



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 12:03 am BST

PDB ID : 4OYH
Title : Structure of Bacillus subtilis MobB
Authors : Kim, D.; Choe, J.
Deposited on : 2014-02-12
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

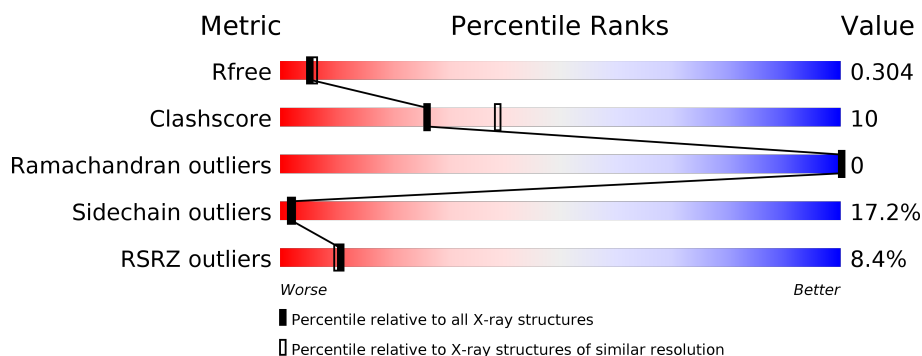
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 on 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	176	<div> <div>4%</div> <div> <div>59%</div> <div>21%</div> <div>5%</div> <div>16%</div> </div> </div>
1	B	176	<div> <div>5%</div> <div> <div>66%</div> <div>17%</div> <div>• •</div> <div>14%</div> </div> </div>
1	C	176	<div> <div>8%</div> <div> <div>56%</div> <div>25%</div> <div>•</div> <div>16%</div> </div> </div>
1	D	176	<div> <div>6%</div> <div> <div>54%</div> <div>24%</div> <div>6%</div> <div>•</div> <div>16%</div> </div> </div>
1	E	176	<div> <div>13%</div> <div> <div>60%</div> <div>24%</div> <div>•</div> <div>15%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6187 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	152	Total	C	N	O	S	0	0	0
			1199	770	203	223	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	150	Total	C	N	O	S	0	0	0
			1186	762	201	220	3			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP E0U3U4
A	2	ALA	-	expression tag	UNP E0U3U4
A	3	SER	-	expression tag	UNP E0U3U4
A	4	MET	-	expression tag	UNP E0U3U4
A	5	ALA	-	expression tag	UNP E0U3U4
A	6	LEU	-	expression tag	UNP E0U3U4
A	7	VAL	-	expression tag	UNP E0U3U4
A	8	ARG	-	expression tag	UNP E0U3U4
A	9	PRO	-	expression tag	UNP E0U3U4
A	10	PHE	-	expression tag	UNP E0U3U4
A	88	LEU	ASN	engineered mutation	UNP E0U3U4
A	166	LEU	PHE	engineered mutation	UNP E0U3U4
B	1	MET	-	expression tag	UNP E0U3U4
B	2	ALA	-	expression tag	UNP E0U3U4
B	3	SER	-	expression tag	UNP E0U3U4
B	4	MET	-	expression tag	UNP E0U3U4
B	5	ALA	-	expression tag	UNP E0U3U4
B	6	LEU	-	expression tag	UNP E0U3U4
B	7	VAL	-	expression tag	UNP E0U3U4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	8	ARG	-	expression tag	UNP E0U3U4
B	9	PRO	-	expression tag	UNP E0U3U4
B	10	PHE	-	expression tag	UNP E0U3U4
B	88	LEU	ASN	engineered mutation	UNP E0U3U4
B	166	LEU	PHE	engineered mutation	UNP E0U3U4
C	1	MET	-	expression tag	UNP E0U3U4
C	2	ALA	-	expression tag	UNP E0U3U4
C	3	SER	-	expression tag	UNP E0U3U4
C	4	MET	-	expression tag	UNP E0U3U4
C	5	ALA	-	expression tag	UNP E0U3U4
C	6	LEU	-	expression tag	UNP E0U3U4
C	7	VAL	-	expression tag	UNP E0U3U4
C	8	ARG	-	expression tag	UNP E0U3U4
C	9	PRO	-	expression tag	UNP E0U3U4
C	10	PHE	-	expression tag	UNP E0U3U4
C	88	LEU	ASN	engineered mutation	UNP E0U3U4
C	166	LEU	PHE	engineered mutation	UNP E0U3U4
D	1	MET	-	expression tag	UNP E0U3U4
D	2	ALA	-	expression tag	UNP E0U3U4
D	3	SER	-	expression tag	UNP E0U3U4
D	4	MET	-	expression tag	UNP E0U3U4
D	5	ALA	-	expression tag	UNP E0U3U4
D	6	LEU	-	expression tag	UNP E0U3U4
D	7	VAL	-	expression tag	UNP E0U3U4
D	8	ARG	-	expression tag	UNP E0U3U4
D	9	PRO	-	expression tag	UNP E0U3U4
D	10	PHE	-	expression tag	UNP E0U3U4
D	88	LEU	ASN	engineered mutation	UNP E0U3U4
D	166	LEU	PHE	engineered mutation	UNP E0U3U4
E	1	MET	-	expression tag	UNP E0U3U4
E	2	ALA	-	expression tag	UNP E0U3U4
E	3	SER	-	expression tag	UNP E0U3U4
E	4	MET	-	expression tag	UNP E0U3U4
E	5	ALA	-	expression tag	UNP E0U3U4
E	6	LEU	-	expression tag	UNP E0U3U4
E	7	VAL	-	expression tag	UNP E0U3U4
E	8	ARG	-	expression tag	UNP E0U3U4
E	9	PRO	-	expression tag	UNP E0U3U4
E	10	PHE	-	expression tag	UNP E0U3U4
E	88	LEU	ASN	engineered mutation	UNP E0U3U4
E	166	LEU	PHE	engineered mutation	UNP E0U3U4

- Molecule 2 is SULFATE ION (three-letter code: 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		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		

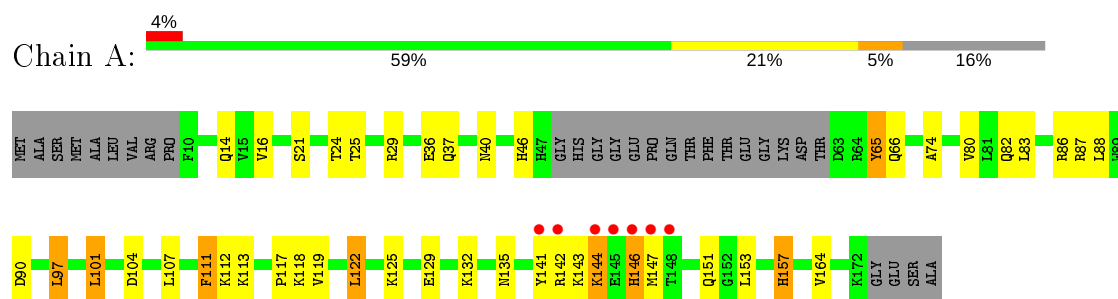
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	27	Total 27	O 27	0	0
3	B	26	Total 26	O 26	0	0
3	C	57	Total 57	O 57	0	0
3	D	64	Total 64	O 64	0	0
3	E	44	Total 44	O 44	0	0

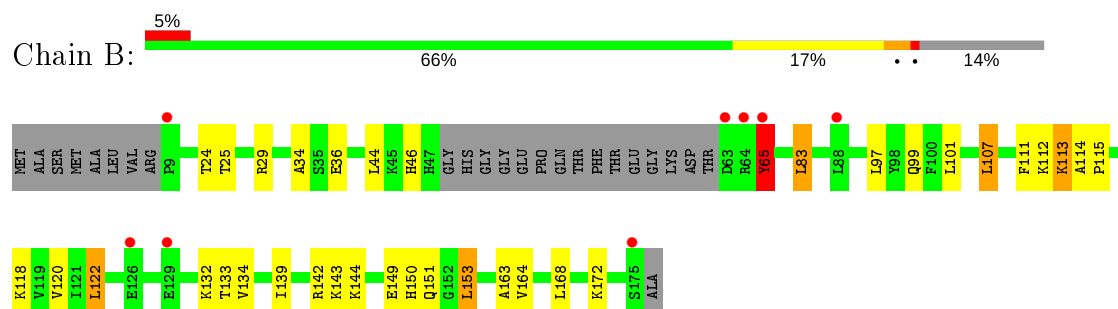
3 Residue-property plots [i](#)

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

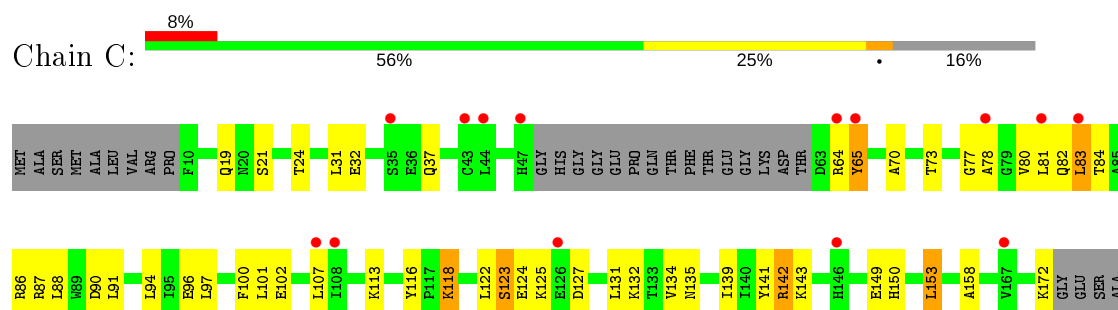
- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B



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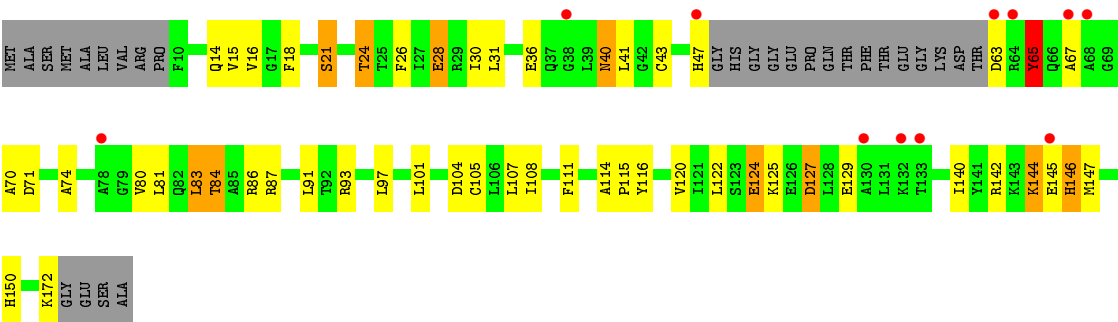


- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B

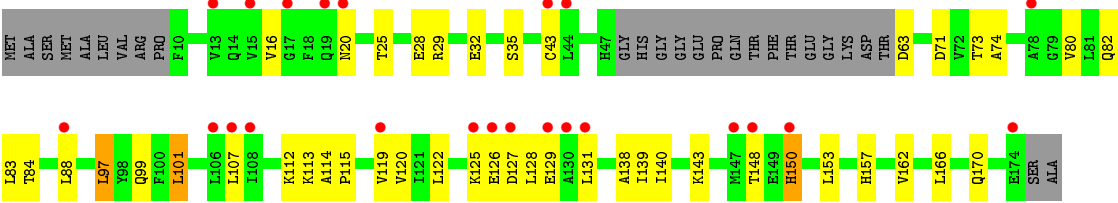


- Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B





● Molecule 1: Molybdopterin-guanine dinucleotide biosynthesis protein B



4 Data and refinement statistics

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)	98.4 (29.27-2.41) 98.4 (29.27-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.42Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.210 , 0.303 0.221 , 0.304	Depositor DCC
R_{free} test set	1682 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 76.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6187	wwPDB-VP
Average B, all atoms (Å ²)	58.0	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.*

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	0.74	1/1193 (0.1%)	0.87	3/1613 (0.2%)
1	B	0.87	2/1220 (0.2%)	0.93	6/1649 (0.4%)
1	C	0.64	1/1193 (0.1%)	0.76	2/1613 (0.1%)
1	D	0.60	0/1193	0.73	1/1613 (0.1%)
1	E	0.52	0/1206	0.67	0/1630
All	All	0.68	4/6005 (0.1%)	0.80	12/8118 (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	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	65	TYR	CD2-CE2	14.16	1.60	1.39
1	B	65	TYR	CD1-CE1	13.98	1.60	1.39
1	C	100	PHE	CG-CD1	7.51	1.50	1.38
1	A	111	PHE	CE1-CZ	5.31	1.47	1.37

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	TYR	CD1-CE1-CZ	10.61	129.35	119.80
1	B	65	TYR	CD1-CG-CD2	-10.25	106.63	117.90
1	B	65	TYR	CE1-CZ-CE2	-9.88	103.99	119.80
1	B	65	TYR	CZ-CE2-CD2	7.43	126.49	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	TYR	CA-CB-CG	6.93	126.57	113.40
1	C	100	PHE	CB-CG-CD2	-6.18	116.47	120.80
1	B	83	LEU	CA-CB-CG	6.12	129.38	115.30
1	C	83	LEU	CA-CB-CG	5.21	127.27	115.30
1	A	65	TYR	CB-CG-CD2	-5.17	117.90	121.00
1	D	65	TYR	CA-CB-CG	5.16	123.20	113.40
1	A	65	TYR	CB-CG-CD1	5.09	124.06	121.00
1	B	142	ARG	NE-CZ-NH2	-5.07	117.77	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	65	TYR	Sidechain

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	1173	0	1202	29	0
1	B	1199	0	1224	16	0
1	C	1173	0	1202	27	0
1	D	1173	0	1202	35	0
1	E	1186	0	1211	25	0
2	A	20	0	0	0	0
2	B	10	0	0	0	0
2	C	10	0	0	0	0
2	D	15	0	0	2	0
2	E	10	0	0	1	0
3	A	27	0	0	3	0
3	B	26	0	0	5	0
3	C	57	0	0	12	0
3	D	64	0	0	6	0
3	E	44	0	0	6	0
All	All	6187	0	6041	125	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 10.

All (125) 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:141:TYR:C	1:A:144:LYS:HZ3	1.71	0.94
1:C:101:LEU:O	1:D:87:ARG:NH2	2.01	0.93
1:C:158:ALA:N	3:C:346:HOH:O	2.02	0.90
1:A:21:SER:O	1:A:142:ARG:NE	2.04	0.90
1:C:141:TYR:O	3:C:346:HOH:O	1.89	0.89
1:C:87:ARG:NH2	3:C:324:HOH:O	2.16	0.78
1:E:84:THR:O	3:E:323:HOH:O	2.02	0.78
1:A:119:VAL:O	3:A:322:HOH:O	2.02	0.77
1:C:118:LYS:NZ	1:C:134:VAL:O	2.15	0.77
1:B:107:LEU:O	3:B:314:HOH:O	2.00	0.77
1:E:143:LYS:NZ	3:E:301:HOH:O	2.16	0.76
1:B:163:ALA:N	3:B:301:HOH:O	2.18	0.76
1:C:135:ASN:OD1	3:C:310:HOH:O	2.03	0.75
1:E:170:GLN:NE2	3:E:302:HOH:O	2.20	0.75
1:C:96:GLU:OE1	3:C:341:HOH:O	2.05	0.73
1:A:142:ARG:N	1:A:144:LYS:HZ3	1.86	0.73
1:E:73:THR:N	3:E:323:HOH:O	2.22	0.71
1:C:131:LEU:O	3:C:334:HOH:O	2.09	0.69
1:C:116:TYR:O	1:C:118:LYS:NZ	2.27	0.68
1:A:144:LYS:HD3	1:A:157:HIS:HA	1.78	0.64
1:C:102:GLU:O	3:C:315:HOH:O	2.13	0.64
1:E:126:GLU:N	1:E:126:GLU:OE2	2.32	0.63
1:D:144:LYS:NZ	1:D:144:LYS:O	2.26	0.63
1:A:141:TYR:HB3	1:A:146:HIS:HE2	1.63	0.63
1:A:122:LEU:O	1:A:142:ARG:N	2.31	0.63
1:E:32:GLU:O	1:E:35:SER:OG	2.16	0.62
1:D:146:HIS:N	3:D:317:HOH:O	2.33	0.60
1:A:141:TYR:HB2	1:A:144:LYS:CE	2.32	0.59
1:D:15:VAL:O	3:D:319:HOH:O	2.18	0.57
1:C:153:LEU:HB3	3:C:355:HOH:O	2.04	0.57
1:D:150:HIS:ND1	3:D:325:HOH:O	2.32	0.56
1:B:44:LEU:N	3:B:314:HOH:O	2.38	0.56
1:D:93:ARG:NH1	3:D:333:HOH:O	2.32	0.56
1:A:144:LYS:HG2	1:A:157:HIS:HB3	1.89	0.55
1:E:120:VAL:HG11	1:E:131:LEU:HD13	1.87	0.55
1:A:46:HIS:HB2	1:A:111:PHE:CE2	2.41	0.55
1:B:44:LEU:HB3	3:B:314:HOH:O	2.06	0.55
1:C:86:ARG:NH1	3:C:328:HOH:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:ALA:HB2	1:D:31:LEU:HD22	1.89	0.54
1:D:124:GLU:OE1	1:D:146:HIS:NE2	2.41	0.53
1:E:74:ALA:HB2	1:E:83:LEU:CD2	2.39	0.53
1:C:123:SER:OG	1:C:142:ARG:NH1	2.38	0.53
1:C:90:ASP:OD1	1:C:90:ASP:N	2.42	0.53
1:A:16:VAL:N	3:A:322:HOH:O	2.41	0.52
1:B:120:VAL:HG12	1:B:122:LEU:HD13	1.91	0.52
1:A:122:LEU:HD23	1:A:141:TYR:CE1	2.44	0.51
1:D:114:ALA:HB1	1:D:115:PRO:HD2	1.91	0.51
1:A:74:ALA:HB2	1:A:83:LEU:HD23	1.93	0.51
1:A:86:ARG:O	1:A:87:ARG:HD3	2.11	0.51
1:C:150:HIS:HB3	1:C:153:LEU:HD11	1.92	0.50
1:C:91:LEU:HA	1:C:94:LEU:HD12	1.94	0.49
1:B:139:ILE:HD12	1:B:153:LEU:HD13	1.94	0.49
1:C:87:ARG:HG2	3:C:354:HOH:O	2.11	0.49
1:D:67:ALA:O	1:D:86:ARG:NH2	2.46	0.49
1:E:139:ILE:HD11	1:E:153:LEU:HD13	1.95	0.48
1:E:74:ALA:HB2	1:E:83:LEU:HD22	1.96	0.48
1:A:122:LEU:HD23	1:A:141:TYR:CD1	2.49	0.48
1:D:24:THR:HG23	2:D:201:SO4:O1	2.13	0.48
3:C:339:HOH:O	1:D:81:LEU:HD22	2.14	0.47
1:E:138:ALA:O	3:E:325:HOH:O	2.20	0.47
1:C:73:THR:HG22	1:D:43:CYS:HB3	1.95	0.47
1:A:141:TYR:CD1	1:A:146:HIS:NE2	2.82	0.47
1:A:142:ARG:HG2	1:A:143:LYS:HE3	1.96	0.47
1:C:65:TYR:CE1	1:D:28:GLU:HG3	2.49	0.47
1:D:111:PHE:N	2:D:202:SO4:O1	2.40	0.46
1:E:97:LEU:HD22	1:E:101:LEU:HD22	1.97	0.46
1:B:25:THR:O	1:B:29:ARG:HG3	2.16	0.46
1:D:26:PHE:CZ	1:D:140:ILE:CD1	2.99	0.46
1:A:141:TYR:HB2	1:A:144:LYS:HE3	1.97	0.46
1:D:18:PHE:O	1:D:21:SER:OG	2.27	0.46
1:D:40:ASN:H	1:D:40:ASN:HD22	1.64	0.46
1:C:139:ILE:HD12	1:C:153:LEU:HD11	1.98	0.46
1:E:83:LEU:HD13	1:E:84:THR:N	2.31	0.46
1:B:111:PHE:HA	1:B:113:LYS:HE3	1.99	0.45
1:C:122:LEU:CD1	1:C:127:ASP:HB2	2.46	0.45
1:A:141:TYR:CB	1:A:146:HIS:HE2	2.28	0.45
1:B:46:HIS:HB2	1:B:111:PHE:CE2	2.51	0.45
1:B:114:ALA:HB1	1:B:115:PRO:HD2	1.99	0.45
1:E:128:LEU:CD2	1:E:150:HIS:CE1	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:TYR:CE1	1:E:28:GLU:OE2	2.70	0.45
1:D:147:MET:N	3:D:317:HOH:O	2.50	0.45
1:D:74:ALA:HB2	1:D:83:LEU:HD23	1.99	0.45
1:D:41:LEU:HD13	1:D:105:CYS:SG	2.58	0.44
1:B:118:LYS:HD2	1:B:133:THR:OG1	2.16	0.44
1:A:14:GLN:HB2	1:A:118:LYS:HB3	1.99	0.44
1:A:141:TYR:HB3	1:A:146:HIS:NE2	2.32	0.44
1:D:105:CYS:SG	3:D:352:HOH:O	2.62	0.44
1:E:162:VAL:O	1:E:166:LEU:N	2.44	0.44
1:A:117:PRO:HA	1:A:135:ASN:O	2.17	0.44
1:D:91:LEU:HD23	1:D:116:TYR:HE2	1.83	0.44
1:C:81:LEU:O	1:D:84:THR:HA	2.17	0.43
1:D:40:ASN:HD21	1:D:104:ASP:CG	2.21	0.43
1:A:97:LEU:HD22	1:A:101:LEU:HD22	2.01	0.43
1:E:139:ILE:HD11	1:E:153:LEU:CD1	2.48	0.43
3:C:339:HOH:O	1:D:81:LEU:HB2	2.17	0.43
1:A:144:LYS:CE	1:A:144:LYS:HA	2.49	0.43
1:B:34:ALA:HB2	1:B:168:LEU:HD21	2.00	0.43
1:D:127:ASP:N	1:D:127:ASP:OD1	2.51	0.42
1:E:114:ALA:HB1	1:E:115:PRO:HD2	2.01	0.42
1:B:150:HIS:ND1	1:B:153:LEU:HD11	2.35	0.42
1:E:122:LEU:HG	1:E:127:ASP:HB2	2.01	0.42
1:A:40:ASN:HB3	1:A:104:ASP:OD2	2.20	0.42
1:A:118:LYS:HB2	3:A:322:HOH:O	2.19	0.42
1:D:124:GLU:HG3	1:D:146:HIS:CE1	2.54	0.42
1:D:16:VAL:CG2	1:D:120:VAL:HG22	2.49	0.42
1:B:150:HIS:HB2	3:B:319:HOH:O	2.19	0.42
1:A:141:TYR:C	1:A:144:LYS:NZ	2.56	0.42
1:D:16:VAL:HG23	1:D:120:VAL:HG22	2.01	0.42
1:E:20:ASN:N	2:E:201:SO4:O4	2.45	0.41
1:A:112:LYS:HB2	1:A:112:LYS:HE3	1.72	0.41
1:E:119:VAL:HG11	1:E:140:ILE:HD12	2.01	0.41
1:D:26:PHE:CE2	1:D:30:ILE:HD11	2.55	0.41
1:E:74:ALA:HB2	1:E:83:LEU:HD23	2.03	0.41
1:B:150:HIS:HB3	1:B:153:LEU:HD11	2.02	0.41
1:E:71:ASP:OD1	1:E:71:ASP:N	2.52	0.41
1:C:123:SER:HB2	1:C:124:GLU:CD	2.42	0.41
1:C:31:LEU:HD22	1:D:70:ALA:HB2	2.03	0.41
1:A:36:GLU:O	1:A:37:GLN:CB	2.68	0.40
1:E:120:VAL:CG1	1:E:131:LEU:HD13	2.50	0.40
1:C:21:SER:HA	1:C:142:ARG:NH1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:TYR:HD1	1:D:65:TYR:H	1.70	0.40
1:E:99:GLN:HG2	3:E:341:HOH:O	2.20	0.40
1:D:14:GLN:HG2	1:D:108:ILE:HB	2.04	0.40
1:C:77:GLY:O	1:C:78:ALA:HB3	2.21	0.40
1:D:74:ALA:HB1	1:D:81:LEU:HD11	2.02	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	144/176 (82%)	133 (92%)	11 (8%)	0	100	100
1	B	148/176 (84%)	140 (95%)	8 (5%)	0	100	100
1	C	144/176 (82%)	135 (94%)	9 (6%)	0	100	100
1	D	144/176 (82%)	143 (99%)	1 (1%)	0	100	100
1	E	146/176 (83%)	141 (97%)	5 (3%)	0	100	100
All	All	726/880 (82%)	692 (95%)	34 (5%)	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	127/147 (86%)	103 (81%)	24 (19%)	1	1
1	B	130/147 (88%)	110 (85%)	20 (15%)	2	3
1	C	127/147 (86%)	104 (82%)	23 (18%)	1	2
1	D	127/147 (86%)	102 (80%)	25 (20%)	1	1
1	E	128/147 (87%)	110 (86%)	18 (14%)	3	4
All	All	639/735 (87%)	529 (83%)	110 (17%)	2	2

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	THR
1	A	25	THR
1	A	29	ARG
1	A	65	TYR
1	A	66	GLN
1	A	80	VAL
1	A	82	GLN
1	A	88	LEU
1	A	90	ASP
1	A	97	LEU
1	A	101	LEU
1	A	107	LEU
1	A	113	LYS
1	A	122	LEU
1	A	125	LYS
1	A	129	GLU
1	A	132	LYS
1	A	144	LYS
1	A	146	HIS
1	A	147	MET
1	A	151	GLN
1	A	153	LEU
1	A	157	HIS
1	A	164	VAL
1	B	24	THR
1	B	36	GLU
1	B	65	TYR
1	B	83	LEU
1	B	97	LEU
1	B	99	GLN
1	B	101	LEU

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Mol	Chain	Res	Type
1	B	107	LEU
1	B	112	LYS
1	B	113	LYS
1	B	122	LEU
1	B	132	LYS
1	B	134	VAL
1	B	143	LYS
1	B	144	LYS
1	B	149	GLU
1	B	151	GLN
1	B	153	LEU
1	B	164	VAL
1	B	172	LYS
1	C	19	GLN
1	C	24	THR
1	C	32	GLU
1	C	37	GLN
1	C	64	ARG
1	C	65	TYR
1	C	80	VAL
1	C	82	GLN
1	C	83	LEU
1	C	84	THR
1	C	88	LEU
1	C	97	LEU
1	C	107	LEU
1	C	113	LYS
1	C	118	LYS
1	C	123	SER
1	C	125	LYS
1	C	132	LYS
1	C	142	ARG
1	C	143	LYS
1	C	149	GLU
1	C	153	LEU
1	C	172	LYS
1	D	21	SER
1	D	24	THR
1	D	28	GLU
1	D	36	GLU
1	D	40	ASN
1	D	47	HIS

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Mol	Chain	Res	Type
1	D	63	ASP
1	D	65	TYR
1	D	71	ASP
1	D	80	VAL
1	D	83	LEU
1	D	84	THR
1	D	97	LEU
1	D	101	LEU
1	D	107	LEU
1	D	122	LEU
1	D	124	GLU
1	D	125	LYS
1	D	127	ASP
1	D	129	GLU
1	D	142	ARG
1	D	144	LYS
1	D	145	GLU
1	D	146	HIS
1	D	172	LYS
1	E	16	VAL
1	E	25	THR
1	E	29	ARG
1	E	43	CYS
1	E	63	ASP
1	E	80	VAL
1	E	82	GLN
1	E	88	LEU
1	E	97	LEU
1	E	101	LEU
1	E	107	LEU
1	E	112	LYS
1	E	113	LYS
1	E	125	LYS
1	E	129	GLU
1	E	148	THR
1	E	150	HIS
1	E	157	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	40	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 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	202	-	4,4,4	0.19	0	6,6,6	0.32	0
2	SO4	C	201	-	4,4,4	0.24	0	6,6,6	0.26	0
2	SO4	E	202	-	4,4,4	0.19	0	6,6,6	0.17	0
2	SO4	D	203	-	4,4,4	0.18	0	6,6,6	0.26	0
2	SO4	D	202	-	4,4,4	0.14	0	6,6,6	0.21	0
2	SO4	B	202	-	4,4,4	0.18	0	6,6,6	0.18	0
2	SO4	A	204	-	4,4,4	0.09	0	6,6,6	0.50	0
2	SO4	A	203	-	4,4,4	0.26	0	6,6,6	0.48	0
2	SO4	B	201	-	4,4,4	0.14	0	6,6,6	0.18	0
2	SO4	A	201	-	4,4,4	0.17	0	6,6,6	0.67	0
2	SO4	D	201	-	4,4,4	0.17	0	6,6,6	0.55	0
2	SO4	E	201	-	4,4,4	0.20	0	6,6,6	0.33	0
2	SO4	C	202	-	4,4,4	0.17	0	6,6,6	0.16	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	202	SO4	1	0
2	D	201	SO4	1	0
2	E	201	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	148/176 (84%)	0.17	7 (4%) 31 30	18, 41, 100, 160	0
1	B	152/176 (86%)	0.29	8 (5%) 26 25	24, 48, 89, 125	0
1	C	148/176 (84%)	0.41	14 (9%) 8 7	25, 54, 88, 107	0
1	D	148/176 (84%)	0.48	11 (7%) 14 13	30, 54, 88, 121	0
1	E	150/176 (85%)	0.80	23 (15%) 2 1	34, 63, 106, 162	0
All	All	746/880 (84%)	0.43	63 (8%) 11 10	18, 53, 97, 162	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	HIS	5.7
1	E	130	ALA	4.8
1	E	127	ASP	4.8
1	B	65	TYR	4.7
1	B	88	LEU	4.5
1	D	63	ASP	4.5
1	A	147	MET	4.4
1	E	125	LYS	4.4
1	C	47	HIS	4.4
1	B	64	ARG	4.0
1	D	47	HIS	4.0
1	E	107	LEU	3.9
1	E	108	ILE	3.7
1	A	141	TYR	3.6
1	B	63	ASP	3.4
1	B	175	SER	3.3
1	D	78	ALA	3.1
1	C	65	TYR	3.1
1	A	144	LYS	3.1
1	D	68	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	20	ASN	3.0
1	E	78	ALA	3.0
1	C	44	LEU	3.0
1	C	35	SER	2.8
1	D	145	GLU	2.8
1	E	15	VAL	2.8
1	C	108	ILE	2.7
1	E	126	GLU	2.7
1	D	64	ARG	2.7
1	E	44	LEU	2.7
1	B	126	GLU	2.6
1	D	132	LYS	2.6
1	C	126	GLU	2.6
1	D	130	ALA	2.6
1	B	9	PRO	2.6
1	C	81	LEU	2.5
1	C	43	CYS	2.5
1	E	13	VAL	2.5
1	C	64	ARG	2.5
1	C	146	HIS	2.5
1	C	78	ALA	2.5
1	D	38	GLY	2.5
1	E	88	LEU	2.4
1	E	148	THR	2.4
1	E	174	GLU	2.4
1	A	145	GLU	2.4
1	E	106	LEU	2.3
1	C	107	LEU	2.3
1	E	147	MET	2.3
1	A	142	ARG	2.3
1	E	129	GLU	2.2
1	E	119	VAL	2.2
1	A	148	THR	2.2
1	C	83	LEU	2.2
1	E	43	CYS	2.2
1	B	129	GLU	2.1
1	D	67	ALA	2.1
1	E	150	HIS	2.1
1	D	133	THR	2.1
1	E	19	GLN	2.1
1	E	17	GLY	2.0
1	E	131	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	167	VAL	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. 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	D	202	5/5	0.88	0.19	92,94,114,114	0
2	SO4	E	201	5/5	0.88	0.19	71,84,95,105	0
2	SO4	A	204	5/5	0.92	0.31	69,75,85,99	0
2	SO4	D	203	5/5	0.93	0.22	78,79,88,92	0
2	SO4	D	201	5/5	0.93	0.16	49,62,75,77	0
2	SO4	A	202	5/5	0.93	0.17	64,78,86,109	0
2	SO4	E	202	5/5	0.95	0.13	70,90,95,104	0
2	SO4	C	201	5/5	0.95	0.10	65,78,88,92	0
2	SO4	C	202	5/5	0.95	0.13	66,68,84,87	0
2	SO4	B	201	5/5	0.97	0.13	49,51,61,70	0
2	SO4	A	201	5/5	0.98	0.09	42,46,51,61	0
2	SO4	B	202	5/5	0.98	0.07	58,61,71,86	0
2	SO4	A	203	5/5	0.99	0.09	29,31,42,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.