



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:06 AM UTC

PDB ID : 5R9G / pdb_00005r9g
Title : PanDDA analysis group deposition Form1 MAP kinase p38-alpha – Fragment
PC587 in complex with MAP kinase p38-alpha
Authors : De Nicola, G.F.; Nichols, C.E.
Deposited on : 2020-03-04
Resolution : 1.73 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

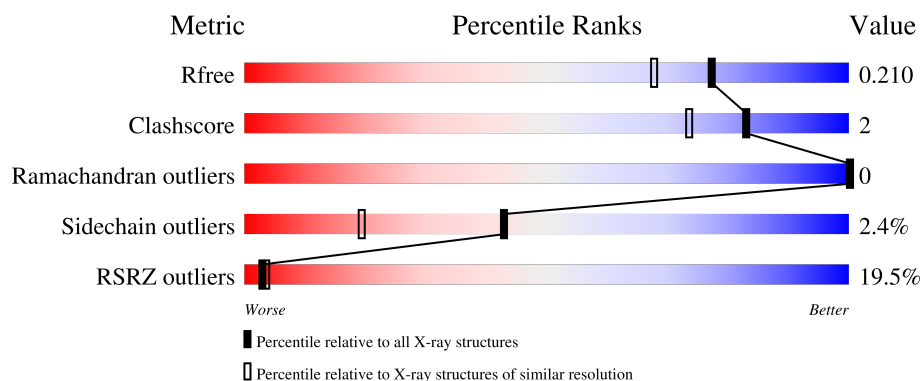
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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}	180053	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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 of 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	360	

2 Entry composition [i](#)

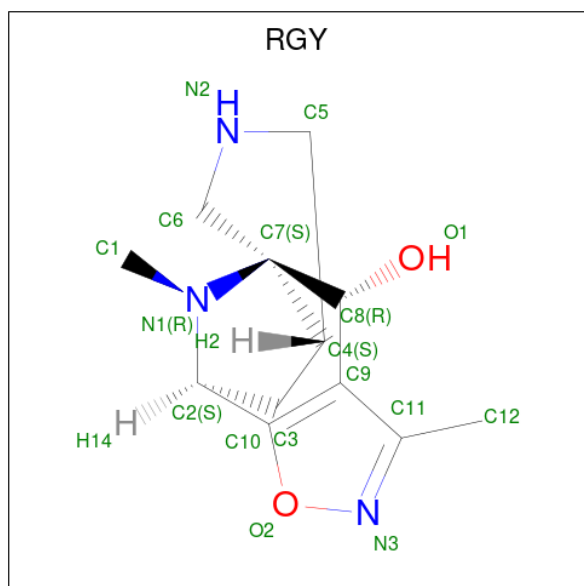
There are 7 unique types of molecules in this entry. The entry contains 3071 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	348	Total	C	N	O	S	0	3	0
			2770	1775	465	515	15			

- Molecule 2 is (4R,4aS,7aS,9S)-3,10-dimethyl-5,6,7,7a,8,9-hexahydro-4H-4a,9-epiminopyrrolo [3',4':5,6]cyclohepta[1,2-d][1,2]oxazol-4-ol (CCD ID: RGY) (formula: C₁₂H₁₇N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			17	12	3	2		

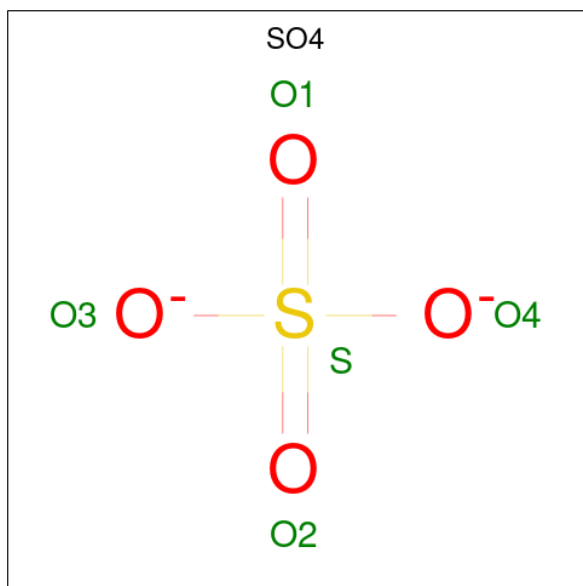
- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	Cl	0	0
			5	5		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

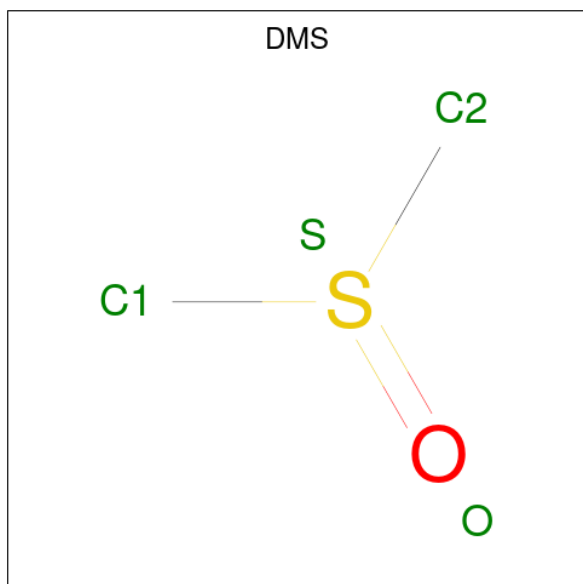
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).

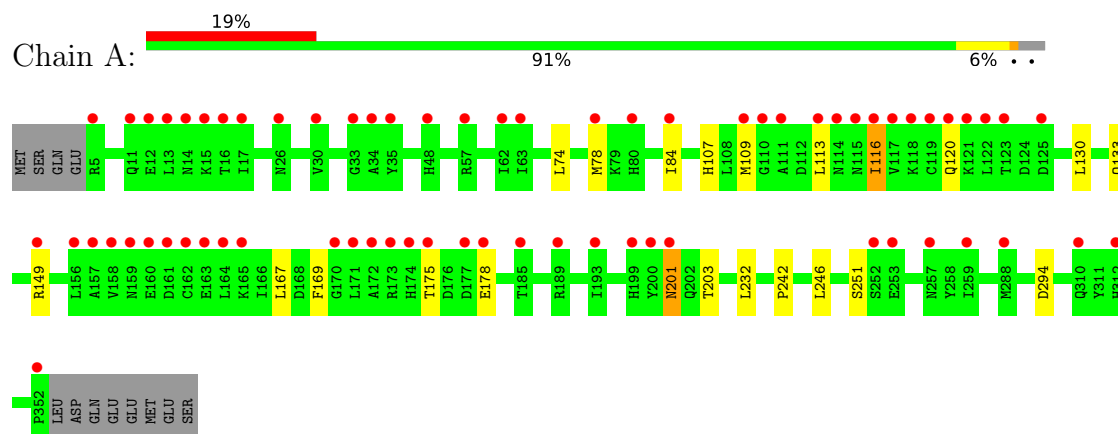


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	269	Total	O	0	0
			269	269		

- Molecule 1: Mitogen-activated protein kinase 14



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.91Å 85.94Å 127.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.34 – 1.73 29.34 – 1.73	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.34-1.73) 99.6 (29.34-1.73)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.176 , 0.195 0.206 , 0.210	Depositor DCC
R_{free} test set	2669 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3071	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% 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: RGY, SO4, CL, DMS, 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	1.37	4/2836 (0.1%)	1.22	1/3859 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	ILE	C-N	24.59	1.64	1.33
1	A	133	GLN	C-O	6.80	1.32	1.24
1	A	130	LEU	C-O	5.29	1.30	1.24
1	A	232	LEU	C-O	5.09	1.30	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	294	ASP	CA-CB-CG	6.79	119.39	112.60

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	2770	0	2690	12	0
2	A	17	0	0	0	0
3	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
5	A	5	0	0	1	0
6	A	4	0	6	0	0
7	A	269	0	0	2	0
All	All	3071	0	2696	13	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 (13) 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)
5:A:408:SO4:O3	7:A:501:HOH:O	2.01	0.78
1:A:78[B]:MET:HE3	1:A:169:PHE:CZ	2.28	0.68
1:A:84:ILE:HD13	1:A:109:MET:HE3	1.85	0.59
1:A:201:ASN:HD22	1:A:201:ASN:C	2.14	0.54
1:A:74:LEU:HD13	1:A:74:LEU:C	2.36	0.50
1:A:175:THR:HG22	1:A:178:GLU:CG	2.43	0.48
1:A:242:PRO:HB3	1:A:246:LEU:HD23	1.94	0.48
1:A:107:HIS:HD2	7:A:534:HOH:O	1.95	0.48
1:A:84:ILE:CD1	1:A:109:MET:HE3	2.44	0.46
1:A:201:ASN:HD22	1:A:203:THR:H	1.67	0.41
1:A:78[B]:MET:HE3	1:A:169:PHE:CE2	2.55	0.41
1:A:201:ASN:ND2	1:A:203:THR:OG1	2.54	0.41
1:A:175:THR:HG23	1:A:178:GLU:H	1.85	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	349/360 (97%)	339 (97%)	10 (3%)	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	294/319 (92%)	287 (98%)	7 (2%)	43	19

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	LEU
1	A	116	ILE
1	A	120	GLN
1	A	149	ARG
1	A	167	LEU
1	A	201	ASN
1	A	251	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	HIS
1	A	60	GLN
1	A	77	HIS
1	A	128	GLN
1	A	201	ASN
1	A	202	GLN
1	A	272	ASN
1	A	310	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\# Z > 2$
6	DMS	A	409	-	3,3,3	0.29	0	3,3,3	0.10	0
5	SO4	A	408	-	4,4,4	0.26	0	6,6,6	0.22	0
2	RGY	A	401	-	15,20,20	1.92	6 (40%)	12,33,33	2.05	5 (41%)

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	RGY	A	401	-	-	-	0/5/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	RGY	O2-N3	-3.87	1.35	1.42
2	A	401	RGY	C9-C10	3.75	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	RGY	C11-N3	2.60	1.36	1.30
2	A	401	RGY	C1-N1	2.28	1.49	1.46
2	A	401	RGY	O2-C10	2.22	1.37	1.34
2	A	401	RGY	C7-N1	2.03	1.52	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	RGY	C9-C11-N3	-3.87	108.45	112.13
2	A	401	RGY	C5-N2-C6	3.27	113.58	105.45
2	A	401	RGY	C12-C11-N3	2.60	124.37	119.86
2	A	401	RGY	O1-C8-C7	-2.52	107.92	111.73
2	A	401	RGY	O2-N3-C11	2.49	108.79	106.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	408	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	116:ILE	C	117:VAL	N	1.64

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	348/360 (96%)	1.66	68 (19%) 3 3	2, 24, 49, 83	33 (9%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	117	VAL	21.4
1	A	123	THR	17.9
1	A	156	LEU	17.3
1	A	122	LEU	16.7
1	A	113	LEU	16.5
1	A	164	LEU	16.0
1	A	116	ILE	15.7
1	A	157	ALA	15.5
1	A	119	CYS	15.5
1	A	175	THR	14.8
1	A	80	HIS	14.3
1	A	162	CYS	14.3
1	A	114	ASN	14.3
1	A	125[A]	ASP	14.2
1	A	158	VAL	14.1
1	A	118	LYS	13.8
1	A	312	HIS	13.2
1	A	78[A]	MET	13.0
1	A	115	ASN	13.0
1	A	177	ASP	12.9
1	A	171	LEU	12.8
1	A	121	LYS	11.9
1	A	165	LYS	11.3
1	A	120	GLN	11.2
1	A	174	HIS	10.5
1	A	161	ASP	9.9
1	A	159	ASN	9.8

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Mol	Chain	Res	Type	RSRZ
1	A	172	ALA	9.6
1	A	149	ARG	9.5
1	A	163	GLU	9.5
1	A	160	GLU	9.4
1	A	173	ARG	7.2
1	A	288[A]	MET	6.7
1	A	13	LEU	5.6
1	A	109	MET	4.5
1	A	33	GLY	4.2
1	A	178	GLU	4.1
1	A	110	GLY	4.1
1	A	34	ALA	4.0
1	A	14	ASN	3.8
1	A	16	THR	3.3
1	A	30	VAL	3.3
1	A	252	SER	3.0
1	A	352	PRO	2.8
1	A	17	ILE	2.8
1	A	111	ALA	2.7
1	A	200	TYR	2.7
1	A	63	ILE	2.6
1	A	257	ASN	2.5
1	A	170	GLY	2.5
1	A	48	HIS	2.5
1	A	26	ASN	2.5
1	A	201	ASN	2.5
1	A	193	ILE	2.5
1	A	259	ILE	2.5
1	A	11	GLN	2.4
1	A	253	GLU	2.4
1	A	199	HIS	2.4
1	A	62	ILE	2.3
1	A	189	ARG	2.3
1	A	310	GLN	2.3
1	A	185	THR	2.3
1	A	15	LYS	2.2
1	A	12	GLU	2.1
1	A	35	TYR	2.1
1	A	84	ILE	2.1
1	A	57	ARG	2.0
1	A	5	ARG	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	RGY	A	401	17/17	0.64	0.34	38,39,40,41	17
6	DMS	A	409	4/4	0.72	0.25	73,77,79,87	0
5	SO4	A	408	5/5	0.86	0.15	52,56,61,82	0
3	CL	A	404	1/1	0.95	0.12	50,50,50,50	0
3	CL	A	405	1/1	0.97	0.13	38,38,38,38	0
4	MG	A	407	1/1	0.97	0.20	31,31,31,31	0
3	CL	A	402	1/1	0.98	0.24	43,43,43,43	0
3	CL	A	403	1/1	0.98	0.10	42,42,42,42	0
3	CL	A	406	1/1	0.98	0.12	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.