Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2023 – 01:42 pm GMT

PDB ID	:	2VBN
Title	:	Molecular basis of human XPC gene recognition and cleavage by engineered homing endonuclease heterodimers
Authors	:	Redondo, P.; Prieto, J.; Munoz, I.G.; Alibes, A.; Stricher, F.; Serrano, L.; Arnould, S.; Perez, C.; Cabaniols, J.P.; Duchateau, P.; Paques, F.; Blanco, F.J.; Montoya, G.
Deposited on	:	2007-09-14
Resolution	:	1.90 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 (1)) were used in the production of this report:

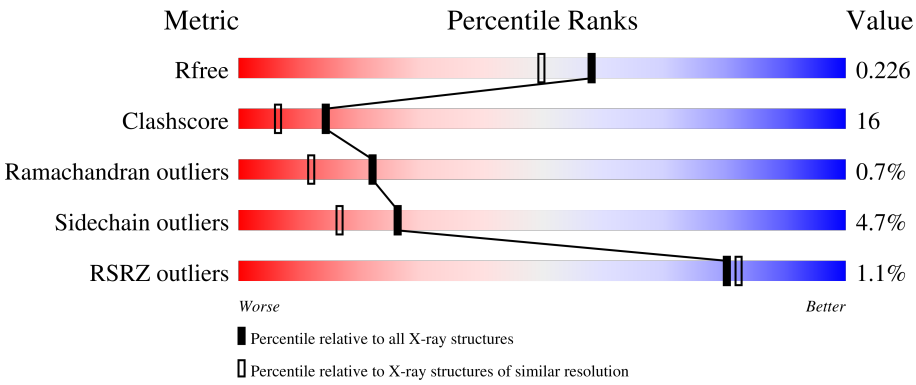
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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% 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	A	153	81% 14% • •
2	B	153	3% 79% 16% • ••
3	C	14	7% 71% 21%
4	E	14	50% 50%
5	S	10	20% 50% 30%

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Mol	Chain	Length	Quality of chain
6	T	10	90% 10%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 3793 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 DNA ENDONUCLEASE I-CREI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	153	1229	788	210	230	1	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	SER	TYR	conflict	UNP P05725
A	38	ARG	GLN	conflict	UNP P05725
A	42	THR	ALA	conflict	UNP P05725
A	70	SER	ARG	conflict	UNP P05725
A	75	ASN	ASP	conflict	UNP P05725
A	110	GLU	TRP	conflict	UNP P05725
A	111	GLN	ARG	conflict	UNP P05725

- Molecule 2 is a protein called DNA ENDONUCLEASE I-CREI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	152	1232	794	207	230	1	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	28	GLU	LYS	conflict	UNP P05725
B	38	ARG	GLN	conflict	UNP P05725
B	40	LYS	SER	conflict	UNP P05725
B	42	THR	ALA	conflict	UNP P05725
B	44	LYS	GLN	conflict	UNP P05725
B	68	SER	ARG	conflict	UNP P05725
B	70	SER	ARG	conflict	UNP P05725
B	75	ASN	ASP	conflict	UNP P05725
B	110	GLU	TRP	conflict	UNP P05725

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Chain	Residue	Modelled	Actual	Comment	Reference
B	111	GLN	ARG	conflict	UNP P05725

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	C	14	282	137	49	83	13	0	0	0

- Molecule 4 is a DNA chain called 5'-D(*TP*CP*TP*GP*CP*CP*TP*TP*TP*TP *TP*TP*GP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	E	14	279	137	40	89	13	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	S	10	211	99	48	54	10	0	0	0

- Molecule 6 is a DNA chain called 5'-D(*AP*GP*GP*AP*TP*CP*CP*TP*AP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
6	T	10	207	98	40	59	10	0	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
7	A	1	1	1	0	0
7	E	2	2	2	0	0

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
8	A	1	1	1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
8	B	1	1	1	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	119	119	119	0	0
			Total	O		
9	B	129	129	129	0	0
			Total	O		
9	C	38	38	38	0	0
			Total	O		
9	E	29	29	29	0	0
			Total	O		
9	S	14	14	14	0	0
			Total	O		
9	T	19	19	19	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 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: DNA ENDONUCLEASE I-CREI

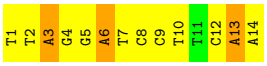
Chain A:

• Molecule 2: DNA ENDONUCLEASE I-CREI

Chain B:

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

Chain C:

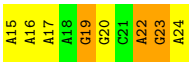


• Molecule 4: 5'-D(*TP*CP*TP*GP*CP*CP*TP*TP*TP*TP *TP*TP*GP*AP)-3'

Chain E:

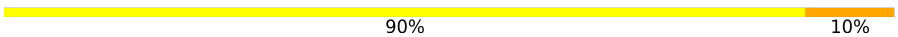
• Molecule 5: 5'-D(*AP*AP*AP*AP*GP*GP*CP*AP*GP*AP)-3'

Chain S:



• Molecule 6: 5'-D(*AP*GP*GP*AP*TP*CP*CP*TP*AP*AP)-3'

Chain T:



A15
G16
G17
A18
T19
C20
C21
T22
A23
A24

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	46.12Å 67.99Å 77.19Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	46.13 – 1.90 46.11 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.5 (46.13-1.90) 93.5 (46.11-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.74 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.141 , 0.223 0.148 , 0.226	Depositor DCC
R_{free} test set	1761 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	24.2	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 54.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3793	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: MG, CA

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	A	0.62	0/1251	0.84	3/1689 (0.2%)
2	B	0.65	0/1255	0.84	3/1693 (0.2%)
3	C	1.15	0/315	2.93	35/484 (7.2%)
4	E	1.01	0/309	2.54	20/475 (4.2%)
5	S	1.17	0/239	2.51	19/367 (5.2%)
6	T	1.23	1/232 (0.4%)	2.48	22/354 (6.2%)
All	All	0.82	1/3601 (0.0%)	1.67	102/5062 (2.0%)

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	A	0	4
2	B	0	3
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	T	15	DA	OP3-P	-10.05	1.49	1.61

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	13	DA	N1-C2-N3	-14.36	122.12	129.30
5	S	16	DA	O4'-C1'-N9	14.33	118.03	108.00
5	S	23	DG	O4'-C1'-N9	14.30	118.01	108.00
4	E	13	DG	O4'-C1'-N9	-13.35	98.66	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	4	DG	O4'-C1'-N9	12.97	117.08	108.00
3	C	10	DT	O4'-C1'-N1	-12.74	99.08	108.00
3	C	3	DA	O4'-C1'-N9	-11.92	99.65	108.00
3	C	5	DG	N1-C6-O6	-11.78	112.83	119.90
3	C	13	DA	O4'-C1'-N9	-10.97	100.32	108.00
3	C	9	DC	O4'-C1'-N1	-10.95	100.34	108.00
3	C	5	DG	N9-C4-C5	10.73	109.69	105.40
4	E	5	DC	O4'-C4'-C3'	-10.50	99.70	106.00
6	T	15	DA	OP1-P-OP2	-10.49	103.86	119.60
4	E	3	DT	P-O3'-C3'	10.38	132.15	119.70
6	T	16	DG	O4'-C1'-N9	10.20	115.14	108.00
4	E	10	DT	O4'-C1'-N1	-10.18	100.87	108.00
3	C	13	DA	C2-N3-C4	9.91	115.55	110.60
3	C	5	DG	N3-C4-C5	-9.56	123.82	128.60
3	C	5	DG	O4'-C1'-N9	9.42	114.59	108.00
4	E	3	DT	N3-C2-O2	-9.06	116.86	122.30
3	C	5	DG	C8-N9-C4	-9.04	102.78	106.40
6	T	22	DT	O4'-C1'-N1	9.00	114.30	108.00
3	C	3	DA	N1-C6-N6	8.64	123.79	118.60
3	C	5	DG	C4-C5-N7	-8.50	107.40	110.80
3	C	6	DA	N9-C4-C5	8.45	109.18	105.80
5	S	22	DA	C3'-C2'-C1'	-8.09	92.80	102.50
6	T	20	DC	C6-N1-C2	7.75	123.40	120.30
6	T	17	DG	O4'-C4'-C3'	-7.74	101.35	106.00
4	E	2	DC	O4'-C1'-N1	-7.70	102.61	108.00
6	T	15	DA	N1-C2-N3	-7.67	125.47	129.30
6	T	22	DT	N3-C2-O2	-7.63	117.72	122.30
3	C	6	DA	C8-N9-C4	-7.42	102.83	105.80
3	C	5	DG	C6-N1-C2	-7.41	120.66	125.10
3	C	9	DC	C5-C6-N1	7.39	124.69	121.00
6	T	23	DA	O4'-C1'-N9	-7.29	102.90	108.00
1	A	130	ASP	CB-CG-OD2	-7.24	111.78	118.30
5	S	22	DA	N1-C6-N6	7.21	122.93	118.60
4	E	7	DT	P-O3'-C3'	7.13	128.26	119.70
3	C	5	DG	C5-C6-O6	7.10	132.86	128.60
5	S	17	DA	N1-C2-N3	-7.08	125.76	129.30
5	S	19	DG	C2-N3-C4	-7.03	108.38	111.90
3	C	5	DG	O4'-C1'-C2'	-7.00	100.30	105.90
3	C	5	DG	C2-N3-C4	6.94	115.37	111.90
5	S	16	DA	N1-C2-N3	-6.71	125.95	129.30
3	C	2	DT	C4-C5-C7	-6.70	114.98	119.00
6	T	19	DT	C6-C5-C7	-6.59	118.94	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	3	DT	N1-C2-N3	6.52	118.51	114.60
6	T	15	DA	P-O5'-C5'	6.51	131.32	120.90
5	S	15	DA	O4'-C1'-C2'	-6.45	100.74	105.90
6	T	21	DC	O4'-C1'-N1	-6.43	103.50	108.00
5	S	19	DG	N3-C4-C5	6.39	131.79	128.60
4	E	3	DT	O3'-P-O5'	-6.26	92.10	104.00
5	S	22	DA	N9-C4-C5	-6.24	103.31	105.80
3	C	10	DT	OP1-P-OP2	6.21	128.91	119.60
3	C	7	DT	C1'-O4'-C4'	-6.17	103.93	110.10
3	C	13	DA	C6-N1-C2	6.08	122.25	118.60
4	E	6	DC	O4'-C1'-N1	6.08	112.26	108.00
1	A	11	LEU	CB-CG-CD2	-6.08	100.66	111.00
5	S	23	DG	N9-C4-C5	6.05	107.82	105.40
3	C	1	DT	O4'-C1'-N1	-6.02	103.79	108.00
6	T	15	DA	C4'-C3'-C2'	5.96	108.46	103.10
3	C	2	DT	C6-C5-C7	5.92	126.45	122.90
3	C	12	DC	N1-C1'-C2'	5.89	123.80	112.60
6	T	20	DC	N3-C4-C5	5.85	124.24	121.90
1	A	130	ASP	CB-CG-OD1	5.83	123.55	118.30
4	E	9	DT	O4'-C1'-N1	-5.79	103.95	108.00
5	S	15	DA	N1-C2-N3	-5.79	126.41	129.30
6	T	15	DA	O5'-P-OP1	5.78	117.64	110.70
5	S	23	DG	O4'-C4'-C3'	5.75	109.45	106.00
3	C	6	DA	O4'-C1'-N9	5.67	111.97	108.00
6	T	24	DA	O4'-C1'-N9	5.62	111.93	108.00
3	C	5	DG	C5-C6-N1	5.62	114.31	111.50
3	C	8	DC	O4'-C1'-C2'	-5.60	101.42	105.90
5	S	15	DA	C6-N1-C2	5.58	121.95	118.60
2	B	52	ARG	CG-CD-NE	-5.58	100.08	111.80
5	S	23	DG	C8-N9-C4	-5.53	104.19	106.40
4	E	4	DG	C5-C6-O6	-5.49	125.31	128.60
3	C	2	DT	O4'-C4'-C3'	-5.46	102.32	104.50
6	T	22	DT	N1-C2-N3	5.44	117.86	114.60
4	E	13	DG	O4'-C1'-C2'	-5.38	101.60	105.90
5	S	22	DA	C4-C5-N7	5.35	113.37	110.70
2	B	58	LEU	CB-CG-CD1	-5.33	101.94	111.00
5	S	19	DG	N3-C4-N9	-5.32	122.81	126.00
5	S	17	DA	C5-C6-N6	-5.31	119.45	123.70
6	T	17	DG	C4-C5-N7	5.29	112.92	110.80
3	C	2	DT	N1-C1'-C2'	5.26	122.59	112.60
3	C	4	DG	O4'-C1'-C2'	-5.22	101.72	105.90
4	E	4	DG	C6-C5-N7	-5.21	127.28	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	T	18	DA	C4'-C3'-C2'	5.18	107.76	103.10
4	E	12	DT	N1-C1'-C2'	5.16	122.41	112.60
4	E	3	DT	C4-C5-C7	-5.16	115.91	119.00
4	E	11	DT	O4'-C1'-C2'	-5.15	101.78	105.90
4	E	1	DT	C6-C5-C7	-5.14	119.81	122.90
6	T	16	DG	N3-C4-N9	-5.12	122.92	126.00
6	T	20	DC	P-O5'-C5'	-5.12	112.70	120.90
2	B	130	ASP	CB-CG-OD1	5.10	122.89	118.30
6	T	15	DA	C2-N3-C4	5.06	113.13	110.60
3	C	9	DC	C6-N1-C2	-5.06	118.28	120.30
4	E	3	DT	N1-C1'-C2'	5.03	122.16	112.60
5	S	17	DA	O4'-C1'-N9	5.03	111.52	108.00
6	T	19	DT	C4-C5-C7	5.03	122.02	119.00
3	C	9	DC	C2-N3-C4	5.01	122.41	119.90

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	MET	Peptide
1	A	149	ARG	Peptide
1	A	150	ALA	Peptide
1	A	152	LEU	Peptide
2	B	149	ARG	Peptide
2	B	150	ALA	Peptide
2	B	152	LEU	Peptide

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	A	1229	0	1259	41	0
2	B	1232	0	1267	32	0
3	C	282	0	160	4	0
4	E	279	0	163	28	0
5	S	211	0	111	11	0
6	T	207	0	113	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	1	0	0	0	0
7	E	2	0	0	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	119	0	0	18	0
9	B	129	0	0	14	0
9	C	38	0	0	1	0
9	E	29	0	0	0	0
9	S	14	0	0	0	0
9	T	19	0	0	2	0
All	All	3793	0	3073	98	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 16.

All (98) 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)
1:A:89:THR:HG23	9:A:2069:HOH:O	1.09	1.24
2:B:69:ASP:HB2	9:B:2071:HOH:O	1.07	1.23
9:A:2021:HOH:O	4:E:3:DT:C7	1.83	1.19
2:B:58:LEU:HG	9:B:2058:HOH:O	0.89	1.07
9:A:2021:HOH:O	4:E:3:DT:H72	1.45	1.06
1:A:100:LYS:HG2	1:A:135:LEU:CD1	1.86	1.06
4:E:6:DC:N4	5:S:19:DG:O6	1.89	1.05
1:A:150:ALA:HA	1:A:152:LEU:H	1.18	1.03
4:E:4:DG:H2"	4:E:5:DC:H5"	1.35	1.03
2:B:69:ASP:CB	9:B:2071:HOH:O	1.72	1.02
5:S:23:DG:H4'	5:S:24:DA:OP1	1.56	1.01
1:A:89:THR:CG2	9:A:2069:HOH:O	1.70	1.01
4:E:6:DC:N3	5:S:19:DG:N1	2.18	0.92
1:A:100:LYS:HG2	1:A:135:LEU:HD13	1.50	0.91
1:A:100:LYS:HG2	1:A:135:LEU:HD11	1.55	0.86
2:B:8:GLU:HG3	9:B:2010:HOH:O	1.75	0.85
4:E:4:DG:H2"	4:E:5:DC:C5'	2.08	0.84
1:A:68:ARG:NH1	4:E:7:DT:OP2	2.10	0.84
1:A:150:ALA:O	9:A:2118:HOH:O	1.95	0.83
1:A:1:MET:CB	9:A:2002:HOH:O	2.27	0.82
5:S:22:DA:O5'	5:S:22:DA:H2'	1.80	0.81
3:C:3:DA:OP2	9:C:2004:HOH:O	1.97	0.81
3:C:6:DA:N6	6:T:19:DT:O4	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ALA:HA	1:A:152:LEU:N	1.97	0.79
1:A:30:ASN:CG	9:A:2020:HOH:O	2.23	0.76
2:B:111:GLN:HG2	9:B:2097:HOH:O	1.86	0.76
1:A:33:SER:OG	9:A:2020:HOH:O	2.05	0.74
1:A:148:VAL:O	1:A:151:VAL:HB	1.88	0.73
1:A:68:ARG:HH21	4:E:7:DT:H2'	1.56	0.71
4:E:4:DG:C2'	4:E:5:DC:H5"	2.15	0.70
5:S:23:DG:C4'	5:S:24:DA:OP1	2.35	0.70
1:A:68:ARG:NH2	4:E:7:DT:H3'	2.09	0.68
1:A:89:THR:CB	9:A:2069:HOH:O	2.23	0.66
1:A:89:THR:OG1	9:A:2069:HOH:O	2.07	0.66
4:E:6:DC:N4	5:S:19:DG:C6	2.53	0.66
2:B:44:LYS:NZ	9:B:2034:HOH:O	2.02	0.65
1:A:68:ARG:HH21	4:E:7:DT:H3'	1.63	0.64
2:B:69:ASP:CG	9:B:2071:HOH:O	2.09	0.61
2:B:151:VAL:C	2:B:153:ASP:H	2.04	0.61
2:B:77:ILE:HD13	9:B:2065:HOH:O	2.00	0.61
5:S:22:DA:O5'	5:S:22:DA:C2'	2.49	0.61
1:A:68:ARG:HH21	4:E:7:DT:C2'	2.13	0.60
4:E:13:DG:H1'	4:E:14:DA:O4'	2.02	0.60
2:B:33:TYR:OH	3:C:3:DA:N7	2.33	0.60
2:B:115:ALA:HA	2:B:121:LYS:HG3	1.84	0.60
1:A:68:ARG:HH21	4:E:7:DT:C3'	2.14	0.59
2:B:92:GLN:HG3	2:B:103:ASN:OD1	2.02	0.58
1:A:92:GLN:HG3	1:A:103:ASN:OD1	2.03	0.58
1:A:150:ALA:N	9:A:2117:HOH:O	2.28	0.58
4:E:5:DC:C5'	4:E:5:DC:H6	2.17	0.58
1:A:149:ARG:O	1:A:152:LEU:HG	2.04	0.57
2:B:38:ARG:HG3	2:B:38:ARG:NH1	2.20	0.56
1:A:1:MET:O	9:A:2001:HOH:O	2.18	0.56
1:A:68:ARG:HH22	4:E:7:DT:P	2.30	0.55
1:A:68:ARG:NH2	4:E:7:DT:O5'	2.39	0.55
2:B:8:GLU:CG	9:B:2010:HOH:O	2.46	0.54
4:E:6:DC:N4	5:S:19:DG:H1	2.07	0.52
1:A:150:ALA:HB3	9:A:2117:HOH:O	2.09	0.52
1:A:150:ALA:CB	9:A:2117:HOH:O	2.57	0.52
2:B:152:LEU:O	2:B:153:ASP:OD1	2.28	0.52
3:C:13:DA:H1'	3:C:14:DA:O4'	2.10	0.52
1:A:80:GLU:HG2	1:A:83:PRO:HD2	1.93	0.51
2:B:30:ASN:HB3	2:B:33:TYR:CD2	2.45	0.51
2:B:150:ALA:O	9:B:2128:HOH:O	2.18	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:5:DC:H6	4:E:5:DC:H5'	1.75	0.50
1:A:63:GLY:O	9:A:2054:HOH:O	2.20	0.49
2:B:151:VAL:C	2:B:153:ASP:N	2.66	0.49
5:S:19:DG:H2"	5:S:20:DG:H5'	1.95	0.48
2:B:82:LYS:HE2	2:B:83:PRO:HD3	1.95	0.48
2:B:107:LYS:HE3	2:B:128:TRP:CZ2	2.48	0.48
2:B:30:ASN:HB3	2:B:33:TYR:HD2	1.79	0.48
9:A:2021:HOH:O	4:E:3:DT:H71	1.78	0.48
1:A:7:LYS:NZ	2:B:8:GLU:OE2	2.30	0.47
4:E:6:DC:N4	5:S:19:DG:N1	2.58	0.47
2:B:38:ARG:HG3	2:B:38:ARG:HH11	1.79	0.47
1:A:32:SER:O	4:E:1:DT:H5'	2.14	0.47
2:B:153:ASP:C	9:B:2129:HOH:O	2.53	0.46
4:E:6:DC:O2	5:S:19:DG:N2	2.38	0.46
1:A:1:MET:O	1:A:2:ASN:HB2	2.15	0.45
2:B:142:LYS:HE2	2:B:142:LYS:HB3	1.56	0.45
2:B:85:HIS:ND1	9:B:2075:HOH:O	2.30	0.45
2:B:121:LYS:O	2:B:121:LYS:HD3	2.17	0.45
1:A:70:SER:HB2	4:E:8:DT:H72	2.00	0.44
6:T:19:DT:H73	9:T:2009:HOH:O	2.17	0.44
1:A:2:ASN:HD22	1:A:2:ASN:N	2.15	0.44
1:A:111:GLN:HG2	9:A:2087:HOH:O	2.18	0.43
2:B:151:VAL:O	2:B:153:ASP:N	2.51	0.43
1:A:68:ARG:NH1	4:E:6:DC:H3'	2.33	0.43
2:B:38:ARG:HH11	2:B:38:ARG:CG	2.32	0.43
2:B:149:ARG:HG2	2:B:152:LEU:HD22	2.01	0.43
1:A:68:ARG:NH2	4:E:7:DT:C3'	2.76	0.42
1:A:127:THR:O	1:A:130:ASP:HB2	2.20	0.41
2:B:4:LYS:HD2	9:B:2079:HOH:O	2.21	0.41
1:A:2:ASN:ND2	9:A:2003:HOH:O	2.51	0.41
2:B:44:LYS:HE3	9:B:2033:HOH:O	2.20	0.41
1:A:128:TRP:N	1:A:128:TRP:CD1	2.86	0.41
4:E:5:DC:C5'	4:E:5:DC:C6	3.02	0.40
6:T:19:DT:O4	9:T:2009:HOH:O	2.22	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	
1	A	151/153 (99%)	142 (94%)	8 (5%)	1 (1%)	22	12
2	B	150/153 (98%)	142 (95%)	7 (5%)	1 (1%)	22	12
All	All	301/306 (98%)	284 (94%)	15 (5%)	2 (1%)	22	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	149	ARG
1	A	151	VAL

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	
1	A	138/140 (99%)	133 (96%)	5 (4%)	35	26
2	B	139/140 (99%)	131 (94%)	8 (6%)	20	10
All	All	277/280 (99%)	264 (95%)	13 (5%)	26	16

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ARG
1	A	64	VAL
1	A	70	SER
1	A	121	LYS

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Mol	Chain	Res	Type
1	A	149	ARG
2	B	38	ARG
2	B	79	SER
2	B	114	SER
2	B	116	LYS
2	B	118	SER
2	B	121	LYS
2	B	152	LEU
2	B	153	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	50	GLN
2	B	2	ASN
2	B	75	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 5 ligands modelled in this entry, 5 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)

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	A	153/153 (100%)	-0.01	0 100 100	18, 28, 52, 70	0
2	B	152/153 (99%)	0.05	4 (2%) 56 58	18, 28, 51, 65	0
3	C	14/14 (100%)	-0.32	0 100 100	21, 28, 35, 39	0
4	E	14/14 (100%)	-0.21	0 100 100	20, 34, 56, 58	0
5	S	10/10 (100%)	-0.23	0 100 100	21, 41, 54, 54	0
6	T	10/10 (100%)	-0.37	0 100 100	21, 37, 43, 43	0
All	All	353/354 (99%)	-0.02	4 (1%) 80 82	18, 28, 52, 70	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	152	LEU	3.0
2	B	33	TYR	2.5
2	B	120	ASP	2.2
2	B	151	VAL	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	CA	B	1154	1/1	0.99	0.14	18,18,18,18	0
7	MG	E	1025	1/1	1.00	0.09	21,21,21,21	0
7	MG	E	1026	1/1	1.00	0.14	9,9,9,9	0
8	CA	A	1155	1/1	1.00	0.10	15,15,15,15	0
7	MG	A	1154	1/1	1.00	0.18	9,9,9,9	0

6.5 Other polymers (i)

There are no such residues in this entry.