



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:53 PM GMT

PDB ID : 1YT5  
Title : Crystal structure of NAD kinase from *Thermotoga maritima*  
Authors : Berkeley Structural Genomics Center (BSGC)  
Deposited on : 2005-02-09  
Resolution : 2.30 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

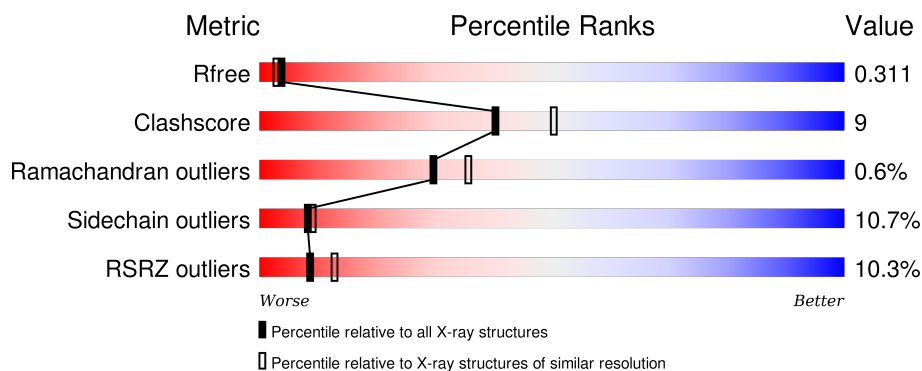
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	258	<div> <div>4%</div> <div>72%</div> <div>23%</div> <div>..</div> </div>
1	B	258	<div> <div>8%</div> <div>77%</div> <div>19%</div> <div>..</div> </div>
1	C	258	<div> <div>19%</div> <div>64%</div> <div>28%</div> <div>5% ..</div> </div>
1	D	258	<div> <div>9%</div> <div>79%</div> <div>17%</div> <div>..</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	304	-	-	-	X
2	SO4	A	309	-	-	-	X
2	SO4	D	311	-	-	-	X
2	SO4	D	314	-	-	-	X
2	SO4	D	315	-	-	-	X

## 2 Entry composition [i](#)

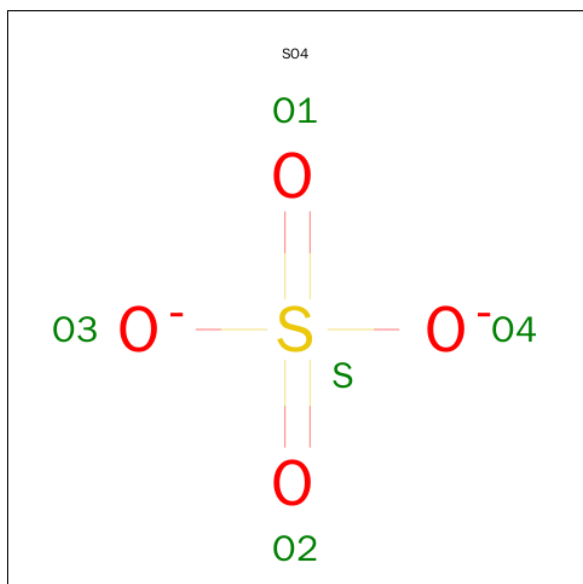
There are 3 unique types of molecules in this entry. The entry contains 8357 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 inorganic polyphosphate/ATP-NAD kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			2044	1306	350	382	6			
1	B	256	Total	C	N	O	S	0	0	0
			2044	1306	350	382	6			
1	C	252	Total	C	N	O	S	0	0	0
			2015	1289	342	378	6			
1	D	256	Total	C	N	O	S	0	0	0
			2044	1306	350	382	6			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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		

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	26	Total O 26 26	0	0
3	B	43	Total O 43 43	0	0
3	C	29	Total O 29 29	0	0

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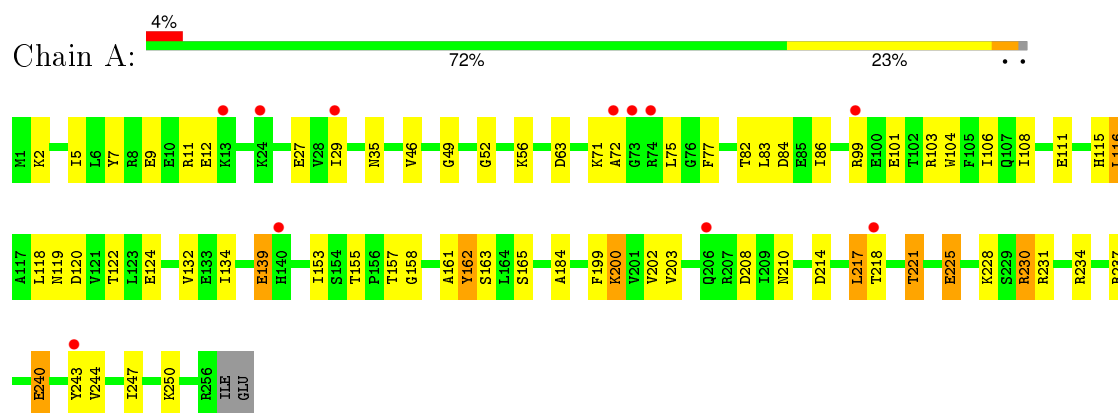
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	22	Total	O	0	0
			22	22		

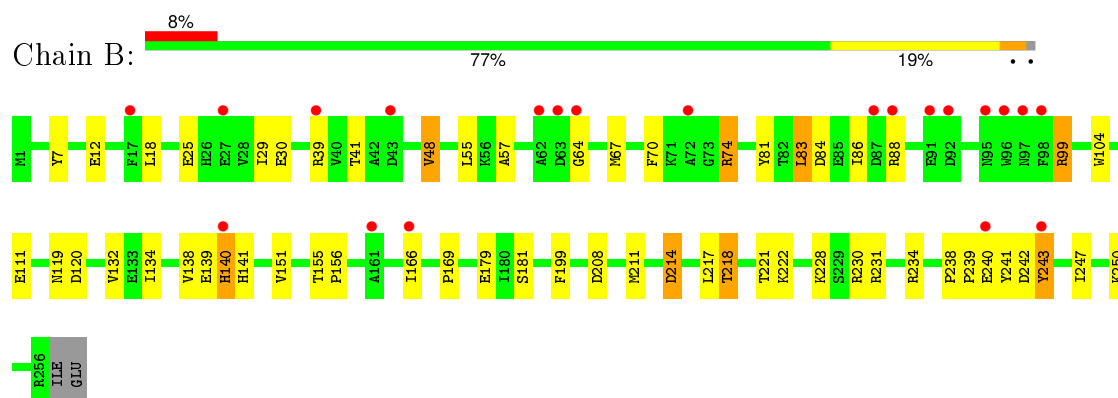
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

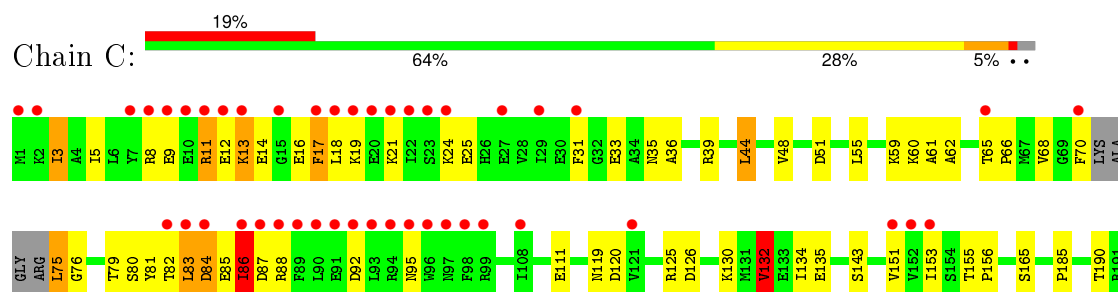
- Molecule 1: inorganic polyphosphate/ATP-NAD kinase

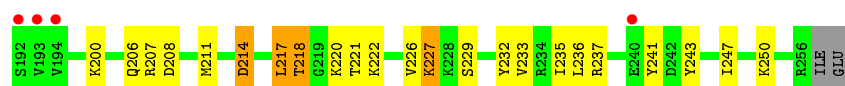


- Molecule 1: inorganic polyphosphate/ATP-NAD kinase

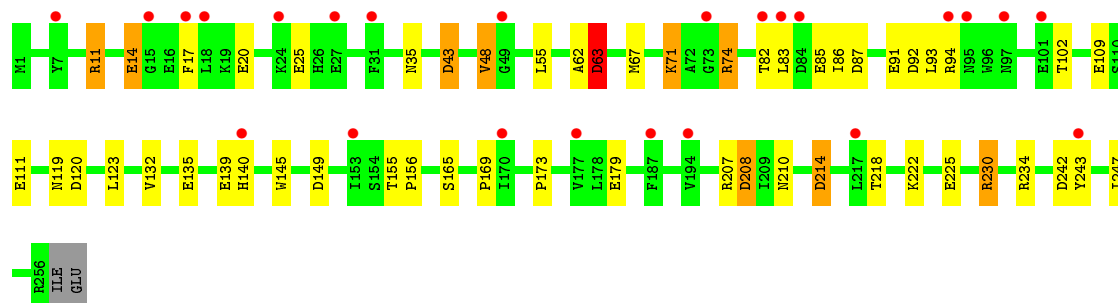
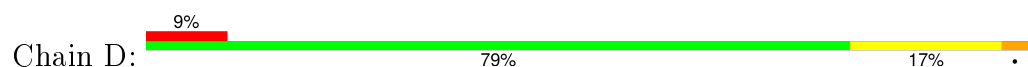


- Molecule 1: inorganic polyphosphate/ATP-NAD kinase





- Molecule 1: inorganic polyphosphate/ATP-NAD kinase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.45Å 137.15Å 58.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.30 49.65 – 2.19	Depositor EDS
% Data completeness (in resolution range)	5.1 (12.00-2.30) 95.7 (49.65-2.19)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.13 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.213 , 0.280 0.254 , 0.311	Depositor DCC
$R_{free}$ test set	2361 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.7	Xtriage
Anisotropy	0.593	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 42.2	EDS
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 52501 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8357	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.17 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.4248e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.78	0/2083	0.93	4/2812 (0.1%)
1	B	0.75	0/2083	0.93	5/2812 (0.2%)
1	C	0.69	0/2053	0.85	7/2772 (0.3%)
1	D	0.71	0/2083	0.90	10/2812 (0.4%)
All	All	0.73	0/8302	0.90	26/11208 (0.2%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	ASP	CB-CG-OD2	8.52	125.96	118.30
1	D	92	ASP	CB-CG-OD2	7.69	125.22	118.30
1	D	87	ASP	CB-CG-OD2	7.32	124.89	118.30
1	B	214	ASP	CB-CG-OD2	7.05	124.65	118.30
1	D	208	ASP	CB-CG-OD2	6.96	124.56	118.30
1	B	120	ASP	CB-CG-OD2	6.92	124.53	118.30
1	A	208	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	120	ASP	CB-CG-OD2	6.67	124.30	118.30
1	D	214	ASP	CB-CG-OD2	6.57	124.21	118.30
1	A	214	ASP	CB-CG-OD2	6.56	124.21	118.30
1	B	84	ASP	CB-CG-OD2	6.52	124.17	118.30
1	C	126	ASP	CB-CG-OD2	6.30	123.97	118.30
1	D	63	ASP	CB-CG-OD2	6.19	123.88	118.30
1	C	120	ASP	CB-CG-OD2	6.16	123.85	118.30
1	C	84	ASP	CB-CG-OD2	6.11	123.80	118.30
1	B	242	ASP	CB-CG-OD2	5.90	123.61	118.30
1	D	140	HIS	CB-CA-C	-5.78	98.83	110.40
1	D	120	ASP	CB-CG-OD2	5.47	123.22	118.30
1	D	43	ASP	CB-CG-OD2	5.40	123.16	118.30
1	C	208	ASP	CB-CG-OD2	5.34	123.11	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	149	ASP	CB-CG-OD2	5.34	123.10	118.30
1	A	84	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	214	ASP	CB-CG-OD2	5.14	122.93	118.30
1	C	132	VAL	CB-CA-C	-5.09	101.73	111.40
1	D	242	ASP	CB-CG-OD1	5.08	122.87	118.30
1	C	51	ASP	CB-CG-OD2	5.05	122.85	118.30

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	2044	0	2069	45	0
1	B	2044	0	2069	30	0
1	C	2015	0	2034	47	0
1	D	2044	0	2069	24	0
2	A	30	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	35	0	0	0	0
3	A	26	0	0	0	0
3	B	43	0	0	0	0
3	C	29	0	0	1	0
3	D	22	0	0	1	0
All	All	8357	0	8241	144	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 9.

All (144) 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:71:LYS:NZ	1:D:74:ARG:O	1.73	1.20
1:A:118:LEU:O	1:A:155:THR:HG21	1.68	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:211:MET:CE	1:C:218:THR:HG21	2.09	0.81
1:C:82:THR:H	1:C:85:GLU:HG3	1.46	0.81
1:C:211:MET:HE3	1:C:218:THR:HG21	1.64	0.79
1:A:71:LYS:NZ	1:A:75:LEU:HD13	2.00	0.77
1:C:111:GLU:HG2	1:C:221:THR:HG23	1.69	0.75
1:A:243:TYR:CE2	1:A:247:ILE:HD11	2.21	0.74
1:B:243:TYR:CE2	1:B:247:ILE:HD11	2.23	0.73
1:B:166:ILE:HD11	1:B:181:SER:HB3	1.72	0.72
1:B:64:GLY:O	1:B:234:ARG:NH1	2.23	0.71
1:A:161:ALA:O	1:A:163:SER:N	2.26	0.67
1:C:61:ALA:HB1	1:C:65:THR:CG2	2.25	0.67
1:A:106:ILE:HD12	1:A:108:ILE:HD11	1.76	0.66
1:A:122:THR:HG22	1:A:124:GLU:HG2	1.78	0.65
1:A:111:GLU:HG2	1:A:221:THR:HG23	1.77	0.65
1:A:115:HIS:NE2	1:A:218:THR:HG21	2.12	0.65
1:A:139:GLU:HG3	1:A:199:PHE:CG	2.32	0.65
1:C:119:ASN:HB2	1:C:214:ASP:OD1	1.97	0.64
1:C:55:LEU:HD11	1:C:214:ASP:OD2	1.98	0.63
1:A:155:THR:CG2	1:A:158:GLY:H	2.12	0.63
1:A:200:LYS:HE2	1:A:225:GLU:OE1	1.98	0.63
1:B:139:GLU:OE2	1:B:199:PHE:HA	2.01	0.61
1:B:18:LEU:HD12	1:B:48:VAL:HG22	1.83	0.61
1:C:18:LEU:CD2	1:C:86:ILE:HG23	2.30	0.60
1:D:55:LEU:HD21	1:D:214:ASP:HB3	1.84	0.60
1:A:71:LYS:HZ3	1:A:75:LEU:HD13	1.66	0.60
1:B:138:VAL:O	1:B:139:GLU:HB2	2.02	0.59
1:C:221:THR:HG22	1:C:222:LYS:H	1.67	0.58
1:C:211:MET:HE2	1:C:218:THR:CG2	2.34	0.58
1:D:11:ARG:HG2	1:D:14:GLU:HG3	1.83	0.58
1:C:82:THR:N	1:C:85:GLU:HG3	2.18	0.58
1:B:18:LEU:HD12	1:B:48:VAL:CG2	2.33	0.58
1:C:18:LEU:HD12	1:C:48:VAL:CG1	2.33	0.58
1:A:119:ASN:O	1:A:155:THR:HG22	2.04	0.58
1:C:18:LEU:HD12	1:C:48:VAL:HG11	1.86	0.58
1:D:119:ASN:HB2	1:D:214:ASP:OD1	2.04	0.57
1:C:75:LEU:HG	1:C:76:GLY:H	1.68	0.57
1:C:243:TYR:CE2	1:C:247:ILE:HD11	2.40	0.56
1:B:119:ASN:HB2	1:B:214:ASP:OD1	2.06	0.55
1:B:238:PRO:HG2	1:B:241:TYR:HB2	1.87	0.55
1:C:211:MET:HE2	1:C:218:THR:HG21	1.87	0.55
1:C:17:PHE:HE2	1:C:83:LEU:HD23	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PHE:O	1:A:237:ARG:NH2	2.32	0.55
1:C:75:LEU:HG	1:C:76:GLY:N	2.22	0.55
1:A:202:VAL:HG22	1:A:225:GLU:CG	2.37	0.54
1:A:9:GLU:OE2	1:A:35:ASN:ND2	2.40	0.54
1:A:230:ARG:HD2	1:C:232:TYR:CD2	2.42	0.54
1:B:88:ARG:NH2	1:B:240:GLU:OE2	2.41	0.54
1:C:44:LEU:HD11	1:C:68:VAL:HG23	1.90	0.54
1:A:244:VAL:HA	1:A:247:ILE:HD12	1.89	0.53
1:A:202:VAL:HG22	1:A:225:GLU:HG2	1.89	0.53
1:C:70:PHE:HA	1:C:81:TYR:O	2.09	0.53
1:C:217:LEU:HG	1:C:218:THR:H	1.73	0.53
1:B:169:PRO:HD2	1:B:179:GLU:OE2	2.08	0.53
1:C:66:PRO:HB3	1:C:236:LEU:HD21	1.90	0.52
1:A:103:ARG:HD2	1:A:157:THR:OG1	2.09	0.52
1:D:243:TYR:CE2	1:D:247:ILE:HD11	2.44	0.52
1:B:211:MET:HE3	1:B:218:THR:HG21	1.92	0.51
1:A:71:LYS:HZ2	1:A:75:LEU:HD13	1.75	0.51
1:D:91:GLU:HA	1:D:94:ARG:NH2	2.25	0.51
1:A:116:LEU:HD21	1:A:231:ARG:HD2	1.92	0.51
1:D:208:ASP:OD1	1:D:222:LYS:HB2	2.11	0.51
1:A:161:ALA:O	1:A:162:TYR:C	2.48	0.51
1:B:74:ARG:NH1	1:B:74:ARG:H	2.09	0.50
1:B:57:ALA:HB1	1:B:67:MET:HE1	1.94	0.50
1:A:155:THR:HG23	1:A:158:GLY:H	1.76	0.49
1:B:166:ILE:HD11	1:B:181:SER:CB	2.42	0.49
1:B:18:LEU:CD1	1:B:48:VAL:HG22	2.42	0.49
1:B:134:ILE:HG21	1:B:151:VAL:CG2	2.42	0.49
1:B:29:ILE:HD12	1:B:30:GLU:HB2	1.95	0.49
1:C:17:PHE:CE2	1:C:83:LEU:HD23	2.48	0.48
1:B:134:ILE:HG21	1:B:151:VAL:HG21	1.94	0.48
1:C:125:ARG:HD3	1:C:130:LYS:O	2.12	0.48
1:D:82:THR:HB	1:D:85:GLU:HG3	1.96	0.48
1:C:227:LYS:HD2	3:C:322:HOH:O	2.13	0.48
1:C:132:VAL:HG13	1:C:207:ARG:NH1	2.29	0.48
1:C:13:LYS:HD3	1:C:13:LYS:HA	1.60	0.47
1:C:61:ALA:HB1	1:C:65:THR:HG21	1.97	0.47
1:C:62:ALA:O	1:C:65:THR:HG22	2.15	0.47
1:C:211:MET:CE	1:C:218:THR:CG2	2.84	0.47
1:B:48:VAL:CG1	1:B:83:LEU:HD11	2.45	0.47
1:C:11:ARG:HB3	1:C:14:GLU:CD	2.35	0.47
1:A:49:GLY:HA2	1:A:72:ALA:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:109:GLU:HG2	1:D:225:GLU:HB3	1.98	0.46
1:C:8:ARG:HB3	1:C:11:ARG:HG3	1.97	0.46
1:A:139:GLU:CG	1:A:199:PHE:CG	2.98	0.46
1:A:104:TRP:CE3	1:A:228:LYS:HG3	2.51	0.46
1:A:2:LYS:HG2	1:A:29:ILE:HD13	1.98	0.46
1:A:139:GLU:HG3	1:A:199:PHE:CD1	2.51	0.46
1:A:11:ARG:HG2	1:A:72:ALA:HB1	1.96	0.46
1:B:48:VAL:HG11	1:B:83:LEU:HD11	1.97	0.46
1:C:36:ALA:O	1:C:60:LYS:HD2	2.15	0.45
1:B:211:MET:CE	1:B:218:THR:HG21	2.47	0.45
1:C:155:THR:HB	1:C:156:PRO:HD2	1.98	0.45
1:A:200:LYS:CE	1:A:225:GLU:OE1	2.64	0.45
1:C:18:LEU:HD23	1:C:86:ILE:CG2	2.47	0.45
1:D:91:GLU:HG3	1:D:94:ARG:NH2	2.32	0.45
1:C:237:ARG:HD2	1:C:241:TYR:CD2	2.52	0.45
1:C:5:ILE:O	1:C:31:PHE:HA	2.17	0.44
1:D:71:LYS:CE	1:D:74:ARG:O	2.63	0.44
1:D:62:ALA:O	1:D:63:ASP:C	2.55	0.44
1:A:184:ALA:HB1	1:D:165:SER:HB3	1.99	0.44
1:C:153:ILE:HG21	1:C:226:VAL:HG11	1.99	0.44
1:C:82:THR:HB	1:C:85:GLU:CG	2.48	0.44
1:D:173:PRO:HD3	1:D:243:TYR:CZ	2.53	0.44
1:A:210:ASN:HB3	1:A:217:LEU:HD11	1.99	0.44
1:A:240:GLU:CD	1:A:240:GLU:H	2.21	0.44
1:B:139:GLU:HB3	1:B:140:HIS:H	1.15	0.44
1:A:7:TYR:CZ	1:A:12:GLU:HG3	2.53	0.44
1:D:11:ARG:HG2	1:D:14:GLU:CG	2.47	0.43
1:C:3:ILE:HG12	1:C:44:LEU:HD23	1.99	0.43
1:B:7:TYR:CE2	1:B:12:GLU:HG3	2.52	0.43
1:D:155:THR:HB	1:D:156:PRO:HD2	1.99	0.43
1:D:135:GLU:HG3	1:D:145:TRP:CE2	2.52	0.43
1:A:52:GLY:O	1:A:56:LYS:HE3	2.19	0.43
1:A:155:THR:HG22	1:A:158:GLY:H	1.81	0.43
1:A:71:LYS:HD2	1:A:75:LEU:HA	2.00	0.43
1:B:57:ALA:O	1:B:67:MET:HE3	2.19	0.43
1:A:82:THR:HG22	1:A:83:LEU:N	2.34	0.43
1:C:217:LEU:HG	1:C:218:THR:N	2.34	0.43
1:C:185:PRO:HD2	1:C:190:THR:HG22	2.01	0.43
1:A:101:GLU:OE1	1:A:103:ARG:NH2	2.48	0.43
1:A:218:THR:O	1:A:218:THR:HG22	2.18	0.42
1:D:74:ARG:HD2	1:D:74:ARG:HH11	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:PRO:HD2	1:D:179:GLU:OE2	2.18	0.42
1:A:5:ILE:HG12	1:A:46:VAL:HB	2.01	0.42
1:C:134:ILE:HG21	1:C:151:VAL:HG21	2.00	0.42
1:A:153:ILE:HD11	1:A:203:VAL:HG21	2.00	0.42
1:B:99:ARG:HG3	1:B:239:PRO:HA	2.02	0.42
1:C:135:GLU:OE2	1:C:143:SER:OG	2.30	0.42
1:A:52:GLY:C	1:A:56:LYS:HE3	2.40	0.42
1:C:82:THR:HB	1:C:85:GLU:HG3	2.01	0.42
1:A:101:GLU:OE1	1:A:103:ARG:NE	2.52	0.42
1:D:135:GLU:HG3	1:D:145:TRP:CZ2	2.55	0.42
1:B:104:TRP:CG	1:B:228:LYS:HE3	2.55	0.42
1:D:74:ARG:HG3	1:D:74:ARG:H	1.50	0.41
1:B:18:LEU:CD2	1:B:86:ILE:HD13	2.50	0.41
1:B:70:PHE:HA	1:B:81:TYR:O	2.21	0.41
1:C:60:LYS:HE3	1:C:60:LYS:HB3	1.88	0.41
1:D:123:LEU:HA	1:D:210:ASN:O	2.20	0.41
1:B:155:THR:HB	1:B:156:PRO:HD2	2.02	0.40
1:D:14:GLU:HB2	1:D:48:VAL:HG11	2.02	0.40
1:D:230:ARG:NH2	3:D:326:HOH:O	2.47	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	254/258 (98%)	235 (92%)	17 (7%)	2 (1%)	24	27
1	B	254/258 (98%)	240 (94%)	13 (5%)	1 (0%)	39	48
1	C	248/258 (96%)	237 (96%)	10 (4%)	1 (0%)	39	48
1	D	254/258 (98%)	241 (95%)	11 (4%)	2 (1%)	24	27
All	All	1010/1032 (98%)	953 (94%)	51 (5%)	6 (1%)	30	36

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	TYR
1	D	139	GLU
1	B	141	HIS
1	D	63	ASP
1	A	139	GLU
1	C	86	ILE

### 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	223/225 (99%)	207 (93%)	16 (7%)	18	22
1	B	223/225 (99%)	204 (92%)	19 (8%)	13	16
1	C	221/225 (98%)	183 (83%)	38 (17%)	2	2
1	D	223/225 (99%)	201 (90%)	22 (10%)	10	11
All	All	890/900 (99%)	795 (89%)	95 (11%)	8	9

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	63	ASP
1	A	86	ILE
1	A	99	ARG
1	A	116	LEU
1	A	132	VAL
1	A	134	ILE
1	A	165	SER
1	A	200	LYS
1	A	217	LEU
1	A	221	THR
1	A	225	GLU
1	A	230	ARG
1	A	234	ARG

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Mol	Chain	Res	Type
1	A	240	GLU
1	A	250	LYS
1	B	25	GLU
1	B	39	ARG
1	B	41	THR
1	B	48	VAL
1	B	55	LEU
1	B	74	ARG
1	B	83	LEU
1	B	99	ARG
1	B	111	GLU
1	B	132	VAL
1	B	140	HIS
1	B	217	LEU
1	B	218	THR
1	B	221	THR
1	B	222	LYS
1	B	230	ARG
1	B	231	ARG
1	B	243	TYR
1	B	250	LYS
1	C	3	ILE
1	C	9	GLU
1	C	11	ARG
1	C	12	GLU
1	C	13	LYS
1	C	16	GLU
1	C	17	PHE
1	C	19	LYS
1	C	21	LYS
1	C	24	LYS
1	C	25	GLU
1	C	33	GLU
1	C	35	ASN
1	C	39	ARG
1	C	44	LEU
1	C	59	LYS
1	C	75	LEU
1	C	79	THR
1	C	80	SER
1	C	83	LEU
1	C	84	ASP

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Mol	Chain	Res	Type
1	C	86	ILE
1	C	87	ASP
1	C	88	ARG
1	C	92	ASP
1	C	95	ASN
1	C	132	VAL
1	C	165	SER
1	C	200	LYS
1	C	206	GLN
1	C	217	LEU
1	C	218	THR
1	C	220	LYS
1	C	227	LYS
1	C	229	SER
1	C	233	VAL
1	C	235	ILE
1	C	250	LYS
1	D	11	ARG
1	D	14	GLU
1	D	17	PHE
1	D	20	GLU
1	D	25	GLU
1	D	35	ASN
1	D	43	ASP
1	D	48	VAL
1	D	63	ASP
1	D	67	MET
1	D	71	LYS
1	D	74	ARG
1	D	83	LEU
1	D	86	ILE
1	D	93	LEU
1	D	102	THR
1	D	111	GLU
1	D	132	VAL
1	D	207	ARG
1	D	218	THR
1	D	230	ARG
1	D	234	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	GLN
1	A	206	GLN
1	C	95	ASN
1	C	186	GLN
1	D	107	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](#)

18 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	301	-	4,4,4	0.24	0	6,6,6	0.35	0
2	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.32	0
2	SO4	A	309	-	4,4,4	0.25	0	6,6,6	0.17	0
2	SO4	A	313	-	4,4,4	0.27	0	6,6,6	0.19	0
2	SO4	A	316	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	A	317	-	4,4,4	0.25	0	6,6,6	0.23	0
2	SO4	B	302	-	4,4,4	0.35	0	6,6,6	0.36	0
2	SO4	B	310	-	4,4,4	0.34	0	6,6,6	0.30	0
2	SO4	B	318	-	4,4,4	0.33	0	6,6,6	0.18	0
2	SO4	C	305	-	4,4,4	0.27	0	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	307	-	4,4,4	0.24	0	6,6,6	0.12	0
2	SO4	D	303	-	4,4,4	0.29	0	6,6,6	0.31	0
2	SO4	D	306	-	4,4,4	0.27	0	6,6,6	0.08	0
2	SO4	D	308	-	4,4,4	0.30	0	6,6,6	0.17	0
2	SO4	D	311	-	4,4,4	0.24	0	6,6,6	0.12	0
2	SO4	D	312	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	D	314	-	4,4,4	0.29	0	6,6,6	0.09	0
2	SO4	D	315	-	4,4,4	0.33	0	6,6,6	0.32	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	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	A	304	-	-	0/0/0/0	0/0/0/0
2	SO4	A	309	-	-	0/0/0/0	0/0/0/0
2	SO4	A	313	-	-	0/0/0/0	0/0/0/0
2	SO4	A	316	-	-	0/0/0/0	0/0/0/0
2	SO4	A	317	-	-	0/0/0/0	0/0/0/0
2	SO4	B	302	-	-	0/0/0/0	0/0/0/0
2	SO4	B	310	-	-	0/0/0/0	0/0/0/0
2	SO4	B	318	-	-	0/0/0/0	0/0/0/0
2	SO4	C	305	-	-	0/0/0/0	0/0/0/0
2	SO4	C	307	-	-	0/0/0/0	0/0/0/0
2	SO4	D	303	-	-	0/0/0/0	0/0/0/0
2	SO4	D	306	-	-	0/0/0/0	0/0/0/0
2	SO4	D	308	-	-	0/0/0/0	0/0/0/0
2	SO4	D	311	-	-	0/0/0/0	0/0/0/0
2	SO4	D	312	-	-	0/0/0/0	0/0/0/0
2	SO4	D	314	-	-	0/0/0/0	0/0/0/0
2	SO4	D	315	-	-	0/0/0/0	0/0/0/0

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.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	256/258 (99%)	0.38	11 (4%) 39 48	6, 18, 32, 44	0
1	B	256/258 (99%)	0.39	21 (8%) 14 20	6, 18, 30, 37	0
1	C	252/258 (97%)	1.25	49 (19%) 1 2	20, 31, 47, 54	0
1	D	256/258 (99%)	0.85	24 (9%) 11 16	21, 33, 45, 53	0
All	All	1020/1032 (98%)	0.72	105 (10%) 9 13	6, 26, 44, 54	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	ARG	10.0
1	C	17	PHE	8.4
1	C	89	PHE	6.9
1	C	22	ILE	6.8
1	D	83	LEU	6.8
1	D	17	PHE	6.6
1	C	86	ILE	6.3
1	C	15	GLY	6.3
1	C	95	ASN	6.3
1	C	82	THR	5.7
1	A	73	GLY	5.5
1	C	18	LEU	5.3
1	C	97	ASN	5.3
1	C	92	ASP	5.3
1	B	63	ASP	5.1
1	C	24	LYS	5.0
1	B	95	ASN	4.9
1	A	72	ALA	4.8
1	C	13	LYS	4.8
1	D	140	HIS	4.6
1	C	88	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
1	C	31	PHE	4.4
1	C	87	ASP	4.4
1	A	140	HIS	4.3
1	D	82	THR	4.3
1	D	95	ASN	4.2
1	C	93	LEU	4.1
1	D	15	GLY	3.9
1	C	96	TRP	3.9
1	C	20	GLU	3.8
1	C	12	GLU	3.7
1	C	27	GLU	3.7
1	C	19	LYS	3.7
1	B	88	ARG	3.6
1	C	10	GLU	3.6
1	C	8	ARG	3.6
1	B	243	TYR	3.4
1	C	23	SER	3.3
1	C	99	ARG	3.3
1	C	90	LEU	3.3
1	B	72	ALA	3.3
1	C	7	TYR	3.2
1	D	84	ASP	3.1
1	D	243	TYR	3.1
1	B	98	PHE	3.1
1	D	94	ARG	3.1
1	B	27	GLU	3.0
1	B	62	ALA	2.9
1	C	9	GLU	2.9
1	D	73	GLY	2.8
1	D	18	LEU	2.8
1	A	206	GLN	2.8
1	B	43	ASP	2.8
1	C	65	THR	2.8
1	B	140	HIS	2.8
1	B	17	PHE	2.7
1	C	11	ARG	2.7
1	C	194	VAL	2.7
1	C	84	ASP	2.7
1	C	83	LEU	2.6
1	D	177	VAL	2.6
1	B	166	ILE	2.6
1	D	24	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	92	ASP	2.6
1	C	91	GLU	2.6
1	C	21	LYS	2.5
1	C	121	VAL	2.5
1	A	13	LYS	2.5
1	B	87	ASP	2.5
1	A	24	LYS	2.4
1	D	187	PHE	2.4
1	B	91	GLU	2.4
1	B	161	ALA	2.4
1	D	194	VAL	2.3
1	C	151	VAL	2.3
1	D	170	ILE	2.3
1	A	218	THR	2.3
1	A	99	ARG	2.3
1	C	94	ARG	2.3
1	B	97	ASN	2.3
1	A	243	TYR	2.3
1	D	49	GLY	2.3
1	D	97	ASN	2.3
1	C	1	MET	2.3
1	B	96	TRP	2.3
1	C	2	LYS	2.2
1	D	27	GLU	2.2
1	C	152	VAL	2.2
1	C	240	GLU	2.2
1	D	217	LEU	2.2
1	C	70	PHE	2.2
1	C	108	ILE	2.1
1	C	98	PHE	2.1
1	C	192	SER	2.1
1	C	193	VAL	2.1
1	A	29	ILE	2.1
1	C	153	ILE	2.1
1	B	240	GLU	2.0
1	D	31	PHE	2.0
1	D	7	TYR	2.0
1	D	101	GLU	2.0
1	C	29	ILE	2.0
1	B	39	ARG	2.0
1	B	64	GLY	2.0
1	D	153	ILE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	D	311	5/5	0.69	0.35	14.25	141,141,141,141	0
2	SO4	A	309	5/5	0.98	0.24	6.05	89,90,91,91	0
2	SO4	D	314	5/5	0.85	0.23	2.66	118,119,119,119	0
2	SO4	D	315	5/5	0.94	0.24	2.11	114,115,115,115	0
2	SO4	A	304	5/5	0.94	0.19	2.00	73,75,76,76	0
2	SO4	D	308	5/5	0.92	0.23	1.97	108,108,109,109	0
2	SO4	B	310	5/5	0.83	0.22	1.62	100,100,101,102	0
2	SO4	D	306	5/5	0.83	0.25	1.48	140,140,141,141	0
2	SO4	B	318	5/5	0.90	0.19	0.60	101,102,103,103	0
2	SO4	C	307	5/5	0.87	0.17	0.55	123,123,124,124	0
2	SO4	A	317	5/5	0.76	0.25	-0.00	122,122,122,122	0
2	SO4	A	313	5/5	0.92	0.14	-	104,104,104,104	0
2	SO4	B	302	5/5	0.91	0.27	-	93,93,93,93	0
2	SO4	A	301	5/5	0.84	0.31	-	80,81,82,83	0
2	SO4	D	312	5/5	0.95	0.17	-	113,113,113,113	0
2	SO4	C	305	5/5	0.91	0.33	-	63,63,64,65	5
2	SO4	A	316	5/5	0.88	0.20	-	120,120,120,120	0
2	SO4	D	303	5/5	0.94	0.15	-	78,78,79,80	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.