



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 15, 2026 – 12:09 PM UTC

PDB ID : 4A0F / pdb_00004a0f
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 wwPDB X-ray Structure Validation Summary 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

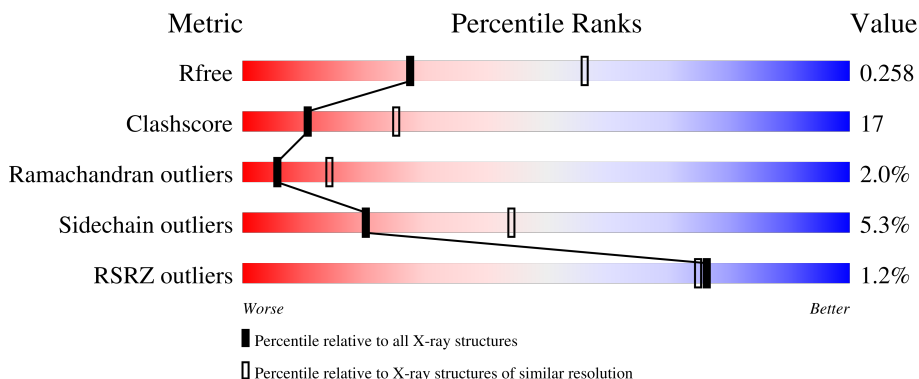
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (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 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	831	
1	B	831	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
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 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 ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE.

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

There are 42 discrepancies between the modelled and reference sequences:

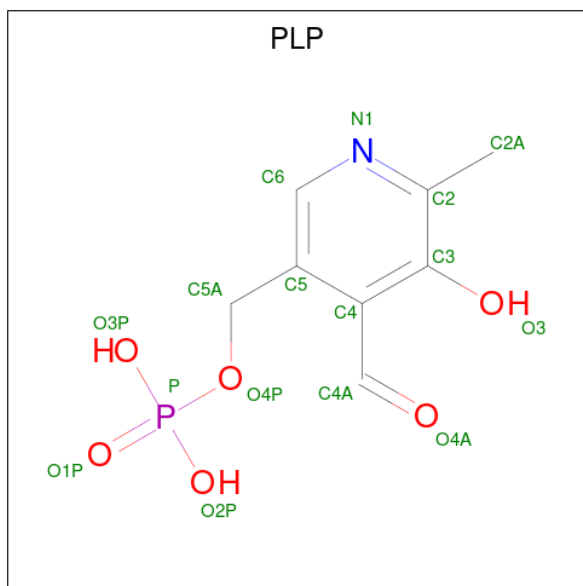
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	GLY	-	expression tag	UNP B0F481
A	-18	SER	-	expression tag	UNP B0F481
A	-17	SER	-	expression tag	UNP B0F481
A	-16	HIS	-	expression tag	UNP B0F481
A	-15	HIS	-	expression tag	UNP B0F481
A	-14	HIS	-	expression tag	UNP B0F481
A	-13	HIS	-	expression tag	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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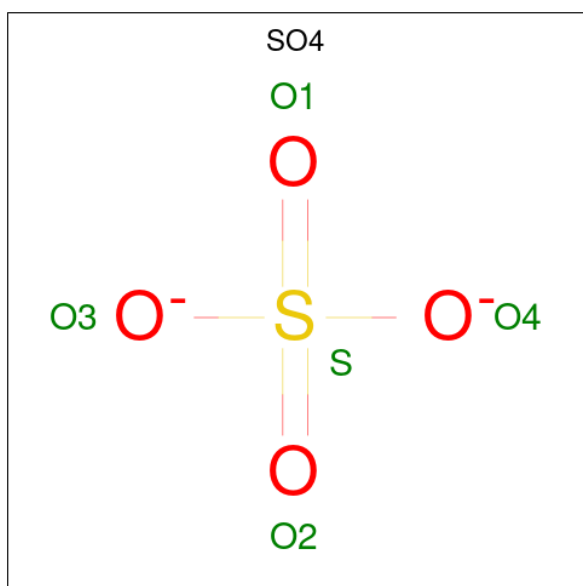
Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP B0F481
B	-15	HIS	-	expression tag	UNP B0F481
B	-14	HIS	-	expression tag	UNP B0F481
B	-13	HIS	-	expression tag	UNP B0F481
B	-12	HIS	-	expression tag	UNP B0F481
B	-11	HIS	-	expression tag	UNP B0F481
B	-10	SER	-	expression tag	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 (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
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 (CCD ID: 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		

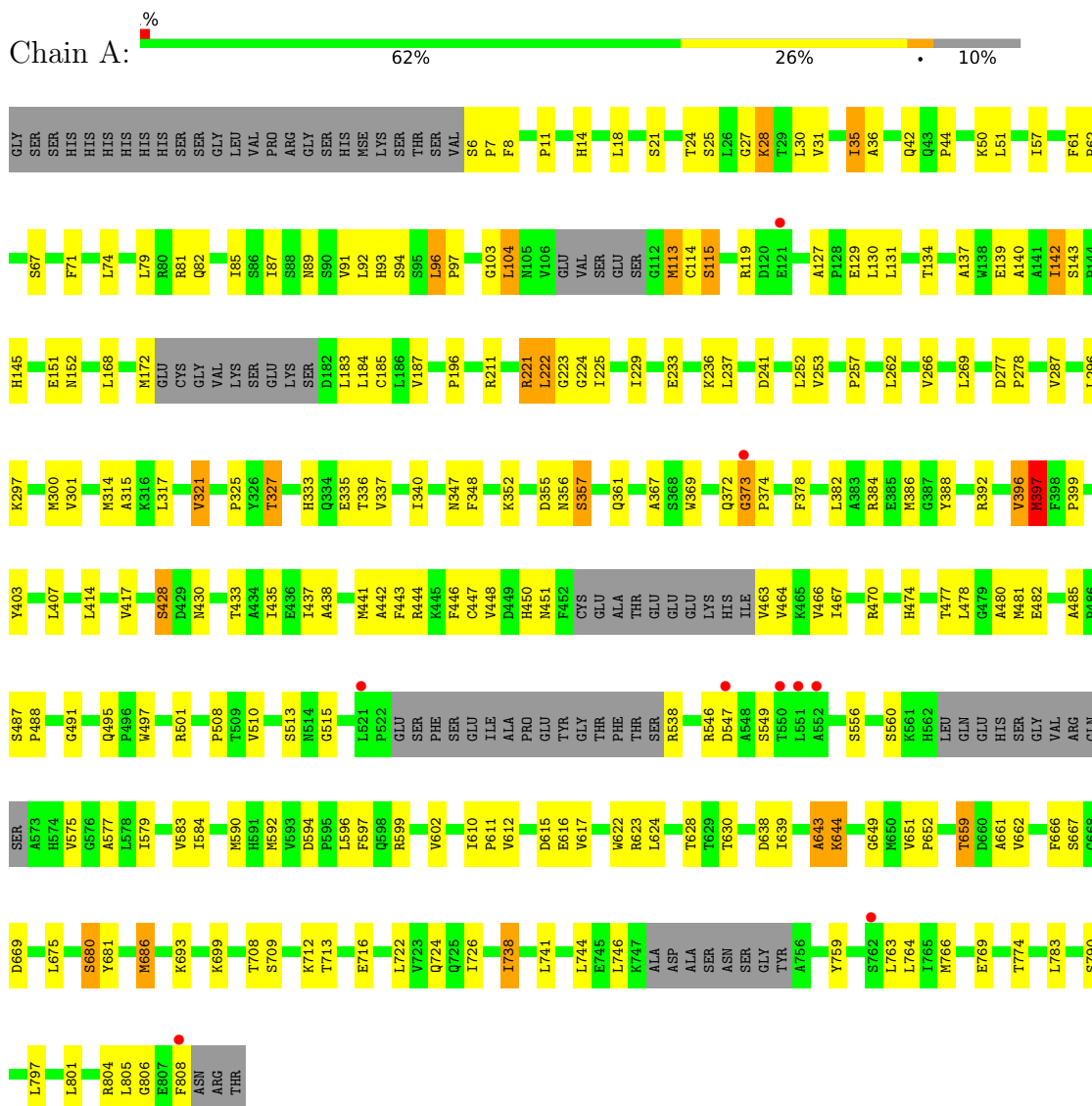
- Molecule 4 is water.

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

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: ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE



- Molecule 1: ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE



GLY	T49	T134	D241	Q361	ALA	S537	T628	L744
SER	K50	L135	L252	A367	THR	R536	T629	E745
HIS	L51	Y136	L253	W369	GLU	R546	T630	L746
HIS	A137	Y138	P257	W372	GLU	D547	K636	LYS
HIS	E139	E139	L262	Q372	LYS	S556	L639	ASP
HIS	G60	T142	V266	P374	HIS	L559	L650	ALA
HIS	F61	S143	L382	L382	V462	S560	A643	SER
SER	P62	P144	L382	L382	V464	K561	R644	ASN
SER	S67	H145	L269	A383	V466	H562	L645	GLY
LEU	F71	L146	D277	R384	I467	I467	M650	TYR
PRO	S72	R150	P278	E385	R470	R470	V651	ALA
ARG	K73	E151	S279	M386	H474	H474	P652	SER
GLY	L74	M152	D280	Y388	L478	G479	T659	ASN
SER	L79	L168	D281	R392	G479	A480	R660	GLY
HIS	R80	M172	L282	H395	M481	A482	A661	TYR
NSE	R81	GLU	V287	V396	E482	A485	F666	ALA
LYS	Q82	CYS	F293	M397	E482	E486	S667	S757
SER	SER	GLY	L296	F398	A485	S487	F666	L758
SER	V5	VAL	K297	P399	E486	P488	S667	L759
S6	S6	LYS	M300	V402	S487	L578	S670	T774
F7	F7	SER	L302	Y403	P488	L579	A671	N779
F8	F8	GLU	L302	Y403	E491	L580	L672	L783
H9	H9	LYS	A315	E411	Q495	V583	L675	L790
L10	L10	SER	R316	L414	P495	L584	S680	L797
P11	P11	D182	L317	V417	W497	M590	L681	L798
L12	L12	L183	V321	L414	R501	H591	M686	L801
N13	N13	L184	P325	S428	P508	M592	K693	R804
H14	H14	C185	T326	M430	F509	D594	T708	L805
L18	L18	L186	T327	T433	V510	P595	S709	G806
S21	S21	V187	K330	I435	S513	F597	Q710	E807
T24	T24	P196	H333	A436	M514	R598	L714	F808
S25	S25	R208	T336	A438	G515	V600	L717	ASN
L26	L26	P209	V337	M441	I519	L601	W718	ARG
G27	G27	F210	I340	A442	S520	V602	D719	THR
K28	K28	R211	F348	F442	F525	I610	V723	
L29	L29	G218	S349	R444	GLU	P611	Q724	
L30	L30	D219	K352	F446	ILE	V612	H729	
L30	L30	G220	K352	C447	ALA	L613	F614	
V31	V31	R221	D355	A448	PRO	F614	D615	
G34	G34	L222	N356	R444	GLU	E616	E616	
I35	I35	G223	S357	K445	TYR	V617	V737	
A36	A36	G224	S357	F445	GLY	F534	I738	
L41	L41	I225	S360	F446	F534	F535	L741	
Q42	Q42	L229		A448	CYS	L624		
O43	O43	E233		V448	GLU			
PRO	PRO	K236		D449	TYR			
SER	SER	L237		M451	GLY			
SER	SER			F452	F534			
S47	S47			GLU	T536			
A48	A48							

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)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.200 , 0.261 0.194 , 0.258	Depositor DCC
R_{free} test set	1990 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtrriage
Anisotropy	0.463	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11317	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage'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.

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: 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	0.57	0/5681	0.88	8/7722 (0.1%)
1	B	0.57	0/5731	0.90	10/7787 (0.1%)
All	All	0.57	0/11412	0.89	18/15509 (0.1%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	111	SER	N-CA-C	-8.38	102.97	113.02
1	A	223	GLY	N-CA-C	-7.86	105.21	115.59
1	B	223	GLY	N-CA-C	-7.47	105.72	115.59
1	B	143	SER	CA-C-N	7.18	127.51	119.32
1	B	143	SER	C-N-CA	7.18	127.51	119.32

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	5568	0	5367	178	0
1	B	5619	0	5425	214	0
2	A	15	0	6	2	0
2	B	15	0	6	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	10	0	0	1	0
3	B	10	0	0	3	0
4	A	50	0	0	1	0
4	B	30	0	0	2	0
All	All	11317	0	10804	369	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 17.

The worst 5 of 369 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:21:SER:HB2	1:A:28:LYS:HD3	1.41	1.01
1:B:21:SER:HB2	1:B:28:LYS:HD3	1.41	1.00
1:A:510:VAL:HB	1:A:592:MSE:HE2	1.48	0.96
1:B:510:VAL:HB	1:B:592:MSE:HE2	1.51	0.91
1:B:766:MSE:HE2	1:B:804:ARG:HD2	1.57	0.86

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	733/831 (88%)	669 (91%)	50 (7%)	14 (2%)	6	15
1	B	734/831 (88%)	672 (92%)	46 (6%)	16 (2%)	5	13
All	All	1467/1662 (88%)	1341 (91%)	96 (6%)	30 (2%)	6	14

5 of 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

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	575/688 (84%)	545 (95%)	30 (5%)	21	45
1	B	583/688 (85%)	552 (95%)	31 (5%)	20	44
All	All	1158/1376 (84%)	1097 (95%)	61 (5%)	20	44

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	738	ILE
1	B	680	SER
1	B	131	LEU
1	B	675	LEU
1	B	738	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	484	GLN
1	B	450	HIS
1	B	42	GLN
1	A	725	GLN
1	B	356	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](#)

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
3	SO4	A	1810	-	4,4,4	0.26	0	6,6,6	0.45	0
3	SO4	B	1810	-	4,4,4	0.36	0	6,6,6	0.31	0
3	SO4	B	1809	-	4,4,4	0.35	0	6,6,6	0.21	0
2	PLP	A	1644	1	15,15,16	1.83	2 (13%)	21,22,23	1.83	5 (23%)
2	PLP	B	1644	1	15,15,16	1.89	3 (20%)	21,22,23	1.73	4 (19%)
3	SO4	A	1809	-	4,4,4	0.33	0	6,6,6	0.28	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	-	5/6/6/8	0/1/1/1
2	PLP	B	1644	1	-	5/6/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1644	PLP	O3-C3	-5.67	1.23	1.36
2	B	1644	PLP	O3-C3	-5.44	1.24	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1644	PLP	C2-N1	2.98	1.39	1.33
2	B	1644	PLP	C6-N1	2.47	1.39	1.34
2	A	1644	PLP	C2-N1	2.43	1.38	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1644	PLP	O4P-C5A-C5	6.13	120.84	109.36
2	B	1644	PLP	O4P-C5A-C5	5.77	120.16	109.36
2	B	1644	PLP	C6-C5-C4	2.65	120.27	118.10
2	B	1644	PLP	O3P-P-O4P	-2.65	99.77	106.67
2	A	1644	PLP	O3P-P-O4P	-2.59	99.91	106.67

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1644	PLP	C4-C5-C5A-O4P
2	A	1644	PLP	C6-C5-C5A-O4P
2	A	1644	PLP	C5A-O4P-P-O2P
2	A	1644	PLP	C5A-O4P-P-O3P
2	B	1644	PLP	C4-C5-C5A-O4P

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1810	SO4	3	0
2	A	1644	PLP	2	0
2	B	1644	PLP	2	0
3	A	1809	SO4	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	731/831 (87%)	-0.05	9 (1%) 76 75	28, 54, 95, 119	0
1	B	735/831 (88%)	-0.04	9 (1%) 76 75	27, 56, 89, 114	0
All	All	1466/1662 (88%)	-0.04	18 (1%) 76 75	27, 55, 92, 119	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	47	SER	3.1
1	B	808	PHE	3.0
1	A	547	ASP	2.9
1	B	43	GLN	2.7
1	B	373	GLY	2.6

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(\AA^2)	Q<0.9
3	SO4	B	1810	5/5	0.81	0.12	57,64,91,114	5
3	SO4	B	1809	5/5	0.85	0.12	52,63,81,83	5
3	SO4	A	1809	5/5	0.86	0.11	48,57,85,89	5
3	SO4	A	1810	5/5	0.95	0.12	31,34,44,57	5
2	PLP	B	1644	15/16	0.96	0.08	34,47,56,60	0
2	PLP	A	1644	15/16	0.97	0.06	44,48,58,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.