



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Dec 9, 2019 – 12:51 PM EST

PDB ID : 6PWW
EMDB ID: : EMD-20513
Title : Cryo-EM structure of MLL1 in complex with RbBP5 and WDR5 bound to the nucleosome
Authors : Park, S.H.; Ayoub, A.; Lee, Y.T.; Xu, J.; Zhang, W.; Zhang, B.; Zhang, Y.; Cianfrocco, M.A.; Su, M.; Dou, Y.; Cho, U.
Deposited on : 2019-07-23
Resolution : 4.40 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

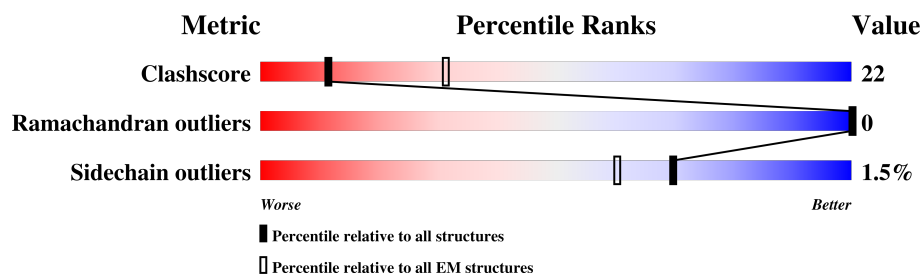
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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.




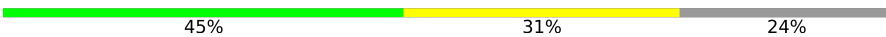


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	538	35% 26% 38%
2	B	313	51% 46% .
3	C	209	38% 35% 27%
4	G	136	35% 37% 28%
4	K	136	34% 38% 28%
5	H	103	39% 39% . 20%
5	L	103	39% 39% . 20%
6	I	129	50% 33% 17%
6	M	129	43% 40% 17%

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Mol	Chain	Length	Quality of chain
7	J	123	 50% 24% 24% .
7	N	123	 45% 31% 24%
8	O	147	 29% 71% .
9	P	147	 34% 64% ..

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 18174 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Retinoblastoma-binding protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	333	Total	C	N	O	S	0	0
			2613	1648	457	493	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q15291

- Molecule 2 is a protein called WD repeat-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	303	Total	C	N	O	S	3	0
			2342	1492	388	451	11		

- Molecule 3 is a protein called Histone-lysine N-methyltransferase 2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	153	Total	C	N	O	S	0	0
			1228	780	218	217	13		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3761	SER	-	expression tag	UNP Q03164
C	3861	ILE	ASN	conflict	UNP Q03164
C	3867	LEU	GLN	conflict	UNP Q03164

- Molecule 4 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	98	Total	C	N	O	S	0	0
			801	506	153	139	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	98	Total	C	N	O	S	0	0
			801	506	153	139	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	102	ALA	GLY	engineered mutation	UNP P84233
K	102	ALA	GLY	engineered mutation	UNP P84233

- Molecule 5 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	82	Total	C	N	O	S	0	0
			653	413	127	112	1		
5	L	82	Total	C	N	O	S	0	0
			653	413	127	112	1		

- Molecule 6 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	107	Total	C	N	O	0	0
			811	510	158	143		
6	M	107	Total	C	N	O	0	0
			815	513	159	143		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	99	ARG	GLY	conflict	UNP P06897
I	123	SER	ALA	conflict	UNP P06897
M	99	ARG	GLY	conflict	UNP P06897
M	123	SER	ALA	conflict	UNP P06897

- Molecule 7 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	93	Total	C	N	O	S	0	0
			718	451	128	137	2		
7	N	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	0	MET	-	initiating methionine	UNP P02281
J	29	THR	SER	engineered mutation	UNP P02281
N	0	MET	-	initiating methionine	UNP P02281
N	29	THR	SER	engineered mutation	UNP P02281

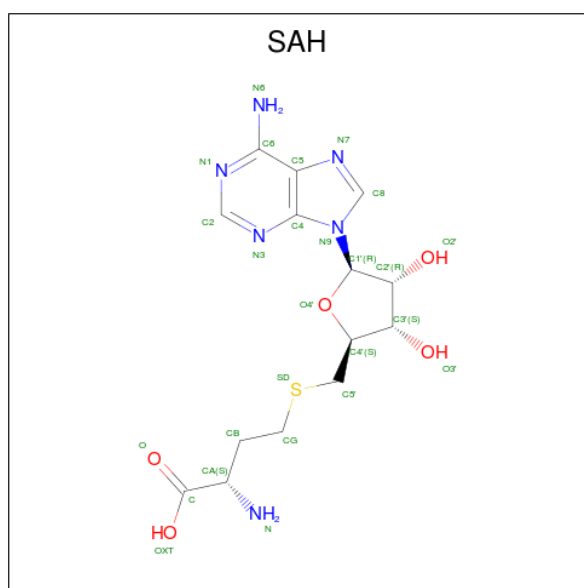
- Molecule 8 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		

- Molecule 9 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		

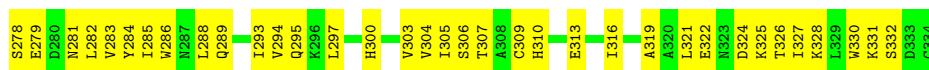
- Molecule 10 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					AltConf
10	C	1	Total	C	N	O	S	0
			26	14	6	5	1	

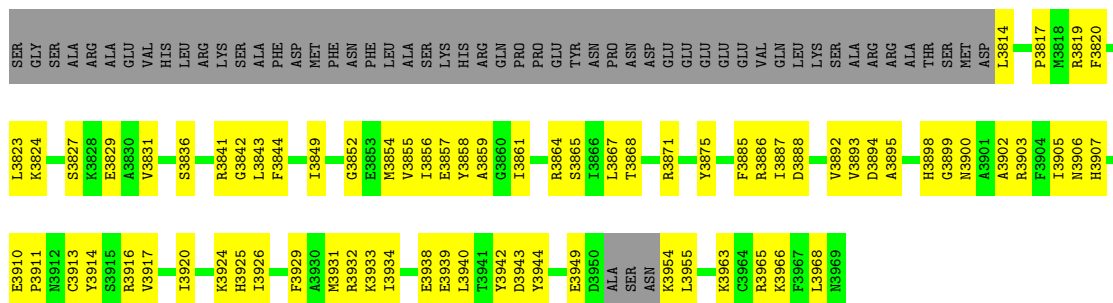
- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		AltConf
11	C	1	Total	Zn	0
			1	1	



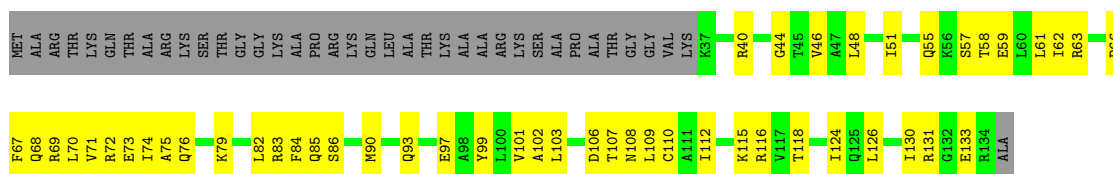
• Molecule 3: Histone-lysine N-methyltransferase 2A

Chain C: 38% 35% 27%



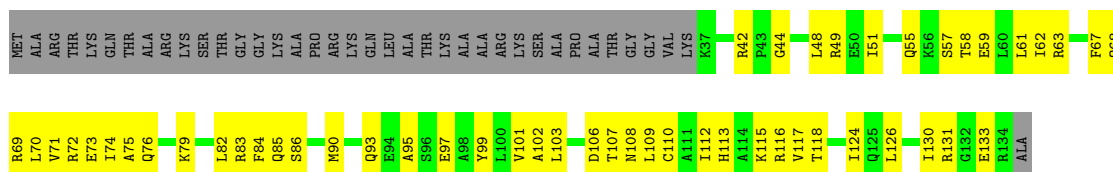
• Molecule 4: Histone H3.2

Chain G: 35% 37% 28%



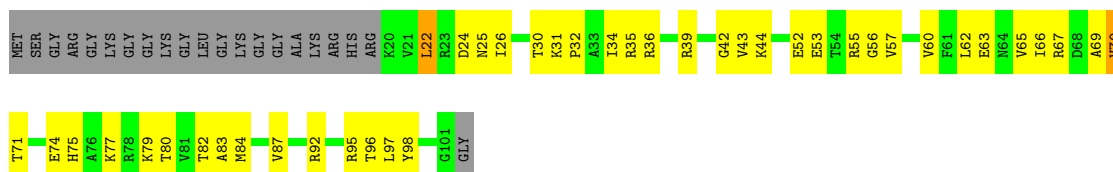
• Molecule 4: Histone H3.2

Chain K: 34% 38% 28%

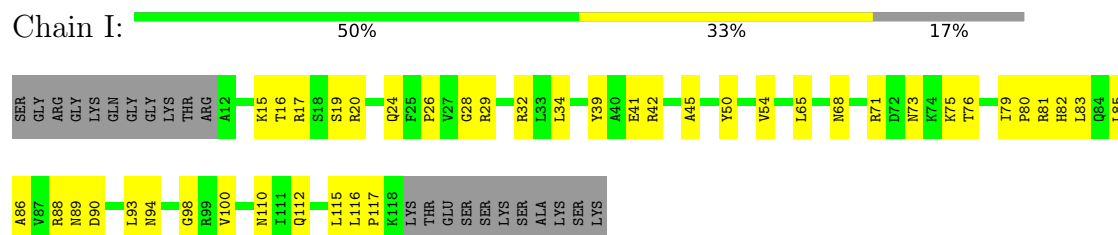


• Molecule 5: Histone H4

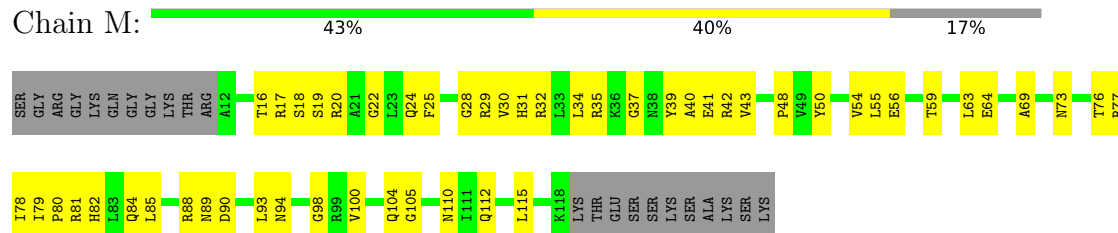
Chain H: 39% 39% 20%



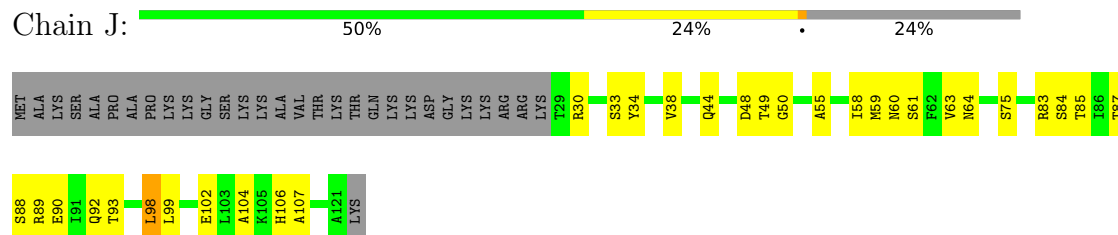
- Molecule 6: Histone H2A type 1



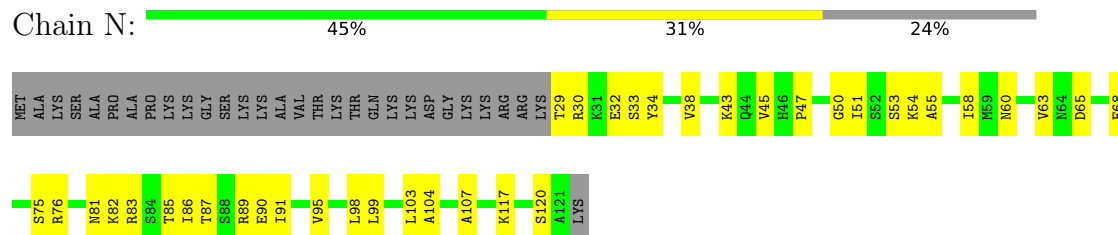
- Molecule 6: Histone H2A type 1



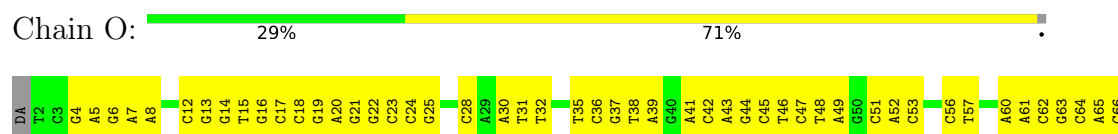
- Molecule 7: Histone H2B 1.1

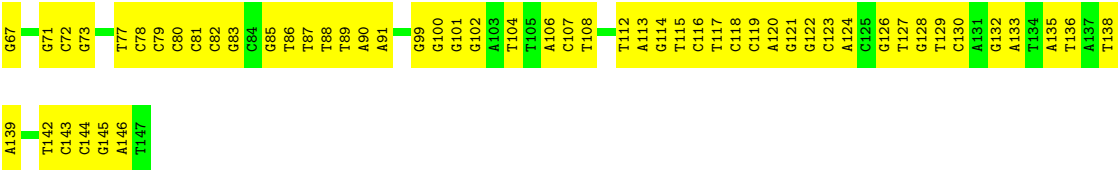


- Molecule 7: Histone H2B 1.1

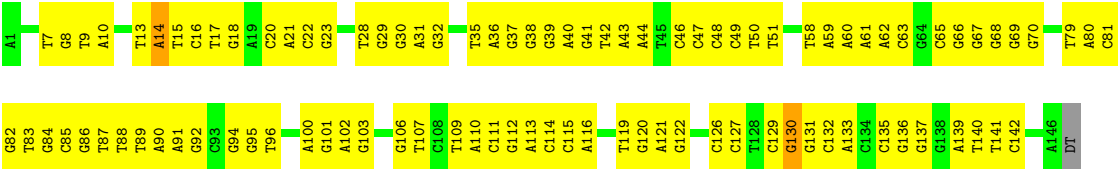
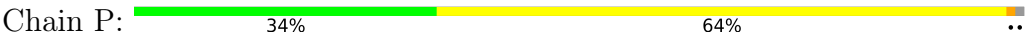


- Molecule 8: DNA (146-MER)





● Molecule 9: DNA (146-MER)



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21114	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.25	0/2667	0.45	0/3620
2	B	0.25	0/2413	0.45	0/3275
3	C	0.25	0/1253	0.41	0/1678
4	G	0.27	0/813	0.41	0/1093
4	K	0.27	0/813	0.41	0/1093
5	H	0.28	0/660	0.44	0/885
5	L	0.28	0/660	0.44	0/885
6	I	0.26	0/821	0.42	0/1112
6	M	0.26	0/825	0.40	0/1116
7	J	0.27	0/729	0.43	1/985 (0.1%)
7	N	0.27	0/737	0.44	1/993 (0.1%)
8	O	0.60	0/3333	0.93	0/5137
9	P	0.62	0/3381	0.92	2/5221 (0.0%)
All	All	0.42	0/19105	0.67	4/27093 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	98	LEU	C-N-CA	-5.83	107.14	121.70
9	P	14	DA	O4'-C4'-C3'	-5.82	102.17	104.50
7	N	98	LEU	C-N-CA	-5.63	107.63	121.70
9	P	130	DG	O4'-C4'-C3'	-5.01	102.50	104.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2613	0	2582	112	0
2	B	2342	0	2298	110	0
3	C	1228	0	1226	65	0
4	G	801	0	831	43	0
4	K	801	0	831	50	0
5	H	653	0	695	45	0
5	L	653	0	695	40	0
6	I	811	0	849	44	0
6	M	815	0	860	53	0
7	J	718	0	725	27	0
7	N	726	0	747	37	0
8	O	2975	0	1639	108	0
9	P	3011	0	1639	119	0
10	C	26	0	18	4	0
11	C	1	0	0	0	0
All	All	18174	0	15635	712	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 22.

All (712) 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)
8:O:83:DG:N2	9:P:65:DC:O2	2.00	0.94
2:B:267:SER:O	2:B:272:LYS:HA	1.67	0.92
7:J:55:ALA:HA	7:J:58:ILE:HD12	1.62	0.81
6:M:112:GLN:HB2	6:M:115:LEU:HD23	1.61	0.81
6:I:42:ARG:HB2	7:J:85:THR:HG22	1.62	0.81
8:O:83:DG:N1	9:P:65:DC:N3	2.31	0.78
8:O:28:DC:N4	9:P:119:DT:C4	2.55	0.75
4:G:55:GLN:O	6:M:81:ARG:NH2	2.20	0.74
2:B:41:LEU:HB2	2:B:327:ILE:HB	1.70	0.73
2:B:194:LEU:HD23	2:B:210:ILE:HD11	1.71	0.73
1:A:329:TRP:HZ2	3:C:3841:ARG:HD3	1.55	0.71
2:B:305:ILE:HB	2:B:321:LEU:HG	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:93:LEU:HD22	7:N:103:LEU:HD11	1.71	0.71
4:G:108:ASN:ND2	5:H:42:GLY:O	2.23	0.71
9:P:47:DC:O2	9:P:48:DC:C2	2.43	0.71
5:L:70:VAL:O	5:L:74:GLU:N	2.23	0.70
9:P:89:DT:H2''	9:P:90:DA:C8	2.26	0.70
3:C:3917:VAL:HG12	3:C:3924:LYS:HD2	1.72	0.70
5:H:36:ARG:NH2	9:P:61:DA:OP1	2.25	0.70
4:K:108:ASN:ND2	5:L:42:GLY:O	2.25	0.70
2:B:238:LEU:HB2	2:B:252:TYR:HB2	1.74	0.69
4:G:79:LYS:HB3	4:G:82:LEU:HD11	1.75	0.69
9:P:102:DA:H5''	5:L:78:ARG:HD2	1.74	0.69
1:A:224:VAL:O	1:A:242:MET:N	2.26	0.69
6:M:34:LEU:HB3	6:M:43:VAL:HG21	1.74	0.69
4:K:79:LYS:HB3	4:K:82:LEU:HD11	1.75	0.68
6:M:54:VAL:HG13	7:N:107:ALA:HB1	1.75	0.68
1:A:219:ASP:OD2	1:A:223:ARG:NH2	2.27	0.68
5:H:70:VAL:O	5:H:74:GLU:N	2.24	0.68
4:G:61:LEU:HD12	5:H:36:ARG:HD2	1.75	0.68
9:P:48:DC:H4'	9:P:49:DC:H5'	1.73	0.68
2:B:41:LEU:N	2:B:327:ILE:O	2.23	0.68
8:O:61:DA:OP1	5:L:36:ARG:NH2	2.26	0.68
1:A:52:ASP:HB2	1:A:59:ALA:HB2	1.75	0.68
2:B:195[B]:CYS:HB2	2:B:209:LEU:HB2	1.75	0.67
2:B:32:LYS:HA	2:B:294:VAL:HB	1.77	0.67
8:O:90:DA:H1'	8:O:91:DA:N7	2.10	0.67
2:B:169:ALA:O	2:B:196:ARG:NH1	2.27	0.67
2:B:283:VAL:HB	2:B:297:LEU:HB2	1.77	0.67
5:H:63:GLU:O	5:H:67:ARG:NH1	2.28	0.67
8:O:28:DC:N4	9:P:119:DT:N3	2.43	0.67
9:P:112:DG:H2''	9:P:113:DA:C8	2.30	0.66
1:A:110:ILE:HA	1:A:127:PRO:HA	1.76	0.66
8:O:45:DC:H2'	8:O:46:DT:C6	2.30	0.66
3:C:3857:GLU:OE2	3:C:3925:HIS:ND1	2.29	0.66
6:M:42:ARG:HG3	7:N:85:THR:HG22	1.77	0.66
7:N:53:SER:N	8:O:20:DA:OP1	2.24	0.66
1:A:339:LEU:HD23	3:C:3898:HIS:HB3	1.78	0.66
5:L:63:GLU:O	5:L:67:ARG:NH1	2.28	0.66
6:I:29:ARG:NH1	7:J:33:SER:O	2.29	0.66
9:P:102:DA:OP1	5:L:79:LYS:N	2.28	0.66
5:H:52:GLU:OE1	5:H:52:GLU:N	2.29	0.66
5:H:66:ILE:O	5:H:69:ALA:HB3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:101:LEU:HD12	2:B:113:ILE:HG22	1.79	0.65
1:A:286:LEU:HD21	1:A:289:ILE:HG13	1.78	0.65
1:A:265:TYR:HB3	1:A:278:ILE:HD11	1.79	0.65
2:B:132:VAL:HA	2:B:148:SER:HA	1.79	0.65
6:I:81:ARG:NH2	4:K:55:GLN:O	2.29	0.65
1:A:329:TRP:CZ2	3:C:3841:ARG:HD3	2.32	0.65
4:K:68:GLN:HE21	4:K:72:ARG:HE	1.45	0.64
5:L:52:GLU:OE1	5:L:52:GLU:N	2.29	0.64
5:L:66:ILE:O	5:L:69:ALA:HB3	1.96	0.64
3:C:3886:ARG:HA	3:C:3892:VAL:HG22	1.79	0.64
6:I:29:ARG:HG3	6:I:32:ARG:HH21	1.62	0.64
5:H:75:HIS:HB2	7:J:93:THR:HG21	1.78	0.64
9:P:37:DG:N2	9:P:38:DG:C2	2.65	0.64
1:A:217:THR:OG1	1:A:219:ASP:OD1	2.15	0.64
2:B:138:ASN:ND2	2:B:142:ASN:OD1	2.29	0.64
4:G:68:GLN:HE21	4:G:72:ARG:HE	1.45	0.64
1:A:220:ARG:HB2	1:A:251:ARG:HH12	1.63	0.63
7:J:83:ARG:HE	9:P:40:DA:H3'	1.63	0.63
1:A:195:THR:OG1	1:A:196:SER:N	2.31	0.63
2:B:217:VAL:HG22	2:B:233:THR:HG22	1.81	0.63
6:I:85:LEU:O	6:I:89:ASN:ND2	2.27	0.63
2:B:157:ASP:OD1	2:B:158:VAL:N	2.29	0.63
1:A:220:ARG:NH1	1:A:251:ARG:O	2.32	0.63
4:G:116:ARG:NH1	4:G:118:THR:O	2.32	0.62
4:K:93:GLN:NE2	4:K:97:GLU:OE2	2.32	0.62
1:A:280:GLU:OE1	1:A:285:ASN:ND2	2.32	0.62
4:K:116:ARG:NH1	4:K:118:THR:O	2.32	0.62
2:B:111:LEU:HB2	2:B:125:LEU:HB2	1.82	0.62
4:G:106:ASP:HB2	4:K:130:ILE:HD12	1.81	0.62
6:M:32:ARG:NH2	7:N:32:GLU:OE2	2.33	0.62
4:G:93:GLN:NE2	4:G:97:GLU:OE2	2.32	0.62
1:A:76:ARG:NH2	1:A:117:PRO:O	2.32	0.62
2:B:90:ILE:HA	2:B:106:SER:HA	1.82	0.62
2:B:303:VAL:HB	2:B:321:LEU:HD12	1.82	0.62
2:B:195[A]:CYS:HB3	2:B:209:LEU:HB2	1.82	0.61
4:G:130:ILE:HD12	4:K:106:ASP:HB2	1.81	0.61
9:P:69:DG:N2	9:P:70:DG:C2	2.68	0.61
2:B:44:HIS:NE2	2:B:62:SER:O	2.32	0.61
6:M:16:THR:HA	8:O:31:DT:H5''	1.81	0.61
4:K:63:ARG:HG2	9:P:91:DA:H4'	1.81	0.61
8:O:106:DA:H2''	8:O:107:DC:H5''	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:263:PHE:O	2:B:307:THR:OG1	2.18	0.61
6:I:54:VAL:HG13	7:J:107:ALA:HB1	1.83	0.61
1:A:273:GLN:NE2	1:A:277:TYR:OH	2.34	0.60
6:I:88:ARG:NH1	6:I:94:ASN:OD1	2.33	0.60
4:K:97:GLU:O	4:K:101:VAL:HG23	2.01	0.60
3:C:3867:LEU:HG	3:C:3871:ARG:HD2	1.84	0.60
2:B:241:TRP:HA	2:B:248:CYS:HA	1.84	0.60
2:B:69:ILE:HD11	2:B:104:SER:HB3	1.83	0.60
6:I:39:TYR:HB3	7:J:75:SER:HB3	1.84	0.60
2:B:149:PHE:HA	2:B:173:PRO:HB3	1.84	0.60
4:K:42:ARG:N	8:O:144:DC:OP1	2.32	0.60
1:A:278:ILE:HG23	1:A:287:VAL:HB	1.84	0.60
6:I:20:ARG:NH2	9:P:32:DG:OP1	2.35	0.60
1:A:251:ARG:O	1:A:272:ARG:NH2	2.34	0.59
5:H:39:ARG:NH1	5:H:43:VAL:O	2.33	0.59
1:A:279:TRP:HA	1:A:286:LEU:HA	1.85	0.59
4:G:75:ALA:HB2	5:H:66:ILE:HD11	1.84	0.59
8:O:60:DA:H2''	8:O:61:DA:H8	1.67	0.59
1:A:33:ASN:ND2	1:A:37:THR:OG1	2.35	0.59
2:B:35:TYR:HB3	2:B:330:TRP:HB3	1.84	0.59
3:C:3819:ARG:NH2	3:C:3852:GLY:O	2.30	0.59
5:L:62:LEU:O	5:L:66:ILE:HG22	2.03	0.59
3:C:3871:ARG:NH1	3:C:3875:TYR:OH	2.36	0.59
6:I:16:THR:HG23	6:I:19:SER:H	1.66	0.59
4:K:72:ARG:HH22	8:O:51:DC:P	2.25	0.59
5:L:39:ARG:NH1	5:L:43:VAL:O	2.33	0.59
3:C:3849:ILE:HG21	3:C:3855:VAL:HG22	1.83	0.59
5:H:82:THR:HG22	5:H:84:MET:H	1.68	0.59
5:L:82:THR:HG22	5:L:84:MET:H	1.68	0.59
1:A:128:MET:HG3	1:A:129:LYS:HG3	1.85	0.59
4:K:117:VAL:N	8:O:71:DG:OP1	2.36	0.59
1:A:47:ARG:HG2	1:A:63:SER:HA	1.84	0.58
7:N:76:ARG:HH22	5:L:91:LYS:HD3	1.68	0.58
4:G:97:GLU:O	4:G:101:VAL:HG23	2.02	0.58
8:O:128:DG:H2'	8:O:129:DT:H71	1.85	0.58
1:A:51:TRP:HA	1:A:58:ILE:HA	1.86	0.58
5:H:62:LEU:O	5:H:66:ILE:HG22	2.03	0.58
6:M:78:ILE:H	7:N:51:ILE:HA	1.68	0.58
9:P:36:DA:H2''	9:P:37:DG:C8	2.38	0.58
1:A:21:LEU:HB2	1:A:318:VAL:HB	1.85	0.58
2:B:255:HIS:HB2	2:B:278:SER:OG	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:76:THR:H	8:O:132:DG:P	2.26	0.58
6:I:16:THR:HA	9:P:31:DA:H5''	1.84	0.58
1:A:247:ASP:HB3	1:A:252:THR:H	1.69	0.58
3:C:3836:SER:HB2	3:C:3842:GLY:HA3	1.85	0.58
4:G:108:ASN:HB2	5:H:43:VAL:HG22	1.86	0.58
3:C:3905:ILE:O	3:C:3944:TYR:OH	2.17	0.58
9:P:106:DG:H2''	9:P:107:DT:H5''	1.86	0.57
3:C:3831:VAL:HG21	3:C:3856:ILE:HD12	1.86	0.57
8:O:126:DG:H2'	8:O:127:DT:H71	1.87	0.57
9:P:111:DC:H2''	9:P:112:DG:C8	2.39	0.57
4:K:69:ARG:NH2	9:P:91:DA:OP1	2.36	0.57
2:B:154:ARG:NH1	2:B:163:CYS:SG	2.76	0.57
4:K:83:ARG:HG2	8:O:51:DC:H5''	1.86	0.57
1:A:272:ARG:NH2	9:P:63:DC:OP1	2.34	0.57
5:H:83:ALA:O	5:H:87:VAL:HG23	2.05	0.57
5:H:74:GLU:O	7:J:89:ARG:NH2	2.36	0.57
7:N:29:THR:OG1	8:O:104:DT:OP1	2.23	0.57
2:B:130:ASN:HB3	2:B:149:PHE:HB3	1.87	0.57
4:G:67:PHE:O	4:G:71:VAL:HG23	2.05	0.57
8:O:30:DA:H2'	8:O:31:DT:H71	1.87	0.57
9:P:79:DT:H2''	9:P:80:DA:C8	2.40	0.57
4:G:126:LEU:O	4:G:130:ILE:HG12	2.05	0.56
4:K:126:LEU:O	4:K:130:ILE:HG12	2.05	0.56
1:A:113:VAL:HG12	1:A:125:VAL:HG22	1.87	0.56
3:C:3913:CYS:HB2	3:C:3942:TYR:HB3	1.87	0.56
3:C:3911:PRO:HG3	3:C:3943:ASP:HB2	1.86	0.56
4:K:67:PHE:O	4:K:71:VAL:HG23	2.05	0.56
8:O:79:DC:N4	9:P:68:DG:O6	2.38	0.56
1:A:233:CYS:HB3	1:A:237:GLY:HA3	1.86	0.56
2:B:101:LEU:HD11	2:B:122:LEU:HD12	1.86	0.56
2:B:240:LEU:HB3	2:B:250:LYS:HB2	1.86	0.56
6:I:73:ASN:O	6:I:75:LYS:NZ	2.24	0.56
2:B:322:GLU:O	2:B:325:LYS:NZ	2.33	0.56
5:H:44:LYS:HB2	6:M:115:LEU:HD12	1.87	0.56
5:L:83:ALA:O	5:L:87:VAL:HG23	2.05	0.56
6:M:29:ARG:NH1	7:N:33:SER:O	2.39	0.56
7:N:81:ASN:O	7:N:83:ARG:NE	2.29	0.56
8:O:36:DC:H2''	8:O:37:DG:C8	2.40	0.56
9:P:15:DT:H4'	9:P:16:DC:OP1	2.05	0.56
3:C:3814:LEU:HB3	3:C:3819:ARG:HG3	1.87	0.56
8:O:132:DG:N2	9:P:17:DT:O2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:272:LYS:HB3	2:B:288:LEU:HD13	1.88	0.56
1:A:252:THR:HG23	1:A:272:ARG:HB3	1.89	0.55
6:M:39:TYR:HB3	7:N:75:SER:HB3	1.88	0.55
8:O:4:DG:H2''	8:O:5:DA:C8	2.40	0.55
9:P:113:DA:C8	9:P:113:DA:H5'	2.41	0.55
9:P:86:DG:H3'	9:P:87:DT:H71	1.88	0.55
1:A:133:VAL:HG11	1:A:142:HIS:HB2	1.88	0.55
1:A:148:ASP:HB2	1:A:176:LEU:HD11	1.87	0.55
5:H:56:GLY:O	5:H:60:VAL:HG23	2.06	0.55
7:J:90:GLU:N	7:J:90:GLU:OE1	2.32	0.55
8:O:129:DT:H2''	8:O:130:DC:C5	2.41	0.55
1:A:171:ALA:HA	1:A:200:ALA:HA	1.88	0.55
9:P:47:DC:O2	9:P:48:DC:O2	2.25	0.55
6:M:41:GLU:N	6:M:41:GLU:OE1	2.40	0.55
9:P:112:DG:H2''	9:P:113:DA:H8	1.72	0.55
1:A:92:GLN:HB3	1:A:101:ASP:HB2	1.88	0.55
2:B:136:ASN:ND2	2:B:177:VAL:O	2.29	0.55
3:C:3914:TYR:HB3	3:C:3931:MET:HG3	1.89	0.55
5:L:56:GLY:O	5:L:60:VAL:HG23	2.06	0.54
6:I:17:ARG:NH2	9:P:31:DA:OP2	2.39	0.54
9:P:102:DA:H5'	5:L:80:THR:HG22	1.89	0.54
9:P:47:DC:C2	9:P:48:DC:C2	2.95	0.54
5:H:36:ARG:NH1	9:P:61:DA:OP2	2.40	0.54
9:P:85:DC:H2''	9:P:86:DG:H8	1.72	0.54
6:I:41:GLU:HB3	7:J:84:SER:HB2	1.89	0.54
9:P:50:DT:H2''	9:P:51:DT:C6	2.42	0.54
9:P:8:DG:H2'	9:P:9:DT:H71	1.89	0.54
7:N:55:ALA:HA	7:N:58:ILE:HD12	1.90	0.54
6:M:79:ILE:HG12	6:M:82:HIS:CE1	2.43	0.54
8:O:7:DA:H2''	8:O:8:DA:C8	2.43	0.54
9:P:109:DT:H2''	9:P:110:DA:C8	2.43	0.54
7:N:33:SER:OG	7:N:34:TYR:N	2.41	0.54
8:O:18:DC:H2''	8:O:19:DG:N7	2.23	0.54
1:A:270:SER:O	1:A:274:HIS:N	2.42	0.53
8:O:112:DT:H2''	8:O:113:DA:H8	1.74	0.53
8:O:66:DC:H2''	8:O:67:DG:C8	2.42	0.53
6:I:28:GLY:HA3	9:P:30:DG:H3'	1.90	0.53
7:J:87:THR:H	7:J:90:GLU:CD	2.10	0.53
1:A:67:HIS:CG	1:A:87:ASP:HB2	2.43	0.53
4:K:83:ARG:HB2	5:L:80:THR:HB	1.90	0.53
8:O:118:DC:N4	9:P:29:DG:O6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:3855:VAL:HG12	3:C:3856:ILE:HG22	1.90	0.53
4:K:75:ALA:HB2	5:L:66:ILE:HD11	1.91	0.53
6:M:16:THR:HG23	6:M:19:SER:H	1.74	0.53
8:O:112:DT:H2''	8:O:113:DA:C8	2.44	0.53
1:A:205:GLU:HB2	1:A:214:LEU:HG	1.91	0.53
3:C:3955:LEU:HB3	3:C:3968:LEU:HB2	1.89	0.53
1:A:177:VAL:HB	1:A:187:ALA:HB3	1.89	0.53
7:N:33:SER:OG	7:N:60:ASN:ND2	2.42	0.53
9:P:17:DT:H2''	9:P:18:DG:C5	2.44	0.53
1:A:112:LYS:NZ	1:A:157:ALA:O	2.34	0.53
2:B:52:LYS:O	2:B:95:TRP:NE1	2.40	0.53
2:B:131:TYR:O	2:B:149:PHE:N	2.41	0.53
2:B:217:VAL:HA	2:B:233:THR:HA	1.90	0.53
2:B:35:TYR:N	2:B:295:GLN:HE22	2.07	0.53
6:M:55:LEU:HD11	7:N:63:VAL:HG22	1.91	0.53
6:I:80:PRO:HA	6:I:83:LEU:HD13	1.89	0.53
7:J:59:MET:O	7:J:63:VAL:HG23	2.09	0.52
2:B:236:ASN:OD1	2:B:257:ASN:N	2.36	0.52
3:C:3843:LEU:O	3:C:3940:LEU:N	2.42	0.52
7:N:99:LEU:HB2	7:N:104:ALA:HB2	1.89	0.52
1:A:195:THR:O	5:H:22:LEU:HD22	2.10	0.52
1:A:300:ASP:HB3	1:A:313:ILE:HB	1.90	0.52
5:H:97:LEU:HD12	5:H:98:TYR:H	1.75	0.52
6:I:112:GLN:HG2	6:I:115:LEU:HD11	1.91	0.52
9:P:65:DC:H2''	9:P:66:DG:C8	2.44	0.52
1:A:100:CYS:SG	1:A:103:ARG:NH2	2.83	0.52
6:I:50:TYR:O	6:I:54:VAL:HG23	2.09	0.52
4:K:48:LEU:HA	4:K:51:ILE:HD12	1.92	0.52
2:B:35:TYR:HB2	2:B:297:LEU:HD21	1.90	0.52
3:C:3843:LEU:HD22	3:C:3905:ILE:HG12	1.91	0.52
5:H:79:LYS:N	8:O:102:DG:OP1	2.37	0.52
2:B:70:LYS:NZ	2:B:82:THR:OG1	2.41	0.52
5:L:31:LYS:HA	5:L:34:ILE:HD12	1.91	0.52
6:M:16:THR:O	6:M:19:SER:OG	2.20	0.52
6:M:50:TYR:O	6:M:54:VAL:HG23	2.09	0.52
8:O:85:DG:H2'	8:O:86:DT:H71	1.92	0.52
3:C:3932:ARG:NH1	3:C:3933:LYS:O	2.43	0.52
7:N:30:ARG:NH1	8:O:28:DC:OP1	2.42	0.52
8:O:72:DC:H2''	8:O:73:DG:C8	2.44	0.52
1:A:26:MET:HB3	1:A:44:ASN:H	1.75	0.52
7:J:34:TYR:H	7:J:60:ASN:ND2	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:N:91:ILE:O	7:N:95:VAL:HG23	2.10	0.52
9:P:30:DG:H2''	9:P:31:DA:H8	1.75	0.52
1:A:294:ARG:NH2	9:P:65:DC:OP1	2.43	0.52
3:C:3907:HIS:O	10:C:4001:SAH:N6	2.43	0.52
4:K:107:THR:HG21	4:K:124:ILE:HG13	1.92	0.52
4:G:48:LEU:HA	4:G:51:ILE:HD12	1.92	0.51
8:O:28:DC:C4	9:P:119:DT:N3	2.78	0.51
1:A:34:ARG:NH1	1:A:34:ARG:O	2.39	0.51
1:A:50:ILE:O	1:A:59:ALA:N	2.40	0.51
1:A:75:SER:HB3	1:A:80:LYS:HB2	1.92	0.51
2:B:34:ASN:H	2:B:332:SER:HG	1.58	0.51
5:H:35:ARG:O	5:H:39:ARG:HG2	2.11	0.51
6:I:110:ASN:H	4:K:55:GLN:NE2	2.08	0.51
8:O:99:DG:H2''	8:O:100:DG:N7	2.25	0.51
2:B:281:ASN:HB3	2:B:300:HIS:O	2.11	0.51
5:H:31:LYS:HA	5:H:34:ILE:HD12	1.91	0.51
8:O:31:DT:H2'	8:O:32:DT:H71	1.93	0.51
7:N:117:LYS:O	7:N:120:SER:OG	2.27	0.51
8:O:60:DA:H2''	8:O:61:DA:C8	2.46	0.51
9:P:9:DT:H2''	9:P:10:DA:C8	2.46	0.51
1:A:278:ILE:O	1:A:287:VAL:N	2.43	0.51
5:H:22:LEU:HD13	5:H:25:ASN:HD21	1.76	0.51
6:I:94:ASN:O	6:I:98:GLY:N	2.44	0.51
5:L:35:ARG:O	5:L:39:ARG:HG2	2.11	0.51
8:O:62:DC:H6	8:O:62:DC:H5'	1.75	0.51
4:G:63:ARG:HH21	9:P:60:DA:H5''	1.75	0.51
8:O:87:DT:O4	9:P:60:DA:N6	2.44	0.51
2:B:155:ILE:O	2:B:164:LEU:N	2.42	0.51
6:M:31:HIS:HD2	6:M:35:ARG:HH11	1.57	0.51
6:M:84:GLN:NE2	6:M:88:ARG:HE	2.09	0.51
5:H:79:LYS:H	8:O:102:DG:P	2.34	0.51
2:B:223:SER:HB3	2:B:228:TYR:HB2	1.93	0.50
3:C:3885:PHE:HD2	3:C:3926:ILE:HD13	1.76	0.50
3:C:3836:SER:OG	3:C:3906:ASN:ND2	2.44	0.50
4:G:107:THR:HG21	4:G:124:ILE:HG13	1.92	0.50
7:N:90:GLU:OE1	7:N:90:GLU:N	2.32	0.50
4:G:46:VAL:HG21	8:O:83:DG:H3'	1.94	0.50
2:B:35:TYR:CG	2:B:332:SER:HB2	2.47	0.50
4:K:63:ARG:HH21	8:O:60:DA:H5''	1.76	0.50
5:H:30:THR:HG21	9:P:61:DA:H5''	1.94	0.50
6:I:76:THR:N	8:O:132:DG:OP1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:28:DT:H1'	9:P:29:DG:C5	2.46	0.50
2:B:192:ASP:O	2:B:214:ASN:ND2	2.38	0.50
3:C:3955:LEU:O	3:C:3968:LEU:N	2.27	0.50
4:K:61:LEU:HD12	5:L:36:ARG:HD2	1.93	0.50
5:L:97:LEU:HD12	5:L:98:TYR:H	1.75	0.50
6:M:32:ARG:NH2	8:O:30:DA:OP1	2.44	0.50
8:O:101:DG:H2''	8:O:102:DG:C8	2.46	0.50
8:O:138:DT:H2''	8:O:139:DA:C8	2.46	0.50
1:A:179:LYS:O	1:A:183:GLN:N	2.40	0.50
2:B:86:HIS:CE1	2:B:112:LYS:HB2	2.46	0.50
6:I:76:THR:O	7:J:50:GLY:N	2.36	0.50
6:M:31:HIS:CD2	6:M:35:ARG:HH11	2.29	0.50
1:A:124:LEU:HD11	1:A:145:LEU:HD11	1.93	0.50
8:O:100:DG:H1'	8:O:101:DG:C8	2.46	0.50
8:O:107:DC:C6	8:O:108:DT:H72	2.47	0.50
9:P:37:DG:C2	9:P:38:DG:C2	3.00	0.50
8:O:101:DG:O6	9:P:46:DC:N4	2.44	0.50
2:B:250:LYS:NZ	2:B:289:GLN:O	2.44	0.49
1:A:258:CYS:SG	1:A:259:PHE:N	2.85	0.49
4:K:133:GLU:OE2	5:L:95:ARG:NH2	2.44	0.49
2:B:267:SER:OG	2:B:271:GLY:O	2.28	0.49
3:C:3827:SER:O	3:C:3831:VAL:HG22	2.12	0.49
3:C:3875:TYR:OH	3:C:3894:ASP:OD2	2.24	0.49
1:A:33:ASN:OD1	1:A:37:THR:N	2.31	0.49
6:I:50:TYR:CZ	7:J:92:GLN:HG2	2.46	0.49
6:M:24:GLN:N	6:M:56:GLU:OE2	2.45	0.49
7:N:82:LYS:HB2	7:N:83:ARG:HH21	1.77	0.49
8:O:41:DA:C8	8:O:41:DA:H5'	2.47	0.49
3:C:3895:ALA:O	3:C:3903:ARG:NH1	2.45	0.49
2:B:160:THR:O	2:B:162:LYS:NZ	2.34	0.49
3:C:3955:LEU:HD23	3:C:3968:LEU:HD22	1.94	0.49
4:G:83:ARG:HB2	5:H:80:THR:HB	1.93	0.49
4:G:85:GLN:HE22	5:H:82:THR:HG23	1.78	0.49
6:M:85:LEU:O	6:M:89:ASN:ND2	2.46	0.49
9:P:136:DG:H2''	9:P:137:DG:OP2	2.13	0.49
1:A:121:ASN:ND2	1:A:138:SER:OG	2.46	0.49
5:L:22:LEU:HD13	5:L:25:ASN:HD21	1.76	0.49
6:M:81:ARG:NH1	6:M:105:GLY:O	2.40	0.49
3:C:3916:ARG:HB2	3:C:3929:PHE:HE1	1.77	0.49
5:H:36:ARG:HH22	9:P:61:DA:P	2.35	0.49
1:A:126:CYS:SG	1:A:157:ALA:N	2.86	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:104:GLN:HG3	7:N:54:LYS:HD3	1.95	0.49
9:P:66:DG:H2''	9:P:67:DG:H5'	1.94	0.49
1:A:307:ARG:HB3	1:A:309:ILE:HG13	1.94	0.49
3:C:3895:ALA:HB1	3:C:3899:GLY:HA3	1.94	0.49
6:I:116:LEU:HD12	6:I:117:PRO:HD2	1.94	0.49
6:I:65:LEU:HB2	6:I:86:ALA:HB1	1.95	0.49
9:P:61:DA:H1'	9:P:62:DA:H5'	1.94	0.49
1:A:167:TYR:CD1	1:A:177:VAL:HG22	2.48	0.48
9:P:100:DA:H1'	9:P:101:DG:O4'	2.13	0.48
2:B:70:LYS:HB3	2:B:72:TRP:HE1	1.76	0.48
7:N:34:TYR:O	7:N:38:VAL:HG23	2.12	0.48
4:K:49:ARG:NH2	9:P:8:DG:H5''	2.29	0.48
1:A:278:ILE:HG23	1:A:288:LYS:H	1.78	0.48
2:B:101:LEU:HD13	2:B:115:ASP:HA	1.93	0.48
2:B:176:ALA:HB3	2:B:189:SER:HB3	1.94	0.48
7:N:65:ASP:O	7:N:68:GLU:HG3	2.13	0.48
1:A:193:THR:HB	1:A:197:ASN:HB3	1.94	0.48
3:C:3859:ALA:HB3	3:C:3900:ASN:HB3	1.96	0.48
5:L:26:ILE:HD11	5:L:55:ARG:HB3	1.94	0.48
9:P:43:DA:H2''	9:P:44:DA:C8	2.48	0.48
1:A:116:HIS:HB3	1:A:119:ASP:O	2.13	0.48
2:B:51:VAL:HB	2:B:60:LEU:HD11	1.94	0.48
9:P:102:DA:P	5:L:79:LYS:H	2.37	0.48
8:O:78:DC:H2''	8:O:79:DC:C6	2.48	0.48
5:H:26:ILE:HD11	5:H:55:ARG:HB3	1.95	0.48
6:I:17:ARG:HA	6:I:20:ARG:HD2	1.95	0.48
8:O:80:DC:H2''	8:O:81:DC:C5	2.48	0.48
9:P:132:DC:H2''	9:P:133:DA:C8	2.49	0.48
9:P:69:DG:H2''	9:P:70:DG:C8	2.49	0.48
2:B:88:LEU:HD12	2:B:108:ASP:HA	1.95	0.48
9:P:13:DT:H2''	9:P:14:DA:C8	2.48	0.48
3:C:3829:GLU:OE1	3:C:3829:GLU:N	2.47	0.48
3:C:3955:LEU:HG	3:C:3968:LEU:HD13	1.96	0.48
4:K:44:GLY:O	4:K:48:LEU:N	2.40	0.48
9:P:42:DT:H1'	9:P:43:DA:H5'	1.96	0.48
1:A:327:GLU:HB3	2:B:204:GLN:HB3	1.95	0.48
7:N:89:ARG:CZ	5:L:77:LYS:HE2	2.44	0.48
1:A:55:THR:OG1	2:B:157:ASP:OD2	2.32	0.47
2:B:283:VAL:HG22	2:B:304:VAL:HG11	1.96	0.47
3:C:3910:GLU:OE2	3:C:3963:LYS:N	2.47	0.47
6:M:94:ASN:O	6:M:98:GLY:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:129:DC:H1'	9:P:130:DG:C5	2.48	0.47
4:K:83:ARG:HG2	8:O:51:DC:C5'	2.44	0.47
8:O:16:DG:H1'	8:O:17:DC:H5'	1.96	0.47
3:C:3871:ARG:NH1	3:C:3894:ASP:OD2	2.47	0.47
8:O:62:DC:C6	8:O:62:DC:H5'	2.50	0.47
1:A:260:SER:HB3	1:A:265:TYR:HB2	1.96	0.47
2:B:93:VAL:HG22	2:B:102:LEU:HD22	1.96	0.47
1:A:256:LYS:HA	1:A:256:LYS:HD2	1.67	0.47
3:C:3823:LEU:HD11	3:C:3856:ILE:HA	1.95	0.47
1:A:270:SER:O	1:A:274:HIS:HA	2.14	0.47
2:B:148:SER:HB3	2:B:150:ASP:OD1	2.14	0.47
2:B:279:GLU:HA	2:B:303:VAL:HG13	1.95	0.47
2:B:51:VAL:HG22	2:B:306:SER:HB2	1.95	0.47
9:P:135:DC:H2''	9:P:136:DG:C8	2.50	0.47
9:P:7:DT:H2''	9:P:8:DG:C8	2.50	0.47
6:M:59:THR:O	6:M:63:LEU:HG	2.15	0.47
1:A:197:ASN:OD1	1:A:198:THR:N	2.44	0.47
1:A:304:HIS:CG	1:A:307:ARG:HB2	2.49	0.47
3:C:3865:SER:O	3:C:3868:THR:OG1	2.21	0.47
4:K:95:ALA:HB2	5:L:97:LEU:HD22	1.97	0.47
9:P:36:DA:H2''	9:P:37:DG:H8	1.76	0.47
9:P:83:DT:H2''	9:P:84:DG:C8	2.50	0.47
8:O:123:DC:H2''	8:O:124:DA:C8	2.50	0.47
8:O:77:DT:H1'	8:O:78:DC:H5'	1.96	0.47
1:A:33:ASN:HA	1:A:74:TRP:CG	2.49	0.47
2:B:48:VAL:HG11	2:B:319:ALA:HB1	1.97	0.47
10:C:4001:SAH:H5'2	10:C:4001:SAH:H8	1.97	0.47
2:B:219:PHE:HB3	2:B:232:ALA:HB3	1.96	0.47
7:J:99:LEU:HB2	7:J:104:ALA:HB2	1.96	0.47
4:K:99:TYR:OH	4:K:133:GLU:OE1	2.33	0.47
6:M:78:ILE:HB	7:N:51:ILE:HG22	1.96	0.47
8:O:43:DA:C6	8:O:44:DG:C6	3.02	0.47
9:P:38:DG:H1'	9:P:39:DG:C5	2.50	0.47
9:P:87:DT:H2'	9:P:88:DT:C6	2.50	0.47
9:P:95:DG:H2''	9:P:96:DT:OP2	2.14	0.47
1:A:160:ASP:N	1:A:160:ASP:OD1	2.45	0.46
2:B:275:VAL:HG13	2:B:285:ILE:HG12	1.97	0.46
4:G:99:TYR:OH	4:G:133:GLU:OE1	2.33	0.46
6:I:90:ASP:HB3	6:I:93:LEU:HB2	1.96	0.46
4:G:44:GLY:O	4:G:48:LEU:N	2.40	0.46
9:P:94:DG:H4'	9:P:95:DG:OP1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:CYS:HB2	1:A:47:ARG:HB2	1.96	0.46
2:B:187:VAL:HG23	2:B:197:ILE:HG13	1.98	0.46
3:C:3949:GLU:O	3:C:3954:LYS:NZ	2.39	0.46
2:B:154:ARG:NH1	2:B:166:THR:OG1	2.48	0.46
7:N:43:LYS:NZ	7:N:47:PRO:O	2.34	0.46
8:O:6:DG:H2''	8:O:7:DA:C8	2.50	0.46
9:P:109:DT:H2''	9:P:110:DA:N7	2.31	0.46
2:B:176:ALA:HB2	2:B:219:PHE:HA	1.96	0.46
2:B:230:LEU:HD11	2:B:238:LEU:HB3	1.98	0.46
2:B:51:VAL:HG12	2:B:62:SER:HA	1.97	0.46
3:C:3887:ILE:HG23	3:C:3917:VAL:HG11	1.98	0.46
8:O:35:DT:H2''	8:O:36:DC:OP2	2.16	0.46
1:A:272:ARG:NH1	9:P:63:DC:H5''	2.30	0.46
3:C:3913:CYS:HA	3:C:3931:MET:H	1.80	0.46
3:C:3849:ILE:HB	3:C:3934:ILE:HB	1.97	0.46
9:P:47:DC:C2	9:P:48:DC:N3	2.84	0.46
2:B:131:TYR:HB2	2:B:149:PHE:HB2	1.98	0.46
2:B:59:TRP:HB2	2:B:95:TRP:CH2	2.51	0.46
8:O:63:DG:H1'	8:O:64:DC:H5'	1.97	0.46
9:P:141:DT:H2''	9:P:142:DC:C5	2.51	0.46
1:A:157:ALA:HA	1:A:167:TYR:O	2.16	0.46
3:C:3968:LEU:HD11	10:C:4001:SAH:C6	2.46	0.46
8:O:145:DG:H2''	8:O:146:DA:C8	2.50	0.46
8:O:65:DA:H1'	8:O:66:DC:H5'	1.97	0.46
1:A:129:LYS:HB3	1:A:153:LEU:HD12	1.98	0.46
2:B:88:LEU:HB2	2:B:108:ASP:N	2.30	0.46
6:I:45:ALA:N	8:O:112:DT:OP1	2.35	0.46
8:O:89:DT:H1'	8:O:90:DA:C4	2.51	0.46
1:A:226:ASP:HB2	1:A:242:MET:HE3	1.98	0.46
4:K:108:ASN:HB2	5:L:43:VAL:HG22	1.98	0.46
8:O:132:DG:H1'	8:O:133:DA:C8	2.52	0.45
8:O:48:DT:H1'	8:O:49:DA:C8	2.51	0.45
1:A:347:GLU:OE1	3:C:3864:ARG:NE	2.49	0.45
3:C:3887:ILE:HD11	3:C:3893:VAL:HG23	1.98	0.45
8:O:48:DT:H1'	8:O:49:DA:C4	2.51	0.45
9:P:121:DA:C6	9:P:122:DG:C6	3.04	0.45
9:P:141:DT:H2''	9:P:142:DC:H5	1.81	0.45
4:G:73:GLU:OE2	5:H:24:ASP:N	2.50	0.45
5:H:96:THR:HG23	6:M:100:VAL:HG13	1.99	0.45
6:M:77:ARG:HA	7:N:50:GLY:C	2.37	0.45
9:P:113:DA:H8	9:P:113:DA:H5'	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:LEU:HD11	1:A:188:SER:HB2	1.98	0.45
7:J:34:TYR:O	7:J:38:VAL:HG23	2.15	0.45
9:P:85:DC:H2''	9:P:86:DG:C8	2.52	0.45
2:B:111:LEU:HD21	2:B:146:SER:HB2	1.99	0.45
2:B:282:LEU:HD22	2:B:284:TYR:CD1	2.51	0.45
1:A:341:GLU:HG2	3:C:3824:LYS:HE2	1.99	0.45
2:B:310:HIS:HB3	2:B:313:GLU:O	2.17	0.45
6:I:79:ILE:HG12	6:I:82:HIS:CG	2.52	0.45
9:P:22:DC:H2''	9:P:23:DG:H8	1.81	0.45
9:P:66:DG:H2''	9:P:67:DG:C8	2.52	0.45
4:G:70:LEU:O	4:G:74:ILE:HG12	2.17	0.45
6:M:18:SER:O	6:M:22:GLY:N	2.50	0.45
7:J:30:ARG:CZ	9:P:28:DT:H5''	2.46	0.45
8:O:38:DT:H2''	8:O:39:DA:N7	2.32	0.45
2:B:89:GLY:O	2:B:107:ASP:N	2.33	0.45
3:C:3965:ARG:C	3:C:3966:LYS:HD2	2.38	0.45
4:K:73:GLU:OE2	5:L:24:ASP:N	2.49	0.45
6:M:42:ARG:NH2	9:P:112:DG:O4'	2.51	0.45
8:O:61:DA:OP2	5:L:36:ARG:NH1	2.49	0.45
4:G:85:GLN:HA	9:P:50:DT:OP1	2.17	0.45
1:A:270:SER:O	1:A:274:HIS:CA	2.65	0.44
6:I:15:LYS:HB3	6:I:20:ARG:NH2	2.32	0.44
7:N:90:GLU:HG3	5:L:75:HIS:CE1	2.52	0.44
6:M:31:HIS:ND1	6:M:48:PRO:HG3	2.32	0.44
9:P:130:DG:H1'	9:P:131:DG:C5	2.52	0.44
1:A:192:THR:OG1	1:A:193:THR:N	2.51	0.44
3:C:3817:PRO:HA	3:C:3920:ILE:HD12	1.99	0.44
4:K:70:LEU:O	4:K:74:ILE:HG12	2.17	0.44
9:P:126:DC:H2''	9:P:127:DC:O5'	2.16	0.44
3:C:3823:LEU:HD22	3:C:3854:MET:HB3	1.99	0.44
8:O:24:DC:H2''	8:O:25:DG:C8	2.53	0.44
8:O:31:DT:C2'	8:O:32:DT:H71	2.46	0.44
8:O:52:DA:H1'	8:O:53:DC:H5'	1.99	0.44
8:O:72:DC:H2''	8:O:73:DG:H8	1.82	0.44
9:P:7:DT:H2''	9:P:8:DG:H8	1.81	0.44
9:P:81:DC:H2''	9:P:82:DG:N7	2.32	0.44
1:A:170:ASN:OD1	1:A:174:LYS:N	2.36	0.44
8:O:121:DG:H2''	8:O:122:DG:C8	2.52	0.44
9:P:113:DA:C5	9:P:114:DC:C4	3.05	0.44
9:P:58:DT:H2''	9:P:59:DA:N7	2.33	0.44
7:J:88:SER:O	7:J:92:GLN:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:O:114:DG:H1'	8:O:115:DT:H5'	2.00	0.44
9:P:28:DT:H1'	9:P:29:DG:C8	2.52	0.44
1:A:121:ASN:OD1	1:A:137:LEU:N	2.50	0.44
1:A:45:ASP:OD2	1:A:47:ARG:NE	2.51	0.44
5:H:52:GLU:O	5:H:55:ARG:HB2	2.18	0.44
8:O:46:DT:H2''	8:O:47:DC:C6	2.52	0.44
1:A:220:ARG:NH1	9:P:63:DC:OP1	2.43	0.44
3:C:3841:ARG:N	10:C:4001:SAH:OXT	2.41	0.44
1:A:195:THR:HG22	5:H:25:ASN:OD1	2.18	0.44
8:O:21:DG:H2''	8:O:22:DG:C8	2.52	0.44
9:P:58:DT:H1'	9:P:59:DA:C4	2.53	0.44
1:A:162:ARG:HB2	1:A:164:GLU:HG2	1.99	0.44
2:B:50[A]:SER:HB2	2:B:263:PHE:HE2	1.82	0.44
6:I:110:ASN:H	4:K:55:GLN:HE22	1.65	0.44
2:B:197:ILE:HG21	2:B:243:TYR:CZ	2.52	0.44
2:B:282:LEU:HD23	2:B:283:VAL:N	2.32	0.44
3:C:3885:PHE:CD2	3:C:3926:ILE:HD13	2.52	0.44
6:M:30:VAL:O	6:M:34:LEU:HD23	2.18	0.44
6:M:90:ASP:OD2	6:M:93:LEU:HD23	2.17	0.44
1:A:155:VAL:HG22	1:A:170:ASN:HA	2.00	0.43
1:A:343:VAL:HB	3:C:3861:ILE:HD13	1.99	0.43
2:B:324:ASP:O	2:B:326:THR:HG23	2.18	0.43
9:P:87:DT:C6	9:P:88:DT:H72	2.53	0.43
4:K:102:ALA:HB1	4:K:131:ARG:HH22	1.84	0.43
8:O:101:DG:H2''	8:O:102:DG:H8	1.82	0.43
8:O:116:DC:H2''	8:O:117:DT:H71	2.00	0.43
2:B:46:LYS:HB2	2:B:66:ASP:HB3	1.99	0.43
5:H:98:TYR:CE2	6:M:100:VAL:HG11	2.53	0.43
1:A:91:SER:HA	1:A:102:GLN:O	2.17	0.43
4:G:102:ALA:HB1	4:G:131:ARG:HH22	1.83	0.43
8:O:142:DT:H2''	8:O:143:DC:C5	2.53	0.43
9:P:115:DC:H2''	9:P:116:DA:H8	1.83	0.43
4:G:108:ASN:ND2	5:H:43:VAL:HA	2.33	0.43
6:I:29:ARG:HG3	6:I:32:ARG:NH2	2.30	0.43
6:M:17:ARG:N	8:O:31:DT:OP1	2.38	0.43
8:O:82:DC:H1'	8:O:83:DG:H5'	2.01	0.43
2:B:138:ASN:OD1	2:B:142:ASN:N	2.52	0.43
2:B:286:TRP:CD1	2:B:293:ILE:HG12	2.53	0.43
2:B:278:SER:H	2:B:304:VAL:HB	1.82	0.43
8:O:36:DC:H2'	8:O:36:DC:OP2	2.19	0.43
4:G:66:PRO:HD3	8:O:91:DA:H3'	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:O:56:DC:H1'	8:O:57:DT:H5'	2.00	0.43
4:K:83:ARG:NH2	9:P:100:DA:H4'	2.34	0.43
1:A:327:GLU:HB3	1:A:328:ASN:H	1.70	0.43
2:B:256:LYS:O	2:B:279:GLU:N	2.44	0.43
3:C:3849:ILE:O	3:C:3934:ILE:N	2.42	0.43
3:C:3911:PRO:HB2	3:C:3913:CYS:O	2.19	0.43
4:G:40:ARG:NH2	8:O:83:DG:O4'	2.52	0.43
6:I:110:ASN:H	4:K:55:GLN:CD	2.22	0.43
6:I:17:ARG:NH2	6:I:28:GLY:HA2	2.34	0.43
5:H:77:LYS:HE2	7:J:89:ARG:CZ	2.49	0.43
5:L:52:GLU:O	5:L:55:ARG:HB2	2.18	0.43
9:P:69:DG:C2	9:P:70:DG:C2	3.06	0.43
9:P:68:DG:H2''	9:P:69:DG:C8	2.53	0.43
1:A:203:SER:OG	1:A:216:ASN:HB3	2.19	0.43
1:A:265:TYR:HD2	1:A:287:VAL:HG21	1.83	0.43
1:A:309:ILE:HG23	1:A:322:ALA:HA	1.99	0.43
2:B:278:SER:HB2	2:B:282:LEU:O	2.19	0.43
7:J:61:SER:HA	7:J:64:ASN:HD22	1.84	0.43
6:I:110:ASN:N	4:K:55:GLN:OE1	2.51	0.43
9:P:28:DT:H2'	9:P:28:DT:H6	1.69	0.43
2:B:193:GLY:HA2	2:B:217:VAL:HG23	1.99	0.43
7:J:48:ASP:OD1	7:J:49:THR:N	2.52	0.43
4:K:72:ARG:HG2	4:K:84:PHE:CE2	2.54	0.43
6:M:37:GLY:HA3	6:M:39:TYR:CE2	2.54	0.43
8:O:47:DC:H2''	8:O:48:DT:H71	2.00	0.43
8:O:90:DA:H1'	8:O:91:DA:C8	2.53	0.43
9:P:102:DA:OP1	5:L:78:ARG:HB3	2.19	0.43
1:A:20:THR:HA	1:A:319:SER:HA	2.00	0.42
7:J:83:ARG:NH2	9:P:41:DG:OP2	2.52	0.42
9:P:43:DA:H2''	9:P:44:DA:H8	1.83	0.42
1:A:308:PRO:HB2	1:A:323:GLN:HB3	2.02	0.42
1:A:52:ASP:OD1	1:A:53:PHE:N	2.51	0.42
2:B:49:SER:HA	2:B:305:ILE:HG12	2.00	0.42
3:C:3932:ARG:NH2	3:C:3938:GLU:OE2	2.49	0.42
6:I:24:GLN:HG3	7:J:44:GLN:HE22	1.84	0.42
9:P:16:DC:H2'	9:P:16:DC:H6	1.62	0.42
1:A:266:ILE:C	1:A:278:ILE:HD12	2.40	0.42
2:B:265:ASN:HB3	2:B:309:CYS:HB2	2.01	0.42
2:B:42:ALA:HB2	2:B:326:THR:HG22	2.01	0.42
3:C:3831:VAL:HG11	3:C:3856:ILE:HB	2.00	0.42
5:H:75:HIS:CE1	7:J:90:GLU:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:42:ARG:O	7:N:85:THR:HA	2.20	0.42
9:P:102:DA:C6	9:P:103:DG:C6	3.07	0.42
9:P:17:DT:H2''	9:P:18:DG:C8	2.54	0.42
3:C:3871:ARG:NH1	3:C:3875:TYR:HH	2.16	0.42
4:G:72:ARG:HG2	4:G:84:PHE:CE2	2.54	0.42
6:I:100:VAL:HG11	5:L:98:TYR:CE2	2.54	0.42
6:M:64:GLU:HB2	7:N:45:VAL:HG21	2.02	0.42
8:O:119:DC:H2''	8:O:120:DA:N7	2.35	0.42
9:P:90:DA:H1'	9:P:91:DA:C8	2.55	0.42
4:G:40:ARG:HH12	8:O:83:DG:H1'	1.85	0.42
4:G:55:GLN:CD	6:M:110:ASN:H	2.23	0.42
6:M:76:THR:O	7:N:50:GLY:N	2.52	0.42
8:O:88:DT:O4	9:P:59:DA:N6	2.52	0.42
9:P:91:DA:H2''	9:P:92:DG:H8	1.84	0.42
1:A:214:LEU:HD23	1:A:259:PHE:CE2	2.54	0.42
5:H:71:THR:O	5:H:74:GLU:HB3	2.19	0.42
6:I:34:LEU:HA	6:I:34:LEU:HD23	1.81	0.42
4:K:73:GLU:O	4:K:76:GLN:HG2	2.20	0.42
5:L:71:THR:O	5:L:74:GLU:HB3	2.19	0.42
6:M:25:PHE:HE2	6:M:55:LEU:HG	1.84	0.42
2:B:47:ALA:HB2	2:B:322:GLU:HB3	2.02	0.42
2:B:51:VAL:HG11	2:B:327:ILE:HG12	2.02	0.42
4:G:86:SER:O	4:G:90:MET:HG2	2.20	0.42
4:G:73:GLU:O	4:G:76:GLN:HG2	2.20	0.42
4:K:57:SER:HB2	4:K:59:GLU:OE1	2.20	0.42
6:M:84:GLN:HE22	6:M:88:ARG:HE	1.66	0.42
2:B:279:GLU:HA	2:B:303:VAL:HG22	2.02	0.42
4:G:68:GLN:NE2	4:G:72:ARG:HH21	2.18	0.42
4:K:118:THR:OG1	8:O:71:DG:H5''	2.20	0.42
6:M:80:PRO:HB2	6:M:104:GLN:HB2	2.02	0.42
1:A:75:SER:OG	1:A:79:HIS:N	2.50	0.42
3:C:3907:HIS:HB2	3:C:3944:TYR:CD2	2.55	0.42
4:G:133:GLU:OE2	5:H:95:ARG:NH2	2.53	0.42
8:O:23:DC:H1'	8:O:24:DC:H5'	2.02	0.42
1:A:110:ILE:HG23	1:A:125:VAL:HG13	2.02	0.41
1:A:202:LYS:N	1:A:216:ASN:O	2.53	0.41
1:A:94:ASP:HB3	1:A:97:SER:OG	2.20	0.41
3:C:3888:ASP:OD1	3:C:3888:ASP:N	2.53	0.41
5:H:32:PRO:O	5:H:35:ARG:HG2	2.20	0.41
5:H:60:VAL:HA	5:H:63:GLU:CD	2.40	0.41
4:K:68:GLN:O	4:K:72:ARG:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:60:VAL:HA	5:L:63:GLU:CD	2.40	0.41
7:N:87:THR:OG1	7:N:90:GLU:OE1	2.27	0.41
9:P:38:DG:H4'	9:P:39:DG:H5'	2.02	0.41
1:A:127:PRO:HD3	1:A:132:PRO:HA	2.01	0.41
1:A:269:GLY:HA2	1:A:276:LEU:HD13	2.01	0.41
2:B:46:LYS:HD2	2:B:66:ASP:HA	2.02	0.41
3:C:3820:PHE:O	3:C:3824:LYS:HG2	2.20	0.41
3:C:3844:PHE:HA	3:C:3939:GLU:HA	2.02	0.41
3:C:3858:TYR:HA	3:C:3902:ALA:HB3	2.02	0.41
4:G:68:GLN:O	4:G:72:ARG:HG3	2.20	0.41
6:M:69:ALA:O	6:M:73:ASN:ND2	2.33	0.41
6:M:20:ARG:NH2	8:O:32:DT:OP1	2.53	0.41
8:O:79:DC:H2''	8:O:80:DC:C6	2.55	0.41
9:P:120:DG:H1'	9:P:121:DA:C5	2.55	0.41
9:P:20:DC:H2''	9:P:21:DA:C8	2.55	0.41
2:B:255:HIS:HA	2:B:284:TYR:CE1	2.56	0.41
3:C:3907:HIS:CE1	3:C:3965:ARG:HH11	2.38	0.41
5:H:53:GLU:O	5:H:57:VAL:HG23	2.20	0.41
4:K:86:SER:O	4:K:90:MET:HG2	2.20	0.41
1:A:135:LEU:HG	1:A:142:HIS:HB3	2.03	0.41
1:A:252:THR:HG21	1:A:270:SER:OG	2.19	0.41
2:B:112:LYS:HD3	2:B:114:TRP:CZ2	2.55	0.41
3:C:3857:GLU:O	3:C:3900:ASN:ND2	2.53	0.41
5:H:92:ARG:NH2	7:J:98:LEU:HA	2.35	0.41
4:K:62:ILE:HG21	4:K:67:PHE:HD2	1.84	0.41
6:M:25:PHE:N	6:M:56:GLU:OE2	2.38	0.41
1:A:75:SER:HB2	1:A:120:GLN:HG3	2.01	0.41
1:A:293:THR:HG23	1:A:296:GLU:HB2	2.03	0.41
2:B:41:LEU:O	2:B:327:ILE:N	2.32	0.41
7:N:43:LYS:HA	7:N:43:LYS:HD3	1.79	0.41
8:O:12:DC:H2''	8:O:13:DG:C8	2.56	0.41
6:I:15:LYS:O	6:I:20:ARG:NE	2.41	0.41
6:I:79:ILE:H	6:I:82:HIS:HD1	1.69	0.41
4:K:68:GLN:NE2	4:K:72:ARG:HH21	2.18	0.41
1:A:118:ARG:HG3	1:A:162:ARG:O	2.20	0.41
2:B:233:THR:HG21	2:B:239:LYS:NZ	2.35	0.41
1:A:133:VAL:HG22	1:A:144:VAL:HG13	2.03	0.41
1:A:71:SER:HB3	1:A:84:ALA:HB3	2.02	0.41
2:B:268:VAL:HA	2:B:272:LYS:HD3	2.02	0.41
2:B:322:GLU:O	2:B:325:LYS:HG3	2.20	0.41
2:B:38:LYS:HE3	2:B:331:LYS:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:57:SER:HB2	4:G:59:GLU:OE1	2.20	0.41
5:L:32:PRO:O	5:L:35:ARG:HG2	2.20	0.41
8:O:100:DG:N2	8:O:101:DG:C2	2.88	0.41
9:P:35:DT:H2''	9:P:36:DA:C8	2.55	0.41
2:B:37:LEU:HD13	2:B:328:LYS:HB3	2.02	0.41
2:B:72:TRP:HA	2:B:80:GLU:H	1.86	0.41
4:G:115:LYS:HD2	4:G:115:LYS:N	2.36	0.41
4:G:62:ILE:HG21	4:G:67:PHE:HD2	1.84	0.41
6:I:68:ASN:O	6:I:71:ARG:HG3	2.21	0.41
5:L:53:GLU:O	5:L:57:VAL:HG23	2.20	0.41
6:M:17:ARG:HH22	6:M:31:HIS:HB2	1.85	0.41
6:M:28:GLY:HA3	8:O:30:DA:H3'	2.02	0.41
6:I:42:ARG:HG2	8:O:113:DA:H5'	2.03	0.41
9:P:139:DA:H1'	9:P:140:DT:H5'	2.03	0.41
4:G:126:LEU:HD22	4:K:113:HIS:CG	2.56	0.41
4:G:69:ARG:NH1	8:O:91:DA:OP2	2.53	0.41
9:P:37:DG:C2	9:P:38:DG:N1	2.90	0.41
1:A:313:ILE:HG12	1:A:318:VAL:HG22	2.03	0.40
2:B:275:VAL:HG11	2:B:316:ILE:HD13	2.03	0.40
7:J:102:GLU:HG3	7:J:106:HIS:CD2	2.56	0.40
4:K:115:LYS:HD2	4:K:115:LYS:N	2.36	0.40
6:M:55:LEU:HD21	7:N:63:VAL:HG13	2.02	0.40
6:M:40:ALA:HB2	7:N:86:ILE:HG13	2.02	0.40
8:O:41:DA:H1'	8:O:42:DC:O4'	2.20	0.40
1:A:160:ASP:OD1	1:A:164:GLU:N	2.54	0.40
1:A:226:ASP:O	1:A:230:ILE:HG12	2.22	0.40
2:B:115:ASP:OD2	2:B:117[B]:SER:OG	2.30	0.40
2:B:178:HIS:HD2	2:B:222:PHE:H	1.68	0.40
2:B:321:LEU:HB3	2:B:322:GLU:H	1.78	0.40
4:G:70:LEU:HD22	5:H:26:ILE:HA	2.02	0.40
7:N:87:THR:O	7:N:91:ILE:HG12	2.21	0.40
8:O:43:DA:N1	9:P:106:DG:N1	2.69	0.40
9:P:37:DG:OP2	9:P:37:DG:H2'	2.21	0.40
1:A:178:LEU:HD23	1:A:185:LEU:HA	2.04	0.40
2:B:256:LYS:HG2	2:B:279:GLU:HB2	2.03	0.40
6:I:26:PRO:HG2	6:I:29:ARG:HB3	2.03	0.40
4:K:62:ILE:HB	4:K:93:GLN:HE21	1.86	0.40
4:K:85:GLN:HE22	5:L:82:THR:HG23	1.87	0.40
8:O:128:DG:H8	8:O:128:DG:P	2.44	0.40
8:O:135:DA:H2''	8:O:136:DT:H71	2.03	0.40
8:O:14:DG:H1'	8:O:15:DT:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:252:TYR:CZ	2:B:274:ILE:HG13	2.57	0.40
5:L:51:TYR:O	5:L:54:THR:HB	2.21	0.40
9:P:35:DT:H2''	9:P:36:DA:H8	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	329/538 (61%)	311 (94%)	18 (6%)	0	100	100
2	B	304/313 (97%)	286 (94%)	18 (6%)	0	100	100
3	C	149/209 (71%)	142 (95%)	7 (5%)	0	100	100
4	G	96/136 (71%)	94 (98%)	2 (2%)	0	100	100
4	K	96/136 (71%)	94 (98%)	2 (2%)	0	100	100
5	H	80/103 (78%)	74 (92%)	6 (8%)	0	100	100
5	L	80/103 (78%)	73 (91%)	7 (9%)	0	100	100
6	I	105/129 (81%)	103 (98%)	2 (2%)	0	100	100
6	M	105/129 (81%)	103 (98%)	2 (2%)	0	100	100
7	J	91/123 (74%)	90 (99%)	1 (1%)	0	100	100
7	N	91/123 (74%)	88 (97%)	3 (3%)	0	100	100
All	All	1526/2042 (75%)	1458 (96%)	68 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	291/462 (63%)	288 (99%)	3 (1%)	78	89
2	B	263/274 (96%)	263 (100%)	0	100	100
3	C	132/182 (72%)	132 (100%)	0	100	100
4	G	84/111 (76%)	79 (94%)	5 (6%)	21	54
4	K	84/111 (76%)	79 (94%)	5 (6%)	21	54
5	H	67/79 (85%)	64 (96%)	3 (4%)	30	61
5	L	67/79 (85%)	64 (96%)	3 (4%)	30	61
6	I	81/101 (80%)	81 (100%)	0	100	100
6	M	82/101 (81%)	82 (100%)	0	100	100
7	J	77/103 (75%)	77 (100%)	0	100	100
7	N	79/103 (77%)	79 (100%)	0	100	100
All	All	1307/1706 (77%)	1288 (98%)	19 (2%)	70	84

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	141	LYS
1	A	294	ARG
4	G	58	THR
4	G	103	LEU
4	G	109	LEU
4	G	110	CYS
4	G	112	ILE
5	H	22	LEU
5	H	65	VAL
5	H	70	VAL
4	K	58	THR
4	K	103	LEU
4	K	109	LEU
4	K	110	CYS
4	K	112	ILE
5	L	22	LEU
5	L	65	VAL
5	L	70	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	HIS
1	A	250	ASN
1	A	273	GLN
1	A	325	GLN
2	B	178	HIS
2	B	204	GLN
2	B	265	ASN
2	B	289	GLN
2	B	323	ASN
3	C	3906	ASN
4	G	39	HIS
4	G	68	GLN
4	G	113	HIS
5	H	25	ASN
5	H	75	HIS
7	J	60	ASN
7	J	64	ASN
7	J	81	ASN
7	J	92	GLN
7	J	106	HIS
4	K	68	GLN
4	K	113	HIS
7	N	46	HIS
7	N	60	ASN
5	L	25	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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$
10	SAH	C	4001	-	20,28,28	1.18	2 (10%)	19,40,40	1.75	2 (10%)

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
10	SAH	C	4001	-	-	2/7/31/31	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	4001	SAH	C2-N3	3.87	1.38	1.32
10	C	4001	SAH	C2-N1	2.38	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	4001	SAH	N3-C2-N1	-5.33	120.09	128.68
10	C	4001	SAH	C5'-SD-CG	-3.58	91.53	102.27

There are no chirality outliers.

All (2) torsion outliers are listed below:

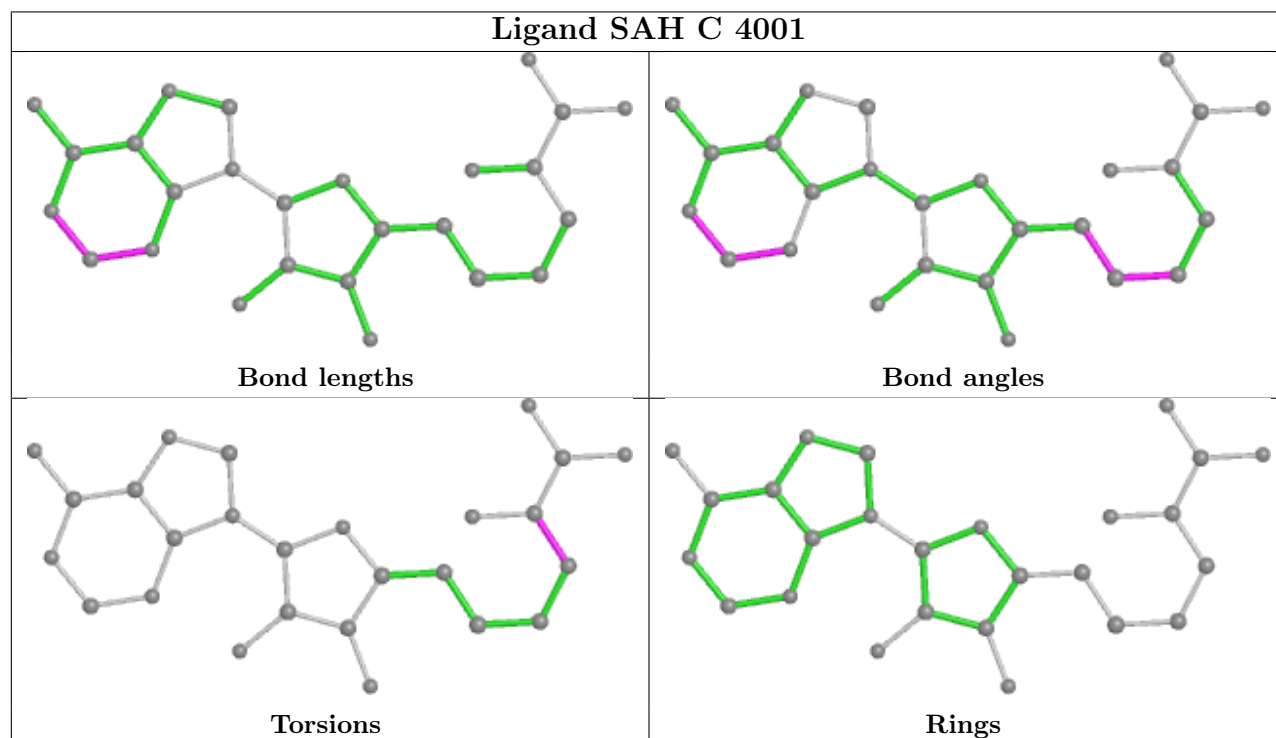
Mol	Chain	Res	Type	Atoms
10	C	4001	SAH	N-CA-CB-CG
10	C	4001	SAH	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	C	4001	SAH	4	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.