Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:02 PM GMT

PDB ID	:	4NKR
Title	:	The Crystal structure of Bacillus subtilis MobB
Authors	:	Choe, J.; Kim, D.; Choi, S.; Kim, H.
Deposited on	:	2013-11-13
Resolution	:	2.41 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

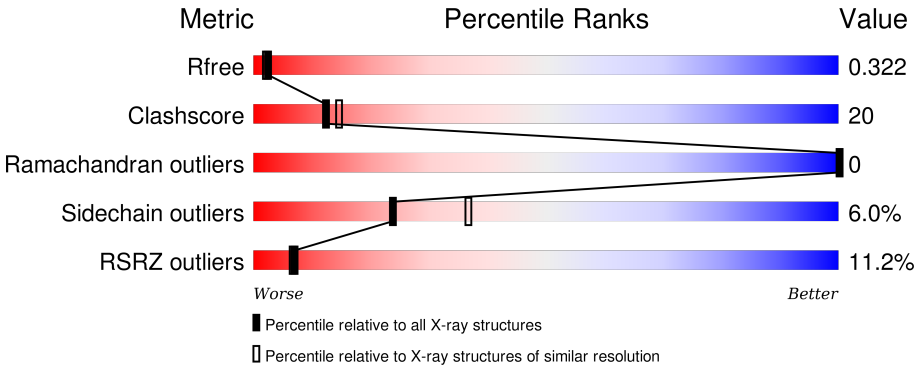
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	3386 (2.44-2.40)
Clashscore	102246	3897 (2.44-2.40)
Ramachandran outliers	100387	3837 (2.44-2.40)
Sidechain outliers	100360	3838 (2.44-2.40)
RSRZ outliers	91569	3396 (2.44-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	166	3% 60% 27% • 11%
1	B	166	8% 64% 24% •• 9%
1	C	166	10% 62% 25% •• 11%
1	D	166	10% 60% 26% • 11%
1	E	166	20% 60% 37% •••

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6285 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.

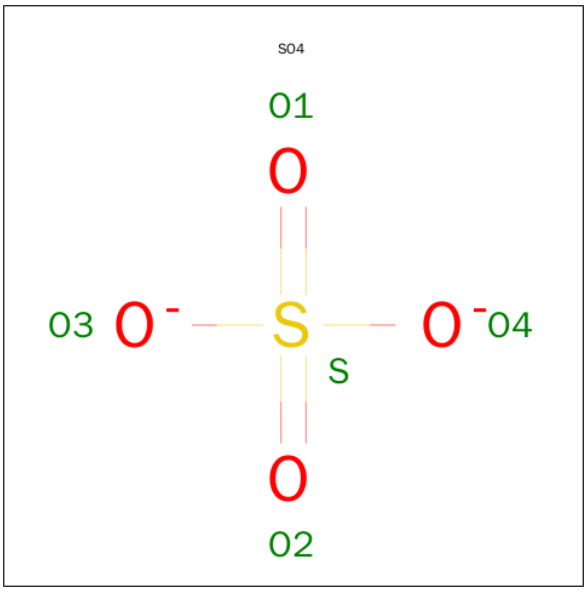
- Molecule 1 is a protein called Molybdopterin-guanine dinucleotide biosynthesis protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	148	Total	C	N	O	S	0	0	0
			1173	755	199	216	3			
1	B	151	Total	C	N	O	S	0	0	0
			1192	765	202	222	3			
1	C	148	Total	C	N	O	S	0	0	0
			1173	755	199	216	3			
1	D	148	Total	C	N	O	S	0	0	0
			1173	755	199	216	3			
1	E	163	Total	C	N	O	S	0	0	0
			1280	819	218	240	3			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	PHE	-	EXPRESSION TAG	UNP E0U3U4
A	88	LEU	ASN	CONFLICT	UNP E0U3U4
A	166	LEU	PHE	CONFLICT	UNP E0U3U4
B	10	PHE	-	EXPRESSION TAG	UNP E0U3U4
B	88	LEU	ASN	CONFLICT	UNP E0U3U4
B	166	LEU	PHE	CONFLICT	UNP E0U3U4
C	10	PHE	-	EXPRESSION TAG	UNP E0U3U4
C	88	LEU	ASN	CONFLICT	UNP E0U3U4
C	166	LEU	PHE	CONFLICT	UNP E0U3U4
D	10	PHE	-	EXPRESSION TAG	UNP E0U3U4
D	88	LEU	ASN	CONFLICT	UNP E0U3U4
D	166	LEU	PHE	CONFLICT	UNP E0U3U4
E	10	PHE	-	EXPRESSION TAG	UNP E0U3U4
E	88	LEU	ASN	CONFLICT	UNP E0U3U4
E	166	LEU	PHE	CONFLICT	UNP E0U3U4

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 3 is water.

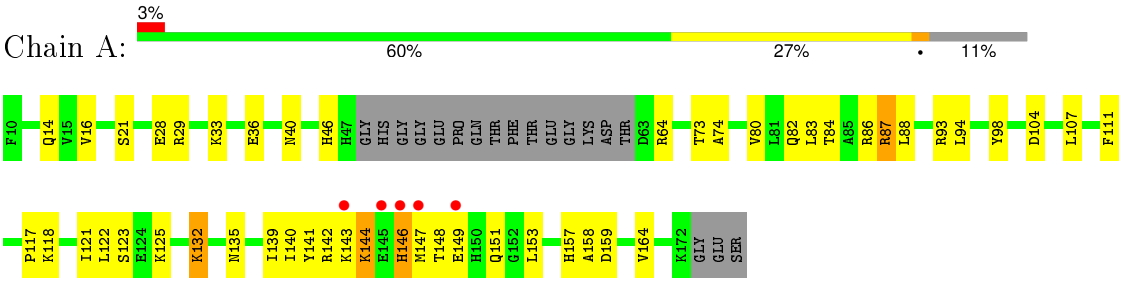
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	32	Total O 32 32	0	0
3	B	37	Total O 37 37	0	0
3	C	55	Total O 55 55	0	0
3	D	64	Total O 64 64	0	0
3	E	41	Total O 41 41	0	0

3 Residue-property plots (i)

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.

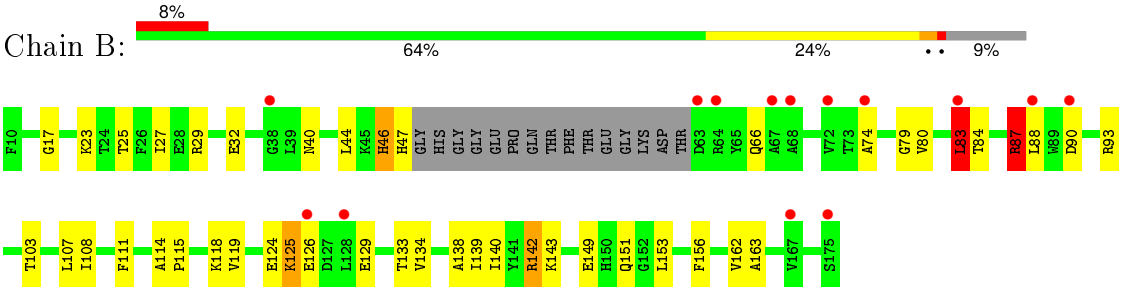
- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B

Chain A:



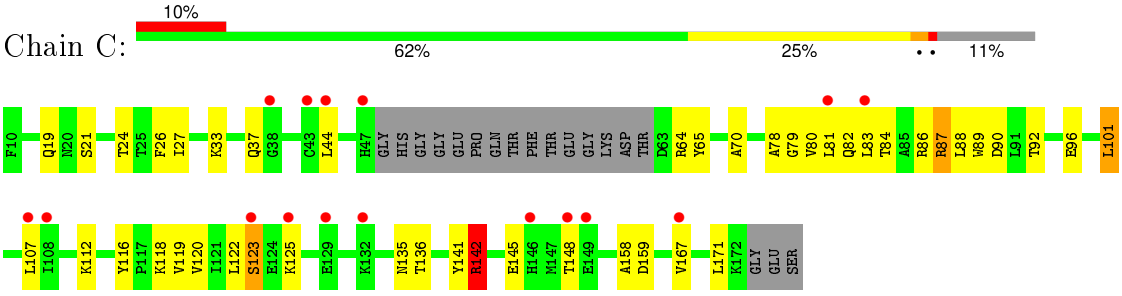
- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B

Chain B:



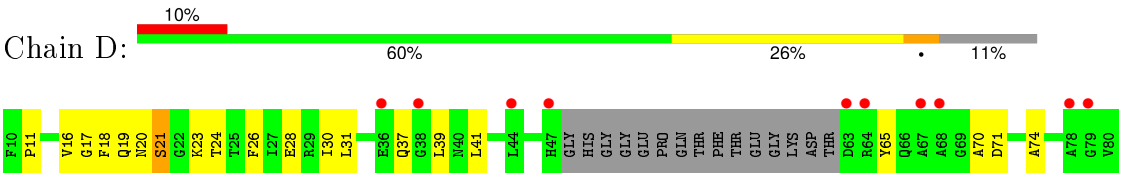
- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B

Chain C:

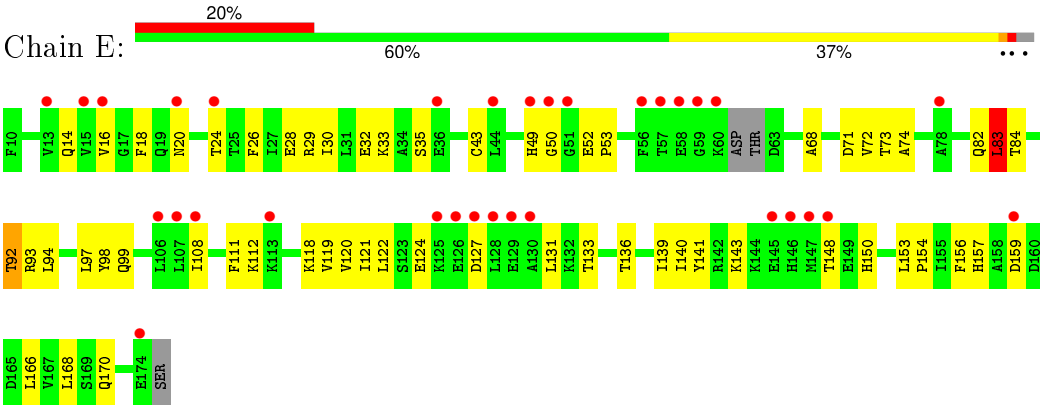


- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B

Chain D:



- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	225.53Å 42.11Å 93.62Å 90.00° 100.99° 90.00°	Depositor
Resolution (Å)	29.27 – 2.41 29.27 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.27-2.41) 98.4 (29.27-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.44 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.227 , 0.321 0.231 , 0.322	Depositor DCC
R_{free} test set	1682 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	44.2	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 63.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 33513 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6285	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.95	0/1193	0.82	0/1613
1	B	0.83	0/1212	0.85	3/1638 (0.2%)
1	C	0.75	0/1193	0.76	1/1613 (0.1%)
1	D	0.79	1/1193 (0.1%)	0.75	0/1613
1	E	0.67	0/1303	0.71	1/1760 (0.1%)
All	All	0.80	1/6094 (0.0%)	0.78	5/8237 (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
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	145	GLU	CD-OE2	6.61	1.32	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	142	ARG	NE-CZ-NH2	-6.77	116.91	120.30
1	C	142	ARG	NE-CZ-NH1	5.45	123.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	142	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	B	83	LEU	CA-CB-CG	5.29	127.46	115.30
1	E	83	LEU	CB-CG-CD1	5.21	119.86	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	ARG	Peptide
1	B	87	ARG	Peptide
1	C	87	ARG	Peptide
1	D	87	ARG	Peptide
1	E	87	ARG	Peptide

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	1173	0	1202	42	1
1	B	1192	0	1216	49	0
1	C	1173	0	1201	43	0
1	D	1173	0	1202	55	0
1	E	1280	0	1293	63	1
2	A	15	0	0	0	0
2	B	15	0	0	1	0
2	C	10	0	0	0	0
2	D	15	0	0	1	0
2	E	10	0	0	2	0
3	A	32	0	0	5	0
3	B	37	0	0	13	0
3	C	55	0	0	20	0
3	D	64	0	0	16	0
3	E	41	0	0	19	0
All	All	6285	0	6114	238	1

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 20.

All (238) 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:142:ARG:NH2	3:D:362:HOH:O	1.82	1.12
1:A:87:ARG:HB3	1:A:88:LEU:HB2	1.33	1.10
1:E:87:ARG:HB3	1:E:88:LEU:HB3	1.33	1.09
1:D:123:SER:OG	1:D:142:ARG:CZ	2.02	1.07
1:C:89:TRP:CE2	3:C:335:HOH:O	2.16	0.97
1:A:139:ILE:HD12	1:A:153:LEU:HD11	1.50	0.94
1:E:111:PHE:HE2	3:E:311:HOH:O	1.48	0.94
1:C:141:TYR:O	3:C:343:HOH:O	1.86	0.92
1:E:111:PHE:CE2	3:E:311:HOH:O	2.22	0.89
1:E:119:VAL:HG23	3:E:302:HOH:O	1.72	0.88
1:C:141:TYR:C	3:C:343:HOH:O	2.13	0.87
1:C:136:THR:C	3:C:308:HOH:O	2.14	0.85
1:B:44:LEU:HB3	3:B:318:HOH:O	1.77	0.83
1:D:65:TYR:O	1:D:70:ALA:HB3	1.80	0.82
1:E:87:ARG:CB	1:E:88:LEU:HB3	2.11	0.78
1:C:26:PHE:CD2	3:C:336:HOH:O	2.36	0.78
1:A:87:ARG:CB	1:A:88:LEU:HB2	2.15	0.77
1:B:163:ALA:N	3:B:313:HOH:O	2.17	0.77
1:A:118:LYS:HB2	3:A:316:HOH:O	1.86	0.76
1:E:87:ARG:NH2	1:E:93:ARG:HD3	2.00	0.76
1:E:131:LEU:HA	3:E:319:HOH:O	1.85	0.76
1:C:135:ASN:C	3:C:308:HOH:O	2.24	0.75
1:D:18:PHE:CD2	3:D:334:HOH:O	2.38	0.75
1:E:112:LYS:HG3	2:E:202:SO4:O1	1.87	0.75
1:E:74:ALA:HB2	1:E:83:LEU:HD22	1.67	0.75
1:C:116:TYR:O	1:C:118:LYS:NZ	2.22	0.72
1:C:158:ALA:HB2	3:C:343:HOH:O	1.88	0.72
1:E:74:ALA:HB2	1:E:83:LEU:CD2	2.20	0.72
1:D:18:PHE:HB2	3:D:334:HOH:O	1.90	0.71
1:E:141:TYR:OH	1:E:150:HIS:NE2	2.24	0.70
1:D:123:SER:OG	1:D:142:ARG:NE	2.24	0.70
1:C:87:ARG:HB3	1:C:88:LEU:HB2	1.74	0.68
1:B:87:ARG:HB3	1:B:88:LEU:HB3	1.75	0.68
1:A:40:ASN:HB3	1:A:104:ASP:OD2	1.94	0.68
1:B:87:ARG:CB	1:B:88:LEU:HB3	2.24	0.67
1:B:107:LEU:O	3:B:318:HOH:O	2.10	0.67
1:E:29:ARG:HH12	1:E:159:ASP:HA	1.60	0.67
1:B:66:GLN:NE2	3:B:322:HOH:O	2.28	0.67
1:A:29:ARG:HH12	1:A:159:ASP:HA	1.59	0.67
1:D:21:SER:HA	1:D:142:ARG:NE	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ASN:HB3	1:A:104:ASP:CG	2.16	0.66
1:D:93:ARG:NH1	3:D:322:HOH:O	2.27	0.66
1:C:78:ALA:HB2	3:C:323:HOH:O	1.96	0.65
1:A:46:HIS:HB2	1:A:111:PHE:CE1	2.32	0.65
1:C:87:ARG:NH2	3:C:321:HOH:O	2.27	0.65
1:B:156:PHE:CD1	3:B:313:HOH:O	2.50	0.64
1:D:123:SER:OG	1:D:142:ARG:NH1	2.30	0.64
1:E:99:GLN:HG2	3:E:337:HOH:O	1.98	0.64
1:A:132:LYS:HE3	1:B:124:GLU:CG	2.28	0.64
1:B:46:HIS:HB2	1:B:111:PHE:CE2	2.33	0.64
1:D:18:PHE:O	1:D:21:SER:OG	2.16	0.64
1:D:87:ARG:HB3	1:D:88:LEU:HB3	1.80	0.64
1:E:124:GLU:HB2	3:E:339:HOH:O	1.98	0.63
1:D:123:SER:HG	1:D:142:ARG:CZ	2.08	0.63
1:A:87:ARG:HB3	1:A:88:LEU:CB	2.21	0.63
1:D:105:CYS:SG	3:D:346:HOH:O	2.56	0.63
1:D:142:ARG:NH2	3:D:321:HOH:O	1.98	0.62
1:B:80:VAL:HG22	1:E:53:PRO:HD2	1.81	0.62
1:C:158:ALA:N	3:C:343:HOH:O	2.30	0.62
1:B:84:THR:HG23	1:E:82:GLN:OE1	1.98	0.62
1:B:25:THR:O	1:B:29:ARG:HG3	2.00	0.61
1:A:144:LYS:HE3	1:A:157:HIS:HB3	1.81	0.61
1:A:123:SER:O	1:A:143:LYS:HD3	1.99	0.61
1:D:122:LEU:HD22	1:D:127:ASP:HB2	1.83	0.61
1:E:87:ARG:HD3	1:E:89:TRP:CZ2	2.36	0.60
1:D:39:LEU:HD11	1:D:105:CYS:SG	2.41	0.60
3:C:335:HOH:O	1:D:81:LEU:HB2	2.02	0.60
1:D:87:ARG:NH2	3:D:308:HOH:O	2.34	0.60
1:D:16:VAL:HG23	1:D:120:VAL:HG22	1.84	0.60
1:A:143:LYS:HB2	1:A:146:HIS:NE2	2.17	0.59
1:C:125:LYS:HG2	1:C:148:THR:HB	1.84	0.59
1:E:73:THR:N	3:E:313:HOH:O	2.35	0.59
1:B:108:ILE:HA	3:B:318:HOH:O	2.01	0.59
1:A:132:LYS:HE3	1:B:124:GLU:HG3	1.85	0.59
1:C:123:SER:HB3	1:C:142:ARG:CZ	2.32	0.59
1:D:114:ALA:HB1	1:D:115:PRO:HD2	1.84	0.58
1:A:28:GLU:OE2	3:A:326:HOH:O	2.17	0.58
1:C:101:LEU:O	1:D:87:ARG:NH2	2.34	0.58
1:C:123:SER:HB3	1:C:142:ARG:NH2	2.19	0.57
1:B:88:LEU:HD21	1:B:93:ARG:NH1	2.19	0.57
1:A:144:LYS:HG3	1:A:147:MET:SD	2.44	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:LYS:HE3	1:A:148:THR:HG21	1.85	0.57
3:B:321:HOH:O	1:E:88:LEU:HD11	2.03	0.57
1:A:86:ARG:O	1:A:87:ARG:HD3	2.05	0.56
1:A:123:SER:O	1:A:143:LYS:CD	2.54	0.56
1:C:142:ARG:HH11	1:C:142:ARG:HG3	1.70	0.56
1:E:154:PRO:HB2	3:E:321:HOH:O	2.06	0.56
1:D:122:LEU:O	1:D:142:ARG:HG3	2.06	0.56
1:D:124:GLU:OE1	1:D:146:HIS:NE2	2.39	0.56
1:C:33:LYS:O	1:C:37:GLN:HG3	2.06	0.56
1:E:139:ILE:HD11	1:E:153:LEU:HD13	1.87	0.56
1:C:89:TRP:CD2	3:C:335:HOH:O	2.46	0.55
1:C:90:ASP:OD1	1:C:90:ASP:N	2.40	0.55
1:B:125:LYS:HE2	1:B:125:LYS:O	2.06	0.55
1:D:87:ARG:HB3	1:D:88:LEU:CB	2.36	0.55
1:E:156:PHE:CZ	3:E:321:HOH:O	2.52	0.55
1:D:19:GLN:HG2	1:D:20:ASN:OD1	2.07	0.55
1:C:87:ARG:HG2	3:C:351:HOH:O	2.05	0.55
1:E:139:ILE:HD11	1:E:153:LEU:CD1	2.37	0.54
1:B:119:VAL:CG1	1:B:140:ILE:HD12	2.36	0.54
1:A:122:LEU:CD1	1:A:141:TYR:CE1	2.89	0.54
1:A:122:LEU:HD12	1:A:141:TYR:CE1	2.43	0.54
1:D:21:SER:O	1:D:142:ARG:HG2	2.07	0.54
1:A:121:ILE:CD1	1:A:140:ILE:HD12	2.38	0.54
1:D:21:SER:HA	1:D:142:ARG:CZ	2.38	0.54
1:E:120:VAL:HB	3:E:315:HOH:O	2.08	0.53
1:D:26:PHE:CZ	1:D:140:ILE:CD1	2.92	0.53
1:B:156:PHE:CE1	3:B:313:HOH:O	2.61	0.53
1:D:124:GLU:HG3	1:D:146:HIS:CE1	2.43	0.53
1:C:158:ALA:CB	3:C:343:HOH:O	2.53	0.53
1:D:17:GLY:O	1:D:23:LYS:HE2	2.09	0.53
1:E:161:PRO:O	1:E:164:VAL:HG22	2.08	0.53
1:A:132:LYS:HE3	1:B:124:GLU:HG2	1.91	0.53
1:C:81:LEU:O	1:D:84:THR:HA	2.09	0.52
1:B:17:GLY:O	1:B:23:LYS:CE	2.57	0.52
1:E:83:LEU:HD13	1:E:84:THR:N	2.24	0.52
1:A:33:LYS:HG3	3:A:301:HOH:O	2.08	0.52
1:E:87:ARG:HE	1:E:88:LEU:HD22	1.74	0.51
1:D:11:PRO:HG3	1:D:172:LYS:HD2	1.92	0.51
1:A:141:TYR:CD2	1:A:147:MET:HB2	2.45	0.51
1:C:86:ARG:NH1	3:C:324:HOH:O	2.42	0.51
1:B:90:ASP:OD1	1:B:90:ASP:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:139:ILE:HG13	3:E:315:HOH:O	2.11	0.51
1:C:70:ALA:HB2	1:D:31:LEU:HD22	1.92	0.51
1:B:40:ASN:HB2	1:E:71:ASP:OD2	2.10	0.51
1:B:17:GLY:O	1:B:23:LYS:HE2	2.11	0.50
1:B:119:VAL:HG11	1:B:140:ILE:HD12	1.92	0.50
1:D:97:LEU:HD23	3:D:340:HOH:O	2.12	0.50
1:B:74:ALA:HB3	1:E:98:TYR:OH	2.11	0.50
1:D:16:VAL:CG2	1:D:120:VAL:HG22	2.42	0.49
1:E:122:LEU:HG	1:E:127:ASP:HB2	1.93	0.49
3:C:335:HOH:O	1:D:81:LEU:HD22	2.11	0.49
1:B:139:ILE:HD13	1:B:153:LEU:CD1	2.42	0.49
1:B:126:GLU:O	1:B:129:GLU:OE2	2.31	0.49
1:A:21:SER:O	1:A:142:ARG:NH2	2.45	0.49
1:A:153:LEU:HD12	1:A:153:LEU:C	2.32	0.49
1:E:156:PHE:CE1	3:E:321:HOH:O	2.66	0.48
1:B:129:GLU:CD	1:B:129:GLU:H	2.17	0.48
1:A:21:SER:O	1:A:142:ARG:NE	2.46	0.48
1:A:94:LEU:O	1:A:98:TYR:HD1	1.95	0.48
1:C:171:LEU:C	3:C:311:HOH:O	2.52	0.48
1:D:147:MET:O	1:D:148:THR:HG23	2.13	0.48
1:E:20:ASN:N	2:E:201:SO4:O4	2.31	0.48
1:E:148:THR:OG1	1:E:150:HIS:CE1	2.66	0.48
1:D:24:THR:HG23	2:D:201:SO4:O1	2.14	0.48
1:C:125:LYS:HD3	1:C:148:THR:HG21	1.95	0.48
1:A:122:LEU:HD12	1:A:141:TYR:CD1	2.49	0.47
1:C:64:ARG:HG2	1:D:28:GLU:OE2	2.13	0.47
1:E:26:PHE:CE2	1:E:30:ILE:HD11	2.48	0.47
1:E:32:GLU:O	1:E:35:SER:OG	2.32	0.47
1:C:65:TYR:N	1:C:65:TYR:CD1	2.79	0.47
1:C:136:THR:N	3:C:308:HOH:O	2.45	0.47
1:C:125:LYS:HD3	1:C:148:THR:CG2	2.45	0.47
1:A:46:HIS:HB2	1:A:111:PHE:CD1	2.50	0.47
1:A:140:ILE:CG2	1:A:158:ALA:HA	2.44	0.47
1:A:121:ILE:HD12	1:A:140:ILE:HD12	1.95	0.46
1:E:18:PHE:N	1:E:18:PHE:CD1	2.82	0.46
1:C:21:SER:HA	1:C:142:ARG:NH1	2.30	0.46
1:A:93:ARG:HD3	3:A:311:HOH:O	2.14	0.46
1:E:118:LYS:HG3	1:E:136:THR:HA	1.97	0.46
1:B:118:LYS:HD2	1:B:133:THR:OG1	2.15	0.46
1:B:88:LEU:HD21	1:B:93:ARG:HH11	1.81	0.46
1:B:129:GLU:HG2	3:B:332:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:148:THR:OG1	1:E:150:HIS:NE2	2.47	0.46
1:D:139:ILE:HD12	1:D:153:LEU:HD13	1.98	0.46
1:B:118:LYS:NZ	1:B:134:VAL:O	2.37	0.46
1:B:27:ILE:HG23	1:B:107:LEU:HD23	1.98	0.45
1:E:74:ALA:HB2	1:E:83:LEU:HD23	1.98	0.45
1:E:112:LYS:O	1:E:133:THR:HG22	2.16	0.45
1:E:24:THR:O	1:E:28:GLU:HB2	2.17	0.45
1:E:33:LYS:HB3	1:E:168:LEU:HD11	1.98	0.45
1:E:14:GLN:HA	1:E:108:ILE:O	2.17	0.45
1:E:94:LEU:O	1:E:97:LEU:HB3	2.16	0.45
1:D:41:LEU:HD13	1:D:105:CYS:SG	2.57	0.45
1:E:92:THR:HG22	3:E:312:HOH:O	2.16	0.45
1:E:49:HIS:HA	1:E:50:GLY:HA2	1.75	0.45
1:E:72:VAL:HG13	3:E:313:HOH:O	2.17	0.45
1:C:27:ILE:HG23	1:C:107:LEU:HD21	1.98	0.45
1:C:119:VAL:HG21	1:C:167:VAL:HG22	1.99	0.44
1:A:148:THR:O	1:A:149:GLU:C	2.56	0.44
1:B:17:GLY:O	1:B:23:LYS:HE3	2.17	0.44
1:E:49:HIS:CG	1:E:50:GLY:HA2	2.52	0.44
1:B:142:ARG:NH2	2:B:203:SO4:O2	2.49	0.44
1:E:162:VAL:O	1:E:166:LEU:N	2.49	0.44
1:B:47:HIS:NE2	3:B:337:HOH:O	2.36	0.44
1:C:21:SER:O	1:C:142:ARG:HG3	2.17	0.44
1:D:74:ALA:HB2	1:D:83:LEU:HD23	1.99	0.44
1:E:154:PRO:CB	3:E:321:HOH:O	2.62	0.44
1:D:21:SER:HA	1:D:142:ARG:HE	1.80	0.44
1:B:119:VAL:HG22	1:B:138:ALA:HB3	2.00	0.43
1:D:18:PHE:CG	3:D:334:HOH:O	2.69	0.43
1:E:84:THR:HG23	3:E:340:HOH:O	2.18	0.43
1:D:167:VAL:CG2	3:D:318:HOH:O	2.66	0.43
3:C:335:HOH:O	1:D:81:LEU:CB	2.65	0.43
1:C:120:VAL:HG12	1:C:122:LEU:HD13	2.01	0.43
1:E:143:LYS:HE2	3:E:329:HOH:O	2.18	0.43
1:D:26:PHE:CE2	1:D:30:ILE:HD11	2.54	0.43
1:E:148:THR:HG1	1:E:150:HIS:CE1	2.37	0.43
1:A:73:THR:OG1	1:A:84:THR:OG1	2.36	0.43
1:E:52:GLU:HB2	1:E:53:PRO:CD	2.49	0.42
1:B:142:ARG:NH2	1:B:143:LYS:HE3	2.34	0.42
1:C:92:THR:O	1:C:96:GLU:HG2	2.18	0.42
1:D:167:VAL:HG21	3:D:318:HOH:O	2.18	0.42
1:B:142:ARG:NH2	1:B:143:LYS:NZ	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:79:GLY:CA	1:D:87:ARG:O	2.68	0.42
1:A:117:PRO:HA	1:A:135:ASN:O	2.20	0.42
1:B:27:ILE:HG23	1:B:107:LEU:CD2	2.50	0.42
1:A:16:VAL:HG13	3:A:316:HOH:O	2.19	0.42
1:E:121:ILE:HD13	1:E:140:ILE:HB	2.00	0.42
1:D:146:HIS:N	3:D:316:HOH:O	2.53	0.42
1:B:87:ARG:CA	1:B:88:LEU:HB3	2.49	0.41
1:B:83:LEU:HD13	1:B:84:THR:N	2.34	0.41
1:C:123:SER:HB3	1:C:142:ARG:NH1	2.35	0.41
1:E:120:VAL:CG2	3:E:332:HOH:O	2.68	0.41
1:D:147:MET:N	3:D:316:HOH:O	2.52	0.41
1:B:44:LEU:N	3:B:318:HOH:O	2.53	0.41
1:E:52:GLU:HB2	1:E:53:PRO:HD2	2.02	0.41
1:C:125:LYS:HG2	1:C:148:THR:CB	2.49	0.41
1:B:88:LEU:CD2	1:B:93:ARG:HH11	2.33	0.41
1:A:147:MET:O	1:A:148:THR:C	2.59	0.41
1:E:166:LEU:O	1:E:170:GLN:HG2	2.20	0.41
1:A:14:GLN:HB2	1:A:118:LYS:HB3	2.01	0.41
1:B:129:GLU:CG	3:B:332:HOH:O	2.69	0.41
1:B:32:GLU:HG3	1:E:68:ALA:HB1	2.03	0.41
1:E:72:VAL:CG1	3:E:313:HOH:O	2.69	0.41
1:D:37:GLN:HG3	3:D:347:HOH:O	2.21	0.41
1:A:29:ARG:NH1	1:A:159:ASP:HA	2.32	0.41
1:B:114:ALA:HB1	1:B:115:PRO:HD2	2.03	0.41
1:C:44:LEU:HD13	3:C:334:HOH:O	2.20	0.41
1:C:145:GLU:CD	1:C:145:GLU:N	2.74	0.40
1:D:18:PHE:HD2	3:D:334:HOH:O	1.89	0.40
1:E:153:LEU:HA	1:E:154:PRO:HD3	1.99	0.40
1:A:74:ALA:HB2	1:A:83:LEU:HD23	2.03	0.40
1:C:142:ARG:CG	1:C:142:ARG:HH11	2.34	0.40
1:D:157:HIS:HB2	3:D:351:HOH:O	2.22	0.40
1:B:79:GLY:O	1:E:87:ARG:O	2.39	0.40
1:B:162:VAL:C	3:B:313:HOH:O	2.52	0.40
1:D:95:ILE:O	1:D:99:GLN:HG3	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:GLU:OE1	1:E:112:LYS:NZ[2_544]	2.06	0.14

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	144/166 (87%)	136 (94%)	8 (6%)	0	100	100
1	B	147/166 (89%)	143 (97%)	4 (3%)	0	100	100
1	C	144/166 (87%)	132 (92%)	12 (8%)	0	100	100
1	D	144/166 (87%)	140 (97%)	4 (3%)	0	100	100
1	E	159/166 (96%)	145 (91%)	14 (9%)	0	100	100
All	All	738/830 (89%)	696 (94%)	42 (6%)	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	127/140 (91%)	118 (93%)	9 (7%)	18	28
1	B	129/140 (92%)	122 (95%)	7 (5%)	27	42
1	C	127/140 (91%)	116 (91%)	11 (9%)	13	18
1	D	127/140 (91%)	120 (94%)	7 (6%)	27	41
1	E	137/140 (98%)	132 (96%)	5 (4%)	42	62
All	All	647/700 (92%)	608 (94%)	39 (6%)	24	37

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	ARG
1	A	80	VAL
1	A	82	GLN
1	A	107	LEU
1	A	132	LYS
1	A	144	LYS
1	A	146	HIS
1	A	151	GLN
1	A	164	VAL
1	B	46	HIS
1	B	83	LEU
1	B	87	ARG
1	B	103	THR
1	B	125	LYS
1	B	149	GLU
1	B	151	GLN
1	C	19	GLN
1	C	24	THR
1	C	80	VAL
1	C	82	GLN
1	C	83	LEU
1	C	84	THR
1	C	101	LEU
1	C	112	LYS
1	C	123	SER
1	C	142	ARG
1	C	159	ASP
1	D	21	SER
1	D	71	ASP
1	D	83	LEU
1	D	88	LEU
1	D	119	VAL
1	D	124	GLU
1	D	127	ASP
1	E	16	VAL
1	E	43	CYS
1	E	83	LEU
1	E	92	THR
1	E	157	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	66	GLN
1	C	66	GLN
1	E	49	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

13 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	201	-	4,4,4	0.61	0	6,6,6	0.66	0
2	SO4	A	202	-	4,4,4	0.55	0	6,6,6	0.27	0
2	SO4	A	203	-	4,4,4	0.42	0	6,6,6	0.44	0
2	SO4	B	201	-	4,4,4	0.45	0	6,6,6	0.22	0
2	SO4	B	202	-	4,4,4	0.27	0	6,6,6	0.31	0
2	SO4	B	203	-	4,4,4	0.44	0	6,6,6	0.52	0
2	SO4	C	201	-	4,4,4	0.71	0	6,6,6	0.22	0
2	SO4	C	202	-	4,4,4	0.47	0	6,6,6	0.11	0
2	SO4	D	201	-	4,4,4	0.75	0	6,6,6	0.62	0
2	SO4	D	202	-	4,4,4	0.44	0	6,6,6	0.38	0
2	SO4	D	203	-	4,4,4	0.50	0	6,6,6	0.40	0
2	SO4	E	201	-	4,4,4	0.67	0	6,6,6	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	SO4	E	202	-	4,4,4	0.42	0	6,6,6	0.13	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	201	-	-	0/0/0/0	0/0/0/0
2	SO4	A	202	-	-	0/0/0/0	0/0/0/0
2	SO4	A	203	-	-	0/0/0/0	0/0/0/0
2	SO4	B	201	-	-	0/0/0/0	0/0/0/0
2	SO4	B	202	-	-	0/0/0/0	0/0/0/0
2	SO4	B	203	-	-	0/0/0/0	0/0/0/0
2	SO4	C	201	-	-	0/0/0/0	0/0/0/0
2	SO4	C	202	-	-	0/0/0/0	0/0/0/0
2	SO4	D	201	-	-	0/0/0/0	0/0/0/0
2	SO4	D	202	-	-	0/0/0/0	0/0/0/0
2	SO4	D	203	-	-	0/0/0/0	0/0/0/0
2	SO4	E	201	-	-	0/0/0/0	0/0/0/0
2	SO4	E	202	-	-	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.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	203	SO4	1	0
2	D	201	SO4	1	0
2	E	201	SO4	1	0
2	E	202	SO4	1	0

5.7 Other polymers (i)

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^{th} 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	148/166 (89%)	0.26	5 (3%) 49 48	18, 37, 83, 142	0
1	B	151/166 (90%)	0.40	14 (9%) 11 10	22, 44, 77, 107	0
1	C	148/166 (89%)	0.56	16 (10%) 8 7	23, 49, 79, 114	0
1	D	148/166 (89%)	0.60	16 (10%) 8 7	27, 50, 83, 115	0
1	E	163/166 (98%)	1.19	34 (20%) 1 1	31, 58, 111, 144	0
All	All	758/830 (91%)	0.61	85 (11%) 7 7	18, 48, 91, 144	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	57	THR	9.4
1	E	60	LYS	8.1
1	E	58	GLU	7.6
1	A	146	HIS	6.5
1	E	59	GLY	6.5
1	B	175	SER	5.8
1	D	88	LEU	5.4
1	E	56	PHE	5.3
1	B	68	ALA	4.5
1	E	78	ALA	4.5
1	B	88	LEU	4.5
1	E	126	GLU	4.3
1	A	145	GLU	4.2
1	D	47	HIS	4.1
1	B	67	ALA	4.0
1	C	125	LYS	3.9
1	B	63	ASP	3.9
1	E	50	GLY	3.9
1	E	129	GLU	3.8
1	A	149	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	E	88	LEU	3.7
1	E	107	LEU	3.7
1	D	145	GLU	3.7
1	E	20	ASN	3.6
1	B	64	ARG	3.5
1	C	81	LEU	3.5
1	E	49	HIS	3.4
1	C	47	HIS	3.4
1	E	108	ILE	3.4
1	A	147	MET	3.3
1	B	74	ALA	3.1
1	D	78	ALA	3.1
1	E	87	ARG	3.1
1	D	67	ALA	3.1
1	E	147	MET	3.1
1	D	79	GLY	3.1
1	E	125	LYS	3.1
1	E	44	LEU	3.0
1	D	63	ASP	3.0
1	E	148	THR	3.0
1	E	51	GLY	2.9
1	D	90	ASP	2.9
1	C	149	GLU	2.8
1	C	123	SER	2.8
1	C	44	LEU	2.7
1	E	15	VAL	2.7
1	D	38	GLY	2.7
1	E	145	GLU	2.7
1	E	106	LEU	2.7
1	E	130	ALA	2.6
1	C	107	LEU	2.6
1	C	108	ILE	2.6
1	D	142	ARG	2.6
1	E	128	LEU	2.6
1	D	44	LEU	2.5
1	D	130	ALA	2.5
1	B	126	GLU	2.5
1	A	143	LYS	2.5
1	E	16	VAL	2.5
1	C	148	THR	2.5
1	C	146	HIS	2.4
1	D	36	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	64	ARG	2.4
1	E	127	ASP	2.4
1	E	159	ASP	2.3
1	B	83	LEU	2.3
1	E	13	VAL	2.2
1	B	72	VAL	2.2
1	D	68	ALA	2.2
1	D	172	LYS	2.2
1	B	128	LEU	2.2
1	C	83	LEU	2.2
1	C	167	VAL	2.2
1	E	146	HIS	2.2
1	C	129	GLU	2.2
1	C	38	GLY	2.1
1	E	36	GLU	2.1
1	C	43	CYS	2.1
1	C	132	LYS	2.1
1	E	24	THR	2.1
1	E	174	GLU	2.1
1	E	113	LYS	2.1
1	B	167	VAL	2.0
1	B	38	GLY	2.0
1	B	90	ASP	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^{th} 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(Å^2)	Q<0.9
2	SO4	D	203	5/5	0.92	0.24	-0.10	70,72,79,81	0
2	SO4	B	201	5/5	0.96	0.14	-0.14	53,54,56,60	0
2	SO4	C	201	5/5	0.89	0.18	-0.17	60,66,75,78	0
2	SO4	D	201	5/5	0.93	0.15	-0.61	45,51,57,60	0
2	SO4	A	201	5/5	0.98	0.10	-0.87	45,46,46,55	0
2	SO4	B	203	5/5	0.99	0.11	-1.11	27,28,35,36	0
2	SO4	A	202	5/5	0.96	0.10	-1.31	48,56,64,76	0
2	SO4	E	201	5/5	0.92	0.18	-1.54	72,76,89,91	0
2	SO4	E	202	5/5	0.95	0.12	-1.68	72,81,89,90	0
2	SO4	D	202	5/5	0.88	0.21	-	78,86,92,92	0
2	SO4	B	202	5/5	0.96	0.10	-	58,62,68,77	0
2	SO4	C	202	5/5	0.97	0.15	-	63,68,72,76	0
2	SO4	A	203	5/5	0.93	0.23	-	66,68,81,95	0

6.5 Other polymers (i)

There are no such residues in this entry.