Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 12:06 AM GMT

PDB ID	:	1ZQX
Title	:	DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7), 31-KD DOMAIN; SOAKED IN THE PRESENCE OF KCL (150 MILLIMOLAR)
Authors	:	Pelletier, H.; Sawaya, M.R.
Deposited on	:	1996-04-19
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

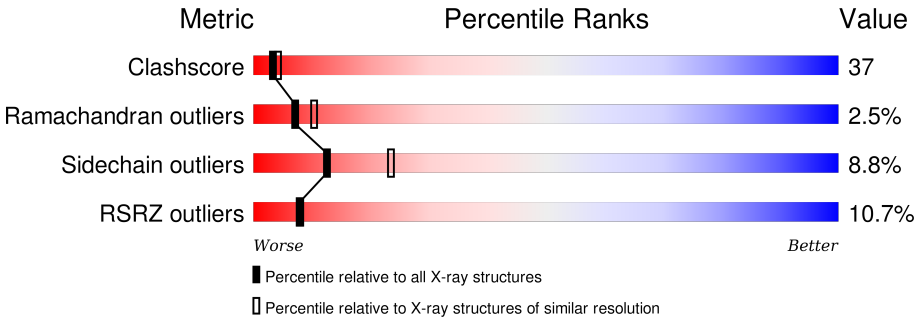
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 >=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 <=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	248	10%, 38%, 44%, 15%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2037 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 DNA POLYMERASE BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	242	1935	1218	342	367	8	0	1	0

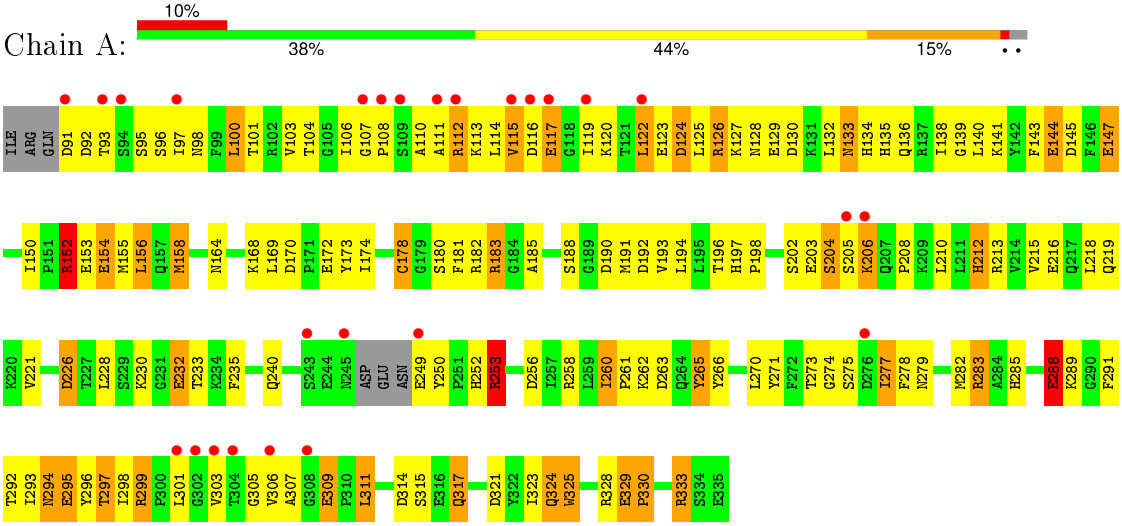
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	102	102	102	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 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: DNA POLYMERASE BETA



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	120.79Å 63.19Å 38.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 27.25 – 2.26	Depositor EDS
% Data completeness (in resolution range)	92.0 (20.00-2.50) 83.9 (27.25-2.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 2.26Å)	Xtriage
Refinement program	TNT V. 5-D	Depositor
R, R_{free}	(Not available) , (Not available) 0.237 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	22.0	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 92.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 12222 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	2037	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.92% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	1.12	13/1973 (0.7%)	1.63	45/2662 (1.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	147	GLU	CD-OE1	6.17	1.32	1.25
1	A	172	GLU	CD-OE1	5.83	1.32	1.25
1	A	117	GLU	CD-OE1	5.78	1.32	1.25
1	A	153	GLU	CD-OE2	5.73	1.31	1.25
1	A	249	GLU	CD-OE1	5.67	1.31	1.25
1	A	216	GLU	CD-OE1	5.62	1.31	1.25
1	A	309	GLU	CD-OE1	5.57	1.31	1.25
1	A	288	GLU	CD-OE1	5.56	1.31	1.25
1	A	329	GLU	CD-OE1	5.26	1.31	1.25
1	A	154	GLU	CD-OE1	5.20	1.31	1.25
1	A	203	GLU	CD-OE1	5.17	1.31	1.25
1	A	144	GLU	CD-OE1	5.14	1.31	1.25
1	A	232	GLU	CD-OE1	5.13	1.31	1.25

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	213	ARG	NE-CZ-NH1	9.26	124.93	120.30
1	A	299[A]	ARG	NE-CZ-NH1	8.39	124.49	120.30
1	A	299[B]	ARG	NE-CZ-NH1	8.39	124.49	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	258	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	A	182	ARG	NE-CZ-NH1	7.83	124.22	120.30
1	A	263	ASP	CB-CG-OD1	-7.73	111.34	118.30
1	A	263	ASP	CB-CG-OD2	7.47	125.03	118.30
1	A	190	ASP	CB-CG-OD1	7.38	124.94	118.30
1	A	253	ARG	NE-CZ-NH2	-7.31	116.64	120.30
1	A	258	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	A	256	ASP	CB-CG-OD2	7.17	124.75	118.30
1	A	130	ASP	CB-CG-OD1	-6.97	112.03	118.30
1	A	112	ARG	NE-CZ-NH1	6.91	123.76	120.30
1	A	190	ASP	CB-CG-OD2	-6.84	112.14	118.30
1	A	321	ASP	CB-CG-OD1	-6.55	112.41	118.30
1	A	314	ASP	CB-CG-OD1	-6.30	112.62	118.30
1	A	213	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	A	235	PHE	CB-CA-C	-6.17	98.05	110.40
1	A	124	ASP	CB-CG-OD1	-6.15	112.77	118.30
1	A	192	ASP	CB-CG-OD1	-6.06	112.85	118.30
1	A	266	TYR	CA-CB-CG	-6.02	101.96	113.40
1	A	178	CYS	CB-CA-C	5.95	122.31	110.40
1	A	235	PHE	CB-CG-CD2	5.93	124.95	120.80
1	A	183	ARG	NE-CZ-NH2	-5.93	117.34	120.30
1	A	260	ILE	CB-CA-C	-5.88	99.85	111.60
1	A	253	ARG	NE-CZ-NH1	5.85	123.23	120.30
1	A	126	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	124	ASP	CB-CG-OD2	5.75	123.47	118.30
1	A	152	ARG	N-CA-CB	5.68	120.82	110.60
1	A	226	ASP	CB-CG-OD1	5.67	123.41	118.30
1	A	145	ASP	CB-CG-OD2	5.66	123.39	118.30
1	A	297	THR	CB-CA-C	-5.60	96.47	111.60
1	A	173	TYR	CA-CB-CG	5.58	124.01	113.40
1	A	226	ASP	N-CA-CB	5.40	120.33	110.60
1	A	126	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	A	299[A]	ARG	CD-NE-CZ	5.31	131.03	123.60
1	A	299[B]	ARG	CD-NE-CZ	5.31	131.03	123.60
1	A	297	THR	N-CA-CB	-5.31	100.22	110.30
1	A	212	HIS	N-CA-CB	5.28	120.11	110.60
1	A	265	TYR	CB-CG-CD1	-5.27	117.84	121.00
1	A	116	ASP	CB-CG-OD2	-5.25	113.58	118.30
1	A	266	TYR	CB-CG-CD1	-5.08	117.95	121.00
1	A	314	ASP	CB-CG-OD2	5.06	122.85	118.30
1	A	333	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	A	283	ARG	NE-CZ-NH1	5.00	122.80	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	152	ARG	CA

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	1935	0	1868	141	0
2	A	102	0	0	7	2
All	All	2037	0	1868	141	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (141) 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:A:317:GLN:NE2	1:A:317:GLN:H	1.41	1.16
1:A:294:ASN:ND2	1:A:296:TYR:H	1.58	1.01
1:A:317:GLN:HE21	1:A:317:GLN:H	0.99	0.96
1:A:294:ASN:HD22	1:A:296:TYR:H	1.08	0.95
1:A:317:GLN:HE21	1:A:317:GLN:N	1.71	0.88
1:A:277:ILE:H	1:A:277:ILE:HD13	1.37	0.87
1:A:133:ASN:HD21	1:A:136:GLN:HG3	1.39	0.86
1:A:103:VAL:HB	1:A:106:ILE:HD13	1.59	0.82
1:A:317:GLN:NE2	1:A:317:GLN:N	2.25	0.81
1:A:279:ASN:O	1:A:283:ARG:HG2	1.81	0.80
1:A:97:ILE:HD11	1:A:112:ARG:HG2	1.67	0.77
1:A:133:ASN:ND2	1:A:136:GLN:H	1.85	0.75
1:A:110:ALA:O	1:A:114:LEU:HD13	1.86	0.75
1:A:104:THR:HG22	2:A:435:HOH:O	1.87	0.74
1:A:154:GLU:O	1:A:158:MET:HG2	1.90	0.71
1:A:122:LEU:HD12	1:A:123:GLU:N	2.04	0.71
1:A:270:LEU:HD21	1:A:282:MET:CE	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:VAL:CB	1:A:106:ILE:HD13	2.20	0.70
1:A:97:ILE:CD1	1:A:112:ARG:HG2	2.22	0.69
1:A:315:SER:HB2	1:A:317:GLN:HE22	1.57	0.69
1:A:133:ASN:ND2	1:A:136:GLN:HG3	2.08	0.69
1:A:98:ASN:O	1:A:101:THR:HG22	1.93	0.68
1:A:92:ASP:O	1:A:95:SER:HB3	1.93	0.68
1:A:144:GLU:OE1	1:A:144:GLU:N	2.28	0.67
1:A:297:THR:O	1:A:299[A]:ARG:NH1	2.28	0.67
1:A:152:ARG:NH2	1:A:181:PHE:O	2.29	0.66
1:A:133:ASN:HD21	1:A:136:GLN:H	1.44	0.66
1:A:112:ARG:O	1:A:115:VAL:HG23	1.97	0.65
1:A:294:ASN:HD22	1:A:296:TYR:N	1.88	0.64
1:A:183:ARG:NE	2:A:499:HOH:O	2.31	0.63
1:A:328:ARG:HG3	2:A:430:HOH:O	1.99	0.62
1:A:113:LYS:O	1:A:117:GLU:HG2	1.99	0.62
1:A:283:ARG:NE	1:A:293:ILE:O	2.31	0.61
1:A:278:PHE:CE2	1:A:282:MET:HE2	2.35	0.61
1:A:215:VAL:O	1:A:219:GLN:HG3	2.00	0.61
1:A:155:MET:HA	1:A:158:MET:HG3	1.83	0.60
1:A:143:PHE:HB3	1:A:144:GLU:OE1	2.00	0.60
1:A:232:GLU:HG3	1:A:233:THR:HG23	1.83	0.60
1:A:262:LYS:O	1:A:262:LYS:HG3	2.02	0.60
1:A:197:HIS:ND1	1:A:198:PRO:HD2	2.16	0.60
1:A:208:PRO:HD2	2:A:473:HOH:O	1.99	0.60
1:A:305:GLY:O	1:A:307:ALA:N	2.35	0.59
1:A:150:ILE:O	1:A:188:SER:N	2.30	0.59
1:A:144:GLU:O	1:A:147:GLU:N	2.29	0.59
1:A:196:THR:HB	1:A:265:TYR:CD1	2.37	0.59
1:A:270:LEU:HD21	1:A:282:MET:HE3	1.85	0.58
1:A:135:HIS:ND1	1:A:228:LEU:HB3	2.19	0.58
1:A:274:GLY:HA2	1:A:279:ASN:OD1	2.03	0.58
1:A:155:MET:HA	1:A:158:MET:CG	2.33	0.58
1:A:126:ARG:HG2	1:A:140:LEU:HD21	1.86	0.58
1:A:100:LEU:O	1:A:103:VAL:HG23	2.03	0.58
1:A:301:LEU:HD12	1:A:301:LEU:N	2.19	0.58
1:A:205:SER:O	1:A:206:LYS:HD3	2.04	0.57
1:A:168:LYS:NZ	1:A:168:LYS:HB2	2.19	0.57
1:A:134:HIS:O	1:A:138:ILE:HG12	2.05	0.57
1:A:103:VAL:HB	1:A:106:ILE:CD1	2.32	0.57
1:A:295:GLU:H	1:A:295:GLU:CD	2.07	0.56
1:A:271:TYR:CG	1:A:295:GLU:HB3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:ASN:H	1:A:136:GLN:NE2	2.02	0.56
1:A:123:GLU:O	1:A:127:LYS:HG2	2.06	0.56
1:A:133:ASN:HD22	1:A:133:ASN:C	2.09	0.55
1:A:253:ARG:NH1	2:A:402:HOH:O	2.28	0.55
1:A:283:ARG:NH2	1:A:294:ASN:HA	2.22	0.55
1:A:107:GLY:O	1:A:111:ALA:N	2.40	0.54
1:A:270:LEU:HD21	1:A:282:MET:HE1	1.89	0.54
1:A:277:ILE:N	1:A:277:ILE:HD13	2.14	0.54
1:A:138:ILE:HB	1:A:228:LEU:HD23	1.88	0.54
1:A:292:THR:HG22	1:A:301:LEU:HD11	1.90	0.52
1:A:289:LYS:NZ	1:A:324:GLN:HG3	2.24	0.52
1:A:285:HIS:HD2	1:A:323:ILE:HD12	1.75	0.52
1:A:122:LEU:O	1:A:126:ARG:HG3	2.10	0.52
1:A:285:HIS:CD2	1:A:323:ILE:HD12	2.45	0.51
1:A:114:LEU:HD12	1:A:114:LEU:N	2.24	0.51
1:A:315:SER:HB2	1:A:317:GLN:NE2	2.25	0.51
1:A:92:ASP:C	1:A:95:SER:HB3	2.30	0.51
1:A:260:ILE:HG22	1:A:261:PRO:N	2.25	0.51
1:A:156:LEU:HD13	1:A:181:PHE:HE1	1.76	0.51
1:A:193:VAL:C	1:A:194:LEU:HD12	2.32	0.51
1:A:288:GLU:N	1:A:288:GLU:OE1	2.43	0.51
1:A:120:LYS:N	1:A:124:ASP:OD2	2.35	0.50
1:A:323:ILE:C	1:A:324:GLN:HG2	2.32	0.50
1:A:218:LEU:HA	1:A:221:VAL:HG22	1.91	0.50
1:A:275:SER:OG	1:A:277:ILE:HG12	2.12	0.49
1:A:298:ILE:HG23	1:A:311:LEU:HB2	1.93	0.49
1:A:294:ASN:C	1:A:294:ASN:HD22	2.16	0.49
1:A:240:GLN:NE2	1:A:252:HIS:CE1	2.80	0.49
1:A:110:ALA:HA	1:A:113:LYS:HE3	1.96	0.48
1:A:315:SER:CB	1:A:317:GLN:NE2	2.76	0.48
1:A:285:HIS:NE2	1:A:325:TRP:CD1	2.82	0.48
1:A:122:LEU:O	1:A:125:LEU:HB2	2.14	0.47
1:A:303:VAL:C	1:A:305:GLY:H	2.17	0.47
1:A:315:SER:OG	1:A:317:GLN:NE2	2.48	0.47
1:A:204:SER:C	1:A:206:LYS:HE2	2.35	0.46
1:A:119:ILE:HA	1:A:124:ASP:OD2	2.15	0.46
1:A:114:LEU:CD1	1:A:114:LEU:N	2.79	0.46
1:A:298:ILE:C	1:A:299[A]:ARG:HG3	2.36	0.46
1:A:100:LEU:HB3	1:A:106:ILE:HG21	1.97	0.45
1:A:174:ILE:HB	1:A:196:THR:HG22	1.98	0.45
1:A:291:PHE:HE1	1:A:311:LEU:HD21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:LYS:O	1:A:128:ASN:ND2	2.50	0.45
1:A:106:ILE:CG2	1:A:111:ALA:HB2	2.46	0.45
1:A:277:ILE:H	1:A:277:ILE:CD1	2.05	0.45
1:A:250:TYR:HB3	2:A:404:HOH:O	2.15	0.45
1:A:301:LEU:C	1:A:307:ALA:HB3	2.37	0.45
1:A:298:ILE:O	1:A:298:ILE:HG23	2.17	0.45
1:A:329:GLU:HB3	1:A:330:PRO:HD2	1.98	0.45
1:A:328:ARG:HD3	1:A:328:ARG:HH11	1.58	0.44
1:A:91:ASP:C	1:A:93:THR:H	2.20	0.44
1:A:294:ASN:HD22	1:A:295:GLU:N	2.15	0.44
1:A:294:ASN:ND2	1:A:296:TYR:N	2.43	0.44
1:A:330:PRO:HA	1:A:333:ARG:HG3	1.99	0.44
1:A:210:LEU:HD23	1:A:210:LEU:HA	1.81	0.44
1:A:103:VAL:CG1	1:A:106:ILE:HD13	2.47	0.44
1:A:158:MET:H	1:A:158:MET:HG2	1.70	0.44
1:A:277:ILE:HG12	1:A:278:PHE:H	1.84	0.43
1:A:156:LEU:CD1	1:A:181:PHE:CE1	3.01	0.43
1:A:315:SER:CB	1:A:317:GLN:HE22	2.28	0.43
1:A:204:SER:CA	1:A:206:LYS:HE2	2.48	0.43
1:A:277:ILE:HG12	1:A:278:PHE:N	2.35	0.42
1:A:197:HIS:CG	1:A:198:PRO:HD2	2.54	0.42
1:A:202:SER:N	1:A:261:PRO:HB3	2.34	0.42
1:A:93:THR:C	1:A:96:SER:H	2.22	0.42
1:A:108:PRO:O	1:A:112:ARG:HG3	2.19	0.42
1:A:93:THR:O	1:A:96:SER:N	2.50	0.42
1:A:240:GLN:HE22	1:A:252:HIS:CE1	2.38	0.42
1:A:122:LEU:HD12	1:A:122:LEU:C	2.40	0.41
1:A:129:GLU:HA	1:A:132:LEU:HD12	2.01	0.41
1:A:205:SER:O	1:A:206:LYS:HB3	2.21	0.41
1:A:212:HIS:CD2	1:A:230:LYS:HE3	2.56	0.41
1:A:252:HIS:C	1:A:253:ARG:HD2	2.40	0.41
1:A:127:LYS:N	1:A:127:LYS:HD3	2.32	0.41
1:A:183:ARG:NH1	1:A:273:THR:O	2.53	0.41
1:A:169:LEU:O	1:A:170:ASP:HB2	2.21	0.41
1:A:113:LYS:HG3	1:A:114:LEU:HD12	2.03	0.41
1:A:104:THR:HG23	1:A:139:GLY:HA3	2.02	0.41
1:A:252:HIS:NE2	2:A:483:HOH:O	2.37	0.41
1:A:180:SER:HB2	1:A:185:ALA:HB2	2.03	0.41
1:A:103:VAL:CG1	1:A:106:ILE:CD1	2.99	0.40
1:A:158:MET:HG3	1:A:191:MET:HE3	2.03	0.40
1:A:138:ILE:HB	1:A:228:LEU:CD2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:HG2	1:A:141:LYS:O	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:477:HOH:O	2:A:477:HOH:O[2_555]	0.45	1.75
2:A:502:HOH:O	2:A:502:HOH:O[2_555]	2.01	0.19

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	239/248 (96%)	207 (87%)	26 (11%)	6 (2%)	7 10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	LYS
1	A	306	VAL
1	A	309	GLU
1	A	204	SER
1	A	324	GLN
1	A	178	CYS

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	206/226 (91%)	188 (91%)	18 (9%)	13 24

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	LEU
1	A	115	VAL
1	A	122	LEU
1	A	133	ASN
1	A	152	ARG
1	A	156	LEU
1	A	158	MET
1	A	164	ASN
1	A	226	ASP
1	A	253	ARG
1	A	277	ILE
1	A	288	GLU
1	A	294	ASN
1	A	295	GLU
1	A	311	LEU
1	A	317	GLN
1	A	325	TRP
1	A	330	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	ASN
1	A	133	ASN
1	A	136	GLN
1	A	157	GLN
1	A	159	GLN
1	A	217	GLN
1	A	240	GLN
1	A	252	HIS
1	A	281	ASN
1	A	285	HIS
1	A	294	ASN
1	A	317	GLN

5.3.3 RNA

There are no RNA molecules 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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	242/248 (97%)	0.56	26 (10%) 8 8	17, 37, 88, 100	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	205	SER	7.9
1	A	94	SER	7.4
1	A	93	THR	6.5
1	A	97	ILE	5.9
1	A	116	ASP	5.8
1	A	243	SER	5.7
1	A	112	ARG	5.2
1	A	306	VAL	5.1
1	A	303	VAL	5.1
1	A	304	THR	4.9
1	A	119	ILE	4.7
1	A	115	VAL	4.7
1	A	91	ASP	4.1
1	A	107	GLY	3.8
1	A	301	LEU	3.7
1	A	108	PRO	3.3
1	A	245	ASN	3.1
1	A	276	ASP	2.9
1	A	302	GLY	2.8
1	A	308	GLY	2.6
1	A	109	SER	2.5
1	A	249	GLU	2.4
1	A	206	LYS	2.4
1	A	111	ALA	2.3
1	A	117	GLU	2.2
1	A	122	LEU	2.2

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.