



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 08:33 am BST

PDB ID : 1TF7  
Title : Crystal Structure of Circadian Clock Protein KaiC  
Authors : Pattanayek, R.; Wang, J.; Mori, T.; Xu, Y.; Johnson, C.H.; Egli, M.  
Deposited on : 2004-05-26  
Resolution : 2.80 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.

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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 : 2.11  
buster-report : 1.1.7 (2018)  
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) : 2.11

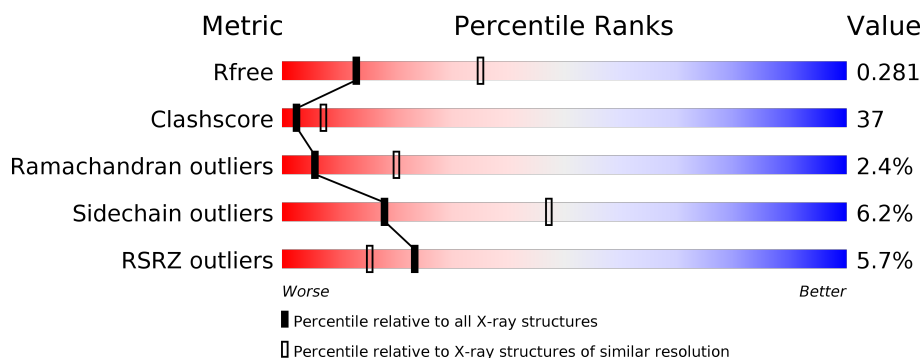
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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	525	<div> <div>8%</div> <div> <div></div> <div>47%</div> <div>40%</div> <div>5%</div> <div>8%</div> </div> </div>
1	B	525	<div> <div>7%</div> <div> <div></div> <div>46%</div> <div>41%</div> <div>5%</div> <div>8%</div> </div> </div>
1	C	525	<div> <div>5%</div> <div> <div></div> <div>41%</div> <div>44%</div> <div>6%</div> <div>8%</div> </div> </div>
1	D	525	<div> <div>4%</div> <div> <div></div> <div>47%</div> <div>40%</div> <div>5%</div> <div>8%</div> </div> </div>
1	E	525	<div> <div>4%</div> <div> <div></div> <div>46%</div> <div>41%</div> <div>6%</div> <div>8%</div> </div> </div>
1	F	525	<div> <div>4%</div> <div> <div></div> <div>43%</div> <div>43%</div> <div>6%</div> <div>8%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23333 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 KaiC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			
1	B	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			
1	C	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			
1	D	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			
1	E	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			
1	F	484	Total	C	N	O	S	0	0	0
			3815	2407	670	723	15			

There are 36 discrepancies between the modelled and reference sequences:

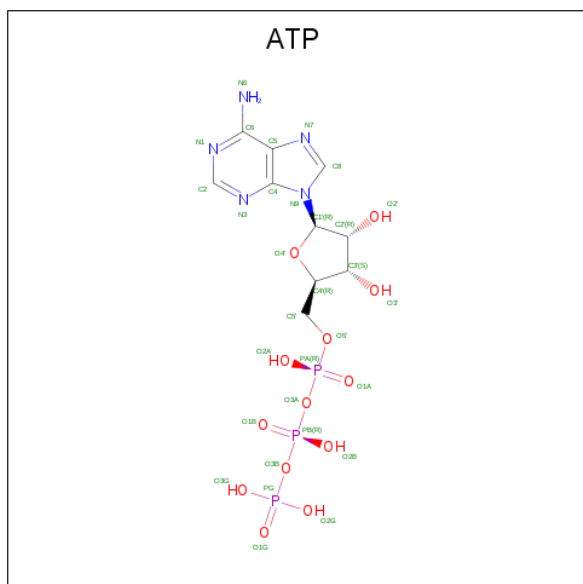
Chain	Residue	Modelled	Actual	Comment	Reference
A	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
A	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
A	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
A	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
A	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
A	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
B	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
C	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
C	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
C	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
C	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
C	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
D	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
E	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	520	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	521	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	522	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	523	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	524	HIS	-	EXPRESSION TAG	UNP Q9Z3H2
F	525	HIS	-	EXPRESSION TAG	UNP Q9Z3H2

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	
			31	10	5	13	3	

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

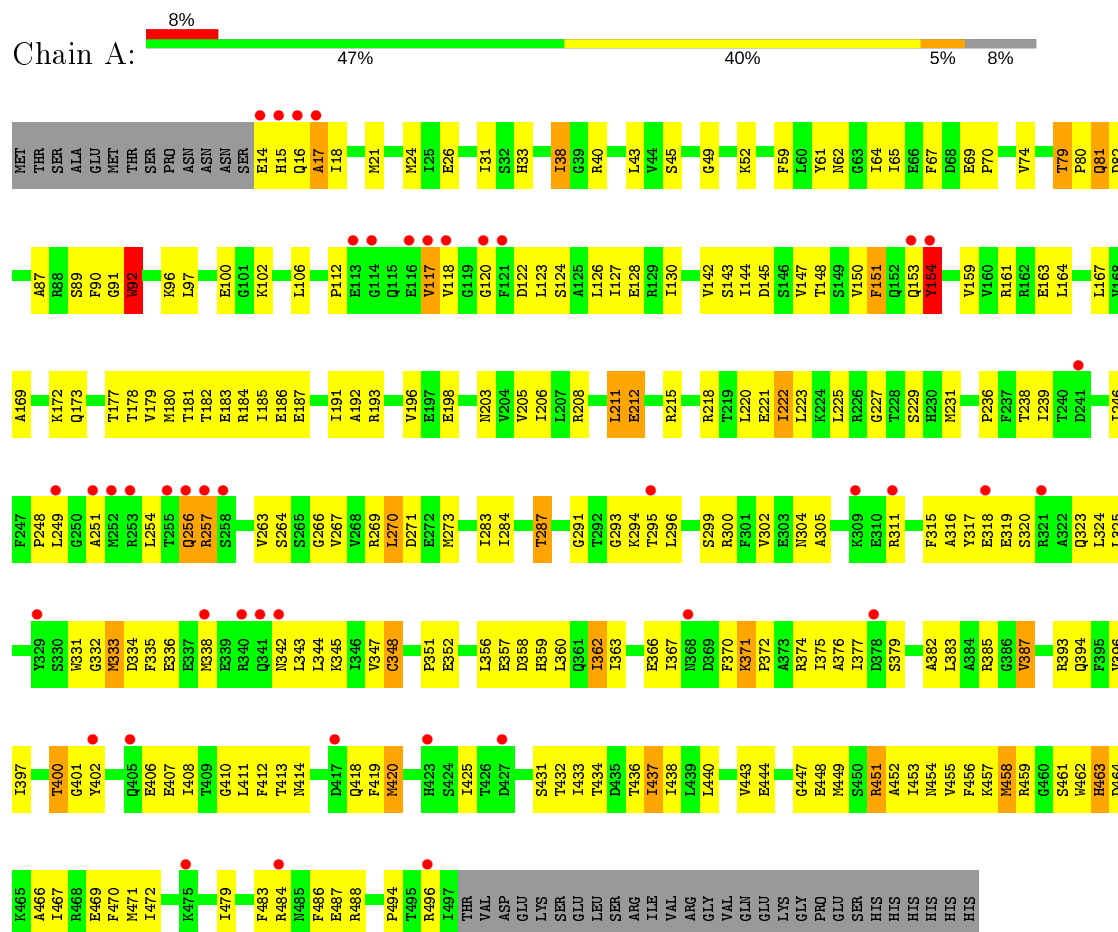
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	7	Total	O	0	0
			7	7		
3	C	7	Total	O	0	0
			7	7		
3	D	13	Total	O	0	0
			13	13		
3	E	12	Total	O	0	0
			12	12		
3	F	23	Total	O	0	0
			23	23		

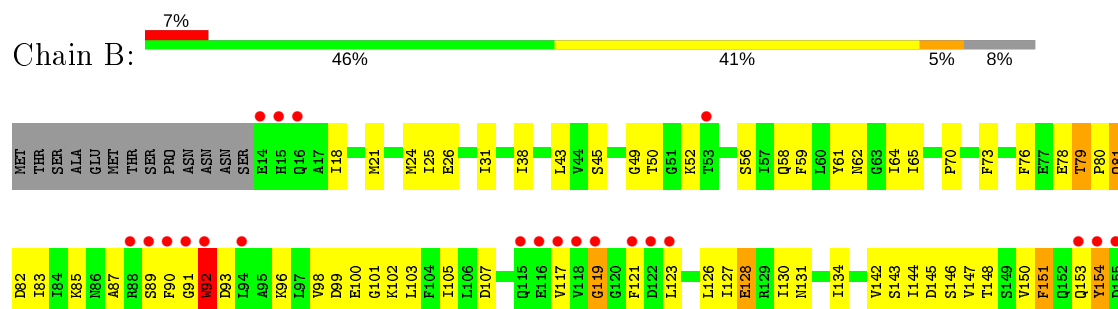
### 3 Residue-property plots

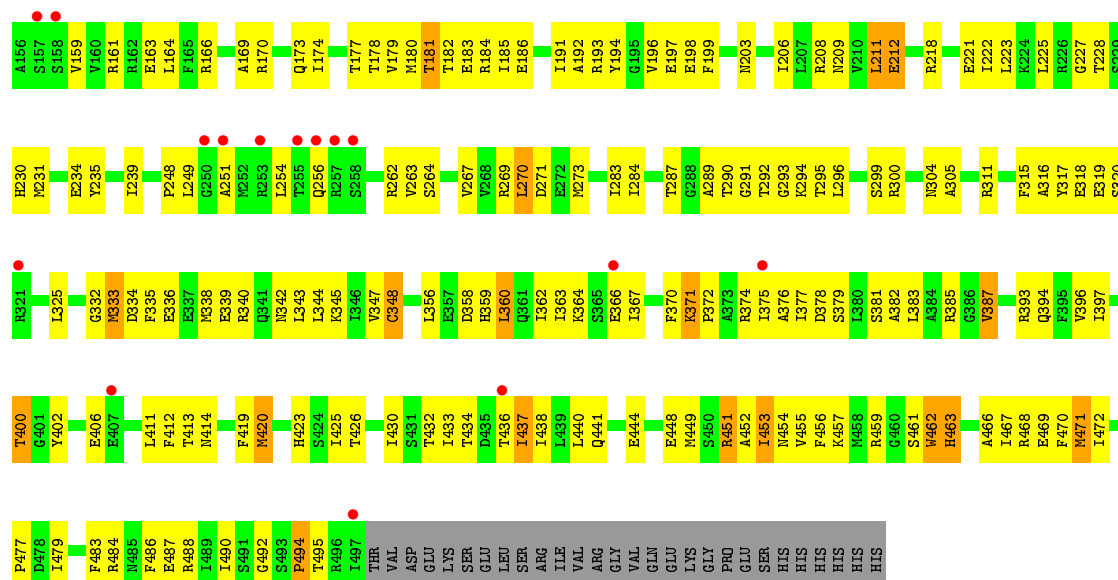
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

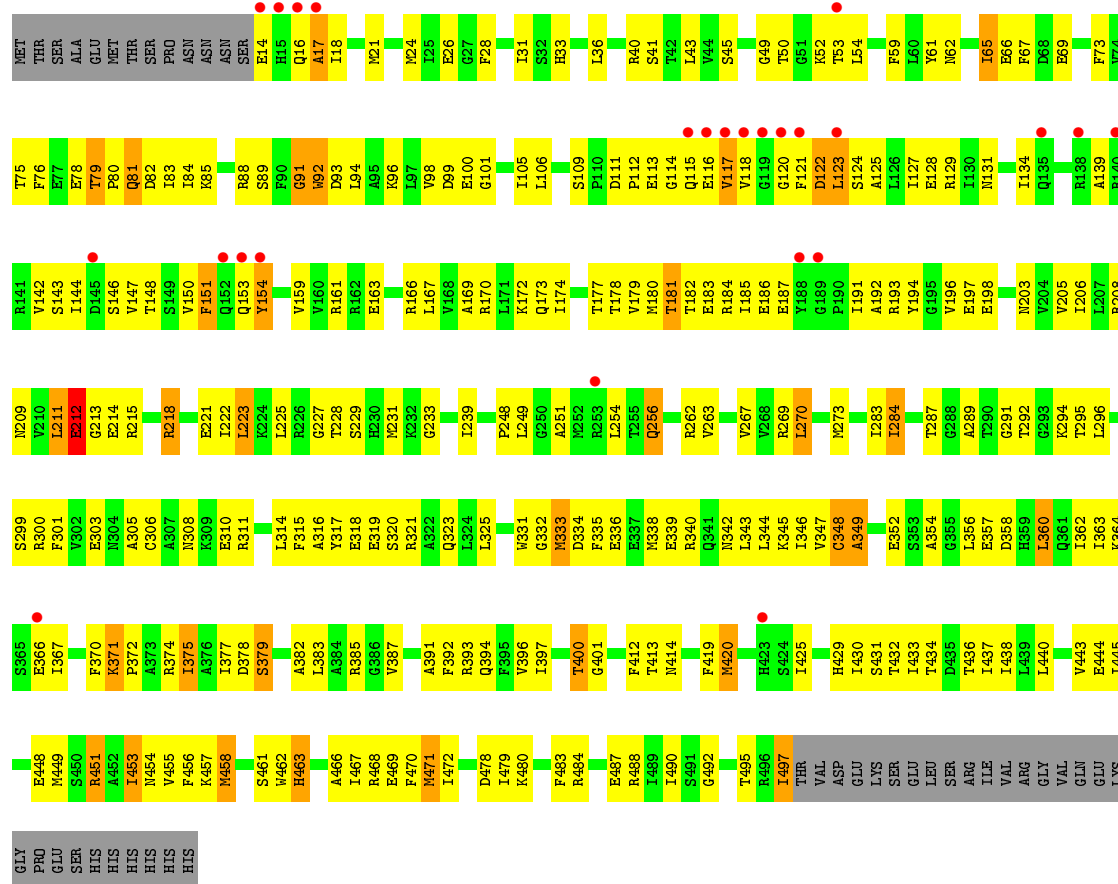
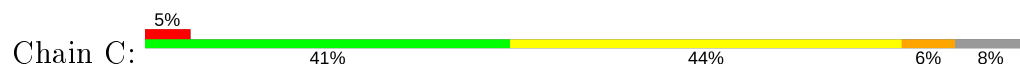


#### • Molecule 1: KaiC

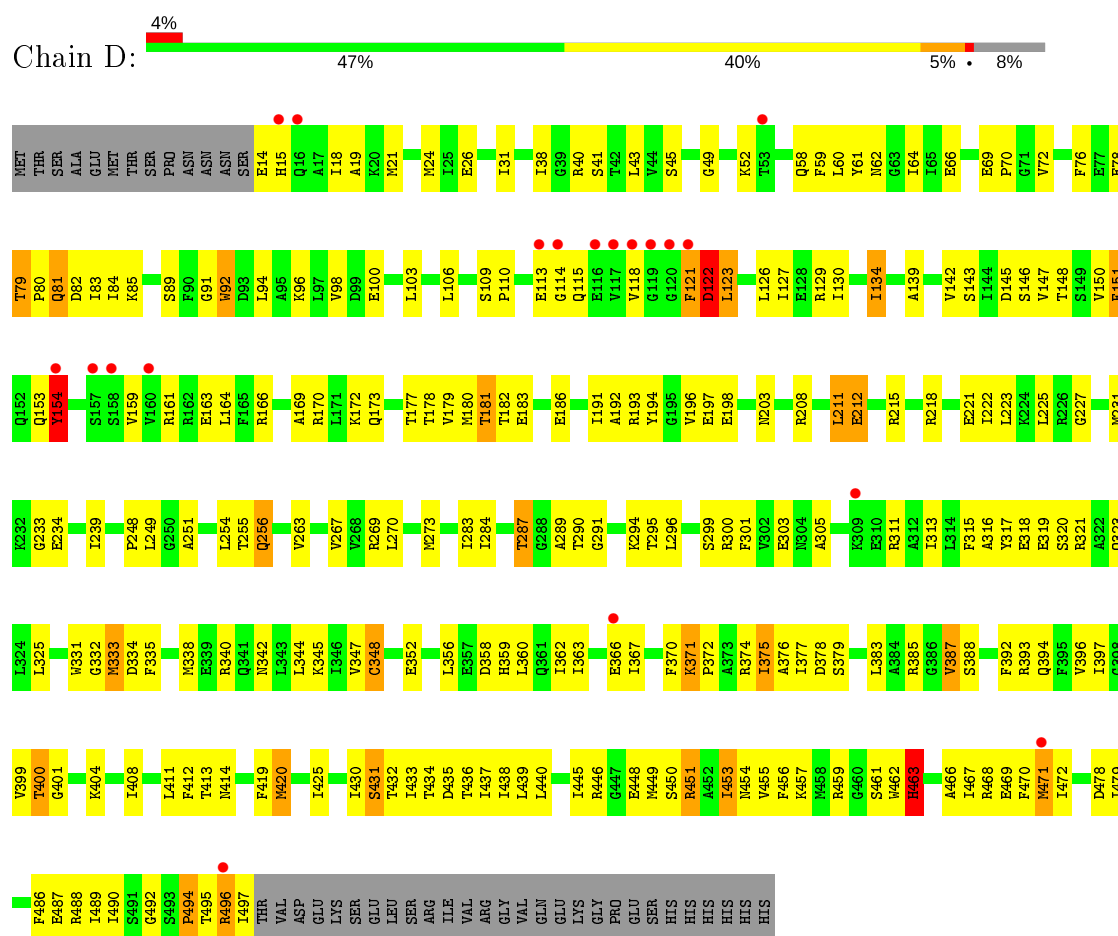




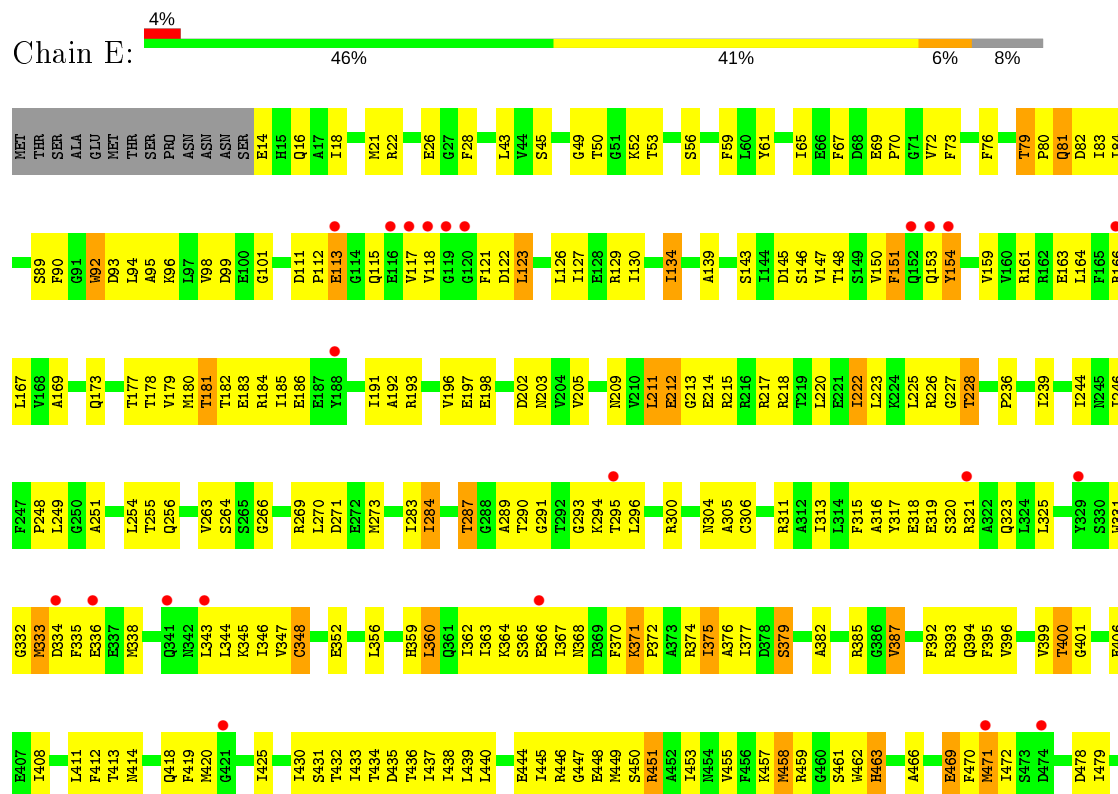
- Molecule 1: KaiC



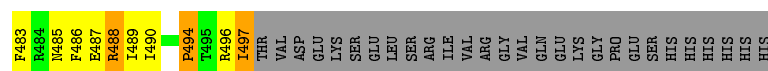
- Molecule 1: KaiC



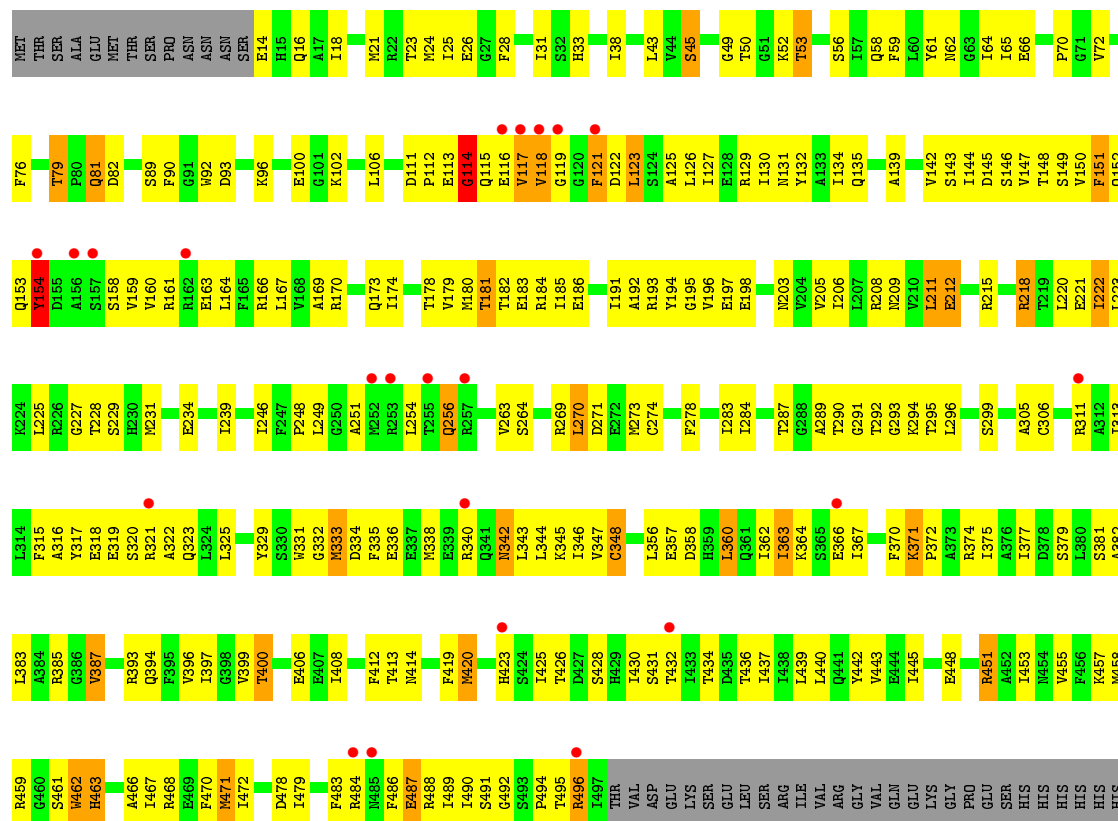
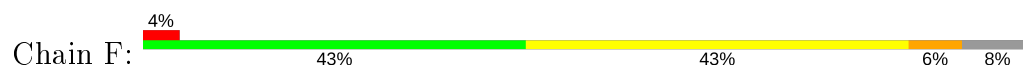
• Molecule 1: KaiC







• Molecule 1: KaiC



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.87Å 135.58Å 204.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 29.73 – 2.83	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.80) 89.7 (29.73-2.83)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.77 (at 2.85Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.240 , 0.280 0.241 , 0.281	Depositor DCC
$R_{free}$ test set	4041 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.8	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 57.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	23333	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.47	3/3880 (0.1%)	0.66	3/5229 (0.1%)
1	B	0.40	1/3880 (0.0%)	0.62	0/5229
1	C	0.45	4/3880 (0.1%)	0.66	6/5229 (0.1%)
1	D	0.46	1/3880 (0.0%)	0.69	5/5229 (0.1%)
1	E	0.43	1/3880 (0.0%)	0.66	1/5229 (0.0%)
1	F	0.40	0/3880	0.64	1/5229 (0.0%)
All	All	0.44	10/23280 (0.0%)	0.66	16/31374 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	TRP	CB-CG	11.02	1.70	1.50
1	A	92	TRP	CA-CB	9.65	1.75	1.53
1	D	91	GLY	C-O	-8.20	1.10	1.23
1	A	92	TRP	CA-C	6.83	1.70	1.52
1	C	91	GLY	CA-C	-6.37	1.41	1.51
1	C	92	TRP	N-CA	-5.54	1.35	1.46
1	B	92	TRP	CD2-CE3	-5.53	1.32	1.40
1	C	92	TRP	CG-CD1	-5.25	1.29	1.36
1	E	92	TRP	CD2-CE3	-5.24	1.32	1.40
1	C	92	TRP	CA-CB	-5.15	1.42	1.53

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	TRP	CB-CG-CD1	8.83	138.48	127.00
1	A	92	TRP	CB-CG-CD2	-7.66	116.64	126.60
1	D	91	GLY	CA-C-O	7.54	134.17	120.60
1	D	92	TRP	CB-CG-CD1	7.49	136.74	127.00
1	D	92	TRP	CA-CB-CG	7.19	127.37	113.70
1	D	92	TRP	CB-CG-CD2	-7.12	117.34	126.60
1	C	91	GLY	CA-C-O	6.73	132.72	120.60
1	C	213	GLY	N-CA-C	-6.58	96.64	113.10
1	E	213	GLY	N-CA-C	-6.37	97.17	113.10
1	D	92	TRP	N-CA-CB	-5.91	99.97	110.60
1	C	92	TRP	CB-CG-CD2	5.85	134.21	126.60
1	C	92	TRP	CG-CD1-NE1	5.39	115.49	110.10
1	F	114	GLY	N-CA-C	5.38	126.56	113.10
1	C	92	TRP	CB-CG-CD1	-5.22	120.21	127.00
1	A	92	TRP	CB-CA-C	5.16	120.72	110.40
1	C	92	TRP	CD1-CG-CD2	-5.04	102.27	106.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	257	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3815	0	3814	287	0
1	B	3815	0	3814	288	0
1	C	3815	0	3814	302	0
1	D	3815	0	3814	318	0
1	E	3815	0	3814	287	0
1	F	3815	0	3814	340	0
2	A	62	0	24	8	0
2	B	62	0	24	10	0
2	C	62	0	24	8	0
2	D	62	0	24	7	0
2	E	62	0	24	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	62	0	24	8	0
3	A	9	0	0	0	0
3	B	7	0	0	0	0
3	C	7	0	0	2	0
3	D	13	0	0	1	0
3	E	12	0	0	2	0
3	F	23	0	0	5	0
All	All	23333	0	23028	1709	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (1709) 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:A:92:TRP:CA	1:A:92:TRP:CB	1.75	1.58
1:A:257:ARG:NH2	1:A:407:GLU:HG2	1.50	1.26
1:F:313:ILE:HB	1:F:375:ILE:CD1	1.74	1.18
1:B:284:ILE:HD12	1:B:436:THR:HB	1.30	1.14
1:D:284:ILE:HD12	1:D:436:THR:HB	1.35	1.09
1:E:263:VAL:HG12	1:E:374:ARG:HH21	1.19	1.07
1:F:305:ALA:HB2	1:F:374:ARG:HD2	1.32	1.06
1:D:60:LEU:O	1:D:64:ILE:HD13	1.57	1.04
1:E:284:ILE:HD12	1:E:436:THR:HB	1.40	1.03
1:F:263:VAL:HG12	1:F:374:ARG:HH21	1.19	1.03
1:D:486:PHE:CB	1:D:489:ILE:HD11	1.89	1.03
1:C:284:ILE:HD12	1:C:436:THR:HB	1.34	1.03
1:C:205:VAL:HG22	1:C:222:ILE:HD13	1.38	1.02
1:E:123:LEU:HD13	1:E:166:ARG:HD2	1.41	1.01
1:A:257:ARG:NH2	1:A:407:GLU:CG	2.22	1.01
1:C:61:TYR:O	1:C:65:ILE:HD13	1.60	1.01
1:A:205:VAL:HG22	1:A:222:ILE:HD12	1.38	1.01
1:D:126:LEU:O	1:D:130:ILE:HD13	1.62	0.99
1:E:205:VAL:HG22	1:E:222:ILE:HD12	1.40	0.99
1:B:263:VAL:HG12	1:B:374:ARG:HH21	1.27	0.99
1:D:147:VAL:HG11	1:D:180:MET:HE3	1.41	0.99
1:F:205:VAL:HG22	1:F:222:ILE:HD12	1.44	0.99
1:A:379:SER:H	1:A:413:THR:HB	1.24	0.98
1:C:287:THR:HG23	1:C:414:ASN:HD22	1.28	0.97
1:D:486:PHE:HB3	1:D:489:ILE:HD11	1.46	0.96
1:A:24:MET:HB2	1:A:62:ASN:HD22	1.32	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ALA:O	1:A:92:TRP:HB2	1.67	0.95
1:B:311:ARG:HD2	1:B:371:LYS:HD2	1.45	0.95
1:B:64:ILE:HD12	1:B:102:LYS:HB3	1.48	0.95
1:A:263:VAL:HG12	1:A:374:ARG:HH21	1.29	0.94
1:A:257:ARG:HH21	1:A:407:GLU:HG2	1.08	0.94
1:D:313:ILE:HD12	1:D:367:ILE:HD13	1.50	0.94
1:E:305:ALA:HB2	1:E:374:ARG:HD2	1.50	0.94
1:D:123:LEU:HD12	1:D:166:ARG:HD2	1.50	0.93
1:D:453:ILE:HG21	1:D:479:ILE:HD12	1.47	0.93
1:E:315:PHE:CE2	1:E:366:GLU:OE1	2.20	0.93
1:A:287:THR:HG23	1:A:414:ASN:HD22	1.31	0.93
1:C:315:PHE:HE2	1:C:366:GLU:OE1	1.52	0.92
1:D:79:THR:HG22	1:D:82:ASP:H	1.32	0.92
1:B:147:VAL:O	1:B:150:VAL:HG12	1.70	0.92
1:F:313:ILE:HB	1:F:375:ILE:HD11	1.50	0.92
1:A:362:ILE:O	1:A:366:GLU:HG3	1.70	0.92
1:C:311:ARG:HD2	1:C:371:LYS:HD2	1.51	0.92
1:E:313:ILE:HD12	1:E:367:ILE:HD13	1.50	0.92
1:C:315:PHE:CE2	1:C:366:GLU:OE1	2.24	0.91
1:D:287:THR:HG23	1:D:414:ASN:HD22	1.36	0.91
1:F:64:ILE:HD12	1:F:102:LYS:HB3	1.52	0.91
1:B:64:ILE:HD11	1:B:70:PRO:HA	1.52	0.90
1:F:434:THR:HG23	1:F:437:ILE:HD11	1.52	0.90
1:D:146:SER:H	1:D:181:THR:HG22	1.36	0.90
1:F:106:LEU:HD11	1:F:129:ARG:CZ	2.02	0.90
1:E:315:PHE:HE2	1:E:366:GLU:OE1	1.55	0.89
1:A:147:VAL:O	1:A:150:VAL:HG12	1.72	0.89
1:A:305:ALA:HB2	1:A:374:ARG:HD2	1.54	0.89
1:B:305:ALA:HB2	1:B:374:ARG:HD2	1.53	0.89
1:F:315:PHE:CE2	1:F:366:GLU:OE1	2.24	0.89
1:F:379:SER:H	1:F:413:THR:HB	1.37	0.89
1:C:84:ILE:HD12	1:C:94:LEU:HB2	1.55	0.89
1:C:147:VAL:O	1:C:150:VAL:HG12	1.72	0.88
1:C:495:THR:HA	1:D:487:GLU:OE2	1.73	0.88
1:C:14:GLU:HG3	1:C:16:GLN:H	1.39	0.88
1:B:31:ILE:HG22	1:B:222:ILE:HD12	1.52	0.87
1:A:257:ARG:HH21	1:A:407:GLU:CG	1.85	0.87
1:E:147:VAL:O	1:E:150:VAL:HG12	1.75	0.86
1:F:123:LEU:HD12	1:F:166:ARG:HD2	1.56	0.86
1:A:147:VAL:HG11	1:A:180:MET:HE3	1.55	0.86
1:D:18:ILE:H	1:D:18:ILE:HD12	1.39	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:VAL:HG11	1:C:180:MET:HE3	1.59	0.85
1:E:79:THR:CG2	1:E:81:GLN:HG2	2.06	0.85
1:D:379:SER:H	1:D:413:THR:HB	1.42	0.85
1:E:287:THR:HG23	1:E:414:ASN:HD22	1.42	0.85
1:C:449:MET:CE	1:D:490:ILE:HD11	2.07	0.84
1:E:147:VAL:HG11	1:E:180:MET:HE2	1.59	0.84
1:D:315:PHE:CE2	1:D:366:GLU:OE1	2.30	0.84
1:E:263:VAL:HG12	1:E:374:ARG:NH2	1.91	0.84
1:B:437:ILE:CD1	1:B:457:LYS:HE2	2.07	0.84
1:A:358:ASP:O	1:A:362:ILE:HD13	1.77	0.83
1:A:311:ARG:HD2	1:A:371:LYS:HD2	1.60	0.83
1:B:263:VAL:HG12	1:B:374:ARG:NH2	1.92	0.83
1:D:147:VAL:O	1:D:150:VAL:HG12	1.78	0.83
1:B:31:ILE:HD13	1:B:231:MET:SD	2.18	0.83
1:F:263:VAL:HG12	1:F:374:ARG:NH2	1.94	0.83
1:D:31:ILE:HG22	1:D:222:ILE:HD12	1.59	0.83
1:A:79:THR:CG2	1:A:81:GLN:HG2	2.09	0.83
1:B:434:THR:HG23	1:B:437:ILE:HD11	1.60	0.83
1:D:446:ARG:N	1:D:496:ARG:HH12	1.75	0.83
1:E:446:ARG:HE	1:E:496:ARG:NH2	1.76	0.82
1:A:434:THR:HG23	1:A:437:ILE:HD11	1.61	0.82
1:D:446:ARG:H	1:D:496:ARG:HH12	1.26	0.82
1:F:147:VAL:O	1:F:150:VAL:HG12	1.79	0.82
1:A:315:PHE:CE2	1:A:366:GLU:OE1	2.32	0.82
1:D:311:ARG:HD2	1:D:371:LYS:HD2	1.61	0.82
1:E:79:THR:HG23	1:E:81:GLN:HG2	1.62	0.82
1:F:347:VAL:HG21	1:F:366:GLU:OE1	1.80	0.82
1:B:191:ILE:HD12	1:B:198:GLU:HG2	1.62	0.82
1:E:449:MET:HG2	1:F:467:ILE:HD11	1.62	0.82
1:C:488:ARG:NH2	1:D:488:ARG:HH21	1.78	0.81
1:F:25:ILE:HD12	1:F:58:GLN:HE21	1.42	0.81
1:B:311:ARG:HD2	1:B:371:LYS:CD	2.10	0.81
1:D:311:ARG:HD2	1:D:371:LYS:CD	2.11	0.81
1:A:117:VAL:HA	1:A:154:TYR:OH	1.79	0.81
1:C:392:PHE:HE2	1:C:430:ILE:HD11	1.45	0.81
1:E:311:ARG:HD2	1:E:371:LYS:HD2	1.62	0.81
1:D:486:PHE:HB2	1:D:489:ILE:HD11	1.60	0.81
1:C:311:ARG:HD2	1:C:371:LYS:CD	2.10	0.81
1:E:379:SER:H	1:E:413:THR:HB	1.43	0.81
1:B:147:VAL:HG11	1:B:180:MET:HE3	1.63	0.81
1:E:283:ILE:HD12	1:E:412:PHE:HE1	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:191:ILE:HB	1:F:198:GLU:CG	2.11	0.81
1:F:263:VAL:CG1	1:F:374:ARG:HH21	1.92	0.81
1:A:79:THR:HG22	1:A:82:ASP:H	1.46	0.81
1:F:315:PHE:HE1	1:F:375:ILE:HD12	1.45	0.81
1:B:436:THR:C	1:B:437:ILE:HD12	2.01	0.80
1:B:444:GLU:OE1	1:C:490:ILE:HD12	1.82	0.80
1:B:64:ILE:CD1	1:B:70:PRO:HA	2.11	0.80
1:F:313:ILE:HD12	1:F:367:ILE:HD13	1.63	0.80
1:F:64:ILE:HD11	1:F:70:PRO:HA	1.63	0.79
1:B:362:ILE:O	1:B:366:GLU:HG3	1.83	0.79
1:E:347:VAL:HG21	1:E:366:GLU:OE1	1.83	0.79
1:D:182:THR:HG21	1:D:192:ALA:HB1	1.65	0.79
1:F:287:THR:HG23	1:F:414:ASN:HD22	1.46	0.79
1:A:436:THR:C	1:A:437:ILE:HD12	2.03	0.78
1:A:451:ARG:HH11	1:A:451:ARG:HG2	1.47	0.78
1:B:45:SER:HB3	1:B:182:THR:HB	1.64	0.78
1:C:263:VAL:HG12	1:C:374:ARG:HH21	1.48	0.78
1:C:347:VAL:HG21	1:C:366:GLU:OE1	1.83	0.78
1:A:263:VAL:HG12	1:A:374:ARG:NH2	1.97	0.78
1:A:311:ARG:HD2	1:A:371:LYS:CD	2.13	0.78
1:F:79:THR:HG22	1:F:82:ASP:H	1.49	0.78
1:D:425:ILE:HD11	1:D:456:PHE:CE2	2.18	0.78
1:C:73:PHE:HB3	1:C:105:ILE:HD13	1.66	0.78
1:E:79:THR:HG22	1:E:82:ASP:H	1.48	0.78
1:A:161:ARG:HB2	1:A:196:VAL:HG11	1.63	0.77
1:B:24:MET:HB2	1:B:62:ASN:HD22	1.47	0.77
1:D:263:VAL:HG12	1:D:374:ARG:HH21	1.50	0.77
1:E:49:GLY:HA2	2:E:5903:ATP:O2B	1.85	0.77
1:F:161:ARG:HB2	1:F:196:VAL:HG11	1.63	0.77
1:F:436:THR:C	1:F:437:ILE:HD12	2.04	0.77
1:F:489:ILE:HA	1:F:494:PRO:HG3	1.65	0.77
1:F:182:THR:HG21	1:F:192:ALA:HB1	1.67	0.77
1:A:74:VAL:HB	1:A:144:ILE:HD12	1.67	0.77
1:D:287:THR:CG2	1:D:414:ASN:HD22	1.97	0.77
1:B:284:ILE:HD12	1:B:436:THR:CB	2.13	0.77
1:B:420:MET:CE	1:C:490:ILE:HD13	2.15	0.77
1:F:25:ILE:HD12	1:F:58:GLN:NE2	1.99	0.77
1:D:495:THR:HA	1:E:487:GLU:OE2	1.85	0.77
1:D:367:ILE:HD12	1:D:375:ILE:HD11	1.66	0.76
1:D:489:ILE:HD13	1:D:494:PRO:HB3	1.65	0.76
1:F:313:ILE:HB	1:F:375:ILE:HD13	1.64	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:191:ILE:HB	1:D:198:GLU:CG	2.16	0.76
1:B:73:PHE:HB3	1:B:105:ILE:HD13	1.65	0.76
1:A:347:VAL:HG21	1:A:366:GLU:OE1	1.85	0.76
1:C:362:ILE:O	1:C:366:GLU:HG3	1.86	0.76
1:C:305:ALA:HB2	1:C:374:ARG:HD2	1.68	0.76
1:A:315:PHE:HE2	1:A:366:GLU:OE1	1.66	0.76
1:C:449:MET:HE3	1:D:490:ILE:HD11	1.66	0.76
1:E:161:ARG:HB2	1:E:196:VAL:HG11	1.65	0.76
1:B:191:ILE:HB	1:B:198:GLU:CG	2.16	0.76
1:B:263:VAL:CG1	1:B:374:ARG:HH21	1.98	0.76
1:B:315:PHE:HE2	1:B:366:GLU:OE1	1.68	0.75
1:B:161:ARG:HB2	1:B:196:VAL:HG11	1.68	0.75
1:A:320:SER:HA	1:B:254:LEU:HG	1.67	0.75
1:A:315:PHE:CD2	1:A:363:ILE:HD12	2.20	0.75
1:C:344:LEU:HD22	1:C:345:LYS:N	2.01	0.75
1:A:92:TRP:CB	1:A:92:TRP:HA	2.11	0.75
1:D:305:ALA:HB2	1:D:374:ARG:HD2	1.69	0.75
1:D:347:VAL:HG21	1:D:366:GLU:OE1	1.87	0.75
1:E:72:VAL:HG21	1:E:134:ILE:HD12	1.69	0.75
1:C:367:ILE:HG12	1:C:375:ILE:HD11	1.67	0.74
1:F:53:THR:HG23	1:F:145:ASP:OD1	1.87	0.74
1:A:257:ARG:HH22	1:A:407:GLU:HG2	1.52	0.74
1:A:437:ILE:CD1	1:A:457:LYS:HE2	2.17	0.74
1:F:203:ASN:HB3	1:F:225:LEU:HD23	1.68	0.74
1:B:43:LEU:HD11	1:B:182:THR:OG1	1.87	0.74
1:B:441:GLN:HE22	1:B:490:ILE:HD13	1.51	0.74
1:B:315:PHE:CE2	1:B:366:GLU:OE1	2.40	0.74
1:D:79:THR:CG2	1:D:81:GLN:HG2	2.18	0.74
1:A:263:VAL:CG1	1:A:374:ARG:HH21	2.01	0.74
1:A:299:SER:HB3	1:A:333:MET:HE1	1.69	0.74
1:C:262:ARG:HH22	1:C:461:SER:HB2	1.52	0.74
1:E:363:ILE:O	1:E:367:ILE:HG12	1.88	0.74
1:F:362:ILE:O	1:F:366:GLU:HG3	1.88	0.74
1:C:284:ILE:HD11	3:C:3910:HOH:O	1.86	0.74
1:B:377:ILE:HD13	1:B:412:PHE:CE2	2.22	0.73
1:D:49:GLY:HA2	2:D:4903:ATP:O2B	1.87	0.73
1:B:347:VAL:HG21	1:B:366:GLU:OE1	1.88	0.73
1:A:64:ILE:HD12	1:A:102:LYS:HB3	1.70	0.73
1:D:284:ILE:HD12	1:D:436:THR:CB	2.17	0.73
1:F:486:PHE:CB	1:F:489:ILE:HD11	2.18	0.73
1:D:299:SER:HB3	1:D:333:MET:HE1	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:123:LEU:HD12	1:E:163:GLU:OE2	1.88	0.73
1:E:269:ARG:HG2	1:E:479:ILE:HB	1.71	0.73
1:B:287:THR:HG23	1:B:414:ASN:HD22	1.53	0.73
1:E:263:VAL:CG1	1:E:374:ARG:HH21	2.00	0.73
1:A:127:ILE:HD11	1:A:167:LEU:HD12	1.70	0.72
1:B:317:TYR:OH	1:B:363:ILE:HD11	1.89	0.72
1:D:375:ILE:CD1	1:D:408:ILE:HG21	2.20	0.72
1:E:191:ILE:HD12	1:E:198:GLU:HG2	1.71	0.72
1:B:49:GLY:HA2	2:B:2903:ATP:O2B	1.90	0.72
1:F:315:PHE:HE2	1:F:366:GLU:OE1	1.68	0.72
1:D:284:ILE:CD1	1:D:436:THR:HB	2.16	0.72
1:A:287:THR:CG2	1:A:414:ASN:HD22	2.02	0.72
1:D:263:VAL:HG12	1:D:374:ARG:NH2	2.05	0.72
1:C:269:ARG:HG2	1:C:479:ILE:HB	1.72	0.72
1:E:311:ARG:HD2	1:E:371:LYS:CD	2.20	0.72
1:D:392:PHE:HE2	1:D:430:ILE:HD11	1.52	0.72
1:F:118:VAL:HG12	1:F:153:GLN:HE22	1.54	0.72
1:F:363:ILE:O	1:F:367:ILE:HG12	1.90	0.72
1:B:127:ILE:HG21	1:B:170:ARG:HG3	1.72	0.71
1:D:315:PHE:HE2	1:D:366:GLU:OE1	1.69	0.71
1:B:420:MET:HE3	1:C:490:ILE:HD13	1.71	0.71
1:E:191:ILE:HB	1:E:198:GLU:CG	2.19	0.71
1:C:392:PHE:CE2	1:C:430:ILE:HD11	2.25	0.71
1:F:191:ILE:HG23	1:F:206:ILE:HD11	1.71	0.71
1:A:254:LEU:HG	1:F:320:SER:HA	1.72	0.71
1:C:487:GLU:HG3	1:C:497:ILE:HD11	1.72	0.71
1:F:344:LEU:HD22	1:F:345:LYS:N	2.06	0.71
1:C:440:LEU:CD2	1:C:453:ILE:HG12	2.20	0.71
1:E:367:ILE:HD12	1:E:375:ILE:HD11	1.73	0.71
1:C:85:LYS:NZ	1:D:14:GLU:HB3	2.05	0.71
1:E:446:ARG:HE	1:E:496:ARG:HH22	1.36	0.71
1:F:437:ILE:HD13	1:F:457:LYS:CE	2.20	0.71
1:A:437:ILE:HD13	1:A:457:LYS:CG	2.21	0.70
1:E:14:GLU:HG3	1:E:16:GLN:H	1.53	0.70
1:A:147:VAL:HG11	1:A:180:MET:CE	2.21	0.70
1:F:269:ARG:HG2	1:F:479:ILE:HB	1.72	0.70
1:E:325:LEU:HD23	1:E:335:PHE:HB2	1.72	0.70
1:F:49:GLY:HA2	2:F:6903:ATP:O2B	1.92	0.70
1:A:150:VAL:HG13	1:A:151:PHE:N	2.06	0.70
1:D:161:ARG:HB2	1:D:196:VAL:HG11	1.72	0.70
1:E:284:ILE:HD11	3:E:5911:HOH:O	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:496:ARG:C	1:E:497:ILE:HD13	2.11	0.70
1:A:64:ILE:HD11	1:A:70:PRO:HA	1.72	0.70
1:B:123:LEU:HD12	1:B:166:ARG:HD2	1.74	0.70
1:B:218:ARG:NH1	1:B:239:ILE:HD12	2.07	0.70
1:F:299:SER:HB3	1:F:333:MET:HE1	1.74	0.70
1:A:377:ILE:HD13	1:A:412:PHE:CE2	2.26	0.69
1:F:79:THR:HG23	1:F:81:GLN:HG2	1.74	0.69
1:A:295:THR:HG21	1:A:319:GLU:OE2	1.92	0.69
1:C:123:LEU:HD12	1:C:163:GLU:OE2	1.92	0.69
1:C:299:SER:C	1:C:333:MET:HE1	2.13	0.69
1:A:211:LEU:O	1:A:212:GLU:HB3	1.92	0.69
1:C:379:SER:H	1:C:413:THR:HB	1.57	0.69
1:A:79:THR:HG23	1:A:81:GLN:HG2	1.72	0.69
1:A:316:ALA:O	1:A:348:CYS:HA	1.92	0.69
1:A:448:GLU:HG2	1:B:466:ALA:HA	1.73	0.69
1:F:325:LEU:HD23	1:F:335:PHE:HB2	1.74	0.69
1:B:287:THR:HG21	1:B:425:ILE:O	1.92	0.69
1:C:150:VAL:HG13	1:C:151:PHE:N	2.07	0.69
1:C:287:THR:HG21	1:C:425:ILE:O	1.91	0.69
1:F:127:ILE:HD11	1:F:167:LEU:HA	1.75	0.69
1:E:214:GLU:HB3	1:F:234:GLU:HB2	1.73	0.69
1:B:448:GLU:HG2	1:C:466:ALA:HA	1.75	0.69
1:B:182:THR:HG21	1:B:192:ALA:HB1	1.73	0.69
1:E:447:GLY:O	1:F:467:ILE:HD13	1.93	0.69
1:A:24:MET:CB	1:A:62:ASN:HD22	2.05	0.69
1:D:375:ILE:HD12	1:D:408:ILE:HG21	1.75	0.69
1:D:72:VAL:HG21	1:D:134:ILE:HD12	1.75	0.68
1:C:377:ILE:HD12	1:C:412:PHE:CE2	2.29	0.68
1:E:93:ASP:OD2	1:E:96:LYS:HB2	1.92	0.68
1:E:61:TYR:CE2	1:E:65:ILE:HG13	2.29	0.68
1:B:79:THR:HG23	1:B:81:GLN:HG2	1.75	0.68
1:C:182:THR:HG21	1:C:192:ALA:HB1	1.76	0.68
1:B:283:ILE:HD13	1:B:400:THR:HG23	1.74	0.68
1:B:437:ILE:HD13	1:B:457:LYS:HE2	1.73	0.68
1:C:191:ILE:HB	1:C:198:GLU:CG	2.23	0.68
1:C:21:MET:HE2	1:C:177:THR:HG21	1.75	0.68
1:C:325:LEU:HD23	1:C:335:PHE:HB2	1.73	0.68
1:F:239:ILE:HB	3:F:6917:HOH:O	1.94	0.68
1:A:437:ILE:N	1:A:437:ILE:HD12	2.08	0.68
1:B:437:ILE:HD11	1:B:457:LYS:HE2	1.75	0.68
1:B:78:GLU:HB2	1:B:83:ILE:HD11	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:LEU:O	1:D:130:ILE:CD1	2.41	0.68
1:F:90:PHE:HB2	1:F:92:TRP:CE2	2.29	0.68
1:B:299:SER:HB3	1:B:333:MET:HE1	1.76	0.68
1:B:449:MET:CE	1:C:490:ILE:HD11	2.24	0.68
1:C:31:ILE:HD13	1:C:231:MET:SD	2.34	0.68
1:C:262:ARG:NH2	1:C:461:SER:HB2	2.10	0.67
1:A:296:LEU:HD13	1:A:331:TRP:CD2	2.28	0.67
1:E:182:THR:HG21	1:E:192:ALA:HB1	1.75	0.67
1:E:43:LEU:HD11	1:E:182:THR:OG1	1.94	0.67
1:B:85:LYS:NZ	1:C:14:GLU:HB3	2.10	0.67
1:A:182:THR:HG21	1:A:192:ALA:HB1	1.76	0.67
1:A:61:TYR:CE2	1:A:65:ILE:HG13	2.30	0.67
1:D:370:PHE:O	1:D:371:LYS:HD3	1.95	0.67
1:E:123:LEU:O	1:E:127:ILE:HG12	1.94	0.67
1:F:16:GLN:HE22	1:F:33:HIS:HB3	1.59	0.67
1:F:486:PHE:HB2	1:F:489:ILE:HD11	1.76	0.67
1:B:61:TYR:CE2	1:B:65:ILE:HG13	2.28	0.67
1:B:441:GLN:NE2	1:B:490:ILE:HD13	2.10	0.67
1:D:377:ILE:HD12	1:D:412:PHE:CE2	2.29	0.67
1:D:453:ILE:HD13	1:D:454:ASN:N	2.10	0.67
1:F:52:LYS:HE3	2:F:6903:ATP:O1B	1.94	0.67
1:A:370:PHE:O	1:A:371:LYS:HD3	1.95	0.67
1:F:144:ILE:CG2	1:F:147:VAL:HG12	2.25	0.67
1:E:318:GLU:OE2	1:F:432:THR:CG2	2.43	0.66
1:E:487:GLU:O	1:E:488:ARG:HB2	1.95	0.66
1:F:370:PHE:O	1:F:371:LYS:HG3	1.95	0.66
1:E:323:GLN:NE2	1:F:459:ARG:HD3	2.10	0.66
1:F:79:THR:CG2	1:F:81:GLN:HG2	2.25	0.66
1:A:92:TRP:HE3	1:A:92:TRP:CA	2.08	0.66
1:C:449:MET:HE1	1:D:490:ILE:HD11	1.76	0.66
1:E:148:THR:OG1	1:E:182:THR:HG23	1.96	0.66
1:F:437:ILE:CD1	1:F:457:LYS:HE2	2.25	0.66
1:B:24:MET:CB	1:B:62:ASN:HD22	2.07	0.66
1:D:150:VAL:HG13	1:D:151:PHE:N	2.10	0.66
1:A:49:GLY:HA2	2:A:1903:ATP:O2B	1.96	0.66
1:B:483:PHE:HB3	1:B:486:PHE:HD1	1.60	0.66
1:C:79:THR:HG23	1:C:81:GLN:HG2	1.76	0.66
1:B:425:ILE:HD11	1:B:456:PHE:CE2	2.30	0.66
1:D:43:LEU:HD11	1:D:182:THR:OG1	1.95	0.66
1:B:169:ALA:O	1:B:173:GLN:HG3	1.95	0.66
1:C:344:LEU:HD11	1:C:346:ILE:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:425:ILE:HD11	1:C:456:PHE:CE2	2.30	0.66
1:C:61:TYR:O	1:C:65:ILE:CD1	2.39	0.66
1:D:114:GLY:O	1:D:115:GLN:HG3	1.96	0.66
1:A:96:LYS:O	1:A:100:GLU:HG3	1.95	0.66
1:C:321:ARG:HG2	1:C:348:CYS:SG	2.36	0.66
1:A:79:THR:HG21	1:A:81:GLN:HG2	1.75	0.65
1:E:290:THR:HG22	2:E:5901:ATP:O1G	1.96	0.65
1:B:150:VAL:HG13	1:B:151:PHE:N	2.11	0.65
1:B:453:ILE:HD13	1:B:454:ASN:N	2.11	0.65
1:D:438:ILE:CD1	1:D:455:VAL:HG22	2.26	0.65
1:D:61:TYR:CE2	1:D:92:TRP:CD1	2.83	0.65
1:E:489:ILE:HA	1:E:494:PRO:HG3	1.77	0.65
1:B:147:VAL:HG11	1:B:180:MET:CE	2.26	0.65
1:C:159:VAL:O	1:C:163:GLU:HG2	1.96	0.65
1:D:85:LYS:NZ	1:E:14:GLU:HB3	2.11	0.65
1:C:453:ILE:HD13	1:C:454:ASN:N	2.11	0.65
1:D:325:LEU:HD23	1:D:335:PHE:HB2	1.79	0.65
1:B:52:LYS:N	2:B:2903:ATP:O1B	2.23	0.65
1:B:79:THR:CG2	1:B:81:GLN:HG2	2.25	0.65
1:F:283:ILE:HG23	1:F:412:PHE:CE1	2.32	0.65
1:E:283:ILE:HD12	1:E:412:PHE:CE1	2.29	0.65
1:E:317:TYR:OH	1:E:363:ILE:HD11	1.97	0.65
1:F:147:VAL:HG11	1:F:180:MET:HE2	1.79	0.65
1:B:440:LEU:CD2	1:B:453:ILE:HG12	2.26	0.65
1:B:449:MET:HE3	1:C:490:ILE:HD11	1.77	0.65
1:C:206:ILE:HD11	1:C:223:LEU:HB2	1.79	0.65
1:E:377:ILE:HD12	1:E:412:PHE:CE2	2.31	0.65
1:F:486:PHE:HE2	1:F:496:ARG:HD2	1.61	0.65
1:C:320:SER:HA	1:D:254:LEU:HG	1.78	0.65
1:D:147:VAL:HG11	1:D:180:MET:CE	2.24	0.65
1:D:362:ILE:O	1:D:366:GLU:HG3	1.97	0.65
1:E:446:ARG:NE	1:E:496:ARG:HH22	1.94	0.65
1:C:65:ILE:N	1:C:65:ILE:HD12	2.12	0.65
1:F:315:PHE:CE1	1:F:375:ILE:HD12	2.29	0.65
1:A:317:TYR:OH	1:A:363:ILE:HD11	1.97	0.64
1:B:437:ILE:HD13	1:B:457:LYS:CE	2.27	0.64
1:D:335:PHE:HA	1:D:338:MET:HG3	1.78	0.64
1:E:150:VAL:HG13	1:E:151:PHE:N	2.13	0.64
1:A:45:SER:HB3	1:A:182:THR:HB	1.79	0.64
1:B:18:ILE:HB	1:B:228:THR:HG23	1.80	0.64
1:E:344:LEU:HD22	1:E:345:LYS:N	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ARG:CZ	1:A:239:ILE:HD12	2.27	0.64
1:B:283:ILE:CD1	1:B:400:THR:HG23	2.27	0.64
1:C:314:LEU:HD23	1:C:346:ILE:HD12	1.79	0.64
1:E:147:VAL:HG11	1:E:180:MET:CE	2.26	0.64
1:F:218:ARG:HD2	3:F:6906:HOH:O	1.97	0.64
1:B:370:PHE:O	1:B:371:LYS:HD3	1.98	0.64
1:D:84:ILE:CD1	1:D:94:LEU:HB2	2.27	0.64
1:F:315:PHE:CE2	1:F:363:ILE:HD12	2.32	0.64
1:B:483:PHE:HB3	1:B:486:PHE:CD1	2.32	0.64
1:C:263:VAL:HG12	1:C:374:ARG:NH2	2.12	0.64
1:D:146:SER:H	1:D:181:THR:CG2	2.08	0.64
1:A:455:VAL:HG11	1:A:463:HIS:HB2	1.80	0.64
1:F:111:ASP:OD1	1:F:112:PRO:HD2	1.97	0.64
1:C:469:GLU:HG3	1:C:480:LYS:HE3	1.79	0.64
1:D:72:VAL:HG21	1:D:134:ILE:CD1	2.28	0.64
1:E:356:LEU:HD22	1:E:387:VAL:HG11	1.80	0.64
1:E:356:LEU:CD2	1:E:387:VAL:HG11	2.28	0.64
1:B:315:PHE:CD2	1:B:363:ILE:HD12	2.33	0.64
1:C:50:THR:HG22	1:C:209:ASN:HB2	1.80	0.64
1:D:487:GLU:OE1	1:D:497:ILE:HD13	1.98	0.64
1:C:121:PHE:O	1:C:125:ALA:HB3	1.97	0.64
1:E:191:ILE:CD1	1:E:198:GLU:HG2	2.27	0.64
1:E:287:THR:CG2	1:E:414:ASN:HD22	2.11	0.63
1:E:269:ARG:HB3	1:E:479:ILE:HD12	1.77	0.63
1:A:64:ILE:CD1	1:A:70:PRO:HA	2.28	0.63
1:B:344:LEU:HD22	1:B:345:LYS:N	2.14	0.63
1:C:218:ARG:NH1	1:C:239:ILE:HD12	2.13	0.63
1:C:296:LEU:CD2	1:C:472:ILE:HD12	2.28	0.63
1:D:146:SER:N	1:D:181:THR:HG22	2.10	0.63
1:A:488:ARG:NE	1:F:488:ARG:HH12	1.96	0.63
1:C:444:GLU:OE1	1:D:490:ILE:HD12	1.98	0.63
1:C:471:MET:O	1:C:472:ILE:HD13	1.97	0.63
1:D:451:ARG:HH11	1:D:451:ARG:HG2	1.63	0.63
1:F:117:VAL:HA	1:F:154:TYR:OH	1.98	0.63
1:D:218:ARG:CZ	1:D:239:ILE:HD12	2.28	0.63
1:F:315:PHE:CD2	1:F:363:ILE:HD12	2.33	0.63
1:F:377:ILE:HD12	1:F:412:PHE:CE2	2.34	0.63
1:C:111:ASP:OD2	1:C:113:GLU:HG2	1.99	0.63
1:C:214:GLU:HB3	1:D:234:GLU:HB2	1.81	0.63
1:E:79:THR:HG21	1:E:81:GLN:HG2	1.79	0.63
1:C:79:THR:CG2	1:C:81:GLN:HG2	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:MET:HB2	1:F:62:ASN:HD22	1.63	0.63
1:F:440:LEU:CD2	1:F:453:ILE:HG13	2.28	0.63
1:A:257:ARG:HH22	1:A:407:GLU:CG	2.09	0.63
1:C:218:ARG:CZ	1:C:239:ILE:HD12	2.29	0.63
1:E:382:ALA:O	1:E:385:ARG:HG3	1.98	0.63
1:F:396:VAL:O	1:F:400:THR:HB	1.99	0.63
1:C:182:THR:HG22	1:C:183:GLU:N	2.13	0.62
1:C:344:LEU:HD22	1:C:345:LYS:H	1.63	0.62
1:C:314:LEU:HB3	1:C:346:ILE:HD13	1.81	0.62
1:D:488:ARG:NH1	1:E:488:ARG:HH21	1.97	0.62
1:F:134:ILE:HD11	1:F:142:VAL:HG22	1.81	0.62
1:A:325:LEU:HD23	1:A:335:PHE:HB2	1.80	0.62
1:A:49:GLY:CA	2:A:1903:ATP:O2B	2.47	0.62
1:C:431:SER:O	1:C:434:THR:HG22	1.99	0.62
1:D:295:THR:HG23	1:D:378:ASP:OD2	1.99	0.62
1:D:393:ARG:O	1:D:397:ILE:HG12	1.99	0.62
1:D:79:THR:HG23	1:D:81:GLN:HG2	1.80	0.62
1:A:249:LEU:HD13	1:A:394:GLN:HG2	1.81	0.62
1:A:437:ILE:HD13	1:A:457:LYS:CE	2.28	0.62
1:B:273:MET:O	1:B:463:HIS:HA	1.99	0.62
1:A:318:GLU:OE2	1:B:432:THR:CG2	2.47	0.62
1:E:191:ILE:HB	1:E:198:GLU:HG2	1.81	0.62
1:E:248:PRO:HB2	1:E:251:ALA:HB3	1.81	0.62
1:B:437:ILE:HD12	1:B:437:ILE:N	2.14	0.62
1:E:377:ILE:HD12	1:E:412:PHE:HE2	1.65	0.62
1:F:437:ILE:HD13	1:F:457:LYS:CG	2.28	0.62
1:F:64:ILE:CD1	1:F:70:PRO:HA	2.28	0.62
1:A:269:ARG:HG2	1:A:479:ILE:HB	1.81	0.62
1:B:438:ILE:HG23	1:B:453:ILE:HD11	1.81	0.62
1:B:437:ILE:HD13	1:B:457:LYS:CG	2.30	0.62
1:D:151:PHE:C	1:D:153:GLN:H	2.00	0.62
1:D:182:THR:HG22	1:D:183:GLU:N	2.15	0.62
1:E:284:ILE:HD12	1:E:436:THR:CB	2.23	0.62
1:C:203:ASN:HB3	1:C:225:LEU:HD23	1.81	0.62
1:C:438:ILE:CD1	1:C:455:VAL:HG22	2.30	0.62
1:E:49:GLY:CA	2:E:5903:ATP:O2B	2.47	0.62
1:A:437:ILE:HD13	1:A:457:LYS:HG2	1.82	0.62
1:A:451:ARG:NH1	1:A:451:ARG:HG2	2.15	0.62
1:A:191:ILE:HB	1:A:198:GLU:CG	2.30	0.61
1:A:184:ARG:O	1:A:185:ILE:HD13	2.00	0.61
1:D:79:THR:HG21	1:D:81:GLN:HG2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:GLN:OE1	1:E:118:VAL:HG21	2.00	0.61
1:F:451:ARG:HH11	1:F:451:ARG:HG2	1.64	0.61
1:F:144:ILE:HG22	1:F:147:VAL:HG12	1.83	0.61
1:B:123:LEU:O	1:B:123:LEU:HD13	2.01	0.61
1:B:379:SER:H	1:B:413:THR:HB	1.64	0.61
1:D:148:THR:CG2	1:D:193:ARG:HD2	2.30	0.61
1:F:370:PHE:C	1:F:371:LYS:HG3	2.20	0.61
1:C:148:THR:CG2	1:C:193:ARG:HD2	2.31	0.61
1:C:289:ALA:HB2	1:C:419:PHE:HA	1.80	0.61
1:D:385:ARG:NH2	1:E:433:ILE:HD11	2.16	0.61
1:F:437:ILE:N	1:F:437:ILE:HD12	2.16	0.61
1:A:21:MET:HB2	1:A:38:ILE:CD1	2.30	0.61
1:A:437:ILE:HD13	1:A:457:LYS:HE2	1.82	0.61
1:F:437:ILE:HD13	1:F:457:LYS:HE2	1.83	0.61
1:B:145:ASP:OD2	1:B:181:THR:HG21	2.00	0.61
1:C:191:ILE:HB	1:C:198:GLU:HG2	1.83	0.61
1:D:321:ARG:HG2	1:D:348:CYS:SG	2.41	0.61
1:F:377:ILE:HD11	1:F:399:VAL:HG11	1.83	0.61
1:B:191:ILE:CD1	1:B:198:GLU:HG2	2.30	0.61
1:A:89:SER:HB2	1:B:227:GLY:O	2.00	0.60
1:B:218:ARG:CZ	1:B:239:ILE:HD12	2.31	0.60
1:A:382:ALA:O	1:A:385:ARG:HG3	2.01	0.60
1:A:92:TRP:CA	1:A:92:TRP:CE3	2.84	0.60
1:C:284:ILE:N	1:C:284:ILE:HD13	2.16	0.60
1:C:61:TYR:CE2	1:C:65:ILE:HG12	2.35	0.60
1:F:127:ILE:HD11	1:F:167:LEU:HD12	1.83	0.60
1:B:18:ILE:HB	1:B:228:THR:CG2	2.31	0.60
1:B:295:THR:HG21	1:B:319:GLU:OE2	2.01	0.60
1:C:287:THR:CG2	1:C:414:ASN:HD22	2.06	0.60
1:D:344:LEU:HD22	1:D:345:LYS:N	2.15	0.60
1:D:315:PHE:CZ	1:D:363:ILE:HG23	2.36	0.60
1:E:79:THR:HG23	1:E:81:GLN:H	1.65	0.60
1:B:123:LEU:O	1:B:127:ILE:HG13	2.00	0.60
1:D:49:GLY:CA	2:D:4903:ATP:O2B	2.49	0.60
1:F:486:PHE:CE2	1:F:496:ARG:HD2	2.36	0.60
1:E:359:HIS:O	1:E:363:ILE:HG12	2.01	0.60
1:F:159:VAL:O	1:F:163:GLU:HG2	2.01	0.60
1:F:461:SER:OG	1:F:462:TRP:N	2.34	0.60
1:D:440:LEU:CD2	1:D:453:ILE:HG12	2.32	0.60
1:D:58:GLN:HG3	1:D:92:TRP:HZ2	1.66	0.60
1:D:79:THR:HG23	1:D:81:GLN:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:467:ILE:N	1:F:467:ILE:HD12	2.17	0.60
1:B:78:GLU:CB	1:B:83:ILE:HD11	2.32	0.60
1:D:194:TYR:O	1:D:196:VAL:HG23	2.01	0.60
1:C:420:MET:CE	1:D:490:ILE:HD13	2.32	0.60
1:D:486:PHE:CE2	1:D:496:ARG:HB3	2.37	0.60
1:E:362:ILE:O	1:E:366:GLU:HG3	2.02	0.60
1:E:451:ARG:HH11	1:E:451:ARG:HG2	1.67	0.60
1:E:293:GLY:HA2	2:E:5901:ATP:O1A	2.02	0.60
1:F:122:ASP:OD2	1:F:123:LEU:N	2.35	0.60
1:A:14:GLU:HG3	1:A:16:GLN:OE1	2.01	0.60
1:C:28:PHE:CZ	1:C:222:ILE:HD11	2.36	0.60
1:D:392:PHE:CE2	1:D:430:ILE:HD11	2.34	0.60
1:A:344:LEU:HD22	1:A:345:LYS:N	2.17	0.60
1:E:159:VAL:O	1:E:163:GLU:HG2	2.02	0.60
1:E:461:SER:OG	1:E:462:TRP:N	2.33	0.60
1:A:79:THR:HG23	1:A:81:GLN:H	1.67	0.59
1:D:489:ILE:HD13	1:D:494:PRO:CB	2.32	0.59
1:F:382:ALA:O	1:F:385:ARG:HG3	2.02	0.59
1:F:293:GLY:HA2	2:F:6901:ATP:O1A	2.02	0.59
1:F:150:VAL:HG13	1:F:151:PHE:N	2.16	0.59
1:A:367:ILE:HG12	1:A:375:ILE:HD11	1.82	0.59
1:A:433:ILE:HD11	1:F:385:ARG:NH2	2.17	0.59
1:A:52:LYS:HE3	2:A:1903:ATP:O1B	2.02	0.59
1:E:396:VAL:O	1:E:400:THR:HB	2.02	0.59
1:F:484:ARG:HH11	1:F:484:ARG:HB3	1.68	0.59
1:A:208:ARG:NH2	1:A:221:GLU:OE2	2.35	0.59
1:B:87:ALA:O	1:B:92:TRP:HB2	2.03	0.59
1:C:205:VAL:CG2	1:C:222:ILE:HD13	2.24	0.59
1:F:437:ILE:CD1	1:F:457:LYS:CE	2.81	0.59
1:B:269:ARG:HG2	1:B:479:ILE:HB	1.83	0.59
1:D:367:ILE:HG23	1:D:372:PRO:HD2	1.85	0.59
1:E:320:SER:HA	1:F:254:LEU:HG	1.83	0.59
1:F:311:ARG:HD2	1:F:371:LYS:HE2	1.84	0.59
1:E:289:ALA:HB2	1:E:419:PHE:HA	1.84	0.59
1:B:453:ILE:HD13	1:B:454:ASN:H	1.66	0.59
1:B:437:ILE:HD13	1:B:457:LYS:HG2	1.84	0.59
1:C:400:THR:HG22	1:C:401:GLY:N	2.18	0.59
1:D:316:ALA:O	1:D:348:CYS:HA	2.02	0.59
1:F:146:SER:H	1:F:181:THR:HG22	1.67	0.59
1:F:49:GLY:CA	2:F:6903:ATP:O2B	2.50	0.59
1:A:74:VAL:CB	1:A:144:ILE:HD12	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:444:GLU:HB2	1:C:490:ILE:CD1	2.33	0.59
1:D:431:SER:O	1:D:434:THR:HG22	2.02	0.59
1:E:148:THR:CG2	1:E:193:ARG:HD2	2.33	0.59
1:F:296:LEU:HD13	1:F:331:TRP:CD2	2.37	0.59
1:A:264:SER:HA	1:A:271:ASP:OD1	2.03	0.58
1:A:437:ILE:HD11	1:A:457:LYS:HE2	1.84	0.58
1:C:84:ILE:CD1	1:C:94:LEU:HB2	2.29	0.58
1:D:400:THR:HG22	1:D:401:GLY:N	2.18	0.58
1:E:273:MET:O	1:E:463:HIS:HA	2.02	0.58
1:E:372:PRO:HB2	1:E:375:ILE:HD11	1.84	0.58
1:A:74:VAL:CG2	1:A:144:ILE:HD12	2.33	0.58
1:B:194:TYR:O	1:B:196:VAL:HG23	2.03	0.58
1:C:52:LYS:HE3	2:C:3903:ATP:O1B	2.02	0.58
1:D:248:PRO:HB2	1:D:251:ALA:HB3	1.85	0.58
1:E:22:ARG:HD3	3:E:5914:HOH:O	2.03	0.58
1:A:437:ILE:CD1	1:A:457:LYS:CE	2.81	0.58
1:C:24:MET:HB2	1:C:62:ASN:HD22	1.67	0.58
1:A:356:LEU:HD13	1:A:387:VAL:HG21	1.85	0.58
1:B:50:THR:HG22	1:B:209:ASN:HB2	1.85	0.58
1:C:273:MET:O	1:C:463:HIS:HA	2.04	0.58
1:D:283:ILE:CD1	1:D:400:THR:HG23	2.33	0.58
1:C:151:PHE:C	1:C:153:GLN:H	2.04	0.58
1:D:14:GLU:CD	1:D:15:HIS:H	2.07	0.58
1:A:377:ILE:N	1:A:377:ILE:HD12	2.18	0.58
1:A:379:SER:N	1:A:413:THR:HB	2.06	0.58
1:A:296:LEU:CD2	1:A:472:ILE:HD12	2.34	0.58
1:B:377:ILE:N	1:B:377:ILE:HD12	2.18	0.58
1:B:49:GLY:CA	2:B:2903:ATP:O2B	2.51	0.58
1:E:315:PHE:CD2	1:E:363:ILE:HD12	2.39	0.58
1:F:194:TYR:O	1:F:196:VAL:HG23	2.04	0.58
1:A:396:VAL:O	1:A:400:THR:HB	2.03	0.58
1:B:451:ARG:HG2	1:B:451:ARG:HH11	1.68	0.58
1:B:269:ARG:HB3	1:B:479:ILE:HD12	1.84	0.58
1:B:85:LYS:HZ3	1:C:14:GLU:HB3	1.68	0.58
1:E:127:ILE:HD11	1:E:167:LEU:HD13	1.84	0.58
1:F:131:ASN:O	1:F:135:GLN:HG3	2.04	0.58
1:A:43:LEU:HD11	1:A:182:THR:OG1	2.04	0.58
1:C:315:PHE:CZ	1:C:363:ILE:HG23	2.38	0.58
1:F:79:THR:HG23	1:F:81:GLN:H	1.68	0.58
1:C:79:THR:HG22	1:C:82:ASP:H	1.69	0.58
1:E:470:PHE:CE1	1:E:472:ILE:HD11	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:316:ALA:O	1:F:348:CYS:HA	2.04	0.58
1:A:372:PRO:O	1:A:408:ILE:HD12	2.03	0.58
1:E:67:PHE:HB2	1:E:69:GLU:HG3	1.86	0.58
1:F:90:PHE:O	1:F:92:TRP:CD1	2.56	0.58
1:B:461:SER:OG	1:B:462:TRP:N	2.37	0.57
1:C:142:VAL:O	1:C:178:THR:HA	2.03	0.57
1:C:221:GLU:HG3	1:C:233:GLY:O	2.03	0.57
1:D:161:ARG:HD2	1:D:196:VAL:HG13	1.86	0.57
1:F:486:PHE:HB3	1:F:489:ILE:HD11	1.86	0.57
1:A:126:LEU:HG	1:A:130:ILE:CD1	2.34	0.57
1:A:315:PHE:CE2	1:A:363:ILE:HD12	2.39	0.57
1:D:367:ILE:HD12	1:D:372:PRO:HG2	1.85	0.57
1:F:147:VAL:HG11	1:F:180:MET:CE	2.34	0.57
1:F:484:ARG:NH1	1:F:484:ARG:HB3	2.18	0.57
1:B:438:ILE:CD1	1:B:455:VAL:HG22	2.34	0.57
1:D:150:VAL:O	1:D:153:GLN:HG3	2.03	0.57
1:C:88:ARG:NE	1:D:15:HIS:HA	2.18	0.57
1:E:169:ALA:O	1:E:173:GLN:HG3	2.03	0.57
1:F:287:THR:CG2	1:F:414:ASN:HD22	2.17	0.57
1:D:470:PHE:CB	1:D:479:ILE:HD13	2.34	0.57
1:F:191:ILE:HB	1:F:198:GLU:CD	2.24	0.57
1:A:273:MET:O	1:A:463:HIS:HA	2.03	0.57
1:E:28:PHE:HE1	1:E:222:ILE:HD11	1.68	0.57
1:E:437:ILE:CD1	1:E:457:LYS:HE2	2.34	0.57
1:A:161:ARG:HD2	1:A:196:VAL:HG13	1.87	0.57
1:A:191:ILE:HG23	1:A:206:ILE:CD1	2.35	0.57
1:F:134:ILE:HD11	1:F:142:VAL:CG2	2.34	0.57
1:F:150:VAL:O	1:F:153:GLN:HG3	2.05	0.57
1:D:363:ILE:O	1:D:367:ILE:HG12	2.05	0.57
1:E:18:ILE:HD11	1:E:227:GLY:C	2.25	0.57
1:E:453:ILE:HB	1:E:470:PHE:CD2	2.40	0.57
1:F:169:ALA:O	1:F:173:GLN:HG3	2.05	0.57
1:A:14:GLU:HG3	1:A:15:HIS:H	1.68	0.57
1:C:484:ARG:HB3	1:C:484:ARG:NH1	2.19	0.57
1:F:14:GLU:HG2	3:F:6924:HOH:O	2.03	0.57
1:F:372:PRO:O	1:F:408:ILE:HD12	2.04	0.57
1:A:459:ARG:HD3	1:F:323:GLN:NE2	2.20	0.57
1:B:89:SER:HB2	1:C:227:GLY:O	2.04	0.57
1:C:148:THR:HG21	1:C:193:ARG:HD2	1.87	0.57
1:C:94:LEU:O	1:C:98:VAL:HG23	2.05	0.57
1:E:370:PHE:O	1:E:371:LYS:HD3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:THR:HG22	1:E:209:ASN:HB2	1.86	0.57
1:A:436:THR:HG23	1:A:458:MET:HG2	1.87	0.56
1:E:76:PHE:HZ	1:E:126:LEU:HD21	1.69	0.56
1:F:420:MET:HE3	1:F:492:GLY:HA3	1.86	0.56
1:A:483:PHE:HB3	1:A:486:PHE:CD1	2.40	0.56
1:B:296:LEU:CD2	1:B:472:ILE:HD12	2.35	0.56
1:B:249:LEU:HD13	1:B:394:GLN:HG2	1.86	0.56
1:C:461:SER:OG	1:C:462:TRP:N	2.36	0.56
1:A:311:ARG:HA	1:A:343:LEU:O	2.05	0.56
1:D:31:ILE:HD13	1:D:231:MET:SD	2.46	0.56
1:D:24:MET:HG3	1:D:66:GLU:HG3	1.87	0.56
1:F:231:MET:CE	1:F:251:ALA:HB2	2.34	0.56
1:B:320:SER:HA	1:C:254:LEU:HG	1.87	0.56
1:C:147:VAL:HG11	1:C:180:MET:CE	2.34	0.56
1:C:440:LEU:HD21	1:C:453:ILE:HG12	1.87	0.56
1:B:367:ILE:HG12	1:B:375:ILE:HD11	1.86	0.56
1:C:150:VAL:HG13	1:C:151:PHE:H	1.70	0.56
1:E:203:ASN:HB3	1:E:225:LEU:HD23	1.86	0.56
1:A:124:SER:O	1:A:128:GLU:HG3	2.05	0.56
1:A:287:THR:HG21	1:A:425:ILE:O	2.06	0.56
1:B:178:THR:HG22	1:B:179:VAL:N	2.20	0.56
1:A:127:ILE:HD11	1:A:167:LEU:CD1	2.34	0.56
1:F:273:MET:O	1:F:463:HIS:HA	2.05	0.56
1:D:21:MET:HE1	1:D:177:THR:HB	1.88	0.56
1:D:487:GLU:OE1	1:D:497:ILE:HG21	2.04	0.56
1:D:317:TYR:CE2	1:D:383:LEU:HD21	2.40	0.56
1:D:453:ILE:HD13	1:D:454:ASN:H	1.69	0.56
1:D:80:PRO:HD2	1:D:81:GLN:NE2	2.21	0.56
1:F:377:ILE:HD12	1:F:412:PHE:HE2	1.70	0.56
1:B:438:ILE:HD13	1:B:455:VAL:HA	1.88	0.56
1:C:218:ARG:HB3	3:C:3906:HOH:O	2.05	0.56
1:C:377:ILE:HD12	1:C:412:PHE:HE2	1.69	0.56
1:D:435:ASP:HA	1:D:459:ARG:HD2	1.86	0.56
1:A:151:PHE:C	1:A:153:GLN:H	2.09	0.56
1:A:362:ILE:HG22	1:A:366:GLU:OE2	2.06	0.56
1:D:320:SER:HA	1:E:254:LEU:HG	1.88	0.56
1:B:56:SER:HB2	1:B:143:SER:HB3	1.87	0.55
1:A:92:TRP:HE3	1:A:92:TRP:N	2.03	0.55
1:F:96:LYS:O	1:F:100:GLU:HG3	2.07	0.55
1:A:466:ALA:HA	1:F:448:GLU:HG2	1.87	0.55
1:B:79:THR:CG2	1:B:82:ASP:H	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:ILE:N	1:A:437:ILE:CD1	2.69	0.55
1:B:117:VAL:O	1:B:117:VAL:HG12	2.07	0.55
1:C:79:THR:CG2	1:C:82:ASP:H	2.18	0.55
1:D:287:THR:HG21	1:D:425:ILE:O	2.06	0.55
1:D:318:GLU:OE2	1:E:432:THR:CG2	2.54	0.55
1:F:338:MET:HB3	1:F:344:LEU:HB3	1.88	0.55
1:F:356:LEU:CD2	1:F:387:VAL:HG11	2.36	0.55
1:A:150:VAL:CG1	1:A:151:PHE:N	2.69	0.55
1:C:150:VAL:O	1:C:153:GLN:HG3	2.06	0.55
1:D:40:ARG:HG2	1:D:172:LYS:HE3	1.88	0.55
1:E:244:ILE:HG22	1:E:246:ILE:HD11	1.89	0.55
1:F:393:ARG:O	1:F:397:ILE:HG12	2.07	0.55
1:B:191:ILE:HB	1:B:198:GLU:CD	2.27	0.55
1:B:148:THR:CG2	1:B:193:ARG:HD2	2.36	0.55
1:B:316:ALA:O	1:B:348:CYS:HA	2.06	0.55
1:C:269:ARG:HB3	1:C:479:ILE:HD13	1.89	0.55
1:D:432:THR:HG22	1:D:432:THR:O	2.05	0.55
1:F:248:PRO:HB2	1:F:251:ALA:HB3	1.87	0.55
1:B:164:LEU:HD11	1:B:197:GLU:HG3	1.88	0.55
1:B:437:ILE:CD1	1:B:437:ILE:N	2.68	0.55
1:F:249:LEU:HD13	1:F:394:GLN:HG2	1.88	0.55
1:C:347:VAL:O	1:C:348:CYS:HB2	2.06	0.55
1:F:284:ILE:N	1:F:284:ILE:HD12	2.22	0.55
1:A:363:ILE:O	1:A:367:ILE:HG13	2.06	0.55
1:B:318:GLU:OE2	1:C:432:THR:CG2	2.55	0.55
1:E:375:ILE:CD1	1:E:408:ILE:HG21	2.37	0.55
1:A:266:GLY:HA3	1:A:300:ARG:O	2.07	0.55
1:B:45:SER:CB	1:B:182:THR:HB	2.37	0.55
1:F:123:LEU:O	1:F:123:LEU:HD13	2.07	0.55
1:A:294:LYS:N	2:A:1901:ATP:O1B	2.40	0.54
1:A:438:ILE:CD1	1:A:455:VAL:HG22	2.37	0.54
1:B:85:LYS:HE3	1:C:17:ALA:O	2.07	0.54
1:C:287:THR:HG23	1:C:414:ASN:ND2	2.11	0.54
1:E:496:ARG:O	1:E:497:ILE:HD13	2.06	0.54
1:B:283:ILE:C	1:B:284:ILE:HD13	2.27	0.54
1:B:52:LYS:HE3	2:B:2903:ATP:O1B	2.07	0.54
1:C:122:ASP:O	1:C:123:LEU:C	2.45	0.54
1:D:96:LYS:O	1:D:100:GLU:HG3	2.07	0.54
1:E:318:GLU:OE2	1:F:432:THR:HG23	2.06	0.54
1:F:313:ILE:CB	1:F:375:ILE:HD11	2.33	0.54
1:A:284:ILE:N	1:A:284:ILE:HD12	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:ILE:O	1:B:433:ILE:HG22	2.07	0.54
1:D:249:LEU:HD13	1:D:394:GLN:HG2	1.89	0.54
1:D:356:LEU:HD13	1:D:387:VAL:HG21	1.89	0.54
1:E:367:ILE:HD12	1:E:375:ILE:CD1	2.38	0.54
1:F:121:PHE:O	1:F:125:ALA:N	2.37	0.54
1:A:295:THR:HB	2:A:1901:ATP:PA	2.48	0.54
1:B:150:VAL:O	1:B:153:GLN:HG3	2.06	0.54
1:C:448:GLU:HG2	1:D:466:ALA:HA	1.90	0.54
1:D:311:ARG:HD2	1:D:371:LYS:HD3	1.87	0.54
1:D:84:ILE:HD12	1:D:94:LEU:HB2	1.87	0.54
1:E:446:ARG:NE	1:E:496:ARG:NH2	2.51	0.54
1:F:191:ILE:HG23	1:F:206:ILE:CD1	2.35	0.54
1:A:203:ASN:HB3	1:A:225:LEU:HD23	1.89	0.54
1:A:440:LEU:HD23	1:A:453:ILE:HG13	1.89	0.54
1:C:451:ARG:HH11	1:C:451:ARG:HG2	1.73	0.54
1:D:52:LYS:HE3	2:D:4903:ATP:O1B	2.08	0.54
1:A:191:ILE:HG23	1:A:206:ILE:HD11	1.88	0.54
1:A:21:MET:HE1	1:A:59:PHE:HZ	1.72	0.54
1:C:370:PHE:O	1:C:371:LYS:HD3	2.08	0.54
1:D:299:SER:CB	1:D:333:MET:HE1	2.38	0.54
1:D:367:ILE:O	1:D:372:PRO:HD3	2.08	0.54
1:F:317:TYR:OH	1:F:363:ILE:HD11	2.07	0.54
1:F:90:PHE:O	1:F:92:TRP:NE1	2.41	0.54
1:D:437:ILE:CD1	1:D:457:LYS:HE2	2.38	0.54
1:D:486:PHE:HB3	1:D:489:ILE:CD1	2.31	0.54
1:E:440:LEU:CD2	1:E:453:ILE:HG13	2.37	0.54
1:E:489:ILE:HD13	1:E:494:PRO:CG	2.37	0.54
1:C:80:PRO:O	1:C:84:ILE:HG12	2.08	0.54
1:D:80:PRO:O	1:D:84:ILE:HG12	2.08	0.54
1:F:151:PHE:C	1:F:153:GLN:H	2.11	0.54
1:A:248:PRO:HB2	1:A:251:ALA:HB3	1.88	0.54
1:A:400:THR:HG22	1:A:401:GLY:N	2.22	0.54
1:C:150:VAL:CG1	1:C:151:PHE:N	2.70	0.54
1:D:148:THR:HG21	1:D:193:ARG:HD2	1.90	0.54
1:D:332:GLY:O	1:D:333:MET:O	2.26	0.54
1:E:153:GLN:O	1:F:158:SER:HB2	2.07	0.54
1:B:150:VAL:HG13	1:B:151:PHE:H	1.73	0.54
1:B:363:ILE:O	1:B:367:ILE:HG13	2.08	0.54
1:C:111:ASP:C	1:C:113:GLU:H	2.12	0.54
1:C:185:ILE:N	1:C:185:ILE:HD12	2.22	0.54
1:D:377:ILE:HD12	1:D:412:PHE:HE2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:294:LYS:N	2:E:5901:ATP:O1B	2.41	0.54
1:F:185:ILE:N	1:F:185:ILE:HD12	2.23	0.54
1:F:377:ILE:CD1	1:F:399:VAL:HG11	2.37	0.54
1:A:169:ALA:O	1:A:173:GLN:HG3	2.08	0.53
1:A:273:MET:O	1:A:464:ASP:N	2.36	0.53
1:E:356:LEU:HD13	1:E:387:VAL:HG21	1.89	0.53
1:F:93:ASP:OD2	1:F:96:LYS:HB2	2.08	0.53
1:B:437:ILE:CD1	1:B:457:LYS:CE	2.83	0.53
1:D:79:THR:CG2	1:D:82:ASP:H	2.14	0.53
1:F:208:ARG:NH2	1:F:221:GLU:OE2	2.41	0.53
1:A:150:VAL:HG13	1:A:151:PHE:H	1.70	0.53
1:A:461:SER:OG	1:A:462:TRP:N	2.41	0.53
1:C:419:PHE:O	1:C:420:MET:HB2	2.08	0.53
1:E:266:GLY:HA2	1:E:304:ASN:HD22	1.73	0.53
1:F:218:ARG:HB3	3:F:6920:HOH:O	2.08	0.53
1:F:347:VAL:O	1:F:348:CYS:HB2	2.08	0.53
1:A:440:LEU:CD2	1:A:453:ILE:HG13	2.38	0.53
1:C:89:SER:HB2	1:D:227:GLY:O	2.08	0.53
1:D:453:ILE:CG2	1:D:479:ILE:HD12	2.29	0.53
1:E:295:THR:HG21	1:E:319:GLU:OE2	2.08	0.53
1:E:448:GLU:HG2	1:F:466:ALA:HA	1.90	0.53
1:F:317:TYR:CD2	1:F:383:LEU:HD21	2.44	0.53
1:E:418:GLN:HB2	1:F:423:HIS:O	2.08	0.53
1:F:24:MET:HG3	1:F:66:GLU:HG3	1.90	0.53
1:C:248:PRO:HB2	1:C:251:ALA:HB3	1.89	0.53
1:C:169:ALA:O	1:C:173:GLN:HG3	2.08	0.53
1:C:470:PHE:HB2	1:C:478:ASP:O	2.08	0.53
1:E:372:PRO:HB2	1:E:375:ILE:CD1	2.39	0.53
1:F:149:SER:HA	1:F:152:GLN:HB2	1.90	0.53
1:A:74:VAL:HG22	1:A:106:LEU:HD23	1.91	0.53
1:C:85:LYS:HZ3	1:D:14:GLU:HB3	1.72	0.53
1:D:299:SER:C	1:D:333:MET:HE1	2.29	0.53
1:D:438:ILE:HG23	1:D:453:ILE:HD11	1.89	0.53
1:E:146:SER:H	1:E:181:THR:HG22	1.74	0.53
1:E:347:VAL:O	1:E:348:CYS:HB2	2.08	0.53
1:F:182:THR:HG22	1:F:183:GLU:N	2.21	0.53
1:F:420:MET:HA	3:F:6916:HOH:O	2.07	0.53
1:A:438:ILE:HD13	1:A:455:VAL:HA	1.91	0.53
1:B:362:ILE:HG22	1:B:366:GLU:OE2	2.09	0.53
1:E:76:PHE:CZ	1:E:126:LEU:HD21	2.44	0.53
1:B:159:VAL:O	1:B:163:GLU:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:334:ASP:OD1	1:C:336:GLU:HB2	2.09	0.53
1:D:375:ILE:HD13	1:D:408:ILE:HG21	1.90	0.53
1:E:202:ASP:HA	1:E:226:ARG:HD2	1.90	0.53
1:E:18:ILE:HG13	1:E:228:THR:HG23	1.91	0.53
1:E:447:GLY:C	1:F:467:ILE:HD13	2.28	0.53
1:F:122:ASP:HA	1:F:125:ALA:HB3	1.91	0.53
1:A:254:LEU:HD23	1:F:348:CYS:HB3	1.91	0.53
1:D:396:VAL:O	1:D:400:THR:HB	2.09	0.53
1:A:21:MET:HE2	1:A:177:THR:HG21	1.90	0.52
1:F:164:LEU:HD11	1:F:197:GLU:HG3	1.90	0.52
1:F:264:SER:O	1:F:374:ARG:NH2	2.41	0.52
1:A:90:PHE:O	1:A:92:TRP:CE3	2.62	0.52
1:D:269:ARG:HG2	1:D:479:ILE:HB	1.89	0.52
1:F:317:TYR:CE2	1:F:383:LEU:HD21	2.43	0.52
1:A:91:GLY:C	1:A:92:TRP:HE3	2.13	0.52
1:B:311:ARG:HA	1:B:343:LEU:O	2.10	0.52
1:C:479:ILE:HD12	1:C:479:ILE:N	2.25	0.52
1:D:294:LYS:N	2:D:4901:ATP:O1B	2.42	0.52
1:E:70:PRO:HB2	1:E:139:ALA:HA	1.92	0.52
1:E:80:PRO:HD2	1:E:81:GLN:NE2	2.24	0.52
1:A:14:GLU:CG	1:A:15:HIS:H	2.21	0.52
1:F:25:ILE:HD13	1:F:62:ASN:ND2	2.25	0.52
1:B:64:ILE:HD11	1:B:102:LYS:O	2.09	0.52
1:D:347:VAL:O	1:D:348:CYS:HB2	2.10	0.52
1:D:446:ARG:H	1:D:496:ARG:NH1	2.03	0.52
1:F:25:ILE:HD12	1:F:58:GLN:HG2	1.92	0.52
1:B:206:ILE:N	1:B:206:ILE:HD12	2.25	0.52
1:B:248:PRO:HB2	1:B:251:ALA:HB3	1.92	0.52
1:C:206:ILE:N	1:C:206:ILE:HD12	2.24	0.52
1:C:65:ILE:N	1:C:65:ILE:CD1	2.70	0.52
1:D:84:ILE:HD13	1:D:94:LEU:HB2	1.90	0.52
1:E:431:SER:O	1:E:434:THR:HG22	2.09	0.52
1:F:184:ARG:HG2	1:F:191:ILE:O	2.10	0.52
1:F:440:LEU:HD23	1:F:453:ILE:HG13	1.90	0.52
1:E:444:GLU:OE1	1:F:490:ILE:HG12	2.09	0.52
1:B:290:THR:HG22	2:B:2901:ATP:O1G	2.10	0.52
1:D:495:THR:O	1:D:497:ILE:HG23	2.10	0.52
1:F:126:LEU:HG	1:F:130:ILE:HD11	1.92	0.52
1:F:406:GLU:HB3	1:F:408:ILE:HG12	1.92	0.52
1:A:126:LEU:HG	1:A:130:ILE:HD11	1.92	0.52
1:A:371:LYS:N	1:A:372:PRO:HD3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:LEU:HD22	1:B:387:VAL:HG11	1.90	0.52
1:A:318:GLU:OE2	1:B:432:THR:HG23	2.09	0.52
1:C:117:VAL:HG12	1:C:117:VAL:O	2.10	0.52
1:D:89:SER:HB2	1:E:227:GLY:O	2.09	0.52
1:E:348:CYS:HB3	1:F:254:LEU:HD23	1.92	0.52
1:F:134:ILE:HD12	1:F:139:ALA:HB3	1.91	0.52
1:A:18:ILE:HD12	1:A:18:ILE:N	2.25	0.52
1:C:311:ARG:HA	1:C:343:LEU:O	2.10	0.52
1:D:267:VAL:CG2	1:D:300:ARG:HG2	2.40	0.52
1:D:472:ILE:HD12	1:D:472:ILE:N	2.24	0.52
1:F:115:GLN:HG3	1:F:116:GLU:N	2.25	0.52
1:A:31:ILE:HD11	1:A:246:ILE:HG21	1.91	0.51
1:C:318:GLU:OE2	1:D:432:THR:CG2	2.58	0.51
1:C:371:LYS:HD3	1:C:371:LYS:O	2.10	0.51
1:D:440:LEU:HD21	1:D:453:ILE:HG12	1.92	0.51
1:F:315:PHE:CZ	1:F:363:ILE:HG23	2.44	0.51
1:B:325:LEU:HD23	1:B:335:PHE:HB2	1.92	0.51
1:B:433:ILE:HD12	1:B:433:ILE:N	2.25	0.51
1:C:49:GLY:HA2	2:C:3903:ATP:O2B	2.10	0.51
1:C:81:GLN:CD	1:C:81:GLN:H	2.13	0.51
1:C:81:GLN:H	1:C:81:GLN:NE2	2.07	0.51
1:D:489:ILE:HA	1:D:494:PRO:HG3	1.92	0.51
1:D:489:ILE:HD13	1:D:494:PRO:CG	2.40	0.51
1:D:21:MET:HE3	1:D:59:PHE:CZ	2.45	0.51
1:E:356:LEU:CD1	1:E:387:VAL:HG21	2.40	0.51
1:F:455:VAL:HG11	1:F:463:HIS:HB2	1.91	0.51
1:F:56:SER:HB2	1:F:143:SER:HB2	1.91	0.51
1:D:287:THR:HG23	1:D:414:ASN:ND2	2.17	0.51
1:E:438:ILE:CD1	1:E:455:VAL:HG22	2.41	0.51
1:F:14:GLU:HG3	1:F:16:GLN:HG3	1.93	0.51
1:E:323:GLN:HE21	1:F:459:ARG:HD3	1.74	0.51
1:B:90:PHE:O	1:B:92:TRP:CZ3	2.63	0.51
1:C:438:ILE:HD13	1:C:455:VAL:HA	1.93	0.51
1:D:106:LEU:HD11	1:D:129:ARG:NH2	2.25	0.51
1:D:170:ARG:HD2	1:D:173:GLN:OE1	2.10	0.51
1:D:367:ILE:CD1	1:D:372:PRO:HG2	2.40	0.51
1:E:300:ARG:HA	1:E:333:MET:HE3	1.93	0.51
1:E:347:VAL:HG12	1:E:348:CYS:N	2.23	0.51
1:A:21:MET:HB2	1:A:38:ILE:HD11	1.93	0.51
1:D:150:VAL:CG1	1:D:151:PHE:N	2.72	0.51
1:E:151:PHE:C	1:E:153:GLN:H	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:316:ALA:O	1:E:348:CYS:HA	2.11	0.51
1:E:496:ARG:HG3	1:E:497:ILE:H	1.75	0.51
1:F:479:ILE:N	1:F:479:ILE:HD12	2.26	0.51
1:A:488:ARG:HE	1:F:488:ARG:HH12	1.56	0.51
1:F:489:ILE:HD13	1:F:494:PRO:CG	2.41	0.51
1:C:111:ASP:O	1:C:113:GLU:N	2.41	0.51
1:D:18:ILE:CD1	1:D:18:ILE:H	2.17	0.51
1:C:420:MET:HE3	1:D:490:ILE:HD13	1.91	0.51
1:E:123:LEU:C	1:E:127:ILE:HG12	2.31	0.51
1:E:126:LEU:O	1:E:129:ARG:HB2	2.11	0.51
1:F:291:GLY:N	2:F:6901:ATP:O2B	2.44	0.51
1:F:287:THR:HG21	1:F:425:ILE:O	2.10	0.51
1:A:266:GLY:HA3	1:A:300:ARG:HG3	1.92	0.51
1:A:449:MET:HG2	1:B:467:ILE:HD11	1.92	0.51
1:B:467:ILE:N	1:B:467:ILE:HD12	2.26	0.51
1:C:191:ILE:H	1:C:191:ILE:HD12	1.75	0.51
1:E:264:SER:O	1:E:374:ARG:NH2	2.44	0.51
1:A:432:THR:CG2	1:F:318:GLU:OE2	2.59	0.51
1:A:150:VAL:CG1	1:A:151:PHE:H	2.23	0.51
1:B:444:GLU:HB2	1:C:490:ILE:HD11	1.93	0.51
1:F:118:VAL:CG1	1:F:153:GLN:HE22	2.23	0.51
1:D:290:THR:HG22	2:D:4901:ATP:O1G	2.11	0.51
1:D:311:ARG:HD3	1:D:370:PHE:CZ	2.45	0.51
1:D:311:ARG:HD3	1:D:370:PHE:CE1	2.46	0.51
1:F:218:ARG:CZ	1:F:239:ILE:HD12	2.41	0.51
1:A:182:THR:HG22	1:A:183:GLU:N	2.26	0.51
1:B:299:SER:C	1:B:333:MET:HE1	2.32	0.51
1:B:264:SER:HB3	1:B:304:ASN:HD21	1.75	0.51
1:B:31:ILE:HA	1:B:231:MET:SD	2.51	0.51
1:C:182:THR:CG2	1:C:183:GLU:N	2.74	0.51
1:C:344:LEU:HD11	1:C:346:ILE:CD1	2.41	0.51
1:D:362:ILE:HG22	1:D:366:GLU:OE2	2.11	0.51
1:F:148:THR:CG2	1:F:193:ARG:HD2	2.41	0.51
1:F:79:THR:CG2	1:F:82:ASP:H	2.22	0.51
1:A:484:ARG:HB3	1:A:484:ARG:NH1	2.25	0.50
1:B:130:ILE:O	1:B:134:ILE:HG13	2.11	0.50
1:E:72:VAL:HG21	1:E:134:ILE:CD1	2.38	0.50
1:E:360:LEU:CD2	1:E:364:LYS:HE3	2.41	0.50
1:E:486:PHE:HB2	1:E:489:ILE:HD11	1.93	0.50
1:A:21:MET:HE3	1:A:59:PHE:CE1	2.47	0.50
1:B:150:VAL:CG1	1:B:151:PHE:N	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LYS:N	2:B:2901:ATP:O1B	2.44	0.50
1:C:31:ILE:HD11	1:C:248:PRO:HB3	1.94	0.50
1:D:127:ILE:HD13	1:D:170:ARG:HG3	1.93	0.50
1:E:284:ILE:N	1:E:284:ILE:HD13	2.26	0.50
1:F:144:ILE:HG21	1:F:147:VAL:HG12	1.93	0.50
1:C:114:GLY:O	1:C:115:GLN:HB3	2.11	0.50
1:C:332:GLY:O	1:C:333:MET:O	2.30	0.50
1:D:60:LEU:O	1:D:64:ILE:CD1	2.46	0.50
1:E:472:ILE:HD12	1:E:472:ILE:N	2.26	0.50
1:A:92:TRP:HA	1:A:92:TRP:CE3	2.47	0.50
1:C:43:LEU:HD11	1:C:182:THR:OG1	2.11	0.50
1:D:169:ALA:O	1:D:173:GLN:HG3	2.10	0.50
1:E:218:ARG:CZ	1:E:239:ILE:HD12	2.42	0.50
1:A:67:PHE:HB2	1:A:69:GLU:HG3	1.93	0.50
1:B:99:ASP:C	1:B:101:GLY:H	2.14	0.50
1:C:49:GLY:O	1:C:218:ARG:NH2	2.43	0.50
1:E:283:ILE:C	1:E:284:ILE:HD13	2.31	0.50
1:E:296:LEU:HD13	1:E:331:TRP:CD2	2.47	0.50
1:E:315:PHE:CZ	1:E:363:ILE:HG23	2.46	0.50
1:F:72:VAL:HG21	1:F:134:ILE:HD13	1.93	0.50
1:F:50:THR:HG22	1:F:209:ASN:HB2	1.92	0.50
1:A:64:ILE:HD11	1:A:102:LYS:O	2.12	0.50
1:B:371:LYS:N	1:B:372:PRO:HD3	2.27	0.50
1:B:92:TRP:CE3	1:B:92:TRP:CA	2.94	0.50
1:D:338:MET:HB3	1:D:344:LEU:HB3	1.93	0.50
1:D:283:ILE:HD13	1:D:400:THR:HG23	1.94	0.50
1:E:332:GLY:O	1:E:333:MET:O	2.30	0.50
1:B:123:LEU:HG	1:B:163:GLU:OE2	2.12	0.50
1:B:184:ARG:HG2	1:B:191:ILE:O	2.11	0.50
1:A:348:CYS:HB3	1:B:254:LEU:HD23	1.93	0.50
1:B:420:MET:SD	1:C:490:ILE:HD13	2.52	0.50
1:D:150:VAL:HG13	1:D:151:PHE:H	1.76	0.50
1:D:430:ILE:HA	1:D:433:ILE:HD13	1.94	0.50
1:F:90:PHE:CB	1:F:92:TRP:CE2	2.94	0.50
1:B:123:LEU:CD1	1:B:166:ARG:HD2	2.40	0.50
1:B:211:LEU:O	1:B:212:GLU:HB3	2.11	0.50
1:C:396:VAL:O	1:C:400:THR:HB	2.12	0.50
1:F:28:PHE:HE1	1:F:222:ILE:HD11	1.77	0.50
1:E:89:SER:HB2	1:F:227:GLY:O	2.12	0.50
1:F:218:ARG:NH1	1:F:239:ILE:HD12	2.27	0.50
1:C:134:ILE:HG23	1:C:139:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:348:CYS:O	1:C:349:ALA:HB2	2.12	0.50
1:D:49:GLY:O	1:D:218:ARG:NH2	2.45	0.50
1:D:344:LEU:HD13	1:D:344:LEU:C	2.32	0.50
1:D:439:LEU:HD12	1:D:440:LEU:N	2.27	0.50
1:D:451:ARG:HG2	1:D:451:ARG:NH1	2.25	0.50
1:C:420:MET:SD	1:D:490:ILE:HD13	2.52	0.50
1:D:64:ILE:HD12	1:D:64:ILE:N	2.27	0.50
1:F:439:LEU:HD12	1:F:440:LEU:N	2.26	0.50
1:A:142:VAL:O	1:A:178:THR:HA	2.12	0.49
1:A:283:ILE:HD12	1:A:412:PHE:HE1	1.77	0.49
1:A:451:ARG:HD2	1:A:451:ARG:N	2.27	0.49
1:B:185:ILE:HD11	1:B:193:ARG:NH1	2.27	0.49
1:C:332:GLY:O	1:C:333:MET:C	2.50	0.49
1:D:420:MET:HE3	1:D:492:GLY:HA3	1.94	0.49
1:D:85:LYS:HZ3	1:E:14:GLU:HB3	1.75	0.49
1:A:356:LEU:CD1	1:A:387:VAL:HG21	2.41	0.49
1:C:150:VAL:CG1	1:C:151:PHE:H	2.24	0.49
1:E:52:LYS:HD3	1:E:182:THR:O	2.12	0.49
1:B:492:GLY:O	1:B:494:PRO:HD3	2.13	0.49
1:C:120:GLY:C	1:C:122:ASP:H	2.16	0.49
1:E:255:THR:HG22	1:E:255:THR:O	2.12	0.49
1:F:283:ILE:HG23	1:F:412:PHE:HE1	1.75	0.49
1:F:360:LEU:CD2	1:F:364:LYS:HE3	2.42	0.49
1:A:90:PHE:O	1:A:92:TRP:CZ3	2.65	0.49
1:E:375:ILE:HD12	1:E:408:ILE:HG21	1.93	0.49
1:E:448:GLU:HA	1:F:467:ILE:CD1	2.43	0.49
1:F:471:MET:HG3	1:F:478:ASP:HB3	1.94	0.49
1:F:496:ARG:HD3	1:F:496:ARG:N	2.27	0.49
1:B:264:SER:HA	1:B:271:ASP:OD1	2.12	0.49
1:C:352:GLU:OE2	1:C:385:ARG:HD2	2.13	0.49
1:C:91:GLY:O	1:C:92:TRP:HE3	1.94	0.49
1:D:203:ASN:HB3	1:D:225:LEU:HD23	1.95	0.49
1:E:130:ILE:O	1:E:134:ILE:HD13	2.11	0.49
1:B:151:PHE:C	1:B:153:GLN:H	2.14	0.49
1:D:433:ILE:HD12	1:D:433:ILE:N	2.28	0.49
1:F:16:GLN:NE2	1:F:33:HIS:HB3	2.27	0.49
1:F:483:PHE:HB3	1:F:486:PHE:CD1	2.47	0.49
1:B:334:ASP:O	1:B:338:MET:HG2	2.13	0.49
1:B:334:ASP:OD1	1:B:336:GLU:HB2	2.12	0.49
1:B:296:LEU:HD21	1:B:477:PRO:HD3	1.94	0.49
1:C:106:LEU:HD11	1:C:129:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:323:GLN:NE2	1:D:459:ARG:HD3	2.27	0.49
1:E:360:LEU:HD21	1:E:364:LYS:HE3	1.93	0.49
1:E:496:ARG:HG3	1:E:497:ILE:N	2.28	0.49
1:B:441:GLN:HE22	1:B:490:ILE:HA	1.78	0.49
1:C:28:PHE:CE1	1:C:222:ILE:HD11	2.48	0.49
1:D:191:ILE:HB	1:D:198:GLU:HG2	1.90	0.49
1:D:451:ARG:NH1	1:D:472:ILE:HD13	2.28	0.49
1:D:94:LEU:O	1:D:98:VAL:HG23	2.11	0.49
1:E:28:PHE:CE1	1:E:222:ILE:HD11	2.47	0.49
1:E:436:THR:HG23	1:E:458:MET:HG2	1.93	0.49
1:E:52:LYS:HE3	2:E:5903:ATP:O1B	2.12	0.49
1:A:338:MET:HB3	1:A:344:LEU:HB3	1.94	0.49
1:B:146:SER:H	1:B:181:THR:CG2	2.26	0.49
1:C:203:ASN:HB3	1:C:225:LEU:CD2	2.43	0.49
1:E:150:VAL:HG13	1:E:151:PHE:H	1.78	0.49
1:A:269:ARG:HB3	1:A:479:ILE:HD12	1.94	0.49
1:B:91:GLY:C	1:B:92:TRP:HE3	2.16	0.49
1:C:440:LEU:HD23	1:C:453:ILE:HG12	1.93	0.49
1:C:469:GLU:CG	1:C:480:LYS:HE3	2.43	0.49
1:D:370:PHE:O	1:D:371:LYS:CD	2.61	0.49
1:D:445:ILE:HD12	1:D:450:SER:OG	2.13	0.49
1:F:451:ARG:NH1	1:F:472:ILE:HD12	2.27	0.49
1:B:182:THR:HG22	1:B:183:GLU:N	2.28	0.48
1:C:191:ILE:HD12	1:C:191:ILE:N	2.28	0.48
1:C:300:ARG:N	1:C:333:MET:HE1	2.28	0.48
1:C:356:LEU:HD22	1:C:387:VAL:HG11	1.94	0.48
1:C:453:ILE:HD13	1:C:454:ASN:H	1.78	0.48
1:D:468:ARG:HH11	1:D:468:ARG:HG2	1.78	0.48
1:F:115:GLN:CG	1:F:116:GLU:H	2.26	0.48
1:F:182:THR:HG21	1:F:192:ALA:CB	2.40	0.48
1:A:344:LEU:HD22	1:A:345:LYS:H	1.77	0.48
1:B:145:ASP:HA	1:B:181:THR:HB	1.95	0.48
1:B:430:ILE:HA	1:B:433:ILE:HD13	1.94	0.48
1:D:182:THR:HG21	1:D:192:ALA:CB	2.40	0.48
1:E:72:VAL:CG2	1:E:134:ILE:HD12	2.41	0.48
1:E:344:LEU:HD22	1:E:345:LYS:H	1.78	0.48
1:F:211:LEU:O	1:F:212:GLU:HB3	2.12	0.48
1:F:453:ILE:HB	1:F:470:PHE:CD2	2.49	0.48
1:A:434:THR:HG23	1:A:437:ILE:CD1	2.36	0.48
1:D:151:PHE:C	1:D:153:GLN:N	2.67	0.48
1:D:255:THR:HG22	1:D:255:THR:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:64:ILE:HD11	1:F:102:LYS:O	2.14	0.48
1:F:23:THR:HB	1:F:25:ILE:HG12	1.95	0.48
1:B:262:ARG:NH2	1:B:461:SER:HB2	2.28	0.48
1:D:267:VAL:HG22	1:D:300:ARG:HG2	1.96	0.48
1:D:468:ARG:NH1	1:D:468:ARG:HG2	2.29	0.48
1:E:306:CYS:SG	1:E:344:LEU:HB2	2.53	0.48
1:A:144:ILE:N	1:A:144:ILE:HD13	2.29	0.48
1:A:419:PHE:O	1:A:420:MET:HB2	2.13	0.48
1:A:454:ASN:CG	1:A:467:ILE:HD13	2.33	0.48
1:A:21:MET:CE	1:A:59:PHE:HZ	2.27	0.48
1:C:49:GLY:CA	2:C:3903:ATP:O2B	2.61	0.48
1:E:291:GLY:N	2:E:5901:ATP:O2B	2.46	0.48
1:F:134:ILE:CD1	1:F:139:ALA:HB3	2.42	0.48
1:F:182:THR:CG2	1:F:183:GLU:N	2.75	0.48
1:F:274:CYS:HG	1:F:278:PHE:HE2	1.60	0.48
1:C:469:GLU:HB3	1:C:483:PHE:CZ	2.48	0.48
1:D:332:GLY:O	1:D:333:MET:C	2.51	0.48
1:D:356:LEU:CD2	1:D:387:VAL:HG11	2.44	0.48
1:E:123:LEU:HD23	1:E:127:ILE:HD11	1.95	0.48
1:E:150:VAL:CG1	1:E:151:PHE:N	2.75	0.48
1:E:182:THR:HG22	1:E:183:GLU:N	2.28	0.48
1:A:14:GLU:HG3	1:A:15:HIS:N	2.29	0.48
1:A:161:ARG:CB	1:A:196:VAL:HG11	2.39	0.48
1:A:487:GLU:OE1	1:F:495:THR:HA	2.14	0.48
1:B:148:THR:HG21	1:B:193:ARG:HD2	1.96	0.48
1:B:208:ARG:NH2	1:B:221:GLU:OE2	2.47	0.48
1:B:79:THR:HG22	1:B:82:ASP:H	1.78	0.48
1:B:93:ASP:OD2	1:B:96:LYS:HB2	2.13	0.48
1:C:296:LEU:HD13	1:C:331:TRP:CD2	2.49	0.48
1:C:438:ILE:HG23	1:C:453:ILE:HD11	1.95	0.48
1:D:130:ILE:N	1:D:130:ILE:HD12	2.28	0.48
1:D:367:ILE:HD12	1:D:375:ILE:CD1	2.41	0.48
1:E:134:ILE:N	1:E:134:ILE:HD13	2.29	0.48
1:E:99:ASP:C	1:E:101:GLY:H	2.17	0.48
1:F:371:LYS:N	1:F:372:PRO:HD3	2.29	0.48
1:F:437:ILE:CD1	1:F:437:ILE:N	2.77	0.48
1:A:347:VAL:O	1:A:348:CYS:HB2	2.14	0.48
1:C:21:MET:HE2	1:C:177:THR:CG2	2.43	0.48
1:C:325:LEU:HD23	1:C:335:PHE:CB	2.43	0.48
1:D:221:GLU:HG3	1:D:233:GLY:O	2.13	0.48
1:D:263:VAL:CG1	1:D:374:ARG:HH21	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:321:ARG:HG2	1:E:348:CYS:SG	2.54	0.48
1:B:87:ALA:HB1	1:B:92:TRP:HB2	1.96	0.48
1:C:283:ILE:C	1:C:284:ILE:HD13	2.33	0.48
1:C:334:ASP:O	1:C:338:MET:HG2	2.14	0.48
1:C:294:LYS:N	2:C:3901:ATP:O1B	2.47	0.48
1:C:433:ILE:HD12	1:C:433:ILE:N	2.29	0.48
1:D:289:ALA:HB2	1:D:419:PHE:HA	1.96	0.48
1:F:21:MET:HE3	1:F:59:PHE:CE1	2.49	0.48
1:F:291:GLY:HA3	1:F:442:TYR:OH	2.14	0.48
1:A:89:SER:CB	1:B:227:GLY:O	2.61	0.48
1:C:185:ILE:HA	3:D:4912:HOH:O	2.13	0.48
1:C:393:ARG:O	1:C:397:ILE:HG12	2.14	0.48
1:D:372:PRO:HB2	1:D:375:ILE:CD1	2.44	0.48
1:F:116:GLU:O	1:F:117:VAL:HB	2.14	0.48
1:F:191:ILE:HB	1:F:198:GLU:HG3	1.94	0.48
1:F:61:TYR:CE2	1:F:65:ILE:HG13	2.48	0.48
1:A:145:ASP:OD2	1:A:181:THR:HG21	2.14	0.47
1:B:150:VAL:CG1	1:B:151:PHE:H	2.27	0.47
1:C:471:MET:HG3	1:C:478:ASP:HB3	1.95	0.47
1:D:372:PRO:HB2	1:D:375:ILE:HD11	1.96	0.47
1:F:106:LEU:CD1	1:F:129:ARG:CZ	2.84	0.47
1:F:127:ILE:CD1	1:F:167:LEU:HD12	2.43	0.47
1:B:197:GLU:CD	1:B:197:GLU:H	2.18	0.47
1:C:144:ILE:CG2	1:C:147:VAL:HG12	2.44	0.47
1:C:18:ILE:HB	1:C:228:THR:HG23	1.96	0.47
1:C:371:LYS:N	1:C:372:PRO:HD3	2.29	0.47
1:D:148:THR:OG1	1:D:182:THR:HG23	2.14	0.47
1:E:451:ARG:NH1	1:E:472:ILE:HD13	2.28	0.47
1:F:299:SER:CB	1:F:333:MET:HE1	2.43	0.47
1:A:488:ARG:NH1	1:B:488:ARG:HH21	2.11	0.47
1:C:73:PHE:HB3	1:C:105:ILE:CD1	2.41	0.47
1:E:148:THR:HG21	1:E:183:GLU:CG	2.45	0.47
1:E:146:SER:H	1:E:181:THR:CG2	2.27	0.47
1:F:311:ARG:HA	1:F:343:LEU:O	2.14	0.47
1:A:402:TYR:O	1:A:406:GLU:HB2	2.13	0.47
1:A:459:ARG:HD3	1:F:323:GLN:HE21	1.79	0.47
1:C:357:GLU:HG3	1:C:358:ASP:N	2.29	0.47
1:C:468:ARG:HG2	1:C:468:ARG:HH11	1.79	0.47
1:F:170:ARG:HD2	1:F:173:GLN:OE1	2.14	0.47
1:F:178:THR:HG22	1:F:179:VAL:N	2.29	0.47
1:F:294:LYS:N	2:F:6901:ATP:O1B	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:GLU:HB3	1:A:408:ILE:HG12	1.97	0.47
1:B:396:VAL:O	1:B:400:THR:HB	2.14	0.47
1:C:84:ILE:HD12	1:C:94:LEU:CB	2.38	0.47
1:D:142:VAL:O	1:D:178:THR:HA	2.13	0.47
1:D:18:ILE:HD13	1:D:227:GLY:O	2.14	0.47
1:E:14:GLU:HG3	1:E:16:GLN:HB2	1.95	0.47
1:E:73:PHE:CE2	1:E:83:ILE:HD13	2.49	0.47
1:F:334:ASP:OD1	1:F:336:GLU:HB2	2.15	0.47
1:F:356:LEU:HD21	1:F:387:VAL:HG11	1.97	0.47
1:A:433:ILE:HD11	1:F:385:ARG:CZ	2.44	0.47
1:F:445:ILE:CD1	1:F:483:PHE:CE2	2.97	0.47
1:F:437:ILE:HD11	1:F:457:LYS:HE2	1.96	0.47
1:B:344:LEU:HD22	1:B:345:LYS:H	1.79	0.47
1:B:262:ARG:HH22	1:B:461:SER:HB2	1.79	0.47
1:C:17:ALA:C	1:C:18:ILE:HD12	2.34	0.47
1:E:143:SER:HA	1:E:179:VAL:O	2.15	0.47
1:E:14:GLU:HG3	1:E:16:GLN:N	2.24	0.47
1:E:311:ARG:HA	1:E:343:LEU:O	2.15	0.47
1:F:344:LEU:HD11	1:F:346:ILE:HG13	1.96	0.47
1:A:143:SER:C	1:A:144:ILE:HD13	2.35	0.47
1:A:16:GLN:O	1:A:17:ALA:O	2.32	0.47
1:C:45:SER:CB	1:C:182:THR:HB	2.44	0.47
1:E:313:ILE:HD12	1:E:367:ILE:CD1	2.35	0.47
1:E:439:LEU:HD12	1:E:440:LEU:N	2.29	0.47
1:F:18:ILE:HG12	1:F:228:THR:HG23	1.96	0.47
1:F:295:THR:HB	2:F:6901:ATP:PA	2.54	0.47
1:F:45:SER:HB2	1:F:182:THR:HB	1.95	0.47
1:C:122:ASP:O	1:C:124:SER:N	2.47	0.47
1:E:287:THR:HG21	1:E:425:ILE:O	2.15	0.47
1:A:211:LEU:HD12	1:A:215:ARG:O	2.15	0.47
1:B:203:ASN:HB3	1:B:225:LEU:HD23	1.97	0.47
1:C:363:ILE:O	1:C:367:ILE:HG13	2.14	0.47
1:C:487:GLU:CG	1:C:497:ILE:HD11	2.44	0.47
1:D:191:ILE:HD12	1:D:191:ILE:N	2.30	0.47
1:D:197:GLU:CD	1:D:197:GLU:H	2.16	0.47
1:D:31:ILE:HD11	1:D:248:PRO:HB3	1.96	0.47
1:F:146:SER:H	1:F:181:THR:CG2	2.27	0.47
1:A:218:ARG:NH1	1:A:239:ILE:HD12	2.29	0.47
1:A:64:ILE:HD13	1:A:69:GLU:O	2.15	0.47
1:C:267:VAL:HB	1:C:270:LEU:HB2	1.97	0.47
1:D:371:LYS:HE2	1:D:371:LYS:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:433:ILE:HG22	1:D:433:ILE:O	2.15	0.47
1:E:127:ILE:CD1	1:E:167:LEU:HD13	2.45	0.47
1:A:334:ASP:OD1	1:A:336:GLU:HB2	2.14	0.47
1:B:191:ILE:HB	1:B:198:GLU:HG2	1.97	0.47
1:B:96:LYS:O	1:B:100:GLU:HG3	2.13	0.47
1:C:131:ASN:OD1	1:C:174:ILE:HD12	2.15	0.47
1:E:440:LEU:HD23	1:E:453:ILE:HG13	1.97	0.47
1:F:150:VAL:CG1	1:F:151:PHE:N	2.78	0.47
1:F:25:ILE:CD1	1:F:58:GLN:HG2	2.45	0.47
1:F:76:PHE:HZ	1:F:126:LEU:HD21	1.80	0.47
1:A:484:ARG:HB3	1:A:484:ARG:HH11	1.79	0.46
1:B:249:LEU:CD1	1:B:394:GLN:HG2	2.45	0.46
1:C:123:LEU:HD13	1:C:166:ARG:HD2	1.96	0.46
1:C:146:SER:H	1:C:181:THR:HG22	1.79	0.46
1:D:143:SER:HA	1:D:179:VAL:O	2.15	0.46
1:D:461:SER:OG	1:D:462:TRP:N	2.47	0.46
1:E:123:LEU:HD21	1:E:167:LEU:HB2	1.96	0.46
1:D:488:ARG:HH12	1:E:488:ARG:HH21	1.61	0.46
1:E:90:PHE:HB2	1:E:92:TRP:CE2	2.50	0.46
1:F:21:MET:HB2	1:F:38:ILE:HG12	1.97	0.46
1:A:332:GLY:O	1:A:333:MET:C	2.53	0.46
1:A:362:ILE:CD1	1:A:362:ILE:N	2.78	0.46
1:B:451:ARG:HG2	1:B:451:ARG:NH1	2.30	0.46
1:C:93:ASP:OD2	1:C:96:LYS:HB2	2.15	0.46
1:D:14:GLU:CG	1:D:15:HIS:H	2.28	0.46
1:E:161:ARG:CB	1:E:196:VAL:HG11	2.38	0.46
1:E:435:ASP:HA	1:E:459:ARG:HD2	1.97	0.46
1:E:21:MET:HE3	1:E:59:PHE:CE1	2.51	0.46
1:A:21:MET:CE	1:A:59:PHE:CZ	2.97	0.46
1:B:142:VAL:O	1:B:178:THR:HA	2.16	0.46
1:B:92:TRP:HE3	1:B:92:TRP:CA	2.27	0.46
1:C:393:ARG:HH21	1:C:429:HIS:HB2	1.80	0.46
1:E:145:ASP:OD2	1:E:181:THR:HG21	2.16	0.46
1:E:486:PHE:CB	1:E:489:ILE:HD11	2.45	0.46
1:F:18:ILE:CG1	1:F:228:THR:HG23	2.45	0.46
1:A:249:LEU:CD1	1:A:394:GLN:HG2	2.44	0.46
1:A:376:ALA:HA	1:A:411:LEU:O	2.16	0.46
1:A:91:GLY:C	1:A:92:TRP:CE3	2.89	0.46
1:B:340:ARG:C	1:B:342:ASN:H	2.18	0.46
1:B:449:MET:CE	1:C:467:ILE:HD11	2.45	0.46
1:C:24:MET:CB	1:C:62:ASN:HD22	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:ILE:CD1	1:D:64:ILE:N	2.78	0.46
1:F:127:ILE:HD12	1:F:170:ARG:HB2	1.97	0.46
1:F:428:SER:OG	1:F:430:ILE:HG12	2.16	0.46
1:F:451:ARG:NH1	1:F:451:ARG:HG2	2.29	0.46
1:A:126:LEU:O	1:A:130:ILE:HG13	2.15	0.46
1:B:130:ILE:HG22	1:B:134:ILE:HD11	1.98	0.46
1:C:314:LEU:HB3	1:C:346:ILE:CD1	2.46	0.46
1:D:178:THR:HG22	1:D:179:VAL:N	2.31	0.46
1:D:301:PHE:CZ	1:D:374:ARG:HD3	2.50	0.46
1:D:64:ILE:HD12	1:D:69:GLU:O	2.15	0.46
1:E:153:GLN:C	1:F:158:SER:HB2	2.36	0.46
1:F:321:ARG:O	1:F:325:LEU:HD12	2.15	0.46
1:A:325:LEU:HD23	1:A:335:PHE:CB	2.45	0.46
1:B:131:ASN:OD1	1:B:174:ILE:HD12	2.16	0.46
1:B:182:THR:HG21	1:B:192:ALA:CB	2.43	0.46
1:B:264:SER:HB3	1:B:304:ASN:ND2	2.31	0.46
1:B:381:SER:HB3	1:B:414:ASN:OD1	2.16	0.46
1:B:393:ARG:O	1:B:397:ILE:HG12	2.16	0.46
1:C:335:PHE:O	1:C:339:GLU:HG3	2.15	0.46
1:C:36:LEU:HD12	1:C:59:PHE:CE1	2.51	0.46
1:D:470:PHE:CE1	1:D:472:ILE:HD11	2.50	0.46
1:E:246:ILE:HD12	1:E:246:ILE:N	2.31	0.46
1:F:106:LEU:CD1	1:F:129:ARG:NH2	2.78	0.46
1:F:356:LEU:HD13	1:F:387:VAL:HG21	1.98	0.46
1:A:183:GLU:HB2	1:B:199:PHE:CE1	2.50	0.46
1:B:332:GLY:O	1:B:333:MET:C	2.54	0.46
1:C:81:GLN:CD	1:C:81:GLN:N	2.69	0.46
1:F:371:LYS:HE3	1:F:371:LYS:O	2.15	0.46
1:F:313:ILE:CB	1:F:375:ILE:CD1	2.69	0.46
1:B:360:LEU:CD2	1:B:364:LYS:HE3	2.46	0.46
1:D:150:VAL:CG1	1:D:151:PHE:H	2.29	0.46
1:D:211:LEU:O	1:D:215:ARG:O	2.32	0.46
1:D:203:ASN:HB3	1:D:225:LEU:CD2	2.45	0.46
1:D:340:ARG:C	1:D:342:ASN:H	2.19	0.46
1:F:115:GLN:HG3	1:F:116:GLU:H	1.80	0.46
1:F:344:LEU:HD22	1:F:345:LYS:H	1.77	0.46
1:F:321:ARG:HG2	1:F:348:CYS:SG	2.56	0.46
1:A:31:ILE:CD1	1:A:246:ILE:HG21	2.46	0.46
1:A:231:MET:CE	1:A:251:ALA:HB2	2.46	0.46
1:B:284:ILE:N	1:B:284:ILE:HD13	2.31	0.46
1:B:430:ILE:HG22	1:B:430:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:GLY:N	2:C:3901:ATP:O2B	2.49	0.46
1:C:78:GLU:HB2	1:C:83:ILE:HD11	1.97	0.46
1:C:88:ARG:HD3	1:D:15:HIS:C	2.37	0.46
1:D:182:THR:CG2	1:D:183:GLU:N	2.79	0.46
1:E:325:LEU:HD23	1:E:335:PHE:CB	2.43	0.46
1:D:495:THR:HG23	1:E:487:GLU:OE2	2.16	0.46
1:A:311:ARG:HD2	1:A:371:LYS:HD3	1.96	0.46
1:B:161:ARG:CB	1:B:196:VAL:HG11	2.42	0.46
1:B:49:GLY:O	1:B:218:ARG:NH2	2.48	0.46
1:C:148:THR:OG1	1:C:182:THR:HG23	2.16	0.46
1:E:344:LEU:C	1:E:344:LEU:HD13	2.36	0.46
1:F:289:ALA:HB2	1:F:419:PHE:HA	1.98	0.46
1:F:72:VAL:CG2	1:F:134:ILE:HD13	2.46	0.46
1:B:377:ILE:HD13	1:B:412:PHE:CD2	2.50	0.45
1:B:92:TRP:N	1:B:92:TRP:HE3	2.13	0.45
1:D:70:PRO:HB2	1:D:139:ALA:HA	1.97	0.45
1:D:273:MET:O	1:D:463:HIS:HA	2.15	0.45
1:E:126:LEU:O	1:E:130:ILE:HG13	2.16	0.45
1:E:21:MET:CE	1:E:59:PHE:CZ	2.99	0.45
1:F:145:ASP:OD2	1:F:181:THR:HG21	2.16	0.45
1:A:150:VAL:O	1:A:153:GLN:HG3	2.16	0.45
1:C:362:ILE:HG22	1:C:366:GLU:OE2	2.16	0.45
1:D:106:LEU:CD1	1:D:129:ARG:NH2	2.79	0.45
1:D:76:PHE:O	1:D:109:SER:HA	2.15	0.45
1:F:129:ARG:O	1:F:132:TYR:HB3	2.16	0.45
1:A:375:ILE:O	1:A:410:GLY:HA2	2.15	0.45
1:B:295:THR:HB	2:B:2901:ATP:PA	2.56	0.45
1:D:387:VAL:HG12	1:D:388:SER:N	2.30	0.45
1:D:377:ILE:HD11	1:D:399:VAL:HG11	1.99	0.45
1:D:448:GLU:HG2	1:E:466:ALA:HA	1.97	0.45
1:F:443:VAL:HG12	1:F:445:ILE:HG13	1.97	0.45
1:A:45:SER:CB	1:A:182:THR:HB	2.46	0.45
1:B:126:LEU:C	1:B:128:GLU:N	2.70	0.45
1:F:356:LEU:HD22	1:F:387:VAL:HG11	1.98	0.45
1:F:484:ARG:CB	1:F:484:ARG:NH1	2.79	0.45
1:F:61:TYR:CE1	1:F:92:TRP:HB3	2.52	0.45
1:A:418:GLN:HB2	1:B:423:HIS:O	2.16	0.45
1:B:79:THR:O	1:B:83:ILE:HG12	2.17	0.45
1:B:90:PHE:O	1:B:92:TRP:CE3	2.69	0.45
1:C:208:ARG:NH2	1:C:221:GLU:OE2	2.50	0.45
1:E:146:SER:N	1:E:181:THR:HG22	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:487:GLU:HB2	1:E:497:ILE:HD11	1.99	0.45
1:F:24:MET:HB2	1:F:62:ASN:ND2	2.30	0.45
1:A:191:ILE:HB	1:A:198:GLU:HG2	1.98	0.45
1:A:323:GLN:NE2	1:B:459:ARG:HD3	2.31	0.45
1:B:359:HIS:O	1:B:363:ILE:HG12	2.17	0.45
1:C:295:THR:HG21	1:C:319:GLU:OE2	2.16	0.45
1:C:305:ALA:HB2	1:C:374:ARG:CD	2.43	0.45
1:B:449:MET:HE1	1:C:490:ILE:HD11	1.95	0.45
1:D:21:MET:CE	1:D:59:PHE:HZ	2.30	0.45
1:D:425:ILE:HD11	1:D:456:PHE:CD2	2.52	0.45
1:E:406:GLU:O	1:E:408:ILE:HG13	2.15	0.45
1:E:469:GLU:HB3	1:E:483:PHE:CZ	2.52	0.45
1:F:292:THR:HB	1:F:440:LEU:HB3	1.98	0.45
1:F:486:PHE:HE2	1:F:496:ARG:CD	2.27	0.45
1:A:80:PRO:HD2	1:A:81:GLN:NE2	2.31	0.45
1:B:161:ARG:HD2	1:B:196:VAL:HG13	1.97	0.45
1:B:317:TYR:CE2	1:B:383:LEU:HD21	2.52	0.45
1:B:484:ARG:NH1	1:B:484:ARG:HB3	2.32	0.45
1:C:451:ARG:NH1	1:C:451:ARG:HG2	2.31	0.45
1:D:492:GLY:O	1:D:494:PRO:HD3	2.17	0.45
1:F:357:GLU:HG3	1:F:358:ASP:N	2.32	0.45
1:A:332:GLY:O	1:A:333:MET:O	2.35	0.45
1:B:452:ALA:HA	1:B:469:GLU:HA	1.99	0.45
1:C:249:LEU:HD13	1:C:394:GLN:HG2	1.99	0.45
1:D:352:GLU:OE2	1:D:385:ARG:HD2	2.17	0.45
1:E:211:LEU:O	1:E:212:GLU:HB3	2.16	0.45
1:E:338:MET:HB3	1:E:344:LEU:HB3	1.98	0.45
1:E:371:LYS:N	1:E:372:PRO:HD3	2.31	0.45
1:F:33:HIS:HD2	1:F:229:SER:OG	1.99	0.45
1:A:118:VAL:HG12	1:A:122:ASP:HB3	1.99	0.45
1:A:148:THR:CG2	1:A:193:ARG:HD2	2.47	0.45
1:A:18:ILE:HD13	1:A:227:GLY:O	2.17	0.45
1:A:351:PRO:HB3	1:A:383:LEU:HD23	1.98	0.45
1:B:469:GLU:HB3	1:B:483:PHE:CZ	2.52	0.45
1:C:443:VAL:HG12	1:C:445:ILE:HG13	1.99	0.45
1:C:437:ILE:CD1	1:C:457:LYS:HE2	2.47	0.45
1:D:164:LEU:HD11	1:D:197:GLU:HG3	1.99	0.45
1:D:371:LYS:HD3	1:D:371:LYS:O	2.16	0.45
1:E:332:GLY:O	1:E:333:MET:C	2.55	0.45
1:F:290:THR:HG22	2:F:6901:ATP:O1G	2.17	0.45
1:F:479:ILE:H	1:F:479:ILE:HD12	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:O	1:A:212:GLU:CB	2.64	0.45
1:A:267:VAL:HB	1:A:270:LEU:HB2	1.98	0.45
1:A:352:GLU:OE2	1:A:385:ARG:HD2	2.17	0.45
1:B:317:TYR:CD2	1:B:383:LEU:HD21	2.51	0.45
1:B:402:TYR:O	1:B:406:GLU:HB2	2.17	0.45
1:C:124:SER:O	1:C:128:GLU:HG3	2.17	0.45
1:C:178:THR:HG22	1:C:179:VAL:N	2.32	0.45
1:C:33:HIS:HD2	1:C:229:SER:OG	2.00	0.45
1:C:24:MET:HG3	1:C:66:GLU:HG3	1.99	0.45
1:D:218:ARG:NH1	1:D:239:ILE:HD12	2.33	0.45
1:D:295:THR:HG21	1:D:319:GLU:OE2	2.17	0.45
1:D:45:SER:HB3	1:D:182:THR:HB	1.98	0.45
1:C:488:ARG:HH22	1:D:488:ARG:HH21	1.61	0.45
1:A:256:GLN:O	1:F:322:ALA:HB3	2.17	0.45
1:F:467:ILE:N	1:F:467:ILE:CD1	2.80	0.45
1:A:362:ILE:O	1:A:366:GLU:CG	2.53	0.44
1:A:315:PHE:CZ	1:A:363:ILE:HG23	2.52	0.44
1:B:92:TRP:CE3	1:B:92:TRP:N	2.86	0.44
1:C:187:GLU:O	1:C:208:ARG:HD3	2.18	0.44
1:D:21:MET:HE3	1:D:59:PHE:CE1	2.52	0.44
1:E:334:ASP:OD1	1:E:336:GLU:HB2	2.17	0.44
1:F:215:ARG:NE	1:F:215:ARG:HA	2.31	0.44
1:B:419:PHE:O	1:B:420:MET:HB2	2.17	0.44
1:C:40:ARG:HG2	1:C:172:LYS:HE3	1.99	0.44
1:C:316:ALA:O	1:C:348:CYS:HA	2.17	0.44
1:E:485:ASN:HD22	1:E:496:ARG:HD3	1.82	0.44
1:E:487:GLU:O	1:E:488:ARG:CB	2.64	0.44
1:F:23:THR:O	1:F:24:MET:HB2	2.17	0.44
1:A:356:LEU:HD22	1:A:387:VAL:HG11	1.98	0.44
1:A:433:ILE:HG22	1:A:433:ILE:O	2.17	0.44
1:C:468:ARG:HG2	1:C:468:ARG:NH1	2.31	0.44
1:D:212:GLU:O	1:D:212:GLU:HG2	2.17	0.44
1:F:21:MET:CE	1:F:59:PHE:CZ	2.99	0.44
1:B:192:ALA:HB3	1:B:197:GLU:OE2	2.18	0.44
1:B:81:GLN:CD	1:B:81:GLN:H	2.20	0.44
1:C:211:LEU:O	1:C:212:GLU:HB3	2.17	0.44
1:E:455:VAL:HG11	1:E:463:HIS:HB2	1.99	0.44
1:E:79:THR:CG2	1:E:82:ASP:H	2.26	0.44
1:F:111:ASP:OD2	1:F:113:GLU:HG3	2.17	0.44
1:E:193:ARG:NH2	1:F:195:GLY:O	2.29	0.44
1:F:363:ILE:N	1:F:363:ILE:HD13	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:360:LEU:HD21	1:F:364:LYS:HE3	1.99	0.44
1:C:449:MET:CE	1:D:467:ILE:HD11	2.48	0.44
1:D:231:MET:CE	1:D:251:ALA:HB2	2.48	0.44
1:E:148:THR:HG21	1:E:193:ARG:HD2	1.99	0.44
1:F:21:MET:HE1	1:F:59:PHE:HZ	1.82	0.44
1:A:227:GLY:O	1:F:89:SER:HB2	2.18	0.44
1:C:146:SER:H	1:C:181:THR:CG2	2.31	0.44
1:C:45:SER:HB3	1:C:182:THR:HB	1.99	0.44
1:D:79:THR:HG23	1:D:81:GLN:N	2.31	0.44
1:E:205:VAL:CG2	1:E:222:ILE:HD12	2.28	0.44
1:F:76:PHE:HZ	1:F:126:LEU:CD2	2.30	0.44
1:B:21:MET:HE3	1:B:59:PHE:CE1	2.53	0.44
1:C:249:LEU:CD1	1:C:394:GLN:HG2	2.48	0.44
1:C:335:PHE:HA	1:C:338:MET:HG3	2.00	0.44
1:D:449:MET:HE3	1:E:490:ILE:HD11	2.00	0.44
1:E:81:GLN:NE2	1:E:81:GLN:H	2.16	0.44
1:F:489:ILE:HD13	1:F:494:PRO:HG2	2.00	0.44
1:A:453:ILE:HB	1:A:470:PHE:CD2	2.52	0.44
1:B:98:VAL:HA	1:B:103:LEU:O	2.17	0.44
1:C:151:PHE:C	1:C:153:GLN:N	2.71	0.44
1:B:495:THR:HG23	1:C:487:GLU:OE2	2.18	0.44
1:C:65:ILE:H	1:C:65:ILE:CD1	2.31	0.44
1:D:31:ILE:HA	1:D:231:MET:SD	2.58	0.44
1:D:21:MET:CE	1:D:59:PHE:CZ	3.01	0.44
1:D:64:ILE:CD1	1:D:64:ILE:H	2.31	0.44
1:E:364:LYS:O	1:E:368:ASN:ND2	2.51	0.44
1:F:43:LEU:HD11	1:F:182:THR:OG1	2.17	0.44
1:B:119:GLY:C	1:B:121:PHE:H	2.21	0.44
1:C:143:SER:HA	1:C:179:VAL:O	2.18	0.44
1:C:88:ARG:HG2	1:C:88:ARG:HH11	1.83	0.44
1:D:122:ASP:HB3	1:D:123:LEU:H	1.43	0.44
1:D:358:ASP:O	1:D:362:ILE:HG12	2.18	0.44
1:D:98:VAL:HA	1:D:103:LEU:O	2.18	0.44
1:E:451:ARG:HG2	1:E:451:ARG:NH1	2.32	0.44
1:E:56:SER:HB2	1:E:143:SER:HB2	1.99	0.44
1:A:14:GLU:CG	1:A:15:HIS:N	2.81	0.43
1:A:357:GLU:HG3	1:A:358:ASP:N	2.32	0.43
1:C:78:GLU:CB	1:C:83:ILE:HD11	2.48	0.43
1:D:106:LEU:CD1	1:D:129:ARG:HH21	2.31	0.43
1:D:211:LEU:HD12	1:D:215:ARG:O	2.18	0.43
1:D:356:LEU:HD22	1:D:387:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:ASP:O	1:E:113:GLU:N	2.51	0.43
1:A:220:LEU:HD21	1:A:222:ILE:CD1	2.47	0.43
1:A:375:ILE:HD12	1:A:408:ILE:HG21	2.00	0.43
1:B:484:ARG:HH11	1:B:484:ARG:HB3	1.83	0.43
1:C:317:TYR:CE2	1:C:383:LEU:HD21	2.54	0.43
1:C:387:VAL:CG1	1:C:391:ALA:HB3	2.48	0.43
1:F:340:ARG:C	1:F:342:ASN:H	2.22	0.43
1:F:381:SER:HB3	1:F:414:ASN:OD1	2.18	0.43
1:A:296:LEU:HD23	1:A:472:ILE:HD12	1.99	0.43
1:B:291:GLY:N	2:B:2901:ATP:O2B	2.51	0.43
1:B:305:ALA:HB2	1:B:374:ARG:CD	2.38	0.43
1:D:106:LEU:HD21	1:D:130:ILE:HD12	2.01	0.43
1:D:14:GLU:CG	1:D:15:HIS:N	2.80	0.43
1:D:21:MET:HE2	1:D:177:THR:HG21	1.99	0.43
1:D:291:GLY:N	2:D:4901:ATP:O2B	2.50	0.43
1:D:440:LEU:HD23	1:D:453:ILE:HG12	2.00	0.43
1:D:470:PHE:HB3	1:D:479:ILE:HD13	2.00	0.43
1:D:81:GLN:H	1:D:81:GLN:CD	2.22	0.43
1:E:211:LEU:HD12	1:E:215:ARG:O	2.18	0.43
1:E:18:ILE:HD11	1:E:228:THR:N	2.33	0.43
1:E:376:ALA:HA	1:E:411:LEU:O	2.17	0.43
1:A:293:GLY:HA2	2:A:1901:ATP:O1A	2.18	0.43
1:A:431:SER:O	1:A:434:THR:HG22	2.19	0.43
1:A:436:THR:CG2	1:A:458:MET:HG2	2.48	0.43
1:B:79:THR:HG21	1:B:81:GLN:HG2	2.01	0.43
1:F:332:GLY:O	1:F:333:MET:C	2.56	0.43
1:A:65:ILE:O	1:A:65:ILE:HG22	2.17	0.43
1:B:432:THR:HG22	1:B:432:THR:O	2.17	0.43
1:B:440:LEU:HD21	1:B:453:ILE:HG12	2.00	0.43
1:B:80:PRO:HD2	1:B:81:GLN:NE2	2.33	0.43
1:B:81:GLN:H	1:B:81:GLN:NE2	2.16	0.43
1:C:215:ARG:NE	1:C:215:ARG:HA	2.32	0.43
1:C:338:MET:HB3	1:C:344:LEU:HB3	2.01	0.43
1:E:385:ARG:HA	1:F:393:ARG:HH12	1.83	0.43
1:E:81:GLN:CD	1:E:81:GLN:H	2.20	0.43
1:A:87:ALA:HB1	1:A:92:TRP:CB	2.49	0.43
1:B:56:SER:O	1:B:59:PHE:HB3	2.18	0.43
1:D:344:LEU:HD22	1:D:345:LYS:H	1.80	0.43
1:D:317:TYR:CD2	1:D:383:LEU:HD21	2.53	0.43
1:E:45:SER:CB	1:E:182:THR:HB	2.48	0.43
1:E:249:LEU:HD13	1:E:394:GLN:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:396:VAL:HG11	1:E:430:ILE:HG21	2.00	0.43
1:F:126:LEU:HG	1:F:130:ILE:CD1	2.47	0.43
1:F:191:ILE:CB	1:F:198:GLU:CG	2.90	0.43
1:F:270:LEU:O	1:F:273:MET:HB2	2.19	0.43
1:A:184:ARG:O	1:B:199:PHE:HZ	2.02	0.43
1:A:291:GLY:N	2:A:1901:ATP:O2B	2.51	0.43
1:A:334:ASP:O	1:A:338:MET:HG2	2.19	0.43
1:A:459:ARG:HH11	1:F:323:GLN:HE22	1.65	0.43
1:C:118:VAL:O	1:C:118:VAL:HG12	2.19	0.43
1:D:387:VAL:CG1	1:D:388:SER:N	2.82	0.43
1:E:21:MET:HE1	1:E:177:THR:HB	2.01	0.43
1:F:419:PHE:O	1:F:420:MET:HB2	2.18	0.43
1:F:468:ARG:NH1	1:F:468:ARG:HG2	2.34	0.43
1:F:81:GLN:N	1:F:81:GLN:CD	2.72	0.43
1:A:178:THR:HG22	1:A:179:VAL:N	2.34	0.43
1:B:378:ASP:O	1:B:379:SER:HB3	2.18	0.43
1:C:340:ARG:C	1:C:342:ASN:H	2.22	0.43
1:D:256:GLN:HG3	1:D:404:LYS:HD3	2.00	0.43
1:E:184:ARG:HG2	1:E:191:ILE:O	2.19	0.43
1:F:148:THR:HG21	1:F:183:GLU:HG3	2.00	0.43
1:F:264:SER:HA	1:F:271:ASP:OD1	2.18	0.43
1:A:299:SER:C	1:A:333:MET:HE1	2.39	0.43
1:A:344:LEU:C	1:A:344:LEU:HD13	2.38	0.43
1:A:447:GLY:C	1:B:467:ILE:HD13	2.39	0.43
1:C:67:PHE:HB2	1:C:69:GLU:HG3	1.99	0.43
1:D:134:ILE:HD13	1:D:134:ILE:N	2.34	0.43
1:E:150:VAL:CG1	1:E:151:PHE:H	2.32	0.43
1:F:431:SER:HA	1:F:434:THR:HG22	1.99	0.43
1:A:218:ARG:O	1:A:236:PRO:HA	2.19	0.43
1:A:362:ILE:CG2	1:A:366:GLU:OE2	2.67	0.43
1:A:406:GLU:O	1:A:407:GLU:HB2	2.19	0.43
1:A:215:ARG:NH2	1:B:234:GLU:O	2.52	0.43
1:B:462:TRP:O	1:B:463:HIS:O	2.35	0.43
1:C:311:ARG:HD2	1:C:371:LYS:HD3	1.96	0.43
1:C:360:LEU:CD2	1:C:364:LYS:HE3	2.49	0.43
1:C:484:ARG:HH11	1:C:484:ARG:HB3	1.82	0.43
1:D:61:TYR:CE2	1:D:92:TRP:HD1	2.37	0.43
1:E:447:GLY:O	1:F:467:ILE:CD1	2.65	0.43
1:F:28:PHE:CE1	1:F:222:ILE:HD11	2.53	0.43
1:A:393:ARG:O	1:A:397:ILE:HG12	2.18	0.42
1:C:184:ARG:HG2	1:C:191:ILE:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:PHE:O	1:C:374:ARG:NH1	2.50	0.42
1:E:294:LYS:HB2	2:E:5901:ATP:O1B	2.19	0.42
1:E:356:LEU:HD21	1:E:387:VAL:HG11	1.99	0.42
1:F:142:VAL:O	1:F:178:THR:HA	2.19	0.42
1:F:180:MET:HB3	1:F:180:MET:HE2	1.84	0.42
1:F:191:ILE:HB	1:F:198:GLU:HG2	1.95	0.42
1:F:25:ILE:HD12	1:F:58:GLN:CG	2.49	0.42
1:A:425:ILE:HD11	1:A:456:PHE:CE2	2.54	0.42
1:D:359:HIS:O	1:D:363:ILE:HG13	2.18	0.42
1:E:203:ASN:HB3	1:E:225:LEU:CD2	2.47	0.42
1:F:106:LEU:HD11	1:F:129:ARG:NH2	2.33	0.42
1:F:425:ILE:HG22	1:F:426:THR:HG23	2.01	0.42
1:A:359:HIS:O	1:A:363:ILE:HG12	2.18	0.42
1:A:317:TYR:CD2	1:A:383:LEU:HD21	2.54	0.42
1:B:264:SER:O	1:B:374:ARG:NH2	2.51	0.42
1:B:21:MET:HB2	1:B:38:ILE:HG12	2.02	0.42
1:C:123:LEU:CD2	1:C:167:LEU:HB2	2.49	0.42
1:C:308:ASN:O	1:C:310:GLU:HG3	2.20	0.42
1:C:356:LEU:CD2	1:C:387:VAL:HG11	2.50	0.42
1:C:52:LYS:N	2:C:3903:ATP:O1B	2.49	0.42
1:C:292:THR:HB	1:C:440:LEU:HB3	2.01	0.42
1:C:75:THR:HG23	1:C:75:THR:O	2.19	0.42
1:D:377:ILE:CD1	1:D:399:VAL:HG11	2.50	0.42
1:D:437:ILE:HD11	1:D:457:LYS:HE2	2.00	0.42
1:E:53:THR:HG23	1:E:145:ASP:OD1	2.18	0.42
1:E:191:ILE:CB	1:E:198:GLU:HG2	2.47	0.42
1:E:400:THR:HG22	1:E:401:GLY:N	2.33	0.42
1:E:446:ARG:HH21	1:E:496:ARG:NH2	2.16	0.42
1:F:111:ASP:OD1	1:F:112:PRO:CD	2.66	0.42
1:F:325:LEU:HD23	1:F:335:PHE:CB	2.45	0.42
1:A:304:ASN:HB3	1:A:374:ARG:HH12	1.84	0.42
1:B:471:MET:O	1:B:472:ILE:HD13	2.19	0.42
1:C:96:LYS:O	1:C:100:GLU:HG3	2.19	0.42
1:C:214:GLU:C	1:C:215:ARG:HE	2.23	0.42
1:D:123:LEU:HA	1:D:123:LEU:HD22	1.84	0.42
1:D:334:ASP:O	1:D:338:MET:HG2	2.19	0.42
1:E:148:THR:HG21	1:E:183:GLU:HG3	2.02	0.42
1:E:164:LEU:HD11	1:E:197:GLU:HG3	2.02	0.42
1:F:115:GLN:CG	1:F:116:GLU:N	2.82	0.42
1:F:121:PHE:HD2	1:F:121:PHE:HA	1.74	0.42
1:F:211:LEU:HD12	1:F:215:ARG:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:295:THR:HG21	1:F:319:GLU:OE2	2.19	0.42
1:F:437:ILE:HD13	1:F:457:LYS:HG2	2.00	0.42
1:A:17:ALA:C	1:A:18:ILE:HD12	2.40	0.42
1:A:33:HIS:HD2	1:A:229:SER:OG	2.02	0.42
1:A:454:ASN:HB2	1:A:467:ILE:HD13	2.02	0.42
1:B:107:ASP:C	1:B:107:ASP:OD1	2.58	0.42
1:B:21:MET:HE2	1:B:177:THR:HG21	2.02	0.42
1:B:289:ALA:HB2	1:B:419:PHE:HA	2.01	0.42
1:C:123:LEU:O	1:C:124:SER:C	2.57	0.42
1:D:323:GLN:NE2	1:E:459:ARG:HD3	2.34	0.42
1:D:45:SER:CB	1:D:182:THR:HB	2.50	0.42
1:F:119:GLY:HA2	1:F:122:ASP:OD1	2.19	0.42
1:F:122:ASP:O	1:F:126:LEU:N	2.33	0.42
1:A:52:LYS:HD3	1:A:182:THR:O	2.20	0.42
1:A:291:GLY:O	2:A:1901:ATP:H4'	2.19	0.42
1:B:315:PHE:CD2	1:B:363:ILE:CD1	3.03	0.42
1:B:336:GLU:OE1	1:B:336:GLU:HA	2.20	0.42
1:B:73:PHE:HB3	1:B:105:ILE:CD1	2.42	0.42
1:C:41:SER:HA	1:C:178:THR:O	2.19	0.42
1:C:420:MET:HE2	1:C:492:GLY:HA3	2.01	0.42
1:D:145:ASP:OD2	1:D:181:THR:HG21	2.20	0.42
1:D:296:LEU:HD13	1:D:331:TRP:CD2	2.55	0.42
1:D:412:PHE:CD1	1:D:412:PHE:N	2.88	0.42
1:E:321:ARG:O	1:E:325:LEU:HD12	2.19	0.42
1:A:377:ILE:HD13	1:A:412:PHE:CD2	2.53	0.42
1:A:488:ARG:NE	1:F:488:ARG:NH1	2.66	0.42
1:B:292:THR:HB	1:B:440:LEU:HB3	2.01	0.42
1:B:487:GLU:O	1:B:494:PRO:HA	2.20	0.42
1:C:116:GLU:O	1:C:117:VAL:HB	2.19	0.42
1:D:362:ILE:CG2	1:D:366:GLU:OE2	2.67	0.42
1:D:387:VAL:HG12	1:D:388:SER:O	2.19	0.42
1:E:396:VAL:HG11	1:E:430:ILE:CG2	2.49	0.42
1:F:306:CYS:SG	1:F:344:LEU:HB2	2.60	0.42
1:A:159:VAL:O	1:A:163:GLU:HG2	2.19	0.42
1:A:443:VAL:CG1	1:A:494:PRO:HG2	2.50	0.42
1:B:146:SER:H	1:B:181:THR:HG22	1.84	0.42
1:C:449:MET:HE3	1:D:467:ILE:HD11	2.02	0.42
1:E:244:ILE:HG22	1:E:246:ILE:CD1	2.50	0.42
1:E:81:GLN:CD	1:E:81:GLN:N	2.72	0.42
1:F:356:LEU:CD1	1:F:387:VAL:HG21	2.50	0.42
1:F:431:SER:O	1:F:434:THR:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:SER:HA	1:B:182:THR:O	2.19	0.42
1:C:161:ARG:HB2	1:C:196:VAL:HG11	2.01	0.42
1:C:283:ILE:CD1	1:C:400:THR:HG23	2.50	0.42
1:D:109:SER:HA	1:D:110:PRO:HD3	1.88	0.42
1:D:41:SER:HA	1:D:178:THR:O	2.20	0.42
1:D:208:ARG:O	1:D:218:ARG:HA	2.20	0.42
1:D:303:GLU:O	1:D:303:GLU:HG2	2.19	0.42
1:D:19:ALA:CB	1:D:38:ILE:HD12	2.49	0.42
1:E:438:ILE:HD13	1:E:455:VAL:HA	2.02	0.42
1:B:267:VAL:HB	1:B:270:LEU:HB2	2.01	0.42
1:B:358:ASP:O	1:B:362:ILE:HG12	2.19	0.42
1:C:197:GLU:OE2	1:C:197:GLU:N	2.36	0.42
1:C:61:TYR:C	1:C:65:ILE:HD13	2.33	0.42
1:E:333:MET:HB2	1:E:333:MET:HE2	1.87	0.42
1:F:336:GLU:HB3	1:F:340:ARG:NH2	2.35	0.42
1:A:437:ILE:HD13	1:A:457:LYS:HG3	2.01	0.41
1:B:126:LEU:C	1:B:128:GLU:H	2.23	0.41
1:C:123:LEU:HD11	1:C:163:GLU:O	2.20	0.41
1:D:489:ILE:CD1	1:D:494:PRO:HB3	2.43	0.41
1:D:78:GLU:OE1	1:D:83:ILE:HD13	2.19	0.41
1:E:344:LEU:HD11	1:E:346:ILE:HG13	2.01	0.41
1:E:84:ILE:HG21	1:E:95:ALA:HB2	2.02	0.41
1:F:440:LEU:HD21	1:F:453:ILE:HG13	2.01	0.41
1:A:316:ALA:CB	1:A:324:LEU:HD11	2.50	0.41
1:B:360:LEU:HD21	1:B:364:LYS:HE3	2.03	0.41
1:D:376:ALA:HA	1:D:411:LEU:O	2.20	0.41
1:E:134:ILE:N	1:E:134:ILE:CD1	2.83	0.41
1:E:371:LYS:HD3	1:E:371:LYS:O	2.20	0.41
1:E:52:LYS:N	2:E:5903:ATP:O1B	2.48	0.41
1:E:21:MET:CE	1:E:59:PHE:HZ	2.34	0.41
1:F:329:TYR:HA	1:F:332:GLY:O	2.20	0.41
1:A:302:VAL:HG13	1:A:344:LEU:HD23	2.03	0.41
1:C:170:ARG:O	1:C:174:ILE:HG12	2.21	0.41
1:C:52:LYS:HD3	1:C:182:THR:O	2.20	0.41
1:F:151:PHE:CZ	1:F:160:VAL:HG13	2.55	0.41
1:A:433:ILE:CD1	1:F:385:ARG:NH2	2.83	0.41
1:B:178:THR:CG2	1:B:179:VAL:N	2.84	0.41
2:B:2901:ATP:H3'	1:C:458:MET:O	2.20	0.41
1:B:85:LYS:HZ2	1:C:14:GLU:HB3	1.82	0.41
1:C:123:LEU:HD11	1:C:163:GLU:CA	2.51	0.41
1:C:123:LEU:HD22	1:C:167:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:THR:HB	2:C:3901:ATP:PA	2.61	0.41
1:E:193:ARG:HH11	1:E:193:ARG:HG2	1.85	0.41
1:E:469:GLU:CB	1:E:483:PHE:CZ	3.03	0.41
1:F:113:GLU:O	1:F:114:GLY:O	2.39	0.41
1:F:131:ASN:OD1	1:F:174:ILE:HD12	2.21	0.41
1:F:161:ARG:CB	1:F:196:VAL:HG11	2.42	0.41
1:F:487:GLU:O	1:F:488:ARG:HB2	2.19	0.41
1:A:40:ARG:HG2	1:A:172:LYS:HE3	2.03	0.41
1:A:451:ARG:CG	1:A:451:ARG:NH1	2.78	0.41
1:B:25:ILE:HG23	1:B:58:GLN:NE2	2.35	0.41
1:C:194:TYR:CD1	1:C:194:TYR:N	2.89	0.41
1:D:72:VAL:CG2	1:D:134:ILE:HD12	2.46	0.41
1:E:377:ILE:HD11	1:E:399:VAL:HG11	2.03	0.41
1:F:468:ARG:HH11	1:F:468:ARG:HG2	1.85	0.41
1:A:87:ALA:HB1	1:A:92:TRP:HB3	2.02	0.41
1:B:449:MET:HE3	1:C:467:ILE:HD11	2.01	0.41
1:B:91:GLY:C	1:B:92:TRP:CE3	2.94	0.41
1:C:306:CYS:SG	1:C:344:LEU:HB2	2.61	0.41
1:D:249:LEU:CD1	1:D:394:GLN:HG2	2.51	0.41
1:E:352:GLU:OE2	1:E:385:ARG:HD2	2.20	0.41
1:E:372:PRO:CB	1:E:375:ILE:HD11	2.48	0.41
1:A:299:SER:CB	1:A:333:MET:HE1	2.43	0.41
1:A:483:PHE:HB3	1:A:486:PHE:HD1	1.85	0.41
1:B:300:ARG:HA	1:B:333:MET:HE3	2.03	0.41
1:B:356:LEU:HD13	1:B:387:VAL:HG21	2.02	0.41
1:D:61:TYR:CZ	1:D:92:TRP:CD1	3.08	0.41
1:D:79:THR:HG22	1:D:82:ASP:N	2.16	0.41
1:E:178:THR:HG22	1:E:179:VAL:N	2.35	0.41
1:E:249:LEU:CD1	1:E:394:GLN:HG2	2.50	0.41
1:F:31:ILE:CD1	1:F:246:ILE:HG21	2.51	0.41
1:A:182:THR:CG2	1:A:183:GLU:N	2.84	0.41
1:A:311:ARG:HB3	1:A:370:PHE:CE2	2.56	0.41
1:B:425:ILE:HG22	1:B:426:THR:HG23	2.03	0.41
1:C:211:LEU:HD12	1:C:215:ARG:O	2.21	0.41
1:C:382:ALA:O	1:C:385:ARG:HG3	2.21	0.41
1:C:296:LEU:HD23	1:C:472:ILE:HD12	2.02	0.41
1:D:488:ARG:HH12	1:E:488:ARG:NH2	2.18	0.41
1:F:118:VAL:O	1:F:118:VAL:HG22	2.20	0.41
1:F:148:THR:HG21	1:F:183:GLU:CG	2.51	0.41
1:A:153:GLN:O	1:A:154:TYR:CB	2.69	0.41
1:B:470:PHE:HE1	1:B:472:ILE:HD11	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:ILE:HG21	1:C:147:VAL:HG12	2.02	0.41
1:C:432:THR:HG22	1:C:432:THR:O	2.20	0.41
1:D:159:VAL:O	1:D:163:GLU:HG2	2.21	0.41
1:D:432:THR:O	1:D:432:THR:CG2	2.69	0.41
1:D:273:MET:CE	1:D:468:ARG:HD2	2.51	0.41
1:E:127:ILE:HD13	1:E:127:ILE:N	2.35	0.41
1:E:365:SER:HA	1:E:368:ASN:HD22	1.86	0.41
1:E:379:SER:N	1:E:413:THR:HB	2.23	0.41
1:F:117:VAL:O	1:F:118:VAL:HB	2.21	0.41
1:F:21:MET:CE	1:F:59:PHE:CE1	3.04	0.41
1:F:220:LEU:C	1:F:220:LEU:HD23	2.41	0.41
1:F:92:TRP:CD1	1:F:92:TRP:N	2.86	0.41
1:A:64:ILE:HG21	1:A:97:LEU:HD22	2.02	0.41
1:B:127:ILE:HG22	1:B:127:ILE:O	2.20	0.41
1:B:148:THR:HA	1:B:151:PHE:CE1	2.56	0.41
1:B:225:LEU:HD12	1:B:230:HIS:HB3	2.03	0.41
1:B:376:ALA:HA	1:B:411:LEU:O	2.21	0.41
1:C:438:ILE:HD12	1:C:455:VAL:HG22	2.03	0.41
1:D:495:THR:O	1:D:495:THR:HG22	2.21	0.41
1:E:217:ARG:HH21	1:E:236:PRO:HB3	1.86	0.41
1:F:269:ARG:HB3	1:F:479:ILE:HD13	2.02	0.41
1:F:375:ILE:HA	1:F:375:ILE:HD13	1.98	0.41
1:A:487:GLU:HG2	1:F:496:ARG:CZ	2.51	0.41
1:F:90:PHE:CB	1:F:92:TRP:CZ2	3.04	0.41
1:A:183:GLU:OE2	1:B:161:ARG:NH1	2.46	0.41
1:B:126:LEU:HG	1:B:130:ILE:CD1	2.51	0.41
1:B:293:GLY:HA2	2:B:2901:ATP:O1A	2.21	0.41
1:C:161:ARG:HD2	1:C:196:VAL:HG13	2.03	0.41
1:D:24:MET:HB2	1:D:62:ASN:HD22	1.86	0.41
1:E:191:ILE:CG2	1:E:198:GLU:HG3	2.51	0.41
1:E:437:ILE:HD12	1:E:457:LYS:HE2	2.01	0.41
1:D:496:ARG:HG2	1:E:487:GLU:OE1	2.20	0.41
1:E:79:THR:HG23	1:E:81:GLN:CG	2.41	0.41
1:F:123:LEU:HA	1:F:123:LEU:HD22	1.82	0.41
1:F:221:GLU:C	1:F:222:ILE:HD13	2.41	0.41
1:F:287:THR:HA	1:F:414:ASN:O	2.21	0.41
1:A:187:GLU:O	1:A:208:ARG:HD3	2.20	0.40
1:B:335:PHE:O	1:B:339:GLU:HG3	2.21	0.40
1:C:123:LEU:HB3	1:C:127:ILE:HD11	2.03	0.40
2:C:3901:ATP:C2	1:D:462:TRP:HA	2.56	0.40
1:C:53:THR:O	1:C:54:LEU:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:PHE:O	1:C:109:SER:HA	2.21	0.40
1:D:471:MET:HG3	1:D:478:ASP:HB3	2.04	0.40
1:E:220:LEU:HD21	1:E:222:ILE:CD1	2.51	0.40
1:E:445:ILE:HD12	1:E:450:SER:OG	2.21	0.40
1:F:357:GLU:HG3	1:F:358:ASP:H	1.86	0.40
1:B:382:ALA:O	1:B:385:ARG:HG3	2.22	0.40
1:B:76:PHE:HE1	1:B:144:ILE:CG2	2.33	0.40
1:C:354:ALA:HB1	1:C:358:ASP:HB2	2.04	0.40
1:C:378:ASP:O	1:C:379:SER:HB3	2.22	0.40
1:D:191:ILE:HB	1:D:198:GLU:CD	2.40	0.40
1:D:325:LEU:HD23	1:D:335:PHE:CB	2.48	0.40
1:D:419:PHE:O	1:D:420:MET:HB2	2.21	0.40
1:E:146:SER:HA	1:E:181:THR:HG22	2.03	0.40
1:E:184:ARG:O	1:E:185:ILE:HD13	2.21	0.40
1:A:164:LEU:HA	1:A:164:LEU:HD23	1.83	0.40
1:A:220:LEU:HD21	1:A:222:ILE:HD11	2.02	0.40
1:A:319:GLU:O	1:B:254:LEU:HD21	2.21	0.40
1:A:444:GLU:O	1:A:494:PRO:HD2	2.21	0.40
1:A:452:ALA:HA	1:A:469:GLU:HA	2.03	0.40
1:B:273:MET:CE	1:B:468:ARG:HD2	2.51	0.40
1:D:121:PHE:N	1:D:121:PHE:CD1	2.89	0.40
1:D:153:GLN:O	1:D:154:TYR:CB	2.69	0.40
1:D:385:ARG:HG2	1:E:393:ARG:NH1	2.36	0.40
1:E:94:LEU:O	1:E:98:VAL:HG23	2.21	0.40
1:F:256:GLN:H	1:F:256:GLN:HG2	1.69	0.40
1:A:283:ILE:HG23	1:A:412:PHE:CE1	2.56	0.40
1:A:90:PHE:HB2	1:A:92:TRP:CG	2.57	0.40
1:B:299:SER:CB	1:B:333:MET:HE1	2.49	0.40
1:B:433:ILE:CG2	1:B:433:ILE:O	2.69	0.40
1:D:61:TYR:CD2	1:D:92:TRP:CD1	3.10	0.40
1:E:264:SER:HA	1:E:271:ASP:OD1	2.22	0.40
1:E:392:PHE:O	1:E:395:PHE:HB3	2.22	0.40
2:D:4901:ATP:C2	1:E:462:TRP:HA	2.56	0.40
1:B:31:ILE:HD12	1:B:235:TYR:CD1	2.56	0.40
1:B:21:MET:HE3	1:B:59:PHE:CZ	2.56	0.40
1:B:92:TRP:CE3	1:B:92:TRP:HA	2.57	0.40
1:B:99:ASP:C	1:B:101:GLY:N	2.74	0.40
1:C:99:ASP:C	1:C:101:GLY:H	2.25	0.40
1:C:256:GLN:H	1:C:256:GLN:HG2	1.70	0.40
1:D:385:ARG:NH2	1:E:433:ILE:CD1	2.83	0.40
1:E:471:MET:HG3	1:E:478:ASP:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:161:ARG:HB2	1:F:196:VAL:CG1	2.43	0.40
1:F:79:THR:HG21	1:F:81:GLN:HG2	2.01	0.40

There are no symmetry-related clashes.

## 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	482/525 (92%)	438 (91%)	33 (7%)	11 (2%)	6	21
1	B	482/525 (92%)	432 (90%)	41 (8%)	9 (2%)	8	26
1	C	482/525 (92%)	431 (89%)	37 (8%)	14 (3%)	4	15
1	D	482/525 (92%)	439 (91%)	32 (7%)	11 (2%)	6	21
1	E	482/525 (92%)	434 (90%)	33 (7%)	15 (3%)	4	14
1	F	482/525 (92%)	436 (90%)	36 (8%)	10 (2%)	7	23
All	All	2892/3150 (92%)	2610 (90%)	212 (7%)	70 (2%)	6	20

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	ALA
1	A	117	VAL
1	A	154	TYR
1	A	211	LEU
1	A	333	MET
1	A	463	HIS
1	B	154	TYR
1	B	333	MET
1	B	463	HIS
1	C	17	ALA

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Mol	Chain	Res	Type
1	C	117	VAL
1	C	122	ASP
1	C	123	LEU
1	C	154	TYR
1	C	333	MET
1	C	463	HIS
1	D	113	GLU
1	D	122	ASP
1	D	154	TYR
1	D	333	MET
1	E	122	ASP
1	E	154	TYR
1	E	211	LEU
1	E	333	MET
1	E	463	HIS
1	F	114	GLY
1	F	118	VAL
1	F	154	TYR
1	F	333	MET
1	F	463	HIS
1	B	119	GLY
1	B	211	LEU
1	D	463	HIS
1	E	113	GLU
1	E	123	LEU
1	E	387	VAL
1	E	420	MET
1	F	211	LEU
1	A	120	GLY
1	A	387	VAL
1	A	420	MET
1	B	420	MET
1	C	112	PRO
1	C	211	LEU
1	C	349	ALA
1	D	211	LEU
1	D	420	MET
1	E	488	ARG
1	F	117	VAL
1	F	420	MET
1	C	420	MET
1	E	494	PRO

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Mol	Chain	Res	Type
1	A	348	CYS
1	B	348	CYS
1	B	494	PRO
1	C	348	CYS
1	C	379	SER
1	D	118	VAL
1	D	387	VAL
1	E	117	VAL
1	E	348	CYS
1	E	379	SER
1	C	212	GLU
1	D	348	CYS
1	D	494	PRO
1	F	348	CYS
1	A	112	PRO
1	E	112	PRO
1	F	387	VAL
1	B	387	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	412/450 (92%)	386 (94%)	26 (6%)	18	46
1	B	412/450 (92%)	391 (95%)	21 (5%)	24	55
1	C	412/450 (92%)	388 (94%)	24 (6%)	20	50
1	D	412/450 (92%)	385 (93%)	27 (7%)	16	44
1	E	412/450 (92%)	386 (94%)	26 (6%)	18	46
1	F	412/450 (92%)	383 (93%)	29 (7%)	15	40
All	All	2472/2700 (92%)	2319 (94%)	153 (6%)	18	47

All (153) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	38	ILE
1	A	79	THR
1	A	81	GLN
1	A	92	TRP
1	A	123	LEU
1	A	151	PHE
1	A	154	TYR
1	A	186	GLU
1	A	212	GLU
1	A	222	ILE
1	A	223	LEU
1	A	238	THR
1	A	256	GLN
1	A	270	LEU
1	A	287	THR
1	A	342	ASN
1	A	360	LEU
1	A	362	ILE
1	A	371	LYS
1	A	400	THR
1	A	437	ILE
1	A	451	ARG
1	A	458	MET
1	A	471	MET
1	A	496	ARG
1	B	26	GLU
1	B	79	THR
1	B	81	GLN
1	B	92	TRP
1	B	128	GLU
1	B	151	PHE
1	B	154	TYR
1	B	181	THR
1	B	186	GLU
1	B	212	GLU
1	B	223	LEU
1	B	256	GLN
1	B	270	LEU
1	B	360	LEU
1	B	371	LYS
1	B	400	THR
1	B	437	ILE

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Mol	Chain	Res	Type
1	B	451	ARG
1	B	453	ILE
1	B	462	TRP
1	B	471	MET
1	C	26	GLU
1	C	65	ILE
1	C	79	THR
1	C	81	GLN
1	C	151	PHE
1	C	154	TYR
1	C	181	THR
1	C	186	GLU
1	C	212	GLU
1	C	218	ARG
1	C	223	LEU
1	C	256	GLN
1	C	270	LEU
1	C	284	ILE
1	C	303	GLU
1	C	360	LEU
1	C	371	LYS
1	C	375	ILE
1	C	400	THR
1	C	451	ARG
1	C	453	ILE
1	C	458	MET
1	C	471	MET
1	C	497	ILE
1	D	26	GLU
1	D	79	THR
1	D	81	GLN
1	D	121	PHE
1	D	122	ASP
1	D	123	LEU
1	D	134	ILE
1	D	151	PHE
1	D	154	TYR
1	D	181	THR
1	D	186	GLU
1	D	212	GLU
1	D	223	LEU
1	D	256	GLN

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Mol	Chain	Res	Type
1	D	270	LEU
1	D	287	THR
1	D	360	LEU
1	D	371	LYS
1	D	375	ILE
1	D	400	THR
1	D	431	SER
1	D	451	ARG
1	D	453	ILE
1	D	463	HIS
1	D	469	GLU
1	D	471	MET
1	D	496	ARG
1	E	26	GLU
1	E	79	THR
1	E	81	GLN
1	E	121	PHE
1	E	134	ILE
1	E	151	PHE
1	E	154	TYR
1	E	181	THR
1	E	186	GLU
1	E	212	GLU
1	E	222	ILE
1	E	223	LEU
1	E	228	THR
1	E	256	GLN
1	E	270	LEU
1	E	284	ILE
1	E	287	THR
1	E	360	LEU
1	E	371	LYS
1	E	375	ILE
1	E	400	THR
1	E	451	ARG
1	E	458	MET
1	E	469	GLU
1	E	471	MET
1	E	497	ILE
1	F	26	GLU
1	F	45	SER
1	F	53	THR

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Mol	Chain	Res	Type
1	F	79	THR
1	F	81	GLN
1	F	121	PHE
1	F	123	LEU
1	F	151	PHE
1	F	154	TYR
1	F	181	THR
1	F	186	GLU
1	F	212	GLU
1	F	218	ARG
1	F	222	ILE
1	F	223	LEU
1	F	256	GLN
1	F	270	LEU
1	F	342	ASN
1	F	360	LEU
1	F	363	ILE
1	F	371	LYS
1	F	400	THR
1	F	451	ARG
1	F	458	MET
1	F	462	TRP
1	F	471	MET
1	F	487	GLU
1	F	491	SER
1	F	496	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	HIS
1	A	62	ASN
1	A	81	GLN
1	A	209	ASN
1	A	361	GLN
1	A	368	ASN
1	A	414	ASN
1	A	441	GLN
1	B	16	GLN
1	B	62	ASN
1	B	81	GLN
1	B	209	ASN

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Mol	Chain	Res	Type
1	B	368	ASN
1	B	414	ASN
1	B	441	GLN
1	C	33	HIS
1	C	62	ASN
1	C	81	GLN
1	C	209	ASN
1	C	368	ASN
1	C	414	ASN
1	D	33	HIS
1	D	81	GLN
1	D	209	ASN
1	D	361	GLN
1	D	368	ASN
1	D	414	ASN
1	E	33	HIS
1	E	81	GLN
1	E	209	ASN
1	E	304	ASN
1	E	361	GLN
1	E	368	ASN
1	E	414	ASN
1	E	441	GLN
1	E	454	ASN
1	F	16	GLN
1	F	33	HIS
1	F	62	ASN
1	F	81	GLN
1	F	153	GLN
1	F	209	ASN
1	F	361	GLN
1	F	368	ASN
1	F	414	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

12 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	ATP	C	3901	-	26,33,33	1.49	5 (19%)	31,52,52	1.88	6 (19%)
2	ATP	D	4903	-	26,33,33	1.38	3 (11%)	31,52,52	1.79	5 (16%)
2	ATP	A	1903	-	26,33,33	1.33	2 (7%)	31,52,52	1.81	6 (19%)
2	ATP	F	6901	-	26,33,33	1.49	5 (19%)	31,52,52	1.95	7 (22%)
2	ATP	B	2903	-	26,33,33	1.36	3 (11%)	31,52,52	1.89	6 (19%)
2	ATP	C	3903	-	26,33,33	1.17	2 (7%)	31,52,52	1.77	4 (12%)
2	ATP	E	5901	-	26,33,33	1.51	5 (19%)	31,52,52	1.98	7 (22%)
2	ATP	D	4901	-	26,33,33	1.49	5 (19%)	31,52,52	1.95	7 (22%)
2	ATP	E	5903	-	26,33,33	1.25	2 (7%)	31,52,52	1.81	5 (16%)
2	ATP	A	1901	-	26,33,33	1.42	5 (19%)	31,52,52	1.94	7 (22%)
2	ATP	B	2901	-	26,33,33	1.39	4 (15%)	31,52,52	1.94	7 (22%)
2	ATP	F	6903	-	26,33,33	1.27	2 (7%)	31,52,52	1.79	5 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	C	3901	-	-	5/18/38/38	0/3/3/3
2	ATP	D	4903	-	-	7/18/38/38	0/3/3/3
2	ATP	A	1903	-	-	7/18/38/38	0/3/3/3
2	ATP	F	6901	-	-	6/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	B	2903	-	-	7/18/38/38	0/3/3/3
2	ATP	C	3903	-	-	8/18/38/38	0/3/3/3
2	ATP	E	5901	-	-	6/18/38/38	0/3/3/3
2	ATP	D	4901	-	-	6/18/38/38	0/3/3/3
2	ATP	E	5903	-	-	7/18/38/38	0/3/3/3
2	ATP	A	1901	-	-	6/18/38/38	0/3/3/3
2	ATP	B	2901	-	-	5/18/38/38	0/3/3/3
2	ATP	F	6903	-	-	8/18/38/38	0/3/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2903	ATP	C2-N3	4.49	1.39	1.32
2	E	5901	ATP	C2-N3	4.33	1.39	1.32
2	F	6903	ATP	C2-N3	4.17	1.38	1.32
2	A	1903	ATP	C2-N3	4.14	1.38	1.32
2	C	3901	ATP	C2-N3	4.12	1.38	1.32
2	D	4903	ATP	C2-N3	4.05	1.38	1.32
2	F	6901	ATP	C2-N3	4.02	1.38	1.32
2	D	4901	ATP	C2-N3	3.91	1.38	1.32
2	A	1901	ATP	C2-N3	3.80	1.38	1.32
2	E	5903	ATP	C2-N3	3.78	1.38	1.32
2	C	3903	ATP	C2-N3	3.72	1.38	1.32
2	B	2901	ATP	C2-N3	3.58	1.37	1.32
2	B	2901	ATP	C2-N1	3.08	1.39	1.33
2	F	6901	ATP	C2-N1	2.95	1.39	1.33
2	E	5901	ATP	C2'-C1'	-2.86	1.49	1.53
2	E	5901	ATP	C2-N1	2.83	1.39	1.33
2	C	3901	ATP	C2-N1	2.80	1.39	1.33
2	A	1901	ATP	O4'-C1'	2.80	1.45	1.41
2	A	1901	ATP	C2-N1	2.76	1.39	1.33
2	F	6901	ATP	O4'-C1'	2.74	1.44	1.41
2	D	4901	ATP	C2-N1	2.70	1.38	1.33
2	F	6901	ATP	C2'-C1'	-2.68	1.49	1.53
2	D	4901	ATP	O4'-C1'	2.67	1.44	1.41
2	C	3901	ATP	O4'-C1'	2.66	1.44	1.41
2	D	4903	ATP	C2'-C1'	-2.60	1.49	1.53
2	D	4901	ATP	O2'-C2'	-2.58	1.36	1.43
2	A	1903	ATP	C2-N1	2.58	1.38	1.33
2	C	3901	ATP	C2'-C1'	-2.49	1.50	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2901	ATP	O4'-C1'	2.47	1.44	1.41
2	D	4901	ATP	C2'-C1'	-2.46	1.50	1.53
2	E	5901	ATP	O2'-C2'	-2.37	1.37	1.43
2	F	6903	ATP	C2-N1	2.34	1.38	1.33
2	B	2903	ATP	C2-N1	2.33	1.38	1.33
2	C	3901	ATP	O2'-C2'	-2.31	1.37	1.43
2	B	2903	ATP	O4'-C1'	2.28	1.44	1.41
2	A	1901	ATP	C2'-C1'	-2.27	1.50	1.53
2	E	5901	ATP	O4'-C1'	2.25	1.44	1.41
2	B	2901	ATP	O2'-C2'	-2.20	1.37	1.43
2	A	1901	ATP	O2'-C2'	-2.17	1.37	1.43
2	F	6901	ATP	O2'-C2'	-2.16	1.37	1.43
2	E	5903	ATP	C2'-C1'	-2.15	1.50	1.53
2	D	4903	ATP	O4'-C4'	-2.12	1.40	1.45
2	C	3903	ATP	C2'-C1'	-2.11	1.50	1.53

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2901	ATP	N3-C2-N1	-5.81	119.59	128.68
2	E	5901	ATP	N3-C2-N1	-5.65	119.85	128.68
2	D	4901	ATP	N3-C2-N1	-5.62	119.90	128.68
2	D	4903	ATP	N3-C2-N1	-5.60	119.93	128.68
2	C	3903	ATP	N3-C2-N1	-5.57	119.97	128.68
2	A	1901	ATP	N3-C2-N1	-5.54	120.01	128.68
2	F	6901	ATP	N3-C2-N1	-5.52	120.05	128.68
2	C	3901	ATP	N3-C2-N1	-5.50	120.08	128.68
2	E	5903	ATP	N3-C2-N1	-5.45	120.17	128.68
2	A	1903	ATP	N3-C2-N1	-5.43	120.20	128.68
2	B	2903	ATP	N3-C2-N1	-5.36	120.30	128.68
2	F	6903	ATP	N3-C2-N1	-5.27	120.44	128.68
2	B	2903	ATP	C5-C6-N6	4.35	126.97	120.35
2	F	6903	ATP	C4-C5-N7	-4.27	104.95	109.40
2	B	2903	ATP	C4-C5-N7	-4.23	105.00	109.40
2	A	1903	ATP	C5-C6-N6	4.13	126.64	120.35
2	D	4903	ATP	C4-C5-N7	-4.10	105.12	109.40
2	F	6903	ATP	C5-C6-N6	4.04	126.50	120.35
2	E	5903	ATP	C4-C5-N7	-4.01	105.22	109.40
2	A	1903	ATP	C4-C5-N7	-3.99	105.24	109.40
2	F	6901	ATP	C4-C5-N7	-3.99	105.24	109.40
2	F	6901	ATP	C5-C6-N6	3.98	126.39	120.35
2	E	5901	ATP	C4-C5-N7	-3.97	105.26	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3901	ATP	C4-C5-N7	-3.94	105.29	109.40
2	A	1901	ATP	C5-C6-N6	3.91	126.29	120.35
2	E	5901	ATP	C5-C6-N6	3.83	126.17	120.35
2	D	4901	ATP	C4-C5-N7	-3.83	105.41	109.40
2	B	2901	ATP	C5-C6-N6	3.82	126.16	120.35
2	C	3903	ATP	C4-C5-N7	-3.80	105.44	109.40
2	E	5903	ATP	C5-C6-N6	3.79	126.11	120.35
2	A	1901	ATP	C4-C5-N7	-3.79	105.45	109.40
2	E	5901	ATP	C3'-C2'-C1'	3.78	106.67	100.98
2	C	3903	ATP	C5-C6-N6	3.73	126.03	120.35
2	D	4903	ATP	C5-C6-N6	3.71	126.00	120.35
2	B	2901	ATP	C4-C5-N7	-3.71	105.53	109.40
2	D	4901	ATP	C3'-C2'-C1'	3.71	106.56	100.98
2	D	4901	ATP	C5-C6-N6	3.70	125.97	120.35
2	C	3901	ATP	C3'-C2'-C1'	3.56	106.34	100.98
2	A	1901	ATP	C3'-C2'-C1'	3.47	106.20	100.98
2	F	6901	ATP	C3'-C2'-C1'	3.44	106.16	100.98
2	C	3901	ATP	C5-C6-N6	3.41	125.53	120.35
2	E	5903	ATP	C3'-C2'-C1'	3.25	105.87	100.98
2	B	2901	ATP	C3'-C2'-C1'	3.25	105.87	100.98
2	B	2903	ATP	C3'-C2'-C1'	2.86	105.28	100.98
2	D	4903	ATP	C3'-C2'-C1'	2.85	105.27	100.98
2	A	1903	ATP	C3'-C2'-C1'	2.84	105.25	100.98
2	B	2901	ATP	PA-O3A-PB	2.80	142.43	132.83
2	D	4901	ATP	PA-O3A-PB	2.77	142.34	132.83
2	C	3901	ATP	PA-O3A-PB	2.76	142.28	132.83
2	E	5901	ATP	PA-O3A-PB	2.71	142.14	132.83
2	F	6901	ATP	PA-O3A-PB	2.67	142.00	132.83
2	A	1901	ATP	PA-O3A-PB	2.67	141.98	132.83
2	B	2901	ATP	O5'-PA-O1A	-2.56	99.08	109.07
2	B	2903	ATP	N6-C6-N1	-2.52	113.33	118.57
2	E	5901	ATP	O5'-PA-O1A	-2.47	99.43	109.07
2	D	4901	ATP	O5'-PA-O1A	-2.45	99.49	109.07
2	F	6903	ATP	C3'-C2'-C1'	2.40	104.59	100.98
2	B	2903	ATP	PB-O3B-PG	-2.29	124.96	132.83
2	F	6901	ATP	O5'-PA-O1A	-2.29	100.13	109.07
2	A	1901	ATP	O5'-PA-O1A	-2.29	100.13	109.07
2	C	3903	ATP	C3'-C2'-C1'	2.25	104.37	100.98
2	A	1901	ATP	PB-O3B-PG	-2.24	125.14	132.83
2	C	3901	ATP	O5'-PA-O1A	-2.23	100.36	109.07
2	F	6901	ATP	PB-O3B-PG	-2.23	125.19	132.83
2	F	6903	ATP	N6-C6-N1	-2.17	114.07	118.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1903	ATP	N6-C6-N1	-2.15	114.10	118.57
2	D	4901	ATP	PB-O3B-PG	-2.13	125.50	132.83
2	E	5903	ATP	N6-C6-N1	-2.12	114.17	118.57
2	A	1903	ATP	PB-O3B-PG	-2.07	125.72	132.83
2	E	5901	ATP	PB-O3B-PG	-2.02	125.89	132.83
2	D	4903	ATP	N6-C6-N1	-2.02	114.38	118.57
2	B	2901	ATP	C2-N1-C6	2.00	122.18	118.75

There are no chirality outliers.

All (78) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	3901	ATP	PB-O3B-PG-O3G
2	C	3901	ATP	PB-O3A-PA-O5'
2	D	4903	ATP	PB-O3B-PG-O3G
2	D	4903	ATP	C5'-O5'-PA-O1A
2	D	4903	ATP	O4'-C4'-C5'-O5'
2	D	4903	ATP	C3'-C4'-C5'-O5'
2	A	1903	ATP	PB-O3B-PG-O3G
2	A	1903	ATP	C5'-O5'-PA-O1A
2	A	1903	ATP	O4'-C4'-C5'-O5'
2	A	1903	ATP	C3'-C4'-C5'-O5'
2	F	6901	ATP	PB-O3B-PG-O3G
2	F	6901	ATP	PB-O3A-PA-O5'
2	B	2903	ATP	PB-O3B-PG-O3G
2	C	3903	ATP	PB-O3B-PG-O3G
2	C	3903	ATP	C5'-O5'-PA-O1A
2	E	5901	ATP	PB-O3B-PG-O3G
2	E	5901	ATP	PB-O3A-PA-O5'
2	D	4901	ATP	PB-O3B-PG-O3G
2	D	4901	ATP	PB-O3A-PA-O5'
2	E	5903	ATP	PB-O3B-PG-O3G
2	E	5903	ATP	C5'-O5'-PA-O1A
2	E	5903	ATP	O4'-C4'-C5'-O5'
2	E	5903	ATP	C3'-C4'-C5'-O5'
2	A	1901	ATP	PB-O3B-PG-O3G
2	A	1901	ATP	PB-O3A-PA-O5'
2	B	2901	ATP	PB-O3B-PG-O3G
2	F	6903	ATP	PB-O3B-PG-O3G
2	F	6903	ATP	C5'-O5'-PA-O1A
2	F	6903	ATP	O4'-C4'-C5'-O5'
2	B	2903	ATP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	B	2903	ATP	C3'-C4'-C5'-O5'
2	C	3903	ATP	O4'-C4'-C5'-O5'
2	C	3903	ATP	C3'-C4'-C5'-O5'
2	F	6903	ATP	C3'-C4'-C5'-O5'
2	A	1903	ATP	PB-O3A-PA-O1A
2	D	4903	ATP	PB-O3A-PA-O5'
2	A	1903	ATP	PB-O3A-PA-O5'
2	B	2903	ATP	PB-O3A-PA-O5'
2	C	3903	ATP	PB-O3A-PA-O5'
2	E	5903	ATP	PB-O3A-PA-O5'
2	B	2901	ATP	PB-O3A-PA-O5'
2	F	6903	ATP	PB-O3A-PA-O5'
2	C	3901	ATP	C5'-O5'-PA-O3A
2	F	6901	ATP	C5'-O5'-PA-O3A
2	D	4901	ATP	C5'-O5'-PA-O3A
2	A	1901	ATP	C5'-O5'-PA-O3A
2	B	2901	ATP	C5'-O5'-PA-O3A
2	C	3901	ATP	PA-O3A-PB-O2B
2	D	4903	ATP	PA-O3A-PB-O2B
2	D	4903	ATP	PB-O3A-PA-O1A
2	A	1903	ATP	PA-O3A-PB-O2B
2	B	2903	ATP	PA-O3A-PB-O2B
2	C	3903	ATP	PA-O3A-PB-O2B
2	E	5901	ATP	PA-O3A-PB-O2B
2	E	5903	ATP	PA-O3A-PB-O2B
2	A	1901	ATP	PA-O3A-PB-O2B
2	F	6903	ATP	PA-O3A-PB-O2B
2	F	6901	ATP	PA-O3A-PB-O2B
2	C	3903	ATP	PB-O3A-PA-O1A
2	D	4901	ATP	PA-O3A-PB-O2B
2	E	5903	ATP	PB-O3A-PA-O1A
2	B	2901	ATP	PA-O3A-PB-O2B
2	B	2903	ATP	PB-O3A-PA-O1A
2	F	6903	ATP	PB-O3A-PA-O1A
2	C	3903	ATP	PB-O3B-PG-O1G
2	F	6903	ATP	PB-O3B-PG-O1G
2	C	3901	ATP	PB-O3B-PG-O2G
2	F	6901	ATP	PB-O3B-PG-O2G
2	E	5901	ATP	PB-O3B-PG-O2G
2	D	4901	ATP	PB-O3B-PG-O2G
2	A	1901	ATP	PB-O3B-PG-O2G
2	B	2901	ATP	PB-O3B-PG-O2G

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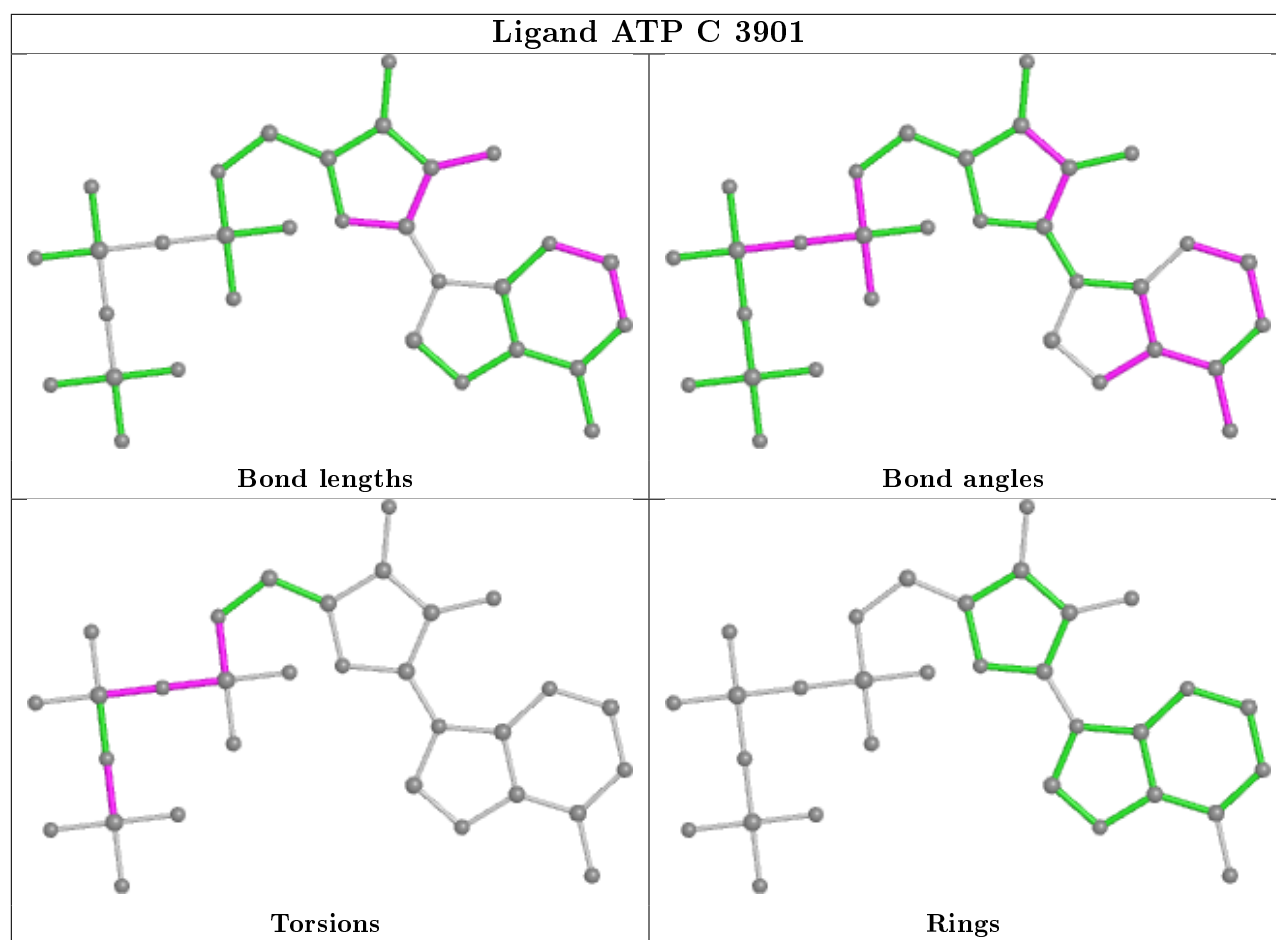
Mol	Chain	Res	Type	Atoms
2	E	5901	ATP	C5'-O5'-PA-O3A
2	D	4901	ATP	PB-O3A-PA-O2A
2	A	1901	ATP	PB-O3A-PA-O2A
2	B	2903	ATP	C5'-O5'-PA-O1A
2	F	6901	ATP	PB-O3B-PG-O1G
2	E	5901	ATP	PB-O3B-PG-O1G

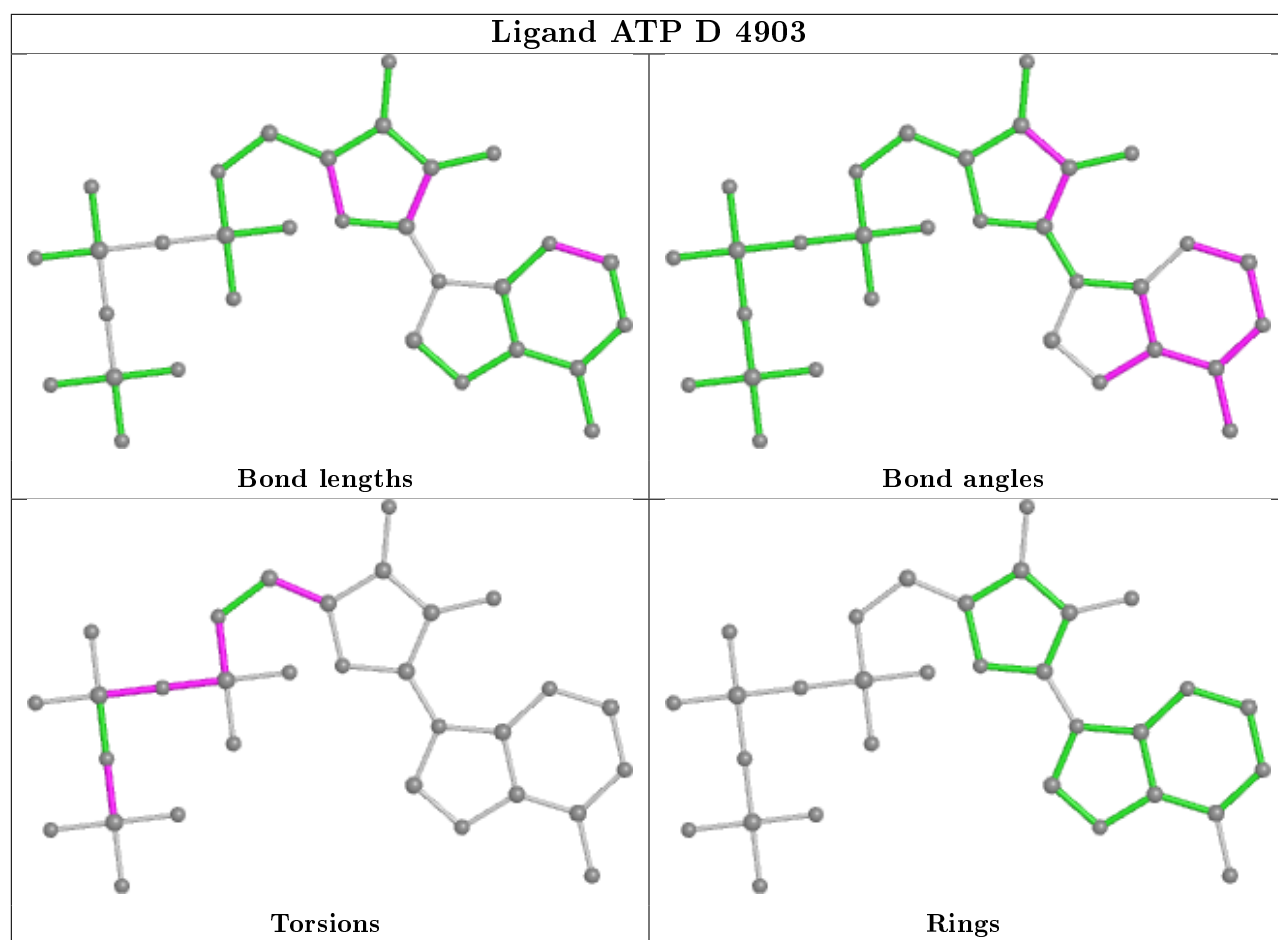
There are no ring outliers.

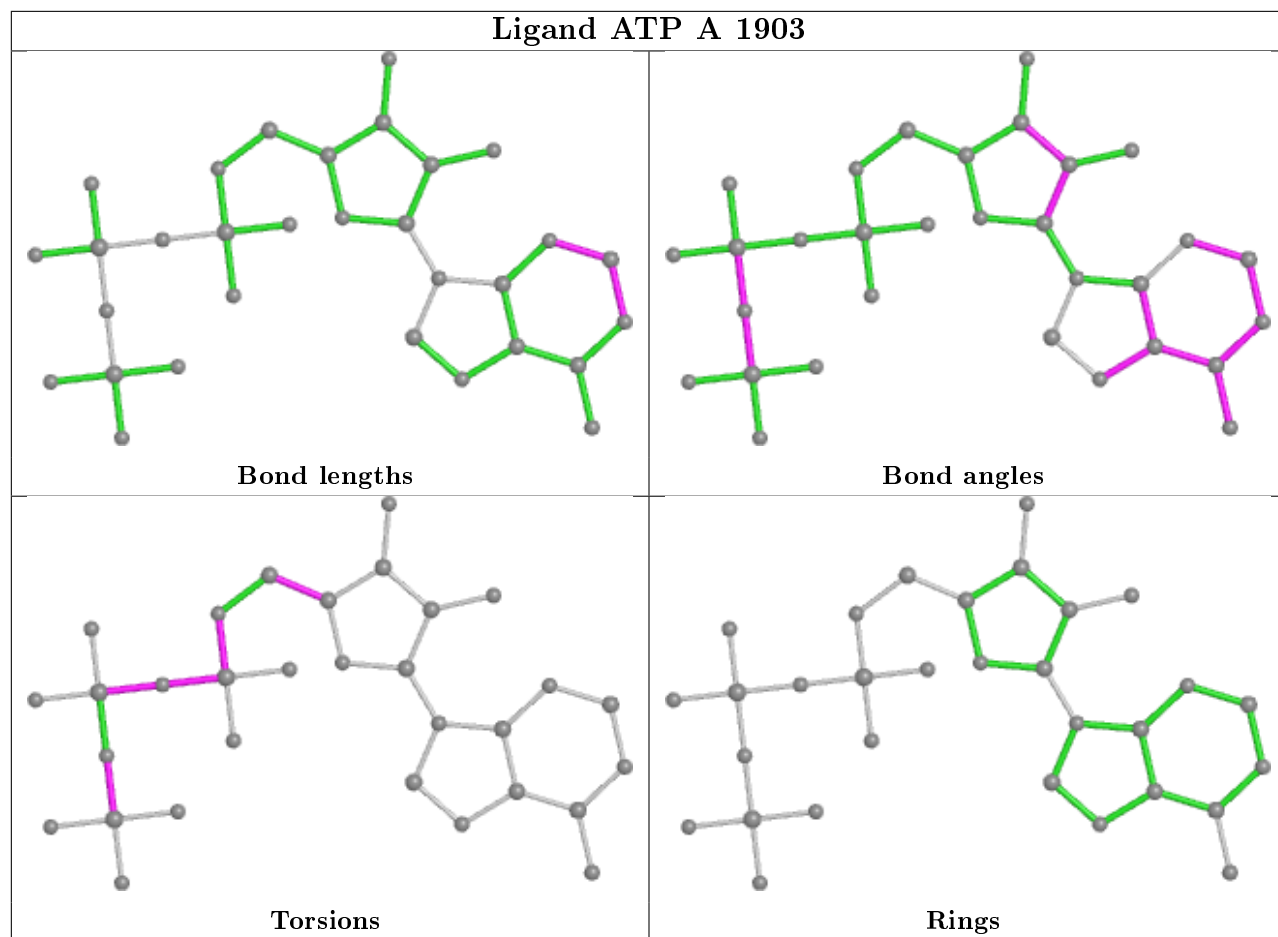
12 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3901	ATP	4	0
2	D	4903	ATP	3	0
2	A	1903	ATP	3	0
2	F	6901	ATP	5	0
2	B	2903	ATP	4	0
2	C	3903	ATP	4	0
2	E	5901	ATP	5	0
2	D	4901	ATP	4	0
2	E	5903	ATP	4	0
2	A	1901	ATP	5	0
2	B	2901	ATP	6	0
2	F	6903	ATP	3	0

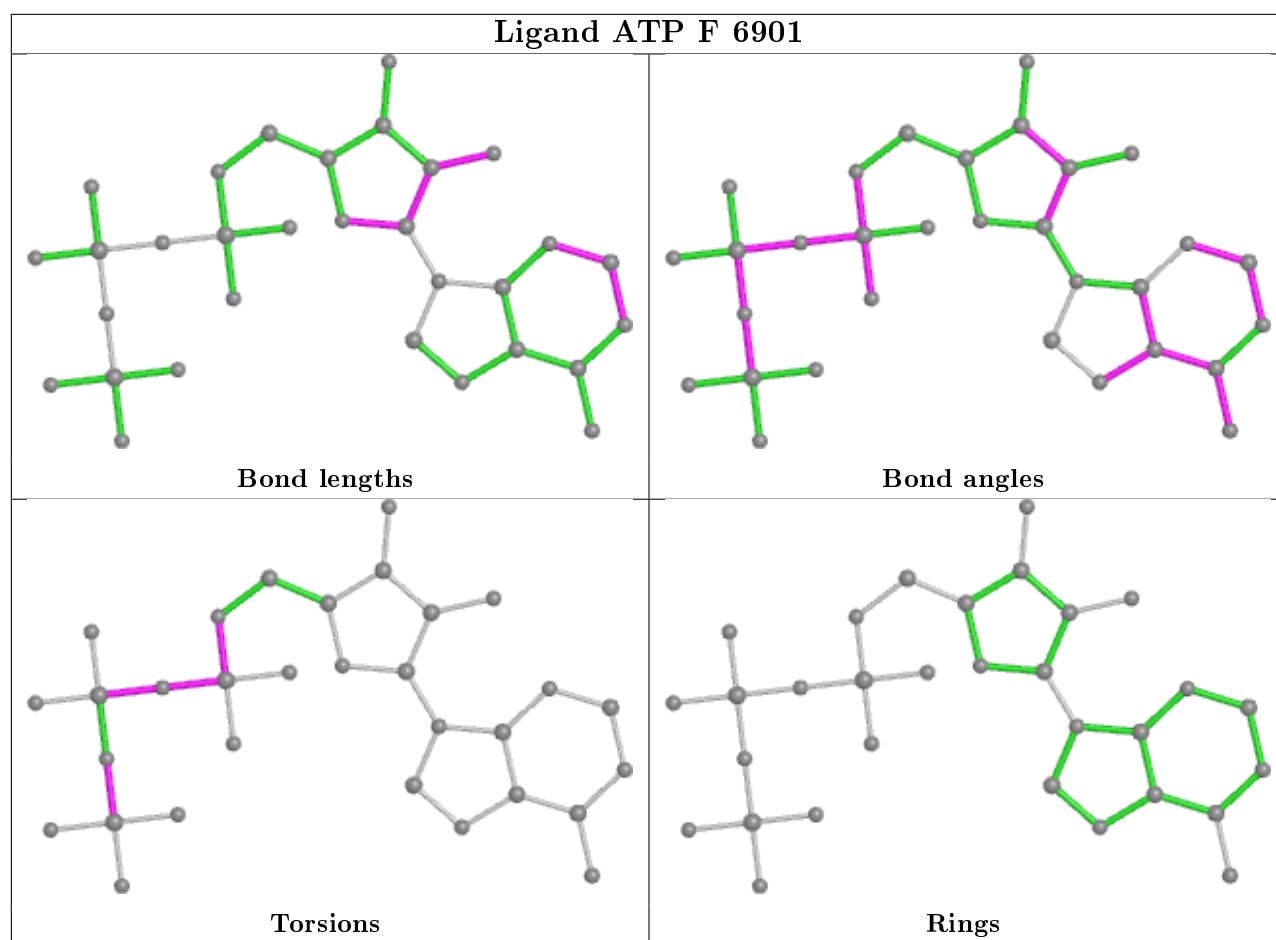
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

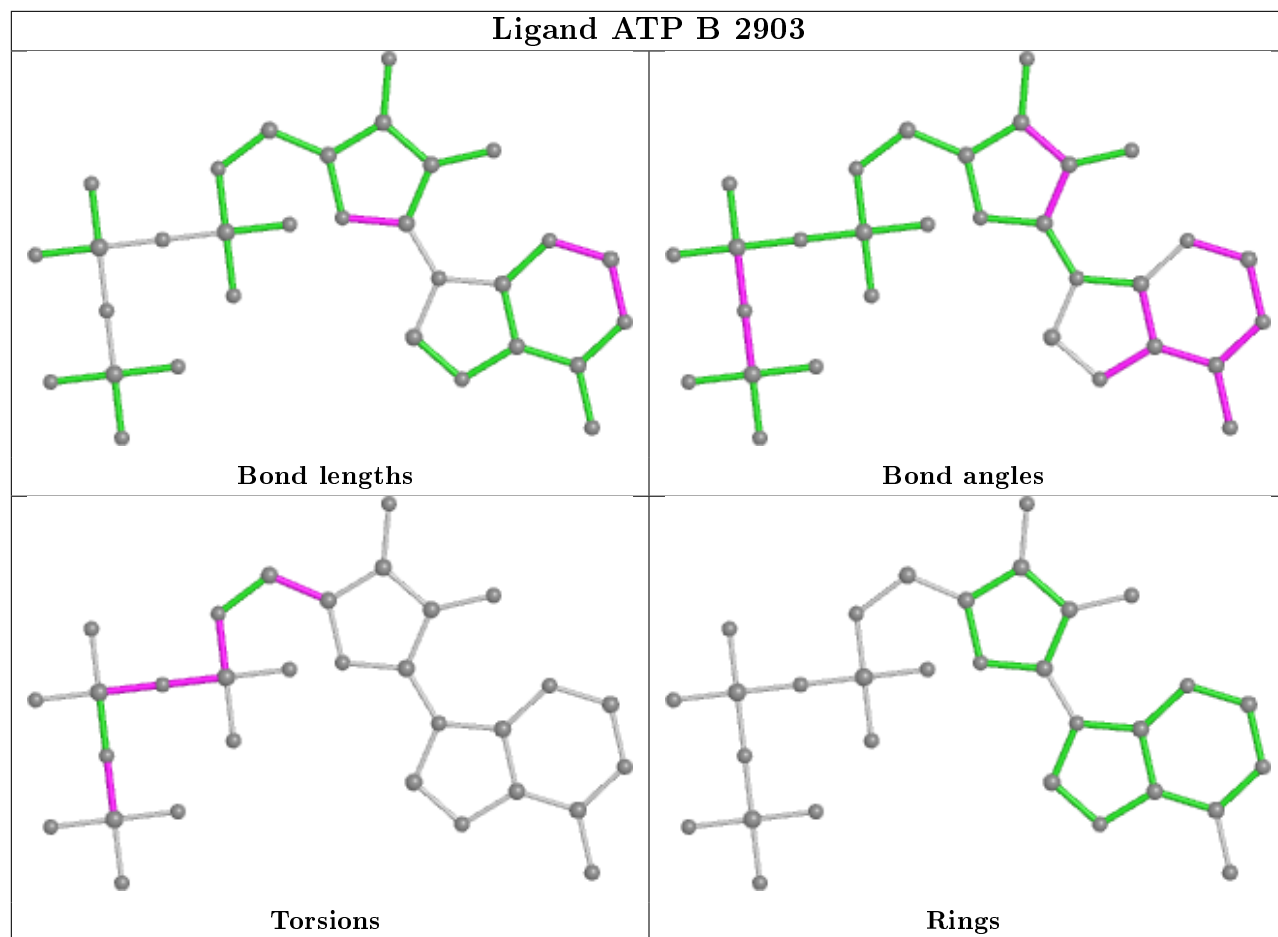


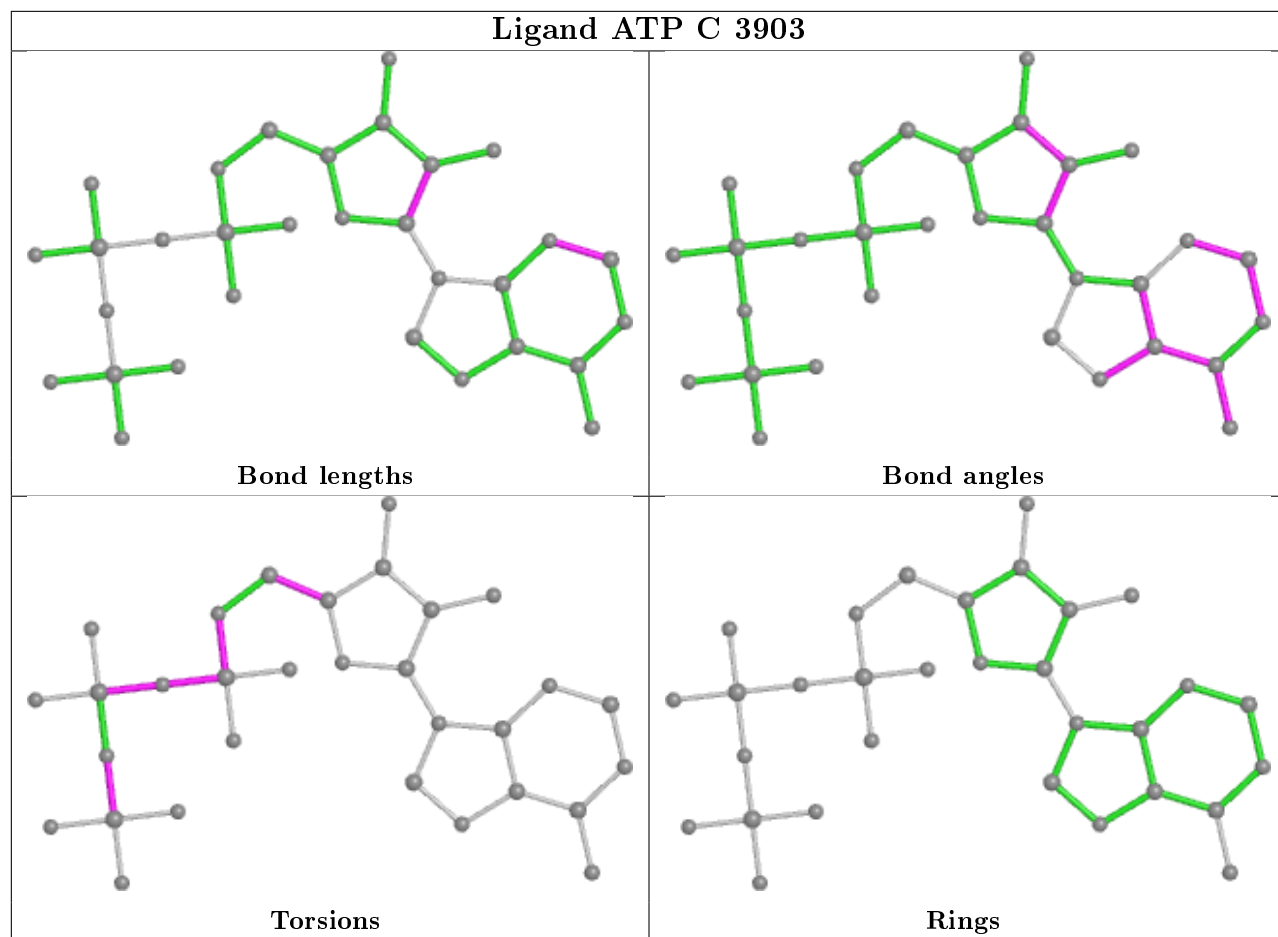


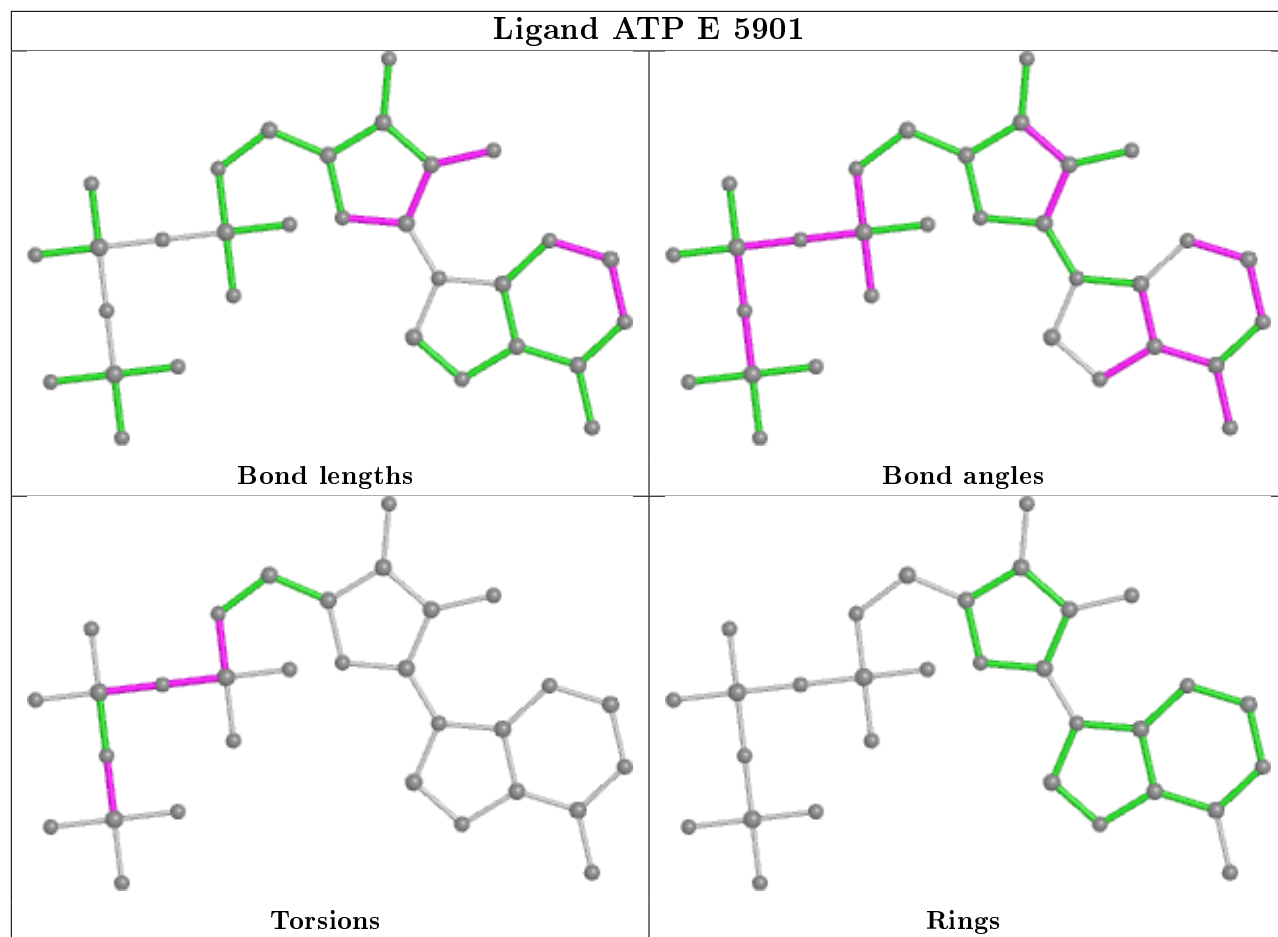


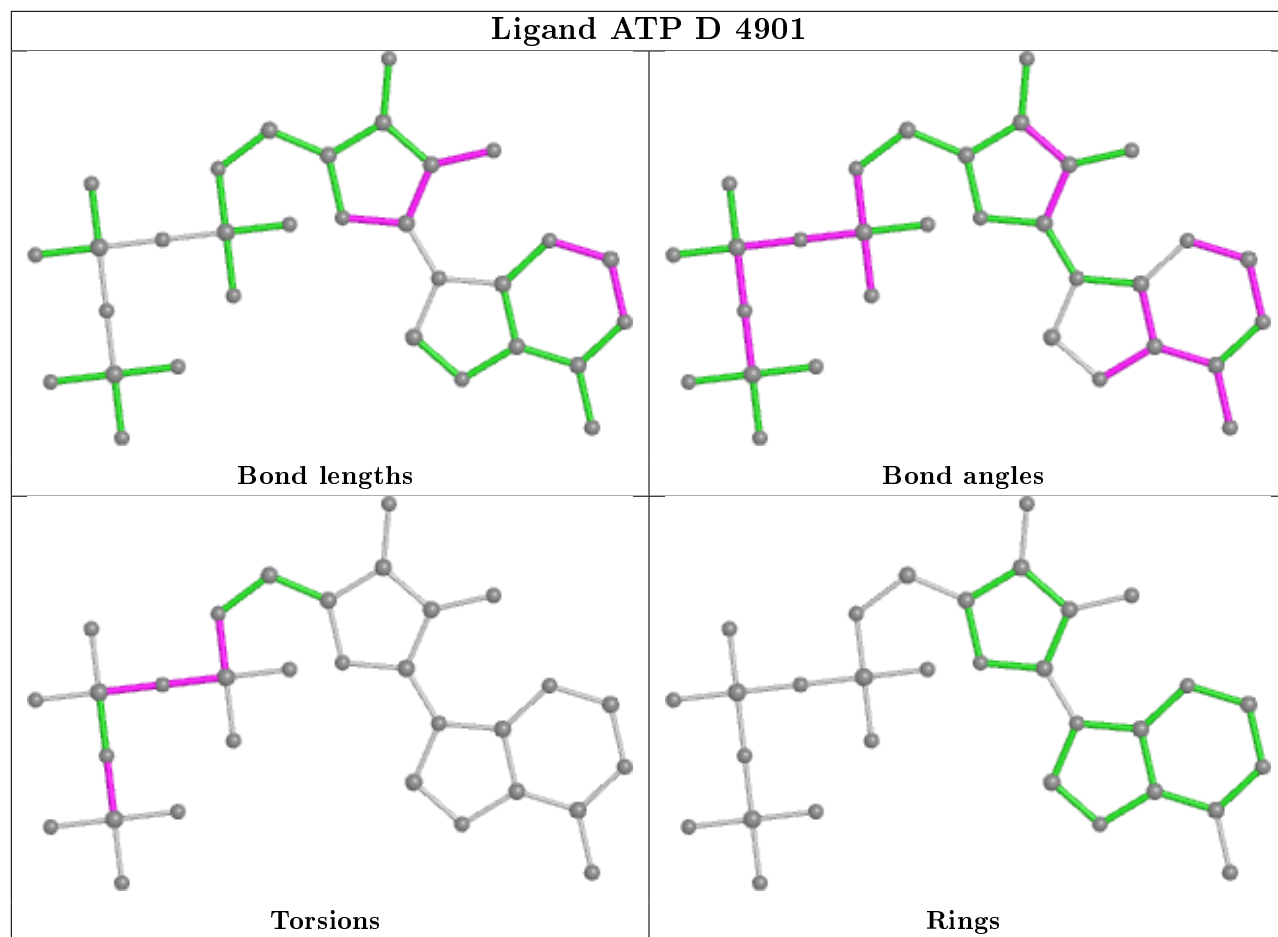


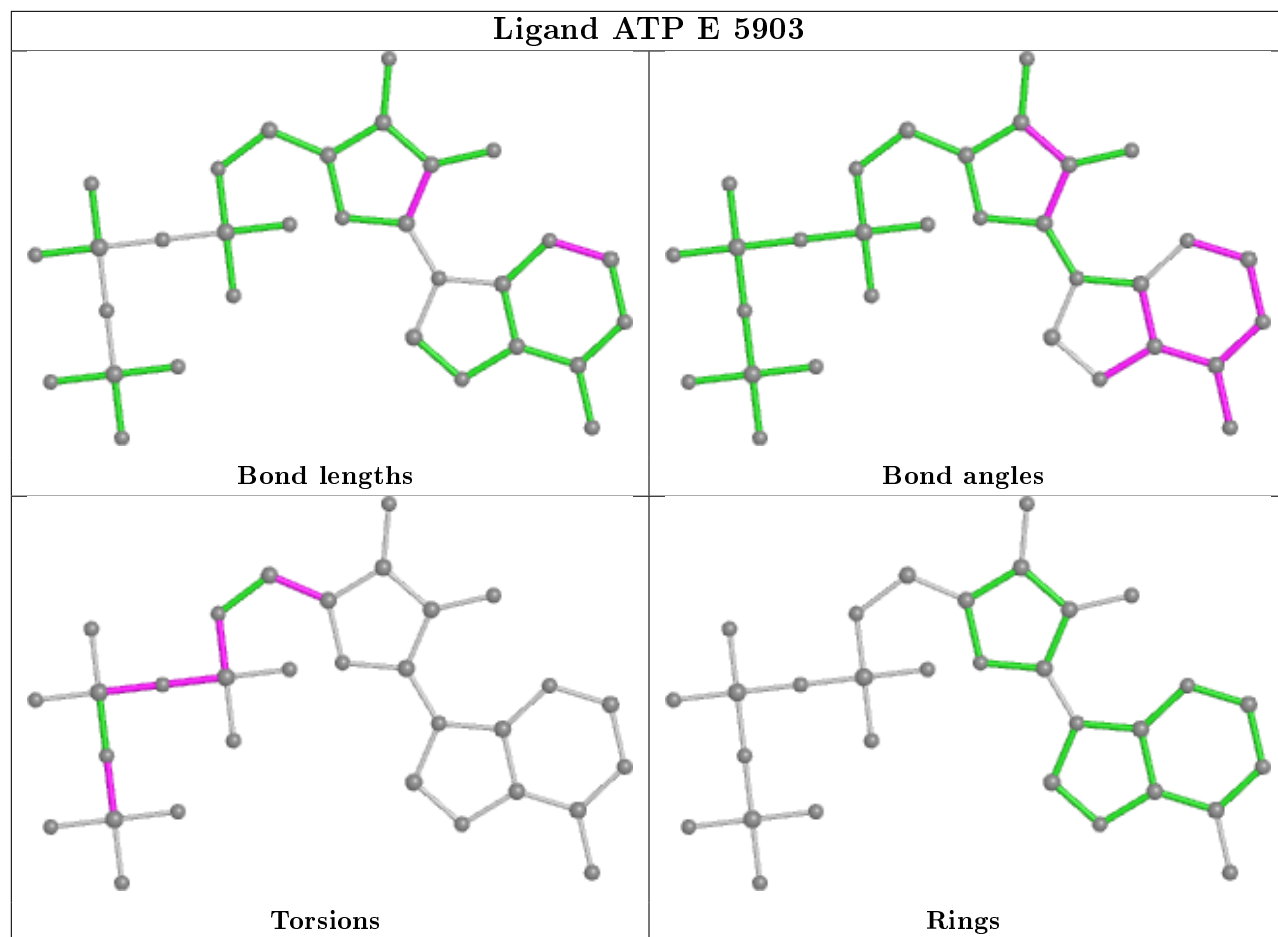


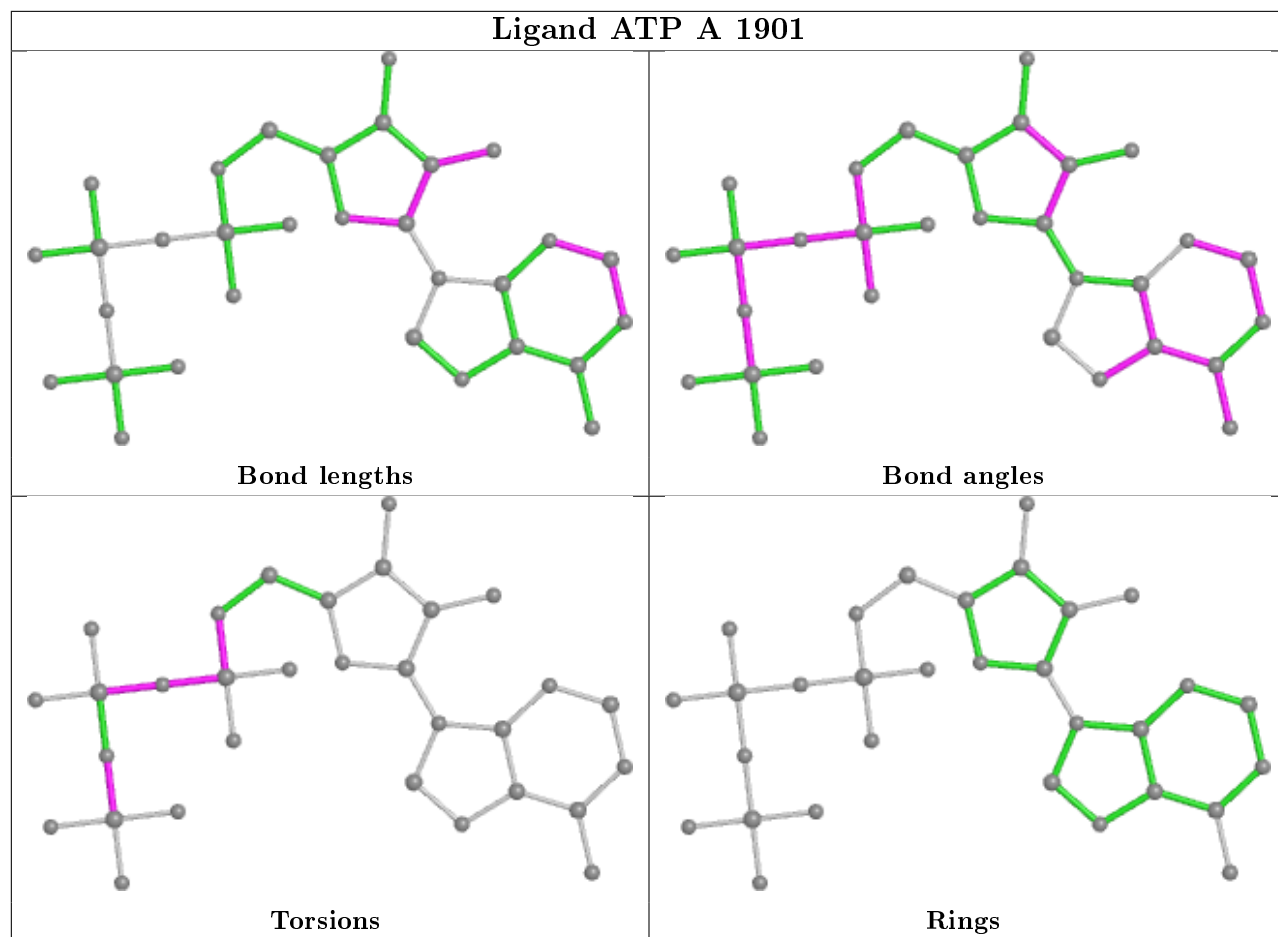


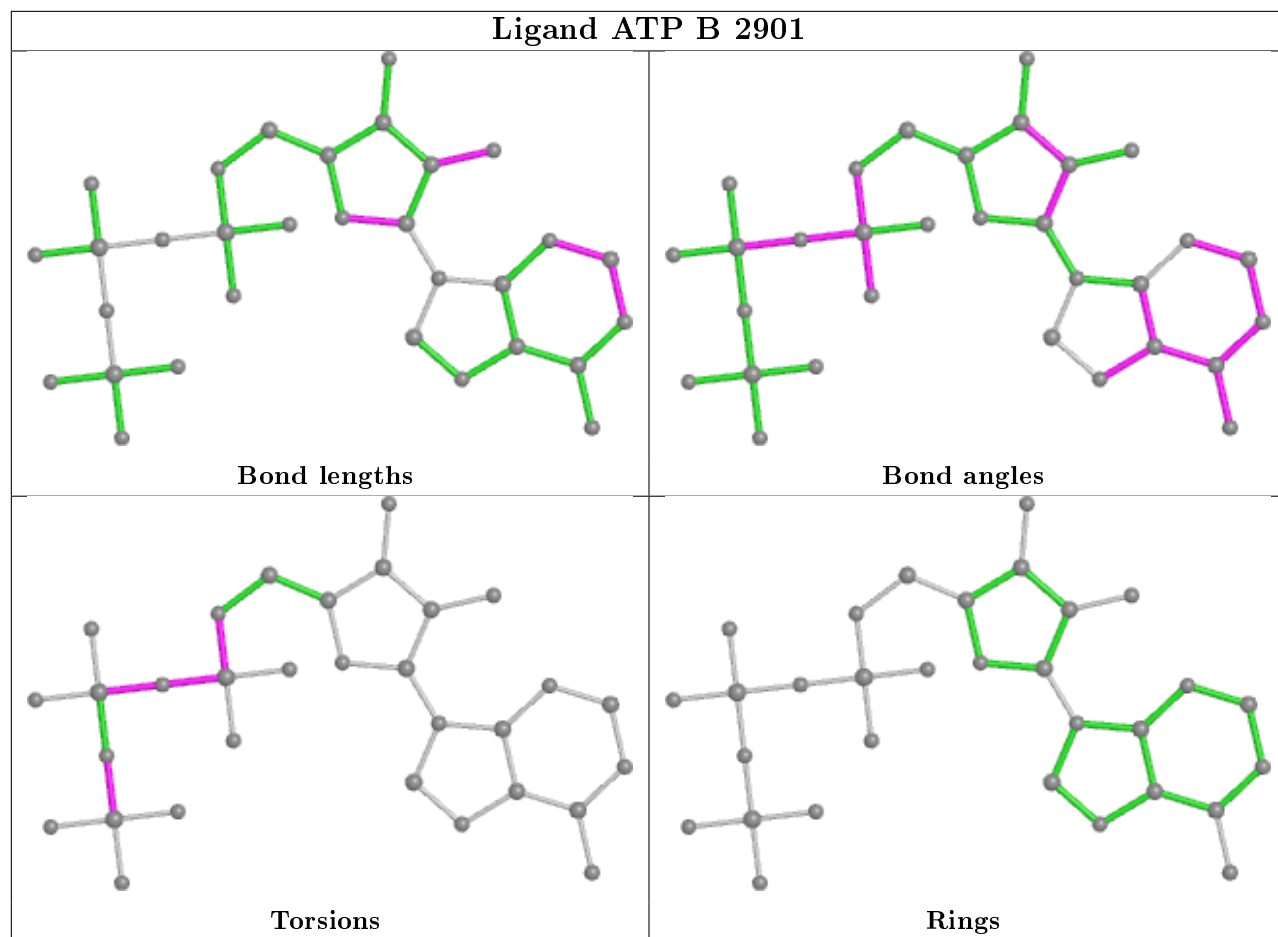




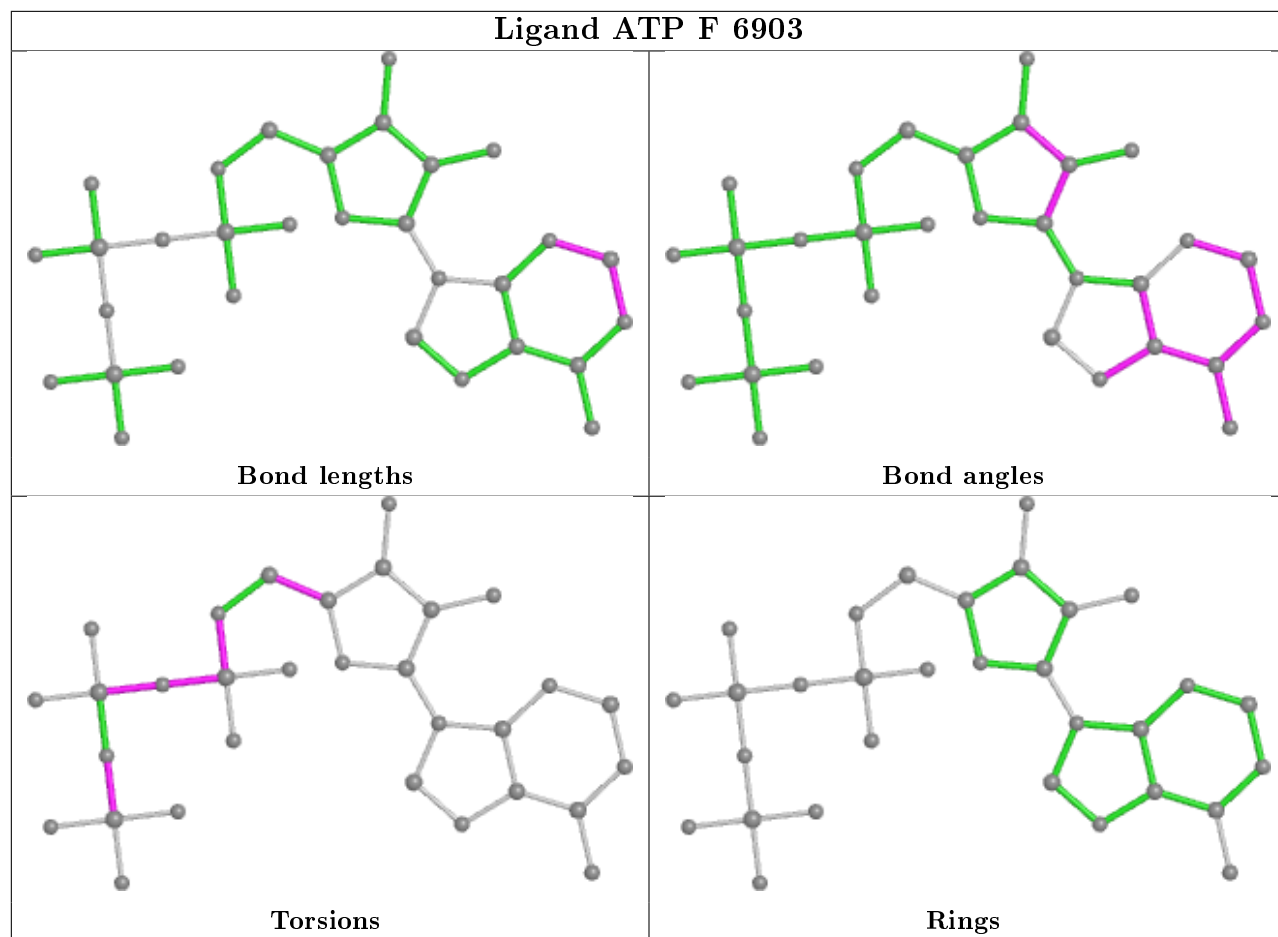












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	484/525 (92%)	0.30	42 (8%)	10 5	31, 77, 129, 156	0
1	B	484/525 (92%)	0.38	36 (7%)	14 8	42, 83, 129, 161	0
1	C	484/525 (92%)	0.19	25 (5%)	27 18	34, 74, 125, 161	0
1	D	484/525 (92%)	-0.03	19 (3%)	39 29	28, 59, 110, 161	0
1	E	484/525 (92%)	-0.03	22 (4%)	33 23	21, 61, 108, 156	0
1	F	484/525 (92%)	0.05	22 (4%)	33 23	21, 69, 116, 159	0
All	All	2904/3150 (92%)	0.15	166 (5%)	23 15	21, 71, 122, 161	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	118	VAL	9.8
1	B	117	VAL	8.6
1	B	118	VAL	8.4
1	B	116	GLU	8.3
1	D	117	VAL	7.8
1	F	117	VAL	7.6
1	F	154	TYR	7.2
1	D	118	VAL	6.7
1	A	121	PHE	6.7
1	C	117	VAL	6.7
1	D	121	PHE	6.6
1	D	120	GLY	6.5
1	C	120	GLY	6.3
1	A	257	ARG	6.1
1	B	121	PHE	6.1
1	D	119	GLY	5.7
1	A	258	SER	5.6
1	C	17	ALA	5.5
1	B	15	HIS	5.4

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Mol	Chain	Res	Type	RSRZ
1	D	113	GLU	4.9
1	E	117	VAL	4.8
1	B	115	GLN	4.8
1	C	119	GLY	4.8
1	B	154	TYR	4.8
1	E	154	TYR	4.5
1	A	154	TYR	4.4
1	D	158	SER	4.3
1	B	258	SER	4.3
1	F	257	ARG	4.1
1	A	253	ARG	4.1
1	B	255	THR	4.0
1	F	366	GLU	4.0
1	B	158	SER	3.9
1	A	295	THR	3.9
1	A	475	LYS	3.9
1	E	118	VAL	3.9
1	D	15	HIS	3.9
1	F	116	GLU	3.9
1	D	154	TYR	3.9
1	C	15	HIS	3.8
1	B	119	GLY	3.7
1	B	366	GLU	3.7
1	F	496	ARG	3.7
1	C	153	GLN	3.6
1	E	329	TYR	3.6
1	B	16	GLN	3.6
1	C	423	HIS	3.6
1	A	251	ALA	3.5
1	C	154	TYR	3.5
1	A	342	ASN	3.5
1	A	120	GLY	3.5
1	E	366	GLU	3.5
1	A	329	TYR	3.5
1	A	311	ARG	3.5
1	B	157	SER	3.4
1	F	311	ARG	3.4
1	B	122	ASP	3.4
1	A	16	GLN	3.3
1	C	152	GLN	3.3
1	D	471	MET	3.3
1	F	118	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	115	GLN	3.3
1	F	255	THR	3.3
1	F	253	ARG	3.3
1	B	321	ARG	3.3
1	E	152	GLN	3.3
1	A	496	ARG	3.2
1	E	153	GLN	3.2
1	C	116	GLU	3.2
1	F	484	ARG	3.2
1	F	485	ASN	3.2
1	B	257	ARG	3.2
1	C	123	LEU	3.2
1	A	417	ASP	3.2
1	C	366	GLU	3.1
1	A	256	GLN	3.1
1	A	341	GLN	3.1
1	C	140	ARG	3.0
1	A	17	ALA	3.0
1	F	156	ALA	3.0
1	D	160	VAL	3.0
1	B	88	ARG	3.0
1	B	253	ARG	2.9
1	F	157	SER	2.9
1	A	309	LYS	2.9
1	A	113	GLU	2.9
1	A	114	GLY	2.9
1	F	321	ARG	2.9
1	B	251	ALA	2.8
1	C	53	THR	2.7
1	E	188	TYR	2.7
1	D	116	GLU	2.7
1	A	153	GLN	2.7
1	C	145	ASP	2.7
1	A	241	ASP	2.7
1	F	121	PHE	2.6
1	C	16	GLN	2.6
1	A	368	ASN	2.6
1	E	321	ARG	2.6
1	A	318	GLU	2.6
1	B	53	THR	2.6
1	A	14	GLU	2.6
1	E	120	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	119	GLY	2.5
1	D	496	ARG	2.5
1	A	402	TYR	2.5
1	B	497	ILE	2.5
1	A	249	LEU	2.5
1	A	321	ARG	2.5
1	C	121	PHE	2.5
1	A	116	GLU	2.4
1	B	90	PHE	2.4
1	D	16	GLN	2.4
1	A	15	HIS	2.4
1	D	366	GLU	2.4
1	E	334	ASP	2.4
1	D	114	GLY	2.4
1	B	250	GLY	2.4
1	E	119	GLY	2.4
1	B	92	TRP	2.4
1	F	423	HIS	2.3
1	A	405	GLN	2.3
1	B	155	ASP	2.3
1	A	117	VAL	2.3
1	A	255	THR	2.3
1	E	113	GLU	2.3
1	E	341	GLN	2.3
1	C	138	ARG	2.3
1	A	378	ASP	2.3
1	A	252	MET	2.3
1	A	118	VAL	2.3
1	C	135	GLN	2.3
1	A	484	ARG	2.3
1	E	295	THR	2.3
1	E	116	GLU	2.3
1	B	89	SER	2.2
1	A	423	HIS	2.2
1	F	162	ARG	2.2
1	B	375	ILE	2.2
1	F	340	ARG	2.2
1	A	427	ASP	2.2
1	E	166	ARG	2.2
1	A	338	MET	2.2
1	C	253	ARG	2.2
1	E	421	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	343	LEU	2.2
1	B	256	GLN	2.2
1	C	188	TYR	2.2
1	B	94	LEU	2.1
1	E	474	ASP	2.1
1	F	252	MET	2.1
1	C	189	GLY	2.1
1	B	123	LEU	2.1
1	E	336	GLU	2.1
1	D	157	SER	2.1
1	C	14	GLU	2.1
1	B	436	THR	2.1
1	B	91	GLY	2.1
1	D	309	LYS	2.1
1	B	153	GLN	2.0
1	F	432	THR	2.0
1	B	407	GLU	2.0
1	D	53	THR	2.0
1	E	471	MET	2.0
1	A	340	ARG	2.0
1	B	14	GLU	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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

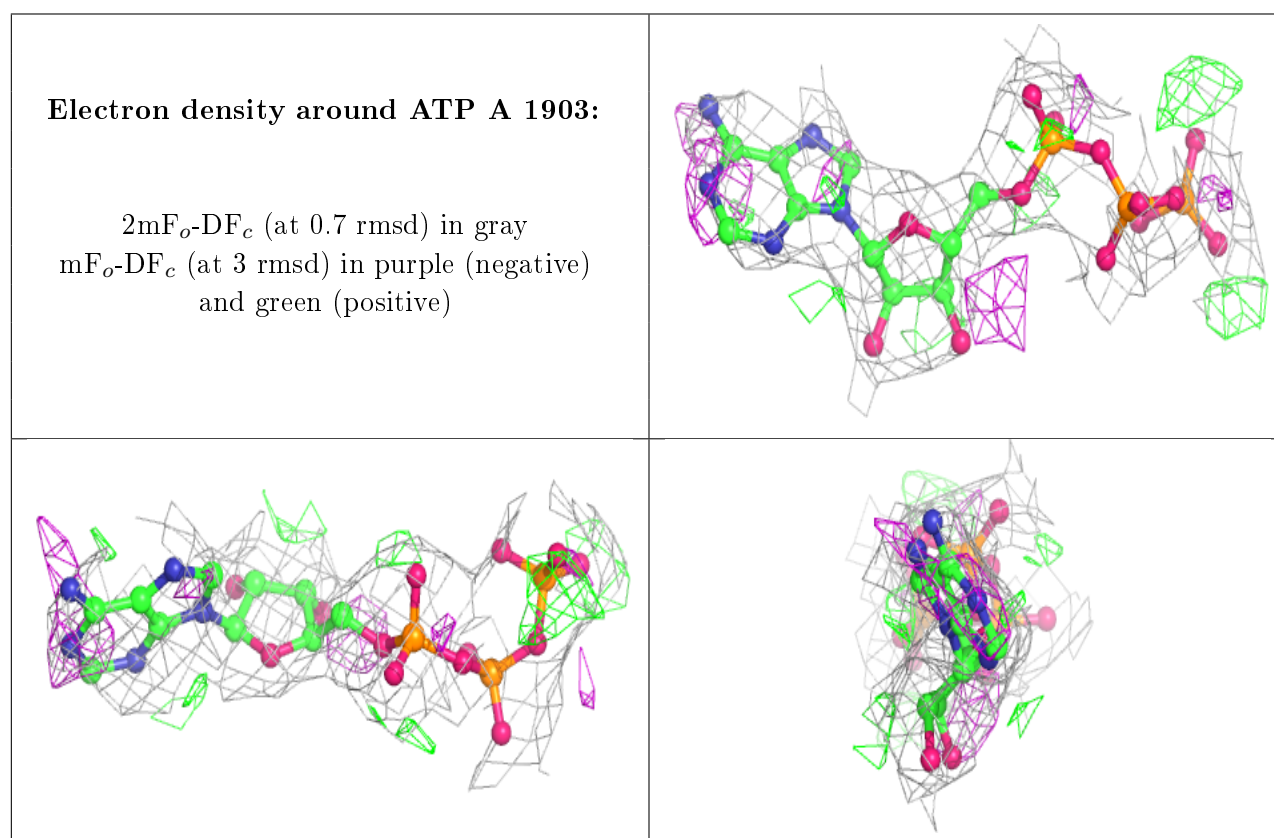
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ATP	A	1903	31/31	0.84	0.24	43,55,77,81	0
2	ATP	B	2903	31/31	0.84	0.22	44,55,77,81	0

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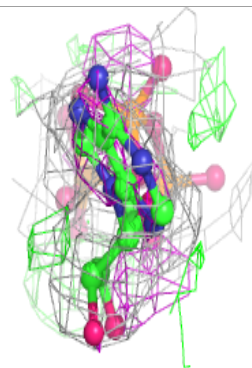
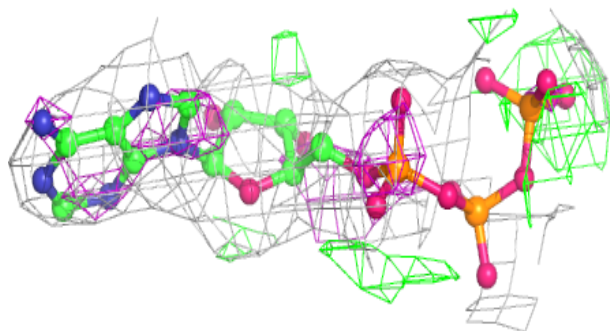
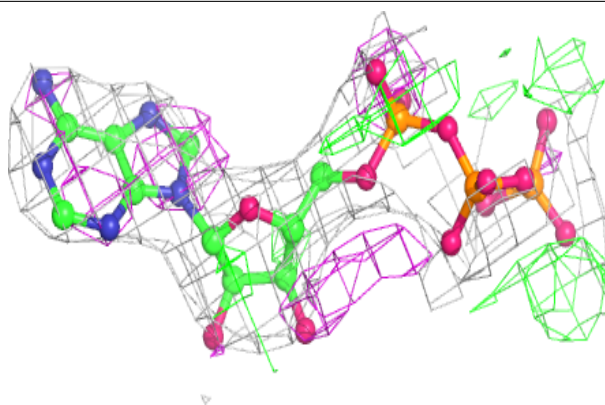
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ATP	A	1901	31/31	0.86	0.29	76,89,103,113	0
2	ATP	F	6901	31/31	0.87	0.27	75,90,115,121	0
2	ATP	C	3903	31/31	0.88	0.23	43,55,77,81	0
2	ATP	E	5901	31/31	0.90	0.23	62,78,101,114	0
2	ATP	D	4903	31/31	0.90	0.28	43,54,77,81	0
2	ATP	B	2901	31/31	0.90	0.24	62,74,110,116	0
2	ATP	F	6903	31/31	0.91	0.23	43,55,77,80	0
2	ATP	C	3901	31/31	0.92	0.21	48,56,97,110	0
2	ATP	D	4901	31/31	0.93	0.24	54,66,90,105	0
2	ATP	E	5903	31/31	0.94	0.25	43,54,77,81	0

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

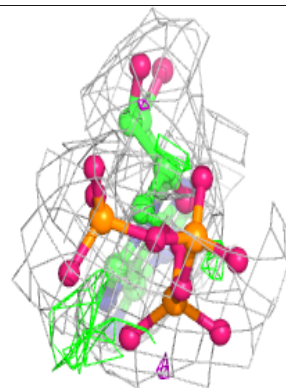
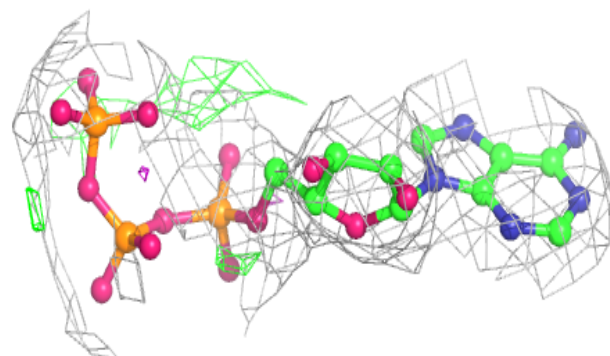
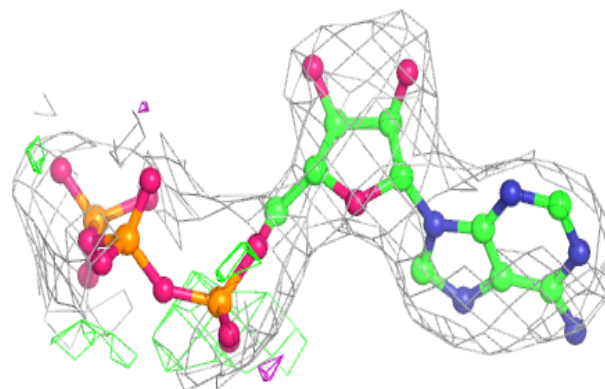


**Electron density around ATP B 2903:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ATP A 1901:**

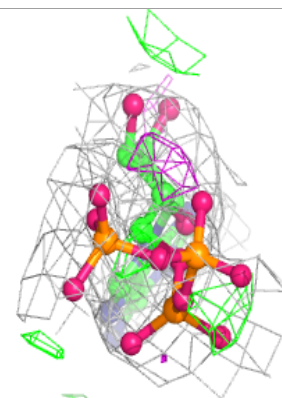
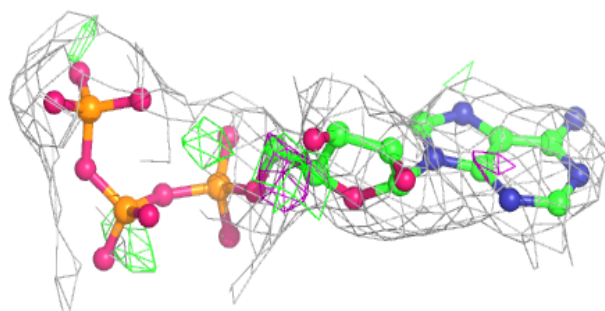
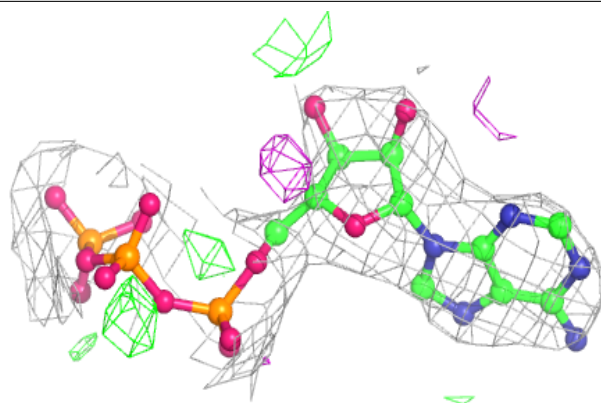
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



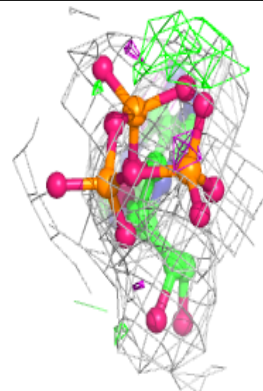
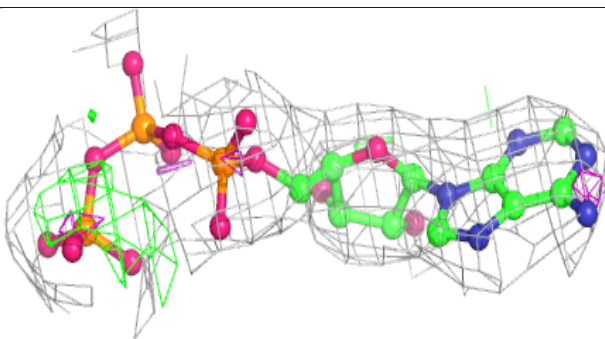
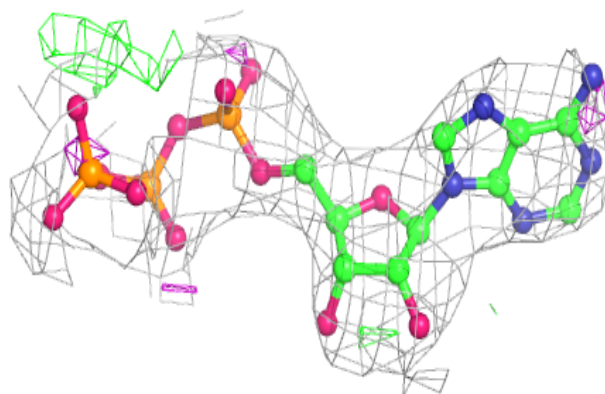


**Electron density around ATP F 6901:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

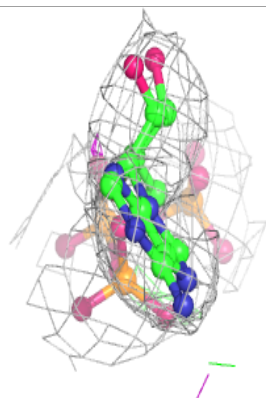
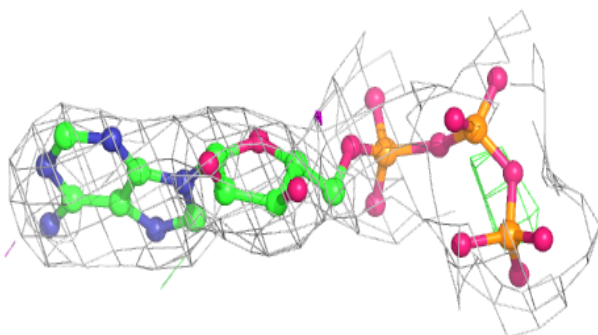
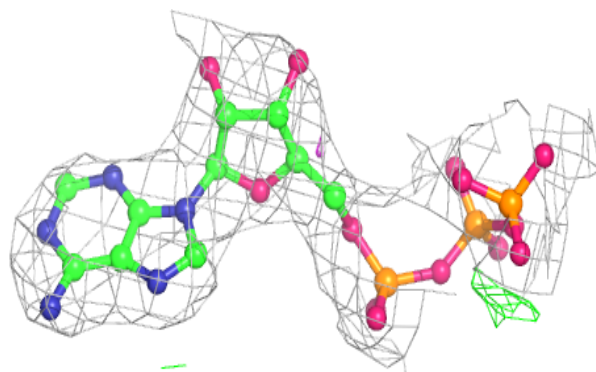
**Electron density around ATP C 3903:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

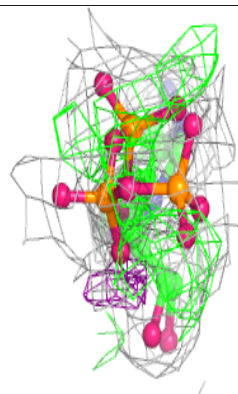
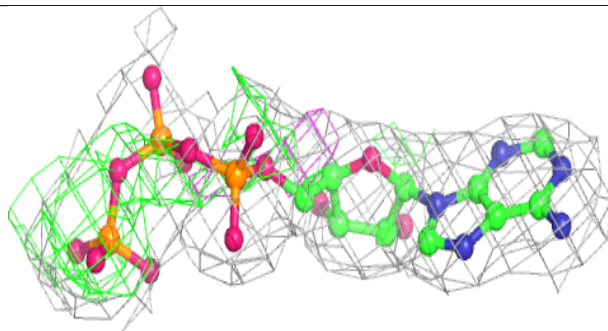
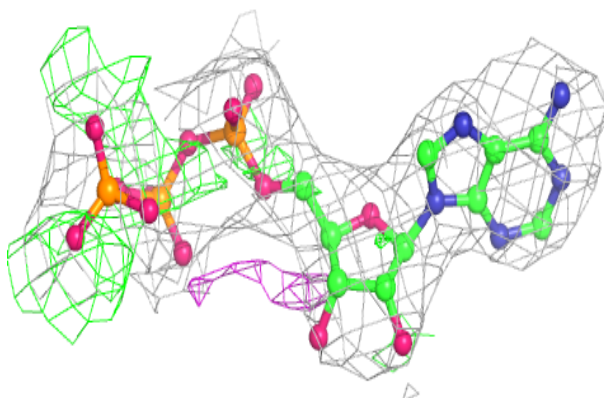


**Electron density around ATP E 5901:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

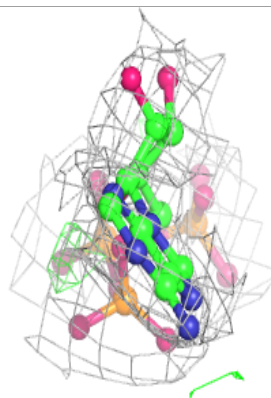
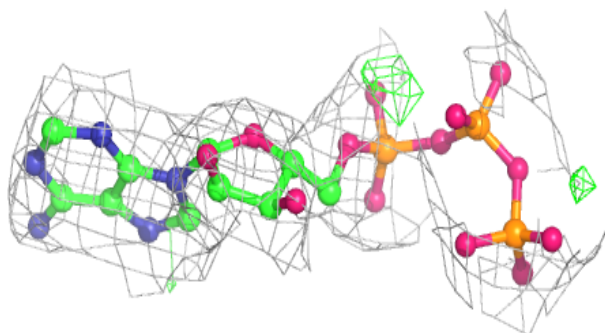
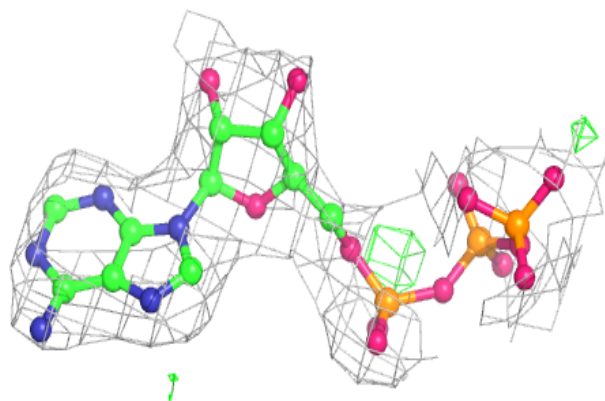
**Electron density around ATP D 4903:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

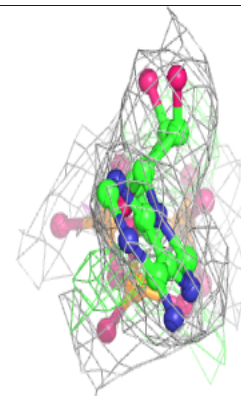
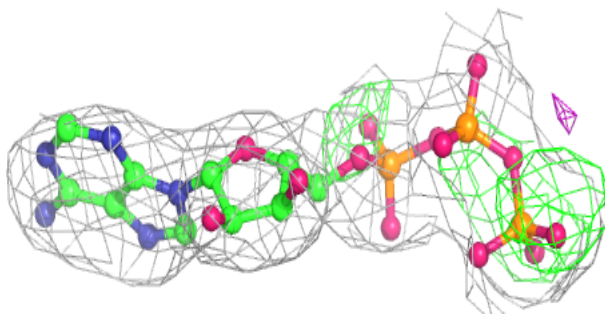
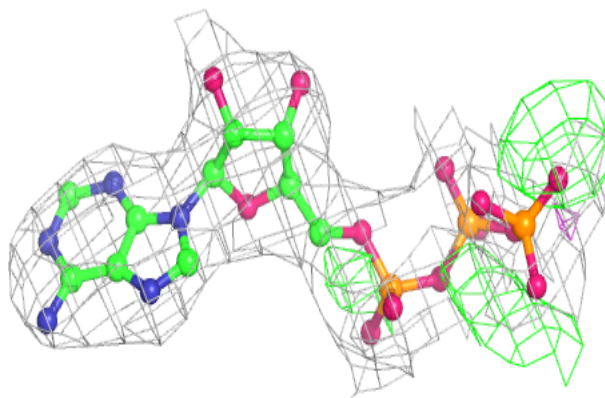


**Electron density around ATP B 2901:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

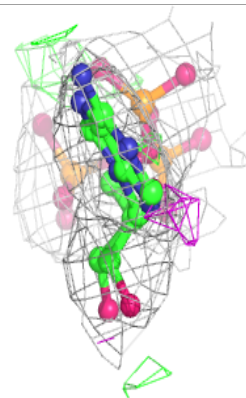
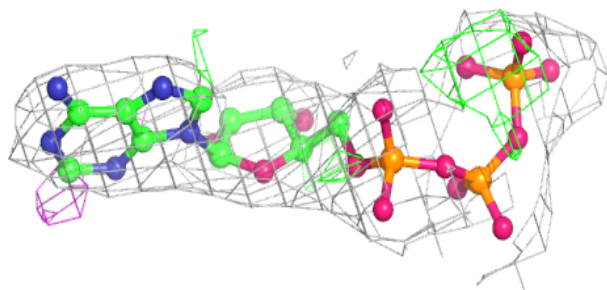
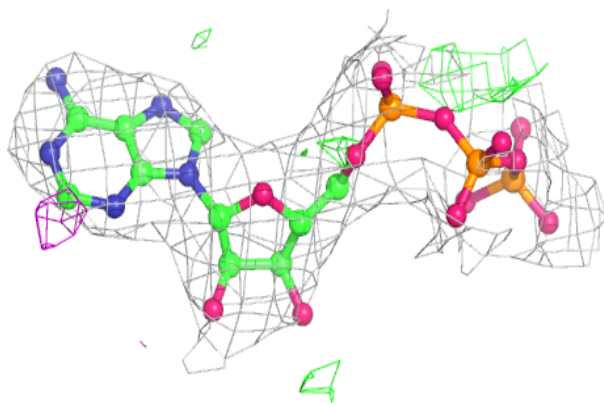
**Electron density around ATP F 6903:**

$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

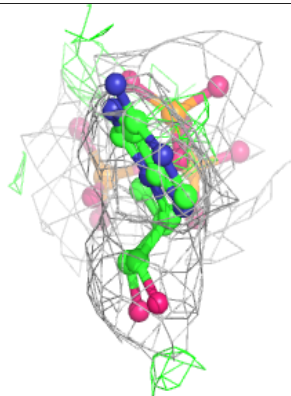
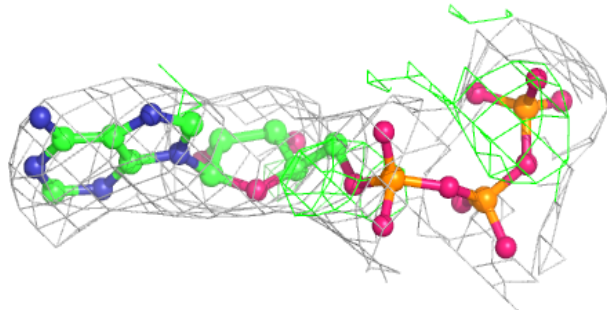
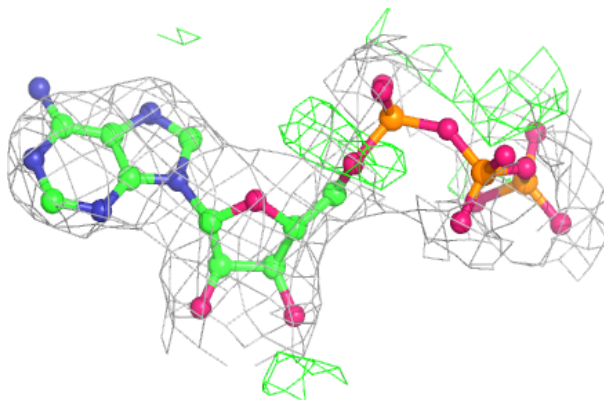


**Electron density around ATP C 3901:**

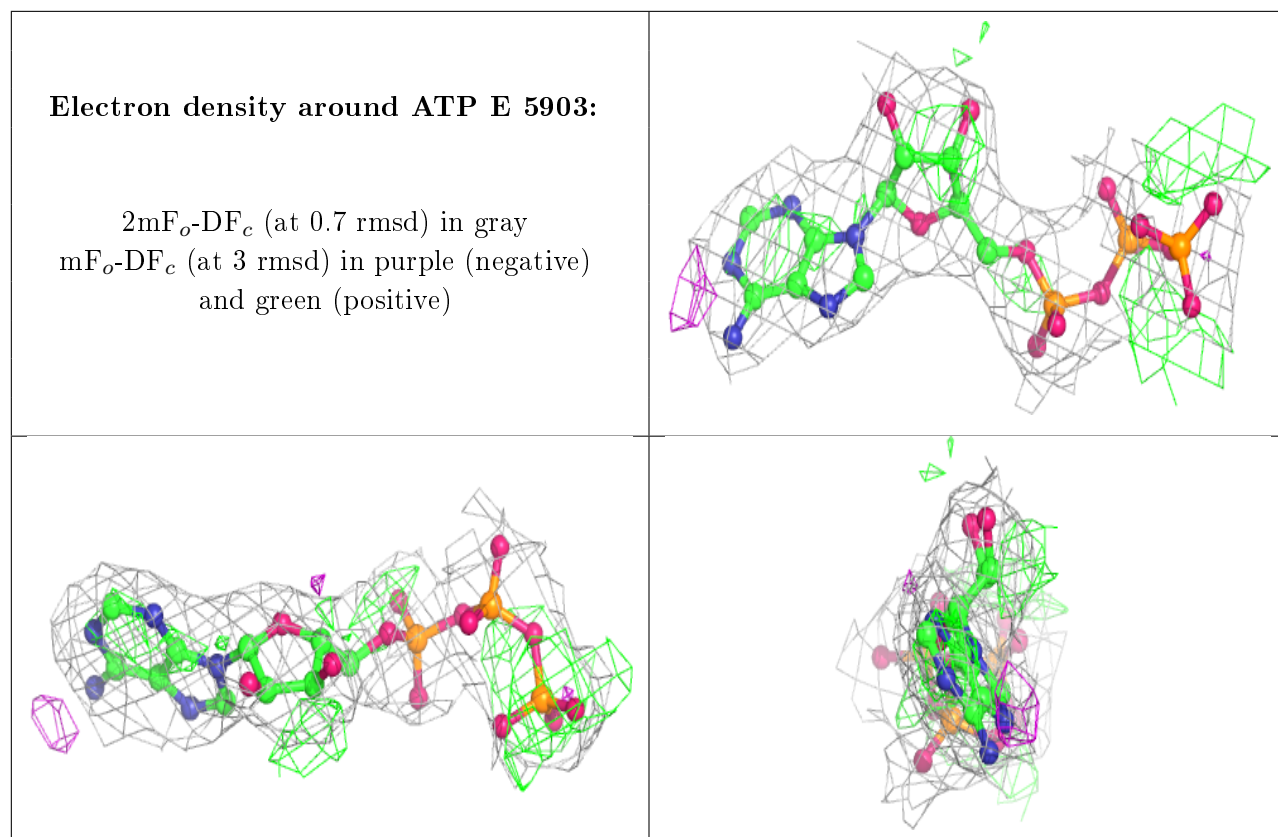
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ATP D 4901:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)







## 6.5 Other polymers [i](#)

There are no such residues in this entry.