



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:37 pm GMT

PDB ID : 2O3S
Title : Structural Basis for Formation and Hydrolysis of Calcium Messenger Cyclic ADP-ribose by Human CD38
Authors : Liu, Q.; Kriksunov, I.A.; Graeff, R.; Lee, H.C.; Hao, Q.
Deposited on : 2006-12-01
Resolution : 1.50 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 : 1.7.2 (RC1), CSD as538be (2017)
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

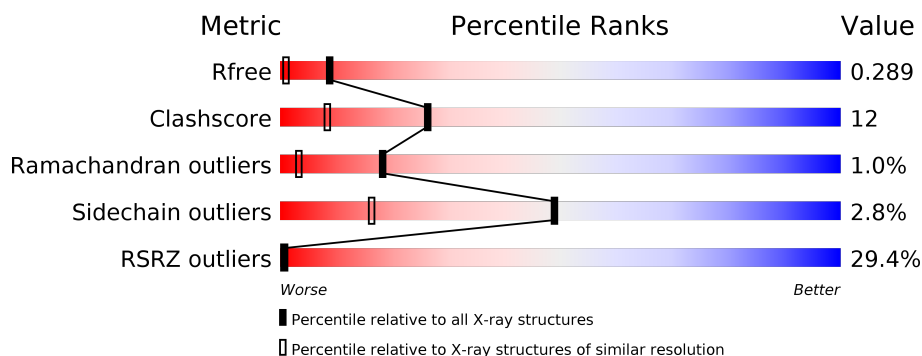
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	2279 (1.50-1.50)
Clashscore	112137	2503 (1.50-1.50)
Ramachandran outliers	110173	2445 (1.50-1.50)
Sidechain outliers	110143	2443 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)

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	A	262	<div> <div>15%</div> <div>79%</div> <div>15%</div> <div>• •</div> </div>
1	B	262	<div> <div>42%</div> <div>76%</div> <div>19%</div> <div>• •</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CXR	A	301	X	-	-	-
2	CXR	B	301	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4808 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 ADP-ribosyl cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2038	1286	352	384	16			
1	B	252	Total	C	N	O	S	0	0	0
			2038	1286	352	384	16			

There are 26 discrepancies between the modelled and reference sequences:

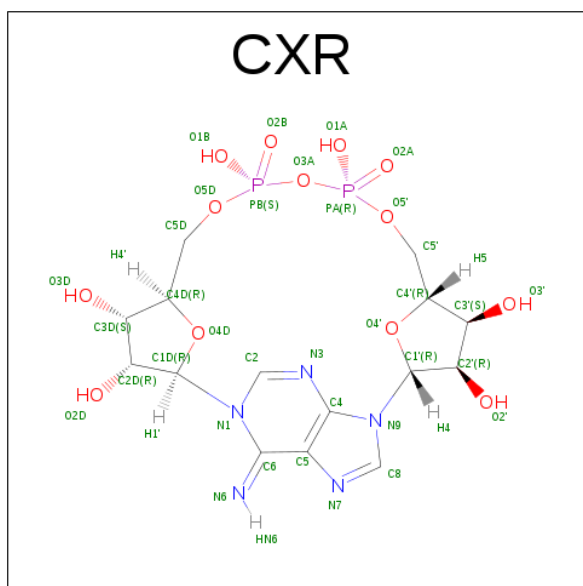
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LYS	-	CLONING ARTIFACT	UNP P28907
A	40	ARG	-	CLONING ARTIFACT	UNP P28907
A	41	GLU	-	CLONING ARTIFACT	UNP P28907
A	42	ALA	-	CLONING ARTIFACT	UNP P28907
A	43	GLU	-	CLONING ARTIFACT	UNP P28907
A	44	ALA	-	CLONING ARTIFACT	UNP P28907
A	45	PHE	ARG	ENGINEERED	UNP P28907
A	49	THR	GLN	ENGINEERED	UNP P28907
A	100	ASP	ASN	ENGINEERED	UNP P28907
A	164	ASP	ASN	ENGINEERED	UNP P28907
A	209	ASP	ASN	ENGINEERED	UNP P28907
A	219	ASP	ASN	ENGINEERED	UNP P28907
A	226	GLY	GLU	ENGINEERED	UNP P28907
B	39	LYS	-	CLONING ARTIFACT	UNP P28907
B	40	ARG	-	CLONING ARTIFACT	UNP P28907
B	41	GLU	-	CLONING ARTIFACT	UNP P28907
B	42	ALA	-	CLONING ARTIFACT	UNP P28907
B	43	GLU	-	CLONING ARTIFACT	UNP P28907
B	44	ALA	-	CLONING ARTIFACT	UNP P28907
B	45	PHE	ARG	ENGINEERED	UNP P28907
B	49	THR	GLN	ENGINEERED	UNP P28907
B	100	ASP	ASN	ENGINEERED	UNP P28907
B	164	ASP	ASN	ENGINEERED	UNP P28907
B	209	ASP	ASN	ENGINEERED	UNP P28907
B	219	ASP	ASN	ENGINEERED	UNP P28907

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Chain	Residue	Modelled	Actual	Comment	Reference
B	226	GLY	GLU	ENGINEERED	UNP P28907

- Molecule 2 is CYCLIC ADENOSINE DIPHOSPHATE-RIBOSE (three-letter code: CXR) (formula: $C_{15}H_{21}N_5O_{13}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 35	C 15	N 5	O 13	P 2	0	0
2	B	1	Total 35	C 15	N 5	O 13	P 2	0	0

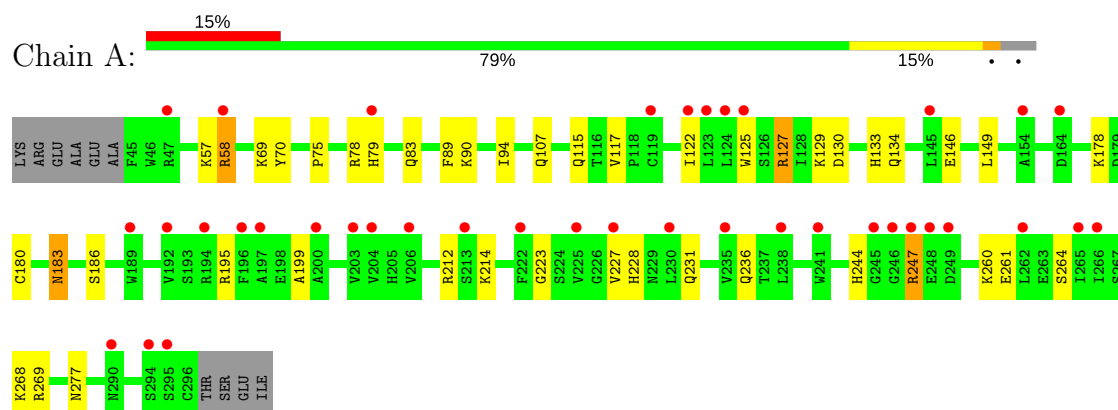
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	386	Total O 386 386	0	0
3	B	276	Total O 276 276	0	0

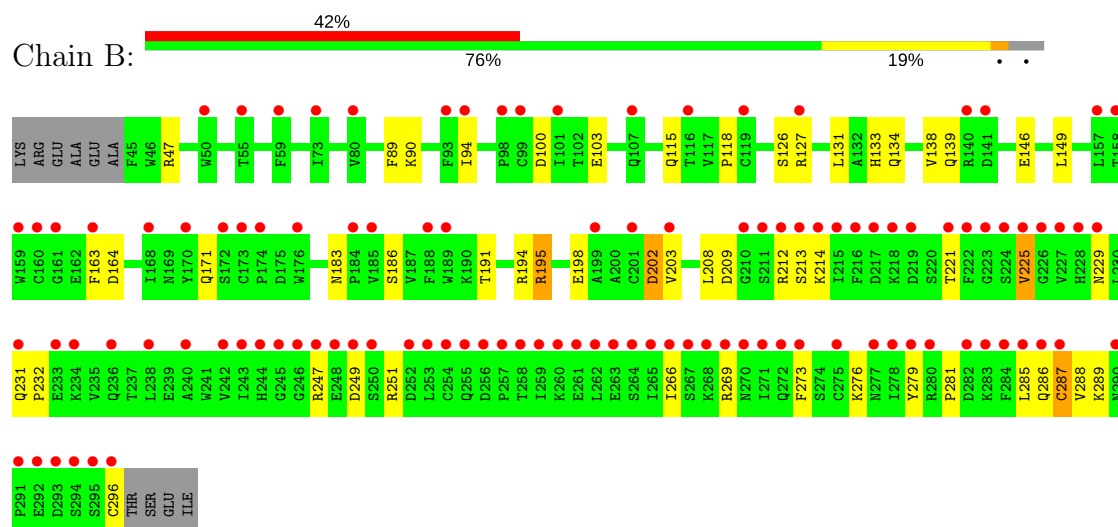
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: ADP-ribosyl cyclase 1



• Molecule 1: ADP-ribosyl cyclase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.35Å 53.79Å 66.83Å 104.97° 91.71° 95.04°	Depositor
Resolution (Å)	20.00 – 1.50 36.18 – 1.50	Depositor EDS
% Data completeness (in resolution range)	86.7 (20.00-1.50) 80.9 (36.18-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.3.0017	Depositor
R, R_{free}	0.189 , 0.238 0.257 , 0.289	Depositor DCC
R_{free} test set	3846 reflections (4.93%)	DCC
Wilson B-factor (Å ²)	20.3	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 63.2	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	0.94	EDS
Total number of atoms	4808	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 7.41% 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: CXR

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.00	1/2090 (0.0%)	0.83	1/2832 (0.0%)
1	B	0.89	2/2090 (0.1%)	0.72	0/2832
All	All	0.95	3/4180 (0.1%)	0.78	1/5664 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	287	CYS	CB-SG	9.46	1.98	1.82
1	B	202	ASP	C-N	5.41	1.46	1.34
1	A	70	TYR	CD1-CE1	5.30	1.47	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	NE-CZ-NH2	-7.87	116.36	120.30

There are no chirality outliers.

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	A	2038	0	1957	47	0
1	B	2038	0	1959	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	35	0	18	0	0
2	B	35	0	19	3	0
3	A	386	0	0	22	0
3	B	276	0	0	8	0
All	All	4808	0	3953	94	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 12.

All (94) 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:58:ARG:HH11	1:A:58:ARG:HG2	1.03	1.18
1:B:195:ARG:HH11	1:B:195:ARG:HG2	0.95	1.11
1:A:268:LYS:HD3	1:B:163:PHE:HE1	1.12	1.05
1:A:268:LYS:HD3	1:B:163:PHE:CE1	1.91	1.05
1:B:195:ARG:HG2	1:B:195:ARG:NH1	1.74	0.93
1:B:287:CYS:HG	1:B:296:CYS:HG	0.95	0.88
1:A:58:ARG:CG	1:A:58:ARG:HH11	1.84	0.87
1:A:58:ARG:NH1	1:A:58:ARG:HG2	1.85	0.84
1:A:115:GLN:HE22	1:A:149:LEU:H	1.26	0.82
1:A:228:HIS:HD2	1:B:100:ASP:OD1	1.62	0.82
1:B:131:LEU:O	1:B:131:LEU:HD23	1.82	0.80
1:B:115:GLN:HE22	1:B:149:LEU:H	1.28	0.79
1:A:268:LYS:CD	1:B:163:PHE:CE1	2.66	0.78
1:A:231:GLN:HG3	3:A:665:HOH:O	1.84	0.77
1:B:195:ARG:HH11	1:B:195:ARG:CG	1.88	0.76
1:A:127:ARG:HB3	1:A:212:ARG:HE	1.50	0.74
1:A:268:LYS:CD	1:B:163:PHE:HE1	1.96	0.73
1:A:261:GLU:HG3	3:A:679:HOH:O	1.90	0.70
1:A:79:HIS:CE1	3:A:608:HOH:O	2.47	0.67
1:A:260:LYS:NZ	3:A:675:HOH:O	2.24	0.64
1:A:199:ALA:HB3	3:A:538:HOH:O	1.98	0.63
1:B:266:ILE:HD11	1:B:273:PHE:HB2	1.81	0.61
1:B:134:GLN:HE21	1:B:285:LEU:HD11	1.67	0.59
1:A:228:HIS:CD2	1:B:100:ASP:OD1	2.52	0.58
1:A:75:PRO:O	1:A:78:ARG:HG2	2.04	0.58
1:B:183:ASN:ND2	1:B:186:SER:H	2.02	0.58
1:B:139:GLN:HE21	1:B:288:VAL:HG13	1.70	0.57
1:B:90:LYS:CG	1:B:94:ILE:HG13	2.36	0.56
1:A:180:CYS:HB2	3:A:426:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ASN:ND2	1:A:186:SER:H	2.05	0.55
1:B:118:PRO:HG2	3:B:435:HOH:O	2.06	0.55
1:B:269:ARG:HH11	1:B:269:ARG:HB3	1.71	0.55
1:A:57:LYS:HG3	3:A:516:HOH:O	2.06	0.54
1:B:90:LYS:HG2	1:B:94:ILE:HG13	1.90	0.54
1:A:195:ARG:NH1	3:A:367:HOH:O	2.39	0.54
1:A:261:GLU:HA	3:A:679:HOH:O	2.08	0.54
1:A:90:LYS:CG	1:A:94:ILE:HG13	2.38	0.53
1:B:221:THR:HG21	2:B:301:CXR:H12	1.89	0.53
1:A:125:TRP:CH2	1:A:129:LYS:HB2	2.44	0.53
1:B:232:PRO:HD3	1:B:269:ARG:HH12	1.73	0.53
1:B:195:ARG:HD3	3:B:431:HOH:O	2.08	0.53
1:B:47:ARG:HH11	1:B:47:ARG:HG2	1.73	0.52
1:A:90:LYS:HG3	1:A:94:ILE:HG13	1.92	0.51
1:B:115:GLN:NE2	1:B:149:LEU:H	2.04	0.51
3:A:679:HOH:O	1:B:163:PHE:HE2	1.93	0.50
1:B:171:GLN:NE2	3:B:563:HOH:O	2.44	0.50
1:B:47:ARG:NH1	1:B:47:ARG:HG2	2.27	0.50
1:A:214:LYS:NZ	3:A:501:HOH:O	2.45	0.50
2:B:301:CXR:H4'	3:B:575:HOH:O	2.13	0.49
1:A:134:GLN:CD	3:A:666:HOH:O	2.50	0.49
1:A:57:LYS:HG2	3:A:620:HOH:O	2.12	0.49
1:B:195:ARG:CG	1:B:195:ARG:NH1	2.56	0.49
1:B:209:ASP:OD2	1:B:212:ARG:HG2	2.12	0.49
1:B:212:ARG:C	1:B:214:LYS:H	2.16	0.49
1:A:58:ARG:CG	1:A:58:ARG:NH1	2.56	0.48
1:B:194:ARG:HG3	1:B:229:ASN:ND2	2.28	0.48
1:B:131:LEU:HD23	1:B:131:LEU:C	2.33	0.48
1:B:171:GLN:NE2	3:B:365:HOH:O	2.45	0.48
1:A:236:GLN:HG2	3:A:376:HOH:O	2.13	0.48
1:B:198:GLU:HG3	1:B:229:ASN:HB3	1.96	0.47
1:A:133:HIS:HE1	1:A:146:GLU:OE1	1.97	0.47
1:A:127:ARG:CB	1:A:212:ARG:HE	2.24	0.47
1:B:90:LYS:HD2	3:B:565:HOH:O	2.14	0.47
1:B:183:ASN:HD21	1:B:186:SER:H	1.63	0.47
1:A:244:HIS:HE1	1:A:277:ASN:OD1	1.98	0.46
1:B:279:TYR:O	1:B:281:PRO:HD3	2.16	0.46
1:A:83:GLN:NE2	3:A:674:HOH:O	2.40	0.45
1:A:122:ILE:CD1	3:A:538:HOH:O	2.63	0.45
1:B:126:SER:HB3	1:B:208:LEU:HD23	1.99	0.45
1:B:212:ARG:C	1:B:214:LYS:N	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:ARG:HA	1:A:247:ARG:HD3	1.77	0.44
1:B:133:HIS:CE1	1:B:146:GLU:HB2	2.53	0.44
1:B:133:HIS:HE1	1:B:146:GLU:OE1	2.00	0.43
1:B:47:ARG:HD2	3:B:529:HOH:O	2.18	0.43
1:A:115:GLN:NE2	1:A:149:LEU:H	2.04	0.43
2:B:301:CXR:H3	2:B:301:CXR:C5D	2.49	0.43
1:B:209:ASP:HB3	1:B:212:ARG:HG2	2.00	0.43
1:A:122:ILE:HD11	3:A:538:HOH:O	2.19	0.42
1:A:78:ARG:NH1	3:A:491:HOH:O	2.52	0.42
1:B:286:GLN:HG3	3:B:495:HOH:O	2.18	0.42
1:A:183:ASN:HD21	1:A:186:SER:H	1.65	0.42
1:B:287:CYS:CB	1:B:296:CYS:HG	2.32	0.42
1:A:264:SER:HB2	1:B:163:PHE:HZ	1.85	0.42
1:B:231:GLN:HA	1:B:232:PRO:HD3	1.90	0.42
1:B:138:VAL:HG11	1:B:289:LYS:HA	2.03	0.41
1:A:90:LYS:HG2	1:A:94:ILE:HG13	2.02	0.41
1:A:223:GLY:O	1:A:227:VAL:CG1	2.69	0.41
1:A:236:GLN:CG	3:A:376:HOH:O	2.67	0.41
1:B:103:GLU:HG3	1:B:191:THR:HG23	2.01	0.41
1:B:221:THR:O	1:B:225:VAL:HB	2.21	0.41
1:A:178:LYS:HG3	3:A:387:HOH:O	2.20	0.40
1:B:202:ASP:HB3	1:B:203:VAL:H	1.57	0.40
1:A:107:GLN:HG2	3:A:609:HOH:O	2.20	0.40
1:A:228:HIS:HE1	3:A:324:HOH:O	2.03	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	250/262 (95%)	237 (95%)	12 (5%)	1 (0%)	38 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	250/262 (95%)	229 (92%)	17 (7%)	4 (2%)	11	1
All	All	500/524 (95%)	466 (93%)	29 (6%)	5 (1%)	18	3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	247	ARG
1	B	225	VAL
1	B	213	SER
1	B	247	ARG
1	B	249	ASP

5.3.2 Protein sidechains ⓘ

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	231/240 (96%)	224 (97%)	7 (3%)	46	14
1	B	231/240 (96%)	225 (97%)	6 (3%)	51	18
All	All	462/480 (96%)	449 (97%)	13 (3%)	49	16

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	ARG
1	A	69	LYS
1	A	89	PHE
1	A	117	VAL
1	A	127	ARG
1	A	130	ASP
1	A	183	ASN
1	B	89	PHE
1	B	127	ARG
1	B	164	ASP
1	B	195	ARG

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Mol	Chain	Res	Type
1	B	251	ARG
1	B	276	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	133	HIS
1	A	134	GLN
1	A	183	ASN
1	A	228	HIS
1	A	231	GLN
1	A	236	GLN
1	A	244	HIS
1	B	48	GLN
1	B	115	GLN
1	B	133	HIS
1	B	134	GLN
1	B	139	GLN
1	B	171	GLN
1	B	183	ASN
1	B	244	HIS

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 ⓘ

2 ligands are 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	CXR	A	301	-	31,39,39	2.08	13 (41%)	31,62,62	1.47	6 (19%)
2	CXR	B	301	-	31,39,39	2.64	10 (32%)	31,62,62	1.26	5 (16%)

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	CXR	A	301	-	1/1/10/10	0/18/58/58	0/0/5/5
2	CXR	B	301	-	1/1/10/10	0/18/58/58	0/0/5/5

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	CXR	C2'-C1'	-3.43	1.48	1.53
2	B	301	CXR	C2'-C1'	-2.66	1.49	1.53
2	B	301	CXR	O2D-C2D	2.20	1.48	1.43
2	B	301	CXR	O4'-C4'	2.25	1.50	1.45
2	B	301	CXR	O3'-C3'	2.41	1.48	1.43
2	A	301	CXR	O4D-C1D	2.50	1.44	1.41
2	A	301	CXR	PB-O2B	2.53	1.60	1.50
2	A	301	CXR	O2D-C2D	2.59	1.48	1.43
2	A	301	CXR	C6-N6	2.76	1.33	1.27
2	A	301	CXR	O3D-C3D	2.80	1.49	1.43
2	A	301	CXR	O4'-C4'	2.91	1.51	1.45
2	A	301	CXR	C6-C5	2.94	1.46	1.41
2	A	301	CXR	C4-N3	2.94	1.39	1.35
2	A	301	CXR	O3'-C3'	2.98	1.49	1.43
2	B	301	CXR	C8-N7	3.17	1.40	1.34
2	A	301	CXR	C2-N3	3.45	1.36	1.30
2	A	301	CXR	O4'-C1'	3.55	1.46	1.41
2	A	301	CXR	C2-N1	3.61	1.43	1.35
2	B	301	CXR	C2-N3	3.67	1.36	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	CXR	C5-C4	4.56	1.50	1.40
2	B	301	CXR	C6-N6	6.03	1.41	1.27
2	B	301	CXR	C2-N1	6.80	1.50	1.35
2	B	301	CXR	O4'-C1'	6.85	1.50	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	CXR	O2'-C2'-C3'	-2.88	102.60	111.83
2	A	301	CXR	O2D-C2D-C1D	-2.43	104.02	111.61
2	B	301	CXR	O2'-C2'-C1'	-2.33	104.31	111.61
2	B	301	CXR	O2'-C2'-C3'	-2.30	104.46	111.83
2	B	301	CXR	O2D-C2D-C1D	-2.12	104.98	111.61
2	A	301	CXR	O2'-C2'-C1'	-2.12	104.98	111.61
2	A	301	CXR	C2'-C3'-C4'	2.29	107.08	102.62
2	B	301	CXR	C2'-C3'-C4'	2.36	107.21	102.62
2	A	301	CXR	C2-N3-C4	2.40	120.09	116.41
2	B	301	CXR	C2-N3-C4	2.58	120.37	116.41
2	A	301	CXR	O3'-C3'-C4'	2.89	119.52	111.09

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	301	CXR	C3'
2	A	301	CXR	C3'

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	CXR	3	0

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	252/262 (96%)	1.05	39 (15%) 2 3	28, 34, 47, 64	0
1	B	252/262 (96%)	2.18	109 (43%) 0 0	26, 38, 64, 71	0
All	All	504/524 (96%)	1.62	148 (29%) 1 1	26, 35, 57, 71	0

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	ILE	11.7
1	B	215	ILE	11.3
1	A	248	GLU	10.8
1	B	249	ASP	10.3
1	A	246	GLY	10.0
1	A	249	ASP	9.9
1	B	246	GLY	9.8
1	B	247	ARG	9.6
1	B	266	ILE	8.6
1	B	225	VAL	8.5
1	B	219	ASP	7.7
1	B	296	CYS	7.7
1	A	247	ARG	7.7
1	B	245	GLY	7.3
1	B	273	PHE	6.5
1	B	248	GLU	6.5
1	B	255	GLN	6.4
1	B	268	LYS	6.3
1	B	73	ILE	6.0
1	B	271	ILE	5.7
1	B	260	LYS	5.7
1	B	270	ASN	5.6
1	B	212	ARG	5.5
1	B	228	HIS	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	262	LEU	5.2
1	B	213	SER	5.1
1	B	231	GLN	5.1
1	B	279	TYR	5.1
1	B	258	THR	5.1
1	B	236	GLN	5.0
1	B	295	SER	4.9
1	B	254	CYS	4.9
1	B	253	LEU	4.9
1	B	210	GLY	4.9
1	B	244	HIS	4.7
1	A	222	PHE	4.6
1	B	264	SER	4.5
1	B	50	TRP	4.5
1	B	275	CYS	4.5
1	B	284	PHE	4.5
1	B	159	TRP	4.5
1	B	234	LYS	4.4
1	B	160	CYS	4.3
1	B	287	CYS	4.2
1	B	294	SER	4.2
1	B	214	LYS	4.1
1	B	223	GLY	4.1
1	A	294	SER	4.1
1	B	283	LYS	4.0
1	B	201	CYS	4.0
1	B	224	SER	4.0
1	A	227	VAL	3.9
1	A	124	LEU	3.9
1	B	278	ILE	3.8
1	B	222	PHE	3.7
1	B	141	ASP	3.7
1	B	269	ARG	3.7
1	B	291	PRO	3.7
1	B	282	ASP	3.5
1	B	185	VAL	3.5
1	B	250	SER	3.5
1	B	293	ASP	3.5
1	B	292	GLU	3.4
1	A	123	LEU	3.4
1	B	218	LYS	3.4
1	B	265	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	286	GLN	3.3
1	B	173	CYS	3.3
1	B	263	GLU	3.3
1	B	267	SER	3.3
1	B	226	GLY	3.2
1	A	245	GLY	3.2
1	B	285	LEU	3.2
1	A	206	VAL	3.2
1	B	163	PHE	3.1
1	B	252	ASP	3.1
1	B	188	PHE	3.1
1	A	122	ILE	3.1
1	B	127	ARG	3.0
1	A	47	ARG	3.0
1	B	199	ALA	3.0
1	B	261	GLU	3.0
1	B	272	GLN	2.9
1	A	119	CYS	2.9
1	B	227	VAL	2.9
1	B	172	SER	2.9
1	A	238	LEU	2.9
1	B	238	LEU	2.9
1	B	217	ASP	2.9
1	B	290	ASN	2.8
1	A	225	VAL	2.8
1	B	233	GLU	2.8
1	A	241	TRP	2.8
1	B	157	LEU	2.7
1	A	235	VAL	2.7
1	B	221	THR	2.7
1	A	295	SER	2.7
1	B	55	THR	2.6
1	B	280	ARG	2.6
1	B	168	ILE	2.6
1	B	140	ARG	2.6
1	A	196	PHE	2.6
1	B	184	PRO	2.6
1	B	240	ALA	2.6
1	B	243	ILE	2.6
1	A	265	ILE	2.6
1	A	200	ALA	2.6
1	B	59	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	99	CYS	2.6
1	B	170	TYR	2.5
1	A	79	HIS	2.5
1	A	197	ALA	2.5
1	A	203	VAL	2.5
1	A	204	VAL	2.5
1	B	80	VAL	2.5
1	B	116	THR	2.4
1	B	161	GLY	2.4
1	A	145	LEU	2.4
1	B	189	TRP	2.4
1	B	216	PHE	2.4
1	B	242	VAL	2.4
1	A	125	TRP	2.4
1	B	158	THR	2.4
1	B	211	SER	2.3
1	B	119	CYS	2.3
1	B	174	PRO	2.3
1	B	93	PHE	2.3
1	B	101	ILE	2.3
1	B	229	ASN	2.3
1	A	230	LEU	2.3
1	B	277	ASN	2.3
1	A	164	ASP	2.3
1	A	262	LEU	2.2
1	B	256	ASP	2.2
1	B	203	VAL	2.2
1	A	154	ALA	2.2
1	A	213	SER	2.2
1	A	58	ARG	2.2
1	B	98	PRO	2.1
1	A	194	ARG	2.1
1	A	266	ILE	2.1
1	B	107	GLN	2.0
1	B	94	ILE	2.0
1	A	192	VAL	2.0
1	A	290	ASN	2.0
1	A	189	TRP	2.0
1	B	176	TRP	2.0
1	B	257	PRO	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, 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
2	CXR	B	301	35/35	0.83	0.15	-0.03	30,44,62,64	0
2	CXR	A	301	35/35	0.94	0.12	-1.14	21,26,39,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.