



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2017 – 05:32 PM EST

PDB ID : 5X5L  
Title : Crystal structure of response regulator AdeR DNA binding domain in complex with an intercistronic region  
Authors : Wen, Y.  
Deposited on : unknown  
Resolution : 2.75 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](mailto: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.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030345

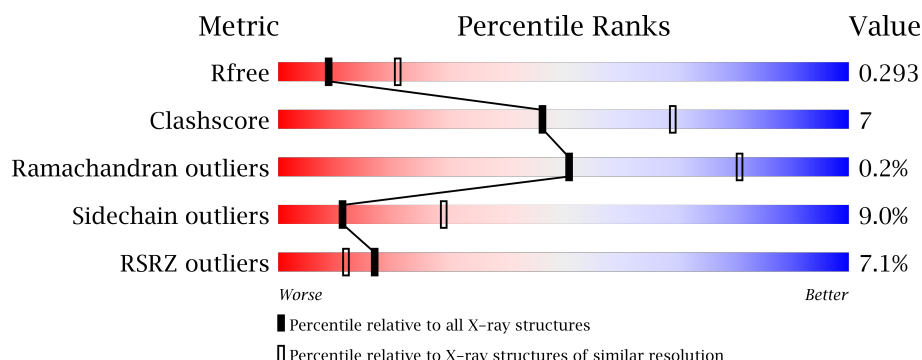
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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))
$R_{free}$	100719	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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  $\geq 3$ , 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	A	109	<div> <div>5%</div> <div>62%</div> <div>20%</div> <div>5%</div> <div>13%</div> </div>
1	B	109	<div> <div>6%</div> <div>70%</div> <div>14%</div> <div>•</div> <div>13%</div> </div>
1	E	109	<div> <div>9%</div> <div>73%</div> <div>14%</div> <div>••</div> <div>10%</div> </div>
1	H	109	<div> <div>11%</div> <div>69%</div> <div>17%</div> <div>•</div> <div>13%</div> </div>
1	M	109	<div> <div>6%</div> <div>70%</div> <div>12%</div> <div>•</div> <div>15%</div> </div>

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Mol	Chain	Length	Quality of chain
1	N	109	<div><div></div><div>6%</div><div>58%</div><div>18%</div><div>5%</div><div>18%</div></div>
2	C	25	<div><div></div><div>68%</div><div>24%</div><div></div></div>
2	F	25	<div><div></div><div>72%</div><div>24%</div><div></div></div>
3	D	25	<div><div></div><div>80%</div><div>20%</div><div></div></div>
3	G	25	<div><div></div><div>4%</div><div>72%</div><div>24%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6667 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 AdeR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	95	Total	C	N	O	S	0	0	0
			782	497	137	143	5			
1	B	95	Total	C	N	O	S	0	0	0
			775	491	135	144	5			
1	E	98	Total	C	N	O	S	0	0	0
			809	511	143	150	5			
1	H	95	Total	C	N	O	S	0	0	0
			779	494	136	144	5			
1	M	93	Total	C	N	O	S	0	0	0
			767	487	135	140	5			
1	N	89	Total	C	N	O	S	0	0	0
			741	471	130	135	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	24	Total	C	N	O	P	0	0	0
			508	240	102	142	24			
2	F	24	Total	C	N	O	P	0	0	0
			508	240	102	142	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	25	Total	C	N	O	P	0	0	0
			496	240	78	153	25			
3	G	25	Total	C	N	O	P	0	0	0
			495	240	78	152	25			

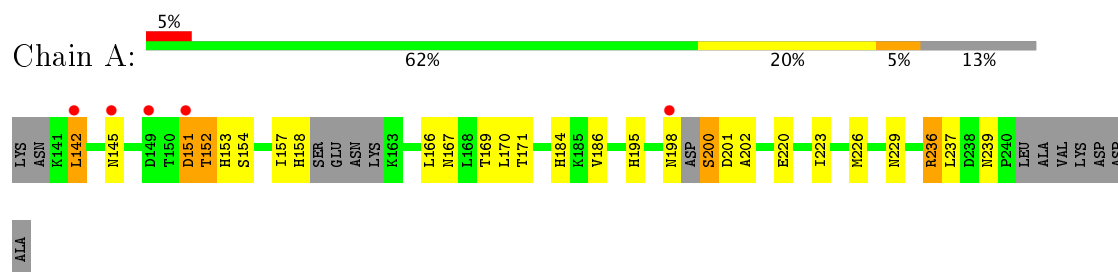
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	2	Total 2	O 2	0	0
4	M	1	Total 1	O 1	0	0
4	N	2	Total 2	O 2	0	0
4	C	2	Total 2	O 2	0	0

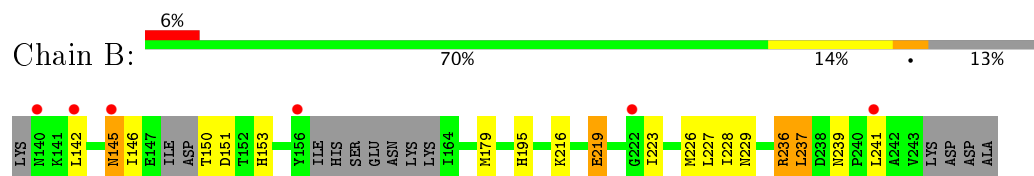
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

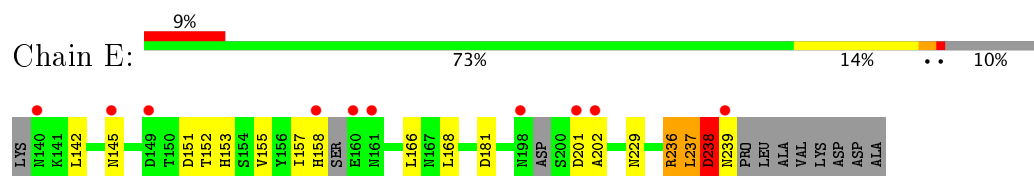
#### • Molecule 1: AdeR



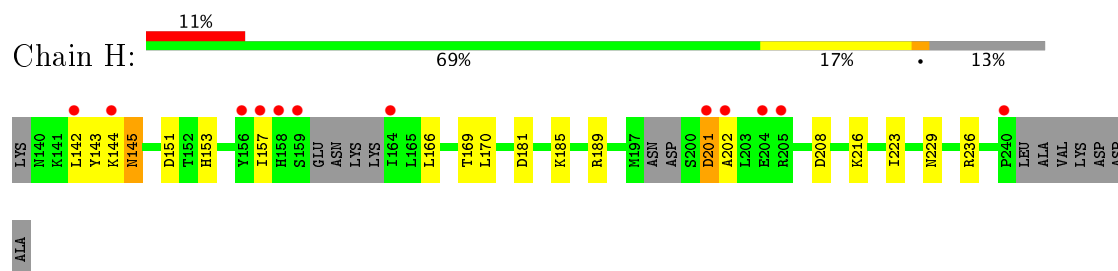
#### • Molecule 1: AdeR



#### • Molecule 1: AdeR

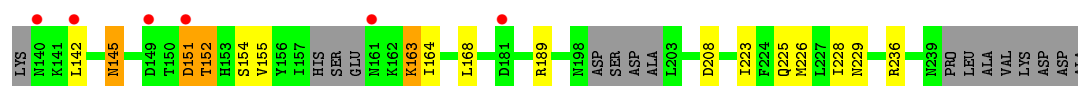


#### • Molecule 1: AdeR

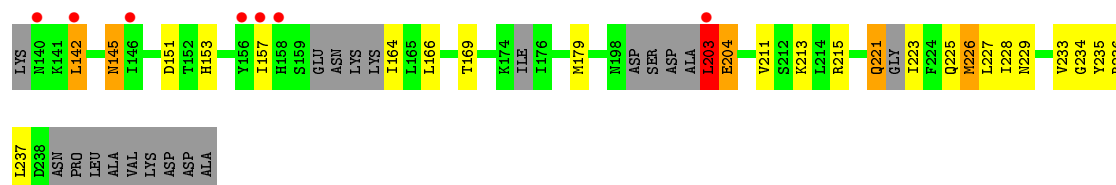


#### • Molecule 1: AdeR





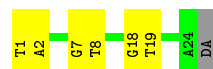
• Molecule 1: AdeR



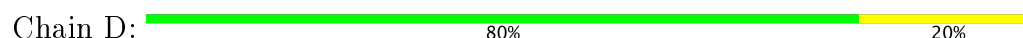
• Molecule 2: DNA (5'-D(P\*TP\*AP\*AP\*AP\*GP\*TP\*GP\*TP\*GP\*GP\*AP\*GP\*TP\*AP\*AP\*G  
P\*TP\*GP\*TP\*GP\*GP\*AP\*GP\*A)-3')



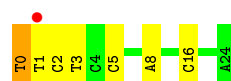
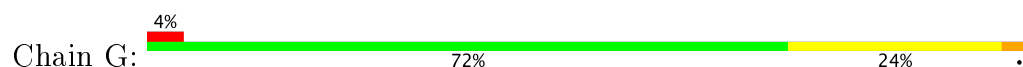
• Molecule 2: DNA (5'-D(P\*TP\*AP\*AP\*AP\*GP\*TP\*GP\*TP\*GP\*GP\*AP\*GP\*TP\*AP\*AP\*G  
P\*TP\*GP\*TP\*GP\*GP\*AP\*GP\*A)-3')



• Molecule 3: DNA (5'-D(P\*TP\*CP\*TP\*CP\*CP\*AP\*CP\*AP\*CP\*TP\*TP\*AP\*CP\*TP\*CP\*C  
P\*AP\*CP\*AP\*CP\*TP\*TP\*TP\*A)-3')



• Molecule 3: DNA (5'-D(P\*TP\*CP\*TP\*CP\*CP\*AP\*CP\*AP\*CP\*TP\*TP\*AP\*CP\*TP\*CP\*C  
P\*AP\*CP\*AP\*CP\*TP\*TP\*TP\*A)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.51Å 71.38Å 78.36Å 101.96° 104.53° 101.86°	Depositor
Resolution (Å)	43.82 – 2.75 43.82 – 2.75	Depositor EDS
% Data completeness (in resolution range)	83.0 (43.82-2.75) 80.3 (43.82-2.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.18 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0171	Depositor
R, $R_{free}$	0.278 , 0.296 0.274 , 0.293	Depositor DCC
$R_{free}$ test set	2000 reflections (9.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.0	Xtriage
Anisotropy	0.921	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 36.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	6667	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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 ⓘ

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	0.61	0/793	1.00	4/1063 (0.4%)
1	B	0.52	0/785	0.81	1/1054 (0.1%)
1	E	0.52	0/819	0.81	1/1096 (0.1%)
1	H	0.50	0/790	0.76	1/1060 (0.1%)
1	M	0.56	0/776	0.85	1/1039 (0.1%)
1	N	0.55	0/749	0.94	4/1000 (0.4%)
2	C	0.59	2/573 (0.3%)	0.86	0/886
2	F	0.49	0/573	0.80	0/886
3	D	0.53	0/551	0.88	1/844 (0.1%)
3	G	0.71	2/550 (0.4%)	0.95	2/841 (0.2%)
All	All	0.56	4/6959 (0.1%)	0.87	15/9769 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	0	DT	P-OP2	9.64	1.65	1.49
2	C	1	DT	C2-N3	5.94	1.42	1.37
3	G	0	DT	P-O5'	5.51	1.65	1.59
2	C	1	DT	C4-O4	5.49	1.28	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	0	DT	OP1-P-OP2	-9.48	105.38	119.60
1	A	236	ARG	CA-CB-CG	9.37	134.02	113.40
1	M	163	LYS	N-CA-C	-9.28	85.94	111.00
1	N	142	LEU	CA-CB-CG	7.73	133.09	115.30
1	E	238	ASP	CB-CG-OD1	-6.88	112.11	118.30
1	B	219	GLU	CA-CB-CG	6.85	128.48	113.40
1	N	203	LEU	CB-CA-C	6.85	123.22	110.20
1	A	200	SER	CB-CA-C	6.19	121.87	110.10
3	G	8	DA	C1'-O4'-C4'	-5.97	104.13	110.10
3	D	8	DA	C1'-O4'-C4'	-5.85	104.25	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	226	MET	CG-SD-CE	5.76	109.41	100.20
1	N	203	LEU	N-CA-C	-5.50	96.15	111.00
1	H	201	ASP	N-CA-CB	5.26	120.07	110.60
1	A	142	LEU	CA-CB-CG	5.23	127.33	115.30
1	A	152	THR	N-CA-C	5.08	124.71	111.00

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	A	782	0	797	26	0
1	B	775	0	786	9	0
1	E	809	0	821	14	0
1	H	779	0	789	16	0
1	M	767	0	783	9	0
1	N	741	0	752	14	0
2	C	508	0	271	5	0
2	F	508	0	271	3	0
3	D	496	0	285	7	0
3	G	495	0	285	8	0
4	C	2	0	0	0	0
4	E	2	0	0	0	0
4	M	1	0	0	0	0
4	N	2	0	0	0	0
All	All	6667	0	5840	90	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 7.

All (90) 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:N:226:MET:O	1:N:237:LEU:O	1.79	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ASP:HA	1:A:152:THR:CG2	2.02	0.89
1:H:169:THR:HG21	3:D:14:DT:OP2	1.73	0.89
1:A:169:THR:HG21	3:G:3:DT:OP2	1.73	0.89
1:A:151:ASP:HA	1:A:152:THR:HG23	1.58	0.84
1:E:166:LEU:HB3	1:E:168:LEU:CD1	2.14	0.78
1:A:186:VAL:HG22	1:A:236:ARG:HG3	1.66	0.75
1:B:226:MET:O	1:B:228:ILE:HD12	1.87	0.74
1:A:198:ASN:HB3	1:H:185:LYS:HE3	1.70	0.72
1:A:151:ASP:CA	1:A:152:THR:HG23	2.22	0.70
1:H:169:THR:HG21	3:D:14:DT:P	2.31	0.70
1:N:203:LEU:HG	1:N:204:GLU:H	1.58	0.68
1:M:223:ILE:CG2	1:M:226:MET:HG3	2.26	0.65
1:M:151:ASP:OD1	1:M:152:THR:N	2.30	0.65
1:A:223:ILE:CG2	1:A:226:MET:HG3	2.28	0.64
1:H:143:TYR:CZ	1:H:144:LYS:HD3	2.32	0.63
1:A:169:THR:HG21	3:G:3:DT:P	2.40	0.61
1:H:169:THR:CG2	3:D:14:DT:P	2.89	0.61
1:M:189:ARG:NH1	1:M:208:ASP:OD1	2.34	0.61
1:A:169:THR:CG2	3:G:3:DT:P	2.89	0.60
1:E:236:ARG:HD3	1:E:239:ASN:ND2	2.17	0.60
1:H:189:ARG:NH1	1:H:208:ASP:OD1	2.34	0.59
1:N:215:ARG:NH1	1:N:227:LEU:O	2.36	0.59
1:A:151:ASP:HA	1:A:152:THR:HG22	1.83	0.59
1:N:164:ILE:N	1:N:164:ILE:HD12	2.19	0.58
2:F:1:DT:H4'	2:F:2:DA:OP1	2.03	0.57
1:A:200:SER:HB2	1:A:202:ALA:N	2.21	0.56
1:E:155:VAL:HG23	1:E:166:LEU:HB2	1.87	0.56
1:A:198:ASN:HB3	1:H:185:LYS:CE	2.35	0.56
1:B:216:LYS:HA	1:B:219:GLU:HG2	1.89	0.55
1:A:167:ASN:HD22	1:N:169:THR:HA	1.73	0.54
1:A:184:HIS:O	1:E:152:THR:HG22	2.07	0.54
1:A:169:THR:HG23	3:G:2:DC:H3'	1.89	0.53
1:A:200:SER:HB3	1:A:201:ASP:CB	2.38	0.53
1:H:216:LYS:NZ	2:C:8:DT:OP1	2.41	0.53
1:M:223:ILE:HG22	1:M:226:MET:HG3	1.91	0.52
1:B:146:ILE:HD12	1:B:226:MET:CE	2.41	0.50
1:H:169:THR:HG22	1:H:170:LEU:N	2.26	0.50
1:B:146:ILE:HD12	1:B:226:MET:HE2	1.93	0.49
1:N:221:GLN:CG	1:N:223:ILE:N	2.77	0.48
3:G:0:DT:H2'	3:G:1:DT:C2	2.49	0.48
1:E:145:ASN:OD1	1:E:158:HIS:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:225:GLN:O	1:M:228:ILE:HD11	2.14	0.48
1:A:145:ASN:OD1	1:A:158:HIS:HB2	2.14	0.47
1:E:157:ILE:HG12	1:E:166:LEU:HD11	1.96	0.47
3:D:0:DT:H2'	3:D:1:DT:C2	2.49	0.47
1:H:145:ASN:HD21	1:H:223:ILE:HD11	1.79	0.47
1:A:169:THR:HG22	1:A:170:LEU:N	2.28	0.47
1:A:157:ILE:HG12	1:A:166:LEU:HD11	1.97	0.47
2:C:1:DT:H2"	2:C:2:DA:C8	2.50	0.47
2:F:18:DG:H2"	2:F:19:DT:H72	1.96	0.46
1:M:145:ASN:HD21	1:M:223:ILE:HD11	1.80	0.46
1:E:155:VAL:HG23	1:E:155:VAL:O	2.15	0.46
1:H:157:ILE:HG12	1:H:166:LEU:HD11	1.97	0.46
1:E:236:ARG:HD3	1:E:239:ASN:HD21	1.80	0.46
1:H:189:ARG:NH2	2:C:5:DG:OP1	2.50	0.45
1:N:221:GLN:HG3	1:N:223:ILE:N	2.31	0.45
1:B:179:MET:HE3	1:B:227:LEU:CD2	2.46	0.45
1:B:236:ARG:HD2	1:B:239:ASN:HA	1.98	0.45
1:E:202:ALA:HB1	3:G:16:DC:OP2	2.16	0.45
1:A:200:SER:CB	1:A:202:ALA:N	2.80	0.45
1:B:145:ASN:HD21	1:B:223:ILE:HD11	1.81	0.45
1:H:169:THR:CG2	3:D:14:DT:OP1	2.65	0.45
1:B:195:HIS:NE2	1:E:181:ASP:OD1	2.50	0.44
1:N:145:ASN:HD21	1:N:223:ILE:HD11	1.83	0.44
1:A:198:ASN:HB2	1:A:200:SER:N	2.33	0.44
1:A:202:ALA:HB1	3:G:5:DC:OP2	2.18	0.44
1:N:225:GLN:O	1:N:228:ILE:HD11	2.18	0.44
2:F:7:DG:H2"	2:F:8:DT:H72	1.99	0.43
1:N:211:VAL:HG11	1:N:235:TYR:CD2	2.53	0.43
1:A:200:SER:HB3	1:A:201:ASP:C	2.38	0.43
1:B:226:MET:HG3	1:B:237:LEU:HD22	1.98	0.43
1:E:155:VAL:CG2	1:E:166:LEU:HB2	2.49	0.43
1:E:237:LEU:O	1:E:238:ASP:C	2.57	0.43
1:H:202:ALA:HB1	3:D:16:DC:OP2	2.19	0.42
1:A:195:HIS:NE2	1:H:181:ASP:OD1	2.53	0.42
1:N:233:VAL:HG22	1:N:234:GLY:N	2.34	0.42
1:N:157:ILE:HG12	1:N:166:LEU:HD11	2.02	0.42
1:M:152:THR:HB	1:M:154:SER:OG	2.20	0.41
2:C:7:DG:H2"	2:C:8:DT:H72	2.01	0.41
1:N:233:VAL:CG2	1:N:234:GLY:N	2.83	0.41
1:N:179:MET:HE1	1:N:227:LEU:HD22	2.01	0.41
1:H:169:THR:HG22	3:D:14:DT:OP1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:236:ARG:HG3	1:E:237:LEU:O	2.20	0.41
2:C:18:DG:H2"	2:C:19:DT:H72	2.03	0.41
1:A:223:ILE:HG22	1:A:226:MET:HG3	2.01	0.41
1:A:169:THR:CG2	3:G:2:DC:H3'	2.51	0.41
1:M:155:VAL:HG21	1:M:168:LEU:HD11	2.02	0.41
1:E:237:LEU:O	1:E:238:ASP:O	2.39	0.41
1:M:163:LYS:H	1:M:164:ILE:HD12	1.85	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	89/109 (82%)	86 (97%)	3 (3%)	0	100	100
1	B	89/109 (82%)	85 (96%)	4 (4%)	0	100	100
1	E	92/109 (84%)	87 (95%)	4 (4%)	1 (1%)	17	43
1	H	89/109 (82%)	85 (96%)	4 (4%)	0	100	100
1	M	87/109 (80%)	83 (95%)	4 (5%)	0	100	100
1	N	79/109 (72%)	75 (95%)	4 (5%)	0	100	100
All	All	525/654 (80%)	501 (95%)	23 (4%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	238	ASP

### 5.3.2 Protein sidechains ⓘ

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	90/102 (88%)	81 (90%)	9 (10%)	9	23
1	B	89/102 (87%)	80 (90%)	9 (10%)	9	23
1	E	93/102 (91%)	86 (92%)	7 (8%)	16	38
1	H	90/102 (88%)	83 (92%)	7 (8%)	15	36
1	M	88/102 (86%)	82 (93%)	6 (7%)	18	43
1	N	86/102 (84%)	76 (88%)	10 (12%)	6	17
All	All	536/612 (88%)	488 (91%)	48 (9%)	11	29

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	LEU
1	A	151	ASP
1	A	153	HIS
1	A	154	SER
1	A	171	THR
1	A	220	GLU
1	A	229	ASN
1	A	237	LEU
1	A	239	ASN
1	B	142	LEU
1	B	145	ASN
1	B	150	THR
1	B	151	ASP
1	B	153	HIS
1	B	229	ASN
1	B	236	ARG
1	B	237	LEU
1	B	241	LEU
1	E	142	LEU
1	E	151	ASP
1	E	153	HIS
1	E	201	ASP

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Mol	Chain	Res	Type
1	E	229	ASN
1	E	236	ARG
1	E	237	LEU
1	H	142	LEU
1	H	145	ASN
1	H	151	ASP
1	H	153	HIS
1	H	201	ASP
1	H	229	ASN
1	H	236	ARG
1	M	142	LEU
1	M	145	ASN
1	M	151	ASP
1	M	152	THR
1	M	229	ASN
1	M	236	ARG
1	N	142	LEU
1	N	145	ASN
1	N	151	ASP
1	N	153	HIS
1	N	203	LEU
1	N	204	GLU
1	N	213	LYS
1	N	221	GLN
1	N	229	ASN
1	N	236	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	ASN
1	A	198	ASN
1	B	145	ASN
1	E	140	ASN
1	E	239	ASN
1	H	145	ASN
1	M	145	ASN
1	N	140	ASN
1	N	145	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	95/109 (87%)	0.61	5 (5%) 27 21	41, 50, 66, 76	0
1	B	95/109 (87%)	0.70	6 (6%) 21 16	43, 52, 73, 87	0
1	E	98/109 (89%)	0.65	10 (10%) 7 5	43, 52, 65, 82	0
1	H	95/109 (87%)	0.77	12 (12%) 4 3	45, 58, 73, 92	0
1	M	93/109 (85%)	0.67	6 (6%) 20 15	45, 55, 68, 75	0
1	N	89/109 (81%)	0.78	7 (7%) 13 9	40, 52, 66, 72	0
2	C	24/25 (96%)	0.46	0 100 100	50, 62, 73, 83	0
2	F	24/25 (96%)	0.46	0 100 100	50, 61, 72, 79	0
3	D	25/25 (100%)	0.28	0 100 100	48, 58, 77, 86	0
3	G	25/25 (100%)	0.54	1 (4%) 39 33	60, 71, 85, 88	0
All	All	663/754 (87%)	0.66	47 (7%) 17 12	40, 55, 73, 92	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	181	ASP	4.4
1	N	142	LEU	4.2
1	M	151	ASP	3.9
1	B	142	LEU	3.8
1	H	202	ALA	3.8
1	A	149	ASP	3.5
1	B	145	ASN	3.4
1	A	198	ASN	3.3
1	H	204	GLU	3.3
1	A	145	ASN	3.2
1	H	144	LYS	3.1
1	B	140	ASN	3.1
1	E	145	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	151	ASP	2.9
1	E	161	ASN	2.8
1	H	201	ASP	2.8
1	H	157	ILE	2.7
1	H	156	TYR	2.7
3	G	1	DT	2.7
1	B	156	TYR	2.7
1	M	142	LEU	2.7
1	E	202	ALA	2.6
1	H	205	ARG	2.5
1	E	140	ASN	2.5
1	E	198	ASN	2.5
1	N	146	ILE	2.5
1	N	203	LEU	2.4
1	E	160	GLU	2.4
1	N	157	ILE	2.4
1	B	222	GLY	2.4
1	E	149	ASP	2.4
1	N	140	ASN	2.4
1	M	140	ASN	2.3
1	A	142	LEU	2.3
1	H	142	LEU	2.2
1	E	201	ASP	2.2
1	E	158	HIS	2.2
1	N	156	TYR	2.2
1	M	161	ASN	2.2
1	H	159	SER	2.1
1	N	158	HIS	2.1
1	H	158	HIS	2.0
1	H	164	ILE	2.0
1	E	239	ASN	2.0
1	H	240	PRO	2.0
1	B	241	LEU	2.0
1	M	149	ASP	2.0

## 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 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.