



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:06 AM GMT

PDB ID : 1ZQV  
Title : DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7), 31-KD DOMAIN;  
SOAKED IN THE PRESENCE OF CACL2 (150 MILLIMOLAR)  
Authors : Pelletier, H.; Sawaya, M.R.  
Deposited on : 1996-04-19  
Resolution : 2.70 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 (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

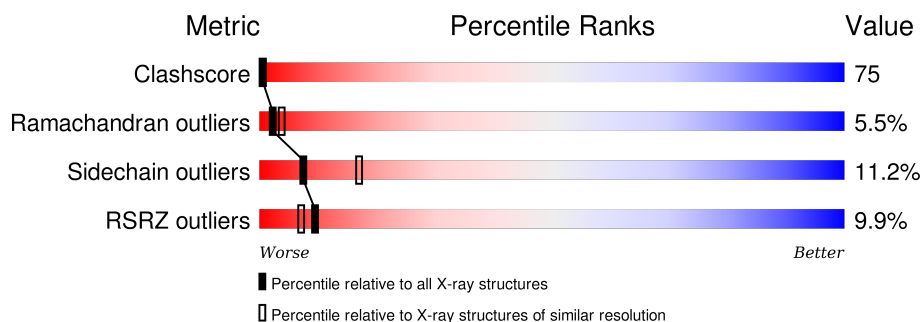
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	248	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2046 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
1	A	242	Total	C	N	O	S	0	1	0
			1939	1221	343	367	8			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

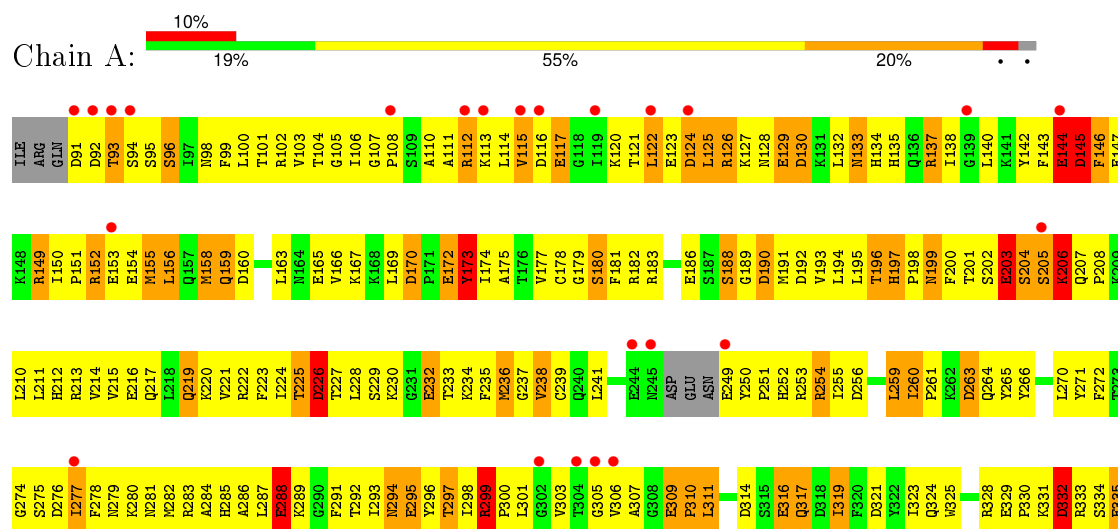
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		

### 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: DNA POLYMERASE BETA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	120.77Å 63.35Å 35.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 9.67 – 2.42	Depositor EDS
% Data completeness (in resolution range)	83.0 (20.00-2.70) 78.0 (9.67-2.42)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.08 (at 2.41Å)	Xtriage
Refinement program	TNT V. 5-D	Depositor
R, $R_{free}$	(Not available) , (Not available) 0.231 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	12.6	Xtriage
Anisotropy	1.326	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 127.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 8589 reflections (0.012%)	Xtriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	2046	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.59% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CA

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	1.23	19/1977 (1.0%)	1.73	52/2666 (2.0%)

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	0	2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	316	GLU	CD-OE1	9.97	1.36	1.25
1	A	172	GLU	CD-OE1	7.80	1.34	1.25
1	A	216	GLU	CD-OE1	7.42	1.33	1.25
1	A	147	GLU	CD-OE1	6.67	1.32	1.25
1	A	249	GLU	CD-OE1	6.64	1.32	1.25
1	A	144	GLU	CD-OE1	6.39	1.32	1.25
1	A	309	GLU	CD-OE1	6.18	1.32	1.25
1	A	335	GLU	CD-OE1	6.16	1.32	1.25
1	A	229	SER	CA-CB	-6.03	1.44	1.52
1	A	295	GLU	CD-OE1	6.02	1.32	1.25
1	A	117	GLU	CD-OE1	5.91	1.32	1.25
1	A	186	GLU	CD-OE1	5.75	1.31	1.25
1	A	153	GLU	CD-OE2	5.67	1.31	1.25
1	A	129	GLU	CD-OE1	5.62	1.31	1.25
1	A	288	GLU	CD-OE1	5.49	1.31	1.25
1	A	165	GLU	CD-OE1	5.36	1.31	1.25
1	A	232	GLU	CD-OE1	5.25	1.31	1.25
1	A	238	VAL	CB-CG2	5.18	1.63	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	203	GLU	CD-OE1	5.18	1.31	1.25

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	ARG	NE-CZ-NH2	-10.82	114.89	120.30
1	A	314	ASP	CB-CG-OD1	-8.13	110.98	118.30
1	A	253	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	A	263	ASP	CB-CG-OD1	-8.12	110.99	118.30
1	A	190	ASP	CB-CG-OD2	-7.92	111.17	118.30
1	A	137	ARG	NE-CZ-NH1	7.55	124.08	120.30
1	A	145	ASP	CB-CG-OD1	-7.50	111.55	118.30
1	A	192	ASP	CB-CG-OD1	-7.34	111.69	118.30
1	A	321	ASP	CB-CG-OD1	-7.21	111.81	118.30
1	A	214	VAL	CB-CA-C	7.09	124.88	111.40
1	A	226	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	A	276	ASP	CB-CG-OD1	-6.88	112.11	118.30
1	A	236	MET	C-N-CA	-6.84	107.93	122.30
1	A	222	ARG	NE-CZ-NH1	6.67	123.63	120.30
1	A	276	ASP	CB-CG-OD2	6.63	124.27	118.30
1	A	116	ASP	CB-CG-OD2	-6.42	112.52	118.30
1	A	145	ASP	CB-CG-OD2	6.35	124.02	118.30
1	A	190	ASP	CB-CG-OD1	6.18	123.86	118.30
1	A	226	ASP	CB-CG-OD1	6.14	123.82	118.30
1	A	124	ASP	CB-CG-OD1	-6.11	112.81	118.30
1	A	297	THR	CA-CB-CG2	-6.01	103.99	112.40
1	A	130	ASP	CB-CG-OD1	-5.96	112.94	118.30
1	A	149	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	160	ASP	CB-CG-OD1	-5.88	113.01	118.30
1	A	214	VAL	CA-CB-CG1	5.87	119.71	110.90
1	A	254	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	A	178	CYS	CA-CB-SG	-5.75	103.65	114.00
1	A	314	ASP	CB-CG-OD2	5.72	123.45	118.30
1	A	152	ARG	N-CA-CB	5.72	120.89	110.60
1	A	319	ILE	CB-CA-C	-5.64	100.32	111.60
1	A	137	ARG	N-CA-CB	5.62	120.72	110.60
1	A	260	ILE	CB-CA-C	-5.59	100.43	111.60
1	A	332	ASP	CB-CG-OD1	-5.55	113.31	118.30
1	A	96	SER	N-CA-CB	5.50	118.76	110.50
1	A	206	LYS	N-CA-CB	-5.45	100.79	110.60
1	A	263	ASP	CB-CG-OD2	5.42	123.17	118.30
1	A	197	HIS	CB-CA-C	-5.41	99.59	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	SER	CB-CA-C	5.39	120.34	110.10
1	A	226	ASP	N-CA-CB	5.32	120.18	110.60
1	A	225	THR	N-CA-CB	5.31	120.38	110.30
1	A	173	TYR	CB-CA-C	-5.25	99.90	110.40
1	A	229	SER	CA-CB-OG	-5.16	97.26	111.20
1	A	299[A]	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	299[B]	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	253	ARG	CB-CA-C	-5.14	100.11	110.40
1	A	124	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	152	ARG	CD-NE-CZ	-5.14	116.41	123.60
1	A	170	ASP	CB-CG-OD1	-5.13	113.68	118.30
1	A	112	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	A	192	ASP	CB-CG-OD2	5.07	122.86	118.30
1	A	266	TYR	CB-CA-C	5.04	120.48	110.40
1	A	173	TYR	CB-CG-CD1	-5.03	117.98	121.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	ASP	Sidechain
1	A	199	ASN	Sidechain

## 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	1939	0	1875	286	1
2	A	1	0	0	0	0
3	A	106	0	0	23	1
All	All	2046	0	1875	286	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 75.

All (286) 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:103:VAL:HB	1:A:106:ILE:HD13	1.19	1.10
1:A:158:MET:HB2	1:A:191:MET:HE1	1.24	1.10
1:A:278:PHE:HE1	1:A:282:MET:HE1	1.15	1.06
1:A:317:GLN:NE2	1:A:317:GLN:H	1.59	1.00
1:A:278:PHE:HE2	1:A:328:ARG:HD2	1.21	1.00
1:A:317:GLN:HE21	1:A:317:GLN:N	1.61	0.97
1:A:133:ASN:ND2	1:A:135:HIS:H	1.63	0.96
1:A:135:HIS:CE1	1:A:228:LEU:HB3	2.05	0.91
1:A:289:LYS:NZ	1:A:324:GLN:HG3	1.85	0.91
1:A:278:PHE:CE1	1:A:282:MET:HE1	2.05	0.91
1:A:133:ASN:HD22	1:A:135:HIS:H	1.12	0.90
1:A:277:ILE:HD13	1:A:277:ILE:H	1.36	0.89
1:A:158:MET:CB	1:A:191:MET:HE1	2.04	0.88
1:A:278:PHE:CE2	1:A:328:ARG:HD2	2.08	0.87
1:A:125:LEU:HB3	1:A:140:LEU:HD22	1.54	0.85
1:A:299[A]:ARG:HG3	1:A:299[A]:ARG:HH11	1.40	0.85
1:A:317:GLN:HE21	1:A:317:GLN:H	0.88	0.83
1:A:270:LEU:HD21	1:A:282:MET:CE	2.10	0.82
1:A:113:LYS:HG3	1:A:114:LEU:HD12	1.60	0.82
1:A:197:HIS:ND1	1:A:199:ASN:HB2	1.95	0.81
1:A:286:ALA:HB2	1:A:323:ILE:HG21	1.63	0.78
1:A:138:ILE:HB	1:A:228:LEU:HD21	1.66	0.77
1:A:217:GLN:O	1:A:221:VAL:HG22	1.84	0.77
1:A:158:MET:HG2	1:A:241:LEU:HD11	1.67	0.76
1:A:234:LYS:HE3	1:A:236:MET:HG3	1.68	0.76
1:A:143:PHE:HB3	1:A:144:GLU:OE1	1.85	0.75
1:A:274:GLY:HA2	1:A:279:ASN:OD1	1.86	0.74
1:A:138:ILE:HB	1:A:228:LEU:CD2	2.17	0.74
1:A:270:LEU:HD21	1:A:282:MET:HE3	1.67	0.74
1:A:103:VAL:CB	1:A:106:ILE:HD13	2.10	0.73
1:A:204:SER:CA	1:A:206:LYS:HE2	2.18	0.73
1:A:158:MET:HB2	1:A:191:MET:CE	2.14	0.72
1:A:299[A]:ARG:HG2	1:A:310:PRO:HA	1.72	0.72
1:A:331:LYS:HG3	1:A:332:ASP:OD1	1.89	0.72
1:A:197:HIS:CG	1:A:198:PRO:HD2	2.25	0.72
1:A:200:PHE:CE2	1:A:259:LEU:HD23	2.25	0.71
1:A:294:ASN:ND2	1:A:297:THR:H	1.88	0.71
1:A:159:GLN:HG3	1:A:177:VAL:CG2	2.21	0.71
1:A:135:HIS:ND1	1:A:228:LEU:HB3	2.06	0.71
1:A:292:THR:HG22	1:A:301:LEU:HD11	1.72	0.71
1:A:133:ASN:HD22	1:A:135:HIS:N	1.87	0.70
1:A:277:ILE:HD13	1:A:277:ILE:N	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ILE:HG22	1:A:261:PRO:O	1.91	0.70
1:A:292:THR:HG22	1:A:301:LEU:CD1	2.20	0.70
1:A:277:ILE:HG12	1:A:335:GLU:HA	1.72	0.70
1:A:329:GLU:HB3	3:A:429:HOH:O	1.93	0.69
1:A:224:ILE:HD13	1:A:235:PHE:CE1	2.27	0.69
1:A:104:THR:HG22	3:A:435:HOH:O	1.93	0.68
1:A:175:ALA:HB2	1:A:195:LEU:HD12	1.76	0.68
1:A:133:ASN:ND2	1:A:135:HIS:N	2.39	0.68
1:A:278:PHE:HB2	1:A:333:ARG:O	1.94	0.68
1:A:159:GLN:HG2	1:A:159:GLN:O	1.92	0.68
1:A:103:VAL:HB	1:A:106:ILE:CD1	2.12	0.68
1:A:108:PRO:O	1:A:112:ARG:HG3	1.94	0.67
1:A:299[A]:ARG:HG3	1:A:299[A]:ARG:NH1	2.10	0.67
1:A:287:LEU:O	1:A:287:LEU:HD12	1.95	0.67
1:A:300:PRO:HD3	1:A:311:LEU:CD2	2.25	0.67
1:A:213:ARG:HD3	3:A:444:HOH:O	1.94	0.66
1:A:144:GLU:N	1:A:144:GLU:OE1	2.29	0.66
1:A:289:LYS:HZ3	1:A:324:GLN:HG3	1.59	0.66
1:A:292:THR:CB	1:A:301:LEU:HD11	2.26	0.66
1:A:137:ARG:NE	3:A:445:HOH:O	2.29	0.65
1:A:204:SER:HA	1:A:206:LYS:HE2	1.78	0.65
1:A:212:HIS:CD2	1:A:230:LYS:HE3	2.32	0.65
1:A:92:ASP:O	1:A:95:SER:HB3	1.95	0.65
1:A:167:LYS:HA	3:A:406:HOH:O	1.97	0.65
1:A:172:GLU:HG2	1:A:198:PRO:HG3	1.80	0.64
1:A:278:PHE:HE1	1:A:282:MET:CE	2.03	0.64
1:A:277:ILE:HD11	1:A:334:SER:O	1.98	0.64
1:A:289:LYS:HD2	1:A:323:ILE:O	1.97	0.64
1:A:172:GLU:CG	1:A:198:PRO:HG3	2.28	0.64
1:A:106:ILE:HG22	1:A:111:ALA:HB2	1.80	0.64
1:A:177:VAL:HG23	3:A:424:HOH:O	1.97	0.64
1:A:292:THR:CG2	1:A:301:LEU:HD11	2.27	0.63
1:A:286:ALA:CB	1:A:323:ILE:HG21	2.28	0.63
1:A:281:ASN:O	1:A:284:ALA:HB3	1.99	0.63
1:A:197:HIS:ND1	1:A:198:PRO:HD2	2.13	0.63
1:A:175:ALA:HB2	1:A:195:LEU:CD1	2.28	0.63
1:A:142:TYR:O	1:A:146:PHE:HB2	1.98	0.63
1:A:114:LEU:HD12	1:A:114:LEU:N	2.15	0.62
1:A:289:LYS:HZ2	1:A:324:GLN:HG3	1.63	0.62
1:A:270:LEU:HD21	1:A:282:MET:HE2	1.79	0.62
1:A:159:GLN:NE2	3:A:514:HOH:O	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:LEU:O	1:A:128:ASN:N	2.32	0.62
1:A:145:ASP:CG	1:A:252:HIS:H	2.03	0.62
1:A:170:ASP:O	1:A:173:TYR:HB2	2.00	0.61
1:A:98:ASN:O	1:A:101:THR:HG22	2.00	0.61
1:A:106:ILE:N	1:A:106:ILE:HD12	2.14	0.61
1:A:155:MET:HB3	1:A:181:PHE:CE2	2.35	0.61
1:A:104:THR:O	1:A:106:ILE:HD12	2.01	0.61
1:A:294:ASN:HD22	1:A:297:THR:H	1.48	0.61
1:A:270:LEU:HD11	1:A:282:MET:HE3	1.83	0.60
1:A:154:GLU:HG2	1:A:250:TYR:HE2	1.65	0.60
1:A:122:LEU:O	1:A:125:LEU:HB2	2.01	0.60
1:A:200:PHE:HD1	1:A:204:SER:HB2	1.66	0.60
1:A:150:ILE:HD11	3:A:411:HOH:O	2.00	0.60
1:A:208:PRO:HB3	1:A:232:GLU:HA	1.84	0.59
1:A:295:GLU:H	1:A:295:GLU:CD	2.06	0.59
1:A:100:LEU:O	1:A:103:VAL:HG23	2.03	0.58
1:A:223:PHE:CE1	1:A:239:CYS:HB2	2.37	0.58
1:A:263:ASP:N	1:A:263:ASP:OD1	2.36	0.58
1:A:270:LEU:CD2	1:A:282:MET:HE3	2.33	0.58
1:A:280:LYS:O	1:A:284:ALA:HB2	2.03	0.58
1:A:331:LYS:O	1:A:333:ARG:N	2.36	0.57
1:A:100:LEU:HD11	1:A:120:LYS:O	2.04	0.57
1:A:212:HIS:HD2	1:A:230:LYS:HE3	1.69	0.57
1:A:137:ARG:HD3	3:A:434:HOH:O	2.03	0.57
1:A:293:ILE:HD11	1:A:298:ILE:HD12	1.87	0.56
1:A:106:ILE:CG2	1:A:111:ALA:HB2	2.35	0.56
1:A:277:ILE:CD1	1:A:277:ILE:H	2.13	0.56
1:A:211:LEU:O	1:A:215:VAL:HG23	2.05	0.56
1:A:283:ARG:NE	1:A:293:ILE:O	2.38	0.56
1:A:328:ARG:HD3	1:A:332:ASP:O	2.06	0.56
1:A:271:TYR:HB2	3:A:403:HOH:O	2.05	0.56
1:A:172:GLU:HG2	1:A:198:PRO:CG	2.35	0.56
1:A:194:LEU:HD21	1:A:272:PHE:CD2	2.40	0.56
1:A:260:ILE:HG21	1:A:265:TYR:HA	1.88	0.56
1:A:291:PHE:CA	1:A:301:LEU:HD13	2.37	0.55
1:A:332:ASP:N	1:A:332:ASP:OD1	2.38	0.55
1:A:110:ALA:O	1:A:113:LYS:HG2	2.06	0.55
1:A:125:LEU:CB	1:A:140:LEU:HD22	2.31	0.54
1:A:122:LEU:HD12	1:A:123:GLU:N	2.22	0.54
1:A:200:PHE:CD1	1:A:204:SER:HB2	2.42	0.54
1:A:132:LEU:HA	3:A:471:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:PHE:O	1:A:102:ARG:HB2	2.08	0.54
1:A:323:ILE:C	1:A:324:GLN:HG2	2.28	0.54
1:A:264:GLN:HG2	3:A:504:HOH:O	2.07	0.54
1:A:188:SER:HB3	3:A:501:HOH:O	2.06	0.54
1:A:239:CYS:SG	1:A:255:ILE:HB	2.48	0.54
1:A:285:HIS:O	1:A:288:GLU:N	2.35	0.54
1:A:92:ASP:HA	1:A:95:SER:HB2	1.90	0.53
1:A:113:LYS:HG3	1:A:114:LEU:CD1	2.35	0.53
1:A:135:HIS:HE1	1:A:228:LEU:HB3	1.68	0.53
1:A:127:LYS:N	1:A:127:LYS:HD3	2.23	0.53
1:A:291:PHE:HA	1:A:301:LEU:HD13	1.91	0.53
1:A:170:ASP:OD2	1:A:197:HIS:NE2	2.27	0.53
1:A:291:PHE:HD1	1:A:300:PRO:HA	1.73	0.53
1:A:193:VAL:O	1:A:194:LEU:HD12	2.08	0.53
1:A:183:ARG:HD2	1:A:333:ARG:HB2	1.91	0.53
1:A:196:THR:HG23	1:A:197:HIS:N	2.23	0.53
1:A:292:THR:HB	1:A:301:LEU:HD11	1.90	0.53
1:A:158:MET:HE2	1:A:191:MET:HE3	1.90	0.52
1:A:285:HIS:CD2	1:A:325:TRP:NE1	2.78	0.52
1:A:301:LEU:HD12	1:A:301:LEU:N	2.23	0.52
1:A:159:GLN:HG3	1:A:177:VAL:HG21	1.90	0.52
1:A:300:PRO:HD3	1:A:311:LEU:HD22	1.92	0.51
1:A:223:PHE:CZ	1:A:239:CYS:HB2	2.45	0.51
1:A:163:LEU:HD13	3:A:506:HOH:O	2.09	0.51
1:A:133:ASN:HD21	1:A:135:HIS:HB3	1.75	0.51
1:A:137:ARG:HB2	3:A:434:HOH:O	2.09	0.51
1:A:142:TYR:CE1	1:A:252:HIS:CG	2.98	0.51
1:A:303:VAL:C	1:A:305:GLY:H	2.14	0.51
1:A:300:PRO:HD3	1:A:311:LEU:HD21	1.92	0.51
1:A:129:GLU:HA	1:A:132:LEU:HD12	1.92	0.51
1:A:207:GLN:O	1:A:210:LEU:HB2	2.11	0.51
1:A:292:THR:N	1:A:301:LEU:HD11	2.25	0.51
1:A:110:ALA:HA	1:A:113:LYS:HE3	1.91	0.51
1:A:174:ILE:HA	3:A:427:HOH:O	2.10	0.51
1:A:133:ASN:HD22	1:A:134:HIS:N	2.09	0.50
1:A:155:MET:SD	1:A:158:MET:HE2	2.52	0.50
1:A:120:LYS:N	1:A:124:ASP:OD2	2.35	0.50
1:A:133:ASN:N	3:A:471:HOH:O	2.45	0.50
1:A:156:LEU:HD12	1:A:181:PHE:CZ	2.47	0.50
1:A:183:ARG:NH1	1:A:275:SER:HA	2.26	0.50
1:A:285:HIS:O	1:A:288:GLU:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:GLU:HG2	1:A:250:TYR:CE2	2.47	0.50
1:A:204:SER:HB3	1:A:207:GLN:HE21	1.77	0.50
1:A:254:ARG:NH1	1:A:256:ASP:OD1	2.45	0.49
1:A:110:ALA:O	1:A:114:LEU:HD13	2.12	0.49
1:A:159:GLN:HB2	1:A:177:VAL:HG21	1.94	0.49
1:A:142:TYR:CE1	1:A:252:HIS:ND1	2.80	0.49
1:A:299[A]:ARG:HG2	1:A:310:PRO:CA	2.42	0.49
1:A:189:GLY:O	1:A:190:ASP:HB3	2.12	0.49
1:A:292:THR:HG22	1:A:301:LEU:HD12	1.93	0.49
1:A:285:HIS:CE1	1:A:289:LYS:HG3	2.48	0.49
1:A:299[B]:ARG:HG2	1:A:310:PRO:HA	1.95	0.49
1:A:172:GLU:HG3	1:A:198:PRO:HG3	1.95	0.49
1:A:291:PHE:CD1	1:A:300:PRO:HA	2.48	0.49
1:A:232:GLU:HG3	1:A:233:THR:HG23	1.95	0.48
1:A:138:ILE:HB	1:A:228:LEU:HD23	1.96	0.48
1:A:235:PHE:CE1	1:A:237:GLY:HA3	2.48	0.48
1:A:270:LEU:CD1	1:A:282:MET:HE3	2.43	0.48
1:A:96:SER:O	1:A:99:PHE:N	2.46	0.48
1:A:234:LYS:O	1:A:234:LYS:HG2	2.12	0.48
1:A:254:ARG:NH2	1:A:256:ASP:OD1	2.44	0.48
1:A:227:THR:HG22	1:A:228:LEU:N	2.28	0.48
1:A:183:ARG:NH1	1:A:275:SER:CA	2.77	0.48
1:A:133:ASN:HD21	1:A:135:HIS:CB	2.26	0.48
1:A:159:GLN:HG3	1:A:177:VAL:HG23	1.94	0.48
1:A:224:ILE:HD13	1:A:235:PHE:CZ	2.47	0.48
1:A:91:ASP:C	1:A:93:THR:H	2.17	0.48
1:A:319:ILE:HG21	1:A:319:ILE:HD13	1.50	0.47
1:A:296:TYR:C	1:A:297:THR:HG23	2.34	0.47
1:A:159:GLN:N	1:A:191:MET:HE2	2.29	0.47
1:A:250:TYR:HB3	1:A:251:PRO:HD2	1.97	0.47
1:A:180:SER:OG	1:A:181:PHE:N	2.47	0.47
1:A:197:HIS:ND1	1:A:198:PRO:CD	2.77	0.47
1:A:215:VAL:HG11	1:A:235:PHE:CD2	2.50	0.47
1:A:223:PHE:CZ	1:A:239:CYS:CB	2.98	0.47
1:A:234:LYS:HE3	1:A:236:MET:CG	2.40	0.47
1:A:299[B]:ARG:HG2	1:A:310:PRO:N	2.29	0.47
1:A:197:HIS:CG	1:A:199:ASN:HB2	2.49	0.47
1:A:158:MET:HE2	1:A:191:MET:CE	2.45	0.47
1:A:328:ARG:HG3	3:A:430:HOH:O	2.14	0.47
1:A:278:PHE:HE2	1:A:328:ARG:CD	2.09	0.47
1:A:212:HIS:CD2	1:A:230:LYS:CE	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:ASP:O	1:A:94:SER:N	2.48	0.46
1:A:330:PRO:HA	1:A:333:ARG:NE	2.30	0.46
1:A:183:ARG:HH12	1:A:275:SER:HA	1.79	0.46
1:A:150:ILE:HA	1:A:151:PRO:HD2	1.69	0.46
1:A:114:LEU:CD1	1:A:114:LEU:N	2.79	0.46
1:A:306:VAL:O	1:A:307:ALA:HB2	2.16	0.46
1:A:331:LYS:HG2	3:A:429:HOH:O	2.14	0.46
1:A:208:PRO:HB3	1:A:232:GLU:CA	2.45	0.46
1:A:294:ASN:HB2	1:A:295:GLU:OE2	2.15	0.46
1:A:232:GLU:C	1:A:233:THR:HG23	2.36	0.45
1:A:201:THR:C	1:A:203:GLU:H	2.19	0.45
1:A:279:ASN:O	1:A:283:ARG:HG2	2.16	0.45
1:A:292:THR:N	1:A:301:LEU:CD1	2.78	0.45
1:A:271:TYR:N	3:A:403:HOH:O	2.50	0.45
1:A:300:PRO:HD3	1:A:311:LEU:CD1	2.46	0.45
1:A:285:HIS:NE2	1:A:289:LYS:HD2	2.31	0.45
1:A:289:LYS:CE	1:A:324:GLN:HG3	2.46	0.45
1:A:91:ASP:O	1:A:94:SER:HB3	2.17	0.45
1:A:323:ILE:O	1:A:324:GLN:HG2	2.17	0.45
1:A:204:SER:O	1:A:205:SER:HB2	2.17	0.45
1:A:149:ARG:HB3	1:A:149:ARG:HE	1.53	0.45
1:A:133:ASN:HD22	1:A:133:ASN:C	2.19	0.45
1:A:227:THR:CG2	1:A:228:LEU:N	2.80	0.45
1:A:163:LEU:CD2	1:A:175:ALA:HB3	2.47	0.45
1:A:163:LEU:HD21	1:A:175:ALA:HB3	1.99	0.45
1:A:179:GLY:O	1:A:182:ARG:N	2.44	0.45
1:A:228:LEU:N	1:A:236:MET:O	2.43	0.45
1:A:121:THR:O	1:A:124:ASP:HB2	2.17	0.44
1:A:122:LEU:O	1:A:125:LEU:N	2.50	0.44
1:A:113:LYS:O	1:A:117:GLU:HG2	2.17	0.44
1:A:104:THR:O	1:A:106:ILE:N	2.50	0.44
1:A:207:GLN:N	1:A:208:PRO:HD3	2.33	0.44
1:A:208:PRO:O	1:A:212:HIS:ND1	2.50	0.44
1:A:163:LEU:HD23	1:A:163:LEU:HA	1.54	0.43
1:A:316:GLU:O	1:A:319:ILE:HB	2.18	0.43
1:A:193:VAL:C	1:A:194:LEU:HD12	2.39	0.43
1:A:111:ALA:O	1:A:115:VAL:HG23	2.18	0.43
1:A:127:LYS:O	1:A:128:ASN:ND2	2.52	0.43
1:A:156:LEU:HD12	1:A:181:PHE:HZ	1.83	0.43
1:A:289:LYS:HD3	1:A:324:GLN:CG	2.49	0.43
1:A:207:GLN:HB2	1:A:210:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:SER:C	1:A:206:LYS:HE2	2.38	0.43
1:A:138:ILE:HD12	1:A:226:ASP:OD2	2.19	0.42
1:A:205:SER:O	1:A:206:LYS:HB3	2.19	0.42
1:A:146:PHE:N	1:A:146:PHE:HD1	2.18	0.42
1:A:107:GLY:O	1:A:111:ALA:N	2.44	0.42
1:A:159:GLN:CG	1:A:177:VAL:HG21	2.49	0.42
1:A:145:ASP:CB	1:A:252:HIS:H	2.32	0.42
1:A:200:PHE:CD2	1:A:259:LEU:HD23	2.53	0.42
1:A:142:TYR:CD1	1:A:252:HIS:HB2	2.54	0.42
1:A:154:GLU:CG	1:A:250:TYR:HE2	2.31	0.42
1:A:105:GLY:HA2	1:A:135:HIS:HD2	1.85	0.42
1:A:250:TYR:CD1	1:A:250:TYR:N	2.86	0.42
1:A:228:LEU:HD23	1:A:228:LEU:HA	1.94	0.42
1:A:300:PRO:C	1:A:301:LEU:HD12	2.40	0.42
1:A:311:LEU:CD1	1:A:311:LEU:N	2.82	0.42
1:A:194:LEU:HB3	1:A:265:TYR:HE1	1.85	0.42
1:A:225:THR:O	1:A:226:ASP:OD1	2.38	0.41
1:A:169:LEU:HD21	1:A:217:GLN:HE21	1.85	0.41
1:A:204:SER:HA	1:A:206:LYS:CE	2.47	0.41
1:A:181:PHE:CD1	1:A:181:PHE:C	2.93	0.41
1:A:299[B]:ARG:HG2	1:A:310:PRO:CA	2.50	0.41
1:A:146:PHE:N	1:A:146:PHE:CD1	2.88	0.41
1:A:122:LEU:O	1:A:126:ARG:HG3	2.20	0.41
1:A:163:LEU:HD21	1:A:175:ALA:O	2.20	0.41
1:A:270:LEU:HD11	1:A:282:MET:CE	2.48	0.41
1:A:193:VAL:HG12	1:A:194:LEU:N	2.34	0.41
1:A:112:ARG:O	1:A:115:VAL:HG23	2.20	0.41
1:A:207:GLN:HA	3:A:473:HOH:O	2.20	0.41
1:A:215:VAL:O	1:A:219:GLN:HG2	2.21	0.41
1:A:114:LEU:H	1:A:114:LEU:HD12	1.86	0.41
1:A:299[B]:ARG:HD2	3:A:459:HOH:O	2.21	0.41
1:A:271:TYR:CG	1:A:295:GLU:HB3	2.56	0.41
1:A:104:THR:N	3:A:435:HOH:O	2.27	0.40
1:A:158:MET:CE	1:A:191:MET:CE	2.99	0.40
1:A:285:HIS:HE2	1:A:289:LYS:HD2	1.86	0.40
1:A:217:GLN:O	1:A:220:LYS:HB3	2.21	0.40
1:A:254:ARG:CZ	1:A:254:ARG:HB3	2.50	0.40
1:A:274:GLY:HA3	1:A:275:SER:HA	1.91	0.40
1:A:166:VAL:CG1	1:A:173:TYR:HB3	2.52	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)
3:A:477:HOH:O	3:A:477:HOH:O[2_555]	0.85	1.35
1:A:206:LYS:NZ	1:A:206:LYS:NZ[2_555]	1.92	0.28

## 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%)	191 (80%)	35 (15%)	13 (5%)	<b>2</b> <b>4</b>

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	GLU
1	A	204	SER
1	A	206	LYS
1	A	309	GLU
1	A	146	PHE
1	A	205	SER
1	A	180	SER
1	A	310	PRO
1	A	145	ASP
1	A	202	SER
1	A	125	LEU
1	A	126	ARG
1	A	238	VAL

### 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	207/226 (92%)	183 (88%)	24 (12%)	7 16

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93	THR
1	A	115	VAL
1	A	122	LEU
1	A	133	ASN
1	A	152	ARG
1	A	155	MET
1	A	156	LEU
1	A	158	MET
1	A	159	GLN
1	A	173	TYR
1	A	188	SER
1	A	196	THR
1	A	203	GLU
1	A	219	GLN
1	A	226	ASP
1	A	259	LEU
1	A	277	ILE
1	A	288	GLU
1	A	294	ASN
1	A	299[A]	ARG
1	A	299[B]	ARG
1	A	311	LEU
1	A	317	GLN
1	A	332	ASP

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

Mol	Chain	Res	Type
1	A	128	ASN
1	A	133	ASN
1	A	135	HIS
1	A	136	GLN
1	A	207	GLN
1	A	217	GLN
1	A	281	ASN
1	A	294	ASN
1	A	317	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	242/248 (97%)	0.63	24 (9%) <b>9</b> <b>7</b>	10, 39, 87, 100	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	91	ASP	8.7
1	A	205	SER	5.3
1	A	92	ASP	4.9
1	A	306	VAL	4.6
1	A	244	GLU	4.3
1	A	304	THR	3.8
1	A	124	ASP	3.7
1	A	245	ASN	3.6
1	A	116	ASP	3.5
1	A	112	ARG	3.3
1	A	108	PRO	3.2
1	A	93	THR	3.2
1	A	122	LEU	3.0
1	A	305	GLY	2.7
1	A	113	LYS	2.6
1	A	302	GLY	2.5
1	A	139	GLY	2.4
1	A	277	ILE	2.3
1	A	249	GLU	2.3
1	A	94	SER	2.2
1	A	115	VAL	2.2
1	A	119	ILE	2.2
1	A	153	GLU	2.2
1	A	144	GLU	2.1

## 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	CA	A	340	1/1	0.84	0.19	-	67,67,67,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.