Full wwPDB X-ray Structure Validation Report (i)

Aug 14, 2023 – 12:32 PM EDT

PDB ID	:	1R4R
Title	:	Crystallographic analysis of the interaction of the glucocorticoid receptor with DNA
Authors	:	Luisi, B.F.; Xu, W.X.; Otwinowski, Z.; Freedman, L.P.; Yamamoto, K.R.; Sigler, P.B.
Deposited on	:	2003-10-07
Resolution	:	3.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

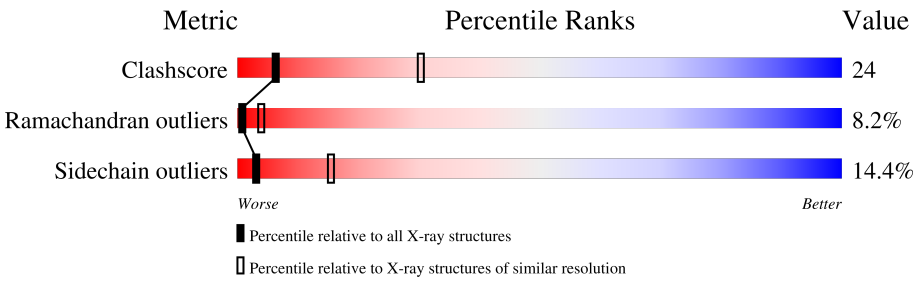
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	19	37% 53% 11%
2	D	19	37% 47% 16%
3	A	92	37% 33% 9% • 21%
3	B	92	41% 34% 8% • 16%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2314 atoms, of which 380 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
1	C	19	422	186	37	69	112	18	0	0	0

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P			
2	D	19	424	186	38	69	113	18	0	0	0

- Molecule 3 is a protein called Glucocorticoid receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	A	73	714	344	149	112	98	11	0	0	0
3	B	77	750	363	156	117	102	12	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	434	MET	-	cloning artifact	UNP P06536
A	435	LYS	-	cloning artifact	UNP P06536
A	436	PRO	-	cloning artifact	UNP P06536
A	437	ALA	-	cloning artifact	UNP P06536
A	438	ARG	-	cloning artifact	UNP P06536
A	439	PRO	-	cloning artifact	UNP P06536
B	434	MET	-	cloning artifact	UNP P06536
B	435	LYS	-	cloning artifact	UNP P06536
B	436	PRO	-	cloning artifact	UNP P06536
B	437	ALA	-	cloning artifact	UNP P06536

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Chain	Residue	Modelled	Actual	Comment	Reference
B	438	ARG	-	cloning artifact	UNP P06536
B	439	PRO	-	cloning artifact	UNP P06536

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	2	2	2	0	0
			Total	Zn		
4	B	2	2	2	0	0

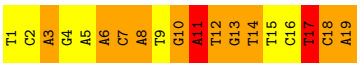
3 Residue-property plots (i)

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

Note EDS was not executed.

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

Chain C: 37% 53% 11%

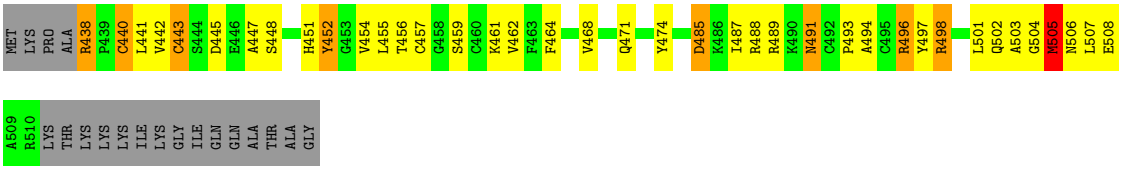


• Molecule 2: 5'-D(*CP*TP*GP*AP*GP*AP*AP*CP*AP*TP*CP*AP*TP*GP*TP*TP*CP*TP*G)-3'

Chain D: 37% 47% 16%

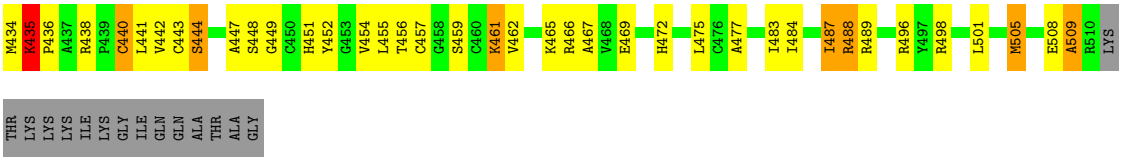
• Molecule 3: Glucocorticoid receptor

Chain A: 37% 33% 9% • 21%



• Molecule 3: Glucocorticoid receptor

Chain B: 41% 34% 8% • 16%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	38.50Å 99.70Å 121.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2314	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	C	2.48	21/431 (4.9%)	3.56	86/663 (13.0%)
2	D	2.29	16/432 (3.7%)	3.36	74/665 (11.1%)
3	A	0.39	0/573	0.70	0/765
3	B	0.40	0/603	0.63	0/805
All	All	1.58	37/2039 (1.8%)	2.39	160/2898 (5.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	4
2	D	0	4
All	All	0	8

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	18	DC	P-O5'	10.92	1.70	1.59
1	C	12	DT	C5-C7	10.24	1.56	1.50
1	C	15	DT	C5-C7	9.22	1.55	1.50
1	C	3	DA	N9-C4	-8.66	1.32	1.37
1	C	12	DT	P-O5'	-7.91	1.51	1.59
1	C	6	DA	C5'-C4'	7.82	1.59	1.51
2	D	10	DT	P-O5'	7.57	1.67	1.59
2	D	11	DC	P-O5'	7.54	1.67	1.59
1	C	17	DT	C5-C7	7.29	1.54	1.50
2	D	17	DC	O3'-P	7.26	1.69	1.61
2	D	7	DA	O3'-P	7.25	1.69	1.61
2	D	9	DA	C5'-C4'	7.05	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	7	DA	P-O5'	6.84	1.66	1.59
2	D	10	DT	C5'-C4'	6.73	1.58	1.51
1	C	14	DT	C5-C7	6.66	1.54	1.50
2	D	1	DC	O3'-P	6.58	1.69	1.61
2	D	7	DA	C5'-C4'	6.58	1.58	1.51
1	C	9	DT	P-O5'	6.53	1.66	1.59
1	C	7	DC	C4'-C3'	6.48	1.59	1.53
1	C	6	DA	N9-C4	6.42	1.41	1.37
1	C	7	DC	O3'-P	6.36	1.68	1.61
1	C	19	DA	C5'-C4'	6.34	1.58	1.51
1	C	16	DC	C3'-C2'	6.21	1.59	1.52
1	C	19	DA	P-O5'	6.10	1.65	1.59
1	C	10	DG	C2'-C1'	-6.02	1.46	1.52
2	D	5	DG	C2-N3	5.84	1.37	1.32
2	D	10	DT	N1-C6	-5.78	1.34	1.38
1	C	9	DT	C5-C7	5.77	1.53	1.50
2	D	8	DC	P-O5'	5.77	1.65	1.59
2	D	3	DG	C5'-C4'	5.66	1.57	1.51
2	D	3	DG	C2'-C1'	-5.57	1.46	1.52
1	C	19	DA	C4'-C3'	5.42	1.58	1.53
2	D	8	DC	C2'-C1'	-5.42	1.46	1.52
1	C	17	DT	P-O5'	5.24	1.65	1.59
2	D	16	DT	P-O5'	5.17	1.65	1.59
1	C	11	DA	C6-N1	-5.11	1.31	1.35
1	C	5	DA	P-O5'	5.04	1.64	1.59

All (160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	19	DG	C1'-O4'-C4'	-19.83	90.27	110.10
2	D	13	DT	O4'-C1'-N1	15.95	119.16	108.00
1	C	11	DA	C1'-O4'-C4'	-15.92	94.18	110.10
2	D	5	DG	C1'-O4'-C4'	-15.04	95.06	110.10
1	C	16	DC	O4'-C1'-C2'	-15.03	93.88	105.90
1	C	10	DG	C1'-O4'-C4'	-15.03	95.07	110.10
1	C	6	DA	O4'-C4'-C3'	-13.94	97.64	106.00
2	D	11	DC	O4'-C4'-C3'	-13.67	97.80	106.00
1	C	11	DA	O4'-C4'-C3'	-13.65	97.81	106.00
1	C	10	DG	O4'-C4'-C3'	-13.44	97.94	106.00
1	C	1	DT	O4'-C4'-C3'	-13.22	98.06	106.00
2	D	5	DG	O4'-C4'-C3'	-13.04	98.17	106.00
2	D	17	DC	C1'-O4'-C4'	-12.46	97.64	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	12	DT	C1'-O4'-C4'	-12.33	97.77	110.10
1	C	15	DT	O4'-C4'-C3'	-12.19	98.69	106.00
2	D	18	DT	O4'-C4'-C3'	-12.10	98.74	106.00
2	D	19	DG	O4'-C4'-C3'	-12.10	98.74	106.00
2	D	1	DC	O4'-C1'-N1	11.64	116.15	108.00
1	C	10	DG	O3'-P-O5'	-11.36	82.42	104.00
2	D	16	DT	O4'-C1'-C2'	-11.31	96.86	105.90
1	C	7	DC	P-O3'-C3'	11.20	133.15	119.70
2	D	5	DG	O4'-C1'-C2'	-11.01	97.10	105.90
1	C	18	DC	N1-C2-O2	10.86	125.42	118.90
1	C	9	DT	N3-C2-O2	-10.82	115.81	122.30
1	C	18	DC	O4'-C4'-C3'	-10.70	99.58	106.00
2	D	4	DA	O4'-C1'-N9	10.47	115.33	108.00
2	D	9	DA	O4'-C1'-C2'	-10.41	97.57	105.90
1	C	18	DC	N3-C2-O2	-10.04	114.87	121.90
2	D	15	DT	C6-C5-C7	-9.74	117.05	122.90
1	C	1	DT	O4'-C1'-C2'	-9.69	98.14	105.90
1	C	9	DT	C4'-C3'-C2'	-9.44	94.60	103.10
2	D	14	DG	O4'-C1'-C2'	-9.40	98.38	105.90
1	C	1	DT	C6-C5-C7	-9.20	117.38	122.90
2	D	8	DC	O4'-C4'-C3'	-9.09	100.55	106.00
1	C	9	DT	O4'-C4'-C3'	-9.07	100.56	106.00
1	C	7	DC	C1'-O4'-C4'	-9.00	101.10	110.10
1	C	14	DT	N1-C2-N3	8.94	119.96	114.60
2	D	1	DC	P-O3'-C3'	8.79	130.25	119.70
1	C	2	DC	O4'-C1'-C2'	-8.70	98.94	105.90
1	C	18	DC	O4'-C1'-C2'	-8.65	98.98	105.90
1	C	17	DT	C6-C5-C7	-8.63	117.72	122.90
2	D	10	DT	C4-C5-C6	8.44	123.06	118.00
1	C	9	DT	C1'-O4'-C4'	-8.43	101.67	110.10
2	D	19	DG	C4'-C3'-C2'	-8.42	95.53	103.10
2	D	13	DT	C6-C5-C7	-8.31	117.92	122.90
2	D	1	DC	N3-C2-O2	-8.21	116.16	121.90
2	D	18	DT	C6-C5-C7	-8.21	117.98	122.90
2	D	10	DT	N3-C2-O2	-8.20	117.38	122.30
1	C	10	DG	O4'-C1'-N9	8.20	113.74	108.00
1	C	9	DT	C4-C5-C6	8.19	122.92	118.00
2	D	15	DT	C4-C5-C6	8.15	122.89	118.00
1	C	9	DT	C6-N1-C2	-8.15	117.23	121.30
2	D	3	DG	O4'-C1'-C2'	-8.15	99.38	105.90
1	C	9	DT	N1-C2-N3	8.10	119.46	114.60
1	C	14	DT	O4'-C4'-C3'	8.07	110.84	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	10	DT	C6-C5-C7	-7.93	118.14	122.90
1	C	9	DT	O4'-C1'-C2'	-7.93	99.56	105.90
1	C	16	DC	N1-C2-O2	7.89	123.63	118.90
1	C	7	DC	C4'-C3'-C2'	-7.84	96.05	103.10
1	C	12	DT	C6-C5-C7	-7.84	118.20	122.90
1	C	16	DC	N3-C2-O2	-7.77	116.46	121.90
2	D	3	DG	O4'-C1'-N9	7.76	113.43	108.00
2	D	11	DC	N3-C2-O2	-7.67	116.53	121.90
1	C	1	DT	N3-C2-O2	-7.61	117.73	122.30
1	C	7	DC	N1-C2-O2	7.47	123.38	118.90
2	D	11	DC	N1-C2-O2	7.33	123.30	118.90
2	D	13	DT	C1'-O4'-C4'	-7.21	102.89	110.10
2	D	6	DA	N1-C6-N6	7.17	122.91	118.60
2	D	19	DG	O4'-C1'-C2'	-7.17	100.17	105.90
2	D	16	DT	N3-C2-O2	-7.14	118.02	122.30
1	C	13	DG	N3-C2-N2	-7.03	114.98	119.90
1	C	4	DG	O4'-C4'-C3'	-7.02	101.69	104.50
1	C	4	DG	P-O3'-C3'	7.01	128.11	119.70
2	D	7	DA	O4'-C1'-N9	7.01	112.91	108.00
1	C	15	DT	C1'-O4'-C4'	-6.99	103.11	110.10
1	C	14	DT	C4-C5-C6	6.95	122.17	118.00
1	C	1	DT	P-O3'-C3'	-6.95	111.36	119.70
2	D	16	DT	C4-C5-C6	6.95	122.17	118.00
2	D	1	DC	N1-C2-O2	6.94	123.06	118.90
2	D	7	DA	O4'-C1'-C2'	-6.89	100.39	105.90
2	D	13	DT	C4-C5-C6	6.85	122.11	118.00
1	C	19	DA	N1-C6-N6	6.81	122.69	118.60
1	C	6	DA	O4'-C1'-C2'	-6.81	100.45	105.90
1	C	7	DC	O4'-C1'-C2'	-6.79	100.47	105.90
2	D	5	DG	O4'-C1'-N9	6.72	112.71	108.00
2	D	6	DA	C5-C6-N6	-6.71	118.33	123.70
1	C	5	DA	C4'-C3'-C2'	-6.62	97.14	103.10
1	C	11	DA	O5'-P-OP2	6.61	118.64	110.70
2	D	8	DC	O4'-C1'-N1	6.52	112.57	108.00
2	D	18	DT	O3'-P-O5'	-6.47	91.71	104.00
1	C	4	DG	C1'-O4'-C4'	-6.46	103.64	110.10
2	D	16	DT	O4'-C1'-N1	6.41	112.48	108.00
1	C	7	DC	O4'-C4'-C3'	6.37	109.82	106.00
1	C	13	DG	N9-C4-C5	6.36	107.94	105.40
1	C	2	DC	N1-C2-O2	6.34	122.70	118.90
1	C	14	DT	C4'-C3'-C2'	-6.34	97.40	103.10
2	D	7	DA	C5-C6-N6	-6.28	118.68	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	9	DT	N1-C1'-C2'	6.27	124.52	112.60
2	D	6	DA	P-O5'-C5'	-6.25	110.89	120.90
1	C	2	DC	P-O5'-C5'	-6.18	111.01	120.90
2	D	17	DC	O4'-C1'-N1	6.18	112.33	108.00
2	D	9	DA	O3'-P-O5'	-6.16	92.29	104.00
1	C	2	DC	O3'-P-O5'	6.15	115.68	104.00
1	C	11	DA	C4'-C3'-C2'	-6.12	97.59	103.10
1	C	13	DG	C8-N9-C4	-6.11	103.95	106.40
1	C	8	DA	P-O3'-C3'	-6.10	112.38	119.70
2	D	6	DA	C4'-C3'-C2'	-6.10	97.61	103.10
2	D	11	DC	P-O5'-C5'	6.05	130.58	120.90
2	D	15	DT	O4'-C4'-C3'	6.05	109.63	106.00
1	C	15	DT	C6-C5-C7	-5.93	119.34	122.90
1	C	1	DT	C4-C5-C6	5.92	121.55	118.00
2	D	9	DA	N9-C4-C5	5.92	108.17	105.80
1	C	10	DG	C4'-C3'-C2'	-5.91	97.78	103.10
2	D	18	DT	C4-C5-C6	5.91	121.55	118.00
1	C	1	DT	O4'-C1'-N1	5.89	112.12	108.00
1	C	12	DT	O4'-C1'-N1	5.89	112.12	108.00
1	C	18	DC	P-O3'-C3'	5.82	126.69	119.70
2	D	15	DT	N3-C2-O2	-5.81	118.81	122.30
2	D	5	DG	C4'-C3'-C2'	-5.79	97.89	103.10
2	D	9	DA	O4'-C1'-N9	5.75	112.03	108.00
1	C	11	DA	O4'-C1'-N9	5.74	112.02	108.00
2	D	2	DT	N3-C2-O2	-5.72	118.87	122.30
1	C	9	DT	N3-C4-C5	-5.71	111.78	115.20
1	C	3	DA	C5-C6-N1	-5.70	114.85	117.70
2	D	16	DT	C5-C6-N1	-5.69	120.28	123.70
1	C	17	DT	O4'-C1'-N1	-5.66	104.04	108.00
2	D	12	DA	O4'-C1'-N9	5.66	111.96	108.00
1	C	12	DT	P-O5'-C5'	-5.66	111.85	120.90
2	D	19	DG	N3-C2-N2	-5.62	115.96	119.90
1	C	4	DG	O4'-C1'-N9	-5.61	104.07	108.00
1	C	9	DT	P-O5'-C5'	5.60	129.86	120.90
2	D	7	DA	C6-N1-C2	-5.56	115.26	118.60
2	D	17	DC	N1-C2-O2	5.53	122.22	118.90
2	D	7	DA	C4'-C3'-C2'	-5.49	98.16	103.10
1	C	3	DA	P-O5'-C5'	-5.47	112.15	120.90
2	D	6	DA	O4'-C1'-C2'	-5.47	101.53	105.90
2	D	15	DT	C5'-C4'-C3'	-5.42	104.35	114.10
2	D	2	DT	C4-C5-C6	5.37	121.22	118.00
2	D	9	DA	C1'-O4'-C4'	-5.34	104.76	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	13	DG	N1-C2-N2	5.32	120.99	116.20
1	C	3	DA	C3'-C2'-C1'	5.26	108.81	102.50
2	D	16	DT	P-O3'-C3'	5.24	125.99	119.70
2	D	7	DA	P-O3'-C3'	5.22	125.97	119.70
1	C	4	DG	C4'-C3'-O3'	-5.21	96.68	109.70
1	C	11	DA	P-O3'-C3'	-5.16	113.50	119.70
1	C	18	DC	C1'-O4'-C4'	5.15	115.25	110.10
1	C	14	DT	C2-N3-C4	-5.15	124.11	127.20
2	D	2	DT	P-O3'-C3'	5.09	125.81	119.70
2	D	9	DA	N1-C2-N3	5.09	131.84	129.30
2	D	19	DG	O4'-C1'-N9	-5.09	104.44	108.00
1	C	12	DT	C5-C4-O4	5.06	128.44	124.90
2	D	15	DT	C5-C4-O4	5.06	128.44	124.90
1	C	14	DT	N3-C2-O2	-5.05	119.27	122.30
1	C	17	DT	C4-C5-C6	5.04	121.02	118.00
1	C	1	DT	C1'-O4'-C4'	-5.03	105.07	110.10
1	C	11	DA	N1-C2-N3	5.02	131.81	129.30
2	D	12	DA	P-O5'-C5'	-5.02	112.87	120.90
2	D	18	DT	C1'-O4'-C4'	-5.02	105.08	110.10
1	C	3	DA	C2-N3-C4	-5.01	108.10	110.60
1	C	6	DA	O4'-C1'-N9	-5.01	104.50	108.00

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	10	DG	Sidechain
1	C	11	DA	Sidechain
1	C	17	DT	Sidechain
1	C	8	DA	Sidechain
2	D	18	DT	Sidechain
2	D	2	DT	Sidechain
2	D	7	DA	Sidechain
2	D	8	DC	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	385	37	217	7	0
2	D	386	38	217	9	0
3	A	565	149	556	35	0
3	B	594	156	590	39	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
All	All	1934	380	1580	83	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (83) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:487:ILE:HD13	3:B:475:LEU:HD12	1.56	0.88
3:B:498:ARG:HH11	3:B:498:ARG:HB3	1.42	0.84
1:C:13:DG:H5'	3:B:489:ARG:HH21	1.47	0.80
3:A:468:VAL:HG11	3:A:507:LEU:HD22	1.65	0.78
3:A:454:VAL:HG21	3:A:503:ALA:O	1.91	0.71
3:A:489:ARG:HD2	3:A:496:ARG:HH12	1.54	0.71
3:A:491:ASN:O	3:A:493:PRO:HD3	1.91	0.70
3:A:452:TYR:HE1	3:A:461:LYS:HG2	1.56	0.70
3:B:435:LYS:N	3:B:436:PRO:HD3	2.08	0.68
3:B:484:ILE:HG22	3:B:484:ILE:O	1.96	0.64
3:B:498:ARG:HB3	3:B:498:ARG:NH1	2.13	0.64
3:A:451:HIS:HB2	3:A:456:THR:OG1	1.98	0.63
3:B:443:CYS:SG	3:B:444:SER:N	2.72	0.62
2:D:1:DC:H2"	2:D:2:DT:O5'	2.01	0.61
3:B:462:VAL:O	3:B:466:ARG:HB2	2.01	0.61
3:A:488:ARG:HG2	3:B:477:ALA:HB2	1.82	0.59
1:C:18:DC:H2'	1:C:19:DA:C8	2.37	0.59
3:B:451:HIS:HB2	3:B:456:THR:OG1	2.02	0.59
3:A:468:VAL:CG1	3:A:507:LEU:HD22	2.33	0.59
2:D:5:DG:H2"	2:D:6:DA:O5'	2.03	0.58
3:A:452:TYR:HB3	3:A:506:ASN:O	2.03	0.58
3:B:435:LYS:CE	3:B:435:LYS:HA	2.35	0.57
2:D:7:DA:H1'	2:D:8:DC:C6	2.40	0.56
3:B:434:MET:C	3:B:436:PRO:HD3	2.25	0.56
1:C:17:DT:H2'	1:C:18:DC:O4'	2.05	0.56
3:A:441:LEU:HD12	3:A:454:VAL:HG13	1.88	0.56
3:B:441:LEU:HD22	3:B:454:VAL:HG21	1.86	0.56
2:D:16:DT:H2"	2:D:17:DC:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:440:CYS:C	3:A:442:VAL:H	2.10	0.55
3:A:456:THR:HG21	3:A:505:MET:HE1	1.89	0.55
3:B:435:LYS:HA	3:B:435:LYS:HE2	1.89	0.54
3:A:452:TYR:HE1	3:A:461:LYS:CG	2.21	0.54
3:B:440:CYS:SG	3:B:442:VAL:HB	2.48	0.54
2:D:4:DA:H2"	2:D:5:DG:H8	1.72	0.53
3:B:456:THR:HG21	3:B:505:MET:SD	2.49	0.53
3:B:457:CYS:SG	3:B:459:SER:HB2	2.49	0.53
3:B:443:CYS:O	3:B:444:SER:HB2	2.09	0.52
3:A:443:CYS:SG	3:A:445:ASP:CB	2.97	0.52
3:A:448:SER:OG	3:A:451:HIS:NE2	2.43	0.52
3:A:474:TYR:CD1	3:A:493:PRO:HB2	2.44	0.51
3:B:448:SER:O	3:B:451:HIS:NE2	2.44	0.51
3:B:454:VAL:HG12	3:B:505:MET:HG2	1.92	0.50
3:A:452:TYR:CE1	3:A:461:LYS:HG2	2.42	0.50
3:A:487:ILE:CD1	3:B:475:LEU:HD12	2.37	0.49
3:B:508:GLU:O	3:B:509:ALA:HB3	2.12	0.48
3:A:443:CYS:SG	3:A:445:ASP:HB3	2.53	0.48
3:B:483:ILE:HD12	3:B:488:ARG:NH1	2.28	0.48
3:A:487:ILE:HG23	3:A:488:ARG:N	2.29	0.48
1:C:6:DA:H4'	1:C:7:DC:OP1	2.14	0.48
3:A:497:TYR:HD2	3:A:498:ARG:NH2	2.12	0.47
2:D:3:DG:H2'	2:D:3:DG:OP2	2.15	0.47
3:A:488:ARG:HG2	3:B:477:ALA:CB	2.45	0.47
3:B:441:LEU:CD2	3:B:454:VAL:HG21	2.45	0.47
3:B:454:VAL:HG22	3:B:455:LEU:N	2.30	0.47
3:B:467:ALA:O	3:B:472:HIS:CE1	2.68	0.47
2:D:14:DG:OP2	3:A:496:ARG:NH2	2.48	0.46
3:B:454:VAL:HG22	3:B:455:LEU:H	1.80	0.46
3:A:443:CYS:SG	3:A:445:ASP:HB2	2.57	0.45
3:B:435:LYS:HA	3:B:435:LYS:NZ	2.31	0.45
1:C:13:DG:C8	1:C:14:DT:H72	2.52	0.44
3:A:485:ASP:O	3:A:489:ARG:HB3	2.17	0.44
3:A:488:ARG:HD3	3:B:477:ALA:HA	2.00	0.44
3:B:452:TYR:OH	3:B:465:LYS:HD3	2.17	0.44
2:D:7:DA:OP2	2:D:7:DA:H2'	2.18	0.44
1:C:3:DA:H8	1:C:3:DA:O5'	2.01	0.43
3:B:441:LEU:HD22	3:B:454:VAL:CG2	2.48	0.43
3:B:435:LYS:HA	3:B:435:LYS:HZ3	1.84	0.43
3:A:494:ALA:O	3:A:498:ARG:NE	2.52	0.42
3:A:447:ALA:HA	3:A:457:CYS:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:442:VAL:HG23	3:B:456:THR:HG22	2.00	0.42
3:B:484:ILE:O	3:B:484:ILE:CG2	2.67	0.42
3:A:438:ARG:N	3:A:438:ARG:HD2	2.35	0.41
1:C:11:DA:H2'	1:C:12:DT:O4'	2.20	0.41
3:A:504:GLY:O	3:A:505:MET:C	2.59	0.41
3:B:508:GLU:O	3:B:509:ALA:CB	2.69	0.41
2:D:7:DA:H4'	2:D:8:DC:OP1	2.20	0.41
3:A:440:CYS:SG	3:A:443:CYS:N	2.80	0.41
3:B:484:ILE:HG21	3:B:496:ARG:HG3	2.01	0.41
3:A:440:CYS:HA	3:A:455:LEU:O	2.21	0.41
3:A:464:PHE:O	3:A:468:VAL:HG23	2.21	0.41
3:B:452:TYR:HE2	3:B:461:LYS:HD3	1.85	0.41
3:A:456:THR:CG2	3:A:505:MET:HE1	2.50	0.40
3:B:487:ILE:H	3:B:487:ILE:HG13	1.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	71/92 (77%)	51 (72%)	15 (21%)	5 (7%)	1 6
3	B	75/92 (82%)	51 (68%)	17 (23%)	7 (9%)	0 3
All	All	146/184 (79%)	102 (70%)	32 (22%)	12 (8%)	1 4

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	491	ASN
3	B	444	SER
3	A	505	MET
3	B	435	LYS

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Mol	Chain	Res	Type
3	B	449	GLY
3	B	509	ALA
3	A	452	TYR
3	B	438	ARG
3	B	447	ALA
3	A	440	CYS
3	A	508	GLU
3	B	488	ARG

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	A	61/75 (81%)	50 (82%)	11 (18%)	1 9
3	B	64/75 (85%)	57 (89%)	7 (11%)	6 25
All	All	125/150 (83%)	107 (86%)	18 (14%)	3 15

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	438	ARG
3	A	443	CYS
3	A	459	SER
3	A	462	VAL
3	A	471	GLN
3	A	485	ASP
3	A	496	ARG
3	A	498	ARG
3	A	501	LEU
3	A	502	GLN
3	A	505	MET
3	B	435	LYS
3	B	440	CYS
3	B	461	LYS
3	B	469	GLU

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Mol	Chain	Res	Type
3	B	487	ILE
3	B	501	LEU
3	B	505	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	480	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.