



Full wwPDB X-ray Structure Validation Report ⓘ

May 30, 2020 – 01:51 am BST

PDB ID : 6IV9
Title : the Cas13d binary complex
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Deposited on : 2018-12-02
Resolution : 1.86 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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

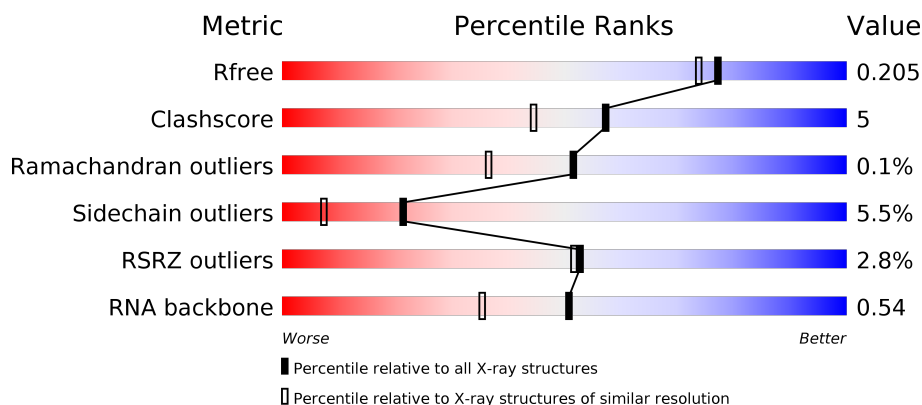
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)
RNA backbone	3102	1026 (2.40-1.32)

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 respectively. 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	930	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>11%</div> <div>6%</div> </div> </div>
2	B	50	<div> <div>4%</div> <div> <div></div> <div>52%</div> <div>38%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8657 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 Cas13d.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	874	Total	C	N	O	S	0	3	0
			7126	4530	1206	1355	35			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	288	ALA	ARG	engineered mutation	UNP A0A1C5SD84
A	823	ALA	ARG	engineered mutation	UNP A0A1C5SD84
A	923	LEU	-	expression tag	UNP A0A1C5SD84
A	924	GLU	-	expression tag	UNP A0A1C5SD84
A	925	HIS	-	expression tag	UNP A0A1C5SD84
A	926	HIS	-	expression tag	UNP A0A1C5SD84
A	927	HIS	-	expression tag	UNP A0A1C5SD84
A	928	HIS	-	expression tag	UNP A0A1C5SD84
A	929	HIS	-	expression tag	UNP A0A1C5SD84
A	930	HIS	-	expression tag	UNP A0A1C5SD84

- Molecule 2 is a RNA chain called crRNA (50-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	50	Total	C	N	O	P	0	0	0
			1054	474	185	345	50			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

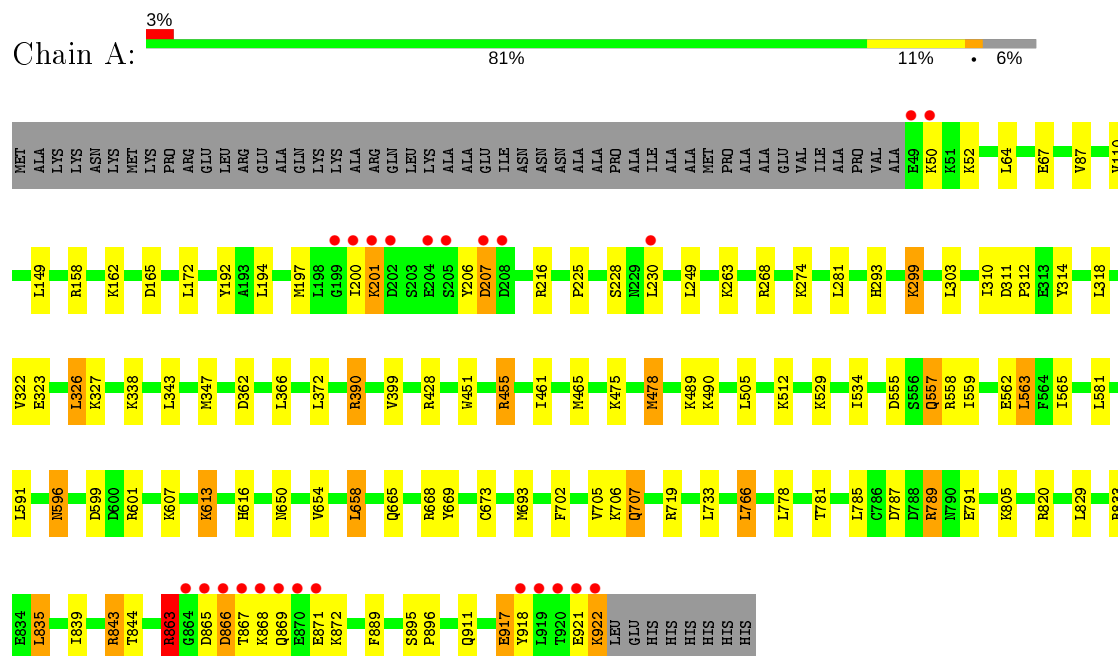
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	358	Total 358	O 358	0	0
4	B	117	Total 117	O 117	0	0

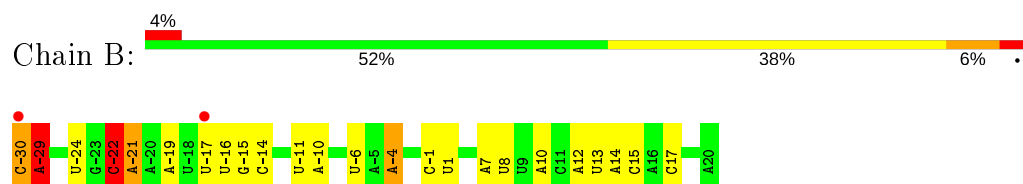
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Cas13d



• Molecule 2: crRNA (50-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.22Å 136.48Å 147.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.11 – 1.86 100.11 – 1.86	Depositor EDS
% Data completeness (in resolution range)	98.7 (100.11-1.86) 98.7 (100.11-1.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.170 , 0.196 0.184 , 0.205	Depositor DCC
R_{free} test set	6055 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8657	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 4.10% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.84	2/7249 (0.0%)	0.74	3/9721 (0.0%)
2	B	1.15	9/1177 (0.8%)	1.09	10/1828 (0.5%)
All	All	0.89	11/8426 (0.1%)	0.80	13/11549 (0.1%)

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	11

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	-14	C	P-OP2	-7.82	1.35	1.49
2	B	-14	C	P-OP1	-7.38	1.36	1.49
2	B	-29	A	O3'-P	-6.74	1.53	1.61
1	A	557[A]	GLN	N-CA	6.43	1.59	1.46
1	A	557[B]	GLN	N-CA	6.43	1.59	1.46
2	B	-4	A	O3'-P	5.99	1.68	1.61
2	B	-22	C	O3'-P	-5.82	1.54	1.61
2	B	-14	C	O3'-P	-5.50	1.54	1.61
2	B	-10	A	P-OP1	-5.16	1.40	1.49
2	B	-21	A	O3'-P	-5.08	1.55	1.61
2	B	-15	G	O3'-P	-5.07	1.55	1.61

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	U	O5'-P-OP2	-6.80	99.58	105.70
2	B	-24	U	O5'-P-OP2	-6.67	99.69	105.70
2	B	17	C	O5'-P-OP2	-6.31	100.02	105.70
1	A	207	ASP	CB-CA-C	6.25	122.90	110.40
2	B	14	A	O5'-P-OP1	6.07	117.98	110.70
2	B	12	A	O5'-P-OP2	-5.95	100.35	105.70
2	B	15	C	O4'-C1'-N1	5.90	112.92	108.20
2	B	-6	U	O5'-P-OP1	-5.79	100.49	105.70
2	B	-1	C	P-O3'-C3'	-5.28	113.36	119.70
1	A	833[A]	ARG	N-CA-C	5.18	124.99	111.00
1	A	833[B]	ARG	N-CA-C	5.18	124.99	111.00
2	B	-4	A	O5'-P-OP2	-5.15	101.07	105.70
2	B	-11	U	O3'-P-O5'	-5.04	94.43	104.00

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	158	ARG	Sidechain
1	A	268	ARG	Sidechain
1	A	390	ARG	Sidechain
1	A	428	ARG	Sidechain
1	A	601	ARG	Sidechain
1	A	668	ARG	Sidechain
1	A	719	ARG	Sidechain
1	A	789	ARG	Sidechain
1	A	820	ARG	Sidechain
1	A	843	ARG	Sidechain
1	A	863	ARG	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	7126	0	7195	70	0
2	B	1054	0	538	12	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	358	0	0	5	0
4	B	117	0	0	0	0
All	All	8657	0	7733	78	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 5.

All (78) 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:B:-22:C:H6	2:B:-22:C:H5''	1.17	1.08
2:B:-22:C:C6	2:B:-22:C:H5''	2.03	0.94
1:A:918:TYR:CD1	2:B:-30:C:N4	2.45	0.83
1:A:201:LYS:HA	1:A:201:LYS:HE2	1.70	0.73
1:A:489:LYS:HE2	4:A:1114:HOH:O	1.90	0.72
1:A:529:LYS:HE2	1:A:557[A]:GLN:HE22	1.57	0.70
2:B:-30:C:H4'	2:B:-29:A:H5'	1.74	0.68
1:A:863:ARG:NH2	1:A:872:LYS:HD2	2.10	0.67
1:A:918:TYR:O	1:A:922:LYS:HD3	1.94	0.67
2:B:-22:C:C5'	2:B:-22:C:H6	2.04	0.64
1:A:581:LEU:HD21	1:A:599:ASP:HB3	1.78	0.64
1:A:362:ASP:HA	1:A:366:LEU:HD23	1.80	0.63
1:A:529:LYS:CE	1:A:557[A]:GLN:NE2	2.62	0.63
1:A:201:LYS:HA	1:A:201:LYS:CE	2.29	0.62
1:A:866:ASP:OD1	1:A:866:ASP:N	2.33	0.62
1:A:529:LYS:CE	1:A:557[A]:GLN:HE22	2.11	0.61
1:A:787:ASP:OD1	1:A:805:LYS:NZ	2.34	0.61
1:A:650:ASN:HB2	4:A:1193:HOH:O	2.00	0.60
1:A:872:LYS:NZ	4:A:1101:HOH:O	2.34	0.60
1:A:607:LYS:O	1:A:616:HIS:HE1	1.86	0.59
1:A:529:LYS:HE2	1:A:557[A]:GLN:NE2	2.18	0.58
1:A:225:PRO:O	1:A:228:SER:HB3	2.03	0.58
1:A:917:GLU:O	1:A:922:LYS:HE2	2.03	0.57
1:A:921:GLU:HG3	2:B:-30:C:N4	2.19	0.57
1:A:785:LEU:HD22	1:A:789:ARG:HD2	1.86	0.56
1:A:52:LYS:HG2	4:A:1281:HOH:O	2.05	0.56
1:A:200:ILE:HD12	1:A:200:ILE:O	2.06	0.55
1:A:323:GLU:O	1:A:327:LYS:HG3	2.06	0.55
1:A:673:CYS:HB3	1:A:693:MET:HE1	1.87	0.55
1:A:216:ARG:HH11	1:A:216:ARG:HG3	1.72	0.55
1:A:707:GLN:HA	1:A:707:GLN:HE21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:LEU:N	1:A:366:LEU:HD22	2.23	0.54
2:B:-30:C:H5'	2:B:-29:A:H5'	1.90	0.54
1:A:766:LEU:HD13	1:A:781:THR:HG21	1.90	0.54
1:A:172:LEU:C	1:A:172:LEU:HD23	2.29	0.53
2:B:-22:C:C5'	2:B:-22:C:C6	2.85	0.52
1:A:654:VAL:HG12	1:A:658:LEU:HD22	1.92	0.52
1:A:451:TRP:HE1	1:A:455:ARG:CZ	2.24	0.51
1:A:702:PHE:O	1:A:705:VAL:HG12	2.10	0.51
1:A:318:LEU:O	1:A:322:VAL:HG23	2.12	0.50
1:A:559:ILE:HG22	1:A:563:LEU:HD22	1.92	0.50
1:A:64:LEU:CD1	1:A:534:ILE:HG21	2.43	0.49
1:A:835:LEU:HD22	1:A:839:ILE:HB	1.95	0.49
1:A:529:LYS:HD3	1:A:557[A]:GLN:NE2	2.28	0.48
2:B:-30:C:C5'	2:B:-29:A:H5'	2.43	0.48
1:A:338:LYS:HB2	1:A:478:MET:HG3	1.95	0.48
1:A:322:VAL:HG12	1:A:326:LEU:HD22	1.95	0.47
1:A:895:SER:N	1:A:896:PRO:CD	2.77	0.47
1:A:596:ASN:HD22	1:A:596:ASN:C	2.16	0.47
1:A:399:VAL:HG21	1:A:465:MET:HB3	1.96	0.47
2:B:-30:C:C4'	2:B:-29:A:H5'	2.44	0.47
1:A:558:ARG:O	1:A:562:GLU:HG3	2.16	0.46
1:A:216:ARG:NH1	1:A:216:ARG:HG3	2.30	0.45
1:A:192:TYR:HA	1:A:206:TYR:OH	2.17	0.45
1:A:613:LYS:HB2	1:A:613:LYS:HE2	1.51	0.45
1:A:665:GLN:HG3	1:A:669:TYR:CE2	2.51	0.45
1:A:293:HIS:CE1	1:A:299:LYS:HD3	2.51	0.45
1:A:310:ILE:HD12	1:A:314:TYR:CG	2.51	0.45
1:A:918:TYR:HB3	1:A:921:GLU:HG2	1.99	0.44
1:A:194:LEU:HD13	1:A:281:LEU:HD22	2.00	0.44
1:A:693:MET:HE3	1:A:693:MET:HB3	1.78	0.44
1:A:216:ARG:NH1	4:A:1106:HOH:O	2.49	0.43
1:A:917:GLU:HB3	1:A:918:TYR:CD2	2.53	0.43
1:A:249:LEU:HD13	1:A:274:LYS:HD3	2.01	0.43
1:A:87:VAL:HG11	1:A:110:VAL:HG11	2.00	0.43
1:A:805:LYS:HA	1:A:805:LYS:HD3	1.74	0.43
1:A:563:LEU:HA	1:A:563:LEU:HD12	1.90	0.43
1:A:201:LYS:HE2	1:A:201:LYS:CA	2.28	0.42
1:A:67:GLU:OE1	1:A:67:GLU:HA	2.21	0.41
1:A:461:ILE:O	1:A:465:MET:HG2	2.21	0.41
1:A:192:TYR:CD2	1:A:829:LEU:HD22	2.55	0.41
1:A:529:LYS:CD	1:A:557[A]:GLN:NE2	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:843:ARG:HG2	1:A:844:THR:HG23	2.02	0.41
1:A:918:TYR:CG	2:B:-30:C:N4	2.76	0.41
1:A:512:LYS:HE3	2:B:8:U:P	2.61	0.41
1:A:490:LYS:HD2	1:A:565:ILE:HD13	2.03	0.40
1:A:200:ILE:CD1	1:A:200:ILE:O	2.70	0.40
1:A:311:ASP:OD1	1:A:312:PRO:HD2	2.21	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
1	A	875/930 (94%)	865 (99%)	9 (1%)	1 (0%)	51 36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	871	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
1	A	791/830 (95%)	748 (95%)	43 (5%)	22 8

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LYS
1	A	149	LEU
1	A	162	LYS
1	A	165	ASP
1	A	197	MET
1	A	201	LYS
1	A	207	ASP
1	A	230	LEU
1	A	263	LYS
1	A	299	LYS
1	A	303	LEU
1	A	326	LEU
1	A	343	LEU
1	A	347	MET
1	A	372	LEU
1	A	390	ARG
1	A	455	ARG
1	A	475	LYS
1	A	478	MET
1	A	505	LEU
1	A	555	ASP
1	A	563	LEU
1	A	591	LEU
1	A	596	ASN
1	A	613	LYS
1	A	658	LEU
1	A	706	LYS
1	A	707	GLN
1	A	733	LEU
1	A	766	LEU
1	A	778	LEU
1	A	791	GLU
1	A	835	LEU
1	A	863	ARG
1	A	865	ASP
1	A	866	ASP
1	A	867	THR
1	A	868	LYS
1	A	869	GLN
1	A	889	PHE
1	A	911	GLN
1	A	917	GLU

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Mol	Chain	Res	Type
1	A	922	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	596	ASN
1	A	616	HIS
1	A	707	GLN
1	A	828	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	50/50 (100%)	10 (20%)	3 (6%)

All (10) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	-29	A
2	B	-22	C
2	B	-21	A
2	B	-19	A
2	B	-17	U
2	B	-16	U
2	B	-4	A
2	B	7	A
2	B	10	A
2	B	13	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	-30	C
2	B	-22	C
2	B	-4	A

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 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 [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	A	874/930 (93%)	0.02	24 (2%) 54 53	20, 35, 66, 140	0
2	B	50/50 (100%)	-0.27	2 (4%) 38 36	24, 34, 77, 127	0
All	All	924/980 (94%)	0.00	26 (2%) 53 52	20, 35, 68, 140	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	867	THR	8.5
1	A	865	ASP	8.2
1	A	866	ASP	6.9
1	A	864	GLY	6.5
1	A	205	SER	5.6
1	A	869	GLN	5.3
1	A	202	ASP	5.2
1	A	201	LYS	4.7
1	A	204	GLU	4.5
1	A	49	GLU	4.4
1	A	200	ILE	4.2
1	A	871	GLU	3.9
1	A	868	LYS	3.7
1	A	921	GLU	3.7
1	A	920	THR	3.6
1	A	199	GLY	3.5
1	A	208	ASP	3.4
1	A	50	LYS	3.1
1	A	919	LEU	3.1
1	A	918	TYR	2.7
2	B	-30	C	2.6
2	B	-17	U	2.5
1	A	922	LYS	2.5
1	A	207	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	870	GLU	2.3
1	A	230	LEU	2.3

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. 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	B-factors(\AA^2)	Q<0.9
3	MG	B	101	1/1	0.81	0.20	51,51,51,51	0
3	MG	A	1001	1/1	0.99	0.09	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.