



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 06:09 pm BST

PDB ID : 1HYO
Title : CRYSTAL STRUCTURE OF FUMARYLACETOACETATE HYDROLASE
COMPLEXED WITH 4-(HYDROXYMETHYLPHOSPHINOYL)-3-OXO-B
UTANOIC ACID
Authors : Bateman, R.L.; Bhanumoorthy, P.; Witte, J.F.; McClard, R.W.; Grompe, M.;
Timm, D.E.
Deposited on : 2001-01-21
Resolution : 1.30 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

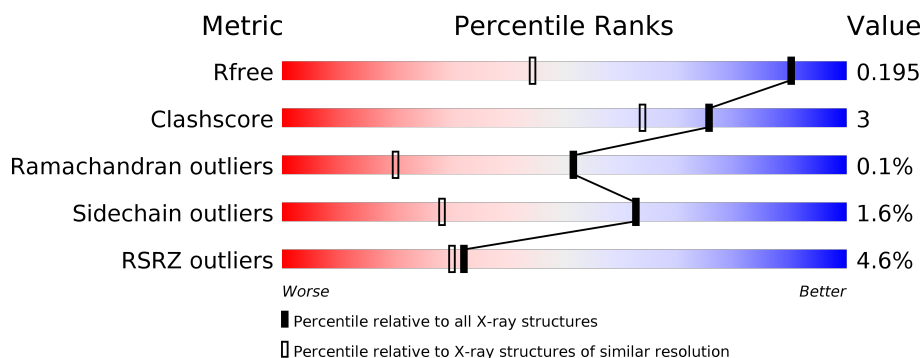
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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}	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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 respectively. 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	421	
1	B	421	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7330 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 FUMARYLACETOACETATE HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3221	2048	562	590	21			
1	B	419	Total	C	N	O	S	0	0	0
			3240	2058	565	595	22			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	CLONING ARTIFACT	UNP P35505
A	0	SER	-	CLONING ARTIFACT	UNP P35505
B	499	GLY	-	CLONING ARTIFACT	UNP P35505
B	500	SER	-	CLONING ARTIFACT	UNP P35505

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

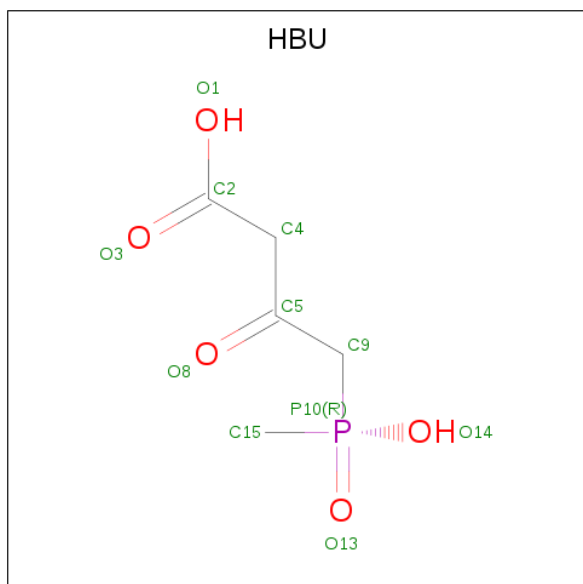
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 5 is 4-[HYDROXY-[METHYL-PHOSPHINOYL]]-3-OXO-BUTANOIC ACID (three-letter code: HBU) (formula: C₅H₉O₅P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	P	0	0
			11	5	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	P	0	0
			11	5	5	1		

- Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Ni	0	0
			1	1		

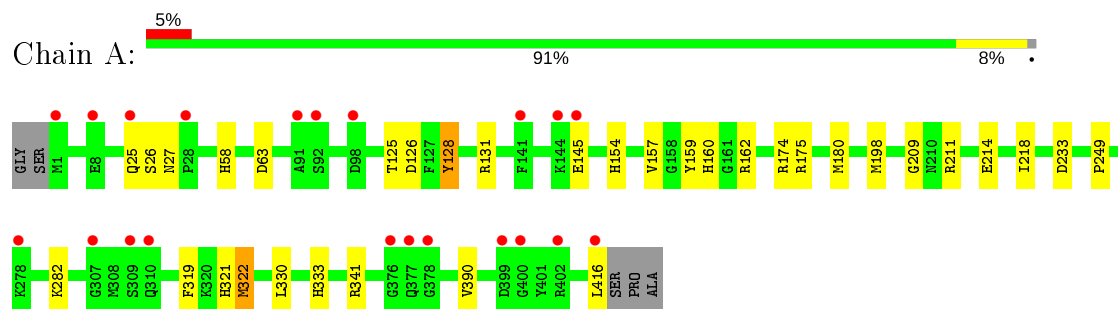
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	392	Total	O	2	0
			392	392		
7	B	442	Total	O	2	0
			442	442		

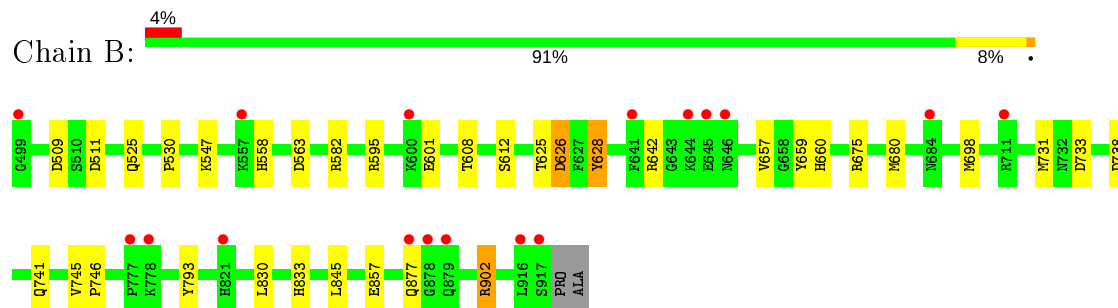
3 Residue-property plots [i](#)

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: FUMARYLACETOACETATE HYDROLASE



• Molecule 1: FUMARYLACETOACETATE HYDROLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.10Å 109.46Å 67.46Å 90.00° 102.37° 90.00°	Depositor
Resolution (Å)	27.00 – 1.30 27.71 – 1.30	Depositor EDS
% Data completeness (in resolution range)	96.6 (27.00-1.30) 97.5 (27.71-1.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 1.30Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.181 , 0.199 0.177 , 0.195	Depositor DCC
R_{free} test set	4361 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	12.1	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7330	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: HBU, NI, MG, CA, ACT

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	0.43	0/3310	0.91	9/4496 (0.2%)
1	B	0.43	0/3329	0.92	9/4520 (0.2%)
All	All	0.43	0/6639	0.92	18/9016 (0.2%)

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	A	0	1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	ARG	NE-CZ-NH2	-7.78	116.41	120.30
1	A	174	ARG	NE-CZ-NH2	-7.54	116.53	120.30
1	A	233	ASP	CB-CG-OD1	7.46	125.01	118.30
1	B	733	ASP	CB-CG-OD1	6.98	124.58	118.30
1	A	341	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	B	675	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	B	626	ASP	CB-CG-OD1	6.27	123.94	118.30
1	B	582	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	B	595	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	B	738	ASP	CB-CG-OD1	5.87	123.58	118.30
1	A	322	MET	CG-SD-CE	-5.72	91.05	100.20
1	A	128	TYR	CA-CB-CG	5.63	124.10	113.40
1	B	675	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	626	ASP	CB-CG-OD2	-5.49	113.36	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ARG	NE-CZ-NH2	-5.31	117.65	120.30
1	A	180	MET	CA-CB-CG	5.29	122.29	113.30
1	B	628	TYR	CA-CB-CG	5.22	123.31	113.40
1	A	175	ARG	NE-CZ-NH1	5.17	122.89	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	209	GLY	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	3221	0	3160	18	0
1	B	3240	0	3177	22	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	11	0	7	0	0
5	B	11	0	7	0	0
6	B	1	0	0	0	0
7	A	392	0	0	8	0
7	B	442	0	0	12	0
All	All	7330	0	6357	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:B:612:SER:HB2	7:B:1363:HOH:O	1.70	0.90
1:B:628:TYR:HB3	1:B:657:VAL:HG23	1.57	0.87
1:A:128:TYR:HB3	1:A:157:VAL:HG23	1.59	0.84
1:B:698:MET:SD	7:B:1426:HOH:O	2.44	0.75
1:A:125:THR:OG1	1:A:333:HIS:HE1	1.73	0.71
1:B:625:THR:OG1	1:B:833:HIS:HE1	1.77	0.68
1:B:741:GLN:HG3	7:B:1430:HOH:O	1.93	0.68
1:B:731:MET:HE3	1:B:845:LEU:HD21	1.77	0.66
1:A:154:HIS:HD2	7:A:1166:HOH:O	1.79	0.63
1:A:58:HIS:HD2	7:A:1304:HOH:O	1.84	0.60
1:B:628:TYR:HB3	1:B:657:VAL:CG2	2.32	0.59
1:B:657:VAL:HG22	7:B:1045:HOH:O	2.03	0.58
1:A:154:HIS:HE1	7:A:1318:HOH:O	1.88	0.56
1:A:319:PHE:O	1:A:322:MET:HG2	2.05	0.56
1:B:857:GLU:HG2	7:B:1344:HOH:O	2.05	0.56
1:B:509:ASP:HA	1:B:902:ARG:HD3	1.88	0.55
1:A:157:VAL:HG22	7:A:1125:HOH:O	2.04	0.55
1:A:145:GLU:HG3	7:A:1200:HOH:O	2.07	0.54
1:B:525:GLN:NE2	7:B:1443:HOH:O	2.44	0.51
1:B:530:PRO:HG3	7:B:1434:HOH:O	2.11	0.51
1:B:558:HIS:HD2	7:B:1322:HOH:O	1.94	0.49
1:A:25:GLN:HG3	1:A:26:SER:N	2.27	0.49
1:A:126:ASP:HB3	1:A:159:TYR:CE2	2.48	0.48
1:A:333:HIS:HD2	1:A:333:HIS:O	1.97	0.47
1:A:160:HIS:HE1	7:B:1101:HOH:O	1.97	0.46
1:B:833:HIS:HD2	1:B:833:HIS:O	1.98	0.46
1:B:511:ASP:OD1	7:B:1166:HOH:O	2.20	0.46
1:B:642:ARG:HH11	1:B:642:ARG:HG3	1.80	0.45
1:A:321:HIS:HE1	7:A:1321:HOH:O	2.00	0.45
1:B:608:THR:HG22	7:B:1363:HOH:O	2.17	0.44
7:A:1123:HOH:O	1:B:660:HIS:HE1	1.99	0.44
1:A:128:TYR:HB3	1:A:157:VAL:CG2	2.38	0.44
1:B:626:ASP:HB3	1:B:659:TYR:CE2	2.53	0.43
1:B:608:THR:CG2	7:B:1363:HOH:O	2.67	0.43
1:A:25:GLN:HG2	7:A:1181:HOH:O	2.19	0.42
1:B:745:VAL:HA	1:B:746:PRO:HA	1.83	0.42
1:A:282:LYS:HB2	1:A:282:LYS:HE3	1.92	0.41
1:B:547:LYS:HE3	1:B:563:ASP:OD2	2.20	0.41
1:A:198:MET:HE3	1:A:390:VAL:HG11	2.04	0.40
1:A:211:ARG:HE	1:A:214:GLU:CD	2.25	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	414/421 (98%)	400 (97%)	14 (3%)	0	100	100
1	B	417/421 (99%)	403 (97%)	13 (3%)	1 (0%)	47	19
All	All	831/842 (99%)	803 (97%)	27 (3%)	1 (0%)	51	20

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	877	GLN

5.3.2 Protein sidechains [i](#)

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	350/354 (99%)	344 (98%)	6 (2%)	60	26
1	B	353/354 (100%)	348 (99%)	5 (1%)	67	34
All	All	703/708 (99%)	692 (98%)	11 (2%)	62	28

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	63	ASP
1	A	218	ILE
1	A	249	PRO
1	A	330	LEU

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Mol	Chain	Res	Type
1	A	416	LEU
1	B	601	GLU
1	B	680	MET
1	B	793	TYR
1	B	830	LEU
1	B	902	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	58	HIS
1	A	86	GLN
1	A	154	HIS
1	A	160	HIS
1	A	241	GLN
1	A	321	HIS
1	A	333	HIS
1	B	525	GLN
1	B	539	GLN
1	B	558	HIS
1	B	660	HIS
1	B	789	HIS
1	B	833	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

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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
5	HBU	B	1011	3	5,10,10	1.46	1 (20%)	2,14,14	1.45	0
4	ACT	B	1010	-	1,3,3	11.15	1 (100%)	0,3,3	0.00	-
4	ACT	A	1009	-	1,3,3	10.64	1 (100%)	0,3,3	0.00	-
5	HBU	A	1012	3	5,10,10	1.50	1 (20%)	2,14,14	2.78	1 (50%)

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
5	HBU	B	1011	3	-	3/5/9/9	-
5	HBU	A	1012	3	-	2/5/9/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1010	ACT	CH3-C	11.15	1.62	1.48
4	A	1009	ACT	CH3-C	10.64	1.62	1.48
5	A	1012	HBU	P10-C9	2.42	1.86	1.81
5	B	1011	HBU	P10-C9	2.36	1.85	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1012	HBU	O8-C5-C4	3.90	126.60	120.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1011	HBU	C2-C4-C5-C9
5	A	1012	HBU	C2-C4-C5-C9
5	B	1011	HBU	C2-C4-C5-O8
5	A	1012	HBU	C2-C4-C5-O8
5	B	1011	HBU	C5-C9-P10-O13

There are no ring outliers.

No monomer is involved in short contacts.

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	416/421 (98%)	0.34	21 (5%) 28 26	8, 14, 31, 38	0
1	B	419/421 (99%)	0.23	17 (4%) 37 34	8, 14, 28, 44	0
All	All	835/842 (99%)	0.28	38 (4%) 32 30	8, 14, 30, 44	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	307	GLY	9.0
1	B	917	SER	7.7
1	B	878	GLY	6.0
1	B	641	PHE	5.0
1	A	416	LEU	4.9
1	A	399	ASP	4.7
1	B	645	GLU	4.6
1	A	141	PHE	4.5
1	A	145	GLU	4.1
1	B	600	LYS	3.9
1	B	916	LEU	3.8
1	B	877	GLN	3.7
1	A	91	ALA	3.6
1	A	1	MET	3.6
1	A	377	GLN	3.5
1	A	25	GLN	3.4
1	A	28	PRO	3.3
1	A	310	GLN	3.2
1	A	92	SER	3.1
1	B	644	LYS	2.8
1	A	400	GLY	2.8
1	B	499	GLY	2.8
1	A	8	GLU	2.8
1	A	278	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	646	ASN	2.7
1	A	402	ARG	2.7
1	A	376	GLY	2.6
1	A	378	GLY	2.6
1	B	557	LYS	2.6
1	B	778	LYS	2.6
1	B	821	HIS	2.5
1	A	98	ASP	2.5
1	B	711	ARG	2.4
1	B	879	GLN	2.2
1	B	684	ASN	2.2
1	A	144	LYS	2.2
1	A	309	SER	2.1
1	B	777	PRO	2.1

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. 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	B-factors(\AA^2)	Q<0.9
4	ACT	A	1009	4/4	0.86	0.13	19,22,22,25	0
4	ACT	B	1010	4/4	0.94	0.13	16,19,19,22	0
6	NI	B	1008	1/1	0.97	0.06	14,14,14,14	0
5	HBU	A	1012	11/11	0.97	0.08	8,9,10,11	0
5	HBU	B	1011	11/11	0.98	0.09	8,9,10,11	0
3	CA	B	1007	1/1	1.00	0.05	8,8,8,8	0
2	MG	B	1005	1/1	1.00	0.05	8,8,8,8	0
2	MG	A	1004	1/1	1.00	0.07	8,8,8,8	0
3	CA	A	1006	1/1	1.00	0.06	7,7,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.