



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 06:20 PM UTC

PDB ID : 7LT1 / pdb_00007lt1
Title : Structure of the cGAS-like receptor human MB21D2
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Deposited on : 2021-02-18
Resolution : 2.40 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

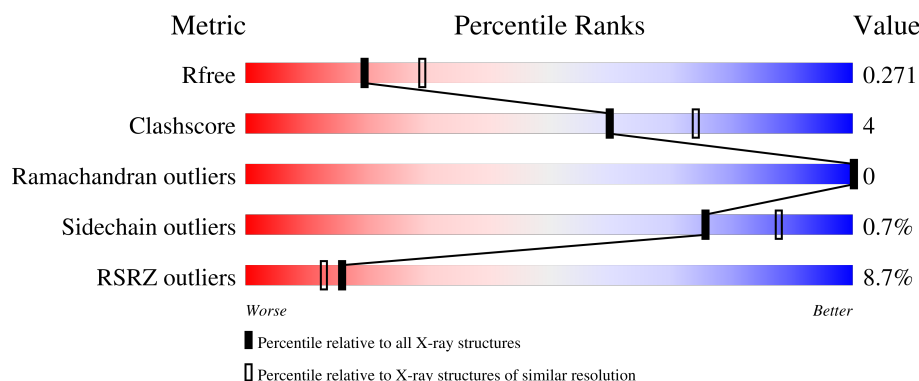
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	464	
1	B	464	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	502	-	-	X	-

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6413 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.

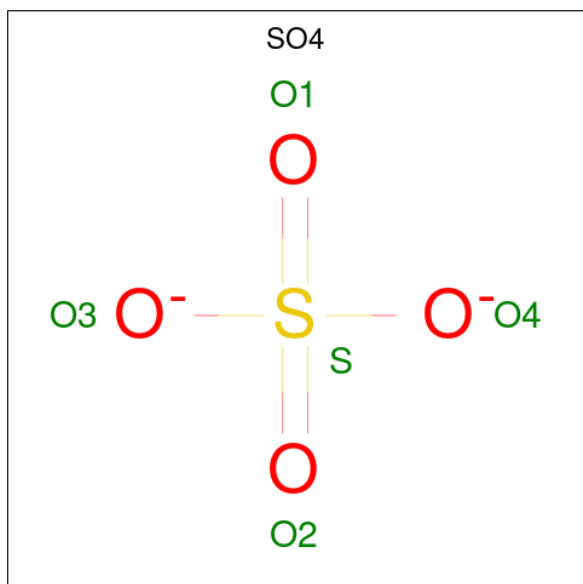
- Molecule 1 is a protein called Protein MB21D2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	Se	0	0	0
			3240	2067	556	594	10	13			
1	B	393	Total	C	N	O	S	Se	0	0	0
			3158	2016	543	576	10	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	SER	-	expression tag	UNP Q8IYB1
B	28	SER	-	expression tag	UNP Q8IYB1

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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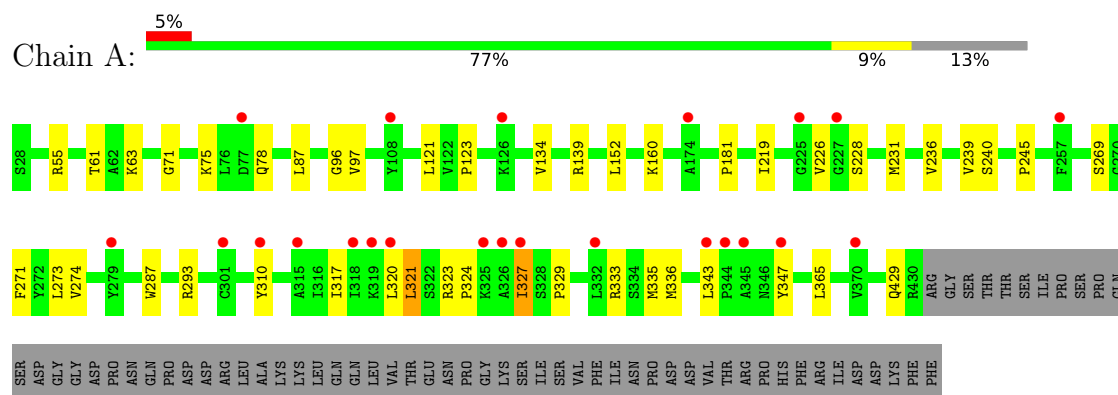
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

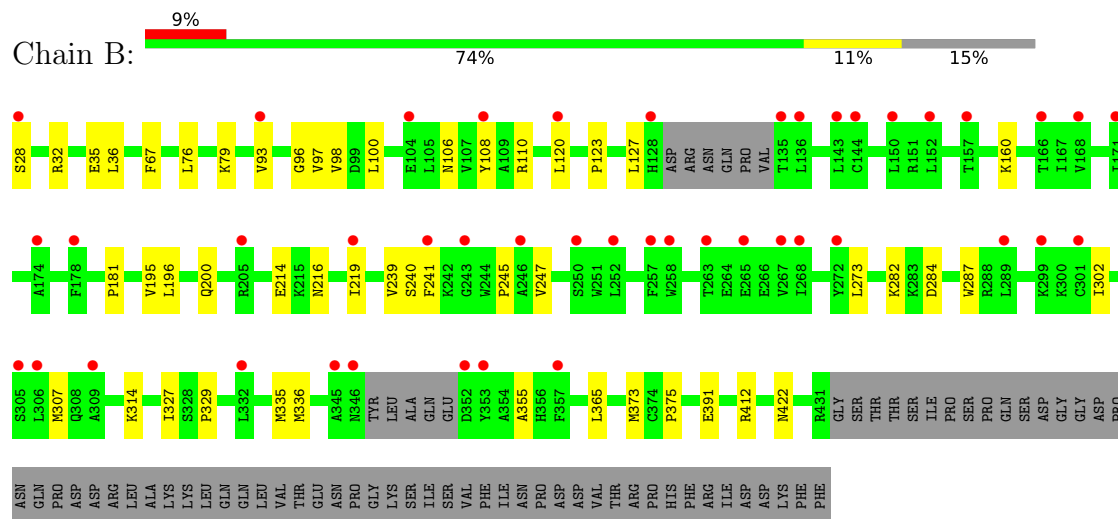
3 Residue-property plots

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: Protein MB21D2



• Molecule 1: Protein MB21D2



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.17Å 127.82Å 198.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.13 – 2.40 46.13 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (46.13-2.40) 99.4 (46.13-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874, PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.247 , 0.267 0.251 , 0.271	Depositor DCC
R_{free} test set	2000 reflections (3.94%)	wwPDB-VP
Wilson B-factor (Å ²)	58.2	Xtriage
Anisotropy	0.742	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6413	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: SO4

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	0.09	0/3299	0.26	0/4441
1	B	0.09	0/3213	0.25	0/4319
All	All	0.09	0/6512	0.25	0/8760

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	3240	0	3243	28	0
1	B	3158	0	3168	27	0
2	A	10	0	0	4	0
2	B	5	0	0	0	0
All	All	6413	0	6411	55	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 4.

All (55) 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:373:MSE:HE3	1:B:375:PRO:HG3	1.77	0.66
1:B:106:ASN:ND2	1:B:216:ASN:OD1	2.32	0.63
1:B:35:GLU:OE2	1:B:412:ARG:NH2	2.33	0.61
1:B:97:VAL:HG23	1:B:98:VAL:HG23	1.83	0.60
1:A:63:LYS:NZ	2:A:502:SO4:O4	2.34	0.60
1:B:110:ARG:NH1	1:B:422:ASN:OD1	2.34	0.60
1:A:139:ARG:NH2	2:A:501:SO4:O2	2.35	0.60
1:A:97:VAL:HG13	1:A:333:ARG:HH22	1.68	0.59
1:B:239:VAL:HB	1:B:273:LEU:HB2	1.83	0.58
1:B:282:LYS:HE2	1:B:284:ASP:HB2	1.86	0.58
1:B:314:LYS:HD2	1:B:329:PRO:HB3	1.86	0.56
1:B:108:TYR:OH	1:B:214:GLU:OE1	2.24	0.56
1:A:335:MSE:HE1	1:A:365:LEU:HD13	1.89	0.55
1:B:96:GLY:HA3	1:B:329:PRO:HB2	1.89	0.55
1:A:320:LEU:HD12	1:A:321:LEU:HD13	1.89	0.54
1:A:87:LEU:HD23	1:A:121:LEU:HD12	1.89	0.54
1:B:67:PHE:HE1	1:B:120:LEU:HD11	1.73	0.54
1:A:63:LYS:NZ	2:A:502:SO4:S	2.80	0.54
1:A:96:GLY:HA3	1:A:329:PRO:HB2	1.89	0.54
1:B:93:VAL:HG21	1:B:219:ILE:HD13	1.91	0.52
1:A:269:SER:OG	1:A:293:ARG:NH2	2.43	0.51
1:A:219:ILE:HD12	1:A:236:VAL:HG22	1.92	0.51
1:B:100:LEU:HD13	1:B:219:ILE:HD11	1.93	0.50
1:A:343:LEU:HD21	1:A:347:TYR:CD2	2.47	0.50
1:B:327:ILE:HG21	1:B:365:LEU:HD11	1.93	0.49
1:A:123:PRO:HB3	1:A:240:SER:HB2	1.94	0.49
1:A:134:VAL:HB	1:A:152:LEU:HD12	1.95	0.49
1:B:335:MSE:HE1	1:B:365:LEU:HB2	1.95	0.49
1:A:228:SER:HB2	1:A:429:GLN:HA	1.94	0.48
1:B:181:PRO:HG3	1:B:287:TRP:CE2	2.48	0.48
1:A:323:ARG:HE	1:A:324:PRO:HA	1.80	0.47
1:B:196:LEU:O	1:B:200:GLN:HG2	2.15	0.47
1:A:239:VAL:HB	1:A:273:LEU:HB2	1.97	0.46
1:B:391:GLU:OE1	1:B:391:GLU:N	2.43	0.46
1:A:317:ILE:O	1:A:321:LEU:HB2	2.16	0.46
1:A:78:GLN:O	1:A:160:LYS:HD2	2.17	0.45
1:B:302:ILE:HG21	1:B:336:MSE:HE2	1.98	0.45
1:A:71:GLY:O	1:A:75:LYS:HG2	2.18	0.44
1:A:343:LEU:HD21	1:A:347:TYR:CE2	2.53	0.43
1:A:343:LEU:HD11	1:A:347:TYR:CD2	2.53	0.43
1:A:245:PRO:HG3	1:A:271:PHE:CG	2.53	0.43
1:A:321:LEU:HD23	1:A:327:ILE:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:THR:HB	1:A:226:VAL:HG11	2.00	0.43
1:A:63:LYS:NZ	2:A:502:SO4:O2	2.34	0.43
1:B:76:LEU:HD22	1:B:195:VAL:HG23	2.01	0.42
1:B:245:PRO:C	1:B:247:VAL:H	2.27	0.42
1:B:28:SER:HB2	1:B:32:ARG:NH2	2.34	0.42
1:B:79:LYS:NZ	1:B:160:LYS:O	2.36	0.42
1:B:36:LEU:HD23	1:B:355:ALA:HB1	2.02	0.42
1:B:123:PRO:HB3	1:B:240:SER:HB2	2.00	0.41
1:B:302:ILE:HD12	1:B:307:MSE:HE1	2.03	0.41
1:A:181:PRO:HG3	1:A:287:TRP:CE2	2.56	0.41
1:B:127:LEU:HD12	1:B:241:PHE:CZ	2.55	0.41
1:A:310:TYR:HB2	1:A:336:MSE:HG3	2.02	0.40
1:A:321:LEU:HB3	1:A:327:ILE:HG22	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	401/464 (86%)	395 (98%)	6 (2%)	0	100	100
1	B	387/464 (83%)	375 (97%)	12 (3%)	0	100	100
All	All	788/928 (85%)	770 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	359/402 (89%)	354 (99%)	5 (1%)	59	79
1	B	350/402 (87%)	350 (100%)	0	100	100
All	All	709/804 (88%)	704 (99%)	5 (1%)	76	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ARG
1	A	231	MSE
1	A	274	VAL
1	A	321	LEU
1	A	327	ILE

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

Mol	Chain	Res	Type
1	A	140	HIS
1	A	255	ASN
1	A	396	HIS
1	A	410	HIS
1	B	106	ASN
1	B	204	GLN
1	B	356	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	A	501	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	B	501	-	4,4,4	0.24	0	6,6,6	0.08	0

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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	SO4	3	0
2	A	501	SO4	1	0

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	390/464 (84%)	0.78	23 (5%) 28 24	66, 88, 117, 139	0
1	B	380/464 (81%)	0.89	44 (11%) 9 7	74, 100, 142, 166	0
All	All	770/928 (82%)	0.83	67 (8%) 16 13	66, 94, 131, 166	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	TYR	4.8
1	A	344	PRO	3.9
1	B	301	CYS	3.8
1	A	77	ASP	3.4
1	B	306	LEU	3.4
1	A	347	TYR	3.3
1	A	345	ALA	3.3
1	B	346	ASN	3.3
1	A	327	ILE	3.2
1	B	171	ILE	3.2
1	B	309	ALA	3.0
1	B	267	VAL	3.0
1	B	357	PHE	3.0
1	A	318	ILE	2.9
1	B	150	LEU	2.8
1	A	343	LEU	2.8
1	B	345	ALA	2.8
1	A	319	LYS	2.8
1	B	299	LYS	2.7
1	B	257	PHE	2.7
1	B	258	TRP	2.7
1	B	289	LEU	2.7
1	B	143	LEU	2.7
1	B	250	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	370	VAL	2.6
1	B	241	PHE	2.6
1	B	268	ILE	2.6
1	B	93	VAL	2.6
1	B	305	SER	2.6
1	B	135	THR	2.6
1	B	263	THR	2.6
1	B	243	GLY	2.5
1	B	128	HIS	2.5
1	B	104	GLU	2.5
1	A	320	LEU	2.4
1	A	326	ALA	2.4
1	B	219	ILE	2.4
1	B	332	LEU	2.4
1	B	174	ALA	2.4
1	A	310	TYR	2.4
1	B	28	SER	2.4
1	B	144	CYS	2.4
1	B	252	LEU	2.3
1	B	272	TYR	2.3
1	B	108	TYR	2.3
1	A	325	LYS	2.3
1	A	315	ALA	2.2
1	A	225	GLY	2.2
1	B	205	ARG	2.2
1	A	257	PHE	2.2
1	B	157	THR	2.2
1	A	174	ALA	2.1
1	A	108	TYR	2.1
1	B	178	PHE	2.1
1	B	265	GLU	2.1
1	A	301	CYS	2.1
1	A	227	GLY	2.1
1	B	136	LEU	2.1
1	B	152	LEU	2.1
1	A	126	LYS	2.1
1	B	352	ASP	2.1
1	B	168	VAL	2.0
1	A	279	TYR	2.0
1	A	332	LEU	2.0
1	B	120	LEU	2.0
1	B	246	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	166	THR	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	SO4	A	502	5/5	0.51	0.11	132,136,151,174	0
2	SO4	B	501	5/5	0.61	0.10	112,126,136,150	0
2	SO4	A	501	5/5	0.90	0.08	97,112,114,130	0

6.5 Other polymers [i](#)

There are no such residues in this entry.