	0.45
5:R:148:LEU:HD12	5:R:148:LEU:N	2.32	0.45
3:U:63:VAL:O	3:U:64:LYS:HB2	2.17	0.45
5:X:12:LEU:HG	5:X:12:LEU:O	2.16	0.44
1:A:196:TYR:O	4:D:66:ARG:NH2	2.49	0.44
1:M:196:TYR:O	4:P:66:ARG:NH2	2.49	0.44
1:S:12:SER:CB	5:X:10:LYS:HZ2	2.30	0.44
3:U:99:TYR:H	3:U:99:TYR:HD1	1.65	0.44
4:W:18:TRP:HE1	4:W:100:ASN:HB2	1.82	0.44
2:N:188:TRP:CH2	2:N:266:TYR:CE1	2.83	0.44
3:C:72:THR:HG22	3:C:75:TYR:H	1.81	0.44
4:D:67:LEU:HD11	4:D:98:PHE:CD2	2.52	0.44
2:N:69:MET:HE3	2:N:87:LEU:HD13	1.98	0.44
3:I:114:TYR:HD2	3:I:144:ASN:HB2	1.82	0.44
3:C:114:TYR:CD2	3:C:144:ASN:HB3	2.52	0.44
1:M:197:SER:O	1:M:198:MET:O	2.34	0.44
3:O:99:TYR:HD1	3:O:99:TYR:H	1.65	0.44
1:S:104:ASP:HA	1:S:108:LYS:HZ3	1.82	0.44
3:U:140:ILE:O	3:U:140:ILE:CG2	2.63	0.44
4:Q:66:ARG:O	4:Q:69:GLU:HB2	2.17	0.44
1:A:114:TRP:CH2	4:D:76:ALA:HA	2.52	0.44
1:M:114:TRP:CH2	4:P:76:ALA:HA	2.52	0.44
4:D:96:LYS:NZ	4:D:100:ASN:ND2	2.65	0.44
1:S:134:THR:OG1	1:S:138:LEU:HB2	2.17	0.44
5:R:69:ARG:O	5:R:72:THR:HG22	2.17	0.44
5:X:15:GLY:N	5:X:102:TRP:CZ3	2.85	0.44
3:I:67:ILE:N	3:I:67:ILE:HD12	2.32	0.44
3:I:54:ILE:CG2	3:I:55:THR:N	2.80	0.44
1:S:124:THR:HG21	3:U:55:THR:HG21	1.98	0.44
1:G:18:GLN:NE2	1:G:18:GLN:O	2.49	0.44
2:B:67:GLN:NE2	2:B:68:GLU:HB2	2.32	0.44
4:P:115:PHE:CE2	4:P:178:VAL:HG21	2.53	0.44
2:B:181:GLN:HG3	2:B:199:LEU:HD23	1.98	0.44
2:H:87:LEU:O	2:H:87:LEU:HD12	2.16	0.44
1:A:50:LEU:HD22	3:C:43:LEU:CD1	2.47	0.44
4:W:114:THR:OG1	4:W:179:LYS:CB	2.65	0.44
4:W:61:TYR:O	4:W:61:TYR:HD2	2.00	0.44
4:K:75:THR:CG2	4:K:93:CYS:SG	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:16:GLU:HG2	4:K:20:ASN:HD22	1.81	0.44
1:M:73:VAL:CG1	1:M:74:GLY:N	2.80	0.44
2:B:200:VAL:O	2:B:200:VAL:HG12	2.17	0.44
2:N:189:SER:HA	2:N:194:HIS:N	2.33	0.44
4:K:31:THR:CG2	4:K:127:PHE:CE2	3.00	0.44
4:D:96:LYS:NZ	4:D:100:ASN:HD21	2.14	0.44
5:X:149:GLU:HG2	5:X:150:THR:N	2.33	0.44
4:K:18:TRP:HE1	4:K:100:ASN:HB2	1.82	0.44
4:K:71:PHE:HE2	4:K:94:ALA:HA	1.81	0.44
4:W:71:PHE:HE2	4:W:94:ALA:HA	1.82	0.44
4:D:115:PHE:CE2	4:D:178:VAL:HG21	2.53	0.44
2:N:67:GLN:NE2	2:N:68:GLU:HB2	2.32	0.44
2:B:188:TRP:CH2	2:B:266:TYR:CE1	2.83	0.44
3:O:48:ILE:CG2	3:O:87:TRP:CD1	3.00	0.44
4:W:25:ILE:HG23	4:W:26:ASN:N	2.32	0.44
5:L:51:GLU:OE1	5:L:56:THR:HA	2.17	0.44
4:Q:16:GLU:HG2	4:Q:20:ASN:HD22	1.82	0.44
5:X:4:GLU:O	5:X:5:TYR:O	2.35	0.44
1:A:186:TYR:CD1	1:A:190:VAL:HG21	2.53	0.44
3:I:3:ILE:CG2	3:I:99:TYR:CE2	2.99	0.44
3:I:72:THR:HG23	3:I:74:LYS:H	1.82	0.44
5:L:145:MET:HE2	5:L:145:MET:HB2	1.92	0.44
5:L:121:ASN:O	5:L:122:LYS:C	2.55	0.44
1:M:132:TYR:HE2	1:M:180:ARG:HA	1.81	0.44
2:B:56:GLU:HB3	4:D:25:ILE:O	2.17	0.44
3:U:11:ARG:HH12	4:W:154:MET:HE1	1.81	0.44
1:A:104:ASP:HA	1:A:108:LYS:HZ3	1.82	0.44
4:Q:25:ILE:HG23	4:Q:26:ASN:N	2.32	0.44
4:E:31:THR:HG21	4:E:127:PHE:CZ	2.52	0.44
1:G:13:GLY:HA3	1:G:41:HIS:CD2	2.53	0.44
4:E:117:LEU:HB2	4:E:176:ILE:O	2.16	0.44
4:P:96:LYS:NZ	4:P:100:ASN:ND2	2.65	0.44
4:P:96:LYS:NZ	4:P:100:ASN:HD21	2.15	0.44
4:Q:11:LYS:HA	4:Q:92:LYS:HB3	1.99	0.44
5:F:77:TYR:HD1	5:F:77:TYR:H	1.64	0.44
1:S:196:TYR:O	4:V:66:ARG:NH2	2.50	0.44
4:K:167:ILE:HD12	4:K:167:ILE:H	1.82	0.44
1:G:196:TYR:O	4:J:66:ARG:NH2	2.49	0.44
3:O:54:ILE:CG2	3:O:55:THR:N	2.80	0.44
2:N:231:TYR:HE2	2:N:251:THR:CA	2.29	0.44
3:I:72:THR:HG22	3:I:75:TYR:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:PHE:CD2	1:A:180:ARG:NH2	2.71	0.44
3:C:114:TYR:HD2	3:C:144:ASN:HB2	1.82	0.44
4:P:118:ILE:CA	4:P:175:GLU:HB3	2.46	0.44
3:U:10:ASP:N	3:U:14:ASN:O	2.50	0.44
5:F:156:THR:HG23	5:F:159:GLU:OE1	2.17	0.44
3:O:131:GLU:HG3	3:O:135:GLN:HB3	2.00	0.44
5:R:88:TYR:HE2	5:R:119:VAL:O	2.00	0.44
2:H:189:SER:HA	2:H:194:HIS:N	2.33	0.44
4:Q:176:ILE:N	4:Q:176:ILE:HD13	2.31	0.44
2:T:265:VAL:HG13	2:T:265:VAL:O	2.17	0.44
1:S:137:GLY:HA2	4:V:188:ILE:CG2	2.31	0.44
4:D:48:ASP:O	4:D:49:PHE:C	2.56	0.44
5:X:77:TYR:HD1	5:X:77:TYR:H	1.64	0.44
3:O:82:THR:HB	3:O:85:GLY:H	1.83	0.44
3:I:99:TYR:H	3:I:99:TYR:HD1	1.66	0.44
4:K:123:PRO:HG2	4:K:124:LEU:H	1.82	0.44
4:D:101:ILE:HG22	4:D:121:GLU:HB2	2.00	0.44
4:P:161:VAL:HA	4:P:177:LYS:O	2.18	0.44
3:U:113:LYS:HB2	3:U:114:TYR:CD1	2.53	0.44
4:D:118:ILE:CA	4:D:175:GLU:HB3	2.46	0.44
1:S:181:LYS:HB3	1:S:214:MET:HE3	2.00	0.44
4:V:29:LEU:C	4:V:29:LEU:HD23	2.37	0.44
4:E:136:LYS:O	4:E:169:ARG:NH1	2.51	0.44
4:P:186:ASP:HB2	5:R:79:ARG:NH2	2.32	0.44
2:T:189:SER:HA	2:T:194:HIS:N	2.33	0.44
2:T:97:ARG:HD3	2:T:100:GLU:OE1	2.18	0.44
4:J:185:LYS:HD2	4:J:185:LYS:C	2.38	0.44
1:S:117:SER:HB3	4:V:191:GLY:H	1.83	0.44
3:C:52:ARG:O	3:C:56:GLN:HG3	2.18	0.44
1:A:8:VAL:HG13	1:A:140:PHE:CD2	2.52	0.44
4:Q:10:LEU:HD21	4:Q:89:VAL:HA	2.00	0.44
4:Q:159:CYS:CB	4:Q:179:LYS:O	2.63	0.44
5:L:149:GLU:HG2	5:L:150:THR:N	2.33	0.44
4:J:129:GLU:O	4:J:131:PRO:CD	2.66	0.44
3:I:83:ALA:HB3	4:K:72:LEU:CD1	2.46	0.44
3:O:120:LEU:HD21	4:W:38:VAL:HG12	1.99	0.44
4:Q:34:TYR:CE2	4:Q:140:TYR:CE2	3.05	0.44
1:G:129:MET:HB2	1:G:143:ILE:CD1	2.47	0.44
4:V:161:VAL:HA	4:V:177:LYS:O	2.18	0.44
4:J:115:PHE:CE2	4:J:178:VAL:HG21	2.53	0.44
4:V:101:ILE:HG22	4:V:121:GLU:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:188:TRP:N	2:T:188:TRP:CD1	2.84	0.44
4:J:101:ILE:O	4:J:101:ILE:HD12	2.18	0.44
1:M:3:ILE:HG21	1:M:6:ILE:HG23	1.99	0.44
3:O:114:TYR:HD2	3:O:144:ASN:HB2	1.82	0.44
4:V:156:GLN:HA	4:V:184:LEU:CD1	2.39	0.44
3:I:48:ILE:CG2	3:I:87:TRP:CD1	3.00	0.44
1:S:50:LEU:HD13	3:U:43:LEU:CD1	2.46	0.44
1:A:50:LEU:HD13	3:C:43:LEU:CD1	2.47	0.44
3:O:10:ASP:N	3:O:14:ASN:O	2.51	0.44
1:S:181:LYS:HB3	1:S:214:MET:CE	2.48	0.44
1:G:104:ASP:HA	1:G:108:LYS:HZ3	1.82	0.44
3:O:72:THR:HG22	3:O:75:TYR:H	1.82	0.44
4:W:66:ARG:O	4:W:69:GLU:HB2	2.18	0.44
4:D:38:VAL:HG11	4:D:140:TYR:HE1	1.74	0.44
5:F:90:VAL:HG13	5:F:129:ARG:NH2	2.33	0.44
5:L:90:VAL:HG13	5:L:129:ARG:NH2	2.33	0.44
4:V:186:ASP:HB2	5:X:79:ARG:NH2	2.32	0.44
2:B:169:MET:HB3	2:B:174:LEU:HD12	1.98	0.44
1:G:38:SER:O	1:G:41:HIS:HB3	2.17	0.44
4:K:79:ARG:O	4:K:80:CYS:C	2.55	0.44
5:R:137:LYS:O	5:R:141:ASP:OD2	2.36	0.44
3:U:83:ALA:HB3	4:W:72:LEU:CD1	2.46	0.44
4:W:155:VAL:O	4:W:155:VAL:CG1	2.64	0.44
4:E:167:ILE:HD12	4:E:167:ILE:H	1.83	0.44
2:T:254:ARG:HG3	2:T:264:THR:HG22	1.99	0.44
3:U:54:ILE:CG2	3:U:55:THR:N	2.81	0.44
2:B:211:ILE:HG21	2:B:268:ILE:HD11	2.00	0.44
1:A:3:ILE:HG21	1:A:6:ILE:HG23	2.00	0.44
1:S:50:LEU:HD22	3:U:43:LEU:CD1	2.48	0.44
4:W:116:SER:CB	4:W:175:GLU:HG3	2.45	0.44
3:C:99:TYR:HD1	3:C:99:TYR:H	1.66	0.44
4:J:25:ILE:HG22	4:J:26:ASN:N	2.32	0.44
3:I:13:CYS:HB3	4:K:188:ILE:HD12	1.99	0.44
4:K:49:PHE:CB	4:K:137:SER:HB3	2.47	0.44
1:S:198:MET:O	1:S:200:MET:N	2.51	0.44
2:N:175:LYS:CG	2:N:176:ILE:N	2.81	0.44
4:J:77:LEU:HB3	4:J:78:PRO:HD2	2.00	0.44
1:S:114:TRP:HH2	4:V:76:ALA:HA	1.83	0.44
2:N:70:ILE:HG22	2:N:74:HIS:HD2	1.79	0.44
1:G:73:VAL:CG1	1:G:74:GLY:N	2.81	0.44
4:V:18:TRP:C	4:V:18:TRP:CD1	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:18:TRP:O	4:J:18:TRP:CD1	2.70	0.44
1:A:133:GLN:O	1:A:133:GLN:HG3	2.18	0.44
4:D:169:ARG:O	4:D:170:GLY:O	2.36	0.44
1:A:190:VAL:CG1	1:A:196:TYR:CE2	3.01	0.44
3:U:82:THR:HB	3:U:85:GLY:H	1.83	0.44
3:U:3:ILE:CG2	3:U:99:TYR:CE2	3.00	0.44
4:E:124:LEU:HD23	4:E:125:ALA:CB	2.48	0.44
4:E:99:LEU:HB2	4:E:101:ILE:CG2	2.45	0.44
2:N:87:LEU:HD12	2:N:87:LEU:O	2.18	0.44
4:E:159:CYS:CB	4:E:179:LYS:O	2.63	0.44
4:J:155:VAL:CG1	4:J:155:VAL:O	2.66	0.44
4:J:156:GLN:HA	4:J:184:LEU:CD1	2.40	0.44
2:B:218:LEU:HB3	2:B:219:THR:H	1.67	0.44
3:U:16:ILE:O	3:U:140:ILE:HG22	2.18	0.44
3:I:140:ILE:CG2	3:I:140:ILE:O	2.63	0.44
2:N:175:LYS:HG2	2:N:176:ILE:H	1.82	0.44
2:H:176:ILE:C	2:H:176:ILE:HD13	2.38	0.44
2:T:176:ILE:HD13	2:T:176:ILE:C	2.38	0.44
2:B:83:PHE:CD1	2:B:83:PHE:C	2.88	0.44
4:Q:31:THR:HG21	4:Q:127:PHE:CZ	2.52	0.44
4:Q:30:PHE:HA	4:W:30:PHE:CD1	2.53	0.44
3:I:110:ILE:HG22	3:I:145:PHE:CE1	2.52	0.44
1:A:117:SER:HB3	4:D:191:GLY:N	2.33	0.44
5:L:66:GLY:O	5:L:70:PHE:HE1	2.01	0.44
2:B:265:VAL:HG13	2:B:265:VAL:O	2.18	0.44
1:A:137:GLY:HA2	4:D:188:ILE:CG2	2.28	0.43
4:Q:105:ILE:HD12	4:Q:115:PHE:CE1	2.53	0.43
4:Q:178:VAL:O	4:Q:178:VAL:HG12	2.18	0.43
3:I:88:PHE:CZ	3:I:107:TYR:HB2	2.53	0.43
4:K:124:LEU:HD23	4:K:125:ALA:HB2	1.99	0.43
4:E:64:GLY:HA2	4:E:147:VAL:HG13	2.00	0.43
3:C:72:THR:HG23	3:C:74:LYS:H	1.82	0.43
1:G:107:PHE:CD2	1:G:180:ARG:NH2	2.73	0.43
4:J:101:ILE:HG22	4:J:121:GLU:HB2	2.00	0.43
4:K:159:CYS:CB	4:K:179:LYS:O	2.62	0.43
3:O:3:ILE:CG2	3:O:99:TYR:CE2	3.01	0.43
4:Q:65:CYS:O	4:Q:68:ILE:HG22	2.17	0.43
4:K:134:ALA:O	4:K:137:SER:N	2.46	0.43
3:O:72:THR:HG23	3:O:74:LYS:H	1.82	0.43
2:T:168:LYS:O	2:T:170:ARG:N	2.51	0.43
5:L:13:LEU:HD21	5:L:25:LEU:CD2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ASN:HB3	1:A:25:GLU:HG2	2.00	0.43
4:E:16:GLU:HG2	4:E:20:ASN:ND2	2.33	0.43
2:B:167:THR:C	2:B:169:MET:H	2.20	0.43
3:I:93:ASP:O	3:I:93:ASP:CG	2.56	0.43
4:V:28:GLU:O	4:V:31:THR:HG22	2.17	0.43
4:P:18:TRP:CD1	4:P:18:TRP:C	2.91	0.43
2:H:247:PRO:HB2	2:H:271:ASP:OD1	2.18	0.43
4:Q:41:LEU:HD22	4:Q:55:HIS:CD2	2.53	0.43
4:V:169:ARG:O	4:V:170:GLY:O	2.36	0.43
5:X:72:THR:HG23	5:X:73:ILE:N	2.33	0.43
5:R:169:ILE:O	5:R:172:SER:HB2	2.18	0.43
1:G:186:TYR:CD1	1:G:190:VAL:HG21	2.53	0.43
2:B:254:ARG:HG3	2:B:264:THR:HG22	1.98	0.43
1:G:129:MET:CE	1:G:143:ILE:HD11	2.48	0.43
4:V:162:TRP:O	4:V:176:ILE:HG23	2.18	0.43
4:V:180:LEU:HD12	4:V:180:LEU:N	2.13	0.43
2:H:237:ILE:HG22	2:H:250:VAL:HG21	1.98	0.43
1:M:20:ASN:ND2	1:M:33:TYR:OH	2.47	0.43
4:V:118:ILE:CA	4:V:175:GLU:HB3	2.46	0.43
1:G:50:LEU:HD22	3:I:43:LEU:CD1	2.48	0.43
4:W:159:CYS:CB	4:W:179:LYS:O	2.62	0.43
3:U:155:PRO:CG	3:U:156:MET:N	2.81	0.43
2:B:176:ILE:HD13	2:B:176:ILE:C	2.37	0.43
4:V:77:LEU:HB3	4:V:78:PRO:HD2	2.01	0.43
4:D:143:ILE:HG23	4:D:144:LEU:N	2.33	0.43
4:J:143:ILE:HG23	4:J:144:LEU:N	2.32	0.43
5:X:148:LEU:HD12	5:X:148:LEU:N	2.33	0.43
5:R:12:LEU:HG	5:R:12:LEU:O	2.18	0.43
4:V:48:ASP:O	4:V:49:PHE:C	2.56	0.43
3:O:77:VAL:O	3:O:78:HIS:C	2.56	0.43
3:U:82:THR:HB	3:U:85:GLY:N	2.32	0.43
4:K:90:LEU:O	4:K:94:ALA:HB3	2.19	0.43
5:L:169:ILE:O	5:L:172:SER:HB2	2.18	0.43
4:P:101:ILE:HG22	4:P:121:GLU:HB2	2.00	0.43
2:T:87:LEU:O	2:T:87:LEU:HD12	2.17	0.43
4:K:61:TYR:HD2	4:K:61:TYR:O	2.01	0.43
1:S:197:SER:O	1:S:198:MET:O	2.36	0.43
4:W:136:LYS:O	4:W:169:ARG:NH1	2.51	0.43
3:I:154:ALA:HB3	3:I:155:PRO:CD	2.48	0.43
1:M:133:GLN:HG3	1:M:133:GLN:O	2.19	0.43
5:L:77:TYR:HD1	5:L:77:TYR:H	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:169:ARG:O	4:P:170:GLY:O	2.36	0.43
4:J:136:LYS:C	4:J:169:ARG:NH1	2.72	0.43
3:C:82:THR:HB	3:C:85:GLY:N	2.33	0.43
4:Q:99:LEU:HB2	4:Q:101:ILE:CG2	2.46	0.43
3:C:72:THR:HG21	3:C:75:TYR:CE2	2.54	0.43
1:S:107:PHE:CD2	1:S:180:ARG:NH2	2.73	0.43
4:V:101:ILE:HD12	4:V:101:ILE:O	2.19	0.43
4:W:104:ASN:O	4:W:105:ILE:HD13	2.18	0.43
3:C:3:ILE:CG2	3:C:99:TYR:CE2	3.01	0.43
2:N:83:PHE:CD1	2:N:83:PHE:C	2.88	0.43
2:T:255:MET:C	2:T:255:MET:SD	2.97	0.43
5:X:90:VAL:HG13	5:X:129:ARG:NH2	2.34	0.43
2:B:70:ILE:HG22	2:B:74:HIS:HD2	1.79	0.43
2:N:194:HIS:O	2:N:195:VAL:C	2.56	0.43
1:M:35:ILE:O	1:M:38:SER:HB2	2.18	0.43
4:J:188:ILE:HA	4:J:189:PRO:HD3	1.76	0.43
3:I:88:PHE:O	3:I:103:LEU:CD2	2.60	0.43
4:W:95:PHE:CD1	4:W:103:PRO:HD3	2.54	0.43
4:W:124:LEU:HD23	4:W:125:ALA:CB	2.48	0.43
2:N:262:GLN:O	2:N:263:ARG:C	2.56	0.43
4:E:18:TRP:HE1	4:E:100:ASN:HB2	1.82	0.43
4:Q:64:GLY:HA2	4:Q:147:VAL:HG13	2.01	0.43
2:B:64:PHE:CD1	4:D:67:LEU:HD13	2.53	0.43
4:V:67:LEU:HD11	4:V:98:PHE:CD2	2.53	0.43
3:U:44:LEU:HD23	3:U:44:LEU:C	2.39	0.43
2:H:56:GLU:HB3	4:J:25:ILE:O	2.19	0.43
1:S:75:MET:HA	1:S:217:ASN:CB	2.48	0.43
3:U:13:CYS:HB3	4:W:188:ILE:HD12	2.00	0.43
3:I:16:ILE:O	3:I:140:ILE:HG22	2.18	0.43
5:R:156:THR:HG23	5:R:159:GLU:OE1	2.18	0.43
4:J:29:LEU:HD23	4:J:29:LEU:C	2.38	0.43
2:N:167:THR:C	2:N:169:MET:H	2.21	0.43
4:E:116:SER:CB	4:E:175:GLU:HG3	2.47	0.43
2:H:200:VAL:O	2:H:200:VAL:HG12	2.18	0.43
2:B:97:ARG:HD3	2:B:100:GLU:OE1	2.18	0.43
4:W:117:LEU:HB2	4:W:176:ILE:O	2.18	0.43
4:J:18:TRP:C	4:J:18:TRP:CD1	2.91	0.43
5:L:143:ASN:O	5:L:144:LYS:HB2	2.17	0.43
4:P:185:LYS:C	4:P:185:LYS:HD2	2.38	0.43
4:D:185:LYS:C	4:D:185:LYS:HD2	2.38	0.43
1:M:8:VAL:HG13	1:M:140:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:8:VAL:HG13	1:S:140:PHE:CD2	2.54	0.43
4:P:137:SER:N	4:P:169:ARG:HH12	2.16	0.43
4:P:48:ASP:O	4:P:49:PHE:C	2.57	0.43
4:K:155:VAL:O	4:K:155:VAL:CG1	2.64	0.43
3:O:82:THR:HG22	3:O:83:ALA:H	1.83	0.43
3:U:77:VAL:O	3:U:78:HIS:C	2.56	0.43
1:S:186:TYR:CD1	1:S:190:VAL:HG21	2.53	0.43
1:S:190:VAL:CG1	1:S:196:TYR:CE2	3.02	0.43
2:B:262:GLN:O	2:B:263:ARG:C	2.55	0.43
4:P:162:TRP:O	4:P:176:ILE:HG23	2.19	0.43
2:B:184:HIS:CB	2:B:211:ILE:HD13	2.48	0.43
2:N:218:LEU:O	2:N:220:GLN:N	2.45	0.43
4:D:17:ILE:HD13	4:D:17:ILE:HA	1.81	0.43
4:W:105:ILE:HD12	4:W:115:PHE:CE1	2.54	0.43
4:E:41:LEU:CB	4:E:52:VAL:HG13	2.49	0.43
1:M:75:MET:HA	1:M:217:ASN:CB	2.48	0.43
4:D:130:LEU:HD23	4:D:168:LEU:HB3	2.00	0.43
4:D:18:TRP:C	4:D:18:TRP:CD1	2.91	0.43
3:C:63:VAL:O	3:C:64:LYS:HB2	2.17	0.43
2:T:247:PRO:HB2	2:T:271:ASP:OD1	2.18	0.43
4:J:48:ASP:O	4:J:49:PHE:C	2.56	0.43
3:U:88:PHE:O	3:U:103:LEU:CD2	2.60	0.43
4:K:64:GLY:HA2	4:K:147:VAL:HG13	2.01	0.43
3:U:72:THR:HG21	3:U:75:TYR:CE2	2.52	0.43
2:N:84:GLU:OE1	2:N:231:TYR:CE1	2.71	0.43
1:A:124:THR:HG21	3:C:55:THR:HG21	2.01	0.43
2:H:67:GLN:NE2	2:H:68:GLU:HB2	2.34	0.43
4:P:22:THR:HG22	4:P:22:THR:O	2.18	0.43
4:E:178:VAL:O	4:E:178:VAL:HG12	2.18	0.43
4:D:156:GLN:HA	4:D:184:LEU:CD1	2.40	0.43
1:G:50:LEU:HD13	3:I:43:LEU:CD1	2.46	0.43
4:J:38:VAL:HG11	4:J:140:TYR:CD1	2.52	0.43
4:D:38:VAL:HG11	4:D:140:TYR:CD1	2.53	0.43
2:T:175:LYS:CG	2:T:176:ILE:H	2.32	0.43
3:U:105:TYR:CE2	3:U:152:PHE:CE1	3.06	0.43
1:G:181:LYS:HD3	1:G:214:MET:CE	2.49	0.43
1:M:38:SER:CB	5:R:45:PHE:CE1	3.02	0.43
2:T:72:GLN:HE21	2:T:72:GLN:HB3	1.56	0.43
4:V:185:LYS:O	4:V:185:LYS:HD2	2.18	0.43
3:C:82:THR:HB	3:C:85:GLY:H	1.84	0.43
4:K:95:PHE:CD1	4:K:103:PRO:HD3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:167:ILE:H	4:W:167:ILE:HD12	1.83	0.43
2:N:211:ILE:HG22	2:N:268:ILE:HD11	1.99	0.43
2:B:84:GLU:OE1	2:B:231:TYR:CE1	2.71	0.43
1:G:7:LEU:HD12	1:G:141:VAL:CB	2.45	0.43
4:P:67:LEU:HD11	4:P:98:PHE:CD2	2.52	0.43
2:T:67:GLN:NE2	2:T:68:GLU:HB2	2.34	0.43
2:T:184:HIS:CB	2:T:211:ILE:HD13	2.47	0.43
2:T:218:LEU:HD21	2:T:232:PHE:HE2	1.83	0.43
4:K:178:VAL:O	4:K:178:VAL:HG12	2.18	0.43
1:M:50:LEU:HD22	3:O:43:LEU:CD1	2.49	0.43
1:S:50:LEU:CB	3:U:43:LEU:HD11	2.42	0.43
4:V:25:ILE:HG22	4:V:26:ASN:N	2.32	0.43
3:O:21:TRP:HH2	3:O:155:PRO:O	2.00	0.43
2:N:99:LEU:N	2:N:99:LEU:HD12	2.31	0.43
4:V:77:LEU:HD22	4:V:78:PRO:CD	2.47	0.43
2:H:185:GLY:HA2	2:H:195:VAL:HG13	2.00	0.43
4:V:130:LEU:HD23	4:V:168:LEU:HB3	2.00	0.43
3:O:63:VAL:O	3:O:64:LYS:HB2	2.18	0.43
3:I:63:VAL:O	3:I:64:LYS:HB2	2.19	0.43
4:P:129:GLU:OE1	4:P:129:GLU:HA	2.19	0.43
5:R:43:VAL:CG2	5:R:43:VAL:O	2.67	0.43
4:Q:41:LEU:CB	4:Q:52:VAL:HG13	2.49	0.43
4:V:136:LYS:C	4:V:169:ARG:NH1	2.73	0.43
4:W:124:LEU:HD13	4:W:141:SER:HB3	2.01	0.43
4:Q:124:LEU:HD23	4:Q:125:ALA:CB	2.49	0.43
4:Q:167:ILE:H	4:Q:167:ILE:HD12	1.84	0.43
2:H:231:TYR:HE2	2:H:252:ALA:H	1.66	0.43
4:P:145:CYS:SG	4:P:176:ILE:HD13	2.59	0.43
1:A:200:MET:CE	5:F:7:TYR:CA	2.92	0.43
2:N:218:LEU:HD21	2:N:232:PHE:HE2	1.84	0.43
4:P:17:ILE:HA	4:P:17:ILE:HD13	1.81	0.43
1:A:132:TYR:HE2	1:A:180:ARG:HA	1.83	0.43
4:K:105:ILE:HD12	4:K:115:PHE:CE1	2.54	0.43
1:S:200:MET:O	1:S:201:PRO:C	2.57	0.43
5:L:28:PHE:O	5:L:28:PHE:CD1	2.72	0.43
4:J:77:LEU:HD22	4:J:78:PRO:CD	2.46	0.43
2:H:255:MET:C	2:H:255:MET:SD	2.97	0.43
5:R:51:GLU:OE1	5:R:56:THR:HA	2.19	0.43
1:M:23:ASN:HB3	1:M:25:GLU:HG2	2.01	0.43
1:M:38:SER:O	1:M:41:HIS:HB3	2.18	0.43
2:N:247:PRO:O	2:N:271:ASP:OD2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:188:ILE:HA	4:V:189:PRO:HD3	1.77	0.43
4:W:36:SER:O	4:W:40:GLN:N	2.46	0.43
1:G:190:VAL:CG1	1:G:196:TYR:CE2	3.02	0.43
4:P:101:ILE:O	4:P:101:ILE:HD12	2.19	0.43
2:T:64:PHE:CD1	4:V:67:LEU:HD13	2.54	0.43
1:A:197:SER:O	1:A:198:MET:O	2.36	0.43
4:K:10:LEU:HD21	4:K:89:VAL:HA	2.00	0.43
1:G:75:MET:HA	1:G:217:ASN:CB	2.48	0.43
4:E:61:TYR:O	4:E:61:TYR:HD2	2.02	0.43
4:W:65:CYS:O	4:W:68:ILE:HG22	2.19	0.43
3:O:72:THR:HG21	3:O:75:TYR:CD2	2.54	0.43
4:V:38:VAL:HG11	4:V:140:TYR:CD1	2.52	0.43
1:A:114:TRP:HH2	4:D:76:ALA:HA	1.83	0.43
2:N:74:HIS:CE1	2:N:83:PHE:CE2	3.07	0.43
4:P:143:ILE:HG23	4:P:144:LEU:N	2.34	0.43
3:O:105:TYR:HE1	3:O:109:HIS:HD1	1.53	0.43
2:T:194:HIS:O	2:T:195:VAL:C	2.57	0.43
2:H:194:HIS:O	2:H:195:VAL:C	2.57	0.43
4:D:28:GLU:O	4:D:31:THR:HG22	2.18	0.43
5:L:62:TRP:N	5:L:62:TRP:CD1	2.87	0.42
4:D:136:LYS:C	4:D:169:ARG:NH1	2.72	0.42
5:R:149:GLU:HG2	5:R:150:THR:H	1.83	0.42
5:X:62:TRP:CD1	5:X:62:TRP:N	2.86	0.42
3:U:107:TYR:HE2	4:W:73:ALA:CA	2.22	0.42
4:E:34:TYR:OH	4:E:140:TYR:O	2.17	0.42
3:I:72:THR:HG21	3:I:75:TYR:CE2	2.53	0.42
4:V:111:ASN:ND2	4:V:113:ASP:OD2	2.39	0.42
2:B:250:VAL:HG12	2:B:266:TYR:HB3	2.00	0.42
2:B:211:ILE:HG22	2:B:268:ILE:HD11	2.00	0.42
3:I:113:LYS:HB2	3:I:114:TYR:CD1	2.54	0.42
1:A:129:MET:HB2	1:A:143:ILE:CD1	2.48	0.42
4:E:105:ILE:HD12	4:E:115:PHE:CE1	2.53	0.42
2:H:218:LEU:HD21	2:H:232:PHE:HE2	1.84	0.42
1:G:198:MET:O	1:G:200:MET:N	2.52	0.42
3:C:16:ILE:O	3:C:140:ILE:HG22	2.19	0.42
4:K:41:LEU:CB	4:K:52:VAL:HG13	2.49	0.42
4:K:36:SER:O	4:K:40:GLN:N	2.46	0.42
2:H:167:THR:C	2:H:169:MET:H	2.22	0.42
4:D:186:ASP:HB2	5:F:79:ARG:NH2	2.33	0.42
1:G:23:ASN:HB3	1:G:25:GLU:HG2	2.00	0.42
5:X:51:GLU:OE1	5:X:56:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:97:ARG:HD3	2:N:100:GLU:OE1	2.18	0.42
4:J:28:GLU:O	4:J:31:THR:HG22	2.18	0.42
5:X:119:VAL:HG12	5:X:120:GLY:N	2.34	0.42
5:F:82:HIS:CB	5:F:169:ILE:HD13	2.49	0.42
4:W:34:TYR:OH	4:W:140:TYR:O	2.18	0.42
3:U:72:THR:HG21	3:U:75:TYR:CD2	2.54	0.42
4:E:95:PHE:CD1	4:E:103:PRO:HD3	2.54	0.42
1:S:3:ILE:HG21	1:S:6:ILE:HG23	2.01	0.42
1:A:131:ILE:HG13	1:A:141:VAL:HG22	2.02	0.42
4:E:10:LEU:HD21	4:E:89:VAL:HA	2.01	0.42
1:G:200:MET:HE1	5:L:7:TYR:CA	2.48	0.42
1:M:50:LEU:CD1	3:O:43:LEU:HD11	2.47	0.42
3:I:10:ASP:N	3:I:14:ASN:O	2.51	0.42
2:H:191:LEU:HD12	2:H:192:PHE:HE1	1.84	0.42
4:E:134:ALA:O	4:E:137:SER:N	2.47	0.42
4:E:49:PHE:CB	4:E:137:SER:HB3	2.49	0.42
2:N:255:MET:SD	2:N:255:MET:C	2.98	0.42
4:V:143:ILE:HG23	4:V:144:LEU:N	2.33	0.42
4:D:65:CYS:HA	4:D:154:MET:HG3	2.01	0.42
1:A:73:VAL:CG1	1:A:74:GLY:N	2.82	0.42
1:M:13:GLY:HA3	1:M:41:HIS:CD2	2.54	0.42
2:T:247:PRO:O	2:T:271:ASP:OD2	2.36	0.42
5:R:72:THR:HG23	5:R:73:ILE:N	2.34	0.42
4:V:129:GLU:O	4:V:131:PRO:CD	2.67	0.42
2:H:262:GLN:O	2:H:263:ARG:C	2.56	0.42
4:Q:124:LEU:CD2	4:Q:124:LEU:C	2.87	0.42
2:H:250:VAL:HG12	2:H:266:TYR:HB3	2.00	0.42
4:V:155:VAL:O	4:V:155:VAL:CG1	2.68	0.42
3:C:113:LYS:HB2	3:C:114:TYR:CD1	2.54	0.42
4:J:118:ILE:CA	4:J:175:GLU:HB3	2.47	0.42
3:O:44:LEU:C	3:O:44:LEU:HD23	2.38	0.42
4:W:10:LEU:HD21	4:W:89:VAL:HA	2.00	0.42
5:R:28:PHE:CD1	5:R:28:PHE:O	2.71	0.42
4:J:125:ALA:HB2	4:J:140:TYR:CE2	2.54	0.42
5:L:53:ASP:C	5:L:55:LYS:N	2.72	0.42
2:B:255:MET:SD	2:B:255:MET:C	2.98	0.42
1:A:185:LEU:HD11	1:A:210:LYS:HD3	2.00	0.42
5:F:51:GLU:OE1	5:F:56:THR:HA	2.19	0.42
1:A:38:SER:O	1:A:41:HIS:HB3	2.18	0.42
2:B:185:GLY:HA2	2:B:195:VAL:HG13	2.01	0.42
4:P:28:GLU:O	4:P:31:THR:HG22	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:247:PRO:HB2	2:N:271:ASP:OD1	2.19	0.42
4:D:188:ILE:O	4:D:188:ILE:HG13	2.18	0.42
4:W:36:SER:O	4:W:40:GLN:CB	2.61	0.42
5:F:149:GLU:HG2	5:F:150:THR:H	1.84	0.42
1:M:190:VAL:CG1	1:M:196:TYR:CE2	3.02	0.42
5:X:169:ILE:O	5:X:172:SER:HB2	2.19	0.42
1:S:120:ARG:HD2	3:U:73:GLY:HA2	2.00	0.42
4:Q:94:ALA:CB	6:Q:194:PLM:H91	2.43	0.42
3:I:114:TYR:HB3	3:I:142:ASN:OD1	2.19	0.42
1:A:20:ASN:ND2	1:A:33:TYR:OH	2.48	0.42
3:O:113:LYS:HB2	3:O:114:TYR:CD1	2.55	0.42
4:P:155:VAL:O	4:P:155:VAL:CG1	2.67	0.42
4:K:104:ASN:O	4:K:105:ILE:HD13	2.19	0.42
4:E:134:ALA:C	4:E:136:LYS:N	2.73	0.42
2:B:99:LEU:HD22	2:B:243:ASN:ND2	2.26	0.42
2:B:175:LYS:CG	2:B:176:ILE:H	2.31	0.42
4:J:33:THR:O	4:J:36:SER:HB3	2.19	0.42
4:P:33:THR:O	4:P:36:SER:HB3	2.19	0.42
4:W:26:ASN:ND2	4:W:28:GLU:H	2.17	0.42
4:P:130:LEU:HD23	4:P:168:LEU:HB3	2.00	0.42
4:J:188:ILE:O	4:J:188:ILE:HG13	2.18	0.42
5:X:149:GLU:HG2	5:X:150:THR:H	1.83	0.42
3:C:77:VAL:O	3:C:78:HIS:C	2.57	0.42
3:C:82:THR:HG22	3:C:83:ALA:H	1.83	0.42
4:J:67:LEU:HD11	4:J:98:PHE:CD2	2.54	0.42
1:M:107:PHE:CD2	1:M:180:ARG:NH2	2.72	0.42
1:M:198:MET:O	1:M:200:MET:N	2.52	0.42
1:S:29:ASN:O	1:S:32:GLU:HG3	2.18	0.42
4:Q:30:PHE:CD1	4:W:30:PHE:HA	2.54	0.42
1:G:117:SER:HB3	4:J:191:GLY:N	2.35	0.42
4:Q:79:ARG:O	4:Q:80:CYS:C	2.56	0.42
3:O:119:LEU:CD2	3:O:119:LEU:N	2.61	0.42
5:R:43:VAL:CG2	5:R:77:TYR:HE2	2.32	0.42
5:F:72:THR:HG23	5:F:73:ILE:N	2.34	0.42
5:R:149:GLU:HG2	5:R:150:THR:N	2.33	0.42
5:R:150:THR:OG1	5:R:158:VAL:CG2	2.68	0.42
5:R:82:HIS:CB	5:R:169:ILE:HD13	2.50	0.42
4:K:124:LEU:HD13	4:K:141:SER:HB3	2.02	0.42
1:A:21:PHE:HZ	1:A:215:VAL:HG11	1.80	0.42
4:V:22:THR:O	4:V:22:THR:HG22	2.19	0.42
4:E:114:THR:OG1	4:E:179:LYS:CB	2.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:156:GLN:HB3	4:D:184:LEU:HB2	2.02	0.42
3:I:133:ARG:H	3:I:133:ARG:CD	2.13	0.42
5:X:28:PHE:CD1	5:X:28:PHE:O	2.72	0.42
4:K:66:ARG:O	4:K:69:GLU:HB2	2.19	0.42
1:A:29:ASN:O	1:A:32:GLU:HG3	2.18	0.42
4:V:33:THR:O	4:V:36:SER:HB3	2.20	0.42
2:H:167:THR:HG22	2:H:167:THR:O	2.18	0.42
2:N:168:LYS:C	2:N:170:ARG:H	2.22	0.42
5:X:13:LEU:HD21	5:X:25:LEU:CD1	2.50	0.42
5:R:13:LEU:HD21	5:R:25:LEU:CD2	2.49	0.42
2:B:74:HIS:CE1	2:B:83:PHE:CE2	3.08	0.42
1:S:23:ASN:HB3	1:S:25:GLU:HG2	2.01	0.42
4:J:130:LEU:HD23	4:J:168:LEU:HB3	2.00	0.42
2:N:241:LEU:HD12	2:N:248:CYS:CB	2.49	0.42
1:G:9:ILE:HG12	1:G:37:ALA:HB1	2.00	0.42
4:P:136:LYS:C	4:P:169:ARG:NH1	2.73	0.42
5:F:149:GLU:HG2	5:F:150:THR:N	2.33	0.42
5:X:66:GLY:O	5:X:70:PHE:HE1	2.03	0.42
3:U:77:VAL:O	3:U:77:VAL:CG2	2.60	0.42
1:S:10:ASN:ND2	1:S:12:SER:N	2.62	0.42
4:E:94:ALA:CB	6:E:194:PLM:H91	2.43	0.42
1:S:28:LEU:CB	1:S:33:TYR:CE1	3.01	0.42
2:T:211:ILE:HG21	2:T:268:ILE:HD11	1.99	0.42
1:M:4:GLU:CG	1:M:143:ILE:HG22	2.44	0.42
4:Q:32:LEU:CD2	3:U:117:ASN:HA	2.49	0.42
2:H:73:LEU:HD11	2:H:86:LYS:HD3	2.01	0.42
2:T:192:PHE:HB3	2:T:217:THR:OG1	2.20	0.42
5:X:93:GLN:HG3	5:X:131:VAL:HG13	2.02	0.42
1:M:114:TRP:HH2	4:P:76:ALA:HA	1.84	0.42
2:B:169:MET:HB3	2:B:174:LEU:CD1	2.50	0.42
2:N:185:GLY:HA2	2:N:195:VAL:HG13	2.02	0.42
2:H:72:GLN:HB3	2:H:72:GLN:HE21	1.58	0.42
4:J:185:LYS:HD2	4:J:185:LYS:O	2.19	0.42
4:P:185:LYS:HD2	4:P:185:LYS:O	2.19	0.42
5:F:143:ASN:O	5:F:144:LYS:HB2	2.19	0.42
5:X:143:ASN:O	5:X:144:LYS:HB2	2.19	0.42
5:F:119:VAL:HG12	5:F:120:GLY:N	2.34	0.42
5:F:62:TRP:N	5:F:62:TRP:CD1	2.87	0.42
3:I:107:TYR:HE2	4:K:73:ALA:CA	2.23	0.42
2:N:254:ARG:HG3	2:N:264:THR:HG22	2.00	0.42
1:S:44:PHE:HD1	1:S:119:LEU:HB3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:LYS:O	1:A:194:PRO:HD3	2.20	0.42
4:J:111:ASN:ND2	4:J:113:ASP:OD2	2.39	0.42
1:A:198:MET:O	1:A:200:MET:N	2.52	0.42
4:Q:61:TYR:HD2	4:Q:61:TYR:O	2.03	0.42
1:A:75:MET:HA	1:A:217:ASN:CB	2.49	0.42
3:C:21:TRP:HH2	3:C:155:PRO:O	2.02	0.42
2:H:180:LEU:HA	2:H:180:LEU:HD12	1.82	0.42
5:F:13:LEU:HD21	5:F:25:LEU:CD2	2.49	0.42
2:H:74:HIS:CE1	2:H:83:PHE:CE2	3.08	0.42
2:T:74:HIS:CE1	2:T:83:PHE:CE2	3.08	0.42
4:V:65:CYS:HA	4:V:154:MET:HG3	2.01	0.42
2:B:247:PRO:O	2:B:271:ASP:OD2	2.38	0.42
2:N:265:VAL:O	2:N:265:VAL:HG13	2.19	0.42
5:L:43:VAL:CG2	5:L:77:TYR:HE2	2.33	0.42
1:S:133:GLN:O	1:S:133:GLN:HG3	2.20	0.42
4:D:133:ASP:HA	4:Q:110:HIS:HA	2.01	0.42
5:L:119:VAL:HG12	5:L:120:GLY:N	2.35	0.42
5:L:150:THR:OG1	5:L:158:VAL:CG2	2.68	0.42
3:U:5:SER:O	3:U:90:LEU:HD12	2.20	0.42
4:Q:95:PHE:CD1	4:Q:103:PRO:HD3	2.55	0.42
2:H:184:HIS:CB	2:H:211:ILE:HD13	2.49	0.42
4:P:180:LEU:O	4:P:181:ASN:C	2.58	0.42
2:N:73:LEU:HD11	2:N:86:LYS:HD3	2.01	0.42
1:M:44:PHE:CD1	1:M:131:ILE:HG21	2.55	0.42
3:C:114:TYR:HB3	3:C:142:ASN:OD1	2.19	0.42
1:G:200:MET:CE	5:L:7:TYR:CA	2.91	0.42
3:U:133:ARG:H	3:U:133:ARG:CD	2.14	0.42
5:L:93:GLN:HG3	5:L:131:VAL:HG13	2.02	0.42
4:Q:49:PHE:CB	4:Q:137:SER:HB3	2.50	0.42
4:D:125:ALA:HB2	4:D:140:TYR:CD2	2.55	0.42
2:H:175:LYS:CG	2:H:176:ILE:N	2.83	0.42
2:T:180:LEU:HA	2:T:180:LEU:HD12	1.81	0.42
4:K:116:SER:CB	4:K:175:GLU:HG3	2.47	0.42
1:M:128:THR:HG22	1:M:130:PHE:CE2	2.54	0.42
4:W:16:GLU:HG2	4:W:20:ASN:HD22	1.83	0.42
2:N:241:LEU:HD12	2:N:248:CYS:HB3	2.02	0.42
1:M:117:SER:HB3	4:P:191:GLY:N	2.34	0.42
2:H:271:ASP:OD2	2:H:271:ASP:N	2.53	0.42
4:E:79:ARG:O	4:E:80:CYS:C	2.57	0.42
4:P:32:LEU:HA	4:P:32:LEU:HD23	1.80	0.42
5:L:158:VAL:O	5:L:161:ALA:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:186:TYR:CD1	1:M:190:VAL:HG21	2.55	0.42
1:A:120:ARG:HD2	3:C:73:GLY:HA2	2.00	0.42
2:B:58:SER:HB3	4:D:98:PHE:HA	2.02	0.42
4:D:101:ILE:O	4:D:101:ILE:HD12	2.19	0.42
4:J:119:LEU:CD1	4:J:120:ASP:N	2.77	0.42
3:U:114:TYR:HB3	3:U:142:ASN:OD1	2.20	0.42
4:D:22:THR:O	4:D:22:THR:HG22	2.20	0.42
2:B:218:LEU:HD21	2:B:232:PHE:HE2	1.84	0.42
3:U:123:TYR:N	3:U:123:TYR:CD1	2.86	0.42
4:E:49:PHE:CD1	4:E:134:ALA:HA	2.55	0.42
2:N:191:LEU:HD12	2:N:192:PHE:HE1	1.85	0.42
3:O:155:PRO:HG2	3:O:156:MET:N	2.25	0.42
2:N:180:LEU:HA	2:N:180:LEU:HD12	1.82	0.42
4:J:125:ALA:HB2	4:J:140:TYR:CD2	2.54	0.42
4:D:125:ALA:HB2	4:D:140:TYR:CE2	2.55	0.42
4:J:143:ILE:CG2	4:J:144:LEU:N	2.83	0.42
4:D:129:GLU:OE1	4:D:129:GLU:HA	2.20	0.41
5:F:66:GLY:O	5:F:70:PHE:HE1	2.03	0.41
5:X:43:VAL:CG2	5:X:77:TYR:HE2	2.32	0.41
4:K:124:LEU:HD23	4:K:125:ALA:CB	2.50	0.41
4:W:99:LEU:HB2	4:W:101:ILE:CG2	2.45	0.41
4:Q:124:LEU:HD13	4:Q:141:SER:HB3	2.02	0.41
1:A:52:PRO:O	1:A:54:ALA:N	2.53	0.41
1:A:31:ASN:O	1:A:34:LEU:HB2	2.20	0.41
1:M:192:LYS:O	1:M:194:PRO:HD3	2.21	0.41
1:M:31:ASN:O	1:M:34:LEU:HB2	2.20	0.41
2:H:211:ILE:HG21	2:H:268:ILE:HD11	2.00	0.41
4:D:119:LEU:CD1	4:D:120:ASP:N	2.77	0.41
4:D:93:CYS:O	4:D:97:ILE:CG1	2.59	0.41
3:U:16:ILE:O	3:U:140:ILE:CG2	2.68	0.41
4:K:134:ALA:C	4:K:136:LYS:N	2.72	0.41
4:P:125:ALA:HB2	4:P:140:TYR:CD2	2.55	0.41
3:C:129:GLU:HB2	3:C:135:GLN:CD	2.41	0.41
5:X:53:ASP:C	5:X:55:LYS:N	2.73	0.41
1:G:128:THR:HG22	1:G:130:PHE:CE2	2.55	0.41
2:H:247:PRO:O	2:H:271:ASP:OD2	2.37	0.41
5:L:62:TRP:O	5:L:64:THR:N	2.45	0.41
5:F:43:VAL:CG2	5:F:43:VAL:O	2.68	0.41
5:F:12:LEU:CB	5:F:62:TRP:HB2	2.48	0.41
5:F:43:VAL:CG2	5:F:77:TYR:HE2	2.33	0.41
5:X:88:TYR:CD1	5:X:96:PHE:HD1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:149:GLU:HG2	5:L:150:THR:H	1.84	0.41
3:I:77:VAL:O	3:I:78:HIS:C	2.58	0.41
3:I:5:SER:O	3:I:90:LEU:HD12	2.21	0.41
3:U:82:THR:CG2	3:U:83:ALA:N	2.82	0.41
5:X:82:HIS:CB	5:X:169:ILE:HD13	2.50	0.41
1:G:14:GLY:N	5:L:10:LYS:HZ3	2.17	0.41
4:W:90:LEU:O	4:W:94:ALA:HB3	2.20	0.41
2:T:262:GLN:O	2:T:263:ARG:C	2.57	0.41
1:G:44:PHE:CD1	1:G:131:ILE:HG21	2.55	0.41
4:J:17:ILE:HA	4:J:17:ILE:HD13	1.82	0.41
4:V:115:PHE:CE2	4:V:178:VAL:HG21	2.55	0.41
2:N:64:PHE:CD1	4:P:67:LEU:HD13	2.54	0.41
4:J:180:LEU:N	4:J:180:LEU:HD12	2.14	0.41
1:S:192:LYS:O	1:S:194:PRO:HD3	2.19	0.41
1:G:200:MET:O	1:G:201:PRO:C	2.58	0.41
1:G:50:LEU:CB	3:I:43:LEU:HD11	2.44	0.41
2:B:191:LEU:HD12	2:B:192:PHE:HE1	1.86	0.41
1:M:75:MET:CE	1:M:181:LYS:NZ	2.83	0.41
4:E:16:GLU:HG2	4:E:20:ASN:HD22	1.84	0.41
4:D:132:MET:HB2	4:Q:109:SER:HA	2.02	0.41
5:R:62:TRP:N	5:R:62:TRP:CD1	2.87	0.41
4:W:41:LEU:CB	4:W:52:VAL:HG13	2.50	0.41
5:X:158:VAL:O	5:X:161:ALA:HB3	2.20	0.41
3:U:88:PHE:CZ	3:U:107:TYR:HB2	2.55	0.41
2:N:250:VAL:HG12	2:N:266:TYR:HB3	2.01	0.41
4:J:180:LEU:O	4:J:181:ASN:C	2.59	0.41
3:O:114:TYR:HB3	3:O:142:ASN:OD1	2.19	0.41
3:C:44:LEU:HD23	3:C:44:LEU:C	2.39	0.41
4:E:65:CYS:O	4:E:68:ILE:HG22	2.20	0.41
4:P:93:CYS:O	4:P:97:ILE:CG1	2.59	0.41
4:K:26:ASN:ND2	4:K:28:GLU:H	2.18	0.41
3:O:105:TYR:CE2	3:O:152:PHE:CE1	3.07	0.41
4:P:105:ILE:H	4:P:105:ILE:HD13	1.84	0.41
1:M:42:GLY:O	1:M:46:ILE:HG13	2.20	0.41
2:B:194:HIS:O	2:B:195:VAL:C	2.58	0.41
4:W:79:ARG:O	4:W:80:CYS:C	2.57	0.41
2:H:206:ASP:OD1	2:H:206:ASP:N	2.51	0.41
5:L:82:HIS:CB	5:L:169:ILE:HD13	2.50	0.41
3:O:120:LEU:HD23	4:W:39:ALA:CB	2.51	0.41
4:V:119:LEU:CD1	4:V:120:ASP:N	2.77	0.41
3:O:141:THR:O	3:O:142:ASN:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:73:LEU:HD11	2:T:86:LYS:HD3	2.01	0.41
4:P:156:GLN:CA	4:P:184:LEU:HD12	2.39	0.41
1:M:200:MET:O	1:M:201:PRO:C	2.58	0.41
2:B:73:LEU:HD11	2:B:86:LYS:HD3	2.02	0.41
1:G:201:PRO:HG2	5:L:6:ASP:O	2.21	0.41
4:W:149:LYS:HD2	4:W:159:CYS:O	2.20	0.41
4:W:178:VAL:O	4:W:178:VAL:HG12	2.20	0.41
3:C:10:ASP:N	3:C:14:ASN:O	2.51	0.41
3:I:16:ILE:O	3:I:138:ARG:HB2	2.20	0.41
3:I:16:ILE:O	3:I:140:ILE:CG2	2.69	0.41
5:F:28:PHE:O	5:F:28:PHE:CD1	2.72	0.41
3:U:154:ALA:HB3	3:U:155:PRO:CD	2.51	0.41
4:D:77:LEU:HB3	4:D:78:PRO:HD2	2.00	0.41
4:V:105:ILE:H	4:V:105:ILE:HD13	1.83	0.41
4:D:105:ILE:HD13	4:D:105:ILE:H	1.85	0.41
2:T:208:GLU:C	2:T:209:TYR:HD2	2.23	0.41
2:B:271:ASP:OD2	2:B:271:ASP:N	2.53	0.41
4:D:32:LEU:HA	4:D:32:LEU:HD23	1.81	0.41
4:D:166:ASP:HB3	4:D:169:ARG:HB2	2.03	0.41
4:V:47:ARG:C	4:V:49:PHE:H	2.23	0.41
5:X:149:GLU:O	5:X:150:THR:CG2	2.66	0.41
5:X:150:THR:OG1	5:X:158:VAL:CG2	2.69	0.41
5:L:149:GLU:O	5:L:150:THR:CG2	2.66	0.41
4:J:129:GLU:OE1	4:J:129:GLU:HA	2.19	0.41
5:F:169:ILE:O	5:F:172:SER:HB2	2.20	0.41
2:H:253:HIS:O	2:H:264:THR:HB	2.20	0.41
4:E:90:LEU:O	4:E:94:ALA:HB3	2.21	0.41
4:Q:18:TRP:HE1	4:Q:100:ASN:HB2	1.84	0.41
1:M:21:PHE:HZ	1:M:215:VAL:HG11	1.81	0.41
1:G:131:ILE:HG13	1:G:141:VAL:HG22	2.03	0.41
1:S:18:GLN:HG3	1:S:33:TYR:CD2	2.55	0.41
5:F:57:VAL:O	5:F:57:VAL:HG12	2.20	0.41
1:A:143:ILE:HA	1:A:143:ILE:HD13	1.90	0.41
4:P:65:CYS:HA	4:P:154:MET:HG3	2.02	0.41
1:G:200:MET:HE1	5:L:7:TYR:CB	2.50	0.41
3:U:16:ILE:O	3:U:138:ARG:HB2	2.21	0.41
3:O:16:ILE:O	3:O:138:ARG:HB2	2.21	0.41
2:H:169:MET:HB3	2:H:174:LEU:HD12	2.02	0.41
1:G:38:SER:CB	5:L:45:PHE:CE1	3.02	0.41
3:I:82:THR:CG2	3:I:83:ALA:N	2.82	0.41
4:K:95:PHE:CD1	4:K:103:PRO:CG	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:64:GLY:HA2	4:W:147:VAL:HG13	2.03	0.41
1:S:52:PRO:O	1:S:54:ALA:N	2.53	0.41
2:N:231:TYR:HE2	2:N:252:ALA:H	1.65	0.41
1:G:120:ARG:HD2	3:I:73:GLY:HA2	2.02	0.41
1:G:44:PHE:HD1	1:G:119:LEU:HB3	1.85	0.41
4:V:180:LEU:O	4:V:181:ASN:C	2.59	0.41
3:U:141:THR:O	3:U:142:ASN:C	2.58	0.41
2:H:218:LEU:HB3	2:H:219:THR:H	1.66	0.41
3:C:16:ILE:O	3:C:138:ARG:HB2	2.21	0.41
3:O:16:ILE:O	3:O:140:ILE:HG22	2.21	0.41
2:N:191:LEU:CB	2:N:192:PHE:CD1	3.04	0.41
2:T:176:ILE:HG23	2:T:177:LEU:H	1.83	0.41
1:M:181:LYS:HD3	1:M:214:MET:CE	2.50	0.41
4:D:75:THR:O	4:D:76:ALA:C	2.58	0.41
2:H:168:LYS:O	2:H:170:ARG:N	2.54	0.41
4:E:26:ASN:ND2	4:E:28:GLU:H	2.18	0.41
4:J:65:CYS:HA	4:J:154:MET:HG3	2.02	0.41
4:Q:185:LYS:HG2	4:Q:186:ASP:N	2.36	0.41
5:F:150:THR:OG1	5:F:158:VAL:CG2	2.69	0.41
1:G:8:VAL:HG13	1:G:140:PHE:CD2	2.56	0.41
4:W:41:LEU:HD22	4:W:55:HIS:CD2	2.55	0.41
4:V:129:GLU:OE1	4:V:129:GLU:HA	2.20	0.41
5:X:68:GLU:C	5:X:70:PHE:N	2.74	0.41
5:L:169:ILE:H	5:L:169:ILE:HG13	1.53	0.41
4:Q:71:PHE:CD1	4:Q:71:PHE:O	2.74	0.41
1:G:3:ILE:HA	1:G:144:SER:HA	2.02	0.41
1:S:192:LYS:HG3	2:T:64:PHE:CE2	2.56	0.41
1:M:200:MET:HE1	5:R:7:TYR:CA	2.49	0.41
1:M:200:MET:HE1	5:R:7:TYR:CB	2.51	0.41
3:I:123:TYR:C	3:I:125:PHE:N	2.66	0.41
2:T:191:LEU:HD12	2:T:192:PHE:HE1	1.85	0.41
2:H:176:ILE:HG23	2:H:177:LEU:H	1.83	0.41
3:O:129:GLU:C	3:O:131:GLU:H	2.24	0.41
4:P:75:THR:O	4:P:76:ALA:C	2.59	0.41
2:T:167:THR:HG22	2:T:169:MET:HB3	2.02	0.41
1:G:42:GLY:O	1:G:46:ILE:HG13	2.21	0.41
2:T:185:GLY:HA2	2:T:195:VAL:HG13	2.02	0.41
4:E:185:LYS:HG2	4:E:186:ASP:N	2.36	0.41
1:A:2:ALA:HB3	1:A:146:SER:HB3	2.02	0.41
4:E:145:CYS:HB2	4:E:163:PHE:HE1	1.85	0.41
4:D:188:ILE:HA	4:D:189:PRO:HD3	1.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:188:ILE:O	4:V:188:ILE:HG13	2.19	0.41
5:R:66:GLY:O	5:R:70:PHE:HE1	2.04	0.41
3:C:107:TYR:HE2	4:E:73:ALA:CA	2.19	0.41
3:I:77:VAL:CG2	3:I:77:VAL:O	2.62	0.41
3:U:80:TYR:CE1	3:U:104:GLN:HA	2.56	0.41
4:E:139:TRP:O	4:E:140:TYR:C	2.58	0.41
1:S:31:ASN:O	1:S:34:LEU:HB2	2.20	0.41
2:H:192:PHE:HB3	2:H:217:THR:OG1	2.21	0.41
4:Q:134:ALA:C	4:Q:136:LYS:N	2.74	0.41
1:M:52:PRO:O	1:M:54:ALA:N	2.54	0.41
4:D:37:ILE:HD12	4:D:37:ILE:HA	1.91	0.41
1:M:189:TYR:HD1	1:M:189:TYR:H	1.67	0.41
5:F:53:ASP:C	5:F:55:LYS:N	2.73	0.41
5:X:13:LEU:HD21	5:X:25:LEU:CD2	2.50	0.41
5:L:13:LEU:HD21	5:L:25:LEU:CD1	2.51	0.41
3:C:105:TYR:CE2	3:C:152:PHE:CE1	3.08	0.41
3:C:105:TYR:HE1	3:C:109:HIS:HD1	1.55	0.41
2:H:208:GLU:C	2:H:209:TYR:HD2	2.23	0.41
1:S:38:SER:CB	5:X:45:PHE:CE1	3.03	0.41
4:V:45:TYR:HE1	4:V:55:HIS:HB2	1.84	0.41
3:C:120:LEU:HD23	3:C:120:LEU:HA	1.91	0.41
1:A:135:LEU:C	1:A:137:GLY:N	2.74	0.41
4:Q:111:ASN:O	4:Q:112:LYS:HB2	2.21	0.41
5:F:12:LEU:HG	5:F:14:ILE:HG23	2.03	0.41
5:X:62:TRP:O	5:X:64:THR:N	2.46	0.41
3:C:88:PHE:CZ	3:C:107:TYR:HB2	2.55	0.41
1:A:10:ASN:ND2	1:A:12:SER:N	2.62	0.41
4:K:95:PHE:HD1	4:K:103:PRO:HD3	1.86	0.41
4:K:71:PHE:O	4:K:71:PHE:CD1	2.73	0.41
4:W:95:PHE:HD1	4:W:103:PRO:HD3	1.86	0.41
4:E:124:LEU:CD2	4:E:124:LEU:C	2.89	0.41
4:Q:90:LEU:O	4:Q:94:ALA:HB3	2.21	0.41
4:Q:39:ALA:CB	3:U:120:LEU:HD23	2.51	0.41
1:G:18:GLN:HG3	1:G:33:TYR:CD2	2.56	0.41
1:G:28:LEU:CB	1:G:33:TYR:CE1	3.03	0.41
4:D:179:LYS:C	4:D:181:ASN:H	2.24	0.41
4:P:179:LYS:C	4:P:181:ASN:H	2.25	0.41
2:T:218:LEU:HB3	2:T:219:THR:H	1.67	0.41
4:P:156:GLN:HB3	4:P:184:LEU:HB2	2.03	0.41
4:P:154:MET:O	4:P:156:GLN:NE2	2.54	0.41
4:P:68:ILE:HG13	4:P:68:ILE:H	1.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:7:TYR:HB2	5:R:57:VAL:HG22	2.03	0.41
5:R:57:VAL:HG12	5:R:57:VAL:O	2.21	0.41
2:H:230:GLU:O	2:H:233:VAL:HG13	2.20	0.41
4:J:156:GLN:HB3	4:J:184:LEU:HB2	2.03	0.41
1:S:181:LYS:HD3	1:S:214:MET:CE	2.51	0.41
1:S:75:MET:CE	1:S:181:LYS:NZ	2.84	0.41
3:C:123:TYR:N	3:C:123:TYR:CD1	2.86	0.41
3:U:123:TYR:C	3:U:125:PHE:N	2.66	0.41
3:I:123:TYR:N	3:I:123:TYR:CD1	2.87	0.41
3:O:123:TYR:N	3:O:123:TYR:CD1	2.87	0.41
2:T:187:LEU:O	2:T:191:LEU:N	2.40	0.41
4:K:49:PHE:CD1	4:K:134:ALA:HA	2.55	0.41
4:Q:49:PHE:CD1	4:Q:134:ALA:HA	2.56	0.41
5:X:7:TYR:HB2	5:X:57:VAL:HG22	2.03	0.41
4:W:49:PHE:CB	4:W:137:SER:HB3	2.50	0.41
1:A:181:LYS:HD3	1:A:214:MET:CE	2.51	0.41
4:P:125:ALA:HB2	4:P:140:TYR:CE2	2.56	0.41
2:N:169:MET:CB	2:N:174:LEU:CD1	2.98	0.41
4:D:33:THR:O	4:D:36:SER:HB3	2.21	0.41
4:K:36:SER:O	4:K:40:GLN:CB	2.63	0.41
5:R:53:ASP:C	5:R:55:LYS:N	2.73	0.41
2:T:168:LYS:O	2:T:172:ARG:NE	2.54	0.41
4:V:68:ILE:HD11	4:V:154:MET:HG3	2.02	0.41
2:B:208:GLU:C	2:B:209:TYR:HD2	2.24	0.41
4:D:45:TYR:HE1	4:D:55:HIS:HB2	1.85	0.41
4:D:185:LYS:O	4:D:185:LYS:HD2	2.20	0.41
2:T:271:ASP:N	2:T:271:ASP:OD2	2.54	0.41
1:G:122:LEU:CD2	1:G:127:PHE:HE1	2.34	0.41
1:G:122:LEU:O	1:G:122:LEU:HD23	2.21	0.41
4:K:130:LEU:HD12	4:K:168:LEU:O	2.21	0.41
2:T:206:ASP:OD1	2:T:206:ASP:N	2.52	0.41
5:R:143:ASN:O	5:R:144:LYS:HB2	2.20	0.41
5:L:14:ILE:HD12	5:L:102:TRP:CE3	2.56	0.41
5:L:12:LEU:HG	5:L:14:ILE:HG23	2.03	0.41
4:V:166:ASP:HB3	4:V:169:ARG:HB2	2.03	0.41
4:E:95:PHE:HD1	4:E:103:PRO:HD3	1.86	0.41
2:T:231:TYR:HE2	2:T:252:ALA:H	1.68	0.41
2:T:250:VAL:HG12	2:T:266:TYR:HB3	2.02	0.41
2:H:64:PHE:CD1	4:J:67:LEU:CD1	3.04	0.41
3:I:141:THR:O	3:I:142:ASN:C	2.58	0.41
4:V:156:GLN:HB3	4:V:184:LEU:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:16:ILE:O	3:C:140:ILE:CG2	2.69	0.41
4:W:134:ALA:O	4:W:137:SER:N	2.48	0.41
2:B:99:LEU:H	2:B:99:LEU:CD1	2.29	0.41
2:B:180:LEU:HD12	2:B:180:LEU:HA	1.82	0.41
3:I:155:PRO:CG	3:I:156:MET:N	2.84	0.41
4:P:37:ILE:HD12	4:P:37:ILE:HA	1.91	0.41
2:H:169:MET:HB2	2:H:174:LEU:HD12	2.02	0.41
4:E:25:ILE:CG2	4:E:26:ASN:N	2.84	0.41
1:G:122:LEU:C	1:G:122:LEU:HD23	2.41	0.41
5:X:8:LEU:HD12	5:X:8:LEU:HA	1.87	0.41
1:M:135:LEU:C	1:M:137:GLY:N	2.75	0.40
4:P:166:ASP:HB3	4:P:169:ARG:HB2	2.03	0.40
5:F:158:VAL:O	5:F:161:ALA:HB3	2.21	0.40
4:Q:77:LEU:HD12	4:Q:89:VAL:CG1	2.52	0.40
3:C:83:ALA:HB3	4:E:72:LEU:CD1	2.46	0.40
5:X:169:ILE:HG13	5:X:169:ILE:H	1.53	0.40
3:C:72:THR:HG21	3:C:75:TYR:CD2	2.56	0.40
1:S:129:MET:HB2	1:S:143:ILE:HD11	2.03	0.40
2:H:64:PHE:CE1	4:J:67:LEU:CD1	3.03	0.40
5:F:7:TYR:HB2	5:F:57:VAL:HG22	2.03	0.40
4:K:114:THR:HG22	4:K:115:PHE:N	2.37	0.40
5:R:29:SER:HA	5:R:48:LYS:CG	2.49	0.40
2:H:187:LEU:O	2:H:191:LEU:N	2.40	0.40
4:W:134:ALA:C	4:W:136:LYS:N	2.73	0.40
4:D:77:LEU:HD22	4:D:78:PRO:CD	2.47	0.40
4:V:143:ILE:CG2	4:V:144:LEU:N	2.84	0.40
1:S:185:LEU:HD11	1:S:210:LYS:HD3	2.03	0.40
4:J:186:ASP:HB2	5:L:79:ARG:NH2	2.36	0.40
2:N:208:GLU:C	2:N:209:TYR:HD2	2.24	0.40
4:P:188:ILE:O	4:P:188:ILE:HG13	2.20	0.40
4:Q:77:LEU:HD12	4:Q:89:VAL:HG11	2.03	0.40
5:R:150:THR:HG22	5:R:157:ASN:HB2	2.03	0.40
1:S:14:GLY:N	5:X:10:LYS:HZ3	2.18	0.40
4:K:99:LEU:HB2	4:K:101:ILE:CG2	2.46	0.40
1:G:10:ASN:ND2	1:G:12:SER:N	2.63	0.40
2:T:253:HIS:O	2:T:264:THR:HB	2.21	0.40
4:Q:38:VAL:HG12	3:U:120:LEU:HD21	2.03	0.40
4:V:17:ILE:HD13	4:V:17:ILE:HA	1.81	0.40
2:T:231:TYR:HE2	2:T:251:THR:CA	2.29	0.40
1:A:44:PHE:HD1	1:A:119:LEU:HB3	1.85	0.40
3:O:117:ASN:HA	4:W:32:LEU:CD2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:155:VAL:HG12	4:P:157:LEU:HD21	2.03	0.40
1:G:200:MET:HE3	1:G:201:PRO:HD2	2.03	0.40
4:W:160:ASP:O	4:W:162:TRP:CE3	2.74	0.40
2:H:99:LEU:HD22	2:H:243:ASN:ND2	2.27	0.40
1:M:29:ASN:O	1:M:32:GLU:HG3	2.21	0.40
1:A:128:THR:HG22	1:A:130:PHE:CE2	2.56	0.40
2:T:241:LEU:O	2:T:244:ALA:HB3	2.21	0.40
1:A:122:LEU:CD2	1:A:127:PHE:HE1	2.34	0.40
3:C:67:ILE:H	3:C:67:ILE:HD12	1.85	0.40
4:Q:139:TRP:O	4:Q:140:TYR:C	2.59	0.40
2:H:84:GLU:OE1	2:H:231:TYR:CE1	2.71	0.40
2:H:68:GLU:CB	4:J:63:ILE:HD11	2.51	0.40
4:P:119:LEU:CD1	4:P:120:ASP:N	2.78	0.40
2:N:73:LEU:HD21	2:N:90:TYR:CE1	2.56	0.40
4:K:77:LEU:HD12	4:K:89:VAL:CG1	2.52	0.40
4:D:155:VAL:O	4:D:157:LEU:HD23	2.22	0.40
4:Q:134:ALA:O	4:Q:137:SER:N	2.50	0.40
2:N:175:LYS:CG	2:N:176:ILE:H	2.34	0.40
3:I:129:GLU:HB2	3:I:135:GLN:CD	2.41	0.40
4:J:75:THR:O	4:J:76:ALA:C	2.59	0.40
4:V:75:THR:O	4:V:76:ALA:C	2.59	0.40
4:Q:26:ASN:ND2	4:Q:28:GLU:H	2.19	0.40
4:W:185:LYS:HG2	4:W:186:ASP:N	2.36	0.40
2:N:206:ASP:OD1	2:N:206:ASP:N	2.51	0.40
1:A:133:GLN:HE22	4:D:188:ILE:CD1	2.24	0.40
3:C:88:PHE:HE1	3:C:107:TYR:CD1	2.39	0.40
3:I:76:ARG:NH1	3:I:94:PHE:CZ	2.90	0.40
4:K:60:GLY:O	4:K:63:ILE:HG13	2.21	0.40
4:W:60:GLY:O	4:W:63:ILE:HG13	2.21	0.40
4:W:71:PHE:CD1	4:W:71:PHE:O	2.74	0.40
4:W:95:PHE:CD1	4:W:103:PRO:CG	3.04	0.40
3:I:72:THR:HG21	3:I:75:TYR:CD2	2.57	0.40
4:V:179:LYS:C	4:V:181:ASN:H	2.25	0.40
1:A:192:LYS:HG3	2:B:64:PHE:CE2	2.56	0.40
4:J:22:THR:HG22	4:J:22:THR:O	2.21	0.40
1:G:50:LEU:HD23	3:I:47:MET:CE	2.51	0.40
4:E:49:PHE:CZ	4:E:134:ALA:N	2.89	0.40
3:C:129:GLU:C	3:C:131:GLU:H	2.25	0.40
4:Q:98:PHE:CD2	4:W:26:ASN:OD1	2.74	0.40
3:U:6:PHE:CZ	3:U:8:ILE:CG1	3.05	0.40
1:S:42:GLY:O	1:S:46:ILE:HG13	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:45:TYR:HE1	4:J:55:HIS:HB2	1.85	0.40
3:U:147:SER:OG	3:U:148:VAL:N	2.54	0.40
1:S:117:SER:HB3	4:V:191:GLY:N	2.37	0.40
2:N:271:ASP:N	2:N:271:ASP:OD2	2.54	0.40
5:X:14:ILE:HD12	5:X:102:TRP:CE3	2.57	0.40
1:M:10:ASN:ND2	1:M:12:SER:N	2.63	0.40
5:R:169:ILE:HG13	5:R:169:ILE:H	1.54	0.40
4:K:124:LEU:C	4:K:124:LEU:CD2	2.90	0.40
4:W:139:TRP:O	4:W:140:TYR:C	2.58	0.40
4:Q:60:GLY:O	4:Q:63:ILE:HG13	2.22	0.40
3:C:141:THR:O	3:C:142:ASN:C	2.60	0.40
4:K:77:LEU:HD12	4:K:89:VAL:HG11	2.03	0.40
5:L:7:TYR:HB2	5:L:57:VAL:HG22	2.04	0.40
4:W:116:SER:HA	4:W:177:LYS:HA	2.03	0.40
5:R:28:PHE:HB3	5:R:48:LYS:HZ1	1.83	0.40
5:X:50:VAL:O	5:X:50:VAL:HG23	2.21	0.40
2:T:99:LEU:HD22	2:T:243:ASN:ND2	2.27	0.40
2:B:191:LEU:CB	2:B:192:PHE:CD1	3.05	0.40
1:A:75:MET:CE	1:A:181:LYS:NZ	2.85	0.40
2:N:169:MET:SD	2:N:179:ILE:HD13	2.61	0.40
4:K:41:LEU:HD12	4:K:52:VAL:HG13	2.03	0.40
3:U:129:GLU:HB2	3:U:135:GLN:CD	2.42	0.40
4:J:37:ILE:HD12	4:J:37:ILE:HA	1.88	0.40
4:P:77:LEU:HB3	4:P:78:PRO:HD2	2.01	0.40
5:F:13:LEU:HD21	5:F:25:LEU:CD1	2.51	0.40
4:W:26:ASN:HD22	4:W:26:ASN:C	2.24	0.40
4:J:105:ILE:H	4:J:105:ILE:HD13	1.83	0.40
4:K:185:LYS:HG2	4:K:186:ASP:N	2.36	0.40
1:A:201:PRO:HG2	5:F:6:ASP:O	2.21	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 X-ray entries followed by that with respect to entries of similar resolution.

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	151/219 (69%)	123 (82%)	21 (14%)	7 (5%)	3	33
1	G	151/219 (69%)	124 (82%)	21 (14%)	6 (4%)	4	38
1	M	151/219 (69%)	124 (82%)	21 (14%)	6 (4%)	4	38
1	S	151/219 (69%)	124 (82%)	21 (14%)	6 (4%)	4	38
2	B	163/283 (58%)	126 (77%)	25 (15%)	12 (7%)	1	21
2	H	163/283 (58%)	126 (77%)	25 (15%)	12 (7%)	1	21
2	N	163/283 (58%)	126 (77%)	24 (15%)	13 (8%)	1	18
2	T	163/283 (58%)	126 (77%)	23 (14%)	14 (9%)	1	16
3	C	139/159 (87%)	107 (77%)	20 (14%)	12 (9%)	1	16
3	I	139/159 (87%)	107 (77%)	20 (14%)	12 (9%)	1	16
3	O	139/159 (87%)	107 (77%)	20 (14%)	12 (9%)	1	16
3	U	139/159 (87%)	106 (76%)	21 (15%)	12 (9%)	1	16
4	D	184/193 (95%)	147 (80%)	22 (12%)	15 (8%)	1	17
4	E	186/193 (96%)	148 (80%)	28 (15%)	10 (5%)	2	29
4	J	184/193 (95%)	146 (79%)	24 (13%)	14 (8%)	1	19
4	K	186/193 (96%)	149 (80%)	27 (14%)	10 (5%)	2	29
4	P	184/193 (95%)	147 (80%)	21 (11%)	16 (9%)	1	16
4	Q	186/193 (96%)	148 (80%)	28 (15%)	10 (5%)	2	29
4	V	184/193 (95%)	146 (79%)	23 (12%)	15 (8%)	1	17
4	W	186/193 (96%)	147 (79%)	29 (16%)	10 (5%)	2	29
5	F	162/206 (79%)	122 (75%)	32 (20%)	8 (5%)	3	32
5	L	162/206 (79%)	122 (75%)	32 (20%)	8 (5%)	3	32
5	R	162/206 (79%)	122 (75%)	32 (20%)	8 (5%)	3	32
5	X	162/206 (79%)	122 (75%)	32 (20%)	8 (5%)	3	32
All	All	3940/5012 (79%)	3092 (78%)	592 (15%)	256 (6%)	1	25

All (256) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	MET
2	B	171	ARG
2	B	224	GLY
3	C	10	ASP
3	C	124	ASP
3	C	125	PHE

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Mol	Chain	Res	Type
3	C	135	GLN
3	C	138	ARG
3	C	155	PRO
4	D	23	GLU
4	D	49	PHE
4	D	132	MET
4	D	172	SER
4	D	181	ASN
4	D	188	ILE
4	E	22	THR
4	E	80	CYS
5	F	5	TYR
5	F	69	ARG
5	F	112	SER
1	G	198	MET
2	H	170	ARG
2	H	171	ARG
2	H	224	GLY
3	I	10	ASP
3	I	124	ASP
3	I	125	PHE
3	I	135	GLN
3	I	138	ARG
3	I	155	PRO
4	J	23	GLU
4	J	49	PHE
4	J	132	MET
4	J	172	SER
4	J	181	ASN
4	J	186	ASP
4	J	188	ILE
4	K	22	THR
4	K	80	CYS
5	L	5	TYR
5	L	69	ARG
5	L	112	SER
1	M	198	MET
2	N	171	ARG
2	N	224	GLY
3	O	10	ASP
3	O	124	ASP
3	O	125	PHE

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Mol	Chain	Res	Type
3	O	135	GLN
3	O	138	ARG
3	O	155	PRO
4	P	23	GLU
4	P	49	PHE
4	P	132	MET
4	P	172	SER
4	P	181	ASN
4	P	188	ILE
4	Q	22	THR
4	Q	80	CYS
5	R	5	TYR
5	R	69	ARG
5	R	112	SER
1	S	198	MET
2	T	170	ARG
2	T	171	ARG
2	T	224	GLY
3	U	10	ASP
3	U	124	ASP
3	U	125	PHE
3	U	135	GLN
3	U	138	ARG
3	U	155	PRO
4	V	23	GLU
4	V	49	PHE
4	V	132	MET
4	V	172	SER
4	V	181	ASN
4	V	186	ASP
4	V	188	ILE
4	W	22	THR
4	W	80	CYS
5	X	5	TYR
5	X	69	ARG
5	X	112	SER
1	A	119	LEU
1	A	199	GLU
2	B	169	MET
2	B	170	ARG
2	B	202	SER
2	B	217	THR

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Mol	Chain	Res	Type
2	B	219	THR
2	B	226	ASN
2	B	258	GLY
3	C	142	ASN
4	D	111	ASN
4	D	170	GLY
4	D	186	ASP
4	E	132	MET
4	E	135	MET
5	F	17	SER
5	F	54	GLY
5	F	122	LYS
5	F	130	VAL
1	G	119	LEU
1	G	199	GLU
2	H	169	MET
2	H	202	SER
2	H	217	THR
2	H	219	THR
2	H	226	ASN
2	H	258	GLY
3	I	142	ASN
4	J	111	ASN
4	J	170	GLY
4	K	132	MET
4	K	135	MET
5	L	17	SER
5	L	54	GLY
5	L	122	LYS
5	L	130	VAL
1	M	119	LEU
1	M	199	GLU
2	N	169	MET
2	N	170	ARG
2	N	202	SER
2	N	217	THR
2	N	219	THR
2	N	226	ASN
2	N	258	GLY
3	O	142	ASN
4	P	111	ASN
4	P	170	GLY

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Mol	Chain	Res	Type
4	P	186	ASP
4	Q	132	MET
4	Q	135	MET
5	R	17	SER
5	R	54	GLY
5	R	122	LYS
5	R	130	VAL
1	S	119	LEU
1	S	199	GLU
2	T	169	MET
2	T	202	SER
2	T	217	THR
2	T	219	THR
2	T	226	ASN
2	T	258	GLY
3	U	142	ASN
4	V	111	ASN
4	V	170	GLY
4	W	132	MET
4	W	135	MET
5	X	17	SER
5	X	54	GLY
5	X	122	LYS
5	X	130	VAL
1	A	10	ASN
3	C	122	PRO
4	D	80	CYS
4	D	171	ASP
1	G	10	ASN
3	I	122	PRO
4	J	80	CYS
4	J	171	ASP
3	O	122	PRO
4	P	80	CYS
4	P	171	ASP
2	T	167	THR
3	U	122	PRO
4	V	80	CYS
4	V	171	ASP
4	V	180	LEU
1	A	53	LYS
3	C	128	ASN

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Mol	Chain	Res	Type
4	D	180	LEU
4	E	124	LEU
4	E	140	TYR
1	G	53	LYS
3	I	128	ASN
4	J	180	LEU
4	K	111	ASN
4	K	124	LEU
4	K	140	TYR
1	M	10	ASN
1	M	53	LYS
4	P	180	LEU
4	Q	111	ASN
4	Q	124	LEU
4	Q	140	TYR
1	S	10	ASN
1	S	53	LYS
2	T	175	LYS
3	U	128	ASN
4	W	124	LEU
4	W	140	TYR
2	B	255	MET
3	C	19	ARG
3	C	119	LEU
4	D	137	SER
4	D	164	VAL
4	E	46	GLU
4	E	49	PHE
4	E	111	ASN
5	F	151	SER
1	G	201	PRO
2	H	255	MET
3	I	19	ARG
4	J	137	SER
4	J	164	VAL
4	K	46	GLU
5	L	151	SER
1	M	201	PRO
2	N	255	MET
3	O	19	ARG
3	O	119	LEU
3	O	128	ASN

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Mol	Chain	Res	Type
4	P	164	VAL
4	Q	49	PHE
5	R	151	SER
1	S	201	PRO
2	T	255	MET
3	U	19	ARG
3	U	119	LEU
4	V	137	SER
4	V	164	VAL
4	W	46	GLU
4	W	49	PHE
4	W	111	ASN
5	X	151	SER
1	A	25	GLU
1	A	201	PRO
3	I	119	LEU
4	K	49	PHE
2	N	175	LYS
4	P	137	SER
4	Q	46	GLU
2	B	249	GLY
2	B	250	VAL
2	H	249	GLY
3	I	136	GLY
2	N	249	GLY
2	T	249	GLY
3	C	136	GLY
4	E	164	VAL
2	N	250	VAL
3	O	136	GLY
2	T	250	VAL
3	U	136	GLY
4	W	164	VAL
2	H	250	VAL
4	K	164	VAL
4	P	128	VAL
4	Q	164	VAL
4	V	118	ILE
4	D	118	ILE
4	P	118	ILE

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 X-ray entries followed by that with respect to entries of similar resolution.

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	145/199 (73%)	120 (83%)	25 (17%)	2	18
1	G	145/199 (73%)	120 (83%)	25 (17%)	2	18
1	M	145/199 (73%)	120 (83%)	25 (17%)	2	18
1	S	145/199 (73%)	121 (83%)	24 (17%)	3	20
2	B	149/249 (60%)	123 (83%)	26 (17%)	2	17
2	H	149/249 (60%)	124 (83%)	25 (17%)	2	19
2	N	149/249 (60%)	124 (83%)	25 (17%)	2	19
2	T	149/249 (60%)	123 (83%)	26 (17%)	2	17
3	C	132/145 (91%)	114 (86%)	18 (14%)	5	30
3	I	132/145 (91%)	114 (86%)	18 (14%)	5	30
3	O	132/145 (91%)	114 (86%)	18 (14%)	5	30
3	U	132/145 (91%)	114 (86%)	18 (14%)	5	30
4	D	171/178 (96%)	151 (88%)	20 (12%)	7	36
4	E	173/178 (97%)	143 (83%)	30 (17%)	2	17
4	J	171/178 (96%)	151 (88%)	20 (12%)	7	36
4	K	173/178 (97%)	143 (83%)	30 (17%)	2	17
4	P	171/178 (96%)	151 (88%)	20 (12%)	7	36
4	Q	173/178 (97%)	142 (82%)	31 (18%)	2	16
4	V	171/178 (96%)	151 (88%)	20 (12%)	7	36
4	W	173/178 (97%)	142 (82%)	31 (18%)	2	16
5	F	148/183 (81%)	135 (91%)	13 (9%)	12	51
5	L	148/183 (81%)	135 (91%)	13 (9%)	12	51
5	R	148/183 (81%)	135 (91%)	13 (9%)	12	51
5	X	148/183 (81%)	135 (91%)	13 (9%)	12	51
All	All	3672/4528 (81%)	3145 (86%)	527 (14%)	4	28

All (527) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	10	ASN
1	A	18	GLN
1	A	21	PHE
1	A	33	TYR
1	A	67	ILE
1	A	70	ILE
1	A	75	MET
1	A	113	ASN
1	A	114	TRP
1	A	120	ARG
1	A	122	LEU
1	A	126	GLN
1	A	133	GLN
1	A	135	LEU
1	A	144	SER
1	A	176	ASP
1	A	180	ARG
1	A	185	LEU
1	A	186	TYR
1	A	189	TYR
1	A	192	LYS
1	A	197	SER
1	A	209	GLU
1	A	214	MET
2	B	64	PHE
2	B	65	LEU
2	B	72	GLN
2	B	73	LEU
2	B	102	LEU
2	B	176	ILE
2	B	178	ASP
2	B	180	LEU
2	B	184	HIS
2	B	187	LEU
2	B	192	PHE
2	B	193	ASN
2	B	210	MET
2	B	215	PHE
2	B	219	THR
2	B	226	ASN
2	B	228	SER
2	B	231	TYR

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Mol	Chain	Res	Type
2	B	233	VAL
2	B	234	CYS
2	B	242	PHE
2	B	246	PHE
2	B	250	VAL
2	B	255	MET
2	B	271	ASP
2	B	282	PHE
3	C	7	TRP
3	C	18	ASP
3	C	19	ARG
3	C	47	MET
3	C	67	ILE
3	C	72	THR
3	C	87	TRP
3	C	89	VAL
3	C	93	ASP
3	C	94	PHE
3	C	101	GLN
3	C	103	LEU
3	C	114	TYR
3	C	119	LEU
3	C	121	SER
3	C	123	TYR
3	C	133	ARG
3	C	142	ASN
4	D	16	GLU
4	D	22	THR
4	D	33	THR
4	D	43	GLN
4	D	57	TYR
4	D	68	ILE
4	D	79	ARG
4	D	93	CYS
4	D	100	ASN
4	D	105	ILE
4	D	149	LYS
4	D	153	GLU
4	D	156	GLN
4	D	157	LEU
4	D	159	CYS
4	D	173	GLN

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Mol	Chain	Res	Type
4	D	175	GLU
4	D	180	LEU
4	D	181	ASN
4	D	192	GLU
4	E	25	ILE
4	E	26	ASN
4	E	27	THR
4	E	55	HIS
4	E	57	TYR
4	E	59	MET
4	E	61	TYR
4	E	62	ASN
4	E	63	ILE
4	E	79	ARG
4	E	82	ASN
4	E	84	VAL
4	E	87	SER
4	E	90	LEU
4	E	93	CYS
4	E	108	TRP
4	E	113	ASP
4	E	115	PHE
4	E	117	LEU
4	E	119	LEU
4	E	144	LEU
4	E	145	CYS
4	E	159	CYS
4	E	160	ASP
4	E	161	VAL
4	E	167	ILE
4	E	174	THR
4	E	175	GLU
4	E	187	GLU
4	E	193	ASP
5	F	13	LEU
5	F	16	ASN
5	F	23	CYS
5	F	41	ILE
5	F	57	VAL
5	F	70	PHE
5	F	77	TYR
5	F	82	HIS

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Mol	Chain	Res	Type
5	F	88	TYR
5	F	95	SER
5	F	102	TRP
5	F	115	LEU
5	F	169	ILE
1	G	7	LEU
1	G	10	ASN
1	G	16	ILE
1	G	18	GLN
1	G	21	PHE
1	G	33	TYR
1	G	67	ILE
1	G	70	ILE
1	G	75	MET
1	G	113	ASN
1	G	114	TRP
1	G	120	ARG
1	G	122	LEU
1	G	126	GLN
1	G	133	GLN
1	G	135	LEU
1	G	176	ASP
1	G	180	ARG
1	G	185	LEU
1	G	186	TYR
1	G	189	TYR
1	G	192	LYS
1	G	197	SER
1	G	209	GLU
1	G	214	MET
2	H	64	PHE
2	H	65	LEU
2	H	72	GLN
2	H	73	LEU
2	H	102	LEU
2	H	176	ILE
2	H	178	ASP
2	H	180	LEU
2	H	184	HIS
2	H	187	LEU
2	H	192	PHE
2	H	193	ASN

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Mol	Chain	Res	Type
2	H	210	MET
2	H	215	PHE
2	H	219	THR
2	H	228	SER
2	H	231	TYR
2	H	233	VAL
2	H	234	CYS
2	H	242	PHE
2	H	246	PHE
2	H	250	VAL
2	H	255	MET
2	H	271	ASP
2	H	282	PHE
3	I	7	TRP
3	I	18	ASP
3	I	19	ARG
3	I	47	MET
3	I	67	ILE
3	I	72	THR
3	I	87	TRP
3	I	89	VAL
3	I	93	ASP
3	I	94	PHE
3	I	101	GLN
3	I	103	LEU
3	I	114	TYR
3	I	119	LEU
3	I	121	SER
3	I	123	TYR
3	I	133	ARG
3	I	142	ASN
4	J	16	GLU
4	J	22	THR
4	J	33	THR
4	J	43	GLN
4	J	57	TYR
4	J	68	ILE
4	J	79	ARG
4	J	93	CYS
4	J	100	ASN
4	J	105	ILE
4	J	149	LYS

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Mol	Chain	Res	Type
4	J	153	GLU
4	J	156	GLN
4	J	157	LEU
4	J	159	CYS
4	J	173	GLN
4	J	175	GLU
4	J	180	LEU
4	J	181	ASN
4	J	192	GLU
4	K	25	ILE
4	K	26	ASN
4	K	27	THR
4	K	33	THR
4	K	55	HIS
4	K	57	TYR
4	K	59	MET
4	K	61	TYR
4	K	62	ASN
4	K	79	ARG
4	K	82	ASN
4	K	84	VAL
4	K	87	SER
4	K	90	LEU
4	K	93	CYS
4	K	108	TRP
4	K	113	ASP
4	K	115	PHE
4	K	117	LEU
4	K	119	LEU
4	K	144	LEU
4	K	145	CYS
4	K	159	CYS
4	K	160	ASP
4	K	161	VAL
4	K	167	ILE
4	K	174	THR
4	K	175	GLU
4	K	187	GLU
4	K	193	ASP
5	L	13	LEU
5	L	16	ASN
5	L	23	CYS

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Mol	Chain	Res	Type
5	L	41	ILE
5	L	57	VAL
5	L	70	PHE
5	L	77	TYR
5	L	82	HIS
5	L	88	TYR
5	L	95	SER
5	L	102	TRP
5	L	115	LEU
5	L	169	ILE
1	M	7	LEU
1	M	10	ASN
1	M	16	ILE
1	M	18	GLN
1	M	21	PHE
1	M	33	TYR
1	M	67	ILE
1	M	70	ILE
1	M	75	MET
1	M	113	ASN
1	M	114	TRP
1	M	120	ARG
1	M	122	LEU
1	M	126	GLN
1	M	133	GLN
1	M	135	LEU
1	M	176	ASP
1	M	180	ARG
1	M	185	LEU
1	M	186	TYR
1	M	189	TYR
1	M	192	LYS
1	M	197	SER
1	M	209	GLU
1	M	214	MET
2	N	64	PHE
2	N	65	LEU
2	N	72	GLN
2	N	73	LEU
2	N	102	LEU
2	N	176	ILE
2	N	178	ASP

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Mol	Chain	Res	Type
2	N	180	LEU
2	N	184	HIS
2	N	187	LEU
2	N	192	PHE
2	N	193	ASN
2	N	210	MET
2	N	215	PHE
2	N	219	THR
2	N	228	SER
2	N	231	TYR
2	N	233	VAL
2	N	234	CYS
2	N	242	PHE
2	N	246	PHE
2	N	250	VAL
2	N	255	MET
2	N	271	ASP
2	N	282	PHE
3	O	7	TRP
3	O	18	ASP
3	O	19	ARG
3	O	47	MET
3	O	67	ILE
3	O	72	THR
3	O	87	TRP
3	O	89	VAL
3	O	93	ASP
3	O	94	PHE
3	O	101	GLN
3	O	103	LEU
3	O	114	TYR
3	O	119	LEU
3	O	121	SER
3	O	123	TYR
3	O	133	ARG
3	O	142	ASN
4	P	16	GLU
4	P	22	THR
4	P	33	THR
4	P	43	GLN
4	P	57	TYR
4	P	68	ILE

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Mol	Chain	Res	Type
4	P	79	ARG
4	P	93	CYS
4	P	100	ASN
4	P	105	ILE
4	P	149	LYS
4	P	153	GLU
4	P	156	GLN
4	P	157	LEU
4	P	159	CYS
4	P	173	GLN
4	P	175	GLU
4	P	180	LEU
4	P	181	ASN
4	P	192	GLU
4	Q	25	ILE
4	Q	26	ASN
4	Q	27	THR
4	Q	33	THR
4	Q	55	HIS
4	Q	57	TYR
4	Q	59	MET
4	Q	61	TYR
4	Q	62	ASN
4	Q	63	ILE
4	Q	79	ARG
4	Q	82	ASN
4	Q	84	VAL
4	Q	87	SER
4	Q	90	LEU
4	Q	93	CYS
4	Q	108	TRP
4	Q	113	ASP
4	Q	115	PHE
4	Q	117	LEU
4	Q	119	LEU
4	Q	144	LEU
4	Q	145	CYS
4	Q	159	CYS
4	Q	160	ASP
4	Q	161	VAL
4	Q	167	ILE
4	Q	174	THR

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Mol	Chain	Res	Type
4	Q	175	GLU
4	Q	187	GLU
4	Q	193	ASP
5	R	13	LEU
5	R	16	ASN
5	R	23	CYS
5	R	41	ILE
5	R	57	VAL
5	R	70	PHE
5	R	77	TYR
5	R	82	HIS
5	R	88	TYR
5	R	95	SER
5	R	102	TRP
5	R	115	LEU
5	R	169	ILE
1	S	7	LEU
1	S	10	ASN
1	S	16	ILE
1	S	18	GLN
1	S	21	PHE
1	S	33	TYR
1	S	67	ILE
1	S	70	ILE
1	S	75	MET
1	S	113	ASN
1	S	114	TRP
1	S	120	ARG
1	S	122	LEU
1	S	126	GLN
1	S	133	GLN
1	S	135	LEU
1	S	176	ASP
1	S	180	ARG
1	S	186	TYR
1	S	189	TYR
1	S	192	LYS
1	S	197	SER
1	S	209	GLU
1	S	214	MET
2	T	64	PHE
2	T	65	LEU

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Mol	Chain	Res	Type
2	T	72	GLN
2	T	73	LEU
2	T	102	LEU
2	T	176	ILE
2	T	178	ASP
2	T	180	LEU
2	T	184	HIS
2	T	187	LEU
2	T	192	PHE
2	T	193	ASN
2	T	210	MET
2	T	215	PHE
2	T	219	THR
2	T	226	ASN
2	T	228	SER
2	T	231	TYR
2	T	233	VAL
2	T	234	CYS
2	T	242	PHE
2	T	246	PHE
2	T	250	VAL
2	T	255	MET
2	T	271	ASP
2	T	282	PHE
3	U	7	TRP
3	U	18	ASP
3	U	19	ARG
3	U	47	MET
3	U	67	ILE
3	U	72	THR
3	U	87	TRP
3	U	89	VAL
3	U	93	ASP
3	U	94	PHE
3	U	101	GLN
3	U	103	LEU
3	U	114	TYR
3	U	119	LEU
3	U	121	SER
3	U	123	TYR
3	U	133	ARG
3	U	142	ASN

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Mol	Chain	Res	Type
4	V	16	GLU
4	V	22	THR
4	V	33	THR
4	V	43	GLN
4	V	57	TYR
4	V	68	ILE
4	V	79	ARG
4	V	93	CYS
4	V	100	ASN
4	V	105	ILE
4	V	149	LYS
4	V	153	GLU
4	V	156	GLN
4	V	157	LEU
4	V	159	CYS
4	V	173	GLN
4	V	175	GLU
4	V	180	LEU
4	V	181	ASN
4	V	192	GLU
4	W	25	ILE
4	W	26	ASN
4	W	27	THR
4	W	33	THR
4	W	55	HIS
4	W	57	TYR
4	W	59	MET
4	W	61	TYR
4	W	62	ASN
4	W	63	ILE
4	W	79	ARG
4	W	82	ASN
4	W	84	VAL
4	W	87	SER
4	W	90	LEU
4	W	93	CYS
4	W	108	TRP
4	W	113	ASP
4	W	115	PHE
4	W	117	LEU
4	W	119	LEU
4	W	144	LEU

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Mol	Chain	Res	Type
4	W	145	CYS
4	W	159	CYS
4	W	160	ASP
4	W	161	VAL
4	W	167	ILE
4	W	174	THR
4	W	175	GLU
4	W	187	GLU
4	W	193	ASP
5	X	13	LEU
5	X	16	ASN
5	X	23	CYS
5	X	41	ILE
5	X	57	VAL
5	X	70	PHE
5	X	77	TYR
5	X	82	HIS
5	X	88	TYR
5	X	95	SER
5	X	102	TRP
5	X	115	LEU
5	X	169	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (111) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	18	GLN
1	A	20	ASN
1	A	133	GLN
1	A	173	GLN
1	A	217	ASN
2	B	72	GLN
2	B	74	HIS
2	B	92	HIS
2	B	214	ASN
2	B	243	ASN
3	C	65	ASN
3	C	104	GLN
3	C	117	ASN
3	C	142	ASN
4	D	55	HIS

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Mol	Chain	Res	Type
4	D	100	ASN
4	D	142	ASN
4	D	156	GLN
4	E	20	ASN
4	E	26	ASN
4	E	111	ASN
4	E	142	ASN
4	E	181	ASN
5	F	93	GLN
5	F	97	ASN
5	F	121	ASN
1	G	10	ASN
1	G	18	GLN
1	G	20	ASN
1	G	133	GLN
1	G	173	GLN
1	G	217	ASN
2	H	72	GLN
2	H	74	HIS
2	H	92	HIS
2	H	214	ASN
2	H	243	ASN
3	I	65	ASN
3	I	104	GLN
3	I	117	ASN
3	I	142	ASN
4	J	55	HIS
4	J	100	ASN
4	J	142	ASN
4	J	156	GLN
4	K	20	ASN
4	K	26	ASN
4	K	111	ASN
4	K	142	ASN
4	K	181	ASN
5	L	93	GLN
5	L	121	ASN
1	M	10	ASN
1	M	18	GLN
1	M	20	ASN
1	M	133	GLN
1	M	173	GLN

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Mol	Chain	Res	Type
1	M	217	ASN
2	N	67	GLN
2	N	72	GLN
2	N	74	HIS
2	N	92	HIS
2	N	214	ASN
2	N	243	ASN
3	O	65	ASN
3	O	104	GLN
3	O	117	ASN
3	O	142	ASN
3	O	144	ASN
4	P	55	HIS
4	P	100	ASN
4	P	142	ASN
4	P	156	GLN
4	Q	20	ASN
4	Q	26	ASN
4	Q	111	ASN
4	Q	142	ASN
4	Q	181	ASN
5	R	93	GLN
5	R	97	ASN
5	R	121	ASN
1	S	10	ASN
1	S	18	GLN
1	S	20	ASN
1	S	133	GLN
1	S	173	GLN
1	S	217	ASN
2	T	67	GLN
2	T	72	GLN
2	T	74	HIS
2	T	92	HIS
2	T	214	ASN
2	T	243	ASN
3	U	65	ASN
3	U	104	GLN
3	U	117	ASN
3	U	142	ASN
3	U	144	ASN
4	V	55	HIS

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Mol	Chain	Res	Type
4	V	100	ASN
4	V	142	ASN
4	V	156	GLN
4	W	20	ASN
4	W	26	ASN
4	W	111	ASN
4	W	142	ASN
4	W	181	ASN
5	X	93	GLN
5	X	97	ASN
5	X	121	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	PLM	E	194	4	16,16,17	1.06	1 (6%)	15,15,17	1.36	3 (20%)
6	PLM	K	194	4	16,16,17	1.06	1 (6%)	15,15,17	1.36	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PLM	Q	194	4	16,16,17	1.08	1 (6%)	15,15,17	1.36	4 (26%)
6	PLM	W	194	4	16,16,17	1.08	1 (6%)	15,15,17	1.35	3 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	PLM	E	194	4	-	0/14/14/15	0/0/0/0
6	PLM	K	194	4	-	0/14/14/15	0/0/0/0
6	PLM	Q	194	4	-	0/14/14/15	0/0/0/0
6	PLM	W	194	4	-	0/14/14/15	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	W	194	PLM	O1-C1	-4.15	1.19	1.42
6	Q	194	PLM	O1-C1	-4.13	1.19	1.42
6	K	194	PLM	O1-C1	-4.08	1.20	1.42
6	E	194	PLM	O1-C1	-4.06	1.20	1.42

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	194	PLM	C9-C8-C7	-2.50	101.60	114.53
6	Q	194	PLM	C9-C8-C7	-2.45	101.86	114.53
6	K	194	PLM	C9-C8-C7	-2.45	101.88	114.53
6	W	194	PLM	C9-C8-C7	-2.40	102.15	114.53
6	Q	194	PLM	CC-CB-CA	-2.19	103.22	114.53
6	W	194	PLM	CC-CB-CA	-2.16	103.39	114.53
6	E	194	PLM	CC-CB-CA	-2.15	103.45	114.53
6	K	194	PLM	CC-CB-CA	-2.09	103.73	114.53
6	K	194	PLM	CE-CD-CC	-2.08	103.77	114.53
6	W	194	PLM	C7-C6-C5	-2.04	104.02	114.53
6	E	194	PLM	CE-CD-CC	-2.03	104.05	114.53
6	Q	194	PLM	CE-CD-CC	-2.03	104.05	114.53
6	Q	194	PLM	C7-C6-C5	-2.02	104.12	114.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	194	PLM	6	0
6	K	194	PLM	5	0
6	Q	194	PLM	7	0
6	W	194	PLM	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	159/219 (72%)	-0.39	0 100 100	83, 114, 159, 168	6 (3%)
1	G	159/219 (72%)	-0.38	0 100 100	83, 116, 159, 167	6 (3%)
1	M	159/219 (72%)	-0.38	0 100 100	81, 116, 159, 168	6 (3%)
1	S	159/219 (72%)	-0.41	0 100 100	80, 115, 159, 168	6 (3%)
2	B	167/283 (59%)	-0.47	0 100 100	92, 131, 179, 188	10 (5%)
2	H	167/283 (59%)	-0.48	1 (0%) 90 83	92, 130, 180, 192	10 (5%)
2	N	167/283 (59%)	-0.46	0 100 100	92, 131, 176, 189	10 (5%)
2	T	167/283 (59%)	-0.46	1 (0%) 90 83	93, 129, 178, 192	10 (5%)
3	C	143/159 (89%)	-0.31	0 100 100	80, 117, 155, 171	2 (1%)
3	I	143/159 (89%)	-0.32	0 100 100	81, 117, 156, 175	3 (2%)
3	O	143/159 (89%)	-0.33	0 100 100	81, 117, 156, 174	2 (1%)
3	U	143/159 (89%)	-0.31	0 100 100	81, 117, 156, 171	3 (2%)
4	D	186/193 (96%)	-0.45	2 (1%) 82 70	94, 134, 168, 185	7 (3%)
4	E	188/193 (97%)	-0.46	3 (1%) 74 60	79, 110, 140, 183	1 (0%)
4	J	186/193 (96%)	-0.46	2 (1%) 82 70	90, 135, 167, 186	7 (3%)
4	K	188/193 (97%)	-0.45	2 (1%) 82 70	79, 111, 140, 183	1 (0%)
4	P	186/193 (96%)	-0.48	1 (0%) 91 86	88, 133, 168, 186	7 (3%)
4	Q	188/193 (97%)	-0.43	3 (1%) 74 60	78, 110, 141, 184	1 (0%)
4	V	186/193 (96%)	-0.47	2 (1%) 82 70	93, 133, 167, 185	7 (3%)
4	W	188/193 (97%)	-0.48	0 100 100	79, 111, 140, 182	1 (0%)
5	F	166/206 (80%)	-0.28	0 100 100	103, 150, 172, 178	7 (4%)
5	L	166/206 (80%)	-0.25	0 100 100	106, 149, 173, 179	7 (4%)
5	R	166/206 (80%)	-0.23	0 100 100	104, 149, 171, 175	7 (4%)
5	X	166/206 (80%)	-0.25	0 100 100	105, 148, 171, 176	7 (4%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	4036/5012 (80%)	-0.40	17 (0%) 93 88	78, 125, 170, 192	134 (3%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	J	193	ASP	4.2
4	D	193	ASP	3.9
4	V	193	ASP	3.8
4	P	193	ASP	3.7
4	K	191	GLY	2.6
4	Q	193	ASP	2.5
4	Q	191	GLY	2.4
4	Q	192	GLU	2.4
4	E	192	GLU	2.3
2	T	165	TYR	2.3
4	E	191	GLY	2.3
4	K	185	LYS	2.2
4	E	193	ASP	2.2
4	J	110	HIS	2.2
4	V	110	HIS	2.1
2	H	165	TYR	2.1
4	D	110	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	PLM	W	194	17/18	0.89	0.22	0.34	107,108,111,111	0
6	PLM	Q	194	17/18	0.89	0.22	0.28	100,103,111,112	0
6	PLM	E	194	17/18	0.91	0.21	0.28	102,105,111,111	0
6	PLM	K	194	17/18	0.91	0.21	0.16	104,106,113,114	0

6.5 Other polymers [i](#)

There are no such residues in this entry.