



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:17 AM GMT

PDB ID : 3E0D
Title : Insights into the Replisome from the Crystal Structure of the Ternary Complex of the Eubacterial DNA Polymerase III alpha-subunit
Authors : Wing, R.A.; Bailey, S.; Steitz, T.A.
Deposited on : 2008-07-31
Resolution : 4.60 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

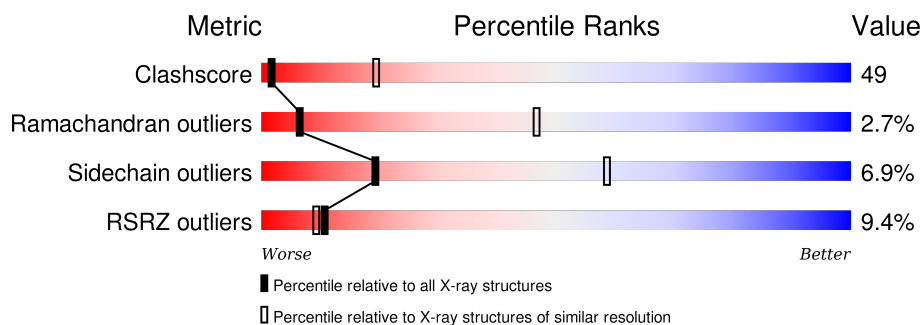
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1004 (5.52-3.64)
Ramachandran outliers	100387	1131 (5.52-3.60)
Sidechain outliers	100360	1112 (5.50-3.60)
RSRZ outliers	91569	1092 (5.52-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	C	27	<div> <div>4%</div> <div>67%</div> <div>26%</div> </div>
1	E	27	<div> <div>70%</div> <div>26%</div> </div>
2	D	21	<div> <div>5%</div> <div>62%</div> <div>19%</div> <div>5%</div> <div>10%</div> </div>
2	F	21	<div> <div>86%</div> <div>5%</div> <div>10%</div> </div>
3	A	1220	<div> <div>10%</div> <div>61%</div> <div>28%</div> <div>6%</div> </div>
3	B	1220	<div> <div>8%</div> <div>61%</div> <div>28%</div> <div>6%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DOC	D	21	-	-	X	-
2	DOC	F	21	-	-	X	-
5	DTP	A	1222	-	-	X	-
5	DTP	B	1222	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19982 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 DNA chain called DNA substrate template strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	20	Total	C	N	O	P	0	0	0
			407	195	69	124	19			
1	E	20	Total	C	N	O	P	0	0	0
			407	195	69	124	19			

- Molecule 2 is a DNA chain called DNA substrate primer strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	19	Total	C	N	O	P	0	0	0
			385	183	78	106	18			
2	F	19	Total	C	N	O	P	0	0	0
			385	183	78	106	18			

- Molecule 3 is a protein called DNA polymerase III subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	1148	Total	C	N	O	S	0	0	0
			9168	5847	1605	1688	28			
3	B	1148	Total	C	N	O	S	0	0	0
			9168	5847	1605	1688	28			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	ASN	ASP	ENGINEERED	UNP Q9XDH5
A	212	ASN	ASP	ENGINEERED	UNP Q9XDH5
A	539	PHE	ILE	ENGINEERED	UNP Q9XDH5
A	540	GLU	GLN	ENGINEERED	UNP Q9XDH5
A	541	ALA	VAL	ENGINEERED	UNP Q9XDH5
A	542	GLU	VAL	ENGINEERED	UNP Q9XDH5
B	20	ASN	ASP	ENGINEERED	UNP Q9XDH5
B	212	ASN	ASP	ENGINEERED	UNP Q9XDH5

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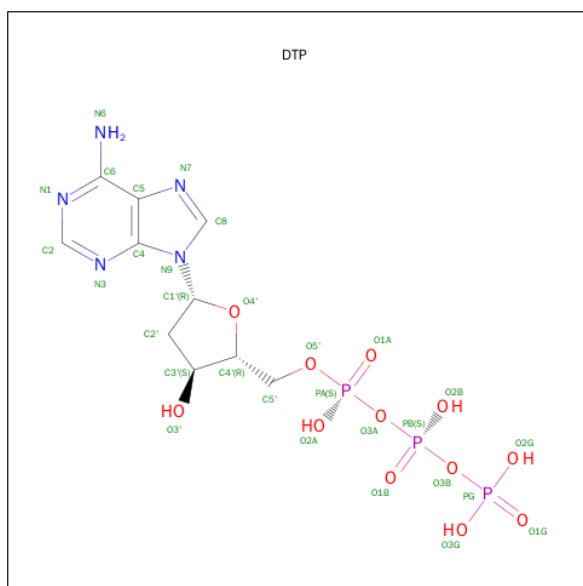
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Chain	Residue	Modelled	Actual	Comment	Reference
B	539	PHE	ILE	ENGINEERED	UNP Q9XDH5
B	540	GLU	GLN	ENGINEERED	UNP Q9XDH5
B	541	ALA	VAL	ENGINEERED	UNP Q9XDH5
B	542	GLU	VAL	ENGINEERED	UNP Q9XDH5

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Ca 1 1	0	0
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: $C_{10}H_{16}N_5O_{12}P_3$).

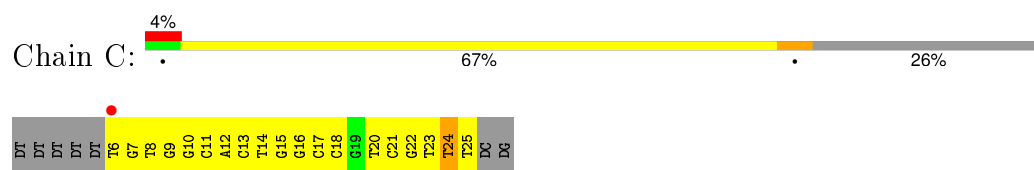


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O P 30 10 5 12 3	0	0
5	B	1	Total C N O P 30 10 5 12 3	0	0

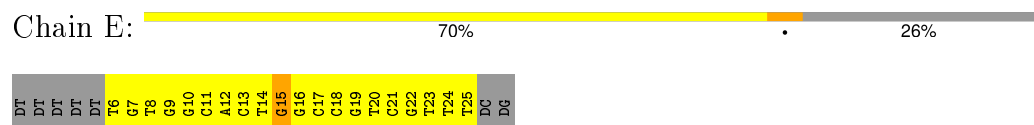
3 Residue-property plots [i](#)

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

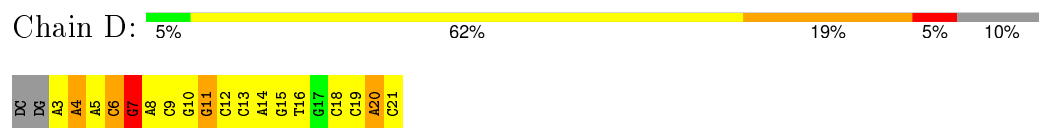
- Molecule 1: DNA substrate template strand



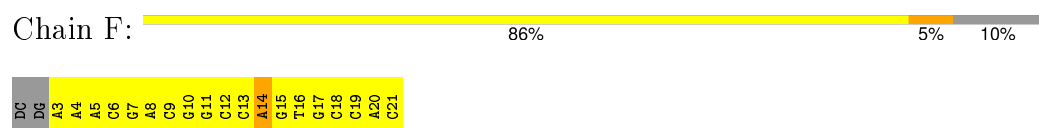
- Molecule 1: DNA substrate template strand



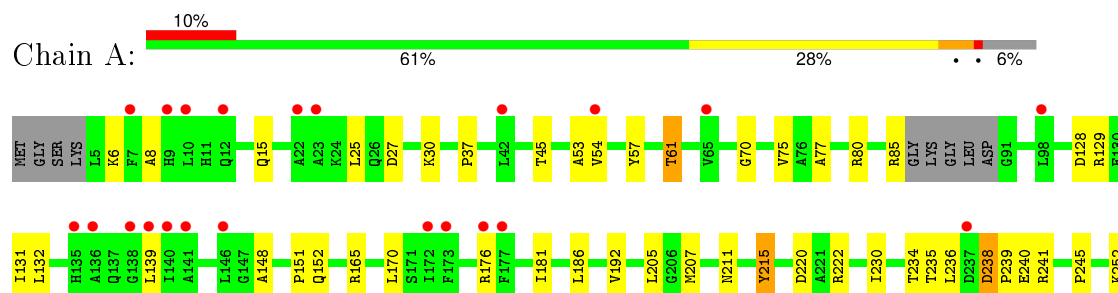
- Molecule 2: DNA substrate primer strand

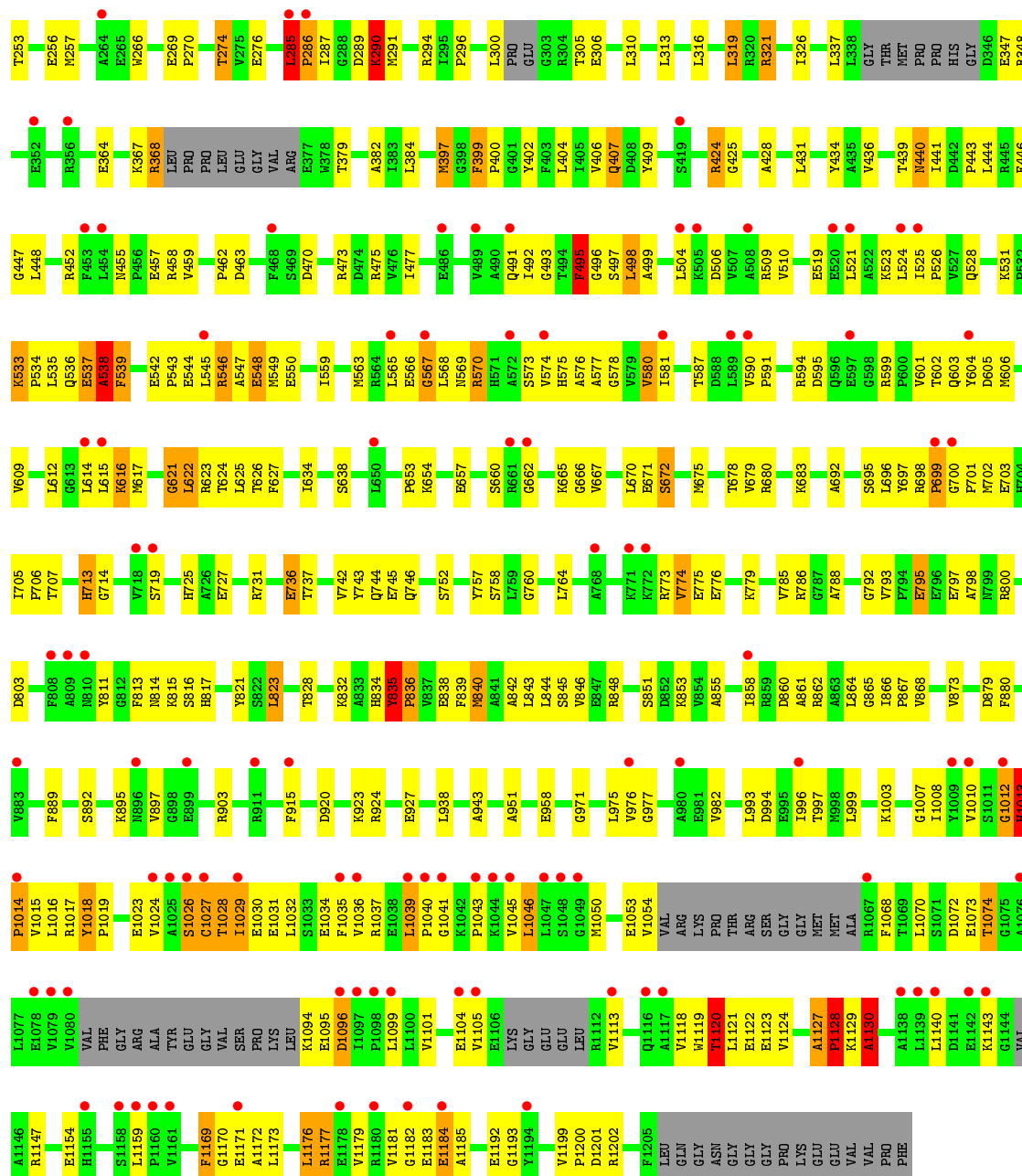


- Molecule 2: DNA substrate primer strand

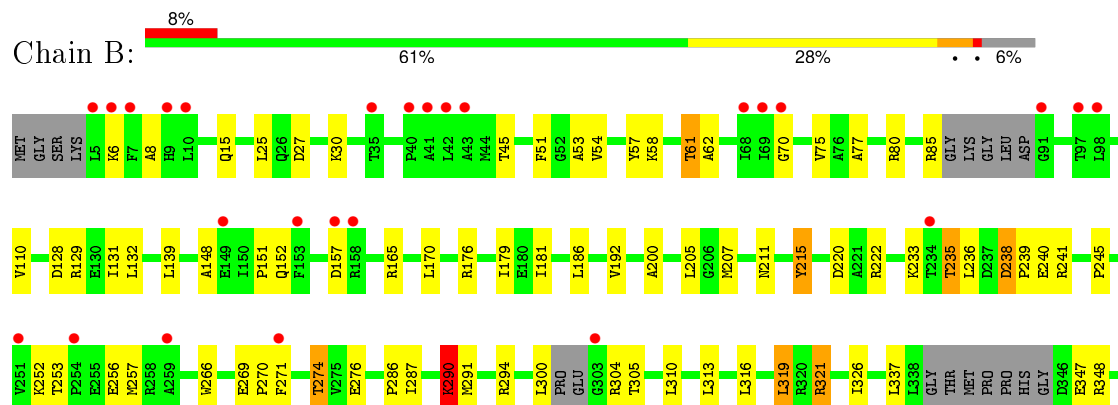


- Molecule 3: DNA polymerase III subunit alpha





- Molecule 3: DNA polymerase III subunit alpha





4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	149.55Å 149.55Å 163.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.60 49.85 – 4.59	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.60) 99.5 (49.85-4.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 4.64Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.287 , 0.271 0.303 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	215.6	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 198.0	EDS
Estimated twinning fraction	0.347 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 20097 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	19982	wwPDB-VP
Average B, all atoms (Å ²)	233.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DOC, CA, DTP

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	C	2.18	1/454 (0.2%)	1.01	3/700 (0.4%)
1	E	0.74	1/454 (0.2%)	0.88	0/700
2	D	1.93	1/413 (0.2%)	1.24	6/635 (0.9%)
2	F	0.85	1/413 (0.2%)	0.95	0/635
3	A	0.68	13/9348 (0.1%)	1.00	21/12615 (0.2%)
3	B	0.79	14/9346 (0.1%)	0.84	20/12608 (0.2%)
All	All	0.84	31/20428 (0.2%)	0.94	50/27893 (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
2	D	0	3
3	A	3	8
3	B	4	11
All	All	7	22

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	24	DT	O3'-P	43.89	2.13	1.61
3	B	713	HIS	C-N	34.20	1.94	1.33
3	B	397	MET	C-N	29.55	1.86	1.33
2	D	3	DA	O3'-P	29.28	1.96	1.61
3	A	567	GLY	C-N	28.47	1.99	1.34
3	B	491	GLN	C-N	23.63	1.88	1.34
3	A	713	HIS	C-N	23.63	1.75	1.33
3	A	699	PRO	C-N	22.99	1.74	1.33
3	B	1127	ALA	C-N	-20.20	0.95	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1026	SER	C-N	-19.57	0.89	1.34
3	A	1127	ALA	C-N	17.08	1.66	1.34
3	B	621	GLY	C-N	-16.52	0.96	1.34
3	B	834	HIS	C-N	-13.91	1.02	1.34
3	A	285	LEU	C-N	-13.02	1.09	1.34
3	A	621	GLY	C-N	-10.70	1.09	1.34
3	A	835	TYR	C-N	10.30	1.53	1.34
3	B	495	PHE	C-N	8.90	1.49	1.33
3	A	544	GLU	CD-OE2	8.04	1.34	1.25
3	B	544	GLU	CD-OE2	8.02	1.34	1.25
3	B	538	ALA	N-CA	7.54	1.61	1.46
3	A	538	ALA	N-CA	7.49	1.61	1.46
3	A	536	GLN	CG-CD	6.58	1.66	1.51
3	B	536	GLN	CG-CD	6.55	1.66	1.51
3	A	397	MET	C-N	6.35	1.44	1.33
2	F	14	DA	C5-C6	-6.11	1.35	1.41
3	B	538	ALA	CA-CB	-5.89	1.40	1.52
3	A	538	ALA	CA-CB	-5.88	1.40	1.52
3	B	835	TYR	C-N	-5.83	1.23	1.34
3	B	533	LYS	C-N	5.75	1.45	1.34
3	A	533	LYS	C-N	5.69	1.45	1.34
1	E	15	DG	C5-C6	-5.50	1.36	1.42

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	495	PHE	O-C-N	-47.05	43.21	123.20
3	A	699	PRO	CA-C-N	-41.86	32.49	116.20
3	A	699	PRO	C-N-CA	-39.91	38.49	122.30
3	A	1127	ALA	C-N-CD	-29.66	55.35	120.60
3	A	495	PHE	C-N-CA	-28.34	62.79	122.30
3	A	1127	ALA	O-C-N	-27.89	68.11	121.10
3	B	1127	ALA	CA-C-N	-26.69	42.36	117.10
3	A	495	PHE	CA-C-N	-24.46	67.27	116.20
3	A	835	TYR	CA-C-N	-19.41	62.77	117.10
3	A	835	TYR	C-N-CA	-19.13	41.67	122.00
3	A	495	PHE	O-C-N	-17.16	94.03	123.20
3	A	699	PRO	O-C-N	16.70	151.59	123.20
3	B	1127	ALA	C-N-CA	-15.28	57.84	122.00
3	B	1013	HIS	C-N-CD	-14.69	88.28	120.60
3	B	1127	ALA	C-N-CD	14.46	158.78	128.40
3	B	834	HIS	O-C-N	-12.76	102.28	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	24	DT	P-O3'-C3'	-12.36	104.86	119.70
3	A	397	MET	O-C-N	12.17	143.89	123.20
3	B	835	TYR	CA-C-N	-12.09	83.24	117.10
3	B	491	GLN	O-C-N	-11.90	103.66	122.70
3	A	1127	ALA	CA-C-N	11.53	149.37	117.10
3	B	835	TYR	C-N-CA	-11.03	75.68	122.00
3	B	1026	SER	O-C-N	-10.63	105.70	122.70
3	A	397	MET	CA-C-N	-10.63	94.95	116.20
3	B	495	PHE	C-N-CA	-10.60	100.05	122.30
3	A	397	MET	C-N-CA	-9.46	102.44	122.30
2	D	3	DA	P-O3'-C3'	9.14	130.67	119.70
3	B	834	HIS	CA-C-N	9.09	137.20	117.20
3	A	1013	HIS	C-N-CD	-8.71	101.44	120.60
3	A	567	GLY	O-C-N	-8.62	108.92	122.70
2	D	6	DC	OP1-P-O3'	8.57	124.06	105.20
3	B	835	TYR	C-N-CD	8.12	145.45	128.40
1	C	24	DT	OP2-P-O3'	7.96	122.71	105.20
3	A	835	TYR	O-C-N	-7.37	107.09	121.10
3	B	491	GLN	C-N-CA	-7.33	103.36	121.70
3	B	834	HIS	C-N-CA	7.20	139.70	121.70
3	B	491	GLN	CA-C-N	-6.86	102.11	117.20
3	A	285	LEU	CA-C-N	-6.85	97.92	117.10
3	A	567	GLY	C-N-CA	-6.68	105.00	121.70
3	A	621	GLY	O-C-N	-6.38	112.49	122.70
3	A	1127	ALA	C-N-CA	6.13	147.76	122.00
2	D	3	DA	OP1-P-O3'	6.13	118.69	105.20
3	B	397	MET	C-N-CA	5.73	134.33	122.30
2	D	7	DG	O5'-P-OP1	-5.71	100.56	105.70
3	B	1026	SER	CA-C-N	-5.70	104.66	117.20
2	D	4	DA	OP1-P-O3'	5.58	117.48	105.20
3	B	397	MET	O-C-N	-5.48	113.88	123.20
3	B	1127	ALA	O-C-N	5.32	131.21	121.10
2	D	3	DA	O3'-P-O5'	-5.07	94.37	104.00
1	C	24	DT	OP1-P-O3'	-5.02	94.16	105.20

All (7) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	538	ALA	CA
3	A	1013	HIS	CA
3	A	1120	THR	CB
3	B	538	ALA	CA

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Mol	Chain	Res	Type	Atom
3	B	866	ILE	CA
3	B	1125	LEU	CA
3	B	1126	GLU	CA

All (22) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	1012	GLY	Peptide
3	A	1120	THR	Peptide
3	A	1128	PRO	Peptide
3	A	1130	ALA	Peptide
3	A	285	LEU	Mainchain
3	A	337	LEU	Mainchain
3	A	495	PHE	Mainchain
3	A	835	TYR	Mainchain
3	B	1012	GLY	Peptide
3	B	1013	HIS	Peptide
3	B	1026	SER	Mainchain
3	B	1124	VAL	Peptide
3	B	1127	ALA	Mainchain
3	B	337	LEU	Mainchain
3	B	495	PHE	Mainchain
3	B	835	TYR	Mainchain,Peptide
3	B	864	LEU	Peptide
3	B	866	ILE	Peptide
2	D	11	DG	Sidechain
2	D	20	DA	Sidechain
2	D	7	DG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	407	0	230	199	0
1	E	407	0	229	139	0
2	D	385	0	212	143	1
2	F	385	0	212	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	9168	0	9186	856	33
3	B	9168	0	9182	793	35
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	30	0	12	24	0
5	B	30	0	11	14	0
All	All	19982	0	19274	1892	36

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 49.

All (1892) 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)
3:A:1013:HIS:CE1	3:A:1073:GLU:HB3	1.26	1.68
3:A:858:ILE:HD11	3:A:889:PHE:CZ	1.24	1.65
3:A:844:LEU:HB3	3:A:880:PHE:CE1	1.24	1.64
3:B:831:VAL:HG12	3:B:839:PHE:CD1	1.14	1.63
3:B:832:LYS:HB2	3:B:839:PHE:CE2	1.26	1.63
3:A:844:LEU:HB3	3:A:880:PHE:CD1	1.20	1.62
3:A:855:ALA:HB2	3:A:1008:ILE:CG2	1.18	1.62
3:A:855:ALA:CB	3:A:1008:ILE:CG2	1.75	1.61
3:B:831:VAL:CG1	3:B:839:PHE:HD1	1.01	1.60
3:A:855:ALA:CB	3:A:1008:ILE:HG22	1.27	1.56
3:B:54:VAL:HG23	3:B:604:TYR:CZ	1.34	1.56
3:A:546:ARG:CZ	3:A:547:ALA:HB2	1.36	1.56
3:B:491:GLN:HB2	3:B:574:VAL:CG1	1.14	1.55
3:A:574:VAL:CG2	3:A:601:VAL:HG22	1.32	1.55
3:B:996:ILE:HD12	3:B:1017:ARG:CD	1.35	1.55
1:C:8:DT:C5'	3:A:622:LEU:HD23	1.10	1.55
3:B:546:ARG:CZ	3:B:547:ALA:HB2	1.34	1.54
3:A:574:VAL:CG2	3:A:601:VAL:CG2	1.79	1.52
3:B:492:ILE:HG13	3:B:580:VAL:CG2	1.35	1.52
1:C:8:DT:H5''	3:A:622:LEU:CD2	1.38	1.51
3:A:575:HIS:CD2	3:A:578:GLY:N	1.78	1.51
3:A:855:ALA:CA	3:A:1008:ILE:HG21	1.33	1.51
3:B:491:GLN:CB	3:B:574:VAL:CG1	1.87	1.51
2:F:21:DOC:H2''	3:B:424:ARG:NH1	1.22	1.51
3:B:574:VAL:HG22	3:B:601:VAL:CG2	1.40	1.50
3:A:844:LEU:HD22	3:A:880:PHE:CZ	1.45	1.50
3:A:1013:HIS:H	3:A:1014:PRO:CD	1.06	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:858:ILE:CD1	3:A:889:PHE:HZ	1.25	1.48
3:B:996:ILE:CD1	3:B:1017:ARG:HD3	1.42	1.48
2:D:21:DOC:H2"	3:A:424:ARG:NH1	1.18	1.47
3:B:996:ILE:CG1	3:B:1017:ARG:HD2	1.44	1.46
1:E:14:DT:P	3:B:509:ARG:HH12	1.38	1.45
3:B:1128:PRO:HG3	3:B:1129:LYS:CE	1.10	1.44
3:A:774:VAL:CB	3:B:778:GLN:HG2	1.46	1.43
3:A:844:LEU:CB	3:A:880:PHE:CD1	2.02	1.41
3:A:858:ILE:CD1	3:A:889:PHE:CZ	1.99	1.41
3:B:1128:PRO:CG	3:B:1129:LYS:HE3	1.22	1.41
3:A:713:HIS:C	3:A:714:GLY:N	1.75	1.40
3:A:1013:HIS:ND1	3:A:1073:GLU:HB3	1.36	1.40
3:B:54:VAL:CG2	3:B:604:TYR:CE1	2.02	1.39
3:B:996:ILE:CD1	3:B:1017:ARG:CD	1.92	1.39
3:A:574:VAL:HG22	3:A:601:VAL:CG2	0.90	1.38
3:B:832:LYS:CB	3:B:839:PHE:CE2	2.07	1.38
3:A:996:ILE:HD11	3:A:1018:TYR:CE2	1.58	1.38
3:B:492:ILE:CG1	3:B:580:VAL:HG22	1.53	1.37
1:C:8:DT:C5'	3:A:622:LEU:CD2	1.96	1.37
3:A:575:HIS:CD2	3:A:578:GLY:H	1.37	1.36
3:A:458:ARG:CZ	3:A:764:LEU:CD2	2.01	1.36
3:A:458:ARG:NH1	3:A:764:LEU:HD22	1.37	1.34
3:A:458:ARG:CZ	3:A:764:LEU:HD22	1.57	1.34
3:A:523:LYS:HD2	3:A:1094:LYS:NZ	1.36	1.33
3:A:458:ARG:NH1	3:A:764:LEU:CD2	1.92	1.33
3:A:575:HIS:HD2	3:A:578:GLY:N	1.09	1.32
3:B:1046:LEU:HD21	3:B:1202:ARG:NH2	1.40	1.32
3:A:832:LYS:HB2	3:A:839:PHE:CE2	1.64	1.31
3:B:710:ARG:NH1	3:B:716:GLU:OE1	1.58	1.31
1:C:9:DG:C4'	3:A:621:GLY:H	1.44	1.31
3:B:699:PRO:HA	3:B:700:GLY:N	1.43	1.31
3:B:844:LEU:HB3	3:B:880:PHE:CD1	1.66	1.30
3:A:1027:CYS:SG	3:A:1031:GLU:HB2	1.72	1.30
3:A:851:SER:OG	3:A:895:LYS:CE	1.80	1.29
1:E:14:DT:OP1	3:B:509:ARG:NH1	1.65	1.29
3:A:744:GLN:N	3:A:813:PHE:N	1.80	1.29
3:A:744:GLN:H	3:A:813:PHE:N	1.26	1.29
1:C:8:DT:C3'	3:A:623:ARG:H	1.46	1.29
3:A:774:VAL:HG23	3:B:778:GLN:CB	1.63	1.28
3:A:230:ILE:CD1	3:A:565:LEU:CD1	2.11	1.28
3:B:397:MET:C	3:B:398:GLY:N	1.86	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:844:LEU:CB	3:A:880:PHE:CE1	2.13	1.28
3:A:1013:HIS:CE1	3:A:1073:GLU:CB	2.18	1.27
1:C:8:DT:P	3:A:623:ARG:HB2	1.73	1.26
3:B:696:LEU:CD2	3:B:742:VAL:HG22	1.66	1.26
3:B:491:GLN:C	3:B:492:ILE:N	1.88	1.26
3:B:996:ILE:CG1	3:B:1017:ARG:CD	2.13	1.25
1:C:9:DG:H4'	3:A:621:GLY:N	1.49	1.25
3:B:543:PRO:O	3:B:546:ARG:HD2	1.28	1.25
3:B:1046:LEU:CD2	3:B:1202:ARG:HH21	1.50	1.25
3:B:321:ARG:HH22	3:B:440:ASN:ND2	1.34	1.24
1:E:14:DT:H4'	3:B:509:ARG:NH2	1.50	1.24
3:A:665:LYS:CB	3:A:860:ASP:OD2	1.85	1.24
3:A:665:LYS:HB3	3:A:860:ASP:OD2	1.06	1.23
3:B:832:LYS:HB2	3:B:839:PHE:CZ	1.73	1.22
3:A:543:PRO:O	3:A:546:ARG:HD2	1.35	1.22
3:B:54:VAL:HG21	3:B:604:TYR:CE1	1.67	1.22
3:A:696:LEU:HD21	3:A:742:VAL:CG2	1.67	1.22
3:B:848:ARG:NE	3:B:879:ASP:OD2	1.72	1.22
3:B:458:ARG:NH1	3:B:764:LEU:HD22	1.56	1.21
3:A:699:PRO:O	3:A:811:TYR:CD2	1.93	1.21
3:A:1013:HIS:ND1	3:A:1073:GLU:CB	2.02	1.20
3:B:54:VAL:HG23	3:B:604:TYR:CE1	1.69	1.20
1:C:8:DT:H4'	3:A:622:LEU:CA	1.70	1.20
1:C:9:DG:N3	3:A:576:ALA:CB	2.05	1.20
3:A:773:ARG:CB	3:B:778:GLN:HE22	1.38	1.20
3:A:1013:HIS:N	3:A:1014:PRO:HD2	1.24	1.20
3:B:699:PRO:CA	3:B:700:GLY:N	2.04	1.20
3:A:1003:LYS:NZ	3:A:1096:ASP:OD1	1.75	1.20
3:A:845:SER:HA	3:A:879:ASP:OD1	1.39	1.20
1:E:14:DT:P	3:B:509:ARG:NH1	2.16	1.19
2:D:21:DOC:H2'	5:A:1222:DTP:O4'	1.36	1.19
1:C:8:DT:C4'	3:A:622:LEU:HA	1.71	1.19
3:B:713:HIS:C	3:B:714:GLY:N	1.94	1.19
3:B:699:PRO:C	3:B:700:GLY:HA3	1.63	1.19
1:E:18:DC:OP1	3:B:933:ARG:HB2	1.40	1.19
3:A:845:SER:OG	3:A:879:ASP:OD2	1.59	1.18
3:A:775:GLU:OE1	3:B:781:ARG:NE	1.74	1.18
3:A:851:SER:OG	3:A:895:LYS:NZ	1.76	1.18
3:B:665:LYS:HD3	3:B:860:ASP:CB	1.73	1.17
3:A:697:TYR:CE1	3:A:702:MET:SD	2.37	1.17
3:B:54:VAL:CG2	3:B:604:TYR:CZ	2.22	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:707:THR:CG2	3:B:716:GLU:OE2	1.92	1.17
3:A:773:ARG:HG2	3:B:778:GLN:NE2	1.57	1.16
3:B:452:ARG:NH2	3:B:766:ARG:CZ	2.08	1.16
3:A:774:VAL:N	3:B:778:GLN:CD	1.74	1.16
3:A:1013:HIS:N	3:A:1014:PRO:CD	1.78	1.16
1:E:8:DT:C4'	3:B:622:LEU:HD23	1.76	1.16
3:A:773:ARG:CG	3:B:778:GLN:NE2	2.08	1.16
3:A:1027:CYS:SG	3:A:1031:GLU:CB	2.33	1.16
3:A:773:ARG:HG2	3:B:778:GLN:CD	1.66	1.15
2:D:21:DOC:C2'	3:A:424:ARG:NH1	2.08	1.15
3:B:714:GLY:O	3:B:715:GLN:HG3	1.44	1.15
3:A:567:GLY:C	3:A:568:LEU:N	1.99	1.15
3:B:665:LYS:HD3	3:B:860:ASP:HB3	1.25	1.15
3:A:230:ILE:CD1	3:A:565:LEU:HD11	1.74	1.15
1:C:10:DG:C4'	3:A:576:ALA:HA	1.76	1.15
1:C:14:DT:O3'	3:A:509:ARG:NH1	1.80	1.15
3:A:634:ILE:CG2	3:A:838:GLU:HB3	1.74	1.15
3:A:455:ASN:HD21	3:A:760:GLY:C	1.47	1.14
2:F:21:DOC:C2'	3:B:424:ARG:NH1	2.09	1.14
2:D:21:DOC:C2'	3:A:424:ARG:HH12	1.60	1.14
3:B:744:GLN:N	3:B:813:PHE:N	1.96	1.13
3:B:996:ILE:HG13	3:B:1017:ARG:CB	1.77	1.13
3:A:698:ARG:O	3:A:701:PRO:CD	1.96	1.13
3:A:1129:LYS:HA	3:A:1200:PRO:CA	1.77	1.13
3:B:1128:PRO:CG	3:B:1129:LYS:CE	1.88	1.13
3:B:744:GLN:H	3:B:813:PHE:C	1.51	1.13
3:B:699:PRO:C	3:B:700:GLY:CA	2.15	1.13
3:A:866:ILE:CG2	3:A:867:PRO:HD2	1.79	1.13
3:B:831:VAL:CG1	3:B:839:PHE:CD1	1.89	1.12
3:A:455:ASN:HD21	3:A:760:GLY:CA	1.61	1.12
3:A:1130:ALA:N	3:A:1199:VAL:O	1.80	1.13
3:B:574:VAL:HG22	3:B:601:VAL:HG22	1.21	1.12
3:B:707:THR:HG23	3:B:716:GLU:OE2	1.47	1.12
3:A:1129:LYS:HA	3:A:1199:VAL:O	1.50	1.12
1:C:8:DT:H3'	3:A:623:ARG:H	1.10	1.12
3:B:844:LEU:HD22	3:B:880:PHE:CE1	1.84	1.12
3:B:831:VAL:HB	3:B:839:PHE:CE1	1.84	1.12
3:B:996:ILE:HG13	3:B:1017:ARG:CG	1.80	1.12
3:A:575:HIS:CG	3:A:578:GLY:H	1.68	1.12
2:D:9:DC:H1'	2:D:10:DG:H5''	1.24	1.11
3:A:523:LYS:CD	3:A:1094:LYS:HZ3	1.63	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:455:ASN:HD21	3:B:760:GLY:C	1.50	1.11
2:F:20:DA:H2''	2:F:21:DOC:H5'	1.30	1.11
3:B:704:HIS:CD2	3:B:808:PHE:HE2	1.68	1.11
3:A:492:ILE:HD12	3:A:616:LYS:HG3	1.27	1.11
3:A:1024:VAL:CG2	3:A:1200:PRO:HD2	1.79	1.11
3:B:665:LYS:CD	3:B:860:ASP:HB3	1.81	1.11
3:A:627:PHE:HE1	3:A:843:LEU:N	1.48	1.11
3:A:696:LEU:CD2	3:A:742:VAL:HG22	1.79	1.11
3:B:696:LEU:HD21	3:B:742:VAL:CG2	1.79	1.10
3:B:452:ARG:NH2	3:B:766:ARG:NH2	2.00	1.10
3:B:704:HIS:NE2	3:B:808:PHE:CZ	2.18	1.10
2:D:20:DA:H2''	2:D:21:DOC:H5'	1.25	1.10
3:A:779:LYS:NZ	3:B:774:VAL:HA	1.67	1.10
3:B:491:GLN:CB	3:B:574:VAL:HG12	1.61	1.10
3:B:546:ARG:CZ	3:B:547:ALA:CB	2.30	1.10
3:B:491:GLN:HB3	3:B:574:VAL:HG12	1.25	1.09
3:B:996:ILE:CB	3:B:1017:ARG:HD2	1.81	1.09
3:B:546:ARG:HD3	3:B:547:ALA:N	1.65	1.09
3:B:701:PRO:HD3	3:B:811:TYR:CD1	1.86	1.09
3:B:699:PRO:C	3:B:701:PRO:HD2	1.73	1.09
1:E:8:DT:H4'	3:B:622:LEU:HD23	1.23	1.09
3:A:574:VAL:HG22	3:A:601:VAL:HG21	1.18	1.09
3:B:699:PRO:C	3:B:700:GLY:N	2.06	1.09
3:A:1129:LYS:HA	3:A:1199:VAL:C	1.71	1.09
3:A:230:ILE:HD11	3:A:565:LEU:HD11	1.33	1.09
3:A:1120:THR:O	3:A:1124:VAL:HG23	1.49	1.08
3:A:844:LEU:CD2	3:A:880:PHE:CZ	2.36	1.08
3:B:493:GLY:H	3:B:602:THR:HB	1.17	1.08
3:A:776:GLU:HG3	3:B:775:GLU:HG3	1.35	1.08
3:A:458:ARG:CZ	3:A:764:LEU:HD21	1.77	1.08
3:A:1129:LYS:CA	3:A:1199:VAL:O	2.01	1.08
3:B:574:VAL:HG22	3:B:601:VAL:HG21	1.24	1.08
3:A:523:LYS:CD	3:A:1094:LYS:NZ	2.16	1.08
1:C:14:DT:N3	2:D:14:DA:N1	2.02	1.08
1:C:9:DG:H3'	3:A:621:GLY:HA3	1.29	1.08
1:E:13:DC:H2''	1:E:14:DT:H5''	1.22	1.08
3:A:866:ILE:HG23	3:A:867:PRO:CD	1.83	1.08
3:A:496:GLY:O	3:A:569:ASN:HA	1.53	1.08
3:B:665:LYS:HZ3	3:B:864:LEU:HD13	1.12	1.07
3:A:546:ARG:CZ	3:A:547:ALA:CB	2.31	1.07
3:A:994:ASP:HB2	3:A:1017:ARG:CZ	1.84	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:999:LEU:HD11	3:B:1013:HIS:N	1.70	1.07
3:A:455:ASN:ND2	3:A:760:GLY:CA	2.16	1.07
3:A:851:SER:OG	3:A:895:LYS:HE2	1.40	1.07
3:A:230:ILE:CD1	3:A:565:LEU:HD13	1.84	1.07
1:E:10:DG:O4'	3:B:576:ALA:HB2	1.55	1.06
1:C:15:DG:C2	2:D:14:DA:C2	2.42	1.06
3:A:855:ALA:HB1	3:A:1008:ILE:HG22	1.34	1.06
2:F:19:DC:H5''	3:B:531:LYS:NZ	1.68	1.06
1:C:24:DT:O3'	1:C:25:DT:P	2.13	1.06
3:A:844:LEU:HD22	3:A:880:PHE:CE1	1.90	1.06
3:A:424:ARG:NH1	5:A:1222:DTP:H4'	1.71	1.06
3:B:866:ILE:CG2	3:B:867:PRO:N	2.19	1.06
3:A:855:ALA:CA	3:A:1008:ILE:CG2	2.14	1.06
3:B:999:LEU:CD1	3:B:1013:HIS:CA	2.10	1.06
3:A:773:ARG:HB3	3:B:778:GLN:HE22	0.92	1.06
3:B:812:GLY:C	3:B:813:PHE:HA	1.74	1.06
1:E:8:DT:H1'	1:E:9:DG:O5'	1.56	1.05
2:D:21:DOC:H3'1	5:A:1222:DTP:H5'1	1.37	1.05
3:A:698:ARG:O	3:A:701:PRO:HD2	1.55	1.05
3:B:455:ASN:HD21	3:B:760:GLY:CA	1.69	1.05
3:B:704:HIS:NE2	3:B:808:PHE:CE2	2.24	1.05
3:B:1035:PHE:HA	3:B:1170:GLY:HA3	1.33	1.05
3:B:996:ILE:HD11	3:B:1017:ARG:HB3	1.34	1.05
3:A:996:ILE:HD11	3:A:1018:TYR:HE2	0.92	1.05
3:A:773:ARG:CB	3:B:778:GLN:NE2	1.99	1.04
3:B:671:GLU:OE2	3:B:853:LYS:NZ	1.91	1.04
3:A:1013:HIS:H	3:A:1014:PRO:HD3	0.91	1.04
1:C:8:DT:C4'	3:A:622:LEU:HD23	1.88	1.04
3:A:523:LYS:HD3	3:A:1054:VAL:HG13	1.39	1.04
3:B:1035:PHE:CE1	3:B:1171:GLU:O	2.11	1.04
3:A:492:ILE:HG13	3:A:580:VAL:HG22	1.35	1.03
1:E:13:DC:C2'	1:E:14:DT:H5''	1.87	1.03
3:A:855:ALA:HB2	3:A:1008:ILE:HG23	1.38	1.03
3:A:230:ILE:HD13	3:A:565:LEU:HD13	1.39	1.03
3:A:457:GLU:OE2	3:A:758:SER:OG	1.75	1.03
3:B:458:ARG:NH1	3:B:764:LEU:CD2	2.22	1.02
3:A:634:ILE:HG22	3:A:838:GLU:CB	1.89	1.02
3:A:492:ILE:CD1	3:A:616:LYS:HG3	1.87	1.02
3:B:491:GLN:HB2	3:B:574:VAL:HG11	1.38	1.02
3:A:774:VAL:HG23	3:B:778:GLN:HB3	1.05	1.02
3:A:321:ARG:HH22	3:A:440:ASN:ND2	1.57	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:574:VAL:CG2	3:B:601:VAL:CG2	2.36	1.02
1:C:9:DG:C4'	3:A:621:GLY:N	2.12	1.02
3:B:817:HIS:CE1	5:B:1222:DTP:H2'1	1.90	1.02
1:E:14:DT:C4'	3:B:509:ARG:HH22	1.73	1.02
1:E:13:DC:H2''	1:E:14:DT:C5'	1.89	1.02
3:A:774:VAL:CG2	3:B:778:GLN:CB	2.38	1.02
1:C:8:DT:C3'	3:A:623:ARG:N	2.23	1.01
3:B:491:GLN:CB	3:B:574:VAL:HG11	1.89	1.01
1:C:8:DT:OP2	3:A:623:ARG:HB2	1.59	1.01
3:A:1129:LYS:CA	3:A:1200:PRO:HA	1.67	1.01
3:B:447:GLY:H	3:B:815:LYS:NZ	1.58	1.01
3:B:1123:GLU:O	3:B:1126:GLU:OE1	1.79	1.01
3:B:704:HIS:CD2	3:B:808:PHE:CE2	2.48	1.01
2:D:21:DOC:H6	2:D:21:DOC:H5''	1.39	1.01
3:A:634:ILE:HG22	3:A:838:GLU:HB3	1.40	1.01
3:B:996:ILE:HG13	3:B:1017:ARG:HD2	1.41	1.01
3:A:455:ASN:OD1	3:A:760:GLY:HA3	1.58	1.01
3:A:1129:LYS:C	3:A:1199:VAL:O	1.99	1.00
3:A:774:VAL:HB	3:B:778:GLN:HG2	1.04	1.00
3:A:1028:THR:O	3:A:1031:GLU:N	1.93	1.00
3:B:743:TYR:C	3:B:813:PHE:N	2.15	1.00
3:A:523:LYS:HD3	3:A:1054:VAL:CG1	1.92	1.00
3:A:743:TYR:HA	3:A:813:PHE:N	1.77	1.00
3:A:745:GLU:OE1	3:A:813:PHE:O	1.78	1.00
2:D:6:DC:H2''	2:D:7:DG:OP2	1.58	1.00
3:A:234:THR:O	3:A:510:VAL:HG13	1.61	1.00
3:A:862:ARG:HE	3:A:868:VAL:HB	1.27	1.00
1:C:8:DT:H1'	1:C:9:DG:O5'	1.60	1.00
3:A:774:VAL:HB	3:B:778:GLN:CG	1.91	1.00
3:A:832:LYS:CB	3:A:839:PHE:CE2	2.45	1.00
3:B:996:ILE:CG1	3:B:1017:ARG:CB	2.39	1.00
3:A:774:VAL:CB	3:B:778:GLN:CG	2.40	0.99
3:A:634:ILE:CG2	3:A:838:GLU:CB	2.39	0.99
3:A:627:PHE:HA	3:A:846:VAL:HG21	1.43	0.99
3:B:1126:GLU:HG3	3:B:1205:PHE:CE2	1.97	0.99
3:A:575:HIS:HB3	3:A:578:GLY:HA3	1.38	0.99
3:A:1046:LEU:HD21	3:A:1202:ARG:HE	1.27	0.99
3:B:996:ILE:HG13	3:B:1017:ARG:CD	1.85	0.99
3:B:832:LYS:HA	3:B:839:PHE:CD2	1.97	0.99
3:B:543:PRO:O	3:B:546:ARG:CD	2.11	0.99
1:C:8:DT:H5'	3:A:622:LEU:CD2	1.88	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1013:HIS:HD2	3:A:1015:VAL:H	1.00	0.99
1:E:8:DT:H5''	3:B:622:LEU:CD2	1.92	0.98
3:B:455:ASN:ND2	3:B:760:GLY:O	1.96	0.98
3:A:496:GLY:O	3:A:569:ASN:CA	2.09	0.98
3:A:424:ARG:NH1	5:A:1222:DTP:C4'	2.25	0.98
3:B:627:PHE:HE1	3:B:843:LEU:N	1.62	0.98
2:D:21:DOC:C2'	5:A:1222:DTP:O4'	2.12	0.98
3:B:58:LYS:CB	3:B:287:ILE:CD1	2.40	0.98
3:A:546:ARG:NE	3:A:547:ALA:HB2	1.78	0.98
3:A:699:PRO:O	3:A:811:TYR:HD2	1.47	0.98
2:D:9:DC:H1'	2:D:10:DG:C5'	1.93	0.98
3:B:546:ARG:NE	3:B:547:ALA:HB2	1.79	0.98
3:A:458:ARG:NE	3:A:764:LEU:HD21	1.78	0.98
3:B:1035:PHE:CE1	3:B:1171:GLU:C	2.37	0.98
2:D:21:DOC:C5'	2:D:21:DOC:H6	1.93	0.97
3:B:455:ASN:ND2	3:B:760:GLY:CA	2.26	0.97
3:A:745:GLU:OE2	3:A:814:ASN:ND2	1.97	0.97
3:A:1129:LYS:HA	3:A:1200:PRO:HA	1.38	0.97
3:B:627:PHE:HA	3:B:846:VAL:HG21	1.46	0.97
3:B:831:VAL:HB	3:B:839:PHE:HE1	1.19	0.97
1:C:11:DC:H4'	3:A:573:SER:HB3	1.45	0.97
3:B:999:LEU:CD1	3:B:1013:HIS:N	2.26	0.97
3:A:844:LEU:HD22	3:A:880:PHE:HZ	1.27	0.97
1:C:8:DT:H5'	3:A:622:LEU:HD23	1.38	0.97
3:A:855:ALA:HA	3:A:1008:ILE:CG2	1.88	0.96
3:A:455:ASN:ND2	3:A:760:GLY:HA2	1.80	0.96
2:F:19:DC:H5''	3:B:531:LYS:HZ1	1.24	0.96
3:B:999:LEU:HD11	3:B:1013:HIS:H	1.29	0.96
3:A:774:VAL:CA	3:B:778:GLN:HG2	1.95	0.96
3:A:773:ARG:C	3:B:778:GLN:NE2	2.00	0.96
3:B:424:ARG:NE	5:B:1222:DTP:H4'	1.81	0.96
3:A:1129:LYS:HA	3:A:1200:PRO:N	1.80	0.96
3:A:996:ILE:CD1	3:A:1018:TYR:HE2	1.79	0.96
3:B:812:GLY:C	3:B:813:PHE:CA	2.33	0.96
3:B:1035:PHE:CD1	3:B:1171:GLU:N	2.33	0.95
1:E:8:DT:O3'	3:B:623:ARG:N	1.98	0.95
3:A:539:PHE:HZ	3:A:559:ILE:CG2	1.79	0.95
3:A:634:ILE:HG21	3:A:838:GLU:HB3	1.49	0.95
3:A:574:VAL:CG2	3:A:601:VAL:HG21	1.73	0.95
3:A:866:ILE:HG23	3:A:867:PRO:HD2	0.95	0.95
3:A:496:GLY:O	3:A:569:ASN:CB	2.14	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:774:VAL:CG2	3:B:778:GLN:HB3	1.95	0.94
3:B:491:GLN:HB2	3:B:574:VAL:HG13	0.95	0.94
1:C:10:DG:H4'	3:A:576:ALA:HA	1.45	0.94
3:B:539:PHE:HZ	3:B:559:ILE:CG2	1.79	0.94
3:A:575:HIS:CD2	3:A:578:GLY:CA	2.50	0.94
3:A:865:GLY:O	3:A:866:ILE:HG13	1.66	0.94
3:A:776:GLU:CG	3:B:775:GLU:HG3	1.98	0.94
2:F:21:DOC:H2''	3:B:424:ARG:HH12	1.29	0.94
3:A:539:PHE:CZ	3:A:559:ILE:CG2	2.51	0.94
3:A:535:LEU:HD23	3:A:539:PHE:HE1	1.30	0.94
3:A:774:VAL:N	3:B:778:GLN:CG	2.31	0.94
3:B:699:PRO:O	3:B:811:TYR:CD1	2.15	0.94
3:A:696:LEU:HG	3:A:742:VAL:CG1	1.96	0.94
1:C:9:DG:C3'	3:A:621:GLY:HA3	1.97	0.94
3:A:543:PRO:O	3:A:546:ARG:CD	2.16	0.94
3:A:455:ASN:ND2	3:A:760:GLY:O	2.01	0.93
3:B:999:LEU:HB3	3:B:1014:PRO:CG	1.97	0.93
3:B:539:PHE:CZ	3:B:559:ILE:CG2	2.51	0.93
3:B:711:ARG:HG2	3:B:716:GLU:O	1.68	0.93
3:B:535:LEU:HD23	3:B:539:PHE:HE1	1.31	0.93
3:A:779:LYS:HZ2	3:B:774:VAL:HA	1.33	0.93
3:B:452:ARG:HH22	3:B:766:ARG:NH2	1.63	0.93
3:B:493:GLY:N	3:B:602:THR:HB	1.83	0.93
1:E:18:DC:P	3:B:933:ARG:HD3	2.09	0.93
3:B:831:VAL:CB	3:B:839:PHE:CD1	2.51	0.93
3:B:546:ARG:NH1	3:B:547:ALA:HB2	1.83	0.93
3:B:58:LYS:HB2	3:B:287:ILE:CD1	1.98	0.93
3:A:1143:LYS:HA	3:A:1147:ARG:HB2	1.50	0.93
3:A:855:ALA:HA	3:A:1008:ILE:HG21	0.94	0.92
3:B:321:ARG:NH2	3:B:440:ASN:HD21	1.68	0.92
3:A:1026:SER:HB3	3:A:1202:ARG:NH2	1.84	0.92
3:A:773:ARG:CG	3:B:778:GLN:CD	2.29	0.92
3:A:844:LEU:CD2	3:A:880:PHE:CE1	2.51	0.92
3:A:1013:HIS:CD2	3:A:1015:VAL:HG12	2.05	0.92
3:A:696:LEU:HG	3:A:742:VAL:HG13	1.51	0.92
3:B:575:HIS:HB3	3:B:578:GLY:HA3	1.48	0.92
3:A:844:LEU:HD13	3:A:880:PHE:CE2	2.05	0.92
1:C:8:DT:OP1	3:A:623:ARG:HB2	1.69	0.92
3:B:707:THR:HG22	3:B:716:GLU:OE2	1.68	0.92
2:D:5:DA:H2''	2:D:6:DC:OP2	1.68	0.92
3:B:54:VAL:HG21	3:B:604:TYR:CD1	2.04	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:831:VAL:HG12	3:B:839:PHE:CG	2.05	0.92
1:E:8:DT:H4'	3:B:622:LEU:CD2	1.99	0.91
3:A:230:ILE:HD11	3:A:565:LEU:CD1	1.90	0.91
3:A:701:PRO:HD3	3:A:811:TYR:HB3	1.52	0.91
3:B:1143:LYS:HA	3:B:1147:ARG:HB2	1.50	0.91
3:A:627:PHE:CA	3:A:846:VAL:HG21	2.00	0.91
3:A:832:LYS:HB2	3:A:839:PHE:CZ	2.04	0.91
3:A:1035:PHE:CD1	3:A:1171:GLU:O	2.23	0.91
3:A:773:ARG:HB3	3:B:778:GLN:NE2	1.74	0.91
3:B:1141:ASP:O	3:B:1143:LYS:N	2.02	0.91
3:B:996:ILE:CD1	3:B:1017:ARG:HB3	1.99	0.91
3:B:447:GLY:H	3:B:815:LYS:HZ2	0.95	0.91
3:B:831:VAL:CB	3:B:839:PHE:CE1	2.53	0.91
3:B:862:ARG:HE	3:B:868:VAL:HB	1.36	0.91
3:B:321:ARG:NH2	3:B:440:ASN:ND2	2.18	0.91
3:A:866:ILE:CG2	3:A:867:PRO:CD	2.45	0.91
2:D:21:DOC:H2''	3:A:424:ARG:HH11	1.16	0.91
1:E:8:DT:C5'	3:B:622:LEU:HD23	2.00	0.91
3:B:866:ILE:HG22	3:B:867:PRO:C	1.92	0.91
3:A:1099:LEU:HD22	3:A:1119:TRP:O	1.71	0.90
3:B:110:VAL:HG11	3:B:587:THR:O	1.71	0.90
1:E:9:DG:H1'	1:E:10:DG:C5'	2.01	0.90
3:B:496:GLY:O	3:B:569:ASN:HA	1.71	0.90
3:A:1013:HIS:HE1	3:A:1073:GLU:HB3	1.35	0.90
3:A:575:HIS:HB3	3:A:578:GLY:CA	2.00	0.90
3:A:775:GLU:CD	3:B:781:ARG:HE	1.74	0.90
3:A:321:ARG:HH22	3:A:440:ASN:HD21	1.18	0.90
1:E:17:DC:O3'	3:B:933:ARG:HD3	1.69	0.90
3:B:452:ARG:HH21	3:B:766:ARG:CZ	1.81	0.90
3:A:1024:VAL:HG23	3:A:1200:PRO:HD2	1.51	0.90
2:F:21:DOC:C2'	3:B:424:ARG:HH12	1.81	0.90
3:B:1126:GLU:HG3	3:B:1205:PHE:CZ	2.07	0.90
3:B:744:GLN:N	3:B:813:PHE:O	2.05	0.90
3:B:458:ARG:NH2	3:B:764:LEU:HD13	1.87	0.90
3:A:627:PHE:CZ	3:A:843:LEU:HG	2.06	0.89
3:A:458:ARG:NH2	3:A:764:LEU:HD13	1.86	0.89
1:E:14:DT:O5'	3:B:509:ARG:NH1	2.03	0.89
3:A:698:ARG:C	3:A:701:PRO:HD2	1.91	0.89
3:B:110:VAL:HG12	3:B:587:THR:HG22	1.52	0.89
3:A:698:ARG:O	3:A:701:PRO:N	2.06	0.89
1:E:10:DG:H4'	3:B:576:ALA:HA	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:58:LYS:HB3	3:B:287:ILE:CD1	2.01	0.89
3:A:289:ASP:HB3	3:B:62:ALA:O	1.73	0.89
3:B:866:ILE:HG22	3:B:867:PRO:N	1.84	0.89
3:A:458:ARG:CD	3:A:764:LEU:HD21	2.03	0.89
3:B:428:ALA:HB3	3:B:816:SER:HB2	1.54	0.89
3:B:665:LYS:NZ	3:B:864:LEU:HD13	1.87	0.89
3:B:999:LEU:HB3	3:B:1014:PRO:HG3	1.55	0.89
3:A:627:PHE:CE1	3:A:843:LEU:HA	2.07	0.89
3:A:862:ARG:NH2	3:A:1010:VAL:HG13	1.87	0.89
3:B:1128:PRO:HG3	3:B:1129:LYS:NZ	1.88	0.89
3:B:492:ILE:CD1	3:B:580:VAL:HG22	2.03	0.88
1:E:14:DT:H4'	3:B:509:ARG:HH22	0.78	0.88
2:D:19:DC:H2'	3:A:531:LYS:NZ	1.87	0.88
3:B:1140:LEU:HD12	3:B:1143:LYS:NZ	1.88	0.88
2:F:20:DA:C2'	2:F:21:DOC:H5'	2.02	0.88
3:B:844:LEU:HD22	3:B:880:PHE:CZ	2.06	0.88
3:A:994:ASP:HB2	3:A:1017:ARG:NH2	1.89	0.88
3:A:492:ILE:HD11	3:A:616:LYS:HB2	1.52	0.88
3:A:696:LEU:CD2	3:A:742:VAL:HG13	2.02	0.88
3:B:235:THR:HA	3:B:510:VAL:O	1.72	0.88
3:B:832:LYS:HB2	3:B:839:PHE:HE2	1.27	0.88
3:B:996:ILE:HG13	3:B:1017:ARG:HB2	1.51	0.88
3:A:627:PHE:CE1	3:A:843:LEU:N	2.41	0.88
1:C:24:DT:H2''	1:C:25:DT:P	2.14	0.88
3:A:539:PHE:CZ	3:A:559:ILE:HG21	2.09	0.87
3:B:665:LYS:CD	3:B:860:ASP:CB	2.46	0.87
3:A:1013:HIS:CD2	3:A:1015:VAL:H	1.92	0.87
3:B:996:ILE:HB	3:B:1017:ARG:HD2	1.55	0.87
3:A:996:ILE:HD11	3:A:1018:TYR:CZ	2.09	0.87
3:B:575:HIS:HB3	3:B:578:GLY:CA	2.03	0.87
3:A:851:SER:HG	3:A:895:LYS:HE2	1.36	0.87
3:B:744:GLN:H	3:B:813:PHE:CA	1.87	0.87
3:B:866:ILE:HG23	3:B:867:PRO:N	1.89	0.87
3:A:627:PHE:HE1	3:A:843:LEU:CA	1.87	0.87
3:A:1129:LYS:CA	3:A:1200:PRO:CA	2.42	0.87
3:B:743:TYR:CA	3:B:813:PHE:N	2.38	0.86
1:C:15:DG:N1	2:D:14:DA:C2	2.42	0.86
3:B:539:PHE:CZ	3:B:559:ILE:HG21	2.09	0.86
1:E:8:DT:H5''	3:B:622:LEU:HD21	1.57	0.86
1:E:14:DT:C4'	3:B:509:ARG:NH2	2.36	0.86
3:A:698:ARG:HG3	3:A:701:PRO:CG	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:8:DT:C5'	3:B:622:LEU:CD2	2.53	0.86
3:B:627:PHE:CE1	3:B:843:LEU:HA	2.10	0.86
1:C:8:DT:O3'	3:A:623:ARG:N	2.09	0.86
3:B:492:ILE:CG1	3:B:580:VAL:CG2	2.26	0.86
3:A:1028:THR:HG23	3:A:1030:GLU:HB3	1.58	0.86
1:C:10:DG:O4'	3:A:576:ALA:HA	1.76	0.86
1:C:9:DG:N3	3:A:576:ALA:HB2	1.91	0.86
1:C:15:DG:C2	2:D:14:DA:N3	2.43	0.86
3:A:1024:VAL:HG22	3:A:1200:PRO:HD2	1.56	0.86
3:B:574:VAL:CG2	3:B:601:VAL:HG22	2.01	0.86
1:E:8:DT:C3'	3:B:623:ARG:H	1.89	0.86
3:B:831:VAL:HG11	3:B:839:PHE:HD1	1.38	0.85
2:F:21:DOC:H4'	3:B:618:ASP:OD1	1.76	0.85
2:D:21:DOC:H3'1	5:A:1222:DTP:C5'	2.06	0.85
3:B:848:ARG:HE	3:B:879:ASP:CG	1.79	0.85
3:B:627:PHE:CA	3:B:846:VAL:HG21	2.06	0.85
3:A:774:VAL:CG2	3:B:778:GLN:HG2	2.06	0.85
3:B:458:ARG:HD2	3:B:764:LEU:HD21	1.58	0.85
3:A:994:ASP:CB	3:A:1017:ARG:NH2	2.39	0.85
1:C:11:DC:H3'	1:C:11:DC:OP1	1.75	0.85
3:A:858:ILE:CD1	3:A:889:PHE:CE1	2.60	0.85
3:B:491:GLN:CG	3:B:574:VAL:HG11	2.07	0.85
3:A:424:ARG:HH11	5:A:1222:DTP:H4'	1.33	0.85
1:C:8:DT:H3'	3:A:623:ARG:N	1.85	0.85
3:B:548:GLU:O	3:B:550:GLU:N	2.10	0.85
3:A:1027:CYS:SG	3:A:1031:GLU:HB3	2.14	0.85
3:B:832:LYS:N	3:B:839:PHE:CE1	2.44	0.85
3:A:627:PHE:CE1	3:A:843:LEU:CA	2.59	0.85
3:A:546:ARG:NH1	3:A:547:ALA:HB2	1.91	0.85
3:B:448:LEU:HD22	3:B:816:SER:N	1.90	0.85
3:B:294:ARG:HB2	3:B:613:GLY:O	1.77	0.85
3:B:321:ARG:HH22	3:B:440:ASN:HD21	0.85	0.85
3:B:866:ILE:HG22	3:B:867:PRO:O	1.76	0.85
3:B:51:PHE:CE2	3:B:603:GLN:HG2	2.11	0.85
3:B:54:VAL:HG23	3:B:604:TYR:CE2	2.09	0.85
3:B:539:PHE:HZ	3:B:559:ILE:HG23	1.42	0.85
3:A:696:LEU:HD21	3:A:742:VAL:HG22	0.89	0.85
3:B:58:LYS:CB	3:B:287:ILE:HD12	2.06	0.85
2:D:20:DA:C2'	2:D:21:DOC:H5'	2.05	0.84
1:C:11:DC:H4'	3:A:573:SER:CB	2.07	0.84
1:E:6:DT:H2"	1:E:7:DG:OP2	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:996:ILE:CD1	3:B:1017:ARG:HD2	1.74	0.84
3:B:744:GLN:HG3	3:B:813:PHE:HA	1.58	0.84
3:A:855:ALA:CB	3:A:1008:ILE:HG21	1.67	0.84
1:E:9:DG:H1'	1:E:10:DG:H5''	1.59	0.84
3:A:844:LEU:HB2	3:A:880:PHE:CD1	2.12	0.84
1:E:9:DG:H2''	1:E:10:DG:C5'	2.08	0.84
1:E:9:DG:H4'	3:B:621:GLY:H	1.41	0.84
3:B:546:ARG:HD3	3:B:546:ARG:C	1.95	0.84
3:B:711:ARG:HD3	3:B:718:VAL:HG22	1.60	0.84
2:F:13:DC:H1'	2:F:14:DA:O5'	1.78	0.84
1:C:9:DG:OP1	3:A:470:ASP:CB	2.26	0.84
3:A:539:PHE:HZ	3:A:559:ILE:HG23	1.42	0.83
3:A:743:TYR:CA	3:A:813:PHE:N	2.41	0.83
3:A:774:VAL:HG23	3:B:778:GLN:CG	2.07	0.83
3:B:447:GLY:N	3:B:815:LYS:HZ2	1.75	0.83
3:A:774:VAL:HG21	3:B:778:GLN:HA	1.61	0.83
3:A:1118:VAL:CG1	3:A:1119:TRP:N	2.41	0.83
3:B:627:PHE:CB	3:B:846:VAL:HG21	2.09	0.83
3:B:832:LYS:CA	3:B:839:PHE:CD2	2.60	0.83
3:A:1024:VAL:CG2	3:A:1200:PRO:CD	2.57	0.83
3:B:858:ILE:CD1	3:B:889:PHE:CZ	2.61	0.83
3:B:424:ARG:CZ	5:B:1222:DTP:C4'	2.56	0.83
1:C:16:DG:O6	2:D:12:DC:N3	2.12	0.82
3:A:671:GLU:OE2	3:A:853:LYS:NZ	2.12	0.82
3:B:1035:PHE:HA	3:B:1170:GLY:CA	2.09	0.82
3:B:858:ILE:HD11	3:B:889:PHE:CZ	2.14	0.82
3:A:862:ARG:NE	3:A:868:VAL:HB	1.93	0.82
3:A:1046:LEU:HD21	3:A:1202:ARG:NE	1.94	0.82
3:B:840:MET:HA	3:B:840:MET:HE2	1.62	0.82
3:A:492:ILE:CD1	3:A:616:LYS:CG	2.58	0.82
1:C:14:DT:H4'	3:A:509:ARG:HH12	1.44	0.82
3:A:627:PHE:CB	3:A:846:VAL:HG21	2.09	0.82
1:C:9:DG:C5'	3:A:621:GLY:N	2.43	0.82
3:A:425:GLY:H	3:A:817:HIS:CD2	1.96	0.82
3:B:743:TYR:HA	3:B:813:PHE:N	1.94	0.82
3:A:858:ILE:HD13	3:A:889:PHE:CZ	2.10	0.82
3:B:424:ARG:CZ	5:B:1222:DTP:H4'	2.10	0.82
2:F:14:DA:H1'	2:F:15:DG:C8	2.15	0.82
3:B:832:LYS:CA	3:B:839:PHE:CE2	2.63	0.82
1:E:9:DG:H2''	1:E:10:DG:H5'	1.61	0.82
3:B:627:PHE:HB2	3:B:846:VAL:HG11	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:521:LEU:HD21	3:A:548:GLU:HG2	1.61	0.81
3:A:776:GLU:HG3	3:B:774:VAL:HG12	1.59	0.81
3:A:696:LEU:CG	3:A:742:VAL:HG13	2.09	0.81
3:B:535:LEU:HD23	3:B:539:PHE:CE1	2.16	0.81
3:A:523:LYS:HD2	3:A:1094:LYS:HZ2	1.42	0.81
3:A:1028:THR:CG2	3:A:1030:GLU:HB3	2.10	0.81
3:A:535:LEU:HD23	3:A:539:PHE:CE1	2.16	0.81
3:A:424:ARG:CZ	5:A:1222:DTP:O3'	2.28	0.81
1:C:9:DG:N3	3:A:576:ALA:HB3	1.93	0.81
1:C:8:DT:OP1	3:A:623:ARG:CB	2.28	0.81
2:D:18:DC:H2''	2:D:19:DC:OP2	1.79	0.81
3:B:458:ARG:CZ	3:B:764:LEU:CD1	2.58	0.81
3:A:234:THR:O	3:A:510:VAL:CG1	2.29	0.81
1:E:17:DC:H2''	1:E:18:DC:OP2	1.80	0.81
2:F:12:DC:H2''	2:F:13:DC:OP2	1.78	0.81
2:D:19:DC:OP2	3:A:531:LYS:HE2	1.79	0.81
3:A:575:HIS:HD2	3:A:578:GLY:CA	1.92	0.81
1:C:8:DT:P	3:A:623:ARG:CB	2.65	0.81
3:B:424:ARG:CZ	5:B:1222:DTP:O4'	2.29	0.81
3:B:696:LEU:HD21	3:B:742:VAL:HG22	0.84	0.81
2:D:19:DC:H2'	3:A:531:LYS:HZ2	1.42	0.81
1:C:15:DG:N2	2:D:14:DA:N3	2.29	0.80
1:C:14:DT:O4	2:D:14:DA:N6	2.14	0.80
3:A:743:TYR:C	3:A:813:PHE:N	2.34	0.80
3:A:492:ILE:HG21	3:A:606:MET:HA	1.61	0.80
3:B:714:GLY:O	3:B:715:GLN:CG	2.29	0.80
3:B:452:ARG:HG3	3:B:748:MET:SD	2.21	0.80
3:B:858:ILE:CD1	3:B:889:PHE:HZ	1.94	0.80
1:C:9:DG:H4'	3:A:621:GLY:H	0.65	0.80
3:A:1028:THR:HG22	3:A:1031:GLU:HG3	1.64	0.80
3:A:845:SER:HG	3:A:879:ASP:CG	1.82	0.80
1:C:9:DG:OP1	3:A:470:ASP:HB2	1.82	0.80
3:A:1013:HIS:ND1	3:A:1073:GLU:HB2	1.95	0.80
3:A:575:HIS:CG	3:A:578:GLY:N	2.40	0.80
3:A:779:LYS:HZ1	3:B:774:VAL:HA	1.47	0.80
3:A:744:GLN:H	3:A:813:PHE:CA	1.95	0.80
3:A:575:HIS:HD2	3:A:577:ALA:C	1.85	0.80
3:B:1125:LEU:O	3:B:1126:GLU:CG	2.30	0.80
3:A:866:ILE:HG22	3:A:867:PRO:N	1.96	0.80
3:B:866:ILE:HG23	3:B:867:PRO:CD	2.11	0.80
3:B:844:LEU:CB	3:B:880:PHE:CD1	2.59	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:743:TYR:H	3:B:746:GLN:HE21	1.30	0.79
2:F:20:DA:H2''	2:F:21:DOC:C5'	2.10	0.79
3:A:774:VAL:CG2	3:B:778:GLN:CG	2.60	0.79
3:A:743:TYR:H	3:A:746:GLN:HE21	1.30	0.79
1:E:8:DT:H5''	3:B:622:LEU:HD23	1.62	0.79
3:A:575:HIS:CB	3:A:578:GLY:HA3	2.11	0.79
2:F:14:DA:H2''	2:F:15:DG:OP2	1.82	0.79
3:A:458:ARG:HD2	3:A:764:LEU:HD21	1.62	0.79
3:A:999:LEU:HD11	3:A:1013:HIS:H	1.46	0.79
3:A:776:GLU:CB	3:B:775:GLU:HG3	2.12	0.79
3:A:523:LYS:NZ	3:A:1054:VAL:HG22	1.97	0.79
3:B:699:PRO:C	3:B:701:PRO:CD	2.51	0.79
2:F:9:DC:H2''	2:F:10:DG:OP2	1.82	0.79
3:B:1123:GLU:O	3:B:1126:GLU:CD	2.21	0.79
3:B:701:PRO:HD3	3:B:811:TYR:CG	2.18	0.79
3:B:1035:PHE:HD1	3:B:1171:GLU:N	1.76	0.79
1:C:9:DG:C4'	3:A:621:GLY:CA	2.60	0.79
3:A:523:LYS:HZ1	3:A:1054:VAL:HG22	1.48	0.79
3:A:566:GLU:O	3:A:568:LEU:N	2.16	0.79
3:B:492:ILE:HG13	3:B:580:VAL:HG22	0.79	0.78
1:C:10:DG:O4'	3:A:576:ALA:CB	2.30	0.78
3:B:546:ARG:CD	3:B:547:ALA:N	2.44	0.78
3:B:1026:SER:OG	3:B:1046:LEU:O	2.01	0.78
3:B:546:ARG:C	3:B:546:ARG:CD	2.51	0.78
3:B:704:HIS:NE2	3:B:808:PHE:HZ	1.80	0.78
3:A:840:MET:HE2	3:A:840:MET:HA	1.64	0.78
3:A:424:ARG:NE	5:A:1222:DTP:O3'	2.17	0.78
2:D:13:DC:H2''	2:D:14:DA:OP2	1.82	0.78
3:B:8:ALA:H	3:B:274:THR:HG21	1.49	0.78
3:B:999:LEU:CB	3:B:1014:PRO:CG	2.61	0.78
3:B:455:ASN:OD1	3:B:760:GLY:HA3	1.83	0.78
3:B:424:ARG:CD	5:B:1222:DTP:H4'	2.14	0.78
3:A:1118:VAL:HG13	3:A:1119:TRP:H	1.49	0.78
3:B:574:VAL:CG2	3:B:601:VAL:HG21	2.09	0.78
2:D:19:DC:P	3:A:531:LYS:NZ	2.57	0.78
1:C:23:DT:H1'	1:C:24:DT:O5'	1.82	0.78
3:A:8:ALA:H	3:A:274:THR:HG21	1.49	0.78
3:B:1046:LEU:HD21	3:B:1202:ARG:HH21	0.65	0.77
3:A:844:LEU:CG	3:A:880:PHE:CE1	2.68	0.77
3:A:574:VAL:HG23	3:A:601:VAL:HG21	1.66	0.77
3:A:230:ILE:HD12	3:A:565:LEU:CD1	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:523:LYS:HD2	3:A:1094:LYS:HZ1	1.43	0.77
2:F:18:DC:H2''	2:F:19:DC:OP2	1.83	0.77
3:A:546:ARG:C	3:A:546:ARG:CD	2.52	0.77
3:B:51:PHE:HE2	3:B:603:GLN:HG2	1.49	0.77
3:B:665:LYS:HD3	3:B:860:ASP:CG	2.04	0.77
2:D:14:DA:H2''	2:D:15:DG:OP2	1.83	0.77
3:A:845:SER:CA	3:A:879:ASP:OD1	2.28	0.77
3:A:627:PHE:HA	3:A:846:VAL:CG2	2.14	0.77
3:A:745:GLU:CD	3:A:814:ASN:HA	2.06	0.77
2:D:21:DOC:H2''	3:A:424:ARG:HH12	0.96	0.77
3:A:699:PRO:O	3:A:811:TYR:CE2	2.37	0.77
3:A:230:ILE:HD13	3:A:565:LEU:CD1	1.97	0.77
3:A:634:ILE:HG21	3:A:838:GLU:CB	2.10	0.76
3:B:665:LYS:CD	3:B:860:ASP:CG	2.50	0.76
3:A:546:ARG:HD3	3:A:546:ARG:C	2.05	0.76
3:A:1099:LEU:CD2	3:A:1119:TRP:O	2.33	0.76
3:A:745:GLU:OE1	3:A:814:ASN:HA	1.86	0.76
3:B:999:LEU:CB	3:B:1014:PRO:HG3	2.15	0.76
1:C:13:DC:H1'	1:C:14:DT:H5''	1.65	0.76
1:C:16:DG:N1	2:D:13:DC:O2	2.18	0.76
3:A:866:ILE:CG2	3:A:867:PRO:N	2.48	0.76
3:B:455:ASN:ND2	3:B:760:GLY:HA2	1.99	0.76
2:F:21:DOC:H2''	3:B:424:ARG:HH11	0.88	0.76
1:C:8:DT:OP2	3:A:623:ARG:CB	2.33	0.76
3:B:844:LEU:HB3	3:B:880:PHE:CE1	2.21	0.76
3:A:865:GLY:O	3:A:866:ILE:CG1	2.33	0.76
3:B:866:ILE:HG23	3:B:867:PRO:HD2	1.68	0.76
1:E:18:DC:OP1	3:B:933:ARG:HD3	1.86	0.76
1:E:17:DC:H5''	3:B:933:ARG:NH2	2.01	0.76
3:B:627:PHE:HA	3:B:846:VAL:CG2	2.15	0.76
3:A:858:ILE:HD11	3:A:889:PHE:CE1	2.16	0.75
3:A:455:ASN:CG	3:A:760:GLY:CA	2.53	0.75
3:A:994:ASP:HB2	3:A:1017:ARG:NH1	2.01	0.75
1:C:15:DG:C2	1:C:16:DG:C5	2.74	0.75
3:A:698:ARG:CG	3:A:701:PRO:CG	2.64	0.75
3:A:862:ARG:HH22	3:A:1010:VAL:HG13	1.51	0.75
3:B:667:VAL:HA	3:B:828:THR:HG21	1.69	0.75
3:A:546:ARG:NH2	3:A:547:ALA:HB2	2.01	0.75
3:B:698:ARG:O	3:B:701:PRO:HD2	1.86	0.75
1:E:15:DG:H1'	1:E:16:DG:H5'	1.67	0.75
3:A:696:LEU:HD11	3:A:742:VAL:HG21	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:DG:O4'	3:A:576:ALA:CA	2.34	0.75
3:A:667:VAL:HA	3:A:828:THR:HG21	1.69	0.75
3:B:627:PHE:HE1	3:B:842:ALA:C	1.90	0.75
2:F:21:DOC:H6	2:F:21:DOC:H5"	1.69	0.75
3:A:574:VAL:CB	3:A:601:VAL:HG22	2.15	0.75
1:C:9:DG:N3	3:A:576:ALA:HB1	2.01	0.75
3:A:1034:GLU:CD	3:A:1170:GLY:HA2	2.07	0.75
2:D:21:DOC:C2'	5:A:1222:DTP:C4'	2.64	0.75
1:E:10:DG:C4'	3:B:576:ALA:CB	2.65	0.74
3:A:539:PHE:CE2	3:A:559:ILE:HG21	2.22	0.74
3:B:627:PHE:HE1	3:B:843:LEU:CA	2.00	0.74
3:A:858:ILE:HD13	3:A:889:PHE:CE1	2.22	0.74
3:A:547:ALA:O	3:A:549:MET:N	2.19	0.74
1:C:15:DG:C6	2:D:14:DA:N1	2.55	0.74
2:D:12:DC:H2"	2:D:13:DC:C6	2.22	0.74
3:A:775:GLU:CD	3:B:781:ARG:HH21	1.90	0.74
3:A:1013:HIS:HD2	3:A:1015:VAL:N	1.82	0.74
3:A:844:LEU:HD13	3:A:880:PHE:CD2	2.21	0.74
2:F:4:DA:H2"	2:F:5:DA:OP2	1.86	0.74
3:A:745:GLU:OE2	3:A:814:ASN:HA	1.85	0.74
3:A:665:LYS:HD3	3:A:860:ASP:CG	2.08	0.74
3:A:230:ILE:HD12	3:A:565:LEU:HD11	1.69	0.74
3:B:539:PHE:CE2	3:B:559:ILE:HG21	2.22	0.74
3:B:1140:LEU:HB2	3:B:1143:LYS:HD2	1.70	0.74
1:C:14:DT:O2	2:D:15:DG:C2	2.40	0.74
1:E:9:DG:C2'	1:E:10:DG:C5'	2.66	0.74
1:C:9:DG:H3'	1:C:9:DG:OP1	1.88	0.74
3:B:1126:GLU:HG3	3:B:1205:PHE:HE2	1.50	0.74
2:F:21:DOC:C2'	3:B:424:ARG:HH11	1.84	0.74
3:A:698:ARG:CG	3:A:701:PRO:HG2	2.18	0.74
3:B:994:ASP:OD2	3:B:1017:ARG:CZ	2.35	0.74
2:D:14:DA:H3'	2:D:14:DA:OP1	1.88	0.74
3:A:774:VAL:CG2	3:B:778:GLN:CA	2.65	0.74
3:B:627:PHE:CE1	3:B:843:LEU:CA	2.70	0.74
3:B:665:LYS:HD2	3:B:860:ASP:HB3	1.70	0.73
3:B:425:GLY:H	3:B:817:HIS:CD2	2.06	0.73
1:E:10:DG:O4'	3:B:576:ALA:CB	2.35	0.73
3:A:1028:THR:O	3:A:1030:GLU:N	2.20	0.73
3:A:1013:HIS:N	3:A:1014:PRO:HD3	1.70	0.73
3:A:538:ALA:O	3:A:539:PHE:CD1	2.42	0.73
2:D:9:DC:Cl'	2:D:10:DG:H5"	2.13	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:538:ALA:O	3:B:539:PHE:CD1	2.42	0.73
3:A:776:GLU:OE1	3:B:775:GLU:OE2	2.06	0.73
3:A:845:SER:OG	3:A:879:ASP:CG	2.26	0.73
3:A:455:ASN:CG	3:A:760:GLY:HA3	2.08	0.73
3:B:817:HIS:CE1	5:B:1222:DTP:C2'	2.69	0.73
1:E:17:DC:H3'	3:B:933:ARG:NH1	2.02	0.73
3:B:58:LYS:HB3	3:B:287:ILE:HD12	1.67	0.73
3:B:660:SER:HB3	3:B:683:LYS:HD3	1.71	0.73
3:A:294:ARG:HB2	3:A:614:LEU:HD23	1.70	0.73
3:B:844:LEU:HB3	3:B:880:PHE:HD1	1.51	0.73
3:A:1046:LEU:CD2	3:A:1202:ARG:HE	2.02	0.73
3:B:448:LEU:HD13	3:B:816:SER:HA	1.70	0.73
2:F:19:DC:H5''	3:B:531:LYS:HZ3	1.54	0.73
3:A:523:LYS:CD	3:A:1054:VAL:HG13	2.17	0.73
3:B:744:GLN:HG3	3:B:813:PHE:CA	2.19	0.73
3:A:660:SER:HB3	3:A:683:LYS:HD3	1.71	0.73
3:B:996:ILE:HD11	3:B:1017:ARG:HD3	1.67	0.73
1:C:16:DG:O6	2:D:12:DC:C2	2.42	0.73
3:A:8:ALA:H	3:A:274:THR:CG2	2.01	0.73
3:A:1035:PHE:HD1	3:A:1171:GLU:O	1.70	0.72
3:B:567:GLY:C	3:B:568:LEU:N	2.42	0.72
3:A:858:ILE:HD12	3:A:1008:ILE:CD1	2.18	0.72
3:B:832:LYS:HA	3:B:839:PHE:CG	2.24	0.72
3:B:996:ILE:CG1	3:B:1017:ARG:HB2	2.14	0.72
3:A:547:ALA:O	3:A:550:GLU:N	2.22	0.72
1:C:9:DG:H3'	3:A:621:GLY:CA	2.14	0.72
3:B:8:ALA:H	3:B:274:THR:CG2	2.01	0.72
3:A:1118:VAL:HG12	3:A:1119:TRP:N	2.03	0.72
3:A:1024:VAL:HG21	3:A:1200:PRO:HG2	1.70	0.72
3:A:407:GLN:HG3	3:A:436:VAL:HG12	1.72	0.72
1:C:9:DG:P	1:C:9:DG:H2'	2.28	0.72
3:A:832:LYS:HB2	3:A:839:PHE:HE2	1.51	0.72
3:A:37:PRO:HB2	3:B:459:VAL:HG21	1.71	0.72
1:C:11:DC:P	1:C:11:DC:H3'	2.30	0.72
3:B:1035:PHE:HB2	3:B:1170:GLY:HA2	1.71	0.72
3:B:832:LYS:N	3:B:839:PHE:CD1	2.58	0.72
1:E:23:DT:H2''	1:E:24:DT:OP2	1.88	0.72
3:A:774:VAL:HG21	3:B:778:GLN:CA	2.20	0.72
3:A:523:LYS:HD3	3:A:1094:LYS:HZ3	1.51	0.72
1:C:9:DG:C3'	3:A:621:GLY:CA	2.67	0.72
3:A:696:LEU:HG	3:A:742:VAL:HG11	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:9:DG:OP1	3:A:470:ASP:HB3	1.90	0.72
1:C:23:DT:H2''	1:C:24:DT:OP2	1.87	0.72
3:B:407:GLN:HG3	3:B:436:VAL:HG12	1.72	0.72
3:A:1026:SER:OG	3:A:1046:LEU:O	2.07	0.71
1:C:16:DG:C6	2:D:13:DC:O2	2.43	0.71
3:B:446:PHE:HB3	3:B:815:LYS:HE2	1.71	0.71
3:B:448:LEU:CD1	3:B:816:SER:HA	2.21	0.71
1:C:8:DT:C4'	3:A:623:ARG:H	2.03	0.71
3:B:996:ILE:HD13	3:B:1018:TYR:CE2	2.25	0.71
3:A:627:PHE:HB2	3:A:846:VAL:HG21	1.70	0.71
3:B:996:ILE:HD12	3:B:1017:ARG:HD3	0.73	0.71
3:A:776:GLU:HG3	3:B:775:GLU:CG	2.18	0.71
3:B:701:PRO:CD	3:B:811:TYR:CD1	2.72	0.71
3:B:458:ARG:CZ	3:B:764:LEU:CD2	2.69	0.71
3:B:832:LYS:CB	3:B:839:PHE:CD2	2.73	0.71
2:F:19:DC:P	3:B:531:LYS:HE2	2.30	0.71
1:C:10:DG:H1'	1:C:11:DC:C5'	2.20	0.71
3:B:458:ARG:CZ	3:B:764:LEU:HD13	2.20	0.71
3:A:699:PRO:C	3:A:701:PRO:CD	2.57	0.71
2:D:9:DC:H2''	2:D:10:DG:OP2	1.90	0.71
1:E:17:DC:H3'	3:B:933:ARG:CZ	2.20	0.71
1:E:20:DT:H2''	1:E:21:DC:OP2	1.89	0.71
3:B:745:GLU:OE2	3:B:814:ASN:ND2	2.24	0.71
3:B:699:PRO:O	3:B:701:PRO:HD2	1.90	0.71
3:A:696:LEU:HD21	3:A:742:VAL:CB	2.21	0.70
3:B:491:GLN:C	3:B:492:ILE:O	2.29	0.70
3:B:492:ILE:HA	3:B:602:THR:OG1	1.91	0.70
1:E:9:DG:H1'	1:E:10:DG:H5'	1.71	0.70
3:B:537:GLU:O	3:B:539:PHE:N	2.24	0.70
3:A:776:GLU:CB	3:B:775:GLU:CG	2.69	0.70
3:B:575:HIS:CB	3:B:578:GLY:HA3	2.03	0.70
3:A:1159:LEU:HD11	3:A:1183:GLU:HG2	1.72	0.70
3:A:858:ILE:HD12	3:A:1008:ILE:HD13	1.72	0.70
1:E:9:DG:H4'	3:B:621:GLY:N	2.06	0.70
3:B:996:ILE:CD1	3:B:1017:ARG:CB	2.65	0.70
2:F:13:DC:H2''	2:F:14:DA:OP2	1.90	0.70
3:B:996:ILE:HD13	3:B:1018:TYR:HE2	1.56	0.70
3:A:1118:VAL:CG1	3:A:1119:TRP:H	2.00	0.70
2:F:21:DOC:C4'	3:B:618:ASP:OD1	2.39	0.70
3:B:546:ARG:NH2	3:B:547:ALA:HB2	2.03	0.70
1:E:18:DC:OP1	3:B:933:ARG:CB	2.31	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:696:LEU:O	3:A:701:PRO:HB2	1.91	0.70
3:B:58:LYS:NZ	3:B:608:ALA:HA	2.06	0.70
3:B:110:VAL:CG1	3:B:587:THR:O	2.40	0.70
3:A:1129:LYS:O	3:A:1130:ALA:HB2	1.92	0.70
3:B:704:HIS:CE1	3:B:808:PHE:HZ	2.10	0.70
3:A:496:GLY:O	3:A:569:ASN:HB3	1.92	0.70
2:D:13:DC:H1'	2:D:14:DA:O5'	1.92	0.69
3:A:835:TYR:O	3:A:839:PHE:HB3	1.91	0.69
3:B:844:LEU:CD2	3:B:880:PHE:CE1	2.72	0.69
3:B:58:LYS:HB2	3:B:287:ILE:HD13	1.72	0.69
3:B:1159:LEU:HD11	3:B:1183:GLU:HG2	1.72	0.69
2:D:12:DC:H3'	2:D:12:DC:OP1	1.92	0.69
1:E:17:DC:O3'	3:B:933:ARG:CD	2.40	0.69
3:A:774:VAL:CG2	3:B:778:GLN:HA	2.21	0.69
3:A:1129:LYS:O	3:A:1130:ALA:CB	2.40	0.69
3:A:994:ASP:HB3	3:A:1017:ARG:HH22	1.56	0.69
3:B:1140:LEU:HD12	3:B:1143:LYS:HZ1	1.54	0.69
3:A:537:GLU:O	3:A:539:PHE:N	2.24	0.69
1:C:8:DT:H5''	3:A:622:LEU:HD23	0.70	0.69
3:B:547:ALA:O	3:B:550:GLU:HB2	1.91	0.69
3:B:1176:LEU:HD23	3:B:1179:VAL:HB	1.75	0.69
1:C:10:DG:H1'	1:C:11:DC:H5'	1.72	0.69
3:A:492:ILE:HG13	3:A:580:VAL:CG2	2.20	0.69
1:C:8:DT:H3'	3:A:623:ARG:HB2	1.75	0.69
3:A:698:ARG:HG2	3:A:701:PRO:HG2	1.73	0.69
3:A:845:SER:HA	3:A:879:ASP:CG	2.12	0.69
3:A:634:ILE:CG2	3:A:838:GLU:HB2	2.22	0.69
3:B:58:LYS:HB3	3:B:287:ILE:HD11	1.74	0.69
3:A:458:ARG:NH2	3:A:764:LEU:CD1	2.56	0.69
3:A:699:PRO:O	3:A:701:PRO:CD	2.41	0.69
3:B:54:VAL:CG2	3:B:604:TYR:CD1	2.69	0.68
3:B:696:LEU:CG	3:B:742:VAL:HG22	2.23	0.68
3:B:866:ILE:HG22	3:B:867:PRO:CA	2.22	0.68
3:B:58:LYS:HB2	3:B:287:ILE:HD12	1.72	0.68
3:B:832:LYS:CB	3:B:839:PHE:CZ	2.57	0.68
3:A:458:ARG:NH2	3:A:764:LEU:HD22	2.08	0.68
3:A:994:ASP:HB3	3:A:1017:ARG:NH2	2.08	0.68
3:B:744:GLN:N	3:B:813:PHE:CA	2.52	0.68
3:B:831:VAL:CG1	3:B:839:PHE:CE1	2.69	0.68
2:F:7:DG:H2''	2:F:8:DA:OP2	1.94	0.68
3:A:845:SER:CB	3:A:879:ASP:CG	2.62	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:14:DA:H1'	2:D:15:DG:C8	2.29	0.68
3:B:1013:HIS:HB3	3:B:1015:VAL:HG12	1.76	0.68
3:A:457:GLU:OE2	3:A:758:SER:CB	2.42	0.68
3:A:1176:LEU:HD23	3:A:1179:VAL:HB	1.75	0.68
3:B:701:PRO:CD	3:B:811:TYR:CG	2.77	0.67
3:B:491:GLN:C	3:B:492:ILE:C	2.53	0.67
3:B:602:THR:HG22	3:B:604:TYR:H	1.60	0.67
2:D:19:DC:H5''	3:A:531:LYS:NZ	2.09	0.67
2:D:19:DC:OP2	3:A:531:LYS:CE	2.41	0.67
2:F:5:DA:H2''	2:F:6:DC:OP2	1.93	0.67
3:B:699:PRO:HB2	3:B:811:TYR:OH	1.94	0.67
1:C:22:DG:C4	2:D:7:DG:N2	2.62	0.67
1:C:9:DG:C2	3:A:576:ALA:CB	2.77	0.67
3:B:1021:LEU:HD23	3:B:1124:VAL:HG11	1.76	0.67
3:A:665:LYS:HD3	3:A:860:ASP:CB	2.25	0.67
3:A:1120:THR:O	3:A:1124:VAL:CG2	2.35	0.67
3:B:627:PHE:CE1	3:B:843:LEU:N	2.54	0.67
3:B:491:GLN:CD	3:B:574:VAL:HG11	2.14	0.67
3:A:638:SER:OG	3:A:838:GLU:OE1	2.11	0.67
3:A:491:GLN:C	3:A:492:ILE:N	2.48	0.67
3:B:546:ARG:HD3	3:B:547:ALA:H	1.59	0.67
1:E:15:DG:C2	2:F:14:DA:C2	2.83	0.67
3:B:1125:LEU:O	3:B:1126:GLU:CB	2.42	0.67
3:B:832:LYS:CG	3:B:839:PHE:CE2	2.78	0.67
3:A:773:ARG:NH1	3:B:775:GLU:OE1	2.28	0.67
1:E:10:DG:H5''	3:B:576:ALA:HB1	1.76	0.67
1:E:15:DG:H1'	1:E:16:DG:C5'	2.25	0.67
3:A:832:LYS:HA	3:A:839:PHE:CD2	2.29	0.67
3:A:698:ARG:HG3	3:A:701:PRO:CD	2.24	0.66
1:C:8:DT:H5'	3:A:622:LEU:HD21	1.75	0.66
3:A:776:GLU:CG	3:B:775:GLU:CG	2.73	0.66
3:A:77:ALA:O	3:A:129:ARG:NH2	2.28	0.66
3:B:999:LEU:HD22	3:B:1012:GLY:O	1.95	0.66
1:C:10:DG:O4'	3:A:576:ALA:HB2	1.93	0.66
3:B:627:PHE:CZ	3:B:843:LEU:HG	2.30	0.66
1:E:8:DT:C1'	1:E:9:DG:O5'	2.37	0.66
3:B:743:TYR:HA	3:B:813:PHE:CA	2.26	0.66
3:B:452:ARG:HH21	3:B:766:ARG:NE	1.93	0.66
3:A:535:LEU:CD2	3:A:539:PHE:CE1	2.78	0.66
1:E:10:DG:H4'	3:B:576:ALA:CA	2.25	0.66
3:B:996:ILE:CD1	3:B:1018:TYR:CE2	2.79	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1019:PRO:O	3:A:1023:GLU:HG2	1.96	0.66
1:E:9:DG:C2'	1:E:10:DG:H5'	2.24	0.66
2:D:21:DOC:C3'	5:A:1222:DTP:H5'1	2.20	0.66
1:C:13:DC:H2''	1:C:14:DT:H5'	1.77	0.66
3:B:1019:PRO:O	3:B:1023:GLU:HG2	1.96	0.66
3:A:425:GLY:H	3:A:817:HIS:HD2	1.40	0.66
1:C:10:DG:H5'	3:A:576:ALA:O	1.96	0.66
3:B:710:ARG:NH1	3:B:716:GLU:CD	2.45	0.66
3:B:744:GLN:OE1	3:B:814:ASN:HB2	1.96	0.66
2:D:5:DA:H1'	2:D:6:DC:O5'	1.95	0.66
3:B:951:ALA:HB2	3:B:993:LEU:HG	1.78	0.66
3:B:996:ILE:CG1	3:B:1017:ARG:HB3	2.17	0.66
3:A:696:LEU:CG	3:A:742:VAL:CG1	2.70	0.66
3:A:285:LEU:HB3	3:A:286:PRO:CD	2.26	0.66
1:E:8:DT:H2''	1:E:9:DG:OP2	1.96	0.65
1:C:15:DG:C4	1:C:16:DG:N7	2.64	0.65
3:B:698:ARG:O	3:B:701:PRO:HG2	1.96	0.65
3:B:77:ALA:O	3:B:129:ARG:NH2	2.28	0.65
1:E:9:DG:C1'	1:E:10:DG:C5'	2.73	0.65
1:C:14:DT:O3'	3:A:509:ARG:CZ	2.43	0.65
3:B:535:LEU:CD2	3:B:539:PHE:CE1	2.78	0.65
3:A:779:LYS:HZ2	3:B:774:VAL:CA	2.08	0.65
3:A:665:LYS:CG	3:A:860:ASP:OD2	2.44	0.65
3:B:448:LEU:HD13	3:B:816:SER:CB	2.26	0.65
3:B:1152:LEU:HB3	3:B:1179:VAL:HG11	1.78	0.65
3:A:602:THR:HG22	3:A:604:TYR:H	1.60	0.65
3:A:776:GLU:OE1	3:B:775:GLU:CD	2.34	0.65
3:B:491:GLN:C	3:B:492:ILE:CA	2.64	0.65
2:F:21:DOC:H6	2:F:21:DOC:C5'	2.26	0.65
3:A:696:LEU:CD2	3:A:742:VAL:CG1	2.75	0.65
3:A:855:ALA:HB2	3:A:1008:ILE:HG22	0.80	0.65
1:E:8:DT:H3'	3:B:623:ARG:HB2	1.79	0.65
1:C:9:DG:H1'	3:A:576:ALA:HB1	1.78	0.65
2:F:3:DA:H2''	2:F:4:DA:OP2	1.97	0.65
3:A:634:ILE:HG22	3:A:838:GLU:HB2	1.78	0.65
1:C:15:DG:H2''	1:C:16:DG:OP2	1.96	0.65
2:D:12:DC:C2'	2:D:13:DC:C6	2.80	0.65
3:A:951:ALA:HB2	3:A:993:LEU:HG	1.78	0.65
3:A:546:ARG:HD3	3:A:547:ALA:N	2.12	0.65
3:A:774:VAL:N	3:B:778:GLN:HG2	2.06	0.65
3:A:999:LEU:HD11	3:A:1013:HIS:N	2.04	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:835:TYR:O	3:B:839:PHE:HB2	1.97	0.65
1:C:17:DC:H2''	1:C:18:DC:OP2	1.96	0.65
3:A:773:ARG:O	3:B:778:GLN:NE2	2.29	0.65
3:B:1142:GLU:O	3:B:1143:LYS:HG3	1.96	0.65
3:B:828:THR:O	3:B:839:PHE:CZ	2.50	0.65
3:A:665:LYS:CD	3:A:860:ASP:CG	2.66	0.64
3:B:700:GLY:HA3	3:B:811:TYR:CE1	2.32	0.64
3:B:858:ILE:HD13	3:B:889:PHE:HZ	1.62	0.64
1:E:8:DT:H4'	3:B:622:LEU:HA	1.78	0.64
1:C:8:DT:H3'	3:A:623:ARG:CB	2.28	0.64
1:C:24:DT:C2'	1:C:25:DT:P	2.85	0.64
3:B:666:GLY:HA3	3:B:843:LEU:HD13	1.80	0.64
1:C:12:DA:H2''	1:C:13:DC:OP2	1.96	0.64
1:C:8:DT:C5'	3:A:622:LEU:HD21	2.18	0.64
3:A:835:TYR:O	3:A:839:PHE:CB	2.46	0.64
3:A:699:PRO:C	3:A:811:TYR:CD2	2.70	0.64
3:B:845:SER:HA	3:B:879:ASP:CG	2.18	0.64
3:B:458:ARG:NE	3:B:764:LEU:HD11	2.12	0.64
3:A:697:TYR:HE1	3:A:702:MET:SD	2.13	0.64
1:E:9:DG:C1'	1:E:10:DG:H5''	2.26	0.64
1:C:14:DT:C4'	3:A:509:ARG:HH12	2.11	0.64
1:C:7:DG:H1'	1:C:8:DT:O5'	1.97	0.64
3:A:458:ARG:HH12	3:A:764:LEU:HD22	1.51	0.64
3:A:1053:GLU:HB3	3:A:1068:PHE:HA	1.80	0.64
3:A:1028:THR:O	3:A:1028:THR:CG2	2.45	0.64
3:B:1035:PHE:HE1	3:B:1171:GLU:C	1.97	0.64
3:B:1023:GLU:O	3:B:1164:ARG:NH2	2.28	0.64
3:A:448:LEU:HD22	3:A:816:SER:HA	1.80	0.64
2:F:19:DC:C6	2:F:19:DC:OP2	2.51	0.64
3:A:697:TYR:CZ	3:A:702:MET:CE	2.80	0.64
3:B:858:ILE:HD13	3:B:889:PHE:CZ	2.31	0.64
3:B:1053:GLU:HB3	3:B:1068:PHE:HA	1.80	0.63
1:E:8:DT:H1'	1:E:9:DG:C5'	2.28	0.63
2:D:19:DC:H6	3:A:531:LYS:CE	2.11	0.63
3:A:575:HIS:CD2	3:A:577:ALA:C	2.67	0.63
3:B:698:ARG:O	3:B:701:PRO:CD	2.45	0.63
3:A:745:GLU:CD	3:A:815:LYS:H	2.02	0.63
3:B:1035:PHE:CZ	3:B:1171:GLU:O	2.50	0.63
3:A:1013:HIS:CD2	3:A:1015:VAL:CG1	2.81	0.63
1:E:9:DG:C2	2:F:20:DA:N1	2.67	0.63
1:C:10:DG:H2''	1:C:11:DC:O5'	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:575:HIS:CB	3:A:578:GLY:H	2.12	0.63
1:C:15:DG:O6	2:D:13:DC:N3	2.32	0.63
1:E:11:DC:H4'	3:B:573:SER:OG	1.99	0.63
2:D:19:DC:C6	2:D:19:DC:OP2	2.51	0.63
3:A:775:GLU:OE2	3:B:806:GLU:OE1	2.16	0.63
3:A:695:SER:HG	3:A:743:TYR:HE2	1.46	0.63
3:A:699:PRO:C	3:A:701:PRO:HD2	2.17	0.63
3:B:458:ARG:CZ	3:B:764:LEU:HD11	2.28	0.63
3:B:627:PHE:CE1	3:B:842:ALA:C	2.72	0.63
2:F:19:DC:C5'	3:B:531:LYS:HZ1	2.07	0.63
3:A:535:LEU:O	3:A:539:PHE:CD1	2.53	0.62
2:D:19:DC:C2'	3:A:531:LYS:NZ	2.60	0.62
2:D:19:DC:H6	2:D:19:DC:OP2	1.82	0.62
3:B:504:LEU:HD12	3:B:525:ILE:HD11	1.81	0.62
3:B:1140:LEU:HD12	3:B:1143:LYS:HZ2	1.63	0.62
3:B:498:LEU:N	3:B:568:LEU:O	2.32	0.62
2:F:20:DA:H4'	3:B:606:MET:HG3	1.81	0.62
1:C:8:DT:H4'	3:A:622:LEU:HA	0.80	0.62
3:B:698:ARG:HG3	3:B:811:TYR:HB3	1.80	0.62
3:A:1028:THR:O	3:A:1029:ILE:C	2.37	0.62
3:B:1140:LEU:HB2	3:B:1143:LYS:HZ2	1.62	0.62
1:C:8:DT:OP1	3:A:624:THR:N	2.33	0.62
1:C:15:DG:N1	1:C:16:DG:C6	2.67	0.62
2:D:11:DG:C2	2:D:12:DC:C2	2.87	0.62
1:C:24:DT:C3'	1:C:25:DT:P	2.86	0.62
3:B:701:PRO:HG3	3:B:811:TYR:CB	2.29	0.62
1:C:9:DG:C6	1:C:10:DG:C6	2.88	0.62
3:A:458:ARG:CZ	3:A:764:LEU:CD1	2.77	0.62
3:B:696:LEU:HG	3:B:742:VAL:HG13	1.81	0.62
3:A:662:GLY:HA3	3:A:680:ARG:HG3	1.82	0.62
3:A:310:LEU:HD22	3:A:400:PRO:HA	1.82	0.62
3:B:1039:LEU:HB3	3:B:1040:PRO:HD2	1.82	0.62
3:A:504:LEU:HD12	3:A:525:ILE:HD11	1.81	0.62
1:E:10:DG:C4'	3:B:576:ALA:HB2	2.28	0.61
2:D:19:DC:H5"	3:A:531:LYS:HZ3	1.63	0.61
2:F:14:DA:H8	2:F:14:DA:OP2	1.83	0.61
3:A:701:PRO:HD3	3:A:811:TYR:CB	2.28	0.61
3:A:1013:HIS:CE1	3:A:1073:GLU:CA	2.83	0.61
3:B:831:VAL:C	3:B:839:PHE:CD1	2.73	0.61
3:B:538:ALA:C	3:B:539:PHE:CD1	2.74	0.61
3:B:458:ARG:CD	3:B:764:LEU:HD21	2.28	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:666:GLY:HA3	3:B:843:LEU:CD1	2.30	0.61
3:B:832:LYS:N	3:B:839:PHE:CZ	2.68	0.61
1:E:16:DG:H1'	1:E:17:DC:H5'	1.82	0.61
3:A:458:ARG:NH1	3:A:764:LEU:HD21	1.90	0.61
3:A:1013:HIS:HE1	3:A:1073:GLU:CA	2.13	0.61
3:A:1013:HIS:O	3:A:1016:LEU:N	2.29	0.61
3:B:996:ILE:CD1	3:B:1017:ARG:CG	2.76	0.61
1:C:14:DT:C2	2:D:14:DA:N1	2.67	0.61
3:B:665:LYS:HB2	3:B:832:LYS:HZ1	1.65	0.61
3:B:492:ILE:HG13	3:B:580:VAL:HG23	1.68	0.61
3:B:535:LEU:O	3:B:539:PHE:CD1	2.53	0.61
1:E:22:DG:H2''	1:E:23:DT:OP2	1.99	0.61
3:A:695:SER:OG	3:A:743:TYR:HE2	1.82	0.61
3:B:447:GLY:N	3:B:815:LYS:NZ	2.40	0.61
3:A:776:GLU:HB2	3:B:775:GLU:HG3	1.81	0.61
3:A:696:LEU:HD23	3:A:742:VAL:HG13	1.82	0.61
3:B:458:ARG:NH2	3:B:764:LEU:CD1	2.60	0.61
3:A:1034:GLU:OE1	3:A:1170:GLY:HA2	2.00	0.61
3:B:662:GLY:HA3	3:B:680:ARG:HG3	1.81	0.61
3:A:999:LEU:CB	3:A:1014:PRO:HG3	2.31	0.61
1:C:8:DT:H4'	3:A:622:LEU:HD23	1.82	0.61
3:A:696:LEU:CD2	3:A:742:VAL:CG2	2.58	0.61
3:B:745:GLU:OE1	3:B:814:ASN:HA	2.00	0.61
3:B:458:ARG:NH1	3:B:764:LEU:HD21	2.14	0.61
1:C:12:DA:H1'	1:C:13:DC:H5'	1.81	0.61
3:B:535:LEU:HB3	3:B:563:MET:CE	2.31	0.61
3:A:1039:LEU:HB3	3:A:1040:PRO:HD2	1.82	0.61
3:A:538:ALA:C	3:A:539:PHE:CD1	2.74	0.60
1:C:12:DA:H1'	1:C:13:DC:C5'	2.31	0.60
3:A:742:VAL:H	3:A:746:GLN:NE2	1.99	0.60
3:B:496:GLY:O	3:B:569:ASN:OD1	2.18	0.60
3:A:574:VAL:CG2	3:A:601:VAL:HG23	2.18	0.60
3:A:424:ARG:NH1	5:A:1222:DTP:O4'	2.34	0.60
2:D:20:DA:H4'	3:A:606:MET:HG3	1.82	0.60
3:A:627:PHE:HE1	3:A:842:ALA:C	2.04	0.60
3:B:492:ILE:HG13	3:B:580:VAL:HG21	1.66	0.60
1:C:8:DT:H5''	3:A:622:LEU:HD22	1.66	0.60
3:A:1024:VAL:CG2	3:A:1200:PRO:CG	2.79	0.60
3:B:667:VAL:HA	3:B:828:THR:CG2	2.31	0.60
3:A:425:GLY:HA2	5:A:1222:DTP:O1B	2.00	0.60
3:A:698:ARG:O	3:A:701:PRO:CG	2.50	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:448:LEU:HD22	3:B:816:SER:CA	2.32	0.60
3:A:493:GLY:N	3:A:602:THR:HB	2.16	0.60
3:A:667:VAL:HA	3:A:828:THR:CG2	2.31	0.60
3:B:1035:PHE:CA	3:B:1170:GLY:HA3	2.21	0.60
3:A:170:LEU:HD21	3:A:205:LEU:HD21	1.84	0.60
3:B:665:LYS:HG2	3:B:860:ASP:OD1	1.96	0.60
3:B:828:THR:O	3:B:839:PHE:CE1	2.54	0.60
3:A:575:HIS:CG	3:A:578:GLY:CA	2.83	0.60
1:E:14:DT:N3	2:F:15:DG:N1	2.50	0.60
3:B:51:PHE:HD2	3:B:603:GLN:HB3	1.66	0.60
3:A:547:ALA:C	3:A:549:MET:N	2.52	0.60
3:B:999:LEU:HD21	3:B:1012:GLY:C	2.21	0.60
3:B:743:TYR:HB2	3:B:746:GLN:HG3	1.83	0.60
3:A:697:TYR:CZ	3:A:702:MET:SD	2.92	0.60
3:A:994:ASP:CB	3:A:1017:ARG:HH22	2.13	0.60
3:B:548:GLU:O	3:B:549:MET:C	2.40	0.60
3:A:701:PRO:CD	3:A:811:TYR:HB3	2.28	0.60
3:B:495:PHE:HZ	3:B:603:GLN:O	1.85	0.60
3:A:535:LEU:HB3	3:A:563:MET:CE	2.31	0.60
1:C:16:DG:O6	2:D:13:DC:O2	2.19	0.60
2:F:8:DA:H2"	2:F:9:DC:OP2	2.02	0.60
3:A:696:LEU:HD11	3:A:742:VAL:CG2	2.31	0.60
3:A:455:ASN:CG	3:A:760:GLY:HA2	2.20	0.60
3:B:313:LEU:HB3	3:B:436:VAL:HG13	1.84	0.60
2:F:12:DC:C2	2:F:13:DC:C4	2.90	0.59
3:B:742:VAL:H	3:B:746:GLN:NE2	1.99	0.59
3:B:402:TYR:HE1	3:B:615:LEU:HD11	1.65	0.59
3:B:458:ARG:HH11	3:B:764:LEU:CD2	2.12	0.59
2:D:4:DA:H2"	2:D:5:DA:OP2	2.02	0.59
3:A:402:TYR:HE1	3:A:615:LEU:HD11	1.65	0.59
3:B:1125:LEU:O	3:B:1126:GLU:HG2	2.01	0.59
3:A:1026:SER:O	3:A:1027:CYS:HB2	2.02	0.59
3:A:743:TYR:HB3	3:A:813:PHE:O	2.02	0.59
3:A:1121:LEU:O	3:A:1124:VAL:N	2.35	0.59
3:A:775:GLU:CD	3:B:781:ARG:NH2	2.55	0.59
3:B:170:LEU:HD21	3:B:205:LEU:HD21	1.83	0.59
1:C:9:DG:H21	3:A:576:ALA:HB3	1.66	0.59
1:C:10:DG:C5	1:C:11:DC:N4	2.70	0.59
3:B:546:ARG:NE	3:B:547:ALA:CB	2.59	0.59
3:B:627:PHE:HB2	3:B:846:VAL:HG21	1.80	0.59
3:A:495:PHE:CE1	3:A:605:ASP:HB3	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:19:DC:OP1	3:B:531:LYS:HE2	2.02	0.59
3:A:186:LEU:HD21	3:A:245:PRO:HB2	1.84	0.59
3:B:535:LEU:HB3	3:B:563:MET:HE1	1.85	0.59
3:A:1034:GLU:HG2	3:A:1170:GLY:CA	2.31	0.59
3:A:148:ALA:O	3:A:152:GLN:HB2	2.03	0.59
3:A:745:GLU:OE2	3:A:815:LYS:N	2.36	0.59
3:B:743:TYR:CA	3:B:813:PHE:O	2.51	0.59
3:B:743:TYR:HB3	3:B:813:PHE:O	2.03	0.59
3:B:845:SER:HA	3:B:879:ASP:OD1	2.03	0.59
3:A:1024:VAL:HG21	3:A:1200:PRO:CG	2.32	0.59
3:B:812:GLY:C	3:B:813:PHE:N	2.56	0.59
3:A:575:HIS:CG	3:A:578:GLY:HA3	2.36	0.58
3:B:491:GLN:CB	3:B:574:VAL:HG13	1.90	0.58
1:E:9:DG:C1'	1:E:10:DG:H5'	2.32	0.58
3:A:743:TYR:HB2	3:A:746:GLN:HG3	1.83	0.58
3:A:858:ILE:CD1	3:A:1008:ILE:CD1	2.81	0.58
3:A:855:ALA:N	3:A:1008:ILE:HG21	2.12	0.58
1:E:9:DG:C6	1:E:10:DG:C6	2.91	0.58
3:B:455:ASN:CG	3:B:760:GLY:CA	2.70	0.58
1:C:8:DT:C1'	1:C:9:DG:O5'	2.43	0.58
3:A:627:PHE:CE1	3:A:842:ALA:C	2.76	0.58
1:C:14:DT:C3'	3:A:509:ARG:HH12	2.17	0.58
3:A:699:PRO:C	3:A:811:TYR:CE2	2.77	0.58
3:B:148:ALA:O	3:B:152:GLN:HB2	2.03	0.58
3:B:470:ASP:OD2	3:B:623:ARG:HA	2.03	0.58
2:D:19:DC:OP2	3:A:531:LYS:NZ	2.35	0.58
3:A:665:LYS:HB2	3:A:832:LYS:HZ1	1.67	0.58
3:B:666:GLY:HA2	3:B:857:TYR:HE2	1.69	0.58
3:A:832:LYS:CA	3:A:839:PHE:CE2	2.86	0.58
3:A:701:PRO:HD3	3:A:811:TYR:CD2	2.38	0.58
2:F:15:DG:H1'	2:F:16:DT:H5'	1.85	0.58
3:A:699:PRO:O	3:A:701:PRO:HD2	2.03	0.58
3:A:848:ARG:HD3	3:A:892:SER:OG	2.03	0.58
2:F:19:DC:OP1	3:B:531:LYS:CE	2.51	0.57
1:C:10:DG:H5''	3:A:473:ARG:NH2	2.19	0.57
3:A:774:VAL:HG21	3:B:781:ARG:HB2	1.85	0.57
1:C:16:DG:O6	2:D:13:DC:C2	2.57	0.57
2:F:6:DC:H2''	2:F:7:DG:OP2	2.04	0.57
2:F:13:DC:H1'	2:F:14:DA:C8	2.39	0.57
3:A:665:LYS:HZ3	3:A:864:LEU:HD13	1.68	0.57
3:B:448:LEU:HD13	3:B:816:SER:CA	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:591:PRO:HG2	3:B:603:GLN:HB2	1.86	0.57
3:A:521:LEU:HD21	3:A:548:GLU:CG	2.33	0.57
1:E:14:DT:OP2	3:B:233:LYS:HE2	2.05	0.57
3:A:523:LYS:CD	3:A:1054:VAL:CG1	2.76	0.57
3:B:51:PHE:HD2	3:B:603:GLN:CB	2.17	0.57
3:A:591:PRO:HG2	3:A:603:GLN:HB2	1.87	0.57
2:D:18:DC:H2''	3:A:531:LYS:HE2	1.86	0.57
1:C:6:DT:H2''	1:C:7:DG:OP2	2.05	0.57
3:A:692:ALA:HA	3:A:743:TYR:OH	2.04	0.57
3:A:448:LEU:HD22	3:A:816:SER:CA	2.35	0.57
3:A:858:ILE:CD1	3:A:1008:ILE:HD11	2.34	0.57
3:A:492:ILE:CD1	3:A:616:LYS:HB2	2.31	0.57
1:E:13:DC:C1'	1:E:14:DT:H5''	2.33	0.57
3:A:523:LYS:HZ3	3:A:1054:VAL:HG13	1.70	0.57
3:A:665:LYS:CG	3:A:860:ASP:CG	2.72	0.57
3:B:51:PHE:HA	3:B:603:GLN:HB3	1.87	0.57
3:B:186:LEU:HD21	3:B:245:PRO:HB2	1.85	0.57
3:B:999:LEU:CD2	3:B:1012:GLY:O	2.52	0.57
3:A:665:LYS:NZ	3:A:864:LEU:HD13	2.20	0.57
3:B:54:VAL:HG23	3:B:604:TYR:OH	1.97	0.57
2:F:19:DC:H2'	3:B:531:LYS:HZ1	1.69	0.57
3:B:539:PHE:CZ	3:B:559:ILE:HG23	2.29	0.57
3:A:575:HIS:CB	3:A:578:GLY:CA	2.76	0.57
3:B:471:ARG:HH12	3:B:630:GLU:CG	2.18	0.57
1:E:9:DG:O5'	1:E:9:DG:H2'	2.04	0.57
3:A:1118:VAL:O	3:A:1119:TRP:CG	2.58	0.57
3:A:851:SER:HB3	3:A:1007:GLY:HA3	1.87	0.57
3:A:539:PHE:CZ	3:A:559:ILE:HG23	2.29	0.56
1:C:8:DT:H2''	1:C:9:DG:OP2	2.05	0.56
1:E:18:DC:OP1	3:B:933:ARG:CD	2.53	0.56
1:E:19:DG:H2''	1:E:20:DT:H71	1.87	0.56
3:A:695:SER:CB	3:A:743:TYR:HE2	2.17	0.56
3:B:627:PHE:CD1	3:B:846:VAL:HG21	2.40	0.56
3:B:491:GLN:CA	3:B:492:ILE:N	2.66	0.56
3:A:996:ILE:CD1	3:A:1018:TYR:OH	2.53	0.56
3:B:742:VAL:O	3:B:813:PHE:HB2	2.05	0.56
3:A:844:LEU:CG	3:A:880:PHE:CZ	2.88	0.56
2:D:21:DOC:H5'	2:D:21:DOC:H6	1.83	0.56
3:A:996:ILE:CD1	3:A:1018:TYR:CE2	2.55	0.56
3:A:845:SER:CB	3:A:879:ASP:OD2	2.51	0.56
3:A:697:TYR:CZ	3:A:702:MET:HE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:455:ASN:OD1	3:A:760:GLY:CA	2.39	0.56
3:B:627:PHE:HD1	3:B:846:VAL:CG2	2.18	0.56
3:B:406:VAL:HA	3:B:409:TYR:CE2	2.40	0.56
2:F:20:DA:C2	2:F:21:DOC:C2	2.88	0.56
2:D:20:DA:H2''	2:D:21:DOC:C5'	2.18	0.56
2:F:19:DC:OP2	3:B:531:LYS:HE2	2.04	0.56
1:E:20:DT:H1'	1:E:21:DC:O5'	2.05	0.56
3:A:1143:LYS:HG2	3:A:1147:ARG:HD2	1.88	0.56
1:C:9:DG:C2	3:A:576:ALA:HB3	2.40	0.56
3:A:627:PHE:HB2	3:A:846:VAL:HG11	1.87	0.56
3:B:455:ASN:CG	3:B:760:GLY:HA3	2.26	0.56
2:F:14:DA:C1'	2:F:15:DG:C8	2.86	0.56
3:A:845:SER:CA	3:A:879:ASP:CG	2.73	0.56
1:C:21:DC:H1'	1:C:22:DG:H5'	1.88	0.56
3:B:402:TYR:HE1	3:B:615:LEU:CD1	2.19	0.56
3:B:703:GLU:O	3:B:706:PRO:HD2	2.06	0.56
3:B:54:VAL:HG21	3:B:612:LEU:HD11	1.87	0.56
3:A:492:ILE:HD11	3:A:616:LYS:CB	2.30	0.56
1:E:15:DG:C1'	1:E:16:DG:H5'	2.36	0.56
3:B:711:ARG:O	3:B:714:GLY:N	2.39	0.56
3:A:1028:THR:HG22	3:A:1031:GLU:H	1.71	0.56
3:B:812:GLY:C	3:B:813:PHE:CB	2.74	0.56
3:B:51:PHE:CD2	3:B:603:GLN:HG2	2.40	0.56
3:B:469:SER:HA	3:B:625:LEU:HB3	1.88	0.56
1:C:14:DT:O2	2:D:15:DG:N2	2.39	0.55
3:A:565:LEU:O	3:A:568:LEU:HG	2.04	0.55
3:B:458:ARG:CZ	3:B:764:LEU:HD22	2.31	0.55
3:A:407:GLN:HG3	3:A:436:VAL:CG1	2.36	0.55
3:B:897:VAL:HG21	3:B:938:LEU:HD13	1.88	0.55
3:A:406:VAL:HA	3:A:409:TYR:CE2	2.40	0.55
2:D:5:DA:C2'	2:D:6:DC:OP2	2.48	0.55
3:A:402:TYR:HE1	3:A:615:LEU:CD1	2.19	0.55
3:A:703:GLU:O	3:A:706:PRO:HD2	2.06	0.55
3:B:424:ARG:HD3	5:B:1222:DTP:H4'	1.85	0.55
3:B:1035:PHE:HD1	3:B:1170:GLY:C	2.09	0.55
2:D:12:DC:C2	2:D:13:DC:C2	2.94	0.55
2:F:9:DC:C2	2:F:10:DG:C8	2.94	0.55
3:A:638:SER:CB	3:A:838:GLU:OE1	2.54	0.55
1:C:21:DC:H2''	1:C:22:DG:OP2	2.05	0.55
3:B:1035:PHE:HE1	3:B:1172:ALA:N	2.03	0.55
3:A:495:PHE:CD1	3:A:605:ASP:HB3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1013:HIS:O	3:A:1014:PRO:C	2.45	0.55
3:A:549:MET:HG2	3:A:559:ILE:HD12	1.89	0.55
3:A:574:VAL:HG21	3:A:601:VAL:CG2	2.20	0.55
3:A:492:ILE:HG12	3:A:609:VAL:HG11	1.88	0.55
1:C:8:DT:C4	1:C:9:DG:C6	2.94	0.55
1:C:9:DG:H2''	1:C:10:DG:OP2	2.04	0.55
3:B:538:ALA:C	3:B:539:PHE:HD1	2.10	0.55
1:E:24:DT:H2''	1:E:25:DT:OP2	2.07	0.55
1:C:9:DG:C2	3:A:576:ALA:HB2	2.42	0.55
2:D:12:DC:C5	2:D:13:DC:N4	2.73	0.55
2:D:12:DC:C6	2:D:13:DC:C4	2.95	0.55
2:F:14:DA:C4	2:F:15:DG:N7	2.75	0.55
3:B:1035:PHE:CA	3:B:1170:GLY:CA	2.83	0.55
3:A:897:VAL:HG21	3:A:938:LEU:HD13	1.88	0.55
3:B:238:ASP:HB3	3:B:239:PRO:CA	2.36	0.55
2:D:11:DG:H2''	2:D:12:DC:C6	2.42	0.55
3:A:665:LYS:HD3	3:A:860:ASP:HB3	1.89	0.55
3:B:711:ARG:HE	3:B:716:GLU:HG2	1.71	0.55
3:B:835:TYR:O	3:B:839:PHE:CB	2.55	0.55
3:B:549:MET:HG2	3:B:559:ILE:HD12	1.89	0.55
3:A:828:THR:O	3:A:839:PHE:CZ	2.60	0.55
3:B:495:PHE:CZ	3:B:603:GLN:O	2.60	0.55
3:B:1126:GLU:CG	3:B:1205:PHE:HE2	2.20	0.55
3:A:458:ARG:NE	3:A:764:LEU:HD11	2.22	0.55
1:E:8:DT:O3'	3:B:622:LEU:HA	2.06	0.54
3:B:471:ARG:HH12	3:B:630:GLU:CD	2.10	0.54
3:A:238:ASP:HB3	3:A:239:PRO:CA	2.36	0.54
3:A:538:ALA:C	3:A:539:PHE:HD1	2.10	0.54
1:C:14:DT:O2	2:D:14:DA:C2	2.60	0.54
3:B:455:ASN:ND2	3:B:760:GLY:HA3	2.20	0.54
3:B:1143:LYS:HG2	3:B:1147:ARG:HD2	1.88	0.54
3:B:407:GLN:HG3	3:B:436:VAL:CG1	2.36	0.54
3:B:665:LYS:NZ	3:B:864:LEU:CD1	2.67	0.54
3:B:831:VAL:HG11	3:B:839:PHE:CD1	2.19	0.54
2:D:19:DC:C5'	3:A:531:LYS:NZ	2.71	0.54
3:A:458:ARG:HH21	3:A:764:LEU:HD13	1.65	0.54
3:A:535:LEU:HB3	3:A:563:MET:HE1	1.89	0.54
1:C:9:DG:N2	3:A:576:ALA:HB3	2.22	0.54
3:B:699:PRO:HG2	3:B:811:TYR:HE2	1.73	0.54
1:E:10:DG:H2''	1:E:11:DC:C6	2.42	0.54
1:C:8:DT:OP2	3:A:623:ARG:CG	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:DG:N2	2:D:14:DA:H5'	2.21	0.54
3:B:492:ILE:HG12	3:B:609:VAL:HG11	1.89	0.54
3:B:699:PRO:HB2	3:B:811:TYR:CZ	2.42	0.54
3:B:866:ILE:CG2	3:B:867:PRO:O	2.52	0.54
3:B:51:PHE:CD2	3:B:603:GLN:CG	2.90	0.54
3:B:424:ARG:NH2	5:B:1222:DTP:O4'	2.41	0.54
3:A:1028:THR:HG22	3:A:1031:GLU:CG	2.36	0.54
3:A:590:VAL:CG1	3:A:602:THR:HG23	2.38	0.54
2:F:14:DA:P	2:F:14:DA:H2'	2.48	0.54
3:A:743:TYR:HD2	3:A:813:PHE:HB3	1.73	0.54
3:A:547:ALA:HA	3:A:550:GLU:OE1	2.08	0.54
1:E:15:DG:N1	2:F:14:DA:C2	2.76	0.54
2:F:21:DOC:OP1	3:B:616:LYS:NZ	2.33	0.54
1:C:11:DC:H2''	1:C:12:DA:OP2	2.07	0.54
1:E:23:DT:H1'	1:E:24:DT:O5'	2.08	0.54
3:A:321:ARG:NH2	3:A:440:ASN:HD21	1.99	0.54
3:B:666:GLY:CA	3:B:857:TYR:HE2	2.21	0.54
3:B:471:ARG:HH12	3:B:630:GLU:HG2	1.71	0.54
3:A:397:MET:CE	3:A:459:VAL:HA	2.38	0.54
3:A:788:ALA:HB1	3:A:793:VAL:HG23	1.90	0.54
3:B:788:ALA:HB1	3:B:793:VAL:HG23	1.90	0.54
1:E:8:DT:C5'	3:B:622:LEU:HD21	2.25	0.53
1:C:14:DT:C2	2:D:15:DG:C2	2.96	0.53
3:A:441:ILE:HD12	3:A:823:LEU:HD12	1.91	0.53
3:B:310:LEU:HD22	3:B:400:PRO:HA	1.89	0.53
3:B:535:LEU:HB2	3:B:563:MET:HB3	1.90	0.53
3:A:497:SER:HA	3:A:569:ASN:OD1	2.09	0.53
3:B:840:MET:HG2	3:B:861:ALA:HB2	1.91	0.53
1:C:13:DC:H2''	1:C:14:DT:C5'	2.38	0.53
1:E:15:DG:C2	1:E:16:DG:C4	2.96	0.53
3:A:535:LEU:HB2	3:A:563:MET:HB3	1.90	0.53
1:C:9:DG:H2'	1:C:9:DG:O5'	2.08	0.53
3:A:575:HIS:CB	3:A:578:GLY:N	2.70	0.53
1:E:12:DA:H2''	1:E:13:DC:OP2	2.06	0.53
2:D:6:DC:C2'	2:D:7:DG:OP2	2.41	0.53
3:B:15:GLN:HE21	3:B:25:LEU:HB2	1.74	0.53
1:E:9:DG:O5'	1:E:9:DG:C2'	2.57	0.53
1:C:9:DG:H21	3:A:576:ALA:CB	2.21	0.53
1:C:22:DG:N3	2:D:7:DG:N2	2.57	0.53
3:B:1034:GLU:O	3:B:1169:PHE:O	2.25	0.53
3:A:1013:HIS:HE1	3:A:1073:GLU:CB	2.01	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:590:VAL:CG1	3:B:602:THR:HG23	2.38	0.53
2:D:19:DC:P	3:A:531:LYS:CE	2.96	0.53
3:A:840:MET:HG2	3:A:861:ALA:HB2	1.91	0.53
2:D:19:DC:P	3:A:531:LYS:HZ1	2.29	0.53
1:E:12:DA:H1'	1:E:13:DC:H5'	1.90	0.53
3:A:775:GLU:CD	3:B:781:ARG:NE	2.45	0.53
3:A:238:ASP:HB3	3:A:239:PRO:C	2.29	0.53
3:A:547:ALA:O	3:A:548:GLU:C	2.47	0.53
2:D:18:DC:H3'	3:A:499:ALA:HB2	1.89	0.53
3:A:996:ILE:HD11	3:A:1018:TYR:OH	2.08	0.53
3:A:547:ALA:C	3:A:549:MET:H	2.13	0.52
3:B:999:LEU:CD2	3:B:1012:GLY:C	2.77	0.52
3:A:1028:THR:HG23	3:A:1028:THR:O	2.09	0.52
3:A:982:VAL:O	3:A:982:VAL:HG13	2.09	0.52
3:A:574:VAL:HG22	3:A:601:VAL:HG22	0.53	0.52
2:D:12:DC:C6	2:D:12:DC:O5'	2.62	0.52
2:D:14:DA:H1'	2:D:15:DG:O5'	2.10	0.52
3:A:1024:VAL:HG22	3:A:1200:PRO:CD	2.30	0.52
3:A:321:ARG:NH1	3:A:434:TYR:O	2.41	0.52
3:B:399:PHE:N	3:B:400:PRO:CD	2.72	0.52
3:B:535:LEU:HD22	3:B:559:ILE:HG23	1.92	0.52
3:B:1140:LEU:CB	3:B:1143:LYS:HD2	2.38	0.52
3:A:399:PHE:N	3:A:400:PRO:CD	2.72	0.52
3:A:1039:LEU:HB3	3:A:1040:PRO:CD	2.39	0.52
3:A:535:LEU:HD22	3:A:559:ILE:HG23	1.92	0.52
3:A:773:ARG:NH1	3:B:774:VAL:HG12	2.25	0.52
3:B:742:VAL:O	3:B:813:PHE:N	2.41	0.52
3:B:788:ALA:HB1	3:B:793:VAL:CG2	2.40	0.52
1:E:8:DT:H4'	3:B:622:LEU:CG	2.39	0.52
3:A:627:PHE:CE1	3:A:843:LEU:HG	2.45	0.52
2:D:11:DG:H1'	2:D:12:DC:O5'	2.10	0.52
1:E:13:DC:C4	1:E:14:DT:C4	2.97	0.52
3:B:699:PRO:C	3:B:811:TYR:CE1	2.61	0.52
3:A:457:GLU:CD	3:A:758:SER:OG	2.47	0.52
3:B:51:PHE:CE2	3:B:593:MET:SD	3.03	0.52
3:A:313:LEU:HB3	3:A:436:VAL:HG13	1.90	0.52
3:A:296:PRO:HD2	3:A:615:LEU:HD23	1.92	0.52
3:B:238:ASP:HB3	3:B:239:PRO:C	2.29	0.52
2:D:13:DC:C4	2:D:14:DA:N6	2.78	0.52
3:A:994:ASP:CB	3:A:1017:ARG:CZ	2.72	0.52
1:C:23:DT:H1'	1:C:24:DT:C5'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:239:PRO:O	3:A:240:GLU:CB	2.58	0.52
3:A:920:ASP:HA	3:A:923:LYS:HE2	1.90	0.52
3:B:698:ARG:O	3:B:701:PRO:CG	2.57	0.52
2:D:6:DC:H1'	2:D:7:DG:O5'	2.09	0.52
1:C:10:DG:C5'	3:A:576:ALA:HA	2.39	0.52
1:C:15:DG:C2	1:C:16:DG:C6	2.98	0.52
3:B:58:LYS:HZ1	3:B:608:ALA:HA	1.73	0.52
2:D:14:DA:H2'	2:D:14:DA:P	2.50	0.52
1:E:15:DG:C6	2:F:14:DA:N1	2.78	0.52
3:B:1126:GLU:O	3:B:1128:PRO:HD3	2.10	0.52
3:A:1128:PRO:HA	3:A:1129:LYS:HE3	1.91	0.52
3:A:496:GLY:O	3:A:569:ASN:CG	2.48	0.52
3:A:1034:GLU:CG	3:A:1170:GLY:HA2	2.39	0.52
3:A:788:ALA:HB1	3:A:793:VAL:CG2	2.40	0.52
3:A:675:MET:O	3:A:679:VAL:HG23	2.10	0.52
3:A:15:GLN:HE21	3:A:25:LEU:HB2	1.74	0.52
3:B:994:ASP:OD2	3:B:1017:ARG:NH2	2.42	0.51
1:C:15:DG:N1	1:C:16:DG:O6	2.43	0.51
3:A:832:LYS:N	3:A:839:PHE:CE1	2.78	0.51
3:A:1028:THR:N	3:A:1031:GLU:OE1	2.44	0.51
3:A:567:GLY:C	3:A:568:LEU:CA	2.76	0.51
3:B:1125:LEU:O	3:B:1126:GLU:CD	2.48	0.51
3:A:773:ARG:HH12	3:B:774:VAL:HB	1.76	0.51
3:A:665:LYS:CD	3:A:860:ASP:HB3	2.41	0.51
3:A:744:GLN:HG3	3:A:813:PHE:HA	1.91	0.51
3:B:982:VAL:O	3:B:982:VAL:HG13	2.09	0.51
3:B:493:GLY:HA3	3:B:602:THR:O	2.09	0.51
3:A:424:ARG:CZ	5:A:1222:DTP:C3'	2.88	0.51
2:D:18:DC:H5'	3:A:499:ALA:CB	2.39	0.51
3:B:920:ASP:HA	3:B:923:LYS:HE2	1.90	0.51
3:B:294:ARG:NH1	3:B:612:LEU:O	2.40	0.51
3:A:498:LEU:HB2	3:A:568:LEU:C	2.30	0.51
3:B:1039:LEU:HB3	3:B:1040:PRO:CD	2.39	0.51
3:A:80:ARG:N	3:A:128:ASP:OD1	2.44	0.51
1:C:9:DG:C2'	1:C:9:DG:O5'	2.57	0.51
2:D:9:DC:C1'	2:D:10:DG:C5'	2.80	0.51
3:A:397:MET:HE3	3:A:459:VAL:HA	1.93	0.51
3:B:80:ARG:N	3:B:128:ASP:OD1	2.44	0.51
1:E:8:DT:H3'	1:E:8:DT:P	2.50	0.51
3:A:458:ARG:HH11	3:A:764:LEU:CD2	2.12	0.51
3:B:239:PRO:O	3:B:240:GLU:CB	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:12:DC:C4	2:F:13:DC:N4	2.78	0.51
3:B:495:PHE:HD1	3:B:605:ASP:HB3	1.75	0.51
3:A:727:GLU:OE2	3:A:731:ARG:NH1	2.44	0.51
3:B:727:GLU:OE2	3:B:731:ARG:NH1	2.44	0.51
3:A:1012:GLY:HA2	3:A:1013:HIS:HB2	1.92	0.51
1:E:8:DT:H3'	3:B:623:ARG:H	1.72	0.51
1:E:18:DC:H6	1:E:18:DC:O5'	1.94	0.51
3:B:714:GLY:C	3:B:715:GLN:HG3	2.24	0.51
3:A:447:GLY:H	3:A:815:LYS:NZ	2.09	0.51
1:E:9:DG:H3'	3:B:621:GLY:HA3	1.92	0.51
1:E:8:DT:OP1	1:E:8:DT:H3'	2.11	0.51
1:E:9:DG:P	1:E:9:DG:H2'	2.50	0.51
2:D:21:DOC:C2'	5:A:1222:DTP:H4'	2.41	0.51
3:B:675:MET:O	3:B:679:VAL:HG23	2.10	0.51
3:A:844:LEU:HD13	3:A:880:PHE:CZ	2.46	0.50
3:B:424:ARG:NH1	5:B:1222:DTP:O4'	2.44	0.50
1:C:15:DG:H5''	3:A:509:ARG:NH2	2.26	0.50
3:A:776:GLU:HB2	3:B:775:GLU:CG	2.40	0.50
3:B:1035:PHE:CE1	3:B:1172:ALA:HA	2.46	0.50
3:B:1035:PHE:HE1	3:B:1172:ALA:HA	1.76	0.50
1:E:8:DT:H2'	1:E:8:DT:OP2	2.11	0.50
2:F:15:DG:H2''	2:F:16:DT:O5'	2.11	0.50
3:A:698:ARG:HG3	3:A:701:PRO:HD2	1.93	0.50
3:A:257:MET:HA	3:A:257:MET:HE2	1.93	0.50
1:C:16:DG:O6	2:D:13:DC:N3	2.44	0.50
2:F:14:DA:C8	2:F:14:DA:O5'	2.65	0.50
3:A:294:ARG:NH1	3:A:612:LEU:O	2.42	0.50
3:A:424:ARG:CZ	5:A:1222:DTP:C4'	2.89	0.50
3:A:473:ARG:NH1	3:A:477:ILE:HD11	2.26	0.50
1:E:21:DC:H2''	1:E:22:DG:OP2	2.11	0.50
3:A:832:LYS:CA	3:A:839:PHE:CD2	2.94	0.50
3:B:58:LYS:CB	3:B:287:ILE:HD11	2.34	0.50
2:D:12:DC:O5'	2:D:12:DC:H6	1.94	0.50
3:B:51:PHE:CE2	3:B:603:GLN:CG	2.91	0.50
3:A:1013:HIS:O	3:A:1015:VAL:N	2.44	0.50
1:C:9:DG:N2	3:A:576:ALA:CB	2.75	0.50
3:B:699:PRO:O	3:B:701:PRO:CD	2.59	0.50
3:A:745:GLU:OE2	3:A:814:ASN:CA	2.57	0.50
3:B:812:GLY:CA	3:B:813:PHE:N	2.75	0.50
3:B:1181:VAL:HG11	3:B:1185:ALA:HB3	1.93	0.50
3:A:1026:SER:OG	3:A:1046:LEU:HG	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:865:GLY:O	3:A:866:ILE:CD1	2.59	0.50
1:C:22:DG:C2	1:C:23:DT:C2	3.00	0.50
3:B:473:ARG:NH1	3:B:477:ILE:HD11	2.26	0.50
1:C:9:DG:C2	2:D:20:DA:N1	2.80	0.50
2:F:19:DC:H6	2:F:19:DC:OP2	1.93	0.50
1:C:8:DT:H3'	1:C:8:DT:P	2.52	0.50
1:C:14:DT:O2	2:D:14:DA:H2	1.94	0.50
2:D:18:DC:C2'	2:D:19:DC:OP2	2.55	0.50
1:E:15:DG:C6	1:E:16:DG:C6	3.00	0.50
3:B:812:GLY:C	3:B:813:PHE:HD1	2.15	0.50
3:A:1140:LEU:H	3:A:1143:LYS:HD2	1.77	0.50
2:D:21:DOC:H2''	5:A:1222:DTP:H4'	1.93	0.49
3:A:744:GLN:HG3	3:A:813:PHE:N	2.27	0.49
3:A:128:ASP:H	3:A:131:ILE:HG12	1.77	0.49
3:A:1181:VAL:HG11	3:A:1185:ALA:HB3	1.93	0.49
1:C:9:DG:P	3:A:621:GLY:C	2.87	0.49
1:C:15:DG:C6	2:D:14:DA:C6	3.00	0.49
3:B:547:ALA:O	3:B:548:GLU:C	2.49	0.49
3:A:699:PRO:O	3:A:701:PRO:HD3	2.11	0.49
1:E:10:DG:H4'	3:B:576:ALA:CB	2.39	0.49
3:B:1140:LEU:HB2	3:B:1143:LYS:CD	2.40	0.49
3:B:425:GLY:N	5:B:1222:DTP:H3'	2.27	0.49
3:A:521:LEU:CD2	3:A:548:GLU:HG2	2.36	0.49
2:D:21:DOC:H2''	5:A:1222:DTP:C4'	2.42	0.49
1:E:13:DC:H1'	1:E:14:DT:H5''	1.93	0.49
3:A:700:GLY:HA3	3:A:811:TYR:CD2	2.42	0.49
3:A:546:ARG:NH2	3:A:547:ALA:CB	2.68	0.49
3:A:286:PRO:HA	3:A:290:LYS:HG3	1.95	0.49
3:B:832:LYS:HE3	3:B:840:MET:HE1	1.93	0.49
3:A:54:VAL:HG13	3:A:287:ILE:HD11	1.95	0.49
1:C:15:DG:C5'	3:A:509:ARG:NH2	2.76	0.49
2:D:9:DC:H1'	2:D:10:DG:H5'	1.91	0.49
3:A:575:HIS:O	3:A:578:GLY:O	2.30	0.49
3:A:851:SER:CB	3:A:895:LYS:HZ3	2.23	0.49
3:A:695:SER:CB	3:A:743:TYR:CE2	2.96	0.49
3:A:492:ILE:CD1	3:A:616:LYS:CB	2.88	0.49
1:C:9:DG:C1'	3:A:576:ALA:HB1	2.42	0.49
2:D:11:DG:H1'	2:D:12:DC:C5'	2.43	0.49
3:A:595:ASP:OD2	3:A:599:ARG:HD2	2.13	0.49
2:D:19:DC:P	3:A:531:LYS:HE2	2.52	0.49
1:C:13:DC:H1'	1:C:14:DT:C5'	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:537:GLU:O	3:B:539:PHE:HB2	2.13	0.49
3:B:701:PRO:HG3	3:B:811:TYR:HB3	1.93	0.49
3:B:1039:LEU:CB	3:B:1040:PRO:CD	2.91	0.49
3:A:319:LEU:HD13	3:A:347:GLU:HG3	1.95	0.49
3:B:319:LEU:HD13	3:B:347:GLU:HG3	1.95	0.49
2:D:19:DC:OP1	3:A:531:LYS:NZ	2.42	0.49
1:C:11:DC:H4'	3:A:573:SER:OG	2.12	0.49
1:C:8:DT:O3'	3:A:622:LEU:C	2.50	0.49
3:A:701:PRO:HD3	3:A:811:TYR:CG	2.48	0.49
3:A:1039:LEU:CB	3:A:1040:PRO:CD	2.91	0.49
3:B:286:PRO:HA	3:B:290:LYS:HG3	1.95	0.49
3:B:425:GLY:HA3	5:B:1222:DTP:O2B	2.13	0.49
3:B:574:VAL:HG13	3:B:601:VAL:HG22	1.95	0.49
1:E:10:DG:C5'	3:B:576:ALA:HB1	2.40	0.49
3:A:537:GLU:O	3:A:539:PHE:HB2	2.13	0.49
2:D:12:DC:C5	2:D:13:DC:C4	3.01	0.49
1:C:15:DG:C6	2:D:14:DA:C2	2.99	0.49
3:B:701:PRO:HG3	3:B:811:TYR:HB2	1.93	0.49
3:B:128:ASP:H	3:B:131:ILE:HG12	1.77	0.49
1:E:9:DG:H3'	1:E:9:DG:OP1	2.13	0.48
3:A:590:VAL:HG11	3:A:602:THR:HG23	1.95	0.48
1:E:17:DC:C3'	3:B:933:ARG:CZ	2.90	0.48
2:F:14:DA:OP1	2:F:14:DA:H3'	2.13	0.48
3:B:1126:GLU:HG3	3:B:1205:PHE:HZ	1.70	0.48
3:A:698:ARG:HG2	3:A:701:PRO:CG	2.37	0.48
3:B:575:HIS:CB	3:B:578:GLY:CA	2.68	0.48
3:A:1034:GLU:CD	3:A:1170:GLY:CA	2.80	0.48
3:A:1039:LEU:HG	3:A:1040:PRO:HD3	1.95	0.48
3:B:367:LYS:O	3:B:368:ARG:HG2	2.13	0.48
3:B:590:VAL:HG11	3:B:602:THR:HG23	1.96	0.48
1:C:15:DG:N2	2:D:14:DA:C4	2.81	0.48
3:A:848:ARG:HE	3:A:879:ASP:CG	2.16	0.48
3:B:1035:PHE:HE1	3:B:1172:ALA:CA	2.26	0.48
3:B:181:ILE:HD13	3:B:266:TRP:CZ3	2.48	0.48
2:F:13:DC:C4	2:F:14:DA:N6	2.81	0.48
3:B:1123:GLU:O	3:B:1126:GLU:CG	2.61	0.48
3:A:37:PRO:HB2	3:B:459:VAL:CG2	2.43	0.48
3:A:496:GLY:O	3:A:569:ASN:OD1	2.31	0.48
3:B:1039:LEU:HG	3:B:1040:PRO:HD3	1.95	0.48
3:B:1050:MET:O	3:B:1070:LEU:HA	2.13	0.48
3:B:1003:LYS:HD2	3:B:1096:ASP:OD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:379:THR:HG23	3:B:382:ALA:H	1.79	0.48
3:B:1105:VAL:HG22	3:B:1113:VAL:HG22	1.96	0.48
1:C:15:DG:OP1	3:A:509:ARG:CZ	2.61	0.48
3:B:742:VAL:O	3:B:813:PHE:CB	2.62	0.48
3:A:181:ILE:HD13	3:A:266:TRP:CZ3	2.48	0.48
1:C:9:DG:OP1	3:A:621:GLY:C	2.52	0.48
2:D:14:DA:C2	2:D:15:DG:C5	3.01	0.48
2:F:11:DG:C2	2:F:12:DC:C2	3.02	0.48
3:B:1128:PRO:HG2	3:B:1129:LYS:CE	2.22	0.48
3:B:448:LEU:HD13	3:B:816:SER:HB3	1.94	0.48
2:F:19:DC:H2'	3:B:531:LYS:NZ	2.29	0.48
1:C:8:DT:C3'	3:A:622:LEU:HA	2.40	0.48
2:F:13:DC:C2	2:F:14:DA:C5	3.01	0.48
3:B:1173:LEU:HD13	3:B:1202:ARG:HH22	1.78	0.48
3:B:704:HIS:CE1	3:B:808:PHE:CZ	2.87	0.48
3:A:367:LYS:O	3:A:368:ARG:HG2	2.13	0.48
3:B:595:ASP:OD2	3:B:599:ARG:HD2	2.13	0.48
1:E:9:DG:H1'	3:B:576:ALA:HB1	1.94	0.48
1:C:12:DA:C1'	1:C:13:DC:H5'	2.43	0.48
3:B:696:LEU:HG	3:B:742:VAL:CG1	2.43	0.48
3:B:812:GLY:C	3:B:813:PHE:CD1	2.87	0.48
3:A:321:ARG:NH2	3:A:440:ASN:ND2	2.42	0.48
1:E:8:DT:C4	1:E:9:DG:C6	3.02	0.48
1:C:12:DA:H1'	1:C:13:DC:O5'	2.14	0.48
3:B:1029:ILE:HG12	3:B:1072:ASP:CG	2.33	0.48
2:D:19:DC:C2'	3:A:531:LYS:HZ1	2.26	0.48
3:B:58:LYS:HZ3	3:B:608:ALA:HA	1.78	0.48
1:E:18:DC:H2''	1:E:19:DG:OP2	2.13	0.47
3:B:364:GLU:HA	3:B:367:LYS:HE2	1.96	0.47
3:A:1105:VAL:HG22	3:A:1113:VAL:HG22	1.96	0.47
2:F:19:DC:P	3:B:531:LYS:CE	3.01	0.47
3:B:1053:GLU:CB	3:B:1068:PHE:HA	2.44	0.47
3:B:996:ILE:HD11	3:B:1018:TYR:CD2	2.48	0.47
1:C:10:DG:C2'	1:C:11:DC:O5'	2.61	0.47
3:A:776:GLU:HG2	3:A:779:LYS:HD2	1.97	0.47
3:A:776:GLU:CB	3:B:775:GLU:HG2	2.44	0.47
3:A:744:GLN:HG3	3:A:813:PHE:CA	2.44	0.47
3:B:58:LYS:HD3	3:B:287:ILE:HD11	1.97	0.47
3:A:535:LEU:HD22	3:A:539:PHE:CZ	2.50	0.47
1:C:8:DT:C6	1:C:9:DG:N7	2.82	0.47
3:A:364:GLU:HA	3:A:367:LYS:HE2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:493:GLY:H	3:A:602:THR:HB	1.79	0.47
3:B:546:ARG:NH1	3:B:547:ALA:CB	2.64	0.47
3:A:1024:VAL:CG2	3:A:1200:PRO:HG2	2.39	0.47
3:B:776:GLU:HG2	3:B:779:LYS:HD2	1.97	0.47
1:E:9:DG:C2'	1:E:10:DG:H5''	2.44	0.47
3:A:535:LEU:HB3	3:A:563:MET:HE2	1.96	0.47
3:B:539:PHE:CE2	3:B:559:ILE:CG2	2.92	0.47
1:E:17:DC:OP1	3:B:933:ARG:NH2	2.46	0.47
3:B:524:LEU:HB2	3:B:545:LEU:HD11	1.97	0.47
3:B:215:TYR:HB2	3:B:220:ASP:HB2	1.96	0.47
3:A:1050:MET:O	3:A:1070:LEU:HA	2.14	0.47
1:C:15:DG:N1	2:D:14:DA:C6	2.83	0.47
2:D:19:DC:C2'	3:A:531:LYS:HZ2	2.18	0.47
2:D:10:DG:H8	2:D:10:DG:H5'	1.79	0.47
2:D:15:DG:H2''	2:D:16:DT:O5'	2.13	0.47
3:B:1125:LEU:O	3:B:1126:GLU:HB3	2.13	0.47
3:A:776:GLU:CG	3:B:774:VAL:HG12	2.39	0.47
3:A:523:LYS:HD3	3:A:1054:VAL:HG11	1.90	0.47
3:A:665:LYS:CB	3:A:860:ASP:CG	2.78	0.47
3:A:498:LEU:HB2	3:A:568:LEU:CA	2.44	0.47
3:B:696:LEU:HD11	3:B:742:VAL:HG21	1.95	0.47
3:B:743:TYR:HA	3:B:813:PHE:O	2.13	0.47
3:B:666:GLY:HA2	3:B:857:TYR:CE2	2.47	0.47
3:A:524:LEU:HB2	3:A:545:LEU:HD11	1.97	0.47
3:A:379:THR:HG23	3:A:382:ALA:H	1.79	0.47
3:A:546:ARG:NH1	3:A:547:ALA:CB	2.66	0.47
3:B:996:ILE:HD11	3:B:1018:TYR:CE2	2.49	0.47
3:A:1121:LEU:O	3:A:1123:GLU:N	2.47	0.47
3:A:1053:GLU:CB	3:A:1068:PHE:HA	2.44	0.47
3:B:528:GLN:HB3	3:B:533:LYS:HE3	1.97	0.47
2:F:17:DG:H2''	2:F:18:DC:C6	2.50	0.47
2:D:21:DOC:C3'	5:A:1222:DTP:C4'	2.93	0.47
3:A:1173:LEU:HD13	3:A:1202:ARG:HH22	1.78	0.47
3:A:851:SER:CB	3:A:895:LYS:NZ	2.74	0.47
3:A:294:ARG:HD3	3:A:614:LEU:HD21	1.96	0.47
3:B:999:LEU:CD2	3:B:1013:HIS:N	2.78	0.46
1:C:15:DG:C6	1:C:16:DG:O6	2.68	0.46
1:E:14:DT:C3'	3:B:509:ARG:NH2	2.78	0.46
3:A:1140:LEU:HD12	3:A:1143:LYS:HE3	1.96	0.46
3:B:1184:GLU:H	3:B:1184:GLU:HG3	1.52	0.46
3:B:492:ILE:HA	3:B:602:THR:CB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:10:DG:H2''	2:D:11:DG:O4'	2.15	0.46
1:C:14:DT:C2	2:D:15:DG:N1	2.84	0.46
3:B:535:LEU:HD22	3:B:539:PHE:CZ	2.50	0.46
3:B:698:ARG:CG	3:B:811:TYR:HB3	2.45	0.46
1:C:24:DT:H1'	1:C:25:DT:H5'	1.98	0.46
3:B:402:TYR:CE2	3:B:462:PRO:HG2	2.50	0.46
3:B:1036:VAL:HG13	3:B:1043:PRO:HG2	1.97	0.46
3:A:54:VAL:CG1	3:A:287:ILE:HD11	2.45	0.46
3:B:548:GLU:C	3:B:550:GLU:N	2.69	0.46
3:B:1123:GLU:O	3:B:1126:GLU:HG2	2.16	0.46
3:B:696:LEU:HD11	3:B:742:VAL:CG2	2.45	0.46
3:B:848:ARG:NE	3:B:879:ASP:CG	2.53	0.46
3:A:1035:PHE:CE1	3:A:1171:GLU:O	2.68	0.46
3:B:425:GLY:HA2	5:B:1222:DTP:O1B	2.15	0.46
3:A:539:PHE:CE2	3:A:559:ILE:CG2	2.92	0.46
3:A:627:PHE:CD1	3:A:843:LEU:HA	2.49	0.46
3:B:627:PHE:CD1	3:B:846:VAL:CG2	2.97	0.46
3:B:492:ILE:N	3:B:580:VAL:HG23	2.31	0.46
1:E:8:DT:OP1	3:B:623:ARG:HB2	2.14	0.46
3:A:744:GLN:H	3:A:813:PHE:C	2.19	0.46
3:B:321:ARG:HG2	3:B:434:TYR:CE2	2.51	0.46
3:A:215:TYR:HB2	3:A:220:ASP:HB2	1.97	0.46
3:A:844:LEU:CB	3:A:880:PHE:CG	2.85	0.46
3:B:665:LYS:HD3	3:B:860:ASP:CA	2.41	0.46
1:C:8:DT:C4'	3:A:623:ARG:N	2.73	0.46
3:B:1124:VAL:O	3:B:1125:LEU:C	2.54	0.46
3:B:448:LEU:HD23	3:B:815:LYS:HD3	1.98	0.46
3:A:1034:GLU:HG2	3:A:1170:GLY:HA2	1.94	0.46
3:B:139:LEU:O	3:B:176:ARG:HD2	2.16	0.46
2:D:12:DC:H1'	2:D:13:DC:O4'	2.16	0.46
1:C:21:DC:H1'	1:C:22:DG:C5'	2.45	0.46
2:D:21:DOC:C2'	3:A:424:ARG:HH11	2.03	0.46
1:C:16:DG:C5	1:C:17:DC:C4	3.04	0.46
2:D:11:DG:H2''	2:D:12:DC:OP2	2.15	0.46
3:A:523:LYS:NZ	3:A:1054:VAL:CG2	2.76	0.46
3:A:828:THR:O	3:A:839:PHE:CE1	2.69	0.46
3:B:695:SER:HB2	3:B:742:VAL:CG1	2.46	0.46
3:A:236:LEU:O	3:A:241:ARG:NE	2.48	0.46
2:F:18:DC:C2'	2:F:19:DC:OP2	2.61	0.46
1:E:12:DA:H1'	1:E:13:DC:C5'	2.45	0.46
3:B:236:LEU:O	3:B:241:ARG:NE	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:DT:OP2	3:A:623:ARG:HG3	2.15	0.46
2:D:14:DA:C2	2:D:15:DG:C4	3.04	0.46
1:E:14:DT:C2	2:F:15:DG:C2	3.04	0.46
3:B:397:MET:HE3	3:B:459:VAL:HA	1.98	0.46
1:C:10:DG:C4'	3:A:576:ALA:CA	2.69	0.45
2:F:13:DC:C1'	2:F:14:DA:O5'	2.58	0.45
3:A:458:ARG:CZ	3:A:764:LEU:CG	2.89	0.45
3:B:458:ARG:CZ	3:B:764:LEU:HD21	2.41	0.45
3:A:402:TYR:CE2	3:A:462:PRO:HG2	2.50	0.45
3:A:785:VAL:HG13	3:A:795:GLU:HB2	1.99	0.45
1:E:8:DT:C4'	3:B:622:LEU:CD2	2.61	0.45
3:A:57:TYR:O	3:A:61:THR:HB	2.17	0.45
3:B:45:THR:HG22	3:B:70:GLY:HA3	1.99	0.45
2:F:19:DC:OP1	3:B:531:LYS:NZ	2.50	0.45
2:F:17:DG:H2'	2:F:18:DC:C5	2.52	0.45
2:D:18:DC:H5'	3:A:499:ALA:HB3	1.97	0.45
1:C:12:DA:H5'	3:A:573:SER:OG	2.16	0.45
3:A:698:ARG:CG	3:A:701:PRO:HG3	2.43	0.45
3:A:528:GLN:HB3	3:A:533:LYS:HE3	1.97	0.45
3:A:139:LEU:O	3:A:176:ARG:HD2	2.16	0.45
1:E:8:DT:H1'	1:E:9:DG:C8	2.51	0.45
3:A:546:ARG:NE	3:A:547:ALA:CB	2.64	0.45
3:A:574:VAL:HA	3:A:601:VAL:HG13	1.99	0.45
1:C:15:DG:P	3:A:509:ARG:CZ	3.05	0.45
1:C:6:DT:H5''	3:A:672:SER:OG	2.16	0.45
1:E:20:DT:H1'	1:E:21:DC:C6	2.51	0.45
3:A:1101:VAL:HG22	3:A:1118:VAL:HG22	1.98	0.45
3:A:698:ARG:HG3	3:A:701:PRO:HG3	1.91	0.45
3:B:743:TYR:CB	3:B:813:PHE:O	2.64	0.45
3:A:1129:LYS:CA	3:A:1199:VAL:C	2.59	0.45
3:A:1036:VAL:HG13	3:A:1043:PRO:HG2	1.98	0.45
3:A:492:ILE:N	3:A:580:VAL:HG23	2.31	0.45
3:A:862:ARG:HH21	3:A:1010:VAL:HG13	1.73	0.45
3:B:151:PRO:HB3	3:B:192:VAL:HG11	1.99	0.45
3:B:838:GLU:H	3:B:838:GLU:CD	2.20	0.45
3:B:57:TYR:O	3:B:61:THR:HB	2.17	0.45
3:B:424:ARG:HA	3:B:817:HIS:HD2	1.81	0.45
3:A:627:PHE:HZ	3:A:843:LEU:HG	1.71	0.45
3:A:448:LEU:CD2	3:A:816:SER:HA	2.46	0.45
3:A:678:THR:CG2	3:A:705:ILE:HG21	2.47	0.45
3:B:546:ARG:NE	3:B:547:ALA:CA	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:45:THR:HG22	3:A:70:GLY:HA3	1.99	0.45
1:E:15:DG:C2	1:E:16:DG:N3	2.84	0.45
3:A:1046:LEU:HA	3:A:1101:VAL:O	2.17	0.45
3:A:1120:THR:OG1	3:A:1121:LEU:N	2.49	0.45
1:C:20:DT:H2''	1:C:21:DC:OP2	2.17	0.45
1:C:25:DT:O2	2:D:4:DA:H2	2.00	0.45
1:E:9:DG:N1	2:F:20:DA:N6	2.64	0.45
2:D:19:DC:C5'	3:A:531:LYS:HZ1	2.30	0.45
3:A:54:VAL:HG23	3:A:604:TYR:CZ	2.52	0.45
1:C:7:DG:OP2	1:C:7:DG:C8	2.70	0.45
3:B:446:PHE:HB3	3:B:815:LYS:CE	2.44	0.45
3:A:269:GLU:HB2	3:A:270:PRO:HD3	1.99	0.45
3:A:424:ARG:HB2	5:A:1222:DTP:O3'	2.17	0.44
2:D:12:DC:C2	2:D:13:DC:N3	2.85	0.44
2:D:19:DC:N3	2:D:20:DA:N6	2.65	0.44
2:D:21:DOC:C5'	2:D:21:DOC:C6	2.82	0.44
2:F:7:DG:H1'	2:F:8:DA:O5'	2.18	0.44
3:A:773:ARG:HH12	3:B:774:VAL:CB	2.30	0.44
3:A:1129:LYS:N	3:A:1201:ASP:H	2.15	0.44
3:B:1035:PHE:CB	3:B:1170:GLY:HA2	2.42	0.44
3:A:151:PRO:HB3	3:A:192:VAL:HG11	1.99	0.44
3:A:835:TYR:O	3:A:839:PHE:HB2	2.16	0.44
3:A:838:GLU:H	3:A:838:GLU:CD	2.21	0.44
3:B:832:LYS:CA	3:B:839:PHE:CG	2.95	0.44
3:B:1102:LEU:HD12	3:B:1119:TRP:HH2	1.83	0.44
3:B:785:VAL:HG13	3:B:795:GLU:HB2	1.98	0.44
3:A:1121:LEU:C	3:A:1123:GLU:N	2.69	0.44
3:B:468:PHE:C	3:B:625:LEU:HD23	2.37	0.44
1:E:13:DC:N3	1:E:14:DT:C4	2.86	0.44
3:B:1128:PRO:HG3	3:B:1129:LYS:HE3	0.44	0.44
3:B:1046:LEU:HA	3:B:1101:VAL:O	2.17	0.44
3:A:321:ARG:CG	3:A:434:TYR:CE2	3.00	0.44
3:B:800:ARG:O	3:B:803:ASP:HB2	2.17	0.44
1:E:18:DC:H5''	3:B:933:ARG:HB3	1.99	0.44
2:F:11:DG:H2''	2:F:12:DC:OP2	2.18	0.44
3:B:1126:GLU:CG	3:B:1205:PHE:CE2	2.84	0.44
3:A:774:VAL:CA	3:B:778:GLN:CG	2.72	0.44
3:B:1152:LEU:CB	3:B:1179:VAL:HG11	2.45	0.44
3:B:492:ILE:CD1	3:B:616:LYS:HG3	2.47	0.44
1:E:10:DG:H2''	1:E:11:DC:C5	2.53	0.44
1:C:9:DG:P	1:C:9:DG:C2'	3.04	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1034:GLU:HG2	3:B:1169:PHE:CA	2.48	0.44
3:B:424:ARG:NH1	5:B:1222:DTP:C4'	2.81	0.44
3:A:575:HIS:NE2	3:A:577:ALA:HB3	2.33	0.44
3:B:269:GLU:HB2	3:B:270:PRO:HD3	1.99	0.44
3:A:623:ARG:HD2	3:A:846:VAL:CG1	2.48	0.44
2:D:19:DC:P	3:A:531:LYS:HZ3	2.31	0.44
3:A:1028:THR:H	3:A:1031:GLU:HB2	1.83	0.43
1:C:24:DT:H2''	1:C:25:DT:O5'	2.17	0.43
3:A:574:VAL:CG1	3:A:601:VAL:HG22	2.47	0.43
1:C:8:DT:H1'	1:C:9:DG:C5'	2.46	0.43
1:E:18:DC:H5''	3:B:933:ARG:CB	2.48	0.43
1:E:23:DT:C2	1:E:24:DT:C4	3.06	0.43
3:B:1128:PRO:HA	3:B:1200:PRO:HA	1.99	0.43
3:A:795:GLU:HA	3:A:798:ALA:HB3	2.01	0.43
3:A:384:LEU:HA	3:A:384:LEU:HD23	1.91	0.43
3:B:639:LYS:HD2	3:B:835:TYR:CD2	2.53	0.43
1:C:11:DC:H2''	1:C:12:DA:C8	2.52	0.43
3:B:535:LEU:HB3	3:B:563:MET:HE2	2.00	0.43
1:E:18:DC:P	3:B:933:ARG:HB2	2.49	0.43
3:A:775:GLU:CD	3:B:781:ARG:CZ	2.86	0.43
3:B:402:TYR:CE1	3:B:615:LEU:CD1	3.01	0.43
3:B:795:GLU:HA	3:B:798:ALA:HB3	2.00	0.43
3:B:495:PHE:CD1	3:B:605:ASP:HB3	2.51	0.43
2:D:21:DOC:C3'	5:A:1222:DTP:C5'	2.87	0.43
3:A:425:GLY:CA	5:A:1222:DTP:O1B	2.65	0.43
1:E:15:DG:H2''	1:E:16:DG:OP2	2.17	0.43
3:A:696:LEU:HD21	3:A:742:VAL:CG1	2.46	0.43
3:A:234:THR:C	3:A:510:VAL:HG13	2.36	0.43
3:B:467:ASP:HB3	3:B:622:LEU:HD12	1.99	0.43
1:E:10:DG:C4'	3:B:576:ALA:HB1	2.47	0.43
3:A:1035:PHE:HE1	3:A:1172:ALA:HA	1.83	0.43
3:B:492:ILE:HG12	3:B:609:VAL:HG21	2.00	0.43
3:B:999:LEU:HB2	3:B:1014:PRO:HG3	1.97	0.43
2:D:19:DC:H6	3:A:531:LYS:HE2	1.82	0.43
1:C:14:DT:C2	2:D:15:DG:N2	2.86	0.43
3:B:458:ARG:HH12	3:B:764:LEU:HD22	1.65	0.43
3:A:296:PRO:HG2	3:A:581:ILE:HG22	2.01	0.43
3:A:800:ARG:O	3:A:803:ASP:HB2	2.17	0.43
1:C:15:DG:C4	1:C:16:DG:C8	3.06	0.43
1:C:9:DG:C5	1:C:10:DG:N7	2.87	0.43
2:D:14:DA:OP2	2:D:14:DA:H8	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:310:LEU:CD2	3:A:400:PRO:HA	2.48	0.43
1:E:8:DT:C1'	1:E:9:DG:C5'	2.97	0.42
3:A:627:PHE:CZ	3:A:843:LEU:CG	2.93	0.42
2:F:5:DA:H1'	2:F:6:DC:C6	2.53	0.42
3:B:1101:VAL:HG22	3:B:1118:VAL:HG22	2.00	0.42
3:A:534:PRO:HA	3:A:566:GLU:OE2	2.19	0.42
3:B:443:PRO:O	3:B:446:PHE:O	2.36	0.42
3:B:1142:GLU:C	3:B:1143:LYS:HG3	2.40	0.42
3:A:428:ALA:HB3	3:A:816:SER:HB2	2.01	0.42
3:A:296:PRO:CG	3:A:581:ILE:HG22	2.49	0.42
3:A:495:PHE:HZ	3:A:603:GLN:O	2.02	0.42
3:A:443:PRO:O	3:A:446:PHE:O	2.36	0.42
3:B:832:LYS:CA	3:B:839:PHE:CZ	2.97	0.42
1:E:10:DG:C2'	1:E:11:DC:C5	3.01	0.42
3:A:1028:THR:C	3:A:1030:GLU:N	2.71	0.42
3:B:866:ILE:CG2	3:B:867:PRO:CD	2.84	0.42
3:B:431:LEU:HA	3:B:443:PRO:HG3	2.01	0.42
3:B:252:LYS:HD2	3:B:257:MET:HE2	2.01	0.42
1:E:9:DG:C4'	3:B:621:GLY:N	2.81	0.42
1:C:14:DT:C3'	3:A:509:ARG:NH1	2.76	0.42
2:D:11:DG:H1'	2:D:12:DC:H5'	2.01	0.42
3:B:526:PRO:CD	3:B:538:ALA:CB	2.97	0.42
3:A:773:ARG:HG2	3:B:778:GLN:CG	2.46	0.42
3:A:1024:VAL:HG23	3:A:1200:PRO:CD	2.34	0.42
1:C:25:DT:O2	2:D:4:DA:C2	2.72	0.42
3:B:492:ILE:HD12	3:B:616:LYS:HG3	2.01	0.42
1:E:8:DT:C3'	1:E:8:DT:P	3.08	0.42
1:C:8:DT:H3'	3:A:623:ARG:CA	2.47	0.42
2:F:14:DA:C4	2:F:15:DG:C5	3.08	0.42
3:B:996:ILE:HA	3:B:1014:PRO:HA	2.01	0.42
3:B:548:GLU:O	3:B:551:LYS:N	2.45	0.42
1:E:24:DT:C2	2:F:5:DA:H2	2.37	0.42
3:A:294:ARG:CB	3:A:614:LEU:HD23	2.46	0.42
3:B:999:LEU:HD21	3:B:1013:HIS:N	2.34	0.42
3:A:252:LYS:HB3	3:A:256:GLU:HB2	2.02	0.42
3:A:252:LYS:HD2	3:A:257:MET:CE	2.50	0.42
3:B:570:ARG:HA	3:B:570:ARG:HD3	1.84	0.42
2:D:19:DC:C6	3:A:531:LYS:CE	2.99	0.42
1:C:14:DT:H2''	1:C:15:DG:O5'	2.19	0.42
2:D:11:DG:H2''	2:D:12:DC:C5	2.55	0.42
3:B:525:ILE:HA	3:B:526:PRO:HD3	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1035:PHE:CB	3:B:1170:GLY:CA	2.98	0.42
3:A:1034:GLU:CG	3:A:1170:GLY:CA	2.96	0.42
3:A:666:GLY:HA3	3:A:843:LEU:CD1	2.50	0.42
1:C:23:DT:H2''	1:C:24:DT:H72	2.02	0.42
1:E:6:DT:C2'	1:E:7:DG:OP2	2.58	0.42
3:B:1039:LEU:HG	3:B:1040:PRO:CD	2.50	0.42
3:A:402:TYR:CE1	3:A:615:LEU:CD1	3.01	0.42
3:B:1036:VAL:O	3:B:1037:ARG:C	2.58	0.42
3:B:252:LYS:HB3	3:B:256:GLU:HB2	2.01	0.42
3:B:534:PRO:HA	3:B:566:GLU:OE2	2.19	0.42
3:A:526:PRO:CD	3:A:538:ALA:CB	2.97	0.42
2:D:19:DC:H2''	2:D:20:DA:C8	2.55	0.42
3:A:1182:GLY:O	3:A:1183:GLU:HB2	2.20	0.42
3:A:752:SER:HA	3:A:757:TYR:HB2	2.02	0.42
3:A:594:ARG:HH11	3:A:594:ARG:HG3	1.84	0.42
3:B:725:HIS:HD2	3:B:797:GLU:OE2	2.03	0.42
3:B:425:GLY:H	3:B:817:HIS:HD2	1.64	0.42
3:A:424:ARG:HB3	3:A:821:TYR:HE1	1.84	0.42
1:C:11:DC:H2'	1:C:11:DC:H6	1.65	0.42
1:E:14:DT:O2	2:F:15:DG:C2	2.72	0.42
3:A:832:LYS:N	3:A:839:PHE:CZ	2.87	0.42
3:B:455:ASN:OD1	3:B:760:GLY:CA	2.61	0.42
2:D:5:DA:H1'	2:D:6:DC:P	2.60	0.42
3:B:448:LEU:CD2	3:B:816:SER:HA	2.50	0.42
3:B:627:PHE:CG	3:B:846:VAL:HG21	2.55	0.42
3:A:1036:VAL:O	3:A:1037:ARG:C	2.58	0.42
3:B:257:MET:HA	3:B:257:MET:HE2	2.00	0.42
3:A:306:GLU:O	3:A:404:LEU:HD11	2.19	0.42
3:A:424:ARG:HD3	5:A:1222:DTP:H4'	2.01	0.41
3:A:1028:THR:CG2	3:A:1031:GLU:H	2.33	0.41
1:E:9:DG:C5	1:E:10:DG:C5	3.08	0.41
1:C:11:DC:H1'	1:C:12:DA:C8	2.55	0.41
3:A:1026:SER:CB	3:A:1202:ARG:NH2	2.69	0.41
3:B:744:GLN:HG3	3:B:813:PHE:C	2.41	0.41
3:A:1128:PRO:N	3:A:1200:PRO:HB3	2.33	0.41
3:B:666:GLY:O	3:B:843:LEU:HD21	2.20	0.41
3:A:542:GLU:HG3	3:A:545:LEU:H	1.85	0.41
2:D:19:DC:C4'	3:A:531:LYS:HZ1	2.32	0.41
3:B:535:LEU:CB	3:B:563:MET:HB3	2.49	0.41
3:A:498:LEU:HD12	3:A:568:LEU:HB2	2.02	0.41
3:B:1035:PHE:HB2	3:B:1170:GLY:CA	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:708:TYR:HD1	3:B:740:ILE:HD12	1.85	0.41
3:B:316:LEU:HD21	3:B:348:ARG:HA	2.02	0.41
3:B:457:GLU:OE2	3:B:758:SER:OG	2.36	0.41
3:B:594:ARG:HG3	3:B:594:ARG:HH11	1.84	0.41
3:A:1184:GLU:HG3	3:A:1184:GLU:H	1.52	0.41
3:A:858:ILE:CD1	3:A:1008:ILE:HD13	2.43	0.41
1:C:11:DC:C3'	1:C:11:DC:P	3.05	0.41
2:D:19:DC:H2'	3:A:531:LYS:HZ1	1.75	0.41
2:D:8:DA:H2''	2:D:9:DC:OP2	2.19	0.41
3:B:699:PRO:HG2	3:B:811:TYR:CE2	2.54	0.41
3:A:1039:LEU:HG	3:A:1040:PRO:CD	2.50	0.41
3:B:1072:ASP:C	3:B:1074:THR:H	2.23	0.41
3:B:524:LEU:HD13	3:B:545:LEU:HG	2.02	0.41
3:A:725:HIS:HD2	3:A:797:GLU:OE2	2.03	0.41
3:A:535:LEU:CB	3:A:563:MET:HB3	2.50	0.41
3:B:696:LEU:CG	3:B:742:VAL:CG2	2.96	0.41
3:B:235:THR:HG23	3:B:510:VAL:O	2.20	0.41
3:B:1182:GLY:O	3:B:1183:GLU:HB2	2.21	0.41
3:A:257:MET:HA	3:A:257:MET:CE	2.50	0.41
3:B:252:LYS:HD2	3:B:257:MET:CE	2.50	0.41
3:A:316:LEU:HD21	3:A:348:ARG:HA	2.02	0.41
3:B:832:LYS:CB	3:B:839:PHE:HE2	2.02	0.41
2:D:13:DC:N4	2:D:14:DA:N6	2.68	0.41
3:B:546:ARG:NH2	3:B:547:ALA:CB	2.74	0.41
3:A:1128:PRO:HB3	3:A:1129:LYS:HE3	2.03	0.41
3:A:27:ASP:HA	3:A:30:LYS:HG2	2.03	0.41
3:B:179:ILE:HG13	3:B:200:ALA:HB2	2.03	0.41
3:A:602:THR:HG21	3:A:609:VAL:CG2	2.51	0.41
1:C:8:DT:O3'	3:A:622:LEU:CA	2.69	0.41
1:C:8:DT:C4	1:C:9:DG:O6	2.74	0.41
3:B:321:ARG:CG	3:B:434:TYR:CE2	3.03	0.41
1:C:23:DT:C1'	1:C:24:DT:O5'	2.62	0.41
3:A:431:LEU:HA	3:A:443:PRO:HG3	2.02	0.41
2:F:17:DG:C2'	2:F:18:DC:C6	3.04	0.41
2:F:20:DA:C3'	2:F:21:DOC:H5'	2.47	0.41
3:A:492:ILE:CG1	3:A:609:VAL:HG11	2.50	0.41
1:C:7:DG:C1'	1:C:8:DT:O5'	2.66	0.41
3:B:1035:PHE:CD1	3:B:1171:GLU:C	2.89	0.41
3:A:524:LEU:HD13	3:A:545:LEU:HG	2.03	0.41
3:A:1072:ASP:C	3:A:1074:THR:H	2.23	0.41
3:A:858:ILE:HD13	3:A:1008:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:602:THR:HG21	3:B:609:VAL:CG2	2.51	0.41
1:C:9:DG:H2'	1:C:9:DG:OP2	2.21	0.41
1:C:9:DG:OP1	3:A:621:GLY:HA3	2.21	0.41
1:E:19:DG:C4	1:E:20:DT:C4	3.08	0.41
3:B:1123:GLU:O	3:B:1125:LEU:O	2.39	0.41
3:A:779:LYS:HZ2	3:B:774:VAL:HG13	1.86	0.41
3:A:458:ARG:NE	3:A:764:LEU:CD1	2.84	0.41
3:A:1023:GLU:HB3	3:A:1199:VAL:HG12	2.03	0.41
3:A:285:LEU:CB	3:A:286:PRO:CD	2.81	0.41
3:B:1034:GLU:HG2	3:B:1169:PHE:CB	2.50	0.41
3:B:257:MET:HA	3:B:257:MET:CE	2.50	0.41
3:B:27:ASP:HA	3:B:30:LYS:HG2	2.03	0.41
3:B:752:SER:HA	3:B:757:TYR:HB2	2.01	0.41
1:E:9:DG:H1	2:F:20:DA:N6	2.19	0.41
1:C:6:DT:C5'	3:A:672:SER:OG	2.69	0.41
1:E:19:DG:C2'	1:E:20:DT:H71	2.51	0.41
3:A:285:LEU:HA	3:A:286:PRO:HD3	1.51	0.41
3:A:402:TYR:CE1	3:A:615:LEU:HD11	2.52	0.41
3:A:834:HIS:O	3:A:836:PRO:HD3	2.21	0.41
3:B:873:VAL:HG22	3:B:943:ALA:O	2.21	0.41
3:B:855:ALA:HA	3:B:1008:ILE:HG21	2.03	0.41
3:A:506:ASP:OD2	3:A:570:ARG:NH2	2.23	0.41
3:B:574:VAL:CG1	3:B:601:VAL:HG22	2.52	0.40
1:E:9:DG:N1	2:F:20:DA:C6	2.88	0.40
2:D:11:DG:H2''	2:D:12:DC:O5'	2.21	0.40
1:E:19:DG:H2''	1:E:20:DT:OP2	2.20	0.40
3:A:290:LYS:HG2	3:A:290:LYS:H	1.47	0.40
3:A:873:VAL:HG22	3:A:943:ALA:O	2.22	0.40
3:B:665:LYS:HG3	3:B:665:LYS:H	1.72	0.40
3:B:602:THR:HG22	3:B:604:TYR:N	2.32	0.40
1:E:8:DT:H2'	1:E:8:DT:P	2.61	0.40
1:E:24:DT:H6	1:E:24:DT:H2'	1.73	0.40
3:A:523:LYS:HZ3	3:A:1054:VAL:HG22	1.80	0.40
3:B:271:PHE:O	3:B:274:THR:HB	2.22	0.40
3:A:915:PHE:HA	3:A:924:ARG:HH21	1.86	0.40
1:C:13:DC:C1'	1:C:14:DT:H5''	2.44	0.40
1:C:16:DG:O6	2:D:12:DC:O2	2.40	0.40
3:B:526:PRO:HD3	3:B:538:ALA:CB	2.52	0.40
3:A:776:GLU:HB3	3:B:775:GLU:HG2	2.03	0.40
3:A:665:LYS:CD	3:A:860:ASP:CB	2.94	0.40
3:B:699:PRO:CB	3:B:811:TYR:CE2	3.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:448:LEU:HD22	3:A:816:SER:N	2.36	0.40
3:B:542:GLU:HG3	3:B:545:LEU:H	1.85	0.40
3:A:492:ILE:N	3:A:580:VAL:CG2	2.84	0.40
3:A:470:ASP:CG	3:A:626:THR:HG1	2.25	0.40
3:B:698:ARG:HD2	3:B:811:TYR:HB3	2.02	0.40
3:B:321:ARG:HD3	3:B:434:TYR:O	2.21	0.40
1:C:22:DG:N2	1:C:23:DT:C2	2.90	0.40
3:B:915:PHE:HA	3:B:924:ARG:HH21	1.85	0.40
3:B:763:ASP:O	3:B:767:ARG:HG2	2.22	0.40
3:B:492:ILE:CG1	3:B:580:VAL:HG21	2.37	0.40
3:A:424:ARG:NH2	5:A:1222:DTP:H1'	2.37	0.40
1:C:14:DT:C4	2:D:14:DA:N6	2.79	0.40
1:C:7:DG:OP2	1:C:7:DG:H8	2.05	0.40
2:D:20:DA:H2''	2:D:21:DOC:H6	2.03	0.40
3:A:737:THR:HG21	3:A:746:GLN:HE22	1.87	0.40
1:C:23:DT:C2'	1:C:24:DT:H72	2.51	0.40
3:B:666:GLY:CA	3:B:857:TYR:CE2	3.03	0.40
3:A:495:PHE:HE1	3:A:605:ASP:HB3	1.85	0.40
3:A:570:ARG:HD3	3:A:570:ARG:HA	1.84	0.40
3:B:1042:LYS:HG2	3:B:1106:GLU:HG2	2.03	0.40

All (36) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1177:ARG:NH2	3:B:972:ARG:CA[3_655]	0.82	1.38
3:A:1154:GLU:O	3:B:157:ASP:OD2[1_655]	0.99	1.21
3:A:657:GLU:OE2	3:B:654:LYS:N[2_655]	1.00	1.20
3:A:1177:ARG:NH2	3:B:972:ARG:CB[3_655]	1.14	1.06
3:A:654:LYS:N	3:B:657:GLU:OE2[2_655]	1.22	0.98
3:A:1169:PHE:CE1	3:B:637:GLU:O[2_655]	1.36	0.84
3:A:1169:PHE:CD1	3:B:638:SER:O[2_655]	1.37	0.83
3:A:657:GLU:OE1	3:B:654:LYS:CG[2_655]	1.41	0.79
3:A:971:GLY:O	3:B:1177:ARG:NH2[3_645]	1.49	0.71
3:A:1169:PHE:CZ	3:B:637:GLU:O[2_655]	1.57	0.63
3:A:653:PRO:C	3:B:657:GLU:OE2[2_655]	1.59	0.61
3:B:347:GLU:OE1	3:B:991:SER:OG[4_554]	1.64	0.56
3:A:1177:ARG:CZ	3:B:972:ARG:C[3_655]	1.66	0.54
3:A:657:GLU:OE2	3:B:654:LYS:CA[2_655]	1.69	0.51
3:A:1177:ARG:CZ	3:B:972:ARG:O[3_655]	1.69	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1041:GLY:N	3:B:982:VAL:CG2[3_655]	1.72	0.48
3:A:1177:ARG:NE	3:B:972:ARG:C[3_655]	1.72	0.48
3:A:1177:ARG:CZ	3:B:972:ARG:CA[3_655]	1.74	0.46
3:A:1177:ARG:NH2	3:B:972:ARG:C[3_655]	1.86	0.34
3:A:653:PRO:CG	3:B:657:GLU:CG[2_655]	1.87	0.33
3:A:657:GLU:CD	3:B:654:LYS:CG[2_655]	1.88	0.32
3:A:653:PRO:CA	3:B:657:GLU:OE2[2_655]	1.94	0.26
3:A:653:PRO:CB	3:B:657:GLU:OE2[2_655]	1.95	0.25
3:A:657:GLU:OE2	3:B:653:PRO:C[2_655]	1.99	0.21
3:A:1177:ARG:NH1	3:B:972:ARG:O[3_655]	2.02	0.18
3:A:1177:ARG:CG	3:B:974:GLY:N[3_655]	2.03	0.17
3:B:304:ARG:NH2	3:B:1017:ARG:CZ[4_554]	2.07	0.13
3:A:1177:ARG:NE	3:B:972:ARG:O[3_655]	2.07	0.13
3:A:1169:PHE:CD1	3:B:638:SER:C[2_655]	2.12	0.08
3:A:971:GLY:O	3:B:1177:ARG:CZ[3_645]	2.13	0.07
3:A:654:LYS:CG	3:B:657:GLU:OE1[2_655]	2.16	0.04
3:A:654:LYS:N	3:B:657:GLU:CD[2_655]	2.17	0.03
3:B:304:ARG:NH2	3:B:1017:ARG:NH2[4_554]	2.18	0.02
2:D:7:DG:OP1	3:A:475:ARG:NH2[4_654]	2.18	0.02
3:A:1154:GLU:O	3:B:157:ASP:CG[1_655]	2.18	0.02
3:A:1154:GLU:C	3:B:157:ASP:OD2[1_655]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	1124/1220 (92%)	1006 (90%)	88 (8%)	30 (3%)	6	47
3	B	1120/1220 (92%)	1007 (90%)	82 (7%)	31 (3%)	6	46
All	All	2244/2440 (92%)	2013 (90%)	170 (8%)	61 (3%)	6	47

All (61) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	286	PRO
3	A	537	GLU
3	A	538	ALA
3	A	774	VAL
3	A	836	PRO
3	A	1013	HIS
3	A	1014	PRO
3	A	1029	ILE
3	A	1039	LEU
3	A	1127	ALA
3	A	1128	PRO
3	A	1130	ALA
3	A	1176	LEU
3	B	492	ILE
3	B	537	GLU
3	B	538	ALA
3	B	549	MET
3	B	774	VAL
3	B	866	ILE
3	B	1014	PRO
3	B	1039	LEU
3	B	1142	GLU
3	B	1176	LEU
3	A	290	LYS
3	A	291	MET
3	A	539	PHE
3	A	548	GLU
3	A	570	ARG
3	A	792	GLY
3	A	975	LEU
3	A	976	VAL
3	A	1122	GLU
3	A	1177	ARG
3	B	290	LYS
3	B	291	MET
3	B	539	PHE
3	B	548	GLU
3	B	570	ARG
3	B	714	GLY
3	B	715	GLN
3	B	792	GLY
3	B	975	LEU
3	B	976	VAL

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Mol	Chain	Res	Type
3	B	1177	ARG
3	B	836	PRO
3	B	1143	LYS
3	A	53	ALA
3	A	238	ASP
3	B	53	ALA
3	B	238	ASP
3	B	867	PRO
3	B	1193	GLY
3	A	736	GLU
3	A	977	GLY
3	A	1027	CYS
3	A	1193	GLY
3	B	736	GLU
3	B	977	GLY
3	B	1125	LEU
3	A	399	PHE
3	B	399	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	953/1008 (94%)	889 (93%)	64 (7%)	20	59
3	B	953/1008 (94%)	886 (93%)	67 (7%)	19	58
All	All	1906/2016 (94%)	1775 (93%)	131 (7%)	19	58

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	6	LYS
3	A	61	THR
3	A	75	VAL
3	A	85	ARG
3	A	132	LEU

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Mol	Chain	Res	Type
3	A	165	ARG
3	A	207	MET
3	A	211	ASN
3	A	215	TYR
3	A	222	ARG
3	A	235	THR
3	A	253	THR
3	A	274	THR
3	A	276	GLU
3	A	290	LYS
3	A	300	LEU
3	A	305	THR
3	A	319	LEU
3	A	321	ARG
3	A	326	ILE
3	A	368	ARG
3	A	407	GLN
3	A	424	ARG
3	A	439	THR
3	A	440	ASN
3	A	444	LEU
3	A	452	ARG
3	A	463	ASP
3	A	498	LEU
3	A	519	GLU
3	A	546	ARG
3	A	580	VAL
3	A	587	THR
3	A	616	LYS
3	A	617	MET
3	A	622	LEU
3	A	625	LEU
3	A	670	LEU
3	A	672	SER
3	A	707	THR
3	A	719	SER
3	A	736	GLU
3	A	786	ARG
3	A	795	GLU
3	A	823	LEU
3	A	840	MET
3	A	903	ARG

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Mol	Chain	Res	Type
3	A	927	GLU
3	A	958	GLU
3	A	997	THR
3	A	1018	TYR
3	A	1026	SER
3	A	1028	THR
3	A	1032	LEU
3	A	1045	VAL
3	A	1046	LEU
3	A	1074	THR
3	A	1095	GLU
3	A	1096	ASP
3	A	1104	GLU
3	A	1120	THR
3	A	1169	PHE
3	A	1184	GLU
3	A	1192	GLU
3	B	6	LYS
3	B	61	THR
3	B	75	VAL
3	B	85	ARG
3	B	132	LEU
3	B	165	ARG
3	B	207	MET
3	B	211	ASN
3	B	215	TYR
3	B	222	ARG
3	B	235	THR
3	B	253	THR
3	B	274	THR
3	B	276	GLU
3	B	290	LYS
3	B	300	LEU
3	B	305	THR
3	B	319	LEU
3	B	321	ARG
3	B	326	ILE
3	B	368	ARG
3	B	407	GLN
3	B	424	ARG
3	B	439	THR
3	B	440	ASN

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Mol	Chain	Res	Type
3	B	444	LEU
3	B	452	ARG
3	B	463	ASP
3	B	498	LEU
3	B	519	GLU
3	B	546	ARG
3	B	580	VAL
3	B	587	THR
3	B	616	LYS
3	B	617	MET
3	B	622	LEU
3	B	625	LEU
3	B	670	LEU
3	B	672	SER
3	B	707	THR
3	B	719	SER
3	B	736	GLU
3	B	786	ARG
3	B	795	GLU
3	B	823	LEU
3	B	840	MET
3	B	866	ILE
3	B	903	ARG
3	B	927	GLU
3	B	958	GLU
3	B	997	THR
3	B	1013	HIS
3	B	1018	TYR
3	B	1027	CYS
3	B	1028	THR
3	B	1032	LEU
3	B	1045	VAL
3	B	1046	LEU
3	B	1074	THR
3	B	1095	GLU
3	B	1096	ASP
3	B	1104	GLU
3	B	1125	LEU
3	B	1142	GLU
3	B	1169	PHE
3	B	1184	GLU
3	B	1192	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	9	HIS
3	A	15	GLN
3	A	440	ASN
3	A	455	ASN
3	A	575	HIS
3	A	725	HIS
3	A	746	GLN
3	A	1013	HIS
3	A	1116	GLN
3	A	1155	HIS
3	B	9	HIS
3	B	15	GLN
3	B	440	ASN
3	B	455	ASN
3	B	569	ASN
3	B	575	HIS
3	B	725	HIS
3	B	746	GLN
3	B	778	GLN
3	B	817	HIS
3	B	1013	HIS
3	B	1116	GLN
3	B	1155	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DOC	D	21	1,2	11,19,20	0.87	1 (9%)	14,26,29	1.30	2 (14%)
2	DOC	F	21	1,2	11,19,20	0.91	1 (9%)	14,26,29	1.27	1 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DOC	D	21	1,2	-	0/3/18/19	0/2/2/2
2	DOC	F	21	1,2	-	0/3/18/19	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	21	DOC	C6-C5	-2.23	1.33	1.38
2	F	21	DOC	C6-C5	-2.16	1.33	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	21	DOC	C3'-C2'-C1'	2.46	105.45	102.71
2	D	21	DOC	C2-N3-C4	3.25	120.19	115.61
2	F	21	DOC	C2-N3-C4	3.27	120.23	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	21	DOC	25	0
2	F	21	DOC	16	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 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	$\# Z > 2$
5	DTP	A	1222	4	24,32,32	1.25	2 (8%)	32,50,50	1.18	4 (12%)
5	DTP	B	1222	4	24,32,32	1.25	2 (8%)	32,50,50	1.18	4 (12%)

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
5	DTP	A	1222	4	-	0/18/34/34	0/3/3/3
5	DTP	B	1222	4	-	0/18/34/34	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1222	DTP	O4'-C1'	-3.01	1.35	1.42
5	A	1222	DTP	O4'-C1'	-3.00	1.35	1.42
5	B	1222	DTP	PA-O2A	-2.88	1.42	1.54
5	A	1222	DTP	PA-O2A	-2.84	1.42	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1222	DTP	C2'-C1'-N9	-2.86	107.20	114.16
5	B	1222	DTP	C2'-C1'-N9	-2.83	107.28	114.16
5	A	1222	DTP	O3G-PG-O3B	-2.20	95.11	105.09
5	B	1222	DTP	O3G-PG-O3B	-2.19	95.17	105.09
5	B	1222	DTP	O2G-PG-O1G	2.21	117.70	110.58
5	A	1222	DTP	O2G-PG-O1G	2.22	117.74	110.58
5	A	1222	DTP	O3'-C3'-C4'	2.75	121.17	110.05
5	B	1222	DTP	O3'-C3'-C4'	2.77	121.23	110.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1222	DTP	24	0
5	B	1222	DTP	14	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95th 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 ²)	Q<0.9
1	C	20/27 (74%)	-0.08	1 (5%) 32 26	228, 228, 228, 228	0
1	E	20/27 (74%)	-0.38	0 100 100	228, 228, 228, 228	0
2	D	18/21 (85%)	-0.26	0 100 100	66, 228, 228, 228	0
2	F	18/21 (85%)	-0.26	0 100 100	228, 228, 228, 228	0
3	A	1148/1220 (94%)	0.41	125 (10%) 7 7	201, 226, 296, 326	0
3	B	1148/1220 (94%)	0.39	97 (8%) 14 11	201, 226, 296, 326	0
All	All	2372/2536 (93%)	0.38	223 (9%) 11 9	66, 226, 296, 326	0

All (223) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	1026	SER	8.4
3	B	496	GLY	8.2
3	B	569	ASN	7.4
3	B	524	LEU	6.8
3	B	1129	LYS	6.6
3	A	23	ALA	6.4
3	B	5	LEU	6.4
3	A	1049	GLY	6.4
3	B	525	ILE	6.2
3	A	1139	LEU	5.8
3	B	574	VAL	5.6
3	B	1172	ALA	5.5
3	A	718	VAL	5.4
3	B	10	LEU	5.4
3	B	447	GLY	5.3
3	A	141	ALA	5.3
3	A	139	LEU	5.2
3	A	1035	PHE	5.0
3	A	1138	ALA	5.0

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Mol	Chain	Res	Type	RSRZ
3	B	497	SER	4.9
3	A	140	ILE	4.9
3	B	6	LYS	4.9
3	A	1040	PRO	4.7
3	B	572	ALA	4.6
3	B	1171	GLU	4.6
3	B	98	LEU	4.6
3	A	22	ALA	4.4
3	B	584	GLU	4.4
3	B	1193	GLY	4.4
3	A	1180	ARG	4.4
3	A	505	LYS	4.4
3	B	254	PRO	4.4
3	A	1140	LEU	4.4
3	B	1048	SER	4.4
3	B	97	THR	4.3
3	B	495	PHE	4.3
3	A	1044	LYS	4.3
3	A	1027	CYS	4.3
3	A	1098	PRO	4.2
3	B	9	HIS	4.2
3	B	1116	GLN	4.2
3	B	1194	TYR	4.2
3	B	1201	ASP	4.1
3	B	1020	GLY	4.0
3	A	1039	LEU	4.0
3	A	1096	ASP	3.9
3	B	149	GLU	3.9
3	B	69	ILE	3.8
3	A	1116	GLN	3.8
3	B	1072	ASP	3.7
3	B	1180	ARG	3.7
3	B	501	LYS	3.7
3	B	570	ARG	3.7
3	A	1041	GLY	3.7
3	A	1048	SER	3.7
3	B	414	ARG	3.6
3	B	1173	LEU	3.6
3	B	522	ALA	3.6
3	B	1005	ALA	3.6
3	B	41	ALA	3.6
3	B	7	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
3	A	996	ILE	3.5
3	B	504	LEU	3.5
3	A	650	LEU	3.5
3	B	303	GLY	3.4
3	B	1075	GLY	3.4
3	A	524	LEU	3.4
3	B	883	VAL	3.4
3	A	1159	LEU	3.4
3	B	1099	LEU	3.4
3	A	146	LEU	3.4
3	A	615	LEU	3.3
3	B	1021	LEU	3.3
3	A	1158	SER	3.3
3	A	1113	VAL	3.3
3	B	1186	LEU	3.3
3	A	1036	VAL	3.3
3	B	895	LYS	3.3
3	A	1099	LEU	3.3
3	A	1194	TYR	3.3
3	B	1013	HIS	3.3
3	A	589	LEU	3.2
3	A	771	LYS	3.2
3	A	10	LEU	3.2
3	A	883	VAL	3.2
3	A	1079	VAL	3.2
3	B	1128	PRO	3.2
3	A	1024	VAL	3.2
3	A	1078	GLU	3.2
3	A	1184	GLU	3.1
3	B	838	GLU	3.1
3	A	1025	ALA	3.1
3	A	453	PHE	3.1
3	B	1121	LEU	3.0
3	A	1080	VAL	3.0
3	B	941	ALA	3.0
3	A	264	ALA	3.0
3	A	1142	GLU	3.0
3	B	157	ASP	3.0
3	B	42	LEU	2.9
3	B	1112	ARG	2.9
3	B	521	LEU	2.9
3	A	42	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
3	A	504	LEU	2.9
3	A	135	HIS	2.9
3	B	568	LEU	2.9
3	A	1161	VAL	2.9
3	A	565	LEU	2.8
3	B	815	LYS	2.8
3	A	768	ALA	2.8
3	A	581	ILE	2.8
3	B	91	GLY	2.8
3	A	590	VAL	2.8
3	A	419	SER	2.7
3	A	567	GLY	2.7
3	A	286	PRO	2.7
3	B	500	SER	2.7
3	B	1159	LEU	2.7
3	A	808	PHE	2.7
3	B	448	LEU	2.7
3	A	700	GLY	2.7
3	B	593	MET	2.7
3	A	486	GLU	2.6
3	A	574	VAL	2.6
3	A	1029	ILE	2.6
3	B	563	MET	2.6
3	A	810	ASN	2.6
3	B	259	ALA	2.6
3	A	1143	LYS	2.6
3	A	468	PHE	2.6
3	A	1105	VAL	2.6
3	A	1043	PRO	2.6
3	B	1067	ARG	2.6
3	A	1009	TYR	2.6
3	A	896	ASN	2.6
3	A	177	PHE	2.5
3	A	614	LEU	2.5
3	B	251	VAL	2.5
3	A	285	LEU	2.5
3	B	1047	LEU	2.5
3	A	489	VAL	2.5
3	B	491	GLN	2.5
3	A	98	LEU	2.5
3	A	699	PRO	2.4
3	B	1158	SER	2.4

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Mol	Chain	Res	Type	RSRZ
3	A	915	PHE	2.4
3	A	911	ARG	2.4
3	A	1155	HIS	2.4
3	B	158	ARG	2.4
3	B	830	TYR	2.4
3	A	1014	PRO	2.4
3	A	809	ALA	2.4
3	B	897	VAL	2.4
3	B	498	LEU	2.4
3	B	571	HIS	2.4
3	B	438	ILE	2.4
3	A	899	GLU	2.4
3	A	719	SER	2.4
3	A	9	HIS	2.4
3	B	530	GLY	2.4
3	A	661	ARG	2.4
3	A	136	ALA	2.4
3	A	520	GLU	2.3
3	A	597	GLU	2.3
3	B	1104	GLU	2.3
3	A	454	LEU	2.3
3	A	491	GLN	2.3
3	A	976	VAL	2.3
3	A	1047	LEU	2.3
3	A	237	ASP	2.3
3	B	68	ILE	2.3
3	B	757	TYR	2.3
3	B	1006	LEU	2.3
3	A	54	VAL	2.3
3	A	508	ALA	2.3
3	A	980	ALA	2.3
3	B	70	GLY	2.2
3	B	271	PHE	2.2
3	A	352	GLU	2.2
3	A	1104	GLU	2.2
3	B	780	HIS	2.2
3	A	1076	ALA	2.2
3	A	173	PHE	2.2
3	B	153	PHE	2.2
3	B	40	PRO	2.2
3	B	837	VAL	2.2
3	A	1010	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	6	DT	2.1
3	A	12	GLN	2.1
3	A	356	ARG	2.1
3	A	1067	ARG	2.1
3	A	525	ILE	2.1
3	B	35	THR	2.1
3	B	234	THR	2.1
3	A	1045	VAL	2.1
3	A	1171	GLU	2.1
3	A	1012	GLY	2.1
3	B	1189	LEU	2.1
3	B	43	ALA	2.1
3	A	138	GLY	2.1
3	B	585	PRO	2.1
3	A	1178	GLU	2.1
3	A	604	TYR	2.1
3	A	1182	GLY	2.1
3	A	7	PHE	2.1
3	B	1022	ARG	2.1
3	A	1160	PRO	2.1
3	A	662	GLY	2.1
3	A	772	LYS	2.1
3	A	1097	ILE	2.1
3	B	1004	GLU	2.1
3	A	172	ILE	2.1
3	B	659	LEU	2.1
3	A	545	LEU	2.0
3	A	572	ALA	2.0
3	B	1130	ALA	2.0
3	A	1117	ALA	2.0
3	B	979	PHE	2.0
3	A	65	VAL	2.0
3	A	858	ILE	2.0
3	A	176	ARG	2.0
3	A	521	LEU	2.0
3	B	1007	GLY	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
2	DOC	D	21	18/19	0.78	0.19	-	227,227,227,227	0
2	DOC	F	21	18/19	0.67	0.26	-	227,227,227,227	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
5	DTP	B	1222	30/30	0.80	0.28	0.38	242,242,242,242	0
5	DTP	A	1222	30/30	0.83	0.25	-0.73	242,242,242,242	0
4	CA	A	1221	1/1	0.97	0.26	-	47,47,47,47	0
4	CA	B	1221	1/1	0.96	0.24	-	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.