



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2018 – 04:42 PM EST

PDB ID : 5OUM
Title : The crystal structure of CK2alpha in complex with compound 21
Authors : Brear, P.; De Fusco, C.; Iegre, J.; Yoshida, M.; Mitchell, S.; Rossmann, M.; Carro, L.; Sore, H.; Hyvonen, M.; Spring, D.
Deposited on : 2017-08-24
Resolution : 2.05 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-20030736
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-20030736

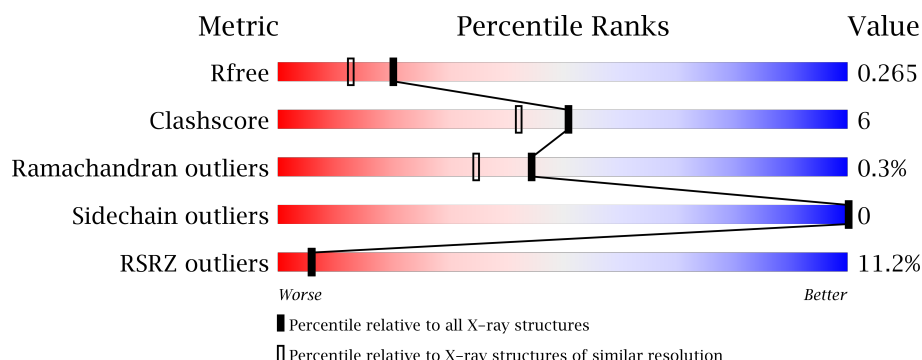
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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	<div> <div>3%</div> <div>80%</div> <div>12%</div> <div>7%</div> </div>
1	B	352	<div> <div>18%</div> <div>81%</div> <div>12%</div> <div>7%</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	ACT	A	403	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5757 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	B	326	Total	C	N	O	S	0	3	0
			2773	1775	487	500	11			
1	A	326	Total	C	N	O	S	0	2	0
			2763	1771	483	498	11			

There are 50 discrepancies between the modelled and reference sequences:

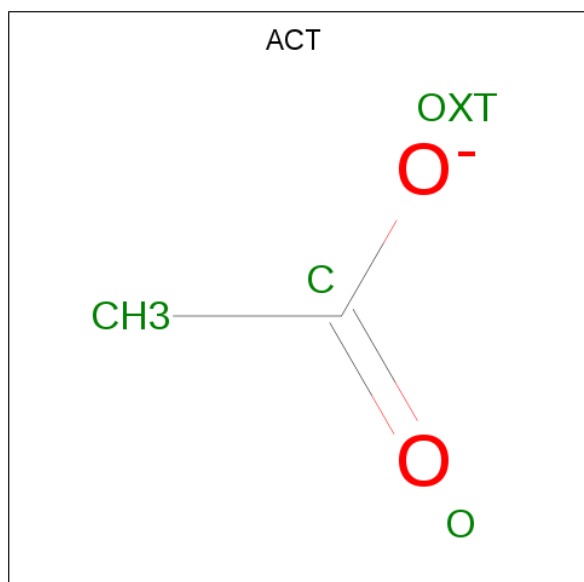
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	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

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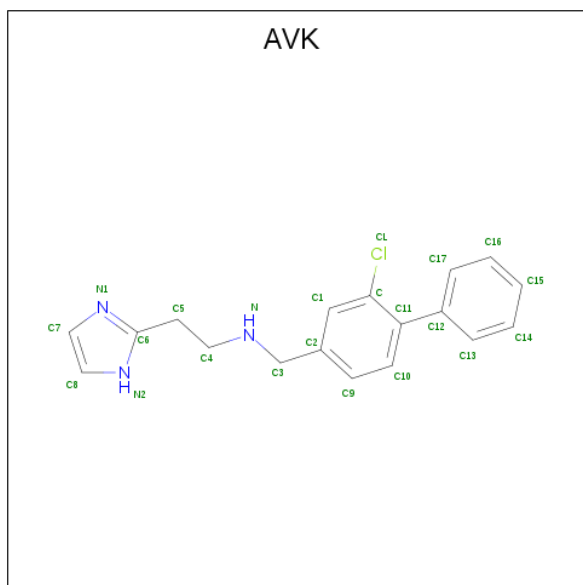
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	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

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 3 is {N}-[(3-chloranyl-4-phenyl-phenyl)methyl]-2-(1 {H}-imidazol-2-yl)ethanamine (three-letter code: AVK) (formula: C₁₈H₁₈ClN₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C Cl N 22 18 1 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	52	Total O 52 52	0	0
4	A	135	Total O 135 135	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	64.24Å 67.57Å 332.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.11 – 2.05 46.11 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.9 (46.11-2.05) 97.9 (46.11-2.05)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.05Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.220 , 0.248 0.240 , 0.265	Depositor DCC
R_{free} test set	2311 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.788	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.067 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5757	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.79% 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: ACT, AVK

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	0.47	0/2838	0.61	0/3840
1	B	0.45	0/2848	0.63	0/3853
All	All	0.46	0/5686	0.62	0/7693

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	2763	0	2700	36	0
1	B	2773	0	2706	36	0
2	A	12	0	9	1	0
3	A	22	0	0	5	0
4	A	135	0	0	4	0
4	B	52	0	0	1	0
All	All	5757	0	5415	71	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 6.

All (71) 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:120:ASP:OD2	4:A:501:HOH:O	1.75	1.02
1:A:225:MET:HG3	3:A:404:AVK:C14	1.95	0.96
1:B:95:ILE:HB	1:B:174:ILE:HG22	1.68	0.74
1:B:33:TRP:CE3	1:B:102:LYS:HG3	2.24	0.73
1:B:68:LYS:HE2	1:B:70:LEU:HD21	1.70	0.72
1:B:122:LYS:HD2	1:B:122:LYS:H	1.57	0.68
1:A:95:ILE:HB	1:A:174:ILE:HG22	1.75	0.68
1:B:122:LYS:HD2	1:B:122:LYS:N	2.11	0.65
1:B:68:LYS:HE2	1:B:70:LEU:CD2	2.26	0.65
1:B:195:ARG:HA	1:B:198:LYS:HD2	1.78	0.63
1:A:225:MET:CG	3:A:404:AVK:C14	2.74	0.62
1:B:36:GLN:HG3	1:B:101:VAL:CG2	2.30	0.61
1:B:258:ILE:HA	1:B:263:ILE:HD12	1.84	0.60
1:A:68:LYS:HE2	1:A:70:LEU:HD21	1.82	0.60
1:A:225:MET:HG3	3:A:404:AVK:C15	2.30	0.59
1:B:128:LEU:CD2	1:B:132:ASP:HB3	2.32	0.59
1:A:84:ILE:HG23	1:A:152:ILE:HD13	1.84	0.59
1:B:122:LYS:H	1:B:122:LYS:CD	2.15	0.58
1:A:103:ASP:HB3	1:A:106:SER:OG	2.03	0.58
1:A:114:GLU:HG3	1:A:114:GLU:O	2.04	0.57
1:B:33:TRP:HD1	1:A:90:GLY:HA3	1.70	0.57
3:A:404:AVK:C13	3:A:404:AVK:CL	2.90	0.57
1:A:50:TYR:HA	1:A:71:LYS:HD2	1.87	0.55
1:B:287:SER:HB2	4:B:425:HOH:O	2.05	0.55
1:A:123:GLN:NE2	4:A:501:HOH:O	2.41	0.54
1:A:285:VAL:HG22	1:A:293:VAL:HG11	1.91	0.53
1:A:196:TYR:CD2	1:A:231:PRO:HG3	2.44	0.53
1:A:148:HIS:CD2	1:A:211:TYR:HB3	2.45	0.52
1:A:124:LEU:CD1	1:A:128:LEU:HD13	2.39	0.52
1:B:125:TYR:HE1	1:B:228:ARG:HG2	1.75	0.51
1:B:121:PHE:CE1	1:B:159:PRO:HB3	2.45	0.51
1:B:33:TRP:CE3	1:B:102:LYS:CG	2.91	0.51
1:A:148:HIS:CG	1:A:211:TYR:HB3	2.47	0.50
1:B:105:VAL:HG13	1:B:106:SER:N	2.26	0.50
1:A:252:GLU:HB2	4:A:569:HOH:O	2.14	0.48
1:B:122:LYS:N	1:B:122:LYS:CD	2.75	0.48
1:A:64:LYS:NZ	1:A:64:LYS:HB2	2.29	0.48
1:B:128:LEU:HD23	1:B:132:ASP:HB3	1.94	0.47
1:B:15:VAL:O	1:B:19[A]:ARG:HG3	2.14	0.47
1:B:226:ILE:HD11	1:B:301:LEU:HD22	1.97	0.47
1:B:5:VAL:HB	1:B:261:TYR:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ALA:HB2	1:A:301:LEU:HD11	1.97	0.47
1:B:120:ASP:HB3	1:B:123:GLN:HB3	1.97	0.46
1:B:36:GLN:HG3	1:B:101:VAL:HG21	1.97	0.46
1:B:95:ILE:CB	1:B:174:ILE:HG22	2.43	0.46
1:A:91:GLY:HA3	1:A:146:TYR:CE2	2.51	0.46
1:A:159:PRO:HA	3:A:404:AVK:CL	2.53	0.45
1:A:22:GLU:CD	1:A:22:GLU:H	2.20	0.45
1:B:104:PRO:HB3	1:A:23:TYR:CE2	2.52	0.45
1:A:285:VAL:CG2	1:A:293:VAL:HG11	2.46	0.45
1:B:223:ALA:HB2	1:B:301:LEU:HD11	1.99	0.45
1:B:36:GLN:HG3	1:B:101:VAL:HG23	1.97	0.45
1:B:15:VAL:O	1:B:19[B]:ARG:HG3	2.17	0.45
1:B:33:TRP:CE3	1:B:100:ILE:HG22	2.52	0.44
1:A:159:PRO:HD3	1:A:221:MET:HG2	2.00	0.44
1:A:96:THR:HB	1:A:114:GLU:HG2	1.99	0.44
1:B:91:GLY:HA3	1:B:146:TYR:CE2	2.52	0.44
1:A:33:TRP:CE3	1:A:100:ILE:HG22	2.53	0.43
1:A:234:HIS:NE2	2:A:403:ACT:H1	2.34	0.43
1:B:22:GLU:H	1:B:22:GLU:CD	2.20	0.43
1:B:316:ARG:HH21	1:B:320:GLU:HG3	1.84	0.43
1:B:36:GLN:OE1	1:B:103:ASP:HB2	2.19	0.42
1:A:127:THR:HG23	4:A:605:HOH:O	2.19	0.42
1:B:50:TYR:HA	1:B:71:LYS:HD2	2.01	0.41
1:A:120:ASP:HB3	1:A:123:GLN:HG2	2.03	0.41
1:A:124:LEU:HD12	1:A:128:LEU:HD13	2.00	0.41
1:A:165:ASP:OD2	1:A:168:HIS:CD2	2.73	0.41
1:A:196:TYR:CE2	1:A:231:PRO:HG3	2.56	0.41
1:B:103:ASP:HA	1:B:104:PRO:HD3	1.95	0.41
1:A:316:ARG:HH21	1:A:320:GLU:HG3	1.86	0.41
1:A:165:ASP:HB3	1:A:170:LYS:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	317 (97%)	9 (3%)	0	100	100
1	B	327/352 (93%)	315 (96%)	10 (3%)	2 (1%)	28	17
All	All	653/704 (93%)	632 (97%)	19 (3%)	2 (0%)	44	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	ARG
1	B	177	GLY

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	302/319 (95%)	302 (100%)	0	100	100
1	B	303/319 (95%)	303 (100%)	0	100	100
All	All	605/638 (95%)	605 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	168	HIS
1	A	186	GLN
1	A	270	ASN

5.3.3 RNA ⓘ

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](#)

4 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	ACT	A	401	-	1,3,3	1.28	0	0,3,3	0.00	-
2	ACT	A	402	-	1,3,3	4.02	1 (100%)	0,3,3	0.00	-
2	ACT	A	403	-	1,3,3	6.12	1 (100%)	0,3,3	0.00	-
3	AVK	A	404	-	22,24,24	0.35	0	24,31,31	0.34	0

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	ACT	A	401	-	-	0/0/0/0	0/0/0/0
2	ACT	A	402	-	-	0/0/0/0	0/0/0/0
2	ACT	A	403	-	-	0/0/0/0	0/0/0/0
3	AVK	A	404	-	-	1/11/11/11	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	402	ACT	CH3-C	4.02	1.53	1.48
2	A	403	ACT	CH3-C	6.12	1.56	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	AVK	C4-C5-C6-N1

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	403	ACT	1	0
3	A	404	AVK	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	326/352 (92%)	0.53	11 (3%) 46 50	27, 42, 78, 124	0
1	B	326/352 (92%)	1.20	62 (19%) 1 1	36, 64, 97, 118	0
All	All	652/704 (92%)	0.86	73 (11%) 6 6	27, 53, 94, 124	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	LEU	11.2
1	B	124	LEU	8.6
1	A	50	TYR	7.8
1	B	123	GLN	6.4
1	B	105	VAL	6.3
1	A	121	PHE	6.2
1	B	257	TYR	5.8
1	B	120	ASP	5.5
1	B	307	TYR	5.4
1	B	126	GLN	5.4
1	A	125	TYR	5.2
1	B	50	TYR	5.1
1	B	270	ASN	4.8
1	B	104	PRO	4.8
1	B	49	LYS	4.7
1	B	283	ARG	4.5
1	B	288	GLU	4.4
1	A	122	LYS	4.4
1	B	122	LYS	4.3
1	B	117	ASN	4.3
1	B	272	ILE	4.1
1	B	325	TYR	4.1
1	A	126	GLN	4.1
1	B	305	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	119	THR	3.9
1	A	33	TRP	3.9
1	B	5	VAL	3.9
1	B	251	THR	3.8
1	B	263	ILE	3.7
1	B	249	LEU	3.7
1	B	316	ARG	3.6
1	B	125	TYR	3.6
1	B	254	LEU	3.6
1	B	22	GLU	3.5
1	B	33	TRP	3.3
1	B	281	TRP	3.3
1	B	59	ILE	3.2
1	B	227	PHE	3.2
1	B	256	ASP	3.1
1	B	258	ILE	3.1
1	A	104	PRO	3.0
1	B	9	ALA	3.0
1	B	188	TYR	2.8
1	B	75	LYS	2.8
1	B	298	LEU	2.8
1	B	178	LEU	2.7
1	B	216	TRP	2.7
1	B	280	ARG	2.7
1	B	252	GLU	2.7
1	B	130	ASP	2.7
1	B	308	ASP	2.6
1	B	107	ARG	2.5
1	B	250	GLY	2.5
1	B	260	LYS	2.5
1	B	255	TYR	2.4
1	B	327	VAL	2.4
1	B	206	TYR	2.4
1	A	123	GLN	2.4
1	A	73	VAL	2.4
1	B	166	HIS	2.3
1	B	8	ARG	2.3
1	B	121	PHE	2.2
1	B	127	THR	2.2
1	B	286	HIS	2.1
1	B	267	PRO	2.1
1	B	88	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	105	VAL	2.1
1	B	100	ILE	2.1
1	B	261	TYR	2.1
1	B	35	ASN	2.0
1	B	322	PRO	2.0
1	B	248	VAL	2.0
1	B	3	GLY	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(Å ²)	Q<0.9
2	ACT	A	403	4/4	0.88	0.24	11.91	50,52,53,56	0
3	AVK	A	404	22/22	0.80	0.24	0.31	55,64,69,74	0
2	ACT	A	401	4/4	0.96	0.13	-0.70	35,41,42,42	0
2	ACT	A	402	4/4	0.90	0.19	-	41,46,47,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.