



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:26 PM UTC

PDB ID : 5R8X / pdb_00005r8x
Title : PanDDA analysis group deposition Form1 MAP kinase p38-alpha – Fragment N11396a 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

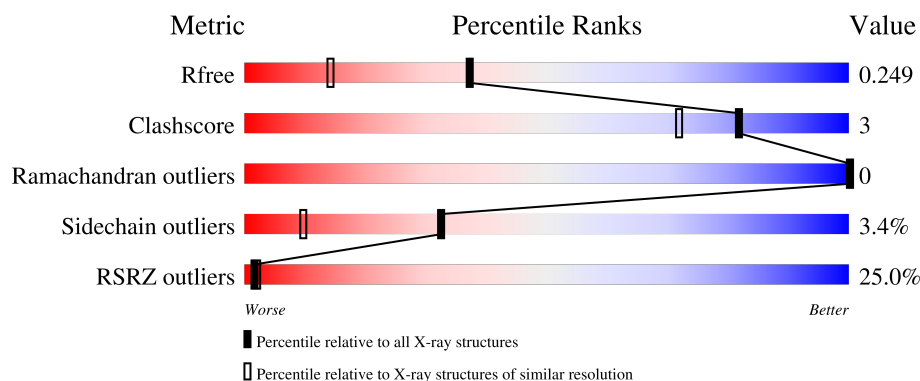
1 Overall quality at a glance

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	24% 89% 7%

2 Entry composition [i](#)

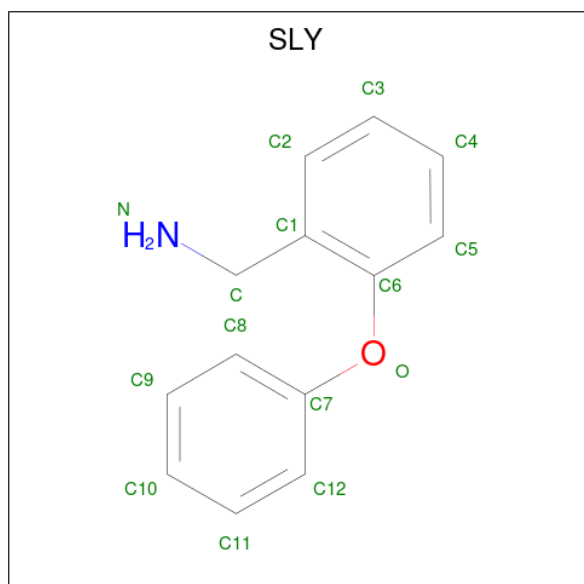
There are 7 unique types of molecules in this entry. The entry contains 3066 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	4	0
			2781	1781	469	516	15			

- Molecule 2 is (2-phenoxyphenyl)methanamine (CCD ID: SLY) (formula: C₁₃H₁₃NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	13	1	1		

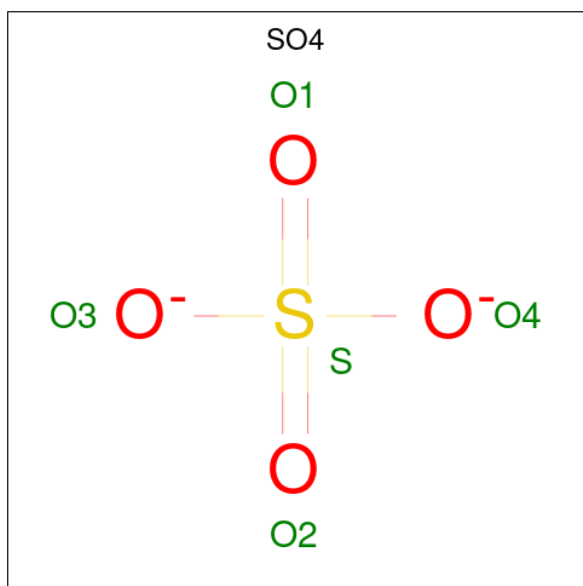
- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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).

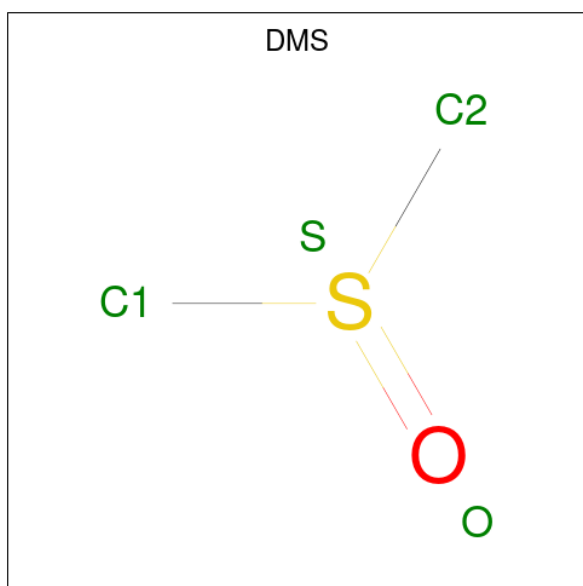
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- 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		

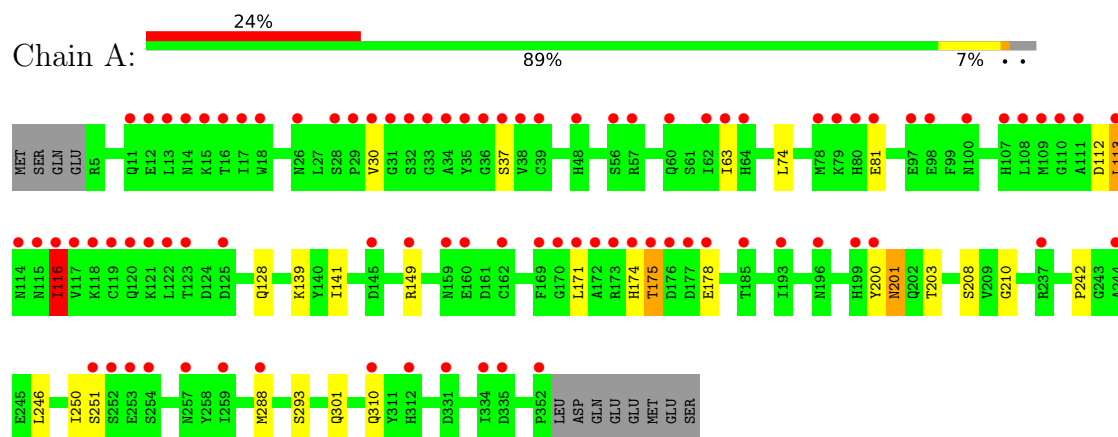
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	255	Total	O	0	0
			255	255		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: 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 86.61Å 127.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.65 – 1.73 71.65 – 1.73	Depositor EDS
% Data completeness (in resolution range)	96.2 (71.65-1.73) 96.2 (71.65-1.73)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.219 , 0.249 (Not available) , 0.249	Depositor DCC
R_{free} test set	2671 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	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	0.92	EDS
Total number of atoms	3066	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CL, DMS, SO4, SLY

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	1.20	5/2847 (0.2%)	1.30	4/3873 (0.1%)

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	A	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	ILE	C-N	6.49	1.42	1.33
1	A	301	GLN	C-O	6.07	1.31	1.24
1	A	141	ILE	C-O	5.70	1.30	1.24
1	A	139	LYS	C-O	5.38	1.30	1.24
1	A	208	SER	C-O	5.10	1.30	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	116	ILE	CA-C-N	-9.56	104.76	121.97
1	A	116	ILE	C-N-CA	-9.56	104.76	121.97
1	A	250	ILE	CA-C-N	5.58	127.76	120.28
1	A	250	ILE	C-N-CA	5.58	127.76	120.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	116	ILE	Mainchain

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	2781	0	2702	14	0
2	A	15	0	0	0	0
3	A	5	0	0	0	0
4	A	1	0	0	0	0
5	A	5	0	0	0	0
6	A	4	0	6	0	0
7	A	255	0	0	2	0
All	All	3066	0	2708	14	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 3.

All (14) 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:A:149[A]:ARG:NH1	1:A:200:TYR:OH	2.28	0.67
1:A:128:GLN:NE2	1:A:310:GLN:OE1	2.36	0.58
1:A:175:THR:HG22	1:A:178:GLU:H	1.69	0.56
1:A:201:ASN:HD22	1:A:201:ASN:C	2.13	0.55
1:A:81:GLU:HG3	7:A:647:HOH:O	2.12	0.49
1:A:112:ASP:OD1	1:A:112:ASP:C	2.56	0.49
1:A:175:THR:CG2	1:A:178:GLU:H	2.26	0.48
1:A:201:ASN:HB2	7:A:658:HOH:O	2.13	0.48
1:A:210:GLY:HA2	1:A:288[B]:MET:HE3	1.98	0.45
1:A:201:ASN:HD22	1:A:203:THR:H	1.64	0.44
1:A:203:THR:OG1	1:A:293:SER:HB2	2.17	0.44
1:A:242:PRO:HB3	1:A:246:LEU:HD23	2.00	0.44
1:A:113:LEU:HD23	1:A:116:ILE:HG12	2.01	0.41
1:A:74:LEU:HD13	1:A:74:LEU:C	2.47	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	350/360 (97%)	342 (98%)	8 (2%)	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%)	285 (97%)	10 (3%)	32	10

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	VAL
1	A	37	SER
1	A	63	ILE
1	A	113	LEU
1	A	116	ILE
1	A	171	LEU
1	A	174	HIS
1	A	175	THR
1	A	201	ASN
1	A	251	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	A	115	ASN
1	A	120	GLN
1	A	128	GLN
1	A	174	HIS
1	A	199	HIS
1	A	201	ASN
1	A	202	GLN
1	A	272	ASN
1	A	310	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	0.21	0	3,3,3	0.08	0
2	SLY	A	401	-	16,16,16	0.84	0	20,20,20	0.85	0
5	SO4	A	408	-	4,4,4	0.43	0	6,6,6	0.29	0

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	SLY	A	401	-	-	1/6/6/6	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	SLY	N-C-C1-C2

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	348/360 (96%)	1.96	87 (25%) 2 2	4, 20, 39, 51	51 (14%)

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	116	ILE	17.4
1	A	34	ALA	16.4
1	A	17	ILE	15.6
1	A	13	LEU	15.4
1	A	35	TYR	15.3
1	A	30	VAL	15.3
1	A	38	VAL	12.8
1	A	33	GLY	12.8
1	A	175	THR	12.7
1	A	31	GLY	12.5
1	A	14	ASN	12.4
1	A	16	THR	12.4
1	A	18	TRP	12.4
1	A	172	ALA	11.8
1	A	171	LEU	11.3
1	A	111	ALA	11.2
1	A	39	CYS	11.1
1	A	29	PRO	10.9
1	A	123	THR	10.8
1	A	115	ASN	10.6
1	A	36	GLY	10.5
1	A	32	SER	10.4
1	A	122	LEU	10.4
1	A	28	SER	9.9
1	A	169	PHE	9.8
1	A	149[A]	ARG	9.7
1	A	37	SER	9.6

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Mol	Chain	Res	Type	RSRZ
1	A	114	ASN	9.5
1	A	110	GLY	9.3
1	A	174	HIS	9.3
1	A	312	HIS	9.2
1	A	11	GLN	9.1
1	A	15	LYS	9.1
1	A	176	ASP	9.0
1	A	12	GLU	8.9
1	A	173	ARG	8.6
1	A	109	MET	8.2
1	A	125[A]	ASP	8.0
1	A	107	HIS	7.8
1	A	80	HIS	7.6
1	A	121	LYS	7.5
1	A	117	VAL	7.3
1	A	79	LYS	7.1
1	A	310	GLN	6.9
1	A	78[A]	MET	6.7
1	A	120	GLN	6.3
1	A	288[A]	MET	6.3
1	A	170	GLY	5.9
1	A	119	CYS	5.5
1	A	81	GLU	5.5
1	A	199	HIS	4.8
1	A	352	PRO	4.5
1	A	48	HIS	4.5
1	A	200	TYR	4.4
1	A	118	LYS	4.1
1	A	251	SER	3.9
1	A	334	ILE	3.9
1	A	331	ASP	3.9
1	A	56	SER	3.7
1	A	160	GLU	3.5
1	A	113	LEU	3.5
1	A	335	ASP	3.5
1	A	178	GLU	3.5
1	A	196	ASN	3.4
1	A	193	ILE	3.2
1	A	145	ASP	3.1
1	A	64	HIS	3.1
1	A	259	ILE	3.1
1	A	162	CYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	253	GLU	2.9
1	A	63	ILE	2.8
1	A	60	GLN	2.8
1	A	97	GLU	2.7
1	A	177	ASP	2.7
1	A	252	SER	2.6
1	A	100	ASN	2.6
1	A	57	ARG	2.6
1	A	159	ASN	2.5
1	A	185	THR	2.5
1	A	26	ASN	2.4
1	A	98	GLU	2.3
1	A	244	ALA	2.3
1	A	108	LEU	2.2
1	A	62	ILE	2.2
1	A	237	ARG	2.2
1	A	257	ASN	2.1
1	A	254	SER	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(Å ²)	Q<0.9
4	MG	A	407	1/1	0.67	0.19	58,58,58,58	0
2	SLY	A	401	15/15	0.72	0.25	29,30,31,32	15
6	DMS	A	409	4/4	0.84	0.32	93,97,99,103	0
5	SO4	A	408	5/5	0.89	0.14	44,45,48,51	0
3	CL	A	402	1/1	0.93	0.20	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CL	A	404	1/1	0.95	0.12	45,45,45,45	0
3	CL	A	403	1/1	0.98	0.08	38,38,38,38	0
3	CL	A	405	1/1	0.98	0.17	38,38,38,38	0
3	CL	A	406	1/1	0.98	0.11	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.