



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:58 AM GMT

PDB ID : 2OWO
Title : Last Stop on the Road to Repair: Structure of E.coli DNA Ligase Bound to Nicked DNA-Adenylate
Authors : Shuman, S.; Nandakumar, J.; Nair, P.A.
Deposited on : 2007-02-16
Resolution : 2.30 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 ⓘ symbol.

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

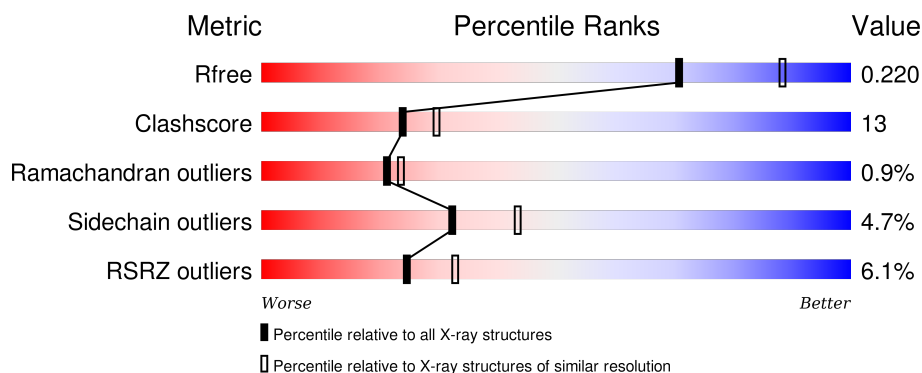
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 $\leq 5\%$. 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	B	26	<div> <div>8%</div> <div>62%</div> <div>31%</div> <div>•</div> <div>•</div> </div>
2	C	13	<div> <div>15%</div> <div>77%</div> <div>23%</div> </div>
3	D	13	<div> <div>100%</div> </div>
4	A	671	<div> <div>5%</div> <div>64%</div> <div>21%</div> <div>•</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5991 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 26-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	26	Total	C	N	O	P	0	0	0
			533	255	96	157	25			

- Molecule 2 is a DNA chain called 5'-D(*AP*CP*AP*AP*TP*TP*GP*CP*GP*AP*CP*(O MC)P*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			262	126	49	75	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	13	Total	C	N	O	P	0	0	0
			267	127	50	77	13			

- Molecule 4 is a protein called DNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	586	Total	C	N	O	S	0	0	0
			4565	2876	814	859	16			

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

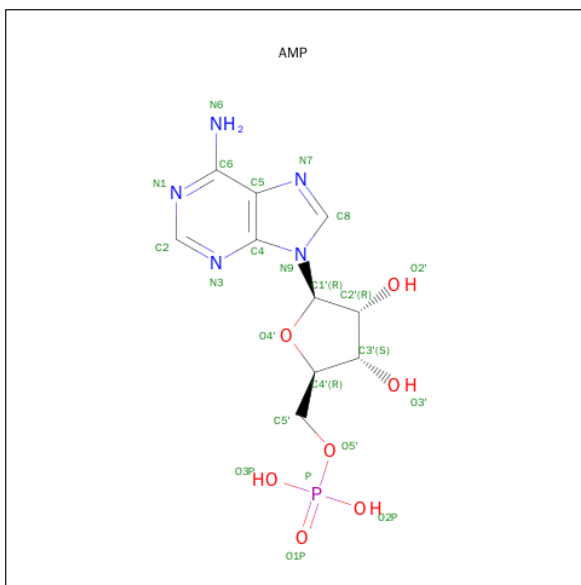
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	255	Total	O	0	0
			255	255		
8	B	43	Total	O	0	0
			43	43		
8	C	11	Total	O	0	0
			11	11		
8	D	11	Total	O	0	0
			11	11		

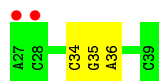
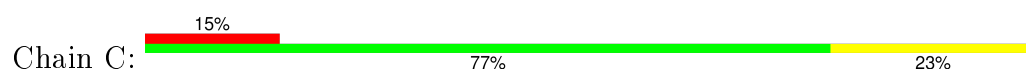
3 Residue-property plots

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: 26-MER



- Molecule 2: 5'-D(*AP*CP*AP*AP*TP*TP*GP*CP*GP*AP*CP*(OMC)P*C)-3'

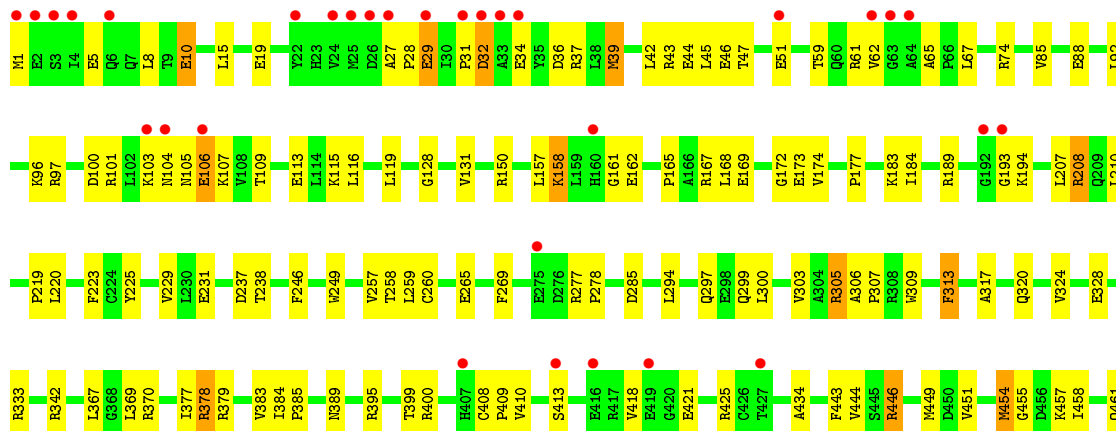


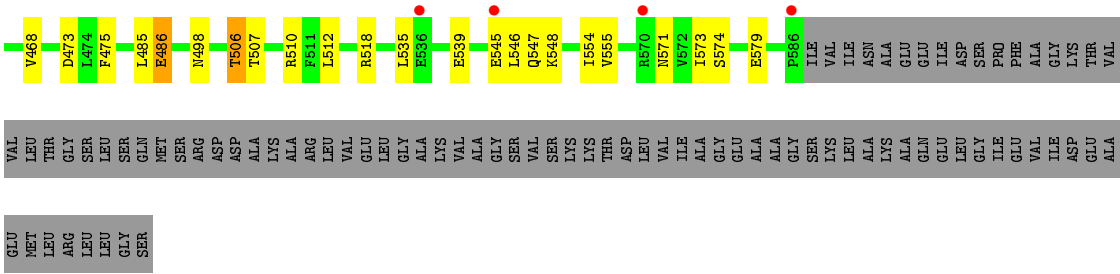
- Molecule 3: 5'-D(*CP*AP*CP*TP*AP*TP*CP*GP*GP*AP*AP*TP*G)-3'



There are no outlier residues recorded for this chain.

- Molecule 4: DNA ligase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	110.44Å 99.27Å 86.25Å 90.00° 105.33° 90.00°	Depositor
Resolution (Å)	30.34 – 2.30 30.34 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.4 (30.34-2.30) 98.5 (30.34-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.217 , 0.254 0.222 , 0.220	Depositor DCC
R_{free} test set	1955 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 39098 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5991	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 5.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: OMC, AMP, ZN, SO4

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	B	0.38	0/597	0.75	1/921 (0.1%)
2	C	0.38	0/270	0.76	0/414
3	D	0.61	0/299	0.77	0/459
4	A	0.34	0/4651	0.61	0/6306
All	All	0.37	0/5817	0.64	1/8100 (0.0%)

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	B	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	13	DG	N9-C1'-C2'	-5.15	102.82	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	12	DT	Sidechain
1	B	13	DG	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	B	533	0	296	12	0
2	C	262	0	149	3	0
3	D	267	0	147	0	0
4	A	4565	0	4566	131	0
5	A	1	0	0	0	0
6	A	20	0	0	0	0
7	D	23	0	12	0	0
8	A	255	0	0	11	0
8	B	43	0	0	2	0
8	C	11	0	0	0	0
8	D	11	0	0	0	0
All	All	5991	0	5170	142	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 13.

All (142) 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)
4:A:444:VAL:HG13	4:A:451:VAL:HB	1.62	0.80
4:A:444:VAL:HG11	4:A:454:MET:HB2	1.62	0.80
4:A:101:ARG:HG2	8:A:903:HOH:O	1.84	0.76
4:A:468:VAL:HG13	4:A:473:ASP:HB2	1.66	0.76
4:A:46:GLU:OE1	4:A:59:THR:HG21	1.85	0.76
4:A:44:GLU:HG2	4:A:131:VAL:HG11	1.68	0.76
4:A:158:LYS:HD3	4:A:158:LYS:N	2.02	0.75
4:A:324:VAL:HG21	4:A:369:LEU:HD11	1.73	0.71
4:A:475:PHE:HB2	4:A:579:GLU:HG2	1.73	0.70
4:A:461:GLN:HE22	4:A:486:GLU:HB2	1.56	0.69
4:A:96:LYS:HG2	4:A:100:ASP:OD2	1.92	0.69
4:A:184:ILE:HD11	4:A:219:PRO:HD2	1.72	0.69
4:A:15:LEU:O	4:A:19:GLU:HG3	1.93	0.69
4:A:189:ARG:HD2	8:A:838:HOH:O	1.92	0.68
4:A:547:GLN:NE2	4:A:554:ILE:HG23	2.10	0.67
4:A:61:ARG:HG2	4:A:65:ALA:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:29:GLU:O	4:A:31:PRO:HD3	1.97	0.65
4:A:174:VAL:HG11	4:A:207:LEU:HD11	1.76	0.65
4:A:67:LEU:HB3	4:A:210:LEU:HD22	1.78	0.64
4:A:169:GLU:HB2	4:A:229:VAL:HG12	1.79	0.63
4:A:303:VAL:HG22	4:A:306:ALA:O	1.98	0.63
4:A:400:ARG:HD2	8:A:708:HOH:O	1.99	0.63
4:A:410:VAL:HG21	4:A:434:ALA:HB2	1.81	0.61
1:B:19:DG:H3'	4:A:210:LEU:HD12	1.82	0.61
4:A:10:GLU:OE1	4:A:10:GLU:HA	2.00	0.61
4:A:377:ILE:HG22	4:A:378:ARG:N	2.15	0.61
1:B:12:DT:H5'	8:B:30:HOH:O	2.02	0.60
4:A:305:ARG:HB3	4:A:305:ARG:HH11	1.67	0.59
4:A:297:GLN:HG3	4:A:309:TRP:CD2	2.37	0.59
4:A:104:ASN:C	4:A:106:GLU:H	2.03	0.59
2:C:34:DC:H3'	4:A:457:LYS:HG3	1.85	0.59
4:A:172:GLY:HA2	4:A:225:TYR:CD2	2.38	0.59
4:A:554:ILE:HD12	4:A:555:VAL:H	1.68	0.58
1:B:2:DA:H1'	1:B:3:DT:H5''	1.85	0.58
4:A:379:ARG:HD2	4:A:383:VAL:O	2.04	0.58
4:A:571:ASN:HA	4:A:574:SER:OG	2.03	0.57
4:A:237:ASP:O	4:A:294:LEU:HD23	2.05	0.57
4:A:535:LEU:O	4:A:539:GLU:HG2	2.04	0.57
4:A:444:VAL:HG12	4:A:444:VAL:O	2.05	0.56
4:A:37:ARG:HB3	4:A:37:ARG:HH11	1.70	0.56
4:A:418:VAL:O	4:A:421:GLU:HG2	2.05	0.56
4:A:43:ARG:O	4:A:47:THR:HG23	2.06	0.56
4:A:32:ASP:OD2	4:A:34:GLU:HB2	2.06	0.56
1:B:1:DC:H2''	1:B:2:DA:C8	2.41	0.56
4:A:446:ARG:NH1	8:A:922:HOH:O	2.39	0.56
4:A:162:GLU:O	4:A:249:TRP:CZ3	2.59	0.55
4:A:105:ASN:ND2	4:A:299:GLN:HE22	2.04	0.55
4:A:101:ARG:C	8:A:903:HOH:O	2.44	0.55
4:A:547:GLN:HE22	4:A:554:ILE:HG23	1.72	0.55
4:A:297:GLN:HG3	4:A:309:TRP:CE2	2.42	0.54
4:A:461:GLN:NE2	4:A:486:GLU:HB2	2.22	0.54
4:A:8:LEU:HD23	4:A:45:LEU:HD23	1.90	0.54
4:A:37:ARG:NH1	4:A:37:ARG:HB3	2.24	0.53
4:A:162:GLU:O	4:A:249:TRP:CH2	2.62	0.52
1:B:12:DT:H2'	8:B:56:HOH:O	2.09	0.52
4:A:535:LEU:HD21	4:A:573:ILE:HG21	1.92	0.52
4:A:115:LYS:HD3	4:A:285:ASP:OD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:258:THR:HG22	4:A:259:LEU:N	2.24	0.51
4:A:498:ASN:HD22	4:A:498:ASN:N	2.08	0.51
4:A:370:ARG:HD2	8:A:697:HOH:O	2.10	0.51
4:A:39:MET:CE	4:A:42:LEU:HD23	2.41	0.51
4:A:461:GLN:HG2	4:A:485:LEU:HD22	1.93	0.50
4:A:104:ASN:HA	4:A:106:GLU:OE2	2.11	0.50
4:A:328:GLU:CD	4:A:342:ARG:HH11	2.14	0.50
4:A:44:GLU:CG	4:A:131:VAL:HG11	2.41	0.50
4:A:246:PHE:HA	4:A:249:TRP:CD1	2.47	0.50
4:A:305:ARG:NH1	4:A:305:ARG:HB3	2.26	0.50
4:A:370:ARG:HG3	4:A:395:ARG:NH2	2.28	0.49
4:A:425:ARG:CZ	4:A:518:ARG:HH21	2.25	0.49
4:A:88:GLU:O	4:A:92:LEU:HG	2.13	0.49
4:A:507:THR:OG1	4:A:510:ARG:HG3	2.13	0.48
4:A:333:ARG:NH1	8:A:872:HOH:O	2.46	0.48
4:A:475:PHE:HB2	4:A:579:GLU:CG	2.41	0.48
4:A:62:VAL:HG13	4:A:62:VAL:O	2.13	0.48
1:B:2:DA:H2''	1:B:3:DT:H5'	1.94	0.48
4:A:150:ARG:HH22	4:A:157:LEU:HD13	1.79	0.48
4:A:177:PRO:HG2	8:A:688:HOH:O	2.13	0.48
1:B:9:DT:H5'	1:B:9:DT:H6	1.79	0.47
4:A:451:VAL:CG1	4:A:454:MET:HG3	2.44	0.47
4:A:74:ARG:HH11	4:A:74:ARG:HG2	1.79	0.47
1:B:2:DA:H2''	1:B:3:DT:C5'	2.45	0.47
4:A:370:ARG:HG3	4:A:395:ARG:CZ	2.44	0.47
4:A:444:VAL:O	4:A:444:VAL:CG1	2.61	0.47
4:A:377:ILE:CG2	4:A:378:ARG:N	2.77	0.47
4:A:29:GLU:OE1	4:A:210:LEU:HD11	2.14	0.47
4:A:105:ASN:HD21	4:A:299:GLN:HE22	1.61	0.47
4:A:208:ARG:NH1	4:A:208:ARG:HG2	2.29	0.47
1:B:7:DG:O5'	4:A:97:ARG:HD3	2.14	0.47
4:A:157:LEU:C	4:A:158:LYS:HD3	2.35	0.47
4:A:258:THR:HG22	4:A:259:LEU:H	1.78	0.47
4:A:61:ARG:HE	4:A:65:ALA:HA	1.80	0.47
4:A:128:GLY:O	4:A:158:LYS:HA	2.15	0.46
4:A:300:LEU:HD12	4:A:309:TRP:HB3	1.97	0.46
4:A:85:VAL:HG23	4:A:313:PHE:HA	1.97	0.46
4:A:150:ARG:NH2	4:A:157:LEU:HD22	2.31	0.46
4:A:208:ARG:CG	4:A:208:ARG:HH11	2.29	0.46
4:A:444:VAL:HG11	4:A:454:MET:CB	2.39	0.45
4:A:506:THR:HG22	4:A:507:THR:H	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:446:ARG:HH11	4:A:446:ARG:HB3	1.82	0.45
4:A:208:ARG:HG2	4:A:208:ARG:HH11	1.81	0.45
4:A:113:GLU:HG2	4:A:257:VAL:HG22	1.99	0.45
4:A:506:THR:HG22	4:A:510:ARG:HD3	1.98	0.45
4:A:277:ARG:N	4:A:278:PRO:HD2	2.32	0.45
4:A:461:GLN:HE22	4:A:486:GLU:H	1.64	0.45
4:A:294:LEU:O	4:A:297:GLN:HB3	2.17	0.45
4:A:165:PRO:HG2	4:A:168:LEU:HB2	1.98	0.45
4:A:34:GLU:CB	4:A:37:ARG:HH12	2.30	0.44
4:A:103:LYS:HE3	4:A:104:ASN:ND2	2.33	0.44
4:A:384:ILE:HA	4:A:385:PRO:HD3	1.94	0.44
4:A:34:GLU:HB3	4:A:37:ARG:HH12	1.82	0.44
1:B:18:DC:H2''	1:B:19:DG:C8	2.53	0.44
4:A:258:THR:HG1	4:A:269:PHE:HE2	1.65	0.43
1:B:12:DT:H2''	1:B:13:DG:OP2	2.17	0.43
4:A:34:GLU:HA	4:A:37:ARG:NH1	2.33	0.43
4:A:109:THR:CG2	4:A:259:LEU:HG	2.49	0.43
4:A:446:ARG:HH11	4:A:446:ARG:CB	2.31	0.43
4:A:167:ARG:HB2	4:A:231:GLU:HB2	2.01	0.43
4:A:317:ALA:HB3	4:A:378:ARG:HG3	2.00	0.42
4:A:554:ILE:HD12	4:A:555:VAL:N	2.32	0.42
4:A:27:ALA:HA	4:A:28:PRO:HD3	1.88	0.42
4:A:395:ARG:HG3	4:A:399:THR:HG21	1.99	0.42
4:A:418:VAL:HB	4:A:421:GLU:CD	2.40	0.42
4:A:183:LYS:HD3	4:A:183:LYS:C	2.40	0.42
2:C:35:DG:H2''	2:C:36:DA:OP2	2.19	0.42
4:A:306:ALA:HB1	4:A:307:PRO:HD2	2.02	0.41
4:A:512:LEU:HD12	4:A:512:LEU:HA	1.84	0.41
4:A:5:GLU:CD	4:A:5:GLU:H	2.23	0.41
4:A:443:PHE:CE2	4:A:449:MET:HG3	2.55	0.41
2:C:34:DC:H3'	4:A:457:LYS:CG	2.49	0.41
4:A:418:VAL:HB	4:A:421:GLU:HG2	2.03	0.41
4:A:342:ARG:NH2	8:A:822:HOH:O	2.53	0.41
4:A:194:LYS:CB	8:A:828:HOH:O	2.68	0.41
4:A:408:CYS:HA	4:A:409:PRO:HD3	1.91	0.41
4:A:367:LEU:HD22	4:A:389:ASN:HA	2.02	0.41
4:A:554:ILE:HG13	8:A:734:HOH:O	2.20	0.40
4:A:32:ASP:C	4:A:34:GLU:H	2.25	0.40
4:A:260:CYS:HB3	4:A:265:GLU:HB2	2.04	0.40
4:A:455:GLY:H	4:A:458:ILE:HG22	1.86	0.40
4:A:454:MET:HA	4:A:458:ILE:HG21	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:DA:C2'	1:B:9:DT:H5''	2.52	0.40
4:A:545:GLU:HG2	4:A:548:LYS:NZ	2.37	0.40
4:A:119:LEU:HD23	4:A:119:LEU:N	2.37	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
4	A	584/671 (87%)	551 (94%)	28 (5%)	5 (1%)	21 24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	106	GLU
4	A	107	LYS
4	A	161	GLY
4	A	413	SER
4	A	193	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
4	A	487/552 (88%)	464 (95%)	23 (5%)	32 43

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	1	MET
4	A	10	GLU
4	A	29	GLU
4	A	32	ASP
4	A	36	ASP
4	A	39	MET
4	A	51	GLU
4	A	116	LEU
4	A	158	LYS
4	A	173	GLU
4	A	208	ARG
4	A	220	LEU
4	A	223	PHE
4	A	238	THR
4	A	305	ARG
4	A	313	PHE
4	A	320	GLN
4	A	378	ARG
4	A	446	ARG
4	A	454	MET
4	A	486	GLU
4	A	506	THR
4	A	546	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	49	HIS
4	A	104	ASN
4	A	105	ASN
4	A	160	HIS
4	A	209	GLN
4	A	297	GLN
4	A	320	GLN
4	A	461	GLN
4	A	494	GLN
4	A	498	ASN
4	A	547	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	OMC	C	38	1,2	13,22,23	0.88	0	20,31,34	1.42	5 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	C	38	1,2	-	0/5/27/28	0/2/2/2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	38	OMC	C5'-C4'-C3'	-2.48	105.35	115.21
2	C	38	OMC	CM2-O2'-C2'	-2.13	108.57	114.59
2	C	38	OMC	O3'-C3'-C4'	-2.04	104.94	111.05
2	C	38	OMC	O3'-C3'-C2'	2.96	119.72	111.16
2	C	38	OMC	C2-N3-C4	3.11	120.00	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	SO4	A	673	-	4,4,4	0.24	0	6,6,6	0.08	0
6	SO4	A	674	-	4,4,4	0.19	0	6,6,6	0.06	0
6	SO4	A	675	-	4,4,4	0.27	0	6,6,6	0.07	0
6	SO4	A	676	-	4,4,4	0.23	0	6,6,6	0.07	0
7	AMP	D	53	3	20,25,25	1.79	3 (15%)	22,38,38	2.74	4 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SO4	A	673	-	-	0/0/0/0	0/0/0/0
6	SO4	A	674	-	-	0/0/0/0	0/0/0/0
6	SO4	A	675	-	-	0/0/0/0	0/0/0/0
6	SO4	A	676	-	-	0/0/0/0	0/0/0/0
7	AMP	D	53	3	-	0/6/26/26	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	53	AMP	C2-N1	3.90	1.41	1.33
7	D	53	AMP	C4-N3	4.25	1.41	1.35
7	D	53	AMP	C2-N3	4.59	1.40	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	53	AMP	N3-C2-N1	-10.83	120.60	128.89
7	D	53	AMP	C4'-O4'-C1'	-3.78	105.57	109.72
7	D	53	AMP	O2'-C2'-C3'	2.43	119.72	111.83
7	D	53	AMP	C1'-N9-C4	2.46	130.66	126.94

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, 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	B	26/26 (100%)	0.07	2 (7%) 16 23	19, 39, 69, 82	0
2	C	12/13 (92%)	0.74	2 (16%) 2 4	22, 42, 86, 88	0
3	D	13/13 (100%)	-0.12	0 100 100	23, 32, 48, 48	0
4	A	586/671 (87%)	0.36	35 (5%) 25 33	15, 36, 68, 92	0
All	All	637/723 (88%)	0.34	39 (6%) 25 33	15, 36, 69, 92	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	62	VAL	8.0
4	A	1	MET	6.1
4	A	2	GLU	5.1
4	A	25	MET	4.9
4	A	106	GLU	4.7
4	A	31	PRO	4.5
4	A	4	ILE	4.4
4	A	24	VAL	4.3
4	A	34	GLU	4.0
4	A	586	PRO	3.7
4	A	63	GLY	3.6
4	A	419	GLU	3.5
4	A	6	GLN	3.5
4	A	27	ALA	3.4
4	A	33	ALA	3.4
4	A	26	ASP	3.3
4	A	545	GLU	3.1
4	A	104	ASN	3.1
2	C	28	DC	3.1
2	C	27	DA	3.1
4	A	29	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
4	A	64	ALA	2.9
4	A	103	LYS	2.8
4	A	51	GLU	2.8
1	B	26	DT	2.7
4	A	3	SER	2.5
4	A	416	GLU	2.4
4	A	407	HIS	2.3
4	A	32	ASP	2.3
1	B	25	DG	2.2
4	A	193	GLY	2.2
4	A	192	GLY	2.1
4	A	275	GLU	2.1
4	A	22	TYR	2.1
4	A	427	THR	2.0
4	A	160	HIS	2.0
4	A	413	SER	2.0
4	A	570	ARG	2.0
4	A	536	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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
2	OMC	C	38	21/22	0.96	0.17	-	18,24,28,33	0

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, 95th 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(\AA^2)	Q<0.9
6	SO4	A	674	5/5	0.97	0.17	0.95	76,76,76,76	0
7	AMP	D	53	23/23	0.95	0.19	0.11	29,33,38,39	0
5	ZN	A	672	1/1	0.99	0.07	-1.80	42,42,42,42	0
6	SO4	A	673	5/5	0.88	0.20	-	83,84,85,85	0
6	SO4	A	675	5/5	0.94	0.21	-	90,90,90,90	0
6	SO4	A	676	5/5	0.94	0.18	-	88,88,89,89	0

6.5 Other polymers [i](#)

There are no such residues in this entry.