



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 04:17 PM GMT

PDB ID : 4A0F
Title : Structure of selenomethionine substituted bifunctional DAPA aminotransferase-dethiobiotin synthetase from *Arabidopsis thaliana* in its apo form.
Authors : Cobessi, D.; Dumas, R.; Pautre, V.; Meinguet, C.; Ferrer, J.L.; Alban, C.
Deposited on : 2011-09-09
Resolution : 2.71 Å (reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

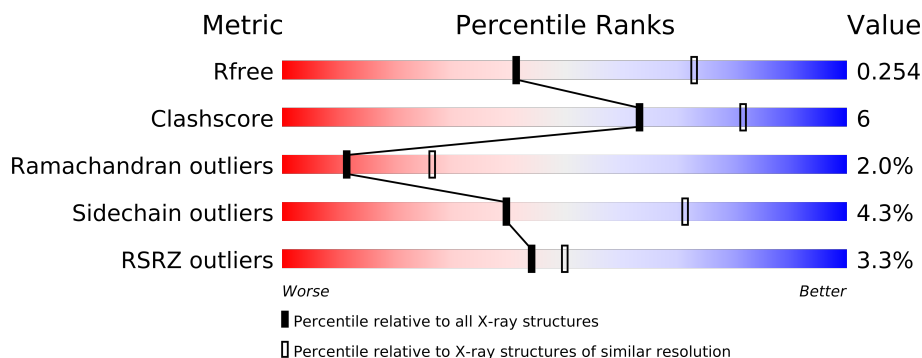
The following versions of software and data (see [references](#)) were used in the production of this report:

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

1 Overall quality at a glance



The reported resolution of this entry is 2.71 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1770 (2.74-2.70)
Clashscore	79885	2183 (2.74-2.70)
Ramachandran outliers	78287	2147 (2.74-2.70)
Sidechain outliers	78261	2148 (2.74-2.70)
RSRZ outliers	66119	1772 (2.74-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	831	
1	B	831	

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

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	A	1809	-	X
3	SO4	A	1810	-	X
3	SO4	B	1810	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11317 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOAT EAMINOTRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	746	Total	C	N	O	S	Se	0	1	0
			5568	3562	937	1037	16	16			
1	B	750	Total	C	N	O	S	Se	0	0	0
			5619	3598	944	1046	16	15			

There are 42 discrepancies between the modelled and reference sequences:

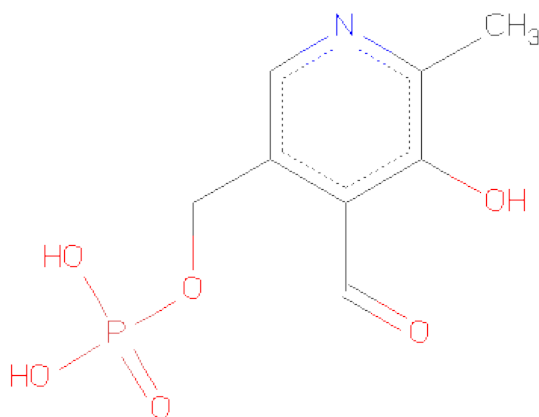
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	GLY	-	EXPRESSION TAG	UNP B0F481
A	-18	SER	-	EXPRESSION TAG	UNP B0F481
A	-17	SER	-	EXPRESSION TAG	UNP B0F481
A	-16	HIS	-	EXPRESSION TAG	UNP B0F481
A	-15	HIS	-	EXPRESSION TAG	UNP B0F481
A	-14	HIS	-	EXPRESSION TAG	UNP B0F481
A	-13	HIS	-	EXPRESSION TAG	UNP B0F481
A	-12	HIS	-	EXPRESSION TAG	UNP B0F481
A	-11	HIS	-	EXPRESSION TAG	UNP B0F481
A	-10	SER	-	EXPRESSION TAG	UNP B0F481
A	-9	SER	-	EXPRESSION TAG	UNP B0F481
A	-8	GLY	-	EXPRESSION TAG	UNP B0F481
A	-7	LEU	-	EXPRESSION TAG	UNP B0F481
A	-6	VAL	-	EXPRESSION TAG	UNP B0F481
A	-5	PRO	-	EXPRESSION TAG	UNP B0F481
A	-4	ARG	-	EXPRESSION TAG	UNP B0F481
A	-3	GLY	-	EXPRESSION TAG	UNP B0F481
A	-2	SER	-	EXPRESSION TAG	UNP B0F481
A	-1	HIS	-	EXPRESSION TAG	UNP B0F481
A	0	MSE	-	EXPRESSION TAG	UNP B0F481
A	326	TYR	PHE	ENGINEERED MUTATION	UNP B0F481
B	-19	GLY	-	EXPRESSION TAG	UNP B0F481
B	-18	SER	-	EXPRESSION TAG	UNP B0F481
B	-17	SER	-	EXPRESSION TAG	UNP B0F481

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	EXPRESSION TAG	UNP B0F481
B	-15	HIS	-	EXPRESSION TAG	UNP B0F481
B	-14	HIS	-	EXPRESSION TAG	UNP B0F481
B	-13	HIS	-	EXPRESSION TAG	UNP B0F481
B	-12	HIS	-	EXPRESSION TAG	UNP B0F481
B	-11	HIS	-	EXPRESSION TAG	UNP B0F481
B	-10	SER	-	EXPRESSION TAG	UNP B0F481
B	-9	SER	-	EXPRESSION TAG	UNP B0F481
B	-8	GLY	-	EXPRESSION TAG	UNP B0F481
B	-7	LEU	-	EXPRESSION TAG	UNP B0F481
B	-6	VAL	-	EXPRESSION TAG	UNP B0F481
B	-5	PRO	-	EXPRESSION TAG	UNP B0F481
B	-4	ARG	-	EXPRESSION TAG	UNP B0F481
B	-3	GLY	-	EXPRESSION TAG	UNP B0F481
B	-2	SER	-	EXPRESSION TAG	UNP B0F481
B	-1	HIS	-	EXPRESSION TAG	UNP B0F481
B	0	MSE	-	EXPRESSION TAG	UNP B0F481
B	326	TYR	PHE	ENGINEERED MUTATION	UNP B0F481

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

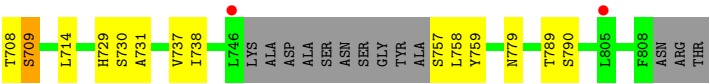
- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	50	Total	O	0	0
			50	50		
4	B	30	Total	O	0	0
			30	30		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	233.67Å 75.97Å 88.63Å 90.00° 109.20° 90.00°	Depositor
Resolution (Å)	41.85 – 2.71 41.85 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.1 (41.85-2.71) 99.1 (41.85-2.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.73Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.200 , 0.261 0.192 , 0.254	Depositor DCC
R_{free} test set	1989 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 39567 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11317	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, PLP

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	0/5681	0.60	1/7722 (0.0%)
1	B	0.45	0/5731	0.60	0/7787
All	All	0.45	0/11412	0.60	1/15509 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	PRO	N-CA-CB	6.07	110.59	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5568	0	0	27	0
1	B	5619	0	0	36	0
2	A	15	0	0	1	0
2	B	15	0	0	1	0
3	A	10	0	0	0	0
3	B	10	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	50	0	0	3	0
4	B	30	0	0	0	0
All	All	11317	0	0	62	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (62) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:538:ARG:NH2	1:A:716:GLU:OE2	2.16	0.78
1:B:708:THR:CG2	1:B:709:SER:N	2.57	0.68
1:B:757:SER:O	1:B:759:TYR:N	2.28	0.66
1:A:103:GLY:O	1:A:104:LEU:C	2.34	0.65
1:A:699:LYS:NZ	4:A:2039:HOH:O	2.33	0.62
1:B:388:TYR:OH	1:B:392:ARG:NH1	2.33	0.61
1:A:708:THR:N	1:A:713:THR:O	2.34	0.60
1:B:28:LYS:NZ	3:B:1809:SO4:O4	2.34	0.60
1:A:143:SER:OG	1:A:145:HIS:ND1	2.35	0.60
1:A:356:ASN:O	1:A:357:SER:O	2.20	0.59
1:B:706:ASN:ND2	1:B:789:THR:O	2.38	0.57
1:A:388:TYR:OH	1:A:392:ARG:NH1	2.39	0.55
1:B:27:GLY:CA	3:B:1810:SO4:O4	2.55	0.54
1:B:446:PHE:CE1	1:B:450:HIS:CD2	2.95	0.54
1:B:644:LYS:NZ	2:B:1644:PLP:O3	2.39	0.54
1:A:547:ASP:OD2	1:A:599:ARG:NH1	2.41	0.54
1:A:446:PHE:CE1	1:A:450:HIS:CD2	2.96	0.53
1:B:473:TYR:OH	1:B:476:ASP:OD1	2.27	0.53
1:A:27:GLY:O	1:A:30:LEU:N	2.42	0.53
1:B:538:ARG:NH1	1:B:737:VAL:O	2.41	0.53
1:B:547:ASP:OD2	1:B:599:ARG:NH1	2.42	0.53
1:A:644:LYS:NZ	2:A:1644:PLP:O3	2.39	0.52
1:B:27:GLY:O	1:B:30:LEU:N	2.41	0.52
1:B:8:PHE:CD1	1:B:8:PHE:C	2.83	0.52
1:B:211:ARG:NH2	1:B:241:ASP:OD2	2.44	0.51
1:B:729:HIS:O	1:B:731:ALA:N	2.43	0.51
1:A:221:ARG:O	1:A:222:LEU:CB	2.58	0.51
1:A:546:ARG:O	1:A:549:SER:OG	2.29	0.51
1:A:211:ARG:NH2	1:A:241:ASP:OD2	2.43	0.51
1:B:221:ARG:O	1:B:222:LEU:CB	2.59	0.50
1:B:546:ARG:O	1:B:549:SER:OG	2.29	0.50
1:B:95:SER:OG	1:B:151:GLU:OE1	2.31	0.48
1:B:622:TRP:CE3	1:B:714:LEU:CD1	2.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:304:ASN:ND2	4:A:2029:HOH:O	2.47	0.48
1:B:41:LEU:O	1:B:42:GLN:NE2	2.47	0.48
1:B:426:TYR:OH	1:B:677:HIS:O	2.32	0.47
1:A:426:TYR:OH	1:A:677:HIS:O	2.31	0.47
1:A:8:PHE:C	1:A:8:PHE:CD1	2.87	0.47
1:B:757:SER:N	1:B:779:ASN:OD1	2.47	0.47
1:A:706:ASN:ND2	1:A:789:THR:O	2.47	0.47
1:A:222:LEU:C	1:A:224:GLY:N	2.67	0.46
1:B:222:LEU:C	1:B:224:GLY:N	2.68	0.46
1:A:113:MSE:CE	1:A:114:CYS:N	2.79	0.46
1:B:280:ASP:OD1	1:B:282:LEU:N	2.49	0.45
1:B:19:ILE:O	1:B:189:THR:OG1	2.35	0.44
1:B:27:GLY:C	3:B:1810:SO4:O4	2.55	0.44
1:A:599:ARG:NE	1:A:633:LEU:O	2.51	0.44
1:A:473:TYR:OH	1:A:476:ASP:OD1	2.36	0.44
1:A:89:ASN:ND2	4:A:2008:HOH:O	2.51	0.43
1:A:644:LYS:O	1:B:681:TYR:OH	2.36	0.43
1:B:281:ASP:O	1:B:282:LEU:CB	2.66	0.43
1:B:221:ARG:O	1:B:252:LEU:CD1	2.67	0.42
1:B:73:LYS:CE	1:B:281:ASP:O	2.67	0.42
1:B:519:ILE:CG1	1:B:535:PHE:CE2	3.02	0.42
1:B:208:ARG:N	1:B:209:PRO:CD	2.84	0.41
1:B:599:ARG:NE	1:B:633:LEU:O	2.54	0.41
1:A:93:HIS:CB	1:A:113:MSE:CE	2.99	0.41
1:A:140:ALA:N	1:A:151:GLU:OE2	2.54	0.41
1:A:95:SER:OG	1:A:151:GLU:OE1	2.38	0.41
1:B:73:LYS:NZ	1:B:281:ASP:O	2.54	0.40
1:B:96:LEU:N	1:B:97:PRO:CD	2.85	0.40
1:B:441:MSE:CE	1:B:639:ILE:CG2	2.99	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	733/831 (88%)	669 (91%)	50 (7%)	14 (2%)	12	28
1	B	734/831 (88%)	672 (92%)	46 (6%)	16 (2%)	10	24
All	All	1467/1662 (88%)	1341 (91%)	96 (6%)	30 (2%)	11	26

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	LEU
1	A	357	SER
1	B	222	LEU
1	B	357	SER
1	B	730	SER
1	B	758	LEU
1	A	355	ASP
1	A	644	LYS
1	B	355	ASP
1	B	644	LYS
1	A	104	LEU
1	A	451	ASN
1	A	643	ALA
1	B	451	ASN
1	B	643	ALA
1	A	397	MSE
1	A	738	ILE
1	B	397	MSE
1	B	491	GLY
1	B	48	ALA
1	B	447	CYS
1	A	28	LYS
1	A	373	GLY
1	A	447	CYS
1	B	583	VAL
1	B	738	ILE
1	A	583	VAL
1	A	491	GLY
1	B	373	GLY
1	B	417	VAL

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	575/688 (84%)	552 (96%)	23 (4%)	42	74
1	B	583/688 (85%)	556 (95%)	27 (5%)	37	69
All	All	1158/1376 (84%)	1108 (96%)	50 (4%)	40	71

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	96	LEU
1	A	113	MSE
1	A	115	SER
1	A	131	LEU
1	A	142	ILE
1	A	183	LEU
1	A	206	LEU
1	A	236	LYS
1	A	321	VAL
1	A	327	THR
1	A	369	TRP
1	A	396	VAL
1	A	397	MSE
1	A	417	VAL
1	A	428	SER
1	A	513	SER
1	A	659	THR
1	A	667	SER
1	A	675	LEU
1	A	680	SER
1	A	686	MSE
1	A	790	SER
1	B	9	HIS
1	B	51	LEU
1	B	67	SER
1	B	96	LEU
1	B	131	LEU
1	B	183	LEU
1	B	206	LEU
1	B	236	LYS
1	B	302	LEU
1	B	321	VAL

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Mol	Chain	Res	Type
1	B	327	THR
1	B	349	SER
1	B	356	ASN
1	B	369	TRP
1	B	396	VAL
1	B	397	MSE
1	B	417	VAL
1	B	428	SER
1	B	513	SER
1	B	624	LEU
1	B	659	THR
1	B	667	SER
1	B	675	LEU
1	B	680	SER
1	B	686	MSE
1	B	709	SER
1	B	790	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	A	1644	1	14,15,16	1.84	2 (14%)	20,22,23	1.69	4 (20%)
3	SO4	A	1809	-	4,4,4	0.23	0	6,6,6	0.33	0
3	SO4	A	1810	-	4,4,4	0.17	0	6,6,6	0.35	0
2	PLP	B	1644	1	14,15,16	1.88	3 (21%)	20,22,23	1.61	3 (15%)
3	SO4	B	1809	-	4,4,4	0.29	0	6,6,6	0.22	0
3	SO4	B	1810	-	4,4,4	0.22	0	6,6,6	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PLP	A	1644	1	-	0/6/6/8	0/1/1/1
3	SO4	A	1809	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1810	-	-	0/0/0/0	0/0/0/0
2	PLP	B	1644	1	-	0/6/6/8	0/1/1/1
3	SO4	B	1809	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1810	-	-	0/0/0/0	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1644	PLP	O3-C3	-5.42	1.23	1.37
2	B	1644	PLP	O3-C3	-5.20	1.24	1.37
2	B	1644	PLP	C2-N1	2.85	1.39	1.33
2	A	1644	PLP	C2-N1	2.33	1.38	1.33
2	B	1644	PLP	C6-N1	2.22	1.39	1.34

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1644	PLP	O4P-C5A-C5	5.70	120.84	109.26
2	B	1644	PLP	O4P-C5A-C5	5.36	120.16	109.26
2	B	1644	PLP	O3P-P-O4P	-2.49	99.77	106.65
2	A	1644	PLP	O3P-P-O4P	-2.44	99.91	106.65
2	A	1644	PLP	C5-C6-N1	-2.17	119.95	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1644	PLP	O3P-P-O2P	2.12	115.88	107.61
2	B	1644	PLP	O3P-P-O2P	2.08	115.69	107.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	746/831 (89%)	0.03	32 (4%) 34 39	28, 54, 95, 119	1 (0%)
1	B	750/831 (90%)	0.01	17 (2%) 57 64	27, 56, 89, 114	0
All	All	1496/1662 (90%)	0.02	49 (3%) 44 50	27, 55, 92, 119	1 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	449	ASP	4.5
1	A	759	TYR	4.5
1	A	512	LEU	4.4
1	A	574	HIS	4.4
1	A	551	LEU	4.1
1	A	766	MSE	3.8
1	B	805	LEU	3.7
1	A	493	LEU	3.6
1	B	448	VAL	3.6
1	A	448	VAL	3.5
1	A	805	LEU	3.4
1	A	746	LEU	3.3
1	B	746	LEU	3.3
1	B	79	LEU	3.3
1	A	450	HIS	3.3
1	A	547	ASP	3.2
1	A	744	LEU	3.1
1	B	81	ARG	3.1
1	A	463	VAL	3.1
1	A	762	SER	3.0
1	A	521	LEU	3.0
1	B	688	CYS	2.9
1	A	45	SER	2.8
1	A	806	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	101	SER	2.7
1	A	106	VAL	2.6
1	A	669	ASP	2.5
1	B	668	GLY	2.5
1	A	576	GLY	2.5
1	A	736	VAL	2.5
1	A	545	SER	2.4
1	A	737	VAL	2.4
1	A	758	LEU	2.4
1	B	96	LEU	2.3
1	A	447	CYS	2.3
1	B	685	ALA	2.3
1	A	451	ASN	2.3
1	A	555	TYR	2.2
1	A	428	SER	2.2
1	B	464	VAL	2.2
1	B	667	SER	2.2
1	B	547	ASP	2.1
1	B	691	ALA	2.1
1	B	687	GLY	2.1
1	A	802	TYR	2.1
1	B	279	SER	2.1
1	B	513	SER	2.1
1	A	434	ALA	2.1
1	A	605	CYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	A	1809	5/5	0.23	3.77	48,57,85,89	5
3	SO4	B	1810	5/5	0.27	2.96	57,64,91,114	5
3	SO4	A	1810	5/5	0.20	2.44	31,34,44,57	5
3	SO4	B	1809	5/5	0.16	1.56	52,63,81,83	5
2	PLP	B	1644	15/16	0.23	0.43	34,47,56,60	0
2	PLP	A	1644	15/16	0.19	0.15	44,48,58,61	0

6.5 Other polymers ⓘ

There are no such residues in this entry.