



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2017 – 10:03 AM EST

PDB ID : 4PX9  
Title : DEAD-box RNA helicase DDX3X Domain 1 with N-terminal ATP-binding Loop  
Authors : Epling, L.B.; Grace, C.R.; Lowe, B.R.; Partridge, J.F.; Enemark, E.J.  
Deposited on : unknown  
Resolution : 2.31 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  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
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

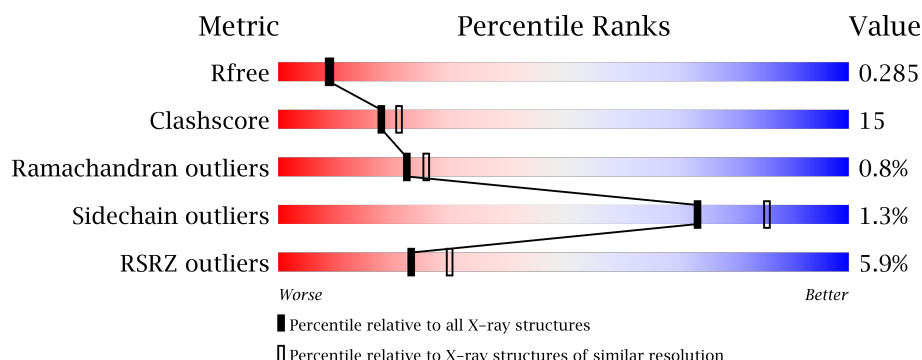
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.31 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	4787 (2.34-2.30)
Clashscore	112137	5439 (2.34-2.30)
Ramachandran outliers	110173	5386 (2.34-2.30)
Sidechain outliers	110143	5385 (2.34-2.30)
RSRZ outliers	101464	4814 (2.34-2.30)

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 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	292	<div> <div>4%</div> <div>62%</div> <div>27%</div> <div>10%</div> </div>
1	B	292	<div> <div>2%</div> <div>64%</div> <div>26%</div> <div>10%</div> </div>
1	C	292	<div> <div>10%</div> <div>61%</div> <div>32%</div> <div>7%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6346 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 ATP-dependent RNA helicase DDX3X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2068	1308	364	379	17			
1	B	262	Total	C	N	O	S	0	0	0
			2068	1308	364	379	17			
1	C	273	Total	C	N	O	S	0	0	0
			2129	1343	377	392	17			

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	116	MET	-	EXPRESSION TAG	UNP O00571
A	117	GLY	-	EXPRESSION TAG	UNP O00571
A	118	SER	-	EXPRESSION TAG	UNP O00571
A	119	SER	-	EXPRESSION TAG	UNP O00571
A	120	HIS	-	EXPRESSION TAG	UNP O00571
A	121	HIS	-	EXPRESSION TAG	UNP O00571
A	122	HIS	-	EXPRESSION TAG	UNP O00571
A	123	HIS	-	EXPRESSION TAG	UNP O00571
A	124	HIS	-	EXPRESSION TAG	UNP O00571
A	125	HIS	-	EXPRESSION TAG	UNP O00571
A	126	SER	-	EXPRESSION TAG	UNP O00571
A	127	SER	-	EXPRESSION TAG	UNP O00571
A	128	GLY	-	EXPRESSION TAG	UNP O00571
A	129	LEU	-	EXPRESSION TAG	UNP O00571
A	130	VAL	-	EXPRESSION TAG	UNP O00571
A	131	PRO	-	EXPRESSION TAG	UNP O00571
A	132	ARG	-	EXPRESSION TAG	UNP O00571
A	133	GLY	-	EXPRESSION TAG	UNP O00571
A	134	SER	-	EXPRESSION TAG	UNP O00571
B	116	MET	-	EXPRESSION TAG	UNP O00571
B	117	GLY	-	EXPRESSION TAG	UNP O00571
B	118	SER	-	EXPRESSION TAG	UNP O00571
B	119	SER	-	EXPRESSION TAG	UNP O00571

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Chain	Residue	Modelled	Actual	Comment	Reference
B	120	HIS	-	EXPRESSION TAG	UNP O00571
B	121	HIS	-	EXPRESSION TAG	UNP O00571
B	122	HIS	-	EXPRESSION TAG	UNP O00571
B	123	HIS	-	EXPRESSION TAG	UNP O00571
B	124	HIS	-	EXPRESSION TAG	UNP O00571
B	125	HIS	-	EXPRESSION TAG	UNP O00571
B	126	SER	-	EXPRESSION TAG	UNP O00571
B	127	SER	-	EXPRESSION TAG	UNP O00571
B	128	GLY	-	EXPRESSION TAG	UNP O00571
B	129	LEU	-	EXPRESSION TAG	UNP O00571
B	130	VAL	-	EXPRESSION TAG	UNP O00571
B	131	PRO	-	EXPRESSION TAG	UNP O00571
B	132	ARG	-	EXPRESSION TAG	UNP O00571
B	133	GLY	-	EXPRESSION TAG	UNP O00571
B	134	SER	-	EXPRESSION TAG	UNP O00571
C	116	MET	-	EXPRESSION TAG	UNP O00571
C	117	GLY	-	EXPRESSION TAG	UNP O00571
C	118	SER	-	EXPRESSION TAG	UNP O00571
C	119	SER	-	EXPRESSION TAG	UNP O00571
C	120	HIS	-	EXPRESSION TAG	UNP O00571
C	121	HIS	-	EXPRESSION TAG	UNP O00571
C	122	HIS	-	EXPRESSION TAG	UNP O00571
C	123	HIS	-	EXPRESSION TAG	UNP O00571
C	124	HIS	-	EXPRESSION TAG	UNP O00571
C	125	HIS	-	EXPRESSION TAG	UNP O00571
C	126	SER	-	EXPRESSION TAG	UNP O00571
C	127	SER	-	EXPRESSION TAG	UNP O00571
C	128	GLY	-	EXPRESSION TAG	UNP O00571
C	129	LEU	-	EXPRESSION TAG	UNP O00571
C	130	VAL	-	EXPRESSION TAG	UNP O00571
C	131	PRO	-	EXPRESSION TAG	UNP O00571
C	132	ARG	-	EXPRESSION TAG	UNP O00571
C	133	GLY	-	EXPRESSION TAG	UNP O00571
C	134	SER	-	EXPRESSION TAG	UNP O00571

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).

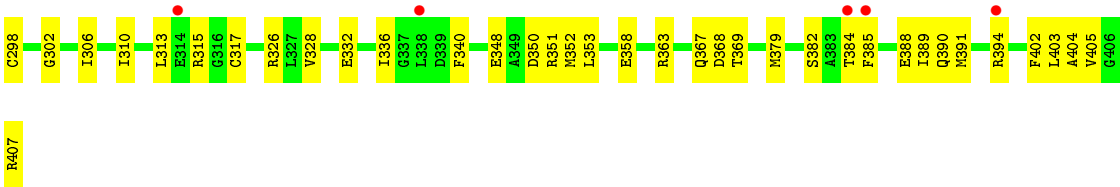


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		



- Molecule 1: ATP-dependent RNA helicase DDX3X





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.64Å 75.64Å 121.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.11 – 2.31 36.11 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.5 (36.11-2.31) 99.6 (36.11-2.31)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.60 (at 2.31Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.255 , 0.285 0.255 , 0.285	Depositor DCC
$R_{free}$ test set	1741 reflections (5.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.8	Xtriage
Anisotropy	0.547	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 31.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l 0.320 for h,-h-k,-l 0.026 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6346	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.05% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.38	0/2110	0.59	0/2846
1	B	0.41	0/2110	0.60	0/2846
1	C	0.34	0/2172	0.59	0/2932
All	All	0.38	0/6392	0.59	0/8624

There are no bond length outliers.

There are no bond angle outliers.

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	2068	0	2068	64	0
1	B	2068	0	2068	64	0
1	C	2129	0	2117	74	0
2	A	27	0	12	1	0
2	B	27	0	12	2	0
2	C	27	0	12	1	0
All	All	6346	0	6289	191	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 15.

All (191) 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:B:140:LEU:HD21	1:B:294:ARG:HE	1.23	0.99
1:C:140:LEU:HD21	1:C:294:ARG:HE	1.32	0.94
1:A:340:PHE:HZ	1:B:340:PHE:HZ	1.14	0.92
1:A:140:LEU:HD21	1:A:294:ARG:HE	1.43	0.83
1:B:140:LEU:HD21	1:B:294:ARG:NE	1.98	0.79
1:A:274:PRO:HB3	1:A:352:MET:HG2	1.66	0.76
1:C:274:PRO:HB3	1:C:352:MET:HG2	1.67	0.76
1:B:274:PRO:HB3	1:B:352:MET:HG2	1.68	0.74
1:C:140:LEU:HD21	1:C:294:ARG:NE	2.01	0.74
1:A:340:PHE:CZ	1:B:340:PHE:HZ	2.04	0.72
1:A:340:PHE:HZ	1:B:340:PHE:CZ	2.04	0.72
1:C:146:LEU:O	1:C:150:LEU:HG	1.90	0.70
1:C:143:SER:O	1:C:147:GLU:HG3	1.92	0.69
1:B:306:ILE:O	1:B:310:ILE:HG13	1.94	0.67
1:C:306:ILE:O	1:C:310:ILE:HG13	1.95	0.67
1:C:223:CYS:HA	1:C:382:SER:O	1.96	0.66
1:A:306:ILE:O	1:A:310:ILE:HG13	1.95	0.65
1:A:223:CYS:HA	1:A:382:SER:O	1.96	0.65
1:B:140:LEU:HB3	1:B:141:PRO:HD2	1.78	0.64
1:B:223:CYS:HA	1:B:382:SER:O	1.97	0.64
1:C:274:PRO:HD2	1:C:278:LEU:HD23	1.81	0.63
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.81	0.63
1:A:144:GLU:O	1:A:148:GLN:HG2	1.98	0.63
1:A:274:PRO:HD2	1:A:278:LEU:HD23	1.80	0.63
1:B:274:PRO:HD2	1:B:278:LEU:HD23	1.80	0.63
1:C:153:GLY:C	1:C:199:ARG:HH12	2.04	0.61
1:B:230:LYS:HB2	2:B:501:ADP:O1B	2.02	0.60
1:A:252:ARG:O	1:A:255:LYS:HG3	2.04	0.58
1:B:252:ARG:O	1:B:255:LYS:HG3	2.04	0.58
1:C:169:GLU:HB3	1:C:404:ALA:HB3	1.86	0.58
1:C:313:LEU:HD22	1:C:336:ILE:HD11	1.86	0.57
1:A:313:LEU:HD22	1:A:336:ILE:HD11	1.86	0.57
1:C:163:TYR:O	1:C:164:ASP:CB	2.51	0.57
1:C:252:ARG:O	1:C:255:LYS:HG3	2.04	0.57
1:B:169:GLU:HB3	1:B:404:ALA:HB3	1.85	0.57
1:A:169:GLU:HB3	1:A:404:ALA:HB3	1.86	0.57
1:B:313:LEU:HD22	1:B:336:ILE:HD11	1.87	0.56
1:B:348:GLU:OE1	1:B:351:ARG:HD3	2.05	0.56
1:A:348:GLU:OE1	1:A:351:ARG:HD3	2.05	0.56
1:B:368:ASP:OD2	1:B:369:THR:HG22	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:LEU:CD2	1:C:294:ARG:HE	2.13	0.56
1:C:146:LEU:O	1:C:149:GLU:HB2	2.06	0.56
1:C:348:GLU:OE1	1:C:351:ARG:HD3	2.05	0.55
1:A:368:ASP:OD2	1:A:369:THR:HG22	2.07	0.55
1:C:258:GLY:C	1:C:259:ARG:HD3	2.27	0.55
1:A:252:ARG:HA	1:A:255:LYS:HE2	1.89	0.54
1:A:370:MET:O	1:B:259:ARG:NH2	2.40	0.54
1:C:368:ASP:OD2	1:C:369:THR:HG22	2.06	0.54
1:B:252:ARG:HA	1:B:255:LYS:HE2	1.89	0.54
1:B:278:LEU:HD22	1:B:348:GLU:OE2	2.08	0.54
1:C:151:PHE:HE1	1:C:198:THR:CG2	2.21	0.54
1:C:403:LEU:CD2	1:C:405:VAL:HG23	2.38	0.54
1:A:403:LEU:CD2	1:A:405:VAL:HG23	2.39	0.53
1:A:254:MET:CE	1:B:339:ASP:HB3	2.38	0.53
1:A:258:GLY:C	1:A:259:ARG:HD3	2.28	0.53
1:B:403:LEU:CD2	1:B:405:VAL:HG23	2.39	0.53
1:A:278:LEU:HD22	1:A:348:GLU:OE2	2.09	0.53
1:B:258:GLY:C	1:B:259:ARG:HD3	2.28	0.53
1:C:252:ARG:HA	1:C:255:LYS:HE2	1.89	0.52
1:C:403:LEU:HD23	1:C:403:LEU:C	2.29	0.52
1:C:278:LEU:HD22	1:C:348:GLU:OE2	2.08	0.52
1:C:136:TRP:CE2	1:C:247:PRO:HD3	2.45	0.52
1:A:403:LEU:HD23	1:A:403:LEU:C	2.29	0.52
1:A:254:MET:HE2	1:B:339:ASP:HB3	1.91	0.52
1:B:250:ALA:HB1	1:B:340:PHE:HE1	1.74	0.52
1:A:250:ALA:HB1	1:A:340:PHE:HE1	1.74	0.51
1:B:403:LEU:C	1:B:403:LEU:HD23	2.29	0.51
1:B:262:ARG:HH11	1:B:262:ARG:HG2	1.75	0.51
1:A:136:TRP:CE2	1:A:247:PRO:HD3	2.46	0.51
1:A:262:ARG:HH11	1:A:262:ARG:HG2	1.75	0.51
1:C:151:PHE:HE1	1:C:198:THR:HG22	1.76	0.51
1:C:243:TYR:OH	1:C:290:SER:HA	2.11	0.51
1:A:243:TYR:OH	1:A:290:SER:HA	2.11	0.50
1:A:350:ASP:HA	1:A:389:ILE:HD11	1.93	0.50
1:C:250:ALA:HB1	1:C:340:PHE:HE1	1.75	0.50
1:C:262:ARG:HG2	1:C:262:ARG:HH11	1.76	0.50
1:C:350:ASP:HA	1:C:389:ILE:HD11	1.93	0.50
1:C:159:ASN:O	1:C:162:LYS:N	2.42	0.50
1:B:350:ASP:HA	1:B:389:ILE:HD11	1.93	0.50
1:C:144:GLU:CG	1:C:145:ARG:N	2.75	0.50
1:C:136:TRP:CD2	1:C:247:PRO:HD3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:403:LEU:HD21	1:C:405:VAL:CG2	2.42	0.49
1:B:243:TYR:OH	1:B:290:SER:HA	2.13	0.49
1:B:302:GLY:HA2	1:B:326:ARG:NH2	2.28	0.48
1:A:339:ASP:OD1	1:B:266:TYR:OH	2.28	0.48
1:B:403:LEU:HD21	1:B:405:VAL:CG2	2.43	0.48
1:C:302:GLY:HA2	1:C:326:ARG:NH2	2.29	0.48
1:B:136:TRP:CE2	1:B:247:PRO:HD3	2.48	0.48
1:B:143:SER:O	1:B:147:GLU:HG3	2.13	0.48
1:A:403:LEU:HD21	1:A:405:VAL:CG2	2.43	0.48
1:A:250:ALA:HB2	1:B:250:ALA:HA	1.96	0.48
1:C:158:ILE:O	1:C:160:PHE:N	2.44	0.48
1:B:192:MET:O	1:B:196:GLU:HG3	2.14	0.47
1:A:198:THR:O	1:A:199:ARG:HB2	2.14	0.47
1:A:302:GLY:HA2	1:A:326:ARG:NH2	2.29	0.47
1:C:140:LEU:HB3	1:C:141:PRO:HD2	1.95	0.47
1:C:144:GLU:HG2	1:C:145:ARG:H	1.80	0.47
1:B:198:THR:O	1:B:199:ARG:HB2	2.14	0.47
1:C:353:LEU:HD22	1:C:358:GLU:HB2	1.96	0.47
1:A:144:GLU:CD	1:A:144:GLU:H	2.17	0.47
1:A:192:MET:O	1:A:196:GLU:HG3	2.15	0.47
1:C:192:MET:O	1:C:196:GLU:HG3	2.14	0.47
1:C:145:ARG:HG2	1:C:145:ARG:HH11	1.78	0.47
1:B:140:LEU:CD2	1:B:294:ARG:HE	2.11	0.47
1:C:153:GLY:O	1:C:155:ASN:N	2.48	0.47
1:C:315:ARG:HH11	1:C:315:ARG:HG3	1.80	0.47
1:A:315:ARG:HG3	1:A:315:ARG:HH11	1.80	0.46
1:B:328:VAL:O	1:B:332:GLU:HG3	2.15	0.46
1:A:353:LEU:HD22	1:A:358:GLU:HB2	1.96	0.46
1:C:144:GLU:CG	1:C:145:ARG:H	2.28	0.46
1:C:198:THR:O	1:C:199:ARG:HB2	2.16	0.46
1:A:328:VAL:O	1:A:332:GLU:HG3	2.16	0.46
1:B:315:ARG:HH11	1:B:315:ARG:HG3	1.81	0.46
1:A:136:TRP:CD2	1:A:247:PRO:HD3	2.51	0.45
1:B:230:LYS:O	1:B:233:ALA:HB3	2.16	0.45
1:B:226:THR:HA	2:B:501:ADP:O2B	2.16	0.45
1:B:353:LEU:HD22	1:B:358:GLU:HB2	1.97	0.45
1:C:328:VAL:O	1:C:332:GLU:HG3	2.16	0.45
1:C:147:GLU:O	1:C:151:PHE:N	2.38	0.45
1:C:156:THR:HG23	1:C:156:THR:O	2.17	0.45
1:C:262:ARG:HG2	1:C:262:ARG:NH1	2.32	0.45
1:A:262:ARG:NH1	1:A:262:ARG:HG2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:ARG:NH1	1:C:145:ARG:HG2	2.32	0.45
1:B:262:ARG:HG2	1:B:262:ARG:NH1	2.32	0.44
1:C:363:ARG:HA	1:C:367:GLN:HB2	1.99	0.44
1:C:230:LYS:HB2	2:C:501:ADP:O1B	2.17	0.44
1:C:385:PHE:CE2	1:C:390:GLN:HG2	2.53	0.44
1:A:363:ARG:HA	1:A:367:GLN:HB2	1.99	0.44
1:B:385:PHE:CE2	1:B:390:GLN:HG2	2.52	0.44
1:B:363:ARG:HA	1:B:367:GLN:HB2	1.99	0.44
1:A:291:TYR:O	1:A:292:ARG:HB2	2.17	0.44
1:C:159:ASN:C	1:C:161:GLU:H	2.20	0.44
1:A:230:LYS:HB2	2:A:601:ADP:O1B	2.18	0.43
1:C:151:PHE:CE1	1:C:198:THR:HG22	2.53	0.43
1:C:230:LYS:O	1:C:233:ALA:HB3	2.18	0.43
1:A:385:PHE:CE2	1:A:390:GLN:HG2	2.53	0.43
1:B:176:PRO:HB3	1:B:216:GLU:HG3	2.00	0.43
1:B:178:HIS:HA	1:B:212:PRO:HG3	2.01	0.43
1:C:176:PRO:CB	1:C:216:GLU:HG3	2.48	0.43
1:C:285:GLU:HG3	1:C:289:PHE:CE2	2.53	0.43
1:B:333:ARG:CZ	1:C:384:THR:HG21	2.48	0.43
1:B:225:GLN:HG3	1:B:407:ARG:HH11	1.84	0.43
1:C:291:TYR:O	1:C:292:ARG:HB2	2.19	0.43
1:B:305:ASP:OD1	1:C:388:GLU:OE1	2.36	0.43
1:A:176:PRO:HB3	1:A:216:GLU:HG3	2.01	0.43
1:A:285:GLU:HG3	1:A:289:PHE:CE2	2.54	0.43
1:B:144:GLU:HG2	1:B:144:GLU:H	1.60	0.43
1:B:258:GLY:O	1:B:259:ARG:HD3	2.18	0.43
1:B:285:GLU:HG3	1:B:289:PHE:CE2	2.54	0.43
1:C:291:TYR:CE2	1:C:292:ARG:HG3	2.54	0.43
1:A:291:TYR:CE2	1:A:292:ARG:HG3	2.54	0.43
1:A:254:MET:HG3	1:A:257:ASN:ND2	2.34	0.42
1:A:258:GLY:O	1:A:259:ARG:HD3	2.19	0.42
1:C:254:MET:HG3	1:C:257:ASN:ND2	2.34	0.42
1:C:258:GLY:O	1:C:259:ARG:HD3	2.18	0.42
1:A:178:HIS:HA	1:A:212:PRO:HG3	2.01	0.42
1:A:214:ILE:HD13	1:A:379:MET:SD	2.59	0.42
1:A:176:PRO:CB	1:A:216:GLU:HG3	2.49	0.42
1:B:291:TYR:CE2	1:B:292:ARG:HG3	2.54	0.42
1:C:176:PRO:HB3	1:C:216:GLU:HG3	2.00	0.42
1:B:254:MET:HG3	1:B:257:ASN:ND2	2.35	0.42
1:C:151:PHE:O	1:C:153:GLY:N	2.47	0.42
1:C:170:ALA:HA	1:C:402:PHE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:178:HIS:HA	1:C:212:PRO:HG3	2.01	0.42
1:C:214:ILE:HD13	1:C:379:MET:SD	2.60	0.42
1:B:176:PRO:CB	1:B:216:GLU:HG3	2.49	0.42
1:A:144:GLU:HG2	1:A:145:ARG:N	2.34	0.42
1:B:291:TYR:O	1:B:292:ARG:HB2	2.19	0.42
1:A:230:LYS:O	1:A:233:ALA:HB3	2.20	0.42
1:A:404:ALA:HB1	1:A:407:ARG:OXT	2.20	0.42
1:C:298:CYS:HB2	1:C:317:CYS:SG	2.60	0.42
1:A:236:LEU:HB2	1:A:237:PRO:CD	2.50	0.41
1:B:136:TRP:CD2	1:B:247:PRO:HD3	2.55	0.41
1:C:403:LEU:HD21	1:C:405:VAL:HG23	2.01	0.41
1:B:170:ALA:HA	1:B:402:PHE:O	2.20	0.41
1:A:250:ALA:HA	1:B:250:ALA:HB2	2.03	0.41
1:A:170:ALA:HA	1:A:402:PHE:O	2.21	0.41
1:A:340:PHE:N	1:A:340:PHE:CD2	2.89	0.41
1:C:154:GLY:O	1:C:155:ASN:HB2	2.21	0.41
1:B:340:PHE:CD2	1:B:340:PHE:N	2.89	0.41
1:A:403:LEU:HD21	1:A:405:VAL:HG23	2.03	0.41
1:B:403:LEU:HD23	1:B:404:ALA:N	2.36	0.41
1:A:363:ARG:HG2	1:A:363:ARG:NH1	2.35	0.40
1:A:403:LEU:HD23	1:A:404:ALA:N	2.36	0.40
1:B:236:LEU:HB2	1:B:237:PRO:CD	2.51	0.40
1:C:236:LEU:HB2	1:C:237:PRO:CD	2.50	0.40
1:A:298:CYS:HB2	1:A:317:CYS:SG	2.61	0.40
1:A:392:LEU:HD11	1:A:396:PHE:CE2	2.56	0.40
1:C:138:LYS:HA	1:C:139:PRO:HD2	1.83	0.40
1:B:363:ARG:NH1	1:B:363:ARG:HG2	2.36	0.40
1:C:158:ILE:HG22	1:C:159:ASN:N	2.37	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	258/292 (88%)	240 (93%)	16 (6%)	2 (1%)	22	26
1	B	258/292 (88%)	240 (93%)	17 (7%)	1 (0%)	38	46
1	C	271/292 (93%)	250 (92%)	18 (7%)	3 (1%)	17	17
All	All	787/876 (90%)	730 (93%)	51 (6%)	6 (1%)	22	26

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	MET
1	B	254	MET
1	C	154	GLY
1	C	254	MET
1	A	165	ASP
1	C	152	SER

### 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	221/250 (88%)	218 (99%)	3 (1%)	71	84
1	B	221/250 (88%)	219 (99%)	2 (1%)	82	91
1	C	225/250 (90%)	221 (98%)	4 (2%)	64	79
All	All	667/750 (89%)	658 (99%)	9 (1%)	73	85

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ILE
1	A	391	MET
1	A	394	ARG
1	B	166	ILE
1	B	394	ARG
1	C	166	ILE
1	C	391	MET

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Mol	Chain	Res	Type
1	C	394	ARG
1	C	407	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	257	ASN
1	B	257	ASN
1	C	257	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](#)

3 ligands are modelled in this entry.

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$
2	ADP	A	601	-	25,29,29	1.17	2 (8%)	24,45,45	1.92	2 (8%)
2	ADP	B	501	-	25,29,29	1.07	2 (8%)	24,45,45	1.95	2 (8%)
2	ADP	C	501	-	25,29,29	1.20	1 (4%)	24,45,45	1.93	3 (12%)



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	A	601	-	-	0/12/32/32	0/3/3/3
2	ADP	B	501	-	-	0/12/32/32	0/3/3/3
2	ADP	C	501	-	-	0/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ADP	C8-N7	-2.30	1.30	1.34
2	B	501	ADP	C8-N7	-2.27	1.30	1.34
2	B	501	ADP	O4'-C1'	3.05	1.45	1.41
2	A	601	ADP	O4'-C1'	3.58	1.46	1.41
2	C	501	ADP	O4'-C1'	3.86	1.46	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	ADP	N3-C2-N1	-8.43	121.52	128.86
2	C	501	ADP	N3-C2-N1	-8.35	121.58	128.86
2	A	601	ADP	N3-C2-N1	-8.31	121.62	128.86
2	A	601	ADP	C4-C5-N7	-2.45	107.04	109.41
2	C	501	ADP	C4-C5-N7	-2.31	107.18	109.41
2	B	501	ADP	C4-C5-N7	-2.21	107.27	109.41
2	C	501	ADP	C2'-C3'-C4'	2.24	106.98	102.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ADP	1	0
2	B	501	ADP	2	0
2	C	501	ADP	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	262/292 (89%)	0.36	12 (4%) 33 40	37, 61, 109, 181	0
1	B	262/292 (89%)	0.16	5 (1%) 67 73	31, 55, 91, 147	0
1	C	273/292 (93%)	0.84	30 (10%) 6 9	48, 79, 141, 274	0
All	All	797/876 (90%)	0.46	47 (5%) 23 30	31, 64, 120, 274	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	260	TYR	11.8
1	C	253	ALA	11.8
1	C	163	TYR	9.3
1	C	261	GLY	8.3
1	C	256	GLU	8.1
1	C	154	GLY	6.1
1	C	257	ASN	5.7
1	A	253	ALA	5.2
1	A	256	GLU	5.0
1	C	255	LYS	4.9
1	A	255	LYS	4.8
1	C	259	ARG	4.6
1	C	263	ARG	3.8
1	C	171	THR	3.6
1	A	202	ARG	3.6
1	C	164	ASP	3.5
1	C	174	ASN	3.2
1	A	334	GLY	3.2
1	B	163	TYR	2.9
1	C	146	LEU	2.9
1	C	262	ARG	2.8
1	A	163	TYR	2.8
1	B	340	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	225	GLN	2.7
1	C	251	LEU	2.7
1	B	351	ARG	2.7
1	A	340	PHE	2.6
1	C	156	THR	2.5
1	C	248	GLY	2.5
1	C	161	GLU	2.5
1	A	394	ARG	2.5
1	C	158	ILE	2.5
1	C	199	ARG	2.4
1	C	385	PHE	2.4
1	B	394	ARG	2.4
1	C	394	ARG	2.3
1	B	403	LEU	2.3
1	C	211	ILE	2.2
1	C	160	PHE	2.1
1	C	384	THR	2.1
1	C	254	MET	2.1
1	A	250	ALA	2.1
1	A	165	ASP	2.1
1	C	314	GLU	2.1
1	A	249	GLU	2.0
1	C	338	LEU	2.0
1	A	164	ASP	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ADP	C	501	27/27	0.77	0.22	0.42	104,104,104,104	0
2	ADP	B	501	27/27	0.86	0.17	0.35	82,82,82,82	0
2	ADP	A	601	27/27	0.81	0.18	0.22	94,94,94,94	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.