



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 11:46 pm BST

PDB ID : 5WRN
Title : Human thymidylate synthase complexed with dCMP
Authors : Chen, D.; Nordlund, P.
Deposited on : 2016-12-02
Resolution : 2.39 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
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

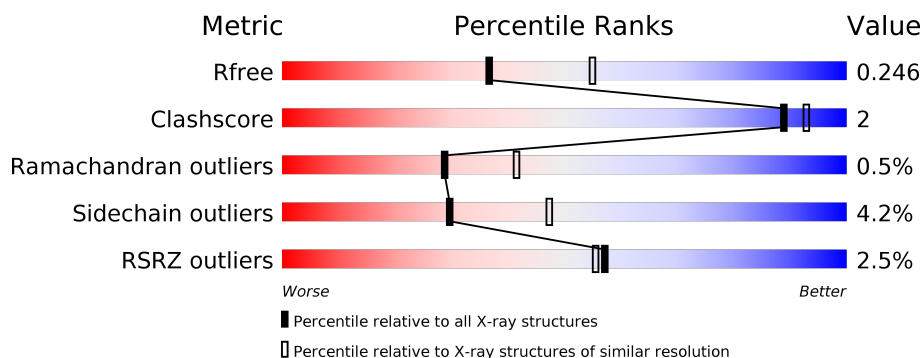
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	289	<div> <div>2%</div> <div>92%</div> <div>5%</div> <div>••</div> </div>
1	B	289	<div> <div>3%</div> <div>87%</div> <div>9%</div> <div>••</div> </div>
1	C	289	<div> <div>2%</div> <div>90%</div> <div>8%</div> <div>•</div> </div>
1	D	289	<div> <div>3%</div> <div>89%</div> <div>8%</div> <div>•••</div> </div>
1	E	289	<div> <div>2%</div> <div>91%</div> <div>6%</div> <div>••</div> </div>
1	F	289	<div> <div>2%</div> <div>86%</div> <div>9%</div> <div>••</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14115 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.

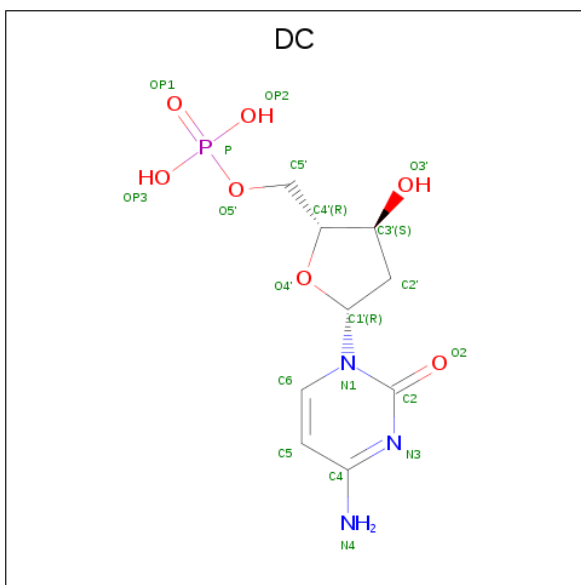
- Molecule 1 is a protein called Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	282	Total	C	N	O	S	0	0	0
			2275	1458	396	409	12			
1	A	284	Total	C	N	O	S	0	0	0
			2288	1463	400	414	11			
1	C	282	Total	C	N	O	S	0	0	0
			2265	1449	396	409	11			
1	D	286	Total	C	N	O	S	0	0	0
			2289	1466	399	412	12			
1	E	286	Total	C	N	O	S	0	0	0
			2301	1471	402	416	12			
1	F	277	Total	C	N	O	S	0	1	0
			2249	1440	394	404	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	25	MET	-	initiating methionine	UNP P04818
A	25	MET	-	initiating methionine	UNP P04818
C	25	MET	-	initiating methionine	UNP P04818
D	25	MET	-	initiating methionine	UNP P04818
E	25	MET	-	initiating methionine	UNP P04818
F	25	MET	-	initiating methionine	UNP P04818

- Molecule 2 is 2'-DEOXYCYTIDINE-5'-MONOPHOSPHATE (three-letter code: DC) (formula: C₉H₁₄N₃O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
2	A	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
2	C	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
2	D	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
2	E	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
2	F	1	Total	C	N	O	P	0	0
			20	9	3	7	1		

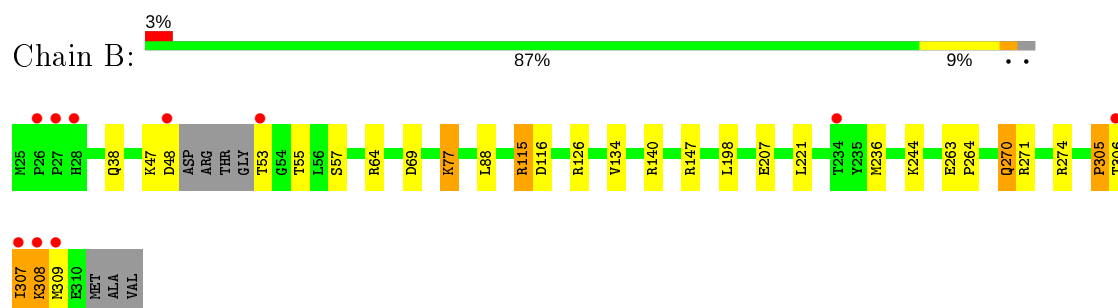
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	50	Total	O	0	0
			50	50		
3	A	47	Total	O	0	0
			47	47		
3	C	45	Total	O	0	0
			45	45		
3	D	54	Total	O	0	0
			54	54		
3	E	64	Total	O	0	0
			64	64		
3	F	68	Total	O	0	0
			68	68		

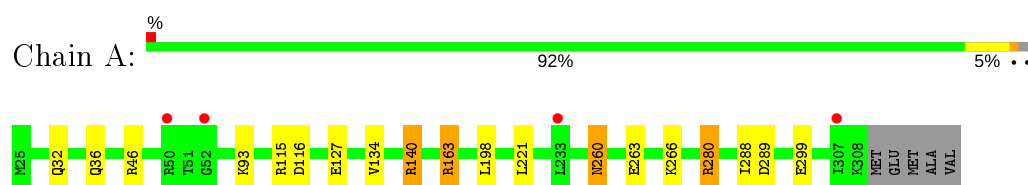
3 Residue-property plots [i](#)

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.

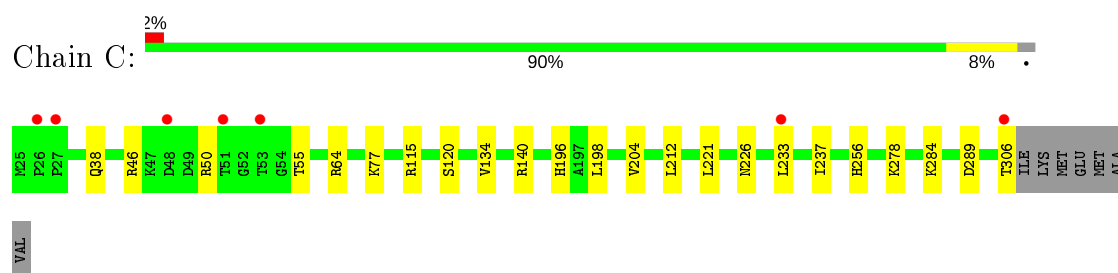
• Molecule 1: Thymidylate synthase



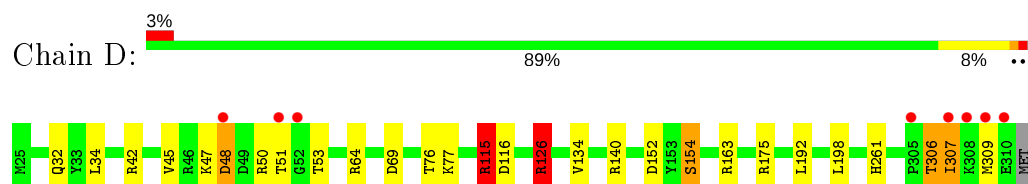
• Molecule 1: Thymidylate synthase



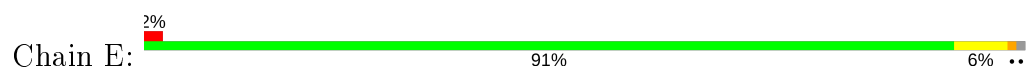
• Molecule 1: Thymidylate synthase

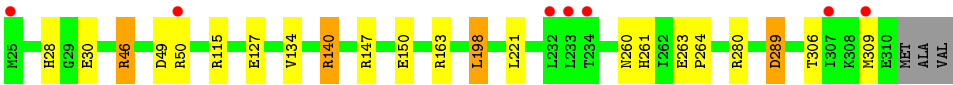


• Molecule 1: Thymidylate synthase

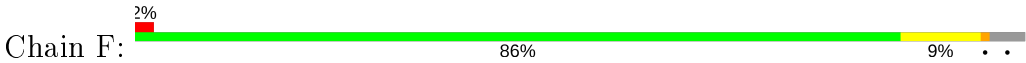


• Molecule 1: Thymidylate synthase





● Molecule 1: Thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	110.10Å 110.10Å 317.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.39 27.05 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.0 (30.00-2.39) 98.1 (27.05-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.63 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.188 , 0.247 0.195 , 0.246	Depositor DCC
R_{free} test set	3757 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14115	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.02 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.3588e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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	0.83	0/2348	0.94	8/3179 (0.3%)
1	B	0.83	0/2334	0.97	8/3157 (0.3%)
1	C	0.76	0/2324	0.88	4/3146 (0.1%)
1	D	0.79	0/2349	0.93	7/3181 (0.2%)
1	E	0.79	0/2361	0.93	5/3196 (0.2%)
1	F	0.76	0/2308	0.90	4/3122 (0.1%)
All	All	0.79	0/14024	0.92	36/18981 (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	B	0	1
1	E	0	2
All	All	0	3

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	140	ARG	NE-CZ-NH2	-10.97	114.82	120.30
1	A	163	ARG	NE-CZ-NH2	9.11	124.86	120.30
1	A	140	ARG	NE-CZ-NH2	-8.26	116.17	120.30
1	E	46	ARG	NE-CZ-NH2	7.99	124.29	120.30
1	B	140	ARG	NE-CZ-NH2	-7.37	116.61	120.30
1	D	115	ARG	NE-CZ-NH1	7.36	123.98	120.30
1	E	140	ARG	NE-CZ-NH2	-7.01	116.80	120.30
1	D	42	ARG	NE-CZ-NH1	6.79	123.69	120.30
1	D	175	ARG	NE-CZ-NH1	-6.75	116.92	120.30
1	D	140	ARG	NE-CZ-NH2	-6.74	116.93	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	115	ARG	NE-CZ-NH1	6.69	123.64	120.30
1	A	115	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	E	115	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	F	140	ARG	NE-CZ-NH1	6.41	123.51	120.30
1	E	198	LEU	CA-CB-CG	6.13	129.40	115.30
1	B	64	ARG	NE-CZ-NH2	-6.11	117.24	120.30
1	B	64	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	D	126	ARG	NE-CZ-NH2	-5.93	117.34	120.30
1	B	48	ASP	CB-CG-OD1	5.76	123.48	118.30
1	A	115	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	C	64	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	198	LEU	CA-CB-CG	5.59	128.16	115.30
1	B	147	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	C	115	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	B	115	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	B	198	LEU	CA-CB-CG	5.48	127.91	115.30
1	A	163	ARG	CD-NE-CZ	5.46	131.24	123.60
1	A	140	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	C	115	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	F	68	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	163	ARG	CG-CD-NE	5.38	123.09	111.80
1	D	115	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	B	274	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	F	115	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	C	64	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	D	175	ARG	NE-CZ-NH2	5.08	122.84	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	53	THR	Peptide
1	E	309	MET	Peptide
1	E	49	ASP	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	2288	0	2249	3	1
1	B	2275	0	2243	16	1
1	C	2265	0	2224	8	0
1	D	2289	0	2245	10	1
1	E	2301	0	2260	6	0
1	F	2249	0	2213	10	0
2	A	20	0	12	0	0
2	B	20	0	12	0	0
2	C	20	0	12	2	0
2	D	20	0	12	0	0
2	E	20	0	12	0	0
2	F	20	0	12	2	0
3	A	47	0	0	0	0
3	B	50	0	0	0	0
3	C	45	0	0	0	0
3	D	54	0	0	0	0
3	E	64	0	0	2	0
3	F	68	0	0	1	0
All	All	14115	0	13506	51	2

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 2.

All (51) 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:271:ARG:HH22	1:B:307:ILE:HD13	1.40	0.87
1:B:271:ARG:NH2	1:B:307:ILE:HD13	2.02	0.74
1:D:115:ARG:NH2	1:D:126:ARG:O	2.21	0.71
1:B:305:PRO:HB2	1:B:307:ILE:HD12	1.76	0.66
1:D:261:HIS:CE1	1:D:309:MET:HB3	2.32	0.65
1:E:140:ARG:NH2	1:E:289:ASP:OD2	2.31	0.63
1:F:297:GLN:HG3	3:F:564:HOH:O	1.99	0.62
1:C:226:ASN:HD21	2:C:400:DC:H42	1.47	0.62
1:D:51:THR:HG23	1:D:53:THR:HG22	1.83	0.60
1:B:77:LYS:HD2	1:B:308:LYS:HG3	1.84	0.59
1:C:226:ASN:ND2	2:C:400:DC:H42	2.01	0.59
1:A:32:GLN:O	1:A:36:GLN:HG3	2.04	0.57
1:B:271:ARG:HH22	1:B:307:ILE:CD1	2.18	0.55
1:F:280[B]:ARG:NH1	1:F:297:GLN:OE1	2.39	0.54
1:F:102:SER:HB2	1:F:110:ASP:OD1	2.06	0.54
1:D:198:LEU:HD12	1:D:198:LEU:C	2.29	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:LEU:HD23	1:B:236:MET:HE1	1.91	0.52
1:D:152:ASP:OD1	1:D:154:SER:OG	2.26	0.50
1:D:32:GLN:NE2	1:D:64:ARG:O	2.32	0.49
1:B:270:GLN:NE2	1:B:270:GLN:HA	2.26	0.49
1:B:263:GLU:N	1:B:264:PRO:CD	2.75	0.49
1:B:115:ARG:NH2	1:B:126:ARG:O	2.34	0.48
1:B:116:ASP:OD1	1:C:306:THR:HG23	2.13	0.48
1:F:226:ASN:HD21	2:F:400:DC:H42	1.62	0.48
1:B:47:LYS:O	1:B:55:THR:OG1	2.26	0.47
1:B:77:LYS:HD2	1:B:308:LYS:CG	2.45	0.47
1:A:140:ARG:NH2	1:A:289:ASP:OD2	2.46	0.46
1:E:127:GLU:HG3	3:E:550:HOH:O	2.15	0.46
1:D:77:LYS:HB2	1:D:307:ILE:HG13	1.98	0.46
1:B:207:GLU:HA	1:B:244:LYS:O	2.16	0.46
1:A:280:ARG:HH21	1:A:299:GLU:CD	2.20	0.46
1:D:47:LYS:O	1:D:48:ASP:CB	2.64	0.46
1:F:196:HIS:HB3	1:F:212:LEU:HD11	1.97	0.45
1:B:77:LYS:NZ	1:B:308:LYS:HD3	2.31	0.45
1:E:263:GLU:N	1:E:264:PRO:CD	2.80	0.44
1:D:34:LEU:HD11	1:D:76:THR:HG21	2.00	0.44
1:E:28:HIS:CD2	1:E:30:GLU:H	2.36	0.43
1:E:261:HIS:HD2	3:E:501:HOH:O	2.01	0.42
1:B:307:ILE:HG22	1:B:307:ILE:O	2.19	0.42
1:E:28:HIS:HD2	1:E:30:GLU:H	1.68	0.42
1:C:196:HIS:HB3	1:C:212:LEU:HD11	2.00	0.42
1:F:226:ASN:ND2	2:F:400:DC:H42	2.19	0.41
1:F:207:GLU:HA	1:F:244:LYS:O	2.20	0.41
1:B:77:LYS:HZ2	1:B:308:LYS:HD3	1.86	0.41
1:C:55:THR:HB	1:C:256:HIS:HB2	2.02	0.41
1:F:151:SER:HB2	1:F:153:TYR:CZ	2.56	0.41
1:C:198:LEU:HD12	1:C:198:LEU:C	2.42	0.40
1:C:204:VAL:HG21	1:D:45:VAL:HG11	2.04	0.40
1:C:233:LEU:HD11	1:C:237:ILE:HD11	2.03	0.40
1:F:93:LYS:HE2	1:F:100:GLU:OE1	2.21	0.40
1:F:140:ARG:NH2	1:F:289:ASP:OD2	2.55	0.40

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ASP:OD1	1:D:306:THR:CG2[1_455]	1.90	0.30

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:GLN:OE1	1:B:270:GLN:OE1[7_555]	2.00	0.20

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	282/289 (98%)	272 (96%)	8 (3%)	2 (1%)	22	32
1	B	278/289 (96%)	271 (98%)	6 (2%)	1 (0%)	34	48
1	C	280/289 (97%)	271 (97%)	8 (3%)	1 (0%)	34	48
1	D	284/289 (98%)	275 (97%)	7 (2%)	2 (1%)	22	32
1	E	284/289 (98%)	274 (96%)	8 (3%)	2 (1%)	22	32
1	F	274/289 (95%)	264 (96%)	9 (3%)	1 (0%)	34	48
All	All	1682/1734 (97%)	1627 (97%)	46 (3%)	9 (0%)	29	41

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	48	ASP
1	E	50	ARG
1	A	260	ASN
1	F	134	VAL
1	B	134	VAL
1	A	134	VAL
1	C	134	VAL
1	D	134	VAL
1	E	134	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	246/252 (98%)	236 (96%)	10 (4%)	30	48
1	B	245/252 (97%)	234 (96%)	11 (4%)	27	44
1	C	242/252 (96%)	232 (96%)	10 (4%)	30	48
1	D	244/252 (97%)	234 (96%)	10 (4%)	30	48
1	E	247/252 (98%)	237 (96%)	10 (4%)	31	49
1	F	242/252 (96%)	230 (95%)	12 (5%)	24	40
All	All	1466/1512 (97%)	1403 (96%)	63 (4%)	30	46

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	38	GLN
1	B	57	SER
1	B	69	ASP
1	B	77	LYS
1	B	221	LEU
1	B	270	GLN
1	B	305	PRO
1	B	306	THR
1	B	307	ILE
1	B	308	LYS
1	B	309	MET
1	A	46	ARG
1	A	93	LYS
1	A	127	GLU
1	A	163	ARG
1	A	221	LEU
1	A	260	ASN
1	A	263	GLU
1	A	266	LYS
1	A	280	ARG
1	A	288	ILE
1	C	38	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	46	ARG
1	C	50	ARG
1	C	77	LYS
1	C	120	SER
1	C	140	ARG
1	C	221	LEU
1	C	278	LYS
1	C	284	LYS
1	C	289	ASP
1	D	50	ARG
1	D	69	ASP
1	D	115	ARG
1	D	116	ASP
1	D	126	ARG
1	D	154	SER
1	D	163	ARG
1	D	192	LEU
1	D	306	THR
1	D	307	ILE
1	E	46	ARG
1	E	147	ARG
1	E	150	GLU
1	E	163	ARG
1	E	198	LEU
1	E	221	LEU
1	E	260	ASN
1	E	280	ARG
1	E	289	ASP
1	E	306	THR
1	F	57	SER
1	F	69	ASP
1	F	82	LYS
1	F	107	LYS
1	F	176	ARG
1	F	185	ARG
1	F	221	LEU
1	F	272	GLU
1	F	280[A]	ARG
1	F	280[B]	ARG
1	F	288	ILE
1	F	306	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	62	GLN
1	B	112	ASN
1	B	211	GLN
1	B	270	GLN
1	A	62	GLN
1	A	112	ASN
1	A	211	GLN
1	A	260	ASN
1	C	62	GLN
1	C	211	GLN
1	D	62	GLN
1	D	112	ASN
1	D	162	GLN
1	D	211	GLN
1	D	261	HIS
1	D	270	GLN
1	E	28	HIS
1	E	62	GLN
1	E	211	GLN
1	E	260	ASN
1	E	261	HIS
1	F	62	GLN
1	F	112	ASN
1	F	205	ASN
1	F	211	GLN
1	F	261	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.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	284/289 (98%)	-0.31	4 (1%) 75 73	18, 31, 57, 99	0
1	B	282/289 (97%)	-0.22	10 (3%) 44 43	18, 32, 61, 111	0
1	C	282/289 (97%)	-0.18	7 (2%) 57 55	21, 36, 62, 82	0
1	D	286/289 (98%)	-0.16	8 (2%) 53 51	23, 37, 65, 115	0
1	E	286/289 (98%)	-0.25	7 (2%) 59 57	22, 35, 62, 96	0
1	F	277/289 (95%)	-0.28	7 (2%) 57 55	20, 33, 57, 92	0
All	All	1697/1734 (97%)	-0.23	43 (2%) 57 55	18, 34, 62, 115	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	309	MET	6.2
1	B	307	ILE	6.1
1	D	52	GLY	4.6
1	B	53	THR	4.4
1	D	307	ILE	4.1
1	A	52	GLY	4.0
1	D	309	MET	3.9
1	C	51	THR	3.9
1	E	50	ARG	3.8
1	A	307	ILE	3.8
1	B	308	LYS	3.8
1	E	309	MET	3.6
1	F	26	PRO	3.2
1	E	307	ILE	3.2
1	B	26	PRO	3.0
1	E	233	LEU	2.9
1	B	28	HIS	2.8
1	C	233	LEU	2.8
1	F	28	HIS	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	51	THR	2.7
1	F	48	ASP	2.6
1	B	27	PRO	2.6
1	D	308	LYS	2.5
1	D	48	ASP	2.5
1	E	234	THR	2.5
1	C	26	PRO	2.5
1	E	25	MET	2.4
1	E	232	LEU	2.4
1	C	306	THR	2.4
1	D	310	GLU	2.4
1	F	230	TYR	2.2
1	C	48	ASP	2.2
1	B	48	ASP	2.2
1	F	25	MET	2.1
1	F	46	ARG	2.1
1	F	210	CYS	2.1
1	D	305	PRO	2.1
1	A	50	ARG	2.0
1	A	233	LEU	2.0
1	B	234	THR	2.0
1	C	27	PRO	2.0
1	B	306	THR	2.0
1	C	53	THR	2.0

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. 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
2	DC	D	400	20/20	0.91	0.17	58,71,95,95	0
2	DC	F	400	20/20	0.92	0.19	53,76,92,93	0
2	DC	E	400	20/20	0.93	0.14	43,56,73,77	0
2	DC	B	400	20/20	0.94	0.14	53,64,80,83	0
2	DC	A	400	20/20	0.95	0.13	39,51,64,67	0
2	DC	C	400	20/20	0.96	0.11	40,52,74,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.