



Full wwPDB NMR Structure Validation Report ⓘ

Mar 24, 2026 – 10:58 PM UTC

PDB ID : 2HDC / pdb_00002hdc
Title : STRUCTURE OF TRANSCRIPTION FACTOR GENESIS/DNA COMPLEX
Authors : Jin, C.; Marsden, I.; Chen, X.; Liao, X.
Deposited on : 1999-05-05

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

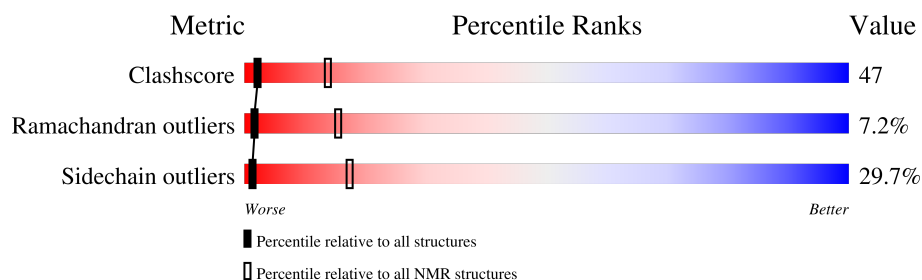
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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	B	17	24% 76%
2	C	17	24% 76%
3	A	97	16% 56% 11% 16%

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:7-A:87 (81)	0.90	6

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20
2	1, 13

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2581 atoms, of which 1080 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*AP*C)-3').

Mol	Chain	Residues	Atoms						Trace
1	B	17	Total	C	H	N	O	P	0
			493	167	145	67	97	17	

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*AP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms						Trace
2	C	17	Total	C	H	N	O	P	0
			484	169	135	56	107	17	

- Molecule 3 is a protein called PROTEIN (TRANSCRIPTION FACTOR).

Mol	Chain	Residues	Atoms						Trace
3	A	97	Total	C	H	N	O	S	0
			1604	517	800	143	140	4	

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

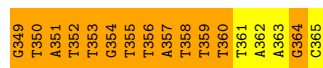
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 



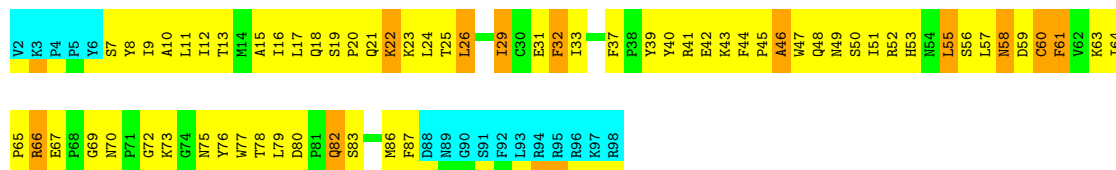
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B:  29% 71%

G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 T263 A264 C265

- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C:  35% 65%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A:  26% 35% 22% 16%

V2 K3 P4 P5 Y6 Y7 Y8 Y9 I10 A11 L12 L13 L14 L15 L16 L17 L18 Q19 S20 P21 Q22 K23 K24 L25 L26 L27 S28 G29 F30 I31 I32 F33 P34 Y35 Y36 Y37 K38 F44 P45 A46 W47 Q48 M49 S50 I51 R52 H53 N54 L55 S56 R57 R58 D59 G60 F61 V62 K63 I64 P65

R66 E67 P68 G69 N70 K71 Y72 Y73 Y74 Y75 Y76 Y77 Y78 L79 D80 F81 Q82 S83 F84 D85 R86 R87 R88 R89 G90 S91 S92 F93 L94 R95 R96 R97 R98

4.2.2 Score per residue for model 2

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B:  35% 65%

G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 T263 A264 C265

- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C:  24% 76%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A:  26% 37% 19% 16%

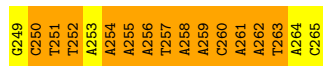
V2 K3 P4 P5 Y6 Y7 Y8 Y9 I10 A11 L12 L13 L14 L15 L16 L17 L18 Q19 S20 P21 Q22 K23 K24 L25 L26 L27 S28 G29 F30 I31 I32 F33 P34 Y35 Y36 Y37 K38 F44 P45 A46 W47 Q48 M49 S50 I51 R52 H53 N54 L55 S56 R57 R58 D59 G60 F61 V62 K63 I64 P65



4.2.3 Score per residue for model 3

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 24% 76%



- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 35% 65%



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

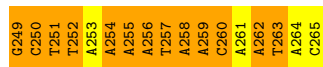
Chain A: 26% 45% 9% 16%



4.2.4 Score per residue for model 4

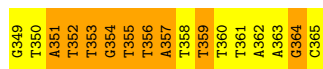
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 24% 76%

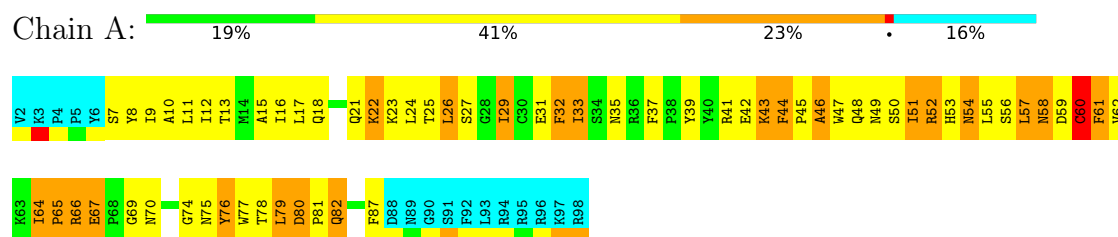


- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 47% 53%



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

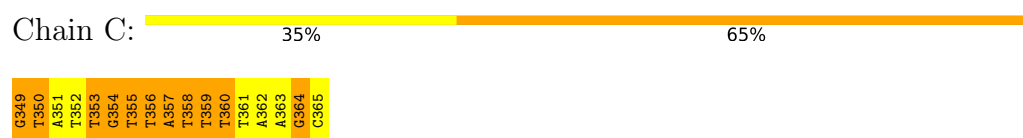


4.2.5 Score per residue for model 5

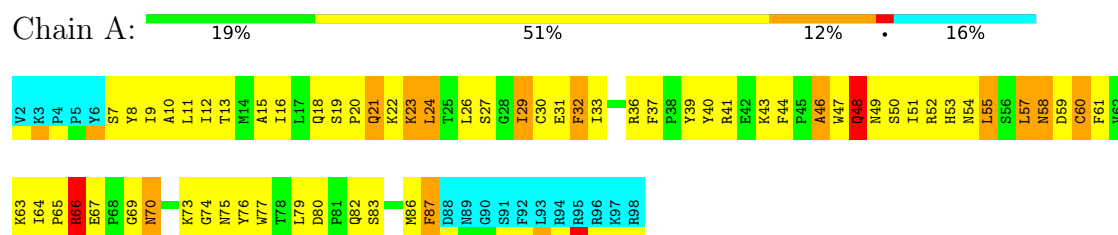
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')



- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)



4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

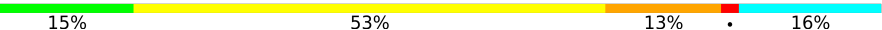


- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 

G349 T350 A351 T352 T353 G354 T355 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 

V2 A3 P4 P5 Y6 S7 Y8 Y9 A10 L11 L12 T13 T14 M14 A15 I16 L17 Q18 S19 P20 Q21 Q22 K23 K24 L24 T25 L26 I29 F32 I33 R34 R35 R36 F37 Y39 Y40 R41 E42 K43 F44 P45 A46 W47 Q48 N49 S50 I51 R52 H53 H54 L55 S56 L57 N58 D59 C60 F61 V62 K63

I64 P65 R66 E67 P68 G69 W70 F71 G72 N75 Y76 W77 T78 L79 D80 P81 Q82 S83 E84 D85 M86 F87 D88 M89 G90 S91 F92 L93 R94 R95 R96 R97 R98

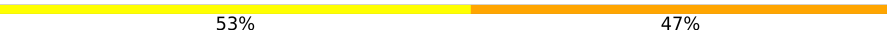
4.2.7 Score per residue for model 7

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 

G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 T263 C265

- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 

G349 T350 A351 T352 T353 G354 T355 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 

V2 A3 P4 P5 Y6 S7 Y8 Y9 A10 L11 L12 T13 T14 M14 A15 I16 L17 Q18 S19 P20 Q21 Q22 K23 K24 L24 T25 L26 I29 F32 I33 R36 F37 Y40 R41 E42 K43 F44 P45 A46 W47 Q48 N49 S50 I51 R52 H53 H54 L55 S56 L57 N58 D59 C60 F61 V62 K63

I64 P65 R66 E67 P68 G69 W70 F71 G72 N75 Y76 W77 T78 L79 D80 P81 Q82 S83 E84 F87 D88 M89 G90 S91 F92 L93 R94 R95 R96 R97 R98

4.2.8 Score per residue for model 8

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B:  24% 76%

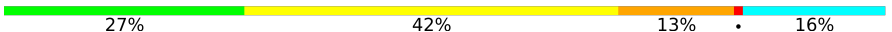
G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 T263 A264 C265

- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C:  35% 65%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A:  27% 42% 13% 16%

V2 K3 P4 P5 Y6 S7 Y8 L11 L12 T13 T14 M15 L16 L17 Q18 L19 P20 K23 L24 T25 L26 L29 F32 I33 S34 N35 N36 R37 F38 Y39 Y40 K43 F44 P45 A46 W47 Q48 L51 R52 H53 N54 L55 S56 L57 N58 D59 C60 F61 V62 K63 I64 P65 R66 E67

P68 G72 K73 G74 N75 Y76 W77 L78 L79 D80 P81 P82 S83 E84 F87 D88 N89 G90 S91 F92 L93 R94 R95 R96 R97 R98

4.2.9 Score per residue for model 9

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B:  24% 76%

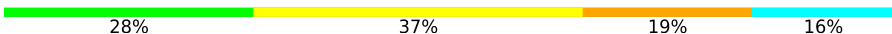
G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 T263 A264 C265

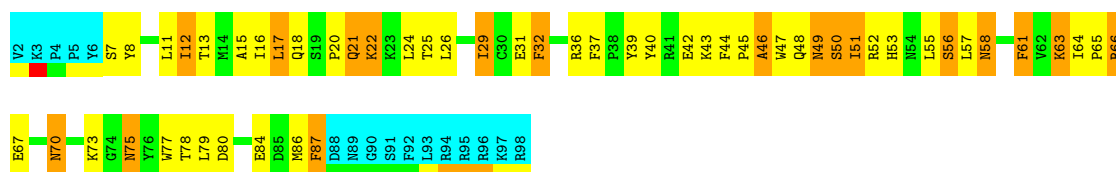
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C:  18% 82%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

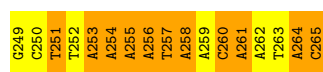
Chain A:  28% 37% 19% 16%



4.2.10 Score per residue for model 10

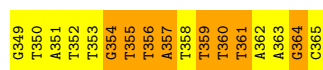
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 35% 65%



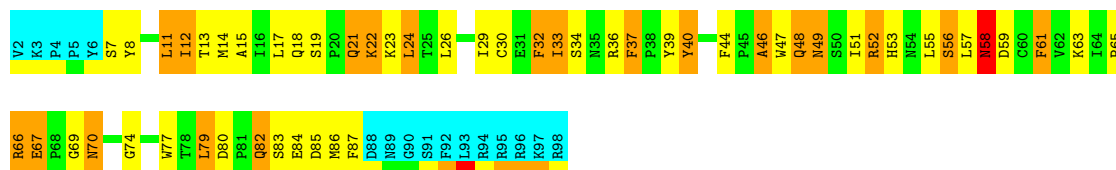
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 53% 47%



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 28% 34% 21% 16%



4.2.11 Score per residue for model 11

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 29% 71%



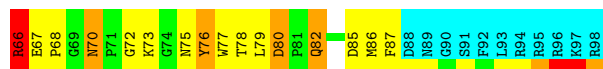
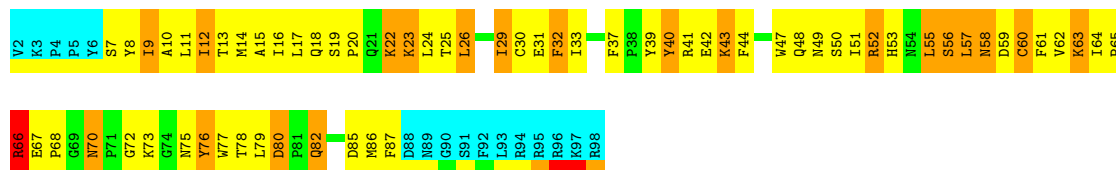
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 35% 65%



• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 16% 45% 21% 16%



4.2.12 Score per residue for model 12

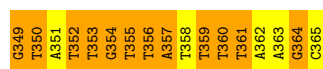
• Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 18% 82%



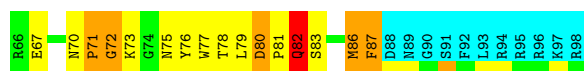
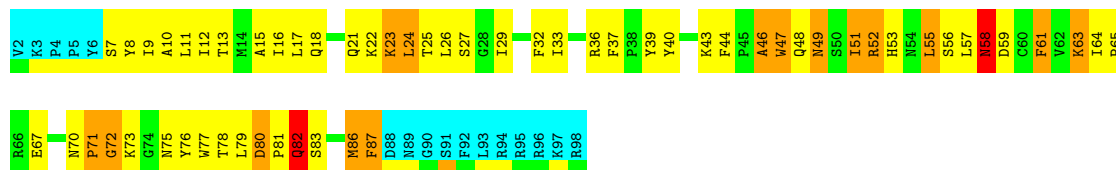
• Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 29% 71%



• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

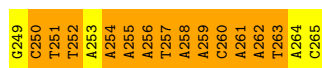
Chain A: 23% 43% 15% 16%



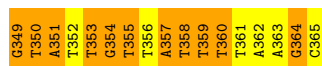
4.2.13 Score per residue for model 13

• Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 24% 76%



- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)



4.2.14 Score per residue for model 14

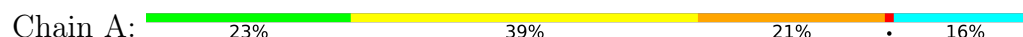
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')



- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)



4.2.15 Score per residue for model 15

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 24% 76%

G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 A263 C265

- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 29% 71%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 22% 49% 10% 16%

V2 R3 P4 P5 Y6 S7 Y8 I9 A10 A11 I12 T13 M14 A15 I16 I17 Q18 S19 P20 Q21 K22 K23 L24 T25 L26 I29 C30 I33 R36 F37 P38 Y39 Y40 R41 E42 K43 F44 P45 A46 W47 Q48 N49 S50 I51 R52 H53 N54 L55 S56 L57 N58 D59 C60 F61 V62 K63 I64
R65 R66 E67 P68 G69 N70 G74 N75 Y76 W77 T78 L79 D80 P81 Q82 D85 W86 F87 D88 N89 G90 S91 F92 L93 R94 R95 R96 K97 R98

4.2.16 Score per residue for model 16

- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 18% 82%

G249 C250 T251 T252 A253 A254 A255 A256 T257 A258 A259 C260 A261 A262 A263 C265

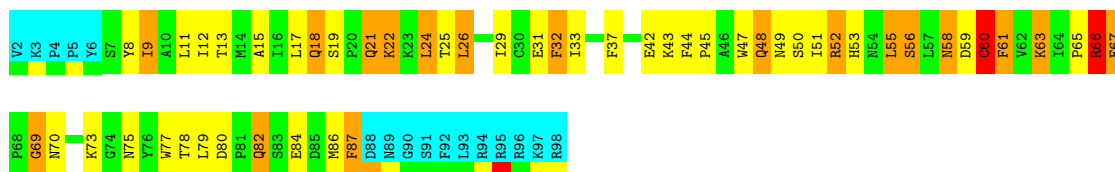
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 47% 53%

G349 T350 A351 T352 T353 G354 T355 T356 A357 T358 T359 T360 T361 A362 A363 G364 C365

- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 30% 33% 19% 16%



4.2.17 Score per residue for model 17

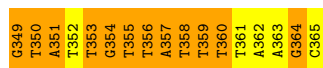
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 12% 88%



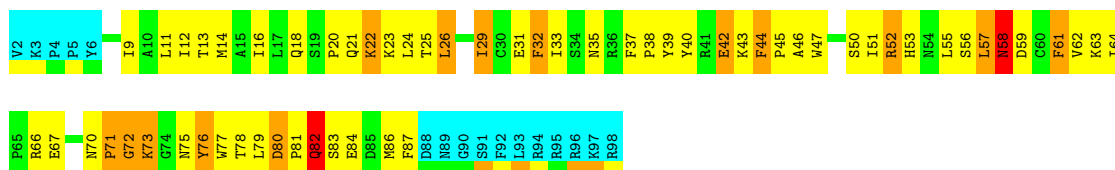
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 29% 71%



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 22% 45% 14% 16%



4.2.18 Score per residue for model 18

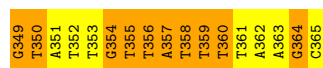
- Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 35% 65%



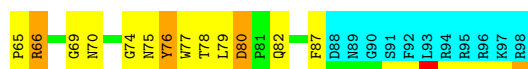
- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 41% 59%



• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

Chain A: 24% 44% 13% 16%



4.2.19 Score per residue for model 19

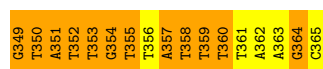
• Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

Chain B: 24% 76%



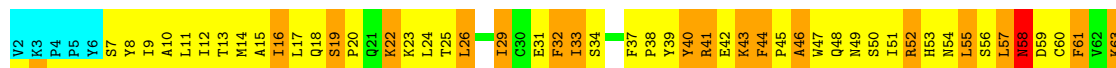
• Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*G P*C)-3')

Chain C: 29% 71%



• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)

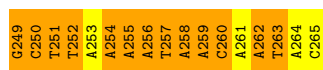
Chain A: 13% 46% 22% 16%



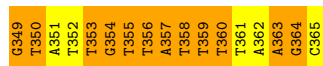
4.2.20 Score per residue for model 20

• Molecule 1: DNA (5'-D(P*GP*CP*TP*TP*AP*AP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A P*C)-3')

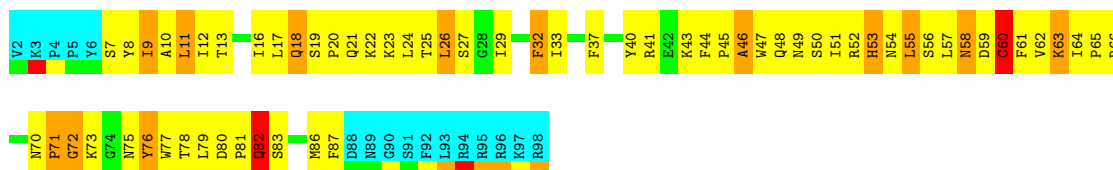
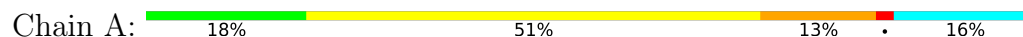
Chain B: 24% 76%



- Molecule 2: DNA (5'-D(P*GP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*TP*TP*AP*AP*GP*C)-3')



- Molecule 3: PROTEIN (TRANSCRIPTION FACTOR)



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DYANA	refinement	1.5
DYANA	structure solution	

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

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 (average) 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	B	2.43±1.13	10±2/391 (2.6± 0.4%)	4.38±0.26	33±1/600 (5.5± 0.2%)
2	C	1.73±0.20	8±2/389 (2.1± 0.4%)	3.58±0.25	29±2/599 (4.9± 0.3%)
3	A	0.70±0.00	0±0/685 (0.0± 0.0%)	1.12±0.01	0±0/930 (0.0± 0.0%)
All	All	1.72	371/29300 (1.3%)	3.10	1246/42580 (2.9%)

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	Planarity
1	B	8.1±1.1	0.0±0.0
2	C	4.2±1.0	0.0±0.0
All	All	246	0

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	B	249	DG	C4'-O4'	138.60	4.22	1.45	20	13
2	C	359	DT	C4'-O4'	30.18	2.05	1.45	18	19
2	C	363	DA	C4'-O4'	22.13	1.89	1.45	9	2
1	B	260	DC	C4'-O4'	20.85	1.87	1.45	3	17
1	B	254	DA	C4'-O4'	-19.08	1.07	1.45	2	20
2	C	360	DT	C4'-O4'	-19.04	1.07	1.45	15	4
1	B	250	DC	C4'-O4'	-18.99	1.07	1.45	7	8
1	B	264	DA	C4'-O4'	-18.70	1.08	1.45	15	4
2	C	358	DT	C4'-O4'	-18.65	1.08	1.45	11	13
1	B	263	DT	C4'-O4'	-18.41	1.08	1.45	15	19
1	B	259	DA	C4'-O4'	-18.38	1.08	1.45	18	15
2	C	352	DT	C4'-O4'	-18.10	1.09	1.45	2	2
1	B	261	DA	C4'-O4'	-18.01	1.09	1.45	12	17

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	B	256	DA	C4'-O4'	18.00	1.81	1.45	6	18
2	C	355	DT	C4'-O4'	-17.79	1.09	1.45	10	6
1	B	257	DT	C4'-O4'	-17.60	1.10	1.45	11	10
1	B	255	DA	C4'-O4'	-17.59	1.10	1.45	11	19
2	C	357	DA	C4'-O4'	-17.58	1.10	1.45	6	14
1	B	258	DA	C4'-O4'	-17.24	1.10	1.45	13	4
1	B	253	DA	C4'-O4'	-16.28	1.12	1.45	19	8
2	C	365	DC	C4'-O4'	-14.49	1.16	1.45	6	20
2	C	364	DG	C4'-O4'	14.41	1.74	1.45	9	20
1	B	251	DT	C4'-O4'	14.33	1.74	1.45	10	15
1	B	265	DC	C4'-O4'	-12.55	1.20	1.45	17	7
2	C	354	DG	C4'-O4'	10.65	1.66	1.45	11	16
1	B	262	DA	C4'-O4'	9.14	1.63	1.45	16	9
2	C	361	DT	C4'-O4'	9.03	1.63	1.45	9	7
2	C	353	DT	C4'-O4'	8.84	1.63	1.45	3	11
2	C	362	DA	C4'-O4'	-8.45	1.28	1.45	20	7
2	C	356	DT	C4'-O4'	-7.78	1.29	1.45	10	6
2	C	350	DT	C4'-O4'	7.20	1.59	1.45	16	18
1	B	252	DT	C4'-O4'	6.98	1.59	1.45	2	3

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	249	DG	C1'-O4'-C4'	-52.46	31.00	109.70	20	10
1	B	249	DG	O4'-C4'-C3'	-48.10	33.25	105.40	20	9
2	C	363	DA	C5'-C4'-O4'	38.25	166.77	109.40	9	2
1	B	263	DT	C5'-C4'-O4'	34.73	161.49	109.40	19	20
1	B	260	DC	C5'-C4'-O4'	34.02	160.43	109.40	6	20
2	C	359	DT	C5'-C4'-O4'	33.98	160.36	109.40	10	18
1	B	256	DA	C5'-C4'-O4'	33.78	160.06	109.40	17	20
1	B	255	DA	C5'-C4'-O4'	33.52	159.67	109.40	19	20
1	B	251	DT	C5'-C4'-O4'	32.16	157.65	109.40	12	20
2	C	358	DT	C5'-C4'-O4'	31.71	156.96	109.40	13	19
2	C	354	DG	C5'-C4'-O4'	31.68	156.93	109.40	9	20
1	B	262	DA	C5'-C4'-O4'	31.57	156.76	109.40	16	20
1	B	257	DT	C5'-C4'-O4'	31.15	156.12	109.40	8	19
1	B	261	DA	C5'-C4'-O4'	31.07	156.01	109.40	11	20
2	C	353	DT	C5'-C4'-O4'	31.03	155.95	109.40	17	20
1	B	253	DA	C5'-C4'-O4'	30.90	155.75	109.40	2	20
1	B	259	DA	C5'-C4'-O4'	30.42	155.03	109.40	14	20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	252	DT	C5'-C4'-O4'	29.93	154.30	109.40	2	20
2	C	361	DT	C5'-C4'-O4'	29.75	154.03	109.40	9	20
2	C	351	DA	C5'-C4'-O4'	29.45	153.57	109.40	2	20
2	C	355	DT	C5'-C4'-O4'	28.93	152.80	109.40	6	20
1	B	264	DA	C5'-C4'-O4'	28.12	151.57	109.40	11	20
1	B	258	DA	C5'-C4'-O4'	27.87	151.21	109.40	6	20
2	C	362	DA	C5'-C4'-O4'	27.54	150.72	109.40	2	20
1	B	265	DC	C5'-C4'-O4'	27.51	150.66	109.40	13	20
2	C	356	DT	C5'-C4'-O4'	27.04	149.97	109.40	20	20
2	C	357	DA	C5'-C4'-O4'	26.68	149.43	109.40	4	20
1	B	254	DA	C5'-C4'-O4'	25.56	147.74	109.40	17	19
2	C	364	DG	C5'-C4'-O4'	24.53	146.20	109.40	9	9
2	C	359	DT	O4'-C4'-C3'	-22.24	72.04	105.40	18	14
2	C	352	DT	C5'-C4'-O4'	18.99	137.88	109.40	7	14
2	C	363	DA	O4'-C4'-C3'	-18.89	77.07	105.40	9	1
1	B	260	DC	O4'-C4'-C3'	-17.61	78.98	105.40	11	20
2	C	360	DT	C5'-C4'-O4'	-17.30	83.45	109.40	2	19
1	B	249	DG	C5'-C4'-O4'	-16.79	84.22	109.40	4	15
1	B	263	DT	O4'-C4'-C3'	-16.73	80.30	105.40	6	17
1	B	255	DA	O4'-C4'-C3'	-16.66	80.42	105.40	18	8
1	B	257	DT	O4'-C4'-C3'	-16.20	81.10	105.40	13	18
2	C	349	DG	C5'-C4'-O4'	15.94	133.30	109.40	17	16
1	B	256	DA	O4'-C4'-C3'	-15.78	81.73	105.40	6	16
2	C	364	DG	O4'-C4'-C3'	-15.29	82.46	105.40	9	20
1	B	251	DT	O4'-C4'-C3'	-15.00	82.90	105.40	10	20
1	B	254	DA	O4'-C4'-C3'	-13.53	85.10	105.40	17	1
2	C	358	DT	O4'-C4'-C3'	-12.77	86.25	105.40	13	14
2	C	353	DT	O4'-C4'-C3'	-12.41	86.78	105.40	19	20
1	B	262	DA	O4'-C4'-C3'	-11.72	87.82	105.40	16	18
2	C	354	DG	O4'-C4'-C3'	-11.66	87.91	105.40	11	20
2	C	365	DC	C5'-C4'-O4'	-11.23	92.55	109.40	20	20
1	B	259	DA	O4'-C4'-C3'	-11.23	88.56	105.40	14	12
1	B	261	DA	O4'-C4'-C3'	-11.22	88.57	105.40	14	18
1	B	253	DA	O4'-C4'-C3'	-10.92	89.02	105.40	3	16
1	B	250	DC	C5'-C4'-O4'	-10.86	93.11	109.40	7	18
1	B	252	DT	O4'-C4'-C3'	-10.66	89.41	105.40	2	14
2	C	360	DT	O4'-C4'-C3'	-10.59	89.51	105.40	13	7
2	C	357	DA	O4'-C4'-C3'	-10.13	90.21	105.40	20	11
2	C	361	DT	O4'-C4'-C3'	-10.01	90.39	105.40	9	19
2	C	351	DA	O4'-C4'-C3'	-9.87	90.60	105.40	2	9
1	B	265	DC	O4'-C4'-C3'	-9.42	91.27	105.40	8	17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	C	360	DT	C1'-O4'-C4'	9.33	123.70	109.70	15	4
1	B	254	DA	C1'-O4'-C4'	9.30	123.65	109.70	2	19
1	B	250	DC	C1'-O4'-C4'	9.24	123.57	109.70	7	8
1	B	263	DT	C1'-O4'-C4'	9.15	123.43	109.70	15	3
2	C	358	DT	C1'-O4'-C4'	9.12	123.38	109.70	11	5
1	B	264	DA	C1'-O4'-C4'	9.06	123.29	109.70	15	8
1	B	264	DA	O4'-C4'-C3'	-9.05	91.82	105.40	11	17
2	C	352	DT	C1'-O4'-C4'	8.87	123.00	109.70	2	1
1	B	259	DA	C1'-O4'-C4'	8.86	122.98	109.70	18	3
1	B	255	DA	C1'-O4'-C4'	8.81	122.91	109.70	17	12
2	C	362	DA	O4'-C4'-C3'	-8.74	92.28	105.40	2	8
1	B	256	DA	C1'-O4'-C4'	8.67	122.71	109.70	20	4
2	C	359	DT	C1'-O4'-C4'	8.60	122.60	109.70	13	5
1	B	258	DA	C1'-O4'-C4'	8.53	122.49	109.70	13	4
2	C	355	DT	O4'-C4'-C3'	-8.50	92.65	105.40	6	10
1	B	258	DA	O4'-C4'-C3'	-8.37	92.84	105.40	8	13
2	C	349	DG	O4'-C4'-C3'	-8.27	92.99	105.40	9	14
1	B	261	DA	C1'-O4'-C4'	8.23	122.04	109.70	12	1
2	C	350	DT	C5'-C4'-O4'	8.16	121.64	109.40	15	20
2	C	363	DA	C1'-O4'-C4'	8.09	121.84	109.70	6	1
2	C	355	DT	C1'-O4'-C4'	7.96	121.64	109.70	10	3
2	C	365	DC	C1'-O4'-C4'	7.93	121.60	109.70	6	20
2	C	350	DT	O4'-C4'-C3'	-7.82	93.67	105.40	9	20
2	C	357	DA	C1'-O4'-C4'	7.76	121.33	109.70	6	6
1	B	257	DT	C1'-O4'-C4'	7.71	121.27	109.70	11	4
2	C	356	DT	O4'-C4'-C3'	-7.34	94.38	105.40	11	11
1	B	250	DC	O4'-C4'-C3'	-7.26	94.50	105.40	19	6
1	B	253	DA	C1'-O4'-C4'	6.94	120.11	109.70	12	2
1	B	265	DC	C1'-O4'-C4'	6.84	119.96	109.70	17	2
3	A	44	PHE	O-C-N	6.44	124.49	121.53	1	1
2	C	356	DT	C1'-O4'-C4'	6.23	119.05	109.70	3	6
2	C	362	DA	C1'-O4'-C4'	6.13	118.90	109.70	17	17
1	B	262	DA	C1'-O4'-C4'	6.12	118.88	109.70	12	1
1	B	252	DT	C1'-O4'-C4'	5.78	118.36	109.70	10	5
2	C	349	DG	C1'-O4'-C4'	5.76	118.34	109.70	3	17
2	C	352	DT	O4'-C4'-C3'	-5.51	97.14	105.40	9	5
2	C	351	DA	C1'-O4'-C4'	5.07	117.31	109.70	15	2
2	C	361	DT	C1'-O4'-C4'	5.00	117.20	109.70	15	1

All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	B	255	DA	C4'	20
1	B	260	DC	C4'	20
1	B	263	DT	C4'	18
2	C	359	DT	C4'	18
2	C	353	DT	C4'	16
2	C	358	DT	C4'	15
1	B	253	DA	C4'	13
1	B	256	DA	C4'	13
1	B	257	DT	C4'	13
2	C	362	DA	C4'	13
1	B	254	DA	C4'	12
1	B	251	DT	C4'	11
1	B	264	DA	C4'	10
1	B	262	DA	C4'	9
1	B	258	DA	C4'	8
2	C	356	DT	C4'	8
1	B	252	DT	C4'	5
2	C	361	DT	C4'	4
2	C	357	DA	C4'	3
1	B	261	DA	C4'	3
1	B	265	DC	C4'	3
1	B	259	DA	C4'	3
2	C	355	DT	C4'	2
2	C	364	DG	C4'	2
2	C	351	DA	C4'	1
1	B	249	DG	C4'	1
2	C	354	DG	C4'	1
2	C	363	DA	C4'	1

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	B	348	145	192	26±6
2	C	349	135	197	22±5
3	A	664	652	652	77±14
All	All	27220	18640	20820	2250

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 47.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:261:DA:O4'	1:B:261:DA:C4'	1.39	1.64	13	8
2:C:361:DT:C4'	2:C:361:DT:O4'	1.38	1.63	9	1
1:B:256:DA:O4'	1:B:256:DA:C4'	1.37	1.64	11	12
2:C:364:DG:O4'	2:C:364:DG:C4'	1.36	1.64	15	8
1:B:251:DT:O4'	1:B:251:DT:C4'	1.35	1.65	3	4
1:B:259:DA:C4'	1:B:259:DA:O4'	1.35	1.65	16	4
1:B:255:DA:O4'	1:B:255:DA:C4'	1.34	1.66	15	7
1:B:249:DG:C4'	1:B:249:DG:O4'	1.34	1.64	17	2
2:C:354:DG:C4'	2:C:354:DG:O4'	1.34	1.66	11	3
1:B:262:DA:O4'	1:B:262:DA:C4'	1.33	1.63	16	1
1:B:257:DT:O4'	1:B:257:DT:C4'	1.33	1.65	6	5
1:B:260:DC:O4'	1:B:260:DC:C4'	1.32	1.70	1	17
2:C:359:DT:C4'	2:C:359:DT:O4'	1.31	1.70	1	14
1:B:265:DC:O4'	1:B:265:DC:C4'	1.29	1.64	8	1
1:B:254:DA:C4'	1:B:254:DA:O4'	1.27	1.68	17	1
1:B:263:DT:C4'	1:B:263:DT:O4'	1.27	1.77	2	8
2:C:358:DT:C4'	2:C:358:DT:O4'	1.19	1.68	13	1
2:C:363:DA:C4'	2:C:363:DA:O4'	1.04	1.89	9	1
3:A:16:ILE:HD12	3:A:24:LEU:HD21	0.95	1.35	14	1
3:A:64:ILE:HG22	3:A:76:TYR:O	0.94	1.62	20	10
3:A:9:ILE:O	3:A:13:THR:HG23	0.90	1.65	19	8
3:A:13:THR:HG21	3:A:87:PHE:CE1	0.90	2.00	12	4
3:A:13:THR:O	3:A:17:LEU:HD23	0.89	1.67	11	10
3:A:12:ILE:HD11	3:A:51:ILE:HD11	0.89	1.42	8	1
3:A:23:LYS:O	3:A:24:LEU:HD22	0.87	1.69	3	4
3:A:9:ILE:HG22	3:A:58:ASN:OD1	0.85	1.71	13	2
3:A:47:TRP:O	3:A:51:ILE:HG23	0.85	1.71	6	1
1:B:249:DG:O4'	1:B:249:DG:C5'	0.85	2.24	17	2
3:A:9:ILE:HD11	3:A:58:ASN:OD1	0.84	1.72	17	2
3:A:26:LEU:HD23	3:A:55:LEU:HD23	0.84	1.49	6	2
3:A:16:ILE:HG21	3:A:79:LEU:HD13	0.83	1.50	13	2
3:A:79:LEU:HD23	3:A:80:ASP:O	0.83	1.72	16	14
3:A:16:ILE:HG12	3:A:79:LEU:HD13	0.82	1.50	1	3
1:B:258:DA:C2	2:C:357:DA:C2	0.82	2.68	15	19
3:A:40:TYR:CD2	3:A:47:TRP:CH2	0.82	2.68	7	7
1:B:250:DC:H2''	1:B:251:DT:H71	0.81	1.52	20	5
3:A:40:TYR:CD2	3:A:47:TRP:CZ2	0.81	2.69	7	3
3:A:86:MET:HE1	3:A:87:PHE:CZ	0.81	2.11	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:356:DT:H72	3:A:57:LEU:HD11	0.81	1.53	14	1
2:C:359:DT:H2'	2:C:360:DT:H71	0.80	1.53	7	3
3:A:40:TYR:CG	3:A:47:TRP:CH2	0.79	2.71	9	2
3:A:44:PHE:CD1	3:A:47:TRP:CD1	0.79	2.71	16	2
3:A:79:LEU:HD22	3:A:80:ASP:N	0.79	1.92	19	1
3:A:11:LEU:HD22	3:A:37:PHE:CE1	0.78	2.14	2	2
3:A:47:TRP:CE3	3:A:51:ILE:HD11	0.78	2.15	1	2
3:A:23:LYS:C	3:A:24:LEU:HD22	0.77	2.04	17	3
3:A:26:LEU:HD11	3:A:52:ARG:NH2	0.77	1.94	15	1
3:A:19:SER:OG	3:A:24:LEU:HD23	0.76	1.79	10	1
3:A:86:MET:HE3	3:A:87:PHE:CD2	0.76	2.14	5	1
3:A:8:TYR:HB3	3:A:51:ILE:HD12	0.75	1.57	3	2
3:A:79:LEU:HD13	3:A:80:ASP:O	0.75	1.82	19	1
3:A:53:HIS:CE1	3:A:57:LEU:HD22	0.75	2.16	13	6
3:A:8:TYR:CE2	3:A:12:ILE:HD11	0.75	2.17	6	2
2:C:359:DT:C4'	2:C:360:DT:OP1	0.74	2.34	2	4
3:A:33:ILE:HG21	3:A:47:TRP:CZ3	0.74	2.17	19	7
1:B:255:DA:H1'	1:B:256:DA:H4'	0.74	1.59	11	7
3:A:47:TRP:CZ3	3:A:51:ILE:HD13	0.74	2.18	19	2
3:A:12:ILE:HD11	3:A:51:ILE:CD1	0.74	2.12	8	2
3:A:25:THR:HG23	3:A:75:ASN:O	0.74	1.83	20	4
3:A:79:LEU:HD22	3:A:80:ASP:H	0.74	1.40	19	1
3:A:12:ILE:HD12	3:A:55:LEU:HD13	0.73	1.56	3	3
3:A:19:SER:OG	3:A:24:LEU:HD22	0.73	1.83	16	4
3:A:13:THR:HG21	3:A:87:PHE:CD1	0.73	2.18	14	1
3:A:44:PHE:O	3:A:44:PHE:CG	0.73	2.42	2	2
3:A:12:ILE:HD12	3:A:55:LEU:HG	0.73	1.58	18	6
3:A:32:PHE:CE2	3:A:33:ILE:HD11	0.72	2.19	17	4
3:A:12:ILE:CD1	3:A:51:ILE:HD11	0.72	2.13	8	2
3:A:75:ASN:C	3:A:76:TYR:CD1	0.72	2.66	6	11
3:A:67:GLU:N	3:A:68:PRO:HD3	0.72	1.99	8	1
3:A:11:LEU:HD21	3:A:37:PHE:CZ	0.71	2.19	10	1
3:A:44:PHE:CD1	3:A:47:TRP:NE1	0.71	2.58	16	1
3:A:16:ILE:HD12	3:A:79:LEU:HD13	0.71	1.62	11	3
3:A:16:ILE:CD1	3:A:24:LEU:HD21	0.71	2.14	14	2
3:A:15:ALA:HB2	3:A:32:PHE:CE2	0.71	2.19	1	4
2:C:351:DA:H2''	2:C:352:DT:H71	0.71	1.60	3	4
3:A:40:TYR:CG	3:A:47:TRP:CZ2	0.71	2.78	7	4
3:A:61:PHE:HB3	3:A:79:LEU:HD23	0.71	1.62	19	1
3:A:8:TYR:CD1	3:A:47:TRP:CZ3	0.70	2.79	5	1
3:A:25:THR:O	3:A:29:ILE:HD13	0.70	1.87	9	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:43:LYS:C	3:A:45:PRO:HD3	0.70	2.10	6	2
2:C:355:DT:H4'	2:C:356:DT:OP1	0.70	1.87	20	3
2:C:364:DG:O4'	2:C:364:DG:C5'	0.70	2.39	10	6
1:B:255:DA:C2	1:B:256:DA:C4	0.70	2.80	9	16
3:A:13:THR:HG21	3:A:87:PHE:CE2	0.69	2.22	13	1
3:A:45:PRO:O	3:A:46:ALA:HB3	0.69	1.86	1	2
1:B:250:DC:C2'	1:B:251:DT:H71	0.69	2.17	20	5
3:A:32:PHE:CE2	3:A:33:ILE:CD1	0.69	2.76	17	4
3:A:44:PHE:CE1	3:A:47:TRP:CB	0.69	2.76	19	1
1:B:257:DT:H73	3:A:53:HIS:ND1	0.69	2.03	6	2
3:A:39:TYR:CE2	3:A:40:TYR:CE1	0.69	2.80	6	2
1:B:255:DA:H2''	1:B:256:DA:OP2	0.68	1.87	19	4
3:A:8:TYR:O	3:A:12:ILE:HD13	0.68	1.87	14	3
1:B:250:DC:H2'	1:B:251:DT:H72	0.68	1.65	6	4
2:C:355:DT:H73	3:A:52:ARG:CZ	0.67	2.19	4	1
3:A:26:LEU:CD2	3:A:55:LEU:HD23	0.67	2.18	6	1
3:A:15:ALA:HB1	3:A:29:ILE:HD11	0.67	1.66	1	2
3:A:11:LEU:HD22	3:A:37:PHE:CZ	0.67	2.23	16	2
3:A:45:PRO:O	3:A:46:ALA:HB2	0.67	1.89	20	8
2:C:354:DG:C8	3:A:52:ARG:NH1	0.67	2.63	19	1
3:A:39:TYR:CD1	3:A:39:TYR:C	0.67	2.73	6	3
3:A:71:PRO:O	3:A:72:GLY:C	0.67	2.37	20	3
1:B:259:DA:H1'	1:B:260:DC:H4'	0.67	1.67	13	1
3:A:24:LEU:HD23	3:A:29:ILE:HD11	0.67	1.65	15	1
2:C:357:DA:N6	3:A:53:HIS:CD2	0.66	2.63	12	9
3:A:43:LYS:O	3:A:45:PRO:N	0.66	2.28	17	1
2:C:358:DT:C4'	2:C:359:DT:OP1	0.66	2.42	5	2
1:B:257:DT:C2	1:B:258:DA:N7	0.66	2.64	13	9
3:A:24:LEU:HD12	3:A:29:ILE:HG12	0.66	1.66	14	1
3:A:75:ASN:O	3:A:76:TYR:CD1	0.66	2.49	20	8
2:C:351:DA:C2'	2:C:352:DT:H71	0.66	2.20	3	4
3:A:46:ALA:HB1	3:A:49:ASN:ND2	0.66	2.05	5	1
1:B:257:DT:H73	3:A:53:HIS:CD2	0.66	2.25	19	4
3:A:53:HIS:CE1	3:A:57:LEU:CD2	0.66	2.79	13	1
3:A:8:TYR:CZ	3:A:50:SER:CB	0.65	2.79	18	1
2:C:359:DT:C2'	2:C:360:DT:H71	0.65	2.21	7	5
2:C:355:DT:H72	3:A:52:ARG:CZ	0.65	2.21	11	1
3:A:16:ILE:HD12	3:A:79:LEU:CD1	0.65	2.21	11	1
1:B:255:DA:C2'	1:B:256:DA:OP2	0.65	2.45	19	1
3:A:43:LYS:O	3:A:44:PHE:C	0.65	2.38	14	11
3:A:14:MET:HE3	3:A:32:PHE:CZ	0.65	2.27	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:249:DG:O4'	1:B:250:DC:C6	0.65	2.49	20	1
1:B:256:DA:C8	1:B:257:DT:H72	0.65	2.27	2	7
3:A:8:TYR:O	3:A:12:ILE:HD12	0.65	1.92	4	3
3:A:79:LEU:HD11	3:A:83:SER:CB	0.64	2.22	1	2
1:B:256:DA:N7	3:A:53:HIS:CE1	0.64	2.65	18	3
1:B:257:DT:O4	3:A:53:HIS:CD2	0.64	2.51	18	6
3:A:61:PHE:CD2	3:A:79:LEU:HD12	0.64	2.26	7	8
3:A:11:LEU:CD2	3:A:37:PHE:CE1	0.64	2.81	10	2
3:A:39:TYR:CE2	3:A:40:TYR:CD1	0.64	2.86	14	1
2:C:358:DT:H4'	2:C:359:DT:OP1	0.64	1.92	18	3
3:A:67:GLU:N	3:A:68:PRO:CD	0.64	2.60	8	1
3:A:55:LEU:O	3:A:61:PHE:CE2	0.64	2.50	9	6
3:A:8:TYR:CZ	3:A:47:TRP:CZ2	0.64	2.85	19	1
2:C:357:DA:N6	3:A:53:HIS:CE1	0.63	2.66	5	5
1:B:257:DT:H71	3:A:53:HIS:CD2	0.63	2.28	1	2
3:A:61:PHE:HD2	3:A:79:LEU:HD12	0.63	1.51	16	9
3:A:55:LEU:HD22	3:A:61:PHE:CZ	0.63	2.28	14	8
1:B:257:DT:O4	3:A:53:HIS:CG	0.63	2.52	19	17
3:A:37:PHE:CB	3:A:40:TYR:CD2	0.63	2.81	1	5
3:A:16:ILE:HD11	3:A:55:LEU:HD11	0.63	1.70	17	2
3:A:39:TYR:CD1	3:A:40:TYR:N	0.63	2.67	2	4
2:C:354:DG:C8	2:C:355:DT:H72	0.62	2.28	4	3
3:A:16:ILE:HD12	3:A:24:LEU:HD22	0.62	1.71	1	1
2:C:358:DT:H2'	2:C:359:DT:H72	0.62	1.71	17	4
3:A:13:THR:HG21	3:A:87:PHE:CZ	0.62	2.29	13	2
2:C:363:DA:C4'	2:C:364:DG:OP1	0.62	2.47	10	19
3:A:83:SER:HA	3:A:86:MET:HE2	0.62	1.71	6	1
2:C:352:DT:H4'	2:C:353:DT:OP1	0.62	1.95	2	1
3:A:51:ILE:HD13	3:A:51:ILE:O	0.62	1.94	8	1
2:C:354:DG:N9	2:C:355:DT:H72	0.62	2.10	4	1
2:C:363:DA:O4'	2:C:364:DG:OP1	0.62	2.17	10	19
3:A:16:ILE:CD1	3:A:79:LEU:HD13	0.62	2.25	7	1
3:A:13:THR:CG2	3:A:87:PHE:CE1	0.62	2.80	12	1
1:B:257:DT:C2	1:B:258:DA:C8	0.62	2.88	10	10
1:B:262:DA:C2'	1:B:263:DT:H71	0.62	2.25	11	1
3:A:75:ASN:ND2	3:A:77:TRP:CD1	0.62	2.68	6	2
3:A:15:ALA:O	3:A:24:LEU:HD13	0.61	1.95	14	1
3:A:55:LEU:O	3:A:61:PHE:CZ	0.61	2.53	4	17
1:B:257:DT:O4	3:A:53:HIS:CE1	0.61	2.53	20	3
2:C:352:DT:H2'	2:C:353:DT:H72	0.61	1.72	2	2
3:A:44:PHE:CE1	3:A:46:ALA:O	0.61	2.53	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:44:PHE:CZ	3:A:47:TRP:CE2	0.61	2.88	16	1
3:A:11:LEU:HD22	3:A:37:PHE:CE2	0.61	2.31	3	2
3:A:62:VAL:HG23	3:A:78:THR:HB	0.61	1.73	15	3
3:A:75:ASN:C	3:A:76:TYR:CG	0.61	2.79	18	8
3:A:46:ALA:HB1	3:A:49:ASN:HD22	0.61	1.54	5	1
3:A:26:LEU:HD11	3:A:52:ARG:CZ	0.61	2.26	15	1
3:A:9:ILE:HD11	3:A:58:ASN:CG	0.61	2.21	17	1
1:B:254:DA:H2''	1:B:255:DA:OP2	0.60	1.96	17	1
3:A:9:ILE:C	3:A:9:ILE:HD12	0.60	2.20	20	2
2:C:354:DG:OP2	3:A:77:TRP:CZ2	0.60	2.55	4	8
3:A:59:ASP:O	3:A:60:CYS:CB	0.60	2.49	5	12
3:A:40:TYR:CD1	3:A:47:TRP:CZ2	0.60	2.89	9	2
1:B:261:DA:C2	2:C:354:DG:C2	0.60	2.89	10	4
2:C:359:DT:O4'	2:C:359:DT:O3'	0.60	2.10	18	4
3:A:8:TYR:HE2	3:A:12:ILE:HD11	0.60	1.55	6	2
3:A:11:LEU:HD11	3:A:37:PHE:CE2	0.60	2.32	12	2
3:A:8:TYR:OH	3:A:47:TRP:CZ2	0.59	2.52	19	2
3:A:45:PRO:O	3:A:46:ALA:CB	0.59	2.49	1	4
3:A:59:ASP:CB	3:A:61:PHE:CD2	0.59	2.84	19	11
3:A:44:PHE:CZ	3:A:46:ALA:O	0.59	2.55	12	2
3:A:8:TYR:CE1	3:A:51:ILE:HG22	0.59	2.32	6	1
1:B:249:DG:C4'	1:B:250:DC:OP1	0.59	2.49	5	3
3:A:64:ILE:HG21	3:A:76:TYR:HD2	0.59	1.58	20	2
2:C:355:DT:C6	2:C:356:DT:H72	0.59	2.33	7	3
2:C:354:DG:C4	2:C:355:DT:H72	0.59	2.32	4	1
3:A:14:MET:HE2	3:A:32:PHE:CZ	0.59	2.32	17	2
2:C:355:DT:H2'	2:C:356:DT:H72	0.59	1.75	10	3
1:B:255:DA:C1'	1:B:256:DA:O5'	0.59	2.51	11	12
2:C:357:DA:H4'	2:C:358:DT:OP1	0.59	1.97	11	5
1:B:256:DA:OP1	3:A:7:SER:HA	0.59	1.97	19	1
3:A:65:PRO:O	3:A:66:ARG:C	0.58	2.43	16	10
3:A:79:LEU:HD11	3:A:83:SER:HB3	0.58	1.75	1	2
1:B:256:DA:OP2	3:A:7:SER:CB	0.58	2.51	8	6
3:A:11:LEU:HD22	3:A:33:ILE:HG23	0.58	1.75	5	1
2:C:355:DT:H72	3:A:52:ARG:NE	0.58	2.11	11	1
3:A:49:ASN:OD1	3:A:50:SER:N	0.58	2.36	11	4
2:C:357:DA:C8	2:C:358:DT:H72	0.58	2.33	15	9
2:C:356:DT:C7	3:A:52:ARG:NH2	0.58	2.66	17	2
3:A:44:PHE:CE2	3:A:47:TRP:CB	0.58	2.87	6	3
3:A:86:MET:HE1	3:A:87:PHE:CE2	0.58	2.32	11	1
3:A:79:LEU:HD21	3:A:83:SER:HB3	0.58	1.75	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:59:ASP:HB2	3:A:61:PHE:CE2	0.58	2.33	19	10
3:A:11:LEU:HB3	3:A:33:ILE:HD12	0.58	1.75	5	1
3:A:44:PHE:CZ	3:A:47:TRP:HB2	0.58	2.33	6	4
3:A:40:TYR:CD1	3:A:47:TRP:CH2	0.58	2.90	9	1
3:A:79:LEU:HD23	3:A:80:ASP:N	0.58	2.13	9	3
2:C:357:DA:H2''	2:C:358:DT:OP2	0.58	1.96	15	1
3:A:16:ILE:CD1	3:A:24:LEU:HD22	0.58	2.28	1	1
3:A:21:GLN:O	3:A:22:LYS:C	0.58	2.46	9	5
3:A:16:ILE:HD12	3:A:24:LEU:HG	0.58	1.73	19	1
3:A:55:LEU:HD23	3:A:77:TRP:CZ3	0.58	2.34	17	2
2:C:356:DT:C7	3:A:57:LEU:HD11	0.58	2.27	14	1
2:C:360:DT:C6	2:C:360:DT:H5'	0.58	2.33	15	1
2:C:359:DT:O4'	2:C:360:DT:OP1	0.57	2.22	2	3
2:C:359:DT:H2'	2:C:360:DT:H72	0.57	1.75	13	4
3:A:51:ILE:O	3:A:55:LEU:N	0.57	2.36	7	10
3:A:8:TYR:CE1	3:A:50:SER:CB	0.57	2.87	18	2
3:A:32:PHE:C	3:A:32:PHE:CD1	0.57	2.82	7	1
3:A:75:ASN:CG	3:A:76:TYR:N	0.57	2.61	3	1
1:B:257:DT:O2	1:B:258:DA:C8	0.57	2.58	10	3
3:A:44:PHE:CE1	3:A:47:TRP:CE2	0.57	2.91	16	1
1:B:250:DC:H4'	1:B:251:DT:OP1	0.57	1.97	6	3
3:A:44:PHE:CD1	3:A:47:TRP:HB2	0.57	2.34	19	3
2:C:355:DT:H72	3:A:52:ARG:CD	0.57	2.30	17	2
1:B:256:DA:H2''	3:A:8:TYR:CE2	0.57	2.34	4	2
3:A:44:PHE:CE2	3:A:47:TRP:HB2	0.57	2.34	6	3
3:A:59:ASP:CB	3:A:61:PHE:CE2	0.57	2.87	12	5
2:C:352:DT:C6	2:C:353:DT:H72	0.57	2.35	7	8
3:A:11:LEU:HD21	3:A:37:PHE:CE1	0.57	2.35	10	2
3:A:44:PHE:CG	3:A:47:TRP:NE1	0.57	2.73	16	1
3:A:52:ARG:NH1	3:A:56:SER:CB	0.56	2.68	4	2
3:A:51:ILE:O	3:A:55:LEU:HB2	0.56	2.00	5	9
1:B:257:DT:H2''	1:B:258:DA:OP2	0.56	2.00	13	1
3:A:33:ILE:CG2	3:A:47:TRP:CZ3	0.56	2.87	18	1
3:A:79:LEU:CD2	3:A:80:ASP:O	0.56	2.54	5	11
3:A:56:SER:HA	3:A:61:PHE:CE1	0.56	2.35	16	10
3:A:57:LEU:O	3:A:58:ASN:CG	0.56	2.49	13	7
3:A:49:ASN:OD1	3:A:49:ASN:C	0.56	2.48	11	2
3:A:17:LEU:HD21	3:A:84:GLU:HB2	0.56	1.78	19	1
2:C:363:DA:C1'	2:C:364:DG:OP1	0.56	2.54	6	19
3:A:52:ARG:CZ	3:A:56:SER:OG	0.56	2.53	4	1
3:A:51:ILE:HG13	3:A:52:ARG:N	0.56	2.16	14	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:24:LEU:CD1	3:A:29:ILE:HD13	0.56	2.31	13	1
2:C:351:DA:C8	2:C:352:DT:H72	0.56	2.35	8	6
3:A:33:ILE:HG21	3:A:47:TRP:HZ3	0.56	1.60	7	2
3:A:37:PHE:HB2	3:A:40:TYR:CD2	0.56	2.34	1	5
3:A:57:LEU:O	3:A:58:ASN:CB	0.56	2.53	9	11
3:A:63:LYS:HG2	3:A:77:TRP:CE3	0.56	2.35	3	8
3:A:24:LEU:CD2	3:A:29:ILE:HD11	0.56	2.30	4	1
3:A:64:ILE:HG21	3:A:76:TYR:CD2	0.56	2.36	5	4
3:A:47:TRP:CZ3	3:A:51:ILE:HD11	0.56	2.36	1	2
3:A:59:ASP:HB3	3:A:61:PHE:CD2	0.56	2.35	12	4
3:A:76:TYR:CD1	3:A:76:TYR:N	0.56	2.74	6	1
1:B:256:DA:H1'	1:B:257:DT:H4'	0.56	1.78	13	4
3:A:59:ASP:C	3:A:60:CYS:SG	0.56	2.89	11	1
3:A:26:LEU:C	3:A:26:LEU:HD13	0.55	2.27	6	5
3:A:26:LEU:C	3:A:26:LEU:CD2	0.55	2.78	11	1
3:A:33:ILE:HG23	3:A:37:PHE:CD1	0.55	2.36	14	1
3:A:11:LEU:CD2	3:A:37:PHE:CZ	0.55	2.88	10	2
3:A:25:THR:CG2	3:A:75:ASN:OD1	0.55	2.54	16	2
1:B:256:DA:P	3:A:7:SER:HA	0.55	2.41	13	2
3:A:8:TYR:CE2	3:A:50:SER:HB3	0.55	2.37	18	5
3:A:27:SER:CB	3:A:73:LYS:O	0.55	2.54	2	3
3:A:11:LEU:HD23	3:A:33:ILE:CG2	0.55	2.31	4	1
1:B:254:DA:C2'	1:B:255:DA:O5'	0.55	2.55	20	18
2:C:357:DA:H2'	2:C:358:DT:H72	0.55	1.78	6	5
3:A:53:HIS:O	3:A:57:LEU:CB	0.55	2.55	5	2
3:A:25:THR:CG2	3:A:75:ASN:O	0.55	2.54	20	3
3:A:26:LEU:HB2	3:A:77:TRP:CE2	0.55	2.37	11	12
2:C:352:DT:O2	3:A:66:ARG:CG	0.55	2.55	4	2
3:A:47:TRP:O	3:A:51:ILE:N	0.55	2.28	5	2
3:A:8:TYR:CD2	3:A:51:ILE:HA	0.55	2.36	6	1
3:A:51:ILE:CG2	3:A:52:ARG:N	0.55	2.70	19	5
3:A:38:PRO:O	3:A:42:GLU:N	0.55	2.40	17	1
1:B:259:DA:N7	3:A:49:ASN:ND2	0.55	2.55	16	11
2:C:359:DT:C1'	2:C:360:DT:OP1	0.55	2.55	6	3
3:A:24:LEU:HD12	3:A:29:ILE:HD11	0.55	1.78	9	1
2:C:354:DG:N7	3:A:52:ARG:NH1	0.54	2.55	14	4
3:A:17:LEU:HD11	3:A:87:PHE:CD2	0.54	2.37	1	1
1:B:262:DA:C8	1:B:263:DT:H72	0.54	2.37	12	11
3:A:65:PRO:O	3:A:67:GLU:N	0.54	2.40	2	7
3:A:25:THR:HG23	3:A:75:ASN:CG	0.54	2.28	16	1
2:C:351:DA:C2'	2:C:352:DT:H72	0.54	2.31	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:354:DG:OP2	3:A:77:TRP:NE1	0.54	2.40	2	6
3:A:37:PHE:CG	3:A:40:TYR:CE2	0.54	2.95	1	3
3:A:49:ASN:O	3:A:53:HIS:CB	0.54	2.55	9	6
3:A:32:PHE:CD1	3:A:32:PHE:C	0.54	2.85	2	4
3:A:37:PHE:CD1	3:A:37:PHE:N	0.54	2.76	15	4
3:A:26:LEU:HD22	3:A:26:LEU:O	0.54	2.03	16	1
3:A:44:PHE:O	3:A:47:TRP:CD1	0.54	2.60	12	2
3:A:12:ILE:HG23	3:A:55:LEU:HD23	0.54	1.79	12	1
3:A:48:GLN:CG	3:A:52:ARG:NH2	0.54	2.71	1	2
3:A:8:TYR:CZ	3:A:50:SER:HB3	0.54	2.37	18	3
1:B:258:DA:N1	2:C:357:DA:C6	0.54	2.75	3	2
3:A:61:PHE:CE1	3:A:77:TRP:CE3	0.54	2.96	7	1
3:A:33:ILE:HG21	3:A:47:TRP:CE3	0.54	2.36	18	1
2:C:354:DG:C4	2:C:355:DT:C5	0.54	2.96	4	5
2:C:359:DT:O4'	2:C:359:DT:C5'	0.54	2.55	18	1
3:A:33:ILE:HG23	3:A:37:PHE:CE1	0.54	2.38	7	2
2:C:354:DG:N7	3:A:52:ARG:NH2	0.54	2.55	6	2
3:A:59:ASP:HB2	3:A:61:PHE:CD2	0.54	2.38	4	5
3:A:64:ILE:CG2	3:A:76:TYR:O	0.54	2.55	18	3
3:A:53:HIS:O	3:A:57:LEU:N	0.53	2.41	7	10
1:B:254:DA:C1'	1:B:255:DA:O5'	0.53	2.56	8	16
2:C:354:DG:OP1	3:A:77:TRP:NE1	0.53	2.41	10	4
3:A:8:TYR:OH	3:A:47:TRP:CE2	0.53	2.61	10	2
1:B:258:DA:N1	2:C:357:DA:N1	0.53	2.56	3	8
1:B:256:DA:OP2	3:A:9:ILE:HG23	0.53	2.03	2	1
1:B:257:DT:C2	1:B:258:DA:C5	0.53	2.96	20	6
3:A:47:TRP:O	3:A:51:ILE:HG22	0.53	2.03	16	3
2:C:359:DT:H4'	2:C:360:DT:OP1	0.53	2.03	6	2
3:A:70:ASN:N	3:A:70:ASN:ND2	0.53	2.57	14	3
1:B:255:DA:H1'	1:B:256:DA:OP2	0.53	2.03	19	1
3:A:15:ALA:HB2	3:A:32:PHE:HE2	0.53	1.57	1	4
3:A:19:SER:OG	3:A:24:LEU:HD13	0.53	2.04	11	2
3:A:24:LEU:O	3:A:77:TRP:N	0.53	2.40	5	9
3:A:15:ALA:O	3:A:18:GLN:CG	0.53	2.56	11	7
3:A:12:ILE:HG13	3:A:55:LEU:HD13	0.53	1.79	17	1
3:A:79:LEU:CD1	3:A:80:ASP:O	0.53	2.55	19	1
3:A:44:PHE:HA	3:A:47:TRP:CD1	0.53	2.39	20	6
1:B:250:DC:C2'	1:B:251:DT:H72	0.53	2.33	19	5
3:A:36:ARG:C	3:A:37:PHE:CD1	0.53	2.86	8	2
3:A:13:THR:O	3:A:17:LEU:HD12	0.53	2.03	9	1
3:A:8:TYR:CE1	3:A:47:TRP:CZ3	0.53	2.97	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:354:DG:H2''	2:C:355:DT:H71	0.53	1.80	15	1
3:A:24:LEU:HD12	3:A:29:ILE:HD13	0.53	1.81	13	1
3:A:44:PHE:CE1	3:A:47:TRP:HB2	0.53	2.38	7	7
3:A:36:ARG:HB2	3:A:37:PHE:CE1	0.53	2.38	15	3
3:A:8:TYR:CE1	3:A:50:SER:HB2	0.53	2.39	18	1
3:A:32:PHE:CE2	3:A:33:ILE:HG13	0.53	2.39	4	6
1:B:257:DT:C2'	1:B:258:DA:O5'	0.53	2.57	11	1
3:A:44:PHE:CE2	3:A:47:TRP:CZ2	0.53	2.97	16	1
3:A:15:ALA:HB1	3:A:29:ILE:CD1	0.53	2.34	1	1
3:A:63:LYS:HG2	3:A:77:TRP:CZ3	0.53	2.39	14	3
3:A:12:ILE:HG23	3:A:55:LEU:HD13	0.53	1.81	8	1
2:C:355:DT:H72	3:A:52:ARG:NH2	0.53	2.19	11	1
3:A:8:TYR:CZ	3:A:51:ILE:HG12	0.53	2.39	5	1
3:A:75:ASN:N	3:A:75:ASN:OD1	0.53	2.40	9	3
3:A:16:ILE:HD13	3:A:24:LEU:CD2	0.53	2.34	11	2
3:A:15:ALA:HB1	3:A:29:ILE:CG1	0.53	2.33	18	1
3:A:64:ILE:HG12	3:A:76:TYR:CB	0.52	2.34	1	1
3:A:44:PHE:O	3:A:47:TRP:HD1	0.52	1.87	12	2
3:A:56:SER:HA	3:A:61:PHE:CZ	0.52	2.39	8	6
1:B:259:DA:C1'	1:B:260:DC:O5'	0.52	2.56	13	4
1:B:258:DA:C2	1:B:259:DA:C5	0.52	2.97	14	3
3:A:61:PHE:HB2	3:A:78:THR:O	0.52	2.03	9	7
3:A:51:ILE:CG1	3:A:52:ARG:N	0.52	2.72	6	3
3:A:11:LEU:HD13	3:A:33:ILE:HD13	0.52	1.82	8	1
2:C:357:DA:N6	3:A:53:HIS:ND1	0.52	2.57	5	3
3:A:61:PHE:C	3:A:61:PHE:CD1	0.52	2.85	2	3
3:A:44:PHE:CD2	3:A:47:TRP:NE1	0.52	2.78	3	2
3:A:44:PHE:CZ	3:A:47:TRP:CB	0.52	2.92	6	2
3:A:55:LEU:HG	3:A:77:TRP:CZ3	0.52	2.40	7	5
2:C:354:DG:OP2	3:A:77:TRP:CE2	0.52	2.63	4	4
3:A:8:TYR:CD2	3:A:12:ILE:HG12	0.52	2.40	6	2
3:A:12:ILE:CG2	3:A:55:LEU:HD13	0.52	2.35	8	1
3:A:52:ARG:CD	3:A:52:ARG:C	0.52	2.83	17	2
1:B:249:DG:O4'	1:B:249:DG:O5'	0.52	2.28	7	1
3:A:55:LEU:HD13	3:A:77:TRP:CZ3	0.52	2.39	11	3
3:A:8:TYR:CE2	3:A:50:SER:CB	0.52	2.93	16	1
3:A:13:THR:CB	3:A:87:PHE:CZ	0.52	2.93	1	2
3:A:29:ILE:HG22	3:A:30:CYS:N	0.52	2.19	11	5
1:B:256:DA:C2'	1:B:257:DT:O5'	0.52	2.58	20	4
2:C:357:DA:N6	3:A:53:HIS:NE2	0.52	2.58	7	3
3:A:44:PHE:CZ	3:A:47:TRP:HB3	0.52	2.40	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:48:GLN:CD	3:A:49:ASN:OD1	0.51	2.53	10	6
3:A:13:THR:HB	3:A:87:PHE:CE1	0.51	2.40	20	1
3:A:8:TYR:O	3:A:12:ILE:CD1	0.51	2.58	14	5
3:A:44:PHE:CE1	3:A:47:TRP:CG	0.51	2.98	19	1
3:A:48:GLN:NE2	3:A:48:GLN:C	0.51	2.68	6	1
3:A:46:ALA:O	3:A:50:SER:CB	0.51	2.57	14	3
3:A:83:SER:O	3:A:87:PHE:CD2	0.51	2.63	7	2
1:B:250:DC:H5''	1:B:250:DC:C6	0.51	2.41	19	1
3:A:41:ARG:HA	3:A:44:PHE:CD1	0.51	2.40	19	1
3:A:13:THR:O	3:A:16:ILE:HG22	0.51	2.06	19	2
3:A:11:LEU:HD22	3:A:37:PHE:HE2	0.51	1.63	3	1
3:A:8:TYR:O	3:A:11:LEU:N	0.51	2.44	11	7
3:A:7:SER:O	3:A:11:LEU:HD23	0.51	2.06	11	1
1:B:257:DT:C7	3:A:54:ASN:OD1	0.51	2.58	14	1
3:A:63:LYS:HD3	3:A:77:TRP:CZ3	0.51	2.40	20	1
3:A:16:ILE:HD12	3:A:24:LEU:CD2	0.51	2.23	14	1
3:A:11:LEU:HD11	3:A:37:PHE:CE1	0.51	2.40	18	2
2:C:355:DT:C2	2:C:356:DT:C5	0.51	2.99	7	5
3:A:12:ILE:HD13	3:A:12:ILE:N	0.51	2.19	11	1
1:B:256:DA:OP2	3:A:7:SER:HA	0.51	2.06	14	1
1:B:255:DA:C1'	1:B:256:DA:OP2	0.51	2.58	19	1
2:C:354:DG:C2'	2:C:355:DT:H71	0.51	2.36	11	11
1:B:259:DA:H4'	1:B:260:DC:OP1	0.51	2.04	4	2
3:A:8:TYR:CE2	3:A:51:ILE:HB	0.51	2.40	6	1
3:A:12:ILE:CG2	3:A:55:LEU:HD23	0.51	2.36	13	1
3:A:63:LYS:HE3	3:A:77:TRP:CH2	0.51	2.40	19	2
1:B:258:DA:C2'	1:B:259:DA:O5'	0.51	2.59	18	1
1:B:257:DT:N3	1:B:258:DA:C5	0.50	2.79	20	4
1:B:264:DA:C2'	1:B:265:DC:O5'	0.50	2.60	15	3
2:C:360:DT:H2'	2:C:361:DT:H72	0.50	1.82	15	1
3:A:44:PHE:CZ	3:A:47:TRP:CZ2	0.50	2.98	16	1
3:A:39:TYR:CD1	3:A:39:TYR:O	0.50	2.64	1	2
3:A:69:GLY:C	3:A:70:ASN:OD1	0.50	2.54	16	2
3:A:71:PRO:O	3:A:73:LYS:N	0.50	2.45	12	3
3:A:26:LEU:HB2	3:A:77:TRP:CZ2	0.50	2.40	15	2
3:A:56:SER:OG	3:A:57:LEU:HD22	0.50	2.06	3	1
1:B:249:DG:H4'	1:B:250:DC:C5'	0.50	2.35	4	4
3:A:24:LEU:C	3:A:25:THR:HG23	0.50	2.32	17	2
1:B:255:DA:H1'	1:B:256:DA:O5'	0.50	2.05	13	4
1:B:250:DC:C6	1:B:251:DT:H72	0.50	2.42	7	12
1:B:259:DA:C2'	1:B:260:DC:O5'	0.50	2.59	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:44:PHE:CD1	3:A:47:TRP:HB3	0.50	2.41	4	1
3:A:32:PHE:O	3:A:32:PHE:CD1	0.50	2.64	5	4
3:A:44:PHE:CD1	3:A:47:TRP:CB	0.50	2.95	19	1
3:A:24:LEU:CD1	3:A:29:ILE:HD11	0.50	2.36	3	1
3:A:79:LEU:HD22	3:A:83:SER:HB2	0.50	1.81	10	1
3:A:24:LEU:HB2	3:A:29:ILE:HD11	0.50	1.82	20	1
3:A:15:ALA:O	3:A:18:GLN:HG3	0.50	2.06	14	8
3:A:48:GLN:O	3:A:52:ARG:HB2	0.50	2.07	12	4
3:A:43:LYS:O	3:A:45:PRO:CD	0.50	2.60	17	1
3:A:44:PHE:CE1	3:A:47:TRP:HB3	0.50	2.42	19	1
3:A:10:ALA:O	3:A:13:THR:OG1	0.50	2.25	6	8
3:A:8:TYR:C	3:A:10:ALA:N	0.50	2.70	4	4
2:C:363:DA:O4'	2:C:363:DA:O3'	0.50	2.25	9	1
3:A:63:LYS:HE3	3:A:77:TRP:CZ3	0.50	2.42	19	1
3:A:21:GLN:O	3:A:22:LYS:HB2	0.50	2.07	3	3
3:A:55:LEU:C	3:A:61:PHE:CZ	0.50	2.90	17	9
1:B:249:DG:H2''	1:B:250:DC:C5'	0.50	2.36	19	1
2:C:359:DT:C2'	2:C:360:DT:H72	0.50	2.37	18	2
3:A:8:TYR:CE2	3:A:12:ILE:CD1	0.50	2.94	6	1
3:A:40:TYR:CE2	3:A:47:TRP:CH2	0.50	2.99	7	2
2:C:354:DG:C2	2:C:355:DT:C4	0.49	3.00	4	1
3:A:67:GLU:HG3	3:A:76:TYR:CE2	0.49	2.41	12	1
3:A:40:TYR:O	3:A:47:TRP:NE1	0.49	2.45	13	1
2:C:353:DT:C2'	3:A:52:ARG:CZ	0.49	2.90	5	1
1:B:255:DA:C2'	1:B:256:DA:O5'	0.49	2.61	3	9
3:A:44:PHE:CG	3:A:47:TRP:HB3	0.49	2.42	4	1
1:B:258:DA:OP2	3:A:46:ALA:HB3	0.49	2.07	10	2
1:B:263:DT:C2'	1:B:264:DA:O5'	0.49	2.60	12	3
3:A:11:LEU:HD13	3:A:33:ILE:HG23	0.49	1.84	12	1
2:C:353:DT:OP1	3:A:74:GLY:N	0.49	2.45	13	1
3:A:70:ASN:CG	3:A:74:GLY:O	0.49	2.56	7	5
1:B:250:DC:H2'	1:B:251:DT:C7	0.49	2.38	7	3
1:B:256:DA:C2'	3:A:7:SER:OG	0.49	2.60	6	1
3:A:13:THR:OG1	3:A:87:PHE:CE1	0.49	2.59	11	1
2:C:355:DT:H71	3:A:52:ARG:HD3	0.49	1.83	19	1
3:A:51:ILE:O	3:A:55:LEU:CB	0.49	2.60	6	3
2:C:358:DT:C2'	2:C:359:DT:O5'	0.49	2.61	15	3
3:A:13:THR:HB	3:A:87:PHE:CZ	0.49	2.43	1	2
3:A:11:LEU:HD11	3:A:40:TYR:CE2	0.49	2.42	6	2
3:A:8:TYR:CE2	3:A:50:SER:HB2	0.49	2.43	7	1
1:B:258:DA:OP2	3:A:44:PHE:CE1	0.49	2.66	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:356:DT:C2	2:C:357:DA:N7	0.49	2.80	3	1
3:A:33:ILE:CG2	3:A:47:TRP:CH2	0.49	2.96	4	1
1:B:256:DA:OP2	3:A:9:ILE:CG2	0.49	2.61	6	1
1:B:254:DA:H1'	1:B:255:DA:H4'	0.49	1.84	15	3
3:A:12:ILE:HG21	3:A:55:LEU:HA	0.49	1.82	13	1
3:A:8:TYR:CD2	3:A:51:ILE:CG2	0.49	2.96	15	1
1:B:256:DA:H62	3:A:53:HIS:HE2	0.49	1.49	18	1
3:A:53:HIS:NE2	3:A:57:LEU:HD22	0.49	2.23	7	2
3:A:47:TRP:CE3	3:A:51:ILE:HD13	0.49	2.43	15	2
2:C:360:DT:H4'	2:C:361:DT:OP1	0.49	2.08	15	1
3:A:51:ILE:HG23	3:A:52:ARG:N	0.49	2.22	19	2
1:B:256:DA:P	3:A:7:SER:CB	0.49	3.01	6	1
3:A:11:LEU:HD13	3:A:14:MET:SD	0.49	2.48	11	1
3:A:16:ILE:CD1	3:A:55:LEU:HD11	0.49	2.37	17	1
1:B:257:DT:C7	3:A:53:HIS:CD2	0.49	2.96	1	2
3:A:37:PHE:CD2	3:A:40:TYR:CE2	0.49	3.01	1	3
3:A:19:SER:OG	3:A:24:LEU:CD1	0.49	2.61	19	2
1:B:256:DA:OP2	3:A:7:SER:OG	0.49	2.30	9	2
3:A:26:LEU:CD1	3:A:52:ARG:CZ	0.49	2.91	15	1
1:B:263:DT:H2''	1:B:264:DA:OP2	0.49	2.08	17	1
3:A:44:PHE:HB3	3:A:47:TRP:CD1	0.48	2.42	4	1
2:C:360:DT:C6	2:C:361:DT:H72	0.48	2.43	10	4
3:A:13:THR:HA	3:A:87:PHE:CZ	0.48	2.43	10	2
3:A:67:GLU:CB	3:A:68:PRO:HD3	0.48	2.38	2	1
3:A:12:ILE:O	3:A:15:ALA:N	0.48	2.46	11	7
3:A:32:PHE:O	3:A:36:ARG:CG	0.48	2.61	18	1
3:A:29:ILE:HD13	3:A:55:LEU:HD11	0.48	1.82	19	1
3:A:61:PHE:CE1	3:A:77:TRP:CZ3	0.48	3.01	13	4
3:A:61:PHE:C	3:A:61:PHE:HD1	0.48	2.16	2	1
3:A:36:ARG:HB3	3:A:37:PHE:CD1	0.48	2.43	6	1
3:A:52:ARG:NH2	3:A:56:SER:OG	0.48	2.46	10	1
2:C:355:DT:H73	3:A:52:ARG:NE	0.48	2.23	4	1
3:A:11:LEU:HD13	3:A:37:PHE:CE2	0.48	2.43	19	1
3:A:12:ILE:HD13	3:A:54:ASN:HB3	0.48	1.84	4	1
2:C:358:DT:H2'	2:C:359:DT:C7	0.48	2.38	15	4
3:A:47:TRP:C	3:A:51:ILE:HG23	0.48	2.32	6	1
3:A:24:LEU:HD12	3:A:29:ILE:CD1	0.48	2.38	7	1
3:A:39:TYR:CE1	3:A:40:TYR:CD1	0.48	3.01	11	1
3:A:13:THR:HG21	3:A:87:PHE:CG	0.48	2.43	14	1
2:C:352:DT:O5'	3:A:72:GLY:O	0.48	2.32	8	6
1:B:249:DG:C2'	1:B:250:DC:O5'	0.48	2.62	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:37:PHE:CG	3:A:40:TYR:CD2	0.48	3.02	1	3
3:A:45:PRO:HD2	3:A:47:TRP:CD1	0.48	2.44	1	3
3:A:8:TYR:OH	3:A:44:PHE:CE2	0.48	2.67	2	2
2:C:353:DT:O3'	3:A:64:ILE:O	0.48	2.31	8	1
2:C:354:DG:OP1	3:A:64:ILE:N	0.48	2.46	11	1
1:B:253:DA:H2''	1:B:254:DA:OP2	0.48	2.08	10	1
1:B:264:DA:C1'	1:B:265:DC:O5'	0.48	2.62	15	3
2:C:354:DG:N9	2:C:355:DT:H71	0.48	2.23	11	1
3:A:26:LEU:HD23	3:A:26:LEU:O	0.48	2.08	11	1
3:A:9:ILE:HD12	3:A:10:ALA:N	0.48	2.23	12	2
3:A:70:ASN:N	3:A:70:ASN:OD1	0.48	2.46	1	2
1:B:256:DA:N6	3:A:53:HIS:CE1	0.48	2.82	5	3
2:C:360:DT:H2''	2:C:361:DT:H71	0.48	1.85	2	1
3:A:24:LEU:O	3:A:25:THR:CG2	0.48	2.62	4	2
3:A:14:MET:O	3:A:18:GLN:CG	0.48	2.62	7	2
3:A:33:ILE:O	3:A:36:ARG:N	0.48	2.42	15	2
3:A:82:GLN:O	3:A:86:MET:CB	0.48	2.62	10	1
3:A:24:LEU:N	3:A:24:LEU:HD23	0.48	2.24	14	2
3:A:63:LYS:CE	3:A:77:TRP:CH2	0.48	2.97	19	1
3:A:63:LYS:HG2	3:A:77:TRP:CD2	0.48	2.44	9	5
3:A:64:ILE:CG1	3:A:76:TYR:O	0.48	2.62	19	2
3:A:65:PRO:O	3:A:67:GLU:OE1	0.48	2.30	4	1
3:A:86:MET:HE3	3:A:87:PHE:CE2	0.48	2.43	5	1
3:A:8:TYR:CE1	3:A:33:ILE:HG13	0.48	2.44	6	1
3:A:11:LEU:HD13	3:A:33:ILE:HD12	0.48	1.86	12	1
1:B:249:DG:C1'	1:B:250:DC:OP1	0.47	2.62	1	3
2:C:349:DG:H2''	2:C:350:DT:OP2	0.47	2.10	12	14
3:A:18:GLN:O	3:A:20:PRO:HD3	0.47	2.09	9	2
3:A:14:MET:HE2	3:A:32:PHE:HZ	0.47	1.65	17	2
3:A:62:VAL:O	3:A:78:THR:O	0.47	2.33	4	6
1:B:257:DT:O4	3:A:53:HIS:ND1	0.47	2.47	13	5
3:A:8:TYR:CZ	3:A:51:ILE:HB	0.47	2.43	6	1
3:A:59:ASP:OD1	3:A:79:LEU:CD1	0.47	2.62	12	2
2:C:349:DG:C8	2:C:350:DT:H72	0.47	2.44	12	3
3:A:11:LEU:CD1	3:A:37:PHE:CE2	0.47	2.97	11	1
2:C:359:DT:C2'	2:C:360:DT:O5'	0.47	2.62	17	1
3:A:32:PHE:CE1	3:A:33:ILE:HG13	0.47	2.44	19	1
3:A:48:GLN:OE1	3:A:49:ASN:OD1	0.47	2.32	2	6
3:A:8:TYR:O	3:A:9:ILE:C	0.47	2.58	18	9
3:A:8:TYR:CE2	3:A:51:ILE:HG23	0.47	2.44	5	1
3:A:44:PHE:CD2	3:A:47:TRP:HB2	0.47	2.44	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:13:THR:O	3:A:17:LEU:CD1	0.47	2.62	9	1
3:A:63:LYS:HB3	3:A:77:TRP:CE2	0.47	2.44	14	2
3:A:79:LEU:C	3:A:79:LEU:HD23	0.47	2.34	1	1
2:C:352:DT:H2'	2:C:353:DT:C7	0.47	2.38	2	2
2:C:359:DT:C2'	2:C:360:DT:C7	0.47	2.93	18	2
3:A:18:GLN:C	3:A:20:PRO:HD3	0.47	2.34	17	10
3:A:13:THR:HG22	3:A:87:PHE:CE1	0.47	2.44	15	1
3:A:52:ARG:CD	3:A:52:ARG:O	0.47	2.63	17	1
3:A:8:TYR:O	3:A:12:ILE:HB	0.47	2.09	8	1
1:B:250:DC:H2''	1:B:251:DT:OP2	0.47	2.07	16	2
2:C:358:DT:C6	2:C:359:DT:H72	0.47	2.45	19	1
1:B:258:DA:C2	2:C:357:DA:N1	0.47	2.82	11	3
3:A:15:ALA:CB	3:A:32:PHE:CE2	0.47	2.97	1	1
1:B:258:DA:N6	2:C:357:DA:N6	0.47	2.62	3	1
3:A:13:THR:HG22	3:A:87:PHE:CZ	0.47	2.45	4	2
3:A:24:LEU:HD12	3:A:29:ILE:CG1	0.47	2.39	14	1
3:A:48:GLN:HG2	3:A:52:ARG:CZ	0.47	2.40	7	4
1:B:256:DA:N6	3:A:53:HIS:NE2	0.47	2.62	4	2
3:A:11:LEU:HG	3:A:37:PHE:CE1	0.47	2.45	4	1
3:A:52:ARG:O	3:A:52:ARG:HD2	0.47	2.09	10	4
3:A:18:GLN:C	3:A:18:GLN:OE1	0.47	2.58	9	2
3:A:75:ASN:OD1	3:A:75:ASN:C	0.47	2.57	8	1
3:A:11:LEU:O	3:A:14:MET:CG	0.47	2.62	11	2
1:B:257:DT:C2'	1:B:258:DA:OP2	0.47	2.62	13	1
3:A:8:TYR:CD2	3:A:51:ILE:HG22	0.47	2.44	15	1
3:A:8:TYR:HB2	3:A:54:ASN:CG	0.47	2.35	7	2
3:A:36:ARG:HB3	3:A:37:PHE:CE1	0.47	2.44	6	3
1:B:256:DA:H2''	1:B:257:DT:O5'	0.47	2.10	20	3
3:A:40:TYR:O	3:A:44:PHE:CB	0.47	2.62	10	1
3:A:15:ALA:HB1	3:A:29:ILE:HG13	0.47	1.87	18	1
3:A:15:ALA:HB2	3:A:32:PHE:CE1	0.47	2.45	19	1
2:C:356:DT:H72	3:A:52:ARG:NH2	0.47	2.25	4	1
3:A:47:TRP:O	3:A:48:GLN:C	0.47	2.57	5	1
3:A:75:ASN:ND2	3:A:77:TRP:NE1	0.47	2.63	11	2
3:A:13:THR:HG21	3:A:87:PHE:HE1	0.47	1.62	12	1
3:A:81:PRO:O	3:A:82:GLN:CB	0.47	2.63	6	8
3:A:8:TYR:OH	3:A:44:PHE:CZ	0.47	2.66	10	1
3:A:9:ILE:HG13	3:A:10:ALA:N	0.47	2.24	13	2
3:A:67:GLU:CB	3:A:68:PRO:CD	0.46	2.93	7	1
3:A:32:PHE:CE1	3:A:36:ARG:HG3	0.46	2.45	9	2
1:B:256:DA:OP2	3:A:7:SER:HB2	0.46	2.10	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:19:SER:CB	3:A:23:LYS:O	0.46	2.63	11	1
3:A:70:ASN:N	3:A:70:ASN:HD22	0.46	2.08	14	1
1:B:256:DA:C1'	1:B:257:DT:O5'	0.46	2.64	10	4
3:A:12:ILE:HG23	3:A:16:ILE:HD13	0.46	1.86	8	1
3:A:21:GLN:O	3:A:22:LYS:CB	0.46	2.63	17	1
3:A:46:ALA:O	3:A:50:SER:OG	0.46	2.32	20	1
3:A:7:SER:OG	3:A:8:TYR:N	0.46	2.49	12	2
3:A:40:TYR:CE2	3:A:47:TRP:CZ2	0.46	3.03	7	1
3:A:24:LEU:O	3:A:77:TRP:O	0.46	2.33	9	2
1:B:261:DA:C2'	1:B:262:DA:O5'	0.46	2.63	12	1
2:C:359:DT:H1'	2:C:360:DT:C5'	0.46	2.40	15	1
3:A:9:ILE:HG22	3:A:54:ASN:CG	0.46	2.35	20	1
1:B:254:DA:H2''	1:B:255:DA:O5'	0.46	2.11	4	11
3:A:57:LEU:O	3:A:58:ASN:ND2	0.46	2.48	1	6
2:C:352:DT:C2'	2:C:353:DT:O5'	0.46	2.64	8	2
2:C:359:DT:C2	2:C:360:DT:C5	0.46	3.03	2	3
3:A:26:LEU:HD11	3:A:51:ILE:HD11	0.46	1.88	6	1
3:A:11:LEU:HB3	3:A:33:ILE:HD11	0.46	1.87	7	1
1:B:262:DA:H2'	1:B:263:DT:H72	0.46	1.87	12	1
2:C:358:DT:C2'	2:C:359:DT:C7	0.46	2.94	2	2
3:A:48:GLN:NE2	3:A:49:ASN:OD1	0.46	2.49	4	4
1:B:253:DA:C2'	1:B:254:DA:O5'	0.46	2.62	19	2
3:A:8:TYR:OH	3:A:47:TRP:NE1	0.46	2.48	10	1
3:A:15:ALA:O	3:A:18:GLN:CB	0.46	2.63	11	1
3:A:59:ASP:O	3:A:60:CYS:SG	0.46	2.74	11	1
3:A:47:TRP:C	3:A:49:ASN:N	0.46	2.72	5	1
3:A:76:TYR:C	3:A:77:TRP:HD1	0.46	2.18	18	2
3:A:11:LEU:CD1	3:A:37:PHE:CE1	0.46	2.99	18	2
3:A:26:LEU:HG	3:A:27:SER:N	0.46	2.26	1	4
2:C:360:DT:C2'	2:C:361:DT:H71	0.46	2.41	2	2
3:A:44:PHE:C	3:A:46:ALA:H	0.46	2.19	8	5
2:C:354:DG:C4	2:C:355:DT:C7	0.46	2.99	11	2
2:C:352:DT:O4'	3:A:66:ARG:CD	0.46	2.63	9	1
3:A:16:ILE:HG13	3:A:24:LEU:HD11	0.46	1.86	4	1
1:B:257:DT:H3'	3:A:44:PHE:CZ	0.46	2.46	10	1
3:A:32:PHE:CE1	3:A:33:ILE:CD1	0.46	2.99	11	1
3:A:64:ILE:HB	3:A:76:TYR:O	0.46	2.11	11	1
1:B:254:DA:C4'	1:B:255:DA:OP1	0.46	2.64	13	2
1:B:254:DA:C2'	1:B:255:DA:OP2	0.46	2.63	17	1
3:A:33:ILE:HG23	3:A:37:PHE:CD2	0.46	2.46	19	1
2:C:352:DT:O3'	3:A:73:LYS:HA	0.45	2.11	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:24:LEU:C	3:A:25:THR:CG2	0.45	2.89	17	2
1:B:257:DT:H72	3:A:50:SER:HA	0.45	1.87	6	2
3:A:9:ILE:HD13	3:A:9:ILE:O	0.45	2.11	7	1
3:A:8:TYR:O	3:A:12:ILE:HG12	0.45	2.11	8	2
3:A:8:TYR:HA	3:A:11:LEU:CG	0.45	2.41	8	1
1:B:257:DT:OP2	3:A:8:TYR:CE2	0.45	2.69	11	2
3:A:39:TYR:CG	3:A:40:TYR:N	0.45	2.84	2	1
3:A:47:TRP:O	3:A:49:ASN:N	0.45	2.50	5	1
2:C:357:DA:H62	3:A:53:HIS:CD2	0.45	2.28	7	5
3:A:52:ARG:HG2	3:A:77:TRP:CH2	0.45	2.45	13	1
1:B:258:DA:N7	3:A:49:ASN:OD1	0.45	2.49	14	2
3:A:32:PHE:CD1	3:A:33:ILE:HG13	0.45	2.46	19	1
3:A:25:THR:HG23	3:A:75:ASN:OD1	0.45	2.11	6	1
1:B:249:DG:O5'	1:B:249:DG:O3'	0.45	2.34	7	1
3:A:49:ASN:O	3:A:53:HIS:N	0.45	2.49	9	2
1:B:264:DA:H5'	3:A:66:ARG:CZ	0.45	2.41	16	1
1:B:258:DA:OP2	3:A:46:ALA:CB	0.45	2.64	19	1
1:B:249:DG:H4'	1:B:250:DC:OP1	0.45	2.11	5	3
2:C:357:DA:H2'	2:C:358:DT:C7	0.45	2.41	3	3
3:A:16:ILE:HD13	3:A:24:LEU:HD21	0.45	1.88	7	1
3:A:63:LYS:HB3	3:A:77:TRP:CD2	0.45	2.46	14	1
3:A:13:THR:HG22	3:A:17:LEU:HD22	0.45	1.88	2	1
3:A:25:THR:HG22	3:A:75:ASN:O	0.45	2.12	12	1
3:A:12:ILE:CG1	3:A:55:LEU:HD13	0.45	2.41	17	1
3:A:41:ARG:O	3:A:41:ARG:NH1	0.45	2.49	3	1
2:C:355:DT:H2'	2:C:356:DT:C7	0.45	2.42	8	2
3:A:11:LEU:HD11	3:A:37:PHE:CZ	0.45	2.47	20	2
1:B:251:DT:C6	1:B:252:DT:H72	0.45	2.47	13	7
2:C:357:DA:C2'	2:C:358:DT:O5'	0.45	2.65	3	1
1:B:257:DT:C7	3:A:50:SER:HA	0.45	2.42	5	1
3:A:83:SER:CA	3:A:86:MET:HE2	0.45	2.40	6	1
3:A:9:ILE:HD12	3:A:9:ILE:C	0.45	2.37	12	1
1:B:258:DA:C2	1:B:259:DA:C6	0.45	3.05	14	1
3:A:26:LEU:CD1	3:A:52:ARG:NH2	0.45	2.75	15	1
2:C:359:DT:C6	2:C:360:DT:H72	0.45	2.47	14	3
3:A:70:ASN:N	3:A:71:PRO:HD3	0.45	2.27	19	1
3:A:65:PRO:HB2	3:A:66:ARG:NH2	0.44	2.27	3	1
3:A:32:PHE:CD1	3:A:32:PHE:O	0.44	2.71	2	1
3:A:11:LEU:HD21	3:A:37:PHE:CE2	0.44	2.46	12	1
3:A:25:THR:O	3:A:26:LEU:C	0.44	2.59	17	3
2:C:355:DT:C7	3:A:52:ARG:HD3	0.44	2.43	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:64:ILE:HD12	3:A:65:PRO:O	0.44	2.13	19	1
3:A:55:LEU:O	3:A:55:LEU:HD12	0.44	2.12	2	1
1:B:250:DC:C2'	1:B:251:DT:O5'	0.44	2.65	17	3
2:C:354:DG:OP2	3:A:52:ARG:HD3	0.44	2.12	14	1
3:A:44:PHE:CE1	3:A:47:TRP:NE1	0.44	2.86	16	1
3:A:44:PHE:CE1	3:A:47:TRP:CD1	0.44	3.05	16	1
1:B:256:DA:OP2	3:A:7:SER:CA	0.44	2.65	1	2
1:B:255:DA:C4'	1:B:256:DA:OP1	0.44	2.64	9	2
2:C:354:DG:C5'	3:A:65:PRO:HB3	0.44	2.42	16	2
3:A:26:LEU:C	3:A:26:LEU:HD12	0.44	2.38	20	2
1:B:256:DA:H2''	1:B:257:DT:OP2	0.44	2.12	14	1
3:A:49:ASN:O	3:A:53:HIS:HB3	0.44	2.12	16	1
3:A:51:ILE:HG23	3:A:52:ARG:H	0.44	1.72	16	1
2:C:358:DT:C2'	2:C:359:DT:H72	0.44	2.43	2	2
2:C:354:DG:OP1	3:A:64:ILE:O	0.44	2.35	8	5
3:A:48:GLN:CG	3:A:52:ARG:CZ	0.44	2.96	6	1
2:C:352:DT:C5'	3:A:72:GLY:O	0.44	2.66	8	1
3:A:70:ASN:ND2	3:A:70:ASN:N	0.44	2.65	13	1
3:A:24:LEU:C	3:A:25:THR:HG1	0.44	2.20	19	1
1:B:249:DG:H4'	1:B:250:DC:H5''	0.44	1.90	12	2
3:A:51:ILE:HD13	3:A:51:ILE:C	0.44	2.38	8	1
1:B:256:DA:C8	1:B:257:DT:H71	0.44	2.48	10	1
3:A:11:LEU:O	3:A:14:MET:HG2	0.44	2.13	19	1
3:A:9:ILE:C	3:A:9:ILE:CD1	0.44	2.89	20	1
2:C:354:DG:OP1	3:A:64:ILE:C	0.44	2.60	8	2
3:A:24:LEU:HD22	3:A:29:ILE:HD11	0.44	1.89	4	1
2:C:354:DG:OP1	3:A:77:TRP:CE2	0.44	2.70	14	1
2:C:359:DT:C1'	2:C:360:DT:O5'	0.44	2.66	17	1
3:A:19:SER:OG	3:A:23:LYS:O	0.44	2.33	11	1
3:A:80:ASP:CG	3:A:81:PRO:HD2	0.43	2.38	6	2
3:A:65:PRO:HB2	3:A:66:ARG:CZ	0.43	2.43	5	1
3:A:12:ILE:CD1	3:A:55:LEU:HD22	0.43	2.42	8	1
3:A:37:PHE:HB3	3:A:40:TYR:CG	0.43	2.49	11	1
3:A:61:PHE:CD1	3:A:61:PHE:N	0.43	2.82	16	1
3:A:53:HIS:ND1	3:A:54:ASN:N	0.43	2.66	20	1
1:B:262:DA:H2'	1:B:263:DT:H71	0.43	1.89	11	1
3:A:37:PHE:HB2	3:A:40:TYR:HB2	0.43	1.89	14	1
3:A:46:ALA:O	3:A:50:SER:HB3	0.43	2.13	14	1
1:B:249:DG:C4	1:B:250:DC:C5	0.43	3.06	18	1
3:A:8:TYR:O	3:A:10:ALA:N	0.43	2.51	5	2
1:B:250:DC:H2''	1:B:251:DT:C7	0.43	2.43	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:29:ILE:CG2	3:A:30:CYS:N	0.43	2.80	11	1
3:A:13:THR:O	3:A:17:LEU:CD2	0.43	2.59	16	1
3:A:16:ILE:HG12	3:A:79:LEU:CD1	0.43	2.43	17	1
1:B:259:DA:H1'	1:B:260:DC:O5'	0.43	2.13	4	1
3:A:14:MET:HE3	3:A:32:PHE:HZ	0.43	1.72	6	1
3:A:11:LEU:HD11	3:A:37:PHE:HE2	0.43	1.72	12	1
1:B:251:DT:C2'	1:B:252:DT:H72	0.43	2.44	13	1
3:A:12:ILE:CD1	3:A:51:ILE:CD1	0.43	2.95	16	1
3:A:9:ILE:CD1	3:A:58:ASN:OD1	0.43	2.62	18	1
3:A:52:ARG:NE	3:A:52:ARG:O	0.43	2.51	4	1
3:A:8:TYR:HE2	3:A:51:ILE:HG23	0.43	1.73	5	1
3:A:52:ARG:HG3	3:A:77:TRP:CH2	0.43	2.49	6	1
3:A:22:LYS:O	3:A:22:LYS:CG	0.43	2.65	9	1
3:A:38:PRO:O	3:A:41:ARG:CG	0.43	2.67	14	1
3:A:52:ARG:CZ	3:A:56:SER:HB3	0.43	2.43	17	1
3:A:47:TRP:O	3:A:51:ILE:HB	0.43	2.14	18	1
3:A:37:PHE:CD2	3:A:40:TYR:CD2	0.43	3.06	1	1
3:A:64:ILE:HG12	3:A:76:TYR:HB2	0.43	1.89	1	1
3:A:11:LEU:HD23	3:A:33:ILE:HG23	0.43	1.90	4	1
3:A:8:TYR:CG	3:A:51:ILE:HG22	0.43	2.49	15	1
2:C:352:DT:C2'	2:C:353:DT:H72	0.43	2.43	16	1
3:A:13:THR:O	3:A:17:LEU:HD13	0.43	2.14	18	1
2:C:351:DA:C2'	2:C:352:DT:C7	0.43	2.96	2	1
3:A:75:ASN:HD21	3:A:77:TRP:CD1	0.43	2.32	11	2
3:A:16:ILE:CG2	3:A:79:LEU:HD13	0.43	2.35	9	1
3:A:13:THR:HG21	3:A:87:PHE:CD2	0.43	2.49	13	1
3:A:9:ILE:HG22	3:A:58:ASN:CG	0.43	2.39	14	1
1:B:263:DT:H4'	1:B:264:DA:OP1	0.43	2.14	11	1
2:C:359:DT:H2'	2:C:360:DT:C7	0.43	2.44	13	1
2:C:353:DT:H2''	2:C:354:DG:OP2	0.43	2.13	14	1
3:A:53:HIS:O	3:A:57:LEU:HB2	0.43	2.14	4	2
3:A:16:ILE:HD13	3:A:24:LEU:CD1	0.43	2.43	9	1
3:A:25:THR:CG2	3:A:75:ASN:CG	0.43	2.92	16	1
3:A:11:LEU:HD13	3:A:37:PHE:CZ	0.43	2.48	19	1
3:A:70:ASN:ND2	3:A:74:GLY:O	0.43	2.52	5	2
1:B:256:DA:H4'	1:B:257:DT:OP1	0.43	2.14	13	1
3:A:43:LYS:O	3:A:45:PRO:HD3	0.43	2.14	16	1
1:B:250:DC:C2'	1:B:251:DT:C7	0.43	2.96	19	1
3:A:34:SER:CB	3:A:41:ARG:HB3	0.43	2.43	19	1
3:A:24:LEU:HD11	3:A:29:ILE:CD1	0.42	2.43	1	1
3:A:55:LEU:HD12	3:A:55:LEU:C	0.42	2.38	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:8:TYR:CD1	3:A:47:TRP:CH2	0.42	3.07	5	1
3:A:16:ILE:CD1	3:A:24:LEU:CD2	0.42	2.97	9	1
2:C:354:DG:H2''	3:A:52:ARG:NH1	0.42	2.28	16	1
1:B:249:DG:H1'	1:B:250:DC:C6	0.42	2.49	18	1
3:A:17:LEU:HD11	3:A:84:GLU:HB2	0.42	1.91	19	1
2:C:355:DT:C7	3:A:52:ARG:NE	0.42	2.82	4	1
3:A:19:SER:C	3:A:21:GLN:H	0.42	2.22	5	2
3:A:12:ILE:HG23	3:A:55:LEU:CD1	0.42	2.44	9	1
3:A:13:THR:HB	3:A:87:PHE:CE2	0.42	2.50	9	1
3:A:64:ILE:HD12	3:A:67:GLU:OE1	0.42	2.14	9	1
1:B:257:DT:O2	1:B:258:DA:N9	0.42	2.51	10	1
3:A:8:TYR:CD2	3:A:51:ILE:HD12	0.42	2.49	10	1
3:A:47:TRP:HA	3:A:47:TRP:CE3	0.42	2.49	13	1
2:C:352:DT:O2	3:A:66:ARG:HG3	0.42	2.13	4	1
3:A:55:LEU:HD12	3:A:61:PHE:CZ	0.42	2.49	6	1
3:A:64:ILE:HG21	3:A:76:TYR:HD1	0.42	1.75	6	1
1:B:255:DA:O4'	1:B:256:DA:OP1	0.42	2.37	7	1
3:A:15:ALA:O	3:A:18:GLN:HG2	0.42	2.14	11	2
1:B:257:DT:H1'	1:B:258:DA:C8	0.42	2.49	13	1
2:C:360:DT:C1'	2:C:361:DT:O5'	0.42	2.68	15	1
3:A:12:ILE:N	3:A:12:ILE:HD13	0.42	2.29	16	1
3:A:62:VAL:C	3:A:63:LYS:HG3	0.42	2.39	3	1
2:C:354:DG:N3	2:C:355:DT:C5	0.42	2.87	4	1
3:A:11:LEU:CD2	3:A:33:ILE:HG23	0.42	2.42	5	1
3:A:11:LEU:N	3:A:11:LEU:HD22	0.42	2.29	7	1
1:B:257:DT:C1'	1:B:258:DA:O5'	0.42	2.67	11	1
3:A:17:LEU:O	3:A:18:GLN:C	0.42	2.61	13	1
3:A:83:SER:O	3:A:86:MET:CG	0.42	2.68	20	1
1:B:265:DC:OP1	3:A:67:GLU:O	0.42	2.37	2	1
2:C:355:DT:C2'	2:C:356:DT:H71	0.42	2.45	9	1
1:B:263:DT:C1'	1:B:264:DA:O5'	0.42	2.68	11	1
3:A:81:PRO:O	3:A:82:GLN:CG	0.42	2.67	12	1
3:A:48:GLN:HE21	3:A:48:GLN:C	0.42	2.22	16	1
3:A:8:TYR:CE2	3:A:51:ILE:HG12	0.42	2.50	5	1
3:A:13:THR:OG1	3:A:87:PHE:CZ	0.42	2.72	5	1
3:A:17:LEU:CD2	3:A:87:PHE:CE2	0.42	3.03	10	1
3:A:86:MET:C	3:A:86:MET:SD	0.42	3.02	13	1
2:C:356:DT:H73	3:A:52:ARG:NH2	0.42	2.28	17	1
3:A:44:PHE:CG	3:A:47:TRP:HB2	0.42	2.50	19	1
3:A:12:ILE:O	3:A:13:THR:C	0.42	2.61	3	5
3:A:9:ILE:HD13	3:A:58:ASN:OD1	0.42	2.15	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:8:TYR:CD2	3:A:12:ILE:CG1	0.42	3.02	6	1
3:A:34:SER:O	3:A:37:PHE:C	0.42	2.62	8	1
3:A:40:TYR:O	3:A:47:TRP:CD1	0.42	2.72	13	1
1:B:258:DA:C4	1:B:259:DA:N7	0.42	2.88	14	1
2:C:359:DT:H2''	2:C:360:DT:O5'	0.42	2.15	17	1
3:A:57:LEU:O	3:A:58:ASN:HB2	0.42	2.13	17	2
3:A:75:ASN:O	3:A:76:TYR:CG	0.42	2.72	19	1
3:A:40:TYR:HB3	3:A:47:TRP:CH2	0.42	2.50	20	1
3:A:44:PHE:CD2	3:A:47:TRP:CD1	0.42	3.07	6	1
1:B:257:DT:O4	3:A:53:HIS:NE2	0.42	2.52	20	1
3:A:53:HIS:C	3:A:55:LEU:N	0.42	2.76	20	1
3:A:44:PHE:CE2	3:A:47:TRP:HB3	0.42	2.50	2	1
1:B:257:DT:H72	3:A:50:SER:O	0.42	2.14	14	2
3:A:11:LEU:CD1	3:A:40:TYR:CE2	0.42	3.03	6	1
3:A:48:GLN:O	3:A:52:ARG:HB3	0.42	2.15	10	1
1:B:258:DA:C4'	1:B:259:DA:OP1	0.42	2.67	13	1
2:C:355:DT:H72	3:A:52:ARG:HD3	0.42	1.92	17	1
3:A:22:LYS:CD	3:A:79:LEU:O	0.42	2.67	19	1
3:A:12:ILE:CD1	3:A:55:LEU:HG	0.42	2.45	5	1
3:A:34:SER:O	3:A:37:PHE:O	0.42	2.37	6	2
2:C:355:DT:C2'	2:C:356:DT:O5'	0.42	2.68	10	1
3:A:19:SER:OG	3:A:24:LEU:HD11	0.41	2.14	19	2
3:A:62:VAL:CG2	3:A:78:THR:HB	0.41	2.45	4	1
3:A:8:TYR:CZ	3:A:33:ILE:HG13	0.41	2.50	6	1
3:A:52:ARG:NH2	3:A:56:SER:HB3	0.41	2.30	16	2
3:A:47:TRP:HZ3	3:A:51:ILE:HD13	0.41	1.69	19	1
3:A:67:GLU:O	3:A:70:ASN:OD1	0.41	2.37	4	2
2:C:353:DT:H2'	3:A:52:ARG:NH2	0.41	2.30	5	1
2:C:353:DT:H2''	3:A:52:ARG:CZ	0.41	2.44	5	1
3:A:52:ARG:O	3:A:52:ARG:CD	0.41	2.69	10	1
2:C:354:DG:OP1	3:A:77:TRP:CZ2	0.41	2.73	14	1
3:A:47:TRP:CD1	3:A:47:TRP:H	0.41	2.33	17	1
1:B:258:DA:N7	3:A:49:ASN:HB2	0.41	2.30	18	1
1:B:256:DA:C4	1:B:257:DT:C5	0.41	3.09	19	1
2:C:351:DA:C4	2:C:352:DT:C4	0.41	3.08	2	1
2:C:353:DT:O3'	3:A:65:PRO:HA	0.41	2.14	12	2
3:A:67:GLU:CD	3:A:67:GLU:C	0.41	2.87	3	1
3:A:25:THR:O	3:A:29:ILE:N	0.41	2.49	4	2
3:A:50:SER:O	3:A:54:ASN:OD1	0.41	2.38	19	3
3:A:26:LEU:C	3:A:26:LEU:HD23	0.41	2.40	11	1
2:C:353:DT:OP1	3:A:73:LYS:C	0.41	2.63	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:12:ILE:HG22	3:A:13:THR:N	0.41	2.31	1	1
1:B:251:DT:H2'	1:B:252:DT:H72	0.41	1.92	6	1
1:B:257:DT:H2''	1:B:258:DA:O5'	0.41	2.14	11	1
1:B:262:DA:H2''	1:B:263:DT:H71	0.41	1.90	11	1
3:A:37:PHE:HB3	3:A:39:TYR:CE1	0.41	2.50	14	1
3:A:39:TYR:HE2	3:A:40:TYR:CE1	0.41	2.33	14	1
1:B:256:DA:P	3:A:7:SER:HB2	0.41	2.56	15	1
3:A:33:ILE:HD13	3:A:51:ILE:HD13	0.41	1.92	16	1
3:A:55:LEU:O	3:A:59:ASP:CG	0.41	2.63	17	1
1:B:256:DA:OP2	3:A:7:SER:HB3	0.41	2.15	20	2
3:A:12:ILE:HG23	3:A:55:LEU:CD2	0.41	2.44	12	1
3:A:14:MET:O	3:A:18:GLN:CB	0.41	2.68	15	1
1:B:255:DA:OP2	1:B:255:DA:C4'	0.41	2.69	17	1
3:A:55:LEU:HG	3:A:61:PHE:CZ	0.41	2.51	17	1
2:C:352:DT:C2'	2:C:353:DT:H71	0.41	2.45	3	1
3:A:16:ILE:HD13	3:A:24:LEU:HD11	0.41	1.93	5	1
3:A:67:GLU:CG	3:A:68:PRO:HD2	0.41	2.45	11	1
1:B:261:DA:H4'	1:B:262:DA:OP1	0.41	2.15	12	1
3:A:17:LEU:C	3:A:19:SER:N	0.41	2.76	1	1
3:A:44:PHE:CG	3:A:47:TRP:CD1	0.41	3.09	10	1
1:B:261:DA:H3'	1:B:261:DA:OP2	0.41	2.16	12	1
3:A:44:PHE:CD1	3:A:47:TRP:CG	0.41	3.08	19	1
3:A:47:TRP:HA	3:A:51:ILE:HD13	0.41	1.92	20	1
3:A:43:LYS:C	3:A:45:PRO:CD	0.41	2.91	6	1
3:A:12:ILE:HG23	3:A:55:LEU:HD12	0.41	1.93	10	1
3:A:86:MET:CE	3:A:87:PHE:CE2	0.41	3.03	11	1
3:A:59:ASP:OD1	3:A:79:LEU:HD11	0.41	2.15	12	1
3:A:21:GLN:O	3:A:22:LYS:HG3	0.41	2.16	16	1
3:A:38:PRO:O	3:A:41:ARG:HG3	0.41	2.16	19	1
1:B:249:DG:O4'	1:B:250:DC:H5''	0.41	2.16	20	1
3:A:13:THR:O	3:A:17:LEU:HD22	0.41	2.16	2	1
3:A:33:ILE:HG22	3:A:47:TRP:CH2	0.41	2.50	4	1
3:A:52:ARG:NH1	3:A:56:SER:HB3	0.41	2.30	4	1
3:A:75:ASN:C	3:A:75:ASN:ND2	0.41	2.79	4	1
2:C:354:DG:OP1	3:A:63:LYS:CB	0.41	2.69	11	1
2:C:355:DT:C7	3:A:52:ARG:CZ	0.41	2.97	11	1
2:C:358:DT:C1'	2:C:359:DT:O5'	0.41	2.69	17	2
1:B:258:DA:C6	2:C:357:DA:N1	0.41	2.88	13	1
3:A:59:ASP:CG	3:A:61:PHE:CE2	0.41	2.99	14	1
3:A:55:LEU:O	3:A:59:ASP:OD1	0.41	2.38	17	1
3:A:49:ASN:HA	3:A:52:ARG:CD	0.41	2.45	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:353:DT:O2	3:A:66:ARG:NH2	0.41	2.54	4	1
2:C:353:DT:H2'	3:A:52:ARG:NH1	0.41	2.31	7	1
3:A:12:ILE:CG1	3:A:51:ILE:HD11	0.41	2.46	8	1
1:B:262:DA:H2''	1:B:263:DT:OP2	0.41	2.15	12	1
2:C:354:DG:C8	2:C:355:DT:C7	0.40	3.04	10	1
3:A:14:MET:HG3	3:A:15:ALA:N	0.40	2.30	10	1
3:A:40:TYR:O	3:A:44:PHE:N	0.40	2.54	10	1
1:B:256:DA:OP2	1:B:256:DA:H2'	0.40	2.17	19	1
3:A:52:ARG:CG	3:A:53:HIS:N	0.40	2.82	19	1
1:B:249:DG:O4'	1:B:250:DC:C5'	0.40	2.69	20	1
2:C:355:DT:OP2	2:C:355:DT:H3'	0.40	2.16	20	1
3:A:79:LEU:HD21	3:A:83:SER:HB2	0.40	1.93	5	1
3:A:12:ILE:HD11	3:A:51:ILE:HG13	0.40	1.92	9	1
1:B:255:DA:H2''	1:B:256:DA:O5'	0.40	2.16	10	1
3:A:17:LEU:HD21	3:A:87:PHE:CD2	0.40	2.51	10	1
3:A:17:LEU:O	3:A:20:PRO:HD3	0.40	2.16	18	1
3:A:24:LEU:C	3:A:25:THR:OG1	0.40	2.65	18	1
3:A:51:ILE:HG22	3:A:55:LEU:HD12	0.40	1.92	18	1
2:C:354:DG:N7	3:A:52:ARG:CZ	0.40	2.85	19	1
1:B:258:DA:OP2	3:A:45:PRO:O	0.40	2.39	1	1
3:A:8:TYR:O	3:A:12:ILE:CB	0.40	2.70	8	1
3:A:82:GLN:O	3:A:82:GLN:CG	0.40	2.69	10	1
3:A:33:ILE:HG13	3:A:51:ILE:CD1	0.40	2.46	11	1
1:B:251:DT:C2'	1:B:252:DT:C7	0.40	2.99	13	1
3:A:8:TYR:CD2	3:A:50:SER:HB3	0.40	2.51	18	1
3:A:29:ILE:O	3:A:32:PHE:N	0.40	2.54	5	1
2:C:357:DA:H62	3:A:53:HIS:CE1	0.40	2.34	9	1
3:A:12:ILE:HD11	3:A:51:ILE:CG1	0.40	2.46	12	1
3:A:82:GLN:O	3:A:86:MET:SD	0.40	2.79	12	1
3:A:17:LEU:HD21	3:A:87:PHE:CG	0.40	2.51	20	1
3:A:70:ASN:OD1	3:A:70:ASN:N	0.40	2.54	20	1
3:A:24:LEU:N	3:A:77:TRP:O	0.40	2.54	2	1
3:A:27:SER:OG	3:A:75:ASN:OD1	0.40	2.36	2	1
1:B:256:DA:O5'	3:A:7:SER:HB2	0.40	2.17	6	1
3:A:8:TYR:CE1	3:A:47:TRP:HB2	0.40	2.52	16	1
3:A:26:LEU:HD23	3:A:75:ASN:ND2	0.40	2.31	19	1
3:A:46:ALA:O	3:A:50:SER:HB2	0.40	2.17	20	1

6.3 Torsion angles [i](#)

6.3.1 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 NMR 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	
3	A	81/97 (84%)	62±2 (77±3%)	13±2 (16±2%)	6±1 (7±2%)	2	15
All	All	1620/1940 (84%)	1244 (77%)	260 (16%)	116 (7%)	2	15

All 16 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
3	A	58	ASN	20
3	A	82	GLN	17
3	A	46	ALA	14
3	A	66	ARG	14
3	A	60	CYS	13
3	A	69	GLY	11
3	A	22	LYS	6
3	A	23	LYS	6
3	A	21	GLN	4
3	A	71	PRO	3
3	A	72	GLY	3
3	A	25	THR	1
3	A	65	PRO	1
3	A	48	GLN	1
3	A	68	PRO	1
3	A	44	PHE	1

6.3.2 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 NMR 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
3	A	74/89 (83%)	52±4 (70±5%)	22±4 (30±5%)	1 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1480/1780 (83%)	1040 (70%)	440 (30%)	1 17

All 62 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
3	A	29	ILE	18
3	A	32	PHE	18
3	A	63	LYS	18
3	A	22	LYS	15
3	A	55	LEU	14
3	A	58	ASN	13
3	A	61	PHE	13
3	A	21	GLN	12
3	A	23	LYS	12
3	A	26	LEU	12
3	A	67	GLU	12
3	A	80	ASP	12
3	A	82	GLN	12
3	A	31	GLU	12
3	A	42	GLU	12
3	A	73	LYS	11
3	A	43	LYS	10
3	A	57	LEU	10
3	A	70	ASN	10
3	A	41	ARG	10
3	A	56	SER	10
3	A	66	ARG	10
3	A	52	ARG	10
3	A	79	LEU	9
3	A	48	GLN	9
3	A	84	GLU	9
3	A	76	TYR	8
3	A	9	ILE	7
3	A	18	GLN	7
3	A	49	ASN	7
3	A	87	PHE	7
3	A	24	LEU	7
3	A	64	ILE	6
3	A	40	TYR	6
3	A	86	MET	6
3	A	60	CYS	5

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Mol	Chain	Res	Type	Models (Total)
3	A	50	SER	4
3	A	17	LEU	4
3	A	37	PHE	4
3	A	33	ILE	4
3	A	51	ILE	4
3	A	11	LEU	4
3	A	12	ILE	4
3	A	35	ASN	3
3	A	30	CYS	3
3	A	85	ASP	3
3	A	19	SER	2
3	A	39	TYR	2
3	A	47	TRP	2
3	A	83	SER	2
3	A	53	HIS	2
3	A	75	ASN	2
3	A	27	SER	2
3	A	44	PHE	2
3	A	14	MET	1
3	A	25	THR	1
3	A	54	ASN	1
3	A	36	ARG	1
3	A	34	SER	1
3	A	13	THR	1
3	A	7	SER	1
3	A	16	ILE	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided