



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:19 PM GMT

PDB ID : 3T72
Title : PhoB(E)-Sigma70(4)-(RNAP-Betha-flap-tip-helix)-DNA Transcription
Activation Sub-Complex
Authors : Blanco, A.G.; Canals, A.; Bernues, J.; Sola, M.; Coll, M.
Deposited on : 2011-07-29
Resolution : 4.33 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

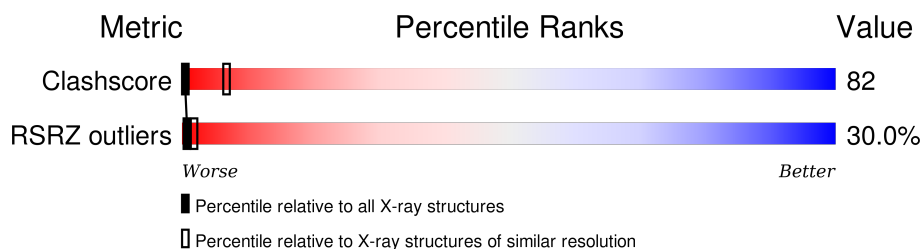
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

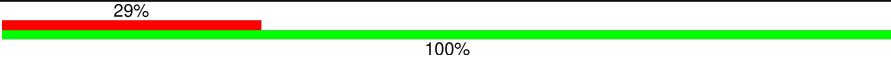
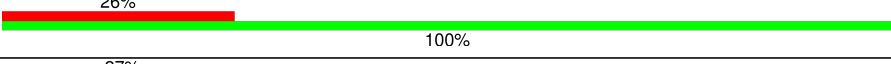
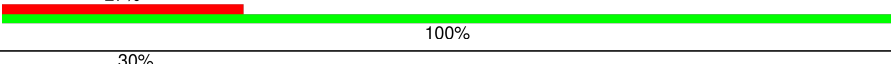
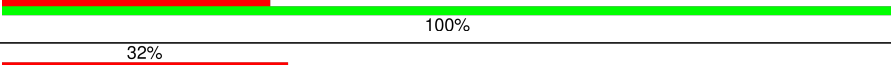
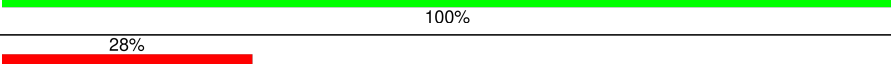

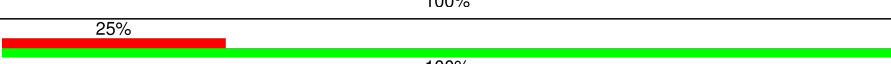
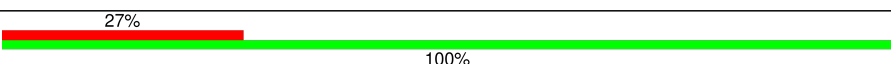

The reported resolution of this entry is 4.33 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1171 (5.08-3.60)
RSRZ outliers	91569	1067 (5.08-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	102	
1	4	102	
1	5	102	
1	8	102	
1	9	102	
1	A	102	
1	B	102	
1	E	102	
1	F	102	

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Mol	Chain	Length	Quality of chain
1	I	102	29% 100%
1	J	102	24% 100%
1	M	102	29% 100%
1	N	102	25% 100%
1	R	102	29% 100%
1	S	102	29% 100%
1	V	102	30% 100%
1	W	102	27% 100%
1	Z	102	28% 100%
1	c	102	31% 100%
1	d	102	22% 100%
1	g	102	25% 100%
1	h	102	29% 100%
1	k	102	30% 100%
1	l	102	24% 100%
2	2	26	50% 100%
2	6	26	27% 92% 8%
2	C	26	35% 96% .
2	G	26	19% 96% .
2	K	26	50% 100%
2	O	26	50% 100%
2	T	26	23% 96% .
2	X	26	42% 100%
2	a	26	35% 81% 19%
2	e	26	38% 92% 8%

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Mol	Chain	Length	Quality of chain
2	i	26	<div> <div>35%</div> <div>96%</div> <div>.</div> </div>
2	m	26	<div> <div>31%</div> <div>88%</div> <div>12%</div> </div>
3	3	26	<div> <div>50%</div> <div>92%</div> <div>8%</div> </div>
3	7	26	<div> <div>31%</div> <div>88%</div> <div>12%</div> </div>
3	D	26	<div> <div>35%</div> <div>92%</div> <div>8%</div> </div>
3	H	26	<div> <div>38%</div> <div>88%</div> <div>12%</div> </div>
3	L	26	<div> <div>46%</div> <div>96%</div> <div>.</div> </div>
3	P	26	<div> <div>50%</div> <div>96%</div> <div>.</div> </div>
3	U	26	<div> <div>31%</div> <div>92%</div> <div>8%</div> </div>
3	Y	26	<div> <div>42%</div> <div>96%</div> <div>.</div> </div>
3	b	26	<div> <div>27%</div> <div>81%</div> <div>19%</div> </div>
3	f	26	<div> <div>38%</div> <div>92%</div> <div>8%</div> </div>
3	j	26	<div> <div>42%</div> <div>92%</div> <div>8%</div> </div>
3	n	26	<div> <div>38%</div> <div>85%</div> <div>15%</div> </div>
4	o	99	<div> <div>35%</div> <div>94%</div> <div>6%</div> </div>
4	q	99	<div> <div>28%</div> <div>94%</div> <div>6%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15354 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Phosphate regulon transcriptional regulatory protein phoB.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	102	Total C 102 102	0	0	102
1	B	102	Total C 102 102	0	0	102
1	E	102	Total C 102 102	0	0	102
1	F	102	Total C 102 102	0	0	102
1	I	102	Total C 102 102	0	0	102
1	J	102	Total C 102 102	0	0	102
1	M	102	Total C 102 102	0	0	102
1	N	102	Total C 102 102	0	0	102
1	R	102	Total C 102 102	0	0	102
1	S	102	Total C 102 102	0	0	102
1	V	102	Total C 102 102	0	0	102
1	W	102	Total C 102 102	0	0	102
1	Z	102	Total C 102 102	0	0	102
1	1	102	Total C 102 102	0	0	102
1	4	102	Total C 102 102	0	0	102
1	5	102	Total C 102 102	0	0	102

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
1	8	102	Total 102	C 102	0	0	102
1	9	102	Total 102	C 102	0	0	102
1	c	102	Total 102	C 102	0	0	102
1	d	102	Total 102	C 102	0	0	102
1	g	102	Total 102	C 102	0	0	102
1	h	102	Total 102	C 102	0	0	102
1	k	102	Total 102	C 102	0	0	102
1	l	102	Total 102	C 102	0	0	102

- Molecule 2 is a DNA chain called PHO BOX DNA (STRAND 1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	G	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	K	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	O	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	T	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	X	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	2	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	6	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	a	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	e	26	Total 534	C 256	N 101	O 152	P 25	0	0	0
2	i	26	Total 534	C 256	N 101	O 152	P 25	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	m	26	Total	C	N	O	P	0	0	0
			534	256	101	152	25			

- Molecule 3 is a DNA chain called PHO BOX DNA (STRAND 2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	H	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	L	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	P	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	U	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	Y	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	3	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	7	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	b	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	f	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	j	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			
3	n	26	Total	C	N	O	P	0	0	0
			526	254	91	156	25			

- Molecule 4 is a protein called RNA polymerase sigma factor rpoD, DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
4	o	93	Total	C	0	0	93
			93	93			
4	q	93	Total	C	0	0	93
			93	93			

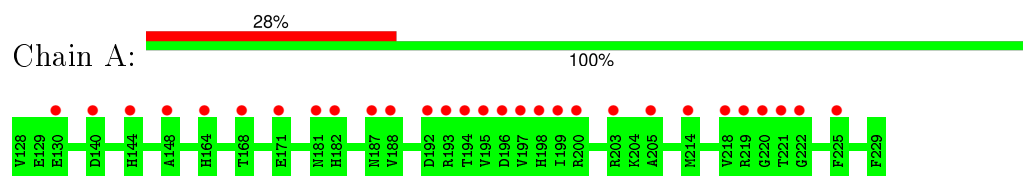
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	532	MET	-	EXPRESSION TAG	UNP P00579
q	890	GLY	-	LINKER	UNP P00579
q	891	SER	-	LINKER	UNP P00579
q	892	SER	-	LINKER	UNP P00579
q	893	GLY	-	LINKER	UNP P00579
q	894	SER	-	LINKER	UNP P00579
q	895	GLY	-	LINKER	UNP P00579
o	532	MET	-	EXPRESSION TAG	UNP P00579
o	890	GLY	-	LINKER	UNP P00579
o	891	SER	-	LINKER	UNP P00579
o	892	SER	-	LINKER	UNP P00579
o	893	GLY	-	LINKER	UNP P00579
o	894	SER	-	LINKER	UNP P00579
o	895	GLY	-	LINKER	UNP P00579

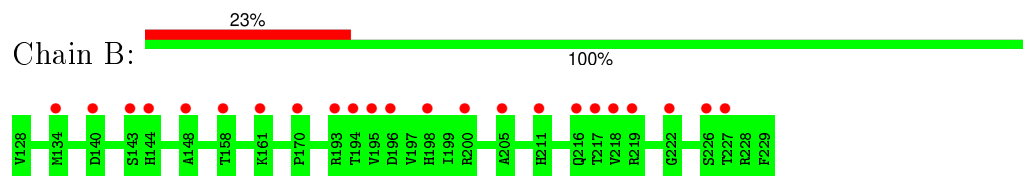
3 Residue-property plots [i](#)

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

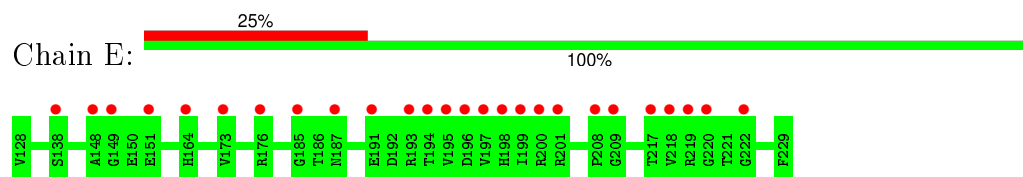
- Molecule 1: Phosphate regulon transcriptional regulatory protein phoB



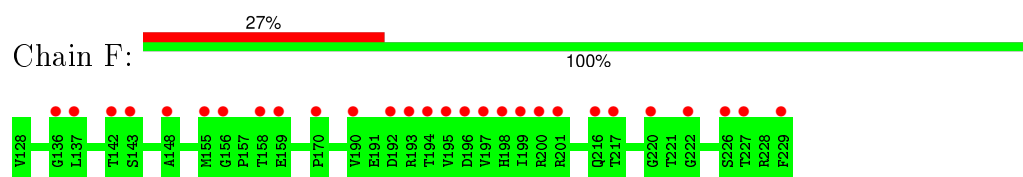
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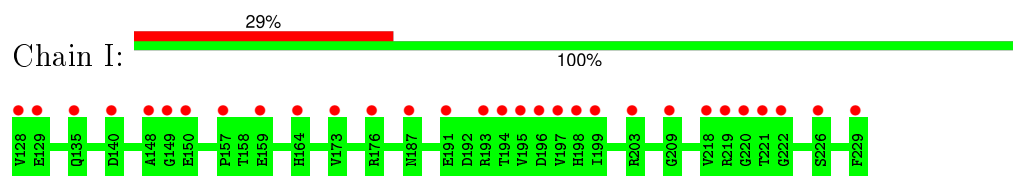
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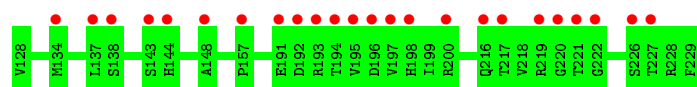
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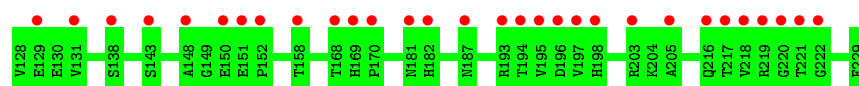
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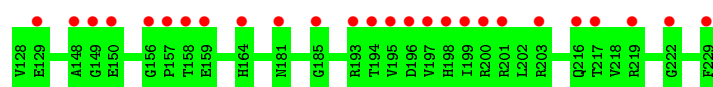
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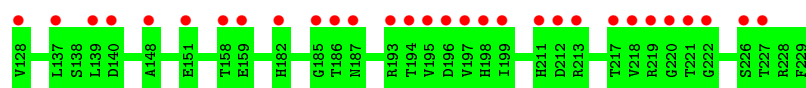
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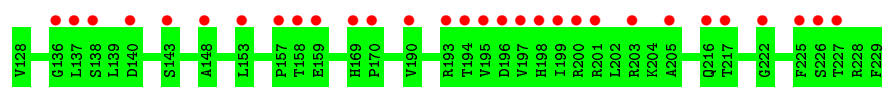
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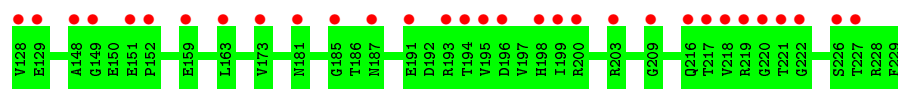
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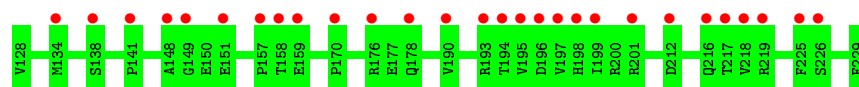
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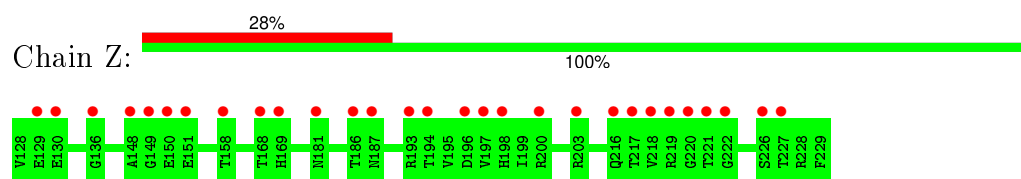
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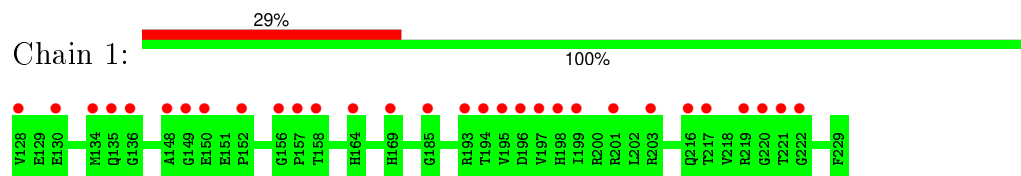
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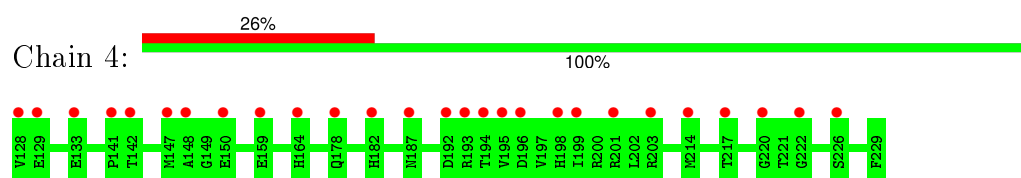
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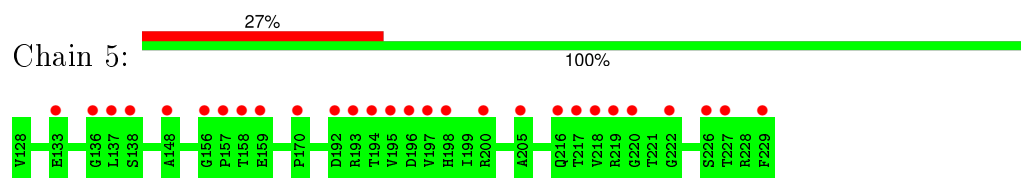
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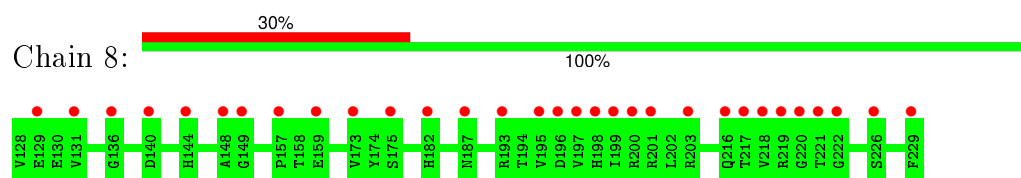
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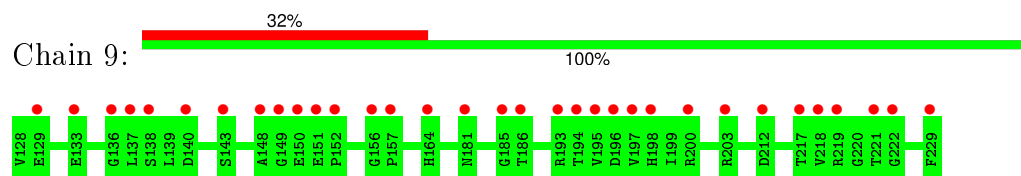
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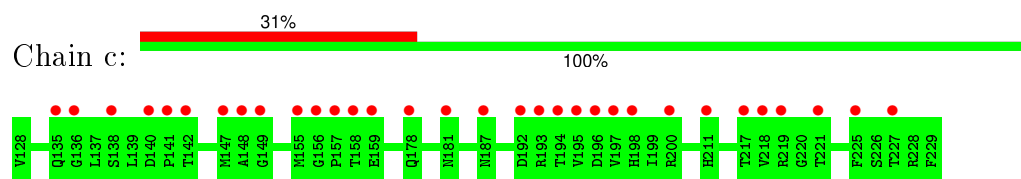
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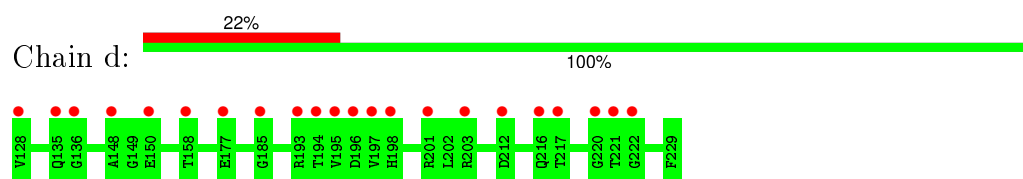
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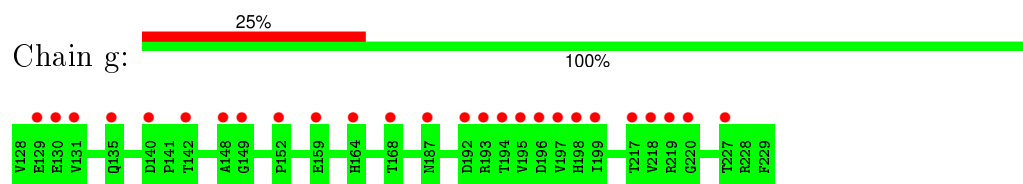
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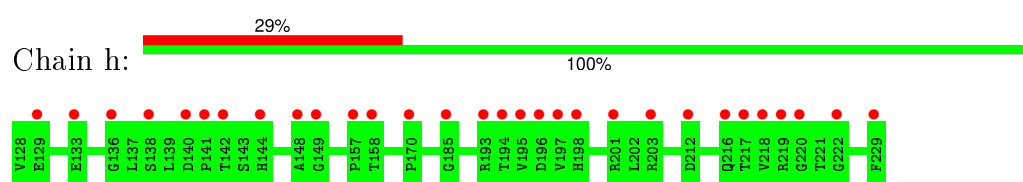
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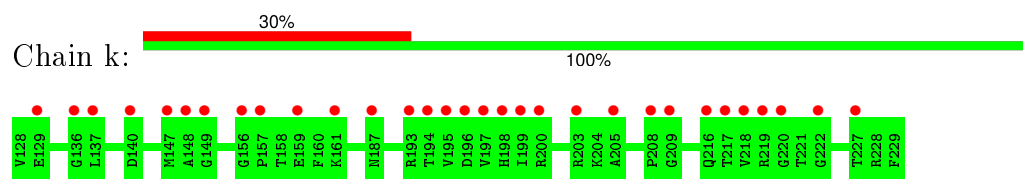
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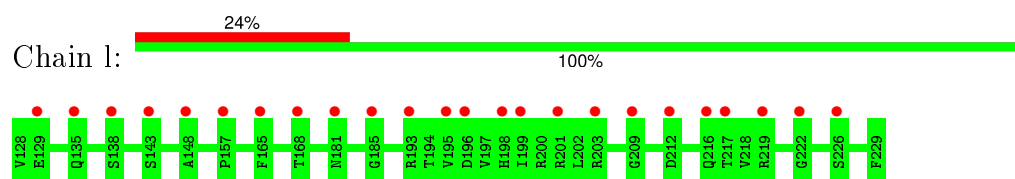
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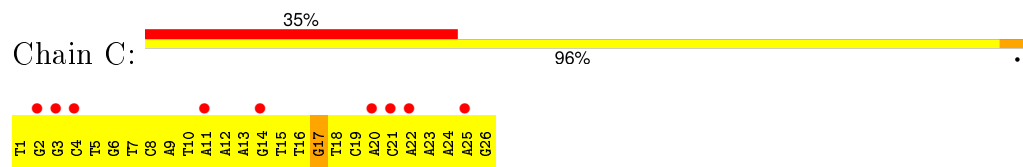
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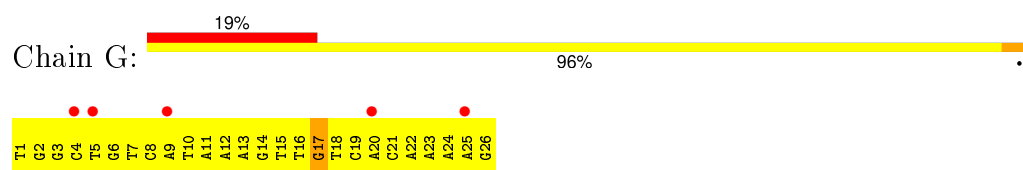
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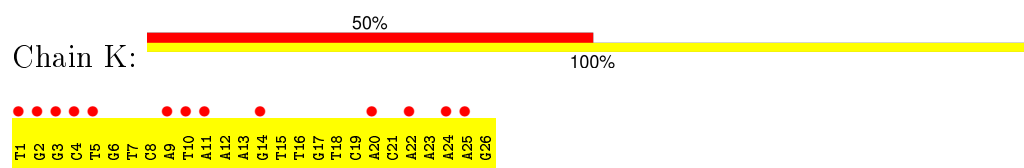
- Molecule 2: PHO BOX DNA (STRAND 1)



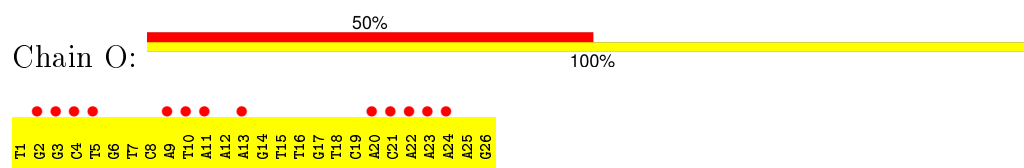
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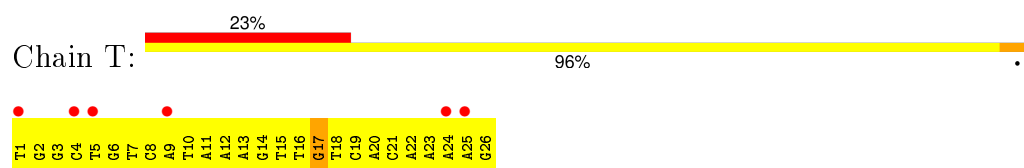
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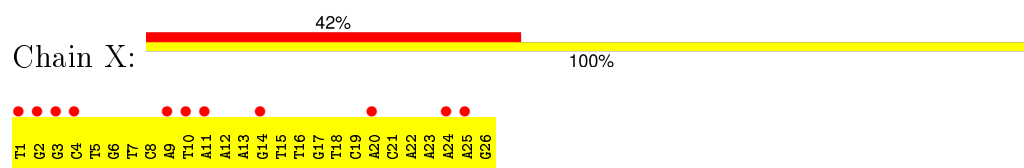
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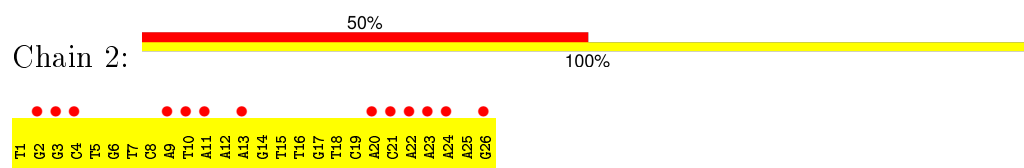
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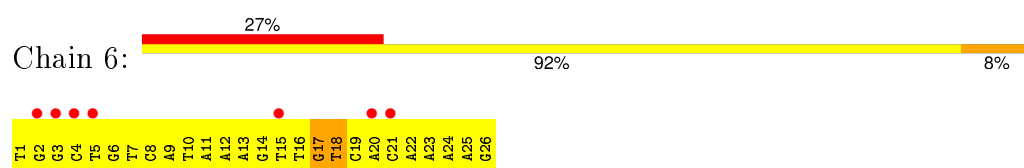
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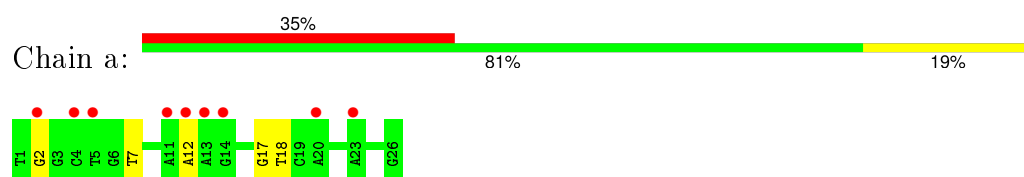
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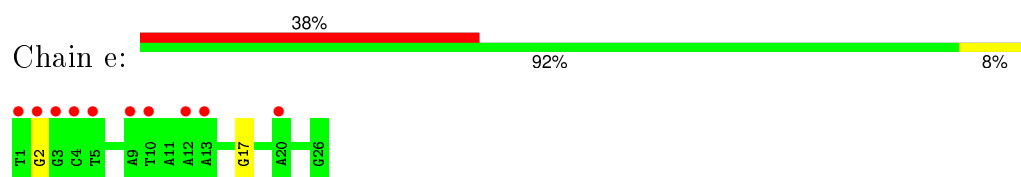
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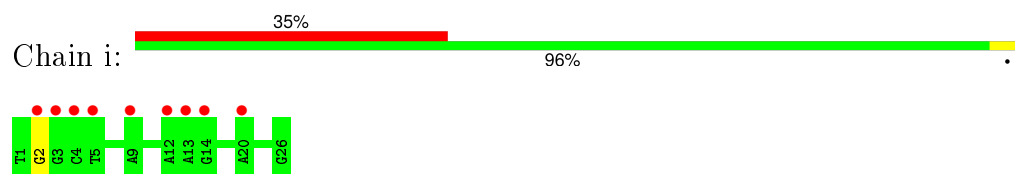
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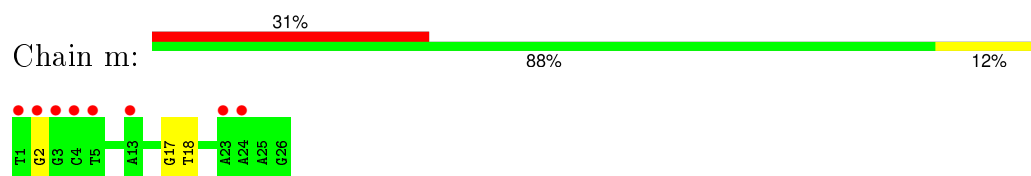
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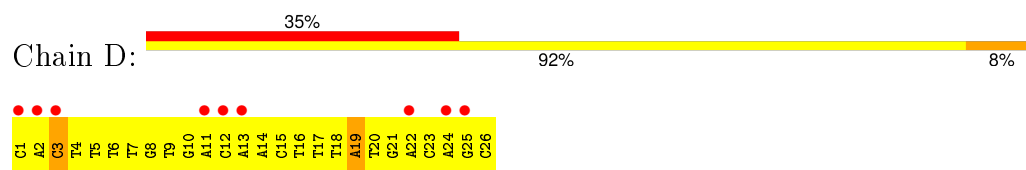
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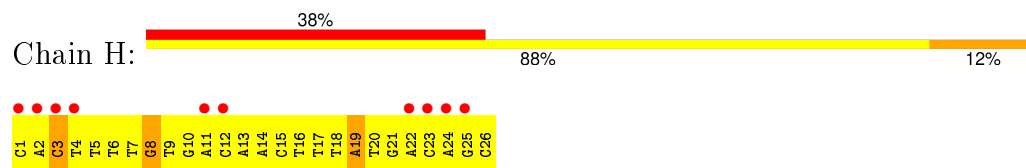
- Molecule 2: PHO BOX DNA (STRAND 1)



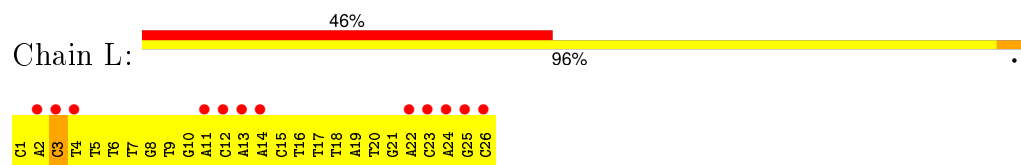
- Molecule 3: PHO BOX DNA (STRAND 2)



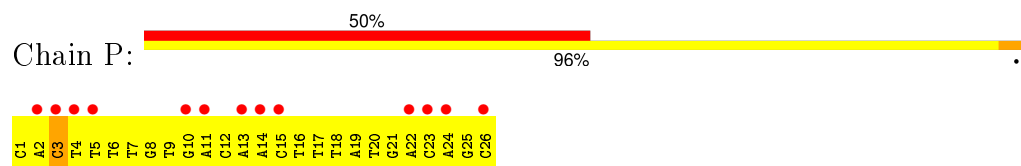
- Molecule 3: PHO BOX DNA (STRAND 2)



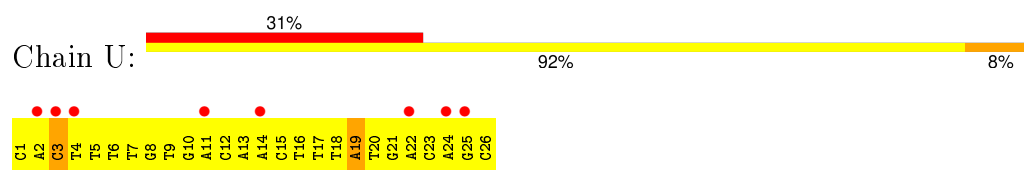
- Molecule 3: PHO BOX DNA (STRAND 2)



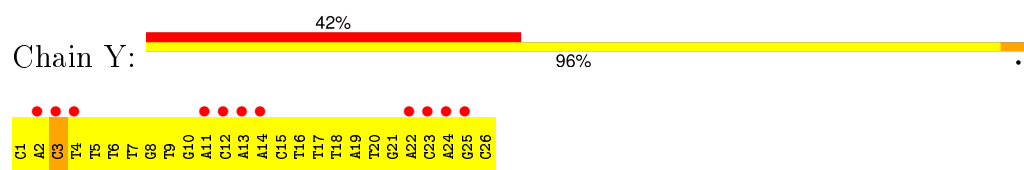
- Molecule 3: PHO BOX DNA (STRAND 2)



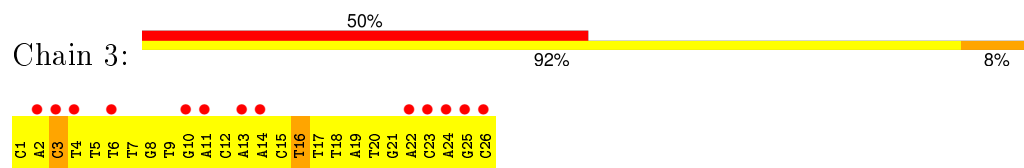
- Molecule 3: PHO BOX DNA (STRAND 2)



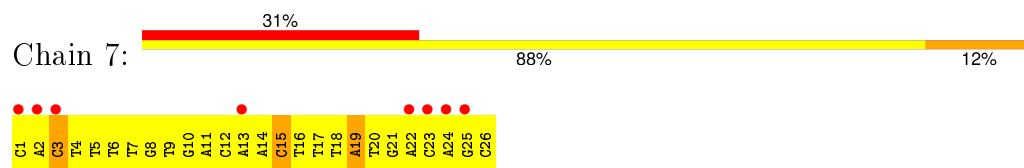
- Molecule 3: PHO BOX DNA (STRAND 2)



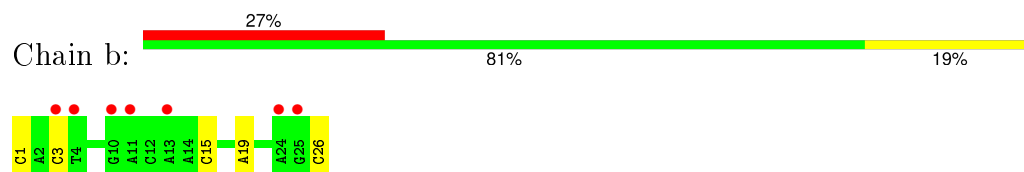
- Molecule 3: PHO BOX DNA (STRAND 2)



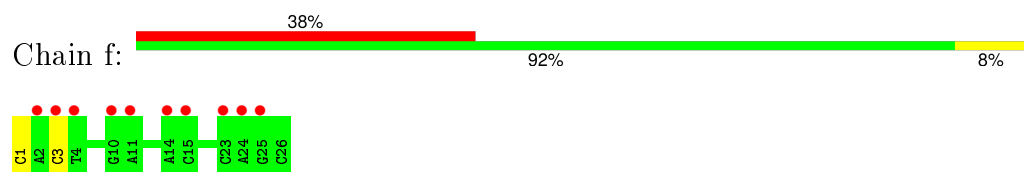
- Molecule 3: PHO BOX DNA (STRAND 2)



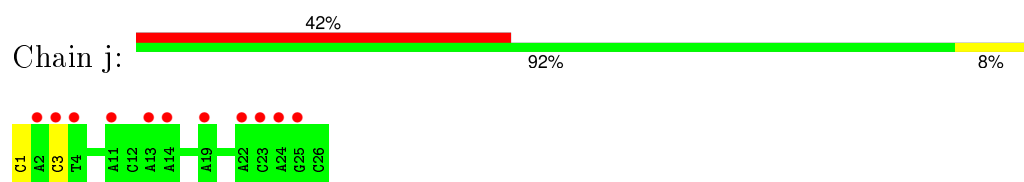
- Molecule 3: PHO BOX DNA (STRAND 2)



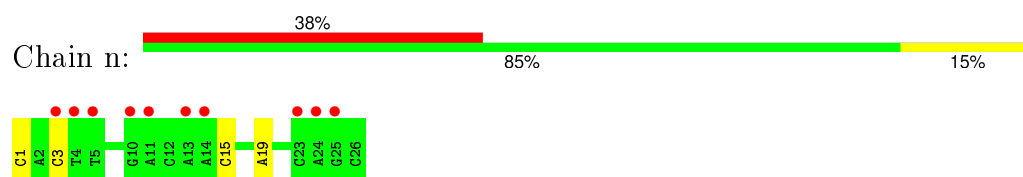
- Molecule 3: PHO BOX DNA (STRAND 2)



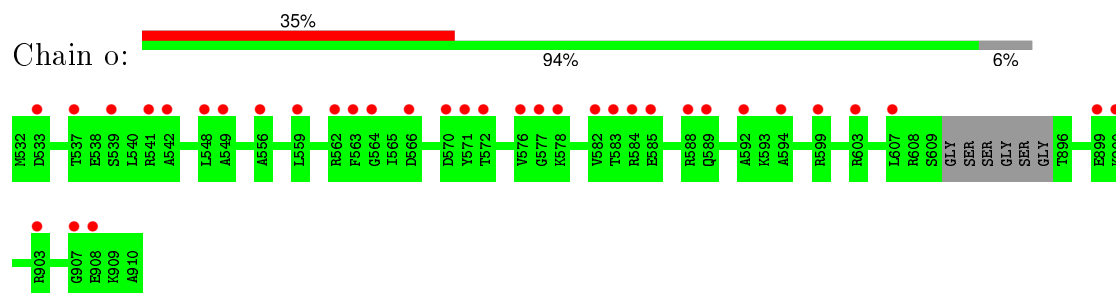
- Molecule 3: PHO BOX DNA (STRAND 2)



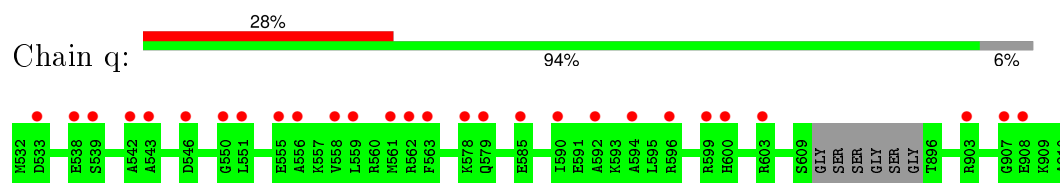
- Molecule 3: PHO BOX DNA (STRAND 2)



- Molecule 4: RNA polymerase sigma factor rpoD, DNA-directed RNA polymerase subunit beta



- Molecule 4: RNA polymerase sigma factor rpoD, DNA-directed RNA polymerase subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	277.30Å 161.40Å 260.10Å 90.00° 91.40° 90.00°	Depositor
Resolution (Å)	50.00 – 4.33 20.00 – 4.33	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-4.33) 96.4 (20.00-4.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 4.36Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	(Not available) , (Not available) 0.485 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	189.2	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	-2.34 , 331.6	EDS
Estimated twinning fraction	0.012 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.013 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.046 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.028 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.019 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 72977 reflections	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	15354	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.19 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 5.1959e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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$
2	2	1.87	0/600	0.94	0/925
2	6	1.85	2/600 (0.3%)	0.96	0/925
2	C	1.85	1/600 (0.2%)	0.96	0/925
2	G	1.97	1/600 (0.2%)	0.90	0/925
2	K	1.83	0/600	0.92	0/925
2	O	1.88	0/600	0.94	0/925
2	T	1.97	1/600 (0.2%)	0.89	0/925
2	X	1.82	0/600	0.93	0/925
2	a	1.99	4/600 (0.7%)	0.91	0/925
2	e	1.78	1/600 (0.2%)	0.89	0/925
2	i	1.79	0/600	0.89	0/925
2	m	1.96	2/600 (0.3%)	0.90	0/925
3	3	1.84	1/588 (0.2%)	0.95	1/905 (0.1%)
3	7	1.85	2/588 (0.3%)	0.96	1/905 (0.1%)
3	D	1.85	1/588 (0.2%)	0.96	1/905 (0.1%)
3	H	1.97	2/588 (0.3%)	0.92	1/905 (0.1%)
3	L	1.79	0/588	0.93	1/905 (0.1%)
3	P	1.83	0/588	0.94	1/905 (0.1%)
3	U	1.96	1/588 (0.2%)	0.92	1/905 (0.1%)
3	Y	1.79	0/588	0.93	1/905 (0.1%)
3	b	1.99	3/588 (0.5%)	0.92	1/905 (0.1%)
3	f	1.74	0/588	0.90	1/905 (0.1%)
3	j	1.75	0/588	0.89	1/905 (0.1%)
3	n	1.99	3/588 (0.5%)	0.92	1/905 (0.1%)
All	All	1.87	25/14256 (0.2%)	0.92	12/21960 (0.1%)

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6	17	DG	N7-C5	-5.82	1.35	1.39
2	m	17	DG	N7-C5	-5.67	1.35	1.39
2	C	17	DG	N7-C5	-5.46	1.35	1.39
2	a	17	DG	N7-C5	-5.41	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	n	15	DC	N3-C4	-5.35	1.30	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	U	3	DC	N1-C1'-C2'	5.88	123.76	112.60
3	H	3	DC	N1-C1'-C2'	5.83	123.68	112.60
3	Y	3	DC	N1-C1'-C2'	5.72	123.47	112.60
3	L	3	DC	N1-C1'-C2'	5.71	123.45	112.60
3	j	3	DC	N1-C1'-C2'	5.71	123.45	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	102	0	0	0	0
1	4	102	0	0	0	0
1	5	102	0	0	0	0
1	8	102	0	0	0	0
1	9	102	0	0	0	0
1	A	102	0	0	0	0
1	B	102	0	0	0	0
1	E	102	0	0	0	0
1	F	102	0	0	0	0
1	I	102	0	0	0	0
1	J	102	0	0	0	0
1	M	102	0	0	0	0
1	N	102	0	0	0	0
1	R	102	0	0	0	0
1	S	102	0	0	0	0
1	V	102	0	0	0	0
1	W	102	0	0	0	0
1	Z	102	0	0	0	0
1	c	102	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	102	0	0	0	0
1	g	102	0	0	0	0
1	h	102	0	0	0	0
1	k	102	0	0	0	0
1	l	102	0	0	0	0
2	2	534	0	295	77	0
2	6	534	0	295	80	0
2	C	534	0	295	80	0
2	G	534	0	295	83	11
2	K	534	0	295	81	8
2	O	534	0	295	85	0
2	T	534	0	295	83	8
2	X	534	0	295	83	8
2	a	534	0	295	0	2
2	e	534	0	295	0	5
2	i	534	0	295	0	1
2	m	534	0	295	0	2
3	3	526	0	297	70	3
3	7	526	0	297	69	0
3	D	526	0	297	69	0
3	H	526	0	297	71	8
3	L	526	0	297	69	8
3	P	526	0	297	75	3
3	U	526	0	297	70	8
3	Y	526	0	297	70	11
3	b	526	0	297	0	7
3	f	526	0	297	0	4
3	j	526	0	297	0	2
3	n	526	0	297	0	1
4	o	93	0	0	0	0
4	q	93	0	0	0	0
All	All	15354	0	7104	1201	50

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 82.

The worst 5 of 1201 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)
2:T:25:DA:H2"	2:T:26:DG:H5"	1.19	1.18
2:K:25:DA:H2"	2:K:26:DG:H5"	1.21	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:25:DA:H2"	2:G:26:DG:H5"	1.19	1.17
3:U:14:DA:H2"	3:U:15:DC:H5"	1.27	1.16
2:6:25:DA:H2"	2:6:26:DG:H5"	1.22	1.15

The worst 5 of 50 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:1:DC:N4	2:X:2:DG:N1[2_456]	0.94	1.26
2:K:2:DG:N1	3:U:1:DC:N4[2_556]	0.97	1.23
2:K:2:DG:N2	3:U:1:DC:N3[2_556]	1.36	0.84
3:H:1:DC:N3	2:X:2:DG:N2[2_456]	1.37	0.83
2:K:2:DG:C6	3:U:1:DC:N4[2_556]	1.43	0.77

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1	102/102 (100%)	1.52	30 (29%) 1 2	56, 70, 90, 95	0
1	4	102/102 (100%)	1.54	27 (26%) 1 2	60, 73, 89, 91	0
1	5	102/102 (100%)	1.49	28 (27%) 1 2	56, 70, 90, 95	0
1	8	102/102 (100%)	1.70	31 (30%) 1 2	60, 73, 89, 91	0
1	9	102/102 (100%)	1.69	33 (32%) 1 2	56, 70, 90, 95	0
1	A	102/102 (100%)	1.59	29 (28%) 1 2	60, 73, 89, 91	0
1	B	102/102 (100%)	1.43	23 (22%) 1 2	56, 70, 90, 95	0
1	E	102/102 (100%)	1.62	26 (25%) 1 2	60, 73, 89, 91	0
1	F	102/102 (100%)	1.58	28 (27%) 1 2	56, 70, 90, 95	0
1	I	102/102 (100%)	1.53	30 (29%) 1 2	60, 73, 89, 91	0
1	J	102/102 (100%)	1.60	24 (23%) 1 2	56, 70, 90, 95	0
1	M	102/102 (100%)	1.69	30 (29%) 1 2	60, 73, 89, 91	0
1	N	102/102 (100%)	1.63	26 (25%) 1 2	56, 70, 90, 95	0
1	R	102/102 (100%)	1.73	30 (29%) 1 2	60, 73, 89, 91	0
1	S	102/102 (100%)	1.68	30 (29%) 1 2	56, 70, 90, 95	0
1	V	102/102 (100%)	1.68	31 (30%) 1 2	60, 73, 89, 91	0
1	W	102/102 (100%)	1.60	28 (27%) 1 2	56, 70, 90, 95	0
1	Z	102/102 (100%)	1.56	29 (28%) 1 2	60, 73, 89, 91	0
1	c	102/102 (100%)	1.63	32 (31%) 1 2	60, 73, 89, 91	0
1	d	102/102 (100%)	1.50	22 (21%) 1 2	56, 70, 90, 95	0
1	g	102/102 (100%)	1.51	26 (25%) 1 2	60, 73, 89, 91	0
1	h	102/102 (100%)	1.65	30 (29%) 1 2	56, 70, 90, 95	0
1	k	102/102 (100%)	1.83	31 (30%) 1 2	60, 73, 89, 91	0
1	l	102/102 (100%)	1.50	24 (23%) 1 2	56, 70, 90, 95	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	2	26/26 (100%)	1.99	13 (50%) 0 1	62, 79, 87, 88	0
2	6	26/26 (100%)	1.74	7 (26%) 1 2	62, 79, 87, 88	0
2	C	26/26 (100%)	1.76	9 (34%) 0 1	62, 79, 87, 88	0
2	G	26/26 (100%)	1.37	5 (19%) 2 3	62, 79, 87, 88	0
2	K	26/26 (100%)	1.90	13 (50%) 0 1	62, 79, 87, 88	0
2	O	26/26 (100%)	2.07	13 (50%) 0 1	62, 79, 87, 88	0
2	T	26/26 (100%)	1.45	6 (23%) 1 2	62, 79, 87, 88	0
2	X	26/26 (100%)	1.79	11 (42%) 0 1	62, 79, 87, 88	0
2	a	26/26 (100%)	1.72	9 (34%) 0 1	62, 79, 87, 88	0
2	e	26/26 (100%)	1.86	10 (38%) 0 1	62, 79, 87, 88	0
2	i	26/26 (100%)	1.78	9 (34%) 0 1	62, 79, 87, 88	0
2	m	26/26 (100%)	1.66	8 (30%) 1 2	62, 79, 87, 88	0
3	3	26/26 (100%)	2.03	13 (50%) 0 1	61, 79, 93, 94	0
3	7	26/26 (100%)	1.60	8 (30%) 1 2	61, 79, 93, 94	0
3	D	26/26 (100%)	1.51	9 (34%) 0 1	61, 79, 93, 94	0
3	H	26/26 (100%)	1.45	10 (38%) 0 1	61, 79, 93, 94	0
3	L	26/26 (100%)	1.71	12 (46%) 0 1	61, 79, 93, 94	0
3	P	26/26 (100%)	1.87	13 (50%) 0 1	61, 79, 93, 94	0
3	U	26/26 (100%)	1.65	8 (30%) 1 2	61, 79, 93, 94	0
3	Y	26/26 (100%)	1.72	11 (42%) 0 1	61, 79, 93, 94	0
3	b	26/26 (100%)	1.65	7 (26%) 1 2	61, 79, 93, 94	0
3	f	26/26 (100%)	1.76	10 (38%) 0 1	61, 79, 93, 94	0
3	j	26/26 (100%)	1.81	11 (42%) 0 1	61, 79, 93, 94	0
3	n	26/26 (100%)	1.79	10 (38%) 0 1	61, 79, 93, 94	0
4	o	93/99 (93%)	1.86	35 (37%) 0 1	19, 23, 79, 88	0
4	q	93/99 (93%)	1.78	28 (30%) 1 2	19, 23, 79, 88	0
All	All	3258/3270 (99%)	1.64	976 (29%) 1 2	19, 73, 90, 95	0

The worst 5 of 976 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	185	GLY	12.4
1	R	187	ASN	11.9

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Mol	Chain	Res	Type	RSRZ
4	o	570	ASP	11.4
4	q	907	GLY	11.3
1	M	129	GLU	10.9

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.