



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:53 PM UTC

PDB ID : 8Y97 / pdb_00008y97
Title : Crystal structure of a heterooligomeric aminotransferase from *Serratia* sp. ATCC 39006, PMP-bound form
Authors : Pramono, H.; Yoshida, A.; Nishiyama, M.
Deposited on : 2024-02-06
Resolution : 2.83 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

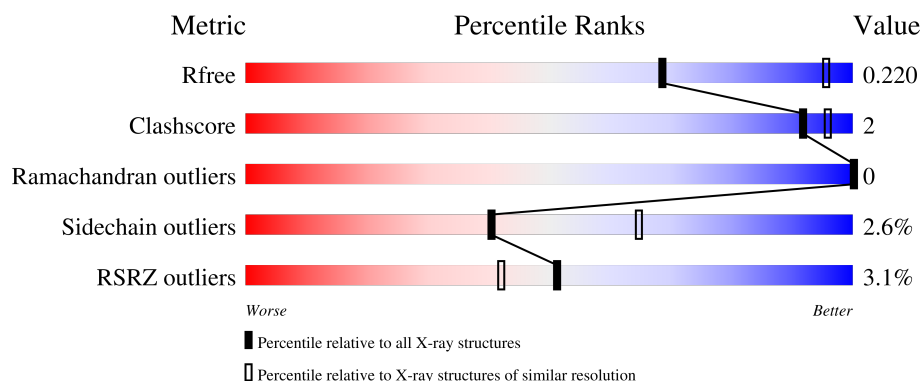
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	443	3% 91% 6% .
1	B	443	2% 90% 6% .
2	C	218	4% 85% . 13%
2	D	218	4% 83% . . 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9733 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 DegT/DnrJ/EryC1/StrS family aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	1	0
			3369	2160	578	614	17			
1	B	428	Total	C	N	O	S	0	0	0
			3370	2160	576	617	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	438	HIS	-	expression tag	UNP A0A2I5TIB4
A	439	HIS	-	expression tag	UNP A0A2I5TIB4
A	440	HIS	-	expression tag	UNP A0A2I5TIB4
A	441	HIS	-	expression tag	UNP A0A2I5TIB4
A	442	HIS	-	expression tag	UNP A0A2I5TIB4
A	443	HIS	-	expression tag	UNP A0A2I5TIB4
B	438	HIS	-	expression tag	UNP A0A2I5TIB4
B	439	HIS	-	expression tag	UNP A0A2I5TIB4
B	440	HIS	-	expression tag	UNP A0A2I5TIB4
B	441	HIS	-	expression tag	UNP A0A2I5TIB4
B	442	HIS	-	expression tag	UNP A0A2I5TIB4
B	443	HIS	-	expression tag	UNP A0A2I5TIB4

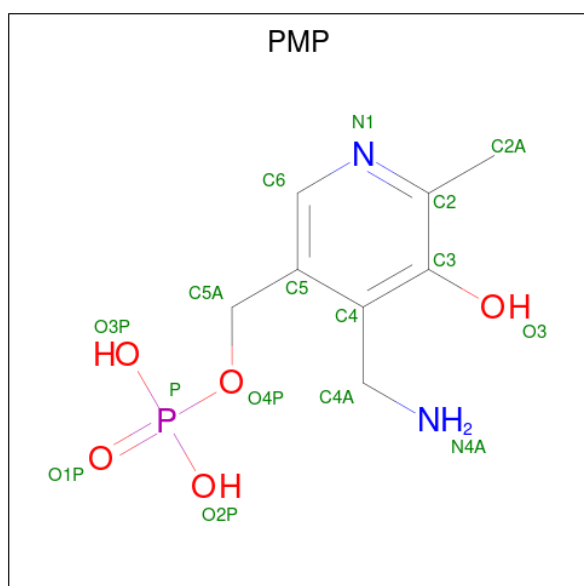
- Molecule 2 is a protein called DegT/DnrJ/EryC1/StrS aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	189	Total	C	N	O	S	0	0	0
			1455	938	243	269	5			
2	D	189	Total	C	N	O	S	0	0	0
			1459	942	242	270	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	initiating methionine	UNP A0A2I5T5Y7
C	1	GLY	-	expression tag	UNP A0A2I5T5Y7
C	212	HIS	-	expression tag	UNP A0A2I5T5Y7
C	213	HIS	-	expression tag	UNP A0A2I5T5Y7
C	214	HIS	-	expression tag	UNP A0A2I5T5Y7
C	215	HIS	-	expression tag	UNP A0A2I5T5Y7
C	216	HIS	-	expression tag	UNP A0A2I5T5Y7
C	217	HIS	-	expression tag	UNP A0A2I5T5Y7
D	0	MET	-	initiating methionine	UNP A0A2I5T5Y7
D	1	GLY	-	expression tag	UNP A0A2I5T5Y7
D	212	HIS	-	expression tag	UNP A0A2I5T5Y7
D	213	HIS	-	expression tag	UNP A0A2I5T5Y7
D	214	HIS	-	expression tag	UNP A0A2I5T5Y7
D	215	HIS	-	expression tag	UNP A0A2I5T5Y7
D	216	HIS	-	expression tag	UNP A0A2I5T5Y7
D	217	HIS	-	expression tag	UNP A0A2I5T5Y7

- Molecule 3 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (CCD ID: PMP) (formula: $C_8H_{13}N_2O_5P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			16	8	2	5	1		
3	B	1	Total	C	N	O	P	0	0
			16	8	2	5	1		

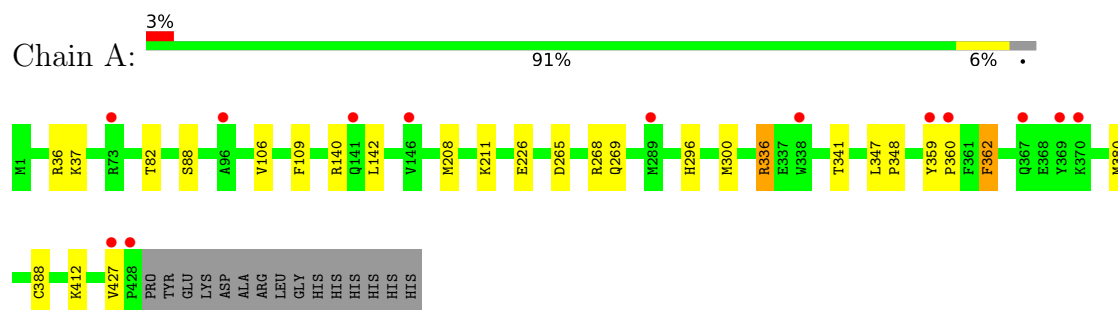
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total 12	O 12	0	0
4	C	10	Total 10	O 10	0	0
4	B	18	Total 18	O 18	0	0
4	D	8	Total 8	O 8	0	0

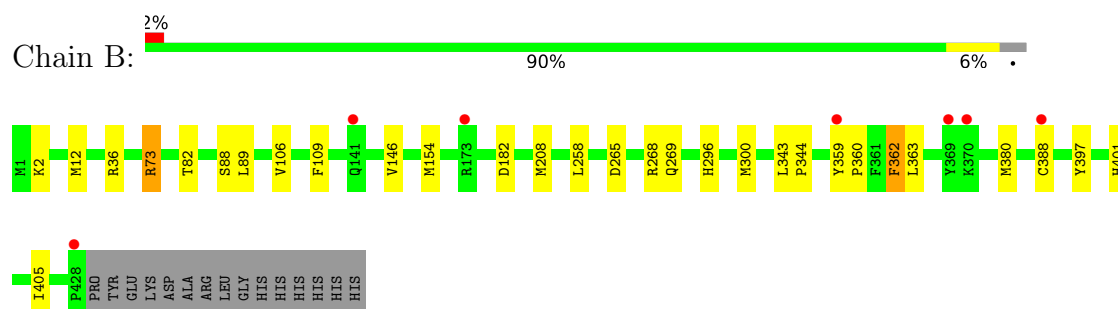
3 Residue-property plots [i](#)

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.

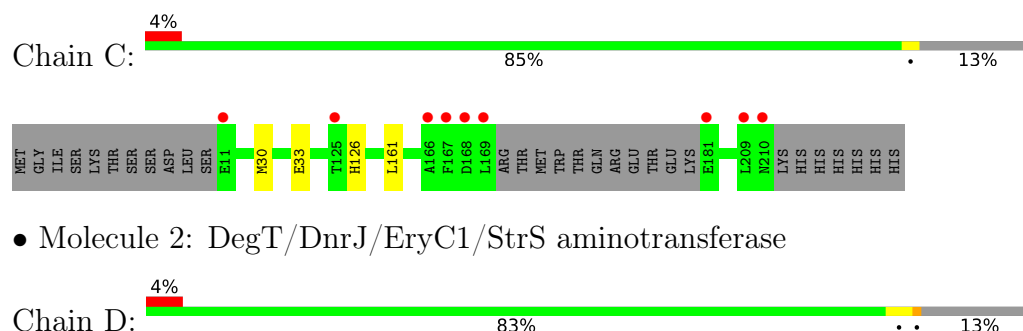
- Molecule 1: DegT/DnrJ/EryC1/StrS family aminotransferase



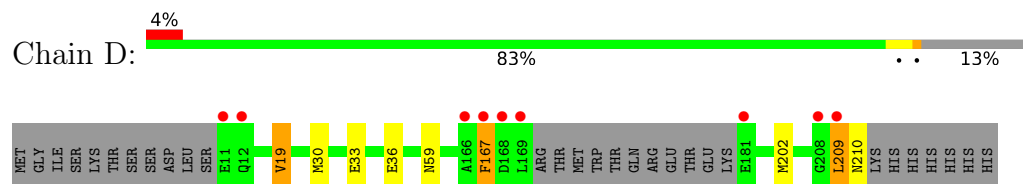
- Molecule 1: DegT/DnrJ/EryC1/StrS family aminotransferase



- Molecule 2: DegT/DnrJ/EryC1/StrS aminotransferase



- Molecule 2: DegT/DnrJ/EryC1/StrS aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.47Å 180.93Å 183.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.63 – 2.83 48.63 – 2.83	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.63-2.83) 100.0 (48.63-2.83)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.228 , 0.257 (Not available) , 0.220	Depositor DCC
R_{free} test set	2056 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	58.2	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9733	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.55% 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: PMP

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	0.46	0/3448	0.88	1/4669 (0.0%)
1	B	0.46	0/3449	0.89	1/4670 (0.0%)
2	C	0.45	0/1481	0.83	0/2003
2	D	0.45	0/1486	0.85	0/2010
All	All	0.46	0/9864	0.87	2/13352 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	362	PHE	CA-CB-CG	5.35	119.15	113.80
1	A	362	PHE	CA-CB-CG	5.16	118.96	113.80

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	3369	0	3357	10	0
1	B	3370	0	3361	15	0
2	C	1455	0	1461	1	0
2	D	1459	0	1462	5	0
3	A	16	0	11	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	16	0	11	1	0
4	A	12	0	0	0	0
4	B	18	0	0	0	0
4	C	10	0	0	0	0
4	D	8	0	0	0	0
All	All	9733	0	9663	31	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 2.

All (31) 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)
2:D:209:LEU:O	2:D:210:ASN:C	2.41	0.63
1:B:182:ASP:OD2	3:B:501:PMP:H2A3	2.02	0.59
1:A:336:ARG:HD2	1:A:388:CYS:SG	2.43	0.58
1:A:211:LYS:HZ1	3:A:501:PMP:HNA1	1.58	0.52
2:D:30:MET:HB2	2:D:33:GLU:HB2	1.92	0.51
2:C:30:MET:HB2	2:C:33:GLU:HB2	1.93	0.51
1:B:359:TYR:HB3	1:B:360:PRO:HD3	1.94	0.49
1:B:265:ASP:OD1	1:B:268:ARG:NH1	2.46	0.49
1:A:359:TYR:HB3	1:A:360:PRO:HD3	1.95	0.48
1:A:265:ASP:OD1	1:A:268:ARG:NH1	2.47	0.48
1:B:89:LEU:HD22	1:B:154:MET:HE2	1.98	0.46
1:B:82:THR:HG21	1:B:88:SER:HB3	1.99	0.45
1:B:300:MET:CE	1:B:388:CYS:SG	3.05	0.45
2:D:167:PHE:N	2:D:167:PHE:CD1	2.85	0.45
2:D:19:VAL:HG21	2:D:202:MET:HB2	1.99	0.45
1:A:300:MET:CE	1:A:388:CYS:SG	3.05	0.44
1:A:82:THR:HG21	1:A:88:SER:HB3	2.00	0.44
1:A:269:GLN:NE2	1:A:296:HIS:O	2.51	0.43
1:B:12:MET:HE1	1:B:397:TYR:HE1	1.84	0.43
1:A:109:PHE:CD1	1:A:380:MET:HE1	2.53	0.43
1:B:73:ARG:HD2	1:B:258:LEU:HD11	2.00	0.43
1:B:109:PHE:CD1	1:B:380:MET:HE1	2.54	0.43
1:B:269:GLN:NE2	1:B:296:HIS:O	2.52	0.42
1:A:109:PHE:CG	1:A:380:MET:HE1	2.55	0.42
1:A:347:LEU:HB2	1:A:348:PRO:HD3	2.02	0.41
1:B:343:LEU:N	1:B:344:PRO:HD2	2.35	0.41
1:B:109:PHE:CG	1:B:380:MET:HE1	2.56	0.41
1:B:343:LEU:N	1:B:344:PRO:CD	2.83	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:59:ASN:OD1	2:D:59:ASN:C	2.64	0.41
1:B:401:HIS:O	1:B:405:ILE:HG12	2.21	0.40
1:B:359:TYR:CD1	1:B:359:TYR:C	3.00	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	427/443 (96%)	417 (98%)	10 (2%)	0	100	100
1	B	426/443 (96%)	415 (97%)	11 (3%)	0	100	100
2	C	185/218 (85%)	176 (95%)	9 (5%)	0	100	100
2	D	185/218 (85%)	176 (95%)	9 (5%)	0	100	100
All	All	1223/1322 (92%)	1184 (97%)	39 (3%)	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	327/369 (89%)	315 (96%)	12 (4%)	30	55
1	B	354/369 (96%)	346 (98%)	8 (2%)	44	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	156/192 (81%)	154 (99%)	2 (1%)	61	79
2	D	157/192 (82%)	153 (98%)	4 (2%)	42	66
All	All	994/1122 (89%)	968 (97%)	26 (3%)	40	65

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	37	LYS
1	A	106	VAL
1	A	140	ARG
1	A	142	LEU
1	A	208	MET
1	A	226	GLU
1	A	336	ARG
1	A	341	THR
1	A	362	PHE
1	A	412	LYS
1	A	427	VAL
2	C	126	HIS
2	C	161	LEU
1	B	2	LYS
1	B	36	ARG
1	B	73	ARG
1	B	106	VAL
1	B	146	VAL
1	B	208	MET
1	B	362	PHE
1	B	363	LEU
2	D	19	VAL
2	D	36	GLU
2	D	167	PHE
2	D	209	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	56	GLN
1	A	269	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	350	GLN
2	C	72	GLN
2	C	83	GLN
2	C	89	GLN
2	C	126	HIS
2	C	150	ASN
1	B	50	GLN
1	B	56	GLN
1	B	72	GLN
1	B	174	GLN
1	B	346	HIS
1	B	350	GLN
2	D	72	GLN
2	D	100	HIS
2	D	120	ASN
2	D	150	ASN

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](#)

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
3	PMP	A	501	-	16,16,16	0.41	0	22,23,23	0.58	0
3	PMP	B	501	-	16,16,16	0.41	0	22,23,23	0.60	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
3	PMP	A	501	-	-	1/8/8/8	0/1/1/1
3	PMP	B	501	-	-	1/8/8/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

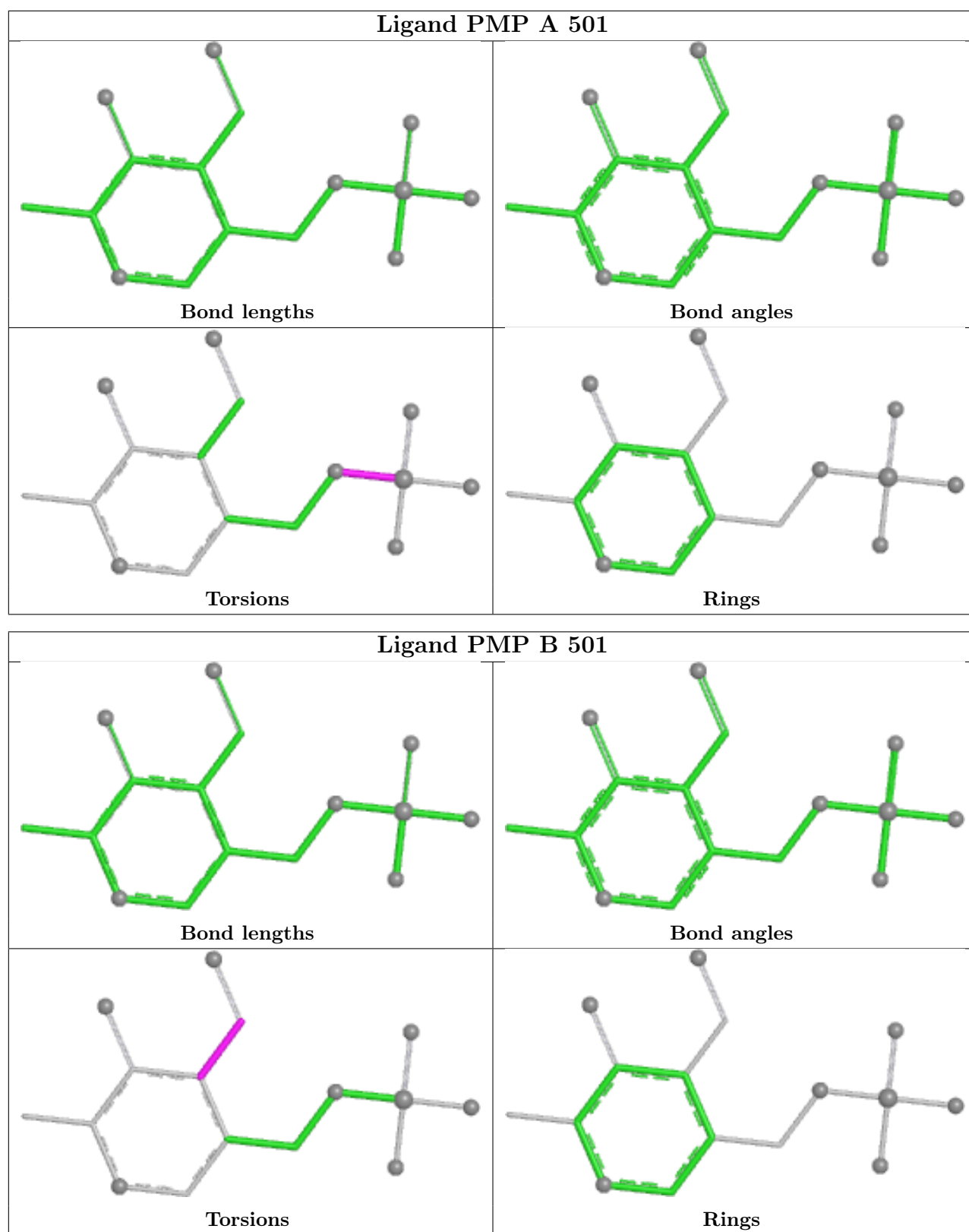
Mol	Chain	Res	Type	Atoms
3	B	501	PMP	C5-C4-C4A-N4A
3	A	501	PMP	C5A-O4P-P-O1P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	PMP	1	0
3	B	501	PMP	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	428/443 (96%)	0.39	13 (3%) 52 43	29, 58, 85, 106	1 (0%)
1	B	428/443 (96%)	0.00	7 (1%) 70 64	34, 50, 70, 111	0
2	C	189/218 (86%)	0.24	9 (4%) 35 29	38, 54, 86, 110	0
2	D	189/218 (86%)	0.43	9 (4%) 35 29	39, 59, 86, 105	0
All	All	1234/1322 (93%)	0.24	38 (3%) 51 42	29, 55, 83, 111	1 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	169	LEU	6.0
1	B	428	PRO	5.2
1	A	141	GLN	4.7
1	A	73[A]	ARG	4.6
2	C	168	ASP	4.5
2	C	167	PHE	4.3
2	C	169	LEU	4.1
1	A	428	PRO	4.0
2	D	167	PHE	3.6
2	D	11	GLU	3.5
2	D	181	GLU	3.4
1	A	367	GLN	3.1
1	A	369	TYR	3.0
2	C	181	GLU	2.9
1	B	141	GLN	2.8
2	D	166	ALA	2.8
2	C	166	ALA	2.8
1	A	370	LYS	2.7
1	A	360	PRO	2.6
2	C	209	LEU	2.6
1	B	370	LYS	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	168	ASP	2.4
1	A	146	VAL	2.4
2	C	11	GLU	2.4
1	A	338	TRP	2.3
2	C	125	THR	2.3
1	B	369	TYR	2.3
1	B	388	CYS	2.2
1	A	427	VAL	2.2
1	A	96	ALA	2.2
1	A	289	MET	2.2
1	A	359	TYR	2.2
2	D	209	LEU	2.1
1	B	173	ARG	2.1
2	D	12	GLN	2.1
2	C	210	ASN	2.1
1	B	359	TYR	2.1
2	D	208	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

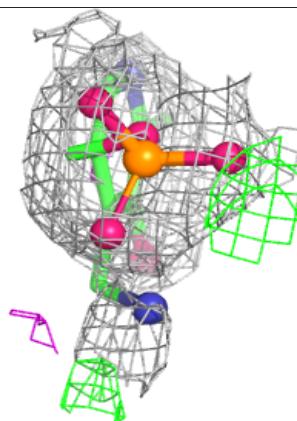
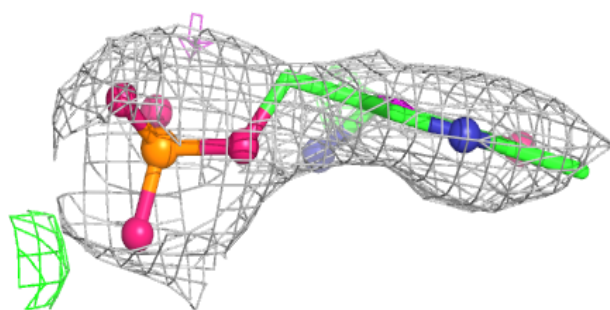
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PMP	A	501	16/16	0.90	0.15	57,68,70,71	0
3	PMP	B	501	16/16	0.93	0.12	41,49,51,51	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.

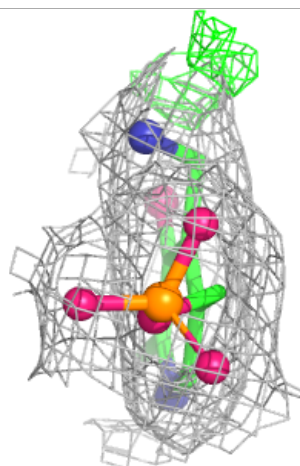
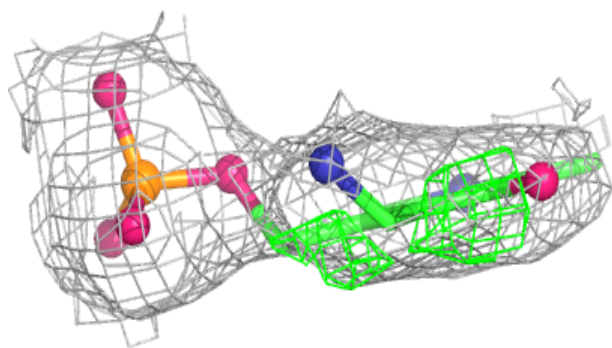
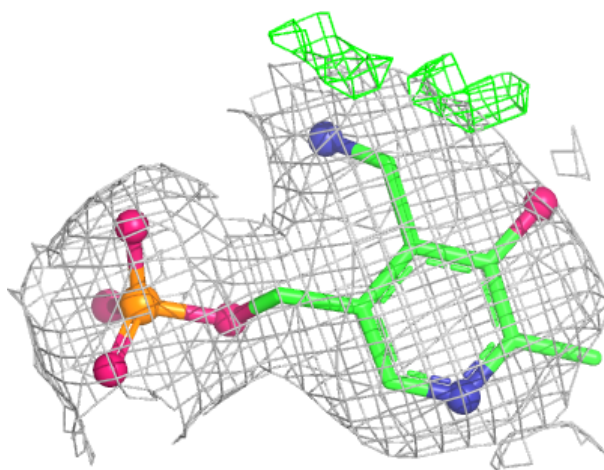
Electron density around PMP A 501:

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



Electron density around PMP B 501:

$2mF_o-DF_c$ (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.