



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:03 PM UTC

PDB ID : 6HRH / pdb_00006hrh
Title : Structure of human erythroid-specific 5'-aminolevulinate synthase, ALAS2
Authors : Bailey, H.J.; Shrestha, L.; Rembeza, E.; Newman, J.; Kupinska, K.; Diaz-saez, L.; Kennedy, E.; Burgess-Brown, N.; von Delft, F.; Arrowsmith, C.; Edwards, A.; Bountra, C.; Yue, W.W.; Structural Genomics Consortium (SGC)
Deposited on : 2018-09-27
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 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

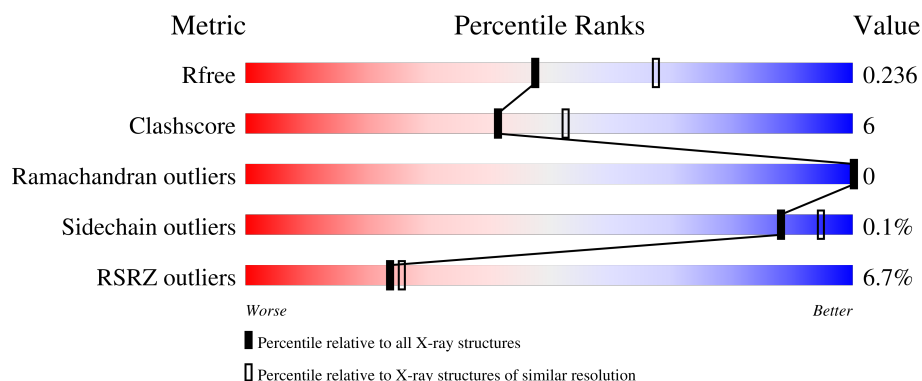
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	469	8% 78% 13% 9%
1	B	469	4% 76% 14% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6901 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 5-aminolevulinate synthase, erythroid-specific, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	428	Total	C	N	O	S	0	1	0
			3299	2101	576	600	22			
1	A	429	Total	C	N	O	S	0	1	0
			3322	2114	587	599	22			

There are 50 discrepancies between the modelled and reference sequences:

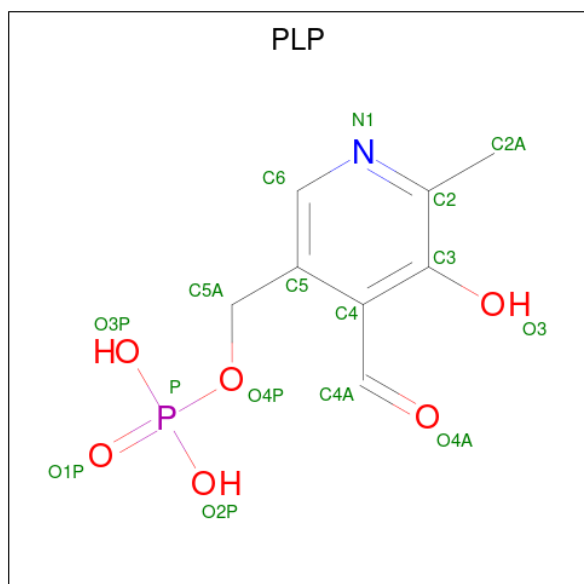
Chain	Residue	Modelled	Actual	Comment	Reference
B	119	MET	-	initiating methionine	UNP P22557
B	120	GLY	-	expression tag	UNP P22557
B	121	HIS	-	expression tag	UNP P22557
B	122	HIS	-	expression tag	UNP P22557
B	123	HIS	-	expression tag	UNP P22557
B	124	HIS	-	expression tag	UNP P22557
B	125	HIS	-	expression tag	UNP P22557
B	126	HIS	-	expression tag	UNP P22557
B	127	SER	-	expression tag	UNP P22557
B	128	SER	-	expression tag	UNP P22557
B	129	GLY	-	expression tag	UNP P22557
B	130	VAL	-	expression tag	UNP P22557
B	131	ASP	-	expression tag	UNP P22557
B	132	LEU	-	expression tag	UNP P22557
B	133	GLY	-	expression tag	UNP P22557
B	134	THR	-	expression tag	UNP P22557
B	135	GLU	-	expression tag	UNP P22557
B	136	ASN	-	expression tag	UNP P22557
B	137	LEU	-	expression tag	UNP P22557
B	138	TYR	-	expression tag	UNP P22557
B	139	PHE	-	expression tag	UNP P22557
B	140	GLN	-	expression tag	UNP P22557
B	141	SER	-	expression tag	UNP P22557
B	142	MET	-	expression tag	UNP P22557
B	221	VAL	ALA	conflict	UNP P22557

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Chain	Residue	Modelled	Actual	Comment	Reference
A	119	MET	-	initiating methionine	UNP P22557
A	120	GLY	-	expression tag	UNP P22557
A	121	HIS	-	expression tag	UNP P22557
A	122	HIS	-	expression tag	UNP P22557
A	123	HIS	-	expression tag	UNP P22557
A	124	HIS	-	expression tag	UNP P22557
A	125	HIS	-	expression tag	UNP P22557
A	126	HIS	-	expression tag	UNP P22557
A	127	SER	-	expression tag	UNP P22557
A	128	SER	-	expression tag	UNP P22557
A	129	GLY	-	expression tag	UNP P22557
A	130	VAL	-	expression tag	UNP P22557
A	131	ASP	-	expression tag	UNP P22557
A	132	LEU	-	expression tag	UNP P22557
A	133	GLY	-	expression tag	UNP P22557
A	134	THR	-	expression tag	UNP P22557
A	135	GLU	-	expression tag	UNP P22557
A	136	ASN	-	expression tag	UNP P22557
A	137	LEU	-	expression tag	UNP P22557
A	138	TYR	-	expression tag	UNP P22557
A	139	PHE	-	expression tag	UNP P22557
A	140	GLN	-	expression tag	UNP P22557
A	141	SER	-	expression tag	UNP P22557
A	142	MET	-	expression tag	UNP P22557
A	221	VAL	ALA	conflict	UNP P22557

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



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	136	Total	O	0	0
			136	136		
3	A	112	Total	O	0	0
			112	112		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.77Å 107.70Å 75.71Å 90.00° 109.05° 90.00°	Depositor
Resolution (Å)	71.53 – 2.30 71.53 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.6 (71.53-2.30) 94.1 (71.53-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.213 , 0.234 0.218 , 0.236	Depositor DCC
R_{free} test set	2008 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6901	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: 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	0.18	0/3403	0.39	1/4608 (0.0%)
1	B	0.20	0/3381	0.45	3/4580 (0.1%)
All	All	0.19	0/6784	0.42	4/9188 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	439	LYS	CB-CG-CD	-7.49	94.08	111.30
1	B	303	ARG	CB-CG-CD	-6.54	96.25	111.30
1	B	501	VAL	CG1-CB-CG2	-5.84	97.95	110.80
1	A	533	VAL	CG1-CB-CG2	-5.20	99.37	110.80

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	3322	0	3215	44	0
1	B	3299	0	3193	45	0
2	A	16	0	8	3	0
2	B	16	0	8	1	0
3	A	112	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	136	0	0	2	0
All	All	6901	0	6424	83	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 6.

All (83) 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:B:194:TRP:HB2	1:B:501:VAL:HG12	1.29	1.09
1:B:194:TRP:HB2	1:B:501:VAL:CG1	2.06	0.86
1:A:299:LYS:HB3	1:A:578:MET:HE1	1.65	0.78
1:A:461:LEU:HD12	1:A:533:VAL:CG1	2.17	0.75
1:B:303:ARG:NH1	3:B:701:HOH:O	2.19	0.75
1:A:194:TRP:CZ3	1:A:457:MET:HE1	2.28	0.69
1:A:388:THR:HG21	1:A:391:LYS:HG3	1.75	0.68
1:B:234:LYS:HB3	1:A:181:PHE:HE2	1.59	0.67
1:B:388:THR:HG21	1:B:391:LYS:HG3	1.80	0.64
1:A:194:TRP:HZ3	1:A:457:MET:HE1	1.65	0.61
1:A:504:ILE:HD12	1:A:517:ARG:HB2	1.84	0.60
1:B:168:VAL:HA	1:B:179:GLN:O	2.03	0.59
1:A:454:VAL:HG21	1:A:474:HIS:HA	1.83	0.59
1:B:175:TYR:HB2	1:B:204:ARG:HD2	1.84	0.58
1:A:534:GLU:O	1:A:538:LEU:HG	2.02	0.58
1:B:272:ILE:HG21	1:B:409:MET:HE2	1.86	0.57
1:B:454:VAL:HG11	1:B:474:HIS:HA	1.88	0.56
1:A:476:ILE:HB	1:A:518:LEU:HB2	1.86	0.56
1:B:426:MET:HE3	1:B:427:VAL:HG23	1.89	0.55
1:A:451:GLN:O	1:A:454:VAL:HG12	2.06	0.55
1:A:239:LEU:HD13	1:A:432:LEU:HG	1.89	0.54
1:B:469:ILE:HB	1:B:477:PRO:HG2	1.90	0.54
1:A:335:GLY:O	1:A:471:CYS:HB3	2.07	0.53
1:A:137:LEU:HD23	1:A:139:PHE:CE1	2.44	0.53
1:A:461:LEU:CD1	1:A:533:VAL:CG1	2.86	0.53
1:B:237:VAL:O	1:B:241:GLN:HG3	2.08	0.53
1:B:476:ILE:HB	1:B:518:LEU:HB2	1.91	0.52
1:B:356:VAL:HG21	1:B:382:ILE:HG12	1.92	0.52
1:A:370:ALA:HB3	1:A:374:GLU:HB2	1.92	0.51
1:B:504:ILE:HD12	1:B:517:ARG:HB2	1.92	0.51
1:B:332:SER:HB3	2:B:601:PLP:H2A1	1.91	0.51
1:B:303:ARG:NE	1:B:306:ASP:OD2	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:ASP:OD2	1:A:511:ARG:NH1	2.40	0.50
1:B:236:HIS:NE2	1:B:422:SER:OG	2.44	0.50
1:A:146:ASP:O	1:A:150:ARG:HG2	2.12	0.50
1:B:529:MET:O	1:B:533:VAL:HG23	2.11	0.49
1:A:493:LEU:HD21	1:A:536:LEU:HA	1.94	0.49
1:A:525:SER:OG	1:A:528:MET:HG3	2.13	0.49
1:A:148:PHE:O	1:A:152:LYS:HG2	2.13	0.48
1:A:356:VAL:HG21	1:A:382:ILE:HG12	1.94	0.48
1:B:460:LEU:O	1:B:464:ARG:HG2	2.14	0.47
1:B:142:MET:HG2	1:B:143:PHE:N	2.28	0.47
1:B:171:TRP:CZ2	1:B:179:GLN:HG3	2.50	0.47
1:B:452:ARG:NH1	3:B:709:HOH:O	2.47	0.46
1:B:349:GLN:HA	1:A:139:PHE:CD1	2.51	0.46
1:A:258:CYS:HA	1:A:261:ALA:HB3	1.97	0.46
1:A:285:HIS:H	1:A:288:MET:HE3	1.81	0.46
1:B:234:LYS:HB3	1:A:181:PHE:CE2	2.45	0.46
1:B:370:ALA:HB3	1:B:374:GLU:HB2	1.97	0.46
1:A:391:LYS:HZ1	2:A:601:PLP:H4A	1.81	0.45
1:B:285:HIS:CE1	1:A:419:PHE:HB3	2.52	0.45
1:B:292:ILE:HG21	1:B:299:LYS:HG3	1.99	0.45
1:B:435:VAL:O	1:B:439:LYS:HB2	2.18	0.44
1:A:221:VAL:O	1:A:424:PRO:HB3	2.17	0.44
1:B:534:GLU:O	1:B:538:LEU:HD23	2.17	0.44
1:A:200:LEU:HD22	1:A:446:LEU:HB3	2.00	0.44
1:A:257:SER:HB2	2:A:601:PLP:O1P	2.18	0.44
1:A:303:ARG:HD2	1:A:306:ASP:OD2	2.18	0.43
1:B:288:MET:HE1	1:B:328:GLU:HG3	2.00	0.43
1:A:278:ILE:HG21	1:A:292:ILE:HG12	2.01	0.43
1:A:444:GLN:HG3	1:A:447:ARG:HH21	1.82	0.43
1:B:221:VAL:O	1:B:424:PRO:HB3	2.18	0.43
1:B:278:ILE:HG21	1:B:292:ILE:HG12	2.01	0.42
1:A:288:MET:HE1	1:A:328:GLU:HG3	2.02	0.42
1:B:348:HIS:O	1:A:139:PHE:HB3	2.18	0.42
1:B:567:MET:HE3	1:B:567:MET:HB2	1.93	0.42
1:A:391:LYS:HZ1	2:A:601:PLP:C4A	2.32	0.42
1:B:234:LYS:HG2	1:A:169:ASN:ND2	2.35	0.42
1:A:461:LEU:CD1	1:A:533:VAL:HG12	2.48	0.42
1:B:142:MET:HE2	1:B:142:MET:HB3	1.85	0.41
1:A:342:GLU:OE1	1:A:342:GLU:N	2.44	0.41
1:B:493:LEU:HD21	1:B:536:LEU:HA	2.02	0.41
1:A:326:ALA:HA	1:A:355:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:TYR:CD2	1:B:364:LEU:HD11	2.56	0.41
1:B:438:LEU:HA	1:B:443:GLY:HA3	2.02	0.41
1:B:449:ALA:HA	1:B:452:ARG:CZ	2.50	0.41
1:A:530:GLU:O	1:A:533:VAL:HG23	2.21	0.41
1:B:321:ILE:O	1:B:323:LYS:NZ	2.52	0.41
1:B:331:HIS:HB3	1:B:334:ASP:OD1	2.20	0.41
1:B:464:ARG:HB3	1:B:537:LEU:HD11	2.03	0.41
1:A:438:LEU:HA	1:A:443:GLY:HA3	2.03	0.40
1:A:529:MET:O	1:A:533:VAL:HG22	2.21	0.40
1:B:385:ILE:HG22	1:B:401:ALA:O	2.21	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	424/469 (90%)	408 (96%)	16 (4%)	0	100	100
1	B	423/469 (90%)	403 (95%)	20 (5%)	0	100	100
All	All	847/938 (90%)	811 (96%)	36 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	347/396 (88%)	347 (100%)	0	100	100
1	B	345/396 (87%)	344 (100%)	1 (0%)	86	93
All	All	692/792 (87%)	691 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	565	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	228	ASN
1	A	207	GLN
1	A	228	ASN
1	A	248	GLN
1	A	456	HIS
1	A	502	GLN
1	A	556	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 oligosaccharides 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	B	601	-	16,16,16	1.17	2 (12%)	20,23,23	1.13	1 (5%)
2	PLP	A	601	-	16,16,16	1.18	2 (12%)	20,23,23	1.11	1 (5%)

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	B	601	-	-	4/8/8/8	0/1/1/1
2	PLP	A	601	-	-	1/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	PLP	C2-N1	2.42	1.38	1.33
2	B	601	PLP	C2-N1	2.40	1.38	1.33
2	B	601	PLP	C4-C4A	2.13	1.51	1.46
2	A	601	PLP	C4-C4A	2.10	1.51	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	PLP	C3-C4-C4A	-3.00	115.72	119.84
2	A	601	PLP	C3-C4-C4A	-2.92	115.83	119.84

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	PLP	C5A-O4P-P-O3P
2	B	601	PLP	C5A-O4P-P-O1P
2	B	601	PLP	C5A-O4P-P-O2P
2	B	601	PLP	C4-C5-C5A-O4P
2	A	601	PLP	C4-C5-C5A-O4P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	PLP	1	0
2	A	601	PLP	3	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	429/469 (91%)	0.69	36 (8%) 17 18	28, 55, 84, 108	1 (0%)
1	B	428/469 (91%)	0.56	21 (4%) 35 36	30, 51, 79, 132	1 (0%)
All	All	857/938 (91%)	0.63	57 (6%) 24 26	28, 52, 82, 132	2 (0%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	558	CYS	5.0
1	A	181	PHE	4.9
1	A	577	ASN	4.6
1	A	459	GLN	4.2
1	B	137	LEU	4.1
1	B	547	LEU	4.1
1	A	137	LEU	4.0
1	B	501	VAL	3.9
1	B	548	GLN	3.7
1	A	191	VAL	3.5
1	A	217	GLN	3.5
1	A	154	MET	3.4
1	A	468	VAL	3.4
1	B	138	TYR	3.3
1	A	557	PHE	3.3
1	A	471	CYS	3.1
1	A	518	LEU	3.0
1	B	538	LEU	2.9
1	A	466	LEU	2.9
1	B	141	SER	2.8
1	A	380[A]	HIS	2.7
1	B	147	GLN	2.7
1	A	146	ASP	2.6
1	A	556	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	138	TYR	2.6
1	A	457	MET	2.6
1	A	467	PRO	2.6
1	A	139	PHE	2.6
1	B	303	ARG	2.5
1	A	159	ASP	2.5
1	A	221	VAL	2.5
1	A	572	ARG	2.5
1	B	578	MET	2.5
1	A	547	LEU	2.5
1	A	561	PRO	2.5
1	A	462	MET	2.4
1	B	146	ASP	2.4
1	A	188	SER	2.4
1	A	142	MET	2.4
1	B	559	ARG	2.4
1	A	546	PRO	2.3
1	B	154	MET	2.3
1	A	461	LEU	2.3
1	A	575	PHE	2.2
1	B	188	SER	2.2
1	A	540	TRP	2.2
1	A	570	TRP	2.2
1	A	463	ASP	2.2
1	B	335	GLY	2.2
1	A	545	LEU	2.1
1	A	576	GLY	2.1
1	B	496	LYS	2.1
1	B	492	LEU	2.1
1	B	577	ASN	2.0
1	B	182	SER	2.0
1	A	566	LEU	2.0
1	B	522	PRO	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(Å ²)	Q<0.9
2	PLP	A	601	16/16	0.90	0.13	63,65,65,66	0
2	PLP	B	601	16/16	0.91	0.12	56,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.