



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:26 PM GMT

PDB ID : 3RAW
Title : Crystal Structure of human CDC-like kinase 3 isoform in complex with leucettine L41
Authors : Filippakopoulos, P.; Fedorov, O.; King, O.; Debdab, M.; Carreaux, F.; Renault, S.; Bullock, A.; Muniz, J.R.C.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.M.; Weigelt, J.; Bountra, C.; Meijer, L.; Bazureau, J.P.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2011-03-28
Resolution : 2.09 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

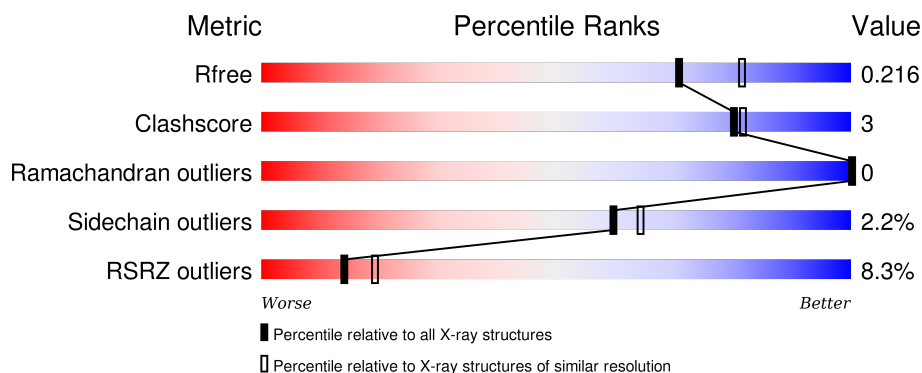
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	381	<div> <div>8%</div> <div>84%</div> <div>8%</div> <div>8%</div> </div>
1	B	381	<div> <div>8%</div> <div>83%</div> <div>8%</div> <div>8%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5928 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 Dual specificity protein kinase CLK3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	3	0
			2839	1822	497	503	17			
1	B	349	Total	C	N	O	S	0	2	0
			2797	1797	490	492	18			

There are 46 discrepancies between the modelled and reference sequences:

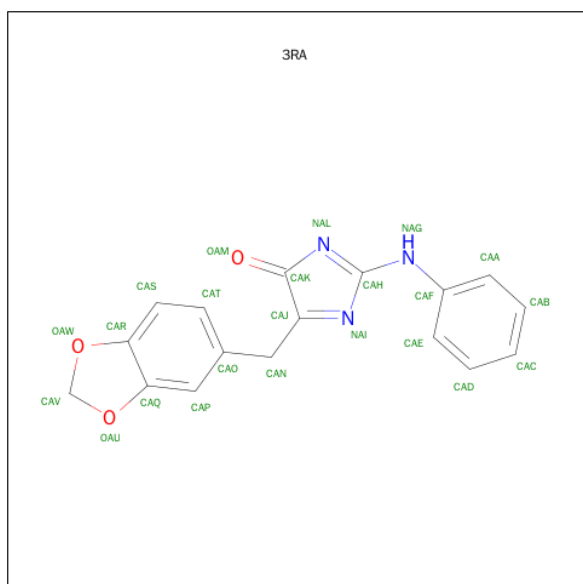
Chain	Residue	Modelled	Actual	Comment	Reference
A	104	MET	-	EXPRESSION TAG	UNP P49761
A	105	HIS	-	EXPRESSION TAG	UNP P49761
A	106	HIS	-	EXPRESSION TAG	UNP P49761
A	107	HIS	-	EXPRESSION TAG	UNP P49761
A	108	HIS	-	EXPRESSION TAG	UNP P49761
A	109	HIS	-	EXPRESSION TAG	UNP P49761
A	110	HIS	-	EXPRESSION TAG	UNP P49761
A	111	SER	-	EXPRESSION TAG	UNP P49761
A	112	SER	-	EXPRESSION TAG	UNP P49761
A	113	GLY	-	EXPRESSION TAG	UNP P49761
A	114	VAL	-	EXPRESSION TAG	UNP P49761
A	115	ASP	-	EXPRESSION TAG	UNP P49761
A	116	LEU	-	EXPRESSION TAG	UNP P49761
A	117	GLY	-	EXPRESSION TAG	UNP P49761
A	118	THR	-	EXPRESSION TAG	UNP P49761
A	119	GLU	-	EXPRESSION TAG	UNP P49761
A	120	ASN	-	EXPRESSION TAG	UNP P49761
A	121	LEU	-	EXPRESSION TAG	UNP P49761
A	122	TYR	-	EXPRESSION TAG	UNP P49761
A	123	PHE	-	EXPRESSION TAG	UNP P49761
A	124	GLN	-	EXPRESSION TAG	UNP P49761
A	125	SER	-	EXPRESSION TAG	UNP P49761
A	126	MET	-	EXPRESSION TAG	UNP P49761
B	104	MET	-	EXPRESSION TAG	UNP P49761
B	105	HIS	-	EXPRESSION TAG	UNP P49761

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Chain	Residue	Modelled	Actual	Comment	Reference
B	106	HIS	-	EXPRESSION TAG	UNP P49761
B	107	HIS	-	EXPRESSION TAG	UNP P49761
B	108	HIS	-	EXPRESSION TAG	UNP P49761
B	109	HIS	-	EXPRESSION TAG	UNP P49761
B	110	HIS	-	EXPRESSION TAG	UNP P49761
B	111	SER	-	EXPRESSION TAG	UNP P49761
B	112	SER	-	EXPRESSION TAG	UNP P49761
B	113	GLY	-	EXPRESSION TAG	UNP P49761
B	114	VAL	-	EXPRESSION TAG	UNP P49761
B	115	ASP	-	EXPRESSION TAG	UNP P49761
B	116	LEU	-	EXPRESSION TAG	UNP P49761
B	117	GLY	-	EXPRESSION TAG	UNP P49761
B	118	THR	-	EXPRESSION TAG	UNP P49761
B	119	GLU	-	EXPRESSION TAG	UNP P49761
B	120	ASN	-	EXPRESSION TAG	UNP P49761
B	121	LEU	-	EXPRESSION TAG	UNP P49761
B	122	TYR	-	EXPRESSION TAG	UNP P49761
B	123	PHE	-	EXPRESSION TAG	UNP P49761
B	124	GLN	-	EXPRESSION TAG	UNP P49761
B	125	SER	-	EXPRESSION TAG	UNP P49761
B	126	MET	-	EXPRESSION TAG	UNP P49761

- Molecule 2 is 5-(1,3-BENZODIOXOL-5-YLMETHYL)-2-(PHENYLAMINO)-4H-IMIDAZO L-4-ONE (three-letter code: 3RA) (formula: C₁₇H₁₃N₃O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	17	3	3		
2	B	1	Total	C	N	O	0	0
			23	17	3	3		

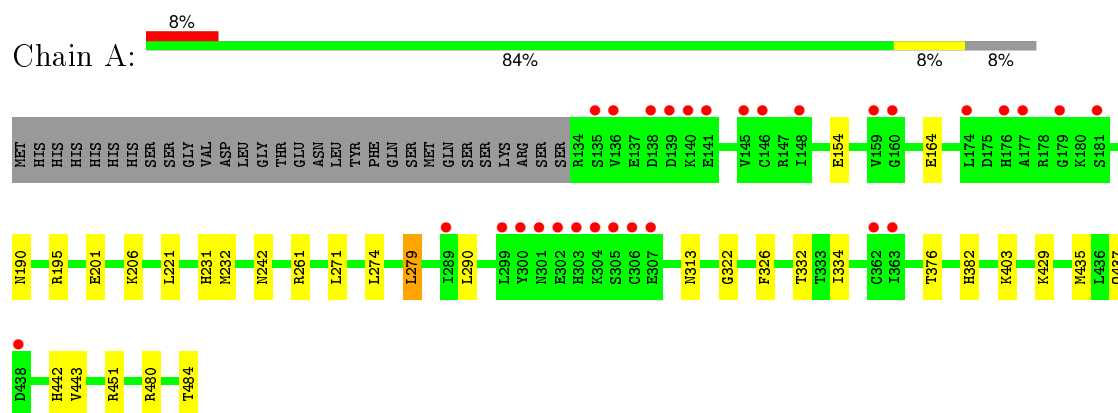
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	128	Total	O	0	0
			128	128		
3	B	118	Total	O	0	0
			118	118		

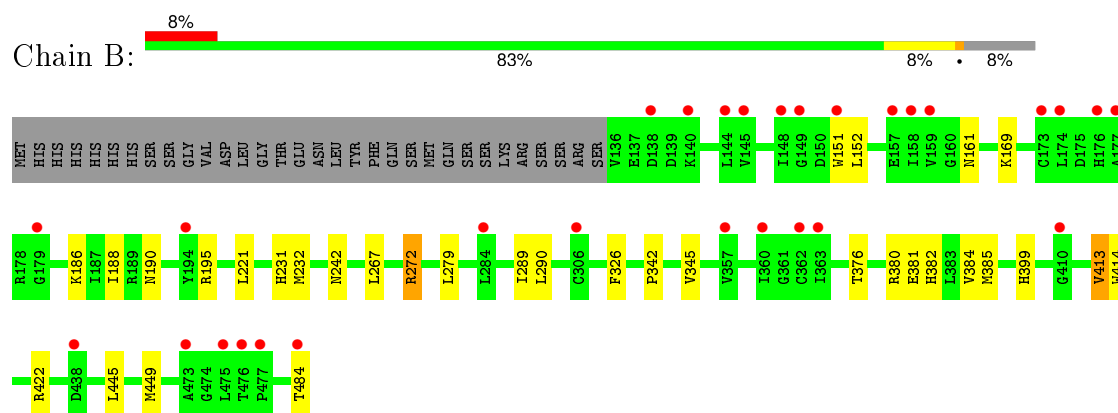
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Dual specificity protein kinase CLK3



- Molecule 1: Dual specificity protein kinase CLK3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.67Å 122.42Å 69.28Å 90.00° 92.60° 90.00°	Depositor
Resolution (Å)	36.26 – 2.09 35.15 – 2.09	Depositor EDS
% Data completeness (in resolution range)	98.1 (36.26-2.09) 98.1 (35.15-2.09)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.181 , 0.219 0.181 , 0.216	Depositor DCC
R_{free} test set	1988 reflections (3.46%)	DCC
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.2	EDS
Estimated twinning fraction	0.058 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 59519 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5928	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3RA

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	0.76	0/2926	0.75	2/3962 (0.1%)
1	B	0.71	0/2879	0.74	0/3900
All	All	0.74	0/5805	0.75	2/7862 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	261	ARG	NE-CZ-NH1	-5.38	117.61	120.30
1	A	261	ARG	NE-CZ-NH2	5.24	122.92	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	2839	0	2707	15	0
1	B	2797	0	2662	21	0
2	A	23	0	13	1	0
2	B	23	0	13	1	0
3	A	128	0	0	3	0
3	B	118	0	0	3	0
All	All	5928	0	5395	38	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 3.

All (38) 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:B:422:ARG:NH2	3:B:84:HOH:O	2.16	0.68
1:B:272[B]:ARG:HD2	3:B:520:HOH:O	2.02	0.59
1:B:380:ARG:NH1	1:B:413:VAL:HG13	2.23	0.53
1:B:186:LYS:HE2	1:B:188:ILE:HD11	1.91	0.52
1:B:380:ARG:HD3	1:B:413:VAL:O	2.12	0.50
1:B:152:LEU:HD12	1:B:152:LEU:N	2.27	0.49
1:A:271:LEU:HD13	1:A:274:LEU:HD12	1.94	0.49
1:B:445:LEU:HD11	1:B:449:MET:HE1	1.94	0.49
1:A:451:ARG:NE	3:A:557:HOH:O	2.38	0.47
1:A:435:MET:HE3	1:A:443:VAL:HA	1.97	0.47
1:B:267:LEU:HD21	1:B:289:ILE:CD1	2.46	0.46
1:B:151:TRP:C	1:B:152:LEU:HD12	2.36	0.46
1:B:384:VAL:HG21	1:B:414:TRP:CG	2.51	0.46
1:B:381:GLU:O	1:B:385:MET:HG3	2.16	0.46
1:A:429:LYS:HE2	3:A:528:HOH:O	2.16	0.45
1:A:190:ASN:HB2	1:A:231:HIS:CE1	2.52	0.45
1:B:195:ARG:HG3	1:B:232:MET:HG2	1.96	0.45
2:A:1:3RA:NAI	2:A:1:3RA:HAE	2.32	0.45
1:B:342:PRO:HG2	1:B:345:VAL:HG23	1.99	0.44
1:A:195:ARG:HG3	1:A:232:MET:HG2	1.98	0.44
1:B:380:ARG:HH12	1:B:413:VAL:HG13	1.83	0.43
2:B:2:3RA:HAE	2:B:2:3RA:NAI	2.34	0.43
1:A:332:THR:HG22	1:A:334:ILE:H	1.84	0.43
1:B:272[A]:ARG:HD3	3:B:520:HOH:O	2.19	0.43
1:B:445:LEU:HD11	1:B:449:MET:CE	2.48	0.43
1:A:279:LEU:HD13	1:A:326:PHE:CD1	2.54	0.43
1:B:190:ASN:OD1	1:B:195:ARG:NH1	2.51	0.42
1:B:190:ASN:HB2	1:B:231:HIS:CE1	2.54	0.42
1:A:451:ARG:NH2	3:A:557:HOH:O	2.48	0.42
1:A:313:ASN:HD21	1:A:484:THR:C	2.22	0.42
1:A:201:GLU:HB2	1:A:322:GLY:HA2	2.02	0.42
1:B:376:THR:HG21	1:B:382:HIS:CG	2.55	0.41
1:B:279:LEU:HD13	1:B:326:PHE:CD1	2.56	0.41
1:A:437:GLN:HB2	1:A:442:HIS:CE1	2.56	0.41
1:A:376:THR:HG21	1:A:382:HIS:CG	2.56	0.40
1:B:242:ASN:HA	1:B:290:LEU:HA	2.03	0.40
1:A:403:LYS:HA	1:A:403:LYS:HD2	1.97	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:ASN:HA	1:A:290:LEU:HA	2.02	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	352/381 (92%)	343 (97%)	9 (3%)	0	100	100
1	B	349/381 (92%)	339 (97%)	10 (3%)	0	100	100
All	All	701/762 (92%)	682 (97%)	19 (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	
1	A	296/345 (86%)	289 (98%)	7 (2%)	57	61
1	B	289/345 (84%)	281 (97%)	8 (3%)	51	55
All	All	585/690 (85%)	570 (97%)	15 (3%)	60	58

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	GLU
1	A	164	GLU
1	A	206	LYS
1	A	221	LEU
1	A	279	LEU
1	A	480[A]	ARG
1	A	480[B]	ARG
1	B	161	ASN
1	B	169	LYS
1	B	221	LEU
1	B	272[A]	ARG
1	B	272[B]	ARG
1	B	399	HIS
1	B	413	VAL
1	B	484	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	377	HIS
1	B	176	HIS
1	B	404	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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](#)

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	3RA	A	1	-	24,26,26	2.84	5 (20%)	27,36,36	2.35	7 (25%)
2	3RA	B	2	-	24,26,26	2.95	5 (20%)	27,36,36	2.21	7 (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	3RA	A	1	-	-	0/8/26/26	0/4/4/4
2	3RA	B	2	-	-	0/8/26/26	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	3RA	CAN-CAJ	-10.27	1.39	1.50
2	A	1	3RA	CAN-CAJ	-10.13	1.39	1.50
2	A	1	3RA	CAN-CAO	-6.33	1.40	1.51
2	B	2	3RA	CAN-CAO	-6.32	1.40	1.51
2	A	1	3RA	CAK-CAJ	-4.97	1.39	1.49
2	B	2	3RA	CAF-NAG	-4.76	1.32	1.41
2	B	2	3RA	CAK-NAL	-3.41	1.31	1.37
2	B	2	3RA	CAK-CAJ	-3.25	1.43	1.49
2	A	1	3RA	CAF-NAG	-2.88	1.36	1.41
2	A	1	3RA	CAK-NAL	-2.13	1.33	1.37

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	3RA	CAN-CAJ-CAK	-8.93	120.27	128.44
2	B	2	3RA	CAN-CAJ-CAK	-7.26	121.79	128.44
2	A	1	3RA	OAW-CAV-OAU	-2.86	103.28	108.12
2	B	2	3RA	CAN-CAO-CAT	-2.74	116.75	120.86
2	A	1	3RA	CAN-CAO-CAT	-2.31	117.40	120.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	3RA	CAP-CAQ-CAR	-2.19	119.01	121.96
2	A	1	3RA	CAN-CAO-CAP	2.19	123.96	120.42
2	B	2	3RA	CAB-CAA-CAF	2.31	122.65	119.72
2	A	1	3RA	OAU-CAQ-CAP	2.46	131.41	127.88
2	A	1	3RA	OAW-CAR-CAS	2.50	131.94	127.96
2	B	2	3RA	CAN-CAO-CAP	2.52	124.50	120.42
2	B	2	3RA	OAU-CAQ-CAP	2.70	131.74	127.88
2	A	1	3RA	CAO-CAN-CAJ	4.62	125.03	113.37
2	B	2	3RA	CAO-CAN-CAJ	5.25	126.62	113.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	3RA	1	0
2	B	2	3RA	1	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	351/381 (92%)	0.23	29 (8%) 14 19	20, 42, 87, 120	0
1	B	349/381 (91%)	0.24	29 (8%) 14 19	22, 43, 87, 110	0
All	All	700/762 (91%)	0.24	58 (8%) 14 19	20, 42, 87, 120	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	306	CYS	6.1
1	B	176	HIS	4.3
1	B	477	PRO	4.2
1	B	148	ILE	4.0
1	A	179	GLY	3.8
1	A	305	SER	3.8
1	A	300	TYR	3.7
1	B	151	TRP	3.6
1	A	303	HIS	3.6
1	A	146	CYS	3.6
1	A	136	VAL	3.5
1	B	484	THR	3.5
1	A	304	LYS	3.4
1	A	145	VAL	3.3
1	B	145	VAL	3.3
1	B	363	ILE	3.2
1	A	140	LYS	3.2
1	B	140	LYS	3.1
1	A	177	ALA	3.1
1	B	144	LEU	3.0
1	B	159	VAL	3.0
1	B	473	ALA	3.0
1	B	174	LEU	3.0
1	A	138	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	148	ILE	2.9
1	A	174	LEU	2.9
1	B	157	GLU	2.8
1	A	302	GLU	2.8
1	B	284	LEU	2.8
1	A	299	LEU	2.7
1	B	475	LEU	2.7
1	A	135	SER	2.7
1	B	177	ALA	2.6
1	A	363	ILE	2.6
1	A	159	VAL	2.6
1	A	301	ASN	2.5
1	A	307	GLU	2.5
1	B	438	ASP	2.4
1	A	160	GLY	2.4
1	A	176	HIS	2.4
1	B	194	TYR	2.4
1	B	306	CYS	2.3
1	B	360	ILE	2.3
1	B	138	ASP	2.3
1	B	149	GLY	2.2
1	A	141	GLU	2.2
1	A	362	CYS	2.2
1	A	289	ILE	2.2
1	A	181	SER	2.2
1	B	357	VAL	2.1
1	B	476	THR	2.1
1	B	362	CYS	2.1
1	B	158	ILE	2.1
1	A	438	ASP	2.1
1	B	410	GLY	2.1
1	A	139	ASP	2.1
1	B	179	GLY	2.0
1	B	173	CYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [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	3RA	B	2	23/23	0.98	0.09	-0.98	26,31,45,48	0
2	3RA	A	1	23/23	0.98	0.08	-1.16	26,34,52,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.