



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 16, 2018 – 01:30 PM EST

PDB ID : 1RQR
Title : Crystal structure and mechanism of a bacterial fluorinating enzyme, product complex
Authors : Dong, C.; Huang, F.; Deng, H.; Schaffrath, C.; Spencer, J.B.; O'Hagan, D.; Naismith, J.H.
Deposited on : 2003-12-07
Resolution : 2.67 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

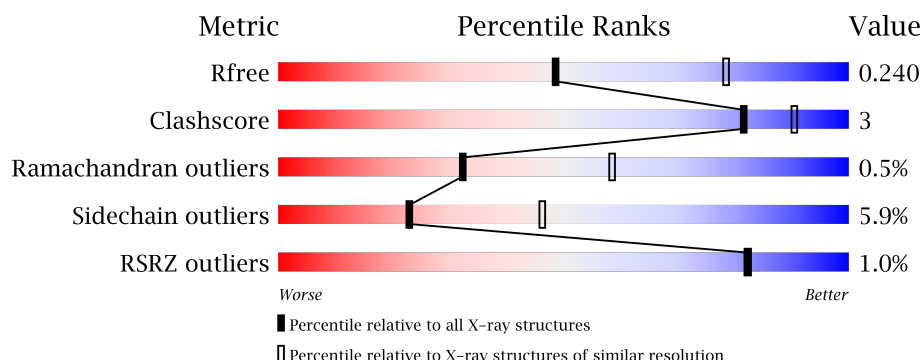
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	3050 (2.70-2.66)
Clashscore	112137	3418 (2.70-2.66)
Ramachandran outliers	110173	3367 (2.70-2.66)
Sidechain outliers	110143	3367 (2.70-2.66)
RSRZ outliers	101464	3069 (2.70-2.66)

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	299	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 84%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 1% 84% 12% 13% </div> </div>
1	B	299	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 82%, grey 14%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 1% 82% 14% 14% </div> </div>
1	C	299	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 83%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 1% 83% 13% 13% </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	5FD	A	500	X	-	-	-
2	5FD	B	500	X	-	-	X
2	5FD	C	500	X	-	-	-
3	MET	B	600	-	-	-	X
3	MET	C	600	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6903 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.

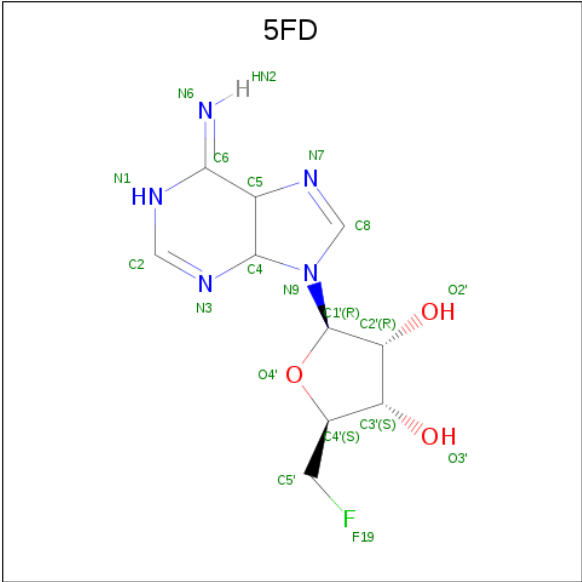
- Molecule 1 is a protein called 5'-fluoro-5'-deoxyadenosine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	Se	0	0	0
			2220	1410	378	424	3	5			
1	B	291	Total	C	N	O	S	Se	0	0	0
			2220	1410	378	424	3	5			
1	C	291	Total	C	N	O	S	Se	0	0	0
			2220	1410	378	424	3	5			

There are 18 discrepancies between the modelled and reference sequences:

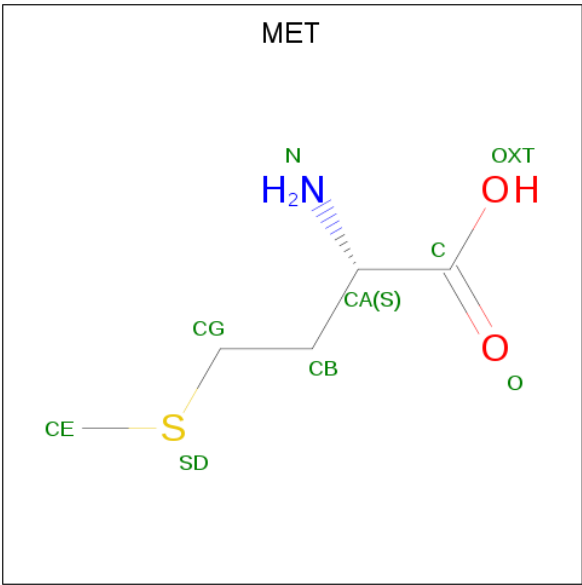
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
A	14	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
A	31	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
A	47	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
A	161	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
A	292	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	14	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	31	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	47	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	161	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
B	292	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	14	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	31	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	47	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	161	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9
C	292	MSE	MET	MODIFIED RESIDUE	UNP Q70GK9

- Molecule 2 is 5'-FLUORO-5'-DEOXYADENOSINE (three-letter code: 5FD) (formula: $C_{10}H_{14}FN_5O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			19	10	1	5	3		
2	B	1	Total	C	F	N	O	0	0
			19	10	1	5	3		
2	C	1	Total	C	F	N	O	0	0
			19	10	1	5	3		

- Molecule 3 is METHIONINE (three-letter code: MET) (formula: C₅H₁₁NO₂S).



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

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

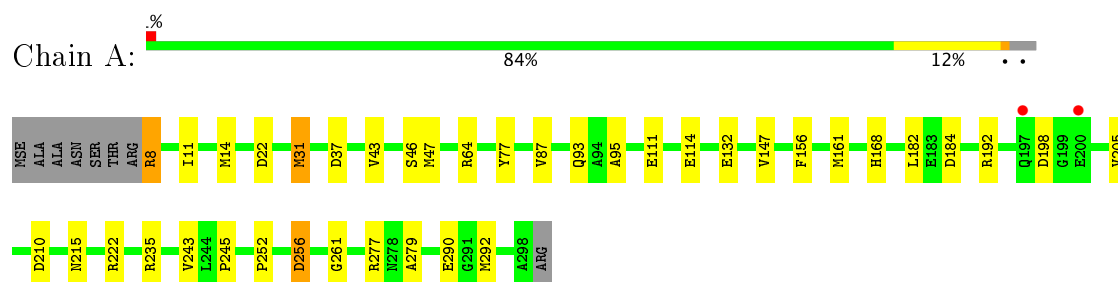
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		
4	B	48	Total	O	0	0
			48	48		
4	C	54	Total	O	0	0
			54	54		

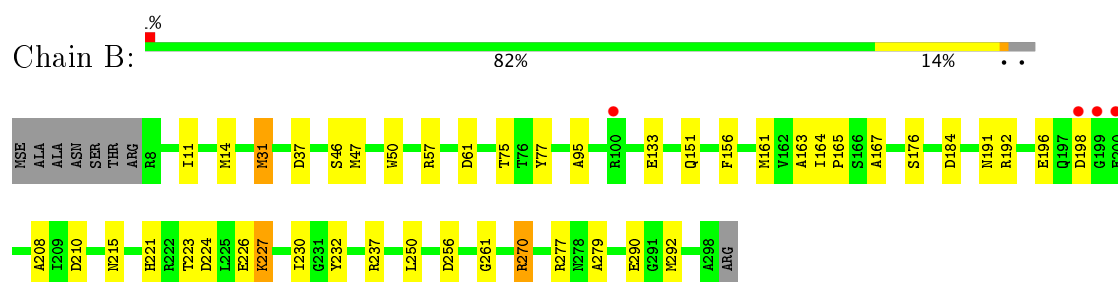
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

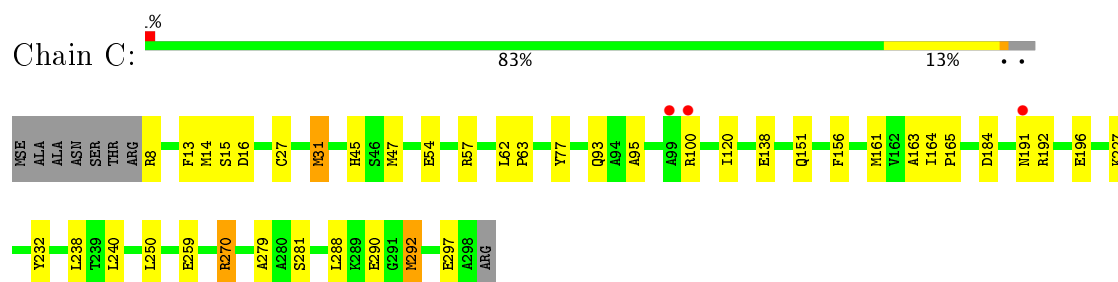
- Molecule 1: 5'-fluoro-5'-deoxyadenosine synthase



- Molecule 1: 5'-fluoro-5'-deoxyadenosine synthase



- Molecule 1: 5'-fluoro-5'-deoxyadenosine synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.18Å 129.92Å 183.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.29 – 2.67 53.46 – 2.67	Depositor EDS
% Data completeness (in resolution range)	98.8 (91.29-2.67) 98.8 (53.46-2.67)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.25 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.173 , 0.232 0.180 , 0.240	Depositor DCC
R_{free} test set	1322 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.033 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6903	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: 5FD

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	0.69	5/2271 (0.2%)	0.77	5/3091 (0.2%)
1	B	0.69	5/2271 (0.2%)	0.80	5/3091 (0.2%)
1	C	0.71	5/2271 (0.2%)	0.80	2/3091 (0.1%)
All	All	0.70	15/6813 (0.2%)	0.79	12/9273 (0.1%)

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	B	0	2
1	C	0	1
All	All	0	3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	47	MSE	C-O	10.63	1.43	1.23
1	C	47	MSE	C-O	10.64	1.43	1.23
1	A	161	MSE	C-O	10.26	1.42	1.23
1	C	31	MSE	C-O	9.91	1.42	1.23
1	B	31	MSE	C-O	9.91	1.42	1.23
1	A	47	MSE	C-O	9.89	1.42	1.23
1	C	161	MSE	C-O	9.84	1.42	1.23
1	A	31	MSE	C-O	9.69	1.41	1.23
1	B	292	MSE	C-O	9.38	1.41	1.23
1	B	161	MSE	C-O	9.37	1.41	1.23
1	B	14	MSE	C-O	9.02	1.40	1.23
1	A	292	MSE	C-O	8.77	1.40	1.23
1	A	14	MSE	C-O	8.74	1.40	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	292	MSE	C-O	8.64	1.39	1.23
1	C	14	MSE	C-O	8.48	1.39	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	ASP	CB-CG-OD2	6.53	124.18	118.30
1	C	16	ASP	CB-CG-OD2	6.44	124.10	118.30
1	B	224	ASP	CB-CG-OD2	6.37	124.04	118.30
1	C	184	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	184	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	256	ASP	CB-CG-OD2	5.45	123.20	118.30
1	B	37	ASP	CB-CG-OD2	5.33	123.10	118.30
1	B	256	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	37	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	22	ASP	CB-CG-OD2	5.28	123.05	118.30
1	B	184	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	198	ASP	CB-CG-OD2	5.15	122.93	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	227	LYS	Peptide
1	B	75	THR	Peptide
1	C	227	LYS	Peptide

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	2220	0	2163	12	0
1	B	2220	0	2163	12	0
1	C	2220	0	2163	13	0
2	A	19	0	11	1	0
2	B	19	0	11	1	0
2	C	19	0	11	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	9	0	8	1	0
3	B	9	0	8	2	0
3	C	9	0	8	2	0
4	A	57	0	0	1	0
4	B	48	0	0	0	0
4	C	54	0	0	1	0
All	All	6903	0	6546	40	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 3.

All (40) 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:C:288:LEU:HD22	1:C:292:MSE:HE1	1.67	0.76
1:B:261:GLY:O	1:B:277:ARG:HD2	1.89	0.72
1:A:261:GLY:O	1:A:277:ARG:HD2	2.04	0.57
2:A:500:5FD:HN1	1:B:279:ALA:H	1.53	0.57
3:C:600:MET:HA	3:C:600:MET:CE	2.35	0.56
1:A:64:ARG:HG2	4:A:653:HOH:O	2.06	0.56
1:A:252:PRO:HD2	1:A:256:ASP:OD2	2.07	0.54
1:A:11:ILE:HG21	1:A:31:MSE:HE2	1.88	0.54
1:A:279:ALA:H	2:C:500:5FD:HN1	1.54	0.54
1:A:87:VAL:HG23	1:A:182:LEU:HD12	1.90	0.54
1:C:232:TYR:O	1:C:250:LEU:O	2.26	0.54
1:A:147:VAL:HA	1:A:168:HIS:CD2	2.43	0.53
1:B:232:TYR:O	1:B:250:LEU:O	2.28	0.52
1:C:120:ILE:HD13	1:C:165:PRO:HB2	1.92	0.51
1:C:164:ILE:HB	1:C:165:PRO:HD3	1.93	0.51
3:B:600:MET:HA	3:B:600:MET:CE	2.42	0.50
3:B:600:MET:O	1:C:270:ARG:NH1	2.45	0.49
1:C:13:PHE:CE2	1:C:31:MSE:HE1	2.48	0.48
1:B:164:ILE:HB	1:B:165:PRO:HD3	1.96	0.48
1:B:226:GLU:O	1:B:227:LYS:HB2	2.15	0.47
1:A:93:GLN:HE21	1:A:114:GLU:HG2	1.80	0.47
1:B:11:ILE:HD11	1:B:167:ALA:HA	1.97	0.47
3:A:600:MET:O	1:B:270:ARG:NH1	2.47	0.47
1:A:8:ARG:N	1:A:8:ARG:CZ	2.79	0.46
1:A:210:ASP:HB3	1:A:215:ASN:HB2	1.98	0.46
1:C:240:LEU:HB3	1:C:292:MSE:HE3	1.99	0.45
1:B:210:ASP:HB3	1:B:215:ASN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:SER:HB2	4:C:606:HOH:O	2.17	0.45
1:C:62:LEU:N	1:C:63:PRO:CD	2.79	0.44
1:C:27:CYS:C	1:C:31:MSE:HE3	2.39	0.43
2:B:500:5FD:HN1	1:C:279:ALA:H	1.66	0.42
1:C:54:GLU:HG3	1:C:57:ARG:NH2	2.35	0.42
1:A:243:VAL:O	1:A:245:PRO:HD3	2.20	0.42
1:B:31:MSE:HE3	1:B:163:ALA:HB1	2.01	0.42
1:C:31:MSE:HE2	1:C:163:ALA:HB1	2.02	0.41
2:C:500:5FD:H5'2	3:C:600:MET:SD	2.60	0.41
1:B:57:ARG:CZ	1:B:208:ALA:HB2	2.51	0.41
1:C:15:SER:O	1:C:45:HIS:HA	2.20	0.41
1:B:221:HIS:HD2	1:B:223:THR:HG23	1.86	0.40
1:B:221:HIS:CD2	1:B:223:THR:H	2.40	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%)	278 (96%)	9 (3%)	2 (1%)	25	50
1	B	289/299 (97%)	277 (96%)	11 (4%)	1 (0%)	44	71
1	C	289/299 (97%)	275 (95%)	13 (4%)	1 (0%)	44	71
All	All	867/897 (97%)	830 (96%)	33 (4%)	4 (0%)	32	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	ALA
1	C	95	ALA
1	B	95	ALA
1	A	43	VAL

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	231/231 (100%)	221 (96%)	10 (4%)	33	61
1	B	231/231 (100%)	216 (94%)	15 (6%)	20	41
1	C	231/231 (100%)	215 (93%)	16 (7%)	18	38
All	All	693/693 (100%)	652 (94%)	41 (6%)	23	46

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	77	TYR
1	A	111	GLU
1	A	132	GLU
1	A	156	PHE
1	A	192	ARG
1	A	205	VAL
1	A	222	ARG
1	A	235	ARG
1	A	290	GLU
1	B	46	SER
1	B	50	TRP
1	B	77	TYR
1	B	133	GLU
1	B	151	GLN
1	B	156	PHE
1	B	176	SER
1	B	191	ASN
1	B	192	ARG
1	B	196	GLU
1	B	198	ASP
1	B	230	ILE
1	B	237	ARG
1	B	270	ARG
1	B	290	GLU
1	C	8	ARG

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Mol	Chain	Res	Type
1	C	77	TYR
1	C	93	GLN
1	C	100	ARG
1	C	138	GLU
1	C	151	GLN
1	C	156	PHE
1	C	191	ASN
1	C	192	ARG
1	C	196	GLU
1	C	238	LEU
1	C	259	GLU
1	C	270	ARG
1	C	281	SER
1	C	290	GLU
1	C	297	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	A	102	GLN
1	A	221	HIS
1	B	102	GLN
1	B	221	HIS
1	C	215	ASN
1	C	221	HIS

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

6 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	5FD	A	500	-	17,21,21	4.16	7 (41%)	17,31,31	1.05	2 (11%)
3	MET	A	600	-	3,8,8	0.34	0	3,9,9	0.71	0
2	5FD	B	500	-	17,21,21	3.90	6 (35%)	17,31,31	1.30	2 (11%)
3	MET	B	600	-	3,8,8	0.17	0	3,9,9	0.63	0
2	5FD	C	500	-	17,21,21	4.10	6 (35%)	17,31,31	1.03	1 (5%)
3	MET	C	600	-	3,8,8	0.17	0	3,9,9	0.32	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	5FD	A	500	-	2/2/8/11	0/4/45/45	0/2/3/3
3	MET	A	600	-	-	0/4/8/8	0/0/0/0
2	5FD	B	500	-	2/2/8/11	0/4/45/45	0/2/3/3
3	MET	B	600	-	-	0/4/8/8	0/0/0/0
2	5FD	C	500	-	2/2/8/11	0/4/45/45	0/2/3/3
3	MET	C	600	-	-	0/4/8/8	0/0/0/0

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	5FD	C5-C6	-10.25	1.37	1.50
2	C	500	5FD	C5-C6	-9.83	1.38	1.50
2	C	500	5FD	C5-N7	-9.17	1.33	1.47
2	A	500	5FD	C5-N7	-9.16	1.33	1.47
2	B	500	5FD	C5-N7	-9.10	1.33	1.47
2	B	500	5FD	C5-C6	-8.66	1.39	1.50
2	C	500	5FD	C4-N3	-8.60	1.34	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	5FD	C4-N3	-8.10	1.35	1.45
2	B	500	5FD	C4-N3	-7.83	1.35	1.45
2	A	500	5FD	C4-N9	-3.77	1.31	1.45
2	C	500	5FD	C4-N9	-3.63	1.32	1.45
2	B	500	5FD	C4-N9	-3.40	1.33	1.45
2	A	500	5FD	C8-N7	2.17	1.33	1.28
2	C	500	5FD	C8-N7	2.23	1.33	1.28
2	C	500	5FD	C6-N6	2.33	1.33	1.27
2	A	500	5FD	C2-N1	2.47	1.40	1.35
2	A	500	5FD	C6-N6	2.55	1.33	1.27
2	B	500	5FD	C6-N6	2.69	1.34	1.27
2	B	500	5FD	C2-N1	2.93	1.41	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	5FD	C4'-O4'-C1'	-2.53	103.83	109.47
2	B	500	5FD	F19-C5'-C4'	-2.30	106.74	109.57
2	A	500	5FD	C4'-O4'-C1'	-2.19	104.59	109.47
2	C	500	5FD	C4'-O4'-C1'	-2.09	104.80	109.47
2	A	500	5FD	C4-C5-N7	2.10	109.66	105.90

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	500	5FD	C4
2	B	500	5FD	C5
2	A	500	5FD	C4
2	A	500	5FD	C5
2	C	500	5FD	C4
2	C	500	5FD	C5

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	5FD	1	0
3	A	600	MET	1	0
2	B	500	5FD	1	0
3	B	600	MET	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	500	5FD	2	0
3	C	600	MET	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	286/299 (95%)	-0.33	2 (0%) 87 88	13, 21, 40, 48	0
1	B	286/299 (95%)	-0.36	4 (1%) 75 75	14, 21, 40, 53	0
1	C	286/299 (95%)	-0.41	3 (1%) 82 82	12, 22, 45, 50	0
All	All	858/897 (95%)	-0.36	9 (1%) 82 82	12, 21, 42, 53	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	198	ASP	3.9
1	B	200	GLU	3.4
1	B	199	GLY	2.5
1	A	200	GLU	2.3
1	C	191	ASN	2.3
1	C	99	ALA	2.2
1	C	100	ARG	2.2
1	A	197	GLN	2.1
1	B	100	ARG	2.1

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
3	MET	B	600	9/9	0.91	0.24	6.46	50,51,51,53	0
3	MET	C	600	9/9	0.98	0.26	3.52	35,36,39,39	0
2	5FD	B	500	19/19	0.97	0.17	2.61	20,23,25,26	0
2	5FD	C	500	19/19	0.98	0.18	1.54	21,23,24,24	0
3	MET	A	600	9/9	0.98	0.14	1.39	31,31,33,34	0
2	5FD	A	500	19/19	0.98	0.12	-0.20	16,20,23,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.