



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:39 PM GMT

PDB ID : 4D08
Title : PDE2a catalytic domain in complex with a brain penetrant inhibitor
Authors : Buijnsters, P.; Andres, J.I.; DeAngelis, M.; Langlois, X.; Rombouts, F.; Sanderson, W.; Tresadern, G.; Trabanco, A.; VanHoof, G.; VanRoosbroeck, Y.
Deposited on : 2014-04-24
Resolution : 1.90 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

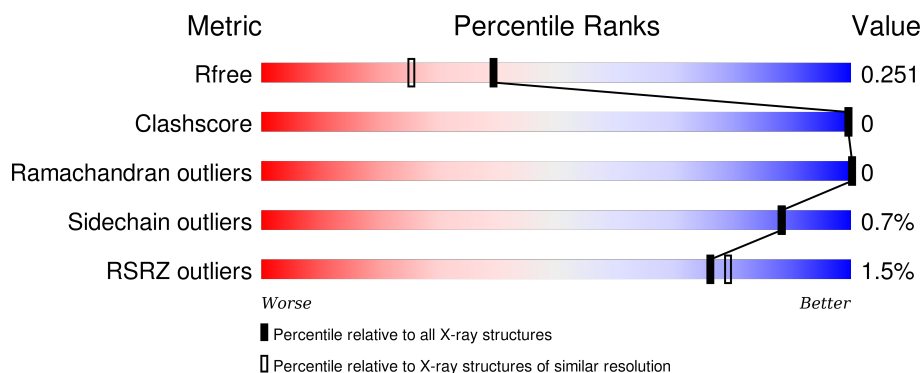
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	353	<div> <div style="width: 95%;"></div> <div>95%</div> </div>
1	B	353	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>
1	C	353	<div> <div style="width: 91%;"></div> <div>91%</div> <div>7%</div> </div>
1	D	353	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11498 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 CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	3	0
			2736	1743	463	505	25			
1	B	337	Total	C	N	O	S	0	0	0
			2699	1723	458	493	25			
1	C	327	Total	C	N	O	S	0	0	0
			2606	1665	440	476	25			
1	D	335	Total	C	N	O	S	0	0	0
			2691	1718	457	491	25			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	576	MET	-	EXPRESSION TAG	UNP O00408
A	577	GLY	-	EXPRESSION TAG	UNP O00408
A	922	ARG	-	EXPRESSION TAG	UNP O00408
A	923	HIS	-	EXPRESSION TAG	UNP O00408
A	924	HIS	-	EXPRESSION TAG	UNP O00408
A	925	HIS	-	EXPRESSION TAG	UNP O00408
A	926	HIS	-	EXPRESSION TAG	UNP O00408
A	927	HIS	-	EXPRESSION TAG	UNP O00408
A	928	HIS	-	EXPRESSION TAG	UNP O00408
B	576	MET	-	EXPRESSION TAG	UNP O00408
B	577	GLY	-	EXPRESSION TAG	UNP O00408
B	922	ARG	-	EXPRESSION TAG	UNP O00408
B	923	HIS	-	EXPRESSION TAG	UNP O00408
B	924	HIS	-	EXPRESSION TAG	UNP O00408
B	925	HIS	-	EXPRESSION TAG	UNP O00408
B	926	HIS	-	EXPRESSION TAG	UNP O00408
B	927	HIS	-	EXPRESSION TAG	UNP O00408
B	928	HIS	-	EXPRESSION TAG	UNP O00408
C	576	MET	-	EXPRESSION TAG	UNP O00408
C	577	GLY	-	EXPRESSION TAG	UNP O00408
C	922	ARG	-	EXPRESSION TAG	UNP O00408

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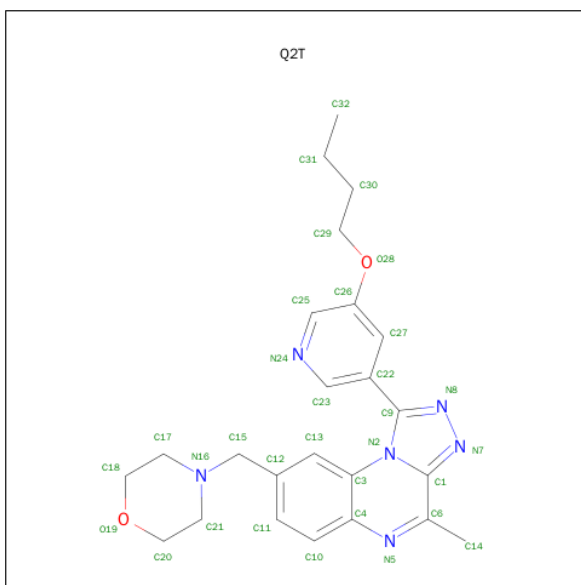
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Chain	Residue	Modelled	Actual	Comment	Reference
C	923	HIS	-	EXPRESSION TAG	UNP O00408
C	924	HIS	-	EXPRESSION TAG	UNP O00408
C	925	HIS	-	EXPRESSION TAG	UNP O00408
C	926	HIS	-	EXPRESSION TAG	UNP O00408
C	927	HIS	-	EXPRESSION TAG	UNP O00408
C	928	HIS	-	EXPRESSION TAG	UNP O00408
D	576	MET	-	EXPRESSION TAG	UNP O00408
D	577	GLY	-	EXPRESSION TAG	UNP O00408
D	922	ARG	-	EXPRESSION TAG	UNP O00408
D	923	HIS	-	EXPRESSION TAG	UNP O00408
D	924	HIS	-	EXPRESSION TAG	UNP O00408
D	925	HIS	-	EXPRESSION TAG	UNP O00408
D	926	HIS	-	EXPRESSION TAG	UNP O00408
D	927	HIS	-	EXPRESSION TAG	UNP O00408
D	928	HIS	-	EXPRESSION TAG	UNP O00408

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

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

- Molecule 3 is 1-(5-BUTOXYPYRIDIN-3-YL)-4-METHYL-8-(MORPHOLIN-4-YLM ETHYL)[1,2,4]TRIAZOLO[4,3-A]QUINOXALINE (three-letter code: Q2T) (formula: C₂₄H₂₈N₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 32	C 24	N 6	O 2	0	0
3	B	1	Total 32	C 24	N 6	O 2	0	0
3	C	1	Total 32	C 24	N 6	O 2	0	0
3	D	1	Total 32	C 24	N 6	O 2	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	173	Total O 173 173	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	168	Total 168	O 168	0	0
5	C	130	Total 130	O 130	0	0
5	D	159	Total 159	O 159	0	0

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.

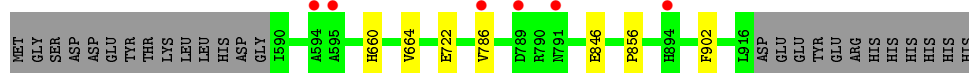
- Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE



- Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE



- Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE



- Molecule 1: CGMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.04Å 74.15Å 92.77Å 109.04° 91.73° 91.34°	Depositor
Resolution (Å)	46.34 – 1.90 46.34 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.0 (46.34-1.90) 83.6 (46.34-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.213 , 0.247 0.219 , 0.251	Depositor DCC
R_{free} test set	5177 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.0	EDS
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 103455 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11498	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.45% 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: ZN, Q2T, MG

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	0.29	0/2806	0.49	1/3800 (0.0%)
1	B	0.30	0/2766	0.50	1/3746 (0.0%)
1	C	0.29	0/2671	0.47	0/3619
1	D	0.30	0/2756	0.50	1/3728 (0.0%)
All	All	0.30	0/10999	0.49	3/14893 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	808	ASP	CB-CG-OD1	5.73	123.46	118.30
1	B	808	ASP	CB-CG-OD1	5.61	123.35	118.30
1	A	808	ASP	CB-CG-OD1	5.45	123.20	118.30

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	2736	0	2610	1	0
1	B	2699	0	2581	3	0
1	C	2606	0	2483	2	0
1	D	2691	0	2582	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	32	0	28	0	0
3	B	32	0	28	0	0
3	C	32	0	28	0	0
3	D	32	0	28	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	173	0	0	0	0
5	B	168	0	0	0	0
5	C	130	0	0	0	0
5	D	159	0	0	0	0
All	All	11498	0	10368	7	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 0.

All (7) 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:864:GLU:OE2	1:B:892:ARG:NH2	2.48	0.46
1:A:596:ILE:HG21	1:A:600:PHE:CE1	2.54	0.42
1:C:660:HIS:O	1:C:664:VAL:HG23	2.20	0.41
1:D:834:GLY:HA3	1:D:848:MET:O	2.20	0.41
1:B:855:ILE:N	1:B:856:PRO:HD2	2.35	0.41
1:C:856:PRO:HG3	1:C:902:PHE:CE1	2.57	0.40
1:B:778:LYS:HD3	1:B:778:LYS:N	2.36	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	340/353 (96%)	338 (99%)	2 (1%)	0	100	100
1	B	335/353 (95%)	333 (99%)	2 (1%)	0	100	100
1	C	325/353 (92%)	320 (98%)	5 (2%)	0	100	100
1	D	331/353 (94%)	330 (100%)	1 (0%)	0	100	100
All	All	1331/1412 (94%)	1321 (99%)	10 (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	295/319 (92%)	295 (100%)	0	100	100
1	B	289/319 (91%)	287 (99%)	2 (1%)	88	88
1	C	278/319 (87%)	275 (99%)	3 (1%)	80	79
1	D	289/319 (91%)	286 (99%)	3 (1%)	82	81
All	All	1151/1276 (90%)	1143 (99%)	8 (1%)	88	88

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

Mol	Chain	Res	Type
1	B	683	ASP
1	B	916	LEU
1	C	722	GLU
1	C	786	VAL
1	C	846	GLU
1	D	617	MET
1	D	633	LYS
1	D	794	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	739	ASN
1	A	794	GLN
1	A	859	GLN
1	B	679	ASN
1	B	842	ASN
1	C	624	GLN
1	C	627	ASN
1	C	630	ASN
1	D	627	ASN
1	D	630	ASN
1	D	842	ASN
1	D	911	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](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
3	Q2T	A	1918	-	28,36,36	0.54	0	38,50,50	0.86	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	Q2T	B	1917	-	28,36,36	0.58	0	38,50,50	0.77	2 (5%)
3	Q2T	C	1917	-	28,36,36	0.53	0	38,50,50	0.80	1 (2%)
3	Q2T	D	1922	-	28,36,36	0.55	0	38,50,50	0.75	2 (5%)

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
3	Q2T	A	1918	-	-	0/13/21/21	0/5/5/5
3	Q2T	B	1917	-	-	0/13/21/21	0/5/5/5
3	Q2T	C	1917	-	-	0/13/21/21	0/5/5/5
3	Q2T	D	1922	-	-	0/13/21/21	0/5/5/5

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1917	Q2T	C6-N5-C4	2.03	119.97	118.43
3	D	1922	Q2T	C6-N5-C4	2.05	119.99	118.43
3	A	1918	Q2T	C6-N5-C4	2.29	120.17	118.43
3	D	1922	Q2T	C9-N8-N7	2.62	108.22	104.89
3	B	1917	Q2T	C9-N8-N7	2.62	108.22	104.89
3	C	1917	Q2T	C9-N8-N7	2.64	108.24	104.89
3	A	1918	Q2T	C9-N8-N7	2.73	108.35	104.89

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	339/353 (96%)	0.08	3 (0%) 85 87	11, 21, 33, 46	0
1	B	337/353 (95%)	0.07	9 (2%) 58 61	12, 21, 37, 47	0
1	C	327/353 (92%)	0.25	6 (1%) 71 74	12, 27, 45, 61	0
1	D	335/353 (94%)	0.05	2 (0%) 90 91	12, 21, 32, 39	0
All	All	1338/1412 (94%)	0.11	20 (1%) 76 79	11, 22, 37, 61	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	791	ASN	3.6
1	D	585	LEU	3.3
1	C	594	ALA	3.0
1	B	717	ALA	2.9
1	B	722	GLU	2.8
1	B	721	SER	2.8
1	A	636	CYS	2.6
1	C	786	VAL	2.6
1	C	789	ASP	2.5
1	B	631	ASN	2.5
1	A	747	ASP	2.4
1	C	595	ALA	2.4
1	B	630	ASN	2.3
1	D	584	LYS	2.3
1	B	589	GLY	2.2
1	B	634	ILE	2.1
1	A	598	SER	2.1
1	B	580	ASP	2.1
1	B	629	ILE	2.0
1	C	894	HIS	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. 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(Å ²)	Q<0.9
3	Q2T	B	1917	32/32	0.90	0.12	1.29	14,18,23,24	0
3	Q2T	A	1918	32/32	0.92	0.11	0.73	17,18,23,24	0
4	MG	D	1923	1/1	0.95	0.09	-0.05	11,11,11,11	0
3	Q2T	D	1922	32/32	0.94	0.10	-0.13	15,16,24,26	0
3	Q2T	C	1917	32/32	0.93	0.10	-0.21	15,17,23,24	0
4	MG	A	1919	1/1	0.97	0.09	-0.71	12,12,12,12	0
4	MG	C	1918	1/1	0.98	0.08	-1.45	11,11,11,11	0
2	ZN	C	1001	1/1	1.00	0.04	-3.55	14,14,14,14	0
2	ZN	A	1001	1/1	1.00	0.04	-4.33	13,13,13,13	0
4	MG	B	1918	1/1	0.97	0.06	-5.33	12,12,12,12	0
2	ZN	D	1001	1/1	1.00	0.03	-6.27	13,13,13,13	0
2	ZN	B	1001	1/1	1.00	0.03	-10.78	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.