Full wwPDB X-ray Structure Validation Report (i)

Feb 13, 2017 – 10:32 pm GMT

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PDB ID	:	3KM8
Title	:	Crystal structuore of adenosine deaminase from mus musculus complexed with 9-deazainosine
Authors	:	Fan, X.; Gao, Y.
Deposited on	:	2009-11-10
Resolution	:	2.00 Å(reported)

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 2.00 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.
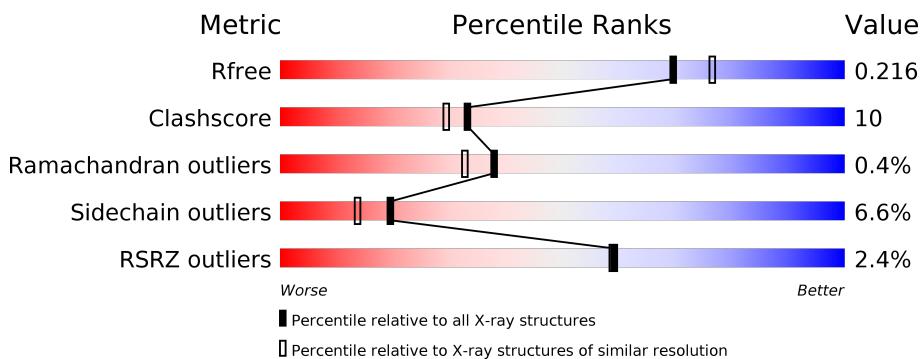
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 <=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	4% / 75% 20% 5% ·
1	B	352	% / 84% 13% · ·
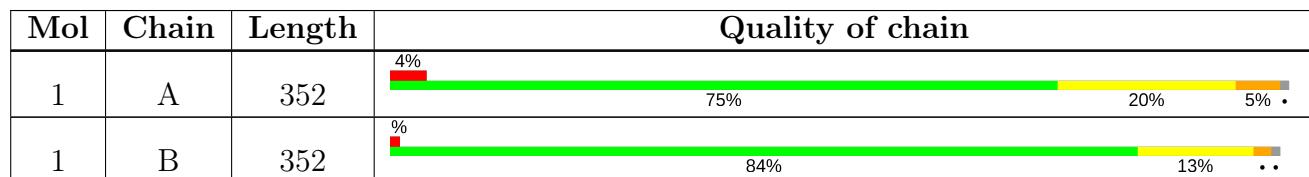
2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 5972 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 Adenosine deaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2788	1774	471	529	14			
1	B	349	Total	C	N	O	S	0	0	0
			2788	1774	471	529	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	217	GLN	GLU	ENGINEERED	UNP P03958
A	240	GLU	TYR	ENGINEERED	UNP P03958
B	217	GLN	GLU	ENGINEERED	UNP P03958
B	240	GLU	TYR	ENGINEERED	UNP P03958

- Molecule 2 is 9-DEAZAINOSINE (three-letter code: 9DI) (formula: $C_{11}H_{13}N_3O_5$).
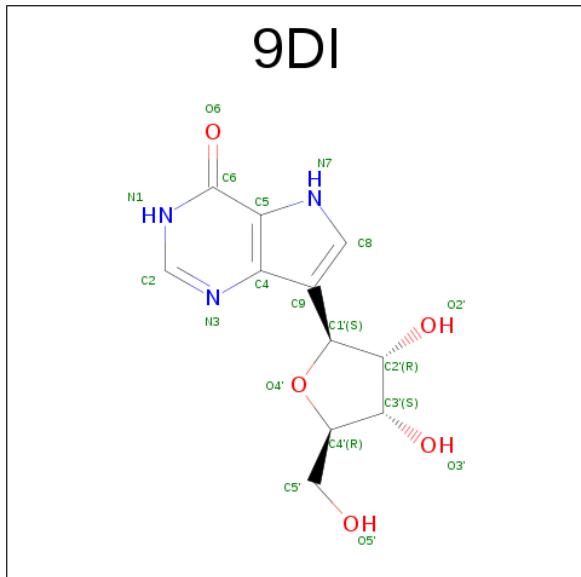
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 19	C 11	N 3	O 5	0	0
2	B	1	Total 19	C 11	N 3	O 5	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Zn 1	0	0
3	A	1	Total 1	Zn 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	173	Total 173	O 173	0	0
4	B	183	Total 183	O 183	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: Adenosine deaminase
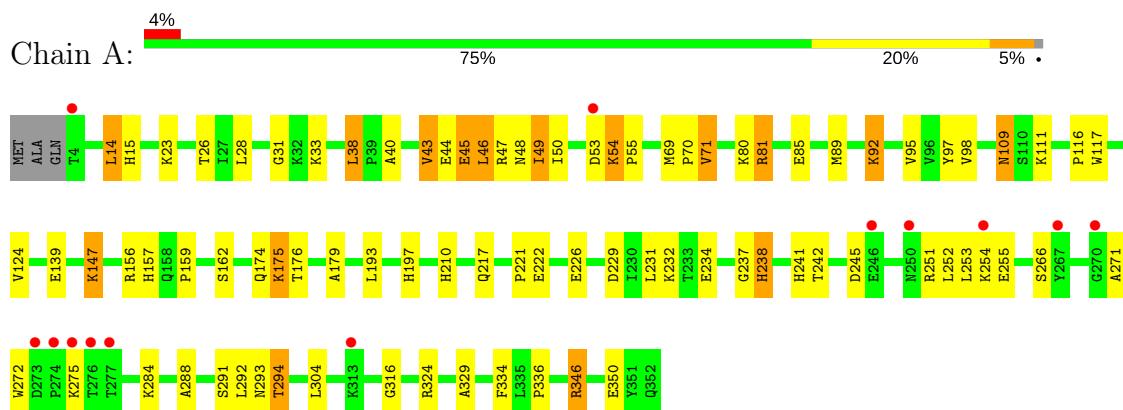
• Molecule 1: Adenosine deaminase
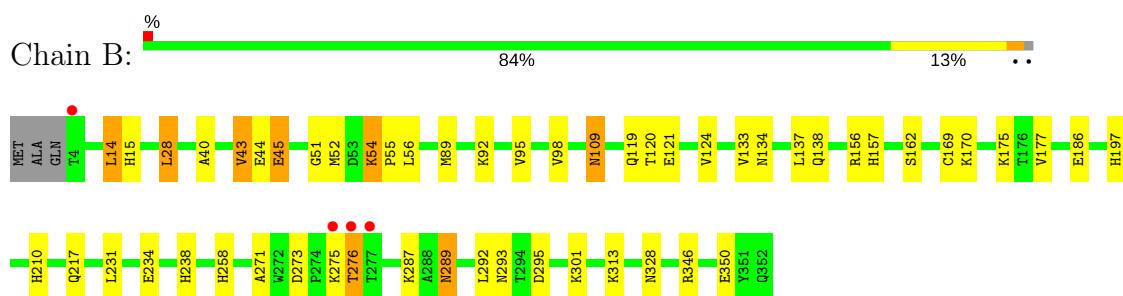
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	100.34Å 93.62Å 85.42Å 90.00° 97.35° 90.00°	Depositor
Resolution (Å)	37.48 – 2.00 34.64 – 2.00	Depositor EDS
% Data completeness (in resolution range)	90.8 (37.48-2.00) 90.8 (34.64-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.96 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.202 , 0.223 0.204 , 0.216	Depositor DCC
R_{free} test set	2445 reflections (5.36%)	DCC
Wilson B-factor (Å^2)	27.0	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 49.9	EDS
L-test for twinning[2]	$< |L| > = 0.53, < L^2 > = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5972	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.84 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.4394e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN, 9DI

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	0.68	0/2851	0.77	3/3858 (0.1%)
1	B	0.70	0/2851	0.77	0/3858
All	All	0.69	0/5702	0.77	3/7716 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	294	THR	N-CA-C	-5.53	96.06	111.00
1	A	294	THR	C-N-CA	-5.08	109.01	121.70
1	A	46	LEU	CA-CB-CG	5.05	126.92	115.30

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	2788	0	2756	69	0
1	B	2788	0	2756	40	0
2	A	19	0	13	0	0
2	B	19	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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WORLDWIDE
wwPDB
PROTEIN DATA BANK

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	173	0	0	20	0
4	B	183	0	0	11	0
All	All	5972	0	5538	109	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 10.

All (109) 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:44:GLU:HG3	4:A:390:HOH:O	1.72	0.89
1:A:174:GLN:C	1:A:175:LYS:HG2	1.93	0.88
1:A:159:PRO:HD2	4:A:415:HOH:O	1.75	0.85
1:B:313:LYS:HG3	4:B:359:HOH:O	1.76	0.84
1:A:284:LYS:HE2	4:A:395:HOH:O	1.78	0.84
1:B:134:ASN:O	1:B:138:GLN:HG3	1.81	0.80
1:B:52:MET:CE	1:B:56:LEU:HD12	2.15	0.77
1:B:273:ASP:O	1:B:276:THR:HB	1.85	0.76
1:A:109:ASN:HD21	1:A:124:VAL:H	1.33	0.76
1:A:210:HIS:HE1	4:A:376:HOH:O	1.69	0.74
1:B:109:ASN:C	1:B:109:ASN:HD22	1.89	0.74
1:B:28:LEU:HD23	1:B:43:VAL:HG12	1.74	0.70
1:B:44:GLU:HB2	4:B:380:HOH:O	1.92	0.68
1:B:109:ASN:HD21	1:B:124:VAL:H	1.40	0.68
1:A:33:LYS:HE3	4:A:506:HOH:O	1.93	0.68
1:A:109:ASN:C	1:A:109:ASN:HD22	1.98	0.67
1:B:170:LYS:CE	4:B:484:HOH:O	2.43	0.67
1:B:15:HIS:H	1:B:293:ASN:ND2	1.93	0.67
1:B:52:MET:HE1	1:B:56:LEU:HD12	1.75	0.67
1:A:174:GLN:O	1:A:175:LYS:HG2	1.93	0.66
1:B:162:SER:OG	1:B:197:HIS:HD2	1.79	0.66
1:A:346:ARG:NH1	1:A:350:GLU:OE1	2.29	0.65
1:A:316:GLY:HA2	4:A:501:HOH:O	1.97	0.65
1:B:14:LEU:H	1:B:293:ASN:HD21	1.43	0.65
1:A:81:ARG:HD2	1:A:85:GLU:OE2	1.96	0.64
1:B:14:LEU:H	1:B:293:ASN:ND2	1.95	0.64
1:B:157:HIS:HB2	4:B:473:HOH:O	1.97	0.63
1:A:89:MET:HG3	4:A:367:HOH:O	1.98	0.63
1:A:294:THR:HG23	1:A:304:LEU:HD13	1.81	0.63
1:A:162:SER:OG	1:A:197:HIS:HD2	1.81	0.63
1:A:237:GLY:O	1:A:238:HIS:HB2	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:HIS:HE1	4:B:487:HOH:O	1.83	0.60
1:A:109:ASN:ND2	1:A:124:VAL:H	2.01	0.59
1:A:54:LYS:HD3	1:A:55:PRO:O	2.03	0.58
1:A:48:ASN:ND2	4:A:369:HOH:O	2.31	0.57
1:A:217:GLN:O	1:A:271:ALA:HB1	2.04	0.57
1:A:288:ALA:O	1:A:324:ARG:NH2	2.34	0.56
1:B:52:MET:HE3	1:B:56:LEU:HD12	1.86	0.56
1:A:251:ARG:HG3	1:A:255:GLU:OE2	2.06	0.55
1:B:346:ARG:NH1	1:B:350:GLU:OE1	2.40	0.55
1:A:162:SER:OG	1:A:197:HIS:CD2	2.60	0.54
1:A:229:ASP:O	1:A:232:LYS:HE2	2.08	0.54
1:A:92:LYS:HD2	4:B:434:HOH:O	2.08	0.54
1:B:170:LYS:HE2	4:B:484:HOH:O	2.07	0.54
1:A:80:LYS:NZ	4:A:497:HOH:O	2.41	0.53
1:A:156:ARG:O	1:A:197:HIS:HE1	1.92	0.53
1:B:15:HIS:H	1:B:293:ASN:HD22	1.57	0.53
1:A:14:LEU:H	1:A:293:ASN:ND2	2.07	0.52
1:B:169:CYS:HA	1:B:177:VAL:HG11	1.91	0.51
1:B:157:HIS:HE1	4:B:442:HOH:O	1.93	0.51
1:A:47:ARG:HD3	4:A:419:HOH:O	2.10	0.50
1:B:109:ASN:C	1:B:109:ASN:ND2	2.60	0.50
1:B:157:HIS:CE1	4:B:442:HOH:O	2.63	0.50
1:A:44:GLU:CG	4:A:390:HOH:O	2.43	0.50
1:A:157:HIS:HE1	4:A:450:HOH:O	1.95	0.49
1:A:174:GLN:NE2	1:A:336:PRO:HD3	2.26	0.49
1:A:251:ARG:O	1:A:255:GLU:HG3	2.12	0.49
1:B:287:LYS:HD3	4:B:411:HOH:O	2.11	0.49
1:A:116:PRO:HB2	1:A:117:TRP:CD1	2.47	0.49
1:A:139:GLU:HG3	4:A:462:HOH:O	2.12	0.48
1:A:31:GLY:HA3	1:A:38:LEU:HD22	1.95	0.48
1:B:54:LYS:HD2	1:B:55:PRO:O	2.14	0.48
1:A:174:GLN:NE2	4:A:416:HOH:O	2.45	0.48
1:A:15:HIS:H	1:A:293:ASN:HD22	1.61	0.47
1:B:162:SER:OG	1:B:197:HIS:CD2	2.62	0.47
1:A:175:LYS:HG3	1:A:175:LYS:HZ2	1.62	0.47
1:B:40:ALA:HB1	1:B:45:GLU:HB3	1.96	0.47
1:B:89:MET:HE1	4:B:417:HOH:O	2.14	0.47
1:A:80:LYS:HB3	1:A:80:LYS:HE2	1.64	0.47
1:B:109:ASN:HB3	1:B:119:GLN:NE2	2.30	0.47
1:A:221:PRO:HG3	1:A:241:HIS:O	2.16	0.47
1:A:26:THR:OG1	1:A:81:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:VAL:HG12	4:A:366:HOH:O	2.15	0.47
1:B:289:ASN:ND2	1:B:328:ASN:HB3	2.31	0.46
1:A:237:GLY:O	1:A:238:HIS:CB	2.61	0.46
1:A:97:TYR:CD1	1:A:147:LYS:HG2	2.50	0.46
1:A:109:ASN:C	1:A:109:ASN:ND2	2.69	0.46
1:A:43:VAL:CG1	4:A:366:HOH:O	2.65	0.45
1:B:217:GLN:O	1:B:271:ALA:HB1	2.15	0.45
1:A:229:ASP:CG	1:A:251:ARG:HH22	2.17	0.45
1:A:291:SER:HB3	1:A:329:ALA:HB2	1.98	0.45
1:A:81:ARG:NH1	1:A:85:GLU:OE2	2.48	0.45
1:B:133:VAL:O	1:B:137:LEU:HG	2.17	0.45
1:A:97:TYR:HD1	1:A:147:LYS:HG2	1.82	0.45
1:A:272:TRP:HB2	4:A:386:HOH:O	2.17	0.44
1:A:245:ASP:OD1	1:A:245:ASP:C	2.55	0.44
1:B:156:ARG:O	1:B:197:HIS:HE1	2.00	0.44
1:B:210:HIS:HD2	1:B:234:GLU:OE1	2.01	0.44
1:B:346:ARG:O	1:B:350:GLU:HG3	2.18	0.44
1:A:49:ILE:CG2	1:A:50:ILE:N	2.81	0.43
1:A:15:HIS:H	1:A:293:ASN:ND2	2.16	0.43
1:A:69:MET:N	1:A:70:PRO:CD	2.82	0.43
1:A:40:ALA:HB1	1:A:45:GLU:HB3	2.01	0.43
1:A:159:PRO:HA	1:A:197:HIS:NE2	2.34	0.43
1:A:242:THR:HG21	1:A:252:LEU:HD12	2.00	0.42
1:A:175:LYS:HA	1:A:176:THR:HA	1.87	0.42
1:A:95:VAL:HG11	1:A:98:VAL:HB	2.02	0.42
1:B:95:VAL:HG11	1:B:98:VAL:HB	2.01	0.42
1:B:52:MET:CE	1:B:56:LEU:HB2	2.49	0.42
1:A:179:ALA:HB2	1:A:334:PHE:CD2	2.55	0.42
1:A:222:GLU:O	1:A:226:GLU:HG3	2.19	0.42
1:A:14:LEU:H	1:A:293:ASN:HD21	1.66	0.41
1:A:23:LYS:HE3	4:A:367:HOH:O	2.20	0.41
1:B:258:HIS:ND1	1:B:289:ASN:ND2	2.68	0.41
1:A:210:HIS:HA	1:A:234:GLU:OE1	2.21	0.41
1:A:47:ARG:CD	4:A:419:HOH:O	2.69	0.41
1:B:51:GLY:HA3	1:B:301:LYS:HD2	2.03	0.41
1:A:31:GLY:HA2	1:A:71:VAL:HG22	2.03	0.41
1:A:47:ARG:NH1	4:A:390:HOH:O	2.54	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	347/352 (99%)	336 (97%)	10 (3%)	1 (0%)	44	40
1	B	347/352 (99%)	338 (97%)	7 (2%)	2 (1%)	28	21
All	All	694/704 (99%)	674 (97%)	17 (2%)	3 (0%)	38	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	238	HIS
1	B	238	HIS
1	B	295	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	304/306 (99%)	280 (92%)	24 (8%)	14	9
1	B	304/306 (99%)	288 (95%)	16 (5%)	26	21
All	All	608/612 (99%)	568 (93%)	40 (7%)	19	14

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	28	LEU
1	A	38	LEU

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Mol	Chain	Res	Type
1	A	43	VAL
1	A	45	GLU
1	A	46	LEU
1	A	49	ILE
1	A	53	ASP
1	A	54	LYS
1	A	71	VAL
1	A	81	ARG
1	A	92	LYS
1	A	109	ASN
1	A	111	LYS
1	A	147	LYS
1	A	175	LYS
1	A	193	LEU
1	A	231	LEU
1	A	253	LEU
1	A	254	LYS
1	A	266	SER
1	A	275	LYS
1	A	292	LEU
1	A	346	ARG
1	B	14	LEU
1	B	28	LEU
1	B	43	VAL
1	B	45	GLU
1	B	54	LYS
1	B	92	LYS
1	B	109	ASN
1	B	120	THR
1	B	121	GLU
1	B	175	LYS
1	B	186	GLU
1	B	231	LEU
1	B	275	LYS
1	B	276	THR
1	B	289	ASN
1	B	292	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	ASN

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Mol	Chain	Res	Type
1	A	119	GLN
1	A	134	ASN
1	A	157	HIS
1	A	158	GLN
1	A	174	GLN
1	A	197	HIS
1	A	210	HIS
1	A	256	ASN
1	A	289	ASN
1	A	293	ASN
1	B	8	ASN
1	B	109	ASN
1	B	119	GLN
1	B	134	ASN
1	B	157	HIS
1	B	158	GLN
1	B	197	HIS
1	B	210	HIS
1	B	289	ASN
1	B	293	ASN

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	9DI	A	353	-	20,21,21	1.04	1 (5%)	20,31,31	3.67	7 (35%)
2	9DI	B	353	-	20,21,21	1.08	2 (10%)	20,31,31	3.27	8 (40%)

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	9DI	A	353	-	-	0/2/22/22	0/3/3/3
2	9DI	B	353	-	-	0/2/22/22	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	353	9DI	C4-N3	-2.16	1.34	1.37
2	A	353	9DI	C6-C5	2.63	1.46	1.41
2	B	353	9DI	C6-C5	3.07	1.47	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	353	9DI	C6-C5-C4	-7.94	112.95	120.84
2	A	353	9DI	C6-C5-C4	-7.47	113.41	120.84
2	A	353	9DI	N3-C2-N1	-6.74	122.99	128.86
2	B	353	9DI	N3-C2-N1	-6.16	123.49	128.86
2	B	353	9DI	C9-C1'-C2'	-5.26	106.48	115.55
2	A	353	9DI	C9-C1'-C2'	-4.96	107.00	115.55
2	A	353	9DI	C9-C4-C5	-2.96	102.34	116.31
2	B	353	9DI	C9-C4-C5	-2.79	103.18	116.31
2	B	353	9DI	C5'-C4'-C3'	-2.10	109.98	115.05
2	B	353	9DI	O4'-C1'-C2'	2.23	108.04	104.45
2	A	353	9DI	O4'-C1'-C2'	2.25	108.06	104.45
2	B	353	9DI	C2-N1-C6	4.27	123.03	115.91
2	A	353	9DI	C2-N1-C6	4.69	123.74	115.91
2	B	353	9DI	O4'-C1'-C9	6.33	113.93	109.64
2	A	353	9DI	O4'-C1'-C9	9.91	116.36	109.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	349/352 (99%)	-0.12	13 (3%)	42	43	14, 27, 48, 72	0
1	B	349/352 (99%)	-0.24	4 (1%)	80	80	16, 25, 41, 61	0
All	All	698/704 (99%)	-0.18	17 (2%)	59	59	14, 26, 45, 72	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	LYS	4.6
1	B	275	LYS	4.1
1	A	4	THR	3.9
1	A	53	ASP	3.6
1	B	276	THR	3.5
1	A	276	THR	3.4
1	A	250	ASN	3.0
1	A	313	LYS	2.8
1	A	277	THR	2.6
1	A	274	PRO	2.5
1	A	273	ASP	2.4
1	A	270	GLY	2.4
1	B	4	THR	2.4
1	A	246	GLU	2.2
1	B	277	THR	2.1
1	A	267	TYR	2.0
1	A	254	LYS	2.0

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

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

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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(Å^2)	Q<0.9
2	9DI	A	353	19/19	0.97	0.14	0.33	14,19,23,24	0
2	9DI	B	353	19/19	0.97	0.13	0.20	11,19,22,26	0
3	ZN	B	400	1/1	1.00	0.08	-1.55	21,21,21,21	0
3	ZN	A	400	1/1	1.00	0.09	-1.92	23,23,23,23	0

6.5　Other polymers ⓘ

There are no such residues in this entry.

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