



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:55 PM EDT

PDB ID : 5QRB / pdb_00005qrb
Title : PanDDA analysis group deposition – Crystal Structure of human ALAS2A in complex with Z2856434868
Authors : Bezerra, G.A.; Foster, W.; Bailey, H.; Shrestha, L.; Krojer, T.; Talon, R.; Brandao-Neto, J.; Douangamath, A.; Nicola, B.B.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Brennan, P.E.; Yue, W.W.
Deposited on : 2019-05-22
Resolution : 1.72 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](#) ①) 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

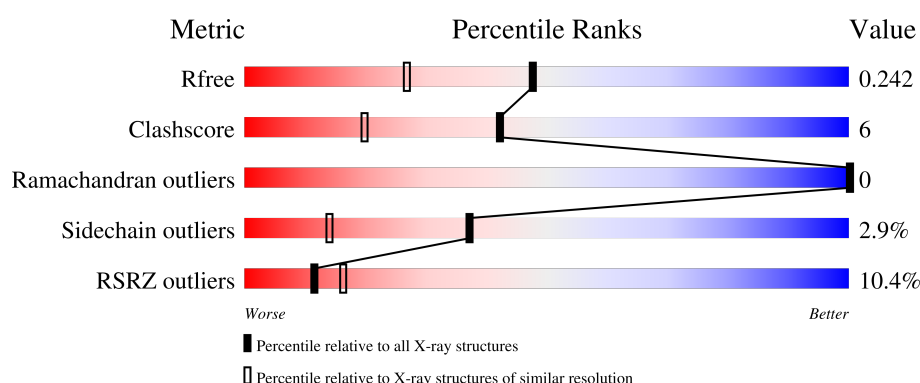
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.72 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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	10% 78% 13% 9%
1	B	469	9% 78% 12% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6920 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
			3302	2102	577	601	22			
1	A	429	Total	C	N	O	S	0	1	0
			3322	2114	587	599	22			

There are 68 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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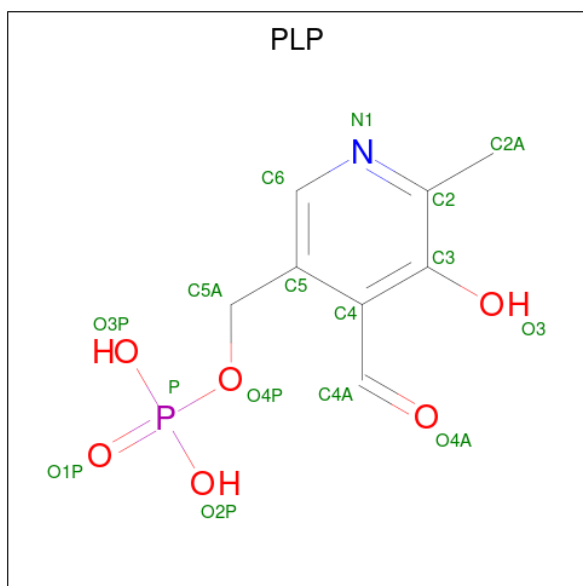
Chain	Residue	Modelled	Actual	Comment	Reference
B	579	GLY	-	expression tag	UNP P22557
B	580	PRO	-	expression tag	UNP P22557
B	581	GLN	-	expression tag	UNP P22557
B	582	TYR	-	expression tag	UNP P22557
B	583	VAL	-	expression tag	UNP P22557
B	584	THR	-	expression tag	UNP P22557
B	585	THR	-	expression tag	UNP P22557
B	586	TYR	-	expression tag	UNP P22557
B	587	ALA	-	expression tag	UNP P22557
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
A	579	GLY	-	expression tag	UNP P22557
A	580	PRO	-	expression tag	UNP P22557
A	581	GLN	-	expression tag	UNP P22557
A	582	TYR	-	expression tag	UNP P22557
A	583	VAL	-	expression tag	UNP P22557
A	584	THR	-	expression tag	UNP P22557
A	585	THR	-	expression tag	UNP P22557
A	586	TYR	-	expression tag	UNP P22557

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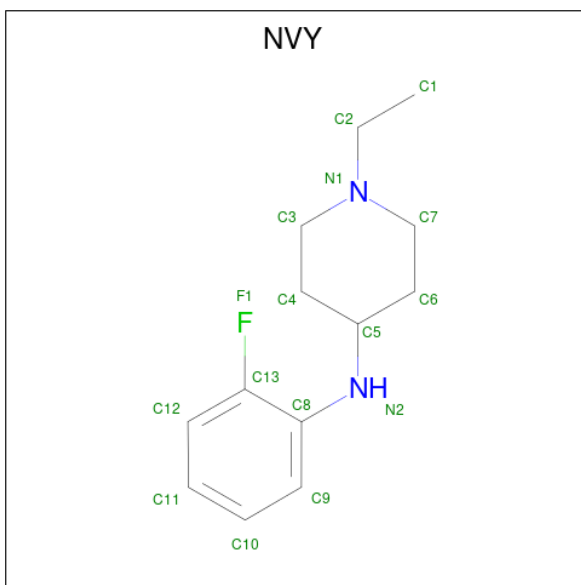
Chain	Residue	Modelled	Actual	Comment	Reference
A	587	ALA	-	expression tag	UNP P22557

- 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 1-ethyl-N-(2-fluorophenyl)piperidin-4-amine (CCD ID: NVY) (formula: $C_{13}H_{19}FN_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	F	N	0	0
			16	13	1	2		

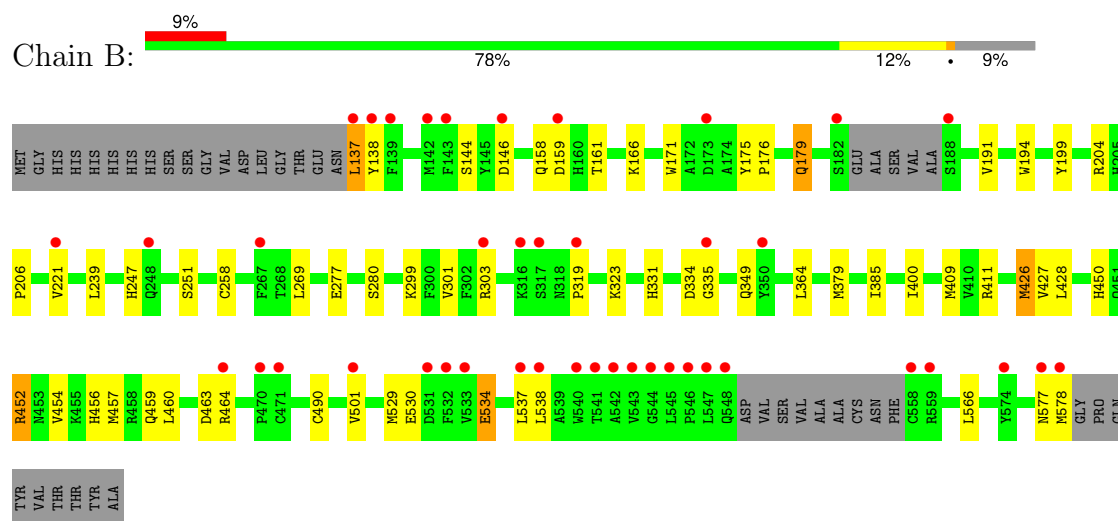
- Molecule 4 is water.

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

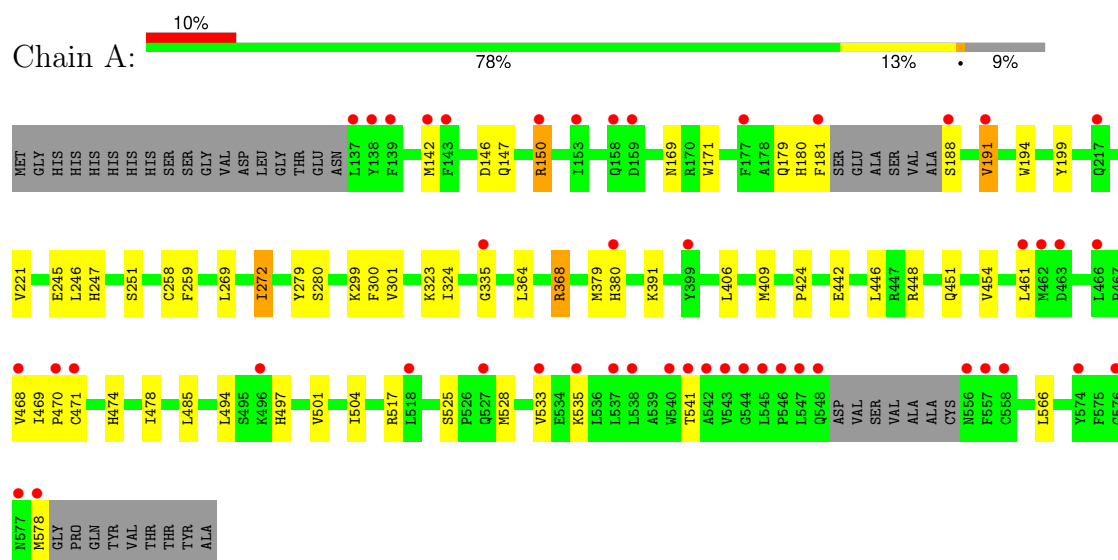
3 Residue-property plots

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: 5-aminolevulinate synthase, erythroid-specific, mitochondrial



- Molecule 1: 5-aminolevulinate synthase, erythroid-specific, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.40Å 108.16Å 75.70Å 90.00° 109.22° 90.00°	Depositor
Resolution (Å)	79.86 – 1.72 79.86 – 1.72	Depositor EDS
% Data completeness (in resolution range)	72.2 (79.86-1.72) 72.2 (79.86-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 1.72Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.206 , 0.237 0.217 , 0.242	Depositor DCC
R_{free} test set	4955 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 24.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6920	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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, NVY

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	1.04	0/3403	1.36	1/4608 (0.0%)
1	B	1.05	2/3381 (0.1%)	1.38	4/4580 (0.1%)
All	All	1.05	2/6784 (0.0%)	1.37	5/9188 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	411	ARG	C-O	6.17	1.31	1.24
1	B	206	PRO	C-O	-5.01	1.18	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	GLN	CB-CA-C	-6.01	100.04	109.84
1	B	452	ARG	CB-CA-C	5.96	120.24	110.88
1	B	158	GLN	CA-C-N	5.77	128.59	120.28
1	B	158	GLN	C-N-CA	5.77	128.59	120.28
1	A	368	ARG	NE-CZ-NH2	5.14	123.83	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	137	LEU	Peptide

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	3322	0	3215	44	0
1	B	3302	0	3192	38	0
2	A	16	0	7	3	0
2	B	16	0	7	2	0
3	B	16	0	0	0	0
4	A	112	0	0	1	0
4	B	136	0	0	8	0
All	All	6920	0	6421	82	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 (82) 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:147:GLN:OE1	1:A:150:ARG:NH1	2.08	0.87
1:B:349:GLN:OE1	4:B:701:HOH:O	2.03	0.76
1:B:464:ARG:HB3	1:B:537:LEU:HD11	1.70	0.73
1:A:497:HIS:ND1	1:A:535:LYS:HE2	2.05	0.72
1:B:175:TYR:HB2	1:B:204:ARG:HD2	1.73	0.70
1:A:146:ASP:O	1:A:150:ARG:HG2	1.92	0.69
1:A:461:LEU:HD21	1:A:478:ILE:HD11	1.74	0.69
1:B:460:LEU:O	1:B:464:ARG:HG2	1.93	0.69
1:A:169:ASN:HD21	1:A:181:PHE:HE2	1.38	0.69
1:B:171:TRP:CZ2	1:B:179:GLN:HG3	2.28	0.68
1:B:194:TRP:HB2	1:B:501:VAL:CG1	2.23	0.67
1:B:175:TYR:CB	1:B:204:ARG:HD2	2.28	0.63
1:B:319:PRO:O	1:A:142:MET:HB3	1.98	0.63
1:A:504:ILE:CD1	1:A:517:ARG:HB2	2.29	0.62
1:B:194:TRP:HB2	1:B:501:VAL:HG12	1.83	0.60
1:B:459:GLN:NE2	4:B:707:HOH:O	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:451:GLN:O	1:A:454:VAL:HG12	2.01	0.59
1:A:504:ILE:HD12	1:A:517:ARG:HB2	1.84	0.59
1:B:303:ARG:NH1	4:B:706:HOH:O	2.34	0.58
1:B:452:ARG:NH1	4:B:710:HOH:O	2.37	0.57
1:B:221:VAL:HG13	1:B:426:MET:HE1	1.87	0.56
1:A:391:LYS:CE	2:A:601:PLP:H4A	2.37	0.55
1:B:258:CYS:HB3	2:B:601:PLP:O4P	2.07	0.54
1:A:258:CYS:HB3	2:A:601:PLP:O4P	2.08	0.53
1:B:456:HIS:HE1	4:B:746:HOH:O	1.92	0.53
1:A:247:HIS:HA	1:A:379:MET:CE	2.39	0.53
1:A:504:ILE:CD1	1:A:517:ARG:CB	2.86	0.52
1:B:166:LYS:HE3	1:B:490:CYS:SG	2.49	0.52
1:A:269:LEU:HB3	1:A:324:ILE:HD11	1.92	0.52
1:A:461:LEU:CD2	1:A:478:ILE:HD11	2.41	0.51
1:B:426:MET:HG2	1:B:427:VAL:N	2.24	0.51
1:A:442:GLU:O	1:A:446:LEU:HD23	2.10	0.51
1:A:191:VAL:HG21	1:A:494:LEU:CD1	2.41	0.51
1:A:194:TRP:HB2	1:A:501:VAL:CG1	2.40	0.51
1:A:461:LEU:HD12	1:A:533:VAL:CG1	2.41	0.50
1:B:247:HIS:HA	1:B:379:MET:CE	2.42	0.50
1:A:194:TRP:HB2	1:A:501:VAL:HG12	1.94	0.49
1:A:299:LYS:HB3	1:A:578:MET:HE1	1.94	0.49
1:B:335:GLY:CA	4:B:756:HOH:O	2.60	0.49
1:B:137:LEU:HD12	1:B:137:LEU:N	2.28	0.49
1:A:461:LEU:HD12	1:A:533:VAL:HG12	1.94	0.48
1:B:277:GLU:O	1:B:323:LYS:HA	2.13	0.48
1:B:331:HIS:HB3	1:B:334:ASP:OD1	2.14	0.48
1:A:525:SER:OG	1:A:528:MET:HG3	2.14	0.48
1:B:194:TRP:HB2	1:B:501:VAL:HG13	1.95	0.47
1:A:171:TRP:CZ2	1:A:179:GLN:HB2	2.49	0.47
1:B:534:GLU:O	1:B:538:LEU:HD23	2.14	0.47
1:A:191:VAL:HG21	1:A:494:LEU:HD12	1.96	0.46
1:A:259:PHE:C	1:A:259:PHE:CD1	2.94	0.46
1:A:246:LEU:O	1:A:368:ARG:NH1	2.43	0.46
1:A:221:VAL:O	1:A:424:PRO:HB3	2.15	0.45
1:A:180:HIS:O	1:A:188:SER:HA	2.16	0.45
1:B:199:TYR:CD2	1:B:364:LEU:HD11	2.51	0.45
1:B:457:MET:HB2	1:B:529:MET:HE3	1.99	0.45
1:B:577:ASN:OD1	1:B:578:MET:N	2.49	0.45
1:A:301:VAL:HG11	1:A:566:LEU:O	2.17	0.45
2:B:601:PLP:O3P	4:B:702:HOH:O	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:VAL:HG21	1:A:474:HIS:HA	1.98	0.44
1:A:406:LEU:C	1:A:406:LEU:HD23	2.42	0.44
1:B:159:ASP:HB3	1:B:161:THR:HG23	1.98	0.44
1:A:279:TYR:HA	1:A:300:PHE:O	2.18	0.44
1:B:280:SER:O	1:B:301:VAL:HA	2.18	0.43
1:B:239:LEU:HD23	1:B:428:LEU:HD22	2.00	0.43
1:A:199:TYR:CD2	1:A:364:LEU:HD11	2.54	0.43
1:A:380[B]:HIS:HE1	4:A:736:HOH:O	2.01	0.43
1:A:391:LYS:HE3	2:A:601:PLP:H4A	2.00	0.42
1:A:272:ILE:HG21	1:A:409:MET:SD	2.60	0.42
1:A:451:GLN:HA	1:A:454:VAL:HG12	2.00	0.41
1:A:469:ILE:HG22	1:A:471:CYS:SG	2.60	0.41
1:A:451:GLN:O	1:A:454:VAL:CG1	2.68	0.41
1:B:269:LEU:HD23	1:B:409:MET:HE1	2.01	0.41
1:B:385:ILE:O	1:B:400:ILE:HA	2.21	0.41
1:B:459:GLN:NE2	1:B:463:ASP:OD1	2.54	0.41
1:A:280:SER:O	1:A:301:VAL:HA	2.21	0.41
1:A:470:PRO:C	1:A:471:CYS:SG	3.04	0.40
1:B:247:HIS:ND1	1:B:385:ILE:HD13	2.37	0.40
1:A:179:GLN:HG3	1:A:188:SER:OG	2.21	0.40
1:B:335:GLY:C	4:B:756:HOH:O	2.64	0.40
1:B:450:HIS:O	1:B:454:VAL:HG23	2.21	0.40
1:B:277:GLU:OE1	1:B:323:LYS:HE3	2.21	0.40
1:B:301:VAL:HG11	1:B:566:LEU:O	2.21	0.40
1:A:335:GLY:O	1:A:471:CYS:HB3	2.22	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	424/469 (90%)	414 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	423/469 (90%)	409 (97%)	14 (3%)	0	100	100
All	All	847/938 (90%)	823 (97%)	24 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	347/396 (88%)	337 (97%)	10 (3%)	37	14
1	B	345/396 (87%)	335 (97%)	10 (3%)	37	14
All	All	692/792 (87%)	672 (97%)	20 (3%)	37	14

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	138	TYR
1	B	144	SER
1	B	146	ASP
1	B	176	PRO
1	B	191	VAL
1	B	251	SER
1	B	299	LYS
1	B	426	MET
1	B	530	GLU
1	B	534	GLU
1	A	150	ARG
1	A	191	VAL
1	A	245	GLU
1	A	251	SER
1	A	272	ILE
1	A	323	LYS
1	A	448	ARG
1	A	468	VAL

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Mol	Chain	Res	Type
1	A	485	LEU
1	A	541	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	180	HIS
1	A	158	GLN
1	A	502	GLN

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](#)

3 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	NVY	B	602	-	17,17,17	0.59	1 (5%)	21,22,22	0.60	0
2	PLP	A	601	-	16,16,16	0.71	0	20,23,23	0.90	1 (5%)
2	PLP	B	601	-	16,16,16	0.84	1 (6%)	20,23,23	1.21	3 (15%)

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
3	NVY	B	602	-	-	2/6/16/16	0/2/2/2
2	PLP	A	601	-	-	2/8/8/8	0/1/1/1
2	PLP	B	601	-	-	3/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	PLP	P-O4P	2.30	1.67	1.60
3	B	602	NVY	C8-C13	2.17	1.41	1.39

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	PLP	C3-C4-C4A	-3.04	115.67	119.84
2	B	601	PLP	O4P-C5A-C5	2.40	113.86	109.36
2	A	601	PLP	C3-C4-C4A	-2.20	116.81	119.84
2	B	601	PLP	O3P-P-O2P	2.02	115.36	107.80

There are no chirality outliers.

All (7) torsion outliers are listed below:

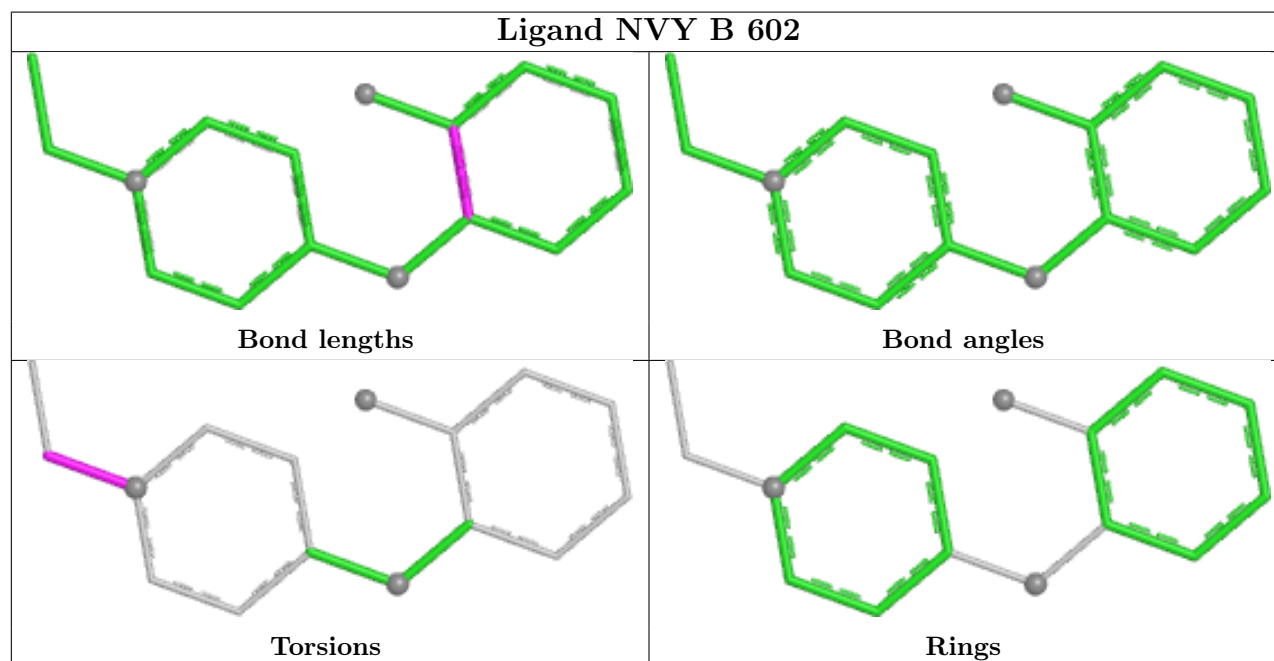
Mol	Chain	Res	Type	Atoms
2	B	601	PLP	C5A-O4P-P-O1P
2	A	601	PLP	C3-C4-C4A-O4A
3	B	602	NVY	C1-C2-N1-C7
3	B	602	NVY	C1-C2-N1-C3
2	A	601	PLP	C5-C4-C4A-O4A
2	B	601	PLP	C3-C4-C4A-O4A
2	B	601	PLP	C5A-O4P-P-O3P

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	PLP	3	0
2	B	601	PLP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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%)	0.59	47 (10%)	10 15	4, 22, 44, 74	5 (1%)
1	B	428/469 (91%)	0.59	42 (9%)	13 18	6, 23, 43, 72	6 (1%)
All	All	857/938 (91%)	0.59	89 (10%)	11 16	4, 22, 44, 74	11 (1%)

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	557	PHE	13.7
1	A	143	PHE	12.2
1	B	143	PHE	12.0
1	B	532	PHE	11.8
1	B	350	TYR	11.6
1	B	267	PHE	11.0
1	A	177	PHE	10.8
1	A	380[A]	HIS	10.7
1	A	399	TYR	9.5
1	B	248[A]	GLN	9.3
1	A	181	PHE	8.8
1	A	137	LEU	8.7
1	B	531	ASP	8.5
1	B	547	LEU	6.9
1	B	138	TYR	6.8
1	B	137	LEU	6.8
1	B	558	CYS	6.3
1	A	545	LEU	5.6
1	A	191	VAL	5.1
1	A	537	LEU	5.1
1	B	548	GLN	5.0
1	B	538	LEU	4.8
1	A	547	LEU	4.7
1	A	548	GLN	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	545	LEU	4.3
1	B	541	THR	4.2
1	B	537	LEU	4.1
1	A	139	PHE	4.1
1	A	188	SER	4.1
1	A	578	MET	4.0
1	B	470	PRO	3.6
1	A	576	GLY	3.6
1	A	470	PRO	3.5
1	A	461	LEU	3.5
1	A	577	ASN	3.4
1	B	546	PRO	3.2
1	A	558	CYS	3.0
1	A	556	ASN	2.9
1	B	577	ASN	2.9
1	A	540	TRP	2.8
1	A	462	MET	2.8
1	B	335	GLY	2.8
1	A	542	ALA	2.8
1	B	221	VAL	2.8
1	A	546	PRO	2.8
1	A	138	TYR	2.7
1	A	541	THR	2.7
1	A	574	TYR	2.7
1	B	471	CYS	2.6
1	B	139	PHE	2.6
1	B	540	TRP	2.6
1	B	182	SER	2.6
1	A	142	MET	2.5
1	A	159	ASP	2.5
1	B	542	ALA	2.5
1	A	543	VAL	2.5
1	B	146	ASP	2.5
1	B	173	ASP	2.5
1	A	538	LEU	2.4
1	B	544	GLY	2.4
1	B	578	MET	2.4
1	A	335	GLY	2.4
1	B	316	LYS	2.3
1	B	142	MET	2.3
1	B	559	ARG	2.3
1	B	159	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	319	PRO	2.3
1	A	527	GLN	2.3
1	B	464	ARG	2.3
1	B	303	ARG	2.2
1	A	535	LYS	2.2
1	A	463	ASP	2.2
1	B	533	VAL	2.2
1	A	153	ILE	2.2
1	B	188	SER	2.2
1	A	217	GLN	2.2
1	A	518	LEU	2.2
1	A	468	VAL	2.1
1	A	544	GLY	2.1
1	A	150	ARG	2.1
1	B	501	VAL	2.1
1	A	158	GLN	2.1
1	A	533	VAL	2.1
1	A	471	CYS	2.1
1	A	466	LEU	2.1
1	B	574	TYR	2.1
1	B	543	VAL	2.0
1	A	496	LYS	2.0
1	B	317	SER	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.

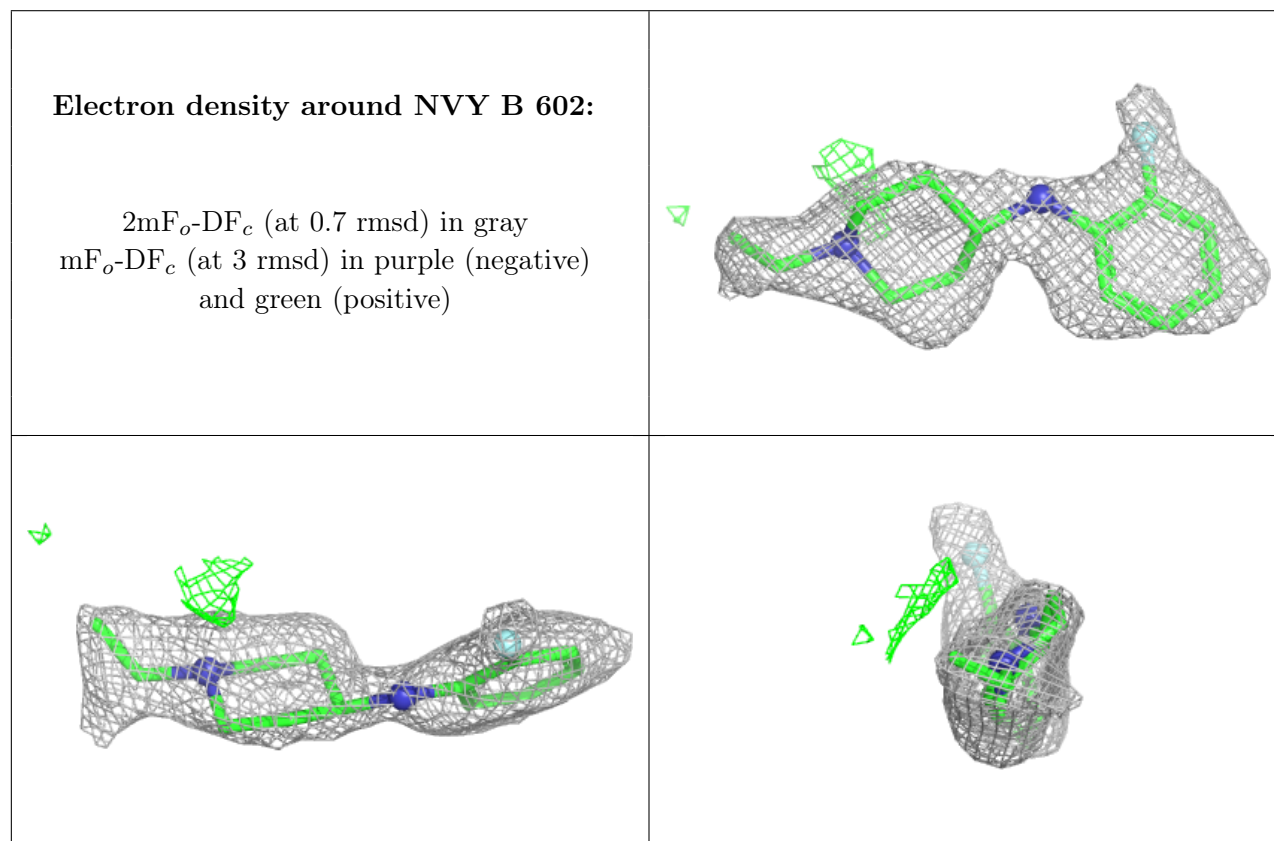
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NVY	B	602	16/16	0.79	0.19	52,53,55,55	0
2	PLP	B	601	16/16	0.86	0.13	22,29,34,41	0
2	PLP	A	601	16/16	0.91	0.11	22,28,34,43	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.