



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:27 AM GMT

PDB ID : 3IJD
Title : Uncharacterized protein Cthe_2304 from Clostridium thermocellum binds two copies of 5-methyl-5,6,7,8-tetrahydrofolic acid
Authors : Bonanno, J.B.; Gilmore, M.; Bain, K.T.; Miller, S.; Ozyurt, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2009-08-04
Resolution : 2.00 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

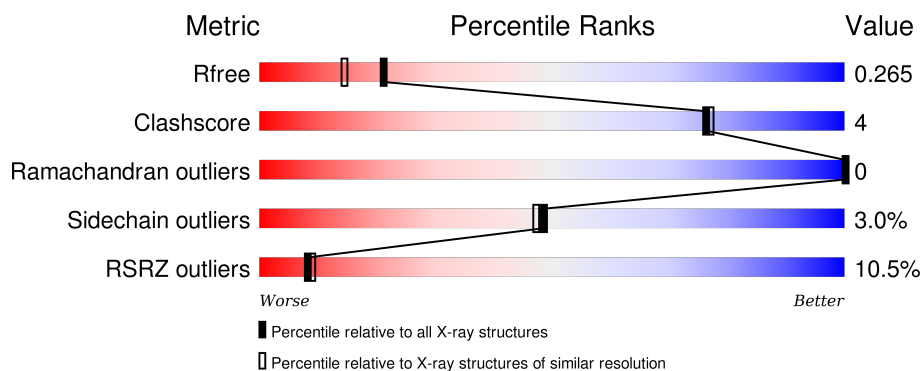
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	315	<div> <div>9%</div> <div> <div></div> <div>82%</div> <div>9%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	315	<div> <div>10%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4725 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.

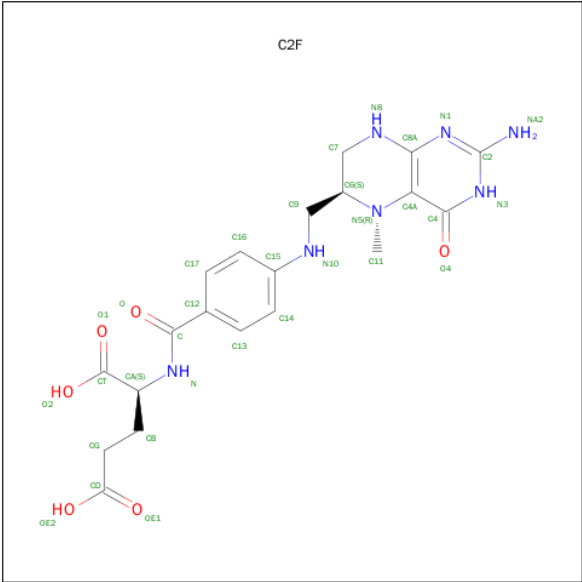
- Molecule 1 is a protein called uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2260	1459	373	416	12			
1	B	285	Total	C	N	O	S	0	0	0
			2223	1436	367	408	12			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP A3DHS7
A	0	SER	-	expression tag	UNP A3DHS7
A	1	LEU	-	expression tag	UNP A3DHS7
A	306	GLU	-	expression tag	UNP A3DHS7
A	307	GLY	-	expression tag	UNP A3DHS7
A	308	HIS	-	expression tag	UNP A3DHS7
A	309	HIS	-	expression tag	UNP A3DHS7
A	310	HIS	-	expression tag	UNP A3DHS7
A	311	HIS	-	expression tag	UNP A3DHS7
A	312	HIS	-	expression tag	UNP A3DHS7
A	313	HIS	-	expression tag	UNP A3DHS7
B	-1	MET	-	expression tag	UNP A3DHS7
B	0	SER	-	expression tag	UNP A3DHS7
B	1	LEU	-	expression tag	UNP A3DHS7
B	306	GLU	-	expression tag	UNP A3DHS7
B	307	GLY	-	expression tag	UNP A3DHS7
B	308	HIS	-	expression tag	UNP A3DHS7
B	309	HIS	-	expression tag	UNP A3DHS7
B	310	HIS	-	expression tag	UNP A3DHS7
B	311	HIS	-	expression tag	UNP A3DHS7
B	312	HIS	-	expression tag	UNP A3DHS7
B	313	HIS	-	expression tag	UNP A3DHS7

- Molecule 2 is 5-METHYL-5,6,7,8-TETRAHYDROFOLIC ACID (three-letter code: C2F) (formula: C₂₀H₂₅N₇O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			33	20	7	6		
2	A	1	Total	C	N	O	0	0
			33	20	7	6		
2	B	1	Total	C	N	O	0	0
			33	20	7	6		
2	B	1	Total	C	N	O	0	0
			33	20	7	6		

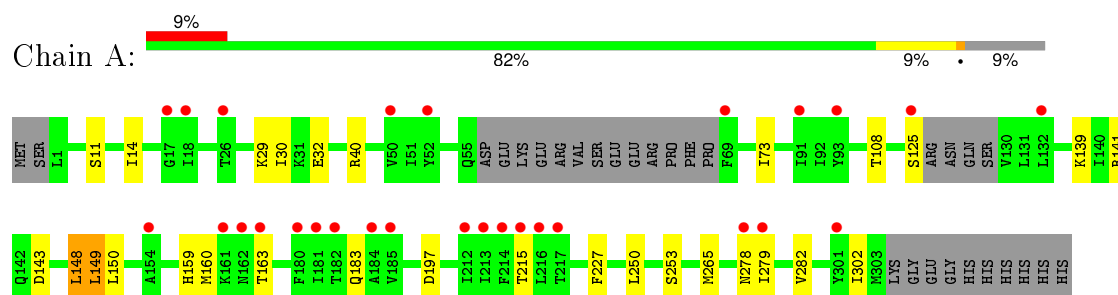
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	56	Total	O	0	0
			56	56		
3	B	54	Total	O	0	0
			54	54		

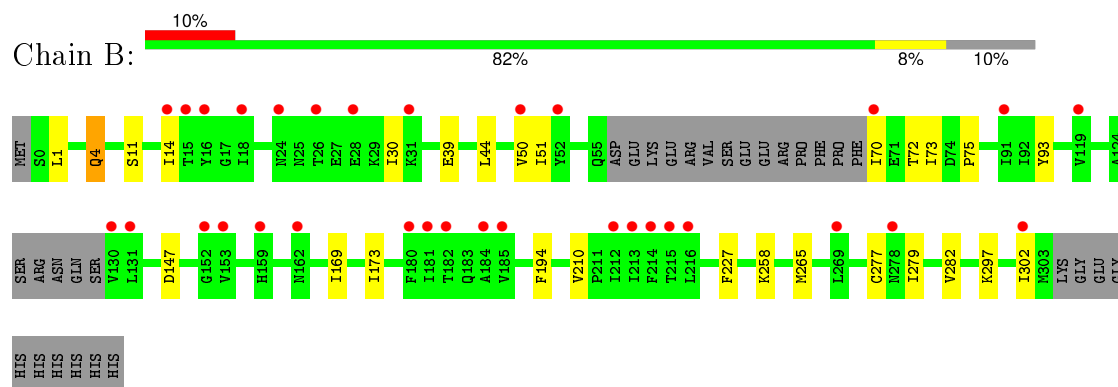
3 Residue-property plots [i](#)

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



- Molecule 1: uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.58Å 52.37Å 60.92Å 94.68° 97.68° 90.57°	Depositor
Resolution (Å)	20.00 – 2.00 29.07 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.0 (20.00-2.00) 93.4 (29.07-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0089	Depositor
R, R_{free}	0.218 , 0.265 0.221 , 0.265	Depositor DCC
R_{free} test set	2095 reflections (5.41%)	DCC
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.872	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 48.5	EDS
Estimated twinning fraction	0.049 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 40855 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4725	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.00% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: C2F

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	0/2300	0.66	0/3107
1	B	0.62	0/2261	0.65	0/3058
All	All	0.63	0/4561	0.65	0/6165

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2260	0	2304	17	0
1	B	2223	0	2260	16	0
2	A	66	0	46	3	0
2	B	66	0	46	2	0
3	A	56	0	0	0	0
3	B	54	0	0	0	0
All	All	4725	0	4656	35	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 4.

All (35) 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:30:ILE:HD13	1:B:73:ILE:HD11	1.67	0.74
1:B:70:ILE:HD11	2:B:315:C2F:H113	1.75	0.68
1:A:40:ARG:NH2	2:A:315:C2F:O1	2.36	0.58
1:B:173:ILE:HD11	1:B:210:VAL:HG22	1.87	0.56
1:A:265:MET:CE	1:A:302:ILE:HG22	2.36	0.56
2:A:314:C2F:H6	2:A:314:C2F:C14	2.38	0.53
1:A:265:MET:HE1	1:A:302:ILE:HG22	1.91	0.53
1:B:30:ILE:CD1	1:B:73:ILE:HD11	2.36	0.51
1:A:279:ILE:HD12	1:A:279:ILE:N	2.26	0.51
1:A:183:GLN:HG2	2:A:314:C2F:H112	1.94	0.50
1:A:215:THR:HA	1:A:278:ASN:O	2.12	0.49
1:B:227:PHE:CD2	1:B:282:VAL:HG22	2.48	0.49
2:B:314:C2F:H6	2:B:314:C2F:C14	2.43	0.49
1:B:14:ILE:HA	1:B:277:CYS:O	2.14	0.48
1:A:265:MET:CE	1:A:302:ILE:CG2	2.92	0.47
1:A:159:HIS:NE2	1:A:197:ASP:OD2	2.40	0.47
1:B:279:ILE:N	1:B:279:ILE:HD12	2.30	0.47
1:A:250:LEU:O	1:A:253:SER:HB2	2.15	0.46
1:A:141:ARG:HD3	1:A:150:LEU:HD22	1.97	0.46
1:B:265:MET:CE	1:B:302:ILE:HG22	2.46	0.46
1:B:265:MET:HE1	1:B:302:ILE:HG22	1.98	0.46
1:A:30:ILE:HD13	1:A:73:ILE:HD11	1.98	0.46
1:B:169:ILE:HD13	1:B:194:PHE:HZ	1.80	0.45
1:B:1:LEU:O	1:B:4:GLN:HG3	2.16	0.45
1:B:44:LEU:HD23	1:B:297:LYS:HE3	1.98	0.45
1:B:51:ILE:HG22	1:B:75:PRO:HB3	1.99	0.44
1:B:50:VAL:HG13	1:B:93:TYR:CE2	2.53	0.44
1:A:148:LEU:HD12	1:A:149:LEU:N	2.32	0.44
1:A:227:PHE:CD2	1:A:282:VAL:HG22	2.53	0.44
1:A:108:THR:HG22	1:A:108:THR:O	2.19	0.43
1:B:227:PHE:HD2	1:B:282:VAL:HG22	1.84	0.43
1:A:14:ILE:O	1:A:14:ILE:HG23	2.18	0.43
1:B:169:ILE:HD13	1:B:194:PHE:CZ	2.55	0.41
1:A:265:MET:HE3	1:A:302:ILE:CG2	2.51	0.41
1:A:163:THR:O	1:A:163:THR:HG22	2.21	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	280/315 (89%)	275 (98%)	5 (2%)	0	100	100
1	B	279/315 (89%)	278 (100%)	1 (0%)	0	100	100
All	All	559/630 (89%)	553 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	250/288 (87%)	241 (96%)	9 (4%)	42	39
1	B	243/288 (84%)	237 (98%)	6 (2%)	55	55
All	All	493/576 (86%)	478 (97%)	15 (3%)	48	47

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	29	LYS
1	A	32	GLU
1	A	125	SER
1	A	139	LYS
1	A	143	ASP
1	A	148	LEU
1	A	149	LEU

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Mol	Chain	Res	Type
1	A	160	MET
1	B	4	GLN
1	B	11	SER
1	B	39	GLU
1	B	72	THR
1	B	147	ASP
1	B	258	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	166	HIS
1	B	4	GLN
1	B	8	ASN
1	B	206	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	C2F	A	314	-	25,35,35	0.73	2 (8%)	27,49,49	2.16	8 (29%)
2	C2F	A	315	-	25,35,35	1.00	1 (4%)	27,49,49	2.01	7 (25%)
2	C2F	B	314	-	25,35,35	0.71	1 (4%)	27,49,49	2.22	8 (29%)
2	C2F	B	315	-	25,35,35	1.02	2 (8%)	27,49,49	1.87	7 (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
2	C2F	A	314	-	-	0/16/35/35	0/3/3/3
2	C2F	A	315	-	-	0/16/35/35	0/3/3/3
2	C2F	B	314	-	-	0/16/35/35	0/3/3/3
2	C2F	B	315	-	-	0/16/35/35	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	314	C2F	C6-N5	-2.06	1.45	1.47
2	A	314	C2F	C4A-C8A	2.06	1.45	1.41
2	B	315	C2F	CB-CA	2.11	1.56	1.53
2	B	314	C2F	C4A-C8A	2.40	1.46	1.41
2	A	315	C2F	C4A-C8A	3.15	1.48	1.41
2	B	315	C2F	C4A-C8A	3.20	1.48	1.41

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	314	C2F	C7-C6-N5	-6.35	101.74	108.79
2	B	314	C2F	C7-C6-N5	-5.95	102.18	108.79
2	A	315	C2F	C7-C6-N5	-4.99	103.25	108.79
2	B	314	C2F	C4A-C4-N3	-4.48	116.56	123.46
2	B	315	C2F	C7-C6-N5	-4.14	104.20	108.79
2	A	315	C2F	C4A-C4-N3	-3.95	117.39	123.46
2	B	315	C2F	C4A-C4-N3	-3.21	118.52	123.46
2	A	314	C2F	C4A-C4-N3	-3.07	118.74	123.46
2	A	314	C2F	C16-C15-N10	-2.22	116.80	121.06
2	B	314	C2F	N3-C2-N1	-2.15	122.00	125.53
2	A	314	C2F	N3-C2-N1	-2.08	122.13	125.53
2	A	315	C2F	C12-C-N	2.07	120.61	116.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	315	C2F	C12-C-N	2.35	121.11	116.93
2	A	315	C2F	C2-N1-C8A	2.40	119.92	114.54
2	B	314	C2F	C9-C6-N5	2.44	116.00	110.90
2	B	314	C2F	C2-N1-C8A	2.45	120.03	114.54
2	A	314	C2F	CG-CB-CA	2.48	118.04	112.99
2	B	314	C2F	C4-C4A-C8A	2.66	116.55	114.43
2	A	315	C2F	C4-C4A-C8A	2.99	116.81	114.43
2	B	315	C2F	C2-N1-C8A	3.01	121.30	114.54
2	A	314	C2F	C2-N1-C8A	3.04	121.36	114.54
2	B	315	C2F	C4-C4A-C8A	3.06	116.87	114.43
2	B	314	C2F	CG-CB-CA	3.08	119.24	112.99
2	B	315	C2F	CG-CB-CA	3.22	119.54	112.99
2	A	314	C2F	C4-C4A-C8A	3.44	117.17	114.43
2	A	315	C2F	CG-CB-CA	3.69	120.49	112.99
2	A	314	C2F	C4-N3-C2	4.06	121.58	115.94
2	B	315	C2F	C4-N3-C2	4.19	121.75	115.94
2	A	315	C2F	C4-N3-C2	5.01	122.89	115.94
2	B	314	C2F	C4-N3-C2	6.01	124.28	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	314	C2F	2	0
2	A	315	C2F	1	0
2	B	314	C2F	1	0
2	B	315	C2F	1	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

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	286/315 (90%)	0.63	28 (9%) 10 10	25, 38, 52, 56	0
1	B	285/315 (90%)	0.67	32 (11%) 7 7	23, 38, 52, 64	0
All	All	571/630 (90%)	0.65	60 (10%) 8 9	23, 38, 52, 64	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	130	VAL	5.9
1	B	131	LEU	5.4
1	A	301	TYR	4.9
1	A	181	ILE	4.7
1	B	50	VAL	4.6
1	A	162	ASN	4.4
1	B	181	ILE	4.2
1	B	162	ASN	3.9
1	A	213	ILE	3.8
1	B	302	ILE	3.7
1	B	212	ILE	3.7
1	A	215	THR	3.5
1	A	163	THR	3.5
1	A	69	PHE	3.4
1	A	91	ILE	3.2
1	B	18	ILE	3.2
1	A	17	GLY	3.2
1	B	26	THR	3.2
1	A	50	VAL	3.2
1	B	216	LEU	3.2
1	A	182	THR	3.1
1	A	125	SER	3.0
1	B	213	ILE	2.8
1	A	279	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	132	LEU	2.8
1	A	161	LYS	2.8
1	B	31	LYS	2.8
1	A	216	LEU	2.7
1	A	52	TYR	2.7
1	A	212	ILE	2.7
1	A	185	VAL	2.7
1	A	214	PHE	2.7
1	B	214	PHE	2.7
1	B	153	VAL	2.6
1	B	152	GLY	2.5
1	B	182	THR	2.5
1	B	278	ASN	2.5
1	B	91	ILE	2.5
1	A	217	THR	2.5
1	A	184	ALA	2.5
1	A	18	ILE	2.5
1	B	184	ALA	2.4
1	B	24	ASN	2.4
1	B	52	TYR	2.4
1	B	215	THR	2.4
1	B	180	PHE	2.3
1	A	26	THR	2.3
1	B	119	VAL	2.3
1	B	70	ILE	2.3
1	A	278	ASN	2.3
1	B	269	LEU	2.3
1	A	93	TYR	2.2
1	B	185	VAL	2.2
1	B	15	THR	2.2
1	B	14	ILE	2.2
1	A	154	ALA	2.1
1	B	16	TYR	2.1
1	B	28	GLU	2.1
1	B	159	HIS	2.1
1	A	180	PHE	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 [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(\AA^2)	Q<0.9
2	C2F	B	315	33/33	0.76	0.20	0.87	60,66,70,71	0
2	C2F	A	315	33/33	0.85	0.14	-0.07	41,46,54,58	0
2	C2F	B	314	33/33	0.87	0.16	-0.08	28,33,49,52	0
2	C2F	A	314	33/33	0.88	0.14	-0.24	25,32,48,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.