



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:58 PM GMT

PDB ID : 4GSA
Title : CRYSTAL STRUCTURE OF GLUTAMATE-1-SEMIALDEHYDE AMINO-MUTASE (AMINOTRANSFERASE) REDUCED WITH CYANOBOROHYDRATE
Authors : Hennig, M.; Jansonius, J.N.
Deposited on : 1997-02-26
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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

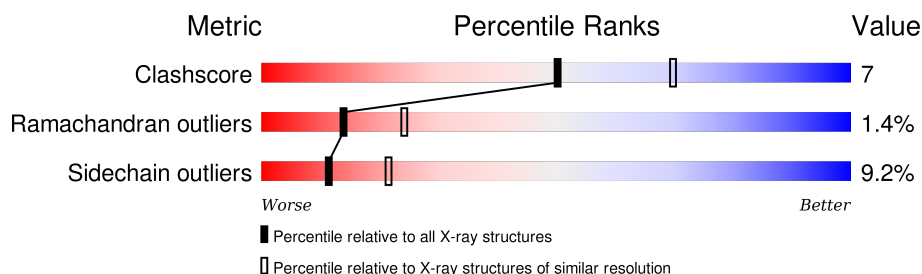
1 Overall quality at a glance

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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	432	 82% 15% ..
1	B	432	 78% 17% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6622 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.

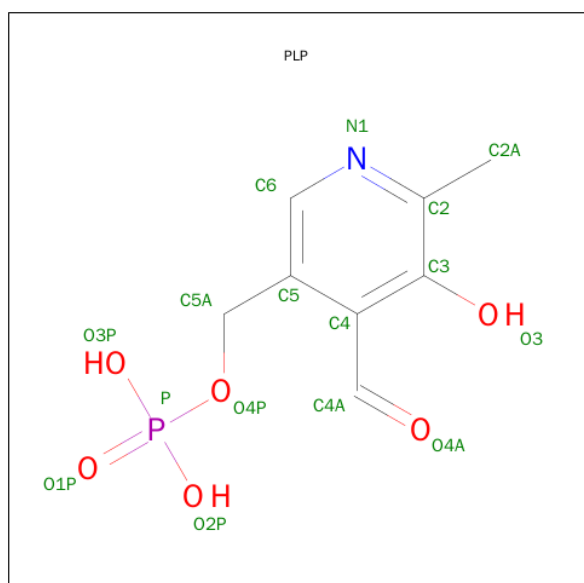
- Molecule 1 is a protein called GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3201	2043	535	604	19			
1	B	427	Total	C	N	O	S	200	0	0
			3201	2043	535	604	19			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	TYR	ILE	CONFLICT	UNP P24630
A	133	LEU	VAL	CONFLICT	UNP P24630
A	134	MET	VAL	CONFLICT	UNP P24630
B	51	TYR	ILE	CONFLICT	UNP P24630
B	133	LEU	VAL	CONFLICT	UNP P24630
B	134	MET	VAL	CONFLICT	UNP P24630

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



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 water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	95	Total	O	0	0
			95	95		
3	B	95	Total	O	0	0
			95	95		

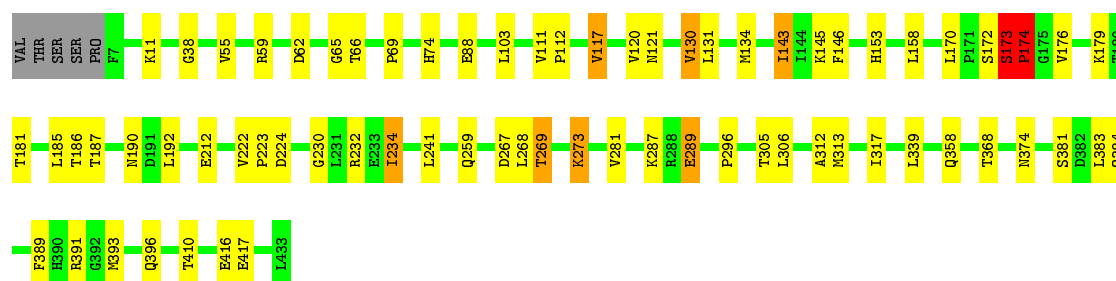
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.


Note EDS was not executed.

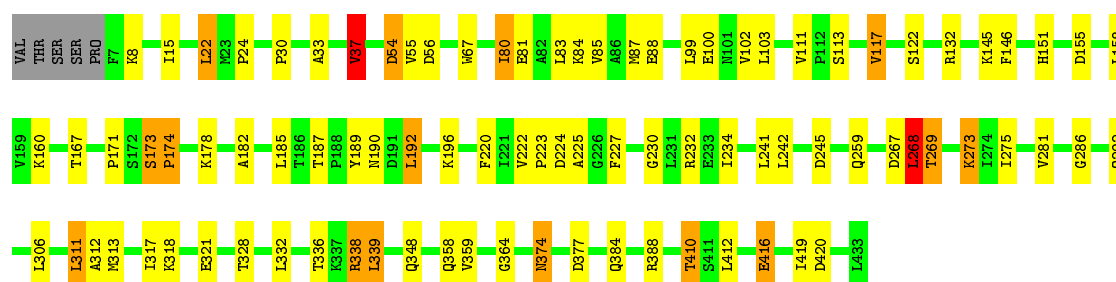
• Molecule 1: GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE

Chain A: 



• Molecule 1: GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.64Å 108.28Å 122.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50	Depositor
% Data completeness (in resolution range)	96.8 (15.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.187 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6622	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

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: 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	0.53	0/3270	0.84	8/4430 (0.2%)
1	B	0.51	0/3270	0.75	5/4430 (0.1%)
All	All	0.52	0/6540	0.80	13/8860 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	SER	C-N-CD	-20.57	75.34	120.60
1	A	173	SER	C-N-CA	10.16	164.66	122.00
1	A	173	SER	N-CA-C	7.67	131.70	111.00
1	B	268	LEU	CA-CB-CG	6.38	129.97	115.30
1	A	174	PRO	CA-N-CD	-6.08	102.99	111.50
1	A	212	GLU	N-CA-C	-5.54	96.03	111.00
1	A	273	LYS	CB-CA-C	5.54	121.47	110.40
1	B	173	SER	N-CA-C	5.47	125.77	111.00
1	A	273	LYS	N-CA-CB	-5.34	100.98	110.60
1	B	273	LYS	CD-CE-NZ	5.33	123.97	111.70
1	B	117	VAL	CB-CA-C	-5.29	101.35	111.40
1	A	117	VAL	CB-CA-C	-5.16	101.61	111.40
1	B	22	LEU	CA-CB-CG	5.07	126.97	115.30

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	3201	0	3180	40	0
1	B	3201	0	3180	56	0
2	A	15	0	7	0	0
2	B	15	0	7	0	0
3	A	95	0	0	1	0
3	B	95	0	0	2	0
All	All	6622	0	6374	87	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 7.

All (87) 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:153:HIS:HD2	1:B:132:ARG:HH22	1.10	0.93
1:A:153:HIS:CD2	1:B:132:ARG:HH22	1.99	0.76
1:A:153:HIS:HD2	1:B:132:ARG:NH2	1.84	0.75
1:A:259:GLN:HE22	1:A:269:THR:HG21	1.53	0.73
1:B:190:ASN:HD21	1:B:224:ASP:H	1.38	0.71
1:A:281:VAL:HG22	1:A:312:ALA:HB1	1.72	0.70
1:A:134:MET:SD	1:A:143:ILE:HD11	2.31	0.70
1:B:232:ARG:HD3	1:B:232:ARG:O	1.93	0.69
1:A:190:ASN:HD21	1:A:224:ASP:H	1.41	0.69
1:A:173:SER:HB3	1:A:176:VAL:HG13	1.75	0.67
1:B:100:GLU:HA	1:B:313:MET:HE3	1.78	0.65
1:A:11:LYS:HB3	1:A:55:VAL:HG13	1.79	0.64
1:B:145:LYS:HG2	1:B:146:PHE:N	2.16	0.61
1:B:332:LEU:HD22	1:B:410:THR:HG22	1.82	0.61
1:B:220:PHE:HB3	1:B:364:GLY:HA3	1.83	0.61
1:B:80:ILE:O	1:B:84:LYS:HG3	2.00	0.61
1:A:222:VAL:HG13	1:A:223:PRO:HD2	1.83	0.60
1:A:281:VAL:CG2	1:A:312:ALA:HB1	2.30	0.60
1:B:259:GLN:HE22	1:B:269:THR:HG21	1.67	0.60
1:B:196:LYS:HG2	1:B:234:ILE:HD12	1.85	0.59
1:A:190:ASN:ND2	1:A:224:ASP:H	2.01	0.58
1:B:54:ASP:HB3	1:B:56:ASP:H	1.69	0.58
1:B:100:GLU:HA	1:B:313:MET:CE	2.34	0.57
1:A:179:LYS:HE2	1:B:182:ALA:HB3	1.86	0.56
1:A:146:PHE:CD1	1:A:187:THR:HG23	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:VAL:CG2	1:B:312:ALA:HB1	2.36	0.56
1:A:172:SER:O	1:A:174:PRO:HD3	2.06	0.56
1:B:85:VAL:O	1:B:88:GLU:HG2	2.07	0.54
1:B:268:LEU:HD12	1:B:286:GLY:HA3	1.89	0.54
1:B:83:LEU:HD22	1:B:311:LEU:HD22	1.88	0.53
1:A:230:GLY:O	1:A:234:ILE:HG23	2.09	0.52
1:A:146:PHE:CE1	1:A:187:THR:HG23	2.44	0.52
1:B:151:HIS:HD2	1:B:245:ASP:OD2	1.93	0.52
1:A:192:LEU:HD11	1:A:230:GLY:HA3	1.92	0.51
1:B:328:THR:HG23	1:B:412:LEU:HD21	1.92	0.51
1:A:145:LYS:O	1:A:186:THR:HA	2.10	0.51
1:B:192:LEU:HD23	1:B:227:PHE:CD1	2.46	0.50
1:A:11:LYS:CB	1:A:55:VAL:HG13	2.43	0.49
1:B:374:ASN:ND2	1:B:377:ASP:H	2.09	0.49
1:A:267:ASP:HA	1:A:287:LYS:HE2	1.95	0.49
1:B:55:VAL:HG12	1:B:55:VAL:O	2.13	0.49
1:B:232:ARG:HD3	1:B:232:ARG:C	2.29	0.48
1:A:305:THR:HG23	1:B:67:TRP:HB2	1.95	0.48
1:B:37:VAL:HG13	1:B:37:VAL:O	2.14	0.48
1:B:232:ARG:HH22	1:B:267:ASP:CG	2.17	0.48
1:A:66:THR:HG23	1:A:69:PRO:HD2	1.96	0.47
1:A:289:GLU:H	1:A:289:GLU:CD	2.18	0.47
1:A:74:HIS:HD2	3:B:2158:HOH:O	1.97	0.47
1:A:130:VAL:O	1:A:134:MET:HG3	2.15	0.47
1:B:190:ASN:ND2	1:B:224:ASP:H	2.08	0.46
1:A:134:MET:CE	1:A:143:ILE:HD11	2.45	0.46
1:B:122:SER:HA	3:B:2091:HOH:O	2.15	0.46
1:B:220:PHE:HZ	1:B:359:VAL:HG23	1.81	0.46
1:B:222:VAL:HG13	1:B:223:PRO:HD2	1.95	0.46
1:A:65:GLY:O	1:A:66:THR:HG22	2.16	0.46
1:A:62:ASP:OD2	1:A:74:HIS:HE1	1.99	0.45
1:B:83:LEU:O	1:B:87:MET:HG2	2.16	0.45
1:A:313:MET:O	1:A:317:ILE:HG13	2.17	0.45
1:B:275:ILE:O	1:B:275:ILE:HG12	2.17	0.45
1:B:338:ARG:NH1	1:B:416:GLU:HG3	2.32	0.45
1:B:113:SER:OG	1:B:269:THR:CG2	2.66	0.44
1:B:339:LEU:HB2	1:B:419:ILE:HD12	1.99	0.44
1:A:368:THR:HB	1:A:381:SER:HA	2.00	0.44
1:A:153:HIS:CD2	1:B:132:ARG:NH2	2.73	0.44
1:B:189:TYR:O	1:B:190:ASN:HB2	2.16	0.44
1:A:179:LYS:CE	1:B:182:ALA:HB3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:VAL:O	1:B:37:VAL:CG1	2.65	0.44
1:A:121:ASN:ND2	3:A:2157:HOH:O	2.50	0.44
1:A:389:PHE:O	1:A:393:MET:HG2	2.18	0.43
1:B:318:LYS:HD2	1:B:318:LYS:HA	1.70	0.43
1:B:192:LEU:HD23	1:B:227:PHE:HD1	1.82	0.43
1:B:281:VAL:HG21	1:B:312:ALA:HB1	2.01	0.43
1:B:338:ARG:NH2	1:B:420:ASP:OD1	2.52	0.43
1:B:332:LEU:HD22	1:B:410:THR:CG2	2.49	0.43
1:A:111:VAL:HA	1:A:112:PRO:HD3	1.83	0.43
1:A:391:ARG:HA	1:A:391:ARG:HD2	1.85	0.42
1:B:102:VAL:HG22	1:B:317:ILE:CD1	2.49	0.42
1:B:230:GLY:O	1:B:234:ILE:HG22	2.20	0.41
1:B:311:LEU:HD23	1:B:311:LEU:HA	1.80	0.41
1:B:374:ASN:C	1:B:374:ASN:HD22	2.24	0.41
1:A:296:PRO:HD3	1:B:30:PRO:HA	2.02	0.41
1:A:296:PRO:HG3	1:B:33:ALA:HB2	2.03	0.41
1:B:317:ILE:O	1:B:321:GLU:HG3	2.22	0.40
1:B:15:ILE:HD12	1:B:55:VAL:HG11	2.03	0.40
1:A:173:SER:CB	1:A:176:VAL:HG13	2.45	0.40
1:B:336:THR:OG1	1:B:410:THR:HG21	2.21	0.40
1:B:384:GLN:HG3	1:B:388:ARG:NH1	2.36	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	425/432 (98%)	398 (94%)	23 (5%)	4 (1%)	21	37
1	B	425/432 (98%)	394 (93%)	23 (5%)	8 (2%)	10	16
All	All	850/864 (98%)	792 (93%)	46 (5%)	12 (1%)	14	24

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	SER
1	A	174	PRO
1	B	173	SER
1	B	174	PRO
1	A	273	LYS
1	B	225	ALA
1	B	273	LYS
1	B	171	PRO
1	B	167	THR
1	B	37	VAL
1	A	38	GLY
1	B	24	PRO

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	330/335 (98%)	301 (91%)	29 (9%)	12	23
1	B	330/335 (98%)	298 (90%)	32 (10%)	10	19
All	All	660/670 (98%)	599 (91%)	61 (9%)	11	21

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	ARG
1	A	88	GLU
1	A	103	LEU
1	A	117	VAL
1	A	120	VAL
1	A	130	VAL
1	A	131	LEU
1	A	143	ILE
1	A	158	LEU
1	A	170	LEU
1	A	174	PRO

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Mol	Chain	Res	Type
1	A	181	THR
1	A	185	LEU
1	A	232	ARG
1	A	234	ILE
1	A	241	LEU
1	A	268	LEU
1	A	269	THR
1	A	289	GLU
1	A	306	LEU
1	A	339	LEU
1	A	358	GLN
1	A	374	ASN
1	A	383	LEU
1	A	384	GLN
1	A	396	GLN
1	A	410	THR
1	A	416	GLU
1	A	417	GLU
1	B	8	LYS
1	B	22	LEU
1	B	37	VAL
1	B	54	ASP
1	B	80	ILE
1	B	81	GLU
1	B	99	LEU
1	B	103	LEU
1	B	111	VAL
1	B	117	VAL
1	B	155	ASP
1	B	158	LEU
1	B	160	LYS
1	B	174	PRO
1	B	178	LYS
1	B	185	LEU
1	B	187	THR
1	B	192	LEU
1	B	241	LEU
1	B	242	LEU
1	B	268	LEU
1	B	269	THR
1	B	292	GLN
1	B	306	LEU

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Mol	Chain	Res	Type
1	B	311	LEU
1	B	338	ARG
1	B	339	LEU
1	B	348	GLN
1	B	358	GLN
1	B	374	ASN
1	B	410	THR
1	B	416	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
1	A	121	ASN
1	A	151	HIS
1	A	153	HIS
1	A	190	ASN
1	A	352	HIS
1	A	374	ASN
1	A	384	GLN
1	B	20	GLN
1	B	58	ASN
1	B	74	HIS
1	B	121	ASN
1	B	151	HIS
1	B	183	ASN
1	B	190	ASN
1	B	217	ASN
1	B	259	GLN
1	B	292	GLN
1	B	334	GLN
1	B	352	HIS
1	B	374	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

2 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	434	1	15,15,16	1.82	3 (20%)	21,22,23	1.80	4 (19%)
2	PLP	B	434	1	15,15,16	1.12	0	21,22,23	2.08	7 (33%)

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	434	1	-	0/6/6/8	0/1/1/1
2	PLP	B	434	1	-	0/6/6/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	434	PLP	C3-C2	-3.35	1.38	1.40
2	A	434	PLP	P-O2P	3.44	1.67	1.54
2	A	434	PLP	C5-C4	3.50	1.44	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	434	PLP	O2P-P-O4P	-5.80	89.87	106.56
2	B	434	PLP	C4A-C4-C3	-2.17	116.43	120.36
2	A	434	PLP	C5-C6-N1	-2.04	120.31	123.86
2	A	434	PLP	C6-C5-C4	2.18	120.00	118.15
2	B	434	PLP	C4A-C4-C5	2.20	123.17	120.88
2	B	434	PLP	O3-C3-C2	2.29	121.64	117.66
2	B	434	PLP	O3P-P-O4P	2.30	113.20	106.56
2	A	434	PLP	C4A-C4-C5	3.32	124.34	120.88
2	B	434	PLP	O3P-P-O1P	3.39	121.49	110.58
2	B	434	PLP	O4P-C5A-C5	4.18	115.91	108.99
2	A	434	PLP	O3P-P-O1P	4.89	126.31	110.58

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 [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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.