



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:18 PM UTC

PDB ID : 2A0U / pdb_00002a0u
Title : Crystal structure of the eukaryotic initiation factor 2B from Leishmania major at 2.1 Å resolution
Authors : Bosch, J.; Hol, W.G.J.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)
Deposited on : 2005-06-17
Resolution : 2.10 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

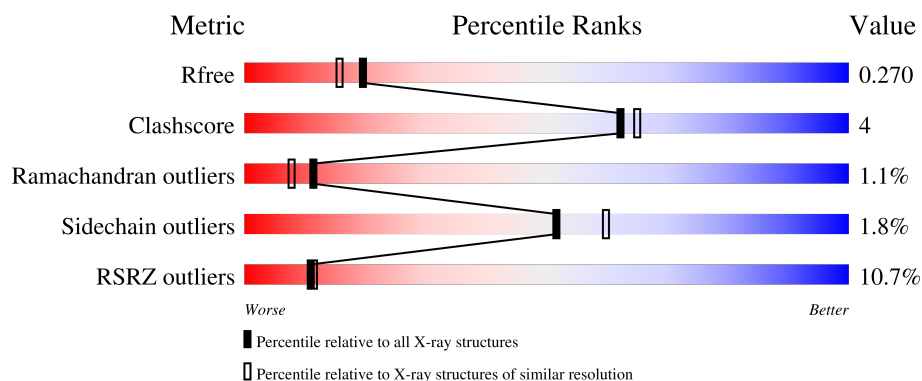
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

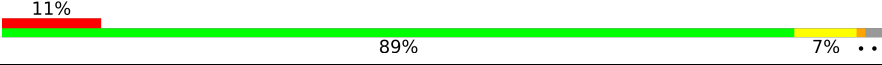
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	383	 11% 89% 7% ..
1	B	383	 9% 87% 8% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5968 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 initiation factor 2B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	Se	0	1	0
			2831	1782	494	543	8	4			
1	B	367	Total	C	N	O	S	Se	0	1	0
			2779	1750	482	535	8	4			

- 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		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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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		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

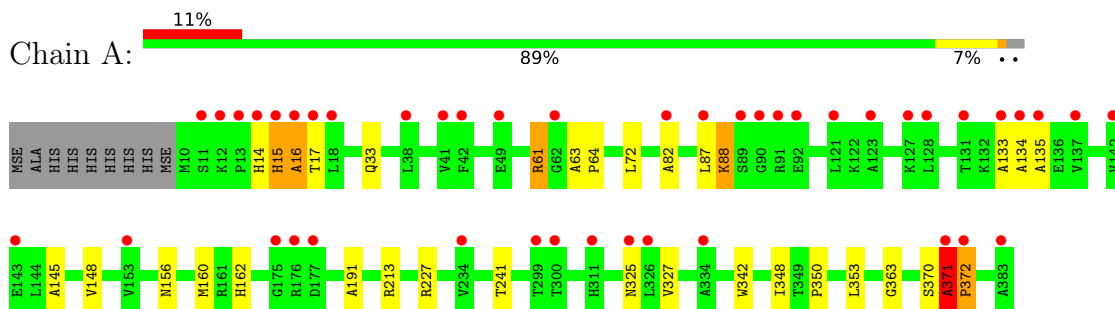
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	159	Total	O	0	0
			159	159		
3	B	149	Total	O	0	0
			149	149		

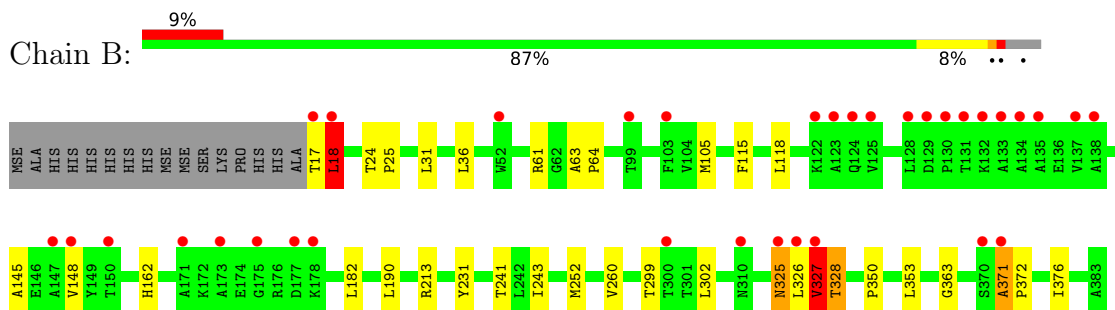
3 Residue-property plots

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: initiation factor 2B



• Molecule 1: initiation factor 2B



4 Data and refinement statistics

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.73Å 164.57Å 172.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.30 – 2.10 15.30 – 2.10	Depositor EDS
% Data completeness (in resolution range)	85.4 (15.30-2.10) 85.4 (15.30-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.214 , 0.264 0.218 , 0.270	Depositor DCC
R_{free} test set	1851 reflections (3.72%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5968	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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	0.46	0/2876	0.85	4/3907 (0.1%)
1	B	0.45	0/2821	0.80	0/3832
All	All	0.45	0/5697	0.82	4/7739 (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	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	THR	CA-C-N	6.47	133.36	121.70
1	A	17	THR	C-N-CA	6.47	133.36	121.70
1	A	17	THR	N-CA-C	-6.29	100.99	110.24
1	A	16	ALA	N-CA-C	5.12	117.58	109.96

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	ALA	Peptide
1	A	371	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	B	17	THR	Peptide
1	B	327	VAL	Peptide

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	2831	0	2870	23	0
1	B	2779	0	2824	24	0
2	A	25	0	0	1	0
2	B	25	0	0	0	0
3	A	159	0	0	0	0
3	B	149	0	0	0	0
All	All	5968	0	5694	46	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 (46) 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:87:LEU:HA	1:A:88:LYS:CB	1.78	1.11
1:B:371:ALA:HB1	1:B:372:PRO:HD2	1.31	1.06
1:A:87:LEU:CA	1:A:88:LYS:HB2	1.90	1.01
1:A:87:LEU:HA	1:A:88:LYS:HB2	0.97	0.97
1:B:252:MSE:HE1	1:B:260:VAL:CG2	2.06	0.85
1:B:371:ALA:HB1	1:B:372:PRO:CD	2.12	0.79
1:B:182:LEU:HD23	1:B:252:MSE:HE3	1.64	0.79
1:A:371:ALA:HB1	1:A:372:PRO:HD2	1.67	0.77
1:B:18:LEU:O	1:B:18:LEU:HG	1.95	0.67
1:B:252:MSE:HE1	1:B:260:VAL:HG21	1.75	0.66
1:B:371:ALA:CB	1:B:372:PRO:HD2	2.19	0.65
1:A:371:ALA:HB1	1:A:372:PRO:CD	2.26	0.65
1:A:61:ARG:HH12	1:A:191:ALA:HB2	1.64	0.62
1:A:87:LEU:CA	1:A:88:LYS:CB	2.61	0.61
1:B:252:MSE:CE	1:B:260:VAL:CG2	2.78	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:LEU:HD21	1:B:36:LEU:HD11	1.88	0.55
1:A:82:ALA:HA	1:A:87:LEU:O	2.08	0.54
1:B:18:LEU:HD13	1:B:231:TYR:CE2	2.44	0.53
1:A:133:ALA:O	1:A:135:ALA:N	2.41	0.52
1:B:63:ALA:HB3	1:B:64:PRO:HD3	1.92	0.52
1:B:213:ARG:HD3	1:B:241:THR:OG1	2.09	0.52
1:B:252:MSE:CE	1:B:260:VAL:HG22	2.39	0.52
1:A:213:ARG:HD3	1:A:241:THR:OG1	2.11	0.51
1:A:33:GLN:O	1:A:227:ARG:NH2	2.45	0.49
1:A:61:ARG:HD2	2:A:402:SO4:O1	2.13	0.48
1:A:63:ALA:HB3	1:A:64:PRO:HD3	1.94	0.48
1:B:299:THR:HA	1:B:302:LEU:HD13	1.96	0.47
1:A:145:ALA:O	1:A:148:VAL:HG22	2.16	0.46
1:B:162:HIS:CG	1:B:363:GLY:HA2	2.51	0.46
1:A:61:ARG:NH1	1:A:191:ALA:HB2	2.29	0.45
1:A:371:ALA:CB	1:A:372:PRO:HD2	2.42	0.45
1:A:370:SER:O	1:A:371:ALA:O	2.35	0.45
1:A:156:ASN:O	1:A:160:MSE:HG3	2.17	0.44
1:B:105:MSE:HE3	1:B:115:PHE:HD2	1.81	0.44
1:A:342:TRP:HB3	1:B:243:ILE:HG22	1.98	0.44
1:A:162:HIS:CG	1:A:363:GLY:HA2	2.53	0.44
1:A:350:PRO:HD2	1:A:353:LEU:HD12	2.00	0.43
1:A:14:HIS:O	1:A:15:HIS:CD2	2.72	0.43
1:B:145:ALA:O	1:B:148:VAL:HG22	2.18	0.42
1:B:371:ALA:CB	1:B:372:PRO:CD	2.86	0.42
1:B:327:VAL:O	1:B:328:THR:CB	2.68	0.42
1:A:325:ASN:C	1:A:327:VAL:H	2.27	0.41
1:B:325:ASN:C	1:B:325:ASN:HD22	2.29	0.41
1:B:350:PRO:HD2	1:B:353:LEU:HD12	2.03	0.41
1:B:24:THR:O	1:B:25:PRO:C	2.64	0.40
1:B:105:MSE:HG3	1:B:118:LEU:HD12	2.04	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	373/383 (97%)	355 (95%)	14 (4%)	4 (1%)	11	8
1	B	366/383 (96%)	351 (96%)	11 (3%)	4 (1%)	11	8
All	All	739/766 (96%)	706 (96%)	25 (3%)	8 (1%)	11	8

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	LYS
1	A	371	ALA
1	A	372	PRO
1	B	18	LEU
1	B	327	VAL
1	B	328	THR
1	B	371	ALA
1	A	134	ALA

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	301/302 (100%)	297 (99%)	4 (1%)	61	69
1	B	296/302 (98%)	289 (98%)	7 (2%)	43	49
All	All	597/604 (99%)	586 (98%)	11 (2%)	51	60

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	61	ARG
1	A	72	LEU
1	A	348	ILE
1	B	18	LEU

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Mol	Chain	Res	Type
1	B	61	ARG
1	B	190	LEU
1	B	325	ASN
1	B	326	LEU
1	B	327	VAL
1	B	376	ILE

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

Mol	Chain	Res	Type
1	A	281	ASN
1	A	289	HIS
1	B	275	ASN
1	B	289	HIS
1	B	311	HIS
1	B	325	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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	B	409	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	A	403	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	A	404	-	4,4,4	0.25	0	6,6,6	0.05	0
2	SO4	A	402	-	4,4,4	0.23	0	6,6,6	0.10	0
2	SO4	A	401	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	B	407	-	4,4,4	0.27	0	6,6,6	0.10	0
2	SO4	B	406	-	4,4,4	0.25	0	6,6,6	0.11	0
2	SO4	B	408	-	4,4,4	0.22	0	6,6,6	0.19	0
2	SO4	A	405	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	B	410	-	4,4,4	0.23	0	6,6,6	0.07	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	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	369/383 (96%)	0.87	44 (11%) 9 9	14, 36, 54, 63	1 (0%)
1	B	363/383 (94%)	0.70	34 (9%) 14 14	14, 36, 54, 64	1 (0%)
All	All	732/766 (95%)	0.79	78 (10%) 11 11	14, 36, 54, 64	2 (0%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	16	ALA	6.3
1	B	371	ALA	5.0
1	B	175	GLY	4.9
1	A	326	LEU	4.6
1	A	17	THR	4.5
1	A	87	LEU	4.5
1	B	173	ALA	4.2
1	A	15	HIS	4.0
1	B	18	LEU	4.0
1	A	11	SER	3.9
1	B	133	ALA	3.8
1	A	133	ALA	3.8
1	A	18	LEU	3.7
1	A	175	GLY	3.6
1	B	326	LEU	3.6
1	A	12	LYS	3.5
1	A	134	ALA	3.5
1	B	128	LEU	3.5
1	A	89	SER	3.4
1	A	13	PRO	3.4
1	A	14	HIS	3.3
1	A	92	GLU	3.2
1	B	130	PRO	3.2
1	B	134	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	131	THR	3.2
1	B	17	THR	3.2
1	B	125	VAL	3.0
1	B	370	SER	2.8
1	B	124	GLN	2.8
1	A	371	ALA	2.8
1	A	383	ALA	2.7
1	B	123	ALA	2.7
1	B	135	ALA	2.7
1	B	300	THR	2.7
1	B	131	THR	2.7
1	B	150	THR	2.7
1	B	138	ALA	2.6
1	A	142	VAL	2.6
1	B	148	VAL	2.6
1	B	147	ALA	2.6
1	B	132	LYS	2.6
1	B	99	THR	2.6
1	A	177	ASP	2.6
1	B	52	TRP	2.6
1	A	325	ASN	2.5
1	B	171	ALA	2.5
1	A	135	ALA	2.5
1	B	178	LYS	2.5
1	A	123	ALA	2.4
1	A	42	PHE	2.4
1	B	103	PHE	2.4
1	B	137	VAL	2.4
1	A	127	LYS	2.4
1	A	299	THR	2.3
1	A	137	VAL	2.3
1	A	176	ARG	2.3
1	A	49	GLU	2.3
1	A	143	GLU	2.3
1	B	310	ASN	2.3
1	A	41	VAL	2.2
1	B	327	VAL	2.2
1	A	82	ALA	2.2
1	A	372	PRO	2.2
1	A	62	GLY	2.1
1	A	121	LEU	2.1
1	B	129	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	177	ASP	2.1
1	A	153	VAL	2.1
1	A	311	HIS	2.1
1	A	128	LEU	2.1
1	B	122	LYS	2.1
1	B	325	ASN	2.1
1	A	91	ARG	2.1
1	A	90	GLY	2.1
1	A	334	ALA	2.1
1	A	234	VAL	2.0
1	A	38	LEU	2.0
1	A	300	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(Å ²)	Q<0.9
2	SO4	B	409	5/5	0.55	0.22	78,79,79,79	0
2	SO4	B	410	5/5	0.65	0.11	95,95,95,95	0
2	SO4	B	406	5/5	0.67	0.17	70,70,71,72	0
2	SO4	A	404	5/5	0.70	0.18	57,58,59,59	0
2	SO4	A	403	5/5	0.77	0.19	57,59,60,60	0
2	SO4	A	401	5/5	0.82	0.19	43,44,45,45	0
2	SO4	A	405	5/5	0.83	0.16	55,56,56,56	0
2	SO4	B	407	5/5	0.83	0.14	37,37,39,39	0
2	SO4	A	402	5/5	0.97	0.11	25,25,29,29	0
2	SO4	B	408	5/5	0.98	0.09	25,26,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.