



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 03:45 AM GMT

PDB ID : 2HGW  
Title : Crystal structure of Cys318Ala mutant of human mitochondrial branched chain aminotransferase  
Authors : Yennawar, N.H.; Hutson, S.M.  
Deposited on : 2006-06-27  
Resolution : 1.98 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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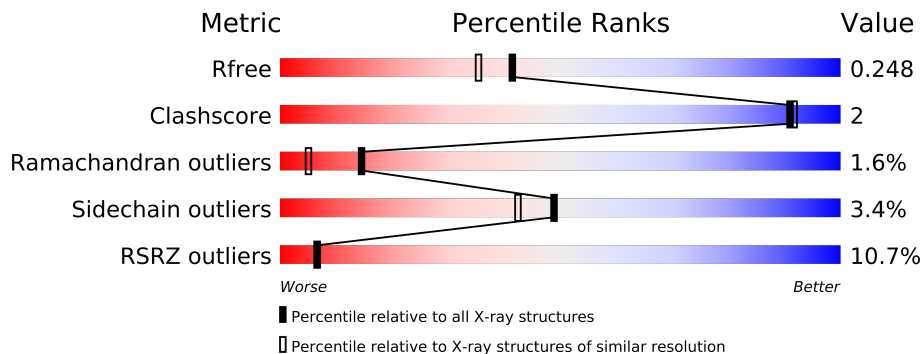
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.98 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	6577 (2.00-1.96)
Clashscore	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)
RSRZ outliers	66119	6578 (2.00-1.96)

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  $\geq 3$ , 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	365	
1	B	365	

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

Mol	Type	Chain	Res	Geometry	Electron density
5	ACY	A	1001	-	X
5	ACY	A	1002	-	X
5	ACY	A	1003	-	X
5	ACY	A	1009	-	X
5	ACY	B	1005	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5983 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.

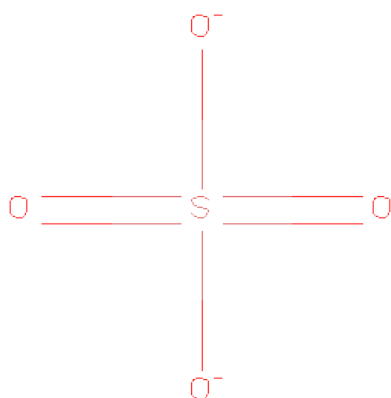
- Molecule 1 is a protein called Branched-chain-amino-acidaminotransferase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2855	1839	499	500	17			
1	B	359	Total	C	N	O	S	0	0	0
			2860	1842	500	501	17			

There are 4 discrepancies between the modelled and reference sequences:

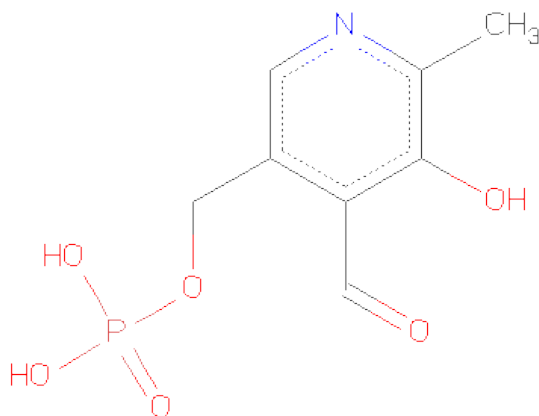
Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ARG	THR	CONFLICT	UNP O15382
A	318	ALA	CYS	ENGINEERED	UNP O15382
B	659	ARG	THR	CONFLICT	UNP O15382
B	818	ALA	CYS	ENGINEERED	UNP O15382

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



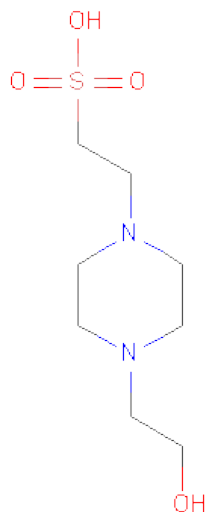
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



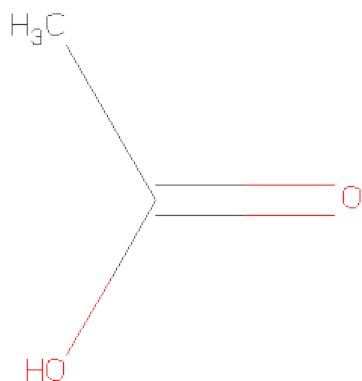
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINEETHANESULFONIC ACID (three-letter code: EPE) (formula:  $C_8H_{18}N_2O_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



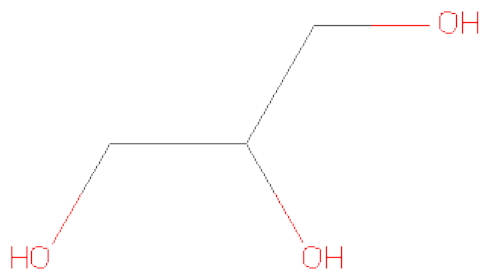
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	89	Total	O	0	0
			89	89		

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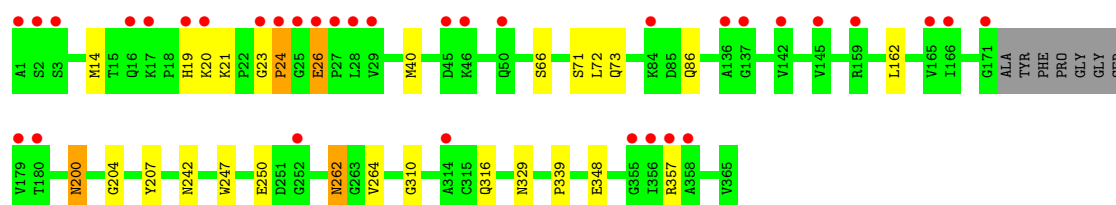
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	83	Total	O	0	0
			83	83		

### 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.

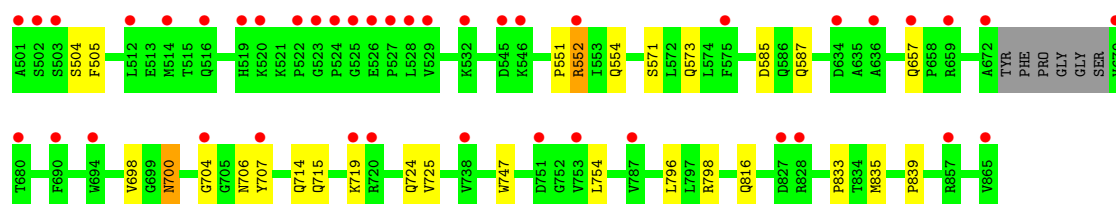
- Molecule 1: Branched-chain-amino-acidaminotransferase, mitochondrial

Chain A: 



- Molecule 1: Branched-chain-amino-acidaminotransferase, mitochondrial

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.67Å 105.58Å 106.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.98 29.48 – 1.98	Depositor EDS
% Data completeness (in resolution range)	95.6 (25.00-1.98) 97.7 (29.48-1.98)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 1.98Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.227 , 0.254 0.238 , 0.248	Depositor DCC
$R_{free}$ test set	2898 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.2	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 41.2	EDS
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57440 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: GOL, ACY, EPE, SO4, PLP

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	0/2928	0.76	1/3974 (0.0%)
1	B	0.63	0/2933	0.74	0/3981
All	All	0.64	0/5861	0.75	1/7955 (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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	23	GLY	C-N-CD	-5.90	107.62	120.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	207	TYR	Sidechain
1	B	707	TYR	Sidechain

## 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	2855	0	2884	13	0
1	B	2860	0	2887	13	0
2	B	5	0	0	0	0
3	A	15	0	6	0	0
3	B	15	0	6	0	0
4	A	15	0	17	1	0
5	A	32	0	24	0	0
5	B	8	0	6	0	0
6	A	6	0	8	0	0
7	A	89	0	0	0	0
7	B	83	0	0	0	0
All	All	5983	0	5838	23	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 2.

All (23) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:700:ASN:HD22	1:B:700:ASN:H	1.13	0.96
1:A:200:ASN:HD22	1:A:200:ASN:H	1.17	0.90
1:B:724:GLN:HE21	1:B:725:VAL:H	1.30	0.80
1:B:700:ASN:HD22	1:B:700:ASN:N	1.93	0.65
1:A:200:ASN:ND2	1:A:200:ASN:H	1.95	0.63
1:B:700:ASN:ND2	1:B:700:ASN:H	1.93	0.62
1:A:71:SER:H	1:B:573:GLN:HE22	1.47	0.61
1:A:73:GLN:HE22	1:B:571:SER:H	1.50	0.59
1:A:66:SER:HB2	1:A:72:LEU:HD12	1.86	0.57
1:B:552:ARG:HD2	1:B:554:GLN:HE21	1.73	0.53
1:A:73:GLN:HE21	1:A:204:GLY:HA3	1.79	0.47
1:B:573:GLN:HE21	1:B:704:GLY:HA3	1.77	0.47
1:B:505:PHE:HB2	1:B:551:PRO:HD3	1.98	0.46
1:B:724:GLN:HE21	1:B:725:VAL:N	2.08	0.45
1:A:71:SER:H	1:B:573:GLN:NE2	2.15	0.44
1:A:200:ASN:N	1:A:200:ASN:HD22	1.97	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:329:ASN:HB2	4:A:1011:EPE:O3S	2.19	0.42
1:B:698:VAL:HG23	1:B:706:ASN:HD21	1.84	0.42
1:A:262:ASN:HD21	1:A:264:VAL:HG22	1.84	0.42
1:B:715:GLN:O	1:B:719:LYS:HG2	2.20	0.41
1:A:242:ASN:O	1:A:310:GLY:HA2	2.19	0.41
1:A:262:ASN:H	1:A:262:ASN:HD22	1.69	0.41
1:A:40:MET:HG2	1:A:162:LEU:HD11	2.02	0.41

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	354/365 (97%)	337 (95%)	11 (3%)	6 (2%)	14	4
1	B	355/365 (97%)	343 (97%)	7 (2%)	5 (1%)	16	6
All	All	709/730 (97%)	680 (96%)	18 (2%)	11 (2%)	14	5

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	24	PRO
1	A	26	GLU
1	B	835	MET
1	A	316	GLN
1	A	21	LYS
1	B	816	GLN
1	B	504	SER
1	B	833	PRO
1	B	839	PRO
1	A	339	PRO

### 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	310/315 (98%)	299 (96%)	11 (4%)	48	41
1	B	310/315 (98%)	300 (97%)	10 (3%)	51	45
All	All	620/630 (98%)	599 (97%)	21 (3%)	49	42

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	MET
1	A	19	HIS
1	A	24	PRO
1	A	26	GLU
1	A	86	GLN
1	A	200	ASN
1	A	247	TRP
1	A	250	GLU
1	A	262	ASN
1	A	348	GLU
1	A	357	ARG
1	B	552	ARG
1	B	585	ASP
1	B	587	GLN
1	B	657	GLN
1	B	700	ASN
1	B	714	GLN
1	B	747	TRP
1	B	754	LEU
1	B	796	LEU
1	B	798	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	73	GLN
1	A	86	GLN

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Mol	Chain	Res	Type
1	A	200	ASN
1	A	206	ASN
1	A	215	GLN
1	A	262	ASN
1	A	272	GLN
1	A	295	GLN
1	B	554	GLN
1	B	573	GLN
1	B	657	GLN
1	B	700	ASN
1	B	706	ASN
1	B	714	GLN
1	B	724	GLN
1	B	742	ASN

### 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 ⓘ

15 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
5	ACY	A	1001	-	3,3,3	1.02	0	3,3,3	1.46	0
5	ACY	A	1002	-	3,3,3	1.03	0	3,3,3	1.52	1 (33%)
5	ACY	A	1003	-	3,3,3	1.00	0	3,3,3	1.42	0
5	ACY	A	1004	-	3,3,3	0.93	0	3,3,3	1.43	0
5	ACY	A	1006	-	3,3,3	1.00	0	3,3,3	1.51	1 (33%)
5	ACY	A	1007	-	3,3,3	1.05	0	3,3,3	1.49	1 (33%)
5	ACY	A	1008	-	3,3,3	1.06	0	3,3,3	1.50	1 (33%)
5	ACY	A	1009	-	3,3,3	1.02	0	3,3,3	1.52	1 (33%)
4	EPE	A	1011	-	15,15,15	1.45	5 (33%)	20,20,20	1.36	4 (20%)
6	GOL	A	2001	-	5,5,5	0.92	0	5,5,5	0.30	0
3	PLP	A	400	1	14,15,16	1.30	3 (21%)	20,22,23	1.64	4 (20%)
5	ACY	B	1005	-	3,3,3	1.05	0	3,3,3	1.47	0
5	ACY	B	1010	-	3,3,3	1.04	0	3,3,3	1.43	0
2	SO4	B	1012	-	4,4,4	0.30	0	6,6,6	0.08	0
3	PLP	B	401	1	14,15,16	1.31	2 (14%)	20,22,23	1.62	3 (15%)

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	ACY	A	1001	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1002	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1003	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1004	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1006	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1007	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1008	-	-	0/0/0/0	0/0/0/0
5	ACY	A	1009	-	-	0/0/0/0	0/0/0/0
4	EPE	A	1011	-	-	0/9/19/19	0/1/1/1
6	GOL	A	2001	-	-	0/4/4/4	0/0/0/0
3	PLP	A	400	1	-	0/6/6/8	0/1/1/1
5	ACY	B	1005	-	-	0/0/0/0	0/0/0/0
5	ACY	B	1010	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1012	-	-	0/0/0/0	0/0/0/0
3	PLP	B	401	1	-	0/6/6/8	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1011	EPE	C7-N4	2.91	1.54	1.47
3	A	400	PLP	P-O1P	-2.41	1.43	1.51
3	B	401	PLP	P-O1P	-2.36	1.43	1.51
4	A	1011	EPE	C2-N1	2.30	1.53	1.47
3	A	400	PLP	C4-C5	2.27	1.43	1.39
4	A	1011	EPE	C6-N1	2.24	1.53	1.47
4	A	1011	EPE	C10-S	2.12	1.80	1.77
3	B	401	PLP	P-O3P	-2.04	1.47	1.54
4	A	1011	EPE	C9-N1	2.02	1.52	1.47
3	A	400	PLP	P-O3P	-2.01	1.47	1.54

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	400	PLP	O4P-C5A-C5	3.59	116.56	109.26
3	B	401	PLP	O4P-C5A-C5	3.56	116.50	109.26
3	A	400	PLP	O3P-P-O1P	3.02	120.32	110.44
3	B	401	PLP	O3P-P-O1P	2.99	120.22	110.44
3	B	401	PLP	O2P-P-O4P	-2.56	99.58	106.65
4	A	1011	EPE	C3-C2-N1	-2.43	105.82	110.61
4	A	1011	EPE	C7-N4-C5	-2.33	105.31	111.32
3	A	400	PLP	O2P-P-O4P	-2.31	100.28	106.65
4	A	1011	EPE	C9-N1-C6	-2.25	105.51	111.32
4	A	1011	EPE	C6-C5-N4	2.12	114.79	110.61
5	A	1009	ACY	O-C-CH3	-2.08	113.00	122.06
5	A	1002	ACY	O-C-CH3	-2.06	113.06	122.06
3	A	400	PLP	C5A-C5-C6	-2.06	115.39	119.28
5	A	1006	ACY	O-C-CH3	-2.05	113.11	122.06
5	A	1008	ACY	O-C-CH3	-2.04	113.14	122.06
5	A	1007	ACY	O-C-CH3	-2.02	113.24	122.06

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	358/365 (98%)	0.78	34 (9%) 8 9	21, 30, 50, 69	0
1	B	359/365 (98%)	0.87	42 (11%) 5 5	22, 31, 49, 65	0
All	All	717/730 (98%)	0.83	76 (10%) 6 7	21, 31, 50, 69	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	503	SER	9.4
1	B	501	ALA	8.7
1	A	24	PRO	8.4
1	A	2	SER	7.8
1	A	27	PRO	7.2
1	A	1	ALA	7.0
1	A	23	GLY	7.0
1	B	502	SER	7.0
1	B	527	PRO	6.9
1	A	26	GLU	6.5
1	B	672	ALA	5.9
1	A	20	LYS	5.8
1	B	524	PRO	5.8
1	B	523	GLY	5.7
1	A	358	ALA	5.2
1	B	520	LYS	5.1
1	B	516	GLN	5.1
1	A	19	HIS	4.9
1	A	25	GLY	4.7
1	A	357	ARG	4.6
1	B	636	ALA	4.5
1	B	546	LYS	4.1
1	B	514	MET	4.1
1	B	525	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	526	GLU	4.0
1	A	84	LYS	3.8
1	A	3	SER	3.8
1	B	827	ASP	3.8
1	A	17	LYS	3.5
1	B	528	LEU	3.5
1	A	252	GLY	3.4
1	B	680	THR	3.3
1	B	679	VAL	3.2
1	A	28	LEU	3.2
1	A	159	ARG	3.2
1	B	659	ARG	3.1
1	A	137	GLY	3.1
1	A	45	ASP	3.0
1	A	136	ALA	2.9
1	B	751	ASP	2.9
1	A	314	ALA	2.9
1	B	512	LEU	2.9
1	A	165	VAL	2.9
1	A	29	VAL	2.8
1	B	545	ASP	2.8
1	A	171	GLY	2.8
1	A	46	LYS	2.7
1	B	519	HIS	2.7
1	B	753	VAL	2.7
1	B	828	ARG	2.7
1	B	720	ARG	2.7
1	B	575	PHE	2.6
1	A	16	GLN	2.6
1	A	145	VAL	2.6
1	A	356	ILE	2.5
1	A	142	VAL	2.5
1	B	865	VAL	2.4
1	B	522	PRO	2.4
1	B	719	LYS	2.4
1	B	529	VAL	2.3
1	A	179	VAL	2.3
1	B	704	GLY	2.3
1	B	694	TRP	2.2
1	B	657	GLN	2.2
1	B	738	VAL	2.2
1	B	690	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	707	TYR	2.1
1	A	50	GLN	2.1
1	B	532	LYS	2.1
1	B	857	ARG	2.1
1	B	787	VAL	2.1
1	A	355	GLY	2.1
1	A	180	THR	2.0
1	A	166	ILE	2.0
1	B	634	ASP	2.0
1	B	552	ARG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	ACY	A	1009	4/4	0.26	6.28	45,47,47,47	0
5	ACY	A	1001	4/4	0.24	6.23	48,50,50,51	0
5	ACY	B	1005	4/4	0.38	5.01	46,48,48,49	0
5	ACY	A	1003	4/4	0.33	4.20	46,46,47,47	0
5	ACY	A	1002	4/4	0.18	2.01	41,43,44,44	0
5	ACY	B	1010	4/4	0.19	1.67	46,46,47,47	0
5	ACY	A	1006	4/4	0.16	1.62	49,49,49,49	0
5	ACY	A	1007	4/4	0.19	1.44	42,43,43,43	0
4	EPE	A	1011	15/15	0.26	1.39	40,45,49,49	0
3	PLP	B	401	15/16	0.21	1.34	24,25,26,28	0
5	ACY	A	1008	4/4	0.17	0.96	44,44,44,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	ACY	A	1004	4/4	0.31	0.92	49,49,49,50	0
3	PLP	A	400	15/16	0.15	0.53	27,28,30,33	0
6	GOL	A	2001	6/6	0.17	0.37	44,44,46,47	0
2	SO4	B	1012	5/5	0.12	-1.10	49,49,49,51	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.