Full wwPDB X-ray Structure Validation Report (i)

Jan 4, 2024 – 01:14 am GMT

PDB ID	:	5AKF
Title	:	THE CRYSTAL STRUCTURE OF I-DMOI Q42AK120M IN COMPLEX WITH ITS TARGET DNA NICKED IN THE CODING STRAND A AND IN THE PRESENCE OF 2MM MN
Authors	:	Molina, R.; Marcaida, M.J.; Redondo, P.; Marenchino, M.; D'Abramo, M.; Montoya, G.; Prieto, J.
Deposited on	:	2015-03-03
Resolution	:	2.45 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:

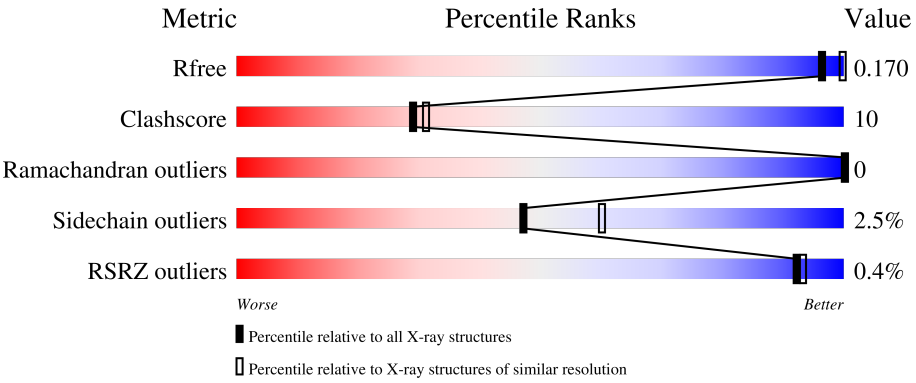
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	199	2% 66% 22% • 10%
1	E	199	73% 15% • 12%
1	I	199	67% 20% • 12%
2	B	14	79% 21%

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Mol	Chain	Length	Quality of chain
2	F	14	71% 29%
2	J	14	50% 36% 14%
3	C	11	45% 55%
3	G	11	27% 64% 9%
3	K	11	18% 64% 18%
4	D	25	56% 40%
4	H	25	60% 32% 8%
4	L	25	36% 52% 12%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 7887 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 HOMING ENDONUCLEASE I-DMOI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	5	0
			1518	978	280	256	4			
1	E	176	Total	C	N	O	S	8	5	0
			1489	960	272	253	4			
1	I	175	Total	C	N	O	S	8	7	0
			1496	968	273	251	4			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP P21505
A	189	ALA	-	expression tag	UNP P21505
A	190	ALA	-	expression tag	UNP P21505
A	191	ALA	-	expression tag	UNP P21505
A	192	LEU	-	expression tag	UNP P21505
A	193	GLU	-	expression tag	UNP P21505
A	194	HIS	-	expression tag	UNP P21505
A	195	HIS	-	expression tag	UNP P21505
A	196	HIS	-	expression tag	UNP P21505
A	197	HIS	-	expression tag	UNP P21505
A	198	HIS	-	expression tag	UNP P21505
A	199	HIS	-	expression tag	UNP P21505
A	42	ALA	GLN	engineered mutation	UNP P21505
A	120	MET	LYS	engineered mutation	UNP P21505
E	1	ALA	-	expression tag	UNP P21505
E	189	ALA	-	expression tag	UNP P21505
E	190	ALA	-	expression tag	UNP P21505
E	191	ALA	-	expression tag	UNP P21505
E	192	LEU	-	expression tag	UNP P21505
E	193	GLU	-	expression tag	UNP P21505
E	194	HIS	-	expression tag	UNP P21505
E	195	HIS	-	expression tag	UNP P21505
E	196	HIS	-	expression tag	UNP P21505

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Chain	Residue	Modelled	Actual	Comment	Reference
E	197	HIS	-	expression tag	UNP P21505
E	198	HIS	-	expression tag	UNP P21505
E	199	HIS	-	expression tag	UNP P21505
E	42	ALA	GLN	engineered mutation	UNP P21505
E	120	MET	LYS	engineered mutation	UNP P21505
I	1	ALA	-	expression tag	UNP P21505
I	189	ALA	-	expression tag	UNP P21505
I	190	ALA	-	expression tag	UNP P21505
I	191	ALA	-	expression tag	UNP P21505
I	192	LEU	-	expression tag	UNP P21505
I	193	GLU	-	expression tag	UNP P21505
I	194	HIS	-	expression tag	UNP P21505
I	195	HIS	-	expression tag	UNP P21505
I	196	HIS	-	expression tag	UNP P21505
I	197	HIS	-	expression tag	UNP P21505
I	198	HIS	-	expression tag	UNP P21505
I	199	HIS	-	expression tag	UNP P21505
I	42	ALA	GLN	engineered mutation	UNP P21505
I	120	MET	LYS	engineered mutation	UNP P21505

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	P	0	0	0
			289	136	53	86	14			
2	F	14	Total	C	N	O	P	0	0	0
			289	136	53	86	14			
2	J	14	Total	C	N	O	P	0	0	0
			289	136	53	86	14			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	P	0	0	0
			227	106	41	69	11			
3	G	11	Total	C	N	O	P	0	0	0
			227	106	41	69	11			
3	K	11	Total	C	N	O	P	0	0	0
			227	106	41	69	11			

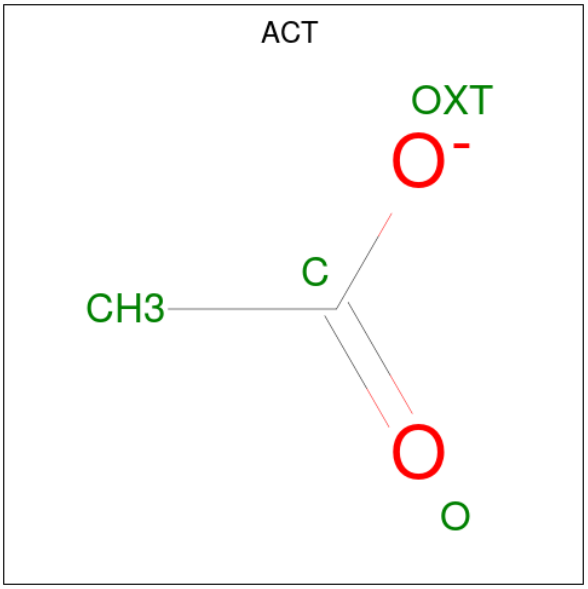
- Molecule 4 is a DNA chain called 25MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	25	Total	C	N	O	P	0	0	0
			508	240	99	145	24			
4	H	25	Total	C	N	O	P	0	0	0
			508	240	99	145	24			
4	L	25	Total	C	N	O	P	0	0	0
			508	240	99	145	24			

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		
5	B	1	Total	Cl	0	0
			1	1		
5	E	1	Total	Cl	0	0
			1	1		
5	I	1	Total	Cl	0	0
			1	1		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Mn 1 1	0	0
7	E	1	Total Mn 1 1	0	0
7	I	1	Total Mn 1 1	0	0

- Molecule 8 is water.

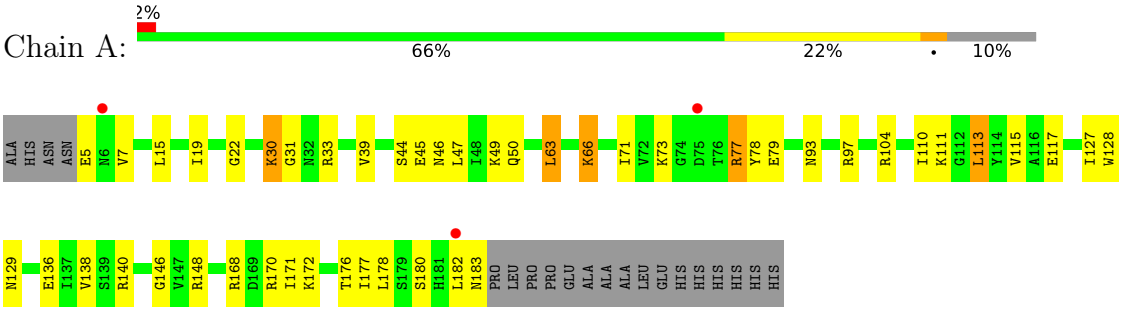
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	55	Total O 55 55	0	0
8	B	9	Total O 9 9	0	0
8	C	19	Total O 19 19	0	0
8	D	8	Total O 8 8	0	0
8	E	46	Total O 46 46	0	0
8	F	11	Total O 11 11	0	0
8	G	11	Total O 11 11	0	0
8	H	5	Total O 5 5	0	0
8	I	87	Total O 87 87	0	0
8	J	12	Total O 12 12	0	0
8	K	15	Total O 15 15	0	0
8	L	23	Total O 23 23	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.

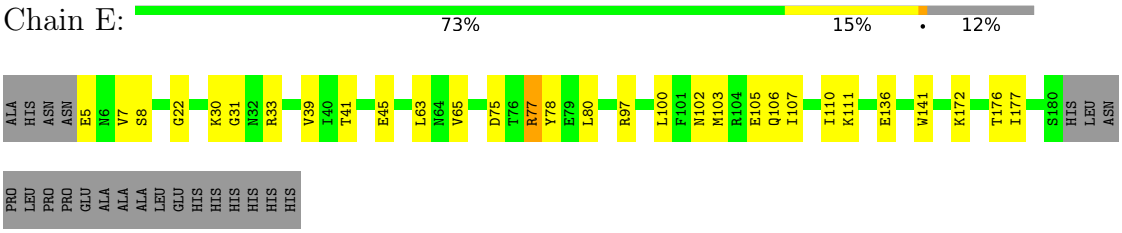
• Molecule 1: HOMING ENDONUCLEASE I-DMOI

Chain A:



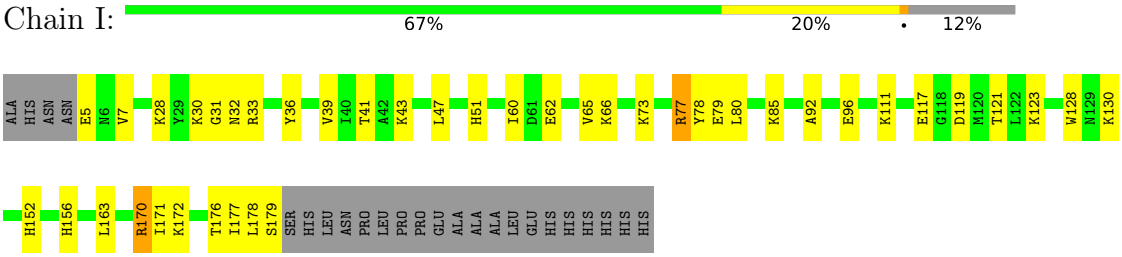
• Molecule 1: HOMING ENDONUCLEASE I-DMOI

Chain E:



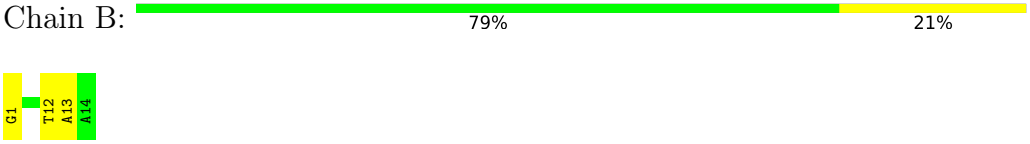
• Molecule 1: HOMING ENDONUCLEASE I-DMOI

Chain I:



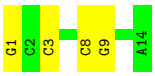
• Molecule 2: 5'-D(*GP*CP*CP*TP*TP*GP*CP*CP*GP*GP*GP*TP*AP*AP)-3'

Chain B:



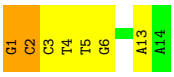
• Molecule 2: 5'-D(*GP*CP*CP*TP*TP*GP*CP*CP*GP*GP*GP*TP*AP*AP)-3'

Chain F:



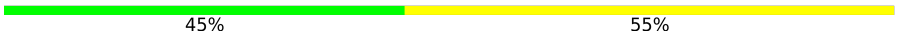
• Molecule 2: 5'-D(*GP*CP*CP*TP*TP*GP*CP*CP*GP*GP*GP*TP*AP*AP)-3'

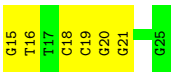
Chain J:



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

Chain C:



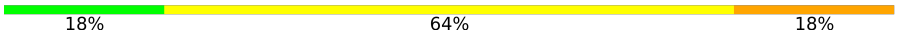


• Molecule 3: 5'-D(*GP*TP*TP*CP*CP*GP*GP*CP*GP*CP*GP)-3'

Chain G:

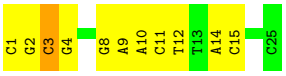
• Molecule 3: 5'-D(*GP*TP*TP*CP*CP*GP*GP*CP*GP*CP*GP)-3'

Chain K:



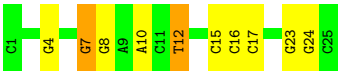
• Molecule 4: 25MER

Chain D:



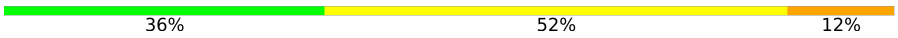
• Molecule 4: 25MER

Chain H:



• Molecule 4: 25MER

Chain L:




C1
G2
C3
G7
G8
A9
A10
C11
T12
T13
A14
C15
C16
C17
G18
G19
C20
A21
A22
G23
G24
C25

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	106.82Å 70.47Å 107.10Å 90.00° 119.88° 90.00°	Depositor
Resolution (Å)	42.65 – 2.45 56.07 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.0 (42.65-2.45) 99.0 (56.07-2.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.83 (at 2.45Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.176 , 0.230 0.167 , 0.170	Depositor DCC
R_{free} test set	2590 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	49.6	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 59.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h-l,k,h 0.018 for l,k,-h-l 0.015 for h,-k,-h-l 0.015 for -h-l,-k,l 0.015 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7887	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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: CL, MN, ACT

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	0.37	0/1553	0.53	0/2085
1	E	0.38	0/1523	0.51	0/2045
1	I	0.41	0/1537	0.55	0/2064
2	B	0.89	1/323 (0.3%)	1.26	0/495
2	F	0.83	1/323 (0.3%)	1.33	1/495 (0.2%)
2	J	0.92	1/323 (0.3%)	1.39	2/495 (0.4%)
3	C	0.98	1/253 (0.4%)	1.27	1/387 (0.3%)
3	G	0.92	1/253 (0.4%)	1.33	1/387 (0.3%)
3	K	0.97	1/253 (0.4%)	1.37	2/387 (0.5%)
4	D	0.65	0/570	1.31	4/877 (0.5%)
4	H	0.73	0/570	1.35	5/877 (0.6%)
4	L	0.75	0/570	1.37	5/877 (0.6%)
All	All	0.61	6/8051 (0.1%)	0.99	21/11471 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	15	DG	OP3-P	-10.73	1.48	1.61
2	F	1	DG	OP3-P	-10.68	1.48	1.61
2	B	1	DG	OP3-P	-10.55	1.48	1.61
2	J	1	DG	OP3-P	-10.55	1.48	1.61
3	K	15	DG	OP3-P	-10.35	1.48	1.61
3	G	15	DG	OP3-P	-10.33	1.48	1.61

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	G	20	DG	O4'-C1'-N9	8.62	114.04	108.00
4	D	14	DA	O4'-C1'-N9	-8.39	102.13	108.00
4	L	2	DG	O4'-C1'-N9	-8.36	102.15	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	K	16	DT	O4'-C1'-N1	-8.13	102.31	108.00
4	H	12	DT	O4'-C4'-C3'	-6.33	101.97	104.50
4	L	14	DA	O4'-C1'-N9	-6.29	103.59	108.00
2	F	3	DC	O4'-C1'-N1	-6.16	103.69	108.00
4	L	13	DT	O4'-C1'-N1	-6.13	103.71	108.00
2	J	4	DT	N3-C4-O4	6.03	123.52	119.90
4	L	18	DG	O4'-C1'-N9	5.93	112.15	108.00
3	K	18	DC	O4'-C1'-N1	5.89	112.12	108.00
2	J	2	DC	C1'-O4'-C4'	-5.60	104.50	110.10
3	C	16	DT	O4'-C1'-N1	-5.58	104.09	108.00
4	H	7	DG	P-O3'-C3'	5.34	126.11	119.70
4	D	1	DC	P-O3'-C3'	5.28	126.03	119.70
4	D	3	DC	O4'-C1'-N1	5.25	111.68	108.00
4	H	12	DT	C4'-C3'-C2'	-5.20	98.42	103.10
4	H	10	DA	O4'-C1'-N9	-5.16	104.39	108.00
4	L	7	DG	O4'-C1'-C2'	-5.15	101.78	105.90
4	D	11	DC	O4'-C1'-N1	5.03	111.52	108.00
4	H	7	DG	O4'-C1'-N9	-5.02	104.49	108.00

There are no chirality outliers.

There are no planarity outliers.

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	1518	0	1602	39	0
1	E	1489	0	1571	21	0
1	I	1496	0	1587	30	1
2	B	289	0	158	1	0
2	F	289	0	158	1	0
2	J	289	0	158	5	0
3	C	227	0	124	4	0
3	G	227	0	124	7	0
3	K	227	0	124	7	0
4	D	508	0	279	7	0
4	H	508	0	279	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	508	0	279	11	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	I	1	0	0	0	0
6	A	4	0	3	1	0
7	A	1	0	0	0	0
7	E	1	0	0	0	0
7	I	1	0	0	0	0
8	A	55	0	0	3	0
8	B	9	0	0	0	0
8	C	19	0	0	0	0
8	D	8	0	0	1	0
8	E	46	0	0	1	0
8	F	11	0	0	0	0
8	G	11	0	0	0	0
8	H	5	0	0	0	0
8	I	87	0	0	3	0
8	J	12	0	0	0	0
8	K	15	0	0	0	0
8	L	23	0	0	1	0
All	All	7887	0	6446	134	1

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 10.

All (134) 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)
4:L:2:DG:H2"	4:L:3:DC:H5"	1.12	1.12
3:G:22:DC:H2"	3:G:23:DG:H5'	1.33	1.09
4:H:16:DC:H2"	4:H:17:DC:H5'	1.41	1.01
4:H:7:DG:H2"	4:H:8:DG:H5"	1.50	0.91
1:A:182:LEU:HA	1:A:183:ASN:HB2	1.51	0.91
1:I:121:THR:HG22	1:I:123:LYS:H	1.41	0.85
1:I:7:VAL:HG11	1:I:62:GLU:HG2	1.62	0.81
1:A:170:ARG:HG2	1:A:171:ILE:HD12	1.64	0.80
1:E:172:LYS:O	1:E:176:THR:HB	1.84	0.78
1:A:183:ASN:H	6:A:1184:ACT:H3	1.50	0.76
4:L:7:DG:H2"	4:L:8:DG:H5"	1.69	0.75
8:E:2006:HOH:O	4:H:15:DC:OP1	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:2:DG:H2"	4:L:3:DC:C5'	2.07	0.73
1:I:73:LYS:HD3	1:I:78:TYR:CZ	2.25	0.72
2:J:1:DG:H2"	2:J:2:DC:O4'	1.91	0.70
1:I:111:LYS:HE2	1:I:177:ILE:O	1.93	0.68
1:A:113:LEU:HD13	1:A:127:ILE:HG21	1.76	0.66
4:H:23:DG:H2'	4:H:24:DG:C8	2.30	0.66
1:E:33:ARG:NH1	3:G:21:DG:O6	2.29	0.65
1:A:45:GLU:HB2	1:A:78:TYR:CE2	2.31	0.65
1:I:5:GLU:HG2	1:I:7:VAL:HG22	1.80	0.64
1:E:111:LYS:HE2	1:E:177:ILE:O	1.98	0.64
1:I:28:LYS:HE3	1:I:32:ASN:HA	1.80	0.62
1:A:128:TRP:O	1:A:129:ASN:HB2	1.99	0.62
8:A:2004:HOH:O	4:D:15:DC:OP1	2.15	0.61
1:A:146:GLY:O	1:A:172:LYS:HE3	2.00	0.61
3:C:19:DC:H2"	3:C:20:DG:H5'	1.85	0.58
1:I:119:ASP:OD1	1:I:121:THR:HB	2.03	0.58
1:A:111:LYS:HE2	1:A:178:LEU:O	2.03	0.58
3:G:24:DC:H2"	3:G:25:DG:C8	2.39	0.58
1:A:46:ASN:O	1:A:50:GLN:HG2	2.04	0.57
4:D:8:DG:H2"	4:D:9:DA:H5'	1.87	0.57
3:K:18:DC:H2"	3:K:19:DC:H5'	1.85	0.57
1:A:5:GLU:HG2	1:A:7:VAL:HG12	1.86	0.57
1:A:93:ASN:O	1:A:97[A]:ARG:HG3	2.05	0.57
1:A:66:LYS:HA	1:A:66:LYS:HE3	1.87	0.57
4:L:23:DG:H2"	4:L:24:DG:OP2	2.05	0.56
1:A:22:GLY:HA3	1:A:39:VAL:O	2.05	0.56
1:A:111:LYS:O	1:A:115:VAL:HG23	2.05	0.56
4:L:20:DC:H2"	4:L:21:DA:C8	2.42	0.54
1:A:148:ARG:HD2	1:A:168:ARG:NH2	2.22	0.54
1:E:33:ARG:HD2	4:H:4:DG:O6	2.08	0.54
1:A:110:ILE:HG12	1:A:138:VAL:HG13	1.90	0.54
1:A:111:LYS:HE3	1:A:177:ILE:O	2.08	0.54
2:F:8:DC:H2"	2:F:9:DG:C8	2.43	0.53
8:A:2053:HOH:O	4:H:12:DT:H4'	2.08	0.53
4:H:16:DC:H2"	4:H:17:DC:C5'	2.27	0.53
4:L:2:DG:C2'	4:L:3:DC:H5"	2.08	0.53
4:H:23:DG:H2'	4:H:24:DG:H8	1.74	0.53
1:I:163:LEU:C	1:I:163:LEU:HD23	2.30	0.52
1:I:172:LYS:O	1:I:176:THR:HB	2.08	0.52
1:E:5:GLU:HG3	1:E:8:SER:H	1.74	0.52
1:E:110:ILE:CG2	1:E:177:ILE:HG21	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:10:DA:H5"	8:L:2009:HOH:O	2.09	0.52
8:I:2010:HOH:O	3:K:15:DG:OP1	2.19	0.52
1:I:156:HIS:HE1	8:I:2078:HOH:O	1.91	0.52
1:A:136:GLU:O	1:A:140:ARG:HG3	2.09	0.52
4:D:2:DG:H2"	4:D:3:DC:H5"	1.91	0.51
4:H:7:DG:C2'	4:H:8:DG:H5"	2.34	0.51
1:A:15:LEU:O	1:A:19:ILE:HG12	2.11	0.51
1:A:45:GLU:HB2	1:A:78:TYR:CD2	2.46	0.51
3:C:19:DC:H2'	3:C:20:DG:C8	2.45	0.51
1:A:73:LYS:HB2	1:A:78:TYR:CE1	2.46	0.51
1:E:102:ASN:OD1	1:E:105:GLU:HG3	2.12	0.50
1:A:182:LEU:HB3	1:A:183:ASN:C	2.32	0.50
4:H:7:DG:H2"	4:H:8:DG:C5'	2.33	0.49
1:I:28:LYS:HD2	1:I:33:ARG:O	2.13	0.49
1:E:41:THR:HB	1:E:77:ARG:HG3	1.94	0.49
1:E:80:LEU:C	1:E:80:LEU:HD23	2.32	0.49
1:A:49:LYS:HG2	1:A:71:ILE:HD13	1.95	0.49
1:I:73:LYS:HD3	1:I:78:TYR:CE2	2.47	0.49
1:A:30:LYS:O	1:A:30:LYS:HD2	2.13	0.48
2:B:12:DT:H2"	2:B:13:DA:C8	2.48	0.48
1:E:97[A]:ARG:HB2	1:E:100:LEU:HD12	1.95	0.48
1:E:103:MET:O	1:E:107:ILE:HG12	2.14	0.48
3:K:24:DC:H2"	3:K:25:DG:C8	2.49	0.48
4:L:12:DT:H1'	4:L:13:DT:H5'	1.95	0.48
4:D:12:DT:H5"	8:D:2004:HOH:O	2.13	0.48
1:I:92:ALA:O	1:I:96:GLU:HG3	2.14	0.48
1:A:33:ARG:NH1	3:C:21:DG:O6	2.46	0.48
1:A:140:ARG:HD2	8:A:2043:HOH:O	2.12	0.48
3:K:18:DC:C2'	3:K:19:DC:H5'	2.44	0.47
1:E:106:GLN:HG2	1:E:141:TRP:CD2	2.50	0.47
4:D:9:DA:H2"	4:D:10:DA:C8	2.50	0.47
3:K:19:DC:H2'	3:K:20:DG:C8	2.49	0.47
1:A:172:LYS:O	1:A:176:THR:HB	2.16	0.46
1:I:41:THR:HB	1:I:77:ARG:HG3	1.97	0.46
3:G:19:DC:H2"	3:G:20:DG:H5'	1.98	0.46
1:I:5:GLU:HG2	1:I:7:VAL:H	1.81	0.46
1:I:39:VAL:HG13	1:I:79:GLU:HG3	1.97	0.45
1:A:33:ARG:HD2	4:D:4:DG:O6	2.16	0.45
1:E:5:GLU:OE1	1:E:7:VAL:HG12	2.16	0.45
1:I:47:LEU:HD12	1:I:51[B]:HIS:ND1	2.32	0.45
1:E:106:GLN:HG2	1:E:141:TRP:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:80:LEU:C	1:I:80:LEU:HD23	2.37	0.44
2:J:5:DT:H2"	2:J:6:DG:C8	2.53	0.44
1:A:113:LEU:CD1	1:A:127:ILE:HG21	2.47	0.44
1:I:152[B]:HIS:HD2	8:I:2072:HOH:O	2.01	0.44
1:A:180:SER:OG	1:A:182:LEU:HD12	2.18	0.44
3:C:18:DC:H5"	3:C:18:DC:H6	1.83	0.43
1:I:60:ILE:HG23	1:I:65:VAL:HB	1.99	0.43
1:E:22:GLY:HA3	1:E:39:VAL:O	2.18	0.43
4:D:8:DG:H2'	4:D:9:DA:C8	2.54	0.43
1:I:66:LYS:HD3	1:I:66:LYS:HA	1.84	0.43
1:I:170:ARG:HG2	1:I:171:ILE:N	2.32	0.43
1:E:30:LYS:HA	1:E:31:GLY:HA2	1.76	0.43
1:I:130:LYS:HG3	4:L:15:DC:OP2	2.19	0.42
1:E:63:LEU:HB2	1:E:65:VAL:HG23	2.01	0.42
1:I:36:TYR:CE1	1:I:85:LYS:HG3	2.54	0.42
1:E:5:GLU:CD	1:E:7:VAL:HG12	2.40	0.42
1:I:128:TRP:CZ3	4:L:16:DC:H2'	2.55	0.42
3:G:22:DC:C2'	3:G:23:DG:H5'	2.25	0.42
1:I:30:LYS:HA	1:I:31:GLY:HA2	1.79	0.42
1:I:33:ARG:NH1	3:K:21:DG:O6	2.52	0.42
1:A:44:SER:HB3	1:A:47:LEU:HB3	2.01	0.42
1:A:170:ARG:HG2	1:A:171:ILE:N	2.34	0.41
1:I:178:LEU:O	1:I:179:SER:C	2.58	0.41
2:J:1:DG:O5'	2:J:1:DG:H8	2.03	0.41
1:I:43:LYS:HB2	2:J:13:DA:H3'	2.02	0.41
4:L:8:DG:H2"	4:L:9:DA:H5'	2.01	0.41
1:A:5:GLU:CG	1:A:7:VAL:HG12	2.50	0.41
1:A:104:ARG:NH2	3:G:19:DC:OP1	2.45	0.41
1:E:106:GLN:O	1:E:110:ILE:HG13	2.21	0.41
1:A:63:LEU:HA	1:A:63:LEU:HD22	1.82	0.41
3:G:19:DC:H2'	3:G:20:DG:C8	2.55	0.41
3:K:17:DT:H1'	3:K:18:DC:C6	2.55	0.41
1:A:39:VAL:HG13	1:A:79:GLU:HG3	2.03	0.41
1:E:110:ILE:HG21	1:E:177:ILE:HG21	2.03	0.41
1:I:7:VAL:CG1	1:I:62:GLU:HG2	2.43	0.41
1:A:77:ARG:N	1:A:77:ARG:HD3	2.36	0.40
2:J:2:DC:H2"	2:J:3:DC:C6	2.57	0.40
1:A:30:LYS:HD2	1:A:30:LYS:C	2.42	0.40
1:A:30:LYS:HA	1:A:31:GLY:HA2	1.87	0.40
1:E:45:GLU:HB2	1:E:78:TYR:CE1	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:62:GLU:OE2	1:I:156:HIS:O[2_455]	2.17	0.03

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	182/199 (92%)	179 (98%)	3 (2%)	0	100	100
1	E	179/199 (90%)	177 (99%)	2 (1%)	0	100	100
1	I	180/199 (90%)	178 (99%)	2 (1%)	0	100	100
All	All	541/597 (91%)	534 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	166/177 (94%)	160 (96%)	6 (4%)	35	46
1	E	163/177 (92%)	160 (98%)	3 (2%)	59	71
1	I	164/177 (93%)	161 (98%)	3 (2%)	59	71
All	All	493/531 (93%)	481 (98%)	12 (2%)	47	61

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LYS
1	A	63	LEU
1	A	66	LYS
1	A	77	ARG
1	A	113	LEU
1	A	117	GLU
1	E	75	ASP
1	E	77	ARG
1	E	136	GLU
1	I	77	ARG
1	I	117	GLU
1	I	170	ARG

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

Mol	Chain	Res	Type
1	E	149	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 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	ACT	A	1184	-	3,3,3	0.79	0	3,3,3	1.34	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1184	ACT	1	0

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, 95^{th} 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	179/199 (89%)	-0.05	3 (1%) 70 67	30, 47, 84, 111	0
1	E	176/199 (88%)	-0.11	0 100 100	27, 47, 79, 102	0
1	I	175/199 (87%)	-0.13	0 100 100	26, 39, 72, 98	0
2	B	14/14 (100%)	-0.48	0 100 100	58, 67, 91, 116	0
2	F	14/14 (100%)	-0.32	0 100 100	42, 75, 97, 118	0
2	J	14/14 (100%)	-0.45	0 100 100	40, 55, 107, 135	0
3	C	11/11 (100%)	-0.44	0 100 100	44, 55, 80, 82	0
3	G	11/11 (100%)	-0.44	0 100 100	44, 56, 74, 76	0
3	K	11/11 (100%)	-0.37	0 100 100	42, 57, 67, 72	0
4	D	25/25 (100%)	-0.43	0 100 100	40, 64, 94, 109	0
4	H	25/25 (100%)	-0.34	0 100 100	39, 61, 114, 125	0
4	L	25/25 (100%)	-0.49	0 100 100	37, 59, 108, 122	0
All	All	680/747 (91%)	-0.17	3 (0%) 92 93	26, 48, 88, 135	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	75	ASP	2.6
1	A	6	ASN	2.5
1	A	182	LEU	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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, 95^{th} 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
5	CL	B	1015	1/1	0.34	0.20	116,116,116,116	0
5	CL	A	1181	1/1	0.76	0.21	90,90,90,90	0
5	CL	E	1181	1/1	0.79	0.22	89,89,89,89	0
6	ACT	A	1184	4/4	0.89	0.14	65,75,75,76	0
5	CL	I	1181	1/1	0.90	0.20	79,79,79,79	0
7	MN	A	1185	1/1	0.97	0.09	49,49,49,49	0
7	MN	I	1180	1/1	0.98	0.14	47,47,47,47	0
7	MN	E	1182	1/1	0.99	0.10	48,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.