



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2017 – 04:37 PM EDT

PDB ID : 5MP8
Title : Crystal Structure of CK2alpha with ZT0432 bound
Authors : Brear, P.; De Fusco, C.; Georgiou, K.; Iegre, J.; Sore, H.; Hyvonen, M.; Spring, D.
Deposited on : unknown
Resolution : 1.92 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 : rb-20029824
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) : rb-20029824

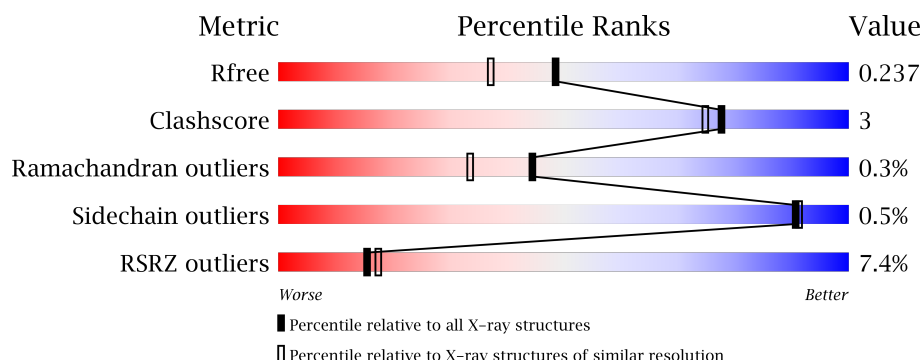
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 1.92 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	6276 (1.94-1.90)
Clashscore	112137	7025 (1.94-1.90)
Ramachandran outliers	110173	6947 (1.94-1.90)
Sidechain outliers	110143	6948 (1.94-1.90)
RSRZ outliers	101464	6332 (1.94-1.90)

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	352	
1	B	352	

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	PO4	A	401	-	-	-	X
4	ACT	A	405	-	-	-	X
5	RKN	A	406[A]	-	-	-	X
5	RKN	B	405	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5849 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	3	0
			2767	1772	486	498	11			
1	B	323	Total	C	N	O	S	0	4	0
			2764	1769	488	496	11			

There are 50 discrepancies between the modelled and reference sequences:

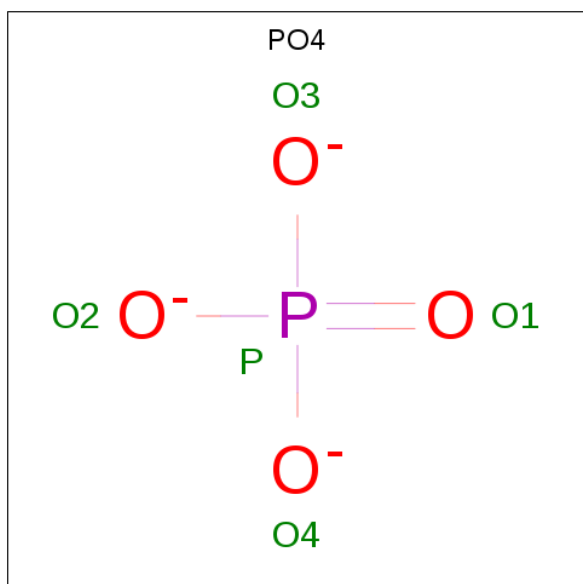
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	UNP P68400
A	-15	ASP	-	expression tag	UNP P68400
A	-14	ASP	-	expression tag	UNP P68400
A	-13	ASP	-	expression tag	UNP P68400
A	-12	ALA	-	expression tag	UNP P68400
A	-11	ASP	-	expression tag	UNP P68400
A	-10	ASP	-	expression tag	UNP P68400
A	-9	ASP	-	expression tag	UNP P68400
A	-8	GLY	-	expression tag	UNP P68400
A	-7	SER	-	expression tag	UNP P68400
A	-6	GLY	-	expression tag	UNP P68400
A	-5	SER	-	expression tag	UNP P68400
A	-4	GLY	-	expression tag	UNP P68400
A	-3	SER	-	expression tag	UNP P68400
A	-2	GLY	-	expression tag	UNP P68400
A	-1	SER	-	expression tag	UNP P68400
A	0	GLY	-	expression tag	UNP P68400
A	1	SER	-	expression tag	UNP P68400
A	21	SER	ARG	engineered mutation	UNP P68400

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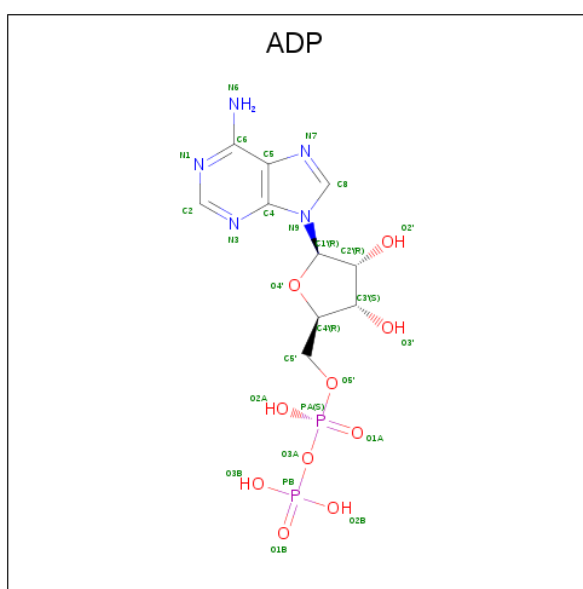
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	UNP P68400
B	-15	ASP	-	expression tag	UNP P68400
B	-14	ASP	-	expression tag	UNP P68400
B	-13	ASP	-	expression tag	UNP P68400
B	-12	ALA	-	expression tag	UNP P68400
B	-11	ASP	-	expression tag	UNP P68400
B	-10	ASP	-	expression tag	UNP P68400
B	-9	ASP	-	expression tag	UNP P68400
B	-8	GLY	-	expression tag	UNP P68400
B	-7	SER	-	expression tag	UNP P68400
B	-6	GLY	-	expression tag	UNP P68400
B	-5	SER	-	expression tag	UNP P68400
B	-4	GLY	-	expression tag	UNP P68400
B	-3	SER	-	expression tag	UNP P68400
B	-2	GLY	-	expression tag	UNP P68400
B	-1	SER	-	expression tag	UNP P68400
B	0	GLY	-	expression tag	UNP P68400
B	1	SER	-	expression tag	UNP P68400
B	21	SER	ARG	engineered mutation	UNP P68400

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



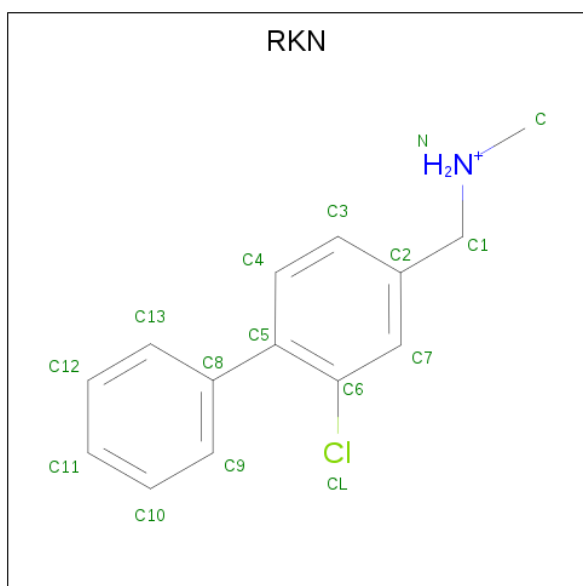
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 27 10 5 10 2	0	0
3	B	1	Total C N O P 27 10 5 10 2	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is (3-chloranyl-4-phenyl-phenyl)methyl-methyl-azanium (three-letter code: RKN) (formula: C₁₄H₁₅ClN).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	0	1
			32	28	2	2		
5	B	1	Total	C	Cl	N	0	0
			16	14	1	1		

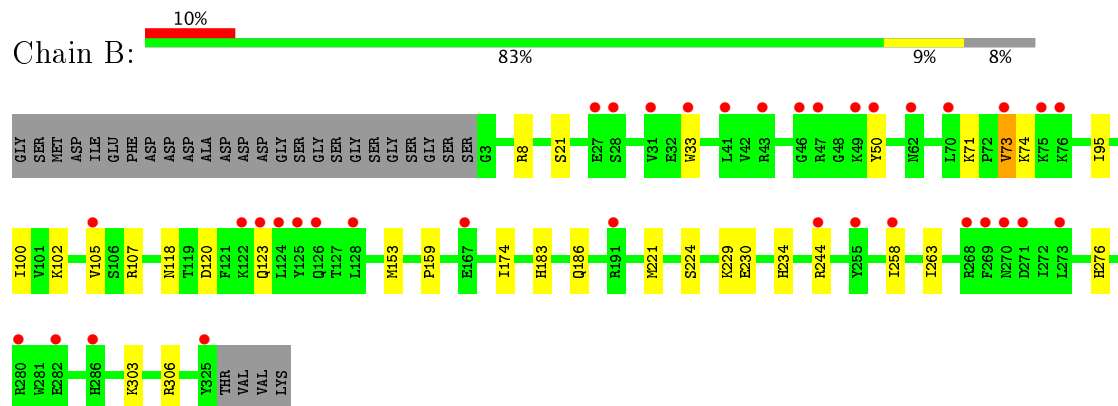
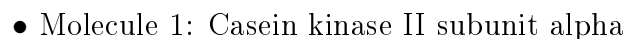
- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	120	Total	O	0	0
			120	120		
7	B	63	Total	O	0	0
			63	63		

- Molecule 1: Casein kinase II subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	65.17Å 68.34Å 331.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.16 – 1.92 47.16 – 1.91	Depositor EDS
% Data completeness (in resolution range)	92.1 (47.16-1.92) 91.6 (47.16-1.91)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 1.91Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.212 , 0.224 0.223 , 0.237	Depositor DCC
R_{free} test set	2664 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.139 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5849	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RKN, MG, PO4, ADP, ACT

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	0.60	0/2842	0.64	0/3845
1	B	0.49	0/2839	0.61	0/3839
All	All	0.55	0/5681	0.62	0/7684

There are no bond length outliers.

There are no bond angle outliers.

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	2767	0	2704	16	1
1	B	2764	0	2700	21	0
2	A	15	0	0	0	0
2	B	5	0	0	1	0
3	A	27	0	12	0	0
3	B	27	0	12	1	0
4	A	4	0	3	0	0
4	B	8	0	6	1	0
5	A	32	0	0	4	0
5	B	16	0	0	2	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	120	0	0	2	0
7	B	63	0	0	2	0
All	All	5849	0	5437	38	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 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:8[B]:ARG:NH2	7:B:501:HOH:O	1.67	1.25
1:A:221:MET:HE1	5:A:406[A]:RKN:CL	2.27	0.72
1:B:118:ASN:HD21	5:B:405:RKN:C	2.05	0.69
1:A:270:ASN:HB3	7:A:570:HOH:O	1.92	0.69
1:A:17:THR:HG22	7:A:556:HOH:O	1.92	0.68
1:A:224:SER:HB2	1:A:230:GLU:HG2	1.83	0.60
1:B:224:SER:HB2	1:B:230:GLU:HG2	1.84	0.59
1:B:303:LYS:HA	1:B:306:ARG:HE	1.70	0.56
1:A:89:ARG:HH11	1:B:107:ARG:HH12	1.53	0.54
1:A:134:ARG:HG2	1:A:323:TYR:CZ	2.43	0.52
1:A:42:VAL:HG12	1:A:43:ARG:HG2	1.92	0.52
1:B:174:ILE:CD1	3:B:402:ADP:H5'2	2.40	0.52
1:B:102:LYS:HD3	1:B:107:ARG:HE	1.75	0.51
5:A:406[A]:RKN:CL	5:A:406[A]:RKN:C9	2.97	0.50
1:B:229:LYS:HE3	1:B:244:ARG:NH2	2.27	0.49
1:A:221:MET:CE	5:A:406[A]:RKN:CL	2.95	0.49
1:A:73:VAL:HG22	1:A:74:LYS:H	1.77	0.49
1:B:234:HIS:NE2	2:B:401:PO4:O4	2.34	0.49
1:B:73:VAL:HG22	1:B:74:LYS:H	1.77	0.49
1:B:258:ILE:HA	1:B:263:ILE:HD12	1.95	0.48
5:B:405:RKN:CL	5:B:405:RKN:C9	2.98	0.48
1:A:258:ILE:HA	1:A:263:ILE:HD12	1.96	0.46
1:A:20:PRO:HD2	1:B:105:VAL:HG11	1.99	0.45
1:B:229:LYS:HE3	1:B:244:ARG:HH21	1.81	0.45
1:A:33:TRP:CE3	1:A:100:ILE:HG22	2.53	0.44
1:B:276:HIS:HA	4:B:404:ACT:O	2.18	0.44
1:A:108:THR:HG23	1:A:109:PRO:HD2	2.00	0.43
1:B:33:TRP:CE3	1:B:100:ILE:HG22	2.54	0.43
1:B:120:ASP:HB3	1:B:123:GLN:HB2	2.00	0.43
1:A:22:GLU:CD	1:A:22:GLU:H	2.22	0.43
1:B:95:ILE:HB	1:B:174:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:HIS:HB2	1:A:186:GLN:HE21	1.83	0.42
1:A:120:ASP:HB3	1:A:123:GLN:HB2	2.01	0.42
1:B:183:HIS:HB2	1:B:186:GLN:HE21	1.84	0.42
1:B:159:PRO:HD3	1:B:221:MET:HG2	2.02	0.41
5:A:406[B]:RKN:CL	5:A:406[B]:RKN:C9	3.06	0.41
1:B:8[B]:ARG:CZ	7:B:501:HOH:O	2.36	0.41
1:B:50:TYR:HA	1:B:71:LYS:HD2	2.04	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)
1:A:264:GLU:OE2	1:A:280:ARG:NH1[8_597]	2.08	0.12

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	326/352 (93%)	316 (97%)	9 (3%)	1 (0%)	44	33
1	B	325/352 (92%)	312 (96%)	12 (4%)	1 (0%)	44	33
All	All	651/704 (92%)	628 (96%)	21 (3%)	2 (0%)	44	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	VAL
1	B	73	VAL

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	302/319 (95%)	301 (100%)	1 (0%)	94	94
1	B	301/319 (94%)	299 (99%)	2 (1%)	87	86
All	All	603/638 (94%)	600 (100%)	3 (0%)	91	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	MET
1	B	21	SER
1	B	153	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	ASN
1	A	118	ASN
1	A	168	HIS
1	A	186	GLN
1	B	118	ASN
1	B	186	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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
2	PO4	A	401	-	4,4,4	2.57	1 (25%)	6,6,6	0.64	0
2	PO4	A	402	-	4,4,4	1.88	1 (25%)	6,6,6	0.54	0
2	PO4	A	403	-	4,4,4	0.79	0	6,6,6	0.38	0
3	ADP	A	404	6	25,29,29	0.64	0	24,45,45	0.79	0
4	ACT	A	405	-	1,3,3	3.49	1 (100%)	0,3,3	0.00	-
5	RKN	A	406[A]	-	16,17,17	0.11	0	22,22,22	0.22	0
5	RKN	A	406[B]	-	16,17,17	0.11	0	22,22,22	0.16	0
2	PO4	B	401	-	4,4,4	2.64	1 (25%)	6,6,6	0.43	0
3	ADP	B	402	-	25,29,29	1.25	3 (12%)	24,45,45	2.54	10 (41%)
4	ACT	B	403	-	1,3,3	4.76	1 (100%)	0,3,3	0.00	-
4	ACT	B	404	-	1,3,3	3.09	1 (100%)	0,3,3	0.00	-
5	RKN	B	405	-	16,17,17	0.69	1 (6%)	22,22,22	0.96	2 (9%)

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	PO4	A	401	-	-	0/0/0/0	0/0/0/0
2	PO4	A	402	-	-	0/0/0/0	0/0/0/0
2	PO4	A	403	-	-	0/0/0/0	0/0/0/0
3	ADP	A	404	6	-	0/12/32/32	0/3/3/3
4	ACT	A	405	-	-	0/0/0/0	0/0/0/0
5	RKN	A	406[A]	-	-	0/6/7/7	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	RKN	A	406[B]	-	-	0/6/7/7	0/2/2/2
2	PO4	B	401	-	-	0/0/0/0	0/0/0/0
3	ADP	B	402	-	-	0/12/32/32	0/3/3/3
4	ACT	B	403	-	-	0/0/0/0	0/0/0/0
4	ACT	B	404	-	-	0/0/0/0	0/0/0/0
5	RKN	B	405	-	-	0/6/7/7	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	405	RKN	C5-C6	-2.56	1.35	1.39
3	B	402	ADP	C5-N7	-2.33	1.31	1.39
2	A	402	PO4	P-O1	2.29	1.55	1.50
3	B	402	ADP	C5'-C4'	2.46	1.59	1.51
4	B	404	ACT	CH3-C	3.09	1.52	1.48
3	B	402	ADP	C5-C4	3.19	1.47	1.40
4	A	405	ACT	CH3-C	3.49	1.53	1.48
2	A	401	PO4	P-O1	4.50	1.60	1.50
2	B	401	PO4	P-O1	4.68	1.60	1.50
4	B	403	ACT	CH3-C	4.76	1.54	1.48

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	ADP	N3-C2-N1	-5.66	123.93	128.86
5	B	405	RKN	C8-C5-C6	-2.84	118.41	123.47
3	B	402	ADP	C4-C5-N7	-2.54	106.95	109.41
3	B	402	ADP	O4'-C4'-C3'	-2.39	100.42	105.17
3	B	402	ADP	O2A-PA-O5'	-2.04	98.49	108.14
3	B	402	ADP	O3B-PB-O2B	2.17	116.39	107.61
3	B	402	ADP	C1'-N9-C4	2.24	130.50	126.64
5	B	405	RKN	C4-C5-C8	2.64	123.63	118.68
3	B	402	ADP	C2-N1-C6	2.82	123.70	118.77
3	B	402	ADP	N6-C6-N1	2.97	124.66	118.77
3	B	402	ADP	O5'-C5'-C4'	3.16	120.20	109.00
3	B	402	ADP	C4'-O4'-C1'	6.91	117.12	109.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	406[A]	RKN	3	0
5	A	406[B]	RKN	1	0
2	B	401	PO4	1	0
3	B	402	ADP	1	0
4	B	404	ACT	1	0
5	B	405	RKN	2	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	325/352 (92%)	0.10	12 (3%) 42 46	7, 24, 60, 82	0
1	B	323/352 (91%)	0.56	36 (11%) 6 7	18, 48, 81, 107	0
All	All	648/704 (92%)	0.33	48 (7%) 15 17	7, 36, 77, 107	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	50	TYR	6.7
1	B	325	TYR	6.4
1	B	125	TYR	5.9
1	B	50	TYR	5.5
1	A	72	PRO	4.9
1	A	33	TRP	4.7
1	B	126	GLN	4.5
1	B	62	ASN	4.3
1	B	280	ARG	3.9
1	B	49	LYS	3.8
1	B	70	LEU	3.7
1	A	325	TYR	3.5
1	B	33	TRP	3.4
1	B	73	VAL	3.2
1	B	128	LEU	3.2
1	B	244	ARG	3.2
1	B	47	ARG	3.1
1	B	271	ASP	3.1
1	A	326	THR	3.1
1	B	258	ILE	3.0
1	A	49	LYS	3.0
1	B	270	ASN	2.9
1	B	76	LYS	2.9
1	B	255	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	124	LEU	2.8
1	B	28	SER	2.7
1	B	75	LYS	2.6
1	B	46	GLY	2.6
1	A	327	VAL	2.6
1	A	74	LYS	2.5
1	B	122	LYS	2.4
1	B	282	GLU	2.4
1	A	70	LEU	2.3
1	B	123	GLN	2.3
1	B	31	VAL	2.3
1	A	71	LYS	2.3
1	B	273	LEU	2.2
1	B	167	GLU	2.2
1	B	41	LEU	2.2
1	B	43	ARG	2.2
1	B	27	GLU	2.2
1	B	269	PHE	2.2
1	B	286	HIS	2.1
1	A	126	GLN	2.1
1	B	191	ARG	2.1
1	B	268	ARG	2.1
1	B	105	VAL	2.1
1	A	123	GLN	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	PO4	A	401	5/5	0.95	0.16	7.30	49,49,51,54	0
5	RKN	A	406[A]	16/16	0.94	0.22	2.52	39,49,53,64	16
4	ACT	A	405	4/4	0.90	0.12	2.51	20,20,20,20	0
5	RKN	B	405	16/16	0.69	0.24	2.06	71,79,83,89	0
5	RKN	A	406[B]	16/16	0.94	0.22	1.97	39,49,53,64	16
3	ADP	B	402	27/27	0.88	0.31	1.66	20,20,20,20	0
4	ACT	B	403	4/4	0.90	0.16	0.90	51,54,54,56	0
2	PO4	B	401	5/5	0.91	0.20	0.63	73,73,74,77	0
3	ADP	A	404	27/27	0.95	0.11	-0.28	35,46,59,65	0
2	PO4	A	403	5/5	0.96	0.25	-	20,20,20,20	0
4	ACT	B	404	4/4	0.87	0.21	-	20,20,20,20	0
6	MG	A	407	1/1	0.95	0.11	-	30,30,30,30	0
2	PO4	A	402	5/5	0.96	0.13	-	56,60,62,62	0

6.5 Other polymers ⓘ

There are no such residues in this entry.