



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 11:35 am BST

PDB ID : 1VBH
Title : Pyruvate Phosphate Dikinase with bound Mg-PEP from Maize
Authors : Nakanishi, T.; Nakatsu, T.; Matsuoka, M.; Sakata, K.; Kato, H.; RIKEN
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

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

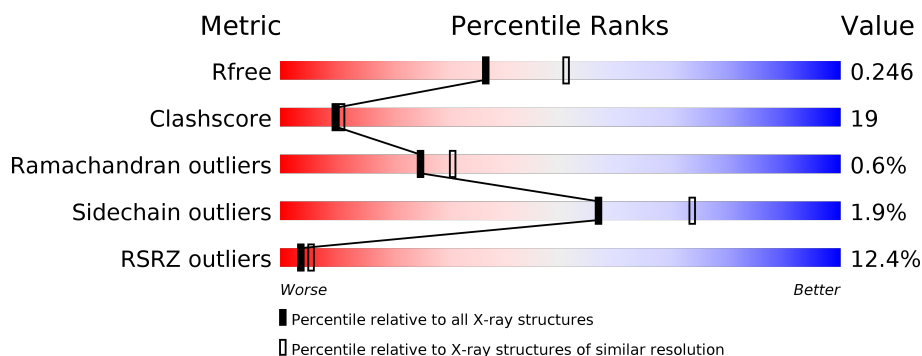
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 ≥ 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>12%</div> <div>69%</div> <div>28%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6665 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	862	6455	4083	1122	1204	46	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).

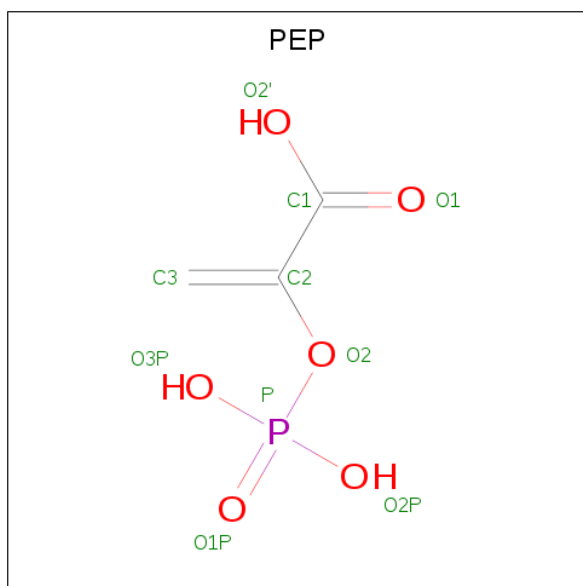
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is PHOSPHOENOLPYRUVATE (three-letter code: PEP) (formula: $C_3H_5O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	194	Total	O	0	0
			194	194		

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.

- Chain A: 12% 69% 28% 1%

The sequence logo displays the conservation of amino acids across 250 positions. The y-axis lists amino acid codes, and the x-axis lists position numbers. The logo is color-coded by region: red (1-12), green (13-109), yellow (110-228), and grey (229-250). The height of each bar indicates the relative frequency of the amino acid at that position. The logo shows a high degree of conservation in the green region, with many positions having a single dominant amino acid. The yellow region shows more variability, with many positions having multiple amino acids at similar frequencies. The red and grey regions show intermediate levels of conservation.

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	109.34Å 100.51Å 108.16Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	45.63 – 2.30 45.62 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (45.63-2.30) 98.1 (45.62-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.230 , 0.259 0.217 , 0.246	Depositor DCC
R_{free} test set	2528 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6665	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PEP, 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	0.44	0/6577	0.63	0/8913

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	6455	0	6308	246	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	10	0	2	2	0
5	A	194	0	0	8	0
All	All	6665	0	6310	246	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 19.

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:131:ARG:HD3	1:A:131:ARG:H	1.21	1.02
1:A:509:ILE:H	1:A:509:ILE:HD12	1.25	1.00
1:A:777:GLN:NE2	1:A:784:ARG:H	1.62	0.97
1:A:777:GLN:HE21	1:A:784:ARG:H	1.04	0.93
1:A:74:LEU:HD12	1:A:75:GLN:N	1.88	0.88
1:A:429:LEU:HD21	1:A:431:ARG:HG3	1.58	0.84
1:A:387:PRO:HA	1:A:390:TYR:CE2	2.13	0.84
1:A:596:ASP:O	1:A:600:PRO:HD3	1.77	0.84
1:A:787:VAL:HG22	1:A:791:ILE:HG12	1.60	0.82
1:A:477:ILE:CG1	1:A:488:ILE:HG12	2.09	0.81
1:A:16:GLY:HA2	1:A:20:MET:HE1	1.61	0.80
1:A:253:THR:HG22	1:A:332:ASN:N	1.98	0.79
1:A:195:LYS:HE2	1:A:195:LYS:HA	1.63	0.78
1:A:396:ALA:HB3	1:A:508:VAL:CG2	2.15	0.76
1:A:396:ALA:HB3	1:A:508:VAL:HG21	1.66	0.76
1:A:668:LEU:HD21	1:A:778[B]:MET:CE	2.16	0.76
1:A:40:SER:H	1:A:311:ASN:HD21	1.31	0.75
1:A:401:ALA:HB1	1:A:460:ALA:CB	2.17	0.75
1:A:372:GLU:H	1:A:375:HIS:HD2	1.33	0.74
1:A:668:LEU:HD21	1:A:778[B]:MET:SD	2.28	0.74
1:A:566:GLU:HG3	1:A:625:PRO:HG3	1.71	0.72
1:A:249:ASN:HA	1:A:278:ASN:ND2	2.06	0.71
1:A:67:TRP:O	1:A:71:VAL:HG23	1.90	0.71
1:A:5:ARG:NH2	1:A:63:PRO:HB2	2.06	0.70
1:A:777:GLN:HE21	1:A:784:ARG:N	1.85	0.70
1:A:276:LEU:HD22	1:A:279:ALA:HB3	1.72	0.69
1:A:509:ILE:HD12	1:A:509:ILE:N	2.04	0.69
1:A:559:GLY:HA2	1:A:613:MET:CE	2.23	0.69
1:A:474:CYS:O	1:A:477:ILE:HG22	1.93	0.68
1:A:431:ARG:HH11	1:A:431:ARG:HG2	1.58	0.68
1:A:626:PRO:HD2	1:A:629:GLU:OE2	1.94	0.68
1:A:321:GLU:CG	1:A:341:THR:HG23	2.24	0.67
1:A:787:VAL:HG22	1:A:791:ILE:CG1	2.25	0.67
1:A:188:LYS:HB3	5:A:3177:HOH:O	1.94	0.67
1:A:520:LEU:O	1:A:520:LEU:HD23	1.94	0.67
1:A:87:ASP:OD1	1:A:89:GLN:HG3	1.93	0.67
1:A:154:SER:HA	1:A:157:GLU:HG2	1.75	0.66
1:A:3:LYS:HZ1	1:A:8:HIS:CE1	2.13	0.66
1:A:401:ALA:HB1	1:A:460:ALA:HB2	1.78	0.66
1:A:509:ILE:CD1	1:A:509:ILE:H	2.00	0.66
1:A:380:LEU:HD13	1:A:865:PRO:HG2	1.77	0.66
1:A:458:HIS:O	1:A:462:VAL:HG23	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:GLU:H	1:A:375:HIS:CD2	2.13	0.65
1:A:125:ALA:HA	1:A:129:GLY:O	1.96	0.65
1:A:249:ASN:HA	1:A:278:ASN:HD22	1.60	0.65
1:A:259:LEU:C	1:A:259:LEU:HD12	2.18	0.64
1:A:390:TYR:HA	1:A:393:GLN:NE2	2.12	0.64
1:A:5:ARG:HH22	1:A:63:PRO:HB2	1.61	0.64
1:A:624:ASP:O	1:A:671[A]:ARG:HB2	1.96	0.64
1:A:310:GLU:O	1:A:314:ILE:HG12	1.98	0.64
1:A:596:ASP:O	1:A:600:PRO:CD	2.44	0.64
1:A:251:GLY:C	5:A:3095:HOH:O	2.35	0.63
1:A:695:ILE:HG21	1:A:737:VAL:HG21	1.80	0.63
1:A:751:ILE:HD13	1:A:778[A]:MET:SD	2.39	0.62
1:A:508:VAL:HG23	1:A:508:VAL:O	1.99	0.61
1:A:603:ARG:NH1	1:A:692:GLU:OE1	2.30	0.61
1:A:494:ARG:O	1:A:497:GLU:HG3	2.02	0.59
1:A:597:ARG:O	1:A:600:PRO:HD2	2.01	0.59
1:A:321:GLU:HG2	1:A:341:THR:HG23	1.83	0.59
1:A:429:LEU:HD23	1:A:429:LEU:C	2.23	0.59
1:A:485:LEU:HB3	1:A:494:ARG:HG2	1.84	0.59
1:A:17:ASN:H	1:A:20:MET:HE3	1.67	0.59
1:A:624:ASP:O	1:A:671[B]:ARG:HB2	2.01	0.59
1:A:429:LEU:CD2	1:A:431:ARG:HG3	2.32	0.58
1:A:89:GLN:C	1:A:91:PRO:HD3	2.23	0.58
1:A:74:LEU:O	1:A:78:GLU:HG3	2.03	0.58
1:A:429:LEU:HD23	1:A:430:VAL:N	2.18	0.57
1:A:380:LEU:CD1	1:A:865:PRO:HG2	2.33	0.57
1:A:733:VAL:O	1:A:737:VAL:HG12	2.05	0.57
1:A:387:PRO:HA	1:A:390:TYR:CZ	2.40	0.57
1:A:599:LEU:HB3	1:A:600:PRO:HD3	1.86	0.57
1:A:654:ALA:O	1:A:658:ILE:HG13	2.04	0.57
1:A:154:SER:HA	1:A:157:GLU:CD	2.25	0.56
1:A:154:SER:HA	1:A:157:GLU:CG	2.35	0.56
1:A:5:ARG:CZ	1:A:54:GLN:HE22	2.19	0.56
1:A:251:GLY:CA	5:A:3095:HOH:O	2.54	0.56
1:A:73:GLY:O	1:A:77:VAL:HG23	2.06	0.56
1:A:55:TYR:O	1:A:60:CYS:HA	2.06	0.55
1:A:62:LEU:HD23	1:A:63:PRO:O	2.06	0.55
1:A:455:MET:O	1:A:464:ARG:NH2	2.39	0.55
1:A:78:GLU:HG2	1:A:92:LEU:CD2	2.37	0.55
1:A:235:LEU:O	1:A:236:ARG:HB3	2.07	0.55
1:A:43:PRO:HG3	1:A:81:MET:HG2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:ASP:O	1:A:173:THR:HB	2.08	0.54
1:A:235:LEU:O	1:A:236:ARG:CB	2.55	0.54
1:A:17:ASN:N	1:A:20:MET:HE3	2.23	0.54
1:A:864:VAL:HB	1:A:865:PRO:HD3	1.89	0.54
1:A:107:MET:HE2	1:A:238:THR:HB	1.89	0.54
1:A:435:SER:HB2	1:A:436:PRO:HD2	1.88	0.54
1:A:480:ASN:O	1:A:483:GLU:O	2.24	0.54
1:A:227:ARG:HD3	1:A:235:LEU:HD12	1.88	0.54
1:A:611[A]:ARG:NH1	1:A:697:MET:SD	2.80	0.54
1:A:197:GLU:HB2	1:A:198:PRO:HD2	1.88	0.54
1:A:566:GLU:CD	1:A:625:PRO:HD3	2.29	0.53
1:A:71:VAL:O	1:A:74:LEU:HG	2.07	0.53
1:A:513:GLN:HA	1:A:513:GLN:HE21	1.73	0.53
1:A:636:ILE:HG23	1:A:637:GLU:N	2.24	0.53
1:A:568:MET:CE	1:A:605:ASP:HB3	2.39	0.53
1:A:85:LEU:HG	1:A:203:PRO:HB3	1.91	0.53
1:A:400:PRO:HG2	1:A:455:MET:SD	2.48	0.53
1:A:732:LYS:NZ	5:A:3161:HOH:O	2.41	0.53
1:A:569:PHE:C	1:A:571:ALA:H	2.12	0.53
1:A:159:LYS:HD3	1:A:186:GLN:HB3	1.91	0.52
1:A:225:LYS:O	1:A:229:ILE:HG13	2.09	0.52
1:A:8:HIS:CE1	1:A:76:TRP:CZ2	2.98	0.52
1:A:401:ALA:HB3	1:A:470:CYS:O	2.10	0.52
1:A:509:ILE:HG22	1:A:510:LEU:N	2.24	0.52
1:A:227:ARG:HA	1:A:232:ILE:HD12	1.92	0.52
1:A:650:ASN:ND2	1:A:653:ASP:H	2.08	0.52
1:A:16:GLY:HA2	1:A:20:MET:CE	2.38	0.52
1:A:131:ARG:N	1:A:131:ARG:HD3	2.06	0.51
1:A:138:ARG:HD2	1:A:183:LEU:HD23	1.90	0.51
1:A:78:GLU:HG2	1:A:92:LEU:HD22	1.91	0.51
1:A:395:ILE:O	1:A:396:ALA:HB2	2.10	0.51
1:A:246:VAL:HG11	1:A:335:TRP:CD1	2.46	0.51
1:A:500:SER:HB2	1:A:509:ILE:HB	1.93	0.51
1:A:668:LEU:CD2	1:A:778[B]:MET:CE	2.88	0.51
1:A:869:LEU:O	1:A:873:GLN:HG3	2.11	0.51
1:A:777:GLN:NE2	1:A:784:ARG:N	2.46	0.51
1:A:104:MET:HE1	1:A:227:ARG:HH21	1.75	0.50
1:A:449:LEU:HD12	1:A:471:VAL:O	2.11	0.50
1:A:107:MET:HE2	1:A:218:TRP:CE3	2.47	0.50
1:A:481:ASP:O	1:A:482:ALA:C	2.50	0.50
1:A:171:ASN:O	1:A:173:THR:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:TYR:CE2	1:A:181:LYS:HE2	2.48	0.49
1:A:230:ASN:HB2	1:A:232:ILE:CG1	2.42	0.49
1:A:860:SER:HB2	1:A:861:PRO:HD2	1.95	0.49
1:A:163:MET:HE2	1:A:179:ASP:HB3	1.93	0.49
1:A:580:ARG:CZ	1:A:632:PRO:HG3	2.42	0.49
1:A:773:ASN:HB2	4:A:3000:PEP:C1	2.42	0.49
1:A:117:ASN:OD1	1:A:120:VAL:HG23	2.13	0.49
1:A:232:ILE:HG22	1:A:235:LEU:HD21	1.94	0.49
1:A:818:LYS:O	1:A:822:GLU:HG3	2.12	0.49
1:A:564:ARG:HH21	4:A:3000:PEP:P	2.36	0.48
1:A:513:GLN:NE2	1:A:513:GLN:HA	2.28	0.48
1:A:251:GLY:HA3	5:A:3095:HOH:O	2.13	0.48
1:A:386:ASN:OD1	1:A:388:SER:HB3	2.12	0.48
1:A:566:GLU:CB	1:A:625:PRO:CG	2.92	0.48
1:A:463:ALA:HB1	1:A:468:LYS:O	2.14	0.48
1:A:611[A]:ARG:NH1	1:A:611[A]:ARG:HB2	2.29	0.48
1:A:707:GLU:HG2	1:A:744:LYS:HB2	1.96	0.48
1:A:107:MET:CE	1:A:218:TRP:CZ3	2.97	0.47
1:A:431:ARG:NH1	1:A:431:ARG:HG2	2.28	0.47
1:A:49:THR:OG1	1:A:236:ARG:HD3	2.13	0.47
1:A:188:LYS:O	5:A:3177:HOH:O	2.20	0.47
1:A:485:LEU:C	1:A:485:LEU:HD12	2.34	0.47
1:A:509:ILE:HG22	1:A:510:LEU:H	1.80	0.47
1:A:451:GLU:CB	1:A:477:ILE:CG2	2.92	0.47
1:A:131:ARG:CD	1:A:131:ARG:H	2.04	0.47
1:A:154:SER:O	1:A:157:GLU:HG2	2.15	0.47
1:A:261:THR:OG1	1:A:322:MET:HG2	2.15	0.47
1:A:7:PHE:O	1:A:45:PHE:HA	2.15	0.47
1:A:135:ASP:OD1	1:A:138:ARG:NH1	2.48	0.46
1:A:138:ARG:CG	1:A:139:ARG:N	2.78	0.46
1:A:114:LEU:HA	1:A:140:PHE:CE1	2.50	0.46
1:A:3:LYS:HB3	1:A:6:VAL:O	2.15	0.46
1:A:321:GLU:HG3	1:A:341:THR:HG23	1.96	0.46
1:A:3:LYS:HD2	1:A:15:GLU:CB	2.46	0.46
1:A:95:SER:HB3	1:A:245:MET:SD	2.56	0.46
1:A:401:ALA:CB	1:A:460:ALA:HB2	2.46	0.45
1:A:791:ILE:HB	1:A:792:PRO:HD3	1.97	0.45
1:A:220:SER:O	1:A:224:LYS:HG3	2.17	0.45
1:A:47:VAL:HB	1:A:240:VAL:HB	1.99	0.45
1:A:704:VAL:HG12	1:A:706:PRO:HD3	1.98	0.45
1:A:278:ASN:C	1:A:278:ASN:HD22	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:MET:HE3	1:A:448:ILE:HG21	1.99	0.45
1:A:5:ARG:NH2	1:A:66:LEU:HB2	2.31	0.45
1:A:660:LYS:HB2	1:A:660:LYS:HE3	1.80	0.45
1:A:311:ASN:HB3	1:A:336:MET:HE3	1.99	0.45
1:A:856:TYR:C	1:A:856:TYR:CD1	2.90	0.45
1:A:163:MET:HE2	1:A:179:ASP:CB	2.47	0.45
1:A:255:GLY:HA3	1:A:275:PHE:CZ	2.52	0.45
1:A:650:ASN:HD21	1:A:653:ASP:H	1.64	0.45
1:A:71:VAL:HA	1:A:74:LEU:HG	1.98	0.45
1:A:108:MET:HG3	1:A:147:VAL:CG1	2.46	0.44
1:A:548:ASP:OD2	5:A:3150:HOH:O	2.21	0.44
1:A:667[B]:MET:CE	1:A:783:SER:HA	2.48	0.44
1:A:348:SER:O	1:A:352:ILE:HG13	2.17	0.44
1:A:3:LYS:HZ1	1:A:8:HIS:CD2	2.34	0.44
1:A:3:LYS:NZ	1:A:8:HIS:CD2	2.85	0.44
1:A:393:GLN:HE21	1:A:393:GLN:N	2.15	0.44
1:A:85:LEU:HG	1:A:203:PRO:CB	2.48	0.44
1:A:597:ARG:C	1:A:600:PRO:HD2	2.38	0.44
1:A:709:MET:SD	1:A:769:SER:HB3	2.57	0.44
1:A:716:PRO:HG3	1:A:760:GLU:HB3	2.00	0.44
1:A:566:GLU:CG	1:A:625:PRO:HG3	2.45	0.44
1:A:106:GLY:N	1:A:222:ARG:HD3	2.33	0.44
1:A:259:LEU:O	1:A:259:LEU:HD12	2.18	0.43
1:A:409:GLN:NE2	1:A:420:TRP:HE1	2.16	0.43
1:A:583:ILE:HG22	1:A:583:ILE:O	2.17	0.43
1:A:624:ASP:H	1:A:625:PRO:HD2	1.83	0.43
1:A:624:ASP:H	1:A:625:PRO:CD	2.31	0.43
1:A:832:LYS:HE3	5:A:3036:HOH:O	2.17	0.43
1:A:114:LEU:HD23	1:A:114:LEU:C	2.39	0.43
1:A:108:MET:H	1:A:217:SER:CB	2.31	0.43
1:A:329:VAL:O	1:A:329:VAL:HG13	2.18	0.43
1:A:773:ASN:O	1:A:777:GLN:HG3	2.19	0.43
1:A:298:LYS:C	1:A:300:LEU:H	2.22	0.43
1:A:276:LEU:HD21	1:A:289:ARG:HD3	2.01	0.43
1:A:34:MET:O	1:A:39:LEU:HB2	2.18	0.43
1:A:402:SER:HA	1:A:403:PRO:HD2	1.88	0.43
1:A:400:PRO:C	1:A:455:MET:SD	2.97	0.43
1:A:395:ILE:HG12	1:A:508:VAL:O	2.18	0.43
1:A:501:LEU:CD2	1:A:508:VAL:HG12	2.49	0.43
1:A:114:LEU:HD23	1:A:115:GLY:N	2.33	0.43
1:A:475:SER:C	1:A:477:ILE:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:622:LEU:O	1:A:711:PRO:HG3	2.19	0.43
1:A:43:PRO:CG	1:A:81:MET:HG2	2.48	0.42
1:A:253:THR:O	1:A:253:THR:HG22	2.19	0.42
1:A:667[B]:MET:HE1	1:A:783:SER:HA	2.00	0.42
1:A:449:LEU:HB2	1:A:501:LEU:HD11	2.01	0.42
1:A:825:ARG:NH2	1:A:855:ASP:OD2	2.47	0.42
1:A:8:HIS:HA	1:A:45:PHE:HA	2.01	0.42
1:A:565:THR:HA	1:A:568:MET:HG3	2.02	0.42
1:A:108:MET:HG3	1:A:147:VAL:HG12	2.02	0.42
1:A:418:GLU:HG3	1:A:441:GLY:HA2	2.01	0.42
1:A:410:VAL:HG23	1:A:497:GLU:O	2.19	0.42
1:A:4:LYS:O	1:A:4:LYS:HG2	2.20	0.42
1:A:249:ASN:CA	1:A:278:ASN:ND2	2.81	0.42
1:A:9:PHE:N	1:A:44:GLY:O	2.50	0.42
1:A:138:ARG:HG2	1:A:139:ARG:N	2.35	0.41
1:A:227:ARG:HG3	1:A:232:ILE:HB	2.01	0.41
1:A:559:GLY:CA	1:A:613:MET:CE	2.96	0.41
1:A:248:GLY:O	1:A:278:ASN:HA	2.20	0.41
1:A:451:GLU:CB	1:A:477:ILE:HG23	2.50	0.41
1:A:65:GLY:O	1:A:68:ALA:HB3	2.20	0.41
1:A:104:MET:CE	1:A:227:ARG:HH21	2.33	0.41
1:A:261:THR:O	1:A:262:ARG:HG2	2.19	0.41
1:A:86:GLY:HA3	1:A:203:PRO:HG2	2.02	0.41
1:A:93:LEU:HD21	1:A:116:LEU:HD13	2.03	0.41
1:A:62:LEU:HD23	1:A:62:LEU:C	2.41	0.41
1:A:107:MET:CE	1:A:218:TRP:HZ3	2.34	0.41
1:A:107:MET:CE	1:A:218:TRP:CE3	3.04	0.41
1:A:253:THR:HG23	1:A:332:ASN:ND2	2.35	0.41
1:A:259:LEU:C	1:A:259:LEU:CD1	2.87	0.41
1:A:584:MET:SD	1:A:657:ARG:HG2	2.60	0.41
1:A:55:TYR:HE2	1:A:216:ASN:ND2	2.19	0.41
1:A:218:TRP:CE2	1:A:237:GLY:HA2	2.56	0.40
1:A:509:ILE:HG21	1:A:513:GLN:HG3	2.02	0.40
1:A:611[A]:ARG:HH11	1:A:611[A]:ARG:HB2	1.86	0.40
1:A:308:LEU:N	1:A:334:LEU:HD22	2.36	0.40
1:A:668:LEU:HD21	1:A:778[B]:MET:HE1	1.98	0.40
1:A:395:ILE:HD13	1:A:510:LEU:HD13	2.04	0.40
1:A:401:ALA:HB1	1:A:460:ALA:CA	2.51	0.40
1:A:568:MET:HE2	1:A:605:ASP:CB	2.51	0.40
1:A:667[A]:MET:O	1:A:668:LEU:HD23	2.22	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	864/876 (99%)	809 (94%)	50 (6%)	5 (1%)	25	31

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	THR
1	A	235	LEU
1	A	236	ARG
1	A	586	PRO
1	A	624	ASP

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	653/707 (92%)	641 (98%)	12 (2%)	59	75

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	131	ARG
1	A	278	ASN
1	A	306	ASP
1	A	390	TYR
1	A	392	ASP

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Mol	Chain	Res	Type
1	A	393	GLN
1	A	420	TRP
1	A	599	LEU
1	A	711	PRO
1	A	809	ASP
1	A	835	ILE

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	252	ASN
1	A	278	ASN
1	A	311	ASN
1	A	318	HIS
1	A	330	GLN
1	A	375	HIS
1	A	393	GLN
1	A	409	GLN
1	A	602	GLN
1	A	650	ASN
1	A	651	GLN
1	A	722	GLN
1	A	764	GLN
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

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	3001	-	4,4,4	0.26	0	6,6,6	0.07	0
4	PEP	A	3000	2	6,9,9	2.23	3 (50%)	8,13,13	0.79	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
4	PEP	A	3000	2	-	1/5/9/9	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3000	PEP	P-O2	4.14	1.65	1.59
4	A	3000	PEP	C3-C2	2.05	1.37	1.33
4	A	3000	PEP	P-O2P	-2.01	1.47	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3000	PEP	C2-O2-P-O1P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3000	PEP	2	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	862/876 (98%)	0.85	107 (12%) 4 5	19, 51, 81, 94	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	235	LEU	8.0
1	A	160	LEU	6.8
1	A	74	LEU	6.7
1	A	92	LEU	5.8
1	A	458	HIS	5.1
1	A	399	LEU	4.9
1	A	232	ILE	4.9
1	A	475	SER	4.9
1	A	59	GLY	4.8
1	A	67	TRP	4.6
1	A	388	SER	4.6
1	A	459	ALA	4.5
1	A	518	PRO	4.4
1	A	91	PRO	4.4
1	A	61	ALA	4.2
1	A	169	LEU	4.2
1	A	460	ALA	4.2
1	A	477	ILE	4.1
1	A	223	ALA	4.0
1	A	80	TYR	3.9
1	A	45	PHE	3.8
1	A	85	LEU	3.8
1	A	229	ILE	3.7
1	A	520	LEU	3.7
1	A	457	SER	3.7
1	A	488	ILE	3.7
1	A	102	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	476	GLY	3.6
1	A	207	LEU	3.6
1	A	473	GLY	3.5
1	A	432	ALA	3.5
1	A	478	ARG	3.5
1	A	586	PRO	3.5
1	A	70	ILE	3.5
1	A	163	MET	3.5
1	A	175	LEU	3.4
1	A	66	LEU	3.4
1	A	60	CYS	3.4
1	A	170	LYS	3.4
1	A	479	VAL	3.3
1	A	519	ALA	3.3
1	A	489	GLY	3.2
1	A	471	VAL	3.2
1	A	124	LEU	3.2
1	A	77	VAL	3.1
1	A	218	TRP	3.1
1	A	233	THR	3.1
1	A	132	PHE	3.1
1	A	455	MET	3.1
1	A	55	TYR	3.0
1	A	252	ASN	3.0
1	A	57	ASP	3.0
1	A	105	PRO	2.9
1	A	226	TYR	2.9
1	A	290	THR	2.9
1	A	62	LEU	2.9
1	A	236	ARG	2.9
1	A	64	ALA	2.9
1	A	276	LEU	2.9
1	A	277	VAL	2.8
1	A	302	PRO	2.8
1	A	234	GLY	2.7
1	A	73	GLY	2.7
1	A	58	ALA	2.7
1	A	76	TRP	2.7
1	A	172	ASP	2.7
1	A	291	PRO	2.7
1	A	401	ALA	2.7
1	A	128	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	562	LEU	2.6
1	A	111	VAL	2.6
1	A	167	LYS	2.6
1	A	819[A]	PHE	2.6
1	A	173	THR	2.6
1	A	23	LEU	2.6
1	A	300	LEU	2.5
1	A	450	THR	2.5
1	A	294	LEU	2.5
1	A	836[A]	CYS	2.4
1	A	154	SER	2.4
1	A	177	ALA	2.4
1	A	168	GLY	2.4
1	A	515	LEU	2.4
1	A	230	ASN	2.4
1	A	106	GLY	2.4
1	A	392	ASP	2.4
1	A	517	PRO	2.4
1	A	9	PHE	2.4
1	A	166	SER	2.3
1	A	540	LEU	2.2
1	A	297	MET	2.2
1	A	508	VAL	2.2
1	A	833	VAL	2.2
1	A	196	GLY	2.2
1	A	171	ASN	2.2
1	A	857	VAL	2.2
1	A	72	ASP	2.2
1	A	451	GLU	2.1
1	A	834	GLY	2.1
1	A	41	VAL	2.1
1	A	174	ASP	2.1
1	A	56	GLN	2.1
1	A	588	LEU	2.1
1	A	3	LYS	2.0
1	A	126	ALA	2.0
1	A	563	CYS	2.0
1	A	89	GLN	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 [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(\AA^2)	Q<0.9
2	MG	A	2000	1/1	0.87	0.21	38,38,38,38	0
4	PEP	A	3000	10/10	0.96	0.16	38,42,45,47	0
3	SO4	A	3001	5/5	0.97	0.12	80,80,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.