



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 06:26 pm BST

PDB ID : 4C30  
Title : Crystal structure of Deinococcus radiodurans UvrD in complex with DNA, form 2  
Authors : Stelter, M.; Acajjaoui, S.; McSweeney, S.; Timmins, J.  
Deposited on : 2013-08-21  
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36.2  
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) : 2.36.2

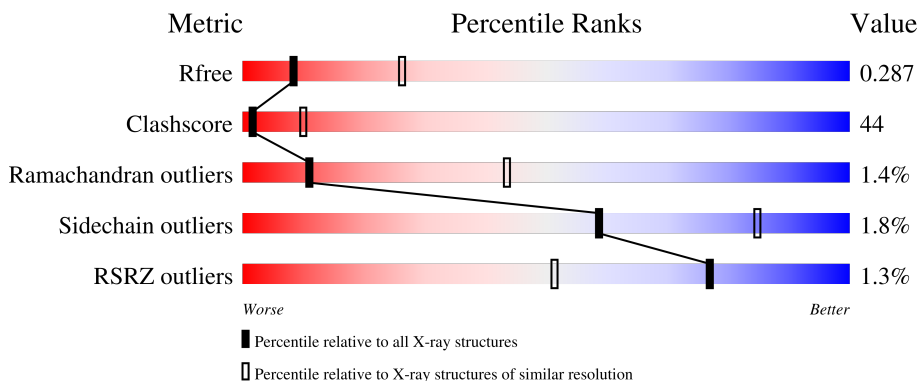
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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

Mol	Chain	Length	Quality of chain
1	A	665	 2% 45% 47% 5%
1	D	665	 48% 46% 2% 4%
1	F	665	 2% 45% 48% 5%
1	I	665	 49% 45% 2% 4%
2	K	25	 52% 40% 8%

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Mol	Chain	Length	Quality of chain
2	X	25	 52% 36% 8%
3	L	25	 48% 40% 8%
3	Y	25	 44% 48% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ANP	F	1663	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 22073 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 DNA HELICASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	631	Total 4970	C 3112	N 898	O 945	S 15	0	0	0
1	D	642	Total 5059	C 3168	N 916	O 961	S 14	0	2	0
1	F	632	Total 4978	C 3118	N 899	O 946	S 15	0	0	0
1	I	638	Total 5025	C 3145	N 909	O 957	S 14	0	1	0

- Molecule 2 is a DNA chain called DNA STRAND FOR25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	K	23	Total 471	C 225	N 78	O 145	P 23	0	0	0
2	X	23	Total 471	C 225	N 78	O 145	P 23	0	0	0

- Molecule 3 is a DNA chain called DNA STRAND REV25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	L	23	Total 467	C 223	N 80	O 141	P 23	0	0	0
3	Y	23	Total 467	C 223	N 80	O 141	P 23	0	0	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula:  $C_{10}H_{17}N_6O_{12}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	F	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		
5	D	1	Total	Mg	0	0
			1	1		
5	F	2	Total	Mg	0	0
			2	2		
5	I	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total	O	0	0
			6	6		
6	D	28	Total	O	0	0
			28	28		
6	F	26	Total	O	0	0
			26	26		

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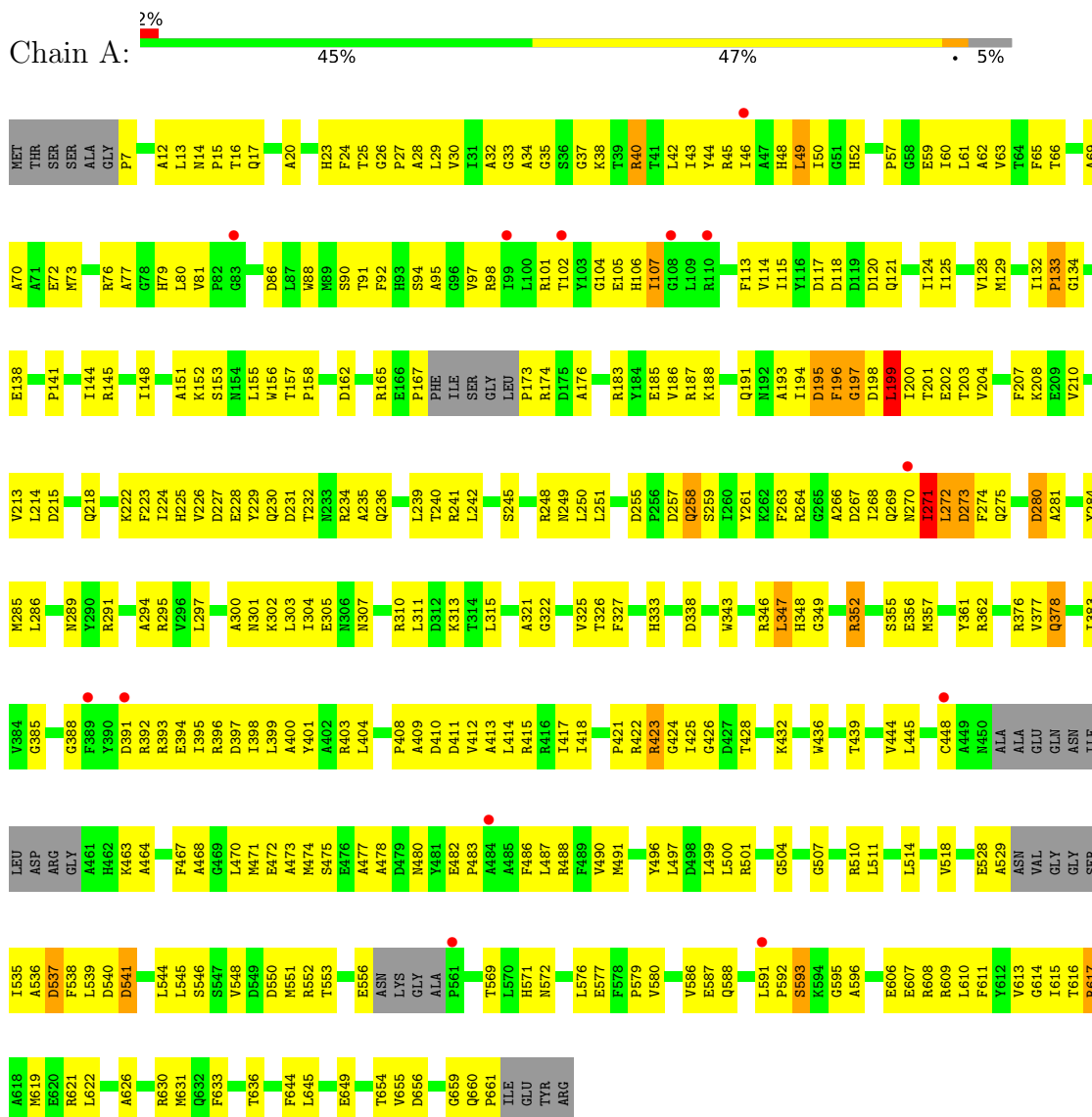
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	I	36	Total	O	0	0
			36	36		
6	Y	1	Total	O	0	0
			1	1		

### 3 Residue-property plots i

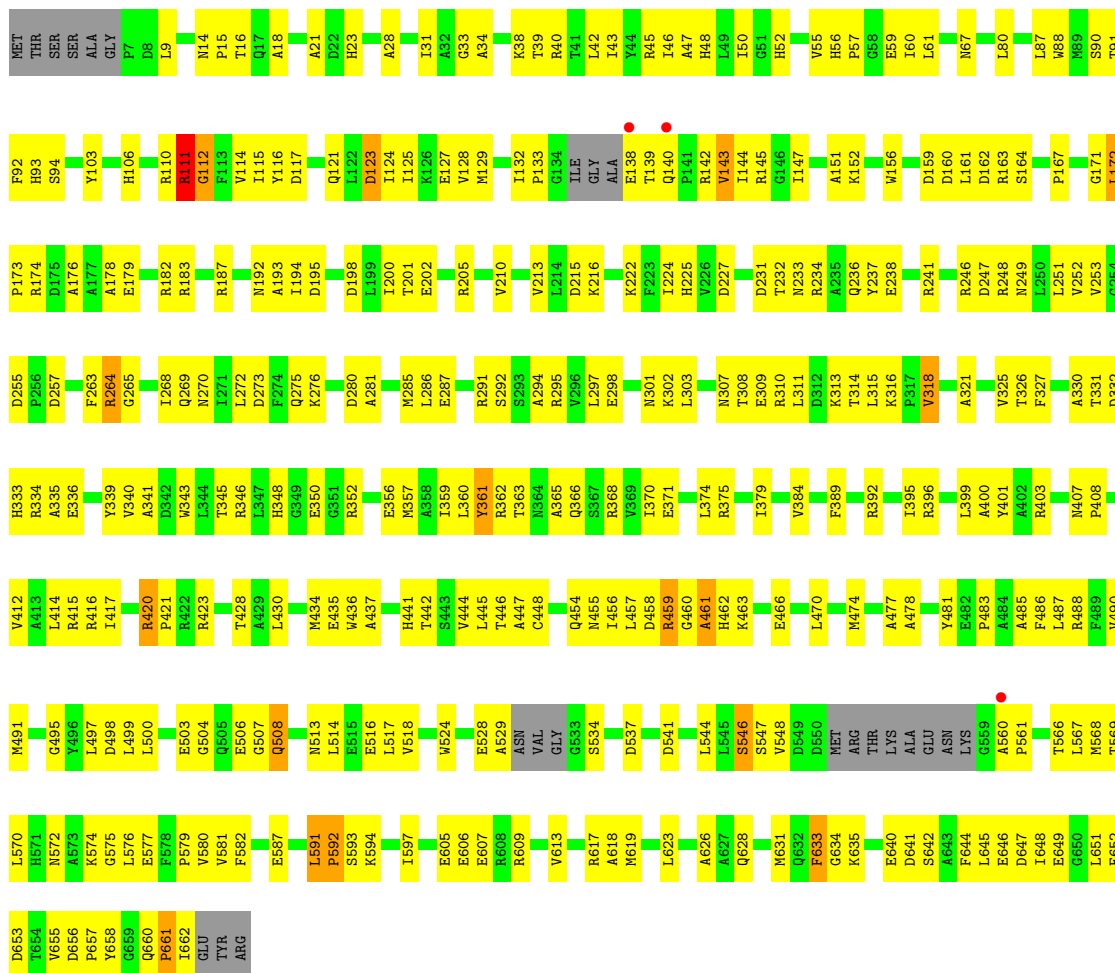
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

#### • Molecule 1: DNA HELICASE II

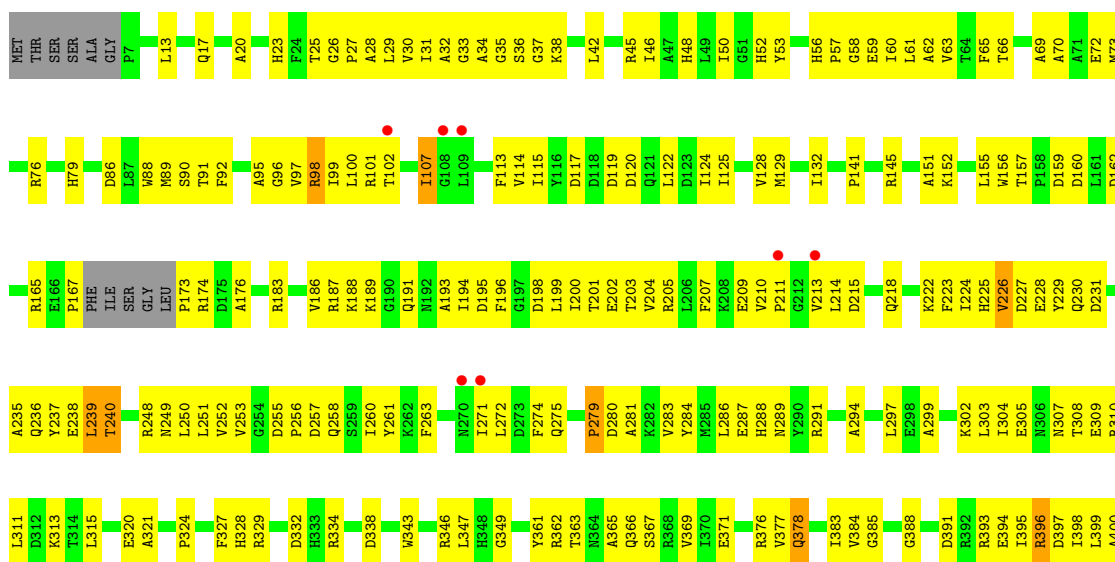
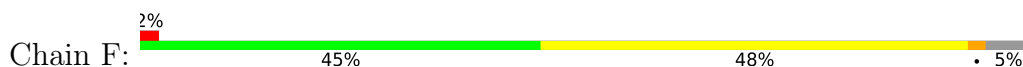


#### • Molecule 1: DNA HELICASE II

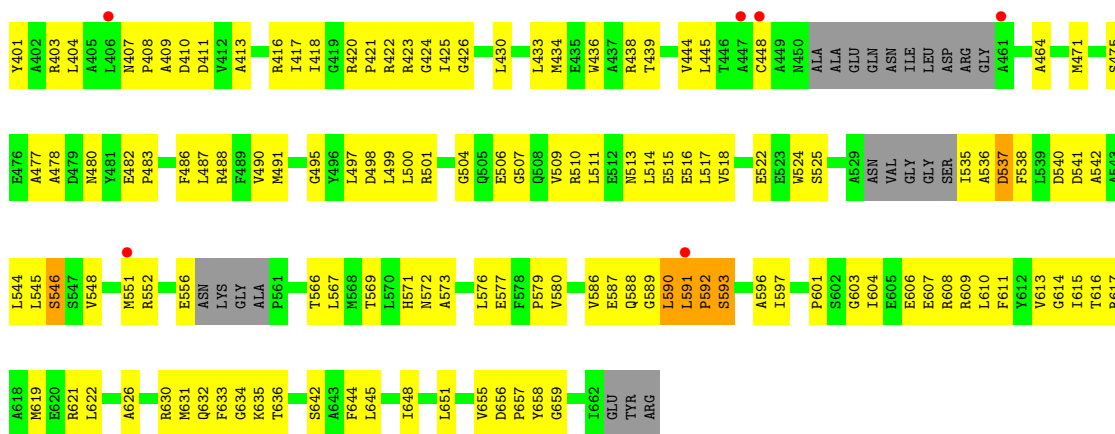




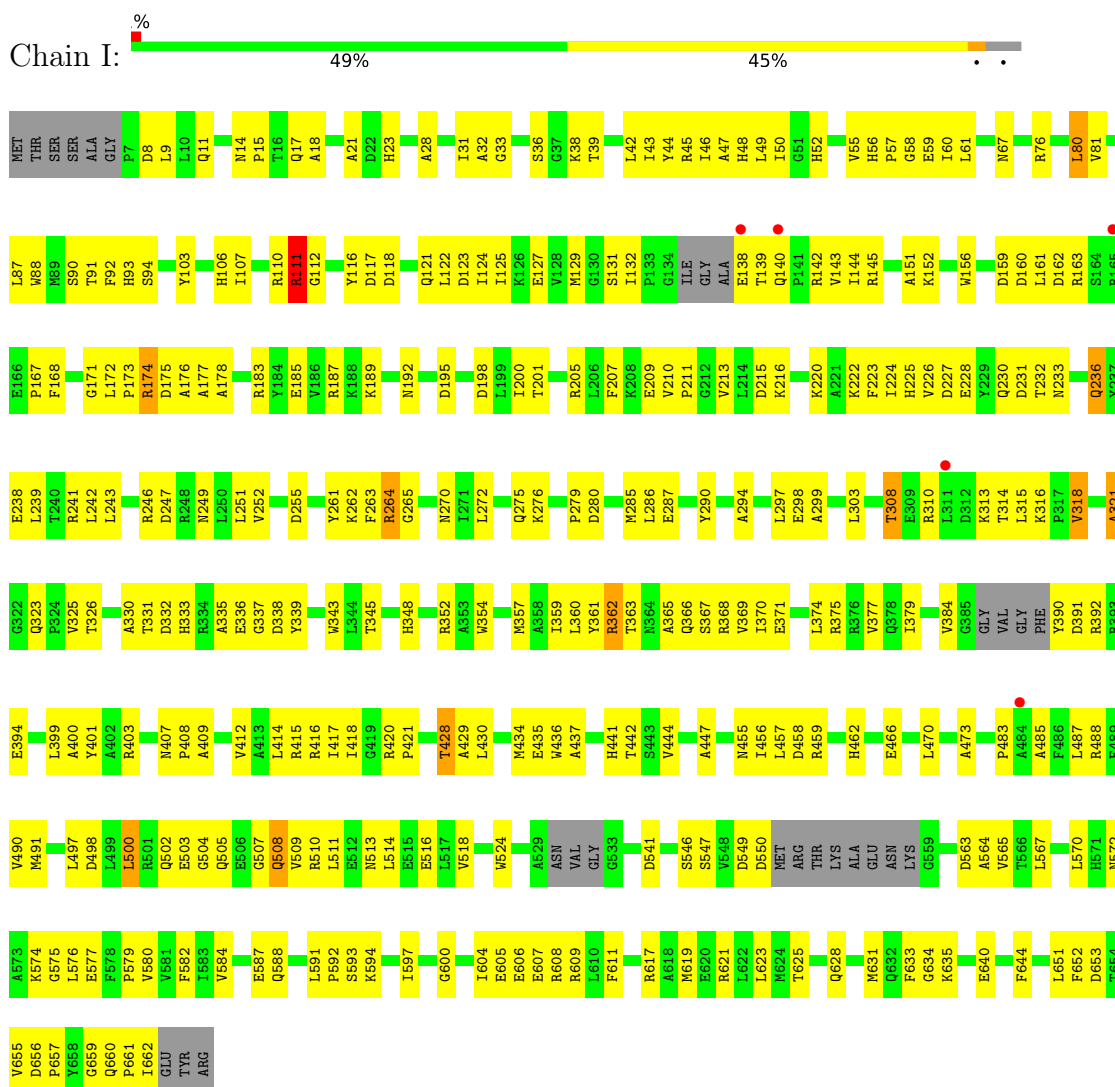
● Molecule 1: DNA HELICASE II







• Molecule 1: DNA HELICASE II

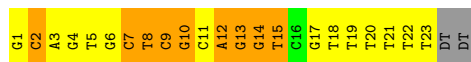


• Molecule 2: DNA STRAND FOR25

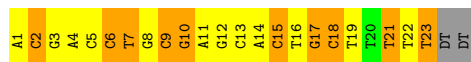
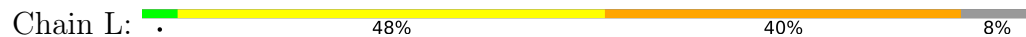




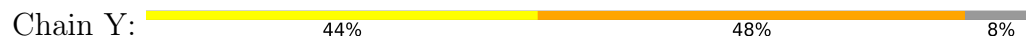
- Molecule 2: DNA STRAND FOR25



- Molecule 3: DNA STRAND REV25



- Molecule 3: DNA STRAND REV25



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.49Å 89.78Å 293.80Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	66.18 – 3.00 66.18 – 3.00	Depositor EDS
% Data completeness (in resolution range)	87.2 (66.18-3.00) 87.2 (66.18-3.00)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.91 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.6.0085	Depositor
R, $R_{free}$	0.228 , 0.288 0.231 , 0.287	Depositor DCC
$R_{free}$ test set	3128 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.2	Xtrriage
Anisotropy	0.942	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 75.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.439 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	22073	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	104.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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 i

### 5.1 Standard geometry i

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

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	0.56	1/5059 (0.0%)	0.74	5/6838 (0.1%)
1	D	0.63	1/5156 (0.0%)	0.78	4/6972 (0.1%)
1	F	0.54	0/5067	0.72	3/6849 (0.0%)
1	I	0.63	0/5117	0.78	2/6919 (0.0%)
2	K	1.29	3/525 (0.6%)	1.76	17/809 (2.1%)
2	X	1.06	0/525	1.68	15/809 (1.9%)
3	L	1.09	0/521	1.62	14/801 (1.7%)
3	Y	1.24	1/521 (0.2%)	1.59	14/801 (1.7%)
All	All	0.67	6/22491 (0.0%)	0.89	74/30798 (0.2%)

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	D	0	2
1	F	0	1
1	I	0	2
All	All	0	5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	2	DC	O3'-P	-15.97	1.42	1.61
3	Y	16	DT	O3'-P	-7.85	1.51	1.61
2	K	12	DA	O3'-P	5.65	1.68	1.61
2	K	6	DG	C4'-O4'	5.29	1.50	1.45
1	D	661	PRO	N-CD	-5.17	1.40	1.47
1	A	133	PRO	N-CD	-5.16	1.40	1.47

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	9	DC	C1'-O4'-C4'	-10.43	99.67	110.10
2	K	9	DC	O4'-C1'-C2'	-9.11	98.61	105.90
3	Y	6	DC	P-O3'-C3'	8.78	130.24	119.70
1	D	112	GLY	N-CA-C	-8.77	91.19	113.10
2	X	9	DC	O4'-C1'-C2'	-8.59	99.03	105.90
2	K	7	DC	C1'-O4'-C4'	-8.57	101.53	110.10
1	F	591	LEU	C-N-CD	-8.56	101.77	120.60
2	X	9	DC	C1'-O4'-C4'	-8.34	101.76	110.10
2	K	3	DA	O4'-C4'-C3'	-8.29	101.03	106.00
3	L	10	DG	C1'-O4'-C4'	-8.06	102.04	110.10
2	K	2	DC	P-O3'-C3'	8.05	129.36	119.70
3	L	7	DT	C1'-O4'-C4'	-7.99	102.11	110.10
2	K	9	DC	O4'-C1'-N1	7.92	113.55	108.00
2	K	15	DT	O4'-C4'-C3'	-7.87	101.28	106.00
2	X	12	DA	O4'-C4'-C3'	-7.70	101.38	106.00
1	F	591	LEU	CB-CA-C	-7.54	95.87	110.20
3	L	15	DC	C1'-O4'-C4'	-7.48	102.62	110.10
2	K	2	DC	O4'-C4'-C3'	-7.45	101.52	104.50
3	L	21	DT	O4'-C4'-C3'	-7.35	101.56	104.50
3	L	9	DC	O4'-C4'-C3'	-7.27	101.59	104.50
2	X	12	DA	O4'-C1'-N9	-7.12	103.02	108.00
2	X	14	DG	O4'-C1'-N9	-7.01	103.10	108.00
2	K	14	DG	O4'-C1'-N9	-6.96	103.13	108.00
3	Y	3	DG	O4'-C4'-C3'	-6.85	101.76	104.50
2	X	7	DC	O4'-C1'-N1	6.72	112.71	108.00
1	F	590	LEU	N-CA-C	6.66	128.98	111.00
2	X	10	DG	C1'-O4'-C4'	-6.64	103.46	110.10
3	Y	18	DC	O4'-C1'-N1	6.46	112.52	108.00
2	K	8	DT	C1'-O4'-C4'	-6.46	103.64	110.10
1	I	500	LEU	CB-CA-C	-6.43	97.98	110.20
1	A	271	ILE	N-CA-C	6.39	128.24	111.00
3	Y	2	DC	C1'-O4'-C4'	-6.37	103.73	110.10
2	X	8	DT	C1'-O4'-C4'	-6.33	103.77	110.10
1	A	347	LEU	CA-CB-CG	6.25	129.69	115.30
2	X	15	DT	O4'-C4'-C3'	-6.16	102.04	104.50
3	L	21	DT	C4'-C3'-C2'	-5.93	97.76	103.10
2	X	2	DC	O4'-C4'-C3'	-5.91	102.14	104.50
3	Y	2	DC	O4'-C1'-C2'	-5.81	101.26	105.90
2	K	2	DC	C1'-O4'-C4'	-5.77	104.33	110.10
2	K	9	DC	C3'-C2'-C1'	-5.76	95.58	102.50
1	A	40	ARG	NE-CZ-NH1	-5.75	117.42	120.30
2	X	7	DC	C3'-C2'-C1'	-5.75	95.60	102.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	9	DC	C3'-C2'-C1'	-5.75	95.60	102.50
3	Y	10	DG	C1'-O4'-C4'	-5.74	104.36	110.10
3	L	17	DG	O4'-C1'-N9	5.74	112.02	108.00
3	Y	4	DA	O4'-C4'-C3'	-5.69	102.22	104.50
3	L	9	DC	C1'-O4'-C4'	-5.69	104.41	110.10
3	Y	21	DT	C4'-C3'-C2'	-5.66	98.00	103.10
3	L	15	DC	O3'-P-O5'	-5.66	93.25	104.00
2	X	2	DC	C1'-O4'-C4'	-5.66	104.44	110.10
3	L	6	DC	O4'-C4'-C3'	-5.61	102.26	104.50
2	K	7	DC	O4'-C1'-C2'	-5.60	101.42	105.90
3	L	23	DT	O4'-C1'-N1	5.55	111.89	108.00
2	K	2	DC	C5'-C4'-O4'	-5.55	98.75	109.30
1	D	111	ARG	CB-CA-C	-5.52	99.36	110.40
2	K	8	DT	O4'-C1'-C2'	-5.51	101.49	105.90
3	Y	18	DC	P-O3'-C3'	-5.49	113.11	119.70
3	L	6	DC	P-O3'-C3'	5.46	126.26	119.70
3	Y	9	DC	O4'-C4'-C3'	-5.45	102.32	104.50
3	L	18	DC	P-O3'-C3'	-5.42	113.19	119.70
1	D	591	LEU	C-N-CD	-5.40	108.73	120.60
2	X	7	DC	O4'-C1'-C2'	-5.39	101.59	105.90
3	Y	23	DT	O4'-C1'-N1	5.37	111.76	108.00
2	X	13	DG	O4'-C1'-N9	-5.34	104.26	108.00
3	Y	14	DA	O4'-C1'-C2'	-5.30	101.66	105.90
2	K	16	DC	O4'-C1'-C2'	-5.24	101.71	105.90
1	A	617	ARG	NE-CZ-NH2	-5.24	117.68	120.30
2	K	7	DC	O4'-C4'-C3'	-5.23	102.41	104.50
3	Y	14	DA	C1'-O4'-C4'	-5.16	104.94	110.10
3	L	2	DC	C1'-O4'-C4'	-5.14	104.96	110.10
1	A	272	LEU	N-CA-C	5.11	124.78	111.00
3	Y	22	DT	N3-C4-O4	5.06	122.94	119.90
1	I	111	ARG	C-N-CA	-5.04	111.71	122.30
1	D	40	ARG	NE-CZ-NH1	5.04	122.82	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	111	ARG	Peptide
1	D	420	ARG	Peptide
1	F	396	ARG	Sidechain
1	I	111	ARG	Peptide
1	I	362	ARG	Sidechain

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4970	0	4901	444	0
1	D	5059	0	4993	368	0
1	F	4978	0	4912	433	0
1	I	5025	0	4955	354	0
2	K	471	0	263	121	0
2	X	471	0	263	88	0
3	L	467	0	261	98	0
3	Y	467	0	261	86	0
4	A	31	0	13	5	0
4	F	31	0	13	11	0
5	A	2	0	0	0	0
5	D	1	0	0	0	0
5	F	2	0	0	0	0
5	I	1	0	0	0	0
6	A	6	0	0	0	0
6	D	28	0	0	7	0
6	F	26	0	0	3	0
6	I	36	0	0	3	0
6	Y	1	0	0	0	0
All	All	22073	0	20835	1889	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 44.

All (1889) 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:D:576:LEU:O	1:D:617:ARG:HD2	1.30	1.30
1:I:171:GLY:O	1:I:172:LEU:HG	1.29	1.26
1:A:401:TYR:OH	1:A:421:PRO:HG2	1.36	1.26
1:D:592:PRO:HD3	1:D:644:PHE:CE2	1.69	1.25
1:A:194:ILE:HD11	1:A:198:ASP:CB	1.65	1.25
1:I:67:ASN:ND2	3:L:23:DT:H5'	1.53	1.23
2:X:2:DC:H2''	2:X:3:DA:C5'	1.68	1.22
1:I:661:PRO:O	1:I:662:ILE:HG13	1.07	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:394:GLU:HB3	1:F:514:LEU:HD11	1.21	1.19
1:A:14:ASN:ND2	1:A:15:PRO:HD2	1.58	1.18
2:X:2:DC:H2''	2:X:3:DA:H5'	1.24	1.17
1:F:401:TYR:OH	1:F:421:PRO:HG2	1.41	1.16
1:F:61:LEU:HD21	1:F:63:VAL:HG13	1.21	1.16
1:A:200:ILE:HG23	1:A:239:LEU:CD1	1.74	1.15
1:I:67:ASN:HD21	3:L:23:DT:H5'	1.00	1.15
3:Y:21:DT:H4'	3:Y:22:DT:OP1	1.43	1.15
3:L:3:DG:H2''	3:L:4:DA:OP2	1.38	1.13
1:A:188:LYS:HD3	1:A:193:ALA:O	1.50	1.12
1:I:661:PRO:O	1:I:662:ILE:CG1	1.97	1.12
3:Y:5:DC:H2''	3:Y:6:DC:O5'	1.25	1.12
1:F:61:LEU:HD21	1:F:63:VAL:CG1	1.77	1.12
1:A:194:ILE:CD1	1:A:198:ASP:HB3	1.80	1.11
1:F:257:ASP:OD2	1:F:313:LYS:HE3	1.50	1.11
3:L:5:DC:H2''	3:L:6:DC:O5'	1.33	1.11
1:A:194:ILE:HD11	1:A:198:ASP:HB3	1.15	1.11
1:F:569:THR:HG21	2:K:22:DT:OP1	1.51	1.11
1:I:174:ARG:HG3	1:I:175:ASP:N	1.63	1.11
1:I:574:LYS:HA	1:I:617:ARG:HH21	1.15	1.10
1:A:34:ALA:CB	1:A:616:THR:HG21	1.79	1.10
2:X:1:DG:H2''	2:X:2:DC:O5'	1.41	1.10
1:A:34:ALA:HB3	1:A:616:THR:HG21	1.26	1.10
1:A:194:ILE:CD1	1:A:198:ASP:CB	2.29	1.10
1:A:194:ILE:CG1	1:A:198:ASP:CB	2.30	1.09
1:I:174:ARG:CG	1:I:175:ASP:H	1.62	1.09
1:D:67:ASN:OD1	3:Y:23:DT:H5'	1.52	1.09
1:F:552:ARG:O	1:F:556:GLU:HG3	1.52	1.09
2:X:12:DA:H2''	2:X:13:DG:O5'	1.49	1.09
1:F:34:ALA:CB	1:F:616:THR:HG21	1.83	1.08
1:A:194:ILE:HD11	1:A:198:ASP:CG	1.74	1.08
2:K:12:DA:H2''	2:K:13:DG:O5'	1.53	1.08
2:X:18:DT:H2''	2:X:19:DT:OP1	1.52	1.08
1:D:591:LEU:CG	1:D:592:PRO:HD2	1.84	1.07
3:L:17:DG:H4'	3:L:18:DC:OP1	1.47	1.07
1:D:210:VAL:HG12	1:D:213:VAL:HG23	1.31	1.07
3:L:6:DC:H2''	3:L:7:DT:O5'	1.55	1.07
1:F:61:LEU:CD2	1:F:63:VAL:HG13	1.85	1.07
1:D:591:LEU:HG	1:D:592:PRO:HD2	1.10	1.06
3:Y:17:DG:H4'	3:Y:18:DC:OP1	1.52	1.06
1:A:132:ILE:HD11	1:A:183:ARG:HH21	1.20	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:394:GLU:HB3	1:F:514:LEU:CD1	1.84	1.05
3:Y:3:DG:H2''	3:Y:4:DA:OP2	1.55	1.05
1:A:198:ASP:HA	1:A:201:THR:OG1	1.57	1.04
1:D:504:GLY:O	1:D:508:GLN:HG3	1.57	1.04
1:D:634:GLY:O	1:D:635:LYS:HG2	1.56	1.04
3:Y:16:DT:H4'	3:Y:17:DG:OP1	1.52	1.04
1:F:426:GLY:HA3	2:K:8:DT:OP1	1.56	1.04
1:D:592:PRO:HD3	1:D:644:PHE:HE2	0.91	1.04
1:D:575:GLY:H	1:D:617:ARG:NH2	1.55	1.03
1:F:589:GLY:O	1:F:593:SER:HA	1.58	1.03
1:F:394:GLU:CB	1:F:514:LEU:HD11	1.87	1.03
1:A:167:PRO:HB2	1:A:173:PRO:HD2	1.35	1.03
1:F:632:GLN:HG2	2:K:19:DT:H72	1.36	1.03
1:D:396:ARG:HB3	6:D:2020:HOH:O	1.58	1.02
1:I:172:LEU:HD13	1:I:176:ALA:HB3	1.38	1.02
1:A:132:ILE:HG23	1:A:133:PRO:HD2	1.41	1.02
2:K:1:DG:H2''	2:K:2:DC:O5'	1.53	1.02
1:I:233:ASN:ND2	1:I:236:GLN:HG3	1.75	1.01
1:I:576:LEU:O	1:I:617:ARG:HD2	1.60	1.01
3:L:12:DG:H2''	3:L:13:DC:C6	1.96	1.01
1:F:362:ARG:NH1	1:F:571:HIS:HE1	1.57	1.01
1:A:200:ILE:HG23	1:A:239:LEU:HD11	1.05	1.00
1:A:194:ILE:CD1	1:A:198:ASP:CG	2.30	1.00
1:I:39:THR:O	1:I:43:ILE:HD12	1.60	1.00
3:Y:5:DC:C2'	3:Y:6:DC:O5'	2.09	1.00
3:L:21:DT:H4'	3:L:22:DT:OP1	1.56	1.00
1:A:545:LEU:HD21	1:A:551:MET:HG3	1.41	0.99
3:L:5:DC:C2'	3:L:6:DC:O5'	2.09	0.99
1:A:194:ILE:CG1	1:A:198:ASP:HB2	1.90	0.99
1:D:232:THR:HG23	1:D:270:ASN:HD22	1.26	0.99
1:I:67:ASN:ND2	3:L:23:DT:C5'	2.24	0.99
1:I:174:ARG:HG3	1:I:175:ASP:H	0.83	0.99
1:D:592:PRO:CD	1:D:644:PHE:CE2	2.45	0.99
1:F:65:PHE:O	1:F:66:THR:HG23	1.63	0.99
1:D:591:LEU:HG	1:D:592:PRO:CD	1.93	0.99
1:I:487:LEU:O	1:I:491:MET:HG3	1.63	0.99
1:F:362:ARG:HH12	1:F:571:HIS:CE1	1.81	0.99
1:F:586:VAL:CG1	1:F:591:LEU:HD22	1.92	0.99
2:K:14:DG:H2''	2:K:15:DT:H5''	1.43	0.99
1:I:67:ASN:HD21	3:L:23:DT:C5'	1.76	0.98
2:K:6:DG:H2''	2:K:7:DC:O5'	1.63	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:592:PRO:O	1:F:607:GLU:HG3	1.62	0.98
1:F:591:LEU:HB3	1:F:592:PRO:HD3	1.45	0.98
1:F:655:VAL:HG13	1:F:659:GLY:HA2	1.44	0.98
2:K:14:DG:H2''	2:K:15:DT:C5'	1.94	0.98
2:K:17:DG:H4'	2:K:18:DT:OP1	1.62	0.98
2:X:14:DG:H2''	2:X:15:DT:H5''	1.44	0.98
2:X:11:DC:H42	3:Y:8:DG:H1	1.08	0.98
1:A:14:ASN:HD22	1:A:15:PRO:HD2	1.26	0.97
1:A:200:ILE:O	1:A:203:THR:HB	1.63	0.97
2:K:1:DG:H1	3:L:18:DC:N4	1.61	0.97
2:X:6:DG:H2''	2:X:7:DC:O5'	1.61	0.97
2:K:9:DC:OP2	2:K:9:DC:H2'	1.64	0.97
3:L:16:DT:H4'	3:L:17:DG:OP1	1.65	0.96
1:A:268:ILE:O	1:A:271:ILE:HG13	1.65	0.96
1:D:56:HIS:CD2	1:D:57:PRO:HD2	1.99	0.96
1:D:655:VAL:HG12	1:D:656:ASP:O	1.64	0.96
2:K:3:DA:H2''	2:K:4:DG:OP2	1.62	0.96
2:K:19:DT:H4'	2:K:20:DT:H5''	1.44	0.96
1:I:232:THR:HG23	1:I:270:ASN:HD22	1.29	0.95
2:K:18:DT:H2''	2:K:19:DT:OP1	1.60	0.95
1:A:43:ILE:HD11	1:A:73:MET:CG	1.96	0.95
1:F:34:ALA:HB3	1:F:616:THR:HG21	1.45	0.95
2:X:1:DG:H1	3:Y:18:DC:N4	1.64	0.95
1:D:592:PRO:CD	1:D:644:PHE:HE2	1.79	0.95
1:A:267:ASP:HB3	1:A:270:ASN:HB2	1.48	0.94
1:A:552:ARG:O	1:A:556:GLU:HG3	1.67	0.94
1:F:32:ALA:HB2	1:F:286:LEU:HB2	1.49	0.94
1:A:198:ASP:HA	1:A:201:THR:HG1	1.30	0.94
1:D:210:VAL:CG1	1:D:213:VAL:HG23	1.96	0.94
1:D:575:GLY:N	1:D:617:ARG:HH21	1.66	0.93
1:A:229:TYR:CE2	1:A:271:ILE:HA	2.04	0.93
3:Y:14:DA:H2'	3:Y:14:DA:OP2	1.67	0.93
1:F:655:VAL:CG1	1:F:659:GLY:HA2	1.99	0.93
3:L:19:DT:O2	3:L:19:DT:H2'	1.65	0.93
1:F:167:PRO:HB2	1:F:173:PRO:HD2	1.50	0.93
1:A:592:PRO:O	1:A:607:GLU:HG3	1.67	0.93
1:D:332:ASP:HB3	1:D:335:ALA:H	1.33	0.92
1:F:303:LEU:HD13	1:F:611:PHE:CE1	2.04	0.92
1:D:294:ALA:HB3	1:D:321:ALA:HA	1.51	0.92
2:X:11:DC:N4	3:Y:8:DG:H1	1.67	0.92
1:I:487:LEU:HA	1:I:490:VAL:HG22	1.47	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:8:DT:H2'	2:X:9:DC:C6	2.04	0.92
1:I:428:THR:HG23	3:L:8:DG:OP2	1.70	0.92
1:A:32:ALA:HB2	1:A:286:LEU:HB2	1.50	0.92
3:L:14:DA:H2'	3:L:14:DA:OP2	1.69	0.92
1:A:257:ASP:OD2	1:A:313:LYS:HE3	1.67	0.92
1:A:591:LEU:HB3	1:A:592:PRO:HD3	1.52	0.91
1:I:127:GLU:HG2	1:I:187:ARG:NH1	1.84	0.91
1:I:592:PRO:HG3	1:I:644:PHE:CE2	2.06	0.91
1:I:462:HIS:O	1:I:466:GLU:HG3	1.70	0.91
1:F:362:ARG:HH12	1:F:571:HIS:HE1	0.92	0.91
2:X:14:DG:H2''	2:X:15:DT:C5'	2.00	0.91
1:F:591:LEU:HD23	1:F:642:SER:CB	2.01	0.91
1:I:31:ILE:HG21	1:I:313:LYS:HD3	1.53	0.91
1:D:487:LEU:HA	1:D:490:VAL:HG22	1.52	0.90
1:F:194:ILE:HG13	1:F:198:ASP:HB3	1.52	0.90
1:A:200:ILE:CG2	1:A:239:LEU:HD11	1.99	0.90
1:A:236:GLN:O	1:A:240:THR:HG23	1.72	0.90
1:A:114:VAL:HG21	1:A:403:ARG:HD2	1.53	0.89
1:D:575:GLY:H	1:D:617:ARG:HH21	0.90	0.89
1:I:331:THR:HA	1:I:628:GLN:HG3	1.51	0.89
1:F:97:VAL:HG11	1:F:544:LEU:HD11	1.53	0.89
1:F:545:LEU:HD21	1:F:551:MET:HG3	1.54	0.89
3:L:14:DA:H1'	3:L:15:DC:OP1	1.73	0.89
1:A:230:GLN:HG2	1:A:255:ASP:H	1.34	0.89
3:Y:13:DC:H2''	3:Y:14:DA:C8	2.08	0.89
3:Y:14:DA:H1'	3:Y:15:DC:OP1	1.73	0.89
2:K:11:DC:H42	3:L:8:DG:H1	1.21	0.89
1:D:164:SER:O	1:D:174:ARG:HD3	1.73	0.88
1:A:234:ARG:CG	1:A:270:ASN:HD21	1.84	0.88
1:F:579:PRO:HA	1:F:619:MET:HB2	1.55	0.88
1:D:524:TRP:CH2	1:D:541:ASP:OD2	2.25	0.88
1:F:200:ILE:HG23	1:F:239:LEU:CD1	2.02	0.88
1:A:43:ILE:HD11	1:A:73:MET:HG3	1.56	0.88
1:I:593:SER:OG	3:L:19:DT:H73	1.73	0.88
1:A:229:TYR:HE2	1:A:271:ILE:HA	1.37	0.87
1:D:661:PRO:O	1:D:662:ILE:HB	1.71	0.87
1:A:194:ILE:HG13	1:A:198:ASP:HB2	1.53	0.87
1:A:591:LEU:HB3	1:A:592:PRO:CD	2.04	0.87
3:L:3:DG:C2'	3:L:4:DA:OP2	2.22	0.87
1:D:576:LEU:O	1:D:617:ARG:CD	2.22	0.87
1:A:267:ASP:HB3	1:A:270:ASN:CB	2.04	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ARG:HG3	1:A:270:ASN:HD21	1.37	0.87
1:I:171:GLY:O	1:I:172:LEU:CG	2.21	0.87
1:D:524:TRP:HH2	1:D:541:ASP:OD2	1.57	0.87
1:I:56:HIS:ND1	1:I:57:PRO:HD2	1.88	0.87
1:F:586:VAL:HG12	1:F:591:LEU:HD22	1.56	0.87
1:D:114:VAL:HG13	1:D:193:ALA:HB2	1.58	0.86
2:X:6:DG:H2''	2:X:7:DC:C5'	2.05	0.86
1:I:160:ASP:HA	1:I:163:ARG:HG3	1.58	0.86
1:A:421:PRO:HA	1:A:499:LEU:HD11	1.56	0.86
1:I:294:ALA:HB3	1:I:321:ALA:HA	1.57	0.86
1:F:606:GLU:HA	1:F:609:ARG:NH1	1.90	0.86
1:I:14:ASN:OD1	1:I:15:PRO:HD2	1.76	0.86
1:A:229:TYR:HE2	1:A:271:ILE:CA	1.90	0.85
1:F:76:ARG:HA	1:F:79:HIS:NE2	1.91	0.85
3:L:12:DG:H2''	3:L:13:DC:C5	2.12	0.85
1:F:586:VAL:HG13	1:F:591:LEU:HD22	1.59	0.85
2:K:21:DT:H5'	2:K:22:DT:OP2	1.77	0.85
1:I:634:GLY:O	1:I:635:LYS:HG2	1.77	0.84
1:A:132:ILE:CG2	1:A:133:PRO:HD2	2.05	0.84
1:D:459:ARG:O	1:D:462:HIS:CE1	2.30	0.84
3:L:12:DG:C2'	3:L:13:DC:C5	2.60	0.84
1:I:233:ASN:ND2	1:I:236:GLN:CG	2.40	0.84
1:F:65:PHE:O	1:F:66:THR:CG2	2.25	0.84
1:I:210:VAL:HG12	1:I:213:VAL:HG23	1.60	0.84
1:D:308:THR:HG22	1:D:605:GLU:OE2	1.77	0.83
1:F:422:ARG:HD2	2:K:9:DC:H3'	1.59	0.83
2:K:19:DT:H2''	2:K:20:DT:O5'	1.76	0.83
1:F:420:ARG:HB2	1:F:421:PRO:HD3	1.61	0.83
1:A:660:GLN:HB2	1:A:661:PRO:HD3	1.60	0.83
1:D:487:LEU:O	1:D:491:MET:HG3	1.76	0.83
1:F:655:VAL:HG12	1:F:656:ASP:O	1.78	0.83
1:A:34:ALA:HB3	1:A:616:THR:CG2	2.08	0.83
1:D:46:ILE:O	1:D:50:ILE:HD12	1.78	0.83
1:D:14:ASN:OD1	1:D:15:PRO:HD2	1.76	0.83
1:F:45:ARG:HD2	1:F:251:LEU:HD22	1.61	0.83
1:A:65:PHE:O	1:A:66:THR:CG2	2.27	0.83
1:D:362:ARG:HH12	1:D:593:SER:HB3	1.44	0.83
1:I:173:PRO:O	1:I:174:ARG:O	1.96	0.82
1:F:32:ALA:CB	1:F:286:LEU:HB2	2.09	0.82
2:K:8:DT:H2'	2:K:9:DC:C6	2.15	0.82
1:F:45:ARG:HD3	1:F:225:HIS:HE1	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:9:LEU:HD23	1:I:18:ALA:O	1.80	0.82
1:F:655:VAL:HG13	1:F:659:GLY:CA	2.10	0.82
2:K:8:DT:C2'	2:K:9:DC:C6	2.62	0.82
1:A:194:ILE:HG13	1:A:198:ASP:CB	2.10	0.81
1:I:574:LYS:HA	1:I:617:ARG:NH2	1.95	0.81
1:A:401:TYR:HH	1:A:421:PRO:HG2	1.41	0.81
2:X:17:DG:H1	3:Y:2:DC:H42	1.27	0.81
1:A:43:ILE:HD11	1:A:73:MET:HG2	1.62	0.81
1:A:229:TYR:CE2	1:A:271:ILE:CA	2.63	0.81
3:Y:13:DC:H2''	3:Y:14:DA:H8	1.43	0.81
1:F:303:LEU:HD13	1:F:611:PHE:CD1	2.15	0.81
1:D:331:THR:HA	1:D:628:GLN:HB2	1.63	0.80
1:F:592:PRO:O	1:F:607:GLU:CG	2.29	0.80
3:L:14:DA:C1'	3:L:15:DC:OP1	2.30	0.80
1:A:24:PHE:CD2	1:A:25:THR:HG23	2.15	0.80
1:A:198:ASP:CA	1:A:201:THR:OG1	2.30	0.80
1:F:200:ILE:HG23	1:F:239:LEU:HD11	1.62	0.80
2:X:12:DA:C2'	2:X:13:DG:O5'	2.30	0.80
3:L:14:DA:C4'	3:L:15:DC:OP1	2.30	0.80
3:L:14:DA:OP2	3:L:14:DA:C2'	2.30	0.80
3:Y:6:DC:H2''	3:Y:7:DT:O5'	1.82	0.80
3:Y:14:DA:C1'	3:Y:15:DC:OP1	2.30	0.80
1:F:194:ILE:CG1	1:F:198:ASP:HB3	2.12	0.80
1:F:611:PHE:CE1	1:F:615:ILE:HD11	2.17	0.79
2:X:6:DG:C2'	2:X:7:DC:O5'	2.30	0.79
1:A:65:PHE:O	1:A:66:THR:HG23	1.82	0.79
1:D:363:THR:O	1:D:366:GLN:HG3	1.80	0.79
1:I:39:THR:O	1:I:43:ILE:CD1	2.29	0.79
1:I:655:VAL:HG12	1:I:656:ASP:O	1.83	0.79
1:D:48:HIS:NE2	1:D:52:HIS:ND1	2.29	0.79
1:D:606:GLU:HA	1:D:609:ARG:NH1	1.96	0.79
3:Y:1:DA:H2''	3:Y:2:DC:O5'	1.81	0.79
1:A:615:ILE:HG23	1:A:622:LEU:HD22	1.65	0.79
1:I:362:ARG:NH1	1:I:593:SER:HB3	1.97	0.79
1:D:631:MET:HB2	1:D:635:LYS:O	1.83	0.79
1:I:172:LEU:HD13	1:I:176:ALA:CB	2.12	0.79
3:Y:6:DC:H2''	3:Y:7:DT:C5'	2.12	0.79
3:Y:14:DA:C4'	3:Y:15:DC:OP1	2.30	0.79
3:Y:14:DA:OP2	3:Y:14:DA:C2'	2.30	0.79
2:K:2:DC:H2''	2:K:3:DA:H5'	1.64	0.79
1:F:122:LEU:HA	1:F:125:ILE:HD12	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:560:ALA:HB1	1:D:561:PRO:HD2	1.65	0.78
2:K:9:DC:OP2	2:K:9:DC:C2'	2.30	0.78
1:D:39:THR:O	1:D:43:ILE:CD1	2.31	0.78
1:F:362:ARG:NH1	1:F:571:HIS:CE1	2.45	0.78
1:A:302:LYS:O	1:A:305:GLU:HG2	1.84	0.78
1:I:357:MET:HG2	1:I:580:VAL:HB	1.64	0.78
1:D:357:MET:HG2	1:D:580:VAL:HB	1.66	0.78
3:Y:3:DG:C2'	3:Y:4:DA:OP2	2.32	0.78
1:A:194:ILE:HG13	1:A:198:ASP:OD2	1.83	0.78
1:D:591:LEU:CB	1:D:592:PRO:HD2	2.14	0.78
2:K:19:DT:C4'	2:K:20:DT:H5''	2.14	0.78
1:A:424:GLY:O	1:A:463:LYS:CD	2.32	0.78
1:F:589:GLY:O	1:F:593:SER:CA	2.32	0.78
1:I:23:HIS:CE1	1:I:28:ALA:HB2	2.18	0.78
3:Y:19:DT:O2	3:Y:19:DT:H2'	1.82	0.78
1:D:389:PHE:HB3	1:D:392:ARG:HB2	1.66	0.77
1:F:569:THR:HG23	1:F:572:ASN:H	1.48	0.77
1:F:488:ARG:HH11	1:F:518:VAL:HG11	1.49	0.77
3:L:11:DA:C4	3:L:12:DG:C8	2.73	0.77
1:A:257:ASP:O	1:A:609:ARG:HG3	1.84	0.77
1:I:399:LEU:O	1:I:403:ARG:HG2	1.83	0.77
1:I:661:PRO:C	1:I:662:ILE:HG13	2.04	0.77
2:X:2:DC:H2''	2:X:3:DA:H5''	1.65	0.77
1:A:655:VAL:HG13	1:A:659:GLY:HA2	1.66	0.77
1:F:248:ARG:HH12	1:F:279:PRO:HD2	1.49	0.77
1:A:26:GLY:HA2	1:A:248:ARG:O	1.84	0.77
1:D:125:ILE:O	1:D:129:MET:HG3	1.85	0.77
1:D:127:GLU:HG2	1:D:187:ARG:NH1	2.00	0.77
3:L:11:DA:C5	3:L:12:DG:N7	2.52	0.77
1:A:586:VAL:HG13	1:A:591:LEU:HD22	1.67	0.77
1:I:48:HIS:NE2	1:I:52:HIS:ND1	2.31	0.77
1:A:579:PRO:HA	1:A:619:MET:HB2	1.66	0.77
1:A:35:GLY:H	4:A:1662:ANP:HNB1	1.33	0.76
1:A:196:PHE:O	1:A:199:LEU:HB2	1.85	0.76
3:L:11:DA:H2''	3:L:12:DG:H5''	1.67	0.76
1:F:634:GLY:HA2	3:L:1:DA:H5'	1.66	0.76
2:K:8:DT:H2''	2:K:9:DC:O4'	1.85	0.76
3:L:12:DG:C4	3:L:13:DC:C4	2.72	0.76
1:D:291:ARG:HH11	1:D:577:GLU:HB3	1.49	0.76
1:I:428:THR:HG21	3:L:7:DT:H3'	1.66	0.76
1:F:591:LEU:CB	1:F:592:PRO:HD3	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:500:LEU:HD22	1:F:511:LEU:HB3	1.65	0.76
3:L:11:DA:C6	3:L:12:DG:C5	2.74	0.76
2:X:2:DC:C2'	2:X:3:DA:C5'	2.60	0.76
2:X:8:DT:H2''	2:X:9:DC:O4'	1.86	0.76
1:A:194:ILE:CD1	1:A:198:ASP:OD2	2.34	0.75
1:F:60:ILE:HG12	1:F:223:PHE:HB2	1.66	0.75
1:I:142:ARG:HE	1:I:145:ARG:HH21	1.33	0.75
3:Y:21:DT:C4'	3:Y:22:DT:OP1	2.23	0.75
2:K:1:DG:C2'	2:K:2:DC:O5'	2.34	0.75
1:D:437:ALA:HA	1:D:442:THR:HG22	1.68	0.75
1:I:47:ALA:HB2	1:I:80:LEU:CD1	2.15	0.75
1:F:393:ARG:HG3	1:F:397:ASP:OD2	1.87	0.75
1:I:279:PRO:O	1:I:280:ASP:OD1	2.05	0.75
1:D:56:HIS:CD2	1:D:57:PRO:CD	2.69	0.75
1:A:32:ALA:CB	1:A:286:LEU:HB2	2.16	0.75
1:I:441:HIS:HD2	6:I:2034:HOH:O	1.70	0.75
1:I:428:THR:CG2	3:L:8:DG:OP2	2.34	0.75
3:L:14:DA:H4'	3:L:15:DC:OP1	1.83	0.75
1:D:660:GLN:HE22	1:I:76:ARG:HG2	1.52	0.74
1:F:34:ALA:CB	1:F:616:THR:CG2	2.63	0.74
1:A:101:ARG:HH22	1:A:536:ALA:HB3	1.52	0.74
1:A:500:LEU:HD22	1:A:511:LEU:HB3	1.66	0.74
1:I:391:ASP:HB2	1:I:547:SER:HA	1.70	0.74
3:Y:3:DG:H1'	3:Y:4:DA:H5'	1.69	0.74
1:D:415:ARG:HB3	1:D:416:ARG:HH11	1.53	0.74
1:D:507:GLY:O	1:D:508:GLN:HB2	1.87	0.74
2:K:19:DT:OP1	2:K:19:DT:O2	2.06	0.74
1:D:142:ARG:O	1:D:145:ARG:N	2.19	0.74
1:F:42:LEU:O	1:F:46:ILE:HD12	1.87	0.74
1:F:45:ARG:HD2	1:F:251:LEU:CD2	2.17	0.74
1:I:331:THR:HA	1:I:628:GLN:CG	2.17	0.74
1:A:587:GLU:CD	1:A:630:ARG:HH12	1.91	0.74
1:I:262:LYS:HB3	1:I:606:GLU:OE1	1.87	0.74
1:D:362:ARG:NH1	1:D:607:GLU:OE2	2.21	0.73
1:I:408:PRO:O	1:I:409:ALA:HB3	1.87	0.73
1:F:569:THR:CG2	1:F:572:ASN:H	2.00	0.73
1:A:268:ILE:HG23	1:A:269:GLN:N	2.03	0.73
1:A:654:THR:O	1:A:661:PRO:C	2.27	0.73
1:I:524:TRP:CH2	1:I:541:ASP:OD2	2.41	0.73
1:I:437:ALA:HA	1:I:442:THR:HG22	1.69	0.73
2:K:14:DG:H2'	2:K:15:DT:H72	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:MET:HG2	1:A:580:VAL:HB	1.70	0.73
3:L:9:DC:H2''	3:L:10:DG:O4'	1.87	0.73
1:I:656:ASP:OD1	1:I:657:PRO:HD2	1.88	0.73
1:A:132:ILE:HD11	1:A:183:ARG:NH2	2.02	0.73
1:I:514:LEU:O	1:I:518:VAL:HG23	1.88	0.73
3:L:12:DG:H2''	3:L:13:DC:H6	1.51	0.73
1:A:26:GLY:H	1:A:249:ASN:HD22	1.36	0.73
1:A:43:ILE:CD1	1:A:73:MET:HG2	2.19	0.73
1:F:422:ARG:NE	2:K:10:DG:OP2	2.22	0.73
2:X:18:DT:C2'	2:X:19:DT:OP1	2.35	0.73
1:I:103:TYR:CD2	1:I:213:VAL:HG13	2.24	0.73
1:A:69:ALA:O	1:A:73:MET:HB2	1.89	0.72
1:A:121:GLN:O	1:A:125:ILE:HD12	1.89	0.72
1:D:264[A]:ARG:HB3	1:D:264[A]:ARG:HH11	1.54	0.72
1:D:362:ARG:NH1	1:D:593:SER:HB3	2.04	0.72
1:F:362:ARG:NH2	1:F:607:GLU:OE2	2.21	0.72
1:A:448:CYS:O	1:A:464:ALA:HB1	1.90	0.72
1:F:289:ASN:OD1	1:F:297:LEU:HD13	1.88	0.72
1:F:426:GLY:CA	2:K:8:DT:OP1	2.37	0.72
1:D:460:GLY:O	1:D:463:LYS:N	2.22	0.72
1:D:294:ALA:O	1:D:298:GLU:HG3	1.90	0.72
1:D:457:LEU:O	1:D:458:ASP:OD1	2.07	0.72
1:F:125:ILE:HD13	1:F:145:ARG:HB3	1.71	0.72
1:F:394:GLU:CB	1:F:514:LEU:CD1	2.57	0.72
1:I:576:LEU:O	1:I:617:ARG:CD	2.34	0.72
2:X:8:DT:C2'	2:X:9:DC:C6	2.73	0.72
1:D:577:GLU:CD	1:D:619:MET:CE	2.58	0.72
1:D:656:ASP:HB2	1:D:657:PRO:HD2	1.69	0.72
1:A:14:ASN:HD22	1:A:15:PRO:CD	2.02	0.72
1:A:57:PRO:HG2	1:A:86:ASP:HB2	1.72	0.72
1:A:188:LYS:CD	1:A:193:ALA:O	2.33	0.72
1:A:34:ALA:CB	1:A:616:THR:CG2	2.65	0.72
1:F:101:ARG:HH22	1:F:536:ALA:HB3	1.55	0.72
1:F:362:ARG:NH2	2:K:21:DT:O2	2.22	0.72
1:F:569:THR:CG2	2:K:22:DT:OP1	2.37	0.72
1:I:9:LEU:HD13	1:I:48:HIS:ND1	2.05	0.72
1:A:569:THR:HG23	1:A:572:ASN:H	1.55	0.71
1:D:462:HIS:O	1:D:466:GLU:HG3	1.90	0.71
1:A:106:HIS:O	1:A:107:ILE:HG22	1.90	0.71
1:A:229:TYR:CD2	1:A:271:ILE:HB	2.25	0.71
1:A:497:LEU:HD21	1:A:501:ARG:CZ	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:34:ALA:HB3	1:F:616:THR:CG2	2.17	0.71
2:X:2:DC:H42	3:Y:17:DG:H1	1.37	0.71
2:K:17:DG:C4'	2:K:18:DT:OP1	2.38	0.71
1:A:66:THR:HG21	1:A:548:VAL:HG22	1.71	0.71
1:D:291:ARG:NH1	1:D:577:GLU:HB3	2.05	0.71
1:F:411:ASP:HB3	1:F:444:VAL:HG11	1.70	0.71
1:I:226:VAL:HG22	1:I:252:VAL:HG12	1.71	0.71
1:I:279:PRO:O	1:I:280:ASP:CG	2.29	0.71
1:F:45:ARG:HD3	1:F:225:HIS:CE1	2.26	0.71
1:D:132:ILE:HD12	1:D:132:ILE:N	2.06	0.71
1:A:606:GLU:HA	1:A:609:ARG:NH1	2.05	0.71
1:D:142:ARG:HE	1:D:145:ARG:NH2	1.89	0.71
1:F:289:ASN:ND2	1:F:291:ARG:H	1.89	0.71
1:A:421:PRO:CA	1:A:499:LEU:HD11	2.20	0.71
1:A:569:THR:CG2	1:A:572:ASN:H	2.03	0.71
1:F:61:LEU:HD12	1:F:88:TRP:CD2	2.26	0.71
1:F:200:ILE:O	1:F:204:VAL:HG23	1.91	0.71
1:F:230:GLN:HG2	1:F:255:ASP:H	1.56	0.71
2:K:2:DC:H2''	2:K:3:DA:C5'	2.19	0.71
1:A:656:ASP:HB3	1:A:661:PRO:HD2	1.71	0.70
1:A:195:ASP:OD1	1:A:198:ASP:CG	2.30	0.70
1:F:426:GLY:HA3	2:K:8:DT:P	2.31	0.70
1:D:318:VAL:HG12	1:D:318:VAL:O	1.89	0.70
1:F:188:LYS:HD3	1:F:193:ALA:O	1.90	0.70
1:A:194:ILE:CG1	1:A:198:ASP:HB3	2.13	0.70
1:F:107:ILE:CG2	1:F:205:ARG:HH22	2.05	0.70
1:F:194:ILE:HG13	1:F:198:ASP:CB	2.20	0.70
2:K:2:DC:H2''	2:K:3:DA:OP2	1.88	0.70
1:D:9:LEU:HD13	1:D:48:HIS:ND1	2.05	0.70
3:Y:18:DC:H2''	3:Y:19:DT:OP2	1.85	0.70
1:A:196:PHE:O	1:A:197:GLY:C	2.30	0.70
2:K:15:DT:H6	2:K:15:DT:H5'	1.56	0.70
1:D:39:THR:O	1:D:43:ILE:HD12	1.90	0.70
1:I:239:LEU:O	1:I:243:LEU:HD12	1.91	0.70
1:I:593:SER:OG	3:L:19:DT:C7	2.40	0.70
2:K:11:DC:N4	3:L:8:DG:H1	1.87	0.70
1:A:535:ILE:HG23	1:A:536:ALA:H	1.56	0.70
1:A:591:LEU:CB	1:A:592:PRO:HD3	2.22	0.70
1:D:232:THR:CG2	1:D:270:ASN:HD22	2.02	0.70
1:A:422:ARG:HG3	2:X:10:DG:OP1	1.91	0.70
2:K:8:DT:H2''	2:K:9:DC:C6	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ARG:NH2	3:Y:4:DA:OP1	2.24	0.70
1:F:61:LEU:HD21	1:F:63:VAL:HG12	1.72	0.70
1:I:574:LYS:CA	1:I:617:ARG:HH21	2.00	0.70
3:Y:11:DA:C6	3:Y:12:DG:C5	2.80	0.70
1:A:195:ASP:CG	1:A:198:ASP:OD2	2.30	0.69
1:D:457:LEU:O	1:D:458:ASP:CG	2.30	0.69
1:F:114:VAL:HG21	1:F:403:ARG:HD3	1.74	0.69
1:D:287:GLU:HG2	1:D:314:THR:H	1.58	0.69
1:F:404:LEU:HD13	1:F:410:ASP:O	1.92	0.69
1:F:436:TRP:HA	1:F:439:THR:HG22	1.73	0.69
1:F:632:GLN:HG2	2:K:19:DT:C7	2.17	0.69
1:F:58:GLY:HA2	1:F:86:ASP:O	1.92	0.69
1:I:9:LEU:CD1	1:I:48:HIS:ND1	2.55	0.69
1:I:31:ILE:CG2	1:I:313:LYS:HD3	2.21	0.69
1:F:591:LEU:HB3	1:F:592:PRO:CD	2.21	0.69
1:I:46:ILE:O	1:I:50:ILE:HD12	1.93	0.69
1:A:422:ARG:NE	2:X:10:DG:OP2	2.26	0.69
1:D:264[A]:ARG:HB3	1:D:264[A]:ARG:NH1	2.07	0.69
1:A:631:MET:HB2	1:A:636:THR:CG2	2.22	0.69
1:D:56:HIS:HB3	1:D:59:GLU:HG3	1.73	0.69
1:D:132:ILE:HG23	1:D:133:PRO:HD2	1.75	0.69
1:D:275:GLN:HE21	1:D:276:LYS:HG3	1.58	0.69
1:D:396:ARG:CB	6:D:2020:HOH:O	2.27	0.69
1:F:608:ARG:HB2	1:F:644:PHE:CE1	2.27	0.69
1:I:210:VAL:CG1	1:I:213:VAL:HG23	2.22	0.69
1:A:194:ILE:HG12	1:A:198:ASP:CB	2.21	0.69
1:A:258:GLN:NE2	4:A:1662:ANP:O2G	2.26	0.69
1:A:417:ILE:O	1:A:421:PRO:HD2	1.92	0.69
1:F:631:MET:HB2	1:F:636:THR:HG22	1.74	0.69
1:I:377:VAL:O	1:I:377:VAL:HG12	1.93	0.69
1:A:231:ASP:HB3	1:A:261:TYR:HB2	1.75	0.69
3:L:11:DA:C6	3:L:12:DG:C6	2.81	0.69
1:A:42:LEU:O	1:A:46:ILE:HD12	1.93	0.68
1:A:229:TYR:CE2	1:A:271:ILE:CB	2.76	0.68
1:F:569:THR:HG22	1:F:572:ASN:HB2	1.75	0.68
1:I:123:ASP:OD2	1:I:415:ARG:NH1	2.26	0.68
1:A:77:ALA:O	1:A:81:VAL:N	2.26	0.68
1:D:142:ARG:HE	1:D:145:ARG:HH21	1.41	0.68
1:A:388:GLY:HA2	1:A:556:GLU:OE2	1.93	0.68
1:A:660:GLN:CB	1:A:661:PRO:HD3	2.24	0.68
1:D:23:HIS:CE1	1:D:28:ALA:HB2	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:655:VAL:C	1:D:662:ILE:HD11	2.14	0.68
1:A:194:ILE:HG12	1:A:198:ASP:HB2	1.72	0.68
1:D:348:HIS:HA	1:D:352:ARG:O	1.94	0.68
1:D:487:LEU:HA	1:D:490:VAL:CG2	2.24	0.68
1:F:631:MET:HB2	1:F:636:THR:CG2	2.23	0.68
1:I:591:LEU:HB3	1:I:592:PRO:HD3	1.76	0.68
3:L:3:DG:H1'	3:L:4:DA:H5'	1.75	0.68
3:L:12:DG:C5	3:L:13:DC:N4	2.62	0.68
1:A:197:GLY:O	1:A:198:ASP:C	2.30	0.68
1:A:229:TYR:CE2	1:A:271:ILE:HB	2.27	0.68
1:D:93:HIS:NE2	3:Y:23:DT:O2	2.27	0.68
1:F:418:ILE:HD11	1:F:425:ILE:HG13	1.76	0.68
2:K:3:DA:H5'	2:K:3:DA:C8	2.29	0.68
1:I:48:HIS:CD2	1:I:52:HIS:HB3	2.30	0.67
2:X:8:DT:H2'	2:X:9:DC:H6	1.54	0.67
1:A:187:ARG:NH2	1:A:411:ASP:OD2	2.27	0.67
1:A:215:ASP:HA	1:A:218:GLN:OE1	1.94	0.67
1:D:231:ASP:OD2	1:D:574:LYS:NZ	2.28	0.67
1:I:336:GLU:HB2	1:I:625:THR:HG21	1.75	0.67
1:I:655:VAL:HG11	1:I:659:GLY:HA2	1.76	0.67
1:D:38:LYS:NZ	1:D:227:ASP:OD1	2.25	0.67
1:F:613:VAL:O	1:F:617:ARG:CD	2.42	0.67
2:X:1:DG:C2'	2:X:2:DC:O5'	2.27	0.67
1:D:294:ALA:HB3	1:D:321:ALA:CA	2.23	0.67
1:F:615:ILE:HG23	1:F:622:LEU:HD22	1.76	0.67
1:I:392:ARG:NH1	1:I:546:SER:HB2	2.09	0.67
1:A:200:ILE:CG2	1:A:239:LEU:CD1	2.64	0.67
1:A:414:LEU:HA	1:A:417:ILE:HD11	1.77	0.67
1:D:67:ASN:OD1	3:Y:23:DT:C5'	2.39	0.67
1:D:416:ARG:O	1:D:420:ARG:NH1	2.27	0.67
1:I:348:HIS:HA	1:I:352:ARG:O	1.95	0.67
2:K:11:DC:H2''	2:K:12:DA:O5'	1.95	0.67
2:K:21:DT:H5''	2:K:22:DT:H72	1.75	0.67
3:L:12:DG:C2'	3:L:13:DC:H5	2.07	0.67
1:A:545:LEU:HD21	1:A:551:MET:CG	2.22	0.67
1:D:399:LEU:O	1:D:403:ARG:HG2	1.95	0.67
1:F:448:CYS:O	1:F:464:ALA:HB1	1.95	0.67
1:F:401:TYR:OH	1:F:421:PRO:CG	2.34	0.67
1:I:500:LEU:O	1:I:504:GLY:HA3	1.95	0.67
1:A:232:THR:HG22	1:A:271:ILE:HG22	1.77	0.67
1:A:257:ASP:OD1	1:A:310:ARG:HD2	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ARG:NE	1:D:145:ARG:NH2	2.43	0.67
1:F:418:ILE:HG12	1:F:425:ILE:HG21	1.77	0.67
1:D:39:THR:O	1:D:43:ILE:HD13	1.95	0.66
1:F:155:LEU:HD23	1:F:201:THR:HG22	1.76	0.66
1:F:224:ILE:HG22	1:F:250:LEU:HD12	1.77	0.66
1:I:631:MET:HB2	1:I:635:LYS:O	1.95	0.66
1:F:291:ARG:NH2	4:F:1663:ANP:HNB1	1.93	0.66
1:F:377:VAL:O	1:F:378:GLN:CG	2.42	0.66
1:F:587:GLU:OE2	1:F:630:ARG:NH2	2.26	0.66
1:F:606:GLU:HA	1:F:609:ARG:HH11	1.57	0.66
1:A:257:ASP:O	1:A:609:ARG:CG	2.44	0.66
1:F:377:VAL:O	1:F:378:GLN:CB	2.43	0.66
1:I:122:LEU:HD21	1:I:145:ARG:HE	1.60	0.66
3:Y:1:DA:C2'	3:Y:2:DC:O5'	2.43	0.66
1:A:72:GLU:O	1:A:76:ARG:HG3	1.94	0.66
1:A:144:ILE:HG22	1:A:148:ILE:HD11	1.77	0.66
1:F:36:SER:N	4:F:1663:ANP:O2B	2.22	0.66
3:Y:6:DC:H2''	3:Y:7:DT:H5''	1.77	0.66
1:A:14:ASN:ND2	1:A:15:PRO:CD	2.47	0.66
1:F:107:ILE:HG21	1:F:205:ARG:HH22	1.60	0.66
1:I:47:ALA:CB	1:I:80:LEU:CD1	2.73	0.66
1:I:233:ASN:HD21	1:I:236:GLN:CG	2.08	0.66
1:A:194:ILE:CG1	1:A:198:ASP:OD2	2.43	0.66
1:D:103:TYR:CD2	1:D:213:VAL:HG13	2.31	0.66
1:F:592:PRO:O	1:F:607:GLU:CD	2.34	0.66
2:K:12:DA:C6	2:K:13:DG:C6	2.84	0.66
1:F:120:ASP:OD1	1:F:396:ARG:NH2	2.29	0.65
1:A:23:HIS:CE1	1:A:28:ALA:HB2	2.31	0.65
1:A:587:GLU:OE2	1:A:630:ARG:NH1	2.24	0.65
1:F:132:ILE:HD11	1:F:183:ARG:HE	1.61	0.65
1:F:633:PHE:CE1	2:K:19:DT:C4	2.83	0.65
1:A:631:MET:HB2	1:A:636:THR:HG22	1.79	0.65
1:D:238:GLU:OE2	1:D:241:ARG:NH2	2.26	0.65
2:X:2:DC:N4	3:Y:17:DG:H1	1.95	0.65
1:A:144:ILE:HG22	1:A:148:ILE:CD1	2.27	0.65
1:A:229:TYR:O	1:A:271:ILE:HG21	1.97	0.65
1:F:591:LEU:HD11	1:F:611:PHE:HD2	1.60	0.65
1:I:549:ASP:O	1:I:550:ASP:HB2	1.96	0.65
1:A:195:ASP:CG	1:A:198:ASP:CG	2.56	0.65
1:D:460:GLY:O	1:D:461:ALA:C	2.35	0.65
1:F:200:ILE:HG22	1:F:235:ALA:HB1	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:258:GLN:HE22	4:F:1663:ANP:PG	2.19	0.65
1:A:60:ILE:HG12	1:A:223:PHE:HB2	1.78	0.65
3:L:11:DA:N6	3:L:12:DG:O6	2.30	0.65
1:D:21:ALA:HA	1:D:45:ARG:HB2	1.79	0.65
1:D:346:ARG:O	1:D:350:GLU:HG2	1.97	0.65
1:F:398:ILE:HD13	1:F:491:MET:HG2	1.78	0.65
1:A:196:PHE:O	1:A:199:LEU:N	2.30	0.64
1:A:198:ASP:O	1:A:200:ILE:N	2.30	0.64
1:A:234:ARG:HG2	1:A:270:ASN:HD21	1.61	0.64
1:F:395:ILE:O	1:F:399:LEU:HG	1.97	0.64
1:F:424:GLY:CA	2:K:9:DC:OP1	2.45	0.64
2:K:9:DC:OP2	2:K:9:DC:C3'	2.45	0.64
1:A:152:LYS:HE3	1:A:195:ASP:OD2	1.96	0.64
1:D:460:GLY:O	1:D:462:HIS:N	2.29	0.64
1:F:334:ARG:NH1	1:F:376:ARG:HH12	1.95	0.64
1:F:632:GLN:CG	2:K:19:DT:H72	2.20	0.64
1:I:142:ARG:HE	1:I:145:ARG:NH2	1.95	0.64
1:I:360:LEU:HD23	1:I:570:LEU:HD23	1.79	0.64
1:I:362:ARG:HH12	1:I:593:SER:HB3	1.59	0.64
1:A:272:LEU:O	1:A:275:GLN:HG3	1.97	0.64
1:D:202:GLU:OE2	1:D:205:ARG:NH1	2.31	0.64
1:D:257:ASP:OD2	1:D:313:LYS:HE2	1.97	0.64
1:I:38:LYS:NZ	1:I:227:ASP:OD1	2.28	0.64
1:I:152:LYS:NZ	1:I:198:ASP:OD1	2.27	0.64
1:F:500:LEU:CD2	1:F:511:LEU:HB3	2.27	0.64
1:A:424:GLY:O	1:A:463:LYS:HD3	1.97	0.64
1:A:591:LEU:HD23	1:A:644:PHE:HD2	1.62	0.64
1:D:459:ARG:O	1:D:462:HIS:ND1	2.29	0.64
2:K:6:DG:C2'	2:K:7:DC:O5'	2.43	0.64
1:A:404:LEU:HD13	1:A:410:ASP:O	1.98	0.64
1:A:606:GLU:HA	1:A:609:ARG:HH11	1.62	0.64
1:D:167:PRO:HA	1:D:174:ARG:HG3	1.79	0.64
1:I:59:GLU:OE1	1:I:222:LYS:HD2	1.97	0.64
1:I:238:GLU:OE2	1:I:241:ARG:NH2	2.31	0.64
1:I:513:ASN:HA	1:I:516:GLU:HB3	1.80	0.64
1:A:59:GLU:HB3	1:A:222:LYS:HB3	1.80	0.63
1:I:462:HIS:O	1:I:466:GLU:CG	2.45	0.63
1:D:232:THR:HG23	1:D:270:ASN:ND2	2.06	0.63
1:F:107:ILE:HG22	1:F:107:ILE:O	1.96	0.63
1:A:32:ALA:O	1:A:38:LYS:HE3	1.98	0.63
3:L:22:DT:H71	3:L:23:DT:H73	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:GLY:O	1:A:38:LYS:NZ	2.22	0.63
1:F:591:LEU:HD23	1:F:642:SER:OG	1.98	0.63
2:K:17:DG:H2''	2:K:18:DT:H71	1.79	0.63
1:D:336:GLU:O	1:D:340:VAL:HG23	1.99	0.63
1:D:436:TRP:CZ3	1:D:442:THR:HG21	2.33	0.63
2:K:19:DT:H4'	2:K:20:DT:C5'	2.23	0.63
1:A:200:ILE:O	1:A:203:THR:N	2.31	0.63
1:F:26:GLY:HA2	1:F:248:ARG:O	1.98	0.63
1:I:394:GLU:CD	1:I:510:ARG:HG2	2.19	0.63
1:D:164:SER:O	1:D:174:ARG:CD	2.47	0.63
2:X:21:DT:H5'	2:X:22:DT:OP2	1.99	0.63
1:F:362:ARG:NH1	1:F:610:LEU:HD22	2.14	0.63
1:A:114:VAL:HG13	1:A:193:ALA:HB2	1.79	0.62
1:A:200:ILE:O	1:A:203:THR:CB	2.43	0.62
1:D:613:VAL:O	1:D:617:ARG:HG2	1.99	0.62
1:F:27:PRO:HA	1:F:250:LEU:O	1.99	0.62
1:F:635:LYS:HB3	1:F:635:LYS:NZ	2.14	0.62
1:A:377:VAL:O	1:A:378:GLN:HB2	1.99	0.62
1:I:90:SER:HB2	1:I:94:SER:HB3	1.82	0.62
3:L:5:DC:H2''	3:L:6:DC:C5'	2.28	0.62
1:A:362:ARG:NH1	1:A:607:GLU:OE1	2.32	0.62
1:F:334:ARG:HH12	1:F:376:ARG:HH12	1.45	0.62
2:K:1:DG:C2'	2:K:2:DC:C6	2.82	0.62
1:I:226:VAL:CG2	1:I:252:VAL:HG12	2.29	0.62
1:F:257:ASP:HB3	1:F:304:ILE:CD1	2.29	0.62
1:A:61:LEU:HA	1:A:88:TRP:O	1.98	0.62
1:F:117:ASP:OD2	1:F:396:ARG:NH2	2.32	0.62
1:I:172:LEU:HD12	1:I:173:PRO:O	1.99	0.62
1:I:332:ASP:HB3	1:I:335:ALA:H	1.65	0.62
1:A:200:ILE:HG21	1:A:235:ALA:HB1	1.82	0.62
1:A:395:ILE:HD13	1:A:514:LEU:HD23	1.81	0.62
1:D:173:PRO:HG2	1:D:176:ALA:CB	2.29	0.62
1:I:142:ARG:NE	1:I:145:ARG:HH21	1.98	0.62
1:A:655:VAL:HG13	1:A:659:GLY:CA	2.29	0.62
2:K:8:DT:H2'	2:K:9:DC:H6	1.65	0.62
1:F:33:GLY:HA2	1:F:313:LYS:HE2	1.80	0.62
1:F:417:ILE:O	1:F:421:PRO:HD2	2.00	0.62
1:I:336:GLU:OE1	1:I:625:THR:CG2	2.48	0.62
1:D:257:ASP:HA	1:D:310[A]:ARG:NH1	2.15	0.61
1:D:287:GLU:HG2	1:D:314:THR:O	2.00	0.61
1:F:57:PRO:HG2	1:F:86:ASP:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:91:THR:HG22	1:F:92:PHE:H	1.65	0.61
3:L:3:DG:H1'	3:L:4:DA:C8	2.34	0.61
1:A:26:GLY:H	1:A:249:ASN:ND2	1.97	0.61
1:D:33:GLY:HA2	1:D:255:ASP:OD2	2.00	0.61
1:F:91:THR:HG22	1:F:92:PHE:N	2.15	0.61
3:L:12:DG:C2	3:L:13:DC:N3	2.68	0.61
1:A:195:ASP:OD1	1:A:198:ASP:N	2.30	0.61
1:A:595:GLY:HA3	2:X:20:DT:H3	1.65	0.61
1:D:462:HIS:O	1:D:466:GLU:CG	2.48	0.61
1:F:36:SER:H	4:F:1663:ANP:PB	2.23	0.61
1:F:421:PRO:HA	1:F:499:LEU:HD11	1.83	0.61
1:F:424:GLY:HA2	2:K:9:DC:OP1	1.99	0.61
1:F:478:ALA:HA	1:F:486:PHE:CE1	2.36	0.61
1:I:313:LYS:O	1:I:314:THR:HG23	1.99	0.61
1:I:335:ALA:HA	1:I:338:ASP:OD2	2.01	0.61
1:I:336:GLU:OE1	1:I:625:THR:HG22	1.99	0.61
1:A:398:ILE:HD12	1:A:514:LEU:HD22	1.80	0.61
1:D:210:VAL:CG1	1:D:213:VAL:CG2	2.75	0.61
3:L:1:DA:H2''	3:L:2:DC:OP2	2.00	0.61
1:A:191:GLN:HG3	1:A:409:ALA:O	2.01	0.61
1:F:66:THR:HG21	1:F:548:VAL:CG2	2.31	0.61
1:D:357:MET:HG2	1:D:580:VAL:CB	2.30	0.61
1:F:29:LEU:HD21	1:F:31:ILE:HB	1.82	0.61
2:K:2:DC:C2'	2:K:3:DA:OP2	2.48	0.61
1:A:65:PHE:O	1:A:66:THR:HG22	2.00	0.61
1:F:23:HIS:CE1	1:F:28:ALA:HB2	2.35	0.61
2:X:6:DG:H2''	2:X:7:DC:H5'	1.82	0.61
1:A:613:VAL:O	1:A:617:ARG:HD2	2.00	0.61
1:F:200:ILE:CG2	1:F:235:ALA:HB1	2.31	0.61
1:I:577:GLU:CD	1:I:619:MET:CE	2.69	0.61
1:I:173:PRO:O	1:I:174:ARG:C	2.39	0.61
1:A:326:THR:OG1	1:A:621:ARG:NH2	2.34	0.61
1:I:56:HIS:HB3	1:I:59:GLU:HG3	1.82	0.61
1:I:363:THR:O	1:I:366:GLN:HG3	2.00	0.61
3:L:12:DG:H2'	3:L:13:DC:H5	1.66	0.61
1:D:9:LEU:CD1	1:D:48:HIS:ND1	2.64	0.60
1:D:132:ILE:HD11	1:D:183:ARG:HD2	1.82	0.60
3:L:10:DG:H2''	3:L:11:DA:C8	2.36	0.60
3:L:11:DA:C4	3:L:12:DG:N7	2.69	0.60
3:Y:22:DT:H71	3:Y:23:DT:H73	1.83	0.60
1:I:415:ARG:HB3	1:I:416:ARG:HH11	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:ALA:HA	1:A:480:ASN:HD21	1.66	0.60
1:D:48:HIS:CD2	1:D:52:HIS:HB3	2.36	0.60
1:A:230:GLN:HE22	1:A:258:GLN:NE2	2.00	0.60
1:D:114:VAL:HG13	1:D:193:ALA:CB	2.29	0.60
1:D:656:ASP:HB2	1:D:657:PRO:CD	2.30	0.60
1:F:59:GLU:HB3	1:F:222:LYS:HB3	1.83	0.60
3:L:11:DA:N1	3:L:12:DG:C5	2.69	0.60
1:D:171:GLY:O	1:D:172:LEU:CB	2.50	0.60
1:D:233:ASN:HD21	1:D:236:GLN:HG3	1.66	0.60
1:D:365:ALA:O	1:D:368:ARG:HG2	2.01	0.60
1:I:491:MET:O	1:I:497:LEU:HD22	2.01	0.60
3:L:3:DG:C1'	3:L:4:DA:H5'	2.31	0.60
1:F:487:LEU:O	1:F:490:VAL:HG22	2.01	0.60
1:I:331:THR:HA	1:I:628:GLN:HB2	1.83	0.60
2:K:12:DA:C2'	2:K:13:DG:O5'	2.41	0.60
1:A:655:VAL:HG12	1:A:656:ASP:O	2.02	0.60
1:I:33:GLY:HA2	1:I:255:ASP:OD2	2.02	0.60
1:A:38:LYS:HE2	1:A:255:ASP:HB2	1.83	0.60
1:A:46:ILE:O	1:A:50:ILE:HD12	2.01	0.60
1:A:411:ASP:O	1:A:415:ARG:HG2	2.02	0.60
1:D:128:VAL:O	1:D:132:ILE:CD1	2.50	0.60
1:D:195:ASP:N	1:D:198:ASP:OD2	2.30	0.60
1:D:257:ASP:OD1	1:D:310[A]:ARG:NH2	2.35	0.60
1:F:229:TYR:HE1	1:F:271:ILE:HA	1.67	0.60
1:F:634:GLY:HA2	3:L:1:DA:C5'	2.31	0.60
1:I:60:ILE:HB	1:I:87:LEU:HD22	1.83	0.60
2:K:12:DA:H2''	2:K:13:DG:C5'	2.31	0.60
1:A:59:GLU:O	1:A:222:LYS:N	2.33	0.60
1:I:172:LEU:CD1	1:I:176:ALA:HB3	2.25	0.60
1:I:408:PRO:O	1:I:409:ALA:CB	2.50	0.60
1:A:66:THR:HG21	1:A:548:VAL:CG2	2.31	0.59
1:D:442:THR:HG1	1:D:446:THR:HG1	1.47	0.59
1:F:114:VAL:HG13	1:F:193:ALA:HB2	1.84	0.59
1:I:195:ASP:N	1:I:198:ASP:OD2	2.32	0.59
1:I:420:ARG:HB2	1:I:421:PRO:HD3	1.83	0.59
1:A:45:ARG:O	1:A:49:LEU:HD12	2.01	0.59
1:F:394:GLU:HB3	1:F:514:LEU:HD13	1.83	0.59
1:F:426:GLY:CA	2:K:8:DT:P	2.90	0.59
1:I:357:MET:HG2	1:I:580:VAL:CB	2.32	0.59
2:X:12:DA:H2'	2:X:13:DG:C8	2.36	0.59
1:A:27:PRO:HD3	1:A:248:ARG:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:GLU:O	1:A:529:ALA:O	2.20	0.59
1:A:571:HIS:CG	2:X:21:DT:H2''	2.38	0.59
1:D:325:VAL:HG23	1:D:652:PHE:CB	2.32	0.59
1:D:421:PRO:HA	1:D:499:LEU:HD13	1.84	0.59
1:F:369:VAL:HG23	6:F:2017:HOH:O	2.01	0.59
1:A:403:ARG:HG2	1:A:539:LEU:HD11	1.83	0.59
1:A:48:HIS:CE1	1:A:52:HIS:CD2	2.90	0.59
1:A:613:VAL:O	1:A:617:ARG:CD	2.50	0.59
1:D:594:LYS:O	1:D:597:ILE:HG22	2.02	0.59
1:A:425:ILE:N	2:X:9:DC:OP1	2.35	0.59
1:I:287:GLU:HB3	1:I:316:LYS:HG2	1.83	0.59
1:A:436:TRP:HA	1:A:439:THR:HG22	1.85	0.59
1:D:47:ALA:HB2	1:D:80:LEU:CD1	2.33	0.59
3:L:12:DG:C4	3:L:13:DC:C5	2.91	0.59
3:Y:11:DA:C4	3:Y:12:DG:C8	2.90	0.59
1:D:401:TYR:OH	1:D:420:ARG:O	2.20	0.59
1:D:660:GLN:NE2	1:I:76:ARG:HG2	2.17	0.59
1:I:444:VAL:O	1:I:447:ALA:HB3	2.02	0.59
2:K:1:DG:C8	2:K:2:DC:C5	2.90	0.59
2:X:15:DT:H6	2:X:15:DT:H5'	1.67	0.59
1:D:171:GLY:O	1:D:172:LEU:HG	2.03	0.59
1:D:444:VAL:O	1:D:447:ALA:HB3	2.02	0.59
1:D:500:LEU:O	1:D:504:GLY:N	2.35	0.59
1:F:66:THR:HG21	1:F:548:VAL:HG22	1.85	0.59
1:F:613:VAL:O	1:F:617:ARG:HD2	2.03	0.59
1:I:116:TYR:CE2	1:I:124:ILE:HD11	2.37	0.58
2:X:6:DG:N2	3:Y:13:DC:N3	2.44	0.58
1:A:577:GLU:HG3	1:A:619:MET:HE3	1.84	0.58
1:F:421:PRO:CA	1:F:499:LEU:HD11	2.33	0.58
2:K:11:DC:H2''	2:K:12:DA:C5'	2.34	0.58
1:D:361:TYR:OH	1:D:567:LEU:HB3	2.04	0.58
1:F:34:ALA:HB1	1:F:616:THR:HG21	1.78	0.58
1:F:633:PHE:CZ	2:K:19:DT:C5	2.91	0.58
1:I:310:ARG:NH2	1:I:605:GLU:OE1	2.36	0.58
1:D:566:THR:HG21	1:D:568:MET:CE	2.33	0.58
1:D:655:VAL:CA	1:D:662:ILE:HD12	2.33	0.58
1:F:46:ILE:O	1:F:50:ILE:HD12	2.03	0.58
1:I:428:THR:OG1	1:I:429:ALA:N	2.34	0.58
1:A:268:ILE:CG2	1:A:269:GLN:N	2.66	0.58
1:A:576:LEU:H	1:A:617:ARG:HH21	1.50	0.58
1:D:116:TYR:CE2	1:D:124:ILE:HD11	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:487:LEU:HA	1:I:490:VAL:CG2	2.27	0.58
1:I:549:ASP:O	1:I:550:ASP:CB	2.51	0.58
1:I:656:ASP:OD1	1:I:657:PRO:CD	2.51	0.58
1:A:496:TYR:HA	1:A:499:LEU:HD12	1.85	0.58
1:D:14:ASN:OD1	1:D:15:PRO:CD	2.50	0.58
2:K:12:DA:H2'	2:K:13:DG:C8	2.39	0.58
1:A:268:ILE:HG23	1:A:269:GLN:H	1.67	0.58
1:A:541:ASP:O	1:A:545:LEU:HG	2.03	0.58
1:I:606:GLU:HG3	1:I:609:ARG:NH1	2.18	0.58
2:K:14:DG:H2'	2:K:15:DT:C7	2.33	0.58
1:F:535:ILE:HG23	1:F:536:ALA:H	1.69	0.58
1:F:656:ASP:C	1:F:656:ASP:OD1	2.41	0.58
1:D:34:ALA:HB1	1:D:291:ARG:HH21	1.68	0.58
1:D:483:PRO:O	1:D:487:LEU:HD12	2.04	0.58
1:D:592:PRO:CG	1:D:644:PHE:CE2	2.87	0.58
1:I:56:HIS:ND1	1:I:57:PRO:CD	2.65	0.57
1:I:591:LEU:HD23	1:I:591:LEU:C	2.25	0.57
1:I:633:PHE:HB3	2:K:1:DG:C2	2.38	0.57
1:D:331:THR:HA	1:D:628:GLN:HG3	1.87	0.57
1:A:195:ASP:OD1	1:A:195:ASP:C	2.42	0.57
1:A:580:VAL:HG22	1:A:621:ARG:HB3	1.86	0.57
1:D:246:ARG:CD	1:D:247:ASP:OD1	2.52	0.57
1:D:392:ARG:NH1	1:D:546:SER:HB2	2.19	0.57
1:F:27:PRO:HD2	1:F:280:ASP:HB2	1.85	0.57
1:F:72:GLU:O	1:F:76:ARG:HG3	2.04	0.57
1:F:632:GLN:CG	2:K:19:DT:C7	2.80	0.57
1:I:503:GLU:O	1:I:507:GLY:N	2.37	0.57
2:K:19:DT:H1'	2:K:20:DT:H5'	1.86	0.57
1:A:614:GLY:O	1:A:617:ARG:HG2	2.03	0.57
1:D:132:ILE:CG2	1:D:133:PRO:HD2	2.35	0.57
1:D:359:ILE:C	1:D:360:LEU:HD12	2.25	0.57
3:Y:17:DG:H1'	3:Y:18:DC:C6	2.39	0.57
1:A:537:ASP:O	1:A:540:ASP:HB2	2.05	0.57
1:D:56:HIS:HD2	1:D:57:PRO:HD2	1.65	0.57
1:I:524:TRP:HH2	1:I:541:ASP:OD2	1.88	0.57
2:K:19:DT:H2''	2:K:20:DT:C5'	2.33	0.57
1:D:128:VAL:O	1:D:132:ILE:HD11	2.05	0.57
1:D:332:ASP:HB3	1:D:335:ALA:N	2.14	0.57
1:F:59:GLU:O	1:F:222:LYS:N	2.37	0.57
1:F:332:ASP:OD1	1:F:334:ARG:HB2	2.05	0.57
1:F:383:ILE:HG22	1:F:384:VAL:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:483:PRO:O	1:I:487:LEU:HD12	2.04	0.57
1:I:656:ASP:HB2	1:I:662:ILE:HD12	1.86	0.57
3:Y:13:DC:C2'	3:Y:14:DA:C8	2.85	0.57
1:F:188:LYS:CD	1:F:193:ALA:O	2.53	0.57
1:F:394:GLU:HG2	1:F:510:ARG:HB3	1.85	0.57
1:F:613:VAL:O	1:F:617:ARG:HD3	2.04	0.57
1:I:287:GLU:HG2	1:I:314:THR:O	2.05	0.57
1:F:362:ARG:HG2	1:F:590:LEU:O	2.05	0.57
1:F:577:GLU:CD	1:F:619:MET:CE	2.73	0.57
1:A:134:GLY:O	1:A:138:GLU:HB2	2.05	0.57
1:A:545:LEU:CD1	1:A:551:MET:HB2	2.35	0.57
1:F:385:GLY:HA2	1:F:552:ARG:NH2	2.20	0.57
1:F:396:ARG:HH11	1:F:396:ARG:HG3	1.69	0.57
2:X:13:DG:H2''	2:X:14:DG:C8	2.40	0.57
1:A:327:PHE:CE1	1:A:645:LEU:HD11	2.40	0.57
1:D:408:PRO:HB3	1:D:445:LEU:HD23	1.87	0.57
1:D:640:GLU:HG3	1:D:641:ASP:H	1.68	0.57
1:F:173:PRO:O	1:F:176:ALA:HB3	2.05	0.57
1:F:334:ARG:HH22	1:F:376:ARG:NH1	2.03	0.57
1:F:343:TRP:O	1:F:347:LEU:HD23	2.05	0.57
1:A:289:ASN:ND2	1:A:291:ARG:H	2.03	0.56
1:I:365:ALA:O	1:I:368:ARG:HG2	2.05	0.56
2:K:1:DG:C5	2:K:2:DC:C4	2.93	0.56
1:A:45:ARG:HD2	1:A:251:LEU:HD22	1.87	0.56
1:A:197:GLY:O	1:A:200:ILE:N	2.30	0.56
1:F:299:ALA:HA	1:F:651:LEU:HD13	1.86	0.56
1:F:592:PRO:HA	1:F:607:GLU:HB3	1.87	0.56
1:I:232:THR:HG23	1:I:270:ASN:ND2	2.09	0.56
1:A:268:ILE:CG2	1:A:269:GLN:H	2.18	0.56
1:D:106:HIS:HD2	1:D:210:VAL:HG11	1.69	0.56
1:D:140:GLN:HB2	1:D:143:VAL:HG23	1.87	0.56
1:D:504:GLY:O	1:D:508:GLN:CG	2.42	0.56
1:F:196:PHE:O	1:F:199:LEU:HB2	2.05	0.56
1:I:42:LEU:HG	1:I:225:HIS:ND1	2.20	0.56
1:I:67:ASN:CG	3:L:23:DT:H5'	2.22	0.56
1:I:92:PHE:HB3	1:I:200:ILE:HD11	1.87	0.56
2:K:15:DT:H5'	2:K:15:DT:C6	2.39	0.56
2:K:21:DT:C5'	2:K:22:DT:OP2	2.52	0.56
2:X:2:DC:H1'	2:X:3:DA:H5''	1.87	0.56
2:X:9:DC:C2	2:X:10:DG:C8	2.94	0.56
3:Y:3:DG:H2'	3:Y:3:DG:O5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Y:11:DA:N6	3:Y:12:DG:C6	2.74	0.56
1:F:69:ALA:O	1:F:73:MET:HG3	2.06	0.56
2:K:14:DG:H2''	2:K:15:DT:O5'	2.02	0.56
1:A:633:PHE:HE1	2:X:19:DT:C4	2.23	0.56
1:F:200:ILE:HD13	1:F:236:GLN:HG3	1.88	0.56
1:D:257:ASP:HA	1:D:310[A]:ARG:HH12	1.69	0.56
1:D:291:ARG:HG2	1:D:619:MET:HG2	1.87	0.56
1:D:656:ASP:N	1:D:662:ILE:HD11	2.20	0.56
1:I:174:ARG:O	1:I:177:ALA:N	2.38	0.56
1:D:504:GLY:O	1:D:508:GLN:N	2.38	0.56
2:X:14:DG:H2'	2:X:15:DT:H72	1.88	0.56
1:D:142:ARG:O	1:D:143:VAL:C	2.44	0.56
2:K:13:DG:H1	3:L:6:DC:H42	1.52	0.56
3:L:17:DG:C4'	3:L:18:DC:OP1	2.37	0.56
1:A:194:ILE:HG23	1:A:194:ILE:O	2.05	0.56
1:A:422:ARG:HD2	2:X:9:DC:H3'	1.87	0.56
1:I:106:HIS:HD2	1:I:210:VAL:HG11	1.70	0.56
1:I:226:VAL:HG23	1:I:226:VAL:O	2.05	0.56
2:K:19:DT:C2'	2:K:20:DT:C5'	2.83	0.56
2:X:17:DG:H1	3:Y:2:DC:N4	2.01	0.56
1:D:656:ASP:OD1	1:D:660:GLN:HB2	2.05	0.56
1:A:167:PRO:HB3	1:A:174:ARG:HB2	1.87	0.55
1:F:187:ARG:NH2	1:F:411:ASP:OD2	2.39	0.55
2:X:14:DG:C2'	2:X:15:DT:H5''	2.28	0.55
1:A:125:ILE:O	1:A:129:MET:HB2	2.06	0.55
1:A:397:ASP:O	1:A:400:ALA:HB3	2.06	0.55
1:D:161:LEU:HD22	1:D:178:ALA:HB2	1.89	0.55
1:D:173:PRO:HG2	1:D:176:ALA:HB2	1.88	0.55
1:D:591:LEU:O	1:D:592:PRO:C	2.42	0.55
1:F:393:ARG:O	1:F:397:ASP:OD2	2.23	0.55
1:I:594:LYS:HA	1:I:597:ILE:HD12	1.88	0.55
3:Y:17:DG:C4'	3:Y:18:DC:OP1	2.42	0.55
1:F:61:LEU:HA	1:F:88:TRP:O	2.06	0.55
2:X:18:DT:H3'	2:X:18:DT:OP2	2.06	0.55
1:A:48:HIS:CE1	1:A:52:HIS:HD2	2.24	0.55
1:D:646:GLU:O	1:D:649:GLU:HG2	2.07	0.55
1:F:577:GLU:CD	1:F:619:MET:HE3	2.26	0.55
1:I:225:HIS:HA	1:I:251:LEU:O	2.07	0.55
1:I:336:GLU:HB2	1:I:625:THR:CG2	2.37	0.55
1:I:502:GLN:O	1:I:505:GLN:HG2	2.06	0.55
1:I:143:VAL:HG23	1:I:144:ILE:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:420:ARG:CB	1:I:421:PRO:HD3	2.37	0.55
2:K:20:DT:C2	2:K:21:DT:N3	2.74	0.55
3:L:22:DT:C7	3:L:23:DT:H73	2.36	0.55
1:D:307:ASN:HB2	1:D:310[A]:ARG:NH2	2.21	0.55
1:F:422:ARG:HG3	2:K:10:DG:OP1	2.07	0.55
1:F:588:GLN:HE21	1:F:597:ILE:HD11	1.71	0.55
2:X:4:DG:H2''	2:X:5:DT:OP2	2.04	0.55
1:A:395:ILE:O	1:A:399:LEU:HG	2.05	0.55
1:D:162:ASP:HB3	1:D:178:ALA:CB	2.37	0.55
1:D:171:GLY:O	1:D:172:LEU:HB2	2.07	0.55
1:I:252:VAL:HG23	1:I:252:VAL:O	2.06	0.55
2:X:19:DT:H4'	2:X:20:DT:H5''	1.87	0.55
1:F:655:VAL:HG11	1:F:659:GLY:HA2	1.87	0.55
1:I:233:ASN:CG	1:I:236:GLN:HG3	2.27	0.55
1:I:459:ARG:O	1:I:462:HIS:ND1	2.39	0.55
3:Y:21:DT:H2''	3:Y:22:DT:C6	2.42	0.55
1:A:97:VAL:HB	1:A:199:LEU:HD13	1.87	0.55
1:A:576:LEU:N	1:A:617:ARG:HH21	2.05	0.55
1:F:59:GLU:HB3	1:F:222:LYS:CB	2.37	0.55
1:F:167:PRO:HB3	1:F:174:ARG:HB2	1.88	0.55
1:I:231:ASP:OD2	1:I:574:LYS:NZ	2.37	0.55
1:D:325:VAL:CG2	1:D:652:PHE:HB3	2.38	0.54
1:F:99:ILE:HG21	1:F:203:THR:HG23	1.88	0.54
2:K:15:DT:C5'	2:K:15:DT:C6	2.90	0.54
1:D:655:VAL:HA	1:D:662:ILE:HD12	1.89	0.54
1:I:331:THR:HA	1:I:628:GLN:CB	2.38	0.54
1:I:588:GLN:HB2	1:I:640:GLU:HB2	1.89	0.54
1:I:275:GLN:HE21	1:I:276:LYS:HG3	1.72	0.54
1:I:436:TRP:CZ3	1:I:442:THR:HG21	2.42	0.54
1:I:588:GLN:HB2	1:I:640:GLU:CB	2.38	0.54
1:A:187:ARG:CZ	1:A:191:GLN:HE22	2.20	0.54
3:Y:21:DT:H2''	3:Y:22:DT:OP1	2.08	0.54
1:D:56:HIS:HD2	1:D:57:PRO:CD	2.19	0.54
1:D:330:ALA:O	1:D:628:GLN:N	2.38	0.54
1:D:362:ARG:NH2	3:Y:19:DT:H6	2.05	0.54
1:D:534:SER:O	1:D:537:ASP:HB2	2.08	0.54
1:A:398:ILE:HD13	1:A:491:MET:HG2	1.89	0.54
1:D:331:THR:HA	1:D:628:GLN:CB	2.35	0.54
1:D:592:PRO:HG3	1:D:644:PHE:CE2	2.43	0.54
1:A:408:PRO:HA	1:A:445:LEU:HD12	1.90	0.54
1:I:172:LEU:HD11	1:I:177:ALA:N	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:487:LEU:CA	1:I:490:VAL:HG22	2.29	0.54
1:I:634:GLY:O	1:I:635:LYS:CG	2.50	0.54
1:A:194:ILE:HD12	1:A:198:ASP:OD2	2.07	0.54
1:A:232:THR:HG22	1:A:271:ILE:CG2	2.38	0.54
1:D:327:PHE:CG	1:D:327:PHE:O	2.60	0.54
1:F:227:ASP:OD1	1:F:228:GLU:N	2.39	0.54
1:I:318:VAL:O	1:I:318:VAL:HG12	2.08	0.54
1:I:497:LEU:HG	1:I:498:ASP:OD1	2.08	0.54
1:I:633:PHE:HB3	2:K:1:DG:N1	2.23	0.54
1:D:132:ILE:HD12	1:D:132:ILE:H	1.73	0.54
3:L:1:DA:H1'	3:L:2:DC:O5'	2.08	0.54
1:A:272:LEU:C	1:A:272:LEU:HD23	2.29	0.54
1:D:159:ASP:OD1	1:D:182:ARG:NH2	2.37	0.54
1:D:399:LEU:O	1:D:403:ARG:N	2.34	0.54
1:D:655:VAL:CG1	1:D:656:ASP:N	2.71	0.54
2:K:1:DG:C1'	2:K:2:DC:C6	2.92	0.54
2:X:11:DC:H2''	2:X:12:DA:O5'	2.08	0.54
1:D:582:PHE:CE1	1:D:623:LEU:HD22	2.42	0.53
1:F:183:ARG:HA	1:F:186:VAL:HG22	1.89	0.53
1:F:591:LEU:CB	1:F:592:PRO:CD	2.85	0.53
1:F:592:PRO:O	1:F:607:GLU:OE1	2.25	0.53
1:I:313:LYS:O	1:I:314:THR:CG2	2.56	0.53
1:I:591:LEU:HD21	1:I:611:PHE:HB2	1.90	0.53
3:L:12:DG:N3	3:L:13:DC:C4	2.75	0.53
1:A:418:ILE:HD13	1:A:467:PHE:CE2	2.43	0.53
1:A:631:MET:HB2	1:A:636:THR:HG23	1.90	0.53
1:D:395:ILE:HG12	1:D:517:LEU:HD22	1.89	0.53
1:D:507:GLY:O	1:D:508:GLN:CB	2.56	0.53
1:I:215:ASP:O	1:I:216:LYS:C	2.45	0.53
1:I:261:TYR:O	1:I:264[B]:ARG:HB2	2.08	0.53
3:Y:17:DG:C4	3:Y:18:DC:C4	2.95	0.53
1:D:285:MET:HE1	1:D:313:LYS:HB2	1.89	0.53
1:D:291:ARG:HD2	1:D:292:SER:OG	2.08	0.53
1:D:318:VAL:O	1:D:318:VAL:CG1	2.56	0.53
1:F:27:PRO:O	1:F:281:ALA:HA	2.09	0.53
1:F:34:ALA:HB1	1:F:616:THR:CG2	2.35	0.53
1:F:257:ASP:HB3	1:F:304:ILE:HD11	1.89	0.53
2:K:14:DG:C2'	2:K:15:DT:H5''	2.30	0.53
3:L:21:DT:C4'	3:L:22:DT:OP1	2.39	0.53
2:X:14:DG:H2''	2:X:15:DT:O5'	2.06	0.53
3:Y:1:DA:H1'	3:Y:2:DC:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:ALA:HA	1:A:480:ASN:ND2	2.24	0.53
1:F:27:PRO:HB2	1:F:281:ALA:HB2	1.90	0.53
1:F:591:LEU:CD2	1:F:642:SER:CB	2.84	0.53
1:A:45:ARG:HD2	1:A:251:LEU:CD2	2.38	0.53
1:A:59:GLU:HB3	1:A:222:LYS:CB	2.39	0.53
1:D:264[B]:ARG:NH2	3:Y:22:DT:H1'	2.24	0.53
1:D:455:ASN:O	1:D:456:ILE:HD13	2.08	0.53
1:F:76:ARG:HA	1:F:79:HIS:CE1	2.44	0.53
1:I:582:PHE:CE2	1:I:623:LEU:HD22	2.43	0.53
3:Y:9:DC:H2''	3:Y:10:DG:O4'	2.08	0.53
1:A:16:THR:HG21	1:A:285:MET:O	2.09	0.53
1:A:267:ASP:CB	1:A:270:ASN:HB2	2.29	0.53
1:A:500:LEU:HD21	1:A:507:GLY:O	2.08	0.53
1:A:569:THR:HG22	1:A:572:ASN:HB2	1.90	0.53
1:D:544:LEU:HB3	3:Y:23:DT:H3'	1.91	0.53
1:F:303:LEU:CD1	1:F:611:PHE:CD1	2.91	0.53
1:F:541:ASP:O	1:F:545:LEU:HG	2.09	0.53
1:I:414:LEU:HD23	1:I:414:LEU:C	2.29	0.53
2:X:6:DG:H1	3:Y:13:DC:H42	1.55	0.53
1:A:474:MET:SD	1:A:490:VAL:HG12	2.49	0.53
1:A:545:LEU:CD2	1:A:551:MET:HB2	2.38	0.53
1:D:593:SER:OG	3:Y:19:DT:H73	2.08	0.53
1:F:38:LYS:NZ	4:F:1663:ANP:O2G	2.34	0.53
1:F:115:ILE:HD12	1:F:540:ASP:OD1	2.09	0.53
3:L:18:DC:H2''	3:L:19:DT:OP2	1.98	0.53
1:F:230:GLN:HB3	1:F:255:ASP:O	2.08	0.53
3:Y:14:DA:H4'	3:Y:15:DC:OP1	1.82	0.53
1:A:609:ARG:O	1:A:613:VAL:HG23	2.08	0.53
1:I:60:ILE:HB	1:I:87:LEU:CD2	2.39	0.53
1:I:91:THR:H	1:I:94:SER:HB3	1.73	0.53
1:A:468:ALA:O	1:A:472:GLU:HB2	2.09	0.53
1:A:490:VAL:HG23	1:A:491:MET:N	2.24	0.53
1:F:132:ILE:CD1	1:F:183:ARG:HE	2.22	0.53
1:I:333:HIS:O	1:I:336:GLU:HG2	2.09	0.53
1:I:577:GLU:CD	1:I:619:MET:HE1	2.28	0.53
1:A:61:LEU:HD22	1:A:88:TRP:CZ3	2.44	0.52
1:A:194:ILE:HG13	1:A:198:ASP:CG	2.28	0.52
1:A:294:ALA:HB3	1:A:321:ALA:HA	1.90	0.52
1:A:428:THR:OG1	2:X:8:DT:OP2	2.27	0.52
1:F:338:ASP:OD1	1:F:376:ARG:NH2	2.42	0.52
1:F:591:LEU:HD23	1:F:642:SER:HB2	1.86	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:285:MET:C	1:I:286:LEU:HD12	2.29	0.52
2:K:18:DT:C2'	2:K:19:DT:OP1	2.46	0.52
3:Y:21:DT:H2'	3:Y:22:DT:C5	2.44	0.52
1:A:214:LEU:HD12	1:A:215:ASP:N	2.23	0.52
1:A:424:GLY:O	1:A:463:LYS:CE	2.57	0.52
1:D:159:ASP:O	1:D:163:ARG:HG3	2.09	0.52
1:D:655:VAL:C	1:D:662:ILE:CD1	2.78	0.52
1:F:377:VAL:C	1:F:378:GLN:HG2	2.28	0.52
1:I:232:THR:CG2	1:I:270:ASN:HD22	2.12	0.52
1:A:424:GLY:O	1:A:463:LYS:HE3	2.10	0.52
1:F:194:ILE:HD11	1:F:202:GLU:HG3	1.90	0.52
1:I:209:GLU:O	1:I:211:PRO:HD3	2.09	0.52
1:I:323:GLN:NE2	1:I:621:ARG:HD2	2.23	0.52
3:L:11:DA:N6	3:L:12:DG:C6	2.77	0.52
1:A:423:ARG:HE	1:A:470:LEU:HD13	1.74	0.52
1:A:478:ALA:HA	1:A:486:PHE:CE2	2.44	0.52
1:A:591:LEU:CB	1:A:592:PRO:CD	2.72	0.52
1:A:608:ARG:HB2	1:A:644:PHE:CE1	2.44	0.52
1:A:392:ARG:HB3	1:A:394:GLU:OE1	2.09	0.52
1:A:497:LEU:HD21	1:A:501:ARG:NH1	2.24	0.52
1:D:121:GLN:O	1:D:125:ILE:HD12	2.10	0.52
1:D:123:ASP:OD1	1:D:415:ARG:NH1	2.42	0.52
1:D:606:GLU:OE1	1:D:609:ARG:NH1	2.42	0.52
1:F:13:LEU:HD23	1:F:17:GLN:OE1	2.09	0.52
1:I:275:GLN:H	1:I:275:GLN:CD	2.12	0.52
1:A:445:LEU:HD21	1:A:467:PHE:HE1	1.73	0.52
1:A:500:LEU:CD2	1:A:511:LEU:HB3	2.36	0.52
1:F:482:GLU:O	1:F:486:PHE:HB2	2.09	0.52
1:I:655:VAL:HG12	1:I:656:ASP:N	2.25	0.52
3:L:13:DC:H2''	3:L:14:DA:C8	2.45	0.52
1:D:55:VAL:HG12	1:D:56:HIS:N	2.25	0.52
1:F:580:VAL:HG22	1:F:621:ARG:HB3	1.91	0.52
1:I:470:LEU:O	1:I:473:ALA:HB3	2.09	0.52
3:L:11:DA:C2	3:L:12:DG:C4	2.98	0.52
2:X:2:DC:C2'	2:X:3:DA:H5''	2.33	0.52
1:A:607:GLU:O	1:A:610:LEU:HB3	2.10	0.52
1:F:403:ARG:HD2	1:F:410:ASP:OD2	2.10	0.52
1:I:152:LYS:NZ	1:I:195:ASP:OD2	2.41	0.52
1:I:412:VAL:O	1:I:416:ARG:HG2	2.09	0.52
1:A:117:ASP:C	1:A:117:ASP:OD1	2.46	0.52
1:A:656:ASP:C	1:A:656:ASP:OD1	2.48	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:61:LEU:HD12	1:D:88:TRP:O	2.10	0.52
1:D:234:ARG:O	1:D:237:TYR:HB3	2.09	0.52
1:F:29:LEU:HD22	1:F:283:VAL:HG23	1.92	0.52
1:F:107:ILE:HG21	1:F:205:ARG:NH2	2.23	0.52
1:F:228:GLU:OE1	1:F:230:GLN:CD	2.47	0.52
1:F:334:ARG:NH2	1:F:376:ARG:HH12	2.07	0.52
1:F:434:MET:O	1:F:438:ARG:HG3	2.10	0.52
1:F:488:ARG:NH1	1:F:518:VAL:HG11	2.20	0.52
1:F:497:LEU:HD21	1:F:501:ARG:CZ	2.39	0.52
3:L:11:DA:C6	3:L:12:DG:N7	2.78	0.52
1:I:392:ARG:HH11	1:I:546:SER:HB2	1.74	0.52
2:K:1:DG:C4	2:K:2:DC:C4	2.99	0.52
1:A:35:GLY:N	4:A:1662:ANP:HNB1	2.04	0.51
1:A:132:ILE:CG1	1:A:183:ARG:HE	2.23	0.51
1:A:259:SER:N	1:A:609:ARG:HD3	2.25	0.51
1:A:473:ALA:O	1:A:477:ALA:N	2.40	0.51
1:D:252:VAL:HG23	1:D:252:VAL:O	2.08	0.51
1:D:500:LEU:O	1:D:504:GLY:CA	2.58	0.51
1:I:152:LYS:HZ1	1:I:198:ASP:CG	2.14	0.51
1:F:210:VAL:HG11	1:F:213:VAL:HG23	1.92	0.51
1:F:656:ASP:OD1	1:F:658:TYR:N	2.42	0.51
1:I:264[A]:ARG:NH1	1:I:264[A]:ARG:HB3	2.25	0.51
2:K:19:DT:C4'	2:K:20:DT:C5'	2.86	0.51
1:A:267:ASP:O	1:A:268:ILE:C	2.48	0.51
1:A:421:PRO:HA	1:A:499:LEU:CD1	2.33	0.51
1:F:302:LYS:O	1:F:305:GLU:HG2	2.09	0.51
1:F:506:GLU:O	1:F:509:VAL:HG12	2.10	0.51
1:I:175:ASP:OD1	1:I:176:ALA:N	2.43	0.51
1:A:30:VAL:HG23	1:A:251:LEU:HD11	1.92	0.51
1:A:34:ALA:HB1	1:A:616:THR:HG21	1.83	0.51
1:D:225:HIS:HA	1:D:251:LEU:O	2.10	0.51
1:F:35:GLY:N	4:F:1663:ANP:N3B	2.55	0.51
2:K:6:DG:H2''	2:K:7:DC:C5'	2.40	0.51
3:Y:11:DA:C6	3:Y:12:DG:C6	2.98	0.51
1:A:230:GLN:O	1:A:271:ILE:HG21	2.11	0.51
1:A:232:THR:CG2	1:A:271:ILE:HG22	2.39	0.51
1:D:92:PHE:HB3	1:D:200:ILE:HD11	1.93	0.51
1:D:291:ARG:HG3	1:D:577:GLU:OE1	2.10	0.51
1:F:97:VAL:HB	1:F:199:LEU:HD13	1.91	0.51
1:I:330:ALA:O	1:I:628:GLN:N	2.40	0.51
2:X:19:DT:C2'	2:X:20:DT:OP2	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:GLY:O	1:A:38:LYS:C	2.48	0.51
1:D:248:ARG:NH2	1:D:280:ASP:OD1	2.43	0.51
1:F:13:LEU:HD22	1:F:17:GLN:HB3	1.93	0.51
1:F:65:PHE:C	1:F:66:THR:HG23	2.28	0.51
1:F:257:ASP:O	1:F:609:ARG:CG	2.58	0.51
1:D:401:TYR:OH	1:D:423:ARG:NH2	2.44	0.51
1:D:577:GLU:OE1	1:D:619:MET:HE2	2.11	0.51
2:X:15:DT:C5'	2:X:15:DT:C6	2.93	0.51
1:A:310:ARG:HG3	1:A:311:LEU:O	2.10	0.51
1:F:397:ASP:O	1:F:400:ALA:HB3	2.11	0.51
1:F:592:PRO:O	1:F:596:ALA:HB3	2.11	0.51
1:A:63:VAL:HG22	1:A:226:VAL:HG22	1.93	0.51
1:D:577:GLU:CD	1:D:619:MET:HE3	2.30	0.51
1:F:363:THR:HG22	1:F:365:ALA:HB3	1.93	0.51
1:I:9:LEU:HD11	1:I:48:HIS:ND1	2.26	0.51
1:A:577:GLU:CD	1:A:619:MET:CE	2.80	0.51
1:F:329:ARG:HA	1:F:626:ALA:O	2.11	0.51
1:A:204:VAL:HG22	1:A:239:LEU:HD12	1.92	0.50
1:A:231:ASP:CB	1:A:261:TYR:HB2	2.39	0.50
1:D:93:HIS:CE1	3:Y:23:DT:O2	2.64	0.50
1:F:510:ARG:O	1:F:514:LEU:HD13	2.10	0.50
1:I:125:ILE:O	1:I:129:MET:HG3	2.10	0.50
1:I:294:ALA:HB3	1:I:321:ALA:CA	2.33	0.50
2:X:2:DC:N4	3:Y:17:DG:C6	2.79	0.50
1:A:7:PRO:HB3	1:A:80:LEU:HD22	1.93	0.50
1:A:61:LEU:HD12	1:A:88:TRP:O	2.12	0.50
1:A:267:ASP:HB3	1:A:270:ASN:H	1.75	0.50
1:A:588:GLN:OE1	1:A:592:PRO:HG2	2.12	0.50
1:D:16:THR:HG22	6:D:2001:HOH:O	2.12	0.50
1:D:396:ARG:C	6:D:2020:HOH:O	2.50	0.50
1:D:513:ASN:HA	1:D:516:GLU:HB3	1.92	0.50
1:F:310:ARG:HG3	1:F:311:LEU:O	2.11	0.50
3:Y:11:DA:C5	3:Y:12:DG:N7	2.79	0.50
1:A:424:GLY:C	1:A:463:LYS:CD	2.79	0.50
1:A:426:GLY:HA3	2:X:8:DT:P	2.52	0.50
1:D:437:ALA:HA	1:D:442:THR:CG2	2.39	0.50
1:F:545:LEU:CD1	1:F:551:MET:HB2	2.41	0.50
1:D:160:ASP:HA	1:D:163:ARG:HG3	1.94	0.50
1:F:511:LEU:O	1:F:515:GLU:N	2.44	0.50
1:F:587:GLU:HG2	1:F:626:ALA:HB1	1.94	0.50
1:I:91:THR:HG22	1:I:92:PHE:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:430:LEU:O	1:I:434:MET:HG3	2.11	0.50
2:K:19:DT:C3'	2:K:20:DT:H5''	2.37	0.50
1:A:194:ILE:O	1:A:195:ASP:O	2.30	0.50
1:A:507:GLY:O	1:A:510:ARG:HB2	2.12	0.50
1:D:167:PRO:HA	1:D:174:ARG:CG	2.41	0.50
1:D:477:ALA:HB1	1:D:481:TYR:HD2	1.77	0.50
1:A:377:VAL:O	1:A:378:GLN:CB	2.60	0.50
1:D:325:VAL:HG23	1:D:652:PHE:HB3	1.93	0.50
1:F:101:ARG:HB2	1:F:113:PHE:HZ	1.75	0.50
1:F:545:LEU:HD21	1:F:551:MET:CG	2.34	0.50
1:I:655:VAL:CG1	1:I:656:ASP:N	2.74	0.50
2:X:1:DG:C4	2:X:2:DC:C5	2.99	0.50
2:X:4:DG:H2'	2:X:4:DG:O5'	2.11	0.50
1:D:297:LEU:HD22	1:D:315:LEU:HD23	1.93	0.50
1:F:157:THR:O	1:F:160:ASP:OD1	2.29	0.50
1:I:325:VAL:CG2	1:I:652:PHE:HB3	2.42	0.50
1:A:60:ILE:HG23	1:A:223:PHE:O	2.12	0.50
1:A:234:ARG:HG2	1:A:270:ASN:ND2	2.25	0.50
1:F:231:ASP:HB3	1:F:261:TYR:HB2	1.93	0.50
1:I:117:ASP:C	1:I:117:ASP:OD1	2.49	0.50
1:I:455:ASN:O	1:I:456:ILE:HD12	2.12	0.50
3:L:9:DC:H2'	3:L:10:DG:C8	2.46	0.50
1:D:90:SER:HB2	1:D:94:SER:HB3	1.94	0.50
2:K:4:DG:O6	3:L:15:DC:N3	2.44	0.50
1:A:424:GLY:C	2:X:9:DC:OP1	2.50	0.49
1:D:514:LEU:O	1:D:518:VAL:HG23	2.12	0.49
1:F:377:VAL:O	1:F:378:GLN:HB2	2.12	0.49
3:Y:14:DA:OP2	3:Y:14:DA:O4'	2.30	0.49
3:Y:19:DT:H2''	3:Y:20:DT:O5'	2.12	0.49
1:A:267:ASP:HB3	1:A:270:ASN:CG	2.33	0.49
1:D:577:GLU:HB2	1:D:619:MET:HE2	1.94	0.49
1:I:31:ILE:CG2	1:I:313:LYS:CD	2.88	0.49
2:K:15:DT:C5'	2:K:15:DT:H6	2.25	0.49
3:Y:3:DG:C2'	3:Y:3:DG:O5'	2.60	0.49
1:D:485:ALA:HA	1:D:488:ARG:HD2	1.93	0.49
1:F:334:ARG:CZ	1:F:376:ARG:HH12	2.25	0.49
1:I:14:ASN:OD1	1:I:15:PRO:CD	2.53	0.49
2:X:17:DG:H4'	2:X:18:DT:O5'	2.11	0.49
1:A:27:PRO:O	1:A:281:ALA:HA	2.12	0.49
1:D:171:GLY:O	1:D:172:LEU:CG	2.60	0.49
1:F:152:LYS:NZ	1:F:198:ASP:CG	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:LYS:HZ3	1:F:198:ASP:CG	2.16	0.49
1:F:195:ASP:O	1:F:198:ASP:HB2	2.11	0.49
1:F:388:GLY:HA2	1:F:556:GLU:OE2	2.13	0.49
1:I:50:ILE:HD13	1:I:81:VAL:HG11	1.92	0.49
1:I:336:GLU:O	1:I:339:TYR:HB3	2.12	0.49
1:I:600:GLY:O	1:I:604:ILE:HG12	2.13	0.49
1:I:655:VAL:HG13	1:I:660:GLN:O	2.13	0.49
3:Y:13:DC:H2''	3:Y:14:DA:OP2	2.11	0.49
1:D:491:MET:O	1:D:497:LEU:HD22	2.12	0.49
1:F:256:PRO:HG2	1:F:311:LEU:HD22	1.95	0.49
1:I:56:HIS:CE1	1:I:57:PRO:HD2	2.47	0.49
2:X:11:DC:N4	3:Y:8:DG:N1	2.37	0.49
1:A:24:PHE:CD2	1:A:25:THR:CG2	2.90	0.49
1:D:152:LYS:NZ	1:D:195:ASP:OD2	2.45	0.49
1:F:499:LEU:HD22	6:F:2021:HOH:O	2.11	0.49
2:K:19:DT:OP1	2:K:19:DT:O4'	2.30	0.49
1:A:195:ASP:OD2	1:A:198:ASP:OD1	2.30	0.49
1:A:346:ARG:O	1:A:349:GLY:N	2.45	0.49
1:A:482:GLU:O	1:A:486:PHE:CB	2.61	0.49
1:A:576:LEU:O	1:A:617:ARG:NH2	2.45	0.49
1:D:634:GLY:O	1:D:635:LYS:CG	2.45	0.49
1:F:524:TRP:CZ3	1:F:541:ASP:OD2	2.65	0.49
1:F:592:PRO:HA	1:F:607:GLU:CB	2.42	0.49
2:X:17:DG:N2	3:Y:3:DG:N2	2.60	0.49
1:A:631:MET:HA	1:A:636:THR:HA	1.93	0.49
1:F:383:ILE:CG2	1:F:384:VAL:N	2.75	0.49
3:L:19:DT:O2	3:L:19:DT:C2'	2.43	0.49
1:A:183:ARG:HA	1:A:186:VAL:HG22	1.95	0.49
1:A:232:THR:H	1:A:266:ALA:HB1	1.78	0.49
1:D:339:TYR:O	1:D:343:TRP:HD1	1.95	0.49
1:F:371:GLU:OE2	1:F:383:ILE:HD11	2.13	0.49
1:I:121:GLN:O	1:I:125:ILE:HD12	2.12	0.49
1:I:593:SER:CB	3:L:19:DT:H73	2.43	0.49
2:X:1:DG:H1	3:Y:18:DC:H42	0.80	0.49
1:A:45:ARG:NH1	1:A:251:LEU:HB3	2.28	0.49
1:A:229:TYR:O	1:A:271:ILE:CG2	2.61	0.49
1:A:343:TRP:O	1:A:347:LEU:HD23	2.12	0.49
1:D:47:ALA:CB	1:D:80:LEU:CD1	2.91	0.49
1:F:404:LEU:HD23	1:F:471:MET:HE2	1.94	0.49
1:F:425:ILE:N	2:K:9:DC:OP1	2.46	0.49
1:F:504:GLY:HA2	1:F:507:GLY:HA3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:47:ALA:HB2	1:I:80:LEU:HD12	1.92	0.49
1:A:42:LEU:O	1:A:46:ILE:CD1	2.60	0.48
1:D:332:ASP:CG	1:D:334:ARG:HB3	2.32	0.48
1:F:23:HIS:HB2	1:F:284:TYR:OH	2.13	0.48
1:F:92:PHE:O	1:F:96:GLY:N	2.27	0.48
2:K:3:DA:OP2	2:K:3:DA:H8	1.96	0.48
2:X:19:DT:H2''	2:X:20:DT:C5'	2.43	0.48
2:K:11:DC:N3	3:L:8:DG:N2	2.52	0.48
3:L:14:DA:OP2	3:L:14:DA:O4'	2.30	0.48
3:Y:21:DT:C2'	3:Y:22:DT:C6	2.96	0.48
1:I:167:PRO:HA	1:I:174:ARG:HB3	1.95	0.48
1:I:174:ARG:CG	1:I:175:ASP:N	2.37	0.48
1:A:66:THR:CG2	1:A:548:VAL:HG22	2.40	0.48
1:A:90:SER:OG	1:A:95:ALA:HB2	2.13	0.48
1:A:195:ASP:N	1:A:198:ASP:OD2	2.46	0.48
1:A:303:LEU:HD11	1:A:611:PHE:HD2	1.78	0.48
1:A:587:GLU:HG2	1:A:626:ALA:HB1	1.96	0.48
1:A:592:PRO:O	1:A:593:SER:CB	2.61	0.48
1:D:325:VAL:HG23	1:D:652:PHE:HB2	1.95	0.48
1:D:655:VAL:HG13	1:D:660:GLN:H	1.78	0.48
1:F:96:GLY:O	1:F:203:THR:OG1	2.31	0.48
1:A:426:GLY:HA2	2:X:8:DT:O5'	2.13	0.48
1:D:132:ILE:N	1:D:132:ILE:CD1	2.75	0.48
1:D:302:LYS:HD2	1:D:651:LEU:CD1	2.43	0.48
1:D:504:GLY:HA2	1:D:508:GLN:H	1.78	0.48
1:F:377:VAL:C	1:F:378:GLN:CG	2.82	0.48
1:F:587:GLU:CD	1:F:630:ARG:HE	2.16	0.48
1:I:513:ASN:HA	1:I:516:GLU:CB	2.44	0.48
2:K:1:DG:H2'	2:K:2:DC:C6	2.49	0.48
1:A:198:ASP:O	1:A:199:LEU:C	2.51	0.48
1:A:482:GLU:O	1:A:486:PHE:N	2.46	0.48
1:D:460:GLY:C	1:D:462:HIS:N	2.67	0.48
1:D:546:SER:O	1:D:547:SER:CB	2.62	0.48
1:F:408:PRO:HA	1:F:445:LEU:HD12	1.96	0.48
1:F:577:GLU:HG3	1:F:619:MET:HE1	1.93	0.48
3:Y:22:DT:OP1	3:Y:22:DT:O4'	2.30	0.48
1:A:33:GLY:HA2	1:A:313:LYS:HE2	1.96	0.48
1:A:343:TRP:O	1:A:347:LEU:CD2	2.62	0.48
1:D:384:VAL:HG12	1:D:572:ASN:ND2	2.29	0.48
1:F:66:THR:CG2	1:F:548:VAL:HG22	2.43	0.48
1:F:302:LYS:HD2	1:F:651:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:91:THR:HB	1:I:94:SER:H	1.78	0.48
3:Y:17:DG:C5	3:Y:18:DC:N4	2.81	0.48
1:A:44:TYR:CE1	1:A:80:LEU:HD21	2.49	0.48
1:A:198:ASP:C	1:A:200:ILE:N	2.67	0.48
1:D:400:ALA:CB	1:D:417:ILE:HG23	2.44	0.48
1:I:139:THR:HG23	1:I:140:GLN:H	1.78	0.48
1:I:332:ASP:HB3	1:I:335:ALA:CB	2.43	0.48
2:X:3:DA:H61	3:Y:16:DT:H3	1.62	0.48
1:D:287:GLU:HB3	1:D:316:LYS:HG2	1.95	0.48
1:F:125:ILE:O	1:F:129:MET:HB2	2.13	0.48
1:F:343:TRP:O	1:F:347:LEU:CD2	2.62	0.48
3:L:11:DA:N3	3:L:12:DG:C8	2.82	0.48
1:A:27:PRO:HA	1:A:250:LEU:O	2.14	0.48
1:A:607:GLU:OE1	1:A:607:GLU:HA	2.13	0.48
1:D:139:THR:HG23	1:D:140:GLN:H	1.78	0.48
1:F:46:ILE:HD12	1:F:46:ILE:H	1.79	0.48
1:F:257:ASP:HB3	1:F:304:ILE:HD13	1.96	0.48
1:I:21:ALA:HA	1:I:45:ARG:HB2	1.96	0.48
1:A:90:SER:HB2	1:A:94:SER:HB2	1.96	0.47
1:A:295:ARG:HG3	1:A:322:GLY:H	1.79	0.47
1:F:297:LEU:HD11	1:F:315:LEU:HD13	1.96	0.47
1:F:334:ARG:HH22	1:F:376:ARG:HH12	1.60	0.47
1:I:238:GLU:OE1	1:I:238:GLU:HA	2.13	0.47
2:X:12:DA:H2''	2:X:13:DG:C5'	2.39	0.47
2:X:19:DT:H4'	2:X:20:DT:C5'	2.44	0.47
1:A:63:VAL:HA	1:A:90:SER:O	2.14	0.47
1:A:121:GLN:C	1:A:125:ILE:HD12	2.34	0.47
1:D:117:ASP:O	1:D:121:GLN:HG3	2.13	0.47
1:D:302:LYS:HD2	1:D:651:LEU:HD11	1.96	0.47
1:F:403:ARG:HG3	1:F:404:LEU:N	2.29	0.47
1:I:32:ALA:HB1	1:I:36:SER:OG	2.15	0.47
1:I:50:ILE:HD13	1:I:81:VAL:CG1	2.44	0.47
1:I:504:GLY:HA2	1:I:508:GLN:H	1.79	0.47
1:A:655:VAL:CG1	1:A:659:GLY:HA2	2.40	0.47
1:D:285:MET:C	1:D:286:LEU:HD12	2.34	0.47
1:D:307:ASN:HB2	1:D:310[A]:ARG:HH21	1.79	0.47
1:D:414:LEU:HD23	1:D:414:LEU:C	2.35	0.47
1:D:421:PRO:HG3	1:D:495:GLY:O	2.13	0.47
1:F:60:ILE:HG23	1:F:223:PHE:O	2.14	0.47
1:I:172:LEU:CD1	1:I:177:ALA:N	2.77	0.47
1:A:65:PHE:C	1:A:66:THR:HG23	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:GLY:C	1:A:463:LYS:HD2	2.34	0.47
1:D:139:THR:HG23	1:D:140:GLN:N	2.30	0.47
1:I:255:ASP:C	1:I:255:ASP:OD1	2.53	0.47
2:X:19:DT:O2	2:X:19:DT:H2'	2.15	0.47
1:A:257:ASP:OD2	1:A:310:ARG:NH1	2.48	0.47
1:I:152:LYS:NZ	1:I:198:ASP:CG	2.67	0.47
1:I:222:LYS:O	1:I:249:ASN:HB2	2.14	0.47
1:A:487:LEU:O	1:A:490:VAL:HG22	2.14	0.47
1:D:361:TYR:O	1:D:569:THR:HA	2.15	0.47
1:F:42:LEU:O	1:F:46:ILE:CD1	2.59	0.47
1:F:210:VAL:CG1	1:F:213:VAL:HG23	2.44	0.47
1:F:226:VAL:CG1	1:F:252:VAL:HG12	2.45	0.47
1:F:631:MET:HA	1:F:636:THR:HA	1.96	0.47
1:I:139:THR:HG23	1:I:140:GLN:N	2.30	0.47
1:A:144:ILE:O	1:A:148:ILE:HG13	2.13	0.47
1:A:210:VAL:HG11	1:A:213:VAL:HG23	1.97	0.47
1:A:591:LEU:HB3	1:A:592:PRO:HD2	1.93	0.47
1:D:356:GLU:HG2	1:D:579:PRO:HG2	1.96	0.47
1:D:362:ARG:HH22	3:Y:19:DT:H73	1.80	0.47
1:D:441:HIS:N	1:D:441:HIS:CD2	2.82	0.47
1:D:660:GLN:HA	1:D:661:PRO:HD2	1.52	0.47
1:F:70:ALA:HB1	1:F:89:MET:HB3	1.97	0.47
1:F:238:GLU:O	1:F:239:LEU:C	2.53	0.47
1:F:362:ARG:CZ	2:K:21:DT:O2	2.62	0.47
1:I:185:GLU:O	1:I:189:LYS:HG3	2.15	0.47
1:I:223:PHE:CE1	1:I:249:ASN:ND2	2.82	0.47
1:I:371:GLU:OE2	1:I:375:ARG:NH2	2.48	0.47
1:I:508:GLN:O	1:I:511:LEU:HG	2.15	0.47
1:I:591:LEU:HD23	1:I:591:LEU:O	2.15	0.47
2:K:8:DT:H2''	2:K:9:DC:C1'	2.45	0.47
2:K:19:DT:C3'	2:K:20:DT:C5'	2.92	0.47
1:A:162:ASP:O	1:A:174:ARG:HD2	2.14	0.47
1:I:246:ARG:HD2	1:I:247:ASP:OD1	2.14	0.47
1:I:660:GLN:OE1	1:I:660:GLN:HA	2.12	0.47
2:X:19:DT:H2''	2:X:20:DT:H5'	1.96	0.47
1:A:198:ASP:O	1:A:201:THR:N	2.48	0.47
1:A:208:LYS:HG3	1:A:242:LEU:HD21	1.97	0.47
1:F:29:LEU:HD23	1:F:29:LEU:C	2.34	0.47
1:F:263:PHE:C	1:F:263:PHE:CD1	2.88	0.47
1:F:393:ARG:NH2	1:F:416:ARG:HB3	2.30	0.47
1:F:576:LEU:N	1:F:617:ARG:HH21	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:336:GLU:HG3	1:I:337:GLY:N	2.30	0.47
3:L:6:DC:C2'	3:L:7:DT:O5'	2.41	0.47
1:A:411:ASP:HA	1:A:444:VAL:HG11	1.95	0.47
1:D:400:ALA:HB3	1:D:417:ILE:CG2	2.45	0.47
1:D:416:ARG:HB3	6:D:2022:HOH:O	2.14	0.47
1:F:132:ILE:HD11	1:F:183:ARG:NE	2.29	0.47
1:I:107:ILE:HB	1:I:205:ARG:HH22	1.80	0.47
1:I:392:ARG:NH1	1:I:546:SER:CB	2.78	0.47
2:X:12:DA:C6	2:X:13:DG:C6	3.03	0.47
1:A:132:ILE:HG13	1:A:183:ARG:HE	1.80	0.46
1:A:240:THR:OG1	1:A:241:ARG:N	2.48	0.46
1:D:331:THR:HA	1:D:628:GLN:CG	2.45	0.46
1:I:58:GLY:O	1:I:220:LYS:HA	2.15	0.46
1:I:415:ARG:O	1:I:416:ARG:NH1	2.48	0.46
2:K:12:DA:C2'	2:K:13:DG:C8	2.98	0.46
1:A:27:PRO:HG2	1:A:280:ASP:HB2	1.97	0.46
1:A:97:VAL:CG1	1:A:98:ARG:N	2.79	0.46
1:A:229:TYR:O	1:A:230:GLN:C	2.54	0.46
1:A:356:GLU:HB3	1:A:579:PRO:HG2	1.96	0.46
1:D:132:ILE:HD11	1:D:183:ARG:CD	2.46	0.46
1:F:395:ILE:HD12	1:F:517:LEU:HB2	1.97	0.46
1:F:404:LEU:HD12	1:F:407:ASN:O	2.15	0.46
1:F:586:VAL:HG13	1:F:591:LEU:CD2	2.37	0.46
1:I:294:ALA:O	1:I:298:GLU:HG3	2.15	0.46
1:I:374:LEU:HB3	1:I:379:ILE:HB	1.97	0.46
1:A:227:ASP:O	1:A:228:GLU:C	2.54	0.46
1:F:388:GLY:O	1:F:391:ASP:HB2	2.15	0.46
1:F:545:LEU:CD2	1:F:551:MET:HB2	2.45	0.46
1:F:611:PHE:HE1	1:F:615:ILE:HD11	1.75	0.46
1:I:8:ASP:HB3	1:I:11:GLN:HB2	1.97	0.46
3:L:1:DA:C1'	3:L:2:DC:O5'	2.63	0.46
1:A:97:VAL:HG11	1:A:544:LEU:HD11	1.98	0.46
1:D:477:ALA:HB1	1:D:481:TYR:CD2	2.49	0.46
1:F:200:ILE:HG21	1:F:235:ALA:CB	2.46	0.46
1:F:421:PRO:HA	1:F:499:LEU:CD1	2.44	0.46
1:F:545:LEU:CD2	1:F:551:MET:HG3	2.36	0.46
1:I:111:ARG:HG2	1:I:112:GLY:N	2.30	0.46
1:I:325:VAL:HG23	1:I:652:PHE:CB	2.46	0.46
2:K:12:DA:C5	2:K:13:DG:C6	3.04	0.46
3:Y:22:DT:C7	3:Y:23:DT:H73	2.45	0.46
1:D:114:VAL:HG21	1:D:403:ARG:HH21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:173:PRO:HG2	1:D:176:ALA:HB3	1.96	0.46
1:D:640:GLU:OE1	1:D:640:GLU:HA	2.14	0.46
1:F:614:GLY:O	1:F:617:ARG:HG2	2.16	0.46
1:A:157:THR:OG1	1:A:158:PRO:HD2	2.15	0.46
1:A:338:ASP:CG	1:A:376:ARG:HH22	2.18	0.46
1:D:222:LYS:O	1:D:249:ASN:HB2	2.16	0.46
1:D:506:GLU:C	1:D:506:GLU:CD	2.74	0.46
1:I:261:TYR:O	1:I:264[A]:ARG:HB2	2.15	0.46
3:L:18:DC:H2''	3:L:19:DT:OP1	2.01	0.46
1:A:538:PHE:CD1	1:A:538:PHE:C	2.89	0.46
1:D:152:LYS:NZ	1:D:198:ASP:OD1	2.48	0.46
1:D:384:VAL:HG12	1:D:572:ASN:HD21	1.80	0.46
1:I:591:LEU:HB3	1:I:592:PRO:CD	2.45	0.46
1:A:66:THR:O	1:A:69:ALA:HB3	2.15	0.46
1:A:114:VAL:CG2	1:A:115:ILE:N	2.79	0.46
1:A:426:GLY:CA	2:X:8:DT:P	3.04	0.46
1:F:29:LEU:HD12	1:F:274:PHE:HD2	1.81	0.46
1:I:362:ARG:NH1	1:I:607:GLU:OE2	2.47	0.46
1:I:458:ASP:C	1:I:458:ASP:OD1	2.54	0.46
3:L:11:DA:C2	3:L:12:DG:C5	3.03	0.46
1:D:524:TRP:CZ3	1:D:541:ASP:OD2	2.69	0.46
1:F:100:LEU:HD21	1:F:202:GLU:C	2.35	0.46
2:K:1:DG:N9	2:K:2:DC:C5	2.84	0.46
1:A:259:SER:H	1:A:609:ARG:HD3	1.81	0.46
1:F:36:SER:HA	1:F:288:HIS:O	2.16	0.46
1:D:633:PHE:HB3	2:X:1:DG:N1	2.31	0.45
1:D:656:ASP:OD2	1:I:44:TYR:OH	2.28	0.45
1:F:101:ARG:HH22	1:F:536:ALA:CB	2.26	0.45
1:F:634:GLY:CA	3:L:1:DA:H5'	2.39	0.45
1:I:287:GLU:HG2	1:I:314:THR:H	1.81	0.45
3:Y:19:DT:O2	3:Y:19:DT:C2'	2.56	0.45
1:A:228:GLU:OE1	1:A:230:GLN:CD	2.54	0.45
1:F:56:HIS:O	1:F:59:GLU:HB2	2.16	0.45
1:F:223:PHE:CD2	1:F:249:ASN:HB3	2.51	0.45
1:I:286:LEU:N	1:I:286:LEU:CD1	2.79	0.45
3:Y:17:DG:H1'	3:Y:18:DC:C5	2.51	0.45
1:A:207:PHE:O	1:A:214:LEU:HD23	2.16	0.45
1:D:117:ASP:C	1:D:117:ASP:OD1	2.55	0.45
1:D:301:ASN:HD21	1:D:315:LEU:HB2	1.80	0.45
1:F:29:LEU:HD12	1:F:274:PHE:CD2	2.50	0.45
1:F:191:GLN:HG3	1:F:409:ALA:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:422:ARG:CD	2:K:9:DC:H3'	2.40	0.45
1:I:161:LEU:C	1:I:161:LEU:HD23	2.37	0.45
1:A:46:ILE:HD12	1:A:46:ILE:H	1.81	0.45
1:A:210:VAL:CG1	1:A:213:VAL:HG23	2.46	0.45
1:D:114:VAL:CG1	1:D:193:ALA:HB2	2.40	0.45
1:F:215:ASP:HA	1:F:218:GLN:OE1	2.17	0.45
1:F:617:ARG:HD2	1:F:617:ARG:N	2.31	0.45
1:I:92:PHE:CD2	1:I:236:GLN:NE2	2.85	0.45
1:I:441:HIS:CD2	6:I:2034:HOH:O	2.55	0.45
3:Y:14:DA:OP2	3:Y:14:DA:C4'	2.65	0.45
1:A:500:LEU:HD22	1:A:511:LEU:HD23	1.98	0.45
1:D:280:ASP:OD1	1:D:280:ASP:N	2.49	0.45
1:D:454:GLN:C	1:D:455:ASN:OD1	2.55	0.45
1:D:591:LEU:CB	1:D:592:PRO:CD	2.92	0.45
1:F:542:ALA:HA	1:F:545:LEU:HG	1.97	0.45
1:F:576:LEU:O	1:F:617:ARG:NH2	2.50	0.45
1:F:635:LYS:HB3	1:F:635:LYS:HZ3	1.82	0.45
1:I:151:ALA:HA	1:I:156:TRP:HE3	1.81	0.45
1:I:252:VAL:O	1:I:252:VAL:CG2	2.64	0.45
1:I:359:ILE:CD1	1:I:565:VAL:HG11	2.46	0.45
3:L:12:DG:C2	3:L:13:DC:C4	3.05	0.45
1:A:249:ASN:HD22	1:A:249:ASN:HA	1.59	0.45
1:A:413:ALA:O	1:A:417:ILE:HG13	2.16	0.45
1:A:488:ARG:HH11	1:A:518:VAL:HG11	1.82	0.45
1:D:9:LEU:HD23	1:D:18:ALA:O	2.16	0.45
1:D:497:LEU:HG	1:D:498:ASP:OD1	2.16	0.45
1:D:500:LEU:O	1:D:504:GLY:HA3	2.17	0.45
1:D:592:PRO:HG3	1:D:644:PHE:CD2	2.51	0.45
1:F:308:THR:O	1:F:309:GLU:HB2	2.16	0.45
1:F:631:MET:HB2	1:F:636:THR:HG23	1.97	0.45
1:I:129:MET:HA	1:I:132:ILE:HG12	1.98	0.45
1:I:263:PHE:C	1:I:265:GLY:H	2.18	0.45
1:I:339:TYR:O	1:I:343:TRP:HD1	2.00	0.45
1:I:579:PRO:HA	1:I:619:MET:HB2	1.97	0.45
1:I:584:VAL:HA	1:I:625:THR:HB	1.97	0.45
1:A:151:ALA:HB1	1:A:156:TRP:HB2	1.99	0.45
1:F:272:LEU:O	1:F:275:GLN:HG3	2.16	0.45
2:K:13:DG:H1	3:L:6:DC:N4	2.14	0.45
1:A:115:ILE:HD12	1:A:540:ASP:OD1	2.16	0.45
1:A:231:ASP:CG	1:A:261:TYR:HB2	2.37	0.45
1:A:325:VAL:HG13	1:A:622:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:PRO:HA	1:A:486:PHE:HB3	1.99	0.45
1:A:577:GLU:CD	1:A:619:MET:HE2	2.37	0.45
1:D:59:GLU:HB3	1:D:222:LYS:HB3	1.99	0.45
1:F:32:ALA:HB3	1:F:38:LYS:HD2	1.99	0.45
1:F:633:PHE:CE1	2:K:18:DT:C2	3.04	0.45
1:F:656:ASP:CB	1:F:657:PRO:CD	2.95	0.45
1:I:330:ALA:HB1	1:I:335:ALA:HB3	1.99	0.45
1:A:228:GLU:OE1	1:A:230:GLN:OE1	2.34	0.45
1:D:61:LEU:HD13	1:D:88:TRP:CD2	2.52	0.45
1:D:132:ILE:CD1	1:D:183:ARG:CZ	2.95	0.45
1:F:30:VAL:HB	1:F:253:VAL:HG12	1.98	0.45
1:F:101:ARG:NH2	1:F:537:ASP:OD1	2.49	0.45
1:F:191:GLN:NE2	1:F:411:ASP:OD1	2.50	0.45
1:F:424:GLY:C	2:K:9:DC:OP1	2.55	0.45
1:F:592:PRO:HG3	1:F:644:PHE:CE2	2.52	0.45
1:I:577:GLU:CD	1:I:619:MET:HE3	2.38	0.45
2:K:6:DG:H2''	2:K:7:DC:O4'	2.16	0.45
1:D:295:ARG:HG2	1:D:321:ALA:HB1	1.99	0.45
1:D:392:ARG:HH11	1:D:546:SER:HB2	1.82	0.45
1:D:430:LEU:O	1:D:434:MET:HG3	2.17	0.45
1:F:257:ASP:O	1:F:609:ARG:HG2	2.17	0.45
1:I:47:ALA:CB	1:I:80:LEU:HD11	2.46	0.45
1:I:361:TYR:OH	1:I:567:LEU:HB3	2.17	0.45
1:D:138:GLU:O	1:D:139:THR:HG22	2.17	0.44
1:D:577:GLU:CD	1:D:619:MET:HE2	2.36	0.44
1:F:35:GLY:H	4:F:1663:ANP:PB	2.41	0.44
1:F:107:ILE:CG2	1:F:107:ILE:O	2.64	0.44
1:F:632:GLN:OE1	1:F:633:PHE:HE2	2.00	0.44
1:I:318:VAL:O	1:I:318:VAL:CG1	2.65	0.44
3:L:8:DG:H2''	3:L:9:DC:O4'	2.16	0.44
1:A:45:ARG:HD3	1:A:225:HIS:CE1	2.52	0.44
1:A:301:ASN:HD21	1:A:315:LEU:HB2	1.82	0.44
1:A:411:ASP:OD1	1:A:412:VAL:N	2.50	0.44
1:A:444:VAL:HG13	1:A:445:LEU:N	2.31	0.44
1:D:60:ILE:HB	1:D:87:LEU:CD2	2.47	0.44
1:D:114:VAL:CG2	1:D:115:ILE:N	2.80	0.44
1:F:576:LEU:H	1:F:617:ARG:HH21	1.66	0.44
1:I:594:LYS:O	1:I:597:ILE:HB	2.17	0.44
3:Y:11:DA:C2	3:Y:12:DG:C4	3.05	0.44
1:A:45:ARG:HH11	1:A:251:LEU:HB3	1.83	0.44
1:A:303:LEU:HD11	1:A:611:PHE:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:ILE:HD12	1:A:383:ILE:N	2.33	0.44
1:A:418:ILE:HD13	1:A:467:PHE:CD2	2.52	0.44
1:D:91:THR:HG22	1:D:92:PHE:N	2.33	0.44
1:D:116:TYR:HE2	1:D:124:ILE:HD11	1.80	0.44
1:D:246:ARG:HD3	1:D:247:ASP:OD1	2.17	0.44
1:D:428:THR:HG1	3:Y:8:DG:P	2.37	0.44
1:D:655:VAL:HG12	1:D:656:ASP:N	2.31	0.44
1:F:25:THR:CG2	1:F:26:GLY:N	2.80	0.44
1:F:257:ASP:O	1:F:609:ARG:HG3	2.17	0.44
1:F:291:ARG:HH22	4:F:1663:ANP:HNB1	1.65	0.44
1:I:111:ARG:HA	1:I:112:GLY:HA2	1.64	0.44
1:I:336:GLU:OE1	1:I:625:THR:HG21	2.17	0.44
2:K:9:DC:C2	2:K:10:DG:C8	3.05	0.44
1:A:26:GLY:CA	1:A:248:ARG:O	2.60	0.44
1:D:269:GLN:NE2	1:D:273:ASP:OD2	2.50	0.44
1:F:124:ILE:O	1:F:128:VAL:HG22	2.17	0.44
1:F:132:ILE:HD11	1:F:183:ARG:HH21	1.83	0.44
1:F:287:GLU:OE2	1:F:288:HIS:CD2	2.70	0.44
1:F:546:SER:HB3	2:K:23:DT:OP1	2.17	0.44
1:F:586:VAL:HG11	1:F:645:LEU:HD21	2.00	0.44
1:I:138:GLU:O	1:I:139:THR:HG22	2.18	0.44
1:I:345:THR:HG23	1:I:379:ILE:HD11	1.98	0.44
2:X:19:DT:C2'	2:X:20:DT:H5'	2.48	0.44
1:F:70:ALA:O	1:F:73:MET:HB2	2.17	0.44
1:F:255:ASP:OD1	1:F:256:PRO:HD2	2.17	0.44
1:F:588:GLN:HE21	1:F:597:ILE:CD1	2.29	0.44
1:I:299:ALA:HA	1:I:651:LEU:HD13	1.99	0.44
1:I:384:VAL:HG12	1:I:572:ASN:ND2	2.33	0.44
1:A:235:ALA:O	1:A:239:LEU:HD12	2.17	0.44
1:D:566:THR:CG2	1:D:568:MET:CE	2.95	0.44
1:F:229:TYR:O	1:F:230:GLN:C	2.56	0.44
1:I:49:LEU:O	1:I:55:VAL:HG23	2.17	0.44
1:I:359:ILE:C	1:I:360:LEU:HD12	2.38	0.44
2:K:4:DG:H2''	2:K:5:DT:OP2	2.17	0.44
3:Y:14:DA:N3	3:Y:15:DC:C6	2.86	0.44
1:A:151:ALA:C	1:A:153:SER:H	2.21	0.44
1:F:477:ALA:HA	1:F:480:ASN:HD21	1.83	0.44
1:I:61:LEU:HD13	1:I:88:TRP:CD2	2.52	0.44
1:I:117:ASP:O	1:I:121:GLN:HG3	2.18	0.44
1:I:407:ASN:C	1:I:408:PRO:O	2.53	0.44
1:I:575:GLY:H	1:I:617:ARG:NH2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:11:DA:N1	3:L:12:DG:C6	2.86	0.44
1:A:224:ILE:HG22	1:A:250:LEU:CD1	2.48	0.44
1:A:291:ARG:NH2	4:A:1662:ANP:O3G	2.45	0.44
1:A:577:GLU:CG	1:A:619:MET:CE	2.95	0.44
1:F:656:ASP:HB2	1:F:657:PRO:CD	2.48	0.44
1:I:110:ARG:H	1:I:192:ASN:HD21	1.66	0.44
1:I:198:ASP:HA	1:I:201:THR:OG1	2.18	0.44
1:D:233:ASN:ND2	1:D:236:GLN:HG3	2.32	0.44
1:F:237:TYR:O	1:F:240:THR:OG1	2.36	0.44
1:F:257:ASP:OD1	1:F:310:ARG:HD2	2.18	0.44
1:F:591:LEU:O	1:F:591:LEU:HG	2.17	0.44
1:F:603:GLY:O	1:F:606:GLU:HB3	2.17	0.44
1:I:116:TYR:HE2	1:I:124:ILE:HD11	1.79	0.44
1:I:333:HIS:CD2	1:I:369:VAL:HG21	2.52	0.44
1:I:524:TRP:CZ3	1:I:541:ASP:OD2	2.70	0.44
2:K:1:DG:C2'	2:K:2:DC:H6	2.27	0.44
1:A:118:ASP:HB2	1:A:145:ARG:NH1	2.33	0.43
1:D:57:PRO:O	1:D:87:LEU:HD23	2.18	0.43
1:F:404:LEU:HD23	1:F:417:ILE:HD11	2.00	0.43
2:K:1:DG:H1'	2:K:2:DC:O4'	2.17	0.43
1:A:104:GLY:C	1:A:106:HIS:H	2.22	0.43
1:D:195:ASP:O	1:D:198:ASP:HB2	2.18	0.43
1:D:303:LEU:HB2	1:D:648:ILE:CG2	2.47	0.43
1:F:320:GLU:HG2	6:F:2010:HOH:O	2.17	0.43
1:F:573:ALA:O	1:F:576:LEU:HD12	2.18	0.43
1:I:143:VAL:CG2	1:I:144:ILE:N	2.80	0.43
1:I:172:LEU:HD11	1:I:177:ALA:CA	2.48	0.43
1:I:308:THR:HG22	1:I:605:GLU:OE2	2.17	0.43
1:I:352:ARG:HD3	1:I:580:VAL:HG21	1.99	0.43
2:K:21:DT:H3'	2:K:22:DT:H72	2.00	0.43
3:L:12:DG:C4	3:L:13:DC:N4	2.85	0.43
1:A:34:ALA:HB1	1:A:616:THR:CG2	2.46	0.43
1:A:62:ALA:HA	1:A:225:HIS:HB2	2.00	0.43
1:A:240:THR:O	1:A:241:ARG:C	2.56	0.43
1:A:338:ASP:OD1	1:A:376:ARG:NH2	2.50	0.43
1:A:545:LEU:HD11	1:A:551:MET:HB2	2.00	0.43
1:F:260:ILE:HG21	1:F:610:LEU:HD12	2.01	0.43
1:F:606:GLU:HA	1:F:609:ARG:HH12	1.79	0.43
1:I:233:ASN:ND2	1:I:236:GLN:CD	2.71	0.43
1:I:457:LEU:O	1:I:458:ASP:CG	2.57	0.43
2:X:15:DT:C5'	2:X:15:DT:H6	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:LEU:CD2	1:A:511:LEU:HD23	2.48	0.43
1:D:152:LYS:O	1:D:201:THR:HG21	2.19	0.43
1:D:179:GLU:O	1:D:182:ARG:HB3	2.19	0.43
1:F:66:THR:HG21	1:F:548:VAL:HG21	2.00	0.43
1:F:162:ASP:O	1:F:174:ARG:HD2	2.18	0.43
1:I:167:PRO:O	1:I:174:ARG:N	2.52	0.43
1:I:303:LEU:O	1:I:608:ARG:HD3	2.18	0.43
2:K:19:DT:C1'	2:K:20:DT:H5'	2.48	0.43
1:A:114:VAL:HG22	1:A:115:ILE:N	2.34	0.43
1:A:232:THR:N	1:A:266:ALA:HB1	2.34	0.43
1:A:269:GLN:O	1:A:273:ASP:CG	2.57	0.43
1:D:31:ILE:HG13	1:D:311:LEU:CD2	2.49	0.43
1:D:161:LEU:C	1:D:161:LEU:HD23	2.39	0.43
1:F:97:VAL:HG11	1:F:544:LEU:CD1	2.36	0.43
1:F:424:GLY:HA2	2:K:9:DC:P	2.58	0.43
1:I:38:LYS:CG	1:I:39:THR:N	2.82	0.43
1:I:161:LEU:HD22	1:I:178:ALA:HB2	2.01	0.43
3:L:14:DA:OP2	3:L:14:DA:C4'	2.66	0.43
2:X:22:DT:C2	2:X:23:DT:C4	3.06	0.43
1:A:13:LEU:CD2	1:A:17:GLN:OE1	2.67	0.43
1:A:194:ILE:C	1:A:195:ASP:O	2.56	0.43
1:A:230:GLN:CD	1:A:258:GLN:HB3	2.39	0.43
1:A:307:ASN:O	1:A:310:ARG:HG2	2.18	0.43
1:A:472:GLU:OE1	1:A:472:GLU:HA	2.17	0.43
1:A:490:VAL:CG2	1:A:491:MET:N	2.82	0.43
1:A:546:SER:HB3	2:X:23:DT:OP1	2.18	0.43
1:D:61:LEU:O	1:D:224:ILE:HA	2.19	0.43
1:D:91:THR:H	1:D:94:SER:HB3	1.84	0.43
1:D:132:ILE:CD1	1:D:132:ILE:H	2.32	0.43
1:D:252:VAL:O	1:D:252:VAL:CG2	2.66	0.43
1:D:577:GLU:HB2	1:D:619:MET:CE	2.49	0.43
1:F:61:LEU:CD2	1:F:63:VAL:CG1	2.62	0.43
1:F:591:LEU:CD2	1:F:642:SER:HB2	2.46	0.43
1:I:354:TRP:HD1	1:I:563:ASP:O	2.01	0.43
1:I:505:GLN:C	1:I:508:GLN:OE1	2.57	0.43
1:A:12:ALA:O	1:A:40:ARG:NH1	2.38	0.43
1:D:280:ASP:O	1:D:281:ALA:C	2.57	0.43
1:D:436:TRP:HZ3	1:D:442:THR:HG21	1.81	0.43
1:F:13:LEU:CD2	1:F:17:GLN:OE1	2.66	0.43
1:F:25:THR:HG22	1:F:26:GLY:N	2.34	0.43
1:F:60:ILE:HG22	1:F:61:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:1:DG:H1	3:L:18:DC:H42	0.77	0.43
1:A:20:ALA:HA	1:A:284:TYR:CE1	2.54	0.43
1:A:144:ILE:CG2	1:A:148:ILE:HD11	2.45	0.43
1:A:195:ASP:OD2	1:A:198:ASP:CG	2.55	0.43
1:A:198:ASP:HB3	1:A:202:GLU:HG2	2.00	0.43
1:A:263:PHE:CE1	1:A:264:ARG:HB2	2.54	0.43
1:A:300:ALA:O	1:A:304:ILE:HG22	2.18	0.43
1:D:210:VAL:HG11	1:D:213:VAL:CG2	2.49	0.43
1:D:470:LEU:O	1:D:474:MET:HG3	2.19	0.43
1:F:224:ILE:HG22	1:F:250:LEU:CD1	2.47	0.43
1:F:228:GLU:OE1	1:F:230:GLN:OE1	2.37	0.43
1:F:566:THR:C	1:F:567:LEU:HD12	2.39	0.43
1:I:264[A]:ARG:HB3	1:I:264[A]:ARG:HH11	1.84	0.43
3:L:14:DA:O4'	3:L:15:DC:OP1	2.35	0.43
1:A:204:VAL:CG2	1:A:239:LEU:HD12	2.48	0.43
1:A:207:PHE:CD1	1:A:214:LEU:HB3	2.53	0.43
1:D:162:ASP:HB3	1:D:178:ALA:HB3	2.00	0.43
1:F:367:SER:HB2	1:F:383:ILE:HD13	2.01	0.43
1:A:401:TYR:OH	1:A:421:PRO:CG	2.31	0.43
1:D:123:ASP:CG	1:D:415:ARG:HH11	2.21	0.43
1:D:162:ASP:HA	1:D:174:ARG:HB3	2.01	0.43
1:D:272:LEU:O	1:D:275:GLN:NE2	2.47	0.43
1:I:377:VAL:O	1:I:377:VAL:CG1	2.66	0.43
3:L:14:DA:OP2	3:L:14:DA:C1'	2.67	0.43
1:A:65:PHE:HE2	1:A:264:ARG:NH1	2.17	0.42
1:A:118:ASP:O	1:A:121:GLN:HB2	2.19	0.42
1:D:111:ARG:HG2	1:D:111:ARG:O	2.12	0.42
1:F:62:ALA:HA	1:F:225:HIS:O	2.19	0.42
1:F:328:HIS:HD2	1:F:655:VAL:O	2.02	0.42
1:I:359:ILE:HD11	1:I:565:VAL:HG11	2.01	0.42
3:L:1:DA:H8	3:L:1:DA:OP2	2.02	0.42
1:A:65:PHE:CE2	1:A:264:ARG:NH1	2.85	0.42
1:A:97:VAL:HG13	1:A:98:ARG:N	2.34	0.42
1:A:297:LEU:HD11	1:A:315:LEU:HB3	2.01	0.42
1:A:497:LEU:HD11	1:A:501:ARG:NH2	2.34	0.42
1:D:263:PHE:C	1:D:265:GLY:H	2.21	0.42
1:D:412:VAL:O	1:D:416:ARG:HG2	2.19	0.42
1:D:587:GLU:HG2	1:D:626:ALA:HB1	2.01	0.42
1:D:623:LEU:N	1:D:623:LEU:HD12	2.33	0.42
1:F:90:SER:OG	1:F:95:ALA:HB2	2.19	0.42
1:F:114:VAL:HG13	1:F:193:ALA:CB	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:436:TRP:HA	1:F:439:THR:CG2	2.47	0.42
1:I:272:LEU:O	1:I:275:GLN:NE2	2.52	0.42
1:I:286:LEU:HD12	1:I:286:LEU:N	2.34	0.42
1:I:326:THR:HA	1:I:653:ASP:O	2.19	0.42
1:A:98:ARG:HG3	1:A:102:THR:HG23	2.00	0.42
1:A:388:GLY:O	1:A:391:ASP:HB2	2.19	0.42
1:F:199:LEU:HA	1:F:199:LEU:HD23	1.69	0.42
1:F:263:PHE:CD1	2:K:21:DT:H71	2.54	0.42
1:F:327:PHE:CE1	1:F:645:LEU:HD11	2.55	0.42
1:F:482:GLU:O	1:F:486:PHE:CB	2.67	0.42
1:F:542:ALA:HA	1:F:545:LEU:CD1	2.49	0.42
1:F:592:PRO:C	1:F:607:GLU:OE1	2.57	0.42
1:I:168:PHE:CD2	1:I:168:PHE:O	2.72	0.42
1:I:500:LEU:HA	1:I:503:GLU:HB2	2.01	0.42
1:A:362:ARG:HH12	1:A:607:GLU:CD	2.23	0.42
1:A:444:VAL:HG13	1:A:445:LEU:H	1.84	0.42
1:F:324:PRO:O	1:F:621:ARG:NH1	2.53	0.42
1:F:483:PRO:O	1:F:487:LEU:HG	2.20	0.42
1:F:632:GLN:OE1	1:F:633:PHE:CE2	2.72	0.42
1:I:401:TYR:CZ	1:I:417:ILE:HB	2.54	0.42
1:I:504:GLY:O	1:I:508:GLN:HG3	2.20	0.42
1:A:44:TYR:O	1:A:45:ARG:C	2.58	0.42
1:A:577:GLU:CG	1:A:619:MET:HE3	2.49	0.42
1:D:327:PHE:O	1:D:327:PHE:CD2	2.73	0.42
1:D:591:LEU:HD12	1:D:591:LEU:HA	1.77	0.42
1:F:37:GLY:O	1:F:38:LYS:C	2.54	0.42
1:F:291:ARG:HB2	4:F:1663:ANP:H4'	2.00	0.42
1:F:418:ILE:HD12	1:F:423:ARG:HD2	2.02	0.42
1:I:107:ILE:HB	1:I:205:ARG:NH2	2.35	0.42
1:I:290:TYR:CD1	1:I:318:VAL:HG11	2.54	0.42
1:I:399:LEU:O	1:I:403:ARG:N	2.46	0.42
1:I:500:LEU:O	1:I:504:GLY:CA	2.66	0.42
1:I:507:GLY:C	1:I:509:VAL:H	2.22	0.42
2:X:2:DC:H2''	2:X:3:DA:OP2	2.16	0.42
1:A:91:THR:HG22	1:A:92:PHE:N	2.34	0.42
1:A:200:ILE:CG2	1:A:235:ALA:HB1	2.49	0.42
1:D:111:ARG:HA	1:D:112:GLY:HA2	1.67	0.42
1:F:65:PHE:O	1:F:66:THR:HG22	2.17	0.42
1:F:601:PRO:O	1:F:604:ILE:N	2.53	0.42
1:I:275:GLN:CD	1:I:275:GLN:N	2.72	0.42
1:I:401:TYR:OH	1:I:421:PRO:CD	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:437:ALA:HA	1:I:442:THR:CG2	2.45	0.42
2:X:23:DT:H6	2:X:23:DT:H2'	1.57	0.42
1:A:424:GLY:CA	2:X:9:DC:OP1	2.68	0.42
1:D:357:MET:CG	1:D:580:VAL:HB	2.44	0.42
1:D:371:GLU:OE2	1:D:375:ARG:NH2	2.53	0.42
1:D:528:GLU:O	1:D:529:ALA:HB3	2.20	0.42
2:K:3:DA:C2	3:L:17:DG:N2	2.88	0.42
2:X:15:DT:H5'	2:X:15:DT:C6	2.49	0.42
1:A:70:ALA:O	1:A:73:MET:HB3	2.20	0.42
1:D:332:ASP:HB3	1:D:335:ALA:CB	2.50	0.42
1:D:487:LEU:O	1:D:491:MET:CG	2.58	0.42
1:F:209:GLU:O	1:F:211:PRO:HD3	2.20	0.42
1:I:261:TYR:HB3	1:I:264[B]:ARG:HB2	2.01	0.42
1:I:420:ARG:HA	1:I:420:ARG:HD3	1.76	0.42
1:A:29:LEU:HB2	1:A:274:PHE:CE2	2.55	0.42
1:A:194:ILE:O	1:A:195:ASP:C	2.56	0.42
1:D:110:ARG:H	1:D:192:ASN:HD21	1.68	0.42
1:F:35:GLY:HA2	4:F:1663:ANP:H5'2	2.01	0.42
1:I:577:GLU:OE2	1:I:619:MET:HE1	2.19	0.42
2:K:15:DT:H2''	2:K:16:DC:O5'	2.19	0.42
2:X:3:DA:H2''	2:X:4:DG:OP2	2.19	0.42
2:X:17:DG:H4'	2:X:18:DT:OP1	2.18	0.42
2:X:17:DG:H1'	2:X:18:DT:C6	2.54	0.42
1:A:65:PHE:HE2	1:A:264:ARG:HH12	1.66	0.42
1:A:173:PRO:O	1:A:176:ALA:HB3	2.19	0.42
1:A:198:ASP:O	1:A:202:GLU:N	2.39	0.42
1:A:199:LEU:O	1:A:203:THR:OG1	2.26	0.42
1:A:550:ASP:HA	1:A:553:THR:OG1	2.20	0.42
1:D:42:LEU:HD21	1:D:253:VAL:HG11	2.01	0.42
1:D:151:ALA:O	1:D:156:TRP:HB2	2.20	0.42
1:D:215:ASP:O	1:D:216:LYS:C	2.56	0.42
1:D:374:LEU:HB3	1:D:379:ILE:HB	2.01	0.42
1:F:27:PRO:HD2	1:F:280:ASP:CB	2.50	0.42
1:F:188:LYS:NZ	1:F:189:LYS:HG2	2.34	0.42
1:I:207:PHE:HB2	1:I:242:LEU:HD23	2.02	0.42
1:I:384:VAL:HG12	1:I:572:ASN:HD21	1.85	0.42
1:I:400:ALA:HB3	1:I:417:ILE:CG2	2.49	0.42
1:A:343:TRP:CD2	1:A:346:ARG:HD2	2.55	0.41
1:F:256:PRO:HG2	1:F:311:LEU:CD2	2.50	0.41
1:F:522:GLU:HA	1:F:525:SER:HB2	2.02	0.41
1:I:93:HIS:NE2	3:L:23:DT:O2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:400:ALA:HA	1:I:403:ARG:HG2	2.00	0.41
1:I:587:GLU:O	1:I:592:PRO:HD2	2.20	0.41
1:A:291:ARG:NH1	4:A:1662:ANP:O3G	2.51	0.41
1:A:424:GLY:HA3	1:A:463:LYS:HD3	2.02	0.41
1:D:194:ILE:HB	1:D:198:ASP:CB	2.50	0.41
1:D:333:HIS:O	1:D:336:GLU:HG2	2.20	0.41
1:D:395:ILE:HD13	1:D:548:VAL:HG22	2.01	0.41
1:D:416:ARG:CB	6:D:2022:HOH:O	2.69	0.41
1:D:416:ARG:N	1:D:416:ARG:HD2	2.35	0.41
1:F:117:ASP:C	1:F:117:ASP:OD1	2.59	0.41
1:F:334:ARG:HH12	1:F:376:ARG:NH1	2.15	0.41
1:F:577:GLU:CG	1:F:619:MET:CE	2.97	0.41
1:I:275:GLN:NE2	1:I:276:LYS:HG3	2.35	0.41
1:I:352:ARG:HD3	1:I:580:VAL:CG2	2.50	0.41
1:I:400:ALA:CB	1:I:417:ILE:HG23	2.50	0.41
1:A:417:ILE:HG13	1:A:417:ILE:H	1.68	0.41
1:D:341:ALA:O	1:D:345:THR:HG23	2.21	0.41
1:D:400:ALA:HB1	1:D:417:ILE:HG23	2.02	0.41
1:D:503:GLU:O	1:D:507:GLY:N	2.53	0.41
1:D:581:VAL:HB	1:D:618:ALA:HB2	2.02	0.41
1:F:48:HIS:CE1	1:F:52:HIS:CD2	3.07	0.41
1:F:114:VAL:HG22	1:F:115:ILE:N	2.35	0.41
1:I:139:THR:OG1	1:I:140:GLN:N	2.53	0.41
1:I:606:GLU:HG3	1:I:609:ARG:HH11	1.83	0.41
1:I:659:GLY:O	1:I:661:PRO:HD3	2.20	0.41
2:K:4:DG:O6	3:L:15:DC:C4	2.73	0.41
2:X:19:DT:C2'	2:X:19:DT:O2	2.68	0.41
1:D:139:THR:OG1	1:D:140:GLN:N	2.53	0.41
1:D:268:ILE:O	1:D:272:LEU:HG	2.20	0.41
1:D:331:THR:CA	1:D:628:GLN:HB2	2.44	0.41
1:D:360:LEU:HD23	1:D:570:LEU:HD23	2.02	0.41
1:D:478:ALA:HB2	1:D:486:PHE:CE1	2.55	0.41
1:F:394:GLU:HB2	1:F:514:LEU:HD11	1.92	0.41
1:F:421:PRO:HA	1:F:499:LEU:HD21	2.02	0.41
1:F:495:GLY:O	1:F:498:ASP:N	2.54	0.41
1:I:428:THR:OG1	3:L:8:DG:OP2	2.38	0.41
2:K:7:DC:H2''	2:K:8:DT:C6	2.55	0.41
3:Y:12:DG:H2'	3:Y:13:DC:C6	2.55	0.41
3:Y:22:DT:C7	3:Y:23:DT:C7	2.98	0.41
1:A:155:LEU:HD23	1:A:201:THR:HG22	2.03	0.41
1:A:234:ARG:CG	1:A:270:ASN:ND2	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:GLU:OE1	1:A:630:ARG:NH1	2.54	0.41
1:D:591:LEU:HB3	1:D:592:PRO:HD2	2.00	0.41
1:F:363:THR:HB	1:F:366:GLN:HG3	2.01	0.41
1:F:422:ARG:HD3	1:F:422:ARG:HA	1.78	0.41
1:I:61:LEU:O	1:I:224:ILE:HA	2.21	0.41
1:I:414:LEU:HD23	1:I:415:ARG:N	2.36	0.41
1:I:457:LEU:O	1:I:458:ASP:OD1	2.38	0.41
3:L:1:DA:C2'	3:L:2:DC:O5'	2.67	0.41
1:D:286:LEU:N	1:D:286:LEU:CD1	2.84	0.41
1:D:575:GLY:H	1:D:617:ARG:CZ	2.24	0.41
1:F:38:LYS:NZ	1:F:255:ASP:HB2	2.35	0.41
1:F:200:ILE:CG2	1:F:235:ALA:CB	2.98	0.41
1:F:513:ASN:O	1:F:516:GLU:HB3	2.20	0.41
1:I:400:ALA:HA	1:I:403:ARG:CG	2.50	0.41
1:I:417:ILE:HG13	1:I:418:ILE:N	2.35	0.41
2:K:12:DA:C6	2:K:13:DG:O6	2.74	0.41
3:L:14:DA:H1'	3:L:15:DC:P	2.59	0.41
3:Y:14:DA:O4'	3:Y:15:DC:OP1	2.37	0.41
1:A:124:ILE:O	1:A:128:VAL:HG22	2.21	0.41
1:A:500:LEU:O	1:A:504:GLY:HA3	2.20	0.41
1:A:616:THR:HG22	1:A:616:THR:O	2.21	0.41
1:D:227:ASP:HA	1:D:253:VAL:HG13	2.03	0.41
1:F:122:LEU:CA	1:F:125:ILE:HD12	2.43	0.41
1:F:632:GLN:HG3	2:K:19:DT:H73	2.02	0.41
1:I:138:GLU:C	1:I:139:THR:HG22	2.41	0.41
1:I:280:ASP:OD1	1:I:280:ASP:C	2.58	0.41
1:I:485:ALA:HA	1:I:488:ARG:HD2	2.02	0.41
2:X:11:DC:N4	3:Y:8:DG:C6	2.75	0.41
3:Y:3:DG:C1'	3:Y:4:DA:H5'	2.46	0.41
1:D:656:ASP:OD1	1:D:658:TYR:O	2.39	0.41
1:F:29:LEU:HB2	1:F:274:PHE:CE2	2.55	0.41
1:F:151:ALA:HB1	1:F:156:TRP:HB2	2.02	0.41
1:I:91:THR:CG2	6:I:2009:HOH:O	2.69	0.41
1:I:325:VAL:HG23	1:I:652:PHE:HB3	2.03	0.41
1:A:76:ARG:HA	1:A:79:HIS:ND1	2.36	0.41
1:A:152:LYS:CE	1:A:195:ASP:OD2	2.68	0.41
1:A:185:GLU:OE1	1:A:188:LYS:HE3	2.21	0.41
1:A:263:PHE:CD1	1:A:263:PHE:C	2.94	0.41
1:A:333:HIS:CE1	1:A:631:MET:HB3	2.55	0.41
1:D:114:VAL:HG21	1:D:403:ARG:NH2	2.36	0.41
1:D:407:ASN:O	1:D:407:ASN:OD1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:548:VAL:O	1:D:548:VAL:HG12	2.20	0.41
1:F:35:GLY:N	4:F:1663:ANP:PB	2.94	0.41
1:F:66:THR:CG2	1:F:548:VAL:CG2	2.99	0.41
1:F:411:ASP:HB3	1:F:444:VAL:CG1	2.44	0.41
1:F:426:GLY:HA2	2:K:8:DT:P	2.60	0.41
1:F:430:LEU:O	1:F:433:LEU:N	2.54	0.41
1:F:524:TRP:HZ3	1:F:541:ASP:OD2	2.04	0.41
1:F:632:GLN:CD	1:F:633:PHE:CE2	2.94	0.41
1:I:297:LEU:HD22	1:I:315:LEU:HD13	2.01	0.41
1:I:354:TRP:HB3	1:I:564:ALA:C	2.41	0.41
1:I:367:SER:O	1:I:370:ILE:HB	2.21	0.41
2:K:8:DT:C2'	2:K:9:DC:H6	2.23	0.41
3:L:12:DG:C2	3:L:13:DC:C2	3.08	0.41
2:X:19:DT:H2''	2:X:20:DT:O5'	2.19	0.41
1:A:97:VAL:HB	1:A:199:LEU:CD1	2.51	0.41
1:A:545:LEU:HD11	1:A:551:MET:CB	2.51	0.41
1:D:326:THR:HA	1:D:653:ASP:O	2.21	0.41
1:F:63:VAL:HA	1:F:90:SER:O	2.21	0.41
1:F:422:ARG:HG3	2:K:10:DG:P	2.61	0.41
1:F:538:PHE:CD1	1:F:538:PHE:C	2.94	0.41
1:F:608:ARG:NE	1:F:644:PHE:CE1	2.89	0.41
1:I:17:GLN:O	1:I:18:ALA:C	2.59	0.41
1:I:131:SER:HB2	1:I:183:ARG:HH22	1.86	0.41
1:I:228:GLU:OE1	1:I:230:GLN:NE2	2.45	0.41
1:I:390:TYR:O	1:I:391:ASP:HB2	2.21	0.41
2:X:12:DA:H2'	2:X:13:DG:H8	1.82	0.41
3:Y:1:DA:C1'	3:Y:2:DC:O5'	2.69	0.41
1:A:27:PRO:CG	1:A:280:ASP:HB2	2.50	0.40
1:A:60:ILE:HG21	1:A:225:HIS:CD2	2.56	0.40
1:A:60:ILE:HG22	1:A:61:LEU:N	2.36	0.40
1:D:138:GLU:C	1:D:139:THR:HG22	2.41	0.40
1:D:366:GLN:O	1:D:370:ILE:HG12	2.21	0.40
1:D:445:LEU:O	1:D:448:CYS:HB2	2.22	0.40
1:F:346:ARG:O	1:F:349:GLY:N	2.54	0.40
1:F:487:LEU:O	1:F:491:MET:HG3	2.20	0.40
1:F:537:ASP:O	1:F:540:ASP:HB2	2.21	0.40
3:Y:21:DT:C2'	3:Y:22:DT:OP1	2.64	0.40
1:D:46:ILE:HG13	1:D:225:HIS:CE1	2.56	0.40
1:D:307:ASN:CB	1:D:310[A]:ARG:NH2	2.84	0.40
1:D:633:PHE:CD1	1:D:633:PHE:N	2.90	0.40
1:F:207:PHE:CD1	1:F:214:LEU:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:294:ALA:HB3	1:F:321:ALA:HA	2.03	0.40
1:F:400:ALA:HB1	1:F:413:ALA:HB1	2.02	0.40
1:F:592:PRO:O	1:F:593:SER:CB	2.69	0.40
1:I:118:ASP:OD1	1:I:118:ASP:N	2.49	0.40
1:A:120:ASP:OD1	1:A:396:ARG:NH2	2.54	0.40
1:A:478:ALA:HA	1:A:486:PHE:HE2	1.87	0.40
1:F:393:ARG:HE	1:F:397:ASP:CG	2.22	0.40
1:I:142:ARG:NE	1:I:145:ARG:NH2	2.63	0.40
1:I:597:ILE:HA	1:I:604:ILE:HD11	2.03	0.40
2:X:2:DC:C2'	2:X:3:DA:OP2	2.69	0.40
1:A:61:LEU:HD22	1:A:88:TRP:CE3	2.55	0.40
1:A:198:ASP:O	1:A:200:ILE:C	2.60	0.40
1:A:348:HIS:HA	1:A:352:ARG:O	2.21	0.40
1:D:144:ILE:HA	1:D:147:ILE:HD12	2.04	0.40
1:F:98:ARG:NH1	1:F:102:THR:HG21	2.36	0.40
1:F:303:LEU:HD21	1:F:608:ARG:HG3	2.04	0.40
1:I:172:LEU:HD11	1:I:177:ALA:HB2	2.03	0.40
1:A:45:ARG:NH1	1:A:251:LEU:CB	2.84	0.40
1:A:113:PHE:CD1	1:A:113:PHE:C	2.95	0.40
1:A:303:LEU:CD1	1:A:611:PHE:CD2	3.04	0.40
1:A:385:GLY:HA2	1:A:552:ARG:NH2	2.36	0.40
1:A:592:PRO:O	1:A:596:ALA:HB3	2.22	0.40
1:D:16:THR:CG2	6:D:2001:HOH:O	2.69	0.40
1:D:173:PRO:HD2	1:D:176:ALA:HB3	2.04	0.40
1:D:325:VAL:CG2	1:D:652:PHE:CB	2.96	0.40
1:D:642:SER:HB3	1:D:645:LEU:HD12	2.04	0.40
1:D:657:PRO:HG2	1:I:11:GLN:O	2.21	0.40
1:F:20:ALA:HA	1:F:284:TYR:CE2	2.56	0.40
1:F:307:ASN:OD1	1:F:608:ARG:HD2	2.22	0.40
1:F:394:GLU:O	1:F:398:ILE:HG13	2.22	0.40
1:I:93:HIS:CE1	3:L:23:DT:O2	2.74	0.40
1:I:162:ASP:HB3	1:I:178:ALA:CB	2.52	0.40
1:I:290:TYR:HD1	1:I:318:VAL:HG11	1.87	0.40
2:K:3:DA:H1'	2:K:4:DG:C8	2.56	0.40
3:L:3:DG:H1'	3:L:4:DA:H8	1.85	0.40
3:Y:14:DA:OP2	3:Y:14:DA:C3'	2.69	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	621/665 (93%)	537 (86%)	71 (11%)	13 (2%)	7	33
1	D	636/665 (96%)	572 (90%)	56 (9%)	8 (1%)	12	45
1	F	622/665 (94%)	553 (89%)	60 (10%)	9 (1%)	11	43
1	I	629/665 (95%)	570 (91%)	54 (9%)	5 (1%)	19	57
All	All	2508/2660 (94%)	2232 (89%)	241 (10%)	35 (1%)	11	43

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	ILE
1	D	143	VAL
1	D	172	LEU
1	D	592	PRO
1	F	107	ILE
1	I	174	ARG
1	A	195	ASP
1	A	197	GLY
1	A	199	LEU
1	A	245	SER
1	D	461	ALA
1	D	647	ASP
1	F	165	ARG
1	F	378	GLN
1	F	592	PRO
1	A	105	GLU
1	A	355	SER
1	A	165	ARG
1	A	196	PHE
1	D	123	ASP
1	F	53	TYR
1	I	264[A]	ARG

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Mol	Chain	Res	Type
1	I	264[B]	ARG
1	I	321	ALA
1	A	378	GLN
1	A	593	SER
1	A	649	GLU
1	D	508	GLN
1	F	593	SER
1	F	279	PRO
1	F	648	ILE
1	F	141	PRO
1	I	318	VAL
1	A	141	PRO
1	D	318	VAL

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	512/536 (96%)	498 (97%)	14 (3%)	44	77
1	D	521/536 (97%)	513 (98%)	8 (2%)	65	87
1	F	513/536 (96%)	503 (98%)	10 (2%)	57	84
1	I	518/536 (97%)	511 (99%)	7 (1%)	67	88
All	All	2064/2144 (96%)	2025 (98%)	39 (2%)	59	84

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	LEU
1	A	199	LEU
1	A	258	GLN
1	A	271	ILE
1	A	273	ASP
1	A	280	ASP
1	A	352	ARG
1	A	361	TYR

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Mol	Chain	Res	Type
1	A	423	ARG
1	A	432	LYS
1	A	471	MET
1	A	475	SER
1	A	537	ASP
1	A	541	ASP
1	D	264[A]	ARG
1	D	264[B]	ARG
1	D	309	GLU
1	D	361	TYR
1	D	435	GLU
1	D	459	ARG
1	D	546	SER
1	D	633	PHE
1	F	98	ARG
1	F	119	ASP
1	F	159	ASP
1	F	226	VAL
1	F	239	LEU
1	F	240	THR
1	F	361	TYR
1	F	475	SER
1	F	537	ASP
1	F	546	SER
1	I	80	LEU
1	I	159	ASP
1	I	236	GLN
1	I	308	THR
1	I	428	THR
1	I	435	GLU
1	I	508	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	48	HIS
1	A	52	HIS
1	A	191	GLN
1	A	225	HIS
1	A	249	ASN
1	A	258	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	270	ASN
1	A	288	HIS
1	A	301	ASN
1	A	328	HIS
1	A	366	GLN
1	A	378	GLN
1	A	480	ASN
1	A	571	HIS
1	D	19	GLN
1	D	56	HIS
1	D	106	HIS
1	D	154	ASN
1	D	192	ASN
1	D	270	ASN
1	D	441	HIS
1	D	450	ASN
1	D	572	ASN
1	D	660	GLN
1	F	52	HIS
1	F	191	GLN
1	F	225	HIS
1	F	258	GLN
1	F	288	HIS
1	F	289	ASN
1	F	328	HIS
1	F	480	ASN
1	F	513	ASN
1	F	571	HIS
1	F	588	GLN
1	F	637	ASN
1	I	67	ASN
1	I	106	HIS
1	I	154	ASN
1	I	192	ASN
1	I	269	GLN
1	I	270	ASN
1	I	301	ASN
1	I	323	GLN
1	I	407	ASN
1	I	440	HIS
1	I	505	GLN
1	I	572	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	ANP	A	1662	5	29,33,33	1.78	7 (24%)	31,52,52	1.44	5 (16%)
4	ANP	F	1663	5	29,33,33	1.72	7 (24%)	31,52,52	1.84	6 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	A	1662	5	-	7/14/38/38	0/3/3/3
4	ANP	F	1663	5	-	9/14/38/38	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1663	ANP	PB-N3B	4.50	1.75	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1662	ANP	PB-N3B	4.35	1.74	1.63
4	A	1662	ANP	PG-N3B	4.03	1.73	1.63
4	F	1663	ANP	PG-N3B	4.01	1.73	1.63
4	A	1662	ANP	PG-O3G	-3.10	1.48	1.56
4	A	1662	ANP	PG-O2G	-2.88	1.49	1.56
4	F	1663	ANP	PG-O2G	-2.83	1.49	1.56
4	A	1662	ANP	PB-O1B	2.61	1.50	1.46
4	F	1663	ANP	PG-O3G	-2.56	1.49	1.56
4	A	1662	ANP	PB-O2B	-2.23	1.50	1.56
4	F	1663	ANP	O4'-C1'	2.23	1.44	1.41
4	F	1663	ANP	C5-C4	2.22	1.46	1.40
4	F	1663	ANP	PB-O2B	-2.19	1.50	1.56
4	A	1662	ANP	C5-C4	2.06	1.46	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1663	ANP	O1G-PG-N3B	-5.15	104.19	111.77
4	F	1663	ANP	PB-O3A-PA	-4.02	118.46	132.62
4	A	1662	ANP	O2B-PB-O1B	3.88	118.05	109.92
4	F	1663	ANP	O2B-PB-O1B	3.86	118.02	109.92
4	F	1663	ANP	N3-C2-N1	-3.08	123.86	128.68
4	F	1663	ANP	O1B-PB-N3B	-3.02	107.32	111.77
4	A	1662	ANP	O2G-PG-O3G	3.00	115.62	107.64
4	A	1662	ANP	C4-C5-N7	-2.88	106.40	109.40
4	F	1663	ANP	C4-C5-N7	-2.79	106.49	109.40
4	A	1662	ANP	N3-C2-N1	-2.78	124.33	128.68
4	A	1662	ANP	PB-O3A-PA	-2.59	123.48	132.62

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1662	ANP	PA-O3A-PB-O1B
4	A	1662	ANP	PA-O3A-PB-O2B
4	A	1662	ANP	C5'-O5'-PA-O1A
4	F	1663	ANP	PB-N3B-PG-O1G
4	F	1663	ANP	PG-N3B-PB-O1B
4	F	1663	ANP	PG-N3B-PB-O3A
4	F	1663	ANP	C5'-O5'-PA-O3A
4	F	1663	ANP	O4'-C4'-C5'-O5'
4	A	1662	ANP	O4'-C4'-C5'-O5'

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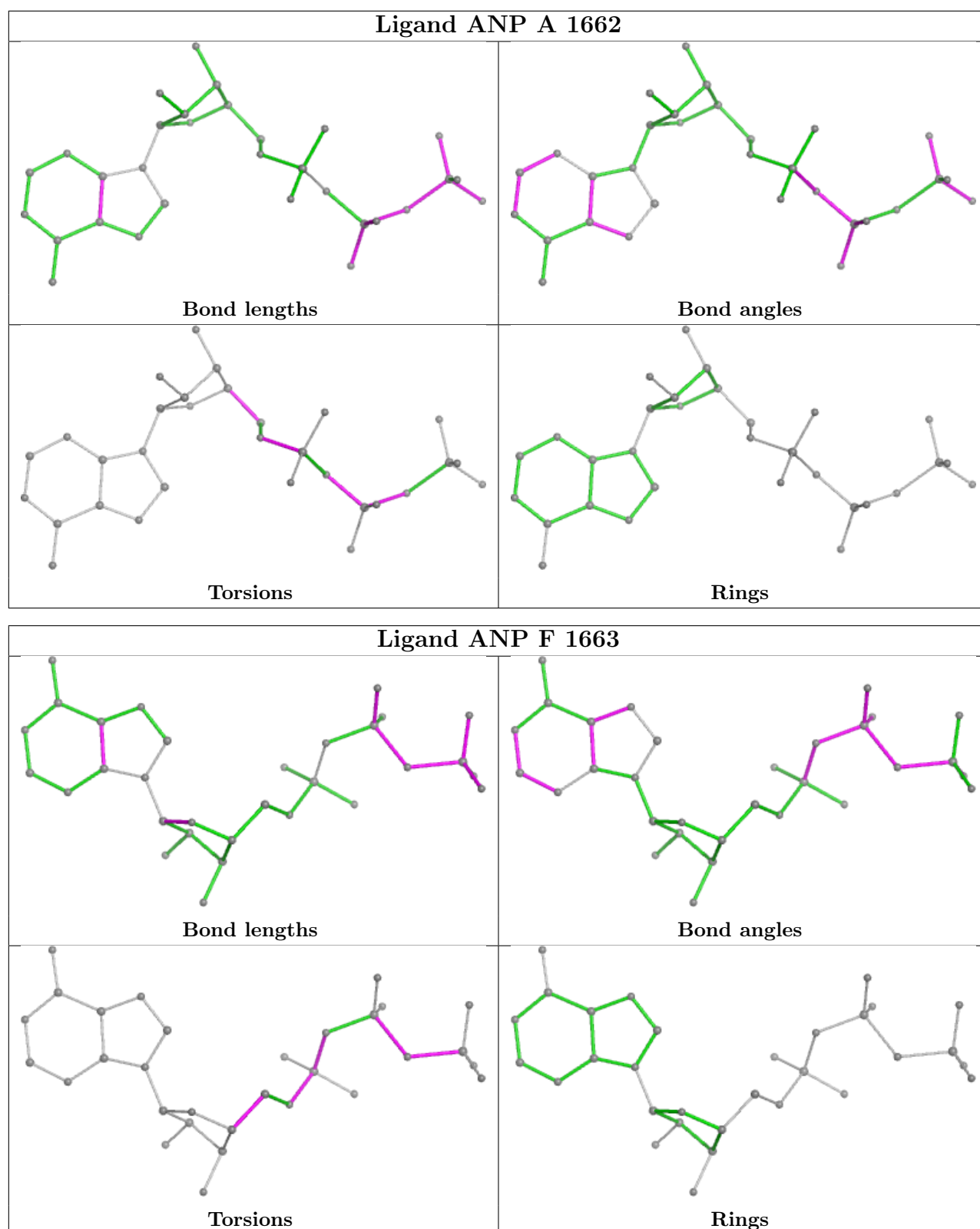
Mol	Chain	Res	Type	Atoms
4	A	1662	ANP	C3'-C4'-C5'-O5'
4	F	1663	ANP	C3'-C4'-C5'-O5'
4	A	1662	ANP	C5'-O5'-PA-O3A
4	F	1663	ANP	C5'-O5'-PA-O1A
4	F	1663	ANP	C5'-O5'-PA-O2A
4	F	1663	ANP	PB-O3A-PA-O2A
4	A	1662	ANP	PG-N3B-PB-O3A

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1662	ANP	5	0
4	F	1663	ANP	11	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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	631/665 (94%)	0.10	13 (2%) 63 34	61, 115, 166, 194	0
1	D	642/665 (96%)	-0.08	3 (0%) 91 75	59, 83, 137, 200	0
1	F	632/665 (95%)	0.08	13 (2%) 63 34	36, 115, 166, 196	0
1	I	638/665 (95%)	-0.06	5 (0%) 86 65	59, 83, 137, 199	0
2	K	23/25 (92%)	-0.35	0 100 100	117, 131, 152, 202	0
2	X	23/25 (92%)	-0.34	0 100 100	110, 125, 145, 187	0
3	L	23/25 (92%)	-0.39	0 100 100	91, 132, 169, 194	0
3	Y	23/25 (92%)	-0.43	0 100 100	89, 130, 147, 165	0
All	All	2635/2760 (95%)	-0.01	34 (1%) 77 51	36, 95, 161, 202	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	406	LEU	3.9
1	A	448	CYS	3.6
1	F	211	PRO	3.5
1	D	560	ALA	3.1
1	A	108	GLY	3.0
1	F	213	VAL	2.9
1	A	83	GLY	2.8
1	I	138	GLU	2.6
1	F	448	CYS	2.6
1	A	46	ILE	2.6
1	A	484	ALA	2.6
1	I	140	GLN	2.5
1	F	102	THR	2.5
1	F	108	GLY	2.5
1	D	138	GLU	2.5
1	A	391	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	109	LEU	2.4
1	I	165	ARG	2.3
1	F	551	MET	2.3
1	A	591	LEU	2.3
1	F	270	ASN	2.3
1	A	389	PHE	2.2
1	F	447	ALA	2.2
1	F	591	LEU	2.2
1	A	99	ILE	2.2
1	A	110	ARG	2.2
1	A	270	ASN	2.2
1	F	271	ILE	2.1
1	D	140	GLN	2.1
1	A	561	PRO	2.1
1	I	311	LEU	2.1
1	I	484	ALA	2.0
1	A	102	THR	2.0
1	F	461	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	MG	A	1663	1/1	0.70	0.15	190,190,190,190	0
5	MG	F	1665	1/1	0.84	0.20	137,137,137,137	0
5	MG	A	1664	1/1	0.90	0.18	112,112,112,112	0
5	MG	F	1664	1/1	0.91	0.17	98,98,98,98	0
4	ANP	F	1663	31/31	0.94	0.17	72,85,91,95	0

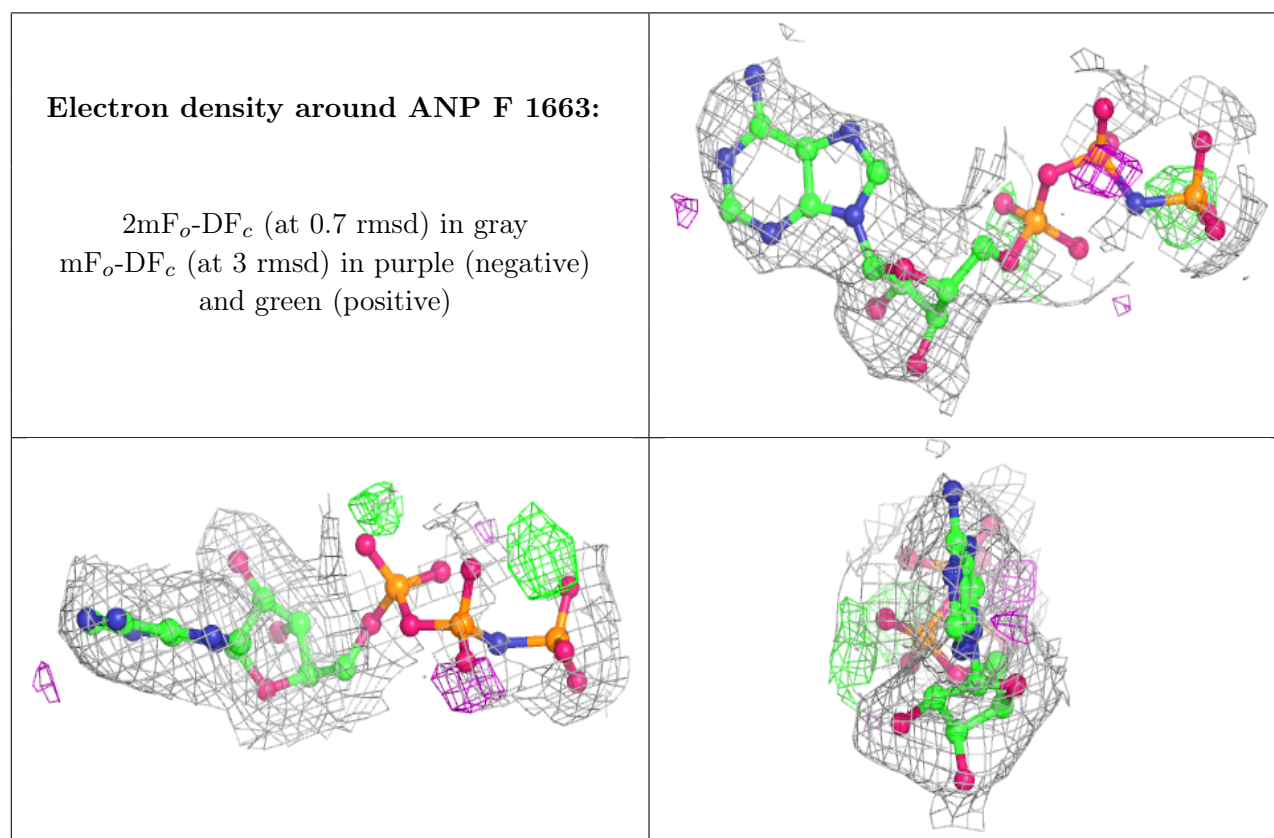
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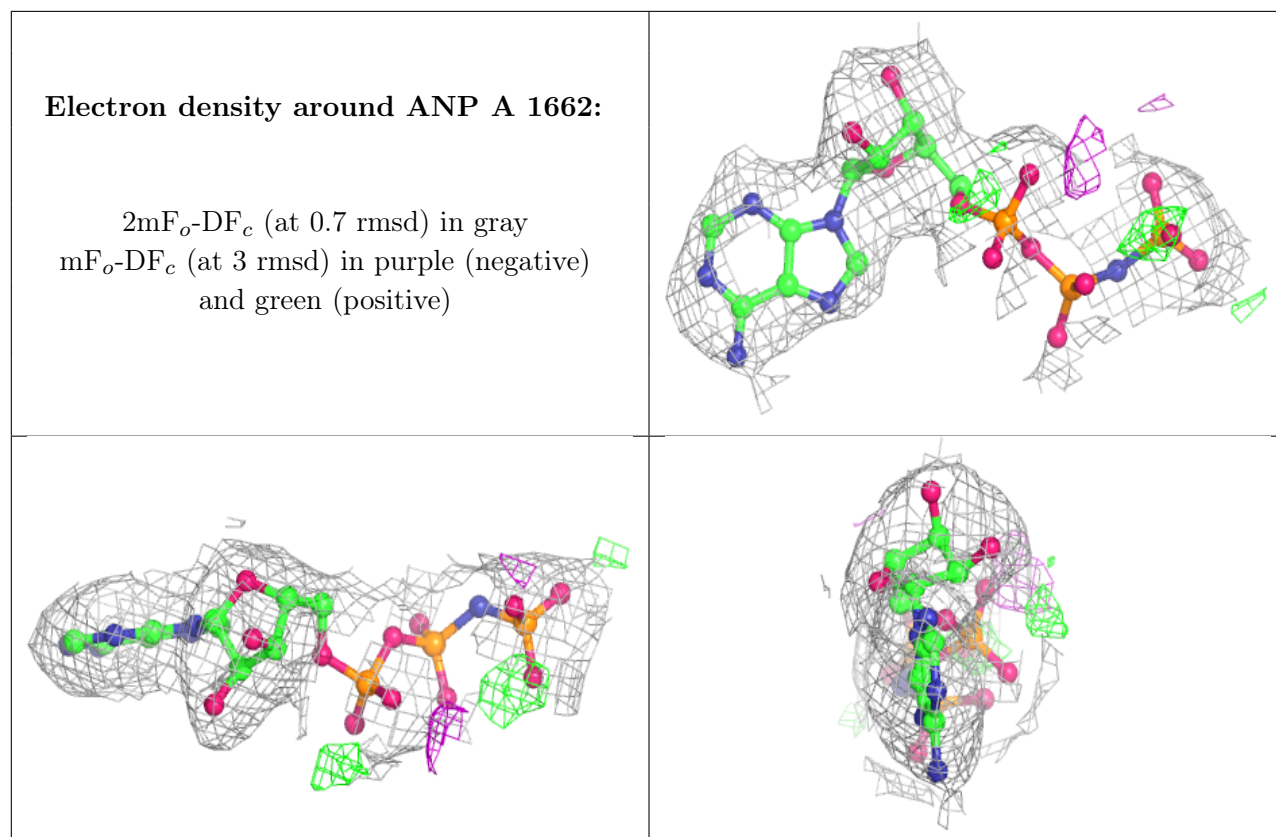


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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MG	D	1663	1/1	0.95	0.07	53,53,53,53	0
5	MG	I	1663	1/1	0.95	0.14	45,45,45,45	0
4	ANP	A	1662	31/31	0.96	0.18	71,82,92,93	0

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.