



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:16 PM GMT

PDB ID : 2WE4
Title : CARBAMATE KINASE FROM ENTEROCOCCUS FAECALIS BOUND TO
A SULFATE ION AND TWO WATER MOLECULES, WHICH MIMIC THE
SUBSTRATE CARBAMYL PHOSPHATE
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Deposited on : 2009-03-27
Resolution : 2.02 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

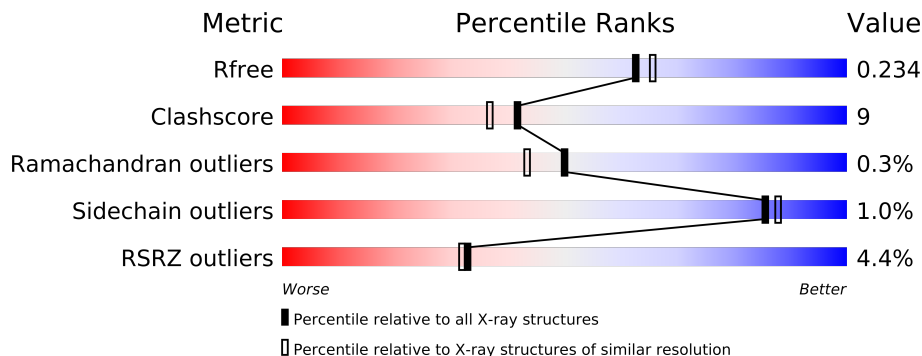
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.02 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}	66092	6003 (2.04-2.00)
Clashscore	79885	7467 (2.04-2.00)
Ramachandran outliers	78287	7370 (2.04-2.00)
Sidechain outliers	78261	7368 (2.04-2.00)
RSRZ outliers	66119	6006 (2.04-2.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	310	
1	B	310	
1	C	310	
1	D	310	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	C	1312	-	X
2	SO4	D	1312	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10190 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CARBAMATE KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	B	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	C	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	D	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			

- 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		

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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	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	C	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	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

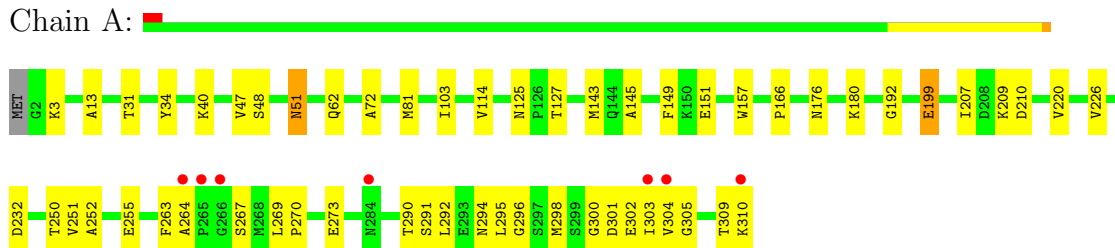
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total	O	0	0
			252	252		
3	B	200	Total	O	0	0
			200	200		
3	C	254	Total	O	0	0
			254	254		
3	D	201	Total	O	0	0
			201	201		

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.

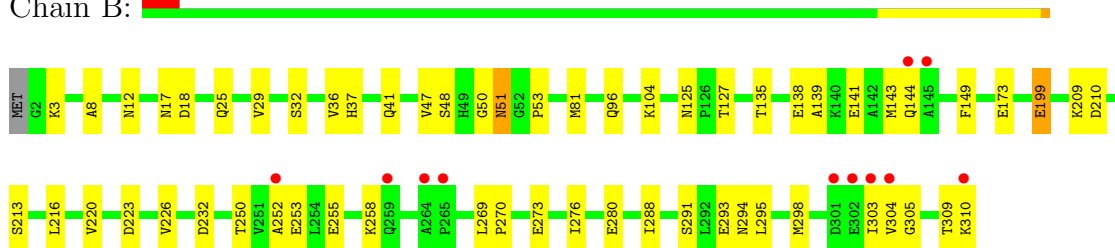
• Molecule 1: CARBAMATE KINASE 1

Chain A:



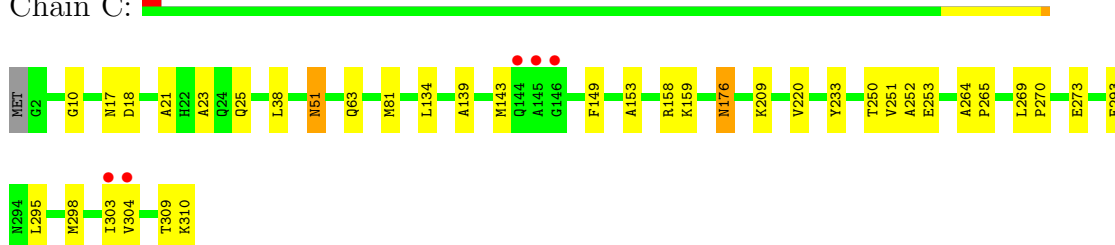
• Molecule 1: CARBAMATE KINASE 1

Chain B:



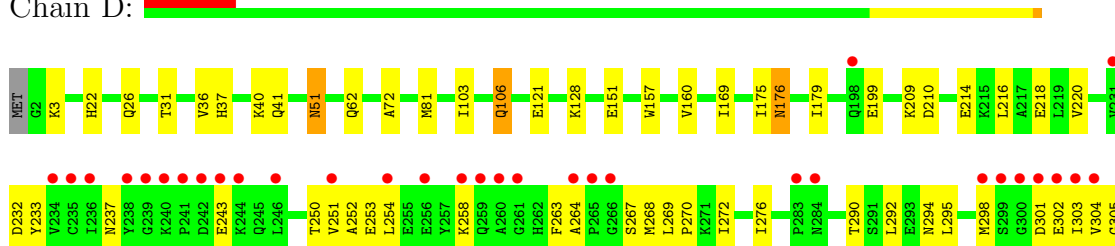
• Molecule 1: CARBAMATE KINASE 1

Chain C:



• Molecule 1: CARBAMATE KINASE 1

Chain D:



T309
K310

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.89Å 172.60Å 98.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.02 49.70 – 2.02	Depositor EDS
% Data completeness (in resolution range)	96.1 (20.00-2.02) 96.2 (49.70-2.02)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.01Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.195 , 0.234 0.195 , 0.234	Depositor DCC
R_{free} test set	4439 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 88281 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10190	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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 23.45 % 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 4.6544e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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	0.29	0/2337	0.57	0/3171
1	B	0.28	0/2337	0.53	0/3171
1	C	0.29	0/2337	0.56	0/3171
1	D	0.28	0/2337	0.55	0/3171
All	All	0.29	0/9348	0.55	0/12684

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2302	0	2337	43	0
1	B	2302	0	2337	48	0
1	C	2302	0	2337	32	0
1	D	2302	0	2337	50	0
2	A	20	0	0	0	0
2	B	20	0	0	1	0
2	C	15	0	0	0	0
2	D	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	252	0	0	4	0
3	B	200	0	0	2	0
3	C	254	0	0	3	0
3	D	201	0	0	0	0
All	All	10190	0	9348	169	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (169) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:176:ASN:HD21	1:D:220:VAL:HA	1.21	1.04
1:A:31:THR:HG23	1:A:292:LEU:HD21	1.39	1.01
1:D:251:VAL:HB	1:D:310:LYS:HD3	1.45	0.99
1:A:252:ALA:HB2	1:A:310:LYS:HE3	1.49	0.94
1:B:252:ALA:HB2	1:B:310:LYS:HE3	1.51	0.90
1:C:251:VAL:HB	1:C:310:LYS:HD3	1.55	0.88
1:C:252:ALA:HB2	1:C:310:LYS:HE3	1.56	0.88
1:B:298:MET:HE2	1:B:303:ILE:HA	1.57	0.87
1:C:298:MET:HE3	1:C:303:ILE:HD12	1.58	0.86
1:B:104:LYS:HA	1:B:104:LYS:HE2	1.60	0.83
1:D:31:THR:HG23	1:D:292:LEU:HD21	1.66	0.78
1:D:252:ALA:HB2	1:D:310:LYS:HE3	1.66	0.75
1:B:309:THR:O	1:B:310:LYS:HB3	1.85	0.75
1:B:81:MET:HE2	1:D:81:MET:HB3	1.67	0.75
1:D:176:ASN:ND2	1:D:220:VAL:HA	2.01	0.73
1:C:309:THR:O	1:C:310:LYS:HB2	1.89	0.73
1:D:106:GLN:HA	1:D:106:GLN:HE21	1.54	0.72
1:D:199:GLU:H	1:D:199:GLU:CD	1.93	0.71
1:B:173:GLU:HG2	3:B:2124:HOH:O	1.92	0.70
1:A:309:THR:O	1:A:310:LYS:HB3	1.92	0.70
1:D:309:THR:O	1:D:310:LYS:HB2	1.91	0.69
1:B:294:ASN:HD21	1:B:304:VAL:HG12	1.61	0.66
1:B:139:ALA:O	1:B:143:MET:HG3	1.96	0.66
1:C:269:LEU:HB3	1:C:270:PRO:HD3	1.79	0.65
1:B:3:LYS:HG3	1:B:223:ASP:HB2	1.80	0.64
1:D:36:VAL:O	1:D:40:LYS:HG3	1.98	0.63
1:B:96:GLN:HG3	3:B:2084:HOH:O	1.98	0.63
1:D:269:LEU:HB3	1:D:270:PRO:HD3	1.81	0.63
1:D:309:THR:O	1:D:310:LYS:CB	2.48	0.62
1:C:139:ALA:O	1:C:143:MET:HG3	2.00	0.62
1:A:250:THR:HB	1:A:310:LYS:HD2	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:255:GLU:OE1	1:B:258:LYS:HE2	1.99	0.62
1:C:309:THR:O	1:C:310:LYS:CB	2.49	0.60
1:D:40:LYS:HG2	1:D:103:ILE:HD11	1.84	0.60
1:C:250:THR:HB	1:C:310:LYS:HD2	1.83	0.60
1:B:294:ASN:HD21	1:B:304:VAL:CG1	2.15	0.60
1:B:17:ASN:CG	1:B:18:ASP:H	2.03	0.60
1:D:237:ASN:HB2	1:D:243:GLU:HA	1.84	0.60
1:C:17:ASN:CG	1:C:18:ASP:H	2.06	0.58
1:D:272:ILE:O	1:D:276:ILE:HG12	2.04	0.58
1:A:31:THR:CG2	1:A:292:LEU:HD21	2.24	0.58
1:B:17:ASN:ND2	1:B:18:ASP:H	2.01	0.58
1:B:199:GLU:H	1:B:199:GLU:CD	2.08	0.57
1:C:252:ALA:CB	1:C:310:LYS:HE3	2.33	0.57
1:A:176:ASN:O	1:A:180:LYS:HG3	2.04	0.57
1:B:269:LEU:O	1:B:273:GLU:HG2	2.05	0.57
1:A:232:ASP:O	1:A:305:GLY:HA2	2.05	0.56
1:D:232:ASP:CG	1:D:294:ASN:HD21	2.08	0.56
1:A:199:GLU:CD	1:A:199:GLU:H	2.08	0.56
1:D:290:THR:HB	1:D:305:GLY:HA3	1.88	0.56
1:C:298:MET:HE2	1:C:303:ILE:HB	1.87	0.56
1:B:141:GLU:HA	1:B:144:GLN:HE21	1.71	0.56
1:A:269:LEU:HB3	1:A:270:PRO:HD3	1.87	0.56
1:D:298:MET:HG3	1:D:302:GLU:O	2.06	0.55
1:C:21:ALA:O	1:C:25:GLN:HG3	2.07	0.55
1:B:226:VAL:HG11	1:B:295:LEU:HD11	1.89	0.55
1:A:81:MET:HB3	1:C:81:MET:HE2	1.88	0.55
1:A:232:ASP:HA	1:A:294:ASN:ND2	2.22	0.54
1:D:36:VAL:HG12	1:D:40:LYS:HE3	1.90	0.53
1:B:252:ALA:CB	1:B:310:LYS:HE3	2.33	0.53
1:A:145:ALA:HB2	3:A:2139:HOH:O	2.07	0.53
1:C:251:VAL:CB	1:C:310:LYS:HD3	2.35	0.52
1:A:13:ALA:HB2	3:A:2007:HOH:O	2.09	0.52
1:A:304:VAL:HA	3:A:2205:HOH:O	2.10	0.52
1:C:38:LEU:HD11	1:C:295:LEU:HD22	1.92	0.51
1:D:295:LEU:HD23	1:D:303:ILE:CD1	2.41	0.51
1:A:232:ASP:HA	1:A:294:ASN:HD21	1.76	0.50
1:A:269:LEU:O	1:A:273:GLU:HG3	2.11	0.50
1:A:51:ASN:N	1:A:51:ASN:HD22	2.10	0.50
1:B:252:ALA:H	1:B:310:LYS:HD3	1.77	0.49
1:D:268:MET:O	1:D:272:ILE:HG12	2.13	0.49
1:D:199:GLU:CD	1:D:199:GLU:N	2.64	0.49
1:B:81:MET:HB3	1:D:81:MET:HE2	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:252:ALA:H	1:A:310:LYS:HD3	1.77	0.48
1:A:81:MET:HE2	1:C:81:MET:HB3	1.94	0.48
1:B:269:LEU:HB3	1:B:270:PRO:HD3	1.95	0.48
1:C:176:ASN:HD21	1:C:220:VAL:HA	1.78	0.48
1:A:250:THR:HB	1:A:310:LYS:CD	2.42	0.48
1:D:209:LYS:HG3	1:D:210:ASP:N	2.29	0.48
1:D:250:THR:HB	1:D:310:LYS:HD2	1.95	0.48
1:B:32:SER:O	1:B:36:VAL:HG23	2.13	0.48
1:C:293:GLU:CD	1:C:293:GLU:H	2.16	0.48
1:B:291:SER:OG	1:B:294:ASN:HB2	2.14	0.48
1:D:3:LYS:HE3	1:D:301:ASP:OD2	2.14	0.48
1:A:294:ASN:OD1	1:A:304:VAL:HB	2.13	0.47
1:B:309:THR:O	1:B:310:LYS:CB	2.61	0.47
1:D:258:LYS:HE3	1:D:269:LEU:HD11	1.96	0.47
1:B:232:ASP:O	1:B:305:GLY:HA2	2.15	0.47
1:B:12:ASN:HA	1:B:53:PRO:HG2	1.97	0.47
1:D:254:LEU:HD12	1:D:276:ILE:HD11	1.97	0.47
1:A:252:ALA:CB	1:A:310:LYS:HE3	2.32	0.47
1:B:216:LEU:O	1:B:220:VAL:HG22	2.15	0.47
1:B:47:VAL:HG12	1:B:48:SER:N	2.30	0.47
1:D:264:ALA:HB3	1:D:267:SER:OG	2.15	0.47
1:D:251:VAL:HG13	1:D:276:ILE:HG23	1.96	0.47
1:A:151:GLU:HB2	1:A:157:TRP:CE2	2.50	0.46
1:A:209:LYS:HG3	1:A:210:ASP:N	2.29	0.46
1:D:151:GLU:HB2	1:D:157:TRP:CE2	2.50	0.46
1:A:34:TYR:HD1	1:A:296:GLY:HA3	1.79	0.46
1:D:37:HIS:O	1:D:41:GLN:HG2	2.16	0.46
1:B:135:THR:OG1	1:B:138:GLU:HG3	2.15	0.46
1:C:134:LEU:HD12	1:C:149:PHE:CE2	2.51	0.46
1:A:166:PRO:HG3	1:A:207:ILE:HG21	1.97	0.46
1:C:18:ASP:HB3	1:C:23:ALA:CB	2.46	0.45
1:D:232:ASP:O	1:D:305:GLY:HA2	2.17	0.45
1:B:209:LYS:HG3	1:B:210:ASP:N	2.32	0.45
1:C:298:MET:CE	1:C:303:ILE:HB	2.45	0.45
1:D:250:THR:OG1	1:D:253:GLU:HG3	2.17	0.45
1:B:8:ALA:HB2	1:B:213:SER:OG	2.17	0.45
1:B:50:GLY:HA3	2:B:1311:SO4:O2	2.17	0.45
1:D:292:LEU:HD12	1:D:295:LEU:HD12	1.98	0.45
1:B:276:ILE:O	1:B:280:GLU:HG3	2.17	0.45
1:B:104:LYS:CA	1:B:104:LYS:HE2	2.41	0.45
1:D:295:LEU:HD23	1:D:303:ILE:HD11	1.99	0.44
1:B:51:ASN:C	1:B:51:ASN:ND2	2.70	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:25:GLN:O	1:B:29:VAL:HG23	2.17	0.44
1:D:51:ASN:N	1:D:51:ASN:HD22	2.14	0.44
1:C:51:ASN:N	1:C:51:ASN:HD22	2.15	0.44
1:B:288:ILE:HD13	1:B:303:ILE:HG21	2.00	0.44
1:A:62:GLN:HB3	1:A:72:ALA:HB1	2.00	0.44
1:C:159:LYS:NZ	3:C:2133:HOH:O	2.50	0.44
1:A:3:LYS:HE3	1:A:301:ASP:OD1	2.18	0.44
1:D:176:ASN:ND2	1:D:220:VAL:HG12	2.33	0.44
1:D:298:MET:CE	1:D:303:ILE:HB	2.48	0.44
1:D:22:HIS:O	1:D:26:GLN:HG3	2.18	0.44
1:B:3:LYS:HG3	1:B:223:ASP:CB	2.45	0.43
1:B:293:GLU:CD	1:B:293:GLU:H	2.21	0.43
1:C:298:MET:HG3	1:C:303:ILE:HB	2.00	0.43
1:C:250:THR:OG1	1:C:253:GLU:HG3	2.18	0.43
1:D:51:ASN:ND2	1:D:51:ASN:C	2.72	0.43
1:A:143:MET:HE3	1:A:149:PHE:H	1.83	0.43
1:A:302:GLU:HA	1:A:302:GLU:OE1	2.19	0.43
1:D:298:MET:HE2	1:D:303:ILE:HB	2.01	0.42
1:C:17:ASN:CG	1:C:18:ASP:N	2.72	0.42
1:D:175:ILE:O	1:D:179:ILE:HG13	2.19	0.42
1:B:37:HIS:O	1:B:41:GLN:HG2	2.18	0.42
1:A:40:LYS:HG2	1:A:103:ILE:HD11	2.01	0.42
1:A:264:ALA:HB3	1:A:267:SER:OG	2.20	0.42
1:B:294:ASN:ND2	1:B:304:VAL:HB	2.34	0.42
1:B:250:THR:OG1	1:B:253:GLU:HG3	2.20	0.42
1:A:47:VAL:HG12	1:A:48:SER:N	2.35	0.42
1:A:298:MET:HG3	1:A:303:ILE:HG22	2.01	0.42
1:B:298:MET:HE1	1:B:303:ILE:HG23	2.02	0.42
1:D:233:TYR:OH	1:D:304:VAL:HG13	2.19	0.42
1:A:290:THR:OG1	1:A:291:SER:N	2.53	0.41
1:A:226:VAL:HG11	1:A:295:LEU:HD11	2.01	0.41
1:D:252:ALA:H	1:D:310:LYS:CD	2.33	0.41
1:A:251:VAL:O	1:A:255:GLU:HG2	2.19	0.41
1:C:264:ALA:HA	1:C:265:PRO:HD3	1.91	0.41
1:A:34:TYR:CD1	1:A:296:GLY:HA3	2.55	0.41
1:B:51:ASN:N	1:B:51:ASN:HD22	2.17	0.41
1:A:114:VAL:CG2	1:A:192:GLY:HA3	2.50	0.41
1:C:10:GLY:HA2	1:C:209:LYS:HE3	2.02	0.41
1:D:169:ILE:HD12	1:D:216:LEU:HA	2.02	0.41
1:B:298:MET:CE	1:B:303:ILE:HG23	2.50	0.41
1:A:176:ASN:HD21	1:A:220:VAL:HA	1.85	0.41
1:C:269:LEU:O	1:C:273:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:233:TYR:OH	1:C:304:VAL:HG13	2.21	0.41
1:D:62:GLN:HB3	1:D:72:ALA:HB1	2.03	0.41
1:A:125:ASN:O	1:A:127:THR:HG23	2.21	0.41
1:D:254:LEU:CD1	1:D:276:ILE:HD11	2.51	0.41
1:B:143:MET:CE	1:B:149:PHE:H	2.34	0.41
1:C:158:ARG:HB2	3:C:2131:HOH:O	2.19	0.41
1:D:128:LYS:O	1:D:160:VAL:HA	2.21	0.40
1:A:298:MET:CE	1:A:303:ILE:HG22	2.51	0.40
1:C:63:GLN:HG3	3:C:2054:HOH:O	2.21	0.40
1:D:214:GLU:O	1:D:218:GLU:HG3	2.22	0.40
1:A:145:ALA:HB3	3:A:2136:HOH:O	2.22	0.40
1:B:125:ASN:O	1:B:127:THR:HG23	2.20	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	307/310 (99%)	299 (97%)	6 (2%)	2 (1%)	30	20
1	B	307/310 (99%)	295 (96%)	12 (4%)	0	100	100
1	C	307/310 (99%)	296 (96%)	10 (3%)	1 (0%)	50	43
1	D	307/310 (99%)	297 (97%)	9 (3%)	1 (0%)	50	43
All	All	1228/1240 (99%)	1187 (97%)	37 (3%)	4 (0%)	50	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	153	ALA
1	D	263	PHE
1	A	263	PHE
1	A	300	GLY

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	248/249 (100%)	246 (99%)	2 (1%)	89	91
1	B	248/249 (100%)	246 (99%)	2 (1%)	89	91
1	C	248/249 (100%)	246 (99%)	2 (1%)	89	91
1	D	248/249 (100%)	244 (98%)	4 (2%)	75	76
All	All	992/996 (100%)	982 (99%)	10 (1%)	85	88

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	199	GLU
1	B	51	ASN
1	B	199	GLU
1	C	51	ASN
1	C	176	ASN
1	D	51	ASN
1	D	106	GLN
1	D	121	GLU
1	D	176	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	170	HIS
1	A	245	GLN
1	B	17	ASN
1	B	51	ASN
1	B	95	ASN
1	B	106	GLN
1	B	144	GLN
1	B	248	ASN
1	B	294	ASN
1	C	12	ASN

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Mol	Chain	Res	Type
1	C	51	ASN
1	C	57	ASN
1	C	170	HIS
1	C	176	ASN
1	C	248	ASN
1	D	51	ASN
1	D	106	GLN
1	D	176	ASN
1	D	294	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

15 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	1311	-	4,4,4	3.43	2 (50%)	6,6,6	0.94	0
2	SO4	A	1312	-	4,4,4	3.46	2 (50%)	6,6,6	0.94	0
2	SO4	A	1313	-	4,4,4	3.44	2 (50%)	6,6,6	0.96	0
2	SO4	A	1314	-	4,4,4	3.43	2 (50%)	6,6,6	0.92	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	B	1311	-	4,4,4	3.39	2 (50%)	6,6,6	0.87	0
2	SO4	B	1312	-	4,4,4	3.42	2 (50%)	6,6,6	0.93	0
2	SO4	B	1313	-	4,4,4	3.35	2 (50%)	6,6,6	0.95	0
2	SO4	B	1314	-	4,4,4	3.42	2 (50%)	6,6,6	0.94	0
2	SO4	C	1311	-	4,4,4	3.46	2 (50%)	6,6,6	0.92	0
2	SO4	C	1312	-	4,4,4	3.47	2 (50%)	6,6,6	0.93	0
2	SO4	C	1313	-	4,4,4	3.37	2 (50%)	6,6,6	0.90	0
2	SO4	D	1311	-	4,4,4	3.42	2 (50%)	6,6,6	0.89	0
2	SO4	D	1312	-	4,4,4	3.47	2 (50%)	6,6,6	0.93	0
2	SO4	D	1313	-	4,4,4	3.41	2 (50%)	6,6,6	0.91	0
2	SO4	D	1314	-	4,4,4	3.44	2 (50%)	6,6,6	0.93	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	1311	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1312	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1313	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1314	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1311	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1312	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1313	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1314	-	-	0/0/0/0	0/0/0/0
2	SO4	C	1311	-	-	0/0/0/0	0/0/0/0
2	SO4	C	1312	-	-	0/0/0/0	0/0/0/0
2	SO4	C	1313	-	-	0/0/0/0	0/0/0/0
2	SO4	D	1311	-	-	0/0/0/0	0/0/0/0
2	SO4	D	1312	-	-	0/0/0/0	0/0/0/0
2	SO4	D	1313	-	-	0/0/0/0	0/0/0/0
2	SO4	D	1314	-	-	0/0/0/0	0/0/0/0

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1311	SO4	O3-S	-5.10	1.29	1.47
2	A	1311	SO4	O3-S	-5.03	1.30	1.47
2	D	1312	SO4	O1-S	4.91	1.63	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1314	SO4	O1-S	4.88	1.63	1.47
2	D	1311	SO4	O3-S	-4.88	1.30	1.47
2	A	1312	SO4	O1-S	4.87	1.62	1.47
2	C	1312	SO4	O3-S	-4.87	1.30	1.47
2	A	1313	SO4	O3-S	-4.86	1.30	1.47
2	D	1314	SO4	O3-S	-4.84	1.30	1.47
2	C	1312	SO4	O1-S	4.83	1.62	1.47
2	B	1314	SO4	O1-S	4.82	1.62	1.47
2	A	1312	SO4	O3-S	-4.80	1.30	1.47
2	D	1312	SO4	O3-S	-4.80	1.31	1.47
2	B	1311	SO4	O3-S	-4.79	1.31	1.47
2	B	1312	SO4	O1-S	4.79	1.62	1.47
2	D	1314	SO4	O1-S	4.78	1.62	1.47
2	D	1313	SO4	O1-S	4.77	1.62	1.47
2	A	1313	SO4	O1-S	4.77	1.62	1.47
2	B	1312	SO4	O3-S	-4.77	1.31	1.47
2	D	1313	SO4	O3-S	-4.76	1.31	1.47
2	B	1314	SO4	O3-S	-4.76	1.31	1.47
2	C	1313	SO4	O3-S	-4.74	1.31	1.47
2	A	1314	SO4	O3-S	-4.73	1.31	1.47
2	B	1313	SO4	O1-S	4.72	1.62	1.47
2	B	1313	SO4	O3-S	-4.66	1.31	1.47
2	B	1311	SO4	O1-S	4.65	1.62	1.47
2	D	1311	SO4	O1-S	4.65	1.62	1.47
2	C	1313	SO4	O1-S	4.63	1.62	1.47
2	C	1311	SO4	O1-S	4.55	1.61	1.47
2	A	1311	SO4	O1-S	4.53	1.61	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	309/310 (99%)	0.14	7 (2%) 57 58	13, 24, 46, 60	0
1	B	309/310 (99%)	0.27	11 (3%) 41 40	14, 27, 50, 73	0
1	C	309/310 (99%)	-0.02	5 (1%) 68 69	13, 22, 43, 65	0
1	D	309/310 (99%)	0.27	32 (10%) 7 6	13, 24, 65, 80	0
All	All	1236/1240 (99%)	0.17	55 (4%) 33 32	13, 24, 52, 80	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	303	ILE	9.8
1	D	241	PRO	6.2
1	A	303	ILE	5.2
1	D	301	ASP	5.0
1	B	145	ALA	4.8
1	D	238	TYR	4.7
1	B	301	ASP	4.5
1	D	239	GLY	4.3
1	C	145	ALA	4.1
1	D	266	GLY	4.0
1	D	243	GLU	3.9
1	B	310	LYS	3.9
1	D	300	GLY	3.8
1	D	304	VAL	3.8
1	D	235	CYS	3.6
1	D	234	VAL	3.6
1	A	264	ALA	3.5
1	B	304	VAL	3.3
1	A	304	VAL	3.2
1	A	310	LYS	3.2
1	C	304	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	302	GLU	3.0
1	D	242	ASP	3.0
1	D	265	PRO	3.0
1	B	302	GLU	3.0
1	D	259	GLN	3.0
1	B	265	PRO	2.9
1	D	251	VAL	2.7
1	B	252	ALA	2.7
1	D	298	MET	2.7
1	C	144	GLN	2.7
1	C	303	ILE	2.7
1	D	240	LYS	2.6
1	D	284	ASN	2.6
1	D	231	VAL	2.6
1	D	236	ILE	2.5
1	D	303	ILE	2.5
1	D	244	LYS	2.5
1	B	264	ALA	2.5
1	D	299	SER	2.5
1	A	266	GLY	2.4
1	C	146	GLY	2.4
1	B	259	GLN	2.4
1	D	264	ALA	2.3
1	D	254	LEU	2.3
1	D	261	GLY	2.3
1	A	265	PRO	2.3
1	D	258	LYS	2.2
1	A	284	ASN	2.2
1	D	246	LEU	2.2
1	D	198	GLN	2.2
1	B	144	GLN	2.2
1	D	283	PRO	2.2
1	D	256	GLU	2.1
1	D	260	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	C	1312	5/5	0.28	3.80	86,87,87,87	0
2	SO4	D	1312	5/5	0.22	3.51	62,62,62,63	0
2	SO4	B	1314	5/5	0.15	1.86	69,70,70,70	0
2	SO4	A	1312	5/5	0.15	0.87	66,67,67,68	0
2	SO4	D	1311	5/5	0.11	0.19	19,23,24,26	0
2	SO4	B	1311	5/5	0.12	0.18	26,27,29,31	0
2	SO4	D	1313	5/5	0.14	0.13	49,49,50,51	0
2	SO4	B	1312	5/5	0.15	0.06	80,80,80,80	0
2	SO4	A	1311	5/5	0.12	-0.04	22,23,24,24	0
2	SO4	B	1313	5/5	0.13	-0.14	39,40,40,41	0
2	SO4	A	1314	5/5	0.13	-0.38	55,56,57,57	0
2	SO4	C	1311	5/5	0.10	-0.52	21,24,26,27	0
2	SO4	A	1313	5/5	0.11	-0.81	34,35,37,40	0
2	SO4	C	1313	5/5	0.07	-1.40	21,23,23,24	0
2	SO4	D	1314	5/5	0.19	-1.61	72,73,73,73	0

6.5 Other polymers ⓘ

There are no such residues in this entry.