



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:25 PM UTC

PDB ID : 8TYH / pdb_00008tyh
Title : Plasmodium vivax PMX
Authors : Hodder, A.N.; Scally, S.W.; Cowman, A.F.
Deposited on : 2023-08-25
Resolution : 1.83 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

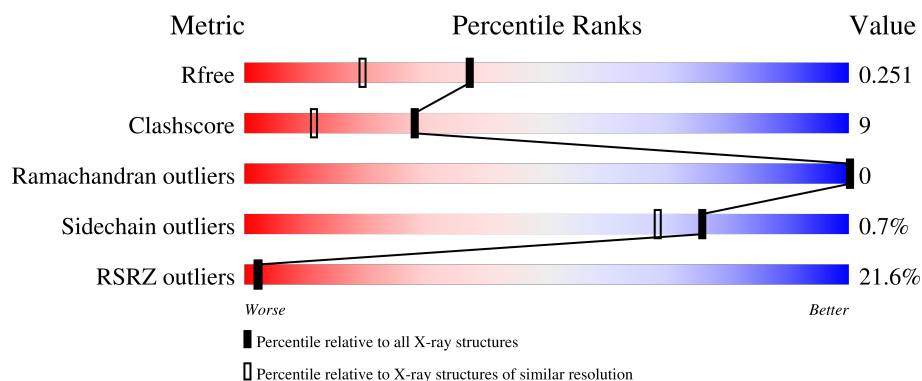
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	538	13% 51% 11% 38%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2834 atoms, of which 9 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.

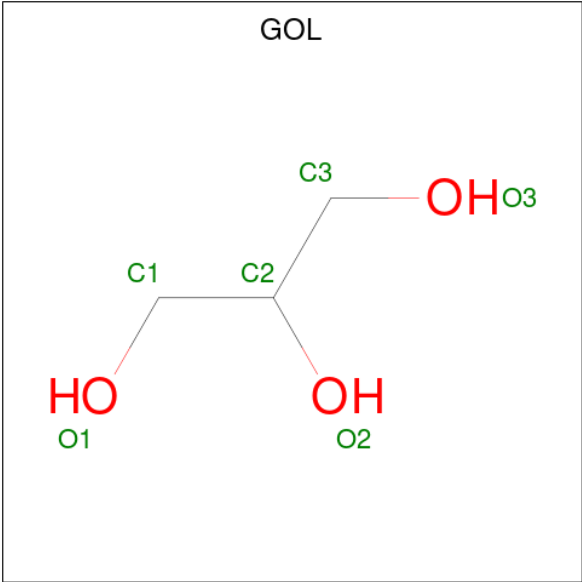
- Molecule 1 is a protein called Aspartyl protease, putative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	333	2651	1709	9	413	506	14	0	2	0

There are 19 discrepancies between the modelled and reference sequences:

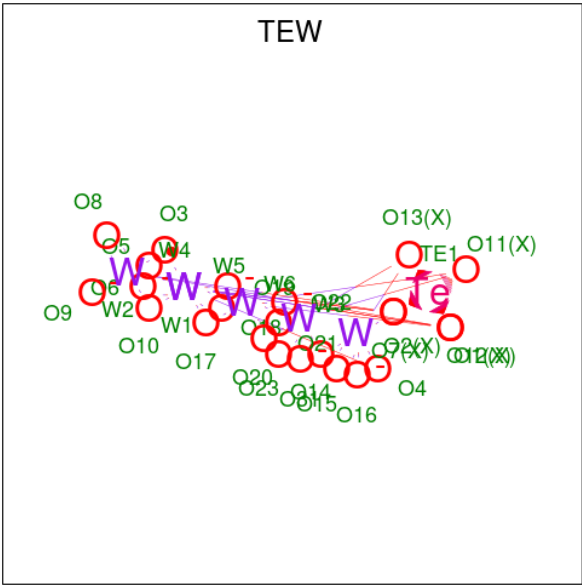
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	expression tag	UNP A5KAC3
A	26	THR	-	expression tag	UNP A5KAC3
A	546	LEU	-	expression tag	UNP A5KAC3
A	547	GLU	-	expression tag	UNP A5KAC3
A	548	ASN	-	expression tag	UNP A5KAC3
A	549	LEU	-	expression tag	UNP A5KAC3
A	550	TYR	-	expression tag	UNP A5KAC3
A	551	PHE	-	expression tag	UNP A5KAC3
A	552	GLN	-	expression tag	UNP A5KAC3
A	553	GLY	-	expression tag	UNP A5KAC3
A	554	ASP	-	expression tag	UNP A5KAC3
A	555	TYR	-	expression tag	UNP A5KAC3
A	556	LYS	-	expression tag	UNP A5KAC3
A	557	ASP	-	expression tag	UNP A5KAC3
A	558	ASP	-	expression tag	UNP A5KAC3
A	559	ASP	-	expression tag	UNP A5KAC3
A	560	ASP	-	expression tag	UNP A5KAC3
A	561	LYS	-	expression tag	UNP A5KAC3
A	562	HIS	-	expression tag	UNP A5KAC3

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 3 is 6-tungstotellurate(VI) (CCD ID: TEW) (formula: $\text{O}_{24}\text{TeW}_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	O	Te	W	0	0
			31	24	1	6		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	132	Total	O	0	0
			132	132		

- Molecule 1: Aspartyl protease, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	136.30Å 136.30Å 45.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.82 – 1.83 42.82 – 1.83	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.82-1.83) 100.0 (42.82-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.228 , 0.251 0.228 , 0.251	Depositor DCC
R_{free} test set	2188 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2834	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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, TEW, NAG

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	0.09	0/2715	0.27	0/3678

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	2642	9	2562	46	0
2	A	6	0	8	1	0
3	A	31	0	0	2	0
4	A	14	0	13	0	0
5	A	132	0	0	3	0
All	All	2825	9	2583	47	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 9.

All (47) 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:210:ASP:HB2	1:A:322:ILE:HG22	1.60	0.84
1:A:434:MET:HA	1:A:434:MET:HE2	1.62	0.80
1:A:429:MET:HB2	1:A:434:MET:HG2	1.74	0.68
1:A:422:THR:HG22	1:A:510:MET:HE1	1.76	0.66
1:A:357:GLN:NE2	1:A:375:GLY:HA2	2.11	0.65
1:A:407:GLU:OE1	1:A:407:GLU:N	2.23	0.64
3:A:702:TEW:W2	3:A:702:TEW:O9	1.43	0.62
1:A:425:SER:HB2	1:A:507:ILE:HD12	1.81	0.62
1:A:434:MET:HA	1:A:434:MET:CE	2.30	0.61
1:A:395:TYR:CE1	1:A:498:LYS:HE2	2.39	0.58
1:A:210:ASP:O	1:A:211:SER:OG	2.18	0.56
1:A:264:ARG:HB3	2:A:701:GOL:H32	1.87	0.55
1:A:306:GLU:OE2	5:A:801:HOH:O	2.18	0.55
1:A:267:PHE:N	3:A:702:TEW:O18	2.36	0.55
1:A:470:ILE:HG23	1:A:513:TYR:CZ	2.45	0.52
1:A:226:ILE:HG13	1:A:228:PRO:HD3	1.91	0.51
1:A:349:SER:O	1:A:352:LYS:HE2	2.10	0.51
1:A:241:THR:HG21	1:A:304:LEU:HB3	1.92	0.51
1:A:199:ASN:OD1	1:A:353:ASN:HB2	2.10	0.51
1:A:240:VAL:HA	1:A:305:VAL:HB	1.92	0.50
1:A:357:GLN:HE21	1:A:375:GLY:HA2	1.75	0.50
1:A:422:THR:HG22	1:A:510:MET:CE	2.42	0.49
1:A:249:CYS:O	1:A:252:VAL:HG22	2.12	0.49
1:A:366:ASP:OD1	1:A:366:ASP:N	2.40	0.49
1:A:461:ILE:HB	1:A:472:LEU:HB2	1.94	0.49
1:A:389:PRO:HA	1:A:527:MET:HG2	1.95	0.49
1:A:422:THR:CG2	1:A:510:MET:HE1	2.42	0.49
1:A:334:GLU:HG3	5:A:874:HOH:O	2.14	0.48
1:A:283:GLY:HA3	1:A:304:LEU:O	2.14	0.48
1:A:493:ASP:OD1	1:A:493:ASP:N	2.36	0.48
1:A:208:LEU:HB2	1:A:210:ASP:OD1	2.14	0.47
1:A:428:THR:HA	1:A:490:MET:O	2.15	0.47
1:A:251:LYS:HD3	5:A:920:HOH:O	2.15	0.46
1:A:353:ASN:HD22	1:A:353:ASN:H	1.63	0.45
1:A:434:MET:HE2	1:A:437:PHE:HB3	1.98	0.45
1:A:202:LEU:HD12	1:A:202:LEU:N	2.32	0.43
1:A:425:SER:HB2	1:A:507:ILE:CD1	2.46	0.43
1:A:483:GLU:O	1:A:483:GLU:HG2	2.19	0.42
1:A:206:LYS:HG2	1:A:208:LEU:HD23	2.02	0.42
1:A:201:PHE:CZ	1:A:373:VAL:HB	2.55	0.42
1:A:372:LEU:HD12	1:A:372:LEU:N	2.35	0.41
1:A:378:LYS:NZ	1:A:383:GLY:O	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:MET:HG2	1:A:394:TYR:CE2	2.56	0.41
1:A:272:LEU:O	1:A:282:SER:HA	2.21	0.41
1:A:411:CYS:HA	1:A:412:CYS:HA	1.74	0.41
1:A:434:MET:HG3	1:A:491:GLN:HB3	2.02	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	331/538 (62%)	323 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	295/459 (64%)	293 (99%)	2 (1%)	76	68

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	434	MET
1	A	493	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	ASN
1	A	357	GLN
1	A	481	ASN
1	A	500	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 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	TEW	A	702	-	24,42,42	1.28	2 (8%)	12,129,129	2.27	5 (41%)
4	NAG	A	703	1	14,14,15	0.28	0	17,19,21	0.40	0
2	GOL	A	701	-	5,5,5	0.96	0	5,5,5	1.09	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	NAG	A	703	1	-	0/6/23/26	0/1/1/1
2	GOL	A	701	-	-	1/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	TEW	W2-O9	-3.48	1.43	2.09
3	A	702	TEW	W6-O14	-2.48	1.74	1.97

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	TEW	O11-TE1-O2	4.27	98.50	94.65
3	A	702	TEW	O11-TE1-O7	-4.03	91.02	94.65
3	A	702	TEW	O13-TE1-O2	-3.13	81.51	85.21
3	A	702	TEW	O1-TE1-O2	-2.26	82.54	85.21
3	A	702	TEW	O7-TE1-O2	2.13	96.57	94.65

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	GOL	C1-C2-C3-O3

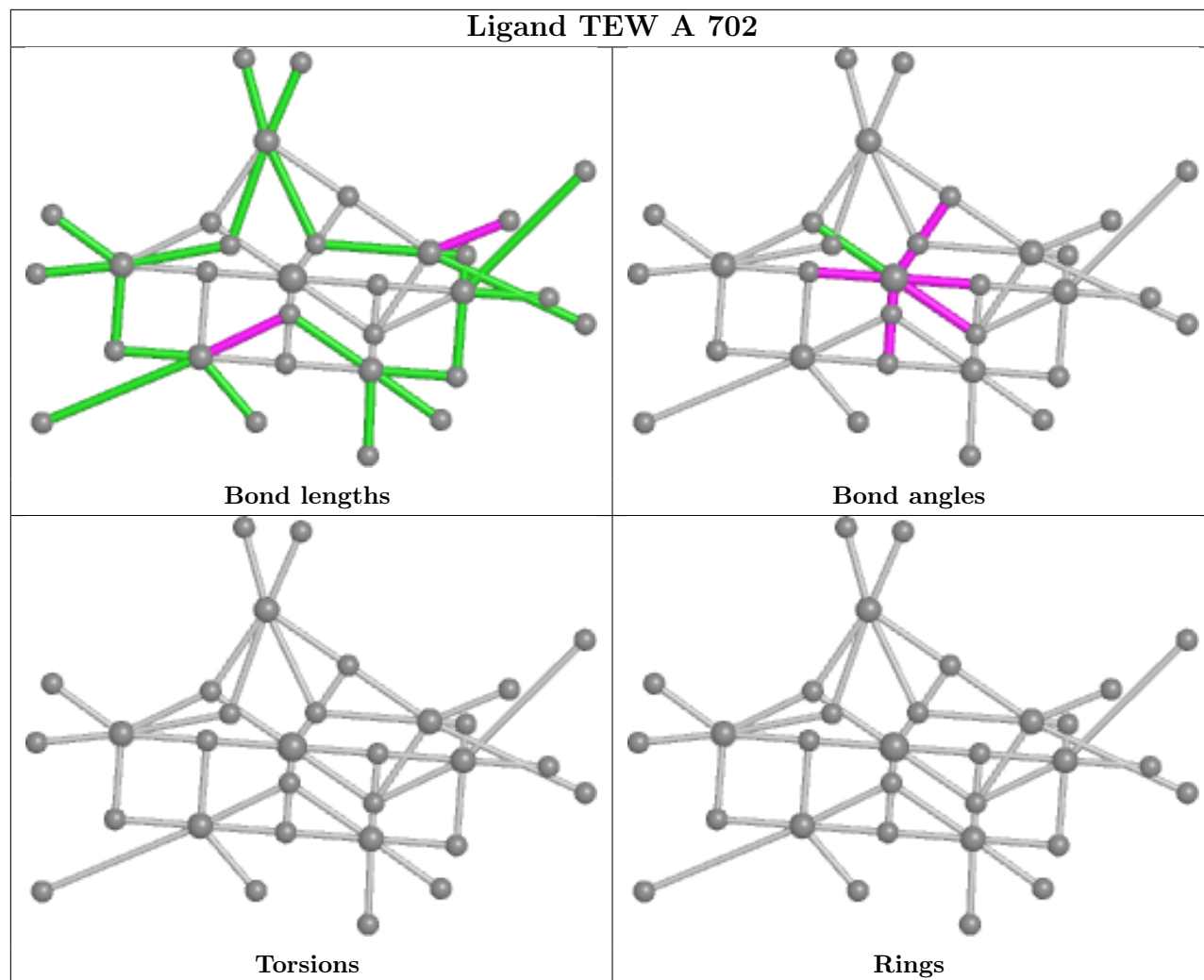
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	TEW	2	0
2	A	701	GOL	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	333/538 (61%)	1.19	72 (21%) 2 2	25, 39, 74, 117	2 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	494	VAL	9.9
1	A	536	ALA	8.1
1	A	321	TYR	5.7
1	A	495	PRO	5.6
1	A	200	VAL	5.2
1	A	535	ALA	5.1
1	A	276	PHE	4.8
1	A	492	ILE	4.8
1	A	277	GLY	4.8
1	A	275	VAL	4.7
1	A	493	ASP	4.5
1	A	451	TYR	4.4
1	A	278	SER	4.3
1	A	309	SER	4.2
1	A	523	GLY	4.1
1	A	198	GLU	4.1
1	A	316	ASP	4.0
1	A	512	HIS	4.0
1	A	273	HIS	3.7
1	A	365	GLU	3.7
1	A	522	GLY	3.5
1	A	521	ALA	3.5
1	A	247	GLU	3.5
1	A	337	SER	3.4
1	A	367	ASN	3.3
1	A	484	SER	3.3
1	A	280	SER	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	448	GLU	3.2
1	A	386	TYR	3.2
1	A	377	SER	3.2
1	A	366	ASP	3.0
1	A	317	ASN	3.0
1	A	480	LEU	3.0
1	A	364	PRO	3.0
1	A	251	LYS	2.9
1	A	467	ASP	2.9
1	A	353	ASN	2.8
1	A	375	GLY	2.8
1	A	207	HIS	2.8
1	A	318	ILE	2.7
1	A	499	ASN	2.7
1	A	379	SER	2.6
1	A	407	GLU	2.6
1	A	483	GLU	2.6
1	A	281	ILE	2.5
1	A	201	PHE	2.4
1	A	322	ILE	2.4
1	A	432	ALA	2.4
1	A	482	GLU	2.4
1	A	268	ILE	2.4
1	A	376	VAL	2.4
1	A	431	SER	2.3
1	A	496	SER	2.3
1	A	534	ARG	2.3
1	A	439	ASP	2.3
1	A	271[A]	ASN	2.3
1	A	378	LYS	2.3
1	A	532	LYS	2.3
1	A	466	GLY	2.2
1	A	507	ILE	2.2
1	A	213	PHE	2.2
1	A	469	VAL	2.2
1	A	425	SER	2.2
1	A	209	ARG	2.2
1	A	440	VAL	2.1
1	A	279	GLY	2.1
1	A	211	SER	2.1
1	A	282	SER	2.1
1	A	412	CYS	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	206	LYS	2.1
1	A	374	GLY	2.0
1	A	245	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

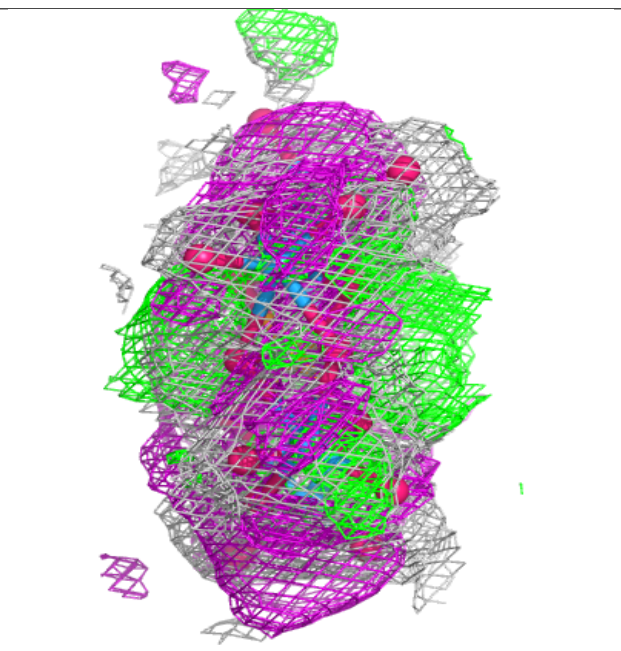
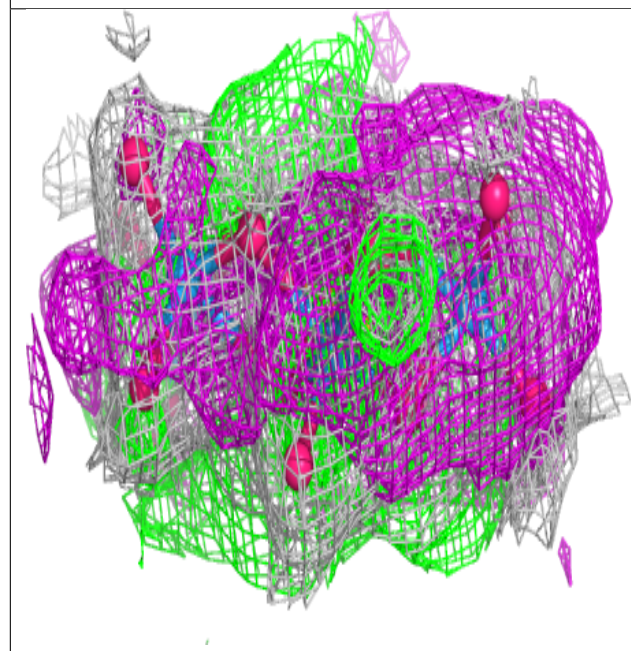
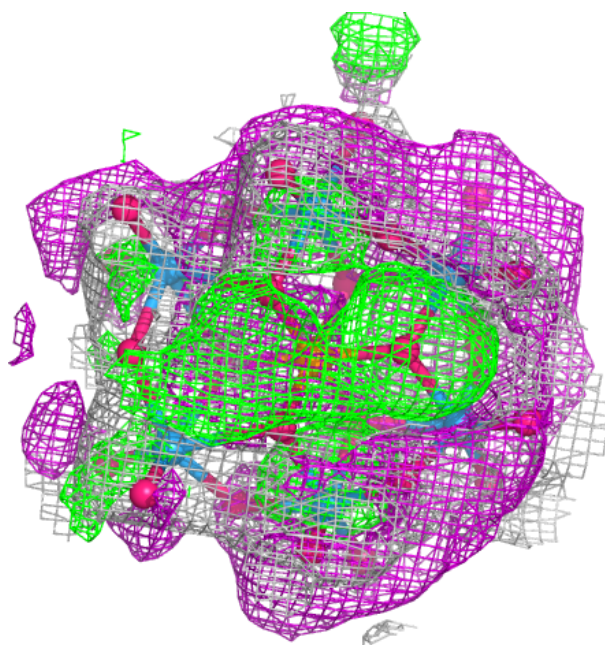
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	703	14/15	0.57	0.21	39,41,50,55	0
2	GOL	A	701	6/6	0.84	0.17	31,33,48,51	0
3	TEW	A	702	31/31	0.95	0.19	0,82,147,171	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 TEW A 702:

$2mF_o-DF_c$ (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.