Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2024 – 03:47 AM EST

PDB ID	:	3ODH
Title	:	Structure of OkrAI/DNA complex
Authors	:	Vanamee, E.S.; Aggarwal, A.K.
Deposited on	:	2010-08-11
Resolution	:	2.30 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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

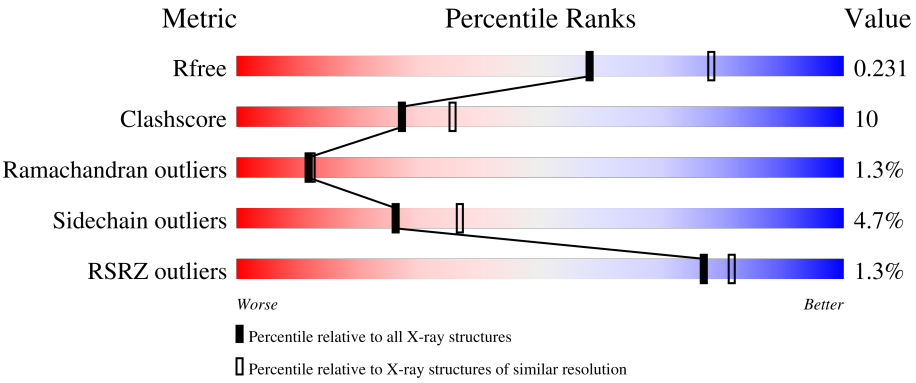
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	194	78% 21%
1	B	194	78% 17%
1	E	194	84% 13%
1	F	194	77% 16% 6%
2	C	12	25% 67% 8%

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Mol	Chain	Length	Quality of chain
2	D	12	17% 67% 17%
2	G	12	25% 58% 17%
2	H	12	33% 58% 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7695 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 OkrAI endonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1506	956	269	271	10			
1	B	192	Total	C	N	O	S	0	0	0
			1471	937	259	266	9			
1	E	194	Total	C	N	O	S	0	0	0
			1516	965	270	271	10			
1	F	194	Total	C	N	O	S	0	0	0
			1514	963	273	268	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			243	118	44	70	11			
2	D	12	Total	C	N	O	P	0	0	0
			243	118	44	70	11			
2	G	12	Total	C	N	O	P	0	0	0
			243	118	44	70	11			
2	H	12	Total	C	N	O	P	0	0	0
			243	118	44	70	11			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	1	Total	Ca	0	0
			1	1		
3	E	1	Total	Ca	0	0
			1	1		
3	F	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Ca 1 1	0	0

- Molecule 4 is water.

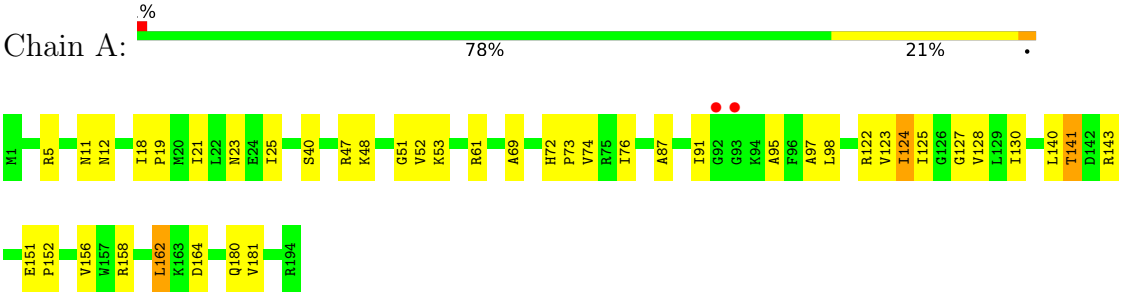
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	159	Total O 159 159	0	0
4	B	108	Total O 108 108	0	0
4	E	170	Total O 170 170	0	0
4	F	151	Total O 151 151	0	0
4	C	35	Total O 35 35	0	0
4	D	27	Total O 27 27	0	0
4	G	30	Total O 30 30	0	0
4	H	30	Total O 30 30	0	0

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.

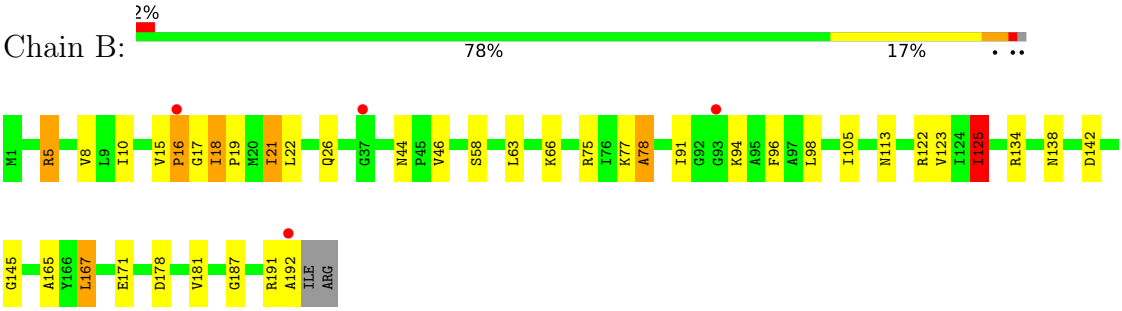
• Molecule 1: OkrAI endonuclease

Chain A:



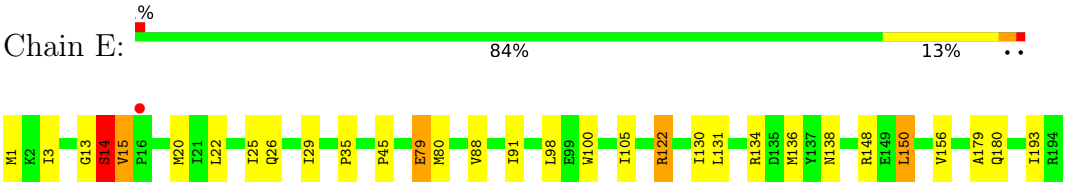
• Molecule 1: OkrAI endonuclease

Chain B:



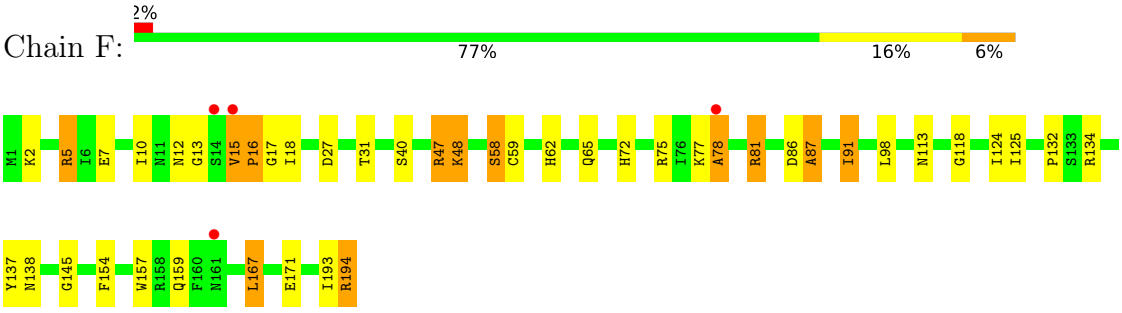
• Molecule 1: OkrAI endonuclease

Chain E:



• Molecule 1: OkrAI endonuclease

Chain F:

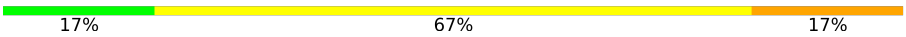


• Molecule 2: DNA (5'-D(*TP*AP*TP*GP*GP*AP*TP*CP*CP*AP*TP*A)-3')

Chain C:

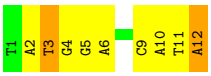
• Molecule 2: DNA (5'-D(*TP*AP*TP*GP*GP*AP*TP*CP*CP*AP*TP*A)-3')

Chain D:



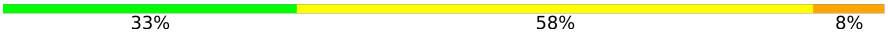
• Molecule 2: DNA (5'-D(*TP*AP*TP*GP*GP*AP*TP*CP*CP*AP*TP*A)-3')

Chain G:



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

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	80.98Å 83.08Å 119.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	88.8 (20.00-2.30) 88.8 (19.96-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	17.56 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.5.0102, CNS	Depositor
R, R_{free}	0.155 , 0.234 0.154 , 0.231	Depositor DCC
R_{free} test set	1624 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	19.9	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 39.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7695	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.77	0/1537	0.83	3/2081 (0.1%)
1	B	0.79	0/1503	0.81	2/2037 (0.1%)
1	E	0.85	0/1548	0.84	2/2092 (0.1%)
1	F	0.84	1/1545 (0.1%)	0.86	1/2086 (0.0%)
2	C	1.46	0/272	2.46	21/418 (5.0%)
2	D	1.44	2/272 (0.7%)	2.30	22/418 (5.3%)
2	G	1.56	2/272 (0.7%)	2.48	25/418 (6.0%)
2	H	1.61	0/272	2.34	18/418 (4.3%)
All	All	0.95	5/7221 (0.1%)	1.24	94/9968 (0.9%)

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	E	0	1
1	F	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	DA	C3'-O3'	-7.21	1.34	1.44
2	G	12	DA	N9-C4	-6.53	1.33	1.37
1	F	59	CYS	CB-SG	-5.31	1.73	1.81
2	D	5	DG	C6-N1	5.13	1.43	1.39
2	G	10	DA	C5-C4	5.13	1.42	1.38

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	12	DA	C5-N7-C8	-12.54	97.63	103.90
2	H	6	DA	O4'-C4'-C3'	-11.24	99.25	106.00
2	G	12	DA	C5-N7-C8	-10.80	98.50	103.90
2	C	12	DA	C4-C5-N7	10.71	116.05	110.70
2	C	12	DA	N7-C8-N9	10.57	119.08	113.80
2	H	7	DT	O4'-C1'-N1	-9.48	101.36	108.00
2	C	1	DT	O4'-C1'-N1	9.39	114.57	108.00
2	C	12	DA	C2-N3-C4	-9.08	106.06	110.60
1	E	122	ARG	NE-CZ-NH2	-8.79	115.90	120.30
2	D	10	DA	O4'-C1'-N9	-8.69	101.92	108.00
2	D	6	DA	O4'-C1'-N9	-8.57	102.00	108.00
2	D	1	DT	C4-C5-C7	-8.26	114.04	119.00
2	H	6	DA	O4'-C1'-N9	-8.21	102.25	108.00
2	H	9	DC	O4'-C1'-N1	-8.10	102.33	108.00
2	C	12	DA	N1-C6-N6	7.95	123.37	118.60
2	D	1	DT	C5-C4-O4	-7.93	119.35	124.90
2	D	1	DT	N3-C4-O4	7.79	124.57	119.90
2	D	2	DA	O5'-P-OP2	-7.66	98.81	105.70
2	G	12	DA	N3-C4-C5	7.62	132.13	126.80
2	H	6	DA	O4'-C1'-C2'	-7.61	99.81	105.90
2	G	12	DA	N7-C8-N9	7.56	117.58	113.80
2	G	12	DA	C2-N3-C4	-7.46	106.87	110.60
2	C	11	DT	O4'-C1'-N1	7.46	113.22	108.00
2	C	12	DA	C6-C5-N7	-7.36	127.15	132.30
2	C	3	DT	N3-C2-O2	-7.34	117.89	122.30
1	E	122	ARG	NE-CZ-NH1	7.27	123.94	120.30
2	D	4	DG	C5-N7-C8	6.92	107.76	104.30
2	C	7	DT	O4'-C4'-C3'	-6.91	101.74	104.50
1	B	75	ARG	NE-CZ-NH1	6.88	123.74	120.30
2	D	5	DG	C2-N3-C4	6.87	115.34	111.90
2	D	5	DG	C5-C6-O6	-6.81	124.51	128.60
2	C	7	DT	C2-N3-C4	-6.78	123.13	127.20
2	G	12	DA	N3-C4-N9	-6.71	122.03	127.40
2	G	3	DT	C4-C5-C7	6.67	123.00	119.00
2	D	9	DC	O4'-C1'-N1	-6.66	103.33	108.00
2	G	3	DT	C6-C5-C7	-6.64	118.92	122.90
2	G	4	DG	O4'-C1'-C2'	-6.59	100.63	105.90
2	C	12	DA	N9-C1'-C2'	6.54	125.03	112.60
2	D	2	DA	P-O5'-C5'	6.45	131.22	120.90
2	G	3	DT	P-O3'-C3'	6.40	127.38	119.70
2	G	12	DA	O4'-C1'-N9	-6.39	103.53	108.00
2	D	4	DG	N7-C8-N9	-6.32	109.94	113.10
2	G	12	DA	C4-C5-N7	6.31	113.85	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	12	DA	O4'-C1'-N9	6.30	112.41	108.00
2	G	9	DC	C5-C6-N1	-6.27	117.86	121.00
2	D	3	DT	C5-C4-O4	-6.25	120.52	124.90
2	G	9	DC	C4-C5-C6	6.22	120.51	117.40
2	C	4	DG	O4'-C1'-N9	6.13	112.29	108.00
2	D	1	DT	C6-C5-C7	6.13	126.58	122.90
2	C	12	DA	C8-N9-C4	-6.08	103.37	105.80
2	H	2	DA	N1-C6-N6	5.99	122.19	118.60
2	H	11	DT	C1'-O4'-C4'	-5.97	104.13	110.10
1	A	143	ARG	NE-CZ-NH2	-5.97	117.32	120.30
2	H	11	DT	OP1-P-OP2	5.96	128.54	119.60
2	H	11	DT	O4'-C4'-C3'	-5.88	102.15	104.50
2	D	8	DC	O4'-C1'-N1	5.85	112.09	108.00
2	G	11	DT	C1'-O4'-C4'	-5.83	104.27	110.10
2	G	12	DA	C5-C6-N1	-5.80	114.80	117.70
1	B	125	ILE	CB-CA-C	-5.78	100.05	111.60
2	G	10	DA	C2-N3-C4	-5.78	107.71	110.60
2	C	10	DA	C8-N9-C4	-5.76	103.49	105.80
2	H	2	DA	C4'-C3'-C2'	5.76	108.28	103.10
2	G	2	DA	O4'-C1'-N9	-5.73	103.99	108.00
2	D	3	DT	N3-C4-O4	5.67	123.30	119.90
2	D	5	DG	C8-N9-C4	-5.64	104.14	106.40
2	G	5	DG	N1-C6-O6	-5.63	116.52	119.90
1	F	81	ARG	NE-CZ-NH2	-5.62	117.49	120.30
2	G	6	DA	N7-C8-N9	5.60	116.60	113.80
2	G	5	DG	C2-N3-C4	5.55	114.68	111.90
2	G	5	DG	O4'-C4'-C3'	-5.54	102.28	104.50
2	H	11	DT	C4-C5-C7	5.53	122.32	119.00
2	C	7	DT	N1-C2-N3	5.53	117.92	114.60
2	G	3	DT	O4'-C1'-N1	5.50	111.85	108.00
2	G	12	DA	C6-N1-C2	5.46	121.88	118.60
2	H	7	DT	C5-C4-O4	-5.45	121.08	124.90
2	D	5	DG	P-O3'-C3'	5.43	126.22	119.70
2	H	2	DA	N1-C2-N3	-5.41	126.59	129.30
2	C	11	DT	C1'-O4'-C4'	-5.38	104.72	110.10
2	H	4	DG	C2-N3-C4	5.30	114.55	111.90
2	H	7	DT	N3-C4-O4	5.25	123.05	119.90
2	C	10	DA	O4'-C1'-C2'	-5.22	101.72	105.90
2	H	8	DC	O4'-C1'-N1	5.22	111.65	108.00
1	A	124	ILE	CG1-CB-CG2	-5.18	100.00	111.40
2	D	5	DG	C6-N1-C2	-5.17	122.00	125.10
1	A	162	LEU	CA-CB-CG	5.16	127.17	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	8	DC	N1-C2-O2	5.15	121.99	118.90
2	D	2	DA	C4'-C3'-C2'	5.08	107.67	103.10
2	C	4	DG	C3'-C2'-C1'	-5.08	96.41	102.50
2	D	7	DT	N3-C4-O4	5.07	122.94	119.90
2	G	4	DG	N1-C2-N3	5.06	126.94	123.90
2	C	5	DG	C2-N3-C4	5.05	114.43	111.90
2	G	5	DG	N3-C4-C5	-5.02	126.09	128.60
2	C	12	DA	N3-C4-C5	5.02	130.31	126.80
2	H	11	DT	C6-C5-C7	-5.00	119.90	122.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	15	VAL	Peptide
1	F	12	ASN	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	1506	0	1505	30	1
1	B	1471	0	1462	36	0
1	E	1516	0	1537	22	0
1	F	1514	0	1534	43	0
2	C	243	0	138	3	0
2	D	243	0	138	5	0
2	G	243	0	138	4	0
2	H	243	0	138	3	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
4	A	159	0	0	9	0
4	B	108	0	0	7	0
4	C	35	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	27	0	0	0	0
4	E	170	0	0	8	2
4	F	151	0	0	10	0
4	G	30	0	0	3	0
4	H	30	0	0	2	0
All	All	7695	0	6590	136	2

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 (136) 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:E:3:ILE:HD12	1:E:26:GLN:HG2	1.23	1.18
1:E:134:ARG:HD2	4:E:709:HOH:O	1.46	1.15
1:B:138:ASN:HB3	4:B:611:HOH:O	1.48	1.11
1:F:47:ARG:HH11	1:F:47:ARG:HB2	1.16	1.06
1:B:16:PRO:HG3	4:B:455:HOH:O	1.56	1.04
1:E:3:ILE:HD12	1:E:26:GLN:CG	1.93	0.97
1:A:21:ILE:HD11	1:A:91:ILE:HD11	1.47	0.96
1:F:47:ARG:HH11	1:F:47:ARG:CB	1.80	0.95
1:B:15:VAL:N	1:B:16:PRO:HD2	1.82	0.93
1:F:87:ALA:N	4:F:614:HOH:O	1.83	0.93
1:F:2:LYS:HE3	4:F:299:HOH:O	1.71	0.91
1:A:23:ASN:HB2	4:A:202:HOH:O	1.75	0.86
1:F:86:ASP:HA	4:F:614:HOH:O	1.79	0.81
1:A:21:ILE:HD11	1:A:91:ILE:CD1	2.10	0.81
2:C:12:DA:H62	2:D:1:DT:H3	1.28	0.81
1:E:3:ILE:CD1	1:E:26:GLN:HG2	2.10	0.80
1:A:141:THR:HG21	2:D:7:DT:OP2	1.82	0.80
1:F:47:ARG:HB2	1:F:47:ARG:NH1	1.96	0.79
2:H:12:DA:C8	4:H:168:HOH:O	2.36	0.79
1:F:86:ASP:CA	4:F:614:HOH:O	2.32	0.78
1:E:15:VAL:CB	4:E:237:HOH:O	2.33	0.77
1:F:86:ASP:O	1:F:98:LEU:O	2.04	0.76
1:B:91:ILE:HG13	1:B:125:ILE:HD11	1.67	0.76
1:F:15:VAL:O	1:F:17:GLY:N	2.18	0.76
2:H:12:DA:H8	4:H:168:HOH:O	1.70	0.75
1:B:15:VAL:H	1:B:16:PRO:HD2	1.50	0.74
1:A:123:VAL:O	1:A:124:ILE:HD12	1.89	0.72
2:G:12:DA:H8	4:G:231:HOH:O	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:13:GLY:HA3	4:F:616:HOH:O	1.95	0.67
1:B:8:VAL:H	1:E:180:GLN:HE21	1.43	0.66
4:F:244:HOH:O	2:H:12:DA:OP1	2.12	0.66
1:F:40:SER:HB3	4:F:560:HOH:O	1.95	0.65
1:F:77:LYS:O	1:F:78:ALA:HB3	1.97	0.65
1:B:122:ARG:CA	4:B:201:HOH:O	2.45	0.64
1:F:48:LYS:HD2	4:F:708:HOH:O	1.97	0.64
1:B:91:ILE:HG13	1:B:125:ILE:CD1	2.28	0.63
1:E:13:GLY:O	1:E:14:SER:C	2.38	0.62
4:E:258:HOH:O	1:F:194:ARG:HD2	2.00	0.61
1:F:47:ARG:HG3	1:F:48:LYS:HD3	1.80	0.61
1:B:91:ILE:CG1	1:B:125:ILE:HD11	2.30	0.61
1:F:77:LYS:O	1:F:78:ALA:CB	2.48	0.61
1:A:53:LYS:HE3	4:A:564:HOH:O	2.01	0.60
1:E:3:ILE:CD1	1:E:26:GLN:CG	2.74	0.60
1:F:2:LYS:CE	4:F:299:HOH:O	2.41	0.60
1:B:17:GLY:O	1:B:21:ILE:HG23	2.01	0.60
1:F:47:ARG:HH11	1:F:47:ARG:CG	2.16	0.59
1:E:79:GLU:HG3	1:E:80:MET:HG3	1.84	0.59
1:E:105:ILE:HD11	1:E:150:LEU:HD13	1.84	0.58
1:E:122:ARG:NH2	4:E:255:HOH:O	2.34	0.58
1:F:47:ARG:HD3	1:F:138:ASN:O	2.04	0.57
1:F:91:ILE:HG12	1:F:125:ILE:HG21	1.86	0.57
1:E:98:LEU:HD11	1:E:130:ILE:HD11	1.86	0.57
2:G:12:DA:H2'	2:G:12:DA:N3	2.20	0.57
1:A:51:GLY:HA2	1:A:141:THR:CG2	2.36	0.56
1:B:187:GLY:O	1:B:192:ALA:HB1	2.07	0.55
1:F:58:SER:O	1:F:62:HIS:HD2	1.90	0.55
1:A:51:GLY:HA2	1:A:141:THR:HG22	1.89	0.55
1:A:40:SER:HB3	4:A:204:HOH:O	2.07	0.54
2:C:12:DA:N6	2:D:1:DT:H3	2.00	0.54
1:B:113:ASN:ND2	4:B:669:HOH:O	2.40	0.53
1:A:5:ARG:HD2	4:A:490:HOH:O	2.08	0.53
1:F:113:ASN:ND2	1:F:157:TRP:HE1	2.06	0.53
1:B:15:VAL:N	1:B:16:PRO:CD	2.66	0.53
1:F:62:HIS:HA	1:F:65:GLN:HE21	1.74	0.52
1:A:25:ILE:HD13	1:A:128:VAL:HG21	1.92	0.52
1:A:98:LEU:HD11	1:A:130:ILE:HD11	1.92	0.51
1:B:16:PRO:HA	1:B:17:GLY:C	2.29	0.51
1:B:125:ILE:O	1:B:165:ALA:HA	2.11	0.51
1:A:158:ARG:NH1	4:A:468:HOH:O	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:7:GLU:HG2	1:F:154:PHE:CE2	2.46	0.50
1:E:193:ILE:O	1:F:194:ARG:HG3	2.11	0.50
1:B:10:ILE:HD12	1:B:167:LEU:HD12	1.94	0.49
1:B:16:PRO:HA	1:B:18:ILE:N	2.28	0.49
1:A:95:ALA:O	1:A:125:ILE:HG22	2.12	0.49
1:B:18:ILE:CB	1:B:19:PRO:HD3	2.43	0.49
1:A:47:ARG:HG2	1:A:48:LYS:HG2	1.93	0.48
2:G:12:DA:C8	4:G:231:HOH:O	2.55	0.48
1:A:69:ALA:O	1:A:87:ALA:HA	2.13	0.48
1:B:22:LEU:O	1:B:26:GLN:HG3	2.14	0.48
1:B:77:LYS:O	1:B:78:ALA:CB	2.61	0.48
1:B:5:ARG:HD3	1:B:171:GLU:OE1	2.14	0.47
1:A:40:SER:CB	4:A:204:HOH:O	2.62	0.47
1:A:18:ILE:HB	1:A:19:PRO:HD3	1.95	0.47
1:B:21:ILE:HD11	1:B:96:PHE:CE2	2.50	0.47
1:B:44:ASN:OD1	1:B:46:VAL:HG23	2.14	0.47
1:E:35:PRO:HB3	4:E:265:HOH:O	2.14	0.47
1:E:138:ASN:ND2	4:E:250:HOH:O	2.46	0.47
1:F:72:HIS:HD2	4:F:215:HOH:O	1.96	0.47
1:E:3:ILE:HD11	1:E:29:ILE:HD12	1.97	0.47
1:F:16:PRO:O	1:F:91:ILE:HD12	2.15	0.46
1:F:86:ASP:O	1:F:87:ALA:O	2.33	0.46
1:B:78:ALA:N	4:B:615:HOH:O	1.84	0.46
1:F:16:PRO:O	1:F:91:ILE:CD1	2.63	0.46
1:E:25:ILE:HG12	1:E:98:LEU:HD12	1.96	0.46
1:B:18:ILE:CB	4:B:704:HOH:O	2.64	0.46
1:E:100:TRP:C	1:E:100:TRP:CD1	2.89	0.46
1:B:21:ILE:HD11	1:B:96:PHE:CZ	2.52	0.45
1:A:151:GLU:N	1:A:152:PRO:CD	2.79	0.45
1:F:47:ARG:NH1	1:F:47:ARG:CG	2.78	0.45
1:B:8:VAL:H	1:E:180:GLN:NE2	2.10	0.45
1:F:5:ARG:HG2	1:F:171:GLU:OE1	2.16	0.45
1:A:76:ILE:HD11	4:A:227:HOH:O	2.17	0.45
1:F:75:ARG:NH1	1:F:78:ALA:HA	2.31	0.45
1:F:10:ILE:HD12	1:F:167:LEU:HD12	2.00	0.44
1:A:141:THR:CG2	2:D:7:DT:OP2	2.61	0.44
1:B:21:ILE:HD11	1:B:96:PHE:CD2	2.52	0.44
1:B:142:ASP:HB3	2:C:8:DC:C5	2.53	0.43
1:A:122:ARG:HH22	1:A:164:ASP:HB2	1.83	0.43
1:F:15:VAL:C	1:F:17:GLY:N	2.71	0.43
1:F:132:PRO:HD2	1:F:145:GLY:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:91:ILE:O	1:F:91:ILE:HG13	2.10	0.43
1:A:48:LYS:HA	1:A:140:LEU:O	2.19	0.43
1:E:1:MET:HE1	1:E:136:MET:SD	2.59	0.43
1:A:72:HIS:HA	1:A:73:PRO:HD3	1.89	0.43
1:F:81:ARG:HB3	2:G:3:DT:H5'	2.01	0.42
4:E:341:HOH:O	1:F:159:GLN:HB3	2.18	0.42
1:F:48:LYS:HE2	4:G:562:HOH:O	2.18	0.42
1:A:5:ARG:NH1	4:A:490:HOH:O	2.22	0.42
1:B:178:ASP:O	1:B:181:VAL:HG22	2.20	0.42
1:A:97:ALA:O	1:A:127:GLY:HA2	2.20	0.42
1:B:63:LEU:HD11	1:B:98:LEU:HD22	2.01	0.41
1:A:141:THR:HG21	2:D:7:DT:P	2.59	0.41
1:A:12:ASN:ND2	4:A:197:HOH:O	2.52	0.41
1:A:74:VAL:HG12	1:A:76:ILE:HG23	2.01	0.41
1:B:91:ILE:CG1	1:B:125:ILE:CD1	2.96	0.41
1:A:52:VAL:HG13	1:A:141:THR:HG23	2.02	0.41
1:E:148:ARG:HD2	4:E:483:HOH:O	2.19	0.41
1:B:105:ILE:HA	1:B:145:GLY:HA2	2.02	0.41
1:B:134:ARG:NH1	4:B:699:HOH:O	2.41	0.41
1:F:27:ASP:O	1:F:31:THR:HG23	2.20	0.41
1:E:45:PRO:HD2	1:E:179:ALA:HA	2.02	0.40
1:F:15:VAL:HA	1:F:18:ILE:HD12	2.02	0.40
1:B:21:ILE:HD11	1:B:96:PHE:CE1	2.56	0.40
1:F:118:GLY:HA3	1:F:124:ILE:HD12	2.03	0.40
1:B:187:GLY:O	1:B:192:ALA:CB	2.70	0.40
1:F:134:ARG:HA	1:F:137:TYR:HB3	2.04	0.40

All (2) 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)
4:E:221:HOH:O	4:C:13:HOH:O[1_565]	1.95	0.25
1:A:11:ASN:ND2	4:E:263:HOH:O[4_455]	2.00	0.20

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	192/194 (99%)	187 (97%)	5 (3%)	0	100 100
1	B	190/194 (98%)	179 (94%)	7 (4%)	4 (2%)	7 5
1	E	192/194 (99%)	182 (95%)	8 (4%)	2 (1%)	15 17
1	F	192/194 (99%)	178 (93%)	10 (5%)	4 (2%)	7 5
All	All	766/776 (99%)	726 (95%)	30 (4%)	10 (1%)	12 12

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	16	PRO
1	E	14	SER
1	F	87	ALA
1	B	78	ALA
1	B	191	ARG
1	F	78	ALA
1	E	91	ILE
1	F	15	VAL
1	F	16	PRO
1	B	18	ILE

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	160/167 (96%)	154 (96%)	6 (4%)	33 47
1	B	155/167 (93%)	147 (95%)	8 (5%)	23 32
1	E	163/167 (98%)	155 (95%)	8 (5%)	25 35
1	F	161/167 (96%)	153 (95%)	8 (5%)	24 34
All	All	639/668 (96%)	609 (95%)	30 (5%)	26 37

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ARG
1	A	141	THR
1	A	156	VAL
1	A	162	LEU
1	A	180	GLN
1	A	181	VAL
1	B	5	ARG
1	B	21	ILE
1	B	58	SER
1	B	66	LYS
1	B	94	LYS
1	B	123	VAL
1	B	125	ILE
1	B	167	LEU
1	E	14	SER
1	E	20	MET
1	E	22	LEU
1	E	79	GLU
1	E	88	VAL
1	E	131	LEU
1	E	150	LEU
1	E	156	VAL
1	F	5	ARG
1	F	47	ARG
1	F	48	LYS
1	F	58	SER
1	F	91	ILE
1	F	167	LEU
1	F	193	ILE
1	F	194	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	64	HIS
1	A	113	ASN
1	A	180	GLN
1	B	12	ASN
1	B	64	HIS
1	B	72	HIS

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Mol	Chain	Res	Type
1	B	113	ASN
1	E	23	ASN
1	E	65	GLN
1	E	113	ASN
1	E	138	ASN
1	E	180	GLN
1	F	62	HIS
1	F	65	GLN
1	F	72	HIS
1	F	113	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 6 ligands modelled in this entry, 6 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

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	194/194 (100%)	-0.69	2 (1%) 82 86	6, 16, 32, 42	0
1	B	192/194 (98%)	-0.50	4 (2%) 63 70	7, 20, 42, 51	0
1	E	194/194 (100%)	-0.84	1 (0%) 91 94	5, 13, 31, 45	0
1	F	194/194 (100%)	-0.69	4 (2%) 63 70	4, 15, 33, 42	0
2	C	12/12 (100%)	-1.21	0 100 100	9, 11, 23, 24	0
2	D	12/12 (100%)	-1.22	0 100 100	7, 12, 24, 28	0
2	G	12/12 (100%)	-0.92	0 100 100	6, 12, 27, 46	0
2	H	12/12 (100%)	-1.20	0 100 100	6, 10, 21, 32	0
All	All	822/824 (99%)	-0.71	11 (1%) 77 81	4, 16, 36, 51	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	192	ALA	4.2
1	A	92	GLY	3.7
1	F	15	VAL	3.3
1	B	93	GLY	3.3
1	A	93	GLY	2.6
1	B	16	PRO	2.4
1	E	16	PRO	2.3
1	F	14	SER	2.3
1	B	37	GLY	2.2
1	F	78	ALA	2.1
1	F	161	ASN	2.1

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
3	CA	H	13	1/1	0.95	0.09	39,39,39,39	0
3	CA	A	196	1/1	0.97	0.05	30,30,30,30	0
3	CA	A	195	1/1	0.98	0.04	10,10,10,10	0
3	CA	F	195	1/1	0.99	0.06	12,12,12,12	0
3	CA	E	195	1/1	0.99	0.06	9,9,9,9	0
3	CA	B	195	1/1	1.00	0.02	15,15,15,15	0

6.5 Other polymers (i)

There are no such residues in this entry.