



Full wwPDB NMR Structure Validation Report ⓘ

Mar 29, 2026 – 03:03 AM UTC

PDB ID : 1WTB / pdb_00001wtb
Title : Complex structure of the C-terminal RNA-binding domain of hnRNP D (AUF1) with telomere DNA
Authors : Enokizono, Y.; Konishi, Y.; Nagata, K.; Ouhashi, K.; Uesugi, S.; Ishikawa, F.; Katahira, M.
Deposited on : 2004-11-22

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

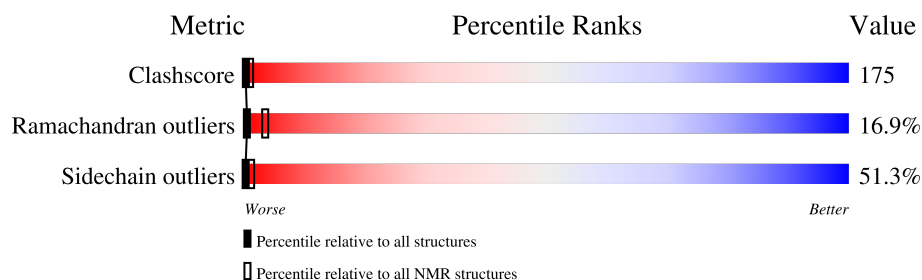
1 Overall quality at a glance

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	4	100%
2	A	79	38% 42% 14%

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:181-A:213, A:223-A:257 (68)	0.21	10

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 4 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1417 atoms, of which 696 are hydrogens and 0 are deuteriums.

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

Mol	Chain	Residues	Atoms						Trace
1	B	4	Total	C	H	N	O	P	0
			130	40	45	17	24	4	

- Molecule 2 is a protein called Heterogeneous nuclear ribonucleoprotein D0.

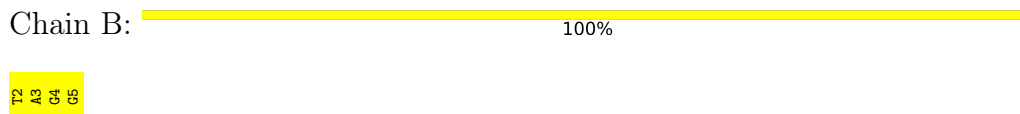
Mol	Chain	Residues	Atoms						Trace
2	A	79	Total	C	H	N	O	S	0
			1287	409	651	105	117	5	

4 Residue-property plots

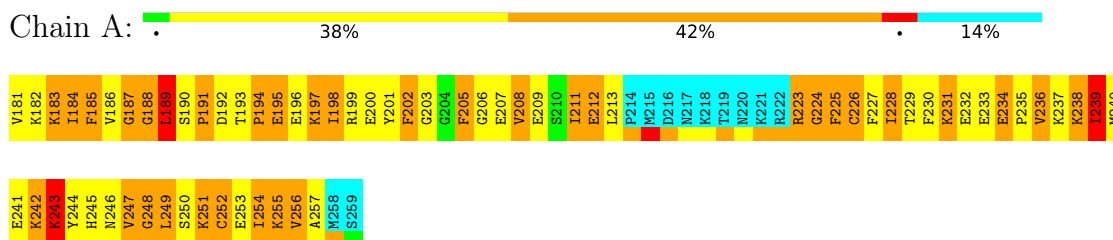
4.1 Average score per residue in the NMR ensemble

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: 5'-D(P*TP*AP*GP*G)-3'



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

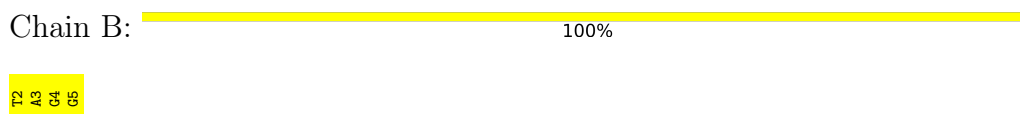


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

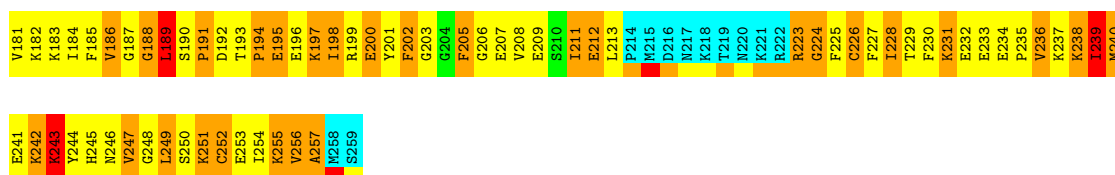
4.2.1 Score per residue for model 1

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0





4.2.2 Score per residue for model 2

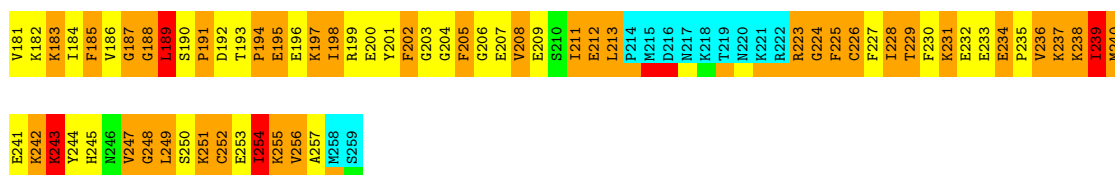
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 34% 44% 5% 14%



4.2.3 Score per residue for model 3

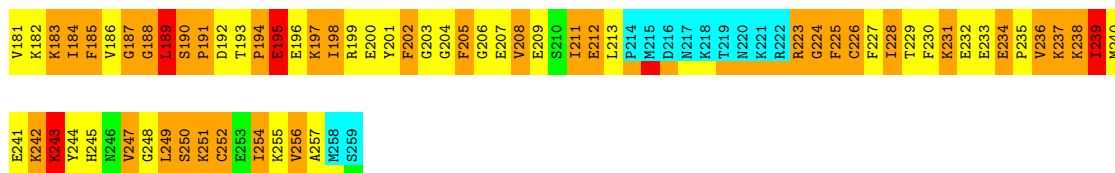
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 35% 42% 5% 14%



4.2.4 Score per residue for model 4

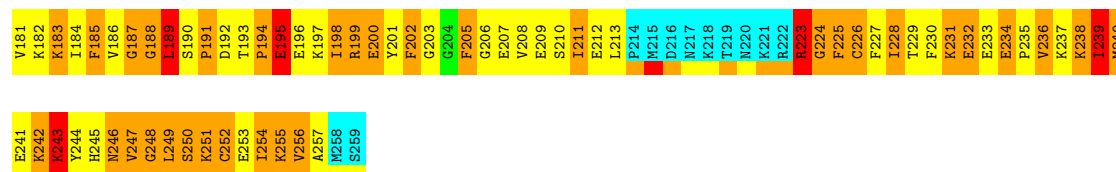
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B:  100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A:  37% 42% 6% 14%



4.2.5 Score per residue for model 5

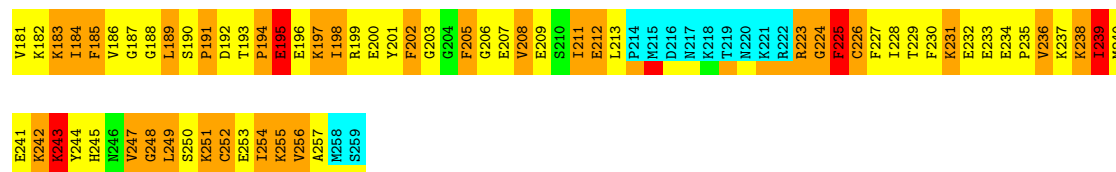
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B:  100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A:  42% 35% 5% 14%



4.2.6 Score per residue for model 6

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B:  100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A:  37% 42% 5% 14%





4.2.7 Score per residue for model 7

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 38% 41% 5% 14%



4.2.8 Score per residue for model 8

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 5% 34% 41% 6% 14%



4.2.9 Score per residue for model 9

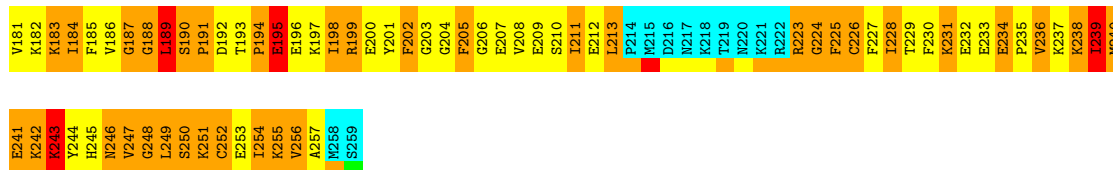
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

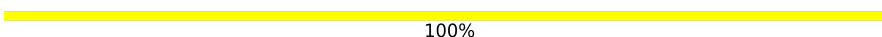
- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 



4.2.10 Score per residue for model 10 (medoid)

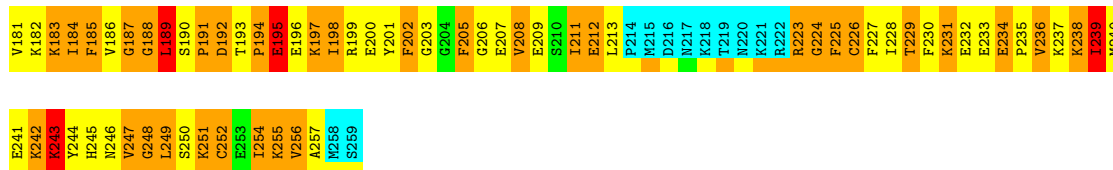
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 

T2
A3
G4
G5

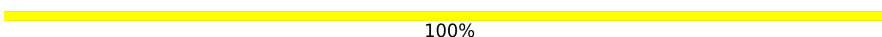
- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 



4.2.11 Score per residue for model 11

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 





4.2.12 Score per residue for model 12

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 43% 33% 8% 14%



4.2.13 Score per residue for model 13

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 35% 44% 5% 14%



4.2.14 Score per residue for model 14

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: . 37% 42% 5% 14%



4.2.15 Score per residue for model 15

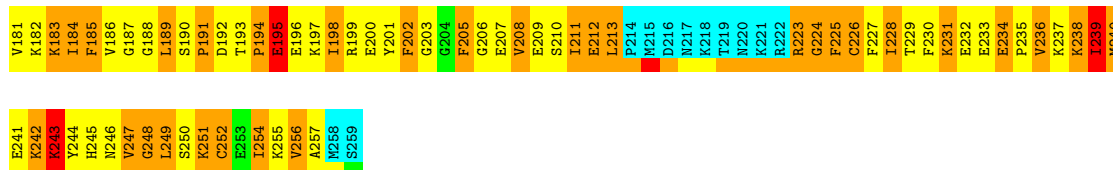
- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: . 41% 39% . 14%



4.2.16 Score per residue for model 16

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

T2
A3
G4
G5

- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: . 34% 41% 8% 14%





4.2.17 Score per residue for model 17

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 35% 44% 5% 14%



4.2.18 Score per residue for model 18

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%



- Molecule 2: Heterogeneous nuclear ribonucleoprotein D0

Chain A: 33% 44% 6% 14%



4.2.19 Score per residue for model 19

- Molecule 1: 5'-D(P*TP*AP*GP*G)-3'

Chain B: 100%

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR	structure solution	3.851
X-PLOR	refinement	3.851

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	0.25±0.01	0±0/95 (0.0± 0.0%)	0.48±0.04	0±0/145 (0.0± 0.0%)
2	A	0.64±0.01	0±0/559 (0.0± 0.0%)	0.93±0.02	0±0/747 (0.0± 0.1%)
All	All	0.60	0/13080 (0.0%)	0.88	4/17840 (0.0%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	254	ILE	N-CA-C	6.32	112.97	106.21	2	4

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in 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	85	45	46	22±4
2	A	547	559	558	208±9
All	All	12640	12080	12080	4321

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 175.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:184:ILE:HD13	2:A:239:ILE:HD12	1.13	1.14	9	19
2:A:198:ILE:HG22	2:A:228:ILE:HD11	1.12	1.15	6	20
2:A:227:PHE:CE2	2:A:257:ALA:HB1	1.06	1.85	12	19
2:A:198:ILE:CG2	2:A:228:ILE:HD11	1.05	1.82	4	20
2:A:198:ILE:HG22	2:A:228:ILE:CD1	1.03	1.83	19	20
2:A:202:PHE:CG	2:A:228:ILE:HD12	1.03	1.89	12	20
1:B:4:DG:N3	1:B:4:DG:H5'	0.99	1.69	10	3
2:A:202:PHE:CD2	2:A:228:ILE:HD12	0.95	1.96	12	20
2:A:198:ILE:HD12	2:A:213:LEU:HD21	0.94	1.37	1	17
2:A:189:LEU:HD22	2:A:193:THR:OG1	0.93	1.64	2	20
2:A:239:ILE:HD13	2:A:245:HIS:CE1	0.93	1.99	13	19
2:A:227:PHE:CE1	2:A:257:ALA:HB1	0.93	1.99	9	1
1:B:3:DA:H4'	1:B:4:DG:O5'	0.93	1.61	8	13
2:A:184:ILE:HD12	2:A:254:ILE:HG21	0.91	1.42	18	20
2:A:184:ILE:CD1	2:A:239:ILE:HD12	0.91	1.95	12	19
1:B:2:DT:H2'	1:B:2:DT:O2	0.91	1.62	8	12
2:A:186:VAL:HG12	2:A:252:CYS:SG	0.89	2.07	3	18
2:A:189:LEU:HD21	2:A:213:LEU:HD12	0.89	1.42	12	18
2:A:186:VAL:HG12	2:A:252:CYS:HB2	0.88	1.41	14	14
2:A:198:ILE:CD1	2:A:213:LEU:HD21	0.88	1.97	17	16
2:A:193:THR:HG22	2:A:198:ILE:CD1	0.88	1.98	2	19
2:A:186:VAL:HG13	2:A:254:ILE:HG12	0.86	1.47	14	19
2:A:235:PRO:O	2:A:239:ILE:HD12	0.84	1.72	18	1
2:A:183:LYS:HD3	2:A:257:ALA:HB3	0.84	1.48	19	3
2:A:185:PHE:N	2:A:257:ALA:HB2	0.83	1.87	13	20
2:A:184:ILE:HD12	2:A:254:ILE:CG2	0.82	2.04	18	20
1:B:4:DG:H2''	1:B:5:DG:O5'	0.82	1.70	16	16
2:A:202:PHE:CE2	2:A:228:ILE:HD12	0.81	2.10	10	20
2:A:193:THR:HG22	2:A:198:ILE:HD11	0.81	1.53	8	20
2:A:245:HIS:CG	2:A:254:ILE:HD12	0.81	2.10	1	20
1:B:4:DG:N2	2:A:227:PHE:CZ	0.80	2.49	2	20
2:A:227:PHE:CD2	2:A:257:ALA:HB1	0.80	2.11	10	19
2:A:239:ILE:CG2	2:A:254:ILE:HG21	0.78	2.09	12	20
2:A:212:GLU:C	2:A:213:LEU:HD22	0.78	2.04	14	2
2:A:184:ILE:CG2	2:A:236:VAL:HG13	0.77	2.09	6	20
1:B:4:DG:N3	1:B:4:DG:C5'	0.76	2.48	10	5
2:A:227:PHE:CD1	2:A:257:ALA:HB1	0.76	2.14	9	1
2:A:189:LEU:HD21	2:A:213:LEU:CD1	0.75	2.11	16	6
2:A:184:ILE:HD11	2:A:202:PHE:CE2	0.74	2.17	12	20
2:A:184:ILE:HG23	2:A:236:VAL:HG13	0.74	1.59	6	18
2:A:183:LYS:CD	2:A:257:ALA:HB3	0.74	2.13	1	3
1:B:4:DG:C2	2:A:227:PHE:CE1	0.73	2.76	16	15

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:195:GLU:HA	2:A:198:ILE:CG1	0.73	2.13	2	20
2:A:184:ILE:C	2:A:257:ALA:HB2	0.73	2.09	1	20
2:A:184:ILE:HD13	2:A:239:ILE:CD1	0.73	2.03	20	3
2:A:202:PHE:CZ	2:A:228:ILE:HD12	0.73	2.18	10	15
1:B:4:DG:C2	2:A:227:PHE:CZ	0.72	2.77	4	20
1:B:4:DG:C5	1:B:5:DG:C6	0.72	2.78	13	2
1:B:4:DG:N7	1:B:5:DG:C6	0.71	2.58	1	8
2:A:202:PHE:CD1	2:A:228:ILE:HD12	0.71	2.20	1	20
2:A:227:PHE:HE2	2:A:257:ALA:HB1	0.71	1.45	11	17
1:B:4:DG:N7	1:B:5:DG:C5	0.71	2.59	1	1
2:A:183:LYS:HB3	2:A:257:ALA:HB3	0.71	1.62	12	17
1:B:3:DA:C6	2:A:185:PHE:CD2	0.71	2.79	12	15
2:A:193:THR:HB	2:A:213:LEU:HD11	0.70	1.63	17	6
2:A:184:ILE:HD13	2:A:239:ILE:HD13	0.70	1.63	18	1
2:A:205:PHE:CE2	2:A:239:ILE:HG13	0.70	2.22	18	1
1:B:4:DG:N1	2:A:227:PHE:CE2	0.69	2.60	19	7
2:A:239:ILE:HG23	2:A:245:HIS:CE1	0.69	2.21	16	19
2:A:227:PHE:CE2	2:A:257:ALA:CB	0.69	2.75	14	19
1:B:4:DG:C5'	1:B:4:DG:N3	0.69	2.55	8	6
2:A:209:GLU:CD	2:A:229:THR:HG21	0.69	2.11	10	7
2:A:249:LEU:N	2:A:249:LEU:HD23	0.69	2.02	6	7
2:A:189:LEU:HD21	2:A:225:PHE:O	0.69	1.87	17	18
2:A:227:PHE:HE1	2:A:257:ALA:HB1	0.69	1.48	9	1
2:A:186:VAL:HG12	2:A:252:CYS:CB	0.69	2.17	14	20
2:A:205:PHE:HB3	2:A:235:PRO:HB3	0.69	1.65	13	20
2:A:183:LYS:O	2:A:184:ILE:HG23	0.69	1.88	5	10
1:B:3:DA:N7	2:A:185:PHE:CE2	0.68	2.62	9	3
2:A:239:ILE:HG23	2:A:245:HIS:NE2	0.68	2.04	16	19
2:A:189:LEU:HD23	2:A:226:CYS:SG	0.68	2.29	1	16
2:A:186:VAL:HG13	2:A:254:ILE:CG1	0.67	2.19	1	19
1:B:4:DG:C2	2:A:227:PHE:CE2	0.67	2.81	9	5
2:A:189:LEU:HD22	2:A:193:THR:HG1	0.67	1.48	1	10
1:B:4:DG:N7	1:B:5:DG:N1	0.67	2.41	16	2
2:A:183:LYS:O	2:A:184:ILE:CG2	0.67	2.43	5	20
1:B:2:DT:C2'	1:B:2:DT:O2	0.67	2.43	11	8
2:A:195:GLU:HA	2:A:198:ILE:HG13	0.67	1.66	2	20
2:A:227:PHE:CE1	2:A:257:ALA:CB	0.67	2.78	9	1
2:A:202:PHE:HA	2:A:205:PHE:HB2	0.67	1.67	2	20
2:A:239:ILE:CG2	2:A:254:ILE:CG2	0.67	2.73	18	20
1:B:3:DA:C5	2:A:185:PHE:CD2	0.66	2.84	1	10
1:B:3:DA:C5'	2:A:225:PHE:CE1	0.66	2.79	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:185:PHE:C	2:A:185:PHE:CD1	0.66	2.72	2	16
1:B:2:DT:O2	1:B:2:DT:C2'	0.66	2.43	18	12
1:B:3:DA:N1	2:A:185:PHE:CD2	0.66	2.62	12	1
2:A:256:VAL:O	2:A:256:VAL:HG13	0.66	1.91	1	5
2:A:239:ILE:HG12	2:A:245:HIS:CE1	0.66	2.24	18	1
2:A:235:PRO:O	2:A:239:ILE:CG1	0.65	2.44	16	19
1:B:4:DG:N3	1:B:4:DG:H5''	0.65	2.05	4	10
2:A:189:LEU:C	2:A:189:LEU:CD1	0.65	2.70	11	20
2:A:185:PHE:CD1	2:A:227:PHE:CE1	0.65	2.85	12	4
2:A:189:LEU:HD13	2:A:190:SER:N	0.65	2.06	14	20
1:B:2:DT:O2	1:B:2:DT:H2'	0.65	1.91	11	6
2:A:181:VAL:HG12	2:A:236:VAL:HB	0.65	1.69	12	20
2:A:197:LYS:HE2	2:A:249:LEU:HD21	0.65	1.67	12	5
2:A:183:LYS:HG3	2:A:229:THR:HG23	0.65	1.68	7	6
2:A:248:GLY:C	2:A:249:LEU:HD23	0.65	2.16	16	2
2:A:184:ILE:HD11	2:A:202:PHE:HE2	0.65	1.48	12	17
2:A:213:LEU:HD13	2:A:226:CYS:SG	0.64	2.32	3	3
1:B:3:DA:C5	2:A:185:PHE:CE2	0.64	2.85	4	9
1:B:3:DA:C5'	2:A:225:PHE:CZ	0.64	2.81	7	10
2:A:245:HIS:CD2	2:A:254:ILE:HD12	0.64	2.26	1	20
2:A:183:LYS:O	2:A:256:VAL:HG23	0.64	1.93	7	20
2:A:186:VAL:HG22	2:A:254:ILE:HD13	0.64	1.69	19	20
2:A:223:ARG:O	2:A:224:GLY:C	0.64	2.41	5	20
2:A:202:PHE:CD1	2:A:202:PHE:N	0.63	2.67	1	20
2:A:183:LYS:HD3	2:A:257:ALA:CB	0.63	2.23	1	3
2:A:181:VAL:O	2:A:233:GLU:CB	0.63	2.47	8	20
2:A:255:LYS:O	2:A:256:VAL:C	0.63	2.42	13	20
2:A:227:PHE:CD2	2:A:257:ALA:CB	0.63	2.82	3	16
2:A:185:PHE:HB2	2:A:227:PHE:CE2	0.63	2.29	6	15
1:B:3:DA:O5'	2:A:225:PHE:CZ	0.62	2.52	11	4
2:A:193:THR:CG2	2:A:198:ILE:HD11	0.62	2.23	8	6
2:A:189:LEU:C	2:A:189:LEU:HD13	0.62	2.20	19	15
2:A:239:ILE:CG1	2:A:245:HIS:CE1	0.62	2.83	18	1
2:A:242:LYS:O	2:A:244:TYR:N	0.62	2.33	7	20
2:A:189:LEU:HD12	2:A:224:GLY:O	0.62	1.94	14	8
2:A:227:PHE:CD1	2:A:257:ALA:CB	0.62	2.83	9	1
1:B:3:DA:OP2	2:A:185:PHE:CE1	0.62	2.53	16	2
2:A:197:LYS:CE	2:A:247:VAL:HG12	0.61	2.25	3	3
1:B:2:DT:C6	1:B:2:DT:OP1	0.61	2.53	15	1
1:B:4:DG:N7	1:B:5:DG:N7	0.61	2.47	11	1
2:A:211:ILE:HG23	2:A:228:ILE:HG12	0.61	1.71	16	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:TYR:HB3	2:A:202:PHE:CD1	0.61	2.31	9	20
1:B:3:DA:OP1	1:B:3:DA:C8	0.61	2.53	4	3
1:B:3:DA:OP2	2:A:225:PHE:CD2	0.61	2.54	11	3
1:B:3:DA:OP2	2:A:225:PHE:CD1	0.61	2.54	12	1
1:B:2:DT:OP2	1:B:2:DT:C6	0.61	2.54	16	1
2:A:198:ILE:CD1	2:A:213:LEU:HD11	0.61	2.26	6	2
2:A:187:GLY:C	2:A:252:CYS:HB3	0.61	2.19	13	19
2:A:185:PHE:HB2	2:A:227:PHE:CE1	0.60	2.31	9	1
1:B:2:DT:OP1	1:B:2:DT:C5	0.60	2.54	15	1
2:A:187:GLY:C	2:A:225:PHE:CB	0.60	2.74	14	3
1:B:2:DT:C5	2:A:187:GLY:O	0.60	2.54	11	4
2:A:245:HIS:CG	2:A:254:ILE:CD1	0.60	2.83	18	20
1:B:3:DA:H4'	2:A:225:PHE:CZ	0.60	2.32	1	5
2:A:184:ILE:HG13	2:A:184:ILE:O	0.60	1.95	20	17
1:B:3:DA:C4'	1:B:4:DG:O5'	0.60	2.49	10	2
1:B:3:DA:OP2	2:A:225:PHE:CE2	0.60	2.55	16	1
1:B:3:DA:H5''	2:A:225:PHE:CE1	0.59	2.31	8	7
2:A:198:ILE:O	2:A:202:PHE:CD1	0.59	2.55	9	20
2:A:185:PHE:CD1	2:A:185:PHE:C	0.59	2.78	12	4
2:A:189:LEU:HG	2:A:225:PHE:HA	0.59	1.74	17	20
1:B:3:DA:O5'	2:A:225:PHE:CE1	0.59	2.55	11	3
2:A:201:TYR:CZ	2:A:245:HIS:HB3	0.59	2.33	5	20
2:A:183:LYS:CG	2:A:229:THR:HG23	0.59	2.28	6	8
2:A:205:PHE:CE1	2:A:238:LYS:HG3	0.59	2.32	14	20
2:A:238:LYS:O	2:A:241:GLU:N	0.59	2.36	3	20
2:A:183:LYS:O	2:A:236:VAL:CG1	0.59	2.51	12	20
2:A:197:LYS:O	2:A:200:GLU:N	0.59	2.36	20	17
2:A:242:LYS:O	2:A:245:HIS:CD2	0.59	2.56	6	20
2:A:183:LYS:HD2	2:A:257:ALA:HB3	0.59	1.74	11	3
2:A:235:PRO:C	2:A:239:ILE:HD12	0.59	2.22	18	1
2:A:247:VAL:O	2:A:249:LEU:N	0.58	2.36	4	20
2:A:225:PHE:CD1	2:A:225:PHE:N	0.58	2.71	18	16
1:B:2:DT:O4'	1:B:2:DT:OP2	0.58	2.21	15	1
2:A:230:PHE:CD2	2:A:235:PRO:HB2	0.58	2.33	18	20
2:A:189:LEU:CD1	2:A:225:PHE:HA	0.58	2.28	20	17
2:A:185:PHE:O	2:A:185:PHE:CG	0.58	2.57	19	5
2:A:183:LYS:CD	2:A:257:ALA:CB	0.58	2.81	1	3
2:A:193:THR:CG2	2:A:198:ILE:CD1	0.58	2.81	8	6
2:A:243:LYS:O	2:A:254:ILE:N	0.58	2.37	4	14
2:A:247:VAL:O	2:A:248:GLY:C	0.58	2.47	5	11
2:A:202:PHE:CD2	2:A:228:ILE:HG21	0.58	2.33	2	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:202:PHE:CE1	2:A:228:ILE:HD12	0.58	2.34	6	16
2:A:185:PHE:CA	2:A:257:ALA:HB2	0.58	2.29	12	20
2:A:183:LYS:HG2	2:A:229:THR:HG23	0.58	1.76	2	3
2:A:230:PHE:CE1	2:A:239:ILE:HD13	0.57	2.34	18	1
2:A:202:PHE:HB3	2:A:230:PHE:CZ	0.57	2.35	11	20
2:A:242:LYS:O	2:A:243:LYS:C	0.57	2.47	5	20
2:A:256:VAL:O	2:A:256:VAL:CG1	0.57	2.52	1	5
1:B:4:DG:N2	2:A:227:PHE:CE1	0.57	2.72	16	12
1:B:4:DG:N7	2:A:212:GLU:OE1	0.57	2.36	2	2
2:A:225:PHE:CE2	2:A:227:PHE:CE2	0.57	2.93	9	1
2:A:239:ILE:CG1	2:A:245:HIS:HE1	0.57	2.11	18	1
2:A:197:LYS:CE	2:A:249:LEU:HD21	0.57	2.30	12	4
1:B:4:DG:OP1	2:A:223:ARG:CZ	0.57	2.53	20	1
2:A:234:GLU:O	2:A:237:LYS:HG2	0.57	2.00	12	9
2:A:195:GLU:OE1	2:A:213:LEU:HD23	0.56	1.99	15	3
1:B:3:DA:H4'	2:A:225:PHE:CE1	0.56	2.35	14	2
2:A:239:ILE:HG23	2:A:254:ILE:HG21	0.56	1.77	1	19
1:B:4:DG:C2'	1:B:5:DG:O5'	0.56	2.52	16	8
1:B:4:DG:O6	2:A:183:LYS:CE	0.56	2.54	18	3
2:A:201:TYR:OH	2:A:245:HIS:ND1	0.56	2.37	18	1
2:A:243:LYS:HE2	2:A:244:TYR:CD2	0.56	2.36	9	6
2:A:203:GLY:O	2:A:206:GLY:O	0.56	2.24	19	20
2:A:186:VAL:HG22	2:A:254:ILE:CD1	0.56	2.30	17	6
2:A:235:PRO:O	2:A:239:ILE:HG13	0.56	2.01	9	19
2:A:239:ILE:O	2:A:242:LYS:N	0.56	2.39	7	20
2:A:202:PHE:CG	2:A:228:ILE:CD1	0.56	2.80	12	9
2:A:230:PHE:CD1	2:A:236:VAL:HG22	0.56	2.36	9	20
2:A:209:GLU:CD	2:A:229:THR:CG2	0.55	2.80	16	7
2:A:186:VAL:CG1	2:A:252:CYS:SG	0.55	2.94	13	17
1:B:2:DT:C2	2:A:187:GLY:HA3	0.55	2.37	13	5
2:A:199:ARG:HG2	2:A:211:ILE:HD11	0.55	1.78	16	10
1:B:3:DA:C2	2:A:257:ALA:HA	0.55	2.36	1	1
2:A:190:SER:O	2:A:192:ASP:N	0.55	2.39	20	20
2:A:200:GLU:CG	2:A:201:TYR:N	0.55	2.69	20	4
2:A:243:LYS:CE	2:A:244:TYR:CD2	0.55	2.90	4	6
1:B:4:DG:C8	1:B:5:DG:C4	0.55	2.94	13	1
1:B:4:DG:H5''	2:A:225:PHE:CZ	0.55	2.37	10	1
2:A:211:ILE:C	2:A:212:GLU:CG	0.55	2.79	19	6
2:A:239:ILE:CG2	2:A:254:ILE:HG22	0.55	2.31	18	5
1:B:4:DG:O5'	2:A:223:ARG:CD	0.55	2.55	10	1
2:A:223:ARG:O	2:A:225:PHE:CD1	0.55	2.59	13	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:4:DG:C8	1:B:5:DG:C5	0.55	2.95	2	3
2:A:201:TYR:CD1	2:A:201:TYR:C	0.55	2.84	18	12
2:A:230:PHE:O	2:A:232:GLU:O	0.55	2.25	19	20
2:A:189:LEU:HD22	2:A:193:THR:CB	0.55	2.32	5	10
2:A:225:PHE:CE2	2:A:227:PHE:CE1	0.55	2.94	20	17
1:B:3:DA:C4'	2:A:225:PHE:CZ	0.55	2.90	10	11
2:A:238:LYS:O	2:A:241:GLU:CG	0.54	2.55	17	19
2:A:187:GLY:O	2:A:252:CYS:CB	0.54	2.55	7	13
2:A:243:LYS:CE	2:A:244:TYR:CG	0.54	2.90	15	4
2:A:243:LYS:HE3	2:A:244:TYR:CG	0.54	2.37	9	5
1:B:3:DA:OP2	2:A:225:PHE:CE1	0.54	2.60	12	1
2:A:183:LYS:C	2:A:184:ILE:HG23	0.54	2.27	6	20
2:A:243:LYS:O	2:A:254:ILE:HG13	0.54	2.01	16	20
2:A:247:VAL:N	2:A:250:SER:O	0.54	2.40	18	15
2:A:185:PHE:CE2	2:A:255:LYS:HD3	0.54	2.37	6	10
1:B:3:DA:OP1	2:A:185:PHE:CZ	0.54	2.60	3	2
1:B:3:DA:C2	2:A:185:PHE:CD2	0.54	2.96	12	1
2:A:243:LYS:HE2	2:A:244:TYR:CG	0.54	2.37	18	1
2:A:187:GLY:C	2:A:225:PHE:HB3	0.54	2.27	14	3
2:A:185:PHE:CE1	2:A:225:PHE:CE2	0.54	2.96	7	13
2:A:202:PHE:CD2	2:A:228:ILE:CD1	0.54	2.84	12	4
2:A:230:PHE:CE2	2:A:235:PRO:CB	0.54	2.90	18	1
2:A:223:ARG:C	2:A:225:PHE:CD1	0.54	2.86	17	10
2:A:195:GLU:HA	2:A:198:ILE:HG12	0.54	1.80	20	3
2:A:195:GLU:CA	2:A:198:ILE:HG12	0.54	2.33	16	3
1:B:3:DA:H5''	2:A:225:PHE:CZ	0.54	2.37	5	5
1:B:4:DG:N7	2:A:212:GLU:CD	0.54	2.66	2	2
1:B:5:DG:OP2	2:A:223:ARG:NH1	0.54	2.41	4	6
2:A:255:LYS:O	2:A:257:ALA:N	0.54	2.41	1	3
1:B:4:DG:C8	2:A:212:GLU:HG2	0.54	2.37	12	2
2:A:186:VAL:CG1	2:A:252:CYS:HB2	0.54	2.33	17	1
2:A:201:TYR:CZ	2:A:245:HIS:ND1	0.54	2.76	18	1
2:A:185:PHE:CZ	2:A:255:LYS:NZ	0.54	2.75	9	4
2:A:189:LEU:CD2	2:A:226:CYS:SG	0.53	2.96	1	15
1:B:2:DT:O2	2:A:255:LYS:NZ	0.53	2.41	17	1
2:A:202:PHE:O	2:A:205:PHE:CB	0.53	2.56	18	20
2:A:209:GLU:OE2	2:A:229:THR:HG21	0.53	2.02	11	5
2:A:184:ILE:HB	2:A:254:ILE:CG2	0.53	2.33	5	18
2:A:213:LEU:CD1	2:A:226:CYS:SG	0.53	2.96	3	3
2:A:194:PRO:HG2	2:A:197:LYS:CD	0.53	2.34	18	9
2:A:187:GLY:O	2:A:188:GLY:O	0.53	2.27	1	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:212:GLU:O	2:A:213:LEU:HD13	0.53	2.04	12	1
2:A:183:LYS:C	2:A:184:ILE:CG2	0.53	2.82	12	19
2:A:184:ILE:HD11	2:A:228:ILE:HB	0.53	1.80	13	9
1:B:3:DA:H5'	2:A:225:PHE:CE1	0.53	2.38	4	1
2:A:185:PHE:HB3	2:A:255:LYS:O	0.53	2.04	14	20
1:B:2:DT:C6	1:B:2:DT:P	0.53	3.02	15	1
2:A:209:GLU:HB2	2:A:231:LYS:N	0.53	2.19	11	20
2:A:184:ILE:HD12	2:A:254:ILE:HG23	0.53	1.80	6	9
2:A:209:GLU:CG	2:A:229:THR:CG2	0.53	2.86	14	4
2:A:199:ARG:HD3	2:A:211:ILE:CD1	0.53	2.34	9	1
2:A:189:LEU:HG	2:A:225:PHE:C	0.53	2.29	20	17
2:A:189:LEU:HD13	2:A:189:LEU:C	0.53	2.29	14	4
2:A:245:HIS:CD2	2:A:254:ILE:CG1	0.53	2.92	13	16
1:B:2:DT:O4'	1:B:2:DT:P	0.53	2.67	20	2
2:A:187:GLY:C	2:A:225:PHE:HB2	0.52	2.30	18	12
2:A:189:LEU:HB3	2:A:252:CYS:SG	0.52	2.44	14	19
1:B:2:DT:C6	2:A:187:GLY:C	0.52	2.88	11	3
2:A:205:PHE:CD2	2:A:239:ILE:HD11	0.52	2.39	18	1
2:A:238:LYS:O	2:A:241:GLU:CB	0.52	2.57	20	13
2:A:183:LYS:HE2	2:A:227:PHE:CD2	0.52	2.39	4	8
1:B:3:DA:H5'	2:A:225:PHE:CZ	0.52	2.39	7	2
2:A:185:PHE:HB2	2:A:227:PHE:CZ	0.52	2.39	12	8
1:B:2:DT:C4	2:A:187:GLY:O	0.52	2.63	19	3
2:A:230:PHE:O	2:A:231:LYS:C	0.52	2.52	2	20
1:B:4:DG:N7	1:B:5:DG:C2	0.52	2.78	13	1
2:A:223:ARG:C	2:A:225:PHE:CD2	0.52	2.88	19	1
2:A:228:ILE:HG22	2:A:229:THR:N	0.52	2.19	5	11
2:A:183:LYS:O	2:A:184:ILE:HG22	0.51	2.05	12	12
2:A:230:PHE:CE2	2:A:235:PRO:HB2	0.51	2.40	18	2
2:A:181:VAL:CG1	2:A:236:VAL:CG1	0.51	2.88	4	14
2:A:181:VAL:O	2:A:182:LYS:HG2	0.51	2.05	2	20
2:A:186:VAL:O	2:A:225:PHE:HB2	0.51	2.05	14	7
2:A:205:PHE:CE2	2:A:239:ILE:HG12	0.51	2.41	14	17
2:A:183:LYS:HE2	2:A:227:PHE:CD1	0.51	2.40	9	1
2:A:184:ILE:HD11	2:A:202:PHE:CD2	0.51	2.41	6	16
2:A:184:ILE:CG2	2:A:236:VAL:CG1	0.51	2.89	10	9
2:A:245:HIS:CD2	2:A:254:ILE:HG13	0.51	2.40	13	11
2:A:187:GLY:O	2:A:252:CYS:HB3	0.51	2.05	11	6
2:A:245:HIS:O	2:A:251:LYS:HA	0.51	2.06	17	16
2:A:195:GLU:O	2:A:199:ARG:N	0.51	2.43	9	1
2:A:225:PHE:HE2	2:A:227:PHE:CE2	0.51	2.24	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:3:DA:C6	2:A:185:PHE:CE2	0.51	2.98	12	1
2:A:184:ILE:C	2:A:257:ALA:CB	0.51	2.83	1	3
2:A:187:GLY:N	2:A:252:CYS:HB2	0.51	2.21	1	10
2:A:188:GLY:O	2:A:252:CYS:SG	0.51	2.69	2	20
2:A:239:ILE:HG23	2:A:254:ILE:CG2	0.51	2.36	18	1
1:B:3:DA:C2'	1:B:4:DG:OP2	0.51	2.58	19	1
1:B:4:DG:O6	2:A:183:LYS:HE3	0.50	2.06	11	3
2:A:184:ILE:HG22	2:A:236:VAL:HG13	0.50	1.82	2	5
1:B:2:DT:H1'	1:B:3:DA:OP2	0.50	2.07	4	3
2:A:253:GLU:O	2:A:255:LYS:HE2	0.50	2.05	16	5
2:A:239:ILE:HG21	2:A:254:ILE:CG2	0.50	2.36	18	4
1:B:4:DG:H3'	2:A:223:ARG:CZ	0.50	2.36	8	8
2:A:205:PHE:CE2	2:A:239:ILE:CG1	0.50	2.93	18	1
2:A:199:ARG:O	2:A:203:GLY:HA3	0.50	2.07	2	20
2:A:243:LYS:HE3	2:A:244:TYR:CD1	0.50	2.41	15	2
2:A:211:ILE:HG23	2:A:228:ILE:CG1	0.50	2.37	9	15
2:A:197:LYS:HD3	2:A:198:ILE:N	0.50	2.22	3	3
2:A:232:GLU:CG	2:A:235:PRO:HD2	0.50	2.37	15	2
1:B:4:DG:H3'	2:A:223:ARG:NH2	0.50	2.22	12	10
2:A:228:ILE:CG2	2:A:229:THR:N	0.50	2.75	5	12
2:A:251:LYS:C	2:A:252:CYS:SG	0.50	2.95	12	16
2:A:193:THR:HB	2:A:213:LEU:CD1	0.50	2.36	13	4
2:A:242:LYS:HG2	2:A:245:HIS:CE1	0.50	2.42	13	5
2:A:185:PHE:CD2	2:A:255:LYS:HE3	0.50	2.42	4	5
2:A:229:THR:C	2:A:230:PHE:CD1	0.50	2.89	10	1
1:B:4:DG:C8	1:B:5:DG:N7	0.50	2.80	11	1
2:A:230:PHE:CZ	2:A:239:ILE:CD1	0.50	2.95	18	1
2:A:256:VAL:O	2:A:257:ALA:O	0.49	2.30	14	3
1:B:4:DG:H2'	1:B:5:DG:C8	0.49	2.41	3	2
1:B:2:DT:H72	2:A:188:GLY:HA3	0.49	1.83	5	2
2:A:249:LEU:N	2:A:249:LEU:CD2	0.49	2.71	6	3
2:A:246:ASN:N	2:A:246:ASN:ND2	0.49	2.58	17	2
2:A:198:ILE:HD12	2:A:213:LEU:CD2	0.49	2.37	17	1
1:B:2:DT:C6	2:A:188:GLY:N	0.49	2.81	1	2
2:A:189:LEU:CD2	2:A:193:THR:OG1	0.49	2.54	12	11
2:A:195:GLU:HA	2:A:198:ILE:CD1	0.49	2.38	19	17
2:A:202:PHE:O	2:A:205:PHE:HB2	0.49	2.08	4	20
2:A:209:GLU:CD	2:A:209:GLU:C	0.49	2.80	17	9
1:B:4:DG:OP1	2:A:223:ARG:NH1	0.49	2.46	20	2
2:A:185:PHE:CE2	2:A:255:LYS:NZ	0.49	2.80	9	5
2:A:182:LYS:HA	2:A:236:VAL:HG21	0.49	1.85	16	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:TYR:HB3	2:A:202:PHE:CE1	0.49	2.43	9	20
2:A:230:PHE:C	2:A:232:GLU:N	0.49	2.69	17	12
2:A:211:ILE:O	2:A:212:GLU:CD	0.49	2.55	16	10
1:B:3:DA:H1'	1:B:4:DG:OP2	0.49	2.07	19	4
2:A:245:HIS:CD2	2:A:254:ILE:CD1	0.49	2.95	18	12
1:B:3:DA:OP2	2:A:185:PHE:CZ	0.49	2.65	16	2
2:A:187:GLY:O	2:A:225:PHE:HB2	0.49	2.07	7	11
2:A:238:LYS:O	2:A:239:ILE:C	0.49	2.56	18	20
2:A:183:LYS:NZ	2:A:212:GLU:OE1	0.49	2.43	2	1
2:A:189:LEU:CD2	2:A:213:LEU:CD1	0.49	2.90	13	2
2:A:194:PRO:HG2	2:A:197:LYS:CE	0.49	2.38	14	1
2:A:211:ILE:C	2:A:212:GLU:CD	0.48	2.81	1	3
2:A:185:PHE:O	2:A:253:GLU:O	0.48	2.31	5	2
2:A:185:PHE:CG	2:A:185:PHE:O	0.48	2.63	1	1
2:A:236:VAL:O	2:A:240:MET:HE2	0.48	2.08	11	1
2:A:245:HIS:O	2:A:251:LYS:HB3	0.48	2.09	18	20
2:A:243:LYS:HD3	2:A:243:LYS:N	0.48	2.23	18	4
2:A:189:LEU:HG	2:A:225:PHE:CA	0.48	2.38	7	17
2:A:244:TYR:CE1	2:A:253:GLU:HG3	0.48	2.44	18	3
2:A:197:LYS:CE	2:A:247:VAL:O	0.48	2.61	8	2
2:A:202:PHE:C	2:A:208:VAL:HG23	0.48	2.33	8	6
1:B:5:DG:OP1	2:A:223:ARG:NH1	0.48	2.46	5	1
2:A:233:GLU:O	2:A:237:LYS:HG3	0.48	2.09	11	11
2:A:235:PRO:HA	2:A:238:LYS:CG	0.48	2.38	11	8
2:A:213:LEU:HD22	2:A:226:CYS:SG	0.48	2.48	17	1
2:A:230:PHE:CE1	2:A:239:ILE:CD1	0.48	2.96	18	1
2:A:197:LYS:HE2	2:A:249:LEU:CD2	0.48	2.38	19	1
2:A:243:LYS:O	2:A:252:CYS:O	0.48	2.32	3	11
2:A:237:LYS:CG	2:A:238:LYS:N	0.48	2.77	7	2
2:A:241:GLU:O	2:A:243:LYS:NZ	0.48	2.43	16	1
2:A:225:PHE:CE1	2:A:227:PHE:CE1	0.48	3.01	19	1
2:A:188:GLY:O	2:A:252:CYS:HB3	0.48	2.09	5	5
2:A:195:GLU:CA	2:A:198:ILE:HG13	0.48	2.39	11	17
2:A:186:VAL:O	2:A:187:GLY:O	0.48	2.32	9	6
2:A:181:VAL:CG1	2:A:236:VAL:HB	0.48	2.39	15	19
2:A:207:GLU:O	2:A:231:LYS:HG3	0.48	2.08	14	20
2:A:211:ILE:HG23	2:A:228:ILE:CD1	0.48	2.39	1	19
2:A:242:LYS:HG2	2:A:245:HIS:NE2	0.48	2.24	13	8
2:A:236:VAL:O	2:A:240:MET:HE3	0.48	2.09	17	1
2:A:190:SER:O	2:A:191:PRO:C	0.48	2.57	2	20
2:A:234:GLU:O	2:A:238:LYS:HG2	0.48	2.09	12	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:189:LEU:HB2	2:A:250:SER:CB	0.48	2.39	5	6
2:A:185:PHE:CE1	2:A:186:VAL:O	0.48	2.67	14	1
2:A:249:LEU:O	2:A:251:LYS:CE	0.48	2.62	17	1
2:A:189:LEU:CD1	2:A:225:PHE:CA	0.47	2.92	20	5
2:A:187:GLY:O	2:A:252:CYS:SG	0.47	2.72	9	9
2:A:183:LYS:HD2	2:A:257:ALA:CB	0.47	2.39	11	3
2:A:188:GLY:N	2:A:225:PHE:HB3	0.47	2.23	1	2
2:A:185:PHE:HE1	2:A:225:PHE:CD2	0.47	2.26	8	14
2:A:230:PHE:HB2	2:A:236:VAL:HG22	0.47	1.86	3	10
2:A:232:GLU:HG3	2:A:235:PRO:HD2	0.47	1.86	19	1
2:A:181:VAL:HG12	2:A:236:VAL:CB	0.47	2.40	1	6
2:A:181:VAL:O	2:A:233:GLU:HB3	0.47	2.09	3	8
1:B:3:DA:OP1	2:A:223:ARG:HA	0.47	2.10	20	6
2:A:230:PHE:HB2	2:A:236:VAL:CG2	0.47	2.39	16	8
1:B:3:DA:C5'	2:A:223:ARG:HG2	0.47	2.39	10	1
2:A:232:GLU:HG3	2:A:235:PRO:CD	0.47	2.39	19	2
2:A:234:GLU:O	2:A:235:PRO:C	0.47	2.57	18	10
2:A:230:PHE:CD2	2:A:235:PRO:CB	0.47	2.98	18	1
2:A:192:ASP:O	2:A:193:THR:C	0.47	2.57	8	19
2:A:189:LEU:CG	2:A:225:PHE:HA	0.47	2.40	17	16
2:A:195:GLU:CA	2:A:198:ILE:CG1	0.47	2.92	2	1
1:B:4:DG:C8	1:B:5:DG:C2	0.47	3.02	16	1
1:B:4:DG:P	2:A:223:ARG:CZ	0.47	3.02	20	1
2:A:240:MET:O	2:A:243:LYS:HG3	0.47	2.09	11	15
2:A:181:VAL:O	2:A:233:GLU:HB2	0.47	2.10	5	11
2:A:239:ILE:O	2:A:243:LYS:N	0.47	2.48	2	5
2:A:201:TYR:CD1	2:A:201:TYR:O	0.47	2.67	18	1
2:A:223:ARG:C	2:A:225:PHE:HD1	0.47	2.18	18	9
1:B:3:DA:H2''	1:B:4:DG:OP2	0.47	2.10	19	1
2:A:238:LYS:O	2:A:241:GLU:HG2	0.46	2.10	3	14
2:A:201:TYR:CE1	2:A:245:HIS:ND1	0.46	2.66	18	4
2:A:188:GLY:O	2:A:251:LYS:O	0.46	2.33	13	3
1:B:3:DA:O4'	1:B:3:DA:P	0.46	2.74	12	1
2:A:186:VAL:HB	2:A:226:CYS:CB	0.46	2.41	12	3
1:B:3:DA:H4'	1:B:4:DG:C5'	0.46	2.41	17	3
2:A:212:GLU:OE2	2:A:213:LEU:C	0.46	2.58	14	1
2:A:200:GLU:O	2:A:201:TYR:C	0.46	2.59	19	7
1:B:3:DA:C8	2:A:185:PHE:CE2	0.46	3.03	9	1
2:A:199:ARG:HG2	2:A:211:ILE:CD1	0.46	2.41	8	9
2:A:211:ILE:O	2:A:212:GLU:OE2	0.46	2.34	15	1
2:A:195:GLU:O	2:A:199:ARG:HG3	0.46	2.10	2	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:196:GLU:O	2:A:200:GLU:OE2	0.46	2.33	9	1
2:A:211:ILE:O	2:A:212:GLU:OE1	0.46	2.34	13	3
2:A:253:GLU:CD	2:A:255:LYS:CE	0.46	2.88	13	1
2:A:183:LYS:HD2	2:A:257:ALA:C	0.46	2.36	19	3
2:A:189:LEU:HD12	2:A:189:LEU:N	0.46	2.25	1	4
1:B:2:DT:C7	2:A:188:GLY:HA3	0.46	2.41	5	3
2:A:200:GLU:HG3	2:A:201:TYR:N	0.46	2.25	20	3
2:A:225:PHE:HE2	2:A:227:PHE:CE1	0.46	2.28	20	8
2:A:192:ASP:O	2:A:192:ASP:OD1	0.46	2.34	2	1
2:A:189:LEU:CD2	2:A:213:LEU:HD12	0.46	2.30	12	1
2:A:184:ILE:HG22	2:A:236:VAL:CG1	0.45	2.41	12	7
2:A:193:THR:HG23	2:A:197:LYS:HZ3	0.45	1.70	8	1
2:A:186:VAL:O	2:A:225:PHE:HD2	0.45	1.94	17	1
2:A:194:PRO:C	2:A:196:GLU:N	0.45	2.74	16	17
1:B:4:DG:N7	2:A:212:GLU:OE2	0.45	2.49	2	1
2:A:239:ILE:CD1	2:A:245:HIS:CE1	0.45	2.88	13	8
2:A:184:ILE:CG1	2:A:228:ILE:HB	0.45	2.41	13	7
1:B:4:DG:C6	1:B:5:DG:O6	0.45	2.69	13	1
2:A:239:ILE:HG13	2:A:245:HIS:HE1	0.45	1.71	18	1
2:A:185:PHE:O	2:A:254:ILE:HA	0.45	2.11	18	8
2:A:239:ILE:HG21	2:A:254:ILE:HG21	0.45	1.87	14	3
2:A:193:THR:HG22	2:A:198:ILE:CG1	0.45	2.40	8	1
2:A:200:GLU:O	2:A:204:GLY:N	0.45	2.40	18	5
2:A:199:ARG:HA	2:A:211:ILE:HD11	0.45	1.89	5	5
2:A:209:GLU:O	2:A:210:SER:OG	0.45	2.35	13	7
2:A:198:ILE:HB	2:A:211:ILE:HG21	0.45	1.89	16	3
2:A:242:LYS:CG	2:A:245:HIS:CE1	0.45	2.99	13	2
2:A:184:ILE:HA	2:A:256:VAL:HA	0.45	1.88	17	6
2:A:250:SER:C	2:A:251:LYS:HG3	0.45	2.36	18	9
2:A:189:LEU:N	2:A:189:LEU:HD12	0.45	2.25	16	6
2:A:185:PHE:CE1	2:A:225:PHE:CD2	0.45	3.04	8	3
2:A:189:LEU:HB2	2:A:250:SER:HB3	0.45	1.88	15	6
2:A:183:LYS:O	2:A:256:VAL:CG2	0.45	2.65	7	2
2:A:202:PHE:HB2	2:A:208:VAL:CG2	0.45	2.42	11	10
2:A:194:PRO:O	2:A:196:GLU:N	0.45	2.49	8	7
2:A:238:LYS:O	2:A:242:LYS:HD2	0.45	2.12	15	4
2:A:239:ILE:O	2:A:242:LYS:HG2	0.45	2.12	2	15
1:B:3:DA:H5''	2:A:223:ARG:CB	0.45	2.42	8	1
2:A:235:PRO:O	2:A:238:LYS:HG2	0.45	2.12	16	13
1:B:4:DG:H4'	2:A:225:PHE:CZ	0.45	2.46	19	1
2:A:193:THR:O	2:A:195:GLU:N	0.44	2.50	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:209:GLU:OE1	2:A:209:GLU:O	0.44	2.35	14	1
2:A:239:ILE:HD13	2:A:245:HIS:HE1	0.44	1.66	1	5
2:A:197:LYS:C	2:A:199:ARG:N	0.44	2.73	2	9
2:A:188:GLY:O	2:A:252:CYS:CB	0.44	2.65	13	3
2:A:234:GLU:N	2:A:234:GLU:CD	0.44	2.74	13	1
2:A:245:HIS:O	2:A:251:LYS:CA	0.44	2.66	14	2
1:B:4:DG:P	2:A:223:ARG:HD3	0.44	2.52	10	1
2:A:226:CYS:SG	2:A:252:CYS:SG	0.44	3.14	20	5
2:A:197:LYS:HE3	2:A:247:VAL:C	0.44	2.37	3	1
1:B:4:DG:O5'	2:A:223:ARG:HD3	0.44	2.11	10	1
2:A:246:ASN:ND2	2:A:246:ASN:N	0.44	2.66	4	4
2:A:199:ARG:CD	2:A:211:ILE:CD1	0.44	2.95	9	1
2:A:209:GLU:OE1	2:A:209:GLU:CA	0.44	2.66	14	1
2:A:243:LYS:HE3	2:A:244:TYR:N	0.44	2.28	15	1
2:A:237:LYS:HA	2:A:240:MET:CE	0.44	2.43	11	1
2:A:247:VAL:HG12	2:A:248:GLY:H	0.44	1.73	16	1
2:A:238:LYS:O	2:A:241:GLU:HG3	0.44	2.13	2	1
1:B:4:DG:O5'	2:A:223:ARG:HD2	0.44	2.12	10	1
2:A:213:LEU:HD22	2:A:213:LEU:N	0.44	2.26	14	1
2:A:207:GLU:O	2:A:232:GLU:OE1	0.44	2.35	15	1
2:A:194:PRO:O	2:A:198:ILE:HG13	0.44	2.12	17	11
1:B:4:DG:O6	2:A:183:LYS:NZ	0.44	2.44	16	3
2:A:198:ILE:O	2:A:202:PHE:HD1	0.44	1.96	13	2
2:A:200:GLU:CD	2:A:200:GLU:C	0.44	2.85	13	1
2:A:202:PHE:CA	2:A:205:PHE:HB2	0.43	2.40	2	14
2:A:184:ILE:CD1	2:A:239:ILE:CD1	0.43	2.86	16	1
2:A:209:GLU:HB3	2:A:230:PHE:N	0.43	2.28	15	7
2:A:184:ILE:CD1	2:A:254:ILE:HG21	0.43	2.39	17	5
2:A:235:PRO:C	2:A:238:LYS:HG2	0.43	2.38	17	10
2:A:182:LYS:C	2:A:236:VAL:HG11	0.43	2.38	12	2
2:A:238:LYS:C	2:A:242:LYS:HD3	0.43	2.38	9	6
2:A:196:GLU:O	2:A:200:GLU:HG3	0.43	2.14	7	1
2:A:187:GLY:O	2:A:188:GLY:C	0.43	2.61	12	2
2:A:186:VAL:CG1	2:A:254:ILE:HG12	0.43	2.35	1	3
2:A:225:PHE:C	2:A:226:CYS:SG	0.43	3.01	5	1
1:B:3:DA:H5''	2:A:223:ARG:HB3	0.43	1.90	8	1
1:B:5:DG:OP2	1:B:5:DG:H2'	0.43	2.14	5	1
2:A:213:LEU:CD1	2:A:226:CYS:HB3	0.43	2.43	7	3
2:A:186:VAL:HA	2:A:253:GLU:O	0.43	2.14	9	1
2:A:199:ARG:CD	2:A:211:ILE:HG13	0.43	2.43	9	1
2:A:193:THR:O	2:A:198:ILE:HD11	0.43	2.13	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:183:LYS:HA	2:A:229:THR:HA	0.43	1.89	6	10
2:A:225:PHE:N	2:A:225:PHE:HD1	0.43	2.10	18	7
2:A:183:LYS:CE	2:A:227:PHE:HB3	0.43	2.44	5	8
2:A:186:VAL:HB	2:A:226:CYS:SG	0.43	2.53	20	7
2:A:195:GLU:C	2:A:198:ILE:HG12	0.43	2.38	16	3
2:A:202:PHE:CG	2:A:228:ILE:HG21	0.43	2.48	2	1
2:A:198:ILE:HD13	2:A:213:LEU:HD11	0.43	1.90	5	1
2:A:253:GLU:CD	2:A:255:LYS:HE2	0.43	2.39	13	1
2:A:212:GLU:OE1	2:A:227:PHE:CB	0.43	2.66	19	1
2:A:181:VAL:HG12	2:A:236:VAL:CG1	0.43	2.43	1	1
2:A:211:ILE:CG2	2:A:228:ILE:HG12	0.43	2.43	9	2
2:A:239:ILE:HA	2:A:245:HIS:CE1	0.43	2.49	8	8
1:B:4:DG:H2''	1:B:5:DG:C5'	0.43	2.44	4	4
2:A:234:GLU:O	2:A:237:LYS:N	0.43	2.52	8	2
2:A:234:GLU:C	2:A:236:VAL:N	0.43	2.73	18	2
2:A:242:LYS:N	2:A:242:LYS:HD2	0.43	2.29	5	5
2:A:211:ILE:C	2:A:212:GLU:HG2	0.43	2.39	8	1
2:A:186:VAL:CG2	2:A:226:CYS:HB2	0.43	2.44	19	1
2:A:201:TYR:C	2:A:201:TYR:CD1	0.42	2.96	19	5
2:A:197:LYS:CD	2:A:198:ILE:HG12	0.42	2.43	3	1
2:A:199:ARG:HD2	2:A:211:ILE:HG13	0.42	1.89	9	1
2:A:205:PHE:O	2:A:235:PRO:HG3	0.42	2.14	17	3
1:B:4:DG:C5'	2:A:225:PHE:CZ	0.42	3.02	10	1
2:A:187:GLY:C	2:A:252:CYS:CB	0.42	2.90	13	1
2:A:189:LEU:CD2	2:A:225:PHE:O	0.42	2.68	15	1
2:A:233:GLU:N	2:A:233:GLU:OE1	0.42	2.52	16	1
2:A:183:LYS:O	2:A:236:VAL:HG13	0.42	2.13	18	1
2:A:183:LYS:HG2	2:A:229:THR:CG2	0.42	2.44	18	1
1:B:2:DT:O4	2:A:253:GLU:HB2	0.42	2.14	14	2
2:A:197:LYS:CE	2:A:247:VAL:CG1	0.42	2.97	3	1
2:A:185:PHE:CE2	2:A:255:LYS:CE	0.42	3.02	4	1
2:A:184:ILE:CD1	2:A:228:ILE:HB	0.42	2.45	13	2
1:B:4:DG:H1'	1:B:5:DG:OP1	0.42	2.13	20	2
2:A:209:GLU:N	2:A:229:THR:O	0.42	2.40	12	1
2:A:188:GLY:O	2:A:189:LEU:CB	0.42	2.67	17	1
2:A:189:LEU:HD13	2:A:190:SER:O	0.42	2.14	13	3
2:A:188:GLY:O	2:A:189:LEU:HB3	0.42	2.14	17	1
2:A:213:LEU:N	2:A:213:LEU:HD22	0.42	2.29	19	1
2:A:205:PHE:CB	2:A:235:PRO:HB3	0.42	2.41	17	3
2:A:238:LYS:NZ	2:A:238:LYS:HB3	0.42	2.28	9	1
2:A:243:LYS:NZ	2:A:244:TYR:CE2	0.42	2.83	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:197:LYS:HD3	2:A:247:VAL:HG12	0.42	1.91	3	1
2:A:184:ILE:CD1	2:A:202:PHE:CE2	0.42	3.03	5	2
1:B:4:DG:O6	2:A:183:LYS:HE2	0.42	2.15	8	1
2:A:183:LYS:HG2	2:A:229:THR:OG1	0.42	2.15	13	1
2:A:235:PRO:O	2:A:239:ILE:CD1	0.42	2.56	18	1
2:A:192:ASP:CG	2:A:192:ASP:O	0.42	2.63	5	1
2:A:184:ILE:CD1	2:A:254:ILE:CG2	0.42	2.93	6	2
2:A:194:PRO:HG2	2:A:197:LYS:CG	0.42	2.44	8	2
2:A:197:LYS:CD	2:A:247:VAL:HG12	0.42	2.45	3	1
2:A:246:ASN:HA	2:A:251:LYS:CB	0.42	2.45	14	1
2:A:211:ILE:C	2:A:212:GLU:OE2	0.42	2.63	15	1
2:A:232:GLU:CD	2:A:234:GLU:OE2	0.42	2.63	16	1
2:A:201:TYR:HE1	2:A:245:HIS:HD1	0.42	1.45	18	1
2:A:195:GLU:HA	2:A:198:ILE:HD12	0.42	1.91	8	4
2:A:230:PHE:O	2:A:232:GLU:N	0.42	2.53	17	1
1:B:4:DG:OP1	2:A:223:ARG:HG2	0.42	2.15	20	1
2:A:234:GLU:O	2:A:237:LYS:HB2	0.41	2.14	20	8
2:A:190:SER:C	2:A:192:ASP:N	0.41	2.78	9	3
2:A:195:GLU:O	2:A:199:ARG:HD3	0.41	2.14	9	1
2:A:184:ILE:CD1	2:A:239:ILE:HG21	0.41	2.45	12	1
2:A:236:VAL:O	2:A:239:ILE:HB	0.41	2.14	14	1
2:A:233:GLU:O	2:A:237:LYS:HB3	0.41	2.15	18	1
2:A:209:GLU:HB3	2:A:229:THR:HB	0.41	1.92	6	3
2:A:197:LYS:HE2	2:A:247:VAL:CG1	0.41	2.46	8	1
2:A:196:GLU:O	2:A:200:GLU:HG2	0.41	2.15	18	2
2:A:181:VAL:O	2:A:182:LYS:CG	0.41	2.69	9	1
2:A:240:MET:SD	2:A:256:VAL:HB	0.41	2.55	11	1
2:A:205:PHE:CZ	2:A:239:ILE:HG12	0.41	2.51	14	1
2:A:189:LEU:HD11	2:A:225:PHE:O	0.41	2.15	17	1
1:B:4:DG:C5	2:A:212:GLU:OE1	0.41	2.73	19	1
2:A:211:ILE:HD13	2:A:228:ILE:HD13	0.41	1.93	9	1
2:A:184:ILE:O	2:A:184:ILE:CG1	0.41	2.68	12	1
2:A:205:PHE:HE2	2:A:245:HIS:CE1	0.41	2.34	17	1
2:A:193:THR:CG2	2:A:250:SER:OG	0.41	2.69	18	1
2:A:197:LYS:HD3	2:A:198:ILE:HG12	0.41	1.93	6	1
2:A:202:PHE:CD1	2:A:228:ILE:CD1	0.41	3.04	11	2
1:B:4:DG:H1'	2:A:212:GLU:CD	0.41	2.39	12	1
2:A:237:LYS:NZ	2:A:237:LYS:CB	0.41	2.83	18	1
1:B:3:DA:C1'	1:B:4:DG:OP2	0.41	2.68	19	1
2:A:225:PHE:CG	2:A:226:CYS:N	0.41	2.87	13	5
2:A:235:PRO:O	2:A:239:ILE:HG12	0.41	2.12	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:3:DA:P	2:A:185:PHE:CZ	0.41	3.14	4	1
2:A:194:PRO:O	2:A:195:GLU:C	0.41	2.64	11	3
1:B:4:DG:C5	1:B:5:DG:N7	0.41	2.89	11	1
2:A:194:PRO:HG2	2:A:197:LYS:HD3	0.41	1.93	14	1
2:A:233:GLU:HG3	2:A:234:GLU:OE2	0.41	2.16	19	1
2:A:193:THR:O	2:A:213:LEU:HG	0.41	2.16	20	1
2:A:238:LYS:O	2:A:241:GLU:HB2	0.41	2.16	1	2
2:A:254:ILE:O	2:A:254:ILE:HG22	0.41	2.16	1	1
1:B:3:DA:H5'	2:A:223:ARG:CB	0.41	2.46	4	1
1:B:4:DG:H1'	1:B:5:DG:H5'	0.41	1.92	5	1
2:A:196:GLU:HA	2:A:199:ARG:HB2	0.41	1.92	9	1
2:A:209:GLU:N	2:A:230:PHE:HA	0.41	2.30	10	1
2:A:197:LYS:HE3	2:A:200:GLU:CD	0.41	2.41	15	1
2:A:185:PHE:CB	2:A:257:ALA:HA	0.41	2.45	19	1
2:A:210:SER:C	2:A:211:ILE:HG12	0.41	2.41	19	1
2:A:197:LYS:O	2:A:198:ILE:C	0.41	2.62	20	1
2:A:184:ILE:HB	2:A:254:ILE:HG22	0.41	1.93	5	2
2:A:205:PHE:CE2	2:A:239:ILE:CD1	0.40	3.05	7	2
2:A:202:PHE:HB3	2:A:230:PHE:CE2	0.40	2.51	18	1
2:A:249:LEU:O	2:A:251:LYS:HE3	0.40	2.16	17	1
2:A:239:ILE:C	2:A:241:GLU:N	0.40	2.78	4	1
1:B:3:DA:OP2	2:A:225:PHE:CG	0.40	2.74	11	1
2:A:253:GLU:CD	2:A:255:LYS:HD2	0.40	2.42	13	1
1:B:3:DA:N3	2:A:227:PHE:HZ	0.40	2.14	17	1
2:A:184:ILE:N	2:A:228:ILE:O	0.40	2.55	17	1
2:A:184:ILE:HA	2:A:257:ALA:H	0.40	1.77	1	3
2:A:209:GLU:CA	2:A:209:GLU:OE1	0.40	2.69	15	1
2:A:236:VAL:O	2:A:240:MET:CE	0.40	2.69	17	1
2:A:189:LEU:HD12	2:A:225:PHE:HA	0.40	1.93	20	1
1:B:3:DA:OP2	2:A:187:GLY:HA2	0.40	2.17	4	1
2:A:230:PHE:CG	2:A:236:VAL:HG22	0.40	2.52	16	1
2:A:183:LYS:HG2	2:A:229:THR:CB	0.40	2.47	18	1
2:A:205:PHE:CZ	2:A:239:ILE:HG13	0.40	2.50	18	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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
2	A	67/79 (85%)	42±2 (62±3%)	14±2 (21±3%)	11±1 (17±2%)	0 3
All	All	1340/1580 (85%)	836 (62%)	277 (21%)	227 (17%)	0 3

All 15 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	A	191	PRO	20
2	A	194	PRO	20
2	A	223	ARG	20
2	A	224	GLY	20
2	A	239	ILE	20
2	A	243	LYS	20
2	A	248	GLY	20
2	A	256	VAL	20
2	A	188	GLY	14
2	A	189	LEU	14
2	A	195	GLU	11
2	A	187	GLY	10
2	A	184	ILE	10
2	A	225	PHE	5
2	A	257	ALA	3

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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
2	A	60/71 (85%)	29±2 (49±4%)	31±2 (51±4%)	0 1
All	All	1200/1420 (85%)	584 (49%)	616 (51%)	0 1

All 47 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)
2	A	189	LEU	20
2	A	198	ILE	20

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Mol	Chain	Res	Type	Models (Total)
2	A	202	PHE	20
2	A	205	PHE	20
2	A	208	VAL	20
2	A	211	ILE	20
2	A	226	CYS	20
2	A	231	LYS	20
2	A	236	VAL	20
2	A	238	LYS	20
2	A	239	ILE	20
2	A	242	LYS	20
2	A	243	LYS	20
2	A	247	VAL	20
2	A	249	LEU	20
2	A	251	LYS	20
2	A	252	CYS	20
2	A	195	GLU	19
2	A	212	GLU	19
2	A	183	LYS	19
2	A	254	ILE	19
2	A	228	ILE	18
2	A	234	GLU	18
2	A	197	LYS	16
2	A	255	LYS	16
2	A	225	PHE	16
2	A	185	PHE	15
2	A	246	ASN	13
2	A	240	MET	11
2	A	250	SER	9
2	A	213	LEU	8
2	A	223	ARG	7
2	A	233	GLU	7
2	A	200	GLU	6
2	A	199	ARG	6
2	A	192	ASP	6
2	A	237	LYS	5
2	A	186	VAL	4
2	A	232	GLU	4
2	A	190	SER	3
2	A	241	GLU	3
2	A	207	GLU	3
2	A	229	THR	2
2	A	196	GLU	1

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Mol	Chain	Res	Type	Models (Total)
2	A	210	SER	1
2	A	256	VAL	1
2	A	209	GLU	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided