



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:56 AM GMT

PDB ID : 1JD2  
Title : Crystal Structure of the yeast 20S Proteasome:TMC-95A complex: A non-covalent Proteasome Inhibitor  
Authors : Groll, M.; Koguchi, Y.; Huber, R.; Kohno, J.  
Deposited on : 2001-06-12  
Resolution : 3.00 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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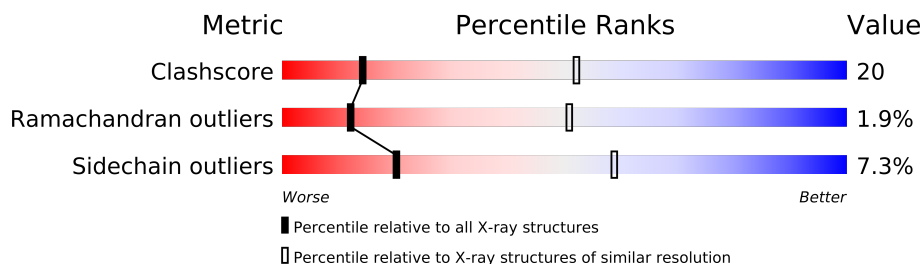
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	250	
1	V	250	
2	B	244	
2	W	244	
3	C	241	
3	X	241	
4	D	242	
4	Y	242	
5	E	233	
5	Z	233	
6	1	244	
6	F	244	
7	2	243	
7	G	243	
8	H	222	
8	O	222	
9	I	204	

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Mol	Chain	Length	Quality of chain
9	P	204	
10	J	198	
10	Q	198	
11	K	212	
11	R	212	
12	L	222	
12	S	222	
13	M	233	
13	T	233	
14	N	196	
14	U	196	
15	8	5	
15	9	5	

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 52549 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PROTEASOME COMPONENT Y7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	V	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called PROTEASOME COMPONENT Y13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1905	1201	321	380	3			
2	W	244	Total	C	N	O	S	0	0	0
			1905	1201	321	380	3			

- Molecule 3 is a protein called PROTEASOME COMPONENT PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1891	1181	331	375	4			
3	X	241	Total	C	N	O	S	0	0	0
			1891	1181	331	375	4			

- Molecule 4 is a protein called PROTEASOME COMPONENT PUP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1862	1162	314	379	7			
4	Y	242	Total	C	N	O	S	0	0	0
			1862	1162	314	379	7			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	121	LEU	-	INSERTION	UNP P32379
D	122	ARG	-	INSERTION	UNP P32379
D	123	PHE	-	INSERTION	UNP P32379
D	123A	GLY	-	INSERTION	UNP P32379
D	123B	GLU	-	INSERTION	UNP P32379
D	123C	GLY	-	INSERTION	UNP P32379
D	123E	SER	-	INSERTION	UNP P32379
D	123F	GLY	-	INSERTION	UNP P32379
D	123G	GLU	-	INSERTION	UNP P32379
D	125	GLU	ALA	CONFLICT	UNP P32379
D	126	ARG	ALA	CONFLICT	UNP P32379
D	127	LEU	ALA	CONFLICT	UNP P32379
Y	121	LEU	-	INSERTION	UNP P32379
Y	122	ARG	-	INSERTION	UNP P32379
Y	123	PHE	-	INSERTION	UNP P32379
Y	123A	GLY	-	INSERTION	UNP P32379
Y	123B	GLU	-	INSERTION	UNP P32379
Y	123C	GLY	-	INSERTION	UNP P32379
Y	123E	SER	-	INSERTION	UNP P32379
Y	123F	GLY	-	INSERTION	UNP P32379
Y	123G	GLU	-	INSERTION	UNP P32379
Y	125	GLU	ALA	CONFLICT	UNP P32379
Y	126	ARG	ALA	CONFLICT	UNP P32379
Y	127	LEU	ALA	CONFLICT	UNP P32379

- Molecule 5 is a protein called PROTEASOME COMPONENT PRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			
5	Z	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	127	TYR	ALA	CONFLICT	UNP P40302
Z	127	TYR	ALA	CONFLICT	UNP P40302

- Molecule 6 is a protein called PROTEASOME COMPONENT C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1897	1205	330	358	4			
6	1	244	Total	C	N	O	S	0	0	0
			1897	1205	330	358	4			

- Molecule 7 is a protein called PROTEASOME COMPONENT C7-ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
7	2	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 8 is a protein called PROTEASOME COMPONENT PUP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			
8	O	222	Total	C	N	O	S	0	0	0
			1685	1061	293	324	7			

- Molecule 9 is a protein called PROTEASOME COMPONENT PUP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	P	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called PROTEASOME COMPONENT C11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			
10	Q	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 11 is a protein called PROTEASOME COMPONENT PRE2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	R	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

- Molecule 12 is a protein called PROTEASOME COMPONENT C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	S	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called PROTEASOME COMPONENT PRE4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	T	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called PROTEASOME COMPONENT PRE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	U	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is a protein called TMC-95A inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	8	5	Total	C	N	O	0	0	0
			49	33	6	10			
15	9	5	Total	C	N	O	0	0	0
			49	33	6	10			

- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	P	1	Total	Mg	0	0
			1	1		
16	G	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	D	1	Total 1	Mg 1	0	0
16	H	1	Total 1	Mg 1	0	0
16	I	2	Total 2	Mg 2	0	0
16	N	1	Total 1	Mg 1	0	0
16	L	1	Total 1	Mg 1	0	0
16	F	2	Total 2	Mg 2	0	0

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	105	Total 105	O 105	0	0
17	B	80	Total 80	O 80	0	0
17	C	69	Total 69	O 69	0	0
17	D	90	Total 90	O 90	0	0
17	E	55	Total 55	O 55	0	0
17	F	99	Total 99	O 99	0	0
17	G	106	Total 106	O 106	0	0
17	H	114	Total 114	O 114	0	0
17	I	107	Total 107	O 107	0	0
17	J	116	Total 116	O 116	0	0
17	K	103	Total 103	O 103	0	0
17	L	140	Total 140	O 140	0	0
17	M	150	Total 150	O 150	0	0

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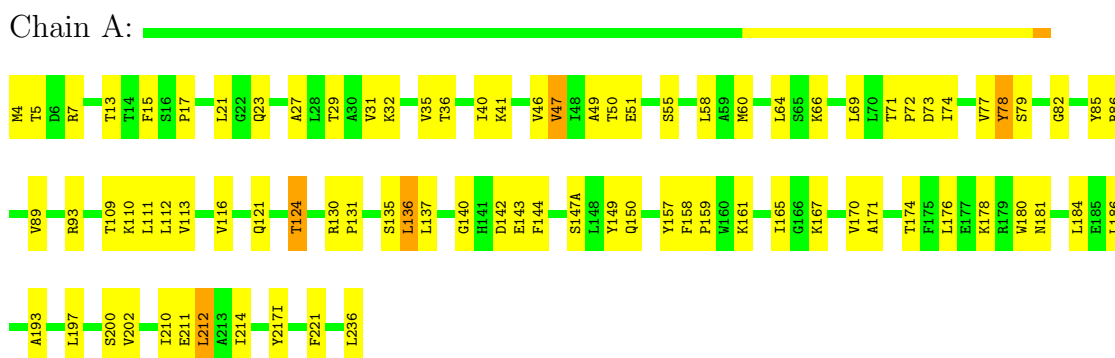
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	N	116	Total 116	O 116	0	0
17	O	121	Total 121	O 121	0	0
17	P	101	Total 101	O 101	0	0
17	Q	121	Total 121	O 121	0	0
17	R	107	Total 107	O 107	0	0
17	S	144	Total 144	O 144	0	0
17	T	142	Total 142	O 142	0	0
17	U	118	Total 118	O 118	0	0
17	V	104	Total 104	O 104	0	0
17	W	74	Total 74	O 74	0	0
17	X	70	Total 70	O 70	0	0
17	Y	89	Total 89	O 89	0	0
17	Z	53	Total 53	O 53	0	0
17	1	93	Total 93	O 93	0	0
17	2	103	Total 103	O 103	0	0
17	8	2	Total 2	O 2	0	0
17	9	1	Total 1	O 1	0	0

### 3 Residue-property plots

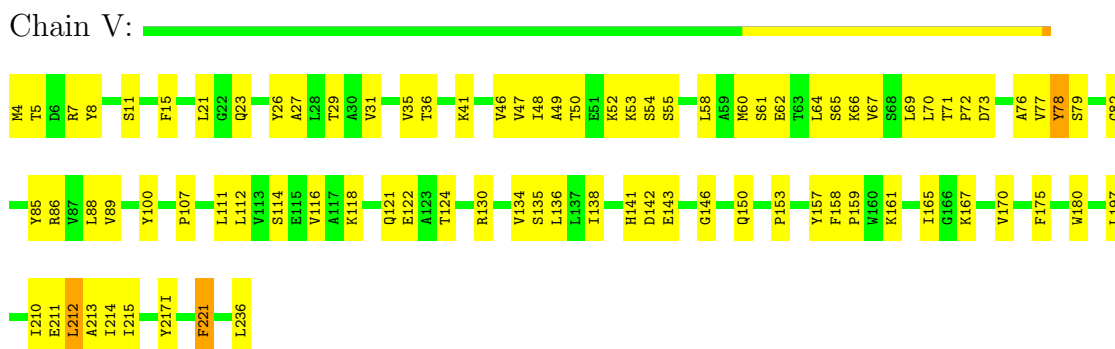
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

#### • Molecule 1: PROTEASOME COMPONENT Y7



#### • Molecule 1: PROTEASOME COMPONENT Y7

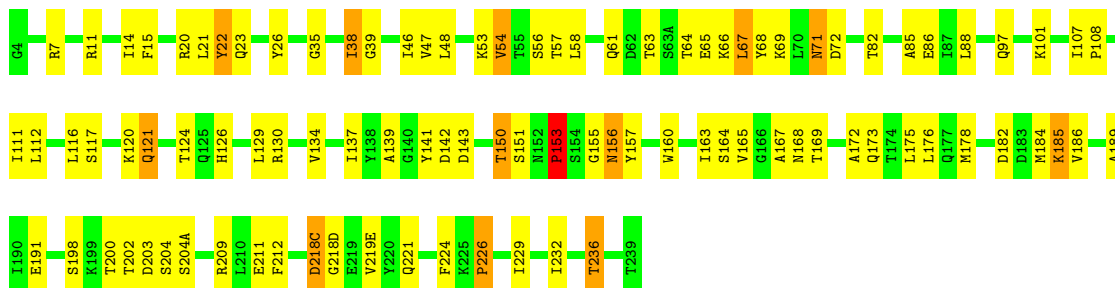


#### • Molecule 2: PROTEASOME COMPONENT Y13



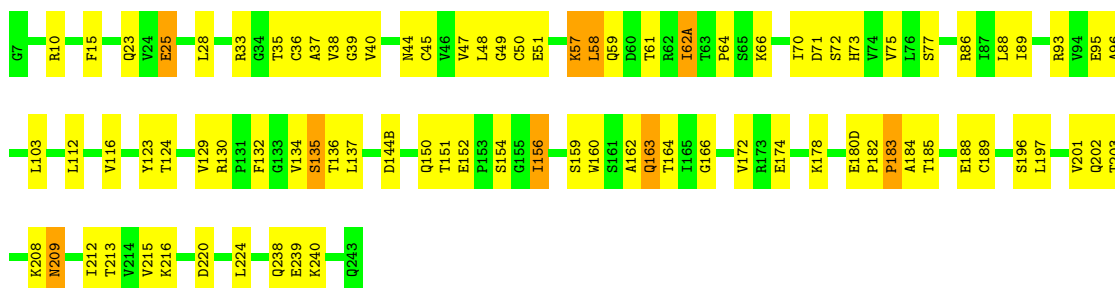
- Molecule 2: PROTEASOME COMPONENT Y13

Chain W:



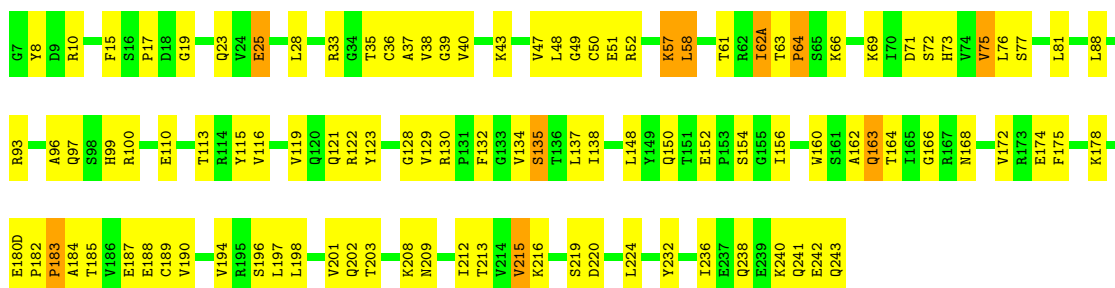
- Molecule 3: PROTEASOME COMPONENT PRE6

Chain C:



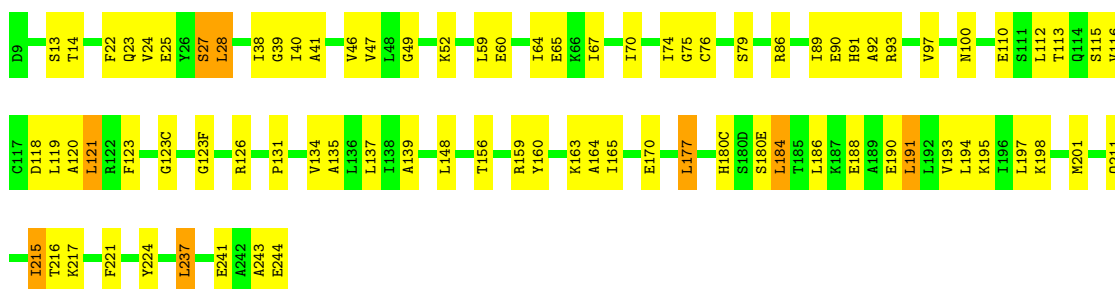
- Molecule 3: PROTEASOME COMPONENT PRE6

Chain X:



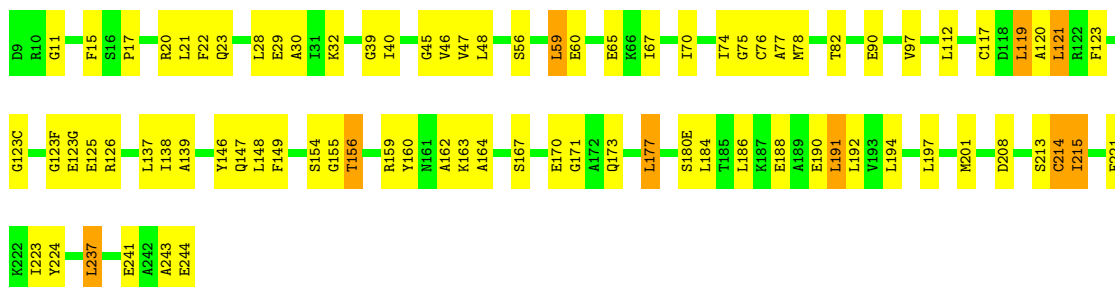
- Molecule 4: PROTEASOME COMPONENT PUP2

Chain D:



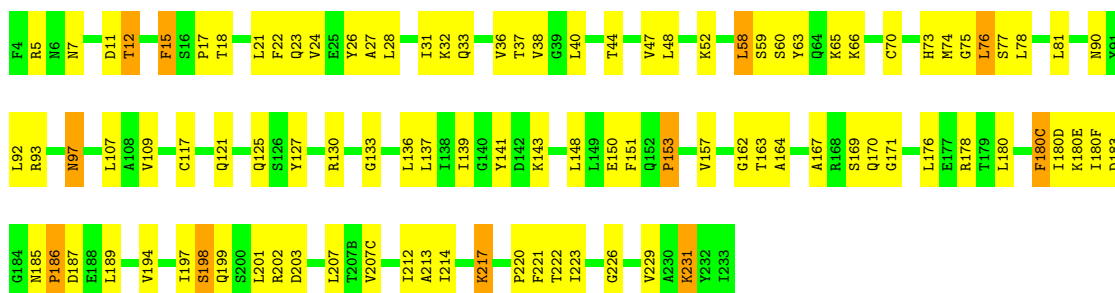
- Molecule 4: PROTEASOME COMPONENT PUP2

Chain Y:



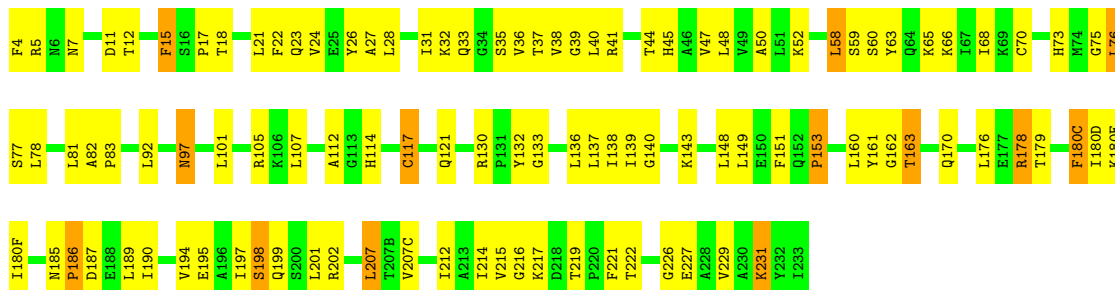
- Molecule 5: PROTEASOME COMPONENT PRE5

Chain E:



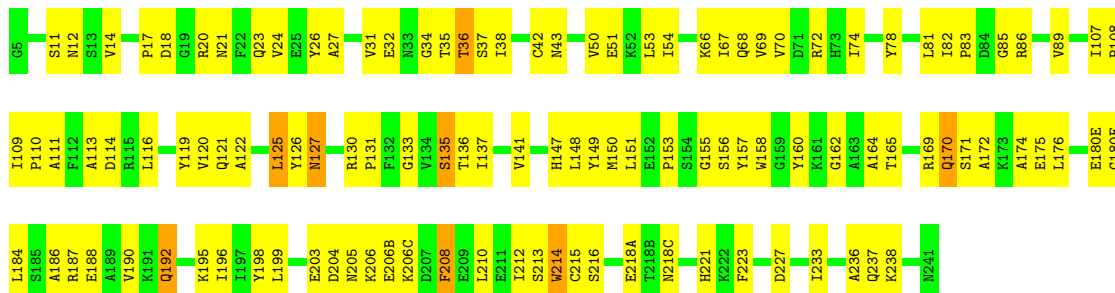
- Molecule 5: PROTEASOME COMPONENT PRE5

Chain Z:



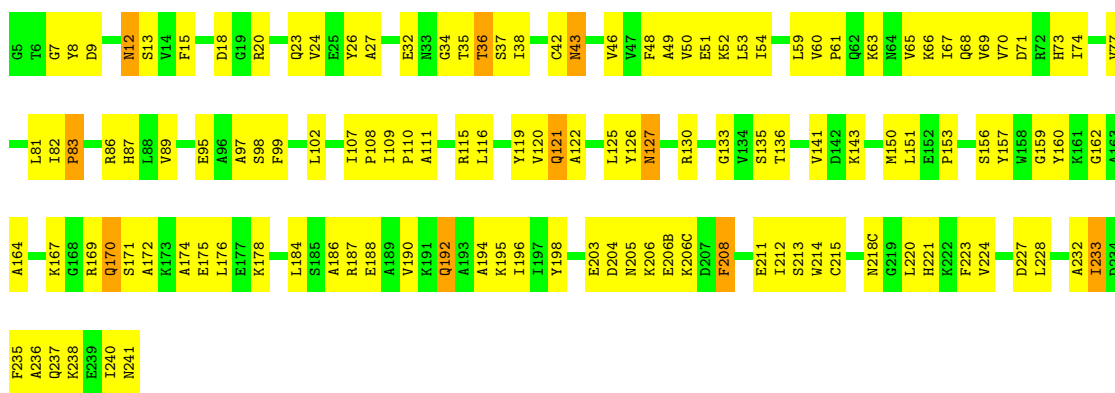
- Molecule 6: PROTEASOME COMPONENT C1

Chain F:



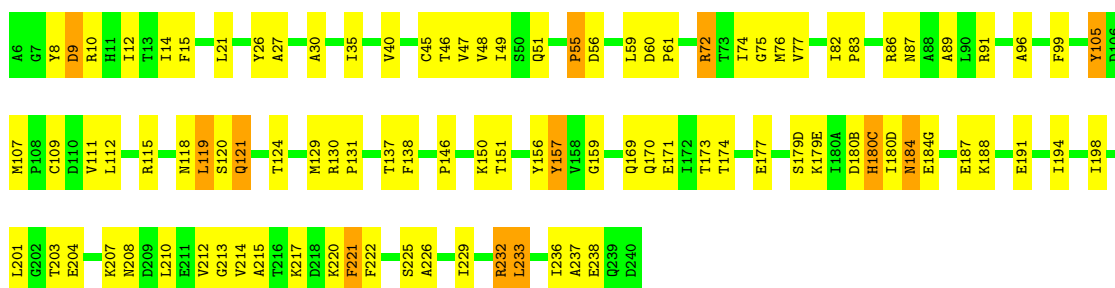
- Molecule 6: PROTEASOME COMPONENT C1

Chain 1:



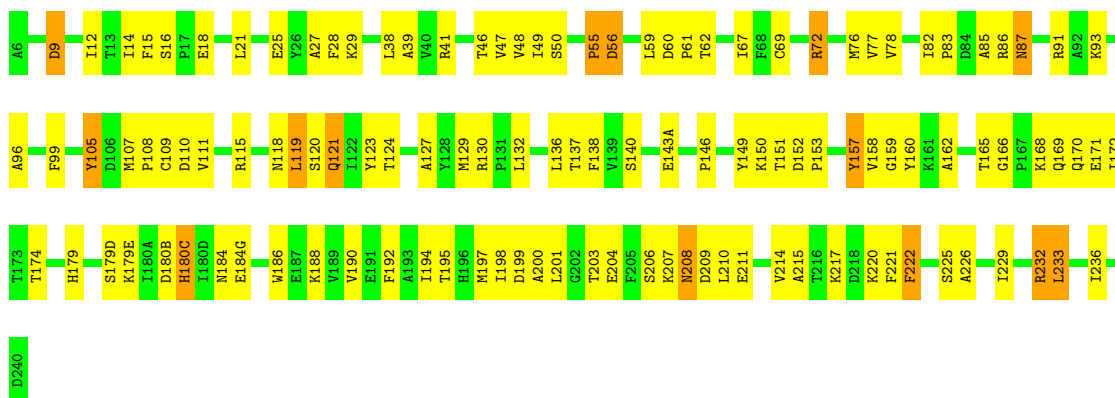
• Molecule 7: PROTEASOME COMPONENT C7-ALPHA

Chain G:



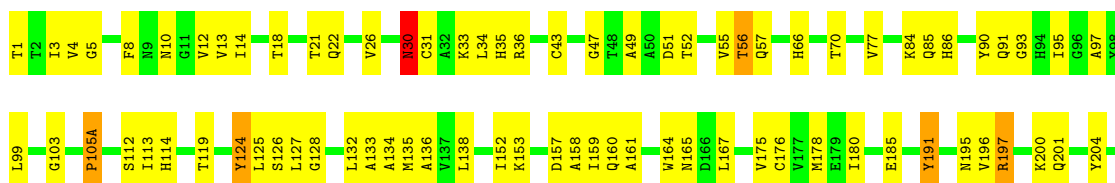
• Molecule 7: PROTEASOME COMPONENT C7-ALPHA

Chain 2:



• Molecule 8: PROTEASOME COMPONENT PUP1

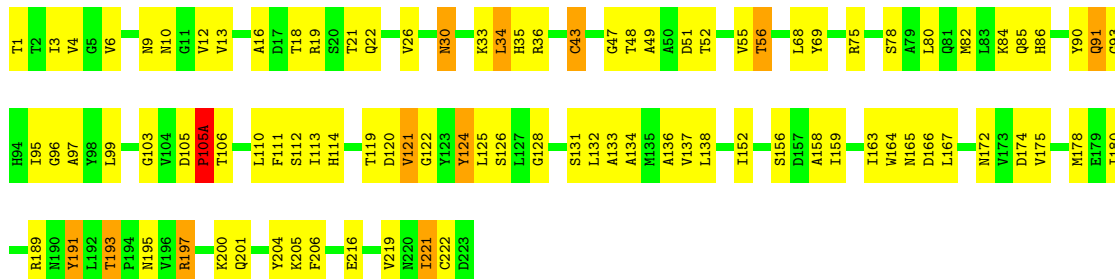
Chain H:





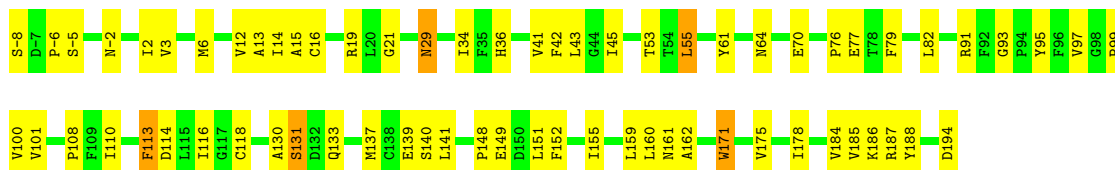
• Molecule 8: PROTEASOME COMPONENT PUP1

Chain O:



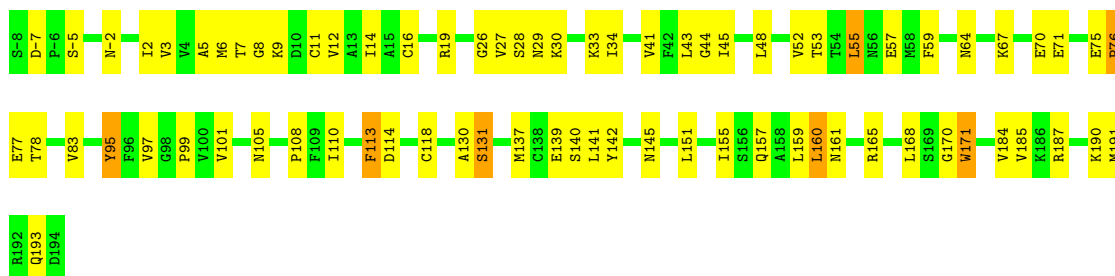
• Molecule 9: PROTEASOME COMPONENT PUP3

Chain I:



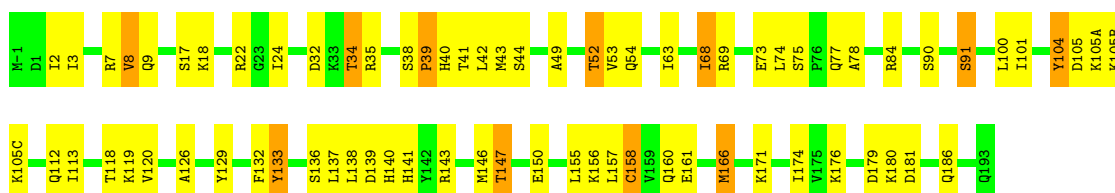
• Molecule 9: PROTEASOME COMPONENT PUP3

Chain P:



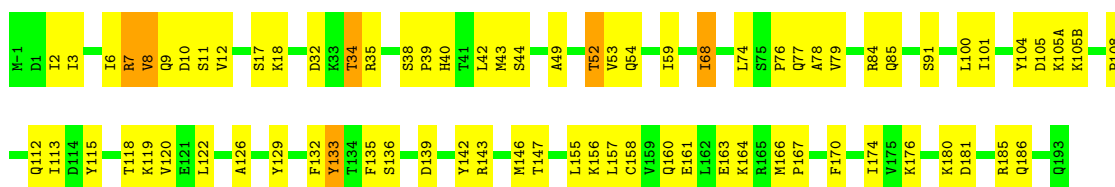
• Molecule 10: PROTEASOME COMPONENT C11

Chain J:



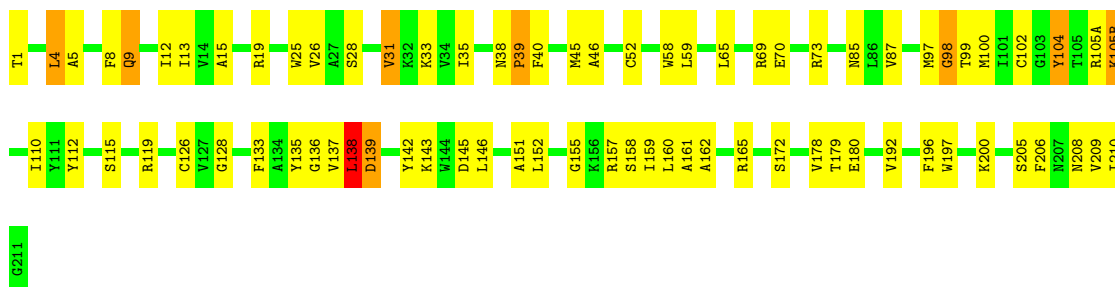
• Molecule 10: PROTEASOME COMPONENT C11

Chain Q:



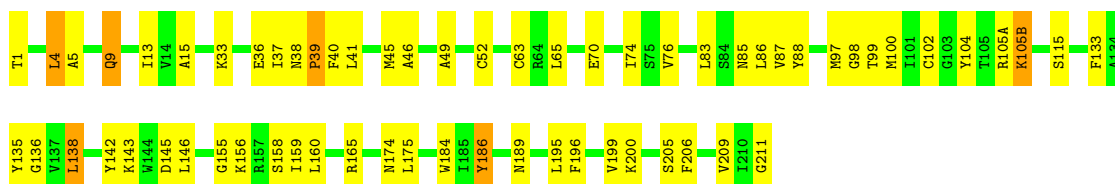
• Molecule 11: PROTEASOME COMPONENT PRE2

Chain K:



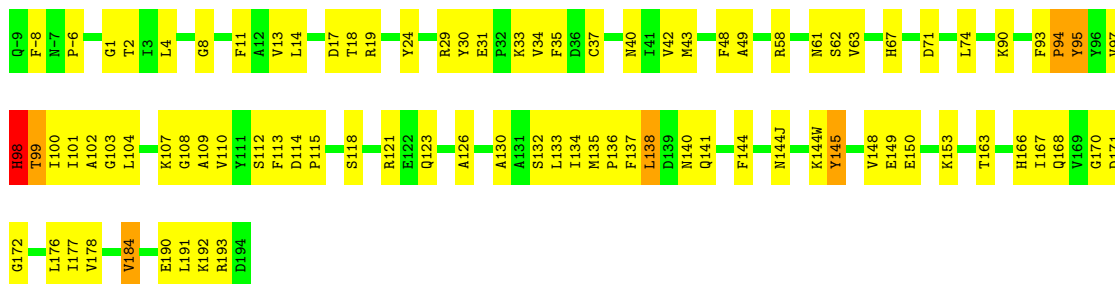
• Molecule 11: PROTEASOME COMPONENT PRE2

Chain R:



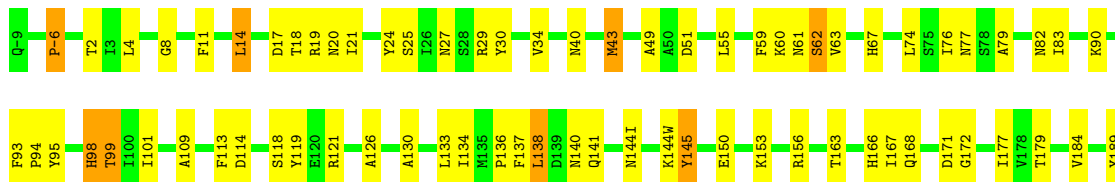
• Molecule 12: PROTEASOME COMPONENT C5

Chain L:



• Molecule 12: PROTEASOME COMPONENT C5

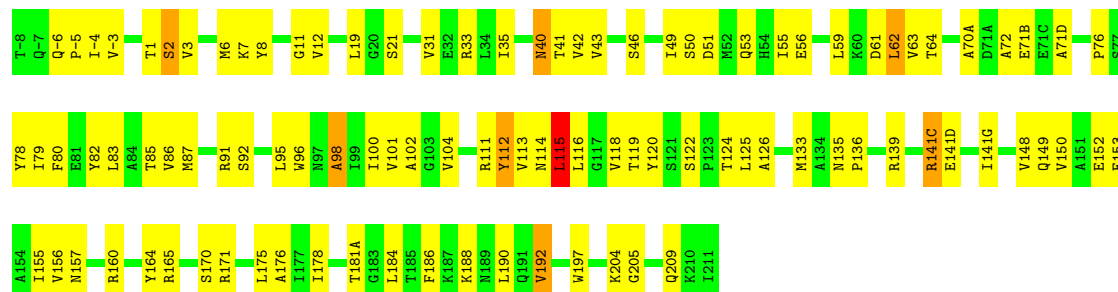
Chain S:



E190  
L191  
K192  
R193  
D194

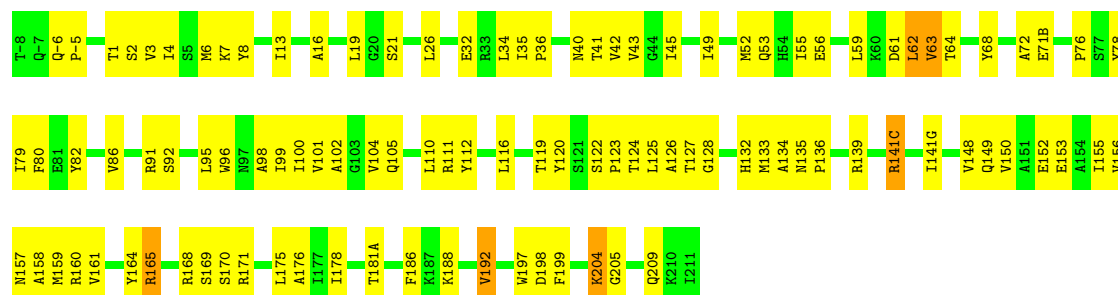
• Molecule 13: PROTEASOME COMPONENT PRE4

Chain M:



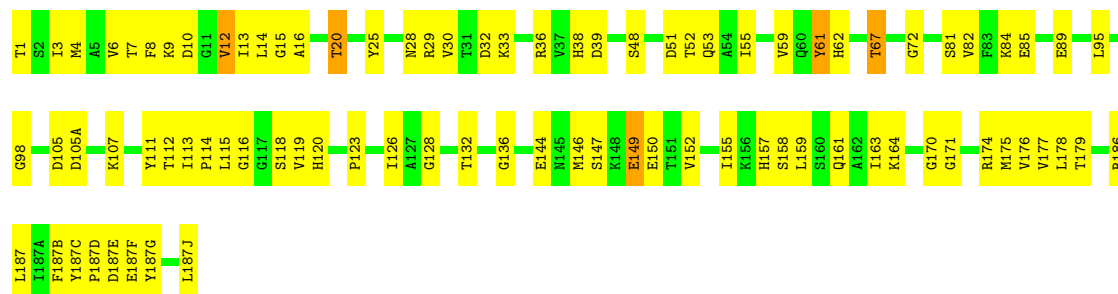
• Molecule 13: PROTEASOME COMPONENT PRE4

Chain T:



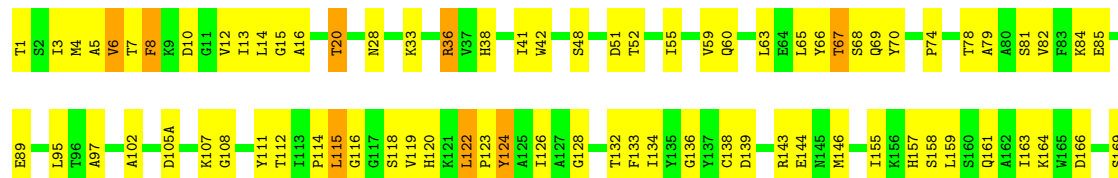
• Molecule 14: PROTEASOME COMPONENT PRE3

Chain N:



• Molecule 14: PROTEASOME COMPONENT PRE3

Chain U:







• Molecule 15: TMC-95A inhibitor



• Molecule 15: TMC-95A inhibitor



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.20Å 301.30Å 144.80Å 90.00° 112.60° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-3.00)	Depositor
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.251 , 0.336	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	52549	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: AKK, MG, 1QQ, R4K

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	0.65	0/1952	0.81	0/2642
1	V	0.62	0/1952	0.79	0/2642
2	B	0.65	0/1935	0.79	0/2618
2	W	0.62	0/1935	0.79	0/2618
3	C	0.65	0/1920	0.80	1/2598 (0.0%)
3	X	0.59	0/1920	0.78	0/2598
4	D	0.63	0/1887	0.78	1/2541 (0.0%)
4	Y	0.63	0/1887	0.78	2/2541 (0.1%)
5	E	0.57	0/1823	0.77	0/2463
5	Z	0.57	0/1823	0.78	0/2463
6	1	0.64	0/1937	0.79	0/2614
6	F	0.61	0/1937	0.78	1/2614 (0.0%)
7	2	0.71	0/1959	0.80	0/2652
7	G	0.65	0/1959	0.80	0/2652
8	H	0.72	0/1716	0.85	0/2326
8	O	0.69	1/1716 (0.1%)	0.81	0/2326
9	I	0.72	0/1611	0.84	0/2174
9	P	0.76	0/1611	0.85	2/2174 (0.1%)
10	J	0.70	1/1613 (0.1%)	0.82	0/2173
10	Q	0.69	0/1613	0.80	0/2173
11	K	0.71	0/1681	0.81	1/2274 (0.0%)
11	R	0.69	0/1681	0.80	0/2274
12	L	0.75	1/1795 (0.1%)	0.82	2/2420 (0.1%)
12	S	0.68	0/1795	0.83	1/2420 (0.0%)
13	M	0.68	0/1855	0.80	1/2514 (0.0%)
13	T	0.70	0/1855	0.84	3/2514 (0.1%)
14	N	0.75	0/1541	0.81	1/2087 (0.0%)
14	U	0.73	0/1541	0.78	1/2087 (0.0%)
15	8	1.96	0/20	2.20	2/26 (7.7%)
15	9	2.53	0/20	2.48	2/26 (7.7%)
All	All	0.67	3/50490 (0.0%)	0.81	21/68244 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	R	0	1
15	8	0	1
15	9	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	L	37	CYS	CB-SG	-5.27	1.73	1.81
8	O	43	CYS	CB-SG	-5.14	1.73	1.81
10	J	158	CYS	CB-SG	-5.06	1.73	1.81

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	9	3	ASN	CB-CG-OD1	-7.24	107.12	121.60
15	8	3	ASN	CB-CG-OD1	-7.21	107.18	121.60
13	T	98	ALA	N-CA-C	-6.22	94.20	111.00
15	9	3	ASN	OD1-CG-ND2	-6.11	107.85	121.90
9	P	95	TYR	N-CA-C	-6.02	94.74	111.00
12	L	98	HIS	N-CA-C	-5.80	95.34	111.00
3	C	103	LEU	CA-CB-CG	5.53	128.01	115.30
6	F	125	LEU	CA-CB-CG	5.49	127.94	115.30
13	M	98	ALA	N-CA-C	-5.45	96.28	111.00
15	8	3	ASN	OD1-CG-ND2	-5.40	109.49	121.90
14	U	122	LEU	CA-CB-CG	5.31	127.51	115.30
4	Y	214	CYS	CA-CB-SG	-5.25	104.55	114.00
4	Y	59	LEU	CA-CB-CG	5.21	127.27	115.30
13	T	116	LEU	CA-CB-CG	5.17	127.20	115.30
12	S	98	HIS	N-CA-C	-5.15	97.10	111.00
12	L	95	TYR	N-CA-C	-5.15	97.10	111.00
4	D	137	LEU	N-CA-C	-5.13	97.14	111.00
13	T	95	LEU	N-CA-C	-5.12	97.17	111.00
14	N	98	GLY	N-CA-C	-5.12	100.30	113.10
11	K	98	GLY	N-CA-C	-5.11	100.31	113.10
9	P	-7	ASP	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	8	3	ASN	Sidechain
15	9	3	ASN	Sidechain
11	R	186	TYR	Sidechain

## 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1926	59	0
1	V	1915	0	1926	71	0
2	B	1905	0	1901	75	0
2	W	1905	0	1901	75	0
3	C	1891	0	1900	68	0
3	X	1891	0	1900	92	0
4	D	1862	0	1836	75	0
4	Y	1862	0	1836	67	0
5	E	1795	0	1797	78	0
5	Z	1795	0	1797	111	0
6	1	1897	0	1886	111	0
6	F	1897	0	1886	101	0
7	2	1921	0	1910	95	0
7	G	1921	0	1910	83	0
8	H	1685	0	1688	75	0
8	O	1685	0	1688	83	0
9	I	1581	0	1574	56	0
9	P	1581	0	1574	67	0
10	J	1585	0	1590	55	0
10	Q	1585	0	1590	62	0
11	K	1644	0	1595	72	0
11	R	1644	0	1595	54	0
12	L	1757	0	1711	79	0
12	S	1757	0	1711	80	0
13	M	1824	0	1832	74	0
13	T	1824	0	1832	90	0
14	N	1512	0	1481	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	U	1512	0	1481	71	0
15	8	49	0	36	8	0
15	9	49	0	36	7	0
16	D	1	0	0	0	0
16	F	2	0	0	0	0
16	G	1	0	0	0	0
16	H	1	0	0	0	0
16	I	2	0	0	0	0
16	L	1	0	0	0	0
16	N	1	0	0	0	0
16	P	1	0	0	0	0
17	1	93	0	0	3	0
17	2	103	0	0	6	0
17	8	2	0	0	0	0
17	9	1	0	0	0	0
17	A	105	0	0	1	0
17	B	80	0	0	1	0
17	C	69	0	0	3	0
17	D	90	0	0	6	0
17	E	55	0	0	3	0
17	F	99	0	0	6	0
17	G	106	0	0	3	0
17	H	114	0	0	2	0
17	I	107	0	0	3	0
17	J	116	0	0	6	0
17	K	103	0	0	4	0
17	L	140	0	0	8	0
17	M	150	0	0	3	0
17	N	116	0	0	5	0
17	O	121	0	0	3	0
17	P	101	0	0	4	0
17	Q	121	0	0	5	0
17	R	107	0	0	4	0
17	S	144	0	0	6	0
17	T	142	0	0	8	0
17	U	118	0	0	1	0
17	V	104	0	0	2	0
17	W	74	0	0	2	0
17	X	70	0	0	4	0
17	Y	89	0	0	5	0
17	Z	53	0	0	2	0
All	All	52549	0	49326	1936	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 20.

All (1936) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:2:123:TYR:O	17:2:2009:HOH:O	1.54	1.25
14:N:136:GLY:HA2	14:U:161:GLN:HE21	1.13	1.10
14:N:161:GLN:HE21	14:U:136:GLY:HA2	1.21	1.05
8:H:21:THR:O	15:8:4:R4K:O33	1.75	1.05
8:O:21:THR:O	15:9:4:R4K:O33	1.75	1.04
3:C:15:PHE:H	4:D:23:GLN:HE22	1.13	0.97
3:C:185:THR:HB	3:C:188:GLU:HG2	1.46	0.96
2:W:202:THR:HG22	2:W:204:SER:H	1.31	0.96
5:Z:52:LYS:HB2	5:Z:63:TYR:HB3	1.45	0.96
7:G:96:ALA:HA	7:G:107:MET:HE2	1.48	0.95
9:P:114:ASP:HB3	15:9:3:ASN:ND2	1.80	0.95
2:B:126:HIS:HB3	3:C:129:VAL:HG12	1.48	0.94
6:1:81:LEU:HD12	6:1:133:GLY:HA3	1.45	0.94
8:O:166:ASP:O	17:O:2015:HOH:O	1.84	0.94
6:1:141:VAL:HG23	6:1:215:CYS:SG	2.09	0.93
5:E:15:PHE:HB2	6:F:23:GLN:HE22	1.33	0.92
9:I:114:ASP:HB3	15:8:3:ASN:HD21	1.35	0.92
5:Z:15:PHE:HB2	6:1:23:GLN:HE22	1.35	0.92
11:K:4:LEU:HD11	11:K:15:ALA:HB3	1.51	0.91
11:K:4:LEU:HD12	11:K:159:ILE:HD11	1.52	0.91
9:I:114:ASP:HB3	15:8:3:ASN:ND2	1.85	0.91
7:2:121:GLN:O	7:2:124:THR:HB	1.70	0.90
14:U:4:MET:HB3	14:U:126:ILE:HG22	1.54	0.90
6:F:141:VAL:HG23	6:F:215:CYS:SG	2.12	0.90
11:R:105(B):LYS:HD2	11:R:105(B):LYS:H	1.34	0.90
13:M:171:ARG:HG3	13:M:192:VAL:HG23	1.53	0.89
11:K:105(B):LYS:HD2	11:K:105(B):LYS:H	1.37	0.88
3:X:152:GLU:HG2	3:X:156:ILE:HG22	1.57	0.87
4:Y:177:LEU:HD22	5:Z:58:LEU:HD22	1.56	0.86
12:S:43:MET:HB2	12:S:101:ILE:HG22	1.55	0.86
13:T:157:ASN:ND2	13:T:160:ARG:HH11	1.73	0.86
13:M:41:THR:OG1	13:M:76:PRO:HG3	1.74	0.86
3:X:88:LEU:HD22	3:X:116:VAL:HG13	1.57	0.86
13:T:171:ARG:HG3	13:T:192:VAL:HG23	1.58	0.85
7:G:151:THR:HG22	7:G:157:TYR:HB2	1.59	0.85
3:C:152:GLU:HG2	3:C:156:ILE:HG22	1.58	0.85
4:Y:214:CYS:HG	4:Y:224:TYR:HE2	0.88	0.84
3:X:185:THR:HB	3:X:188:GLU:HG2	1.55	0.84
6:1:186:ALA:O	6:1:190:VAL:HG23	1.77	0.84

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:76:MET:SD	7:G:138:PHE:CE2	2.70	0.84
6:1:37:SER:HB3	6:1:50:VAL:HG23	1.60	0.84
12:S:18:THR:HG22	12:S:30:TYR:HA	1.59	0.84
3:C:35:THR:HB	3:C:51:GLU:HG3	1.61	0.83
1:V:124:THR:HG22	2:W:130:ARG:HH21	1.41	0.83
10:Q:176:LYS:HE2	10:Q:186:GLN:HE21	1.44	0.82
5:E:194:VAL:O	5:E:197:ILE:HG22	1.79	0.82
8:H:21:THR:HG22	8:H:26:VAL:HA	1.62	0.81
10:Q:113:ILE:HG12	10:Q:119:LYS:HG3	1.60	0.81
14:N:136:GLY:HA2	14:U:161:GLN:NE2	1.94	0.81
13:M:104:VAL:HG23	13:M:178:ILE:HG22	1.62	0.81
10:Q:133:TYR:CZ	10:Q:166:MET:HG3	2.15	0.81
9:I:194:ASP:O	17:I:2016:HOH:O	1.99	0.81
4:D:46:VAL:HG11	4:D:139:ALA:HB1	1.63	0.80
11:K:142:TYR:O	11:K:143:LYS:HD2	1.82	0.79
6:F:81:LEU:HD12	6:F:133:GLY:HA3	1.62	0.79
3:X:163:GLN:HE21	3:X:164:THR:H	1.30	0.79
13:T:133:MET:O	13:T:136:PRO:HD2	1.81	0.79
5:E:81:LEU:HB2	5:E:133:GLY:O	1.83	0.79
14:N:4:MET:HB3	14:N:126:ILE:HG22	1.65	0.79
5:E:75:GLY:HA3	5:E:221:PHE:CE2	2.17	0.79
14:U:157:HIS:CD2	14:U:187(J):LEU:HD13	2.18	0.79
3:X:163:GLN:NE2	3:X:164:THR:H	1.82	0.78
6:F:122:ALA:HA	6:F:125:LEU:HD12	1.65	0.78
5:Z:81:LEU:HB2	5:Z:133:GLY:O	1.84	0.78
9:P:114:ASP:HB3	15:9:3:ASN:HD21	1.48	0.77
10:Q:32:ASP:OD2	10:Q:34:THR:HG22	1.84	0.77
5:Z:52:LYS:HD2	5:Z:63:TYR:O	1.84	0.77
2:B:202:THR:HG22	2:B:204:SER:H	1.48	0.77
5:E:176:LEU:HD22	5:E:180(C):PHE:HE2	1.50	0.77
10:Q:18:LYS:HD3	10:Q:174:ILE:HG13	1.63	0.77
12:S:190:GLU:O	12:S:191:LEU:HD23	1.85	0.77
13:T:41:THR:OG1	13:T:76:PRO:HG3	1.85	0.77
6:F:37:SER:HB3	6:F:50:VAL:HG23	1.67	0.77
7:G:77:VAL:HG12	7:G:137:THR:HB	1.67	0.76
10:J:90:SER:O	10:J:91:SER:HB3	1.85	0.76
3:C:163:GLN:HE21	3:C:164:THR:H	1.32	0.76
11:R:143:LYS:O	11:R:146:LEU:HD13	1.86	0.76
7:2:96:ALA:HA	7:2:107:MET:HE2	1.67	0.75
13:M:152:GLU:O	13:M:156:VAL:HG23	1.87	0.75
5:E:143:LYS:HE3	13:M:78:TYR:OH	1.85	0.75
7:G:170:GLN:HE21	7:G:174:THR:HG23	1.52	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:76:MET:SD	7:G:138:PHE:HE2	2.09	0.75
4:Y:70:ILE:HB	4:Y:74:ILE:HG22	1.68	0.75
3:C:57:LYS:HD2	3:C:58:LEU:N	2.02	0.75
10:J:113:ILE:HG12	10:J:119:LYS:HG3	1.69	0.74
7:2:198:ILE:HG23	7:2:203:THR:O	1.87	0.74
14:N:161:GLN:NE2	14:U:136:GLY:HA2	2.00	0.74
1:V:7:ARG:HH22	4:Y:123(C):GLY:HA3	1.52	0.74
9:I:41:VAL:HG22	9:I:76:PRO:HG3	1.67	0.74
5:E:198:SER:HA	5:E:201:LEU:HG	1.69	0.74
7:G:77:VAL:CG1	7:G:137:THR:HB	2.18	0.74
5:Z:52:LYS:CB	5:Z:63:TYR:HB3	2.16	0.73
3:X:15:PHE:H	4:Y:23:GLN:HE22	1.36	0.73
7:2:59:LEU:O	7:2:61:PRO:HD3	1.88	0.73
3:X:36:CYS:SG	3:X:37:ALA:N	2.61	0.73
7:G:220:LYS:HG2	7:G:221:PHE:H	1.52	0.73
14:U:157:HIS:HD2	14:U:187(J):LEU:HD13	1.51	0.73
3:C:71:ASP:HA	10:J:68:ILE:HD11	1.71	0.73
5:Z:130:ARG:HH11	5:Z:130:ARG:HG3	1.52	0.73
12:S:8:GLY:HA3	12:S:11:PHE:CE2	2.23	0.73
4:D:75:GLY:HA3	4:D:221:PHE:CE2	2.24	0.73
8:H:197:ARG:HH21	9:I:139:GLU:HG3	1.52	0.73
8:H:197:ARG:NH2	9:I:139:GLU:HG3	2.03	0.73
12:S:18:THR:HG21	12:S:30:TYR:CD1	2.23	0.72
9:I:2:ILE:HG21	9:I:130:ALA:HB3	1.72	0.72
11:K:45:MET:HG2	11:K:52:CYS:HB3	1.71	0.72
5:Z:15:PHE:HB2	6:1:23:GLN:NE2	2.04	0.72
4:Y:40:ILE:HG23	4:Y:162:ALA:HB2	1.71	0.72
6:1:221:HIS:HE1	6:1:223:PHE:CE1	2.06	0.72
8:H:175:VAL:HG21	8:H:191:TYR:HD1	1.53	0.72
1:V:15:PHE:H	2:W:23:GLN:HE22	1.37	0.72
1:A:130:ARG:HH21	7:G:124:THR:HG22	1.55	0.72
11:R:4:LEU:HD12	11:R:159:ILE:HD11	1.71	0.71
7:2:233:LEU:O	7:2:236:ILE:HG13	1.91	0.71
10:Q:43:MET:SD	10:Q:101:ILE:HD11	2.30	0.71
13:T:160:ARG:HA	13:T:192:VAL:HG11	1.72	0.71
14:U:112:THR:HG22	14:U:120:HIS:HB2	1.72	0.71
12:L:43:MET:HB2	12:L:101:ILE:HG22	1.71	0.71
8:O:112:SER:HB3	8:O:125:LEU:HD13	1.72	0.71
13:M:42:VAL:HG23	13:M:178:ILE:HD11	1.72	0.70
14:U:163:ILE:HG23	14:U:170:GLY:HA2	1.71	0.70
9:P:131:SER:OG	17:P:2011:HOH:O	2.10	0.70
4:Y:163:LYS:HG3	4:Y:164:ALA:N	2.07	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:198:ILE:HG23	7:G:203:THR:O	1.91	0.70
3:X:35:THR:HB	3:X:51:GLU:HG3	1.72	0.70
12:L:137:PHE:CE1	12:L:141:GLN:HG3	2.26	0.70
5:E:130:ARG:HH11	5:E:130:ARG:HG3	1.54	0.70
7:2:96:ALA:HA	7:2:107:MET:CE	2.22	0.70
12:L:18:THR:HG21	12:L:30:TYR:CD1	2.26	0.70
6:F:42:CYS:HB2	6:F:184:LEU:O	1.91	0.70
2:B:124:THR:HG22	3:C:130:ARG:HH21	1.56	0.70
8:O:175:VAL:HG21	8:O:191:TYR:HD1	1.57	0.70
9:P:7:THR:HG23	9:P:110:ILE:HD13	1.74	0.69
13:M:124:THR:O	13:M:125:LEU:HD23	1.92	0.69
13:T:80:PHE:CE1	13:T:111:ARG:HD3	2.28	0.69
6:1:35:THR:HG21	6:1:51:GLU:O	1.92	0.69
11:R:87:VAL:HG11	11:R:115:SER:HA	1.73	0.69
6:F:36:THR:O	6:F:50:VAL:HG23	1.93	0.69
10:J:44:SER:OG	10:J:100:LEU:HB2	1.92	0.69
10:Q:105(B):LYS:HE2	2:W:143:ASP:OD2	1.93	0.69
13:T:6:MET:HG2	13:T:155:ILE:HD11	1.74	0.69
6:1:172:ALA:O	6:1:176:LEU:HD23	1.91	0.69
7:2:91:ARG:HH21	7:2:115:ARG:HH21	1.38	0.69
14:N:4:MET:CB	14:N:126:ILE:HG22	2.22	0.69
8:H:167:LEU:HD22	12:S:167:ILE:O	1.93	0.69
4:D:97:VAL:HG21	11:K:65:LEU:HD12	1.72	0.69
4:D:163:LYS:HG3	4:D:164:ALA:N	2.08	0.69
10:J:113:ILE:HA	10:J:118:THR:O	1.93	0.69
8:H:214:LEU:HD22	11:R:211:GLY:HA2	1.74	0.69
8:H:33:LYS:HE2	15:8:5:AKK:HA1	1.74	0.69
1:A:112:LEU:O	1:A:116:VAL:HG23	1.93	0.69
4:D:160:TYR:CE1	4:D:163:LYS:HD3	2.28	0.69
6:1:126:TYR:HE1	7:2:129:MET:SD	2.16	0.69
4:Y:45:GLY:HA2	4:Y:146:TYR:CE1	2.29	0.68
14:N:6:VAL:HG23	14:N:155:ILE:HD11	1.76	0.68
5:Z:75:GLY:HA3	5:Z:221:PHE:CE2	2.28	0.68
4:Y:46:VAL:HG11	4:Y:139:ALA:HB1	1.75	0.68
5:Z:194:VAL:O	5:Z:197:ILE:HG22	1.93	0.68
3:X:156:ILE:HD11	4:Y:82:THR:OG1	1.93	0.68
7:2:105:TYR:H	7:2:105:TYR:HD2	1.41	0.68
12:L:166:HIS:HD2	12:L:168:GLN:H	1.41	0.68
13:M:175:LEU:HD23	13:M:176:ALA:N	2.09	0.68
4:D:70:ILE:HB	4:D:74:ILE:HG22	1.75	0.68
12:L:109:ALA:HB2	12:L:121:ARG:NH2	2.08	0.68
14:N:163:ILE:HG23	14:N:170:GLY:HA2	1.76	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:66:LYS:HA	5:E:78:LEU:HD21	1.75	0.68
6:1:38:ILE:HG22	6:1:164:ALA:CB	2.23	0.68
13:T:4:ILE:HD11	13:T:159:MET:SD	2.33	0.68
2:B:126:HIS:CB	3:C:129:VAL:HG12	2.22	0.67
11:K:143:LYS:O	11:K:146:LEU:HD13	1.94	0.67
12:S:29:ARG:NH1	12:S:193:ARG:HB3	2.09	0.67
1:A:49:ALA:HB2	1:A:212:LEU:HG	1.77	0.67
14:N:157:HIS:HD2	14:N:187(J):LEU:HD13	1.60	0.67
13:T:175:LEU:HD23	13:T:176:ALA:N	2.10	0.67
5:Z:180(C):PHE:HD1	5:Z:180(D):ILE:N	1.93	0.67
4:D:75:GLY:HA3	4:D:221:PHE:CD2	2.30	0.67
9:I:178:ILE:HG23	9:I:184:VAL:HG22	1.77	0.67
4:D:97:VAL:HG21	11:K:65:LEU:CD1	2.23	0.67
5:E:97:ASN:HD21	12:L:61:ASN:HD21	1.42	0.67
10:Q:133:TYR:OH	10:Q:166:MET:HG3	1.93	0.67
3:C:163:GLN:NE2	3:C:164:THR:H	1.91	0.67
7:G:184(G):GLU:HG2	7:G:188:LYS:CB	2.25	0.67
8:O:197:ARG:NH2	9:P:139:GLU:HG3	2.10	0.67
11:R:65:LEU:HD12	4:Y:97:VAL:HG21	1.76	0.67
2:W:69:LYS:HG3	2:W:221:GLN:OE1	1.95	0.66
6:F:82:ILE:HB	6:F:83:PRO:HD3	1.77	0.66
6:1:69:VAL:HG12	17:1:2563:HOH:O	1.94	0.66
12:L:90:LYS:HD3	12:L:95:TYR:CE1	2.29	0.66
11:K:196:PHE:HZ	11:K:209:VAL:HG21	1.59	0.66
12:S:163:THR:O	17:S:2012:HOH:O	2.12	0.66
7:G:105:TYR:HD2	7:G:105:TYR:H	1.41	0.66
4:D:215:ILE:HG22	4:D:221:PHE:HD2	1.60	0.66
7:G:12:ILE:HA	17:G:538:HOH:O	1.95	0.66
7:2:12:ILE:HG13	7:2:14:ILE:HG23	1.77	0.66
2:W:175:LEU:HB3	17:W:2109:HOH:O	1.95	0.66
3:X:38:VAL:HG22	3:X:39:GLY:N	2.11	0.66
2:W:88:LEU:HD22	2:W:116:LEU:HD22	1.77	0.66
12:S:109:ALA:HB2	12:S:121:ARG:NH2	2.11	0.66
6:F:78:TYR:CE1	6:F:85:GLY:HA3	2.31	0.66
7:G:150:LYS:O	7:G:157:TYR:HA	1.95	0.65
2:B:150:THR:O	2:B:157:TYR:HA	1.95	0.65
7:G:233:LEU:O	7:G:236:ILE:HG13	1.96	0.65
2:W:15:PHE:HB2	3:X:23:GLN:HE22	1.61	0.65
14:N:157:HIS:CD2	14:N:187(J):LEU:HD13	2.31	0.65
13:M:135:ASN:O	13:M:139:ARG:HG3	1.97	0.65
14:N:51:ASP:O	14:N:55:ILE:HG13	1.96	0.65
1:A:50:THR:HG21	1:A:66:LYS:HE2	1.78	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:T:78:TYR:OH	5:Z:143:LYS:HE3	1.96	0.65
9:P:64:ASN:HD22	2:W:97:GLN:HE22	1.44	0.65
10:Q:68:ILE:CD1	3:X:71:ASP:HA	2.27	0.65
7:G:184(G):GLU:HG2	7:G:188:LYS:HB2	1.79	0.65
9:I:14:ILE:HG23	9:I:34:ILE:HD13	1.78	0.65
14:N:4:MET:SD	14:N:159:LEU:HD21	2.37	0.65
5:Z:161:TYR:CE2	6:1:60:VAL:HA	2.31	0.65
1:A:15:PHE:H	2:B:23:GLN:HE22	1.42	0.65
5:Z:198:SER:HA	5:Z:201:LEU:HG	1.79	0.65
1:A:217(I):TYR:CE1	8:H:36:ARG:HD2	2.32	0.65
1:V:49:ALA:HB2	1:V:212:LEU:HG	1.78	0.64
14:N:30:VAL:HG11	13:T:199:PHE:HE2	1.62	0.64
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.79	0.64
11:R:105(A):ARG:HB3	11:R:105(B):LYS:HE3	1.78	0.64
6:F:24:VAL:O	6:F:27:ALA:HB3	1.98	0.64
5:Z:22:PHE:HD1	5:Z:26:TYR:HE1	1.46	0.64
12:S:4:LEU:HD13	12:S:126:ALA:HB2	1.80	0.64
3:X:57:LYS:HD2	3:X:58:LEU:N	2.11	0.64
2:W:126:HIS:HB3	3:X:129:VAL:HG12	1.79	0.64
6:F:126:TYR:HE1	7:G:129:MET:SD	2.20	0.64
3:C:71:ASP:HA	10:J:68:ILE:CD1	2.27	0.64
6:1:221:HIS:HE1	6:1:223:PHE:HE1	1.46	0.64
6:F:221:HIS:HE1	6:F:223:PHE:CE1	2.16	0.64
5:Z:117:CYS:SG	6:1:86:ARG:HD3	2.38	0.64
14:U:6:VAL:HG23	14:U:155:ILE:HD11	1.80	0.64
12:S:144(W):LYS:HG2	12:S:145:TYR:N	2.13	0.63
4:Y:214:CYS:SG	4:Y:224:TYR:CE2	2.87	0.63
14:N:59:VAL:HG13	14:N:82:VAL:HG11	1.79	0.63
8:O:80:LEU:HD12	8:O:113:ILE:HD11	1.80	0.63
7:G:220:LYS:HG2	7:G:221:PHE:N	2.13	0.63
13:T:152:GLU:O	13:T:156:VAL:HG23	1.98	0.63
12:L:24:TYR:HA	8:O:167:LEU:HD12	1.81	0.63
7:G:121:GLN:O	7:G:124:THR:HB	1.99	0.63
8:H:18:THR:HB	8:H:30:ASN:HA	1.81	0.63
3:C:40:VAL:HG12	3:C:162:ALA:HB1	1.81	0.63
5:Z:48:LEU:HD13	5:Z:77:SER:HB3	1.80	0.63
8:O:113:ILE:HG12	8:O:119:THR:HG22	1.79	0.63
12:L:29:ARG:NH1	12:L:193:ARG:HB3	2.13	0.63
4:D:180(C):HIS:CD2	4:D:184:LEU:HG	2.34	0.63
12:L:133:LEU:O	12:L:136:PRO:HD2	1.99	0.63
14:N:67:THR:HA	14:N:72:GLY:O	1.99	0.63
13:T:91:ARG:HG3	13:T:92:SER:N	2.13	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:1:184:LEU:HD11	6:1:188:GLU:HB3	1.81	0.63
4:Y:46:VAL:HG11	4:Y:139:ALA:CB	2.29	0.63
12:L:109:ALA:HB2	12:L:121:ARG:HH21	1.63	0.63
3:C:163:GLN:HG3	3:C:164:THR:N	2.14	0.62
10:J:39:PRO:HD3	17:J:3265:HOH:O	1.99	0.62
6:F:186:ALA:O	6:F:190:VAL:HG23	2.00	0.62
3:X:197:LEU:O	3:X:201:VAL:HG23	1.98	0.62
3:X:134:VAL:HG12	3:X:135:SER:N	2.14	0.62
12:S:29:ARG:HD3	12:S:171:ASP:OD1	1.99	0.62
7:2:207:LYS:HG3	7:2:208:ASN:OD1	1.99	0.62
6:1:160:TYR:HB3	6:1:162:GLY:O	1.99	0.62
2:B:6:ARG:HG3	5:E:127:TYR:OH	1.99	0.62
4:Y:65:GLU:HA	17:Y:2028:HOH:O	1.99	0.62
1:V:130:ARG:HH21	7:2:124:THR:HG22	1.65	0.62
13:M:-5:PRO:HD3	13:M:96:TRP:CD2	2.35	0.62
2:W:229:ILE:O	2:W:232:ILE:HG22	1.99	0.62
6:F:12:ASN:ND2	6:F:131:PRO:HD3	2.14	0.62
11:K:5:ALA:HA	11:K:13:ILE:O	2.00	0.62
2:W:71:ASN:HD22	2:W:72:ASP:H	1.48	0.62
8:H:197:ARG:NH1	8:H:200:LYS:HD3	2.15	0.62
5:Z:226:GLY:O	5:Z:229:VAL:HG22	1.99	0.62
12:L:144(W):LYS:HG2	12:L:145:TYR:N	2.15	0.62
3:X:47:VAL:O	3:X:48:LEU:HD23	1.99	0.62
2:B:71:ASN:HD22	2:B:72:ASP:H	1.47	0.62
6:1:37:SER:HB3	6:1:50:VAL:CG2	2.29	0.62
4:D:38:ILE:HD12	4:D:197:LEU:HG	1.80	0.62
6:1:13:SER:HB2	7:2:130:ARG:HB3	1.81	0.62
8:O:49:ALA:HB1	9:P:118:CYS:SG	2.40	0.62
2:B:163:ILE:HG13	2:B:164:SER:H	1.65	0.62
10:J:133:TYR:CZ	10:J:166:MET:HG3	2.35	0.62
4:Y:78:MET:SD	4:Y:82:THR:HG22	2.40	0.62
12:L:190:GLU:O	12:L:191:LEU:HD23	2.00	0.62
5:E:52:LYS:HB3	5:E:63:TYR:HB3	1.80	0.62
13:M:6:MET:HG2	13:M:155:ILE:HD11	1.81	0.62
14:N:10:ASP:O	14:N:179:THR:HG22	2.00	0.62
9:P:114:ASP:HB3	15:9:3:ASN:HD22	1.64	0.61
8:O:35:HIS:HB3	8:O:56:THR:HG21	1.82	0.61
13:M:104:VAL:HG23	13:M:178:ILE:CG2	2.29	0.61
12:S:61:ASN:HD21	5:Z:97:ASN:HD21	1.47	0.61
10:Q:113:ILE:HA	10:Q:118:THR:O	2.00	0.61
9:I:113:PHE:CD2	9:I:113:PHE:N	2.68	0.61
9:I:137:MET:HE3	9:I:141:LEU:HD11	1.81	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:X:190:VAL:O	3:X:194:VAL:HG23	2.00	0.61
11:K:112:TYR:O	11:K:119:ARG:HA	2.01	0.61
7:2:91:ARG:NH2	7:2:115:ARG:HH21	1.98	0.61
5:Z:161:TYR:OH	6:1:61:PRO:HD2	2.00	0.61
13:M:80:PHE:CE1	13:M:111:ARG:HD3	2.35	0.61
10:Q:176:LYS:HE2	10:Q:186:GLN:NE2	2.15	0.61
3:X:36:CYS:HA	3:X:166:GLY:HA3	1.83	0.61
4:Y:214:CYS:SG	4:Y:224:TYR:HE2	2.08	0.61
6:F:119:TYR:O	6:F:122:ALA:HB3	2.00	0.61
6:1:176:LEU:HD22	6:1:196:ILE:HD13	1.82	0.61
12:S:134:ILE:HG22	12:S:138:LEU:HD22	1.82	0.61
14:U:134:ILE:HD12	14:U:158:SER:HB3	1.82	0.61
2:W:124:THR:HG22	3:X:130:ARG:HH21	1.66	0.61
13:M:82:TYR:O	13:M:86:VAL:HG23	2.00	0.61
3:C:38:VAL:HG22	3:C:39:GLY:N	2.16	0.61
6:F:35:THR:HG21	6:F:51:GLU:O	2.01	0.60
6:1:122:ALA:HA	6:1:125:LEU:HD12	1.83	0.60
8:O:84:LYS:HG3	8:O:85:GLN:N	2.14	0.60
5:E:52:LYS:HD2	5:E:63:TYR:O	2.01	0.60
7:G:212:VAL:HG12	7:G:213:GLY:N	2.16	0.60
7:2:220:LYS:HG2	7:2:221:PHE:H	1.67	0.60
2:W:71:ASN:ND2	2:W:72:ASP:H	1.99	0.60
10:Q:180:LYS:HG3	10:Q:181:ASP:OD1	2.01	0.60
5:E:180(C):PHE:HD1	5:E:180(D):ILE:N	2.00	0.60
12:S:-6:PRO:HB2	13:T:91:ARG:NH1	2.15	0.60
14:U:13:ILE:HG12	14:U:177:VAL:HG13	1.83	0.60
14:U:4:MET:CB	14:U:126:ILE:HG22	2.27	0.60
8:H:47:GLY:O	15:8:5:AKK:ND	2.34	0.60
7:G:12:ILE:HG13	7:G:14:ILE:HG23	1.83	0.60
13:M:133:MET:O	13:M:136:PRO:HD2	2.01	0.60
4:Y:215:ILE:HG13	4:Y:215:ILE:O	2.00	0.60
14:U:55:ILE:O	14:U:59:VAL:HG23	2.01	0.60
12:S:177:ILE:N	12:S:177:ILE:HD12	2.16	0.60
1:A:130:ARG:HH21	7:G:124:THR:CG2	2.14	0.60
7:G:229:ILE:O	7:G:232:ARG:HB2	2.01	0.60
8:H:4:VAL:HG22	8:H:159:ILE:HD11	1.83	0.60
10:J:180:LYS:HG3	10:J:181:ASP:OD1	2.01	0.60
6:F:184:LEU:HD11	6:F:188:GLU:CB	2.32	0.60
6:F:151:LEU:HD11	6:F:155:GLY:HA2	1.83	0.60
12:S:166:HIS:HD2	12:S:168:GLN:H	1.47	0.60
5:E:47:VAL:HG12	5:E:48:LEU:N	2.17	0.60
5:E:73:HIS:HE1	5:E:107:LEU:O	1.83	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:S:43:MET:CB	12:S:101:ILE:HG22	2.31	0.60
14:N:51:ASP:OD2	14:N:95:LEU:HA	2.01	0.60
11:R:38:ASN:O	11:R:40:PHE:N	2.34	0.60
9:I:6:MET:HB3	9:I:151:LEU:HD11	1.83	0.60
5:Z:70:CYS:SG	5:Z:92:LEU:HD23	2.42	0.60
10:Q:68:ILE:HD11	3:X:71:ASP:HA	1.84	0.60
8:O:78:SER:O	8:O:82:MET:HG3	2.01	0.60
8:H:152:ILE:CG2	8:H:191:TYR:HE1	2.14	0.59
12:S:133:LEU:O	12:S:136:PRO:HD2	2.02	0.59
8:H:200:LYS:HE3	9:I:140:SER:O	2.03	0.59
11:K:102:CYS:SG	11:K:110:ILE:HG23	2.42	0.59
5:E:198:SER:HA	5:E:201:LEU:CG	2.30	0.59
10:J:43:MET:SD	10:J:101:ILE:HD11	2.43	0.59
11:K:165:ARG:NH1	9:P:171:TRP:HH2	2.00	0.59
2:B:121:GLN:O	2:B:124:THR:HB	2.03	0.59
4:Y:237:LEU:HD22	4:Y:241:GLU:HG3	1.84	0.59
7:G:173:THR:O	7:G:177:GLU:HG3	2.03	0.59
13:M:149:GLN:NE2	13:M:149:GLN:H	2.00	0.59
5:Z:136:LEU:HD12	5:Z:151:PHE:CD2	2.37	0.59
8:H:3:ILE:O	8:H:3:ILE:HG13	2.02	0.59
11:R:5:ALA:HA	11:R:13:ILE:O	2.01	0.59
7:G:59:LEU:O	7:G:61:PRO:HD3	2.02	0.59
13:M:197:TRP:CH2	14:U:171:GLY:HA2	2.37	0.59
11:K:196:PHE:CE2	11:K:206:PHE:CD2	2.91	0.59
12:S:-6:PRO:HB2	13:T:91:ARG:HH11	1.65	0.59
8:H:84:LYS:HG3	8:H:85:GLN:N	2.18	0.59
12:L:134:ILE:HG22	12:L:138:LEU:HD22	1.84	0.59
3:X:163:GLN:HE21	3:X:164:THR:N	1.99	0.59
13:T:-5:PRO:HD3	13:T:96:TRP:CD2	2.36	0.59
13:T:3:VAL:HG22	13:T:16:ALA:HB2	1.83	0.59
6:F:38:ILE:HG22	6:F:164:ALA:HA	1.85	0.59
3:X:116:VAL:O	3:X:119:VAL:HB	2.02	0.59
5:Z:48:LEU:HG	5:Z:139:ILE:HD13	1.85	0.59
7:2:214:VAL:HG12	7:2:215:ALA:N	2.17	0.59
4:Y:197:LEU:O	4:Y:201:MET:HG3	2.02	0.59
3:C:71:ASP:O	3:C:73:HIS:N	2.36	0.59
4:Y:75:GLY:HA3	4:Y:221:PHE:CE2	2.38	0.59
5:E:77:SER:OG	5:E:137:LEU:HB2	2.02	0.59
9:P:70:GLU:HB3	17:P:2524:HOH:O	2.02	0.59
7:2:229:ILE:O	7:2:232:ARG:HB2	2.03	0.59
7:2:105:TYR:N	7:2:105:TYR:CD2	2.69	0.58
12:L:19:ARG:HB2	12:L:171:ASP:HB2	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:X:76:LEU:HD12	3:X:138:ILE:HG12	1.84	0.58
8:O:69:TYR:O	8:O:69:TYR:CD1	2.56	0.58
3:X:115:TYR:O	3:X:119:VAL:HG23	2.04	0.58
5:E:52:LYS:CB	5:E:63:TYR:HB3	2.33	0.58
1:A:79:SER:HB2	1:A:165:ILE:HD12	1.85	0.58
2:B:181:LYS:O	2:B:184:MET:HG3	2.02	0.58
6:1:171:SER:O	6:1:174:ALA:HB3	2.02	0.58
4:Y:67:ILE:HD13	4:Y:213:SER:OG	2.03	0.58
3:C:57:LYS:O	3:C:58:LEU:HB2	2.03	0.58
4:Y:160:TYR:CE1	4:Y:163:LYS:HD3	2.38	0.58
7:G:188:LYS:O	7:G:191:GLU:HB2	2.03	0.58
13:T:4:ILE:HD11	13:T:159:MET:HG2	1.85	0.58
6:1:42:CYS:HB2	6:1:184:LEU:O	2.02	0.58
2:W:160:TRP:CE3	2:W:163:ILE:HD13	2.39	0.58
1:V:27:ALA:O	1:V:31:VAL:HG23	2.02	0.58
7:2:67:ILE:HD12	7:2:211:GLU:HG2	1.83	0.58
8:O:10:ASN:OD1	8:O:180:ILE:HD12	2.04	0.58
8:H:52:THR:O	8:H:56:THR:HB	2.04	0.58
1:A:79:SER:HA	17:A:252:HOH:O	2.01	0.58
1:A:78:TYR:CE2	1:A:82:GLY:HA2	2.39	0.58
9:I:55:LEU:HD21	9:I:95:TYR:CD1	2.39	0.58
12:L:49:ALA:HA	17:L:531:HOH:O	2.02	0.58
11:R:65:LEU:CD1	4:Y:97:VAL:HG21	2.34	0.58
2:B:229:ILE:O	2:B:232:ILE:HG22	2.04	0.58
14:N:114:PRO:HD2	14:N:118:SER:O	2.03	0.58
12:S:109:ALA:HB2	12:S:121:ARG:HH21	1.67	0.58
13:T:124:THR:O	13:T:125:LEU:HD23	2.03	0.58
11:K:1:THR:HG23	11:K:33:LYS:NZ	2.19	0.58
13:T:4:ILE:CD1	13:T:159:MET:SD	2.92	0.58
11:K:196:PHE:CE1	9:P:193:GLN:HG3	2.39	0.58
13:M:87:MET:SD	13:M:95:LEU:HD12	2.44	0.58
8:O:172:ASN:HD22	8:O:193:THR:HA	1.69	0.58
12:L:-8:PHE:HE1	13:M:115:LEU:HD12	1.68	0.58
2:B:49:ALA:HB2	2:B:212:PHE:CE1	2.39	0.57
4:D:65:GLU:HA	17:D:246:HOH:O	2.04	0.57
8:O:36:ARG:HD2	1:V:217(I):TYR:CE1	2.39	0.57
13:M:141(C):ARG:HH11	13:M:141(C):ARG:HG3	1.70	0.57
6:1:36:THR:O	6:1:50:VAL:HG23	2.04	0.57
12:S:18:THR:CG2	12:S:30:TYR:HA	2.32	0.57
10:J:68:ILE:HG22	10:J:69:ARG:N	2.18	0.57
7:2:105:TYR:N	7:2:105:TYR:HD2	2.01	0.57
1:A:181:ASN:HD21	1:A:184:LEU:HD21	1.69	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:151:THR:HG22	7:G:157:TYR:CB	2.31	0.57
7:G:130:ARG:HG3	7:G:131:PRO:O	2.04	0.57
1:V:78:TYR:CE2	1:V:82:GLY:HA2	2.39	0.57
13:M:104:VAL:CG2	13:M:178:ILE:HG22	2.33	0.57
6:1:68:GLN:HE22	6:1:86:ARG:NH1	2.02	0.57
11:R:195:LEU:O	11:R:199:VAL:HG23	2.04	0.57
11:K:126:CYS:SG	11:K:135:TYR:CE2	2.96	0.57
4:D:97:VAL:HG11	11:K:65:LEU:CD1	2.34	0.57
4:D:159:ARG:HB3	5:E:60:SER:HB3	1.85	0.57
6:1:175:GLU:O	6:1:178:LYS:HB2	2.05	0.57
5:E:180(C):PHE:HA	5:E:180(F):ILE:HG13	1.86	0.57
5:Z:148:LEU:HD12	5:Z:149:LEU:N	2.19	0.57
2:B:20:ARG:HE	3:C:33:ARG:HH21	1.52	0.57
3:C:36:CYS:SG	3:C:37:ALA:N	2.78	0.57
4:Y:39:GLY:HA2	4:Y:47:VAL:O	2.03	0.57
4:D:46:VAL:HG11	4:D:139:ALA:CB	2.33	0.57
6:1:69:VAL:HG23	6:1:74:ILE:O	2.05	0.57
3:X:57:LYS:O	3:X:58:LEU:HB2	2.03	0.57
1:V:77:VAL:HG22	1:V:78:TYR:H	1.70	0.57
2:B:97:GLN:HE22	9:I:64:ASN:HD22	1.52	0.57
1:V:86:ARG:HH21	7:2:118:ASN:HD22	1.53	0.57
6:F:170:GLN:H	6:F:170:GLN:CD	2.08	0.57
11:K:105(B):LYS:HD2	11:K:105(B):LYS:N	2.14	0.57
13:T:76:PRO:HD2	13:T:105:GLN:OE1	2.04	0.57
14:U:163:ILE:HG21	14:U:187(G):TYR:OH	2.05	0.57
13:T:63:VAL:HG12	13:T:64:THR:N	2.19	0.57
10:Q:35:ARG:O	10:Q:42:LEU:HD12	2.04	0.57
4:D:177:LEU:HD22	5:E:58:LEU:HD22	1.86	0.57
7:G:46:THR:OG1	7:G:146:PRO:HB3	2.04	0.57
13:M:53:GLN:O	13:M:56:GLU:HB2	2.04	0.57
1:A:130:ARG:O	1:A:130:ARG:HG3	2.04	0.57
5:Z:78:LEU:HA	5:Z:136:LEU:HD23	1.87	0.57
5:E:17:PRO:HA	6:F:26:TYR:CD2	2.40	0.57
14:N:187(D):PRO:HA	14:N:187(G):TYR:CE2	2.40	0.57
11:R:142:TYR:O	11:R:143:LYS:HD2	2.05	0.57
4:Y:160:TYR:CZ	4:Y:163:LYS:HD3	2.40	0.57
3:C:160:TRP:CZ2	4:D:59:LEU:HD23	2.40	0.57
13:T:141(C):ARG:HH11	13:T:141(C):ARG:HG3	1.70	0.57
1:V:124:THR:CG2	2:W:130:ARG:HH21	2.15	0.56
5:Z:214:ILE:O	5:Z:221:PHE:HA	2.05	0.56
8:O:197:ARG:HH21	9:P:139:GLU:HG3	1.69	0.56
6:1:198:TYR:CE2	6:1:208:PHE:HZ	2.23	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:2:49:ILE:N	7:2:49:ILE:HD12	2.20	0.56
2:W:53:LYS:HG2	2:W:54:VAL:HG23	1.87	0.56
11:R:1:THR:HG23	11:R:33:LYS:NZ	2.20	0.56
12:L:192:LYS:HE3	8:O:195:ASN:HB3	1.87	0.56
7:2:220:LYS:HG2	7:2:221:PHE:N	2.21	0.56
2:W:163:ILE:HG13	2:W:164:SER:H	1.70	0.56
4:D:39:GLY:HA2	4:D:47:VAL:O	2.06	0.56
5:Z:24:VAL:O	5:Z:27:ALA:HB3	2.05	0.56
3:C:136:THR:O	3:C:150:GLN:HA	2.05	0.56
9:P:9:LYS:HD3	9:P:145:ASN:ND2	2.20	0.56
10:J:161:GLU:OE1	11:R:136:GLY:HA2	2.05	0.56
12:L:166:HIS:CD2	12:L:168:GLN:HB2	2.40	0.56
5:Z:73:HIS:HE1	5:Z:107:LEU:O	1.88	0.56
8:H:165:ASN:OD1	13:T:136:PRO:HA	2.05	0.56
5:Z:198:SER:HA	5:Z:201:LEU:CG	2.36	0.56
5:E:48:LEU:HD13	5:E:77:SER:HB3	1.87	0.56
14:U:85:GLU:O	14:U:89:GLU:HB2	2.06	0.56
12:S:63:VAL:HG22	12:S:74:LEU:HD23	1.86	0.56
14:U:10:ASP:O	14:U:179:THR:HG22	2.06	0.56
15:8:4:R4K:N	15:8:4:R4K:C32	2.69	0.56
4:D:215:ILE:O	4:D:215:ILE:HG13	2.05	0.56
9:P:101:VAL:O	9:P:110:ILE:HA	2.05	0.56
12:L:4:LEU:HD11	12:L:138:LEU:HD21	1.87	0.56
14:U:8:PHE:CZ	14:U:10:ASP:HB2	2.40	0.56
14:U:114:PRO:HD2	14:U:118:SER:O	2.06	0.56
1:V:4:MET:SD	1:V:5:THR:N	2.77	0.56
6:1:127:ASN:HD22	6:1:127:ASN:C	2.09	0.56
6:F:127:ASN:HD22	6:F:127:ASN:C	2.09	0.56
5:Z:114:HIS:HB3	6:1:86:ARG:NH2	2.21	0.56
6:F:38:ILE:HG22	6:F:164:ALA:CB	2.36	0.56
12:S:55:LEU:HD13	12:S:95:TYR:CD1	2.41	0.56
5:E:186:PRO:HG2	5:E:187:ASP:H	1.71	0.56
12:L:114:ASP:HB2	12:L:118:SER:HB3	1.88	0.56
1:A:4:MET:SD	1:A:5:THR:N	2.78	0.56
12:L:43:MET:CB	12:L:101:ILE:HG22	2.36	0.56
7:2:39:ALA:HB2	7:2:48:VAL:HG12	1.86	0.56
10:Q:44:SER:OG	10:Q:100:LEU:HB2	2.05	0.56
12:L:18:THR:HG22	12:L:30:TYR:HA	1.87	0.56
1:A:74:ILE:HG12	1:A:140:GLY:HA3	1.88	0.56
2:B:69:LYS:HG3	2:B:221:GLN:OE1	2.05	0.56
3:X:152:GLU:CG	3:X:156:ILE:HG22	2.34	0.56
6:1:70:VAL:HB	6:1:74:ILE:HB	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:8:PHE:CE1	13:M:115:LEU:HD12	2.41	0.56
12:L:140:ASN:O	12:L:144:PHE:HA	2.05	0.56
2:B:46:ILE:HD11	2:B:146:TYR:HB3	1.87	0.56
4:Y:188:GLU:O	4:Y:191:LEU:HB2	2.06	0.56
12:S:144(W):LYS:HG2	12:S:145:TYR:H	1.71	0.55
5:Z:148:LEU:HD12	5:Z:149:LEU:H	1.70	0.55
7:2:48:VAL:C	7:2:49:ILE:HD12	2.26	0.55
13:T:55:ILE:O	13:T:59:LEU:HG	2.06	0.55
7:G:48:VAL:C	7:G:49:ILE:HD12	2.26	0.55
5:E:78:LEU:HA	5:E:136:LEU:HD23	1.87	0.55
9:I:91:ARG:CD	9:I:116:ILE:HD12	2.36	0.55
9:I:186:LYS:HE2	9:I:188:TYR:OH	2.05	0.55
13:T:157:ASN:ND2	13:T:160:ARG:NH1	2.49	0.55
12:L:4:LEU:HD13	12:L:126:ALA:HB2	1.89	0.55
8:H:216:GLU:HG3	9:I:187:ARG:HG2	1.89	0.55
7:2:186:TRP:O	7:2:190:VAL:HG23	2.06	0.55
7:G:214:VAL:HG12	7:G:215:ALA:N	2.21	0.55
8:H:12:VAL:HG22	8:H:13:VAL:N	2.21	0.55
13:M:43:VAL:HG22	13:M:101:VAL:HG22	1.88	0.55
2:W:156:ASN:HD22	2:W:157:TYR:H	1.55	0.55
5:Z:40:LEU:HD23	5:Z:40:LEU:N	2.22	0.55
12:L:19:ARG:HD2	12:L:168:GLN:O	2.05	0.55
9:I:12:VAL:HG13	9:I:108:PRO:HB3	1.89	0.55
6:1:82:ILE:HB	6:1:83:PRO:HD3	1.87	0.55
13:T:165:ARG:HD2	13:T:165:ARG:N	2.20	0.55
2:B:15:PHE:HB2	3:C:23:GLN:HE22	1.72	0.55
1:A:13:THR:O	2:B:130:ARG:HD3	2.07	0.55
6:1:150:MET:HE1	6:1:160:TYR:CE2	2.42	0.55
1:A:86:ARG:HE	7:G:118:ASN:HD21	1.53	0.55
9:I:161:ASN:HD21	12:S:140:ASN:ND2	2.04	0.55
13:M:7:LYS:HD2	13:M:141(G):ILE:HD13	1.88	0.55
2:W:65:GLU:HG3	2:W:66:LYS:HG3	1.87	0.55
5:Z:186:PRO:HG2	5:Z:187:ASP:H	1.72	0.55
14:U:112:THR:CG2	14:U:120:HIS:HB2	2.37	0.55
9:I:8:SER:O	9:I:6:PRO:HD3	2.06	0.55
7:2:77:VAL:CG1	7:2:137:THR:HB	2.36	0.55
2:B:24:VAL:O	2:B:28:LEU:HD12	2.06	0.55
9:P:6:MET:HB3	9:P:151:LEU:HD11	1.89	0.55
13:M:46:SER:OG	13:M:98:ALA:HB3	2.06	0.55
7:2:180(B):ASP:O	7:2:180(C):HIS:HB3	2.06	0.55
13:T:45:ILE:HG12	13:T:99:ILE:HG12	1.89	0.55
10:J:129:TYR:O	10:J:132:PHE:HB2	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:Q:112:GLN:HE22	10:Q:126:ALA:H	1.54	0.55
4:D:160:TYR:CD2	5:E:59:SER:HB3	2.42	0.55
2:B:163:ILE:HG13	2:B:164:SER:N	2.21	0.55
8:O:105:ASP:HB2	8:O:105(A):PRO:HD2	1.89	0.55
9:P:12:VAL:CG1	9:P:108:PRO:HB3	2.37	0.55
9:I:97:VAL:HG23	9:I:99:PRO:HD3	1.89	0.55
10:Q:85:GLN:HE21	2:W:101:LYS:HZ2	1.54	0.55
9:P:113:PHE:CD2	9:P:113:PHE:N	2.75	0.55
7:2:72:ARG:HH11	7:2:72:ARG:HB2	1.71	0.55
6:F:50:VAL:HG22	6:F:51:GLU:N	2.22	0.54
4:Y:163:LYS:HE3	4:Y:164:ALA:O	2.06	0.54
14:U:48:SER:HB3	14:U:51:ASP:HB2	1.89	0.54
2:B:161:LYS:HE3	3:C:59:GLN:O	2.06	0.54
10:J:104:TYR:HD2	10:J:179:ASP:HA	1.72	0.54
14:N:38:HIS:CD2	17:N:352:HOH:O	2.59	0.54
5:Z:140:GLY:HA2	5:Z:215:VAL:HG11	1.88	0.54
8:H:49:ALA:HB1	9:I:118:CYS:SG	2.47	0.54
8:O:204:TYR:CD2	8:O:204:TYR:N	2.75	0.54
9:I:171:TRP:HH2	11:R:165:ARG:NH1	2.04	0.54
6:F:68:GLN:OE1	6:F:89:VAL:HG21	2.07	0.54
13:M:100:ILE:HD13	13:M:125:LEU:HB2	1.88	0.54
8:O:49:ALA:CB	9:P:118:CYS:SG	2.96	0.54
4:Y:20:ARG:NH1	5:Z:33:GLN:HE22	2.05	0.54
2:W:212:PHE:O	2:W:224:PHE:HB2	2.08	0.54
5:Z:76:LEU:HD23	5:Z:76:LEU:O	2.07	0.54
5:E:48:LEU:O	5:E:212:ILE:HG23	2.08	0.54
3:C:88:LEU:HD22	3:C:116:VAL:HG13	1.90	0.54
11:R:37:ILE:HB	11:R:41:LEU:O	2.08	0.54
13:T:153:GLU:HG3	17:T:1470:HOH:O	2.07	0.54
3:X:40:VAL:HG12	3:X:162:ALA:HB1	1.88	0.54
13:T:133:MET:C	13:T:136:PRO:HD2	2.27	0.54
11:R:4:LEU:O	11:R:4:LEU:HD13	2.07	0.54
6:1:38:ILE:HG22	6:1:164:ALA:HB2	1.89	0.54
6:1:24:VAL:O	6:1:27:ALA:HB3	2.08	0.54
3:X:187:GLU:HA	3:X:232:TYR:OH	2.07	0.54
2:W:126:HIS:CB	3:X:129:VAL:HG12	2.37	0.54
12:S:166:HIS:CD2	12:S:168:GLN:HB2	2.43	0.54
1:V:69:LEU:HD23	1:V:70:LEU:N	2.22	0.54
8:H:158:ALA:O	8:H:161:ALA:HB3	2.08	0.54
8:O:4:VAL:HG12	8:O:126:SER:HB2	1.90	0.54
11:K:4:LEU:CD1	11:K:15:ALA:HB3	2.31	0.54
5:E:150:GLU:O	5:E:157:VAL:HA	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:10:ASN:OD1	8:H:180:ILE:HD12	2.08	0.54
6:F:212:ILE:HG22	6:F:213:SER:H	1.72	0.54
11:K:25:TRP:CH2	12:L:132:SER:HA	2.43	0.54
3:X:43:LYS:O	3:X:43:LYS:HG2	2.08	0.54
3:X:180(D):GLU:N	3:X:182:PRO:HD3	2.23	0.54
11:R:200:LYS:HE3	11:R:206:PHE:O	2.08	0.54
5:E:15:PHE:HB2	6:F:23:GLN:NE2	2.12	0.54
11:K:105(A):ARG:HB3	11:K:105(B):LYS:HE3	1.90	0.54
12:L:90:LYS:HE3	12:L:93:PHE:O	2.08	0.54
10:J:32:ASP:OD2	10:J:34:THR:HG22	2.07	0.54
8:O:103:GLY:HA2	8:O:178:MET:SD	2.48	0.54
12:S:49:ALA:HA	17:S:2531:HOH:O	2.07	0.54
2:W:137:ILE:HD11	2:W:165:VAL:HG22	1.89	0.54
12:S:137:PHE:CE1	12:S:141:GLN:HG3	2.43	0.54
7:G:96:ALA:HA	7:G:107:MET:CE	2.29	0.53
2:B:212:PHE:O	2:B:224:PHE:HB2	2.08	0.53
14:U:114:PRO:O	14:U:116:GLY:N	2.41	0.53
12:L:-6:PRO:O	13:M:91:ARG:NH1	2.41	0.53
4:D:67:ILE:HD12	4:D:211:GLN:HE21	1.73	0.53
7:2:69:CYS:O	7:2:93:LYS:HE2	2.08	0.53
2:B:81:LEU:HD22	2:B:81:LEU:H	1.71	0.53
12:L:24:TYR:O	8:O:167:LEU:HG	2.08	0.53
8:O:200:LYS:HE3	9:P:140:SER:O	2.08	0.53
5:Z:162:GLY:O	5:Z:163:THR:HB	2.07	0.53
4:D:59:LEU:HD13	4:D:60:GLU:N	2.22	0.53
8:O:133:ALA:O	8:O:136:ALA:HB3	2.09	0.53
4:D:52:LYS:HG3	4:D:64:ILE:HG21	1.91	0.53
4:D:188:GLU:O	4:D:191:LEU:HB2	2.08	0.53
6:F:11:SER:O	6:F:14:VAL:HG23	2.08	0.53
9:P:45:ILE:HG22	9:P:52:VAL:HG22	1.90	0.53
1:V:76:ALA:HB2	1:V:138:ILE:HG12	1.89	0.53
8:H:132:LEU:HD11	14:N:25:TYR:CE1	2.43	0.53
14:N:3:ILE:HG22	14:N:16:ALA:CB	2.38	0.53
6:F:37:SER:HB3	6:F:50:VAL:CG2	2.38	0.53
12:S:61:ASN:HD21	5:Z:97:ASN:ND2	2.05	0.53
6:F:171:SER:O	6:F:174:ALA:HB3	2.08	0.53
3:C:44:ASN:O	3:C:45:CYS:HB3	2.09	0.53
13:T:186:PHE:HE1	13:T:188:LYS:HG3	1.74	0.53
7:G:109:CYS:HB3	17:G:754:HOH:O	2.08	0.53
5:E:141:TYR:OH	5:E:217:LYS:HG3	2.09	0.53
4:Y:221:PHE:CE1	4:Y:223:ILE:HG13	2.42	0.53
10:J:52:THR:CG2	10:J:53:VAL:N	2.72	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:121:LEU:HB2	17:D:3156:HOH:O	2.09	0.53
11:K:157:ARG:O	11:K:160:LEU:HB3	2.09	0.53
8:H:112:SER:HB3	8:H:125:LEU:HD13	1.91	0.53
14:N:55:ILE:O	14:N:59:VAL:HG23	2.09	0.53
8:H:35:HIS:CB	8:H:56:THR:HG21	2.38	0.53
4:D:186:LEU:O	4:D:190:GLU:HG3	2.08	0.53
6:1:65:VAL:HG12	6:1:66:LYS:N	2.23	0.53
8:H:43:CYS:SG	8:H:99:LEU:HD22	2.49	0.53
14:N:61:TYR:CD2	14:N:62:HIS:N	2.77	0.53
8:H:195:ASN:HB3	12:S:192:LYS:HE3	1.89	0.53
8:H:134:ALA:HB1	8:H:158:ALA:HB1	1.89	0.53
8:O:3:ILE:O	8:O:3:ILE:HG13	2.07	0.53
3:X:33:ARG:HB2	3:X:33:ARG:HH11	1.73	0.53
14:N:84:LYS:HD3	17:N:920:HOH:O	2.07	0.53
4:Y:15:PHE:HB2	5:Z:23:GLN:OE1	2.08	0.53
12:L:103:GLY:HA2	12:L:178:VAL:HG11	1.89	0.53
9:I:3:VAL:HG22	9:I:16:CYS:HB3	1.89	0.53
7:G:72:ARG:HH11	7:G:72:ARG:HB2	1.72	0.53
2:B:120:LYS:HZ1	2:B:136:PHE:HD1	1.57	0.53
10:Q:85:GLN:NE2	2:W:101:LYS:NZ	2.56	0.53
1:V:23:GLN:OE1	7:2:15:PHE:HB2	2.09	0.53
10:Q:166:MET:HG2	10:Q:167:PRO:HD2	1.91	0.53
14:N:159:LEU:O	14:N:163:ILE:HG13	2.09	0.53
13:T:41:THR:HG21	13:T:79:ILE:HD12	1.91	0.53
2:B:173:GLN:HA	2:B:176:LEU:HD12	1.91	0.53
8:O:34:LEU:HD22	8:O:174:ASP:HB3	1.90	0.53
12:S:114:ASP:HB2	12:S:118:SER:HB3	1.91	0.53
7:2:77:VAL:HG12	7:2:137:THR:HB	1.90	0.53
1:A:27:ALA:O	1:A:31:VAL:HG23	2.08	0.53
3:X:93:ARG:O	3:X:96:ALA:HB3	2.09	0.53
9:P:6:MET:HE3	9:P:155:ILE:HB	1.90	0.52
14:N:84:LYS:HB2	14:N:119:VAL:CG2	2.39	0.52
5:E:214:ILE:O	5:E:221:PHE:HA	2.09	0.52
1:V:15:PHE:N	2:W:23:GLN:HE22	2.06	0.52
5:E:130:ARG:NH1	5:E:130:ARG:HG3	2.23	0.52
6:F:184:LEU:HD11	6:F:188:GLU:HB3	1.91	0.52
3:X:38:VAL:CG2	3:X:39:GLY:N	2.73	0.52
13:M:133:MET:C	13:M:136:PRO:HD2	2.29	0.52
6:1:224:VAL:HG13	6:1:228:LEU:HD23	1.91	0.52
14:N:14:LEU:O	14:N:175:MET:HA	2.09	0.52
6:1:220:LEU:HD23	6:1:220:LEU:N	2.24	0.52
5:Z:160:LEU:HD13	5:Z:163:THR:HB	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:S:90:LYS:HE3	12:S:93:PHE:O	2.09	0.52
9:P:43:LEU:HD11	9:P:99:PRO:HB3	1.91	0.52
5:E:22:PHE:HD1	5:E:26:TYR:HE1	1.57	0.52
5:E:24:VAL:O	5:E:27:ALA:HB3	2.08	0.52
12:L:163:THR:HB	17:L:2651:HOH:O	2.09	0.52
2:W:191:GLU:HG3	2:W:236:THR:HG22	1.91	0.52
4:D:215:ILE:HG22	4:D:221:PHE:CD2	2.42	0.52
7:G:105:TYR:OH	8:H:66:HIS:HE1	1.93	0.52
13:M:113:VAL:HA	13:M:118:VAL:O	2.09	0.52
11:K:4:LEU:HD13	11:K:4:LEU:O	2.09	0.52
2:B:46:ILE:HG21	2:B:139:ALA:HB1	1.92	0.52
11:K:38:ASN:O	11:K:40:PHE:N	2.42	0.52
4:D:90:GLU:HA	17:D:509:HOH:O	2.08	0.52
11:R:105(B):LYS:HD2	11:R:105(B):LYS:N	2.14	0.52
7:G:105:TYR:N	7:G:105:TYR:CD2	2.77	0.52
13:M:112:TYR:O	13:M:119:THR:HA	2.09	0.52
9:P:2:ILE:HG21	9:P:130:ALA:HB3	1.92	0.52
10:J:176:LYS:HE2	10:J:186:GLN:HE21	1.75	0.52
5:Z:52:LYS:O	5:Z:63:TYR:HD2	1.92	0.52
12:L:140:ASN:ND2	9:P:161:ASN:HD21	2.06	0.52
12:S:79:ALA:O	12:S:83:ILE:HG13	2.10	0.52
8:O:134:ALA:O	8:O:137:VAL:N	2.43	0.52
5:E:223:ILE:HG22	5:E:223:ILE:O	2.09	0.52
12:S:43:MET:HB2	12:S:101:ILE:CG2	2.33	0.52
11:K:165:ARG:HH11	9:P:171:TRP:HH2	1.57	0.52
5:E:36:VAL:HG22	5:E:37:THR:N	2.24	0.52
7:2:108:PRO:HB2	7:2:111:VAL:HG23	1.91	0.52
7:2:109:CYS:HB3	17:2:2754:HOH:O	2.09	0.52
5:Z:207:LEU:H	5:Z:207:LEU:HD23	1.74	0.52
3:X:163:GLN:HG3	3:X:164:THR:N	2.25	0.52
5:Z:22:PHE:HD1	5:Z:26:TYR:CE1	2.27	0.52
1:V:8:TYR:CD1	7:2:127:ALA:HB3	2.45	0.52
3:C:238:GLN:C	3:C:240:LYS:H	2.13	0.52
13:T:104:VAL:HG23	13:T:178:ILE:HG22	1.92	0.52
1:A:55:SER:HB2	17:G:3268:HOH:O	2.10	0.52
11:R:105(B):LYS:CD	11:R:105(B):LYS:H	2.13	0.52
5:Z:180(C):PHE:C	5:Z:180(E):LYS:H	2.14	0.52
2:B:38:ILE:HG23	2:B:164:SER:HB3	1.92	0.52
4:Y:48:LEU:HD23	4:Y:77:ALA:HB2	1.92	0.52
7:G:47:VAL:HG12	7:G:48:VAL:N	2.24	0.52
1:A:124:THR:HG22	2:B:130:ARG:HH21	1.73	0.52
8:O:219:VAL:HG23	9:P:184:VAL:HG12	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:O:221:ILE:HG22	8:O:222:CYS:N	2.25	0.52
5:E:180:LEU:HD12	5:E:180(C):PHE:HE1	1.75	0.51
8:O:172:ASN:ND2	8:O:193:THR:HA	2.23	0.51
4:D:123:PHE:CE1	4:D:131:PRO:HG3	2.44	0.51
2:B:141:TYR:CD1	2:B:219(E):VAL:HG21	2.45	0.51
12:L:97:VAL:O	12:L:115:PRO:HB3	2.10	0.51
9:I:79:PHE:O	9:I:82:LEU:HB3	2.10	0.51
6:1:151:LEU:HD12	6:1:156:SER:O	2.10	0.51
10:J:18:LYS:HD3	10:J:174:ILE:HG13	1.90	0.51
8:O:172:ASN:ND2	8:O:193:THR:HG22	2.25	0.51
3:X:33:ARG:HB2	3:X:33:ARG:NH1	2.25	0.51
8:H:113:ILE:HG12	8:H:119:THR:HG22	1.91	0.51
7:2:47:VAL:HG12	7:2:48:VAL:N	2.26	0.51
2:W:150:THR:O	2:W:157:TYR:HA	2.10	0.51
10:J:35:ARG:O	10:J:42:LEU:HD12	2.10	0.51
2:W:185:LYS:HD3	2:W:186:VAL:N	2.26	0.51
12:S:14:LEU:CD1	12:S:34:VAL:HG13	2.40	0.51
10:J:147:THR:HG23	10:J:150:GLU:HG3	1.93	0.51
7:G:187:GLU:O	7:G:191:GLU:HG3	2.10	0.51
12:S:-6:PRO:O	13:T:91:ARG:NH1	2.43	0.51
6:1:121:GLN:HG2	7:2:83:PRO:HB2	1.91	0.51
6:1:130:ARG:HG3	6:1:130:ARG:HH11	1.75	0.51
2:W:15:PHE:HB2	3:X:23:GLN:NE2	2.24	0.51
2:B:160:TRP:CD2	2:B:163:ILE:HD13	2.45	0.51
4:Y:75:GLY:HA3	4:Y:221:PHE:CD2	2.45	0.51
8:H:221:ILE:HG22	8:H:222:CYS:N	2.25	0.51
1:V:71:THR:O	1:V:73:ASP:N	2.44	0.51
14:N:161:GLN:O	14:N:164:LYS:HB3	2.10	0.51
13:M:135:ASN:ND2	13:M:139:ARG:NH2	2.59	0.51
11:K:12:ILE:HB	11:K:178:VAL:HB	1.92	0.51
9:P:-2:ASN:OD1	9:P:48:LEU:HD12	2.11	0.51
6:F:21:ASN:HB2	17:F:547:HOH:O	2.10	0.51
13:T:150:VAL:HG21	17:T:2869:HOH:O	2.10	0.51
11:R:45:MET:HG2	11:R:52:CYS:HB3	1.92	0.51
13:T:112:TYR:O	13:T:119:THR:HA	2.10	0.51
14:U:187(D):PRO:O	14:U:187(F):GLU:N	2.44	0.51
7:G:91:ARG:HH21	7:G:115:ARG:HH21	1.57	0.51
14:N:8:PHE:CE1	14:N:10:ASP:HB2	2.46	0.51
12:L:177:ILE:N	12:L:177:ILE:HD12	2.26	0.51
14:U:14:LEU:HD21	14:U:102:ALA:HB3	1.91	0.51
11:K:8:PHE:HE2	11:K:13:ILE:HG12	1.75	0.51
11:K:126:CYS:SG	11:K:135:TYR:CD2	2.87	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:86:ARG:HH21	7:G:118:ASN:HD22	1.59	0.51
6:1:95:GLU:HG3	6:1:115:ARG:HH11	1.75	0.51
4:Y:186:LEU:O	4:Y:190:GLU:HG3	2.11	0.51
4:Y:112:LEU:HD13	4:Y:112:LEU:C	2.31	0.51
4:Y:160:TYR:CE2	5:Z:59:SER:HB3	2.46	0.51
6:F:68:GLN:HE22	6:F:86:ARG:NH1	2.09	0.51
13:M:164:TYR:C	13:M:165:ARG:HD2	2.31	0.51
14:N:15:GLY:HA2	14:N:174:ARG:O	2.10	0.51
1:A:46:VAL:HG12	1:A:47:VAL:N	2.25	0.51
7:2:14:ILE:O	7:2:21:LEU:HD23	2.11	0.51
14:N:30:VAL:HG11	13:T:199:PHE:CE2	2.43	0.51
12:L:115:PRO:HA	17:L:613:HOH:O	2.11	0.51
12:S:14:LEU:HD12	12:S:34:VAL:HG13	1.93	0.51
7:2:38:LEU:HD23	7:2:197:MET:CE	2.41	0.51
1:A:137:LEU:HA	1:A:149:TYR:O	2.11	0.51
7:2:222:PHE:N	7:2:222:PHE:CD2	2.79	0.51
14:U:14:LEU:O	14:U:175:MET:HA	2.10	0.50
8:H:51:ASP:HB3	8:H:95:ILE:HG23	1.93	0.50
6:1:109:ILE:O	6:1:110:PRO:C	2.49	0.50
1:A:35:VAL:HG12	1:A:36:THR:N	2.26	0.50
9:P:28:SER:HA	17:P:1086:HOH:O	2.11	0.50
8:O:197:ARG:NH2	9:P:139:GLU:O	2.44	0.50
4:D:180(C):HIS:NE2	4:D:184:LEU:HG	2.25	0.50
3:X:76:LEU:HD12	3:X:138:ILE:CG1	2.41	0.50
6:F:68:GLN:HG2	17:F:407:HOH:O	2.11	0.50
12:L:153:LYS:HG2	8:O:201:GLN:HG2	1.93	0.50
10:J:24:ILE:HG12	10:J:24:ILE:O	2.11	0.50
8:H:167:LEU:HG	12:S:24:TYR:O	2.12	0.50
9:P:160:LEU:HD11	9:P:191:MET:HB3	1.93	0.50
10:J:143:ARG:O	10:J:146:MET:HG3	2.11	0.50
5:Z:45:HIS:HB2	5:Z:189:LEU:HD12	1.92	0.50
1:A:110:LYS:HG3	1:A:111:LEU:N	2.27	0.50
5:Z:41:ARG:HG3	5:Z:41:ARG:O	2.11	0.50
5:Z:15:PHE:H	6:1:23:GLN:HE22	1.59	0.50
5:E:180(C):PHE:C	5:E:180(E):LYS:H	2.15	0.50
5:Z:207:LEU:H	5:Z:207:LEU:CD2	2.25	0.50
11:K:104:TYR:CD1	11:K:180:GLU:HG3	2.45	0.50
14:N:7:THR:HA	14:N:12:VAL:HG23	1.93	0.50
4:D:41:ALA:HA	4:D:46:VAL:HG22	1.92	0.50
8:H:47:GLY:H	15:8:5:AKK:HC1	1.76	0.50
13:M:8:TYR:CE2	13:M:148:VAL:HG22	2.46	0.50
7:2:179:HIS:CD2	7:2:192:PHE:HZ	2.29	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:34:VAL:HG12	12:L:176:LEU:HD22	1.92	0.50
13:T:32:GLU:OE1	13:T:34:LEU:HB2	2.11	0.50
2:B:124:THR:CG2	3:C:130:ARG:HH21	2.22	0.50
6:1:68:GLN:OE1	6:1:89:VAL:HG21	2.11	0.50
4:D:197:LEU:O	4:D:201:MET:HG3	2.12	0.50
9:I:171:TRP:HH2	11:R:165:ARG:HH11	1.59	0.50
4:D:112:LEU:C	4:D:112:LEU:HD13	2.32	0.50
4:D:14:THR:HA	17:D:3133:HOH:O	2.12	0.50
6:1:18:ASP:OD1	6:1:20:ARG:HD3	2.12	0.50
5:Z:47:VAL:HG12	5:Z:48:LEU:N	2.26	0.50
11:K:1:THR:HG23	11:K:33:LYS:HZ2	1.76	0.50
11:R:196:PHE:CE2	11:R:206:PHE:CD2	3.00	0.50
14:U:1:THR:HG23	14:U:33:LYS:NZ	2.26	0.50
4:D:100:ASN:HB3	17:D:252:HOH:O	2.11	0.50
8:O:128:GLY:O	8:O:131:SER:HB2	2.11	0.50
7:G:180(B):ASP:O	7:G:180(C):HIS:HB3	2.12	0.50
7:G:180(D):ILE:HG22	7:G:184:ASN:N	2.27	0.50
14:N:28:ASN:HA	17:N:319:HOH:O	2.10	0.50
6:F:198:TYR:CE2	6:F:208:PHE:HZ	2.29	0.50
6:F:54:ILE:HG13	6:F:208:PHE:HA	1.93	0.50
10:Q:155:LEU:O	10:Q:158:CYS:HB2	2.12	0.50
3:C:134:VAL:HG12	3:C:135:SER:N	2.26	0.50
5:Z:130:ARG:NH1	5:Z:130:ARG:HG3	2.20	0.50
13:T:4:ILE:HD11	13:T:159:MET:CG	2.41	0.50
11:R:200:LYS:HG3	11:R:205:SER:O	2.12	0.50
10:J:38:SER:O	10:J:40:HIS:N	2.45	0.50
11:R:174:ASN:HD21	11:R:189:ASN:HB2	1.76	0.50
6:1:49:ALA:HB2	6:1:212:ILE:HG23	1.93	0.50
5:E:5:ARG:C	5:E:7:ASN:H	2.15	0.50
6:1:240:ILE:HG23	6:1:241:ASN:ND2	2.26	0.50
4:D:79:SER:HB3	4:D:165:ILE:HD12	1.94	0.50
14:N:163:ILE:CG2	14:N:170:GLY:HA2	2.41	0.49
5:E:97:ASN:ND2	12:L:61:ASN:HD21	2.07	0.49
6:F:150:MET:O	6:F:157:TYR:HA	2.12	0.49
2:B:86:GLU:HB2	17:B:863:HOH:O	2.11	0.49
3:C:216:LYS:HB2	3:C:220:ASP:HB3	1.93	0.49
2:W:134:VAL:O	2:W:153:PRO:HD3	2.11	0.49
6:1:35:THR:HG22	6:1:36:THR:N	2.26	0.49
6:1:184:LEU:HD11	6:1:188:GLU:CB	2.42	0.49
14:U:59:VAL:HG13	14:U:82:VAL:HG11	1.93	0.49
7:G:49:ILE:HD12	7:G:49:ILE:N	2.27	0.49
14:N:175:MET:HE3	14:N:187(B):PHE:CE2	2.47	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:O:134:ALA:HB1	8:O:158:ALA:HB1	1.94	0.49
10:J:8:VAL:HG23	10:J:9:GLN:N	2.26	0.49
5:E:125:GLN:HG3	6:F:130:ARG:HG2	1.93	0.49
6:F:66:LYS:HA	17:F:670:HOH:O	2.10	0.49
13:M:41:THR:HG21	13:M:79:ILE:HD12	1.94	0.49
6:1:221:HIS:CE1	6:1:223:PHE:CE1	2.95	0.49
8:H:213:VAL:HG12	8:H:214:LEU:N	2.27	0.49
12:S:19:ARG:HB2	12:S:171:ASP:HB2	1.93	0.49
5:Z:138:ILE:O	5:Z:148:LEU:HD12	2.11	0.49
2:B:81:LEU:HD22	2:B:81:LEU:N	2.27	0.49
9:I:15:ALA:CB	9:I:175:VAL:HG22	2.41	0.49
8:H:55:VAL:HG23	8:H:86:HIS:HD2	1.77	0.49
1:V:11:SER:OG	2:W:129:LEU:HA	2.12	0.49
14:N:112:THR:HG22	14:N:120:HIS:HB2	1.94	0.49
3:X:212:ILE:HG22	3:X:213:THR:N	2.27	0.49
2:B:39:GLY:HA2	2:B:47:VAL:O	2.12	0.49
9:P:8:GLY:HA3	9:P:11:CYS:SG	2.52	0.49
11:K:35:ILE:CD1	11:K:45:MET:SD	3.01	0.49
6:1:69:VAL:HG22	6:1:70:VAL:N	2.27	0.49
13:M:35:ILE:HD13	13:M:56:GLU:HG2	1.94	0.49
8:H:55:VAL:HG23	8:H:86:HIS:CD2	2.45	0.49
3:X:160:TRP:CZ2	4:Y:59:LEU:HD23	2.48	0.49
2:W:86:GLU:HB2	17:W:2863:HOH:O	2.11	0.49
12:L:29:ARG:HD3	12:L:171:ASP:OD1	2.12	0.49
5:Z:180(C):PHE:CD1	5:Z:180(D):ILE:N	2.79	0.49
12:L:123:GLN:HG3	12:L:145:TYR:OH	2.13	0.49
6:F:38:ILE:HA	6:F:137:ILE:HD13	1.94	0.49
8:H:114:HIS:HE1	17:H:544:HOH:O	1.96	0.49
5:Z:132:TYR:O	5:Z:153:PRO:HB3	2.13	0.49
9:P:41:VAL:HG22	9:P:76:PRO:HG3	1.94	0.49
3:X:81:LEU:HB3	17:X:1414:HOH:O	2.12	0.49
7:G:82:ILE:N	7:G:83:PRO:HD2	2.28	0.49
15:9:4:R4K:N	15:9:4:R4K:C32	2.75	0.49
7:G:105:TYR:HD2	7:G:105:TYR:N	2.09	0.49
6:F:126:TYR:CE1	7:G:129:MET:SD	3.04	0.49
12:L:134:ILE:HG22	12:L:138:LEU:CD2	2.43	0.49
8:H:77:VAL:HG13	17:H:952:HOH:O	2.12	0.49
10:Q:6:ILE:HD11	10:Q:142:TYR:CE1	2.47	0.49
3:X:154:SER:HB3	17:X:1000:HOH:O	2.12	0.49
7:G:151:THR:HA	7:G:156:TYR:O	2.13	0.49
3:C:36:CYS:HA	3:C:166:GLY:HA3	1.94	0.49
6:F:148:LEU:HD12	6:F:149:TYR:N	2.27	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:W:46:ILE:HG21	2:W:139:ALA:HB1	1.95	0.49
2:W:48:LEU:HD11	2:W:139:ALA:HB3	1.93	0.49
8:O:111:PHE:HD1	8:O:121:VAL:HB	1.77	0.49
4:Y:173:GLN:HB3	17:Y:1455:HOH:O	2.11	0.49
2:W:64:THR:HG23	2:W:67:LEU:O	2.13	0.49
3:X:216:LYS:HB2	3:X:220:ASP:HB3	1.95	0.49
2:B:53:LYS:HG2	2:B:54:VAL:HG23	1.94	0.49
2:B:65:GLU:HG3	2:B:66:LYS:HG3	1.94	0.49
14:N:161:GLN:HE22	14:U:139:ASP:HB3	1.77	0.49
13:M:160:ARG:HA	13:M:192:VAL:HG11	1.95	0.49
2:B:71:ASN:ND2	2:B:72:ASP:H	2.10	0.49
3:C:39:GLY:HA2	3:C:47:VAL:O	2.12	0.49
9:P:76:PRO:O	9:P:77:GLU:C	2.51	0.49
2:W:11:ARG:O	2:W:14:ILE:HG12	2.13	0.49
4:Y:121:LEU:HB2	17:Y:1156:HOH:O	2.12	0.49
5:Z:77:SER:OG	5:Z:137:LEU:HB2	2.13	0.49
10:Q:112:GLN:NE2	10:Q:126:ALA:H	2.11	0.49
6:1:97:ALA:O	6:1:99:PHE:N	2.46	0.49
6:F:236:ALA:O	6:F:238:LYS:N	2.46	0.49
7:G:207:LYS:HG3	7:G:208:ASN:OD1	2.12	0.49
1:V:221:PHE:C	1:V:221:PHE:CD2	2.86	0.49
3:C:57:LYS:HG3	3:C:208:LYS:NZ	2.28	0.49
6:F:78:TYR:HB3	6:F:136:THR:HG23	1.95	0.49
4:D:112:LEU:O	4:D:116:VAL:HG23	2.13	0.49
4:Y:59:LEU:HD13	4:Y:60:GLU:N	2.27	0.49
8:H:90:TYR:O	8:H:93:GLY:N	2.46	0.49
1:V:112:LEU:O	1:V:116:VAL:HG23	2.13	0.49
14:U:41:ILE:HD13	14:U:79:ALA:HB2	1.93	0.49
13:T:157:ASN:O	13:T:160:ARG:N	2.46	0.48
13:T:13:ILE:HG23	13:T:175:LEU:HD21	1.95	0.48
5:Z:66:LYS:HA	5:Z:78:LEU:HD21	1.95	0.48
14:N:8:PHE:CZ	14:N:10:ASP:HB2	2.48	0.48
12:S:51:ASP:OD1	12:S:95:TYR:HA	2.12	0.48
9:I:43:LEU:HD11	9:I:99:PRO:HB3	1.94	0.48
11:K:40:PHE:CD1	11:K:73:ARG:NH1	2.80	0.48
13:T:112:TYR:HE1	13:T:127:THR:HG22	1.78	0.48
8:O:86:HIS:CE1	8:O:90:TYR:HE2	2.30	0.48
12:S:76:ILE:HG23	12:S:77:ASN:N	2.27	0.48
12:L:166:HIS:HE1	17:L:233:HOH:O	1.95	0.48
6:F:221:HIS:HE1	6:F:223:PHE:HE1	1.59	0.48
2:W:38:ILE:HG23	2:W:164:SER:HB3	1.95	0.48
12:L:49:ALA:HB1	17:M:965:HOH:O	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:Y:77:ALA:HB3	4:Y:137:LEU:HB2	1.94	0.48
1:A:13:THR:HG22	1:A:21:LEU:HD22	1.95	0.48
1:A:46:VAL:CG1	1:A:47:VAL:N	2.75	0.48
14:N:111:TYR:HA	14:N:120:HIS:O	2.12	0.48
6:F:31:VAL:O	6:F:34:GLY:N	2.46	0.48
4:D:237:LEU:HD22	4:D:241:GLU:HG3	1.95	0.48
12:S:2:THR:HG21	12:S:130:ALA:HB3	1.94	0.48
13:M:40:ASN:HD22	13:M:40:ASN:N	2.11	0.48
3:C:71:ASP:CA	10:J:68:ILE:HD11	2.42	0.48
1:A:77:VAL:HG22	1:A:78:TYR:N	2.28	0.48
4:Y:170:GLU:HG2	4:Y:171:GLY:N	2.27	0.48
14:U:143:ARG:O	14:U:146:MET:HG3	2.13	0.48
11:K:208:ASN:O	9:P:30:LYS:NZ	2.46	0.48
2:W:121:GLN:O	2:W:124:THR:HB	2.13	0.48
1:A:85:TYR:O	1:A:89:VAL:HG23	2.12	0.48
10:J:132:PHE:HD1	11:R:133:PHE:CZ	2.31	0.48
10:Q:156:LYS:O	10:Q:160:GLN:HG3	2.13	0.48
13:T:19:LEU:HD11	13:T:26:LEU:HB3	1.96	0.48
3:C:159:SER:HB2	17:C:245:HOH:O	2.13	0.48
8:H:124:TYR:N	8:H:124:TYR:CD1	2.81	0.48
1:A:130:ARG:NH1	1:A:131:PRO:O	2.46	0.48
11:K:200:LYS:HG3	11:K:205:SER:O	2.13	0.48
2:W:88:LEU:HD22	2:W:116:LEU:CD2	2.43	0.48
13:T:78:TYR:CE1	5:Z:105:ARG:HB2	2.48	0.48
14:N:175:MET:HE3	14:N:187(B):PHE:HE2	1.78	0.48
5:E:40:LEU:HD23	5:E:40:LEU:N	2.28	0.48
8:O:18:THR:HB	8:O:30:ASN:HA	1.95	0.48
14:N:1:THR:HG23	14:N:33:LYS:NZ	2.29	0.48
1:V:150:GLN:O	1:V:157:TYR:HA	2.14	0.48
7:2:143(A):GLU:HG2	17:2:1127:HOH:O	2.12	0.48
8:H:1:THR:O	8:H:128:GLY:HA3	2.13	0.48
4:D:160:TYR:CZ	4:D:163:LYS:HD3	2.48	0.48
8:H:208:ARG:NH1	9:I:149:GLU:HB2	2.28	0.48
6:1:43:ASN:N	6:1:43:ASN:HD22	2.12	0.48
3:C:95:GLU:HG3	3:C:95:GLU:O	2.13	0.48
3:C:15:PHE:N	4:D:23:GLN:HE22	1.96	0.48
1:V:121:GLN:O	1:V:124:THR:HB	2.13	0.48
14:U:8:PHE:CE1	14:U:10:ASP:HB2	2.49	0.48
14:N:12:VAL:HG12	14:N:178:LEU:HB2	1.96	0.48
2:B:117:SER:HB3	2:B:155:GLY:O	2.13	0.48
1:V:197:LEU:HD23	1:V:210:ILE:HD12	1.96	0.48
2:W:107:ILE:HD11	2:W:111:ILE:HG22	1.94	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:2:76:MET:SD	7:2:138:PHE:CE2	3.07	0.48
5:E:70:CYS:SG	5:E:92:LEU:HD23	2.53	0.48
14:U:28:ASN:HA	17:U:2319:HOH:O	2.14	0.48
9:P:19:ARG:HB2	9:P:170:GLY:O	2.14	0.48
14:U:51:ASP:OD2	14:U:95:LEU:HA	2.13	0.48
7:2:179:HIS:CD2	7:2:192:PHE:CZ	3.01	0.48
3:C:201:VAL:O	3:C:202:GLN:HB2	2.14	0.48
11:R:46:ALA:HB3	11:R:98:GLY:O	2.14	0.48
3:X:134:VAL:CG1	3:X:135:SER:N	2.77	0.48
5:E:180:LEU:HD12	5:E:180(C):PHE:CE1	2.49	0.48
7:2:198:ILE:O	7:2:200:ALA:N	2.47	0.48
5:Z:180(C):PHE:HA	5:Z:180(F):ILE:HG13	1.96	0.48
6:1:136:THR:O	6:1:150:MET:HA	2.14	0.48
6:F:151:LEU:HD12	6:F:156:SER:O	2.14	0.48
1:A:124:THR:CG2	2:B:130:ARG:HH21	2.27	0.48
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.95	0.48
6:F:158:TRP:HB2	6:F:160:TYR:HE1	1.78	0.48
14:N:147:SER:OG	14:N:149:GLU:HG3	2.14	0.48
8:O:51:ASP:HB3	8:O:95:ILE:HG23	1.95	0.48
12:L:99:THR:HG23	12:L:113:PHE:HB2	1.96	0.48
2:W:117:SER:HB3	2:W:155:GLY:O	2.14	0.48
12:L:135:MET:CE	9:P:165:ARG:NH2	2.77	0.48
7:2:151:THR:HG22	7:2:157:TYR:HB2	1.95	0.48
3:X:57:LYS:CG	3:X:208:LYS:NZ	2.77	0.48
2:W:160:TRP:CD2	2:W:163:ILE:HD13	2.49	0.48
6:F:148:LEU:HD12	6:F:149:TYR:H	1.79	0.48
14:N:146:MET:HE3	14:N:150:GLU:HB3	1.95	0.48
12:L:104:LEU:HD23	12:L:108:GLY:HA2	1.94	0.48
7:2:170:GLN:HE21	7:2:174:THR:HG23	1.78	0.48
13:M:157:ASN:ND2	13:M:160:ARG:HH11	2.12	0.47
13:T:157:ASN:HD22	13:T:160:ARG:NH1	2.11	0.47
12:L:93:PHE:N	12:L:94:PRO:HD3	2.29	0.47
1:A:121:GLN:O	1:A:124:THR:HB	2.14	0.47
9:I:43:LEU:HD12	9:I:100:VAL:O	2.13	0.47
10:Q:113:ILE:CG1	10:Q:119:LYS:HG3	2.37	0.47
8:O:152:ILE:CG2	8:O:191:TYR:HE1	2.27	0.47
12:S:134:ILE:HG22	12:S:138:LEU:CD2	2.43	0.47
14:U:14:LEU:N	14:U:14:LEU:HD12	2.29	0.47
14:U:51:ASP:O	14:U:55:ILE:HG13	2.15	0.47
11:K:31:VAL:HG12	11:K:33:LYS:HG3	1.96	0.47
12:L:-6:PRO:HB2	13:M:91:ARG:NH1	2.29	0.47
4:D:52:LYS:HE3	4:D:211:GLN:HB2	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:2:206:SER:O	7:2:209:ASP:HB2	2.15	0.47
6:1:192:GLN:O	6:1:195:LYS:HB3	2.15	0.47
5:E:117:CYS:SG	6:F:86:ARG:HD3	2.55	0.47
5:E:162:GLY:O	5:E:163:THR:HB	2.14	0.47
9:I:101:VAL:O	9:I:110:ILE:HA	2.13	0.47
1:V:52:LYS:O	1:V:54:SER:N	2.47	0.47
5:E:38:VAL:HG22	5:E:164:ALA:HB2	1.96	0.47
3:C:212:ILE:HG22	3:C:213:THR:N	2.28	0.47
12:S:25:SER:HB3	17:S:2284:HOH:O	2.14	0.47
11:R:83:LEU:O	11:R:86:LEU:HB3	2.14	0.47
13:T:1:THR:OG1	13:T:2:SER:N	2.47	0.47
1:A:58:LEU:HD23	1:A:58:LEU:HA	1.60	0.47
4:Y:160:TYR:CD2	5:Z:59:SER:HB3	2.49	0.47
9:I:178:ILE:HG23	9:I:184:VAL:CG2	2.44	0.47
1:A:41:LYS:HA	1:A:46:VAL:HG22	1.96	0.47
6:F:18:ASP:OD1	6:F:20:ARG:HD3	2.14	0.47
8:H:103:GLY:HA2	8:H:178:MET:SD	2.55	0.47
11:K:19:ARG:HA	11:K:28:SER:O	2.13	0.47
10:Q:185:ARG:HG2	10:Q:185:ARG:HH11	1.79	0.47
6:F:35:THR:CG2	6:F:36:THR:N	2.78	0.47
6:F:35:THR:HG23	6:F:51:GLU:HB3	1.96	0.47
8:H:167:LEU:HD12	12:S:24:TYR:HA	1.97	0.47
4:D:97:VAL:HG11	11:K:65:LEU:HD11	1.95	0.47
5:E:28:LEU:O	5:E:31:ILE:HB	2.15	0.47
8:O:124:TYR:N	8:O:124:TYR:CD1	2.82	0.47
3:C:123:TYR:CD1	3:C:132:PHE:HE1	2.33	0.47
3:X:135:SER:OG	3:X:152:GLU:HA	2.14	0.47
6:F:38:ILE:HG22	6:F:164:ALA:CA	2.44	0.47
2:B:20:ARG:NH2	3:C:33:ARG:HE	2.13	0.47
8:O:55:VAL:HG23	8:O:86:HIS:HD2	1.80	0.47
8:H:201:GLN:CG	12:S:153:LYS:HG2	2.44	0.47
2:W:56:SER:OG	2:W:57:THR:N	2.45	0.47
10:Q:135:PHE:HZ	17:Q:2596:HOH:O	1.98	0.47
5:E:65:LYS:HG3	5:E:65:LYS:O	2.15	0.47
13:M:62:LEU:HD23	13:M:62:LEU:HA	1.66	0.47
2:B:157:TYR:CD2	3:C:86:ARG:NH1	2.82	0.47
3:X:71:ASP:O	3:X:73:HIS:N	2.48	0.47
6:1:83:PRO:O	6:1:86:ARG:N	2.48	0.47
5:Z:38:VAL:HG12	5:Z:39:GLY:N	2.30	0.47
7:2:67:ILE:CD1	7:2:211:GLU:HG2	2.45	0.47
8:O:3:ILE:HG22	8:O:16:ALA:HB2	1.97	0.47
9:P:75:GLU:OE1	9:P:105:ASN:HA	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:19:LEU:HD22	13:M:170:SER:HB2	1.96	0.47
4:D:89:ILE:HG22	4:D:93:ARG:HD2	1.96	0.47
11:K:46:ALA:HB3	11:K:98:GLY:O	2.15	0.47
6:1:170:GLN:H	6:1:170:GLN:CD	2.17	0.47
7:2:179(D):SER:O	7:2:179(E):LYS:HB2	2.15	0.47
1:A:7:ARG:HH22	4:D:123(C):GLY:HA3	1.79	0.47
13:T:205:GLY:HA3	13:T:209:GLN:HB3	1.97	0.47
9:I:-2:ASN:HA	9:I:21:GLY:O	2.15	0.47
7:2:136:LEU:O	7:2:150:LYS:HA	2.14	0.47
4:Y:29:GLU:OE2	4:Y:32:LYS:HD2	2.15	0.47
14:N:186:ARG:NH2	13:T:204:LYS:HB2	2.30	0.47
9:P:53:THR:HG22	10:Q:84:ARG:NH2	2.30	0.47
3:C:49:GLY:C	3:C:50:CYS:SG	2.93	0.47
5:Z:65:LYS:HG3	5:Z:65:LYS:O	2.15	0.47
13:M:111:ARG:HG3	13:M:120:TYR:O	2.15	0.47
13:T:161:VAL:O	13:T:164:TYR:HB2	2.14	0.47
14:N:152:VAL:HG13	14:N:175:MET:HE1	1.96	0.47
11:R:138:LEU:HD13	11:R:158:SER:OG	2.15	0.47
17:1:2420:HOH:O	7:2:86:ARG:HD2	2.14	0.47
6:F:109:ILE:HB	6:F:110:PRO:HD3	1.95	0.47
14:U:3:ILE:HG22	14:U:16:ALA:HB2	1.96	0.47
5:E:97:ASN:HD21	12:L:61:ASN:ND2	2.12	0.47
13:M:112:TYR:CD2	13:M:120:TYR:CZ	3.03	0.47
6:1:115:ARG:HG2	17:1:2418:HOH:O	2.14	0.47
1:V:210:ILE:HG22	1:V:211:GLU:N	2.30	0.47
3:X:123:TYR:CD1	3:X:132:PHE:HE1	2.33	0.47
4:Y:148:LEU:HD12	4:Y:149:PHE:H	1.81	0.46
13:T:-6:GLN:O	13:T:-6:GLN:HG3	2.15	0.46
13:T:19:LEU:HD22	13:T:170:SER:HB2	1.95	0.46
9:P:3:VAL:HG22	9:P:16:CYS:HB3	1.97	0.46
9:P:71:GLU:HG2	17:P:2213:HOH:O	2.13	0.46
10:J:74:LEU:HD22	10:J:78:ALA:HB1	1.97	0.46
1:V:146:GLY:HA3	17:V:2772:HOH:O	2.15	0.46
11:K:136:GLY:HA2	10:Q:161:GLU:OE1	2.15	0.46
6:F:53:LEU:HD23	6:F:53:LEU:HA	1.71	0.46
2:B:192:LEU:HD23	2:B:192:LEU:O	2.15	0.46
2:B:51:GLU:OE2	2:B:202:THR:HG23	2.16	0.46
8:H:197:ARG:HH12	8:H:200:LYS:HD3	1.79	0.46
4:Y:139:ALA:HB2	4:Y:148:LEU:HD13	1.97	0.46
9:I:12:VAL:CG1	9:I:108:PRO:HB3	2.45	0.46
13:T:100:ILE:HD13	13:T:125:LEU:HB2	1.96	0.46
8:O:204:TYR:O	8:O:206:PHE:CD2	2.69	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:91:ARG:HG3	13:M:92:SER:N	2.30	0.46
8:O:219:VAL:CG2	9:P:184:VAL:HG12	2.45	0.46
6:F:157:TYR:CE2	7:G:86:ARG:NH1	2.83	0.46
11:R:155:GLY:O	11:R:156:LYS:C	2.54	0.46
9:P:67:LYS:O	9:P:71:GLU:N	2.48	0.46
17:S:1438:HOH:O	13:T:132:HIS:HE1	1.98	0.46
14:U:84:LYS:HE3	14:U:119:VAL:HG23	1.98	0.46
5:E:139:ILE:HG22	5:E:148:LEU:HD13	1.97	0.46
3:C:163:GLN:CG	3:C:164:THR:N	2.78	0.46
12:S:166:HIS:HE1	17:S:2233:HOH:O	1.99	0.46
1:A:77:VAL:HG22	1:A:78:TYR:H	1.79	0.46
1:A:142:ASP:O	1:A:144:PHE:N	2.49	0.46
13:T:198:ASP:HB3	17:T:3406:HOH:O	2.15	0.46
12:S:67:HIS:HD2	17:Z:2864:HOH:O	1.97	0.46
5:E:207:LEU:H	5:E:207:LEU:HD23	1.80	0.46
14:N:161:GLN:HE21	14:U:136:GLY:CA	2.10	0.46
10:Q:18:LYS:CD	10:Q:174:ILE:HG13	2.38	0.46
2:B:78:VAL:HG22	2:B:136:PHE:CE2	2.51	0.46
14:N:187(D):PRO:O	14:N:187(F):GLU:N	2.48	0.46
3:C:163:GLN:HE21	3:C:164:THR:N	2.05	0.46
3:C:38:VAL:CG2	3:C:39:GLY:N	2.78	0.46
1:V:66:LYS:HG2	1:V:78:TYR:HE1	1.80	0.46
12:S:60:LYS:O	12:S:63:VAL:HB	2.16	0.46
9:P:97:VAL:HG23	9:P:99:PRO:HD3	1.97	0.46
12:L:-6:PRO:HB2	13:M:91:ARG:HH11	1.81	0.46
7:2:82:ILE:N	7:2:83:PRO:HD2	2.30	0.46
6:1:109:ILE:HB	6:1:110:PRO:HD3	1.97	0.46
4:D:89:ILE:HA	4:D:89:ILE:HD13	1.74	0.46
14:U:3:ILE:HG22	14:U:16:ALA:CB	2.45	0.46
9:P:59:PHE:CZ	9:P:83:VAL:HG22	2.50	0.46
4:D:25:GLU:O	4:D:28:LEU:HB2	2.16	0.46
12:L:102:ALA:HB2	12:L:110:VAL:HG22	1.97	0.46
13:M:55:ILE:O	13:M:59:LEU:HG	2.15	0.46
6:F:69:VAL:HG23	6:F:74:ILE:O	2.14	0.46
13:T:35:ILE:HA	13:T:36:PRO:HD3	1.82	0.46
13:T:53:GLN:O	13:T:56:GLU:HB2	2.15	0.46
11:R:99:THR:HA	17:R:2444:HOH:O	2.16	0.46
7:2:119:LEU:HA	7:2:119:LEU:HD12	1.79	0.46
1:V:175:PHE:CD1	1:V:175:PHE:O	2.68	0.46
3:X:35:THR:HB	3:X:51:GLU:CG	2.43	0.46
5:Z:47:VAL:O	5:Z:48:LEU:HD23	2.16	0.46
13:T:164:TYR:C	13:T:165:ARG:HD2	2.36	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:P:6:MET:SD	9:P:142:TYR:HD1	2.38	0.46
13:T:42:VAL:HG23	13:T:178:ILE:HD11	1.96	0.46
11:R:174:ASN:ND2	11:R:189:ASN:HB2	2.30	0.46
2:W:39:GLY:HA2	2:W:47:VAL:O	2.16	0.46
12:S:20:ASN:O	12:S:27:ASN:HB2	2.16	0.46
3:C:93:ARG:O	3:C:96:ALA:HB3	2.16	0.46
6:F:206(B):GLU:HG3	6:F:206(C):LYS:HG3	1.97	0.46
10:J:155:LEU:O	10:J:158:CYS:HB2	2.16	0.46
11:K:155:GLY:O	11:K:158:SER:N	2.49	0.46
7:2:168:LYS:O	7:2:172:ILE:HG13	2.15	0.46
6:1:235:PHE:O	6:1:235:PHE:CD2	2.69	0.46
9:P:7:THR:HG23	9:P:110:ILE:CD1	2.45	0.46
12:S:19:ARG:NE	12:S:171:ASP:OD2	2.46	0.46
3:X:57:LYS:HG3	3:X:208:LYS:NZ	2.30	0.46
9:P:99:PRO:HB2	9:P:113:PHE:CE2	2.51	0.46
6:F:67:ILE:HG22	6:F:68:GLN:N	2.30	0.46
6:1:120:VAL:HG21	6:1:151:LEU:HD21	1.97	0.46
3:X:150:GLN:HE21	3:X:160:TRP:HE1	1.64	0.46
6:1:15:PHE:CE2	7:2:27:ALA:HB2	2.51	0.46
12:L:98:HIS:HE1	12:L:112:SER:HB2	1.80	0.46
11:K:87:VAL:HG11	11:K:115:SER:HA	1.98	0.46
10:Q:129:TYR:O	10:Q:132:PHE:HB2	2.16	0.46
6:F:141:VAL:CG2	6:F:215:CYS:SG	2.96	0.46
3:C:154:SER:OG	3:C:156:ILE:HB	2.16	0.46
3:C:208:LYS:HE3	3:C:209:ASN:HD22	1.81	0.46
11:K:200:LYS:HE3	11:K:206:PHE:O	2.16	0.46
2:B:120:LYS:NZ	2:B:136:PHE:HD1	2.14	0.46
2:W:163:ILE:HG13	2:W:164:SER:N	2.31	0.46
6:F:32:GLU:C	6:F:34:GLY:H	2.19	0.46
1:A:150:GLN:O	1:A:157:TYR:HA	2.15	0.46
7:2:55:PRO:HG2	7:2:56:ASP:H	1.81	0.46
4:D:110:GLU:O	4:D:113:THR:HB	2.16	0.46
12:L:18:THR:HG22	12:L:31:GLU:H	1.80	0.46
14:N:48:SER:HB3	14:N:51:ASP:HB2	1.98	0.46
5:Z:37:THR:OG1	5:Z:50:ALA:HB2	2.16	0.46
13:T:125:LEU:HA	17:T:2278:HOH:O	2.16	0.46
10:Q:35:ARG:NH2	17:Q:2774:HOH:O	2.49	0.46
10:J:2:ILE:O	10:J:3:ILE:HD13	2.15	0.46
13:T:43:VAL:HG22	13:T:101:VAL:HG22	1.98	0.46
14:U:7:THR:HA	14:U:12:VAL:HG23	1.98	0.46
2:W:112:LEU:C	2:W:112:LEU:HD23	2.36	0.46
6:1:35:THR:CG2	6:1:36:THR:N	2.78	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:Y:17:PRO:HA	5:Z:26:TYR:CD2	2.51	0.45
6:1:86:ARG:HH11	6:1:86:ARG:HG2	1.81	0.45
14:N:175:MET:CE	14:N:187(B):PHE:HE2	2.29	0.45
2:W:184:MET:HE1	2:W:189:ALA:HA	1.99	0.45
4:D:40:ILE:HD11	4:D:193:VAL:HG23	1.96	0.45
6:F:180(E):GLU:HG3	6:F:180(F):GLY:O	2.16	0.45
9:P:55:LEU:HD21	9:P:95:TYR:CD1	2.50	0.45
13:M:3:VAL:O	13:M:126:ALA:HA	2.16	0.45
7:G:99:PHE:CE1	7:G:107:MET:HA	2.51	0.45
6:1:50:VAL:HG22	6:1:51:GLU:N	2.30	0.45
7:2:91:ARG:NH2	7:2:115:ARG:NH2	2.63	0.45
8:H:33:LYS:HE2	15:8:5:AKK:CA	2.43	0.45
11:K:196:PHE:HE2	11:K:206:PHE:CD2	2.35	0.45
5:Z:47:VAL:HG11	5:Z:190:ILE:HG12	1.98	0.45
3:C:47:VAL:O	3:C:48:LEU:HD23	2.16	0.45
5:E:212:ILE:HG22	5:E:213:ALA:N	2.31	0.45
8:H:126:SER:O	8:H:127:LEU:HD23	2.16	0.45
1:V:31:VAL:HG13	1:V:79:SER:O	2.16	0.45
14:N:113:ILE:HA	14:N:118:SER:O	2.15	0.45
8:O:4:VAL:HG22	8:O:159:ILE:HD11	1.97	0.45
2:B:141:TYR:CG	2:B:142:ASP:N	2.85	0.45
13:M:153:GLU:HG3	17:M:3470:HOH:O	2.15	0.45
5:Z:17:PRO:HA	6:1:26:TYR:CD2	2.51	0.45
13:T:102:ALA:HB2	13:T:110:LEU:HD12	1.98	0.45
11:R:88:TYR:HB2	17:R:2144:HOH:O	2.17	0.45
10:J:156:LYS:O	10:J:160:GLN:HG3	2.17	0.45
3:X:198:LEU:HA	3:X:198:LEU:HD23	1.61	0.45
4:D:139:ALA:HB2	4:D:148:LEU:CD1	2.46	0.45
8:H:152:ILE:O	8:H:153:LYS:C	2.54	0.45
5:E:52:LYS:O	5:E:63:TYR:HD2	2.00	0.45
6:F:127:ASN:ND2	6:F:127:ASN:C	2.69	0.45
12:S:49:ALA:HB1	17:T:2965:HOH:O	2.17	0.45
4:Y:32:LYS:O	4:Y:167:SER:HA	2.17	0.45
13:T:35:ILE:HD13	13:T:56:GLU:HG2	1.98	0.45
9:P:55:LEU:N	9:P:55:LEU:HD23	2.31	0.45
8:H:218:ILE:HG22	8:H:219:VAL:N	2.32	0.45
12:L:8:GLY:HA3	12:L:11:PHE:CE2	2.51	0.45
4:Y:117:CYS:HB3	4:Y:155:GLY:O	2.16	0.45
5:Z:5:ARG:C	5:Z:7:ASN:H	2.20	0.45
12:S:8:GLY:HA3	12:S:11:PHE:CZ	2.52	0.45
6:1:67:ILE:HG13	6:1:211:GLU:OE1	2.15	0.45
7:2:214:VAL:HG12	7:2:215:ALA:H	1.80	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:O:3:ILE:HG22	8:O:16:ALA:CB	2.47	0.45
2:B:176:LEU:C	2:B:178:MET:N	2.69	0.45
13:T:112:TYR:CD2	13:T:120:TYR:CZ	3.05	0.45
10:Q:12:VAL:HG23	10:Q:108:PRO:HB2	1.98	0.45
4:D:115:SER:O	4:D:118:ASP:HB2	2.16	0.45
3:C:25:GLU:O	3:C:28:LEU:HB2	2.16	0.45
4:Y:123(G):GLU:HG2	4:Y:125:GLU:H	1.80	0.45
4:D:224:TYR:N	4:D:224:TYR:CD2	2.84	0.45
3:C:57:LYS:HG3	3:C:208:LYS:HZ1	1.82	0.45
7:G:221:PHE:CD1	7:G:221:PHE:C	2.90	0.45
10:Q:43:MET:HG3	10:Q:101:ILE:CG1	2.46	0.45
14:U:84:LYS:HB2	14:U:119:VAL:CG2	2.46	0.45
10:Q:129:TYR:HA	10:Q:132:PHE:HD2	1.82	0.45
4:Y:90:GLU:HA	17:Y:2509:HOH:O	2.16	0.45
6:1:107:ILE:HA	6:1:108:PRO:HD3	1.76	0.45
4:Y:194:LEU:HA	4:Y:194:LEU:HD12	1.77	0.45
11:K:210:ILE:N	17:K:2742:HOH:O	2.50	0.45
2:W:71:ASN:HD22	2:W:72:ASP:N	2.14	0.45
6:1:54:ILE:HG13	6:1:208:PHE:HA	1.98	0.45
11:R:138:LEU:HA	11:R:138:LEU:HD12	1.67	0.45
4:Y:156:THR:HG23	5:Z:83:PRO:HD3	1.97	0.45
3:X:238:GLN:C	3:X:240:LYS:H	2.20	0.45
12:L:184:VAL:O	12:L:184:VAL:HG12	2.16	0.45
5:E:198:SER:HA	5:E:201:LEU:CD1	2.47	0.45
9:I:6:MET:HE1	9:I:155:ILE:HA	1.99	0.45
2:B:15:PHE:HB2	3:C:23:GLN:NE2	2.30	0.45
9:P:45:ILE:CG2	9:P:52:VAL:HG22	2.47	0.45
7:G:72:ARG:NH2	14:N:39:ASP:OD2	2.50	0.45
7:2:38:LEU:HD23	7:2:197:MET:HE3	1.98	0.45
8:H:124:TYR:HB2	8:H:138:LEU:HD13	1.99	0.45
8:H:5:GLY:O	8:H:124:TYR:HA	2.16	0.45
10:J:171:LYS:NZ	10:Q:163:GLU:O	2.50	0.45
6:1:236:ALA:O	6:1:238:LYS:N	2.50	0.45
1:V:134:VAL:O	1:V:153:PRO:HG3	2.17	0.45
6:F:36:THR:HG22	6:F:51:GLU:OE2	2.17	0.45
3:C:57:LYS:CG	3:C:208:LYS:NZ	2.80	0.45
11:R:87:VAL:CG1	11:R:115:SER:HA	2.43	0.45
8:H:35:HIS:CG	8:H:56:THR:HG21	2.52	0.45
6:1:52:LYS:HD2	6:1:211:GLU:OE2	2.16	0.45
2:W:124:THR:CG2	3:X:130:ARG:HH21	2.29	0.45
6:F:120:VAL:HG21	6:F:151:LEU:HD21	1.99	0.45
6:F:176:LEU:HD22	6:F:196:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:23:GLN:OE1	7:G:15:PHE:HB2	2.16	0.45
9:P:33:LYS:O	9:P:44:GLY:HA2	2.17	0.45
13:M:136:PRO:HA	8:O:165:ASN:OD1	2.17	0.45
14:U:51:ASP:OD2	14:U:95:LEU:HD23	2.17	0.45
9:I:161:ASN:ND2	12:S:140:ASN:ND2	2.64	0.45
11:K:104:TYR:CD2	11:K:179:THR:HA	2.51	0.45
6:F:208:PHE:HD2	6:F:208:PHE:H	1.64	0.45
14:U:65:LEU:HG	14:U:69:GLN:HE21	1.80	0.45
10:J:140:HIS:HD2	10:J:141:HIS:CE1	2.35	0.45
10:Q:54:GLN:OE1	11:R:85:ASN:ND2	2.50	0.45
13:T:8:TYR:CE2	13:T:148:VAL:HG22	2.51	0.45
13:M:11:GLY:HA3	13:M:178:ILE:O	2.17	0.45
5:Z:92:LEU:HD12	5:Z:92:LEU:HA	1.85	0.45
11:R:1:THR:HG23	11:R:33:LYS:HZ2	1.82	0.45
3:X:160:TRP:CE2	4:Y:59:LEU:HD23	2.51	0.45
8:H:201:GLN:HG2	12:S:153:LYS:HG2	1.97	0.45
14:U:36:ARG:HG2	14:U:38:HIS:H	1.82	0.45
5:Z:28:LEU:O	5:Z:31:ILE:HB	2.17	0.45
2:W:141:TYR:CG	2:W:142:ASP:N	2.85	0.45
2:B:186:VAL:HG12	2:B:187:ASP:N	2.32	0.45
4:D:160:TYR:CE2	5:E:59:SER:HB3	2.51	0.44
8:H:13:VAL:HG22	8:H:14:ILE:N	2.31	0.44
3:X:148:LEU:HD23	3:X:160:TRP:O	2.17	0.44
5:E:31:ILE:HD11	5:E:153:PRO:HD2	1.99	0.44
14:N:32:ASP:OD1	13:T:204:LYS:HA	2.17	0.44
12:L:42:VAL:HG22	12:L:102:ALA:O	2.17	0.44
2:W:21:LEU:O	2:W:22:TYR:C	2.54	0.44
14:N:144:GLU:HG2	17:N:485:HOH:O	2.17	0.44
6:1:32:GLU:C	6:1:34:GLY:H	2.20	0.44
2:W:82:THR:O	2:W:85:ALA:HB3	2.17	0.44
10:Q:136:SER:HA	17:Q:194:HOH:O	2.17	0.44
7:G:111:VAL:HG22	8:H:70:THR:HG22	1.98	0.44
4:Y:119:LEU:O	4:Y:119:LEU:HD23	2.17	0.44
12:L:90:LYS:HD3	12:L:95:TYR:CZ	2.51	0.44
8:H:8:PHE:CE2	8:H:12:VAL:N	2.85	0.44
6:F:172:ALA:O	6:F:176:LEU:HD23	2.18	0.44
7:2:194:ILE:HD13	7:2:210:LEU:HD12	1.99	0.44
10:Q:74:LEU:HD22	10:Q:78:ALA:CB	2.48	0.44
4:D:134:VAL:HG22	4:D:135:ALA:N	2.32	0.44
7:G:55:PRO:HG2	7:G:56:ASP:H	1.82	0.44
5:E:226:GLY:O	5:E:229:VAL:HG22	2.17	0.44
3:X:39:GLY:HA2	3:X:47:VAL:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:O:206:PHE:CE1	9:P:157:GLN:HG3	2.53	0.44
13:T:186:PHE:CE1	13:T:188:LYS:HG3	2.52	0.44
7:G:72:ARG:NH1	7:G:72:ARG:HB2	2.32	0.44
11:R:49:ALA:HB1	12:S:118:SER:OG	2.17	0.44
11:R:85:ASN:ND2	17:R:2153:HOH:O	2.49	0.44
2:B:197:LEU:HA	2:B:200:THR:OG1	2.17	0.44
10:Q:10:ASP:O	10:Q:11:SER:HB3	2.18	0.44
8:H:157:ASP:O	8:H:160:GLN:HB2	2.17	0.44
1:A:32:LYS:HE2	1:A:32:LYS:HA	1.98	0.44
3:X:69:LYS:HA	3:X:75:VAL:HG12	2.00	0.44
5:E:74:MET:HE1	5:E:109:VAL:HA	1.98	0.44
3:C:180(D):GLU:N	3:C:182:PRO:HD3	2.31	0.44
3:X:215:VAL:HG22	3:X:215:VAL:O	2.16	0.44
10:Q:43:MET:HG3	10:Q:101:ILE:HG13	1.99	0.44
8:O:52:THR:O	8:O:56:THR:HB	2.17	0.44
10:Q:85:GLN:HE21	2:W:101:LYS:NZ	2.16	0.44
6:F:158:TRP:HB2	6:F:160:TYR:CE1	2.52	0.44
3:C:89:ILE:HG22	3:C:93:ARG:HD2	1.99	0.44
3:X:168:ASN:O	3:X:172:VAL:HG12	2.17	0.44
10:J:105:ASP:O	10:J:105(B):LYS:N	2.51	0.44
10:Q:8:VAL:HG23	10:Q:9:GLN:N	2.32	0.44
4:D:216:THR:O	4:D:217:LYS:C	2.56	0.44
1:V:141:HIS:CG	1:V:142:ASP:N	2.86	0.44
3:X:219:SER:N	17:X:2958:HOH:O	2.50	0.44
4:Y:159:ARG:HB3	5:Z:60:SER:HB3	1.99	0.44
13:T:157:ASN:O	13:T:158:ALA:C	2.56	0.44
11:K:206:PHE:CE1	10:Q:139:ASP:HB3	2.53	0.44
7:G:86:ARG:O	7:G:89:ALA:HB3	2.17	0.44
8:O:124:TYR:HD2	8:O:138:LEU:HB3	1.82	0.44
8:O:48:THR:HG22	17:O:2636:HOH:O	2.18	0.44
7:2:184(G):GLU:HG2	7:2:188:LYS:CB	2.47	0.44
6:F:107:ILE:HA	6:F:108:PRO:HD3	1.76	0.44
7:G:8:TYR:C	7:G:10:ARG:H	2.21	0.44
2:B:67:LEU:HD12	2:B:77:ALA:HA	1.99	0.44
5:Z:21:LEU:HA	5:Z:21:LEU:HD23	1.82	0.44
3:C:135:SER:OG	3:C:152:GLU:HA	2.17	0.44
7:G:194:ILE:HG23	7:G:210:LEU:HD11	2.00	0.44
6:1:151:LEU:HD13	6:1:157:TYR:HB3	1.99	0.44
10:J:74:LEU:HD22	10:J:78:ALA:CB	2.47	0.44
4:D:40:ILE:CD1	4:D:193:VAL:HG23	2.47	0.44
10:J:75:SER:HB2	17:J:835:HOH:O	2.18	0.44
10:J:112:GLN:NE2	10:J:126:ALA:H	2.15	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:136:SER:HA	17:J:2114:HOH:O	2.18	0.44
6:1:232:ALA:O	6:1:233:ILE:C	2.55	0.44
9:P:137:MET:HE3	9:P:141:LEU:HD11	2.00	0.44
3:X:110:GLU:O	3:X:113:THR:HB	2.17	0.44
3:X:62(A):ILE:HG12	3:X:62(A):ILE:H	1.64	0.44
1:V:124:THR:HG22	1:V:124:THR:O	2.18	0.44
14:U:177:VAL:HG23	14:U:185:GLU:HB3	2.00	0.44
14:U:59:VAL:O	14:U:60:GLN:C	2.56	0.44
5:E:73:HIS:CE1	5:E:107:LEU:O	2.68	0.44
11:K:1:THR:O	11:K:128:GLY:HA3	2.17	0.44
5:E:151:PHE:HA	5:E:157:VAL:HG22	2.00	0.44
12:L:17:ASP:HA	12:L:172:GLY:O	2.17	0.44
2:W:172:ALA:HB2	2:W:200:THR:HG21	1.99	0.44
12:L:2:THR:HG21	12:L:130:ALA:HB3	2.00	0.44
14:N:9:LYS:O	14:N:107:LYS:HD3	2.17	0.44
13:M:-6:GLN:O	13:M:-6:GLN:HG3	2.16	0.44
2:B:71:ASN:HD22	2:B:72:ASP:N	2.13	0.44
10:J:35:ARG:NH2	17:J:774:HOH:O	2.51	0.44
6:F:69:VAL:HG12	17:F:563:HOH:O	2.16	0.44
1:A:71:THR:O	1:A:73:ASP:N	2.51	0.44
13:M:1:THR:OG1	13:M:2:SER:N	2.51	0.44
11:R:63:CYS:SG	11:R:74:ILE:HD13	2.58	0.44
11:K:137:VAL:HG21	11:K:161:ALA:HB2	2.00	0.44
2:B:112:LEU:HD23	2:B:112:LEU:C	2.38	0.44
14:N:157:HIS:O	14:N:158:SER:C	2.55	0.44
5:Z:180(C):PHE:O	5:Z:180(E):LYS:N	2.51	0.44
14:U:6:VAL:CG2	14:U:155:ILE:HD11	2.47	0.44
3:X:33:ARG:CB	3:X:33:ARG:HH11	2.30	0.44
7:2:109:CYS:HB2	7:2:140:SER:OG	2.17	0.44
12:L:8:GLY:HA3	12:L:11:PHE:CZ	2.53	0.44
2:B:82:THR:O	2:B:85:ALA:HB3	2.18	0.44
11:R:36:GLU:HG2	11:R:184:TRP:CZ2	2.53	0.44
1:V:124:THR:O	1:V:124:THR:CG2	2.65	0.43
13:T:135:ASN:HB3	13:T:139:ARG:NE	2.33	0.43
1:V:15:PHE:H	2:W:23:GLN:NE2	2.12	0.43
7:2:233:LEU:HD12	7:2:233:LEU:HA	1.80	0.43
5:Z:66:LYS:HA	5:Z:78:LEU:CD2	2.48	0.43
13:M:35:ILE:CD1	13:M:56:GLU:HG2	2.48	0.43
13:M:141(D):GLU:O	13:M:141(G):ILE:HG13	2.18	0.43
4:D:195:LYS:O	4:D:198:LYS:HB3	2.18	0.43
1:V:48:ILE:HG13	1:V:213:ALA:HB3	1.99	0.43
1:V:60:MET:HG3	7:2:159:GLY:O	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:167:ILE:O	8:O:167:LEU:HD22	2.17	0.43
2:W:202:THR:HG22	2:W:204:SER:N	2.14	0.43
7:G:76:MET:HB2	7:G:138:PHE:CD2	2.53	0.43
7:G:75:GLY:HA3	7:G:221:PHE:CE2	2.53	0.43
8:H:197:ARG:NH2	9:I:139:GLU:O	2.51	0.43
2:W:15:PHE:H	3:X:23:GLN:HE22	1.66	0.43
3:C:40:VAL:HA	3:C:162:ALA:HA	2.00	0.43
5:Z:148:LEU:HD23	5:Z:162:GLY:HA2	2.00	0.43
12:S:55:LEU:HD13	12:S:95:TYR:CE1	2.53	0.43
14:N:3:ILE:HG22	14:N:16:ALA:HB2	2.00	0.43
1:V:8:TYR:CE1	7:2:127:ALA:HB1	2.54	0.43
13:T:19:LEU:HD23	13:T:168:ARG:O	2.18	0.43
6:F:172:ALA:C	6:F:176:LEU:HD23	2.38	0.43
6:F:175:GLU:HG3	6:F:199:LEU:HD23	2.00	0.43
2:B:10:SER:O	2:B:11:ARG:C	2.56	0.43
12:L:1:GLY:N	17:L:866:HOH:O	2.51	0.43
1:A:161:LYS:HD3	1:A:180:TRP:CH2	2.53	0.43
9:P:114:ASP:CB	15:9:3:ASN:ND2	2.67	0.43
11:R:105(A):ARG:HB3	11:R:105(B):LYS:CE	2.46	0.43
14:U:173:ILE:HB	14:U:187(B):PHE:HB2	2.00	0.43
5:Z:37:THR:HG23	5:Z:137:LEU:HD12	2.00	0.43
14:N:114:PRO:O	14:N:116:GLY:N	2.50	0.43
9:I:15:ALA:HB2	9:I:175:VAL:HG22	2.01	0.43
12:S:114:ASP:HB2	12:S:118:SER:CB	2.48	0.43
6:1:95:GLU:HG2	6:1:115:ARG:HB3	1.99	0.43
10:Q:7:ARG:HB2	10:Q:12:VAL:HG22	1.99	0.43
1:A:29:THR:O	1:A:32:LYS:HB2	2.18	0.43
6:F:108:PRO:O	6:F:111:ALA:HB3	2.19	0.43
6:1:46:VAL:HG23	6:1:48:PHE:CE1	2.53	0.43
13:M:205:GLY:HA3	13:M:209:GLN:HB3	2.00	0.43
8:O:112:SER:OG	8:O:120:ASP:HB2	2.18	0.43
12:L:18:THR:CG2	12:L:30:TYR:HA	2.48	0.43
6:1:176:LEU:CD2	6:1:196:ILE:HD13	2.47	0.43
11:K:196:PHE:CZ	11:K:209:VAL:HG21	2.46	0.43
6:1:159:GLY:C	6:1:160:TYR:HD1	2.21	0.43
12:L:144(W):LYS:CG	12:L:145:TYR:N	2.81	0.43
2:B:160:TRP:CE3	2:B:163:ILE:HD13	2.54	0.43
13:T:126:ALA:N	17:T:2278:HOH:O	2.46	0.43
6:1:127:ASN:ND2	6:1:127:ASN:C	2.72	0.43
9:P:99:PRO:HB2	9:P:113:PHE:CD2	2.52	0.43
7:2:72:ARG:HB2	7:2:72:ARG:NH1	2.32	0.43
6:F:198:TYR:CE2	6:F:208:PHE:CZ	3.06	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:1:212:ILE:HG22	6:1:213:SER:H	1.84	0.43
6:F:148:LEU:HD23	6:F:160:TYR:O	2.18	0.43
14:U:7:THR:HG23	14:U:123:PRO:O	2.17	0.43
7:G:8:TYR:O	7:G:10:ARG:N	2.51	0.43
5:E:169:SER:O	5:E:171:GLY:N	2.51	0.43
6:F:116:LEU:HA	6:F:116:LEU:HD23	1.69	0.43
7:2:110:ASP:HB3	7:2:149:TYR:CZ	2.53	0.43
6:F:72:ARG:HD2	13:M:64:THR:OG1	2.18	0.43
6:1:102:LEU:O	6:1:102:LEU:HG	2.17	0.43
12:S:184:VAL:HG12	12:S:184:VAL:O	2.18	0.43
4:Y:192:LEU:H	4:Y:192:LEU:HD12	1.83	0.43
7:G:119:LEU:HD12	7:G:119:LEU:HA	1.74	0.43
14:U:4:MET:SD	14:U:159:LEU:HD21	2.59	0.43
10:Q:133:TYR:OH	10:Q:166:MET:CG	2.63	0.43
8:O:75:ARG:CZ	7:2:105:TYR:CD1	3.02	0.43
5:Z:180(D):ILE:HG13	5:Z:180(D):ILE:O	2.18	0.43
8:H:56:THR:HG22	8:H:57:GLN:N	2.34	0.43
5:E:47:VAL:HG12	5:E:48:LEU:H	1.84	0.43
13:M:51:ASP:OD1	13:M:95:LEU:HA	2.18	0.43
12:S:90:LYS:HD3	12:S:95:TYR:CZ	2.53	0.43
14:U:20:THR:OG1	14:U:28:ASN:HB3	2.19	0.43
4:D:28:LEU:HA	4:D:28:LEU:HD12	1.76	0.43
6:F:70:VAL:HB	6:F:74:ILE:HB	2.00	0.43
10:Q:76:PRO:O	10:Q:78:ALA:N	2.52	0.43
14:N:85:GLU:O	14:N:89:GLU:HB2	2.19	0.43
2:W:167:ALA:O	2:W:168:ASN:HB2	2.18	0.43
7:2:78:VAL:HG11	7:2:85:ALA:HB2	2.00	0.43
2:B:40:ILE:CD1	2:B:193:ALA:HB2	2.48	0.43
1:V:88:LEU:HD23	1:V:88:LEU:HA	1.68	0.43
5:E:176:LEU:HD22	5:E:180(C):PHE:CE2	2.40	0.43
5:Z:161:TYR:CZ	6:1:60:VAL:HG13	2.54	0.43
11:K:40:PHE:HB3	11:K:73:ARG:NH2	2.34	0.43
9:P:76:PRO:O	9:P:78:THR:N	2.51	0.43
4:Y:121:LEU:HD23	4:Y:123:PHE:HE1	1.84	0.43
6:F:236:ALA:C	6:F:238:LYS:H	2.22	0.43
5:Z:17:PRO:HG3	6:1:26:TYR:CE2	2.53	0.43
1:V:41:LYS:HA	1:V:46:VAL:HG22	2.01	0.43
6:1:206(B):GLU:HG3	6:1:206(C):LYS:HG3	2.00	0.43
1:V:111:LEU:O	1:V:114:SER:HB3	2.18	0.43
3:X:8:TYR:CE2	3:X:128:GLY:HA2	2.53	0.43
13:M:31:VAL:HG12	13:M:33:ARG:HG2	2.00	0.43
1:V:130:ARG:HH21	7:2:124:THR:CG2	2.30	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:4:MET:SD	14:N:159:LEU:CD2	3.07	0.43
12:S:8:GLY:HA2	12:S:145:TYR:CE1	2.53	0.43
7:G:236:ILE:C	7:G:238:GLU:H	2.21	0.43
6:1:119:TYR:O	6:1:122:ALA:HB3	2.18	0.43
1:A:82:GLY:O	1:A:85:TYR:HB3	2.18	0.43
14:N:1:THR:O	14:N:128:GLY:HA3	2.19	0.43
11:R:155:GLY:O	11:R:158:SER:N	2.52	0.43
14:U:107:LYS:HG2	14:U:108:GLY:N	2.33	0.43
8:O:216:GLU:HG3	9:P:187:ARG:HG2	2.00	0.43
8:O:43:CYS:SG	8:O:99:LEU:HD22	2.59	0.43
11:K:133:PHE:CB	11:K:162:ALA:HA	2.48	0.43
9:P:14:ILE:HG23	9:P:34:ILE:HD13	2.00	0.43
11:K:26:VAL:HG12	11:K:26:VAL:O	2.17	0.43
2:B:7:ARG:HH11	2:B:7:ARG:HG3	1.83	0.43
11:K:4:LEU:HD13	11:K:15:ALA:O	2.19	0.43
4:D:97:VAL:HG21	11:K:65:LEU:HD11	2.00	0.43
2:B:136:PHE:O	2:B:150:THR:HA	2.19	0.43
9:I:151:LEU:HG	9:I:151:LEU:O	2.19	0.43
6:F:137:ILE:HD11	6:F:165:THR:HG22	2.00	0.43
7:G:45:CYS:O	7:G:146:PRO:HB3	2.19	0.43
6:F:11:SER:HA	17:F:379:HOH:O	2.18	0.43
5:E:22:PHE:HD1	5:E:26:TYR:CE1	2.35	0.43
9:P:165:ARG:HD3	9:P:165:ARG:HA	1.85	0.43
1:V:52:LYS:NZ	1:V:61:SER:HB2	2.33	0.43
5:E:38:VAL:HG22	5:E:164:ALA:CB	2.48	0.43
9:P:53:THR:O	9:P:57:GLU:HG3	2.18	0.43
7:G:15:PHE:CD1	7:G:21:LEU:HD21	2.53	0.43
7:2:194:ILE:O	7:2:195:THR:C	2.57	0.43
11:K:172:SER:HA	11:K:192:VAL:HG23	2.00	0.43
17:C:3453:HOH:O	4:D:86:ARG:HB3	2.19	0.43
14:U:15:GLY:HA2	14:U:174:ARG:O	2.19	0.43
10:J:22:ARG:HD3	10:J:22:ARG:HA	1.85	0.43
2:B:205:LEU:HA	2:B:205:LEU:HD12	1.82	0.43
5:E:12:THR:HG23	5:E:23:GLN:HB2	2.01	0.43
4:D:24:VAL:O	4:D:27:SER:HB3	2.19	0.43
11:R:159:ILE:O	11:R:160:LEU:C	2.58	0.43
14:U:134:ILE:HD12	14:U:138:CYS:SG	2.59	0.43
11:R:38:ASN:OD1	11:R:38:ASN:C	2.57	0.43
1:V:66:LYS:HG2	1:V:78:TYR:CE1	2.54	0.43
6:1:195:LYS:O	6:1:198:TYR:N	2.51	0.43
12:S:59:PHE:O	12:S:60:LYS:C	2.57	0.43
10:Q:85:GLN:NE2	2:W:101:LYS:HZ1	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:52:THR:HG22	10:J:53:VAL:H	1.83	0.43
8:O:111:PHE:CD1	8:O:121:VAL:HB	2.54	0.43
9:P:19:ARG:HD3	9:P:168:LEU:O	2.18	0.43
2:W:141:TYR:CD1	2:W:219(E):VAL:HG21	2.54	0.43
10:Q:76:PRO:HD2	17:Q:2835:HOH:O	2.19	0.43
5:E:21:LEU:HD23	5:E:21:LEU:HA	1.81	0.43
5:Z:21:LEU:HA	17:Z:2539:HOH:O	2.19	0.43
5:Z:15:PHE:HE1	5:Z:21:LEU:HG	1.84	0.43
3:X:163:GLN:HE21	3:X:163:GLN:HA	1.84	0.43
13:T:135:ASN:HB2	13:T:136:PRO:HD3	2.00	0.43
11:K:35:ILE:HD11	11:K:45:MET:SD	2.58	0.43
14:U:155:ILE:HG22	14:U:175:MET:HE2	2.01	0.43
11:R:196:PHE:HZ	11:R:209:VAL:HG21	1.84	0.43
2:B:175:LEU:O	2:B:178:MET:HB3	2.19	0.43
5:E:40:LEU:HA	5:E:162:GLY:HA2	1.99	0.43
8:O:1:THR:HG23	8:O:33:LYS:NZ	2.33	0.43
14:U:67:THR:O	14:U:68:SER:C	2.57	0.43
11:K:197:TRP:CE2	9:P:190:LYS:HE3	2.54	0.43
7:G:222:PHE:N	7:G:222:PHE:CD2	2.86	0.43
6:F:214:TRP:N	6:F:214:TRP:CD1	2.85	0.43
8:O:19:ARG:NH1	8:O:167:LEU:O	2.52	0.42
6:1:77:VAL:O	6:1:136:THR:HG23	2.19	0.42
12:S:93:PHE:N	12:S:94:PRO:HD3	2.33	0.42
9:I:43:LEU:HD21	9:I:45:ILE:HD11	2.00	0.42
5:Z:68:ILE:HB	5:Z:76:LEU:CD2	2.48	0.42
11:K:38:ASN:OD1	11:K:38:ASN:C	2.57	0.42
10:J:105:ASP:OD1	10:J:105(C):LYS:HB2	2.19	0.42
7:2:184(G):GLU:HG2	7:2:188:LYS:HB2	2.01	0.42
1:V:67:VAL:HG11	1:V:213:ALA:HB2	2.01	0.42
7:2:46:THR:OG1	7:2:146:PRO:HB3	2.18	0.42
9:I:36:HIS:HB3	9:I:42:PHE:CD2	2.54	0.42
5:E:44:THR:CG2	5:E:183:ASP:HB3	2.49	0.42
1:A:17:PRO:HG3	2:B:26:TYR:CE2	2.54	0.42
7:2:87:ASN:HD22	7:2:87:ASN:C	2.22	0.42
4:D:97:VAL:CB	11:K:65:LEU:HD11	2.49	0.42
11:K:209:VAL:HA	17:K:2742:HOH:O	2.19	0.42
6:1:68:GLN:NE2	6:1:86:ARG:NH1	2.67	0.42
6:F:157:TYR:CZ	7:G:86:ARG:NH1	2.87	0.42
8:O:95:ILE:O	8:O:97:ALA:N	2.47	0.42
6:1:32:GLU:O	6:1:167:LYS:HG3	2.19	0.42
14:U:5:ALA:O	14:U:124:TYR:HB2	2.19	0.42
12:L:35:PHE:HZ	17:L:458:HOH:O	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:X:97:GLN:C	3:X:99:HIS:N	2.72	0.42
13:M:42:VAL:CG2	13:M:178:ILE:HD11	2.45	0.42
1:V:21:LEU:HA	1:V:21:LEU:HD23	1.83	0.42
12:S:4:LEU:HA	12:S:126:ALA:HA	2.01	0.42
12:S:4:LEU:CD1	12:S:138:LEU:HD21	2.49	0.42
1:V:86:ARG:HH21	7:2:118:ASN:ND2	2.16	0.42
6:1:157:TYR:C	6:1:157:TYR:CD1	2.92	0.42
1:V:71:THR:C	1:V:73:ASP:H	2.22	0.42
14:U:1:THR:O	14:U:128:GLY:HA3	2.20	0.42
2:W:64:THR:HG22	2:W:68:TYR:CE1	2.54	0.42
4:D:237:LEU:HA	4:D:237:LEU:HD23	1.87	0.42
6:F:69:VAL:HG22	6:F:70:VAL:N	2.35	0.42
4:D:224:TYR:HD2	4:D:224:TYR:N	2.17	0.42
9:I:53:THR:HG22	10:J:84:ARG:NH2	2.34	0.42
13:T:7:LYS:HD2	13:T:141(G):ILE:HD13	2.01	0.42
2:W:209:ARG:HH11	2:W:209:ARG:HG2	1.84	0.42
6:1:223:PHE:N	6:1:223:PHE:CD1	2.85	0.42
1:V:15:PHE:CE1	1:V:21:LEU:HD21	2.54	0.42
5:Z:198:SER:HA	5:Z:201:LEU:CD1	2.49	0.42
5:Z:38:VAL:HG13	5:Z:163:THR:O	2.19	0.42
12:S:61:ASN:ND2	5:Z:101:LEU:HD21	2.35	0.42
2:W:163:ILE:HD12	2:W:173:GLN:NE2	2.34	0.42
8:H:132:LEU:CD1	14:N:25:TYR:CE1	3.02	0.42
10:J:52:THR:HG22	10:J:53:VAL:N	2.34	0.42
8:O:110:LEU:HD23	8:O:122:GLY:O	2.19	0.42
6:1:7:GLY:O	6:1:9:ASP:N	2.53	0.42
2:B:137:ILE:HD11	2:B:165:VAL:HG22	2.00	0.42
1:V:214:ILE:O	1:V:215:ILE:HD13	2.19	0.42
3:X:77:SER:OG	3:X:137:LEU:HB2	2.19	0.42
13:T:49:ILE:O	13:T:52:MET:N	2.52	0.42
6:1:12:ASN:C	6:1:12:ASN:OD1	2.58	0.42
6:F:210:LEU:HD12	6:F:210:LEU:HA	1.84	0.42
14:U:161:GLN:O	14:U:164:LYS:N	2.51	0.42
13:T:13:ILE:CG2	13:T:175:LEU:HD21	2.48	0.42
5:Z:66:LYS:O	5:Z:77:SER:HA	2.20	0.42
6:1:194:ALA:O	6:1:198:TYR:HD1	2.03	0.42
5:Z:76:LEU:HD23	5:Z:76:LEU:C	2.40	0.42
12:L:163:THR:HG23	12:L:170:GLY:HA2	2.01	0.42
12:L:13:VAL:HG12	12:L:177:ILE:HG13	2.02	0.42
4:D:89:ILE:O	4:D:92:ALA:HB3	2.20	0.42
2:B:172:ALA:HB2	2:B:200:THR:HG21	2.01	0.42
13:T:62:LEU:HD23	13:T:62:LEU:HA	1.76	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:V:58:LEU:HD23	1:V:58:LEU:HA	1.77	0.42
2:W:7:ARG:HG3	2:W:7:ARG:HH11	1.85	0.42
11:R:105(B):LYS:N	11:R:105(B):LYS:CD	2.80	0.42
4:Y:70:ILE:HB	4:Y:74:ILE:CG2	2.44	0.42
7:2:9:ASP:HA	7:2:14:ILE:HD11	2.00	0.42
7:2:41:ARG:NH2	7:2:180(B):ASP:O	2.51	0.42
3:X:25:GLU:O	3:X:28:LEU:HB2	2.20	0.42
1:A:186:LEU:HD21	1:A:214:ILE:HD12	2.02	0.42
8:O:12:VAL:HG22	8:O:13:VAL:N	2.34	0.42
14:N:29:ARG:HD2	13:T:197:TRP:CH2	2.54	0.42
14:U:42:TRP:CD1	14:U:42:TRP:N	2.85	0.42
1:V:15:PHE:HB2	2:W:23:GLN:NE2	2.35	0.42
11:R:4:LEU:HD11	11:R:15:ALA:HB3	2.02	0.42
6:F:82:ILE:O	6:F:83:PRO:C	2.58	0.42
8:O:84:LYS:HE2	8:O:119:THR:HG23	2.02	0.42
5:E:107:LEU:HD12	17:E:389:HOH:O	2.19	0.42
3:X:182:PRO:HA	3:X:183:PRO:HD3	1.97	0.42
4:D:211:GLN:HA	17:D:916:HOH:O	2.19	0.42
10:J:53:VAL:O	10:J:54:GLN:C	2.58	0.42
8:O:55:VAL:HG23	8:O:86:HIS:CD2	2.53	0.42
8:H:160:GLN:O	8:H:164:TRP:CD1	2.73	0.42
7:2:25:GLU:O	7:2:28:PHE:HB2	2.20	0.42
7:G:179(D):SER:O	7:G:179(E):LYS:HB2	2.19	0.42
12:L:58:ARG:NH2	17:L:3067:HOH:O	2.53	0.42
3:X:63:THR:HG23	3:X:64:PRO:HD2	2.02	0.42
1:A:197:LEU:O	1:A:202:VAL:HG23	2.20	0.42
3:C:15:PHE:CE2	4:D:27:SER:HB2	2.55	0.42
13:T:171:ARG:CG	13:T:192:VAL:HG23	2.38	0.42
12:L:43:MET:HB2	12:L:101:ILE:CG2	2.44	0.42
6:1:67:ILE:HG22	6:1:68:GLN:N	2.34	0.42
4:D:180(C):HIS:O	4:D:184:LEU:HD12	2.20	0.42
5:Z:92:LEU:HD11	5:Z:112:ALA:HB1	2.01	0.42
9:P:12:VAL:HG13	9:P:108:PRO:HB3	2.01	0.42
2:W:20:ARG:HE	3:X:33:ARG:HH21	1.67	0.42
3:X:212:ILE:CG2	3:X:213:THR:N	2.83	0.42
3:X:81:LEU:HA	3:X:81:LEU:HD23	1.86	0.42
14:U:78:THR:O	14:U:79:ALA:C	2.58	0.42
2:W:107:ILE:HG13	2:W:108:PRO:HD2	2.02	0.42
6:1:108:PRO:O	6:1:111:ALA:HB3	2.19	0.42
1:V:46:VAL:HG12	1:V:47:VAL:N	2.34	0.42
3:X:97:GLN:O	3:X:99:HIS:N	2.53	0.42
13:T:128:GLY:HA3	17:T:2312:HOH:O	2.18	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:70:ILE:HG21	3:C:112:LEU:HD21	2.00	0.42
8:O:47:GLY:O	15:9:5:AKK:ND	2.52	0.42
4:D:243:ALA:O	4:D:244:GLU:HG2	2.20	0.42
6:F:135:SER:HA	17:F:408:HOH:O	2.20	0.42
1:A:221:PHE:CD2	1:A:221:PHE:C	2.93	0.42
12:S:144(W):LYS:CG	12:S:145:TYR:N	2.83	0.42
14:U:111:TYR:HA	14:U:120:HIS:O	2.20	0.42
4:Y:138:ILE:O	4:Y:148:LEU:HD12	2.20	0.42
2:W:66:LYS:HB2	2:W:211:GLU:OE1	2.20	0.42
8:O:90:TYR:O	8:O:93:GLY:N	2.53	0.42
3:C:197:LEU:O	3:C:201:VAL:HG23	2.20	0.42
6:F:113:ALA:O	6:F:116:LEU:N	2.52	0.42
7:2:16:SER:O	7:2:18:GLU:N	2.53	0.42
14:U:63:LEU:O	14:U:66:TYR:HB3	2.20	0.42
8:O:19:ARG:HG2	8:O:21:THR:HG23	2.02	0.42
8:H:152:ILE:HG21	8:H:191:TYR:HE1	1.84	0.42
8:H:167:LEU:HB3	12:S:167:ILE:HB	2.02	0.42
5:Z:180(C):PHE:C	5:Z:180(E):LYS:N	2.72	0.42
7:G:212:VAL:CG1	7:G:213:GLY:N	2.82	0.42
8:O:34:LEU:HA	8:O:34:LEU:HD12	1.78	0.42
14:N:187(C):TYR:CE1	13:T:198:ASP:HA	2.55	0.42
6:1:7:GLY:C	6:1:9:ASP:H	2.22	0.42
1:V:35:VAL:HG12	1:V:36:THR:N	2.35	0.42
7:G:74:ILE:HG21	7:G:112:LEU:HD23	2.02	0.42
11:K:151:ALA:O	11:K:152:LEU:C	2.58	0.42
6:1:53:LEU:HD23	6:1:53:LEU:HA	1.77	0.41
10:Q:166:MET:HA	10:Q:167:PRO:HD3	1.88	0.41
3:X:163:GLN:CG	3:X:164:THR:N	2.82	0.41
10:J:119:LYS:HG2	10:J:120:VAL:N	2.35	0.41
13:M:135:ASN:HB2	13:M:136:PRO:HD3	2.02	0.41
3:X:52:ARG:HD2	3:X:208:LYS:O	2.20	0.41
5:Z:139:ILE:HG22	5:Z:148:LEU:HD13	2.02	0.41
11:R:41:LEU:HA	11:R:41:LEU:HD23	1.75	0.41
3:X:33:ARG:O	3:X:33:ARG:HG2	2.19	0.41
1:V:221:PHE:HD2	1:V:221:PHE:O	2.01	0.41
13:M:-4:ILE:HG22	13:M:-3:VAL:N	2.34	0.41
1:V:72:PRO:HB3	17:V:1013:HOH:O	2.20	0.41
3:X:49:GLY:C	3:X:50:CYS:SG	2.98	0.41
7:G:27:ALA:O	7:G:30:ALA:N	2.51	0.41
1:A:69:LEU:O	1:A:93:ARG:NH2	2.51	0.41
14:N:52:THR:O	14:N:53:GLN:C	2.58	0.41
3:C:62(A):ILE:HG12	3:C:62(A):ILE:H	1.71	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:157:ASN:O	13:M:160:ARG:N	2.53	0.41
6:1:51:GLU:OE1	6:1:53:LEU:HD21	2.20	0.41
3:X:201:VAL:O	3:X:202:GLN:HB2	2.19	0.41
9:I:13:ALA:CB	9:I:151:LEU:HD21	2.51	0.41
9:I:152:PHE:O	9:I:155:ILE:HG22	2.20	0.41
6:1:208:PHE:H	6:1:208:PHE:HD2	1.67	0.41
11:R:52:CYS:SG	11:R:97:MET:CB	3.08	0.41
1:V:65:SER:HA	1:V:211:GLU:OE1	2.19	0.41
12:S:156:ARG:HD2	12:S:189:TYR:CE1	2.55	0.41
1:V:118:LYS:O	1:V:122:GLU:HG3	2.20	0.41
1:A:176:LEU:O	1:A:178:LYS:N	2.53	0.41
1:A:210:ILE:HG22	1:A:211:GLU:N	2.35	0.41
10:Q:143:ARG:O	10:Q:146:MET:HG3	2.20	0.41
6:F:216:SER:HB3	6:F:218(A):GLU:HB2	2.02	0.41
1:V:26:TYR:O	1:V:29:THR:HB	2.20	0.41
8:O:91:GLN:NE2	8:O:91:GLN:HA	2.35	0.41
12:L:107:LYS:HA	12:L:107:LYS:HD3	1.86	0.41
11:K:142:TYR:C	11:K:143:LYS:HD2	2.39	0.41
7:G:120:SER:O	7:G:121:GLN:C	2.57	0.41
5:Z:215:VAL:HG23	5:Z:221:PHE:N	2.35	0.41
10:J:133:TYR:C	17:J:441:HOH:O	2.58	0.41
8:O:35:HIS:CB	8:O:56:THR:HG21	2.50	0.41
10:J:43:MET:HG3	10:J:101:ILE:HG13	2.02	0.41
1:V:86:ARG:HE	7:2:118:ASN:HD21	1.69	0.41
4:Y:15:PHE:CE1	4:Y:21:LEU:HG	2.54	0.41
10:J:38:SER:OG	10:J:41:THR:HB	2.20	0.41
11:K:133:PHE:HB2	11:K:162:ALA:HA	2.02	0.41
7:2:225:SER:O	7:2:226:ALA:C	2.58	0.41
6:1:116:LEU:HA	6:1:116:LEU:HD23	1.81	0.41
13:T:134:ALA:O	13:T:135:ASN:C	2.58	0.41
10:J:44:SER:HG	10:J:100:LEU:HB2	1.84	0.41
9:I:12:VAL:HG23	9:I:178:ILE:HD12	2.02	0.41
9:I:55:LEU:HD21	9:I:95:TYR:CE1	2.56	0.41
7:2:49:ILE:HG22	7:2:50:SER:N	2.35	0.41
7:2:179:HIS:C	7:2:179:HIS:ND1	2.73	0.41
3:X:172:VAL:O	3:X:175:PHE:HB3	2.20	0.41
6:F:113:ALA:O	6:F:114:ASP:C	2.55	0.41
2:B:40:ILE:HD12	2:B:193:ALA:HB2	2.01	0.41
10:J:73:GLU:HG2	17:J:870:HOH:O	2.19	0.41
1:V:85:TYR:O	1:V:89:VAL:HG23	2.21	0.41
1:A:171:ALA:O	1:A:174:THR:HB	2.21	0.41
1:A:40:ILE:HD12	1:A:193:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:2:160:TYR:HB3	7:2:162:ALA:O	2.20	0.41
5:E:76:LEU:C	5:E:76:LEU:HD23	2.40	0.41
12:S:177:ILE:N	12:S:177:ILE:CD1	2.84	0.41
9:I:13:ALA:HB2	9:I:151:LEU:HD21	2.02	0.41
10:Q:112:GLN:NE2	10:Q:126:ALA:N	2.68	0.41
14:N:112:THR:CG2	14:N:120:HIS:HB2	2.49	0.41
14:U:38:HIS:NE2	14:U:74:PRO:HD2	2.35	0.41
9:I:131:SER:HB2	17:I:3153:HOH:O	2.20	0.41
9:I:133:GLN:HB3	9:I:162:ALA:HB1	2.02	0.41
5:E:90:ASN:O	5:E:93:ARG:N	2.53	0.41
13:T:149:GLN:H	13:T:149:GLN:NE2	2.18	0.41
7:G:194:ILE:O	7:G:198:ILE:HG13	2.20	0.41
8:O:175:VAL:HG21	8:O:191:TYR:CD1	2.46	0.41
5:Z:176:LEU:C	5:Z:178:ARG:N	2.73	0.41
12:S:59:PHE:O	12:S:62:SER:N	2.53	0.41
9:I:29:ASN:HB3	9:I:171:TRP:CE3	2.56	0.41
12:L:113:PHE:N	12:L:113:PHE:CD1	2.89	0.41
13:M:186:PHE:HE1	13:M:188:LYS:HG3	1.86	0.41
13:M:49:ILE:O	13:M:50:SER:C	2.57	0.41
4:D:194:LEU:HD12	4:D:194:LEU:HA	1.74	0.41
11:K:138:LEU:HD12	11:K:138:LEU:HA	1.89	0.41
1:V:15:PHE:O	2:W:26:TYR:HD2	2.04	0.41
12:L:100:ILE:HG22	12:L:101:ILE:N	2.36	0.41
14:U:163:ILE:CG2	14:U:170:GLY:HA2	2.44	0.41
7:G:9:ASP:HA	7:G:14:ILE:HD11	2.02	0.41
5:Z:48:LEU:O	5:Z:212:ILE:HG23	2.20	0.41
3:X:183:PRO:HB3	3:X:189:CYS:HA	2.03	0.41
12:S:20:ASN:OD1	12:S:27:ASN:HB2	2.21	0.41
2:W:176:LEU:C	2:W:178:MET:H	2.24	0.41
14:U:133:PHE:HE2	14:U:166:ASP:HB2	1.83	0.41
12:L:63:VAL:HG22	12:L:74:LEU:HD23	2.02	0.41
7:2:132:LEU:O	7:2:153:PRO:HG3	2.20	0.41
11:K:85:ASN:HA	11:K:85:ASN:HD22	1.74	0.41
7:2:165:THR:HG22	7:2:166:GLY:N	2.36	0.41
7:2:120:SER:HA	7:2:123:TYR:CD2	2.56	0.41
3:C:185:THR:CB	3:C:188:GLU:HG2	2.34	0.41
7:2:59:LEU:O	7:2:61:PRO:CD	2.64	0.41
8:O:197:ARG:NH1	8:O:200:LYS:HD3	2.35	0.41
3:X:58:LEU:HG	3:X:58:LEU:O	2.20	0.41
5:Z:138:ILE:O	5:Z:148:LEU:HA	2.21	0.41
13:M:149:GLN:CD	13:M:149:GLN:H	2.23	0.41
6:F:26:TYR:N	6:F:26:TYR:CD1	2.87	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:124:THR:CG2	1:A:124:THR:O	2.69	0.41
8:O:105:ASP:O	8:O:106:THR:N	2.53	0.41
8:O:6:VAL:O	8:O:13:VAL:HG12	2.21	0.41
5:Z:121:GLN:NE2	6:1:87:HIS:ND1	2.69	0.41
13:T:68:TYR:OH	6:1:71:ASP:N	2.50	0.41
1:V:161:LYS:HD3	1:V:180:TRP:CH2	2.55	0.41
13:T:169:SER:HB2	17:T:2472:HOH:O	2.20	0.41
7:G:35:ILE:HG23	7:G:51:GLN:HB2	2.03	0.41
8:O:132:LEU:N	8:O:132:LEU:CD1	2.84	0.41
8:O:21:THR:HG22	8:O:26:VAL:HA	2.03	0.41
5:E:220:PRO:O	5:E:221:PHE:C	2.59	0.41
6:F:35:THR:HG22	6:F:36:THR:N	2.34	0.41
4:Y:45:GLY:HA2	4:Y:146:TYR:CD1	2.56	0.41
14:N:6:VAL:CG2	14:N:155:ILE:HD11	2.46	0.41
12:S:29:ARG:HB2	17:S:2276:HOH:O	2.21	0.41
5:Z:176:LEU:HD22	5:Z:180(C):PHE:HE2	1.86	0.41
7:2:12:ILE:HA	17:2:2538:HOH:O	2.20	0.41
2:W:15:PHE:CB	3:X:23:GLN:HE22	2.31	0.41
4:Y:215:ILE:HG22	4:Y:221:PHE:HD2	1.84	0.41
11:R:40:PHE:HB2	17:R:2501:HOH:O	2.20	0.41
11:K:165:ARG:NH1	9:P:26:GLY:O	2.53	0.41
10:J:43:MET:HG3	10:J:101:ILE:CG1	2.50	0.41
1:V:50:THR:HG21	1:V:66:LYS:HE2	2.03	0.41
4:Y:47:VAL:HG12	4:Y:48:LEU:N	2.36	0.41
5:Z:73:HIS:CE1	5:Z:107:LEU:O	2.72	0.41
2:B:15:PHE:N	3:C:23:GLN:HE22	2.18	0.41
8:H:49:ALA:CB	9:I:118:CYS:SG	3.09	0.41
2:B:175:LEU:HD23	2:B:175:LEU:HA	1.88	0.41
2:B:176:LEU:C	2:B:178:MET:H	2.23	0.41
3:X:96:ALA:O	3:X:100:ARG:HG3	2.21	0.41
8:O:221:ILE:N	8:O:221:ILE:CD1	2.84	0.41
11:R:52:CYS:SG	11:R:97:MET:HB2	2.60	0.41
14:N:174:ARG:HD2	17:N:564:HOH:O	2.21	0.41
1:A:147(A):SER:HB2	1:A:149:TYR:CE2	2.56	0.41
5:Z:44:THR:O	5:Z:45:HIS:ND1	2.53	0.41
6:F:160:TYR:HB3	6:F:162:GLY:O	2.21	0.41
6:F:147:HIS:HB3	6:F:149:TYR:HE2	1.86	0.41
1:A:136:LEU:O	1:A:150:GLN:HA	2.21	0.41
2:B:64:THR:HG23	2:B:67:LEU:O	2.20	0.41
14:U:107:LYS:HG2	14:U:108:GLY:H	1.86	0.41
9:P:5:ALA:HB2	9:P:14:ILE:HG13	2.03	0.41
2:B:207:TYR:CG	2:B:208:ASP:N	2.89	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:Y:147:GLN:HA	17:Y:1042:HOH:O	2.21	0.41
8:H:133:ALA:O	8:H:136:ALA:HB3	2.21	0.41
5:Z:35:SER:OG	5:Z:36:VAL:N	2.54	0.41
1:V:100:TYR:CE1	1:V:107:PRO:HA	2.56	0.41
13:M:150:VAL:HG21	17:M:869:HOH:O	2.21	0.41
11:K:58:TRP:O	11:K:59:LEU:C	2.59	0.41
12:L:148:VAL:HG13	12:L:149:GLU:N	2.36	0.41
12:S:113:PHE:CD2	12:S:119:TYR:HB3	2.56	0.41
10:Q:3:ILE:HA	10:Q:3:ILE:HD13	1.85	0.41
10:J:137:LEU:HD23	10:J:137:LEU:HA	1.84	0.41
10:J:157:LEU:HA	10:J:157:LEU:HD12	1.80	0.41
5:Z:161:TYR:CE2	6:1:61:PRO:HD3	2.56	0.41
12:S:4:LEU:CD1	12:S:126:ALA:HB2	2.48	0.41
5:Z:160:LEU:CD2	6:1:59:LEU:HD12	2.51	0.41
11:R:41:LEU:HD21	11:R:76:VAL:HG22	2.02	0.41
4:D:121:LEU:HD23	4:D:123:PHE:HE1	1.85	0.41
13:M:165:ARG:HD2	13:M:165:ARG:N	2.36	0.41
7:2:158:VAL:HG22	7:2:159:GLY:N	2.36	0.41
2:B:70:LEU:CD2	2:B:89:ILE:HG23	2.50	0.41
11:K:139:ASP:OD2	10:Q:164:LYS:HD3	2.21	0.41
8:O:163:ILE:HG22	8:O:164:TRP:CE3	2.55	0.41
1:A:109:THR:O	1:A:113:VAL:HG23	2.21	0.41
3:C:183:PRO:HB3	3:C:189:CYS:HA	2.02	0.41
5:E:180(C):PHE:C	5:E:180(E):LYS:N	2.74	0.40
6:F:50:VAL:CG2	6:F:51:GLU:N	2.84	0.40
10:Q:105:ASP:O	10:Q:105(B):LYS:N	2.53	0.40
3:X:57:LYS:HG3	3:X:208:LYS:HZ1	1.86	0.40
1:A:149:TYR:CE1	1:A:159:PRO:HB3	2.57	0.40
3:C:212:ILE:CG2	3:C:213:THR:N	2.84	0.40
5:E:28:LEU:HA	5:E:31:ILE:HD12	2.03	0.40
5:Z:4:PHE:O	5:Z:7:ASN:HB2	2.21	0.40
4:Y:243:ALA:O	4:Y:244:GLU:HG2	2.20	0.40
1:V:55:SER:HB2	17:2:1268:HOH:O	2.21	0.40
1:A:60:MET:HG3	7:G:159:GLY:O	2.21	0.40
10:Q:52:THR:CG2	10:Q:53:VAL:N	2.84	0.40
6:F:192:GLN:O	6:F:195:LYS:HB3	2.21	0.40
11:K:99:THR:HA	17:K:444:HOH:O	2.21	0.40
13:M:83:LEU:HA	13:M:83:LEU:HD23	1.87	0.40
10:J:63:ILE:HD13	10:J:63:ILE:HA	1.91	0.40
5:Z:15:PHE:HD1	5:Z:15:PHE:HA	1.75	0.40
12:L:18:THR:HG22	12:L:31:GLU:N	2.36	0.40
5:Z:194:VAL:O	5:Z:195:GLU:C	2.60	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:T:78:TYR:CD1	5:Z:105:ARG:HB2	2.55	0.40
13:M:82:TYR:O	13:M:85:THR:HB	2.21	0.40
1:V:79:SER:HB2	1:V:165:ILE:HD12	2.02	0.40
7:G:130:ARG:HG3	7:G:130:ARG:HH11	1.86	0.40
6:1:198:TYR:CE2	6:1:208:PHE:CZ	3.06	0.40
3:C:150:GLN:HG2	3:C:151:THR:N	2.36	0.40
7:G:214:VAL:HG12	7:G:215:ALA:H	1.87	0.40
8:H:13:VAL:CG2	8:H:14:ILE:N	2.85	0.40
9:I:19:ARG:HB2	9:I:171:TRP:HB2	2.04	0.40
8:O:3:ILE:O	8:O:126:SER:HA	2.22	0.40
9:P:53:THR:CG2	10:Q:84:ARG:CZ	2.99	0.40
5:Z:82:ALA:O	5:Z:83:PRO:C	2.60	0.40
8:O:114:HIS:HD2	17:O:2814:HOH:O	2.03	0.40
3:C:77:SER:OG	3:C:137:LEU:HB2	2.21	0.40
6:F:17:PRO:HA	7:G:26:TYR:CD2	2.57	0.40
10:Q:120:VAL:HG13	10:Q:122:LEU:HG	2.02	0.40
17:E:864:HOH:O	12:L:67:HIS:HD2	2.03	0.40
13:M:12:VAL:HG21	13:M:102:ALA:HB1	2.03	0.40
2:B:116:LEU:HD23	2:B:116:LEU:HA	1.84	0.40
10:Q:157:LEU:HA	10:Q:157:LEU:HD12	1.87	0.40
12:L:167:ILE:HA	17:L:2973:HOH:O	2.21	0.40
12:S:18:THR:O	12:S:18:THR:HG22	2.21	0.40
4:Y:160:TYR:HA	5:Z:59:SER:HA	2.03	0.40
14:U:175:MET:CE	14:U:187(B):PHE:HE2	2.34	0.40
13:T:122:SER:N	13:T:125:LEU:HD21	2.36	0.40
1:V:77:VAL:HG22	1:V:78:TYR:N	2.35	0.40
13:T:55:ILE:O	13:T:55:ILE:HG22	2.22	0.40
9:I:19:ARG:NH1	17:I:211:HOH:O	2.55	0.40
3:X:232:TYR:O	3:X:236:ILE:HG13	2.21	0.40
6:1:63:LYS:O	6:1:65:VAL:N	2.53	0.40
5:Z:207:LEU:N	5:Z:207:LEU:HD23	2.36	0.40
14:N:20:THR:OG1	14:N:28:ASN:HB3	2.22	0.40
6:1:236:ALA:C	6:1:238:LYS:H	2.25	0.40
17:C:2999:HOH:O	4:D:86:ARG:HG3	2.21	0.40
2:W:176:LEU:C	2:W:178:MET:N	2.74	0.40
7:G:225:SER:O	7:G:226:ALA:C	2.59	0.40
10:Q:38:SER:O	10:Q:40:HIS:N	2.54	0.40
2:B:225:LYS:O	2:B:228:GLU:HB2	2.20	0.40
13:M:70(A):ALA:O	13:M:71(D):ALA:HB2	2.21	0.40
1:V:62:GLU:H	1:V:62:GLU:CD	2.24	0.40
10:Q:59:ILE:HG23	10:Q:59:ILE:HD12	1.86	0.40
4:D:91:HIS:CD2	4:D:91:HIS:O	2.74	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:V:130:ARG:O	1:V:130:ARG:HG3	2.20	0.40
4:D:139:ALA:HB2	4:D:148:LEU:HD13	2.04	0.40
3:C:208:LYS:HE3	3:C:209:ASN:ND2	2.37	0.40
9:I:76:PRO:O	9:I:77:GLU:C	2.60	0.40
11:K:196:PHE:CE2	11:K:206:PHE:CG	3.09	0.40
5:Z:161:TYR:OH	6:1:61:PRO:CD	2.66	0.40
8:H:3:ILE:HD11	8:H:127:LEU:HB2	2.04	0.40
7:G:59:LEU:O	7:G:61:PRO:CD	2.70	0.40
13:T:-6:GLN:HA	13:T:-5:PRO:HD2	1.93	0.40
8:H:13:VAL:HG23	8:H:176:CYS:O	2.20	0.40
4:D:49:GLY:HA2	4:D:211:GLN:O	2.22	0.40
9:I:3:VAL:HA	9:I:15:ALA:O	2.21	0.40
13:T:42:VAL:CG2	13:T:178:ILE:HD11	2.51	0.40
7:2:82:ILE:O	7:2:83:PRO:C	2.59	0.40
14:U:187(D):PRO:C	14:U:187(F):GLU:N	2.75	0.40
14:N:112:THR:O	14:N:112:THR:HG23	2.21	0.40
13:M:63:VAL:HG12	13:M:64:THR:N	2.35	0.40
7:2:87:ASN:N	17:2:2404:HOH:O	2.54	0.40
11:K:85:ASN:ND2	17:K:227:HOH:O	2.53	0.40
12:S:99:THR:HG23	12:S:113:PHE:HB2	2.03	0.40
13:T:82:TYR:O	13:T:86:VAL:HG23	2.21	0.40
12:S:17:ASP:HA	12:S:172:GLY:O	2.22	0.40
11:R:175:LEU:O	11:R:186:TYR:HD1	2.05	0.40
14:U:52:THR:HG22	14:U:97:ALA:HB1	2.03	0.40
3:X:19:GLY:O	4:Y:30:ALA:HB2	2.22	0.40
2:B:189:ALA:O	2:B:190:ILE:C	2.59	0.40
3:X:241:GLN:C	3:X:243:GLN:H	2.25	0.40
8:H:204:TYR:N	8:H:204:TYR:CD2	2.89	0.40
5:Z:179:THR:HG22	5:Z:179:THR:O	2.21	0.40
14:N:187:LEU:HD23	14:N:187:LEU:HA	1.90	0.40
7:2:99:PHE:CE1	7:2:107:MET:HA	2.57	0.40
1:A:50:THR:OG1	1:A:51:GLU:N	2.55	0.40
2:W:71:ASN:ND2	2:W:72:ASP:N	2.68	0.40
6:F:38:ILE:HG22	6:F:164:ALA:HB2	2.03	0.40
8:H:95:ILE:O	8:H:97:ALA:N	2.52	0.40
6:F:198:TYR:CD2	6:F:208:PHE:HZ	2.40	0.40
1:V:197:LEU:HA	1:V:197:LEU:HD12	1.79	0.40
9:P:27:VAL:HG13	17:Q:2596:HOH:O	2.20	0.40
10:Q:78:ALA:O	10:Q:79:VAL:C	2.60	0.40
14:N:171:GLY:HA2	13:T:197:TRP:CH2	2.56	0.40
5:Z:216:GLY:O	5:Z:219:THR:N	2.50	0.40
10:Q:2:ILE:HD12	10:Q:170:PHE:CG	2.55	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:13:ILE:HG12	14:N:177:VAL:HG13	2.04	0.40
10:J:138:LEU:O	10:J:139:ASP:C	2.57	0.40
3:X:122:ARG:NH2	17:X:2046:HOH:O	2.55	0.40
13:M:114:ASN:O	13:M:116:LEU:N	2.55	0.40
2:W:120:LYS:NZ	2:W:151:SER:OG	2.53	0.40
12:S:21:ILE:C	12:S:21:ILE:HD12	2.41	0.40
5:E:167:ALA:HB3	17:E:982:HOH:O	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	207 (84%)	38 (15%)	3 (1%)	19	64
1	V	248/250 (99%)	212 (86%)	32 (13%)	4 (2%)	14	56
2	B	242/244 (99%)	210 (87%)	26 (11%)	6 (2%)	9	40
2	W	242/244 (99%)	209 (86%)	24 (10%)	9 (4%)	5	28
3	C	239/241 (99%)	207 (87%)	25 (10%)	7 (3%)	7	35
3	X	239/241 (99%)	203 (85%)	29 (12%)	7 (3%)	7	35
4	D	240/242 (99%)	205 (85%)	30 (12%)	5 (2%)	11	47
4	Y	240/242 (99%)	210 (88%)	24 (10%)	6 (2%)	9	40
5	E	231/233 (99%)	196 (85%)	30 (13%)	5 (2%)	10	45
5	Z	231/233 (99%)	196 (85%)	28 (12%)	7 (3%)	7	34
6	1	242/244 (99%)	203 (84%)	33 (14%)	6 (2%)	9	40
6	F	242/244 (99%)	206 (85%)	34 (14%)	2 (1%)	27	76
7	2	241/243 (99%)	211 (88%)	24 (10%)	6 (2%)	9	40
7	G	241/243 (99%)	209 (87%)	27 (11%)	5 (2%)	11	47
8	H	220/222 (99%)	192 (87%)	25 (11%)	3 (1%)	16	60
8	O	220/222 (99%)	198 (90%)	17 (8%)	5 (2%)	10	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	202/204 (99%)	181 (90%)	20 (10%)	1 (0%)	38	84
9	P	202/204 (99%)	185 (92%)	16 (8%)	1 (0%)	38	84
10	J	196/198 (99%)	175 (89%)	17 (9%)	4 (2%)	11	48
10	Q	196/198 (99%)	175 (89%)	16 (8%)	5 (3%)	8	39
11	K	210/212 (99%)	190 (90%)	17 (8%)	3 (1%)	16	60
11	R	210/212 (99%)	187 (89%)	21 (10%)	2 (1%)	22	70
12	L	220/222 (99%)	191 (87%)	27 (12%)	2 (1%)	25	73
12	S	220/222 (99%)	196 (89%)	23 (10%)	1 (0%)	38	84
13	M	231/233 (99%)	202 (87%)	25 (11%)	4 (2%)	14	54
13	T	231/233 (99%)	200 (87%)	29 (13%)	2 (1%)	25	73
14	N	194/196 (99%)	175 (90%)	16 (8%)	3 (2%)	15	58
14	U	194/196 (99%)	171 (88%)	20 (10%)	3 (2%)	15	58
15	8	1/5 (20%)	1 (100%)	0	0	100	100
15	9	1/5 (20%)	1 (100%)	0	0	100	100
All	All	6314/6378 (99%)	5504 (87%)	693 (11%)	117 (2%)	12	51

All (117) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	GLU
1	A	167	LYS
2	B	54	VAL
2	B	204(A)	SER
3	C	58	LEU
3	C	72	SER
3	C	183	PRO
3	C	203	THR
5	E	217	LYS
8	H	91	GLN
10	J	39	PRO
13	M	71(B)	GLU
8	O	91	GLN
11	R	39	PRO
1	V	167	LYS
2	W	54	VAL
2	W	204(A)	SER
2	W	218(C)	ASP

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Mol	Chain	Res	Type
3	X	58	LEU
3	X	183	PRO
3	X	203	THR
5	Z	217	LYS
2	B	219(C)	ASP
3	C	184	ALA
4	D	120	ALA
4	D	121	LEU
4	D	180(E)	SER
5	E	202	ARG
5	E	231	LYS
7	G	9	ASP
7	G	180(C)	HIS
10	J	49	ALA
14	N	115	LEU
10	Q	105(A)	LYS
13	T	71(B)	GLU
14	U	115	LEU
1	V	53	LYS
1	V	143	GLU
2	W	182	ASP
3	X	72	SER
4	Y	120	ALA
4	Y	180(E)	SER
5	Z	163	THR
5	Z	202	ARG
5	Z	231	LYS
7	2	9	ASP
7	2	55	PRO
7	2	180(C)	HIS
2	B	11	ARG
4	D	22	PHE
5	E	170	GLN
6	F	206	LYS
6	F	237	GLN
8	H	30	ASN
10	J	105(A)	LYS
11	K	9	GLN
11	K	39	PRO
12	L	71	ASP
13	M	2	SER
14	N	187(E)	ASP

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Mol	Chain	Res	Type
8	O	205	LYS
10	Q	8	VAL
10	Q	49	ALA
11	R	9	GLN
14	U	187(E)	ASP
2	W	35	GLY
3	X	184	ALA
4	Y	22	PHE
4	Y	121	LEU
5	Z	227	GLU
6	1	8	TYR
6	1	143	LYS
6	1	237	GLN
5	E	186	PRO
7	G	55	PRO
7	G	237	ALA
13	M	72	ALA
8	O	9	ASN
10	Q	39	PRO
10	Q	115	TYR
3	X	64	PRO
5	Z	170	GLN
5	Z	186	PRO
6	1	12	ASN
6	1	206	LYS
7	2	199	ASP
2	B	219(D)	GLY
3	C	239	GLU
9	I	93	GLY
11	K	138	LEU
13	M	115	LEU
14	U	67	THR
2	W	22	TYR
3	X	242	GLU
6	1	98	SER
1	A	72	PRO
14	N	67	THR
8	O	105(A)	PRO
9	P	76	PRO
13	T	72	ALA
2	W	226	PRO
7	2	60	ASP

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Mol	Chain	Res	Type
7	2	208	ASN
7	G	60	ASP
8	H	105(A)	PRO
10	J	8	VAL
8	O	96	GLY
2	W	153	PRO
3	C	64	PRO
1	V	159	PRO
2	W	218(D)	GLY
4	Y	123(F)	GLY
2	B	186	VAL
4	D	123(F)	GLY
12	L	94	PRO
12	S	-6	PRO
4	Y	11	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	198 (95%)	11 (5%)	32	74
1	V	209/209 (100%)	200 (96%)	9 (4%)	40	82
2	B	203/203 (100%)	188 (93%)	15 (7%)	20	58
2	W	203/203 (100%)	186 (92%)	17 (8%)	16	51
3	C	213/213 (100%)	194 (91%)	19 (9%)	14	48
3	X	213/213 (100%)	196 (92%)	17 (8%)	17	53
4	D	198/198 (100%)	185 (93%)	13 (7%)	24	64
4	Y	198/198 (100%)	185 (93%)	13 (7%)	24	64
5	E	192/192 (100%)	171 (89%)	21 (11%)	9	35
5	Z	192/192 (100%)	173 (90%)	19 (10%)	11	40
6	1	201/201 (100%)	181 (90%)	20 (10%)	11	39
6	F	201/201 (100%)	183 (91%)	18 (9%)	14	47
7	2	207/207 (100%)	188 (91%)	19 (9%)	13	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	207/207 (100%)	191 (92%)	16 (8%)	18	56
8	H	181/181 (100%)	169 (93%)	12 (7%)	24	64
8	O	181/181 (100%)	167 (92%)	14 (8%)	18	56
9	I	172/172 (100%)	160 (93%)	12 (7%)	21	62
9	P	172/172 (100%)	163 (95%)	9 (5%)	32	75
10	J	175/175 (100%)	164 (94%)	11 (6%)	25	66
10	Q	175/175 (100%)	165 (94%)	10 (6%)	29	71
11	K	169/169 (100%)	156 (92%)	13 (8%)	18	56
11	R	169/169 (100%)	158 (94%)	11 (6%)	24	65
12	L	185/185 (100%)	173 (94%)	12 (6%)	24	65
12	S	185/185 (100%)	173 (94%)	12 (6%)	24	65
13	M	199/199 (100%)	186 (94%)	13 (6%)	24	65
13	T	199/199 (100%)	188 (94%)	11 (6%)	30	73
14	N	162/162 (100%)	152 (94%)	10 (6%)	26	67
14	U	162/162 (100%)	147 (91%)	15 (9%)	13	45
15	8	2/2 (100%)	2 (100%)	0	100	100
15	9	2/2 (100%)	2 (100%)	0	100	100
All	All	5336/5336 (100%)	4944 (93%)	392 (7%)	20	59

All (392) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	VAL
1	A	64	LEU
1	A	78	TYR
1	A	124	THR
1	A	135	SER
1	A	136	LEU
1	A	158	PHE
1	A	170	VAL
1	A	200	SER
1	A	212	LEU
1	A	236	LEU
2	B	58	LEU
2	B	61	GLN
2	B	63	THR

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Mol	Chain	Res	Type
2	B	65	GLU
2	B	67	LEU
2	B	71	ASN
2	B	150	THR
2	B	156	ASN
2	B	169	THR
2	B	185	LYS
2	B	198	SER
2	B	203	ASP
2	B	206	THR
2	B	226	PRO
2	B	236	THR
3	C	10	ARG
3	C	25	GLU
3	C	57	LYS
3	C	61	THR
3	C	62(A)	ILE
3	C	66	LYS
3	C	75	VAL
3	C	124	THR
3	C	135	SER
3	C	144(B)	ASP
3	C	156	ILE
3	C	163	GLN
3	C	172	VAL
3	C	174	GLU
3	C	178	LYS
3	C	196	SER
3	C	209	ASN
3	C	215	VAL
3	C	224	LEU
4	D	13	SER
4	D	27	SER
4	D	28	LEU
4	D	76	CYS
4	D	119	LEU
4	D	126	ARG
4	D	156	THR
4	D	170	GLU
4	D	177	LEU
4	D	184	LEU
4	D	191	LEU

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Mol	Chain	Res	Type
4	D	215	ILE
4	D	237	LEU
5	E	11	ASP
5	E	12	THR
5	E	15	PHE
5	E	18	THR
5	E	32	LYS
5	E	33	GLN
5	E	58	LEU
5	E	76	LEU
5	E	97	ASN
5	E	121	GLN
5	E	153	PRO
5	E	178	ARG
5	E	180(C)	PHE
5	E	185	ASN
5	E	189	LEU
5	E	198	SER
5	E	199	GLN
5	E	203	ASP
5	E	207(C)	VAL
5	E	222	THR
5	E	231	LYS
6	F	36	THR
6	F	43	ASN
6	F	121	GLN
6	F	127	ASN
6	F	135	SER
6	F	153	PRO
6	F	169	ARG
6	F	170	GLN
6	F	187	ARG
6	F	192	GLN
6	F	203	GLU
6	F	204	ASP
6	F	205	ASN
6	F	208	PHE
6	F	214	TRP
6	F	218(C)	ASN
6	F	227	ASP
6	F	233	ILE
7	G	40	VAL

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Mol	Chain	Res	Type
7	G	72	ARG
7	G	87	ASN
7	G	105	TYR
7	G	119	LEU
7	G	121	GLN
7	G	157	TYR
7	G	169	GLN
7	G	171	GLU
7	G	184	ASN
7	G	201	LEU
7	G	204	GLU
7	G	217	LYS
7	G	221	PHE
7	G	232	ARG
7	G	233	LEU
8	H	22	GLN
8	H	30	ASN
8	H	31	CYS
8	H	34	LEU
8	H	56	THR
8	H	105(A)	PRO
8	H	124	TYR
8	H	135	MET
8	H	185	GLU
8	H	191	TYR
8	H	196	VAL
8	H	197	ARG
9	I	-5	SER
9	I	29	ASN
9	I	55	LEU
9	I	61	TYR
9	I	70	GLU
9	I	113	PHE
9	I	131	SER
9	I	148	PRO
9	I	159	LEU
9	I	160	LEU
9	I	171	TRP
9	I	185	VAL
10	J	7	ARG
10	J	17	SER
10	J	34	THR

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Mol	Chain	Res	Type
10	J	52	THR
10	J	68	ILE
10	J	77	GLN
10	J	91	SER
10	J	104	TYR
10	J	133	TYR
10	J	147	THR
10	J	166	MET
11	K	4	LEU
11	K	9	GLN
11	K	31	VAL
11	K	39	PRO
11	K	69	ARG
11	K	70	GLU
11	K	97	MET
11	K	100	MET
11	K	104	TYR
11	K	105(B)	LYS
11	K	138	LEU
11	K	139	ASP
11	K	145	ASP
12	L	14	LEU
12	L	33	LYS
12	L	40	ASN
12	L	48	PHE
12	L	62	SER
12	L	98	HIS
12	L	99	THR
12	L	138	LEU
12	L	144(J)	ASN
12	L	145	TYR
12	L	150	GLU
12	L	184	VAL
13	M	21	SER
13	M	40	ASN
13	M	61	ASP
13	M	62	LEU
13	M	112	TYR
13	M	115	LEU
13	M	122	SER
13	M	141(C)	ARG
13	M	181(A)	THR

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Mol	Chain	Res	Type
13	M	184	LEU
13	M	190	LEU
13	M	192	VAL
13	M	204	LYS
14	N	12	VAL
14	N	20	THR
14	N	36	ARG
14	N	61	TYR
14	N	81	SER
14	N	105	ASP
14	N	105(A)	ASP
14	N	123	PRO
14	N	132	THR
14	N	149	GLU
8	O	22	GLN
8	O	30	ASN
8	O	34	LEU
8	O	56	THR
8	O	68	LEU
8	O	105(A)	PRO
8	O	121	VAL
8	O	124	TYR
8	O	156	SER
8	O	189	ARG
8	O	191	TYR
8	O	193	THR
8	O	197	ARG
8	O	221	ILE
9	P	-5	SER
9	P	29	ASN
9	P	55	LEU
9	P	113	PHE
9	P	131	SER
9	P	159	LEU
9	P	160	LEU
9	P	171	TRP
9	P	185	VAL
10	Q	7	ARG
10	Q	17	SER
10	Q	34	THR
10	Q	52	THR
10	Q	68	ILE

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Mol	Chain	Res	Type
10	Q	77	GLN
10	Q	91	SER
10	Q	104	TYR
10	Q	133	TYR
10	Q	147	THR
11	R	4	LEU
11	R	9	GLN
11	R	39	PRO
11	R	70	GLU
11	R	100	MET
11	R	102	CYS
11	R	104	TYR
11	R	105(B)	LYS
11	R	135	TYR
11	R	138	LEU
11	R	145	ASP
12	S	14	LEU
12	S	40	ASN
12	S	43	MET
12	S	62	SER
12	S	82	ASN
12	S	98	HIS
12	S	99	THR
12	S	138	LEU
12	S	144(I)	ASN
12	S	145	TYR
12	S	150	GLU
12	S	179	THR
13	T	21	SER
13	T	40	ASN
13	T	61	ASP
13	T	62	LEU
13	T	63	VAL
13	T	123	PRO
13	T	141(C)	ARG
13	T	165	ARG
13	T	181(A)	THR
13	T	192	VAL
13	T	204	LYS
14	U	6	VAL
14	U	8	PHE
14	U	20	THR

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Mol	Chain	Res	Type
14	U	36	ARG
14	U	70	TYR
14	U	81	SER
14	U	105(A)	ASP
14	U	115	LEU
14	U	122	LEU
14	U	124	TYR
14	U	132	THR
14	U	144	GLU
14	U	169	SER
14	U	177	VAL
14	U	178	LEU
1	V	64	LEU
1	V	78	TYR
1	V	135	SER
1	V	136	LEU
1	V	158	PHE
1	V	170	VAL
1	V	212	LEU
1	V	221	PHE
1	V	236	LEU
2	W	38	ILE
2	W	58	LEU
2	W	61	GLN
2	W	63	THR
2	W	67	LEU
2	W	71	ASN
2	W	121	GLN
2	W	150	THR
2	W	153	PRO
2	W	156	ASN
2	W	169	THR
2	W	185	LYS
2	W	198	SER
2	W	203	ASP
2	W	218(C)	ASP
2	W	226	PRO
2	W	236	THR
3	X	10	ARG
3	X	17	PRO
3	X	25	GLU
3	X	57	LYS

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Mol	Chain	Res	Type
3	X	61	THR
3	X	62(A)	ILE
3	X	66	LYS
3	X	75	VAL
3	X	121	GLN
3	X	135	SER
3	X	163	GLN
3	X	174	GLU
3	X	178	LYS
3	X	196	SER
3	X	209	ASN
3	X	215	VAL
3	X	224	LEU
4	Y	28	LEU
4	Y	56	SER
4	Y	76	CYS
4	Y	119	LEU
4	Y	126	ARG
4	Y	154	SER
4	Y	156	THR
4	Y	177	LEU
4	Y	184	LEU
4	Y	191	LEU
4	Y	208	ASP
4	Y	215	ILE
4	Y	237	LEU
5	Z	11	ASP
5	Z	12	THR
5	Z	15	PHE
5	Z	18	THR
5	Z	32	LYS
5	Z	58	LEU
5	Z	76	LEU
5	Z	97	ASN
5	Z	117	CYS
5	Z	153	PRO
5	Z	178	ARG
5	Z	180(C)	PHE
5	Z	185	ASN
5	Z	198	SER
5	Z	199	GLN
5	Z	207	LEU

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Mol	Chain	Res	Type
5	Z	207(C)	VAL
5	Z	222	THR
5	Z	231	LYS
6	1	36	THR
6	1	43	ASN
6	1	73	HIS
6	1	83	PRO
6	1	121	GLN
6	1	127	ASN
6	1	135	SER
6	1	153	PRO
6	1	169	ARG
6	1	170	GLN
6	1	187	ARG
6	1	192	GLN
6	1	203	GLU
6	1	204	ASP
6	1	205	ASN
6	1	208	PHE
6	1	214	TRP
6	1	218(C)	ASN
6	1	227	ASP
6	1	233	ILE
7	2	29	LYS
7	2	56	ASP
7	2	62	THR
7	2	72	ARG
7	2	87	ASN
7	2	105	TYR
7	2	119	LEU
7	2	121	GLN
7	2	152	ASP
7	2	157	TYR
7	2	169	GLN
7	2	171	GLU
7	2	184	ASN
7	2	201	LEU
7	2	204	GLU
7	2	217	LYS
7	2	222	PHE
7	2	232	ARG
7	2	233	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (187) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	HIS
1	A	145	ASN
2	B	23	GLN
2	B	71	ASN
2	B	97	GLN
2	B	121	GLN
2	B	125	GLN
2	B	156	ASN
2	B	177	GLN
3	C	23	GLN
3	C	82	ASN
3	C	97	GLN
3	C	120	GLN
3	C	150	GLN
3	C	163	GLN
3	C	209	ASN
3	C	235	GLN
4	D	23	GLN
4	D	99	HIS
4	D	108	ASN
4	D	150	HIS
4	D	211	GLN
4	D	226	ASN
5	E	6	ASN
5	E	7	ASN
5	E	33	GLN
5	E	73	HIS
5	E	97	ASN
5	E	121	GLN
5	E	123	ASN
5	E	125	GLN
5	E	152	GLN
5	E	185	ASN
5	E	199	GLN
6	F	23	GLN
6	F	43	ASN
6	F	90	ASN
6	F	121	GLN
6	F	123	HIS
6	F	221	HIS
6	F	241	ASN

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Mol	Chain	Res	Type
7	G	34(A)	ASN
7	G	87	ASN
7	G	118	ASN
7	G	121	GLN
7	G	125	GLN
7	G	170	GLN
7	G	184	ASN
8	H	22	GLN
8	H	30	ASN
8	H	66	HIS
8	H	86	HIS
8	H	109	HIS
8	H	114	HIS
8	H	144	GLN
8	H	172	ASN
8	H	190	ASN
9	I	29	ASN
9	I	81	GLN
9	I	145	ASN
10	J	54	GLN
10	J	64	GLN
10	J	77	GLN
10	J	85	GLN
10	J	112	GLN
10	J	140	HIS
10	J	141	HIS
10	J	186	GLN
11	K	85	ASN
11	K	174	ASN
12	L	-7	ASN
12	L	40	ASN
12	L	67	HIS
12	L	70(A)	ASN
12	L	123	GLN
12	L	140	ASN
12	L	141	GLN
12	L	144(B)	ASN
12	L	144(J)	ASN
12	L	166	HIS
13	M	10	ASN
13	M	40	ASN
13	M	89	GLN

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Mol	Chain	Res	Type
13	M	93	ASN
13	M	135	ASN
13	M	149	GLN
13	M	157	ASN
13	M	172	ASN
13	M	191	GLN
14	N	38	HIS
14	N	62	HIS
14	N	157	HIS
14	N	161	GLN
8	O	22	GLN
8	O	30	ASN
8	O	66	HIS
8	O	91	GLN
8	O	114	HIS
8	O	144	GLN
8	O	172	ASN
8	O	190	ASN
9	P	29	ASN
9	P	81	GLN
9	P	145	ASN
10	Q	54	GLN
10	Q	64	GLN
10	Q	77	GLN
10	Q	85	GLN
10	Q	112	GLN
10	Q	141	HIS
10	Q	186	GLN
11	R	9	GLN
11	R	85	ASN
11	R	174	ASN
12	S	40	ASN
12	S	61	ASN
12	S	70(A)	ASN
12	S	140	ASN
12	S	141	GLN
12	S	144(B)	ASN
12	S	144(I)	ASN
12	S	166	HIS
13	T	10	ASN
13	T	40	ASN
13	T	89	GLN

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Mol	Chain	Res	Type
13	T	93	ASN
13	T	132	HIS
13	T	135	ASN
13	T	149	GLN
13	T	157	ASN
13	T	172	ASN
13	T	191	GLN
14	U	69	GLN
14	U	161	GLN
1	V	97	HIS
1	V	145	ASN
1	V	181	ASN
1	V	217(B)	ASN
2	W	23	GLN
2	W	71	ASN
2	W	97	GLN
2	W	121	GLN
2	W	125	GLN
2	W	156	ASN
2	W	177	GLN
2	W	227	GLN
3	X	23	GLN
3	X	82	ASN
3	X	97	GLN
3	X	150	GLN
3	X	163	GLN
3	X	209	ASN
4	Y	23	GLN
4	Y	108	ASN
4	Y	150	HIS
4	Y	211	GLN
4	Y	226	ASN
5	Z	6	ASN
5	Z	7	ASN
5	Z	33	GLN
5	Z	54	ASN
5	Z	73	HIS
5	Z	121	GLN
5	Z	123	ASN
5	Z	125	GLN
5	Z	152	GLN
5	Z	185	ASN

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Mol	Chain	Res	Type
5	Z	199	GLN
6	1	23	GLN
6	1	43	ASN
6	1	90	ASN
6	1	121	GLN
6	1	123	HIS
6	1	147	HIS
6	1	192	GLN
6	1	241	ASN
7	2	33	GLN
7	2	34(A)	ASN
7	2	87	ASN
7	2	118	ASN
7	2	121	GLN
7	2	125	GLN
7	2	170	GLN
7	2	184	ASN
7	2	239	GLN
15	8	3	ASN
15	9	3	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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$
15	R4K	8	4	15	18,18,19	5.71	6 (33%)	25,27,29	2.13	8 (32%)
15	R4K	9	4	15	18,18,19	4.98	9 (50%)	25,27,29	3.31	12 (48%)



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
15	R4K	8	4	15	-	0/10/28/30	0/0/2/2
15	R4K	9	4	15	-	0/10/28/30	0/0/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	8	4	R4K	O-C	21.19	1.26	1.11
15	9	4	R4K	O-C	15.59	1.22	1.11
15	9	4	R4K	C32-N31	-8.05	1.24	1.35
15	8	4	R4K	C29-C50	-7.73	1.41	1.51
15	9	4	R4K	C55-C50	-6.84	1.30	1.39
15	8	4	R4K	C55-C50	-5.23	1.32	1.39
15	8	4	R4K	C32-N31	-4.83	1.28	1.35
15	9	4	R4K	CB-CA	4.59	1.61	1.53
15	9	4	R4K	C29-C32	-4.40	1.45	1.54
15	9	4	R4K	C55-N31	-3.92	1.31	1.38
15	9	4	R4K	C29-C50	-3.81	1.46	1.51
15	8	4	R4K	C51-C50	3.25	1.44	1.39
15	9	4	R4K	C51-C50	2.67	1.43	1.39
15	9	4	R4K	O33-C32	2.21	1.27	1.22
15	8	4	R4K	C29-C32	-2.02	1.50	1.54

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	9	4	R4K	C51-C50-C55	10.42	128.82	119.75
15	9	4	R4K	C54-C55-C50	-6.59	115.56	121.98
15	9	4	R4K	CB-CA-N	6.29	117.39	109.22
15	8	4	R4K	CB-CA-N	4.72	115.35	109.22
15	8	4	R4K	C51-C50-C55	4.70	123.84	119.75
15	9	4	R4K	C50-C55-N31	4.36	112.56	109.60
15	8	4	R4K	C54-C55-C50	-4.02	118.06	121.98
15	8	4	R4K	C55-N31-C32	-3.26	110.05	111.87
15	8	4	R4K	O33-C32-N31	3.19	129.51	126.26
15	9	4	R4K	C55-N31-C32	-2.94	110.23	111.87
15	9	4	R4K	C51-C50-C29	-2.74	124.91	130.80
15	9	4	R4K	C52-C51-C50	-2.66	114.98	120.02
15	9	4	R4K	C52-C53-C54	2.39	124.15	120.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	8	4	R4K	C29-CB-CA	-2.36	109.84	115.57
15	9	4	R4K	C-CA-N	-2.33	108.15	111.94
15	8	4	R4K	O30-C29-C32	2.25	114.59	109.43
15	9	4	R4K	C29-CB-CA	-2.10	110.47	115.57
15	9	4	R4K	C29-C32-N31	2.07	110.65	108.06
15	8	4	R4K	C50-C29-CB	-2.03	106.16	112.67
15	9	4	R4K	O30-C29-C32	2.02	114.06	109.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.