



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:17 PM UTC

PDB ID : 3CUE / pdb\_00003cue  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

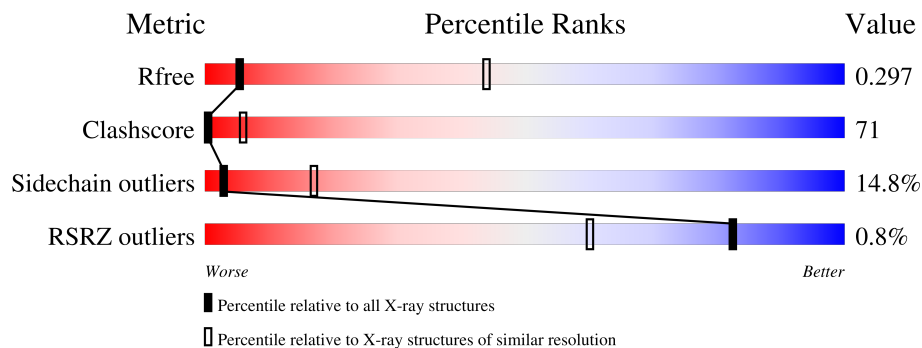
# 1 Overall quality at a glance

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.



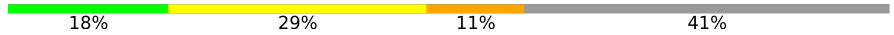
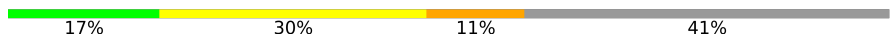
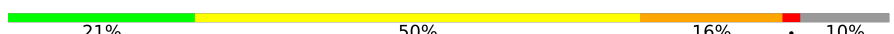
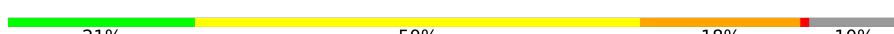
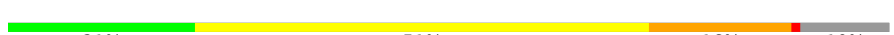

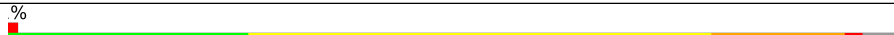
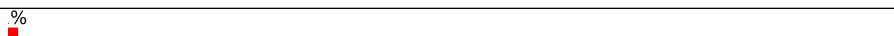
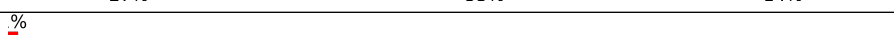
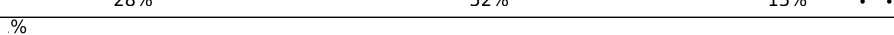
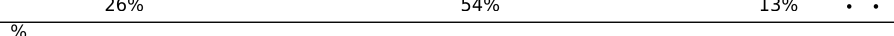

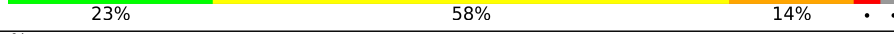

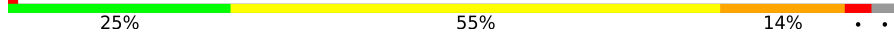
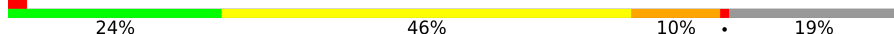
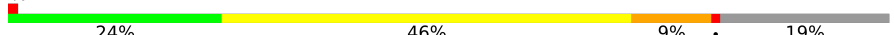
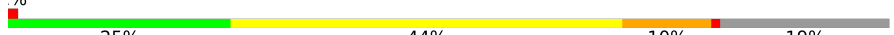
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the 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	
2	H	283	

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
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 [i](#)

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
			Total	C	N	O	S			
1	A	159	1285	833	204	239	9	27	0	0
1	G	159	1285	833	204	239	9	27	0	0
1	M	159	1285	833	204	239	9	27	0	0
1	S	159	1285	833	204	239	9	27	0	0

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

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

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

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

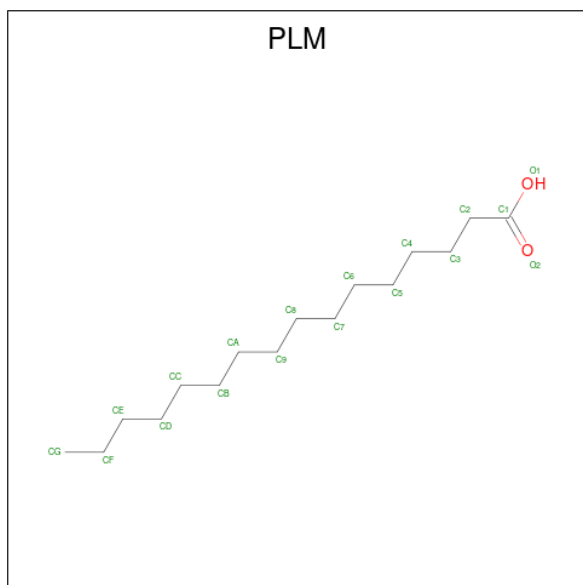
- Molecule 4 is a protein called Transport protein particle 22 kDa subunit.

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 (CCD ID: PLM) (formula: C<sub>16</sub>H<sub>32</sub>O<sub>2</sub>).

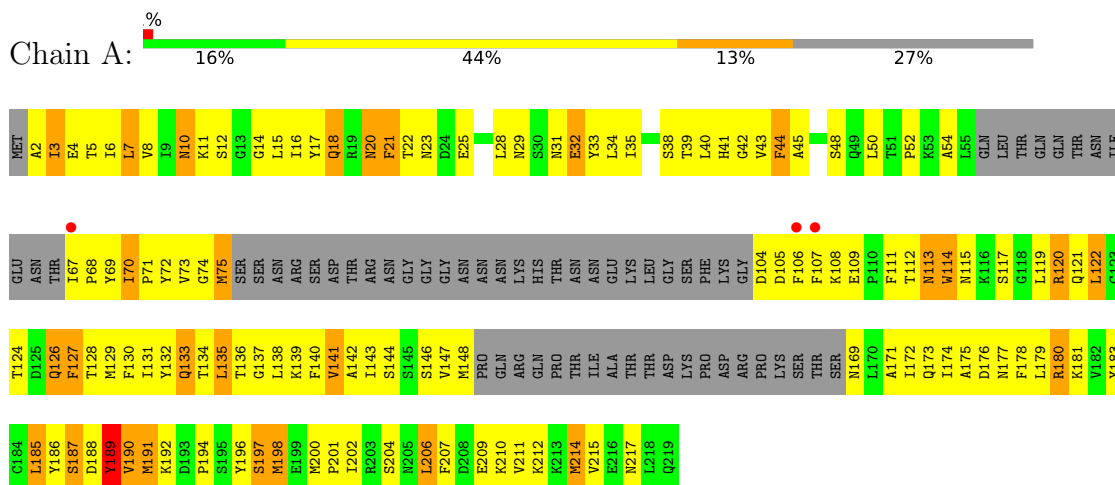


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			17	16	1		
6	K	1	Total	C	O	0	0
			17	16	1		
6	Q	1	Total	C	O	0	0
			17	16	1		
6	W	1	Total	C	O	0	0
			17	16	1		

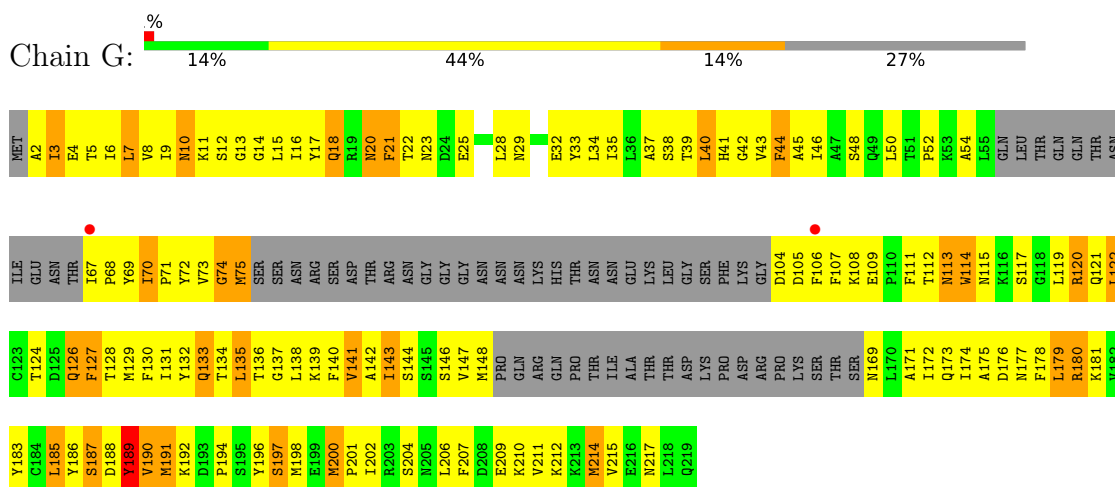
### 3 Residue-property plots [i](#)

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

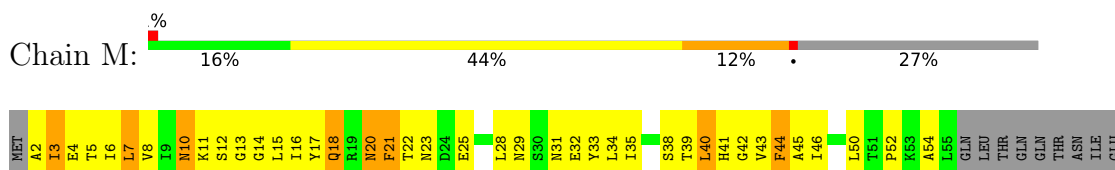
- Molecule 1: Transport protein particle 23 kDa subunit

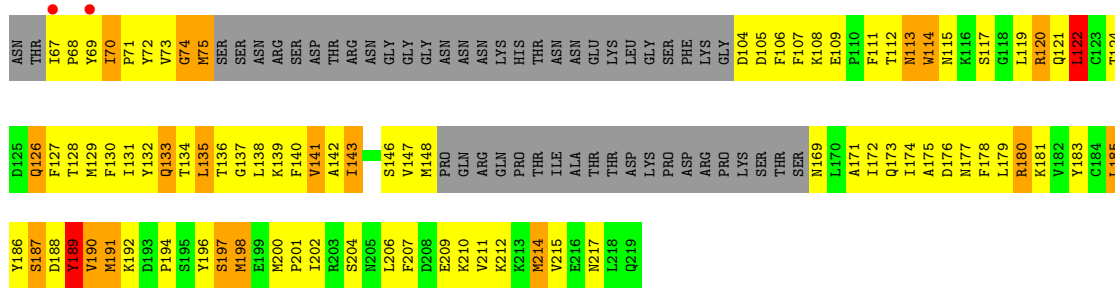


- Molecule 1: Transport protein particle 23 kDa subunit

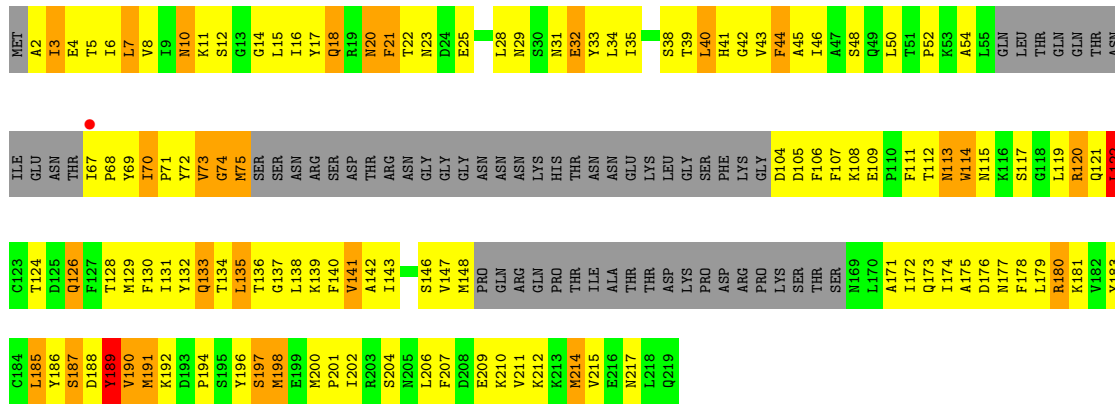
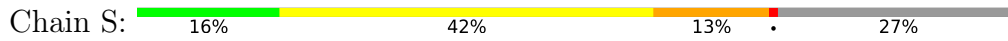


- Molecule 1: Transport protein particle 23 kDa subunit

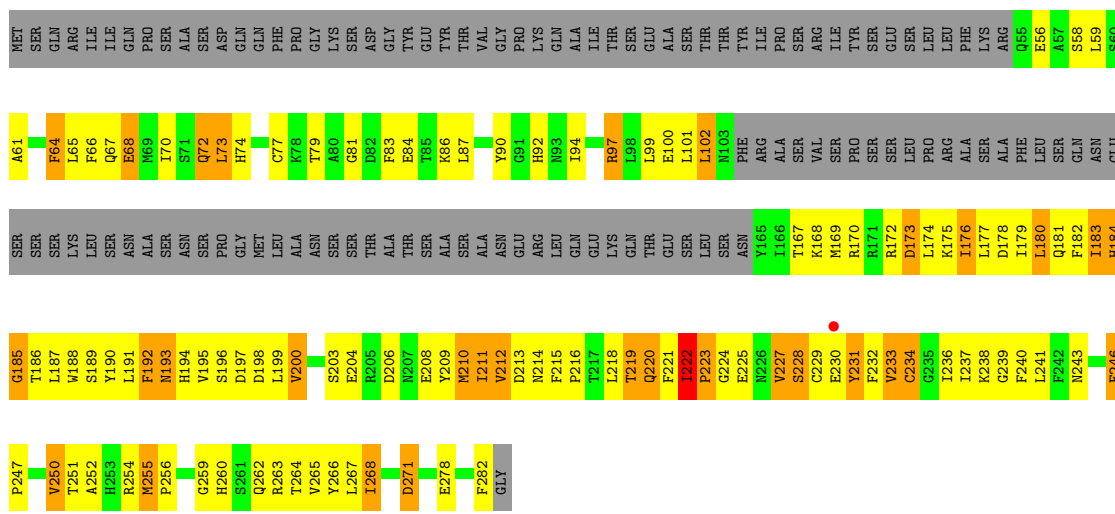
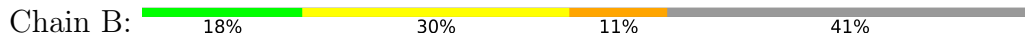




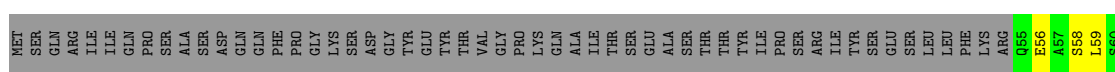
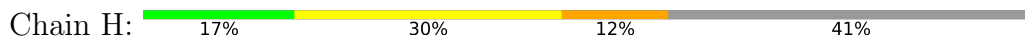
● Molecule 1: Transport protein particle 23 kDa subunit

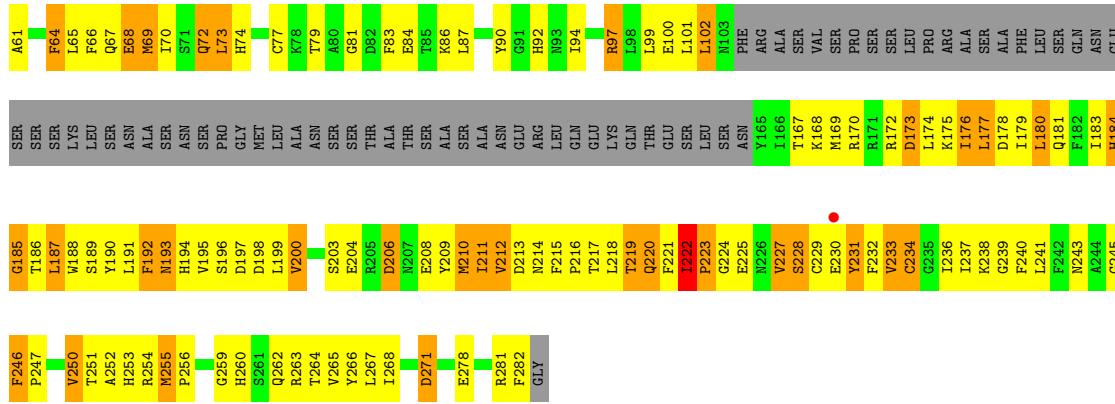


● Molecule 2: Transport protein particle 31 kDa subunit



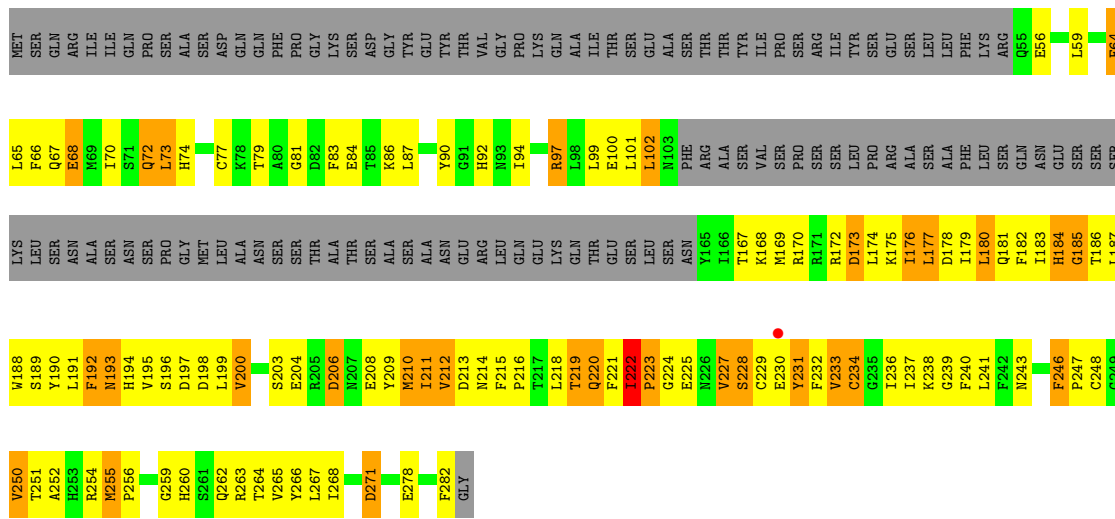
● Molecule 2: Transport protein particle 31 kDa subunit





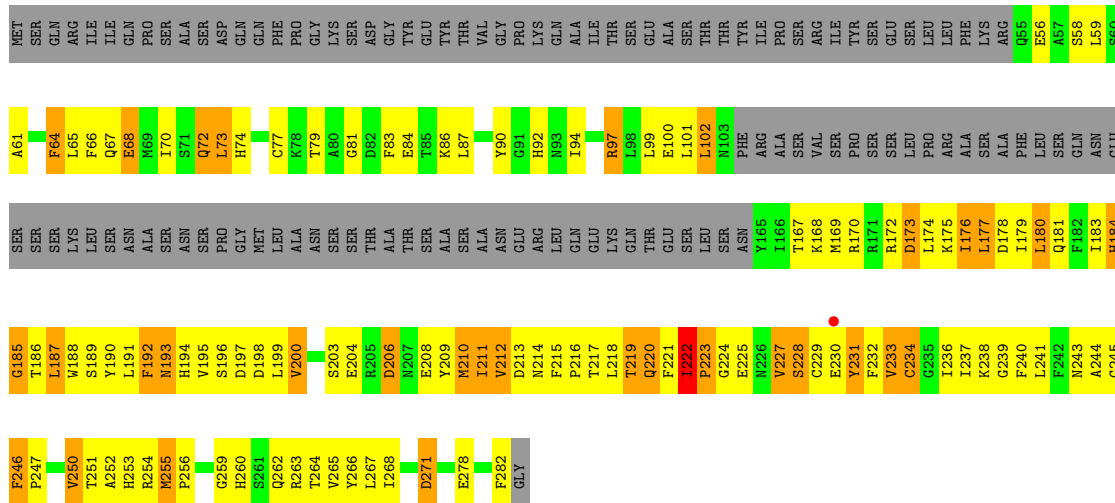
• Molecule 2: Transport protein particle 31 kDa subunit

Chain N: 18% 29% 11% 41%



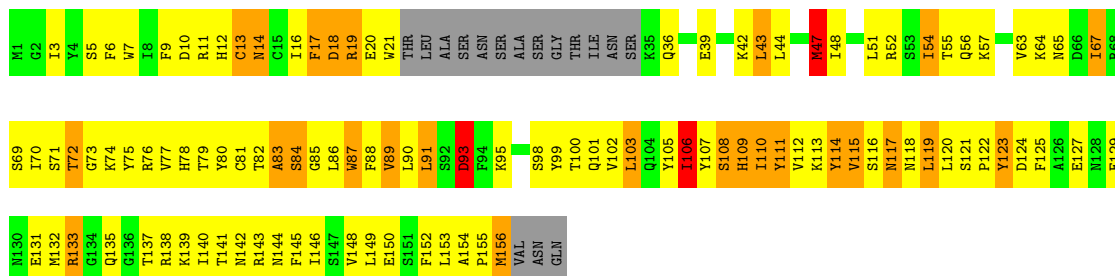
• Molecule 2: Transport protein particle 31 kDa subunit

Chain T: 17% 30% 11% 41%



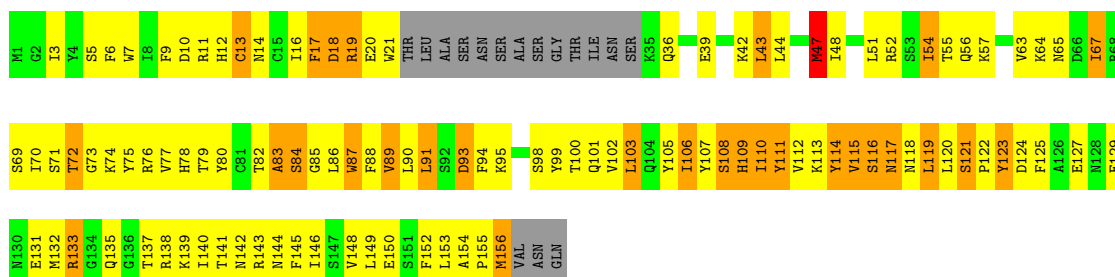
- Molecule 3: Transport protein particle 18 kDa subunit

Chain C: 21% 50% 16% 10%



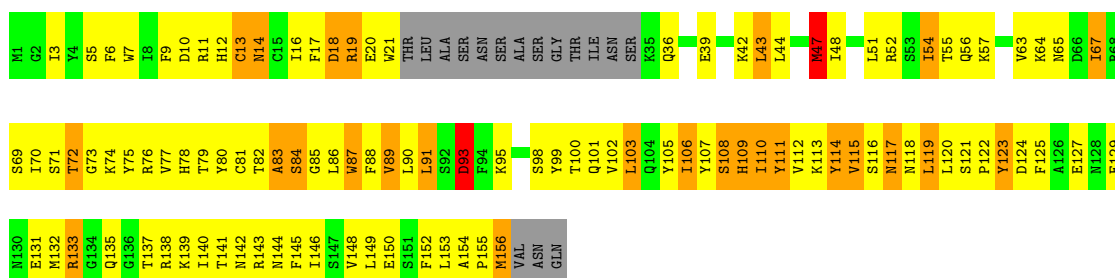
- Molecule 3: Transport protein particle 18 kDa subunit

Chain I: 21% 50% 18% 10%



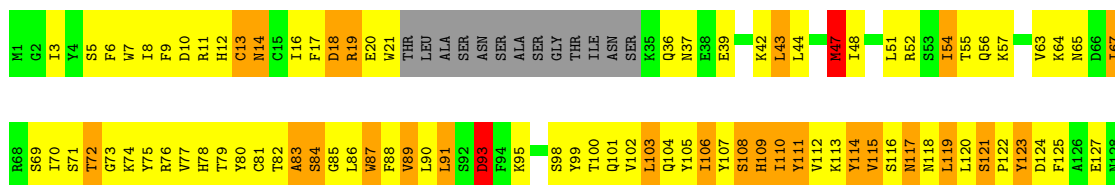
- Molecule 3: Transport protein particle 18 kDa subunit

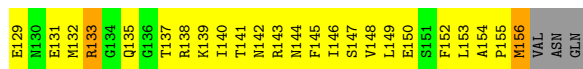
Chain O: 21% 51% 16% 10%



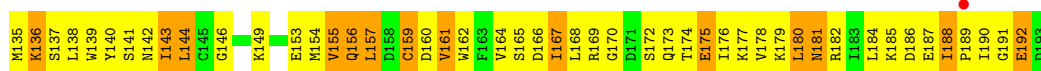
- Molecule 3: Transport protein particle 18 kDa subunit

Chain U: 19% 53% 17% 10%





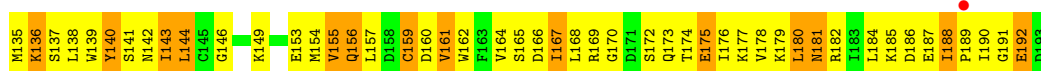
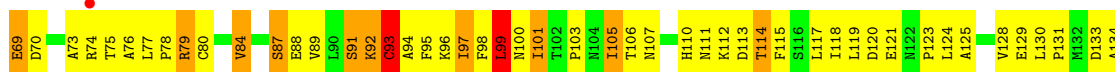
- Molecule 4: Transport protein particle 22 kDa subunit



- Molecule 4: Transport protein particle 22 kDa subunit

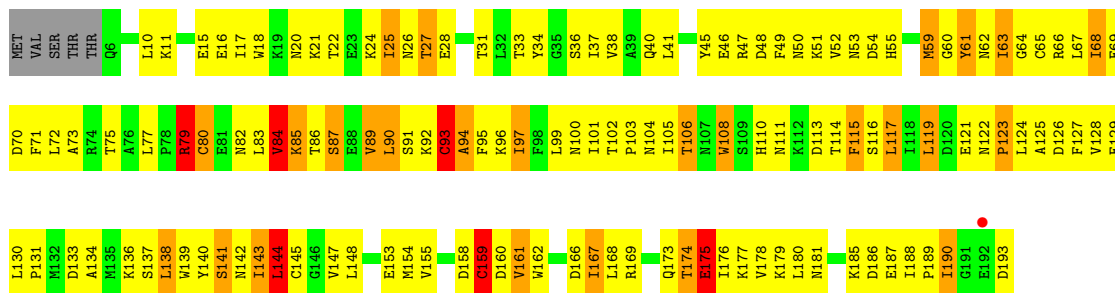


- Molecule 4: Transport protein particle 22 kDa subunit

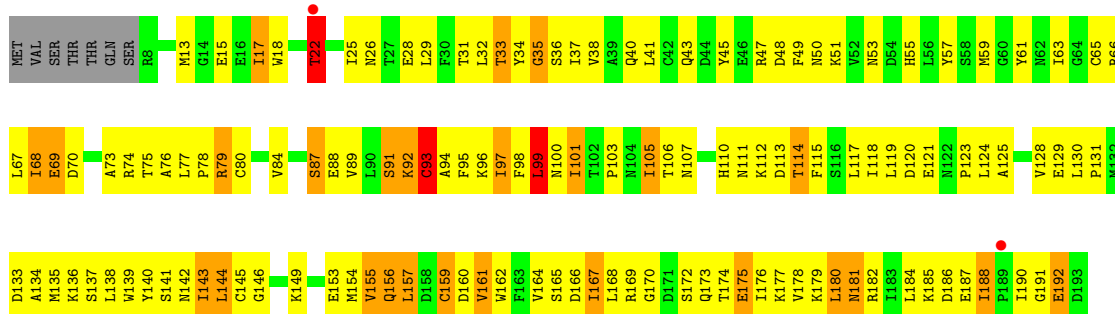


- Molecule 4: Transport protein particle 22 kDa subunit

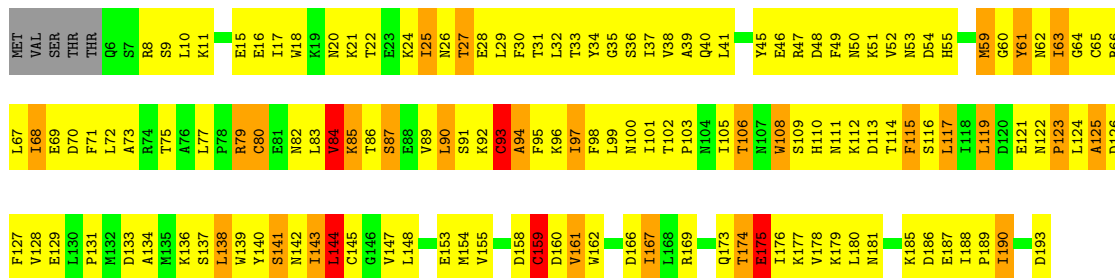




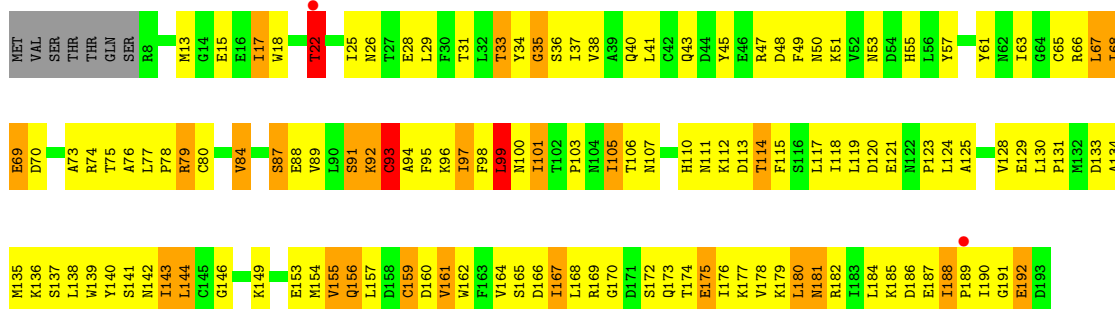
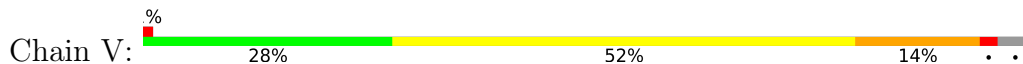
• Molecule 4: Transport protein particle 22 kDa subunit



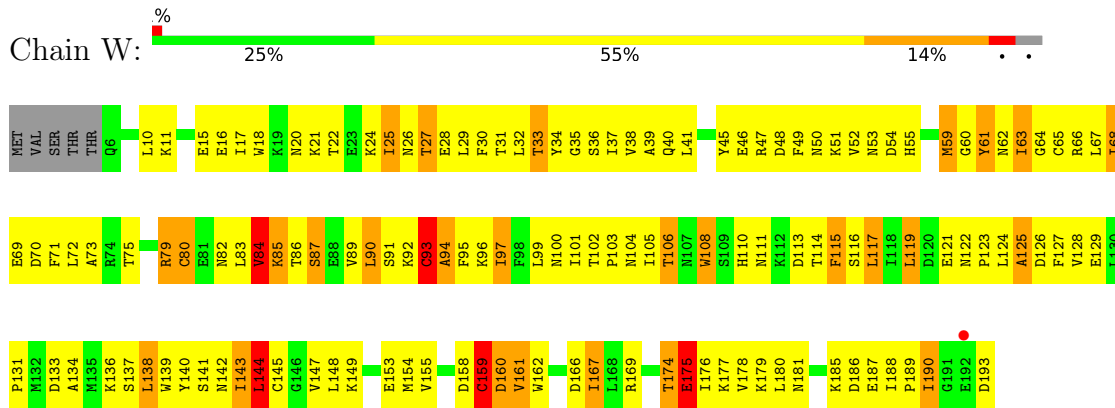
• Molecule 4: Transport protein particle 22 kDa subunit



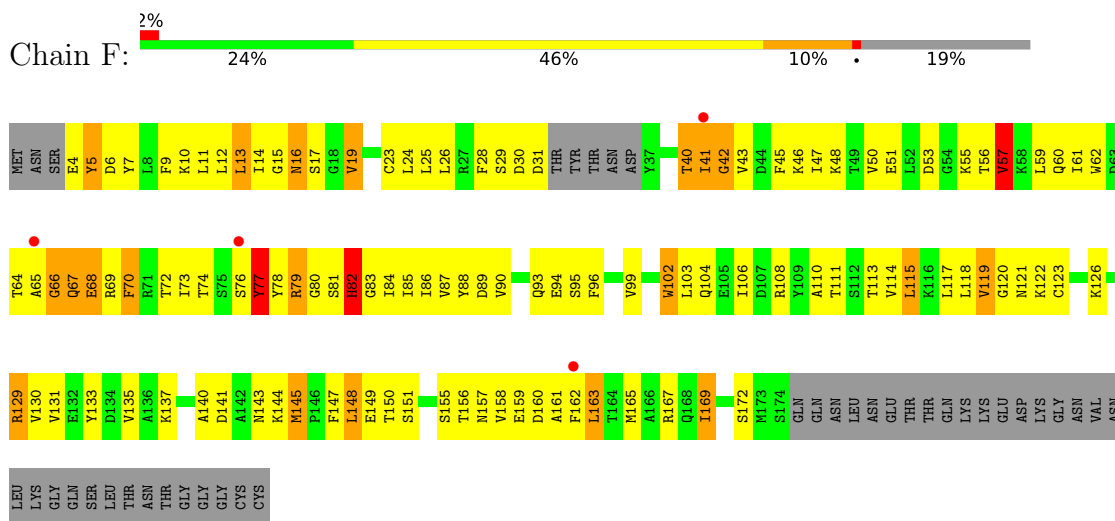
• Molecule 4: Transport protein particle 22 kDa subunit



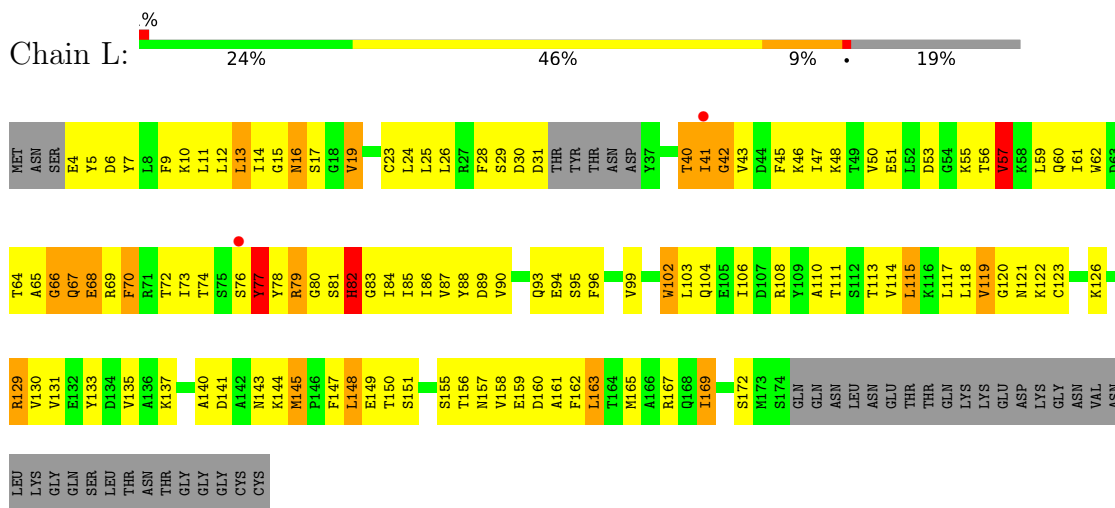
• Molecule 4: Transport protein particle 22 kDa subunit



• Molecule 5: GTP-binding protein YPT1

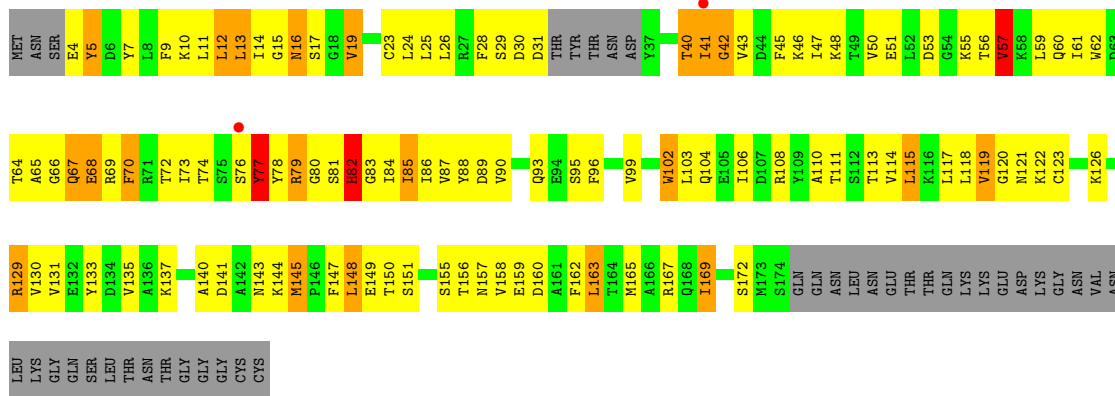


• Molecule 5: GTP-binding protein YPT1

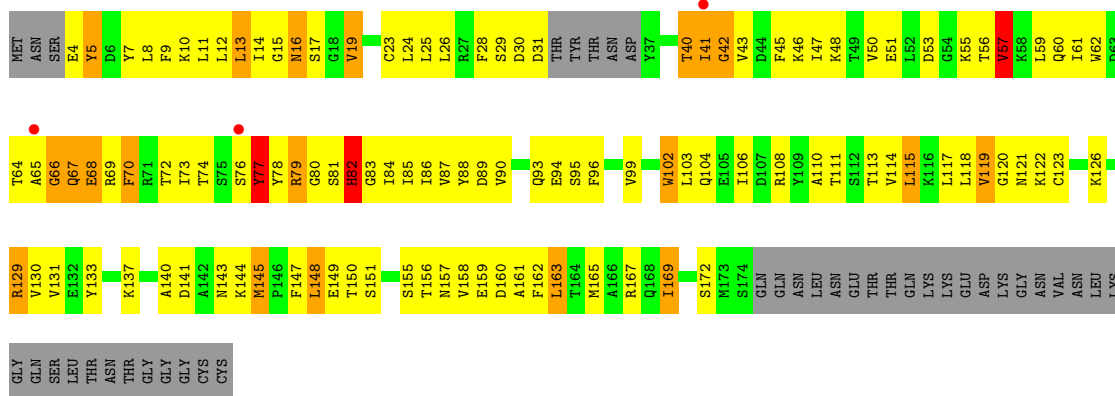
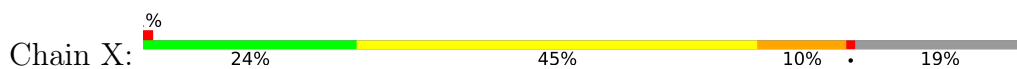


• Molecule 5: GTP-binding protein YPT1





• Molecule 5: GTP-binding protein YPT1



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.12Å 115.40Å 290.07Å 90.00° 90.28° 90.00°	Depositor
Resolution (Å)	25.00 – 3.70 25.00 – 3.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (25.00-3.70) 96.9 (25.00-3.70)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.53 (at 3.74Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.265 , 0.299 0.268 , 0.297	Depositor DCC
$R_{free}$ test set	5685 reflections (7.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	128.9	Xtrriage
Anisotropy	0.158	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , 56.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.387 for -k,-h,-l 0.398 for k,h,-l 0.397 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	32776	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	128.0	wwPDB-VP

Xtrriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.80	1/1309 (0.1%)	1.25	12/1764 (0.7%)
1	G	0.80	1/1309 (0.1%)	1.25	13/1764 (0.7%)
1	M	0.81	1/1309 (0.1%)	1.26	14/1764 (0.8%)
1	S	0.81	1/1309 (0.1%)	1.25	14/1764 (0.8%)
2	B	0.72	0/1388	1.32	19/1869 (1.0%)
2	H	0.72	1/1388 (0.1%)	1.31	17/1869 (0.9%)
2	N	0.71	0/1388	1.32	17/1869 (0.9%)
2	T	0.72	0/1388	1.31	17/1869 (0.9%)
3	C	0.83	0/1218	1.44	18/1640 (1.1%)
3	I	0.81	0/1218	1.44	15/1640 (0.9%)
3	O	0.83	0/1218	1.44	16/1640 (1.0%)
3	U	0.82	0/1218	1.45	17/1640 (1.0%)
4	D	0.75	1/1527 (0.1%)	1.32	20/2063 (1.0%)
4	E	0.87	1/1542 (0.1%)	1.37	21/2083 (1.0%)
4	J	0.76	1/1527 (0.1%)	1.32	20/2063 (1.0%)
4	K	0.86	0/1542	1.37	21/2083 (1.0%)
4	P	0.77	2/1527 (0.1%)	1.31	18/2063 (0.9%)
4	Q	0.87	0/1542	1.37	21/2083 (1.0%)
4	V	0.75	1/1527 (0.1%)	1.31	19/2063 (0.9%)
4	W	0.85	0/1542	1.36	19/2083 (0.9%)
5	F	0.75	4/1348 (0.3%)	1.48	29/1815 (1.6%)
5	L	0.75	6/1348 (0.4%)	1.44	28/1815 (1.5%)
5	R	0.71	3/1348 (0.2%)	1.43	28/1815 (1.5%)
5	X	0.73	5/1348 (0.4%)	1.45	28/1815 (1.5%)
All	All	0.78	29/33328 (0.1%)	1.36	461/44936 (1.0%)

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

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

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	67	GLN	C-N	-7.46	1.23	1.33
5	F	67	GLN	C-N	-7.44	1.23	1.33
5	L	68	GLU	CA-C	-7.21	1.43	1.52
5	F	67	GLN	CA-C	-7.17	1.42	1.52
5	L	68	GLU	N-CA	-6.70	1.37	1.46
5	L	67	GLN	N-CA	-6.59	1.38	1.46
5	X	67	GLN	N-CA	-6.55	1.38	1.46
5	L	66	GLY	C-N	-6.53	1.24	1.33
5	F	66	GLY	C-N	-6.44	1.24	1.33
5	R	67	GLN	CA-C	-5.99	1.44	1.52
5	L	67	GLN	CA-C	-5.92	1.44	1.52
5	L	67	GLN	C-N	-5.89	1.25	1.33
4	P	59	MET	SD-CE	-5.84	1.65	1.79
5	X	67	GLN	C-N	-5.81	1.25	1.33
4	D	22	THR	CA-CB	5.81	1.59	1.53
5	X	66	GLY	C-N	-5.69	1.25	1.33
5	X	68	GLU	N-CA	-5.64	1.39	1.46
2	H	69	MET	SD-CE	-5.58	1.65	1.79
1	A	198	MET	SD-CE	5.56	1.93	1.79
5	F	67	GLN	N-CA	-5.43	1.39	1.46
4	J	22	THR	CA-CB	5.41	1.59	1.53
1	G	200	MET	SD-CE	-5.35	1.66	1.79
4	V	22	THR	CA-CB	5.30	1.59	1.53
5	X	67	GLN	CA-C	-5.25	1.45	1.52
4	P	22	THR	CA-CB	5.24	1.59	1.53
4	E	125	ALA	CA-CB	-5.12	1.48	1.53
5	R	68	GLU	CA-C	-5.10	1.46	1.52
1	M	198	MET	SD-CE	5.05	1.92	1.79
1	S	198	MET	SD-CE	5.01	1.92	1.79

All (461) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	93	CYS	N-CA-C	18.20	130.80	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	93	CYS	N-CA-C	18.14	130.73	111.14
4	J	93	CYS	N-CA-C	18.04	130.62	111.14
4	P	93	CYS	N-CA-C	17.87	130.44	111.14
4	Q	93	CYS	N-CA-C	16.04	128.46	111.14
4	W	93	CYS	N-CA-C	15.93	128.34	111.14
4	E	93	CYS	N-CA-C	15.91	128.32	111.14
4	K	93	CYS	N-CA-C	15.81	128.22	111.14
3	U	115	VAL	N-CA-C	15.15	124.78	110.53
3	C	115	VAL	N-CA-C	15.06	124.69	110.53
3	I	115	VAL	N-CA-C	14.93	124.57	110.53
3	O	115	VAL	N-CA-C	14.79	124.43	110.53
5	F	67	GLN	N-CA-C	-14.73	96.19	114.75
5	F	74	THR	N-CA-C	13.81	126.05	111.14
5	R	74	THR	N-CA-C	13.76	126.00	111.14
5	X	74	THR	N-CA-C	13.68	125.91	111.14
5	L	74	THR	N-CA-C	13.56	125.78	111.14
3	C	110	ILE	N-CA-C	12.61	122.38	110.53
3	U	110	ILE	N-CA-C	12.60	122.38	110.53
3	I	110	ILE	N-CA-C	12.54	122.31	110.53
3	O	110	ILE	N-CA-C	12.50	122.28	110.53
5	X	67	GLN	N-CA-C	-12.01	99.62	114.75
1	A	189	TYR	N-CA-C	11.59	123.66	111.14
1	S	189	TYR	N-CA-C	11.43	123.49	111.14
5	L	67	GLN	N-CA-C	-11.38	100.41	114.75
2	H	186	THR	N-CA-C	11.31	123.35	111.14
2	T	186	THR	N-CA-C	11.30	123.34	111.14
1	M	189	TYR	N-CA-C	11.29	123.33	111.14
1	G	189	TYR	N-CA-C	11.22	123.26	111.14
2	B	186	THR	N-CA-C	11.19	123.23	111.14
2	N	186	THR	N-CA-C	11.09	123.11	111.14
5	L	77	TYR	N-CA-C	10.82	122.83	111.14
5	F	77	TYR	N-CA-C	10.74	122.74	111.14
5	X	77	TYR	N-CA-C	10.67	122.66	111.14
5	R	77	TYR	N-CA-C	10.63	122.62	111.14
5	X	79	ARG	N-CA-C	10.07	122.26	111.28
5	R	79	ARG	N-CA-C	9.95	122.13	111.28
5	F	79	ARG	N-CA-C	9.88	122.05	111.28
5	F	67	GLN	CA-C-N	-9.85	102.72	121.54
5	F	67	GLN	C-N-CA	-9.85	102.72	121.54
5	L	79	ARG	N-CA-C	9.81	121.98	111.28
5	X	67	GLN	OE1-CD-NE2	-9.76	112.84	122.60
5	F	67	GLN	OE1-CD-NE2	-9.73	112.87	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	67	GLN	OE1-CD-NE2	-9.72	112.88	122.60
5	R	67	GLN	OE1-CD-NE2	-9.66	112.94	122.60
3	I	109	HIS	N-CA-C	9.58	121.49	111.14
3	U	109	HIS	N-CA-C	9.42	121.32	111.14
4	W	91	SER	N-CA-C	9.40	121.30	111.14
5	R	78	TYR	N-CA-C	9.39	121.52	111.28
3	C	109	HIS	N-CA-C	9.38	121.27	111.14
3	O	109	HIS	N-CA-C	9.36	121.25	111.14
5	L	78	TYR	N-CA-C	9.35	121.48	111.28
5	F	78	TYR	N-CA-C	9.29	121.41	111.28
5	X	78	TYR	N-CA-C	9.26	121.37	111.28
3	O	84	SER	N-CA-C	-9.13	102.14	113.38
4	K	91	SER	N-CA-C	9.12	121.00	111.14
2	T	222	ILE	CA-C-N	9.10	131.22	119.84
2	T	222	ILE	C-N-CA	9.10	131.22	119.84
3	O	108	SER	N-CA-C	9.06	120.93	111.14
3	U	108	SER	N-CA-C	9.06	120.92	111.14
3	C	108	SER	N-CA-C	8.98	120.84	111.14
3	U	84	SER	N-CA-C	-8.96	102.36	113.38
2	H	222	ILE	CA-C-N	8.95	131.02	119.84
2	H	222	ILE	C-N-CA	8.95	131.02	119.84
3	I	108	SER	N-CA-C	8.94	120.79	111.14
3	I	84	SER	N-CA-C	-8.92	102.41	113.38
3	C	84	SER	N-CA-C	-8.88	102.46	113.38
4	Q	91	SER	N-CA-C	8.76	120.60	111.14
2	N	222	ILE	CA-C-N	8.71	130.72	119.84
2	N	222	ILE	C-N-CA	8.71	130.72	119.84
4	E	91	SER	N-CA-C	8.64	120.47	111.14
3	I	111	TYR	N-CA-C	8.62	120.45	111.14
5	R	67	GLN	N-CA-C	-8.61	101.55	114.64
2	B	222	ILE	CA-C-N	8.54	130.51	119.84
2	B	222	ILE	C-N-CA	8.54	130.51	119.84
3	U	111	TYR	N-CA-C	8.47	120.28	111.14
3	O	111	TYR	N-CA-C	8.35	120.16	111.14
3	C	111	TYR	N-CA-C	8.33	120.13	111.14
2	B	206	ASP	N-CA-C	8.31	122.52	112.38
2	H	206	ASP	N-CA-C	8.31	122.51	112.38
1	S	44	PHE	N-CA-C	-8.28	102.26	111.28
2	N	206	ASP	N-CA-C	8.27	122.47	112.38
2	T	206	ASP	N-CA-C	8.26	122.46	112.38
2	T	200	VAL	N-CA-C	8.20	119.73	107.51
2	N	200	VAL	N-CA-C	8.19	119.71	107.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	44	PHE	N-CA-C	-8.15	102.39	111.28
2	H	200	VAL	N-CA-C	8.15	119.66	107.51
3	C	54	ILE	N-CA-C	-8.12	102.34	110.62
1	A	44	PHE	N-CA-C	-8.10	102.45	111.28
2	B	200	VAL	N-CA-C	8.10	119.58	107.51
5	R	76	SER	N-CA-C	8.06	119.84	111.14
3	U	54	ILE	N-CA-C	-8.04	102.42	110.62
3	I	13	CYS	N-CA-C	-8.02	103.44	113.23
5	F	76	SER	N-CA-C	8.00	119.78	111.14
5	R	148	LEU	N-CA-C	-7.99	97.75	110.14
5	X	148	LEU	N-CA-C	-7.99	97.76	110.14
3	I	54	ILE	N-CA-C	-7.92	102.55	110.62
1	G	44	PHE	N-CA-C	-7.87	102.70	111.28
5	L	148	LEU	N-CA-C	-7.86	97.95	110.14
5	X	76	SER	N-CA-C	7.85	119.62	111.14
3	O	54	ILE	N-CA-C	-7.83	102.64	110.62
5	F	148	LEU	N-CA-C	-7.80	98.04	110.14
4	W	159	CYS	N-CA-C	7.74	121.51	110.14
5	L	76	SER	N-CA-C	7.72	119.48	111.14
4	Q	159	CYS	N-CA-C	7.64	121.37	110.14
4	K	159	CYS	N-CA-C	7.63	121.36	110.14
5	X	67	GLN	CA-C-N	-7.63	106.97	121.54
5	X	67	GLN	C-N-CA	-7.63	106.97	121.54
4	E	159	CYS	N-CA-C	7.60	121.31	110.14
3	O	13	CYS	N-CA-C	-7.56	104.00	113.23
1	A	190	VAL	N-CA-C	7.55	117.63	110.53
5	R	67	GLN	CA-C-N	-7.48	107.26	121.54
5	R	67	GLN	C-N-CA	-7.48	107.26	121.54
1	M	190	VAL	N-CA-C	7.43	117.52	110.53
5	L	17	SER	N-CA-C	7.41	126.58	110.80
5	X	17	SER	N-CA-C	7.41	126.58	110.80
5	R	17	SER	N-CA-C	7.35	126.46	110.80
4	D	188	ILE	CA-C-N	7.30	128.96	119.84
4	D	188	ILE	C-N-CA	7.30	128.96	119.84
5	F	17	SER	N-CA-C	7.29	126.34	110.80
1	S	190	VAL	N-CA-C	7.24	117.33	110.53
4	E	68	ILE	N-CA-C	-7.18	103.30	110.62
1	G	190	VAL	N-CA-C	7.17	117.27	110.53
4	W	68	ILE	N-CA-C	-7.16	103.32	110.62
4	V	188	ILE	CA-C-N	7.14	128.76	119.84
4	V	188	ILE	C-N-CA	7.14	128.76	119.84
3	O	47	MET	N-CA-C	-7.12	103.52	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	67	GLN	CA-C-N	-7.09	107.99	121.54
5	L	67	GLN	C-N-CA	-7.09	107.99	121.54
4	P	188	ILE	CA-C-N	7.09	128.70	119.84
4	P	188	ILE	C-N-CA	7.09	128.70	119.84
2	H	212	VAL	N-CA-C	7.09	118.49	108.36
4	J	188	ILE	CA-C-N	7.07	128.68	119.84
4	J	188	ILE	C-N-CA	7.07	128.68	119.84
2	N	212	VAL	N-CA-C	7.06	118.46	108.36
2	B	212	VAL	N-CA-C	7.03	118.42	108.36
2	T	212	VAL	N-CA-C	7.01	118.39	108.36
3	C	83	ALA	N-CA-C	-7.00	104.77	113.38
4	K	68	ILE	N-CA-C	-7.00	103.48	110.62
4	Q	68	ILE	N-CA-C	-6.98	103.50	110.62
4	W	94	ALA	N-CA-C	6.96	118.65	111.14
3	U	83	ALA	N-CA-C	-6.88	104.92	113.38
3	O	83	ALA	N-CA-C	-6.85	104.95	113.38
5	R	81	SER	N-CA-C	6.84	120.00	108.02
3	I	83	ALA	N-CA-C	-6.83	104.98	113.38
2	N	173	ASP	N-CA-C	6.82	120.27	110.24
4	P	99	LEU	N-CA-C	-6.80	98.97	109.24
5	F	81	SER	N-CA-C	6.80	119.92	108.02
4	J	99	LEU	N-CA-C	-6.80	98.97	109.24
4	D	172	SER	N-CA-C	6.79	125.27	110.80
2	N	77	CYS	N-CA-C	6.79	120.21	110.10
5	L	81	SER	N-CA-C	6.78	119.89	108.02
4	P	172	SER	N-CA-C	6.75	125.18	110.80
4	K	94	ALA	N-CA-C	6.72	118.40	111.14
5	X	81	SER	N-CA-C	6.72	119.78	108.02
4	Q	94	ALA	N-CA-C	6.71	118.38	111.14
5	R	70	PHE	N-CA-C	-6.70	103.98	111.28
4	J	172	SER	N-CA-C	6.69	125.05	110.80
2	B	229	CYS	CA-C-N	6.69	129.24	120.28
2	B	229	CYS	C-N-CA	6.69	129.24	120.28
4	E	94	ALA	N-CA-C	6.68	118.36	111.14
4	D	99	LEU	N-CA-C	-6.68	99.16	109.24
3	U	117	ASN	N-CA-C	-6.67	106.08	114.56
5	R	67	GLN	CG-CD-NE2	6.67	126.40	116.40
2	T	77	CYS	N-CA-C	6.66	119.96	109.96
5	F	70	PHE	N-CA-C	-6.66	104.02	111.28
4	J	35	GLY	N-CA-C	-6.65	104.75	112.73
2	H	77	CYS	N-CA-C	6.63	119.91	109.96
4	V	172	SER	N-CA-C	6.63	124.93	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	U	47	MET	N-CA-C	-6.63	104.06	111.28
4	V	99	LEU	N-CA-C	-6.62	99.25	109.24
2	B	77	CYS	N-CA-C	6.62	119.89	109.96
5	L	70	PHE	N-CA-C	-6.61	104.08	111.28
3	I	117	ASN	N-CA-C	-6.60	106.17	114.56
5	X	70	PHE	N-CA-C	-6.59	104.10	111.28
3	O	36	GLN	CA-C-N	6.56	129.06	120.28
3	O	36	GLN	C-N-CA	6.56	129.06	120.28
3	I	36	GLN	CA-C-N	6.54	129.05	120.28
3	I	36	GLN	C-N-CA	6.54	129.05	120.28
3	C	47	MET	N-CA-C	-6.54	104.15	111.28
4	P	35	GLY	N-CA-C	-6.54	104.89	112.73
3	C	117	ASN	N-CA-C	-6.52	106.28	114.56
3	C	36	GLN	CA-C-N	6.52	129.02	120.28
3	C	36	GLN	C-N-CA	6.52	129.02	120.28
3	U	13	CYS	N-CA-C	-6.51	103.83	113.40
2	H	225	GLU	N-CA-C	6.50	118.25	111.03
5	R	119	VAL	N-CA-C	6.45	119.37	108.86
2	H	173	ASP	N-CA-C	6.42	119.67	110.10
3	C	13	CYS	N-CA-C	-6.42	103.97	113.40
5	L	119	VAL	N-CA-C	6.42	119.32	108.86
3	O	117	ASN	N-CA-C	-6.41	106.42	114.56
4	Q	85	LYS	N-CA-C	-6.40	104.31	111.28
3	U	36	GLN	CA-C-N	6.39	128.84	120.28
3	U	36	GLN	C-N-CA	6.39	128.84	120.28
2	N	229	CYS	CA-C-N	6.38	128.83	120.28
2	N	229	CYS	C-N-CA	6.38	128.83	120.28
4	K	85	LYS	N-CA-C	-6.37	104.34	111.28
2	T	173	ASP	N-CA-C	6.37	119.22	110.24
3	I	47	MET	N-CA-C	-6.36	104.35	111.28
1	A	20	ASN	N-CA-C	-6.36	98.85	108.96
4	E	143	ILE	CB-CA-C	-6.32	103.60	112.14
5	F	119	VAL	N-CA-C	6.31	119.14	108.86
4	V	35	GLY	N-CA-C	-6.31	105.16	112.73
4	W	138	LEU	N-CA-C	6.29	119.38	110.50
1	G	20	ASN	N-CA-C	-6.28	98.98	108.96
4	K	138	LEU	N-CA-C	6.27	119.34	110.50
2	B	173	ASP	N-CA-C	6.27	119.08	110.24
2	T	225	GLU	N-CA-C	6.26	117.98	111.03
4	V	143	ILE	N-CA-C	-6.26	104.23	110.62
5	F	68	GLU	O-C-N	6.26	130.92	122.59
5	X	119	VAL	N-CA-C	6.25	119.04	108.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	225	GLU	N-CA-C	6.24	117.96	111.03
4	E	79	ARG	N-CA-C	6.24	124.08	110.80
1	S	20	ASN	N-CA-C	-6.23	99.06	108.96
4	Q	138	LEU	N-CA-C	6.22	119.27	110.50
4	D	35	GLY	N-CA-C	-6.22	105.27	112.73
5	X	82	HIS	N-CA-C	-6.21	105.28	112.92
5	F	82	HIS	N-CA-C	-6.20	105.30	112.92
1	M	20	ASN	N-CA-C	-6.20	99.11	108.96
2	T	224	GLY	N-CA-C	6.17	127.80	113.18
5	F	67	GLN	CG-CD-NE2	6.16	125.65	116.40
4	J	167	ILE	N-CA-C	-6.16	104.50	110.42
2	T	229	CYS	CA-C-N	6.16	128.54	120.28
2	T	229	CYS	C-N-CA	6.16	128.54	120.28
4	W	106	THR	N-CA-C	6.16	116.22	108.45
2	N	225	GLU	N-CA-C	6.13	117.83	111.03
2	N	224	GLY	N-CA-C	6.11	127.66	113.18
4	E	106	THR	N-CA-C	6.11	116.14	108.45
2	H	224	GLY	N-CA-C	6.09	127.61	113.18
2	H	229	CYS	CA-C-N	6.09	128.44	120.28
2	H	229	CYS	C-N-CA	6.09	128.44	120.28
4	K	80	CYS	CA-CB-SG	-6.09	100.39	114.40
4	P	167	ILE	N-CA-C	-6.09	104.58	110.42
4	E	138	LEU	N-CA-C	6.08	119.07	110.50
4	W	85	LYS	N-CA-C	-6.08	104.65	111.28
4	Q	106	THR	N-CA-C	6.08	116.11	108.45
4	K	143	ILE	CB-CA-C	-6.07	103.94	112.14
4	V	91	SER	N-CA-C	6.07	117.70	111.14
2	B	224	GLY	N-CA-C	6.07	127.57	113.18
4	Q	79	ARG	N-CA-C	6.06	123.72	110.80
4	P	143	ILE	N-CA-C	-6.05	104.45	110.62
5	L	67	GLN	CG-CD-NE2	6.04	125.46	116.40
4	E	85	LYS	N-CA-C	-6.04	104.70	111.28
5	X	67	GLN	CG-CD-NE2	6.04	125.45	116.40
4	D	97	ILE	N-CA-C	6.03	116.81	110.72
4	V	167	ILE	N-CA-C	-6.02	104.64	110.42
4	D	143	ILE	N-CA-C	-6.01	104.49	110.62
4	D	167	ILE	N-CA-C	-6.01	104.65	110.42
4	K	106	THR	N-CA-C	6.01	116.02	108.45
4	D	91	SER	N-CA-C	6.01	117.63	111.14
4	V	97	ILE	N-CA-C	6.01	116.79	110.72
4	P	91	SER	N-CA-C	6.00	117.61	111.14
4	W	79	ARG	N-CA-C	5.99	123.56	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	80	CYS	CA-CB-SG	-5.98	100.65	114.40
4	Q	143	ILE	CB-CA-C	-5.97	104.08	112.14
4	J	143	ILE	N-CA-C	-5.97	104.53	110.62
4	W	80	CYS	CA-CB-SG	-5.96	100.68	114.40
4	K	79	ARG	N-CA-C	5.96	123.50	110.80
4	W	175	GLU	N-CA-C	5.96	117.98	107.61
5	L	82	HIS	N-CA-C	-5.93	105.63	112.92
4	K	84	VAL	N-CA-C	5.91	116.09	110.42
4	J	97	ILE	N-CA-C	5.86	116.64	110.72
4	E	175	GLU	N-CA-C	5.86	117.81	107.61
5	R	82	HIS	N-CA-C	-5.86	105.71	112.92
5	F	133	TYR	N-CA-C	5.86	117.67	111.28
5	L	133	TYR	N-CA-C	5.86	117.67	111.28
1	A	3	ILE	N-CA-C	5.86	117.14	109.58
4	E	80	CYS	CA-CB-SG	-5.84	100.96	114.40
4	K	175	GLU	N-CA-C	5.84	117.77	107.61
2	H	185	GLY	N-CA-C	5.84	119.55	112.49
5	X	133	TYR	N-CA-C	5.81	117.62	111.28
2	B	185	GLY	N-CA-C	5.80	119.51	112.49
5	F	40	THR	N-CA-C	5.80	118.55	107.75
4	Q	175	GLU	N-CA-C	5.80	117.70	107.61
1	M	191	MET	N-CA-C	5.79	117.67	111.36
1	G	3	ILE	N-CA-C	5.78	117.04	109.58
4	J	91	SER	N-CA-C	5.78	117.38	111.14
1	M	3	ILE	N-CA-C	5.78	117.03	109.58
1	G	191	MET	N-CA-C	5.77	117.64	111.36
5	L	40	THR	N-CA-C	5.75	118.45	107.75
4	Q	84	VAL	N-CA-C	5.74	115.93	110.42
2	T	185	GLY	N-CA-C	5.74	119.43	112.49
5	R	40	THR	N-CA-C	5.73	118.41	107.75
5	R	133	TYR	N-CA-C	5.73	117.53	111.28
2	N	185	GLY	N-CA-C	5.73	119.42	112.49
4	W	143	ILE	CB-CA-C	-5.73	104.41	112.14
4	P	97	ILE	N-CA-C	5.70	116.48	110.72
1	A	21	PHE	N-CA-C	5.69	122.92	110.80
5	X	40	THR	N-CA-C	5.68	118.31	107.75
4	K	97	ILE	N-CA-C	5.68	116.45	110.72
4	E	54	ASP	N-CA-C	-5.67	105.10	111.28
1	S	21	PHE	N-CA-C	5.63	122.80	110.80
1	M	21	PHE	N-CA-C	5.63	122.78	110.80
4	Q	54	ASP	N-CA-C	-5.62	105.16	111.28
4	W	84	VAL	N-CA-C	5.61	115.81	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	21	PHE	N-CA-C	5.61	122.75	110.80
1	S	3	ILE	N-CA-C	5.60	116.80	109.58
1	S	187	SER	CA-C-N	-5.58	112.84	120.44
1	S	187	SER	C-N-CA	-5.58	112.84	120.44
4	E	84	VAL	N-CA-C	5.58	115.78	110.42
5	F	99	VAL	N-CA-C	5.58	116.31	110.62
5	R	99	VAL	N-CA-C	5.56	116.29	110.62
4	D	155	VAL	N-CA-C	-5.55	106.97	111.91
5	F	68	GLU	CA-C-O	5.53	128.42	120.51
4	W	190	ILE	CB-CG1-CD1	-5.53	102.18	113.80
4	E	190	ILE	CB-CG1-CD1	-5.52	102.20	113.80
4	K	173	GLN	CB-CA-C	-5.52	106.53	114.87
5	L	99	VAL	N-CA-C	5.52	116.25	110.62
5	X	129	ARG	N-CA-C	5.52	118.05	109.60
4	Q	190	ILE	CB-CG1-CD1	-5.52	102.22	113.80
5	R	42	GLY	N-CA-C	-5.51	100.12	113.18
5	L	42	GLY	N-CA-C	-5.51	100.12	113.18
4	J	155	VAL	N-CA-C	-5.50	107.02	111.91
4	K	190	ILE	CB-CG1-CD1	-5.49	102.27	113.80
4	E	173	GLN	CB-CA-C	-5.48	106.59	114.87
4	V	87	SER	N-CA-C	5.48	116.94	111.07
2	B	220	GLN	N-CA-C	5.47	119.94	111.56
4	W	97	ILE	N-CA-C	5.47	116.25	110.72
5	X	42	GLY	N-CA-C	-5.47	100.22	113.18
1	G	127	PHE	N-CA-C	5.46	115.04	107.73
2	B	227	VAL	N-CA-C	5.46	116.23	110.72
2	T	220	GLN	N-CA-C	5.45	119.89	111.56
3	U	93	ASP	N-CA-C	-5.45	104.89	112.03
1	S	191	MET	N-CA-C	5.44	117.29	111.36
1	A	187	SER	CA-C-N	-5.43	113.05	120.44
1	A	187	SER	C-N-CA	-5.43	113.05	120.44
4	D	101	ILE	N-CA-C	5.43	117.22	108.85
5	L	129	ARG	N-CA-C	5.43	117.91	109.60
1	G	187	SER	CA-C-N	-5.43	113.06	120.44
1	G	187	SER	C-N-CA	-5.43	113.06	120.44
2	T	97	ARG	N-CA-C	5.42	117.19	111.28
5	X	99	VAL	N-CA-C	5.42	116.15	110.62
4	P	91	SER	CA-C-N	-5.42	113.07	120.44
4	P	91	SER	C-N-CA	-5.42	113.07	120.44
2	N	220	GLN	N-CA-C	5.41	119.84	111.56
4	Q	97	ILE	N-CA-C	5.41	116.19	110.72
4	K	54	ASP	N-CA-C	-5.41	105.39	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	187	SER	CA-C-N	-5.41	113.08	120.44
1	M	187	SER	C-N-CA	-5.41	113.08	120.44
2	B	97	ARG	N-CA-C	5.40	117.17	111.28
4	Q	173	GLN	CB-CA-C	-5.39	106.73	114.87
4	J	87	SER	N-CA-C	5.39	116.84	111.07
4	P	101	ILE	N-CA-C	5.38	117.14	108.85
4	K	144	LEU	CA-CB-CG	5.38	135.13	116.30
5	X	26	LEU	N-CA-C	5.38	117.14	111.28
5	R	129	ARG	N-CA-C	5.37	117.82	109.60
4	D	87	SER	N-CA-C	5.36	116.81	111.07
3	U	81	CYS	N-CA-C	5.36	118.48	109.95
4	D	114	THR	N-CA-C	5.36	117.00	108.79
1	G	204	SER	N-CA-C	5.36	118.36	109.46
2	N	227	VAL	N-CA-C	5.36	116.13	110.72
4	V	101	ILE	N-CA-C	5.36	117.10	108.85
2	T	227	VAL	N-CA-C	5.35	116.13	110.72
5	X	163	LEU	N-CA-C	-5.35	105.44	111.28
1	A	191	MET	N-CA-C	5.35	117.19	111.36
4	E	97	ILE	N-CA-C	5.34	116.12	110.72
5	F	42	GLY	N-CA-C	-5.34	100.53	113.18
3	O	81	CYS	N-CA-C	5.33	118.43	109.95
4	P	114	THR	N-CA-C	5.32	116.94	108.79
5	F	129	ARG	N-CA-C	5.31	117.73	109.60
4	E	123	PRO	N-CA-C	-5.31	105.87	113.47
4	D	91	SER	CA-C-N	-5.30	113.23	120.44
4	D	91	SER	C-N-CA	-5.30	113.23	120.44
1	S	204	SER	N-CA-C	5.30	118.26	109.46
5	L	68	GLU	O-C-N	5.30	129.64	122.59
4	V	114	THR	N-CA-C	5.29	116.89	108.79
4	J	101	ILE	N-CA-C	5.28	116.98	108.85
2	N	97	ARG	N-CA-C	5.27	117.03	111.28
4	J	114	THR	N-CA-C	5.27	116.86	108.79
1	M	204	SER	N-CA-C	5.27	118.21	109.46
5	R	26	LEU	N-CA-C	5.27	117.03	111.28
4	W	144	LEU	CA-CB-CG	5.27	134.75	116.30
1	A	127	PHE	N-CA-C	5.27	114.79	107.73
4	P	87	SER	N-CA-C	5.27	116.71	111.07
2	H	97	ARG	N-CA-C	5.26	117.01	111.28
2	H	220	GLN	N-CA-C	5.26	119.61	111.56
4	J	140	TYR	N-CA-C	5.26	117.09	111.36
4	E	144	LEU	CA-CB-CG	5.25	134.69	116.30
4	J	91	SER	CA-C-N	-5.25	113.30	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	91	SER	C-N-CA	-5.25	113.30	120.44
2	T	68	GLU	N-CA-C	-5.24	105.65	111.36
5	F	163	LEU	N-CA-C	-5.24	105.57	111.28
4	K	123	PRO	N-CA-C	-5.23	105.99	113.47
4	V	91	SER	CA-C-N	-5.23	113.33	120.44
4	V	91	SER	C-N-CA	-5.23	113.33	120.44
1	M	74	GLY	N-CA-C	-5.22	100.80	113.18
5	F	26	LEU	N-CA-C	5.21	116.96	111.28
4	Q	144	LEU	CA-CB-CG	5.20	134.50	116.30
2	H	227	VAL	N-CA-C	5.20	115.97	110.72
5	R	5	TYR	N-CA-C	5.19	121.86	110.80
4	J	136	LYS	N-CA-C	-5.19	106.97	113.72
1	S	40	LEU	N-CA-C	-5.19	105.62	111.28
2	H	68	GLU	N-CA-C	-5.19	105.71	111.36
1	G	74	GLY	N-CA-C	-5.18	100.90	113.18
5	L	68	GLU	CA-C-O	5.18	127.91	120.51
5	R	163	LEU	N-CA-C	-5.17	105.64	111.28
3	I	17	PHE	N-CA-C	5.17	117.84	109.06
2	B	68	GLU	N-CA-C	-5.16	105.73	111.36
4	K	89	VAL	CB-CA-C	-5.16	105.17	112.14
5	L	19	VAL	N-CA-C	5.16	115.89	108.93
5	X	5	TYR	N-CA-C	5.16	121.79	110.80
5	L	163	LEU	N-CA-C	-5.16	105.66	111.28
1	G	40	LEU	N-CA-C	-5.16	105.66	111.28
4	Q	123	PRO	N-CA-C	-5.16	106.10	113.47
5	F	5	TYR	N-CA-C	5.15	121.77	110.80
5	X	57	VAL	N-CA-C	5.15	115.47	107.28
3	O	93	ASP	N-CA-C	-5.14	105.29	112.03
4	W	125	ALA	N-CA-C	5.14	117.01	107.60
3	C	14	ASN	N-CA-C	5.14	118.44	110.17
4	E	190	ILE	CG1-CB-CG2	5.14	126.12	110.70
4	Q	190	ILE	CG1-CB-CG2	5.14	126.12	110.70
4	D	84	VAL	CB-CA-C	-5.13	105.40	111.97
4	W	54	ASP	N-CA-C	-5.13	105.69	111.28
4	K	190	ILE	CG1-CB-CG2	5.13	126.08	110.70
3	C	81	CYS	N-CA-C	5.12	118.10	109.95
1	M	122	LEU	N-CA-C	-5.12	99.93	108.34
4	W	190	ILE	CG1-CB-CG2	5.12	126.08	110.70
3	U	14	ASN	N-CA-C	5.12	118.42	110.17
5	L	57	VAL	N-CA-C	5.12	115.42	107.28
5	X	94	GLU	N-CA-C	-5.12	105.70	111.28
5	F	94	GLU	N-CA-C	-5.12	105.70	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	40	LEU	N-CA-C	-5.12	105.70	111.28
4	P	155	VAL	N-CA-C	-5.12	107.36	111.91
5	R	12	LEU	N-CA-C	5.11	116.96	108.02
1	S	74	GLY	N-CA-C	-5.10	101.09	113.18
1	A	206	LEU	N-CA-C	5.10	116.92	111.36
4	Q	125	ALA	N-CA-C	5.10	116.93	107.60
4	D	92	LYS	N-CA-C	5.09	116.64	111.14
5	L	26	LEU	N-CA-C	5.09	116.83	111.28
4	P	92	LYS	N-CA-C	5.09	116.64	111.14
1	S	122	LEU	N-CA-C	-5.09	100.00	108.34
5	X	68	GLU	CA-C-O	5.08	127.78	120.51
5	R	57	VAL	N-CA-C	5.08	115.36	107.28
5	L	94	GLU	N-CA-C	-5.07	105.75	111.28
1	M	127	PHE	N-CA-C	5.07	114.52	107.73
5	R	68	GLU	O-C-N	5.07	129.33	122.59
2	N	68	GLU	N-CA-C	-5.06	105.84	111.36
3	U	37	ASN	N-CA-C	5.06	116.80	111.28
4	J	92	LYS	N-CA-C	5.06	116.60	111.14
4	D	136	LYS	N-CA-C	-5.05	107.15	113.72
5	X	19	VAL	N-CA-C	5.05	115.75	108.93
5	F	57	VAL	N-CA-C	5.05	115.31	107.28
3	O	14	ASN	N-CA-C	5.04	118.29	110.17
5	F	19	VAL	N-CA-C	5.04	115.73	108.93
5	R	19	VAL	N-CA-C	5.04	115.74	108.93
3	C	17	PHE	N-CA-C	5.04	117.62	109.06
2	B	268	ILE	N-CA-C	5.03	119.80	109.34
4	V	92	LYS	N-CA-C	5.03	116.57	111.14
3	C	106	ILE	CB-CA-C	-5.02	105.54	111.97
4	D	67	LEU	N-CA-C	5.02	116.75	111.28
1	A	204	SER	N-CA-C	5.02	117.79	109.46
1	S	73	VAL	N-CA-C	5.02	116.22	108.44
4	V	84	VAL	CB-CA-C	-5.02	105.55	111.97
3	C	93	ASP	N-CA-C	-5.01	105.46	112.03
3	I	116	SER	N-CA-C	5.01	116.87	110.61
4	J	84	VAL	CB-CA-C	-5.01	105.56	111.97
4	V	67	LEU	N-CA-C	5.01	116.74	111.28
2	B	183	ILE	CB-CA-C	-5.01	105.56	111.97
4	V	155	VAL	N-CA-C	-5.01	107.45	111.91
4	E	173	GLN	N-CA-C	5.00	114.24	108.49
4	P	188	ILE	N-CA-C	5.00	119.68	108.88

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1285	0	1290	232	0
1	G	1285	0	1290	235	0
1	M	1285	0	1290	231	0
1	S	1285	0	1290	232	0
2	B	1359	0	1335	171	0
2	H	1359	0	1335	177	0
2	N	1359	0	1335	173	0
2	T	1359	0	1335	178	0
3	C	1190	0	1166	221	0
3	I	1190	0	1166	223	0
3	O	1190	0	1166	220	0
3	U	1190	0	1166	233	0
4	D	1500	0	1500	220	0
4	E	1515	0	1512	185	0
4	J	1500	0	1500	219	0
4	K	1515	0	1512	195	0
4	P	1500	0	1500	218	0
4	Q	1515	0	1512	207	0
4	V	1500	0	1500	217	0
4	W	1515	0	1512	209	0
5	F	1328	0	1329	187	0
5	L	1328	0	1329	187	0
5	R	1328	0	1329	184	0
5	X	1328	0	1329	190	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	32776	0	32652	4510	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 71.

All (4510) 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
5:X:103:LEU:HD21	5:X:145:MET:HE1	1.26	1.16
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
5:L:103:LEU:HD21	5:L:145:MET:HE1	1.26	1.16
3:O:119:LEU:HD23	3:O:119:LEU:H	1.06	1.15
3:O:39:GLU:HA	3:O:42:LYS:HE2	1.24	1.15
5:F:120:GLY:HA3	5:F:149:GLU:HG3	1.17	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
3:C:119:LEU:HD23	3:C:119:LEU:H	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:D:49:PHE:HB3	4:D:138:LEU:HD12	1.18	1.14
4:J:79:ARG:HH21	4:J:190:ILE:HD12	1.02	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:R:103:LEU:HD21	5:R:145:MET:HE1	1.25	1.12
5:F:103:LEU:HD21	5:F:145:MET:HE1	1.26	1.11
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
4:J:49:PHE:HB3	4:J:138:LEU:HD12	1.17	1.10
5:R:68:GLU:HG2	5:R:69:ARG:H	1.08	1.10
5:X:68:GLU:HG2	5:X:69:ARG:H	1.05	1.09
1:A:10:ASN:HD22	1:A:11:LYS:N	1.50	1.09
3:C:77:VAL:HG12	3:C:91:LEU:HD22	1.35	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:77:VAL:HG12	3:I:91:LEU:HD22	1.34	1.09
3:I:82:THR:HG22	3:I:84:SER:H	1.12	1.08
3:O:77:VAL:HG12	3:O:91:LEU:HD22	1.35	1.08
1:M:10:ASN:HD22	1:M:11:LYS:N	1.51	1.08
3:C:82:THR:HG22	3:C:84:SER:H	1.14	1.08
5:R:69:ARG:HB2	5:R:72:THR:HG22	1.28	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
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
1:G:10:ASN:HD22	1:G:11:LYS:N	1.52	1.05
4:K:60:GLY:HA2	4:K:63:ILE:HD11	1.37	1.05
4:W:60:GLY:HA2	4:W:63:ILE:HD11	1.38	1.05
2:B:214:ASN:HA	2:B:263:ARG:HG3	1.39	1.04
2:H:214:ASN:HA	2:H:263:ARG:HG3	1.39	1.04
5:L:69:ARG:HB2	5:L:72:THR:HG22	1.36	1.04
5:F:150:THR:HB	5:F:155:SER:CB	1.88	1.03
3:C:11:ARG:HH12	4:E:154:MET:HE1	1.20	1.03
4:E:60:GLY:HA2	4:E:63:ILE:HD11	1.38	1.03
3:I:11:ARG:HH12	4:K:154:MET:HE1	1.23	1.03
2:N:214:ASN:HA	2:N:263:ARG:HG3	1.39	1.03
3:O:7:TRP:HB2	3:O:89:VAL:HG12	1.38	1.03
5:R:150:THR:HB	5:R:155:SER:CB	1.88	1.03
1:S:120:ARG:HB3	1:S:120:ARG:HH11	1.23	1.03
3:C:7:TRP:HB2	3:C:89:VAL:HG12	1.38	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
5:X:150:THR:HB	5:X:155:SER:CB	1.87	1.03
3:O:11:ARG:HH12	4:Q:154:MET:HE1	1.22	1.03
2:T:214:ASN:HA	2:T:263:ARG:HG3	1.40	1.03
1:M:147:VAL:HG12	1:M:148:MET:H	1.21	1.02
5:X:150:THR:CB	5:X:155:SER:HB2	1.89	1.02
5:L:150:THR:CB	5:L:155:SER:HB2	1.89	1.02
5:R:69:ARG:HB2	5:R:72:THR:CG2	1.88	1.02
1:A:75:MET:HE1	1:A:105:ASP:HB3	1.40	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:150:THR:CB	5:R:155:SER:HB2	1.90	1.02
1:S:75:MET:HE1	1:S:105:ASP:HB3	1.41	1.02
5:F:150:THR:CB	5:F:155:SER:HB2	1.90	1.02
1:M:120:ARG:HB3	1:M:120:ARG:HH11	1.24	1.02
4:Q:60:GLY:HA2	4:Q:63:ILE:HD11	1.40	1.02
1:S:137:GLY:HA2	4:V:188:ILE:HG21	1.42	1.02
1:A:137:GLY:HA2	4:D:188:ILE:HG21	1.38	1.01
1:M:75:MET:HE1	1:M:105:ASP:HB3	1.40	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:75:MET:HE1	1:G:105:ASP:HB3	1.40	1.00
1:G:120:ARG:HB3	1:G:120:ARG:HH11	1.25	1.00
3:U:11:ARG:HH12	4:W:154:MET:HE1	1.24	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
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
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
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
1:G:15:LEU:HB3	1:G:34:LEU:HD23	1.46	0.97
5:L:68:GLU:HG2	5:L:69:ARG:N	1.71	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
5:L:110:ALA:HB1	5:L:114:VAL:HG21	1.44	0.96
4:P:106:THR:HG22	4:P:107:ASN:H	1.30	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
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:15:LEU:HB3	1:S:34:LEU:HD23	1.47	0.96
1:S:147:VAL:HG12	1:S:148:MET:H	1.29	0.96
1:M:15:LEU:HB3	1:M:34:LEU:HD23	1.48	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
5:F:47:ILE:HG12	5:F:60:GLN:HA	1.47	0.95
4:V:99:LEU:HD12	4:V:101:ILE:HD11	1.48	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:J:106:THR:HG22	4:J:107:ASN:H	1.29	0.94
4:V:119:LEU:HD12	4:V:120:ASP:H	1.31	0.94
4:W:119:LEU:O	4:W:174:THR:HG21	1.68	0.94
4:D:119:LEU:HD12	4:D: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
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
2:N:188:TRP:HH2	2:N:266:TYR:HE1	1.09	0.93
5:X:68:GLU:HG2	5:X:69:ARG:N	1.75	0.93
1:M:10:ASN:HB3	1:M:14:GLY:H	1.30	0.93
4:J:99:LEU:HD12	4:J:101:ILE:HD11	1.50	0.93
5:X:47:ILE:HG12	5:X:60:GLN:HA	1.47	0.93
2:B:188:TRP:HH2	2:B:266:TYR:HE1	1.09	0.92
3:C:102:VAL:HG11	3:C:156:MET:HE1	1.51	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:I:102:VAL:HG11	3:I:156:MET:HE1	1.51	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
1:M:200:MET:HE1	5:R:7:TYR:HA	1.49	0.92
3:U:102:VAL:HG11	3:U:156:MET:HE1	1.52	0.92
5:L:89:ASP:HA	5:L:121:ASN:HD21	1.32	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
1:A:10:ASN:HB3	1:A:14:GLY:H	1.32	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:9:PHE:HB2	5:L:59:LEU:HD23	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
2:B:262:GLN:O	2:B:264:THR:HG23	1.70	0.91
4:K:119:LEU:O	4:K:174:THR:HG21	1.71	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
3:I:112:VAL:HG12	3:I:117:ASN:ND2	1.84	0.91
4:P:79:ARG:NH2	4:P:190:ILE:HD12	1.86	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
1:A:142:ALA:HB2	1:A:179:LEU:HD21	1.51	0.90
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
3:C:119:LEU:HD23	3:C:119:LEU:N	1.85	0.90
1:G:200:MET:HE1	5:L:7:TYR:HA	1.52	0.90
4:D:22:THR:HB	4:D:74:ARG:HH12	1.35	0.90
3:O:112:VAL:HG12	3:O:117:ASN:ND2	1.85	0.90
4:Q:161:VAL:HG13	4:Q:178:VAL:HG22	1.53	0.90
4:V:155:VAL:O	4:V:156:GLN:HG2	1.70	0.90
3:O:102:VAL:HG11	3:O:156:MET:HE1	1.54	0.90
2:T:232:PHE:O	2:T:236:ILE:HD12	1.70	0.90
1:G:194:PRO:HG3	2:H:67:GLN:HB2	1.51	0.90
2:T:262:GLN:O	2:T:264:THR:HG23	1.70	0.90
4:P:155:VAL:O	4:P:156:GLN:HG2	1.70	0.90
4:V:79:ARG:NH2	4:V:190:ILE:HD12	1.87	0.90
4:E:119:LEU:O	4:E:174:THR:HG21	1.70	0.90
5:F:9:PHE:HB2	5:F:59:LEU:HD23	1.51	0.90
5:F:11:LEU:HD11	5:F:59:LEU:HD22	1.53	0.90
1:G:142:ALA:HB2	1:G:179:LEU:HD21	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: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:22:THR:HB	4:J:74:ARG:HH12	1.35	0.90
3:U:112:VAL:HG12	3:U:117:ASN:HD21	1.36	0.90
5:F:12:LEU:HD23	5:F:12:LEU:H	1.37	0.90
4:J:79:ARG:NH2	4:J:190:ILE:HD12	1.87	0.90
5:X:11:LEU:HD11	5:X:59:LEU:HD22	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:9:PHE:HB2	5:R:59:LEU:HD23	1.52	0.89
1:A:194:PRO:HG3	2:B:67:GLN:HB2	1.54	0.89
1:S:142:ALA:HB2	1:S:179:LEU:HD21	1.54	0.89
4:K:161:VAL:HG13	4:K:178:VAL:HG22	1.52	0.89
2:H:232:PHE:O	2:H:236:ILE:HD12	1.72	0.89
3:I:82:THR:HG21	3:I:84:SER:OG	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: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:112:VAL:HG12	3:I:117:ASN:HD21	1.37	0.89
4:P:188:ILE:HD11	4:P:190:ILE:HD11	1.53	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:D:155:VAL:O	4:D:156:GLN:HG2	1.72	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: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
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
4:D:164:VAL:HB	4:D:175:GLU:OE2	1.73	0.88
3:O:82:THR:HG21	3:O:84:SER:OG	1.74	0.88
5:X:14:ILE:HG22	5:X:64:THR:HG21	1.55	0.88
4:J:188:ILE:HD11	4:J:190:ILE:HD11	1.54	0.88
5:R:11:LEU:HD11	5:R:59:LEU:HD22	1.55	0.88
5:R:150:THR:HB	5:R:155:SER:HB2	0.94	0.88
3:U:119:LEU:HD23	3:U:119:LEU:N	1.87	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:L:150:THR:HB	5:L:155:SER:HB2	0.93	0.87
5:R:123:CYS:HB3	5:R:151:SER:HA	1.57	0.87
3:O:9:PHE:HB2	3:O:87:TRP:HB2	1.56	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
3:O:119:LEU:HD23	3:O:119:LEU:N	1.88	0.87
3:C:11:ARG:NH1	4:E:154:MET:HE1	1.89	0.87
5:L:11:LEU:HD11	5:L:59:LEU:HD22	1.55	0.87
1:A:200:MET:HE1	5:F:7:TYR:HA	1.53	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:156:GLN:HA	4:P:184:LEU:HD12	1.55	0.87
2:T:188:TRP:CH2	2:T:266:TYR:HE1	1.92	0.87
4:V:188:ILE:CD1	4:V:190:ILE:HD11	2.05	0.87
5:R:12:LEU:HD23	5:R:12:LEU:H	1.40	0.86
1:S:200:MET:HE1	5:X:7:TYR:HA	1.55	0.86
3:I:9:PHE:HB2	3:I:87:TRP:HB2	1.55	0.86
5:X:12:LEU:HD23	5:X:12:LEU:H	1.39	0.86
5:X:118:LEU:HB3	5:X:147:PHE:HB2	1.57	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:43:LEU:HD12	3:I:44:LEU:N	1.90	0.86
3:I:119:LEU:HD23	3:I:119:LEU:N	1.89	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:HD23	5:L:12:LEU:H	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
3:C:43:LEU:HD12	3:C:44:LEU:N	1.89	0.85
3:C:82:THR:HG21	3:C:84:SER:OG	1.77	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
4:J:156:GLN:HA	4:J:184:LEU:HD12	1.56	0.85
4:P:67:LEU:HD11	4:P:98:PHE:CE2	2.12	0.85
3:C:119:LEU:H	3:C:119:LEU:CD2	1.83	0.85
1:S:133:GLN:CB	1:S:139:LYS:HG2	2.06	0.85
3:C:3:ILE:HB	3:C:90:LEU:HD11	1.56	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
2:N:231:TYR:HD2	2:N:234:CYS:HG	1.21	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
1:G:181:LYS:HB3	1:G:214:MET:HE1	1.59	0.85
1:M:181:LYS:HB3	1:M:214:MET:HE1	1.59	0.85
4:E:143:ILE:O	4:E:147:VAL:HG23	1.76	0.85
1:G:75:MET:HE1	1:G:105:ASP:CB	2.06	0.85
5:L:123:CYS:HB3	5:L:151:SER:HA	1.57	0.85
5:L:108:ARG:NH1	5:L:108:ARG:HB2	1.92	0.84
3:C:71:SER:OG	3:C:76:ARG:HD3	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:75:MET:HE1	1:A:105:ASP:CB	2.06	0.84
4:D:67:LEU:HD11	4:D:98:PHE:CE2	2.13	0.84
5:L:118:LEU:HB3	5:L:147:PHE:HB2	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
1:S:21:PHE:HD1	1:S:22:THR:N	1.75	0.84
4:W:143:ILE:O	4:W:147:VAL:HG23	1.77	0.84
2:B:59:LEU:HD13	4:D:25:ILE:HD11	1.57	0.84
5:F:108:ARG:NH1	5:F:108:ARG:HB2	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:R:108:ARG:NH1	5:R:108:ARG:HB2	1.92	0.84
5:X:123:CYS:HB3	5:X:151:SER:HA	1.58	0.84
3:O:11:ARG:NH1	4:Q:154:MET:HE1	1.92	0.84
2:T:231:TYR:HD2	2:T:234:CYS:HG	1.20	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
3:U:11:ARG:NH1	4:W:154:MET:HE1	1.92	0.83
3:O:133:ARG:H	3:O:133:ARG:HD2	1.42	0.83
5:R:118:LEU:HB3	5:R:147:PHE:HB2	1.60	0.83
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
1:M:75:MET:HE1	1:M:105:ASP:CB	2.07	0.83
2:N:59:LEU:HD13	4:P:25:ILE:HD11	1.59	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:G:21:PHE:HD1	1:G:22:THR:N	1.76	0.83
4:K:143:ILE:O	4:K:147:VAL:HG23	1.78	0.83
1:S:75:MET:HE1	1:S:105:ASP:CB	2.08	0.83
3:C:123:TYR:O	3:C:125:PHE:N	2.10	0.83
3:U:39:GLU:HA	3:U:42:LYS:CE	2.07	0.83
3:C:72:THR:HG23	3:C:73:GLY:N	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
4:P:159:CYS:HB3	4:P:180:LEU:HA	1.60	0.83
1:S:133:GLN:HE22	4:V:188:ILE:HD12	1.44	0.83
3:C:133:ARG:H	3:C:133:ARG:HD2	1.43	0.83
1:M:21:PHE:HD1	1:M:22:THR:N	1.76	0.83
3:U:82:THR:HG21	3:U:84:SER:OG	1.78	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
3:I:11:ARG:NH1	4:K:154:MET:HE1	1.92	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
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:O:119:LEU:H	3:O:119:LEU:CD2	1.86	0.82
1:S:181:LYS:HB3	1:S:214:MET:HE1	1.61	0.82
4:V:111:ASN:ND2	4:V:113:ASP:HB2	1.95	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
1:G:200:MET:CE	5:L:7:TYR:HA	2.08	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:I:123:TYR:O	3:I:125:PHE:N	2.11	0.82
3:O:71:SER:OG	3:O:76:ARG:HD3	1.79	0.82
4:V:79:ARG:HH21	4:V:190:ILE:CD1	1.88	0.82
3:C:88:PHE:O	3:C:103:LEU:HD21	1.80	0.82
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
1:A:70:ILE:HD12	1:A:108:LYS:HA	1.60	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LYS:HB3	1:A:214:MET:HE1	1.62	0.82
4:E:21:LYS:O	4:E:22:THR:HG23	1.79	0.82
2:N:87:LEU:HD11	2:N:232:PHE:HB2	1.62	0.82
2:N:254:ARG:HA	2:N:264:THR:HG22	1.60	0.82
2:T:192:PHE:HD1	2:T:192:PHE:H	1.28	0.82
3:U:119:LEU:H	3:U:119:LEU:CD2	1.85	0.82
2:B:222:ILE:H	2:B:222:ILE:HD12	1.43	0.81
3:U:72:THR:HG23	3:U:73:GLY:N	1.95	0.81
4:V:93:CYS:O	4:V:97:ILE:HG13	1.79	0.81
4:V:139:TRP:HB2	4:V:142:ASN:HD21	1.45	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:A:200:MET:CE	5:F:7:TYR:HA	2.10	0.81
2:B:188:TRP:HH2	2:B:266:TYR:CE1	1.97	0.81
1:G:107:PHE:HB3	1:G:180:ARG:HH12	1.46	0.81
1:M:133:GLN:HE22	4:P:188:ILE:HD12	1.45	0.81
2:N:188:TRP:HH2	2:N:266:TYR:CE1	1.97	0.81
4:P:111:ASN:ND2	4:P:113:ASP:HB2	1.93	0.81
3:U:88:PHE:O	3:U:103:LEU:HD21	1.81	0.81
5:X:68:GLU:HG3	5:X:69:ARG:N	1.96	0.81
2:H:192:PHE:HD1	2:H:192:PHE:H	1.29	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
5:R:68:GLU:HG3	5:R:69:ARG:N	1.95	0.81
2:H:188:TRP:HH2	2:H:266:TYR:CE1	1.97	0.81
3:O:107:TYR:HE2	4:Q:73:ALA:HA	1.45	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
4:E:49:PHE:CZ	4:E:133:ASP:HB3	2.16	0.81
1:G:50:LEU:HB2	3:I:43:LEU:HD11	1.63	0.81
4:J:159:CYS:HB3	4:J:180:LEU:HA	1.60	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
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
5:L:93:GLN:HE21	5:L:131:VAL:HG12	1.44	0.81
3:U:107:TYR:HE2	4:W:73:ALA:HA	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
4:K:49:PHE:HZ	4:K:133:ASP:HB3	1.45	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:222:ILE:H	2:N:222:ILE:HD12	1.44	0.80
1:S:107:PHE:HB3	1:S:180:ARG:HH12	1.46	0.80
2:T:222:ILE:H	2:T:222:ILE:HD12	1.43	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
3:O:48:ILE:HG21	3:O:87:TRP:HD1	1.47	0.80
2:T:87:LEU:HD11	2:T:232:PHE:HB2	1.63	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
1:S:200:MET:CE	5:X:7:TYR:HA	2.11	0.80
3:U:48:ILE:HG21	3:U:87:TRP:HD1	1.46	0.80
3:U:155:PRO:HG2	3:U:156:MET:H	1.46	0.80
3:C:122:PRO:HA	4:E:66:ARG:HH22	1.47	0.80
5:F:28:PHE:CD2	5:F:48:LYS:HD3	2.16	0.80
1:A:133:GLN:NE2	4:D:188:ILE:HD12	1.97	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
4:W:94:ALA:HB1	6:W:194:PLM:H91	1.63	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
2:H:99:LEU:HD22	2:H:243:ASN:HD22	1.47	0.79
4:K:49:PHE:CZ	4:K:133:ASP:HB3	2.17	0.79
1:M:50:LEU:HB2	3:O:43:LEU:HD11	1.63	0.79
1:M:107:PHE:HB3	1:M:180:ARG:HH12	1.45	0.79
4:E:188:ILE:HG23	4:E:188:ILE:O	1.82	0.79
3:I:48:ILE:HG21	3:I:87:TRP:HD1	1.47	0.79
1:S:133:GLN:NE2	4:V:188:ILE:HD12	1.97	0.79
5:X:93:GLN:HE21	5:X:131:VAL:HG12	1.45	0.79
2:N:192:PHE:H	2:N:192:PHE:HD1	1.27	0.79
4:Q:188:ILE:HG23	4:Q:188:ILE:O	1.82	0.79
1:G:133:GLN:HE22	4:J:188:ILE:HD12	1.48	0.79
5:L:68:GLU:HG3	5:L:69:ARG:N	1.97	0.79
2:H:87:LEU:HD11	2:H:232:PHE:HB2	1.64	0.79
4:Q:87:SER:HB2	4:Q:115:PHE:CE1	2.18	0.79
4:W:49:PHE:HZ	4:W:133:ASP:HB3	1.46	0.79
4:K:87:SER:HB2	4:K:115:PHE:CE1	2.17	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:113:LYS:HA	3:C:117:ASN:HD22	1.48	0.79
5:L:29:SER:N	5:L:48:LYS:HE2	1.97	0.79
4:Q:114:THR:HG23	4:Q:179:LYS:N	1.98	0.79
2:T:99:LEU:HD22	2:T:243:ASN:HD22	1.48	0.79
4:J:49:PHE:CB	4:J:138:LEU:HD12	2.09	0.79
2:B:99:LEU:HD22	2:B:243:ASN:HD22	1.47	0.78
4:E:87:SER:HB2	4:E:115:PHE:CE1	2.18	0.78
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
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:192:PHE:HD1	2:B:192:PHE:H	1.28	0.78
1:G:137:GLY:CA	4:J:188:ILE:HG21	2.13	0.78
5:L:30:ASP:OD1	5:L:48:LYS:HA	1.83	0.78
3:O:113:LYS:HA	3:O:117:ASN:HD22	1.49	0.78
4:Q:95:PHE:HB3	4:Q:101:ILE:HG23	1.65	0.78
5:R:28:PHE:CD2	5:R:48:LYS:HD3	2.18	0.78
4:V:138:LEU:H	4:V:169:ARG:NH2	1.81	0.78
4:W:144:LEU:HD23	6:W:194:PLM:HF2	1.65	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
3:I:122:PRO:HA	4:K:66:ARG:HH22	1.49	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: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
4:D:101:ILE:HG21	4:D:121:GLU:O	1.84	0.78
3:I:113:LYS:HA	3:I:117:ASN:HD22	1.48	0.78
4:K:144:LEU:HD23	6:K:194:PLM:HF2	1.66	0.78
5:L:28:PHE:CD2	5:L:48:LYS:HD3	2.18	0.78
4:W:86:THR:HA	6:W:194:PLM:O1	1.83	0.78
4:W:188:ILE:HG23	4:W:188:ILE:O	1.82	0.77
3:I:127:GLU:C	3:I:129:GLU:H	1.93	0.77
4:K:188:ILE:O	4:K:188:ILE:HG23	1.82	0.77
4:Q:86:THR:HA	6:Q:194:PLM:O1	1.83	0.77
2:B:175:LYS:HG3	2:B:278:GLU:OE2	1.83	0.77
3:U:127:GLU:C	3:U:129:GLU:H	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:101:ILE:HG21	4:J:121:GLU:O	1.84	0.77
4:K:86:THR:HA	6:K:194:PLM:O1	1.84	0.77
4:P:38:VAL:HG11	4:P:140:TYR:CE1	2.19	0.77
5:R:84:ILE:HD11	5:R:114:VAL:HG11	1.64	0.77
1:A:40:LEU:HD21	1:A:129:MET:SD	2.25	0.77
2:B:256:PRO:HG2	2:B:263:ARG:HH21	1.50	0.77
4:D:119:LEU:HD12	4:D:120:ASP:N	1.99	0.77
5:F:84:ILE:HD11	5:F:114:VAL:HG11	1.65	0.77
3:O:122:PRO:HA	4:Q:66:ARG:HH22	1.49	0.77
5:F:30:ASP:OD1	5:F:48:LYS:HA	1.84	0.77
2:N:86:LYS:NZ	2:N:90:TYR:HE1	1.83	0.77
3:O:20:GLU:O	3:O:21:TRP:HB2	1.83	0.77
1:A:50:LEU:HB2	3:C:43:LEU:HD11	1.67	0.77
5:F:117:LEU:HD23	5:F:118:LEU:N	1.99	0.77
2:H:86:LYS:HZ2	2:H:90:TYR:HE1	1.33	0.77
4:Q:144:LEU:HD23	6:Q:194:PLM:HF2	1.67	0.77
5:R:117:LEU:HD23	5:R:118:LEU:N	1.99	0.77
3:C:155:PRO:HG2	3:C:156:MET:H	1.50	0.77
4:E:86:THR:HA	6:E:194:PLM:O1	1.84	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
3:I:155:PRO:HG2	3:I:156:MET:H	1.50	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
4:V:49:PHE:CB	4:V:138:LEU:HD12	2.11	0.77
4:E:95:PHE:HB3	4:E:101:ILE:HG23	1.67	0.76
4:E:114:THR:HG23	4:E:179:LYS:N	2.00	0.76
4:J:38:VAL:HG11	4:J:140:TYR:CE1	2.20	0.76
2:T:86:LYS:NZ	2:T:90:TYR:HE1	1.83	0.76
2:B:86:LYS:NZ	2:B:90:TYR:HE1	1.83	0.76
2:H:86:LYS:NZ	2:H:90:TYR:HE1	1.83	0.76
2:H:256:PRO:HG2	2:H:263:ARG:HH21	1.50	0.76
1:M:200:MET:HE1	5:R:7:TYR:CA	2.14	0.76
3:O:155:PRO:HG2	3:O:156:MET:H	1.50	0.76
4:P:95:PHE:O	4:P:99:LEU:O	2.03	0.76
3:U:113:LYS:HA	3:U:117:ASN:HD22	1.50	0.76
1:M:181:LYS:CB	1:M:214:MET:HE1	2.16	0.76
3:C:20:GLU:O	3:C:21:TRP:HB2	1.84	0.76
4:V:119:LEU:HD12	4:V:120:ASP:N	1.99	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:T:256:PRO:HG2	2:T:263:ARG:HH21	1.50	0.76
3:U:122:PRO:HA	4:W:66:ARG:HH22	1.51	0.76
2:H:222:ILE:HD12	2:H:222:ILE:H	1.48	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
4:V:101:ILE:HG21	4:V:121:GLU:O	1.86	0.76
4:D:38:VAL:HG11	4:D:140:TYR:CE1	2.20	0.76
4:J:119:LEU:HD12	4:J:120:ASP:N	1.99	0.76
4:Q:141:SER:O	4:Q:144:LEU:HB3	1.86	0.76
1:A:174:ILE:HG13	1:A:175:ALA:N	2.01	0.76
3:I:20:GLU:O	3:I:21:TRP:HB2	1.84	0.76
5:L:93:GLN:HB2	5:L:130:VAL:HG11	1.68	0.76
3:O:127:GLU:C	3:O:129:GLU:H	1.93	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
1:M:10:ASN:HD22	1:M:10:ASN:C	1.88	0.76
5:X:117:LEU:HD23	5:X:118:LEU:N	2.00	0.76
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:101:ILE:HD12	4:K:121:GLU:O	1.85	0.75
4:K:159:CYS:HB3	4:K:179:LYS:O	1.85	0.75
5:R:28:PHE:HB3	5:R:48:LYS:HZ3	1.51	0.75
3:U:82:THR:OG1	3:U:86:LEU:HB2	1.86	0.75
4:W:75:THR:HG21	4:W:93:CYS:SG	2.26	0.75
4:W:159:CYS:HB3	4:W:179:LYS:O	1.85	0.75
1:S:52:PRO:C	1:S:54:ALA:H	1.94	0.75
4:Q:110:HIS:O	4:Q:111:ASN:CB	2.34	0.75
5:F:85:ILE:HD12	5:F:85:ILE:H	1.51	0.75
1:G:181:LYS:CB	1:G:214:MET:HE1	2.14	0.75
2:T:87:LEU:CD1	2:T:232:PHE:HB2	2.16	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
4:J:138:LEU:H	4:J:169:ARG:NH2	1.85	0.75
1:M:133:GLN:HB2	1:M:139:LYS:HG2	1.67	0.75
3:O:133:ARG:HE	4:Q:189:PRO:HD2	1.52	0.75
4:P:119:LEU:HD12	4:P:120:ASP:N	2.01	0.75
1:S:10:ASN:HD22	1:S:10:ASN:C	1.89	0.75
3:U:39:GLU:CA	3:U:42:LYS:HE2	2.12	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ASN:HD22	1:A:10:ASN:C	1.88	0.75
3:C:127:GLU:C	3:C:129:GLU:H	1.94	0.75
4:D:49:PHE:CB	4:D:138:LEU:HD12	2.10	0.75
4:E:110:HIS:O	4:E:111:ASN:CB	2.35	0.75
1:G:200:MET:HE1	5:L:7:TYR:CA	2.16	0.75
1:M:174:ILE:HG13	1:M:175:ALA:N	2.01	0.75
4:P:49:PHE:CB	4:P:138:LEU:HD12	2.10	0.75
4:P:155:VAL:C	4:P:156:GLN:HG2	2.11	0.75
1:S:29:ASN:HB3	1:S:32:GLU:OE2	1.87	0.75
1:S:137:GLY:CA	4:V:188:ILE:HG21	2.15	0.75
5:F:68:GLU:HG3	5:F:69:ARG:N	2.02	0.75
5:L:117:LEU:HD23	5:L:118:LEU:N	2.01	0.75
4:W:37:ILE:O	4:W:41:LEU:HG	1.86	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:S:15:LEU:HD21	1:S:18:GLN:HB2	1.69	0.75
5:F:93:GLN:HB2	5:F:130:VAL:HG11	1.69	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: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
2:B:87:LEU:CD1	2:B:232:PHE:HB2	2.18	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
3:I:107:TYR:CE2	4:K:73:ALA:HA	2.22	0.74
1:S:133:GLN:HB2	1:S:139:LYS:HG2	1.67	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
4:E:75:THR:HG21	4:E:93:CYS:SG	2.26	0.74
3:I:39:GLU:CA	3:I:42:LYS:HE2	2.13	0.74
4:P:34:TYR:O	4:P:37:ILE:HG22	1.88	0.74
3:U:107:TYR:CE2	4:W:73:ALA:HA	2.23	0.74
1:A:52:PRO:C	1:A:54:ALA:H	1.94	0.74
2:H:87:LEU:CD1	2:H:232:PHE:HB2	2.17	0.74
3:I:83:ALA:HB3	4:K:72:LEU:HD11	1.70	0.74
4:K:139:TRP:HB2	4:K:142:ASN:ND2	2.01	0.74
5:L:120:GLY:CA	5:L:149:GLU:HG3	2.09	0.74
3:C:102:VAL:CG1	3:C:156:MET:HE1	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:37:ILE:O	4:E:41:LEU:HG	1.87	0.74
1:S:133:GLN:HB3	1:S:139:LYS:HG2	1.69	0.74
2:T:175:LYS:HG3	2:T:278:GLU:OE2	1.88	0.74
1:A:133:GLN:HB3	1:A:139:LYS:HG2	1.70	0.74
1:G:7:LEU:HD12	1:G:141:VAL:HB	1.69	0.74
1:M:52:PRO:C	1:M:54:ALA:H	1.94	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:A:200:MET:HE1	5:F:7:TYR:CA	2.17	0.74
1:G:10:ASN:HD22	1:G:10:ASN:C	1.91	0.74
3:I:7:TRP:HB2	3:I:89:VAL:CG1	2.16	0.74
3:I:82:THR:OG1	3:I:86:LEU:HB2	1.88	0.74
1:M:183:TYR:CE2	4:P:73:ALA:HB2	2.23	0.74
1:A:181:LYS:CB	1:A:214:MET:HE1	2.18	0.74
1:A:189:TYR:N	1:A:189:TYR:CD1	2.55	0.74
4:K:122:ASN:HB3	4:K:126:ASP:CG	2.13	0.74
4:P:22:THR:HB	4:P:74:ARG:NH1	2.02	0.74
3:U:83:ALA:HB3	4:W:72:LEU:HD11	1.70	0.74
1:A:29:ASN:HB3	1:A:32:GLU:OE2	1.88	0.73
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
4:E:122:ASN:HB3	4:E:126:ASP:CG	2.13	0.73
1:G:183:TYR:CE2	4:J:73:ALA:HB2	2.23	0.73
3:O:107:TYR:CE2	4:Q:73:ALA:HA	2.23	0.73
4:Q:37:ILE:O	4:Q:41:LEU:HG	1.88	0.73
5:R:103:LEU:HD21	5:R:145:MET:CE	2.13	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
4:D:22:THR:HB	4:D:74:ARG:NH1	2.03	0.73
1:G:133:GLN:HB3	1:G:139:LYS:HG2	1.69	0.73
1:G:174:ILE:HG13	1:G:175:ALA:N	2.00	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: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
4:D:155:VAL:C	4:D:156:GLN:HG2	2.13	0.73
4:K:141:SER:O	4:K:144:LEU:HB3	1.87	0.73
5:X:120:GLY:CA	5:X:149:GLU:HG3	2.09	0.73
1:A:133:GLN:HB2	1:A:139:LYS:HG2	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:139:TRP:HB2	4:E:142:ASN:ND2	2.03	0.73
1:G:50:LEU:HD23	3:I:47:MET:HE2	1.71	0.73
2:H:94:ILE:HD11	4:J:33:THR:HA	1.71	0.73
3:U:102:VAL:CG1	3:U:156:MET:HE1	2.19	0.73
4:W:84:VAL:HG23	4:W:108:TRP:CH2	2.23	0.73
3:I:102:VAL:CG1	3:I:156:MET:HE1	2.19	0.73
4:W:101:ILE:HD12	4:W:121:GLU:O	1.88	0.73
5:F:85:ILE:HG12	5:F:162:PHE:CZ	2.24	0.73
5:F:93:GLN:HG2	5:F:93:GLN:O	1.88	0.73
4:J:162:TRP:NE1	4:J:177:LYS:HB2	2.04	0.73
1:M:15:LEU:HD21	1:M:18:GLN:HB2	1.69	0.73
3:O:102:VAL:CG1	3:O:156:MET:HE1	2.19	0.73
5:R:85:ILE:HG12	5:R:162:PHE:CZ	2.24	0.73
1:S:40:LEU:HD21	1:S:129:MET:SD	2.29	0.73
1:A:10:ASN:ND2	1:A:12:SER:H	1.86	0.73
3:C:133:ARG:HE	4:E:189:PRO:HD2	1.54	0.73
1:G:10:ASN:ND2	1:G:12:SER:H	1.87	0.73
3:O:131:GLU:HB3	3:O:135:GLN:OE1	1.89	0.73
4:P:111:ASN:O	4:P:112:LYS:HG2	1.89	0.73
4:Q:37:ILE:HD11	4:W:37:ILE:CD1	2.09	0.73
4:Q:122:ASN:HB3	4:Q:126:ASP:CG	2.14	0.73
1:S:194:PRO:HG3	2:T:67:GLN:CB	2.18	0.73
4:W:122:ASN:HB3	4:W:126:ASP:CG	2.14	0.73
5:X:85:ILE:H	5:X:85:ILE:HD12	1.54	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
4:V:34:TYR:O	4:V:37:ILE:HG22	1.89	0.72
2:B:170:ARG:O	2:B:172:ARG:N	2.20	0.72
5:F:93:GLN:HE21	5:F:131:VAL:CG1	2.01	0.72
1:S:189:TYR:CD1	1:S:189:TYR:N	2.54	0.72
1:S:200:MET:HE1	5:X:7:TYR:CA	2.19	0.72
4:V:155:VAL:C	4:V:156:GLN:HG2	2.12	0.72
1:A:6:ILE:HG22	1:A:142:ALA:HA	1.69	0.72
4:E:141:SER:O	4:E:144:LEU:HB3	1.89	0.72
1:G:189:TYR:N	1:G:189:TYR:CD1	2.54	0.72
5:R:93:GLN:O	5:R:93:GLN:HG2	1.88	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
5:X:93:GLN:O	5:X:93:GLN:HG2	1.88	0.72
3:C:131:GLU:HB3	3:C:135:GLN:OE1	1.90	0.72
4:E:36:SER:O	4:E:40:GLN:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:103:LEU:HD21	5:F:145:MET:CE	2.15	0.72
5:L:111:THR:O	5:L:114:VAL:HG23	1.89	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
4:W:141:SER:O	4:W:144:LEU:HB3	1.88	0.72
1:A:15:LEU:HD21	1:A:18:GLN:HB2	1.69	0.72
5:L:165:MET:O	5:L:169:ILE:HG13	1.90	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
5:L:93:GLN:O	5:L:93:GLN:HG2	1.89	0.72
3:O:82:THR:OG1	3:O:86:LEU:HB2	1.90	0.72
3:I:5:SER:HG	3:I:7:TRP:HZ3	1.37	0.72
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
4:E:119:LEU:O	4:E:174:THR:CG2	2.37	0.72
3:O:83:ALA:HB3	4:Q:72:LEU:HD11	1.72	0.72
2:T:86:LYS:HZ2	2:T:90:TYR:HE1	1.38	0.72
4:W:99:LEU:HB2	4:W:101:ILE:HG22	1.72	0.72
2:B:94:ILE:HD11	4:D:33:THR:HA	1.71	0.72
2:B:170:ARG:C	2:B:172:ARG:H	1.97	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
4:Q:36:SER:O	4:Q:40:GLN:HB2	1.90	0.72
4:J:34:TYR:O	4:J:37:ILE:HG22	1.89	0.72
2:N:86:LYS:HZ2	2:N:90:TYR:HE1	1.38	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
1:A:10:ASN:ND2	1:A:11:LYS:N	2.34	0.71
1:A:197:SER:O	1:A:200:MET:HB2	1.89	0.71
4:J:106:THR:HG22	4:J:107:ASN:N	2.03	0.71
4:K:119:LEU:O	4:K:174:THR:CG2	2.38	0.71
3:O:5:SER:HG	3:O:7:TRP:HZ3	1.37	0.71
4:Q:139:TRP:HB2	4:Q:142:ASN:ND2	2.04	0.71
2:B:84:GLU:HB3	2:B:231:TYR:CD1	2.25	0.71
2:B:213:ASP:O	2:B:263:ARG:HG2	1.90	0.71
4:D:111:ASN:O	4:D:112:LYS:HG2	1.90	0.71
1:G:52:PRO:C	1:G:54:ALA:H	1.96	0.71
3:I:106:ILE:HD11	3:I:153:LEU:HD21	1.71	0.71
2:N:191:LEU:HB2	2:N:192:PHE:HD1	1.55	0.71
4:Q:75:THR:HG21	4:Q:93:CYS:SG	2.28	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:93:GLN:HE21	5:R:131:VAL:CG1	2.01	0.71
1:S:189:TYR:N	1:S:189:TYR:HD1	1.89	0.71
4:W:116:SER:HB3	4:W:175:GLU:HG3	1.72	0.71
1:G:189:TYR:N	1:G:189:TYR:HD1	1.89	0.71
1:M:10:ASN:ND2	1:M:12:SER:H	1.88	0.71
4:P:138:LEU:H	4:P:169:ARG:NH2	1.87	0.71
1:S:28:LEU:HD21	3:U:57:LYS:HD2	1.73	0.71
4:D:138:LEU:N	4:D:169:ARG:NH2	2.39	0.71
4:D:162:TRP:NE1	4:D:177:LYS:HB2	2.06	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:K:99:LEU:HB2	4:K:101:ILE:HG22	1.73	0.71
2:T:94:ILE:HD11	4:V:33:THR:HA	1.73	0.71
4:V:162:TRP:NE1	4:V:177:LYS:HB2	2.05	0.71
2:B:86:LYS:HZ2	2:B:90:TYR:HE1	1.39	0.71
4:D:95:PHE:HB3	4:D:101:ILE:HD12	1.72	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
2:N:213:ASP:O	2:N:263:ARG:HG2	1.90	0.71
4:P:161:VAL:HG12	4:P:176:ILE:CG2	2.20	0.71
4:Q:84:VAL:HG23	4:Q:108:TRP:CH2	2.24	0.71
4:Q:116:SER:HB3	4:Q:175:GLU:HG3	1.72	0.71
4:Q:119:LEU:O	4:Q:174:THR:CG2	2.37	0.71
4:V:106:THR:HG22	4:V:107:ASN:N	2.03	0.71
4:V:111:ASN:O	4:V:112:LYS:HG2	1.90	0.71
4:J:155:VAL:C	4:J:156:GLN:HG2	2.13	0.71
1:M:50:LEU:HD23	3:O:47:MET:HE2	1.71	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
1:S:181:LYS:CB	1:S:214:MET:HE1	2.19	0.71
4:V:138:LEU:H	4:V:169:ARG:CZ	2.02	0.71
4:W:37:ILE:HG21	4:W:59:MET:HE1	1.72	0.71
5:X:165:MET:O	5:X:169:ILE:HG13	1.90	0.71
3:C:123:TYR:C	3:C:125:PHE:H	1.99	0.71
1:G:29:ASN:HB3	1:G:32:GLU:OE2	1.91	0.71
5:L:85:ILE:H	5:L:85:ILE:HD12	1.55	0.71
3:U:82:THR:HG22	3:U:84:SER:N	1.99	0.71
1:A:183:TYR:CE2	4:D:73:ALA:HB2	2.26	0.71
2:H:84:GLU:HG2	2:H:228:SER:HB3	1.71	0.71
3:I:70:ILE:HB	3:I:77:VAL:CG2	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
5:L:68:GLU:CG	5:L:69:ARG:H	1.66	0.71
4:W:139:TRP:HB2	4:W:142:ASN:ND2	2.04	0.71
4:D:99:LEU:HB2	4:D:101:ILE:HG13	1.71	0.71
1:M:194:PRO:HG3	2:N:67:GLN:CB	2.20	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
3:U:7:TRP:HB2	3:U:89:VAL:CG1	2.18	0.71
4:V:138:LEU:N	4:V:169:ARG:NH2	2.39	0.71
1:A:194:PRO:HG3	2:B:67:GLN:CB	2.20	0.71
2:B:216:PRO:C	2:B:218:LEU:H	1.99	0.71
3:C:77:VAL:HG23	3:C:77:VAL:O	1.89	0.71
4:D:161:VAL:HG12	4:D:176:ILE:CG2	2.21	0.71
3:I:123:TYR:C	3:I:125:PHE:H	1.99	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
2:T:84:GLU:HB3	2:T:231:TYR:CD1	2.26	0.71
3:C:11:ARG:NH1	3:C:125:PHE:HE1	1.89	0.70
2:N:84:GLU:HG2	2:N:228:SER:HB3	1.71	0.70
2:N:94:ILE:HD11	4:P:33:THR:HA	1.73	0.70
4:P:95:PHE:HB3	4:P:101:ILE:HD12	1.72	0.70
1:S:183:TYR:CE2	4:V:73:ALA:HB2	2.26	0.70
5:F:29:SER:OG	5:F:46:LYS:HB3	1.90	0.70
1:G:147:VAL:HG12	1:G:148:MET:N	2.01	0.70
5:L:87:VAL:HG22	5:L:119:VAL:HB	1.73	0.70
5:X:28:PHE:HB2	5:X:159:GLU:OE2	1.89	0.70
1:A:114:TRP:HZ3	4:D:77:LEU:O	1.75	0.70
1:A:189:TYR:N	1:A:189:TYR:HD1	1.90	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
5:R:111:THR:O	5:R:114:VAL:HG23	1.91	0.70
2:T:213:ASP:O	2:T:263:ARG:HG2	1.92	0.70
4:V:139:TRP:HB2	4:V:142:ASN:ND2	2.05	0.70
2:B:191:LEU:HB2	2:B:192:PHE:HD1	1.56	0.70
5:F:69:ARG:CB	5:F:72:THR:HG22	2.16	0.70
4:J:99:LEU:HB2	4:J:101:ILE:HG13	1.71	0.70
3:O:77:VAL:HG23	3:O:77:VAL:O	1.90	0.70
1:S:126:GLN:HG3	3:U:65:ASN:CB	2.21	0.70
3:U:123:TYR:C	3:U:125:PHE:H	2.00	0.70
1:M:5:THR:HB	1:M:143:ILE:HB	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:10:ASN:ND2	1:M:11:LYS:N	2.34	0.70
3:O:123:TYR:C	3:O:125:PHE:H	2.00	0.70
1:S:50:LEU:HD23	3:U:47:MET:HE2	1.72	0.70
5:X:111:THR:O	5:X:114:VAL:HG23	1.91	0.70
1:A:21:PHE:CZ	1:A:215:VAL:HG11	2.26	0.70
3:I:82:THR:HB	3:I:86:LEU:H	1.56	0.70
5:R:149:GLU:O	5:R:150:THR:HG23	1.91	0.70
3:U:77:VAL:O	3:U:77:VAL:HG23	1.90	0.70
4:E:84:VAL:HG23	4:E:108:TRP:CH2	2.26	0.70
4:E:116:SER:HB3	4:E:175:GLU:HG3	1.74	0.70
5:L:108:ARG:HB2	5:L:108:ARG:HH11	1.54	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:J:161:VAL:HG12	4:J:176:ILE:CG2	2.20	0.70
4:K:116:SER:HB3	4:K:175:GLU:HG3	1.74	0.70
4:V:161:VAL:HG12	4:V:176:ILE:CG2	2.20	0.70
5:X:108:ARG:HB2	5:X:108:ARG:HH11	1.55	0.70
4:D:161:VAL:HG12	4:D:176:ILE:HG21	1.74	0.70
3:U:70:ILE:HB	3:U:77:VAL:CG2	2.21	0.70
5:X:29:SER:OG	5:X:46:LYS:HB3	1.90	0.70
2:B:84:GLU:HG2	2:B:228:SER:HB3	1.72	0.70
2:B:176:ILE:O	2:B:179:ILE:HG22	1.92	0.70
2:B:231:TYR:HE2	2:B:251:THR:HA	1.57	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
4:K:155:VAL:O	4:K:155:VAL:HG12	1.92	0.70
4:Q:180:LEU:HD23	4:Q:181:ASN:N	2.07	0.70
2:T:176:ILE:O	2:T:179:ILE:HG22	1.92	0.70
3:U:5:SER:HG	3:U:7:TRP:HZ3	1.38	0.70
1:G:114:TRP:HZ3	4:J:77:LEU:O	1.74	0.69
3:I:80:TYR:HB3	3:I:103:LEU:HD23	1.74	0.69
3:I:85:GLY:C	3:I:86:LEU:HD12	2.18	0.69
3:I:111:TYR:O	3:I:115:VAL:HB	1.91	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
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
5:X:87:VAL:HG22	5:X:119:VAL:HB	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:7:TRP:HB2	3:C:89:VAL:CG1	2.18	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:28:PHE:HB2	5:F:159:GLU:OE2	1.92	0.69
5:F:165:MET:O	5:F:169:ILE:HG13	1.91	0.69
2:H:238:LYS:HB2	2:H:250:VAL:HG23	1.74	0.69
5:L:16:ASN:O	5:L:19:VAL:HG23	1.92	0.69
1:M:171:ALA:O	1:M:174:ILE:HG12	1.92	0.69
3:O:140:ILE:HG23	3:O:140:ILE:O	1.91	0.69
3:U:133:ARG:HG2	4:W:188:ILE:HA	1.74	0.69
5:X:149:GLU:O	5:X:150:THR:HG23	1.93	0.69
1:A:3:ILE:HG23	1:A:143:ILE:O	1.92	0.69
1:A:147:VAL:HG12	1:A:148:MET:N	2.04	0.69
3:C:70:ILE:HB	3:C:77:VAL:CG2	2.22	0.69
5:F:87:VAL:HG22	5:F:119:VAL:HB	1.73	0.69
3:I:70:ILE:HB	3:I:77:VAL:HG22	1.74	0.69
4:P:106:THR:HG22	4:P:107:ASN:N	2.04	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
2:H:68:GLU:HG2	4:J:63:ILE:HD11	1.74	0.69
1:M:114:TRP:HZ3	4:P:77:LEU:O	1.76	0.69
2:N:170:ARG:C	2:N:172:ARG:H	2.00	0.69
4:W:180:LEU:HD23	4:W:181:ASN:N	2.07	0.69
4:D:111:ASN:HD22	4:D:113:ASP:CG	2.01	0.69
5:L:29:SER:OG	5:L:46:LYS:HB3	1.91	0.69
1:M:147:VAL:HG12	1:M:148:MET:N	2.01	0.69
2:N:238:LYS:HB2	2:N:250:VAL:HG23	1.74	0.69
3:O:82:THR:HG22	3:O:84:SER:N	1.97	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
2:B:238:LYS:HB2	2:B:250:VAL:HG23	1.74	0.69
1:G:21:PHE:CZ	1:G:215:VAL:HG11	2.27	0.69
2:H:173:ASP:O	2:H:174:LEU:HD23	1.93	0.69
3:I:11:ARG:NH1	3:I:125:PHE:HE1	1.90	0.69
1:S:21:PHE:CZ	1:S:215:VAL:HG11	2.27	0.69
3:U:11:ARG:NH1	3:U:125:PHE:HE1	1.90	0.69
4:W:110:HIS:O	4:W:111:ASN:HB3	1.92	0.69
4:E:99:LEU:HB2	4:E:101:ILE:HG22	1.73	0.69
1:G:212:LYS:O	1:G:215:VAL:HG22	1.92	0.69
5:L:149:GLU:O	5:L:150:THR:HG23	1.93	0.69
2:N:216:PRO:C	2:N:218:LEU:H	2.01	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:99:LEU:HB2	4:Q:101:ILE:HG22	1.72	0.69
1:S:114:TRP:HZ3	4:V:77:LEU:O	1.75	0.69
1:S:120:ARG:HH11	1:S:120:ARG:CB	2.04	0.69
2:T:84:GLU:HG2	2:T:228:SER:HB3	1.73	0.69
1:A:126:GLN:HG3	3:C:65:ASN:CB	2.22	0.69
4:D:77:LEU:HD22	4:D:78:PRO:HD2	1.75	0.69
4:E:122:ASN:OD1	4:E:124:LEU:HB3	1.93	0.69
5:F:16:ASN:O	5:F:19:VAL:HG23	1.93	0.69
5:F:53:ASP:O	5:F:55:LYS:N	2.26	0.69
2:H:87:LEU:CG	2:H:232:PHE:HB2	2.22	0.69
3:I:77:VAL:HG23	3:I:77:VAL:O	1.91	0.69
4:J:49:PHE:CZ	4:J:133:ASP:OD2	2.46	0.69
4:J:95:PHE:HB3	4:J:101:ILE:HD12	1.74	0.69
4:J:138:LEU:H	4:J:169:ARG:CZ	2.05	0.69
4:J:161:VAL:HG12	4:J:176:ILE:HG21	1.74	0.69
5:L:14:ILE:HG22	5:L:64:THR:CG2	2.23	0.69
5:L:53:ASP:O	5:L:55:LYS:N	2.26	0.69
4:P:138:LEU:H	4:P:169:ARG:CZ	2.05	0.69
5:R:16:ASN:O	5:R:19:VAL:HG23	1.93	0.69
3:U:111:TYR:O	3:U:115:VAL:HB	1.92	0.69
4:V:95:PHE:HB3	4:V:101:ILE:HD12	1.73	0.69
4:E:110:HIS:O	4:E:111:ASN:HB3	1.93	0.69
4:K:37:ILE:HG21	4:K:59:MET:HE1	1.75	0.69
1:M:21:PHE:CZ	1:M:215:VAL:HG11	2.27	0.69
2:N:231:TYR:HE2	2:N:251:THR:HA	1.58	0.69
3:O:7:TRP:HB2	3:O:89:VAL:CG1	2.18	0.69
3:O:106:ILE:HD11	3:O:153:LEU:HD21	1.73	0.69
4:Q:110:HIS:O	4:Q:111:ASN:HB3	1.93	0.69
3:U:10:ASP:OD2	3:U:12:HIS:HB2	1.93	0.69
5:X:69:ARG:CB	5:X:72:THR:HG22	2.18	0.69
1:A:75:MET:HA	1:A:217:ASN:ND2	2.07	0.69
2:B:99:LEU:H	2:B:99:LEU:HD12	1.57	0.69
5:F:14:ILE:HG22	5:F:64:THR:CG2	2.23	0.69
5:F:149:GLU:O	5:F:150:THR:HG23	1.93	0.69
4:K:180:LEU:HD23	4:K:181:ASN:N	2.07	0.69
5:R:120:GLY:CA	5:R:149:GLU:HG3	2.09	0.69
2:T:170:ARG:C	2:T:172:ARG:H	2.00	0.69
2:T:173:ASP:O	2:T:174:LEU:HD23	1.92	0.69
3:U:140:ILE:HG23	3:U:140:ILE:O	1.94	0.69
4:V:161:VAL:HG12	4:V:176:ILE:HG21	1.74	0.69
3:C:82:THR:HG22	3:C:84:SER:N	1.99	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:106:ILE:HD11	3:C:153:LEU:HD21	1.73	0.68
1:G:75:MET:HA	1:G:217:ASN:ND2	2.08	0.68
4:K:75:THR:HG21	4:K:93:CYS:SG	2.32	0.68
4:K:110:HIS:O	4:K:111:ASN:HB3	1.93	0.68
2:N:176:ILE:O	2:N:179:ILE:HG22	1.93	0.68
5:R:28:PHE:HB2	5:R:159:GLU:OE2	1.93	0.68
1:S:10:ASN:HD22	1:S:11:LYS:H	1.42	0.68
1:G:10:ASN:HD22	1:G:11:LYS:H	1.41	0.68
2:H:176:ILE:O	2:H:179:ILE:HG22	1.93	0.68
4:P:111:ASN:HD22	4:P:113:ASP:CG	2.01	0.68
5:R:53:ASP:O	5:R:55:LYS:N	2.26	0.68
5:X:53:ASP:O	5:X:55:LYS:N	2.26	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
1:G:197:SER:O	1:G:200:MET:HB2	1.92	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:S:70:ILE:HG12	1:S:72:TYR:H	1.57	0.68
3:C:140:ILE:HG23	3:C:140:ILE:O	1.93	0.68
4:E:180:LEU:HD23	4:E:181:ASN:N	2.08	0.68
5:F:108:ARG:HB2	5:F:108:ARG:HH11	1.55	0.68
2:H:255:MET:O	2:H:255:MET:SD	2.51	0.68
3:I:10:ASP:OD2	3:I:12:HIS:HB2	1.94	0.68
5:L:28:PHE:HB2	5:L:159:GLU:OE2	1.92	0.68
5:R:108:ARG:HB2	5:R:108:ARG:HH11	1.56	0.68
1:S:212:LYS:O	1:S:215:VAL:HG22	1.93	0.68
3:U:70:ILE:HB	3:U:77:VAL:HG22	1.74	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:V:111:ASN:HD22	4:V:113:ASP:CG	2.02	0.68
4:E:37:ILE:HG21	4:E:59:MET:HE1	1.74	0.68
1:G:120:ARG:HH11	1:G:120:ARG:CB	2.05	0.68
1:M:75:MET:HA	1:M:217:ASN:ND2	2.08	0.68
2:N:87:LEU:CG	2:N:232:PHE:HB2	2.23	0.68
3:I:112:VAL:HG11	4:K:70:ASP:HB2	1.74	0.68
5:L:41:ILE:H	5:L:41:ILE:HD12	1.59	0.68
4:P:77:LEU:HD22	4:P:78:PRO:HD2	1.76	0.68
1:S:28:LEU:HB2	1:S:33:TYR:CE1	2.28	0.68
1:S:75:MET:HA	1:S:217:ASN:ND2	2.08	0.68
2:T:231:TYR:HE2	2:T:251:THR:HA	1.57	0.68
5:X:14:ILE:HG22	5:X:64:THR:CG2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:17:TYR:HB2	1:G:202:ILE:HD12	1.76	0.68
3:O:85:GLY:C	3:O:86:LEU:HD12	2.19	0.68
5:R:14:ILE:HG22	5:R:64:THR:CG2	2.24	0.68
3:C:85:GLY:C	3:C:86:LEU:HD12	2.19	0.68
3:I:140:ILE:HG23	3:I:140:ILE:O	1.94	0.68
4:J:111:ASN:HD22	4:J:113:ASP:CG	2.02	0.68
1:M:28:LEU:HD21	3:O:57:LYS:HD2	1.76	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
2:N:184:HIS:HB2	2:N:211:ILE:CD1	2.24	0.68
3:O:111:TYR:O	3:O:115:VAL:HB	1.93	0.68
3:O:133:ARG:HG2	4:Q:188:ILE:HA	1.76	0.68
3:U:106:ILE:HD11	3:U:153:LEU:HD21	1.74	0.68
4:V:77:LEU:HD22	4:V:78:PRO:HD2	1.75	0.68
1:M:120:ARG:HH11	1:M:120:ARG:CB	2.05	0.67
1:S:50:LEU:HD13	3:U:43:LEU:HD11	1.74	0.67
1:A:17:TYR:HB2	1:A:202:ILE:HD12	1.75	0.67
1:A:28:LEU:HB2	1:A:33:TYR:CE1	2.29	0.67
1:A:50:LEU:HD13	3:C:43:LEU:HD11	1.74	0.67
2:B:87:LEU:CG	2:B:232:PHE:HB2	2.24	0.67
5:F:113:THR:O	5:F:115:LEU:HD23	1.94	0.67
2:H:170:ARG:C	2:H:172:ARG:H	2.02	0.67
3:I:44:LEU:O	3:I:44:LEU:HD23	1.95	0.67
4:J:77:LEU:HD22	4:J:78:PRO:HD2	1.75	0.67
1:M:70:ILE:HG12	1:M:72:TYR:H	1.58	0.67
3:O:3:ILE:CB	3:O:90:LEU:HD11	2.24	0.67
4:Q:49:PHE:CD2	4:Q:134:ALA:HB2	2.30	0.67
5:R:85:ILE:HD12	5:R:85:ILE:N	2.08	0.67
1:S:136:THR:HG21	4:V:69:GLU:OE1	1.94	0.67
3:U:112:VAL:HG11	4:W:70:ASP:HB2	1.75	0.67
4:W:122:ASN:OD1	4:W:124:LEU:HB3	1.95	0.67
1:G:70:ILE:HG12	1:G:72:TYR:H	1.59	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
1:S:133:GLN:HA	1:S:138:LEU:O	1.94	0.67
2:T:99:LEU:H	2:T:99:LEU:HD12	1.58	0.67
3:U:133:ARG:CB	4:W:188:ILE:HG13	2.24	0.67
4:V:49:PHE:CZ	4:V:133:ASP:OD2	2.48	0.67
1:A:192:LYS:HE2	2:B:64:PHE:CZ	2.30	0.67
4:D:131:PRO:O	4:D:133:ASP:N	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:50:LEU:HD13	3:I:43:LEU:HD11	1.75	0.67
2:H:216:PRO:C	2:H:218:LEU:H	2.00	0.67
3:I:114:TYR:CD1	3:I:114:TYR:N	2.62	0.67
4:K:114:THR:OG1	4:K:179:LYS:HB2	1.94	0.67
5:L:113:THR:O	5:L:115:LEU:HD23	1.94	0.67
1:S:17:TYR:HB2	1:S:202:ILE:HD12	1.76	0.67
3:U:114:TYR:N	3:U:114:TYR:CD1	2.62	0.67
4:E:155:VAL:HG12	4:E:155:VAL:O	1.93	0.67
3:I:108:SER:HB3	4:K:73:ALA:HB1	1.74	0.67
1:M:136:THR:HG21	4:P:69:GLU:OE1	1.93	0.67
2:N:170:ARG:O	2:N:172:ARG:N	2.27	0.67
3:O:70:ILE:HB	3:O:77:VAL:HG22	1.75	0.67
5:X:113:THR:O	5:X:115:LEU:HD23	1.94	0.67
1:A:130:PHE:CE1	1:A:172:ILE:HA	2.30	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
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:V:131:PRO:O	4:V:133:ASP:N	2.27	0.67
3:C:10:ASP:OD2	3:C:12:HIS:HB2	1.94	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
1:M:130:PHE:CE1	1:M:172:ILE:HA	2.30	0.67
4:P:131:PRO:O	4:P:133:ASP:N	2.27	0.67
2:T:216:PRO:C	2:T:218:LEU:H	2.01	0.67
3:U:133:ARG:NE	4:W:189:PRO:HD2	2.08	0.67
1:A:212:LYS:O	1:A:215:VAL:HG22	1.95	0.67
3:C:3:ILE:CB	3:C:90:LEU:HD11	2.25	0.67
1:G:126:GLN:HG3	3:I:65:ASN:CB	2.25	0.67
3:I:84:SER:OG	3:I:86:LEU:HD13	1.95	0.67
3:O:137:THR:O	3:O:139:LYS:N	2.28	0.67
4:P:138:LEU:N	4:P:169:ARG:NH2	2.43	0.67
1:S:10:ASN:ND2	1:S:11:LYS:N	2.34	0.67
3:U:85:GLY:C	3:U:86:LEU:HD12	2.20	0.67
4:V:114:THR:HG22	4:V:115:PHE:N	2.10	0.67
5:X:85:ILE:HD12	5:X:85:ILE:N	2.09	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:HD12	5:F:41:ILE:H	1.58	0.67
1:G:39:THR:O	1:G:43:VAL:HG23	1.95	0.67
4:K:122:ASN:OD1	4:K:124:LEU:HB3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:Q:34:TYR:CE1	4:Q:143:ILE:HG21	2.30	0.67
2:T:238:LYS:HB2	2:T:250:VAL:HG23	1.77	0.67
1:A:133:GLN:HA	1:A:138:LEU:O	1.95	0.66
3:I:98:SER:HB2	3:I:100:THR:HG23	1.77	0.66
4:J:47:ARG:HB3	4:J:49:PHE:CE2	2.30	0.66
4:J:131:PRO:O	4:J:133:ASP:N	2.27	0.66
3:O:98:SER:HB2	3:O:100:THR:HG23	1.77	0.66
4:Q:37:ILE:HG21	4:Q:59:MET:HE1	1.76	0.66
2:T:87:LEU:CG	2:T:232:PHE:HB2	2.24	0.66
3:U:80:TYR:HB3	3:U:103:LEU:HD23	1.76	0.66
4:V:47:ARG:HB3	4:V:49:PHE:CE2	2.30	0.66
1:G:28:LEU:HB2	1:G:33:TYR:CE1	2.30	0.66
3:I:137:THR:O	3:I:139:LYS:N	2.28	0.66
1:M:28:LEU:HB2	1:M:33:TYR:CE1	2.30	0.66
1:M:107:PHE:HB3	1:M:180:ARG:NH1	2.10	0.66
3:O:10:ASP:OD2	3:O:12:HIS:HB2	1.94	0.66
2:T:233:VAL:HA	2:T:236:ILE:HD13	1.77	0.66
5:X:14:ILE:HB	5:X:102:TRP:HZ3	1.59	0.66
5:F:120:GLY:CA	5:F:149:GLU:HG3	2.10	0.66
1:G:130:PHE:CE1	1:G:172:ILE:HA	2.30	0.66
4:K:49:PHE:CD2	4:K:134:ALA:HB2	2.28	0.66
4:P:114:THR:HG22	4:P:115:PHE:N	2.10	0.66
3:C:137:THR:O	3:C:139:LYS:N	2.28	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
5:R:14:ILE:HB	5:R:102:TRP:HZ3	1.59	0.66
1:M:133:GLN:HA	1:M:138:LEU:O	1.95	0.66
5:R:113:THR:O	5:R:115:LEU:HD23	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
3:U:137:THR:O	3:U:139:LYS:N	2.29	0.66
5:X:108:ARG:HH11	5:X:108:ARG:CB	2.09	0.66
1:A:50:LEU:HD23	3:C:47:MET:HE2	1.76	0.66
3:C:98:SER:HB2	3:C:100:THR:HG23	1.77	0.66
2:H:99:LEU:H	2:H:99:LEU:HD12	1.59	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
1:G:107:PHE:HB3	1:G:180:ARG:NH1	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:129:GLU:O	4:J:131:PRO:HD3	1.96	0.66
4:Q:124:LEU:HD23	4:Q:124:LEU:C	2.20	0.66
1:A:129:MET:HG2	1:A:131:ILE:HD12	1.77	0.66
2:B:184:HIS:HB2	2:B:211:ILE:CD1	2.26	0.66
5:F:13:LEU:CD2	5:F:25:LEU:HD11	2.26	0.66
5:F:14:ILE:HB	5:F:102:TRP:HZ3	1.60	0.66
1:G:192:LYS:HE2	2:H:64:PHE:CZ	2.30	0.66
1:S:5:THR:HB	1:S:143:ILE:HB	1.75	0.66
1:A:70:ILE:HG12	1:A:72:TYR:H	1.60	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:G:114:TRP:CZ3	4:J:77:LEU:O	2.49	0.66
5:L:108:ARG:HH11	5:L:108:ARG:CB	2.09	0.66
1:M:17:TYR:HB2	1:M:202:ILE:HD12	1.77	0.66
2:N:66:PHE:CZ	2:N:70:ILE:HD11	2.30	0.66
5:R:130:VAL:HG12	5:R:131:VAL:N	2.11	0.66
5:X:13:LEU:CD2	5:X:25:LEU:HD11	2.26	0.66
2:B:214:ASN:HA	2:B:263:ARG:CG	2.23	0.66
3:C:133:ARG:HG2	4:E:188:ILE:HA	1.78	0.66
4:D:114:THR:HG22	4:D:115:PHE:N	2.10	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:H:216:PRO:O	2:H:218:LEU:N	2.29	0.66
3:I:142:ASN:C	3:I:142:ASN:HD22	2.04	0.66
4:K:87:SER:HB2	4:K:115:PHE:CD1	2.31	0.66
5:L:85:ILE:HD12	5:L:85:ILE:N	2.10	0.66
4:P:47:ARG:HB3	4:P:49:PHE:CE2	2.31	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
2:N:218:LEU:HD23	2:N:233:VAL:HG12	1.78	0.65
3:U:3:ILE:CB	3:U:90:LEU:HD11	2.26	0.65
3:U:84:SER:OG	3:U:86:LEU:HD13	1.96	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
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
1:M:10:ASN:C	1:M:10:ASN:ND2	2.55	0.65
2:N:173:ASP:O	2:N:174:LEU:HD23	1.97	0.65
3:O:133:ARG:CB	4:Q:188:ILE:HG13	2.26	0.65
4:Q:122:ASN:OD1	4:Q:124:LEU:HB3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:255:MET:O	2:T:255:MET:SD	2.54	0.65
2:H:184:HIS:HB2	2:H:211:ILE:CD1	2.27	0.65
3:O:119:LEU:HD11	4:W:36:SER:N	2.11	0.65
3:O:133:ARG:NE	4:Q:189:PRO:HD2	2.10	0.65
1:A:7:LEU:HD12	1:A:141:VAL:HB	1.76	0.65
5:F:28:PHE:HB3	5:F:48:LYS:NZ	2.11	0.65
3:I:7:TRP:CB	3:I:89:VAL:HG12	2.20	0.65
2:N:192:PHE:CD1	2:N:192:PHE:N	2.65	0.65
4:P:129:GLU:O	4:P:131:PRO:HD3	1.96	0.65
5:R:28:PHE:HB3	5:R:48:LYS:NZ	2.11	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:10:ASN:C	1:A:10:ASN:ND2	2.55	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
3:I:133:ARG:HG2	4:K:188:ILE:HA	1.79	0.65
2:N:255:MET:O	2:N:255:MET:SD	2.54	0.65
3:O:118:ASN:CG	3:O:118:ASN:O	2.40	0.65
4:Q:114:THR:OG1	4:Q:179:LYS:HB2	1.95	0.65
5:X:28:PHE:HB3	5:X:48:LYS:NZ	2.11	0.65
1:A:114:TRP:CZ3	4:D:77:LEU:O	2.49	0.65
3:C:72:THR:CG2	3:C:73:GLY:N	2.60	0.65
5:X:68:GLU:HG2	5:X:69:ARG:HB3	1.79	0.65
3:C:43:LEU:HD12	3:C:43:LEU:C	2.22	0.65
3:I:106:ILE:HD13	3:I:149:LEU:HD11	1.78	0.65
2:N:216:PRO:O	2:N:218:LEU:N	2.29	0.65
3:O:44:LEU:O	3:O:44:LEU:HD23	1.97	0.65
4:V:129:GLU:O	4:V:131:PRO:HD3	1.97	0.65
1:A:120:ARG:HH11	1:A:120:ARG:CB	2.07	0.65
2:H:64:PHE:CE1	4:J:67:LEU:HD12	2.32	0.65
4:K:34:TYR:CE1	4:K:143:ILE:HG21	2.32	0.65
4:K:115:PHE:CE2	4:K:178:VAL:HB	2.31	0.65
2:N:233:VAL:HA	2:N:236:ILE:HD13	1.79	0.65
3:O:7:TRP:CB	3:O:89:VAL:HG12	2.22	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
5:F:90:VAL:O	5:F:90:VAL:HG12	1.97	0.65
4:Q:114:THR:HG23	4:Q:178:VAL:C	2.21	0.65
4:Q:115:PHE:CE2	4:Q:178:VAL:HB	2.31	0.65
5:R:86:ILE:HD11	5:R:106:ILE:HD11	1.79	0.65
4:W:34:TYR:CE1	4:W:143:ILE:HG21	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4:GLU:HG3	1:G:143:ILE:HG22	1.77	0.64
1:M:129:MET:HG2	1:M:131:ILE:HD12	1.79	0.64
2:N:184:HIS:HB2	2:N:211:ILE:HD11	1.79	0.64
3:O:108:SER:HB3	4:Q:73:ALA:HB1	1.77	0.64
1:S:114:TRP:CZ3	4:V:77:LEU:O	2.50	0.64
2:T:216:PRO:O	2:T:218:LEU:N	2.30	0.64
1:A:28:LEU:HD21	3:C:57:LYS:HD2	1.79	0.64
3:C:142:ASN:C	3:C:142:ASN:HD22	2.04	0.64
5:F:108:ARG:HH11	5:F:108:ARG:CB	2.08	0.64
3:O:133:ARG:HB3	4:Q:188:ILE:HG13	1.78	0.64
2:B:192:PHE:CD1	2:B:192:PHE:N	2.66	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
4:K:124:LEU:C	4:K:124:LEU:HD23	2.23	0.64
4:K:129:GLU:HG3	4:K:129:GLU:O	1.96	0.64
4:W:87:SER:HB2	4:W:115:PHE:CD1	2.32	0.64
2:B:175:LYS:HG2	2:B:176:ILE:N	2.12	0.64
2:B:255:MET:SD	2:B:255:MET:O	2.55	0.64
3:C:114:TYR:N	3:C:114:TYR:CD1	2.63	0.64
4:E:143:ILE:HG23	4:E:144:LEU:N	2.12	0.64
3:I:85:GLY:O	3:I:86:LEU:HD12	1.98	0.64
5:L:90:VAL:O	5:L:90:VAL:HG12	1.98	0.64
1:M:114:TRP:CZ3	4:P:77:LEU:O	2.50	0.64
3:O:114:TYR:N	3:O:114:TYR:CD1	2.63	0.64
3:U:44:LEU:HD23	3:U:44:LEU:O	1.98	0.64
5:X:69:ARG:HB2	5:X:72:THR:HG21	1.79	0.64
4:E:124:LEU:HD23	4:E:124:LEU:C	2.22	0.64
2:H:66:PHE:CZ	2:H:70:ILE:HD11	2.32	0.64
3:I:3:ILE:CB	3:I:90:LEU:HD11	2.28	0.64
5:L:28:PHE:HB3	5:L:48:LYS:NZ	2.12	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:R:43:VAL:HG23	5:R:43:VAL:O	1.96	0.64
1:S:192:LYS:HE2	2:T:64:PHE:CZ	2.32	0.64
4:W:114:THR:HG23	4:W:178:VAL:C	2.21	0.64
3:C:7:TRP:CB	3:C:89:VAL:HG12	2.22	0.64
3:C:137:THR:O	3:C:139:LYS:HG3	1.98	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
5:R:90:VAL:HG12	5:R:90:VAL:O	1.97	0.64
4:W:48:ASP:OD1	4:W:51:LYS:HG3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:99:LEU:CD1	4:D:101:ILE:HD11	2.27	0.64
1:M:187:SER:O	1:M:191:MET:HB2	1.98	0.64
4:V:99:LEU:CD1	4:V:101:ILE:HD11	2.27	0.64
4:W:124:LEU:HD23	4:W:124:LEU:C	2.23	0.64
3:C:44:LEU:HD23	3:C:44:LEU:O	1.98	0.64
4:D:47:ARG:HB3	4:D:49:PHE:CE2	2.32	0.64
1:G:124:THR:CB	3:I:65:ASN:HD21	2.11	0.64
2:H:170:ARG:O	2:H:172:ARG:N	2.28	0.64
1:M:43:VAL:HG11	3:O:51:LEU:HG	1.78	0.64
4:P:99:LEU:CD1	4:P:101:ILE:HD11	2.26	0.64
4:W:49:PHE:CD2	4:W:134:ALA:HB2	2.31	0.64
4:W:102:THR:O	4:W:102:THR:HG22	1.97	0.64
3:I:133:ARG:CB	4:K:188:ILE:HG13	2.28	0.64
4:K:114:THR:HG23	4:K:178:VAL:C	2.21	0.64
3:O:85:GLY:O	3:O:86:LEU:HD12	1.98	0.64
4:Q:129:GLU:HG3	4:Q:129:GLU:O	1.97	0.64
2:B:86:LYS:NZ	2:B:90:TYR:CE1	2.66	0.64
4:D:179:LYS:HE2	4:D:181:ASN:HB3	1.80	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:R:108:ARG:HH11	5:R:108:ARG:CB	2.09	0.64
4:V:48:ASP:O	4:V:50:ASN:N	2.31	0.64
5:X:90:VAL:O	5:X:90:VAL:HG12	1.98	0.64
2:B:66:PHE:CZ	2:B:70:ILE:HD11	2.33	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
4:J:48:ASP:O	4:J:50:ASN:N	2.31	0.63
5:R:12:LEU:HD23	5:R:12:LEU:N	2.09	0.63
5:R:13:LEU:CD2	5:R:25:LEU:HD11	2.28	0.63
1:S:23:ASN:HB3	1:S:25:GLU:CD	2.23	0.63
3:U:108:SER:HB3	4:W:73:ALA:HB1	1.78	0.63
3:C:108:SER:HB3	4:E:73:ALA:HB1	1.79	0.63
3:C:112:VAL:HG11	4:E:70:ASP:CB	2.28	0.63
3:C:133:ARG:CB	4:E:188:ILE:HG13	2.28	0.63
4:D:61:TYR:HA	4:D:146:GLY:O	1.98	0.63
4:E:101:ILE:CD1	4:E:121:GLU:O	2.46	0.63
4:E:129:GLU:HG3	4:E:129:GLU:O	1.97	0.63
1:G:23:ASN:HB3	1:G:25:GLU:CD	2.23	0.63
3:U:7:TRP:CB	3:U:89:VAL:HG12	2.22	0.63
4:V:179:LYS:HE2	4:V:181:ASN:HB3	1.80	0.63
4:W:17:ILE:HG21	4:W:97:ILE:CD1	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:14:ASN:ND2	3:C:132:MET:O	2.31	0.63
4:D:111:ASN:HD22	4:D:113:ASP:HB2	1.63	0.63
5:F:86:ILE:HD11	5:F:106:ILE:HD11	1.80	0.63
1:G:178:PHE:HD2	1:G:179:LEU:HD23	1.63	0.63
2:H:214:ASN:HA	2:H:263:ARG:CG	2.23	0.63
2:H:233:VAL:HA	2:H:236:ILE:HD13	1.80	0.63
5:L:86:ILE:HD11	5:L:106:ILE:HD11	1.79	0.63
3:O:39:GLU:CA	3:O:42:LYS:HE2	2.14	0.63
3:O:106:ILE:HD13	3:O:149:LEU:HD11	1.80	0.63
1:S:124:THR:CB	3:U:65:ASN:HD21	2.12	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
4:E:17:ILE:HG21	4:E:97:ILE:CD1	2.28	0.63
3:I:82:THR:CG2	3:I:84:SER:H	2.02	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
5:R:12:LEU:HB3	5:R:62:TRP:HB2	1.80	0.63
1:S:52:PRO:HD3	3:U:75:TYR:CE2	2.34	0.63
3:C:84:SER:OG	3:C:86:LEU:HD13	1.98	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
5:L:53:ASP:C	5:L:55:LYS:H	2.07	0.63
1:M:52:PRO:HD3	3:O:75:TYR:CE2	2.34	0.63
3:O:142:ASN:HD22	3:O:142:ASN:C	2.06	0.63
2:T:191:LEU:HB2	2:T:192:PHE:CD1	2.34	0.63
3:U:137:THR:O	3:U:139:LYS:HG3	1.98	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
4:W:129:GLU:HG3	4:W:129:GLU:O	1.97	0.63
4:E:34:TYR:CE1	4:E:143:ILE:HG21	2.33	0.63
4:E:87:SER:HB2	4:E:115:PHE:CD1	2.33	0.63
4:E:102:THR:O	4:E:102:THR:HG22	1.98	0.63
3:I:72:THR:CG2	3:I:73:GLY:N	2.61	0.63
4:J:134:ALA:HB1	4:J:138:LEU:HD13	1.81	0.63
1:M:39:THR:O	1:M:43:VAL:HG23	1.99	0.63
3:O:112:VAL:HG11	4:Q:70:ASP:CB	2.28	0.63
4:Q:87:SER:HB2	4:Q:115:PHE:CD1	2.33	0.63
4:W:95:PHE:CD1	4:W:103:PRO:HG3	2.34	0.63
5:X:12:LEU:HD23	5:X:12:LEU:N	2.09	0.63
4:E:115:PHE:CE2	4:E:178:VAL:HB	2.33	0.63
3:O:84:SER:OG	3:O:86:LEU:HD13	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:111:ASN:HD22	4:P:113:ASP:HB2	1.63	0.63
4:Q:48:ASP:OD1	4:Q:51:LYS:HG3	1.99	0.63
4:V:118:ILE:HA	4:V:175:GLU:HB3	1.81	0.63
1:A:23:ASN:HB3	1:A:25:GLU:CD	2.23	0.63
1:G:43:VAL:HG11	3:I:51:LEU:HG	1.80	0.63
4:Q:99:LEU:HB3	4:Q:123:PRO:HG3	1.81	0.63
3:U:106:ILE:HD13	3:U:149:LEU:HD11	1.81	0.63
3:U:118:ASN:O	3:U:118:ASN:CG	2.42	0.63
4:W:114:THR:OG1	4:W:179:LYS:HB2	1.99	0.63
3:C:118:ASN:CG	3:C:118:ASN:O	2.42	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
4:P:155:VAL:C	4:P:156:GLN:HE21	2.07	0.63
3:U:72:THR:CG2	3:U:73:GLY:N	2.61	0.63
3:U:127:GLU:O	3:U:129:GLU:N	2.29	0.63
5:X:53:ASP:C	5:X:55:LYS:H	2.07	0.63
1:A:134:THR:HG21	1:A:183:TYR:CD1	2.34	0.62
2:B:99:LEU:HD11	2:B:240:PHE:HA	1.81	0.62
5:F:12:LEU:HB3	5:F:62:TRP:HB2	1.80	0.62
5:F:43:VAL:HG23	5:F:43:VAL:O	1.98	0.62
3:I:105:TYR:CD2	3:I:152:PHE:CZ	2.87	0.62
3:I:118:ASN:CG	3:I:118:ASN:O	2.42	0.62
4:J:99:LEU:CD1	4:J:101:ILE:HD11	2.27	0.62
1:S:134:THR:HG21	1:S:183:TYR:CD1	2.33	0.62
3:U:112:VAL:HG11	4:W:70:ASP:CB	2.28	0.62
1:A:52:PRO:HD3	3:C:75:TYR:CE2	2.34	0.62
1:A:178:PHE:HD2	1:A:179:LEU:HD23	1.63	0.62
2:B:68:GLU:HG2	4:D:63:ILE:HD11	1.80	0.62
3:C:133:ARG:NE	4:E:189:PRO:HD2	2.13	0.62
4:E:114:THR:OG1	4:E:179:LYS:HB2	1.97	0.62
3:O:48:ILE:HG21	3:O:87:TRP:CD1	2.33	0.62
4:P:48:ASP:O	4:P:50:ASN:N	2.32	0.62
2:T:175:LYS:HG2	2:T:176:ILE:N	2.14	0.62
4:V:155:VAL:C	4:V:156:GLN:HE21	2.07	0.62
2:B:218:LEU:HD23	2:B:233:VAL:HG12	1.81	0.62
1:G:10:ASN:C	1:G:10:ASN:ND2	2.57	0.62
3:I:112:VAL:HG11	4:K:70:ASP:CB	2.28	0.62
3:I:137:THR:O	3:I:139:LYS:HG3	1.99	0.62
4:K:60:GLY:HA2	4:K:63:ILE:CD1	2.23	0.62
1:M:23:ASN:HB3	1:M:25:GLU:CD	2.24	0.62
1:M:140:PHE:CZ	1:M:183:TYR:HA	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:43:LEU:HD12	3:O:43:LEU:C	2.24	0.62
4:D:141:SER:O	4:D:144:LEU:HB2	2.00	0.62
3:I:44:LEU:O	3:I:48:ILE:HG12	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
2:N:99:LEU:HD11	2:N:240:PHE:HA	1.81	0.62
4:Q:102:THR:HG22	4:Q:102:THR:O	1.99	0.62
1:S:140:PHE:CZ	1:S:183:TYR:HA	2.34	0.62
3:U:14:ASN:ND2	3:U:132:MET:O	2.32	0.62
4:V:190:ILE:O	4:V:190:ILE:HG22	2.00	0.62
5:X:93:GLN:HG3	5:X:131:VAL:CG1	2.29	0.62
1:A:72:TYR:CD2	1:A:72:TYR:O	2.52	0.62
2:H:86:LYS:NZ	2:H:90:TYR:CE1	2.66	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
5:L:12:LEU:HB3	5:L:62:TRP:HB2	1.80	0.62
1:M:72:TYR:O	1:M:72:TYR:CD2	2.52	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
3:U:82:THR:HB	3:U:86:LEU:N	2.14	0.62
2:B:231:TYR:HD2	2:B:234:CYS:HG	1.46	0.62
3:C:142:ASN:C	3:C:142:ASN:ND2	2.56	0.62
4:D:48:ASP:O	4:D:50:ASN:N	2.33	0.62
4:D:155:VAL:C	4:D:156:GLN:HE21	2.07	0.62
4:E:99:LEU:HB3	4:E:123:PRO:HG3	1.82	0.62
5:F:83:GLY:HA2	5:F:165:MET:HE1	1.82	0.62
5:F:93:GLN:HG3	5:F:131:VAL:CG1	2.28	0.62
3:I:82:THR:HB	3:I:86:LEU:N	2.14	0.62
4:J:190:ILE:HG22	4:J:190:ILE:O	2.00	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
4:P:155:VAL:CA	4:P:156:GLN:HE21	2.12	0.62
5:R:83:GLY:HA2	5:R:165:MET:HE1	1.82	0.62
1:S:178:PHE:HD2	1:S:179:LEU:HD23	1.65	0.62
1:A:124:THR:CB	3:C:65:ASN:HD21	2.12	0.62
1:A:187:SER:O	1:A:191:MET:HB2	2.00	0.62
4:E:95:PHE:CD1	4:E:103:PRO:HG3	2.35	0.62
3:I:127:GLU:O	3:I:129:GLU:N	2.29	0.62
3:I:133:ARG:HB3	4:K:188:ILE:HG13	1.80	0.62
4:K:102:THR:HG22	4:K:102:THR:O	1.99	0.62
5:L:12:LEU:HD23	5:L:12:LEU:N	2.10	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:82:THR:HG22	3:O:83:ALA:N	2.15	0.62
3:O:119:LEU:HD21	4:W:35:GLY:HA3	1.81	0.62
4:P:179:LYS:HE2	4:P:181:ASN:HB3	1.82	0.62
1:S:39:THR:O	1:S:43:VAL:HG23	1.99	0.62
2:T:66:PHE:CZ	2:T:70:ILE:HD11	2.34	0.62
2:T:86:LYS:NZ	2:T:90:TYR:CE1	2.67	0.62
2:T:184:HIS:HB2	2:T:211:ILE:HD11	1.82	0.62
3:C:44:LEU:O	3:C:48:ILE:HG12	2.00	0.62
5:F:68:GLU:HG2	5:F:69:ARG:HB3	1.81	0.62
5:L:43:VAL:HG23	5:L:43:VAL:O	1.98	0.62
5:L:130:VAL:HG12	5:L:131:VAL:N	2.12	0.62
2:N:70:ILE:HG22	2:N:74:HIS:CD2	2.35	0.62
2:N:191:LEU:HB2	2:N:192:PHE:CD1	2.34	0.62
4:Q:143:ILE:HG23	4:Q:144:LEU:N	2.14	0.62
2:T:99:LEU:HD11	2:T:240:PHE:HA	1.81	0.62
4:V:141:SER:O	4:V:144:LEU:HB2	2.00	0.62
4:W:26:ASN:HD22	4:W:27:THR:N	1.97	0.62
5:X:86:ILE:HD11	5:X:106:ILE:HD11	1.80	0.62
4:D:141:SER:HB3	4:D:144:LEU:HD12	1.82	0.62
1:G:140:PHE:CZ	1:G:183:TYR:HA	2.35	0.62
4:K:148:LEU:HD12	4:K:161:VAL:HG11	1.81	0.62
3:O:72:THR:CG2	3:O:73:GLY:N	2.62	0.62
5:R:93:GLN:HG3	5:R:131:VAL:CG1	2.29	0.62
1:S:21:PHE:CD1	1:S:22:THR:N	2.60	0.62
1:S:187:SER:O	1:S:191:MET:HB2	1.99	0.62
2:T:214:ASN:HA	2:T:263:ARG:CG	2.25	0.62
2:T:218:LEU:HD23	2:T:233:VAL:HG12	1.82	0.62
3:U:44:LEU:O	3:U:48:ILE:HG12	2.00	0.62
3:U:82:THR:HG22	3:U:83:ALA:N	2.15	0.62
4:W:101:ILE:CD1	4:W:121:GLU:O	2.48	0.62
5:X:89:ASP:HA	5:X:121:ASN:ND2	2.12	0.62
1:A:140:PHE:CZ	1:A:183:TYR:HA	2.35	0.62
2:B:184:HIS:HB2	2:B:211:ILE:HD11	1.82	0.62
2:B:191:LEU:HB2	2:B:192:PHE:CD1	2.35	0.62
4:E:114:THR:HG23	4:E:178:VAL:C	2.24	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
4:J:118:ILE:HA	4:J:175:GLU:HB3	1.82	0.62
4:K:99:LEU:HB3	4:K:123:PRO:HG3	1.82	0.62
5:X:12:LEU:HB3	5:X:62:TRP:HB2	1.80	0.62
1:A:10:ASN:HD22	1:A:11:LYS:H	1.42	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:52:PRO:HD3	3:I:75:TYR:CD2	2.36	0.61
2:H:99:LEU:HD11	2:H:240:PHE:HA	1.81	0.61
2:N:87:LEU:HG	2:N:232:PHE:HB2	1.80	0.61
3:U:142:ASN:HD22	3:U:142:ASN:C	2.08	0.61
4:W:48:ASP:CG	4:W:51:LYS:HG3	2.24	0.61
5:X:43:VAL:O	5:X:43:VAL:HG23	1.98	0.61
3:I:43:LEU:HD12	3:I:43:LEU:C	2.24	0.61
3:I:82:THR:HG22	3:I:83:ALA:N	2.16	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:X:68:GLU:HG2	5:X:69:ARG:CB	2.30	0.61
1:A:107:PHE:HE1	4:D:17:ILE:HD11	1.64	0.61
4:D:155:VAL:CA	4:D:156:GLN:HE21	2.13	0.61
5:F:89:ASP:HA	5:F:121:ASN:ND2	2.11	0.61
3:I:6:PHE:H	3:I:19:ARG:HB3	1.64	0.61
4:J:155:VAL:C	4:J:156:GLN:HE21	2.08	0.61
5:L:68:GLU:HG2	5:L:69:ARG:CB	2.30	0.61
5:L:89:ASP:HA	5:L:121:ASN:ND2	2.12	0.61
1:S:107:PHE:HE1	4:V:17:ILE:HD11	1.65	0.61
4:V:155:VAL:HA	4:V:156:GLN:HE21	1.64	0.61
1:A:21:PHE:CD1	1:A:22:THR:N	2.60	0.61
1:A:136:THR:HG21	4:D:69:GLU:OE1	1.99	0.61
2:B:70:ILE:HG22	2:B:74:HIS:CD2	2.35	0.61
3:C:133:ARG:HH11	3:C:133:ARG:HG3	1.65	0.61
4:E:26:ASN:HD22	4:E:27:THR:N	1.97	0.61
2:H:184:HIS:HB2	2:H:211:ILE:HD11	1.83	0.61
2:H:231:TYR:HD2	2:H:234:CYS:HG	1.48	0.61
4:J:141:SER:HB3	4:J:144:LEU:HD12	1.81	0.61
4:Q:95:PHE:CD1	4:Q:103:PRO:HG3	2.35	0.61
5:R:53:ASP:C	5:R:55:LYS:H	2.07	0.61
5:R:150:THR:CG2	5:R:157:ASN:HB2	2.31	0.61
2:T:233:VAL:HA	2:T:236:ILE:CD1	2.30	0.61
3:U:43:LEU:HD12	3:U:43:LEU:C	2.24	0.61
4:V:61:TYR:HA	4:V:146:GLY:O	2.00	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
5:F:53:ASP:C	5:F:55:LYS:H	2.07	0.61
1:G:107:PHE:HE1	4:J:17:ILE:HD11	1.65	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
3:O:82:THR:HB	3:O:86:LEU:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:211:ILE:CG2	2:T:268:ILE:HD11	2.30	0.61
2:B:64:PHE:O	2:B:67:GLN:HG3	1.99	0.61
3:C:69:SER:OG	3:C:76:ARG:HD2	2.00	0.61
5:L:103:LEU:HD21	5:L:145:MET:CE	2.15	0.61
1:M:126:GLN:HG3	3:O:65:ASN:CB	2.26	0.61
2:N:233:VAL:HA	2:N:236:ILE:CD1	2.31	0.61
4:Q:36:SER:N	3:U:119:LEU:HD11	2.14	0.61
1:S:129:MET:HG2	1:S:131:ILE:CD1	2.31	0.61
3:C:5:SER:OG	3:C:7:TRP:HZ3	1.84	0.61
4:D:190:ILE:O	4:D:190:ILE:HG22	1.99	0.61
4:E:48:ASP:OD1	4:E:51:LYS:HG3	2.01	0.61
4:E:148:LEU:HD12	4:E:161:VAL:HG11	1.82	0.61
4:J:179:LYS:HE2	4:J:181:ASN:HB3	1.82	0.61
4:K:48:ASP:OD1	4:K:51:LYS:HG3	2.01	0.61
1:M:10:ASN:HB3	1:M:14:GLY:N	2.12	0.61
1:M:178:PHE:HD2	1:M:179:LEU:HD23	1.65	0.61
3:O:129:GLU:HB2	3:O:135:GLN:HE22	1.65	0.61
3:O:142:ASN:C	3:O:142:ASN:ND2	2.58	0.61
1:S:12:SER:HB3	5:X:10:LYS:HZ1	1.65	0.61
2:B:87:LEU:HG	2:B:232:PHE:HB2	1.81	0.61
3:C:5:SER:HB2	3:C:7:TRP:CZ3	2.36	0.61
3:C:11:ARG:NH1	4:E:154:MET:CE	2.63	0.61
4:D:155:VAL:O	4:D:155:VAL:HG12	2.01	0.61
4:D:155:VAL:HA	4:D:156:GLN:HE21	1.65	0.61
4:J:95:PHE:HB3	4:J:101:ILE:CD1	2.31	0.61
4:J:141:SER:O	4:J:144:LEU:HB2	2.01	0.61
1:M:21:PHE:CD1	1:M:22:THR:N	2.60	0.61
4:P:190:ILE:HG22	4:P:190:ILE:O	1.99	0.61
5:R:89:ASP:HA	5:R:121:ASN:ND2	2.11	0.61
3:U:105:TYR:CD2	3:U:152:PHE:CZ	2.89	0.61
5:X:130:VAL:HG12	5:X:131:VAL:N	2.13	0.61
3:C:127:GLU:O	3:C:129:GLU:N	2.30	0.61
4:D:95:PHE:HB3	4:D:101:ILE:CD1	2.31	0.61
4:D:135:MET:O	4:D:135:MET:HG2	2.00	0.61
4:K:26:ASN:HD22	4:K:27:THR:N	1.98	0.61
3:O:70:ILE:O	3:O:76:ARG:HG3	2.01	0.61
3:C:82:THR:HB	3:C:86:LEU:N	2.16	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:87:LEU:HG	2:T:232:PHE:HB2	1.81	0.61
4:V:155:VAL:CA	4:V:156:GLN:HE21	2.13	0.61
2:H:218:LEU:HD23	2:H:233:VAL:HG12	1.84	0.60
3:I:69:SER:OG	3:I:76:ARG:HD2	2.01	0.60
4:J:155:VAL:HA	4:J:156:GLN:HE21	1.65	0.60
5:L:150:THR:CG2	5:L:157:ASN:HB2	2.31	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
4:V:134:ALA:HB1	4:V:138:LEU:HD13	1.83	0.60
1:A:207:PHE:O	1:A:211:VAL:HG22	2.01	0.60
3:C:129:GLU:HB2	3:C:135:GLN:HE22	1.65	0.60
4:D:134:ALA:HB1	4:D:138:LEU:HD13	1.83	0.60
4:E:53:ASN:OD1	4:E:138:LEU:HD12	2.01	0.60
1:G:21:PHE:CD1	1:G:22:THR:N	2.60	0.60
1:G:207:PHE:O	1:G:211:VAL:HG22	2.00	0.60
2:H:68:GLU:HG2	4:J:63:ILE:CD1	2.31	0.60
3:I:133:ARG:HG3	3:I:133:ARG:HH11	1.65	0.60
4:J:99:LEU:HB2	4:J:101:ILE:CG1	2.31	0.60
4:J:155:VAL:O	4:J:155:VAL:HG12	2.00	0.60
4:P:155:VAL:O	4:P:155:VAL:HG12	2.01	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
3:C:7:TRP:HA	3:C:17:PHE:O	2.01	0.60
3:C:133:ARG:HB3	4:E:188:ILE:HG13	1.82	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:I:5:SER:OG	3:I:7:TRP:HZ3	1.83	0.60
3:I:108:SER:CB	4:K:73:ALA:HB1	2.31	0.60
5:L:82:HIS:HB2	5:L:169:ILE:HD13	1.83	0.60
4:Q:48:ASP:CG	4:Q:51:LYS:HG3	2.26	0.60
2:B:184:HIS:ND1	2:B:199:LEU:HB2	2.16	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
4:P:141:SER:O	4:P:144:LEU:HB2	2.01	0.60
4:Q:35:GLY:HA3	3:U:119:LEU:HD21	1.83	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
3:C:82:THR:HG22	3:C:83:ALA:N	2.16	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
2:H:216:PRO:C	2:H:218:LEU:N	2.59	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:142:ASN:C	3:I:142:ASN:ND2	2.56	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
4:Q:148:LEU:HD12	4:Q:161:VAL:HG11	1.82	0.60
1:S:43:VAL:HG11	3:U:51:LEU:HG	1.82	0.60
3:I:7:TRP:HA	3:I:17:PHE:O	2.01	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:6:PHE:H	3:U:19:ARG:HB3	1.66	0.60
3:U:114:TYR:HD1	3:U:114:TYR:H	1.49	0.60
4:W:71:PHE:C	4:W:71:PHE:CD1	2.78	0.60
5:X:82:HIS:HB2	5:X:169:ILE:HD13	1.84	0.60
5:X:103:LEU:HD21	5:X:145:MET:CE	2.15	0.60
2:B:233:VAL:HA	2:B:236:ILE:CD1	2.31	0.60
3:I:114:TYR:H	3:I:114:TYR:HD1	1.49	0.60
3:I:142:ASN:ND2	3:I:144:ASN:H	2.00	0.60
1:M:10:ASN:HD22	1:M:11:LYS:H	1.42	0.60
5:R:29:SER:HA	5:R:48:LYS:HG2	1.83	0.60
5:X:150:THR:CG2	5:X:157:ASN:HB2	2.31	0.60
4:J:155:VAL:CA	4:J:156:GLN:HE21	2.14	0.60
3:O:7:TRP:HA	3:O:17:PHE:O	2.01	0.60
4:P:141:SER:HB3	4:P:144:LEU:HD12	1.84	0.60
4:W:143:ILE:HG23	4:W:144:LEU:N	2.14	0.60
1:A:129:MET:HG2	1:A:131:ILE:CD1	2.32	0.60
4:K:16:GLU:OE2	4:K:20:ASN:HB2	2.01	0.60
3:O:127:GLU:O	3:O:129:GLU:N	2.31	0.60
3:O:133:ARG:HH11	3:O:133:ARG:HG3	1.67	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:V:99:LEU:HB2	4:V:101:ILE:CD1	2.32	0.60
4:V:141:SER:HB3	4:V:144:LEU:HD12	1.83	0.60
4:E:84:VAL:CG1	4:E:85:LYS:N	2.65	0.60
4:J:98:PHE:C	4:J:99:LEU:HD23	2.26	0.60
1:M:185:LEU:HB3	1:M:207:PHE:HE1	1.67	0.60
2:N:256:PRO:HG2	2:N:263:ARG:NH2	2.15	0.60
4:Q:84:VAL:CG1	4:Q:85:LYS:N	2.65	0.60
4:V:135:MET:HG2	4:V:135:MET:O	2.00	0.60
4:V:155:VAL:O	4:V:155:VAL:HG12	2.01	0.60
3:C:105:TYR:CD2	3:C:152:PHE:CZ	2.90	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:5:SER:HB2	3:I:7:TRP:CZ3	2.36	0.59
2:T:70:ILE:HG22	2:T:74:HIS:CD2	2.37	0.59
4:D:114:THR:HA	4:D:178:VAL:O	2.02	0.59
4:E:175:GLU:O	4:E:175:GLU:HG2	2.02	0.59
1:G:129:MET:HG2	1:G:131:ILE:CD1	2.32	0.59
4:K:61:TYR:HD2	4:K:61:TYR:C	2.10	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:V:22:THR:CB	4:V:74:ARG:HH12	2.13	0.59
1:A:10:ASN:C	1:A:12:SER:H	2.10	0.59
2:B:211:ILE:CG2	2:B:268:ILE:HD11	2.32	0.59
4:D:111:ASN:HD22	4:D:113:ASP:CB	2.15	0.59
4:P:134:ALA:HB1	4:P:138:LEU:HD13	1.84	0.59
4:Q:17:ILE:HG21	4:Q:97:ILE:CD1	2.32	0.59
1:S:10:ASN:C	1:S:12:SER:H	2.10	0.59
2:B:216:PRO:C	2:B:218:LEU:N	2.58	0.59
2:B:256:PRO:HG2	2:B:263:ARG:NH2	2.15	0.59
4:J:68:ILE:HD13	4:J:154:MET:HB3	1.84	0.59
4:J:99:LEU:HB2	4:J:101:ILE:CD1	2.32	0.59
2:T:64:PHE:O	2:T:67:GLN:HG3	2.01	0.59
3:U:133:ARG:HH11	3:U:133:ARG:HG3	1.67	0.59
2:B:252:ALA:HA	2:B:266:TYR:HA	1.85	0.59
3:C:114:TYR:HD1	3:C:114:TYR:H	1.49	0.59
4:D:98:PHE:C	4:D:99:LEU:HD23	2.26	0.59
5:F:68:GLU:C	5:F:70:PHE:H	2.10	0.59
4:J:22:THR:CB	4:J:74:ARG:HH12	2.13	0.59
4:J:114:THR:HA	4:J:178:VAL:O	2.02	0.59
3:O:6:PHE:H	3:O:19:ARG:HB3	1.67	0.59
4:P:87:SER:HB2	4:P:115:PHE:CE1	2.38	0.59
3:U:7:TRP:HA	3:U:17:PHE:O	2.02	0.59
3:U:127:GLU:C	3:U:129:GLU:N	2.61	0.59
5:X:28:PHE:HB3	5:X:48:LYS:HZ3	1.65	0.59
1:A:183:TYR:CD2	4:D:73:ALA:HB2	2.38	0.59
5:F:68:GLU:HG2	5:F:69:ARG:CB	2.32	0.59
3:I:127:GLU:C	3:I:129:GLU:N	2.61	0.59
5:L:69:ARG:HB2	5:L:72:THR:HG21	1.84	0.59
1:M:129:MET:HG2	1:M:131:ILE:CD1	2.33	0.59
3:O:5:SER:OG	3:O:7:TRP:HZ3	1.86	0.59
4:Q:71:PHE:C	4:Q:71:PHE:CD1	2.79	0.59
5:R:67:GLN:OE1	5:R:67:GLN:HA	2.01	0.59
1:S:52:PRO:HD3	3:U:75:TYR:CD2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
4:W:148:LEU:HD12	4:W:161:VAL:HG11	1.83	0.59
4:E:60:GLY:O	4:E:147:VAL:HA	2.02	0.59
4:K:99:LEU:O	4:K:100:ASN:C	2.45	0.59
4:K:162:TRP:CZ2	4:K:177:LYS:HD3	2.37	0.59
5:L:14:ILE:CB	5:L:102:TRP:HZ3	2.16	0.59
3:O:105:TYR:CD2	3:O:152:PHE:CZ	2.90	0.59
4:P:114:THR:HA	4:P:178:VAL:O	2.03	0.59
2:T:216:PRO:C	2:T:218:LEU:N	2.60	0.59
2:B:102:LEU:HD23	2:B:102:LEU:C	2.28	0.59
4:E:48:ASP:CG	4:E:51:LYS:HG3	2.27	0.59
4:K:71:PHE:CD1	4:K:71:PHE:C	2.80	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: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:10:ASN:C	1:S:10:ASN:ND2	2.55	0.59
4:W:17:ILE:HG21	4:W:97:ILE:HD13	1.84	0.59
4:W:84:VAL:CG1	4:W:85:LYS:N	2.64	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
3:C:70:ILE:O	3:C:76:ARG:HG3	2.02	0.59
4:D:22:THR:CB	4:D:74:ARG:HH12	2.13	0.59
4:D:99:LEU:HD12	4:D:101:ILE:CD1	2.28	0.59
4:D:186:ASP:HB2	5:F:79:ARG:CZ	2.33	0.59
5:F:82:HIS:HB2	5:F:169:ILE:HD13	1.84	0.59
1:G:10:ASN:C	1:G:12:SER:H	2.11	0.59
1:G:10:ASN:C	1:G:12:SER:N	2.59	0.59
2:H:256:PRO:HG2	2:H:263:ARG:NH2	2.16	0.59
3:I:70:ILE:O	3:I:76:ARG:HG3	2.02	0.59
4:J:99:LEU:HD12	4:J:101:ILE:CD1	2.29	0.59
4:P:99:LEU:HD12	4:P:101:ILE:CD1	2.28	0.59
1:S:183:TYR:CD2	4:V:73:ALA:HB2	2.38	0.59
3:U:70:ILE:O	3:U:76:ARG:HG3	2.02	0.59
1:A:198:MET:O	1:A:200:MET:HG2	2.03	0.59
2:H:102:LEU:HD23	2:H:102:LEU:C	2.28	0.59
4:K:48:ASP:CG	4:K:51:LYS:HG3	2.27	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:82:HIS:HB2	5:R:169:ILE:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:111:ASN:HD22	4:V:113:ASP:HB2	1.64	0.59
5:X:157:ASN:HA	5:X:160:ASP:OD2	2.03	0.59
3:C:142:ASN:ND2	3:C:144:ASN:H	2.01	0.58
4:D:99:LEU:HB2	4:D:101:ILE:CD1	2.33	0.58
1:G:189:TYR:CD2	1:G:206:LEU:HB3	2.37	0.58
4:J:111:ASN:HD22	4:J:113:ASP:HB2	1.64	0.58
4:K:17:ILE:HG21	4:K:97:ILE:CD1	2.33	0.58
3:O:129:GLU:HB2	3:O:135:GLN:NE2	2.18	0.58
4:P:68:ILE:HD13	4:P:154:MET:HB3	1.83	0.58
4:P:111:ASN:HD22	4:P:113:ASP:CB	2.15	0.58
5:R:65:ALA:O	5:R:73:ILE:HG13	2.03	0.58
2:T:102:LEU:HD23	2:T:102:LEU:C	2.28	0.58
4:W:53:ASN:OD1	4:W:138:LEU:HD12	2.03	0.58
4:W:99:LEU:O	4:W:100:ASN:C	2.45	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
1:A:10:ASN:HB3	1:A:14:GLY:N	2.13	0.58
4:K:61:TYR:C	4:K:61:TYR:CD2	2.81	0.58
5:L:13:LEU:HD21	5:L:25:LEU:CG	2.32	0.58
1:M:10:ASN:C	1:M:12:SER:H	2.10	0.58
2:N:211:ILE:CG2	2:N:268:ILE:HD11	2.32	0.58
2:B:175:LYS:HG3	2:B:278:GLU:CD	2.28	0.58
3:C:82:THR:CG2	3:C:84:SER:H	2.03	0.58
3:C:129:GLU:HB2	3:C:135:GLN:NE2	2.18	0.58
4:E:71:PHE:CD1	4:E:71:PHE:C	2.80	0.58
1:G:185:LEU:HD21	1:G:210:LYS:HB3	1.86	0.58
2:H:228:SER:O	2:H:231:TYR:HB2	2.04	0.58
5:L:28:PHE:HB3	5:L:48:LYS:HZ3	1.66	0.58
5:L:83:GLY:HA2	5:L:165:MET:HE1	1.84	0.58
3:O:114:TYR:HD1	3:O:114:TYR:H	1.50	0.58
1:S:10:ASN:C	1:S:12:SER:N	2.59	0.58
3:U:5:SER:OG	3:U:7:TRP:HZ3	1.85	0.58
4:V:49:PHE:HB3	4:V:138:LEU:CD1	2.13	0.58
4:W:16:GLU:OE2	4:W:20:ASN:HB2	2.02	0.58
3:C:85:GLY:O	3:C:86:LEU:HD12	2.03	0.58
4:D:128:VAL:O	4:D:128:VAL:HG22	2.04	0.58
4:E:16:GLU:OE2	4:E:20:ASN:HB2	2.02	0.58
4:J:49:PHE:HZ	4:J:133:ASP:OD2	1.87	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:W:61:TYR:HD2	4:W:61:TYR:C	2.11	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:10:LYS:H	5:X:82:HIS:CE1	2.21	0.58
1:A:124:THR:O	1:A:147:VAL:HG13	2.03	0.58
4:D:49:PHE:HB3	4:D:138:LEU:CD1	2.12	0.58
4:E:61:TYR:HD2	4:E:61:TYR:C	2.11	0.58
5:F:13:LEU:HD21	5:F:25:LEU:CG	2.33	0.58
5:F:65:ALA:O	5:F:73:ILE:HG13	2.03	0.58
1:G:185:LEU:HB3	1:G:207:PHE:HE1	1.67	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:60:GLY:HA2	4:Q:63:ILE:CD1	2.25	0.58
4:Q:175:GLU:HG2	4:Q:175:GLU:O	2.03	0.58
1:S:133:GLN:HA	1:S:139:LYS:HA	1.84	0.58
2:T:256:PRO:HG2	2:T:263:ARG:NH2	2.16	0.58
3:U:5:SER:HB2	3:U:7:TRP:CZ3	2.38	0.58
5:X:83:GLY:HA2	5:X:165:MET:HE1	1.84	0.58
1:A:189:TYR:CD2	1:A:206:LEU:HB3	2.38	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
5:R:69:ARG:CB	5:R:72:THR:HG22	2.18	0.58
1:S:185:LEU:HD21	1:S:210:LYS:HB3	1.86	0.58
4:V:105:ILE:HD13	4:V:105:ILE:N	2.18	0.58
1:A:7:LEU:CD1	1:A:141:VAL:HB	2.33	0.58
4:D:68:ILE:HD13	4:D:154:MET:HB3	1.84	0.58
1:G:3:ILE:HG23	1:G:143:ILE:O	2.03	0.58
4:J:135:MET:O	4:J:135:MET:HG2	2.02	0.58
3:U:142:ASN:C	3:U:142:ASN:ND2	2.59	0.58
4:V:186:ASP:HB2	5:X:79:ARG:CZ	2.33	0.58
1:A:185:LEU:HD21	1:A:210:LYS:HB3	1.85	0.58
3:C:106:ILE:HD13	3:C:149:LEU:CD1	2.33	0.58
5:F:29:SER:HA	5:F:48:LYS:HG2	1.85	0.58
2:H:252:ALA:HA	2:H:266:TYR:HA	1.86	0.58
3:I:106:ILE:HD13	3:I:149:LEU:CD1	2.33	0.58
3:I:124:ASP:O	3:I:125:PHE:C	2.46	0.58
4:K:60:GLY:O	4:K:147:VAL:HA	2.04	0.58
1:M:185:LEU:HD21	1:M:210:LYS:HB3	1.86	0.58
2:N:102:LEU:C	2:N:102:LEU:HD23	2.29	0.58
4:Q:83:LEU:O	4:Q:86:THR:HB	2.03	0.58
5:R:10:LYS:H	5:R:82:HIS:CE1	2.21	0.58
5:X:13:LEU:HD21	5:X:25:LEU:CG	2.32	0.58
2:B:228:SER:O	2:B:231:TYR:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:15:GLU:HG2	4:E:96:LYS:HE2	1.86	0.58
1:G:119:LEU:C	1:G:119:LEU:HD23	2.29	0.58
3:I:5:SER:OG	3:I:7:TRP:CZ3	2.56	0.58
4:J:186:ASP:HB2	5:L:79:ARG:CZ	2.33	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
2:N:216:PRO:C	2:N:218:LEU:N	2.59	0.58
4:V:114:THR:HA	4:V:178:VAL:O	2.03	0.58
5:X:29:SER:HA	5:X:48:LYS:HG2	1.84	0.58
1:A:43:VAL:HG11	3:C:51:LEU:HG	1.84	0.58
5:L:43:VAL:HG22	5:L:77:TYR:HE2	1.68	0.58
5:L:51:GLU:OE1	5:L:56:THR:HG23	2.04	0.58
3:O:108:SER:CB	4:Q:73:ALA:HB1	2.34	0.58
4:Q:61:TYR:HD2	4:Q:61:TYR:C	2.12	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
5:X:151:SER:N	5:X:155:SER:HB3	2.18	0.58
1:A:189:TYR:HD2	1:A:206:LEU:HB3	1.68	0.57
4:E:17:ILE:HG21	4:E:97:ILE:HD13	1.86	0.57
1:G:147:VAL:CG1	1:G:148:MET:H	2.06	0.57
3:O:11:ARG:NH1	4:Q:154:MET:CE	2.66	0.57
3:O:124:ASP:O	3:O:125:PHE:C	2.47	0.57
4:P:49:PHE:HB3	4:P:138:LEU:CD1	2.12	0.57
4:P:114:THR:CG2	4:P:115:PHE:N	2.67	0.57
4:Q:16:GLU:OE2	4:Q:20:ASN:HB2	2.03	0.57
4:Q:60:GLY:O	4:Q:147:VAL:HA	2.03	0.57
4:Q:180:LEU:HD23	4:Q:181:ASN:H	1.68	0.57
1:S:7:LEU:HD12	1:S:141:VAL:HB	1.85	0.57
3:U:124:ASP:O	3:U:125:PHE:C	2.46	0.57
1:A:52:PRO:HD3	3:C:75:TYR:CD2	2.38	0.57
2:B:191:LEU:HB3	4:D:29:LEU:HD12	1.86	0.57
3:C:124:ASP:O	3:C:125:PHE:C	2.47	0.57
4:D:70:ASP:O	4:D:74:ARG:HB2	2.04	0.57
5:F:14:ILE:CB	5:F:102:TRP:HZ3	2.17	0.57
4:K:83:LEU:O	4:K:86:THR:HB	2.03	0.57
4:K:122:ASN:HB3	4:K:126:ASP:OD2	2.04	0.57
1:M:7:LEU:HD12	1:M:141:VAL:HB	1.86	0.57
1:M:134:THR:O	1:M:137:GLY:N	2.32	0.57
4:Q:53:ASN:OD1	4:Q:138:LEU:HD12	2.05	0.57
5:R:14:ILE:CB	5:R:102:TRP:HZ3	2.17	0.57
1:S:185:LEU:HB3	1:S:207:PHE:HE1	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:207:PHE:O	1:S:211:VAL:HG22	2.03	0.57
4:W:61:TYR:C	4:W:61:TYR:CD2	2.82	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:HD13	4:J:105:ILE:N	2.19	0.57
2:N:175:LYS:HG3	2:N:278:GLU:CD	2.29	0.57
2:T:228:SER:O	2:T:231:TYR:HB2	2.05	0.57
1:A:191:MET:SD	4:D:69:GLU:HG3	2.45	0.57
2:B:173:ASP:O	2:B:174:LEU:HD23	2.04	0.57
3:C:5:SER:OG	3:C:7:TRP:CZ3	2.57	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
4:Q:17:ILE:HG21	4:Q:97:ILE:HD13	1.87	0.57
1:S:5:THR:OG1	1:S:20:ASN:ND2	2.37	0.57
1:S:189:TYR:CD2	1:S:206:LEU:HB3	2.38	0.57
4:V:49:PHE:HZ	4:V:133:ASP:OD2	1.87	0.57
4:V:98:PHE:C	4:V:99:LEU:HD23	2.29	0.57
3:C:133:ARG:HG3	3:C:133:ARG:NH1	2.18	0.57
4:D:98:PHE:O	4:D:99:LEU:HD23	2.04	0.57
1:G:121:GLN:OE1	1:G:172:ILE:HG12	2.04	0.57
5:L:151:SER:N	5:L:155:SER:HB3	2.19	0.57
1:M:189:TYR:HD2	1:M:206:LEU:HB3	1.69	0.57
1:M:198:MET:O	1:M:200:MET:HG2	2.05	0.57
2:N:252:ALA:HA	2:N:266:TYR:HA	1.87	0.57
4:Q:32:LEU:HD21	3:U:117:ASN:OD1	2.04	0.57
4:Q:162:TRP:CZ2	4:Q:177:LYS:HD3	2.39	0.57
1:S:73:VAL:HG12	1:S:74:GLY:N	2.19	0.57
3:U:5:SER:OG	3:U:7:TRP:CZ3	2.57	0.57
4:W:122:ASN:HB3	4:W:126:ASP:OD2	2.04	0.57
4:E:60:GLY:HA2	4:E:63:ILE:CD1	2.25	0.57
1:G:10:ASN:HB3	1:G:14:GLY:N	2.11	0.57
5:L:126:LYS:HG2	5:L:129:ARG:HD2	1.86	0.57
1:M:52:PRO:HD3	3:O:75:TYR:CD2	2.38	0.57
1:M:147:VAL:CG1	1:M:148:MET:H	2.05	0.57
4:P:105:ILE:HD13	4:P:105:ILE:N	2.19	0.57
4:Q:15:GLU:HG2	4:Q:96:LYS:HE2	1.87	0.57
5:R:13:LEU:HD21	5:R:25:LEU:CG	2.33	0.57
5:R:14:ILE:HB	5:R:102:TRP:CZ3	2.40	0.57
2:T:175:LYS:HG3	2:T:278:GLU:CD	2.29	0.57
3:U:11:ARG:NH1	4:W:154:MET:CE	2.66	0.57
4:W:60:GLY:O	4:W:147:VAL:HA	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ASN:C	1:A:12:SER:N	2.60	0.57
3:C:108:SER:CB	4:E:73:ALA:HB1	2.35	0.57
4:D:114:THR:CG2	4:D:115:PHE:N	2.68	0.57
4:E:61:TYR:C	4:E:61:TYR:CD2	2.82	0.57
2:H:198:ASP:OD2	2:H:200:VAL:HG23	2.04	0.57
3:I:77:VAL:CG1	3:I:91:LEU:HD22	2.24	0.57
5:L:69:ARG:CB	5:L:72:THR:HG22	2.24	0.57
2:N:231:TYR:CE2	2:N:251:THR:HA	2.40	0.57
3:U:48:ILE:HG21	3:U:87:TRP:CD1	2.33	0.57
4:V:110:HIS:C	4:V:112:LYS:H	2.12	0.57
1:A:121:GLN:OE1	1:A:172:ILE:HG12	2.04	0.57
5:F:151:SER:N	5:F:155:SER:HB3	2.19	0.57
3:I:11:ARG:NH1	4:K:154:MET:CE	2.66	0.57
3:I:129:GLU:HB2	3:I:135:GLN:NE2	2.18	0.57
4:J:111:ASN:HD22	4:J:113:ASP:CB	2.17	0.57
1:M:69:TYR:HD1	1:M:173:GLN:NE2	2.03	0.57
4:Q:50:ASN:HA	4:Q:53:ASN:HD22	1.69	0.57
4:V:111:ASN:HD22	4:V:113:ASP:CB	2.17	0.57
5:X:68:GLU:C	5:X:70:PHE:H	2.12	0.57
3:C:72:THR:HG23	3:C:73:GLY:H	1.69	0.57
4:E:162:TRP:CZ2	4:E:177:LYS:HD3	2.40	0.57
5:F:14:ILE:HB	5:F:102:TRP:CZ3	2.40	0.57
5:L:14:ILE:HB	5:L:102:TRP:CZ3	2.39	0.57
1:M:50:LEU:HG	1:M:50:LEU:O	2.04	0.57
1:M:73:VAL:HG12	1:M:74:GLY:N	2.20	0.57
1:M:121:GLN:OE1	1:M:172:ILE:HG12	2.04	0.57
3:O:142:ASN:ND2	3:O:144:ASN:H	2.03	0.57
4:Q:59:MET:O	4:Q:63:ILE:HG12	2.04	0.57
5:R:157:ASN:HA	5:R:160:ASP:OD2	2.04	0.57
1:S:121:GLN:OE1	1:S:172:ILE:HG12	2.04	0.57
3:U:154:ALA:HB3	3:U:155:PRO:HD3	1.87	0.57
4:W:162:TRP:CZ2	4:W:177:LYS:HD3	2.40	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
4:D:110:HIS:C	4:D:112:LYS:H	2.12	0.57
1:G:134:THR:O	1:G:137:GLY:N	2.34	0.57
4:J:70:ASP:O	4:J:74:ARG:HB2	2.05	0.57
4:J:114:THR:CG2	4:J:115:PHE:N	2.67	0.57
1:M:10:ASN:C	1:M:12:SER:N	2.60	0.57
1:M:133:GLN:HA	1:M:139:LYS:HA	1.86	0.57
3:O:133:ARG:HG3	3:O:133:ARG:NH1	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:120:ARG:HB3	1:S:120:ARG:NH1	2.07	0.57
2:T:192:PHE:CD1	2:T:192:PHE:N	2.66	0.57
4:V:87:SER:HB2	4:V:115:PHE:CE1	2.39	0.57
1:A:177:ASN:O	1:A:181:LYS:HG3	2.04	0.56
5:F:43:VAL:HG22	5:F:77:TYR:HE2	1.69	0.56
2:H:167:THR:HG22	2:H:169:MET:HB3	1.86	0.56
2:H:209:TYR:C	2:H:210:MET:HG2	2.29	0.56
5:R:43:VAL:HG22	5:R:77:TYR:HE2	1.69	0.56
1:S:75:MET:HA	1:S:217:ASN:HD22	1.69	0.56
2:H:64:PHE:HE1	4:J:67:LEU:HD12	1.70	0.56
4:K:50:ASN:HA	4:K:53:ASN:HD22	1.69	0.56
5:L:29:SER:HA	5:L:48:LYS:HG2	1.85	0.56
1:M:12:SER:HB3	5:R:10:LYS:HZ1	1.68	0.56
1:M:200:MET:HE2	5:R:7:TYR:CD2	2.40	0.56
3:O:106:ILE:HD13	3:O:149:LEU:CD1	2.34	0.56
2:T:84:GLU:OE1	2:T:231:TYR:HE1	1.88	0.56
4:V:114:THR:CG2	4:V:115:PHE:N	2.67	0.56
2:B:209:TYR:C	2:B:210:MET:HG2	2.29	0.56
2:B:227:VAL:O	2:B:230:GLU:HB3	2.04	0.56
4:D:87:SER:HB2	4:D:115:PHE:CE1	2.41	0.56
4:D:105:ILE:HD13	4:D:105:ILE:N	2.20	0.56
5:F:10:LYS:H	5:F:82:HIS:CE1	2.22	0.56
1:G:189:TYR:HD2	1:G:206:LEU:HB3	1.68	0.56
3:I:82:THR:CB	3:I:86:LEU:H	2.17	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
4:J:110:HIS:C	4:J:112:LYS:H	2.13	0.56
4:K:84:VAL:CG1	4:K:85:LYS:N	2.67	0.56
1:M:3:ILE:HG23	1:M:143:ILE:O	2.04	0.56
3:O:154:ALA:HB3	3:O:155:PRO:HD3	1.87	0.56
4:Q:61:TYR:C	4:Q:61:TYR:CD2	2.83	0.56
5:R:85:ILE:HG12	5:R:162:PHE:CE1	2.40	0.56
1:S:50:LEU:HG	1:S:50:LEU:O	2.05	0.56
3:U:106:ILE:HD13	3:U:149:LEU:CD1	2.34	0.56
3:U:129:GLU:HB2	3:U:135:GLN:NE2	2.19	0.56
5:X:51:GLU:OE1	5:X:56:THR:HG23	2.04	0.56
5:X:85:ILE:HG12	5:X:162:PHE:CE1	2.41	0.56
4:E:188:ILE:O	4:E:188:ILE:CG2	2.54	0.56
1:G:71:PRO:HD2	1:G:177:ASN:OD1	2.05	0.56
2:H:227:VAL:O	2:H:230:GLU:HB3	2.04	0.56
3:I:133:ARG:HG3	3:I:133:ARG:NH1	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5:SER:OG	3:O:7:TRP:CZ3	2.58	0.56
3:O:120:LEU:HD23	4:W:39:ALA:HB2	1.88	0.56
4:P:70:ASP:O	4:P:74:ARG:HB2	2.05	0.56
4:P:98:PHE:C	4:P:99:LEU:HD23	2.29	0.56
4:P:110:HIS:C	4:P:112:LYS:H	2.13	0.56
4:P:113:ASP:O	4:P:179:LYS:HA	2.06	0.56
4:P:128:VAL:O	4:P:128:VAL:HG22	2.06	0.56
4:Q:188:ILE:O	4:Q:188:ILE:CG2	2.54	0.56
5:R:151:SER:N	5:R:155:SER:HB3	2.19	0.56
2:T:196:SER:OG	2:T:211:ILE:HD11	2.06	0.56
1:A:71:PRO:HD2	1:A:177:ASN:OD1	2.05	0.56
1:A:133:GLN:HA	1:A:139:LYS:HA	1.86	0.56
2:B:260:HIS:HB2	2:B:263:ARG:HB2	1.87	0.56
3:C:112:VAL:HG11	4:E:70:ASP:OD1	2.06	0.56
4:E:67:LEU:HD23	4:E:67:LEU:C	2.31	0.56
4:E:180:LEU:HD23	4:E:181:ASN:H	1.70	0.56
5:F:157:ASN:HA	5:F:160:ASP:OD2	2.05	0.56
1:G:192:LYS:HE2	2:H:64:PHE:CE1	2.40	0.56
3:I:48:ILE:HG21	3:I:87:TRP:CD1	2.34	0.56
4:K:61:TYR:CE2	4:K:65:CYS:SG	2.99	0.56
3:O:127:GLU:C	3:O:129:GLU:N	2.62	0.56
5:R:126:LYS:HG2	5:R:129:ARG:HD2	1.87	0.56
1:S:177:ASN:O	1:S:181:LYS:HG3	2.06	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
4:W:180:LEU:HD23	4:W:181:ASN:H	1.68	0.56
3:C:11:ARG:HH11	3:C:125:PHE:HE1	1.53	0.56
1:G:73:VAL:HG12	1:G:74:GLY:N	2.21	0.56
2:N:228:SER:O	2:N:231:TYR:HB2	2.05	0.56
5:R:68:GLU:HG2	5:R:69:ARG:HB3	1.87	0.56
1:S:134:THR:O	1:S:137:GLY:N	2.35	0.56
4:W:15:GLU:HG2	4:W:96:LYS:HE2	1.88	0.56
2:B:176:ILE:HG23	2:B:177:LEU:N	2.20	0.56
1:G:177:ASN:O	1:G:181:LYS:HG3	2.06	0.56
2:H:84:GLU:OE1	2:H:231:TYR:HE1	1.89	0.56
3:I:133:ARG:HD2	3:I:133:ARG:N	2.18	0.56
4:K:175:GLU:HG2	4:K:175:GLU:O	2.04	0.56
4:Q:99:LEU:O	4:Q:100:ASN:C	2.47	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
4:V:155:VAL:C	4:V:156:GLN:CG	2.78	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:LYS:HE2	2:B:64:PHE:CE1	2.41	0.56
2:B:170:ARG:C	2:B:172:ARG:N	2.64	0.56
2:B:198:ASP:OD2	2:B:200:VAL:HG23	2.06	0.56
4:E:59:MET:O	4:E:63:ILE:HG12	2.05	0.56
4:E:122:ASN:HB3	4:E:126:ASP:OD2	2.05	0.56
5:L:68:GLU:HG2	5:L:69:ARG:CA	2.35	0.56
2:N:84:GLU:OE1	2:N:231:TYR:HE1	1.89	0.56
2:N:176:ILE:HG23	2:N:177:LEU:N	2.20	0.56
2:N:209:TYR:C	2:N:210:MET:HG2	2.29	0.56
4:P:180:LEU:H	4:P:180:LEU:CD1	2.12	0.56
1:S:124:THR:O	1:S:147:VAL:HG13	2.05	0.56
2:T:198:ASP:OD2	2:T:200:VAL:HG23	2.05	0.56
3:U:108:SER:CB	4:W:73:ALA:HB1	2.35	0.56
4:V:50:ASN:HA	4:V:53:ASN:HD22	1.71	0.56
4:W:61:TYR:CE2	4:W:65:CYS:SG	2.99	0.56
4:W:175:GLU:O	4:W:175:GLU:HG2	2.03	0.56
2:B:84:GLU:OE1	2:B:231:TYR:HE1	1.89	0.56
4:D:50:ASN:HA	4:D:53:ASN:HD22	1.71	0.56
5:L:50:VAL:HG23	5:L:57:VAL:HG12	1.87	0.56
2:N:198:ASP:OD2	2:N:200:VAL:HG23	2.06	0.56
3:U:82:THR:CB	3:U:86:LEU:H	2.18	0.56
4:V:128:VAL:HG22	4:V:128:VAL:O	2.05	0.56
5:X:126:LYS:HG2	5:X:129:ARG:HD2	1.88	0.56
1:A:50:LEU:O	1:A:50:LEU:HG	2.06	0.56
1:A:130:PHE:HE1	1:A:172:ILE:HA	1.68	0.56
3:C:127:GLU:C	3:C:129:GLU:N	2.62	0.56
5:F:126:LYS:HG2	5:F:129:ARG:HD2	1.87	0.56
1:G:200:MET:HE2	5:L:7:TYR:CD2	2.41	0.56
2:H:192:PHE:CD1	2:H:192:PHE:N	2.66	0.56
3:I:112:VAL:HG21	4:K:70:ASP:HA	1.89	0.56
4:K:59:MET:O	4:K:63:ILE:HG12	2.05	0.56
4:K:180:LEU:HD23	4:K:181:ASN:H	1.69	0.56
1:M:15:LEU:HD11	1:M:17:TYR:O	2.05	0.56
1:M:130:PHE:HE1	1:M:172:ILE:HA	1.67	0.56
3:O:3:ILE:HG21	3:O:90:LEU:HD21	1.87	0.56
3:O:93:ASP:OD1	3:O:95:LYS:HB2	2.06	0.56
1:S:12:SER:HB3	5:X:10:LYS:NZ	2.21	0.56
1:S:119:LEU:HD23	1:S:119:LEU:C	2.31	0.56
4:W:83:LEU:O	4:W:86:THR:HB	2.05	0.56
5:X:11:LEU:O	5:X:61:ILE:HA	2.06	0.56
4:D:37:ILE:O	4:D:41:LEU:HG	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:113:ASP:O	4:D:179:LYS:HA	2.06	0.55
4:E:83:LEU:O	4:E:86:THR:HB	2.06	0.55
5:F:51:GLU:OE1	5:F:56:THR:HG23	2.06	0.55
2:H:260:HIS:HB2	2:H:263:ARG:HB2	1.88	0.55
4:J:128:VAL:O	4:J:128:VAL:HG22	2.06	0.55
2:N:254:ARG:CA	2:N:264:THR:HG22	2.35	0.55
4:Q:122:ASN:HB3	4:Q:126:ASP:OD2	2.05	0.55
1:S:69:TYR:HD1	1:S:173:GLN:NE2	2.03	0.55
3:U:77:VAL:CG1	3:U:91:LEU:HD22	2.24	0.55
4:V:98:PHE:O	4:V:99:LEU:HD23	2.06	0.55
1:A:42:GLY:O	1:A:45:ALA:HB3	2.06	0.55
4:D:136:LYS:C	4:D:169:ARG:HH12	2.14	0.55
4:E:99:LEU:O	4:E:100:ASN:C	2.47	0.55
2:H:176:ILE:HG23	2:H:177:LEU:N	2.20	0.55
3:I:18:ASP:OD2	3:I:18:ASP:N	2.38	0.55
2:N:68:GLU:HG2	4:P:63:ILE:CD1	2.36	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:T:231:TYR:CE2	2:T:251:THR:HA	2.40	0.55
3:U:93:ASP:OD1	3:U:95:LYS:HB2	2.06	0.55
4:V:137:SER:HA	4:V:169:ARG:HH22	1.71	0.55
2:B:231:TYR:HD2	2:B:234:CYS:SG	2.29	0.55
5:L:50:VAL:CG2	5:L:57:VAL:HG12	2.36	0.55
2:N:175:LYS:HG2	2:N:176:ILE:N	2.21	0.55
5:R:68:GLU:HG2	5:R:69:ARG:CB	2.36	0.55
3:U:133:ARG:HD2	3:U:133:ARG:N	2.19	0.55
4:V:160:ASP:HB3	4:V:162:TRP:CZ3	2.42	0.55
5:X:24:LEU:HD11	5:X:158:VAL:HG21	1.88	0.55
1:A:69:TYR:HD1	1:A:173:GLN:NE2	2.05	0.55
1:A:129:MET:HE2	1:A:143:ILE:HD11	1.89	0.55
2:B:64:PHE:HE1	4:D:67:LEU:HD12	1.70	0.55
5:F:24:LEU:HD11	5:F:158:VAL:HG21	1.88	0.55
2:N:190:TYR:O	4:P:26:ASN:ND2	2.38	0.55
1:S:189:TYR:HD2	1:S:206:LEU:HB3	1.69	0.55
3:U:133:ARG:HG3	3:U:133:ARG:NH1	2.20	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
5:F:28:PHE:HB3	5:F:48:LYS:HZ3	1.70	0.55
1:G:15:LEU:HD11	1:G:17:TYR:O	2.06	0.55
4:J:106:THR:CG2	4:J:107:ASN:H	2.10	0.55
4:J:113:ASP:O	4:J:179:LYS:HA	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:85:LYS:O	4:K:89:VAL:HG23	2.06	0.55
4:K:188:ILE:O	4:K:188:ILE:CG2	2.54	0.55
3:O:98:SER:C	3:O:100:THR:H	2.14	0.55
4:P:155:VAL:C	4:P:156:GLN:CG	2.77	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
2:T:250:VAL:HG13	2:T:268:ILE:HG12	1.88	0.55
4:W:34:TYR:CE2	4:W:124:LEU:HD21	2.42	0.55
1:A:119:LEU:HD23	1:A:119:LEU:C	2.32	0.55
2:B:190:TYR:O	4:D:26:ASN:ND2	2.39	0.55
2:H:175:LYS:HG3	2:H:278:GLU:CD	2.30	0.55
2:H:231:TYR:CE2	2:H:251:THR:HA	2.40	0.55
5:R:50:VAL:CG2	5:R:57:VAL:HG12	2.36	0.55
1:S:192:LYS:HE2	2:T:64:PHE:CE1	2.41	0.55
2:T:176:ILE:HG23	2:T:177:LEU:N	2.21	0.55
4:W:188:ILE:O	4:W:188:ILE:CG2	2.54	0.55
1:A:73:VAL:HG12	1:A:74:GLY:N	2.22	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:D:49:PHE:HZ	4:D:133:ASP:OD2	1.87	0.55
4:E:85:LYS:O	4:E:89:VAL:HG23	2.07	0.55
2:H:190:TYR:O	4:J:26:ASN:ND2	2.40	0.55
3:I:98:SER:C	3:I:100:THR:H	2.14	0.55
4:J:160:ASP:HB3	4:J:162:TRP:CZ3	2.42	0.55
2:N:227:VAL:O	2:N:230:GLU:HB3	2.06	0.55
3:O:20:GLU:O	3:O:21:TRP:CB	2.54	0.55
3:O:116:SER:O	4:Q:66:ARG:HB3	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
5:R:77:TYR:N	5:R:77:TYR:CD1	2.73	0.55
5:R:140:ALA:HB1	5:R:145:MET:O	2.06	0.55
1:S:130:PHE:HE1	1:S:172:ILE:HA	1.68	0.55
2:T:68:GLU:HG2	4:V:63:ILE:CD1	2.36	0.55
2:T:190:TYR:O	4:V:26:ASN:ND2	2.40	0.55
3:U:98:SER:C	3:U:100:THR:H	2.14	0.55
2:B:72:GLN:HE22	4:D:55:HIS:CE1	2.24	0.55
5:F:85:ILE:HG12	5:F:162:PHE:CE1	2.42	0.55
1:G:5:THR:OG1	1:G:20:ASN:ND2	2.40	0.55
4:K:67:LEU:HD23	4:K:67:LEU:C	2.32	0.55
1:M:71:PRO:HD2	1:M:177:ASN:OD1	2.07	0.55
1:M:119:LEU:HD23	1:M:119:LEU:C	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:50:ASN:HA	4:P:53:ASN:HD22	1.72	0.55
2:T:168:LYS:C	2:T:170:ARG:H	2.15	0.55
4:W:67:LEU:C	4:W:67:LEU:HD23	2.32	0.55
5:X:50:VAL:CG2	5:X:57:VAL:HG12	2.37	0.55
2:B:254:ARG:CA	2:B:264:THR:HG22	2.36	0.55
1:G:133:GLN:HA	1:G:139:LYS:HA	1.88	0.55
3:I:5:SER:CB	3:I:7:TRP:CZ3	2.90	0.55
4:J:162:TRP:HE1	4:J:177:LYS:HB2	1.70	0.55
4:J:187:GLU:HG3	4:J:187:GLU:O	2.07	0.55
3:O:131:GLU:O	3:O:135:GLN:HG2	2.07	0.55
1:S:42:GLY:O	1:S:45:ALA:HB3	2.06	0.55
1:S:194:PRO:HG3	2:T:67:GLN:CA	2.37	0.55
2:T:191:LEU:HB3	4:V:29:LEU:HD12	1.89	0.55
3:U:76:ARG:O	3:U:91:LEU:HA	2.06	0.55
4:V:37:ILE:O	4:V:41:LEU:HG	2.07	0.55
4:V:70:ASP:O	4:V:74:ARG:HB2	2.07	0.55
4:V:113:ASP:O	4:V:179:LYS:HA	2.06	0.55
4:V:136:LYS:C	4:V:169:ARG:HH12	2.14	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
1:G:107:PHE:CB	1:G:180:ARG:HH12	2.18	0.55
3:I:72:THR:CG2	3:I:74:LYS:H	2.20	0.55
3:I:93:ASP:OD1	3:I:95:LYS:HB2	2.07	0.55
3:I:116:SER:O	4:K:66:ARG:HB3	2.07	0.55
4:J:136:LYS:C	4:J:169:ARG:HH12	2.14	0.55
4:K:49:PHE:HB2	4:K:137:SER:HB3	1.89	0.55
1:M:5:THR:OG1	1:M:20:ASN:ND2	2.39	0.55
1:M:177:ASN:O	1:M:181:LYS:HG3	2.06	0.55
4:P:29:LEU:O	4:P:29:LEU:HD23	2.07	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
2:T:267:LEU:HD23	2:T:267:LEU:C	2.32	0.55
1:A:5:THR:OG1	1:A:20:ASN:ND2	2.39	0.54
1:A:107:PHE:CB	1:A:180:ARG:HH12	2.17	0.54
4:E:61:TYR:CE2	4:E:65:CYS:SG	3.01	0.54
5:F:68:GLU:HG2	5:F:69:ARG:CA	2.36	0.54
5:F:89:ASP:HB2	5:F:95:SER:HB3	1.89	0.54
5:F:140:ALA:HB1	5:F:145:MET:O	2.07	0.54
2:H:250:VAL:HG13	2:H:268:ILE:HG12	1.89	0.54
4:J:155:VAL:C	4:J:156:GLN:CG	2.79	0.54
2:N:256:PRO:CG	2:N:263:ARG:NH2	2.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:67:LEU:HD23	4:Q:67:LEU:C	2.33	0.54
1:S:71:PRO:HD2	1:S:177:ASN:OD1	2.07	0.54
5:X:82:HIS:HB3	5:X:169:ILE:HG21	1.88	0.54
5:X:89:ASP:HB2	5:X:95:SER:HB3	1.89	0.54
3:C:20:GLU:O	3:C:21:TRP:CB	2.55	0.54
3:C:98:SER:C	3:C:100:THR:H	2.15	0.54
1:G:42:GLY:O	1:G:45:ALA:HB3	2.07	0.54
1:M:120:ARG:HB3	1:M:120:ARG:NH1	2.08	0.54
3:O:112:VAL:HG11	4:Q:70:ASP:OD1	2.07	0.54
2:T:209:TYR:C	2:T:210:MET:HG2	2.31	0.54
4:V:162:TRP:HE1	4:V:177:LYS:HB2	1.71	0.54
5:X:77:TYR:N	5:X:77:TYR:CD1	2.74	0.54
2:B:90:TYR:CZ	4:D:40:GLN:HG2	2.42	0.54
2:B:282:PHE:C	2:B:282:PHE:CD1	2.85	0.54
3:C:131:GLU:O	3:C:135:GLN:HG2	2.07	0.54
5:F:93:GLN:HG3	5:F:131:VAL:HG11	1.89	0.54
2:H:179:ILE:HG23	2:H:180:LEU:N	2.23	0.54
3:I:72:THR:HG23	3:I:73:GLY:H	1.72	0.54
4:K:166:ASP:O	4:K:167:ILE:C	2.50	0.54
5:L:11:LEU:O	5:L:61:ILE:HA	2.07	0.54
5:L:89:ASP:HB2	5:L:95:SER:HB3	1.90	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
3:U:155:PRO:HG2	3:U:156:MET:N	2.20	0.54
5:F:68:GLU:O	5:F:70:PHE:N	2.28	0.54
1:G:191:MET:SD	4:J:69:GLU:HG3	2.46	0.54
1:M:191:MET:SD	4:P:69:GLU:HG3	2.47	0.54
1:M:192:LYS:HE2	2:N:64:PHE:CE1	2.43	0.54
3:U:11:ARG:HH11	3:U:125:PHE:HE1	1.54	0.54
4:V:106:THR:CG2	4:V:107:ASN:H	2.10	0.54
4:V:192:GLU:O	4:V:192:GLU:HG2	2.07	0.54
4:W:50:ASN:HA	4:W:53:ASN:HD22	1.70	0.54
4:W:60:GLY:HA2	4:W:63:ILE:CD1	2.25	0.54
1:A:15:LEU:HD11	1:A:17:TYR:O	2.07	0.54
2:B:250:VAL:HG13	2:B:268:ILE:HG12	1.89	0.54
3:C:67:ILE:HG21	3:C:70:ILE:HD11	1.90	0.54
3:C:133:ARG:HD2	3:C:133:ARG:N	2.19	0.54
4:D:160:ASP:HB3	4:D:162:TRP:CZ3	2.43	0.54
5:F:77:TYR:N	5:F:77:TYR:CD1	2.74	0.54
1:G:12:SER:HB3	5:L:10:LYS:NZ	2.23	0.54
2:H:196:SER:OG	2:H:211:ILE:HD11	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:67:ILE:HD13	3:I:79:THR:HG21	1.88	0.54
3:I:131:GLU:O	3:I:135:GLN:HG2	2.08	0.54
5:L:24:LEU:HD11	5:L:158:VAL:HG21	1.89	0.54
1:M:107:PHE:CB	1:M:180:ARG:HH12	2.18	0.54
3:O:67:ILE:HD13	3:O:79:THR:HG21	1.90	0.54
3:C:116:SER:O	4:E:66:ARG:HB3	2.08	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: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
2:N:231:TYR:HD2	2:N:234:CYS:SG	2.27	0.54
1:S:107:PHE:CB	1:S:180:ARG:HH12	2.19	0.54
3:U:116:SER:O	4:W:66:ARG:HB3	2.07	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:E:49:PHE:HB2	4:E:137:SER:HB3	1.90	0.54
4:E:131:PRO:C	4:E:133:ASP:H	2.16	0.54
1:G:50:LEU:HD21	3:I:44:LEU:HG	1.90	0.54
2:H:87:LEU:O	2:H:90:TYR:HB2	2.08	0.54
3:I:111:TYR:CZ	3:I:115:VAL:HG11	2.43	0.54
4:J:94:ALA:O	4:J:98:PHE:HD1	1.91	0.54
4:K:49:PHE:CE2	4:K:134:ALA:HB2	2.42	0.54
2:N:191:LEU:HB3	4:P:29:LEU:HD12	1.90	0.54
2:N:282:PHE:CD1	2:N:282:PHE:C	2.85	0.54
3:O:76:ARG:O	3:O:91:LEU:HA	2.08	0.54
4:P:160:ASP:HB3	4:P:162:TRP:CZ3	2.43	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
4:W:166:ASP:O	4:W:167:ILE:C	2.51	0.54
2:B:175:LYS:HG2	2:B:176:ILE:H	1.72	0.54
3:C:5:SER:CB	3:C:7:TRP:CZ3	2.90	0.54
3:C:76:ARG:O	3:C:91:LEU:HA	2.08	0.54
2:H:267:LEU:C	2:H:267:LEU:HD23	2.33	0.54
2:H:282:PHE:CD1	2:H:282:PHE:C	2.86	0.54
1:M:42:GLY:O	1:M:45:ALA:HB3	2.08	0.54
1:M:52:PRO:C	1:M:54:ALA:N	2.61	0.54
3:O:11:ARG:HH11	3:O:125:PHE:HE1	1.54	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:24:LEU:HD11	5:R:158:VAL:HG21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:89:ASP:HB2	5:R:95:SER:HB3	1.90	0.54
1:S:191:MET:SD	4:V:69:GLU:HG3	2.46	0.54
5:X:50:VAL:HG23	5:X:57:VAL:HG12	1.89	0.54
1:A:135:LEU:HD21	4:D:79:ARG:NH1	2.23	0.54
3:C:93:ASP:OD1	3:C:95:LYS:HB2	2.08	0.54
4:D:94:ALA:O	4:D:98:PHE:HD1	1.91	0.54
4:E:50:ASN:HA	4:E:53:ASN:HD22	1.72	0.54
4:E:90:LEU:HD12	6:E:194:PLM:H52	1.90	0.54
5:F:11:LEU:O	5:F:61:ILE:HA	2.07	0.54
2:H:254:ARG:CA	2:H:264:THR:HG22	2.36	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
4:Q:166:ASP:O	4:Q:167:ILE:C	2.50	0.54
5:X:68:GLU:HG2	5:X:69:ARG:CA	2.37	0.54
1:A:12:SER:CB	5:F:10:LYS:HZ2	2.21	0.54
2:B:256:PRO:CG	2:B:263:ARG:NH2	2.71	0.54
3:C:88:PHE:CE1	3:C:107:TYR:CD1	2.96	0.54
4:D:29:LEU:HD23	4:D:29:LEU:O	2.08	0.54
4:D:192:GLU:O	4:D:192:GLU:HG2	2.07	0.54
4:E:34:TYR:CE2	4:E:124:LEU:HD21	2.43	0.54
4:J:137:SER:HA	4:J:169:ARG:HH22	1.73	0.54
2:N:72:GLN:HE22	4:P:55:HIS:CE1	2.25	0.54
2:N:167:THR:HG22	2:N:169:MET:HB3	1.89	0.54
2:N:170:ARG:C	2:N:172:ARG:N	2.66	0.54
2:N:196:SER:OG	2:N:211:ILE:HD11	2.07	0.54
2:N:214:ASN:HA	2:N:263:ARG:CG	2.25	0.54
3:U:131:GLU:O	3:U:135:GLN:HG2	2.08	0.54
4:E:144:LEU:HD23	6:E:194:PLM:CF	2.37	0.53
5:F:13:LEU:H	5:F:13:LEU:HD12	1.72	0.53
5:F:50:VAL:HG23	5:F:57:VAL:HG12	1.89	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
4:K:144:LEU:HD23	6:K:194:PLM:CF	2.37	0.53
1:M:194:PRO:HG3	2:N:67:GLN:CA	2.39	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
3:U:18:ASP:OD2	3:U:18:ASP:N	2.40	0.53
1:A:38:SER:HB3	5:F:45:PHE:CE1	2.43	0.53
5:F:82:HIS:HB3	5:F:169:ILE:HG21	1.89	0.53
1:G:69:TYR:HD1	1:G:173:GLN:NE2	2.05	0.53
1:G:131:ILE:HG22	1:G:131:ILE:O	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:191:LEU:HB3	4:J:29:LEU:HD12	1.90	0.53
4:J:50:ASN:HA	4:J:53:ASN:HD22	1.73	0.53
4:J:192:GLU:HG2	4:J:192:GLU:O	2.08	0.53
4:K:17:ILE:HG21	4:K:97:ILE:HD13	1.90	0.53
2:N:260:HIS:HB2	2:N:263:ARG:HB2	1.89	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
2:T:282:PHE:CD1	2:T:282:PHE:C	2.86	0.53
3:C:107:TYR:CE2	4:E:73:ALA:CA	2.90	0.53
2:H:256:PRO:CG	2:H:263:ARG:NH2	2.71	0.53
4:K:15:GLU:HG2	4:K:96:LYS:HE2	1.91	0.53
4:K:34:TYR:CE2	4:K:124:LEU:HD21	2.43	0.53
5:L:77:TYR:CD1	5:L:77:TYR:N	2.75	0.53
1:M:12:SER:HB3	5:R:10:LYS:NZ	2.23	0.53
2:N:87:LEU:O	2:N:90:TYR:HB2	2.08	0.53
2:N:189:SER:O	2:N:193:ASN:HA	2.08	0.53
2:T:179:ILE:HG23	2:T:180:LEU:N	2.24	0.53
2:T:260:HIS:HB2	2:T:263:ARG:HB2	1.89	0.53
4:V:29:LEU:O	4:V:29:LEU:HD23	2.09	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:B:168:LYS:C	2:B:170:ARG:H	2.15	0.53
2:B:189:SER:O	2:B:193:ASN:HA	2.08	0.53
2:B:196:SER:OG	2:B:211:ILE:HD11	2.07	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
3:C:112:VAL:HG21	4:E:70:ASP:HA	1.91	0.53
4:D:155:VAL:C	4:D:156:GLN:CG	2.79	0.53
2:H:231:TYR:HD2	2:H:234:CYS:SG	2.30	0.53
4:K:34:TYR:OH	4:K:140:TYR:O	2.17	0.53
4:K:111:ASN:OD1	4:K:111:ASN:O	2.26	0.53
5:L:13:LEU:H	5:L:13:LEU:HD12	1.73	0.53
4:P:48:ASP:O	4:P:51:LYS:N	2.40	0.53
4:P:136:LYS:C	4:P:169:ARG:HH12	2.16	0.53
4:P:192:GLU:HG2	4:P:192:GLU:O	2.08	0.53
4:Q:49:PHE:HB2	4:Q:137:SER:HB3	1.91	0.53
5:R:13:LEU:HD12	5:R:13:LEU:N	2.23	0.53
5:R:86:ILE:HD11	5:R:106:ILE:CD1	2.38	0.53
1:S:129:MET:HE2	1:S:143:ILE:HD11	1.90	0.53
5:X:13:LEU:HD12	5:X:13:LEU:H	1.73	0.53
5:X:89:ASP:HB2	5:X:95:SER:CB	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:ASN:O	1:A:32:GLU:CG	2.56	0.53
3:C:82:THR:CB	3:C:86:LEU:H	2.20	0.53
4:E:111:ASN:OD1	4:E:111:ASN:O	2.27	0.53
4:E:166:ASP:O	4:E:167:ILE:C	2.51	0.53
5:F:89:ASP:HB2	5:F:95:SER:CB	2.39	0.53
3:I:82:THR:CG2	3:I:84:SER:OG	2.52	0.53
1:M:128:THR:O	1:M:130:PHE:CE2	2.62	0.53
3:O:67:ILE:HG21	3:O:70:ILE:HD11	1.91	0.53
3:O:72:THR:CG2	3:O:74:LYS:H	2.21	0.53
4:Q:34:TYR:CE2	4:Q:124:LEU:HD21	2.44	0.53
1:S:38:SER:HB3	5:X:45:PHE:CE1	2.43	0.53
2:T:64:PHE:HE1	4:V:67:LEU:HD12	1.73	0.53
2:T:256:PRO:CG	2:T:263:ARG:NH2	2.71	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
4:E:34:TYR:OH	4:E:140:TYR:O	2.17	0.53
4:J:188:ILE:HD12	4:J:190:ILE:HD11	1.90	0.53
2:N:250:VAL:HG13	2:N:268:ILE:HG12	1.89	0.53
4:Q:34:TYR:OH	4:Q:143:ILE:HG22	2.09	0.53
4:Q:139:TRP:HE3	4:Q:142:ASN:HD21	1.57	0.53
5:R:93:GLN:HG3	5:R:131:VAL:HG11	1.90	0.53
1:S:134:THR:HG21	1:S:183:TYR:CE1	2.44	0.53
3:U:82:THR:CG2	3:U:84:SER:H	2.04	0.53
3:U:112:VAL:HG21	4:W:70:ASP:HA	1.91	0.53
4:W:111:ASN:OD1	4:W:111:ASN:O	2.26	0.53
4:W:114:THR:HG23	4:W:179:LYS:CA	2.39	0.53
2:B:267:LEU:HD23	2:B:267:LEU:C	2.32	0.53
3:C:88:PHE:CE1	3:C:107:TYR:HB2	2.43	0.53
5:F:50:VAL:CG2	5:F:57:VAL:HG12	2.38	0.53
2:H:72:GLN:HE22	4:J:55:HIS:CE1	2.26	0.53
4:K:131:PRO:C	4:K:133:ASP:H	2.17	0.53
5:L:88:TYR:CE2	5:L:119:VAL:O	2.62	0.53
5:L:89:ASP:HB2	5:L:95:SER:CB	2.38	0.53
4:Q:111:ASN:O	4:Q:111:ASN:OD1	2.27	0.53
4:Q:131:PRO:C	4:Q:133:ASP:H	2.17	0.53
5:R:82:HIS:HB3	5:R:169:ILE:HG21	1.90	0.53
2:T:87:LEU:O	2:T:90:TYR:HB2	2.09	0.53
2:T:254:ARG:CA	2:T:264:THR:HG22	2.37	0.53
3:U:112:VAL:HG11	4:W:70:ASP:OD1	2.08	0.53
4:V:187:GLU:HG3	4:V:187:GLU:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:95:PHE:HE1	4:W:119:LEU:CD2	2.22	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
2:B:87:LEU:O	2:B:90:TYR:HB2	2.09	0.53
2:B:227:VAL:O	2:B:230:GLU:CB	2.57	0.53
3:C:80:TYR:CB	3:C:103:LEU:HD23	2.38	0.53
4:E:128:VAL:HG12	4:E:129:GLU:N	2.24	0.53
5:F:28:PHE:HD2	5:F:48:LYS:HZ3	1.56	0.53
2:N:267:LEU:HD23	2:N:267:LEU:C	2.33	0.53
3:O:82:THR:CB	3:O:86:LEU:H	2.20	0.53
3:O:105:TYR:CE1	3:O:109:HIS:ND1	2.67	0.53
3:O:111:TYR:CZ	3:O:115:VAL:HG11	2.43	0.53
4:P:137:SER:HA	4:P:169:ARG:HH22	1.74	0.53
4:Q:49:PHE:CE2	4:Q:134:ALA:HB2	2.43	0.53
5:R:83:GLY:CA	5:R:165:MET:HE1	2.39	0.53
5:X:88:TYR:CE2	5:X:119:VAL:O	2.61	0.53
5:F:88:TYR:CE2	5:F:119:VAL:O	2.61	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
5:L:140:ALA:HB1	5:L:145:MET:O	2.08	0.53
1:M:131:ILE:O	1:M:131:ILE:HG22	2.09	0.53
4:P:37:ILE:O	4:P:41:LEU:HG	2.08	0.53
4:Q:31:THR:CG2	4:Q:127:PHE:CZ	2.92	0.53
1:S:29:ASN:O	1:S:32:GLU:CG	2.56	0.53
5:X:140:ALA:HB1	5:X:145:MET:O	2.08	0.53
1:A:200:MET:HE2	5:F:7:TYR:CD2	2.44	0.53
4:E:18:TRP:NE1	4:E:100:ASN:HB2	2.23	0.53
5:F:86:ILE:HD11	5:F:106:ILE:CD1	2.39	0.53
3:I:80:TYR:CB	3:I:103:LEU:HD23	2.38	0.53
3:O:129:GLU:CB	3:O:135:GLN:OE1	2.57	0.53
5:R:47:ILE:HG12	5:R:60:GLN:CA	2.30	0.53
3:U:105:TYR:CE1	3:U:109:HIS:ND1	2.68	0.53
4:W:49:PHE:HB2	4:W:137:SER:HB3	1.91	0.53
1:A:12:SER:HB3	5:F:10:LYS:NZ	2.24	0.52
4:D:48:ASP:O	4:D:51:LYS:N	2.41	0.52
4:D:114:THR:HG21	4:D:177:LYS:HE2	1.91	0.52
1:G:38:SER:HB3	5:L:45:PHE:CE1	2.44	0.52
1:G:186:TYR:O	1:G:190:VAL:HB	2.08	0.52
5:L:73:ILE:O	5:L:77:TYR:HB2	2.09	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:68:PRO:HD2	1:S:111:PHE:O	2.10	0.52
2:T:189:SER:O	2:T:193:ASN:HA	2.09	0.52
5:X:86:ILE:HD11	5:X:106:ILE:CD1	2.39	0.52
1:G:12:SER:HB3	5:L:10:LYS:HZ1	1.73	0.52
4:K:18:TRP:NE1	4:K:100:ASN:HB2	2.24	0.52
2:N:90:TYR:CZ	4:P:40:GLN:HG2	2.44	0.52
2:N:227:VAL:O	2:N:230:GLU:CB	2.57	0.52
3:O:5:SER:CB	3:O:7:TRP:CZ3	2.92	0.52
5:R:68:GLU:HG2	5:R:69:ARG:CA	2.39	0.52
5:R:84:ILE:CD1	5:R:114:VAL:HG11	2.38	0.52
1:S:50:LEU:HD21	3:U:44:LEU:HG	1.92	0.52
4:V:117:LEU:O	4:V:118:ILE:C	2.53	0.52
3:C:155:PRO:O	3:C:156:MET:O	2.27	0.52
4:E:38:VAL:HG11	4:E:140:TYR:CE1	2.44	0.52
1:G:135:LEU:HD21	4:J:79:ARG:NH1	2.24	0.52
3:I:105:TYR:CE1	3:I:109:HIS:ND1	2.69	0.52
5:L:93:GLN:HG3	5:L:131:VAL:HG11	1.90	0.52
1:M:107:PHE:CB	1:M:180:ARG:NH1	2.72	0.52
2:N:72:GLN:HE22	4:P:55:HIS:HE1	1.57	0.52
4:P:95:PHE:HB3	4:P:101:ILE:O	2.09	0.52
4:V:114:THR:HG21	4:V:177:LYS:HE2	1.91	0.52
1:A:21:PHE:CE2	1:A:215:VAL:HG11	2.44	0.52
2:B:267:LEU:HD23	2:B:267:LEU:O	2.09	0.52
4:D:138:LEU:HD23	4:D:138:LEU:C	2.35	0.52
2:H:189:SER:O	2:H:193:ASN:HA	2.10	0.52
1:M:21:PHE:CE2	1:M:215:VAL:HG11	2.44	0.52
1:M:104:ASP:HA	1:M:108:LYS:NZ	2.25	0.52
4:P:114:THR:HG21	4:P:177:LYS:HE2	1.92	0.52
4:P:187:GLU:O	4:P:187:GLU:HG3	2.09	0.52
4:Q:144:LEU:HD23	6:Q:194:PLM:CF	2.38	0.52
5:R:69:ARG:HB2	5:R:72:THR:HG21	1.83	0.52
1:S:52:PRO:C	1:S:54:ALA:N	2.61	0.52
4:V:94:ALA:O	4:V:98:PHE:HD1	1.92	0.52
1:A:135:LEU:C	1:A:137:GLY:H	2.17	0.52
3:C:122:PRO:HA	4:E:66:ARG:NH2	2.22	0.52
4:E:123:PRO:HG2	4:E:124:LEU:H	1.74	0.52
1:G:129:MET:SD	1:G:131:ILE:HD11	2.50	0.52
2:H:175:LYS:HG2	2:H:176:ILE:N	2.25	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
3:I:88:PHE:CE1	3:I:107:TYR:HB2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:10:ASN:CB	1:M:14:GLY:O	2.58	0.52
1:M:38:SER:HB3	5:R:45:PHE:CE1	2.43	0.52
1:M:50:LEU:HD21	3:O:44:LEU:HG	1.92	0.52
1:M:135:LEU:HD21	4:P:79:ARG:NH1	2.25	0.52
2:N:64:PHE:HE1	4:P:67:LEU:HD12	1.73	0.52
3:O:18:ASP:OD2	3:O:18:ASP:N	2.41	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
3:U:129:GLU:CB	3:U:135:GLN:OE1	2.57	0.52
4:V:138:LEU:HD23	4:V:138:LEU:C	2.35	0.52
5:F:28:PHE:CE2	5:F:48:LYS:HD3	2.44	0.52
3:O:112:VAL:HG21	4:Q:70:ASP:HA	1.92	0.52
5:R:13:LEU:H	5:R:13:LEU:CD1	2.22	0.52
4:W:131:PRO:C	4:W:133:ASP:H	2.18	0.52
1:A:29:ASN:O	1:A:32:GLU:HG2	2.10	0.52
1:A:68:PRO:HD2	1:A:111:PHE:O	2.10	0.52
3:I:129:GLU:CB	3:I:135:GLN:OE1	2.57	0.52
3:I:155:PRO:O	3:I:156:MET:O	2.26	0.52
4:P:162:TRP:HE1	4:P:177:LYS:HB2	1.71	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
2:T:92:HIS:NE2	2:T:239:GLY:HA2	2.24	0.52
2:T:197:ASP:HB3	2:T:212:VAL:O	2.10	0.52
3:U:3:ILE:HG23	3:U:99:TYR:CE2	2.44	0.52
1:A:194:PRO:HG3	2:B:67:GLN:CA	2.40	0.52
4:E:49:PHE:CE2	4:E:134:ALA:HB2	2.45	0.52
4:J:29:LEU:HD23	4:J:29:LEU:O	2.10	0.52
4:J:88:GLU:O	4:J:92:LYS:HG2	2.10	0.52
4:K:31:THR:CG2	4:K:127:PHE:CZ	2.93	0.52
3:O:123:TYR:C	3:O:125:PHE:N	2.67	0.52
1:S:7:LEU:CD1	1:S:141:VAL:HB	2.40	0.52
4:V:48:ASP:O	4:V:51:LYS:N	2.40	0.52
4:V:88:GLU:O	4:V:92:LYS:HG2	2.09	0.52
5:X:73:ILE:O	5:X:77:TYR:HB2	2.10	0.52
5:X:93:GLN:HG3	5:X:131:VAL:HG11	1.91	0.52
3:C:105:TYR:CE1	3:C:109:HIS:ND1	2.68	0.52
4:D:162:TRP:HE1	4:D:177:LYS:HB2	1.72	0.52
5:F:84:ILE:CD1	5:F:114:VAL:HG11	2.39	0.52
1:G:132:TYR:HB3	1:G:179:LEU:HD12	1.92	0.52
1:G:134:THR:HG21	1:G:183:TYR:CE1	2.45	0.52
4:J:138:LEU:HD23	4:J:138:LEU:C	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:35:GLY:HA2	4:P:140:TYR:OH	2.10	0.52
4:Q:128:VAL:HG12	4:Q:129:GLU:N	2.25	0.52
1:S:4:GLU:HG3	1:S:143:ILE:HG22	1.91	0.52
1:S:29:ASN:O	1:S:32:GLU:HG2	2.10	0.52
1:S:132:TYR:HB3	1:S:179:LEU:HD12	1.92	0.52
1:S:186:TYR:O	1:S:190:VAL:HB	2.09	0.52
1:S:200:MET:HE2	5:X:7:TYR:CD2	2.45	0.52
2:B:79:THR:HG22	2:B:81:GLY:H	1.75	0.52
4:D:187:GLU:HG3	4:D:187:GLU:O	2.09	0.52
1:G:107:PHE:CB	1:G:180:ARG:NH1	2.73	0.52
5:L:68:GLU:CG	5:L:69:ARG:CA	2.85	0.52
1:M:106:PHE:N	1:M:106:PHE:CD1	2.78	0.52
2:T:72:GLN:HE22	4:V:55:HIS:CE1	2.28	0.52
2:T:227:VAL:O	2:T:230:GLU:CB	2.57	0.52
4:W:144:LEU:HD23	6:W:194:PLM:CF	2.38	0.52
2:B:179:ILE:HG23	2:B:180:LEU:N	2.23	0.51
4:E:95:PHE:HE1	4:E:119:LEU:CD2	2.23	0.51
4:E:139:TRP:HE3	4:E:142:ASN:HD21	1.58	0.51
4:J:162:TRP:CD1	4:J:177:LYS:HB2	2.45	0.51
5:L:28:PHE:CE2	5:L:48:LYS:HD3	2.45	0.51
4:P:117:LEU:O	4:P:118:ILE:C	2.53	0.51
4:P:138:LEU:HD23	4:P:138:LEU:C	2.35	0.51
5:R:68:GLU:C	5:R:70:PHE:H	2.17	0.51
1:S:107:PHE:CB	1:S:180:ARG:NH1	2.73	0.51
3:U:3:ILE:HG21	3:U:90:LEU:HD21	1.91	0.51
3:U:67:ILE:HD13	3:U:79:THR:HG21	1.90	0.51
1:A:128:THR:O	1:A:130:PHE:CE2	2.63	0.51
2:B:220:GLN:HG3	2:B:221:PHE:H	1.74	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:G:106:PHE:N	1:G:106:PHE:CD1	2.78	0.51
3:O:155:PRO:O	3:O:156:MET:O	2.28	0.51
4:Q:46:GLU:O	4:Q:47:ARG:HB2	2.10	0.51
3:U:93:ASP:CG	3:U:93:ASP:O	2.53	0.51
2:B:92:HIS:NE2	2:B:239:GLY:HA2	2.25	0.51
3:C:77:VAL:CG1	3:C:91:LEU:HD22	2.24	0.51
3:C:111:TYR:CZ	3:C:115:VAL:HG11	2.45	0.51
4:E:17:ILE:O	4:E:21:LYS:O	2.28	0.51
5:F:13:LEU:HD12	5:F:13:LEU:N	2.25	0.51
3:I:88:PHE:CE1	3:I:107:TYR:CD1	2.98	0.51
4:K:139:TRP:HE3	4:K:142:ASN:HD21	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:N:259:GLY:C	2:N:260:HIS:CG	2.88	0.51
4:Q:114:THR:HG23	4:Q:179:LYS:CA	2.40	0.51
1:S:112:THR:HG22	1:S:113:ASN:O	2.10	0.51
4:V:188:ILE:HD12	4:V:190:ILE:HD11	1.92	0.51
1:A:106:PHE:N	1:A:106:PHE:CD1	2.78	0.51
2:B:231:TYR:CE2	2:B:251:THR:HA	2.40	0.51
4:J:117:LEU:O	4:J:118:ILE:C	2.54	0.51
2:N:79:THR:HG22	2:N:81:GLY:H	1.76	0.51
1:S:104:ASP:HA	1:S:108:LYS:NZ	2.26	0.51
4:W:85:LYS:O	4:W:89:VAL:HG23	2.10	0.51
5:F:156:THR:O	5:F:156:THR:HG22	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
5:L:13:LEU:HD12	5:L:13:LEU:N	2.25	0.51
1:M:12:SER:OG	5:R:80:GLY:HA3	2.11	0.51
1:M:135:LEU:C	1:M:137:GLY:H	2.18	0.51
4:Q:85:LYS:O	4:Q:89:VAL:HG23	2.10	0.51
3:C:3:ILE:HG23	3:C:99:TYR:CE2	2.45	0.51
3:C:18:ASP:OD2	3:C:18:ASP:N	2.42	0.51
4:E:84:VAL:HG13	4:E:85:LYS:N	2.25	0.51
5:F:47:ILE:HG12	5:F:60:GLN:CA	2.31	0.51
1:G:120:ARG:HB3	1:G:120:ARG:NH1	2.10	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
1:M:132:TYR:HB3	1:M:179:LEU:HD12	1.91	0.51
1:M:134:THR:HG21	1:M:183:TYR:CE1	2.44	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
2:T:99:LEU:HD22	2:T:243:ASN:HB3	1.93	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
5:X:28:PHE:CE2	5:X:48:LYS:HD3	2.46	0.51
1:A:10:ASN:CB	1:A:14:GLY:O	2.59	0.51
5:F:13:LEU:H	5:F:13:LEU:CD1	2.23	0.51
5:F:85:ILE:H	5:F:85:ILE:CD1	2.23	0.51
2:H:68:GLU:CG	4:J:63:ILE:HD11	2.40	0.51
2:H:72:GLN:HE22	4:J:55:HIS:HE1	1.59	0.51
4:K:114:THR:HG23	4:K:179:LYS:CA	2.41	0.51
1:M:29:ASN:O	1:M:32:GLU:CG	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:68:PRO:HD2	1:M:111:PHE:O	2.11	0.51
2:N:184:HIS:HB2	2:N:211:ILE:HD13	1.93	0.51
3:O:93:ASP:O	3:O:93:ASP:CG	2.54	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:128:THR:O	1:S:130:PHE:CE2	2.64	0.51
4:W:84:VAL:HG13	4:W:85:LYS:N	2.24	0.51
2:B:72:GLN:HE22	4:D:55:HIS:HE1	1.58	0.51
4:D:180:LEU:HD12	4:D:180:LEU:N	2.13	0.51
1:G:12:SER:CB	5:L:10:LYS:HZ2	2.24	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
2:H:218:LEU:O	2:H:220:GLN:N	2.43	0.51
4:K:128:VAL:HG12	4:K:129:GLU:N	2.26	0.51
5:L:28:PHE:HD2	5:L:48:LYS:HZ3	1.56	0.51
3:O:88:PHE:CE1	3:O:107:TYR:CD1	2.99	0.51
3:O:117:ASN:OD1	4:W:32:LEU:HD21	2.11	0.51
1:S:21:PHE:CE2	1:S:215:VAL:HG11	2.44	0.51
4:W:49:PHE:CE2	4:W:134:ALA:HB2	2.45	0.51
5:X:68:GLU:O	5:X:70:PHE:N	2.33	0.51
1:A:104:ASP:HA	1:A:108:LYS:NZ	2.26	0.51
1:A:186:TYR:O	1:A:190:VAL:HB	2.10	0.51
3:C:93:ASP:O	3:C:93:ASP:CG	2.54	0.51
4:D:47:ARG:HG3	4:Q:84:VAL:HG21	1.92	0.51
4:D:88:GLU:O	4:D:92:LYS:HG2	2.10	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: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
3:O:77:VAL:CG1	3:O:91:LEU:HD22	2.25	0.51
4:P:88:GLU:O	4:P:92:LYS:HG2	2.10	0.51
5:R:28:PHE:CE2	5:R:48:LYS:HD3	2.46	0.51
1:S:106:PHE:N	1:S:106:PHE:CD1	2.78	0.51
2:T:184:HIS:HB2	2:T:211:ILE:HD13	1.93	0.51
4:D:117:LEU:O	4:D:118:ILE:C	2.54	0.51
4:D:130:LEU:CD2	4:D:168:LEU:HB3	2.41	0.51
4:E:114:THR:HG23	4:E:179:LYS:CA	2.41	0.51
1:G:68:PRO:HD2	1:G:111:PHE:O	2.11	0.51
1:G:124:THR:HG21	3:I:55:THR:CG2	2.41	0.51
2:H:79:THR:HG22	2:H:81:GLY:H	1.76	0.51
2:H:90:TYR:CZ	4:J:40:GLN:HG2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:197:ASP:HB3	2:H:212:VAL:O	2.11	0.51
4:K:38:VAL:HG11	4:K:140:TYR:CE1	2.45	0.51
1:M:186:TYR:O	1:M:190:VAL:HB	2.10	0.51
1:S:10:ASN:CB	1:S:14:GLY:O	2.59	0.51
2:T:59:LEU:HD12	2:T:59:LEU:O	2.11	0.51
2:T:79:THR:HG22	2:T:81:GLY:H	1.76	0.51
3:U:79:THR:HG22	3:U:80:TYR:N	2.26	0.51
3:U:80:TYR:CB	3:U:103:LEU:HD23	2.41	0.51
3:U:88:PHE:CE1	3:U:107:TYR:CD1	2.99	0.51
3:U:111:TYR:CZ	3:U:115:VAL:HG11	2.46	0.51
4:W:128:VAL:HG12	4:W:129:GLU:N	2.26	0.51
4:W:139:TRP:HE3	4:W:142:ASN:HD21	1.59	0.51
1:A:112:THR:HG22	1:A:113:ASN:O	2.10	0.50
2:B:221:PHE:O	2:B:223:PRO:HD3	2.11	0.50
3:C:142:ASN:HD22	3:C:143:ARG:N	2.09	0.50
2:H:99:LEU:HD22	2:H:243:ASN:HB3	1.93	0.50
4:J:35:GLY:HA2	4:J:140:TYR:OH	2.10	0.50
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
4:V:38:VAL:HG11	4:V:140:TYR:HE1	1.74	0.50
4:W:31:THR:HG21	4:W:127:PHE:CE2	2.46	0.50
2:B:167:THR:HG22	2:B:167:THR:O	2.11	0.50
2:B:184:HIS:HB2	2:B:211:ILE:HD13	1.93	0.50
1:G:12:SER:CB	5:L:10:LYS:NZ	2.75	0.50
1:G:29:ASN:O	1:G:32:GLU:CG	2.59	0.50
1:G:135:LEU:C	1:G:137:GLY:H	2.17	0.50
2:H:59:LEU:HD12	2:H:59:LEU:O	2.11	0.50
3:I:79:THR:HG22	3:I:80:TYR:N	2.26	0.50
1:M:29:ASN:O	1:M:32:GLU:HG2	2.11	0.50
4:Q:84:VAL:HG13	4:Q:85:LYS:N	2.26	0.50
3:U:99:TYR:N	3:U:99:TYR:CD1	2.79	0.50
4:W:34:TYR:OH	4:W:143:ILE:HG22	2.11	0.50
5:F:41:ILE:HD12	5:F:41:ILE:N	2.26	0.50
1:G:29:ASN:O	1:G:32:GLU:HG2	2.11	0.50
1:G:190:VAL:HG12	1:G:191:MET:CE	2.42	0.50
4:K:90:LEU:HD12	6:K:194:PLM:H52	1.93	0.50
5:L:13:LEU:H	5:L:13:LEU:CD1	2.24	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
2:N:179:ILE:HG23	2:N:180:LEU:N	2.24	0.50
1:S:135:LEU:HD21	4:V:79:ARG:NH1	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:92:HIS:CD2	2:T:239:GLY:HA2	2.46	0.50
4:W:75:THR:CG2	4:W:93:CYS:SG	3.00	0.50
1:A:52:PRO:C	1:A:54:ALA:N	2.61	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
5:F:67:GLN:OE1	5:F:67:GLN:HA	2.10	0.50
2:H:83:PHE:CD1	2:H:83:PHE:C	2.88	0.50
2:H:267:LEU:HD23	2:H:267:LEU:O	2.11	0.50
3:I:155:PRO:HG2	3:I:156:MET:N	2.24	0.50
3:O:99:TYR:N	3:O:99:TYR:CD1	2.79	0.50
4:P:29:LEU:HD23	4:P:29:LEU:C	2.36	0.50
4:P:106:THR:CG2	4:P:107:ASN:H	2.11	0.50
4:V:185:LYS:HD2	4:V:185:LYS:C	2.37	0.50
5:X:13:LEU:H	5:X:13:LEU:CD1	2.24	0.50
2:B:99:LEU:HD22	2:B:243:ASN:HB3	1.93	0.50
2:B:167:THR:HG22	2:B:169:MET:HB3	1.92	0.50
3:C:129:GLU:HB2	3:C:135:GLN:OE1	2.11	0.50
4:D:111:ASN:ND2	4:D:113:ASP:OD2	2.37	0.50
5:F:121:ASN:O	5:F:122:LYS:C	2.54	0.50
1:G:12:SER:OG	5:L:80:GLY:HA3	2.11	0.50
2:H:168:LYS:C	2:H:170:ARG:H	2.20	0.50
3:I:142:ASN:HD22	3:I:143:ARG:N	2.09	0.50
4:K:134:ALA:O	4:K:136:LYS:N	2.45	0.50
1:M:112:THR:HG22	1:M:113:ASN:O	2.10	0.50
3:O:132:MET:HB2	3:O:133:ARG:NH1	2.27	0.50
5:R:13:LEU:HD21	5:R:25:LEU:HD21	1.94	0.50
2:T:169:MET:CB	2:T:174:LEU:HD12	2.42	0.50
2:T:231:TYR:CD2	2:T:234:CYS:SG	3.02	0.50
3:U:83:ALA:O	4:W:155:VAL:HG13	2.11	0.50
3:U:88:PHE:CE1	3:U:107:TYR:HB2	2.46	0.50
4:V:35:GLY:HA2	4:V:140:TYR:OH	2.11	0.50
4:V:91:SER:HB2	4:V:103:PRO:HG2	1.93	0.50
4:W:34:TYR:CE1	4:W:143:ILE:CG2	2.93	0.50
2:B:84:GLU:HB3	2:B:231:TYR:CE1	2.46	0.50
2:B:92:HIS:CD2	2:B:239:GLY:HA2	2.47	0.50
5:F:83:GLY:CA	5:F:165:MET:HE1	2.42	0.50
2:H:220:GLN:HG3	2:H:221:PHE:H	1.77	0.50
2:H:259:GLY:C	2:H:260:HIS:CG	2.89	0.50
3:I:3:ILE:HG21	3:I:90:LEU:HD21	1.92	0.50
4:J:160:ASP:HB2	4:J:179:LYS:HB3	1.92	0.50
4:K:99:LEU:O	4:K:101:ILE:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:176:ILE:HD11	2:N:180:LEU:HD22	1.93	0.50
2:N:197:ASP:HB3	2:N:212:VAL:O	2.11	0.50
3:O:79:THR:HG22	3:O:80:TYR:N	2.25	0.50
3:O:80:TYR:CB	3:O:103:LEU:HD23	2.41	0.50
3:O:83:ALA:O	4:Q:155:VAL:HG13	2.12	0.50
4:P:130:LEU:CD2	4:P:168:LEU:HB3	2.42	0.50
5:R:73:ILE:O	5:R:77:TYR:HB2	2.11	0.50
5:R:121:ASN:O	5:R:122:LYS:C	2.54	0.50
2:T:259:GLY:C	2:T:260:HIS:CG	2.89	0.50
3:U:155:PRO:O	3:U:156:MET:O	2.28	0.50
4:W:17:ILE:O	4:W:21:LYS:O	2.29	0.50
5:X:47:ILE:HD11	5:X:60:GLN:HG3	1.93	0.50
3:C:99:TYR:N	3:C:99:TYR:CD1	2.79	0.50
4:E:75:THR:CG2	4:E:93:CYS:SG	2.99	0.50
5:F:73:ILE:O	5:F:77:TYR:HB2	2.11	0.50
1:G:52:PRO:C	1:G:54:ALA:N	2.63	0.50
2:H:92:HIS:NE2	2:H:239:GLY:HA2	2.26	0.50
2:H:184:HIS:HB2	2:H:211:ILE:HD13	1.94	0.50
4:J:48:ASP:O	4:J:51:LYS:N	2.42	0.50
1:M:7:LEU:CD1	1:M:141:VAL:HB	2.41	0.50
4:P:180:LEU:HD12	4:P:180:LEU:N	2.13	0.50
1:S:12:SER:CB	5:X:10:LYS:NZ	2.75	0.50
3:U:12:HIS:O	3:U:13:CYS:HB2	2.12	0.50
5:X:28:PHE:HD2	5:X:48:LYS:HZ3	1.57	0.50
5:X:68:GLU:CG	5:X:69:ARG:CA	2.88	0.50
1:A:70:ILE:HG23	1:A:70:ILE:O	2.10	0.50
3:C:79:THR:HG22	3:C:80:TYR:N	2.25	0.50
4:D:106:THR:CG2	4:D:107:ASN:H	2.11	0.50
4:E:131:PRO:O	4:E:133:ASP:N	2.45	0.50
5:F:13:LEU:HD21	5:F:25:LEU:HD21	1.93	0.50
4:K:17:ILE:O	4:K:21:LYS:O	2.29	0.50
5:L:163:LEU:O	5:L:167:ARG:HG3	2.11	0.50
3:O:88:PHE:CE1	3:O:107:TYR:HB2	2.46	0.50
3:U:132:MET:HB2	3:U:133:ARG:NH1	2.27	0.50
5:X:121:ASN:O	5:X:122:LYS:C	2.54	0.50
1:A:50:LEU:HD21	3:C:44:LEU:HG	1.94	0.50
1:A:119:LEU:CD2	1:A:131:ILE:HD13	2.42	0.50
4:D:29:LEU:HD23	4:D:29:LEU:C	2.37	0.50
1:G:119:LEU:HD23	1:G:119:LEU:O	2.12	0.50
1:G:128:THR:O	1:G:130:PHE:CE2	2.65	0.50
3:I:83:ALA:O	4:K:155:VAL:HG13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:99:TYR:N	3:I:99:TYR:CD1	2.80	0.50
1:M:129:MET:SD	1:M:131:ILE:HD11	2.52	0.50
2:N:59:LEU:HD12	2:N:59:LEU:O	2.12	0.50
2:N:92:HIS:CD2	2:N:239:GLY:HA2	2.47	0.50
2:N:176:ILE:HD13	2:N:176:ILE:C	2.36	0.50
3:O:110:ILE:HD13	3:O:148:VAL:HG13	1.93	0.50
5:R:85:ILE:H	5:R:85:ILE:CD1	2.24	0.50
1:S:124:THR:HG21	3:U:55:THR:CG2	2.42	0.50
1:S:131:ILE:O	1:S:131:ILE:HG22	2.11	0.50
4:V:130:LEU:CD2	4:V:168:LEU:HB3	2.42	0.50
1:A:4:GLU:HG3	1:A:143:ILE:HG22	1.93	0.49
5:F:47:ILE:HD11	5:F:60:GLN:HG3	1.94	0.49
1:G:112:THR:HG22	1:G:113:ASN:O	2.12	0.49
1:G:181:LYS:CD	1:G:214:MET:HE1	2.42	0.49
2:N:267:LEU:HD23	2:N:267:LEU:O	2.12	0.49
2:T:83:PHE:C	2:T:83:PHE:CD1	2.88	0.49
2:T:267:LEU:HD23	2:T:267:LEU:O	2.11	0.49
4:D:165:SER:O	4:D:174:THR:HA	2.12	0.49
3:I:44:LEU:HD23	3:I:44:LEU:C	2.37	0.49
3:I:110:ILE:HD13	3:I:148:VAL:HG13	1.93	0.49
1:M:10:ASN:HB2	1:M:14:GLY:O	2.13	0.49
1:M:28:LEU:CD2	3:O:57:LYS:HD2	2.42	0.49
1:S:132:TYR:CE2	1:S:180:ARG:HA	2.47	0.49
4:W:99:LEU:O	4:W:101:ILE:N	2.46	0.49
5:X:13:LEU:HD21	5:X:25:LEU:HG	1.94	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:88:TYR:CD1	5:X:96:PHE:CD1	2.99	0.49
5:X:156:THR:HG22	5:X:156:THR:O	2.12	0.49
1:A:119:LEU:HD23	1:A:119:LEU:O	2.11	0.49
2:B:169:MET:CB	2:B:174:LEU:HD12	2.43	0.49
4:E:34:TYR:OH	4:E:143:ILE:HG22	2.13	0.49
4:J:38:VAL:HG11	4:J:140:TYR:HE1	1.75	0.49
4:J:187:GLU:O	4:J:188:ILE:O	2.30	0.49
1:M:12:SER:CB	5:R:10:LYS:NZ	2.75	0.49
4:P:68:ILE:CD1	4:P:154:MET:HB3	2.42	0.49
4:Q:90:LEU:HD12	6:Q:194:PLM:H52	1.94	0.49
3:U:3:ILE:HD12	3:U:90:LEU:HD11	1.94	0.49
4:V:165:SER:O	4:V:174:THR:HA	2.12	0.49
1:A:129:MET:SD	1:A:131:ILE:HD11	2.53	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)
2:B:197:ASP:HB3	2:B:212:VAL:O	2.12	0.49
3:C:83:ALA:O	4:E:155:VAL:HG13	2.12	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
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
4:J:130:LEU:CD2	4:J:168:LEU:HB3	2.43	0.49
4:K:46:GLU:O	4:K:47:ARG:HB2	2.11	0.49
4:K:61:TYR:HE2	4:K:65:CYS:SG	2.35	0.49
1:M:124:THR:HG21	3:O:55:THR:CG2	2.43	0.49
1:M:190:VAL:HG12	1:M:191:MET:CE	2.42	0.49
4:P:165:SER:O	4:P:174:THR:HA	2.13	0.49
2:T:72:GLN:HE22	4:V:55:HIS:HE1	1.60	0.49
2:T:221:PHE:O	2:T:223:PRO:HD3	2.12	0.49
4:D:110:HIS:O	4:D:112:LYS:N	2.46	0.49
4:E:34:TYR:CE1	4:E:143:ILE:CG2	2.94	0.49
5:F:120:GLY:O	5:F:150:THR:O	2.31	0.49
1:G:104:ASP:HA	1:G:108:LYS:NZ	2.28	0.49
4:K:84:VAL:HG13	4:K:85:LYS:N	2.26	0.49
5:L:47:ILE:HD11	5:L:60:GLN:HG3	1.93	0.49
3:O:114:TYR:HD2	3:O:144:ASN:CB	2.25	0.49
4:P:91:SER:HB2	4:P:103:PRO:HG2	1.94	0.49
3:U:72:THR:HG23	3:U:73:GLY:H	1.72	0.49
3:U:114:TYR:HD2	3:U:144:ASN:CB	2.25	0.49
4:W:46:GLU:O	4:W:47:ARG:HB2	2.11	0.49
5:X:40:THR:HG22	5:X:69:ARG:HH12	1.78	0.49
5:X:163:LEU:O	5:X:167:ARG:HG3	2.12	0.49
4:D:137:SER:N	4:D:169:ARG:NH1	2.61	0.49
4:E:108:TRP:CE2	4:E:115:PHE:HB3	2.48	0.49
1:G:106:PHE:HD1	1:G:106:PHE:H	1.61	0.49
2:H:183:ILE:CD1	2:H:241:LEU:HD21	2.43	0.49
3:I:107:TYR:CE2	4:K:73:ALA:CA	2.94	0.49
3:I:112:VAL:HG11	4:K:70:ASP:OD1	2.11	0.49
4:J:180:LEU:O	4:J:182:ARG:N	2.45	0.49
4:K:143:ILE:CG2	4:K:144:LEU:N	2.76	0.49
1:M:107:PHE:CE1	4:P:17:ILE:HD11	2.45	0.49
5:R:68:GLU:CG	5:R:69:ARG:CA	2.88	0.49
5:R:163:LEU:O	5:R:167:ARG:HG3	2.12	0.49
4:W:108:TRP:CE2	4:W:115:PHE:HB3	2.48	0.49
5:X:14:ILE:HA	5:X:64:THR:HG23	1.94	0.49
1:A:181:LYS:CD	1:A:214:MET:HE1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:3:ILE:HD12	3:C:90:LEU:HD11	1.94	0.49
4:E:143:ILE:CG2	4:E:144:LEU:N	2.75	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
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:V:68:ILE:CD1	4:V:154:MET:HB3	2.43	0.49
4:D:91:SER:HB2	4:D:103:PRO:HG2	1.94	0.49
4:E:99:LEU:O	4:E:101:ILE:N	2.45	0.49
1:G:188:ASP:HA	1:G:192:LYS:HD3	1.94	0.49
3:I:132:MET:HB2	3:I:133:ARG:NH1	2.27	0.49
4:K:34:TYR:OH	4:K:143:ILE:HG22	2.13	0.49
5:L:121:ASN:O	5:L:122:LYS:C	2.55	0.49
1:M:188:ASP:HA	1:M:192:LYS:HD3	1.93	0.49
2:N:99:LEU:HD22	2:N:243:ASN:HB3	1.94	0.49
3:O:12:HIS:O	3:O:13:CYS:HB2	2.13	0.49
4:P:113:ASP:O	4:P:180:LEU:HD12	2.13	0.49
1:S:50:LEU:HD11	3:U:44:LEU:HD12	1.95	0.49
1:S:119:LEU:HD23	1:S:119:LEU:O	2.12	0.49
3:U:129:GLU:HB2	3:U:135:GLN:OE1	2.13	0.49
5:X:104:GLN:HG3	5:X:108:ARG:NH2	2.28	0.49
2:B:220:GLN:HG3	2:B:221:PHE:N	2.28	0.49
2:B:259:GLY:C	2:B:260:HIS:CG	2.91	0.49
4:D:137:SER:HA	4:D:169:ARG:HH12	1.78	0.49
4:K:108:TRP:CE2	4:K:115:PHE:HB3	2.48	0.49
5:L:14:ILE:HA	5:L:64:THR:HG23	1.94	0.49
1:M:132:TYR:CE2	1:M:180:ARG:HA	2.48	0.49
1:M:212:LYS:O	1:M:215:VAL:CG2	2.61	0.49
4:Q:161:VAL:HA	4:Q:177:LYS:O	2.13	0.49
5:R:62:TRP:O	5:R:64:THR:N	2.44	0.49
2:T:97:ARG:O	2:T:101:LEU:HG	2.13	0.49
4:V:99:LEU:HB2	4:V:101:ILE:HD11	1.94	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
3:C:110:ILE:HD13	3:C:148:VAL:HG13	1.95	0.49
3:C:114:TYR:HD2	3:C:144:ASN:CB	2.26	0.49
4:D:48:ASP:O	4:D:49:PHE:C	2.56	0.49
4:D:162:TRP:CD1	4:D:177:LYS:HB2	2.47	0.49
2:H:173:ASP:OD2	2:H:281:ARG:NH1	2.40	0.49
3:I:129:GLU:HB2	3:I:135:GLN:OE1	2.13	0.49
4:J:185:LYS:HD2	4:J:185:LYS:C	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
3:O:129:GLU:HB2	3:O:135:GLN:OE1	2.13	0.49
4:P:110:HIS:O	4:P:112:LYS:N	2.46	0.49
4:Q:108:TRP:CE2	4:Q:115:PHE:HB3	2.48	0.49
5:R:13:LEU:HD21	5:R:25:LEU:HG	1.95	0.49
5:R:40:THR:HG22	5:R:69:ARG:HH12	1.78	0.49
5:R:120:GLY:O	5:R:150:THR:O	2.31	0.49
5:R:156:THR:O	5:R:156:THR:HG22	2.13	0.49
2:T:176:ILE:HD11	2:T:180:LEU:HD22	1.95	0.49
2:T:183:ILE:CD1	2:T:241:LEU:HD21	2.43	0.49
5:X:12:LEU:N	5:X:12:LEU:CD2	2.76	0.49
1:A:107:PHE:CE1	4:D:17:ILE:HD11	2.46	0.48
1:A:174:ILE:CG1	1:A:175:ALA:N	2.74	0.48
4:D:68:ILE:CD1	4:D:154:MET:HB3	2.43	0.48
5:F:43:VAL:CG1	5:F:64:THR:HA	2.44	0.48
5:F:163:LEU:O	5:F:167:ARG:HG3	2.13	0.48
1:G:10:ASN:HB2	1:G:14:GLY:O	2.13	0.48
4:K:79:ARG:O	4:K:80:CYS:C	2.55	0.48
1:M:2:ALA:HB3	1:M:146:SER:HB3	1.95	0.48
5:R:10:LYS:HB2	5:R:80:GLY:O	2.13	0.48
1:S:129:MET:CE	1:S:143:ILE:HD11	2.43	0.48
2:T:84:GLU:HB3	2:T:231:TYR:CE1	2.47	0.48
2:T:220:GLN:HG3	2:T:221:PHE:N	2.27	0.48
4:V:29:LEU:HD23	4:V:29:LEU:C	2.37	0.48
4:V:65:CYS:O	4:V:68:ILE:CD1	2.61	0.48
5:X:10:LYS:HB2	5:X:80:GLY:O	2.13	0.48
1:A:23:ASN:HB3	1:A:25:GLU:OE1	2.14	0.48
1:A:72:TYR:O	1:A:72:TYR:CG	2.66	0.48
4:E:46:GLU:O	4:E:47:ARG:HB2	2.13	0.48
5:F:13:LEU:HD21	5:F:25:LEU:HG	1.95	0.48
1:G:50:LEU:HD11	3:I:44:LEU:HD12	1.95	0.48
1:G:132:TYR:CE2	1:G:180:ARG:HA	2.48	0.48
2:N:169:MET:CB	2:N:174:LEU:HD12	2.44	0.48
4:Q:131:PRO:O	4:Q:133:ASP:N	2.47	0.48
5:R:14:ILE:HA	5:R:64:THR:HG23	1.96	0.48
5:R:29:SER:CA	5:R:48:LYS:HE2	2.43	0.48
2:T:175:LYS:CG	2:T:176:ILE:N	2.76	0.48
4:V:18:TRP:CD1	4:V:18:TRP:C	2.90	0.48
5:X:13:LEU:HD21	5:X:25:LEU:HD11	1.95	0.48
5:X:29:SER:CA	5:X:48:LYS:HE2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:VAL:HG12	1:A:191:MET:CE	2.43	0.48
2:B:83:PHE:CD1	2:B:83:PHE:C	2.88	0.48
2:B:183:ILE:CD1	2:B:241:LEU:HD21	2.43	0.48
4:D:160:ASP:HB2	4:D:179:LYS:HB3	1.94	0.48
4:D:187:GLU:O	4:D:188:ILE:O	2.30	0.48
4:E:24:LYS:O	4:E:25:ILE:HD12	2.13	0.48
2:H:84:GLU:HB3	2:H:231:TYR:CE1	2.47	0.48
2:H:176:ILE:C	2:H:176:ILE:HD13	2.38	0.48
3:I:93:ASP:O	3:I:93:ASP:CG	2.56	0.48
4:J:93:CYS:O	4:J:97:ILE:CG1	2.58	0.48
4:J:113:ASP:O	4:J:180:LEU:HD12	2.13	0.48
5:L:69:ARG:O	5:L:72:THR:HG22	2.12	0.48
1:M:72:TYR:O	1:M:72:TYR:CG	2.66	0.48
4:P:99:LEU:HB2	4:P:101:ILE:HD11	1.94	0.48
4:P:187:GLU:O	4:P:188:ILE:O	2.30	0.48
5:R:104:GLN:HG3	5:R:108:ARG:NH2	2.28	0.48
1:S:133:GLN:CA	1:S:138:LEU:O	2.61	0.48
3:U:142:ASN:HD22	3:U:143:ARG:N	2.11	0.48
4:V:110:HIS:O	4:V:112:LYS:N	2.46	0.48
5:X:83:GLY:CA	5:X:165:MET:HE1	2.43	0.48
2:B:84:GLU:HB3	2:B:231:TYR:HD1	1.76	0.48
2:B:167:THR:C	2:B:169:MET:H	2.20	0.48
2:B:176:ILE:HD11	2:B:180:LEU:HD22	1.94	0.48
3:C:12:HIS:O	3:C:13:CYS:HB2	2.14	0.48
5:F:13:LEU:HD22	5:F:25:LEU:HD11	1.96	0.48
5:F:40:THR:HG22	5:F:69:ARG:HH12	1.78	0.48
1:G:11:LYS:HG3	1:G:136:THR:O	2.14	0.48
1:G:70:ILE:HG23	1:G:70:ILE:O	2.12	0.48
5:L:13:LEU:CD1	5:L:25:LEU:HD11	2.44	0.48
5:L:43:VAL:CG1	5:L:64:THR:HA	2.43	0.48
5:L:104:GLN:HG3	5:L:108:ARG:NH2	2.28	0.48
1:M:119:LEU:HD23	1:M:119:LEU:O	2.12	0.48
3:O:11:ARG:NH1	3:O:125:PHE:CE1	2.77	0.48
4:P:18:TRP:CD1	4:P:18:TRP:C	2.91	0.48
4:P:111:ASN:ND2	4:P:113:ASP:OD2	2.39	0.48
2:T:176:ILE:HD13	2:T:176:ILE:C	2.38	0.48
2:T:268:ILE:O	2:T:268:ILE:HG22	2.14	0.48
3:U:107:TYR:CE2	4:W:73:ALA:CA	2.94	0.48
3:U:123:TYR:O	3:U:123:TYR:HD1	1.95	0.48
4:W:134:ALA:O	4:W:136:LYS:N	2.46	0.48
5:X:85:ILE:H	5:X:85:ILE:CD1	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:THR:HG21	3:C:55:THR:CG2	2.44	0.48
2:B:97:ARG:O	2:B:101:LEU:HG	2.14	0.48
4:D:167:ILE:CG2	4:D:168:LEU:N	2.76	0.48
4:E:134:ALA:O	4:E:136:LYS:N	2.47	0.48
3:I:12:HIS:O	3:I:13:CYS:HB2	2.14	0.48
4:J:165:SER:O	4:J:174:THR:HA	2.13	0.48
4:K:24:LYS:O	4:K:25:ILE:HD12	2.14	0.48
4:K:49:PHE:HB2	4:K:137:SER:CB	2.43	0.48
5:L:10:LYS:HB2	5:L:80:GLY:O	2.14	0.48
5:L:120:GLY:O	5:L:150:THR:O	2.30	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
4:Q:38:VAL:HG11	4:Q:140:TYR:CE1	2.48	0.48
5:R:41:ILE:HD12	5:R:41:ILE:N	2.25	0.48
1:S:18:GLN:NE2	1:S:18:GLN:O	2.45	0.48
4:V:162:TRP:CD1	4:V:177:LYS:HB2	2.49	0.48
4:W:108:TRP:NE1	4:W:115:PHE:HB3	2.29	0.48
2:B:176:ILE:C	2:B:176:ILE:HD13	2.37	0.48
5:F:10:LYS:HB2	5:F:80:GLY:O	2.13	0.48
5:F:29:SER:CA	5:F:48:LYS:HE2	2.43	0.48
5:F:68:GLU:CG	5:F:69:ARG:CA	2.87	0.48
5:F:88:TYR:CD1	5:F:96:PHE:CD1	3.01	0.48
1:G:124:THR:O	1:G:147:VAL:HG13	2.13	0.48
2:H:92:HIS:CD2	2:H:239:GLY:HA2	2.48	0.48
4:K:108:TRP:NE1	4:K:115:PHE:HB3	2.29	0.48
1:M:119:LEU:CD2	1:M:131:ILE:HD13	2.44	0.48
1:M:194:PRO:HG3	2:N:67:GLN:HA	1.95	0.48
3:O:77:VAL:O	3:O:78:HIS:C	2.56	0.48
3:O:102:VAL:HG21	3:O:156:MET:SD	2.53	0.48
3:O:142:ASN:HD22	3:O:143:ARG:N	2.11	0.48
4:Q:99:LEU:O	4:Q:101:ILE:N	2.46	0.48
1:S:12:SER:OG	5:X:80:GLY:HA3	2.13	0.48
3:U:11:ARG:NH1	3:U:125:PHE:CE1	2.77	0.48
4:V:34:TYR:CD2	4:V:124:LEU:HG	2.48	0.48
4:V:48:ASP:O	4:V:49:PHE:C	2.56	0.48
4:V:180:LEU:O	4:V:182:ARG:N	2.47	0.48
5:X:88:TYR:H	5:X:88:TYR:HD2	1.61	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
2:B:268:ILE:HG22	2:B:268:ILE:O	2.13	0.48
5:F:12:LEU:N	5:F:12:LEU:CD2	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:52:PRO:CD	3:I:75:TYR:CD2	2.96	0.48
1:G:72:TYR:O	1:G:72:TYR:CG	2.66	0.48
3:I:105:TYR:CE2	3:I:152:PHE:CZ	3.01	0.48
4:J:99:LEU:HB2	4:J:101:ILE:HD11	1.95	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:L:47:ILE:HG12	5:L:60:GLN:CA	2.34	0.48
2:N:83:PHE:CD1	2:N:83:PHE:C	2.88	0.48
2:N:194:HIS:O	2:N:195:VAL:C	2.56	0.48
3:O:110:ILE:HG22	3:O:145:PHE:CE1	2.49	0.48
4:Q:24:LYS:O	4:Q:25:ILE:HD12	2.14	0.48
4:Q:30:PHE:HE1	4:W:33:THR:HG1	1.56	0.48
2:T:255:MET:SD	2:T:255:MET:C	2.97	0.48
3:U:44:LEU:HD23	3:U:44:LEU:C	2.39	0.48
5:X:41:ILE:HD12	5:X:41:ILE:N	2.24	0.48
5:X:43:VAL:CG1	5:X:64:THR:HA	2.43	0.48
5:X:67:GLN:OE1	5:X:67:GLN:HA	2.13	0.48
4:D:185:LYS:C	4:D:185:LYS:HD2	2.38	0.48
4:E:108:TRP:NE1	4:E:115:PHE:HB3	2.29	0.48
3:I:11:ARG:NH1	3:I:125:PHE:CE1	2.78	0.48
4:J:18:TRP:CD1	4:J:18:TRP:C	2.91	0.48
5:L:12:LEU:N	5:L:12:LEU:CD2	2.77	0.48
5:L:88:TYR:CD1	5:L:96:PHE:CD1	3.01	0.48
2:N:167:THR:C	2:N:169:MET:H	2.21	0.48
2:N:200:VAL:HG12	2:N:210:MET:HG3	1.96	0.48
2:N:220:GLN:HG3	2:N:221:PHE:H	1.77	0.48
2:N:262:GLN:O	2:N:263:ARG:C	2.56	0.48
4:P:48:ASP:O	4:P:49:PHE:C	2.57	0.48
4:P:185:LYS:HD2	4:P:185:LYS:C	2.38	0.48
5:R:88:TYR:H	5:R:88:TYR:HD2	1.60	0.48
1:S:35:ILE:O	1:S:38:SER:HB2	2.13	0.48
1:S:70:ILE:HG23	1:S:70:ILE:O	2.12	0.48
2:T:56:GLU:HB3	4:V:25:ILE:O	2.14	0.48
4:W:123:PRO:HG2	4:W:124:LEU:H	1.78	0.48
1:A:188:ASP:HA	1:A:192:LYS:HD3	1.94	0.48
2:B:262:GLN:O	2:B:263:ARG:C	2.55	0.48
4:D:18:TRP:CD1	4:D:18:TRP:C	2.91	0.48
4:J:29:LEU:HD23	4:J:29:LEU:C	2.38	0.48
4:J:34:TYR:CE2	4:J:124:LEU:HG	2.49	0.48
3:O:123:TYR:O	3:O:123:TYR:HD1	1.96	0.48
4:P:162:TRP:CD1	4:P:177:LYS:HB2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:17:ILE:O	4:Q:21:LYS:O	2.31	0.48
4:Q:101:ILE:HG12	4:Q:102:THR:N	2.28	0.48
1:S:107:PHE:CE1	4:V:17:ILE:HD11	2.47	0.48
1:S:135:LEU:C	1:S:137:GLY:H	2.19	0.48
3:U:72:THR:HG22	3:U:75:TYR:H	1.79	0.48
3:U:77:VAL:O	3:U:78:HIS:C	2.56	0.48
4:W:143:ILE:CG2	4:W:144:LEU:N	2.77	0.48
5:X:84:ILE:CD1	5:X:114:VAL:HG11	2.38	0.48
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
1:G:10:ASN:O	1:G:12:SER:N	2.47	0.48
4:J:48:ASP:O	4:J:49:PHE:C	2.56	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
2:N:68:GLU:CG	4:P:63:ILE:HD11	2.44	0.48
4:P:167:ILE:CG2	4:P:168:LEU:N	2.76	0.48
4:P:180:LEU:O	4:P:182:ARG:N	2.46	0.48
4:Q:143:ILE:CG2	4:Q:144:LEU:N	2.77	0.48
5:R:88:TYR:CD1	5:R:96:PHE:CD1	3.01	0.48
1:S:106:PHE:HD1	1:S:106:PHE:H	1.62	0.48
2:T:218:LEU:O	2:T:220:GLN:N	2.46	0.48
3:U:82:THR:CG2	3:U:84:SER:OG	2.58	0.48
4:V:96:LYS:HZ1	4:V:100:ASN:HD21	1.61	0.48
4:V:137:SER:N	4:V:169:ARG:NH1	2.61	0.48
4:V:167:ILE:CG2	4:V:168:LEU:N	2.76	0.48
1:A:10:ASN:HB2	1:A:14:GLY:O	2.14	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:J:137:SER:HA	4:J:169:ARG:HH12	1.79	0.47
4:K:131:PRO:O	4:K:133:ASP:N	2.47	0.47
5:L:40:THR:HG22	5:L:69:ARG:HH12	1.79	0.47
1:M:18:GLN:O	1:M:18:GLN:NE2	2.47	0.47
3:O:44:LEU:HD23	3:O:44:LEU:C	2.38	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
4:V:187:GLU:O	4:V:188:ILE:O	2.32	0.47
4:W:31:THR:CG2	4:W:127:PHE:CE2	2.97	0.47
4:W:158:ASP:O	4:W:181:ASN:HB2	2.14	0.47
5:X:120:GLY:O	5:X:150:THR:O	2.31	0.47
3:C:102:VAL:HG21	3:C:156:MET:SD	2.53	0.47
3:C:132:MET:HB2	3:C:133:ARG:NH1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:13:LEU:HD21	5:F:25:LEU:HD11	1.96	0.47
1:G:28:LEU:CD2	3:I:57:LYS:HD2	2.44	0.47
2:H:176:ILE:HD11	2:H:180:LEU:HD22	1.96	0.47
2:H:255:MET:SD	2:H:255:MET:C	2.97	0.47
3:I:20:GLU:O	3:I:21:TRP:CB	2.55	0.47
1:S:23:ASN:HB3	1:S:25:GLU:OE1	2.14	0.47
1:S:72:TYR:O	1:S:72:TYR:CG	2.67	0.47
1:S:181:LYS:CD	1:S:214:MET:HE1	2.44	0.47
1:S:200:MET:O	1:S:201:PRO:C	2.57	0.47
3:U:110:ILE:HD13	3:U:148:VAL:HG13	1.95	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
5:X:13:LEU:HD21	5:X:25:LEU:HD21	1.96	0.47
1:A:12:SER:OG	5:F:80:GLY:HA3	2.15	0.47
3:C:123:TYR:O	3:C:123:TYR:HD1	1.96	0.47
1:G:107:PHE:CE1	4:J:17:ILE:HD11	2.47	0.47
2:H:194:HIS:O	2:H:195:VAL:C	2.57	0.47
3:I:79:THR:CG2	3:I:80:TYR:N	2.77	0.47
3:O:140:ILE:O	3:O:140:ILE:CG2	2.61	0.47
4:Q:31:THR:HG21	4:Q:127:PHE:CE2	2.49	0.47
4:Q:61:TYR:HE2	4:Q:65:CYS:SG	2.36	0.47
5:R:12:LEU:N	5:R:12:LEU:CD2	2.77	0.47
5:R:30:ASP:O	5:R:31:ASP:HB2	2.14	0.47
5:R:77:TYR:N	5:R:77:TYR:HD1	2.12	0.47
2:T:194:HIS:O	2:T:195:VAL:C	2.57	0.47
3:U:20:GLU:O	3:U:21:TRP:CB	2.56	0.47
4:V:113:ASP:O	4:V:180:LEU:HD12	2.14	0.47
3:C:17:PHE:HZ	3:C:146:ILE:HG22	1.79	0.47
4:D:136:LYS:C	4:D:169:ARG:NH1	2.72	0.47
4:E:31:THR:HG21	4:E:127:PHE:CE2	2.49	0.47
1:G:186:TYR:CE1	1:G:190:VAL:HG11	2.49	0.47
2:H:167:THR:C	2:H:169:MET:H	2.22	0.47
3:I:82:THR:HB	3:I:85:GLY:H	1.79	0.47
4:J:136:LYS:C	4:J:169:ARG:NH1	2.72	0.47
5:L:120:GLY:N	5:L:147:PHE:HE1	2.12	0.47
1:M:10:ASN:O	1:M:12:SER:N	2.46	0.47
4:Q:134:ALA:O	4:Q:136:LYS:N	2.48	0.47
5:R:13:LEU:HD22	5:R:25:LEU:HD11	1.97	0.47
1:S:10:ASN:O	1:S:12:SER:N	2.47	0.47
1:G:174:ILE:CG1	1:G:175:ALA:N	2.73	0.47
3:I:123:TYR:O	3:I:123:TYR:HD1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:23:ASN:HB3	1:M:25:GLU:OE1	2.15	0.47
1:M:134:THR:OG1	1:M:138:LEU:HB2	2.15	0.47
2:N:255:MET:SD	2:N:255:MET:C	2.98	0.47
4:Q:29:LEU:HD21	6:W:194:PLM:HG3	1.97	0.47
4:Q:108:TRP:NE1	4:Q:115:PHE:HB3	2.29	0.47
1:S:134:THR:N	1:S:138:LEU:O	2.39	0.47
2:T:84:GLU:HB3	2:T:231:TYR:HD1	1.77	0.47
4:V:34:TYR:CE2	4:V:124:LEU:HG	2.49	0.47
5:X:120:GLY:N	5:X:147:PHE:HE1	2.12	0.47
2:B:255:MET:SD	2:B:255:MET:C	2.98	0.47
5:F:13:LEU:CD1	5:F:25:LEU:HD11	2.45	0.47
5:F:68:GLU:C	5:F:70:PHE:N	2.70	0.47
5:F:88:TYR:H	5:F:88:TYR:HD2	1.61	0.47
2:H:179:ILE:CG2	2:H:180:LEU:N	2.78	0.47
4:J:45:TYR:OH	4:J:55:HIS:CD2	2.67	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
4:K:161:VAL:HA	4:K:177:LYS:O	2.14	0.47
5:L:4:GLU:O	5:L:5:TYR:O	2.32	0.47
5:L:83:GLY:CA	5:L:165:MET:HE1	2.44	0.47
3:O:124:ASP:OD2	3:O:140:ILE:HB	2.14	0.47
4:P:13:MET:HE1	4:P:77:LEU:HD21	1.96	0.47
4:P:34:TYR:CE2	4:P:124:LEU:HG	2.50	0.47
4:P:50:ASN:HA	4:P:53:ASN:ND2	2.29	0.47
4:P:137:SER:HA	4:P:169:ARG:HH12	1.79	0.47
4:Q:75:THR:CG2	4:Q:93:CYS:SG	3.02	0.47
4:Q:124:LEU:C	4:Q:124:LEU:CD2	2.87	0.47
1:S:188:ASP:HA	1:S:192:LYS:HD3	1.96	0.47
4:V:137:SER:HA	4:V:169:ARG:HH12	1.79	0.47
1:A:12:SER:CB	5:F:10:LYS:NZ	2.77	0.47
2:B:59:LEU:HD12	2:B:59:LEU:O	2.15	0.47
3:C:77:VAL:O	3:C:78:HIS:C	2.57	0.47
3:C:110:ILE:HG22	3:C:145:PHE:CE1	2.50	0.47
4:D:34:TYR:CE2	4:D:124:LEU:HG	2.50	0.47
4:D:137:SER:N	4:D:169:ARG:HH12	2.12	0.47
4:D:180:LEU:O	4:D:182:ARG:N	2.47	0.47
4:E:61:TYR:HE2	4:E:65:CYS:SG	2.37	0.47
4:E:126:ASP:OD2	4:E:167:ILE:HD13	2.14	0.47
5:F:120:GLY:N	5:F:147:PHE:HE1	2.12	0.47
5:F:148:LEU:HD12	5:F:148:LEU:N	2.30	0.47
2:H:97:ARG:O	2:H:101:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:82:THR:HB	3:I:85:GLY:N	2.29	0.47
4:J:65:CYS:O	4:J:68:ILE:CD1	2.63	0.47
4:J:96:LYS:HZ1	4:J:100:ASN:HD21	1.62	0.47
4:J:167:ILE:CG2	4:J:168:LEU:N	2.76	0.47
4:K:117:LEU:HB2	4:K:176:ILE:O	2.15	0.47
4:K:190:ILE:HA	4:K:190:ILE:HD13	1.67	0.47
5:L:53:ASP:C	5:L:55:LYS:N	2.72	0.47
5:L:68:GLU:C	5:L:70:PHE:H	2.22	0.47
1:M:200:MET:HE3	5:R:7:TYR:HA	1.95	0.47
2:N:169:MET:HB3	2:N:174:LEU:HD12	1.96	0.47
4:P:160:ASP:HB2	4:P:179:LYS:HB3	1.96	0.47
4:Q:25:ILE:HD13	4:W:27:THR:OG1	2.14	0.47
4:Q:79:ARG:O	4:Q:80:CYS:C	2.56	0.47
5:R:13:LEU:CD1	5:R:25:LEU:HD11	2.45	0.47
5:R:43:VAL:CG1	5:R:64:THR:HA	2.45	0.47
1:S:174:ILE:CG1	1:S:175:ALA:N	2.73	0.47
4:V:136:LYS:C	4:V:169:ARG:NH1	2.73	0.47
4:V:137:SER:N	4:V:169:ARG:HH12	2.12	0.47
3:C:129:GLU:HB3	3:C:135:GLN:OE1	2.14	0.47
4:D:34:TYR:CD2	4:D:124:LEU:HG	2.49	0.47
5:F:12:LEU:HG	5:F:12:LEU:O	2.14	0.47
1:G:4:GLU:CG	1:G:143:ILE:HG22	2.45	0.47
1:G:23:ASN:HB3	1:G:25:GLU:OE1	2.15	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
5:L:88:TYR:H	5:L:88:TYR:HD2	1.63	0.47
1:M:181:LYS:CD	1:M:214:MET:HE1	2.44	0.47
2:N:168:LYS:C	2:N:170:ARG:H	2.22	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
3:U:72:THR:HG23	3:U:74:LYS:H	1.80	0.47
4:V:28:GLU:HA	4:V:31:THR:HG22	1.97	0.47
4:V:96:LYS:NZ	4:V:100:ASN:HD21	2.12	0.47
1:A:106:PHE:H	1:A:106:PHE:HD1	1.62	0.47
4:E:68:ILE:HG21	4:E:154:MET:CB	2.45	0.47
4:E:134:ALA:C	4:E:136:LYS:N	2.73	0.47
5:F:77:TYR:N	5:F:77:TYR:HD1	2.12	0.47
2:H:262:GLN:O	2:H:263:ARG:C	2.56	0.47
5:L:13:LEU:HD21	5:L:25:LEU:HD11	1.97	0.47
1:M:52:PRO:CD	3:O:75:TYR:CD2	2.98	0.47
2:N:97:ARG:O	2:N:101:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:72:THR:HG21	3:O:75:TYR:CE2	2.50	0.47
4:P:136:LYS:C	4:P:169:ARG:NH1	2.73	0.47
1:S:2:ALA:HB3	1:S:146:SER:HB3	1.96	0.47
1:S:11:LYS:HG3	1:S:136:THR:O	2.15	0.47
1:S:133:GLN:HE22	4:V:188:ILE:CD1	2.22	0.47
1:S:194:PRO:HG3	2:T:67:GLN:HA	1.95	0.47
4:V:68:ILE:H	4:V:68:ILE:HG13	1.35	0.47
3:C:107:TYR:O	3:C:111:TYR:HB3	2.14	0.47
4:D:13:MET:HE1	4:D:77:LEU:HD21	1.97	0.47
4:D:166:ASP:HB3	4:D:169:ARG:CG	2.45	0.47
4:E:79:ARG:O	4:E:80:CYS:C	2.57	0.47
5:F:104:GLN:HG3	5:F:108:ARG:NH2	2.30	0.47
1:G:133:GLN:CA	1:G:138:LEU:O	2.63	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:O:17:PHE:HZ	3:O:146:ILE:HG22	1.80	0.47
3:C:67:ILE:HD12	3:C:67:ILE:N	2.30	0.46
1:G:45:ALA:O	1:G:48:SER:OG	2.31	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
4:J:28:GLU:HA	4:J:31:THR:HG22	1.97	0.46
1:M:69:TYR:CD1	1:M:69:TYR:N	2.83	0.46
4:P:180:LEU:O	4:P:181:ASN:C	2.58	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:V:47:ARG:C	4:V:49:PHE:H	2.23	0.46
4:V:160:ASP:HB2	4:V:179:LYS:HB3	1.96	0.46
4:V:167:ILE:HG23	4:V:168:LEU:N	2.30	0.46
4:W:101:ILE:HG12	4:W:102:THR:N	2.30	0.46
2:B:175:LYS:CG	2:B:176:ILE:N	2.77	0.46
3:C:44:LEU:HD23	3:C:44:LEU:C	2.39	0.46
4:D:99:LEU:HB2	4:D:101:ILE:HD11	1.96	0.46
4:E:190:ILE:HD13	4:E:190:ILE:HA	1.67	0.46
5:F:169:ILE:HG13	5:F:169:ILE:H	1.54	0.46
1:G:194:PRO:HG3	2:H:67:GLN:HA	1.96	0.46
3:I:107:TYR:O	3:I:111:TYR:HB3	2.15	0.46
3:I:121:SER:HA	3:I:122:PRO:HD2	1.79	0.46
3:I:129:GLU:HB3	3:I:135:GLN:OE1	2.15	0.46
4:J:68:ILE:H	4:J:68:ILE:HG13	1.36	0.46
4:J:159:CYS:CB	4:J:179:LYS:O	2.63	0.46
4:K:134:ALA:C	4:K:136:LYS:N	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:84:ILE:CD1	5:L:114:VAL:HG11	2.40	0.46
2:N:56:GLU:HB3	4:P:25:ILE:O	2.15	0.46
3:U:79:THR:CG2	3:U:80:TYR:N	2.78	0.46
3:U:105:TYR:HE1	3:U:109:HIS:HD1	1.54	0.46
5:X:13:LEU:HD22	5:X:25:LEU:HD11	1.97	0.46
5:X:88:TYR:HD1	5:X:96:PHE:HB2	1.79	0.46
5:X:137:LYS:O	5:X:141:ASP:OD2	2.33	0.46
1:A:50:LEU:HD11	3:C:44:LEU:HD12	1.97	0.46
1:A:69:TYR:CD1	1:A:69:TYR:N	2.83	0.46
2:B:68:GLU:CG	4:D:63:ILE:HD11	2.46	0.46
2:B:246:PHE:CD1	2:B:246:PHE:N	2.83	0.46
3:C:79:THR:CG2	3:C:80:TYR:N	2.77	0.46
5:F:30:ASP:O	5:F:31:ASP:HB2	2.15	0.46
2:H:231:TYR:CD2	2:H:234:CYS:SG	3.08	0.46
3:I:114:TYR:CD2	3:I:144:ASN:HB3	2.51	0.46
3:I:131:GLU:HG3	3:I:135:GLN:HB3	1.97	0.46
5:L:137:LYS:O	5:L:141:ASP:OD2	2.34	0.46
3:O:79:THR:CG2	3:O:80:TYR:N	2.78	0.46
1:S:10:ASN:HB2	1:S:14:GLY:O	2.15	0.46
2:T:262:GLN:O	2:T:263:ARG:C	2.57	0.46
5:X:53:ASP:C	5:X:55:LYS:N	2.73	0.46
4:D:28:GLU:HA	4:D:31:THR:HG22	1.98	0.46
1:G:114:TRP:CH2	4:J:76:ALA:HA	2.51	0.46
1:G:134:THR:N	1:G:138:LEU:O	2.41	0.46
1:G:200:MET:O	1:G:201:PRO:C	2.58	0.46
3:I:77:VAL:O	3:I:78:HIS:C	2.58	0.46
4:J:50:ASN:HA	4:J:53:ASN:ND2	2.30	0.46
4:K:101:ILE:HG12	4:K:102:THR:N	2.30	0.46
5:L:41:ILE:HD12	5:L:41:ILE:N	2.26	0.46
1:M:70:ILE:HG23	1:M:70:ILE:O	2.14	0.46
1:M:129:MET:HB2	1:M:143:ILE:HD11	1.97	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:Q:29:LEU:CD2	4:W:99:LEU:HD21	2.45	0.46
2:T:70:ILE:HG22	2:T:74:HIS:HD2	1.81	0.46
3:U:17:PHE:HZ	3:U:146:ILE:HG22	1.80	0.46
5:X:77:TYR:N	5:X:77:TYR:HD1	2.12	0.46
1:A:10:ASN:O	1:A:12:SER:N	2.47	0.46
1:A:35:ILE:O	1:A:38:SER:HB2	2.14	0.46
2:B:194:HIS:O	2:B:195:VAL:C	2.58	0.46
2:B:200:VAL:HG12	2:B:210:MET:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:131:GLU:HG3	3:C:135:GLN:HB3	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
1:G:69:TYR:CD1	1:G:69:TYR:N	2.83	0.46
3:I:52:ARG:O	3:I:56:GLN:HG3	2.16	0.46
4:J:180:LEU:O	4:J:181:ASN:C	2.59	0.46
5:L:15:GLY:N	5:L:102:TRP:CZ3	2.83	0.46
1:M:178:PHE:CD2	1:M:179:LEU:HD23	2.49	0.46
2:N:220:GLN:HG3	2:N:221:PHE:N	2.31	0.46
4:P:28:GLU:HA	4:P:31:THR:HG22	1.98	0.46
4:P:137:SER:N	4:P:169:ARG:NH1	2.64	0.46
4:Q:123:PRO:HG2	4:Q:124:LEU:H	1.79	0.46
4:Q:136:LYS:O	4:Q:169:ARG:NH1	2.48	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
3:U:67:ILE:N	3:U:67:ILE:HD12	2.30	0.46
4:V:18:TRP:CD1	4:V:18:TRP:O	2.68	0.46
4:V:45:TYR:OH	4:V:55:HIS:CD2	2.68	0.46
4:W:31:THR:HG21	4:W:127:PHE:CZ	2.50	0.46
4:W:79:ARG:O	4:W:80:CYS:C	2.57	0.46
1:A:129:MET:CE	1:A:143:ILE:HD11	2.45	0.46
4:E:101:ILE:HG12	4:E:102:THR:N	2.30	0.46
1:G:117:SER:HB3	4:J:191:GLY:H	1.81	0.46
3:I:105:TYR:HE1	3:I:109:HIS:HD1	1.56	0.46
5:L:77:TYR:N	5:L:77:TYR:HD1	2.13	0.46
2:N:181:GLN:HG3	2:N:199:LEU:HD23	1.97	0.46
3:O:13:CYS:HB3	4:Q:188:ILE:HD12	1.97	0.46
3:O:141:THR:O	3:O:142:ASN:C	2.59	0.46
4:Q:117:LEU:HB2	4:Q:176:ILE:O	2.15	0.46
5:R:68:GLU:O	5:R:70:PHE:N	2.38	0.46
3:U:105:TYR:CE2	3:U:152:PHE:CZ	3.03	0.46
3:U:119:LEU:N	3:U:119:LEU:CD2	2.60	0.46
1:A:52:PRO:CD	3:C:75:TYR:CD2	2.99	0.46
2:B:208:GLU:C	2:B:209:TYR:HD2	2.24	0.46
2:B:237:ILE:HG22	2:B:250:VAL:HG21	1.98	0.46
3:C:140:ILE:O	3:C:140:ILE:CG2	2.62	0.46
4:D:65:CYS:O	4:D:68:ILE:CD1	2.64	0.46
4:E:71:PHE:HE2	4:E:94:ALA:HA	1.80	0.46
4:E:124:LEU:HD23	4:E:125:ALA:HB2	1.97	0.46
5:F:69:ARG:O	5:F:72:THR:HG22	2.15	0.46
2:H:265:VAL:HG13	2:H:265:VAL:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:102:VAL:HG21	3:I:156:MET:SD	2.55	0.46
4:K:68:ILE:HG21	4:K:154:MET:CB	2.46	0.46
1:M:50:LEU:HD13	3:O:43:LEU:CD1	2.45	0.46
1:M:133:GLN:HE22	4:P:188:ILE:CD1	2.23	0.46
3:O:67:ILE:N	3:O:67:ILE:HD12	2.31	0.46
3:O:107:TYR:O	3:O:111:TYR:HB3	2.15	0.46
4:Q:16:GLU:HG2	4:Q:20:ASN:ND2	2.30	0.46
1:S:52:PRO:CD	3:U:75:TYR:CD2	2.98	0.46
3:U:52:ARG:O	3:U:56:GLN:HG3	2.16	0.46
3:U:129:GLU:HB3	3:U:135:GLN:OE1	2.16	0.46
3:U:141:THR:O	3:U:142:ASN:C	2.58	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
5:X:69:ARG:O	5:X:72:THR:HG22	2.15	0.46
1:A:134:THR:OG1	1:A:138:LEU:HB2	2.16	0.46
4:D:75:THR:O	4:D:76:ALA:C	2.58	0.46
4:E:36:SER:O	4:E:40:GLN:CB	2.63	0.46
5:F:15:GLY:N	5:F:102:TRP:CZ3	2.84	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
2:H:246:PHE:CD1	2:H:246:PHE:N	2.84	0.46
3:I:17:PHE:HZ	3:I:146:ILE:HG22	1.81	0.46
4:K:176:ILE:HD13	4:K:176:ILE:N	2.31	0.46
4:P:45:TYR:OH	4:P:55:HIS:CD2	2.69	0.46
1:S:69:TYR:CD1	1:S:69:TYR:N	2.83	0.46
2:T:167:THR:O	2:T:167:THR:HG22	2.15	0.46
2:T:208:GLU:C	2:T:209:TYR:HD2	2.23	0.46
4:V:180:LEU:O	4:V:181:ASN:C	2.59	0.46
1:A:133:GLN:CA	1:A:138:LEU:O	2.62	0.46
2:B:179:ILE:CG2	2:B:180:LEU:N	2.79	0.46
3:C:54:ILE:CG2	3:C:55:THR:N	2.79	0.46
4:D:159:CYS:CB	4:D:179:LYS:O	2.63	0.46
4:E:139:TRP:O	4:E:140:TYR:C	2.58	0.46
1:G:20:ASN:ND2	1:G:33:TYR:OH	2.49	0.46
3:I:105:TYR:CE2	3:I:152:PHE:CE1	3.04	0.46
4:J:162:TRP:O	4:J:176:ILE:HG23	2.15	0.46
4:K:34:TYR:CE2	4:K:140:TYR:CE2	3.04	0.46
1:M:134:THR:N	1:M:138:LEU:O	2.40	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:O:114:TYR:CD2	3:O:144:ASN:HB3	2.51	0.46
4:P:75:THR:O	4:P:76:ALA:C	2.59	0.46
4:P:159:CYS:CB	4:P:179:LYS:O	2.63	0.46
1:S:73:VAL:CG1	1:S:74:GLY:N	2.79	0.46
2:T:170:ARG:C	2:T:172:ARG:N	2.67	0.46
2:T:181:GLN:HG3	2:T:199:LEU:HD23	1.97	0.46
4:W:190:ILE:HA	4:W:190:ILE:HD13	1.67	0.46
5:X:68:GLU:C	5:X:70:PHE:N	2.74	0.46
1:A:194:PRO:HG3	2:B:67:GLN:HA	1.98	0.46
2:H:70:ILE:HG22	2:H:74:HIS:HD2	1.81	0.46
2:H:268:ILE:O	2:H:268:ILE:HG22	2.16	0.46
2:N:169:MET:HB3	2:N:174:LEU:CD1	2.46	0.46
2:N:208:GLU:C	2:N:209:TYR:HD2	2.24	0.46
3:O:129:GLU:C	3:O:131:GLU:H	2.24	0.46
1:S:129:MET:SD	1:S:131:ILE:HD11	2.57	0.46
1:S:212:LYS:HA	1:S:215:VAL:HG22	1.98	0.46
2:T:179:ILE:CG2	2:T:180:LEU:N	2.79	0.46
2:T:237:ILE:HG22	2:T:250:VAL:HG21	1.96	0.46
3:U:110:ILE:HG22	3:U:145:PHE:CE1	2.51	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
4:V:159:CYS:CB	4:V:179:LYS:O	2.64	0.46
4:V:166:ASP:HB3	4:V:169:ARG:CG	2.46	0.46
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
4:D:179:LYS:C	4:D:181:ASN:H	2.24	0.45
4:E:49:PHE:HB2	4:E:137:SER:CB	2.46	0.45
5:F:53:ASP:C	5:F:55:LYS:N	2.73	0.45
1:G:212:LYS:HA	1:G:215:VAL:HG22	1.98	0.45
4:J:167:ILE:HG23	4:J:168:LEU:N	2.31	0.45
4:K:136:LYS:O	4:K:169:ARG:NH1	2.48	0.45
5:L:57:VAL:HG12	5:L:57:VAL:O	2.16	0.45
5:L:67:GLN:HA	5:L:67:GLN:OE1	2.16	0.45
1:M:12:SER:CB	5:R:10:LYS:HZ2	2.29	0.45
3:O:129:GLU:HB3	3:O:135:GLN:OE1	2.16	0.45
4:P:166:ASP:HB3	4:P:169:ARG:CG	2.46	0.45
4:Q:49:PHE:HB2	4:Q:137:SER:CB	2.46	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
4:V:96:LYS:NZ	4:V:100:ASN:ND2	2.63	0.45
4:W:68:ILE:HG21	4:W:154:MET:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:W:161:VAL:HA	4:W:177:LYS:O	2.16	0.45
1:A:212:LYS:O	1:A:215:VAL:CG2	2.64	0.45
3:C:11:ARG:NH1	3:C:125:PHE:CE1	2.77	0.45
4:E:124:LEU:C	4:E:124:LEU:CD2	2.89	0.45
4:E:158:ASP:O	4:E:181:ASN:HB2	2.16	0.45
1:G:35:ILE:O	1:G:38:SER:HB2	2.16	0.45
1:G:114:TRP:HH2	4:J:76:ALA:HA	1.81	0.45
1:G:124:THR:HG21	3:I:55:THR:HG21	1.98	0.45
2:H:208:GLU:C	2:H:209:TYR:HD2	2.23	0.45
3:I:141:THR:O	3:I:142:ASN:C	2.58	0.45
4:J:166:ASP:HB3	4:J:169:ARG:CG	2.46	0.45
4:K:158:ASP:O	4:K:181:ASN:HB2	2.16	0.45
1:M:11:LYS:HG3	1:M:136:THR:O	2.16	0.45
2:N:179:ILE:CG2	2:N:180:LEU:N	2.79	0.45
3:O:52:ARG:O	3:O:56:GLN:HG3	2.17	0.45
3:O:88:PHE:O	3:O:103:LEU:CD2	2.59	0.45
4:P:179:LYS:C	4:P:181:ASN:H	2.25	0.45
4:Q:31:THR:CG2	4:Q:127:PHE:CE2	2.99	0.45
4:Q:71:PHE:HE2	4:Q:94:ALA:HA	1.80	0.45
4:Q:190:ILE:HD13	4:Q:190:ILE:HA	1.67	0.45
5:R:53:ASP:C	5:R:55:LYS:N	2.73	0.45
5:R:88:TYR:HD1	5:R:96:PHE:HB2	1.80	0.45
2:T:175:LYS:HG2	2:T:176:ILE:H	1.80	0.45
2:T:200:VAL:HG12	2:T:210:MET:HG3	1.97	0.45
3:U:102:VAL:HG21	3:U:156:MET:SD	2.55	0.45
4:W:126:ASP:OD2	4:W:167:ILE:HD13	2.16	0.45
5:X:57:VAL:HG12	5:X:57:VAL:O	2.16	0.45
5:X:156:THR:HG23	5:X:159:GLU:OE1	2.16	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
1:G:122:LEU:HD23	1:G:122:LEU:C	2.41	0.45
3:I:119:LEU:N	3:I:119:LEU:CD2	2.61	0.45
4:J:47:ARG:C	4:J:49:PHE:H	2.25	0.45
4:J:96:LYS:NZ	4:J:100:ASN:HD21	2.13	0.45
4:K:65:CYS:O	4:K:68:ILE:HG22	2.17	0.45
5:L:12:LEU:HG	5:L:12:LEU:O	2.16	0.45
5:L:148:LEU:HD12	5:L:148:LEU:N	2.32	0.45
1:M:124:THR:HG21	3:O:55:THR:HG21	1.98	0.45
3:O:155:PRO:CG	3:O:156:MET:H	2.24	0.45
4:P:167:ILE:HG23	4:P:168:LEU:N	2.30	0.45
4:P:188:ILE:HD12	4:P:190:ILE:HD11	1.91	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:134:ALA:C	4:Q:136:LYS:N	2.74	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
4:W:34:TYR:CE2	4:W:140:TYR:CE2	3.04	0.45
2:B:247:PRO:HB2	2:B:271:ASP:OD1	2.16	0.45
3:C:124:ASP:OD2	3:C:140:ILE:HB	2.16	0.45
4:E:34:TYR:CE2	4:E:140:TYR:CE2	3.03	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
2:H:181:GLN:HG3	2:H:199:LEU:HD23	1.97	0.45
2:H:220:GLN:HG3	2:H:221:PHE:N	2.30	0.45
3:I:123:TYR:C	3:I:125:PHE:N	2.66	0.45
4:J:96:LYS:NZ	4:J:100:ASN:ND2	2.64	0.45
4:K:25:ILE:HG23	4:K:26:ASN:N	2.31	0.45
5:L:88:TYR:HD1	5:L:96:PHE:HB2	1.80	0.45
1:M:133:GLN:CA	1:M:138:LEU:O	2.62	0.45
1:M:190:VAL:HG12	1:M:191:MET:HE2	1.98	0.45
2:N:167:THR:HG22	2:N:167:THR:O	2.15	0.45
2:N:188:TRP:N	2:N:188:TRP:CD1	2.82	0.45
5:R:4:GLU:O	5:R:5:TYR:O	2.35	0.45
5:R:15:GLY:N	5:R:102:TRP:CZ3	2.85	0.45
2:T:246:PHE:N	2:T:246:PHE:CD1	2.84	0.45
3:U:114:TYR:N	3:U:114:TYR:HD1	2.08	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:W:134:ALA:C	4:W:136:LYS:N	2.73	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:A:200:MET:HE3	5:F:7:TYR:HA	1.97	0.45
1:A:212:LYS:HA	1:A:215:VAL:HG22	1.98	0.45
2:B:168:LYS:O	2:B:170:ARG:N	2.49	0.45
2:B:218:LEU:O	2:B:220:GLN:N	2.43	0.45
3:C:105:TYR:CE2	3:C:152:PHE:CZ	3.04	0.45
3:C:119:LEU:N	3:C:119:LEU:CD2	2.58	0.45
4:D:162:TRP:O	4:D:176:ILE:HG23	2.17	0.45
4:D:167:ILE:HG23	4:D:168:LEU:N	2.30	0.45
1:G:200:MET:HE3	5:L:7:TYR:HA	1.95	0.45
2:H:211:ILE:HG22	2:H:268:ILE:HD11	1.98	0.45
2:N:268:ILE:O	2:N:268:ILE:HG22	2.16	0.45
4:P:18:TRP:CD1	4:P:18:TRP:O	2.69	0.45
4:P:38:VAL:HG11	4:P:140:TYR:HE1	1.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:36:SER:O	4:Q:40:GLN:CB	2.63	0.45
4:Q:158:ASP:O	4:Q:181:ASN:HB2	2.16	0.45
1:S:38:SER:O	1:S:41:HIS:HB3	2.16	0.45
1:S:186:TYR:CE1	1:S:190:VAL:HG11	2.51	0.45
4:W:49:PHE:HB2	4:W:137:SER:CB	2.46	0.45
5:X:88:TYR:HE2	5:X:119:VAL:O	1.99	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
4:D:18:TRP:CD1	4:D:18:TRP:O	2.69	0.45
4:D:25:ILE:HG22	4:D:26:ASN:N	2.32	0.45
5:F:88:TYR:HD1	5:F:96:PHE:HB2	1.80	0.45
1:G:3:ILE:HG21	1:G:6:ILE:HG23	1.98	0.45
3:I:129:GLU:HB2	3:I:135:GLN:CD	2.41	0.45
4:J:75:THR:O	4:J:76:ALA:C	2.59	0.45
4:J:169:ARG:O	4:J:170:GLY:O	2.35	0.45
4:K:11:LYS:HA	4:K:92:LYS:HB3	1.98	0.45
5:L:88:TYR:HE2	5:L:119:VAL:O	2.00	0.45
1:M:50:LEU:HD11	3:O:44:LEU:HD12	1.99	0.45
4:P:25:ILE:HG22	4:P:26:ASN:N	2.32	0.45
4:Q:139:TRP:O	4:Q:140:TYR:C	2.59	0.45
3:U:21:TRP:HH2	3:U:155:PRO:O	2.00	0.45
3:U:107:TYR:O	3:U:111:TYR:HB3	2.16	0.45
3:U:114:TYR:HD2	3:U:144:ASN:HB2	1.82	0.45
4:V:75:THR:O	4:V:76:ALA:C	2.59	0.45
3:C:48:ILE:CG2	3:C:87:TRP:CD1	3.00	0.45
4:D:188:ILE:HD12	4:D:190:ILE:HD11	1.91	0.45
4:E:161:VAL:HA	4:E:177:LYS:O	2.17	0.45
5:F:88:TYR:HE2	5:F:119:VAL:O	1.99	0.45
3:I:124:ASP:OD2	3:I:140:ILE:HB	2.16	0.45
5:L:72:THR:HG23	5:L:73:ILE:N	2.31	0.45
1:M:104:ASP:HA	1:M:108:LYS:HZ3	1.82	0.45
1:M:117:SER:HB3	4:P:191:GLY:H	1.81	0.45
4:P:65:CYS:O	4:P:68:ILE:CD1	2.65	0.45
4:Q:116:SER:CB	4:Q:175:GLU:HG3	2.45	0.45
5:R:90:VAL:HG13	5:R:129:ARG:NH2	2.32	0.45
1:S:114:TRP:CH2	4:V:76:ALA:HA	2.52	0.45
3:U:121:SER:HA	3:U:122:PRO:HD2	1.80	0.45
4:V:179:LYS:C	4:V:181:ASN:H	2.25	0.45
4:W:16:GLU:HG2	4:W:20:ASN:ND2	2.31	0.45
4:W:26:ASN:HD22	4:W:26:ASN:C	2.24	0.45
2:B:188:TRP:N	2:B:188:TRP:CD1	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:88:PHE:O	3:C:103:LEU:CD2	2.60	0.45
3:C:141:THR:O	3:C:142:ASN:C	2.60	0.45
4:E:11:LYS:HA	4:E:92:LYS:HB3	1.99	0.45
4:E:25:ILE:HG23	4:E:26:ASN:N	2.31	0.45
2:H:170:ARG:C	2:H:172:ARG:N	2.67	0.45
2:H:254:ARG:HG3	2:H:264:THR:HG22	1.98	0.45
4:J:137:SER:N	4:J:169:ARG:HH12	2.14	0.45
4:K:124:LEU:C	4:K:124:LEU:CD2	2.90	0.45
1:M:200:MET:O	1:M:201:PRO:C	2.58	0.45
2:N:176:ILE:HG23	2:N:177:LEU:H	1.82	0.45
4:Q:68:ILE:HG21	4:Q:154:MET:CB	2.47	0.45
5:R:77:TYR:HD1	5:R:77:TYR:H	1.63	0.45
3:U:123:TYR:C	3:U:125:PHE:N	2.66	0.45
3:U:129:GLU:HB2	3:U:135:GLN:CD	2.42	0.45
3:U:129:GLU:C	3:U:131:GLU:H	2.25	0.45
3:U:131:GLU:HG3	3:U:135:GLN:HB3	1.99	0.45
4:W:139:TRP:O	4:W:140:TYR:C	2.58	0.45
1:A:18:GLN:NE2	1:A:18:GLN:O	2.50	0.45
1:A:75:MET:CE	1:A:105:ASP:CB	2.88	0.45
2:B:189:SER:HA	2:B:194:HIS:N	2.32	0.45
3:C:129:GLU:C	3:C:131:GLU:H	2.25	0.45
4:D:161:VAL:HA	4:D:177:LYS:O	2.17	0.45
4:D:180:LEU:O	4:D:181:ASN:C	2.60	0.45
4:E:41:LEU:HD22	4:E:55:HIS:CD2	2.52	0.45
4:E:176:ILE:HD13	4:E:176:ILE:N	2.31	0.45
5:F:137:LYS:O	5:F:141:ASP:OD2	2.35	0.45
1:G:132:TYR:HE2	1:G:180:ARG:HA	1.81	0.45
1:G:134:THR:OG1	1:G:138:LEU:HB2	2.17	0.45
2:H:188:TRP:N	2:H:188:TRP:CD1	2.83	0.45
3:I:114:TYR:N	3:I:114:TYR:HD1	2.08	0.45
3:I:129:GLU:C	3:I:131:GLU:H	2.25	0.45
4:J:179:LYS:C	4:J:181:ASN:H	2.25	0.45
5:L:156:THR:HG23	5:L:159:GLU:OE1	2.17	0.45
1:M:129:MET:HB2	1:M:143:ILE:CD1	2.46	0.45
1:M:186:TYR:CE1	1:M:190:VAL:HG11	2.52	0.45
3:O:105:TYR:CE2	3:O:152:PHE:CZ	3.04	0.45
4:P:38:VAL:HG11	4:P:140:TYR:CD1	2.51	0.45
4:Q:114:THR:OG1	4:Q:179:LYS:CB	2.62	0.45
3:U:48:ILE:CG2	3:U:87:TRP:CD1	3.00	0.45
4:V:13:MET:HE1	4:V:77:LEU:HD21	1.98	0.45
1:A:38:SER:CB	5:F:45:PHE:CE1	3.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:LEU:C	1:A:137:GLY:N	2.74	0.45
1:A:190:VAL:HG12	1:A:191:MET:HE2	1.99	0.45
4:E:66:ARG:O	4:E:69:GLU:HB2	2.17	0.45
2:H:200:VAL:HG12	2:H:210:MET:HG3	1.98	0.45
3:I:21:TRP:HH2	3:I:155:PRO:O	2.00	0.45
4:J:161:VAL:HA	4:J:177:LYS:O	2.17	0.45
4:K:31:THR:HG21	4:K:127:PHE:CZ	2.52	0.45
4:K:41:LEU:HD22	4:K:55:HIS:CD2	2.52	0.45
2:N:184:HIS:CB	2:N:211:ILE:HD13	2.47	0.45
2:N:218:LEU:HB3	2:N:219:THR:H	1.66	0.45
2:N:231:TYR:CD2	2:N:234:CYS:SG	3.06	0.45
3:O:82:THR:HB	3:O:85:GLY:N	2.32	0.45
4:Q:124:LEU:HD23	4:Q:125:ALA:HB2	1.98	0.45
5:R:13:LEU:HD21	5:R:25:LEU:HD11	1.99	0.45
5:R:148:LEU:N	5:R:148:LEU:HD12	2.32	0.45
1:S:178:PHE:CD2	1:S:179:LEU:HD23	2.48	0.45
2:T:169:MET:HB3	2:T:174:LEU:CD1	2.47	0.45
3:U:63:VAL:O	3:U:64:LYS:HB2	2.17	0.45
4:W:124:LEU:HD23	4:W:125:ALA:HB2	1.98	0.45
1:A:114:TRP:CH2	4:D:76:ALA:HA	2.52	0.44
1:A:196:TYR:O	4:D:66:ARG:NH2	2.49	0.44
3:C:72:THR:HG22	3:C:75:TYR:H	1.81	0.44
3:C:114:TYR:CD2	3:C:144:ASN:HB3	2.52	0.44
4:D:67:LEU:HD11	4:D:98:PHE:CD2	2.52	0.44
4:D:96:LYS:NZ	4:D:100:ASN:ND2	2.65	0.44
3:I:114:TYR:HD2	3:I:144:ASN:HB2	1.82	0.44
1:M:114:TRP:CH2	4:P:76:ALA:HA	2.52	0.44
1:M:196:TYR:O	4:P:66:ARG:NH2	2.49	0.44
1:M:197:SER:O	1:M:198:MET:O	2.34	0.44
2:N:188:TRP:CH2	2:N:266:TYR:CE1	2.83	0.44
3:O:99:TYR:HD1	3:O:99:TYR:H	1.65	0.44
4:Q:66:ARG:O	4:Q:69:GLU:HB2	2.17	0.44
1:S:12:SER:CB	5:X:10:LYS:HZ2	2.30	0.44
1:S:104:ASP:HA	1:S:108:LYS:HZ3	1.82	0.44
3:U:99:TYR:HD1	3:U:99:TYR:H	1.65	0.44
3:U:140:ILE:O	3:U:140:ILE:CG2	2.63	0.44
4:W:18:TRP:HE1	4:W:100:ASN:HB2	1.82	0.44
5:X:12:LEU:O	5:X:12:LEU:HG	2.16	0.44
5:X:42:GLY:C	5:X:43:VAL:HG13	2.43	0.44
1:A:50:LEU:HD22	3:C:43:LEU:CD1	2.47	0.44
2:B:67:GLN:NE2	2:B:68:GLU:HB2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:181:GLN:HG3	2:B:199:LEU:HD23	1.98	0.44
3:C:129:GLU:HB2	3:C:135:GLN:CD	2.41	0.44
4:D:96:LYS:NZ	4:D:100:ASN:HD21	2.14	0.44
1:G:18:GLN:O	1:G:18:GLN:NE2	2.49	0.44
2:H:87:LEU:O	2:H:87:LEU:HD12	2.16	0.44
3:I:54:ILE:CG2	3:I:55:THR:N	2.80	0.44
3:I:67:ILE:HD12	3:I:67:ILE:N	2.32	0.44
4:K:16:GLU:HG2	4:K:20:ASN:HD22	1.81	0.44
4:K:31:THR:CG2	4:K:127:PHE:CE2	3.00	0.44
4:K:75:THR:CG2	4:K:93:CYS:SG	3.05	0.44
1:M:73:VAL:CG1	1:M:74:GLY:N	2.80	0.44
1:M:135:LEU:C	1:M:137:GLY:N	2.75	0.44
2:N:189:SER:HA	2:N:194:HIS:N	2.33	0.44
4:P:115:PHE:CE2	4:P:178:VAL:HG21	2.53	0.44
5:R:69:ARG:O	5:R:72:THR:HG22	2.17	0.44
1:S:124:THR:HG21	3:U:55:THR:HG21	1.98	0.44
1:S:134:THR:OG1	1:S:138:LEU:HB2	2.17	0.44
4:W:61:TYR:HD2	4:W:61:TYR:O	2.00	0.44
4:W:114:THR:OG1	4:W:179:LYS:CB	2.65	0.44
5:X:15:GLY:N	5:X:102:TRP:CZ3	2.85	0.44
1:A:12:SER:HB3	5:F:10:LYS:HZ1	1.82	0.44
2:B:188:TRP:CH2	2:B:266:TYR:CE1	2.83	0.44
4:D:115:PHE:CE2	4:D:178:VAL:HG21	2.53	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:K:131:PRO:C	4:K:133:ASP:N	2.76	0.44
5:L:51:GLU:OE1	5:L:56:THR:HA	2.17	0.44
1:M:212:LYS:C	1:M:215:VAL:HG22	2.43	0.44
2:N:67:GLN:NE2	2:N:68:GLU:HB2	2.32	0.44
3:O:48:ILE:CG2	3:O:87:TRP:CD1	3.00	0.44
3:O:129:GLU:HB2	3:O:135:GLN:CD	2.41	0.44
4:Q:16:GLU:HG2	4:Q:20:ASN:HD22	1.82	0.44
5:R:42:GLY:C	5:R:43:VAL:HG13	2.42	0.44
4:W:25:ILE:HG23	4:W:26:ASN:N	2.32	0.44
4:W:71:PHE:HE2	4:W:94:ALA:HA	1.82	0.44
5:X:4:GLU:O	5:X:5:TYR:O	2.35	0.44
5:X:149:GLU:HG2	5:X:150:THR:N	2.33	0.44
1:A:104:ASP:HA	1:A:108:LYS:HZ3	1.82	0.44
1:A:186:TYR:CD1	1:A:190:VAL:HG21	2.53	0.44
2:B:56:GLU:HB3	4:D:25:ILE:O	2.17	0.44
4:E:31:THR:HG21	4:E:127:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:117:LEU:HB2	4:E:176:ILE:O	2.16	0.44
1:G:13:GLY:HA3	1:G:41:HIS:CD2	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
1:M:108:LYS:C	1:M:109:GLU:HG3	2.42	0.44
1:M:132:TYR:HE2	1:M:180:ARG:HA	1.81	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:P:155:VAL:C	4:P:156:GLN:NE2	2.75	0.44
4:Q:11:LYS:HA	4:Q:92:LYS:HB3	1.99	0.44
4:Q:25:ILE:HG23	4:Q:26:ASN:N	2.32	0.44
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
5:F:77:TYR:HD1	5:F:77:TYR:H	1.64	0.44
5:F:156:THR:HG23	5:F:159:GLU:OE1	2.17	0.44
1:G:196:TYR:O	4:J:66:ARG:NH2	2.49	0.44
2:H:189:SER:HA	2:H:194:HIS:N	2.33	0.44
3:I:72:THR:HG22	3:I:75:TYR:H	1.83	0.44
4:K:167:ILE:H	4:K:167:ILE:HD12	1.82	0.44
2:N:231:TYR:HE2	2:N:251:THR:CA	2.29	0.44
3:O:54:ILE:CG2	3:O:55:THR:N	2.80	0.44
3:O:131:GLU:HG3	3:O:135:GLN:HB3	2.00	0.44
4:P:47:ARG:C	4:P:49:PHE:H	2.25	0.44
4:P:118:ILE:CA	4:P:175:GLU:HB3	2.46	0.44
4:Q:176:ILE:HD13	4:Q:176:ILE:N	2.31	0.44
5:R:88:TYR:HE2	5:R:119:VAL:O	2.00	0.44
1:S:108:LYS:C	1:S:109:GLU:HG3	2.43	0.44
1:S:196:TYR:O	4:V:66:ARG:NH2	2.50	0.44
2:T:265:VAL:O	2:T:265:VAL:HG13	2.17	0.44
3:U:10:ASP:N	3:U:14:ASN:O	2.50	0.44
3:C:52:ARG:O	3:C:56:GLN:HG3	2.18	0.44
4:D:101:ILE:HG22	4:D:121:GLU:HB2	2.00	0.44
4:D:118:ILE:CA	4:D:175:GLU:HB3	2.46	0.44
4:E:26:ASN:HD22	4:E:26:ASN:C	2.25	0.44
4:E:136:LYS:O	4:E:169:ARG:NH1	2.51	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
1:M:12:SER:C	5:R:10:LYS:NZ	2.76	0.44
3:O:82:THR:HB	3:O:85:GLY:H	1.83	0.44
4:P:161:VAL:HA	4:P:177:LYS:O	2.18	0.44
4:P:186:ASP:HB2	5:R:79:ARG:NH2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:117:SER:HB3	4:V:191:GLY:H	1.83	0.44
1:S:137:GLY:HA2	4:V:188:ILE:CG2	2.31	0.44
2:T:97:ARG:HD3	2:T:100:GLU:OE1	2.18	0.44
2:T:189:SER:HA	2:T:194:HIS:N	2.33	0.44
3:U:113:LYS:HB2	3:U:114:TYR:CD1	2.53	0.44
4:W:124:LEU:C	4:W:124:LEU:CD2	2.90	0.44
5:X:77:TYR:HD1	5:X:77:TYR:H	1.64	0.44
1:A:8:VAL:HG13	1:A:140:PHE:CD2	2.52	0.44
1:A:50:LEU:HD13	3:C:43:LEU:CD1	2.47	0.44
2:B:169:MET:HB3	2:B:174:LEU:HD12	1.98	0.44
4:D:38:VAL:HG11	4:D:140:TYR:HE1	1.74	0.44
4:D:110:HIS:C	4:D:112:LYS:N	2.76	0.44
5:F:90:VAL:HG13	5:F:129:ARG:NH2	2.33	0.44
1:G:38:SER:O	1:G:41:HIS:HB3	2.17	0.44
1:G:129:MET:HB2	1:G:143:ILE:CD1	2.47	0.44
3:I:48:ILE:CG2	3:I:87:TRP:CD1	3.00	0.44
3:I:83:ALA:HB3	4:K:72:LEU:CD1	2.46	0.44
4:J:101:ILE:HD12	4:J:101:ILE:O	2.18	0.44
4:J:115:PHE:CE2	4:J:178:VAL:HG21	2.53	0.44
4:J:129:GLU:O	4:J:131:PRO:CD	2.66	0.44
5:L:90:VAL:HG13	5:L:129:ARG:NH2	2.33	0.44
5:L:149:GLU:HG2	5:L:150:THR:N	2.33	0.44
1:M:3:ILE:HG21	1:M:6:ILE:HG23	1.99	0.44
1:M:75:MET:CE	1:M:105:ASP:CB	2.89	0.44
3:O:10:ASP:N	3:O:14:ASN:O	2.51	0.44
3:O:72:THR:HG22	3:O:75:TYR:H	1.82	0.44
3:O:114:TYR:HD2	3:O:144:ASN:HB2	1.82	0.44
3:O:120:LEU:HD21	4:W:38:VAL:HG12	1.99	0.44
4:Q:10:LEU:HD21	4:Q:89:VAL:HA	2.00	0.44
4:Q:34:TYR:CE2	4:Q:140:TYR:CE2	3.05	0.44
4:Q:159:CYS:CB	4:Q:179:LYS:O	2.63	0.44
5:R:117:LEU:HD23	5:R:118:LEU:C	2.43	0.44
5:R:137:LYS:O	5:R:141:ASP:OD2	2.36	0.44
1:S:50:LEU:HD13	3:U:43:LEU:CD1	2.46	0.44
2:T:188:TRP:CD1	2:T:188:TRP:N	2.84	0.44
4:V:101:ILE:HG22	4:V:121:GLU:HB2	2.00	0.44
4:V:156:GLN:HA	4:V:184:LEU:CD1	2.39	0.44
4:V:161:VAL:HA	4:V:177:LYS:O	2.18	0.44
4:V:186:ASP:HB2	5:X:79:ARG:NH2	2.32	0.44
4:W:66:ARG:O	4:W:69:GLU:HB2	2.18	0.44
1:A:3:ILE:HG21	1:A:6:ILE:HG23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:211:ILE:HG21	2:B:268:ILE:HD11	2.00	0.44
3:C:99:TYR:HD1	3:C:99:TYR:H	1.66	0.44
4:E:131:PRO:C	4:E:133:ASP:N	2.76	0.44
4:E:167:ILE:HD12	4:E:167:ILE:H	1.83	0.44
5:F:117:LEU:HD23	5:F:117:LEU:C	2.42	0.44
1:G:73:VAL:CG1	1:G:74:GLY:N	2.81	0.44
3:I:13:CYS:HB3	4:K:188:ILE:HD12	1.99	0.44
4:J:18:TRP:CD1	4:J:18:TRP:O	2.70	0.44
4:J:25:ILE:HG22	4:J:26:ASN:N	2.32	0.44
4:J:77:LEU:HB3	4:J:78:PRO:HD2	2.00	0.44
4:K:49:PHE:CB	4:K:137:SER:HB3	2.47	0.44
2:N:70:ILE:HG22	2:N:74:HIS:HD2	1.79	0.44
2:N:175:LYS:CG	2:N:176:ILE:N	2.81	0.44
1:S:50:LEU:HD22	3:U:43:LEU:CD1	2.48	0.44
1:S:114:TRP:HH2	4:V:76:ALA:HA	1.83	0.44
1:S:198:MET:O	1:S:200:MET:N	2.51	0.44
1:S:200:MET:HE3	5:X:7:TYR:HA	1.96	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
3:U:83:ALA:HB3	4:W:72:LEU:CD1	2.46	0.44
4:V:110:HIS:C	4:V:112:LYS:N	2.76	0.44
4:W:116:SER:CB	4:W:175:GLU:HG3	2.45	0.44
4:W:155:VAL:O	4:W:155:VAL:CG1	2.64	0.44
5:X:117:LEU:HD23	5:X:118:LEU:C	2.43	0.44
1:A:108:LYS:C	1:A:109:GLU:HG3	2.43	0.44
1:A:117:SER:HB3	4:D:191:GLY:N	2.33	0.44
1:A:122:LEU:HD23	1:A:122:LEU:C	2.43	0.44
1:A:133:GLN:O	1:A:133:GLN:HG3	2.18	0.44
1:A:190:VAL:CG1	1:A:196:TYR:CE2	3.01	0.44
2:B:218:LEU:HB3	2:B:219:THR:H	1.67	0.44
2:B:265:VAL:HG13	2:B:265:VAL:O	2.18	0.44
4:D:169:ARG:O	4:D:170:GLY:O	2.36	0.44
4:E:99:LEU:HB2	4:E:101:ILE:CG2	2.45	0.44
4:E:124:LEU:HD23	4:E:125:ALA:CB	2.48	0.44
4:E:159:CYS:CB	4:E:179:LYS:O	2.63	0.44
3:I:110:ILE:HG22	3:I:145:PHE:CE1	2.52	0.44
3:I:140:ILE:O	3:I:140:ILE:CG2	2.63	0.44
4:J:110:HIS:C	4:J:112:LYS:N	2.76	0.44
4:J:155:VAL:O	4:J:155:VAL:CG1	2.66	0.44
4:J:156:GLN:HA	4:J:184:LEU:CD1	2.40	0.44
5:L:66:GLY:O	5:L:70:PHE:HE1	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:87:LEU:O	2:N:87:LEU:HD12	2.18	0.44
2:N:175:LYS:HG2	2:N:176:ILE:H	1.82	0.44
4:P:110:HIS:C	4:P:112:LYS:N	2.76	0.44
4:Q:30:PHE:HA	4:W:30:PHE:CD1	2.53	0.44
4:Q:31:THR:HG21	4:Q:127:PHE:CZ	2.52	0.44
3:U:3:ILE:CG2	3:U:99:TYR:CE2	3.00	0.44
3:U:16:ILE:O	3:U:140:ILE:HG22	2.18	0.44
3:U:82:THR:HB	3:U:85:GLY:H	1.83	0.44
1:A:23:ASN:HB3	1:A:25:GLU:HG2	2.00	0.43
1:A:137:GLY:HA2	4:D:188:ILE:CG2	2.28	0.43
3:C:72:THR:HG23	3:C:74:LYS:H	1.82	0.43
4:E:16:GLU:HG2	4:E:20:ASN:ND2	2.33	0.43
4:E:64:GLY:HA2	4:E:147:VAL:HG13	2.00	0.43
5:F:117:LEU:HD23	5:F:118:LEU:C	2.43	0.43
1:G:107:PHE:CD2	1:G:180:ARG:NH2	2.73	0.43
2:H:247:PRO:HB2	2:H:271:ASP:OD1	2.18	0.43
3:I:88:PHE:CZ	3:I:107:TYR:HB2	2.53	0.43
4:J:101:ILE:HG22	4:J:121:GLU:HB2	2.00	0.43
4:K:124:LEU:HD23	4:K:125:ALA:HB2	1.99	0.43
4:K:134:ALA:O	4:K:137:SER:N	2.46	0.43
4:K:159:CYS:CB	4:K:179:LYS:O	2.62	0.43
5:L:13:LEU:HD21	5:L:25:LEU:CD2	2.48	0.43
3:O:3:ILE:CG2	3:O:99:TYR:CE2	3.01	0.43
3:O:72:THR:HG23	3:O:74:LYS:H	1.82	0.43
4:Q:65:CYS:O	4:Q:68:ILE:HG22	2.17	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
1:S:122:LEU:C	1:S:122:LEU:HD23	2.43	0.43
2:T:168:LYS:O	2:T:170:ARG:N	2.51	0.43
4:V:28:GLU:O	4:V:31:THR:HG22	2.17	0.43
4:W:45:TYR:O	4:W:46:GLU:C	2.61	0.43
2:B:254:ARG:HG3	2:B:264:THR:HG22	1.98	0.43
4:D:47:ARG:C	4:D:49:PHE:H	2.26	0.43
4:D:143:ILE:HG23	4:D:144:LEU:N	2.33	0.43
1:G:12:SER:C	5:L:10:LYS:NZ	2.76	0.43
1:G:50:LEU:HD22	3:I:43:LEU:CD1	2.48	0.43
1:G:108:LYS:C	1:G:109:GLU:HG3	2.43	0.43
1:G:129:MET:CE	1:G:143:ILE:HD11	2.48	0.43
1:G:186:TYR:CD1	1:G:190:VAL:HG21	2.53	0.43
2:H:237:ILE:HG22	2:H:250:VAL:HG21	1.98	0.43
4:J:143:ILE:HG23	4:J:144:LEU:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:20:ASN:ND2	1:M:33:TYR:OH	2.47	0.43
2:N:200:VAL:HG12	2:N:200:VAL:O	2.15	0.43
4:Q:41:LEU:HD22	4:Q:55:HIS:CD2	2.53	0.43
5:R:28:PHE:HD2	5:R:48:LYS:HZ3	1.64	0.43
5:R:169:ILE:O	5:R:172:SER:HB2	2.18	0.43
4:V:77:LEU:HB3	4:V:78:PRO:HD2	2.01	0.43
4:V:118:ILE:CA	4:V:175:GLU:HB3	2.46	0.43
4:V:162:TRP:O	4:V:176:ILE:HG23	2.18	0.43
4:V:169:ARG:O	4:V:170:GLY:O	2.36	0.43
4:V:180:LEU:HD12	4:V:180:LEU:N	2.13	0.43
4:W:159:CYS:CB	4:W:179:LYS:O	2.62	0.43
5:X:148:LEU:N	5:X:148:LEU:HD12	2.33	0.43
1:G:75:MET:CE	1:G:105:ASP:CB	2.89	0.43
1:G:115:ASN:O	1:G:115:ASN:CG	2.61	0.43
3:I:154:ALA:HB3	3:I:155:PRO:CD	2.48	0.43
4:K:61:TYR:HD2	4:K:61:TYR:O	2.01	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
5:R:12:LEU:HG	5:R:12:LEU:O	2.18	0.43
1:S:197:SER:O	1:S:198:MET:O	2.36	0.43
2:T:87:LEU:O	2:T:87:LEU:HD12	2.17	0.43
3:U:82:THR:HB	3:U:85:GLY:N	2.32	0.43
4:V:185:LYS:C	4:V:185:LYS:CD	2.92	0.43
4:W:131:PRO:C	4:W:133:ASP:N	2.77	0.43
4:W:136:LYS:O	4:W:169:ARG:NH1	2.51	0.43
2:B:70:ILE:HG22	2:B:74:HIS:HD2	1.79	0.43
3:C:3:ILE:CG2	3:C:99:TYR:CE2	3.01	0.43
3:C:72:THR:HG21	3:C:75:TYR:CE2	2.54	0.43
3:C:82:THR:HB	3:C:85:GLY:N	2.33	0.43
5:F:42:GLY:C	5:F:43:VAL:HG13	2.43	0.43
1:G:135:LEU:C	1:G:137:GLY:N	2.75	0.43
4:K:26:ASN:HD22	4:K:26:ASN:C	2.25	0.43
5:L:77:TYR:HD1	5:L:77:TYR:H	1.65	0.43
1:M:35:ILE:O	1:M:38:SER:HB2	2.18	0.43
1:M:133:GLN:O	1:M:133:GLN:HG3	2.19	0.43
4:P:169:ARG:O	4:P:170:GLY:O	2.36	0.43
4:Q:99:LEU:HB2	4:Q:101:ILE:CG2	2.46	0.43
4:Q:131:PRO:C	4:Q:133:ASP:N	2.76	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:123:PRO:C	4:V:125:ALA:N	2.77	0.43
4:W:104:ASN:O	4:W:105:ILE:HD13	2.18	0.43
5:X:90:VAL:HG13	5:X:129:ARG:NH2	2.34	0.43
2:B:64:PHE:CD1	4:D:67:LEU:HD13	2.53	0.43
2:B:97:ARG:HD3	2:B:100:GLU:OE1	2.18	0.43
4:E:18:TRP:HE1	4:E:100:ASN:HB2	1.82	0.43
4:E:116:SER:CB	4:E:175:GLU:HG3	2.47	0.43
2:H:56:GLU:HB3	4:J:25:ILE:O	2.19	0.43
3:I:16:ILE:O	3:I:140:ILE:HG22	2.18	0.43
3:I:88:PHE:O	3:I:103:LEU:CD2	2.60	0.43
4:J:188:ILE:HA	4:J:189:PRO:HD3	1.76	0.43
5:L:143:ASN:O	5:L:144:LYS:HB2	2.17	0.43
4:P:123:PRO:C	4:P:125:ALA:H	2.27	0.43
4:Q:64:GLY:HA2	4:Q:147:VAL:HG13	2.01	0.43
5:R:156:THR:HG23	5:R:159:GLU:OE1	2.18	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
4:V:67:LEU:HD11	4:V:98:PHE:CD2	2.53	0.43
4:W:95:PHE:CD1	4:W:103:PRO:HD3	2.54	0.43
4:W:117:LEU:HB2	4:W:176:ILE:O	2.18	0.43
4:W:124:LEU:HD23	4:W:125:ALA:CB	2.48	0.43
1:A:200:MET:O	1:A:201:PRO:C	2.59	0.43
2:B:184:HIS:CB	2:B:211:ILE:HD13	2.48	0.43
3:C:63:VAL:O	3:C:64:LYS:HB2	2.17	0.43
4:D:17:ILE:HD13	4:D:17:ILE:HA	1.81	0.43
4:D:130:LEU:HD23	4:D:168:LEU:HB3	2.00	0.43
4:E:41:LEU:CB	4:E:52:VAL:HG13	2.49	0.43
4:K:155:VAL:O	4:K:155:VAL:CG1	2.64	0.43
1:M:8:VAL:HG13	1:M:140:PHE:CD2	2.53	0.43
1:M:29:ASN:H	1:M:32:GLU:CD	2.26	0.43
1:M:75:MET:HA	1:M:217:ASN:CB	2.48	0.43
2:N:218:LEU:O	2:N:220:GLN:N	2.45	0.43
3:O:82:THR:HG22	3:O:83:ALA:H	1.83	0.43
4:P:137:SER:N	4:P:169:ARG:HH12	2.16	0.43
4:P:162:TRP:O	4:P:176:ILE:HG23	2.19	0.43
5:R:117:LEU:HD23	5:R:117:LEU:C	2.43	0.43
1:S:8:VAL:HG13	1:S:140:PHE:CD2	2.54	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:T:247:PRO:HB2	2:T:271:ASP:OD1	2.18	0.43
4:W:105:ILE:HD12	4:W:115:PHE:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:THR:HG21	3:C:55:THR:HG21	2.01	0.43
2:B:231:TYR:CD2	2:B:234:CYS:SG	3.07	0.43
4:D:38:VAL:HG11	4:D:140:TYR:CD1	2.53	0.43
4:D:123:PRO:C	4:D:125:ALA:H	2.27	0.43
4:D:155:VAL:C	4:D:156:GLN:NE2	2.76	0.43
4:D:156:GLN:HA	4:D:184:LEU:CD1	2.40	0.43
4:E:178:VAL:O	4:E:178:VAL:HG12	2.18	0.43
1:G:50:LEU:HD13	3:I:43:LEU:CD1	2.46	0.43
1:G:181:LYS:HD3	1:G:214:MET:CE	2.49	0.43
2:H:67:GLN:NE2	2:H:68:GLU:HB2	2.34	0.43
4:J:38:VAL:HG11	4:J:140:TYR:CD1	2.52	0.43
4:K:64:GLY:HA2	4:K:147:VAL:HG13	2.01	0.43
1:M:38:SER:CB	5:R:45:PHE:CE1	3.02	0.43
2:N:84:GLU:OE1	2:N:231:TYR:CE1	2.71	0.43
4:P:22:THR:O	4:P:22:THR:HG22	2.18	0.43
1:S:190:VAL:HG12	1:S:191:MET:HE2	2.01	0.43
2:T:72:GLN:HE21	2:T:72:GLN:HB3	1.56	0.43
2:T:175:LYS:CG	2:T:176:ILE:H	2.32	0.43
3:U:72:THR:HG21	3:U:75:TYR:CE2	2.52	0.43
3:U:88:PHE:O	3:U:103:LEU:CD2	2.60	0.43
3:U:105:TYR:CE2	3:U:152:PHE:CE1	3.06	0.43
4:V:185:LYS:HD2	4:V:185:LYS:O	2.18	0.43
5:X:72:THR:HG23	5:X:73:ILE:N	2.33	0.43
2:B:84:GLU:OE1	2:B:231:TYR:CE1	2.71	0.43
3:C:82:THR:HB	3:C:85:GLY:H	1.84	0.43
1:G:7:LEU:HD12	1:G:141:VAL:CB	2.45	0.43
1:G:190:VAL:HG12	1:G:191:MET:HE2	2.01	0.43
2:H:185:GLY:HA2	2:H:195:VAL:HG13	2.00	0.43
3:I:63:VAL:O	3:I:64:LYS:HB2	2.19	0.43
4:K:95:PHE:CD1	4:K:103:PRO:HD3	2.54	0.43
1:M:50:LEU:HD22	3:O:43:LEU:CD1	2.49	0.43
2:N:99:LEU:HD12	2:N:99:LEU:N	2.31	0.43
2:N:211:ILE:HG22	2:N:268:ILE:HD11	1.99	0.43
3:O:21:TRP:HH2	3:O:155:PRO:O	2.00	0.43
3:O:63:VAL:O	3:O:64:LYS:HB2	2.18	0.43
4:P:67:LEU:HD11	4:P:98:PHE:CD2	2.52	0.43
1:S:29:ASN:H	1:S:32:GLU:CD	2.27	0.43
1:S:50:LEU:CB	3:U:43:LEU:HD11	2.42	0.43
1:S:115:ASN:CG	1:S:115:ASN:O	2.62	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:218:LEU:HD21	2:T:232:PHE:HE2	1.83	0.43
4:V:25:ILE:HG22	4:V:26:ASN:N	2.32	0.43
4:V:77:LEU:HD22	4:V:78:PRO:CD	2.47	0.43
4:V:130:LEU:HD23	4:V:168:LEU:HB3	2.00	0.43
4:W:167:ILE:H	4:W:167:ILE:HD12	1.83	0.43
1:A:132:TYR:HE2	1:A:180:ARG:HA	1.83	0.43
2:H:231:TYR:HE2	2:H:252:ALA:H	1.66	0.43
2:H:243:ASN:C	2:H:245:GLY:N	2.76	0.43
4:J:77:LEU:HD22	4:J:78:PRO:CD	2.46	0.43
4:K:105:ILE:HD12	4:K:115:PHE:CE1	2.54	0.43
5:L:28:PHE:O	5:L:28:PHE:CD1	2.72	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:218:LEU:HD21	2:N:232:PHE:HE2	1.84	0.43
2:N:247:PRO:O	2:N:271:ASP:OD2	2.37	0.43
4:P:17:ILE:HD13	4:P:17:ILE:HA	1.81	0.43
4:P:129:GLU:OE1	4:P:129:GLU:HA	2.19	0.43
4:P:145:CYS:SG	4:P:176:ILE:HD13	2.59	0.43
4:Q:41:LEU:CB	4:Q:52:VAL:HG13	2.49	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
5:R:43:VAL:O	5:R:43:VAL:CG2	2.67	0.43
5:R:51:GLU:OE1	5:R:56:THR:HA	2.19	0.43
4:W:124:LEU:HD13	4:W:141:SER:HB3	2.01	0.43
1:A:114:TRP:HH2	4:D:76:ALA:HA	1.83	0.43
1:A:197:SER:O	1:A:198:MET:O	2.36	0.43
4:D:28:GLU:O	4:D:31:THR:HG22	2.18	0.43
4:E:61:TYR:HD2	4:E:61:TYR:O	2.02	0.43
1:G:75:MET:HA	1:G:217:ASN:CB	2.48	0.43
1:G:181:LYS:HD3	1:G:214:MET:HE1	2.00	0.43
1:G:190:VAL:CG1	1:G:196:TYR:CE2	3.02	0.43
4:J:13:MET:HE1	4:J:77:LEU:HD21	2.00	0.43
4:J:123:PRO:C	4:J:125:ALA:N	2.77	0.43
4:J:185:LYS:C	4:J:185:LYS:CD	2.92	0.43
4:K:10:LEU:HD21	4:K:89:VAL:HA	2.00	0.43
5:L:117:LEU:HD23	5:L:118:LEU:C	2.44	0.43
2:N:74:HIS:CE1	2:N:83:PHE:CE2	3.07	0.43
3:O:72:THR:HG21	3:O:75:TYR:CD2	2.54	0.43
3:O:105:TYR:HE1	3:O:109:HIS:HD1	1.53	0.43
4:P:101:ILE:HD12	4:P:101:ILE:O	2.19	0.43
4:P:143:ILE:HG23	4:P:144:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:64:PHE:CD1	4:V:67:LEU:HD13	2.54	0.43
2:T:243:ASN:C	2:T:245:GLY:N	2.76	0.43
4:V:38:VAL:HG11	4:V:140:TYR:CD1	2.52	0.43
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
4:W:65:CYS:O	4:W:68:ILE:HG22	2.19	0.43
1:A:129:MET:HB2	1:A:143:ILE:CD1	2.48	0.42
2:B:211:ILE:HG22	2:B:268:ILE:HD11	2.00	0.42
2:B:250:VAL:HG12	2:B:266:TYR:HB3	2.00	0.42
3:C:16:ILE:O	3:C:140:ILE:HG22	2.19	0.42
3:C:43:LEU:C	3:C:43:LEU:CD1	2.92	0.42
4:D:186:ASP:HB2	5:F:79:ARG:NH2	2.33	0.42
4:E:105:ILE:HD12	4:E:115:PHE:CE1	2.53	0.42
1:G:23:ASN:HB3	1:G:25:GLU:HG2	2.00	0.42
1:G:129:MET:HE2	1:G:143:ILE:HD11	2.00	0.42
1:G:198:MET:O	1:G:200:MET:N	2.52	0.42
2:H:218:LEU:HD21	2:H:232:PHE:HE2	1.84	0.42
3:I:72:THR:HG21	3:I:75:TYR:CE2	2.53	0.42
3:I:113:LYS:HB2	3:I:114:TYR:CD1	2.54	0.42
4:J:28:GLU:O	4:J:31:THR:HG22	2.18	0.42
4:K:36:SER:O	4:K:40:GLN:N	2.46	0.42
4:K:41:LEU:CB	4:K:52:VAL:HG13	2.49	0.42
5:L:62:TRP:N	5:L:62:TRP:CD1	2.87	0.42
1:M:122:LEU:HD23	1:M:122:LEU:C	2.44	0.42
2:N:97:ARG:HD3	2:N:100:GLU:OE1	2.18	0.42
4:P:100:ASN:HD22	4:P:100:ASN:C	2.27	0.42
5:R:149:GLU:HG2	5:R:150:THR:H	1.83	0.42
1:S:191:MET:HE2	1:S:191:MET:HA	2.01	0.42
3:U:107:TYR:HE2	4:W:73:ALA:CA	2.22	0.42
4:V:111:ASN:ND2	4:V:113:ASP:OD2	2.39	0.42
5:X:51:GLU:OE1	5:X:56:THR:HA	2.19	0.42
5:X:62:TRP:N	5:X:62:TRP:CD1	2.86	0.42
1:A:73:VAL:CG1	1:A:74:GLY:N	2.82	0.42
1:A:131:ILE:HG13	1:A:141:VAL:HG22	2.02	0.42
4:D:65:CYS:HA	4:D:154:MET:HG3	2.01	0.42
4:E:10:LEU:HD21	4:E:89:VAL:HA	2.01	0.42
4:E:49:PHE:CB	4:E:137:SER:HB3	2.49	0.42
4:E:95:PHE:CD1	4:E:103:PRO:HD3	2.54	0.42
4:E:134:ALA:O	4:E:137:SER:N	2.47	0.42
5:F:82:HIS:CB	5:F:169:ILE:HD13	2.49	0.42
1:G:104:ASP:HA	1:G:108:LYS:HZ3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:191:LEU:HD12	2:H:192:PHE:HE1	1.84	0.42
3:I:10:ASP:N	3:I:14:ASN:O	2.51	0.42
4:K:45:TYR:O	4:K:46:GLU:C	2.63	0.42
1:M:13:GLY:HA3	1:M:41:HIS:CD2	2.54	0.42
1:M:50:LEU:CD1	3:O:43:LEU:HD11	2.47	0.42
4:Q:26:ASN:HD22	4:Q:26:ASN:C	2.27	0.42
4:Q:154:MET:HE2	4:Q:154:MET:HA	2.00	0.42
1:S:3:ILE:HG21	1:S:6:ILE:HG23	2.01	0.42
1:S:12:SER:C	5:X:10:LYS:NZ	2.77	0.42
2:T:247:PRO:O	2:T:271:ASP:OD2	2.36	0.42
3:U:72:THR:HG21	3:U:75:TYR:CD2	2.54	0.42
4:V:143:ILE:HG23	4:V:144:LEU:N	2.33	0.42
4:W:34:TYR:OH	4:W:140:TYR:O	2.18	0.42
4:W:99:LEU:C	4:W:101:ILE:N	2.77	0.42
4:W:105:ILE:C	4:W:106:THR:CG2	2.93	0.42
5:X:119:VAL:HG12	5:X:120:GLY:N	2.34	0.42
1:A:38:SER:O	1:A:41:HIS:HB3	2.18	0.42
1:A:185:LEU:HD11	1:A:210:LYS:HD3	2.00	0.42
2:B:185:GLY:HA2	2:B:195:VAL:HG13	2.01	0.42
3:C:113:LYS:HB2	3:C:114:TYR:CD1	2.54	0.42
5:F:51:GLU:OE1	5:F:56:THR:HA	2.19	0.42
2:H:250:VAL:HG12	2:H:266:TYR:HB3	2.00	0.42
4:J:118:ILE:CA	4:J:175:GLU:HB3	2.47	0.42
4:J:125:ALA:HB2	4:J:140:TYR:CE2	2.54	0.42
2:N:247:PRO:HB2	2:N:271:ASP:OD1	2.19	0.42
3:O:98:SER:C	3:O:100:THR:N	2.77	0.42
4:P:28:GLU:O	4:P:31:THR:HG22	2.18	0.42
5:R:28:PHE:O	5:R:28:PHE:CD1	2.71	0.42
1:S:135:LEU:C	1:S:137:GLY:N	2.76	0.42
4:V:129:GLU:O	4:V:131:PRO:CD	2.67	0.42
4:V:155:VAL:O	4:V:155:VAL:CG1	2.68	0.42
4:W:10:LEU:HD21	4:W:89:VAL:HA	2.00	0.42
1:A:20:ASN:ND2	1:A:33:TYR:OH	2.48	0.42
1:A:29:ASN:H	1:A:32:GLU:CD	2.27	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:D:188:ILE:O	4:D:188:ILE:HG13	2.18	0.42
5:F:149:GLU:HG2	5:F:150:THR:H	1.84	0.42
3:I:114:TYR:HB3	3:I:142:ASN:OD1	2.19	0.42
4:J:33:THR:O	4:J:36:SER:HB3	2.19	0.42
4:K:104:ASN:O	4:K:105:ILE:HD13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:154:MET:HE2	4:K:154:MET:HA	2.00	0.42
1:M:148:MET:HE3	1:M:169:ASN:N	2.34	0.42
1:M:190:VAL:CG1	1:M:196:TYR:CE2	3.02	0.42
1:M:200:MET:HE1	5:R:7:TYR:CB	2.50	0.42
3:O:113:LYS:HB2	3:O:114:TYR:CD1	2.55	0.42
4:P:33:THR:O	4:P:36:SER:HB3	2.19	0.42
4:P:130:LEU:HD23	4:P:168:LEU:HB3	2.00	0.42
4:P:155:VAL:O	4:P:155:VAL:CG1	2.67	0.42
4:Q:94:ALA:CB	6:Q:194:PLM:H91	2.43	0.42
1:S:120:ARG:HD2	3:U:73:GLY:HA2	2.00	0.42
4:W:26:ASN:ND2	4:W:28:GLU:H	2.17	0.42
4:W:36:SER:O	4:W:40:GLN:CB	2.61	0.42
5:X:28:PHE:O	5:X:29:SER:C	2.63	0.42
5:X:169:ILE:O	5:X:172:SER:HB2	2.19	0.42
3:C:82:THR:HG22	3:C:83:ALA:H	1.83	0.42
1:G:117:SER:HB3	4:J:191:GLY:N	2.35	0.42
4:J:67:LEU:HD11	4:J:98:PHE:CD2	2.54	0.42
4:J:188:ILE:O	4:J:188:ILE:HG13	2.18	0.42
4:K:178:VAL:O	4:K:178:VAL:HG12	2.18	0.42
5:L:42:GLY:C	5:L:43:VAL:HG13	2.45	0.42
1:M:14:GLY:N	5:R:10:LYS:HZ3	2.17	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
4:P:123:PRO:C	4:P:125:ALA:N	2.76	0.42
4:Q:30:PHE:CD1	4:W:30:PHE:HA	2.54	0.42
1:S:29:ASN:O	1:S:32:GLU:HG3	2.18	0.42
4:V:79:ARG:O	4:V:80:CYS:C	2.62	0.42
5:X:149:GLU:HG2	5:X:150:THR:H	1.83	0.42
1:A:21:PHE:HZ	1:A:215:VAL:HG11	1.80	0.42
1:A:29:ASN:O	1:A:32:GLU:HG3	2.18	0.42
2:B:74:HIS:CE1	2:B:83:PHE:CE2	3.08	0.42
3:C:123:TYR:C	3:C:125:PHE:N	2.66	0.42
4:D:100:ASN:HD22	4:D:100:ASN:C	2.28	0.42
4:D:156:GLN:HB3	4:D:184:LEU:HB2	2.02	0.42
4:E:114:THR:OG1	4:E:179:LYS:CB	2.64	0.42
5:F:72:THR:HG23	5:F:73:ILE:N	2.34	0.42
1:G:9:ILE:HG12	1:G:37:ALA:HB1	2.00	0.42
2:H:167:THR:HG22	2:H:167:THR:O	2.18	0.42
3:I:133:ARG:H	3:I:133:ARG:CD	2.13	0.42
4:J:100:ASN:C	4:J:100:ASN:HD22	2.27	0.42
4:J:130:LEU:HD23	4:J:168:LEU:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:66:ARG:O	4:K:69:GLU:HB2	2.19	0.42
4:K:99:LEU:C	4:K:101:ILE:N	2.78	0.42
4:K:124:LEU:HD13	4:K:141:SER:HB3	2.02	0.42
2:N:241:LEU:HD12	2:N:248:CYS:CB	2.49	0.42
3:O:119:LEU:N	3:O:119:LEU:CD2	2.61	0.42
4:P:185:LYS:C	4:P:185:LYS:CD	2.92	0.42
5:R:13:LEU:HD21	5:R:25:LEU:CD2	2.49	0.42
5:R:43:VAL:CG2	5:R:77:TYR:HE2	2.32	0.42
5:R:82:HIS:CB	5:R:169:ILE:HD13	2.50	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
1:S:23:ASN:HB3	1:S:25:GLU:HG2	2.01	0.42
4:V:22:THR:O	4:V:22:THR:HG22	2.19	0.42
4:V:33:THR:O	4:V:36:SER:HB3	2.20	0.42
4:V:123:PRO:C	4:V:125:ALA:H	2.28	0.42
5:X:13:LEU:HD21	5:X:25:LEU:CD1	2.50	0.42
5:X:28:PHE:O	5:X:28:PHE:CD1	2.72	0.42
2:B:169:MET:HB3	2:B:174:LEU:CD1	2.50	0.42
4:D:123:PRO:C	4:D:125:ALA:N	2.77	0.42
4:E:94:ALA:CB	6:E:194:PLM:H91	2.43	0.42
5:F:143:ASN:O	5:F:144:LYS:HB2	2.19	0.42
5:F:149:GLU:HG2	5:F:150:THR:N	2.33	0.42
2:H:72:GLN:HE21	2:H:72:GLN:HB3	1.58	0.42
2:H:73:LEU:HD11	2:H:86:LYS:HD3	2.01	0.42
3:I:118:ASN:C	3:I:120:LEU:H	2.28	0.42
4:J:185:LYS:HD2	4:J:185:LYS:O	2.19	0.42
4:K:139:TRP:O	4:K:140:TYR:C	2.61	0.42
1:M:4:GLU:CG	1:M:143:ILE:HG22	2.44	0.42
1:M:114:TRP:HH2	4:P:76:ALA:HA	1.84	0.42
2:N:185:GLY:HA2	2:N:195:VAL:HG13	2.02	0.42
4:P:185:LYS:HD2	4:P:185:LYS:O	2.19	0.42
4:Q:8:ARG:O	4:Q:9:SER:C	2.62	0.42
4:Q:32:LEU:CD2	3:U:117:ASN:HA	2.49	0.42
1:S:10:ASN:ND2	1:S:12:SER:N	2.62	0.42
1:S:28:LEU:CB	1:S:33:TYR:CE1	3.01	0.42
2:T:169:MET:O	2:T:170:ARG:C	2.62	0.42
2:T:192:PHE:HB3	2:T:217:THR:OG1	2.20	0.42
2:T:211:ILE:HG21	2:T:268:ILE:HD11	1.99	0.42
3:U:77:VAL:O	3:U:77:VAL:CG2	2.60	0.42
5:X:66:GLY:O	5:X:70:PHE:HE1	2.03	0.42
5:X:93:GLN:HG3	5:X:131:VAL:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:143:ASN:O	5:X:144:LYS:HB2	2.19	0.42
1:A:75:MET:HA	1:A:217:ASN:CB	2.49	0.42
1:A:148:MET:HE3	1:A:169:ASN:N	2.35	0.42
1:A:192:LYS:O	1:A:194:PRO:HD3	2.20	0.42
1:A:198:MET:O	1:A:200:MET:N	2.52	0.42
2:B:247:PRO:O	2:B:271:ASP:OD2	2.38	0.42
3:C:21:TRP:HH2	3:C:155:PRO:O	2.02	0.42
5:F:13:LEU:HD21	5:F:25:LEU:CD2	2.49	0.42
5:F:62:TRP:N	5:F:62:TRP:CD1	2.87	0.42
5:F:119:VAL:HG12	5:F:120:GLY:N	2.34	0.42
1:G:148:MET:HE3	1:G:169:ASN:N	2.35	0.42
1:G:191:MET:HE2	1:G:191:MET:HA	2.01	0.42
2:H:74:HIS:CE1	2:H:83:PHE:CE2	3.08	0.42
2:H:180:LEU:HD12	2:H:180:LEU:HA	1.82	0.42
3:I:107:TYR:HE2	4:K:73:ALA:CA	2.23	0.42
4:J:79:ARG:O	4:J:80:CYS:C	2.62	0.42
4:J:111:ASN:ND2	4:J:113:ASP:OD2	2.39	0.42
2:N:254:ARG:HG3	2:N:264:THR:HG22	2.00	0.42
2:N:265:VAL:HG13	2:N:265:VAL:O	2.19	0.42
4:Q:61:TYR:HD2	4:Q:61:TYR:O	2.03	0.42
4:Q:105:ILE:C	4:Q:106:THR:CG2	2.93	0.42
5:R:72:THR:HG23	5:R:73:ILE:N	2.34	0.42
1:S:44:PHE:HD1	1:S:119:LEU:HB3	1.83	0.42
1:S:75:MET:CE	1:S:105:ASP:CB	2.90	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
1:A:212:LYS:C	1:A:215:VAL:HG22	2.45	0.42
3:C:114:TYR:HB3	3:C:142:ASN:OD1	2.19	0.42
4:D:125:ALA:HB2	4:D:140:TYR:CD2	2.55	0.42
4:D:133:ASP:HA	4:Q:110:HIS:HA	2.01	0.42
2:H:69:MET:HE1	2:H:87:LEU:HD11	2.02	0.42
2:H:175:LYS:CG	2:H:176:ILE:N	2.83	0.42
2:H:184:HIS:CB	2:H:211:ILE:HD13	2.49	0.42
2:H:271:ASP:OD2	2:H:271:ASP:N	2.53	0.42
4:J:123:PRO:C	4:J:125:ALA:H	2.28	0.42
4:K:116:SER:CB	4:K:175:GLU:HG3	2.47	0.42
5:L:28:PHE:O	5:L:29:SER:C	2.63	0.42
5:L:43:VAL:CG2	5:L:77:TYR:HE2	2.33	0.42
5:L:93:GLN:HG3	5:L:131:VAL:HG13	2.02	0.42
5:L:117:LEU:HD23	5:L:117:LEU:C	2.43	0.42
5:L:119:VAL:HG12	5:L:120:GLY:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:150:THR:OG1	5:L:158:VAL:CG2	2.68	0.42
1:M:44:PHE:CD1	1:M:131:ILE:HG21	2.55	0.42
1:M:117:SER:HB3	4:P:191:GLY:N	2.34	0.42
1:M:128:THR:HG22	1:M:130:PHE:CE2	2.54	0.42
2:N:73:LEU:HD11	2:N:86:LYS:HD3	2.01	0.42
2:N:241:LEU:HD12	2:N:248:CYS:HB3	2.02	0.42
4:P:32:LEU:HD23	4:P:32:LEU:HA	1.80	0.42
4:Q:49:PHE:CB	4:Q:137:SER:HB3	2.50	0.42
4:Q:95:PHE:CD1	4:Q:103:PRO:HD3	2.55	0.42
1:S:133:GLN:O	1:S:133:GLN:HG3	2.20	0.42
2:T:180:LEU:HD12	2:T:180:LEU:HA	1.81	0.42
2:T:200:VAL:HG12	2:T:200:VAL:O	2.16	0.42
3:U:5:SER:O	3:U:90:LEU:HD12	2.20	0.42
3:U:133:ARG:H	3:U:133:ARG:CD	2.14	0.42
4:W:16:GLU:HG2	4:W:20:ASN:HD22	1.83	0.42
1:A:120:ARG:HD2	3:C:73:GLY:HA2	2.00	0.42
1:A:181:LYS:HD3	1:A:214:MET:HE1	2.01	0.42
2:B:58:SER:HB3	4:D:98:PHE:HA	2.02	0.42
2:B:218:LEU:HD21	2:B:232:PHE:HE2	1.84	0.42
4:D:22:THR:HG22	4:D:22:THR:O	2.20	0.42
4:D:101:ILE:HD12	4:D:101:ILE:O	2.19	0.42
4:D:125:ALA:HB2	4:D:140:TYR:CE2	2.55	0.42
4:E:49:PHE:CD1	4:E:134:ALA:HA	2.55	0.42
3:I:98:SER:C	3:I:100:THR:N	2.77	0.42
4:J:119:LEU:CD1	4:J:120:ASP:N	2.77	0.42
4:J:125:ALA:HB2	4:J:140:TYR:CD2	2.54	0.42
4:J:143:ILE:CG2	4:J:144:LEU:N	2.83	0.42
4:K:105:ILE:C	4:K:106:THR:CG2	2.93	0.42
5:L:158:VAL:O	5:L:161:ALA:HB3	2.20	0.42
1:M:129:MET:HE2	1:M:143:ILE:HD11	2.01	0.42
1:M:186:TYR:CD1	1:M:190:VAL:HG21	2.55	0.42
1:M:191:MET:HE2	1:M:191:MET:HA	2.01	0.42
2:N:180:LEU:HD12	2:N:180:LEU:HA	1.82	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
4:P:79:ARG:O	4:P:80:CYS:C	2.62	0.42
3:U:98:SER:C	3:U:100:THR:N	2.77	0.42
3:U:114:TYR:HB3	3:U:142:ASN:OD1	2.20	0.42
3:U:123:TYR:N	3:U:123:TYR:CD1	2.86	0.42
1:A:31:ASN:O	1:A:34:LEU:HB2	2.20	0.41
1:A:52:PRO:O	1:A:54:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:182:PHE:CD2	2:B:182:PHE:C	2.98	0.41
2:B:203:SER:C	2:B:204:GLU:HG2	2.45	0.41
3:C:80:TYR:C	3:C:80:TYR:CD2	2.98	0.41
3:C:98:SER:C	3:C:100:THR:N	2.78	0.41
4:D:93:CYS:O	4:D:97:ILE:CG1	2.59	0.41
4:D:119:LEU:CD1	4:D:120:ASP:N	2.77	0.41
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
1:G:128:THR:HG22	1:G:130:PHE:CE2	2.55	0.41
2:H:211:ILE:HG21	2:H:268:ILE:HD11	2.00	0.41
2:H:247:PRO:O	2:H:271:ASP:OD2	2.37	0.41
4:K:124:LEU:HD23	4:K:125:ALA:CB	2.50	0.41
1:M:31:ASN:O	1:M:34:LEU:HB2	2.20	0.41
1:M:192:LYS:O	1:M:194:PRO:HD3	2.21	0.41
4:P:125:ALA:HB2	4:P:140:TYR:CD2	2.55	0.41
4:Q:124:LEU:HD13	4:Q:141:SER:HB3	2.02	0.41
1:S:126:GLN:HG3	3:U:65:ASN:CG	2.45	0.41
3:U:16:ILE:O	3:U:140:ILE:CG2	2.68	0.41
4:W:99:LEU:HB2	4:W:101:ILE:CG2	2.45	0.41
5:X:43:VAL:CG2	5:X:77:TYR:HE2	2.32	0.41
1:A:126:GLN:HG3	3:C:65:ASN:CG	2.45	0.41
2:B:191:LEU:HD12	2:B:192:PHE:HE1	1.86	0.41
2:B:200:VAL:HG12	2:B:200:VAL:O	2.17	0.41
4:D:132:MET:HB2	4:Q:109:SER:HA	2.02	0.41
4:E:16:GLU:HG2	4:E:20:ASN:HD22	1.84	0.41
5:F:12:LEU:CB	5:F:62:TRP:HB2	2.48	0.41
5:F:43:VAL:O	5:F:43:VAL:CG2	2.68	0.41
5:F:43:VAL:CG2	5:F:77:TYR:HE2	2.33	0.41
1:G:10:ASN:O	1:G:11:LYS:C	2.64	0.41
1:G:44:PHE:CD1	1:G:131:ILE:HG21	2.55	0.41
1:G:50:LEU:CB	3:I:43:LEU:HD11	2.44	0.41
3:I:5:SER:O	3:I:90:LEU:HD12	2.21	0.41
4:J:17:ILE:HD13	4:J:17:ILE:HA	1.82	0.41
4:J:180:LEU:HD12	4:J:180:LEU:N	2.14	0.41
5:L:62:TRP:O	5:L:64:THR:N	2.45	0.41
5:L:149:GLU:HG2	5:L:150:THR:H	1.84	0.41
1:M:75:MET:CE	1:M:181:LYS:NZ	2.83	0.41
2:N:64:PHE:CD1	4:P:67:LEU:HD13	2.54	0.41
1:S:192:LYS:O	1:S:194:PRO:HD3	2.19	0.41
3:U:82:THR:CG2	3:U:83:ALA:N	2.82	0.41
3:U:118:ASN:C	3:U:120:LEU:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:115:PHE:CE2	4:V:178:VAL:HG21	2.55	0.41
4:W:90:LEU:O	4:W:94:ALA:HB3	2.20	0.41
5:X:82:HIS:CB	5:X:169:ILE:HD13	2.50	0.41
5:X:88:TYR:CD1	5:X:96:PHE:HD1	2.37	0.41
1:A:115:ASN:CG	1:A:115:ASN:O	2.63	0.41
4:E:45:TYR:O	4:E:46:GLU:C	2.63	0.41
4:E:65:CYS:O	4:E:68:ILE:HG22	2.20	0.41
4:E:105:ILE:C	4:E:106:THR:CG2	2.93	0.41
1:G:198:MET:C	1:G:200:MET:N	2.78	0.41
2:H:206:ASP:OD1	2:H:206:ASP:N	2.51	0.41
4:K:26:ASN:ND2	4:K:28:GLU:H	2.18	0.41
1:M:42:GLY:O	1:M:46:ILE:HG13	2.20	0.41
2:N:250:VAL:HG12	2:N:266:TYR:HB3	2.01	0.41
3:O:105:TYR:CE2	3:O:152:PHE:CE1	3.07	0.41
3:O:114:TYR:HB3	3:O:142:ASN:OD1	2.19	0.41
4:P:93:CYS:O	4:P:97:ILE:CG1	2.59	0.41
4:P:105:ILE:HD13	4:P:105:ILE:H	1.84	0.41
5:R:62:TRP:N	5:R:62:TRP:CD1	2.87	0.41
1:S:181:LYS:HD3	1:S:214:MET:HE1	2.02	0.41
1:S:198:MET:C	1:S:200:MET:N	2.78	0.41
3:U:88:PHE:CZ	3:U:107:TYR:HB2	2.55	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
1:A:12:SER:C	5:F:10:LYS:NZ	2.78	0.41
2:B:73:LEU:HD11	2:B:86:LYS:HD3	2.02	0.41
2:B:271:ASP:OD2	2:B:271:ASP:N	2.53	0.41
3:C:10:ASP:N	3:C:14:ASN:O	2.51	0.41
4:D:32:LEU:HD23	4:D:32:LEU:HA	1.81	0.41
4:D:77:LEU:HB3	4:D:78:PRO:HD2	2.00	0.41
4:D:105:ILE:HD13	4:D:105:ILE:H	1.85	0.41
5:F:28:PHE:O	5:F:28:PHE:CD1	2.72	0.41
1:G:201:PRO:HG2	5:L:6:ASP:O	2.21	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: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:P:156:GLN:CA	4:P:184:LEU:HD12	2.39	0.41
2:T:73:LEU:HD11	2:T:86:LYS:HD3	2.01	0.41
2:T:167:THR:C	2:T:169:MET:H	2.27	0.41
3:U:154:ALA:HB3	3:U:155:PRO:CD	2.51	0.41
4:V:105:ILE:HD13	4:V:105:ILE:H	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:119:LEU:CD1	4:V:120:ASP:N	2.77	0.41
4:W:149:LYS:HD2	4:W:159:CYS:O	2.20	0.41
1:A:143:ILE:HD13	1:A:143:ILE:HA	1.90	0.41
4:D:79:ARG:O	4:D:80:CYS:C	2.63	0.41
4:D:166:ASP:HB3	4:D:169:ARG:HB2	2.03	0.41
4:E:90:LEU:O	4:E:94:ALA:HB3	2.21	0.41
5:F:57:VAL:HG12	5:F:57:VAL:O	2.20	0.41
5:F:169:ILE:O	5:F:172:SER:HB2	2.20	0.41
1:G:38:SER:CB	5:L:45:PHE:CE1	3.02	0.41
1:G:131:ILE:HG13	1:G:141:VAL:HG22	2.03	0.41
2:H:58:SER:HG	2:H:61:ALA:H	1.66	0.41
2:H:169:MET:HB3	2:H:174:LEU:HD12	2.02	0.41
2:H:253:HIS:O	2:H:264:THR:HB	2.20	0.41
4:J:129:GLU:HA	4:J:129:GLU:OE1	2.19	0.41
5:L:149:GLU:O	5:L:150:THR:CG2	2.66	0.41
1:M:21:PHE:HZ	1:M:215:VAL:HG11	1.81	0.41
3:O:16:ILE:O	3:O:138:ARG:HB2	2.21	0.41
3:O:80:TYR:C	3:O:80:TYR:CD2	2.98	0.41
4:P:65:CYS:HA	4:P:154:MET:HG3	2.02	0.41
4:Q:18:TRP:HE1	4:Q:100:ASN:HB2	1.84	0.41
5:R:28:PHE:O	5:R:29:SER:C	2.64	0.41
1:S:18:GLN:HG3	1:S:33:TYR:CD2	2.55	0.41
3:U:16:ILE:O	3:U:138:ARG:HB2	2.21	0.41
4:V:100:ASN:C	4:V:100:ASN:HD22	2.28	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
3:C:16:ILE:O	3:C:138:ARG:HB2	2.21	0.41
4:E:26:ASN:ND2	4:E:28:GLU:H	2.18	0.41
5:F:28:PHE:O	5:F:29:SER:C	2.64	0.41
1:G:44:PHE:HD1	1:G:119:LEU:HB3	1.85	0.41
1:G:120:ARG:HD2	3:I:73:GLY:HA2	2.02	0.41
2:H:168:LYS:O	2:H:170:ARG:N	2.54	0.41
2:H:218:LEU:HB3	2:H:219:THR:H	1.66	0.41
3:I:82:THR:CG2	3:I:83:ALA:N	2.82	0.41
4:J:65:CYS:HA	4:J:154:MET:HG3	2.02	0.41
4:K:95:PHE:CD1	4:K:103:PRO:CG	3.03	0.41
1:M:181:LYS:HD3	1:M:214:MET:CE	2.50	0.41
2:N:191:LEU:CB	2:N:192:PHE:CD1	3.04	0.41
2:N:231:TYR:HE2	2:N:252:ALA:H	1.65	0.41
3:O:16:ILE:O	3:O:140:ILE:HG22	2.21	0.41
4:Q:185:LYS:HG2	4:Q:186:ASP:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:52:PRO:O	1:S:54:ALA:N	2.53	0.41
2:T:176:ILE:HG23	2:T:177:LEU:H	1.83	0.41
4:W:64:GLY:HA2	4:W:147:VAL:HG13	2.03	0.41
5:X:117:LEU:HD23	5:X:117:LEU:C	2.44	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:E:185:LYS:HG2	4:E:186:ASP:N	2.36	0.41
5:F:150:THR:OG1	5:F:158:VAL:CG2	2.69	0.41
1:G:3:ILE:HA	1:G:144:SER:HA	2.02	0.41
1:G:8:VAL:HG13	1:G:140:PHE:CD2	2.56	0.41
1:G:42:GLY:O	1:G:46:ILE:HG13	2.21	0.41
1:G:200:MET:HE1	5:L:7:TYR:CB	2.51	0.41
1:G:212:LYS:C	1:G:215:VAL:HG22	2.44	0.41
2:H:176:ILE:HG23	2:H:177:LEU:H	1.83	0.41
5:L:169:ILE:HG13	5:L:169:ILE:H	1.53	0.41
1:S:192:LYS:HG3	2:T:64:PHE:CE2	2.56	0.41
1:S:212:LYS:C	1:S:215:VAL:HG22	2.44	0.41
2:T:167:THR:HG22	2:T:169:MET:HB3	2.02	0.41
2:T:185:GLY:HA2	2:T:195:VAL:HG13	2.02	0.41
2:T:191:LEU:HD12	2:T:192:PHE:HE1	1.85	0.41
4:V:129:GLU:OE1	4:V:129:GLU:HA	2.20	0.41
4:W:41:LEU:HD22	4:W:55:HIS:CD2	2.55	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
3:C:107:TYR:HE2	4:E:73:ALA:CA	2.19	0.41
3:C:120:LEU:HD23	3:C:120:LEU:HA	1.91	0.41
4:D:37:ILE:HD12	4:D:37:ILE:HA	1.91	0.41
4:D:188:ILE:HA	4:D:189:PRO:HD3	1.76	0.41
4:E:8:ARG:O	4:E:9:SER:C	2.63	0.41
2:H:192:PHE:HB3	2:H:217:THR:OG1	2.21	0.41
3:I:77:VAL:CG2	3:I:77:VAL:O	2.62	0.41
5:L:13:LEU:HD21	5:L:25:LEU:CD1	2.51	0.41
1:M:52:PRO:O	1:M:54:ALA:N	2.54	0.41
1:M:115:ASN:CG	1:M:115:ASN:O	2.64	0.41
1:M:189:TYR:HD1	1:M:189:TYR:H	1.67	0.41
2:N:101:LEU:O	2:N:102:LEU:C	2.63	0.41
3:O:43:LEU:C	3:O:43:LEU:CD1	2.94	0.41
5:R:66:GLY:O	5:R:70:PHE:HE1	2.04	0.41
1:S:31:ASN:O	1:S:34:LEU:HB2	2.20	0.41
1:S:38:SER:CB	5:X:45:PHE:CE1	3.03	0.41
2:T:101:LEU:O	2:T:102:LEU:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U:80:TYR:CE1	3:U:104:GLN:HA	2.56	0.41
4:V:45:TYR:HE1	4:V:55:HIS:HB2	1.84	0.41
4:V:188:ILE:O	4:V:188:ILE:HG13	2.19	0.41
5:X:13:LEU:HD21	5:X:25:LEU:CD2	2.50	0.41
1:A:10:ASN:ND2	1:A:12:SER:N	2.62	0.41
1:A:181:LYS:HD3	1:A:214:MET:CE	2.51	0.41
1:A:198:MET:C	1:A:200:MET:N	2.79	0.41
2:B:168:LYS:C	2:B:170:ARG:N	2.79	0.41
3:C:88:PHE:CZ	3:C:107:TYR:HB2	2.55	0.41
3:C:123:TYR:CD1	3:C:123:TYR:N	2.86	0.41
4:D:33:THR:O	4:D:36:SER:HB3	2.21	0.41
4:D:45:TYR:HE1	4:D:55:HIS:HB2	1.85	0.41
4:D:185:LYS:HD2	4:D:185:LYS:O	2.20	0.41
5:F:12:LEU:HG	5:F:14:ILE:HG23	2.03	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
1:G:29:ASN:H	1:G:32:GLU:CD	2.29	0.41
1:G:122:LEU:HD23	1:G:122:LEU:O	2.21	0.41
1:G:122:LEU:CD2	1:G:127:PHE:HE1	2.34	0.41
2:H:101:LEU:O	2:H:102:LEU:C	2.63	0.41
2:H:230:GLU:O	2:H:233:VAL:HG13	2.20	0.41
3:I:123:TYR:N	3:I:123:TYR:CD1	2.87	0.41
4:J:156:GLN:HB3	4:J:184:LEU:HB2	2.03	0.41
4:K:36:SER:O	4:K:40:GLN:CB	2.63	0.41
4:K:49:PHE:CD1	4:K:134:ALA:HA	2.55	0.41
4:K:71:PHE:CD1	4:K:71:PHE:O	2.73	0.41
4:K:95:PHE:HD1	4:K:103:PRO:HD3	1.86	0.41
4:K:130:LEU:HD12	4:K:168:LEU:O	2.21	0.41
1:M:181:LYS:HD3	1:M:214:MET:HE1	2.02	0.41
1:M:198:MET:C	1:M:200:MET:N	2.79	0.41
2:N:169:MET:CB	2:N:174:LEU:CD1	2.98	0.41
3:O:118:ASN:C	3:O:120:LEU:H	2.28	0.41
3:O:123:TYR:N	3:O:123:TYR:CD1	2.87	0.41
4:P:68:ILE:H	4:P:68:ILE:HG13	1.36	0.41
4:P:125:ALA:HB2	4:P:140:TYR:CE2	2.56	0.41
4:P:154:MET:O	4:P:156:GLN:NE2	2.54	0.41
4:P:156:GLN:HB3	4:P:184:LEU:HB2	2.03	0.41
4:Q:39:ALA:CB	3:U:120:LEU:HD23	2.51	0.41
4:Q:45:TYR:O	4:Q:46:GLU:C	2.64	0.41
4:Q:49:PHE:CD1	4:Q:134:ALA:HA	2.56	0.41
4:Q:71:PHE:CD1	4:Q:71:PHE:O	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:90:LEU:O	4:Q:94:ALA:HB3	2.21	0.41
4:Q:111:ASN:O	4:Q:112:LYS:HB2	2.21	0.41
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
5:R:143:ASN:O	5:R:144:LYS:HB2	2.20	0.41
1:S:75:MET:CE	1:S:181:LYS:NZ	2.84	0.41
1:S:181:LYS:HD3	1:S:214:MET:CE	2.51	0.41
2:T:168:LYS:O	2:T:172:ARG:NE	2.54	0.41
2:T:187:LEU:O	2:T:191:LEU:N	2.40	0.41
2:T:206:ASP:OD1	2:T:206:ASP:N	2.52	0.41
2:T:218:LEU:HB3	2:T:219:THR:H	1.67	0.41
2:T:271:ASP:OD2	2:T:271:ASP:N	2.54	0.41
4:V:68:ILE:HD11	4:V:154:MET:HG3	2.02	0.41
4:W:49:PHE:CB	4:W:137:SER:HB3	2.50	0.41
4:W:95:PHE:HD1	4:W:103:PRO:HD3	1.86	0.41
4:W:178:VAL:O	4:W:178:VAL:HG12	2.20	0.41
5:X:7:TYR:HB2	5:X:57:VAL:HG22	2.03	0.41
5:X:62:TRP:O	5:X:64:THR:N	2.46	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:C:16:ILE:O	3:C:140:ILE:CG2	2.69	0.41
4:E:95:PHE:HD1	4:E:103:PRO:HD3	1.86	0.41
2:H:64:PHE:CD1	4:J:67:LEU:CD1	3.04	0.41
2:H:169:MET:HB2	2:H:174:LEU:HD12	2.02	0.41
5:L:12:LEU:HG	5:L:14:ILE:HG23	2.03	0.41
5:L:14:ILE:HD12	5:L:102:TRP:CE3	2.56	0.41
4:P:37:ILE:HD12	4:P:37:ILE:HA	1.91	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:T:255:MET:HE3	2:T:255:MET:HB3	1.99	0.41
4:V:156:GLN:HB3	4:V:184:LEU:HB2	2.03	0.41
4:V:166:ASP:HB3	4:V:169:ARG:HB2	2.03	0.41
4:W:134:ALA:O	4:W:137:SER:N	2.48	0.41
5:X:8:LEU:HA	5:X:8:LEU:HD12	1.87	0.41
3:C:72:THR:HG21	3:C:75:TYR:CD2	2.56	0.40
3:C:83:ALA:HB3	4:E:72:LEU:CD1	2.46	0.40
4:D:77:LEU:HD22	4:D:78:PRO:CD	2.47	0.40
5:F:7:TYR:HB2	5:F:57:VAL:HG22	2.03	0.40
5:F:158:VAL:O	5:F:161:ALA:HB3	2.21	0.40
2:H:64:PHE:CE1	4:J:67:LEU:CD1	3.03	0.40
2:H:187:LEU:O	2:H:191:LEU:N	2.40	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:186:ASP:HB2	5:L:79:ARG:NH2	2.36	0.40
4:K:114:THR:HG22	4:K:115:PHE:N	2.37	0.40
2:N:182:PHE:CD2	2:N:182:PHE:C	2.99	0.40
4:P:166:ASP:HB3	4:P:169:ARG:HB2	2.03	0.40
4:Q:77:LEU:HD12	4:Q:89:VAL:CG1	2.52	0.40
5:R:29:SER:HA	5:R:48:LYS:CG	2.49	0.40
1:S:129:MET:HB2	1:S:143:ILE:HD11	2.03	0.40
1:S:185:LEU:HD11	1:S:210:LYS:HD3	2.03	0.40
2:T:203:SER:C	2:T:204:GLU:HG2	2.46	0.40
3:U:155:PRO:CG	3:U:156:MET:N	2.81	0.40
4:V:143:ILE:CG2	4:V:144:LEU:N	2.84	0.40
5:X:169:ILE:HG13	5:X:169:ILE:H	1.53	0.40
1:A:44:PHE:HD1	1:A:119:LEU:HB3	1.85	0.40
1:A:45:ALA:O	1:A:48:SER:OG	2.28	0.40
1:A:122:LEU:CD2	1:A:127:PHE:HE1	2.34	0.40
1:A:128:THR:HG22	1:A:130:PHE:CE2	2.56	0.40
2:B:58:SER:HG	2:B:61:ALA:H	1.68	0.40
3:C:112:VAL:HG11	4:E:70:ASP:CG	2.46	0.40
1:G:10:ASN:ND2	1:G:12:SER:N	2.63	0.40
2:H:99:LEU:HD22	2:H:243:ASN:ND2	2.27	0.40
4:K:99:LEU:HB2	4:K:101:ILE:CG2	2.46	0.40
1:M:29:ASN:O	1:M:32:GLU:HG3	2.21	0.40
3:O:117:ASN:HA	4:W:32:LEU:CD2	2.51	0.40
4:P:155:VAL:HG12	4:P:157:LEU:HD21	2.03	0.40
4:P:188:ILE:O	4:P:188:ILE:HG13	2.20	0.40
4:Q:38:VAL:HG12	3:U:120:LEU:HD21	2.03	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
2:T:231:TYR:HE2	2:T:251:THR:CA	2.29	0.40
2:T:241:LEU:O	2:T:244:ALA:HB3	2.21	0.40
2:T:253:HIS:O	2:T:264:THR:HB	2.21	0.40
4:V:17:ILE:HA	4:V:17:ILE:HD13	1.81	0.40
4:W:160:ASP:O	4:W:162:TRP:CE3	2.74	0.40
3:C:67:ILE:HD12	3:C:67:ILE:H	1.85	0.40
3:C:118:ASN:C	3:C:120:LEU:H	2.28	0.40
4:D:155:VAL:O	4:D:157:LEU:HD23	2.22	0.40
2:H:68:GLU:CB	4:J:63:ILE:HD11	2.51	0.40
2:H:84:GLU:OE1	2:H:231:TYR:CE1	2.71	0.40
2:H:200:VAL:HG12	2:H:200:VAL:O	2.18	0.40
4:K:77:LEU:HD12	4:K:89:VAL:CG1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:73:LEU:HD21	2:N:90:TYR:CE1	2.56	0.40
2:N:175:LYS:CG	2:N:176:ILE:H	2.34	0.40
2:N:206:ASP:OD1	2:N:206:ASP:N	2.51	0.40
4:P:119:LEU:CD1	4:P:120:ASP:N	2.78	0.40
4:Q:26:ASN:ND2	4:Q:28:GLU:H	2.19	0.40
4:Q:134:ALA:O	4:Q:137:SER:N	2.50	0.40
2:T:58:SER:HG	2:T:61:ALA:H	1.67	0.40
4:W:185:LYS:HG2	4:W:186:ASP:N	2.36	0.40
1:A:133:GLN:HE22	4:D:188:ILE:CD1	2.24	0.40
1:A:192:LYS:HG3	2:B:64:PHE:CE2	2.56	0.40
3:C:88:PHE:HE1	3:C:107:TYR:CD1	2.39	0.40
4:E:49:PHE:CZ	4:E:134:ALA:N	2.89	0.40
3:I:72:THR:HG21	3:I:75:TYR:CD2	2.57	0.40
3:I:76:ARG:NH1	3:I:94:PHE:CZ	2.90	0.40
3:I:111:TYR:CD2	3:I:111:TYR:C	2.99	0.40
4:J:22:THR:O	4:J:22:THR:HG22	2.21	0.40
4:J:45:TYR:HE1	4:J:55:HIS:HB2	1.85	0.40
4:K:60:GLY:O	4:K:63:ILE:HG13	2.21	0.40
2:N:271:ASP:OD2	2:N:271:ASP:N	2.54	0.40
4:Q:98:PHE:CD2	4:W:26:ASN:OD1	2.74	0.40
1:S:42:GLY:O	1:S:46:ILE:HG13	2.22	0.40
1:S:117:SER:HB3	4:V:191:GLY:N	2.37	0.40
3:U:6:PHE:CZ	3:U:8:ILE:CG1	3.05	0.40
3:U:147:SER:OG	3:U:148:VAL:N	2.54	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
1:A:75:MET:CE	1:A:181:LYS:NZ	2.85	0.40
1:A:201:PRO:HG2	5:F:6:ASP:O	2.21	0.40
2:B:191:LEU:CB	2:B:192:PHE:CD1	3.05	0.40
5:F:13:LEU:HD21	5:F:25:LEU:CD1	2.51	0.40
2:H:203:SER:C	2:H:204:GLU:HG2	2.46	0.40
4:J:37:ILE:HD12	4:J:37:ILE:HA	1.88	0.40
4:J:105:ILE:HD13	4:J:105:ILE:H	1.83	0.40
4:K:41:LEU:HD12	4:K:52:VAL:HG13	2.03	0.40
4:K:77:LEU:HD12	4:K:89:VAL:HG11	2.03	0.40
4:K:185:LYS:HG2	4:K:186:ASP:N	2.36	0.40
5:L:7:TYR:HB2	5:L:57:VAL:HG22	2.04	0.40
1:M:10:ASN:ND2	1:M:12:SER:N	2.63	0.40
2:N:169:MET:SD	2:N:179:ILE:HD13	2.61	0.40
2:N:203:SER:C	2:N:204:GLU:HG2	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:77:LEU:HB3	4:P:78:PRO:HD2	2.01	0.40
4:Q:60:GLY:O	4:Q:63:ILE:HG13	2.22	0.40
5:R:169:ILE:HG13	5:R:169:ILE:H	1.54	0.40
1:S:45:ALA:O	1:S:48:SER:OG	2.29	0.40
2:T:99:LEU:HD22	2:T:243:ASN:ND2	2.27	0.40
4:W:116:SER:HA	4:W:177:LYS:HA	2.03	0.40
5:X:14:ILE:HD12	5:X:102:TRP:CE3	2.57	0.40
5:X:50:VAL:HG23	5:X:50:VAL:O	2.21	0.40

There are no symmetry-related clashes.

### 5.3 Torsion angles [i](#)

#### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

#### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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%)	121 (83%)	24 (17%)	2	14
1	G	145/199 (73%)	121 (83%)	24 (17%)	2	14
1	M	145/199 (73%)	122 (84%)	23 (16%)	2	15
1	S	145/199 (73%)	122 (84%)	23 (16%)	2	15
2	B	149/249 (60%)	123 (83%)	26 (17%)	2	12
2	H	149/249 (60%)	122 (82%)	27 (18%)	2	12
2	N	149/249 (60%)	122 (82%)	27 (18%)	2	12
2	T	149/249 (60%)	122 (82%)	27 (18%)	2	12
3	C	132/145 (91%)	112 (85%)	20 (15%)	3	16
3	I	132/145 (91%)	112 (85%)	20 (15%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	O	132/145 (91%)	112 (85%)	20 (15%)	3	16
3	U	132/145 (91%)	112 (85%)	20 (15%)	3	16
4	D	171/178 (96%)	146 (85%)	25 (15%)	3	17
4	E	173/178 (97%)	146 (84%)	27 (16%)	2	15
4	J	171/178 (96%)	146 (85%)	25 (15%)	3	17
4	K	173/178 (97%)	143 (83%)	30 (17%)	2	12
4	P	171/178 (96%)	146 (85%)	25 (15%)	3	17
4	Q	173/178 (97%)	144 (83%)	29 (17%)	2	13
4	V	171/178 (96%)	146 (85%)	25 (15%)	3	17
4	W	173/178 (97%)	145 (84%)	28 (16%)	2	14
5	F	148/183 (81%)	136 (92%)	12 (8%)	11	36
5	L	148/183 (81%)	136 (92%)	12 (8%)	11	36
5	R	148/183 (81%)	135 (91%)	13 (9%)	9	33
5	X	148/183 (81%)	137 (93%)	11 (7%)	13	39
All	All	3672/4528 (81%)	3129 (85%)	543 (15%)	3	17

All (543) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	10	ASN
1	A	16	ILE
1	A	18	GLN
1	A	32	GLU
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	141	VAL
1	A	144	SER
1	A	176	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	180	ARG
1	A	185	LEU
1	A	189	TYR
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	211	ILE
2	B	215	PHE
2	B	219	THR
2	B	222	ILE
2	B	223	PRO
2	B	228	SER
2	B	231	TYR
2	B	233	VAL
2	B	234	CYS
2	B	246	PHE
2	B	250	VAL
2	B	255	MET
2	B	271	ASP
3	C	18	ASP
3	C	19	ARG
3	C	43	LEU
3	C	47	MET
3	C	67	ILE
3	C	72	THR
3	C	87	TRP
3	C	89	VAL
3	C	91	LEU
3	C	93	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	101	GLN
3	C	103	LEU
3	C	106	ILE
3	C	114	TYR
3	C	119	LEU
3	C	121	SER
3	C	123	TYR
3	C	133	ARG
3	C	150	GLU
3	C	156	MET
4	D	15	GLU
4	D	17	ILE
4	D	22	THR
4	D	33	THR
4	D	43	GLN
4	D	68	ILE
4	D	69	GLU
4	D	79	ARG
4	D	84	VAL
4	D	89	VAL
4	D	93	CYS
4	D	99	LEU
4	D	105	ILE
4	D	144	LEU
4	D	149	LYS
4	D	153	GLU
4	D	156	GLN
4	D	157	LEU
4	D	159	CYS
4	D	161	VAL
4	D	173	GLN
4	D	175	GLU
4	D	180	LEU
4	D	181	ASN
4	D	192	GLU
4	E	25	ILE
4	E	27	THR
4	E	33	THR
4	E	59	MET
4	E	61	TYR
4	E	62	ASN
4	E	63	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
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	77	TYR
5	F	82	HIS
5	F	102	TRP
5	F	115	LEU
5	F	135	VAL
5	F	145	MET
5	F	169	ILE
1	G	7	LEU
1	G	10	ASN
1	G	16	ILE
1	G	18	GLN
1	G	67	ILE
1	G	70	ILE
1	G	75	MET
1	G	113	ASN
1	G	114	TRP
1	G	120	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	G	122	LEU
1	G	126	GLN
1	G	133	GLN
1	G	135	LEU
1	G	141	VAL
1	G	143	ILE
1	G	176	ASP
1	G	179	LEU
1	G	180	ARG
1	G	185	LEU
1	G	189	TYR
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	177	LEU
2	H	178	ASP
2	H	180	LEU
2	H	184	HIS
2	H	187	LEU
2	H	192	PHE
2	H	193	ASN
2	H	210	MET
2	H	211	ILE
2	H	215	PHE
2	H	219	THR
2	H	222	ILE
2	H	223	PRO
2	H	228	SER
2	H	231	TYR
2	H	233	VAL
2	H	234	CYS
2	H	246	PHE
2	H	250	VAL
2	H	255	MET
2	H	271	ASP
3	I	18	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	I	19	ARG
3	I	43	LEU
3	I	47	MET
3	I	67	ILE
3	I	72	THR
3	I	87	TRP
3	I	89	VAL
3	I	91	LEU
3	I	93	ASP
3	I	101	GLN
3	I	103	LEU
3	I	106	ILE
3	I	114	TYR
3	I	119	LEU
3	I	121	SER
3	I	123	TYR
3	I	133	ARG
3	I	150	GLU
3	I	156	MET
4	J	15	GLU
4	J	17	ILE
4	J	22	THR
4	J	33	THR
4	J	43	GLN
4	J	68	ILE
4	J	69	GLU
4	J	79	ARG
4	J	84	VAL
4	J	89	VAL
4	J	93	CYS
4	J	99	LEU
4	J	105	ILE
4	J	144	LEU
4	J	149	LYS
4	J	153	GLU
4	J	156	GLN
4	J	157	LEU
4	J	159	CYS
4	J	161	VAL
4	J	173	GLN
4	J	175	GLU
4	J	180	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	J	181	ASN
4	J	192	GLU
4	K	25	ILE
4	K	27	THR
4	K	33	THR
4	K	59	MET
4	K	61	TYR
4	K	62	ASN
4	K	63	ILE
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	141	SER
4	K	144	LEU
4	K	145	CYS
4	K	153	GLU
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
5	L	41	ILE
5	L	57	VAL
5	L	77	TYR
5	L	82	HIS
5	L	102	TRP
5	L	115	LEU
5	L	135	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	L	145	MET
5	L	169	ILE
1	M	7	LEU
1	M	10	ASN
1	M	16	ILE
1	M	18	GLN
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	141	VAL
1	M	143	ILE
1	M	176	ASP
1	M	180	ARG
1	M	185	LEU
1	M	189	TYR
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	177	LEU
2	N	178	ASP
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	211	ILE
2	N	215	PHE
2	N	219	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	N	222	ILE
2	N	223	PRO
2	N	228	SER
2	N	231	TYR
2	N	233	VAL
2	N	234	CYS
2	N	246	PHE
2	N	250	VAL
2	N	255	MET
2	N	271	ASP
3	O	18	ASP
3	O	19	ARG
3	O	43	LEU
3	O	47	MET
3	O	67	ILE
3	O	72	THR
3	O	87	TRP
3	O	89	VAL
3	O	91	LEU
3	O	93	ASP
3	O	101	GLN
3	O	103	LEU
3	O	106	ILE
3	O	114	TYR
3	O	119	LEU
3	O	121	SER
3	O	123	TYR
3	O	133	ARG
3	O	150	GLU
3	O	156	MET
4	P	15	GLU
4	P	17	ILE
4	P	22	THR
4	P	33	THR
4	P	43	GLN
4	P	68	ILE
4	P	69	GLU
4	P	79	ARG
4	P	84	VAL
4	P	89	VAL
4	P	93	CYS
4	P	99	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	P	105	ILE
4	P	144	LEU
4	P	149	LYS
4	P	153	GLU
4	P	156	GLN
4	P	157	LEU
4	P	159	CYS
4	P	161	VAL
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	27	THR
4	Q	33	THR
4	Q	59	MET
4	Q	61	TYR
4	Q	62	ASN
4	Q	63	ILE
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	141	SER
4	Q	144	LEU
4	Q	145	CYS
4	Q	153	GLU
4	Q	159	CYS
4	Q	160	ASP
4	Q	161	VAL
4	Q	167	ILE
4	Q	174	THR
4	Q	175	GLU
4	Q	187	GLU
4	Q	193	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	R	13	LEU
5	R	16	ASN
5	R	23	CYS
5	R	41	ILE
5	R	57	VAL
5	R	77	TYR
5	R	82	HIS
5	R	85	ILE
5	R	102	TRP
5	R	115	LEU
5	R	135	VAL
5	R	145	MET
5	R	169	ILE
1	S	7	LEU
1	S	10	ASN
1	S	16	ILE
1	S	18	GLN
1	S	32	GLU
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	141	VAL
1	S	176	ASP
1	S	180	ARG
1	S	185	LEU
1	S	189	TYR
1	S	197	SER
1	S	209	GLU
1	S	214	MET
2	T	64	PHE
2	T	65	LEU
2	T	72	GLN
2	T	73	LEU
2	T	102	LEU
2	T	176	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	T	177	LEU
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	211	ILE
2	T	215	PHE
2	T	219	THR
2	T	222	ILE
2	T	223	PRO
2	T	228	SER
2	T	231	TYR
2	T	233	VAL
2	T	234	CYS
2	T	246	PHE
2	T	250	VAL
2	T	255	MET
2	T	271	ASP
3	U	18	ASP
3	U	19	ARG
3	U	43	LEU
3	U	47	MET
3	U	67	ILE
3	U	72	THR
3	U	87	TRP
3	U	89	VAL
3	U	91	LEU
3	U	93	ASP
3	U	101	GLN
3	U	103	LEU
3	U	106	ILE
3	U	114	TYR
3	U	119	LEU
3	U	121	SER
3	U	123	TYR
3	U	133	ARG
3	U	150	GLU
3	U	156	MET
4	V	15	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	V	17	ILE
4	V	22	THR
4	V	33	THR
4	V	43	GLN
4	V	68	ILE
4	V	69	GLU
4	V	79	ARG
4	V	84	VAL
4	V	89	VAL
4	V	93	CYS
4	V	99	LEU
4	V	105	ILE
4	V	144	LEU
4	V	149	LYS
4	V	153	GLU
4	V	156	GLN
4	V	157	LEU
4	V	159	CYS
4	V	161	VAL
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	27	THR
4	W	33	THR
4	W	59	MET
4	W	61	TYR
4	W	62	ASN
4	W	63	ILE
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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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	W	145	CYS
4	W	153	GLU
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	77	TYR
5	X	82	HIS
5	X	102	TRP
5	X	115	LEU
5	X	145	MET
5	X	169	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (119) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	10	ASN
1	A	18	GLN
1	A	20	ASN
1	A	126	GLN
1	A	133	GLN
1	A	217	ASN
2	B	72	GLN
2	B	74	HIS
2	B	92	HIS
2	B	193	ASN
2	B	214	ASN
2	B	243	ASN
2	B	262	GLN
3	C	65	ASN
3	C	104	GLN
3	C	117	ASN
3	C	142	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	D	55	HIS
4	D	100	ASN
4	D	142	ASN
4	D	156	GLN
4	E	20	ASN
4	E	26	ASN
4	E	50	ASN
4	E	111	ASN
4	E	142	ASN
4	E	181	ASN
5	F	93	GLN
5	F	121	ASN
5	F	168	GLN
1	G	10	ASN
1	G	18	GLN
1	G	20	ASN
1	G	126	GLN
1	G	133	GLN
1	G	217	ASN
2	H	72	GLN
2	H	74	HIS
2	H	92	HIS
2	H	193	ASN
2	H	214	ASN
2	H	243	ASN
2	H	262	GLN
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	50	ASN
4	K	111	ASN
4	K	142	ASN
4	K	181	ASN
5	L	93	GLN
5	L	121	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	L	168	GLN
1	M	10	ASN
1	M	18	GLN
1	M	20	ASN
1	M	126	GLN
1	M	133	GLN
1	M	217	ASN
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	50	ASN
4	Q	111	ASN
4	Q	142	ASN
4	Q	181	ASN
5	R	93	GLN
5	R	121	ASN
5	R	168	GLN
1	S	10	ASN
1	S	18	GLN
1	S	20	ASN
1	S	126	GLN
1	S	133	GLN
2	T	72	GLN
2	T	74	HIS
2	T	92	HIS
2	T	193	ASN
2	T	214	ASN
2	T	243	ASN
2	T	262	GLN

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Mol	Chain	Res	Type
3	U	65	ASN
3	U	104	GLN
3	U	117	ASN
3	U	142	ASN
3	U	144	ASN
4	V	55	HIS
4	V	100	ASN
4	V	142	ASN
4	V	156	GLN
4	W	20	ASN
4	W	26	ASN
4	W	50	ASN
4	W	111	ASN
4	W	142	ASN
4	W	181	ASN
5	X	93	GLN
5	X	121	ASN
5	X	168	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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	Q	194	4	16,16,17	1.14	1 (6%)	15,15,17	1.38	4 (26%)
6	PLM	K	194	4	16,16,17	1.13	1 (6%)	15,15,17	1.38	4 (26%)
6	PLM	W	194	4	16,16,17	1.15	1 (6%)	15,15,17	1.37	3 (20%)
6	PLM	E	194	4	16,16,17	1.12	1 (6%)	15,15,17	1.37	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	Q	194	4	-	1/14/14/15	-
6	PLM	K	194	4	-	1/14/14/15	-
6	PLM	W	194	4	-	1/14/14/15	-
6	PLM	E	194	4	-	1/14/14/15	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	W	194	PLM	O1-C1	-4.41	1.19	1.42
6	Q	194	PLM	O1-C1	-4.39	1.19	1.42
6	K	194	PLM	O1-C1	-4.34	1.20	1.42
6	E	194	PLM	O1-C1	-4.31	1.20	1.42

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	194	PLM	C9-C8-C7	-2.53	101.60	114.37
6	Q	194	PLM	C9-C8-C7	-2.48	101.86	114.37
6	K	194	PLM	C9-C8-C7	-2.47	101.88	114.37
6	W	194	PLM	C9-C8-C7	-2.42	102.15	114.37
6	Q	194	PLM	CC-CB-CA	-2.21	103.22	114.37
6	W	194	PLM	CC-CB-CA	-2.17	103.39	114.37
6	E	194	PLM	CC-CB-CA	-2.16	103.45	114.37
6	K	194	PLM	CC-CB-CA	-2.10	103.73	114.37
6	K	194	PLM	CE-CD-CC	-2.10	103.77	114.37
6	W	194	PLM	C7-C6-C5	-2.05	104.02	114.37
6	E	194	PLM	CE-CD-CC	-2.04	104.05	114.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Q	194	PLM	CE-CD-CC	-2.04	104.05	114.37
6	Q	194	PLM	C7-C6-C5	-2.03	104.12	114.37
6	K	194	PLM	C7-C6-C5	-2.01	104.22	114.37

There are no chirality outliers.

All (4) torsion outliers are listed below:

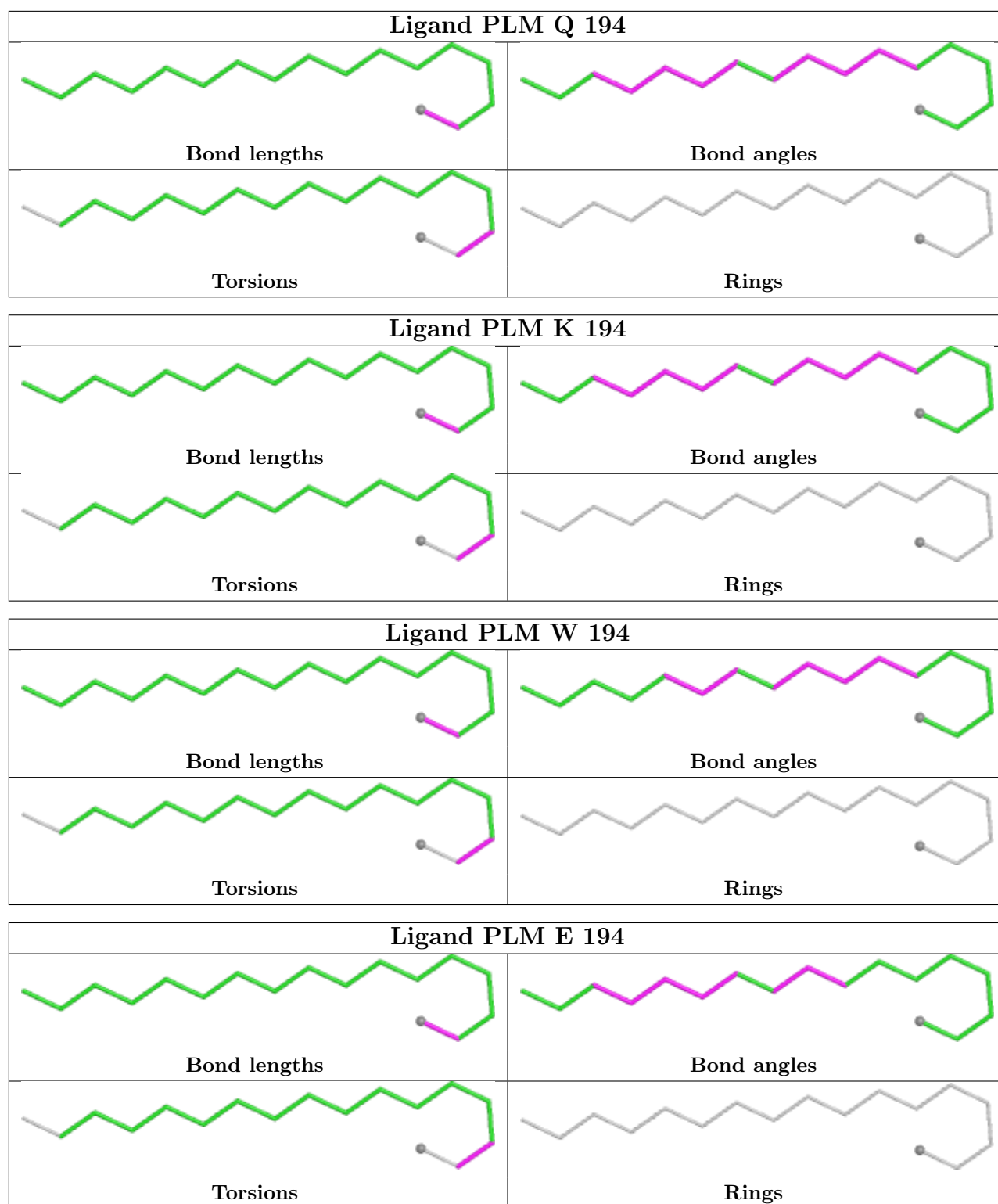
Mol	Chain	Res	Type	Atoms
6	E	194	PLM	O1-C1-C2-C3
6	K	194	PLM	O1-C1-C2-C3
6	Q	194	PLM	O1-C1-C2-C3
6	W	194	PLM	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 24 short contacts:

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

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data i

### 6.1 Protein, DNA and RNA chains i

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	159/219 (72%)	-0.08	3 (1%) 66 42	54, 111, 158, 168	6 (3%)
1	G	159/219 (72%)	-0.09	2 (1%) 75 50	56, 114, 159, 167	6 (3%)
1	M	159/219 (72%)	-0.08	2 (1%) 75 50	55, 112, 158, 168	6 (3%)
1	S	159/219 (72%)	-0.10	1 (0%) 85 66	55, 112, 159, 168	6 (3%)
2	B	167/283 (59%)	-0.20	1 (0%) 85 66	58, 128, 172, 188	10 (5%)
2	H	167/283 (59%)	-0.21	1 (0%) 85 66	57, 128, 171, 192	10 (5%)
2	N	167/283 (59%)	-0.19	1 (0%) 85 66	57, 128, 171, 189	10 (5%)
2	T	167/283 (59%)	-0.24	1 (0%) 85 66	58, 126, 172, 192	10 (5%)
3	C	143/159 (89%)	-0.17	0 100 100	41, 116, 155, 171	2 (1%)
3	I	143/159 (89%)	-0.16	0 100 100	43, 117, 155, 175	3 (2%)
3	O	143/159 (89%)	-0.16	0 100 100	42, 117, 156, 174	2 (1%)
3	U	143/159 (89%)	-0.15	0 100 100	41, 116, 152, 171	3 (2%)
4	D	186/193 (96%)	-0.21	2 (1%) 78 53	56, 132, 168, 185	7 (3%)
4	E	188/193 (97%)	-0.24	1 (0%) 87 69	79, 110, 140, 183	1 (0%)
4	J	186/193 (96%)	-0.20	2 (1%) 78 53	56, 133, 167, 186	7 (3%)
4	K	188/193 (97%)	-0.23	1 (0%) 87 69	79, 111, 140, 183	1 (0%)
4	P	186/193 (96%)	-0.19	2 (1%) 78 53	57, 132, 168, 186	7 (3%)
4	Q	188/193 (97%)	-0.21	0 100 100	78, 110, 141, 184	1 (0%)
4	V	186/193 (96%)	-0.20	2 (1%) 78 53	56, 132, 167, 185	7 (3%)
4	W	188/193 (97%)	-0.22	1 (0%) 87 69	79, 111, 140, 182	1 (0%)
5	F	166/206 (80%)	-0.02	4 (2%) 59 37	57, 145, 172, 178	7 (4%)
5	L	166/206 (80%)	-0.03	2 (1%) 76 51	57, 146, 173, 179	7 (4%)
5	R	166/206 (80%)	-0.01	2 (1%) 76 51	56, 146, 171, 175	7 (4%)
5	X	166/206 (80%)	-0.04	3 (1%) 67 42	57, 146, 171, 176	7 (4%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	4036/5012 (80%)	-0.15	34 (0%) 82 60	41, 123, 169, 192	134 (3%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	X	76	SER	4.0
5	R	76	SER	3.6
5	L	76	SER	3.4
5	F	76	SER	3.2
5	L	41	ILE	2.9
4	P	189	PRO	2.9
4	V	189	PRO	2.8
2	N	230	GLU	2.7
2	T	230	GLU	2.7
5	F	41	ILE	2.6
5	X	41	ILE	2.6
1	G	67	ILE	2.5
4	P	22	THR	2.5
4	D	189	PRO	2.5
2	H	230	GLU	2.5
4	W	192	GLU	2.4
2	B	230	GLU	2.4
1	G	106	PHE	2.4
1	M	69	TYR	2.3
4	V	22	THR	2.3
5	F	162	PHE	2.3
5	R	41	ILE	2.2
5	F	65	ALA	2.2
4	K	192	GLU	2.2
1	S	67	ILE	2.2
4	J	74	ARG	2.1
4	E	187	GLU	2.1
1	A	106	PHE	2.1
1	A	67	ILE	2.1
1	M	67	ILE	2.1
4	J	189	PRO	2.1
5	X	65	ALA	2.1
1	A	107	PHE	2.1
4	D	22	THR	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](#)

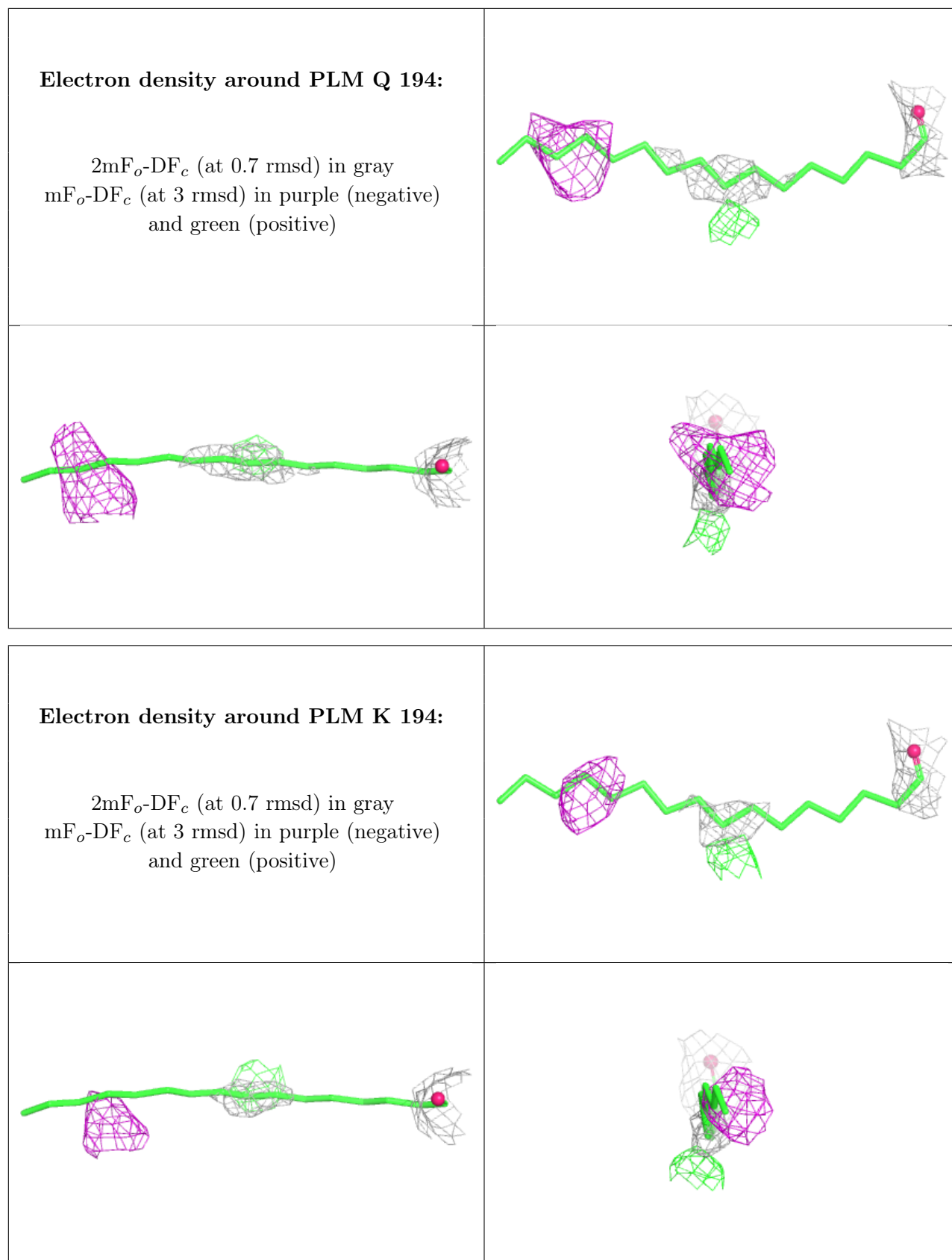
There are no oligosaccharides in this entry.

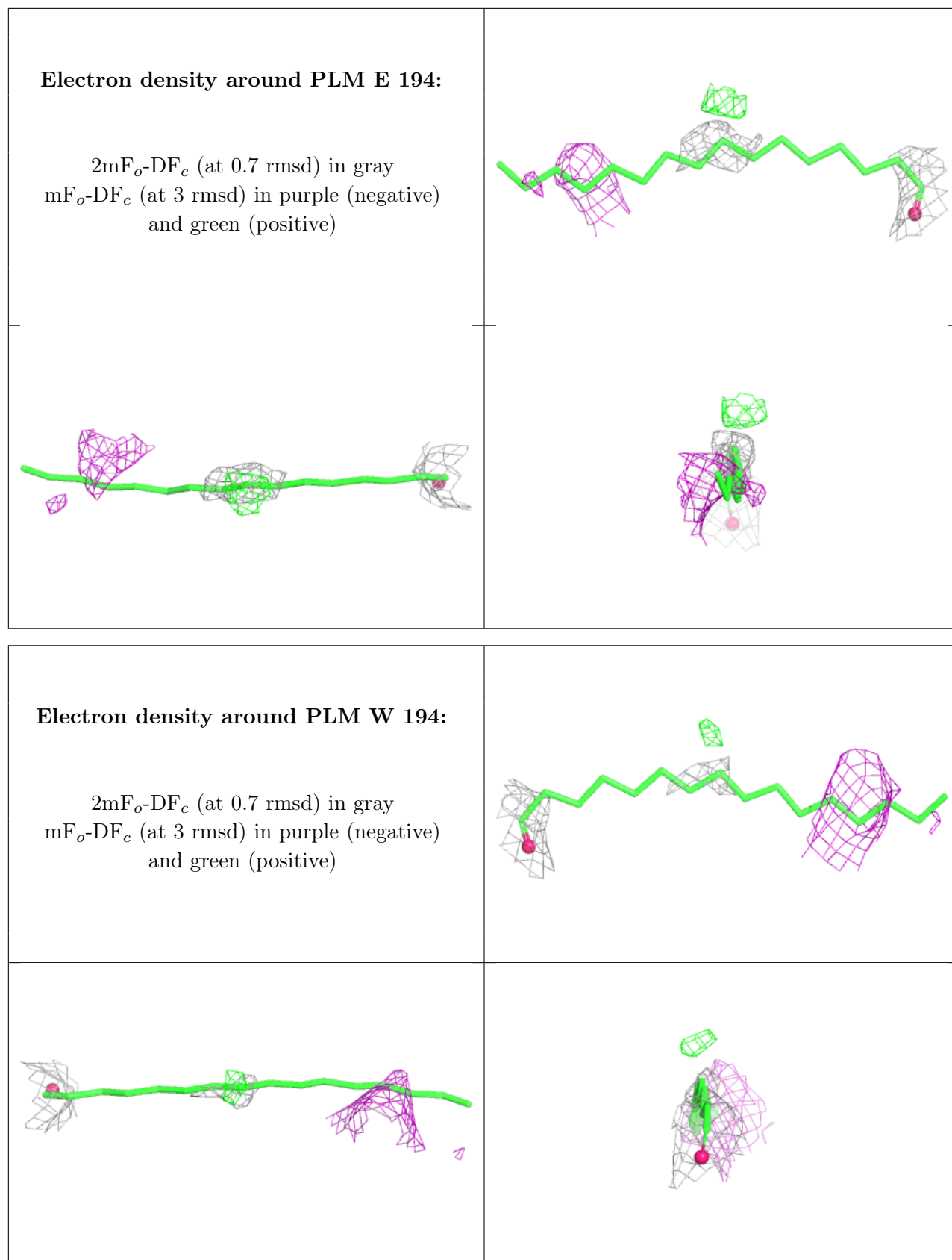
## 6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
6	PLM	Q	194	17/18	0.89	0.29	100,103,111,112	0
6	PLM	K	194	17/18	0.91	0.28	104,106,113,114	0
6	PLM	E	194	17/18	0.91	0.28	102,105,111,111	0
6	PLM	W	194	17/18	0.91	0.30	107,108,111,111	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.