



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4AJF
Title : Identification and structural characterization of PDE10 fragment inhibitors
Authors : Johansson, P.; Albert, J.S.; Spadola, L.; Akerud, T.; Back, E.; Hillertz, P.;
Horsefeld, R.; Scott, C.; Spear, N.; Tian, G.; Tigerstrom, A.; Aharony, D.;
Geschwindner, S.
Deposited on : 2012-02-16
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

<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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

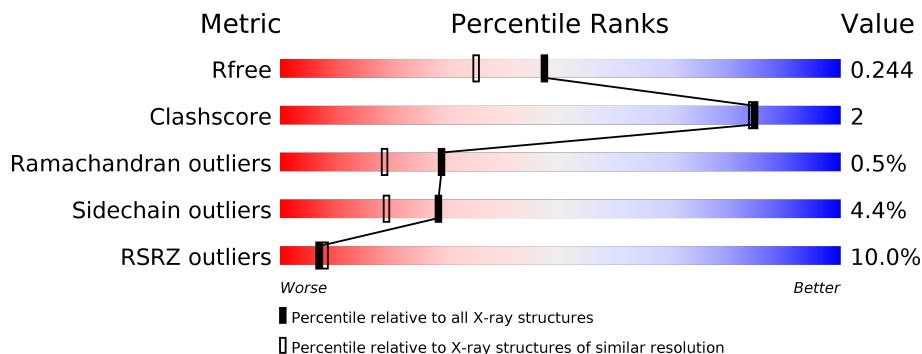
1 Overall quality at a glance i

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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (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 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	328	 4% 90% 10%
1	D	328	 16% 87% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5666 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 CAMP AND CAMP-INHIBITED CGMP 3', 5'-CYCLIC PHOSPHODIESTERASE 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	328	2654	1694	451	485	24	0	0	0
1	D	324	2624	1674	446	480	24	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	447	ASN	-	expression tag	UNP Q9Y233
A	448	ALA	-	expression tag	UNP Q9Y233
D	447	ASN	-	expression tag	UNP Q9Y233
D	448	ALA	-	expression tag	UNP Q9Y233

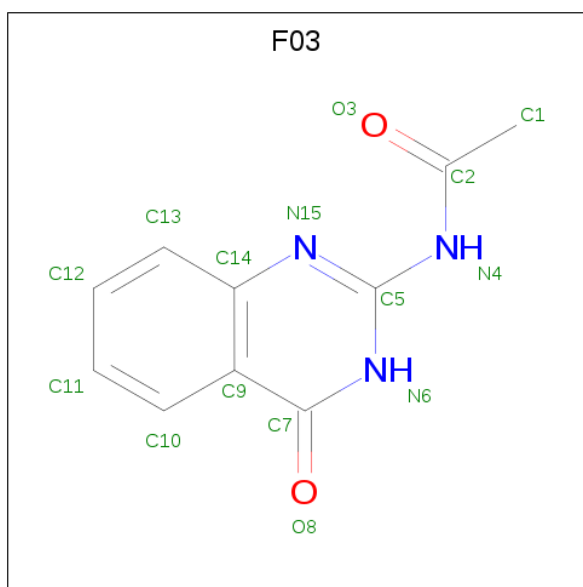
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is N-(4-OXO-3H-QUINAZOLIN-2-YL)ACETAMIDE (three-letter code: F03) (formula: C₁₀H₉N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	15	10	3	2	0	0

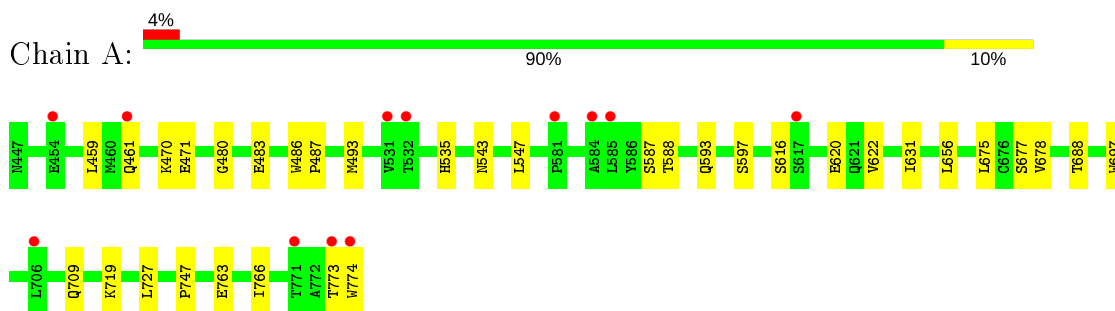
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	217	217	217	0	0
5	D	152	152	152	0	0

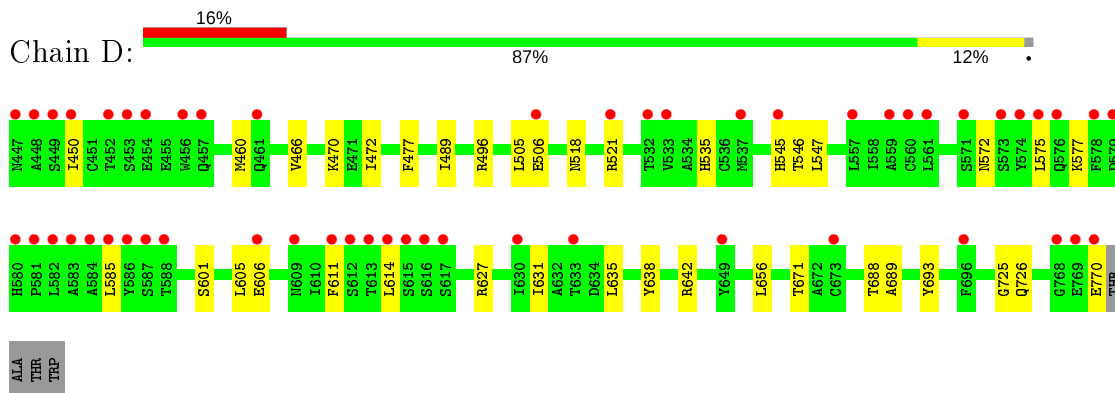
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: CAMP AND CAMP-INHIBITED CGMP 3', 5'-CYCLIC PHOSPHODIESTERASE 10A



- Molecule 1: CAMP AND CAMP-INHIBITED CGMP 3', 5'-CYCLIC PHOSPHODIESTERASE 10A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.37Å 81.80Å 156.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.25 – 1.90 29.25 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.25-1.90) 99.5 (29.25-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.91Å)	Xtrriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.213 , 0.248 0.206 , 0.244	Depositor DCC
R_{free} test set	2563 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	30.2	Xtrriage
Anisotropy	0.508	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5666	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: MG, ZN, F03

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	0.52	0/2719	0.62	0/3683
1	D	0.50	0/2688	0.65	0/3640
All	All	0.51	0/5407	0.63	0/7323

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 [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 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	2654	0	2607	12	0
1	D	2624	0	2583	12	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
4	A	15	0	9	0	0
5	A	217	0	0	0	0
5	D	152	0	0	1	0
All	All	5666	0	5199	24	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 2.

All (24) 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:D:450:ILE:HG22	1:D:605:LEU:HD13	1.84	0.59
1:D:472:ILE:HD11	1:D:489:ILE:HG23	1.89	0.55
1:A:727:LEU:HD11	1:A:763:GLU:HG3	1.89	0.53
1:D:496:ARG:NH2	5:D:2031:HOH:O	2.34	0.50
1:A:483:GLU:HA	1:A:486:TRP:CE2	2.49	0.48
1:A:459:LEU:HD13	1:A:487:PRO:HB2	1.96	0.48
1:A:727:LEU:HD13	1:A:766:ILE:HD12	1.95	0.47
1:D:506:GLU:H	1:D:506:GLU:CD	2.18	0.47
1:D:693:TYR:OH	1:D:725:GLY:HA3	2.15	0.46
1:D:572:ASN:HA	1:D:575:LEU:HD12	1.98	0.44
1:D:460:MET:HG2	1:D:505:LEU:HG	2.00	0.44
1:D:627:ARG:O	1:D:631:ILE:HG12	2.17	0.44
1:A:697:TRP:CZ2	1:A:719:LYS:HG2	2.53	0.43
1:D:689:ALA:O	1:D:726:GLN:NE2	2.52	0.43
1:A:675:LEU:O	1:A:678:VAL:HG22	2.19	0.42
1:A:727:LEU:HD11	1:A:763:GLU:CG	2.49	0.42
1:D:638:TYR:CD1	1:D:671:THR:HG21	2.54	0.42
1:A:593:GLN:HG2	1:A:631:ILE:HD11	2.03	0.41
1:A:547:LEU:HD22	1:A:656:LEU:HD22	2.02	0.41
1:D:611:PHE:HB3	1:D:614:LEU:HD12	2.03	0.41
1:D:477:PHE:HB3	1:D:535:HIS:CE1	2.55	0.41
1:A:677:SER:OG	1:A:688:THR:HG21	2.22	0.40
1:A:493:MET:SD	1:A:535:HIS:HA	2.61	0.40
1:A:543:ASN:HB3	1:A:747:PRO:HB2	2.04	0.40

There are no symmetry-related clashes.

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	325/328 (99%)	318 (98%)	6 (2%)	1 (0%)	41	31
1	D	322/328 (98%)	310 (96%)	10 (3%)	2 (1%)	25	15
All	All	647/656 (99%)	628 (97%)	16 (2%)	3 (0%)	29	18

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	577	LYS
1	D	518	ASN
1	A	480	GLY

5.3.2 Protein sidechains [i](#)

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	294/295 (100%)	282 (96%)	12 (4%)	30	21
1	D	292/295 (99%)	278 (95%)	14 (5%)	25	16
All	All	586/590 (99%)	560 (96%)	26 (4%)	28	19

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	461	GLN
1	A	470	LYS
1	A	471	GLU
1	A	587	SER
1	A	588	THR
1	A	597	SER
1	A	616	SER
1	A	620	GLU
1	A	622	VAL
1	A	709	GLN
1	A	773	THR
1	A	774	TRP
1	D	466	VAL

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Mol	Chain	Res	Type
1	D	470	LYS
1	D	521	ARG
1	D	545	HIS
1	D	546	THR
1	D	547	LEU
1	D	585	LEU
1	D	601	SER
1	D	606	GLU
1	D	635	LEU
1	D	642	ARG
1	D	656	LEU
1	D	688	THR
1	D	770	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	598	GLN
1	A	743	GLN
1	D	709	GLN
1	D	724	GLN
1	D	743	GLN
1	D	761	GLN

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 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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
4	F03	A	1777	-	15,16,16	1.57	3 (20%)	20,22,22	3.23	7 (35%)

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
4	F03	A	1777	-	-	0/4/4/4	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1777	F03	C12-C13	3.51	1.44	1.36
4	A	1777	F03	C7-N6	2.72	1.37	1.33
4	A	1777	F03	C5-N4	-2.18	1.36	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1777	F03	C9-C7-N6	-11.59	116.32	124.40
4	A	1777	F03	C7-N6-C5	4.14	122.59	115.18
4	A	1777	F03	C10-C9-C14	3.09	122.05	117.55
4	A	1777	F03	C1-C2-N4	-2.89	110.75	114.98
4	A	1777	F03	C9-C14-N15	-2.79	122.08	123.60
4	A	1777	F03	O3-C2-N4	2.58	126.44	123.04
4	A	1777	F03	C5-N4-C2	-2.37	126.68	130.28

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, 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	328/328 (100%)	0.20	12 (3%) 41 44	20, 34, 61, 72	3 (0%)
1	D	324/328 (98%)	0.80	53 (16%) 1 1	22, 43, 73, 93	3 (0%)
All	All	652/656 (99%)	0.50	65 (9%) 7 8	20, 38, 70, 93	6 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	448	ALA	6.5
1	D	584	ALA	5.6
1	D	452	THR	5.5
1	D	450	ILE	5.4
1	D	585	LEU	5.0
1	D	456	TRP	4.5
1	A	584	ALA	4.4
1	D	579	ASP	4.3
1	D	586	TYR	4.0
1	A	771	THR	3.8
1	A	774	TRP	3.6
1	D	447	ASN	3.6
1	D	559	ALA	3.5
1	D	616	SER	3.5
1	D	769	GLU	3.4
1	D	583	ALA	3.3
1	D	449	SER	3.2
1	D	575	LEU	3.1
1	D	613	THR	3.1
1	D	673	CYS	3.1
1	A	581	PRO	3.0
1	D	588	THR	3.0
1	D	587	SER	3.0
1	D	453	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	560	CYS	2.9
1	D	506	GLU	2.8
1	D	581	PRO	2.8
1	D	606	GLU	2.8
1	A	585	LEU	2.7
1	D	521	ARG	2.7
1	D	461	GLN	2.7
1	A	706	LEU	2.5
1	D	533	VAL	2.5
1	D	561	LEU	2.5
1	D	614	LEU	2.5
1	D	582	LEU	2.4
1	D	457	GLN	2.4
1	D	580	HIS	2.4
1	A	454	GLU	2.4
1	D	630	ILE	2.4
1	D	571	SER	2.4
1	D	454	GLU	2.4
1	A	531	VAL	2.4
1	D	578	PHE	2.3
1	D	696	PHE	2.3
1	D	576	GLN	2.3
1	D	768	GLY	2.2
1	A	532	THR	2.2
1	A	617	SER	2.2
1	D	612	SER	2.2
1	A	773	THR	2.2
1	D	574	TYR	2.1
1	D	609	ASN	2.1
1	D	615	SER	2.1
1	D	545	HIS	2.1
1	A	461	GLN	2.1
1	D	649	TYR	2.1
1	D	611	PHE	2.1
1	D	633	THR	2.0
1	D	532	THR	2.0
1	D	617	SER	2.0
1	D	557	LEU	2.0
1	D	537	MET	2.0
1	D	573	SER	2.0
1	D	770	GLU	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
3	MG	D	1772	1/1	0.92	0.07	31,31,31,31	0
4	F03	A	1777	15/15	0.95	0.12	33,37,39,39	0
3	MG	A	1776	1/1	0.98	0.14	22,22,22,22	0
2	ZN	D	1771	1/1	1.00	0.06	35,35,35,35	0
2	ZN	A	1775	1/1	1.00	0.07	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.