



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1VBG  
Title : Pyruvate Phosphate Dikinase from Maize  
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Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2004-02-26  
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (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

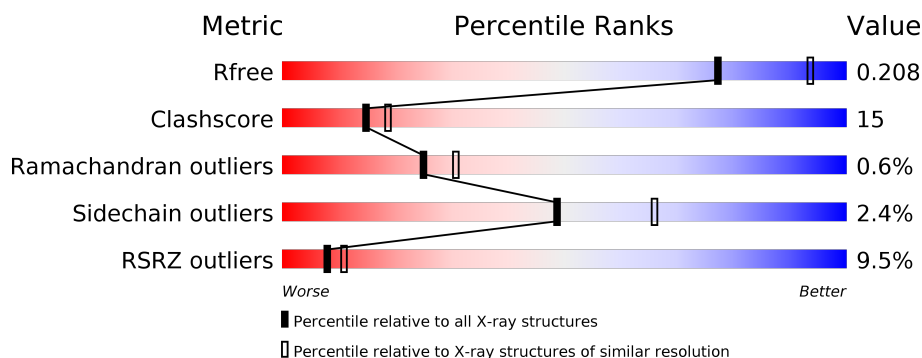
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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	876	<div> <div>9%</div> <div>72%</div> <div>26%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6866 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 pyruvate,orthophosphate dikinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	874	6602	4168	1145	1246	43	0	8	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	819	PHE	LEU	SEE REMARK 999	UNP P11155

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

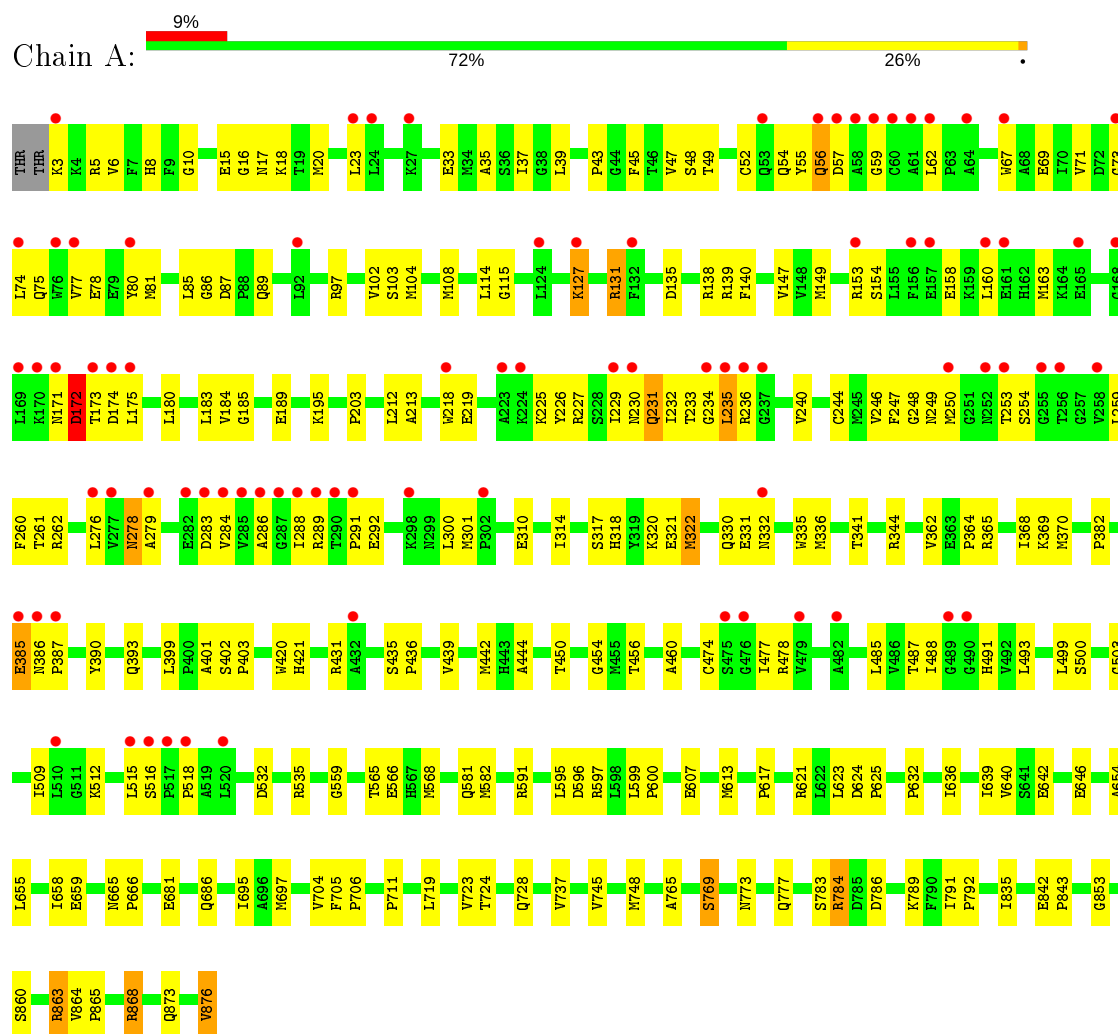
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	248	Total	O	0	0
			248	248		

### 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: pyruvate,orthophosphate dikinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.16Å 100.22Å 108.41Å 90.00° 96.53° 90.00°	Depositor
Resolution (Å)	46.03 – 2.30 62.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.03-2.30) 99.8 (62.90-2.30)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.56 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.209 , 0.237 0.210 , 0.208	Depositor DCC
$R_{free}$ test set	2546 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.7	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 59.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6866	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 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: MG, 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	0.47	0/6727	0.68	8/9114 (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

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	863	ARG	NE-CZ-NH2	7.35	123.98	120.30
1	A	535	ARG	NE-CZ-NH2	7.26	123.93	120.30
1	A	868	ARG	NE-CZ-NH2	6.77	123.68	120.30
1	A	97	ARG	NE-CZ-NH2	6.73	123.67	120.30
1	A	784	ARG	NE-CZ-NH2	5.97	123.29	120.30
1	A	262	ARG	NE-CZ-NH2	5.76	123.18	120.30
1	A	621	ARG	NE-CZ-NH2	5.72	123.16	120.30
1	A	322	MET	CG-SD-CE	5.16	108.45	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	783	SER	Mainchain

## 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	6602	0	6517	199	0
2	A	1	0	0	0	0
3	A	15	0	0	0	0
4	A	248	0	0	2	0
All	All	6866	0	6517	199	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 15.

All (199) 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:565:THR:HA	1:A:568:MET:HE2	1.33	1.09
1:A:131:ARG:H	1:A:131:ARG:HD3	1.21	1.02
1:A:108:MET:HE2	1:A:147:VAL:HG12	1.42	1.01
1:A:365:ARG:HG3	1:A:876:VAL:HG22	1.41	0.98
1:A:695:ILE:HG21	1:A:737:VAL:HG11	1.46	0.94
1:A:17:ASN:H	1:A:20:MET:HE3	1.37	0.88
1:A:623:LEU:H	1:A:686:GLN:HE22	1.20	0.85
1:A:777:GLN:HE21	1:A:784:ARG:H	1.27	0.81
1:A:226:TYR:O	1:A:230:ASN:HB2	1.81	0.80
1:A:74:LEU:HD12	1:A:75:GLN:N	1.97	0.80
1:A:607:GLU:HB3	1:A:697:MET:HE3	1.63	0.79
1:A:87:ASP:OD1	1:A:89:GLN:HG2	1.83	0.78
1:A:596:ASP:O	1:A:600:PRO:HD3	1.82	0.78
1:A:230:ASN:O	1:A:232:ILE:HG13	1.84	0.77
1:A:247:PHE:H	1:A:330:GLN:NE2	1.82	0.77
1:A:3:LYS:HZ1	1:A:8:HIS:CE1	2.04	0.75
1:A:439:VAL:HA	1:A:442:MET:HE2	1.68	0.75
1:A:47:VAL:HB	1:A:240:VAL:CG1	2.17	0.74
1:A:565:THR:HG22	1:A:568:MET:CE	2.18	0.74
1:A:131:ARG:CD	1:A:131:ARG:H	2.00	0.72
1:A:382:PRO:HG3	1:A:518[B]:PRO:HD3	1.71	0.71
1:A:279:ALA:HB1	1:A:283:ASP:OD2	1.90	0.71
1:A:565:THR:HG22	1:A:568:MET:HE3	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:GLY:HA2	1:A:20:MET:HE1	1.73	0.70
1:A:321:GLU:CG	1:A:341:THR:HG23	2.21	0.70
1:A:47:VAL:HB	1:A:240:VAL:HG12	1.73	0.70
1:A:597:ARG:O	1:A:600:PRO:HD2	1.91	0.69
1:A:478:ARG:HB2	1:A:487:THR:HG22	1.74	0.69
1:A:596:ASP:O	1:A:600:PRO:CD	2.39	0.69
1:A:17:ASN:N	1:A:20:MET:HE3	2.08	0.69
1:A:108:MET:HE1	1:A:213:ALA:CB	2.23	0.68
1:A:704:VAL:HG12	1:A:706:PRO:HD3	1.74	0.68
1:A:3:LYS:HZ1	1:A:8:HIS:CD2	2.13	0.67
1:A:108:MET:CE	1:A:147:VAL:HG12	2.22	0.67
1:A:135:ASP:OD1	1:A:138:ARG:NH1	2.28	0.65
1:A:3:LYS:HB3	1:A:6:VAL:O	1.96	0.65
1:A:624:ASP:HB3	1:A:625:PRO:HD3	1.77	0.65
1:A:321:GLU:HG2	1:A:341:THR:HG23	1.78	0.64
1:A:276:LEU:HD11	1:A:289:ARG:HG3	1.79	0.64
1:A:249:ASN:HA	1:A:278:ASN:HD22	1.63	0.64
1:A:597:ARG:C	1:A:600:PRO:HD2	2.18	0.63
1:A:276:LEU:HD11	1:A:289:ARG:CG	2.28	0.62
1:A:225:LYS:HB3	1:A:229:ILE:HD12	1.81	0.61
1:A:74:LEU:O	1:A:78:GLU:HG3	2.00	0.61
1:A:456:THR:O	1:A:456:THR:HG22	1.99	0.61
1:A:229:ILE:O	1:A:229:ILE:HG22	2.00	0.61
1:A:5:ARG:HD3	1:A:69:GLU:OE2	2.01	0.60
1:A:180:LEU:O	1:A:184:VAL:HG23	2.01	0.60
1:A:108:MET:HE1	1:A:213:ALA:HB1	1.83	0.60
1:A:246:VAL:HG11	1:A:335:TRP:CD1	2.37	0.60
1:A:163:MET:HG2	1:A:175:LEU:HD21	1.84	0.59
1:A:365:ARG:HG3	1:A:876:VAL:CG2	2.24	0.59
1:A:474:CYS:O	1:A:477:ILE:HG12	2.02	0.59
1:A:33:GLU:OE2	1:A:318:HIS:HE1	1.85	0.59
1:A:625:PRO:HG3	4:A:3246:HOH:O	2.02	0.59
1:A:229:ILE:O	1:A:230:ASN:ND2	2.36	0.58
1:A:259:LEU:HD12	1:A:259:LEU:C	2.23	0.58
1:A:253:THR:HG22	1:A:332:ASN:N	2.18	0.58
1:A:102:VAL:HG12	1:A:103:SER:N	2.19	0.58
1:A:864:VAL:HB	1:A:865:PRO:HD3	1.86	0.57
1:A:500:SER:HB2	1:A:509:ILE:HB	1.87	0.57
1:A:385:GLU:HG2	1:A:516[A]:SER:HA	1.88	0.56
1:A:127:LYS:CG	1:A:250:MET:HB3	2.35	0.56
1:A:512:LYS:O	1:A:512:LYS:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:MET:HE1	1:A:227:ARG:HD3	1.87	0.56
1:A:493:LEU:CD2	1:A:499:LEU:HD13	2.36	0.55
1:A:153:ARG:HH11	1:A:153:ARG:HB2	1.72	0.55
1:A:786:ASP:O	1:A:789:LYS:HE2	2.06	0.55
1:A:369:LYS:NZ	1:A:876:VAL:HG13	2.21	0.55
1:A:655:LEU:O	1:A:659:GLU:HG3	2.07	0.55
1:A:108:MET:CE	1:A:213:ALA:HB1	2.37	0.54
1:A:10:GLY:O	1:A:35:ALA:HB1	2.08	0.54
1:A:43:PRO:HG3	1:A:81:MET:HG2	1.90	0.54
1:A:171:ASN:O	1:A:173:THR:N	2.41	0.54
1:A:85:LEU:HG	1:A:203:PRO:HB3	1.90	0.54
1:A:487:THR:HA	1:A:491:HIS:O	2.08	0.53
1:A:581:GLN:HE22	1:A:597:ARG:HH12	1.55	0.53
1:A:43:PRO:HB3	1:A:80:TYR:CD2	2.44	0.53
1:A:235:LEU:O	1:A:236:ARG:HG2	2.09	0.53
1:A:6:VAL:HG22	1:A:47:VAL:HG22	1.91	0.53
1:A:85:LEU:HG	1:A:203:PRO:CB	2.38	0.53
1:A:642:GLU:O	1:A:646:GLU:HG3	2.09	0.52
1:A:138:ARG:HD2	1:A:183:LEU:HD23	1.90	0.52
1:A:478:ARG:HB2	1:A:487:THR:CG2	2.38	0.52
1:A:723:VAL:HG22	1:A:745:VAL:HG11	1.91	0.51
1:A:232:ILE:HG22	1:A:233:THR:N	2.26	0.51
1:A:225:LYS:O	1:A:229:ILE:N	2.43	0.51
1:A:153:ARG:NH1	1:A:153:ARG:HB2	2.25	0.51
1:A:385:GLU:HA	1:A:516[A]:SER:OG	2.11	0.51
1:A:748:MET:HG3	1:A:769:SER:O	2.10	0.51
1:A:399:LEU:CD1	1:A:454:GLY:HA2	2.40	0.51
1:A:127:LYS:HG2	1:A:250:MET:HB3	1.92	0.51
1:A:399:LEU:HD12	1:A:454:GLY:HA2	1.92	0.51
1:A:632:PRO:HG2	1:A:639:ILE:HG23	1.92	0.50
1:A:566:GLU:HG3	1:A:625:PRO:HG3	1.93	0.50
1:A:253:THR:HG22	1:A:253:THR:O	2.12	0.50
1:A:276:LEU:HD13	1:A:291:PRO:HA	1.93	0.50
1:A:532:ASP:OD1	1:A:868:ARG:HD2	2.11	0.50
1:A:439:VAL:HA	1:A:442:MET:CE	2.38	0.49
1:A:5:ARG:HH21	1:A:54:GLN:NE2	2.11	0.49
1:A:369:LYS:HZ2	1:A:876:VAL:HG13	1.76	0.49
1:A:431:ARG:O	1:A:450:THR:HA	2.12	0.49
1:A:104:MET:HG2	1:A:218:TRP:CZ3	2.48	0.49
1:A:261:THR:OG1	1:A:322:MET:HG2	2.13	0.49
1:A:135:ASP:O	1:A:138:ARG:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLN:NE2	1:A:219:GLU:HG2	2.27	0.48
1:A:791:ILE:HB	1:A:792:PRO:HD3	1.95	0.48
1:A:235:LEU:O	1:A:236:ARG:CG	2.61	0.48
1:A:18:LYS:HB3	1:A:33:GLU:HB2	1.94	0.48
1:A:87:ASP:OD1	1:A:89:GLN:CG	2.59	0.48
1:A:439:VAL:CA	1:A:442:MET:HE2	2.41	0.48
1:A:108:MET:HE1	1:A:213:ALA:HB3	1.93	0.48
1:A:248:GLY:HA2	1:A:254:SER:HB3	1.95	0.48
1:A:565:THR:HA	1:A:568:MET:CE	2.24	0.48
1:A:172:ASP:C	1:A:174:ASP:H	2.17	0.48
1:A:3:LYS:HZ2	1:A:15:GLU:CB	2.27	0.48
1:A:364:PRO:O	1:A:368:ILE:HG12	2.14	0.48
1:A:160:LEU:O	1:A:160:LEU:HD23	2.13	0.47
1:A:3:LYS:NZ	1:A:8:HIS:CD2	2.82	0.47
1:A:719:LEU:HD21	1:A:765:ALA:HB2	1.96	0.47
1:A:127:LYS:HG3	1:A:250:MET:HB3	1.96	0.47
1:A:62:LEU:HD12	1:A:212:LEU:HD21	1.97	0.47
1:A:114:LEU:HD23	1:A:115:GLY:N	2.30	0.47
1:A:73:GLY:O	1:A:77:VAL:HG23	2.15	0.47
1:A:493:LEU:HD21	1:A:499:LEU:HD13	1.97	0.46
1:A:67:TRP:O	1:A:71:VAL:HG23	2.15	0.46
1:A:3:LYS:NZ	1:A:15:GLU:CB	2.78	0.46
1:A:596:ASP:O	1:A:600:PRO:HD2	2.15	0.46
1:A:185:GLY:O	1:A:189:GLU:HG3	2.15	0.46
1:A:485:LEU:C	1:A:485:LEU:HD12	2.36	0.46
1:A:234:GLY:O	1:A:235:LEU:C	2.54	0.46
1:A:86:GLY:HA3	1:A:203:PRO:HG2	1.97	0.46
1:A:52:CYS:O	1:A:55:TYR:HB3	2.16	0.46
1:A:636:ILE:O	1:A:640:VAL:HG23	2.15	0.46
1:A:487:THR:O	1:A:487:THR:HG23	2.15	0.45
1:A:43:PRO:CG	1:A:81:MET:HG2	2.46	0.45
1:A:365:ARG:CG	1:A:876:VAL:HG22	2.29	0.45
1:A:276:LEU:HD11	1:A:289:ARG:HG2	1.97	0.45
1:A:860:SER:OG	1:A:863:ARG:HG2	2.17	0.45
1:A:300:LEU:C	1:A:301:MET:HG3	2.37	0.45
1:A:5:ARG:NH2	1:A:54:GLN:HE22	2.14	0.45
1:A:654:ALA:O	1:A:658:ILE:HG13	2.17	0.45
1:A:160:LEU:C	1:A:160:LEU:HD23	2.36	0.45
1:A:86:GLY:CA	1:A:203:PRO:HG2	2.46	0.45
1:A:331:GLU:O	1:A:332:ASN:HB2	2.15	0.45
1:A:310:GLU:O	1:A:314:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:724:THR:O	1:A:728:GLN:HG3	2.17	0.45
1:A:362:VAL:HG21	1:A:370:MET:HE3	1.99	0.45
1:A:773:ASN:HD21	1:A:784:ARG:HH11	1.65	0.44
1:A:138:ARG:CG	1:A:139:ARG:N	2.80	0.44
1:A:477:ILE:HG22	1:A:488:ILE:HG23	1.99	0.44
1:A:387:PRO:HA	1:A:390:TYR:CE2	2.53	0.44
1:A:515[A]:LEU:HD23	1:A:515[A]:LEU:HA	1.81	0.44
1:A:317:SER:O	1:A:320:LYS:HE2	2.18	0.43
1:A:218:TRP:HH2	1:A:235:LEU:HD13	1.83	0.43
1:A:235:LEU:O	1:A:236:ARG:CB	2.67	0.43
1:A:286:ALA:HB3	1:A:288:ILE:HG13	2.00	0.43
1:A:172:ASP:C	1:A:174:ASP:N	2.72	0.43
1:A:382:PRO:HG3	1:A:518[B]:PRO:CD	2.45	0.43
1:A:114:LEU:C	1:A:114:LEU:HD23	2.39	0.43
1:A:559:GLY:HA2	1:A:613:MET:HE2	2.01	0.43
1:A:607:GLU:CB	1:A:697:MET:HE3	2.41	0.43
1:A:102:VAL:CG1	1:A:103:SER:N	2.82	0.42
1:A:149:MET:O	1:A:195:LYS:HE3	2.19	0.42
1:A:477:ILE:HA	1:A:487:THR:O	2.20	0.42
1:A:114:LEU:HA	1:A:140:PHE:CE1	2.55	0.42
1:A:387:PRO:HA	1:A:390:TYR:CD2	2.54	0.42
1:A:8:HIS:HA	1:A:45:PHE:HA	2.00	0.42
1:A:559:GLY:HA2	1:A:613:MET:CE	2.49	0.42
1:A:260:PHE:HD2	1:A:322:MET:CE	2.33	0.42
1:A:368:ILE:HG22	1:A:873:GLN:HG2	2.02	0.42
1:A:853:GLY:HA3	4:A:3216:HOH:O	2.20	0.42
1:A:108:MET:CE	1:A:213:ALA:CB	2.96	0.42
1:A:591:ARG:NH1	1:A:681:GLU:OE2	2.53	0.42
1:A:57:ASP:C	1:A:59:GLY:H	2.22	0.42
1:A:402:SER:HA	1:A:403:PRO:HD2	1.93	0.42
1:A:278:ASN:O	1:A:279:ALA:HB2	2.20	0.41
1:A:284:VAL:HG22	1:A:291:PRO:HD3	2.02	0.41
1:A:421:HIS:HB2	1:A:444:ALA:HB1	2.02	0.41
1:A:581:GLN:OE1	1:A:597:ARG:NH1	2.53	0.41
1:A:773:ASN:O	1:A:777:GLN:HG3	2.20	0.41
1:A:401:ALA:HB1	1:A:460:ALA:CB	2.49	0.41
1:A:582:MET:SD	1:A:595:LEU:HD13	2.59	0.41
1:A:37:ILE:HG13	1:A:39:LEU:HG	2.02	0.41
1:A:43:PRO:HG3	1:A:80:TYR:HD2	1.84	0.41
1:A:246:VAL:CG1	1:A:330:GLN:HB2	2.50	0.41
1:A:402:SER:O	1:A:503:GLY:HA3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LEU:O	1:A:49:THR:HG23	2.20	0.41
1:A:71:VAL:HA	1:A:74:LEU:HG	2.03	0.41
1:A:456:THR:O	1:A:456:THR:CG2	2.67	0.41
1:A:127:LYS:HG3	1:A:250:MET:CB	2.51	0.41
1:A:154:SER:O	1:A:158:GLU:HB2	2.21	0.41
1:A:336:MET:HB3	1:A:336:MET:HE2	1.79	0.40
1:A:842:GLU:HA	1:A:843:PRO:HD3	1.90	0.40
1:A:276:LEU:HD13	1:A:291:PRO:CA	2.51	0.40
1:A:665:ASN:HA	1:A:666:PRO:HD2	1.93	0.40
1:A:617:PRO:HA	1:A:705:PHE:HB2	2.03	0.40
1:A:230:ASN:O	1:A:231:GLN:C	2.60	0.40
1:A:435:SER:HB2	1:A:436:PRO:HD2	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	880/876 (100%)	835 (95%)	40 (4%)	5 (1%)	25	31

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	ASP
1	A	235	LEU
1	A	231	GLN
1	A	385	GLU
1	A	48	SER

### 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	681/707 (96%)	665 (98%)	16 (2%)	50 67

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	127	LYS
1	A	131	ARG
1	A	172	ASP
1	A	244	CYS
1	A	278	ASN
1	A	292	GLU
1	A	344	ARG
1	A	386	ASN
1	A	393	GLN
1	A	420	TRP
1	A	599	LEU
1	A	711	PRO
1	A	769	SER
1	A	835	ILE
1	A	876	VAL

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

Mol	Chain	Res	Type
1	A	54	GLN
1	A	216	ASN
1	A	230	ASN
1	A	241	ASN
1	A	252	ASN
1	A	278	ASN
1	A	318	HIS
1	A	330	GLN
1	A	332	ASN

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Mol	Chain	Res	Type
1	A	386	ASN
1	A	393	GLN
1	A	602	GLN
1	A	686	GLN
1	A	722	GLN
1	A	773	ASN
1	A	777	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	$\# Z  > 2$
3	SO4	A	3000	-	4,4,4	0.22	0	6,6,6	0.13	0
3	SO4	A	3002	-	4,4,4	0.27	0	6,6,6	0.04	0
3	SO4	A	3001	-	4,4,4	0.27	0	6,6,6	0.13	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	874/876 (99%)	0.69	83 (9%)	8 11	12, 37, 66, 81	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	ALA	10.3
1	A	169	LEU	7.6
1	A	173	THR	7.3
1	A	283	ASP	7.3
1	A	168	GLY	7.2
1	A	127	LYS	5.9
1	A	174	ASP	5.7
1	A	289	ARG	5.6
1	A	284	VAL	5.5
1	A	229	ILE	5.2
1	A	160	LEU	5.1
1	A	170	LYS	5.1
1	A	285	VAL	5.1
1	A	234	GLY	4.9
1	A	288	ILE	4.8
1	A	255	GLY	4.7
1	A	432	ALA	4.5
1	A	490	GLY	4.4
1	A	80	TYR	4.3
1	A	235	LEU	4.2
1	A	161	GLU	4.1
1	A	61	ALA	4.0
1	A	59	GLY	4.0
1	A	386	ASN	4.0
1	A	489	GLY	3.8
1	A	67	TRP	3.7
1	A	516[A]	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	385	GLU	3.5
1	A	476	GLY	3.5
1	A	165	GLU	3.5
1	A	282	GLU	3.5
1	A	279	ALA	3.4
1	A	62	LEU	3.4
1	A	76	TRP	3.3
1	A	56	GLN	3.3
1	A	517[A]	PRO	3.3
1	A	475	SER	3.3
1	A	124	LEU	3.2
1	A	250	MET	3.2
1	A	171	ASN	3.2
1	A	157	GLU	3.1
1	A	290	THR	3.0
1	A	479	VAL	3.0
1	A	276	LEU	3.0
1	A	74	LEU	2.9
1	A	287	GLY	2.9
1	A	60	CYS	2.8
1	A	224	LYS	2.8
1	A	277	VAL	2.8
1	A	23	LEU	2.8
1	A	92	LEU	2.8
1	A	518[A]	PRO	2.7
1	A	58	ALA	2.7
1	A	237	GLY	2.7
1	A	57	ASP	2.7
1	A	515[A]	LEU	2.6
1	A	3	LYS	2.6
1	A	64	ALA	2.5
1	A	520[A]	LEU	2.5
1	A	153	ARG	2.5
1	A	77	VAL	2.5
1	A	218	TRP	2.5
1	A	24	LEU	2.4
1	A	332	ASN	2.4
1	A	27	LYS	2.4
1	A	253	THR	2.4
1	A	230	ASN	2.4
1	A	482	ALA	2.4
1	A	223	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	258	VAL	2.3
1	A	298	LYS	2.3
1	A	302	PRO	2.3
1	A	175	LEU	2.2
1	A	252	ASN	2.2
1	A	256	THR	2.2
1	A	73	GLY	2.2
1	A	156	PHE	2.1
1	A	132	PHE	2.1
1	A	387	PRO	2.1
1	A	53	GLN	2.1
1	A	510	LEU	2.1
1	A	291	PRO	2.1
1	A	236	ARG	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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	A	2000	1/1	0.97	0.15	14,14,14,14	0
3	SO4	A	3002	5/5	0.97	0.23	89,89,91,92	0
3	SO4	A	3000	5/5	0.99	0.18	22,24,25,28	0
3	SO4	A	3001	5/5	0.99	0.16	31,37,39,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.