

Full wwPDB X-ray Structure Validation Report (i)

Nov 20, 2023 – 09:25 PM JST

PDB ID	:	7DLY
Title	:	Crystal structure of Arabidopsis ACS7 mutant in complex with PPG
Authors	:	Hao, B.; Zhang, Y.; Li, X.; Rao, Z.
Deposited on		
Resolution	:	2.94 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 (i) 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:

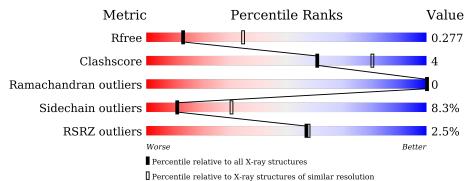
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.94 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$		
R _{free}	130704	2969 (2.98-2.90)		
Clashscore	141614	3218 (2.98-2.90)		
Ramachandran outliers	138981	3122 (2.98-2.90)		
Sidechain outliers	138945	3124 (2.98-2.90)		
RSRZ outliers	127900	2902 (2.98-2.90)		

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 <=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	А	447	2% 74%	14%	•	11%
1	В	447	75%	14%	•	10%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6428 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	400	Total	С	Ν	0	\mathbf{S}	0	0	0
	I A	400	3186	2010	554	606	16	0	0	0
1	В	401	Total	С	Ν	0	S	0	0	0
	D	401	3190	2011	555	608	16	0	0	0

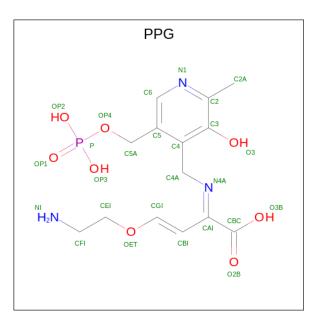
• Molecule 1 is a protein called 1-aminocyclopropane-1-carboxylate synthase 7.

Residue	Modelled	Actual	Comment	Reference
97	TYR	PHE	engineered mutation	UNP Q9STR4
98	GLY	GLN	engineered mutation	UNP Q9STR4
99	ASN	ASP	engineered mutation	UNP Q9STR4
100	PHE	TYR	engineered mutation	UNP Q9STR4
101	ARG	HIS	engineered mutation	UNP Q9STR4
103	GLY	LEU	engineered mutation	UNP Q9STR4
104	GLU	LYS	engineered mutation	UNP Q9STR4
97	TYR	PHE	engineered mutation	UNP Q9STR4
98	GLY	GLN	engineered mutation	UNP Q9STR4
99	ASN	ASP	engineered mutation	UNP Q9STR4
100	PHE	TYR	engineered mutation	UNP Q9STR4
101	ARG	HIS	engineered mutation	UNP Q9STR4
103	GLY	LEU	engineered mutation	UNP Q9STR4
104	GLU	LYS	engineered mutation	UNP Q9STR4
	97 98 99 100 101 103 104 97 98 99 100 101 103	97 TYR 98 GLY 99 ASN 100 PHE 101 ARG 103 GLY 104 GLU 97 TYR 98 GLY 99 ASN 101 ARG 103 GLY 104 GLU 97 TYR 98 GLY 99 ASN 100 PHE 101 ARG 103 GLY	97 TYR PHE 98 GLY GLN 99 ASN ASP 100 PHE TYR 101 ARG HIS 103 GLY LEU 104 GLU LYS 97 TYR PHE 98 GLY GLN 99 ASN ASP 101 ARG HIS 103 GLY LEU 104 GLY LYS 97 TYR PHE 98 GLY GLN 99 ASN ASP 100 PHE TYR 101 ARG HIS 103 GLY LEU	97TYRPHEengineered mutation98GLYGLNengineered mutation99ASNASPengineered mutation100PHETYRengineered mutation101ARGHISengineered mutation103GLYLEUengineered mutation104GLULYSengineered mutation97TYRPHEengineered mutation98GLYGLNengineered mutation99ASNASPengineered mutation100PHETYRengineered mutation101ARGHISengineered mutation103GLYLEUengineered mutation

There are 14 discrepancies between the modelled and reference sequences:

• Molecule 2 is $(2E,3E)-4-(2-aminoethoxy)-2-[({3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}methyl)imino]but-3-enoic acid (three-letter code: PPG) (formula: C₁₄H₂₀N₃O₈P) (labeled as "Ligand of Interest" by depositor).$



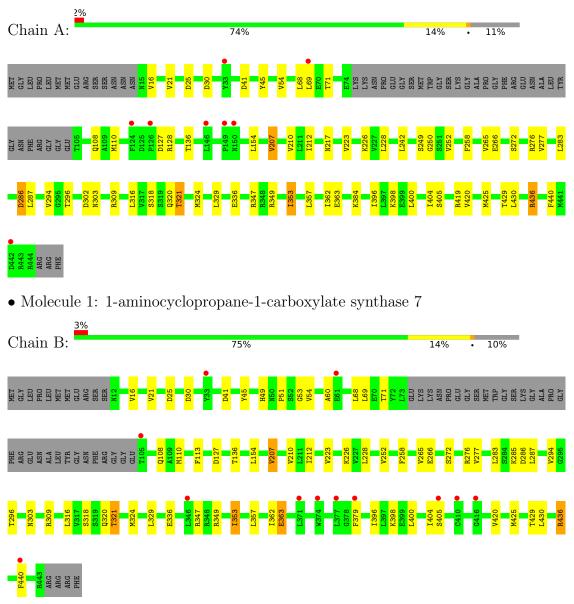


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	٨	1	1 Total C N O P		0	0				
	Z A		26	14	3	8	1	0	0	
0	D	1	Total	С	Ν	Ο	Р	0	0	
	2 B	В І		14	3	8	1	0	0	



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: 1-aminocyclopropane-1-carboxylate synthase 7



4 Data and refinement statistics (i)

Property	Value	Source
Space group	Н 3	Depositor
Cell constants a, b, c, α , β , γ	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Depositor
Resolution (Å)	$\begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	Depositor EDS
% Data completeness	95.5 (47.16-2.94)	Depositor
(in resolution range)	95.5 (47.47-2.94)	EDS
R _{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.80 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
D D	0.224 , 0.277	Depositor
R, R_{free}	0.225 , 0.277	DCC
R_{free} test set	1947 reflections $(9.73%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	111.5	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27,48.1	EDS
L-test for $twinning^2$	$< L > = 0.53, < L^2 > = 0.36$	Xtriage
Estimated twinning fraction	$\begin{array}{c} 0.000 \; {\rm for} \; -2/3^{*}{\rm h}-1/3^{*}{\rm k}-4/3^{*}{\rm l}, -1/3^{*}{\rm h}-2/3^{*}{\rm k}+\\ & 4/3^{*}{\rm l}, -1/3^{*}{\rm h}+1/3^{*}{\rm k}+1/3^{*}{\rm l}\\ 0.000 \; {\rm for} \; -{\rm h}, 1/3^{*}{\rm h}-1/3^{*}{\rm k}-4/3^{*}{\rm l}, -1/3^{*}{\rm h}-2/3^{*}{\rm k}\\ & +1/3^{*}{\rm l}\\ 0.000 \; {\rm for} \; -1/3^{*}{\rm h}+1/3^{*}{\rm k}+4/3^{*}{\rm l}, -{\rm k}, 2/3^{*}{\rm h}+1/\\ & 3^{*}{\rm k}+1/3^{*}{\rm l}\\ 0.000 \; {\rm for} \; -{\rm h}, 2/3^{*}{\rm h}+1/3^{*}{\rm k}+4/3^{*}{\rm l}, -{\rm k}, 2/3^{*}{\rm h}+2/3\\ & {\rm k}-1/3^{*}{\rm l}\\ 0.000 \; {\rm for} \; -1/3^{*}{\rm h}-2/3^{*}{\rm k}+4/3^{*}{\rm l}, -2/3^{*}{\rm h}-1/3^{*}{\rm k}-\\ & 4/3^{*}{\rm l}, 1/3^{*}{\rm h}-1/3^{*}{\rm k}-1/3^{*}{\rm l}\\ 0.000 \; {\rm for} \; 1/3^{*}{\rm h}+2/3^{*}{\rm k}-4/3^{*}{\rm l}, -{\rm k}, -2/3^{*}{\rm h}-1/3^{*}{\rm k}-\\ & {\rm k}-1/3^{*}{\rm l}\\ 0.015 \; {\rm for} \; {\rm h}, -{\rm h}-{\rm k}, -{\rm l}\\ \end{array}$	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6428	wwPDB-VP
Average B, all atoms $(Å^2)$	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.65% of the height of the origin peak. No significant pseudotranslation is detected.

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.



 $^{^1 \}mathrm{Intensities}$ estimated from amplitudes.

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: PPG

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	Mol Chain		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.56	0/3250	0.75	0/4399	
1	В	0.52	0/3254	0.73	0/4406	
All	All	0.54	0/6504	0.74	0/8805	

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	А	3186	0	3131	31	0
1	В	3190	0	3130	33	0
2	А	26	0	17	1	0
2	В	26	0	16	2	0
All	All	6428	0	6294	57	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 (57) 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:384:LYS:O	1:A:384:LYS:HG2	1.81	0.80	
1:A:321:THR:HG21	1:B:318:SER:OG	1.95	0.66	
1:A:136:THR:HG23	2:A:1001:PPG:H5A2	1.79	0.64	
1:A:318:SER:OG	1:B:321:THR:HG21	1.98	0.63	
1:A:320:GLN:HE22	1:B:324:MET:CG	2.12	0.62	
1:B:136:THR:HG23	2:B:1001:PPG:H5A2	1.82	0.61	
1:A:320:GLN:HE22	1:B:324:MET:HG2	1.65	0.60	
1:A:324:MET:CG	1:B:320:GLN:HE22	2.14	0.60	
1:B:252:VAL:HG11	1:B:258:PHE:HB2	1.84	0.60	
1:A:252:VAL:HG11	1:A:258:PHE:HB2	1.85	0.57	
1:A:110:MET:HG2	1:A:296:THR:HG21	1.87	0.56	
1:B:353:ILE:HG12	1:B:430:LEU:HD11	1.87	0.56	
1:A:324:MET:HG2	1:B:320:GLN:HE22	1.70	0.56	
1:A:353:ILE:HG12	1:A:430:LEU:HD11	1.87	0.55	
1:B:110:MET:HG2	1:B:296:THR:HG21	1.88	0.55	
1:B:272:SER:O	1:B:276:ARG:NH1	2.39	0.55	
1:A:223:VAL:HG21	1:A:228:LEU:HD21	1.88	0.54	
1:B:223:VAL:HG21	1:B:228:LEU:HD21	1.88	0.54	
1:A:45:TYR:CE1	1:A:429:THR:HG22	2.43	0.54	
1:B:396:ILE:HA	1:B:400:LEU:HD23	1.88	0.54	
1:A:396:ILE:HA	1:A:400:LEU:HD23	1.88	0.54	
1:B:45:TYR:CE1	1:B:429:THR:HG22	2.43	0.53	
1:A:272:SER:O	1:A:276:ARG:NH1	2.40	0.53	
1:B:45:TYR:CD2	1:B:51:PRO:O	2.62	0.53	
1:B:265:VAL:HG21	1:B:277:VAL:HG21	1.94	0.50	
1:A:265:VAL:HG21	1:A:277:VAL:HG21	1.94	0.49	
1:B:287:LEU:HD21	1:B:329:LEU:HD21	1.95	0.49	
1:B:154:LEU:HD11	1:B:207:VAL:HG11	1.95	0.49	
1:B:357:LEU:HB3	1:B:362:ILE:HB	1.95	0.48	
1:A:287:LEU:HD21	1:A:329:LEU:HD21	1.96	0.48	
1:A:400:LEU:O	1:A:436:ARG:NH1	2.47	0.48	
1:A:357:LEU:HB3	1:A:362:ILE:HB	1.95	0.47	
1:A:154:LEU:HD11	1:A:207:VAL:HG11	1.97	0.47	
1:B:400:LEU:O	1:B:436:ARG:NH1	2.48	0.46	
1:B:285:LYS:HE2	2:B:1001:PPG:H4A2	1.99	0.45	
1:A:349:ARG:NH1	1:A:425:MET:O	2.50	0.44	
1:A:400:LEU:HD11	1:A:440:PHE:HB2	2.00	0.44	
1:B:349:ARG:NH1	1:B:425:MET:O	2.51	0.44	
1:B:400:LEU:HD11	1:B:440:PHE:HB2	1.99	0.44	
1:A:68:LEU:HA	1:A:71:THR:HG22	2.00	0.44	
1:B:68:LEU:HA	1:B:71:THR:HG22	2.00	0.43	
1:A:250:GLY:N	1:A:286:ASP:OD2	2.45	0.42	



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ASP:O	1:A:309:ARG:NH2	2.49	0.42
1:B:51:PRO:C	1:B:53:GLY:N	2.73	0.42
1:A:324:MET:SD	1:B:320:GLN:NE2	2.88	0.42
1:B:45:TYR:HD2	1:B:51:PRO:O	2.02	0.42
1:B:51:PRO:C	1:B:53:GLY:H	2.22	0.42
1:A:353:ILE:CG1	1:A:430:LEU:HD11	2.50	0.41
1:B:127:ASP:O	1:B:309:ARG:NH2	2.50	0.41
1:B:353:ILE:CG1	1:B:430:LEU:HD11	2.50	0.41
1:B:363:GLU:H	1:B:363:GLU:HG3	1.66	0.41
1:A:217:ASN:HD21	1:A:419:ARG:HH11	1.67	0.41
1:B:113:PHE:CZ	1:B:287:LEU:HD13	2.56	0.41
1:A:128:ARG:NH2	1:A:302:ASP:OD1	2.54	0.40
1:A:242:LEU:HD23	1:A:242:LEU:C	2.42	0.40
1:A:249:SER:O	1:A:252:VAL:HG12	2.22	0.40
1:B:60:ALA:O	1:B:285:LYS:HE3	2.21	0.40

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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	А	396/447~(89%)	365~(92%)	31 (8%)	0	100 100
1	В	397/447~(89%)	362 (91%)	35~(9%)	0	100 100
All	All	793/894~(89%)	727 (92%)	66 (8%)	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	А	351/388~(90%)	323~(92%)	28~(8%)	12 32
1	В	352/388~(91%)	322~(92%)	30 (8%)	10 29
All	All	703/776~(91%)	645~(92%)	58~(8%)	11 30

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	16	VAL
1	А	21	VAL
1	А	25	ASP
1	А	30	ASP
1	А	41	ASP
1	A A	54	VAL
1	А	69	LEU
1	А	108	GLN
1	А	207	VAL
1	A A	210	VAL
1	А	212	ILE
1	А	226	LYS
1	A A	266	GLU
1	А	283	LEU
1	А	286	ASP
1	А	294	VAL
1	A A A	303	ASN
1	А	316	LEU
1	А	321	THR
1	А	336	GLU
1	A A	347	ARG
1	А	353	ILE
1	А	363	GLU
1	А	398	LYS
1	A A A	404	ILE
1	А	405	SER
1	А	420	VAL
1	А	436	ARG
1	В	16	VAL
1	В	21	VAL
1	В	25	ASP



1B 30 ASP1B 41 ASP1B 49 HIS1B 54 VAL1B 69 LEU1B 108 GLN1B 207 VAL1B 210 VAL1B 212 ILE1B 226 LYS1B 226 LYS1B 283 LEU1B 286 ASP1B 294 VAL1B 303 ASN1B 316 LEU1B 321 THR1B 336 GLU1B 353 ILE1B 363 GLU1B 379 PHE1B 398 LYS1B 404 ILE1B 405 SER1B 420 VAL1B 436 ARG	Mol	Chain	Res	Type
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	30	ASP
1 B 54 VAL 1 B 69 LEU 1 B 108 GLN 1 B 207 VAL 1 B 210 VAL 1 B 212 ILE 1 B 226 LYS 1 B 226 GLU 1 B 283 LEU 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 404 ILE 1 <t< td=""><td>1</td><td>В</td><td>41</td><td>ASP</td></t<>	1	В	41	ASP
1 B 69 LEU 1 B 108 GLN 1 B 207 VAL 1 B 210 VAL 1 B 210 VAL 1 B 212 ILE 1 B 226 LYS 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 <	1	В	49	HIS
1 B 108 GLN 1 B 207 VAL 1 B 210 VAL 1 B 212 ILE 1 B 226 LYS 1 B 226 LYS 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 353 ILE 1 B 363 GLU 1 B 379 PHE 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	54	VAL
1 B 207 VAL 1 B 210 VAL 1 B 212 ILE 1 B 226 LYS 1 B 266 GLU 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 316 LEU 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 373 ILE 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	69	LEU
1 B 210 VAL 1 B 212 ILE 1 B 226 LYS 1 B 266 GLU 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	108	GLN
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	207	VAL
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	210	VAL
1 B 266 GLU 1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 353 ILE 1 B 363 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	212	ILE
1 B 283 LEU 1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 363 GLU 1 B 363 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	226	LYS
1 B 286 ASP 1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 321 THR 1 B 336 GLU 1 B 353 ILE 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	266	GLU
1 B 294 VAL 1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 336 GLU 1 B 363 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	283	LEU
1 B 303 ASN 1 B 316 LEU 1 B 321 THR 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 347 ARG 1 B 353 ILE 1 B 363 GLU 1 B 363 GLU 1 B 363 LYS 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	286	ASP
1 B 316 LEU 1 B 321 THR 1 B 336 GLU 1 B 336 GLU 1 B 347 ARG 1 B 353 ILE 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	294	VAL
1 B 321 THR 1 B 336 GLU 1 B 347 ARG 1 B 353 ILE 1 B 363 GLU 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	303	ASN
1 B 336 GLU 1 B 347 ARG 1 B 353 ILE 1 B 363 GLU 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	316	LEU
1 B 347 ARG 1 B 353 ILE 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	321	THR
1 B 353 ILE 1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	336	GLU
1 B 363 GLU 1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	347	ARG
1 B 379 PHE 1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	353	ILE
1 B 398 LYS 1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	363	GLU
1 B 404 ILE 1 B 405 SER 1 B 420 VAL	1	В	379	PHE
1 B 405 SER 1 B 420 VAL	1	В	398	LYS
1 B 420 VAL	1	В	404	ILE
	1	В	405	SER
1 B 436 ARG	1	В	420	VAL
	1	В	436	ARG

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

Mol	Chain	Res	Type
1	А	224	GLN
1	А	320	GLN
1	В	224	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 monosaccharides 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).

Mal	Turne	Chain	Dec	Res Link Bond lengths				Bond angles		
Mol	Type	Chain	Res		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	PPG	В	1001	-	$25,\!26,\!26$	2.52	6 (24%)	$26,\!35,\!35$	2.66	7 (26%)
2	PPG	А	1001	-	$25,\!26,\!26$	2.64	7 (28%)	$26,\!35,\!35$	2.26	6 (23%)

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	PPG	В	1001	-	-	12/20/21/21	0/1/1/1
2	PPG	А	1001	-	-	14/20/21/21	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	А	1001	PPG	C3-C2	8.04	1.49	1.40
2	В	1001	PPG	C5-C4	7.25	1.50	1.40
2	А	1001	PPG	C5-C4	6.01	1.48	1.40
2	В	1001	PPG	C3-C2	5.77	1.46	1.40
2	В	1001	PPG	C3-C4	5.61	1.48	1.40
2	А	1001	PPG	C3-C4	5.31	1.48	1.40



Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	А	1001	PPG	CAI-CBC	4.08	1.52	1.48
2	В	1001	PPG	CBI-CAI	2.93	1.52	1.43
2	В	1001	PPG	CAI-CBC	2.92	1.51	1.48
2	В	1001	PPG	OET-CGI	2.87	1.47	1.36
2	А	1001	PPG	OET-CGI	2.66	1.46	1.36
2	А	1001	PPG	CBI-CAI	2.32	1.50	1.43
2	А	1001	PPG	C6-C5	2.21	1.42	1.37

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All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	1001	PPG	CBC-CAI-N4A	-10.57	109.85	121.84
2	А	1001	PPG	CBC-CAI-N4A	-8.58	112.11	121.84
2	В	1001	PPG	C4A-C4-C5	4.00	124.56	119.73
2	А	1001	PPG	O3B-CBC-CAI	3.49	119.17	113.42
2	В	1001	PPG	C2A-C2-C3	-3.17	116.97	120.89
2	А	1001	PPG	C4A-C4-C5	3.08	123.45	119.73
2	В	1001	PPG	OP4-C5A-C5	2.89	114.86	109.35
2	А	1001	PPG	OP4-C5A-C5	2.68	114.46	109.35
2	В	1001	PPG	O3B-CBC-CAI	2.68	117.83	113.42
2	В	1001	PPG	C2A-C2-N1	2.63	122.80	117.67
2	А	1001	PPG	OP4-P-OP1	-2.61	99.17	106.47
2	В	1001	PPG	C6-N1-C2	2.22	123.27	119.17
2	А	1001	PPG	O3-C3-C2	2.06	121.98	117.49

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	1001	PPG	C3-C4-C4A-N4A
2	А	1001	PPG	C5-C4-C4A-N4A
2	А	1001	PPG	C5A-OP4-P-OP1
2	А	1001	PPG	C5A-OP4-P-OP2
2	А	1001	PPG	C5A-OP4-P-OP3
2	А	1001	PPG	CBI-CAI-N4A-C4A
2	А	1001	PPG	CBI-CAI-CBC-O2B
2	А	1001	PPG	CBI-CAI-CBC-O3B
2	А	1001	PPG	N4A-CAI-CBI-CGI
2	А	1001	PPG	CBI-CGI-OET-CEI
2	А	1001	PPG	OET-CEI-CFI-NI
2	В	1001	PPG	C5A-OP4-P-OP1
2	В	1001	PPG	C5A-OP4-P-OP2



Mol	Chain	\mathbf{Res}	Type	Atoms
2	В	1001	PPG	C5A-OP4-P-OP3
2	В	1001	PPG	CBI-CAI-N4A-C4A
2	В	1001	PPG	CBI-CAI-CBC-O2B
2	В	1001	PPG	CBI-CAI-CBC-O3B
2	В	1001	PPG	N4A-CAI-CBI-CGI
2	В	1001	PPG	OET-CEI-CFI-NI
2	А	1001	PPG	CBC-CAI-CBI-CGI
2	В	1001	PPG	C3-C4-C4A-N4A
2	В	1001	PPG	C5-C4-C4A-N4A
2	А	1001	PPG	N4A-CAI-CBC-O2B
2	В	1001	PPG	CBI-CGI-OET-CEI
2	А	1001	PPG	CFI-CEI-OET-CGI
2	В	1001	PPG	CBC-CAI-CBI-CGI

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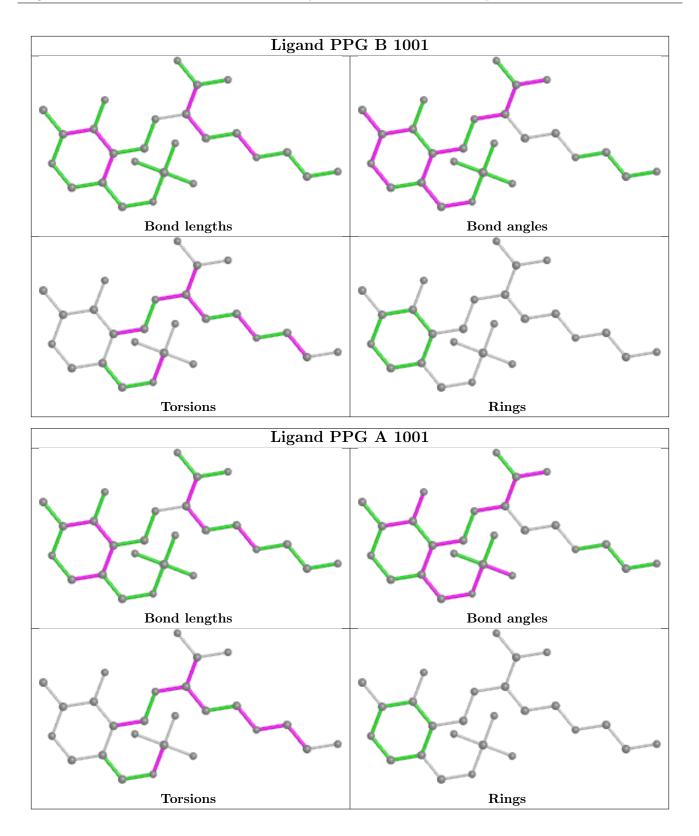
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1001	PPG	2	0
2	А	1001	PPG	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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	400/447~(89%)	0.17	8 (2%) 65 66	6 70, 94, 125, 161	0
1	В	401/447 (89%)	0.23	12 (2%) 50 4	9 75, 108, 145, 171	0
All	All	801/894 (89%)	0.20	20 (2%) 57 5	8 70, 101, 140, 171	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	33	TYR	4.4
1	В	61	GLU	3.7
1	В	379	PHE	3.4
1	А	33	TYR	3.2
1	А	149	PRO	2.8
1	А	124	PHE	2.6
1	А	146	LEU	2.6
1	В	416	GLY	2.5
1	В	410	CYS	2.5
1	В	371	LEU	2.5
1	А	69	LEU	2.5
1	В	377	LEU	2.3
1	А	126	PRO	2.3
1	В	374	TRP	2.2
1	В	440	PHE	2.2
1	А	150	ASN	2.2
1	В	105	THR	2.2
1	В	405	SER	2.1
1	В	346	LEU	2.1
1	А	442	ASP	2.1



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.

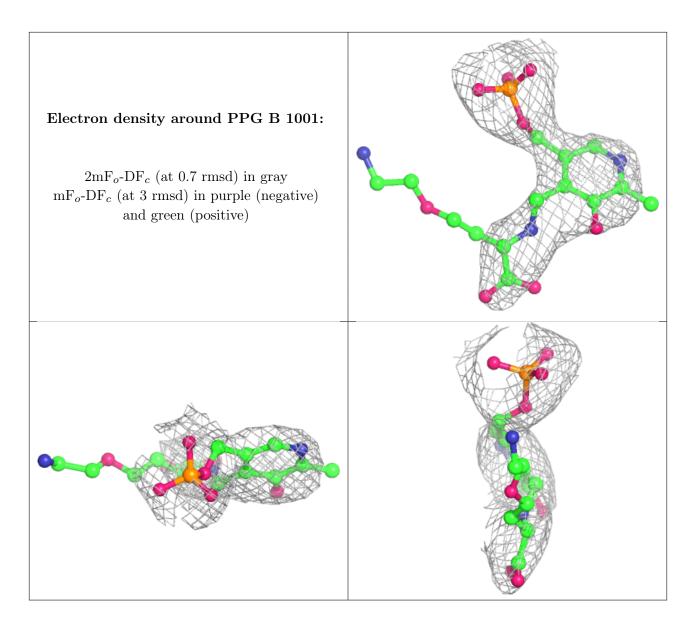
6.4 Ligands (i)

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, 95^{th} 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.

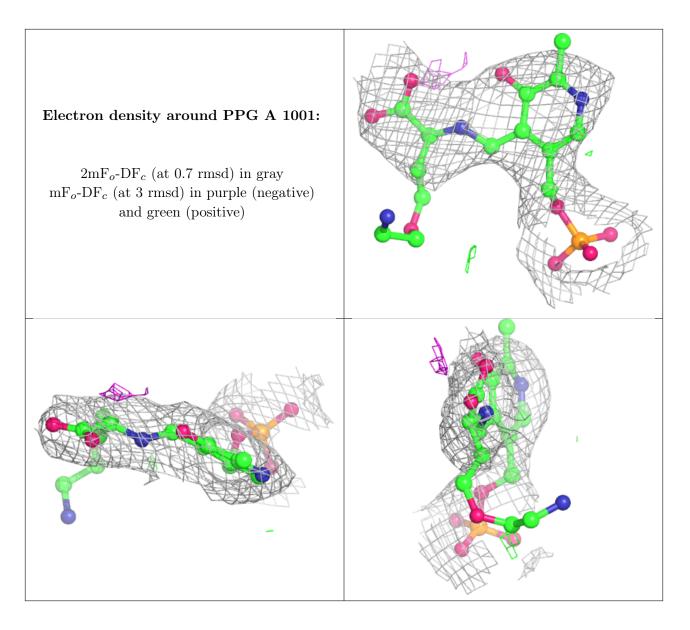
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
2	PPG	В	1001	26/26	0.94	0.30	88,102,141,143	0
2	PPG	А	1001	26/26	0.95	0.22	79,87,123,126	0

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.

