Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 12:06 AM GMT

PDB ID	:	1ZQO
Title	:	DNA POLYMERASE BETA (POL B) (E.C.2.7.7.7) COMPLEXED WITH SEVEN BASE PAIRS OF DNA; SOAKED IN THE PRESENCE OF CACL2 (15 MILLIMOLAR) AND NACL (15 MILLIMOLAR)
Authors	:	Pelletier, H.; Sawaya, M.R.
Deposited on	:	1996-04-12
Resolution	:	3.20 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:

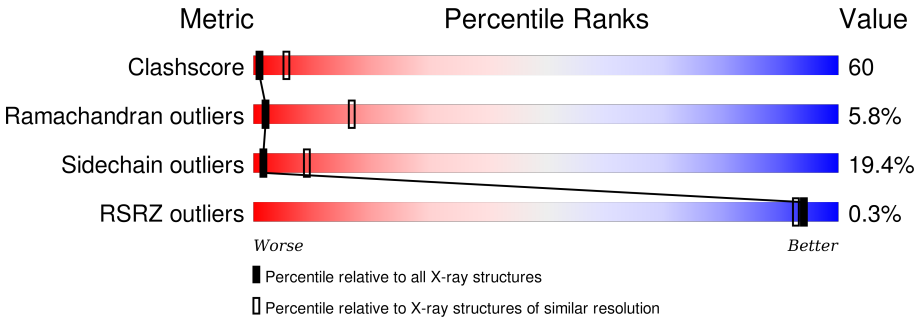
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	T	8	13% 13% 75%
2	P	7	14% 86%
3	A	335	21% 47% 25%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3059 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 DNA chain called DNA (5'-D(*CP*AP*TP*TP*AP*GP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	8	Total	C	N	O	P	0	0	0
			145	69	27	42	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	P	0	0	0
			144	69	24	44	7			

- Molecule 3 is a protein called PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	327	Total	C	N	O	S	18	0	0
			2623	1657	458	499	9			

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Na	0	0
			2	2		

- Molecule 5 is water.

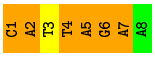
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	108	Total	O	0	0
			108	108		
5	P	22	Total	O	0	0
			22	22		
5	T	15	Total	O	0	0
			15	15		

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.

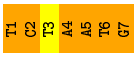
- Molecule 1: DNA (5'-D(*CP*AP*TP*TP*AP*GP*AP*A)-3')

Chain T:



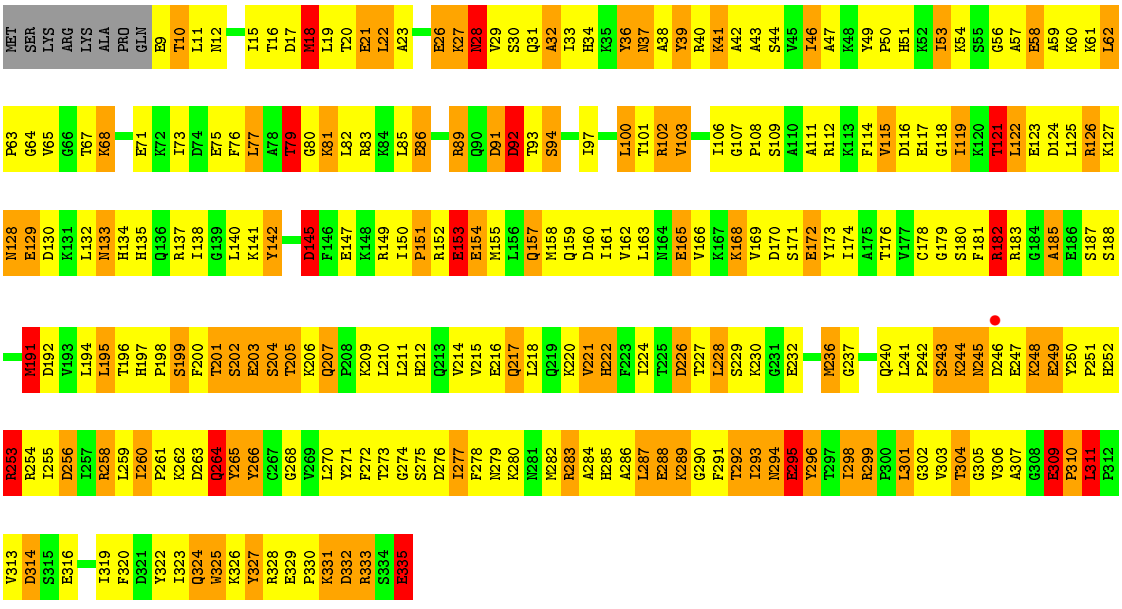
- Molecule 2: DNA (5'-D(*TP*CP*TP*AP*AP*TP*G)-3')

Chain P:



- Molecule 3: PROTEIN (DNA POLYMERASE BETA (E.C.2.7.7.7))

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	178.69Å 57.74Å 48.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 9.73 – 2.64	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-3.20) 86.6 (9.73-2.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.35 (at 2.63Å)	Xtriage
Refinement program	TNT V. 5-D	Depositor
R, R_{free}	0.159 , (Not available) 0.155 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	24.8	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.11 , 117.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.23$	Xtriage
Outliers	1 of 13035 reflections (0.008%)	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	3059	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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

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

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	T	2.83	10/162 (6.2%)	3.18	13/249 (5.2%)
2	P	2.93	14/160 (8.8%)	3.25	11/243 (4.5%)
3	A	1.25	26/2672 (1.0%)	1.97	71/3590 (2.0%)
All	All	1.52	50/2994 (1.7%)	2.16	95/4082 (2.3%)

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
3	A	3	0

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	6	DG	C3'-O3'	-13.54	1.26	1.44
2	P	3	DT	N1-C6	-9.89	1.31	1.38
2	P	2	DC	C1'-N1	9.74	1.61	1.49
1	T	5	DA	P-O5'	9.29	1.69	1.59
2	P	1	DT	C1'-N1	-9.22	1.34	1.47
1	T	1	DC	C3'-O3'	9.16	1.55	1.44
3	A	147	GLU	CD-OE2	8.68	1.35	1.25
3	A	129	GLU	CD-OE1	8.62	1.35	1.25
1	T	5	DA	N3-C4	8.31	1.39	1.34
3	A	153	GLU	CD-OE2	8.20	1.34	1.25
2	P	3	DT	C5-C7	7.99	1.54	1.50
2	P	5	DA	N9-C4	7.76	1.42	1.37
3	A	71	GLU	CD-OE1	7.65	1.34	1.25
3	A	288	GLU	CD-OE2	7.55	1.33	1.25
3	A	86	GLU	CD-OE1	7.51	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	117	GLU	CD-OE2	7.39	1.33	1.25
3	A	58	GLU	CD-OE1	7.12	1.33	1.25
1	T	4	DT	N1-C6	-7.11	1.33	1.38
3	A	154	GLU	CD-OE2	6.70	1.33	1.25
3	A	172	GLU	CD-OE2	6.64	1.32	1.25
3	A	249	GLU	CD-OE2	6.60	1.32	1.25
1	T	4	DT	C3'-C2'	6.58	1.60	1.52
3	A	335	GLU	CD-OE2	6.53	1.32	1.25
3	A	26	GLU	CD-OE1	6.49	1.32	1.25
3	A	203	GLU	CD-OE1	6.47	1.32	1.25
3	A	75	GLU	CD-OE1	6.44	1.32	1.25
1	T	5	DA	C1'-N9	-6.42	1.38	1.47
2	P	5	DA	N3-C4	6.19	1.38	1.34
3	A	232	GLU	CD-OE2	6.04	1.32	1.25
3	A	295	GLU	CD-OE2	6.04	1.32	1.25
2	P	5	DA	C3'-C2'	6.02	1.59	1.52
3	A	309	GLU	CD-OE2	5.97	1.32	1.25
1	T	5	DA	C6-N1	5.93	1.39	1.35
3	A	216	GLU	CD-OE2	5.92	1.32	1.25
2	P	2	DC	C5'-C4'	5.79	1.57	1.51
3	A	329	GLU	CD-OE2	5.69	1.31	1.25
2	P	4	DA	C3'-O3'	-5.67	1.36	1.44
3	A	123	GLU	CD-OE1	5.67	1.31	1.25
2	P	3	DT	N3-C4	-5.54	1.34	1.38
2	P	3	DT	N1-C2	5.48	1.42	1.38
3	A	165	GLU	CD-OE2	5.46	1.31	1.25
1	T	5	DA	C4'-O4'	-5.42	1.39	1.45
2	P	5	DA	C3'-O3'	-5.35	1.36	1.44
2	P	3	DT	C2-N3	-5.34	1.33	1.37
3	A	147	GLU	CD-OE1	-5.32	1.19	1.25
3	A	247	GLU	CD-OE1	5.30	1.31	1.25
3	A	9	GLU	CD-OE2	5.16	1.31	1.25
1	T	4	DT	C1'-N1	-5.13	1.40	1.47
2	P	1	DT	C4'-O4'	-5.12	1.40	1.45
3	A	21	GLU	CD-OE1	5.04	1.31	1.25

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	T	6	DG	C8-N9-C1'	21.36	154.76	127.00
1	T	6	DG	C4-N9-C1'	-21.19	98.95	126.50
2	P	7	DG	C8-N9-C1'	20.14	153.18	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	P	7	DG	C4-N9-C1'	-19.73	100.85	126.50
2	P	1	DT	C6-N1-C1'	-17.49	94.16	120.40
1	T	7	DA	C4-N9-C1'	-16.49	96.62	126.30
1	T	7	DA	C8-N9-C1'	16.23	156.91	127.70
2	P	1	DT	C2-N1-C1'	15.71	143.33	118.20
1	T	4	DT	C6-N1-C1'	-15.44	97.25	120.40
2	P	6	DT	C6-N1-C1'	-14.34	98.89	120.40
1	T	4	DT	C2-N1-C1'	13.79	140.26	118.20
2	P	6	DT	C2-N1-C1'	13.47	139.75	118.20
2	P	2	DC	C2-N1-C1'	13.20	133.32	118.80
3	A	258	ARG	NE-CZ-NH1	12.72	126.66	120.30
3	A	182	ARG	NE-CZ-NH1	12.72	126.66	120.30
2	P	2	DC	C6-N1-C1'	-11.77	106.67	120.80
2	P	5	DA	C4-N9-C1'	10.55	145.30	126.30
2	P	5	DA	C8-N9-C1'	-10.38	109.01	127.70
3	A	192	ASP	CB-CG-OD2	-9.93	109.36	118.30
3	A	258	ARG	NE-CZ-NH2	-9.74	115.43	120.30
3	A	256	ASP	CB-CG-OD2	-9.31	109.92	118.30
3	A	130	ASP	CB-CG-OD2	-9.24	109.98	118.30
3	A	299	ARG	NE-CZ-NH1	9.13	124.86	120.30
3	A	173	TYR	CB-CG-CD1	-8.79	115.73	121.00
3	A	116	ASP	CB-CG-OD1	8.77	126.19	118.30
3	A	224	ILE	CA-CB-CG1	-8.69	94.50	111.00
3	A	126	ARG	NE-CZ-NH2	-8.64	115.98	120.30
3	A	145	ASP	CB-CG-OD2	-8.59	110.57	118.30
3	A	39	TYR	CB-CG-CD1	-8.10	116.14	121.00
3	A	263	ASP	CB-CG-OD2	-8.03	111.08	118.30
3	A	57	ALA	N-CA-CB	-8.00	98.90	110.10
3	A	79	THR	CA-CB-CG2	-8.00	101.20	112.40
1	T	5	DA	C4-N9-C1'	-7.93	112.03	126.30
3	A	332	ASP	CB-CG-OD1	-7.92	111.17	118.30
3	A	116	ASP	CB-CG-OD2	-7.79	111.28	118.30
3	A	192	ASP	CB-CG-OD1	7.70	125.23	118.30
3	A	333	ARG	NE-CZ-NH1	7.69	124.14	120.30
3	A	253	ARG	NE-CZ-NH2	-7.67	116.47	120.30
3	A	256	ASP	CB-CG-OD1	7.66	125.19	118.30
3	A	283	ARG	NE-CZ-NH1	7.45	124.03	120.30
3	A	91	ASP	CB-CG-OD1	-7.37	111.67	118.30
3	A	39	TYR	CB-CG-CD2	7.37	125.42	121.00
3	A	253	ARG	NE-CZ-NH1	7.31	123.95	120.30
1	T	5	DA	C8-N9-C1'	7.20	140.66	127.70
3	A	168	LYS	N-CA-CB	7.17	123.50	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	264	GLN	N-CA-CB	7.08	123.34	110.60
3	A	160	ASP	CB-CG-OD2	-6.81	112.17	118.30
3	A	195	LEU	CB-CG-CD1	-6.79	99.45	111.00
3	A	18	MET	CG-SD-CE	-6.75	89.41	100.20
3	A	333	ARG	NE-CZ-NH2	-6.73	116.93	120.30
3	A	116	ASP	CB-CA-C	6.35	123.10	110.40
3	A	121	THR	CA-CB-CG2	-6.34	103.53	112.40
3	A	103	VAL	CA-CB-CG1	-6.27	101.49	110.90
3	A	28	ASN	CA-CB-CG	-6.27	99.61	113.40
3	A	157	GLN	N-CA-CB	6.26	121.88	110.60
3	A	226	ASP	CB-CG-OD1	6.21	123.89	118.30
3	A	266	TYR	CA-CB-CG	-6.16	101.69	113.40
3	A	130	ASP	CB-CG-OD1	6.12	123.81	118.30
3	A	222	HIS	N-CA-CB	6.11	121.60	110.60
1	T	5	DA	O4'-C1'-N9	-6.07	103.75	108.00
3	A	296	TYR	CB-CG-CD2	-5.85	117.49	121.00
3	A	151	PRO	N-CA-CB	5.84	110.31	103.30
1	T	2	DA	C4-N9-C1'	-5.78	115.89	126.30
3	A	142	TYR	CG-CD1-CE1	-5.78	116.67	121.30
3	A	157	GLN	CB-CA-C	5.77	121.95	110.40
3	A	243	SER	CB-CA-C	5.77	121.06	110.10
3	A	246	ASP	CB-CG-OD1	-5.72	113.15	118.30
3	A	53	ILE	CB-CA-C	5.71	123.02	111.60
3	A	314	ASP	CB-CG-OD1	-5.67	113.20	118.30
3	A	241	LEU	CB-CG-CD1	-5.65	101.39	111.00
3	A	160	ASP	CB-CG-OD1	5.64	123.38	118.30
3	A	89	ARG	NE-CZ-NH1	5.60	123.10	120.30
3	A	36	TYR	CB-CG-CD2	-5.59	117.64	121.00
3	A	126	ARG	NE-CZ-NH1	5.59	123.09	120.30
3	A	227	THR	N-CA-CB	5.56	120.86	110.30
3	A	17	ASP	CB-CA-C	5.55	121.51	110.40
1	T	3	DT	C2-N1-C1'	-5.54	109.34	118.20
3	A	92	ASP	CB-CG-OD1	-5.50	113.35	118.30
3	A	102	ARG	CD-NE-CZ	-5.46	115.95	123.60
3	A	68	LYS	CB-CA-C	5.44	121.28	110.40
3	A	260	ILE	CB-CA-C	-5.40	100.79	111.60
3	A	122	LEU	CB-CG-CD2	-5.38	101.85	111.00
3	A	27	LYS	N-CA-CB	-5.32	101.02	110.60
3	A	115	VAL	CA-CB-CG1	-5.31	102.93	110.90
3	A	40	ARG	N-CA-CB	5.31	120.16	110.60
3	A	116	ASP	N-CA-CB	5.28	120.11	110.60
1	T	3	DT	C6-N1-C1'	5.23	128.25	120.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	T	2	DA	C8-N9-C1'	5.17	137.01	127.70
3	A	176	THR	CA-CB-CG2	-5.17	105.16	112.40
3	A	253	ARG	CD-NE-CZ	5.14	130.79	123.60
3	A	263	ASP	CB-CG-OD1	5.13	122.92	118.30
2	P	3	DT	C5-C6-N1	-5.12	120.62	123.70
3	A	311	LEU	CB-CG-CD2	-5.11	102.32	111.00
3	A	102	ARG	CA-CB-CG	-5.07	102.24	113.40
3	A	191	MET	N-CA-CB	5.02	119.63	110.60

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	68	LYS	CA
3	A	205	THR	CA
3	A	264	GLN	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	T	145	0	80	8	0
2	P	144	0	81	20	0
3	A	2623	0	2641	317	0
4	A	2	0	0	0	0
5	A	108	0	0	15	0
5	P	22	0	0	3	0
5	T	15	0	0	1	0
All	All	3059	0	2802	342	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 60.

All (342) 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)
2:P:6:DT:H2"	2:P:7:DG:H5"	1.18	1.12
2:P:5:DA:H2"	2:P:6:DT:H5"	1.33	1.09
3:A:182:ARG:HG2	3:A:182:ARG:HH11	1.25	1.02
3:A:165:GLU:HB3	3:A:217:GLN:HG3	1.41	1.02
3:A:245:ASN:ND2	3:A:245:ASN:H	1.62	0.97
3:A:41:LYS:HE2	3:A:64:GLY:HA3	1.46	0.96
1:T:6:DG:H2"	1:T:7:DA:C8	2.02	0.95
3:A:245:ASN:N	3:A:245:ASN:HD22	1.54	0.94
2:P:5:DA:H2"	2:P:6:DT:C5'	1.98	0.93
3:A:201:THR:HA	3:A:261:PRO:HB3	1.52	0.92
3:A:293:ILE:HD13	3:A:298:ILE:HG13	1.51	0.90
3:A:243:SER:HB3	3:A:249:GLU:HA	1.56	0.88
3:A:103:VAL:HB	3:A:106:ILE:HD12	1.57	0.86
3:A:73:ILE:HG22	3:A:77:LEU:HD22	1.57	0.85
3:A:178:CYS:SG	3:A:194:LEU:HD22	2.16	0.84
3:A:49:TYR:CD1	3:A:50:PRO:HD2	2.14	0.82
3:A:255:ILE:HG12	3:A:256:ASP:N	1.96	0.81
3:A:330:PRO:HA	3:A:333:ARG:CG	2.10	0.81
3:A:197:HIS:CD2	3:A:198:PRO:HD2	2.17	0.80
3:A:29:VAL:HG21	3:A:94:SER:HB2	1.65	0.79
2:P:6:DT:C2'	2:P:7:DG:H5"	2.09	0.78
3:A:41:LYS:HE2	3:A:64:GLY:CA	2.14	0.77
3:A:127:LYS:HB2	3:A:128:ASN:ND2	2.00	0.77
3:A:155:MET:HE2	3:A:188:SER:HB2	1.66	0.76
3:A:165:GLU:HA	3:A:168:LYS:HG2	1.68	0.75
3:A:180:SER:HB3	3:A:183:ARG:HH21	1.52	0.74
3:A:201:THR:HA	3:A:261:PRO:CB	2.18	0.74
3:A:19:LEU:HD23	3:A:43:ALA:HA	1.69	0.73
3:A:26:GLU:HA	3:A:30:SER:OG	1.87	0.73
3:A:331:LYS:HG2	3:A:332:ASP:N	2.02	0.73
1:T:1:DC:H2"	1:T:2:DA:OP2	1.89	0.73
3:A:245:ASN:HD22	3:A:245:ASN:H	0.78	0.72
3:A:330:PRO:HA	3:A:333:ARG:HG2	1.71	0.72
3:A:293:ILE:CD1	3:A:298:ILE:HG13	2.18	0.72
3:A:18:MET:HE1	3:A:76:PHE:HB2	1.72	0.72
3:A:59:ALA:O	3:A:62:LEU:HB2	1.90	0.71
3:A:11:LEU:HD23	3:A:11:LEU:H	1.54	0.71
3:A:31:GLN:NE2	3:A:112:ARG:HH12	1.89	0.71
3:A:28:ASN:ND2	3:A:28:ASN:N	2.34	0.70
3:A:278:PHE:CE2	3:A:333:ARG:HD2	2.25	0.70
2:P:6:DT:H2"	2:P:7:DG:C5'	2.10	0.70
3:A:294:ASN:O	3:A:296:TYR:N	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:330:PRO:HA	3:A:333:ARG:HG3	1.74	0.70
3:A:277:ILE:HD11	3:A:335:GLU:HB3	1.74	0.70
3:A:323:ILE:O	3:A:324:GLN:HG2	1.91	0.69
3:A:155:MET:CE	3:A:188:SER:HB2	2.22	0.69
3:A:29:VAL:HG21	3:A:94:SER:CB	2.22	0.69
3:A:15:ILE:HB	3:A:46:ILE:HD11	1.74	0.69
3:A:289:LYS:N	3:A:289:LYS:HD3	2.07	0.68
3:A:16:THR:HG21	3:A:47:ALA:HB2	1.76	0.68
3:A:92:ASP:HB3	5:A:647:HOH:O	1.94	0.67
3:A:73:ILE:HG22	3:A:77:LEU:CD2	2.24	0.67
3:A:306:VAL:HG22	5:A:650:HOH:O	1.93	0.67
3:A:172:GLU:HB3	3:A:197:HIS:NE2	2.08	0.67
3:A:182:ARG:NH1	3:A:182:ARG:HG2	1.97	0.67
3:A:108:PRO:O	3:A:112:ARG:HG3	1.95	0.67
3:A:29:VAL:HA	3:A:97:ILE:HD12	1.76	0.67
3:A:128:ASN:N	3:A:128:ASN:HD22	1.93	0.66
3:A:180:SER:CB	3:A:183:ARG:HH21	2.07	0.66
3:A:140:LEU:HD12	3:A:140:LEU:O	1.96	0.66
3:A:327:TYR:HD1	3:A:328:ARG:N	1.92	0.66
3:A:49:TYR:CG	3:A:50:PRO:HD2	2.30	0.66
3:A:253:ARG:NH1	5:A:503:HOH:O	2.29	0.66
3:A:180:SER:CA	3:A:183:ARG:HH21	2.08	0.66
3:A:295:GLU:OE1	3:A:295:GLU:N	2.28	0.66
3:A:323:ILE:C	3:A:324:GLN:HG2	2.15	0.66
3:A:128:ASN:N	3:A:128:ASN:ND2	2.45	0.65
3:A:12:ASN:HD21	3:A:53:ILE:H	1.44	0.65
3:A:121:THR:HG23	3:A:124:ASP:OD1	1.97	0.65
3:A:169:VAL:HG13	3:A:170:ASP:H	1.62	0.64
3:A:180:SER:HA	3:A:183:ARG:HH21	1.62	0.64
3:A:291:PHE:HD2	3:A:323:ILE:HG22	1.61	0.64
3:A:217:GLN:HA	3:A:217:GLN:NE2	2.12	0.64
3:A:236:MET:HG3	3:A:256:ASP:OD1	1.98	0.64
3:A:180:SER:HB3	3:A:183:ARG:NH2	2.12	0.63
3:A:157:GLN:HE22	3:A:244:LYS:NZ	1.95	0.63
3:A:277:ILE:CG1	3:A:335:GLU:HB2	2.28	0.63
3:A:133:ASN:ND2	3:A:135:HIS:H	1.94	0.63
3:A:159:GLN:O	3:A:163:LEU:HG	1.97	0.63
3:A:182:ARG:NH1	3:A:273:THR:OG1	2.29	0.63
3:A:93:THR:HG22	3:A:94:SER:N	2.12	0.63
3:A:285:HIS:NE2	3:A:289:LYS:HG2	2.13	0.63
3:A:201:THR:CA	3:A:261:PRO:HB3	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:23:ALA:HB2	3:A:39:TYR:HB2	1.80	0.63
3:A:15:ILE:O	3:A:19:LEU:HB2	1.98	0.63
3:A:83:ARG:O	3:A:86:GLU:N	2.31	0.63
3:A:27:LYS:HB2	3:A:36:TYR:CD1	2.34	0.63
3:A:169:VAL:HG13	3:A:170:ASP:N	2.12	0.63
3:A:270:LEU:HD21	3:A:282:MET:CE	2.29	0.62
3:A:204:SER:O	3:A:206:LYS:N	2.32	0.62
3:A:320:PHE:CE2	3:A:328:ARG:HG3	2.34	0.62
3:A:286:ALA:CB	3:A:323:ILE:HG21	2.30	0.62
3:A:18:MET:CE	3:A:76:PHE:HB2	2.29	0.62
3:A:58:GLU:O	3:A:61:LYS:HG3	2.00	0.62
3:A:211:LEU:O	3:A:211:LEU:HD12	1.99	0.62
3:A:12:ASN:HA	5:A:553:HOH:O	2.00	0.62
3:A:23:ALA:HB2	3:A:39:TYR:CB	2.28	0.62
3:A:242:PRO:HB2	5:A:589:HOH:O	1.98	0.62
3:A:248:LYS:HG2	3:A:248:LYS:O	1.99	0.62
3:A:260:ILE:HG23	3:A:261:PRO:HD2	1.82	0.62
3:A:79:THR:O	3:A:81:LYS:N	2.32	0.62
3:A:125:LEU:HD22	3:A:132:LEU:HD21	1.82	0.61
3:A:327:TYR:HE1	3:A:333:ARG:HH21	1.46	0.61
3:A:197:HIS:CG	3:A:198:PRO:HD2	2.36	0.61
3:A:253:ARG:HG3	3:A:253:ARG:HH11	1.66	0.61
3:A:243:SER:CB	3:A:249:GLU:HA	2.28	0.61
3:A:27:LYS:HG3	3:A:28:ASN:ND2	2.15	0.60
2:P:5:DA:H1'	5:P:565:HOH:O	1.99	0.60
3:A:38:ALA:O	3:A:41:LYS:HD3	2.02	0.60
3:A:278:PHE:HB2	3:A:333:ARG:O	2.01	0.60
3:A:111:ALA:O	3:A:115:VAL:HG23	2.00	0.60
3:A:209:LYS:HA	3:A:212:HIS:HB2	1.84	0.60
3:A:264:GLN:NE2	3:A:296:TYR:HB3	2.17	0.60
3:A:28:ASN:HD22	3:A:28:ASN:N	1.79	0.59
3:A:82:LEU:HB3	3:A:85:LEU:HB2	1.84	0.59
3:A:41:LYS:HD3	3:A:42:ALA:H	1.67	0.59
3:A:254:ARG:NH2	5:A:657:HOH:O	2.35	0.59
3:A:82:LEU:HD23	3:A:85:LEU:HB2	1.84	0.59
3:A:16:THR:O	3:A:20:THR:HG23	2.03	0.59
3:A:328:ARG:O	3:A:333:ARG:NE	2.30	0.58
3:A:292:THR:O	3:A:298:ILE:HA	2.04	0.58
3:A:174:ILE:O	3:A:195:LEU:HD12	2.03	0.58
3:A:18:MET:O	3:A:21:GLU:HB2	2.03	0.58
3:A:163:LEU:N	3:A:163:LEU:HD23	2.15	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:31:GLN:N	5:A:641:HOH:O	2.28	0.58
3:A:207:GLN:HB3	3:A:210:LEU:HG	1.85	0.58
3:A:31:GLN:HE21	3:A:112:ARG:HH12	1.50	0.58
3:A:270:LEU:HA	3:A:316:GLU:OE2	2.04	0.57
3:A:129:GLU:HG2	3:A:137:ARG:HD3	1.86	0.57
3:A:121:THR:HG23	3:A:124:ASP:CG	2.24	0.57
3:A:119:ILE:CG2	3:A:124:ASP:HB3	2.35	0.57
3:A:49:TYR:CE2	3:A:51:HIS:HB2	2.40	0.57
3:A:217:GLN:HA	3:A:217:GLN:HE21	1.70	0.57
3:A:124:ASP:O	3:A:128:ASN:ND2	2.38	0.56
3:A:149:ARG:NH2	3:A:188:SER:HA	2.20	0.56
3:A:286:ALA:HB2	3:A:323:ILE:HG21	1.87	0.56
3:A:97:ILE:HG23	3:A:111:ALA:HB1	1.87	0.56
3:A:287:LEU:HD13	3:A:291:PHE:O	2.05	0.56
3:A:141:LYS:HE2	3:A:142:TYR:CZ	2.40	0.56
3:A:316:GLU:O	3:A:320:PHE:HD1	1.89	0.56
3:A:202:SER:N	3:A:261:PRO:HB3	2.21	0.56
3:A:291:PHE:CD2	3:A:323:ILE:HG22	2.41	0.56
3:A:286:ALA:O	3:A:291:PHE:N	2.38	0.56
3:A:133:ASN:O	3:A:137:ARG:HG3	2.06	0.56
3:A:60:LYS:HA	3:A:65:VAL:HG12	1.87	0.56
3:A:299:ARG:CD	3:A:310:PRO:HD3	2.36	0.56
3:A:103:VAL:CB	3:A:106:ILE:HD12	2.32	0.56
2:P:4:DA:H5'	5:P:569:HOH:O	2.07	0.55
3:A:262:LYS:HG3	3:A:262:LYS:O	2.06	0.55
3:A:260:ILE:HG22	3:A:261:PRO:N	2.21	0.55
3:A:276:ASP:O	3:A:280:LYS:HG3	2.06	0.55
3:A:309:GLU:N	3:A:309:GLU:OE1	2.40	0.54
3:A:274:GLY:O	3:A:278:PHE:HD2	1.91	0.54
3:A:254:ARG:NH1	3:A:254:ARG:HB3	2.22	0.54
3:A:56:GLY:O	3:A:59:ALA:HB3	2.08	0.54
3:A:319:ILE:O	3:A:322:TYR:HB2	2.07	0.54
3:A:34:HIS:O	3:A:38:ALA:N	2.39	0.53
3:A:76:PHE:HD1	3:A:77:LEU:HD12	1.73	0.53
1:T:5:DA:H2"	1:T:6:DG:O5'	2.08	0.53
3:A:255:ILE:HG12	3:A:256:ASP:H	1.72	0.53
1:T:4:DT:H2"	1:T:5:DA:C8	2.43	0.53
3:A:253:ARG:HH11	3:A:253:ARG:CG	2.21	0.53
3:A:152:ARG:HA	3:A:155:MET:HB2	1.90	0.53
2:P:2:DC:H1'	5:P:635:HOH:O	2.08	0.53
3:A:244:LYS:HB3	3:A:245:ASN:HD22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:330:PRO:CA	3:A:333:ARG:HG2	2.38	0.52
3:A:18:MET:HE1	3:A:76:PHE:CB	2.40	0.52
3:A:151:PRO:HB2	3:A:153:GLU:HG2	1.91	0.52
2:P:6:DT:H2'	2:P:7:DG:C8	2.44	0.52
3:A:33:ILE:O	3:A:36:TYR:HD2	1.93	0.52
3:A:260:ILE:CG2	3:A:261:PRO:HD2	2.40	0.52
3:A:271:TYR:CE1	3:A:283:ARG:NH2	2.78	0.52
3:A:181:PHE:HD1	5:A:530:HOH:O	1.93	0.52
3:A:288:GLU:C	3:A:290:GLY:H	2.14	0.52
3:A:180:SER:HB2	3:A:185:ALA:CB	2.40	0.52
3:A:53:ILE:HG21	3:A:59:ALA:HB2	1.92	0.52
3:A:240:GLN:NE2	3:A:252:HIS:CE1	2.78	0.51
2:P:5:DA:H2'	2:P:6:DT:H71	1.93	0.51
3:A:270:LEU:HD21	3:A:282:MET:HE1	1.92	0.51
3:A:293:ILE:HA	5:A:593:HOH:O	2.09	0.51
2:P:5:DA:C2'	2:P:6:DT:H5"	2.22	0.51
3:A:311:LEU:HB3	3:A:322:TYR:CE2	2.45	0.51
3:A:33:ILE:HG23	3:A:34:HIS:H	1.76	0.51
3:A:295:GLU:HA	5:A:592:HOH:O	2.11	0.51
3:A:73:ILE:O	3:A:77:LEU:HD13	2.11	0.51
3:A:254:ARG:NH1	3:A:255:ILE:N	2.58	0.51
3:A:197:HIS:CE1	3:A:199:SER:HB3	2.46	0.51
3:A:244:LYS:HB3	3:A:245:ASN:ND2	2.26	0.50
3:A:201:THR:HA	3:A:261:PRO:CA	2.41	0.50
3:A:121:THR:O	3:A:124:ASP:HB2	2.11	0.50
3:A:150:ILE:HG21	3:A:158:MET:HE1	1.93	0.50
3:A:183:ARG:HH11	3:A:275:SER:HB3	1.76	0.50
3:A:220:LYS:O	3:A:220:LYS:HG2	2.09	0.50
3:A:282:MET:HB2	3:A:325:TRP:CZ3	2.46	0.50
3:A:240:GLN:NE2	3:A:250:TYR:O	2.44	0.50
3:A:135:HIS:O	3:A:138:ILE:HB	2.12	0.50
3:A:277:ILE:HD11	3:A:335:GLU:CB	2.41	0.50
3:A:277:ILE:HG13	3:A:335:GLU:HB2	1.94	0.49
3:A:302:GLY:N	3:A:307:ALA:HB2	2.26	0.49
3:A:326:LYS:O	3:A:328:ARG:HG2	2.11	0.49
3:A:46:ILE:HD13	3:A:53:ILE:HD12	1.93	0.49
3:A:127:LYS:HB2	3:A:128:ASN:HD21	1.73	0.49
3:A:273:THR:O	3:A:273:THR:HG22	2.11	0.49
3:A:19:LEU:HD23	3:A:43:ALA:CA	2.40	0.49
3:A:180:SER:HB2	3:A:185:ALA:HB2	1.96	0.48
3:A:119:ILE:HG23	3:A:124:ASP:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:271:TYR:CD1	3:A:283:ARG:NH2	2.81	0.48
3:A:299:ARG:HG2	3:A:310:PRO:N	2.29	0.48
1:T:6:DG:O6	2:P:2:DC:N3	2.46	0.48
3:A:150:ILE:CD1	3:A:253:ARG:HG2	2.44	0.48
3:A:265:TYR:HD2	3:A:266:TYR:CE1	2.31	0.48
3:A:157:GLN:HE22	3:A:244:LYS:HZ1	1.61	0.48
3:A:207:GLN:O	3:A:210:LEU:N	2.46	0.48
3:A:200:PHE:CE2	3:A:261:PRO:HD3	2.48	0.48
3:A:133:ASN:HD22	3:A:135:HIS:H	1.58	0.48
3:A:245:ASN:N	3:A:245:ASN:ND2	2.30	0.47
3:A:23:ALA:HB2	3:A:39:TYR:HB3	1.96	0.47
3:A:15:ILE:CB	3:A:46:ILE:HD11	2.42	0.47
3:A:56:GLY:O	3:A:59:ALA:N	2.48	0.47
3:A:309:GLU:HA	3:A:310:PRO:HD2	1.48	0.47
3:A:182:ARG:NH2	3:A:316:GLU:OE1	2.47	0.47
3:A:259:LEU:HA	3:A:259:LEU:HD12	1.50	0.47
3:A:22:LEU:HA	3:A:22:LEU:HD13	1.61	0.47
3:A:203:GLU:O	3:A:205:THR:N	2.48	0.47
3:A:180:SER:HA	3:A:183:ARG:HE	1.80	0.46
3:A:11:LEU:N	3:A:11:LEU:HD23	2.22	0.46
1:T:4:DT:H2"	1:T:5:DA:H8	1.81	0.46
3:A:133:ASN:HD22	3:A:134:HIS:N	2.12	0.46
3:A:133:ASN:ND2	3:A:135:HIS:N	2.63	0.46
3:A:243:SER:O	3:A:244:LYS:O	2.33	0.46
2:P:1:DT:H2'	2:P:2:DC:C6	2.51	0.46
3:A:183:ARG:HB2	3:A:183:ARG:HE	1.41	0.46
3:A:77:LEU:CD1	3:A:77:LEU:N	2.78	0.46
3:A:207:GLN:O	3:A:210:LEU:HB2	2.16	0.46
3:A:157:GLN:O	3:A:161:ILE:HG13	2.16	0.46
3:A:36:TYR:CD2	3:A:37:ASN:N	2.84	0.46
1:T:4:DT:H71	5:T:663:HOH:O	2.16	0.46
3:A:49:TYR:HA	3:A:50:PRO:HD3	1.21	0.46
3:A:114:PHE:HB3	3:A:119:ILE:HB	1.98	0.46
3:A:299:ARG:HD2	3:A:310:PRO:HD3	1.98	0.46
3:A:171:SER:O	3:A:171:SER:OG	2.32	0.46
2:P:1:DT:H2"	2:P:2:DC:C5'	2.45	0.46
3:A:237:GLY:O	3:A:254:ARG:NH1	2.49	0.46
3:A:145:ASP:OD1	3:A:145:ASP:N	2.49	0.45
3:A:286:ALA:HB1	3:A:293:ILE:HD11	1.98	0.45
3:A:122:LEU:CD2	3:A:126:ARG:CZ	2.95	0.45
3:A:81:LYS:NZ	3:A:86:GLU:HB2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:266:TYR:HB2	3:A:313:VAL:HG11	1.98	0.45
3:A:121:THR:OG1	3:A:122:LEU:N	2.49	0.45
3:A:254:ARG:HB3	3:A:254:ARG:CZ	2.46	0.45
3:A:26:GLU:HB3	3:A:32:ALA:HB3	1.99	0.45
2:P:5:DA:P	3:A:109:SER:HB3	2.56	0.45
2:P:6:DT:C2'	2:P:7:DG:C8	3.00	0.45
3:A:243:SER:OG	3:A:249:GLU:HG3	2.16	0.45
3:A:85:LEU:HA	3:A:85:LEU:HD12	1.49	0.45
3:A:62:LEU:HA	3:A:62:LEU:HD12	1.55	0.45
3:A:286:ALA:CB	3:A:293:ILE:HD11	2.47	0.45
3:A:115:VAL:O	3:A:118:GLY:N	2.50	0.45
3:A:19:LEU:HB3	3:A:43:ALA:HB2	1.99	0.45
3:A:81:LYS:NZ	3:A:86:GLU:CB	2.80	0.45
2:P:6:DT:H5'	2:P:6:DT:H6	1.82	0.45
3:A:138:ILE:HD12	3:A:228:LEU:CD1	2.47	0.45
2:P:5:DA:H2"	2:P:6:DT:H5'	1.95	0.44
3:A:114:PHE:CZ	3:A:132:LEU:HD23	2.51	0.44
3:A:149:ARG:NH2	3:A:188:SER:CA	2.80	0.44
3:A:154:GLU:C	3:A:158:MET:HE3	2.37	0.44
3:A:194:LEU:CD1	3:A:258:ARG:HD3	2.48	0.44
3:A:194:LEU:CD1	3:A:194:LEU:N	2.79	0.44
3:A:191:MET:HG3	3:A:255:ILE:HG13	2.00	0.44
3:A:298:ILE:HA	5:A:593:HOH:O	2.17	0.44
3:A:254:ARG:NH1	3:A:255:ILE:H	2.15	0.44
3:A:282:MET:HG2	5:A:555:HOH:O	2.17	0.44
3:A:33:ILE:HG23	3:A:34:HIS:N	2.33	0.44
3:A:154:GLU:O	3:A:158:MET:HE3	2.17	0.44
3:A:250:TYR:HA	3:A:251:PRO:HD3	1.84	0.44
3:A:149:ARG:NH2	3:A:187:SER:O	2.52	0.43
3:A:149:ARG:HH21	3:A:187:SER:C	2.22	0.43
3:A:288:GLU:O	3:A:290:GLY:N	2.51	0.43
3:A:214:VAL:CG2	3:A:215:VAL:N	2.77	0.43
3:A:202:SER:H	3:A:261:PRO:HB3	1.82	0.43
3:A:133:ASN:O	3:A:137:ARG:N	2.49	0.43
3:A:162:VAL:O	3:A:166:VAL:HG23	2.19	0.43
3:A:301:LEU:HD12	3:A:301:LEU:HA	1.55	0.43
3:A:286:ALA:O	3:A:291:PHE:HB2	2.18	0.43
3:A:270:LEU:HD21	3:A:282:MET:HE3	1.98	0.43
3:A:194:LEU:HD12	3:A:194:LEU:N	2.33	0.43
3:A:294:ASN:HB2	3:A:295:GLU:OE1	2.19	0.43
3:A:169:VAL:CG1	3:A:170:ASP:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:15:ILE:CG2	3:A:46:ILE:HD11	2.49	0.43
2:P:5:DA:O5'	3:A:107:GLY:HA3	2.19	0.43
3:A:119:ILE:H	3:A:119:ILE:HG12	1.42	0.43
3:A:11:LEU:H	3:A:11:LEU:CD2	2.27	0.43
3:A:134:HIS:O	3:A:138:ILE:HG13	2.19	0.43
3:A:62:LEU:HA	3:A:63:PRO:HD3	1.77	0.42
3:A:212:HIS:CD2	3:A:212:HIS:N	2.86	0.42
3:A:302:GLY:N	3:A:307:ALA:CB	2.82	0.42
3:A:298:ILE:N	5:A:578:HOH:O	2.51	0.42
3:A:217:GLN:O	3:A:221:VAL:HG13	2.19	0.42
3:A:196:THR:OG1	3:A:197:HIS:N	2.51	0.42
3:A:12:ASN:HB3	3:A:46:ILE:HD12	2.02	0.42
3:A:179:GLY:O	3:A:182:ARG:HB3	2.20	0.42
3:A:278:PHE:HZ	3:A:320:PHE:HZ	1.67	0.42
3:A:270:LEU:HD22	3:A:319:ILE:HD13	2.01	0.42
3:A:119:ILE:HA	3:A:124:ASP:HB3	2.01	0.42
3:A:299:ARG:HG2	3:A:310:PRO:HD3	2.00	0.42
3:A:285:HIS:NE2	3:A:289:LYS:CG	2.81	0.42
3:A:152:ARG:O	3:A:155:MET:HB2	2.20	0.42
3:A:284:ALA:O	3:A:287:LEU:HB2	2.20	0.42
3:A:155:MET:HE3	3:A:188:SER:CB	2.50	0.42
1:T:1:DC:H6	1:T:1:DC:H2'	1.59	0.42
3:A:265:TYR:HB3	3:A:266:TYR:H	1.74	0.42
3:A:266:TYR:N	5:A:508:HOH:O	2.52	0.42
3:A:181:PHE:HA	5:A:530:HOH:O	2.19	0.41
3:A:100:LEU:HD12	3:A:100:LEU:HA	1.42	0.41
3:A:330:PRO:O	3:A:333:ARG:HG2	2.20	0.41
3:A:21:GLU:OE1	3:A:85:LEU:HG	2.20	0.41
3:A:77:LEU:HA	3:A:77:LEU:HD12	1.77	0.41
3:A:125:LEU:CD2	3:A:132:LEU:HD21	2.50	0.41
3:A:15:ILE:CG2	3:A:46:ILE:CD1	2.98	0.41
3:A:15:ILE:HG22	3:A:19:LEU:HD22	2.02	0.41
3:A:275:SER:N	3:A:278:PHE:HB3	2.35	0.41
3:A:183:ARG:HH11	3:A:275:SER:CB	2.34	0.41
3:A:289:LYS:HA	3:A:289:LYS:HD3	1.47	0.41
3:A:68:LYS:HB2	3:A:68:LYS:NZ	2.34	0.41
3:A:165:GLU:CB	3:A:217:GLN:HG3	2.30	0.41
3:A:165:GLU:HA	3:A:168:LYS:CG	2.45	0.41
3:A:332:ASP:OD1	3:A:332:ASP:O	2.39	0.41
3:A:327:TYR:CD1	3:A:328:ARG:N	2.80	0.41
3:A:254:ARG:HH11	3:A:254:ARG:CA	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:1:DT:H2"	2:P:2:DC:H5'	2.03	0.41
3:A:299:ARG:HG2	3:A:310:PRO:CD	2.51	0.41
3:A:230:LYS:HB3	3:A:230:LYS:HE2	1.69	0.41
3:A:228:LEU:O	3:A:229:SER:HB3	2.20	0.41
3:A:79:THR:C	3:A:81:LYS:H	2.21	0.41
3:A:150:ILE:HG21	3:A:158:MET:CE	2.51	0.40
3:A:311:LEU:HB3	3:A:322:TYR:HE2	1.86	0.40
3:A:133:ASN:HD21	3:A:135:HIS:CB	2.35	0.40
3:A:265:TYR:O	3:A:268:GLY:N	2.54	0.40
3:A:303:VAL:O	3:A:305:GLY:N	2.54	0.40
3:A:254:ARG:HH11	3:A:255:ILE:N	2.17	0.40
3:A:133:ASN:HD21	3:A:135:HIS:HB3	1.85	0.40
3:A:271:TYR:C	3:A:271:TYR:CD2	2.94	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
3	A	325/335 (97%)	274 (84%)	32 (10%)	19 (6%)	2 17

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	202	SER
3	A	204	SER
3	A	205	THR
3	A	244	LYS
3	A	289	LYS
3	A	295	GLU
3	A	32	ALA
3	A	80	GLY

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Mol	Chain	Res	Type
3	A	185	ALA
3	A	265	TYR
3	A	304	THR
3	A	222	HIS
3	A	298	ILE
3	A	10	THR
3	A	91	ASP
3	A	28	ASN
3	A	207	GLN
3	A	310	PRO
3	A	309	GLU

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
3	A	288/295 (98%)	232 (81%)	56 (19%)	2 9

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	10	THR
3	A	18	MET
3	A	22	LEU
3	A	37	ASN
3	A	41	LYS
3	A	44	SER
3	A	46	ILE
3	A	54	LYS
3	A	62	LEU
3	A	67	THR
3	A	77	LEU
3	A	79	THR
3	A	81	LYS
3	A	89	ARG
3	A	92	ASP

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Mol	Chain	Res	Type
3	A	94	SER
3	A	100	LEU
3	A	101	THR
3	A	102	ARG
3	A	119	ILE
3	A	121	THR
3	A	128	ASN
3	A	133	ASN
3	A	145	ASP
3	A	153	GLU
3	A	182	ARG
3	A	191	MET
3	A	199	SER
3	A	201	THR
3	A	217	GLN
3	A	218	LEU
3	A	221	VAL
3	A	226	ASP
3	A	228	LEU
3	A	236	MET
3	A	245	ASN
3	A	248	LYS
3	A	253	ARG
3	A	264	GLN
3	A	272	PHE
3	A	277	ILE
3	A	279	ASN
3	A	287	LEU
3	A	292	THR
3	A	293	ILE
3	A	294	ASN
3	A	301	LEU
3	A	304	THR
3	A	309	GLU
3	A	311	LEU
3	A	314	ASP
3	A	324	GLN
3	A	325	TRP
3	A	327	TYR
3	A	331	LYS
3	A	335	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such

sidechains are listed below:

Mol	Chain	Res	Type
3	A	12	ASN
3	A	28	ASN
3	A	31	GLN
3	A	37	ASN
3	A	128	ASN
3	A	133	ASN
3	A	135	HIS
3	A	136	GLN
3	A	157	GLN
3	A	212	HIS
3	A	213	GLN
3	A	217	GLN
3	A	240	GLN
3	A	245	ASN
3	A	252	HIS
3	A	264	GLN
3	A	279	ASN

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

Of 2 ligands modelled in this entry, 2 are 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

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	T	8/8 (100%)	-0.80	0	100	100	14, 39, 92, 98	0
2	P	7/7 (100%)	-1.03	0	100	100	12, 26, 46, 70	0
3	A	325/335 (97%)	-1.02	1 (0%)	94	93	3, 31, 83, 100	0
All	All	340/350 (97%)	-1.02	1 (0%)	94	93	3, 31, 85, 100	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	246	ASP	2.4

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

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^{th} 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(Å^2)	Q<0.9
4	NA	A	342	1/1	0.94	0.14	-0.30	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
4	NA	A	341	1/1	0.97	0.08	-0.89	13,13,13,13	0

6.5 Other polymers (i)

There are no such residues in this entry.