



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:26 AM UTC

PDB ID : 3IF2 / pdb_00003if2
Title : Crystal structure of Putative amino-acid aminotransferase (YP_265399.1)
from Psychrobacter arcticum 273-4 at 2.50 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2009-07-23
Resolution : 2.50 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

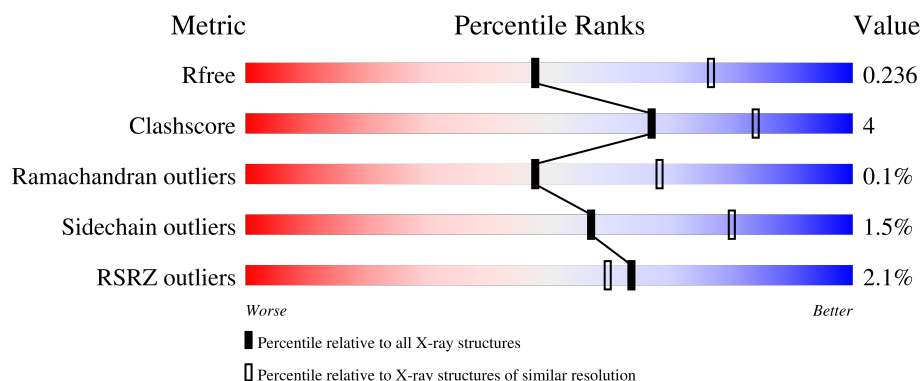
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

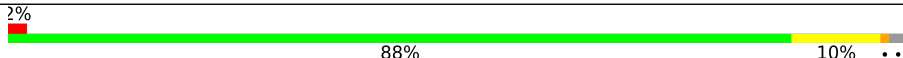
The reported resolution of this entry is 2.50 Å.

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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. 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	444	
1	B	444	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7113 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.

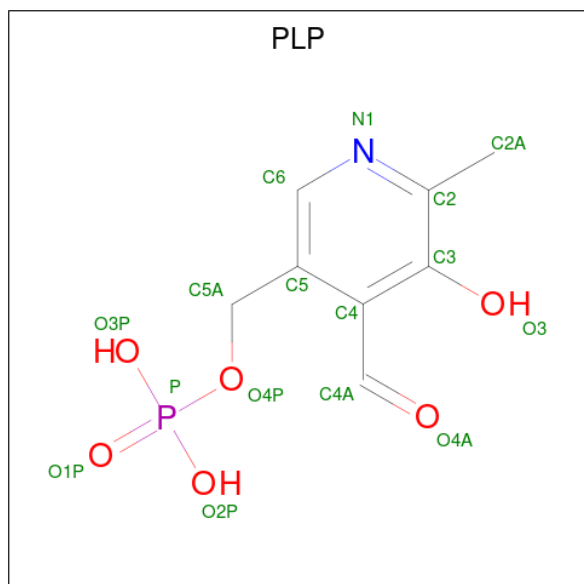
- Molecule 1 is a protein called Aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	Se	0	9	0
			3436	2205	566	651	4	10			
1	B	437	Total	C	N	O	S	Se	0	7	0
			3426	2196	561	655	4	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q4FPU3
B	0	GLY	-	expression tag	UNP Q4FPU3

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



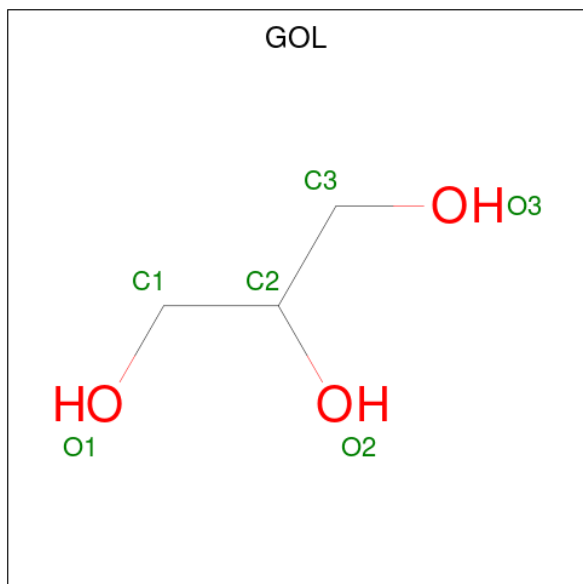
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

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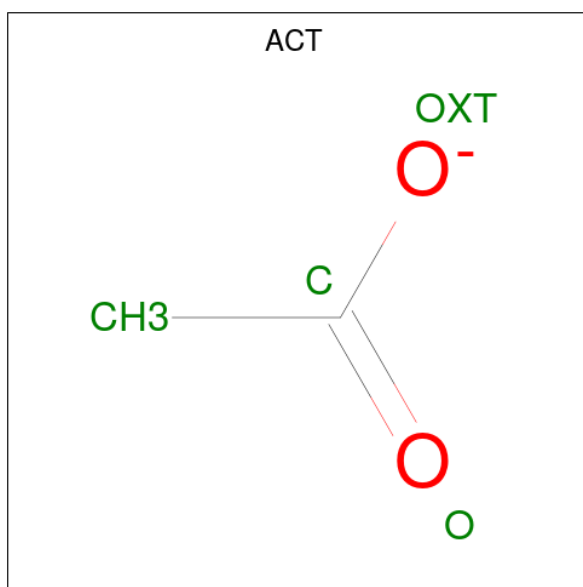
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

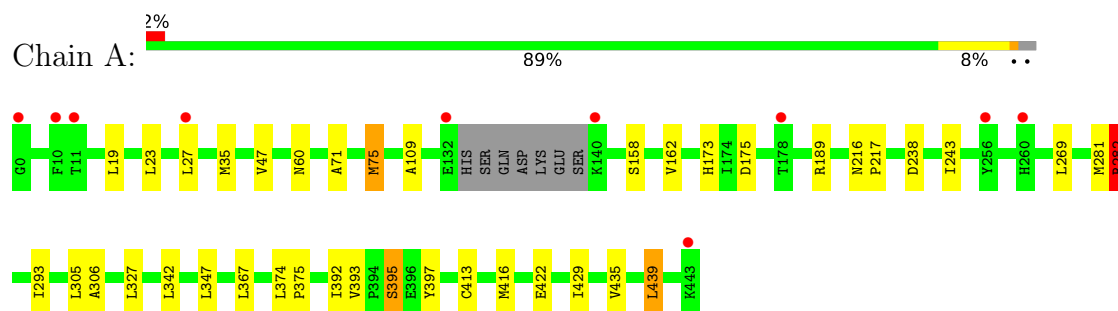
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	105	Total	O	0	0
			105	105		
5	B	98	Total	O	0	0
			98	98		

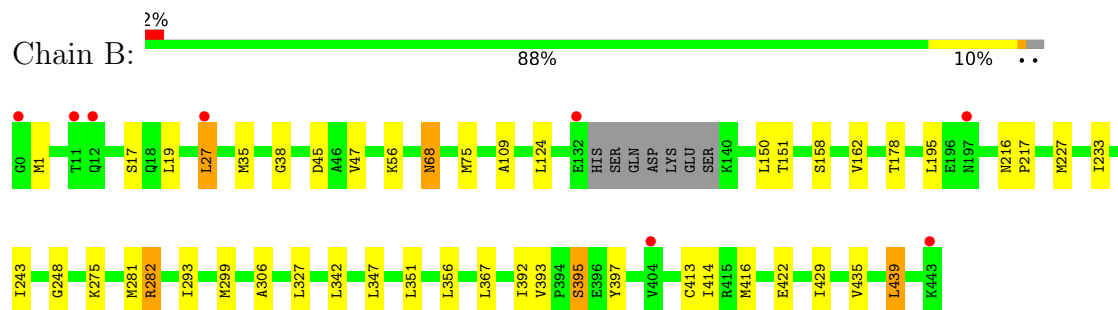
3 Residue-property plots [i](#)

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: Aminotransferase



- Molecule 1: Aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	152.81Å 152.81Å 100.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 2.50 29.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.98-2.50) 98.8 (29.98-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0053, PHENIX	Depositor
R, R_{free}	0.178 , 0.221 0.190 , 0.236	Depositor DCC
R_{free} test set	1986 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7113	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PLP, ACT

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	0.91	0/3532	1.10	8/4781 (0.2%)
1	B	0.96	0/3513	1.13	6/4756 (0.1%)
All	All	0.94	0/7045	1.12	14/9537 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	ASN	N-CA-C	-8.66	97.07	109.62
1	B	216	ASN	N-CA-C	-6.96	98.46	109.04
1	B	68	ASN	N-CA-C	6.59	124.84	110.80
1	B	395	SER	N-CA-C	6.29	120.22	112.54
1	A	395	SER	N-CA-C	6.14	118.95	111.82
1	B	248	GLY	N-CA-C	5.74	119.67	112.79
1	A	173[A]	HIS	N-CA-C	-5.36	101.81	110.32
1	A	173[B]	HIS	N-CA-C	-5.36	101.81	110.32
1	A	75	MSE	CB-CA-C	-5.29	102.58	110.88
1	B	158	SER	N-CA-C	5.22	119.98	111.37
1	B	45	ASP	N-CA-C	5.09	116.52	111.07
1	A	75	MSE	N-CA-C	5.09	116.52	111.07
1	A	158	SER	N-CA-C	5.05	121.57	110.80
1	A	282	ARG	NE-CZ-NH2	-5.04	114.66	119.20

There are no chirality outliers.

There are no planarity outliers.

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	3436	0	3376	29	0
1	B	3426	0	3349	33	0
2	A	16	0	8	1	0
2	B	16	0	8	2	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	B	4	0	3	0	0
5	A	105	0	0	0	0
5	B	98	0	0	0	0
All	All	7113	0	6760	51	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 4.

All (51) 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:VAL:HG11	1:B:162:VAL:HG11	1.20	1.11
1:B:27:LEU:HD11	1:B:35:MSE:HE2	1.67	0.75
1:A:109:ALA:HB2	1:A:293:ILE:HG23	1.75	0.69
1:A:281:MSE:HE2	1:B:75:MSE:CG	2.23	0.68
1:A:75:MSE:CG	1:B:281:MSE:HE2	2.24	0.67
1:A:75:MSE:HG2	1:B:281:MSE:HE2	1.79	0.64
1:B:275:LYS:HZ1	2:B:500:PLP:C4A	2.17	0.58
1:A:19:LEU:HD21	1:A:393:VAL:HG13	1.85	0.58
1:A:60:ASN:OD1	1:B:56:LYS:NZ	2.37	0.58
1:A:162:VAL:CG1	1:B:162:VAL:HG11	2.14	0.57
1:B:342:LEU:HD21	1:B:422:GLU:HG3	1.86	0.57
1:B:195:LEU:HD22	1:B:233:ILE:HD13	1.87	0.56
1:A:281:MSE:HE2	1:B:75:MSE:HG2	1.88	0.55
1:A:282:ARG:NH2	2:A:500:PLP:O3P	2.35	0.53
1:A:342:LEU:HD21	1:A:422:GLU:HG3	1.91	0.52
1:B:19:LEU:HD21	1:B:393:VAL:HG13	1.91	0.52
1:B:351:LEU:HD12	1:B:356:LEU:HD22	1.91	0.51
1:A:19:LEU:HD22	1:A:397:TYR:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:ALA:HB2	1:B:293:ILE:HG23	1.91	0.50
1:A:27:LEU:HD11	1:A:35:MSE:HE2	1.93	0.49
1:A:162:VAL:HG11	1:B:162:VAL:CG1	2.14	0.49
1:B:275:LYS:NZ	2:B:500:PLP:C4A	2.75	0.48
1:B:47:VAL:HA	1:B:327:LEU:HD11	1.94	0.48
1:A:435:VAL:O	1:A:439:LEU:HD13	2.14	0.48
1:A:306:ALA:O	1:B:282:ARG:HD3	2.15	0.47
1:B:367:LEU:HD12	1:B:416:MSE:CE	2.45	0.47
1:A:281:MSE:HE2	1:B:75:MSE:HG3	1.96	0.46
1:B:124:LEU:HB2	1:B:299:MSE:HE1	1.98	0.46
1:A:175[B]:ASP:OD2	1:A:189[B]:ARG:HD2	2.17	0.45
1:B:19:LEU:HD22	1:B:397:TYR:CD2	2.52	0.45
1:B:392:ILE:HD13	1:B:414:ILE:HB	1.98	0.44
1:A:367:LEU:HB2	1:A:416:MSE:HE2	1.99	0.44
1:B:47:VAL:HG22	1:B:327:LEU:HD11	2.00	0.44
1:A:71:ALA:O	1:A:75:MSE:HE3	2.18	0.44
1:A:395:SER:HB3	1:A:413:CYS:HB2	2.01	0.42
1:A:282:ARG:HD3	1:B:306:ALA:O	2.18	0.42
1:B:347:LEU:HD23	1:B:429:ILE:HG23	2.02	0.42
1:B:367:LEU:HB2	1:B:416:MSE:HE2	2.01	0.42
1:A:47:VAL:HA	1:A:327:LEU:HD11	2.02	0.42
1:A:243:ILE:HB	1:A:269:LEU:HD23	2.02	0.41
1:A:347:LEU:HD23	1:A:429:ILE:HG23	2.01	0.41
1:A:374:LEU:HD12	1:A:375:PRO:HD2	2.02	0.41
1:B:150:LEU:C	1:B:150:LEU:HD23	2.45	0.41
1:B:227:MSE:HE2	1:B:243:ILE:HD13	2.03	0.41
1:B:395:SER:HB3	1:B:413:CYS:HB2	2.02	0.41
1:B:150:LEU:HD23	1:B:151:THR:N	2.36	0.41
1:B:35:MSE:HE3	1:B:38:GLY:HA3	2.03	0.41
1:A:392:ILE:C	1:A:392:ILE:HD12	2.46	0.41
1:B:435:VAL:O	1:B:439:LEU:HD13	2.21	0.41
1:A:305:LEU:HD12	1:A:305:LEU:HA	1.98	0.40
1:A:23:LEU:O	1:A:27:LEU:HD13	2.21	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	442/444 (100%)	426 (96%)	16 (4%)	0	100	100
1	B	440/444 (99%)	425 (97%)	14 (3%)	1 (0%)	43	63
All	All	882/888 (99%)	851 (96%)	30 (3%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	ASN

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	369/362 (102%)	365 (99%)	4 (1%)	65	84
1	B	368/362 (102%)	361 (98%)	7 (2%)	50	76
All	All	737/724 (102%)	726 (98%)	11 (2%)	57	80

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	217	PRO
1	A	238	ASP
1	A	282	ARG
1	A	439	LEU
1	B	1	MSE

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Mol	Chain	Res	Type
1	B	17	SER
1	B	27	LEU
1	B	178	THR
1	B	217	PRO
1	B	282	ARG
1	B	439	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	115	GLN
1	A	197	ASN
1	A	245	ASN
1	A	265	ASN
1	A	423	GLN
1	B	8	GLN
1	B	245	ASN
1	B	304	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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
3	GOL	A	444	-	5,5,5	0.54	0	5,5,5	0.76	0
3	GOL	B	445	-	5,5,5	0.32	0	5,5,5	0.49	0
2	PLP	B	500	-	16,16,16	1.36	2 (12%)	20,23,23	1.30	2 (10%)
4	ACT	B	444	-	3,3,3	0.79	0	3,3,3	1.94	2 (66%)
2	PLP	A	500	-	16,16,16	1.38	2 (12%)	20,23,23	1.71	4 (20%)

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
3	GOL	B	445	-	-	2/4/4/4	-
2	PLP	B	500	-	-	5/8/8/8	0/1/1/1
3	GOL	A	444	-	-	1/4/4/4	-
2	PLP	A	500	-	-	6/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	PLP	C4-C4A	2.84	1.53	1.46
2	A	500	PLP	C4-C4A	2.76	1.52	1.46
2	B	500	PLP	C2-N1	2.59	1.38	1.33
2	A	500	PLP	C2-N1	2.50	1.38	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	PLP	O4P-P-O1P	5.05	120.09	106.44
2	B	500	PLP	O4P-P-O1P	2.71	113.77	106.44
2	B	500	PLP	C2A-C2-C3	2.54	123.78	120.80
4	B	444	ACT	OXT-C-O	-2.54	112.60	122.03
2	A	500	PLP	O4P-C5A-C5	2.41	113.88	109.36
4	B	444	ACT	OXT-C-CH3	2.19	124.22	115.05
2	A	500	PLP	O2P-P-O4P	-2.11	101.18	106.67
2	A	500	PLP	O3-C3-C2	2.02	121.76	117.58

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	PLP	C5A-O4P-P-O1P
2	A	500	PLP	C5A-O4P-P-O2P
2	A	500	PLP	C5A-O4P-P-O3P
2	B	500	PLP	C5A-O4P-P-O1P
2	B	500	PLP	C5A-O4P-P-O2P
2	B	500	PLP	C5A-O4P-P-O3P
2	A	500	PLP	C3-C4-C4A-O4A
2	B	500	PLP	C3-C4-C4A-O4A
3	B	445	GOL	C1-C2-C3-O3
3	B	445	GOL	O2-C2-C3-O3
2	A	500	PLP	C5-C4-C4A-O4A
2	A	500	PLP	C4-C5-C5A-O4P
3	A	444	GOL	C1-C2-C3-O3
2	B	500	PLP	C5-C4-C4A-O4A

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	PLP	2	0
2	A	500	PLP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	427/444 (96%)	0.14	10 (2%) 61 57	21, 37, 51, 66	9 (2%)
1	B	427/444 (96%)	0.04	8 (1%) 66 62	17, 37, 52, 64	7 (1%)
All	All	854/888 (96%)	0.09	18 (2%) 63 59	17, 37, 52, 66	16 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	TYR	3.0
1	B	443	LYS	2.9
1	B	27	LEU	2.9
1	B	197	ASN	2.8
1	A	11	THR	2.8
1	A	27	LEU	2.8
1	B	132	GLU	2.7
1	A	443	LYS	2.4
1	B	12	GLN	2.3
1	A	140	LYS	2.3
1	B	404	VAL	2.3
1	B	0	GLY	2.2
1	A	132	GLU	2.2
1	A	260	HIS	2.1
1	A	178	THR	2.1
1	B	11	THR	2.1
1	A	10	PHE	2.1
1	A	0	GLY	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	ACT	B	444	4/4	0.82	0.18	60,60,61,62	0
3	GOL	B	445	6/6	0.86	0.16	59,59,60,60	0
3	GOL	A	444	6/6	0.89	0.14	56,57,57,57	0
2	PLP	A	500	16/16	0.95	0.11	38,49,53,54	0
2	PLP	B	500	16/16	0.96	0.09	37,47,50,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.