Full wwPDB X-ray Structure Validation Report (i)

Feb 28, 2014 – 10:52 AM GMT

PDB ID : 4GEV

Title : E. coli thymidylate synthase Y209W variant in complex with substrate and a cofactor analog

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Deposited on : 2012-08-02

Resolution : 1.30 Å(reported)

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 1.30 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	Percentile Ranks	Value
Rfree		0.146
Clashscore		5
Ramachandran outliers		0.4%
Sidechain outliers		1.1%
RSRZ outliers		3.9%

Worse   Better

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
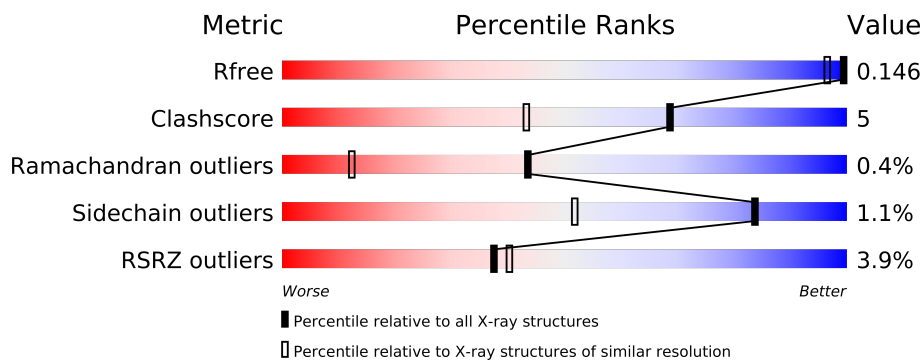
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1025 (1.34-1.26)
Clashscore	79885	1140 (1.34-1.26)
Ramachandran outliers	78287	1093 (1.34-1.26)
Sidechain outliers	78261	1092 (1.34-1.26)
RSRZ outliers	66119	1025 (1.34-1.26)

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	264	
1	B	264	

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 9394 atoms, of which 4280 are hydrogens 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 Thymidylate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	264	Total 4285	C 1388	H 2114	N 376	O 395	S 12	0	3	0
1	B	264	Total 4260	C 1382	H 2100	N 372	O 394	S 12	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	TRP	TYR	ENGINEERED MUTATION	UNP P0A884
B	209	TRP	TYR	ENGINEERED MUTATION	UNP P0A884

- Molecule 2 is 2'-DEOXY-5'-URIDYLIC ACID (three-letter code: UMC) (formula: $C_9H_{15}N_2O_8P$).
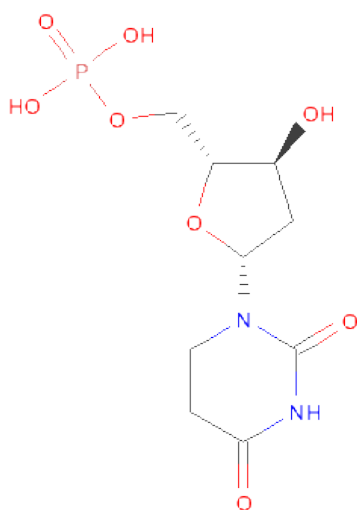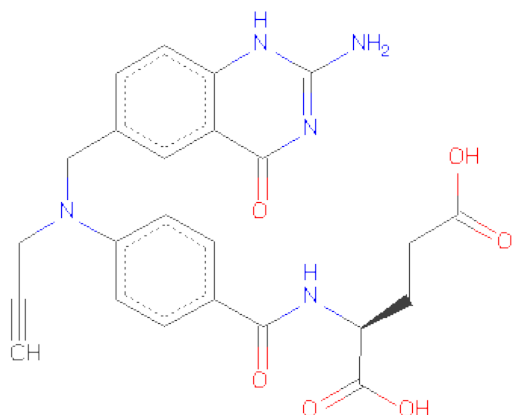

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 32	C 9	H 12	N 2	O 8	P 1	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
2	B	1	32	9	12	2	8	1	0	0

- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLICACID (three-letter code: CB3) (formula: $C_{24}H_{23}N_5O_6$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
3	A	1	56	24	21	5	6	0	0
3	B	1	56	24	21	5	6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	385	385	385	0	0
4	B	288	288	288	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 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.
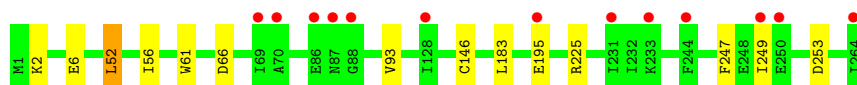
• Molecule 1: Thymidylate synthase

Chain A:
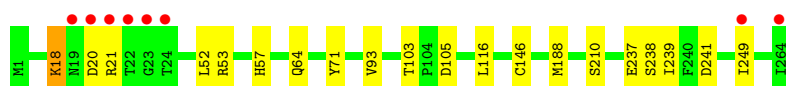
• Molecule 1: Thymidylate synthase

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	125.78Å 125.78Å 66.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.83 – 1.30 45.83 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.83-1.30) 99.8 (45.83-1.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 1.30Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.127 , 0.151 0.121 , 0.146	Depositor DCC
R_{free} test set	7364 reflections (5.01%)	DCC
Wilson B-factor (Å^2)	13.4	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 44.6	EDS
Estimated twinning fraction	0.024 for h,-h-k,-l	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 146991 reflections	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	9394	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CB3, CXM, UMC

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	0.44	0/2232	0.65	0/3031
1	B	0.39	0/2213	0.62	0/3006
All	All	0.42	0/4445	0.63	0/6037

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts (i)

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	2171	2114	0	17	0
1	B	2160	2100	0	11	0
2	A	20	12	0	1	0
2	B	20	12	0	1	0
3	A	35	21	0	6	0
3	B	35	21	0	6	0
4	A	385	0	0	4	3
4	B	288	0	0	2	1
All	All	5114	4280	0	40	3

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 5.

All (40) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:146:CYS:SG	4:B:1188:HOH:O	2.43	0.76
1:A:18:LYS:HB2	4:A:986:HOH:O	1.87	0.74
1:A:116:LEU:HG	1:A:188:MET:HE1	1.71	0.71
1:A:64:GLN:NE2	4:A:1135:HOH:O	2.28	0.66
1:A:57:HIS:HD1	1:A:71:TYR:HH	1.49	0.61
1:A:210:SER:O	4:A:1126:HOH:O	2.16	0.60
1:A:52:LEU:CD2	1:A:249:ILE:HG13	2.31	0.60
1:A:116:LEU:CG	1:A:188:MET:HE1	2.32	0.59
1:A:52:LEU:HD22	1:A:249:ILE:HG13	1.84	0.58
1:A:116:LEU:CD2	1:A:188:MET:HE1	2.35	0.56
1:A:116:LEU:CD2	1:A:188:MET:CE	2.84	0.55
1:A:146:CYS:SG	2:A:701:UMC:C5	2.92	0.54
1:A:116:LEU:HD11	1:A:239:ILE:HB	1.90	0.54
3:B:802:CB3:H13	3:B:802:CB3:C6	2.39	0.52
3:A:702:CB3:C6	3:A:702:CB3:H15	2.41	0.50
1:B:2:LYS:NZ	1:B:6:GLU:OE2	2.45	0.50
1:A:237:GLU:HG2	1:A:241:ASP:OD2	2.13	0.49
1:A:53:ARG:HD2	4:A:974:HOH:O	2.13	0.48
1:B:195:GLU:HG2	4:B:1127:HOH:O	2.13	0.48
1:B:52:LEU:HD11	1:B:249:ILE:HG13	1.95	0.48
1:B:52:LEU:HD13	1:B:56:ILE:HD11	1.96	0.48
1:A:116:LEU:HD23	1:A:188:MET:CE	2.45	0.46
1:A:103:THR:OG1	1:A:105:ASP:OD1	2.32	0.46
1:B:146:CYS:SG	2:B:801:UMC:C5	2.97	0.46
3:B:802:CB3:H16	3:B:802:CB3:HN	1.77	0.44
3:B:802:CB3:C5	3:B:802:CB3:C14	2.94	0.44
3:B:802:CB3:H15	3:B:802:CB3:HP12	1.83	0.43
3:A:702:CB3:HP11	3:A:702:CB3:H13	1.91	0.43
3:B:802:CB3:C5	3:B:802:CB3:C13	2.97	0.43
3:A:702:CB3:C5	3:A:702:CB3:C15	2.97	0.43
1:B:183:LEU:HD11	1:B:247:PHE:CE2	2.53	0.43
1:B:52:LEU:CD1	1:B:249:ILE:HG13	2.48	0.43
3:A:702:CB3:C5	3:A:702:CB3:C14	2.96	0.42
3:A:702:CB3:HN	3:A:702:CB3:H12	1.77	0.42
1:B:225:ARG:HD2	1:B:253:ASP:O	2.19	0.42
3:A:702:CB3:C6	3:A:702:CB3:C15	2.98	0.42
1:B:52:LEU:HD23	1:B:52:LEU:HA	1.95	0.41
1:B:61:TRP:CD1	1:B:66:ASP:HB3	2.57	0.40
3:B:802:CB3:C6	3:B:802:CB3:C13	2.96	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:116:LEU:CD2	1:A:188:MET:HE3	2.51	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:1089:HOH:O	4:A:1141:HOH:O[6_544]	2.14	0.06
4:A:950:HOH:O	4:A:1141:HOH:O[6_544]	2.18	0.02
4:A:1089:HOH:O	4:B:1096:HOH:O[6_544]	2.19	0.01

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	265/264 (100%)	261 (98%)	3 (1%)	1 (0%)	43	12
1	B	263/264 (100%)	257 (98%)	5 (2%)	1 (0%)	43	12
All	All	528/528 (100%)	518 (98%)	8 (2%)	2 (0%)	43	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	93	VAL
1	B	93	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	235/232 (101%)	231 (98%)	4 (2%)	73	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	233/232 (100%)	232 (100%)	1 (0%)	95	80
All	All	468/464 (101%)	463 (99%)	5 (1%)	84	52

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LYS
1	A	20	ASP
1	A	21	ARG
1	A	238	SER
1	B	52	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	76	ASN
1	A	117	ASN
1	B	19	ASN
1	B	75	ASN
1	B	76	ASN
1	B	121	ASN
1	B	217	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CXM	A	1	1	10,10,11	5.53	3 (30%)	8,11,13	2.13	2 (25%)
1	CXM	B	1	1	10,10,11	5.81	2 (20%)	8,11,13	2.00	2 (25%)

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
1	CXM	A	1	1	-	0/8/10/12	0/0/0/0
1	CXM	B	1	1	-	0/8/10/12	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	CXM	O-C	18.03	1.23	1.11
1	A	1	CXM	O-C	17.15	1.23	1.11
1	B	1	CXM	CA-C	2.37	1.52	1.48
1	A	1	CXM	ON1-CN	2.29	1.26	1.21
1	A	1	CXM	CA-C	2.08	1.52	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1	CXM	ON2-CN-N	3.99	121.30	116.33
1	A	1	CXM	ON1-CN-N	-3.94	117.87	124.90
1	B	1	CXM	ON2-CN-N	3.86	121.14	116.33
1	B	1	CXM	ON1-CN-N	-3.49	118.67	124.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 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	UMC	A	701	1	21,21,21	0.78	0	31,31,31	1.37	3 (9%)
3	CB3	A	702	-	37,37,37	1.20	3 (8%)	49,51,51	1.41	6 (12%)
2	UMC	B	801	1	21,21,21	0.99	2 (9%)	31,31,31	1.47	5 (16%)
3	CB3	B	802	-	37,37,37	1.21	3 (8%)	49,51,51	1.42	7 (14%)

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	UMC	A	701	1	-	0/10/35/35	0/2/2/2
3	CB3	A	702	-	-	0/27/28/28	0/1/3/3
2	UMC	B	801	1	-	0/10/35/35	0/2/2/2
3	CB3	B	802	-	-	0/27/28/28	0/1/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	802	CB3	O-C	4.16	1.31	1.23
3	B	802	CB3	C2-N3	4.06	1.38	1.33
3	A	702	CB3	O-C	3.54	1.30	1.23
3	A	702	CB3	C2-N3	3.32	1.37	1.33
2	B	801	UMC	C4-N3	-2.45	1.33	1.37
3	A	702	CB3	CP1-CP2	2.18	1.50	1.47
3	B	802	CB3	CP1-CP2	2.07	1.50	1.47
2	B	801	UMC	C2-N1	-2.01	1.32	1.35

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	802	CB3	C6-C9-N10	-4.50	107.75	114.44
2	B	801	UMC	C6-N1-C1'	-4.29	114.46	119.81
3	A	702	CB3	C6-C9-N10	-4.28	108.06	114.44
2	A	701	UMC	C6-N1-C1'	-3.92	114.92	119.81
3	B	802	CB3	C4A-C4-N3	-3.86	119.20	123.72
3	B	802	CB3	C4-N3-C2	3.75	120.97	116.91
3	A	702	CB3	C4-N3-C2	3.53	120.72	116.91
2	A	701	UMC	C5-C4-N3	3.45	120.00	116.76
3	A	702	CB3	NA2-C2-N1	3.35	121.55	117.86
3	B	802	CB3	C9-N10-C14	3.29	126.50	120.71
3	A	702	CB3	C9-N10-C14	3.17	126.28	120.71
3	A	702	CB3	C8-C8A-C4A	-3.14	119.80	121.72
3	A	702	CB3	C4A-C4-N3	-3.09	120.10	123.72
2	B	801	UMC	C5-C4-N3	2.68	119.28	116.76
2	B	801	UMC	N3-C2-N1	2.51	119.17	116.71
2	B	801	UMC	C1'-N1-C2	2.45	121.39	117.93
2	B	801	UMC	O2-C2-N1	-2.31	120.19	123.25
3	B	802	CB3	C8-C8A-C4A	-2.20	120.38	121.72
3	B	802	CB3	C15-C14-N10	-2.18	118.27	121.37
2	A	701	UMC	O4'-C1'-N1	2.08	111.18	108.42
3	B	802	CB3	OE2-CD-CG	2.01	121.33	114.22

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	264/264 (100%)	-0.15	8 (3%)	48	52	8, 13, 25, 36	0
1	B	264/264 (100%)	0.20	13 (4%)	28	29	8, 19, 32, 38	0
All	All	528/528 (100%)	0.03	21 (3%)	37	38	8, 15, 29, 38	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	THR	6.8
1	A	23	GLY	5.1
1	B	69	ILE	5.0
1	B	249	ILE	4.8
1	B	264	ILE	4.7
1	B	86	GLU	4.7
1	A	264	ILE	4.6
1	A	24	THR	4.0
1	B	231	ILE	3.6
1	B	88	GLY	3.2
1	A	21	ARG	3.2
1	A	19	ASN	3.2
1	B	233	LYS	3.0
1	A	20	ASP	2.7
1	B	70	ALA	2.7
1	A	249	ILE	2.6
1	B	244	PHE	2.3
1	B	87	ASN	2.3
1	B	250	GLU	2.2
1	B	128	ILE	2.2
1	B	195	GLU	2.0

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

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
1	CXM	B	1	11/12	0.05	-0.85	16,18,23,23	0
1	CXM	A	1	11/12	0.04	-1.20	10,12,18,18	0

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
3	CB3	A	702	35/35	0.10	0.17	13,16,25,27	0
3	CB3	B	802	35/35	0.08	0.01	15,21,33,36	0
2	UMC	A	701	20/20	0.06	-0.38	10,12,15,15	0
2	UMC	B	801	20/20	0.04	-1.28	13,14,18,18	0

6.5 Other polymers ⓘ

There are no such residues in this entry.