



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2026 – 04:08 AM UTC

PDB ID : 4PB3 / pdb_00004pb3
Title : D-threo-3-hydroxyaspartate dehydratase H351A mutant
Authors : Yasutake, Y.; Matsumoto, Y.; Wada, M.
Deposited on : 2014-04-11
Resolution : 1.70 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

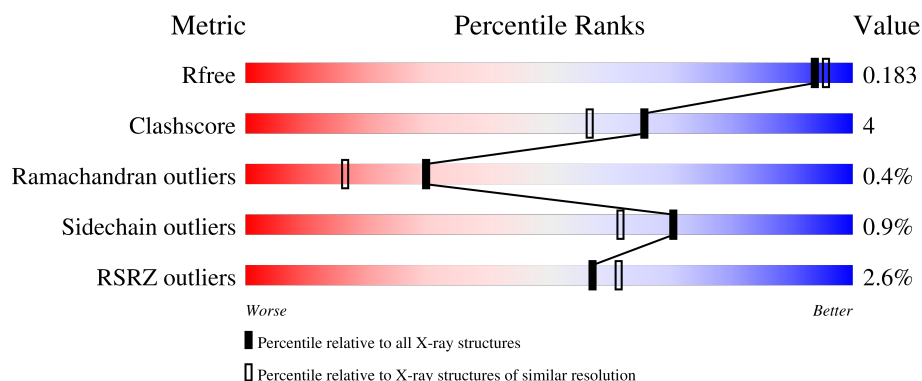
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	390	% 84% 12% ..
1	B	390	4% 86% 13% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6362 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 D-threo-3-hydroxyaspartate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	6	0
			2857	1775	533	534	15			
1	B	389	Total	C	N	O	S	0	5	0
			2932	1821	549	544	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	GLY	-	expression tag	UNP B2DFG5
A	-8	HIS	-	expression tag	UNP B2DFG5
A	-7	HIS	-	expression tag	UNP B2DFG5
A	-6	HIS	-	expression tag	UNP B2DFG5
A	-5	HIS	-	expression tag	UNP B2DFG5
A	-4	HIS	-	expression tag	UNP B2DFG5
A	-3	HIS	-	expression tag	UNP B2DFG5
A	-2	ALA	-	expression tag	UNP B2DFG5
A	-1	MET	-	expression tag	UNP B2DFG5
A	0	SER	-	expression tag	UNP B2DFG5
A	351	ALA	HIS	engineered mutation	UNP B2DFG5
B	-9	GLY	-	expression tag	UNP B2DFG5
B	-8	HIS	-	expression tag	UNP B2DFG5
B	-7	HIS	-	expression tag	UNP B2DFG5
B	-6	HIS	-	expression tag	UNP B2DFG5
B	-5	HIS	-	expression tag	UNP B2DFG5
B	-4	HIS	-	expression tag	UNP B2DFG5
B	-3	HIS	-	expression tag	UNP B2DFG5
B	-2	ALA	-	expression tag	UNP B2DFG5
B	-1	MET	-	expression tag	UNP B2DFG5
B	0	SER	-	expression tag	UNP B2DFG5
B	351	ALA	HIS	engineered mutation	UNP B2DFG5

- 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
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	2	Total	Mg	0	0
			2	2		

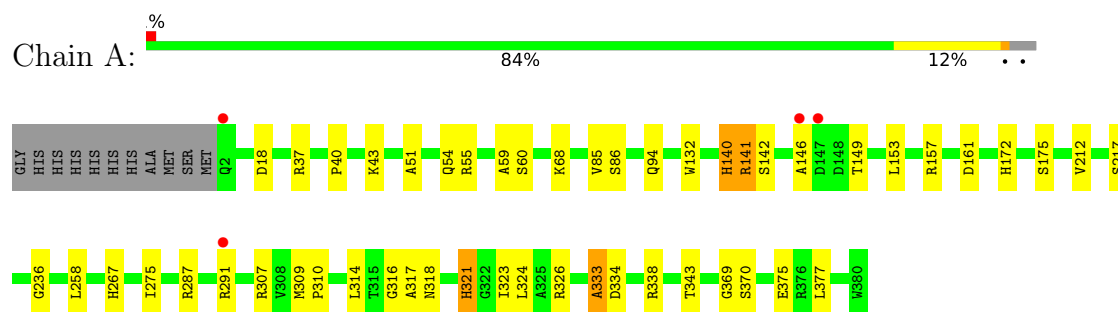
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	276	Total	O	0	0
			276	276		
4	B	264	Total	O	0	0
			264	264		

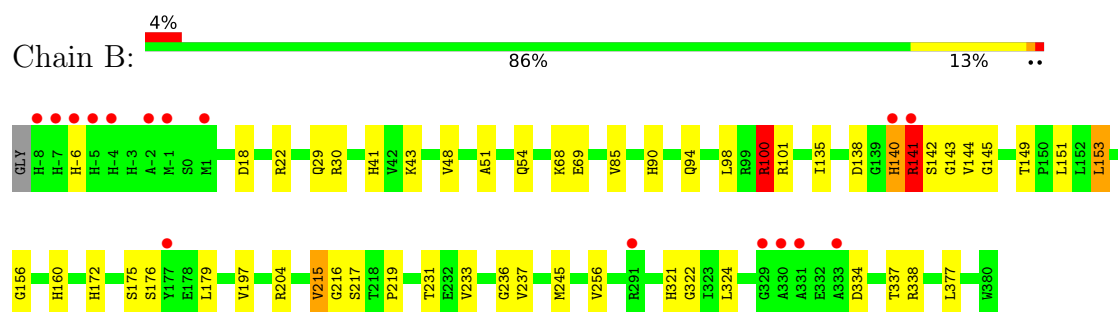
3 Residue-property plots [i](#)

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: D-threo-3-hydroxyaspartate dehydratase



- Molecule 1: D-threo-3-hydroxyaspartate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	157.60Å 157.60Å 157.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.70 40.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.00-1.70) 99.6 (40.00-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.65 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.166 , 0.185 0.164 , 0.183	Depositor DCC
R_{free} test set	5375 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 38.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h 0.002 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6362	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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: PLP, MG

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	1.64	22/2921 (0.8%)	1.44	17/3962 (0.4%)
1	B	1.73	33/2999 (1.1%)	1.45	19/4066 (0.5%)
All	All	1.69	55/5920 (0.9%)	1.45	36/8028 (0.4%)

All (55) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	267	HIS	ND1-CE1	12.21	1.44	1.32
1	B	204	ARG	CD-NE	-9.42	1.33	1.46
1	B	41	HIS	CE1-NE2	9.09	1.41	1.32
1	A	172	HIS	ND1-CE1	8.64	1.41	1.32
1	A	314	LEU	N-CA	8.21	1.57	1.46
1	A	172	HIS	CG-CD2	8.16	1.44	1.35
1	B	172	HIS	ND1-CE1	7.72	1.40	1.32
1	A	321	HIS	ND1-CE1	7.68	1.40	1.32
1	B	321	HIS	ND1-CE1	7.22	1.39	1.32
1	B	98	LEU	N-CA	6.85	1.54	1.46
1	B	216	GLY	N-CA	6.72	1.52	1.45
1	B	231	THR	CB-OG1	-6.68	1.33	1.43
1	A	140	HIS	ND1-CE1	6.60	1.39	1.32
1	B	140	HIS	CG-CD2	6.41	1.42	1.35
1	B	29	GLN	N-CA	6.40	1.54	1.46
1	B	145	GLY	N-CA	6.33	1.54	1.45
1	A	317	ALA	N-CA	6.30	1.53	1.46
1	A	309	MET	CA-CB	6.30	1.61	1.53
1	B	140	HIS	CE1-NE2	6.16	1.38	1.32
1	B	85	VAL	N-CA	6.14	1.53	1.46
1	B	172	HIS	CG-CD2	6.14	1.42	1.35
1	A	140	HIS	CG-CD2	6.07	1.42	1.35
1	A	175	SER	N-CA	6.05	1.54	1.46
1	A	307	ARG	N-CA	5.98	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	41	HIS	CG-CD2	5.81	1.42	1.35
1	B	175	SER	N-CA	5.77	1.53	1.46
1	B	176	SER	N-CA	5.74	1.53	1.46
1	B	236	GLY	N-CA	5.74	1.53	1.45
1	B	41	HIS	ND1-CE1	5.73	1.38	1.32
1	B	156	GLY	CA-C	5.72	1.58	1.52
1	B	30	ARG	CZ-NH2	5.67	1.40	1.33
1	B	256	VAL	CA-CB	5.65	1.60	1.53
1	A	375	GLU	C-O	5.64	1.31	1.23
1	B	94	GLN	CA-C	5.58	1.60	1.52
1	A	258	LEU	N-CA	5.53	1.52	1.46
1	A	343	THR	N-CA	5.47	1.52	1.46
1	A	321	HIS	CG-CD2	5.45	1.41	1.35
1	B	141	ARG	CZ-NH2	5.40	1.40	1.33
1	A	370	SER	N-CA	5.39	1.52	1.45
1	B	172	HIS	CE1-NE2	5.34	1.37	1.32
1	A	287	ARG	CZ-NH2	5.32	1.40	1.33
1	B	179	LEU	N-CA	5.27	1.51	1.45
1	A	326	ARG	CD-NE	5.27	1.53	1.46
1	B	90	HIS	CE1-NE2	5.24	1.37	1.32
1	A	321	HIS	CA-C	-5.22	1.46	1.52
1	A	172	HIS	CE1-NE2	5.20	1.37	1.32
1	A	316	GLY	N-CA	5.19	1.50	1.45
1	B	135	ILE	CA-CB	5.13	1.61	1.54
1	B	140	HIS	ND1-CE1	5.08	1.37	1.32
1	B	322	GLY	N-CA	5.08	1.51	1.45
1	A	43	LYS	N-CA	5.02	1.52	1.46
1	B	98	LEU	CA-C	5.02	1.59	1.52
1	B	197	VAL	C-O	5.02	1.30	1.24
1	B	160	HIS	ND1-CE1	5.01	1.37	1.32
1	B	-6	HIS	CG-CD2	5.01	1.41	1.35

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	141	ARG	NE-CZ-NH1	-9.40	112.10	121.50
1	B	204	ARG	NE-CZ-NH2	-8.93	111.16	119.20
1	A	310	PRO	CA-C-N	-7.42	111.63	122.46
1	A	310	PRO	C-N-CA	-7.42	111.63	122.46
1	B	100	ARG	NE-CZ-NH2	7.41	125.86	119.20
1	B	140	HIS	N-CA-C	7.30	118.88	111.07
1	B	149	THR	CA-C-N	-7.21	111.00	118.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	THR	C-N-CA	-7.21	111.00	118.85
1	B	215	VAL	CA-C-N	-7.12	112.93	122.54
1	B	215	VAL	C-N-CA	-7.12	112.93	122.54
1	B	231	THR	OG1-CB-CG2	-6.75	95.81	109.30
1	A	321	HIS	CB-CA-C	-6.73	97.52	109.70
1	A	55	ARG	NE-CZ-NH2	6.41	124.97	119.20
1	B	30	ARG	NE-CZ-NH1	-6.39	115.11	121.50
1	A	146	ALA	CA-C-N	-6.27	112.62	122.65
1	A	146	ALA	C-N-CA	-6.27	112.62	122.65
1	A	217	SER	N-CA-C	-6.21	99.71	108.96
1	A	338	ARG	CG-CD-NE	-5.96	98.88	112.00
1	B	204	ARG	CB-CG-CD	-5.88	97.78	111.30
1	B	143	GLY	N-CA-C	5.86	119.39	111.72
1	A	149	THR	CA-C-N	-5.84	112.57	119.05
1	A	149	THR	C-N-CA	-5.84	112.57	119.05
1	A	140	HIS	N-CA-C	5.69	117.29	111.14
1	B	69	GLU	CB-CG-CD	-5.68	102.94	112.60
1	A	333	ALA	CA-C-N	-5.60	114.40	122.36
1	A	333	ALA	C-N-CA	-5.60	114.40	122.36
1	A	287	ARG	NE-CZ-NH1	-5.57	115.93	121.50
1	A	307	ARG	NE-CZ-NH2	-5.53	114.23	119.20
1	B	143	GLY	CA-C-O	5.51	126.51	121.77
1	A	369	GLY	N-CA-C	-5.48	107.75	115.32
1	B	217	SER	N-CA-C	-5.42	101.07	109.14
1	B	153	LEU	CD1-CG-CD2	5.34	122.54	110.80
1	A	55	ARG	NE-CZ-NH1	-5.15	116.35	121.50
1	B	140	HIS	N-CA-CB	-5.11	102.61	110.01
1	B	48	VAL	O-C-N	5.04	123.65	120.42
1	B	101	ARG	CG-CD-NE	5.03	123.06	112.00

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	2857	0	2866	19	0
1	B	2932	0	2925	30	0
2	A	15	0	6	0	0
2	B	15	0	7	0	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
4	A	276	0	0	2	0
4	B	264	0	0	1	0
All	All	6362	0	5804	44	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 (44) 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:100:ARG:HH11	1:B:100:ARG:HG2	0.96	1.13
1:B:100:ARG:HG2	1:B:100:ARG:NH1	1.78	0.95
1:B:100:ARG:HH11	1:B:100:ARG:CG	1.84	0.88
1:B:334:ASP:OD1	1:B:337:THR:HG23	1.74	0.87
1:B:68[A]:LYS:HG2	1:B:377:LEU:HD21	1.68	0.76
1:A:51:ALA:HA	1:A:54:GLN:HE21	1.60	0.66
1:B:18:ASP:HB3	1:B:22:ARG:NH2	2.10	0.66
1:A:94[A]:GLN:HG3	4:A:695:HOH:O	1.97	0.65
1:B:51:ALA:HA	1:B:54:GLN:HE21	1.62	0.64
1:B:68[A]:LYS:HD3	1:B:377:LEU:HD11	1.80	0.64
1:B:141:ARG:CG	1:B:142:SER:H	2.18	0.57
1:B:68[A]:LYS:CD	1:B:377:LEU:HD11	2.35	0.55
1:B:141:ARG:HG2	1:B:142:SER:N	2.21	0.55
1:B:245[B]:MET:HE3	1:B:245[B]:MET:HA	1.91	0.53
1:B:68[A]:LYS:CG	1:B:377:LEU:HD21	2.38	0.53
1:A:321:HIS:NE2	1:B:141:ARG:HD3	2.25	0.52
1:A:153:LEU:O	1:A:157[B]:ARG:HG3	2.10	0.51
1:A:333:ALA:O	1:A:334:ASP:C	2.53	0.50
1:B:141:ARG:CG	1:B:142:SER:N	2.74	0.49
1:A:68:LYS:HG2	1:A:377:LEU:HD21	1.95	0.48
1:A:37[B]:ARG:HD3	1:A:60:SER:OG	2.13	0.48
1:B:100:ARG:NH1	1:B:100:ARG:CG	2.56	0.48
1:A:324:LEU:HD23	1:A:324:LEU:C	2.38	0.48
1:B:219:PRO:HG3	1:B:245[B]:MET:HE1	1.96	0.47
1:B:138:ASP:OD1	1:B:140:HIS:CB	2.63	0.46
1:B:141:ARG:HG2	1:B:142:SER:H	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:HIS:HD2	4:A:744:HOH:O	1.99	0.45
1:B:138:ASP:OD1	1:B:140:HIS:HB3	2.16	0.45
1:B:324:LEU:C	1:B:324:LEU:HD23	2.42	0.45
1:A:321:HIS:CE1	1:B:141:ARG:HD3	2.53	0.44
1:A:321:HIS:CD2	1:B:141:ARG:HD3	2.53	0.44
1:A:275:ILE:HD12	1:A:323:ILE:HD12	2.01	0.43
1:B:144:VAL:HG13	1:B:151:LEU:HD23	2.01	0.43
1:A:318:ASN:HD22	1:B:141:ARG:HG3	1.83	0.43
1:B:237:VAL:HG11	1:B:245[A]:MET:HE3	2.00	0.43
1:A:40:PRO:CD	1:A:59:ALA:HB1	2.49	0.42
1:B:43:LYS:NZ	4:B:758:HOH:O	2.36	0.42
1:A:85:VAL:O	1:A:86:SER:C	2.63	0.41
1:A:318:ASN:ND2	1:B:141:ARG:HG3	2.35	0.41
1:B:338:ARG:HA	1:B:338:ARG:HD3	1.83	0.41
1:B:215:VAL:O	1:B:233:VAL:HA	2.21	0.40
1:A:132:TRP:CH2	1:A:212:VAL:HG11	2.56	0.40
1:A:140:HIS:CD2	1:A:141:ARG:HB2	2.55	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	383/390 (98%)	374 (98%)	7 (2%)	2 (0%)	24	12
1	B	392/390 (100%)	383 (98%)	8 (2%)	1 (0%)	36	22
All	All	775/780 (99%)	757 (98%)	15 (2%)	3 (0%)	30	16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	ARG

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Mol	Chain	Res	Type
1	B	141	ARG
1	A	236	GLY

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	285/288 (99%)	282 (99%)	3 (1%)	65	54
1	B	293/288 (102%)	291 (99%)	2 (1%)	76	69
All	All	578/576 (100%)	573 (99%)	5 (1%)	70	62

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	A	142	SER
1	A	291	ARG
1	B	100	ARG
1	B	153	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	54	GLN
1	A	140	HIS
1	A	305	GLN
1	A	318	ASN
1	B	-3	HIS
1	B	28	GLN
1	B	54	GLN
1	B	94	GLN
1	B	305	GLN
1	B	363	GLN

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 ⓘ

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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	401	1	15,15,16	2.42	4 (26%)	21,22,23	1.79	7 (33%)
2	PLP	B	401	1	15,15,16	1.79	3 (20%)	21,22,23	1.58	4 (19%)

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	401	1	-	0/6/6/8	0/1/1/1
2	PLP	B	401	1	-	0/6/6/8	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PLP	C5-C4	6.84	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PLP	C3-C2	3.96	1.45	1.41
2	B	401	PLP	C5-C4	3.79	1.44	1.40
2	B	401	PLP	C6-C5	3.32	1.44	1.37
2	B	401	PLP	C3-C2	3.18	1.44	1.41
2	A	401	PLP	C3-C4	3.03	1.45	1.40
2	A	401	PLP	C6-C5	2.22	1.42	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	PLP	C2A-C2-C3	-3.60	116.59	120.80
2	A	401	PLP	C4A-C4-C3	3.35	126.12	120.52
2	B	401	PLP	C6-C5-C4	-2.89	115.72	118.10
2	B	401	PLP	C4A-C4-C5	-2.72	118.14	120.94
2	A	401	PLP	O4P-C5A-C5	-2.71	104.27	109.36
2	A	401	PLP	C4A-C4-C5	-2.71	118.14	120.94
2	A	401	PLP	C3-C2-N1	-2.70	117.56	120.96
2	B	401	PLP	C2A-C2-N1	2.64	122.62	117.64
2	A	401	PLP	C3-C4-C5	-2.47	115.62	118.59
2	A	401	PLP	C2A-C2-N1	2.32	122.01	117.64
2	A	401	PLP	C4-C3-C2	2.01	122.89	119.89

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

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	379/390 (97%)	-0.34	4 (1%) 78 81	7, 20, 39, 58	6 (1%)
1	B	389/390 (99%)	-0.26	16 (4%) 41 45	8, 19, 44, 72	5 (1%)
All	All	768/780 (98%)	-0.30	20 (2%) 57 61	7, 20, 40, 72	11 (1%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-8	HIS	4.7
1	A	2	GLN	3.9
1	B	-7	HIS	3.8
1	B	330	ALA	3.7
1	B	291	ARG	3.5
1	B	-5	HIS	3.3
1	B	333	ALA	3.2
1	B	-1	MET	3.1
1	B	331	ALA	2.9
1	B	1	MET	2.5
1	A	291	ARG	2.4
1	A	147	ASP	2.3
1	B	140	HIS	2.2
1	B	329	GLY	2.2
1	B	-4	HIS	2.2
1	B	141	ARG	2.1
1	A	146	ALA	2.1
1	B	-6	HIS	2.1
1	B	-2	ALA	2.0
1	B	177	TYR	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
3	MG	A	402	1/1	0.92	0.06	14,14,14,14	1
3	MG	B	402	1/1	0.95	0.04	11,11,11,11	1
3	MG	B	403	1/1	0.98	0.14	17,17,17,17	1
2	PLP	B	401	15/16	0.99	0.03	12,14,17,20	0
2	PLP	A	401	15/16	0.99	0.04	14,16,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.