



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 22, 2022 – 03:38 pm BST

PDB ID : 7AYQ
Title : Crystal structure of DPP8 in complex with a 4-oxo-b-lactam based inhibitor, B114
Authors : Ross, B.; Huber, R.
Deposited on : 2020-11-13
Resolution : 2.45 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.30
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.30

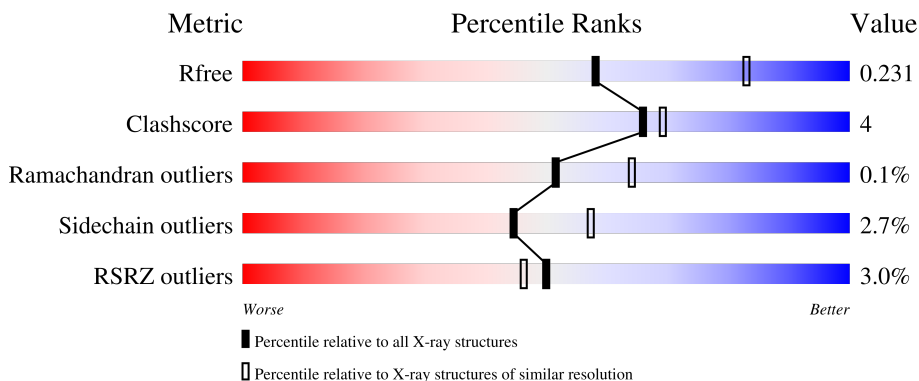
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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}	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	898	 3% 80% 10% • 10%
1	B	898	 3% 80% 10% • 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	903	-	-	-	X
4	GOL	B	903	-	-	-	X

2 Entry composition [i](#)

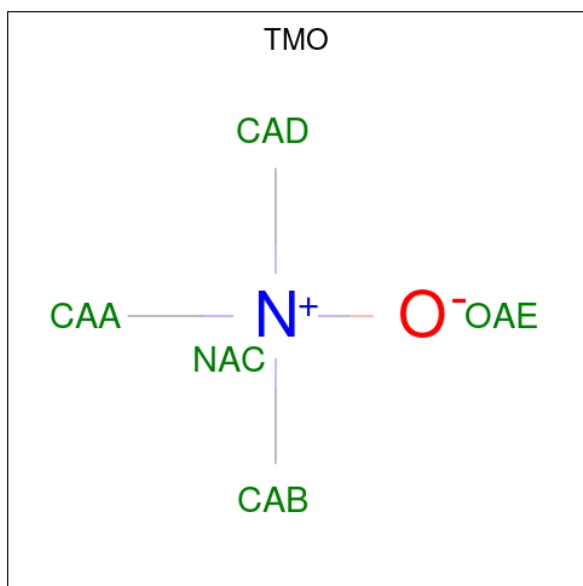
There are 6 unique types of molecules in this entry. The entry contains 13428 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dipeptidyl peptidase 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	808	6584	4238	1098	1222	26	0	3	0
1	B	811	6583	4238	1094	1224	27	9	1	0

- Molecule 2 is trimethylamine oxide (three-letter code: TMO) (formula: C_3H_9NO).



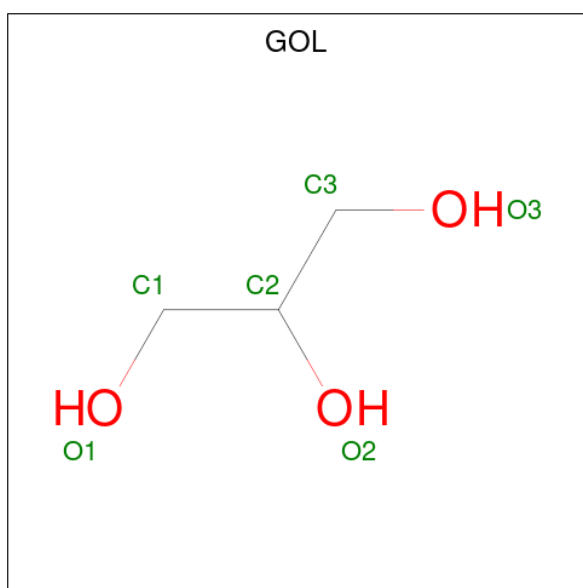
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	5	3	1	1	0	0
2	B	1	5	3	1	1	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



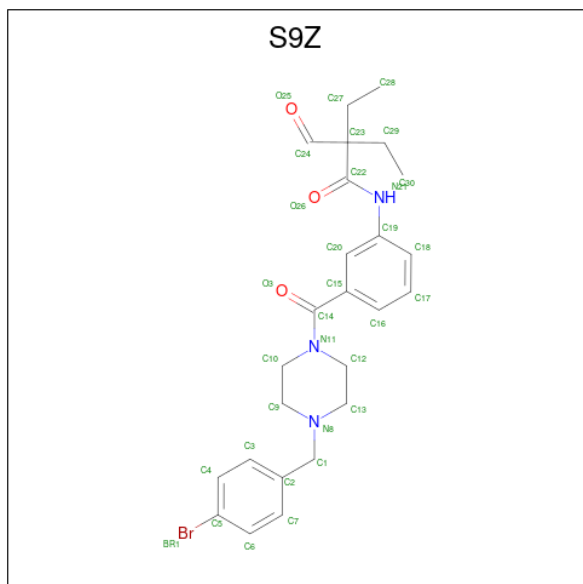
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

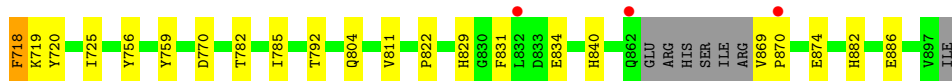
- Molecule 5 is {N}-[3-[4-[(4-bromophenyl)methyl]piperazin-1-yl]carbonylphenyl]-2-ethyl-1-2-methanoyl-butanamide (three-letter code: S9Z) (formula: C₂₅H₃₀BrN₃O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	N	O		
5	A	1	Total	Br	C	N	O	0	0
			32	1	25	3	3		
5	B	1	Total	Br	C	N	O	0	0
			32	1	25	3	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	108	Total	O	0	0
			108	108		
6	B	57	Total	O	0	0
			57	57		



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	149.50Å 149.50Å 269.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.94 – 2.45 48.94 – 2.45	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.94-2.45) 100.0 (48.94-2.45)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.45Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.193 , 0.228 0.198 , 0.231	Depositor DCC
R_{free} test set	6228 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	64.2	Xtrriage
Anisotropy	0.268	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.028 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13428	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.93% 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: GOL, TMO, PO4, S9Z

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	0.70	0/6774	0.85	0/9191
1	B	0.70	0/6768	0.85	0/9185
All	All	0.70	0/13542	0.85	0/18376

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 [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	6584	0	6395	57	0
1	B	6583	0	6385	50	0
2	A	5	0	9	0	0
2	B	5	0	9	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	32	0	0	1	0
5	B	32	0	0	1	0
6	A	108	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	57	0	0	0	0
All	All	13428	0	12814	103	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 (103) 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:829:HIS:HD2	1:A:841:THR:OG1	1.64	0.81
1:A:334:THR:CG2	1:A:785:ILE:HA	2.13	0.78
1:A:173:GLN:HE22	1:A:579:GLN:HE22	1.40	0.70
1:B:376:GLU:HG2	1:B:397:ARG:HB2	1.75	0.69
1:A:882:HIS:CE1	1:B:822:PRO:HG3	2.28	0.68
1:A:705:ARG:HD3	1:A:729:ASP:OD2	1.96	0.66
1:A:317:THR:HB	1:A:832:LEU:HD21	1.78	0.65
1:B:304:GLU:CD	1:B:306:ASN:HD21	2.05	0.60
1:A:123:ASN:ND2	1:A:125:ALA:H	2.00	0.59
1:B:423:GLN:HA	1:B:426:ILE:HD12	1.85	0.59
1:A:348:ILE:HG22	1:A:350:ILE:HD11	1.83	0.59
1:B:651:TYR:HB2	1:B:699:VAL:HB	1.85	0.58
1:A:822:PRO:HG3	1:B:882:HIS:CE1	2.39	0.57
1:A:348:ILE:HG22	1:A:350:ILE:CD1	2.34	0.57
1:A:500:ALA:HB1	1:A:501:PRO:HD2	1.86	0.57
1:A:767:GLN:O	1:A:768:ARG:HD2	2.05	0.56
1:B:211:CYS:HB3	1:B:232:HIS:CD2	2.40	0.56
1:B:252:VAL:HG13	1:B:264:ARG:HB3	1.87	0.56
1:B:481:LYS:HB2	1:B:514:ILE:HD11	1.90	0.53
1:B:687:PHE:O	1:B:690:ASN:HB3	2.09	0.53
1:B:164:VAL:HG21	1:B:183:GLY:CA	2.38	0.53
1:B:487:LYS:HG3	1:B:488:GLU:O	2.08	0.53
1:A:421:GLU:HA	1:A:421:GLU:OE1	2.08	0.52
1:A:719:LYS:HE3	1:A:720:TYR:CZ	2.45	0.52
1:B:629:ASP:OD1	1:B:629:ASP:N	2.38	0.51
1:A:519:TRP:CG	1:A:544:LYS:HA	2.46	0.50
1:A:123:ASN:HD21	1:A:125:ALA:HB3	1.76	0.50
1:A:402:LEU:C	1:A:402:LEU:HD23	2.31	0.50
1:B:462:GLU:HA	1:B:486:LEU:HB2	1.93	0.50
1:A:351:ASP:OD1	1:A:353:GLU:HG2	2.10	0.50
1:A:252:VAL:CG1	1:A:264:ARG:HB3	2.42	0.50
1:B:882:HIS:CE1	1:B:886:GLU:HG3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:PHE:CZ	1:A:275:GLU:HG3	2.47	0.49
1:A:719:LYS:HE3	1:A:720:TYR:CE2	2.47	0.49
1:B:69:ARG:CZ	1:B:874:GLU:HG2	2.42	0.49
1:A:273:LEU:HD22	1:A:279:ARG:NH2	2.28	0.48
1:A:627:LEU:HB2	1:A:630:TYR:HB3	1.96	0.48
1:A:99:ILE:O	1:A:115:TYR:HA	2.13	0.48
1:A:252:VAL:HG13	1:A:264:ARG:HB3	1.95	0.48
1:A:536:ARG:HA	1:A:557:TYR:CE2	2.48	0.48
1:B:376:GLU:CG	1:B:397:ARG:HB2	2.42	0.48
1:A:123:ASN:ND2	1:A:123:ASN:C	2.67	0.48
1:A:473:LYS:NZ	1:A:511:GLU:OE2	2.30	0.48
1:B:400:THR:O	1:B:442:THR:HA	2.14	0.48
1:B:519:TRP:CG	1:B:544:LYS:HA	2.49	0.48
5:A:904:S9Z:C12	5:A:904:S9Z:C16	2.91	0.47
1:B:756:TYR:O	1:B:759:TYR:HB3	2.14	0.47
1:A:303:TYR:CZ	1:A:344:LYS:HB2	2.49	0.47
1:B:258:ASN:HD22	1:B:258:ASN:N	2.13	0.47
1:B:869:VAL:HG22	1:B:870:PRO:HD2	1.95	0.47
1:B:365:ILE:HD12	1:B:429:VAL:HG21	1.96	0.47
1:A:782:THR:H	1:A:840:HIS:CD2	2.33	0.46
1:A:123:ASN:C	1:A:123:ASN:HD22	2.18	0.46
1:A:782:THR:H	1:A:840:HIS:HD2	1.61	0.46
1:A:882:HIS:CE1	1:A:886:GLU:HG3	2.51	0.46
1:B:192:GLY:HA2	1:B:197:PHE:CE1	2.51	0.46
1:A:49:GLU:O	1:A:660:LYS:HA	2.15	0.46
1:B:286:CYS:HB2	1:B:383:TRP:CZ2	2.51	0.46
1:B:460:HIS:CE1	1:B:462:GLU:HG2	2.51	0.45
1:B:465:GLU:OE1	1:B:481:LYS:HE2	2.17	0.45
1:B:782:THR:H	1:B:840:HIS:HD2	1.64	0.45
1:A:882:HIS:CE1	1:B:822:PRO:CG	2.98	0.45
5:B:904:S9Z:C12	5:B:904:S9Z:C16	2.94	0.45
1:A:69:ARG:CZ	1:A:874:GLU:HG2	2.47	0.45
1:A:734:LEU:HD12	1:A:734:LEU:HA	1.81	0.45
1:A:129:MET:HE1	1:A:622:ASP:HB2	1.98	0.45
1:A:829:HIS:HE1	1:A:836:VAL:O	1.99	0.45
1:A:882:HIS:NE2	1:B:822:PRO:HG3	2.32	0.44
1:A:400:THR:O	1:A:442:THR:HA	2.18	0.44
1:A:334:THR:HG22	1:A:785:ILE:HA	1.96	0.44
1:A:422:ARG:NH1	1:A:426:ILE:HD11	2.32	0.44
1:B:433:VAL:O	1:B:433:VAL:HG12	2.18	0.44
1:A:736:TYR:OH	1:A:740:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:VAL:HG12	1:A:871:GLU:HG2	2.00	0.44
1:B:770:ASP:OD1	1:B:770:ASP:N	2.49	0.44
1:B:465:GLU:OE1	1:B:481:LYS:CE	2.66	0.44
1:A:84:MET:SD	1:A:171:TYR:CD2	3.11	0.43
1:A:353:GLU:CG	1:A:355:ARG:HG2	2.49	0.43
1:B:804:GLN:NE2	1:B:804:GLN:HA	2.34	0.43
1:A:302:LEU:HD22	1:A:390:ALA:HB1	2.00	0.43
1:B:693:ALA:HA	1:B:697:TYR:O	2.19	0.43
1:A:178:PHE:O	1:A:188:HIS:HA	2.19	0.42
1:A:353:GLU:HG3	1:A:355:ARG:HG2	2.00	0.42
1:A:693:ALA:HA	1:A:697:TYR:O	2.19	0.42
1:A:706:GLY:HA3	1:A:718:PHE:CE2	2.54	0.42
1:B:706:GLY:HA3	1:B:718:PHE:CE2	2.54	0.42
1:B:719:LYS:HG2	1:B:720:TYR:CD2	2.54	0.42
1:B:782:THR:HA	1:B:811:VAL:HG13	2.01	0.42
1:B:334:THR:CG2	1:B:785:ILE:HA	2.50	0.42
1:A:211:CYS:HB3	1:A:232:HIS:CD2	2.54	0.42
1:A:273:LEU:HD22	1:A:279:ARG:HH21	1.84	0.42
1:B:99:ILE:O	1:B:115:TYR:HA	2.19	0.42
1:B:416:GLU:HG2	1:B:421:GLU:HG3	2.02	0.41
1:B:411:LEU:HD21	1:B:434:THR:HA	2.02	0.41
1:B:608:ASP:OD1	1:B:610:THR:HB	2.20	0.41
1:A:831:PHE:CZ	1:B:831:PHE:CZ	3.09	0.41
1:A:446:TRP:HZ2	1:A:715:GLU:HG2	1.86	0.40
1:B:372:PHE:HE1	1:B:405:VAL:HG11	1.87	0.40
1:B:243:THR:O	1:B:244:ARG:HB2	2.21	0.40
1:B:402:LEU:HD12	1:B:447:ILE:HG21	2.03	0.40
1:A:820:SER:O	1:B:58:TRP:HB3	2.22	0.40
1:B:418:ASP:OD1	1:B:420:MET:HB2	2.22	0.40
1:B:524:ARG:HA	1:B:524:ARG:HD2	1.90	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	801/898 (89%)	774 (97%)	26 (3%)	1 (0%)	51	64
1	B	804/898 (90%)	775 (96%)	28 (4%)	1 (0%)	51	64
All	All	1605/1796 (89%)	1549 (96%)	54 (3%)	2 (0%)	51	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	ILE
1	B	445	ILE

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	719/795 (90%)	702 (98%)	17 (2%)	49	61
1	B	718/795 (90%)	697 (97%)	21 (3%)	42	53
All	All	1437/1590 (90%)	1399 (97%)	38 (3%)	44	58

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	HIS
1	A	123	ASN
1	A	139	PHE
1	A	261	GLU
1	A	273	LEU
1	A	294	SER
1	A	312	GLU
1	A	434	THR
1	A	473	LYS
1	A	510	GLU
1	A	545	ASP

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Mol	Chain	Res	Type
1	A	694	SER
1	A	704	ASN
1	A	718	PHE
1	A	829	HIS
1	A	835	ASN
1	A	876	TYR
1	B	110	GLU
1	B	164	VAL
1	B	252	VAL
1	B	258	ASN
1	B	294	SER
1	B	304	GLU
1	B	376	GLU
1	B	420	MET
1	B	464	ILE
1	B	490	LYS
1	B	545	ASP
1	B	559	ASN
1	B	569	ARG
1	B	603	SER
1	B	614	LYS
1	B	694	SER
1	B	718	PHE
1	B	725	ILE
1	B	792	THR
1	B	829	HIS
1	B	834	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	A	123	ASN
1	A	173	GLN
1	A	200	GLN
1	A	403	GLN
1	A	423	GLN
1	A	829	HIS
1	A	835	ASN
1	A	840	HIS
1	A	882	HIS
1	B	111	ASN

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Mol	Chain	Res	Type
1	B	173	GLN
1	B	199	GLN
1	B	200	GLN
1	B	213	ASN
1	B	258	ASN
1	B	306	ASN
1	B	460	HIS
1	B	595	HIS
1	B	804	GLN
1	B	840	HIS
1	B	882	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	$\# Z > 2$
5	S9Z	B	904	1	32,34,34	0.74	0	43,47,47	1.82	10 (23%)
4	GOL	B	903	-	5,5,5	0.29	0	5,5,5	0.60	0
3	PO4	B	902	-	4,4,4	0.62	0	6,6,6	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	TMO	B	901	-	4,4,4	1.06	0	6,6,6	0.62	0
3	PO4	A	902	-	4,4,4	0.60	0	6,6,6	0.48	0
4	GOL	A	903	-	5,5,5	0.40	0	5,5,5	0.74	0
5	S9Z	A	904	1	32,34,34	0.71	0	43,47,47	1.66	9 (20%)
2	TMO	A	901	-	4,4,4	1.36	0	6,6,6	0.49	0

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
4	GOL	B	903	-	-	2/4/4/4	-
4	GOL	A	903	-	-	1/4/4/4	-
5	S9Z	A	904	1	-	4/28/41/41	0/3/3/3
5	S9Z	B	904	1	-	2/28/41/41	0/3/3/3

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	904	S9Z	BR1-C5-C4	4.56	125.92	119.30
5	A	904	S9Z	C23-C22-N21	4.50	122.11	115.43
5	B	904	S9Z	C15-C14-N11	4.41	124.32	118.72
5	B	904	S9Z	BR1-C5-C6	-4.18	113.22	119.30
5	A	904	S9Z	C10-C9-N8	-3.59	103.29	110.64
5	B	904	S9Z	O3-C14-C15	-3.13	114.15	120.23
5	B	904	S9Z	C12-N11-C10	2.81	118.03	112.62
5	B	904	S9Z	C1-N8-C13	-2.78	104.87	111.06
5	B	904	S9Z	C1-C2-C7	-2.70	115.69	120.77
5	A	904	S9Z	C7-C2-C3	2.65	122.33	118.17
5	A	904	S9Z	O26-C22-C23	-2.63	116.98	121.21
5	A	904	S9Z	C18-C19-C20	-2.58	116.59	119.65
5	A	904	S9Z	C12-N11-C10	2.54	117.52	112.62
5	B	904	S9Z	O26-C22-C23	-2.37	117.39	121.21
5	A	904	S9Z	C13-N8-C9	-2.32	103.60	108.83
5	B	904	S9Z	C23-C22-N21	2.23	118.74	115.43
5	B	904	S9Z	C28-C27-C23	-2.20	111.82	114.38
5	A	904	S9Z	C20-C19-N21	2.12	127.11	120.18
5	A	904	S9Z	C6-C7-C2	-2.06	118.19	121.03

There are no chirality outliers.

All (9) torsion outliers are listed below:

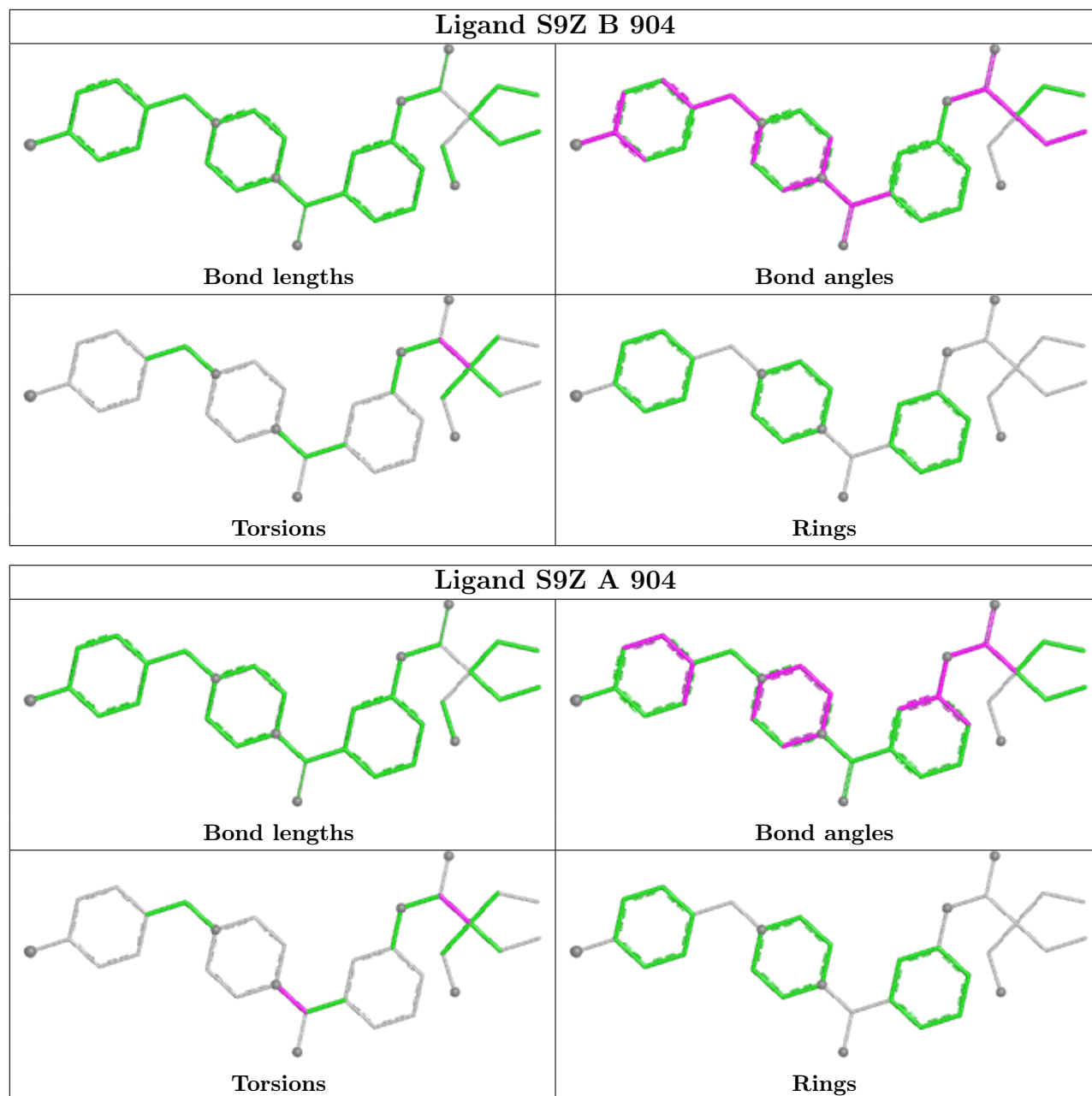
Mol	Chain	Res	Type	Atoms
5	A	904	S9Z	N21-C22-C23-C27
4	B	903	GOL	O1-C1-C2-C3
4	B	903	GOL	O1-C1-C2-O2
5	A	904	S9Z	O3-C14-N11-C10
5	B	904	S9Z	O26-C22-C23-C27
5	A	904	S9Z	O26-C22-C23-C27
5	A	904	S9Z	O26-C22-C23-C29
5	B	904	S9Z	N21-C22-C23-C27
4	A	903	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	904	S9Z	1	0
5	A	904	S9Z	1	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	808/898 (89%)	0.04	23 (2%) 53 49	45, 62, 111, 154	0
1	B	811/898 (90%)	0.07	25 (3%) 49 45	48, 67, 115, 159	2 (0%)
All	All	1619/1796 (90%)	0.05	48 (2%) 50 46	45, 64, 113, 159	2 (0%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	420	MET	5.1
1	B	256	LEU	4.8
1	B	258	ASN	4.6
1	B	260	GLU	4.4
1	B	317	THR	4.3
1	B	259	MET	4.1
1	A	317	THR	4.1
1	A	256	LEU	3.9
1	A	108	ASN	3.9
1	A	420	MET	3.8
1	B	108	ASN	3.7
1	A	139	PHE	3.6
1	A	71	TYR	3.5
1	A	105	SER	3.5
1	A	261	GLU	3.5
1	A	70	LYS	3.5
1	A	259	MET	3.4
1	A	293	PRO	3.2
1	A	138	LEU	3.2
1	A	316	VAL	3.1
1	A	110	GLU	3.1
1	B	487	LYS	3.0
1	B	870	PRO	3.0
1	B	261	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	105	SER	2.9
1	B	832	LEU	2.7
1	B	862	GLN	2.6
1	A	753	GLY	2.5
1	B	490	LYS	2.5
1	B	524	ARG	2.4
1	B	316	VAL	2.4
1	A	258	ASN	2.4
1	A	862	GLN	2.4
1	B	315	HIS	2.3
1	B	327	ASP	2.3
1	B	525	HIS	2.3
1	A	490	LYS	2.3
1	B	71	TYR	2.2
1	A	315	HIS	2.2
1	A	381	ALA	2.2
1	B	523	GLY	2.2
1	A	524	ARG	2.1
1	B	106	GLY	2.1
1	A	523	GLY	2.1
1	A	72	HIS	2.1
1	B	655	ASP	2.1
1	B	485	ILE	2.0
1	B	526	GLY	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](#)

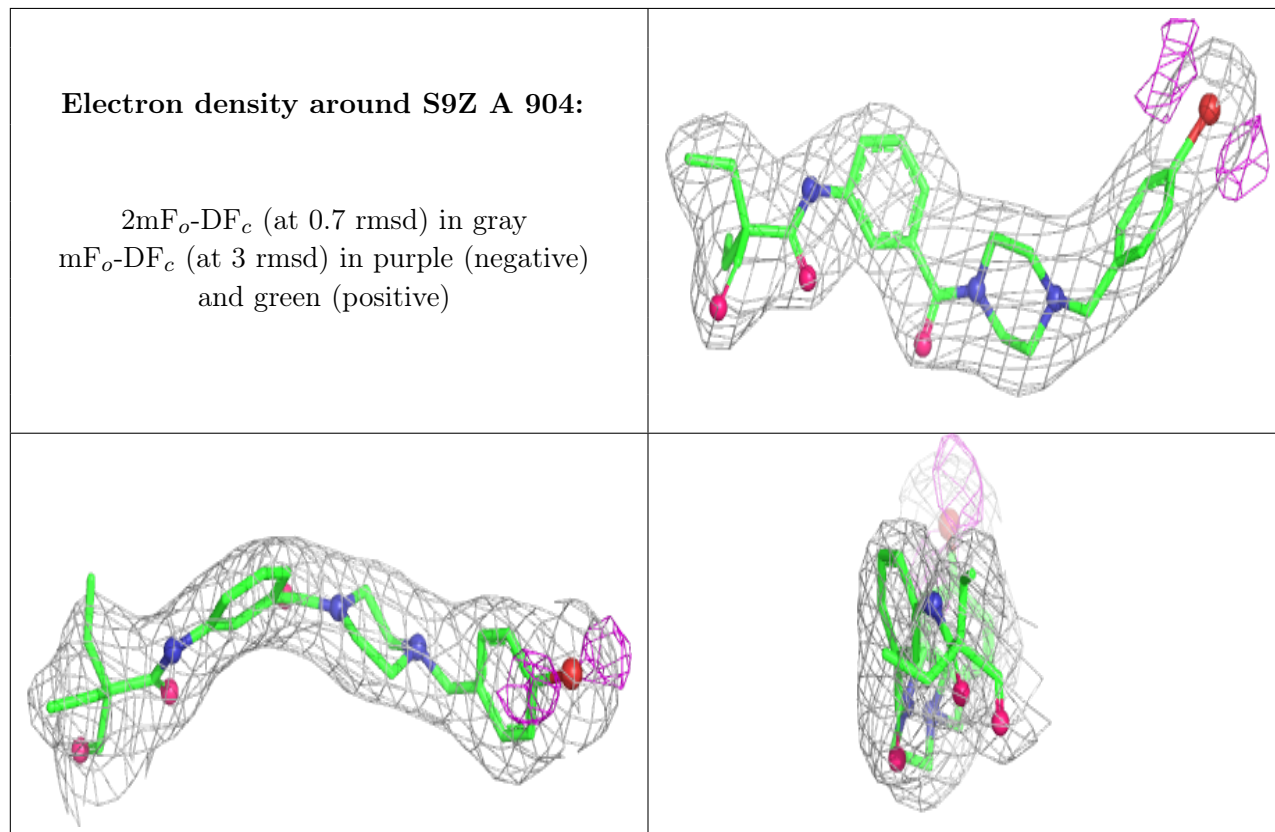
There are no monosaccharides in this entry.

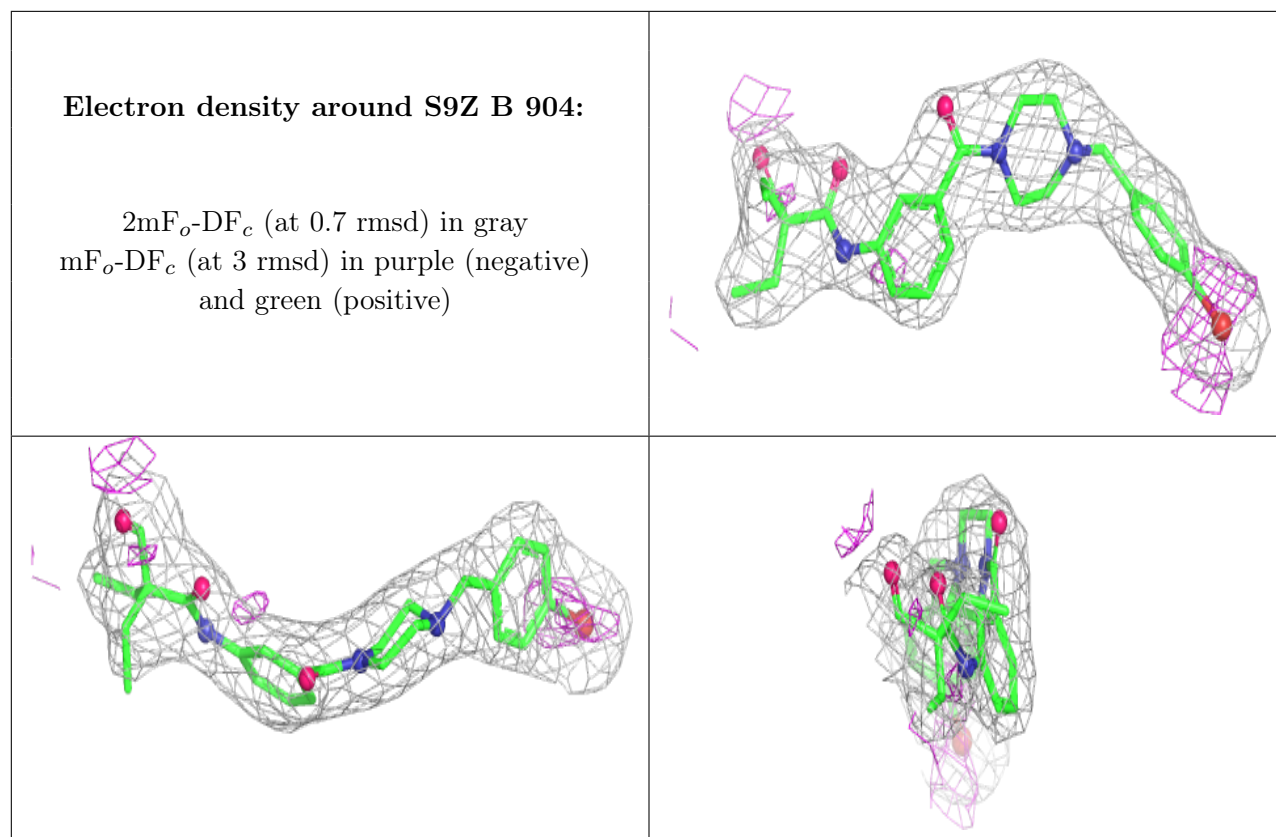
6.4 Ligands [i](#)

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
4	GOL	B	903	6/6	0.63	0.57	83,89,102,102	0
4	GOL	A	903	6/6	0.75	0.54	71,80,98,99	0
3	PO4	A	902	5/5	0.94	0.27	101,110,123,124	0
3	PO4	B	902	5/5	0.94	0.34	91,94,113,114	0
5	S9Z	A	904	32/32	0.94	0.20	53,69,79,109	0
5	S9Z	B	904	32/32	0.95	0.16	45,67,76,93	0
2	TMO	A	901	5/5	0.97	0.38	57,62,70,71	0
2	TMO	B	901	5/5	0.98	0.29	61,64,72,74	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.