Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 06:24 AM EDT

PDB ID	:	2E28
Title	:	Crystal structure analysis of pyruvate kinase from Bacillus stearothermophilus
Authors	:	Suzuki, K.
Deposited on	:	2006-11-09
Resolution	:	2.40 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

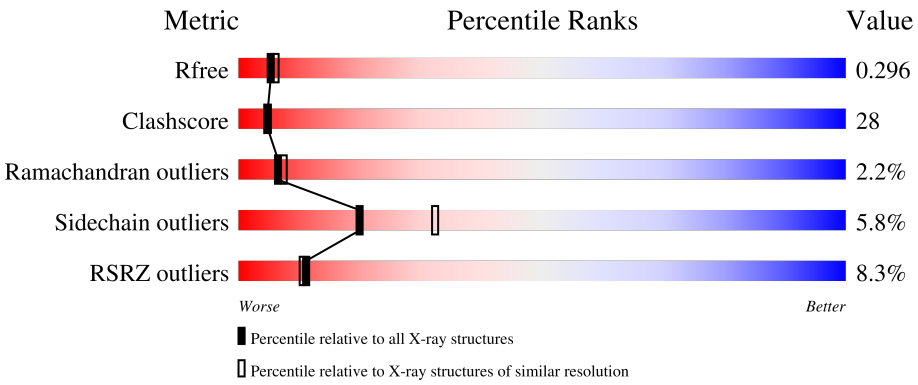
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.40 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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	587	8% 58% 35% 6% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4522 atoms, of which 4 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.

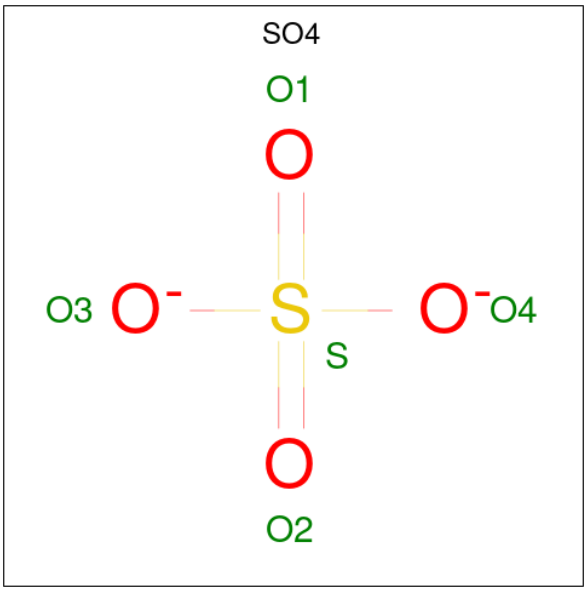
- Molecule 1 is a protein called Pyruvate kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	587	4364	2725	4	770	848	17	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	SER	CYS	engineered mutation	UNP Q02499
A	268	SER	CYS	engineered mutation	UNP Q02499

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



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

- Molecule 3 is water.

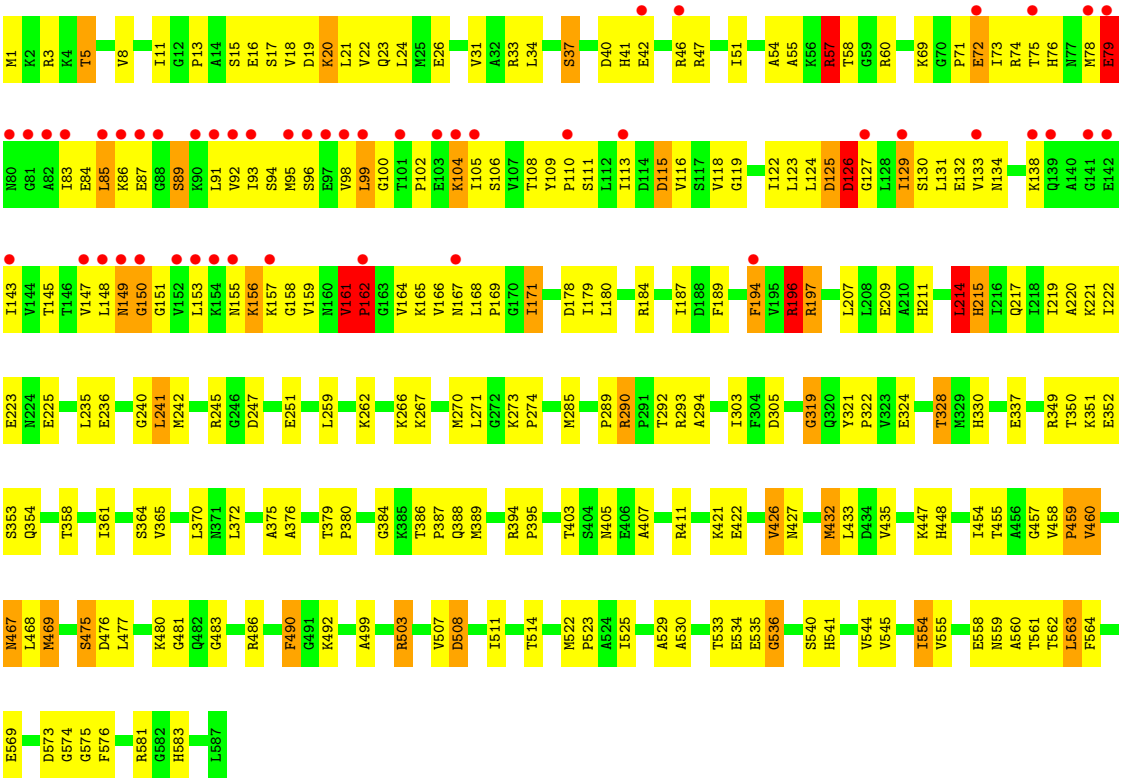
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	153	153	153	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Pyruvate kinase

Chain A: 8% 58% 35% 6%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α, β, γ	145.97Å 145.97Å 118.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.40 47.78 – 2.49	Depositor EDS
% Data completeness (in resolution range)	97.7 (50.00-2.40) 98.4 (47.78-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	7.17 (at 2.48Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.226 , 0.294 0.235 , 0.296	Depositor DCC
R_{free} test set	2552 reflections (9.81%)	wwPDB-VP
Wilson B-factor (Å^2)	48.0	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 58.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4522	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.65	13/4408 (0.3%)	0.94	35/5969 (0.6%)

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	1	4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	196	ARG	C-N	-14.69	1.00	1.34
1	A	33	ARG	C-N	-13.17	1.03	1.34
1	A	104	LYS	C-N	-9.83	1.11	1.34
1	A	184	ARG	C-N	-9.17	1.12	1.34
1	A	486	ARG	C-N	-9.17	1.12	1.34
1	A	499	ALA	C-N	-7.89	1.15	1.34
1	A	490	PHE	C-N	-6.67	1.21	1.33
1	A	167	ASN	C-N	-6.57	1.19	1.34
1	A	126	ASP	C-N	-6.31	1.21	1.33
1	A	426	VAL	C-N	-6.28	1.19	1.34
1	A	161	VAL	C-N	5.89	1.45	1.34
1	A	125	ASP	C-N	-5.38	1.21	1.34
1	A	169	PRO	N-CD	5.29	1.55	1.47

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	162	PRO	C-N-CA	12.56	148.67	122.30
1	A	104	LYS	O-C-N	-11.59	104.15	122.70
1	A	167	ASN	O-C-N	-11.22	104.75	122.70
1	A	33	ARG	C-N-CA	10.42	147.76	121.70
1	A	486	ARG	CB-CA-C	9.80	130.01	110.40
1	A	33	ARG	O-C-N	-8.92	108.42	122.70
1	A	168	LEU	C-N-CD	8.71	146.70	128.40
1	A	215	HIS	CA-C-N	-8.68	98.10	117.20
1	A	427	ASN	O-C-N	-7.97	109.95	122.70
1	A	104	LYS	CA-C-N	7.51	133.72	117.20
1	A	486	ARG	O-C-N	-7.30	111.01	122.70
1	A	126	ASP	O-C-N	-7.09	111.15	123.20
1	A	167	ASN	CA-C-N	6.71	131.97	117.20
1	A	72	GLU	CB-CA-C	-6.45	97.51	110.40
1	A	554	ILE	CB-CA-C	6.43	124.46	111.60
1	A	162	PRO	N-CA-C	6.28	128.42	112.10
1	A	57	ARG	CB-CA-C	6.27	122.94	110.40
1	A	194	PHE	CB-CG-CD2	6.11	125.08	120.80
1	A	215	HIS	O-C-N	6.10	132.46	122.70
1	A	197	ARG	CB-CA-C	-6.09	98.23	110.40
1	A	34	LEU	CB-CA-C	6.00	121.59	110.20
1	A	169	PRO	CA-N-CD	-5.98	103.13	111.50
1	A	47	ARG	CB-CA-C	5.85	122.10	110.40
1	A	33	ARG	CA-C-N	5.84	130.06	117.20
1	A	427	ASN	CA-C-N	5.80	129.95	117.20
1	A	126	ASP	CA-C-N	5.73	127.65	116.20
1	A	184	ARG	C-N-CA	5.60	135.70	121.70
1	A	196	ARG	O-C-N	-5.54	113.83	122.70
1	A	499	ALA	C-N-CA	5.51	135.47	121.70
1	A	161	VAL	O-C-N	-5.45	110.74	121.10
1	A	72	GLU	CA-C-O	5.45	131.54	120.10
1	A	499	ALA	O-C-N	-5.44	114.00	122.70
1	A	503	ARG	CB-CA-C	5.42	121.24	110.40
1	A	161	VAL	CA-CB-CG2	5.40	119.00	110.90
1	A	194	PHE	CB-CG-CD1	-5.10	117.23	120.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	162	PRO	CA

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	161	VAL	Mainchain
1	A	162	PRO	Mainchain
1	A	214	LEU	Mainchain
1	A	72	GLU	Mainchain

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	4360	4	4507	246	1
2	A	5	0	0	0	0
3	A	153	0	0	4	1
All	All	4518	4	4507	246	2

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 28.

All (246) 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:162:PRO:HG3	1:A:251:GLU:CD	1.34	1.47
1:A:162:PRO:CG	1:A:251:GLU:CD	1.86	1.41
1:A:162:PRO:HG2	1:A:251:GLU:CG	1.51	1.40
1:A:162:PRO:HG2	1:A:251:GLU:CB	1.73	1.19
1:A:162:PRO:CG	1:A:251:GLU:OE2	1.89	1.17
1:A:535:GLU:HG3	1:A:536:GLY:H	0.98	1.13
1:A:162:PRO:HG3	1:A:251:GLU:OE2	1.48	1.11
1:A:162:PRO:CG	1:A:251:GLU:CG	2.30	1.06
1:A:197:ARG:NH2	3:A:642:HOH:O	1.97	0.97
1:A:40:ASP:OD1	1:A:42:GLU:HG2	1.67	0.94
1:A:535:GLU:HG3	1:A:536:GLY:N	1.82	0.94
1:A:534:GLU:OE2	1:A:561:THR:HG22	1.66	0.94
1:A:197:ARG:CZ	3:A:642:HOH:O	2.16	0.93
1:A:162:PRO:HG2	1:A:251:GLU:HB3	1.48	0.92
1:A:535:GLU:CG	1:A:536:GLY:H	1.74	0.92
1:A:222:ILE:HG12	1:A:241:LEU:HD21	1.50	0.91
1:A:476:ASP:HB2	1:A:581:ARG:NH1	1.86	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:SER:HA	1:A:20:LYS:HG2	1.55	0.89
1:A:57:ARG:HH21	1:A:57:ARG:HB2	1.37	0.88
1:A:162:PRO:HG2	1:A:251:GLU:CD	1.66	0.88
1:A:116:VAL:HG11	1:A:143:ILE:HD12	1.56	0.86
1:A:3:ARG:HE	1:A:330:HIS:HD2	1.24	0.86
1:A:3:ARG:HE	1:A:330:HIS:CD2	1.94	0.85
1:A:71:PRO:HG2	1:A:196:ARG:HH12	1.39	0.85
1:A:476:ASP:HB2	1:A:581:ARG:HH12	1.43	0.83
1:A:129:ILE:HD13	1:A:150:GLY:HA2	1.60	0.81
1:A:365:VAL:HA	1:A:469:MET:HE3	1.62	0.80
1:A:162:PRO:HG3	1:A:251:GLU:OE1	1.81	0.80
1:A:26:GLU:HA	1:A:60:ARG:HH22	1.46	0.79
1:A:133:VAL:HA	1:A:145:THR:HG22	1.63	0.79
1:A:86:LYS:HG2	1:A:87:GLU:H	1.47	0.79
1:A:71:PRO:HG2	1:A:196:ARG:NH1	1.97	0.79
1:A:448:HIS:HD2	1:A:475:SER:HA	1.47	0.78
1:A:459:PRO:O	1:A:460:VAL:HG22	1.85	0.77
1:A:194:PHE:CD2	1:A:223:GLU:OE1	2.37	0.77
1:A:162:PRO:HG2	1:A:251:GLU:HG2	1.64	0.77
1:A:156:LYS:HD2	1:A:156:LYS:O	1.84	0.76
1:A:20:LYS:HE3	1:A:20:LYS:HA	1.69	0.75
1:A:447:LYS:HD3	1:A:448:HIS:N	2.00	0.75
1:A:78:MET:HB3	1:A:83:ILE:HG12	1.67	0.74
1:A:559:ASN:HB3	1:A:562:THR:CG2	2.19	0.72
1:A:40:ASP:OD1	1:A:42:GLU:CG	2.37	0.72
1:A:74:ARG:HG3	1:A:75:THR:H	1.54	0.71
1:A:458:VAL:H	1:A:467:ASN:HD21	1.37	0.71
1:A:18:VAL:O	1:A:22:VAL:HG23	1.89	0.71
1:A:162:PRO:CB	1:A:251:GLU:OE2	2.38	0.70
1:A:432:MET:HE1	1:A:433:LEU:HD23	1.72	0.70
1:A:5:THR:HG23	1:A:337:GLU:OE2	1.91	0.70
1:A:129:ILE:HD11	1:A:147:VAL:HG13	1.74	0.69
1:A:432:MET:HE2	1:A:432:MET:O	1.93	0.69
1:A:189:PHE:CD1	1:A:217:GLN:HB2	2.29	0.68
1:A:54:ALA:O	1:A:58:THR:HG22	1.94	0.68
1:A:511:ILE:HD12	1:A:530:ALA:HB3	1.76	0.67
1:A:83:ILE:HG22	1:A:84:GLU:N	2.10	0.67
1:A:171:ILE:HD13	1:A:171:ILE:H	1.60	0.67
1:A:481:GLY:C	1:A:554:ILE:HD11	2.15	0.67
1:A:98:VAL:HG22	1:A:106:SER:HB3	1.76	0.66
1:A:57:ARG:HB2	1:A:57:ARG:NH2	2.07	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:THR:HG22	1:A:294:ALA:H	1.59	0.66
1:A:490:PHE:O	1:A:511:ILE:CG1	2.44	0.66
1:A:83:ILE:HG22	1:A:84:GLU:H	1.61	0.65
1:A:222:ILE:CG1	1:A:241:LEU:HD21	2.26	0.64
1:A:241:LEU:HD23	1:A:242:MET:H	1.62	0.64
1:A:490:PHE:O	1:A:511:ILE:HG12	1.96	0.64
1:A:459:PRO:O	1:A:460:VAL:HG13	1.97	0.64
1:A:133:VAL:HG22	1:A:143:ILE:HD11	1.79	0.64
1:A:157:LYS:HE2	1:A:157:LYS:HA	1.78	0.64
1:A:161:VAL:N	1:A:162:PRO:HD3	2.13	0.63
1:A:492:LYS:HG2	1:A:569:GLU:OE1	1.99	0.62
1:A:351:LYS:O	1:A:352:GLU:HG2	1.98	0.62
1:A:458:VAL:HA	1:A:459:PRO:C	2.20	0.61
1:A:221:LYS:HG2	1:A:242:MET:HB3	1.83	0.61
1:A:354:GLN:HE21	1:A:354:GLN:HA	1.64	0.61
1:A:26:GLU:HA	1:A:60:ARG:NH2	2.16	0.61
1:A:361:ILE:HG13	1:A:467:ASN:HA	1.81	0.61
1:A:575:GLY:O	1:A:576:PHE:HB2	2.00	0.61
1:A:384:GLY:O	1:A:387:PRO:HD2	2.01	0.60
1:A:321:TYR:HB3	1:A:324:GLU:HB2	1.81	0.60
1:A:83:ILE:HG23	1:A:102:PRO:HG3	1.83	0.60
1:A:354:GLN:HA	1:A:354:GLN:NE2	2.16	0.60
1:A:477:LEU:HD21	1:A:480:LYS:HE2	1.84	0.60
1:A:73:ILE:O	1:A:159:VAL:HB	2.01	0.60
1:A:241:LEU:HD23	1:A:242:MET:N	2.16	0.60
1:A:525:ILE:HG21	1:A:545:VAL:HG11	1.82	0.60
1:A:8:VAL:HG22	1:A:31:VAL:HB	1.84	0.59
1:A:235:LEU:HB3	1:A:271:LEU:CD1	2.32	0.59
1:A:74:ARG:HG3	1:A:75:THR:N	2.16	0.59
1:A:125:ASP:HA	1:A:157:LYS:HB3	1.83	0.59
1:A:162:PRO:CG	1:A:251:GLU:HB3	2.25	0.58
1:A:73:ILE:HG13	1:A:109:TYR:HB2	1.84	0.58
1:A:507:VAL:HG12	1:A:508:ASP:H	1.68	0.58
1:A:132:GLU:HG2	1:A:148:LEU:HD11	1.86	0.58
1:A:60:ARG:HH21	1:A:60:ARG:HG3	1.69	0.57
1:A:235:LEU:HB3	1:A:271:LEU:HD12	1.86	0.57
1:A:1:MET:HE2	3:A:699:HOH:O	2.04	0.57
1:A:162:PRO:CG	1:A:251:GLU:HG2	2.26	0.56
1:A:476:ASP:CB	1:A:581:ARG:HH12	2.17	0.56
1:A:93:ILE:HB	1:A:143:ILE:HG23	1.89	0.55
1:A:468:LEU:C	1:A:468:LEU:HD23	2.26	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:THR:HG22	1:A:389:MET:HG3	1.89	0.55
1:A:384:GLY:C	1:A:387:PRO:HD2	2.26	0.55
1:A:42:GLU:O	1:A:46:ARG:HG3	2.07	0.55
1:A:93:ILE:HB	1:A:143:ILE:CG2	2.37	0.55
1:A:124:LEU:HA	1:A:158:GLY:O	2.07	0.55
1:A:324:GLU:O	1:A:328:THR:HG23	2.08	0.54
1:A:55:ALA:O	1:A:58:THR:O	2.23	0.54
1:A:21:LEU:HA	1:A:24:LEU:HD23	1.90	0.54
1:A:132:GLU:HG3	1:A:148:LEU:HD21	1.90	0.54
1:A:17:SER:OG	1:A:20:LYS:HB2	2.09	0.53
1:A:20:LYS:O	1:A:24:LEU:HD22	2.08	0.53
1:A:129:ILE:HA	1:A:149:ASN:O	2.09	0.53
1:A:541:HIS:CE1	1:A:545:VAL:HG21	2.44	0.53
1:A:85:LEU:HB3	1:A:147:VAL:HG21	1.91	0.53
1:A:108:THR:HG22	1:A:108:THR:O	2.09	0.53
1:A:535:GLU:CG	1:A:536:GLY:N	2.48	0.53
1:A:490:PHE:CD2	1:A:583:HIS:CG	2.97	0.52
1:A:540:SER:O	1:A:544:VAL:HG23	2.09	0.52
1:A:92:VAL:O	1:A:104:LYS:HA	2.10	0.52
1:A:365:VAL:HA	1:A:469:MET:CE	2.35	0.52
1:A:379:THR:OG1	1:A:387:PRO:HG3	2.10	0.52
1:A:507:VAL:HG12	1:A:508:ASP:N	2.25	0.52
1:A:79:GLU:H	1:A:99:LEU:HD22	1.75	0.51
1:A:514:THR:O	1:A:533:THR:HA	2.10	0.51
1:A:285:MET:SD	1:A:328:THR:HG21	2.51	0.51
1:A:405:ASN:OD1	1:A:407:ALA:N	2.43	0.51
1:A:215:HIS:O	1:A:411:ARG:NH2	2.44	0.51
1:A:468:LEU:HD23	1:A:469:MET:N	2.26	0.51
1:A:403:THR:O	1:A:422:GLU:HA	2.10	0.51
1:A:432:MET:HE2	1:A:432:MET:C	2.31	0.51
1:A:91:LEU:HD12	1:A:131:LEU:HD13	1.93	0.51
1:A:245:ARG:H	1:A:245:ARG:HD3	1.75	0.51
1:A:41:HIS:HE1	1:A:178:ASP:OD2	1.94	0.50
1:A:511:ILE:CD1	1:A:529:ALA:HB3	2.41	0.50
1:A:73:ILE:HD11	1:A:166:VAL:HG11	1.92	0.50
1:A:123:LEU:HB3	1:A:127:GLY:HA2	1.94	0.50
1:A:126:ASP:O	1:A:126:ASP:OD2	2.29	0.50
1:A:575:GLY:O	1:A:576:PHE:CB	2.59	0.50
1:A:358:THR:CG2	1:A:389:MET:HG3	2.41	0.50
1:A:349:ARG:O	1:A:353:SER:HB2	2.12	0.49
1:A:380:PRO:HG2	1:A:432:MET:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:ARG:N	1:A:395:PRO:HD3	2.27	0.49
1:A:457:GLY:HA2	1:A:467:ASN:ND2	2.27	0.49
1:A:241:LEU:CD2	1:A:242:MET:N	2.76	0.49
1:A:267:LYS:HA	1:A:270:MET:HE2	1.93	0.49
1:A:350:THR:O	1:A:353:SER:HB3	2.13	0.49
1:A:266:LYS:O	1:A:270:MET:HG3	2.12	0.49
1:A:79:GLU:HG3	1:A:83:ILE:HD11	1.94	0.49
1:A:109:TYR:CZ	1:A:166:VAL:HG13	2.48	0.49
1:A:5:THR:HG21	1:A:303:ILE:HD13	1.95	0.49
1:A:289:PRO:HG3	1:A:321:TYR:CZ	2.48	0.49
1:A:83:ILE:HD12	1:A:102:PRO:HD3	1.95	0.49
1:A:113:ILE:HD11	1:A:138:LYS:HA	1.95	0.49
1:A:483:GLY:HA3	1:A:574:GLY:O	2.12	0.49
1:A:563:LEU:HD12	1:A:564:PHE:CE1	2.48	0.49
1:A:534:GLU:HG2	1:A:560:ALA:HB3	1.95	0.48
1:A:79:GLU:HA	1:A:99:LEU:HD21	1.95	0.48
1:A:365:VAL:CA	1:A:469:MET:HE3	2.39	0.48
1:A:116:VAL:CG2	1:A:133:VAL:HG21	2.43	0.48
1:A:321:TYR:N	1:A:322:PRO:HD3	2.28	0.48
1:A:75:THR:O	1:A:156:LYS:HA	2.13	0.48
1:A:180:LEU:HD21	1:A:211:HIS:CD2	2.48	0.48
1:A:559:ASN:HB3	1:A:562:THR:HG22	1.93	0.48
1:A:13:PRO:HA	1:A:16:GLU:OE2	2.14	0.47
1:A:116:VAL:HG21	1:A:133:VAL:HG21	1.96	0.47
1:A:432:MET:HE1	1:A:454:ILE:HG21	1.96	0.47
1:A:563:LEU:HD12	1:A:564:PHE:CD1	2.49	0.47
1:A:86:LYS:HG2	1:A:87:GLU:OE2	2.15	0.47
1:A:324:GLU:O	1:A:328:THR:CG2	2.62	0.47
1:A:426:VAL:HG11	1:A:435:VAL:HG21	1.97	0.47
1:A:219:ILE:HD12	1:A:240:GLY:HA3	1.97	0.47
1:A:5:THR:CG2	1:A:337:GLU:OE2	2.62	0.47
1:A:78:MET:HE1	1:A:153:LEU:HD23	1.97	0.47
1:A:448:HIS:CD2	1:A:475:SER:HA	2.37	0.47
1:A:267:LYS:HA	1:A:270:MET:CE	2.45	0.47
1:A:78:MET:HE1	1:A:153:LEU:CD2	2.45	0.47
1:A:375:ALA:O	1:A:376:ALA:HB2	2.15	0.46
1:A:459:PRO:O	1:A:460:VAL:CG2	2.60	0.46
1:A:319:GLY:HA3	3:A:613:HOH:O	2.16	0.46
1:A:541:HIS:O	1:A:545:VAL:HG23	2.15	0.46
1:A:179:ILE:HG21	1:A:207:LEU:HD23	1.98	0.46
1:A:503:ARG:NH1	1:A:503:ARG:HG3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:VAL:HG12	1:A:164:VAL:HG12	1.97	0.46
1:A:89:SER:HB2	1:A:147:VAL:CG2	2.45	0.46
1:A:129:ILE:HD12	1:A:130:SER:N	2.30	0.46
1:A:222:ILE:HG12	1:A:241:LEU:CD2	2.34	0.46
1:A:83:ILE:CG2	1:A:84:GLU:H	2.29	0.45
1:A:78:MET:HE3	1:A:83:ILE:HG13	1.98	0.45
1:A:122:ILE:C	1:A:123:LEU:HD12	2.37	0.45
1:A:292:THR:HG22	1:A:293:ARG:N	2.30	0.45
1:A:511:ILE:HD11	1:A:529:ALA:HB3	1.97	0.45
1:A:559:ASN:O	1:A:562:THR:HG22	2.17	0.45
1:A:194:PHE:CE2	1:A:223:GLU:OE1	2.68	0.45
1:A:83:ILE:CG2	1:A:84:GLU:N	2.79	0.44
1:A:554:ILE:HD12	1:A:555:VAL:N	2.32	0.44
1:A:75:THR:HG22	1:A:76:HIS:N	2.32	0.44
1:A:223:GLU:HB3	1:A:247:ASP:HB3	1.99	0.44
1:A:79:GLU:HB3	1:A:99:LEU:HD13	2.00	0.44
1:A:119:GLY:N	1:A:133:VAL:O	2.43	0.44
1:A:481:GLY:CA	1:A:554:ILE:HD11	2.47	0.44
1:A:457:GLY:O	1:A:460:VAL:HA	2.17	0.43
1:A:490:PHE:HB2	1:A:583:HIS:ND1	2.32	0.43
1:A:37:SER:OG	1:A:69:LYS:HG3	2.18	0.43
1:A:109:TYR:CZ	1:A:111:SER:HB2	2.53	0.43
1:A:386:THR:HB	1:A:387:PRO:HD3	2.01	0.43
1:A:21:LEU:HD13	1:A:51:ILE:HD13	2.00	0.43
1:A:109:TYR:C	1:A:111:SER:H	2.22	0.43
1:A:380:PRO:HG2	1:A:432:MET:CE	2.48	0.43
1:A:262:LYS:HG2	1:A:305:ASP:OD1	2.17	0.43
1:A:180:LEU:HD21	1:A:211:HIS:NE2	2.34	0.43
1:A:76:HIS:HD2	1:A:106:SER:OG	2.00	0.43
1:A:447:LYS:HD3	1:A:448:HIS:H	1.80	0.43
1:A:388:GLN:HE21	1:A:388:GLN:HB3	1.54	0.43
1:A:573:ASP:OD1	1:A:575:GLY:O	2.36	0.43
1:A:94:SER:C	1:A:96:SER:H	2.23	0.43
1:A:379:THR:HG22	1:A:455:THR:HG23	2.01	0.43
1:A:74:ARG:HD2	1:A:156:LYS:O	2.19	0.42
1:A:84:GLU:O	1:A:151:GLY:O	2.37	0.42
1:A:118:VAL:HG13	1:A:134:ASN:O	2.19	0.42
1:A:123:LEU:HD12	1:A:123:LEU:N	2.34	0.42
1:A:379:THR:HG22	1:A:455:THR:CG2	2.49	0.42
1:A:91:LEU:HD13	1:A:91:LEU:C	2.39	0.42
1:A:290:ARG:HH11	1:A:290:ARG:HB2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ILE:O	1:A:131:LEU:N	2.51	0.42
1:A:155:ASN:O	1:A:156:LYS:HG3	2.20	0.42
1:A:95:MET:HE2	1:A:95:MET:HA	2.01	0.42
1:A:129:ILE:CD1	1:A:147:VAL:HG13	2.46	0.42
1:A:96:SER:O	1:A:98:VAL:HG13	2.20	0.42
1:A:273:LYS:HA	1:A:274:PRO:HD3	1.91	0.42
1:A:432:MET:CE	1:A:454:ILE:HG21	2.50	0.42
1:A:20:LYS:O	1:A:23:GLN:HB2	2.20	0.41
1:A:458:VAL:HA	1:A:460:VAL:N	2.34	0.41
1:A:171:ILE:H	1:A:171:ILE:CD1	2.32	0.41
1:A:133:VAL:CG2	1:A:143:ILE:HD11	2.48	0.41
1:A:209:GLU:HA	1:A:214:LEU:HG	2.02	0.41
1:A:220:ALA:O	1:A:241:LEU:HD23	2.21	0.41
1:A:162:PRO:HB2	1:A:225:GLU:OE2	2.20	0.41
1:A:11:ILE:HD12	1:A:21:LEU:HD21	2.02	0.41
1:A:73:ILE:HD12	1:A:73:ILE:N	2.36	0.41
1:A:79:GLU:HG3	1:A:100:GLY:O	2.21	0.41
1:A:115:ASP:O	1:A:164:VAL:HG21	2.21	0.41
1:A:522:MET:HB2	1:A:523:PRO:HD3	2.02	0.40
1:A:187:ILE:HD12	1:A:189:PHE:O	2.21	0.40
1:A:490:PHE:O	1:A:511:ILE:HG13	2.20	0.40
1:A:79:GLU:HA	1:A:99:LEU:CD2	2.52	0.40
1:A:100:GLY:HA2	1:A:105:ILE:HA	2.04	0.40
1:A:180:LEU:HD23	1:A:180:LEU:HA	1.93	0.40

All (2) 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)
3:A:737:HOH:O	3:A:737:HOH:O[12_566]	1.53	0.67
1:A:364:SER:OG	1:A:364:SER:OG[10_665]	1.87	0.33

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	585/587 (100%)	522 (89%)	50 (8%)	13 (2%)	6 7

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	LEU
1	A	459	PRO
1	A	460	VAL
1	A	79	GLU
1	A	89	SER
1	A	536	GLY
1	A	115	ASP
1	A	558	GLU
1	A	150	GLY
1	A	85	LEU
1	A	319	GLY
1	A	475	SER
1	A	110	PRO

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	469/471 (100%)	442 (94%)	27 (6%)	20 32

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	19	ASP
1	A	20	LYS
1	A	37	SER
1	A	57	ARG
1	A	79	GLU

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Mol	Chain	Res	Type
1	A	99	LEU
1	A	126	ASP
1	A	129	ILE
1	A	149	ASN
1	A	156	LYS
1	A	165	LYS
1	A	171	ILE
1	A	196	ARG
1	A	236	GLU
1	A	241	LEU
1	A	259	LEU
1	A	290	ARG
1	A	328	THR
1	A	370	LEU
1	A	372	LEU
1	A	421	LYS
1	A	432	MET
1	A	467	ASN
1	A	469	MET
1	A	508	ASP
1	A	563	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	50	ASN
1	A	76	HIS
1	A	77	ASN
1	A	134	ASN
1	A	139	GLN
1	A	149	ASN
1	A	230	ASN
1	A	280	GLN
1	A	330	HIS
1	A	331	GLN
1	A	338	GLN
1	A	354	GLN
1	A	388	GLN
1	A	448	HIS
1	A	467	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	588	-	4,4,4	0.25	0	6,6,6	0.12	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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	8

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	426:VAL	C	427:ASN	N	1.19
1	A	167:ASN	C	168:LEU	N	1.18
1	A	499:ALA	C	500:GLU	N	1.15
1	A	486:ARG	C	487:LYS	N	1.13
1	A	184:ARG	C	185:GLN	N	1.12
1	A	104:LYS	C	105:ILE	N	1.11
1	A	33:ARG	C	34:LEU	N	1.03
1	A	196:ARG	C	197:ARG	N	1.00

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	587/587 (100%)	0.31	49 (8%) 11 10	18, 47, 107, 151	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	80	ASN	9.0
1	A	90	LYS	6.0
1	A	86	LYS	5.7
1	A	87	GLU	5.4
1	A	152	VAL	5.2
1	A	78	MET	4.9
1	A	83	ILE	4.6
1	A	93	ILE	4.6
1	A	88	GLY	4.6
1	A	153	LEU	4.5
1	A	72	GLU	4.5
1	A	141	GLY	4.4
1	A	79	GLU	4.3
1	A	75	THR	4.3
1	A	82	ALA	4.2
1	A	99	LEU	4.2
1	A	103	GLU	3.8
1	A	139	GLN	3.5
1	A	147	VAL	3.5
1	A	91	LEU	3.4
1	A	97	GLU	3.3
1	A	155	ASN	3.3
1	A	96	SER	3.2
1	A	162	PRO	3.1
1	A	138	LYS	3.1
1	A	85	LEU	3.0
1	A	81	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	154	LYS	2.9
1	A	150	GLY	2.9
1	A	104	LYS	2.9
1	A	148	LEU	2.8
1	A	95	MET	2.7
1	A	101	THR	2.7
1	A	157	LYS	2.6
1	A	194	PHE	2.5
1	A	149	ASN	2.5
1	A	167	ASN	2.3
1	A	98	VAL	2.3
1	A	133	VAL	2.3
1	A	142	GLU	2.3
1	A	105	ILE	2.2
1	A	92	VAL	2.2
1	A	110	PRO	2.1
1	A	46	ARG	2.1
1	A	127	GLY	2.1
1	A	113	ILE	2.1
1	A	42	GLU	2.0
1	A	129	ILE	2.0
1	A	143	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 monosaccharides 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	A	588	5/5	0.99	0.17	38,38,45,49	0

6.5 Other polymers (i)

There are no such residues in this entry.