



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:48 AM GMT

PDB ID : 3G15
Title : Crystal structure of human choline kinase alpha in complex with hemicholinium-3 and ADP
Authors : Hong, B.S.; Tempel, W.; Rabeh, W.M.; MacKenzie, F.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Bochkarev, A.; Park, H.W.; Structural Genomics Consortium (SGC)
Deposited on : 2009-01-29
Resolution : 1.70 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

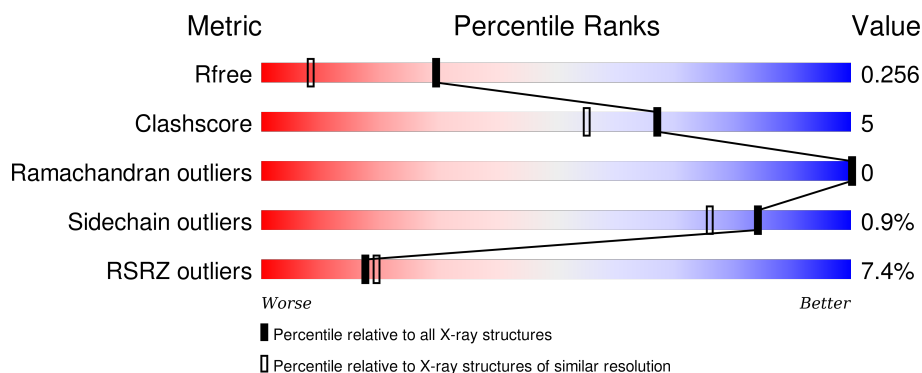
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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	401	<div> <div>5%</div> <div>84%</div> <div>12%</div> </div>
1	B	401	<div> <div>7%</div> <div>70%</div> <div>6%</div> <div>24%</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
5	SO4	A	604	-	-	-	X
6	UNX	A	12	-	-	-	X
6	UNX	A	13	-	-	-	X
6	UNX	A	16	-	-	-	X
6	UNX	A	3	-	-	-	X
6	UNX	A	4	-	-	-	X
6	UNX	A	606	-	-	-	X
6	UNX	B	15	-	-	-	X
6	UNX	B	606	-	-	-	X
6	UNX	B	9	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5861 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 Choline kinase alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	2	0
			2858	1861	470	510	17			
1	B	306	Total	C	N	O	S	0	6	0
			2530	1661	403	448	18			

There are 42 discrepancies between the modelled and reference sequences:

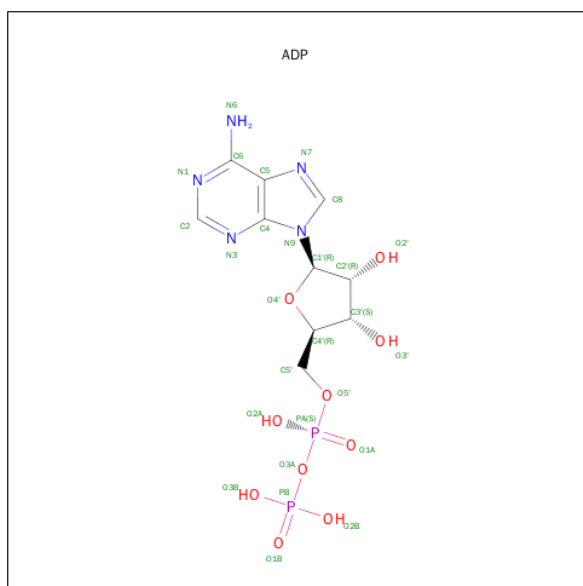
Chain	Residue	Modelled	Actual	Comment	Reference
A	57	GLY	-	EXPRESSION TAG	UNP P35790
A	58	SER	-	EXPRESSION TAG	UNP P35790
A	59	SER	-	EXPRESSION TAG	UNP P35790
A	60	HIS	-	EXPRESSION TAG	UNP P35790
A	61	HIS	-	EXPRESSION TAG	UNP P35790
A	62	HIS	-	EXPRESSION TAG	UNP P35790
A	63	HIS	-	EXPRESSION TAG	UNP P35790
A	64	HIS	-	EXPRESSION TAG	UNP P35790
A	65	HIS	-	EXPRESSION TAG	UNP P35790
A	66	SER	-	EXPRESSION TAG	UNP P35790
A	67	SER	-	EXPRESSION TAG	UNP P35790
A	68	GLY	-	EXPRESSION TAG	UNP P35790
A	69	LEU	-	EXPRESSION TAG	UNP P35790
A	70	VAL	-	EXPRESSION TAG	UNP P35790
A	71	PRO	-	EXPRESSION TAG	UNP P35790
A	72	ARG	-	EXPRESSION TAG	UNP P35790
A	73	GLY	-	EXPRESSION TAG	UNP P35790
A	74	SER	-	EXPRESSION TAG	UNP P35790
A	154	MET	VAL	VARIANT	UNP P35790
A	220	SER	GLY	VARIANT	UNP P35790
A	422	LEU	GLN	VARIANT	UNP P35790
B	57	GLY	-	EXPRESSION TAG	UNP P35790
B	58	SER	-	EXPRESSION TAG	UNP P35790
B	59	SER	-	EXPRESSION TAG	UNP P35790
B	60	HIS	-	EXPRESSION TAG	UNP P35790

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Chain	Residue	Modelled	Actual	Comment	Reference
B	61	HIS	-	EXPRESSION TAG	UNP P35790
B	62	HIS	-	EXPRESSION TAG	UNP P35790
B	63	HIS	-	EXPRESSION TAG	UNP P35790
B	64	HIS	-	EXPRESSION TAG	UNP P35790
B	65	HIS	-	EXPRESSION TAG	UNP P35790
B	66	SER	-	EXPRESSION TAG	UNP P35790
B	67	SER	-	EXPRESSION TAG	UNP P35790
B	68	GLY	-	EXPRESSION TAG	UNP P35790
B	69	LEU	-	EXPRESSION TAG	UNP P35790
B	70	VAL	-	EXPRESSION TAG	UNP P35790
B	71	PRO	-	EXPRESSION TAG	UNP P35790
B	72	ARG	-	EXPRESSION TAG	UNP P35790
B	73	GLY	-	EXPRESSION TAG	UNP P35790
B	74	SER	-	EXPRESSION TAG	UNP P35790
B	154	MET	VAL	VARIANT	UNP P35790
B	220	SER	GLY	VARIANT	UNP P35790
B	422	LEU	GLN	VARIANT	UNP P35790

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 3 | B | 2 | Total Mg
2 2 | 0 | 0 |
| 3 | A | 2 | Total Mg
2 2 | 0 | 0 |

- HC6
-
- The chemical structure of HC6 is a complex molecule featuring two quaternary ammonium cations (N⁺) and multiple chiral centers. The structure is composed of several interconnected rings and side chains, including a central benzene ring and a cyclohexane ring. The molecule is highly symmetrical and contains numerous stereocenters, indicated by wedge and dash bonds. The structure is labeled with various abbreviations (e.g., CAZ, CAX, CAU, CAQ, CAM, CAI, CAH, CAG, CAD(S), CAC, CBA, CBB, CBF, CAE, CAG, CAM, CAU, CAI, CAH, CAG, CAD(S), CAC, CBA, CBB, CBF, CAE) and includes a central benzene ring and a cyclohexane ring. The molecule is highly symmetrical and contains numerous stereocenters, indicated by wedge and dash bonds.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 30	C 24	N 2	O 4	0	0
4	B	1	Total 30	C 24	N 2	O 4	0	0

- 



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

- Molecule 6 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	9	Total	X	0	0
			9	9		
6	A	12	Total	X	0	0
			12	12		

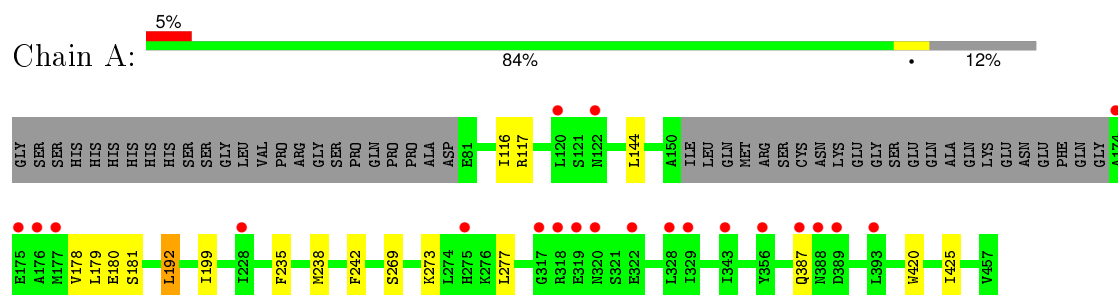
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	169	Total	O	0	0
			169	169		
7	B	155	Total	O	0	0
			155	155		

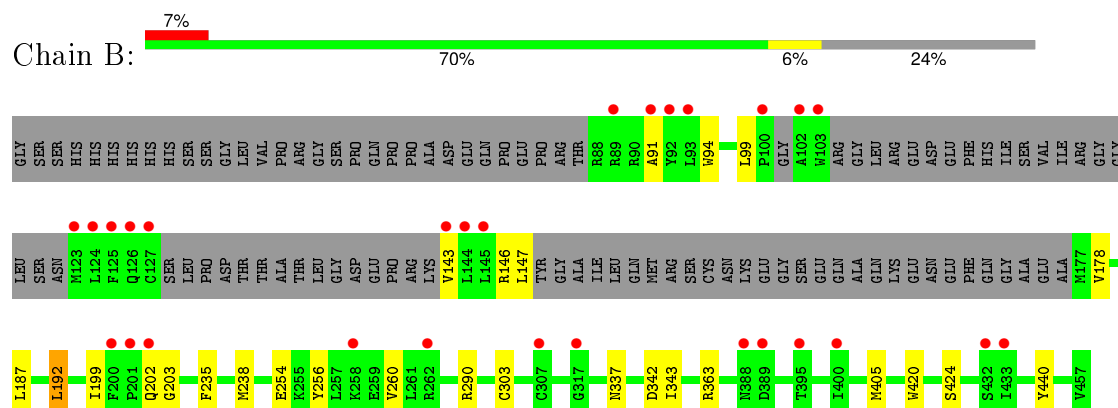
3 Residue-property plots [i](#)

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: Choline kinase alpha



• Molecule 1: Choline kinase alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.80 Å 118.99 Å 131.04 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.70 29.78 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.7 (30.00-1.70) 96.7 (29.78-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 1.70 Å)	Xtriage
Refinement program	REFMAC 5.4.0069, coot, molprobity, arp/warp	Depositor
R, R_{free}	0.220 , 0.257 0.222 , 0.256	Depositor DCC
R_{free} test set	2122 reflections (2.32%)	DCC
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 93408 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5861	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UNX, MG, HC6, SO4, ADP

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	0.70	0/2940	0.71	0/3972
1	B	0.72	0/2611	0.71	0/3518
All	All	0.71	0/5551	0.71	0/7490

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	2858	0	2768	16	0
1	B	2530	0	2451	31	0
2	A	27	0	12	1	0
2	B	27	0	12	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	30	0	34	5	0
4	B	30	0	34	3	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	9	0	0	0	0
7	A	169	0	0	1	0
7	B	155	0	0	1	0
All	All	5861	0	5311	52	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 (52) 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:192:LEU:HD22	1:B:238[B]:MET:CE	1.12	1.56
1:B:192:LEU:CD2	1:B:238[B]:MET:CE	1.98	1.40
1:B:192:LEU:CD2	1:B:238[B]:MET:HE1	1.55	1.31
1:B:192:LEU:HD22	1:B:238[B]:MET:HE2	1.41	1.02
1:A:192:LEU:HD22	1:A:238[B]:MET:CE	1.94	0.98
1:B:192:LEU:CD2	1:B:238[B]:MET:HE2	1.88	0.97
1:B:424[B]:SER:HG	1:B:440:TYR:HD2	1.08	0.96
1:A:192:LEU:HD22	1:A:238[B]:MET:HE1	1.49	0.93
1:B:192:LEU:HD21	1:B:238[B]:MET:HE2	1.67	0.75
4:B:603:HC6:HBAB	4:B:603:HC6:OBC	1.96	0.65
1:A:235:PHE:HA	1:A:238[B]:MET:HE2	1.81	0.62
4:A:603:HC6:OBD	4:A:603:HC6:HAZB	1.99	0.62
1:B:146:ARG:O	1:B:203:GLY:CA	2.47	0.62
1:A:192:LEU:HD22	1:A:238[B]:MET:HE2	1.77	0.61
1:B:91:ALA:HA	1:B:94:TRP:CE3	2.35	0.61
1:B:192:LEU:HD22	1:B:238[B]:MET:HE1	0.61	0.60
1:A:192:LEU:CD2	1:A:238[B]:MET:CE	2.76	0.59
4:A:603:HC6:OBC	4:A:603:HC6:HBAB	2.04	0.58
1:B:91:ALA:HA	1:B:94:TRP:HE3	1.70	0.57
1:A:235:PHE:HA	1:A:238[B]:MET:CE	2.36	0.55
1:A:192:LEU:CD2	1:A:238[B]:MET:HE2	2.36	0.54
1:B:94:TRP:CZ2	1:B:202:GLN:HB2	2.43	0.53
1:B:146:ARG:O	1:B:203:GLY:HA3	2.08	0.53
1:A:420:TRP:CE3	4:A:603:HC6:HABA	2.44	0.53
1:B:235:PHE:HA	1:B:238[B]:MET:HE3	1.91	0.52
1:A:180:GLU:HG3	7:A:534:HOH:O	2.10	0.52
1:B:187:LEU:CD2	1:B:238[B]:MET:SD	2.99	0.51
1:A:116:ILE:HD12	1:A:144:LEU:CD1	2.40	0.51
1:B:192:LEU:HD22	1:B:238[B]:MET:HE3	1.60	0.50
1:B:147:LEU:HA	1:B:202:GLN:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:LEU:CD2	1:B:238[B]:MET:HE3	2.28	0.48
1:B:254[B]:GLU:OE2	1:B:290:ARG:NH2	2.47	0.47
1:B:256:TYR:O	1:B:260:VAL:HG23	2.14	0.47
1:B:363:ARG:NH1	7:B:533:HOH:O	2.47	0.47
1:A:117:ARG:NH2	2:A:601:ADP:O3B	2.48	0.47
1:A:181:SER:HB3	1:A:199:ILE:CD1	2.45	0.47
1:B:343:ILE:CD1	1:B:405:MET:CE	2.94	0.46
1:B:420:TRP:CD2	4:B:603:HC6:HABA	2.51	0.46
1:B:146:ARG:O	1:B:203:GLY:HA2	2.16	0.46
4:A:603:HC6:OBD	4:A:603:HC6:CAZ	2.64	0.45
1:B:235:PHE:HA	1:B:238[B]:MET:CE	2.48	0.44
1:B:187:LEU:HD21	1:B:238[B]:MET:SD	2.58	0.44
1:B:303:CYS:SG	1:B:337:ASN:HB3	2.58	0.43
1:A:277:LEU:HD13	1:A:425:ILE:HD11	2.01	0.43
4:B:603:HC6:OBC	4:B:603:HC6:CBA	2.66	0.42
1:A:269:SER:O	1:A:273:LYS:HG3	2.20	0.42
1:A:179:LEU:HD22	1:A:242:PHE:CE1	2.54	0.42
1:B:192:LEU:CG	1:B:238[B]:MET:HE1	2.40	0.42
4:A:603:HC6:OBC	4:A:603:HC6:CBA	2.67	0.41
1:B:99:LEU:HD11	1:B:143:VAL:HG21	2.02	0.40
1:A:178:VAL:HG22	1:B:178:VAL:HG22	2.03	0.40
1:B:94:TRP:CH2	1:B:202:GLN:HB2	2.56	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	352/401 (88%)	346 (98%)	6 (2%)	0	100	100
1	B	302/401 (75%)	292 (97%)	10 (3%)	0	100	100
All	All	654/802 (82%)	638 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	296/357 (83%)	294 (99%)	2 (1%)	88	82
1	B	265/357 (74%)	262 (99%)	3 (1%)	80	69
All	All	561/714 (79%)	556 (99%)	5 (1%)	84	76

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	192	LEU
1	A	387	GLN
1	B	192	LEU
1	B	199	ILE
1	B	342	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

Of 31 ligands modelled in this entry, 21 are unknown and 4 are monoatomic - leaving 6 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	ADP	A	601	3	22,29,29	1.18	2 (9%)	27,45,45	1.80	2 (7%)
4	HC6	A	603	-	31,33,33	2.42	12 (38%)	38,52,52	1.11	3 (7%)
5	SO4	A	604	3	4,4,4	0.38	0	6,6,6	0.81	0
2	ADP	B	601	3	22,29,29	1.03	2 (9%)	27,45,45	1.78	3 (11%)
4	HC6	B	603	-	31,33,33	2.10	10 (32%)	38,52,52	1.21	3 (7%)
5	SO4	B	604	3	4,4,4	0.62	0	6,6,6	0.17	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	ADP	A	601	3	-	0/12/32/32	0/3/3/3
4	HC6	A	603	-	-	0/16/44/44	0/4/4/4
5	SO4	A	604	3	-	0/0/0/0	0/0/0/0
2	ADP	B	601	3	-	0/12/32/32	0/3/3/3
4	HC6	B	603	-	-	0/16/44/44	0/4/4/4
5	SO4	B	604	3	-	0/0/0/0	0/0/0/0

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	HC6	CAS-CAP	-5.03	1.47	1.52
4	A	603	HC6	CAD-CAG	-3.97	1.48	1.52
4	A	603	HC6	CAX-NAW	-3.38	1.48	1.51
4	A	603	HC6	CAB-NAA	-2.66	1.45	1.51
4	B	603	HC6	CAS-CAP	-2.63	1.49	1.52
4	A	603	HC6	CAM-CAJ	-2.61	1.42	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	603	HC6	CAM-CAJ	-2.32	1.43	1.49
4	A	603	HC6	CAC-NAA	-2.26	1.49	1.51
4	B	603	HC6	CAD-CAG	-2.25	1.50	1.52
4	B	603	HC6	CAC-NAA	-2.21	1.49	1.51
4	B	603	HC6	CAB-NAA	-2.16	1.46	1.51
4	A	603	HC6	OAT-CAU	2.15	1.47	1.44
4	B	603	HC6	CAQ-CAR	2.19	1.42	1.38
2	B	601	ADP	O4'-C1'	2.29	1.44	1.41
4	A	603	HC6	OAE-CAF	2.67	1.48	1.44
2	A	601	ADP	C5-C4	2.70	1.46	1.40
4	A	603	HC6	OAE-CAD	2.75	1.45	1.42
4	B	603	HC6	OAT-CAS	2.78	1.45	1.42
2	B	601	ADP	C5-C4	3.02	1.47	1.40
2	A	601	ADP	O4'-C1'	3.55	1.45	1.41
4	B	603	HC6	OAE-CAD	3.60	1.46	1.42
4	A	603	HC6	OBC-CAD	3.87	1.44	1.40
4	A	603	HC6	OBD-CAS	4.06	1.44	1.40
4	B	603	HC6	OBC-CAD	4.21	1.44	1.40
4	B	603	HC6	OBD-CAS	6.21	1.46	1.40
4	A	603	HC6	OAT-CAS	6.26	1.48	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	ADP	N3-C2-N1	-7.67	123.02	128.89
2	A	601	ADP	N3-C2-N1	-7.63	123.06	128.89
4	B	603	HC6	CAD-CAC-NAA	-4.58	112.42	114.28
4	A	603	HC6	CAD-CAC-NAA	-3.27	112.95	114.28
4	B	603	HC6	OAE-CAF-CAB	-2.99	109.03	111.47
2	B	601	ADP	C4-C5-N7	-2.60	107.09	109.48
4	A	603	HC6	CAY-NAW-CAZ	2.01	111.11	107.84
2	A	601	ADP	N6-C6-N1	2.02	123.54	119.20
4	B	603	HC6	CAS-CAX-NAW	2.13	115.14	114.28
2	B	601	ADP	C2-N1-C6	2.17	122.65	118.77
4	A	603	HC6	CBB-NAA-CBA	2.99	112.72	107.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ADP	1	0
4	A	603	HC6	5	0
4	B	603	HC6	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	354/401 (88%)	0.24	21 (5%) 26 27	14, 25, 46, 61	0
1	B	306/401 (76%)	0.39	28 (9%) 11 12	14, 24, 49, 67	0
All	All	660/802 (82%)	0.31	49 (7%) 17 19	14, 25, 48, 67	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	317	GLY	5.1
1	B	123	MET	4.8
1	A	174	ALA	4.8
1	B	100	PRO	4.8
1	B	103	TRP	4.5
1	B	395	THR	4.4
1	B	93	LEU	4.4
1	B	124	LEU	4.3
1	B	202	GLN	4.1
1	B	102	ALA	4.0
1	B	126	GLN	3.9
1	A	175	GLU	3.9
1	A	319	GLU	3.8
1	B	89	ARG	3.8
1	A	320	ASN	3.5
1	B	125	PHE	3.5
1	A	389	ASP	3.4
1	B	258	LYS	3.4
1	B	201	PRO	3.2
1	B	388	ASN	3.0
1	A	122	ASN	2.9
1	B	262	ARG	2.9
1	A	388	ASN	2.8
1	A	176	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	275	HIS	2.8
1	B	143	VAL	2.6
1	B	433	ILE	2.6
1	A	387	GLN	2.6
1	B	400	ILE	2.6
1	B	144	LEU	2.6
1	A	393	LEU	2.6
1	B	389	ASP	2.5
1	A	356	TYR	2.4
1	A	329	ILE	2.4
1	B	92	TYR	2.4
1	B	200	PHE	2.3
1	A	322	GLU	2.3
1	A	177	MET	2.3
1	B	307[A]	CYS	2.3
1	B	432	SER	2.3
1	A	328	LEU	2.2
1	B	317	GLY	2.2
1	A	228	ILE	2.2
1	A	120	LEU	2.1
1	B	145	LEU	2.1
1	B	127	CYS	2.1
1	A	318	ARG	2.1
1	B	91	ALA	2.1
1	A	343	ILE	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
6	UNX	A	13	1/1	0.01	3.39	167.81	2,2,2,2	1
6	UNX	B	15	1/1	-0.09	1.99	105.78	2,2,2,2	1
6	UNX	A	16	1/1	0.30	2.88	92.58	2,2,2,2	1
6	UNX	A	4	1/1	-0.31	1.88	87.62	2,2,2,2	1
6	UNX	A	606	1/1	-0.31	1.81	83.86	2,2,2,2	1
6	UNX	B	606	1/1	-0.33	2.24	80.38	2,2,2,2	1
6	UNX	A	3	1/1	0.09	1.61	67.55	2,2,2,2	1
6	UNX	B	9	1/1	0.08	1.42	55.99	2,2,2,2	1
6	UNX	A	12	1/1	0.09	2.44	52.84	2,2,2,2	1
5	SO4	A	604	5/5	0.81	0.26	17.10	28,28,35,38	0
4	HC6	B	603	30/30	0.83	0.14	0.43	23,28,32,34	0
4	HC6	A	603	30/30	0.88	0.10	0.15	22,29,32,33	0
5	SO4	B	604	5/5	0.94	0.12	0.13	24,24,29,32	0
2	ADP	A	601	27/27	0.90	0.11	-0.24	28,32,37,40	0
2	ADP	B	601	27/27	0.97	0.06	-1.28	24,30,33,34	0
6	UNX	B	10	1/1	-0.29	2.88	-	2,2,2,2	1
6	UNX	A	17	1/1	-0.39	1.70	-	2,2,2,2	1
3	MG	B	605	1/1	1.00	0.09	-	24,24,24,24	0
6	UNX	A	19	1/1	-0.35	3.66	-	2,2,2,2	1
6	UNX	B	8	1/1	0.42	2.69	-	2,2,2,2	1
3	MG	B	602	1/1	0.97	0.06	-	25,25,25,25	0
6	UNX	B	7	1/1	-0.02	1.98	-	2,2,2,2	1
6	UNX	A	20	1/1	0.05	2.77	-	2,2,2,2	1
6	UNX	A	2	1/1	0.76	2.04	-	2,2,2,2	1
6	UNX	A	14	1/1	-0.23	2.37	-	2,2,2,2	1
6	UNX	B	18	1/1	-0.17	1.62	-	2,2,2,2	1
6	UNX	A	1	1/1	0.23	2.42	-	2,2,2,2	1
6	UNX	B	5	1/1	-0.10	2.19	-	2,2,2,2	1
3	MG	A	602	1/1	0.99	0.07	-	27,27,27,27	0
3	MG	A	605	1/1	0.96	0.19	-	33,33,33,33	0
6	UNX	B	6	1/1	0.56	2.59	-	2,2,2,2	1

6.5 Other polymers ⓘ

There are no such residues in this entry.