



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:51 am GMT

PDB ID : 4UN3  
Title : Crystal structure of Cas9 bound to PAM-containing DNA target  
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Deposited on : 2014-05-25  
Resolution : 2.59 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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

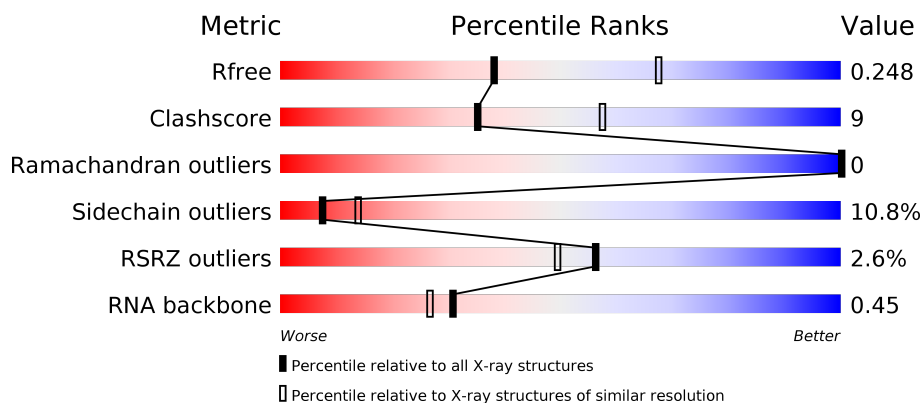
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)
RNA backbone	2435	1140 (3.00-2.20)

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	83	
2	B	1372	
3	C	28	
4	D	12	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13629 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 RNA chain called SGRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	81	Total	C	N	O	P	0	0	0
			1732	778	318	555	81			

- Molecule 2 is a protein called CRISPR-ASSOCIATED ENDONUCLEASE CAS9/CSN1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1306	Total	C	N	O	S	0	0	0
			10690	6816	1854	1998	22			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	EXPRESSION TAG	UNP Q99ZW2
B	-2	ALA	-	EXPRESSION TAG	UNP Q99ZW2
B	-1	ALA	-	EXPRESSION TAG	UNP Q99ZW2
B	0	SER	-	EXPRESSION TAG	UNP Q99ZW2
B	840	ALA	HIS	ENGINEERED MUTATION	UNP Q99ZW2

- Molecule 3 is a DNA chain called TARGET DNA STRAND.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total	C	N	O	P	0	0	0
			567	276	96	168	27			

- Molecule 4 is a DNA chain called NON-TARGET DNA STRAND.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	11	Total	C	N	O	P	0	0	0
			227	110	43	64	10			

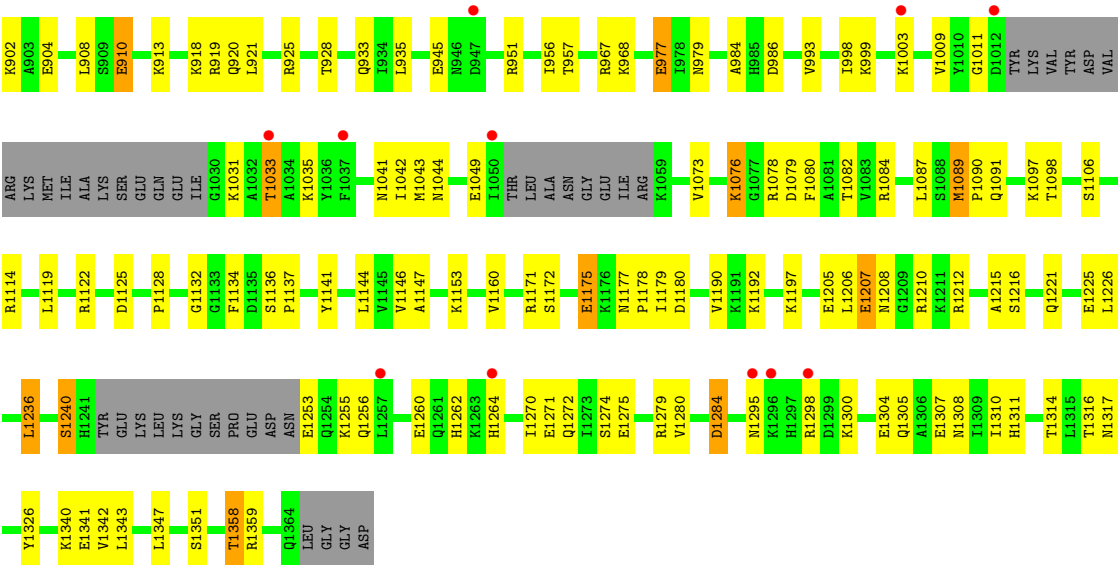
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	4	Total 4	Mg 4	0	0
5	A	4	Total 4	Mg 4	0	0

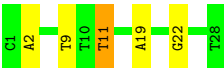
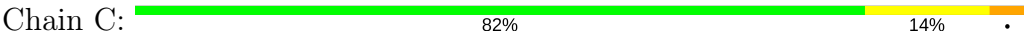
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	146	Total 146	O 146	0	0
6	B	246	Total 246	O 246	0	0
6	C	11	Total 11	O 11	0	0
6	D	2	Total 2	O 2	0	0

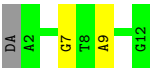




● Molecule 3: TARGET DNA STRAND



● Molecule 4: NON-TARGET DNA STRAND



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	177.72Å 68.14Å 188.23Å 90.00° 111.17° 90.00°	Depositor
Resolution (Å)	48.15 – 2.59 48.15 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.15-2.59) 99.3 (48.15-2.59)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.03 (at 2.58Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.2_1309)	Depositor
R, $R_{free}$	0.217 , 0.252 0.215 , 0.248	Depositor DCC
$R_{free}$ test set	3260 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.0	Xtriage
Anisotropy	0.620	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 47.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	13629	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.28	0/1942	0.81	0/3023
2	B	0.24	0/10877	0.43	0/14612
3	C	0.48	0/634	1.27	3/976 (0.3%)
4	D	0.48	0/255	1.10	0/393
All	All	0.27	0/13708	0.60	3/19004 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	DA	O4'-C1'-N9	6.68	112.67	108.00
3	C	11	DT	O4'-C4'-C3'	-5.99	102.11	104.50
3	C	22	DG	O4'-C1'-N9	5.22	111.66	108.00

There are no chirality outliers.

There are no planarity outliers.

### 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	1732	0	869	40	0
2	B	10690	0	10858	202	0
3	C	567	0	322	5	0
4	D	227	0	127	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	0	0	0
5	B	4	0	0	0	0
6	A	146	0	0	10	0
6	B	246	0	0	27	1
6	C	11	0	0	0	0
6	D	2	0	0	0	0
All	All	13629	0	12176	234	1

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 9.

All (234) 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:9:A:OP1	6:A:2016:HOH:O	1.83	0.97
2:B:587:PHE:O	6:B:2124:HOH:O	1.86	0.92
2:B:1084:ARG:O	6:B:2182:HOH:O	1.92	0.85
2:B:1225:GLU:OE2	6:B:2230:HOH:O	1.94	0.85
6:A:2121:HOH:O	2:B:69:ARG:NH2	2.11	0.82
2:B:601:ILE:HD12	2:B:603:ASP:H	1.45	0.82
6:B:2032:HOH:O	3:C:9:DT:O4	1.97	0.82
2:B:523:GLU:O	6:B:2119:HOH:O	1.97	0.81
6:A:2078:HOH:O	2:B:102:GLU:O	1.98	0.81
6:A:2141:HOH:O	2:B:1098:THR:O	2.00	0.80
2:B:577:SER:OG	6:B:2127:HOH:O	1.94	0.76
2:B:614:ASP:OD1	6:B:2136:HOH:O	2.02	0.76
1:A:41:A:OP1	6:A:2067:HOH:O	2.04	0.76
2:B:442:LYS:HE3	2:B:476:TRP:HD1	1.50	0.75
2:B:1132:GLY:O	6:B:2202:HOH:O	2.04	0.75
1:A:18:A:OP2	2:B:71:ARG:NH1	2.20	0.74
2:B:557:ARG:NH2	2:B:596:ASP:OD1	2.21	0.74
2:B:1316:THR:O	6:B:2229:HOH:O	2.04	0.74
2:B:60:GLU:OE1	6:B:2028:HOH:O	2.06	0.73
2:B:1215:ALA:HB2	2:B:1221:GLN:HG3	1.68	0.73
2:B:263:LYS:NZ	6:B:2072:HOH:O	2.14	0.73
2:B:1212:ARG:NH2	2:B:1280:VAL:O	2.22	0.72
2:B:1295:ASN:OD1	2:B:1298:ARG:NH1	2.22	0.71
2:B:307:ARG:NH2	2:B:397:ASP:OD2	2.24	0.70
2:B:1300:LYS:O	2:B:1305:GLN:NE2	2.26	0.69
2:B:1207:GLU:OE2	2:B:1210:ARG:NH1	2.26	0.69
2:B:1076:LYS:HG3	2:B:1080:PHE:HE2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:182:ASP:H	2:B:209:LYS:HE2	1.58	0.69
2:B:1236:LEU:O	2:B:1240:SER:OG	2.10	0.68
2:B:54:ASP:OD2	6:B:2023:HOH:O	2.11	0.68
2:B:1212:ARG:NH1	6:B:2224:HOH:O	2.20	0.68
2:B:212:LEU:HD12	2:B:246:LEU:HD21	1.76	0.67
2:B:184:LEU:O	6:B:2063:HOH:O	2.13	0.67
2:B:516:GLU:HA	2:B:519:THR:HG22	1.76	0.67
2:B:1125:ASP:OD1	6:B:2203:HOH:O	2.14	0.66
2:B:672:ASP:HA	2:B:703:THR:HG22	1.78	0.66
1:A:77:A:OP1	2:B:721:HIS:NE2	2.29	0.65
2:B:365:GLY:O	6:B:2086:HOH:O	2.14	0.65
2:B:165:ARG:NH2	2:B:446:PHE:O	2.30	0.65
2:B:780:ARG:NH1	2:B:806:LEU:O	2.29	0.65
1:A:73:G:H3'	1:A:74:A:H5''	1.80	0.63
1:A:75:A:H2'	1:A:76:A:C8	2.32	0.63
2:B:778:ARG:NH2	3:C:11:DT:OP1	2.31	0.63
2:B:1042:ILE:HG23	2:B:1043:MET:HG2	1.82	0.62
2:B:1256:GLN:NE2	2:B:1260:GLU:OE2	2.33	0.61
2:B:1304:GLU:O	2:B:1308:ASN:ND2	2.28	0.61
2:B:521:TYR:O	2:B:525:THR:OG1	2.18	0.61
2:B:967:ARG:NH1	2:B:986:ASP:OD1	2.34	0.61
2:B:1009:VAL:O	6:B:2176:HOH:O	2.16	0.61
2:B:1205:GLU:OE1	2:B:1359:ARG:NH2	2.34	0.60
2:B:817:GLN:O	2:B:882:TYR:OH	2.19	0.60
1:A:20:A:OP2	2:B:403:ARG:NH1	2.34	0.60
2:B:776:ASN:N	6:B:2154:HOH:O	2.35	0.59
2:B:817:GLN:NE2	6:B:2156:HOH:O	2.10	0.59
2:B:437:ARG:NH1	6:B:2095:HOH:O	2.36	0.59
2:B:119:PHE:HE2	2:B:128:TYR:HB2	1.67	0.59
2:B:217:SER:OG	2:B:220:ARG:NH1	2.35	0.59
2:B:525:THR:HG22	2:B:690:ASN:HB3	1.83	0.59
2:B:699:ASP:OD1	2:B:701:SER:OG	2.22	0.58
1:A:67:C:OP2	2:B:1097:LYS:NZ	2.34	0.58
1:A:32:A:H61	1:A:37:U:H3	1.51	0.58
2:B:442:LYS:HE3	2:B:476:TRP:CD1	2.37	0.58
1:A:8:A:H2'	1:A:9:A:C8	2.39	0.58
2:B:179:SER:O	2:B:209:LYS:NZ	2.30	0.57
2:B:22:THR:HG22	2:B:23:ASP:H	1.67	0.57
2:B:1141:TYR:OH	2:B:1175:GLU:OE1	2.23	0.57
2:B:849:ASP:HB3	2:B:854:ASN:HD22	1.68	0.57
3:C:19:DA:H5''	3:C:19:DA:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:719:SER:N	6:B:2147:HOH:O	2.37	0.57
1:A:59:U:OP2	2:B:467:ARG:NH2	2.38	0.56
2:B:525:THR:HG23	2:B:545:LYS:HZ1	1.70	0.56
2:B:788:ILE:HG23	2:B:793:SER:HB3	1.87	0.56
1:A:3:A:H2'	1:A:4:A:C8	2.39	0.56
2:B:489:GLN:HG3	2:B:625:LEU:HD21	1.86	0.56
2:B:161:MET:HE3	2:B:419:LEU:HD12	1.87	0.56
6:A:2024:HOH:O	2:B:462:PHE:O	2.18	0.56
2:B:35:LEU:HB2	2:B:1358:THR:HB	1.88	0.56
2:B:75:ARG:HD3	2:B:163:LYS:HG2	1.88	0.55
1:A:33:G:H2'	1:A:34:A:H5''	1.87	0.55
1:A:76:A:C5	1:A:77:A:H1'	2.42	0.55
1:A:27:G:N2	1:A:44:U:OP2	2.38	0.55
2:B:977:GLU:HG3	2:B:1310:ILE:HG23	1.89	0.55
1:A:5:C:OP1	2:B:515:TYR:OH	2.21	0.54
1:A:81:G:N2	6:A:2142:HOH:O	2.29	0.54
2:B:1208:ASN:O	2:B:1279:ARG:NH1	2.39	0.54
2:B:908:LEU:O	2:B:913:LYS:NZ	2.41	0.54
1:A:56:U:OP1	6:A:2104:HOH:O	2.18	0.54
1:A:42:A:O2'	1:A:43:G:OP1	2.22	0.54
2:B:1206:LEU:HD11	2:B:1341:GLU:HG3	1.89	0.54
1:A:15:A:OP2	2:B:70:ARG:NH2	2.36	0.54
2:B:1317:ASN:ND2	6:B:2171:HOH:O	2.32	0.53
2:B:832:ARG:NH1	2:B:835:ASP:OD2	2.39	0.53
2:B:519:THR:HG23	2:B:589:ALA:HB1	1.90	0.53
2:B:502:LEU:HD21	2:B:670:ILE:HD11	1.91	0.53
2:B:48:ILE:HG12	2:B:984:ALA:HB1	1.90	0.53
2:B:324:ARG:HB2	2:B:402:GLN:HE22	1.74	0.53
2:B:378:PRO:O	2:B:382:LYS:HG2	2.09	0.53
2:B:597:LEU:O	2:B:601:ILE:HG13	2.08	0.52
2:B:870:VAL:HG23	2:B:908:LEU:HG	1.90	0.52
6:A:2021:HOH:O	2:B:63:ARG:NH1	2.42	0.52
2:B:1119:LEU:HB3	2:B:1128:PRO:HB2	1.91	0.52
2:B:1179:ILE:HD11	2:B:1192:LYS:HD3	1.92	0.52
2:B:290:PHE:O	6:B:2074:HOH:O	2.19	0.52
2:B:139:ARG:NH1	2:B:418:GLU:OE1	2.43	0.52
2:B:1177:ASN:ND2	2:B:1180:ASP:OD2	2.43	0.51
2:B:539:PHE:HB3	2:B:690:ASN:ND2	2.25	0.51
2:B:845:SER:O	2:B:920:GLN:NE2	2.33	0.51
2:B:1340:LYS:HA	2:B:1343:LEU:HD12	1.92	0.51
1:A:26:A:N7	6:A:2057:HOH:O	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1307:GLU:O	2:B:1310:ILE:HB	2.12	0.50
2:B:999:LYS:HB3	2:B:1073:VAL:HG12	1.94	0.50
2:B:215:ARG:NH2	2:B:395:ARG:O	2.42	0.50
1:A:36:A:H2'	1:A:37:U:H5'	1.92	0.50
2:B:1284:ASP:OD1	2:B:1284:ASP:N	2.23	0.50
1:A:71:U:H3	1:A:78:A:H61	1.59	0.49
2:B:137:HIS:HA	2:B:322:ILE:HD11	1.94	0.49
2:B:623:LEU:HG	2:B:654:ARG:O	2.13	0.49
2:B:584:GLU:O	2:B:586:ARG:N	2.45	0.49
1:A:27:G:H4'	1:A:28:A:OP2	2.12	0.49
2:B:1114:ARG:NH1	4:D:9:DA:OP1	2.45	0.49
1:A:18:A:OP1	2:B:165:ARG:HD3	2.13	0.49
2:B:951:ARG:NH1	2:B:1011:GLY:HA3	2.28	0.49
2:B:136:TYR:HA	2:B:139:ARG:HG3	1.95	0.49
2:B:290:PHE:HB3	6:B:2074:HOH:O	2.11	0.49
2:B:1079:ASP:O	2:B:1082:THR:OG1	2.25	0.48
2:B:910:GLU:HG2	2:B:1033:THR:HG23	1.96	0.48
2:B:826:GLN:NE2	2:B:859:ARG:HD3	2.28	0.48
1:A:69:A:H1'	2:B:1358:THR:HG21	1.96	0.48
1:A:73:G:C3'	1:A:74:A:H5''	2.43	0.48
1:A:73:G:H3'	1:A:74:A:C5'	2.42	0.48
2:B:215:ARG:HG3	2:B:307:ARG:CZ	2.43	0.47
2:B:901:THR:O	2:B:904:GLU:HG2	2.14	0.47
2:B:133:PRO:HG2	2:B:137:HIS:CE1	2.50	0.47
3:C:19:DA:H5''	3:C:19:DA:C8	2.49	0.47
2:B:814:TYR:CZ	2:B:830:ILE:HG23	2.50	0.47
2:B:1210:ARG:HA	2:B:1280:VAL:HG22	1.97	0.46
2:B:190:GLN:O	2:B:194:GLN:HG2	2.15	0.46
2:B:536:LYS:HG2	2:B:537:PRO:HD2	1.98	0.46
2:B:893:THR:HG23	2:B:896:LYS:H	1.80	0.46
2:B:69:ARG:O	2:B:73:THR:HG23	2.16	0.46
2:B:212:LEU:O	2:B:221:ARG:NE	2.48	0.46
1:A:68:A:HO2'	1:A:69:A:P	2.39	0.46
2:B:979:ASN:ND2	2:B:1226:LEU:O	2.47	0.45
2:B:1271:GLU:O	2:B:1275:GLU:HG3	2.15	0.45
2:B:238:PHE:HA	2:B:241:LEU:HD12	1.97	0.45
2:B:803:ASN:N	2:B:803:ASN:OD1	2.49	0.45
2:B:306:LEU:O	2:B:320:SER:HB3	2.16	0.45
1:A:37:U:H2'	1:A:38:A:O4'	2.17	0.45
2:B:1308:ASN:HB3	2:B:1326:TYR:O	2.16	0.45
2:B:794:GLN:HG2	2:B:794:GLN:H	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:910:GLU:HA	2:B:913:LYS:HD3	1.99	0.45
2:B:665:LYS:HA	2:B:669:GLY:HA3	1.99	0.45
1:A:28:A:N3	2:B:122:ILE:HG21	2.32	0.44
2:B:398:LEU:HG	2:B:399:LEU:HG	1.99	0.44
2:B:78:ARG:NH1	2:B:162:ILE:O	2.50	0.44
2:B:877:LYS:HE3	2:B:877:LYS:HB2	1.70	0.44
2:B:830:ILE:HG13	2:B:830:ILE:H	1.42	0.44
2:B:231:GLY:N	6:B:2068:HOH:O	2.51	0.44
2:B:1153:LYS:HB2	2:B:1153:LYS:HE3	1.69	0.44
2:B:1041:ASN:HB3	2:B:1044:ASN:ND2	2.33	0.44
2:B:178:ASN:O	2:B:178:ASN:ND2	2.47	0.44
2:B:349:GLU:HG2	2:B:356:LYS:HG3	2.00	0.44
2:B:896:LYS:NZ	6:B:2156:HOH:O	2.46	0.43
1:A:48:A:H2'	1:A:49:A:C8	2.52	0.43
2:B:1119:LEU:HA	2:B:1119:LEU:HD12	1.82	0.43
2:B:44:LYS:HG3	2:B:44:LYS:O	2.19	0.43
2:B:652:LYS:HE3	2:B:652:LYS:HB3	1.77	0.43
2:B:1171:ARG:O	2:B:1175:GLU:HG2	2.17	0.43
2:B:211:ILE:O	2:B:221:ARG:HD2	2.17	0.43
2:B:216:LEU:O	2:B:221:ARG:NH1	2.50	0.43
2:B:869:ASN:OD1	2:B:870:VAL:N	2.48	0.43
2:B:1136:SER:HA	4:D:7:DG:O3'	2.18	0.43
2:B:551:LEU:HD22	2:B:572:ILE:HD11	2.01	0.43
2:B:925:ARG:HB3	2:B:928:THR:HG23	2.00	0.43
2:B:373:TYR:O	2:B:377:LYS:HG3	2.19	0.43
2:B:561:VAL:HG22	2:B:583:VAL:HG13	2.01	0.43
2:B:746:GLU:OE2	2:B:1351:SER:HB3	2.17	0.43
1:A:68:A:O2'	1:A:69:A:OP1	2.30	0.43
2:B:566:GLU:O	2:B:570:LYS:HB3	2.19	0.42
2:B:1262:HIS:HA	2:B:1264:HIS:CE1	2.54	0.42
2:B:977:GLU:HG3	2:B:1310:ILE:CG2	2.48	0.42
1:A:47:A:O2'	2:B:101:LEU:O	2.34	0.42
2:B:1076:LYS:HG3	2:B:1080:PHE:CE2	2.47	0.42
2:B:956:ILE:HD11	2:B:998:ILE:HD13	2.00	0.42
2:B:79:ILE:HD11	2:B:163:LYS:HG3	2.02	0.42
2:B:234:LYS:HG2	2:B:234:LYS:H	1.50	0.42
4:D:7:DG:C8	4:D:7:DG:H5'	2.55	0.42
1:A:74:A:C2'	1:A:75:A:H5'	2.49	0.42
2:B:993:VAL:HG13	2:B:1043:MET:HE1	2.01	0.42
2:B:497:ASN:HD21	3:C:19:DA:P	2.43	0.42
2:B:1206:LEU:HD13	2:B:1210:ARG:HH12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:144:ASP:O	2:B:425:ARG:NH2	2.53	0.42
2:B:646:LYS:HE2	2:B:650:GLN:HG3	2.02	0.42
2:B:730:SER:O	2:B:733:ILE:HG22	2.19	0.42
2:B:400:ARG:NH2	2:B:406:ASP:OD2	2.53	0.42
2:B:787:GLY:O	2:B:791:LEU:HB2	2.19	0.42
1:A:27:G:H5'	1:A:28:A:C5'	2.50	0.41
2:B:1177:ASN:HA	2:B:1178:PRO:HD2	1.92	0.41
2:B:273:ASP:OD1	2:B:653:ARG:NH2	2.52	0.41
2:B:870:VAL:HG21	2:B:902:LYS:HB3	2.00	0.41
2:B:1206:LEU:HB3	2:B:1207:GLU:H	1.63	0.41
2:B:187:GLN:O	2:B:191:THR:HG23	2.20	0.41
2:B:448:ILE:HD13	2:B:455:LEU:HD13	2.01	0.41
2:B:1147:ALA:HB2	2:B:1190:VAL:HA	2.02	0.41
2:B:1308:ASN:O	2:B:1311:HIS:HB2	2.19	0.41
2:B:525:THR:HG23	2:B:545:LYS:NZ	2.33	0.41
2:B:1255:LYS:HG2	2:B:1255:LYS:H	1.62	0.41
2:B:442:LYS:HA	2:B:445:THR:HB	2.01	0.41
2:B:535:ARG:H	2:B:535:ARG:HG2	1.74	0.41
2:B:1122:ARG:HG3	2:B:1134:PHE:CE2	2.55	0.41
2:B:317:LEU:O	2:B:320:SER:OG	2.25	0.41
2:B:586:ARG:NH1	6:B:2129:HOH:O	2.53	0.41
2:B:1106:SER:HB3	2:B:1137:PRO:HA	2.02	0.41
2:B:531:THR:HG21	2:B:575:PHE:CZ	2.56	0.41
2:B:524:LEU:HD22	2:B:540:LEU:HD23	2.02	0.41
2:B:813:LEU:O	2:B:817:GLN:HG3	2.20	0.41
2:B:820:ARG:NH1	2:B:827:GLU:HG3	2.36	0.41
2:B:4:LYS:HB2	2:B:4:LYS:HE2	1.86	0.41
2:B:629:ARG:CZ	2:B:653:ARG:HA	2.50	0.41
2:B:272:ASP:HB2	2:B:653:ARG:NH2	2.35	0.41
1:A:35:A:H2'	1:A:36:A:C8	2.55	0.40
2:B:165:ARG:O	2:B:412:HIS:HA	2.21	0.40
2:B:251:ASN:HB2	2:B:263:LYS:HG2	2.02	0.40
2:B:749:LYS:HB3	2:B:749:LYS:HE2	1.84	0.40
1:A:25:U:H1'	2:B:104:SER:O	2.20	0.40
2:B:116:HIS:HA	2:B:117:PRO:HD3	1.78	0.40
2:B:528:LYS:HE3	2:B:539:PHE:CE1	2.56	0.40
2:B:558:LYS:HE2	2:B:586:ARG:HH12	1.86	0.40
1:A:33:G:N2	1:A:36:A:OP2	2.54	0.40
2:B:635:ARG:HG3	2:B:635:ARG:HH11	1.86	0.40
2:B:735:LYS:O	2:B:739:GLN:HG2	2.22	0.40
2:B:1089:MET:HA	2:B:1090:PRO:HD3	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:614:ASP:OD1	2:B:664:ARG:NH2	2.52	0.40
1:A:71:U:H3	1:A:78:A:N6	2.19	0.40

All (1) 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)
6:B:2016:HOH:O	6:B:2092:HOH:O[3_445]	2.18	0.02

## 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	
2	B	1292/1372 (94%)	1249 (97%)	43 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
2	B	1174/1227 (96%)	1047 (89%)	127 (11%)	7	14

All (127) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	13	THR
2	B	22	THR
2	B	27	VAL
2	B	29	SER
2	B	39	ASP
2	B	41	HIS
2	B	44	LYS
2	B	64	LEU
2	B	65	LYS
2	B	73	THR
2	B	82	LEU
2	B	87	SER
2	B	101	LEU
2	B	102	GLU
2	B	106	LEU
2	B	139	ARG
2	B	141	LYS
2	B	146	THR
2	B	165	ARG
2	B	173	ASP
2	B	174	LEU
2	B	178	ASN
2	B	188	LEU
2	B	197	GLU
2	B	198	GLU
2	B	212	LEU
2	B	215	ARG
2	B	220	ARG
2	B	226	ILE
2	B	244	LEU
2	B	257	ASP
2	B	300	ILE
2	B	304	ASP
2	B	311	GLU
2	B	321	MET
2	B	334	LEU
2	B	345	GLU
2	B	387	GLU
2	B	419	LEU
2	B	425	ARG
2	B	438	GLU
2	B	465	MET
2	B	466	THR

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Mol	Chain	Res	Type
2	B	471	GLU
2	B	502	LEU
2	B	514	LEU
2	B	530	VAL
2	B	536	LYS
2	B	540	LEU
2	B	543	GLU
2	B	557	ARG
2	B	579	GLU
2	B	581	SER
2	B	598	LEU
2	B	599	LYS
2	B	602	LYS
2	B	610	GLU
2	B	623	LEU
2	B	627	GLU
2	B	630	GLU
2	B	635	ARG
2	B	638	THR
2	B	643	PHE
2	B	661	ARG
2	B	666	LEU
2	B	696	LEU
2	B	699	ASP
2	B	703	THR
2	B	707	ASP
2	B	709	GLN
2	B	726	ASN
2	B	735	LYS
2	B	738	LEU
2	B	751	MET
2	B	782	LYS
2	B	785	GLU
2	B	794	GLN
2	B	801	VAL
2	B	803	ASN
2	B	811	LEU
2	B	830	ILE
2	B	856	VAL
2	B	859	ARG
2	B	861	ASP
2	B	867	SER

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Mol	Chain	Res	Type
2	B	884	ARG
2	B	887	LEU
2	B	894	GLN
2	B	910	GLU
2	B	918	LYS
2	B	919	ARG
2	B	921	LEU
2	B	933	GLN
2	B	935	LEU
2	B	945	GLU
2	B	957	THR
2	B	968	LYS
2	B	977	GLU
2	B	1003	LYS
2	B	1031	LYS
2	B	1033	THR
2	B	1035	LYS
2	B	1049	GLU
2	B	1076	LYS
2	B	1078	ARG
2	B	1087	LEU
2	B	1089	MET
2	B	1091	GLN
2	B	1144	LEU
2	B	1146	VAL
2	B	1160	VAL
2	B	1172	SER
2	B	1175	GLU
2	B	1197	LYS
2	B	1207	GLU
2	B	1216	SER
2	B	1236	LEU
2	B	1240	SER
2	B	1253	GLU
2	B	1270	ILE
2	B	1272	GLN
2	B	1274	SER
2	B	1284	ASP
2	B	1314	THR
2	B	1342	VAL
2	B	1347	LEU
2	B	1358	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	402	GLN
2	B	1256	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	80/83 (96%)	21 (26%)	0

All (21) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	A
1	A	20	A
1	A	28	A
1	A	29	G
1	A	31	U
1	A	32	A
1	A	34	A
1	A	35	A
1	A	37	U
1	A	38	A
1	A	40	C
1	A	42	A
1	A	43	G
1	A	51	A
1	A	56	U
1	A	59	U
1	A	68	A
1	A	69	A
1	A	74	A
1	A	75	A
1	A	79	G

There are no RNA pucker outliers to report.

## 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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 [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	81/83 (97%)	-0.26	0 100 100	16, 38, 96, 112	0
2	B	1306/1372 (95%)	0.17	37 (2%) 53 46	12, 43, 76, 100	0
3	C	28/28 (100%)	-0.30	0 100 100	24, 38, 66, 85	0
4	D	11/12 (91%)	0.34	0 100 100	37, 47, 86, 97	0
All	All	1426/1495 (95%)	0.14	37 (2%) 56 49	12, 43, 77, 112	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	178	ASN	3.6
2	B	1296	LYS	3.4
2	B	200	PRO	3.2
2	B	803	ASN	3.0
2	B	804	THR	2.9
2	B	1264	HIS	2.9
2	B	382	LYS	2.9
2	B	204	SER	2.8
2	B	1257	LEU	2.8
2	B	197	GLU	2.7
2	B	377	LYS	2.7
2	B	1033	THR	2.7
2	B	199	ASN	2.6
2	B	530	VAL	2.6
2	B	807	GLN	2.5
2	B	1295	ASN	2.5
2	B	242	ILE	2.5
2	B	868	ASP	2.4
2	B	1037	PHE	2.4
2	B	1050	ILE	2.4
2	B	198	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	848	LYS	2.3
2	B	469	SER	2.3
2	B	1298	ARG	2.2
2	B	529	TYR	2.2
2	B	692	ASN	2.2
2	B	580	ILE	2.1
2	B	688	PHE	2.1
2	B	584	GLU	2.1
2	B	347	TYR	2.1
2	B	697	ILE	2.1
2	B	424	ARG	2.1
2	B	1012	ASP	2.1
2	B	947	ASP	2.0
2	B	205	GLY	2.0
2	B	398	LEU	2.0
2	B	1003	LYS	2.0

## 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(Å <sup>2</sup> )	Q<0.9
5	MG	A	1082	1/1	0.86	0.17	1.00	27,27,27,27	0
5	MG	B	2368	1/1	0.58	0.25	0.60	36,36,36,36	0
5	MG	B	2367	1/1	0.71	0.17	-0.09	15,15,15,15	0
5	MG	B	2366	1/1	0.87	0.11	-0.99	25,25,25,25	0
5	MG	A	1083	1/1	0.98	0.11	-2.87	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MG	B	2365	1/1	0.58	0.28	-	53,53,53,53	0
5	MG	A	1084	1/1	0.91	0.12	-	27,27,27,27	0
5	MG	A	1085	1/1	0.79	0.51	-	53,53,53,53	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.