



Full wwPDB X-ray Structure Validation Report ⓘ

May 20, 2026 – 08:13 PM EDT

PDB ID : 9Y91 / pdb_00009y91
Title : Nanorana parkeri saxiphilin:STX-C13-NBz (co-crystal)
Authors : Zakrzewska, S.; Minor, D.L.
Deposited on : 2025-09-12
Resolution : 1.95 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
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

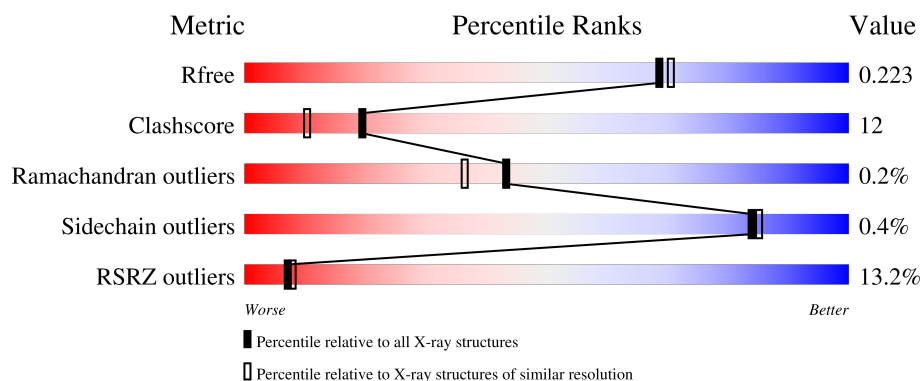
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	854	<div> <div>13%</div> <div>77%</div> <div>19%</div> <div>.</div> </div>

2 Entry composition [i](#)

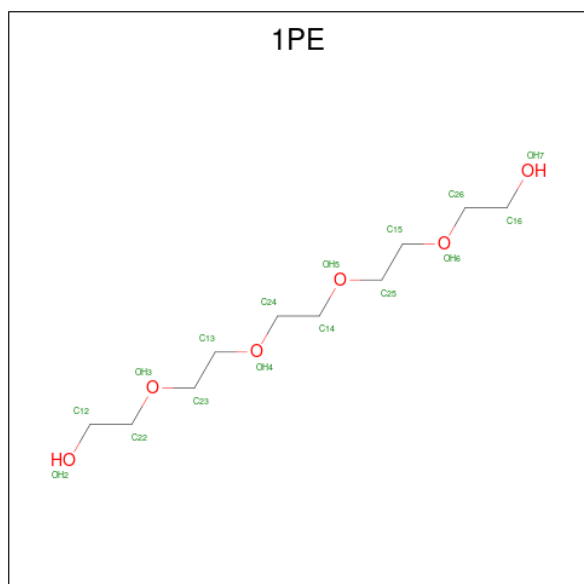
There are 4 unique types of molecules in this entry. The entry contains 6848 atoms, of which 22 are hydrogens and 0 are deuteriums.

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 Saxiphilin.

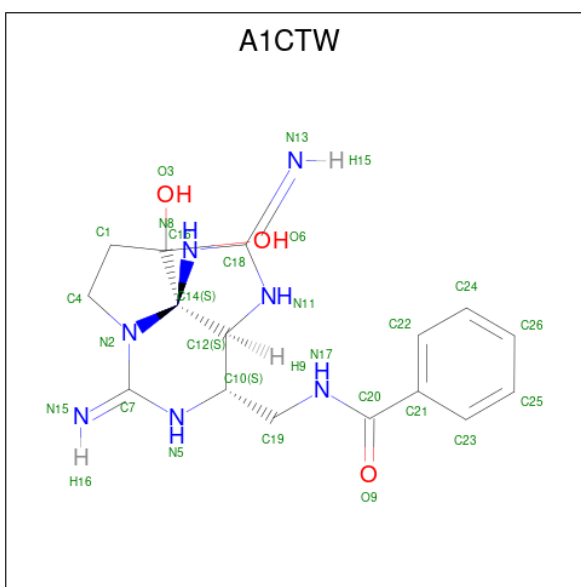
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	821	Total	C	N	O	S	0	2	0
			6384	4000	1105	1220	59			

- Molecule 2 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			38	10	22	6		

- Molecule 3 is N-{[(2Z,3aS,4S,6Z,7R,10aS)-10,10-dihydroxy-2,6-diiminooctahydro-1H,8H-pyrrolo[1,2-c]purin-4-yl]methyl}benzamide (CCD ID: A1CTW) (formula: $C_{16}H_{21}N_7O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			26	16	7	3		

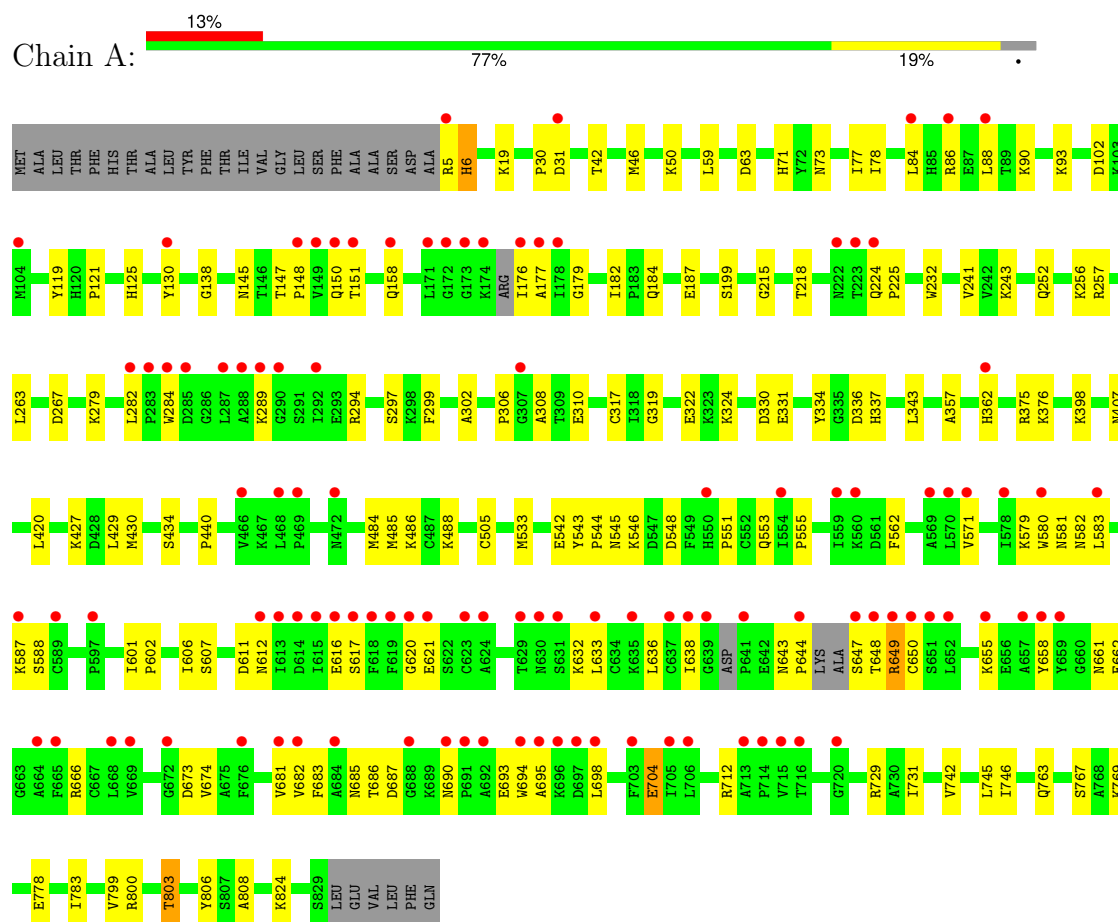
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	400	Total O 400 400	0	0

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: Saxiphilin



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	228.98Å 228.98Å 67.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.27 – 1.95 43.27 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.27-1.95) 99.9 (43.27-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 1.95Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, R_{free}	0.194 , 0.223 0.194 , 0.223	Depositor DCC
R_{free} test set	4751 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.013 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6848	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: 1PE, A1CTW

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	0.39	0/6539	0.56	0/8841

There are no bond length outliers.

There are no bond angle outliers.

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	6384	0	6186	146	0
2	A	16	22	22	0	0
3	A	26	0	0	0	0
4	A	400	0	0	18	0
All	All	6826	22	6208	146	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 12.

All (146) 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:330:ASP:OD2	4:A:1001:HOH:O	1.69	1.08
1:A:102:ASP:H	1:A:803:THR:HG21	1.05	1.08
1:A:662:GLU:HG3	1:A:685:ASN:HD21	1.27	0.95
1:A:90:LYS:NZ	4:A:1002:HOH:O	2.02	0.93
1:A:616:GLU:HA	1:A:633:LEU:HD21	1.50	0.92
1:A:693:GLU:OE1	1:A:693:GLU:N	2.02	0.91
1:A:102:ASP:N	1:A:803:THR:HG21	1.87	0.88
1:A:218:THR:HG23	1:A:362[C]:HIS:HE1	1.40	0.85
1:A:484:MET:HE3	1:A:488:LYS:HE3	1.61	0.83
1:A:571:VAL:HG12	1:A:673:ASP:O	1.80	0.82
1:A:177:ALA:HB3	1:A:182:ILE:HD11	1.62	0.79
1:A:799:VAL:O	1:A:803:THR:HG23	1.84	0.78
1:A:661:ASN:HB3	1:A:681:VAL:HG22	1.66	0.77
1:A:362[C]:HIS:NE2	4:A:1006:HOH:O	2.16	0.77
1:A:662:GLU:HG3	1:A:685:ASN:ND2	1.99	0.77
1:A:638:ILE:HG13	1:A:658:TYR:CE2	2.21	0.74
1:A:322:GLU:N	1:A:322:GLU:OE2	2.17	0.74
1:A:187:GLU:HA	1:A:187:GLU:OE1	1.87	0.73
1:A:147:THR:HB	1:A:148:PRO:HD2	1.71	0.73
1:A:661:ASN:HB3	1:A:681:VAL:CG2	2.18	0.72
1:A:125:HIS:ND1	1:A:611:ASP:OD1	2.18	0.72
1:A:643:ASN:OD1	1:A:649:ARG:NH2	2.22	0.72
1:A:225:PRO:HG3	1:A:362[A]:HIS:ND1	2.05	0.71
1:A:86:ARG:HG2	1:A:86:ARG:HH11	1.54	0.71
1:A:337[B]:HIS:CD2	1:A:427:LYS:HD2	2.26	0.70
1:A:73:ASN:HA	1:A:398:LYS:HE3	1.73	0.70
1:A:542:GLU:OE1	4:A:1003:HOH:O	2.10	0.70
1:A:86:ARG:HD3	1:A:232:TRP:CE2	2.27	0.69
1:A:484:MET:HG3	1:A:488:LYS:NZ	2.07	0.68
1:A:179:GLY:HA2	1:A:199:SER:OG	1.93	0.68
1:A:151:THR:HG22	4:A:1351:HOH:O	1.94	0.68
1:A:505:CYS:SG	4:A:1381:HOH:O	2.51	0.67
1:A:587:LYS:N	1:A:587:LYS:HD2	2.09	0.67
1:A:224:GLN:OE1	1:A:225:PRO:HD2	1.95	0.66
1:A:602:PRO:O	1:A:606:ILE:HG12	1.96	0.65
1:A:434:SER:OG	4:A:1005:HOH:O	2.15	0.65
1:A:147:THR:H	1:A:150:GLN:NE2	1.95	0.64
1:A:362[A]:HIS:HD2	4:A:1343:HOH:O	1.81	0.64
1:A:86:ARG:HD2	4:A:1332:HOH:O	1.97	0.64
1:A:218:THR:HG23	1:A:362[C]:HIS:CE1	2.30	0.63
1:A:647:SER:HB2	1:A:655:LYS:HE3	1.81	0.62
1:A:224:GLN:HG3	1:A:225:PRO:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:GLN:O	1:A:256:LYS:NZ	2.30	0.62
1:A:543:TYR:HB2	1:A:783:ILE:HD12	1.81	0.62
1:A:579:LYS:H	1:A:582:ASN:HD21	1.46	0.62
1:A:30:PRO:O	1:A:31:ASP:HB2	1.99	0.61
1:A:225:PRO:HG3	1:A:362[B]:HIS:ND1	2.15	0.60
1:A:218:THR:CG2	1:A:362[C]:HIS:HE1	2.14	0.60
1:A:130:TYR:CE1	1:A:147:THR:HG22	2.36	0.60
1:A:694:TRP:O	1:A:698:LEU:HD21	2.01	0.60
1:A:362[C]:HIS:CE1	4:A:1006:HOH:O	2.54	0.60
1:A:88:LEU:HD23	1:A:93:LYS:HD3	1.84	0.59
1:A:806:TYR:OH	4:A:1004:HOH:O	2.14	0.58
1:A:46:MET:CE	1:A:63:ASP:HB3	2.35	0.57
1:A:763:GLN:NE2	4:A:1016:HOH:O	2.38	0.56
1:A:648:THR:O	1:A:649:ARG:HB2	2.05	0.56
1:A:695:ALA:C	1:A:698:LEU:HD23	2.30	0.56
1:A:224:GLN:OE1	1:A:225:PRO:CD	2.53	0.56
1:A:50:LYS:HE2	1:A:71:HIS:O	2.06	0.56
1:A:284:TRP:HA	1:A:289:LYS:HD3	1.88	0.56
1:A:485:MET:HE3	1:A:769:LYS:HD3	1.88	0.55
1:A:542:GLU:OE1	1:A:729:ARG:HD3	2.06	0.55
1:A:376:LYS:HE2	4:A:1231:HOH:O	2.07	0.55
1:A:484:MET:HG3	1:A:488:LYS:HZ2	1.68	0.55
1:A:742:VAL:O	1:A:746:ILE:HG12	2.07	0.55
1:A:621:GLU:HB3	1:A:636:LEU:CD1	2.37	0.55
1:A:644:PRO:HD3	1:A:647:SER:HB3	1.89	0.55
1:A:620:GLY:O	1:A:632:LYS:HE2	2.08	0.54
1:A:661:ASN:O	1:A:681:VAL:HG11	2.07	0.54
1:A:544:PRO:HD2	1:A:562:PHE:O	2.08	0.53
1:A:553:GLN:O	1:A:555:PRO:HD3	2.08	0.53
1:A:579:LYS:H	1:A:582:ASN:ND2	2.06	0.52
1:A:84:LEU:HD22	1:A:824:LYS:HE2	1.91	0.52
1:A:587:LYS:HA	1:A:621:GLU:O	2.09	0.52
1:A:362[B]:HIS:HD2	4:A:1343:HOH:O	1.92	0.52
1:A:621:GLU:C	1:A:636:LEU:HD13	2.35	0.52
1:A:704:GLU:OE2	1:A:712:ARG:NH2	2.43	0.52
1:A:317:CYS:HB3	1:A:331:GLU:OE1	2.10	0.52
1:A:638:ILE:O	1:A:649:ARG:HG2	2.10	0.52
1:A:695:ALA:HA	1:A:698:LEU:HD23	1.93	0.51
1:A:176:ILE:HD12	1:A:176:ILE:O	2.11	0.50
1:A:86:ARG:HG2	1:A:86:ARG:NH1	2.26	0.50
1:A:607:SER:HB2	1:A:612:ASN:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:601:ILE:HB	1:A:602:PRO:HD3	1.92	0.50
1:A:215:GLY:O	1:A:362[C]:HIS:HB3	2.12	0.50
1:A:687:ASP:N	1:A:698:LEU:O	2.41	0.49
1:A:682:VAL:HG13	1:A:683:PHE:N	2.26	0.49
1:A:580:TRP:CE3	1:A:583:LEU:HD11	2.47	0.49
1:A:102:ASP:OD2	1:A:800:ARG:NE	2.44	0.48
1:A:666:ARG:HG2	1:A:694:TRP:CH2	2.48	0.48
1:A:282:LEU:HD21	1:A:299:PHE:HB2	1.95	0.48
1:A:294:ARG:HG2	1:A:310:GLU:OE2	2.13	0.48
1:A:130:TYR:CZ	1:A:147:THR:HG22	2.49	0.48
1:A:587:LYS:HD2	1:A:673:ASP:OD1	2.13	0.48
1:A:647:SER:N	1:A:655:LYS:O	2.47	0.48
1:A:121:PRO:HG3	1:A:158:GLN:HG2	1.96	0.47
1:A:306:PRO:HG2	1:A:334:TYR:HA	1.95	0.47
1:A:533:MET:HE2	4:A:1145:HOH:O	2.15	0.47
1:A:546:LYS:NZ	1:A:778:GLU:OE1	2.38	0.47
1:A:587:LYS:HB2	1:A:673:ASP:OD1	2.14	0.47
1:A:145:ASN:ND2	4:A:1009:HOH:O	2.31	0.47
1:A:638:ILE:HD11	1:A:658:TYR:OH	2.15	0.47
1:A:282:LEU:CD2	1:A:299:PHE:HB2	2.45	0.47
1:A:294:ARG:O	1:A:297:SER:HB3	2.15	0.47
1:A:543:TYR:CZ	1:A:545:ASN:HB3	2.51	0.46
1:A:685:ASN:HD22	1:A:694:TRP:HH2	1.63	0.46
1:A:686:THR:HB	1:A:698:LEU:O	2.16	0.46
1:A:119:TYR:CZ	1:A:138:GLY:HA3	2.51	0.46
1:A:19:LYS:NZ	1:A:420:LEU:O	2.40	0.45
1:A:279:LYS:NZ	4:A:1026:HOH:O	2.49	0.45
1:A:182:ILE:O	1:A:184:GLN:NE2	2.48	0.45
1:A:616:GLU:OE1	1:A:617:SER:N	2.50	0.45
1:A:42:THR:HG22	1:A:46:MET:HE3	1.98	0.45
1:A:319:GLY:O	1:A:324:LYS:HB2	2.16	0.45
1:A:263:LEU:HD22	1:A:308:ALA:HA	1.97	0.45
1:A:579:LYS:HG3	1:A:582:ASN:HD21	1.82	0.45
1:A:661:ASN:HB3	1:A:681:VAL:HG21	1.95	0.45
1:A:731:ILE:HD12	1:A:731:ILE:N	2.32	0.44
1:A:5:ARG:O	1:A:6:HIS:HB2	2.17	0.44
1:A:86:ARG:HD3	1:A:232:TRP:NE1	2.31	0.44
1:A:362[C]:HIS:HD2	4:A:1343:HOH:O	2.01	0.44
1:A:429:LEU:O	1:A:430:MET:HB2	2.18	0.44
1:A:46:MET:HE2	1:A:59:LEU:HD13	1.98	0.43
1:A:666:ARG:HG2	1:A:694:TRP:CZ2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:616:GLU:HB2	1:A:633:LEU:HD11	2.01	0.43
1:A:241:VAL:HG13	1:A:343:LEU:HD22	2.02	0.42
1:A:695:ALA:CA	1:A:698:LEU:HD23	2.48	0.42
1:A:267:ASP:OD2	1:A:336:ASP:OD1	2.37	0.42
1:A:803:THR:HG22	1:A:808:ALA:HB2	2.02	0.42
1:A:336:ASP:HB3	1:A:357:ALA:CB	2.50	0.42
1:A:548:ASP:OD1	1:A:551:PRO:HD3	2.20	0.42
1:A:588:SER:HA	1:A:674:VAL:O	2.20	0.42
1:A:745:LEU:HD23	1:A:745:LEU:HA	1.90	0.42
1:A:77:ILE:C	1:A:78:ILE:HG13	2.45	0.42
1:A:693:GLU:HG2	1:A:694:TRP:N	2.34	0.42
1:A:587:LYS:CD	1:A:673:ASP:OD1	2.67	0.41
1:A:486:LYS:HD2	1:A:767:SER:HB2	2.03	0.41
1:A:257:ARG:HA	1:A:302:ALA:O	2.21	0.41
1:A:579:LYS:HG3	1:A:582:ASN:ND2	2.35	0.41
1:A:690:ASN:HB3	1:A:695:ALA:CB	2.50	0.41
1:A:243:LYS:O	1:A:375:ARG:NH2	2.54	0.41
1:A:803:THR:HA	1:A:808:ALA:N	2.36	0.41
1:A:579:LYS:NZ	1:A:581:ASN:HD21	2.19	0.41
1:A:30:PRO:O	1:A:31:ASP:CB	2.68	0.40
1:A:694:TRP:O	1:A:698:LEU:CD2	2.69	0.40
1:A:407:ASN:OD1	1:A:440:PRO:HB3	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	816/854 (96%)	780 (96%)	34 (4%)	2 (0%)	43 36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	649	ARG

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	708/731 (97%)	705 (100%)	3 (0%)	84 85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	650	CYS
1	A	704	GLU
1	A	803	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	96	GLN
1	A	120	HIS
1	A	150	GLN
1	A	188	GLN
1	A	274	ASN
1	A	379	ASN
1	A	437	HIS
1	A	553	GLN
1	A	608	ASN
1	A	661	ASN
1	A	685	ASN
1	A	788	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 ⓘ

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	1PE	A	901	-	15,15,15	0.30	0	14,14,14	0.40	0
3	A1CTW	A	902	-	23,29,29	0.52	0	22,45,45	1.07	4 (18%)

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	1PE	A	901	-	-	4/13/13/13	-
3	A1CTW	A	902	-	-	0/9/57/57	0/4/4/4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	A1CTW	N8-C14-N2	-2.50	108.13	112.45
3	A	902	A1CTW	C4-N2-C7	2.23	125.76	122.11
3	A	902	A1CTW	C12-C10-N5	2.20	111.29	108.86
3	A	902	A1CTW	N8-C18-N11	2.15	111.40	109.21

There are no chirality outliers.

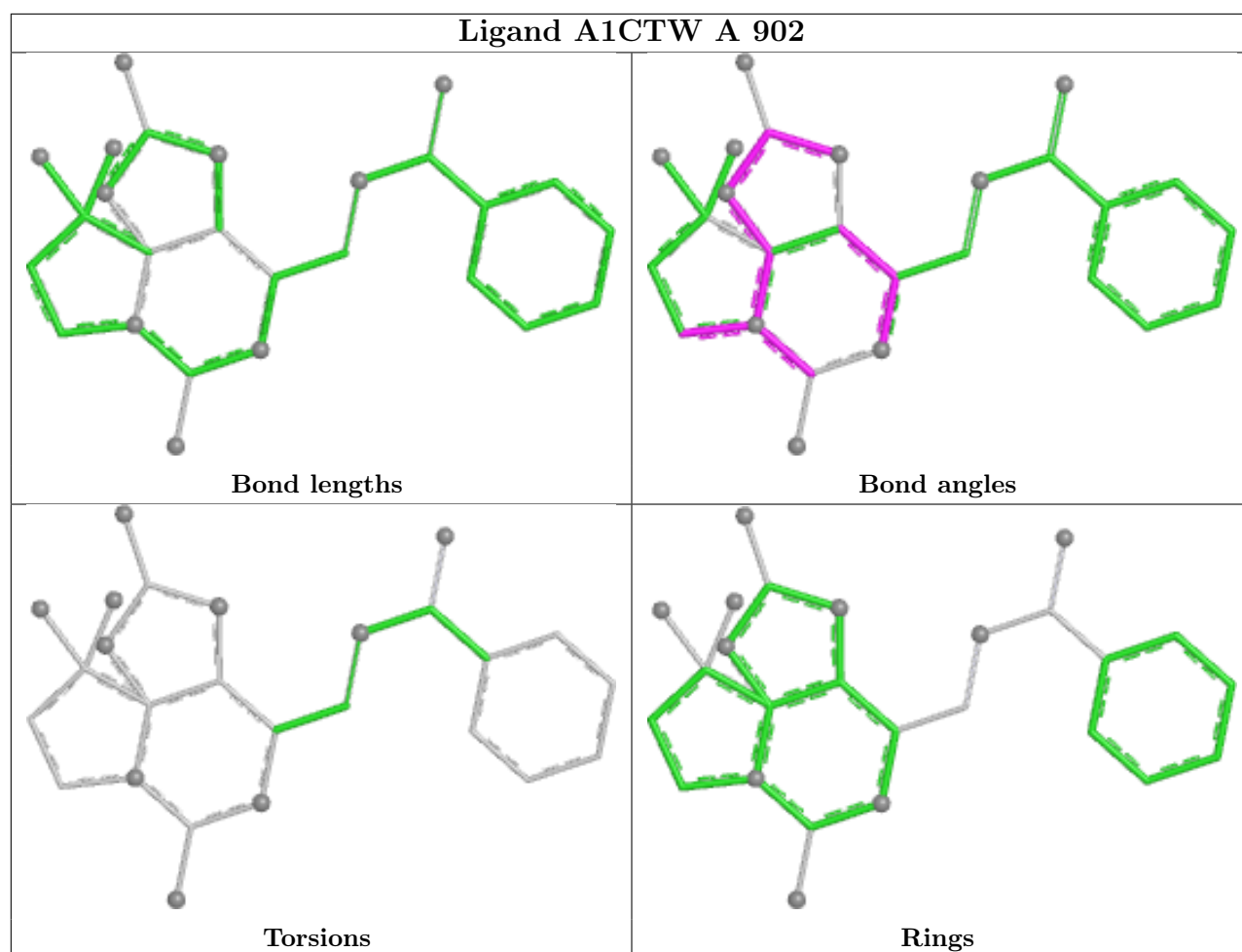
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	1PE	OH6-C15-C25-OH5
2	A	901	1PE	C25-C15-OH6-C26
2	A	901	1PE	C23-C13-OH4-C24
2	A	901	1PE	OH5-C14-C24-OH4

There are no ring outliers.

No monomer is involved in short contacts.

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	821/854 (96%)	0.80	108 (13%) 7 8	21, 52, 105, 139	2 (0%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	ILE	8.4
1	A	613	ILE	6.8
1	A	641	PRO	6.5
1	A	638	ILE	4.7
1	A	285	ASP	4.6
1	A	466	VAL	4.3
1	A	177	ALA	4.3
1	A	284	TRP	4.2
1	A	644	PRO	4.2
1	A	657	ALA	4.1
1	A	639	GLY	3.9
1	A	287	LEU	3.8
1	A	554	ILE	3.8
1	A	149	VAL	3.7
1	A	665	PHE	3.7
1	A	714	PRO	3.7
1	A	570	LEU	3.6
1	A	692	ALA	3.6
1	A	698	LEU	3.6
1	A	647	SER	3.6
1	A	559	ILE	3.5
1	A	223	THR	3.4
1	A	658	TYR	3.4
1	A	224	GLN	3.4
1	A	669	VAL	3.3
1	A	569	ALA	3.3
1	A	468	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	283	PRO	3.3
1	A	635	LYS	3.3
1	A	694	TRP	3.3
1	A	580	TRP	3.3
1	A	648	THR	3.2
1	A	288	ALA	3.2
1	A	158	GLN	3.2
1	A	178	ILE	3.1
1	A	171	LEU	3.1
1	A	633	LEU	3.1
1	A	713	ALA	3.1
1	A	571	VAL	3.1
1	A	682	VAL	3.0
1	A	86	ARG	3.0
1	A	616	GLU	3.0
1	A	655	LYS	3.0
1	A	174	LYS	2.9
1	A	578	ILE	2.9
1	A	615	ILE	2.9
1	A	173	GLY	2.8
1	A	620	GLY	2.8
1	A	630	ASN	2.8
1	A	629	THR	2.8
1	A	148	PRO	2.8
1	A	651	SER	2.7
1	A	624	ALA	2.7
1	A	623	CYS	2.7
1	A	697	ASP	2.7
1	A	222	ASN	2.7
1	A	589	CYS	2.6
1	A	289	LYS	2.6
1	A	681	VAL	2.6
1	A	150	GLN	2.6
1	A	676	PHE	2.6
1	A	652	LEU	2.6
1	A	290	GLY	2.6
1	A	715	VAL	2.6
1	A	151	THR	2.6
1	A	550	HIS	2.5
1	A	469	PRO	2.5
1	A	659	TYR	2.5
1	A	695	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	614	ASP	2.5
1	A	618	PHE	2.5
1	A	705	ILE	2.5
1	A	703	PHE	2.4
1	A	621	GLU	2.4
1	A	649	ARG	2.4
1	A	282	LEU	2.4
1	A	691	PRO	2.4
1	A	472	ASN	2.4
1	A	84	LEU	2.4
1	A	690	ASN	2.3
1	A	688	GLY	2.3
1	A	637	CYS	2.3
1	A	619	PHE	2.3
1	A	612	ASN	2.3
1	A	716	THR	2.3
1	A	172	GLY	2.3
1	A	672	GLY	2.3
1	A	104	MET	2.3
1	A	668	LEU	2.3
1	A	696	LYS	2.3
1	A	587	LYS	2.2
1	A	5	ARG	2.2
1	A	650	CYS	2.2
1	A	307	GLY	2.2
1	A	684	ALA	2.2
1	A	130	TYR	2.2
1	A	362[A]	HIS	2.2
1	A	664	ALA	2.2
1	A	617	SER	2.1
1	A	88	LEU	2.1
1	A	292	ILE	2.1
1	A	560	LYS	2.1
1	A	31	ASP	2.1
1	A	597	PRO	2.1
1	A	583	LEU	2.1
1	A	631	SER	2.0
1	A	720	GLY	2.0
1	A	706	LEU	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](#)

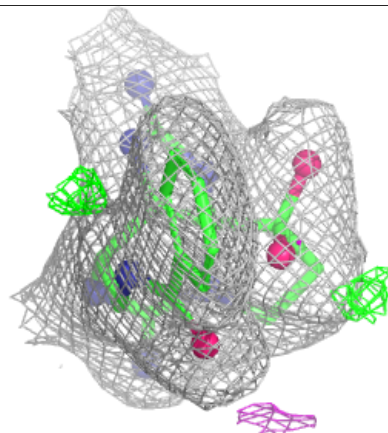
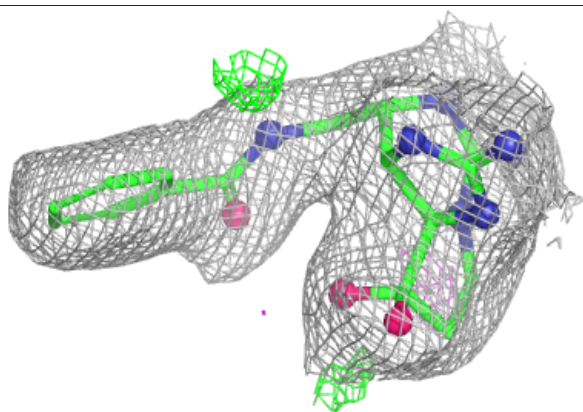
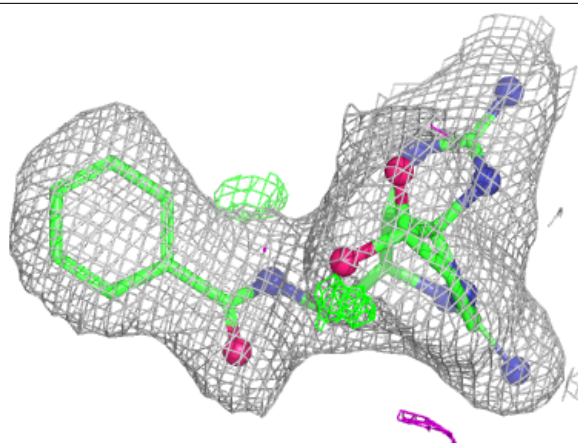
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	1PE	A	901	16/16	0.82	0.16	66,84,102,103	0
3	A1CTW	A	902	26/26	0.95	0.08	48,54,66,74	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.

Electron density around A1CTW A 902:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.