



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 04:04 PM GMT

PDB ID : 2C5H
Title : X-RAY CRYSTAL STRUCTURE OF 5'-FLUORODEOXYADENOSIN
ESYNTHASE FROM STREPTOMYCES CATTLEYA COMPLEXED WITH
2'DEOXY-ADENOSINE
Authors : Mcewan, A.R.; Deng, H.; McGlinchey, R.P.; Robinson, D.R.; O'Hagan, D.;
Naismith, J.H.; Spencer, J.
Deposited on : 2005-10-27
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

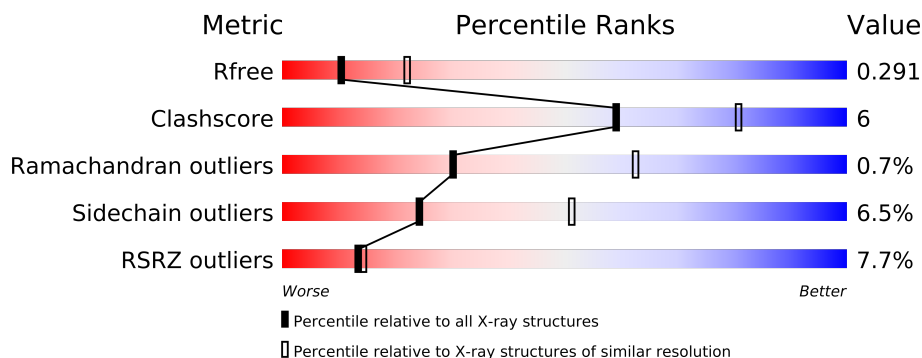
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	299	
1	B	299	
1	C	299	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	CL	A	1302	-	X

2 Entry composition i

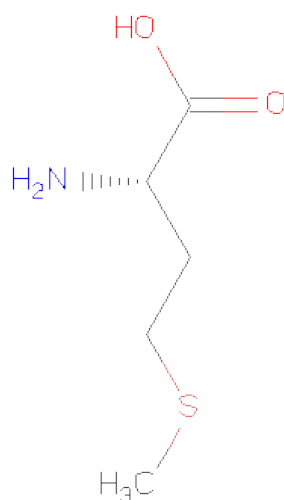
There are 5 unique types of molecules in this entry. The entry contains 6829 atoms, of which 0 are hydrogen and 0 are deuterium.

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 5'-FLUORO-5'-DEOXYADENOSINESYNTHASE.

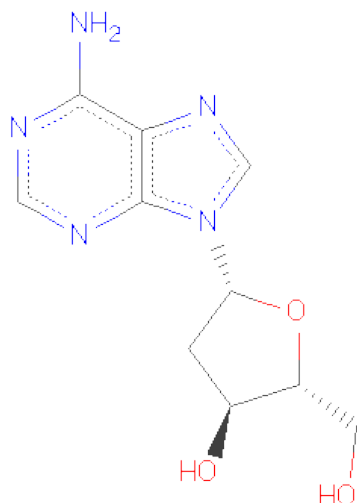
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2220	1410	378	424	8			
1	B	291	Total	C	N	O	S	0	0	0
			2220	1410	378	424	8			
1	C	291	Total	C	N	O	S	0	0	0
			2220	1410	378	424	8			

- Molecule 2 is METHIONINE (three-letter code: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		
2	B	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

- Molecule 3 is (2R,3S,5R)-5-(6-AMINO-9H-PURIN-9-YL)-TETRAHYDRO-2-(HYDROXY METHYL)FURAN-3-OL (three-letter code: 3D1) (formula: C₁₀H₁₃N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	10	5	3		
3	B	1	Total	C	N	O	0	0
			18	10	5	3		
3	C	1	Total	C	N	O	0	0
			18	10	5	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

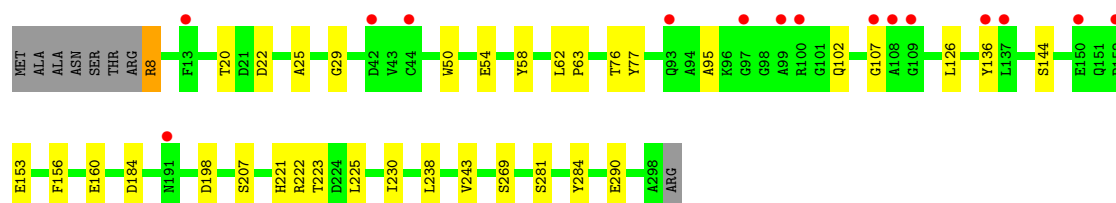
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	33	Total	O	0	0
			33	33		
5	B	36	Total	O	0	0
			36	36		
5	C	27	Total	O	0	0
			27	27		

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 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.

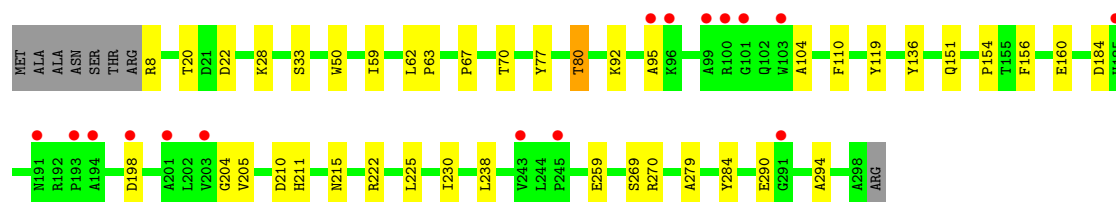
• Molecule 1: 5'-FLUORO-5'-DEOXYADENOSINESYNTHASE

Chain A: 



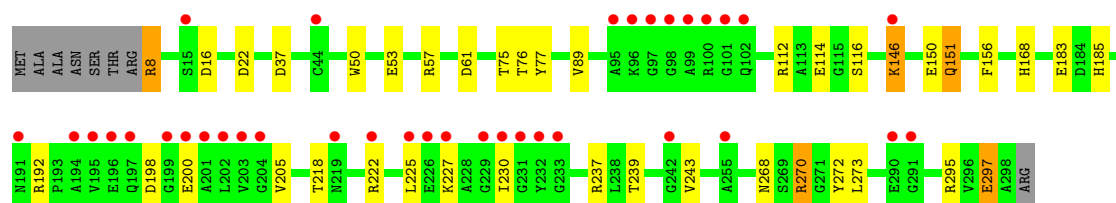
• Molecule 1: 5'-FLUORO-5'-DEOXYADENOSINESYNTHASE

Chain B: 



• Molecule 1: 5'-FLUORO-5'-DEOXYADENOSINESYNTHASE

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	74.54Å 126.70Å 181.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 37.04 – 2.70	Depositor EDS
% Data completeness (in resolution range)	94.6 (50.00-2.70) 94.6 (37.04-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.228 , 0.293 0.233 , 0.291	Depositor DCC
R_{free} test set	1146 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.795	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , -5.6	EDS
Estimated twinning fraction	0.059 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.059 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	1 of 22702 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6829	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3D1, CL

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	0.64	0/2276	0.75	1/3106 (0.0%)
1	B	0.65	0/2276	0.76	1/3106 (0.0%)
1	C	0.66	0/2276	0.77	0/3106
All	All	0.65	0/6828	0.76	2/9318 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	LEU	CA-CB-CG	5.87	128.81	115.30
1	B	238	LEU	CA-CB-CG	5.50	127.94	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	75	THR	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2220	0	0	14	0
1	B	2220	0	0	17	0
1	C	2220	0	0	15	0
2	A	9	0	0	0	0
2	B	9	0	0	1	0
3	A	18	0	0	1	0
3	B	18	0	0	1	0
3	C	18	0	0	0	0
4	A	1	0	0	0	0
5	A	33	0	0	1	0
5	B	36	0	0	1	0
5	C	27	0	0	1	0
All	All	6829	0	0	41	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (41) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:183:GLU:OE1	1:C:185:HIS:CE1	2.43	0.71
1:B:211:HIS:ND1	1:B:284:TYR:OH	2.26	0.69
1:C:218:THR:OG1	1:C:273:LEU:O	2.13	0.67
1:A:136:TYR:OH	1:A:184:ASP:OD1	2.13	0.67
1:B:22:ASP:OD1	1:C:270:ARG:NH2	2.29	0.65
1:A:54:GLU:OE2	1:A:58:TYR:OH	2.16	0.64
1:A:102:GLN:NE2	1:C:151:GLN:O	2.35	0.59
1:C:239:THR:N	1:C:295:ARG:O	2.35	0.59
1:B:80:THR:OG1	1:B:154:PRO:O	2.21	0.58
1:B:204:GLY:N	1:B:294:ALA:O	2.39	0.56
1:A:281:SER:OG	1:A:284:TYR:CD2	2.63	0.51
1:B:136:TYR:OH	1:B:184:ASP:OD1	2.28	0.51
1:B:222:ARG:O	1:B:225:LEU:N	2.47	0.48
1:A:153:GLU:N	1:A:160:GLU:OE1	2.46	0.48
1:C:222:ARG:O	1:C:225:LEU:N	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:269:SER:N	5:A:2027:HOH:O	2.48	0.47
1:A:207:SER:O	1:A:290:GLU:OE2	2.32	0.47
1:C:268:ASN:OD1	1:C:272:TYR:N	2.47	0.47
1:B:59:ILE:O	1:B:119:TYR:OH	2.34	0.46
3:B:500:3D1:O3'	1:C:16:ASP:OD1	2.34	0.46
1:C:237:ARG:N	1:C:297:GLU:O	2.49	0.46
1:C:8:ARG:N	5:C:2001:HOH:O	2.50	0.45
3:A:500:3D1:N1	1:B:279:ALA:N	2.65	0.45
1:A:222:ARG:O	1:A:225:LEU:N	2.49	0.45
1:A:22:ASP:OD1	1:B:270:ARG:NH2	2.50	0.44
1:B:62:LEU:N	1:B:63:PRO:CD	2.80	0.44
1:C:146:LYS:O	1:C:168:HIS:CE1	2.70	0.44
1:A:107:GLY:O	1:C:150:GLU:N	2.51	0.44
1:B:104:ALA:O	1:B:110:PHE:N	2.52	0.43
1:B:210:ASP:OD2	1:B:215:ASN:ND2	2.52	0.43
1:B:269:SER:OG	2:B:1299:MET:O	2.36	0.42
1:B:67:PRO:O	1:B:70:THR:OG1	2.38	0.41
1:C:22:ASP:OD1	1:C:22:ASP:N	2.53	0.41
1:A:25:ALA:O	1:A:29:GLY:N	2.54	0.41
1:A:62:LEU:N	1:A:63:PRO:CD	2.83	0.41
1:B:33:SER:OG	1:C:112:ARG:NH2	2.53	0.41
1:A:221:HIS:CD2	1:A:223:THR:OG1	2.74	0.41
1:C:237:ARG:O	1:C:297:GLU:N	2.54	0.41
1:A:8:ARG:N	1:A:8:ARG:NE	2.69	0.41
1:B:28:LYS:NZ	5:B:2005:HOH:O	2.54	0.40
1:B:22:ASP:N	1:B:22:ASP:OD1	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	289/299 (97%)	266 (92%)	21 (7%)	2 (1%)	30 62
1	B	289/299 (97%)	268 (93%)	18 (6%)	3 (1%)	22 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	289/299 (97%)	269 (93%)	19 (7%)	1 (0%)	50	82
All	All	867/897 (97%)	803 (93%)	58 (7%)	6 (1%)	30	62

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	230	ILE
1	A	95	ALA
1	A	230	ILE
1	B	92	LYS
1	B	95	ALA
1	C	230	ILE

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	231/237 (98%)	221 (96%)	10 (4%)	40	72
1	B	231/237 (98%)	219 (95%)	12 (5%)	32	63
1	C	231/237 (98%)	209 (90%)	22 (10%)	12	28
All	All	693/711 (98%)	649 (94%)	44 (6%)	24	53

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	20	THR
1	A	50	TRP
1	A	76	THR
1	A	77	TYR
1	A	126	LEU
1	A	144	SER
1	A	156	PHE
1	A	198	ASP
1	A	243	VAL

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Mol	Chain	Res	Type
1	B	8	ARG
1	B	20	THR
1	B	50	TRP
1	B	77	TYR
1	B	80	THR
1	B	151	GLN
1	B	156	PHE
1	B	160	GLU
1	B	198	ASP
1	B	205	VAL
1	B	259	GLU
1	B	290	GLU
1	C	8	ARG
1	C	37	ASP
1	C	50	TRP
1	C	53	GLU
1	C	57	ARG
1	C	61	ASP
1	C	76	THR
1	C	77	TYR
1	C	89	VAL
1	C	114	GLU
1	C	116	SER
1	C	146	LYS
1	C	151	GLN
1	C	156	PHE
1	C	192	ARG
1	C	198	ASP
1	C	200	GLU
1	C	205	VAL
1	C	227	LYS
1	C	243	VAL
1	C	270	ARG
1	C	297	GLU

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 chains 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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	MET	A	1301	-	8,8,8	0.72	0	9,9,9	1.88	2 (22%)
3	3D1	A	500	-	20,20,20	1.29	2 (10%)	29,29,29	2.03	4 (13%)
2	MET	B	1299	-	8,8,8	0.68	0	9,9,9	1.59	3 (33%)
3	3D1	B	500	-	20,20,20	1.08	1 (5%)	29,29,29	2.78	10 (34%)
3	3D1	C	500	-	20,20,20	1.18	2 (10%)	29,29,29	2.34	8 (27%)

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	MET	A	1301	-	-	0/8/8/8	0/0/0/0
3	3D1	A	500	-	-	0/4/18/18	0/1/3/3
2	MET	B	1299	-	-	0/8/8/8	0/0/0/0
3	3D1	B	500	-	-	0/4/18/18	0/1/3/3
3	3D1	C	500	-	-	0/4/18/18	0/1/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	3D1	C4-N9	-3.70	1.32	1.37
3	C	500	3D1	C4-N9	-3.44	1.32	1.37
3	B	500	3D1	C4-N9	-2.73	1.33	1.37
3	A	500	3D1	O4'-C1'	2.23	1.47	1.42
3	C	500	3D1	C8-N9	-2.15	1.33	1.36

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	500	3D1	N3-C2-N1	-9.60	120.68	128.71
3	C	500	3D1	N3-C2-N1	-8.94	121.24	128.71
3	A	500	3D1	N3-C2-N1	-8.60	121.52	128.71
3	B	500	3D1	O4'-C1'-N9	5.34	117.71	107.68
3	B	500	3D1	N3-C4-N9	4.36	133.30	125.43
3	C	500	3D1	N3-C4-N9	4.26	133.13	125.43
3	B	500	3D1	C2'-C1'-N9	-4.03	103.62	114.08
3	A	500	3D1	N3-C4-N9	3.66	132.03	125.43
2	A	1301	MET	C-CA-N	3.53	115.20	109.36
2	A	1301	MET	OXT-C-O	-3.28	116.65	124.07
3	B	500	3D1	O4'-C4'-C3'	-3.18	97.61	105.66
2	B	1299	MET	C-CA-N	3.14	114.56	109.36
3	B	500	3D1	O4'-C4'-C5'	-3.13	102.45	109.15
3	C	500	3D1	C2'-C3'-C4'	-3.04	95.93	102.73
3	C	500	3D1	C4'-O4'-C1'	-2.91	102.08	109.44
3	C	500	3D1	C5-C4-N3	-2.89	119.41	125.70
3	C	500	3D1	C2-N3-C4	2.73	121.77	114.01
3	B	500	3D1	C2'-C3'-C4'	-2.64	96.81	102.73
3	B	500	3D1	C5-C4-N3	-2.62	120.00	125.70
3	C	500	3D1	C4-C5-N7	-2.60	107.29	109.52
3	A	500	3D1	C5-C4-N3	-2.42	120.43	125.70
2	B	1299	MET	OXT-C-CA	2.35	122.16	116.88
3	A	500	3D1	O4'-C4'-C3'	-2.32	99.78	105.66
3	B	500	3D1	C2-N3-C4	2.25	120.41	114.01
3	B	500	3D1	C4'-O4'-C1'	-2.24	103.77	109.44
3	C	500	3D1	O5'-C5'-C4'	-2.19	103.84	111.36
2	B	1299	MET	OXT-C-O	-2.13	119.26	124.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	291/299 (97%)	0.50	15 (5%) 26 29	2, 8, 22, 31	0
1	B	291/299 (97%)	0.45	16 (5%) 24 26	2, 8, 22, 31	0
1	C	291/299 (97%)	0.72	36 (12%) 5 5	2, 8, 23, 31	0
All	All	873/897 (97%)	0.56	67 (7%) 13 14	2, 8, 23, 31	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	201	ALA	8.9
1	C	99	ALA	6.3
1	C	200	GLU	6.2
1	C	195	VAL	6.2
1	C	197	GLN	6.0
1	C	229	GLY	5.6
1	C	225	LEU	5.5
1	C	202	LEU	5.4
1	C	97	GLY	4.2
1	B	100	ARG	4.1
1	C	204	GLY	4.0
1	A	100	ARG	3.8
1	C	232	TYR	3.8
1	C	194	ALA	3.8
1	C	226	GLU	3.7
1	B	201	ALA	3.6
1	C	98	GLY	3.6
1	C	100	ARG	3.6
1	B	103	TRP	3.5
1	C	227	LYS	3.5
1	C	203	VAL	3.4
1	C	199	GLY	3.3
1	C	222	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	230	ILE	3.2
1	C	101	GLY	3.2
1	B	99	ALA	3.1
1	C	242	GLY	3.1
1	C	196	GLU	2.9
1	A	108	ALA	2.9
1	C	191	ASN	2.9
1	A	150	GLU	2.9
1	A	107	GLY	2.8
1	B	245	PRO	2.8
1	B	101	GLY	2.8
1	B	95	ALA	2.7
1	B	243	VAL	2.7
1	C	146	LYS	2.7
1	A	44	CYS	2.6
1	A	109	GLY	2.6
1	B	291	GLY	2.6
1	A	137	LEU	2.6
1	C	233	GLY	2.6
1	A	191	ASN	2.5
1	B	193	PRO	2.5
1	C	95	ALA	2.5
1	C	44	CYS	2.4
1	C	231	GLY	2.4
1	B	191	ASN	2.4
1	B	198	ASP	2.4
1	C	102	GLN	2.4
1	A	99	ALA	2.3
1	A	42	ASP	2.3
1	B	203	VAL	2.2
1	A	136	TYR	2.2
1	C	15	SER	2.2
1	C	255	ALA	2.1
1	C	291	GLY	2.1
1	B	194	ALA	2.1
1	A	13	PHE	2.1
1	A	93	GLN	2.1
1	C	96	LYS	2.1
1	B	185	HIS	2.1
1	A	152	PRO	2.0
1	A	97	GLY	2.0
1	B	96	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	290	GLU	2.0
1	C	219	ASN	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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	CL	A	1302	1/1	0.51	5.71	58,58,58,58	0
3	3D1	C	500	18/18	0.21	1.12	2,2,4,6	0
2	MET	A	1301	9/9	0.22	0.89	8,9,11,12	0
2	MET	B	1299	9/9	0.23	0.45	18,18,19,19	0
3	3D1	B	500	18/18	0.17	-0.08	2,2,4,5	0
3	3D1	A	500	18/18	0.16	-0.97	2,3,6,7	0

6.5 Other polymers ⓘ

There are no such residues in this entry.