



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2024 – 10:48 PM EST

PDB ID : 5W6J  
Title : Agrobacterium tumefaciens ADP-glucose pyrophosphorylase  
Authors : Mascarenhas, R.N.; Hill, B.L.; Wu, R.; Ballicora, M.A.; Liu, D.  
Deposited on : 2017-06-16  
Resolution : 1.78 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

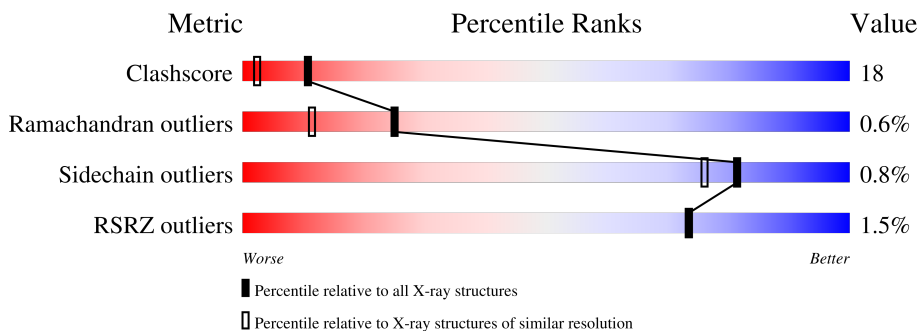
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 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	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	420	
1	B	420	
1	C	420	
1	D	420	
1	E	420	
1	F	420	

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Mol	Chain	Length	Quality of chain	
1	G	420		•
1	H	420		••
1	I	420		••
1	J	420		•
1	K	420		•
1	L	420		••
1	M	420		•
1	N	420		••
1	O	420		•
1	P	420		•
1	Q	420		••
1	R	420		••
1	T	420		••
1	U	420		•

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	502	-	-	X	-
2	SO4	C	502	-	-	X	-
2	SO4	D	502	-	-	X	-
2	SO4	L	502	-	-	X	-
2	SO4	O	502	-	-	X	-
2	SO4	T	501	-	-	X	-
2	SO4	T	502	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 75925 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Glucose-1-phosphate adenylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	415	Total 3252	C 2062	N 564	O 613	S 13	0	1	0
1	B	415	Total 3262	C 2068	N 567	O 614	S 13	0	3	0
1	C	413	Total 3240	C 2055	N 562	O 610	S 13	0	1	0
1	D	412	Total 3226	C 2047	N 558	O 608	S 13	0	0	0
1	E	409	Total 3202	C 2035	N 549	O 605	S 13	0	1	0
1	H	409	Total 3202	C 2034	N 549	O 606	S 13	0	0	0
1	I	409	Total 3212	C 2040	N 552	O 607	S 13	0	1	0
1	J	415	Total 3250	C 2062	N 561	O 614	S 13	3	2	0
1	K	410	Total 3213	C 2040	N 553	O 607	S 13	0	0	0
1	L	410	Total 3222	C 2045	N 554	O 610	S 13	0	1	0
1	N	415	Total 3253	C 2061	N 562	O 617	S 13	0	0	0
1	O	411	Total 3212	C 2040	N 551	O 608	S 13	0	0	0
1	P	409	Total 3212	C 2040	N 552	O 607	S 13	0	1	0
1	Q	409	Total 3212	C 2040	N 552	O 607	S 13	0	1	0
1	R	409	Total 3202	C 2034	N 549	O 606	S 13	0	0	0
1	F	408	Total 3214	C 2042	N 554	O 605	S 13	5	1	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	410	Total	C	N	O	S	0	1	0
			3227	2048	559	607	13			
1	M	410	Total	C	N	O	S	4	1	0
			3210	2037	553	607	13			
1	T	415	Total	C	N	O	S	0	1	0
			3252	2062	562	615	13			
1	U	415	Total	C	N	O	S	0	1	0
			3244	2058	559	614	13			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	221	LEU	VAL	conflict	UNP P39669
B	221	LEU	VAL	conflict	UNP P39669
C	221	LEU	VAL	conflict	UNP P39669
D	221	LEU	VAL	conflict	UNP P39669
E	221	LEU	VAL	conflict	UNP P39669
H	221	LEU	VAL	conflict	UNP P39669
I	221	LEU	VAL	conflict	UNP P39669
J	221	LEU	VAL	conflict	UNP P39669
K	221	LEU	VAL	conflict	UNP P39669
L	221	LEU	VAL	conflict	UNP P39669
N	221	LEU	VAL	conflict	UNP P39669
O	221	LEU	VAL	conflict	UNP P39669
P	221	LEU	VAL	conflict	UNP P39669
Q	221	LEU	VAL	conflict	UNP P39669
R	221	LEU	VAL	conflict	UNP P39669
F	221	LEU	VAL	conflict	UNP P39669
G	221	LEU	VAL	conflict	UNP P39669
M	221	LEU	VAL	conflict	UNP P39669
T	221	LEU	VAL	conflict	UNP P39669
U	221	LEU	VAL	conflict	UNP P39669

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	I	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	J	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	K	1	5	4	1	0	0
2	L	1	5	4	1	0	0
2	L	1	5	4	1	0	0
2	N	1	5	4	1	0	0
2	N	1	5	4	1	0	0
2	O	1	5	4	1	0	0
2	O	1	5	4	1	0	0
2	P	1	5	4	1	0	0
2	P	1	5	4	1	0	0
2	Q	1	5	4	1	0	0
2	Q	1	5	4	1	0	0
2	R	1	5	4	1	0	0
2	R	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	F	1	5	4	1	0	0
2	G	1	5	4	1	0	0
2	G	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	M	1	Total	O	S	0	0
			5	4	1		
2	M	1	Total	O	S	0	0
			5	4	1		
2	T	1	Total	O	S	0	0
			5	4	1		
2	T	1	Total	O	S	0	0
			5	4	1		
2	T	1	Total	O	S	0	0
			5	4	1		
2	U	1	Total	O	S	0	0
			5	4	1		
2	U	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	514	Total	O	0	0
			514	514		
3	B	531	Total	O	0	0
			531	531		
3	C	619	Total	O	0	0
			619	619		
3	D	573	Total	O	0	0
			573	573		
3	E	587	Total	O	0	0
			587	587		
3	H	544	Total	O	0	0
			544	544		
3	I	623	Total	O	0	0
			623	623		
3	J	654	Total	O	0	0
			654	654		
3	K	545	Total	O	0	0
			545	545		
3	L	514	Total	O	0	0
			514	514		
3	N	503	Total	O	0	0
			503	503		
3	O	603	Total	O	0	0
			603	603		

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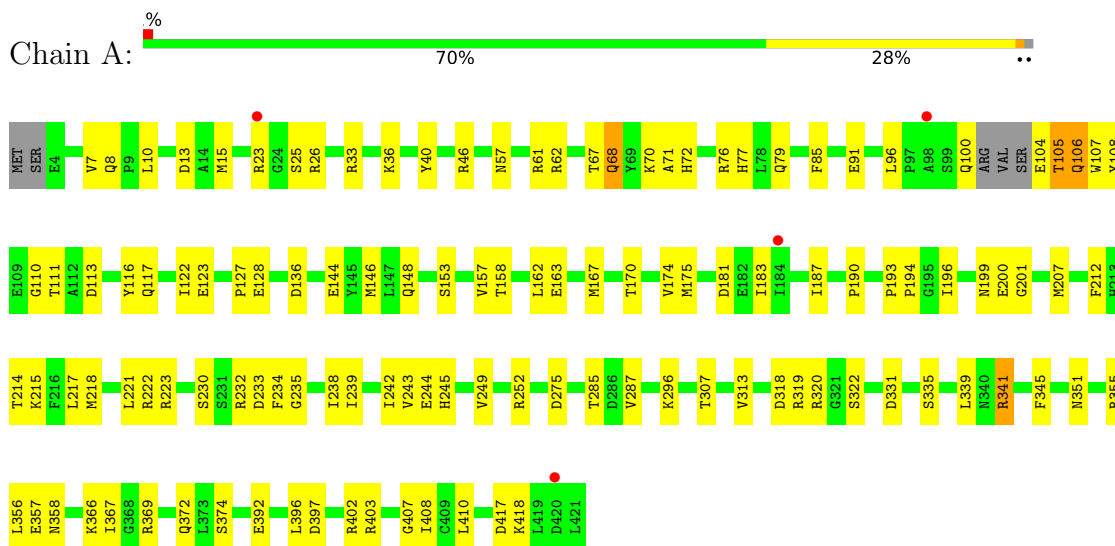
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	511	Total O 511 511	0	0
3	Q	557	Total O 557 557	0	0
3	R	597	Total O 597 597	0	0
3	F	545	Total O 545 545	0	0
3	G	489	Total O 489 489	0	0
3	M	559	Total O 559 559	0	0
3	T	589	Total O 589 589	0	0
3	U	539	Total O 539 539	0	0

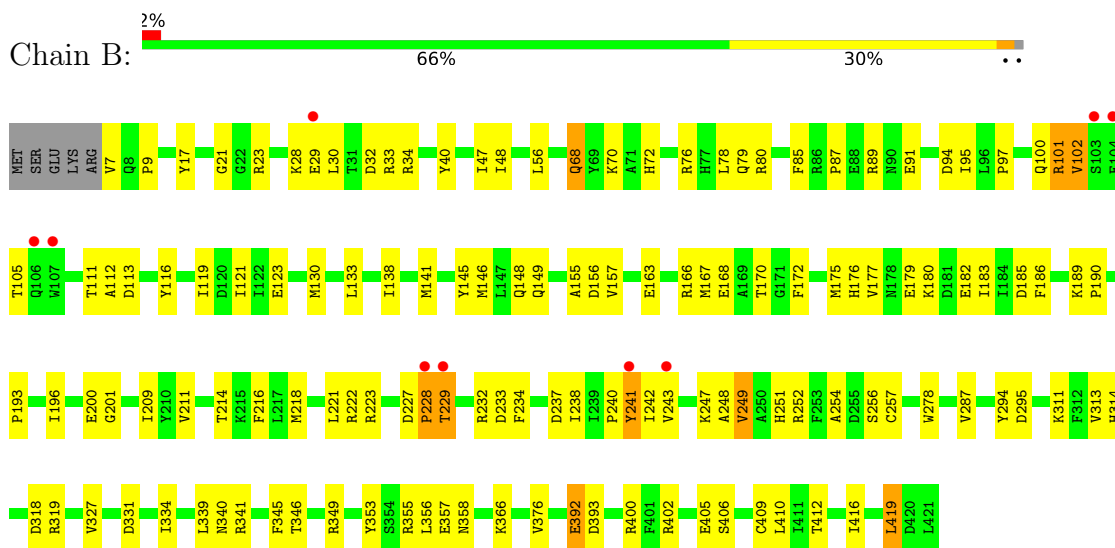
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glucose-1-phosphate adenylyltransferase



- Molecule 1: Glucose-1-phosphate adenylyltransferase

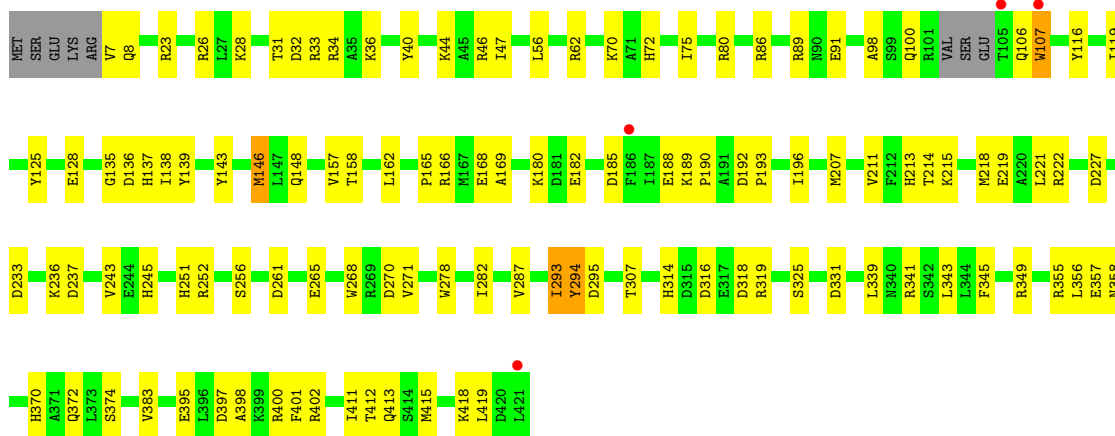


- Molecule 1: Glucose-1-phosphate adenylyltransferase

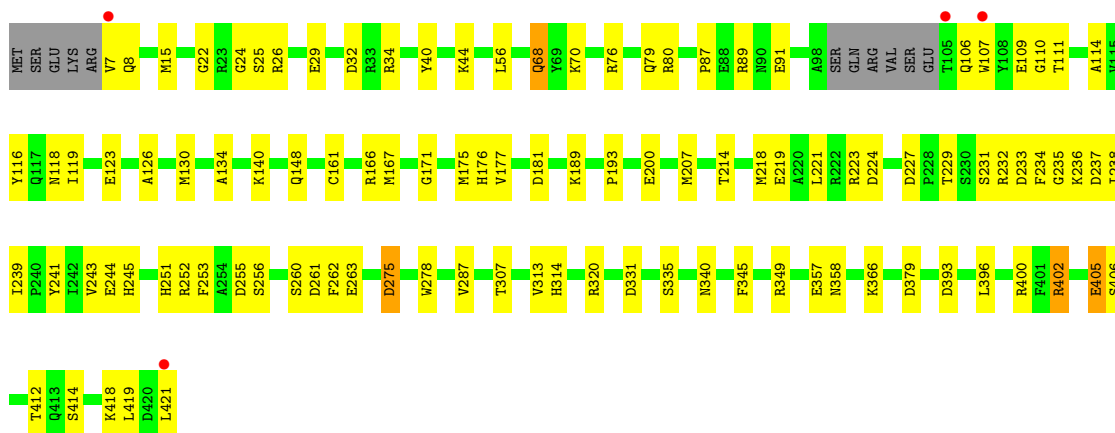




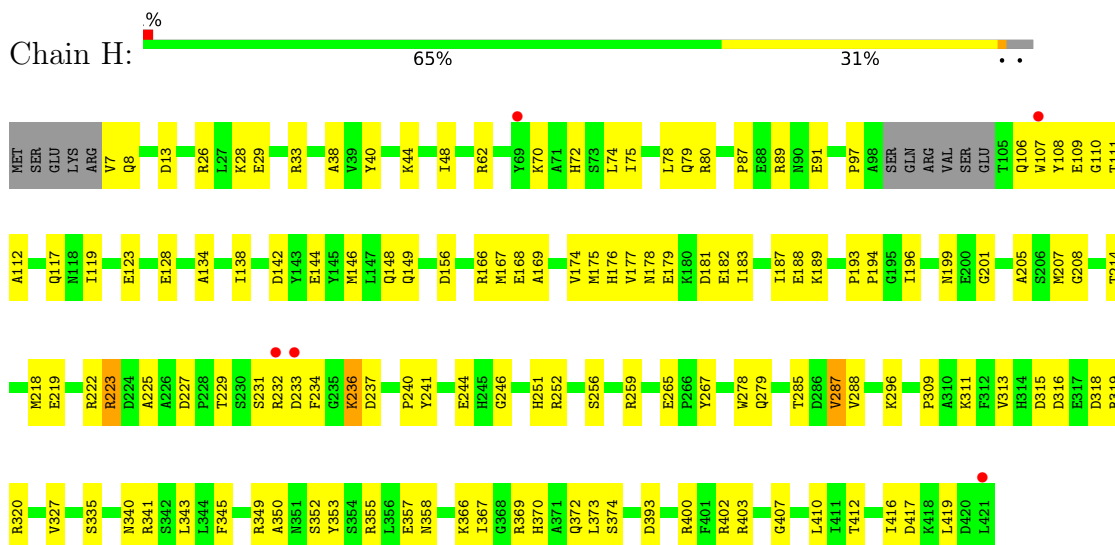
- Molecule 1: Glucose-1-phosphate adenylyltransferase



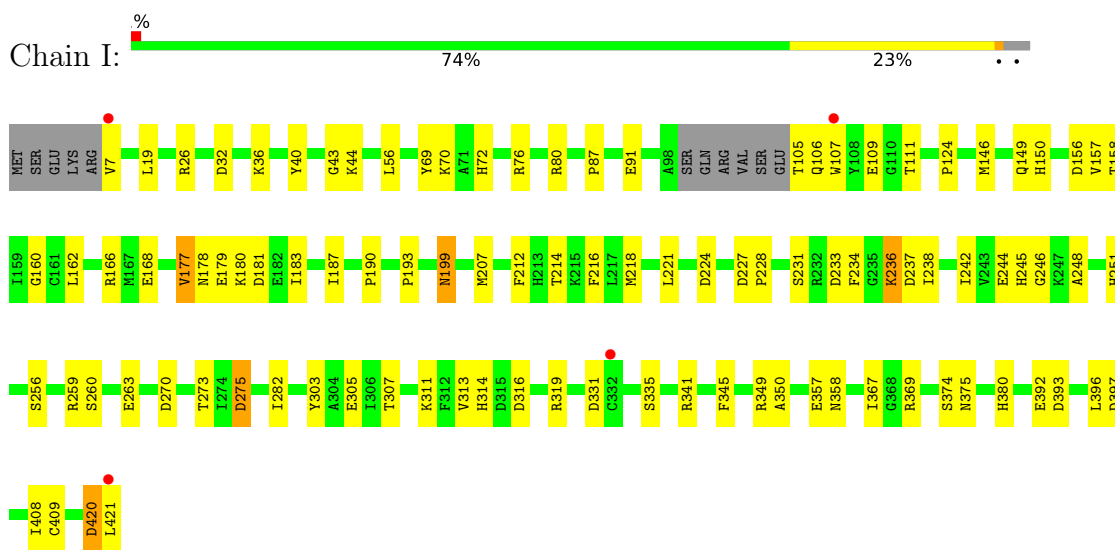
- Molecule 1: Glucose-1-phosphate adenylyltransferase



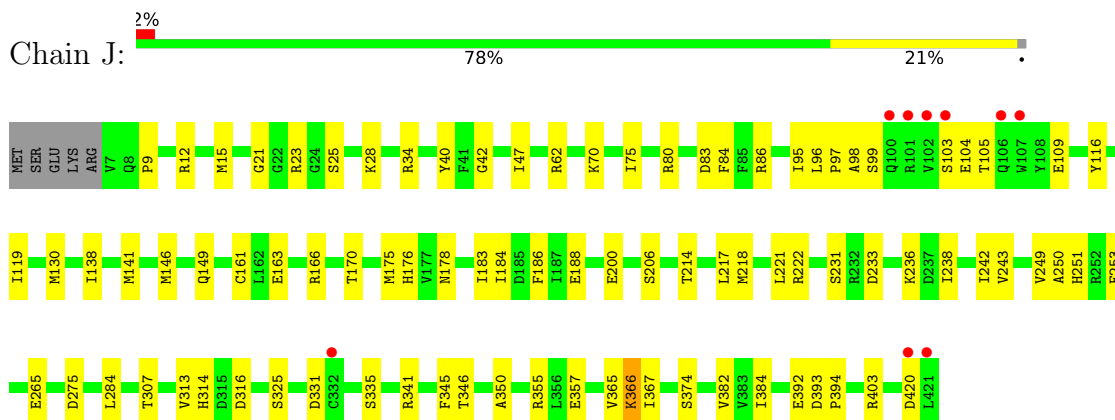
- Molecule 1: Glucose-1-phosphate adenylyltransferase



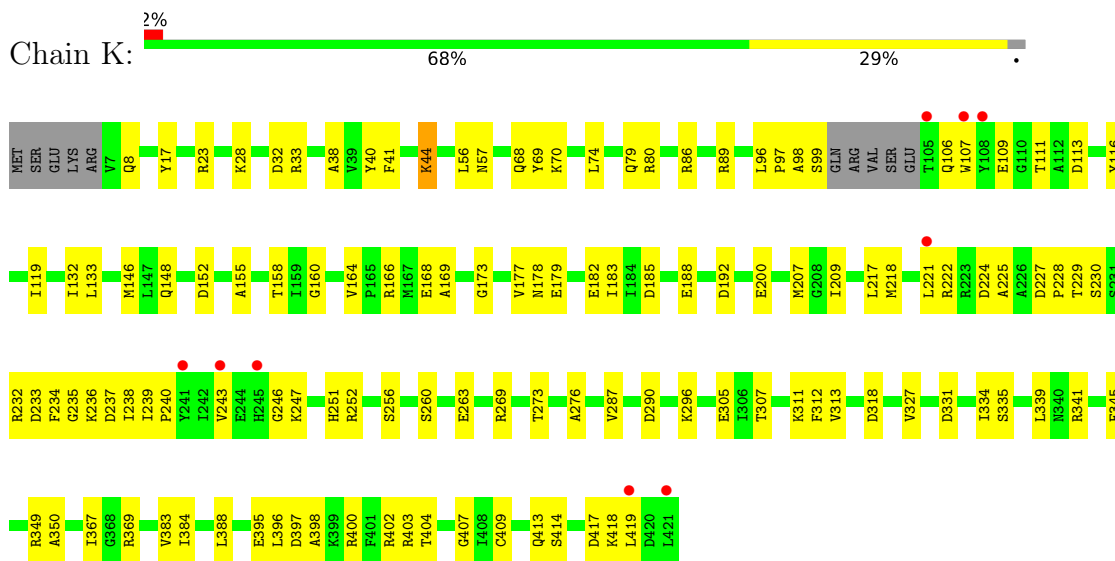
- Molecule 1: Glucose-1-phosphate adenylyltransferase



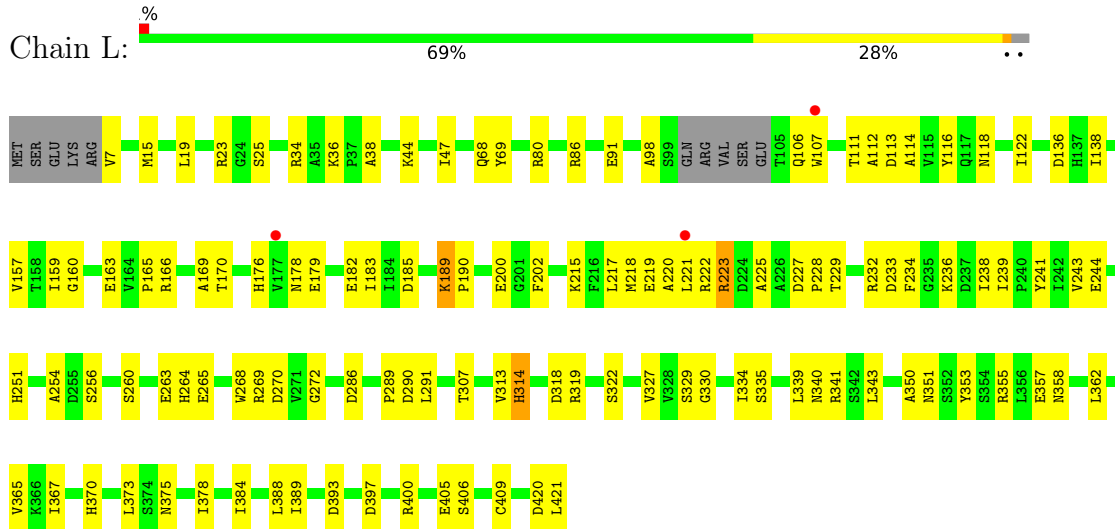
- Molecule 1: Glucose-1-phosphate adenylyltransferase



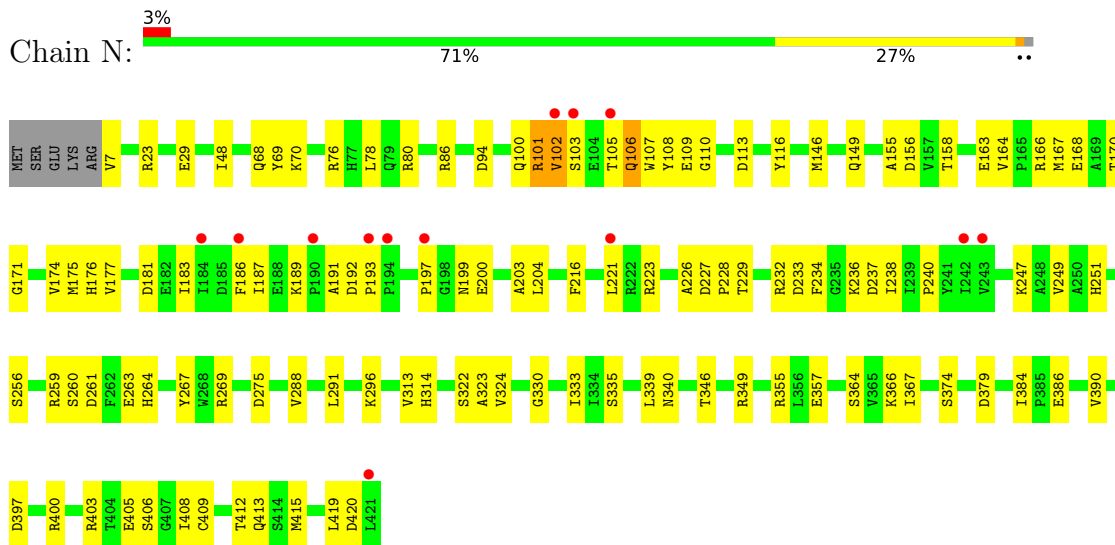
- Molecule 1: Glucose-1-phosphate adenylyltransferase



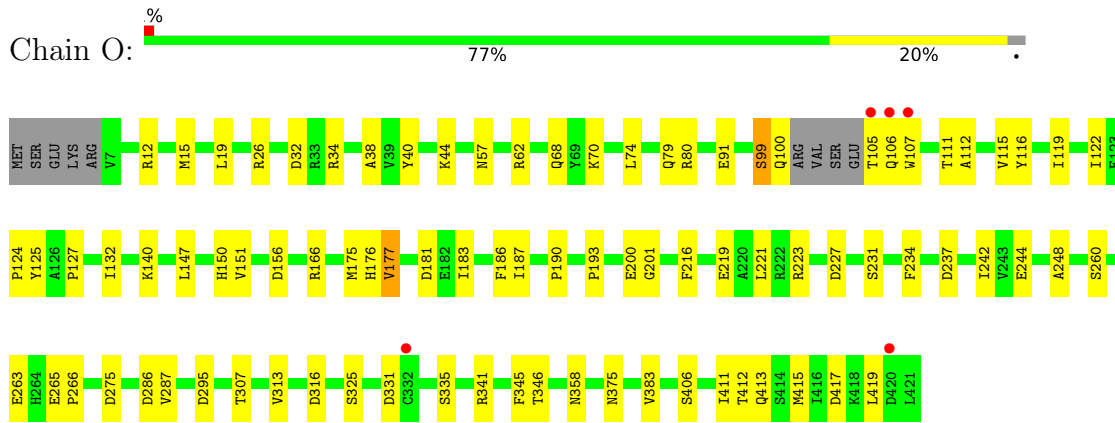
- Molecule 1: Glucose-1-phosphate adenylyltransferase



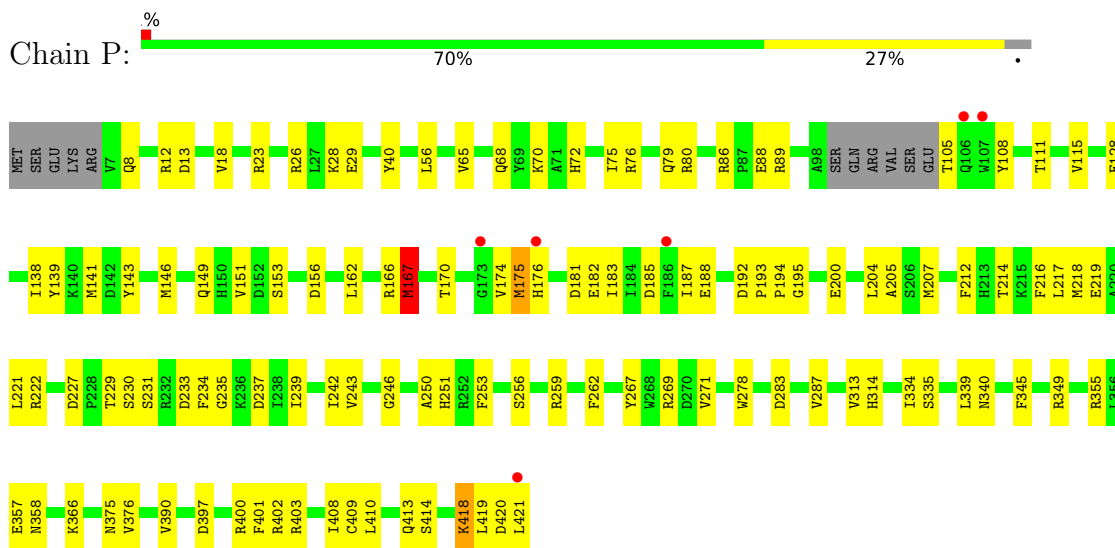
- Molecule 1: Glucose-1-phosphate adenylyltransferase



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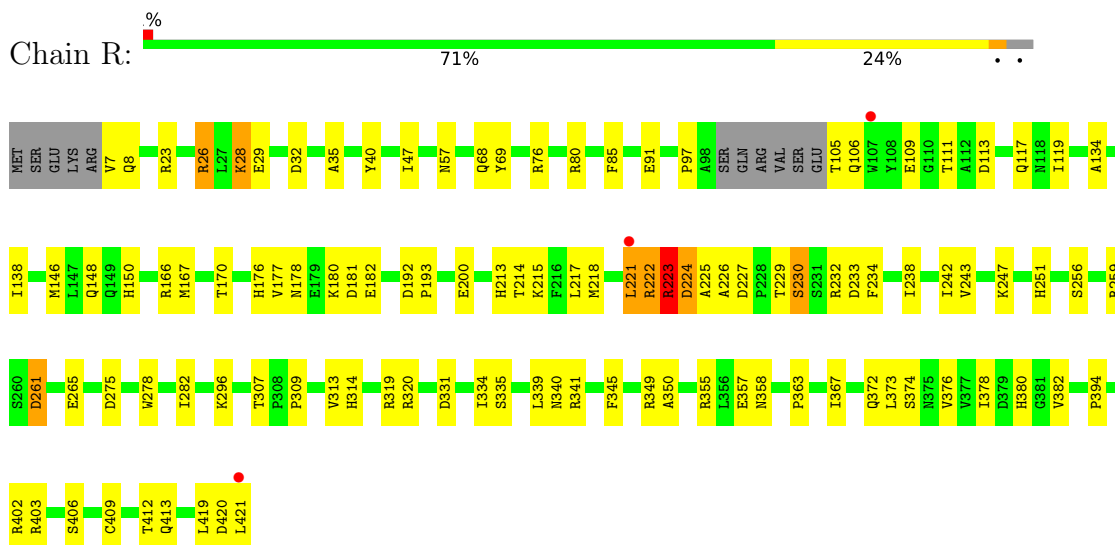
- Molecule 1: Glucose-1-phosphate adenylyltransferase



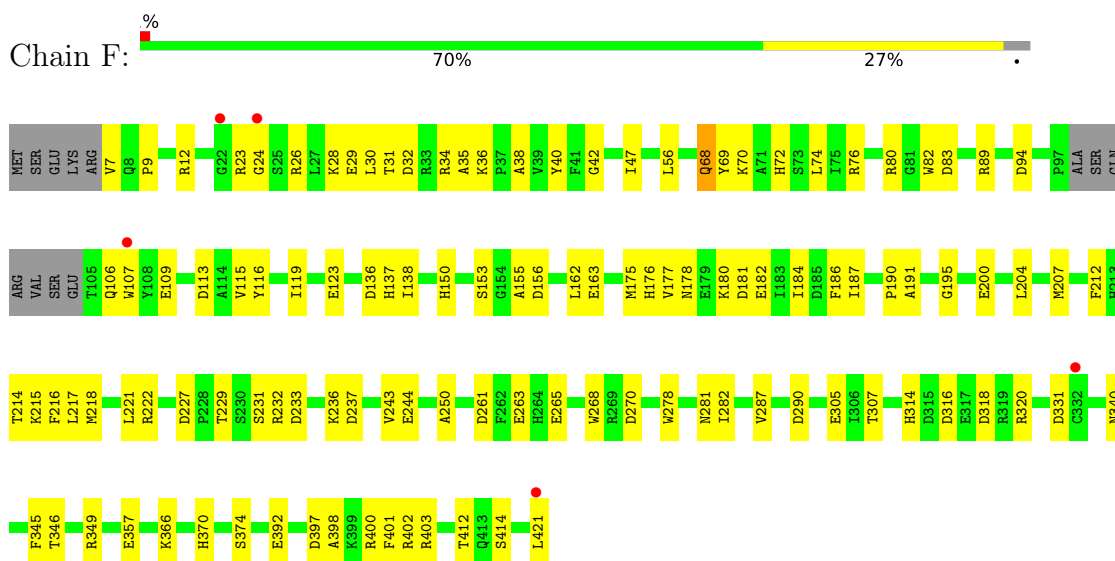
- Molecule 1: Glucose-1-phosphate adenylyltransferase



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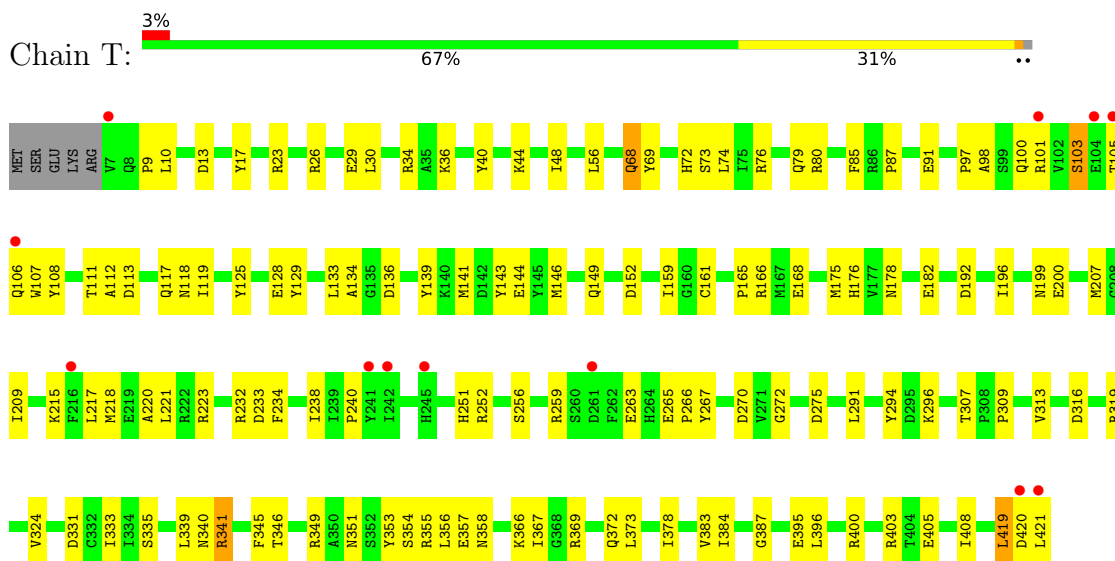




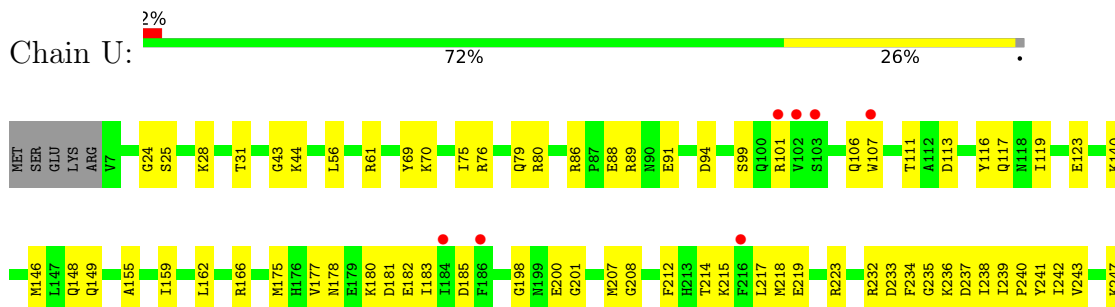
- Molecule 1: Glucose-1-phosphate adenylyltransferase



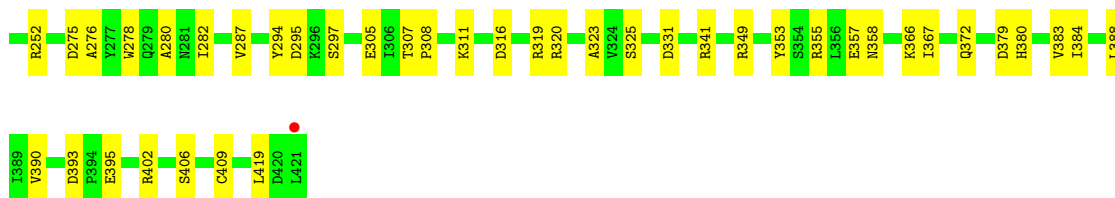
- Molecule 1: Glucose-1-phosphate adenylyltransferase



- Molecule 1: Glucose-1-phosphate adenylyltransferase







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.44Å 140.69Å 228.49Å 72.04° 78.19° 89.98°	Depositor
Resolution (Å)	36.55 – 1.78 36.55 – 1.78	Depositor EDS
% Data completeness (in resolution range)	97.0 (36.55-1.78) 89.6 (36.55-1.78)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 1.78Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, $R_{free}$	0.200 , 0.229 0.174 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtrriage
Anisotropy	0.438	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.467 for h,-k,h-l 0.468 for -h,k,k-l 0.467 for -h,-k,-h-k+l	Xtrriage
Reported twinning fraction	0.450 for h,-k,h-l	Depositor
Outliers	0 of 1003130 reflections	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	75925	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 61.29 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3393e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.32	0/3331	0.50	0/4523
1	B	0.40	3/3348 (0.1%)	0.54	0/4548
1	C	0.33	0/3319	0.49	0/4507
1	D	0.70	7/3302 (0.2%)	0.89	7/4485 (0.2%)
1	E	0.34	0/3281	0.50	0/4460
1	F	0.34	0/3293	0.49	0/4473
1	G	0.33	0/3306	0.49	0/4490
1	H	0.40	2/3278 (0.1%)	0.51	1/4455 (0.0%)
1	I	0.34	0/3291	0.50	0/4472
1	J	0.36	1/3333 (0.0%)	0.51	1/4530 (0.0%)
1	K	0.32	0/3289	0.49	0/4469
1	L	0.33	0/3298	0.50	0/4481
1	M	0.35	0/3288	0.51	1/4468 (0.0%)
1	N	0.37	0/3330	0.53	2/4525 (0.0%)
1	O	0.33	0/3288	0.49	0/4469
1	P	0.37	1/3291 (0.0%)	0.53	2/4472 (0.0%)
1	Q	0.41	1/3291 (0.0%)	0.64	7/4472 (0.2%)
1	R	0.48	3/3278 (0.1%)	0.61	5/4455 (0.1%)
1	T	0.34	0/3332	0.50	0/4528
1	U	0.32	0/3324	0.49	0/4518
All	All	0.38	18/66091 (0.0%)	0.54	26/89800 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	N	0	1
1	O	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Q	0	1
1	R	0	2
1	T	0	1
All	All	0	7

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	294	TYR	CE1-CZ	-24.51	1.06	1.38
1	D	294	TYR	CG-CD2	-17.56	1.16	1.39
1	R	223	ARG	CZ-NH1	16.09	1.53	1.33
1	D	294	TYR	CD1-CE1	-12.35	1.20	1.39
1	H	236	LYS	CB-CG	8.52	1.75	1.52
1	D	294	TYR	CD2-CE2	7.21	1.50	1.39
1	H	236	LYS	CG-CD	-7.03	1.28	1.52
1	P	167	MET	CG-SD	-6.75	1.63	1.81
1	D	294	TYR	CE2-CZ	-6.08	1.30	1.38
1	Q	23	ARG	CZ-NH2	6.04	1.40	1.33
1	B	392	GLU	CD-OE1	-5.84	1.19	1.25
1	R	223	ARG	CB-CG	5.58	1.67	1.52
1	D	295	ASP	CB-CG	-5.57	1.40	1.51
1	D	294	TYR	CB-CG	5.56	1.59	1.51
1	B	249	VAL	CB-CG1	-5.42	1.41	1.52
1	R	223	ARG	CD-NE	-5.28	1.37	1.46
1	J	366	LYS	CD-CE	-5.21	1.38	1.51
1	B	392	GLU	CG-CD	5.10	1.59	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	294	TYR	CB-CG-CD1	33.54	141.12	121.00
1	D	294	TYR	CB-CG-CD2	-28.05	104.17	121.00
1	R	223	ARG	NE-CZ-NH1	-17.47	111.56	120.30
1	Q	23	ARG	NE-CZ-NH2	-15.28	112.66	120.30
1	Q	23	ARG	NE-CZ-NH1	14.61	127.61	120.30
1	D	294	TYR	CG-CD2-CE2	-12.87	111.01	121.30
1	P	167	MET	CG-SD-CE	-10.96	82.66	100.20
1	Q	223	ARG	NE-CZ-NH2	10.37	125.49	120.30
1	D	294	TYR	CZ-CE2-CD2	8.97	127.88	119.80
1	D	294	TYR	CG-CD1-CE1	8.29	127.94	121.30
1	D	146	MET	CG-SD-CE	-7.18	88.71	100.20
1	D	294	TYR	CD1-CE1-CZ	6.63	125.76	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	223	ARG	NE-CZ-NH2	6.54	123.57	120.30
1	Q	223	ARG	NE-CZ-NH1	-6.46	117.07	120.30
1	R	26	ARG	NE-CZ-NH1	-6.43	117.09	120.30
1	N	366	LYS	CD-CE-NZ	-6.39	96.99	111.70
1	J	366	LYS	CG-CD-CE	-6.36	92.81	111.90
1	Q	204	LEU	CB-CG-CD1	-6.00	100.80	111.00
1	Q	23	ARG	NH1-CZ-NH2	-5.78	113.04	119.40
1	Q	204	LEU	CA-CB-CG	-5.72	102.15	115.30
1	R	26	ARG	NE-CZ-NH2	5.61	123.11	120.30
1	P	167	MET	CB-CG-SD	5.43	128.71	112.40
1	M	417	ASP	CB-CG-OD1	5.38	123.15	118.30
1	R	221	LEU	CA-CB-CG	5.19	127.23	115.30
1	H	236	LYS	CA-CB-CG	5.11	124.64	113.40
1	N	366	LYS	CG-CD-CE	-5.09	96.64	111.90

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	419	LEU	Peptide
1	N	419	LEU	Peptide
1	O	419	LEU	Peptide
1	Q	23	ARG	Sidechain
1	R	222	ARG	Peptide
1	R	223	ARG	Peptide
1	T	419	LEU	Peptide

## 5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3252	0	3146	121	0
1	B	3262	0	3165	153	0
1	C	3240	0	3143	109	0
1	D	3226	0	3124	135	0
1	E	3202	0	3105	112	0
1	F	3214	0	3130	140	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3227	0	3139	105	0
1	H	3202	0	3102	145	0
1	I	3212	0	3120	94	0
1	J	3250	0	3147	86	0
1	K	3213	0	3115	112	1
1	L	3222	0	3120	120	0
1	M	3210	0	3115	134	0
1	N	3253	0	3151	137	0
1	O	3212	0	3106	89	0
1	P	3212	0	3120	116	0
1	Q	3212	0	3120	116	0
1	R	3202	0	3102	118	0
1	T	3252	0	3152	133	0
1	U	3244	0	3136	108	0
2	A	10	0	0	1	0
2	B	10	0	0	3	0
2	C	10	0	0	3	0
2	D	10	0	0	3	0
2	E	15	0	0	1	0
2	F	10	0	0	0	0
2	G	10	0	0	0	0
2	H	10	0	0	0	0
2	I	10	0	0	2	0
2	J	10	0	0	1	0
2	K	10	0	0	2	0
2	L	10	0	0	3	0
2	M	10	0	0	1	0
2	N	10	0	0	0	0
2	O	10	0	0	3	0
2	P	10	0	0	0	0
2	Q	10	0	0	1	0
2	R	10	0	0	0	0
2	T	15	0	0	5	0
2	U	10	0	0	0	0
3	A	514	0	0	77	5
3	B	531	0	0	63	2
3	C	619	0	0	66	2
3	D	573	0	0	72	3
3	E	587	0	0	66	8
3	F	545	0	0	76	1
3	G	489	0	0	66	1
3	H	544	0	0	80	9

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	623	0	0	44	2
3	J	654	0	0	56	23
3	K	545	0	0	61	0
3	L	514	0	0	61	16
3	M	559	0	0	60	5
3	N	503	0	0	62	26
3	O	603	0	0	54	20
3	P	511	0	0	69	11
3	Q	557	0	0	54	1
3	R	597	0	0	58	17
3	T	589	0	0	71	8
3	U	539	0	0	61	5
All	All	75925	0	62558	2326	83

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (2326) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:236:LYS:CB	1:H:236:LYS:CG	1.75	1.63
1:C:259:ARG:NH2	3:C:601:HOH:O	1.81	1.11
1:N:113:ASP:OD1	1:N:232:ARG:NH1	1.82	1.11
1:A:223:ARG:NH2	3:A:601:HOH:O	1.81	1.11
1:N:113:ASP:OD2	1:N:232:ARG:NH2	1.85	1.08
1:N:113:ASP:OD1	1:N:232:ARG:CZ	2.02	1.06
1:R:224:ASP:HA	1:R:227:ASP:HB3	1.30	1.06
1:T:215:LYS:NZ	3:T:602:HOH:O	1.84	1.04
1:H:149:GLN:NE2	3:H:606:HOH:O	1.93	1.00
1:N:296:LYS:O	3:N:601:HOH:O	1.77	1.00
1:N:187:ILE:HD12	1:N:189:LYS:H	1.25	0.99
1:M:252:ARG:NH1	3:M:609:HOH:O	1.94	0.99
1:D:116:TYR:HB2	1:D:221:LEU:HD13	1.44	0.99
1:A:15:MET:SD	3:A:986:HOH:O	2.19	0.99
1:U:232:ARG:NH1	3:U:610:HOH:O	1.96	0.99
1:I:80:ARG:NH2	3:I:601:HOH:O	1.87	0.99
1:J:23:ARG:NH1	3:J:601:HOH:O	1.82	0.99
1:T:79:GLN:NE2	3:T:603:HOH:O	1.93	0.99
1:N:166:ARG:NH2	3:N:605:HOH:O	1.93	0.99
1:M:222:ARG:NH1	3:M:603:HOH:O	1.88	0.99
1:C:247:LYS:NZ	3:C:606:HOH:O	1.94	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:166:ARG:NH1	1:N:192:ASP:OD1	1.95	0.98
1:M:223:ARG:NH1	3:M:610:HOH:O	1.95	0.98
1:U:44:LYS:NZ	3:U:604:HOH:O	1.89	0.98
1:M:395:GLU:OE1	3:M:601:HOH:O	1.80	0.97
1:T:396:LEU:O	3:T:601:HOH:O	1.83	0.97
1:I:7:VAL:N	3:I:605:HOH:O	1.97	0.97
1:E:320:ARG:NH1	3:E:608:HOH:O	1.97	0.96
1:N:187:ILE:CD1	1:N:189:LYS:H	1.78	0.96
1:P:105:THR:OG1	3:P:601:HOH:O	1.84	0.96
1:L:179:GLU:N	3:L:606:HOH:O	1.98	0.95
1:A:61:ARG:NH2	3:A:607:HOH:O	1.97	0.95
1:A:358:ASN:OD1	3:A:603:HOH:O	1.85	0.95
1:R:238:ILE:O	3:R:601:HOH:O	1.83	0.95
1:U:79:GLN:NE2	3:U:611:HOH:O	1.99	0.95
1:G:141:MET:SD	3:G:1040:HOH:O	2.24	0.95
1:A:113:ASP:OD1	3:A:602:HOH:O	1.84	0.95
1:D:215:LYS:NZ	3:D:605:HOH:O	2.00	0.95
1:T:355:ARG:NH1	3:T:608:HOH:O	2.00	0.94
1:T:165:PRO:HG2	1:T:168:GLU:HG3	1.45	0.94
1:C:115:VAL:O	3:C:602:HOH:O	1.85	0.94
1:R:28:LYS:HE3	1:R:29:GLU:HB2	1.48	0.94
1:E:76:ARG:NH2	3:E:611:HOH:O	2.00	0.94
1:N:113:ASP:CG	1:N:232:ARG:CZ	2.35	0.94
1:H:80:ARG:NH1	3:H:609:HOH:O	1.97	0.94
1:H:182:GLU:OE1	3:H:601:HOH:O	1.85	0.94
1:N:113:ASP:CG	1:N:232:ARG:NH2	2.20	0.94
1:P:259:ARG:NH2	3:P:602:HOH:O	1.85	0.93
1:R:223:ARG:HH12	1:R:232:ARG:HA	1.33	0.93
1:L:254:ALA:O	3:L:601:HOH:O	1.85	0.93
1:Q:167:MET:O	3:Q:601:HOH:O	1.85	0.93
1:E:414:SER:OG	3:E:601:HOH:O	1.87	0.93
1:F:265:GLU:O	3:F:601:HOH:O	1.85	0.93
1:M:141:MET:SD	3:M:1081:HOH:O	2.25	0.93
1:D:401:PHE:N	3:D:604:HOH:O	1.99	0.93
1:T:161:CYS:SG	3:T:920:HOH:O	2.28	0.92
1:C:222:ARG:NH1	3:C:610:HOH:O	1.98	0.92
1:O:15:MET:SD	3:O:1101:HOH:O	2.26	0.92
1:A:403:ARG:NH1	3:A:610:HOH:O	2.01	0.92
1:H:349:ARG:NH2	3:H:613:HOH:O	2.02	0.92
1:O:91:GLU:OE1	3:O:601:HOH:O	1.84	0.92
1:N:174:VAL:HG11	1:N:189:LYS:HD2	1.52	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:296:LYS:NZ	3:T:612:HOH:O	2.02	0.91
1:L:80:ARG:NH1	3:L:607:HOH:O	2.03	0.91
1:O:147:LEU:O	3:O:602:HOH:O	1.87	0.91
1:R:419:LEU:O	3:R:602:HOH:O	1.87	0.91
1:I:341:ARG:NH1	3:I:607:HOH:O	2.01	0.91
1:M:192:ASP:OD2	3:M:602:HOH:O	1.87	0.91
1:P:181:ASP:HB3	3:P:613:HOH:O	1.70	0.91
1:H:241:TYR:O	3:H:602:HOH:O	1.86	0.91
1:A:351:ASN:OD1	3:A:604:HOH:O	1.87	0.91
1:B:28:LYS:HD2	1:B:402:ARG:HE	1.35	0.91
1:U:69:TYR:OH	3:U:603:HOH:O	1.88	0.91
1:M:109:GLU:OE2	3:M:604:HOH:O	1.88	0.91
1:H:123:GLU:OE1	3:H:603:HOH:O	1.88	0.90
1:R:355:ARG:NH1	3:R:608:HOH:O	2.01	0.90
1:K:41:PHE:O	3:K:601:HOH:O	1.89	0.90
1:N:322:SER:OG	3:N:603:HOH:O	1.89	0.90
1:I:224:ASP:OD1	3:I:602:HOH:O	1.89	0.90
1:C:207:MET:SD	3:C:1118:HOH:O	2.30	0.90
1:Q:392:GLU:OE1	3:Q:602:HOH:O	1.90	0.90
1:O:375:ASN:OD1	3:O:603:HOH:O	1.90	0.90
1:G:98:ALA:O	3:G:601:HOH:O	1.89	0.90
1:U:323:ALA:O	3:U:602:HOH:O	1.88	0.89
1:B:166:ARG:O	3:B:602:HOH:O	1.89	0.89
1:C:68:GLN:OE1	3:C:603:HOH:O	1.88	0.89
1:I:316:ASP:OD1	3:I:603:HOH:O	1.90	0.89
1:K:235:GLY:O	3:K:602:HOH:O	1.90	0.89
1:O:34:ARG:NH2	3:O:612:HOH:O	2.04	0.89
1:T:36:LYS:NZ	3:T:607:HOH:O	2.06	0.89
1:K:397:ASP:OD1	3:K:603:HOH:O	1.91	0.89
1:P:235:GLY:O	3:P:603:HOH:O	1.90	0.89
1:U:319:ARG:NH1	3:U:621:HOH:O	2.06	0.89
1:I:179:GLU:OE1	3:I:604:HOH:O	1.90	0.89
1:B:116:TYR:HB2	1:B:221:LEU:HD11	1.54	0.88
1:Q:23:ARG:H	1:Q:23:ARG:HD3	1.38	0.88
1:A:215:LYS:NZ	3:A:620:HOH:O	2.07	0.88
1:D:32:ASP:OD1	3:D:601:HOH:O	1.89	0.88
2:A:501:SO4:O4	3:A:604:HOH:O	1.92	0.88
1:U:200:GLU:O	3:U:606:HOH:O	1.90	0.88
1:N:113:ASP:OD2	1:N:232:ARG:CZ	2.21	0.88
1:P:420:ASP:OD1	3:P:605:HOH:O	1.91	0.88
1:D:158:THR:O	3:D:602:HOH:O	1.90	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:THR:HG23	1:Q:228:PRO:O	1.74	0.88
1:E:405:GLU:OE2	3:E:604:HOH:O	1.92	0.88
1:M:123:GLU:OE2	1:M:215:LYS:NZ	2.05	0.88
1:B:68:GLN:O	3:B:603:HOH:O	1.90	0.88
1:K:407:GLY:O	3:K:604:HOH:O	1.91	0.88
1:O:115:VAL:O	3:O:604:HOH:O	1.92	0.87
1:G:264:HIS:O	3:G:602:HOH:O	1.92	0.87
1:B:241:TYR:OH	3:B:604:HOH:O	1.92	0.87
1:U:76:ARG:O	3:U:605:HOH:O	1.90	0.87
1:R:233:ASP:OD2	3:R:603:HOH:O	1.90	0.87
1:B:80:ARG:NH1	3:B:617:HOH:O	2.07	0.87
1:D:62:ARG:NH1	3:D:611:HOH:O	2.06	0.87
1:Q:128:GLU:OE1	3:Q:603:HOH:O	1.91	0.87
1:Q:141:MET:SD	3:Q:935:HOH:O	2.32	0.87
1:M:255:ASP:O	3:M:607:HOH:O	1.92	0.86
1:P:230:SER:N	3:P:610:HOH:O	2.07	0.86
1:K:404:THR:O	3:K:605:HOH:O	1.93	0.86
1:L:291:LEU:O	3:L:602:HOH:O	1.91	0.86
1:U:149:GLN:OE1	3:U:607:HOH:O	1.92	0.86
1:A:117:GLN:NE2	3:A:622:HOH:O	2.08	0.86
1:L:15:MET:SD	3:L:977:HOH:O	2.34	0.86
1:P:166:ARG:O	3:P:606:HOH:O	1.93	0.86
1:H:240:PRO:O	3:H:607:HOH:O	1.93	0.86
1:M:397:ASP:OD2	3:M:606:HOH:O	1.91	0.86
1:M:163:GLU:OE1	3:M:605:HOH:O	1.91	0.86
1:T:80:ARG:NH1	3:T:619:HOH:O	2.09	0.86
1:U:247:LYS:NZ	3:U:627:HOH:O	2.08	0.86
1:M:375:ASN:OD1	3:M:608:HOH:O	1.94	0.86
1:E:224:ASP:OD1	3:E:603:HOH:O	1.91	0.86
1:T:146:MET:SD	3:T:1175:HOH:O	2.31	0.86
1:B:29:GLU:O	3:B:605:HOH:O	1.94	0.86
1:J:84:PHE:O	3:J:603:HOH:O	1.94	0.86
1:J:243:VAL:O	3:J:602:HOH:O	1.92	0.85
1:D:7:VAL:N	3:D:612:HOH:O	2.08	0.85
1:L:313:VAL:HG12	1:L:335:SER:HA	1.58	0.85
1:U:235:GLY:O	3:U:608:HOH:O	1.93	0.85
1:C:392:GLU:OE1	3:C:605:HOH:O	1.93	0.85
1:C:123:GLU:OE2	3:C:607:HOH:O	1.95	0.85
2:E:502:SO4:O2	3:E:605:HOH:O	1.93	0.85
1:N:221:LEU:HD21	1:N:238:ILE:HD13	1.58	0.85
1:R:105:THR:O	3:R:605:HOH:O	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ARG:NH2	3:A:623:HOH:O	2.09	0.84
1:H:97:PRO:O	3:H:608:HOH:O	1.95	0.84
1:F:281:ASN:ND2	3:F:619:HOH:O	2.11	0.84
1:C:23:ARG:HH12	1:C:70:LYS:HB2	1.41	0.84
1:L:7:VAL:O	3:L:603:HOH:O	1.94	0.84
1:G:412:THR:OG1	3:G:604:HOH:O	1.95	0.84
1:U:106:GLN:O	3:U:609:HOH:O	1.95	0.84
1:N:296:LYS:NZ	3:N:619:HOH:O	2.10	0.84
1:O:106:GLN:O	3:O:606:HOH:O	1.95	0.84
1:O:227:ASP:O	3:O:605:HOH:O	1.95	0.84
1:A:70:LYS:O	3:A:605:HOH:O	1.96	0.84
1:O:34:ARG:NH1	2:O:502:SO4:O1	2.11	0.83
1:F:28:LYS:HG3	1:F:29:GLU:H	1.41	0.83
1:G:397:ASP:OD1	3:G:605:HOH:O	1.95	0.83
1:J:200:GLU:O	3:J:605:HOH:O	1.95	0.83
1:P:403:ARG:NH2	3:P:607:HOH:O	1.99	0.83
2:K:502:SO4:O1	3:K:607:HOH:O	1.97	0.83
1:N:260:SER:O	3:N:607:HOH:O	1.95	0.83
1:A:33:ARG:O	3:A:606:HOH:O	1.96	0.83
1:R:97:PRO:O	3:R:606:HOH:O	1.96	0.83
1:U:409:CYS:SG	3:U:998:HOH:O	2.35	0.83
1:E:238:ILE:O	3:E:606:HOH:O	1.97	0.83
1:N:275:ASP:OD2	3:N:609:HOH:O	1.97	0.83
1:F:403:ARG:NH1	3:F:620:HOH:O	2.11	0.83
1:A:76:ARG:NH1	3:A:626:HOH:O	2.12	0.83
1:C:198:GLY:O	3:C:609:HOH:O	1.97	0.83
1:R:232:ARG:NE	3:R:604:HOH:O	1.92	0.83
1:M:175:MET:HE3	1:M:183:ILE:HG21	1.61	0.83
1:L:160:GLY:O	3:L:604:HOH:O	1.97	0.83
1:A:372:GLN:NE2	3:A:627:HOH:O	2.12	0.82
1:O:112:ALA:O	3:O:609:HOH:O	1.97	0.82
1:O:231:SER:OG	3:O:607:HOH:O	1.96	0.82
1:F:26:ARG:NH2	3:F:602:HOH:O	1.88	0.82
1:C:13:ASP:OD2	3:C:608:HOH:O	1.96	0.82
1:J:98:ALA:O	3:J:606:HOH:O	1.96	0.82
1:N:228:PRO:O	3:N:608:HOH:O	1.96	0.82
1:O:417:ASP:OD2	3:O:608:HOH:O	1.96	0.82
1:G:33:ARG:NH1	3:G:616:HOH:O	2.04	0.82
1:C:68:GLN:NE2	3:C:622:HOH:O	2.11	0.82
1:K:349:ARG:NH1	3:K:623:HOH:O	2.13	0.82
1:F:163:GLU:OE1	3:F:604:HOH:O	1.98	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:400:ARG:O	3:F:603:HOH:O	1.96	0.82
1:M:275:ASP:OD2	3:M:611:HOH:O	1.98	0.82
1:G:105:THR:O	3:G:606:HOH:O	1.97	0.81
1:T:105:THR:OG1	3:T:605:HOH:O	1.97	0.81
1:H:366:LYS:NZ	3:H:625:HOH:O	2.12	0.81
1:R:222:ARG:NH1	3:R:611:HOH:O	2.08	0.81
1:L:222:ARG:O	3:L:605:HOH:O	1.98	0.81
1:F:178:ASN:ND2	1:F:182:GLU:O	2.14	0.81
1:E:76:ARG:NH1	3:E:602:HOH:O	1.88	0.81
1:P:141:MET:SD	3:P:938:HOH:O	2.37	0.81
1:P:251:HIS:NE2	1:P:256:SER:OG	2.14	0.81
1:N:379:ASP:OD2	3:N:610:HOH:O	1.97	0.81
1:B:76:ARG:NH1	3:B:628:HOH:O	2.13	0.81
1:K:290:ASP:OD1	3:K:608:HOH:O	1.98	0.81
1:N:23:ARG:NH1	3:N:628:HOH:O	2.14	0.81
1:N:187:ILE:HD12	1:N:189:LYS:N	1.95	0.81
1:C:62:ARG:NH1	3:C:617:HOH:O	2.08	0.81
1:R:243:VAL:O	3:R:607:HOH:O	1.99	0.81
1:C:223:ARG:NH2	3:C:630:HOH:O	2.14	0.80
1:K:179:GLU:OE1	3:K:609:HOH:O	1.99	0.80
1:I:397:ASP:OD2	3:I:606:HOH:O	1.97	0.80
1:D:383:VAL:H	1:D:413:GLN:HE22	1.28	0.80
1:O:412:THR:H	1:O:415:MET:HE2	1.44	0.80
1:A:397:ASP:OD1	3:A:608:HOH:O	1.99	0.80
1:N:364:SER:OG	3:N:606:HOH:O	1.94	0.80
1:K:403:ARG:NH1	3:K:627:HOH:O	2.15	0.80
1:T:73:SER:OG	3:T:606:HOH:O	1.99	0.80
1:U:178:ASN:ND2	3:U:634:HOH:O	2.15	0.80
1:B:400:ARG:O	3:B:609:HOH:O	1.99	0.80
1:D:318:ASP:N	3:D:603:HOH:O	2.15	0.80
1:A:418:LYS:NZ	3:A:617:HOH:O	2.04	0.80
1:F:153:SER:OG	3:F:606:HOH:O	1.99	0.79
1:F:305:GLU:OE1	3:F:605:HOH:O	1.99	0.79
1:U:101:ARG:O	3:U:614:HOH:O	2.00	0.79
1:G:200:GLU:OE2	3:G:608:HOH:O	2.00	0.79
1:M:223:ARG:NH2	3:M:630:HOH:O	2.16	0.79
1:U:208:GLY:O	3:U:612:HOH:O	2.00	0.79
1:U:419:LEU:O	3:U:613:HOH:O	2.00	0.79
1:D:136:ASP:N	3:D:619:HOH:O	2.14	0.79
1:B:180:LYS:O	3:B:608:HOH:O	1.99	0.79
1:J:250:ALA:O	3:J:607:HOH:O	1.99	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:270:ASP:O	3:T:607:HOH:O	1.99	0.79
1:A:407:GLY:O	3:A:609:HOH:O	2.00	0.79
1:F:177:VAL:HG13	1:F:181:ASP:HA	1.62	0.79
1:B:168:GLU:OE1	3:B:610:HOH:O	1.99	0.79
1:F:397:ASP:OD2	3:F:607:HOH:O	2.00	0.79
1:D:211:VAL:N	3:D:602:HOH:O	2.14	0.78
1:P:204:LEU:O	3:P:608:HOH:O	2.00	0.78
1:U:406:SER:OG	3:U:615:HOH:O	2.00	0.78
1:K:173:GLY:N	3:K:622:HOH:O	2.15	0.78
1:F:191:ALA:O	3:F:609:HOH:O	2.02	0.78
1:B:180:LYS:HG2	3:B:608:HOH:O	1.83	0.78
1:P:390:VAL:O	3:P:609:HOH:O	2.01	0.78
1:U:395:GLU:O	3:U:616:HOH:O	2.01	0.78
1:E:200:GLU:O	3:E:613:HOH:O	2.02	0.78
1:H:148:GLN:NE2	3:H:629:HOH:O	2.16	0.78
1:N:23:ARG:NH2	3:N:630:HOH:O	2.16	0.78
1:T:421:LEU:O	3:T:609:HOH:O	2.00	0.78
1:Q:275:ASP:OD1	3:Q:605:HOH:O	2.01	0.78
1:G:265:GLU:OE2	3:G:610:HOH:O	2.02	0.78
1:T:152:ASP:OD2	3:T:610:HOH:O	2.01	0.78
1:H:416:ILE:O	3:H:611:HOH:O	2.01	0.77
1:G:403:ARG:HG3	3:G:774:HOH:O	1.84	0.77
1:A:123:GLU:O	3:A:612:HOH:O	2.02	0.77
1:K:188:GLU:OE2	3:K:612:HOH:O	2.02	0.77
1:L:334:ILE:HD12	1:L:339:LEU:HD11	1.66	0.77
1:N:405:GLU:OE2	3:N:611:HOH:O	2.03	0.77
1:T:29:GLU:OE1	3:T:613:HOH:O	2.02	0.77
1:J:403:ARG:NH2	3:J:614:HOH:O	2.11	0.77
1:R:28:LYS:HD3	1:R:29:GLU:H	1.50	0.77
1:C:101:ARG:NH2	1:H:79:GLN:OE1	2.17	0.77
1:C:236:LYS:NZ	3:C:637:HOH:O	2.17	0.77
1:L:341:ARG:NH1	3:L:613:HOH:O	2.16	0.77
1:H:128:GLU:OE1	3:H:612:HOH:O	2.01	0.77
1:R:109:GLU:OE1	3:R:609:HOH:O	2.02	0.77
1:U:357:GLU:OE2	3:U:617:HOH:O	2.01	0.77
1:K:44:LYS:NZ	3:K:628:HOH:O	2.17	0.77
1:Q:68:GLN:OE1	3:Q:606:HOH:O	2.02	0.77
1:G:235:GLY:O	3:G:614:HOH:O	2.03	0.77
1:D:192:ASP:OD2	3:D:606:HOH:O	2.02	0.77
1:F:397:ASP:O	3:F:608:HOH:O	2.02	0.77
1:R:382:VAL:HA	3:R:617:HOH:O	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:LEU:O	3:A:613:HOH:O	2.02	0.76
1:H:168:GLU:O	3:H:615:HOH:O	2.03	0.76
1:K:414:SER:OG	3:K:610:HOH:O	2.01	0.76
1:B:33:ARG:NH1	3:B:635:HOH:O	2.18	0.76
1:B:232:ARG:NE	3:B:607:HOH:O	1.97	0.76
1:U:295:ASP:O	3:U:618:HOH:O	2.03	0.76
1:U:393:ASP:OD2	3:U:619:HOH:O	2.03	0.76
1:B:7:VAL:O	3:B:612:HOH:O	2.04	0.76
1:C:72:HIS:ND1	3:C:636:HOH:O	2.17	0.76
1:D:401:PHE:HA	1:D:415:MET:HE2	1.67	0.76
1:Q:223:ARG:NH2	3:Q:626:HOH:O	2.17	0.76
1:T:111:THR:HG23	1:T:234:PHE:HD2	1.49	0.76
1:A:153:SER:OG	3:A:614:HOH:O	2.03	0.76
1:B:29:GLU:HA	1:B:32:ASP:HB2	1.66	0.76
1:D:214:THR:O	1:D:218:MET:HG2	1.85	0.76
1:E:134:ALA:O	3:E:617:HOH:O	2.04	0.76
1:H:355:ARG:O	3:H:616:HOH:O	2.04	0.76
1:K:400:ARG:NH1	3:K:611:HOH:O	2.01	0.76
1:O:383:VAL:H	1:O:413:GLN:HE22	1.32	0.76
1:A:318:ASP:OD1	3:A:615:HOH:O	2.03	0.76
1:K:396:LEU:HG	1:K:400:ARG:HE	1.51	0.76
1:E:114:ALA:O	3:E:614:HOH:O	2.04	0.76
1:E:118:ASN:ND2	3:E:614:HOH:O	2.18	0.76
1:F:7:VAL:N	3:F:630:HOH:O	2.19	0.76
1:G:166:ARG:NH2	3:G:628:HOH:O	2.17	0.76
1:U:372:GLN:NE2	3:U:623:HOH:O	2.06	0.76
1:N:76:ARG:NH2	3:N:614:HOH:O	2.06	0.76
1:H:236:LYS:CB	1:H:236:LYS:CD	2.60	0.76
1:M:97:PRO:O	3:M:612:HOH:O	2.03	0.76
1:U:349:ARG:NH2	3:U:631:HOH:O	2.10	0.76
1:A:100:GLN:O	3:A:618:HOH:O	2.04	0.75
1:A:105:THR:O	3:A:616:HOH:O	2.04	0.75
1:D:270:ASP:OD2	3:D:609:HOH:O	2.04	0.75
1:I:44:LYS:NZ	3:I:608:HOH:O	2.02	0.75
1:R:227:ASP:OD1	1:R:229:THR:HG22	1.84	0.75
1:G:275:ASP:OD2	3:G:612:HOH:O	2.03	0.75
1:B:76:ARG:NH2	3:B:615:HOH:O	2.06	0.75
1:J:231:SER:OG	3:J:609:HOH:O	2.04	0.75
1:N:390:VAL:O	3:N:612:HOH:O	2.03	0.75
1:M:414:SER:HA	3:M:634:HOH:O	1.84	0.75
1:N:187:ILE:CD1	1:N:189:LYS:N	2.49	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:178:ASN:HD21	1:F:182:GLU:HB2	1.52	0.75
1:M:379:ASP:OD1	3:M:613:HOH:O	2.03	0.75
1:C:34:ARG:NH1	2:C:502:SO4:O1	2.20	0.75
1:C:370:HIS:ND1	3:C:629:HOH:O	2.14	0.75
1:C:419:LEU:O	3:C:611:HOH:O	2.02	0.75
1:L:223:ARG:NE	3:L:633:HOH:O	2.19	0.75
1:N:146:MET:HB2	3:N:765:HOH:O	1.86	0.75
1:U:80:ARG:NH1	3:U:638:HOH:O	2.20	0.75
1:N:189:LYS:HG3	1:N:193:PRO:HD2	1.67	0.75
1:C:101:ARG:HD3	3:H:663:HOH:O	1.86	0.75
1:Q:23:ARG:HH11	1:Q:24:GLY:H	1.32	0.75
1:E:287:VAL:O	3:E:618:HOH:O	2.05	0.74
1:E:393:ASP:OD2	3:E:616:HOH:O	2.04	0.74
1:L:169:ALA:O	3:L:608:HOH:O	2.04	0.74
1:N:413:GLN:NE2	3:N:632:HOH:O	2.18	0.74
1:E:307:THR:OG1	3:E:619:HOH:O	2.05	0.74
1:J:23:ARG:NH2	3:J:615:HOH:O	2.12	0.74
1:K:341:ARG:NH1	3:K:634:HOH:O	2.19	0.74
1:D:116:TYR:HA	1:D:119:ILE:HD11	1.69	0.74
1:O:12:ARG:O	3:O:613:HOH:O	2.05	0.74
1:G:286:ASP:O	3:G:618:HOH:O	2.04	0.74
1:M:293:ILE:O	3:M:614:HOH:O	2.05	0.74
1:T:346[B]:THR:HG23	3:T:615:HOH:O	1.85	0.74
1:U:280:ALA:N	3:U:625:HOH:O	2.07	0.74
1:E:175:MET:O	3:E:615:HOH:O	2.04	0.74
1:F:318:ASP:OD1	3:F:610:HOH:O	2.03	0.74
1:G:400:ARG:O	3:G:617:HOH:O	2.04	0.74
1:D:261:ASP:OD1	3:D:608:HOH:O	2.04	0.74
1:E:123:GLU:O	3:E:620:HOH:O	2.05	0.74
1:E:219:GLU:OE1	3:E:622:HOH:O	2.06	0.74
1:R:193:PRO:O	3:R:610:HOH:O	2.04	0.74
1:U:252:ARG:NE	3:U:636:HOH:O	2.19	0.74
1:I:246:GLY:O	3:I:611:HOH:O	2.05	0.74
1:P:397:ASP:HA	3:P:708:HOH:O	1.87	0.74
1:M:33:ARG:NH2	3:M:641:HOH:O	2.21	0.74
1:A:355:ARG:NH1	3:A:638:HOH:O	2.20	0.74
1:B:222:ARG:NH1	3:B:636:HOH:O	2.20	0.74
1:Q:161:CYS:HB3	1:Q:204:LEU:HD22	1.69	0.74
1:F:106:GLN:OE1	3:F:612:HOH:O	2.05	0.74
1:M:315:ASP:OD2	3:M:618:HOH:O	2.06	0.74
1:M:421:LEU:O	3:M:617:HOH:O	2.06	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:199:ASN:OD1	3:T:616:HOH:O	2.05	0.74
1:U:43:GLY:O	3:U:620:HOH:O	2.06	0.74
1:F:177:VAL:HG21	1:F:204:LEU:HD12	1.68	0.73
1:M:149:GLN:OE1	3:M:616:HOH:O	2.06	0.73
1:A:366:LYS:NZ	3:A:639:HOH:O	2.21	0.73
1:D:125:TYR:OH	3:D:610:HOH:O	2.05	0.73
1:H:232:ARG:NH1	3:H:637:HOH:O	2.19	0.73
1:F:162:LEU:HG	1:F:207:MET:HG2	1.69	0.73
1:C:57:ASN:OD1	3:C:613:HOH:O	2.05	0.73
1:P:176:HIS:O	3:P:611:HOH:O	2.07	0.73
1:R:166:ARG:NH2	3:R:610:HOH:O	2.04	0.73
1:A:79:GLN:OE1	3:A:619:HOH:O	2.07	0.73
1:H:109:GLU:OE2	3:H:619:HOH:O	2.06	0.73
1:Q:68:GLN:O	3:Q:609:HOH:O	2.06	0.73
1:M:118:ASN:OD1	3:M:615:HOH:O	2.06	0.73
1:E:26:ARG:NH2	3:E:637:HOH:O	2.21	0.73
1:I:124:PRO:HB2	3:I:926:HOH:O	1.88	0.73
1:L:98:ALA:O	3:L:610:HOH:O	2.05	0.73
1:E:44:LYS:O	3:E:621:HOH:O	2.06	0.73
1:H:207:MET:SD	3:H:864:HOH:O	2.44	0.73
1:N:68:GLN:NE2	1:N:107:TRP:HB3	2.02	0.73
1:R:80:ARG:NH1	3:R:628:HOH:O	2.21	0.73
1:R:213:HIS:ND1	3:R:631:HOH:O	2.22	0.73
1:B:295:ASP:O	3:B:614:HOH:O	2.05	0.73
1:H:175:MET:HG3	1:H:183:ILE:HD12	1.69	0.73
1:G:69:TYR:OH	3:G:615:HOH:O	2.04	0.73
1:U:123:GLU:OE2	3:U:622:HOH:O	2.06	0.73
1:P:193:PRO:HG2	3:P:606:HOH:O	1.88	0.73
1:Q:286:ASP:OD1	3:Q:608:HOH:O	2.06	0.72
1:R:313:VAL:HG12	1:R:335:SER:HA	1.70	0.72
1:O:346:THR:OG1	3:O:614:HOH:O	2.06	0.72
1:F:214:THR:O	1:F:218:MET:HG2	1.89	0.72
1:T:294:TYR:O	3:T:617:HOH:O	2.06	0.72
1:F:109:GLU:OE2	3:F:614:HOH:O	2.07	0.72
1:N:233:ASP:OD2	3:N:613:HOH:O	2.06	0.72
1:P:26:ARG:NH1	3:P:630:HOH:O	2.21	0.72
1:F:320:ARG:NH1	3:F:634:HOH:O	2.21	0.72
1:H:419:LEU:O	3:H:618:HOH:O	2.06	0.72
1:J:105:THR:N	3:J:627:HOH:O	2.22	0.72
1:L:286:ASP:OD1	3:L:613:HOH:O	2.08	0.72
1:Q:50:PHE:O	3:Q:610:HOH:O	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:250:ALA:O	3:F:615:HOH:O	2.07	0.72
1:D:245:HIS:NE2	3:D:628:HOH:O	2.22	0.72
1:H:236:LYS:HB3	1:H:236:LYS:HE3	1.71	0.72
1:K:224:ASP:HB2	3:K:688:HOH:O	1.88	0.72
1:K:395:GLU:O	3:K:614:HOH:O	2.06	0.72
1:B:121:ILE:HD11	3:D:631:HOH:O	1.90	0.72
1:E:251:HIS:NE2	1:E:256:SER:OG	2.20	0.72
1:M:129:TYR:O	3:M:621:HOH:O	2.08	0.72
1:C:307:THR:OG1	3:C:615:HOH:O	2.08	0.72
1:J:21:GLY:O	3:J:610:HOH:O	2.06	0.72
1:N:355:ARG:NH1	3:N:637:HOH:O	2.22	0.72
1:Q:316:ASP:O	3:Q:613:HOH:O	2.08	0.72
1:T:316:ASP:OD2	3:T:618:HOH:O	2.07	0.72
1:B:145:TYR:CE2	1:M:7:VAL:HG11	2.25	0.72
1:E:110:GLY:O	3:E:623:HOH:O	2.07	0.72
1:H:319:ARG:N	3:H:623:HOH:O	2.21	0.72
1:N:386:GLU:OE2	3:N:615:HOH:O	2.07	0.72
1:U:316:ASP:O	3:U:628:HOH:O	2.08	0.72
1:C:200:GLU:OE1	3:C:616:HOH:O	2.08	0.72
1:B:146:MET:HG2	1:B:211:VAL:HG21	1.72	0.71
1:H:219:GLU:OE1	3:H:620:HOH:O	2.08	0.71
1:J:170:THR:O	3:J:611:HOH:O	2.08	0.71
1:L:355:ARG:HD2	3:P:889:HOH:O	1.90	0.71
1:M:317:GLU:OE2	3:M:619:HOH:O	2.07	0.71
1:T:403:ARG:NH1	3:T:639:HOH:O	2.23	0.71
1:B:189:LYS:O	1:B:189:LYS:HG3	1.89	0.71
1:L:106:GLN:OE1	3:L:612:HOH:O	2.07	0.71
1:L:200[B]:GLU:OE2	3:L:614:HOH:O	2.08	0.71
1:N:187:ILE:CD1	1:N:189:LYS:HA	2.20	0.71
1:P:111:THR:O	3:P:612:HOH:O	2.07	0.71
1:P:139:TYR:HD2	3:P:674:HOH:O	1.72	0.71
1:P:149:GLN:NE2	3:P:636:HOH:O	2.24	0.71
1:M:251:HIS:O	3:M:622:HOH:O	2.09	0.71
1:T:111:THR:HG21	3:T:1025:HOH:O	1.89	0.71
1:E:34:ARG:NH2	1:E:379:ASP:OD1	2.24	0.71
1:E:44:LYS:NZ	3:E:639:HOH:O	2.23	0.71
1:Q:395:GLU:O	3:Q:614:HOH:O	2.08	0.71
1:R:7:VAL:O	3:R:612:HOH:O	2.08	0.71
1:G:409:CYS:SG	3:G:774:HOH:O	2.48	0.71
1:A:200:GLU:OE2	3:A:621:HOH:O	2.08	0.71
1:B:148:GLN:CD	1:M:7:VAL:HG23	2.10	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:215:LYS:NZ	3:D:632:HOH:O	2.24	0.71
1:I:409:CYS:SG	3:I:678:HOH:O	2.47	0.71
1:R:296:LYS:NZ	3:R:637:HOH:O	2.24	0.71
1:D:400:ARG:O	3:D:613:HOH:O	2.09	0.71
1:U:198:GLY:O	3:U:626:HOH:O	2.08	0.71
1:C:318:ASP:O	3:C:614:HOH:O	2.08	0.71
1:E:176:HIS:CD2	1:E:177:VAL:H	2.09	0.71
1:J:366:LYS:HB2	3:J:1074:HOH:O	1.90	0.71
1:U:25:SER:N	3:U:644:HOH:O	2.23	0.71
1:B:123:GLU:OE1	3:B:618:HOH:O	2.07	0.71
1:C:7:VAL:N	3:C:650:HOH:O	2.24	0.71
1:D:106:GLN:NE2	3:D:617:HOH:O	2.12	0.71
1:D:355:ARG:HB2	1:D:372:GLN:HG2	1.72	0.71
1:K:106:GLN:HG3	1:K:107:TRP:H	1.55	0.71
1:N:168:GLU:O	3:N:616:HOH:O	2.08	0.71
1:P:349:ARG:NH1	3:P:634:HOH:O	2.23	0.71
1:N:386:GLU:OE1	3:N:618:HOH:O	2.09	0.71
1:F:401:PHE:N	3:F:608:HOH:O	2.01	0.71
1:T:141:MET:SD	3:T:1013:HOH:O	2.48	0.71
1:D:185:ASP:HA	1:D:243:VAL:HG11	1.73	0.70
1:B:113:ASP:OD2	3:B:622:HOH:O	2.09	0.70
1:E:252:ARG:NH1	3:E:643:HOH:O	2.24	0.70
1:G:233:ASP:OD2	3:G:619:HOH:O	2.08	0.70
1:U:276:ALA:O	3:U:625:HOH:O	2.08	0.70
1:J:109:GLU:OE2	3:J:612:HOH:O	2.09	0.70
1:B:29:GLU:HB2	1:B:412[B]:THR:HG21	1.73	0.70
1:C:97:PRO:HG2	1:C:101:ARG:HA	1.73	0.70
1:I:331:ASP:OD2	3:I:612:HOH:O	2.09	0.70
1:L:322:SER:OG	3:L:616:HOH:O	2.09	0.70
1:E:106:GLN:HB3	3:E:627:HOH:O	1.91	0.70
1:H:205:ALA:HA	3:H:671:HOH:O	1.90	0.70
1:K:168:GLU:O	3:K:617:HOH:O	2.09	0.70
1:B:28:LYS:HE3	1:B:29:GLU:HG3	1.74	0.70
1:C:153:SER:OG	3:C:618:HOH:O	2.09	0.70
1:Q:129:TYR:O	3:Q:612:HOH:O	2.08	0.70
1:R:225:ALA:O	3:R:613:HOH:O	2.09	0.70
1:T:200:GLU:OE2	3:T:621:HOH:O	2.10	0.70
1:T:232:ARG:NH2	3:T:620:HOH:O	2.09	0.70
1:U:155:ALA:O	3:U:624:HOH:O	2.07	0.70
1:B:392:GLU:OE2	3:B:620:HOH:O	2.08	0.70
1:U:44:LYS:O	3:U:629:HOH:O	2.08	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:HIS:ND1	3:A:643:HOH:O	2.23	0.70
1:K:68:GLN:OE1	3:K:616:HOH:O	2.08	0.70
1:N:174:VAL:HG13	1:N:176:HIS:CE1	2.26	0.70
1:Q:166:ARG:HH22	1:Q:200:GLU:HB3	1.56	0.70
1:A:196:ILE:O	3:A:624:HOH:O	2.09	0.70
1:H:79:GLN:O	3:H:622:HOH:O	2.09	0.70
1:L:219:GLU:OE1	3:L:615:HOH:O	2.09	0.70
1:G:142:ASP:O	3:G:620:HOH:O	2.08	0.70
1:G:403:ARG:NH1	3:G:634:HOH:O	2.25	0.70
1:A:68:GLN:HE22	1:A:108:TYR:H	1.40	0.70
1:D:72:HIS:NE2	3:D:631:HOH:O	2.24	0.70
1:I:80:ARG:NH1	3:I:624:HOH:O	2.25	0.70
1:Q:25:SER:OG	3:Q:617:HOH:O	2.10	0.70
1:R:413:GLN:HB2	3:R:617:HOH:O	1.92	0.70
1:A:68:GLN:NE2	3:A:625:HOH:O	2.10	0.69
1:A:10:LEU:HD13	1:A:148:GLN:HG2	1.74	0.69
1:C:119:ILE:N	3:C:602:HOH:O	2.24	0.69
1:C:294:TYR:OH	3:C:619:HOH:O	2.10	0.69
1:N:275:ASP:OD1	3:N:617:HOH:O	2.09	0.69
1:B:148:GLN:NE2	1:M:7:VAL:HG23	2.07	0.69
1:B:392:GLU:OE2	3:B:621:HOH:O	2.09	0.69
1:Q:106:GLN:NE2	3:Q:642:HOH:O	2.25	0.69
1:R:341:ARG:NH2	3:R:638:HOH:O	2.24	0.69
1:L:38:ALA:O	3:L:617:HOH:O	2.10	0.69
1:Q:375:ASN:HB3	1:Q:408:ILE:HD13	1.75	0.69
1:H:222:ARG:HD3	3:H:648:HOH:O	1.92	0.69
1:K:417:ASP:OD1	3:K:620:HOH:O	2.11	0.69
1:G:398:ALA:HB2	1:G:403:ARG:HD3	1.73	0.69
1:M:62:ARG:HG3	3:M:833:HOH:O	1.91	0.69
1:M:254:ALA:N	3:M:605:HOH:O	2.23	0.69
1:A:369:ARG:NH2	3:A:641:HOH:O	2.21	0.69
1:C:161:CYS:SG	3:C:967:HOH:O	2.50	0.69
1:F:261:ASP:OD2	3:F:618:HOH:O	2.10	0.69
1:H:407:GLY:O	3:H:621:HOH:O	2.08	0.69
1:K:160:GLY:O	3:K:618:HOH:O	2.09	0.69
1:O:34:ARG:NH1	2:O:502:SO4:S	2.65	0.69
1:F:116:TYR:HA	1:F:119:ILE:HD11	1.74	0.69
1:F:233:ASP:OD2	3:F:616:HOH:O	2.08	0.69
1:B:100:GLN:O	1:B:102:VAL:N	2.23	0.69
1:E:80:ARG:NH2	3:E:628:HOH:O	2.16	0.69
1:E:106:GLN:NE2	3:E:645:HOH:O	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:246:GLY:HA3	3:H:638:HOH:O	1.92	0.69
1:H:355:ARG:NH1	3:H:655:HOH:O	2.25	0.69
1:O:80:ARG:NH2	3:O:631:HOH:O	2.22	0.69
1:G:395:GLU:N	3:G:609:HOH:O	2.24	0.69
1:I:244:GLU:OE2	3:I:614:HOH:O	2.11	0.69
1:R:394:PRO:O	3:R:614:HOH:O	2.10	0.69
1:C:89:ARG:HD2	1:G:56:LEU:HD21	1.73	0.69
1:P:253:PHE:HE1	3:P:674:HOH:O	1.76	0.69
1:G:177:VAL:HG13	1:G:181:ASP:HA	1.74	0.69
1:G:318:ASP:O	3:G:624:HOH:O	2.11	0.69
1:C:8:GLN:OE1	3:C:621:HOH:O	2.11	0.68
1:I:109:GLU:OE1	3:I:613:HOH:O	2.10	0.68
1:N:149:GLN:OE1	3:N:621:HOH:O	2.11	0.68
1:Q:28:LYS:HG2	1:Q:402:ARG:CZ	2.22	0.68
1:Q:111:THR:HG23	1:Q:234:PHE:H	1.57	0.68
1:G:404:THR:CG2	1:G:408:ILE:H	2.06	0.68
1:M:197:PRO:O	3:M:624:HOH:O	2.11	0.68
1:B:167:MET:SD	3:B:870:HOH:O	2.50	0.68
1:C:259:ARG:NH1	3:C:653:HOH:O	2.25	0.68
1:E:233:ASP:OD2	3:E:624:HOH:O	2.10	0.68
1:F:263:GLU:OE1	3:F:617:HOH:O	2.10	0.68
1:M:29:GLU:OE2	3:M:623:HOH:O	2.10	0.68
1:T:125:TYR:O	3:T:623:HOH:O	2.11	0.68
1:U:297:SER:OG	3:U:630:HOH:O	2.09	0.68
1:C:216:PHE:HB3	3:C:990:HOH:O	1.93	0.68
1:N:200:GLU:OE1	3:N:623:HOH:O	2.12	0.68
1:P:23:ARG:NH2	3:P:642:HOH:O	2.26	0.68
1:M:332:CYS:N	3:M:637:HOH:O	2.25	0.68
1:D:355:ARG:NH2	3:D:636:HOH:O	2.26	0.68
1:B:130:MET:SD	3:B:644:HOH:O	2.50	0.68
1:L:290:ASP:OD2	3:L:618:HOH:O	2.11	0.68
1:F:200:GLU:OE1	3:F:621:HOH:O	2.12	0.68
1:A:67:THR:N	3:A:613:HOH:O	2.24	0.68
1:B:166:ARG:NH2	3:B:606:HOH:O	1.97	0.68
1:I:341:ARG:NE	3:I:625:HOH:O	2.26	0.68
1:C:390:VAL:O	3:C:625:HOH:O	2.12	0.68
1:I:251:HIS:NE2	1:I:256:SER:OG	2.25	0.68
1:O:106:GLN:O	3:O:616:HOH:O	2.12	0.68
1:U:117:GLN:NE2	3:U:639:HOH:O	2.20	0.68
2:B:501:SO4:O2	3:B:624:HOH:O	2.10	0.68
1:K:313:VAL:HG12	1:K:335:SER:HA	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:196:ILE:O	3:B:627:HOH:O	2.12	0.68
1:C:237:ASP:O	3:C:624:HOH:O	2.12	0.68
1:H:316:ASP:O	3:H:623:HOH:O	2.12	0.68
1:J:163:GLU:O	3:J:613:HOH:O	2.10	0.68
1:T:106:GLN:O	3:T:622:HOH:O	2.10	0.68
1:U:113:ASP:OD1	1:U:232:ARG:NH2	2.27	0.68
1:U:384:ILE:O	3:U:632:HOH:O	2.12	0.68
1:A:100:GLN:N	3:A:618:HOH:O	2.21	0.68
1:C:369:ARG:NH2	3:C:654:HOH:O	2.26	0.68
1:R:403:ARG:NH2	3:R:642:HOH:O	2.26	0.68
1:D:116:TYR:CB	1:D:221:LEU:HD13	2.21	0.67
1:N:163:GLU:OE1	3:N:622:HOH:O	2.11	0.67
1:M:105:THR:N	3:M:652:HOH:O	2.27	0.67
1:E:44:LYS:NZ	3:E:649:HOH:O	2.27	0.67
1:E:167:MET:N	3:E:650:HOH:O	2.27	0.67
1:H:134:ALA:N	3:H:624:HOH:O	2.12	0.67
1:I:259:ARG:NH2	1:I:263:GLU:O	2.26	0.67
1:K:243:VAL:O	3:K:621:HOH:O	2.12	0.67
1:L:68:GLN:HE21	1:L:107:TRP:HB3	1.60	0.67
1:R:192:ASP:OD2	3:R:615:HOH:O	2.12	0.67
1:B:237:ASP:OD1	3:B:625:HOH:O	2.11	0.67
1:F:23:ARG:NH2	3:F:624:HOH:O	2.16	0.67
1:C:32:ASP:OD1	3:C:626:HOH:O	2.13	0.67
1:D:116:TYR:HB2	1:D:221:LEU:CD1	2.21	0.67
1:H:279:GLN:NE2	3:H:656:HOH:O	2.27	0.67
1:I:316:ASP:HB2	3:I:640:HOH:O	1.94	0.67
1:M:163:GLU:OE2	3:M:625:HOH:O	2.12	0.67
1:C:395:GLU:HG3	3:C:744:HOH:O	1.95	0.67
1:L:286:ASP:O	3:L:619:HOH:O	2.12	0.67
1:N:103:SER:OG	3:N:620:HOH:O	2.11	0.67
1:N:171:GLY:O	3:N:626:HOH:O	2.13	0.67
1:Q:241:TYR:OH	3:Q:618:HOH:O	2.10	0.67
1:R:28:LYS:CD	1:R:29:GLU:H	2.08	0.67
1:G:352:SER:O	3:G:623:HOH:O	2.11	0.67
1:K:188:GLU:OE2	3:K:622:HOH:O	2.12	0.67
1:O:32:ASP:OD2	3:O:617:HOH:O	2.13	0.67
1:O:34:ARG:NE	3:O:612:HOH:O	2.27	0.67
1:F:222:ARG:NE	3:F:626:HOH:O	2.27	0.67
1:B:346[B]:THR:OG1	3:B:601:HOH:O	1.84	0.67
1:D:165:PRO:O	3:D:616:HOH:O	2.11	0.67
1:K:32:ASP:OD1	3:K:619:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ARG:NH1	3:C:657:HOH:O	2.28	0.67
1:N:227:ASP:HB2	1:N:229:THR:HG22	1.77	0.67
1:I:392:GLU:OE2	1:J:200:GLU:N	2.27	0.67
1:K:155:ALA:HA	1:K:247:LYS:HG2	1.77	0.67
1:B:318:ASP:OD1	1:B:318:ASP:N	2.28	0.66
1:C:116:TYR:HA	1:C:221:LEU:HD21	1.76	0.66
1:C:233:ASP:HB3	3:C:705:HOH:O	1.95	0.66
1:I:150:HIS:O	3:I:615:HOH:O	2.13	0.66
1:I:311:LYS:NZ	3:I:626:HOH:O	2.26	0.66
1:K:183:ILE:O	3:K:621:HOH:O	2.13	0.66
1:L:166:ARG:NH2	3:L:639:HOH:O	2.26	0.66
1:M:372:GLN:OE1	3:M:626:HOH:O	2.13	0.66
1:A:57:ASN:OD1	3:A:628:HOH:O	2.13	0.66
1:P:222:ARG:NH1	3:P:643:HOH:O	2.27	0.66
1:C:124:PRO:O	3:C:623:HOH:O	2.11	0.66
1:C:156:ASP:OD1	3:C:627:HOH:O	2.13	0.66
1:D:26:ARG:NH2	3:D:635:HOH:O	2.26	0.66
1:E:243:VAL:O	3:E:625:HOH:O	2.12	0.66
1:H:72:HIS:ND1	3:H:663:HOH:O	2.29	0.66
1:P:250:ALA:O	3:P:613:HOH:O	2.12	0.66
1:E:262:PHE:N	3:E:651:HOH:O	2.27	0.66
1:Q:116:TYR:HA	1:Q:119:ILE:HD11	1.76	0.66
1:Q:421:LEU:O	3:Q:621:HOH:O	2.13	0.66
1:G:185:ASP:O	3:G:622:HOH:O	2.11	0.66
1:B:29:GLU:OE1	3:B:629:HOH:O	2.13	0.66
1:E:176:HIS:HD2	1:E:177:VAL:H	1.44	0.66
1:P:253:PHE:CE1	3:P:674:HOH:O	2.48	0.66
1:U:146:MET:SD	3:U:1098:HOH:O	2.53	0.66
1:N:166:ARG:CZ	1:N:192:ASP:OD1	2.43	0.66
1:D:89:ARG:NH2	3:D:624:HOH:O	2.28	0.66
1:H:319:ARG:NH1	3:H:642:HOH:O	2.21	0.66
1:J:97:PRO:O	3:J:616:HOH:O	2.12	0.66
1:K:44:LYS:O	3:K:624:HOH:O	2.14	0.66
1:N:94:ASP:OD1	3:N:625:HOH:O	2.13	0.66
1:F:28:LYS:HD3	1:F:402:ARG:NH2	2.10	0.66
1:U:223:ARG:HG2	1:U:223:ARG:HH11	1.61	0.66
1:B:247:LYS:NZ	3:B:611:HOH:O	2.00	0.66
1:E:106:GLN:OE1	3:E:627:HOH:O	2.14	0.66
1:P:402:ARG:O	3:P:616:HOH:O	2.13	0.66
1:H:79:GLN:NE2	3:H:657:HOH:O	2.28	0.66
1:Q:320:ARG:O	3:Q:622:HOH:O	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:GLU:OE2	3:B:626:HOH:O	2.12	0.65
1:D:316:ASP:OD2	3:D:618:HOH:O	2.13	0.65
1:L:69:TYR:HE1	1:L:107:TRP:CD2	2.14	0.65
1:N:7:VAL:O	3:N:627:HOH:O	2.13	0.65
1:Q:264:HIS:O	3:Q:623:HOH:O	2.15	0.65
1:F:72:HIS:CG	1:T:101:ARG:HG2	2.31	0.65
1:D:397:ASP:O	3:D:604:HOH:O	2.14	0.65
1:J:275:ASP:OD1	3:J:617:HOH:O	2.14	0.65
1:O:119:ILE:HG13	3:O:604:HOH:O	1.97	0.65
1:P:262:PHE:O	3:P:615:HOH:O	2.13	0.65
1:Q:270:ASP:OD2	3:Q:620:HOH:O	2.13	0.65
1:M:109:GLU:OE1	3:M:628:HOH:O	2.14	0.65
1:M:176:HIS:HD2	1:M:177:VAL:H	1.41	0.65
1:A:79:GLN:OE1	3:A:630:HOH:O	2.13	0.65
1:H:214:THR:O	1:H:218:MET:HG2	1.96	0.65
1:I:168:GLU:OE2	1:I:168:GLU:N	2.29	0.65
1:P:413:GLN:OE1	3:P:617:HOH:O	2.13	0.65
1:R:111:THR:OG1	1:R:233:ASP:OD1	2.13	0.65
1:M:90:ASN:ND2	3:M:645:HOH:O	2.24	0.65
1:D:157:VAL:HG23	3:D:620:HOH:O	1.97	0.65
1:L:420:ASP:OD2	3:L:620:HOH:O	2.13	0.65
1:P:70:LYS:O	3:P:619:HOH:O	2.15	0.65
1:D:211:VAL:O	3:D:620:HOH:O	2.15	0.65
1:D:316:ASP:HB2	3:D:603:HOH:O	1.96	0.65
1:N:261:ASP:OD2	3:N:624:HOH:O	2.12	0.65
1:F:237:ASP:OD2	3:F:623:HOH:O	2.15	0.65
1:M:315:ASP:OD1	3:M:627:HOH:O	2.13	0.65
2:T:501:SO4:O2	3:T:624:HOH:O	2.12	0.65
1:P:26:ARG:NH2	3:P:645:HOH:O	2.27	0.65
1:R:170:THR:OG1	3:R:616:HOH:O	2.13	0.65
1:M:313:VAL:HG12	1:M:335:SER:HA	1.78	0.65
1:K:69:TYR:HH	1:K:107:TRP:HE1	1.44	0.65
1:O:275:ASP:OD1	3:O:618:HOH:O	2.13	0.65
1:P:400:ARG:HB2	3:P:708:HOH:O	1.95	0.65
1:Q:133:LEU:HD23	1:Q:209:ILE:HG23	1.79	0.65
1:M:46:ARG:NH1	2:M:502:SO4:O2	2.26	0.65
1:M:119:ILE:HG21	1:M:222:ARG:NH2	2.11	0.65
1:B:23:ARG:HH22	1:B:70:LYS:HG3	1.62	0.65
1:B:28:LYS:CE	1:B:29:GLU:HG3	2.27	0.65
1:C:417:ASP:OD1	3:C:631:HOH:O	2.14	0.65
1:J:166:ARG:NH1	3:J:608:HOH:O	2.04	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:389:ILE:HD11	1:P:166:ARG:HH21	1.62	0.65
1:Q:23:ARG:HH11	1:Q:24:GLY:N	1.94	0.65
1:R:413:GLN:OE1	3:R:617:HOH:O	2.15	0.65
1:G:406:SER:HB3	3:G:612:HOH:O	1.97	0.65
1:M:332:CYS:C	3:M:637:HOH:O	2.35	0.65
1:T:101:ARG:O	3:T:626:HOH:O	2.14	0.65
1:A:7:VAL:O	3:A:629:HOH:O	2.13	0.65
1:H:222:ARG:NH1	3:H:659:HOH:O	2.28	0.65
1:O:44:LYS:NZ	3:O:637:HOH:O	2.28	0.65
1:F:70:LYS:NZ	3:F:635:HOH:O	2.21	0.65
1:B:97:PRO:HG2	1:B:101:ARG:H	1.60	0.65
1:P:182:GLU:OE1	3:P:618:HOH:O	2.14	0.65
1:T:313:VAL:HG12	1:T:335:SER:HA	1.78	0.65
1:U:80:ARG:HD2	3:U:968:HOH:O	1.96	0.65
1:N:408:ILE:HD11	3:N:836:HOH:O	1.94	0.64
1:O:105:THR:N	3:O:625:HOH:O	2.30	0.64
1:H:142:ASP:OD2	3:H:628:HOH:O	2.14	0.64
1:H:166:ARG:NH2	3:H:661:HOH:O	2.29	0.64
1:J:15:MET:SD	3:J:1188:HOH:O	2.55	0.64
1:K:383:VAL:H	1:K:413:GLN:HE22	1.46	0.64
1:L:116:TYR:OH	3:L:609:HOH:O	2.04	0.64
1:M:146:MET:HG2	1:M:211:VAL:HG21	1.78	0.64
1:B:9:PRO:HB3	1:M:9:PRO:HG3	1.78	0.64
1:B:227:ASP:OD2	3:B:630:HOH:O	2.14	0.64
1:H:117:GLN:NE2	3:H:662:HOH:O	2.29	0.64
1:K:227:ASP:OD2	3:K:625:HOH:O	2.14	0.64
1:F:366:LYS:NZ	3:F:622:HOH:O	2.12	0.64
1:A:187:ILE:HB	1:A:190:PRO:HG3	1.78	0.64
1:D:166:ARG:HB2	1:D:193:PRO:HG2	1.79	0.64
1:F:137:HIS:ND1	3:F:625:HOH:O	2.30	0.64
1:G:115:VAL:HB	1:G:221:LEU:HD21	1.79	0.64
1:T:220:ALA:N	3:T:604:HOH:O	1.97	0.64
1:T:240:PRO:O	3:T:628:HOH:O	2.14	0.64
1:B:238:ILE:HD11	3:B:799:HOH:O	1.96	0.64
1:L:163:GLU:OE2	3:L:622:HOH:O	2.15	0.64
1:F:28:LYS:HG3	1:F:29:GLU:N	2.10	0.64
1:T:17:TYR:OH	1:T:118:ASN:ND2	2.30	0.64
1:D:227:ASP:OD2	3:D:621:HOH:O	2.15	0.64
1:E:214:THR:O	1:E:218:MET:HG2	1.98	0.64
1:E:218:MET:SD	3:E:1027:HOH:O	2.54	0.64
1:T:200:GLU:OE2	3:T:629:HOH:O	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ARG:HB3	1:A:70:LYS:HE2	1.78	0.64
1:Q:86:ARG:NH1	3:Q:619:HOH:O	2.11	0.64
1:B:228:PRO:O	3:B:631:HOH:O	2.14	0.64
1:K:44:LYS:HE3	3:K:868:HOH:O	1.97	0.64
1:N:269:ARG:NH2	3:N:648:HOH:O	2.28	0.64
1:O:132:ILE:HG12	3:O:656:HOH:O	1.97	0.64
1:K:296:LYS:NZ	3:K:642:HOH:O	2.25	0.64
1:L:241:TYR:O	3:L:623:HOH:O	2.15	0.64
1:P:376:VAL:HG12	1:P:409:CYS:HB2	1.78	0.64
1:R:419:LEU:HG	1:R:421:LEU:H	1.62	0.64
1:R:420:ASP:O	3:R:618:HOH:O	2.15	0.64
1:A:106:GLN:OE1	3:A:631:HOH:O	2.15	0.63
1:D:401:PHE:O	3:D:604:HOH:O	2.15	0.63
1:J:355:ARG:NH2	3:J:638:HOH:O	2.31	0.63
1:K:148:GLN:OE1	3:K:626:HOH:O	2.14	0.63
1:N:199:ASN:OD1	3:N:622:HOH:O	2.15	0.63
1:R:421:LEU:HB2	3:R:641:HOH:O	1.97	0.63
1:G:49:ASP:HB2	3:G:701:HOH:O	1.98	0.63
1:H:236:LYS:CB	1:H:236:LYS:HE3	2.28	0.63
1:J:384:ILE:HG12	3:J:622:HOH:O	1.98	0.63
1:R:28:LYS:CE	1:R:29:GLU:HB2	2.24	0.63
1:O:34:ARG:CZ	3:O:612:HOH:O	2.40	0.63
1:M:26:ARG:HA	1:M:28:LYS:HE2	1.80	0.63
1:Q:23:ARG:HD3	1:Q:23:ARG:N	2.04	0.63
1:M:113:ASP:OD2	3:M:629:HOH:O	2.15	0.63
1:M:417:ASP:HB2	3:M:634:HOH:O	1.99	0.63
1:D:383:VAL:H	1:D:413:GLN:NE2	1.94	0.63
1:D:398:ALA:HB3	3:D:734:HOH:O	1.97	0.63
1:N:267:TYR:CE1	1:N:291:LEU:HB2	2.34	0.63
1:J:206:SER:O	3:J:619:HOH:O	2.15	0.63
1:O:79:GLN:OE1	3:O:619:HOH:O	2.15	0.63
1:Q:199:ASN:ND2	3:Q:637:HOH:O	2.23	0.63
1:M:215:LYS:HZ2	1:M:218:MET:HG3	1.63	0.63
1:N:68:GLN:HE21	1:N:107:TRP:HB3	1.62	0.63
1:J:420:ASP:N	3:J:635:HOH:O	2.29	0.63
1:L:218:MET:HB2	3:L:632:HOH:O	1.97	0.63
1:N:187:ILE:CD1	1:N:189:LYS:CA	2.77	0.63
1:G:149:GLN:NE2	3:G:644:HOH:O	2.31	0.63
1:T:366:LYS:HE2	1:T:383:VAL:HG13	1.80	0.63
1:L:260:SER:HB3	1:L:263:GLU:HG3	1.81	0.63
1:L:272:GLY:N	3:L:635:HOH:O	2.20	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:235:GLY:N	3:E:656:HOH:O	2.31	0.62
1:N:251:HIS:NE2	1:N:256:SER:OG	2.31	0.62
1:N:323:ALA:HA	1:N:339:LEU:HB2	1.79	0.62
1:O:175:MET:HG3	1:O:183:ILE:HG12	1.80	0.62
1:G:26:ARG:NH1	3:G:647:HOH:O	2.32	0.62
1:C:178:ASN:ND2	3:C:661:HOH:O	2.32	0.62
1:P:86:ARG:HB3	3:P:667:HOH:O	1.99	0.62
1:Q:180:LYS:HG3	1:Q:182:GLU:HG3	1.81	0.62
1:F:392:GLU:N	3:F:607:HOH:O	2.17	0.62
1:R:180:LYS:NZ	3:R:645:HOH:O	2.28	0.62
1:F:236:LYS:HD3	3:F:616:HOH:O	1.99	0.62
1:A:111:THR:HG22	1:A:233:ASP:HA	1.81	0.62
1:E:244:GLU:HG2	1:E:245:HIS:CD2	2.33	0.62
1:P:80:ARG:NH1	3:P:648:HOH:O	2.31	0.62
1:A:175:MET:HE1	3:A:952:HOH:O	1.99	0.62
1:C:94:ASP:OD1	1:H:80:ARG:NH2	2.31	0.62
1:O:127:PRO:HG3	3:O:1101:HOH:O	1.99	0.62
1:F:115:VAL:HB	1:F:221:LEU:HD21	1.81	0.62
1:G:353:TYR:HB2	3:G:623:HOH:O	2.00	0.62
1:T:48:ILE:HD13	1:T:74:LEU:HD11	1.82	0.62
1:D:80:ARG:NH2	3:D:614:HOH:O	2.10	0.62
1:G:313:VAL:HG12	1:G:335:SER:HA	1.81	0.62
1:A:36:LYS:HD3	1:A:136:ASP:HB2	1.82	0.62
1:C:91:GLU:OE2	3:C:633:HOH:O	2.16	0.62
1:Q:109:GLU:OE1	1:Q:232:ARG:NH1	2.33	0.62
1:O:57:ASN:OD1	3:O:621:HOH:O	2.16	0.62
1:T:44:LYS:NZ	1:U:307:THR:O	2.29	0.62
1:D:218:MET:O	1:D:222:ARG:HG3	2.00	0.62
1:R:7:VAL:HG23	1:R:8:GLN:HG3	1.81	0.62
1:H:353:TYR:OH	3:H:626:HOH:O	2.14	0.61
1:O:200:GLU:O	3:O:620:HOH:O	2.16	0.61
1:Q:105:THR:HG22	1:Q:106:GLN:H	1.63	0.61
1:C:34:ARG:NH1	2:C:502:SO4:S	2.74	0.61
1:K:80:ARG:NH2	3:K:652:HOH:O	2.32	0.61
1:K:207:MET:N	3:K:618:HOH:O	2.31	0.61
1:F:244:GLU:N	3:F:638:HOH:O	2.23	0.61
1:I:244:GLU:OE1	1:I:245:HIS:NE2	2.33	0.61
1:J:86:ARG:NH1	3:J:640:HOH:O	2.34	0.61
1:U:24:GLY:HA2	3:U:995:HOH:O	1.98	0.61
1:L:362:LEU:N	3:L:629:HOH:O	2.25	0.61
1:P:229:THR:N	3:P:610:HOH:O	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:227:ASP:CG	1:R:229:THR:HG22	2.20	0.61
1:T:251:HIS:NE2	1:T:256:SER:OG	2.28	0.61
1:D:196:ILE:HD13	1:D:252:ARG:HH12	1.65	0.61
1:N:68:GLN:NE2	1:N:108:TYR:H	1.98	0.61
1:U:75:ILE:O	1:U:79:GLN:HG3	2.01	0.61
1:D:91:GLU:OE1	3:D:624:HOH:O	2.16	0.61
1:H:265:GLU:OE2	3:H:630:HOH:O	2.16	0.61
1:L:222:ARG:NH2	3:L:651:HOH:O	2.32	0.61
1:R:229:THR:HG23	1:R:230:SER:H	1.65	0.61
1:E:109:GLU:OE1	1:E:232:ARG:NH1	2.34	0.61
1:J:392:GLU:OE2	3:J:621:HOH:O	2.16	0.61
1:K:80:ARG:NH1	3:K:654:HOH:O	2.33	0.61
1:O:125:TYR:OH	3:O:622:HOH:O	2.16	0.61
1:F:28:LYS:HB2	3:F:831:HOH:O	2.00	0.61
1:C:395:GLU:HG2	3:C:687:HOH:O	2.00	0.61
1:L:223:ARG:NH1	3:L:644:HOH:O	2.28	0.61
1:C:245:HIS:O	3:C:634:HOH:O	2.16	0.61
1:G:305:GLU:OE2	3:G:625:HOH:O	2.16	0.61
1:H:373:LEU:HG	3:H:616:HOH:O	2.01	0.61
1:J:249:VAL:HG23	3:J:681:HOH:O	1.99	0.61
1:A:285:THR:OG1	1:A:341:ARG:NH1	2.34	0.60
1:B:101:ARG:HB3	1:D:75:ILE:HD12	1.83	0.60
1:D:33:ARG:NH1	3:D:649:HOH:O	2.33	0.60
1:H:369:ARG:NH2	3:H:642:HOH:O	2.34	0.60
1:B:145:TYR:OH	3:B:633:HOH:O	2.16	0.60
1:C:76:ARG:NH1	3:C:620:HOH:O	2.10	0.60
1:P:29:GLU:OE2	3:P:620:HOH:O	2.16	0.60
1:A:318:ASP:N	3:A:611:HOH:O	2.34	0.60
1:B:85:PHE:HD2	1:B:91:GLU:HB3	1.64	0.60
1:I:181:ASP:O	3:I:617:HOH:O	2.16	0.60
1:Q:166:ARG:HD3	1:Q:193:PRO:O	2.01	0.60
1:R:223:ARG:CZ	1:R:224:ASP:HB3	2.31	0.60
1:F:24:GLY:HA3	1:F:31:THR:HG21	1.82	0.60
1:F:42:GLY:N	3:F:619:HOH:O	2.20	0.60
1:H:251:HIS:CE1	1:H:256:SER:HG	2.19	0.60
1:L:307:THR:OG1	3:L:624:HOH:O	2.16	0.60
1:B:193:PRO:HG2	3:B:602:HOH:O	2.02	0.60
1:N:259:ARG:HB3	3:N:607:HOH:O	2.01	0.60
1:P:170:THR:N	3:P:606:HOH:O	2.33	0.60
1:F:28:LYS:NZ	3:F:648:HOH:O	2.33	0.60
1:G:70:LYS:O	3:G:627:HOH:O	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:249:VAL:HB	3:G:703:HOH:O	2.00	0.60
1:J:275:ASP:OD1	3:J:620:HOH:O	2.15	0.60
1:P:349:ARG:NE	3:P:614:HOH:O	2.12	0.60
1:D:265:GLU:OE1	3:D:623:HOH:O	2.16	0.60
1:L:289:PRO:HG3	3:L:619:HOH:O	2.02	0.60
1:F:28:LYS:HD3	1:F:402:ARG:HH21	1.66	0.60
1:B:79:GLN:OE1	3:B:634:HOH:O	2.17	0.60
1:C:210:TYR:O	3:C:635:HOH:O	2.17	0.60
1:D:116:TYR:HD1	1:D:221:LEU:HD12	1.66	0.60
1:N:106:GLN:NE2	3:N:645:HOH:O	2.28	0.60
1:G:222:ARG:HD3	3:G:629:HOH:O	2.02	0.60
1:B:214:THR:O	1:B:218:MET:HG3	2.01	0.60
1:J:86:ARG:NH2	3:J:631:HOH:O	2.28	0.60
1:F:180:LYS:NZ	3:F:632:HOH:O	2.20	0.60
1:J:178:ASN:HB3	1:J:184:ILE:HD11	1.82	0.60
1:T:196:ILE:HA	3:T:686:HOH:O	2.01	0.60
1:L:80:ARG:NH2	3:L:654:HOH:O	2.34	0.59
1:Q:44:LYS:NZ	3:Q:615:HOH:O	2.09	0.59
1:G:415:MET:N	3:G:604:HOH:O	2.16	0.59
1:C:34:ARG:NH1	2:C:502:SO4:O4	2.34	0.59
1:L:225:ALA:N	3:L:605:HOH:O	2.34	0.59
1:Q:119:ILE:HG23	1:Q:218:MET:HE3	1.84	0.59
1:F:403:ARG:NH1	3:F:649:HOH:O	2.33	0.59
1:C:97:PRO:O	1:C:99:SER:N	2.35	0.59
1:J:149:GLN:NE2	3:J:607:HOH:O	2.35	0.59
1:L:23:ARG:NH1	3:L:653:HOH:O	2.34	0.59
1:F:30:LEU:HD12	1:F:34:ARG:HH21	1.67	0.59
1:F:94:ASP:OD1	1:T:76:ARG:NH2	2.35	0.59
1:G:366:LYS:HD3	3:G:903:HOH:O	2.02	0.59
1:L:228:PRO:O	3:L:625:HOH:O	2.16	0.59
1:P:128:GLU:OE2	3:P:621:HOH:O	2.16	0.59
1:H:319:ARG:HD3	1:H:352:SER:HB3	1.85	0.59
1:O:244:GLU:OE1	3:O:623:HOH:O	2.17	0.59
1:D:401:PHE:HA	1:D:415:MET:CE	2.33	0.59
1:E:223:ARG:NH2	1:E:241:TYR:OH	2.36	0.59
1:H:187:ILE:HD12	1:H:194:PRO:HG3	1.85	0.59
1:N:187:ILE:HD13	1:N:189:LYS:H	1.66	0.59
1:N:340:ASN:HB3	1:N:357:GLU:HG2	1.83	0.59
3:T:612:HOH:O	1:U:308:PRO:HD3	2.02	0.59
1:A:232:ARG:HD2	3:A:690:HOH:O	2.02	0.59
1:H:313:VAL:CG2	1:H:335:SER:HA	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:116:TYR:O	1:F:119:ILE:HG12	2.03	0.59
1:F:331:ASP:O	1:F:349:ARG:NH1	2.27	0.59
1:T:36:LYS:HE2	1:T:136:ASP:HB2	1.85	0.59
1:T:346[A]:THR:OG1	3:T:615:HOH:O	2.05	0.59
1:B:101:ARG:NH2	3:B:658:HOH:O	2.35	0.59
3:D:937:HOH:O	1:M:311:LYS:HE2	2.01	0.59
1:I:259:ARG:NE	3:I:621:HOH:O	2.21	0.59
1:J:188:GLU:HG3	3:J:1010:HOH:O	2.02	0.59
1:G:393:ASP:OD1	3:G:609:HOH:O	2.16	0.59
1:T:420:ASP:OD2	3:T:630:HOH:O	2.17	0.59
1:C:355:ARG:HB2	1:C:372:GLN:HG2	1.84	0.59
1:G:370:HIS:N	3:G:623:HOH:O	2.36	0.59
1:B:341:ARG:NH1	3:B:653:HOH:O	2.26	0.58
1:E:320:ARG:NH1	3:E:659:HOH:O	2.34	0.58
1:O:116:TYR:HA	1:O:221:LEU:HD13	1.86	0.58
1:Q:351:ASN:ND2	1:Q:367:ILE:O	2.34	0.58
1:C:116:TYR:HB2	1:C:221:LEU:HD11	1.85	0.58
1:E:7:VAL:HG13	1:E:8:GLN:HG3	1.85	0.58
1:A:72:HIS:CE1	3:A:626:HOH:O	2.56	0.58
1:A:181:ASP:OD1	1:A:252:ARG:NH2	2.35	0.58
1:B:112:ALA:HB1	3:B:799:HOH:O	2.02	0.58
1:C:229:THR:HG21	1:M:229:THR:HA	1.84	0.58
1:P:89:ARG:HG3	3:P:667:HOH:O	2.03	0.58
1:Q:7:VAL:N	3:Q:656:HOH:O	2.36	0.58
1:Q:153:SER:O	1:Q:155:ALA:N	2.37	0.58
1:H:13:ASP:HB3	1:H:128:GLU:HB2	1.84	0.58
1:K:350:ALA:HA	1:K:367:ILE:HB	1.85	0.58
1:A:8:GLN:NE2	3:A:663:HOH:O	2.36	0.58
1:A:71:ALA:HA	3:A:605:HOH:O	2.03	0.58
1:D:402:ARG:H	1:D:415:MET:HE3	1.67	0.58
1:T:141:MET:HE2	1:T:143:TYR:HE1	1.68	0.58
1:T:372:GLN:HG2	3:T:698:HOH:O	2.02	0.58
1:D:219:GLU:OE2	1:D:222:ARG:NE	2.37	0.58
1:J:313:VAL:HG12	1:J:335:SER:HA	1.85	0.58
1:K:57:ASN:ND2	3:K:660:HOH:O	2.37	0.58
1:K:178:ASN:HD21	1:K:182:GLU:HB2	1.69	0.58
1:P:313:VAL:HG12	1:P:335:SER:HA	1.85	0.58
1:T:91:GLU:OE2	3:T:631:HOH:O	2.17	0.58
1:D:418:LYS:NZ	3:D:659:HOH:O	2.37	0.58
1:L:159:ILE:HD13	1:L:183:ILE:HD12	1.85	0.58
2:L:502:SO4:O2	3:L:626:HOH:O	2.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:238:ILE:HG23	3:T:826:HOH:O	2.02	0.58
1:B:331:ASP:O	1:B:349[B]:ARG:NH1	2.34	0.58
1:I:76:ARG:NE	3:I:647:HOH:O	2.36	0.58
1:B:327:VAL:HG22	1:K:311:LYS:HG3	1.84	0.58
1:D:146:MET:HE2	3:D:602:HOH:O	2.03	0.58
1:E:7:VAL:N	3:E:660:HOH:O	2.35	0.58
1:F:195:GLY:O	3:F:627:HOH:O	2.17	0.58
1:B:189:LYS:NZ	3:B:659:HOH:O	2.36	0.57
1:R:222:ARG:NH2	3:R:639:HOH:O	2.24	0.57
1:K:218:MET:O	1:K:222:ARG:HG3	2.04	0.57
1:L:36:LYS:HD3	1:L:136:ASP:HB2	1.86	0.57
1:E:400:ARG:NH1	3:E:629:HOH:O	2.16	0.57
1:Q:89:ARG:HD2	1:T:56:LEU:HD21	1.86	0.57
1:A:167:MET:O	3:A:633:HOH:O	2.17	0.57
1:B:80:ARG:NH2	3:B:616:HOH:O	2.06	0.57
1:I:40:TYR:HH	1:I:380:HIS:HD1	1.52	0.57
1:T:119:ILE:HG12	1:T:218:MET:SD	2.45	0.57
1:A:417:ASP:O	3:A:632:HOH:O	2.17	0.57
1:A:116:TYR:HB3	3:A:602:HOH:O	2.03	0.57
1:B:89:ARG:HD2	1:M:56:LEU:HD21	1.85	0.57
1:H:33:ARG:HA	1:H:70:LYS:HE2	1.86	0.57
1:H:236:LYS:CB	1:H:236:LYS:CE	2.81	0.57
1:F:28:LYS:HD3	1:F:402:ARG:NE	2.20	0.57
1:M:286:ASP:OD1	3:M:631:HOH:O	2.17	0.57
1:A:339:LEU:HD22	1:A:356:LEU:HD12	1.85	0.57
1:B:116:TYR:CB	1:B:221:LEU:HD11	2.31	0.57
1:N:333:ILE:HB	1:N:349:ARG:HD3	1.86	0.57
1:O:287:VAL:HA	3:O:627:HOH:O	2.02	0.57
1:R:150:HIS:NE2	3:R:631:HOH:O	2.27	0.57
1:G:177:VAL:CG1	1:G:181:ASP:HA	2.34	0.57
1:M:180:LYS:HB3	1:M:182:GLU:HG3	1.86	0.57
1:E:255:ASP:OD2	3:E:632:HOH:O	2.18	0.57
1:N:400:ARG:NH1	3:N:666:HOH:O	2.37	0.57
1:B:28:LYS:HE3	1:B:29:GLU:CG	2.35	0.57
1:L:330:GLY:HA2	3:L:666:HOH:O	2.04	0.57
1:O:80:ARG:NH1	3:O:651:HOH:O	2.38	0.57
1:F:68:GLN:HB3	3:F:611:HOH:O	2.04	0.57
1:M:34:ARG:NH2	3:M:613:HOH:O	2.38	0.57
1:B:133:LEU:HD23	1:B:209:ILE:HG23	1.85	0.56
1:C:393:ASP:HB3	1:C:396:LEU:HB3	1.87	0.56
1:E:111:THR:HG23	1:E:234:PHE:HD2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:331:ASP:O	1:E:349:ARG:NH1	2.35	0.56
1:H:227:ASP:OD1	1:H:229:THR:N	2.37	0.56
1:I:319:ARG:N	3:I:640:HOH:O	2.33	0.56
1:L:86:ARG:NH2	3:L:661:HOH:O	2.38	0.56
1:F:218:MET:O	3:F:626:HOH:O	2.17	0.56
1:A:62:ARG:NH1	3:A:651:HOH:O	2.28	0.56
1:D:395:GLU:HG3	3:D:669:HOH:O	2.06	0.56
1:L:406:SER:OG	3:L:627:HOH:O	2.17	0.56
1:Q:397:ASP:OD2	3:Q:624:HOH:O	2.17	0.56
1:T:134:ALA:O	3:T:632:HOH:O	2.17	0.56
1:B:416:ILE:O	1:B:419:LEU:HB2	2.06	0.56
1:C:44:LYS:NZ	3:C:670:HOH:O	2.38	0.56
1:C:229:THR:CG2	1:M:229:THR:HA	2.34	0.56
1:H:350:ALA:HA	1:H:367:ILE:HB	1.87	0.56
1:I:43:GLY:O	1:I:44:LYS:HG3	2.05	0.56
1:I:231:SER:O	3:I:618:HOH:O	2.18	0.56
1:Q:116:TYR:O	1:Q:119:ILE:HG12	2.05	0.56
1:R:80:ARG:HD3	3:R:969:HOH:O	2.05	0.56
1:F:119:ILE:HG23	1:F:218:MET:CE	2.34	0.56
1:G:176:HIS:N	3:G:622:HOH:O	2.37	0.56
1:T:85:PHE:HD2	1:T:91:GLU:HB3	1.70	0.56
1:U:111:THR:HG23	1:U:234:PHE:HD1	1.70	0.56
1:U:166:ARG:CZ	3:U:695:HOH:O	2.53	0.56
1:U:234:PHE:HA	1:U:238:ILE:HD12	1.87	0.56
1:B:376:VAL:HG12	1:B:409:CYS:HB2	1.86	0.56
1:E:262:PHE:CG	3:E:651:HOH:O	2.53	0.56
1:H:374:SER:O	3:H:632:HOH:O	2.18	0.56
1:I:156:ASP:OD1	3:I:619:HOH:O	2.18	0.56
1:I:369:ARG:NH2	2:I:501:SO4:O2	2.30	0.56
1:K:119:ILE:HG12	1:K:218:MET:CE	2.35	0.56
1:O:151:VAL:N	3:O:602:HOH:O	2.02	0.56
1:R:76:ARG:NH2	3:R:662:HOH:O	2.38	0.56
1:T:111:THR:CG2	1:T:234:PHE:H	2.18	0.56
1:D:319:ARG:N	3:D:603:HOH:O	1.93	0.56
1:R:331:ASP:OD1	1:R:349:ARG:NH2	2.39	0.56
1:P:400:ARG:HB3	1:P:419:LEU:HD21	1.88	0.56
1:Q:413:GLN:NE2	3:Q:662:HOH:O	2.38	0.56
1:T:97:PRO:HG2	1:T:100:GLN:HG3	1.87	0.56
1:A:23:ARG:CZ	3:A:623:HOH:O	2.48	0.56
1:B:340:ASN:HB3	1:B:357:GLU:HG2	1.88	0.56
1:C:33:ARG:NH2	3:C:665:HOH:O	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:319:ARG:NH1	1:C:352:SER:OG	2.38	0.56
1:K:224:ASP:OD1	3:K:629:HOH:O	2.18	0.56
1:B:116:TYR:HA	1:B:221:LEU:HD21	1.88	0.56
1:L:220:ALA:O	1:L:223:ARG:NH2	2.39	0.56
1:O:150:HIS:N	3:O:602:HOH:O	2.38	0.56
1:R:309:PRO:O	3:R:619:HOH:O	2.18	0.56
1:T:217:LEU:O	1:T:221:LEU:HG	2.05	0.56
1:U:119:ILE:HG23	1:U:218:MET:HE3	1.88	0.56
1:A:68:GLN:OE1	1:A:107:TRP:HB3	2.06	0.56
1:A:199:ASN:N	3:A:624:HOH:O	2.39	0.56
1:I:158:THR:N	3:I:632:HOH:O	2.38	0.56
1:I:313:VAL:HG12	1:I:335:SER:HA	1.88	0.56
1:J:366:LYS:HE3	3:J:1074:HOH:O	2.06	0.56
1:G:404:THR:HG23	1:G:407:GLY:H	1.70	0.56
1:A:122:ILE:HG23	3:A:986:HOH:O	2.05	0.56
1:D:7:VAL:N	3:D:662:HOH:O	2.39	0.56
1:N:259:ARG:NH1	1:N:263:GLU:O	2.39	0.56
1:Q:111:THR:CG2	1:Q:234:PHE:H	2.19	0.56
1:T:113:ASP:HA	3:T:620:HOH:O	2.05	0.56
1:B:180:LYS:O	1:B:180:LYS:HG2	2.05	0.55
1:C:188:GLU:N	3:C:671:HOH:O	2.39	0.55
1:E:255:ASP:OD2	3:E:633:HOH:O	2.18	0.55
1:E:366:LYS:NZ	3:E:666:HOH:O	2.38	0.55
1:Q:217:LEU:HA	3:Q:666:HOH:O	2.05	0.55
1:G:134:ALA:N	3:G:621:HOH:O	2.09	0.55
1:E:140:LYS:HE3	3:E:708:HOH:O	2.05	0.55
1:H:259:ARG:NH2	3:H:667:HOH:O	2.31	0.55
1:I:166:ARG:NH2	1:I:193:PRO:O	2.39	0.55
1:I:180:LYS:NZ	3:I:629:HOH:O	2.28	0.55
1:Q:214:THR:O	1:Q:218:MET:HG2	2.05	0.55
1:R:29:GLU:HB3	1:R:412:THR:HG21	1.88	0.55
1:G:367:ILE:HA	1:G:384:ILE:HB	1.88	0.55
1:E:24:GLY:O	1:E:26:ARG:N	2.38	0.55
1:H:80:ARG:CZ	3:H:609:HOH:O	2.48	0.55
1:K:403:ARG:HG3	1:K:409:CYS:SG	2.46	0.55
1:P:76:ARG:NH1	3:P:658:HOH:O	2.38	0.55
1:P:218:MET:HB3	1:P:222:ARG:NH1	2.20	0.55
1:R:28:LYS:HG3	1:R:402:ARG:NE	2.22	0.55
1:R:226:ALA:O	3:R:620:HOH:O	2.18	0.55
1:F:180:LYS:NZ	3:F:629:HOH:O	2.19	0.55
1:M:417:ASP:OD2	3:M:634:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:275:ASP:OD1	1:T:408:ILE:HD13	2.07	0.55
1:B:223:ARG:NH2	3:B:664:HOH:O	2.39	0.55
1:B:346[A]:THR:HG22	3:B:797:HOH:O	2.05	0.55
1:C:75:ILE:O	1:C:79:GLN:HG3	2.07	0.55
1:H:8:GLN:OE1	3:H:633:HOH:O	2.18	0.55
1:J:275:ASP:HB2	3:J:675:HOH:O	2.06	0.55
1:N:288:VAL:HG12	3:N:985:HOH:O	2.07	0.55
1:R:259:ARG:NH2	3:R:666:HOH:O	2.39	0.55
1:T:272:GLY:HA2	3:T:607:HOH:O	2.06	0.55
1:D:395:GLU:HA	3:D:734:HOH:O	2.07	0.55
1:I:146:MET:HB2	3:I:697:HOH:O	2.06	0.55
1:O:295:ASP:N	3:O:652:HOH:O	2.39	0.55
1:M:111:THR:HG23	1:M:234:PHE:HD2	1.70	0.55
1:M:119:ILE:HD13	1:M:218:MET:CE	2.35	0.55
1:D:148:GLN:OE1	3:D:625:HOH:O	2.18	0.55
1:D:293:ILE:HG22	3:D:1139:HOH:O	2.05	0.55
1:O:70:LYS:O	3:O:626:HOH:O	2.18	0.55
1:G:149:GLN:HG2	3:G:736:HOH:O	2.05	0.55
1:M:198:GLY:O	3:M:633:HOH:O	2.18	0.55
1:T:367:ILE:HA	1:T:384:ILE:HB	1.88	0.55
1:E:119:ILE:HD11	1:E:221:LEU:HD11	1.87	0.55
1:H:70:LYS:NZ	3:H:684:HOH:O	2.40	0.55
1:O:116:TYR:N	3:O:609:HOH:O	2.40	0.55
1:O:286:ASP:O	3:O:627:HOH:O	2.18	0.55
1:P:192:ASP:O	3:P:623:HOH:O	2.18	0.55
1:R:223:ARG:HG3	1:R:225:ALA:H	1.71	0.55
1:F:222:ARG:CZ	3:F:626:HOH:O	2.55	0.55
1:I:162:LEU:HG	1:I:207:MET:HG2	1.87	0.55
1:K:192:ASP:OD2	3:K:632:HOH:O	2.18	0.55
1:O:383:VAL:H	1:O:413:GLN:NE2	2.04	0.55
1:P:162:LEU:O	1:P:205:ALA:N	2.33	0.55
1:M:218:MET:O	1:M:222:ARG:HG3	2.07	0.55
1:A:402:ARG:HD3	3:A:925:HOH:O	2.06	0.55
1:N:29:GLU:HB3	1:N:412:THR:HG21	1.89	0.55
1:F:7:VAL:N	3:F:659:HOH:O	2.40	0.55
1:E:229:THR:HG22	3:E:868:HOH:O	2.06	0.55
1:D:34:ARG:NH1	2:D:502:SO4:O1	2.40	0.54
1:E:232:ARG:HA	3:E:667:HOH:O	2.07	0.54
1:L:355:ARG:NH2	1:L:357:GLU:OE1	2.39	0.54
1:O:219:GLU:HG2	3:O:845:HOH:O	2.07	0.54
1:P:414:SER:O	1:P:418:LYS:HD3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:282:ILE:HG23	3:R:699:HOH:O	2.06	0.54
1:U:116:TYR:O	1:U:119:ILE:HG12	2.07	0.54
1:D:116:TYR:O	1:D:119:ILE:HG12	2.08	0.54
1:D:251:HIS:NE2	1:D:256:SER:OG	2.38	0.54
1:I:331:ASP:O	1:I:349:ARG:NH1	2.36	0.54
1:N:100:GLN:O	1:N:102:VAL:N	2.41	0.54
3:Q:847:HOH:O	1:U:88:GLU:HB2	2.06	0.54
1:F:28:LYS:HD3	1:F:402:ARG:CZ	2.38	0.54
1:E:227:ASP:OD1	1:E:229:THR:HB	2.08	0.54
1:H:107:TRP:O	3:H:634:HOH:O	2.19	0.54
1:G:376:VAL:HG12	1:G:409:CYS:HB2	1.88	0.54
1:U:278:TRP:HZ2	1:U:358:ASN:HB3	1.72	0.54
1:E:176:HIS:CD2	1:E:177:VAL:N	2.75	0.54
1:L:25:SER:N	3:L:674:HOH:O	2.41	0.54
1:N:259:ARG:NH2	3:N:675:HOH:O	2.40	0.54
1:N:420:ASP:HA	3:N:728:HOH:O	2.06	0.54
1:Q:397:ASP:N	3:Q:625:HOH:O	2.39	0.54
1:R:224:ASP:OD2	1:R:230:SER:OG	2.26	0.54
1:G:404:THR:OG1	1:G:405:GLU:N	2.41	0.54
1:H:327:VAL:HG23	1:H:343:LEU:HA	1.90	0.54
1:T:263:GLU:OE1	3:T:633:HOH:O	2.18	0.54
1:D:40:TYR:HB3	1:D:345:PHE:CE2	2.42	0.54
1:L:318:ASP:OD2	3:L:628:HOH:O	2.18	0.54
1:O:166:ARG:NH2	1:O:201:GLY:H	2.05	0.54
1:P:141:MET:HB2	3:P:674:HOH:O	2.07	0.54
1:P:242:ILE:O	1:P:246:GLY:N	2.37	0.54
1:B:254:ALA:HB2	3:B:932:HOH:O	2.08	0.54
1:I:149:GLN:OE1	1:I:251:HIS:ND1	2.38	0.54
1:R:225:ALA:N	3:R:604:HOH:O	2.39	0.54
1:U:214:THR:O	1:U:218:MET:HG2	2.08	0.54
1:A:170:THR:HG23	3:A:920:HOH:O	2.08	0.54
1:B:175:MET:HB3	1:B:183:ILE:CG2	2.37	0.54
1:C:23:ARG:NH1	1:C:70:LYS:HB2	2.17	0.54
1:K:273:THR:HG23	1:K:276:ALA:H	1.72	0.54
1:O:115:VAL:HB	3:O:609:HOH:O	2.08	0.54
1:P:259:ARG:NH1	3:P:660:HOH:O	2.39	0.54
1:M:176:HIS:CD2	1:M:177:VAL:N	2.76	0.54
1:M:212:PHE:CG	1:M:217:LEU:HD13	2.42	0.54
1:E:29:GLU:OE2	1:E:402:ARG:HD2	2.08	0.54
1:H:400:ARG:HD3	1:H:419:LEU:HD21	1.89	0.54
1:J:382:VAL:O	3:J:622:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:189:LYS:NZ	3:N:602:HOH:O	1.87	0.54
1:U:111:THR:HG22	1:U:233:ASP:HA	1.89	0.54
1:B:349[A]:ARG:HD3	1:B:366:LYS:HZ1	1.72	0.54
1:C:369:ARG:H	1:C:386:GLU:HG2	1.73	0.54
1:E:26:ARG:NH2	3:E:671:HOH:O	2.41	0.54
1:G:218:MET:HB2	3:G:680:HOH:O	2.07	0.54
1:A:116:TYR:HD2	3:A:602:HOH:O	1.91	0.53
1:H:166:ARG:HD3	1:H:201:GLY:H	1.73	0.53
1:J:175:MET:SD	1:J:183:ILE:HD13	2.47	0.53
1:P:13:ASP:OD1	3:P:626:HOH:O	2.19	0.53
1:R:227:ASP:O	3:R:622:HOH:O	2.19	0.53
1:G:177:VAL:HG21	1:G:204:LEU:HD12	1.90	0.53
1:B:119:ILE:HD11	1:B:221:LEU:HD23	1.90	0.53
1:C:105:THR:O	3:C:638:HOH:O	2.19	0.53
1:E:7:VAL:O	3:E:636:HOH:O	2.19	0.53
1:E:237:ASP:HB3	3:E:603:HOH:O	2.08	0.53
1:R:57:ASN:ND2	3:R:668:HOH:O	2.40	0.53
1:G:402:ARG:NH1	3:G:603:HOH:O	1.94	0.53
1:G:404:THR:HG22	1:G:408:ILE:O	2.08	0.53
1:T:72:HIS:HB3	3:T:857:HOH:O	2.07	0.53
1:D:89:ARG:HD2	1:K:56:LEU:HD21	1.91	0.53
1:E:80:ARG:NH2	3:E:638:HOH:O	2.22	0.53
1:J:307:THR:HB	1:J:331:ASP:HB2	1.91	0.53
1:K:164:VAL:HG13	1:K:169:ALA:HB2	1.89	0.53
1:M:33:ARG:NH2	3:M:657:HOH:O	2.28	0.53
1:A:127:PRO:HG3	3:A:986:HOH:O	2.08	0.53
1:I:106:GLN:HG3	1:I:107:TRP:H	1.74	0.53
1:L:378:ILE:O	3:L:629:HOH:O	2.18	0.53
1:P:205:ALA:HA	3:P:653:HOH:O	2.08	0.53
1:M:250:ALA:HB2	3:M:1100:HOH:O	2.07	0.53
1:T:400:ARG:NH2	1:T:421:LEU:O	2.37	0.53
1:L:15:MET:HE1	1:L:122:ILE:HG12	1.89	0.53
1:L:68:GLN:HA	3:L:721:HOH:O	2.09	0.53
1:O:186:PHE:O	3:O:628:HOH:O	2.19	0.53
1:P:195:GLY:HA3	1:P:200:GLU:HG3	1.89	0.53
1:T:68:GLN:OE1	1:T:108:TYR:N	2.41	0.53
1:B:392:GLU:HG3	1:B:393:ASP:N	2.23	0.53
1:D:185:ASP:HA	1:D:243:VAL:CG1	2.38	0.53
1:H:175:MET:CG	1:H:183:ILE:HD12	2.39	0.53
1:K:109:GLU:OE2	1:K:232:ARG:HG3	2.08	0.53
1:L:327:VAL:HB	1:L:343:LEU:HG	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:PRO:HG2	3:C:613:HOH:O	2.07	0.53
1:H:176:HIS:N	3:H:691:HOH:O	2.41	0.53
1:M:29:GLU:OE1	1:M:29:GLU:N	2.38	0.53
1:I:393:ASP:HB3	1:I:396:LEU:HB3	1.90	0.53
1:K:69:TYR:OH	1:K:107:TRP:NE1	2.42	0.53
1:N:166:ARG:NH2	1:N:192:ASP:OD1	2.42	0.53
1:A:418:LYS:HG2	1:A:418:LYS:O	2.09	0.53
1:B:182:GLU:HA	1:B:249:VAL:HG12	1.91	0.53
1:H:316:ASP:OD2	3:H:635:HOH:O	2.19	0.53
1:L:189:LYS:C	1:L:189:LYS:HD3	2.29	0.53
1:O:166:ARG:HH22	1:O:201:GLY:H	1.57	0.53
1:O:307:THR:HB	1:O:331:ASP:HB2	1.91	0.53
1:Q:267:TYR:HA	3:Q:714:HOH:O	2.09	0.53
1:R:119:ILE:HG12	1:R:218:MET:CE	2.39	0.53
1:R:180:LYS:HB2	1:R:182:GLU:HG3	1.91	0.53
1:G:209:ILE:HG13	3:G:621:HOH:O	2.09	0.53
1:J:28:LYS:HE3	3:J:1122:HOH:O	2.07	0.53
1:J:236:LYS:NZ	3:J:651:HOH:O	2.39	0.53
1:Q:196:ILE:HD11	1:Q:252:ARG:HH12	1.74	0.53
1:Q:393:ASP:OD1	1:Q:395:GLU:HG2	2.08	0.53
1:T:26:ARG:NH2	3:T:646:HOH:O	2.27	0.53
1:T:420:ASP:OD1	3:T:634:HOH:O	2.18	0.53
1:A:33:ARG:NE	3:A:666:HOH:O	2.38	0.52
1:L:111:THR:HG22	1:L:233:ASP:HA	1.90	0.52
1:R:221:LEU:HA	1:R:223:ARG:HB3	1.89	0.52
1:M:180:LYS:CB	1:M:182:GLU:HG3	2.39	0.52
1:U:79:GLN:N	3:U:605:HOH:O	2.42	0.52
1:C:403:ARG:NH2	3:C:641:HOH:O	2.19	0.52
1:P:75:ILE:O	1:P:79:GLN:HG3	2.10	0.52
1:Q:313:VAL:HG21	1:F:287:VAL:HA	1.92	0.52
1:G:26:ARG:NH2	3:G:660:HOH:O	2.41	0.52
1:M:176:HIS:HD2	1:M:177:VAL:N	2.05	0.52
1:M:332:CYS:O	3:M:637:HOH:O	2.19	0.52
1:A:23:ARG:NH1	3:A:668:HOH:O	2.40	0.52
1:A:244:GLU:HG2	1:A:245:HIS:CD2	2.45	0.52
1:B:190:PRO:HG2	1:B:193:PRO:HG3	1.91	0.52
1:C:116:TYR:HE1	1:C:222:ARG:HG2	1.74	0.52
1:H:89:ARG:HD2	1:I:56:LEU:HD21	1.90	0.52
1:H:148:GLN:HG3	1:I:7:VAL:HG23	1.90	0.52
1:Q:220:ALA:HB1	1:Q:223:ARG:NH2	2.24	0.52
1:R:229:THR:HG23	1:R:230:SER:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:333:ILE:HD12	1:T:349:ARG:NE	2.25	0.52
3:T:716:HOH:O	1:U:311:LYS:HE2	2.09	0.52
1:B:355:ARG:NH1	3:B:613:HOH:O	2.04	0.52
1:I:157:VAL:CG2	3:I:632:HOH:O	2.57	0.52
1:R:181:ASP:OD2	3:R:621:HOH:O	2.19	0.52
1:M:161:CYS:N	3:M:622:HOH:O	2.24	0.52
1:A:319:ARG:N	3:A:611:HOH:O	2.02	0.52
1:B:240:PRO:HA	1:B:243:VAL:HG22	1.90	0.52
1:D:341:ARG:HD3	1:D:358:ASN:HD21	1.75	0.52
1:E:171:GLY:HA2	1:E:189:LYS:HG2	1.91	0.52
1:E:262:PHE:CD2	3:E:651:HOH:O	2.62	0.52
1:K:152:ASP:HB2	3:K:636:HOH:O	2.10	0.52
1:O:62:ARG:NH2	3:O:642:HOH:O	2.30	0.52
1:O:156:ASP:HB3	1:O:216:PHE:CZ	2.44	0.52
1:Q:247:LYS:NZ	3:Q:670:HOH:O	2.42	0.52
1:F:82:TRP:N	3:F:663:HOH:O	2.42	0.52
1:B:101:ARG:HD2	1:D:72:HIS:HA	1.91	0.52
1:C:8:GLN:NE2	3:C:628:HOH:O	2.13	0.52
1:D:34:ARG:NH1	2:D:502:SO4:O4	2.42	0.52
1:E:405:GLU:H	1:E:405:GLU:CD	2.12	0.52
1:H:278:TRP:HZ2	1:H:358:ASN:HB3	1.75	0.52
1:P:8:GLN:OE1	1:P:12:ARG:NH1	2.42	0.52
1:Q:259:ARG:NH2	3:Q:668:HOH:O	2.39	0.52
1:E:44:LYS:NZ	3:E:609:HOH:O	1.98	0.52
1:K:397:ASP:OD2	3:K:627:HOH:O	2.19	0.52
1:L:91:GLU:OE2	3:L:630:HOH:O	2.18	0.52
1:L:405:GLU:O	3:L:631:HOH:O	2.19	0.52
1:O:231:SER:HB2	3:O:807:HOH:O	2.10	0.52
1:P:181:ASP:O	3:P:613:HOH:O	2.18	0.52
1:L:340:ASN:O	1:L:357:GLU:HA	2.10	0.52
1:C:414:SER:OG	3:C:640:HOH:O	2.19	0.52
1:H:28:LYS:NZ	3:H:695:HOH:O	2.43	0.52
1:H:119:ILE:HD12	1:H:218:MET:SD	2.50	0.52
1:H:236:LYS:NZ	3:H:604:HOH:O	1.88	0.52
1:R:113:ASP:OD1	1:R:117:GLN:NE2	2.36	0.52
1:F:357:GLU:O	1:F:374:SER:HA	2.09	0.52
1:U:31:THR:O	1:U:70:LYS:NZ	2.43	0.52
1:B:177:VAL:HG12	1:B:183:ILE:HA	1.92	0.52
1:K:318:ASP:OD1	3:K:630:HOH:O	2.18	0.52
1:O:26:ARG:NE	3:O:660:HOH:O	2.43	0.52
1:G:307:THR:HB	1:G:331:ASP:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:355:ARG:NH1	3:U:674:HOH:O	2.42	0.52
1:B:311:LYS:HE2	3:K:732:HOH:O	2.11	0.51
1:D:119:ILE:HD12	1:D:218:MET:CE	2.40	0.51
1:N:264:HIS:NE2	3:N:657:HOH:O	2.34	0.51
1:M:316:ASP:OD2	3:M:635:HOH:O	2.19	0.51
1:A:287:VAL:HA	1:P:313:VAL:HG21	1.91	0.51
1:E:148:GLN:OE1	3:E:634:HOH:O	2.18	0.51
1:K:200:GLU:HG3	3:K:727:HOH:O	2.09	0.51
1:K:369:ARG:NH2	2:K:501:SO4:O2	2.40	0.51
1:Q:212:PHE:CG	1:Q:217:LEU:HD13	2.45	0.51
1:A:367:ILE:HG12	3:A:650:HOH:O	2.09	0.51
1:B:80:ARG:NH2	3:D:610:HOH:O	2.43	0.51
1:B:222:ARG:NH2	3:B:619:HOH:O	2.08	0.51
1:E:234:PHE:HA	1:E:238:ILE:HB	1.92	0.51
1:J:350:ALA:HA	1:J:367:ILE:HB	1.92	0.51
1:L:15:MET:CE	1:L:122:ILE:HG23	2.40	0.51
1:L:47:ILE:HG12	1:L:138:ILE:HD11	1.92	0.51
1:G:176:HIS:CD2	3:G:961:HOH:O	2.63	0.51
1:G:349[A]:ARG:NH1	3:G:655:HOH:O	2.37	0.51
1:A:217:LEU:O	1:A:221:LEU:HD23	2.11	0.51
1:H:112:ALA:HA	1:H:234:PHE:CE1	2.45	0.51
1:H:188:GLU:HG3	3:H:699:HOH:O	2.09	0.51
1:J:166:ARG:HD2	3:J:608:HOH:O	2.10	0.51
1:B:340:ASN:O	1:B:357:GLU:HA	2.10	0.51
1:E:313:VAL:HG12	1:E:335:SER:HA	1.91	0.51
1:L:179:GLU:CD	3:L:606:HOH:O	2.49	0.51
1:O:316:ASP:OD2	3:O:629:HOH:O	2.19	0.51
1:R:225:ALA:CA	3:R:604:HOH:O	2.58	0.51
1:U:353:TYR:HB3	3:U:672:HOH:O	2.10	0.51
1:E:68:GLN:HG3	3:E:732:HOH:O	2.10	0.51
1:I:369:ARG:NH2	3:I:646:HOH:O	2.35	0.51
1:K:334:ILE:HD12	1:K:339:LEU:HD11	1.92	0.51
1:K:403:ARG:HG2	3:K:605:HOH:O	2.09	0.51
1:M:244:GLU:HB2	3:M:783:HOH:O	2.11	0.51
1:M:357:GLU:OE2	3:M:638:HOH:O	2.19	0.51
1:D:168:GLU:HG3	3:D:616:HOH:O	2.10	0.51
1:I:105:THR:HA	3:I:954:HOH:O	2.10	0.51
1:P:175:MET:O	3:P:627:HOH:O	2.19	0.51
1:M:243:VAL:O	3:M:632:HOH:O	2.18	0.51
1:U:383:VAL:O	3:U:635:HOH:O	2.19	0.51
1:A:25:SER:OG	3:A:636:HOH:O	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:375:ASN:HB3	1:I:408:ILE:HD13	1.92	0.51
1:P:278:TRP:HZ2	1:P:358:ASN:HB3	1.75	0.51
1:Q:40:TYR:HB3	1:Q:345:PHE:CE2	2.46	0.51
1:G:116:TYR:O	1:G:119:ILE:HG12	2.11	0.51
1:M:176:HIS:CD2	1:M:177:VAL:H	2.27	0.51
1:M:178:ASN:ND2	1:M:182:GLU:O	2.44	0.51
1:B:141:MET:HG3	1:B:256:SER:HB3	1.92	0.51
1:B:243:VAL:HG12	1:B:248:ALA:HB3	1.92	0.51
1:D:190:PRO:HG2	1:D:193:PRO:HB3	1.93	0.51
1:J:265:GLU:HB2	3:J:896:HOH:O	2.10	0.51
1:L:113:ASP:OD1	1:L:232:ARG:NH1	2.42	0.51
1:N:68:GLN:HE22	1:N:108:TYR:H	1.59	0.51
1:N:187:ILE:HD12	1:N:187:ILE:C	2.31	0.51
1:B:257:CYS:HB3	3:B:840:HOH:O	2.11	0.51
1:B:287:VAL:HG22	1:K:313:VAL:HG22	1.91	0.51
1:E:116:TYR:HA	1:E:221:LEU:HD13	1.93	0.51
1:H:156:ASP:OD2	3:H:638:HOH:O	2.20	0.51
1:N:170:THR:HA	3:N:646:HOH:O	2.09	0.51
1:N:227:ASP:O	3:N:634:HOH:O	2.20	0.51
1:N:367:ILE:HA	1:N:384:ILE:HB	1.92	0.51
1:R:217:LEU:O	1:R:221:LEU:HG	2.11	0.51
1:D:72:HIS:CE1	3:D:631:HOH:O	2.61	0.50
1:K:400:ARG:HG2	3:K:611:HOH:O	2.10	0.50
1:N:177:VAL:HG21	1:N:181:ASP:HA	1.94	0.50
1:N:313:VAL:HG12	1:N:335:SER:HA	1.92	0.50
1:Q:23:ARG:NH2	3:Q:675:HOH:O	2.43	0.50
1:R:148:GLN:OE1	3:R:623:HOH:O	2.19	0.50
1:R:251:HIS:HE1	1:R:256:SER:OG	1.94	0.50
1:F:243:VAL:O	3:F:631:HOH:O	2.20	0.50
1:M:180:LYS:HD3	1:M:182:GLU:OE2	2.11	0.50
1:T:313:VAL:HG22	1:U:287:VAL:HG22	1.92	0.50
1:J:23:ARG:HB3	3:J:751:HOH:O	2.11	0.50
1:J:40:TYR:HB3	1:J:345:PHE:CE2	2.47	0.50
1:N:229:THR:O	3:N:633:HOH:O	2.19	0.50
1:R:215:LYS:HE3	3:R:664:HOH:O	2.12	0.50
1:F:175:MET:HG2	1:F:186:PHE:HD1	1.76	0.50
1:A:111:THR:HG21	3:A:966:HOH:O	2.11	0.50
1:A:113:ASP:HA	3:A:602:HOH:O	2.11	0.50
1:K:384:ILE:HG23	1:K:388:LEU:HD23	1.93	0.50
1:Q:180:LYS:HD3	1:Q:182:GLU:OE1	2.11	0.50
1:G:349[A]:ARG:NH2	3:G:611:HOH:O	2.03	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:207:MET:HE2	3:T:758:HOH:O	2.10	0.50
1:I:221:LEU:HA	1:I:224:ASP:HB3	1.92	0.50
1:J:365:VAL:HG13	3:J:622:HOH:O	2.11	0.50
1:N:101:ARG:NH2	3:N:650:HOH:O	2.30	0.50
1:R:214:THR:O	1:R:218:MET:HG2	2.11	0.50
1:M:111:THR:CG2	1:M:234:PHE:H	2.24	0.50
1:B:222:ARG:NH2	3:B:654:HOH:O	2.29	0.50
1:D:36:LYS:HE2	3:D:666:HOH:O	2.12	0.50
1:E:278:TRP:HZ2	1:E:358:ASN:HB3	1.77	0.50
1:K:217:LEU:HD23	3:K:1079:HOH:O	2.12	0.50
1:L:264:HIS:CD2	1:L:265:GLU:HG2	2.45	0.50
1:N:177:VAL:HG12	1:N:183:ILE:HA	1.93	0.50
1:O:124:PRO:HA	3:O:790:HOH:O	2.11	0.50
1:O:156:ASP:HB3	1:O:216:PHE:CE2	2.46	0.50
1:Q:123:GLU:OE2	3:Q:627:HOH:O	2.20	0.50
1:Q:400:ARG:NH1	3:Q:654:HOH:O	2.35	0.50
3:A:707:HOH:O	1:B:167:MET:HB3	2.11	0.50
1:D:56:LEU:HD21	1:K:89:ARG:HD2	1.92	0.50
1:D:157:VAL:HA	3:D:620:HOH:O	2.10	0.50
1:L:215:LYS:O	3:L:632:HOH:O	2.19	0.50
1:P:88:GLU:HG2	3:P:667:HOH:O	2.11	0.50
1:F:155:ALA:HB3	3:F:606:HOH:O	2.12	0.50
1:T:178:ASN:HB2	1:T:182:GLU:HB3	1.93	0.50
1:T:341:ARG:NE	3:T:678:HOH:O	2.43	0.50
1:B:170:THR:HG23	3:B:602:HOH:O	2.10	0.50
1:E:419:LEU:C	1:E:421:LEU:H	2.14	0.50
1:I:40:TYR:OH	2:I:502:SO4:O1	2.28	0.50
1:O:325:SER:O	1:O:341:ARG:HA	2.12	0.50
1:R:146:MET:HB2	3:R:788:HOH:O	2.10	0.50
1:E:275:ASP:OD2	1:E:406:SER:OG	2.27	0.50
1:H:146:MET:HB2	3:H:776:HOH:O	2.12	0.50
1:K:398:ALA:HB2	1:K:403:ARG:HD3	1.92	0.50
1:N:263:GLU:HB2	3:N:607:HOH:O	2.12	0.50
1:G:17:TYR:CE2	1:G:115:VAL:HG22	2.47	0.50
1:G:44:LYS:HG3	1:G:302:THR:HG21	1.93	0.50
1:T:215:LYS:HE3	3:T:856:HOH:O	2.10	0.50
1:U:76:ARG:HD2	3:U:638:HOH:O	2.12	0.50
1:U:316:ASP:OD2	3:U:637:HOH:O	2.20	0.50
1:C:229:THR:HG23	1:M:228:PRO:O	2.12	0.50
1:E:166:ARG:C	3:E:650:HOH:O	2.49	0.50
1:N:412:THR:OG1	1:N:415:MET:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:313:VAL:HG13	1:O:335:SER:HA	1.93	0.50
1:R:28:LYS:NZ	3:R:671:HOH:O	2.42	0.50
1:R:223:ARG:HG3	1:R:224:ASP:N	2.27	0.50
1:D:237:ASP:HB3	3:D:738:HOH:O	2.10	0.49
1:E:126:ALA:HB2	3:E:620:HOH:O	2.11	0.49
1:J:141:MET:HB2	1:J:253:PHE:HE1	1.77	0.49
1:L:176:HIS:N	1:L:185:ASP:O	2.43	0.49
1:P:146:MET:HB2	3:P:707:HOH:O	2.11	0.49
1:R:340:ASN:O	1:R:357:GLU:HA	2.11	0.49
1:B:17:TYR:HB2	3:B:644:HOH:O	2.12	0.49
1:B:163:GLU:OE1	1:B:252:ARG:NH1	2.45	0.49
2:B:502:SO4:O3	3:B:615:HOH:O	2.20	0.49
1:H:62:ARG:NH2	3:H:653:HOH:O	2.24	0.49
1:J:393:ASP:OD2	3:J:623:HOH:O	2.18	0.49
1:L:15:MET:HE1	1:L:122:ILE:HG23	1.94	0.49
1:L:178:ASN:ND2	1:L:182:GLU:HB2	2.27	0.49
1:F:346:THR:OG1	3:F:613:HOH:O	2.06	0.49
1:T:111:THR:HG22	1:T:234:PHE:H	1.77	0.49
1:J:346[B]:THR:CG2	3:J:745:HOH:O	2.60	0.49
1:P:188:GLU:HG3	3:P:903:HOH:O	2.12	0.49
1:Q:313:VAL:HG12	1:Q:335:SER:HA	1.92	0.49
1:F:28:LYS:HD3	1:F:402:ARG:HE	1.75	0.49
1:G:355:ARG:HD3	3:G:889:HOH:O	2.11	0.49
1:M:323:ALA:HA	1:M:339:LEU:HB2	1.93	0.49
1:T:405:GLU:OE1	1:T:405:GLU:N	2.41	0.49
1:D:33:ARG:HA	1:D:70:LYS:HE2	1.94	0.49
1:K:227:ASP:OD2	1:K:229:THR:HG22	2.12	0.49
1:L:223:ARG:HG2	1:L:223:ARG:O	2.13	0.49
1:P:89:ARG:N	3:P:667:HOH:O	2.43	0.49
1:Q:155:ALA:HA	1:Q:247:LYS:HG2	1.93	0.49
1:R:234:PHE:HA	1:R:238:ILE:HB	1.94	0.49
1:R:320:ARG:NH2	3:R:676:HOH:O	2.46	0.49
1:F:70:LYS:CE	3:F:635:HOH:O	2.58	0.49
1:B:339:LEU:HD22	1:B:356:LEU:HD12	1.93	0.49
1:C:181:ASP:OD2	3:C:642:HOH:O	2.19	0.49
1:C:200:GLU:O	3:C:643:HOH:O	2.20	0.49
1:M:23:ARG:HD2	1:M:69:TYR:CD1	2.47	0.49
1:M:233:ASP:O	1:M:237:ASP:HB2	2.13	0.49
1:T:313:VAL:HG21	1:U:287:VAL:HA	1.94	0.49
1:U:146:MET:HB2	3:U:715:HOH:O	2.12	0.49
1:C:115:VAL:HG12	1:C:221:LEU:HD22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:111:THR:CG2	1:O:234:PHE:H	2.26	0.49
1:Q:255:ASP:HB3	3:Q:835:HOH:O	2.12	0.49
1:F:421:LEU:HA	3:F:945:HOH:O	2.11	0.49
1:C:10:LEU:HG	3:C:799:HOH:O	2.12	0.49
1:H:156:ASP:CG	3:H:638:HOH:O	2.50	0.49
1:L:116:TYR:HE1	1:L:222:ARG:HD3	1.78	0.49
1:F:29:GLU:HB2	1:F:412:THR:HG21	1.95	0.49
1:G:166:ARG:CZ	3:G:628:HOH:O	2.60	0.49
1:A:287:VAL:HG22	1:P:313:VAL:HG22	1.95	0.49
1:A:320:ARG:O	3:A:634:HOH:O	2.18	0.49
1:D:162:LEU:HG	1:D:207:MET:HG2	1.94	0.49
1:L:178:ASN:O	3:L:634:HOH:O	2.20	0.49
1:N:187:ILE:HD13	1:N:189:LYS:HA	1.94	0.49
1:Q:107:TRP:CD1	1:Q:107:TRP:N	2.78	0.49
1:R:32:ASP:OD1	3:R:624:HOH:O	2.19	0.49
1:A:111:THR:HG23	1:A:234:PHE:HD2	1.78	0.49
1:B:313:VAL:HG21	1:K:287:VAL:HA	1.95	0.49
1:H:403:ARG:HD3	3:H:855:HOH:O	2.11	0.49
1:N:100:GLN:HB2	1:N:103:SER:HB2	1.93	0.49
1:F:40:TYR:HB3	1:F:345:PHE:CE2	2.48	0.49
1:F:178:ASN:HD21	1:F:182:GLU:CB	2.24	0.49
1:F:233:ASP:CG	3:F:616:HOH:O	2.48	0.49
1:F:401:PHE:O	3:F:608:HOH:O	2.19	0.49
1:G:182:GLU:CD	3:G:643:HOH:O	2.50	0.49
1:M:207:MET:HE2	1:M:253:PHE:HB2	1.93	0.49
1:M:316:ASP:HB2	1:M:318:ASP:OD1	2.12	0.49
1:A:13:ASP:HB3	1:A:128:GLU:HB2	1.94	0.49
1:A:174:VAL:HG11	1:A:194:PRO:HD2	1.95	0.49
1:C:119:ILE:O	3:C:644:HOH:O	2.20	0.49
1:J:104:GLU:HA	1:J:105:THR:HA	1.56	0.49
1:Q:240:PRO:O	1:Q:243:VAL:HG12	2.13	0.49
1:F:215:LYS:CE	1:F:215:LYS:HA	2.43	0.49
1:A:163:GLU:OE2	3:A:637:HOH:O	2.20	0.48
1:D:86:ARG:N	3:D:624:HOH:O	2.37	0.48
1:H:318:ASP:HB2	1:H:353:TYR:HE1	1.78	0.48
1:P:334:ILE:HD12	1:P:339:LEU:HD11	1.94	0.48
1:R:119:ILE:HG12	1:R:218:MET:HE3	1.95	0.48
1:G:149:GLN:HG3	3:G:999:HOH:O	2.12	0.48
1:E:236:LYS:HB3	3:E:995:HOH:O	2.13	0.48
1:H:223:ARG:N	3:H:704:HOH:O	2.47	0.48
1:L:165:PRO:HA	1:L:202:PHE:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:13:ASP:OD2	3:G:631:HOH:O	2.19	0.48
1:A:111:THR:CG2	1:A:234:PHE:H	2.26	0.48
1:D:233:ASP:O	1:D:237:ASP:HB2	2.12	0.48
1:H:29:GLU:HB3	1:H:412:THR:HG21	1.96	0.48
1:H:189:LYS:NZ	3:H:699:HOH:O	2.45	0.48
1:H:311:LYS:NZ	3:G:618:HOH:O	2.46	0.48
1:L:111:THR:CG2	1:L:234:PHE:H	2.27	0.48
1:N:189:LYS:HE2	1:N:193:PRO:HD2	1.95	0.48
1:G:379:ASP:HB2	1:G:412:THR:HG22	1.95	0.48
1:M:116:TYR:HD2	1:M:117:GLN:HE21	1.61	0.48
1:M:212:PHE:CD2	1:M:217:LEU:HD13	2.49	0.48
1:A:222:ARG:NH1	3:A:635:HOH:O	2.19	0.48
1:A:313:VAL:HG21	1:P:287:VAL:HA	1.94	0.48
1:B:406:SER:O	3:B:638:HOH:O	2.20	0.48
1:H:111:THR:O	3:H:640:HOH:O	2.20	0.48
1:H:296:LYS:HE3	3:G:778:HOH:O	2.12	0.48
1:N:176:HIS:CD2	1:N:204:LEU:H	2.31	0.48
1:Q:350:ALA:HA	1:Q:367:ILE:HB	1.96	0.48
1:R:350:ALA:HA	1:R:367:ILE:HB	1.96	0.48
1:M:62:ARG:HH21	1:M:92:SER:HB3	1.78	0.48
1:A:357:GLU:O	1:A:374:SER:HA	2.14	0.48
1:C:223:ARG:NH1	3:C:612:HOH:O	2.04	0.48
1:E:8:GLN:NE2	3:E:688:HOH:O	2.46	0.48
1:I:70:LYS:HD3	3:I:857:HOH:O	2.12	0.48
1:J:47:ILE:HG12	1:J:138:ILE:HD11	1.95	0.48
1:Q:86:ARG:NH2	1:U:305:GLU:HG2	2.29	0.48
1:Q:126:ALA:HA	3:Q:988:HOH:O	2.13	0.48
1:R:419:LEU:HG	1:R:421:LEU:N	2.27	0.48
1:F:56:LEU:HD21	1:U:89:ARG:HD2	1.95	0.48
1:M:379:ASP:OD2	3:M:639:HOH:O	2.20	0.48
1:B:101:ARG:HD3	1:D:75:ILE:HB	1.94	0.48
1:B:400:ARG:CD	1:B:419:LEU:HD21	2.44	0.48
1:E:421:LEU:HG	3:E:648:HOH:O	2.14	0.48
1:H:285:THR:HG22	1:H:327:VAL:HG22	1.94	0.48
1:H:372:GLN:NE2	3:H:605:HOH:O	1.89	0.48
1:J:141:MET:HB3	3:J:712:HOH:O	2.13	0.48
1:Q:29:GLU:HB3	1:Q:412:THR:HG21	1.95	0.48
1:F:156:ASP:HB3	1:F:216:PHE:CZ	2.48	0.48
1:A:402:ARG:HB3	1:A:410:LEU:HB3	1.94	0.48
1:E:56:LEU:HD21	1:P:89:ARG:HD2	1.95	0.48
1:E:402:ARG:NH2	3:E:692:HOH:O	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:ARG:HG3	3:H:825:HOH:O	2.13	0.48
1:J:62:ARG:HG3	3:J:857:HOH:O	2.14	0.48
1:J:346[B]:THR:HG23	3:J:745:HOH:O	2.12	0.48
1:O:176:HIS:ND1	3:O:624:HOH:O	2.17	0.48
1:P:68:GLN:OE1	1:P:108:TYR:HB2	2.13	0.48
1:P:170:THR:HG23	3:P:606:HOH:O	2.14	0.48
1:H:108:TYR:O	1:H:110:GLY:N	2.45	0.48
1:N:108:TYR:O	1:N:110:GLY:N	2.47	0.48
1:N:187:ILE:HG23	3:N:779:HOH:O	2.14	0.48
1:Q:340:ASN:O	1:Q:357:GLU:HA	2.14	0.48
1:M:231:SER:OG	1:M:236:LYS:HD2	2.13	0.48
1:B:172:PHE:HA	3:B:729:HOH:O	2.12	0.48
1:L:393:ASP:HB2	3:L:702:HOH:O	2.13	0.48
1:O:223:ARG:NH2	3:O:633:HOH:O	2.23	0.48
1:T:103:SER:O	3:T:605:HOH:O	2.20	0.48
1:U:402:ARG:NH2	3:U:678:HOH:O	2.45	0.48
1:D:44:LYS:HE3	3:D:660:HOH:O	2.14	0.48
1:H:223:ARG:NH2	3:H:705:HOH:O	2.47	0.48
1:I:275:ASP:HB2	3:I:792:HOH:O	2.13	0.48
1:K:185:ASP:OD1	3:K:635:HOH:O	2.19	0.48
1:M:396:LEU:HG	1:M:400:ARG:HD2	1.95	0.48
1:T:85:PHE:CD2	1:T:91:GLU:HB3	2.48	0.48
1:T:98:ALA:O	1:T:103:SER:N	2.31	0.48
1:K:251:HIS:HE1	1:K:256:SER:OG	1.97	0.47
1:L:170:THR:O	1:L:189:LYS:HE2	2.14	0.47
1:T:40:TYR:HB3	1:T:345:PHE:CE2	2.49	0.47
1:T:199:ASN:HB3	3:T:792:HOH:O	2.13	0.47
1:T:369:ARG:NH2	2:T:502:SO4:O2	2.46	0.47
1:B:175:MET:HB3	1:B:183:ILE:HG21	1.96	0.47
1:N:403:ARG:HB3	3:N:816:HOH:O	2.13	0.47
1:Q:36:LYS:HD3	1:Q:136:ASP:HB2	1.96	0.47
1:R:176:HIS:HD2	1:R:177:VAL:H	1.62	0.47
1:G:404:THR:CG2	1:G:408:ILE:N	2.77	0.47
1:T:111:THR:HG22	1:T:233:ASP:HA	1.96	0.47
1:A:200:GLU:HG2	1:A:201:GLY:H	1.78	0.47
1:A:313:VAL:HG12	1:A:335:SER:HA	1.95	0.47
1:B:28:LYS:HB3	1:B:29:GLU:H	1.27	0.47
1:J:238:ILE:O	1:J:242:ILE:HD13	2.14	0.47
1:L:178:ASN:HD21	1:L:182:GLU:HB2	1.78	0.47
1:P:214:THR:O	1:P:218:MET:HG2	2.13	0.47
1:Q:178:ASN:O	3:Q:630:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:223:ARG:HE	1:R:238:ILE:HG12	1.80	0.47
1:F:72:HIS:HB2	1:T:100:GLN:HB3	1.96	0.47
1:F:218:MET:HB3	3:F:626:HOH:O	2.14	0.47
1:T:44:LYS:HE2	3:T:839:HOH:O	2.14	0.47
1:T:100:GLN:NE2	3:T:689:HOH:O	2.46	0.47
1:B:40:TYR:HB3	1:B:345:PHE:CE2	2.49	0.47
1:D:341:ARG:HB3	1:D:358:ASN:HD22	1.80	0.47
1:H:240:PRO:C	3:H:607:HOH:O	2.45	0.47
1:J:233:ASP:N	3:J:636:HOH:O	2.30	0.47
1:J:394:PRO:HB3	1:J:403:ARG:CZ	2.44	0.47
1:M:28:LYS:HG3	1:M:402:ARG:CZ	2.44	0.47
1:C:23:ARG:NH2	1:C:32:ASP:O	2.47	0.47
1:D:316:ASP:C	3:D:603:HOH:O	2.52	0.47
1:E:224:ASP:HB2	1:E:238:ILE:HD11	1.96	0.47
1:H:341:ARG:NH2	3:H:614:HOH:O	2.02	0.47
1:G:176:HIS:HE1	3:G:863:HOH:O	1.96	0.47
1:G:339:LEU:HD22	1:G:356:LEU:HD12	1.95	0.47
1:T:159:ILE:HG21	1:T:175:MET:HE1	1.97	0.47
1:U:162:LEU:HG	1:U:207:MET:HG2	1.97	0.47
1:A:162:LEU:HG	1:A:207:MET:HG2	1.97	0.47
1:C:241:TYR:HB2	3:C:624:HOH:O	2.14	0.47
1:J:70:LYS:O	3:J:625:HOH:O	2.20	0.47
1:J:161:CYS:SG	1:J:175:MET:HG3	2.54	0.47
1:J:341:ARG:NH2	3:J:666:HOH:O	2.45	0.47
1:N:174:VAL:HG13	1:N:176:HIS:HE1	1.75	0.47
1:P:401:PHE:HB2	3:P:616:HOH:O	2.15	0.47
1:R:265:GLU:OE1	3:R:626:HOH:O	2.20	0.47
1:U:116:TYR:HA	1:U:119:ILE:HD11	1.97	0.47
1:A:174:VAL:HG21	1:A:193:PRO:HB3	1.96	0.47
1:A:234:PHE:HA	1:A:238:ILE:HB	1.97	0.47
1:B:166:ARG:HG3	1:B:201:GLY:C	2.35	0.47
1:C:119:ILE:HG12	3:C:602:HOH:O	2.14	0.47
1:D:278:TRP:CE2	1:D:282:ILE:HG13	2.50	0.47
1:D:341:ARG:HD3	1:D:358:ASN:ND2	2.29	0.47
1:H:110:GLY:N	3:H:706:HOH:O	2.47	0.47
1:I:69:TYR:CZ	1:I:70:LYS:HG2	2.49	0.47
1:L:400:ARG:HD3	1:L:421:LEU:O	2.15	0.47
1:Q:15:MET:HB3	3:Q:612:HOH:O	2.14	0.47
1:Q:54:ASN:N	3:Q:610:HOH:O	2.47	0.47
1:Q:119:ILE:HD12	1:Q:218:MET:CE	2.44	0.47
1:R:105:THR:HG22	1:R:106:GLN:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:315:ASP:OD1	1:G:320:ARG:NE	2.48	0.47
1:M:227:ASP:OD1	1:M:229:THR:OG1	2.31	0.47
1:T:26:ARG:NH1	3:T:646:HOH:O	2.36	0.47
1:E:116:TYR:O	1:E:119:ILE:HG13	2.15	0.47
1:I:187:ILE:HG21	1:I:190:PRO:HB3	1.97	0.47
3:I:734:HOH:O	1:J:166:ARG:HD3	2.15	0.47
1:O:411:ILE:HA	1:O:415:MET:HE3	1.97	0.47
1:Q:86:ARG:HH21	1:U:305:GLU:HG2	1.79	0.47
1:F:123:GLU:OE2	1:F:222:ARG:NH2	2.46	0.47
1:G:140:LYS:NZ	3:G:613:HOH:O	2.03	0.47
1:G:176:HIS:O	3:G:622:HOH:O	2.21	0.47
1:B:145:TYR:CZ	1:M:7:VAL:HG11	2.48	0.47
1:C:333:ILE:HB	1:C:349:ARG:HD3	1.96	0.47
1:D:218:MET:HG3	3:D:949:HOH:O	2.14	0.47
1:E:32:ASP:O	1:E:70:LYS:HD2	2.14	0.47
1:E:40:TYR:HB3	1:E:345:PHE:CE2	2.50	0.47
1:H:370:HIS:O	3:H:641:HOH:O	2.20	0.47
1:K:111:THR:HG22	1:K:233:ASP:HA	1.97	0.47
1:N:223:ARG:NH2	3:N:665:HOH:O	2.37	0.47
1:N:233:ASP:OD1	1:N:234:PHE:N	2.48	0.47
1:P:340:ASN:O	1:P:357:GLU:HA	2.15	0.47
1:R:40:TYR:HB3	1:R:345:PHE:CE2	2.49	0.47
1:M:398:ALA:HB2	1:M:403:ARG:HD3	1.97	0.47
1:U:384:ILE:HG23	1:U:388:LEU:HD23	1.96	0.47
1:A:61:ARG:NH1	3:A:684:HOH:O	2.49	0.47
1:A:85:PHE:HD2	1:A:91:GLU:HB3	1.79	0.47
1:E:239:ILE:HA	3:E:606:HOH:O	2.15	0.47
1:K:38:ALA:HB2	1:K:74:LEU:HB2	1.97	0.47
1:L:223:ARG:NH1	3:L:701:HOH:O	2.48	0.47
1:P:349:ARG:NH1	3:P:604:HOH:O	1.90	0.47
1:Q:156:ASP:HB3	1:Q:216:PHE:CZ	2.50	0.47
1:R:8:GLN:HA	3:R:773:HOH:O	2.15	0.47
1:M:253:PHE:N	3:M:622:HOH:O	2.48	0.47
1:U:159:ILE:HD11	1:U:239:ILE:HD12	1.96	0.47
1:A:79:GLN:HG2	1:E:79:GLN:HG2	1.97	0.46
1:D:119:ILE:HD11	1:D:221:LEU:HD11	1.96	0.46
1:D:233:ASP:HB2	1:D:236:LYS:HG2	1.98	0.46
1:H:232:ARG:HD3	3:H:706:HOH:O	2.14	0.46
1:I:214:THR:O	1:I:218:MET:HG2	2.14	0.46
1:N:186:PHE:HZ	3:N:1020:HOH:O	1.99	0.46
1:P:185:ASP:O	3:P:611:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:278:TRP:HZ2	1:R:358:ASN:HB3	1.80	0.46
1:T:405:GLU:CD	1:T:405:GLU:H	2.11	0.46
1:U:367:ILE:HA	1:U:384:ILE:HB	1.98	0.46
1:D:213:HIS:HD2	3:D:668:HOH:O	1.98	0.46
1:I:282:ILE:HG23	3:I:625:HOH:O	2.15	0.46
1:O:19:LEU:HD13	1:O:111:THR:OG1	2.16	0.46
1:R:85:PHE:HD2	1:R:91:GLU:HB3	1.79	0.46
1:R:261:ASP:O	3:R:627:HOH:O	2.21	0.46
1:F:12:ARG:NE	3:F:674:HOH:O	2.47	0.46
1:F:113:ASP:HB2	1:F:232:ARG:HB3	1.97	0.46
1:F:316:ASP:O	3:F:633:HOH:O	2.20	0.46
1:B:419:LEU:HD23	1:B:419:LEU:HA	1.46	0.46
1:D:188:GLU:HG3	1:D:189:LYS:HG3	1.97	0.46
1:E:89:ARG:HD2	1:P:56:LEU:HD21	1.97	0.46
1:P:231:SER:OG	1:P:237:ASP:OD1	2.33	0.46
1:P:283:ASP:HB3	3:P:804:HOH:O	2.16	0.46
1:M:215:LYS:HZ2	1:M:218:MET:CG	2.27	0.46
1:T:196:ILE:HG21	1:T:252:ARG:HH22	1.80	0.46
1:B:28:LYS:CD	1:B:402:ARG:HE	2.16	0.46
1:B:157:VAL:HG12	1:B:242:ILE:HG21	1.97	0.46
1:D:28:LYS:HD2	1:D:402:ARG:NH1	2.30	0.46
1:H:187:ILE:HD13	3:H:1105:HOH:O	2.16	0.46
1:J:175:MET:HE2	1:J:186:PHE:CD1	2.51	0.46
1:K:177:VAL:HG12	1:K:183:ILE:HG12	1.98	0.46
1:Q:416:ILE:HD13	1:Q:419:LEU:HD22	1.96	0.46
1:F:83:ASP:N	3:F:663:HOH:O	2.47	0.46
1:G:404:THR:HG21	3:G:612:HOH:O	2.14	0.46
1:M:124:PRO:HG3	3:M:993:HOH:O	2.14	0.46
1:U:175:MET:SD	1:U:183:ILE:HD13	2.55	0.46
1:U:275:ASP:HB2	3:U:615:HOH:O	2.15	0.46
1:B:334:ILE:HD12	1:B:339:LEU:HD11	1.96	0.46
1:D:398:ALA:C	3:D:604:HOH:O	2.53	0.46
1:H:187:ILE:CD1	1:H:194:PRO:HG3	2.45	0.46
1:J:325:SER:O	1:J:341:ARG:HA	2.16	0.46
1:L:397:ASP:HB3	1:L:409:CYS:SG	2.55	0.46
1:N:197:PRO:HG3	3:N:898:HOH:O	2.15	0.46
1:O:122:ILE:HG23	3:O:1101:HOH:O	2.15	0.46
1:P:138:ILE:HG22	1:P:267:TYR:HE1	1.80	0.46
1:R:314:HIS:CG	1:R:319:ARG:HD2	2.50	0.46
1:F:83:ASP:HB3	3:F:663:HOH:O	2.15	0.46
1:M:44:LYS:HG3	1:M:45:ALA:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:VAL:HG21	3:A:614:HOH:O	2.15	0.46
1:A:322:SER:HB3	3:A:634:HOH:O	2.16	0.46
1:B:287:VAL:HA	1:K:313:VAL:HG21	1.98	0.46
1:B:319:ARG:HB3	1:B:353:TYR:CE1	2.50	0.46
1:C:275:ASP:OD1	3:C:645:HOH:O	2.20	0.46
1:I:32:ASP:OD1	3:I:620:HOH:O	2.20	0.46
1:N:186:PHE:CD2	1:N:240:PRO:HG3	2.50	0.46
1:P:28:LYS:HG2	1:P:402:ARG:CZ	2.45	0.46
1:Q:183:ILE:O	1:Q:243:VAL:HG23	2.15	0.46
1:A:110:GLY:H	1:A:113:ASP:HB3	1.80	0.46
1:H:40:TYR:HB3	1:H:345:PHE:CE2	2.51	0.46
1:P:40:TYR:HB3	1:P:345:PHE:CE2	2.50	0.46
1:P:141:MET:HB3	1:P:141:MET:HE2	1.80	0.46
1:P:355:ARG:HD2	3:P:969:HOH:O	2.16	0.46
1:P:366:LYS:NZ	3:P:651:HOH:O	2.34	0.46
1:Q:311:LYS:NZ	3:Q:648:HOH:O	2.31	0.46
1:F:178:ASN:ND2	1:F:178:ASN:H	2.14	0.46
1:M:196:ILE:HD13	1:M:252:ARG:NH2	2.31	0.46
1:T:259:ARG:NH2	1:T:263:GLU:O	2.48	0.46
1:J:218:MET:O	1:J:222:ARG:HG3	2.16	0.46
1:K:68:GLN:HB3	3:K:890:HOH:O	2.16	0.46
1:N:167:MET:HE3	3:N:935:HOH:O	2.16	0.46
1:N:186:PHE:HD2	1:N:240:PRO:HG3	1.81	0.46
1:N:259:ARG:CZ	3:N:675:HOH:O	2.63	0.46
1:Q:150:HIS:CD2	3:Q:727:HOH:O	2.68	0.46
1:B:47:ILE:HG12	1:B:138:ILE:HD11	1.98	0.46
1:D:370:HIS:HE1	3:D:852:HOH:O	1.99	0.46
1:K:116:TYR:HA	1:K:221:LEU:HD21	1.97	0.46
1:K:252:ARG:NH2	3:K:687:HOH:O	2.49	0.46
1:N:113:ASP:HA	1:N:116:TYR:HB3	1.98	0.46
1:Q:23:ARG:NH2	3:Q:616:HOH:O	2.09	0.46
1:Q:179:GLU:C	1:Q:181:ASP:H	2.18	0.46
1:F:187:ILE:HA	3:F:789:HOH:O	2.15	0.46
1:M:307:THR:HB	1:M:331:ASP:HB2	1.97	0.46
1:T:166:ARG:NH1	1:T:192:ASP:OD1	2.26	0.46
1:U:166:ARG:HG3	1:U:201:GLY:C	2.36	0.46
1:A:214:THR:O	1:A:218:MET:HG2	2.16	0.46
1:E:177:VAL:CG2	1:E:181:ASP:HA	2.46	0.46
1:I:36:LYS:NZ	1:I:270:ASP:O	2.31	0.46
1:I:260:SER:HB3	1:I:263:GLU:HG3	1.98	0.46
1:J:75:ILE:HG23	1:J:95:ILE:HG21	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:269:ARG:NH1	3:L:611:HOH:O	2.07	0.46
1:N:23:ARG:HH21	1:N:69:TYR:HB3	1.80	0.46
1:P:111:THR:HG22	1:P:233:ASP:HA	1.98	0.46
1:C:88:GLU:O	3:C:646:HOH:O	2.20	0.45
1:D:215:LYS:N	3:D:615:HOH:O	2.49	0.45
1:H:166:ARG:O	1:H:193:PRO:HG2	2.15	0.45
1:N:106:GLN:HB3	1:N:107:TRP:H	1.61	0.45
1:R:35:ALA:HB2	1:R:69:TYR:O	2.16	0.45
1:G:283:ASP:HB3	3:G:810:HOH:O	2.16	0.45
1:M:111:THR:HG22	1:M:234:PHE:H	1.81	0.45
1:U:61:ARG:HA	3:U:987:HOH:O	2.16	0.45
1:B:100:GLN:C	1:B:102:VAL:N	2.69	0.45
1:D:116:TYR:CB	1:D:221:LEU:CD1	2.89	0.45
1:E:340:ASN:O	1:E:357:GLU:HA	2.16	0.45
1:K:419:LEU:HB3	3:K:611:HOH:O	2.16	0.45
1:N:234:PHE:HA	1:N:238:ILE:CG1	2.46	0.45
1:O:34:ARG:NH1	2:O:502:SO4:O4	2.31	0.45
1:O:242:ILE:HA	3:O:727:HOH:O	2.16	0.45
1:Q:215:LYS:NZ	3:Q:632:HOH:O	2.22	0.45
1:R:215:LYS:NZ	3:R:684:HOH:O	2.50	0.45
1:T:107:TRP:HD1	3:T:952:HOH:O	1.99	0.45
1:T:294:TYR:OH	1:U:311:LYS:HB2	2.17	0.45
1:A:392:GLU:OE2	1:B:200:GLU:N	2.24	0.45
1:F:278:TRP:CE2	1:F:282:ILE:HG13	2.51	0.45
1:T:106:GLN:HB3	3:T:952:HOH:O	2.16	0.45
1:A:235:GLY:HA2	3:A:874:HOH:O	2.16	0.45
1:B:95:ILE:HB	1:B:101:ARG:HH22	1.82	0.45
1:C:176:HIS:ND1	3:C:648:HOH:O	2.23	0.45
1:E:393:ASP:HB3	1:E:396:LEU:HB3	1.97	0.45
1:I:183:ILE:HG13	3:I:617:HOH:O	2.16	0.45
1:J:403:ARG:NH1	3:J:667:HOH:O	2.46	0.45
1:N:23:ARG:CZ	3:N:628:HOH:O	2.58	0.45
1:N:234:PHE:HA	1:N:238:ILE:HG13	1.98	0.45
1:Q:69:TYR:HB2	3:Q:651:HOH:O	2.17	0.45
1:D:137:HIS:N	3:D:619:HOH:O	2.32	0.45
1:H:44:LYS:HE3	1:G:307:THR:O	2.16	0.45
1:I:40:TYR:HB3	1:I:345:PHE:CE2	2.51	0.45
1:I:375:ASN:ND2	3:I:679:HOH:O	2.49	0.45
1:J:9:PRO:HG2	1:J:12:ARG:HG3	1.99	0.45
1:J:86:ARG:NH2	3:J:642:HOH:O	2.35	0.45
1:L:351:ASN:HB3	2:L:502:SO4:O3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:316:ASP:HB3	3:O:610:HOH:O	2.15	0.45
1:F:89:ARG:HD2	1:U:56:LEU:HD21	1.98	0.45
1:F:236:LYS:NZ	3:F:616:HOH:O	2.49	0.45
1:T:354:SER:O	1:T:355:ARG:HD3	2.15	0.45
1:H:225:ALA:N	3:H:704:HOH:O	2.50	0.45
1:K:28:LYS:HG2	1:K:402:ARG:CZ	2.46	0.45
1:K:111:THR:CG2	1:K:234:PHE:H	2.29	0.45
1:K:228:PRO:HB3	3:K:1088:HOH:O	2.16	0.45
1:K:234:PHE:HA	1:K:238:ILE:HB	1.99	0.45
1:L:34:ARG:HD3	2:L:501:SO4:O3	2.17	0.45
1:P:176:HIS:HB3	1:P:194:PRO:HB2	1.98	0.45
1:Q:146:MET:HB2	3:Q:750:HOH:O	2.17	0.45
1:R:222:ARG:NE	3:R:639:HOH:O	2.45	0.45
1:R:357:GLU:O	1:R:374:SER:HA	2.16	0.45
1:F:119:ILE:HD12	1:F:218:MET:CE	2.47	0.45
1:A:40:TYR:HB3	1:A:345:PHE:CE2	2.51	0.45
1:H:402:ARG:HB3	1:H:410:LEU:HB3	1.99	0.45
1:J:176:HIS:O	1:J:184:ILE:N	2.45	0.45
1:K:32:ASP:OD2	3:K:639:HOH:O	2.21	0.45
1:K:246:GLY:O	3:K:637:HOH:O	2.21	0.45
1:N:68:GLN:HE22	1:N:108:TYR:N	2.14	0.45
1:R:47:ILE:HG12	1:R:138:ILE:HD11	1.99	0.45
1:M:119:ILE:HD13	1:M:218:MET:HE2	1.99	0.45
1:T:23:ARG:HA	1:T:69:TYR:CD2	2.52	0.45
1:D:331:ASP:O	1:D:349:ARG:NH1	2.45	0.45
1:I:157:VAL:HG22	3:I:632:HOH:O	2.17	0.45
1:I:350:ALA:HA	1:I:367:ILE:HB	1.98	0.45
1:K:97:PRO:O	1:K:99:SER:N	2.50	0.45
1:N:80:ARG:NE	3:N:706:HOH:O	2.50	0.45
1:O:223:ARG:NH2	3:O:676:HOH:O	2.49	0.45
1:P:183:ILE:O	1:P:243:VAL:HG23	2.17	0.45
1:P:218:MET:O	1:P:222:ARG:HG3	2.17	0.45
1:Q:9:PRO:HB3	1:T:9:PRO:HB3	1.98	0.45
1:F:119:ILE:HB	3:F:806:HOH:O	2.16	0.45
1:U:238:ILE:O	1:U:242:ILE:HG12	2.17	0.45
1:D:135:GLY:C	3:D:619:HOH:O	2.52	0.45
1:H:244:GLU:N	3:H:602:HOH:O	2.49	0.45
1:I:19:LEU:HD13	1:I:111:THR:OG1	2.17	0.45
1:I:358:ASN:HD22	1:I:375:ASN:HD21	1.63	0.45
1:J:34:ARG:NH2	2:J:502:SO4:O4	2.48	0.45
1:L:157:VAL:HG13	1:L:159:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:373:LEU:HD12	1:R:378:ILE:HD11	1.99	0.45
1:G:340:ASN:O	1:G:357:GLU:HA	2.16	0.45
1:G:404:THR:HG23	1:G:407:GLY:N	2.31	0.45
1:T:339:LEU:HD22	1:T:356:LEU:HD12	1.99	0.45
1:C:251:HIS:NE2	1:C:256:SER:OG	2.34	0.45
1:D:325:SER:O	1:D:341:ARG:HA	2.17	0.45
1:H:106:GLN:HG3	1:H:107:TRP:H	1.82	0.45
1:L:98:ALA:HB1	1:L:107:TRP:HA	1.99	0.45
1:N:221:LEU:CD2	1:N:238:ILE:HG21	2.47	0.45
1:N:259:ARG:NH1	3:N:675:HOH:O	2.50	0.45
1:O:40:TYR:HB3	1:O:345:PHE:CE2	2.52	0.45
1:O:140:LYS:NZ	3:O:683:HOH:O	2.50	0.45
1:P:267:TYR:CZ	1:P:269:ARG:HG3	2.52	0.45
1:F:109:GLU:CD	3:F:614:HOH:O	2.53	0.45
1:F:195:GLY:HA3	1:F:200:GLU:HG3	1.99	0.45
1:F:227:ASP:OD1	1:F:229:THR:HB	2.17	0.45
1:M:128:GLU:OE2	3:M:640:HOH:O	2.21	0.45
1:M:331:ASP:C	3:M:637:HOH:O	2.54	0.45
1:T:103:SER:C	1:T:105:THR:H	2.21	0.45
1:T:233:ASP:HB3	3:T:726:HOH:O	2.16	0.45
1:C:34:ARG:HG2	1:C:38:ALA:HB3	2.00	0.44
1:D:169:ALA:N	3:D:616:HOH:O	2.49	0.44
1:H:251:HIS:NE2	1:H:256:SER:OG	2.33	0.44
1:O:183:ILE:HD12	1:O:248:ALA:HB1	1.99	0.44
1:R:166:ARG:HD2	1:R:200:GLU:O	2.17	0.44
1:R:223:ARG:HD2	1:R:238:ILE:HD11	1.99	0.44
1:F:29:GLU:HG2	1:F:32:ASP:OD2	2.18	0.44
1:F:215:LYS:HG2	3:F:1045:HOH:O	2.17	0.44
1:G:40:TYR:HB3	1:G:345:PHE:CE2	2.52	0.44
1:G:145:TYR:HB2	1:G:256:SER:HB3	1.98	0.44
1:T:87:PRO:HA	1:T:91:GLU:O	2.17	0.44
1:B:155:ALA:HA	1:B:247:LYS:HD3	2.00	0.44
1:B:185:ASP:HA	3:B:779:HOH:O	2.17	0.44
1:E:307:THR:HB	1:E:331:ASP:HB2	1.99	0.44
1:H:26:ARG:NH1	3:H:714:HOH:O	2.49	0.44
1:H:178:ASN:OD1	1:H:179:GLU:N	2.51	0.44
1:H:320:ARG:O	3:H:636:HOH:O	2.19	0.44
1:F:176:HIS:HD2	1:F:177:VAL:N	2.16	0.44
1:M:161:CYS:SG	3:M:1100:HOH:O	2.50	0.44
1:C:238:ILE:O	1:C:242:ILE:HG13	2.18	0.44
1:E:261:ASP:HB2	3:E:651:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:83:ASP:OD2	3:J:626:HOH:O	2.21	0.44
1:K:232:ARG:N	1:K:237:ASP:OD2	2.50	0.44
1:N:156:ASP:HB3	1:N:216:PHE:CZ	2.52	0.44
1:T:267:TYR:CD1	1:T:291:LEU:HD13	2.53	0.44
1:U:282:ILE:HD11	1:U:341:ARG:O	2.18	0.44
1:U:320:ARG:NH2	3:U:692:HOH:O	2.49	0.44
1:C:133:LEU:HD23	1:C:209:ILE:HG23	1.99	0.44
1:C:211:VAL:HG13	3:C:709:HOH:O	2.17	0.44
1:E:207:MET:HA	3:E:668:HOH:O	2.18	0.44
1:I:234:PHE:HA	1:I:238:ILE:HB	1.98	0.44
1:K:33:ARG:HA	1:K:70:LYS:HE2	2.00	0.44
1:K:200:GLU:OE1	3:K:638:HOH:O	2.21	0.44
1:L:185:ASP:HA	3:L:801:HOH:O	2.17	0.44
1:G:166:ARG:NE	3:G:628:HOH:O	2.51	0.44
1:T:133:LEU:HD23	1:T:209:ILE:HG23	1.99	0.44
1:T:387:GLY:HA3	3:T:708:HOH:O	2.15	0.44
1:U:215:LYS:O	1:U:219:GLU:HG3	2.18	0.44
1:A:175:MET:HG3	1:A:183:ILE:HG23	1.98	0.44
1:B:48:ILE:HD13	1:B:78:LEU:HD21	2.00	0.44
1:C:319:ARG:HB3	1:C:353:TYR:CE1	2.52	0.44
1:H:7:VAL:N	3:H:715:HOH:O	2.49	0.44
1:L:19:LEU:HD13	1:L:111:THR:OG1	2.17	0.44
1:L:319:ARG:HB3	1:L:353:TYR:CE1	2.52	0.44
1:N:48:ILE:HD13	1:N:78:LEU:HD21	1.98	0.44
1:N:70:LYS:HE2	1:N:70:LYS:HB3	1.72	0.44
1:N:158:THR:HA	1:N:249:VAL:O	2.18	0.44
1:N:340:ASN:O	1:N:357:GLU:HA	2.17	0.44
1:O:106:GLN:HG2	1:O:107:TRP:H	1.83	0.44
1:P:217:LEU:O	1:P:221:LEU:HD13	2.17	0.44
1:U:366:LYS:HD3	1:U:383:VAL:HG13	2.00	0.44
1:B:170:THR:N	3:B:602:HOH:O	2.50	0.44
1:E:340:ASN:HB3	1:E:357:GLU:HG2	2.00	0.44
1:H:40:TYR:OH	3:H:627:HOH:O	2.14	0.44
1:I:260:SER:N	3:I:683:HOH:O	2.51	0.44
1:J:214:THR:O	1:J:218:MET:HG2	2.18	0.44
1:O:412:THR:OG1	1:O:415:MET:HG3	2.17	0.44
1:F:29:GLU:HA	1:F:32:ASP:CG	2.38	0.44
1:F:314:HIS:HE1	3:F:669:HOH:O	2.00	0.44
1:T:10:LEU:HD22	1:T:129:TYR:OH	2.18	0.44
1:T:307:THR:HB	1:T:331:ASP:HB2	1.98	0.44
1:A:275:ASP:OD1	1:A:408:ILE:HD13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:HIS:HE1	3:B:979:HOH:O	2.00	0.44
1:B:311:LYS:HG3	1:K:327:VAL:HG22	2.00	0.44
1:D:265:GLU:HB2	3:D:869:HOH:O	2.18	0.44
1:E:22:GLY:N	3:E:684:HOH:O	2.45	0.44
1:E:349:ARG:HB2	1:E:366:LYS:HG3	2.00	0.44
1:I:313:VAL:HG22	1:I:314:HIS:N	2.32	0.44
1:J:80:ARG:NH2	3:J:660:HOH:O	2.43	0.44
1:K:225:ALA:HA	1:K:232:ARG:HD3	2.00	0.44
1:L:44:LYS:HE2	1:L:329:SER:HB3	1.99	0.44
1:L:69:TYR:HB2	3:L:679:HOH:O	2.18	0.44
1:N:76:ARG:HG3	1:N:80:ARG:NH1	2.33	0.44
1:R:278:TRP:CE2	1:R:282:ILE:HG13	2.53	0.44
1:F:398:ALA:C	3:F:608:HOH:O	2.55	0.44
1:T:395:GLU:OE1	3:T:636:HOH:O	2.21	0.44
1:U:86:ARG:O	1:U:91:GLU:HG2	2.17	0.44
1:U:212:PHE:CD1	1:U:217:LEU:HD13	2.52	0.44
1:A:61:ARG:HB3	1:A:91:GLU:HG2	2.00	0.44
1:B:346[B]:THR:HG22	3:B:797:HOH:O	2.18	0.44
1:B:400:ARG:HD3	1:B:419:LEU:HD21	1.99	0.44
1:D:40:TYR:OH	1:D:46:ARG:NH2	2.51	0.44
1:J:25:SER:HA	3:J:751:HOH:O	2.18	0.44
1:K:23:ARG:HG2	3:K:710:HOH:O	2.17	0.44
1:P:250:ALA:N	3:P:613:HOH:O	2.51	0.44
1:G:353:TYR:HD2	3:G:623:HOH:O	2.01	0.44
1:G:356:LEU:HD11	1:G:367:ILE:HD13	2.00	0.44
1:T:372:GLN:NE2	3:T:660:HOH:O	2.36	0.44
1:U:185:ASP:OD1	3:U:640:HOH:O	2.21	0.44
1:J:130:MET:HG3	1:J:217:LEU:HD23	1.99	0.44
1:K:17:TYR:HB3	1:K:132:ILE:HD13	1.99	0.44
1:L:239:ILE:O	1:L:243:VAL:HG23	2.17	0.44
1:P:420:ASP:OD1	1:P:421:LEU:N	2.51	0.44
1:R:23:ARG:HA	1:R:69:TYR:CD2	2.52	0.44
1:F:150:HIS:HA	3:F:606:HOH:O	2.18	0.44
1:F:177:VAL:CG1	1:F:181:ASP:HA	2.41	0.44
1:D:294:TYR:HB2	3:D:810:HOH:O	2.17	0.43
1:K:146:MET:HE1	1:K:209:ILE:HG22	2.00	0.43
1:N:200:GLU:CD	1:N:200:GLU:H	2.21	0.43
1:O:412:THR:H	1:O:415:MET:CE	2.23	0.43
1:Q:317:GLU:OE2	3:Q:628:HOH:O	2.20	0.43
1:R:242:ILE:N	3:R:601:HOH:O	1.99	0.43
1:R:307:THR:HB	1:R:331:ASP:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:376:VAL:HG12	1:R:409:CYS:HB2	2.00	0.43
1:T:223:ARG:HG2	3:T:1087:HOH:O	2.18	0.43
1:B:34:ARG:NH2	2:B:502:SO4:O4	2.28	0.43
1:B:156:ASP:HB3	1:B:216:PHE:CZ	2.53	0.43
1:B:247:LYS:HZ2	1:B:247:LYS:HG3	1.57	0.43
1:D:128:GLU:HG3	3:D:678:HOH:O	2.17	0.43
1:H:138:ILE:HG22	1:H:267:TYR:HE1	1.83	0.43
1:N:187:ILE:HD13	1:N:189:LYS:N	2.29	0.43
1:P:151:VAL:N	3:P:625:HOH:O	2.51	0.43
1:R:275:ASP:OD2	1:R:406:SER:OG	2.28	0.43
1:F:268:TRP:NE1	3:F:625:HOH:O	2.16	0.43
1:M:40:TYR:HB3	1:M:345:PHE:CE2	2.54	0.43
1:M:253:PHE:HB3	3:M:605:HOH:O	2.18	0.43
1:M:358:ASN:N	1:M:358:ASN:HD22	2.16	0.43
1:M:384:ILE:HG23	1:M:388:LEU:HD23	1.98	0.43
1:T:324:VAL:HG12	1:T:340:ASN:HD22	1.82	0.43
1:U:241:TYR:HD1	1:U:242:ILE:HD13	1.83	0.43
1:C:40:TYR:HB3	1:C:345:PHE:CE2	2.53	0.43
1:C:108:TYR:CD1	1:C:114:ALA:HA	2.54	0.43
1:E:177:VAL:HB	3:E:615:HOH:O	2.18	0.43
1:L:373:LEU:HD11	1:L:384:ILE:HG21	2.00	0.43
1:N:324:VAL:HG23	1:N:340:ASN:OD1	2.18	0.43
1:O:175:MET:SD	1:O:183:ILE:HG21	2.58	0.43
1:P:80:ARG:CZ	3:P:648:HOH:O	2.67	0.43
1:P:355:ARG:NH1	3:P:629:HOH:O	2.20	0.43
1:Q:42:GLY:H	1:Q:281:ASN:ND2	2.16	0.43
1:F:80:ARG:NH1	3:F:684:HOH:O	2.50	0.43
1:F:370:HIS:HE1	3:F:878:HOH:O	2.00	0.43
1:H:208:GLY:O	3:H:624:HOH:O	2.21	0.43
1:Q:313:VAL:HG22	1:F:287:VAL:HG22	2.00	0.43
1:U:390:VAL:HG13	3:U:998:HOH:O	2.17	0.43
1:B:30:LEU:HD13	1:B:410:LEU:HD11	1.99	0.43
1:C:130:MET:HG3	1:C:217:LEU:HD23	1.99	0.43
1:D:419:LEU:O	3:D:626:HOH:O	2.21	0.43
1:K:239:ILE:O	1:K:243:VAL:HG13	2.19	0.43
1:O:111:THR:HG23	1:O:234:PHE:H	1.83	0.43
1:P:18:VAL:HB	1:P:65:VAL:HG22	1.99	0.43
1:F:36:LYS:NZ	1:F:270:ASP:O	2.39	0.43
1:G:26:ARG:NH1	3:G:638:HOH:O	2.28	0.43
1:M:320:ARG:HD3	3:M:920:HOH:O	2.17	0.43
1:B:111:THR:HG23	1:B:234:PHE:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:TRP:HZ2	1:B:358:ASN:HB3	1.84	0.43
1:D:412:THR:OG1	1:D:415:MET:SD	2.58	0.43
1:E:207:MET:HE1	1:E:253:PHE:CD1	2.53	0.43
1:H:313:VAL:HG23	1:H:335:SER:HA	1.99	0.43
1:H:315:ASP:OD2	3:H:643:HOH:O	2.21	0.43
1:I:26:ARG:HE	1:I:273:THR:HG22	1.84	0.43
1:I:156:ASP:HB3	1:I:216:PHE:CZ	2.53	0.43
1:J:146:MET:HG3	1:J:251:HIS:CG	2.53	0.43
1:L:170:THR:OG1	1:L:190:PRO:O	2.24	0.43
1:N:233:ASP:HB2	3:N:660:HOH:O	2.17	0.43
1:P:212:PHE:CG	1:P:217:LEU:HD13	2.54	0.43
1:R:28:LYS:HG3	1:R:402:ARG:HE	1.82	0.43
1:R:372:GLN:C	1:R:373:LEU:HD23	2.38	0.43
1:T:101:ARG:NH1	3:T:704:HOH:O	2.52	0.43
1:U:180:LYS:HB2	1:U:182:GLU:HG3	2.00	0.43
1:U:240:PRO:O	1:U:243:VAL:HG22	2.18	0.43
1:A:68:GLN:CD	1:A:107:TRP:HB3	2.38	0.43
1:B:111:THR:HG22	1:B:233:ASP:OD1	2.19	0.43
1:D:180:LYS:HG3	1:D:182:GLU:HG3	1.99	0.43
1:H:28:LYS:HD2	1:H:402:ARG:NH1	2.34	0.43
1:L:68:GLN:NE2	1:L:107:TRP:HB3	2.32	0.43
1:L:268:TRP:CH2	1:L:270:ASP:HB2	2.53	0.43
1:P:187:ILE:HD13	1:P:194:PRO:HG2	2.00	0.43
1:Q:212:PHE:CD1	1:Q:217:LEU:HD13	2.53	0.43
1:G:128:GLU:HG3	3:G:700:HOH:O	2.17	0.43
1:U:325:SER:O	1:U:341:ARG:HA	2.17	0.43
1:E:15:MET:HB3	1:E:130:MET:SD	2.59	0.43
1:K:148:GLN:O	3:K:636:HOH:O	2.20	0.43
1:K:240:PRO:HA	1:K:243:VAL:HG22	2.00	0.43
1:L:370:HIS:ND1	1:P:167:MET:HG2	2.33	0.43
1:Q:86:ARG:NH2	3:U:647:HOH:O	2.52	0.43
1:G:159:ILE:HD11	1:G:239:ILE:HD12	2.00	0.43
1:M:28:LYS:HG3	1:M:402:ARG:NH2	2.33	0.43
1:M:215:LYS:NZ	1:M:218:MET:HG3	2.33	0.43
1:A:146:MET:HB2	3:A:691:HOH:O	2.19	0.43
1:D:139:TYR:HB3	1:D:268:TRP:CD1	2.54	0.43
1:E:231:SER:OG	1:E:237:ASP:OD1	2.30	0.43
1:H:417:ASP:N	1:H:417:ASP:OD1	2.52	0.43
1:J:98:ALA:HB1	1:J:99:SER:HA	2.01	0.43
1:L:122:ILE:HG21	1:L:218:MET:CE	2.49	0.43
1:N:406:SER:OG	3:N:635:HOH:O	2.20	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:139:TYR:HE2	1:Q:141:MET:HE2	1.84	0.43
1:Q:156:ASP:HB3	1:Q:216:PHE:CE2	2.54	0.43
1:R:178:ASN:HB2	3:R:914:HOH:O	2.19	0.43
1:F:9:PRO:HG2	1:F:12:ARG:HG3	2.01	0.43
1:F:28:LYS:HE2	3:F:852:HOH:O	2.18	0.43
1:M:17:TYR:HB3	1:M:132:ILE:HD13	2.01	0.43
1:A:40:TYR:OH	1:A:46:ARG:NH2	2.52	0.43
1:A:104:GLU:O	3:A:616:HOH:O	2.21	0.43
1:A:307:THR:HB	1:A:331:ASP:HB2	1.99	0.43
1:I:420:ASP:HB3	1:I:421:LEU:H	1.72	0.43
1:L:314:HIS:N	3:L:698:HOH:O	2.48	0.43
1:N:86:ARG:NH2	3:N:708:HOH:O	2.51	0.43
1:Q:76:ARG:NH2	2:Q:502:SO4:O3	2.51	0.43
1:Q:393:ASP:HB3	1:Q:396:LEU:HB3	2.00	0.43
1:R:224:ASP:CG	1:R:230:SER:OG	2.57	0.43
1:F:35:ALA:HB2	1:F:69:TYR:O	2.19	0.43
1:F:243:VAL:N	3:F:638:HOH:O	2.52	0.43
1:F:307:THR:HB	1:F:331:ASP:HB2	2.01	0.43
1:G:52:LEU:HD22	1:G:63:ILE:HG21	1.99	0.43
1:M:111:THR:HG22	1:M:233:ASP:HA	2.00	0.43
1:T:34:ARG:NH2	2:T:501:SO4:O1	2.32	0.43
1:T:319:ARG:HB3	1:T:353:TYR:CE1	2.53	0.43
1:U:223:ARG:HG2	1:U:223:ARG:NH1	2.33	0.43
1:A:230:SER:O	3:A:640:HOH:O	2.21	0.42
1:B:180:LYS:NZ	3:B:611:HOH:O	2.00	0.42
1:C:101:ARG:N	3:C:686:HOH:O	2.46	0.42
1:H:110:GLY:HA3	1:H:232:ARG:HB3	2.01	0.42
1:Q:119:ILE:HD12	1:Q:218:MET:HE3	2.00	0.42
1:F:265:GLU:OE2	3:F:636:HOH:O	2.22	0.42
1:U:94:ASP:OD1	3:U:641:HOH:O	2.22	0.42
1:U:177:VAL:HG12	1:U:183:ILE:HA	2.01	0.42
1:B:29:GLU:HB3	3:B:629:HOH:O	2.18	0.42
1:E:80:ARG:NE	3:E:628:HOH:O	2.52	0.42
1:E:313:VAL:O	1:E:314:HIS:HB2	2.19	0.42
1:H:38:ALA:HB2	1:H:74:LEU:HB2	2.01	0.42
1:H:318:ASP:N	3:H:623:HOH:O	2.52	0.42
1:Q:119:ILE:HG23	1:Q:218:MET:CE	2.47	0.42
1:M:35:ALA:HB2	1:M:69:TYR:O	2.18	0.42
1:M:212:PHE:CD1	1:M:217:LEU:HD13	2.53	0.42
1:T:13:ASP:HB3	1:T:128:GLU:HB3	2.01	0.42
1:B:177:VAL:HG12	1:B:183:ILE:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:144:GLU:O	1:H:148:GLN:HG2	2.19	0.42
1:I:111:THR:HG23	1:I:234:PHE:H	1.84	0.42
1:L:222:ARG:HD2	3:L:890:HOH:O	2.19	0.42
1:L:358:ASN:HD22	1:L:375:ASN:HD21	1.67	0.42
1:R:26:ARG:HD2	3:R:1022:HOH:O	2.18	0.42
1:T:341:ARG:O	1:T:358:ASN:HA	2.19	0.42
1:T:346[B]:THR:CG2	3:T:839:HOH:O	2.66	0.42
1:T:351:ASN:HB3	2:T:502:SO4:O3	2.19	0.42
1:A:402:ARG:HA	3:A:925:HOH:O	2.20	0.42
1:C:95:ILE:HB	1:C:101:ARG:HH12	1.84	0.42
1:C:224:ASP:CG	3:C:655:HOH:O	2.58	0.42
1:D:98:ALA:HB1	1:D:107:TRP:HA	2.00	0.42
1:H:231:SER:N	1:H:237:ASP:OD2	2.30	0.42
1:K:269:ARG:NH1	3:K:678:HOH:O	2.46	0.42
1:L:179:GLU:OE2	3:L:636:HOH:O	2.20	0.42
1:P:375:ASN:HB3	1:P:408:ILE:HD13	2.02	0.42
1:Q:283:ASP:HB3	3:Q:699:HOH:O	2.18	0.42
1:R:176:HIS:CD2	1:R:177:VAL:N	2.87	0.42
1:F:38:ALA:HB2	1:F:74:LEU:HB2	2.00	0.42
1:F:184:ILE:HG23	3:F:692:HOH:O	2.18	0.42
1:F:340:ASN:O	1:F:357:GLU:HA	2.20	0.42
1:T:117:GLN:NE2	3:T:707:HOH:O	2.53	0.42
1:T:139:TYR:HE2	1:T:141:MET:HE2	1.83	0.42
1:T:356:LEU:HD11	1:T:367:ILE:HD12	2.01	0.42
1:U:379:ASP:OD1	1:U:380:HIS:N	2.49	0.42
1:H:313:VAL:HG12	3:G:618:HOH:O	2.19	0.42
1:K:113:ASP:OD1	1:K:232:ARG:NH2	2.52	0.42
1:L:234:PHE:HA	1:L:238:ILE:CD1	2.50	0.42
1:O:166:ARG:HG2	1:O:193:PRO:HD2	2.01	0.42
1:M:418:LYS:O	1:M:419:LEU:HD12	2.20	0.42
1:T:44:LYS:NZ	3:T:644:HOH:O	2.25	0.42
1:T:340:ASN:O	1:T:357:GLU:HA	2.20	0.42
1:A:157:VAL:HG12	1:A:242:ILE:HG21	2.00	0.42
1:A:158:THR:HG23	1:A:249:VAL:HG13	2.00	0.42
1:B:94:ASP:HA	3:D:614:HOH:O	2.18	0.42
1:C:56:LEU:HD21	1:G:89:ARG:HD2	2.00	0.42
1:D:339:LEU:HD22	1:D:356:LEU:HD12	2.02	0.42
1:D:411:ILE:HA	1:D:415:MET:HE1	2.02	0.42
1:H:251:HIS:CE1	1:H:256:SER:OG	2.73	0.42
1:I:183:ILE:HB	1:I:248:ALA:HB3	2.00	0.42
1:L:111:THR:HG23	1:L:234:PHE:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:178:ASN:CG	3:L:606:HOH:O	2.57	0.42
1:P:193:PRO:HA	1:P:194:PRO:HD3	1.90	0.42
1:G:267:TYR:CD1	1:G:291:LEU:HD13	2.55	0.42
1:D:34:ARG:NH1	2:D:502:SO4:S	2.93	0.42
1:D:116:TYR:CA	1:D:221:LEU:HD13	2.49	0.42
1:E:106:GLN:HB3	1:E:107:TRP:H	1.74	0.42
1:I:157:VAL:HG23	3:I:632:HOH:O	2.20	0.42
1:J:217:LEU:O	1:J:221:LEU:HG	2.19	0.42
1:L:114:ALA:O	1:L:118:ASN:ND2	2.40	0.42
1:N:236:LYS:O	1:N:240:PRO:HG2	2.20	0.42
1:N:296:LYS:NZ	3:N:683:HOH:O	2.51	0.42
1:Q:355:ARG:HD3	1:Q:372:GLN:OE1	2.19	0.42
1:F:26:ARG:NH2	3:F:624:HOH:O	2.43	0.42
1:G:65:VAL:HG11	1:G:78:LEU:HD11	2.02	0.42
1:G:396:LEU:N	3:G:609:HOH:O	2.01	0.42
1:M:115:VAL:HB	1:M:221:LEU:CD2	2.49	0.42
1:M:415:MET:O	1:M:419:LEU:HD13	2.20	0.42
2:T:501:SO4:O4	3:T:637:HOH:O	2.21	0.42
1:B:227:ASP:O	1:B:229:THR:N	2.52	0.42
1:I:166:ARG:O	1:I:193:PRO:HG2	2.19	0.42
1:I:303:TYR:OH	1:I:305:GLU:OE2	2.29	0.42
1:P:156:ASP:HB3	1:P:216:PHE:CE2	2.55	0.42
1:Q:166:ARG:HH21	1:Q:195:GLY:HA3	1.85	0.42
1:F:72:HIS:ND1	1:T:101:ARG:HG2	2.34	0.42
1:F:212:PHE:CD1	1:F:217:LEU:HD13	2.55	0.42
1:G:116:TYR:HE1	1:G:222:ARG:HG2	1.84	0.42
1:B:179:GLU:H	1:B:179:GLU:CD	2.23	0.42
1:E:130:MET:HG2	1:E:214:THR:OG1	2.19	0.42
1:N:330:GLY:O	1:N:346:THR:HG23	2.20	0.42
1:O:231:SER:HB3	1:O:237:ASP:OD2	2.20	0.42
1:Q:168:GLU:OE2	3:Q:631:HOH:O	2.21	0.42
1:A:212:PHE:CG	1:A:217:LEU:HD13	2.55	0.42
1:B:72:HIS:HB2	1:D:100:GLN:O	2.20	0.42
1:C:119:ILE:CD1	1:C:218:MET:HG2	2.50	0.42
1:D:80:ARG:HG2	3:D:842:HOH:O	2.20	0.42
1:H:169:ALA:HB1	1:H:174:VAL:CG2	2.50	0.42
1:J:116:TYR:O	1:J:119:ILE:HG12	2.19	0.42
1:L:112:ALA:HB2	1:L:238:ILE:CD1	2.50	0.42
1:L:384:ILE:HG23	1:L:388:LEU:HD23	2.00	0.42
1:N:175:MET:HG3	1:N:183:ILE:HG21	2.02	0.42
1:O:38:ALA:HB2	1:O:74:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:341:ARG:NH2	3:O:632:HOH:O	2.46	0.42
1:P:192:ASP:C	3:P:623:HOH:O	2.57	0.42
1:P:233:ASP:OD1	1:P:235:GLY:N	2.53	0.42
1:M:215:LYS:HA	1:M:218:MET:HG2	2.01	0.42
1:T:76:ARG:CZ	3:T:821:HOH:O	2.68	0.42
1:T:144:GLU:OE1	3:T:635:HOH:O	2.21	0.42
1:B:23:ARG:HH12	1:B:70:LYS:CG	2.33	0.41
1:J:70:LYS:NZ	3:J:618:HOH:O	2.15	0.41
1:J:146:MET:HB2	3:J:684:HOH:O	2.20	0.41
1:N:166:ARG:NH1	3:N:602:HOH:O	2.47	0.41
1:P:115:VAL:HB	1:P:221:LEU:HD21	2.01	0.41
1:R:334:ILE:HD12	1:R:339:LEU:HD11	2.01	0.41
1:F:231:SER:OG	3:F:623:HOH:O	2.14	0.41
1:T:265:GLU:HG3	1:T:266:PRO:O	2.20	0.41
1:U:307:THR:HB	1:U:331:ASP:HB2	2.02	0.41
1:B:21:GLY:O	3:B:642:HOH:O	2.22	0.41
1:B:87:PRO:HA	1:B:91:GLU:O	2.20	0.41
1:D:146:MET:HB2	3:D:805:HOH:O	2.19	0.41
1:H:196:ILE:HB	1:H:199:ASN:HB3	2.02	0.41
1:H:287:VAL:HB	1:G:313:VAL:HG21	2.02	0.41
1:K:133:LEU:HD23	1:K:209:ILE:HG23	2.02	0.41
1:L:217:LEU:HD12	1:L:221:LEU:HD13	2.02	0.41
1:O:99:SER:HA	1:O:100:GLN:HA	1.65	0.41
1:R:230:SER:N	3:R:622:HOH:O	2.54	0.41
1:F:156:ASP:HB3	1:F:216:PHE:CE2	2.56	0.41
1:U:99:SER:HB2	3:U:955:HOH:O	2.19	0.41
1:U:166:ARG:NH1	3:U:695:HOH:O	2.51	0.41
1:A:26:ARG:NH1	3:A:645:HOH:O	2.24	0.41
1:C:405:GLU:H	1:C:405:GLU:CD	2.24	0.41
1:I:233:ASP:OD2	1:I:236:LYS:HB3	2.20	0.41
1:K:40:TYR:HB3	1:K:345:PHE:CE2	2.55	0.41
1:K:79:GLN:HE21	1:M:79:GLN:HE21	1.67	0.41
1:K:158:THR:HG23	3:K:712:HOH:O	2.19	0.41
1:N:221:LEU:HD21	1:N:238:ILE:HG21	2.01	0.41
1:Q:345:PHE:HB3	1:Q:363:PRO:HG3	2.02	0.41
1:R:223:ARG:CD	1:R:238:ILE:HD11	2.50	0.41
1:R:363:PRO:O	1:R:380:HIS:HD2	2.04	0.41
1:F:116:TYR:HA	1:F:119:ILE:CD1	2.48	0.41
1:F:263:GLU:HG2	1:F:290:ASP:O	2.20	0.41
1:G:35:ALA:HB1	1:G:37:PRO:HD2	2.02	0.41
1:U:140:LYS:NZ	3:U:654:HOH:O	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ARG:NH2	3:A:687:HOH:O	2.49	0.41
1:A:76:ARG:HD2	3:A:626:HOH:O	2.21	0.41
1:A:144:GLU:O	1:A:148:GLN:HG3	2.21	0.41
1:B:23:ARG:NH2	1:B:32:ASP:O	2.52	0.41
1:B:251:HIS:NE2	1:B:256:SER:OG	2.32	0.41
1:C:106:GLN:HG3	1:C:107:TRP:H	1.85	0.41
1:H:287:VAL:HG22	1:H:288:VAL:HG23	2.03	0.41
1:H:319:ARG:HG3	1:H:353:TYR:CE1	2.55	0.41
1:I:357:GLU:O	1:I:374:SER:HA	2.21	0.41
1:O:187:ILE:HG21	1:O:190:PRO:HB3	2.01	0.41
1:P:174:VAL:N	1:P:187:ILE:O	2.51	0.41
1:Q:204:LEU:HA	1:Q:204:LEU:HD23	1.30	0.41
1:M:156:ASP:HB3	1:M:216:PHE:CZ	2.55	0.41
1:T:309:PRO:O	1:U:294:TYR:OH	2.31	0.41
1:T:387:GLY:N	3:T:708:HOH:O	2.53	0.41
1:B:121:ILE:HA	1:B:121:ILE:HD13	1.72	0.41
1:B:405:GLU:CD	1:B:405:GLU:H	2.24	0.41
1:C:28:LYS:HA	1:C:28:LYS:HD3	1.86	0.41
1:D:23:ARG:HB3	3:D:737:HOH:O	2.19	0.41
1:D:23:ARG:NH1	1:D:31:THR:O	2.39	0.41
1:D:47:ILE:HG12	1:D:138:ILE:HD11	2.02	0.41
1:E:193:PRO:HG2	3:E:650:HOH:O	2.21	0.41
1:I:238:ILE:O	1:I:242:ILE:HG13	2.20	0.41
1:K:86:ARG:NH1	3:K:690:HOH:O	2.51	0.41
1:K:305:GLU:HB3	1:M:88:GLU:CG	2.51	0.41
1:L:112:ALA:HB2	1:L:238:ILE:HD11	2.02	0.41
1:N:175:MET:SD	1:N:186:PHE:HB2	2.61	0.41
1:N:236:LYS:HG2	1:N:237:ASP:OD1	2.21	0.41
1:O:177:VAL:HG13	1:O:181:ASP:HA	2.01	0.41
1:O:265:GLU:HG2	1:O:266:PRO:HD2	2.03	0.41
1:F:178:ASN:N	3:F:692:HOH:O	2.52	0.41
1:G:106:GLN:HG2	1:G:107:TRP:CE3	2.56	0.41
1:M:178:ASN:HD21	1:M:182:GLU:HB2	1.86	0.41
1:M:233:ASP:HB3	3:M:878:HOH:O	2.20	0.41
1:C:287:VAL:HG22	1:I:313:VAL:CG2	2.50	0.41
1:D:116:TYR:CD1	1:D:221:LEU:HD12	2.51	0.41
1:D:307:THR:HB	1:D:331:ASP:HB2	2.03	0.41
1:E:161:CYS:N	1:E:251:HIS:O	2.50	0.41
1:E:176:HIS:HD2	3:E:751:HOH:O	2.02	0.41
1:I:87:PRO:HA	1:I:91:GLU:O	2.21	0.41
1:I:146:MET:HE3	1:I:160:GLY:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:42:GLY:HA2	1:J:284:LEU:CD1	2.50	0.41
1:K:307:THR:HB	1:K:331:ASP:HB2	2.02	0.41
1:L:112:ALA:CB	1:L:238:ILE:HD11	2.50	0.41
1:O:260:SER:HB3	1:O:263:GLU:HG3	2.01	0.41
1:P:111:THR:CG2	1:P:234:PHE:H	2.34	0.41
1:P:410:LEU:N	3:P:616:HOH:O	2.53	0.41
1:Q:269:ARG:HD2	3:Q:1009:HOH:O	2.19	0.41
1:F:36:LYS:HD3	1:F:136:ASP:HB2	2.02	0.41
1:F:236:LYS:HB3	1:F:236:LYS:HE2	1.92	0.41
1:G:217:LEU:O	1:G:221:LEU:HD13	2.21	0.41
1:M:259:ARG:HD2	1:M:265:GLU:C	2.40	0.41
1:D:219:GLU:HA	1:D:222:ARG:HD2	2.02	0.41
1:E:260:SER:HB3	1:E:263:GLU:HG3	2.03	0.41
1:H:181:ASP:CG	1:H:252:ARG:HH21	2.24	0.41
1:J:357:GLU:O	1:J:374:SER:HA	2.20	0.41
1:L:233:ASP:O	1:L:238:ILE:HD12	2.20	0.41
1:L:236:LYS:HB3	3:L:779:HOH:O	2.21	0.41
1:L:365:VAL:HG21	3:L:629:HOH:O	2.20	0.41
1:P:174:VAL:HA	3:P:653:HOH:O	2.21	0.41
1:P:212:PHE:CD1	1:P:217:LEU:HD13	2.55	0.41
1:R:29:GLU:HA	1:R:32:ASP:CG	2.41	0.41
1:R:341:ARG:NE	3:R:699:HOH:O	2.54	0.41
1:F:47:ILE:HG12	1:F:138:ILE:HD11	2.02	0.41
1:F:314:HIS:CE1	3:F:669:HOH:O	2.73	0.41
1:A:212:PHE:CD2	1:A:217:LEU:HD13	2.56	0.41
1:B:256:SER:OG	3:B:639:HOH:O	2.21	0.41
1:H:48:ILE:HD13	1:H:78:LEU:HD21	2.02	0.41
1:H:87:PRO:HA	1:H:91:GLU:O	2.21	0.41
1:I:111:THR:CG2	1:I:234:PHE:H	2.34	0.41
1:I:313:VAL:O	1:I:314:HIS:HB2	2.21	0.41
1:L:227:ASP:OD1	1:L:229:THR:HG22	2.21	0.41
1:P:141:MET:HE2	1:P:143:TYR:HE1	1.86	0.41
1:P:239:ILE:HD13	1:P:239:ILE:HA	1.95	0.41
1:F:305:GLU:CD	3:F:605:HOH:O	2.54	0.41
1:G:307:THR:OG1	3:G:633:HOH:O	2.22	0.41
1:A:296:LYS:HE3	3:P:801:HOH:O	2.20	0.41
1:B:28:LYS:HE2	1:B:29:GLU:HG3	2.01	0.41
1:B:56:LEU:HD12	3:B:750:HOH:O	2.21	0.41
1:B:185:ASP:OD1	1:B:186:PHE:N	2.52	0.41
1:B:294:TYR:OH	1:K:311:LYS:HB2	2.20	0.41
1:C:80:ARG:HB3	1:C:303:TYR:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ARG:HG3	1:H:75:ILE:HD12	2.03	0.41
1:D:8:GLN:NE2	3:D:689:HOH:O	2.53	0.41
1:D:357:GLU:O	1:D:374:SER:HA	2.21	0.41
1:I:231:SER:OG	1:I:237:ASP:OD2	2.28	0.41
1:I:313:VAL:HG22	1:I:314:HIS:H	1.85	0.41
1:K:230:SER:O	3:K:640:HOH:O	2.22	0.41
1:K:260:SER:HB3	1:K:263:GLU:HG3	2.02	0.41
1:L:23:ARG:NH2	1:L:69:TYR:HB3	2.36	0.41
1:N:324:VAL:O	1:N:340:ASN:HA	2.21	0.41
1:O:68:GLN:OE1	1:O:107:TRP:HB3	2.21	0.41
1:O:341:ARG:O	1:O:358:ASN:HA	2.21	0.41
1:F:187:ILE:HG21	1:F:190:PRO:HB3	2.02	0.41
1:F:215:LYS:HA	1:F:215:LYS:HE3	2.03	0.41
1:M:47:ILE:HG12	1:M:138:ILE:HD11	2.03	0.41
1:T:9:PRO:HB2	3:T:1136:HOH:O	2.20	0.41
1:T:373:LEU:HD22	1:T:378:ILE:HD11	2.03	0.41
1:U:111:THR:CG2	1:U:234:PHE:H	2.33	0.41
1:U:282:ILE:HD12	1:U:282:ILE:HA	1.86	0.41
1:D:8:GLN:H	1:D:8:GLN:HG3	1.72	0.41
1:D:287:VAL:HA	1:M:313:VAL:HG21	2.03	0.41
1:D:294:TYR:CE2	1:M:308:PRO:CB	3.05	0.41
1:H:309:PRO:HB3	1:G:329:SER:HA	2.02	0.41
1:H:313:VAL:HG22	1:H:335:SER:HA	2.01	0.41
1:I:76:ARG:HB2	3:I:647:HOH:O	2.20	0.41
1:I:177:VAL:HG13	1:I:178:ASN:O	2.20	0.41
1:I:307:THR:HB	1:I:331:ASP:HB2	2.03	0.41
1:K:227:ASP:HB2	3:K:790:HOH:O	2.20	0.41
1:L:251:HIS:NE2	1:L:256:SER:OG	2.34	0.41
1:L:370:HIS:O	1:P:166:ARG:NH2	2.53	0.41
1:N:357:GLU:O	1:N:374:SER:HA	2.21	0.41
1:Q:23:ARG:HG2	1:Q:25:SER:N	2.36	0.41
1:Q:68:GLN:HB3	3:Q:606:HOH:O	2.22	0.41
1:R:223:ARG:HG3	1:R:225:ALA:N	2.35	0.41
1:T:112:ALA:HA	1:T:234:PHE:CE2	2.55	0.41
1:D:23:ARG:HA	1:D:23:ARG:HD2	1.92	0.40
1:D:278:TRP:HZ2	1:D:358:ASN:HB3	1.86	0.40
1:H:233:ASP:O	1:H:237:ASP:HB2	2.21	0.40
1:O:346:THR:HG22	3:O:840:HOH:O	2.20	0.40
1:Q:44:LYS:HB2	3:Q:1062:HOH:O	2.20	0.40
1:Q:196:ILE:CD1	1:Q:252:ARG:HH12	2.34	0.40
1:F:70:LYS:HB3	1:F:70:LYS:HE3	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:76:ARG:NH2	3:F:696:HOH:O	2.54	0.40
1:G:44:LYS:HD2	1:G:304:ALA:HB2	2.02	0.40
1:G:396:LEU:HD11	1:G:400:ARG:CZ	2.51	0.40
1:M:36:LYS:HG2	1:M:136:ASP:HB2	2.02	0.40
1:T:149:GLN:HB2	3:T:654:HOH:O	2.20	0.40
1:U:215:LYS:HD3	3:U:981:HOH:O	2.19	0.40
1:D:341:ARG:HB3	1:D:358:ASN:ND2	2.36	0.40
1:H:177:VAL:HB	1:H:181:ASP:HA	2.03	0.40
1:H:340:ASN:O	1:H:357:GLU:HA	2.22	0.40
1:I:227:ASP:HA	1:I:228:PRO:HD3	1.96	0.40
1:J:231:SER:HB3	3:J:636:HOH:O	2.21	0.40
1:K:166:ARG:HD2	3:K:727:HOH:O	2.21	0.40
1:K:236:LYS:HA	1:K:240:PRO:HG2	2.03	0.40
1:P:227:ASP:C	3:P:610:HOH:O	2.59	0.40
1:Q:242:ILE:HG23	3:Q:1072:HOH:O	2.21	0.40
1:R:134:ALA:O	3:R:630:HOH:O	2.22	0.40
1:F:178:ASN:ND2	1:F:182:GLU:HB2	2.29	0.40
1:A:239:ILE:O	1:A:243:VAL:HG13	2.21	0.40
1:B:149:GLN:HG2	3:B:794:HOH:O	2.22	0.40
1:C:151:VAL:HG23	1:C:152:ASP:OD1	2.21	0.40
1:D:162:LEU:HB3	3:D:888:HOH:O	2.21	0.40
1:H:13:ASP:OD2	3:H:645:HOH:O	2.22	0.40
1:H:357:GLU:O	1:H:374:SER:HA	2.20	0.40
1:H:393:ASP:OD1	3:H:644:HOH:O	2.21	0.40
1:J:313:VAL:O	1:J:314:HIS:HB2	2.22	0.40
1:J:316:ASP:O	3:J:628:HOH:O	2.22	0.40
1:L:178:ASN:CB	3:L:606:HOH:O	2.68	0.40
1:Q:242:ILE:HG22	1:Q:246:GLY:HA3	2.03	0.40
1:F:176:HIS:HD2	1:F:177:VAL:H	1.69	0.40
1:M:62:ARG:NH2	1:M:92:SER:HB3	2.36	0.40
1:D:143:TYR:HA	3:D:805:HOH:O	2.21	0.40
1:E:87:PRO:HA	1:E:91:GLU:O	2.22	0.40
1:I:341:ARG:HB3	3:I:625:HOH:O	2.21	0.40
1:N:155:ALA:HA	1:N:247:LYS:HG2	2.03	0.40
1:N:223:ARG:NH2	3:N:720:HOH:O	2.55	0.40
1:N:397:ASP:HB3	1:N:409:CYS:SG	2.62	0.40
1:P:72:HIS:CE1	3:P:685:HOH:O	2.75	0.40
1:G:36:LYS:HA	1:G:39:VAL:HG23	2.03	0.40
1:T:30:LEU:HD12	1:T:30:LEU:HA	1.91	0.40
1:U:236:LYS:HG3	1:U:237:ASP:OD1	2.21	0.40
1:D:166:ARG:H	1:D:166:ARG:HG2	1.76	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:259:ARG:HE	1:H:259:ARG:HB2	1.62	0.40
1:I:199:ASN:ND2	3:I:676:HOH:O	2.48	0.40
1:K:312:PHE:CE2	1:K:334:ILE:HG13	2.56	0.40
1:L:350:ALA:HA	1:L:367:ILE:HB	2.02	0.40
1:N:164:VAL:O	1:N:203:ALA:N	2.49	0.40
1:Q:353:TYR:OH	3:Q:604:HOH:O	1.96	0.40
1:G:225:ALA:HA	1:G:232:ARG:HD2	2.04	0.40
1:T:400:ARG:HG2	1:T:419:LEU:HD11	2.04	0.40
1:U:239:ILE:O	1:U:243:VAL:HG13	2.21	0.40

All (83) 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	Interatomic distance (Å)	Clash overlap (Å)
3:M:1066:HOH:O	3:U:1036:HOH:O[1_565]	1.68	0.52
3:J:1187:HOH:O	3:L:1071:HOH:O[1_546]	1.69	0.51
3:J:831:HOH:O	3:N:787:HOH:O[1_655]	1.71	0.49
3:I:648:HOH:O	3:J:742:HOH:O[1_455]	1.74	0.46
3:J:1031:HOH:O	3:N:1056:HOH:O[1_655]	1.79	0.41
3:J:1171:HOH:O	3:L:859:HOH:O[1_546]	1.81	0.39
3:N:823:HOH:O	3:R:1024:HOH:O[1_446]	1.82	0.38
3:N:841:HOH:O	3:R:1133:HOH:O[1_446]	1.82	0.38
3:N:831:HOH:O	3:R:993:HOH:O[1_446]	1.84	0.36
3:J:1242:HOH:O	3:R:1160:HOH:O[1_546]	1.87	0.33
3:M:1055:HOH:O	3:U:1047:HOH:O[1_465]	1.87	0.33
3:E:1016:HOH:O	3:O:1028:HOH:O[1_654]	1.88	0.32
3:H:733:HOH:O	3:T:972:HOH:O[1_465]	1.88	0.32
3:H:806:HOH:O	3:T:915:HOH:O[1_565]	1.88	0.32
3:M:1149:HOH:O	3:U:1093:HOH:O[1_565]	1.88	0.32
3:O:1187:HOH:O	3:P:1074:HOH:O[1_456]	1.89	0.31
3:L:928:HOH:O	3:N:1065:HOH:O[1_664]	1.91	0.29
3:D:1096:HOH:O	3:E:1026:HOH:O[1_565]	1.92	0.28
3:H:1069:HOH:O	3:T:1073:HOH:O[1_465]	1.92	0.28
3:N:1025:HOH:O	3:R:1174:HOH:O[1_446]	1.92	0.28
3:O:906:HOH:O	3:P:751:HOH:O[1_456]	1.92	0.28
3:J:1126:HOH:O	3:L:985:HOH:O[1_546]	1.93	0.27
3:O:622:HOH:O	3:P:648:HOH:O[1_456]	1.93	0.27
3:A:946:HOH:O	3:O:1081:HOH:O[1_654]	1.94	0.26
3:J:831:HOH:O	3:N:758:HOH:O[1_655]	1.95	0.25
3:L:1016:HOH:O	3:N:1061:HOH:O[1_664]	1.95	0.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:990:HOH:O	3:R:1035:HOH:O[1_446]	1.95	0.25
3:J:1026:HOH:O	3:L:906:HOH:O[1_546]	1.98	0.22
3:N:1044:HOH:O	3:G:1013:HOH:O[1_445]	1.98	0.22
3:H:1038:HOH:O	3:T:1074:HOH:O[1_465]	1.99	0.21
3:M:1110:HOH:O	3:U:1048:HOH:O[1_565]	2.00	0.20
3:O:965:HOH:O	3:P:685:HOH:O[1_456]	2.01	0.19
3:N:759:HOH:O	3:R:730:HOH:O[1_446]	2.02	0.18
3:O:818:HOH:O	3:P:901:HOH:O[1_456]	2.02	0.18
3:A:624:HOH:O	3:B:621:HOH:O[1_655]	2.03	0.17
3:C:900:HOH:O	3:F:879:HOH:O[1_455]	2.03	0.17
3:E:1054:HOH:O	3:O:690:HOH:O[1_654]	2.03	0.17
3:L:945:HOH:O	3:N:918:HOH:O[1_664]	2.04	0.16
3:O:901:HOH:O	3:P:751:HOH:O[1_456]	2.06	0.14
3:D:916:HOH:O	3:E:616:HOH:O[1_465]	2.07	0.13
3:D:993:HOH:O	3:E:834:HOH:O[1_465]	2.07	0.13
3:E:618:HOH:O	3:O:1002:HOH:O[1_654]	2.07	0.13
3:J:698:HOH:O	3:R:657:HOH:O[1_546]	2.07	0.13
3:J:843:HOH:O	3:N:782:HOH:O[1_655]	2.07	0.13
3:O:970:HOH:O	3:R:1157:HOH:O[1_546]	2.07	0.13
3:A:803:HOH:O	3:O:912:HOH:O[1_654]	2.08	0.12
3:N:906:HOH:O	3:R:733:HOH:O[1_446]	2.08	0.12
3:H:904:HOH:O	3:T:1089:HOH:O[1_565]	2.09	0.11
3:L:707:HOH:O	3:N:964:HOH:O[1_664]	2.09	0.11
3:N:964:HOH:O	3:R:785:HOH:O[1_446]	2.09	0.11
3:A:898:HOH:O	3:O:959:HOH:O[1_654]	2.10	0.10
3:E:1080:HOH:O	3:O:1189:HOH:O[1_654]	2.10	0.10
3:J:853:HOH:O	3:L:723:HOH:O[1_546]	2.10	0.10
3:J:1127:HOH:O	3:R:1018:HOH:O[1_546]	2.10	0.10
3:N:878:HOH:O	3:R:680:HOH:O[1_446]	2.10	0.10
3:E:950:HOH:O	3:O:922:HOH:O[1_654]	2.11	0.09
3:L:666:HOH:O	3:N:902:HOH:O[1_664]	2.11	0.09
3:O:713:HOH:O	3:P:948:HOH:O[1_456]	2.11	0.09
3:J:838:HOH:O	3:N:893:HOH:O[1_655]	2.12	0.08
3:J:1124:HOH:O	3:L:974:HOH:O[1_546]	2.12	0.08
3:O:1031:HOH:O	3:P:987:HOH:O[1_456]	2.12	0.08
3:H:791:HOH:O	3:T:700:HOH:O[1_465]	2.13	0.07
3:J:869:HOH:O	3:N:958:HOH:O[1_655]	2.13	0.07
3:O:1024:HOH:O	3:P:750:HOH:O[1_456]	2.13	0.07
3:A:892:HOH:O	3:B:1019:HOH:O[1_655]	2.14	0.06
3:H:742:HOH:O	3:T:1078:HOH:O[1_565]	2.14	0.06
3:J:779:HOH:O	3:R:1063:HOH:O[1_546]	2.14	0.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:994:HOH:O	3:N:827:HOH:O[1_664]	2.14	0.06
3:J:1126:HOH:O	3:L:1028:HOH:O[1_546]	2.15	0.05
3:N:900:HOH:O	3:R:1004:HOH:O[1_446]	2.15	0.05
3:N:1077:HOH:O	3:R:1168:HOH:O[1_446]	2.15	0.05
3:M:660:HOH:O	3:U:623:HOH:O[1_565]	2.15	0.05
3:H:1038:HOH:O	3:T:844:HOH:O[1_465]	2.17	0.03
3:J:793:HOH:O	3:L:974:HOH:O[1_546]	2.17	0.03
1:K:200:GLU:O	3:Q:602:HOH:O[1_455]	2.17	0.03
3:C:1206:HOH:O	3:H:1120:HOH:O[1_655]	2.18	0.02
3:J:756:HOH:O	3:R:826:HOH:O[1_546]	2.18	0.02
3:J:989:HOH:O	3:L:845:HOH:O[1_546]	2.18	0.02
3:L:1046:HOH:O	3:N:996:HOH:O[1_664]	2.18	0.02
3:I:719:HOH:O	3:J:864:HOH:O[1_455]	2.19	0.01
3:J:631:HOH:O	3:N:696:HOH:O[1_655]	2.19	0.01
3:O:901:HOH:O	3:P:984:HOH:O[1_456]	2.19	0.01
3:O:940:HOH:O	3:P:987:HOH:O[1_456]	2.19	0.01

## 5.3 Torsion angles [i](#)

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

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	412/420 (98%)	384 (93%)	25 (6%)	3 (1%)	22	9
1	B	416/420 (99%)	384 (92%)	25 (6%)	7 (2%)	9	2
1	C	410/420 (98%)	391 (95%)	16 (4%)	3 (1%)	22	9
1	D	408/420 (97%)	387 (95%)	17 (4%)	4 (1%)	15	4
1	E	406/420 (97%)	387 (95%)	17 (4%)	2 (0%)	29	14
1	F	405/420 (96%)	380 (94%)	24 (6%)	1 (0%)	47	32
1	G	407/420 (97%)	388 (95%)	19 (5%)	0	100	100
1	H	405/420 (96%)	378 (93%)	26 (6%)	1 (0%)	47	32
1	I	406/420 (97%)	385 (95%)	19 (5%)	2 (0%)	29	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	415/420 (99%)	395 (95%)	19 (5%)	1 (0%)	47	32
1	K	406/420 (97%)	384 (95%)	19 (5%)	3 (1%)	22	9
1	L	407/420 (97%)	383 (94%)	21 (5%)	3 (1%)	22	9
1	M	407/420 (97%)	384 (94%)	22 (5%)	1 (0%)	47	32
1	N	413/420 (98%)	377 (91%)	28 (7%)	8 (2%)	8	1
1	O	407/420 (97%)	392 (96%)	14 (3%)	1 (0%)	47	32
1	P	406/420 (97%)	383 (94%)	21 (5%)	2 (0%)	29	14
1	Q	406/420 (97%)	378 (93%)	24 (6%)	4 (1%)	15	4
1	R	405/420 (96%)	385 (95%)	18 (4%)	2 (0%)	29	14
1	T	414/420 (99%)	390 (94%)	22 (5%)	2 (0%)	29	14
1	U	414/420 (99%)	396 (96%)	18 (4%)	0	100	100
All	All	8175/8400 (97%)	7711 (94%)	414 (5%)	50 (1%)	25	11

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	102	VAL
1	B	105	THR
1	C	98	ALA
1	L	244	GLU
1	N	102	VAL
1	N	105	THR
1	Q	154	GLY
1	R	224	ASP
1	C	335	SER
1	I	420	ASP
1	K	98	ALA
1	K	418	LYS
1	Q	107	TRP
1	B	101	ARG
1	B	228	PRO
1	B	229	THR
1	C	99	SER
1	E	25	SER
1	E	68	GLN
1	H	223	ARG
1	N	101	ARG
1	N	226	ALA

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Mol	Chain	Res	Type
1	O	99	SER
1	Q	106	GLN
1	A	68	GLN
1	A	106	GLN
1	B	68	GLN
1	I	236	LYS
1	N	109	GLU
1	N	191	ALA
1	Q	70	LYS
1	T	68	GLN
1	A	105	THR
1	K	8	GLN
1	L	314	HIS
1	N	314	HIS
1	P	314	HIS
1	R	68	GLN
1	F	68	GLN
1	M	107	TRP
1	T	103	SER
1	B	314	HIS
1	D	107	TRP
1	D	314	HIS
1	J	103	SER
1	L	189	LYS
1	N	106	GLN
1	D	293	ILE
1	P	271	VAL
1	D	271	VAL

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

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	340/352 (97%)	338 (99%)	2 (1%)	86	82
1	B	342/352 (97%)	341 (100%)	1 (0%)	92	90
1	C	340/352 (97%)	335 (98%)	5 (2%)	65	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	338/352 (96%)	337 (100%)	1 (0%)	92	90
1	E	337/352 (96%)	331 (98%)	6 (2%)	59	45
1	F	340/352 (97%)	338 (99%)	2 (1%)	86	82
1	G	340/352 (97%)	340 (100%)	0	100	100
1	H	337/352 (96%)	335 (99%)	2 (1%)	86	82
1	I	339/352 (96%)	334 (98%)	5 (2%)	65	53
1	J	341/352 (97%)	340 (100%)	1 (0%)	92	90
1	K	338/352 (96%)	336 (99%)	2 (1%)	86	82
1	L	339/352 (96%)	338 (100%)	1 (0%)	92	90
1	M	338/352 (96%)	335 (99%)	3 (1%)	78	72
1	N	343/352 (97%)	343 (100%)	0	100	100
1	O	337/352 (96%)	335 (99%)	2 (1%)	86	82
1	P	339/352 (96%)	333 (98%)	6 (2%)	59	45
1	Q	339/352 (96%)	336 (99%)	3 (1%)	78	72
1	R	337/352 (96%)	332 (98%)	5 (2%)	65	53
1	T	342/352 (97%)	340 (99%)	2 (1%)	86	82
1	U	340/352 (97%)	336 (99%)	4 (1%)	71	62
All	All	6786/7040 (96%)	6733 (99%)	53 (1%)	81	76

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	341	ARG
1	A	396	LEU
1	B	241	TYR
1	C	96	LEU
1	C	117	GLN
1	C	177	VAL
1	C	412[A]	THR
1	C	412[B]	THR
1	D	343	LEU
1	E	275	ASP
1	E	402	ARG
1	E	405	GLU
1	E	412[A]	THR
1	E	412[B]	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	418	LYS
1	H	167	MET
1	H	287	VAL
1	I	72	HIS
1	I	177	VAL
1	I	199	ASN
1	I	212	PHE
1	I	275	ASP
1	J	96	LEU
1	K	44	LYS
1	K	96	LEU
1	L	223	ARG
1	O	177	VAL
1	O	406	SER
1	P	153	SER
1	P	167	MET
1	P	175	MET
1	P	207	MET
1	P	219	GLU
1	P	418	LYS
1	Q	23	ARG
1	Q	176	HIS
1	Q	223	ARG
1	R	28	LYS
1	R	167	MET
1	R	230	SER
1	R	247	LYS
1	R	261	ASP
1	F	107	TRP
1	F	414	SER
1	M	261	ASP
1	M	341	ARG
1	M	402	ARG
1	T	176	HIS
1	T	341	ARG
1	U	28	LYS
1	U	107	TRP
1	U	148	GLN
1	U	181	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	68	GLN
1	A	148	GLN
1	A	245	HIS
1	A	351	ASN
1	B	148	GLN
1	B	372	GLN
1	C	8	GLN
1	C	54	ASN
1	C	79	GLN
1	C	117	GLN
1	C	358	ASN
1	C	372	GLN
1	D	149	GLN
1	D	358	ASN
1	D	413	GLN
1	E	106	GLN
1	E	117	GLN
1	E	176	HIS
1	H	149	GLN
1	H	176	HIS
1	I	199	ASN
1	I	375	ASN
1	J	351	ASN
1	K	57	ASN
1	K	68	GLN
1	K	79	GLN
1	K	90	ASN
1	K	251	HIS
1	K	351	ASN
1	K	413	GLN
1	L	314	HIS
1	L	372	GLN
1	L	375	ASN
1	N	68	GLN
1	N	413	GLN
1	O	279	GLN
1	O	413	GLN
1	P	57	ASN
1	P	149	GLN
1	P	372	GLN
1	Q	72	HIS
1	Q	281	ASN

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Mol	Chain	Res	Type
1	R	57	ASN
1	R	176	HIS
1	R	251	HIS
1	R	370	HIS
1	F	149	GLN
1	F	176	HIS
1	F	178	ASN
1	F	281	ASN
1	F	314	HIS
1	F	351	ASN
1	F	370	HIS
1	G	79	GLN
1	G	213	HIS
1	G	245	HIS
1	M	90	ASN
1	M	117	GLN
1	M	176	HIS
1	M	199	ASN
1	M	358	ASN
1	M	372	GLN
1	T	79	GLN
1	T	117	GLN
1	T	340	ASN
1	U	68	GLN
1	U	148	GLN
1	U	351	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry

42 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	B	501	-	4,4,4	0.17	0	6,6,6	0.32	0
2	SO4	L	502	-	4,4,4	0.15	0	6,6,6	0.12	0
2	SO4	R	501	-	4,4,4	0.19	0	6,6,6	0.13	0
2	SO4	R	502	-	4,4,4	0.15	0	6,6,6	0.24	0
2	SO4	U	501	-	4,4,4	0.19	0	6,6,6	0.31	0
2	SO4	A	502	-	4,4,4	0.13	0	6,6,6	0.06	0
2	SO4	D	501	-	4,4,4	0.23	0	6,6,6	0.22	0
2	SO4	H	501	-	4,4,4	0.17	0	6,6,6	0.15	0
2	SO4	K	502	-	4,4,4	0.15	0	6,6,6	0.28	0
2	SO4	J	501	-	4,4,4	0.20	0	6,6,6	0.25	0
2	SO4	C	501	-	4,4,4	0.23	0	6,6,6	0.15	0
2	SO4	Q	501	-	4,4,4	0.20	0	6,6,6	0.23	0
2	SO4	J	502	-	4,4,4	0.18	0	6,6,6	0.19	0
2	SO4	N	501	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	P	501	-	4,4,4	0.15	0	6,6,6	0.28	0
2	SO4	C	502	-	4,4,4	0.15	0	6,6,6	0.14	0
2	SO4	Q	502	-	4,4,4	0.15	0	6,6,6	0.14	0
2	SO4	T	503	-	4,4,4	0.17	0	6,6,6	0.21	0
2	SO4	N	502	-	4,4,4	0.18	0	6,6,6	0.23	0
2	SO4	F	501	-	4,4,4	0.19	0	6,6,6	0.14	0
2	SO4	P	502	-	4,4,4	0.17	0	6,6,6	0.14	0
2	SO4	G	502	-	4,4,4	0.19	0	6,6,6	0.11	0
2	SO4	M	501	-	4,4,4	0.17	0	6,6,6	0.14	0
2	SO4	O	501	-	4,4,4	0.21	0	6,6,6	0.15	0
2	SO4	I	501	-	4,4,4	0.24	0	6,6,6	0.22	0
2	SO4	B	502	-	4,4,4	0.15	0	6,6,6	0.26	0
2	SO4	I	502	-	4,4,4	0.20	0	6,6,6	0.13	0
2	SO4	L	501	-	4,4,4	0.19	0	6,6,6	0.07	0
2	SO4	U	502	-	4,4,4	0.15	0	6,6,6	0.16	0
2	SO4	F	502	-	4,4,4	0.17	0	6,6,6	0.19	0
2	SO4	E	501	-	4,4,4	0.21	0	6,6,6	0.14	0
2	SO4	T	502	-	4,4,4	0.19	0	6,6,6	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	501	-	4,4,4	0.17	0	6,6,6	0.18	0
2	SO4	D	502	-	4,4,4	0.21	0	6,6,6	0.13	0
2	SO4	G	501	-	4,4,4	0.15	0	6,6,6	0.15	0
2	SO4	M	502	-	4,4,4	0.17	0	6,6,6	0.13	0
2	SO4	E	502	-	4,4,4	0.15	0	6,6,6	0.10	0
2	SO4	H	502	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	O	502	-	4,4,4	0.14	0	6,6,6	0.14	0
2	SO4	E	503	-	4,4,4	0.18	0	6,6,6	0.15	0
2	SO4	T	501	-	4,4,4	0.21	0	6,6,6	0.30	0
2	SO4	K	501	-	4,4,4	0.21	0	6,6,6	0.18	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	SO4	1	0
2	L	502	SO4	2	0
2	K	502	SO4	1	0
2	J	502	SO4	1	0
2	C	502	SO4	3	0
2	Q	502	SO4	1	0
2	I	501	SO4	1	0
2	B	502	SO4	2	0
2	I	502	SO4	1	0
2	L	501	SO4	1	0
2	T	502	SO4	2	0
2	A	501	SO4	1	0
2	D	502	SO4	3	0
2	M	502	SO4	1	0
2	E	502	SO4	1	0
2	O	502	SO4	3	0
2	T	501	SO4	3	0
2	K	501	SO4	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	415/420 (98%)	-0.25	4 (0%) 82 82	19, 32, 52, 62	0
1	B	415/420 (98%)	-0.16	9 (2%) 62 61	19, 32, 53, 70	0
1	C	413/420 (98%)	-0.28	6 (1%) 73 73	17, 28, 44, 58	0
1	D	412/420 (98%)	-0.26	4 (0%) 82 82	16, 29, 46, 58	0
1	E	409/420 (97%)	-0.27	4 (0%) 82 82	17, 29, 44, 60	0
1	F	408/420 (97%)	-0.25	5 (1%) 79 79	16, 29, 49, 59	0
1	G	410/420 (97%)	-0.22	4 (0%) 82 82	18, 32, 51, 62	0
1	H	409/420 (97%)	-0.23	5 (1%) 79 79	19, 32, 53, 69	0
1	I	409/420 (97%)	-0.30	4 (0%) 82 82	16, 26, 44, 57	0
1	J	415/420 (98%)	-0.24	9 (2%) 62 61	15, 25, 42, 74	0
1	K	410/420 (97%)	-0.18	9 (2%) 62 61	17, 32, 52, 62	0
1	L	410/420 (97%)	-0.18	3 (0%) 87 88	19, 33, 51, 63	0
1	M	410/420 (97%)	-0.19	6 (1%) 73 73	18, 32, 50, 67	0
1	N	415/420 (98%)	-0.10	13 (3%) 49 47	17, 33, 61, 82	0
1	O	411/420 (97%)	-0.30	5 (1%) 79 79	15, 25, 42, 65	0
1	P	409/420 (97%)	-0.18	6 (1%) 73 73	19, 33, 53, 66	0
1	Q	409/420 (97%)	-0.19	4 (0%) 82 82	19, 32, 50, 68	0
1	R	409/420 (97%)	-0.25	3 (0%) 87 88	15, 25, 47, 66	0
1	T	415/420 (98%)	-0.16	12 (2%) 51 50	18, 32, 55, 73	0
1	U	415/420 (98%)	-0.16	8 (1%) 66 67	18, 32, 51, 70	0
All	All	8228/8400 (97%)	-0.22	123 (1%) 73 73	15, 30, 51, 82	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	107	TRP	8.4
1	U	102	VAL	8.2
1	U	421	LEU	7.7
1	H	421	LEU	6.9
1	J	102	VAL	6.4
1	U	103	SER	6.1
1	B	229	THR	6.1
1	Q	421	LEU	6.0
1	G	421	LEU	5.5
1	Q	107	TRP	5.4
1	T	105	THR	5.3
1	B	103	SER	5.1
1	N	190	PRO	5.1
1	N	194	PRO	5.0
1	I	421	LEU	4.9
1	E	421	LEU	4.8
1	Q	106	GLN	4.6
1	T	421	LEU	4.5
1	N	193	PRO	4.4
1	R	421	LEU	4.4
1	L	107	TRP	4.4
1	C	105	THR	4.4
1	N	102	VAL	4.3
1	J	103	SER	4.2
1	J	100	GLN	3.9
1	D	421	LEU	3.8
1	P	421	LEU	3.8
1	N	186	PHE	3.8
1	B	104	GLU	3.8
1	H	107	TRP	3.7
1	A	420	ASP	3.7
1	P	176	HIS	3.6
1	D	107	TRP	3.5
1	J	421	LEU	3.5
1	G	107	TRP	3.5
1	A	98	ALA	3.4
1	J	101	ARG	3.3
1	Q	7	VAL	3.3
1	L	177	VAL	3.3
1	N	421	LEU	3.3
1	O	107	TRP	3.3
1	K	421	LEU	3.2
1	F	22	GLY	3.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	J	107	TRP	3.2
1	P	107	TRP	3.2
1	L	221	LEU	3.1
1	U	107	TRP	3.1
1	U	186	PHE	3.1
1	O	105	THR	3.1
1	O	106	GLN	3.0
1	C	101	ARG	3.0
1	A	184	ILE	3.0
1	N	103	SER	3.0
1	B	106	GLN	3.0
1	K	107	TRP	2.9
1	I	332	CYS	2.8
1	H	69	TYR	2.8
1	K	241	TYR	2.8
1	I	7	VAL	2.8
1	C	420	ASP	2.8
1	O	332	CYS	2.8
1	B	29	GLU	2.7
1	K	245	HIS	2.7
1	N	105	THR	2.7
1	C	421	LEU	2.7
1	N	243	VAL	2.7
1	I	107	TRP	2.7
1	T	420	ASP	2.7
1	G	184	ILE	2.7
1	T	241	TYR	2.6
1	K	105	THR	2.6
1	U	184	ILE	2.6
1	M	106	GLN	2.6
1	P	106	GLN	2.6
1	B	107	TRP	2.5
1	E	105	THR	2.5
1	E	7	VAL	2.5
1	N	221	LEU	2.5
1	A	23	ARG	2.5
1	H	232	ARG	2.5
1	T	101	ARG	2.5
1	M	105	THR	2.4
1	F	332	CYS	2.4
1	K	243	VAL	2.4
1	T	7	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	107	TRP	2.4
1	P	173	GLY	2.4
1	B	228	PRO	2.4
1	E	107	TRP	2.4
1	N	242	ILE	2.3
1	R	221	LEU	2.3
1	T	216	PHE	2.3
1	T	261	ASP	2.3
1	F	107	TRP	2.3
1	T	104	GLU	2.3
1	T	242	ILE	2.3
1	G	420	ASP	2.3
1	M	22	GLY	2.3
1	F	421	LEU	2.3
1	D	105	THR	2.3
1	T	106	GLN	2.2
1	N	184	ILE	2.2
1	H	233	ASP	2.2
1	B	241	TYR	2.2
1	J	332	CYS	2.2
1	R	107	TRP	2.2
1	D	186	PHE	2.1
1	K	221	LEU	2.1
1	C	100	GLN	2.1
1	J	106	GLN	2.1
1	U	101	ARG	2.1
1	O	420	ASP	2.1
1	B	243	VAL	2.1
1	N	197	PRO	2.1
1	K	419	LEU	2.1
1	J	420	ASP	2.1
1	M	318	ASP	2.1
1	P	186	PHE	2.0
1	T	245	HIS	2.0
1	K	108	TYR	2.0
1	M	221	LEU	2.0
1	U	216	PHE	2.0
1	F	24	GLY	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	A	501	5/5	0.98	0.07	38,38,39,39	0
2	SO4	G	501	5/5	0.98	0.07	38,40,41,46	0
2	SO4	T	503	5/5	0.98	0.07	28,32,34,35	0
2	SO4	B	502	5/5	0.99	0.08	21,26,29,29	0
2	SO4	C	502	5/5	0.99	0.07	21,26,26,34	0
2	SO4	D	502	5/5	0.99	0.08	20,22,23,27	0
2	SO4	E	502	5/5	0.99	0.05	30,30,34,44	0
2	SO4	E	503	5/5	0.99	0.09	32,33,33,34	0
2	SO4	H	501	5/5	0.99	0.07	24,26,28,31	0
2	SO4	H	502	5/5	0.99	0.09	43,43,44,44	0
2	SO4	I	501	5/5	0.99	0.10	20,24,25,28	0
2	SO4	I	502	5/5	0.99	0.08	39,39,41,42	0
2	SO4	J	501	5/5	0.99	0.08	19,23,25,25	0
2	SO4	K	501	5/5	0.99	0.08	27,27,27,28	0
2	SO4	K	502	5/5	0.99	0.05	28,29,31,33	0
2	SO4	L	501	5/5	0.99	0.08	28,30,32,32	0
2	SO4	L	502	5/5	0.99	0.06	31,32,32,35	0
2	SO4	N	501	5/5	0.99	0.07	22,24,29,30	0
2	SO4	N	502	5/5	0.99	0.08	30,31,31,33	0
2	SO4	O	502	5/5	0.99	0.06	26,28,29,32	0
2	SO4	P	501	5/5	0.99	0.07	21,21,25,25	0
2	SO4	P	502	5/5	0.99	0.08	39,40,41,46	0
2	SO4	Q	501	5/5	0.99	0.08	19,22,23,29	0
2	SO4	Q	502	5/5	0.99	0.09	38,39,39,44	0
2	SO4	R	502	5/5	0.99	0.07	33,34,34,39	0
2	SO4	F	501	5/5	0.99	0.09	23,23,23,28	0
2	SO4	F	502	5/5	0.99	0.06	30,31,33,34	0
2	SO4	A	502	5/5	0.99	0.05	43,44,45,45	0
2	SO4	M	501	5/5	0.99	0.06	26,26,27,29	0
2	SO4	M	502	5/5	0.99	0.08	31,31,34,41	0
2	SO4	T	501	5/5	0.99	0.09	23,24,30,39	0
2	SO4	B	501	5/5	0.99	0.07	26,27,30,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	U	501	5/5	0.99	0.09	23,24,27,28	0
2	SO4	U	502	5/5	0.99	0.07	33,34,34,35	0
2	SO4	G	502	5/5	1.00	0.06	29,30,31,31	0
2	SO4	O	501	5/5	1.00	0.10	21,21,22,24	0
2	SO4	R	501	5/5	1.00	0.08	21,21,24,26	0
2	SO4	D	501	5/5	1.00	0.08	19,22,25,25	0
2	SO4	T	502	5/5	1.00	0.07	27,28,29,30	0
2	SO4	J	502	5/5	1.00	0.06	19,21,26,27	0
2	SO4	C	501	5/5	1.00	0.09	19,25,25,28	0
2	SO4	E	501	5/5	1.00	0.07	23,25,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.