



Full wwPDB X-ray Structure Validation Report

Jul 22, 2014 – 11:42 AM EDT

PDB ID : 4V4E
Title : Crystal Structure of Pyrogallol-PhloroglucinolTranshydroxylase from Pelobacter acidigallici complexed with inhibitor 1,2,4,5-tetrahydroxy-benzene
Authors : Messerschmidt, A.; Niessen, H.; Abt, D.; Einsle, O.; Schink, B.; Kroneck, P.M.H.
Deposited on : 2004-06-02
Resolution : 2.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

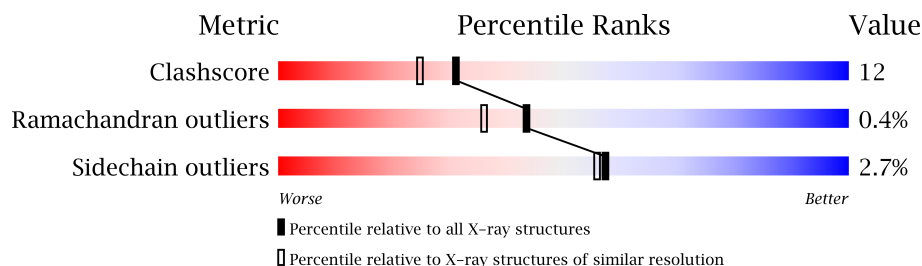
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 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) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)








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 ≥ 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	875	<div><div></div><div></div></div>
1	C	875	<div><div></div><div></div></div>
1	E	875	<div><div></div><div></div></div>
1	G	875	<div><div></div><div></div></div>
1	I	875	<div><div></div><div></div></div>
1	K	875	<div><div></div><div></div></div>
1	M	875	<div><div></div><div></div></div>
1	O	875	<div><div></div><div></div></div>
1	Q	875	<div><div></div><div></div></div>
1	S	875	<div><div></div><div></div></div>
1	U	875	<div><div></div><div></div></div>
1	W	875	<div><div></div><div></div></div>
2	B	274	<div><div></div><div></div></div>
2	D	274	<div><div></div><div></div></div>
2	F	274	<div><div></div><div></div></div>
2	H	274	<div><div></div><div></div></div>
2	J	274	<div><div></div><div></div></div>

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Mol	Chain	Length	Quality of chain
2	L	274	
2	N	274	
2	P	274	
2	R	274	
2	T	274	
2	V	274	
2	X	274	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
6	BTT	S	905	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 121823 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 Pyrogallol hydroxytransferase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	C	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	E	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	G	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	I	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	K	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	M	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	O	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	Q	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	S	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	U	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			
1	W	875	Total	C	N	O	S	0	0	0
			6998	4464	1189	1297	48			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP P80563
C	1	MET	-	INITIATING METHIONINE	UNP P80563
E	1	MET	-	INITIATING METHIONINE	UNP P80563
G	1	MET	-	INITIATING METHIONINE	UNP P80563
I	1	MET	-	INITIATING METHIONINE	UNP P80563

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1	MET	-	INITIATING METHIONINE	UNP P80563
M	1	MET	-	INITIATING METHIONINE	UNP P80563
O	1	MET	-	INITIATING METHIONINE	UNP P80563
Q	1	MET	-	INITIATING METHIONINE	UNP P80563
S	1	MET	-	INITIATING METHIONINE	UNP P80563
U	1	MET	-	INITIATING METHIONINE	UNP P80563
W	1	MET	-	INITIATING METHIONINE	UNP P80563

- Molecule 2 is a protein called Pyrogallol hydroxytransferase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	D	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	F	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	H	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	J	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	L	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	N	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	P	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	R	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	T	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	V	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			
2	X	274	Total	C	N	O	S	0	0	0
			2182	1371	364	423	24			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total	Ca	0	0
			1	1		
3	K	1	Total	Ca	0	0
			1	1		

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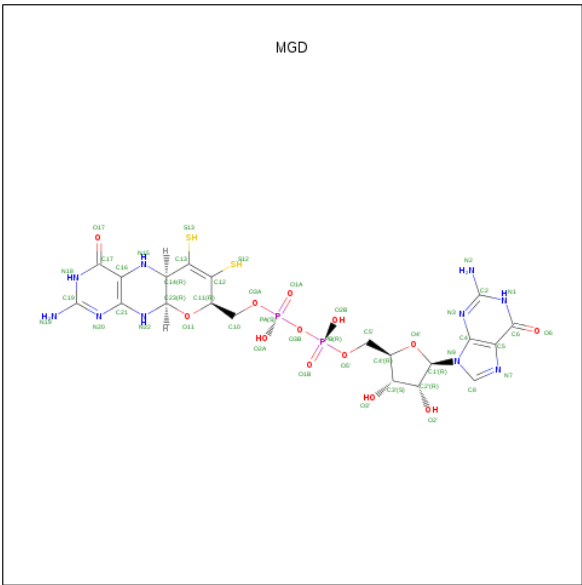
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Ca 1	0	0
3	W	1	Total 1	Ca 1	0	0
3	N	1	Total 1	Ca 1	0	0
3	X	1	Total 1	Ca 1	0	0
3	S	1	Total 1	Ca 1	0	0
3	J	1	Total 1	Ca 1	0	0
3	E	1	Total 1	Ca 1	0	0
3	V	1	Total 1	Ca 1	0	0
3	A	1	Total 1	Ca 1	0	0
3	R	1	Total 1	Ca 1	0	0
3	M	1	Total 1	Ca 1	0	0
3	D	1	Total 1	Ca 1	0	0
3	I	1	Total 1	Ca 1	0	0
3	U	1	Total 1	Ca 1	0	0
3	L	1	Total 1	Ca 1	0	0
3	G	1	Total 1	Ca 1	0	0
3	Q	1	Total 1	Ca 1	0	0
3	H	1	Total 1	Ca 1	0	0
3	C	1	Total 1	Ca 1	0	0
3	T	1	Total 1	Ca 1	0	0
3	O	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	1	Total	Ca	0	0
			1	1		

- Molecule 4 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONEGUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	E	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	E	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	G	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	G	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	I	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	I	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	K	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	K	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	M	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	M	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	O	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	O	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	Q	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	Q	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	S	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	S	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	U	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	U	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	W	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	W	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 5 is MOLYBDENUM(IV) ION (three-letter code: 4MO) (formula: Mo).

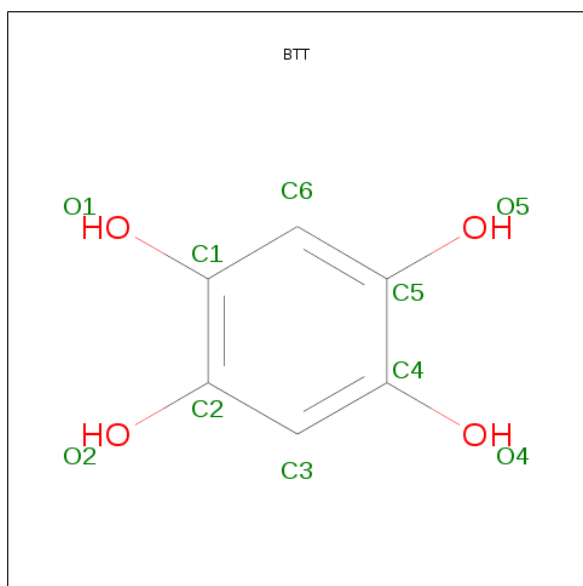
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	1	Total	Mo	0	0
			1	1		
5	Q	1	Total	Mo	0	0
			1	1		
5	K	1	Total	Mo	0	0
			1	1		
5	E	1	Total	Mo	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	1	Total	Mo	0	0
			1	1		
5	C	1	Total	Mo	0	0
			1	1		
5	W	1	Total	Mo	0	0
			1	1		
5	A	1	Total	Mo	0	0
			1	1		
5	U	1	Total	Mo	0	0
			1	1		
5	O	1	Total	Mo	0	0
			1	1		
5	S	1	Total	Mo	0	0
			1	1		
5	M	1	Total	Mo	0	0
			1	1		

- Molecule 6 is BENZENE-1,2,4,5-TETROL (three-letter code: BTT) (formula: $C_6H_6O_4$).



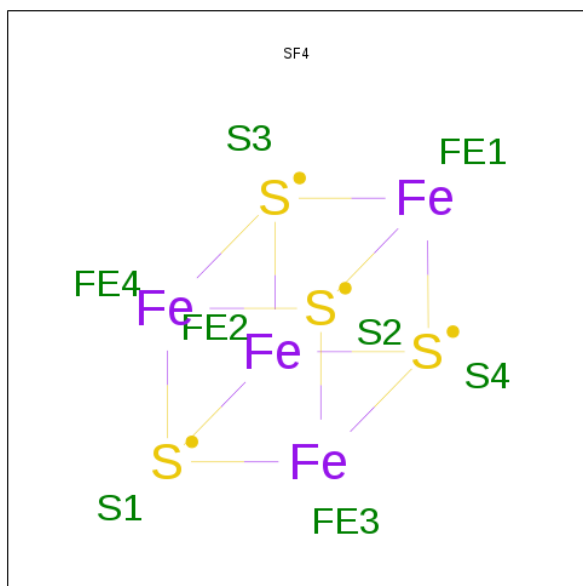
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	C	1	Total	C	O	0	0
			10	6	4		
6	E	1	Total	C	O	0	0
			10	6	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	1	Total	C	O	0	0
			10	6	4		
6	I	1	Total	C	O	0	0
			10	6	4		
6	K	1	Total	C	O	0	0
			10	6	4		
6	M	1	Total	C	O	0	0
			10	6	4		
6	O	1	Total	C	O	0	0
			10	6	4		
6	Q	1	Total	C	O	0	0
			10	6	4		
6	S	1	Total	C	O	0	0
			10	6	4		
6	U	1	Total	C	O	0	0
			10	6	4		
6	W	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		
7	B	1	Total	Fe	S	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total 8	Fe 4	S 4	0	0
7	D	1	Total 8	Fe 4	S 4	0	0
7	D	1	Total 8	Fe 4	S 4	0	0
7	D	1	Total 8	Fe 4	S 4	0	0
7	F	1	Total 8	Fe 4	S 4	0	0
7	F	1	Total 8	Fe 4	S 4	0	0
7	F	1	Total 8	Fe 4	S 4	0	0
7	H	1	Total 8	Fe 4	S 4	0	0
7	H	1	Total 8	Fe 4	S 4	0	0
7	H	1	Total 8	Fe 4	S 4	0	0
7	J	1	Total 8	Fe 4	S 4	0	0
7	J	1	Total 8	Fe 4	S 4	0	0
7	J	1	Total 8	Fe 4	S 4	0	0
7	L	1	Total 8	Fe 4	S 4	0	0
7	L	1	Total 8	Fe 4	S 4	0	0
7	L	1	Total 8	Fe 4	S 4	0	0
7	N	1	Total 8	Fe 4	S 4	0	0
7	N	1	Total 8	Fe 4	S 4	0	0
7	N	1	Total 8	Fe 4	S 4	0	0
7	P	1	Total 8	Fe 4	S 4	0	0
7	P	1	Total 8	Fe 4	S 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	P	1	Total 8	Fe 4	S 4	0	0
7	R	1	Total 8	Fe 4	S 4	0	0
7	R	1	Total 8	Fe 4	S 4	0	0
7	R	1	Total 8	Fe 4	S 4	0	0
7	T	1	Total 8	Fe 4	S 4	0	0
7	T	1	Total 8	Fe 4	S 4	0	0
7	T	1	Total 8	Fe 4	S 4	0	0
7	V	1	Total 8	Fe 4	S 4	0	0
7	V	1	Total 8	Fe 4	S 4	0	0
7	V	1	Total 8	Fe 4	S 4	0	0
7	X	1	Total 8	Fe 4	S 4	0	0
7	X	1	Total 8	Fe 4	S 4	0	0
7	X	1	Total 8	Fe 4	S 4	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	681	Total 681	O 681	0	0
8	B	169	Total 169	O 169	0	0
8	C	684	Total 684	O 684	0	0
8	D	162	Total 162	O 162	0	0
8	E	688	Total 688	O 688	0	0
8	F	160	Total 160	O 160	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	G	682	Total 682	O 682	0	0
8	H	161	Total 161	O 161	0	0
8	I	671	Total 671	O 671	0	0
8	J	168	Total 168	O 168	0	0
8	K	681	Total 681	O 681	0	0
8	L	165	Total 165	O 165	0	0
8	M	682	Total 682	O 682	0	0
8	N	160	Total 160	O 160	0	0
8	O	675	Total 675	O 675	0	0
8	P	160	Total 160	O 160	0	0
8	Q	693	Total 693	O 693	0	0
8	R	158	Total 158	O 158	0	0
8	S	665	Total 665	O 665	0	0
8	T	162	Total 162	O 162	0	0
8	U	670	Total 670	O 670	0	0
8	V	154	Total 154	O 154	0	0
8	W	675	Total 675	O 675	0	0
8	X	165	Total 165	O 165	0	0

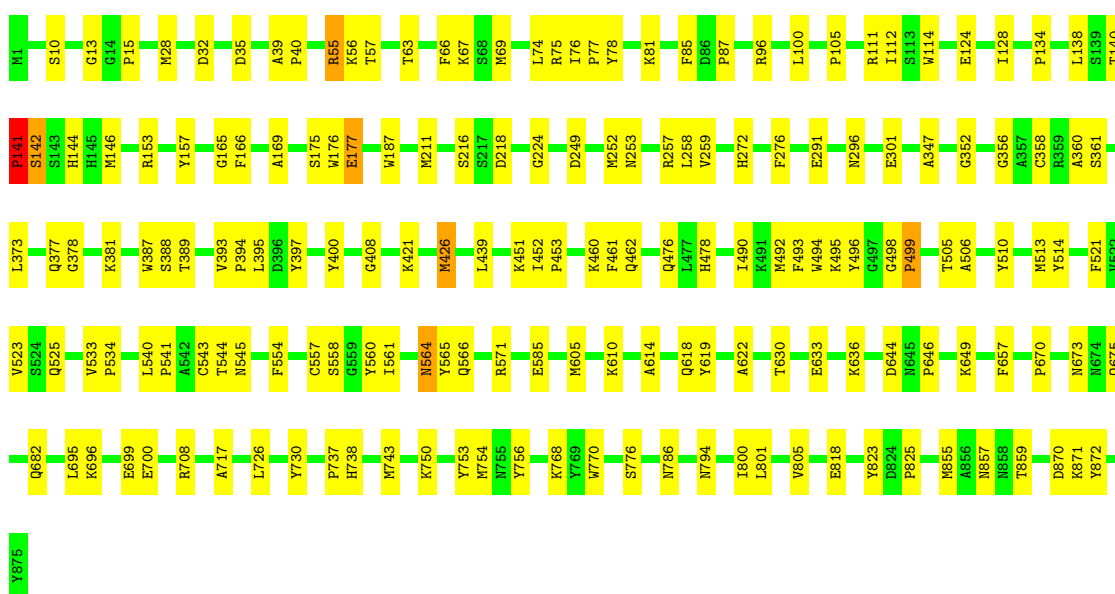
3 Residue-property plots

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.

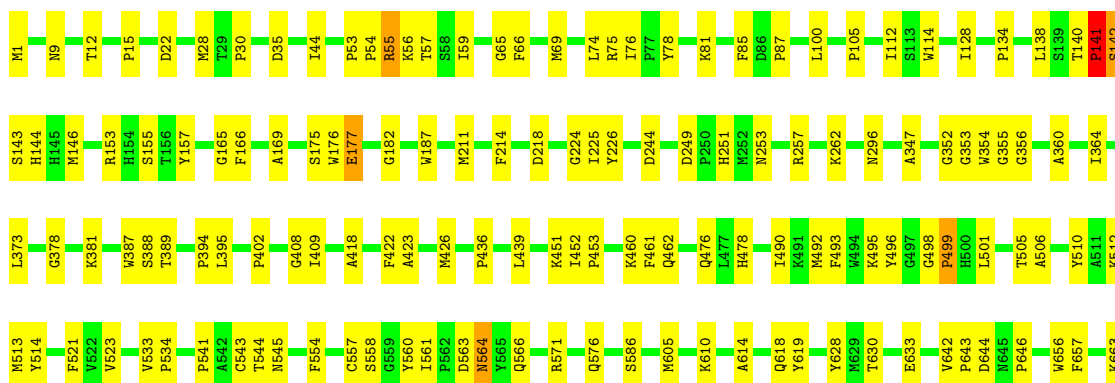
• Molecule 1: Pyrogallol hydroxytransferase large subunit

Chain A:



• Molecule 1: Pyrogallol hydroxytransferase large subunit

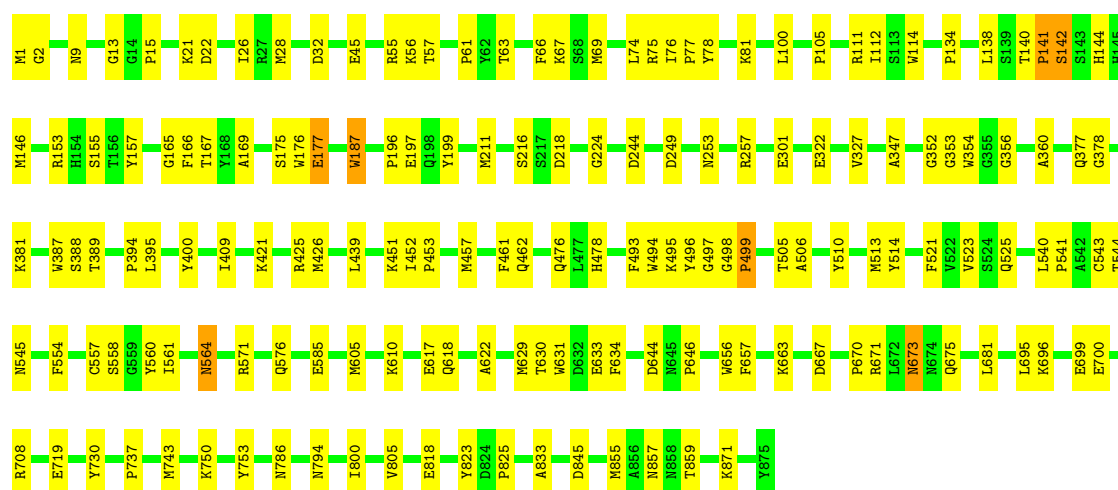
Chain C:





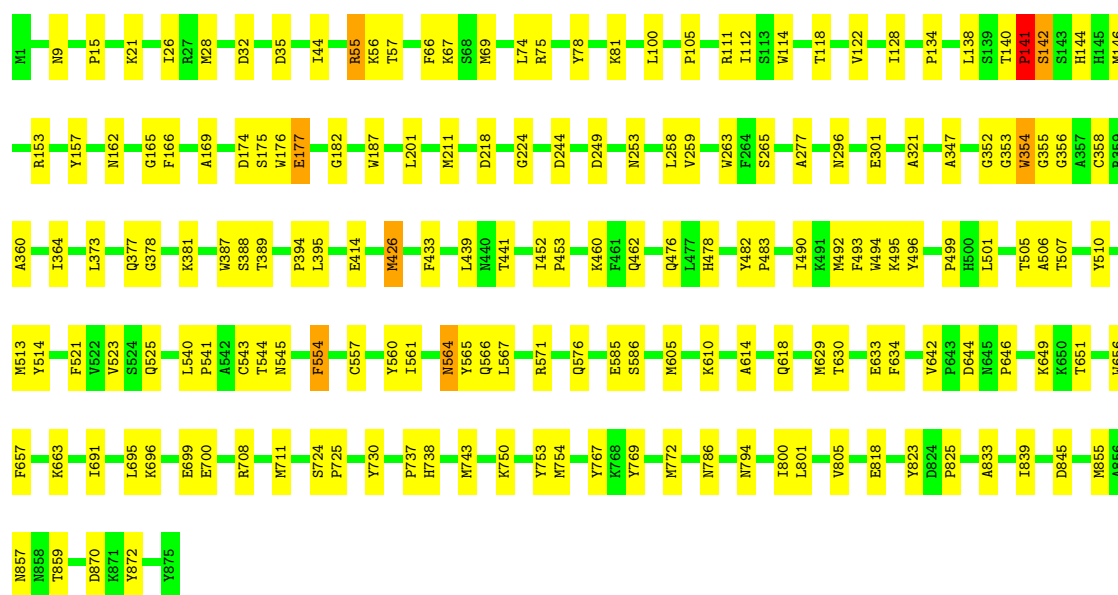
• Molecule 1: Pyrogallol hydroxytransferase large subunit

Chain E:



• Molecule 1: Pyrogallol hydroxytransferase large subunit

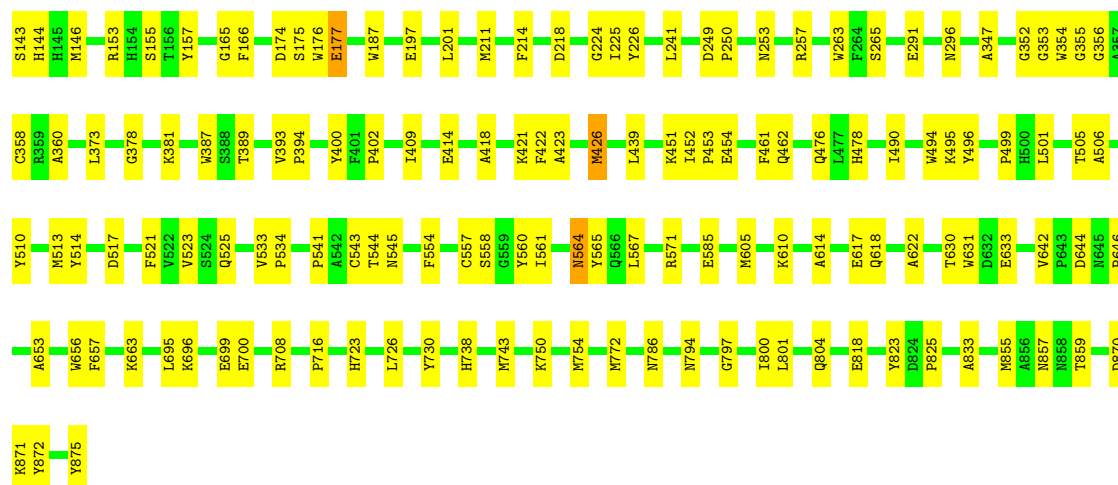
Chain G:



• Molecule 1: Pyrogallol hydroxytransferase large subunit

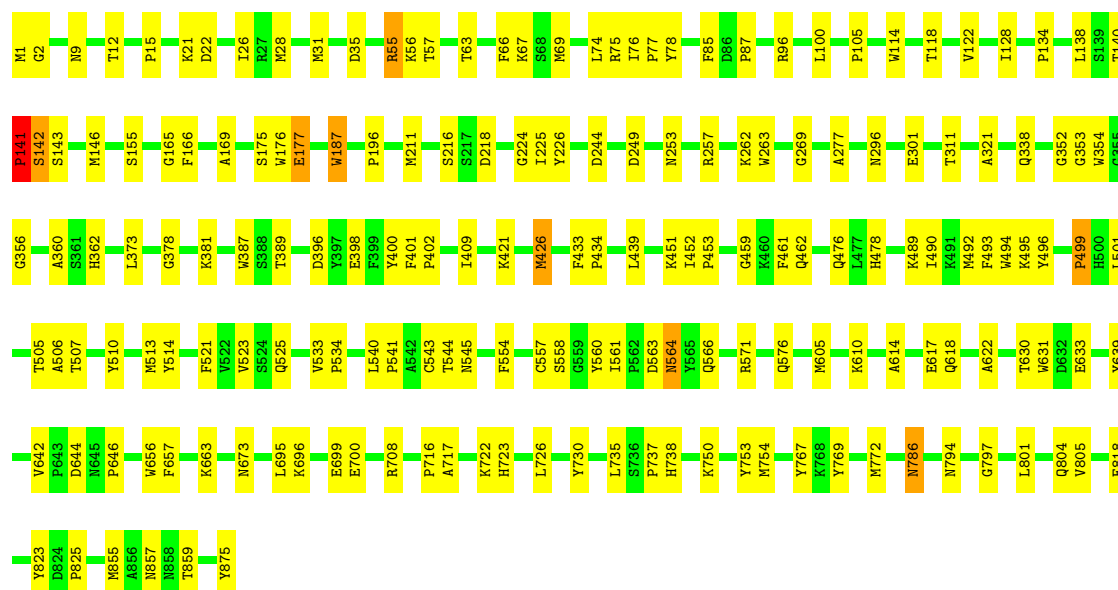
Chain I:





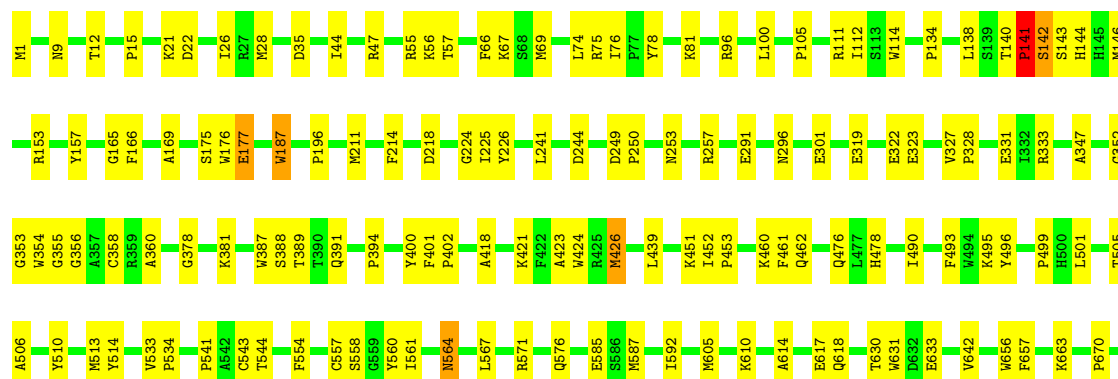
• Molecule 1: Pyrogallol hydroxytransferase large subunit

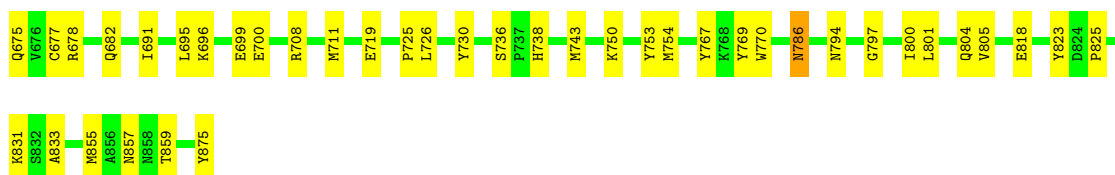
Chain K:



• Molecule 1: Pyrogallol hydroxytransferase large subunit

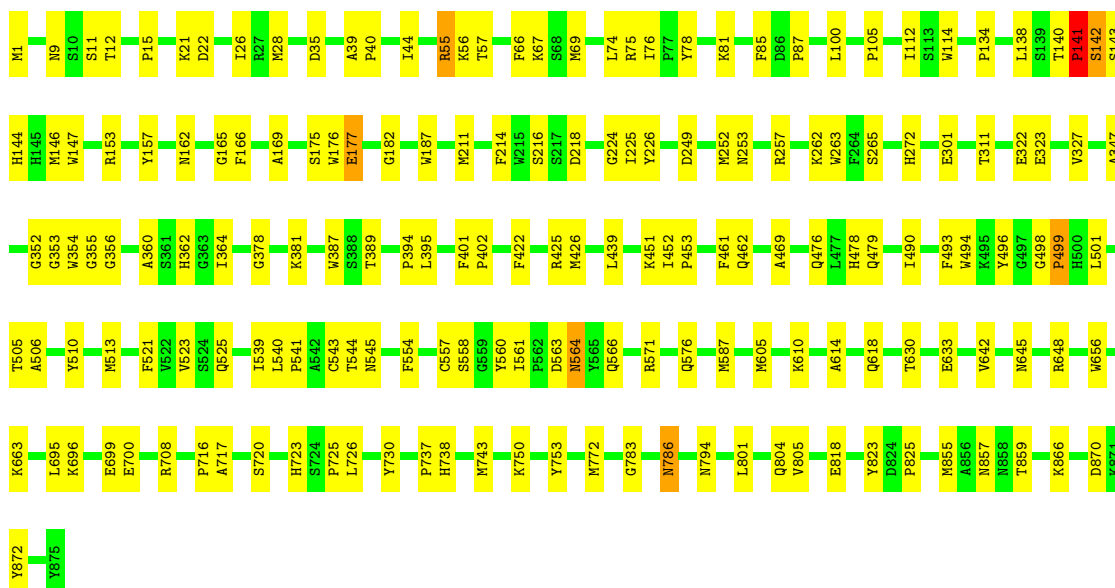
Chain M:





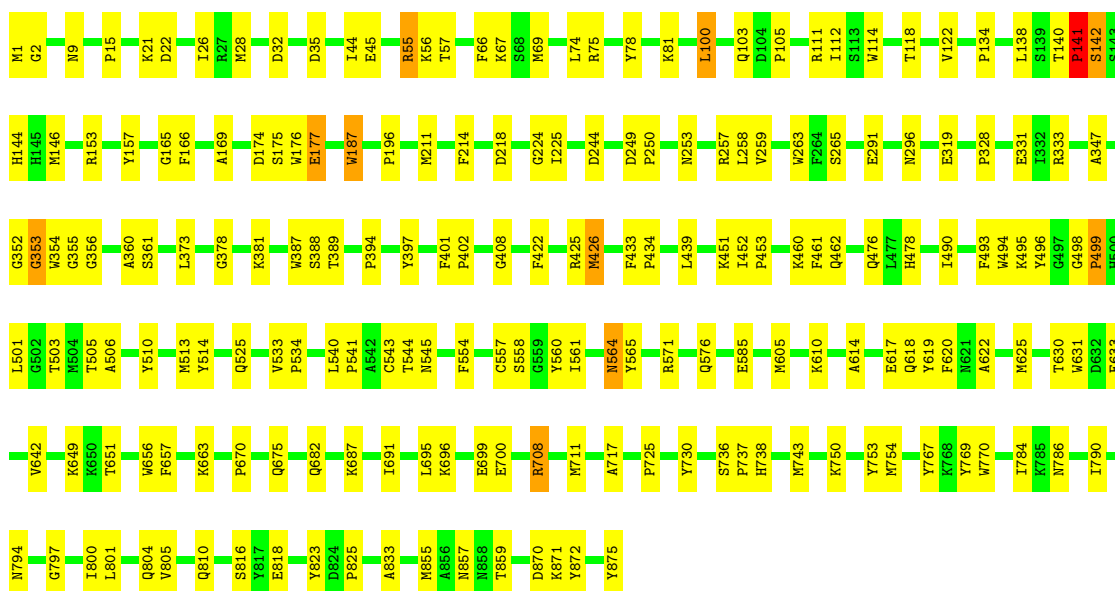
• Molecule 1: Pyrogallol hydroxytransferase large subunit

Chain O:



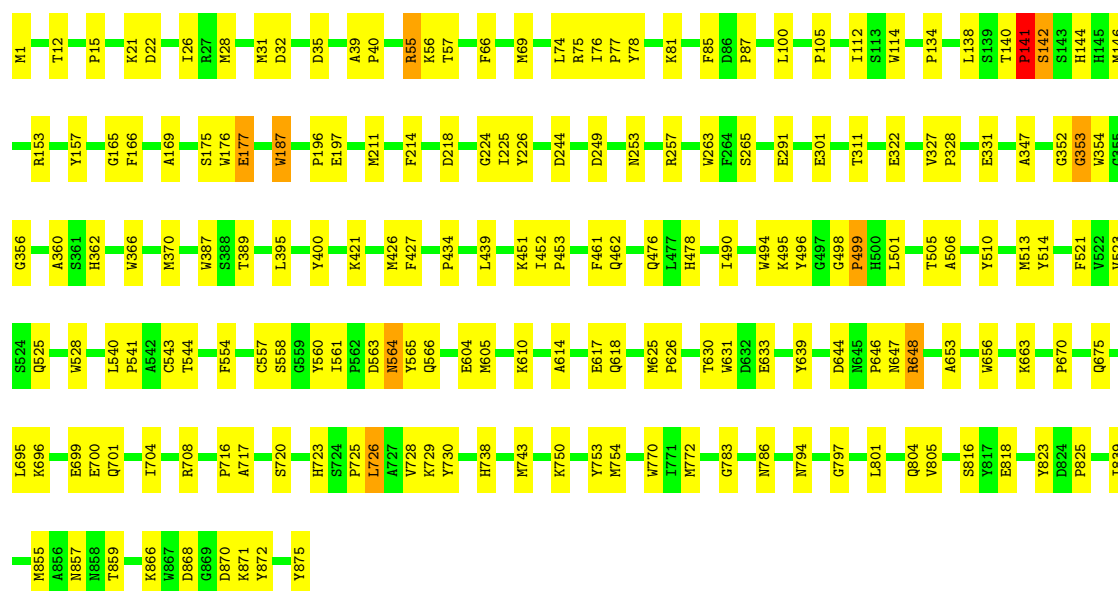
• Molecule 1: Pyrogallol hydroxytransferase large subunit

Chain Q:



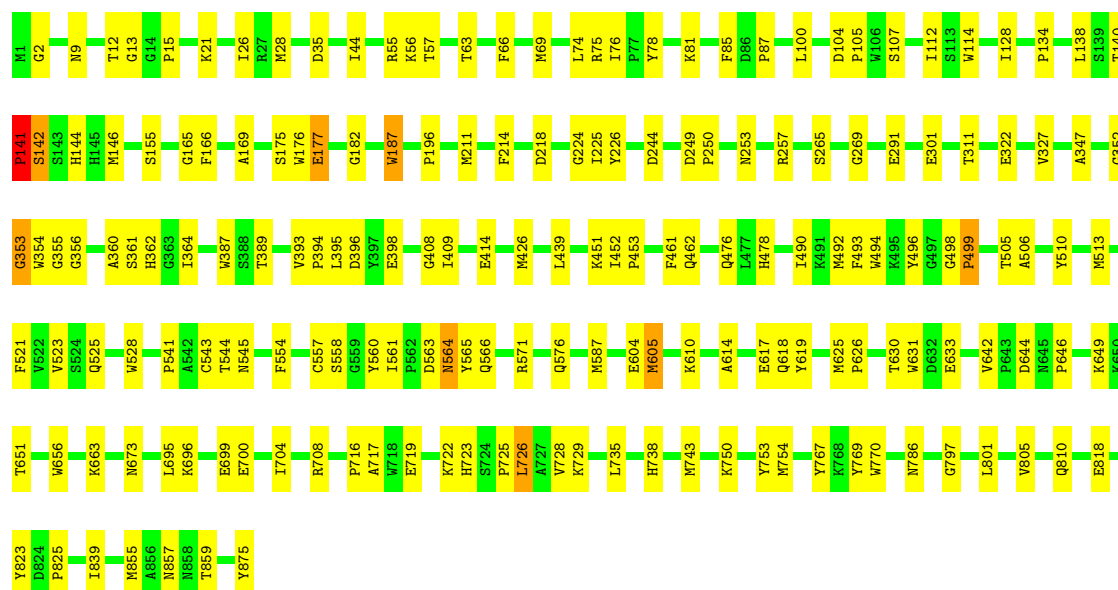
• Molecule 1: Pyrogallol hydroxytransferase large subunit

Chain S:



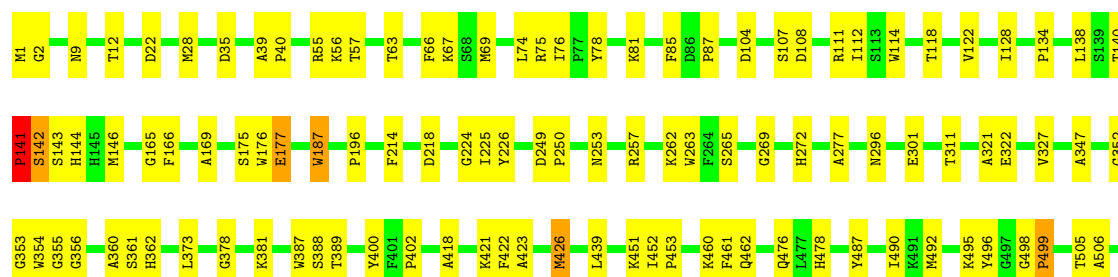
• Molecule 1: Pyrogallol hydroxytransferase large subunit

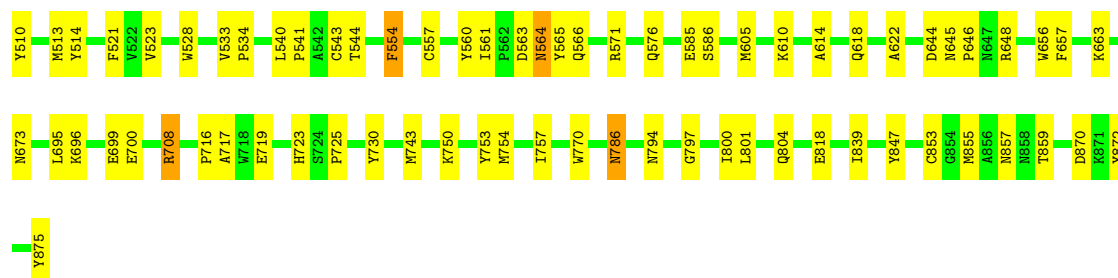
Chain U:



• Molecule 1: Pyrogallol hydroxytransferase large subunit

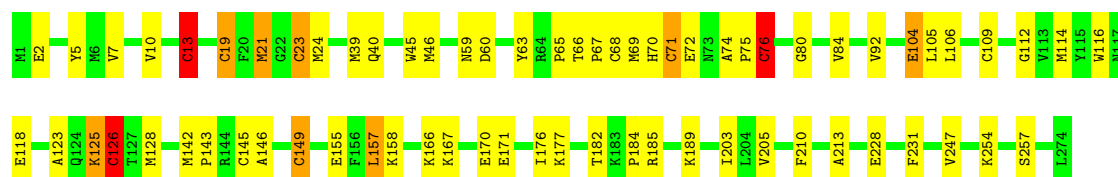
Chain W:





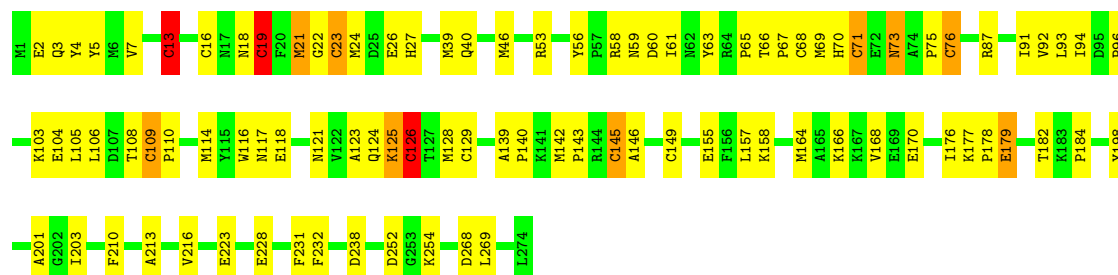
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain B:



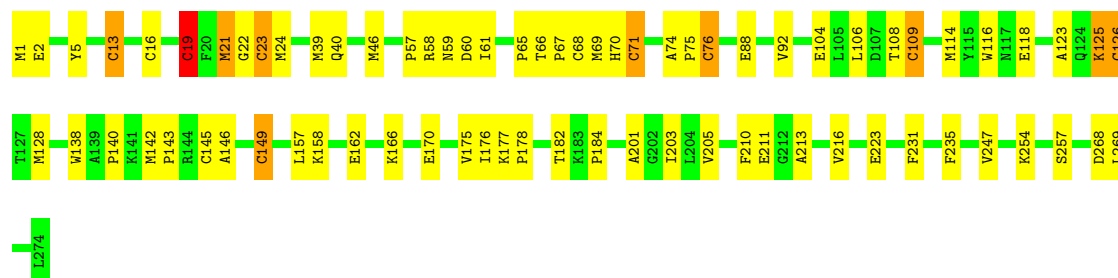
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain D:



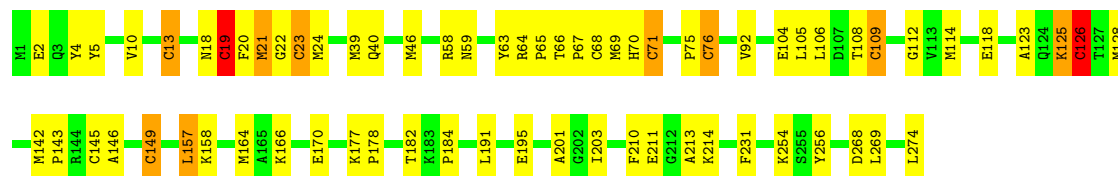
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain F:



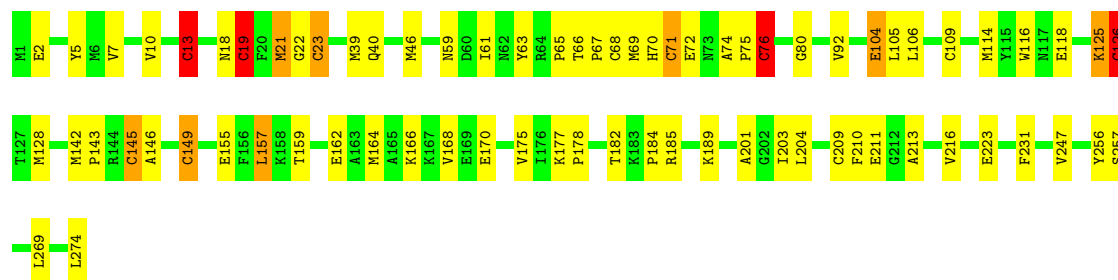
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain H:



- Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain J:



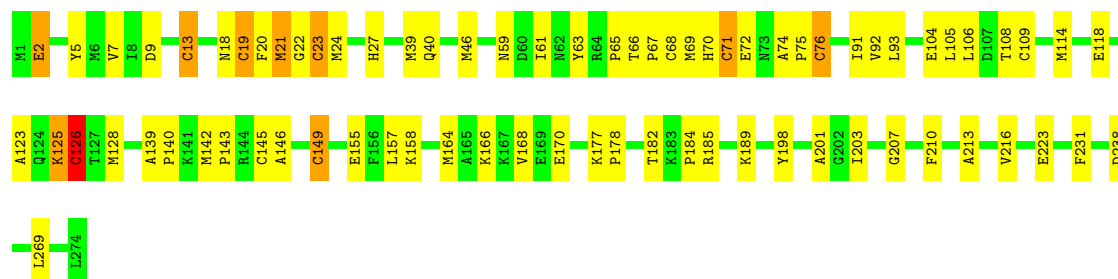
- Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain L:



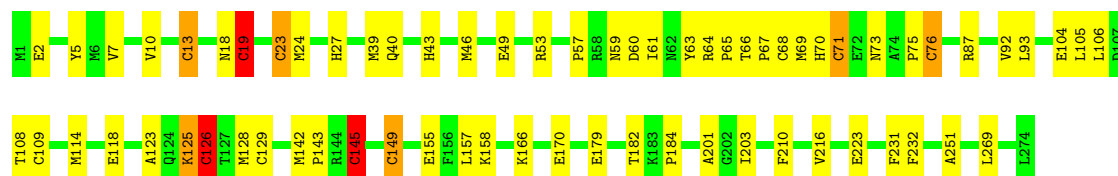
- Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain N:



- Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain P:



- Molecule 2: Pyrogallol hydroxytransferase small subunit

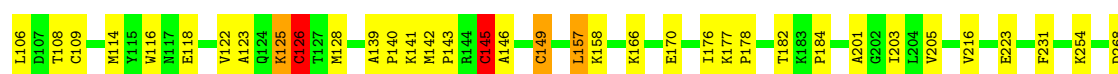
Chain R:





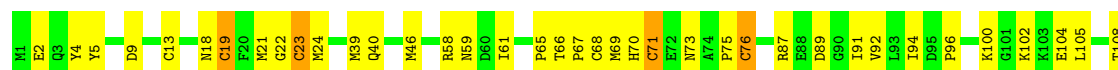
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain T:



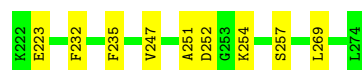
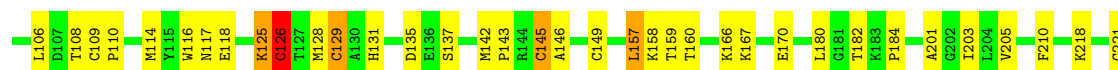
• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain V:



• Molecule 2: Pyrogallol hydroxytransferase small subunit

Chain X:



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	Depositor
Cell constants a, b, c, α , β , γ	172.57Å 178.44Å 179.66Å 63.83° 64.40° 65.04°	Depositor
Resolution (Å)	24.99 – 2.00	Depositor
% Data completeness (in resolution range)	96.5 (24.99-2.00)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.172 , 0.203	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	121823	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: BTT, SF4, 4MO, CA, MGD

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	0.33	0/7219	0.63	3/9786 (0.0%)
1	C	0.32	0/7219	0.61	3/9786 (0.0%)
1	E	0.33	0/7219	0.63	2/9786 (0.0%)
1	G	0.33	0/7219	0.63	3/9786 (0.0%)
1	I	0.32	0/7219	0.62	3/9786 (0.0%)
1	K	0.33	0/7219	0.63	4/9786 (0.0%)
1	M	0.33	0/7219	0.63	3/9786 (0.0%)
1	O	0.33	0/7219	0.62	3/9786 (0.0%)
1	Q	0.33	0/7219	0.63	4/9786 (0.0%)
1	S	0.32	0/7219	0.62	4/9786 (0.0%)
1	U	0.32	0/7219	0.62	4/9786 (0.0%)
1	W	0.32	0/7219	0.61	3/9786 (0.0%)
2	B	0.55	5/2231 (0.2%)	0.73	6/3009 (0.2%)
2	D	0.44	4/2231 (0.2%)	0.64	2/3009 (0.1%)
2	F	0.54	5/2231 (0.2%)	0.72	5/3009 (0.2%)
2	H	0.54	4/2231 (0.2%)	0.72	5/3009 (0.2%)
2	J	0.52	4/2231 (0.2%)	0.70	5/3009 (0.2%)
2	L	0.52	4/2231 (0.2%)	0.71	4/3009 (0.1%)
2	N	0.51	4/2231 (0.2%)	0.70	4/3009 (0.1%)
2	P	0.51	4/2231 (0.2%)	0.68	4/3009 (0.1%)
2	R	0.55	4/2231 (0.2%)	0.71	5/3009 (0.2%)
2	T	0.48	4/2231 (0.2%)	0.67	5/3009 (0.2%)
2	V	0.45	3/2231 (0.1%)	0.65	2/3009 (0.1%)
2	X	0.43	3/2231 (0.1%)	0.61	2/3009 (0.1%)
All	All	0.38	48/113400 (0.0%)	0.64	88/153540 (0.1%)

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	19	CYS	CB-SG	-9.78	1.65	1.82
2	P	23	CYS	CB-SG	-9.55	1.66	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	19	CYS	CB-SG	-9.47	1.66	1.82
2	J	23	CYS	CB-SG	-9.47	1.66	1.82
2	H	23	CYS	CB-SG	-9.46	1.66	1.82
2	F	23	CYS	CB-SG	-9.18	1.66	1.82
2	R	19	CYS	CB-SG	-9.11	1.66	1.82
2	L	145	CYS	CB-SG	-9.10	1.66	1.82
2	R	23	CYS	CB-SG	-9.02	1.67	1.82
2	B	145	CYS	CB-SG	-8.98	1.67	1.82
2	R	145	CYS	CB-SG	-8.94	1.67	1.82
2	B	19	CYS	CB-SG	-8.89	1.67	1.82
2	B	23	CYS	CB-SG	-8.84	1.67	1.82
2	L	23	CYS	CB-SG	-8.64	1.67	1.82
2	F	145	CYS	CB-SG	-8.57	1.67	1.82
2	T	23	CYS	CB-SG	-8.44	1.67	1.82
2	N	23	CYS	CB-SG	-8.43	1.68	1.82
2	L	19	CYS	CB-SG	-8.13	1.68	1.82
2	J	19	CYS	CB-SG	-8.07	1.68	1.82
2	V	19	CYS	CB-SG	-7.83	1.69	1.82
2	H	145	CYS	CB-SG	-7.81	1.69	1.82
2	N	145	CYS	CB-SG	-7.79	1.69	1.82
2	T	19	CYS	CB-SG	-7.78	1.69	1.82
2	N	19	CYS	CB-SG	-7.77	1.69	1.82
2	B	126	CYS	CB-SG	-7.76	1.69	1.82
2	P	126	CYS	CB-SG	-7.71	1.69	1.82
2	V	23	CYS	CB-SG	-7.71	1.69	1.82
2	N	126	CYS	CB-SG	-7.68	1.69	1.82
2	X	19	CYS	CB-SG	-7.66	1.69	1.82
2	J	76	CYS	CB-SG	-7.48	1.69	1.82
2	F	126	CYS	CB-SG	-7.37	1.69	1.82
2	P	19	CYS	CB-SG	-7.36	1.69	1.82
2	R	126	CYS	CB-SG	-7.36	1.69	1.82
2	B	76	CYS	CB-SG	-7.30	1.69	1.82
2	H	126	CYS	CB-SG	-7.16	1.70	1.82
2	D	19	CYS	CB-SG	-7.00	1.70	1.82
2	T	145	CYS	CB-SG	-6.97	1.70	1.82
2	D	23	CYS	CB-SG	-6.93	1.70	1.82
2	J	126	CYS	CB-SG	-6.90	1.70	1.82
2	D	126	CYS	CB-SG	-6.77	1.70	1.82
2	T	126	CYS	CB-SG	-6.71	1.70	1.82
2	V	126	CYS	CB-SG	-6.60	1.71	1.82
2	X	23	CYS	CB-SG	-6.29	1.71	1.82
2	L	126	CYS	CB-SG	-6.26	1.71	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	126	CYS	CB-SG	-5.92	1.72	1.81
2	F	109	CYS	CB-SG	-5.91	1.72	1.81
2	D	16	CYS	CB-SG	-5.08	1.73	1.81
2	P	145	CYS	CB-SG	-5.05	1.73	1.81

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	352	GLY	N-CA-C	-9.07	90.42	113.10
1	I	352	GLY	N-CA-C	-8.62	91.55	113.10
1	Q	352	GLY	N-CA-C	-8.60	91.61	113.10
1	A	352	GLY	N-CA-C	-8.54	91.74	113.10
1	E	352	GLY	N-CA-C	-8.48	91.90	113.10
1	W	352	GLY	N-CA-C	-8.46	91.96	113.10
1	K	352	GLY	N-CA-C	-8.41	92.06	113.10
1	C	352	GLY	N-CA-C	-8.36	92.19	113.10
1	G	352	GLY	N-CA-C	-8.33	92.28	113.10
1	S	352	GLY	N-CA-C	-8.31	92.32	113.10
1	O	352	GLY	N-CA-C	-8.19	92.63	113.10
1	U	352	GLY	N-CA-C	-7.96	93.19	113.10
2	F	19	CYS	CB-CA-C	-7.25	95.89	110.40
2	H	19	CYS	CB-CA-C	-7.24	95.93	110.40
2	B	23	CYS	CB-CA-C	-7.22	95.95	110.40
2	L	19	CYS	CB-CA-C	-7.07	96.27	110.40
2	R	19	CYS	CB-CA-C	-7.03	96.33	110.40
2	B	19	CYS	CB-CA-C	-6.97	96.45	110.40
2	T	19	CYS	CB-CA-C	-6.74	96.93	110.40
2	N	19	CYS	CB-CA-C	-6.73	96.94	110.40
2	J	19	CYS	CB-CA-C	-6.72	96.96	110.40
2	N	23	CYS	CB-CA-C	-6.70	97.00	110.40
2	J	23	CYS	CB-CA-C	-6.69	97.01	110.40
1	I	224	GLY	N-CA-C	-6.66	96.46	113.10
1	Q	224	GLY	N-CA-C	-6.64	96.50	113.10
2	P	23	CYS	CB-CA-C	-6.61	97.18	110.40
2	P	19	CYS	CB-CA-C	-6.59	97.22	110.40
2	N	145	CYS	CB-CA-C	-6.54	97.31	110.40
2	R	23	CYS	CB-CA-C	-6.49	97.41	110.40
1	A	224	GLY	N-CA-C	-6.47	96.92	113.10
2	H	145	CYS	CB-CA-C	-6.47	97.47	110.40
2	L	23	CYS	CB-CA-C	-6.46	97.47	110.40
1	O	224	GLY	N-CA-C	-6.46	96.95	113.10
2	F	145	CYS	CB-CA-C	-6.43	97.54	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	145	CYS	CB-CA-C	-6.41	97.59	110.40
2	R	145	CYS	CB-CA-C	-6.38	97.64	110.40
2	F	23	CYS	CB-CA-C	-6.37	97.66	110.40
2	L	145	CYS	CB-CA-C	-6.35	97.70	110.40
1	G	224	GLY	N-CA-C	-6.25	97.46	113.10
2	X	19	CYS	CB-CA-C	-6.25	97.91	110.40
1	E	224	GLY	N-CA-C	-6.21	97.58	113.10
2	V	19	CYS	CB-CA-C	-6.21	97.98	110.40
1	K	224	GLY	N-CA-C	-6.20	97.60	113.10
2	F	149	CYS	CB-CA-C	-6.18	98.04	110.40
1	W	224	GLY	N-CA-C	-6.12	97.81	113.10
2	B	149	CYS	CB-CA-C	-6.11	98.19	110.40
1	U	224	GLY	N-CA-C	-6.10	97.86	113.10
2	L	149	CYS	CB-CA-C	-6.09	98.22	110.40
2	H	23	CYS	CB-CA-C	-6.07	98.26	110.40
1	G	141	PRO	N-CA-C	-5.95	96.63	112.10
1	M	224	GLY	N-CA-C	-5.93	98.28	113.10
1	S	224	GLY	N-CA-C	-5.88	98.41	113.10
2	R	149	CYS	CB-CA-C	-5.72	98.96	110.40
2	D	19	CYS	CB-CA-C	-5.71	98.97	110.40
1	A	141	PRO	N-CA-C	-5.70	97.28	112.10
2	D	13	CYS	CA-CB-SG	-5.70	103.74	114.00
2	H	149	CYS	CB-CA-C	-5.67	99.05	110.40
2	N	149	CYS	CB-CA-C	-5.67	99.07	110.40
1	C	224	GLY	N-CA-C	-5.66	98.96	113.10
1	Q	141	PRO	N-CA-C	-5.63	97.45	112.10
2	J	76	CYS	CB-CA-C	-5.58	99.25	110.40
2	P	13	CYS	CA-CB-SG	-5.57	103.97	114.00
2	T	145	CYS	CB-CA-C	-5.53	99.33	110.40
2	X	13	CYS	CA-CB-SG	-5.53	104.05	114.00
2	P	149	CYS	CB-CA-C	-5.53	99.35	110.40
2	T	23	CYS	CB-CA-C	-5.51	99.39	110.40
2	B	76	CYS	CB-CA-C	-5.48	99.44	110.40
2	T	13	CYS	CA-CB-SG	-5.48	104.13	114.00
1	K	141	PRO	N-CA-C	-5.48	97.86	112.10
1	S	141	PRO	N-CA-C	-5.41	98.03	112.10
1	I	141	PRO	N-CA-C	-5.39	98.09	112.10
1	K	507	THR	N-CA-C	5.37	125.50	111.00
2	H	13	CYS	CA-CB-SG	-5.36	104.36	114.00
2	R	13	CYS	CA-CB-SG	-5.33	104.40	114.00
2	J	149	CYS	CB-CA-C	-5.33	99.75	110.40
1	U	141	PRO	N-CA-C	-5.25	98.45	112.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	23	CYS	CB-CA-C	-5.23	99.94	110.40
1	W	141	PRO	N-CA-C	-5.21	98.55	112.10
1	U	353	GLY	N-CA-C	-5.20	100.09	113.10
2	B	13	CYS	CA-CB-SG	-5.17	104.69	114.00
1	O	141	PRO	N-CA-C	-5.17	98.67	112.10
1	M	141	PRO	N-CA-C	-5.15	98.72	112.10
1	S	353	GLY	N-CA-C	-5.12	100.30	113.10
1	C	141	PRO	N-CA-C	-5.09	98.85	112.10
1	Q	353	GLY	N-CA-C	-5.07	100.41	113.10
2	F	13	CYS	CA-CB-SG	-5.02	104.97	114.00
2	J	13	CYS	CA-CB-SG	-5.02	104.97	114.00
2	T	149	CYS	CB-CA-C	-5.01	100.38	110.40

There are no chirality outliers.

There are no planarity outliers.

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	6998	0	6632	150	0
1	C	6998	0	6632	157	0
1	E	6998	0	6632	140	0
1	G	6998	0	6632	141	0
1	I	6998	0	6632	141	0
1	K	6998	0	6632	149	0
1	M	6998	0	6632	152	0
1	O	6998	0	6632	140	1
1	Q	6998	0	6632	160	0
1	S	6998	0	6632	155	0
1	U	6998	0	6632	151	0
1	W	6998	0	6632	139	0
2	B	2182	0	2077	64	0
2	D	2182	0	2077	88	0
2	F	2182	0	2077	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	2182	0	2077	67	0
2	J	2182	0	2077	70	0
2	L	2182	0	2077	75	0
2	N	2182	0	2077	73	0
2	P	2182	0	2077	61	0
2	R	2182	0	2077	64	0
2	T	2182	0	2077	61	0
2	V	2182	0	2077	66	0
2	X	2182	0	2077	74	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
3	Q	1	0	0	0	0
3	R	1	0	0	0	0
3	S	1	0	0	0	0
3	T	1	0	0	0	0
3	U	1	0	0	0	0
3	V	1	0	0	0	0
3	W	1	0	0	0	0
3	X	1	0	0	0	0
4	A	94	0	44	11	0
4	C	94	0	44	15	0
4	E	94	0	44	13	0
4	G	94	0	44	15	0
4	I	94	0	44	10	0
4	K	94	0	44	14	0
4	M	94	0	44	16	0
4	O	94	0	44	17	0
4	Q	94	0	44	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	S	94	0	44	11	0
4	U	94	0	44	15	0
4	W	94	0	44	14	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
5	I	1	0	0	0	0
5	K	1	0	0	0	0
5	M	1	0	0	0	0
5	O	1	0	0	0	0
5	Q	1	0	0	0	0
5	S	1	0	0	0	0
5	U	1	0	0	0	0
5	W	1	0	0	0	0
6	A	10	0	2	1	0
6	C	10	0	2	1	0
6	E	10	0	2	1	0
6	G	10	0	2	1	0
6	I	10	0	2	1	0
6	K	10	0	2	1	0
6	M	10	0	2	1	0
6	O	10	0	2	1	0
6	Q	10	0	2	1	0
6	S	10	0	2	1	0
6	U	10	0	2	1	0
6	W	10	0	2	1	0
7	B	24	0	0	3	0
7	D	24	0	0	4	0
7	F	24	0	0	4	0
7	H	24	0	0	4	0
7	J	24	0	0	4	0
7	L	24	0	0	4	0
7	N	24	0	0	5	0
7	P	24	0	0	4	0
7	R	24	0	0	4	0
7	T	24	0	0	4	0
7	V	24	0	0	4	0
7	X	24	0	0	4	0
8	A	681	0	0	13	2
8	B	169	0	0	4	0
8	C	684	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	162	0	0	1	0
8	E	688	0	0	14	0
8	F	160	0	0	1	0
8	G	682	0	0	9	0
8	H	161	0	0	1	0
8	I	671	0	0	6	0
8	J	168	0	0	2	0
8	K	681	0	0	6	0
8	L	165	0	0	3	0
8	M	682	0	0	11	0
8	N	160	0	0	1	0
8	O	675	0	0	12	1
8	P	160	0	0	3	0
8	Q	693	0	0	13	0
8	R	158	0	0	2	0
8	S	665	0	0	13	0
8	T	162	0	0	1	0
8	U	670	0	0	9	0
8	V	154	0	0	0	0
8	W	675	0	0	8	0
8	X	165	0	0	2	0
All	All	121823	0	105060	2542	2

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 12.

All (2542) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:U:426:MET:HE1	1:U:618:GLN:HG2	1.31	1.10
1:I:356:GLY:N	4:I:903:MGD:O1B	1.86	1.09
1:C:356:GLY:N	4:C:903:MGD:O1B	1.86	1.09
1:C:557:CYS:H	1:C:564:ASN:HD21	1.08	1.00
2:D:19:CYS:HB3	2:D:145:CYS:HB3	1.44	1.00
1:S:356:GLY:N	4:S:903:MGD:O1B	1.94	0.99
1:I:557:CYS:H	1:I:564:ASN:HD21	1.11	0.99
1:K:557:CYS:H	1:K:564:ASN:HD21	1.05	0.98
2:F:46:MET:HE3	2:F:66:THR:H	1.27	0.98
2:R:68:CYS:HB2	2:R:126:CYS:HB3	1.46	0.98
1:A:426:MET:HA	1:A:426:MET:HE3	1.44	0.97
2:F:68:CYS:HB2	2:F:126:CYS:HB3	1.44	0.97
1:M:557:CYS:H	1:M:564:ASN:HD21	1.08	0.97
1:Q:557:CYS:H	1:Q:564:ASN:HD21	1.06	0.97

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:N:68:CYS:HB2	2:N:126:CYS:HB3	1.45	0.97
2:N:207:GLY:HA2	1:S:728:VAL:HG12	1.49	0.95
1:O:557:CYS:H	1:O:564:ASN:HD21	1.11	0.95
2:P:2:GLU:HG2	2:P:158:LYS:HG2	1.48	0.95
1:S:753:TYR:HB3	2:T:24:MET:HE3	1.47	0.95
1:W:426:MET:HA	1:W:426:MET:HE3	1.49	0.95
1:W:557:CYS:H	1:W:564:ASN:HD21	1.14	0.94
1:M:426:MET:HE3	1:M:426:MET:HA	1.49	0.93
1:O:426:MET:HE3	1:O:426:MET:HA	1.48	0.93
1:E:557:CYS:H	1:E:564:ASN:HD21	1.08	0.93
2:N:46:MET:HE3	2:N:66:THR:H	1.33	0.92
1:Q:319:GLU:HG2	1:U:726:LEU:HD13	1.48	0.92
1:U:557:CYS:H	1:U:564:ASN:HD21	1.10	0.92
2:P:68:CYS:HB2	2:P:126:CYS:HB3	1.52	0.92
1:M:319:GLU:HG2	1:S:726:LEU:HD13	1.52	0.92
1:S:426:MET:HE1	1:S:618:GLN:HG2	1.50	0.92
1:Q:426:MET:HE3	1:Q:426:MET:HA	1.50	0.92
2:H:68:CYS:HB2	2:H:126:CYS:HB3	1.50	0.91
2:T:68:CYS:HB2	2:T:126:CYS:HB3	1.52	0.91
1:I:426:MET:HA	1:I:426:MET:HE3	1.52	0.91
1:S:557:CYS:H	1:S:564:ASN:HD21	1.03	0.91
2:D:68:CYS:HB2	2:D:126:CYS:HB3	1.53	0.90
1:A:557:CYS:H	1:A:564:ASN:HD21	1.09	0.90
2:R:207:GLY:HA2	1:U:728:VAL:HG12	1.49	0.90
2:B:68:CYS:HB2	2:B:126:CYS:CB	2.02	0.90
2:F:70:HIS:HD2	2:F:92:VAL:H	1.19	0.89
1:G:426:MET:HA	1:G:426:MET:HE3	1.54	0.89
1:E:426:MET:HE1	1:E:618:GLN:HG2	1.52	0.89
2:T:68:CYS:HB2	2:T:126:CYS:CB	2.03	0.89
2:H:46:MET:HE3	2:H:66:THR:H	1.37	0.89
1:Q:355:GLY:HA2	4:Q:903:MGD:O2B	1.71	0.89
2:L:68:CYS:HB2	2:L:126:CYS:CB	2.02	0.88
2:N:70:HIS:HD2	2:N:92:VAL:H	1.18	0.88
1:M:66:PHE:CD1	1:M:69:MET:HE3	2.08	0.88
2:T:2:GLU:HG2	2:T:158:LYS:HG2	1.54	0.88
2:J:68:CYS:HB2	2:J:126:CYS:HB3	1.53	0.88
1:G:355:GLY:HA2	4:G:903:MGD:O2B	1.75	0.87
2:R:46:MET:HE3	2:R:66:THR:H	1.38	0.87
2:B:70:HIS:HD2	2:B:92:VAL:H	1.16	0.87
2:V:68:CYS:HB2	2:V:126:CYS:HB3	1.57	0.87
1:G:557:CYS:H	1:G:564:ASN:HD21	1.14	0.87
2:J:68:CYS:HB2	2:J:126:CYS:CB	2.05	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:68:CYS:HB2	2:B:126:CYS:HB3	1.53	0.87
2:R:70:HIS:HD2	2:R:92:VAL:H	1.22	0.87
1:U:66:PHE:CD1	1:U:69:MET:HE3	2.09	0.87
1:A:66:PHE:CD1	1:A:69:MET:HE3	2.09	0.87
2:L:70:HIS:HD2	2:L:92:VAL:H	1.16	0.86
2:P:68:CYS:HB2	2:P:126:CYS:CB	2.03	0.86
1:C:360:ALA:HB1	1:C:859:THR:HG23	1.54	0.86
2:H:68:CYS:HB2	2:H:126:CYS:CB	2.06	0.86
1:C:426:MET:HE3	1:C:426:MET:HA	1.57	0.86
1:G:146:MET:HE1	1:G:544:THR:HB	1.58	0.86
1:K:426:MET:HA	1:K:426:MET:HE3	1.56	0.86
2:N:68:CYS:HB2	2:N:126:CYS:CB	2.05	0.86
2:L:68:CYS:HB2	2:L:126:CYS:HB3	1.57	0.86
2:F:68:CYS:HB2	2:F:126:CYS:CB	2.05	0.85
1:W:66:PHE:CD1	1:W:69:MET:HE3	2.11	0.85
2:J:46:MET:HE3	2:J:66:THR:H	1.41	0.85
2:R:68:CYS:HB2	2:R:126:CYS:CB	2.05	0.85
1:G:141:PRO:HA	1:G:496:TYR:HB3	1.59	0.85
2:J:106:LEU:HD23	2:J:114:MET:HE3	1.59	0.85
2:J:70:HIS:HD2	2:J:92:VAL:H	1.22	0.85
1:S:360:ALA:HB1	1:S:859:THR:HG23	1.57	0.85
1:G:66:PHE:CD1	1:G:69:MET:HE3	2.11	0.85
2:V:68:CYS:HB2	2:V:126:CYS:CB	2.07	0.85
2:P:70:HIS:HD2	2:P:92:VAL:H	1.26	0.84
2:X:106:LEU:HD11	2:X:116:TRP:HB2	1.60	0.84
1:Q:66:PHE:CD1	1:Q:69:MET:HE3	2.13	0.84
1:S:426:MET:HE3	1:S:426:MET:HA	1.60	0.84
1:M:355:GLY:HA2	4:M:903:MGD:O1B	1.77	0.83
2:T:70:HIS:HD2	2:T:92:VAL:H	1.26	0.83
2:P:46:MET:HE3	2:P:66:THR:H	1.43	0.83
1:O:695:LEU:O	1:O:699:GLU:HG2	1.79	0.83
2:P:19:CYS:HB3	2:P:145:CYS:HB3	1.61	0.83
1:U:28:MET:HE1	1:U:66:PHE:HB3	1.60	0.83
1:C:610:LYS:NZ	1:C:618:GLN:HE22	1.77	0.83
2:R:40:GLN:HE22	2:R:118:GLU:H	1.24	0.83
1:A:360:ALA:HB1	1:A:859:THR:HG23	1.61	0.83
1:E:426:MET:HA	1:E:426:MET:HE3	1.61	0.83
1:E:141:PRO:HA	1:E:496:TYR:HB3	1.61	0.82
2:H:70:HIS:HD2	2:H:92:VAL:H	1.26	0.82
2:T:46:MET:HE3	2:T:66:THR:H	1.44	0.82
1:A:141:PRO:HA	1:A:496:TYR:HB3	1.61	0.82
1:K:695:LEU:O	1:K:699:GLU:HG2	1.80	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:610:LYS:NZ	1:Q:618:GLN:HE22	1.77	0.82
1:C:66:PHE:CD1	1:C:69:MET:HE3	2.14	0.82
1:E:66:PHE:CD1	1:E:69:MET:HE3	2.14	0.82
1:Q:66:PHE:HD1	1:Q:69:MET:HE3	1.45	0.82
2:L:40:GLN:HE22	2:L:118:GLU:H	1.24	0.82
2:N:40:GLN:HE22	2:N:118:GLU:H	1.23	0.82
1:E:426:MET:CE	1:E:618:GLN:HG2	2.09	0.81
1:Q:141:PRO:HA	1:Q:496:TYR:HB3	1.62	0.81
1:E:360:ALA:HB1	1:E:859:THR:HG23	1.63	0.81
1:U:426:MET:CE	1:U:618:GLN:HG2	2.11	0.81
1:U:360:ALA:HB1	1:U:859:THR:HG23	1.60	0.81
1:C:141:PRO:HA	1:C:496:TYR:HB3	1.62	0.81
1:I:66:PHE:CD1	1:I:69:MET:HE3	2.16	0.81
2:V:76:CYS:HB3	2:V:108:THR:OG1	1.80	0.81
1:I:426:MET:CE	1:I:618:GLN:HG2	2.10	0.81
2:B:46:MET:HE3	2:B:66:THR:H	1.46	0.81
1:S:426:MET:CE	1:S:618:GLN:HG2	2.10	0.80
1:O:66:PHE:CD1	1:O:69:MET:HE3	2.17	0.80
1:O:141:PRO:HA	1:O:496:TYR:HB3	1.64	0.80
1:U:356:GLY:N	4:U:903:MGD:O1B	2.13	0.80
2:F:40:GLN:HE22	2:F:118:GLU:H	1.27	0.79
1:W:141:PRO:HA	1:W:496:TYR:HB3	1.64	0.79
1:U:146:MET:HE1	1:U:544:THR:HB	1.62	0.79
1:Q:610:LYS:HZ2	1:Q:618:GLN:HE22	1.28	0.79
1:U:695:LEU:O	1:U:699:GLU:HG2	1.83	0.79
1:A:823:TYR:CZ	1:A:825:PRO:HG3	2.18	0.79
1:I:141:PRO:HA	1:I:496:TYR:HB3	1.64	0.79
2:X:46:MET:HE3	2:X:66:THR:H	1.47	0.79
1:E:216:SER:OG	4:E:903:MGD:H5'2	1.83	0.78
2:L:46:MET:HE3	2:L:66:THR:H	1.47	0.78
1:M:695:LEU:O	1:M:699:GLU:HG2	1.81	0.78
1:O:426:MET:CE	1:O:618:GLN:HG2	2.13	0.78
1:M:610:LYS:NZ	1:M:618:GLN:HE22	1.82	0.78
1:K:146:MET:CE	1:K:544:THR:HB	2.13	0.78
1:G:610:LYS:NZ	1:G:618:GLN:HE22	1.81	0.78
1:S:66:PHE:CD1	1:S:69:MET:HE3	2.18	0.78
1:E:610:LYS:NZ	1:E:618:GLN:HE22	1.82	0.78
1:K:360:ALA:HB1	1:K:859:THR:HG23	1.66	0.78
1:C:28:MET:HE1	1:C:66:PHE:HB3	1.65	0.78
1:K:426:MET:CE	1:K:618:GLN:HG2	2.13	0.78
1:O:823:TYR:CZ	1:O:825:PRO:HG3	2.18	0.78
2:D:70:HIS:HD2	2:D:92:VAL:H	1.30	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:786:ASN:HD22	1:E:805:VAL:H	1.30	0.77
1:K:66:PHE:CD1	1:K:69:MET:HE3	2.19	0.77
1:C:695:LEU:O	1:C:699:GLU:HG2	1.81	0.77
1:I:360:ALA:HB1	1:I:859:THR:HG23	1.65	0.77
1:U:146:MET:CE	1:U:544:THR:HB	2.15	0.77
1:A:753:TYR:HB3	2:B:24:MET:HE3	1.66	0.77
1:K:165:GLY:HA3	1:K:166:PHE:HB3	1.67	0.76
2:D:76:CYS:HB3	2:D:108:THR:OG1	1.85	0.76
1:G:823:TYR:CZ	1:G:825:PRO:HG3	2.20	0.76
1:K:141:PRO:HA	1:K:496:TYR:HB3	1.67	0.76
1:Q:426:MET:CE	1:Q:618:GLN:HG2	2.14	0.76
2:F:46:MET:HE3	2:F:66:THR:N	2.00	0.76
2:H:46:MET:HE3	2:H:66:THR:N	2.00	0.76
1:I:165:GLY:HA3	1:I:166:PHE:HB3	1.67	0.76
2:P:128:MET:HA	7:P:303:SF4:S1	2.26	0.76
2:B:40:GLN:HE22	2:B:118:GLU:H	1.34	0.76
1:A:426:MET:CE	1:A:618:GLN:HG2	2.16	0.75
2:B:46:MET:HE1	2:B:65:PRO:HA	1.68	0.75
1:M:426:MET:CE	1:M:618:GLN:HG2	2.15	0.75
2:D:68:CYS:HB2	2:D:126:CYS:CB	2.16	0.75
2:F:40:GLN:NE2	2:F:118:GLU:H	1.83	0.75
1:O:360:ALA:HB1	1:O:859:THR:HG23	1.68	0.75
1:S:610:LYS:NZ	1:S:618:GLN:HE22	1.83	0.75
1:U:141:PRO:HA	1:U:496:TYR:HB3	1.66	0.75
1:C:426:MET:CE	1:C:618:GLN:HG2	2.16	0.75
1:G:426:MET:CE	1:G:618:GLN:HG2	2.17	0.75
1:A:146:MET:CE	1:A:544:THR:HB	2.17	0.75
1:A:695:LEU:O	1:A:699:GLU:HG2	1.86	0.75
1:I:426:MET:HE1	1:I:618:GLN:HG2	1.69	0.75
1:K:823:TYR:CZ	1:K:825:PRO:HG3	2.20	0.75
1:M:426:MET:HE1	1:M:618:GLN:HG2	1.69	0.75
2:V:19:CYS:HB3	2:V:145:CYS:HB3	1.68	0.74
1:A:786:ASN:HD22	1:A:805:VAL:H	1.34	0.74
2:D:2:GLU:HG2	2:D:158:LYS:HG2	1.67	0.74
2:H:142:MET:HE2	2:H:146:ALA:HB1	1.68	0.74
1:M:66:PHE:HD1	1:M:69:MET:HE3	1.52	0.74
1:G:146:MET:CE	1:G:544:THR:HB	2.17	0.74
2:R:68:CYS:HB3	2:R:70:HIS:CE1	2.23	0.74
1:Q:360:ALA:HB1	1:Q:859:THR:HG23	1.69	0.74
2:X:68:CYS:HB2	2:X:126:CYS:HB3	1.69	0.74
2:N:40:GLN:NE2	2:N:118:GLU:H	1.84	0.74
1:Q:146:MET:HE1	1:Q:544:THR:HB	1.70	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:128:MET:HA	7:D:303:SF4:S1	2.26	0.74
1:W:360:ALA:HB1	1:W:859:THR:HG23	1.70	0.74
1:U:610:LYS:NZ	1:U:618:GLN:HE22	1.86	0.74
2:V:128:MET:HA	7:V:303:SF4:S1	2.27	0.74
1:G:695:LEU:O	1:G:699:GLU:HG2	1.86	0.73
2:N:68:CYS:HB3	2:N:70:HIS:CE1	2.22	0.73
2:D:75:PRO:HD2	7:D:304:SF4:S4	2.27	0.73
2:T:128:MET:HA	7:T:303:SF4:S1	2.28	0.73
1:W:610:LYS:NZ	1:W:618:GLN:HE22	1.86	0.73
1:K:146:MET:HE1	1:K:544:THR:HB	1.69	0.73
1:W:426:MET:CE	1:W:618:GLN:HG2	2.18	0.73
1:K:66:PHE:HD1	1:K:69:MET:HE3	1.50	0.73
1:S:557:CYS:N	1:S:564:ASN:HD21	1.85	0.73
1:S:823:TYR:CZ	1:S:825:PRO:HG3	2.23	0.73
2:T:76:CYS:HB3	2:T:108:THR:OG1	1.89	0.73
2:X:68:CYS:HB2	2:X:126:CYS:CB	2.17	0.73
1:A:66:PHE:HD1	1:A:69:MET:HE3	1.52	0.73
1:I:695:LEU:O	1:I:699:GLU:HG2	1.89	0.73
1:G:100:LEU:HD12	1:G:105:PRO:HG3	1.71	0.73
1:M:141:PRO:HA	1:M:496:TYR:HB3	1.68	0.73
2:N:46:MET:HE3	2:N:66:THR:N	2.04	0.72
1:A:610:LYS:NZ	1:A:618:GLN:HE22	1.86	0.72
2:R:40:GLN:NE2	2:R:118:GLU:H	1.86	0.72
1:C:146:MET:HE1	1:C:544:THR:HB	1.71	0.72
1:E:66:PHE:HD1	1:E:69:MET:HE3	1.54	0.72
1:G:165:GLY:HA3	1:G:166:PHE:HB3	1.71	0.72
1:A:146:MET:HE1	1:A:544:THR:HB	1.70	0.72
1:A:28:MET:HE1	1:A:66:PHE:HB3	1.72	0.72
2:X:68:CYS:CB	2:X:126:CYS:HB3	2.19	0.72
2:B:40:GLN:NE2	2:B:118:GLU:H	1.86	0.72
2:D:69:MET:HB3	2:D:184:PRO:HB3	1.70	0.72
1:E:146:MET:HE1	1:E:544:THR:HB	1.72	0.72
1:S:141:PRO:HA	1:S:496:TYR:HB3	1.70	0.72
2:T:68:CYS:HB3	2:T:70:HIS:CE1	2.25	0.72
2:R:46:MET:HE3	2:R:66:THR:N	2.05	0.72
2:N:142:MET:CE	2:N:146:ALA:HB1	2.19	0.71
1:C:823:TYR:CZ	1:C:825:PRO:HG3	2.24	0.71
2:L:106:LEU:HD11	2:L:116:TRP:HB2	1.72	0.71
1:Q:165:GLY:HA3	1:Q:166:PHE:HB3	1.72	0.71
1:I:610:LYS:NZ	1:I:618:GLN:HE22	1.88	0.71
2:X:128:MET:HA	7:X:303:SF4:S1	2.29	0.71
1:W:695:LEU:O	1:W:699:GLU:HG2	1.88	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:142:MET:CE	2:H:146:ALA:HB1	2.20	0.71
1:S:695:LEU:O	1:S:699:GLU:HG2	1.90	0.71
2:V:70:HIS:HD2	2:V:92:VAL:H	1.38	0.71
1:O:610:LYS:NZ	1:O:618:GLN:HE22	1.89	0.71
2:J:128:MET:HA	7:J:303:SF4:S1	2.30	0.71
2:N:142:MET:HE2	2:N:146:ALA:HB1	1.73	0.71
1:E:394:PRO:HG3	8:E:1323:HOH:O	1.91	0.71
1:O:28:MET:HE1	1:O:66:PHE:HB3	1.73	0.71
1:O:786:ASN:ND2	1:O:805:VAL:H	1.88	0.71
1:U:355:GLY:HA2	4:U:903:MGD:O1B	1.91	0.71
2:L:46:MET:HE1	2:L:65:PRO:HA	1.70	0.71
2:T:68:CYS:CB	2:T:126:CYS:HB3	2.21	0.71
2:P:68:CYS:HB3	2:P:70:HIS:CE1	2.26	0.71
1:A:561:ILE:HG22	1:A:564:ASN:HB3	1.72	0.70
2:B:68:CYS:HB3	2:B:70:HIS:CE1	2.26	0.70
1:E:100:LEU:HD12	1:E:105:PRO:HG3	1.73	0.70
1:O:146:MET:HE1	1:O:544:THR:HB	1.73	0.70
2:J:68:CYS:HB3	2:J:70:HIS:CE1	2.26	0.70
2:L:166:LYS:O	2:L:170:GLU:HG3	1.92	0.70
1:M:823:TYR:CZ	1:M:825:PRO:HG3	2.26	0.70
2:V:68:CYS:CB	2:V:126:CYS:HB3	2.20	0.70
1:W:610:LYS:HZ2	1:W:618:GLN:HE22	1.39	0.70
1:W:645:ASN:ND2	1:W:648:ARG:HB3	2.06	0.70
2:L:5:TYR:HB2	2:L:157:LEU:CD1	2.20	0.70
1:O:146:MET:CE	1:O:544:THR:HB	2.22	0.70
1:E:146:MET:CE	1:E:544:THR:HB	2.21	0.70
2:J:40:GLN:NE2	2:J:118:GLU:H	1.90	0.70
1:C:394:PRO:HG3	8:C:1323:HOH:O	1.91	0.70
1:G:426:MET:HE2	1:G:618:GLN:HG2	1.74	0.70
1:Q:146:MET:CE	1:Q:544:THR:HB	2.21	0.70
2:L:68:CYS:HB2	2:L:126:CYS:HB2	1.71	0.70
1:G:360:ALA:HB1	1:G:859:THR:HG23	1.74	0.70
2:J:71:CYS:HB2	2:J:182:THR:O	1.92	0.70
2:N:2:GLU:HG2	2:N:158:LYS:HG2	1.73	0.70
2:P:46:MET:HE1	2:P:65:PRO:HA	1.74	0.70
1:Q:823:TYR:CZ	1:Q:825:PRO:HG3	2.27	0.70
1:U:823:TYR:CZ	1:U:825:PRO:HG3	2.26	0.70
2:F:76:CYS:HB3	2:F:108:THR:OG1	1.92	0.70
2:L:104:GLU:H	2:L:104:GLU:CD	1.95	0.70
1:O:66:PHE:HD1	1:O:69:MET:HE3	1.56	0.70
1:A:165:GLY:HA3	1:A:166:PHE:HB3	1.71	0.70
2:H:142:MET:HE2	2:H:146:ALA:CB	2.21	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:823:TYR:CZ	1:I:825:PRO:HG3	2.27	0.70
1:O:394:PRO:HG3	8:O:1319:HOH:O	1.91	0.69
1:C:146:MET:CE	1:C:544:THR:HB	2.23	0.69
1:G:66:PHE:HD1	1:G:69:MET:HE3	1.57	0.69
1:K:249:ASP:OD1	4:K:903:MGD:H1'	1.92	0.69
1:M:360:ALA:HB1	1:M:859:THR:HG23	1.73	0.69
2:J:46:MET:HE3	2:J:66:THR:N	2.07	0.69
2:L:128:MET:HA	7:L:303:SF4:S1	2.32	0.69
1:G:146:MET:HE2	1:G:545:ASN:H	1.57	0.69
2:H:71:CYS:HB2	2:H:182:THR:O	1.92	0.69
2:H:40:GLN:HE22	2:H:118:GLU:H	1.40	0.69
2:J:68:CYS:CB	2:J:126:CYS:HB3	2.21	0.69
1:C:165:GLY:HA3	1:C:166:PHE:HB3	1.75	0.69
1:I:146:MET:CE	1:I:544:THR:HB	2.23	0.69
1:O:249:ASP:OD1	4:O:903:MGD:H1'	1.91	0.69
1:U:66:PHE:HD1	1:U:69:MET:HE3	1.57	0.69
1:S:561:ILE:HG22	1:S:564:ASN:HB3	1.73	0.69
1:W:644:ASP:OD1	1:W:646:PRO:HG3	1.93	0.69
2:B:68:CYS:HB2	2:B:126:CYS:HB2	1.75	0.69
2:B:71:CYS:HB2	2:B:182:THR:O	1.92	0.69
2:D:40:GLN:HE22	2:D:118:GLU:H	1.41	0.69
1:K:426:MET:HE1	1:K:618:GLN:HG2	1.74	0.69
2:R:46:MET:HE1	2:R:65:PRO:HA	1.73	0.69
1:W:165:GLY:HA3	1:W:166:PHE:HB3	1.73	0.69
2:J:104:GLU:CD	2:J:104:GLU:H	1.97	0.68
1:G:753:TYR:HB3	2:H:24:MET:HE3	1.74	0.68
2:D:68:CYS:CB	2:D:126:CYS:HB3	2.24	0.68
2:H:68:CYS:HB3	2:H:70:HIS:CE1	2.28	0.68
1:W:356:GLY:N	4:W:903:MGD:O2B	2.26	0.68
2:H:114:MET:HE2	2:H:123:ALA:HB1	1.74	0.68
2:J:5:TYR:HB2	2:J:157:LEU:CD1	2.23	0.68
2:F:68:CYS:HB3	2:F:70:HIS:CE1	2.27	0.68
1:M:28:MET:HE1	1:M:66:PHE:HB3	1.75	0.68
2:P:76:CYS:HB3	2:P:108:THR:OG1	1.93	0.68
2:X:71:CYS:HA	2:X:184:PRO:HA	1.75	0.68
2:X:76:CYS:HB3	2:X:108:THR:OG1	1.94	0.68
1:E:753:TYR:HB3	2:F:24:MET:HE3	1.76	0.68
2:V:142:MET:HE2	2:V:146:ALA:CB	2.23	0.68
1:W:561:ILE:HG22	1:W:564:ASN:HB3	1.75	0.68
1:Q:753:TYR:HB3	2:R:24:MET:HE3	1.76	0.67
1:E:695:LEU:O	1:E:699:GLU:HG2	1.94	0.67
1:M:610:LYS:HZ3	1:M:618:GLN:HE22	1.40	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:68:CYS:CB	2:H:126:CYS:HB3	2.23	0.67
1:K:74:LEU:HD12	1:K:750:LYS:HA	1.76	0.67
2:P:68:CYS:CB	2:P:126:CYS:HB3	2.22	0.67
2:R:68:CYS:CB	2:R:126:CYS:HB3	2.22	0.67
2:P:46:MET:HE3	2:P:66:THR:N	2.10	0.67
2:R:5:TYR:HB2	2:R:157:LEU:HD13	1.77	0.67
1:C:355:GLY:HA2	4:C:903:MGD:O1B	1.95	0.67
1:E:823:TYR:CZ	1:E:825:PRO:HG3	2.30	0.67
2:J:46:MET:HE1	2:J:65:PRO:HA	1.75	0.67
1:O:165:GLY:HA3	1:O:166:PHE:HB3	1.75	0.67
1:Q:695:LEU:O	1:Q:699:GLU:HG2	1.95	0.67
2:T:46:MET:HE3	2:T:66:THR:N	2.08	0.67
1:O:211:MET:HE1	2:P:231:PHE:HZ	1.60	0.67
1:E:165:GLY:HA3	1:E:166:PHE:HB3	1.75	0.67
2:L:68:CYS:HB3	2:L:70:HIS:CE1	2.30	0.67
1:E:610:LYS:HZ3	1:E:618:GLN:HE22	1.42	0.66
1:Q:28:MET:HE1	1:Q:66:PHE:HB3	1.77	0.66
2:B:46:MET:HE1	2:B:65:PRO:CA	2.25	0.66
1:U:753:TYR:HB3	2:V:24:MET:HE3	1.75	0.66
1:G:355:GLY:CA	4:G:903:MGD:O2B	2.43	0.66
2:L:69:MET:HB3	2:L:184:PRO:HB3	1.78	0.66
1:O:753:TYR:HB3	2:P:24:MET:HE3	1.77	0.66
2:B:68:CYS:CB	2:B:126:CYS:HB3	2.24	0.66
1:C:426:MET:HE1	1:C:618:GLN:HG2	1.78	0.66
1:G:211:MET:HE2	1:G:244:ASP:HB2	1.75	0.66
1:O:426:MET:HE1	1:O:618:GLN:HG2	1.75	0.66
1:A:216:SER:OG	4:A:903:MGD:H5'2	1.96	0.66
1:C:561:ILE:HG22	1:C:564:ASN:HB3	1.76	0.66
2:F:5:TYR:HB2	2:F:157:LEU:HD11	1.77	0.66
2:J:40:GLN:HE22	2:J:118:GLU:H	1.42	0.66
1:S:146:MET:CE	1:S:544:THR:HB	2.25	0.66
2:B:46:MET:CE	2:B:66:THR:H	2.09	0.66
2:B:75:PRO:HD2	7:B:304:SF4:S4	2.36	0.66
2:F:128:MET:HA	7:F:303:SF4:S1	2.36	0.66
1:G:32:ASP:OD2	8:G:1659:HOH:O	2.13	0.66
2:H:46:MET:HE1	2:H:65:PRO:HA	1.78	0.66
1:W:74:LEU:HD12	1:W:750:LYS:HA	1.76	0.66
1:E:630:THR:OG1	1:E:633:GLU:HG3	1.94	0.66
1:W:142:SER:HB3	4:W:902:MGD:H5'2	1.76	0.66
1:S:138:LEU:HB2	1:S:490:ILE:HD12	1.78	0.66
1:A:142:SER:OG	4:A:902:MGD:O1A	2.13	0.65
2:D:68:CYS:HB3	2:D:70:HIS:CE1	2.30	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:356:GLY:N	4:G:903:MGD:O2B	2.28	0.65
1:K:610:LYS:NZ	1:K:618:GLN:HE22	1.95	0.65
1:M:165:GLY:HA3	1:M:166:PHE:HB3	1.77	0.65
2:T:46:MET:HE1	2:T:65:PRO:HA	1.78	0.65
1:M:74:LEU:HD12	1:M:750:LYS:HA	1.79	0.65
1:Q:134:PRO:HB2	1:Q:439:LEU:HD11	1.76	0.65
2:H:2:GLU:HG2	2:H:158:LYS:HG2	1.78	0.65
1:I:211:MET:HE1	2:J:231:PHE:HZ	1.59	0.65
1:K:630:THR:OG1	1:K:633:GLU:HG3	1.97	0.65
2:R:142:MET:CE	2:R:146:ALA:HB1	2.27	0.65
1:S:75:ARG:HH21	1:S:543:CYS:HA	1.62	0.65
1:C:696:LYS:HD3	8:C:1680:HOH:O	1.96	0.65
2:D:114:MET:HA	2:D:125:LYS:HB3	1.78	0.65
1:G:394:PRO:HG3	8:G:1321:HOH:O	1.97	0.65
2:L:71:CYS:HB2	2:L:182:THR:O	1.97	0.65
2:T:75:PRO:HD2	7:T:304:SF4:S4	2.37	0.65
2:X:69:MET:HB3	2:X:184:PRO:HB3	1.78	0.65
2:L:46:MET:HE3	2:L:66:THR:N	2.11	0.65
1:A:394:PRO:HG3	8:A:1320:HOH:O	1.96	0.65
1:O:355:GLY:HA2	4:O:903:MGD:O2B	1.96	0.65
1:S:28:MET:HE1	1:S:66:PHE:HB3	1.78	0.65
2:B:128:MET:HA	7:B:303:SF4:S1	2.37	0.64
1:C:610:LYS:HZ2	1:C:618:GLN:HE22	1.43	0.64
4:Q:903:MGD:O1B	4:Q:903:MGD:H4'	1.96	0.64
1:I:478:HIS:HD2	8:I:1202:HOH:O	1.80	0.64
2:N:76:CYS:HB3	2:N:108:THR:OG1	1.97	0.64
2:N:114:MET:HE2	2:N:123:ALA:HB1	1.79	0.64
2:R:128:MET:HA	7:R:303:SF4:S1	2.38	0.64
2:X:59:ASN:H	2:X:59:ASN:HD22	1.46	0.64
2:P:125:LYS:HD2	2:P:126:CYS:O	1.96	0.64
1:Q:394:PRO:HG3	8:Q:1320:HOH:O	1.96	0.64
2:X:46:MET:HE3	2:X:66:THR:N	2.13	0.64
2:N:68:CYS:CB	2:N:126:CYS:HB3	2.24	0.64
2:P:40:GLN:HE22	2:P:118:GLU:H	1.45	0.64
1:U:165:GLY:HA3	1:U:166:PHE:HB3	1.78	0.64
1:I:394:PRO:HG3	8:I:1318:HOH:O	1.98	0.64
1:K:478:HIS:HD2	8:K:1201:HOH:O	1.80	0.64
2:P:75:PRO:HD2	7:P:304:SF4:S4	2.37	0.64
2:N:128:MET:HA	7:N:303:SF4:S1	2.38	0.64
1:Q:426:MET:HE1	1:Q:618:GLN:HG2	1.79	0.64
1:U:35:ASP:OD1	1:U:55:ARG:HD3	1.98	0.64
2:V:68:CYS:HB3	2:V:70:HIS:CE1	2.33	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:V:69:MET:HB3	2:V:184:PRO:HB3	1.79	0.64
1:G:28:MET:HE1	1:G:66:PHE:HB3	1.79	0.64
2:N:46:MET:HE1	2:N:65:PRO:HA	1.79	0.64
2:P:69:MET:HB3	2:P:184:PRO:HB3	1.80	0.64
2:D:71:CYS:HB2	2:D:182:THR:O	1.98	0.64
1:E:197:GLU:HG3	1:E:199:TYR:CD1	2.34	0.64
2:R:157:LEU:HD12	2:R:157:LEU:H	1.62	0.64
2:B:46:MET:HE3	2:B:66:THR:N	2.12	0.63
1:K:561:ILE:HG22	1:K:564:ASN:HB3	1.80	0.63
1:A:301:GLU:CD	1:A:301:GLU:H	2.00	0.63
1:M:561:ILE:HG22	1:M:564:ASN:HB3	1.79	0.63
2:J:105:LEU:C	2:J:114:MET:HE2	2.18	0.63
1:M:100:LEU:HD12	1:M:105:PRO:HG3	1.80	0.63
2:T:68:CYS:HB2	2:T:126:CYS:HB2	1.78	0.63
1:A:495:LYS:HD3	8:A:1105:HOH:O	1.98	0.63
1:I:66:PHE:HA	1:I:69:MET:HE3	1.80	0.63
1:M:134:PRO:HB2	1:M:439:LEU:HD11	1.80	0.63
2:V:75:PRO:HD2	7:V:304:SF4:S4	2.38	0.63
2:X:46:MET:HE1	2:X:65:PRO:HA	1.78	0.63
1:G:146:MET:HE1	1:G:544:THR:CB	2.26	0.63
1:I:146:MET:HE1	1:I:544:THR:HB	1.81	0.63
1:I:75:ARG:HH21	1:I:543:CYS:HA	1.63	0.63
2:L:68:CYS:CB	2:L:126:CYS:HB3	2.28	0.63
1:M:146:MET:HE3	1:M:544:THR:HA	1.81	0.63
1:Q:114:TRP:CZ2	1:Q:541:PRO:HD2	2.33	0.63
2:T:71:CYS:HB2	2:T:182:THR:O	1.99	0.63
1:U:561:ILE:HG22	1:U:564:ASN:HB3	1.80	0.63
1:Q:100:LEU:HD13	1:Q:105:PRO:HG3	1.80	0.63
1:E:211:MET:HE2	1:E:244:ASP:HB2	1.81	0.63
2:L:70:HIS:CD2	2:L:92:VAL:H	2.08	0.63
1:S:478:HIS:HD2	8:S:1205:HOH:O	1.82	0.63
2:P:104:GLU:CD	2:P:104:GLU:H	2.00	0.63
1:S:165:GLY:HA3	1:S:166:PHE:HB3	1.80	0.63
2:X:2:GLU:HG2	2:X:158:LYS:HG2	1.79	0.63
1:G:66:PHE:HA	1:G:69:MET:HE3	1.81	0.62
1:E:800:ILE:HD12	1:E:800:ILE:N	2.15	0.62
1:I:66:PHE:HA	1:I:69:MET:CE	2.29	0.62
1:S:558:SER:H	1:S:564:ASN:ND2	1.97	0.62
2:X:59:ASN:H	2:X:59:ASN:ND2	1.96	0.62
2:D:7:VAL:HB	2:D:155:GLU:HB3	1.82	0.62
1:G:249:ASP:OD1	4:G:903:MGD:H1'	1.99	0.62
1:M:356:GLY:N	4:M:903:MGD:O1B	2.31	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:333:ARG:NH1	1:U:729:LYS:HE3	2.14	0.62
2:N:69:MET:HB3	2:N:184:PRO:HB3	1.81	0.62
1:Q:249:ASP:OD1	4:Q:903:MGD:H1'	1.98	0.62
1:U:138:LEU:HB2	1:U:490:ILE:HD12	1.80	0.62
2:J:75:PRO:HD2	7:J:304:SF4:S4	2.39	0.62
1:Q:319:GLU:CG	1:U:726:LEU:HD13	2.27	0.62
1:W:311:THR:HG21	8:W:1499:HOH:O	1.98	0.62
1:U:311:THR:HG21	8:U:1502:HOH:O	2.00	0.62
2:V:46:MET:CE	2:V:66:THR:H	2.12	0.62
2:X:143:PRO:HB3	7:X:303:SF4:S1	2.39	0.62
2:V:46:MET:HE1	2:V:65:PRO:HA	1.82	0.62
1:I:75:ARG:NH2	1:I:543:CYS:HA	2.15	0.62
2:L:46:MET:CE	2:L:66:THR:H	2.12	0.62
2:N:142:MET:HE2	2:N:146:ALA:CB	2.29	0.62
1:S:610:LYS:HZ2	1:S:618:GLN:HE22	1.46	0.62
1:K:301:GLU:CD	1:K:301:GLU:H	2.04	0.62
1:Q:708:ARG:HD2	8:Q:1043:HOH:O	1.98	0.62
1:M:725:PRO:HA	1:S:704:ILE:HG13	1.82	0.62
1:U:478:HIS:HD2	8:U:1207:HOH:O	1.83	0.62
1:A:249:ASP:OD1	4:A:903:MGD:H1'	2.00	0.61
2:V:2:GLU:HG2	2:V:158:LYS:HG2	1.82	0.61
2:X:125:LYS:HD2	2:X:126:CYS:O	2.00	0.61
2:V:68:CYS:HB2	2:V:126:CYS:HB2	1.80	0.61
2:H:21:MET:HE2	2:H:21:MET:HA	1.81	0.61
2:J:68:CYS:HB2	2:J:126:CYS:HB2	1.81	0.61
2:L:75:PRO:HD2	7:L:304:SF4:S4	2.41	0.61
2:P:68:CYS:HB2	2:P:126:CYS:HB2	1.79	0.61
1:S:81:LYS:HB2	1:S:112:ILE:HD13	1.82	0.61
2:B:205:VAL:HG13	2:B:254:LYS:NZ	2.16	0.61
2:F:114:MET:HE2	2:F:123:ALA:HB1	1.82	0.61
2:F:21:MET:HE2	2:F:21:MET:HA	1.82	0.61
2:J:21:MET:HA	2:J:21:MET:HE2	1.81	0.61
2:N:75:PRO:HD2	7:N:304:SF4:S4	2.41	0.61
4:A:903:MGD:O2B	4:A:903:MGD:O1A	2.18	0.61
1:E:561:ILE:HG22	1:E:564:ASN:HB3	1.82	0.61
1:G:162:ASN:HA	8:G:1364:HOH:O	1.99	0.61
2:L:59:ASN:H	2:L:59:ASN:ND2	1.99	0.61
2:F:68:CYS:CB	2:F:126:CYS:HB3	2.23	0.61
1:C:786:ASN:ND2	1:C:805:VAL:H	1.99	0.61
2:F:5:TYR:HB2	2:F:157:LEU:CD1	2.30	0.61
2:N:71:CYS:HB2	2:N:182:THR:O	2.00	0.61
2:T:40:GLN:HE22	2:T:118:GLU:H	1.47	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:426:MET:HE2	1:A:618:GLN:HG2	1.83	0.60
2:P:142:MET:HE1	8:P:428:HOH:O	2.00	0.60
1:O:257:ARG:HD3	2:P:61:ILE:HG21	1.83	0.60
1:Q:696:LYS:O	1:Q:700:GLU:HG3	2.00	0.60
1:U:426:MET:HE3	1:U:426:MET:HA	1.82	0.60
1:A:426:MET:CA	1:A:426:MET:HE3	2.27	0.60
2:R:104:GLU:H	2:R:104:GLU:CD	2.05	0.60
1:S:311:THR:HG21	8:S:1495:HOH:O	2.01	0.60
1:A:81:LYS:HB2	1:A:112:ILE:HD13	1.84	0.60
1:C:610:LYS:HZ3	1:C:618:GLN:HE22	1.48	0.60
1:C:644:ASP:C	1:C:646:PRO:HD3	2.22	0.60
2:H:128:MET:HA	7:H:303:SF4:S1	2.42	0.60
2:L:1:MET:HG3	2:L:88:GLU:HB3	1.83	0.60
1:M:696:LYS:O	1:M:700:GLU:HG3	2.01	0.60
1:O:557:CYS:N	1:O:564:ASN:HD21	1.93	0.60
1:M:319:GLU:CG	1:S:726:LEU:HD13	2.30	0.60
2:D:143:PRO:HB3	7:D:303:SF4:S1	2.41	0.60
1:E:696:LYS:O	1:E:700:GLU:HG3	2.01	0.60
4:K:903:MGD:O1A	4:K:903:MGD:O2B	2.18	0.60
1:O:74:LEU:HD12	1:O:750:LYS:HA	1.83	0.60
2:P:106:LEU:HD23	2:P:114:MET:HE3	1.84	0.60
1:S:786:ASN:HD22	1:S:805:VAL:H	1.48	0.60
1:W:249:ASP:OD1	4:W:903:MGD:H1'	2.01	0.60
1:K:216:SER:OG	4:K:903:MGD:H5'2	2.01	0.60
1:I:786:ASN:ND2	1:I:804:GLN:HA	2.16	0.60
2:J:76:CYS:O	2:J:80:GLY:N	2.35	0.60
1:Q:557:CYS:N	1:Q:564:ASN:HD21	1.88	0.60
2:R:125:LYS:HD2	2:R:126:CYS:O	2.02	0.60
2:X:70:HIS:HD2	2:X:92:VAL:H	1.48	0.60
1:A:495:LYS:HD2	1:A:514:TYR:OH	2.01	0.60
2:F:46:MET:HE1	2:F:65:PRO:HA	1.83	0.60
1:C:610:LYS:HB3	1:C:614:ALA:HB3	1.84	0.60
2:H:40:GLN:NE2	2:H:118:GLU:H	1.99	0.60
2:R:59:ASN:ND2	2:R:59:ASN:H	2.00	0.60
1:C:557:CYS:N	1:C:564:ASN:HD21	1.89	0.59
2:F:166:LYS:O	2:F:170:GLU:HG3	2.02	0.59
1:O:211:MET:HE1	2:P:231:PHE:CZ	2.35	0.59
1:Q:800:ILE:HD12	1:Q:800:ILE:N	2.17	0.59
1:U:134:PRO:HB2	1:U:439:LEU:HD11	1.83	0.59
2:B:166:LYS:HG2	2:B:170:GLU:OE2	2.01	0.59
1:E:28:MET:HE1	1:E:66:PHE:HB3	1.83	0.59
2:T:114:MET:HE3	2:T:123:ALA:HB1	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:691:ILE:HD11	1:G:711:MET:HE3	1.83	0.59
1:K:557:CYS:N	1:K:564:ASN:HD21	1.88	0.59
2:L:142:MET:HE1	8:L:430:HOH:O	2.03	0.59
1:W:645:ASN:HD22	1:W:648:ARG:HB3	1.65	0.59
1:M:356:GLY:H	4:M:903:MGD:H5'2	1.67	0.59
1:I:114:TRP:CZ2	1:I:541:PRO:HD2	2.36	0.59
1:Q:649:LYS:HE3	1:Q:651:THR:HG22	1.84	0.59
1:G:786:ASN:HD22	1:G:805:VAL:H	1.50	0.59
2:H:201:ALA:HB2	2:H:269:LEU:HB2	1.84	0.59
2:L:103:LYS:HE2	2:L:116:TRP:NE1	2.18	0.59
1:M:211:MET:HE2	1:M:244:ASP:HB2	1.85	0.59
1:M:630:THR:OG1	1:M:633:GLU:HG3	2.02	0.59
1:M:800:ILE:HD12	1:M:800:ILE:N	2.17	0.59
1:U:249:ASP:CG	4:U:903:MGD:H1'	2.23	0.59
1:A:15:PRO:HD2	8:A:1003:HOH:O	2.01	0.59
1:A:55:ARG:HD2	8:A:1637:HOH:O	2.03	0.59
1:O:561:ILE:HG22	1:O:564:ASN:HB3	1.82	0.59
1:W:708:ARG:HD2	8:W:1044:HOH:O	2.03	0.59
1:E:197:GLU:OE2	1:E:667:ASP:HB2	2.03	0.59
1:G:134:PRO:HB2	1:G:439:LEU:HD11	1.84	0.59
1:M:610:LYS:HB3	1:M:614:ALA:HB3	1.85	0.59
1:Q:823:TYR:CE2	1:Q:825:PRO:HG3	2.38	0.59
1:Q:871:LYS:HG2	8:Q:1230:HOH:O	2.02	0.59
1:W:35:ASP:OD1	1:W:55:ARG:HD3	2.03	0.59
2:B:105:LEU:C	2:B:114:MET:HE2	2.23	0.59
2:B:70:HIS:CD2	2:B:92:VAL:H	2.09	0.58
1:C:478:HIS:HD2	8:C:1205:HOH:O	1.86	0.58
1:S:753:TYR:HB3	2:T:24:MET:CE	2.29	0.58
2:X:5:TYR:HB2	2:X:157:LEU:CD1	2.33	0.58
1:G:144:HIS:HB2	4:G:902:MGD:O1B	2.03	0.58
1:G:610:LYS:HB3	1:G:614:ALA:HB3	1.84	0.58
2:L:46:MET:HE1	2:L:65:PRO:CA	2.32	0.58
1:Q:44:ILE:HD11	1:Q:394:PRO:HG2	1.85	0.58
1:Q:691:ILE:HD11	1:Q:711:MET:HE3	1.85	0.58
2:T:46:MET:CE	2:T:66:THR:H	2.16	0.58
2:B:114:MET:HA	2:B:125:LYS:HB3	1.85	0.58
1:C:726:LEU:HD23	8:C:1194:HOH:O	2.02	0.58
1:Q:55:ARG:HD2	8:Q:1636:HOH:O	2.02	0.58
1:Q:800:ILE:HD11	1:Q:833:ALA:HB1	1.84	0.58
1:S:249:ASP:CG	4:S:903:MGD:H1'	2.24	0.58
2:B:21:MET:HE2	2:B:21:MET:HA	1.85	0.58
1:Q:146:MET:HG2	4:Q:902:MGD:N7	2.19	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:510:TYR:O	1:S:513:MET:HG2	2.03	0.58
1:K:311:THR:HG21	8:K:1495:HOH:O	2.02	0.58
1:K:400:TYR:CE1	1:K:421:LYS:HD2	2.39	0.58
1:U:85:PHE:CE2	1:U:87:PRO:HG3	2.38	0.58
2:X:23:CYS:HB3	2:X:39:MET:HE3	1.84	0.58
2:F:205:VAL:HG13	2:F:254:LYS:NZ	2.18	0.58
1:O:138:LEU:HB2	1:O:490:ILE:HD12	1.85	0.58
1:Q:738:HIS:HE2	4:Q:902:MGD:H15	1.52	0.58
1:S:647:ASN:O	1:S:648:ARG:O	2.21	0.58
1:U:610:LYS:HZ2	1:U:618:GLN:HE22	1.51	0.58
1:C:785:LYS:HB2	1:C:785:LYS:NZ	2.18	0.58
1:G:66:PHE:HA	1:G:69:MET:CE	2.34	0.58
1:M:75:ARG:NH2	1:M:543:CYS:HA	2.18	0.58
1:O:696:LYS:O	1:O:700:GLU:HG3	2.02	0.58
1:O:786:ASN:ND2	1:O:804:GLN:HA	2.19	0.58
4:O:903:MGD:O1B	4:O:903:MGD:H4'	2.04	0.58
1:U:214:PHE:HA	1:U:347:ALA:HB3	1.86	0.58
1:W:426:MET:HE1	1:W:618:GLN:HG2	1.86	0.58
1:A:211:MET:HE1	2:B:231:PHE:HZ	1.68	0.58
2:D:40:GLN:NE2	2:D:117:ASN:HA	2.18	0.58
1:I:494:TRP:HE1	1:I:525:GLN:HE21	1.52	0.58
2:P:5:TYR:HB2	2:P:157:LEU:CD1	2.34	0.58
1:S:66:PHE:HA	1:S:69:MET:CE	2.34	0.58
2:D:70:HIS:CD2	2:D:92:VAL:H	2.16	0.58
1:G:870:ASP:HB3	1:G:872:TYR:CE1	2.39	0.58
1:M:691:ILE:HD11	1:M:711:MET:HE3	1.85	0.58
1:C:74:LEU:HD12	1:C:750:LYS:HA	1.85	0.57
1:G:114:TRP:CZ2	1:G:541:PRO:HD2	2.39	0.57
2:J:46:MET:CE	2:J:66:THR:H	2.15	0.57
1:K:66:PHE:HA	1:K:69:MET:HE2	1.86	0.57
2:N:5:TYR:HB2	2:N:157:LEU:CD1	2.34	0.57
1:O:100:LEU:HD12	1:O:105:PRO:HG3	1.86	0.57
1:S:1:MET:H3	1:S:22:ASP:CG	2.07	0.57
1:S:754:MET:HG3	8:S:1652:HOH:O	2.04	0.57
1:C:823:TYR:CE2	1:C:825:PRO:HG3	2.39	0.57
2:F:104:GLU:CD	2:F:104:GLU:H	2.07	0.57
2:H:59:ASN:H	2:H:59:ASN:ND2	2.03	0.57
4:O:903:MGD:O1A	4:O:903:MGD:O2B	2.21	0.57
1:U:696:LYS:O	1:U:700:GLU:HG3	2.04	0.57
1:W:66:PHE:HD1	1:W:69:MET:HE3	1.64	0.57
2:D:106:LEU:HD11	2:D:116:TRP:HB2	1.86	0.57
1:E:134:PRO:HB2	1:E:439:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:100:LEU:HD12	1:I:105:PRO:HG3	1.85	0.57
1:K:610:LYS:HB3	1:K:614:ALA:HB3	1.84	0.57
1:Q:426:MET:HE2	1:Q:618:GLN:HG2	1.86	0.57
1:W:510:TYR:O	1:W:513:MET:HG2	2.05	0.57
2:X:75:PRO:HD2	7:X:304:SF4:S4	2.45	0.57
2:B:59:ASN:H	2:B:59:ASN:ND2	2.02	0.57
1:K:786:ASN:ND2	1:K:805:VAL:H	2.03	0.57
2:L:40:GLN:NE2	2:L:118:GLU:H	1.97	0.57
1:M:211:MET:HE3	2:N:231:PHE:CZ	2.39	0.57
1:M:35:ASP:OD1	1:M:55:ARG:HD3	2.04	0.57
1:Q:100:LEU:CD1	1:Q:105:PRO:HG3	2.34	0.57
2:T:166:LYS:HG2	2:T:170:GLU:OE2	2.04	0.57
1:K:823:TYR:CE2	1:K:825:PRO:HG3	2.40	0.57
1:O:479:GLN:HG2	8:O:1176:HOH:O	2.04	0.57
1:E:800:ILE:HD11	1:E:833:ALA:HB1	1.86	0.57
1:I:557:CYS:N	1:I:564:ASN:HD21	1.92	0.57
2:J:19:CYS:HB3	2:J:145:CYS:HB3	1.86	0.57
2:L:105:LEU:HB3	2:L:114:MET:CE	2.35	0.57
1:Q:211:MET:HE2	1:Q:244:ASP:HB2	1.84	0.57
1:S:140:THR:HB	1:S:169:ALA:HB3	1.86	0.57
2:X:19:CYS:HB3	2:X:145:CYS:HB3	1.85	0.57
2:B:142:MET:HE1	8:B:429:HOH:O	2.03	0.57
2:N:70:HIS:CD2	2:N:92:VAL:H	2.10	0.57
2:H:76:CYS:HB3	2:H:108:THR:OG1	2.05	0.57
2:J:106:LEU:HD11	2:J:116:TRP:HB2	1.87	0.57
1:M:823:TYR:CE2	1:M:825:PRO:HG3	2.39	0.57
2:T:106:LEU:HD11	2:T:116:TRP:HB2	1.86	0.57
1:A:218:ASP:OD2	1:A:253:ASN:HB2	2.05	0.57
1:E:249:ASP:OD1	4:E:903:MGD:H1'	2.04	0.57
2:F:69:MET:HB3	2:F:184:PRO:HB3	1.87	0.57
2:H:105:LEU:HB3	2:H:114:MET:HE3	1.85	0.57
2:J:5:TYR:HB2	2:J:157:LEU:HD11	1.85	0.57
1:I:211:MET:HE1	2:J:231:PHE:CZ	2.39	0.57
1:O:823:TYR:CE2	1:O:825:PRO:HG3	2.40	0.57
1:Q:100:LEU:HD22	1:Q:534:PRO:HB2	1.87	0.57
1:Q:503:THR:HG21	4:Q:902:MGD:O2A	2.04	0.57
1:U:394:PRO:HG3	8:U:1322:HOH:O	2.04	0.57
2:V:46:MET:CE	2:V:66:THR:N	2.68	0.57
1:C:100:LEU:HD12	1:C:105:PRO:HG3	1.87	0.57
1:E:114:TRP:CZ2	1:E:541:PRO:HD2	2.40	0.57
1:U:100:LEU:HD12	1:U:105:PRO:HG3	1.87	0.57
1:G:74:LEU:HD12	1:G:750:LYS:HA	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:R:70:HIS:CD2	2:R:92:VAL:H	2.13	0.56
1:S:66:PHE:HD1	1:S:69:MET:HE3	1.69	0.56
1:I:708:ARG:HD2	8:I:1043:HOH:O	2.03	0.56
1:K:737:PRO:CG	4:K:903:MGD:H2'	2.35	0.56
2:D:46:MET:HE1	2:D:66:THR:N	2.21	0.56
4:E:903:MGD:O2B	8:E:1287:HOH:O	2.18	0.56
1:O:140:THR:HB	1:O:169:ALA:HB3	1.87	0.56
2:R:75:PRO:HD2	7:R:304:SF4:S4	2.45	0.56
2:X:68:CYS:HB3	2:X:70:HIS:CE1	2.40	0.56
1:K:356:GLY:H	4:K:903:MGD:C5'	2.19	0.56
1:Q:69:MET:HE2	1:Q:754:MET:HE1	1.87	0.56
1:S:146:MET:HE1	1:S:544:THR:HB	1.85	0.56
4:E:903:MGD:O2B	4:E:903:MGD:O1A	2.24	0.56
1:G:378:GLY:O	1:G:381:LYS:HG2	2.04	0.56
2:H:75:PRO:HD2	7:H:304:SF4:S4	2.45	0.56
1:M:753:TYR:HB3	2:N:24:MET:HE3	1.87	0.56
1:O:146:MET:HE2	1:O:545:ASN:H	1.70	0.56
1:U:253:ASN:O	1:U:257:ARG:HG3	2.06	0.56
1:A:478:HIS:HD2	8:A:1203:HOH:O	1.87	0.56
1:A:610:LYS:HZ1	1:A:618:GLN:HE22	1.53	0.56
1:A:737:PRO:HG3	4:A:903:MGD:H2'	1.87	0.56
1:E:56:LYS:HG2	1:E:57:THR:O	2.05	0.56
1:Q:356:GLY:N	4:Q:903:MGD:O2B	2.38	0.56
1:U:76:ILE:HG22	1:U:541:PRO:HG3	1.88	0.56
2:V:40:GLN:HE22	2:V:118:GLU:H	1.51	0.56
1:W:140:THR:HB	1:W:169:ALA:HB3	1.88	0.56
1:C:66:PHE:HD1	1:C:69:MET:HE3	1.68	0.56
1:G:708:ARG:HD2	8:G:1044:HOH:O	2.05	0.56
1:U:510:TYR:O	1:U:513:MET:HG2	2.06	0.56
1:W:426:MET:HE2	1:W:618:GLN:HG2	1.88	0.56
1:W:696:LYS:O	1:W:700:GLU:HG3	2.06	0.56
2:X:40:GLN:HE22	2:X:118:GLU:H	1.53	0.56
2:D:125:LYS:HD2	2:D:126:CYS:O	2.05	0.56
1:E:510:TYR:O	1:E:513:MET:HG2	2.06	0.56
1:M:786:ASN:ND2	1:M:804:GLN:HA	2.21	0.56
1:O:478:HIS:HD2	8:O:1204:HOH:O	1.89	0.56
1:S:74:LEU:HD12	1:S:750:LYS:HA	1.86	0.56
1:S:142:SER:OG	4:S:902:MGD:O1A	2.20	0.56
2:V:104:GLU:H	2:V:104:GLU:CD	2.09	0.56
1:A:630:THR:OG1	1:A:633:GLU:HG3	2.06	0.56
1:G:610:LYS:HZ3	1:G:618:GLN:HE22	1.50	0.56
1:G:786:ASN:ND2	1:G:805:VAL:H	2.03	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:P:46:MET:HE1	2:P:65:PRO:CA	2.36	0.56
1:S:696:LYS:O	1:S:700:GLU:HG3	2.05	0.56
1:I:495:LYS:HD2	1:I:514:TYR:OH	2.06	0.56
1:M:478:HIS:HD2	8:M:1205:HOH:O	1.89	0.56
1:Q:478:HIS:HD2	8:Q:1203:HOH:O	1.88	0.56
2:R:166:LYS:HG2	2:R:170:GLU:OE2	2.06	0.56
1:W:610:LYS:HB3	1:W:614:ALA:HB3	1.87	0.56
2:X:252:ASP:C	2:X:254:LYS:H	2.09	0.56
1:C:725:PRO:HD2	8:C:1194:HOH:O	2.06	0.56
1:G:610:LYS:HZ1	1:G:618:GLN:HE22	1.52	0.56
1:K:753:TYR:HB3	2:L:24:MET:HE3	1.88	0.56
1:O:143:SER:N	4:O:902:MGD:O1A	2.39	0.56
1:M:333:ARG:NH1	1:S:729:LYS:HE3	2.20	0.56
2:X:95:ASP:HB3	2:X:98:LYS:HB2	1.88	0.56
2:F:70:HIS:CD2	2:F:92:VAL:H	2.10	0.55
2:J:69:MET:HB3	2:J:184:PRO:HB3	1.87	0.55
2:L:254:LYS:HD2	2:L:274:LEU:OXT	2.06	0.55
1:G:301:GLU:CD	1:G:301:GLU:H	2.08	0.55
1:K:426:MET:HE3	1:K:622:ALA:HB2	1.88	0.55
2:L:59:ASN:H	2:L:59:ASN:HD22	1.54	0.55
1:O:311:THR:HG21	8:O:1498:HOH:O	2.06	0.55
1:Q:319:GLU:HG2	1:U:726:LEU:CD1	2.30	0.55
1:W:557:CYS:N	1:W:564:ASN:HD21	1.95	0.55
1:A:66:PHE:HA	1:A:69:MET:CE	2.37	0.55
1:I:426:MET:HE1	1:I:618:GLN:O	2.06	0.55
1:E:146:MET:HG2	4:E:902:MGD:N7	2.22	0.55
2:J:142:MET:HE1	8:J:928:HOH:O	2.06	0.55
2:L:114:MET:HA	2:L:125:LYS:HB3	1.87	0.55
1:Q:561:ILE:HG22	1:Q:564:ASN:HB3	1.87	0.55
1:E:301:GLU:CD	1:E:301:GLU:H	2.09	0.55
2:H:157:LEU:N	2:H:157:LEU:HD12	2.21	0.55
2:J:59:ASN:H	2:J:59:ASN:ND2	2.04	0.55
2:R:68:CYS:HB2	2:R:126:CYS:HB2	1.88	0.55
2:R:207:GLY:CA	1:U:728:VAL:HG12	2.29	0.55
1:C:451:LYS:HG3	1:C:461:PHE:CE2	2.42	0.55
1:C:533:VAL:HB	1:C:534:PRO:HD3	1.88	0.55
1:Q:56:LYS:HG2	1:Q:57:THR:O	2.06	0.55
2:V:46:MET:HE1	2:V:65:PRO:CA	2.37	0.55
1:C:356:GLY:H	4:C:903:MGD:H5'2	1.70	0.55
2:F:201:ALA:HB2	2:F:269:LEU:HB2	1.89	0.55
1:G:142:SER:OG	4:G:902:MGD:O1A	2.20	0.55
1:Q:15:PRO:HD2	8:Q:1003:HOH:O	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:U:301:GLU:CD	1:U:301:GLU:H	2.10	0.55
1:U:610:LYS:HB3	1:U:614:ALA:HB3	1.89	0.55
2:V:143:PRO:HB3	7:V:303:SF4:S1	2.47	0.55
1:W:770:TRP:HB3	1:W:801:LEU:HD23	1.89	0.55
2:X:68:CYS:HB2	2:X:126:CYS:HB2	1.86	0.55
1:E:823:TYR:CE2	1:E:825:PRO:HG3	2.42	0.55
2:L:166:LYS:HG2	2:L:170:GLU:OE2	2.07	0.55
1:M:800:ILE:HD11	1:M:833:ALA:HB1	1.89	0.55
1:S:855:MET:HB2	1:S:857:ASN:OD1	2.07	0.55
1:C:75:ARG:HH21	1:C:543:CYS:HA	1.72	0.55
1:C:249:ASP:CG	4:C:903:MGD:H1'	2.28	0.55
1:C:355:GLY:CA	4:C:903:MGD:O1B	2.55	0.55
2:D:53:ARG:HB2	2:D:60:ASP:OD1	2.07	0.55
1:G:476:GLN:OE1	1:G:708:ARG:NH2	2.40	0.55
1:O:301:GLU:H	1:O:301:GLU:CD	2.10	0.55
2:B:106:LEU:HD23	2:B:114:MET:HE3	1.89	0.54
1:C:426:MET:HE2	1:C:618:GLN:HG2	1.86	0.54
2:F:114:MET:HG2	2:F:125:LYS:HG2	1.89	0.54
1:I:610:LYS:HZ2	1:I:618:GLN:HE22	1.54	0.54
1:I:28:MET:HE1	1:I:66:PHE:HB3	1.89	0.54
1:O:563:ASP:O	1:O:566:GLN:HG2	2.07	0.54
1:O:855:MET:HB2	1:O:857:ASN:OD1	2.08	0.54
1:G:249:ASP:CG	4:G:903:MGD:H1'	2.28	0.54
1:M:394:PRO:HG3	8:M:1322:HOH:O	2.07	0.54
1:O:708:ARG:HD2	8:O:1043:HOH:O	2.07	0.54
2:R:142:MET:HE2	2:R:146:ALA:CB	2.37	0.54
2:V:46:MET:HE3	2:V:66:THR:H	1.72	0.54
2:B:46:MET:CE	2:B:66:THR:N	2.70	0.54
1:C:253:ASN:O	1:C:257:ARG:HG3	2.07	0.54
1:C:426:MET:HE1	1:C:618:GLN:O	2.08	0.54
1:G:211:MET:HE2	1:G:244:ASP:CB	2.37	0.54
1:M:476:GLN:OE1	1:M:708:ARG:NH2	2.40	0.54
2:P:59:ASN:HD22	2:P:59:ASN:H	1.54	0.54
2:J:114:MET:HA	2:J:125:LYS:HB3	1.88	0.54
1:K:426:MET:HA	1:K:426:MET:CE	2.33	0.54
1:M:426:MET:CA	1:M:426:MET:HE3	2.33	0.54
1:M:81:LYS:HB2	1:M:112:ILE:HD13	1.90	0.54
1:M:356:GLY:N	4:M:903:MGD:PB	2.80	0.54
1:O:426:MET:HE2	1:O:618:GLN:HG2	1.86	0.54
1:S:563:ASP:O	1:S:566:GLN:HG2	2.07	0.54
1:W:249:ASP:CG	4:W:903:MGD:H1'	2.27	0.54
1:G:141:PRO:CA	1:G:496:TYR:HB3	2.35	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:175:SER:HB2	1:I:176:TRP:CE3	2.43	0.54
1:O:253:ASN:O	1:O:257:ARG:HG3	2.08	0.54
1:U:146:MET:HE2	1:U:545:ASN:H	1.72	0.54
1:G:800:ILE:N	1:G:800:ILE:HD12	2.23	0.54
2:H:21:MET:CE	2:H:21:MET:HA	2.38	0.54
1:I:800:ILE:HD12	1:I:800:ILE:N	2.23	0.54
1:Q:855:MET:HB2	1:Q:857:ASN:OD1	2.07	0.54
1:U:249:ASP:OD1	4:U:903:MGD:H1'	2.07	0.54
2:V:125:LYS:HD2	2:V:126:CYS:O	2.07	0.54
1:W:28:MET:HE1	1:W:66:PHE:HB3	1.90	0.54
1:A:114:TRP:CZ2	1:A:541:PRO:HD2	2.43	0.54
2:B:5:TYR:HB2	2:B:157:LEU:CD1	2.37	0.54
1:G:730:TYR:CE1	1:G:794:ASN:HA	2.43	0.54
2:P:59:ASN:ND2	2:P:59:ASN:H	2.05	0.54
2:R:157:LEU:HD12	2:R:157:LEU:N	2.23	0.54
1:C:476:GLN:OE1	1:C:708:ARG:NH2	2.41	0.54
1:I:823:TYR:CE2	1:I:825:PRO:HG3	2.43	0.54
1:Q:786:ASN:HD22	1:Q:805:VAL:H	1.55	0.54
1:Q:355:GLY:CA	4:Q:903:MGD:O2B	2.49	0.54
1:S:75:ARG:NH2	1:S:543:CYS:HA	2.23	0.54
2:V:87:ARG:HG3	2:V:91:ILE:O	2.08	0.54
2:X:18:ASN:HB2	7:X:302:SF4:S1	2.48	0.54
1:C:871:LYS:HG2	8:C:1233:HOH:O	2.07	0.54
2:H:68:CYS:HB2	2:H:126:CYS:HB2	1.85	0.54
1:M:356:GLY:H	4:M:903:MGD:PB	2.31	0.54
1:U:753:TYR:HB3	2:V:24:MET:CE	2.38	0.54
1:E:673:ASN:H	1:E:673:ASN:HD22	1.56	0.54
1:K:426:MET:HE2	1:K:618:GLN:HG2	1.89	0.54
2:R:5:TYR:O	2:R:157:LEU:HD12	2.07	0.54
1:A:387:TRP:CE2	1:A:389:THR:HA	2.43	0.53
2:D:164:MET:O	2:D:168:VAL:HG23	2.08	0.53
2:H:46:MET:CE	2:H:66:THR:H	2.15	0.53
2:L:114:MET:HE3	2:L:123:ALA:HB1	1.89	0.53
1:M:249:ASP:CG	4:M:903:MGD:H1'	2.28	0.53
2:P:216:VAL:HG13	2:P:223:GLU:HG3	1.89	0.53
1:Q:291:GLU:CD	1:Q:291:GLU:H	2.11	0.53
1:E:737:PRO:CG	4:E:903:MGD:H2'	2.38	0.53
2:J:164:MET:O	2:J:168:VAL:HG23	2.09	0.53
2:N:5:TYR:HB2	2:N:157:LEU:HD11	1.89	0.53
1:Q:426:MET:HE3	1:Q:426:MET:CA	2.33	0.53
1:Q:649:LYS:HE3	1:Q:651:THR:CG2	2.38	0.53
2:R:142:MET:HE1	2:R:146:ALA:HB1	1.90	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:476:GLN:OE1	1:A:708:ARG:NH2	2.41	0.53
1:E:478:HIS:HD2	8:E:1205:HOH:O	1.92	0.53
1:O:146:MET:HG2	4:O:902:MGD:N7	2.24	0.53
1:C:81:LYS:HB2	1:C:112:ILE:HD13	1.91	0.53
1:C:85:PHE:CE2	1:C:87:PRO:HG3	2.43	0.53
1:G:571:ARG:HB2	1:G:642:VAL:HB	1.91	0.53
2:H:211:GLU:HB2	2:H:231:PHE:HA	1.89	0.53
1:I:426:MET:HE2	1:I:618:GLN:HG2	1.88	0.53
1:Q:425:ARG:HD3	1:Q:622:ALA:O	2.08	0.53
1:S:35:ASP:OD1	1:S:55:ARG:HD3	2.08	0.53
2:T:39:MET:HE2	2:T:45:TRP:CD2	2.44	0.53
1:W:75:ARG:NH2	1:W:543:CYS:HA	2.23	0.53
1:A:800:ILE:N	1:A:800:ILE:HD12	2.23	0.53
1:C:510:TYR:O	1:C:513:MET:HG2	2.08	0.53
2:L:201:ALA:HB2	2:L:269:LEU:HB2	1.90	0.53
1:O:66:PHE:HA	1:O:69:MET:CE	2.39	0.53
1:U:140:THR:HB	1:U:169:ALA:HB3	1.89	0.53
1:W:218:ASP:OD2	1:W:253:ASN:HB2	2.08	0.53
1:C:211:MET:HE2	1:C:244:ASP:HB2	1.90	0.53
1:C:505:THR:O	1:C:506:ALA:C	2.46	0.53
2:F:203:ILE:N	2:F:203:ILE:HD12	2.24	0.53
1:O:825:PRO:HD2	8:O:1332:HOH:O	2.08	0.53
1:U:44:ILE:HD11	1:U:394:PRO:HG2	1.89	0.53
2:B:203:ILE:N	2:B:203:ILE:HD12	2.24	0.53
1:C:15:PRO:HD3	1:C:554:PHE:CD1	2.43	0.53
2:F:75:PRO:HD2	7:F:304:SF4:S4	2.49	0.53
2:H:70:HIS:CD2	2:H:92:VAL:H	2.16	0.53
2:J:46:MET:HE1	2:J:65:PRO:CA	2.38	0.53
1:K:610:LYS:HZ2	1:K:618:GLN:HE22	1.57	0.53
1:O:81:LYS:HB2	1:O:112:ILE:HD13	1.91	0.53
1:G:353:GLY:O	1:G:354:TRP:HB2	2.07	0.53
1:G:478:HIS:HD2	8:G:1203:HOH:O	1.91	0.53
2:H:69:MET:HB3	2:H:184:PRO:HB3	1.90	0.53
2:J:143:PRO:HB3	7:J:303:SF4:S1	2.49	0.53
1:K:510:TYR:O	1:K:513:MET:HG2	2.09	0.53
1:K:28:MET:HE1	1:K:67:LYS:N	2.24	0.53
2:V:58:ARG:HD2	2:V:268:ASP:OD1	2.07	0.53
1:C:140:THR:HB	1:C:169:ALA:HB3	1.91	0.53
1:I:66:PHE:HZ	1:I:146:MET:CE	2.22	0.53
1:I:426:MET:HA	1:I:426:MET:CE	2.31	0.53
1:M:142:SER:CB	4:M:902:MGD:O1A	2.57	0.53
1:O:451:LYS:HG3	1:O:461:PHE:CE2	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:645:ASN:ND2	1:O:648:ARG:HB3	2.23	0.53
1:Q:460:LYS:HE2	8:Q:1022:HOH:O	2.09	0.53
2:R:203:ILE:HD12	2:R:203:ILE:N	2.24	0.53
1:W:478:HIS:HD2	8:W:1206:HOH:O	1.92	0.53
1:W:144:HIS:HB2	4:W:902:MGD:O1B	2.09	0.53
2:X:203:ILE:HD12	2:X:203:ILE:N	2.23	0.53
2:X:87:ARG:HG3	2:X:91:ILE:O	2.08	0.53
1:A:737:PRO:CG	4:A:903:MGD:H2'	2.39	0.53
1:E:671:ARG:HB2	8:E:1099:HOH:O	2.09	0.53
1:I:510:TYR:O	1:I:513:MET:HG2	2.09	0.53
1:M:460:LYS:HE2	8:M:1023:HOH:O	2.09	0.53
1:M:730:TYR:CE1	1:M:794:ASN:HA	2.44	0.53
2:P:143:PRO:HB3	7:P:303:SF4:S1	2.49	0.53
2:R:142:MET:HE2	2:R:146:ALA:HB1	1.91	0.53
1:S:610:LYS:HZ3	1:S:618:GLN:HE22	1.56	0.53
1:W:75:ARG:HH21	1:W:543:CYS:HA	1.74	0.53
1:C:138:LEU:HB2	1:C:490:ILE:HD12	1.91	0.52
1:C:355:GLY:C	4:C:903:MGD:O1B	2.47	0.52
1:M:557:CYS:N	1:M:564:ASN:HD21	1.92	0.52
1:Q:249:ASP:CG	4:Q:903:MGD:H1'	2.30	0.52
1:S:528:TRP:CD2	1:S:750:LYS:HD3	2.44	0.52
2:T:59:ASN:H	2:T:59:ASN:ND2	2.07	0.52
1:U:610:LYS:HZ3	1:U:618:GLN:HE22	1.57	0.52
1:A:610:LYS:HZ3	1:A:618:GLN:HE22	1.57	0.52
1:K:211:MET:HE1	1:K:338:GLN:HG2	1.91	0.52
2:N:104:GLU:CD	2:N:104:GLU:H	2.12	0.52
1:W:753:TYR:HB3	2:X:24:MET:HE3	1.89	0.52
1:C:153:ARG:O	1:C:157:TYR:HB3	2.08	0.52
1:E:197:GLU:HG3	1:E:199:TYR:HD1	1.73	0.52
1:K:617:GLU:HG3	1:K:631:TRP:CG	2.44	0.52
1:K:708:ARG:HD2	8:K:1043:HOH:O	2.09	0.52
2:N:59:ASN:H	2:N:59:ASN:ND2	2.06	0.52
2:P:201:ALA:HB2	2:P:269:LEU:HB2	1.90	0.52
1:Q:146:MET:HE1	1:Q:544:THR:CB	2.39	0.52
1:S:823:TYR:CE2	1:S:825:PRO:HG3	2.44	0.52
1:C:387:TRP:CE2	1:C:389:THR:HA	2.44	0.52
1:C:630:THR:OG1	1:C:633:GLU:HG3	2.10	0.52
2:D:114:MET:HE3	2:D:123:ALA:HB1	1.91	0.52
1:E:495:LYS:HD2	1:E:514:TYR:OH	2.10	0.52
2:F:1:MET:SD	2:F:88:GLU:HB3	2.49	0.52
1:I:855:MET:HB2	1:I:857:ASN:OD1	2.08	0.52
1:Q:175:SER:HB2	1:Q:176:TRP:CE3	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:786:ASN:ND2	1:S:805:VAL:H	2.08	0.52
2:T:69:MET:HB3	2:T:184:PRO:HB3	1.89	0.52
1:W:85:PHE:CE2	1:W:87:PRO:HG3	2.45	0.52
2:B:7:VAL:HB	2:B:155:GLU:HB3	1.92	0.52
1:C:378:GLY:O	1:C:381:LYS:HG2	2.09	0.52
1:G:182:GLY:HA3	1:G:364:ILE:HG23	1.91	0.52
1:I:144:HIS:HB2	4:I:902:MGD:O1B	2.09	0.52
2:L:162:GLU:H	2:L:162:GLU:CD	2.13	0.52
2:L:18:ASN:HB2	7:L:302:SF4:S1	2.50	0.52
1:M:400:TYR:CE1	1:M:421:LYS:HD2	2.44	0.52
1:Q:825:PRO:HD2	8:Q:1334:HOH:O	2.10	0.52
2:T:104:GLU:CD	2:T:104:GLU:H	2.12	0.52
1:C:144:HIS:HB2	4:C:902:MGD:O1B	2.09	0.52
2:D:59:ASN:H	2:D:59:ASN:ND2	2.07	0.52
1:E:55:ARG:HD2	8:E:1644:HOH:O	2.10	0.52
1:I:143:SER:N	4:I:902:MGD:O1A	2.42	0.52
1:K:28:MET:CE	1:K:66:PHE:HB3	2.40	0.52
1:O:783:GLY:O	1:O:866:LYS:HD2	2.10	0.52
2:P:46:MET:CE	2:P:66:THR:H	2.18	0.52
2:V:201:ALA:HB2	2:V:269:LEU:HB2	1.90	0.52
1:I:249:ASP:CG	4:I:903:MGD:H1'	2.30	0.52
2:L:46:MET:CE	2:L:66:THR:N	2.72	0.52
2:N:7:VAL:HB	2:N:155:GLU:HB3	1.92	0.52
1:O:134:PRO:HB2	1:O:439:LEU:HD11	1.91	0.52
2:V:46:MET:HE1	2:V:66:THR:N	2.24	0.52
2:X:129:CYS:HB3	2:X:131:HIS:CE1	2.44	0.52
2:F:106:LEU:HD11	2:F:116:TRP:HB2	1.91	0.52
2:L:40:GLN:NE2	2:L:117:ASN:HA	2.24	0.52
2:L:58:ARG:HD2	2:L:268:ASP:OD1	2.10	0.52
1:Q:75:ARG:NH2	1:Q:543:CYS:HA	2.25	0.52
2:V:205:VAL:HG13	2:V:254:LYS:HZ2	1.75	0.52
2:V:5:TYR:HB2	2:V:157:LEU:CD1	2.40	0.52
2:B:205:VAL:HG13	2:B:254:LYS:HZ2	1.74	0.52
1:C:495:LYS:HD2	1:C:514:TYR:OH	2.10	0.52
1:M:825:PRO:HD2	8:M:1336:HOH:O	2.09	0.52
1:O:356:GLY:H	4:O:903:MGD:C5'	2.22	0.52
1:U:146:MET:HG2	4:U:902:MGD:N7	2.25	0.52
2:V:142:MET:HE2	2:V:146:ALA:HB3	1.92	0.52
1:W:143:SER:N	4:W:902:MGD:O1A	2.42	0.52
2:X:166:LYS:O	2:X:170:GLU:HG3	2.09	0.52
1:C:211:MET:HE1	2:D:231:PHE:HZ	1.75	0.52
2:D:201:ALA:HB2	2:D:269:LEU:HB2	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:630:THR:OG1	1:I:633:GLU:HG3	2.10	0.52
1:M:114:TRP:CZ2	1:M:541:PRO:HD2	2.45	0.52
2:N:72:GLU:HG2	2:N:185:ARG:NH2	2.25	0.52
2:P:2:GLU:CG	2:P:158:LYS:HG2	2.33	0.52
2:X:68:CYS:HB3	2:X:126:CYS:HB3	1.91	0.52
2:D:103:LYS:HG2	2:D:116:TRP:CD2	2.45	0.51
1:E:387:TRP:CE2	1:E:389:THR:HA	2.46	0.51
2:J:21:MET:HA	2:J:21:MET:CE	2.40	0.51
1:S:134:PRO:HB2	1:S:439:LEU:HD11	1.91	0.51
1:S:717:ALA:HB3	1:S:720:SER:HB3	1.92	0.51
1:U:257:ARG:HD3	2:V:61:ILE:HG21	1.92	0.51
1:A:32:ASP:HB2	8:A:1658:HOH:O	2.10	0.51
2:B:76:CYS:O	2:B:80:GLY:N	2.43	0.51
1:G:823:TYR:CE2	1:G:825:PRO:HG3	2.45	0.51
1:K:696:LYS:O	1:K:700:GLU:HG3	2.10	0.51
1:O:630:THR:OG1	1:O:633:GLU:HG3	2.11	0.51
1:S:253:ASN:O	1:S:257:ARG:HG3	2.09	0.51
1:S:617:GLU:HG3	1:S:631:TRP:CG	2.46	0.51
1:S:708:ARG:HD2	8:S:1046:HOH:O	2.11	0.51
2:T:125:LYS:HD2	2:T:126:CYS:O	2.10	0.51
2:V:142:MET:HE2	2:V:146:ALA:HB1	1.92	0.51
2:V:71:CYS:HB2	2:V:182:THR:O	2.09	0.51
1:W:104:ASP:OD2	1:W:107:SER:HB3	2.10	0.51
1:C:563:ASP:O	1:C:566:GLN:HG2	2.11	0.51
2:D:166:LYS:HE2	2:D:170:GLU:OE2	2.10	0.51
1:G:56:LYS:HG2	1:G:57:THR:O	2.10	0.51
1:K:353:GLY:O	1:K:354:TRP:HB2	2.11	0.51
2:L:105:LEU:HB3	2:L:114:MET:HE1	1.92	0.51
1:S:146:MET:HG2	4:S:902:MGD:N7	2.25	0.51
2:T:203:ILE:HD12	2:T:203:ILE:N	2.24	0.51
1:E:457:MET:HE3	8:E:1513:HOH:O	2.09	0.51
1:G:855:MET:HB2	1:G:857:ASN:OD1	2.10	0.51
2:J:105:LEU:HB3	2:J:114:MET:HE2	1.91	0.51
1:K:146:MET:HG2	4:K:902:MGD:N7	2.25	0.51
1:K:533:VAL:HB	1:K:534:PRO:HD3	1.93	0.51
1:Q:100:LEU:CD2	1:Q:534:PRO:HB2	2.39	0.51
2:T:23:CYS:O	2:T:27:HIS:N	2.40	0.51
1:W:418:ALA:HB1	1:W:423:ALA:HB2	1.92	0.51
1:A:510:TYR:O	1:A:513:MET:HG2	2.10	0.51
1:C:155:SER:OG	1:C:409:ILE:HG12	2.09	0.51
1:I:81:LYS:HB2	1:I:112:ILE:HD13	1.93	0.51
2:J:211:GLU:HB2	2:J:231:PHE:HA	1.91	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:2:GLU:HG2	2:L:158:LYS:HG2	1.92	0.51
1:O:610:LYS:HZ2	1:O:618:GLN:HE22	1.59	0.51
1:Q:111:ARG:NH2	1:Q:585:GLU:OE2	2.37	0.51
1:S:144:HIS:HB2	4:S:902:MGD:O1B	2.10	0.51
1:U:187:TRP:CH2	1:U:196:PRO:HB3	2.46	0.51
1:U:353:GLY:O	1:U:354:TRP:HB2	2.11	0.51
2:X:40:GLN:NE2	8:X:942:HOH:O	2.43	0.51
1:A:253:ASN:O	1:A:257:ARG:HG3	2.11	0.51
1:A:494:TRP:HE1	1:A:525:GLN:HE21	1.58	0.51
1:C:66:PHE:HA	1:C:69:MET:CE	2.41	0.51
1:I:111:ARG:NH2	1:I:585:GLU:OE2	2.42	0.51
1:K:140:THR:HB	1:K:169:ALA:HB3	1.92	0.51
1:M:175:SER:OG	6:M:905:BTT:C5	2.59	0.51
2:P:71:CYS:HB2	2:P:182:THR:O	2.10	0.51
2:P:23:CYS:HB3	2:P:39:MET:HE3	1.93	0.51
1:Q:649:LYS:HE2	8:Q:1459:HOH:O	2.10	0.51
1:Q:730:TYR:CE1	1:Q:794:ASN:HA	2.45	0.51
1:S:387:TRP:CE2	1:S:389:THR:HA	2.45	0.51
1:C:786:ASN:ND2	1:C:804:GLN:HA	2.26	0.51
2:F:71:CYS:HB2	2:F:182:THR:O	2.10	0.51
2:H:254:LYS:HD2	2:H:274:LEU:OXT	2.10	0.51
1:K:825:PRO:HD2	8:K:1330:HOH:O	2.10	0.51
1:M:100:LEU:CD1	1:M:105:PRO:HG3	2.40	0.51
2:N:68:CYS:HB2	2:N:126:CYS:HB2	1.90	0.51
1:S:66:PHE:HA	1:S:69:MET:HE3	1.92	0.51
1:S:797:GLY:HA2	1:S:875:TYR:CE2	2.45	0.51
2:T:143:PRO:HB3	7:T:303:SF4:S1	2.51	0.51
1:A:142:SER:CB	4:A:902:MGD:O1A	2.59	0.51
1:C:628:TYR:CE2	1:C:643:PRO:HG2	2.45	0.51
1:I:15:PRO:HD3	1:I:554:PHE:CD1	2.46	0.51
1:I:610:LYS:HZ3	1:I:618:GLN:HE22	1.57	0.51
2:R:71:CYS:HB2	2:R:182:THR:O	2.11	0.51
2:V:18:ASN:HB2	7:V:302:SF4:S1	2.51	0.51
2:B:114:MET:HE3	2:B:123:ALA:HB1	1.93	0.51
1:I:47:ARG:HD2	1:I:241:LEU:HD22	1.91	0.51
1:K:451:LYS:HG3	1:K:461:PHE:CE2	2.46	0.51
1:K:673:ASN:H	1:K:673:ASN:HD22	1.59	0.51
1:O:510:TYR:O	1:O:513:MET:HG2	2.09	0.51
1:Q:138:LEU:HB2	1:Q:490:ILE:HD12	1.93	0.51
2:X:4:TYR:CE2	2:X:158:LYS:HD2	2.45	0.51
1:A:644:ASP:O	1:A:646:PRO:HD3	2.11	0.51
2:H:46:MET:HE1	2:H:65:PRO:CA	2.41	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:44:ILE:HD11	1:I:394:PRO:HG2	1.92	0.51
1:O:476:GLN:OE1	1:O:708:ARG:NH2	2.44	0.51
1:Q:510:TYR:O	1:Q:513:MET:HG2	2.11	0.51
1:U:146:MET:HE1	1:U:544:THR:CB	2.39	0.51
1:W:56:LYS:HG2	1:W:57:THR:O	2.11	0.51
1:C:218:ASP:OD2	1:C:253:ASN:HB2	2.11	0.50
1:C:696:LYS:O	1:C:700:GLU:HG3	2.11	0.50
1:C:708:ARG:HD2	8:C:1044:HOH:O	2.11	0.50
1:C:753:TYR:HB3	2:D:24:MET:CE	2.42	0.50
1:G:81:LYS:HB2	1:G:112:ILE:HD13	1.93	0.50
1:I:644:ASP:C	1:I:646:PRO:HD3	2.32	0.50
1:O:85:PHE:CE2	1:O:87:PRO:HG3	2.46	0.50
1:A:855:MET:HB2	1:A:857:ASN:OD1	2.10	0.50
1:E:175:SER:OG	6:E:905:BTT:C5	2.59	0.50
1:G:258:LEU:HG	1:G:259:VAL:HG13	1.93	0.50
2:H:106:LEU:HD23	2:H:114:MET:CE	2.41	0.50
1:M:451:LYS:HG3	1:M:461:PHE:CE2	2.46	0.50
1:M:75:ARG:HH21	1:M:543:CYS:HA	1.77	0.50
1:O:100:LEU:CD1	1:O:105:PRO:HG3	2.42	0.50
2:B:5:TYR:HB2	2:B:157:LEU:HD13	1.94	0.50
2:D:203:ILE:N	2:D:203:ILE:HD12	2.26	0.50
2:D:5:TYR:HB2	2:D:157:LEU:CD1	2.42	0.50
1:E:211:MET:HE3	2:F:231:PHE:CZ	2.46	0.50
2:F:166:LYS:HG2	2:F:170:GLU:OE2	2.12	0.50
1:G:166:PHE:HD2	8:G:1364:HOH:O	1.94	0.50
1:G:142:SER:CB	4:G:902:MGD:O1A	2.59	0.50
2:J:203:ILE:N	2:J:203:ILE:HD12	2.27	0.50
1:K:100:LEU:HD12	1:K:105:PRO:HG3	1.93	0.50
1:K:716:PRO:HB3	1:K:723:HIS:CD2	2.46	0.50
1:Q:296:ASN:HB3	1:Q:657:PHE:CZ	2.47	0.50
1:Q:451:LYS:HG3	1:Q:461:PHE:CE2	2.46	0.50
1:Q:175:SER:OG	6:Q:905:BTT:C5	2.60	0.50
1:U:56:LYS:HG2	1:U:57:THR:O	2.11	0.50
2:V:96:PRO:O	2:V:100:LYS:HG3	2.11	0.50
1:C:146:MET:HE2	1:C:545:ASN:H	1.76	0.50
2:D:142:MET:CE	2:D:146:ALA:HB1	2.41	0.50
1:G:505:THR:O	1:G:506:ALA:C	2.50	0.50
1:G:510:TYR:O	1:G:513:MET:HG2	2.10	0.50
1:I:387:TRP:CE2	1:I:389:THR:HA	2.46	0.50
1:I:134:PRO:HB2	1:I:439:LEU:HD11	1.92	0.50
1:K:387:TRP:CE2	1:K:389:THR:HA	2.46	0.50
1:M:69:MET:HE1	1:M:754:MET:HE3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:387:TRP:CE2	1:O:389:THR:HA	2.46	0.50
1:Q:770:TRP:HB3	1:Q:801:LEU:HD23	1.93	0.50
1:S:142:SER:CB	4:S:902:MGD:O1A	2.59	0.50
1:W:353:GLY:O	1:W:354:TRP:HB2	2.11	0.50
1:W:400:TYR:CE1	1:W:421:LYS:HD2	2.47	0.50
1:E:786:ASN:ND2	1:E:805:VAL:H	2.04	0.50
1:G:630:THR:OG1	1:G:633:GLU:HG3	2.11	0.50
1:K:146:MET:HE2	1:K:545:ASN:H	1.77	0.50
1:M:166:PHE:N	1:M:439:LEU:HD12	2.27	0.50
1:O:75:ARG:NH2	1:O:543:CYS:HA	2.26	0.50
2:R:59:ASN:H	2:R:59:ASN:HD22	1.59	0.50
2:V:5:TYR:HB2	2:V:157:LEU:HD11	1.93	0.50
1:W:797:GLY:HA2	1:W:875:TYR:CE2	2.46	0.50
2:B:5:TYR:O	2:B:157:LEU:HD12	2.11	0.50
1:E:476:GLN:OE1	1:E:708:ARG:NH2	2.45	0.50
2:H:166:LYS:HG2	2:H:170:GLU:OE2	2.11	0.50
1:I:610:LYS:HB3	1:I:614:ALA:HB3	1.92	0.50
1:M:296:ASN:HB3	1:M:657:PHE:CZ	2.46	0.50
2:N:21:MET:HE2	2:N:21:MET:HA	1.93	0.50
1:O:610:LYS:HB3	1:O:614:ALA:HB3	1.93	0.50
8:Q:1681:HOH:O	1:S:871:LYS:HE2	2.12	0.50
1:A:426:MET:HE1	1:A:618:GLN:HG2	1.91	0.50
2:B:105:LEU:HB3	2:B:114:MET:CE	2.42	0.50
1:C:35:ASP:OD1	1:C:55:ARG:HD3	2.11	0.50
2:F:68:CYS:HB2	2:F:126:CYS:HB2	1.91	0.50
1:G:561:ILE:HG22	1:G:564:ASN:HB3	1.93	0.50
1:K:56:LYS:HG2	1:K:57:THR:O	2.11	0.50
2:N:143:PRO:HB3	7:N:303:SF4:S1	2.52	0.50
1:S:729:LYS:HD2	8:S:1134:HOH:O	2.11	0.50
1:U:144:HIS:HB2	4:U:902:MGD:O1B	2.12	0.50
1:W:146:MET:HE3	1:W:544:THR:HA	1.92	0.50
1:E:187:TRP:CH2	1:E:196:PRO:HB3	2.46	0.50
1:E:144:HIS:HB2	4:E:902:MGD:O1B	2.12	0.50
2:H:166:LYS:O	2:H:170:GLU:HG3	2.11	0.50
1:I:146:MET:HE2	1:I:545:ASN:H	1.77	0.50
1:I:28:MET:HE1	1:I:67:LYS:N	2.27	0.50
1:M:510:TYR:O	1:M:513:MET:HG2	2.12	0.50
1:M:738:HIS:HE2	4:M:902:MGD:H15	1.60	0.50
1:O:501:LEU:HD13	1:O:823:TYR:CD2	2.47	0.50
1:O:146:MET:HE3	1:O:545:ASN:OD1	2.12	0.50
1:O:737:PRO:HG3	4:O:903:MGD:H2'	1.94	0.50
2:P:18:ASN:HB2	7:P:302:SF4:S1	2.52	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:T:46:MET:HE1	2:T:65:PRO:CA	2.41	0.50
1:A:100:LEU:CD1	1:A:105:PRO:HG3	2.42	0.50
1:E:81:LYS:HB2	1:E:112:ILE:HD13	1.92	0.50
2:F:216:VAL:HG13	2:F:223:GLU:HG3	1.93	0.50
2:F:68:CYS:HB3	2:F:70:HIS:ND1	2.27	0.50
2:H:46:MET:CE	2:H:66:THR:N	2.74	0.50
1:I:356:GLY:H	4:I:903:MGD:H5'2	1.75	0.50
2:J:210:PHE:HD2	2:J:213:ALA:HB2	1.77	0.50
2:N:114:MET:CE	2:N:123:ALA:HB1	2.42	0.50
1:A:356:GLY:H	4:A:903:MGD:C5'	2.23	0.49
1:A:823:TYR:CE2	1:A:825:PRO:HG3	2.46	0.49
2:B:104:GLU:H	2:B:104:GLU:CD	2.12	0.49
1:C:800:ILE:HD12	1:C:800:ILE:N	2.27	0.49
1:I:561:ILE:HG22	1:I:564:ASN:HB3	1.93	0.49
1:K:735:LEU:H	1:K:735:LEU:HD23	1.77	0.49
1:U:557:CYS:N	1:U:564:ASN:HD21	1.93	0.49
1:A:708:ARG:HD2	8:A:1044:HOH:O	2.11	0.49
1:I:218:ASP:OD2	1:I:253:ASN:HB2	2.12	0.49
1:M:770:TRP:HB3	1:M:801:LEU:HD23	1.94	0.49
1:Q:144:HIS:HB2	4:Q:902:MGD:O1B	2.13	0.49
1:S:263:TRP:CZ2	1:S:265:SER:HB2	2.47	0.49
1:U:81:LYS:HB2	1:U:112:ILE:HD13	1.94	0.49
1:A:696:LYS:O	1:A:700:GLU:HG3	2.11	0.49
1:E:140:THR:HB	1:E:169:ALA:HB3	1.93	0.49
1:E:426:MET:HA	1:E:426:MET:CE	2.40	0.49
1:G:377:GLN:O	1:G:381:LYS:HE2	2.12	0.49
1:K:269:GLY:HA2	1:K:362:HIS:CE1	2.47	0.49
1:K:141:PRO:CA	1:K:496:TYR:HB3	2.41	0.49
1:M:355:GLY:CA	4:M:903:MGD:O1B	2.56	0.49
1:O:21:LYS:HB3	1:O:26:ILE:HD11	1.93	0.49
1:S:211:MET:HE3	1:S:244:ASP:HB2	1.94	0.49
1:A:561:ILE:CG2	1:A:564:ASN:HB3	2.41	0.49
1:E:74:LEU:HD12	1:E:750:LYS:HA	1.94	0.49
1:G:426:MET:HE1	1:G:618:GLN:HG2	1.92	0.49
1:O:142:SER:HB3	4:O:902:MGD:H5'2	1.95	0.49
1:O:610:LYS:HZ3	1:O:618:GLN:HE22	1.57	0.49
1:A:426:MET:HE1	1:A:618:GLN:O	2.12	0.49
1:A:75:ARG:NH2	1:A:543:CYS:HA	2.27	0.49
1:A:870:ASP:HB3	1:A:872:TYR:CE1	2.47	0.49
1:M:505:THR:O	1:M:506:ALA:C	2.50	0.49
1:M:617:GLU:HG3	1:M:631:TRP:CG	2.47	0.49
1:S:738:HIS:HE2	4:S:902:MGD:H15	1.58	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:753:TYR:HB3	2:X:24:MET:CE	2.41	0.49
1:A:505:THR:O	1:A:506:ALA:C	2.51	0.49
1:E:557:CYS:N	1:E:564:ASN:HD21	1.92	0.49
1:G:495:LYS:HD2	1:G:514:TYR:OH	2.12	0.49
1:M:767:TYR:HB3	1:M:769:TYR:CE1	2.47	0.49
1:O:426:MET:HE3	1:O:426:MET:CA	2.32	0.49
1:Q:214:PHE:HA	1:Q:347:ALA:HB3	1.95	0.49
1:S:505:THR:O	1:S:506:ALA:C	2.50	0.49
1:S:700:GLU:HG2	8:S:1561:HOH:O	2.12	0.49
2:T:70:HIS:CD2	2:T:92:VAL:H	2.18	0.49
2:D:46:MET:CE	2:D:66:THR:N	2.76	0.49
1:G:165:GLY:HA3	1:G:166:PHE:CB	2.40	0.49
1:G:656:TRP:CD2	1:G:663:LYS:HA	2.48	0.49
1:G:175:SER:OG	6:G:905:BTT:C5	2.60	0.49
1:I:66:PHE:CZ	1:I:146:MET:HE3	2.48	0.49
1:I:175:SER:OG	6:I:905:BTT:C5	2.60	0.49
1:K:2:GLY:O	1:K:21:LYS:HE3	2.13	0.49
1:K:786:ASN:ND2	1:K:804:GLN:HA	2.28	0.49
1:M:142:SER:HB3	4:M:902:MGD:O1A	2.12	0.49
1:Q:146:MET:HE2	1:Q:545:ASN:H	1.77	0.49
1:S:21:LYS:HB3	1:S:26:ILE:HD11	1.94	0.49
1:U:182:GLY:HA3	1:U:364:ILE:HG23	1.95	0.49
2:V:211:GLU:HB2	2:V:231:PHE:HA	1.95	0.49
2:V:71:CYS:HA	2:V:184:PRO:HA	1.95	0.49
1:W:387:TRP:CE2	1:W:389:THR:HA	2.48	0.49
2:H:109:CYS:HB3	2:H:112:GLY:H	1.78	0.49
1:I:644:ASP:O	1:I:646:PRO:HD3	2.13	0.49
1:M:211:MET:CE	2:N:231:PHE:CZ	2.95	0.49
1:M:328:PRO:HB2	1:M:331:GLU:HG3	1.95	0.49
1:M:708:ARG:HD2	8:M:1044:HOH:O	2.12	0.49
1:O:469:ALA:HA	8:O:1516:HOH:O	2.12	0.49
1:S:100:LEU:HD12	1:S:105:PRO:HG3	1.94	0.49
1:U:114:TRP:CZ2	1:U:541:PRO:HD2	2.48	0.49
1:U:75:ARG:NH2	1:U:543:CYS:HA	2.28	0.49
1:A:111:ARG:NH2	1:A:585:GLU:OE2	2.45	0.49
2:B:59:ASN:H	2:B:59:ASN:HD22	1.58	0.49
2:D:13:CYS:HB3	2:D:63:TYR:HB2	1.95	0.49
2:F:114:MET:CE	2:F:123:ALA:HB1	2.42	0.49
1:G:414:GLU:OE2	1:G:441:THR:HA	2.12	0.49
1:G:426:MET:HE1	1:G:618:GLN:O	2.12	0.49
1:G:629:MET:HE1	1:G:634:PHE:HA	1.94	0.49
1:I:96:ARG:HD2	1:I:514:TYR:O	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:35:ASP:OD1	1:K:55:ARG:HD3	2.11	0.49
2:L:5:TYR:HB2	2:L:157:LEU:HD11	1.94	0.49
1:Q:1:MET:H3	1:Q:22:ASP:CG	2.15	0.49
1:Q:378:GLY:O	1:Q:381:LYS:HG2	2.12	0.49
2:T:94:ILE:O	2:T:96:PRO:HD3	2.13	0.49
1:W:253:ASN:O	1:W:257:ARG:HG3	2.12	0.49
1:W:561:ILE:CG2	1:W:564:ASN:HB3	2.41	0.49
1:C:146:MET:HE3	1:C:545:ASN:OD1	2.13	0.49
1:C:753:TYR:HB3	2:D:24:MET:HE3	1.94	0.49
1:M:400:TYR:CZ	1:M:421:LYS:HD2	2.48	0.49
1:O:786:ASN:HD21	1:O:804:GLN:HA	1.77	0.49
1:W:426:MET:HE3	1:W:426:MET:CA	2.33	0.49
2:X:23:CYS:O	2:X:27:HIS:N	2.41	0.49
2:B:106:LEU:HD11	2:B:116:TRP:HB2	1.95	0.48
1:E:146:MET:HE2	1:E:545:ASN:H	1.77	0.48
1:G:541:PRO:HB2	1:G:586:SER:HA	1.95	0.48
1:I:153:ARG:O	1:I:157:TYR:HB3	2.13	0.48
1:I:402:PRO:HG2	1:I:422:PHE:CE1	2.48	0.48
2:N:210:PHE:HD2	2:N:213:ALA:HB2	1.78	0.48
1:O:558:SER:H	1:O:564:ASN:ND2	2.11	0.48
1:Q:630:THR:OG1	1:Q:633:GLU:HG3	2.13	0.48
1:C:355:GLY:N	4:C:903:MGD:O2A	2.43	0.48
1:E:395:LEU:HD13	1:E:571:ARG:HG3	1.95	0.48
1:E:400:TYR:CZ	1:E:421:LYS:HD2	2.49	0.48
1:I:452:ILE:HB	1:I:453:PRO:HD3	1.95	0.48
2:P:106:LEU:HD23	2:P:114:MET:CE	2.42	0.48
1:Q:452:ILE:HB	1:Q:453:PRO:HD3	1.95	0.48
1:Q:257:ARG:HD3	2:R:61:ILE:HG21	1.95	0.48
1:S:476:GLN:OE1	1:S:708:ARG:NH2	2.46	0.48
1:S:56:LYS:HG2	1:S:57:THR:O	2.13	0.48
1:S:644:ASP:O	1:S:646:PRO:HD3	2.13	0.48
1:U:104:ASP:OD2	1:U:107:SER:HB3	2.12	0.48
1:U:558:SER:H	1:U:564:ASN:ND2	2.11	0.48
1:U:801:LEU:HD11	1:U:839:ILE:HD11	1.95	0.48
2:X:7:VAL:HG21	2:X:167:LYS:NZ	2.27	0.48
1:A:377:GLN:O	1:A:381:LYS:HE2	2.14	0.48
1:A:673:ASN:H	1:A:673:ASN:HD22	1.61	0.48
1:A:146:MET:HG2	4:A:902:MGD:N7	2.27	0.48
1:K:476:GLN:OE1	1:K:708:ARG:NH2	2.47	0.48
1:K:644:ASP:C	1:K:646:PRO:HD3	2.33	0.48
1:O:505:THR:O	1:O:506:ALA:C	2.52	0.48
1:U:563:ASP:O	1:U:566:GLN:HG2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:U:708:ARG:HD2	8:U:1047:HOH:O	2.12	0.48
1:A:452:ILE:HB	1:A:453:PRO:HD3	1.95	0.48
1:E:737:PRO:HG3	4:E:903:MGD:H2'	1.95	0.48
2:H:106:LEU:CD2	2:H:114:MET:HB3	2.44	0.48
2:L:106:LEU:HD23	2:L:114:MET:HE3	1.95	0.48
1:O:479:GLN:N	8:O:1176:HOH:O	2.37	0.48
1:O:725:PRO:HD2	8:O:1193:HOH:O	2.14	0.48
2:P:203:ILE:N	2:P:203:ILE:HD12	2.28	0.48
2:R:207:GLY:HA2	1:U:728:VAL:CG1	2.34	0.48
2:R:46:MET:HE1	2:R:65:PRO:CA	2.39	0.48
1:S:696:LYS:HD3	8:S:1660:HOH:O	2.13	0.48
1:S:716:PRO:HB3	1:S:723:HIS:CD2	2.49	0.48
1:S:85:PHE:CE2	1:S:87:PRO:HG3	2.48	0.48
1:U:15:PRO:HD3	1:U:554:PHE:CD1	2.48	0.48
1:W:696:LYS:HD3	8:W:1670:HOH:O	2.12	0.48
1:A:426:MET:HA	1:A:426:MET:CE	2.32	0.48
1:A:69:MET:HE1	1:A:754:MET:HE3	1.95	0.48
1:A:175:SER:OG	6:A:905:BTT:C5	2.61	0.48
2:D:71:CYS:HA	2:D:184:PRO:HA	1.95	0.48
1:I:400:TYR:CE1	1:I:421:LYS:HD2	2.49	0.48
2:J:70:HIS:CD2	2:J:92:VAL:H	2.14	0.48
1:O:218:ASP:OD2	1:O:253:ASN:HB2	2.13	0.48
1:O:214:PHE:HA	1:O:347:ALA:HB3	1.95	0.48
2:R:46:MET:CE	2:R:66:THR:H	2.17	0.48
1:A:636:LYS:HE3	2:X:166:LYS:HE2	1.96	0.48
1:E:353:GLY:O	1:E:354:TRP:HB2	2.14	0.48
2:F:210:PHE:HD2	2:F:213:ALA:HB2	1.79	0.48
1:K:165:GLY:CA	1:K:166:PHE:HB3	2.41	0.48
1:M:797:GLY:HA2	1:M:875:TYR:CE2	2.49	0.48
2:N:68:CYS:HB3	2:N:70:HIS:ND1	2.29	0.48
1:O:35:ASP:OD1	1:O:55:ARG:HD3	2.13	0.48
1:Q:670:PRO:HB3	1:Q:682:GLN:HB2	1.96	0.48
1:W:451:LYS:HG3	1:W:461:PHE:CE2	2.48	0.48
1:A:673:ASN:CG	8:A:1584:HOH:O	2.52	0.48
2:B:10:VAL:HG13	2:B:63:TYR:O	2.14	0.48
1:E:610:LYS:HZ1	1:E:618:GLN:HE22	1.57	0.48
1:G:387:TRP:CE2	1:G:389:THR:HA	2.48	0.48
1:K:426:MET:HE1	1:K:618:GLN:O	2.14	0.48
1:O:28:MET:HE1	1:O:67:LYS:N	2.29	0.48
1:O:141:PRO:CA	1:O:496:TYR:HB3	2.41	0.48
2:P:166:LYS:O	2:P:170:GLU:HG3	2.13	0.48
2:P:40:GLN:HB3	2:P:43:HIS:CE1	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:561:ILE:CG2	1:S:564:ASN:HB3	2.42	0.48
1:S:870:ASP:HB3	1:S:872:TYR:CE1	2.48	0.48
2:T:18:ASN:HB2	7:T:302:SF4:S1	2.53	0.48
2:T:58:ARG:HD2	2:T:268:ASP:OD1	2.13	0.48
1:U:28:MET:HE1	1:U:66:PHE:CB	2.38	0.48
1:U:291:GLU:CD	1:U:291:GLU:H	2.17	0.48
1:C:134:PRO:HB2	1:C:439:LEU:HD11	1.96	0.48
1:E:111:ARG:NH2	1:E:585:GLU:OE2	2.44	0.48
1:E:356:GLY:H	4:E:903:MGD:C5'	2.27	0.48
2:F:59:ASN:ND2	2:F:59:ASN:H	2.12	0.48
2:H:256:TYR:HB2	2:H:274:LEU:HD21	1.95	0.48
2:L:211:GLU:HB2	2:L:231:PHE:HA	1.95	0.48
1:M:153:ARG:O	1:M:157:TYR:HB3	2.14	0.48
1:M:452:ILE:N	1:M:453:PRO:CD	2.76	0.48
2:N:46:MET:HE1	2:N:65:PRO:CA	2.43	0.48
2:T:5:TYR:HB2	2:T:157:LEU:CD1	2.43	0.48
1:U:426:MET:HE2	1:U:426:MET:O	2.13	0.48
1:U:825:PRO:HD2	8:U:1336:HOH:O	2.14	0.48
1:U:823:TYR:CE2	1:U:825:PRO:HG3	2.48	0.48
1:U:142:SER:CB	4:U:902:MGD:O1A	2.62	0.48
1:W:716:PRO:HB3	1:W:723:HIS:CD2	2.49	0.48
2:X:114:MET:HA	2:X:125:LYS:HB3	1.94	0.48
2:X:46:MET:HE1	2:X:65:PRO:CA	2.44	0.48
1:C:114:TRP:CZ2	1:C:541:PRO:HD2	2.49	0.48
1:E:257:ARG:HD3	2:F:61:ILE:HG21	1.96	0.48
2:H:106:LEU:HD22	2:H:114:MET:HB3	1.95	0.48
1:K:134:PRO:HB2	1:K:439:LEU:HD11	1.96	0.48
1:O:426:MET:CE	1:O:426:MET:HA	2.33	0.48
2:P:49:GLU:HG3	2:P:64:ARG:NH2	2.29	0.48
1:Q:387:TRP:CE2	1:Q:389:THR:HA	2.49	0.48
1:W:563:ASP:O	1:W:566:GLN:HG2	2.14	0.48
2:D:142:MET:HE2	2:D:146:ALA:HB1	1.96	0.48
2:D:46:MET:CE	2:D:66:THR:H	2.26	0.48
1:E:730:TYR:CE1	1:E:794:ASN:HA	2.49	0.48
1:E:142:SER:CB	4:E:902:MGD:O1A	2.62	0.48
1:U:716:PRO:HB3	1:U:723:HIS:CD2	2.49	0.48
1:U:356:GLY:N	4:U:903:MGD:PB	2.86	0.48
1:W:28:MET:CE	1:W:66:PHE:HB3	2.44	0.48
2:X:205:VAL:HG11	2:X:252:ASP:OD1	2.14	0.48
1:C:1:MET:H3	1:C:22:ASP:CG	2.17	0.47
2:D:58:ARG:HD2	2:D:268:ASP:OD1	2.14	0.47
1:G:175:SER:HB2	1:G:176:TRP:CE3	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:258:LEU:HG	1:Q:259:VAL:HG13	1.96	0.47
1:W:128:ILE:CD1	1:W:492:MET:HB2	2.43	0.47
1:W:28:MET:HE1	1:W:67:LYS:N	2.29	0.47
1:W:347:ALA:CB	1:W:388:SER:HA	2.44	0.47
2:D:198:TYR:HB3	2:D:238:ASP:HA	1.95	0.47
2:D:23:CYS:O	2:D:26:GLU:N	2.47	0.47
1:E:175:SER:HB2	1:E:176:TRP:CE3	2.49	0.47
1:I:138:LEU:HB2	1:I:490:ILE:HD12	1.95	0.47
1:I:296:ASN:HB3	1:I:657:PHE:CZ	2.50	0.47
1:I:797:GLY:HA2	1:I:875:TYR:CE2	2.50	0.47
1:M:175:SER:HB2	1:M:176:TRP:CE3	2.48	0.47
1:M:831:LYS:HD3	8:M:1576:HOH:O	2.13	0.47
1:M:855:MET:HB2	1:M:857:ASN:OD1	2.14	0.47
2:N:19:CYS:O	2:N:22:GLY:N	2.48	0.47
2:N:203:ILE:HD12	2:N:203:ILE:N	2.28	0.47
1:Q:353:GLY:O	1:Q:354:TRP:HB2	2.14	0.47
1:Q:81:LYS:HB2	1:Q:112:ILE:HD13	1.95	0.47
1:U:855:MET:HB2	1:U:857:ASN:OD1	2.14	0.47
1:W:356:GLY:H	4:W:903:MGD:PB	2.37	0.47
1:A:451:LYS:HG3	1:A:461:PHE:CE2	2.49	0.47
2:B:247:VAL:O	2:B:257:SER:HA	2.14	0.47
1:G:174:ASP:OD1	1:G:175:SER:N	2.47	0.47
1:I:617:GLU:HG3	1:I:631:TRP:CG	2.50	0.47
2:J:18:ASN:HB2	7:J:302:SF4:S1	2.54	0.47
2:N:106:LEU:HD22	2:N:114:MET:HB3	1.95	0.47
2:N:166:LYS:O	2:N:170:GLU:HG3	2.13	0.47
1:U:563:ASP:HA	1:U:565:TYR:CE1	2.48	0.47
2:V:46:MET:HE1	2:V:66:THR:H	1.80	0.47
2:V:46:MET:HE3	2:V:66:THR:N	2.28	0.47
1:W:439:LEU:HD21	1:W:487:TYR:CE2	2.49	0.47
1:A:258:LEU:HG	1:A:259:VAL:HG13	1.95	0.47
1:G:44:ILE:HD11	1:G:394:PRO:HG2	1.97	0.47
1:M:558:SER:H	1:M:564:ASN:ND2	2.13	0.47
1:O:494:TRP:HE1	1:O:525:GLN:HE21	1.62	0.47
1:O:56:LYS:HG2	1:O:57:THR:O	2.14	0.47
1:Q:153:ARG:O	1:Q:157:TYR:HB3	2.14	0.47
1:U:725:PRO:HD2	8:U:1197:HOH:O	2.15	0.47
2:V:114:MET:HA	2:V:125:LYS:HB3	1.96	0.47
2:V:23:CYS:HB3	2:V:39:MET:HE3	1.97	0.47
1:A:66:PHE:HA	1:A:69:MET:HE2	1.96	0.47
2:D:73:ASN:HB3	2:D:182:THR:HA	1.96	0.47
1:E:1:MET:H3	1:E:22:ASP:CG	2.17	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:56:LYS:HG2	1:I:57:THR:O	2.15	0.47
2:J:189:LYS:HD2	8:J:997:HOH:O	2.15	0.47
1:K:85:PHE:CE2	1:K:87:PRO:HG3	2.50	0.47
1:M:187:TRP:CH2	1:M:196:PRO:HB3	2.50	0.47
1:M:533:VAL:HB	1:M:534:PRO:HD3	1.96	0.47
2:N:164:MET:O	2:N:168:VAL:HG23	2.15	0.47
2:N:23:CYS:HB3	2:N:39:MET:HE3	1.97	0.47
1:O:146:MET:HE1	1:O:544:THR:CB	2.42	0.47
1:Q:558:SER:H	1:Q:564:ASN:ND2	2.13	0.47
1:S:211:MET:HE1	2:T:231:PHE:CZ	2.49	0.47
1:U:211:MET:HE3	1:U:244:ASP:HB2	1.97	0.47
1:A:138:LEU:HB2	1:A:490:ILE:HD12	1.96	0.47
1:A:730:TYR:CE1	1:A:794:ASN:HA	2.49	0.47
1:C:717:ALA:HB3	1:C:720:SER:HB3	1.97	0.47
1:E:505:THR:O	1:E:506:ALA:C	2.53	0.47
1:E:855:MET:HB2	1:E:857:ASN:OD1	2.14	0.47
1:G:296:ASN:HB3	1:G:657:PHE:CZ	2.49	0.47
2:J:23:CYS:HB3	2:J:39:MET:HE3	1.97	0.47
1:M:426:MET:HE2	1:M:618:GLN:HG2	1.96	0.47
1:O:738:HIS:HE2	4:O:902:MGD:H15	1.62	0.47
1:S:610:LYS:HB3	1:S:614:ALA:HB3	1.96	0.47
2:N:207:GLY:CA	1:S:728:VAL:HG12	2.31	0.47
2:V:203:ILE:HD12	2:V:203:ILE:N	2.29	0.47
1:W:476:GLN:OE1	1:W:708:ARG:NH2	2.48	0.47
1:W:28:MET:HE3	1:W:63:THR:O	2.14	0.47
1:A:291:GLU:H	1:A:291:GLU:CD	2.18	0.47
1:C:146:MET:HG2	4:C:902:MGD:N7	2.29	0.47
2:D:213:ALA:O	2:D:228:GLU:HA	2.14	0.47
2:D:216:VAL:HG13	2:D:223:GLU:HG3	1.97	0.47
1:E:21:LYS:CB	1:E:26:ILE:HD11	2.44	0.47
1:K:15:PRO:HD3	1:K:554:PHE:CD1	2.50	0.47
1:M:218:ASP:OD2	1:M:253:ASN:HB2	2.14	0.47
1:M:56:LYS:HG2	1:M:57:THR:O	2.14	0.47
2:R:23:CYS:HB3	2:R:39:MET:HE3	1.95	0.47
1:S:114:TRP:CZ2	1:S:541:PRO:HD2	2.49	0.47
1:S:495:LYS:HD2	1:S:514:TYR:OH	2.15	0.47
1:W:730:TYR:CE1	1:W:794:ASN:HA	2.49	0.47
2:X:46:MET:CE	2:X:66:THR:H	2.21	0.47
1:C:571:ARG:HB2	1:C:642:VAL:HB	1.96	0.47
2:D:104:GLU:H	2:D:104:GLU:CD	2.18	0.47
2:D:23:CYS:HB3	2:D:39:MET:HE3	1.97	0.47
2:F:142:MET:HE1	8:F:428:HOH:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:J:166:LYS:HG2	2:J:170:GLU:OE2	2.15	0.47
1:K:730:TYR:CE1	1:K:794:ASN:HA	2.50	0.47
1:O:114:TRP:CZ2	1:O:541:PRO:HD2	2.50	0.47
1:Q:786:ASN:ND2	1:Q:804:GLN:HA	2.29	0.47
1:S:214:PHE:HA	1:S:347:ALA:HB3	1.97	0.47
2:V:68:CYS:CB	2:V:126:CYS:CB	2.84	0.47
1:W:673:ASN:HD22	1:W:673:ASN:H	1.61	0.47
1:W:146:MET:HG2	4:W:902:MGD:N7	2.29	0.47
1:A:347:ALA:CB	1:A:388:SER:HA	2.44	0.47
1:G:69:MET:HE2	1:G:754:MET:HE1	1.97	0.47
1:G:737:PRO:CG	4:G:903:MGD:H2'	2.45	0.47
1:I:66:PHE:HZ	1:I:146:MET:HE3	1.78	0.47
2:J:142:MET:HE2	2:J:146:ALA:HB1	1.97	0.47
1:K:118:THR:O	1:K:122:VAL:HG23	2.15	0.47
2:N:216:VAL:HG13	2:N:223:GLU:HG3	1.96	0.47
1:O:44:ILE:HD11	1:O:394:PRO:HG2	1.97	0.47
2:P:70:HIS:CD2	2:P:92:VAL:H	2.17	0.47
1:Q:218:ASP:OD2	1:Q:253:ASN:HB2	2.14	0.47
1:S:153:ARG:O	1:S:157:TYR:HB3	2.14	0.47
1:S:55:ARG:HD2	8:S:1627:HOH:O	2.15	0.47
1:U:387:TRP:CE2	1:U:389:THR:HA	2.49	0.47
1:U:476:GLN:OE1	1:U:708:ARG:NH2	2.48	0.47
1:W:786:ASN:ND2	1:W:804:GLN:HA	2.30	0.47
2:D:23:CYS:HB3	2:D:39:MET:CE	2.45	0.47
1:E:28:MET:HE1	1:E:67:LYS:N	2.29	0.47
1:E:495:LYS:HD3	8:E:1107:HOH:O	2.15	0.47
1:E:617:GLU:HG3	1:E:631:TRP:CG	2.49	0.47
1:G:218:ASP:OD2	1:G:253:ASN:HB2	2.14	0.47
1:G:644:ASP:C	1:G:646:PRO:HD3	2.34	0.47
2:J:166:LYS:O	2:J:170:GLU:HG3	2.14	0.47
2:R:143:PRO:HB3	7:R:303:SF4:S1	2.55	0.47
2:T:46:MET:CE	2:T:66:THR:N	2.77	0.47
1:W:644:ASP:C	1:W:646:PRO:HD3	2.35	0.47
1:W:361:SER:OG	1:W:717:ALA:HB1	2.15	0.47
2:B:105:LEU:HB3	2:B:114:MET:HE2	1.97	0.47
1:C:56:LYS:HG2	1:C:57:THR:O	2.15	0.47
1:C:75:ARG:NH2	1:C:543:CYS:HA	2.30	0.47
2:D:106:LEU:HD23	2:D:114:MET:HE3	1.96	0.47
1:G:395:LEU:HD12	1:G:566:GLN:HA	1.97	0.47
1:K:1:MET:H3	1:K:22:ASP:CG	2.18	0.47
1:K:142:SER:HB3	4:K:902:MGD:O1A	2.14	0.47
1:M:495:LYS:HD2	1:M:514:TYR:OH	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:N:201:ALA:HB2	2:N:269:LEU:HB2	1.97	0.47
1:Q:75:ARG:HH21	1:Q:543:CYS:HA	1.80	0.47
1:U:176:TRP:O	1:U:177:GLU:C	2.53	0.47
2:V:142:MET:CE	2:V:146:ALA:HB1	2.45	0.47
1:W:499:PRO:HG3	4:W:902:MGD:O5'	2.15	0.47
1:W:870:ASP:HB3	1:W:872:TYR:CE1	2.50	0.47
1:A:100:LEU:HD12	1:A:105:PRO:HG3	1.97	0.46
1:C:452:ILE:HB	1:C:453:PRO:HD3	1.98	0.46
1:E:378:GLY:O	1:E:381:LYS:HG2	2.15	0.46
2:F:21:MET:CA	2:F:21:MET:HE2	2.45	0.46
1:I:13:GLY:HA3	1:I:63:THR:OG1	2.15	0.46
1:I:738:HIS:HE2	4:I:902:MGD:H15	1.63	0.46
1:K:253:ASN:O	1:K:257:ARG:HG3	2.16	0.46
1:K:521:PHE:CE2	1:K:523:VAL:CG2	2.99	0.46
2:L:68:CYS:CB	2:L:126:CYS:CB	2.85	0.46
2:L:143:PRO:HB3	7:L:303:SF4:S1	2.55	0.46
1:M:656:TRP:CD2	1:M:663:LYS:HA	2.50	0.46
1:O:9:ASN:HA	1:O:576:GLN:HA	1.97	0.46
1:O:66:PHE:HA	1:O:69:MET:HE2	1.98	0.46
1:S:563:ASP:HA	1:S:565:TYR:CE1	2.49	0.46
2:T:68:CYS:CB	2:T:126:CYS:CB	2.84	0.46
1:U:166:PHE:N	1:U:439:LEU:HD12	2.30	0.46
2:V:59:ASN:ND2	2:V:59:ASN:H	2.13	0.46
1:W:800:ILE:N	1:W:800:ILE:HD12	2.30	0.46
2:X:23:CYS:HB3	2:X:39:MET:CE	2.45	0.46
1:A:644:ASP:C	1:A:646:PRO:HD3	2.36	0.46
1:E:9:ASN:HA	1:E:576:GLN:HA	1.96	0.46
2:F:23:CYS:HB3	2:F:39:MET:HE3	1.97	0.46
1:I:495:LYS:CD	1:I:514:TYR:OH	2.63	0.46
2:J:10:VAL:HG13	2:J:63:TYR:O	2.15	0.46
2:J:216:VAL:HG13	2:J:223:GLU:HG3	1.96	0.46
1:M:96:ARG:HD2	1:M:514:TYR:O	2.15	0.46
1:M:146:MET:HE3	1:M:544:THR:CB	2.44	0.46
1:M:66:PHE:HA	1:M:69:MET:CE	2.45	0.46
1:O:175:SER:OG	6:O:905:BTT:C5	2.64	0.46
2:P:5:TYR:HB2	2:P:157:LEU:HD11	1.97	0.46
1:U:604:GLU:HB3	1:U:605:MET:CE	2.45	0.46
1:A:211:MET:HE1	2:B:231:PHE:CZ	2.48	0.46
1:E:15:PRO:HD3	1:E:554:PHE:CD1	2.50	0.46
2:F:2:GLU:HG2	2:F:158:LYS:HG2	1.98	0.46
1:O:356:GLY:N	4:O:903:MGD:O5'	2.39	0.46
2:P:210:PHE:CE2	2:P:251:ALA:HB1	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:644:ASP:C	1:S:646:PRO:HD3	2.35	0.46
1:A:35:ASP:OD1	1:A:55:ARG:HD3	2.15	0.46
1:A:56:LYS:HG2	1:A:57:THR:O	2.16	0.46
1:C:644:ASP:O	1:C:646:PRO:HD3	2.15	0.46
1:G:146:MET:HG2	4:G:902:MGD:N7	2.30	0.46
1:I:214:PHE:HA	1:I:347:ALA:HB3	1.96	0.46
1:K:175:SER:OG	6:K:905:BTT:C5	2.63	0.46
2:L:162:GLU:CD	2:L:162:GLU:N	2.69	0.46
1:Q:140:THR:HB	1:Q:169:ALA:HB3	1.97	0.46
1:S:426:MET:CE	1:S:426:MET:HA	2.38	0.46
1:S:656:TRP:CD2	1:S:663:LYS:HA	2.51	0.46
1:U:521:PHE:CE2	1:U:523:VAL:CG2	2.98	0.46
2:V:205:VAL:HG13	2:V:254:LYS:NZ	2.29	0.46
1:G:28:MET:HE1	1:G:67:LYS:N	2.29	0.46
2:J:13:CYS:HB3	2:J:63:TYR:HB2	1.97	0.46
1:K:146:MET:HE2	1:K:544:THR:HB	1.97	0.46
1:O:165:GLY:HA3	1:O:166:PHE:CB	2.41	0.46
1:O:353:GLY:O	1:O:354:TRP:HB2	2.16	0.46
1:O:182:GLY:HA3	1:O:364:ILE:HG23	1.98	0.46
1:Q:610:LYS:NZ	1:Q:618:GLN:NE2	2.56	0.46
1:Q:753:TYR:HB3	2:R:24:MET:CE	2.43	0.46
2:R:76:CYS:O	2:R:80:GLY:N	2.49	0.46
1:S:69:MET:HE1	1:S:754:MET:HE3	1.98	0.46
1:S:501:LEU:HD13	1:S:823:TYR:CG	2.50	0.46
1:U:528:TRP:CD2	1:U:750:LYS:HD3	2.51	0.46
2:V:5:TYR:CD2	2:V:164:MET:HG2	2.51	0.46
1:W:165:GLY:HA3	1:W:166:PHE:CB	2.40	0.46
1:E:644:ASP:C	1:E:646:PRO:HD3	2.36	0.46
1:E:656:TRP:CD2	1:E:663:LYS:HA	2.51	0.46
2:H:59:ASN:HD22	2:H:59:ASN:H	1.64	0.46
1:I:253:ASN:O	1:I:257:ARG:HG3	2.14	0.46
1:K:146:MET:HE1	1:K:544:THR:CB	2.44	0.46
1:K:155:SER:OG	1:K:409:ILE:HG12	2.16	0.46
1:K:499:PRO:HG3	4:K:902:MGD:O5'	2.14	0.46
2:L:203:ILE:N	2:L:203:ILE:HD12	2.30	0.46
1:M:144:HIS:HB2	4:M:902:MGD:O1B	2.16	0.46
1:M:610:LYS:HZ1	1:M:618:GLN:HE22	1.59	0.46
1:Q:505:THR:O	1:Q:506:ALA:C	2.53	0.46
4:Q:903:MGD:O1B	4:Q:903:MGD:C4'	2.62	0.46
2:T:205:VAL:HG13	2:T:254:LYS:NZ	2.30	0.46
1:U:617:GLU:HG3	1:U:631:TRP:CG	2.51	0.46
1:A:15:PRO:HD3	1:A:554:PHE:CD1	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:75:ARG:HH21	1:A:543:CYS:HA	1.80	0.46
2:D:106:LEU:N	2:D:114:MET:HE2	2.31	0.46
1:E:400:TYR:CE1	1:E:421:LYS:HD2	2.51	0.46
1:E:75:ARG:NH2	1:E:543:CYS:HA	2.30	0.46
1:I:12:THR:O	1:I:226:TYR:HA	2.16	0.46
1:O:176:TRP:O	1:O:177:GLU:C	2.54	0.46
1:O:144:HIS:HB2	4:O:902:MGD:O1B	2.15	0.46
1:Q:118:THR:O	1:Q:122:VAL:HG23	2.15	0.46
2:V:102:LYS:HB3	2:V:104:GLU:OE2	2.16	0.46
1:W:146:MET:HE3	1:W:544:THR:CB	2.46	0.46
1:C:767:TYR:HB3	1:C:769:TYR:CE1	2.50	0.46
1:E:253:ASN:O	1:E:257:ARG:HG3	2.16	0.46
2:F:142:MET:CE	2:F:146:ALA:HB1	2.45	0.46
1:G:738:HIS:HE2	4:G:902:MGD:H15	1.64	0.46
1:M:353:GLY:O	1:M:354:TRP:HB2	2.16	0.46
1:M:460:LYS:HG3	8:M:1232:HOH:O	2.16	0.46
1:Q:460:LYS:HG3	8:Q:1229:HOH:O	2.16	0.46
2:R:68:CYS:HB3	2:R:70:HIS:ND1	2.30	0.46
2:T:142:MET:CE	2:T:146:ALA:HB1	2.46	0.46
1:U:362:HIS:HB3	1:U:717:ALA:HB2	1.97	0.46
1:W:452:ILE:HB	1:W:453:PRO:HD3	1.98	0.46
2:B:176:ILE:HG22	2:B:177:LYS:HG3	1.97	0.46
1:C:561:ILE:CG2	1:C:564:ASN:HB3	2.45	0.46
2:D:70:HIS:HD2	2:D:92:VAL:N	2.08	0.46
1:E:561:ILE:CG2	1:E:564:ASN:HB3	2.46	0.46
2:F:143:PRO:HB3	7:F:303:SF4:S1	2.56	0.46
1:K:495:LYS:HD2	1:K:514:TYR:OH	2.16	0.46
1:K:142:SER:CB	4:K:902:MGD:O1A	2.64	0.46
1:M:12:THR:O	1:M:226:TYR:HA	2.16	0.46
1:M:257:ARG:HD3	2:N:61:ILE:HG21	1.97	0.46
1:O:323:GLU:HB2	8:O:1569:HOH:O	2.15	0.46
2:R:87:ARG:HG3	2:R:91:ILE:O	2.15	0.46
2:T:216:VAL:HG13	2:T:223:GLU:HG3	1.97	0.46
1:U:265:SER:O	1:U:810:GLN:NE2	2.49	0.46
1:W:460:LYS:HE3	8:W:1232:HOH:O	2.16	0.46
1:W:426:MET:HE3	1:W:622:ALA:HB2	1.97	0.46
1:C:100:LEU:CD1	1:C:105:PRO:HG3	2.45	0.46
2:D:106:LEU:HD23	2:D:114:MET:CE	2.46	0.46
1:G:460:LYS:HE3	8:G:1230:HOH:O	2.16	0.46
4:G:903:MGD:O2A	4:G:903:MGD:O2B	2.34	0.46
2:P:105:LEU:C	2:P:114:MET:HE2	2.36	0.46
2:P:105:LEU:HB3	2:P:114:MET:CE	2.45	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:328:PRO:HB2	1:Q:331:GLU:HG3	1.98	0.46
2:R:58:ARG:HD2	2:R:268:ASP:OD1	2.16	0.46
1:S:528:TRP:CG	1:S:750:LYS:HD3	2.51	0.46
1:U:452:ILE:N	1:U:453:PRO:CD	2.79	0.46
2:X:142:MET:HE2	2:X:146:ALA:HB1	1.97	0.46
1:A:395:LEU:HD12	1:A:566:GLN:HA	1.98	0.45
1:A:13:GLY:HA3	1:A:63:THR:OG1	2.16	0.45
1:C:408:GLY:HA2	1:C:619:TYR:HE1	1.80	0.45
1:E:13:GLY:HA3	1:E:63:THR:OG1	2.16	0.45
1:E:708:ARG:HD2	8:E:1044:HOH:O	2.16	0.45
1:G:452:ILE:HB	1:G:453:PRO:HD3	1.98	0.45
1:I:696:LYS:O	1:I:700:GLU:HG3	2.16	0.45
1:K:28:MET:HE1	1:K:66:PHE:HB3	1.96	0.45
1:S:521:PHE:CE2	1:S:523:VAL:CG2	2.99	0.45
1:U:12:THR:O	1:U:226:TYR:HA	2.16	0.45
1:U:561:ILE:CG2	1:U:564:ASN:HB3	2.46	0.45
1:U:738:HIS:HE2	4:U:902:MGD:H15	1.64	0.45
1:W:400:TYR:CZ	1:W:421:LYS:HD2	2.51	0.45
1:A:452:ILE:N	1:A:453:PRO:CD	2.80	0.45
1:A:825:PRO:HD2	8:A:1333:HOH:O	2.15	0.45
1:A:96:ARG:HD2	1:A:514:TYR:O	2.16	0.45
1:C:44:ILE:HD11	1:C:394:PRO:HG2	1.98	0.45
1:E:153:ARG:O	1:E:157:TYR:HB3	2.16	0.45
1:G:128:ILE:CD1	1:G:492:MET:HB2	2.46	0.45
2:H:210:PHE:HD2	2:H:213:ALA:HB2	1.81	0.45
1:I:452:ILE:N	1:I:453:PRO:CD	2.79	0.45
1:K:452:ILE:N	1:K:453:PRO:CD	2.79	0.45
1:K:501:LEU:HD13	1:K:823:TYR:CD2	2.52	0.45
1:K:505:THR:O	1:K:506:ALA:C	2.55	0.45
1:Q:2:GLY:O	1:Q:21:LYS:HE3	2.16	0.45
2:R:142:MET:HE1	8:R:429:HOH:O	2.16	0.45
1:S:197:GLU:HG3	1:S:653:ALA:HB1	1.98	0.45
1:U:498:GLY:N	1:U:499:PRO:HD3	2.31	0.45
1:A:378:GLY:O	1:A:381:LYS:HG2	2.16	0.45
2:B:112:GLY:HA2	8:B:519:HOH:O	2.16	0.45
2:B:68:CYS:CB	2:B:126:CYS:CB	2.84	0.45
1:C:418:ALA:HB1	1:C:423:ALA:HB2	1.97	0.45
1:E:66:PHE:HA	1:E:69:MET:HE2	1.98	0.45
1:K:738:HIS:HE2	4:K:902:MGD:H15	1.64	0.45
1:M:786:ASN:HD21	1:M:804:GLN:HA	1.80	0.45
1:M:730:TYR:CZ	1:M:794:ASN:HA	2.51	0.45
2:N:2:GLU:CG	2:N:158:LYS:HG2	2.43	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:15:PRO:HD3	1:O:554:PHE:CD1	2.51	0.45
1:O:870:ASP:HB3	1:O:872:TYR:CE1	2.51	0.45
1:U:13:GLY:HA3	1:U:63:THR:OG1	2.17	0.45
1:U:21:LYS:CB	1:U:26:ILE:HD11	2.45	0.45
1:U:356:GLY:H	4:U:903:MGD:PB	2.38	0.45
2:V:213:ALA:O	2:V:228:GLU:HA	2.16	0.45
1:W:505:THR:O	1:W:506:ALA:C	2.54	0.45
2:X:99:ALA:HA	2:X:102:LYS:HD2	1.97	0.45
2:X:68:CYS:CB	2:X:126:CYS:CB	2.87	0.45
2:X:97:GLU:OE2	2:X:100:LYS:HE2	2.16	0.45
2:B:228:GLU:OE2	2:H:214:LYS:NZ	2.50	0.45
1:C:460:LYS:HE3	8:C:1232:HOH:O	2.16	0.45
1:E:2:GLY:N	1:E:22:ASP:OD1	2.50	0.45
1:I:402:PRO:HG2	1:I:422:PHE:CD1	2.51	0.45
1:K:187:TRP:CH2	1:K:196:PRO:HB3	2.51	0.45
1:K:218:ASP:OD2	1:K:253:ASN:HB2	2.16	0.45
1:K:28:MET:HE3	1:K:63:THR:O	2.16	0.45
1:M:587:MET:HG3	1:M:592:ILE:HG13	1.99	0.45
2:N:142:MET:CE	2:N:146:ALA:CB	2.90	0.45
1:Q:533:VAL:HB	1:Q:534:PRO:HD3	1.98	0.45
1:Q:656:TRP:CD2	1:Q:663:LYS:HA	2.51	0.45
1:S:100:LEU:CD1	1:S:105:PRO:HG3	2.46	0.45
2:T:5:TYR:HB2	2:T:157:LEU:HD12	1.99	0.45
1:W:134:PRO:HB2	1:W:439:LEU:HD11	1.98	0.45
1:W:855:MET:HB2	1:W:857:ASN:OD1	2.16	0.45
1:E:451:LYS:HG3	1:E:461:PHE:CE2	2.52	0.45
1:E:644:ASP:O	1:E:646:PRO:HD3	2.16	0.45
1:G:201:LEU:HD13	1:G:387:TRP:HB2	1.98	0.45
2:H:105:LEU:HB3	2:H:114:MET:CE	2.46	0.45
1:I:426:MET:HE3	1:I:622:ALA:HB2	1.98	0.45
1:K:114:TRP:CZ2	1:K:541:PRO:HD2	2.52	0.45
1:K:138:LEU:HB2	1:K:490:ILE:HD12	1.98	0.45
1:M:66:PHE:HZ	1:M:146:MET:HE1	1.82	0.45
1:O:561:ILE:CG2	1:O:564:ASN:HB3	2.47	0.45
1:Q:408:GLY:HA2	1:Q:619:TYR:HE1	1.82	0.45
2:R:142:MET:CE	2:R:146:ALA:CB	2.93	0.45
2:T:145:CYS:HB2	2:T:146:ALA:H	1.33	0.45
2:T:40:GLN:HB3	2:T:43:HIS:CE1	2.51	0.45
1:U:21:LYS:HB3	1:U:26:ILE:HD11	1.97	0.45
1:U:9:ASN:HA	1:U:576:GLN:HA	1.98	0.45
1:U:722:LYS:HG2	8:U:1560:HOH:O	2.16	0.45
1:W:426:MET:HE1	1:W:618:GLN:O	2.15	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:66:PHE:HA	1:W:69:MET:CE	2.46	0.45
2:X:142:MET:CE	2:X:146:ALA:HB1	2.46	0.45
1:A:66:PHE:HZ	1:A:146:MET:CE	2.30	0.45
1:A:28:MET:HE1	1:A:67:LYS:N	2.32	0.45
1:A:670:PRO:HG2	1:A:675:GLN:CD	2.37	0.45
2:B:210:PHE:HD2	2:B:213:ALA:HB2	1.81	0.45
1:C:501:LEU:HD13	1:C:823:TYR:CD2	2.51	0.45
1:C:142:SER:CB	4:C:902:MGD:O1A	2.65	0.45
1:K:737:PRO:HG2	4:K:903:MGD:H2'	1.98	0.45
2:N:106:LEU:HD23	2:N:114:MET:CE	2.46	0.45
2:N:142:MET:HE1	2:N:146:ALA:HB1	1.97	0.45
1:U:649:LYS:O	1:U:649:LYS:HG3	2.16	0.45
2:V:19:CYS:O	2:V:22:GLY:N	2.50	0.45
1:W:498:GLY:N	1:W:499:PRO:HD3	2.31	0.45
1:C:670:PRO:HB3	1:C:682:GLN:HB2	1.99	0.45
1:E:825:PRO:HD2	8:E:1337:HOH:O	2.16	0.45
1:G:138:LEU:HB2	1:G:490:ILE:HD12	1.99	0.45
1:I:505:THR:O	1:I:506:ALA:C	2.55	0.45
2:J:74:ALA:HA	2:J:75:PRO:HD3	1.86	0.45
1:K:75:ARG:NH2	1:K:543:CYS:HA	2.32	0.45
1:M:250:PRO:HD3	4:M:903:MGD:C2	2.46	0.45
1:O:395:LEU:HD12	1:O:566:GLN:HA	1.99	0.45
1:O:737:PRO:CG	4:O:903:MGD:H2'	2.46	0.45
1:Q:35:ASP:OD1	1:Q:55:ARG:HD3	2.17	0.45
1:U:571:ARG:HB2	1:U:642:VAL:HB	1.97	0.45
1:U:361:SER:OG	1:U:717:ALA:HB1	2.16	0.45
1:A:146:MET:HE2	1:A:545:ASN:H	1.80	0.45
1:C:211:MET:HE1	2:D:231:PHE:CZ	2.52	0.45
1:C:402:PRO:HG2	1:C:422:PHE:CE1	2.51	0.45
1:E:800:ILE:CD1	1:E:833:ALA:HB1	2.47	0.45
1:G:540:LEU:HA	1:G:541:PRO:HD3	1.79	0.45
1:G:696:LYS:O	1:G:700:GLU:HG3	2.17	0.45
2:H:114:MET:CE	2:H:123:ALA:HB1	2.43	0.45
1:I:69:MET:HE2	1:I:754:MET:CE	2.47	0.45
2:J:247:VAL:O	2:J:257:SER:HA	2.17	0.45
1:K:855:MET:HB2	1:K:857:ASN:OD1	2.16	0.45
1:M:378:GLY:O	1:M:381:LYS:HG2	2.17	0.45
1:O:175:SER:HB2	1:O:176:TRP:CE3	2.52	0.45
1:Q:296:ASN:O	1:Q:687:LYS:HB3	2.16	0.45
1:S:452:ILE:N	1:S:453:PRO:CD	2.80	0.45
1:S:630:THR:OG1	1:S:633:GLU:HG3	2.17	0.45
1:S:66:PHE:HA	1:S:69:MET:HE2	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:U:155:SER:OG	1:U:409:ILE:HG12	2.17	0.45
1:W:111:ARG:NH2	1:W:585:GLU:OE2	2.46	0.45
4:W:903:MGD:O2A	4:W:903:MGD:O2B	2.34	0.45
2:X:110:PRO:HB3	2:X:180:LEU:HD13	1.98	0.45
1:C:541:PRO:HB2	1:C:586:SER:HA	1.99	0.45
1:K:66:PHE:HA	1:K:69:MET:CE	2.46	0.45
1:K:753:TYR:HB3	2:L:24:MET:CE	2.47	0.45
1:K:76:ILE:HG22	1:K:541:PRO:HG3	1.99	0.45
1:U:142:SER:OG	4:U:902:MGD:O1A	2.31	0.45
1:C:12:THR:O	1:C:226:TYR:HA	2.17	0.45
1:C:177:GLU:OE2	1:C:177:GLU:HA	2.17	0.45
1:K:100:LEU:CD1	1:K:105:PRO:HG3	2.47	0.45
1:K:561:ILE:CG2	1:K:564:ASN:HB3	2.45	0.45
1:K:69:MET:HE2	1:K:754:MET:HE1	1.99	0.45
1:Q:617:GLU:HG3	1:Q:631:TRP:CG	2.52	0.45
1:S:21:LYS:CB	1:S:26:ILE:HD11	2.47	0.45
1:S:730:TYR:CE1	1:S:794:ASN:HA	2.52	0.45
1:W:847:TYR:CZ	1:W:853:CYS:HB3	2.52	0.45
1:A:66:PHE:HA	1:A:69:MET:HE3	1.98	0.44
2:D:4:TYR:CE2	2:D:158:LYS:HD2	2.51	0.44
1:I:21:LYS:CB	1:I:26:ILE:HD11	2.46	0.44
1:I:656:TRP:CD2	1:I:663:LYS:HA	2.52	0.44
2:J:59:ASN:H	2:J:59:ASN:HD22	1.64	0.44
1:K:656:TRP:CD2	1:K:663:LYS:HA	2.52	0.44
1:O:55:ARG:HD2	8:O:1636:HOH:O	2.17	0.44
1:S:366:TRP:O	1:S:370:MET:HG2	2.16	0.44
2:X:70:HIS:CD2	2:X:92:VAL:H	2.32	0.44
1:A:738:HIS:HE2	4:A:902:MGD:H15	1.64	0.44
2:D:23:CYS:O	2:D:27:HIS:N	2.40	0.44
2:D:94:ILE:O	2:D:96:PRO:HD3	2.17	0.44
1:E:347:ALA:CB	1:E:388:SER:HA	2.47	0.44
1:E:521:PHE:CE2	1:E:523:VAL:CG2	3.00	0.44
2:F:205:VAL:HG13	2:F:254:LYS:HZ1	1.82	0.44
2:H:203:ILE:HD12	2:H:203:ILE:N	2.32	0.44
1:I:825:PRO:HD2	8:I:1332:HOH:O	2.17	0.44
2:J:256:TYR:HB2	2:J:274:LEU:HD21	1.98	0.44
1:M:501:LEU:HD13	1:M:823:TYR:CD2	2.52	0.44
2:P:5:TYR:HB2	2:P:157:LEU:HD12	1.98	0.44
1:Q:265:SER:O	1:Q:810:GLN:NE2	2.50	0.44
1:S:176:TRP:O	1:S:177:GLU:C	2.56	0.44
1:S:783:GLY:O	1:S:866:LYS:HD2	2.18	0.44
1:U:146:MET:HE3	1:U:545:ASN:OD1	2.16	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:U:735:LEU:H	1:U:735:LEU:HD23	1.81	0.44
1:U:356:GLY:H	4:U:903:MGD:H5'2	1.83	0.44
2:X:201:ALA:HB2	2:X:269:LEU:HB2	1.99	0.44
1:C:770:TRP:HB3	1:C:801:LEU:HD23	1.99	0.44
1:E:494:TRP:HE1	1:E:525:GLN:HE21	1.65	0.44
1:I:501:LEU:HD13	1:I:823:TYR:CD2	2.51	0.44
2:L:60:ASP:OD1	2:L:60:ASP:C	2.56	0.44
1:O:177:GLU:HA	1:O:177:GLU:OE2	2.16	0.44
1:O:571:ARG:HB2	1:O:642:VAL:HB	1.99	0.44
1:O:656:TRP:CD2	1:O:663:LYS:HA	2.53	0.44
1:U:218:ASP:OD2	1:U:253:ASN:HB2	2.17	0.44
1:U:786:ASN:HD22	1:U:805:VAL:H	1.64	0.44
1:A:74:LEU:HD12	1:A:750:LYS:HA	2.00	0.44
1:C:870:ASP:HB3	1:C:872:TYR:CE1	2.53	0.44
2:D:91:ILE:HG22	2:D:93:LEU:HG	1.98	0.44
1:E:66:PHE:HA	1:E:69:MET:CE	2.47	0.44
2:F:166:LYS:HE2	2:F:170:GLU:OE2	2.17	0.44
1:G:146:MET:CE	1:G:545:ASN:OD1	2.66	0.44
1:G:146:MET:HE3	1:G:545:ASN:OD1	2.16	0.44
2:H:5:TYR:CD2	2:H:164:MET:HG2	2.52	0.44
2:J:105:LEU:O	2:J:114:MET:HE2	2.17	0.44
2:J:46:MET:CE	2:J:66:THR:N	2.76	0.44
1:K:21:LYS:HB3	1:K:26:ILE:HD11	1.98	0.44
1:K:362:HIS:HB3	1:K:717:ALA:HB2	1.98	0.44
1:M:9:ASN:HA	1:M:576:GLN:HA	1.98	0.44
2:P:43:HIS:ND1	8:P:404:HOH:O	2.36	0.44
1:Q:211:MET:HE1	2:R:231:PHE:HZ	1.81	0.44
1:S:301:GLU:CD	1:S:301:GLU:H	2.20	0.44
1:S:540:LEU:HA	1:S:541:PRO:HD3	1.79	0.44
1:S:647:ASN:O	1:S:648:ARG:HG2	2.18	0.44
1:U:505:THR:HG22	1:U:857:ASN:ND2	2.33	0.44
1:C:656:TRP:CD2	1:C:663:LYS:HA	2.53	0.44
2:D:166:LYS:HG2	2:D:170:GLU:OE2	2.17	0.44
1:E:138:LEU:HD12	1:E:167:THR:O	2.17	0.44
1:E:671:ARG:HD2	8:E:1099:HOH:O	2.17	0.44
1:I:521:PHE:CE2	1:I:523:VAL:HG22	2.53	0.44
1:K:610:LYS:HZ3	1:K:618:GLN:HE22	1.66	0.44
2:L:103:LYS:HE2	2:L:116:TRP:CE2	2.53	0.44
1:M:146:MET:HE3	1:M:544:THR:CA	2.47	0.44
1:M:347:ALA:CB	1:M:388:SER:HA	2.48	0.44
1:Q:253:ASN:O	1:Q:257:ARG:HG3	2.17	0.44
1:Q:15:PRO:HD3	1:Q:554:PHE:CD1	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:R:210:PHE:HD2	2:R:213:ALA:HB2	1.82	0.44
2:V:105:LEU:HB3	2:V:114:MET:HE1	1.99	0.44
1:W:114:TRP:CZ2	1:W:541:PRO:HD2	2.51	0.44
1:A:153:ARG:O	1:A:157:TYR:HB3	2.18	0.44
2:B:74:ALA:HA	2:B:75:PRO:HD3	1.86	0.44
1:C:797:GLY:HA2	1:C:875:TYR:CE2	2.52	0.44
2:D:103:LYS:HE2	2:D:116:TRP:NE1	2.33	0.44
1:E:629:MET:HE1	1:E:634:PHE:HA	1.98	0.44
2:F:21:MET:CA	2:F:21:MET:CE	2.95	0.44
2:F:46:MET:HB2	7:F:303:SF4:S2	2.58	0.44
8:E:1394:HOH:O	2:F:60:ASP:HB2	2.17	0.44
1:I:772:MET:HB2	1:I:801:LEU:HD13	1.99	0.44
1:I:871:LYS:HE2	8:I:1230:HOH:O	2.18	0.44
2:L:10:VAL:HG13	2:L:63:TYR:O	2.18	0.44
1:O:1:MET:N	1:O:22:ASP:OD1	2.44	0.44
1:Q:620:PHE:CZ	1:Q:625:MET:HB3	2.52	0.44
2:X:135:ASP:OD1	2:X:137:SER:HB2	2.17	0.44
2:B:76:CYS:HB2	2:B:84:VAL:HG11	1.99	0.44
1:C:176:TRP:O	1:C:177:GLU:C	2.56	0.44
1:C:214:PHE:HA	1:C:347:ALA:HB3	1.99	0.44
2:D:18:ASN:HB2	7:D:302:SF4:S1	2.58	0.44
2:D:46:MET:HE1	2:D:65:PRO:CA	2.47	0.44
2:H:106:LEU:HD23	2:H:114:MET:HE1	2.00	0.44
1:I:165:GLY:CA	1:I:166:PHE:HB3	2.44	0.44
1:I:146:MET:HG2	4:I:902:MGD:N7	2.33	0.44
1:K:66:PHE:HZ	1:K:146:MET:CE	2.31	0.44
1:M:610:LYS:NZ	1:M:618:GLN:NE2	2.60	0.44
1:Q:401:PHE:HA	1:Q:402:PRO:HD3	1.82	0.44
1:U:142:SER:HB3	4:U:902:MGD:O1A	2.18	0.44
1:W:452:ILE:N	1:W:453:PRO:CD	2.81	0.44
1:W:76:ILE:HG22	1:W:541:PRO:HG3	1.99	0.44
2:B:39:MET:HE2	2:B:45:TRP:CD2	2.53	0.44
1:E:177:GLU:OE2	1:E:177:GLU:HA	2.17	0.44
1:E:498:GLY:N	1:E:499:PRO:HD3	2.33	0.44
1:E:610:LYS:NZ	1:E:618:GLN:NE2	2.58	0.44
1:E:75:ARG:HH21	1:E:543:CYS:HA	1.83	0.44
1:G:737:PRO:HG2	4:G:903:MGD:H2'	1.99	0.44
1:G:767:TYR:HB3	1:G:769:TYR:CE1	2.53	0.44
4:G:903:MGD:H4'	4:G:903:MGD:O1B	2.16	0.44
1:I:870:ASP:HB3	1:I:872:TYR:CE1	2.52	0.44
2:J:201:ALA:HB2	2:J:269:LEU:HB2	1.99	0.44
1:K:165:GLY:HA3	1:K:166:PHE:CB	2.37	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:563:ASP:O	1:K:566:GLN:HG2	2.18	0.44
1:K:571:ARG:HB2	1:K:642:VAL:HB	2.00	0.44
1:O:66:PHE:HZ	1:O:146:MET:CE	2.30	0.44
2:R:7:VAL:HB	2:R:155:GLU:HB3	2.00	0.44
1:S:218:ASP:OD2	1:S:253:ASN:HB2	2.18	0.44
1:U:128:ILE:CD1	1:U:492:MET:HB2	2.48	0.44
1:U:505:THR:O	1:U:506:ALA:C	2.56	0.44
1:U:74:LEU:HD12	1:U:750:LYS:HA	1.99	0.44
1:W:214:PHE:HA	1:W:347:ALA:HB3	2.00	0.44
1:A:10:SER:HA	1:A:15:PRO:HA	2.00	0.44
1:A:177:GLU:HA	1:A:177:GLU:OE2	2.18	0.44
1:A:460:LYS:HG3	8:A:1230:HOH:O	2.18	0.44
2:B:21:MET:CA	2:B:21:MET:HE2	2.48	0.44
1:C:262:LYS:HG2	2:D:232:PHE:CE1	2.53	0.44
1:C:66:PHE:HA	1:C:69:MET:HE3	1.99	0.44
2:D:46:MET:HE1	2:D:65:PRO:HA	2.00	0.44
2:J:105:LEU:HB3	2:J:114:MET:CE	2.48	0.44
1:M:211:MET:HE3	2:N:231:PHE:CE1	2.53	0.44
1:M:426:MET:HA	1:M:426:MET:CE	2.34	0.44
1:M:47:ARG:HD2	1:M:241:LEU:HD22	2.00	0.44
2:P:114:MET:HE3	2:P:123:ALA:HB1	2.00	0.44
2:P:166:LYS:HE2	2:P:170:GLU:OE2	2.18	0.44
1:Q:187:TRP:CH2	1:Q:196:PRO:HB3	2.53	0.44
1:Q:786:ASN:ND2	1:Q:805:VAL:H	2.16	0.44
1:S:12:THR:O	1:S:226:TYR:HA	2.18	0.44
1:S:451:LYS:HG3	1:S:461:PHE:CE2	2.52	0.44
2:T:142:MET:HE2	2:T:146:ALA:CB	2.48	0.44
2:T:201:ALA:HB2	2:T:269:LEU:HB2	2.00	0.44
1:U:494:TRP:HE1	1:U:525:GLN:HE21	1.64	0.44
1:U:649:LYS:HE3	1:U:651:THR:CG2	2.48	0.44
2:V:94:ILE:O	2:V:96:PRO:HD3	2.17	0.44
1:W:322:GLU:HG3	1:W:327:VAL:O	2.17	0.44
1:W:257:ARG:HD3	2:X:61:ILE:HG21	1.99	0.44
2:X:80:GLY:O	2:X:81:ASN:HB3	2.18	0.44
1:C:557:CYS:H	1:C:564:ASN:ND2	1.93	0.43
1:C:786:ASN:HA	1:C:786:ASN:HD22	1.57	0.43
2:F:211:GLU:HB2	2:F:231:PHE:HA	2.00	0.43
2:F:21:MET:HA	2:F:21:MET:CE	2.48	0.43
1:I:353:GLY:O	1:I:354:TRP:HB2	2.18	0.43
1:I:451:LYS:HA	1:I:454:GLU:OE1	2.17	0.43
2:J:204:LEU:HD23	2:J:209:CYS:HA	2.00	0.43
1:K:716:PRO:HB3	1:K:723:HIS:CG	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:213:ALA:O	2:L:228:GLU:HA	2.18	0.43
2:P:105:LEU:HB3	2:P:114:MET:HE1	1.99	0.43
1:Q:347:ALA:CB	1:Q:388:SER:HA	2.48	0.43
1:Q:737:PRO:CG	4:Q:903:MGD:H2'	2.48	0.43
1:Q:767:TYR:HB3	1:Q:769:TYR:CE1	2.52	0.43
1:S:187:TRP:CH2	1:S:196:PRO:HB3	2.53	0.43
1:S:249:ASP:OD1	4:S:903:MGD:H1'	2.18	0.43
1:S:32:ASP:HB2	8:S:1643:HOH:O	2.16	0.43
1:S:427:PHE:CG	1:S:434:PRO:HG3	2.53	0.43
1:S:141:PRO:CA	1:S:496:TYR:HB3	2.43	0.43
2:T:59:ASN:H	2:T:59:ASN:HD22	1.65	0.43
1:U:451:LYS:HG3	1:U:461:PHE:CE2	2.53	0.43
1:W:725:PRO:HD2	8:W:1195:HOH:O	2.18	0.43
1:A:272:HIS:O	1:A:276:PHE:HD1	2.01	0.43
2:B:142:MET:HE2	2:B:146:ALA:HB1	1.99	0.43
2:B:68:CYS:HB3	2:B:70:HIS:ND1	2.33	0.43
1:C:30:PRO:HG3	1:C:59:ILE:HG12	1.99	0.43
1:C:673:ASN:H	1:C:673:ASN:HD22	1.65	0.43
1:E:100:LEU:CD1	1:E:105:PRO:HG3	2.46	0.43
1:E:176:TRP:O	1:E:177:GLU:C	2.57	0.43
1:E:377:GLN:O	1:E:381:LYS:HE2	2.17	0.43
1:I:83:LYS:HE3	1:I:109:TYR:O	2.18	0.43
1:I:716:PRO:HB3	1:I:723:HIS:CD2	2.53	0.43
2:J:21:MET:CA	2:J:21:MET:CE	2.96	0.43
1:Q:494:TRP:HE1	1:Q:525:GLN:HE21	1.66	0.43
1:Q:571:ARG:HB2	1:Q:642:VAL:HB	1.99	0.43
1:Q:797:GLY:HA2	1:Q:875:TYR:CE2	2.53	0.43
2:R:247:VAL:O	2:R:257:SER:HA	2.18	0.43
1:U:729:LYS:HD2	8:U:1134:HOH:O	2.18	0.43
1:W:263:TRP:CZ2	1:W:265:SER:HB2	2.53	0.43
2:X:39:MET:HG2	2:X:40:GLN:N	2.32	0.43
1:A:176:TRP:O	1:A:177:GLU:C	2.56	0.43
1:A:66:PHE:HZ	1:A:146:MET:HE1	1.84	0.43
1:C:356:GLY:N	4:C:903:MGD:PB	2.88	0.43
1:C:558:SER:H	1:C:564:ASN:ND2	2.15	0.43
1:C:785:LYS:HZ3	1:C:785:LYS:HB2	1.83	0.43
1:C:249:ASP:OD1	4:C:903:MGD:H1'	2.19	0.43
1:G:21:LYS:HB3	1:G:26:ILE:HD11	2.00	0.43
1:I:146:MET:HE1	1:I:544:THR:CB	2.47	0.43
1:I:176:TRP:O	1:I:177:GLU:C	2.56	0.43
1:K:21:LYS:CB	1:K:26:ILE:HD11	2.49	0.43
1:K:96:ARG:HD2	1:K:514:TYR:O	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:146:MET:HG2	4:M:902:MGD:N7	2.33	0.43
1:O:216:SER:OG	4:O:903:MGD:H5'2	2.18	0.43
1:Q:21:LYS:HB3	1:Q:26:ILE:HD11	2.00	0.43
1:Q:540:LEU:HA	1:Q:541:PRO:HD3	1.84	0.43
1:Q:725:PRO:HA	1:U:704:ILE:HG13	2.00	0.43
1:Q:69:MET:HE1	1:Q:754:MET:HE3	2.00	0.43
1:S:175:SER:HB2	1:S:176:TRP:CE3	2.53	0.43
1:S:142:SER:HB3	4:S:902:MGD:O1A	2.18	0.43
2:T:176:ILE:HG22	2:T:177:LYS:HG3	2.01	0.43
1:W:716:PRO:HB3	1:W:723:HIS:CG	2.54	0.43
2:X:7:VAL:HG21	2:X:167:LYS:HZ2	1.83	0.43
1:A:871:LYS:HE2	8:A:1231:HOH:O	2.18	0.43
1:C:816:SER:OG	1:C:839:ILE:HG13	2.18	0.43
1:E:66:PHE:HZ	1:E:146:MET:CE	2.31	0.43
1:G:15:PRO:HD3	1:G:554:PHE:CD1	2.52	0.43
2:H:142:MET:HE2	2:H:146:ALA:HB3	1.99	0.43
1:I:378:GLY:O	1:I:381:LYS:HG2	2.17	0.43
2:J:70:HIS:HD2	2:J:92:VAL:N	2.03	0.43
1:K:767:TYR:HB3	1:K:769:TYR:CE1	2.53	0.43
1:M:111:ARG:NH2	1:M:585:GLU:OE2	2.44	0.43
2:N:21:MET:HE2	2:N:21:MET:CA	2.48	0.43
1:O:12:THR:O	1:O:226:TYR:HA	2.19	0.43
1:O:716:PRO:HB3	1:O:723:HIS:CD2	2.53	0.43
2:R:159:THR:OG1	2:R:160:THR:N	2.51	0.43
2:R:19:CYS:O	2:R:22:GLY:N	2.52	0.43
2:R:5:TYR:CD2	2:R:164:MET:HG2	2.53	0.43
1:S:175:SER:OG	6:S:905:BTT:C5	2.66	0.43
1:U:656:TRP:CD2	1:U:663:LYS:HA	2.53	0.43
1:W:673:ASN:H	1:W:673:ASN:ND2	2.17	0.43
1:A:770:TRP:HB3	1:A:801:LEU:HD23	2.01	0.43
2:B:69:MET:HB3	2:B:184:PRO:HB3	1.99	0.43
1:C:757:ILE:CG1	2:D:21:MET:HE1	2.48	0.43
2:D:176:ILE:HG22	2:D:177:LYS:HG3	2.01	0.43
1:E:871:LYS:HE2	8:E:1233:HOH:O	2.19	0.43
2:F:247:VAL:O	2:F:257:SER:HA	2.19	0.43
1:G:35:ASP:OD1	1:G:55:ARG:HD3	2.19	0.43
1:G:75:ARG:NH2	1:G:543:CYS:HA	2.33	0.43
1:G:772:MET:HB2	1:G:801:LEU:HD13	1.99	0.43
2:H:21:MET:CA	2:H:21:MET:CE	2.96	0.43
1:K:494:TRP:HE1	1:K:525:GLN:HE21	1.67	0.43
1:M:141:PRO:CA	1:M:496:TYR:HB3	2.43	0.43
1:M:15:PRO:HD3	1:M:554:PHE:CD1	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:66:PHE:HA	1:M:69:MET:HE2	1.99	0.43
1:M:143:SER:N	4:M:902:MGD:O1A	2.52	0.43
2:N:91:ILE:HG22	2:N:93:LEU:HG	2.01	0.43
1:O:165:GLY:CA	1:O:166:PHE:HB3	2.46	0.43
1:Q:28:MET:HE1	1:Q:67:LYS:N	2.34	0.43
1:Q:74:LEU:HD12	1:Q:750:LYS:HA	2.01	0.43
1:S:825:PRO:HD2	8:S:1331:HOH:O	2.19	0.43
2:T:122:VAL:HG22	2:T:123:ALA:N	2.34	0.43
1:W:262:LYS:HG2	2:X:232:PHE:CE1	2.53	0.43
1:W:39:ALA:HA	1:W:40:PRO:HD3	1.88	0.43
1:W:528:TRP:CD2	1:W:750:LYS:HD3	2.54	0.43
1:W:355:GLY:HA2	4:W:903:MGD:O1B	2.18	0.43
2:X:73:ASN:O	2:X:75:PRO:HD3	2.18	0.43
1:C:512:LYS:HE3	1:C:830:GLY:O	2.18	0.43
2:F:176:ILE:HG22	2:F:177:LYS:HG3	2.00	0.43
1:G:176:TRP:O	1:G:177:GLU:C	2.57	0.43
1:G:142:SER:HB3	4:G:902:MGD:O1A	2.18	0.43
2:H:19:CYS:O	2:H:22:GLY:N	2.51	0.43
1:I:558:SER:H	1:I:564:ASN:ND2	2.16	0.43
2:N:23:CYS:O	2:N:27:HIS:N	2.49	0.43
1:Q:166:PHE:N	1:Q:439:LEU:HD12	2.34	0.43
1:Q:452:ILE:N	1:Q:453:PRO:CD	2.81	0.43
1:S:291:GLU:CD	1:S:291:GLU:H	2.21	0.43
1:S:501:LEU:HD13	1:S:823:TYR:CD2	2.53	0.43
1:A:400:TYR:CE1	1:A:421:LYS:HD2	2.54	0.43
1:A:141:PRO:CA	1:A:496:TYR:HB3	2.39	0.43
1:C:426:MET:CA	1:C:426:MET:HE3	2.39	0.43
1:E:146:MET:HE1	1:E:544:THR:CB	2.45	0.43
1:G:9:ASN:HA	1:G:576:GLN:HA	2.01	0.43
2:H:143:PRO:HB3	7:H:303:SF4:S1	2.58	0.43
1:K:378:GLY:O	1:K:381:LYS:HG2	2.17	0.43
2:L:106:LEU:HD23	2:L:114:MET:CE	2.49	0.43
2:P:68:CYS:CB	2:P:126:CYS:CB	2.85	0.43
1:Q:426:MET:HE1	1:Q:618:GLN:O	2.18	0.43
1:Q:356:GLY:H	4:Q:903:MGD:H5'2	1.84	0.43
2:T:49:GLU:HG3	2:T:64:ARG:NH2	2.33	0.43
1:W:1:MET:H2	1:W:22:ASP:CG	2.21	0.43
1:W:347:ALA:HB1	1:W:388:SER:HA	2.01	0.43
1:W:533:VAL:HB	1:W:534:PRO:HD3	1.99	0.43
2:X:247:VAL:O	2:X:257:SER:HA	2.19	0.43
1:A:69:MET:HE2	1:A:754:MET:HE1	2.00	0.43
1:A:76:ILE:HA	1:A:77:PRO:HD3	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:144:HIS:HB2	4:A:902:MGD:O1B	2.18	0.43
1:C:495:LYS:CD	1:C:514:TYR:OH	2.67	0.43
1:C:9:ASN:HA	1:C:576:GLN:HA	1.99	0.43
1:C:175:SER:OG	6:C:905:BTT:C5	2.66	0.43
1:E:15:PRO:HD2	8:E:1003:HOH:O	2.17	0.43
1:E:211:MET:CE	2:F:231:PHE:CZ	3.01	0.43
1:E:857:ASN:HB3	4:E:902:MGD:N19	2.34	0.43
2:H:166:LYS:HE2	2:H:170:GLU:OE2	2.19	0.43
1:I:69:MET:HE2	1:I:754:MET:HE1	2.01	0.43
2:L:105:LEU:C	2:L:114:MET:HE2	2.39	0.43
1:M:69:MET:CE	1:M:754:MET:HE3	2.49	0.43
1:S:39:ALA:HA	1:S:40:PRO:HD3	1.87	0.43
1:U:100:LEU:CD1	1:U:105:PRO:HG3	2.48	0.43
1:A:557:CYS:N	1:A:564:ASN:HD21	1.93	0.43
1:A:571:ARG:HA	8:A:1026:HOH:O	2.18	0.43
1:C:66:PHE:HZ	1:C:146:MET:CE	2.32	0.43
1:C:165:GLY:CA	1:C:166:PHE:HB3	2.46	0.43
1:C:69:MET:HE1	1:C:754:MET:HE3	2.01	0.43
1:E:452:ILE:N	1:E:453:PRO:CD	2.81	0.43
1:G:69:MET:HE2	1:G:754:MET:CE	2.48	0.43
1:G:825:PRO:HD2	8:G:1335:HOH:O	2.19	0.43
2:H:58:ARG:HD2	2:H:268:ASP:OD1	2.19	0.43
1:I:565:TYR:C	1:I:567:LEU:H	2.22	0.43
1:I:74:LEU:HD12	1:I:750:LYS:HA	2.00	0.43
2:J:175:VAL:HG23	2:J:178:PRO:HG3	2.00	0.43
2:J:5:TYR:HB2	2:J:157:LEU:HD12	1.98	0.43
1:K:722:LYS:HE3	1:K:722:LYS:HB2	1.86	0.43
1:O:378:GLY:O	1:O:381:LYS:HG2	2.19	0.43
1:O:540:LEU:HA	1:O:541:PRO:HD3	1.82	0.43
2:P:87:ARG:HD3	2:P:93:LEU:HD12	2.01	0.43
1:Q:433:PHE:HA	1:Q:434:PRO:HD3	1.84	0.43
1:W:81:LYS:HB2	1:W:112:ILE:HD13	2.00	0.43
1:W:176:TRP:O	1:W:177:GLU:C	2.58	0.43
2:X:69:MET:O	2:X:70:HIS:C	2.56	0.43
1:A:252:MET:HE3	8:B:470:HOH:O	2.19	0.43
2:B:189:LYS:HD2	8:B:499:HOH:O	2.19	0.43
2:B:72:GLU:HG2	2:B:185:ARG:NH2	2.34	0.43
1:E:558:SER:H	1:E:564:ASN:ND2	2.17	0.43
1:G:482:TYR:CD1	1:G:483:PRO:HA	2.54	0.43
2:H:114:MET:HA	2:H:125:LYS:HB3	2.01	0.43
1:I:35:ASP:OD1	1:I:55:ARG:HD3	2.19	0.43
1:I:476:GLN:OE1	1:I:708:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:142:SER:OG	4:M:902:MGD:O1A	2.31	0.43
2:N:166:LYS:HG2	2:N:170:GLU:OE2	2.18	0.43
1:U:177:GLU:HA	1:U:177:GLU:OE2	2.18	0.43
1:U:644:ASP:C	1:U:646:PRO:HD3	2.39	0.43
1:U:770:TRP:HB3	1:U:801:LEU:HD23	2.01	0.43
1:A:146:MET:HE3	1:A:545:ASN:OD1	2.19	0.42
1:C:353:GLY:O	1:C:354:TRP:HB2	2.19	0.42
2:D:5:TYR:HB2	2:D:157:LEU:HD11	2.01	0.42
1:G:505:THR:HG22	1:G:857:ASN:ND2	2.35	0.42
2:H:68:CYS:HB3	2:H:70:HIS:ND1	2.34	0.42
1:I:355:GLY:C	4:I:903:MGD:O1B	2.53	0.42
1:K:176:TRP:O	1:K:177:GLU:C	2.57	0.42
1:K:459:GLY:O	1:K:489:LYS:HE2	2.19	0.42
1:K:146:MET:HE3	1:K:545:ASN:OD1	2.19	0.42
1:M:21:LYS:CB	1:M:26:ILE:HD11	2.49	0.42
1:O:263:TRP:CZ2	1:O:265:SER:HB2	2.54	0.42
1:O:401:PHE:HA	1:O:402:PRO:HD3	1.83	0.42
1:O:452:ILE:N	1:O:453:PRO:CD	2.81	0.42
2:P:53:ARG:HB2	2:P:60:ASP:OD1	2.19	0.42
1:S:211:MET:CE	2:T:231:PHE:CZ	3.02	0.42
1:U:393:VAL:HA	1:U:394:PRO:HD3	1.84	0.42
1:W:356:GLY:N	4:W:903:MGD:PB	2.91	0.42
1:A:128:ILE:CD1	1:A:492:MET:HB2	2.49	0.42
1:A:521:PHE:CE2	1:A:523:VAL:CG2	3.01	0.42
1:C:165:GLY:HA3	1:C:166:PHE:CB	2.42	0.42
1:C:296:ASN:HB3	1:C:657:PHE:CZ	2.55	0.42
1:C:724:SER:HA	1:C:725:PRO:HD3	1.94	0.42
2:D:109:CYS:HA	2:D:110:PRO:HD3	1.89	0.42
1:E:61:PRO:HG3	2:F:16:CYS:HB2	2.01	0.42
1:G:177:GLU:HA	1:G:177:GLU:OE2	2.19	0.42
1:G:347:ALA:CB	1:G:388:SER:HA	2.50	0.42
1:G:494:TRP:HE1	1:G:525:GLN:HE21	1.66	0.42
2:H:177:LYS:N	2:H:178:PRO:HD3	2.33	0.42
1:I:165:GLY:HA3	1:I:166:PHE:CB	2.37	0.42
1:I:76:ILE:HA	1:I:77:PRO:HD3	1.78	0.42
1:K:9:ASN:HA	1:K:576:GLN:HA	2.01	0.42
1:K:786:ASN:HA	1:K:786:ASN:HD22	1.58	0.42
2:N:2:GLU:HB3	2:N:158:LYS:HE2	2.01	0.42
2:N:74:ALA:HA	2:N:75:PRO:HD3	1.86	0.42
1:O:717:ALA:HB3	1:O:720:SER:HB3	2.00	0.42
2:P:10:VAL:HG13	2:P:63:TYR:O	2.19	0.42
1:S:670:PRO:HG2	1:S:675:GLN:CD	2.39	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:V:177:LYS:N	2:V:178:PRO:HD3	2.34	0.42
1:W:521:PHE:CE2	1:W:523:VAL:CG2	3.01	0.42
1:A:540:LEU:HA	1:A:541:PRO:HD3	1.77	0.42
1:A:69:MET:CE	1:A:754:MET:HE3	2.49	0.42
1:C:347:ALA:CB	1:C:388:SER:HA	2.48	0.42
1:C:521:PHE:CE2	1:C:523:VAL:CG2	3.03	0.42
1:I:155:SER:OG	1:I:409:ILE:HG12	2.19	0.42
1:I:28:MET:CE	1:I:66:PHE:HB3	2.48	0.42
1:K:772:MET:HB2	1:K:801:LEU:HD13	2.01	0.42
1:M:28:MET:HE2	8:M:1399:HOH:O	2.19	0.42
1:M:319:GLU:HG2	1:S:726:LEU:CD1	2.36	0.42
2:N:114:MET:HA	2:N:125:LYS:HB3	2.00	0.42
2:N:19:CYS:HB2	2:N:20:PHE:H	1.51	0.42
1:O:252:MET:HE3	8:P:469:HOH:O	2.19	0.42
2:P:106:LEU:N	2:P:114:MET:HE2	2.35	0.42
1:Q:250:PRO:HD3	4:Q:903:MGD:C2	2.49	0.42
1:Q:356:GLY:H	4:Q:903:MGD:C5'	2.32	0.42
2:R:106:LEU:HD11	2:R:116:TRP:HB2	2.01	0.42
2:R:27:HIS:HE1	8:R:469:HOH:O	2.01	0.42
1:S:725:PRO:HD2	8:S:1195:HOH:O	2.20	0.42
1:S:770:TRP:HB3	1:S:801:LEU:HD23	2.01	0.42
1:U:269:GLY:HA2	1:U:362:HIS:CE1	2.54	0.42
1:W:554:PHE:HB3	8:W:1025:HOH:O	2.19	0.42
1:A:361:SER:OG	1:A:717:ALA:HB1	2.20	0.42
2:B:13:CYS:HB3	2:B:63:TYR:HB2	2.01	0.42
1:C:182:GLY:HA3	1:C:364:ILE:HG23	2.01	0.42
1:C:855:MET:HB2	1:C:857:ASN:OD1	2.20	0.42
2:D:179:GLU:OE1	2:D:179:GLU:N	2.52	0.42
1:E:426:MET:HE2	1:E:618:GLN:HG2	1.97	0.42
1:I:1:MET:H3	1:I:22:ASP:CG	2.22	0.42
1:I:291:GLU:H	1:I:291:GLU:CD	2.23	0.42
1:K:262:LYS:HG2	2:L:232:PHE:CE1	2.53	0.42
1:K:557:CYS:H	1:K:564:ASN:ND2	1.90	0.42
2:P:7:VAL:HB	2:P:155:GLU:HB3	2.02	0.42
2:P:46:MET:CE	2:P:66:THR:N	2.78	0.42
1:Q:211:MET:CE	2:R:231:PHE:CZ	3.02	0.42
1:Q:495:LYS:HD2	1:Q:514:TYR:OH	2.20	0.42
1:U:66:PHE:HA	1:U:69:MET:CE	2.50	0.42
1:U:250:PRO:HD3	4:U:903:MGD:C2	2.50	0.42
1:A:610:LYS:HB3	1:A:614:ALA:HB3	2.01	0.42
1:C:65:GLY:HA3	2:D:21:MET:HG3	2.01	0.42
1:E:495:LYS:HE3	1:E:497:GLY:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:F:114:MET:HA	2:F:125:LYS:HB3	2.02	0.42
2:F:138:TRP:CD2	2:F:140:PRO:HD2	2.54	0.42
2:F:177:LYS:N	2:F:178:PRO:HD3	2.35	0.42
1:G:521:PHE:CE2	1:G:523:VAL:CG2	3.02	0.42
1:G:69:MET:HE1	1:G:754:MET:HE3	2.02	0.42
2:H:191:LEU:HG	2:H:195:GLU:HG3	2.01	0.42
1:I:100:LEU:CD1	1:I:105:PRO:HG3	2.49	0.42
1:K:433:PHE:HA	1:K:434:PRO:HD3	1.79	0.42
1:K:76:ILE:HA	1:K:77:PRO:HD3	1.76	0.42
1:M:561:ILE:CG2	1:M:564:ASN:HB3	2.47	0.42
1:O:521:PHE:CE2	1:O:523:VAL:CG2	3.02	0.42
1:Q:21:LYS:CB	1:Q:26:ILE:HD11	2.49	0.42
1:Q:141:PRO:CA	1:Q:496:TYR:HB3	2.40	0.42
2:D:118:GLU:HB3	1:S:604:GLU:CD	2.40	0.42
1:S:76:ILE:HG22	1:S:541:PRO:HG3	2.02	0.42
2:V:40:GLN:NE2	2:V:118:GLU:H	2.17	0.42
2:V:210:PHE:HD2	2:V:213:ALA:HB2	1.85	0.42
1:A:347:ALA:HB1	1:A:388:SER:HA	2.01	0.42
1:E:322:GLU:HG3	1:E:327:VAL:O	2.20	0.42
1:G:21:LYS:CB	1:G:26:ILE:HD11	2.50	0.42
1:G:482:TYR:HA	1:G:483:PRO:C	2.39	0.42
2:H:104:GLU:H	2:H:104:GLU:CD	2.22	0.42
1:I:517:ASP:HB3	8:I:1203:HOH:O	2.19	0.42
1:M:146:MET:CE	1:M:544:THR:HG22	2.49	0.42
1:M:347:ALA:HB1	1:M:388:SER:HA	2.01	0.42
2:N:106:LEU:CD2	2:N:114:MET:HB3	2.50	0.42
1:O:114:TRP:CZ2	1:O:587:MET:HG2	2.55	0.42
1:S:362:HIS:HB3	1:S:717:ALA:HB2	2.01	0.42
1:U:355:GLY:CA	4:U:903:MGD:O1B	2.64	0.42
1:A:296:ASN:HB3	1:A:657:PHE:CZ	2.55	0.42
2:D:105:LEU:C	2:D:114:MET:HE2	2.40	0.42
2:D:19:CYS:HB2	2:D:46:MET:HG2	2.01	0.42
2:D:46:MET:HE1	2:D:66:THR:H	1.84	0.42
1:C:257:ARG:HD3	2:D:61:ILE:HG21	2.01	0.42
1:E:673:ASN:ND2	1:E:673:ASN:H	2.17	0.42
1:E:142:SER:OG	4:E:902:MGD:O1A	2.29	0.42
1:G:165:GLY:CA	1:G:166:PHE:HB3	2.46	0.42
1:G:495:LYS:CD	1:G:514:TYR:OH	2.68	0.42
1:G:644:ASP:OD1	1:G:646:PRO:HG3	2.20	0.42
2:L:119:GLU:HB2	8:L:442:HOH:O	2.19	0.42
2:L:247:VAL:O	2:L:257:SER:HA	2.19	0.42
2:L:76:CYS:O	2:L:80:GLY:N	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:140:THR:HB	1:M:169:ALA:HB3	2.01	0.42
1:Q:476:GLN:OE1	1:Q:708:ARG:NH2	2.52	0.42
1:Q:501:LEU:HD13	1:Q:823:TYR:CD2	2.54	0.42
2:R:46:MET:CE	2:R:66:THR:N	2.78	0.42
2:T:177:LYS:N	2:T:178:PRO:HD3	2.34	0.42
1:U:630:THR:OG1	1:U:633:GLU:HG3	2.20	0.42
1:W:356:GLY:H	4:W:903:MGD:H5'2	1.83	0.42
1:A:673:ASN:H	1:A:673:ASN:ND2	2.17	0.42
1:C:735:LEU:HD23	1:C:735:LEU:H	1.85	0.42
1:C:142:SER:HB3	4:C:902:MGD:O1A	2.20	0.42
1:G:263:TRP:CZ2	1:G:265:SER:HB2	2.55	0.42
1:I:730:TYR:CE1	1:I:794:ASN:HA	2.54	0.42
2:J:19:CYS:O	2:J:22:GLY:N	2.53	0.42
1:M:401:PHE:HA	1:M:402:PRO:HD3	1.87	0.42
1:M:670:PRO:HB3	1:M:682:GLN:HB2	2.02	0.42
1:O:322:GLU:HG3	1:O:327:VAL:O	2.19	0.42
2:T:4:TYR:CE2	2:T:158:LYS:HD2	2.55	0.42
1:U:76:ILE:CG2	1:U:541:PRO:HG3	2.47	0.42
2:V:4:TYR:CE2	2:V:158:LYS:HD2	2.55	0.42
2:X:142:MET:HE1	8:X:930:HOH:O	2.20	0.42
1:A:15:PRO:HD3	1:A:554:PHE:CE1	2.54	0.42
1:A:786:ASN:ND2	1:A:805:VAL:H	2.10	0.42
1:C:738:HIS:HE2	4:C:902:MGD:H15	1.68	0.42
2:D:3:GLN:O	2:D:158:LYS:HA	2.20	0.42
1:G:452:ILE:N	1:G:453:PRO:CD	2.83	0.42
1:G:111:ARG:NH2	1:G:585:GLU:OE2	2.45	0.42
2:H:18:ASN:HB2	7:H:302:SF4:S1	2.60	0.42
1:I:211:MET:CE	2:J:231:PHE:CZ	3.03	0.42
1:K:296:ASN:HB3	1:K:657:PHE:CZ	2.54	0.42
1:M:495:LYS:CD	1:M:514:TYR:OH	2.67	0.42
2:N:5:TYR:HB2	2:N:157:LEU:HD12	2.02	0.42
1:O:15:PRO:HD3	1:O:554:PHE:CE1	2.55	0.42
1:O:66:PHE:HA	1:O:69:MET:HE3	2.01	0.42
1:Q:498:GLY:N	1:Q:499:PRO:HD3	2.34	0.42
2:R:176:ILE:HG22	2:R:177:LYS:HG3	2.02	0.42
1:S:257:ARG:HD3	2:T:61:ILE:HG21	2.02	0.42
1:U:395:LEU:HD12	1:U:566:GLN:HA	2.01	0.42
1:U:797:GLY:HA2	1:U:875:TYR:CE2	2.54	0.42
1:W:187:TRP:CH2	1:W:196:PRO:HB3	2.54	0.42
1:W:9:ASN:HA	1:W:576:GLN:HA	2.01	0.42
1:A:426:MET:HE3	1:A:622:ALA:HB2	2.01	0.42
2:D:210:PHE:HD2	2:D:213:ALA:HB2	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:218:ASP:OD2	1:E:253:ASN:HB2	2.19	0.42
1:G:501:LEU:HD13	1:G:823:TYR:CD2	2.55	0.42
1:I:263:TRP:CZ2	1:I:265:SER:HB2	2.55	0.42
1:K:143:SER:N	4:K:902:MGD:O1A	2.52	0.42
1:K:15:PRO:HD2	8:K:1003:HOH:O	2.19	0.42
1:K:797:GLY:HA2	1:K:875:TYR:CE2	2.55	0.42
1:M:28:MET:HE1	1:M:67:LYS:N	2.35	0.42
1:O:75:ARG:HH21	1:O:543:CYS:HA	1.85	0.42
1:Q:176:TRP:O	1:Q:177:GLU:C	2.58	0.42
1:Q:610:LYS:HB3	1:Q:614:ALA:HB3	2.01	0.42
2:R:177:LYS:N	2:R:178:PRO:HD3	2.34	0.42
2:R:18:ASN:HB2	7:R:302:SF4:S1	2.59	0.42
2:R:70:HIS:HD2	2:R:92:VAL:N	2.02	0.42
1:S:66:PHE:HZ	1:S:146:MET:CE	2.33	0.42
1:U:66:PHE:HZ	1:U:146:MET:CE	2.32	0.42
1:U:396:ASP:OD2	1:U:398:GLU:HB2	2.20	0.42
2:V:23:CYS:HB3	2:V:39:MET:CE	2.50	0.42
1:C:670:PRO:HG2	1:C:675:GLN:CD	2.40	0.41
2:D:19:CYS:O	2:D:22:GLY:N	2.53	0.41
2:H:19:CYS:HB2	2:H:20:PHE:H	1.38	0.41
1:I:257:ARG:HD3	2:J:61:ILE:HG21	2.02	0.41
1:I:418:ALA:HB1	1:I:423:ALA:HB2	2.01	0.41
1:I:77:PRO:HB2	1:I:78:TYR:CD2	2.54	0.41
1:K:175:SER:HB2	1:K:176:TRP:CE3	2.55	0.41
1:K:177:GLU:HA	1:K:177:GLU:OE2	2.20	0.41
2:N:13:CYS:HB3	2:N:63:TYR:HB2	2.02	0.41
2:N:18:ASN:HB2	7:N:302:SF4:S1	2.60	0.41
1:O:153:ARG:O	1:O:157:TYR:HB3	2.20	0.41
1:O:772:MET:HB2	1:O:801:LEU:HD13	2.00	0.41
1:O:249:ASP:CG	4:O:903:MGD:H1'	2.39	0.41
1:S:353:GLY:O	1:S:354:TRP:HB2	2.20	0.41
2:V:105:LEU:HB3	2:V:114:MET:CE	2.50	0.41
1:A:670:PRO:HB3	1:A:682:GLN:HB2	2.03	0.41
1:C:143:SER:N	4:C:902:MGD:O1A	2.53	0.41
1:E:211:MET:HE3	2:F:231:PHE:CE1	2.55	0.41
2:H:10:VAL:HG13	2:H:63:TYR:O	2.20	0.41
2:H:68:CYS:CB	2:H:126:CYS:CB	2.88	0.41
1:I:201:LEU:HD13	1:I:387:TRP:HB2	2.01	0.41
1:I:74:LEU:HA	1:I:74:LEU:HD23	1.90	0.41
1:I:142:SER:CB	4:I:902:MGD:O1A	2.68	0.41
2:J:162:GLU:CD	2:J:162:GLU:H	2.23	0.41
2:J:177:LYS:N	2:J:178:PRO:HD3	2.35	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:21:LYS:CB	1:O:26:ILE:HD11	2.50	0.41
2:R:13:CYS:HB3	2:R:63:TYR:HB2	2.01	0.41
2:T:142:MET:HE2	2:T:146:ALA:HB1	2.01	0.41
1:U:211:MET:CE	2:V:231:PHE:CZ	3.02	0.41
1:U:722:LYS:HB2	1:U:722:LYS:HE3	1.88	0.41
2:V:9:ASP:HA	2:V:189:LYS:HB3	2.02	0.41
1:W:165:GLY:CA	1:W:166:PHE:HB3	2.45	0.41
1:W:138:LEU:HB2	1:W:490:ILE:HD12	2.03	0.41
1:A:165:GLY:HA3	1:A:166:PHE:CB	2.40	0.41
1:C:498:GLY:N	1:C:499:PRO:HD3	2.35	0.41
2:D:56:TYR:HA	2:D:59:ASN:HD22	1.85	0.41
1:E:142:SER:HB3	4:E:902:MGD:O1A	2.20	0.41
1:G:140:THR:HB	1:G:169:ALA:HB3	2.02	0.41
2:H:4:TYR:CE2	2:H:158:LYS:HD2	2.55	0.41
1:I:250:PRO:HD3	4:I:903:MGD:C2	2.51	0.41
1:K:211:MET:HE3	1:K:244:ASP:HB2	2.01	0.41
2:L:216:VAL:HG13	2:L:223:GLU:HG3	2.02	0.41
2:L:218:LYS:HG2	2:L:223:GLU:HA	2.03	0.41
1:M:677:CYS:C	1:M:678:ARG:HG2	2.39	0.41
1:O:1:MET:H3	1:O:22:ASP:CG	2.22	0.41
1:Q:174:ASP:OD1	1:Q:175:SER:N	2.49	0.41
1:Q:670:PRO:HG2	1:Q:675:GLN:CD	2.40	0.41
1:S:400:TYR:CE1	1:S:421:LYS:HD2	2.55	0.41
1:S:495:LYS:CD	1:S:514:TYR:OH	2.68	0.41
1:E:21:LYS:HB2	1:E:26:ILE:HD11	2.03	0.41
1:E:15:PRO:HD3	1:E:554:PHE:CE1	2.55	0.41
1:E:657:PHE:CE1	1:E:681:LEU:HG	2.54	0.41
1:E:76:ILE:HA	1:E:77:PRO:HD3	1.80	0.41
1:G:724:SER:HA	1:G:725:PRO:HD3	1.91	0.41
1:I:800:ILE:CD1	1:I:833:ALA:HB1	2.50	0.41
2:L:142:MET:HE2	2:L:146:ALA:HB1	2.03	0.41
1:M:28:MET:HE1	1:M:66:PHE:CB	2.48	0.41
1:M:301:GLU:CD	1:M:301:GLU:H	2.23	0.41
2:P:179:GLU:OE1	2:P:179:GLU:N	2.45	0.41
1:Q:495:LYS:HD3	8:Q:1105:HOH:O	2.19	0.41
1:Q:361:SER:OG	1:Q:717:ALA:HB1	2.20	0.41
1:S:395:LEU:HD12	1:S:566:GLN:HA	2.02	0.41
1:S:786:ASN:ND2	1:S:804:GLN:HA	2.34	0.41
2:T:142:MET:HE1	8:T:927:HOH:O	2.21	0.41
1:W:301:GLU:H	1:W:301:GLU:CD	2.24	0.41
2:X:235:PHE:C	2:X:235:PHE:CD1	2.94	0.41
1:A:140:THR:HB	1:A:169:ALA:HB3	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:85:PHE:CE2	1:A:87:PRO:HG3	2.56	0.41
1:C:868:ASP:OD1	1:C:870:ASP:HB2	2.20	0.41
1:E:165:GLY:HA3	1:E:166:PHE:CB	2.43	0.41
1:E:540:LEU:HA	1:E:541:PRO:HD3	1.84	0.41
1:I:21:LYS:HB2	1:I:26:ILE:HD11	2.02	0.41
1:K:263:TRP:HZ3	2:L:59:ASN:HD21	1.68	0.41
1:K:857:ASN:HB3	4:K:902:MGD:N19	2.35	0.41
2:L:40:GLN:HE21	2:L:117:ASN:HA	1.85	0.41
1:M:291:GLU:H	1:M:291:GLU:CD	2.22	0.41
1:M:322:GLU:HG3	1:M:327:VAL:O	2.20	0.41
1:M:387:TRP:CE2	1:M:389:THR:HA	2.55	0.41
1:M:786:ASN:ND2	1:M:805:VAL:H	2.18	0.41
1:O:262:LYS:HG2	2:P:232:PHE:CE1	2.55	0.41
1:Q:402:PRO:HG2	1:Q:422:PHE:CE1	2.56	0.41
1:Q:142:SER:OG	4:Q:902:MGD:O1A	2.15	0.41
1:S:452:ILE:HB	1:S:453:PRO:HD3	2.03	0.41
1:S:868:ASP:HA	8:S:1002:HOH:O	2.21	0.41
1:U:625:MET:N	1:U:626:PRO:CD	2.83	0.41
1:W:495:LYS:HD2	1:W:514:TYR:OH	2.20	0.41
2:X:19:CYS:O	2:X:22:GLY:N	2.54	0.41
1:A:124:GLU:HG3	1:A:521:PHE:CD2	2.55	0.41
1:A:558:SER:H	1:A:564:ASN:ND2	2.19	0.41
1:C:53:PRO:HA	1:C:54:PRO:HD3	1.91	0.41
1:C:825:PRO:HD2	8:C:1337:HOH:O	2.21	0.41
2:F:205:VAL:HG13	2:F:254:LYS:HZ2	1.82	0.41
1:G:501:LEU:HA	1:G:507:THR:HB	2.03	0.41
1:I:174:ASP:OD1	1:I:175:SER:N	2.50	0.41
2:J:72:GLU:HG2	2:J:185:ARG:NH2	2.36	0.41
1:K:31:MET:HE1	1:K:639:TYR:CG	2.56	0.41
1:K:558:SER:H	1:K:564:ASN:ND2	2.18	0.41
1:K:673:ASN:H	1:K:673:ASN:ND2	2.18	0.41
2:L:256:TYR:HB2	2:L:274:LEU:HD21	2.01	0.41
1:M:15:PRO:HD2	8:M:1003:HOH:O	2.20	0.41
1:M:421:LYS:HA	1:M:424:TRP:HD1	1.86	0.41
1:O:498:GLY:N	1:O:499:PRO:HD3	2.36	0.41
2:P:23:CYS:O	2:P:27:HIS:N	2.45	0.41
2:R:95:ASP:HB3	2:R:98:LYS:HB2	2.03	0.41
1:S:625:MET:N	1:S:626:PRO:CD	2.83	0.41
1:S:857:ASN:HB3	4:S:902:MGD:N19	2.35	0.41
1:U:610:LYS:NZ	1:U:618:GLN:NE2	2.64	0.41
1:W:2:GLY:N	1:W:22:ASP:OD1	2.53	0.41
1:W:563:ASP:HA	1:W:565:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:296:ASN:HB3	1:W:657:PHE:CZ	2.55	0.41
2:X:210:PHE:CE2	2:X:251:ALA:HB1	2.55	0.41
1:A:39:ALA:HA	1:A:40:PRO:HD3	1.90	0.41
1:A:649:LYS:O	1:A:649:LYS:HG3	2.21	0.41
2:D:56:TYR:HA	2:D:59:ASN:ND2	2.36	0.41
1:E:21:LYS:HB3	1:E:26:ILE:HD11	2.03	0.41
1:E:670:PRO:HG2	1:E:675:GLN:CD	2.41	0.41
1:G:69:MET:CE	1:G:754:MET:HE3	2.50	0.41
1:I:175:SER:HB2	1:I:176:TRP:CZ3	2.56	0.41
1:I:451:LYS:HG3	1:I:461:PHE:CE2	2.54	0.41
1:I:521:PHE:CE2	1:I:523:VAL:CG2	3.04	0.41
1:K:269:GLY:HA2	1:K:362:HIS:CG	2.55	0.41
1:K:277:ALA:HB2	1:K:321:ALA:HB2	2.03	0.41
1:K:401:PHE:HA	1:K:402:PRO:HD3	1.90	0.41
1:M:165:GLY:CA	1:M:166:PHE:HB3	2.48	0.41
1:M:571:ARG:HB2	1:M:642:VAL:HB	2.03	0.41
2:N:105:LEU:HB3	2:N:114:MET:CE	2.50	0.41
1:Q:32:ASP:HB2	8:Q:1658:HOH:O	2.21	0.41
1:Q:736:SER:HA	1:Q:816:SER:O	2.21	0.41
1:S:328:PRO:HB2	1:S:331:GLU:HG3	2.03	0.41
1:S:816:SER:OG	1:S:839:ILE:HG13	2.19	0.41
2:T:10:VAL:HG13	2:T:63:TYR:O	2.20	0.41
2:V:167:LYS:HZ3	2:V:171:GLU:CD	2.24	0.41
1:W:541:PRO:HB2	1:W:586:SER:HA	2.02	0.41
1:W:66:PHE:HA	1:W:69:MET:HE2	2.03	0.41
2:D:139:ALA:HB3	2:D:140:PRO:HD3	2.02	0.41
2:D:252:ASP:C	2:D:254:LYS:H	2.23	0.41
2:D:87:ARG:HG3	2:D:91:ILE:O	2.21	0.41
1:E:155:SER:OG	1:E:409:ILE:HG12	2.21	0.41
2:F:175:VAL:HG23	2:F:178:PRO:HG3	2.02	0.41
2:F:74:ALA:HA	2:F:75:PRO:HD3	1.85	0.41
1:G:118:THR:O	1:G:122:VAL:HG23	2.21	0.41
2:H:64:ARG:NH1	8:H:417:HOH:O	2.48	0.41
1:I:393:VAL:HA	1:I:394:PRO:HD3	1.83	0.41
1:M:138:LEU:HB2	1:M:490:ILE:HD12	2.03	0.41
1:O:39:ALA:HA	1:O:40:PRO:HD3	1.90	0.41
1:Q:103:GLN:CD	1:Q:103:GLN:N	2.74	0.41
1:S:701:GLN:HG3	8:S:1644:HOH:O	2.19	0.41
8:N:1045:HOH:O	1:S:729:LYS:HE2	2.20	0.41
1:S:738:HIS:ND1	4:S:903:MGD:N15	2.65	0.41
2:T:139:ALA:HB3	2:T:140:PRO:HD3	2.01	0.41
1:U:69:MET:HE1	1:U:754:MET:HE3	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:269:GLY:HA2	1:W:362:HIS:CG	2.56	0.41
1:W:571:ARG:HA	8:W:1025:HOH:O	2.20	0.41
2:X:60:ASP:OD1	2:X:60:ASP:C	2.58	0.41
1:A:408:GLY:HA2	1:A:619:TYR:HE1	1.86	0.41
2:B:2:GLU:HG2	2:B:158:LYS:HG2	2.02	0.41
1:C:128:ILE:CD1	1:C:492:MET:HB2	2.51	0.41
1:C:395:LEU:HD13	1:C:571:ARG:CG	2.50	0.41
2:F:162:GLU:CD	2:F:162:GLU:H	2.23	0.41
1:G:277:ALA:HB2	1:G:321:ALA:HB2	2.02	0.41
2:H:23:CYS:HB3	2:H:39:MET:HE3	2.03	0.41
1:K:134:PRO:HD2	8:K:1354:HOH:O	2.20	0.41
1:K:128:ILE:CD1	1:K:492:MET:HB2	2.51	0.41
1:K:737:PRO:HG3	4:K:903:MGD:H2'	2.03	0.41
2:L:110:PRO:HB2	2:L:180:LEU:HD13	2.02	0.41
2:L:219:SER:C	2:L:221:GLY:H	2.25	0.41
1:K:211:MET:CE	2:L:231:PHE:CZ	3.04	0.41
2:L:74:ALA:HA	2:L:75:PRO:HD3	1.92	0.41
1:M:323:GLU:HB3	8:M:1109:HOH:O	2.21	0.41
1:M:670:PRO:HG2	1:M:675:GLN:CD	2.41	0.41
2:N:46:MET:CE	2:N:66:THR:N	2.82	0.41
4:O:903:MGD:C4'	4:O:903:MGD:O1B	2.68	0.41
2:T:114:MET:HA	2:T:125:LYS:HB3	2.02	0.41
2:V:19:CYS:CB	2:V:145:CYS:HB3	2.46	0.41
1:W:402:PRO:HG2	1:W:422:PHE:CE1	2.56	0.41
1:A:146:MET:HE1	1:A:544:THR:CB	2.47	0.41
1:A:776:SER:HA	1:A:805:VAL:HG13	2.02	0.41
1:E:800:ILE:CD1	1:E:800:ILE:N	2.84	0.41
2:F:201:ALA:HB3	2:F:235:PHE:CE2	2.56	0.41
1:G:134:PRO:HB2	1:G:439:LEU:CD1	2.51	0.41
1:G:565:TYR:C	1:G:567:LEU:H	2.24	0.41
1:K:75:ARG:HH21	1:K:543:CYS:HA	1.86	0.41
2:L:105:LEU:HB3	2:L:114:MET:HE2	2.03	0.41
1:M:418:ALA:HB1	1:M:423:ALA:HB2	2.03	0.41
1:M:55:ARG:HD2	8:M:1638:HOH:O	2.20	0.41
1:M:76:ILE:HG22	1:M:541:PRO:HG3	2.03	0.41
2:N:106:LEU:HD23	2:N:114:MET:HE2	2.02	0.41
1:Q:426:MET:HA	1:Q:426:MET:CE	2.37	0.41
1:Q:74:LEU:HA	1:Q:74:LEU:HD23	1.91	0.41
1:S:494:TRP:HE1	1:S:525:GLN:HE21	1.69	0.41
1:U:15:PRO:HD2	8:U:1006:HOH:O	2.20	0.41
1:U:2:GLY:O	1:U:21:LYS:HE3	2.21	0.41
1:U:175:SER:OG	6:U:905:BTT:C5	2.68	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:250:PRO:HD3	4:W:903:MGD:C2	2.51	0.41
1:W:656:TRP:CD2	1:W:663:LYS:HA	2.56	0.41
1:W:175:SER:OG	6:W:905:BTT:C5	2.69	0.41
2:X:71:CYS:HB2	2:X:182:THR:O	2.20	0.41
1:A:301:GLU:CD	1:A:301:GLU:N	2.72	0.41
1:A:495:LYS:CD	1:A:514:TYR:OH	2.68	0.41
2:D:114:MET:HB3	2:D:125:LYS:HG2	2.02	0.41
1:E:425:ARG:HD3	1:E:622:ALA:O	2.21	0.41
2:F:58:ARG:HD2	2:F:268:ASP:OD1	2.20	0.41
2:F:60:ASP:OD1	2:F:60:ASP:C	2.60	0.41
1:I:197:GLU:HG3	1:I:653:ALA:HB1	2.03	0.41
1:I:800:ILE:CD1	1:I:800:ILE:N	2.84	0.41
2:L:119:GLU:O	2:L:119:GLU:HG2	2.21	0.41
2:L:164:MET:O	2:L:168:VAL:HG23	2.21	0.41
2:L:23:CYS:HB3	2:L:39:MET:HE3	2.02	0.41
1:M:176:TRP:O	1:M:177:GLU:C	2.59	0.41
2:N:177:LYS:N	2:N:178:PRO:HD3	2.36	0.41
1:O:425:ARG:NH2	8:O:1082:HOH:O	2.51	0.41
1:S:15:PRO:HD3	1:S:554:PHE:CD1	2.56	0.41
1:S:177:GLU:OE2	1:S:177:GLU:HA	2.21	0.41
2:V:87:ARG:HB2	2:V:89:ASP:OD2	2.21	0.41
1:W:118:THR:O	1:W:122:VAL:HG23	2.21	0.41
1:W:272:HIS:ND1	1:W:272:HIS:N	2.69	0.41
1:W:757:ILE:CG1	2:X:21:MET:HE1	2.51	0.41
1:A:533:VAL:HB	1:A:534:PRO:HD3	2.03	0.40
2:B:167:LYS:HZ3	2:B:171:GLU:CD	2.23	0.40
2:B:21:MET:CA	2:B:21:MET:CE	2.99	0.40
2:B:60:ASP:OD1	2:B:60:ASP:C	2.60	0.40
1:C:730:TYR:CE1	1:C:794:ASN:HA	2.56	0.40
1:C:211:MET:CE	2:D:231:PHE:CZ	3.04	0.40
1:I:533:VAL:HB	1:I:534:PRO:HD3	2.03	0.40
1:I:66:PHE:HA	1:I:69:MET:HE2	2.02	0.40
1:K:69:MET:HE1	1:K:754:MET:HE3	2.04	0.40
2:L:103:LYS:HG2	2:L:116:TRP:CD2	2.56	0.40
1:M:1:MET:H3	1:M:22:ASP:CG	2.25	0.40
1:O:11:SER:HA	1:O:147:TRP:HB2	2.03	0.40
1:O:362:HIS:HB3	1:O:717:ALA:HB2	2.02	0.40
1:O:402:PRO:HG2	1:O:422:PHE:CE1	2.56	0.40
1:S:322:GLU:HG3	1:S:327:VAL:O	2.21	0.40
1:U:408:GLY:HA2	1:U:619:TYR:HE1	1.85	0.40
1:W:277:ALA:HB2	1:W:321:ALA:HB2	2.02	0.40
1:W:378:GLY:O	1:W:381:LYS:HG2	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:W:540:LEU:HA	1:W:541:PRO:HD3	1.82	0.40
1:W:362:HIS:HB3	1:W:717:ALA:HB2	2.03	0.40
2:X:53:ARG:HB2	2:X:60:ASP:OD1	2.22	0.40
1:A:165:GLY:CA	1:A:166:PHE:HB3	2.45	0.40
1:A:495:LYS:HE3	1:A:495:LYS:HB3	1.90	0.40
1:C:175:SER:HB2	1:C:176:TRP:CE3	2.56	0.40
1:C:436:PRO:HG3	8:C:1460:HOH:O	2.21	0.40
1:C:564:ASN:H	1:C:564:ASN:HD22	1.69	0.40
1:C:69:MET:CE	1:C:754:MET:HE3	2.51	0.40
2:D:68:CYS:HB2	2:D:126:CYS:HB2	2.02	0.40
1:E:571:ARG:HA	8:E:1026:HOH:O	2.22	0.40
1:G:433:PHE:CD1	1:G:433:PHE:N	2.89	0.40
1:G:649:LYS:HE3	1:G:651:THR:CG2	2.51	0.40
1:G:845:ASP:OD2	1:G:845:ASP:N	2.51	0.40
1:I:414:GLU:O	1:I:414:GLU:HG3	2.21	0.40
1:I:15:PRO:HD3	1:I:554:PHE:CE1	2.56	0.40
1:M:44:ILE:HD11	1:M:394:PRO:CG	2.51	0.40
2:N:9:ASP:HA	2:N:189:LYS:HB3	2.02	0.40
1:Q:501:LEU:HD13	1:Q:823:TYR:CG	2.56	0.40
1:Q:870:ASP:HB3	1:Q:872:TYR:CE1	2.56	0.40
2:R:69:MET:HB3	2:R:184:PRO:HB3	2.04	0.40
1:U:322:GLU:HG3	1:U:327:VAL:O	2.22	0.40
1:U:114:TRP:CZ2	1:U:587:MET:HG2	2.56	0.40
1:U:673:ASN:HD22	1:U:673:ASN:H	1.69	0.40
1:U:786:ASN:ND2	1:U:805:VAL:H	2.19	0.40
1:W:839:ILE:HD13	1:W:839:ILE:HA	1.96	0.40
2:X:218:LYS:HG2	2:X:223:GLU:HA	2.02	0.40
1:A:696:LYS:HD3	8:A:1677:HOH:O	2.20	0.40
1:A:800:ILE:N	1:A:800:ILE:CD1	2.83	0.40
2:B:143:PRO:HB3	7:B:303:SF4:S1	2.61	0.40
1:C:251:HIS:HA	1:C:809:LEU:HD23	2.04	0.40
1:C:395:LEU:HD13	1:C:571:ARG:HG2	2.03	0.40
1:C:76:ILE:HG22	1:C:541:PRO:HG3	2.02	0.40
1:G:15:PRO:HD2	8:G:1003:HOH:O	2.20	0.40
2:J:7:VAL:HB	2:J:155:GLU:HB3	2.03	0.40
1:K:12:THR:O	1:K:226:TYR:HA	2.21	0.40
1:M:391:GLN:HG2	1:M:567:LEU:HD23	2.03	0.40
1:M:736:SER:O	4:M:902:MGD:N18	2.54	0.40
1:O:142:SER:CB	4:O:902:MGD:O1A	2.70	0.40
1:Q:397:TYR:HA	1:Q:565:TYR:OH	2.21	0.40
1:Q:9:ASN:HA	1:Q:576:GLN:HA	2.03	0.40
1:S:76:ILE:HA	1:S:77:PRO:HD3	1.79	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:T:139:ALA:O	2:T:141:LYS:HG3	2.20	0.40
2:T:53:ARG:HB2	2:T:60:ASP:OD1	2.22	0.40
2:V:122:VAL:HG22	2:V:123:ALA:N	2.36	0.40
1:A:134:PRO:HG2	1:A:439:LEU:HD11	2.03	0.40
1:A:393:VAL:HA	1:A:394:PRO:HD3	1.80	0.40
1:C:387:TRP:CZ2	1:C:389:THR:HA	2.56	0.40
2:D:124:GLN:O	2:D:125:LYS:HB3	2.21	0.40
2:J:68:CYS:CB	2:J:126:CYS:CB	2.85	0.40
1:K:396:ASP:OD2	1:K:398:GLU:HB2	2.21	0.40
1:K:540:LEU:HA	1:K:541:PRO:HD3	1.81	0.40
2:N:139:ALA:HB3	2:N:140:PRO:HD3	2.03	0.40
2:N:198:TYR:HB3	2:N:238:ASP:HA	2.04	0.40
1:O:76:ILE:HD13	1:O:539:ILE:CG2	2.51	0.40
1:O:730:TYR:CE1	1:O:794:ASN:HA	2.57	0.40
1:Q:263:TRP:CZ2	1:Q:265:SER:HB2	2.57	0.40
1:S:31:MET:HE1	1:S:639:TYR:CG	2.56	0.40
1:U:141:PRO:CA	1:U:496:TYR:HB3	2.43	0.40
1:U:767:TYR:HB3	1:U:769:TYR:CE1	2.57	0.40
1:W:12:THR:O	1:W:226:TYR:HA	2.22	0.40
1:W:69:MET:CE	1:W:754:MET:HE3	2.51	0.40
1:W:719:GLU:HG2	1:W:859:THR:O	2.21	0.40
2:X:159:THR:OG1	2:X:160:THR:N	2.53	0.40
2:X:40:GLN:NE2	2:X:117:ASN:HA	2.35	0.40
2:X:46:MET:CE	2:X:66:THR:N	2.82	0.40
1:A:498:GLY:N	1:A:499:PRO:HD3	2.37	0.40
1:A:397:TYR:HA	1:A:565:TYR:OH	2.22	0.40
1:A:756:TYR:CE2	1:A:768:LYS:HE2	2.57	0.40
2:D:142:MET:HE1	8:D:927:HOH:O	2.21	0.40
2:D:177:LYS:N	2:D:178:PRO:HD3	2.37	0.40
1:E:32:ASP:OD2	1:E:32:ASP:N	2.54	0.40
1:E:45:GLU:OE2	1:E:45:GLU:N	2.55	0.40
1:E:845:ASP:N	1:E:845:ASP:OD2	2.53	0.40
2:F:19:CYS:O	2:F:22:GLY:N	2.55	0.40
1:G:153:ARG:O	1:G:157:TYR:HB3	2.22	0.40
1:G:69:MET:CE	1:G:754:MET:CE	2.99	0.40
1:G:801:LEU:HD11	1:G:839:ILE:HD11	2.03	0.40
1:G:800:ILE:CD1	1:G:833:ALA:HB1	2.51	0.40
1:I:571:ARG:HB2	1:I:642:VAL:HB	2.03	0.40
2:J:2:GLU:HG3	2:J:159:THR:C	2.42	0.40
1:K:400:TYR:CZ	1:K:421:LYS:HD2	2.56	0.40
2:L:27:HIS:HE1	8:L:473:HOH:O	2.04	0.40
1:M:214:PHE:HA	1:M:347:ALA:HB3	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:N:46:MET:HB2	7:N:303:SF4:S2	2.62	0.40
1:Q:45:GLU:OE2	1:Q:45:GLU:N	2.55	0.40
1:Q:784:ILE:HD13	1:Q:790:ILE:HG21	2.04	0.40
2:R:201:ALA:HB2	2:R:269:LEU:HB2	2.04	0.40
1:S:498:GLY:N	1:S:499:PRO:HD3	2.36	0.40
1:S:772:MET:HB2	1:S:801:LEU:HD13	2.04	0.40
1:W:495:LYS:CD	1:W:514:TYR:OH	2.70	0.40
2:X:59:ASN:HD22	2:X:59:ASN:N	2.17	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:A:1584:HOH:O	8:O:1361:HOH:O[1_644]	2.06	0.14
1:O:162:ASN:O	8:A:1584:HOH:O[1_466]	2.19	0.01

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	873/875 (100%)	827 (95%)	44 (5%)	2 (0%)	56	51
1	C	873/875 (100%)	833 (95%)	37 (4%)	3 (0%)	50	44
1	E	873/875 (100%)	832 (95%)	39 (4%)	2 (0%)	56	51
1	G	873/875 (100%)	833 (95%)	37 (4%)	3 (0%)	50	44
1	I	873/875 (100%)	826 (95%)	44 (5%)	3 (0%)	50	44
1	K	873/875 (100%)	831 (95%)	39 (4%)	3 (0%)	50	44
1	M	873/875 (100%)	829 (95%)	41 (5%)	3 (0%)	50	44
1	O	873/875 (100%)	827 (95%)	43 (5%)	3 (0%)	50	44
1	Q	873/875 (100%)	835 (96%)	35 (4%)	3 (0%)	50	44
1	S	873/875 (100%)	826 (95%)	43 (5%)	4 (0%)	38	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	U	873/875 (100%)	829 (95%)	41 (5%)	3 (0%)	50	44
1	W	873/875 (100%)	826 (95%)	44 (5%)	3 (0%)	50	44
2	B	272/274 (99%)	260 (96%)	11 (4%)	1 (0%)	43	36
2	D	272/274 (99%)	259 (95%)	12 (4%)	1 (0%)	43	36
2	F	272/274 (99%)	259 (95%)	11 (4%)	2 (1%)	30	20
2	H	272/274 (99%)	258 (95%)	12 (4%)	2 (1%)	30	20
2	J	272/274 (99%)	261 (96%)	10 (4%)	1 (0%)	43	36
2	L	272/274 (99%)	259 (95%)	11 (4%)	2 (1%)	30	20
2	N	272/274 (99%)	262 (96%)	9 (3%)	1 (0%)	43	36
2	P	272/274 (99%)	260 (96%)	11 (4%)	1 (0%)	43	36
2	R	272/274 (99%)	260 (96%)	10 (4%)	2 (1%)	30	20
2	T	272/274 (99%)	259 (95%)	11 (4%)	2 (1%)	30	20
2	V	272/274 (99%)	258 (95%)	13 (5%)	1 (0%)	43	36
2	X	272/274 (99%)	252 (93%)	18 (7%)	2 (1%)	30	20
All	All	13740/13788 (100%)	13061 (95%)	626 (5%)	53 (0%)	43	36

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	177	GLU
1	C	177	GLU
1	E	177	GLU
1	G	177	GLU
1	K	177	GLU
1	M	177	GLU
1	O	177	GLU
1	S	177	GLU
1	S	648	ARG
1	U	177	GLU
1	W	177	GLU
1	E	141	PRO
1	I	177	GLU
1	Q	177	GLU
1	A	141	PRO
1	C	141	PRO
1	G	141	PRO
1	I	141	PRO

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Mol	Chain	Res	Type
1	K	141	PRO
1	M	141	PRO
1	O	141	PRO
1	Q	141	PRO
1	S	141	PRO
2	T	145	CYS
1	U	141	PRO
1	W	141	PRO
2	X	221	GLY
2	L	145	CYS
1	C	225	ILE
2	D	67	PRO
2	F	19	CYS
2	H	67	PRO
2	L	67	PRO
2	N	67	PRO
2	R	145	CYS
2	V	67	PRO
2	X	67	PRO
2	F	67	PRO
1	G	354	TRP
2	H	19	CYS
2	J	67	PRO
1	M	225	ILE
2	P	67	PRO
2	R	67	PRO
2	T	67	PRO
2	B	67	PRO
1	K	225	ILE
1	O	225	ILE
1	S	225	ILE
1	I	225	ILE
1	U	225	ILE
1	W	225	ILE
1	Q	225	ILE

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	729/729 (100%)	713 (98%)	16 (2%)	64	65
1	C	729/729 (100%)	713 (98%)	16 (2%)	64	65
1	E	729/729 (100%)	716 (98%)	13 (2%)	71	73
1	G	729/729 (100%)	713 (98%)	16 (2%)	64	65
1	I	729/729 (100%)	714 (98%)	15 (2%)	66	67
1	K	729/729 (100%)	714 (98%)	15 (2%)	66	67
1	M	729/729 (100%)	713 (98%)	16 (2%)	64	65
1	O	729/729 (100%)	714 (98%)	15 (2%)	66	67
1	Q	729/729 (100%)	713 (98%)	16 (2%)	64	65
1	S	729/729 (100%)	717 (98%)	12 (2%)	75	77
1	U	729/729 (100%)	715 (98%)	14 (2%)	69	71
1	W	729/729 (100%)	713 (98%)	16 (2%)	64	65
2	B	235/235 (100%)	223 (95%)	12 (5%)	33	26
2	D	235/235 (100%)	221 (94%)	14 (6%)	27	20
2	F	235/235 (100%)	227 (97%)	8 (3%)	49	45
2	H	235/235 (100%)	226 (96%)	9 (4%)	44	39
2	J	235/235 (100%)	223 (95%)	12 (5%)	33	26
2	L	235/235 (100%)	225 (96%)	10 (4%)	40	33
2	N	235/235 (100%)	226 (96%)	9 (4%)	44	39
2	P	235/235 (100%)	223 (95%)	12 (5%)	33	26
2	R	235/235 (100%)	227 (97%)	8 (3%)	49	45
2	T	235/235 (100%)	224 (95%)	11 (5%)	36	29
2	V	235/235 (100%)	225 (96%)	10 (4%)	40	33
2	X	235/235 (100%)	223 (95%)	12 (5%)	33	26
All	All	11568/11568 (100%)	11261 (97%)	307 (3%)	57	56

All (307) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	78	TYR
1	A	142	SER
1	A	187	TRP
1	A	358	CYS
1	A	373	LEU

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Mol	Chain	Res	Type
1	A	426	MET
1	A	462	GLN
1	A	493	PHE
1	A	499	PRO
1	A	560	TYR
1	A	564	ASN
1	A	605	MET
1	A	726	LEU
1	A	743	MET
1	A	818	GLU
2	B	13	CYS
2	B	19	CYS
2	B	21	MET
2	B	23	CYS
2	B	71	CYS
2	B	76	CYS
2	B	104	GLU
2	B	109	CYS
2	B	125	LYS
2	B	126	CYS
2	B	149	CYS
2	B	157	LEU
1	C	55	ARG
1	C	78	TYR
1	C	142	SER
1	C	187	TRP
1	C	373	LEU
1	C	462	GLN
1	C	493	PHE
1	C	499	PRO
1	C	560	TYR
1	C	564	ASN
1	C	605	MET
1	C	743	MET
1	C	786	ASN
1	C	801	LEU
1	C	818	GLU
1	C	870	ASP
2	D	13	CYS
2	D	19	CYS
2	D	21	MET
2	D	71	CYS

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Mol	Chain	Res	Type
2	D	73	ASN
2	D	76	CYS
2	D	109	CYS
2	D	121	ASN
2	D	125	LYS
2	D	126	CYS
2	D	129	CYS
2	D	145	CYS
2	D	149	CYS
2	D	179	GLU
1	E	78	TYR
1	E	142	SER
1	E	187	TRP
1	E	462	GLN
1	E	493	PHE
1	E	499	PRO
1	E	560	TYR
1	E	564	ASN
1	E	605	MET
1	E	673	ASN
1	E	719	GLU
1	E	743	MET
1	E	818	GLU
2	F	13	CYS
2	F	21	MET
2	F	57	PRO
2	F	71	CYS
2	F	76	CYS
2	F	109	CYS
2	F	125	LYS
2	F	149	CYS
1	G	55	ARG
1	G	78	TYR
1	G	142	SER
1	G	187	TRP
1	G	358	CYS
1	G	373	LEU
1	G	426	MET
1	G	462	GLN
1	G	493	PHE
1	G	499	PRO
1	G	554	PHE

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Mol	Chain	Res	Type
1	G	560	TYR
1	G	564	ASN
1	G	605	MET
1	G	743	MET
1	G	818	GLU
2	H	13	CYS
2	H	21	MET
2	H	71	CYS
2	H	76	CYS
2	H	109	CYS
2	H	125	LYS
2	H	126	CYS
2	H	149	CYS
2	H	157	LEU
1	I	55	ARG
1	I	78	TYR
1	I	142	SER
1	I	187	TRP
1	I	358	CYS
1	I	373	LEU
1	I	426	MET
1	I	462	GLN
1	I	499	PRO
1	I	560	TYR
1	I	564	ASN
1	I	605	MET
1	I	726	LEU
1	I	743	MET
1	I	818	GLU
2	J	13	CYS
2	J	19	CYS
2	J	21	MET
2	J	71	CYS
2	J	76	CYS
2	J	104	GLU
2	J	109	CYS
2	J	125	LYS
2	J	126	CYS
2	J	145	CYS
2	J	149	CYS
2	J	157	LEU
1	K	55	ARG

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Mol	Chain	Res	Type
1	K	78	TYR
1	K	142	SER
1	K	187	TRP
1	K	373	LEU
1	K	426	MET
1	K	462	GLN
1	K	493	PHE
1	K	499	PRO
1	K	560	TYR
1	K	564	ASN
1	K	605	MET
1	K	726	LEU
1	K	786	ASN
1	K	818	GLU
2	L	13	CYS
2	L	19	CYS
2	L	71	CYS
2	L	73	ASN
2	L	76	CYS
2	L	109	CYS
2	L	125	LYS
2	L	126	CYS
2	L	149	CYS
2	L	157	LEU
1	M	78	TYR
1	M	142	SER
1	M	187	TRP
1	M	358	CYS
1	M	426	MET
1	M	462	GLN
1	M	493	PHE
1	M	499	PRO
1	M	560	TYR
1	M	564	ASN
1	M	605	MET
1	M	719	GLU
1	M	726	LEU
1	M	743	MET
1	M	786	ASN
1	M	818	GLU
2	N	2	GLU
2	N	13	CYS

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Mol	Chain	Res	Type
2	N	21	MET
2	N	71	CYS
2	N	76	CYS
2	N	109	CYS
2	N	125	LYS
2	N	126	CYS
2	N	149	CYS
1	O	55	ARG
1	O	78	TYR
1	O	142	SER
1	O	187	TRP
1	O	272	HIS
1	O	462	GLN
1	O	493	PHE
1	O	499	PRO
1	O	560	TYR
1	O	564	ASN
1	O	605	MET
1	O	726	LEU
1	O	743	MET
1	O	786	ASN
1	O	818	GLU
2	P	13	CYS
2	P	19	CYS
2	P	57	PRO
2	P	71	CYS
2	P	73	ASN
2	P	76	CYS
2	P	109	CYS
2	P	125	LYS
2	P	126	CYS
2	P	129	CYS
2	P	145	CYS
2	P	149	CYS
1	Q	55	ARG
1	Q	78	TYR
1	Q	100	LEU
1	Q	142	SER
1	Q	187	TRP
1	Q	373	LEU
1	Q	426	MET
1	Q	462	GLN

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Mol	Chain	Res	Type
1	Q	493	PHE
1	Q	499	PRO
1	Q	560	TYR
1	Q	564	ASN
1	Q	605	MET
1	Q	708	ARG
1	Q	743	MET
1	Q	818	GLU
2	R	13	CYS
2	R	21	MET
2	R	71	CYS
2	R	76	CYS
2	R	109	CYS
2	R	125	LYS
2	R	149	CYS
2	R	157	LEU
1	S	55	ARG
1	S	78	TYR
1	S	142	SER
1	S	187	TRP
1	S	462	GLN
1	S	499	PRO
1	S	560	TYR
1	S	564	ASN
1	S	605	MET
1	S	726	LEU
1	S	743	MET
1	S	818	GLU
2	T	13	CYS
2	T	19	CYS
2	T	21	MET
2	T	71	CYS
2	T	73	ASN
2	T	76	CYS
2	T	109	CYS
2	T	125	LYS
2	T	126	CYS
2	T	149	CYS
2	T	157	LEU
1	U	78	TYR
1	U	142	SER
1	U	187	TRP

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Mol	Chain	Res	Type
1	U	414	GLU
1	U	462	GLN
1	U	493	PHE
1	U	499	PRO
1	U	560	TYR
1	U	564	ASN
1	U	605	MET
1	U	719	GLU
1	U	726	LEU
1	U	743	MET
1	U	818	GLU
2	V	13	CYS
2	V	21	MET
2	V	71	CYS
2	V	73	ASN
2	V	76	CYS
2	V	109	CYS
2	V	125	LYS
2	V	126	CYS
2	V	145	CYS
2	V	149	CYS
1	W	78	TYR
1	W	108	ASP
1	W	142	SER
1	W	187	TRP
1	W	373	LEU
1	W	426	MET
1	W	462	GLN
1	W	499	PRO
1	W	554	PHE
1	W	560	TYR
1	W	564	ASN
1	W	605	MET
1	W	708	ARG
1	W	743	MET
1	W	786	ASN
1	W	818	GLU
2	X	13	CYS
2	X	19	CYS
2	X	21	MET
2	X	59	ASN
2	X	71	CYS

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Mol	Chain	Res	Type
2	X	109	CYS
2	X	125	LYS
2	X	126	CYS
2	X	129	CYS
2	X	145	CYS
2	X	149	CYS
2	X	157	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (229) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
1	A	171	HIS
1	A	222	ASN
1	A	462	GLN
1	A	478	HIS
1	A	525	GLN
1	A	564	ASN
1	A	618	GLN
1	A	673	ASN
1	A	697	ASN
1	A	701	GLN
1	A	721	GLN
1	A	786	ASN
2	B	27	HIS
2	B	40	GLN
2	B	59	ASN
2	B	70	HIS
2	B	73	ASN
1	C	162	ASN
1	C	222	ASN
1	C	478	HIS
1	C	525	GLN
1	C	564	ASN
1	C	618	GLN
1	C	673	ASN
1	C	697	ASN
1	C	701	GLN
1	C	721	GLN
1	C	786	ASN
2	D	27	HIS
2	D	40	GLN

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Mol	Chain	Res	Type
2	D	59	ASN
2	D	70	HIS
2	D	73	ASN
2	D	81	ASN
1	E	162	ASN
1	E	171	HIS
1	E	222	ASN
1	E	462	GLN
1	E	478	HIS
1	E	525	GLN
1	E	564	ASN
1	E	576	GLN
1	E	618	GLN
1	E	673	ASN
1	E	697	ASN
1	E	701	GLN
1	E	721	GLN
1	E	786	ASN
2	F	27	HIS
2	F	40	GLN
2	F	59	ASN
2	F	70	HIS
2	F	73	ASN
2	F	81	ASN
1	G	162	ASN
1	G	171	HIS
1	G	222	ASN
1	G	415	ASN
1	G	440	ASN
1	G	462	GLN
1	G	478	HIS
1	G	525	GLN
1	G	564	ASN
1	G	576	GLN
1	G	618	GLN
1	G	673	ASN
1	G	697	ASN
1	G	701	GLN
1	G	721	GLN
1	G	786	ASN
2	H	27	HIS
2	H	40	GLN

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Mol	Chain	Res	Type
2	H	59	ASN
2	H	70	HIS
2	H	73	ASN
2	H	81	ASN
1	I	162	ASN
1	I	171	HIS
1	I	222	ASN
1	I	462	GLN
1	I	478	HIS
1	I	525	GLN
1	I	564	ASN
1	I	618	GLN
1	I	673	ASN
1	I	697	ASN
1	I	701	GLN
1	I	721	GLN
1	I	786	ASN
2	J	27	HIS
2	J	40	GLN
2	J	59	ASN
2	J	70	HIS
2	J	73	ASN
2	J	81	ASN
2	J	86	GLN
1	K	162	ASN
1	K	171	HIS
1	K	222	ASN
1	K	462	GLN
1	K	478	HIS
1	K	525	GLN
1	K	564	ASN
1	K	618	GLN
1	K	673	ASN
1	K	697	ASN
1	K	701	GLN
1	K	721	GLN
1	K	786	ASN
2	L	27	HIS
2	L	40	GLN
2	L	59	ASN
2	L	70	HIS
2	L	73	ASN

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Mol	Chain	Res	Type
2	L	81	ASN
1	M	162	ASN
1	M	171	HIS
1	M	462	GLN
1	M	478	HIS
1	M	525	GLN
1	M	564	ASN
1	M	618	GLN
1	M	673	ASN
1	M	697	ASN
1	M	701	GLN
1	M	721	GLN
1	M	786	ASN
2	N	27	HIS
2	N	40	GLN
2	N	59	ASN
2	N	70	HIS
2	N	73	ASN
2	N	81	ASN
1	O	130	HIS
1	O	162	ASN
1	O	171	HIS
1	O	222	ASN
1	O	478	HIS
1	O	525	GLN
1	O	564	ASN
1	O	618	GLN
1	O	673	ASN
1	O	697	ASN
1	O	701	GLN
1	O	721	GLN
1	O	786	ASN
2	P	27	HIS
2	P	40	GLN
2	P	59	ASN
2	P	70	HIS
2	P	81	ASN
1	Q	162	ASN
1	Q	171	HIS
1	Q	222	ASN
1	Q	462	GLN
1	Q	478	HIS

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Mol	Chain	Res	Type
1	Q	525	GLN
1	Q	564	ASN
1	Q	618	GLN
1	Q	697	ASN
1	Q	701	GLN
1	Q	721	GLN
1	Q	786	ASN
2	R	27	HIS
2	R	40	GLN
2	R	59	ASN
2	R	70	HIS
2	R	73	ASN
2	R	81	ASN
1	S	130	HIS
1	S	162	ASN
1	S	171	HIS
1	S	222	ASN
1	S	478	HIS
1	S	525	GLN
1	S	564	ASN
1	S	618	GLN
1	S	673	ASN
1	S	697	ASN
1	S	701	GLN
1	S	721	GLN
1	S	786	ASN
2	T	27	HIS
2	T	40	GLN
2	T	59	ASN
2	T	70	HIS
2	T	73	ASN
2	T	81	ASN
1	U	130	HIS
1	U	162	ASN
1	U	171	HIS
1	U	222	ASN
1	U	462	GLN
1	U	478	HIS
1	U	525	GLN
1	U	564	ASN
1	U	576	GLN
1	U	618	GLN

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Mol	Chain	Res	Type
1	U	673	ASN
1	U	697	ASN
1	U	701	GLN
1	U	721	GLN
1	U	786	ASN
2	V	27	HIS
2	V	40	GLN
2	V	59	ASN
2	V	70	HIS
2	V	73	ASN
2	V	81	ASN
1	W	162	ASN
1	W	171	HIS
1	W	222	ASN
1	W	462	GLN
1	W	478	HIS
1	W	525	GLN
1	W	564	ASN
1	W	618	GLN
1	W	645	ASN
1	W	673	ASN
1	W	697	ASN
1	W	701	GLN
1	W	721	GLN
1	W	786	ASN
2	X	27	HIS
2	X	40	GLN
2	X	59	ASN
2	X	70	HIS
2	X	73	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 108 ligands modelled in this entry, 36 are monoatomic - leaving 72 for Mogul analysis.

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
4	MGD	A	902	5	52,52,52	2.21	18 (34%)	73,81,81	3.46	19 (26%)
4	MGD	A	903	5	52,52,52	2.50	21 (40%)	73,81,81	2.79	25 (34%)
6	BTT	A	905	5	10,10,10	8.59	6 (60%)	14,14,14	2.19	3 (21%)
7	SF4	B	302	2	12,12,12	10.63	11 (91%)	0,24,24	0.00	-
7	SF4	B	303	2	12,12,12	10.69	8 (66%)	0,24,24	0.00	-
7	SF4	B	304	2	12,12,12	10.72	9 (75%)	0,24,24	0.00	-
4	MGD	C	902	5	52,52,52	2.28	18 (34%)	73,81,81	3.48	20 (27%)
4	MGD	C	903	5	52,52,52	2.42	18 (34%)	73,81,81	3.24	19 (26%)
6	BTT	C	905	5	10,10,10	8.61	6 (60%)	14,14,14	2.24	3 (21%)
7	SF4	D	302	2	12,12,12	10.85	10 (83%)	0,24,24	0.00	-
7	SF4	D	303	2	12,12,12	11.29	8 (66%)	0,24,24	0.00	-
7	SF4	D	304	2	12,12,12	10.53	10 (83%)	0,24,24	0.00	-
4	MGD	E	902	5	52,52,52	2.22	17 (32%)	73,81,81	3.21	22 (30%)
4	MGD	E	903	5	52,52,52	2.43	19 (36%)	73,81,81	2.91	24 (32%)
6	BTT	E	905	5	10,10,10	8.64	6 (60%)	14,14,14	2.16	3 (21%)
7	SF4	F	302	2	12,12,12	10.47	9 (75%)	0,24,24	0.00	-
7	SF4	F	303	2	12,12,12	11.18	8 (66%)	0,24,24	0.00	-
7	SF4	F	304	2	12,12,12	10.14	10 (83%)	0,24,24	0.00	-
4	MGD	G	902	5	52,52,52	2.23	17 (32%)	73,81,81	3.20	19 (26%)
4	MGD	G	903	5	52,52,52	2.34	20 (38%)	73,81,81	3.20	25 (34%)
6	BTT	G	905	5	10,10,10	8.60	6 (60%)	14,14,14	2.15	3 (21%)
7	SF4	H	302	2	12,12,12	10.40	8 (66%)	0,24,24	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SF4	H	303	2	12,12,12	11.44	8 (66%)	0,24,24	0.00	-
7	SF4	H	304	2	12,12,12	10.31	9 (75%)	0,24,24	0.00	-
4	MGD	I	902	5	52,52,52	2.18	18 (34%)	73,81,81	3.20	21 (28%)
4	MGD	I	903	5	52,52,52	2.36	18 (34%)	73,81,81	3.22	18 (24%)
6	BTT	I	905	5	10,10,10	8.56	6 (60%)	14,14,14	2.22	3 (21%)
7	SF4	J	302	2	12,12,12	10.29	9 (75%)	0,24,24	0.00	-
7	SF4	J	303	2	12,12,12	10.87	8 (66%)	0,24,24	0.00	-
7	SF4	J	304	2	12,12,12	10.85	9 (75%)	0,24,24	0.00	-
4	MGD	K	902	5	52,52,52	2.28	17 (32%)	73,81,81	3.22	17 (23%)
4	MGD	K	903	5	52,52,52	2.46	21 (40%)	73,81,81	2.69	25 (34%)
6	BTT	K	905	5	10,10,10	8.59	6 (60%)	14,14,14	2.24	3 (21%)
7	SF4	L	302	2	12,12,12	10.79	9 (75%)	0,24,24	0.00	-
7	SF4	L	303	2	12,12,12	11.46	8 (66%)	0,24,24	0.00	-
7	SF4	L	304	2	12,12,12	10.55	9 (75%)	0,24,24	0.00	-
4	MGD	M	902	5	52,52,52	2.18	15 (28%)	73,81,81	3.25	21 (28%)
4	MGD	M	903	5	52,52,52	2.31	17 (32%)	73,81,81	3.23	21 (28%)
6	BTT	M	905	5	10,10,10	8.55	6 (60%)	14,14,14	2.18	3 (21%)
7	SF4	N	302	2	12,12,12	10.26	10 (83%)	0,24,24	0.00	-
7	SF4	N	303	2	12,12,12	11.02	8 (66%)	0,24,24	0.00	-
7	SF4	N	304	2	12,12,12	10.53	9 (75%)	0,24,24	0.00	-
4	MGD	O	902	5	52,52,52	2.28	19 (36%)	73,81,81	3.49	22 (30%)
4	MGD	O	903	5	52,52,52	2.43	20 (38%)	73,81,81	3.17	28 (38%)
6	BTT	O	905	5	10,10,10	8.58	6 (60%)	14,14,14	2.22	3 (21%)
7	SF4	P	302	2	12,12,12	11.15	10 (83%)	0,24,24	0.00	-
7	SF4	P	303	2	12,12,12	10.95	8 (66%)	0,24,24	0.00	-
7	SF4	P	304	2	12,12,12	10.09	9 (75%)	0,24,24	0.00	-
4	MGD	Q	902	5	52,52,52	2.25	18 (34%)	73,81,81	3.22	18 (24%)
4	MGD	Q	903	5	52,52,52	2.34	16 (30%)	73,81,81	3.52	25 (34%)
6	BTT	Q	905	5	10,10,10	8.59	6 (60%)	14,14,14	2.17	3 (21%)
7	SF4	R	302	2	12,12,12	11.03	9 (75%)	0,24,24	0.00	-
7	SF4	R	303	2	12,12,12	11.02	8 (66%)	0,24,24	0.00	-
7	SF4	R	304	2	12,12,12	10.32	9 (75%)	0,24,24	0.00	-
4	MGD	S	902	5	52,52,52	2.25	18 (34%)	73,81,81	3.33	20 (27%)
4	MGD	S	903	5	52,52,52	2.28	18 (34%)	73,81,81	3.27	18 (24%)
6	BTT	S	905	5	10,10,10	8.63	6 (60%)	14,14,14	2.22	4 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SF4	T	302	2	12,12,12	10.79	9 (75%)	0,24,24	0.00	-
7	SF4	T	303	2	12,12,12	11.71	8 (66%)	0,24,24	0.00	-
7	SF4	T	304	2	12,12,12	10.04	9 (75%)	0,24,24	0.00	-
4	MGD	U	902	5	52,52,52	2.31	17 (32%)	73,81,81	3.39	22 (30%)
4	MGD	U	903	5	52,52,52	2.25	16 (30%)	73,81,81	3.09	21 (28%)
6	BTT	U	905	5	10,10,10	8.58	6 (60%)	14,14,14	2.25	3 (21%)
7	SF4	V	302	2	12,12,12	10.92	9 (75%)	0,24,24	0.00	-
7	SF4	V	303	2	12,12,12	11.50	8 (66%)	0,24,24	0.00	-
7	SF4	V	304	2	12,12,12	10.34	10 (83%)	0,24,24	0.00	-
4	MGD	W	902	5	52,52,52	2.25	17 (32%)	73,81,81	3.24	20 (27%)
4	MGD	W	903	5	52,52,52	2.35	20 (38%)	73,81,81	3.29	24 (32%)
6	BTT	W	905	5	10,10,10	8.58	6 (60%)	14,14,14	2.22	3 (21%)
7	SF4	X	302	2	12,12,12	11.35	9 (75%)	0,24,24	0.00	-
7	SF4	X	303	2	12,12,12	11.70	8 (66%)	0,24,24	0.00	-
7	SF4	X	304	2	12,12,12	10.31	11 (91%)	0,24,24	0.00	-

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
4	MGD	A	902	5	-	0/22/66/66	0/6/6/6
4	MGD	A	903	5	-	2/22/66/66	0/6/6/6
6	BTT	A	905	5	-	0/0/0/0	0/1/1/1
7	SF4	B	302	2	-	0/0/48/48	0/6/5/5
7	SF4	B	303	2	-	0/0/48/48	0/6/5/5
7	SF4	B	304	2	-	0/0/48/48	0/6/5/5
4	MGD	C	902	5	-	0/22/66/66	0/6/6/6
4	MGD	C	903	5	-	0/22/66/66	0/6/6/6
6	BTT	C	905	5	-	0/0/0/0	0/1/1/1
7	SF4	D	302	2	-	0/0/48/48	0/6/5/5
7	SF4	D	303	2	-	0/0/48/48	0/6/5/5
7	SF4	D	304	2	-	0/0/48/48	0/6/5/5
4	MGD	E	902	5	-	0/22/66/66	0/6/6/6
4	MGD	E	903	5	-	2/22/66/66	0/6/6/6
6	BTT	E	905	5	-	0/0/0/0	0/1/1/1
7	SF4	F	302	2	-	0/0/48/48	0/6/5/5
7	SF4	F	303	2	-	0/0/48/48	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	SF4	F	304	2	-	0/0/48/48	0/6/5/5
4	MGD	G	902	5	-	0/22/66/66	0/6/6/6
4	MGD	G	903	5	-	0/22/66/66	0/6/6/6
6	BTT	G	905	5	-	0/0/0/0	0/1/1/1
7	SF4	H	302	2	-	0/0/48/48	0/6/5/5
7	SF4	H	303	2	-	0/0/48/48	0/6/5/5
7	SF4	H	304	2	-	0/0/48/48	0/6/5/5
4	MGD	I	902	5	-	0/22/66/66	0/6/6/6
4	MGD	I	903	5	-	0/22/66/66	0/6/6/6
6	BTT	I	905	5	-	0/0/0/0	0/1/1/1
7	SF4	J	302	2	-	0/0/48/48	0/6/5/5
7	SF4	J	303	2	-	0/0/48/48	0/6/5/5
7	SF4	J	304	2	-	0/0/48/48	0/6/5/5
4	MGD	K	902	5	-	0/22/66/66	0/6/6/6
4	MGD	K	903	5	-	1/22/66/66	0/6/6/6
6	BTT	K	905	5	-	0/0/0/0	0/1/1/1
7	SF4	L	302	2	-	0/0/48/48	0/6/5/5
7	SF4	L	303	2	-	0/0/48/48	0/6/5/5
7	SF4	L	304	2	-	0/0/48/48	0/6/5/5
4	MGD	M	902	5	-	0/22/66/66	0/6/6/6
4	MGD	M	903	5	-	0/22/66/66	0/6/6/6
6	BTT	M	905	5	-	0/0/0/0	0/1/1/1
7	SF4	N	302	2	-	0/0/48/48	0/6/5/5
7	SF4	N	303	2	-	0/0/48/48	0/6/5/5
7	SF4	N	304	2	-	0/0/48/48	0/6/5/5
4	MGD	O	902	5	-	0/22/66/66	0/6/6/6
4	MGD	O	903	5	-	1/22/66/66	0/6/6/6
6	BTT	O	905	5	-	0/0/0/0	0/1/1/1
7	SF4	P	302	2	-	0/0/48/48	0/6/5/5
7	SF4	P	303	2	-	0/0/48/48	0/6/5/5
7	SF4	P	304	2	-	0/0/48/48	0/6/5/5
4	MGD	Q	902	5	-	0/22/66/66	0/6/6/6
4	MGD	Q	903	5	-	0/22/66/66	0/6/6/6
6	BTT	Q	905	5	-	0/0/0/0	0/1/1/1
7	SF4	R	302	2	-	0/0/48/48	0/6/5/5
7	SF4	R	303	2	-	0/0/48/48	0/6/5/5
7	SF4	R	304	2	-	0/0/48/48	0/6/5/5
4	MGD	S	902	5	-	0/22/66/66	0/6/6/6
4	MGD	S	903	5	-	0/22/66/66	0/6/6/6
6	BTT	S	905	5	-	0/0/0/0	0/1/1/1
7	SF4	T	302	2	-	0/0/48/48	0/6/5/5
7	SF4	T	303	2	-	0/0/48/48	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	SF4	T	304	2	-	0/0/48/48	0/6/5/5
4	MGD	U	902	5	-	0/22/66/66	0/6/6/6
4	MGD	U	903	5	-	0/22/66/66	0/6/6/6
6	BTT	U	905	5	-	0/0/0/0	0/1/1/1
7	SF4	V	302	2	-	0/0/48/48	0/6/5/5
7	SF4	V	303	2	-	0/0/48/48	0/6/5/5
7	SF4	V	304	2	-	0/0/48/48	0/6/5/5
4	MGD	W	902	5	-	0/22/66/66	0/6/6/6
4	MGD	W	903	5	-	0/22/66/66	0/6/6/6
6	BTT	W	905	5	-	0/0/0/0	0/1/1/1
7	SF4	X	302	2	-	0/0/48/48	0/6/5/5
7	SF4	X	303	2	-	0/0/48/48	0/6/5/5
7	SF4	X	304	2	-	0/0/48/48	0/6/5/5

All (826) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	302	SF4	S1-FE4	-20.60	2.19	2.33
7	X	302	SF4	S1-FE4	-20.03	2.19	2.33
7	X	302	SF4	S3-FE1	-19.96	2.19	2.33
7	F	303	SF4	S1-FE4	-19.83	2.19	2.33
7	V	302	SF4	S1-FE4	-19.83	2.19	2.33
7	X	303	SF4	S1-FE4	-19.73	2.20	2.33
7	P	302	SF4	S1-FE4	-19.53	2.20	2.33
7	P	303	SF4	S1-FE4	-19.47	2.20	2.33
7	R	302	SF4	S1-FE4	-19.24	2.20	2.33
7	L	302	SF4	S1-FE4	-18.91	2.20	2.33
7	N	303	SF4	S1-FE4	-18.88	2.20	2.33
7	J	302	SF4	S1-FE4	-18.58	2.20	2.33
7	N	302	SF4	S1-FE4	-18.35	2.20	2.33
7	X	302	SF4	S4-FE1	-18.35	2.20	2.33
7	T	302	SF4	S1-FE4	-18.31	2.20	2.33
7	L	302	SF4	S3-FE1	-18.22	2.21	2.33
7	R	302	SF4	S3-FE1	-18.06	2.21	2.33
7	R	302	SF4	S4-FE1	-18.02	2.21	2.33
7	H	302	SF4	S1-FE4	-17.93	2.21	2.33
7	T	303	SF4	S1-FE4	-17.93	2.21	2.33
7	B	302	SF4	S1-FE4	-17.89	2.21	2.33
7	V	303	SF4	S1-FE4	-17.86	2.21	2.33
7	P	302	SF4	S4-FE1	-17.83	2.21	2.33
7	J	304	SF4	S3-FE1	-17.80	2.21	2.33
7	H	303	SF4	S1-FE4	-17.80	2.21	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	303	SF4	S3-FE1	-17.76	2.21	2.33
7	L	303	SF4	S1-FE4	-17.67	2.21	2.33
7	V	304	SF4	S3-FE4	-17.54	2.21	2.33
7	V	303	SF4	S3-FE1	-17.51	2.21	2.33
7	V	302	SF4	S4-FE1	-17.49	2.21	2.33
7	B	304	SF4	S3-FE1	-17.48	2.21	2.33
7	T	302	SF4	S3-FE1	-17.42	2.21	2.33
7	B	302	SF4	S4-FE1	-17.25	2.21	2.33
7	L	303	SF4	S3-FE1	-17.21	2.21	2.33
7	F	302	SF4	S3-FE1	-17.20	2.21	2.33
7	L	302	SF4	S4-FE1	-17.06	2.21	2.33
7	N	303	SF4	S3-FE1	-17.03	2.21	2.33
7	T	302	SF4	S4-FE1	-17.01	2.21	2.33
7	P	304	SF4	S3-FE4	-16.99	2.21	2.33
7	X	304	SF4	S1-FE4	-16.97	2.21	2.33
7	D	303	SF4	S1-FE4	-16.94	2.21	2.33
7	J	303	SF4	S1-FE4	-16.90	2.21	2.33
7	D	304	SF4	S1-FE4	-16.87	2.21	2.33
7	D	303	SF4	S3-FE1	-16.86	2.21	2.33
7	H	302	SF4	S4-FE1	-16.84	2.21	2.33
7	J	304	SF4	S1-FE4	-16.82	2.21	2.33
7	D	304	SF4	S3-FE4	-16.76	2.22	2.33
7	R	303	SF4	S3-FE1	-16.75	2.22	2.33
7	F	302	SF4	S1-FE4	-16.72	2.22	2.33
7	H	303	SF4	S3-FE1	-16.70	2.22	2.33
7	L	304	SF4	S3-FE4	-16.69	2.22	2.33
7	R	304	SF4	S3-FE1	-16.62	2.22	2.33
7	B	302	SF4	S3-FE1	-16.59	2.22	2.33
7	V	302	SF4	S3-FE1	-16.58	2.22	2.33
7	J	304	SF4	S3-FE4	-16.56	2.22	2.33
7	P	302	SF4	S3-FE1	-16.52	2.22	2.33
7	D	302	SF4	S4-FE1	-16.51	2.22	2.33
7	H	304	SF4	S1-FE4	-16.36	2.22	2.33
7	L	304	SF4	S3-FE1	-16.32	2.22	2.33
7	B	303	SF4	S1-FE4	-16.31	2.22	2.33
7	N	304	SF4	S1-FE4	-16.26	2.22	2.33
7	B	304	SF4	S3-FE4	-16.26	2.22	2.33
7	R	303	SF4	S1-FE4	-16.15	2.22	2.33
6	E	905	BTT	C3-C2	16.12	1.61	1.38
7	V	304	SF4	S3-FE1	-16.09	2.22	2.33
6	A	905	BTT	C3-C2	16.07	1.61	1.38
6	S	905	BTT	C3-C2	16.07	1.61	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	P	303	SF4	S3-FE1	-16.06	2.22	2.33
6	K	905	BTT	C3-C2	16.04	1.61	1.38
7	T	304	SF4	S3-FE4	-16.04	2.22	2.33
7	R	304	SF4	S3-FE4	-16.03	2.22	2.33
7	H	304	SF4	S3-FE4	-16.01	2.22	2.33
7	N	304	SF4	S3-FE4	-15.99	2.22	2.33
7	L	303	SF4	S4-FE1	-15.98	2.22	2.33
7	F	304	SF4	S1-FE4	-15.96	2.22	2.33
7	B	304	SF4	S1-FE4	-15.95	2.22	2.33
6	G	905	BTT	C3-C2	15.95	1.61	1.38
6	O	905	BTT	C3-C2	15.87	1.61	1.38
6	Q	905	BTT	C3-C2	15.86	1.61	1.38
7	H	302	SF4	S3-FE1	-15.85	2.22	2.33
6	C	905	BTT	C3-C2	15.81	1.60	1.38
7	T	303	SF4	S4-FE1	-15.79	2.22	2.33
6	W	905	BTT	C3-C2	15.78	1.60	1.38
7	X	304	SF4	S3-FE4	-15.78	2.22	2.33
7	F	304	SF4	S3-FE4	-15.78	2.22	2.33
6	M	905	BTT	C3-C2	15.77	1.60	1.38
6	U	905	BTT	C3-C2	15.77	1.60	1.38
7	N	302	SF4	S4-FE1	-15.74	2.22	2.33
6	I	905	BTT	C3-C2	15.73	1.60	1.38
7	N	302	SF4	S3-FE1	-15.63	2.22	2.33
7	D	304	SF4	S3-FE1	-15.61	2.22	2.33
7	L	304	SF4	S1-FE4	-15.59	2.22	2.33
7	X	303	SF4	S3-FE1	-15.58	2.22	2.33
7	D	303	SF4	S1-FE3	-15.54	2.22	2.33
7	J	302	SF4	S3-FE1	-15.52	2.22	2.33
7	B	303	SF4	S3-FE1	-15.48	2.22	2.33
7	P	304	SF4	S1-FE4	-15.46	2.22	2.33
7	J	302	SF4	S4-FE1	-15.46	2.22	2.33
7	F	303	SF4	S3-FE1	-15.45	2.22	2.33
7	J	303	SF4	S3-FE1	-15.44	2.22	2.33
7	H	304	SF4	S3-FE1	-15.42	2.22	2.33
7	F	302	SF4	S4-FE1	-15.40	2.22	2.33
7	V	303	SF4	S4-FE1	-15.33	2.22	2.33
7	T	304	SF4	S3-FE1	-15.32	2.22	2.33
7	T	304	SF4	S1-FE4	-15.19	2.23	2.33
7	V	304	SF4	S1-FE4	-15.18	2.23	2.33
7	H	303	SF4	S4-FE1	-15.10	2.23	2.33
7	D	302	SF4	S3-FE1	-15.08	2.23	2.33
7	T	303	SF4	S3-FE4	-14.92	2.23	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	N	304	SF4	S3-FE1	-14.83	2.23	2.33
6	E	905	BTT	C6-C5	14.76	1.59	1.38
6	G	905	BTT	C6-C5	14.75	1.59	1.38
6	M	905	BTT	C6-C5	14.68	1.59	1.38
6	W	905	BTT	C6-C5	14.67	1.59	1.38
6	Q	905	BTT	C6-C5	14.62	1.59	1.38
6	A	905	BTT	C6-C5	14.55	1.59	1.38
7	X	304	SF4	S3-FE1	-14.54	2.23	2.33
7	P	303	SF4	S4-FE1	-14.51	2.23	2.33
7	F	303	SF4	S4-FE1	-14.49	2.23	2.33
6	S	905	BTT	C6-C5	14.47	1.59	1.38
6	K	905	BTT	C6-C5	14.46	1.59	1.38
6	C	905	BTT	C6-C5	14.44	1.59	1.38
6	O	905	BTT	C6-C5	14.42	1.59	1.38
6	I	905	BTT	C6-C5	14.37	1.58	1.38
6	U	905	BTT	C6-C5	14.36	1.58	1.38
7	D	303	SF4	S2-FE4	-14.36	2.23	2.33
7	X	303	SF4	S3-FE4	-14.33	2.23	2.33
7	F	304	SF4	S3-FE1	-14.32	2.23	2.33
7	H	303	SF4	S3-FE4	-14.26	2.23	2.33
7	J	303	SF4	S4-FE1	-14.26	2.23	2.33
7	N	303	SF4	S4-FE1	-14.23	2.23	2.33
7	B	303	SF4	S4-FE1	-14.21	2.23	2.33
7	P	304	SF4	S3-FE1	-14.19	2.23	2.33
7	R	303	SF4	S4-FE1	-14.11	2.23	2.33
7	X	303	SF4	S2-FE1	-14.08	2.23	2.33
7	X	303	SF4	S2-FE4	-14.07	2.23	2.33
7	J	303	SF4	S3-FE4	-14.03	2.23	2.33
7	V	303	SF4	S1-FE3	-14.02	2.23	2.33
7	V	303	SF4	S2-FE4	-13.92	2.23	2.33
7	R	304	SF4	S1-FE4	-13.90	2.23	2.33
7	R	303	SF4	S3-FE4	-13.89	2.23	2.33
7	B	303	SF4	S3-FE4	-13.88	2.23	2.33
7	L	303	SF4	S3-FE4	-13.85	2.23	2.33
7	X	303	SF4	S4-FE1	-13.79	2.24	2.33
7	F	303	SF4	S1-FE3	-13.65	2.24	2.33
7	D	303	SF4	S4-FE1	-13.50	2.24	2.33
7	F	303	SF4	S3-FE4	-13.48	2.24	2.33
7	D	302	SF4	S2-FE1	-13.45	2.24	2.33
7	N	304	SF4	S2-FE1	-13.40	2.24	2.33
7	L	303	SF4	S1-FE3	-13.38	2.24	2.33
7	T	303	SF4	S1-FE3	-13.34	2.24	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	303	SF4	S1-FE3	-13.26	2.24	2.33
7	R	303	SF4	S1-FE3	-13.19	2.24	2.33
7	J	304	SF4	S4-FE1	-13.15	2.24	2.33
7	P	303	SF4	S1-FE3	-13.02	2.24	2.33
7	N	303	SF4	S1-FE3	-12.96	2.24	2.33
7	H	303	SF4	S1-FE3	-12.85	2.24	2.33
7	H	303	SF4	S2-FE4	-12.71	2.24	2.33
7	P	303	SF4	S3-FE4	-12.70	2.24	2.33
7	V	303	SF4	S3-FE4	-12.59	2.24	2.33
7	T	303	SF4	S2-FE1	-12.56	2.24	2.33
7	B	304	SF4	S4-FE1	-12.52	2.24	2.33
7	L	304	SF4	S2-FE1	-12.42	2.24	2.33
7	B	303	SF4	S1-FE3	-12.27	2.25	2.33
7	L	303	SF4	S2-FE4	-12.24	2.25	2.33
7	V	302	SF4	S2-FE1	-12.18	2.25	2.33
7	D	303	SF4	S3-FE4	-12.17	2.25	2.33
7	P	302	SF4	S2-FE1	-12.16	2.25	2.33
7	R	303	SF4	S2-FE4	-12.16	2.25	2.33
7	P	304	SF4	S2-FE1	-12.15	2.25	2.33
7	J	303	SF4	S2-FE4	-12.15	2.25	2.33
7	N	304	SF4	S4-FE1	-12.13	2.25	2.33
7	D	304	SF4	S2-FE1	-11.99	2.25	2.33
7	V	304	SF4	S2-FE1	-11.91	2.25	2.33
7	X	303	SF4	S1-FE3	-11.88	2.25	2.33
7	T	302	SF4	S2-FE1	-11.87	2.25	2.33
7	N	303	SF4	S3-FE4	-11.87	2.25	2.33
7	T	304	SF4	S2-FE1	-11.86	2.25	2.33
7	H	304	SF4	S4-FE1	-11.84	2.25	2.33
7	L	304	SF4	S4-FE1	-11.82	2.25	2.33
7	N	303	SF4	S2-FE4	-11.78	2.25	2.33
7	P	304	SF4	S4-FE1	-11.74	2.25	2.33
7	N	302	SF4	S2-FE1	-11.67	2.25	2.33
7	F	302	SF4	S3-FE4	-11.62	2.25	2.33
7	R	304	SF4	S4-FE1	-11.61	2.25	2.33
7	B	302	SF4	S2-FE1	-11.56	2.25	2.33
7	F	304	SF4	S4-FE1	-11.53	2.25	2.33
7	F	304	SF4	S2-FE1	-11.52	2.25	2.33
7	T	303	SF4	S2-FE4	-11.50	2.25	2.33
7	T	304	SF4	S4-FE1	-11.40	2.25	2.33
7	H	303	SF4	S2-FE1	-11.37	2.25	2.33
7	X	304	SF4	S4-FE1	-11.34	2.25	2.33
7	R	304	SF4	S2-FE1	-11.33	2.25	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	304	SF4	S4-FE1	-11.23	2.25	2.33
7	H	302	SF4	S2-FE1	-11.19	2.25	2.33
7	F	303	SF4	S2-FE4	-11.17	2.25	2.33
7	B	303	SF4	S2-FE4	-11.15	2.25	2.33
7	H	302	SF4	S3-FE4	-11.11	2.25	2.33
7	L	303	SF4	S2-FE1	-11.10	2.25	2.33
7	X	304	SF4	S2-FE1	-11.06	2.25	2.33
7	J	302	SF4	S3-FE4	-11.03	2.25	2.33
7	X	304	SF4	S2-FE4	-11.00	2.25	2.33
7	V	304	SF4	S4-FE1	-10.97	2.25	2.33
7	B	304	SF4	S2-FE1	-10.92	2.25	2.33
7	H	304	SF4	S2-FE1	-10.82	2.26	2.33
7	D	302	SF4	S3-FE4	-10.81	2.26	2.33
7	F	304	SF4	S2-FE4	-10.81	2.26	2.33
7	R	304	SF4	S2-FE4	-10.80	2.26	2.33
6	C	905	BTT	C2-C1	10.76	1.59	1.40
7	B	304	SF4	S2-FE4	-10.72	2.26	2.33
6	U	905	BTT	C2-C1	10.71	1.59	1.40
7	J	304	SF4	S2-FE1	-10.70	2.26	2.33
6	I	905	BTT	C2-C1	10.68	1.59	1.40
6	S	905	BTT	C2-C1	10.66	1.59	1.40
7	R	303	SF4	S2-FE1	-10.65	2.26	2.33
7	D	303	SF4	S2-FE1	-10.65	2.26	2.33
6	O	905	BTT	C2-C1	10.63	1.59	1.40
6	Q	905	BTT	C2-C1	10.61	1.59	1.40
6	E	905	BTT	C2-C1	10.60	1.59	1.40
6	K	905	BTT	C2-C1	10.54	1.59	1.40
6	G	905	BTT	C2-C1	10.51	1.58	1.40
7	P	302	SF4	S3-FE4	-10.49	2.26	2.33
6	A	905	BTT	C2-C1	10.48	1.58	1.40
7	B	302	SF4	S3-FE4	-10.47	2.26	2.33
7	R	302	SF4	S3-FE4	-10.46	2.26	2.33
6	M	905	BTT	C2-C1	10.46	1.58	1.40
7	P	303	SF4	S2-FE1	-10.43	2.26	2.33
7	L	304	SF4	S2-FE4	-10.42	2.26	2.33
7	F	302	SF4	S2-FE1	-10.41	2.26	2.33
6	W	905	BTT	C2-C1	10.40	1.58	1.40
7	J	302	SF4	S2-FE1	-10.37	2.26	2.33
7	N	303	SF4	S2-FE1	-10.35	2.26	2.33
7	H	304	SF4	S2-FE4	-10.27	2.26	2.33
7	V	304	SF4	S2-FE4	-10.24	2.26	2.33
7	L	302	SF4	S3-FE4	-10.21	2.26	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	N	302	SF4	S3-FE4	-10.20	2.26	2.33
7	P	303	SF4	S2-FE4	-10.15	2.26	2.33
7	B	303	SF4	S2-FE1	-10.14	2.26	2.33
7	J	303	SF4	S2-FE1	-10.08	2.26	2.33
7	N	304	SF4	S2-FE4	-10.08	2.26	2.33
7	R	302	SF4	S2-FE1	-10.08	2.26	2.33
7	R	302	SF4	S1-FE3	-9.93	2.26	2.33
7	F	303	SF4	S2-FE1	-9.91	2.26	2.33
7	T	304	SF4	S2-FE4	-9.83	2.26	2.33
7	D	304	SF4	S2-FE4	-9.66	2.26	2.33
7	V	303	SF4	S2-FE1	-9.64	2.26	2.33
7	T	302	SF4	S3-FE4	-9.63	2.26	2.33
7	X	302	SF4	S3-FE4	-9.52	2.26	2.33
7	L	302	SF4	S2-FE1	-9.51	2.26	2.33
7	B	303	SF4	S4-FE3	-9.49	2.26	2.33
7	P	302	SF4	S2-FE4	-9.46	2.26	2.33
7	X	302	SF4	S2-FE1	-9.41	2.26	2.33
7	P	302	SF4	S1-FE3	-9.39	2.26	2.33
7	B	304	SF4	S1-FE3	-9.37	2.27	2.33
7	J	304	SF4	S2-FE4	-9.36	2.27	2.33
7	X	302	SF4	S1-FE3	-9.34	2.27	2.33
7	X	304	SF4	S4-FE3	-9.33	2.27	2.33
7	T	302	SF4	S4-FE3	-9.33	2.27	2.33
7	X	302	SF4	S2-FE4	-9.31	2.27	2.33
7	R	304	SF4	S1-FE3	-9.30	2.27	2.33
7	F	302	SF4	S2-FE4	-9.27	2.27	2.33
7	V	302	SF4	S2-FE4	-9.25	2.27	2.33
7	H	303	SF4	S4-FE3	-9.16	2.27	2.33
7	L	302	SF4	S1-FE3	-9.14	2.27	2.33
7	J	302	SF4	S4-FE3	-9.12	2.27	2.33
7	V	302	SF4	S3-FE4	-9.10	2.27	2.33
7	D	304	SF4	S4-FE3	-9.06	2.27	2.33
7	J	304	SF4	S1-FE3	-9.03	2.27	2.33
7	R	303	SF4	S4-FE3	-9.01	2.27	2.33
7	V	303	SF4	S4-FE3	-8.96	2.27	2.33
6	I	905	BTT	O2-C2	-8.92	1.17	1.36
7	F	302	SF4	S1-FE3	-8.91	2.27	2.33
7	F	302	SF4	S4-FE3	-8.86	2.27	2.33
6	U	905	BTT	C5-C4	8.84	1.55	1.40
7	T	302	SF4	S1-FE3	-8.81	2.27	2.33
6	W	905	BTT	O2-C2	-8.81	1.18	1.36
6	G	905	BTT	O2-C2	-8.80	1.18	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	905	BTT	O2-C2	-8.79	1.18	1.36
6	M	905	BTT	O2-C2	-8.74	1.18	1.36
6	A	905	BTT	O2-C2	-8.74	1.18	1.36
6	O	905	BTT	O2-C2	-8.73	1.18	1.36
6	O	905	BTT	C5-C4	8.73	1.55	1.40
6	C	905	BTT	C5-C4	8.72	1.55	1.40
6	Q	905	BTT	O2-C2	-8.71	1.18	1.36
6	S	905	BTT	O2-C2	-8.70	1.18	1.36
6	K	905	BTT	O2-C2	-8.69	1.18	1.36
6	E	905	BTT	O2-C2	-8.69	1.18	1.36
6	U	905	BTT	O2-C2	-8.68	1.18	1.36
7	P	304	SF4	S2-FE4	-8.67	2.27	2.33
7	H	304	SF4	S1-FE3	-8.65	2.27	2.33
6	W	905	BTT	C5-C4	8.63	1.55	1.40
7	J	304	SF4	S4-FE3	-8.63	2.27	2.33
6	I	905	BTT	C5-C4	8.59	1.55	1.40
7	N	304	SF4	S4-FE3	-8.56	2.27	2.33
6	S	905	BTT	C5-C4	8.56	1.55	1.40
7	X	303	SF4	S4-FE3	-8.55	2.27	2.33
6	Q	905	BTT	C5-C4	8.51	1.55	1.40
6	K	905	BTT	C5-C4	8.41	1.55	1.40
7	L	304	SF4	S4-FE3	-8.41	2.27	2.33
7	F	304	SF4	S1-FE3	-8.40	2.27	2.33
6	M	905	BTT	C5-C4	8.40	1.55	1.40
6	E	905	BTT	C5-C4	8.39	1.55	1.40
6	A	905	BTT	C5-C4	8.36	1.55	1.40
6	G	905	BTT	C5-C4	8.36	1.55	1.40
7	J	302	SF4	S2-FE4	-8.31	2.27	2.33
7	H	302	SF4	S4-FE3	-8.29	2.27	2.33
7	D	302	SF4	S4-FE3	-8.29	2.27	2.33
7	T	303	SF4	S4-FE3	-8.21	2.27	2.33
7	P	304	SF4	S4-FE3	-8.17	2.27	2.33
7	N	304	SF4	S1-FE3	-8.17	2.27	2.33
7	B	302	SF4	S2-FE4	-8.16	2.27	2.33
7	L	304	SF4	S1-FE3	-8.16	2.27	2.33
7	L	302	SF4	S2-FE4	-8.16	2.27	2.33
7	F	303	SF4	S4-FE3	-8.14	2.27	2.33
7	L	303	SF4	S4-FE3	-8.10	2.27	2.33
7	N	302	SF4	S1-FE3	-8.08	2.27	2.33
7	D	303	SF4	S4-FE3	-8.04	2.27	2.33
7	V	302	SF4	S4-FE3	-8.02	2.27	2.33
7	R	304	SF4	S4-FE3	-7.97	2.27	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	302	SF4	S1-FE3	-7.96	2.27	2.33
7	H	302	SF4	S1-FE3	-7.94	2.27	2.33
7	T	302	SF4	S2-FE4	-7.93	2.27	2.33
7	V	302	SF4	S1-FE3	-7.93	2.27	2.33
7	J	303	SF4	S4-FE3	-7.91	2.27	2.33
7	V	304	SF4	S4-FE3	-7.86	2.28	2.33
7	L	302	SF4	S4-FE3	-7.83	2.28	2.33
7	B	302	SF4	S4-FE3	-7.80	2.28	2.33
7	D	302	SF4	S2-FE4	-7.80	2.28	2.33
7	H	304	SF4	S4-FE3	-7.75	2.28	2.33
7	N	302	SF4	S2-FE4	-7.75	2.28	2.33
7	T	304	SF4	S1-FE3	-7.71	2.28	2.33
7	B	304	SF4	S4-FE3	-7.69	2.28	2.33
7	F	304	SF4	S4-FE3	-7.67	2.28	2.33
7	P	302	SF4	S4-FE3	-7.66	2.28	2.33
7	D	304	SF4	S1-FE3	-7.64	2.28	2.33
7	P	304	SF4	S1-FE3	-7.50	2.28	2.33
7	R	302	SF4	S4-FE3	-7.50	2.28	2.33
7	H	302	SF4	S2-FE4	-7.41	2.28	2.33
7	X	304	SF4	S1-FE3	-7.38	2.28	2.33
7	R	302	SF4	S2-FE4	-7.35	2.28	2.33
7	T	304	SF4	S4-FE3	-7.22	2.28	2.33
7	J	302	SF4	S1-FE3	-7.10	2.28	2.33
7	N	303	SF4	S4-FE3	-7.10	2.28	2.33
7	P	303	SF4	S4-FE3	-6.63	2.28	2.33
7	X	302	SF4	S4-FE3	-6.51	2.28	2.33
7	D	302	SF4	S1-FE3	-6.48	2.28	2.33
7	V	304	SF4	S1-FE3	-6.44	2.28	2.33
4	A	903	MGD	C14-N15	6.37	1.54	1.45
4	Q	903	MGD	C14-N15	6.30	1.54	1.45
4	S	903	MGD	C14-N15	6.29	1.54	1.45
7	N	302	SF4	S4-FE3	-6.28	2.29	2.33
4	K	903	MGD	C14-N15	6.19	1.54	1.45
4	C	903	MGD	C14-N15	6.16	1.54	1.45
4	I	903	MGD	C14-N15	6.15	1.54	1.45
4	G	903	MGD	C14-N15	6.15	1.54	1.45
4	O	903	MGD	C14-N15	6.12	1.54	1.45
4	C	902	MGD	C23-C14	6.11	1.58	1.53
4	U	903	MGD	C14-N15	6.06	1.54	1.45
4	M	903	MGD	C14-N15	6.01	1.54	1.45
4	W	903	MGD	C14-N15	5.97	1.53	1.45
4	K	902	MGD	C23-C14	5.91	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	903	MGD	C14-N15	5.87	1.53	1.45
4	M	903	MGD	C6-N1	5.85	1.45	1.36
4	G	902	MGD	C23-C14	5.84	1.58	1.53
4	K	903	MGD	C6-N1	5.79	1.45	1.36
4	U	902	MGD	C23-C14	5.72	1.58	1.53
4	O	902	MGD	C23-C14	5.67	1.58	1.53
4	E	903	MGD	C6-N1	5.66	1.44	1.36
4	M	902	MGD	C23-C14	5.61	1.58	1.53
4	A	902	MGD	C23-C14	5.58	1.58	1.53
4	Q	903	MGD	C6-N1	5.51	1.44	1.36
4	E	902	MGD	C23-C14	5.51	1.58	1.53
4	A	903	MGD	C6-N1	5.49	1.44	1.36
4	Q	902	MGD	C17-N18	5.49	1.44	1.36
4	M	902	MGD	C17-N18	5.43	1.44	1.36
4	O	903	MGD	C6-N1	5.42	1.44	1.36
4	I	903	MGD	C6-N1	5.41	1.44	1.36
4	U	902	MGD	C17-N18	5.41	1.44	1.36
4	W	903	MGD	C6-N1	5.39	1.44	1.36
4	S	902	MGD	C17-N18	5.38	1.44	1.36
4	G	903	MGD	C6-N1	5.38	1.44	1.36
4	O	903	MGD	C17-N18	5.33	1.44	1.36
4	O	902	MGD	C17-N18	5.33	1.44	1.36
4	C	902	MGD	C17-N18	5.33	1.44	1.36
4	K	902	MGD	C17-N18	5.30	1.44	1.36
4	C	903	MGD	C6-N1	5.26	1.44	1.36
4	W	902	MGD	C23-C14	5.25	1.57	1.53
4	I	902	MGD	C17-N18	5.23	1.44	1.36
4	A	903	MGD	C17-N18	5.22	1.44	1.36
4	W	903	MGD	C17-N18	5.22	1.44	1.36
4	G	903	MGD	C17-N18	5.22	1.44	1.36
4	E	903	MGD	C17-N18	5.20	1.44	1.36
4	A	902	MGD	C17-N18	5.20	1.44	1.36
4	M	903	MGD	C17-N18	5.16	1.44	1.36
4	I	902	MGD	C23-C14	5.16	1.57	1.53
4	C	903	MGD	C17-N18	5.15	1.44	1.36
4	G	902	MGD	C17-N18	5.07	1.44	1.36
4	E	902	MGD	C17-N18	5.06	1.44	1.36
4	W	902	MGD	C17-N18	5.06	1.44	1.36
4	U	903	MGD	C17-N18	5.05	1.44	1.36
4	S	903	MGD	C6-N1	5.05	1.44	1.36
4	A	902	MGD	C6-N1	5.04	1.43	1.36
4	E	903	MGD	PB-O3B	4.97	1.68	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	903	MGD	C17-N18	4.96	1.43	1.36
4	E	903	MGD	C23-C14	4.95	1.57	1.53
4	S	903	MGD	C17-N18	4.91	1.43	1.36
4	I	903	MGD	C17-N18	4.90	1.43	1.36
4	U	903	MGD	C6-N1	4.84	1.43	1.36
4	C	903	MGD	C23-C14	4.79	1.57	1.53
4	C	902	MGD	C6-N1	4.78	1.43	1.36
4	U	903	MGD	C8-N9	4.78	1.43	1.36
4	U	902	MGD	C6-N1	4.76	1.43	1.36
4	Q	903	MGD	C23-C14	4.76	1.57	1.53
4	Q	902	MGD	C23-C14	4.74	1.57	1.53
4	Q	902	MGD	O11-C11	4.74	1.50	1.43
4	I	902	MGD	C6-N1	4.70	1.43	1.36
4	W	902	MGD	C6-N1	4.63	1.43	1.36
7	N	304	SF4	S1-FE2	-4.62	2.30	2.33
4	A	903	MGD	PB-O3B	4.60	1.68	1.59
4	O	903	MGD	C23-C14	4.58	1.57	1.53
4	K	903	MGD	PB-O3B	4.57	1.68	1.59
4	K	903	MGD	C17-N18	4.57	1.43	1.36
4	S	902	MGD	C23-C14	4.56	1.57	1.53
4	M	902	MGD	C6-N1	4.54	1.43	1.36
4	G	903	MGD	C23-C14	4.54	1.57	1.53
4	G	903	MGD	C2-N2	4.52	1.39	1.32
4	K	902	MGD	C6-N1	4.52	1.43	1.36
4	M	903	MGD	C23-C14	4.51	1.57	1.53
4	U	903	MGD	C23-C14	4.50	1.57	1.53
4	A	903	MGD	C23-C14	4.47	1.57	1.53
4	K	903	MGD	C23-C14	4.47	1.57	1.53
4	W	902	MGD	C2-N2	4.41	1.38	1.32
4	Q	902	MGD	C6-N1	4.41	1.43	1.36
4	C	903	MGD	C8-N9	4.40	1.43	1.36
4	S	902	MGD	C6-N1	4.39	1.43	1.36
4	G	902	MGD	C6-N1	4.38	1.43	1.36
4	W	903	MGD	C8-N9	4.38	1.43	1.36
4	M	903	MGD	C8-N9	4.33	1.43	1.36
4	W	902	MGD	O4'-C1'	4.33	1.46	1.41
4	A	903	MGD	C2-N2	4.31	1.38	1.32
4	K	903	MGD	O4'-C1'	-4.30	1.35	1.41
4	I	903	MGD	C23-C14	4.30	1.57	1.53
4	M	902	MGD	C2-N2	4.29	1.38	1.32
4	E	902	MGD	C6-N1	4.29	1.42	1.36
4	O	902	MGD	C6-N1	4.29	1.42	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	902	MGD	C2-N2	4.28	1.38	1.32
7	R	304	SF4	S1-FE2	-4.27	2.30	2.33
4	K	903	MGD	C2-N2	4.25	1.38	1.32
4	E	902	MGD	O11-C11	4.21	1.50	1.43
4	U	902	MGD	O11-C11	4.17	1.50	1.43
4	S	902	MGD	O11-C11	4.17	1.50	1.43
4	C	902	MGD	C2-N2	4.16	1.38	1.32
4	K	902	MGD	O11-C11	4.14	1.50	1.43
4	W	902	MGD	O11-C11	4.13	1.50	1.43
4	E	903	MGD	C2-N2	4.12	1.38	1.32
4	W	903	MGD	C23-C14	4.12	1.56	1.53
4	S	902	MGD	C14-N15	4.10	1.51	1.45
4	K	902	MGD	C2-N2	4.09	1.38	1.32
4	Q	903	MGD	C8-N9	4.09	1.42	1.36
4	I	903	MGD	C8-N9	4.09	1.42	1.36
4	G	902	MGD	C14-N15	4.08	1.51	1.45
4	C	903	MGD	O11-C11	4.08	1.49	1.43
7	B	302	SF4	S2-FE3	-4.07	2.30	2.33
4	U	902	MGD	C2-N2	4.05	1.38	1.32
4	Q	902	MGD	C14-N15	4.03	1.51	1.45
4	I	902	MGD	C2-N2	4.01	1.38	1.32
4	G	903	MGD	C8-N9	4.01	1.42	1.36
4	Q	902	MGD	C2-N2	4.00	1.38	1.32
7	R	302	SF4	S2-FE3	-3.99	2.30	2.33
7	H	304	SF4	S1-FE2	-3.99	2.30	2.33
4	S	903	MGD	C23-C14	3.98	1.56	1.53
7	B	304	SF4	S1-FE2	-3.97	2.30	2.33
4	W	902	MGD	C8-N9	3.97	1.42	1.36
4	C	902	MGD	C8-N9	3.96	1.42	1.36
4	E	902	MGD	C2-N2	3.95	1.38	1.32
4	S	902	MGD	C2-N2	3.95	1.38	1.32
4	A	902	MGD	C2-N2	3.95	1.38	1.32
4	M	903	MGD	C2-N2	3.94	1.38	1.32
4	E	902	MGD	C14-N15	3.94	1.51	1.45
4	O	903	MGD	C2-N2	3.94	1.38	1.32
4	M	902	MGD	O11-C11	3.93	1.49	1.43
4	S	903	MGD	C8-N9	3.93	1.42	1.36
4	O	903	MGD	O4'-C1'	-3.93	1.36	1.41
4	O	903	MGD	C16-N15	3.93	1.47	1.38
4	S	903	MGD	C2-N1	3.92	1.42	1.36
4	O	902	MGD	C14-N15	3.91	1.51	1.45
4	K	903	MGD	C8-N9	3.91	1.42	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	902	MGD	O4'-C1'	3.91	1.46	1.41
4	A	902	MGD	C16-N15	3.89	1.47	1.38
4	C	903	MGD	C16-N15	3.89	1.47	1.38
4	C	902	MGD	O11-C11	3.89	1.49	1.43
4	I	903	MGD	O11-C11	3.87	1.49	1.43
4	A	903	MGD	C16-N15	3.86	1.47	1.38
4	K	902	MGD	O4'-C1'	3.86	1.46	1.41
4	O	902	MGD	O11-C11	3.85	1.49	1.43
4	Q	903	MGD	C16-N15	3.85	1.47	1.38
4	M	903	MGD	C16-N15	3.84	1.47	1.38
4	U	902	MGD	C14-N15	3.84	1.50	1.45
4	C	902	MGD	O4'-C1'	3.84	1.46	1.41
4	I	903	MGD	C16-N15	3.84	1.47	1.38
7	N	302	SF4	S2-FE3	-3.83	2.30	2.33
4	I	903	MGD	C2-N2	3.83	1.38	1.32
4	I	902	MGD	O11-C11	3.82	1.49	1.43
4	G	902	MGD	C16-N15	3.81	1.47	1.38
4	S	902	MGD	C16-N15	3.81	1.47	1.38
4	G	903	MGD	C16-N15	3.81	1.47	1.38
4	U	902	MGD	C8-N9	3.80	1.42	1.36
4	U	902	MGD	O4'-C1'	3.80	1.46	1.41
4	G	902	MGD	O11-C11	3.79	1.49	1.43
4	K	903	MGD	C16-N15	3.77	1.47	1.38
4	I	902	MGD	C8-N9	3.77	1.42	1.36
4	A	902	MGD	C14-N15	3.77	1.50	1.45
4	W	903	MGD	C16-N15	3.76	1.46	1.38
4	Q	902	MGD	C8-N9	3.76	1.42	1.36
4	C	903	MGD	C2-N1	3.75	1.42	1.36
4	A	903	MGD	O4'-C1'	-3.74	1.36	1.41
4	W	902	MGD	C14-N15	3.73	1.50	1.45
4	M	903	MGD	C2-N1	3.72	1.42	1.36
4	G	902	MGD	C2-N2	3.71	1.37	1.32
4	M	902	MGD	C14-N15	3.71	1.50	1.45
4	Q	902	MGD	C16-N15	3.71	1.46	1.38
4	Q	902	MGD	O4'-C1'	3.70	1.45	1.41
4	E	903	MGD	C16-N15	3.69	1.46	1.38
4	O	902	MGD	C8-N9	3.69	1.42	1.36
4	I	903	MGD	C2-N1	3.67	1.42	1.36
7	X	302	SF4	S2-FE3	-3.66	2.30	2.33
4	S	903	MGD	O4'-C1'	3.66	1.45	1.41
4	S	902	MGD	C8-N9	3.64	1.42	1.36
4	U	902	MGD	C16-N15	3.64	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	903	MGD	C2-N2	3.63	1.37	1.32
4	A	903	MGD	C21-N22	3.63	1.41	1.35
4	Q	903	MGD	O4'-C1'	-3.62	1.36	1.41
4	O	903	MGD	PA-O3B	3.62	1.66	1.59
4	S	902	MGD	O4'-C1'	3.60	1.45	1.41
4	E	903	MGD	C21-N22	3.58	1.41	1.35
4	K	902	MGD	C16-N15	3.58	1.46	1.38
4	U	903	MGD	C16-N15	3.55	1.46	1.38
4	S	903	MGD	C16-N15	3.54	1.46	1.38
4	W	903	MGD	C21-N22	3.54	1.41	1.35
4	G	903	MGD	C2-N1	3.54	1.42	1.36
4	K	903	MGD	C2-N1	3.52	1.42	1.36
4	O	903	MGD	C14-C13	3.52	1.56	1.51
4	C	903	MGD	C2-N2	3.52	1.37	1.32
4	E	902	MGD	C8-N9	3.50	1.42	1.36
7	F	302	SF4	S2-FE3	-3.50	2.30	2.33
4	O	902	MGD	C16-N15	3.50	1.46	1.38
4	M	903	MGD	C14-C13	3.49	1.56	1.51
4	E	903	MGD	C14-C13	3.49	1.56	1.51
4	E	902	MGD	C16-N15	3.49	1.46	1.38
4	W	902	MGD	C2-N1	3.49	1.42	1.36
4	Q	903	MGD	C14-C13	3.47	1.56	1.51
4	W	903	MGD	C2-N2	3.47	1.37	1.32
4	C	903	MGD	PB-O3B	-3.47	1.53	1.59
4	M	902	MGD	C16-N15	3.44	1.46	1.38
4	G	902	MGD	C8-N9	3.44	1.41	1.36
4	C	903	MGD	C21-N22	3.44	1.41	1.35
4	G	902	MGD	O4'-C1'	3.44	1.45	1.41
4	I	902	MGD	C16-N15	3.44	1.46	1.38
4	G	903	MGD	C14-C13	3.43	1.56	1.51
4	I	902	MGD	O4'-C1'	3.43	1.45	1.41
4	W	902	MGD	C16-N15	3.42	1.46	1.38
4	A	902	MGD	O4'-C1'	3.42	1.45	1.41
4	A	903	MGD	C8-N9	3.42	1.41	1.36
4	U	903	MGD	C2-N2	3.41	1.37	1.32
4	W	903	MGD	C2-N1	3.41	1.42	1.36
4	C	902	MGD	C16-N15	3.40	1.46	1.38
4	O	903	MGD	C2-N1	3.40	1.42	1.36
4	S	903	MGD	O11-C11	3.39	1.48	1.43
4	U	902	MGD	C2-N1	3.38	1.41	1.36
4	M	902	MGD	C8-N9	3.38	1.41	1.36
4	E	903	MGD	C8-N9	3.37	1.41	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	O	903	MGD	C19-N19	3.38	1.37	1.32
6	S	905	BTT	O5-C5	-3.38	1.29	1.36
7	P	302	SF4	S2-FE3	-3.36	2.31	2.33
4	C	902	MGD	C14-N15	3.35	1.50	1.45
4	O	902	MGD	O4'-C1'	3.34	1.45	1.41
4	U	902	MGD	C19-N19	3.35	1.37	1.32
4	U	903	MGD	C2-N1	3.34	1.41	1.36
6	U	905	BTT	O5-C5	-3.31	1.29	1.36
4	I	903	MGD	C21-N22	3.30	1.41	1.35
4	W	903	MGD	C14-C13	3.30	1.56	1.51
4	K	903	MGD	C21-N22	3.30	1.41	1.35
4	O	903	MGD	C8-N9	3.29	1.41	1.36
4	I	902	MGD	C14-N15	3.29	1.50	1.45
4	G	902	MGD	C21-N22	3.28	1.41	1.35
4	A	903	MGD	C14-C13	3.28	1.56	1.51
4	E	902	MGD	C11-C12	3.28	1.56	1.51
4	G	903	MGD	C21-N22	3.27	1.41	1.35
4	E	903	MGD	C2-N1	3.26	1.41	1.36
4	W	902	MGD	C21-N22	3.26	1.41	1.35
4	K	902	MGD	C14-N15	3.25	1.50	1.45
4	W	903	MGD	C19-N19	3.25	1.37	1.32
4	O	903	MGD	PB-O3B	3.25	1.65	1.59
6	K	905	BTT	O5-C5	-3.24	1.29	1.36
4	K	902	MGD	C8-N9	3.24	1.41	1.36
4	S	902	MGD	C21-N22	3.23	1.41	1.35
4	W	903	MGD	O11-C11	3.23	1.48	1.43
4	I	903	MGD	O11-C23	3.23	1.48	1.43
4	Q	903	MGD	C2-N2	3.23	1.37	1.32
4	M	902	MGD	C19-N19	3.21	1.37	1.32
4	A	902	MGD	C2-N1	3.20	1.41	1.36
4	Q	903	MGD	PA-O3B	3.20	1.65	1.59
4	W	903	MGD	C21-N20	3.20	1.40	1.34
4	O	902	MGD	C21-N22	3.20	1.41	1.35
7	D	304	SF4	S1-FE2	-3.19	2.31	2.33
4	Q	903	MGD	C21-N22	3.19	1.41	1.35
4	S	902	MGD	C11-C12	3.19	1.56	1.51
4	C	903	MGD	C21-N20	3.19	1.40	1.34
4	C	902	MGD	C2-N1	3.18	1.41	1.36
4	A	902	MGD	O11-C11	3.17	1.48	1.43
4	A	903	MGD	C21-N20	3.17	1.40	1.34
4	A	902	MGD	C8-N9	3.16	1.41	1.36
4	M	903	MGD	O11-C11	3.16	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	903	MGD	C14-C13	3.16	1.56	1.51
7	J	302	SF4	S2-FE3	-3.15	2.31	2.33
4	O	903	MGD	C21-N22	3.15	1.41	1.35
4	C	903	MGD	O4'-C1'	3.14	1.45	1.41
4	U	903	MGD	C21-N22	3.14	1.41	1.35
6	C	905	BTT	O5-C5	-3.14	1.29	1.36
4	M	902	MGD	O4'-C1'	3.13	1.45	1.41
4	K	902	MGD	C4-N9	3.13	1.42	1.37
4	C	903	MGD	C14-C13	3.13	1.55	1.51
4	M	902	MGD	C11-C12	3.13	1.56	1.51
4	C	902	MGD	C21-N22	3.11	1.40	1.35
4	S	902	MGD	C2-N1	3.11	1.41	1.36
4	Q	902	MGD	C2-N1	3.09	1.41	1.36
4	G	902	MGD	C19-N19	3.09	1.37	1.32
6	W	905	BTT	O5-C5	-3.09	1.30	1.36
7	V	304	SF4	S1-FE2	-3.08	2.31	2.33
4	S	903	MGD	C19-N19	3.07	1.37	1.32
4	Q	903	MGD	C2-N1	3.07	1.41	1.36
4	E	902	MGD	C2-N1	3.06	1.41	1.36
4	I	903	MGD	C19-N19	3.05	1.36	1.32
4	U	903	MGD	C14-C13	3.05	1.55	1.51
4	E	902	MGD	C19-N19	3.04	1.36	1.32
4	I	903	MGD	O4'-C1'	3.04	1.45	1.41
4	U	902	MGD	C21-N22	3.04	1.40	1.35
4	K	902	MGD	C19-N19	3.04	1.36	1.32
4	C	903	MGD	O11-C23	3.03	1.48	1.43
4	E	903	MGD	C21-N20	3.03	1.40	1.34
4	I	902	MGD	C11-C12	3.03	1.56	1.51
4	G	902	MGD	C11-C12	3.02	1.56	1.51
4	K	903	MGD	C5-N7	3.02	1.41	1.38
4	U	903	MGD	C19-N19	3.01	1.36	1.32
4	Q	902	MGD	C21-N22	3.01	1.40	1.35
7	N	302	SF4	S1-FE2	-3.00	2.31	2.33
4	S	903	MGD	C14-C13	2.99	1.55	1.51
4	O	902	MGD	C11-C12	2.99	1.56	1.51
4	A	903	MGD	PA-O3B	2.99	1.65	1.59
4	A	903	MGD	C19-N19	2.99	1.36	1.32
6	O	905	BTT	O5-C5	-2.99	1.30	1.36
4	M	903	MGD	C21-N22	2.98	1.40	1.35
4	E	903	MGD	C19-N19	2.98	1.36	1.32
4	U	903	MGD	O11-C11	2.98	1.48	1.43
4	C	903	MGD	C19-N19	2.98	1.36	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	905	BTT	O5-C5	-2.97	1.30	1.36
4	I	902	MGD	C19-N19	2.96	1.36	1.32
7	V	302	SF4	S2-FE3	-2.96	2.31	2.33
4	O	902	MGD	C2-N1	2.95	1.41	1.36
4	G	902	MGD	C2-N1	2.95	1.41	1.36
4	O	902	MGD	C21-N20	2.95	1.40	1.34
4	S	903	MGD	C21-N22	2.95	1.40	1.35
6	Q	905	BTT	O5-C5	-2.95	1.30	1.36
4	K	902	MGD	C2-N3	2.94	1.37	1.33
4	I	903	MGD	C14-C13	2.94	1.55	1.51
4	Q	903	MGD	C21-N20	2.94	1.40	1.34
4	M	903	MGD	C19-N19	2.91	1.36	1.32
7	B	302	SF4	S4-FE2	2.90	2.35	2.33
4	M	902	MGD	C2-N1	2.89	1.41	1.36
7	D	302	SF4	S4-FE2	2.89	2.35	2.33
4	A	903	MGD	O11-C11	2.89	1.48	1.43
4	E	902	MGD	C21-N22	2.89	1.40	1.35
7	F	304	SF4	S1-FE2	-2.88	2.31	2.33
4	G	903	MGD	C21-N20	2.87	1.40	1.34
4	K	902	MGD	C2-N1	2.86	1.41	1.36
4	K	903	MGD	C21-N20	2.86	1.40	1.34
7	P	302	SF4	S3-FE2	-2.86	2.31	2.33
4	G	903	MGD	O11-C11	2.86	1.48	1.43
6	E	905	BTT	O5-C5	-2.86	1.30	1.36
4	W	902	MGD	C21-N20	2.85	1.40	1.34
4	U	902	MGD	C11-C12	2.85	1.56	1.51
4	Q	902	MGD	C19-N19	2.85	1.36	1.32
4	I	902	MGD	C2-N1	2.84	1.41	1.36
4	W	903	MGD	C2'-C1'	2.85	1.57	1.53
4	M	903	MGD	C21-N20	2.84	1.40	1.34
4	O	902	MGD	C19-N19	2.84	1.36	1.32
4	C	902	MGD	C19-N19	2.83	1.36	1.32
4	K	902	MGD	C21-N22	2.83	1.40	1.35
4	Q	903	MGD	C19-N19	2.82	1.36	1.32
4	S	902	MGD	C21-N20	2.80	1.40	1.34
4	W	902	MGD	C19-N19	2.79	1.36	1.32
6	I	905	BTT	O5-C5	-2.79	1.30	1.36
4	A	902	MGD	C19-N19	2.79	1.36	1.32
4	O	903	MGD	C21-N20	2.78	1.39	1.34
4	K	903	MGD	C19-N19	2.78	1.36	1.32
4	O	903	MGD	O11-C11	2.76	1.47	1.43
4	A	902	MGD	C21-N20	2.76	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	905	BTT	O5-C5	-2.75	1.30	1.36
6	G	905	BTT	O5-C5	-2.75	1.30	1.36
7	L	304	SF4	S1-FE2	-2.75	2.31	2.33
4	M	903	MGD	PB-O3B	-2.74	1.55	1.59
4	K	902	MGD	C21-N20	2.74	1.39	1.34
4	M	902	MGD	C21-N22	2.72	1.40	1.35
4	S	903	MGD	O11-C23	2.71	1.47	1.43
4	E	903	MGD	C5-N7	2.71	1.41	1.38
4	A	903	MGD	C5-N7	2.71	1.41	1.38
4	C	902	MGD	C21-N20	2.70	1.39	1.34
4	A	902	MGD	C21-N22	2.68	1.40	1.35
4	I	902	MGD	C21-N20	2.68	1.39	1.34
4	E	902	MGD	C21-N20	2.67	1.39	1.34
4	Q	902	MGD	C21-N20	2.66	1.39	1.34
4	A	902	MGD	C2-N3	2.64	1.36	1.33
4	A	903	MGD	C2-N1	2.64	1.40	1.36
4	C	902	MGD	C11-C12	2.64	1.55	1.51
4	A	903	MGD	C19-N18	2.63	1.40	1.36
4	K	903	MGD	O11-C11	2.63	1.47	1.43
4	I	902	MGD	C21-N22	2.63	1.40	1.35
4	G	902	MGD	C21-N20	2.62	1.39	1.34
4	S	902	MGD	C19-N19	2.62	1.36	1.32
4	G	903	MGD	C19-N19	2.61	1.36	1.32
4	O	902	MGD	C5-N7	2.60	1.41	1.38
4	U	902	MGD	C5-N7	2.60	1.41	1.38
4	U	902	MGD	C21-N20	2.58	1.39	1.34
7	D	304	SF4	S4-FE2	-2.58	2.31	2.33
7	D	302	SF4	S2-FE3	-2.58	2.31	2.33
4	I	903	MGD	C21-N20	2.56	1.39	1.34
4	O	902	MGD	C2-N3	2.56	1.36	1.33
4	O	902	MGD	C4-N9	2.55	1.41	1.37
4	W	903	MGD	C19-N20	2.53	1.36	1.33
4	E	903	MGD	O4'-C1'	-2.53	1.38	1.41
4	M	902	MGD	C5-N7	2.50	1.41	1.38
4	U	903	MGD	C21-N20	2.50	1.39	1.34
4	K	903	MGD	PA-O3B	2.50	1.64	1.59
4	C	902	MGD	C5-N7	2.49	1.41	1.38
7	P	304	SF4	S1-FE2	-2.47	2.31	2.33
4	U	903	MGD	O11-C23	2.47	1.47	1.43
4	A	902	MGD	C5-N7	2.46	1.41	1.38
4	G	903	MGD	C19-N18	2.45	1.40	1.36
4	U	903	MGD	C5-N7	2.45	1.40	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	903	MGD	C19-N18	2.43	1.40	1.36
4	M	902	MGD	C21-N20	2.41	1.39	1.34
7	T	302	SF4	S2-FE3	-2.41	2.31	2.33
4	O	903	MGD	C5-N7	2.39	1.40	1.38
4	W	903	MGD	C5'-C4'	-2.39	1.43	1.51
4	S	903	MGD	C2'-C1'	2.38	1.56	1.53
4	I	902	MGD	C2-N3	2.38	1.36	1.33
4	E	903	MGD	O11-C11	2.38	1.47	1.43
4	Q	903	MGD	C19-N18	2.38	1.40	1.36
4	S	902	MGD	C5-N7	2.36	1.40	1.38
4	C	903	MGD	C19-N18	2.35	1.40	1.36
4	A	902	MGD	C11-C12	2.34	1.55	1.51
4	Q	903	MGD	O11-C11	2.34	1.47	1.43
4	G	903	MGD	O4'-C1'	-2.34	1.38	1.41
4	W	903	MGD	C19-N18	2.33	1.40	1.36
4	U	902	MGD	C2-N3	2.33	1.36	1.33
4	E	903	MGD	C19-N18	2.33	1.40	1.36
4	W	903	MGD	PB-O3B	-2.31	1.55	1.59
4	W	903	MGD	C2'-C3'	2.30	1.59	1.53
7	L	302	SF4	S2-FE3	-2.29	2.31	2.33
4	S	902	MGD	C19-N20	2.29	1.36	1.33
4	I	902	MGD	C5-N7	2.29	1.40	1.38
7	X	304	SF4	S4-FE2	-2.28	2.31	2.33
4	C	902	MGD	C19-N20	2.28	1.36	1.33
4	A	903	MGD	O4'-C4'	-2.27	1.39	1.45
7	F	304	SF4	S4-FE2	-2.26	2.31	2.33
4	C	902	MGD	C2-N3	2.26	1.36	1.33
4	A	903	MGD	O11-C23	2.26	1.47	1.43
4	Q	902	MGD	C5-N7	2.26	1.40	1.38
4	G	902	MGD	C4-N9	2.25	1.41	1.37
4	S	902	MGD	C12-S12	2.25	1.82	1.75
4	S	903	MGD	C21-N20	2.25	1.38	1.34
7	J	304	SF4	S1-FE2	-2.25	2.31	2.33
4	E	902	MGD	C5-N7	2.24	1.40	1.38
4	O	903	MGD	C19-N18	2.24	1.40	1.36
4	M	903	MGD	O11-C23	2.23	1.47	1.43
4	S	903	MGD	C19-N18	2.22	1.40	1.36
4	A	903	MGD	C19-N20	2.22	1.36	1.33
4	U	903	MGD	C19-N18	2.22	1.40	1.36
4	I	902	MGD	C4-N9	2.20	1.41	1.37
4	M	903	MGD	C5'-C4'	-2.20	1.44	1.51
4	C	903	MGD	C19-N20	2.19	1.36	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	903	MGD	O11-C23	2.19	1.47	1.43
4	Q	902	MGD	C2-N3	2.18	1.36	1.33
4	W	902	MGD	C19-N20	2.17	1.36	1.33
4	I	903	MGD	PB-O3B	-2.16	1.56	1.59
4	O	902	MGD	C19-N18	2.16	1.40	1.36
4	G	903	MGD	O11-C23	2.16	1.47	1.43
4	K	903	MGD	O11-C23	2.16	1.47	1.43
4	O	903	MGD	C8-N7	-2.15	1.30	1.34
4	K	903	MGD	C8-N7	-2.13	1.30	1.34
4	E	902	MGD	C2-N3	2.13	1.36	1.33
4	W	903	MGD	C5-N7	2.13	1.40	1.38
4	Q	902	MGD	C11-C12	2.12	1.54	1.51
4	E	903	MGD	C19-N20	2.12	1.36	1.33
4	G	902	MGD	C2-N3	2.12	1.36	1.33
4	O	903	MGD	C19-N20	2.11	1.36	1.33
4	G	902	MGD	C5-N7	2.11	1.40	1.38
4	I	903	MGD	C8-N7	-2.11	1.30	1.34
4	K	902	MGD	C19-N20	2.10	1.36	1.33
4	I	903	MGD	C19-N18	2.10	1.39	1.36
4	G	903	MGD	C4-N3	2.10	1.39	1.35
4	W	902	MGD	C11-C12	2.10	1.54	1.51
4	S	902	MGD	C2-N3	2.09	1.36	1.33
7	X	304	SF4	S2-FE3	-2.08	2.31	2.33
4	K	903	MGD	C19-N18	2.08	1.39	1.36
4	I	902	MGD	C19-N18	2.08	1.39	1.36
4	C	902	MGD	C4-N9	2.08	1.40	1.37
7	B	302	SF4	S3-FE2	-2.08	2.31	2.33
4	K	902	MGD	C5-N7	2.07	1.40	1.38
7	V	304	SF4	S4-FE2	-2.07	2.31	2.33
4	W	902	MGD	C2'-C1'	2.07	1.56	1.53
7	X	304	SF4	S1-FE2	-2.06	2.31	2.33
4	G	903	MGD	C8-N7	-2.06	1.30	1.34
4	A	902	MGD	C19-N18	2.05	1.39	1.36
4	U	902	MGD	C19-N20	2.05	1.36	1.33
4	S	903	MGD	C5'-C4'	-2.04	1.45	1.51
4	G	903	MGD	C2'-C3'	2.02	1.59	1.53
4	O	902	MGD	C4-N3	2.02	1.39	1.35
4	E	902	MGD	C4-N9	2.02	1.40	1.37
4	W	902	MGD	C5-N7	2.02	1.40	1.38
4	K	903	MGD	O4'-C4'	-2.02	1.40	1.45
7	T	304	SF4	S4-FE2	-2.01	2.31	2.33
4	G	903	MGD	PA-O3B	2.01	1.63	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	902	MGD	C19-N20	2.01	1.36	1.33
4	Q	902	MGD	C19-N18	2.01	1.39	1.36
4	A	902	MGD	C19-N20	2.00	1.36	1.33

All (551) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	902	MGD	C6-C5-N7	-23.09	131.03	134.14
4	A	902	MGD	C6-C5-N7	-23.03	131.04	134.14
4	O	902	MGD	C6-C5-N7	-22.85	131.06	134.14
4	U	902	MGD	C6-C5-N7	-21.95	131.18	134.14
4	S	902	MGD	C6-C5-N7	-21.29	131.27	134.14
4	K	902	MGD	C6-C5-N7	-21.08	131.30	134.14
4	Q	902	MGD	C6-C5-N7	-20.43	131.39	134.14
4	M	902	MGD	C6-C5-N7	-20.30	131.41	134.14
4	W	902	MGD	C6-C5-N7	-20.15	131.43	134.14
4	G	902	MGD	C6-C5-N7	-20.13	131.43	134.14
4	E	902	MGD	C6-C5-N7	-20.08	131.44	134.14
4	S	903	MGD	C6-C5-N7	-19.78	131.48	134.14
4	I	902	MGD	C6-C5-N7	-19.68	131.49	134.14
4	C	903	MGD	C6-C5-N7	-19.55	131.51	134.14
4	I	903	MGD	C6-C5-N7	-19.29	131.54	134.14
4	Q	903	MGD	C6-C5-N7	-18.59	131.64	134.14
4	W	903	MGD	C6-C5-N7	-17.59	131.77	134.14
4	M	903	MGD	C6-C5-N7	-16.78	131.88	134.14
4	U	903	MGD	C6-C5-N7	-16.33	131.94	134.14
4	O	903	MGD	C6-C5-N7	-14.44	132.20	134.14
4	G	903	MGD	C6-C5-N7	-14.24	132.22	134.14
4	E	903	MGD	C6-C5-N7	-11.88	132.54	134.14
4	W	902	MGD	O3B-PA-O3A	8.78	126.17	102.91
4	I	902	MGD	O3B-PA-O3A	8.62	125.76	102.91
4	O	902	MGD	O3B-PA-O3A	8.62	125.75	102.91
4	E	903	MGD	O11-C23-C14	-8.54	102.28	108.99
4	A	903	MGD	C6-C5-N7	-8.51	132.99	134.14
4	Q	903	MGD	PA-O3B-PB	-8.50	108.38	131.93
4	O	903	MGD	O11-C23-C14	-8.47	102.34	108.99
4	G	903	MGD	PA-O3B-PB	-8.47	108.48	131.93
4	S	902	MGD	O3B-PA-O3A	8.43	125.26	102.91
4	G	903	MGD	O11-C23-C14	-8.43	102.37	108.99
4	M	902	MGD	O3B-PA-O3A	8.37	125.08	102.91
4	G	902	MGD	O3B-PA-O3A	8.28	124.84	102.91
4	U	902	MGD	O3B-PA-O3A	8.26	124.81	102.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	902	MGD	O3B-PA-O3A	8.19	124.60	102.91
4	C	902	MGD	O3B-PA-O3A	8.15	124.52	102.91
4	A	903	MGD	O11-C23-C14	-8.10	102.63	108.99
4	Q	903	MGD	O11-C23-C14	-8.09	102.63	108.99
4	K	903	MGD	O11-C23-C14	-8.08	102.64	108.99
4	W	903	MGD	PA-O3B-PB	-8.06	109.60	131.93
4	M	903	MGD	O11-C23-C14	-7.97	102.72	108.99
4	A	902	MGD	O3B-PA-O3A	7.91	123.88	102.91
4	Q	902	MGD	O3B-PA-O3A	7.85	123.70	102.91
4	K	903	MGD	C6-C5-N7	-7.65	133.11	134.14
4	W	903	MGD	O11-C23-C14	-7.63	103.00	108.99
4	U	903	MGD	O11-C23-C14	-7.46	103.13	108.99
4	M	903	MGD	PA-O3B-PB	-7.34	111.61	131.93
4	I	903	MGD	O11-C23-C14	-7.19	103.34	108.99
4	Q	903	MGD	C6-N1-C2	7.04	124.18	120.20
4	E	903	MGD	C6-N1-C2	7.03	124.17	120.20
4	O	903	MGD	PA-O3B-PB	-6.97	112.61	131.93
4	A	903	MGD	C6-N1-C2	6.93	124.11	120.20
4	C	903	MGD	O11-C23-C14	-6.82	103.63	108.99
4	S	903	MGD	O11-C23-C14	-6.81	103.64	108.99
4	G	903	MGD	O4'-C4'-C5'	-6.80	85.22	109.37
4	K	902	MGD	O3B-PA-O3A	6.77	120.84	102.91
4	G	903	MGD	C6-N1-C2	6.70	123.98	120.20
4	O	903	MGD	C6-N1-C2	6.61	123.93	120.20
4	Q	903	MGD	O4'-C4'-C5'	-6.61	85.90	109.37
4	M	903	MGD	O4'-C4'-C5'	-6.57	86.02	109.37
4	O	903	MGD	O4'-C4'-C5'	-6.49	86.31	109.37
4	K	903	MGD	C6-N1-C2	6.36	123.79	120.20
4	U	903	MGD	PA-O3B-PB	-6.32	114.44	131.93
4	W	903	MGD	C6-N1-C2	6.27	123.74	120.20
4	I	903	MGD	C6-N1-C2	6.25	123.73	120.20
4	C	903	MGD	C6-N1-C2	6.23	123.72	120.20
4	M	903	MGD	C6-N1-C2	6.23	123.72	120.20
4	W	903	MGD	O4'-C4'-C5'	-6.13	87.61	109.37
4	U	903	MGD	O4'-C4'-C5'	-6.11	87.67	109.37
4	K	903	MGD	C4'-O4'-C1'	6.11	116.43	109.72
6	U	905	BTT	O5-C5-C6	-6.09	103.24	119.43
4	C	903	MGD	O4'-C4'-C5'	-6.07	87.82	109.37
4	I	903	MGD	O4'-C4'-C5'	-6.06	87.84	109.37
4	U	903	MGD	C6-N1-C2	6.04	123.61	120.20
6	O	905	BTT	O5-C5-C6	-5.99	103.52	119.43
4	E	903	MGD	C13-C14-N15	-5.97	100.43	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	905	BTT	O5-C5-C6	-5.96	103.59	119.43
6	I	905	BTT	O5-C5-C6	-5.94	103.65	119.43
6	W	905	BTT	O5-C5-C6	-5.93	103.69	119.43
6	K	905	BTT	O5-C5-C6	-5.92	103.70	119.43
6	S	905	BTT	O5-C5-C6	-5.88	103.81	119.43
4	O	903	MGD	C4'-O4'-C1'	5.82	116.11	109.72
4	A	903	MGD	C4'-O4'-C1'	5.82	116.11	109.72
4	S	903	MGD	C6-N1-C2	5.81	123.48	120.20
6	Q	905	BTT	O5-C5-C6	-5.73	104.19	119.43
4	K	903	MGD	O4'-C4'-C5'	-5.73	89.01	109.37
6	M	905	BTT	O5-C5-C6	-5.73	104.21	119.43
6	A	905	BTT	O5-C5-C6	-5.71	104.26	119.43
4	E	903	MGD	C4'-O4'-C1'	5.70	115.98	109.72
4	S	903	MGD	O4'-C4'-C5'	-5.66	89.26	109.37
6	G	905	BTT	O5-C5-C6	-5.66	104.40	119.43
6	E	905	BTT	O5-C5-C6	-5.63	104.46	119.43
4	A	903	MGD	O4'-C4'-C5'	-5.58	89.57	109.37
4	G	903	MGD	C4'-O4'-C1'	5.55	115.81	109.72
4	A	903	MGD	PA-O3B-PB	-5.49	116.73	131.93
4	S	903	MGD	C13-C14-N15	-5.48	101.35	111.70
4	A	902	MGD	O2A-PA-O3B	-5.46	79.22	105.14
4	K	903	MGD	C13-C14-N15	-5.44	101.44	111.70
4	W	902	MGD	O2A-PA-O3B	-5.43	79.35	105.14
4	I	902	MGD	O2A-PA-O3B	-5.42	79.41	105.14
4	Q	903	MGD	C4'-O4'-C1'	5.41	115.66	109.72
4	U	903	MGD	C13-C14-N15	-5.40	101.52	111.70
4	U	902	MGD	O2A-PA-O3B	-5.39	79.58	105.14
4	Q	902	MGD	O2A-PA-O3B	-5.38	79.60	105.14
4	G	903	MGD	C13-C14-N15	-5.37	101.57	111.70
4	K	902	MGD	O2A-PA-O3B	-5.37	79.68	105.14
4	G	902	MGD	O2A-PA-O3B	-5.36	79.70	105.14
4	A	903	MGD	C13-C14-N15	-5.36	101.59	111.70
4	W	903	MGD	C13-C14-N15	-5.34	101.63	111.70
4	C	903	MGD	PA-O3B-PB	-5.30	117.25	131.93
4	C	902	MGD	C6-N1-C2	5.29	123.19	120.20
4	U	902	MGD	C6-N1-C2	5.29	123.19	120.20
4	U	903	MGD	C17-N18-C19	5.28	123.18	120.20
4	M	902	MGD	O2A-PA-O3B	-5.26	80.16	105.14
4	M	903	MGD	C13-C14-N15	-5.26	101.77	111.70
4	C	902	MGD	O2A-PA-O3B	-5.26	80.18	105.14
4	Q	903	MGD	C17-N18-C19	5.26	123.17	120.20
4	E	902	MGD	O2A-PA-O3B	-5.24	80.26	105.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	903	MGD	PA-O3B-PB	-5.22	117.49	131.93
4	K	903	MGD	C17-N18-C19	5.21	123.14	120.20
4	O	903	MGD	C13-C14-N15	-5.21	101.86	111.70
4	S	902	MGD	O2A-PA-O3B	-5.20	80.45	105.14
4	I	903	MGD	C17-N18-C19	5.18	123.13	120.20
4	S	902	MGD	C6-N1-C2	5.18	123.12	120.20
4	C	903	MGD	C13-C14-N15	-5.15	101.98	111.70
4	C	903	MGD	C17-N18-C19	5.15	123.11	120.20
4	S	903	MGD	C17-N18-C19	5.14	123.10	120.20
4	W	902	MGD	C6-N1-C2	5.13	123.10	120.20
4	Q	902	MGD	O2A-PA-O3A	-5.13	82.64	108.51
4	M	903	MGD	C17-N18-C19	5.13	123.09	120.20
4	Q	902	MGD	C6-N1-C2	5.11	123.09	120.20
4	O	902	MGD	O2A-PA-O3B	-5.11	80.89	105.14
4	I	902	MGD	C6-N1-C2	5.10	123.08	120.20
4	O	903	MGD	C17-N18-C19	5.09	123.07	120.20
4	E	902	MGD	C6-N1-C2	5.06	123.06	120.20
4	C	902	MGD	C17-C16-C21	5.06	119.14	114.56
4	K	902	MGD	C17-C16-C21	5.03	119.12	114.56
4	E	903	MGD	O4'-C4'-C5'	-4.98	91.67	109.37
4	O	902	MGD	C17-C16-C21	4.98	119.07	114.56
4	O	902	MGD	C6-N1-C2	4.98	123.01	120.20
4	I	902	MGD	C17-C16-C21	4.98	119.07	114.56
4	G	902	MGD	C6-N1-C2	4.98	123.01	120.20
4	W	903	MGD	O3B-PB-O5'	4.98	116.10	102.91
4	A	902	MGD	O2A-PA-O3A	-4.95	83.57	108.51
4	W	903	MGD	C17-N18-C19	4.94	122.99	120.20
4	S	902	MGD	O2A-PA-O3A	-4.94	83.61	108.51
4	K	902	MGD	C6-N1-C2	4.93	122.99	120.20
4	M	903	MGD	O11-C23-N22	-4.92	103.39	109.03
4	E	903	MGD	C17-C16-C21	4.89	118.99	114.56
4	I	903	MGD	C13-C14-N15	-4.89	102.48	111.70
4	E	903	MGD	C17-N18-C19	4.88	122.96	120.20
4	A	902	MGD	C17-C16-C21	4.88	118.98	114.56
4	Q	903	MGD	C13-C14-N15	-4.87	102.50	111.70
4	M	902	MGD	C17-C16-C21	4.87	118.97	114.56
4	A	902	MGD	C6-N1-C2	4.87	122.95	120.20
4	W	903	MGD	C17-C16-C21	4.87	118.97	114.56
4	G	903	MGD	C17-N18-C19	4.87	122.95	120.20
4	W	902	MGD	C17-C16-C21	4.87	118.97	114.56
4	A	903	MGD	C17-N18-C19	4.85	122.94	120.20
4	E	902	MGD	C17-C16-C21	4.85	118.95	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	902	MGD	O2A-PA-O3A	-4.84	84.09	108.51
4	S	902	MGD	C17-C16-C21	4.84	118.95	114.56
4	E	903	MGD	O11-C23-N22	-4.81	103.52	109.03
4	I	903	MGD	PA-O3B-PB	-4.79	118.65	131.93
4	U	902	MGD	C17-C16-C21	4.78	118.89	114.56
4	Q	902	MGD	C17-C16-C21	4.76	118.87	114.56
4	I	902	MGD	O2A-PA-O3A	-4.74	84.59	108.51
4	G	902	MGD	O2A-PA-O3A	-4.74	84.60	108.51
4	M	902	MGD	O2A-PA-O3A	-4.74	84.62	108.51
4	E	903	MGD	C5-C4-N3	4.73	131.52	126.07
4	G	903	MGD	C17-C16-C21	4.73	118.84	114.56
4	A	903	MGD	C5-C4-N3	4.71	131.49	126.07
4	W	902	MGD	O2A-PA-O3A	-4.70	84.80	108.51
4	K	903	MGD	C17-C16-C21	4.70	118.82	114.56
4	A	903	MGD	C17-C16-C21	4.69	118.81	114.56
4	G	902	MGD	C17-C16-C21	4.69	118.80	114.56
4	O	903	MGD	C17-C16-C21	4.67	118.79	114.56
4	K	902	MGD	O2A-PA-O3A	-4.66	85.04	108.51
4	W	902	MGD	C17-N18-C19	4.65	122.83	120.20
4	U	902	MGD	O2A-PA-O3A	-4.65	85.06	108.51
4	O	902	MGD	O2A-PA-O3A	-4.62	85.19	108.51
4	C	903	MGD	C17-C16-C21	4.60	118.73	114.56
4	E	902	MGD	O2A-PA-O3A	-4.59	85.39	108.51
4	M	903	MGD	C17-C16-C21	4.57	118.70	114.56
4	S	903	MGD	PA-O3B-PB	-4.56	119.30	131.93
4	S	903	MGD	C17-C16-C21	4.56	118.69	114.56
4	Q	903	MGD	C17-C16-C21	4.55	118.68	114.56
4	O	902	MGD	PA-O3B-PB	-4.53	119.37	131.93
4	M	902	MGD	C17-N18-C19	4.50	122.74	120.20
4	U	903	MGD	C17-C16-C21	4.50	118.63	114.56
4	M	903	MGD	C5-C4-N3	4.49	131.24	126.07
4	Q	903	MGD	O11-C23-N22	-4.48	103.89	109.03
4	E	902	MGD	C17-N18-C19	4.47	122.72	120.20
4	Q	903	MGD	C5-C4-N3	4.42	131.15	126.07
4	K	903	MGD	C5-C4-N3	4.39	131.13	126.07
4	O	903	MGD	C5-C4-N3	4.38	131.11	126.07
4	U	902	MGD	C17-N18-C19	4.38	122.67	120.20
4	G	903	MGD	O11-C23-N22	-4.36	104.04	109.03
4	G	902	MGD	C17-N18-C19	4.35	122.66	120.20
4	U	903	MGD	O11-C23-N22	-4.34	104.06	109.03
4	O	903	MGD	O11-C23-N22	-4.33	104.07	109.03
4	E	903	MGD	PA-O3B-PB	-4.29	120.04	131.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	903	MGD	C5-C4-N3	4.29	131.01	126.07
4	I	903	MGD	C5-C4-N3	4.28	131.00	126.07
4	K	903	MGD	O11-C23-N22	-4.27	104.13	109.03
4	S	903	MGD	O11-C23-N22	-4.27	104.14	109.03
4	C	902	MGD	C17-N18-C19	4.26	122.61	120.20
4	A	903	MGD	O11-C23-N22	-4.25	104.16	109.03
4	Q	902	MGD	O2A-PA-O1A	-4.25	88.62	112.14
4	W	903	MGD	C5-C4-N3	4.24	130.95	126.07
4	I	903	MGD	C17-C16-C21	4.22	118.38	114.56
4	I	902	MGD	C17-N18-C19	4.20	122.57	120.20
4	A	902	MGD	C17-N18-C19	4.19	122.57	120.20
4	O	902	MGD	C17-N18-C19	4.19	122.57	120.20
4	K	902	MGD	C17-N18-C19	4.05	122.49	120.20
4	M	902	MGD	C6-N1-C2	4.04	122.48	120.20
4	C	903	MGD	C5-C4-N3	4.03	130.71	126.07
4	S	902	MGD	C17-N18-C19	4.02	122.47	120.20
4	G	903	MGD	C5-C4-N3	3.95	130.61	126.07
4	S	902	MGD	O2A-PA-O1A	-3.94	90.34	112.14
4	A	902	MGD	O2A-PA-O1A	-3.90	90.54	112.14
4	Q	903	MGD	O3B-PB-O5'	3.90	113.25	102.91
4	M	903	MGD	O3B-PB-O5'	3.90	113.23	102.91
4	G	902	MGD	O2A-PA-O1A	-3.84	90.89	112.14
4	A	903	MGD	C2'-C1'-N9	3.82	123.76	113.35
4	K	902	MGD	O2A-PA-O1A	-3.81	91.05	112.14
4	Q	902	MGD	C17-N18-C19	3.81	122.35	120.20
4	U	902	MGD	O2A-PA-O1A	-3.79	91.16	112.14
4	K	902	MGD	C16-N15-C14	-3.78	108.86	118.66
4	M	902	MGD	PA-O3B-PB	-3.77	121.49	131.93
4	A	902	MGD	C16-N15-C14	-3.74	108.96	118.66
4	C	902	MGD	C16-N15-C14	-3.73	109.00	118.66
4	C	902	MGD	O2A-PA-O1A	-3.71	91.61	112.14
4	E	902	MGD	O2A-PA-O1A	-3.69	91.71	112.14
4	S	902	MGD	C16-N15-C14	-3.69	109.09	118.66
4	Q	902	MGD	C16-N15-C14	-3.68	109.11	118.66
4	U	902	MGD	C16-N15-C14	-3.68	109.12	118.66
4	E	902	MGD	C16-N15-C14	-3.66	109.17	118.66
4	U	903	MGD	C5-C4-N3	3.65	130.27	126.07
4	O	902	MGD	C16-N15-C14	-3.64	109.22	118.66
4	M	902	MGD	O2A-PA-O1A	-3.63	92.05	112.14
4	W	902	MGD	C16-N15-C14	-3.63	109.26	118.66
4	W	903	MGD	O11-C23-N22	-3.60	104.90	109.03
4	G	903	MGD	O5'-C5'-C4'	3.57	122.08	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	902	MGD	C16-N15-C14	-3.56	109.42	118.66
4	A	903	MGD	O4'-C1'-N9	-3.56	100.35	108.10
4	G	902	MGD	C16-N15-C14	-3.55	109.46	118.66
4	S	903	MGD	C2-N3-C4	-3.54	111.05	115.30
4	M	903	MGD	C16-C21-N20	3.52	125.14	118.43
4	I	902	MGD	PA-O3B-PB	-3.52	122.18	131.93
4	W	902	MGD	PA-O3B-PB	-3.51	122.20	131.93
4	C	903	MGD	O11-C23-N22	-3.51	105.00	109.03
4	O	903	MGD	O4'-C1'-N9	-3.51	100.47	108.10
4	U	903	MGD	C16-C21-N20	3.50	125.11	118.43
4	O	902	MGD	O2A-PA-O1A	-3.50	92.77	112.14
4	I	902	MGD	C16-N15-C14	-3.50	109.58	118.66
4	S	903	MGD	C16-C21-N20	3.50	125.10	118.43
4	Q	903	MGD	C2-N3-C4	-3.50	111.11	115.30
4	I	903	MGD	C2-N3-C4	-3.49	111.11	115.30
4	O	903	MGD	C16-C21-N20	3.45	125.00	118.43
4	U	903	MGD	O3B-PB-O5'	3.43	112.01	102.91
4	W	902	MGD	O2A-PA-O1A	-3.42	93.22	112.14
4	A	902	MGD	C16-C21-N20	3.41	124.93	118.43
4	I	903	MGD	C16-C21-N20	3.40	124.91	118.43
4	I	902	MGD	C16-C21-N20	3.39	124.89	118.43
4	M	902	MGD	C16-C21-N20	3.38	124.88	118.43
4	W	903	MGD	C16-C21-N20	3.38	124.88	118.43
4	M	903	MGD	C2-N3-C4	-3.37	111.26	115.30
4	G	903	MGD	C16-C21-N20	3.37	124.86	118.43
4	Q	903	MGD	C16-C21-N20	3.37	124.85	118.43
4	U	902	MGD	C16-C21-N20	3.35	124.82	118.43
4	I	902	MGD	O2A-PA-O1A	-3.34	93.64	112.14
4	K	902	MGD	C16-C21-N20	3.34	124.80	118.43
4	Q	902	MGD	C23-C14-N15	3.34	113.03	108.34
4	C	903	MGD	C16-C21-N20	3.33	124.79	118.43
4	O	902	MGD	C16-C21-N20	3.33	124.77	118.43
4	W	902	MGD	C23-C14-N15	3.32	113.01	108.34
4	O	903	MGD	C16-N15-C14	-3.32	110.05	118.66
4	Q	902	MGD	C16-C21-N20	3.32	124.75	118.43
4	E	902	MGD	C16-C21-N20	3.31	124.75	118.43
4	G	903	MGD	O3B-PB-O5'	3.31	111.69	102.91
4	Q	903	MGD	O5'-C5'-C4'	3.31	121.13	108.96
4	W	903	MGD	C4'-O4'-C1'	3.31	113.36	109.72
4	K	903	MGD	C16-C21-N20	3.31	124.74	118.43
4	E	902	MGD	PA-O3B-PB	-3.30	122.79	131.93
4	C	902	MGD	C23-C14-N15	3.30	112.98	108.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	903	MGD	C16-C21-N20	3.30	124.71	118.43
4	K	902	MGD	C23-C14-N15	3.29	112.97	108.34
4	C	902	MGD	C16-C21-N20	3.29	124.71	118.43
4	G	902	MGD	C16-C21-N20	3.28	124.69	118.43
4	Q	903	MGD	C16-N15-C14	-3.27	110.17	118.66
4	E	903	MGD	C16-C21-N20	3.27	124.67	118.43
4	S	902	MGD	C16-C21-N20	3.27	124.66	118.43
4	O	903	MGD	C2-N3-C4	-3.26	111.39	115.30
4	W	903	MGD	C2-N3-C4	-3.26	111.39	115.30
4	W	902	MGD	C16-C21-N20	3.25	124.62	118.43
4	C	903	MGD	C2-N3-C4	-3.25	111.41	115.30
4	G	902	MGD	O3A-C10-C11	-3.25	100.21	108.87
4	M	903	MGD	C16-N15-C14	-3.23	110.28	118.66
4	U	903	MGD	O5'-C5'-C4'	3.23	120.84	108.96
4	G	903	MGD	C16-N15-C14	-3.22	110.30	118.66
4	K	903	MGD	C16-N15-C14	-3.22	110.31	118.66
4	G	902	MGD	C23-C14-N15	3.22	112.86	108.34
4	U	903	MGD	C16-N15-C14	-3.22	110.32	118.66
4	M	902	MGD	C23-C14-N15	3.21	112.85	108.34
4	E	902	MGD	C23-C14-N15	3.20	112.84	108.34
4	O	902	MGD	C23-C14-N15	3.20	112.83	108.34
4	W	903	MGD	C16-N15-C14	-3.19	110.38	118.66
4	A	902	MGD	O3A-C10-C11	-3.19	100.36	108.87
4	M	903	MGD	O5'-C5'-C4'	3.18	120.65	108.96
4	O	903	MGD	O2B-PB-O5'	-3.18	92.47	108.51
4	S	903	MGD	C16-N15-C14	-3.17	110.44	118.66
4	O	903	MGD	C2'-C1'-N9	3.17	121.97	113.35
4	I	903	MGD	C16-N15-C14	-3.17	110.45	118.66
4	C	903	MGD	C16-N15-C14	-3.17	110.45	118.66
4	U	902	MGD	C23-C14-N15	3.16	112.79	108.34
4	K	903	MGD	C2'-C1'-N9	3.16	121.95	113.35
4	A	902	MGD	C23-C14-N15	3.15	112.78	108.34
4	A	903	MGD	C1'-N9-C4	-3.16	121.18	126.64
4	S	903	MGD	O3B-PB-O5'	3.16	111.27	102.91
4	U	902	MGD	C5-C4-N3	3.16	129.70	126.07
4	E	903	MGD	C2'-C1'-N9	3.15	121.92	113.35
4	A	902	MGD	C5-C4-N3	3.14	129.69	126.07
4	K	903	MGD	O4'-C1'-N9	-3.14	101.26	108.10
4	A	903	MGD	C2-N3-C4	-3.13	111.54	115.30
4	I	903	MGD	O11-C23-N22	-3.13	105.44	109.03
4	A	903	MGD	C8-N9-C1'	3.13	132.04	126.15
4	E	903	MGD	O11-C11-C10	-3.13	100.74	108.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	903	MGD	C2-N3-C4	-3.12	111.56	115.30
4	A	903	MGD	C16-N15-C14	-3.12	110.57	118.66
4	W	902	MGD	C5-C4-N3	3.11	129.65	126.07
4	I	902	MGD	C23-C14-N15	3.11	112.71	108.34
4	S	902	MGD	C23-C14-N15	3.07	112.65	108.34
4	E	903	MGD	C2-N3-C4	-3.06	111.63	115.30
4	E	903	MGD	C16-N15-C14	-3.06	110.72	118.66
4	S	902	MGD	C5-C4-N3	3.05	129.59	126.07
4	Q	903	MGD	O2B-PB-O5'	-3.05	93.12	108.51
4	U	903	MGD	C2-N3-C4	-3.05	111.65	115.30
4	M	902	MGD	C5-C4-N3	3.03	129.56	126.07
4	Q	902	MGD	O3A-C10-C11	-3.02	100.81	108.87
4	Q	902	MGD	C5-C4-N3	3.01	129.53	126.07
6	W	905	BTT	O5-C5-C4	-3.00	110.69	118.47
4	U	902	MGD	PA-O3B-PB	-3.00	123.63	131.93
4	W	903	MGD	O5'-C5'-C4'	2.98	119.93	108.96
4	Q	903	MGD	O11-C11-C10	-2.95	101.21	108.81
4	C	902	MGD	PA-O3B-PB	-2.95	123.77	131.93
4	C	902	MGD	C5-C4-N3	2.94	129.45	126.07
6	K	905	BTT	O5-C5-C4	-2.93	110.88	118.47
4	S	903	MGD	C16-C21-N22	2.92	121.40	118.34
6	C	905	BTT	O5-C5-C4	-2.92	110.89	118.47
4	M	903	MGD	C4'-O4'-C1'	2.91	112.92	109.72
6	O	905	BTT	O5-C5-C4	-2.91	110.92	118.47
6	Q	905	BTT	O5-C5-C4	-2.90	110.94	118.47
4	O	903	MGD	O11-C11-C10	-2.90	101.33	108.81
4	M	903	MGD	C3'-C2'-C1'	2.89	105.46	100.92
4	A	903	MGD	O2B-PB-O5'	-2.89	93.94	108.51
4	U	902	MGD	O3A-C10-C11	-2.89	101.17	108.87
4	C	903	MGD	O3B-PB-O5'	2.88	110.54	102.91
4	U	903	MGD	C4'-O4'-C1'	2.87	112.88	109.72
4	S	902	MGD	PA-O3B-PB	-2.87	123.97	131.93
6	A	905	BTT	O5-C5-C4	-2.86	111.03	118.47
4	U	903	MGD	C3'-C2'-C1'	2.86	105.40	100.92
4	A	903	MGD	O11-C11-C10	-2.85	101.45	108.81
4	Q	903	MGD	O4'-C1'-N9	-2.85	101.89	108.10
4	K	903	MGD	O11-C11-C10	-2.84	101.47	108.81
6	U	905	BTT	O5-C5-C4	-2.84	111.10	118.47
4	I	903	MGD	C16-C21-N22	2.84	121.31	118.34
4	M	902	MGD	O3A-C10-C11	-2.83	101.31	108.87
4	U	903	MGD	C16-C21-N22	2.83	121.30	118.34
6	G	905	BTT	O5-C5-C4	-2.83	111.14	118.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	903	MGD	O4'-C4'-C3'	2.82	110.90	105.16
4	E	902	MGD	C5-C4-N3	2.82	129.31	126.07
6	S	905	BTT	O5-C5-C4	-2.81	111.17	118.47
4	I	902	MGD	C5-C4-N3	2.81	129.30	126.07
6	M	905	BTT	O5-C5-C4	-2.81	111.18	118.47
4	G	903	MGD	O11-C11-C10	-2.80	101.58	108.81
6	E	905	BTT	O5-C5-C4	-2.78	111.25	118.47
4	W	903	MGD	C3'-C2'-C1'	2.78	105.28	100.92
6	I	905	BTT	O5-C5-C4	-2.77	111.28	118.47
4	I	903	MGD	O3B-PB-O5'	2.77	110.26	102.91
4	O	902	MGD	C2-N3-C4	-2.77	111.98	115.30
4	O	902	MGD	C5-C4-N3	2.77	129.25	126.07
4	M	902	MGD	C16-C21-N22	2.76	121.23	118.34
4	I	903	MGD	C3'-C2'-C1'	2.76	105.25	100.92
4	K	903	MGD	O2B-PB-O5'	-2.74	94.70	108.51
4	S	902	MGD	O3A-C10-C11	-2.74	101.56	108.87
4	Q	903	MGD	C16-C21-N22	2.73	121.20	118.34
6	U	905	BTT	O1-C1-C2	2.73	125.56	118.47
4	C	902	MGD	O3A-C10-C11	-2.73	101.59	108.87
4	K	902	MGD	C16-C21-N22	2.73	121.20	118.34
4	Q	903	MGD	C3'-C2'-C1'	2.73	105.19	100.92
6	I	905	BTT	O1-C1-C2	2.71	125.52	118.47
4	G	903	MGD	C16-C21-N22	2.71	121.18	118.34
6	S	905	BTT	O1-C1-C2	2.71	125.50	118.47
4	U	902	MGD	C2-N3-C4	-2.71	112.06	115.30
4	Q	903	MGD	C2'-C1'-N9	2.70	120.71	113.35
4	A	902	MGD	C2-N3-C4	-2.70	112.07	115.30
4	G	902	MGD	O4'-C4'-C5'	-2.69	99.83	109.37
4	U	902	MGD	C16-C21-N22	2.68	121.15	118.34
6	C	905	BTT	O1-C1-C2	2.68	125.43	118.47
6	K	905	BTT	O1-C1-C2	2.68	125.43	118.47
4	C	903	MGD	C3'-C2'-C1'	2.67	105.12	100.92
6	O	905	BTT	O1-C1-C2	2.67	125.41	118.47
4	G	902	MGD	C5-C4-N3	2.67	129.14	126.07
4	S	902	MGD	C2-N3-C4	-2.67	112.10	115.30
4	M	903	MGD	C16-C21-N22	2.66	121.12	118.34
4	G	903	MGD	C3'-C2'-C1'	2.65	105.07	100.92
4	K	903	MGD	C16-C21-N22	2.64	121.11	118.34
4	Q	902	MGD	C2-N3-C4	-2.63	112.14	115.30
6	G	905	BTT	O1-C1-C2	2.63	125.31	118.47
4	E	903	MGD	C8-N9-C1'	2.63	131.10	126.15
4	A	903	MGD	N3-C4-N9	-2.62	123.06	126.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	903	MGD	C1'-N9-C4	-2.62	122.11	126.64
4	A	903	MGD	O5'-PB-O1B	2.62	119.62	109.37
4	O	903	MGD	O5'-PB-O1B	2.62	119.62	109.37
6	A	905	BTT	O1-C1-C2	2.61	125.26	118.47
4	E	902	MGD	O3A-C10-C11	-2.61	101.89	108.87
4	C	903	MGD	C16-C21-N22	2.61	121.08	118.34
4	E	902	MGD	C2-N3-C4	-2.61	112.17	115.30
6	Q	905	BTT	O1-C1-C2	2.61	125.24	118.47
4	E	903	MGD	C1'-N9-C4	-2.60	122.14	126.64
6	E	905	BTT	O1-C1-C2	2.60	125.22	118.47
4	M	902	MGD	O5'-C5'-C4'	-2.59	99.44	108.96
4	K	903	MGD	C2-N3-C4	-2.59	112.20	115.30
4	E	903	MGD	O4'-C1'-N9	-2.59	102.47	108.10
4	E	903	MGD	N3-C4-N9	-2.58	123.11	126.91
4	Q	902	MGD	C16-C21-N22	2.58	121.05	118.34
6	M	905	BTT	O1-C1-C2	2.58	125.16	118.47
4	C	902	MGD	C2-N3-C4	-2.57	112.21	115.30
4	S	902	MGD	C10-C11-C12	2.57	114.02	110.98
4	K	902	MGD	C5-C4-N3	2.57	129.03	126.07
4	S	903	MGD	C3'-C2'-C1'	2.57	104.94	100.92
4	C	902	MGD	C16-C21-N22	2.56	121.02	118.34
6	W	905	BTT	O1-C1-C2	2.56	125.12	118.47
4	G	902	MGD	C16-C21-N22	2.54	121.00	118.34
4	W	902	MGD	C16-C21-N22	2.54	121.00	118.34
4	K	903	MGD	O5'-PB-O1B	2.53	119.28	109.37
4	I	902	MGD	O3A-C10-C11	-2.53	102.12	108.87
4	O	902	MGD	C16-C21-N22	2.52	120.97	118.34
4	G	903	MGD	O2B-PB-O5'	-2.51	95.83	108.51
4	Q	903	MGD	O5'-PB-O1B	2.51	119.22	109.37
4	I	902	MGD	O4'-C4'-C5'	-2.51	100.47	109.37
4	G	903	MGD	C2'-C1'-N9	2.51	120.17	113.35
4	E	902	MGD	C16-C21-N22	2.50	120.96	118.34
4	W	902	MGD	C2-N3-C4	-2.50	112.31	115.30
4	M	903	MGD	N3-C4-N9	-2.50	123.24	126.91
4	A	903	MGD	C16-C21-N22	2.49	120.95	118.34
4	O	903	MGD	C16-C21-N22	2.49	120.95	118.34
4	O	903	MGD	O5'-C5'-C4'	2.49	118.11	108.96
4	O	902	MGD	C13-C14-N15	-2.48	107.01	111.70
4	G	902	MGD	C2-N3-C4	-2.48	112.33	115.30
4	A	902	MGD	C16-C21-N22	2.48	120.94	118.34
4	U	902	MGD	O4'-C4'-C5'	-2.46	100.62	109.37
4	I	902	MGD	C16-C21-N22	2.46	120.92	118.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	902	MGD	C16-C21-N22	2.44	120.90	118.34
4	M	902	MGD	C10-C11-C12	2.42	113.84	110.98
4	M	903	MGD	O11-C11-C10	-2.42	102.56	108.81
4	G	903	MGD	O4'-C1'-N9	-2.42	102.82	108.10
4	E	903	MGD	C16-C21-N22	2.41	120.86	118.34
4	W	903	MGD	O11-C11-C10	-2.40	102.61	108.81
4	S	902	MGD	O4'-C4'-C5'	-2.39	100.88	109.37
4	O	902	MGD	O11-C11-C10	-2.38	102.66	108.81
4	K	903	MGD	C8-N9-C1'	2.38	130.63	126.15
4	I	902	MGD	C2-N3-C4	-2.38	112.45	115.30
4	G	903	MGD	C8-N9-C1'	2.38	130.62	126.15
4	W	903	MGD	N3-C4-N9	-2.37	123.42	126.91
4	E	903	MGD	O2B-PB-O5'	-2.37	96.56	108.51
4	I	902	MGD	C10-C11-C12	2.37	113.77	110.98
4	C	903	MGD	O5'-C5'-C4'	2.36	117.65	108.96
4	M	903	MGD	PB-O5'-C5'	-2.36	105.05	122.03
4	C	902	MGD	C3'-C2'-C1'	2.36	104.62	100.92
4	Q	902	MGD	O4'-C4'-C5'	-2.35	101.01	109.37
4	W	903	MGD	C16-C21-N22	2.35	120.80	118.34
4	A	903	MGD	O3B-PA-O3A	2.35	109.14	102.91
4	O	903	MGD	C8-N9-C1'	2.35	130.58	126.15
4	C	903	MGD	C4'-O4'-C1'	2.35	112.30	109.72
4	I	902	MGD	C13-C14-N15	-2.34	107.28	111.70
4	U	903	MGD	O11-C11-C10	-2.33	102.79	108.81
4	K	902	MGD	C2-N3-C4	-2.31	112.53	115.30
4	W	902	MGD	C13-C14-N15	-2.31	107.35	111.70
4	Q	903	MGD	C8-N9-C1'	2.29	130.47	126.15
4	O	903	MGD	O3B-PA-O3A	2.29	108.99	102.91
4	G	902	MGD	PA-O3B-PB	-2.29	125.58	131.93
4	S	903	MGD	N3-C4-N9	-2.29	123.54	126.91
4	I	903	MGD	O4'-C4'-C3'	2.29	109.81	105.16
4	E	902	MGD	C10-C11-C12	2.28	113.67	110.98
4	K	902	MGD	C13-C14-N15	-2.28	107.40	111.70
4	G	903	MGD	O5'-PB-O1B	2.28	118.31	109.37
4	O	903	MGD	C1'-N9-C4	-2.27	122.71	126.64
4	M	902	MGD	C2-N3-C4	-2.26	112.59	115.30
4	S	902	MGD	O5'-C5'-C4'	-2.26	100.65	108.96
4	W	903	MGD	PB-O5'-C5'	-2.26	105.79	122.03
4	O	903	MGD	C3'-C2'-C1'	2.26	104.46	100.92
4	O	902	MGD	O3A-C10-C11	-2.24	102.90	108.87
4	E	902	MGD	O11-C23-C14	2.24	110.75	108.99
4	E	902	MGD	C13-C14-N15	-2.23	107.48	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	902	MGD	C13-C14-N15	-2.23	107.49	111.70
4	G	902	MGD	C10-C11-C12	2.22	113.60	110.98
4	O	902	MGD	O5'-C5'-C4'	-2.21	100.83	108.96
4	C	902	MGD	O4'-C4'-C5'	-2.20	101.55	109.37
4	W	902	MGD	O11-C11-C10	-2.20	103.13	108.81
4	Q	903	MGD	N3-C4-N9	-2.19	123.69	126.91
4	A	902	MGD	C4-C5-N7	2.19	111.53	109.41
4	Q	902	MGD	O11-C23-C14	2.19	110.72	108.99
4	K	903	MGD	O3A-PA-O1A	-2.18	100.82	109.37
4	O	902	MGD	O4'-C4'-C5'	-2.17	101.65	109.37
4	M	902	MGD	C13-C14-N15	-2.17	107.60	111.70
4	U	902	MGD	O5'-C5'-C4'	-2.17	100.99	108.96
4	A	902	MGD	O5'-C5'-C4'	-2.15	101.06	108.96
4	K	902	MGD	O4'-C4'-C5'	-2.15	101.73	109.37
4	C	902	MGD	C4-C5-N7	2.15	111.49	109.41
4	E	902	MGD	C3'-C2'-C1'	2.14	104.28	100.92
4	M	902	MGD	C4-C5-N7	2.14	111.48	109.41
4	W	903	MGD	O4'-C4'-C3'	2.14	109.51	105.16
4	C	903	MGD	N3-C4-N9	-2.14	123.77	126.91
4	U	903	MGD	C8-N9-C1'	2.14	130.18	126.15
4	O	902	MGD	C4-C5-N7	2.14	111.47	109.41
4	W	903	MGD	C8-N9-C1'	2.14	130.17	126.15
4	K	903	MGD	N3-C4-N9	-2.13	123.78	126.91
4	K	902	MGD	O3A-C10-C11	-2.13	103.19	108.87
4	U	902	MGD	C3'-C2'-C1'	2.12	104.25	100.92
4	A	902	MGD	C10-C11-C12	2.12	113.48	110.98
4	W	902	MGD	C3'-C2'-C1'	2.12	104.25	100.92
4	E	903	MGD	O3B-PA-O3A	2.12	108.52	102.91
4	E	902	MGD	O5'-C5'-C4'	-2.11	101.22	108.96
4	U	903	MGD	PB-O5'-C5'	-2.10	106.91	122.03
4	C	902	MGD	O5'-C5'-C4'	-2.10	101.25	108.96
4	I	903	MGD	N3-C4-N9	-2.10	123.83	126.91
4	E	902	MGD	O4'-C4'-C5'	-2.09	101.94	109.37
4	I	902	MGD	C3'-C2'-C1'	2.09	104.20	100.92
4	Q	902	MGD	O5'-C5'-C4'	-2.08	101.30	108.96
4	O	903	MGD	O3A-PA-O1A	-2.08	101.22	109.37
4	K	903	MGD	O3B-PA-O3A	2.08	108.42	102.91
4	U	902	MGD	C4-C5-N7	2.08	111.42	109.41
4	M	902	MGD	C3'-C2'-C1'	2.07	104.17	100.92
4	E	903	MGD	O3A-PA-O1A	-2.07	101.26	109.37
4	S	902	MGD	C3'-C2'-C1'	2.07	104.16	100.92
4	A	902	MGD	C3'-C2'-C1'	2.06	104.15	100.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	W	902	MGD	O5'-C5'-C4'	-2.05	101.42	108.96
4	O	902	MGD	C10-C11-C12	2.05	113.39	110.98
4	O	903	MGD	O3B-PB-O5'	2.04	108.33	102.91
4	W	902	MGD	C4-C5-N7	2.04	111.38	109.41
4	U	902	MGD	C10-C11-C12	2.04	113.39	110.98
4	G	903	MGD	N3-C4-N9	-2.04	123.92	126.91
4	O	903	MGD	N3-C4-N9	-2.03	123.93	126.91
4	W	903	MGD	C2'-C1'-N9	2.02	118.86	113.35
4	G	902	MGD	C3'-C2'-C1'	2.01	104.08	100.92
4	A	903	MGD	O3A-PA-O1A	-2.01	101.51	109.37
6	S	905	BTT	C3-C2-C1	-2.01	118.04	119.80
4	I	902	MGD	O11-C11-C10	-2.01	103.64	108.81

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	903	MGD	PB-O5'-C5'-C4'
4	K	903	MGD	PB-O5'-C5'-C4'
4	E	903	MGD	PB-O5'-C5'-C4'
4	O	903	MGD	PB-O5'-C5'-C4'
4	E	903	MGD	C2'-C1'-N9-C8
4	A	903	MGD	C2'-C1'-N9-C8

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.