



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 01:36 am BST

PDB ID : 2W4L  
Title : Human dCMP deaminase  
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Deposited on : 2008-11-28  
Resolution : 2.10 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](mailto: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.

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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  
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

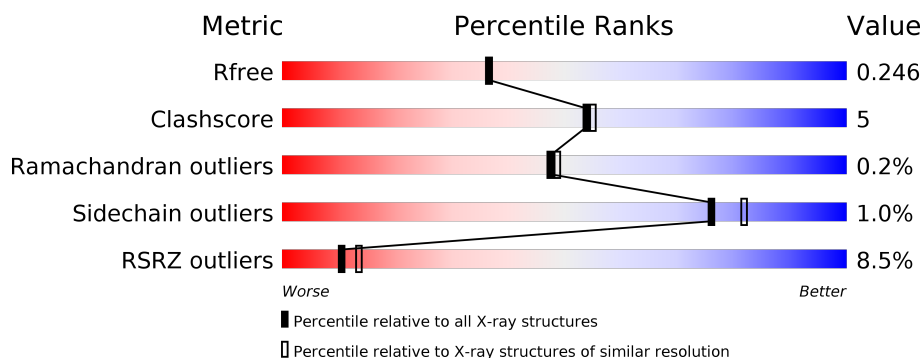
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 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	178	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>6%</div> <div>10%</div> </div> </div>
1	B	178	<div> <div>8%</div> <div> <div></div> <div>74%</div> <div>14%</div> <div>12%</div> </div> </div>
1	C	178	<div> <div>4%</div> <div> <div></div> <div>67%</div> <div>13%</div> <div>20%</div> </div> </div>
1	D	178	<div> <div>13%</div> <div> <div></div> <div>75%</div> <div>10%</div> <div>16%</div> </div> </div>
1	E	178	<div> <div>10%</div> <div> <div></div> <div>84%</div> <div>6%</div> <div>9%</div> </div> </div>
1	F	178	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>6%</div> <div>11%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7539 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 DEOXYCYTIDYLATE DEAMINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	0	4	0
			1264	808	209	232	15			
1	B	157	Total	C	N	O	S	0	0	0
			1225	782	202	228	13			
1	C	142	Total	C	N	O	S	0	1	0
			1097	703	177	204	13			
1	D	150	Total	C	N	O	S	0	0	0
			1174	753	195	213	13			
1	E	162	Total	C	N	O	S	0	0	0
			1267	806	212	236	13			
1	F	159	Total	C	N	O	S	0	2	0
			1250	797	208	231	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	LEU	SER	conflict	UNP P32321
B	95	LEU	SER	conflict	UNP P32321
C	95	LEU	SER	conflict	UNP P32321
D	95	LEU	SER	conflict	UNP P32321
E	95	LEU	SER	conflict	UNP P32321
F	95	LEU	SER	conflict	UNP P32321

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Cl 1	0	0
3	A	2	Total 2	Cl 2	0	0
3	E	1	Total 1	Cl 1	0	0

- Molecule 4 is water.

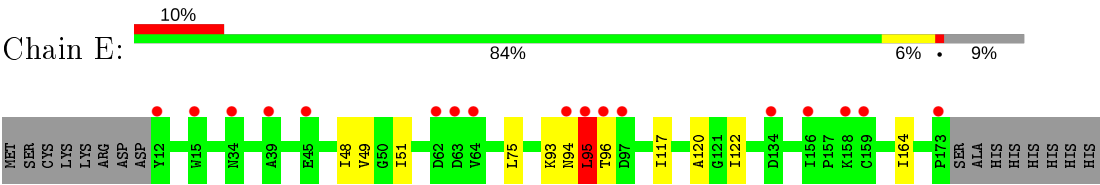
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total 49	O 49	0	0
4	B	35	Total 35	O 35	0	0
4	C	37	Total 37	O 37	0	0
4	D	36	Total 36	O 36	0	0
4	E	44	Total 44	O 44	0	0
4	F	51	Total 51	O 51	0	0



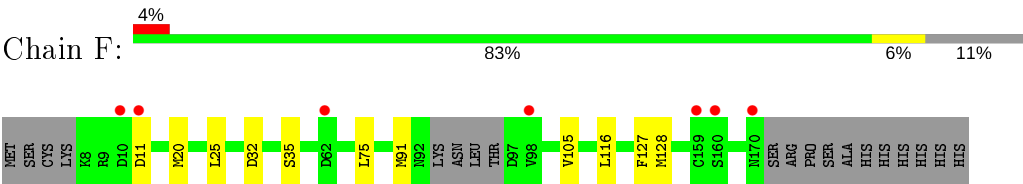
- Molecule 1: DEOXYCYTIDYLATE DEAMINASE



● Molecule 1: DEOXYCYTIDYLATE DEAMINASE



● Molecule 1: DEOXYCYTIDYLATE DEAMINASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.23Å 80.07Å 96.24Å 90.00° 94.34° 90.00°	Depositor
Resolution (Å)	29.70 – 2.10 29.68 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.70-2.10) 99.7 (29.68-2.10)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.05 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.200 , 0.243 0.204 , 0.246	Depositor DCC
$R_{free}$ test set	2924 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7539	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ZN, CL

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	0.40	0/1302	0.51	0/1757
1	B	0.38	0/1251	0.54	0/1691
1	C	0.39	0/1122	0.52	0/1514
1	D	0.38	0/1198	0.51	0/1615
1	E	0.39	0/1295	0.54	0/1753
1	F	0.40	0/1282	0.54	0/1731
All	All	0.39	0/7450	0.53	0/10061

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	1264	0	1252	7	0
1	B	1225	0	1192	25	0
1	C	1097	0	1074	25	0
1	D	1174	0	1157	23	0
1	E	1267	0	1243	10	0
1	F	1250	0	1226	7	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
4	A	49	0	0	1	0
4	B	35	0	0	0	0
4	C	37	0	0	1	0
4	D	36	0	0	0	0
4	E	44	0	0	0	0
4	F	51	0	0	0	0
All	All	7539	0	7144	77	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 5.

All (77) 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)
4:C:2016:HOH:O	1:D:147:MET:SD	2.15	1.03
1:C:128:MET:HE2	1:C:155:PHE:HD2	1.34	0.91
1:C:128:MET:HE2	1:C:155:PHE:CD2	2.21	0.74
1:C:112:GLU:O	1:C:116:LEU:HD13	1.92	0.69
1:B:51:ILE:CD1	1:C:48:ILE:HD12	2.23	0.68
1:C:91:MET:HE2	1:D:120:ALA:HA	1.75	0.68
1:D:25:LEU:HD13	1:E:164:ILE:HD11	1.76	0.67
1:D:143:LEU:HG	1:D:147:MET:CE	2.28	0.64
1:D:143:LEU:HG	1:D:147:MET:HE2	1.79	0.62
1:C:49:VAL:O	1:C:93:LYS:HB3	1.99	0.62
1:B:48:ILE:HD12	1:C:51:ILE:CD1	2.29	0.62
1:B:51:ILE:HD12	1:C:48:ILE:HD12	1.81	0.62
1:D:112:GLU:O	1:D:116:LEU:HD12	2.00	0.62
1:D:98:VAL:HG21	1:D:120:ALA:HB1	1.82	0.61
1:C:92:ASN:O	1:C:93:LYS:HB2	2.01	0.61
1:D:98:VAL:HG23	1:D:120:ALA:O	2.00	0.61
1:C:48:ILE:HG21	1:C:51:ILE:HD11	1.82	0.60
1:B:56:MET:HG3	1:B:61:SER:HB2	1.84	0.59
1:C:103:MET:HG2	1:C:105:VAL:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:MET:HG2	1:A:105:VAL:HG13	1.84	0.58
1:B:166:PHE:HB3	1:C:128:MET:HE3	1.85	0.57
1:D:48:ILE:HD12	1:E:51:ILE:HD12	1.88	0.56
1:D:112:GLU:O	1:D:116:LEU:CD1	2.54	0.56
1:A:164:ILE:HD11	1:F:25:LEU:HD13	1.87	0.56
1:B:130:ASP:OD2	1:B:133:HIS:HD2	1.88	0.55
1:B:117:ILE:HG23	1:B:122:ILE:HB	1.89	0.55
1:B:48:ILE:HD12	1:C:51:ILE:HD13	1.88	0.54
1:C:81:TYR:CE1	1:D:147:MET:HE1	2.43	0.53
1:D:113:CYS:HA	1:D:116:LEU:HD13	1.93	0.51
1:A:136:ASP:HB3	1:B:75:LEU:HD11	1.93	0.51
1:B:90:ILE:HG22	1:B:91:MET:HE3	1.93	0.51
1:B:56:MET:HG3	1:B:61:SER:CB	2.41	0.50
1:C:91:MET:CE	1:D:120:ALA:HA	2.42	0.50
1:D:48:ILE:HD12	1:E:51:ILE:CD1	2.41	0.50
1:E:94:ASN:O	1:E:96:THR:N	2.44	0.50
1:C:128:MET:CE	1:C:155:PHE:HD2	2.16	0.49
1:B:90:ILE:HG22	1:B:91:MET:CE	2.43	0.49
1:C:104:TYR:CZ	1:C:126:ILE:HD13	2.48	0.48
1:A:130:ASP:OD2	1:A:133:HIS:HD2	1.96	0.48
1:E:49:VAL:O	1:E:93:LYS:HB3	2.12	0.48
1:F:105:VAL:O	1:F:127:PHE:HA	2.14	0.48
1:E:95:LEU:O	1:E:95:LEU:HD13	2.14	0.47
1:E:120:ALA:HA	1:F:91:MET:HE2	1.96	0.47
1:D:51:ILE:CD1	1:E:48:ILE:HD12	2.45	0.47
1:C:139:THR:HG21	1:D:74:LYS:HE3	1.97	0.47
1:D:98:VAL:CG2	1:D:120:ALA:HB1	2.43	0.47
1:C:87:LEU:HD23	1:C:87:LEU:C	2.35	0.46
1:B:143:LEU:HG	1:B:147:MET:HE3	1.97	0.46
1:B:143:LEU:CG	1:B:147:MET:HE3	2.46	0.45
1:B:49:VAL:O	1:B:93:LYS:HB3	2.16	0.45
1:B:106:ALA:O	1:B:128:MET:HB3	2.16	0.45
1:E:95:LEU:CD1	1:E:95:LEU:O	2.65	0.44
1:F:11:ASP:OD1	1:F:11:ASP:N	2.49	0.44
1:E:117:ILE:HG23	1:E:122:ILE:HB	1.99	0.44
1:D:93:LYS:CB	1:D:98:VAL:HG13	2.46	0.44
1:B:41:ILE:HG22	1:B:49:VAL:CG2	2.48	0.44
1:B:60:CYS:O	1:B:61:SER:C	2.56	0.44
1:B:166:PHE:HB3	1:C:128:MET:CE	2.49	0.43
1:C:130:ASP:OD2	1:C:133:HIS:HD2	2.02	0.43
1:B:15:TRP:HB2	1:B:16:PRO:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ILE:HD13	1:C:18:TYR:OH	2.19	0.43
1:F:91:MET:HE3	1:F:91:MET:HA	2.00	0.43
1:A:87:LEU:HD23	1:A:87:LEU:C	2.39	0.42
1:D:87:LEU:HD23	1:D:87:LEU:C	2.40	0.42
1:C:117:ILE:HG23	1:C:122[A]:ILE:HB	2.01	0.42
1:A:127:PHE:CE1	1:A:130:ASP:HB2	2.54	0.42
1:D:93:LYS:CB	1:D:98:VAL:CG1	2.98	0.41
1:F:32:ASP:HB3	1:F:35:SER:O	2.20	0.41
1:A:62:ASP:OD1	4:A:2019:HOH:O	2.20	0.41
1:C:91:MET:HE2	1:D:120:ALA:CA	2.49	0.41
1:B:51:ILE:HG21	1:C:18:TYR:OH	2.21	0.41
1:D:41:ILE:HG22	1:D:49:VAL:CG2	2.51	0.41
1:D:143:LEU:HG	1:D:147:MET:HE3	2.01	0.40
1:B:98:VAL:CG2	1:B:120:ALA:HB1	2.51	0.40
1:B:92:ASN:O	1:B:93:LYS:HB2	2.21	0.40
1:B:128:MET:HE1	1:B:157:PRO:HG3	2.03	0.40
1:F:20:MET:HG2	1:F:128[B]:MET:CE	2.52	0.40

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	160/178 (90%)	157 (98%)	3 (2%)	0	100	100
1	B	153/178 (86%)	149 (97%)	3 (2%)	1 (1%)	22	18
1	C	137/178 (77%)	136 (99%)	1 (1%)	0	100	100
1	D	142/178 (80%)	138 (97%)	4 (3%)	0	100	100
1	E	160/178 (90%)	156 (98%)	3 (2%)	1 (1%)	25	21
1	F	157/178 (88%)	156 (99%)	1 (1%)	0	100	100
All	All	909/1068 (85%)	892 (98%)	15 (2%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	61	SER
1	E	95	LEU

### 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	139/155 (90%)	138 (99%)	1 (1%)	84	88
1	B	132/155 (85%)	132 (100%)	0	100	100
1	C	120/155 (77%)	119 (99%)	1 (1%)	81	86
1	D	127/155 (82%)	125 (98%)	2 (2%)	62	69
1	E	139/155 (90%)	137 (99%)	2 (1%)	67	73
1	F	136/155 (88%)	134 (98%)	2 (2%)	65	71
All	All	793/930 (85%)	785 (99%)	8 (1%)	76	82

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	LEU
1	C	156	ILE
1	D	73	ASN
1	D	158	LYS
1	E	75	LEU
1	E	95	LEU
1	F	75	LEU
1	F	116	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	HIS
1	A	146	ASN

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Mol	Chain	Res	Type
1	B	133	HIS
1	C	133	HIS
1	D	73	ASN
1	D	133	HIS
1	F	133	HIS

### 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](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

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 [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, 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	160/178 (89%)	0.41	10 (6%) 20 24	15, 24, 40, 47	0
1	B	157/178 (88%)	0.58	14 (8%) 9 12	14, 25, 46, 49	0
1	C	142/178 (79%)	0.31	8 (5%) 24 29	17, 23, 39, 46	0
1	D	150/178 (84%)	0.75	23 (15%) 2 3	17, 28, 57, 60	0
1	E	162/178 (91%)	0.52	17 (10%) 6 8	16, 25, 39, 45	0
1	F	159/178 (89%)	0.38	7 (4%) 34 40	13, 23, 39, 44	0
All	All	930/1068 (87%)	0.49	79 (8%) 10 13	13, 25, 44, 60	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	96	THR	7.9
1	D	79	TYR	7.4
1	B	62	ASP	5.4
1	B	169	ILE	5.2
1	A	6	CYS	5.2
1	B	61	SER	5.2
1	C	34	ASN	5.1
1	C	33	PRO	4.9
1	B	170	ASN	4.7
1	D	69	ARG	4.4
1	B	72	GLU	4.4
1	D	77	THR	4.2
1	D	34	ASN	4.2
1	F	159	CYS	4.2
1	E	15	TRP	4.1
1	E	62	ASP	4.1
1	F	10	ASP	3.9
1	D	78	LYS	3.9
1	B	64	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
1	E	173	PRO	3.8
1	F	170	ASN	3.7
1	D	98	VAL	3.6
1	D	159	CYS	3.6
1	E	12	TYR	3.5
1	E	94	ASN	3.4
1	D	169	ILE	3.4
1	B	12	TYR	3.3
1	D	68	ARG	3.3
1	B	97	ASP	3.2
1	A	98	VAL	3.2
1	B	11	ASP	3.2
1	F	62	ASP	3.1
1	D	12	TYR	3.1
1	F	11	ASP	3.0
1	F	160	SER	3.0
1	D	99	LYS	3.0
1	A	97	ASP	2.9
1	E	95	LEU	2.9
1	D	64	VAL	2.9
1	D	81	TYR	2.8
1	E	158	LYS	2.8
1	E	97	ASP	2.8
1	B	158	LYS	2.7
1	C	35	SER	2.6
1	D	11	ASP	2.6
1	B	98	VAL	2.6
1	A	73	ASN	2.6
1	E	156	ILE	2.6
1	D	33	PRO	2.6
1	D	74	LYS	2.5
1	D	158	LYS	2.5
1	D	65	LEU	2.5
1	A	63	ASP	2.5
1	D	136	ASP	2.5
1	E	63	ASP	2.5
1	E	64	VAL	2.4
1	B	73	ASN	2.3
1	A	99	LYS	2.3
1	D	73	ASN	2.3
1	E	34	ASN	2.3
1	D	35	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	11	ASP	2.3
1	A	45	GLU	2.3
1	E	134	ASP	2.2
1	A	70	THR	2.2
1	E	159	CYS	2.2
1	C	45	GLU	2.1
1	C	156	ILE	2.1
1	C	158	LYS	2.1
1	F	98	VAL	2.1
1	B	70	THR	2.1
1	A	100	GLY	2.1
1	D	72	GLU	2.0
1	E	39	ALA	2.0
1	E	45	GLU	2.0
1	B	63	ASP	2.0
1	C	160	SER	2.0
1	D	160	SER	2.0
1	A	39	ALA	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, 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	E	1175	1/1	0.90	0.07	51,51,51,51	0
3	CL	B	1172	1/1	0.91	0.08	39,39,39,39	0
3	CL	A	1172	1/1	0.93	0.08	38,38,38,38	0
3	CL	A	1171	1/1	0.96	0.13	60,60,60,60	0
2	ZN	C	1170	1/1	1.00	0.09	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	F	1171	1/1	1.00	0.09	19,19,19,19	0
2	ZN	A	1170	1/1	1.00	0.09	19,19,19,19	0
2	ZN	B	1171	1/1	1.00	0.07	21,21,21,21	0
2	ZN	E	1174	1/1	1.00	0.08	18,18,18,18	0
2	ZN	D	1170	1/1	1.00	0.07	23,23,23,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.