Full wwPDB X-ray Structure Validation Report (i)

Nov 2, 2023 – 03:04 PM EDT

PDB ID	:	3VH0
Title	:	Crystal structure of E. coli YncE complexed with DNA
Authors	:	Kagawa, W.; Sagawa, T.; Niki, H.; Kurumizaka, H.
Deposited on	:	2011-08-23
Resolution	:	2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

The following versions of software and data (see references (1)) were used in the production of this report:

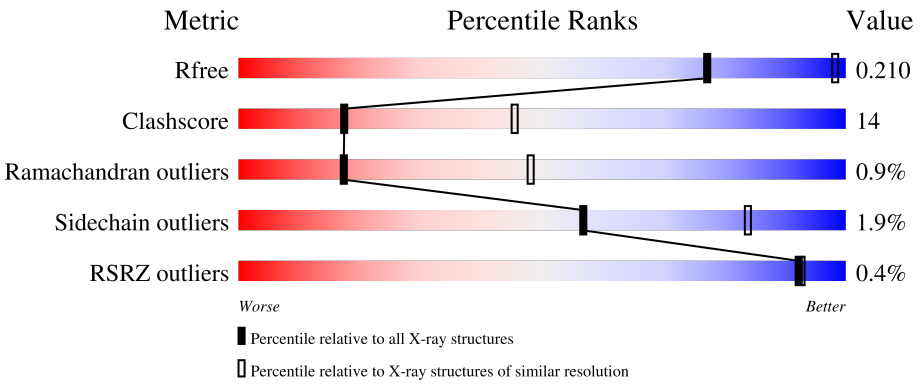
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (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 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	353	67% 24% • 9%
1	B	353	66% 23% • 9%
1	C	353	68% 20% • 9%
1	D	353	66% 24% • 9%
2	E	11	27% 18% 82%

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Mol	Chain	Length	Quality of chain
2	F	11	18% 18% 82%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10388 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 Uncharacterized protein YncE.

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

- 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
			Total	C	N	O	P			
2	E	11	224	107	43	64	10	0	0	0
2	F	11	224	107	43	64	10	0	0	0

- Molecule 3 is water.

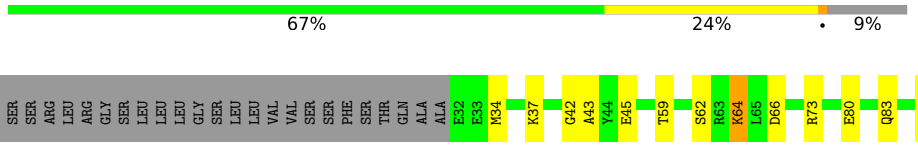
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	5	5	5	0	0
3	B	11	11	11	0	0
3	C	9	9	9	0	0
3	D	5	5	5	0	0

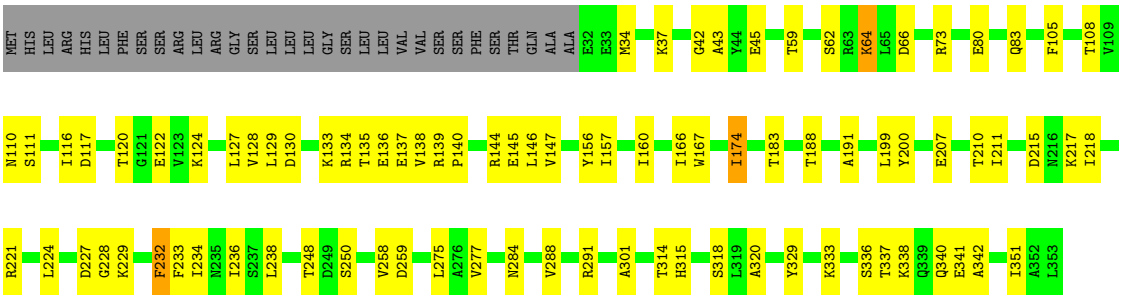
3 Residue-property plots (i)

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: Uncharacterized protein YncE

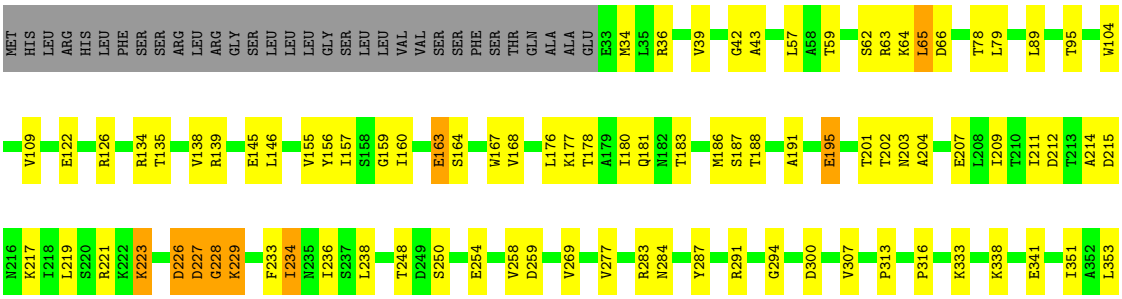
Chain A:





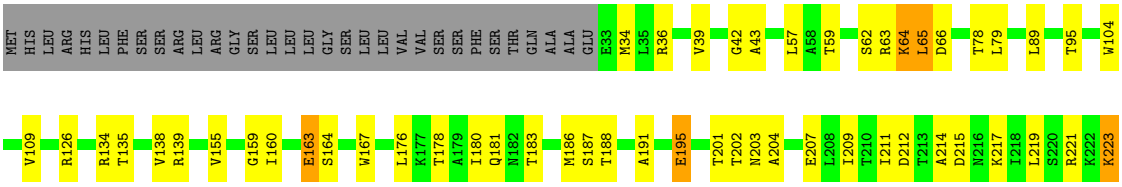
- Molecule 1: Uncharacterized protein YncE

Chain B:



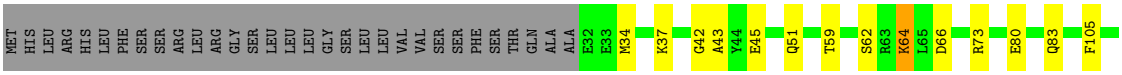
- Molecule 1: Uncharacterized protein YncE

Chain C:



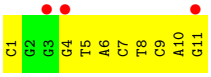
• Molecule 1: Uncharacterized protein YncE

Chain D:



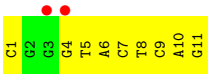
• Molecule 2: DNA (5'-D(*CP*GP*GP*GP*TP*AP*CP*TP*CP*AP*G)-3')

Chain E:



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

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α, β, γ	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
$< I/\sigma(I) >$ [1]	5.50 (at 2.91Å)	Xtriage
Refinement program	CNS 1.21	Depositor
R, R_{free}	0.210 , 0.234 0.212 , 0.210	Depositor DCC
R_{free} test set	2860 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	62.7	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 27.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
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
F_o,F_c correlation	0.93	EDS
Total number of atoms	10388	wwPDB-VP
Average B, all atoms (Å^2)	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.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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 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	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
3	C	9	0	0	0	0
3	D	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10388	0	10358	283	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 14.

All (283) 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: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:A:135:THR:OG1	1:A:138:VAL:HG12	1.89	0.73
1:D:135:THR:OG1	1:D:138:VAL:HG12	1.88	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:HD13	1:C:234:ILE:N	2.10	0.66
1:C:234:ILE:HD13	1:C:234:ILE:H	1.61	0.66
1:D:166:ILE:HG13	1:D:183:THR:HG21	1.77	0.66
1:B:234:ILE:HD13	1:B:234:ILE:H	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	Interatomic distance (Å)	Clash overlap (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:37:LYS:HE2	1:D:80:GLU:OE2	1.99	0.63
1:D:314:THR:HG22	1:D:315:HIS:CD2	2.33	0.63
1:D:207:GLU:OE2	1:D:221:ARG:HD3	1.98	0.63
1:D:340:GLN:HA	1:D:340:GLN:NE2	2.14	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
1:D:174:ILE:HG22	1:D:174:ILE:O	2.00	0.61
2:F:10:DA:H1'	2:F:11:DG:H5"	1.82	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:73:ARG:HB3	1:A:83:GLN:HB3	1.84	0.59
1:A:174:ILE:HG22	1:A:174:ILE:O	2.01	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:HH11	1:C:139:ARG:HG3	1.68	0.58
1:B:63:ARG:NH1	1:B:338:LYS:HE2	2.19	0.58
1:B:139:ARG:HG3	1:B:139:ARG:HH11	1.68	0.58
1:D:145:GLU:C	1:D:146:LEU:HD12	2.23	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:B:234:ILE:H	1:B:234:ILE:CD1	2.16	0.57
1:C:63:ARG:NH1	1:C:338:LYS:HE2	2.19	0.57
1:C:234:ILE:H	1:C:234:ILE:CD1	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:HB2	1:B:223:LYS:NZ	2.20	0.56
2:E:7:DC:H2"	2:E:8:DT:OP1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:LEU:HD13	1:D:167:TRP:CE3	2.41	0.55
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:108:THR:HG1	2:E:9:DC:H5	1.57	0.53
1:D:117:ASP:HB2	1:D:124:LYS:HD3	1.90	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
2:F:7:DC:H1'	2:F:8:DT:OP1	2.08	0.53
1:A:42:GLY:O	1:A:59:THR:HA	2.08	0.53
1:C:234:ILE:HD11	1:C:250:SER:H	1.71	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
1:A:277:VAL:HG23	1:A:288:VAL:HG22	1.92	0.52
1:D:134:ARG:HG2	1:D:140:PRO:CD	2.39	0.52
2:F:10:DA:H2"	2:F:11:DG:C5'	2.39	0.52
1:A:117:ASP:HB2	1:A:124:LYS:HD3	1.90	0.52
1:B:212:ASP:OD1	1:B:214:ALA:HB3	2.09	0.52
2:E:10:DA:H2"	2:E:11:DG:C5'	2.40	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:O	1:C:163:GLU:HG2	2.11	0.51
1:A:136:GLU:HB3	1:A:137:GLU:OE2	2.11	0.51
1:B:234:ILE:HD11	1:B:250:SER:N	2.26	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:HD12	1:A:146:LEU:N	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:GLU:O	1:B:163:GLU:HG2	2.12	0.50
1:D:136:GLU:HB3	1:D:137:GLU:OE2	2.12	0.50
2:F:4:DG:H2"	2:F:5:DT:C7	2.41	0.50
1:A:336:SER:HB2	1:A:342:ALA:HB2	1.94	0.49
1:B:122:GLU:HA	3:B:354:HOH:O	2.12	0.49
1:D:146:LEU:HD12	1:D:146:LEU:N	2.27	0.49
1:B:34:MET:HG2	1:B:351:ILE:HG12	1.94	0.49
2:E:4:DG:H2"	2:E:5:DT:H71	1.95	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:B:39:VAL:HG11	1:B:57:LEU:HD23	1.95	0.49
1:C:187:SER:HA	1:C:203:ASN:HB3	1.94	0.49
1:C:202:THR:HB	1:C:233:PHE:HB2	1.93	0.49
1:C:300:ASP:HB2	1:C:307:VAL:CG1	2.43	0.49
1:D:291:ARG:HH11	1:D:291:ARG:HG2	1.78	0.49
1:D:337:THR:OG1	1:D:340:GLN:HB3	2.13	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:HG2	1:A:291:ARG:HH11	1.78	0.48
1:C:195:GLU:OE2	1:C:195:GLU:HA	2.13	0.48
1:B:195:GLU:OE2	1:B:195:GLU:HA	2.13	0.48
1:D:215:ASP:O	1:D:217:LYS:HG3	2.14	0.48
2:F:4:DG:H2"	2:F:5:DT:H71	1.95	0.48
1:D:34:MET:HG2	1:D:351:ILE:HG12	1.96	0.48
1:A:250:SER:OG	2:F:11:DG:H2"	2.14	0.48
1:D:133:LYS:O	1:D:135:THR:HG23	2.14	0.48
1:B:226:ASP:O	1:B:228:GLY:N	2.47	0.48
1:D:340:GLN:HA	1:D:340:GLN:HE21	1.78	0.48
2:E:7:DC:C2'	2:E:8:DT:OP1	2.61	0.48
1:A:139:ARG:NH2	2:E:1:DC:C5	2.81	0.48
2:E:4:DG:H2"	2:E:5:DT:C7	2.43	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:HA	1:A:340:GLN:HE21	1.78	0.47
1:C:227:ASP:O	1:C:229:LYS:N	2.42	0.47
1:D:160:ILE:HG21	1:D:188:THR:HG22	1.97	0.47
1:D:338:LYS:HG2	2:E:8:DT:P	2.53	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:215:ASP:O	1:A:217:LYS:HG3	2.16	0.46
2:F:7:DC:C2'	2:F:8:DT:OP1	2.63	0.46
1:A:258:VAL:HG12	1:A:259:ASP:N	2.30	0.46
1:B:291:ARG:HH11	1:B:291:ARG:HG2	1.81	0.46
1:D:248:THR:HG23	1:D:277:VAL:HB	1.97	0.46
1:D:45:GLU:HG2	1:D:318:SER:OG	2.16	0.46
1:D:258:VAL:HG12	1:D:259:ASP:N	2.30	0.46
1:B:227:ASP:O	1:B:229:LYS:N	2.41	0.46
1:C:300:ASP:HB2	1:C:307:VAL:HG13	1.97	0.46
1:D:139:ARG:NH2	2:F:1:DC:C5	2.84	0.46
1:A:110:ASN:O	1:A:111:SER:C	2.54	0.45
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: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: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:D:232:PHE:HB3	1:D:250:SER:OG	2.16	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:B:300:ASP:HB2	1:B:307:VAL:HG13	1.97	0.45
1:D:248:THR:CG2	1:D:277:VAL:HB	2.47	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:C:164:SER:HB2	1:C:183:THR:OG1	2.17	0.44
1:D:227:ASP:C	1:D:229:LYS:H	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:127:LEU:HD22	1:A:174:ILE:O	2.19	0.43
2:E:5:DT:H72	2:E:6:DA:H62	1.80	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:B:164:SER:HB2	1:B:183:THR:OG1	2.17	0.43
1:C:95:THR:CG2	1:C:104:TRP:HB2	2.48	0.43
1:A:284:ASN:O	1:A:301:ALA:HB3	2.18	0.43
1:B:223:LYS:HB2	1:B:223:LYS:HZ3	1.84	0.43
1:A:211:ILE:HG12	1:A:218:ILE:HA	1.99	0.43
1:B:180:ILE:HD13	1:B:211:ILE:HG21	2.00	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
1:B:186:MET:HB2	1:B:204:ALA:HB2	2.01	0.42
1:C:104:TRP:CD2	1:C:155:VAL:HG21	2.54	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
2:E:5:DT:H2'	2:E:6:DA:C8	2.54	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:51:GLN:HE21	1:D:51:GLN:HB3	1.65	0.42
1:D:191:ALA:HB1	1:D:238:LEU:HG	2.01	0.42
1:A:236:ILE:HG23	1:A:236:ILE:O	2.19	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:B:254:GLU:HA	1:B:269:VAL:O	2.19	0.42
1:C:287:TYR:OH	1:C:353:LEU:HD13	2.19	0.42
1:D:236:ILE:HG23	1:D:236:ILE:O	2.19	0.42
1:C:186:MET:HB2	1:C:204:ALA:HB2	2.02	0.42
1:A:234:ILE:HG21	1:A:275:LEU:HD12	2.00	0.42
1:C:254:GLU:HA	1:C:269:VAL:O	2.19	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
1:B:248:THR:HG23	1:B:277:VAL:HB	2.02	0.42
2:F:4:DG:C2'	2:F:5:DT:C7	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:5:DT:H2'	2:F:6:DA:C8	2.55	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:163:GLU:H	1:B:163:GLU:CD	2.23	0.41
1:B:234:ILE:HD11	1:B:250:SER:CB	2.50	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
1:C:248:THR:HG23	1:C:277:VAL:HB	2.03	0.41
1:D:127:LEU:HD22	1:D:174:ILE:O	2.20	0.41
2:E:4:DG:C2'	2:E:5:DT:C7	2.98	0.41
1:A:146:LEU:HG	1:A:157:ILE:HG12	2.03	0.41
1:A:337:THR:OG1	1:A:340:GLN:N	2.51	0.41
1:B:65:LEU:HD22	1:B:65:LEU:HA	1.89	0.41
1:D:337:THR:OG1	1:D:340:GLN:N	2.51	0.41
1:B:168:VAL:O	1:B:177:LYS:HB2	2.20	0.41
1:C:78:THR:O	1:C:79:LEU:HB2	2.20	0.41
1:C:201:THR:CG2	1:C:209:ILE:HB	2.50	0.41
1:D:215:ASP:HB2	1:D:217:LYS:HE3	2.02	0.41
1:B:78:THR:O	1:B:79:LEU:HB2	2.20	0.41
1:B:104:TRP:CD2	1:B:155:VAL:HG21	2.54	0.41
1:B:146:LEU:HG	1:B:157:ILE:HG23	2.01	0.41
1:D:221:ARG:O	1:D:221:ARG:HG3	2.20	0.41
1:B:134:ARG:NH2	1:B:139:ARG:NE	2.68	0.41
1:D:120:THR:OG1	1:D:122:GLU:HG3	2.20	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:339:GLN:NE2	2:E:7:DC:H5'	2.35	0.41
1:A:320:ALA:HB3	1:A:329:TYR:HB2	2.03	0.41
1:D:144:ARG:HD2	2:E:9:DC:C4	2.56	0.41
1:C:64:LYS:CE	1:C:65:LEU:HD23	2.51	0.40
1:D:144:ARG:NH1	1:D:160:ILE:CD1	2.84	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
1:D:337:THR:C	1:D:338:LYS:HD2	2.42	0.40
1:A:224:LEU:HD12	1:A:233:PHE:CE2	2.56	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:145:GLU:C	1:B:146:LEU:HD12	2.42	0.40
1:B:233:PHE:HA	1:B:248:THR:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:5:DT:H2'	2:F:6:DA:N7	2.37	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 (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	320/353 (91%)	289 (90%)	29 (9%)	2 (1%)	25	58
1	B	319/353 (90%)	289 (91%)	26 (8%)	4 (1%)	12	37
1	C	319/353 (90%)	289 (91%)	26 (8%)	4 (1%)	12	37
1	D	320/353 (91%)	289 (90%)	29 (9%)	2 (1%)	25	58
All	All	1278/1412 (90%)	1156 (90%)	110 (9%)	12 (1%)	17	48

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

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Mol	Chain	Res	Type
1	A	228	GLY

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	270/297 (91%)	268 (99%)	2 (1%)	84 95
1	B	269/297 (91%)	261 (97%)	8 (3%)	41 75
1	C	269/297 (91%)	261 (97%)	8 (3%)	41 75
1	D	270/297 (91%)	268 (99%)	2 (1%)	84 95
All	All	1078/1188 (91%)	1058 (98%)	20 (2%)	57 84

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

Sometimes 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
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 (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)

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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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	322/353 (91%)	0.07	0	100	100	39, 61, 85, 107	0
1	B	321/353 (90%)	0.08	0	100	100	36, 59, 86, 108	0
1	C	321/353 (90%)	0.08	0	100	100	37, 59, 86, 108	0
1	D	322/353 (91%)	0.10	0	100	100	39, 62, 85, 107	0
2	E	11/11 (100%)	1.25	3 (27%)	0	0	120, 145, 192, 196	0
2	F	11/11 (100%)	0.88	2 (18%)	1	1	120, 146, 192, 197	0
All	All	1308/1434 (91%)	0.10	5 (0%)	92	93	36, 61, 93, 197	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	4	DG	4.1
2	E	11	DG	2.7
2	E	3	DG	2.5
2	F	4	DG	2.5
2	F	3	DG	2.5

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 monosaccharides 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.