



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:42 PM GMT

PDB ID : 3VH0  
Title : Crystal structure of E. coli YncE complexed with DNA  
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Deposited on : 2011-08-23  
Resolution : 2.90 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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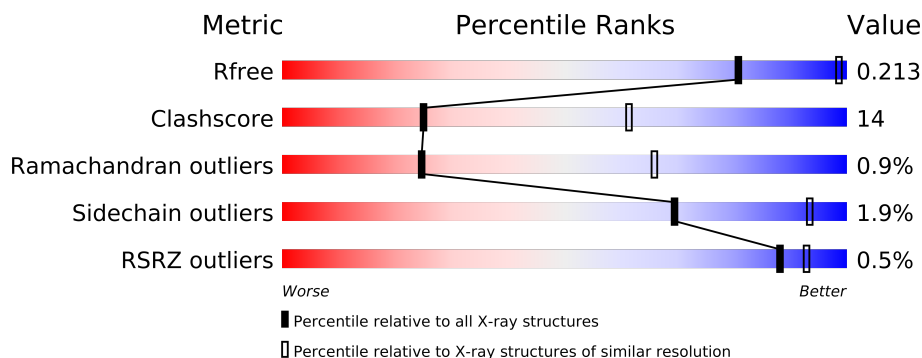
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	353	
1	B	353	
1	C	353	
1	D	353	
2	E	11	
2	F	11	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10388 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Uncharacterized protein YncE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2482	1552	438	489	3			
1	B	321	Total	C	N	O	S	0	0	0
			2473	1547	437	486	3			
1	C	321	Total	C	N	O	S	0	0	0
			2473	1547	437	486	3			
1	D	322	Total	C	N	O	S	0	0	0
			2482	1552	438	489	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	P	0	0	0
			224	107	43	64	10			
2	F	11	Total	C	N	O	P	0	0	0
			224	107	43	64	10			

- Molecule 3 is water.

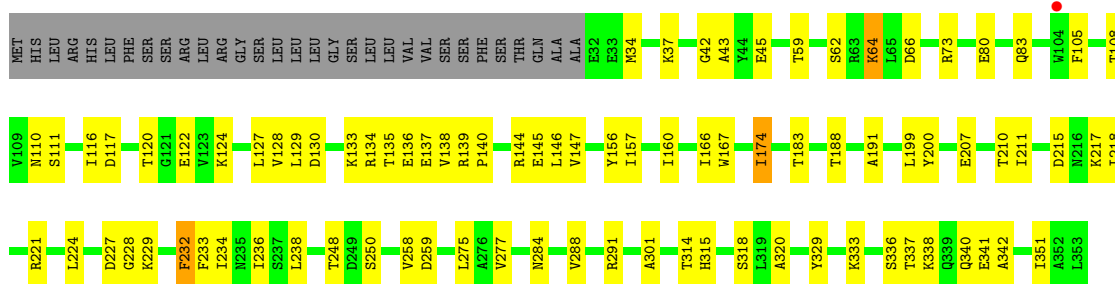
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	11	Total	O	0	0
			11	11		
3	C	9	Total	O	0	0
			9	9		
3	D	5	Total	O	0	0
			5	5		

### 3 Residue-property plots

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

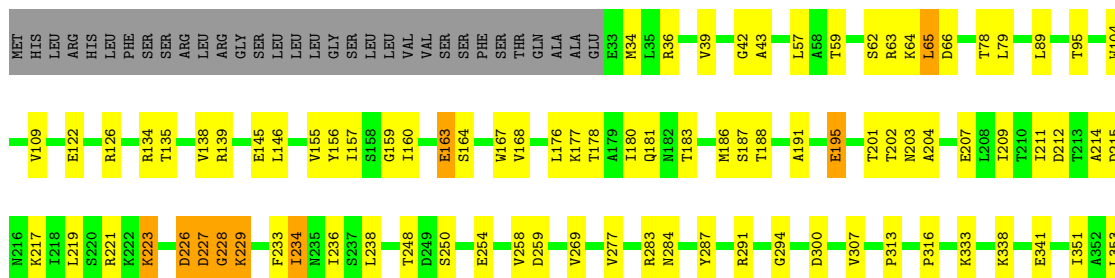
- Molecule 1: Uncharacterized protein YncE

Chain A:



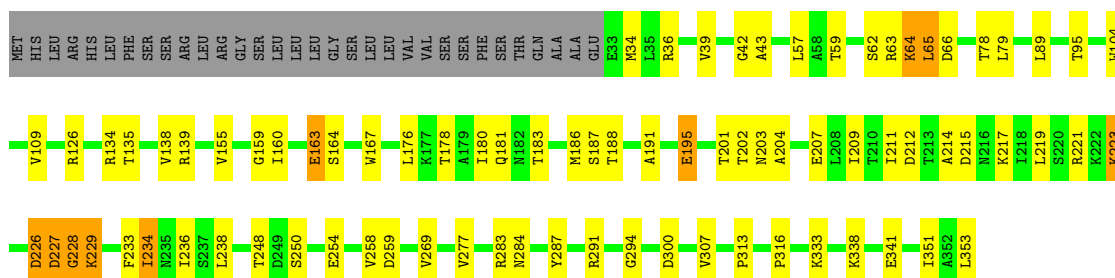
- Molecule 1: Uncharacterized protein YncE

Chain B:



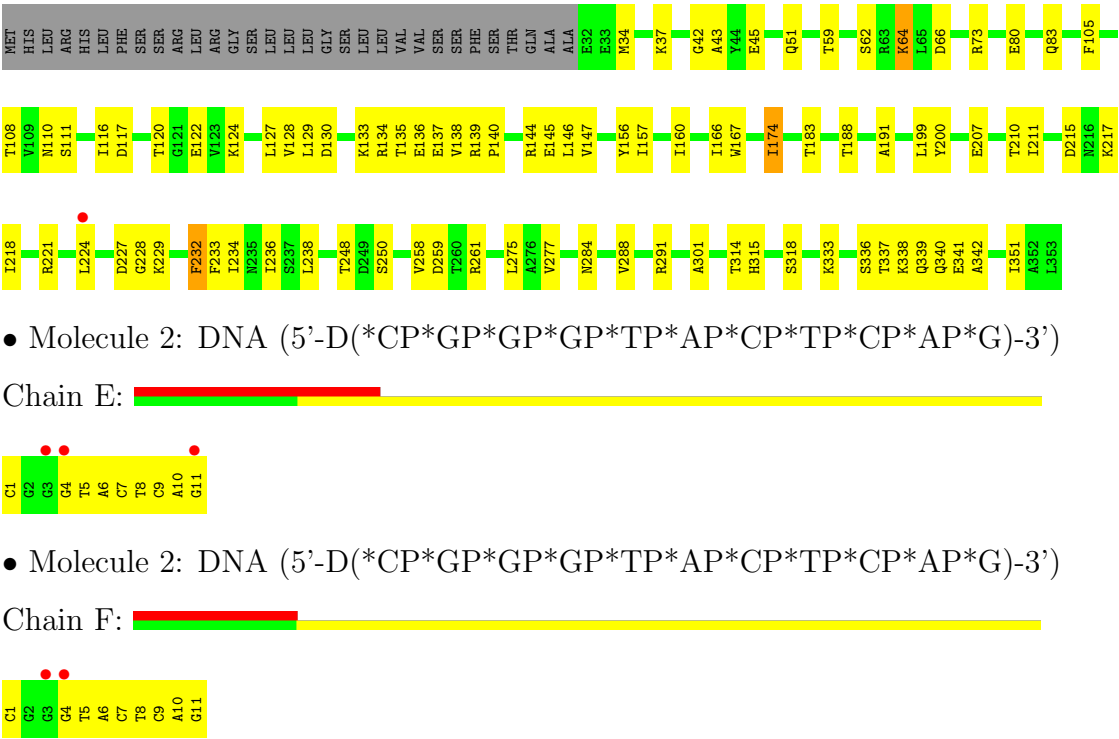
- Molecule 1: Uncharacterized protein YncE

Chain C:



- Molecule 1: Uncharacterized protein YncE

Chain D:



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	171.17Å 171.17Å 177.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.90 46.19 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.90) 99.9 (46.19-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.50 (at 2.91Å)	Xtriage
Refinement program	CNS 1.21	Depositor
R, $R_{free}$	0.210 , 0.234 0.214 , 0.213	Depositor DCC
$R_{free}$ test set	2860 reflections (5.08%)	DCC
Wilson B-factor (Å <sup>2</sup> )	62.7	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 25.7	EDS
Estimated twinning fraction	0.001 for l,-k,h 0.003 for -l,-k,-h 0.001 for -h,-l,-k 0.000 for -h,l,k 0.487 for -h,k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 56543 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10388	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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	0.38	0/2515	0.68	0/3406
1	B	0.40	0/2506	0.69	0/3394
1	C	0.40	0/2506	0.69	0/3394
1	D	0.38	0/2515	0.68	0/3406
2	E	0.44	0/251	0.69	0/386
2	F	0.43	0/251	0.71	0/386
All	All	0.39	0/10544	0.69	0/14372

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2482	0	2530	64	0
1	B	2473	0	2524	67	0
1	C	2473	0	2524	60	0
1	D	2482	0	2530	67	0
2	E	224	0	125	21	0
2	F	224	0	125	22	0
3	A	5	0	0	0	0
3	B	11	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	9	0	0	0	0
3	D	5	0	0	0	0
All	All	10388	0	10358	283	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 14.

All (283) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:207:GLU:OE2	1:C:221:ARG:HD3	1.74	0.86
1:B:207:GLU:OE2	1:B:221:ARG:HD3	1.73	0.86
1:B:160:ILE:HG21	1:B:188:THR:HG22	1.65	0.78
2:F:5:DT:H72	2:F:6:DA:N6	1.98	0.78
2:E:5:DT:H72	2:E:6:DA:N6	1.98	0.78
1:C:160:ILE:HG21	1:C:188:THR:HG22	1.66	0.77
1:A:147:VAL:HG23	1:A:156:TYR:HB2	1.67	0.75
1:D:147:VAL:HG23	1:D:156:TYR:HB2	1.67	0.75
1:D:62:SER:HB3	1:D:66:ASP:OD1	1.86	0.75
1:D:338:LYS:N	1:D:338:LYS:HD2	2.03	0.74
1:A:62:SER:HB3	1:A:66:ASP:OD1	1.87	0.74
1:A:338:LYS:HD2	1:A:338:LYS:N	2.04	0.73
1:D:135:THR:OG1	1:D:138:VAL:HG12	1.88	0.73
1:A:135:THR:OG1	1:A:138:VAL:HG12	1.89	0.73
1:D:291:ARG:HD3	2:E:11:DG:OP1	1.88	0.72
1:C:43:ALA:O	1:C:333:LYS:HE2	1.90	0.71
2:F:10:DA:H2''	2:F:11:DG:H5'	1.73	0.70
1:A:291:ARG:HD3	2:F:11:DG:OP1	1.91	0.70
1:B:43:ALA:O	1:B:333:LYS:HE2	1.92	0.69
2:E:10:DA:H2''	2:E:11:DG:H5'	1.73	0.68
1:A:166:ILE:HG13	1:A:183:THR:HG21	1.76	0.68
1:B:63:ARG:HH12	1:B:338:LYS:HE2	1.59	0.68
1:A:43:ALA:O	1:A:333:LYS:HE2	1.94	0.68
1:C:63:ARG:HH12	1:C:338:LYS:HE2	1.59	0.68
1:C:89:LEU:HD12	1:C:126:ARG:HD3	1.76	0.67
1:B:89:LEU:HD12	1:B:126:ARG:HD3	1.76	0.66
1:D:43:ALA:O	1:D:333:LYS:HE2	1.95	0.66
1:B:234:ILE:HD13	1:B:234:ILE:N	2.11	0.66
1:C:234:ILE:N	1:C:234:ILE:HD13	2.10	0.66
1:C:234:ILE:H	1:C:234:ILE:HD13	1.61	0.66
1:D:166:ILE:HG13	1:D:183:THR:HG21	1.77	0.66
1:B:234:ILE:H	1:B:234:ILE:HD13	1.61	0.64
1:B:212:ASP:HB2	1:B:219:LEU:HD11	1.79	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:212:ASP:HB2	1:C:219:LEU:HD11	1.79	0.64
1:B:95:THR:HG23	1:B:104:TRP:HB2	1.81	0.63
1:C:95:THR:HG23	1:C:104:TRP:HB2	1.80	0.63
1:D:314:THR:HG22	1:D:315:HIS:CD2	2.33	0.63
1:D:37:LYS:HE2	1:D:80:GLU:OE2	1.99	0.63
1:D:340:GLN:NE2	1:D:340:GLN:HA	2.14	0.63
1:D:207:GLU:OE2	1:D:221:ARG:HD3	1.98	0.63
1:A:314:THR:HG22	1:A:315:HIS:CD2	2.33	0.62
1:A:207:GLU:OE2	1:A:221:ARG:HD3	1.98	0.62
1:C:135:THR:OG1	1:C:138:VAL:HG12	2.00	0.62
1:A:340:GLN:HA	1:A:340:GLN:NE2	2.14	0.61
2:F:10:DA:H1'	2:F:11:DG:H5''	1.82	0.61
1:D:174:ILE:O	1:D:174:ILE:HG22	2.00	0.61
1:A:37:LYS:HE2	1:A:80:GLU:OE2	2.00	0.61
1:B:135:THR:OG1	1:B:138:VAL:HG12	2.00	0.61
1:A:134:ARG:HG2	1:A:140:PRO:HD2	1.83	0.60
1:A:145:GLU:C	1:A:146:LEU:HD12	2.22	0.60
1:A:174:ILE:HG22	1:A:174:ILE:O	2.01	0.59
1:A:73:ARG:HB3	1:A:83:GLN:HB3	1.84	0.59
2:E:10:DA:H1'	2:E:11:DG:H5''	1.83	0.59
1:A:338:LYS:HG2	2:F:7:DC:O3'	2.02	0.59
1:D:134:ARG:HG2	1:D:140:PRO:HD2	1.83	0.59
1:D:338:LYS:HG2	2:E:7:DC:O3'	2.01	0.59
1:C:42:GLY:O	1:C:59:THR:HA	2.04	0.58
1:D:73:ARG:HB3	1:D:83:GLN:HB3	1.84	0.58
1:C:139:ARG:HG3	1:C:139:ARG:HH11	1.68	0.58
1:B:63:ARG:NH1	1:B:338:LYS:HE2	2.19	0.58
1:D:145:GLU:C	1:D:146:LEU:HD12	2.23	0.58
1:B:139:ARG:HG3	1:B:139:ARG:HH11	1.68	0.58
2:E:7:DC:H1'	2:E:8:DT:OP1	2.04	0.58
1:C:223:LYS:HB2	1:C:223:LYS:NZ	2.20	0.57
1:B:42:GLY:O	1:B:59:THR:HA	2.04	0.57
1:C:63:ARG:NH1	1:C:338:LYS:HE2	2.19	0.57
1:B:234:ILE:H	1:B:234:ILE:CD1	2.16	0.57
1:C:234:ILE:CD1	1:C:234:ILE:H	2.16	0.57
1:D:200:TYR:CE1	1:D:210:THR:HG23	2.40	0.56
1:A:129:LEU:HD13	1:A:167:TRP:CE3	2.41	0.56
2:F:7:DC:H2''	2:F:8:DT:OP1	2.06	0.56
1:C:36:ARG:NH2	1:C:313:PRO:O	2.39	0.56
1:B:223:LYS:NZ	1:B:223:LYS:HB2	2.20	0.56
2:E:7:DC:H2''	2:E:8:DT:OP1	2.05	0.56
1:D:129:LEU:HD13	1:D:167:TRP:CE3	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:191:ALA:HB1	1:B:238:LEU:HG	1.88	0.55
1:B:234:ILE:HD11	1:B:250:SER:H	1.71	0.55
1:A:200:TYR:CE1	1:A:210:THR:HG23	2.41	0.54
1:D:117:ASP:HB2	1:D:124:LYS:HD3	1.90	0.53
1:D:108:THR:HG1	2:E:9:DC:H5	1.57	0.53
2:F:7:DC:H1'	2:F:8:DT:OP1	2.08	0.53
1:B:36:ARG:NH2	1:B:313:PRO:O	2.41	0.53
1:B:159:GLY:HA3	1:B:167:TRP:CZ3	2.44	0.53
1:C:234:ILE:HD11	1:C:250:SER:H	1.71	0.53
1:A:42:GLY:O	1:A:59:THR:HA	2.08	0.53
1:C:191:ALA:HB1	1:C:238:LEU:HG	1.89	0.53
1:C:212:ASP:OD1	1:C:214:ALA:HB3	2.08	0.53
1:A:134:ARG:HG2	1:A:140:PRO:CD	2.39	0.53
1:B:191:ALA:HB2	1:B:236:ILE:HG23	1.91	0.52
1:D:42:GLY:O	1:D:59:THR:HA	2.09	0.52
2:F:10:DA:H2''	2:F:11:DG:C5'	2.39	0.52
1:D:134:ARG:HG2	1:D:140:PRO:CD	2.39	0.52
1:A:277:VAL:HG23	1:A:288:VAL:HG22	1.92	0.52
1:A:117:ASP:HB2	1:A:124:LYS:HD3	1.90	0.52
2:E:10:DA:H2''	2:E:11:DG:C5'	2.40	0.52
1:B:212:ASP:OD1	1:B:214:ALA:HB3	2.09	0.52
1:C:159:GLY:HA3	1:C:167:TRP:CZ3	2.44	0.52
1:C:191:ALA:HB2	1:C:236:ILE:HG23	1.91	0.52
1:D:277:VAL:HG23	1:D:288:VAL:HG22	1.92	0.52
1:C:234:ILE:HD11	1:C:250:SER:N	2.26	0.51
1:C:258:VAL:HG12	1:C:259:ASP:N	2.25	0.51
1:A:108:THR:HG1	2:F:9:DC:H5	1.59	0.51
1:C:163:GLU:HG2	1:C:163:GLU:O	2.11	0.51
1:B:234:ILE:HD11	1:B:250:SER:N	2.26	0.51
1:A:136:GLU:HB3	1:A:137:GLU:OE2	2.11	0.51
1:A:156:TYR:CD2	1:A:199:LEU:HD22	2.46	0.50
1:B:226:ASP:C	1:B:228:GLY:H	2.14	0.50
1:C:176:LEU:HD11	1:C:178:THR:O	2.11	0.50
1:D:156:TYR:CD2	1:D:199:LEU:HD22	2.46	0.50
1:B:176:LEU:HD11	1:B:178:THR:O	2.12	0.50
1:D:336:SER:HB2	1:D:342:ALA:HB2	1.94	0.50
1:B:258:VAL:HG12	1:B:259:ASP:N	2.25	0.50
1:A:146:LEU:N	1:A:146:LEU:HD12	2.27	0.50
1:C:34:MET:HG2	1:C:351:ILE:HG12	1.94	0.50
1:C:226:ASP:C	1:C:228:GLY:H	2.14	0.50
2:F:4:DG:H2''	2:F:5:DT:C7	2.41	0.50
1:D:136:GLU:HB3	1:D:137:GLU:OE2	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:163:GLU:HG2	1:B:163:GLU:O	2.12	0.50
1:D:146:LEU:N	1:D:146:LEU:HD12	2.27	0.49
1:B:122:GLU:HA	3:B:354:HOH:O	2.12	0.49
1:A:336:SER:HB2	1:A:342:ALA:HB2	1.94	0.49
2:E:4:DG:H2"	2:E:5:DT:H71	1.95	0.49
1:B:34:MET:HG2	1:B:351:ILE:HG12	1.94	0.49
1:B:202:THR:HB	1:B:233:PHE:HB2	1.94	0.49
1:B:187:SER:HA	1:B:203:ASN:HB3	1.93	0.49
1:C:39:VAL:HG11	1:C:57:LEU:HD23	1.94	0.49
1:A:337:THR:OG1	1:A:340:GLN:HB3	2.13	0.49
1:C:187:SER:HA	1:C:203:ASN:HB3	1.94	0.49
1:B:39:VAL:HG11	1:B:57:LEU:HD23	1.95	0.49
1:C:202:THR:HB	1:C:233:PHE:HB2	1.93	0.49
1:D:337:THR:OG1	1:D:340:GLN:HB3	2.13	0.49
1:D:291:ARG:HH11	1:D:291:ARG:HG2	1.78	0.49
1:C:300:ASP:HB2	1:C:307:VAL:CG1	2.43	0.49
1:A:338:LYS:HG2	2:F:8:DT:P	2.53	0.48
1:B:300:ASP:HB2	1:B:307:VAL:CG1	2.43	0.48
1:A:291:ARG:HH11	1:A:291:ARG:HG2	1.78	0.48
1:C:195:GLU:HA	1:C:195:GLU:OE2	2.13	0.48
1:B:195:GLU:HA	1:B:195:GLU:OE2	2.13	0.48
2:F:4:DG:H2"	2:F:5:DT:H71	1.95	0.48
1:D:215:ASP:O	1:D:217:LYS:HG3	2.14	0.48
1:D:34:MET:HG2	1:D:351:ILE:HG12	1.96	0.48
1:D:133:LYS:O	1:D:135:THR:HG23	2.14	0.48
1:A:250:SER:OG	2:F:11:DG:H2"	2.14	0.48
1:D:340:GLN:HE21	1:D:340:GLN:HA	1.78	0.48
2:E:7:DC:C2'	2:E:8:DT:OP1	2.61	0.48
1:B:226:ASP:O	1:B:228:GLY:N	2.47	0.48
2:E:4:DG:H2"	2:E:5:DT:C7	2.43	0.48
1:A:139:ARG:NH2	2:E:1:DC:C5	2.81	0.48
1:A:133:LYS:O	1:A:135:THR:HG23	2.14	0.48
1:D:250:SER:OG	2:E:11:DG:H2"	2.14	0.47
1:A:340:GLN:HE21	1:A:340:GLN:HA	1.78	0.47
1:C:227:ASP:O	1:C:229:LYS:N	2.42	0.47
1:D:338:LYS:HG2	2:E:8:DT:P	2.53	0.47
1:D:160:ILE:HG21	1:D:188:THR:HG22	1.97	0.47
1:A:128:VAL:HG12	1:A:130:ASP:H	1.80	0.47
1:A:160:ILE:HG21	1:A:188:THR:HG22	1.96	0.47
1:C:89:LEU:HD12	1:C:126:ARG:CD	2.45	0.47
1:B:294:GLY:HA2	1:B:316:PRO:CD	2.45	0.47
1:A:34:MET:HG2	1:A:351:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:89:LEU:HD12	1:B:126:ARG:CD	2.44	0.46
1:B:234:ILE:N	1:B:234:ILE:CD1	2.76	0.46
1:D:110:ASN:O	1:D:111:SER:C	2.54	0.46
1:D:128:VAL:HG12	1:D:130:ASP:H	1.79	0.46
1:A:291:ARG:HD3	2:F:11:DG:P	2.55	0.46
2:F:7:DC:C2'	2:F:8:DT:OP1	2.63	0.46
1:A:215:ASP:O	1:A:217:LYS:HG3	2.16	0.46
1:D:248:THR:HG23	1:D:277:VAL:HB	1.97	0.46
1:B:291:ARG:HH11	1:B:291:ARG:HG2	1.81	0.46
1:A:258:VAL:HG12	1:A:259:ASP:N	2.30	0.46
1:D:258:VAL:HG12	1:D:259:ASP:N	2.30	0.46
1:D:45:GLU:HG2	1:D:318:SER:OG	2.16	0.46
1:C:300:ASP:HB2	1:C:307:VAL:HG13	1.97	0.46
1:B:227:ASP:O	1:B:229:LYS:N	2.41	0.46
1:D:139:ARG:NH2	2:F:1:DC:C5	2.84	0.46
1:A:232:PHE:HB3	1:A:250:SER:OG	2.16	0.45
1:A:248:THR:HG23	1:A:277:VAL:HB	1.97	0.45
1:A:110:ASN:O	1:A:111:SER:C	2.54	0.45
1:C:294:GLY:HA2	1:C:316:PRO:CD	2.45	0.45
1:B:62:SER:HB3	1:B:66:ASP:OD1	2.16	0.45
2:F:5:DT:H72	2:F:6:DA:H62	1.80	0.45
1:D:232:PHE:HB3	1:D:250:SER:OG	2.16	0.45
1:C:226:ASP:O	1:C:228:GLY:N	2.48	0.45
1:C:291:ARG:HG2	1:C:291:ARG:HH11	1.82	0.45
1:C:62:SER:HB3	1:C:66:ASP:OD1	2.17	0.45
1:A:45:GLU:HG2	1:A:318:SER:OG	2.17	0.45
1:B:283:ARG:O	1:B:284:ASN:C	2.55	0.45
1:D:248:THR:CG2	1:D:277:VAL:HB	2.47	0.45
1:B:300:ASP:HB2	1:B:307:VAL:HG13	1.97	0.45
1:A:64:LYS:HD2	1:A:341:GLU:OE2	2.17	0.44
1:A:248:THR:CG2	1:A:277:VAL:HB	2.48	0.44
1:D:211:ILE:HG12	1:D:218:ILE:HA	1.99	0.44
1:B:294:GLY:HA2	1:B:316:PRO:HD3	1.99	0.44
1:C:283:ARG:O	1:C:284:ASN:C	2.56	0.44
1:D:227:ASP:C	1:D:229:LYS:H	2.21	0.44
1:C:164:SER:HB2	1:C:183:THR:OG1	2.17	0.44
1:A:105:PHE:CE2	1:A:116:ILE:HD12	2.53	0.44
1:D:284:ASN:O	1:D:301:ALA:HB3	2.18	0.44
1:D:147:VAL:CG2	1:D:156:TYR:HB2	2.44	0.44
1:D:291:ARG:HD3	2:E:11:DG:P	2.58	0.44
1:B:287:TYR:OH	1:B:353:LEU:HD13	2.18	0.43
1:D:64:LYS:HD2	1:D:341:GLU:OE2	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:227:ASP:C	1:A:229:LYS:H	2.21	0.43
1:B:215:ASP:OD1	1:B:217:LYS:HB2	2.18	0.43
2:E:5:DT:H72	2:E:6:DA:H62	1.80	0.43
1:A:127:LEU:HD22	1:A:174:ILE:O	2.19	0.43
1:C:234:ILE:HD11	1:C:250:SER:HB3	2.01	0.43
1:D:105:PHE:CE2	1:D:116:ILE:HD12	2.53	0.43
1:C:95:THR:CG2	1:C:104:TRP:HB2	2.48	0.43
1:B:164:SER:HB2	1:B:183:THR:OG1	2.17	0.43
1:B:223:LYS:HZ3	1:B:223:LYS:HB2	1.84	0.43
1:A:284:ASN:O	1:A:301:ALA:HB3	2.18	0.43
1:B:180:ILE:HD13	1:B:211:ILE:HG21	2.00	0.43
1:A:211:ILE:HG12	1:A:218:ILE:HA	1.99	0.43
1:D:234:ILE:HG21	1:D:275:LEU:HD12	2.00	0.43
1:A:120:THR:OG1	1:A:122:GLU:HG3	2.19	0.43
1:B:234:ILE:HD11	1:B:250:SER:HB3	2.01	0.42
2:E:5:DT:H2'	2:E:6:DA:C8	2.54	0.42
1:C:104:TRP:CD2	1:C:155:VAL:HG21	2.54	0.42
1:B:186:MET:HB2	1:B:204:ALA:HB2	2.01	0.42
1:C:180:ILE:HD13	1:C:211:ILE:HG21	2.00	0.42
1:C:215:ASP:OD1	1:C:217:LYS:HB2	2.18	0.42
1:A:147:VAL:CG2	1:A:156:TYR:HB2	2.45	0.42
1:B:95:THR:CG2	1:B:104:TRP:HB2	2.49	0.42
1:D:191:ALA:HB1	1:D:238:LEU:HG	2.01	0.42
1:D:51:GLN:HB3	1:D:51:GLN:HE21	1.65	0.42
1:C:134:ARG:NH2	1:C:139:ARG:NE	2.67	0.42
1:C:163:GLU:CD	1:C:163:GLU:H	2.23	0.42
1:A:236:ILE:O	1:A:236:ILE:HG23	2.19	0.42
1:B:254:GLU:HA	1:B:269:VAL:O	2.19	0.42
1:D:236:ILE:HG23	1:D:236:ILE:O	2.19	0.42
1:C:287:TYR:OH	1:C:353:LEU:HD13	2.19	0.42
1:C:186:MET:HB2	1:C:204:ALA:HB2	2.02	0.42
1:C:254:GLU:HA	1:C:269:VAL:O	2.19	0.42
1:A:234:ILE:HG21	1:A:275:LEU:HD12	2.00	0.42
1:C:234:ILE:HD11	1:C:250:SER:CB	2.50	0.42
1:C:294:GLY:HA2	1:C:316:PRO:HD3	2.00	0.42
2:F:4:DG:C2'	2:F:5:DT:C7	2.98	0.42
2:F:5:DT:H2'	2:F:6:DA:C8	2.55	0.42
1:B:248:THR:HG23	1:B:277:VAL:HB	2.02	0.42
1:A:191:ALA:HB1	1:A:238:LEU:HG	2.01	0.42
1:A:144:ARG:HD2	2:F:9:DC:C4	2.54	0.41
1:B:234:ILE:HD11	1:B:250:SER:CB	2.50	0.41
1:B:163:GLU:CD	1:B:163:GLU:H	2.23	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:127:LEU:HD22	1:D:174:ILE:O	2.20	0.41
1:C:248:THR:HG23	1:C:277:VAL:HB	2.03	0.41
1:A:215:ASP:HB2	1:A:217:LYS:HE3	2.02	0.41
1:B:156:TYR:CD2	1:B:168:VAL:HG22	2.55	0.41
1:B:201:THR:CG2	1:B:209:ILE:HB	2.51	0.41
2:E:4:DG:C2'	2:E:5:DT:C7	2.98	0.41
1:D:337:THR:OG1	1:D:340:GLN:N	2.51	0.41
1:A:337:THR:OG1	1:A:340:GLN:N	2.51	0.41
1:A:146:LEU:HG	1:A:157:ILE:HG12	2.03	0.41
1:B:65:LEU:HA	1:B:65:LEU:HD22	1.89	0.41
1:D:215:ASP:HB2	1:D:217:LYS:HE3	2.02	0.41
1:B:168:VAL:O	1:B:177:LYS:HB2	2.20	0.41
1:C:201:THR:CG2	1:C:209:ILE:HB	2.50	0.41
1:C:78:THR:O	1:C:79:LEU:HB2	2.20	0.41
1:B:104:TRP:CD2	1:B:155:VAL:HG21	2.54	0.41
1:D:221:ARG:HG3	1:D:221:ARG:O	2.20	0.41
1:B:78:THR:O	1:B:79:LEU:HB2	2.20	0.41
1:B:146:LEU:HG	1:B:157:ILE:HG23	2.01	0.41
1:D:339:GLN:NE2	2:E:7:DC:H5'	2.35	0.41
1:B:134:ARG:NH2	1:B:139:ARG:NE	2.68	0.41
1:D:146:LEU:HG	1:D:157:ILE:HG12	2.03	0.41
1:D:224:LEU:HD12	1:D:233:PHE:CE2	2.55	0.41
1:D:120:THR:OG1	1:D:122:GLU:HG3	2.20	0.41
1:D:144:ARG:HD2	2:E:9:DC:C4	2.56	0.41
1:A:320:ALA:HB3	1:A:329:TYR:HB2	2.03	0.41
1:D:144:ARG:NH1	1:D:160:ILE:CD1	2.84	0.40
1:C:64:LYS:CE	1:C:65:LEU:HD23	2.51	0.40
1:D:337:THR:C	1:D:338:LYS:HD2	2.42	0.40
1:A:144:ARG:NH1	1:A:160:ILE:CD1	2.84	0.40
1:A:144:ARG:NH2	2:F:11:DG:N7	2.69	0.40
1:C:134:ARG:NH2	1:C:139:ARG:HE	2.18	0.40
2:F:5:DT:H2'	2:F:6:DA:N7	2.37	0.40
1:B:63:ARG:HB3	1:B:341:GLU:OE2	2.21	0.40
1:B:126:ARG:HD2	3:B:363:HOH:O	2.22	0.40
1:B:233:PHE:HA	1:B:248:THR:O	2.22	0.40
1:B:145:GLU:C	1:B:146:LEU:HD12	2.42	0.40
1:A:224:LEU:HD12	1:A:233:PHE:CE2	2.56	0.40
1:C:63:ARG:HB3	1:C:341:GLU:OE2	2.20	0.40
1:C:233:PHE:HA	1:C:248:THR:O	2.21	0.40
1:D:259:ASP:OD1	1:D:261:ARG:HB2	2.22	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	320/353 (91%)	289 (90%)	29 (9%)	2 (1%)	33	76
1	B	319/353 (90%)	289 (91%)	26 (8%)	4 (1%)	18	54
1	C	319/353 (90%)	289 (91%)	26 (8%)	4 (1%)	18	54
1	D	320/353 (91%)	289 (90%)	29 (9%)	2 (1%)	33	76
All	All	1278/1412 (90%)	1156 (90%)	110 (9%)	12 (1%)	25	66

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	227	ASP
1	C	227	ASP
1	B	229	LYS
1	C	229	LYS
1	A	174	ILE
1	D	174	ILE
1	B	109	VAL
1	B	228	GLY
1	C	109	VAL
1	C	228	GLY
1	D	228	GLY
1	A	228	GLY

### 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	270/297 (91%)	268 (99%)	2 (1%)	91	98
1	B	269/297 (91%)	261 (97%)	8 (3%)	53	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	269/297 (91%)	261 (97%)	8 (3%)	53	89
1	D	270/297 (91%)	268 (99%)	2 (1%)	91	98
All	All	1078/1188 (91%)	1058 (98%)	20 (2%)	69	93

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	LYS
1	A	232	PHE
1	B	64	LYS
1	B	65	LEU
1	B	163	GLU
1	B	181	GLN
1	B	195	GLU
1	B	223	LYS
1	B	226	ASP
1	B	234	ILE
1	C	64	LYS
1	C	65	LEU
1	C	163	GLU
1	C	181	GLN
1	C	195	GLU
1	C	223	LYS
1	C	226	ASP
1	C	234	ILE
1	D	64	LYS
1	D	232	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	61	GLN
1	A	142	GLN
1	A	216	ASN
1	A	315	HIS
1	A	339	GLN
1	A	340	GLN
1	B	51	GLN
1	B	216	ASN

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Mol	Chain	Res	Type
1	B	264	ASN
1	B	315	HIS
1	B	317	ASN
1	B	340	GLN
1	C	51	GLN
1	C	216	ASN
1	C	264	ASN
1	C	315	HIS
1	C	317	ASN
1	C	340	GLN
1	D	51	GLN
1	D	61	GLN
1	D	216	ASN
1	D	315	HIS
1	D	339	GLN
1	D	340	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

### 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	322/353 (91%)	0.14	1 (0%) 91 95	39, 61, 85, 107	0
1	B	321/353 (90%)	0.17	0 100 100	36, 59, 86, 108	0
1	C	321/353 (90%)	0.16	0 100 100	37, 59, 86, 108	0
1	D	322/353 (91%)	0.18	1 (0%) 91 95	39, 62, 85, 107	0
2	E	11/11 (100%)	1.37	3 (27%) 1 1	120, 145, 192, 196	0
2	F	11/11 (100%)	0.99	2 (18%) 2 3	120, 146, 192, 197	0
All	All	1308/1434 (91%)	0.18	7 (0%) 88 93	36, 61, 93, 197	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	4	DG	4.2
2	E	11	DG	3.1
2	F	3	DG	2.8
2	F	4	DG	2.8
2	E	3	DG	2.7
1	D	224	LEU	2.2
1	A	104	TRP	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.